# Oligonucleotide for reducing the expression of leucine-rich repeat kinase 2 (LRRK2) and its use for preventing and/or treating human diseases

The present invention refers to oligonucleotides, in particular antisense oligonucleotides, comprising one or more modified nucleotides and hybridizing with the LRRK2 mRNA and/or pre-mRNA. The oligonucleotides inhibit the expression of LRRK2, LRRK2 mRNA and/or LRRK2 pre-mRNA and are used for preventing and/or treating a human disease such as Parkinson´s disease (PD) and other neurodegenerative diseases.

## Technical background

A neurodegenerative disease is caused by the progressive loss of structure or function of neurons, in the process known as neurodegeneration. Such neuronal damage may ultimately involve cell death. Neurodegenerative diseases include amyotrophic lateral sclerosis, multiple sclerosis, Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple system atrophy, and prion diseases. Neurodegeneration can be found in the brain at many different levels of neuronal circuitry.

Parkinson's disease (PD) is the second most common neurodegenerative disease and affects approximately 1 in 100 people over the age of 60. A disease-modifying or neuroprotective therapy is highly desired, as the current standard of care is limited to symptomatic treatment (Lees, Hardy, & Revesz, 2009). Pathological hallmarks of PD include accumulation of α-synuclein (α-syn) into Lewy bodies (LBs) and Lewy neurites (LNs), and progressive loss of dopaminergic (DA) neurons in the substantia nigra pars compacta (SNpc) (Trojanowski & Lee, 1998).

Currently a variety of medications provide some relief from the symptoms of the neurodegenerative diseases such as Parkinson's disease. However, there is a lack of effective / acceptable treatment for such disease.

Understanding of the genetics of PD has identified a number of genetic alleles causing or associated with disease on-set and progression (Chang et al., 2017; Gasser, Hardy, & Mizuno, 2011; Hardy, 2010; Lunati, Lesage, & Brice, 2018). The human genetic evidence

demonstrates a direct involvement of LRRK2 function in risk to develop PD, the underlying disease pathology and progression of PD and thus validate LRRK2 as an attractive therapeutic target. LRRK2 is a 2527 amino acid large protein that is widely expressed throughout the body with its highest level being detected in lung and kidney tissues. The LRKK2 protein consists of multiple functional domains, including a Ras of complex proteins (ROC)-type GTP-binding domain, a carboxyl terminal of ROC (COR) domain, and a serine/threonine protein kinase domain (Cookson, 2017). Collectively, LRRK2 appears to regulate aspects of intracellular vesicle trafficking, maintenance of cellular organelles including the Golgi, endosomes and lysosomes.

Altered LRRK2 functions due to genetic, epigenetic or environmental factors, and similarly mutations in or around the LRRK2 gene are directly involved in development and progression of diseases, including synucleopathies such as PD. Therefore, suppression of its expression could provide an effective treatment opportunity for these diseases. Suppression of LRRK2 expression can be achieved for example by targeted degradation of the mRNA coding for LRRK2 or by blocking of its translation.

Two competing technologies are predominantly described for specific suppression of mRNA expression: siRNA and antisense oligonucleotides (ASOs). siRNAs target the mRNA in the cytoplasm. In contrast, RNase H dependent ASOs target the mRNA and/or pre-mRNA in the nucleus. Thereby also intronic regions can be targeted by ASOs that are not accessible to siRNA resulting in a significantly larger target space for ASOs.

Moreover, due to its double stranded nature, siRNA does not cross the cell membrane by itself and delivery systems are required for its activity *in vitro* and *in vivo*. While delivery systems for siRNA exist that efficiently deliver siRNA to liver cells *in vivo*, there is currently no system that can deliver siRNA *in vivo* to extra-hepatic tissues with sufficient efficacy. In contrast, modified ASOs can enter many cell types *in vitro* without transfection or delivery methods in sufficient amounts, resulting in potent and sequence specific target knockdown. *In vivo*, naked unconjugated ASOs achieve target knockdown in several different relevant tissues after systemic administration. After direct administration, ASOs achieve a potent and long-lasting target knockdown in the central nervous system (CNS) indicating the strong potential of ASOs for treatment of CNS diseases such as neurodegenerative diseases (e.g., Geary et al., Adv Drug Deliv Rev. 2015 Jun 29; 87:46-51).

The present invention refers to oligonucleotides such as antisense oligonucleotides (ASOs) resulting in significant reduction of LRRK2 mRNA and protein expressions in CNS as a therapeutic treatment option for PD.

The mode of action of an oligonucleotide differs from the mode of action of an antibody or small molecule, and oligonucleotides are highly advantageous regarding, for example,
(i) the penetration of tissue such as brain tissue which is better than penetration of antibodies due to the substantially smaller size (e.g., Pizzo et al., J Physiol. 2018 Feb 1; 596(3):445-475; Noguchi et al., MAbs. 2017 Oct; 9(7): 1210-1215),
(ii) prolonged retention and effect duration in the brain after direct administration,
(iii) the blocking of multiple functions and activities, respectively, of a target,
(iv) the combination of oligonucleotides with each other or an antibody or a small molecule, and
(v) the inhibition of intracellular effects which are not accessible for an antibody or not inhibitable via a small molecule.

Thus, a need exists for new and improved therapies for the treatment of disease (e.g., PD) that are capable of reducing the amount of LRRK2 mRNA and protein, with minimal toxic side effects.

**Summary of the invention**

The present invention refers to an oligonucleotide comprising 10 to 25 nucleotides, at least one nucleotide having a modification selected from the group consisting of a bridged nucleic acid such as LNA, ENA, cET, a 2'Fluoro modified nucleotide, a 2´ O-Methyl modified nucleotide, a 2´ O-Methoxy modified nucleotide, a FANA and a combination thereof, wherein said modification is located in a sequence of 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide and wherein the oligonucleotide hybridizes with a transcript or an mRNA of leucine-rich repeat kinase 2 (LRRK2) of SEQ ID NO.1 and/or with pre-mRNA of LRRK2 of SEQ ID NO.2 and/or a fragment thereof. The fragment results from a biological process including but not limited to alternative splicing. The oligonucleotide hybridizes, for example, outside a hybridizing active region or within a hybridizing active region of position 102001 to 102500, position 27001 to 27500, position 80501 to 81000, position 24501 to 25000, position 114001 to 114500, position 92001 to 92500, position 99501 to 100000, position 67001 to 67500, position 15001 to 15500,

position 24001 to 24500, position 26501 to 27000, position 79501 to 80000, position 87001 to 87500, position 120501 to 121000, position 142001 to 142500, position 135001 to 135500, position 71001 to 71500, position 140501 to 141000 or a combination thereof.

The oligonucleotide comprises or consists of, for example, SEQ ID NO.210, SEQ ID NO.69, SEQ ID NO.164, SEQ ID NO.254, SEQ ID NO.222, SEQ ID NO.186, SEQ ID NO.204, SEQ ID NO.142, SEQ ID NO.209, SEQ ID NO.255, SEQ ID NO.45, SEQ ID NO.46, SEQ ID NO.60, SEQ ID NO.66, SEQ ID NO.162, SEQ ID NO.171, SEQ ID NO.224, SEQ ID NO.241, SEQ ID NO.250, SEQ ID NO.149, SEQ ID NO.256, SEQ ID NO.239, or a combination thereof. The sequence comprises at least one modification.

For example the oligonucleotide is selected from the group consisting of
+T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C (A57208Hi; SEQ ID NO.210),
+A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C (A57067Hi; SEQ ID NO.69),
+G*+T*+C*A*T*A*A*G*T*T*G*T*C*A*G*+T*+A*+T (A57162Hi; SEQ ID NO.164),
+G*+A*+C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57252H; SEQ ID NO.254),
+C*+T*+T*T*G*C*T*T*A*T*T*C*G*T*G*+A*+C*+T (A57220Hi; SEQ ID NO.222),
+T*+T*+T*A*T*T*G*C*A*G*T*C*A*T*A*G*+T*+G*+A (A57184Hi; SEQ ID NO.186),
+C*+T*+T*T*G*T*A*A*A*T*G*A*C*G*T*T*+T*+C*+C (A57202Hi; SEQ ID NO.204),
+T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A*+C*+A (A57140Hi, SEQ ID NO.142),
+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A (A57207Hi; SEQ ID NO.209),
+G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57253H; SEQ ID NO.255),
+C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*A*G*+T*+T*+C (A57043Hi; SEQ ID NO.45),
+T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*C*+A*+G*+T (A57044Hi; SEQ ID NO.46),
+G*+T*+G*T*A*A*C*T*A*A*G*T*G*A*T*+C*+T*+C (A57058Hi; SEQ ID NO.60),
+G*+A*+T*A*T*T*G*A*C*A*A*C*C*T*G*+C*+T*+G (A57064Hi; SEQ ID NO.66),
+T*+G*+T*G*T*T*A*C*C*A*T*A*T*C*C*A*+T*+T*+T (A57160Hi; SEQ ID NO.162),
+C*+T*+G*T*G*A*C*T*T*T*G*C*A*T*C*A*+A*+C*+T (A57169Hi; SEQ ID NO.171),
+C*+A*+A*T*G*T*A*T*A*C*C*A*T*G*C*+A*+G*+T (A57222Hi; SEQ ID NO.224),
+T*+T*+C*C*T*G*A*T*T*A*T*A*C*C*A*T*+A*+T*+G (A57239Hi; SEQ ID NO.241),
+A*+T*+G*C*T*C*T*T*A*T*C*C*A*C*A*A*+T*+C*+C (A57248Hi; SEQ ID NO.250),
+T*+T*+T*G*A*T*C*T*G*T*A*G*T*A*C*A*+T*+A*+C (A57147Hi; SEQ ID NO.149),
+A*+T*+G*G*A*C*T*T*C*G*T*T*T*A*A*T*+A*+C*+C (A57254H; SEQ ID NO.256),
+G*+G*+A*C*A*T*G*T*A*T*C*T*T*A*A*T*+A*+G*+T (A57237Hi; SEQ ID NO.239),

and a combination thereof, wherein + indicates an LNA nucleotide and * indicates a phosphorothioate (PTO) linkage between the nucleotides. Alternatively, the oligonucleotide has 80 to 99 %, 85 to 98 %, 90 to 95 or 93 % sequence identity to any one of the oligonucleotides of SEQ ID NO.3 to SEQ ID NO.5301 of the present invention.

Furthermore, the oligonucleotide comprises or consists of, for example, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21 or at least 22 nucleotides of any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301 of the present invention. The nucleotides are for example contiguous nucleotides.

The oligonucleotide of the present invention inhibits, for example, the expression of LRRK2, a LRRK2 mRNA, a LRRK2 pre-mRNA or a combination thereof at a nanomolar or micromolar concentration.

The present invention is further directed to a pharmaceutical composition comprising or consisting of an oligonucleotide of the present invention and a pharmaceutically acceptable carrier, excipient, dilutant, stimulant such as an adjuvant, or a combination thereof. The pharmaceutical composition can comprise an additional therapeutically active agent. The oligonucleotide and the pharmaceutical composition, respectively, of the present invention is, for example, for use in a method of preventing and/or treating a human disease such as a neurodegenerative disease. The neurodegenerative disease is, for example, selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease. The pharmaceutically acceptable carrier, excipient, adjuvant, or a combination thereof, or the therapeutically active agent is for example administrated separately before or after delivery of the oligonucleotide, or is for example administered simultaneously via different delivery methods. The delivery methods are for example orally, sublingually, nasally, subcutaneously, intravenously, intraperitoneally, intramuscularly, intratumorally, intrathecally, intraventricularly, transdermal and/or rectally.

The oligonucleotide and pharmaceutical composition, respectively, of the present invention is, for example, for local or systemic administration.

The present invention further relates to a method of preventing and/or treating a human disease comprising administering a therapeutically effective amount of an oligonucleotide of the present invention or a pharmaceutical composition comprising such oligonucleotide. The human disease, such as a neurological disease, can be selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease. The oligonucleotide or pharmaceutical composition can be administered locally or systemically.

All documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

## Description of figures

**Fig. 1** shows RefSeq ID NM_198578 of LRRK2 mRNA (SEQ ID NO.1).

**Fig. 2** depicts GRCh38:12:40224997:40369285, in particular LRRK2_GRCh38:12:40224997:40369285:1_seqGenomicENST00000298910.12 (LRRK2 pre-mRNA of SEQ ID NO.2).

**Fig. 3A** to **3D** depict the screening of human LRRK2- specific ASOs in A549 cells (human lung carcinoma).

**Figs. 4A** to **4D** show the screening of human LRRK2- specific ASOs in MDA-MB-231 cells (human breast adenocarcinoma).

## Detailed description

The present invention provides oligonucleotides, which hybridize with mRNA and/or pre-mRNA sequences of the leucine-rich repeat kinase 2 (LRRK2) for example of human origin. These oligonucleotides hybridize with an intron and/or an exon and/or an exon-exon junction and/or an exon-intron junction of the LRRK2 pre-mRNA for example in a neuronal cell or a tumor cell or other mammalian cell. Via recruitment of enzymes such as RNase H the pre mRNA is degraded and the levels of LRRK2 mRNA are reduced. As a consequence the production of LRRK2 protein is prevented and levels of LRRK2 protein are reduced, for example in a neuronal cell or a tumor cell or other mammalian cell. In consequence, the level of LRRK2 protein and its downstream effects decreases. The oligonucleotides of the present invention represent a promising and highly efficient tool for use in methods of preventing and/or treating disorders (e.g., neurodegenerative disorders), where the LRRK2 protein expression, function, and/or activity, respectively, is involved in disease development and progression.

The oligonucleotides of the present invention hybridize, for example, with LRRK2 mRNA of SEQ ID NO.1 (RefSeq ID NM_198578) and/or LRRK2 pre-mRNA of SEQ ID NO.2 (GRCh38:12:40224997:40369285).

In the following, the elements of the present invention will be described in more detail. These elements are listed with specific embodiments, however, it should be understood that they may be combined in any manner and in any number to create additional embodiments. The examples and embodiments provided herein are not intended to limit the present invention to only the explicitly described embodiments. This description should be understood to support and encompass embodiments which combine the explicitly described embodiments with any number of the disclosed elements. Furthermore, any permutations or combinations of all described elements in this application should be considered disclosed by the description of the present application unless the context indicates otherwise.

Throughout this specification and the claims, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated member, integer or step or group of members, integers or steps but not the exclusion of any other member, integer or step or

group of members, integers or steps. The terms "a" and "an" and "the" and similar reference used in the context of describing the invention (especially in the context of the claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by the context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as", “for example”), provided herein is intended merely to better illustrate the invention and does not pose a limitation on the scope of the invention otherwise claimed. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the invention.

Oligonucleotides of the present invention are for example antisense oligonucleotides consisting of or comprising about 10 to about 25 nucleotides, about 10 to about 15 nucleotides, about 15 to about 20 nucleotides, about 12 to about 19 nucleotides, or about 14 to about 18 nucleotides. The oligonucleotides for example consist of or comprise about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides. The oligonucleotides of the present invention comprise at least one nucleotide which is modified. The modified nucleotide may be, for example, a bridged nucleotide such as a locked nucleic acid (LNA, e.g., 2´,4´-LNA), cET, ENA, a 2´Fluoro modified nucleotide, a 2´O-Methyl modified nucleotide or combinations thereof. The oligonucleotide of the present invention comprises nucleotides having for example one or more, two or more, three or more or four or more of the same or different modifications. Further, the oligonucleotide of the present invention comprises optionally a modified phosphate backbone, wherein the phosphate is, for example, a phosphodiester, a phosphorothioate, methylphosphonate, methyl phosphorothioate, phosphoramidate, phosphorodiamidate, thiophosphoramidate, mesyl phosphoramidate or a combination thereof.

“Reducing” according to the present invention includes inhibiting an effect such as expression in different percentages and amounts, respectively.

The present invention refers to the provision of an oligonucleotide such as an antisense oligonucleotide, mediating the limitation of available LRKK2 mRNA for protein expression. In order to limit protein expression, the oligonucleotide requires the presence of a complementary nucleic acid sequence representing a hybridization target, which allows the formation of heteroduplexes. The oligonucleotides of the present invention hybridize with RNAs of SEQ ID NO.1 and/or pre-mRNAs of SEQ ID NO.2. The formation of a heteroduplex between the oligonucleotide and the target RNA leads to enzymes such as RNaseH-mediated degradation or inactivation of the target RNA or termination of transcription, and thus, limits the amount of available LRKK2 mRNA for protein expression.

Further, the present invention relates to an oligonucleotide of the present invention comprising, for example, the one or more, two or more, three or more or four or more modified nucleotide(s) at the 3´- and/or 5´- end of the oligonucleotide and/or at any position within the oligonucleotide, wherein modified nucleotides follow in a row of about 1, 2, 3, 4, 5, or 6 modified nucleotides, or a modified nucleotide is combined with one or more, two or more, three or more or four or more unmodified nucleotides. The following Table 1 presents embodiments of oligonucleotides comprising modified nucleotides, for example, LNA which are indicated by (+) and phosphorothioate (PTO) indicated by (*). The oligonucleotides consisting of or comprising the sequences of Table 1 may comprise any other modified nucleotide and any other combination of modified and unmodified nucleotides. Oligonucleotides of Table 1 hybridize with human LRKK2 mRNA:

| SEQ ID | Antisense Sequence 5'-3' | Name | Antisense Sequence 5'-3' with PTO (*) and LNA (+) | Position on pre-mRNA (GRCh38, Chr 12, 40224997_40369285) | Length |
|---|---|---|---|---|---|
| 3 | AAGTCACAATCCACAGCAC | A57001Hi | +A*+A*+G*T*C*A*C*A*A*T*C*C*A*C*A*G*+C*+A*+C | 509 | 19 |
| 4 | ACGTCTCCTTCCAAACAGA | A57002Hi | +A*+C*+G*T*C*T*C*C*T*T*C*C*A*A*A*C*+A*+G*+A | 681 | 19 |
| 5 | AACTAAAGGCTAGAAATCT | A57003Hi | +A*+A*+C*T*A*A*A*G*G*C*T*A*G*A*A*A*+T*+C*+T | 1112 | 19 |
| 6 | ACTTTCTTTAGATACTACA | A57004Hi | +A*+C*+T*T*T*C*T*T*T*A*G*A*T*A*C*T*+A*+C*+A | 1142 | 19 |
| 7 | ATCATTCTTAATTACCATT | A57005Hi | +A*+T*+C*A*T*T*C*T*T*A*A*T*T*A*C*C*+A*+T*+T | 1299 | 19 |
| 8 | AACATTGGCTTTCTGACTG | A57006Hi | +A*+A*+C*A*T*T*G*G*C*T*T*T*C*T*G*A*+C*+T*+G | 1459 | 19 |
| 9 | TTTATTATGCCTCCATCTT | A57007Hi | +T*+T*+T*A*T*T*A*T*G*C*C*T*C*C*A*T*+C*+T*+T | 1718 | 19 |
| 10 | TCTTTATTATGCCTCCATC | A57008Hi | +T*+C*+T*T*T*A*T*T*A*T*G*C*C*T*C*C*+A*+T*+C | 1720 | 19 |
| 11 | TCCGACTTTGAGTCTTAA | A57009Hi | +T*+C*+C*G*A*C*T*T*T*G*A*G*T*C*T*+T*+A*+A | 1749 | 18 |

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|---|---|---|---|---|---|
| 12 | GTGACTCATATTCCACAGG | A57010Hi | +G*+T*+G*A*C*T*C*A*T*A*T*T*C*C*A*C*+A*+G*+G | 1773 | 19 |
| 13 | AATTGATGTCATTGTACCT | A57011Hi | +A*+A*+T*T*G*A*T*G*T*C*A*T*T*G*T*A*+C*+C*+T | 4070 | 19 |
| 14 | TACTTACAGTAATTATACT | A57012Hi | +T*+A*+C*T*T*A*C*A*G*T*A*A*T*T*A*T*+A*+C*+T | 4195 | 19 |
| 15 | CAGGCAACTGAGCTCTCCA | A57013Hi | +C*+A*+G*G*C*A*A*C*T*G*A*G*C*T*C*T*+C*+C*+A | 4829 | 19 |
| 16 | CACATAGGATGCCAAACTC | A57014Hi | +C*+A*+C*A*T*A*G*G*A*T*G*C*C*A*A*A*+C*+T*+C | 4939 | 19 |
| 17 | TCACATAGGATGCCAAACT | A57015Hi | +T*+C*+A*C*A*T*A*G*G*A*T*G*C*C*A*A*+A*+C*+T | 4940 | 19 |
| 18 | CAATCCAGCTGTCATAGA | A57016Hi | +C*+A*+A*T*C*C*A*G*C*T*G*T*C*A*T*+A*+G*+A | 5077 | 18 |
| 19 | CCACGTAAGCTGAACAGA | A57017Hi | +C*+C*+A*C*G*T*A*A*G*C*T*G*A*A*C*+A*+G*+A | 5101 | 18 |
| 20 | CCTCCACGTAAGCTGAAC | A57018Hi | +C*+C*+T*C*C*A*C*G*T*A*A*G*C*T*G*+A*+A*+C | 5104 | 18 |
| 21 | ACATCCTCCTCCACGTAAG | A57019Hi | +A*+C*+A*T*C*C*T*C*C*T*C*C*A*C*G*T*+A*+A*+G | 5110 | 19 |
| 22 | GCTATTTCTACCTATACT | A57020Hi | +G*+C*+T*A*T*T*T*C*T*A*C*C*T*A*T*+A*+C*+T | 5140 | 18 |
| 23 | AAGTTGCTCTTTACCTCTG | A57021Hi | +A*+A*+G*T*T*G*C*T*C*T*T*T*T*A*C*C*T*+C*+T*+G | 5827 | 19 |
| 24 | GTATATCTTCACTCAGTC | A57022Hi | +G*+T*+A*T*A*T*C*T*T*C*A*C*T*C*A*+G*+T*+C | 5870 | 18 |
| 25 | GTAGAACTCCTCAATGGCT | A57023Hi | +G*+T*+A*G*A*A*C*T*C*C*T*C*A*A*T*G*+G*+C*+T | 5996 | 19 |
| 26 | GGTTGTACCAAGATTATT | A57024Hi | +G*+G*+T*T*G*T*A*C*C*A*A*G*A*T*T*T*+A*+T*+T | 6644 | 18 |
| 27 | TCAACTTTCAAATTACTAC | A57025Hi | +T*+C*+A*A*C*T*T*T*C*A*A*A*T*T*A*C*+T*+A*+C | 7773 | 19 |
| 28 | ATTATGCTGCAAACTGCAA | A57026Hi | +A*+T*+T*A*T*G*C*T*G*C*A*A*A*C*T*G*+C*+A*+A | 7944 | 19 |
| 29 | GTTGCATAATCTCCATTTG | A57027Hi | +G*+T*+T*G*C*A*T*A*A*T*C*T*C*C*A*T*+T*+T*+G | 9182 | 19 |
| 30 | AACGTTGCATAATCTCCAT | A57028Hi | +A*+A*+C*G*T*T*G*C*A*T*A*A*T*C*T*C*+C*+A*+T | 9185 | 19 |
| 31 | TTATTGATTGCTACTGTTT | A57029Hi | +T*+T*+A*T*T*G*A*T*T*G*C*T*A*C*T*G*+T*+T*+T | 9717 | 19 |
| 32 | TATGGCATACTCCAGAACA | A57030Hi | +T*+A*+T*G*G*C*A*T*A*C*T*C*C*A*G*A*+A*+C*+A | 11171 | 19 |
| 33 | ATTATGGCATACTCCAGA | A57031Hi | +A*+T*+T*A*T*G*G*C*A*T*A*C*T*C*C*+A*+G*+A | 11174 | 18 |
| 34 | CTCATACTCTCATCTTCCT | A57032Hi | +C*+T*+C*A*T*A*C*T*C*T*C*A*T*C*T*T*+C*+C*+T | 11731 | 19 |
| 35 | CACATTGTCTTCACTCCAA | A57033Hi | +C*+A*+C*A*T*T*G*T*C*T*T*C*A*C*T*C*+C*+A*+A | 12157 | 19 |
| 36 | ACACATCTTGAAGATTCCT | A57034Hi | +A*+C*+A*C*A*T*C*T*T*G*A*A*G*A*T*T*+C*+C*+T | 12449 | 19 |
| 37 | TCTCCTACACATCTTGAAG | A57035Hi | +T*+C*+T*C*C*T*A*C*A*C*A*T*C*T*T*G*+A*+A*+G | 12455 | 19 |
| 38 | TCTTCATCAATGATACCAT | A57036Hi | +T*+C*+T*T*C*A*T*C*A*A*T*G*A*T*A*C*+C*+A*+T | 12590 | 19 |
| 39 | CTCTTAGACAACATCTGA | A57037Hi | +C*+T*+C*T*T*A*G*A*C*A*A*C*A*T*C*+T*+G*+A | 12652 | 18 |
| 40 | GAAATACATTCTTATGCCT | A57038Hi | +G*+A*+A*A*T*A*C*A*T*T*C*T*T*A*T*G*+C*+C*+T | 12668 | 19 |
| 41 | CAAGGACTCCAACCAACTC | A57039Hi | +C*+A*+A*G*G*A*C*T*C*C*A*A*C*C*A*A*+C*+T*+C | 13583 | 19 |
| 42 | AGACTAAACAAGGACTCCA | A57040Hi | +A*+G*+A*C*T*A*A*A*C*A*A*G*G*A*C*T*+C*+C*+A | 13591 | 19 |
| 43 | TGGTAAACTGATAACTGAC | A57041Hi | +T*+G*+G*T*A*A*A*C*T*G*A*T*A*A*C*T*+G*+A*+C | 13785 | 19 |
| 44 | TTTCAGTTCAAGAGTTGTC | A57042Hi | +T*+T*+T*C*A*G*T*T*C*A*A*G*A*G*T*T*+G*+T*+C | 15055 | 19 |
| 45 | CGGCTAAATGTTTCAGTTC | A57043Hi | +C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*A*G*+T*+T*+C | 15065 | 19 |
| 46 | TCGGCTAAATGTTTCAGT | A57044Hi | +T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*C*+A*+G*+T | 15067 | 18 |

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| 47 | ATTGTACTACAAGCTCTGA | A57045Hi | +A*+T*+T*G*T*A*C*T*A*C*A*A*G*C*T*C*+T*+G*+A | 15852 | 19 |
| 48 | TTGCCTCTGTCAATGAAAC | A57046Hi | +T*+T*+G*C*C*T*C*T*G*T*C*A*A*T*G*A*+A*+A*+C | 16213 | 19 |
| 49 | AGTGATTTCCATATCTGAA | A57047Hi | +A*+G*+T*G*A*T*T*T*C*C*A*T*A*T*C*T*+G*+A*+A | 16735 | 19 |
| 50 | TCCTGTTTCTTGGCTTAAA | A57048Hi | +T*+C*+C*T*G*T*T*T*C*T*T*G*G*C*T*T*+A*+A*+A | 18310 | 19 |
| 51 | TGTCAATATGCTACTTATC | A57049Hi | +T*+G*+T*C*A*A*T*A*T*G*C*T*A*C*T*T*+A*+T*+C | 18767 | 19 |
| 52 | GAAACAGGTGAACCTCTA | A57050Hi | +G*+A*+A*A*C*A*G*G*T*G*A*A*C*C*T*+C*+T*+A | 20304 | 18 |
| 53 | TTTGTGCAATTCCAGTCAA | A57051Hi | +T*+T*+T*G*T*G*C*A*A*T*T*C*C*A*G*T*+C*+A*+A | 20604 | 19 |
| 54 | TCAGACTGTCATTATTTAC | A57052Hi | +T*+C*+A*G*A*C*T*G*T*C*A*T*T*A*T*T*+T*+A*+C | 20895 | 19 |
| 55 | AGAACTCAGACTGTCATTA | A57053Hi | +A*+G*+A*A*C*T*C*A*G*A*C*T*G*T*C*A*+T*+T*+A | 20900 | 19 |
| 56 | TCTTTAATTTAAGTCCTCA | A57054Hi | +T*+C*+T*T*T*A*A*T*T*T*A*A*G*T*C*C*+T*+C*+A | 21645 | 19 |
| 57 | GAGCATCTTTAATTTAAGT | A57055Hi | +G*+A*+G*C*A*T*C*T*T*T*A*A*T*T*T*A*+A*+G*+T | 21650 | 19 |
| 58 | AATATTCCTGGTTATCCTT | A57056Hi | +A*+A*+T*A*T*T*C*C*T*G*G*T*T*A*T*C*+C*+T*+T | 22023 | 19 |
| 59 | TTACCAGCTTGTCTAAACT | A57057Hi | +T*+T*+A*C*C*A*G*C*T*T*G*T*C*T*A*A*+A*+C*+T | 23835 | 19 |
| 60 | GTGTAACTAAGTGATCTC | A57058Hi | +G*+T*+G*T*A*A*C*T*A*A*G*T*G*A*T*+C*+T*+C | 24080 | 18 |
| 61 | AAGTGTAACTAAGTGATCT | A57059Hi | +A*+A*+G*T*G*T*A*A*C*T*A*A*G*T*G*A*+T*+C*+T | 24081 | 19 |
| 62 | TTGTCTATGATGATCTCAG | A57060Hi | +T*+T*+G*T*C*T*A*T*G*A*T*G*A*T*C*T*+C*+A*+G | 24338 | 19 |
| 63 | TTACTTAGACAATGGAAGT | A57061Hi | +T*+T*+A*C*T*T*A*G*A*C*A*A*T*G*G*A*+A*+G*+T | 24615 | 19 |
| 64 | ATCTTACTTAGACAATGGA | A57062Hi | +A*+T*+C*T*T*A*C*T*T*A*G*A*C*A*A*T*+G*+G*+A | 24618 | 19 |
| 65 | ATCTCTCAATAATAACTCT | A57063Hi | +A*+T*+C*T*C*T*C*A*A*T*A*A*T*A*A*C*+T*+C*+T | 26745 | 19 |
| 66 | GATATTGACAACCTGCTG | A57064Hi | +G*+A*+T*A*T*T*G*A*C*A*A*C*C*T*G*+C*+T*+G | 26913 | 18 |
| 67 | AGGTCAACTCTGTCACAT | A57065Hi | +A*+G*+G*T*C*A*A*C*T*C*T*G*T*C*A*+C*+A*+T | 26978 | 18 |
| 68 | ATGACAGCTTCAAATAACC | A57066Hi | +A*+T*+G*A*C*A*G*C*T*T*C*A*A*A*T*A*+A*+C*+C | 27011 | 19 |
| 69 | AATACTACTATTTGTTTCC | A57067Hi | +A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575301Hi | +A*+A*T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575302Hi | +A*A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575304Hi | +A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575307Hi | +A*+A*+T*+A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575308Hi | +A*+A*+T*+A*C*T*A*C*T*A*T*T*T*G*T*T*T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575309Hi | +A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*+T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575310Hi | +A*+A*T*A*C*T*A*C*T*A*T*T*T*G*T*+T*+T*+C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575312Hi | +A*+A*+T*+A*C*T*A*C*T*A*T*T*T*G*T*T*+T*C*+C | 27238 | 19 |
| 69 | AATACTACTATTTGTTTCC | A575313Hi | +A*A*+T*A*C*T*A*C*T*A*T*T*T*G*T*+T*+T*+C*+C | 27238 | 19 |
| 70 | CCTTGCTCAACATGAGATT | A57068Hi | +C*+C*+T*T*G*C*T*C*A*A*C*A*T*G*A*G*+A*+T*+T | 27406 | 19 |
| 71 | TTTGAGCAGCCTGAACCAT | A57069Hi | +T*+T*+T*G*A*G*C*A*G*C*C*T*G*A*A*C*+C*+A*+T | 29066 | 19 |
| 72 | TCTTAACTGCCTCAAATAT | A57070Hi | +T*+C*+T*T*A*A*C*T*G*C*C*T*C*A*A*A*+T*+A*+T | 30217 | 19 |

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| 73 | ACACTGTGATTCAAC ACTT | A57071Hi | +A*+C*+A*C*T*G*T*G*A*T*T*C*A*A*C*A*+ C*+T*+T | 31035 | 19 |
| 74 | GATATATTCTGTACA AGTT | A57072Hi | +G*+A*+T*A*T*A*T*T*C*T*G*T*A*C*A*A*+ G*+T*+T | 32398 | 19 |
| 75 | TAAGTCTATGGTACT AGT | A57073Hi | +T*+A*+A*G*T*C*T*A*T*G*G*T*A*C*T*+A* +G*+T | 32529 | 18 |
| 76 | GTTTCCACAATCTTG CCAT | A57074Hi | +G*+T*+T*T*C*C*A*C*A*A*T*C*T*T*G*C*+ C*+A*+T | 32569 | 19 |
| 77 | GTCAACATCAAGCAT CAG | A57075Hi | +G*+T*+C*A*A*C*A*T*C*A*A*G*C*A*T*+C* +A*+G | 32611 | 18 |
| 78 | TCTAAGCTTACAACT TTCA | A57076Hi | +T*+C*+T*A*A*G*C*T*T*A*C*A*A*C*T*T*+ T*+C*+A | 33116 | 19 |
| 79 | ACATTCTAAGCTTAC AACT | A57077Hi | +A*+C*+A*T*T*C*T*A*A*G*C*T*T*A*C*A*+ A*+C*+T | 33120 | 19 |
| 80 | ACATCACTGGACTTC TTAT | A57078Hi | +A*+C*+A*T*C*A*C*T*G*G*A*C*T*T*C*T*+ T*+A*+T | 34021 | 19 |
| 81 | GATTAACATCACTGG ACTT | A57079Hi | +G*+A*+T*T*A*A*C*A*T*C*A*C*T*G*G*A*+ C*+T*+T | 34026 | 19 |
| 82 | CTTCCTCTTCCAGATT AAC | A57080Hi | +C*+T*+T*C*C*T*C*T*T*C*C*A*G*A*T*T*+ A*+A*+C | 34038 | 19 |
| 83 | TAGCTAATAGTACAA TTCA | A57081Hi | +T*+A*+G*C*T*A*A*T*A*G*T*A*C*A*A*T*+ T*+C*+A | 34942 | 19 |
| 84 | ACAGTCCTCAAGTGA TTA | A57082Hi | +A*+C*+A*G*T*C*C*T*C*A*A*G*T*G*A*+T* +T*+A | 36460 | 18 |
| 85 | ATGCAATATGCTATC CTTA | A57083Hi | +A*+T*+G*C*A*A*T*A*T*G*C*T*A*T*C*C*+ T*+T*+A | 36843 | 19 |
| 86 | ACTAGATGCAATATG CTAT | A57084Hi | +A*+C*+T*A*G*A*T*G*C*A*A*T*A*T*G*C*+ T*+A*+T | 36848 | 19 |
| 87 | AACTAGCAGTAACTC AAGA | A57085Hi | +A*+A*+C*T*A*G*C*A*G*T*A*A*C*T*C*A*+ A*+G*+A | 37013 | 19 |
| 88 | GACCAAATGAACATT CCTG | A57086Hi | +G*+A*+C*C*A*A*A*T*G*A*A*C*A*T*T*C*+ C*+T*+G | 37688 | 19 |
| 89 | TCAAAGAGGTTCTGA CATT | A57087Hi | +T*+C*+A*A*A*G*A*G*G*T*T*C*T*G*A*C*+ A*+T*+T | 37896 | 19 |
| 90 | ATCTTCCACTTTAATA ATC | A57088Hi | +A*+T*+C*T*T*C*C*A*C*T*T*T*A*A*T*A*+ A*+T*+C | 38085 | 19 |
| 91 | TACACTTAGCTGGAC TTA | A57089Hi | +T*+A*+C*A*C*T*T*A*G*C*T*G*G*A*C*+T* +T*+A | 39087 | 18 |
| 92 | ATTCTTGCCATACTC AAGG | A57090Hi | +A*+T*+T*C*T*T*G*C*C*A*T*A*C*T*C*A*+ A*+G*+G | 40151 | 19 |
| 93 | ACTGTGGCAATCTTA CTG | A57091Hi | +A*+C*+T*G*T*G*G*C*A*A*T*C*T*T*A*+C* +T*+G | 42242 | 18 |
| 94 | AGAGTAAGACATGCA ATCA | A57092Hi | +A*+G*+A*G*T*A*A*G*A*C*A*T*G*C*A*A*+ T*+C*+A | 42832 | 19 |
| 95 | TCTGCAATATTTGGA CCTA | A57093Hi | +T*+C*+T*G*C*A*A*T*A*T*T*T*G*G*A*C*+ C*+T*+A | 42880 | 19 |
| 96 | CTCCAAGTTTAGATG TATT | A57094Hi | +C*+T*+C*C*A*A*G*T*T*T*A*G*A*T*G*T*+ A*+T*+T | 42922 | 19 |
| 97 | CTCAAGTTCTACCTT ATTT | A57095Hi | +C*+T*+C*A*A*G*T*T*C*T*A*C*C*T*T*A*+ T*+T*+T | 42952 | 19 |
| 98 | ATCTCAAGTTCTACC TTAT | A57096Hi | +A*+T*+C*T*C*A*A*G*T*T*C*T*A*C*C*T*+ T*+A*+T | 42954 | 19 |
| 99 | TTGAATCTCAAGTTC TACC | A57097Hi | +T*+T*+G*A*A*T*C*T*C*A*A*G*T*T*C*T*+ A*+C*+C | 42958 | 19 |
| 100 | CAGGCATAAATGGAA CATC | A57098Hi | +C*+A*+G*G*C*A*T*A*A*A*T*G*G*A*A*C*+ A*+T*+C | 43090 | 19 |
| 101 | ACTGGATTTCCTCAC TGAA | A57099Hi | +A*+C*+T*G*G*A*T*T*T*C*C*T*C*A*C*T*+ G*+A*+A | 43259 | 19 |
| 102 | CTTTACTGGATTTCCT CAC | A57100Hi | +C*+T*+T*T*A*C*T*G*G*A*T*T*T*C*C*T*+ C*+A*+C | 43263 | 19 |
| 103 | GTTAGTTGTTCCAAC ACA | A57101Hi | +G*+T*+T*A*G*T*T*G*T*T*C*C*A*A*C*+A* +C*+A | 43904 | 18 |
| 104 | ATGAGCAAGTATATC TAC | A57102Hi | +A*+T*+G*A*G*C*A*A*G*T*A*T*A*T*C*+T* +A*+C | 44172 | 18 |
| 105 | TTCAACCTAACTACT AAAT | A57103Hi | +T*+T*+C*A*A*C*C*T*A*A*C*T*A*C*T*A*+ A*+A*+T | 44337 | 19 |
| 106 | ACCACAAACTTAGCT ATTA | A57104Hi | +A*+C*+C*A*C*A*A*A*C*T*T*A*G*C*T*A*+ T*+T*+A | 44934 | 19 |
| 107 | CCAGTTCTACTTCCA AACT | A57105Hi | +C*+C*+A*G*T*T*C*T*A*C*T*T*C*C*A*A*+ A*+C*+T | 45910 | 19 |

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| 108 | GATTGTCATTCTGAACTTT | A57106Hi | +G*+A*+T*T*G*T*C*A*T*T*C*T*G*A*A*C*+T*+T*+T | 47251 | 19 |
| 109 | TAATTGCTCAGCTTGGAC | A57107Hi | +T*+A*+A*T*T*G*C*T*C*A*G*C*T*T*G*+G*+A*+C | 48387 | 18 |
| 110 | CTCTCAGTGAACAGATTTC | A57108Hi | +C*+T*+C*T*C*A*G*T*G*A*A*C*A*G*A*T*+T*+T*+C | 48522 | 19 |
| 111 | TTTCTGTACTCTCAGTGAA | A57109Hi | +T*+T*+T*C*T*G*T*A*C*T*C*T*C*A*G*T*+G*+A*+A | 48530 | 19 |
| 112 | AGATAATCCAAAGAGCTGA | A57110Hi | +A*+G*+A*T*A*A*T*C*C*A*A*A*G*A*G*C*+T*+G*+A | 48605 | 19 |
| 113 | CTCCACTCCAAAGACGTG | A57111Hi | +C*+T*+C*C*A*C*T*C*C*A*A*A*G*A*C*+G*+T*+G | 48638 | 18 |
| 114 | CTAACTCTTATTCTGGTC | A57112Hi | +C*+T*+A*A*C*T*C*T*T*A*T*T*C*T*G*+G*+T*+C | 48812 | 18 |
| 115 | TCTAACTCTTATTCTGGT | A57113Hi | +T*+C*+T*A*A*C*T*C*T*T*A*T*T*C*T*+G*+G*+T | 48813 | 18 |
| 116 | CCATCCTACTCATCAACCA | A57114Hi | +C*+C*+A*T*C*C*T*A*C*T*C*A*T*C*A*A*+C*+C*+A | 48851 | 19 |
| 117 | CCATCCTACTCATCAACC | A57115Hi | +C*+C*+A*T*C*C*T*A*C*T*C*A*T*C*A*+A*+C*+C | 48852 | 18 |
| 118 | ATCCAACCTCTTTAATCTG | A57116Hi | +A*+T*+C*C*A*A*C*C*T*C*T*T*T*A*A*T*+C*+T*+G | 48933 | 19 |
| 119 | CATCCAACCTCTTTAATCT | A57117Hi | +C*+A*+T*C*C*A*A*C*C*T*C*T*T*T*A*A*+T*+C*+T | 48934 | 19 |
| 120 | GAGATCTTAATACTTACC | A57118Hi | +G*+A*+G*A*T*C*T*T*A*A*T*A*C*T*T*+A*+C*+C | 49537 | 18 |
| 121 | TCCAAGATAATGCACATAC | A57119Hi | +T*+C*+C*A*A*G*A*T*A*A*T*G*C*A*C*A*+T*+A*+C | 49998 | 19 |
| 122 | AGATGAATTAATCCAGAGT | A57120Hi | +A*+G*+A*T*G*A*A*T*T*A*A*T*C*C*A*G*+A*+G*+T | 51201 | 19 |
| 123 | TAGAACCACCTTAAGCAC | A57121Hi | +T*+A*+G*A*A*C*C*A*C*C*T*T*A*A*G*+C*+A*+C | 52279 | 18 |
| 124 | TCACACAACTCACCAAGTA | A57122Hi | +T*+C*+A*C*A*C*C*A*A*C*T*C*A*C*C*A*A*+G*+T*+A | 53941 | 19 |
| 125 | TCTGGCACAAATAAGGTAC | A57123Hi | +T*+C*+T*G*G*C*A*C*A*A*A*T*A*A*G*G*+T*+A*+C | 54906 | 19 |
| 126 | TTTCCACTGTGATTTGATG | A57124Hi | +T*+T*+T*C*C*A*C*T*G*T*G*A*T*T*T*T*G*+A*+T*+G | 55121 | 19 |
| 127 | TTCAGACTTCACTATACTT | A57125Hi | +T*+T*+C*A*G*A*C*T*T*C*A*C*T*A*T*A*+C*+T*+T | 55140 | 19 |
| 128 | CACCACTACCATGAATCT | A57126Hi | +C*+A*+C*C*A*C*T*A*C*C*A*T*G*A*A*+T*+C*+T | 56373 | 18 |
| 129 | TACCACCACTACCATGAAT | A57127Hi | +T*+A*+C*C*A*C*C*A*C*T*A*C*C*A*T*G*+A*+A*+T | 56375 | 19 |
| 130 | CTTTAAATCCTACAGAGTC | A57128Hi | +C*+T*+T*T*A*A*A*T*C*C*T*A*C*A*G*A*+G*+T*+C | 56645 | 19 |
| 131 | AAGCTGACTTTAGGCATAT | A57129Hi | +A*+A*+G*C*T*G*A*C*T*T*T*A*G*G*C*A*+T*+A*+T | 56742 | 19 |
| 132 | ACTATCCAAGCTGACTTTA | A57130Hi | +A*+C*+T*A*T*C*C*A*A*G*C*T*G*A*C*T*+T*+T*+A | 56749 | 19 |
| 133 | TCCTCAAAGATATACCTTG | A57131Hi | +T*+C*+C*T*C*A*A*A*G*A*T*A*T*A*C*C*+T*+T*+G | 58333 | 19 |
| 134 | CAAGATCTCTGTTTACATC | A57132Hi | +C*+A*+A*G*A*T*C*T*C*T*G*T*T*T*A*C*+A*+T*+C | 58587 | 19 |
| 135 | ATCCAAACCTTTGCAATAT | A57133Hi | +A*+T*+C*C*A*A*A*C*C*T*T*T*G*C*A*A*+T*+A*+T | 59248 | 19 |
| 136 | TAGATTCCTAACAGTACA | A57134Hi | +T*+A*+G*A*T*T*C*C*T*A*A*C*A*G*T*+A*+C*+A | 60574 | 18 |
| 137 | AAGTGTTCTTTACTCAGAC | A57135Hi | +A*+A*+G*T*G*T*T*C*T*T*T*A*C*T*C*A*+G*+A*+C | 61211 | 19 |
| 138 | ATTCTTCTCACAACTTCAT | A57136Hi | +A*+T*+T*C*T*T*C*T*C*A*C*A*A*C*T*T*+C*+A*+T | 61793 | 19 |
| 139 | CTCTCAAATATCCTTATTC | A57137Hi | +C*+T*+C*T*C*A*A*A*T*A*T*C*C*T*T*A*+T*+T*+C | 63162 | 19 |
| 140 | GTATAAATCAGTGGCACA | A57138Hi | +G*+T*+A*T*A*A*A*T*C*A*G*T*G*G*C*+A*+C*+A | 64255 | 18 |
| 141 | AACATCCAATACAACACAC | A57139Hi | +A*+A*+C*A*T*C*C*A*A*T*A*C*A*A*C*A*+C*+A*+C | 64669 | 19 |
| 142 | TGAAATGTCTATTAGCACA | A57140Hi | +T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A*+C*+A | 67470 | 19 |

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| 142 | TGAAATGTCTATTAG CACA | A575315Hi | +T*+G*A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A *+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575316Hi | +T*G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A *+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575318Hi | +T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+ A*C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575321Hi | +T*+G*+A*+A*A*T*G*T*C*T*A*T*T*A*G*C* +A*+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575322Hi | +T*+G*+A*+A*A*T*G*T*C*T*A*T*T*A*G*C* A*+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575323Hi | +T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*+C* +A*+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575324Hi | +T*+G*A*A*A*T*G*T*C*T*A*T*T*A*G*+C*+ A*+C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575326Hi | +T*+G*+A*+A*A*T*G*T*C*T*A*T*T*A*G*C* +A*C*+A | 67470 | 19 |
| 142 | TGAAATGTCTATTAG CACA | A575327Hi | +T*G*+A*A*A*T*G*T*C*T*A*T*T*A*G*+C*+ A*+C*+A | 67470 | 19 |
| 143 | CCTACTCTTTATCTTA GAA | A57141Hi | +C*+C*+T*A*C*T*C*T*T*T*A*T*C*T*T*A*+ G*+A*+A | 67740 | 19 |
| 144 | TACTCAATCATAAGA TCC | A57142Hi | +T*+A*+C*T*C*A*A*T*C*A*T*A*A*G*A*+T* +C*+C | 68485 | 18 |
| 145 | GATTTCTAGCTAAAG TGTT | A57143Hi | +G*+A*+T*T*T*C*T*A*G*C*T*A*A*A*G*T*+ G*+T*+T | 69023 | 19 |
| 146 | ACATCACACAGACTA AGAT | A57144Hi | +A*+C*+A*T*C*A*C*A*C*A*G*A*C*T*A*A*+ G*+A*+T | 70797 | 19 |
| 147 | TACCAAACCAGGTCT AATT | A57145Hi | +T*+A*+C*C*A*A*A*C*C*A*G*G*T*C*T*A*+ A*+T*+T | 70984 | 19 |
| 148 | CAGAGCCAGTACTAC CAAA | A57146Hi | +C*+A*+G*A*G*C*C*A*G*T*A*C*T*A*C*C*+ A*+A*+A | 70996 | 19 |
| 149 | TTTGATCTGTAGTAC ATAC | A57147Hi | +T*+T*+T*G*A*T*C*T*G*T*A*G*T*A*C*A*+ T*+A*+C | 71257 | 19 |
| 150 | AAGCCTGAAACAAGT CCTG | A57148Hi | +A*+A*+G*C*C*T*G*A*A*A*C*A*A*G*T*C*+ C*+T*+G | 72080 | 19 |
| 151 | TTTACTGAGTCAGGT ATA | A57149Hi | +T*+T*+T*A*C*T*G*A*G*T*C*A*G*G*T*+A* +T*+A | 75451 | 18 |
| 152 | GATCATTATTAGTTTC TGA | A57150Hi | +G*+A*+T*C*A*T*T*A*T*T*A*G*T*T*T*C*+ T*+G*+A | 75543 | 19 |
| 153 | ATGGCTTTGATCATT ATTA | A57151Hi | +A*+T*+G*G*C*T*T*T*G*A*T*C*A*T*T*A*+ T*+T*+A | 75551 | 19 |
| 154 | AACTTAATCACAAGT TCCT | A57152Hi | +A*+A*+C*T*T*A*A*T*C*A*C*A*A*G*T*T*+ C*+C*+T | 75722 | 19 |
| 155 | ACAGAGCATCCTGAA ACTT | A57153Hi | +A*+C*+A*G*A*G*C*A*T*C*C*T*G*A*A*A*+ C*+T*+T | 75814 | 19 |
| 156 | TCTCAAATGTAAGAC CACT | A57154Hi | +T*+C*+T*C*A*A*A*T*G*T*A*A*G*A*C*C*+ A*+C*+T | 76162 | 19 |
| 157 | GATTCTCCACTTAAG ACTT | A57155Hi | +G*+A*+T*T*C*T*C*C*A*C*T*T*A*A*G*A*+ C*+T*+T | 76526 | 19 |
| 158 | TTTATCTAGACAATCT TCA | A57156Hi | +T*+T*+T*A*T*C*T*A*G*A*C*A*A*T*C*T*+ T*+C*+A | 76645 | 19 |
| 159 | GTTTCTAAAGGTTCT GTTC | A57157Hi | +G*+T*+T*T*C*T*A*A*A*G*G*T*T*C*T*G*+ T*+T*+C | 77928 | 19 |
| 160 | TAGCCAGTATAATCT CATT | A57158Hi | +T*+A*+G*C*C*A*G*T*A*T*A*A*T*C*T*C*+ A*+T*+T | 78143 | 19 |
| 161 | TGAGCTAGTACTATA AAGA | A57159Hi | +T*+G*+A*G*C*T*A*G*T*A*C*T*A*T*A*A*+ A*+G*+A | 79662 | 19 |
| 162 | TGTGTTACCATATCC ATTT | A57160Hi | +T*+G*+T*G*T*T*A*C*C*A*T*A*T*C*C*A*+ T*+T*+T | 79809 | 19 |
| 163 | AACATACTTCATCTCT TCA | A57161Hi | +A*+A*+C*A*T*A*C*T*T*C*A*T*C*T*C*T*+ T*+C*+A | 80509 | 19 |
| 164 | GTCATAAGTTGTCAG TAT | A57162Hi | +G*+T*+C*A*T*A*A*G*T*T*G*T*C*A*G*+T* +A*+T | 80622 | 18 |
| 165 | TCCAAAGGTTTGTCA TAAG | A57163Hi | +T*+C*+C*A*A*A*G*G*T*T*T*G*T*C*A*T*+ A*+A*+G | 80632 | 19 |
| 166 | TATTTCTTAAGAATG CACC | A57164Hi | +T*+A*+T*T*T*C*T*T*A*A*G*A*A*T*G*C*+ A*+C*+C | 82190 | 19 |
| 167 | TCCTGATGATATGAC CAAA | A57165Hi | +T*+C*+C*T*G*A*T*G*A*T*A*T*G*A*C*C*+ A*+A*+A | 82232 | 19 |
| 168 | GTGGTCTTCATGACT AAAT | A57166Hi | +G*+T*+G*G*T*C*T*T*C*A*T*G*A*C*T*A*+ A*+A*+T | 86182 | 19 |

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| 169 | GACTAAGTGAAATTC ATCA | A57167Hi | +G*+A*+C*T*A*A*G*T*G*A*A*A*T*T*C*A*+ T*+C*+A | 86462 | 19 |
| 170 | ACAAATGGCTCATTA GGTT | A57168Hi | +A*+C*+A*A*A*T*G*G*C*T*C*A*T*T*A*G*+ G*+T*+T | 86707 | 19 |
| 171 | CTGTGACTTTGCATC AACT | A57169Hi | +C*+T*+G*T*G*A*C*T*T*T*G*C*A*T*C*A*+ A*+C*+T | 87122 | 19 |
| 172 | AATTCAGGTTGAAGC ACCT | A57170Hi | +A*+A*+T*T*C*A*G*G*T*T*G*A*A*G*C*A*+ C*+C*+T | 87444 | 19 |
| 173 | CAACCATAACCATTA CTTC | A57171Hi | +C*+A*+A*C*C*A*T*A*A*C*C*A*T*T*A*C*+ T*+T*+C | 87994 | 19 |
| 174 | AGACAACCATAACCA TTAC | A57172Hi | +A*+G*+A*C*A*A*C*C*A*T*A*A*C*C*A*T*+ T*+A*+C | 87997 | 19 |
| 175 | TGGCAAATTCAGTGC TAAC | A57173Hi | +T*+G*+G*C*A*A*A*T*T*C*A*G*T*G*C*T*+ A*+A*+C | 88896 | 19 |
| 176 | TCAAATGGTTGGCAA ATTC | A57174Hi | +T*+C*+A*A*A*T*G*G*T*T*G*G*C*A*A*A*+ T*+T*+C | 88905 | 19 |
| 177 | ACTCCTAGGTGATTT CTAA | A57175Hi | +A*+C*+T*C*C*T*A*G*G*T*G*A*T*T*T*C*+ T*+A*+A | 89376 | 19 |
| 178 | ACACAATTAGCACTG AAGT | A57176Hi | +A*+C*+A*C*A*A*T*T*A*G*C*A*C*T*G*A*+ A*+G*+T | 89684 | 19 |
| 179 | ACTTACTCTAGTACT ATCA | A57177Hi | +A*+C*+T*T*A*C*T*C*T*A*G*T*A*C*T*A*+ T*+C*+A | 89742 | 19 |
| 180 | AGGAACAGATCATAA ACC | A57178Hi | +A*+G*+G*A*A*C*A*G*A*T*C*A*T*A*A*+A* +C*+C | 89817 | 18 |
| 181 | TCTATGCTTTGACCA TAAC | A57179Hi | +T*+C*+T*A*T*G*C*T*T*T*G*A*C*C*A*T*+ A*+A*+C | 90335 | 19 |
| 182 | AGTCTTCTATGTGAA ATGT | A57180Hi | +A*+G*+T*C*T*T*C*T*A*T*G*T*G*A*A*A*+ T*+G*+T | 90437 | 19 |
| 183 | AGTGAACTCAAGACA TCTT | A57181Hi | +A*+G*+T*G*A*A*C*T*C*A*A*G*A*C*A*T*+ C*+T*+T | 90482 | 19 |
| 184 | TCTAGATAGAGGTTT CAC | A57182Hi | +T*+C*+T*A*G*A*T*A*G*A*G*G*T*T*T*+C* +A*+C | 90672 | 18 |
| 185 | CAGCTACCTACACAT CTTT | A57183Hi | +C*+A*+G*C*T*A*C*C*T*A*C*A*C*A*T*C*+ T*+T*+T | 91810 | 19 |
| 186 | TTTATTGCAGTCATA GTGA | A57184Hi | +T*+T*+T*A*T*T*G*C*A*G*T*C*A*T*A*G*+ T*+G*+A | 92086 | 19 |
| 187 | CTGCCTTAATGGTAC CTTT | A57185Hi | +C*+T*+G*C*C*T*T*A*A*T*G*G*T*A*C*C*+ T*+T*+T | 92545 | 19 |
| 188 | ACAGTTAAATGAGTC TTGT | A57186Hi | +A*+C*+A*G*T*T*A*A*A*T*G*A*A*G*T*C*T*+ T*+G*+T | 92574 | 19 |
| 189 | GTACTTTATAGCAAT TCC | A57187Hi | +G*+T*+A*C*T*T*T*A*T*A*G*C*A*A*T*+T* +C*+C | 93827 | 18 |
| 190 | TCTCAGAACTTGCTT AATA | A57188Hi | +T*+C*+T*C*A*G*A*A*C*T*T*G*C*T*T*A*+ A*+T*+A | 95512 | 19 |
| 191 | ACACTATGGTTATAC AGC | A57189Hi | +A*+C*+A*C*T*A*T*G*G*T*T*A*T*A*C*C+A* +G*+C | 96006 | 18 |
| 192 | AGTGATTGTAATACA GATC | A57190Hi | +A*+G*+T*G*A*T*T*G*T*A*A*T*A*C*A*G*+ A*+T*+C | 96949 | 19 |
| 193 | TTGTCTAAACCTCAT ACT | A57191Hi | +T*+T*+G*T*C*T*A*A*A*C*C*T*C*A*T*+A* +C*+T | 97276 | 18 |
| 194 | CTTGTCTAAACCTCA TAC | A57192Hi | +C*+T*+T*G*T*C*T*A*A*A*C*C*T*C*A*+T* +A*+C | 97277 | 18 |
| 195 | ATCCTAGTCTACATG ATTA | A57193Hi | +A*+T*+C*C*T*A*G*T*C*T*A*C*A*T*G*A*+ T*+T*+A | 98498 | 19 |
| 196 | CATGATAATCTCATC CTCA | A57194Hi | +C*+A*+T*G*A*T*A*A*T*C*T*C*A*T*C*C*+ T*+C*+A | 98522 | 19 |
| 197 | ATAGCTAAACTTCTC CATT | A57195Hi | +A*+T*+A*G*C*T*A*A*A*C*T*T*C*T*C*C*+ A*+T*+T | 99316 | 19 |
| 198 | TATGTCCTGACTGAC AGA | A57196Hi | +T*+A*+T*G*T*C*C*T*G*A*C*T*G*A*C*+A* +G*+A | 99612 | 18 |
| 199 | ACTAATACATTAACTT CCT | A57197Hi | +A*+C*+T*A*A*T*A*C*A*T*T*A*A*C*T*T*+ C*+C*+T | 99754 | 19 |
| 200 | GTCCATTCATCTGAA ACAC | A57198Hi | +G*+T*+C*C*A*T*T*C*A*T*C*T*G*A*A*A*+ C*+A*+C | 99941 | 19 |
| 201 | CGTTTCCACATACAC TACT | A57199Hi | +C*+G*+T*T*T*C*C*A*C*A*T*A*C*A*C*T*+ A*+C*+T | 99968 | 19 |
| 202 | CGTTTCCACATACAC TAC | A57200Hi | +C*+G*+T*T*T*C*C*A*C*A*T*A*C*A*C*+T* +A*+C | 99969 | 18 |
| 203 | ACGTTTCCACATACA CTAC | A57201Hi | +A*+C*+G*T*T*T*C*C*A*C*A*T*A*C*A*C*+ T*+A*+C | 99969 | 19 |

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| 204 | CTTTGTAAATGACGTTTCC | A57202Hi | +C*+T*+T*T*G*T*A*A*A*T*G*A*C*G*T*T*+T*+C*+C | 99980 | 19 |
| 205 | AACTCCTATCTAGACTGC | A57203Hi | +A*+A*+C*T*C*C*T*A*T*C*T*A*G*A*C*+T*+G*+C | 100415 | 18 |
| 206 | CCTTATCTTTGGCAACATC | A57204Hi | +C*+C*+T*T*A*T*C*T*T*T*G*G*C*A*A*C*+A*+T*+C | 100594 | 19 |
| 207 | TCACTGCATAATAGTTAC | A57205Hi | +T*+C*+A*C*T*G*C*A*T*A*A*T*A*G*T*+T*+A*+C | 100809 | 18 |
| 208 | TCACTTGATGGATATAAGT | A57206Hi | +T*+C*+A*C*T*T*G*A*T*G*G*A*T*A*T*A*+A*+G*+T | 102072 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A57207Hi | +A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575329Hi | +A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575330Hi | +A*C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575332Hi | +A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575335Hi | +A*+C*+A*+A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575336Hi | +A*+C*+A*+A*T*A*T*T*T*A*T*G*G*T*T*C*T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575337Hi | +A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575338Hi | +A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575340Hi | +A*+C*+A*+A*T*A*T*T*T*A*T*G*G*T*T*C*+T*C*+A | 102111 | 19 |
| 209 | ACAATATTTATGGTTCTCA | A575341Hi | +A*C*+A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C*+A | 102111 | 19 |
| 210 | TACAATATTTATGGTTCTC | A57208Hi | +T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575343Hi | +T*+A*C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575344Hi | +T*A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575346Hi | +T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575349Hi | +T*+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575350Hi | +T*+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575351Hi | +T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*+T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575352Hi | +T*+A*C*A*A*T*A*T*T*T*A*T*G*G*T*+T*+C*+T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575354Hi | +T*+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*+C*T*+C | 102112 | 19 |
| 210 | TACAATATTTATGGTTCTC | A575355Hi | +T*A*+C*A*A*T*A*T*T*T*A*T*G*G*T*+T*+C*+T*+C | 102112 | 19 |
| 211 | TGTACAATATTTATGGTTC | A57209Hi | +T*+G*+T*A*C*A*A*T*A*T*T*T*A*T*G*G*+T*+T*+C | 102114 | 19 |
| 212 | GTGCTCTAGACAAACCG | A57210Hi | +G*+T*+G*C*T*C*T*A*G*A*C*A*A*A*+C*+C*+G | 102304 | 17 |
| 213 | ATTCAGCTCCATAGTCATA | A57211Hi | +A*+T*+T*C*A*G*C*T*C*C*A*T*A*G*T*C*+A*+T*+A | 102569 | 19 |
| 214 | CTTCCATATAGCTGATGA | A57212Hi | +C*+T*+T*C*C*A*T*A*T*A*G*C*T*G*A*+T*+G*+A | 102915 | 18 |
| 215 | AACTCAATCACAGCCTAT | A57213Hi | +A*+A*+C*T*C*A*A*T*C*A*C*A*G*C*C*+T*+A*+T | 102980 | 18 |
| 216 | TTATAGCCACCTCCTAAG | A57214Hi | +T*+T*+A*T*A*G*C*C*A*C*C*T*C*C*T*+A*+A*+G | 103051 | 18 |
| 217 | CTTCTGTGACTTCATCTAT | A57215Hi | +C*+T*+T*C*T*G*T*G*A*C*T*T*C*A*T*C*+T*+A*+T | 103101 | 19 |
| 218 | AATTATGTCATCCACTTCT | A57216Hi | +A*+A*+T*T*A*T*G*T*C*A*T*C*C*A*C*T*+T*+C*+T | 103115 | 19 |
| 219 | AACTAGATATAGGCTCCA | A57217Hi | +A*+A*+C*T*A*G*A*T*A*T*A*G*G*C*T*+C*+C*+A | 105711 | 18 |
| 220 | CACGTATCTCCTTCTTTA | A57218Hi | +C*+A*+C*G*T*A*T*C*T*C*C*T*T*C*T*+T*+T*+A | 109904 | 18 |

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| 221 | CCTGATCCAACTTTC ATG | A57219Hi | +C*+C*+T*G*A*T*C*C*A*A*C*T*T*T*C*+A* +T*+G | 111091 | 18 |
| 222 | CTTTGCTTATTCGTG ACT | A57220Hi | +C*+T*+T*T*G*C*T*T*A*T*T*C*G*T*G*+A* +C*+T | 114218 | 18 |
| 223 | CCTAATAAAGTGCAC CTG | A57221Hi | +C*+C*+T*A*A*T*A*A*A*G*T*G*C*A*C*+C* +T*+G | 119686 | 18 |
| 224 | CAATGTATACCATGC AGT | A57222Hi | +C*+A*+A*T*G*T*A*T*A*C*C*A*T*G*C*+A* +G*+T | 120997 | 18 |
| 225 | TCTTGCCTAGTATAT GTT | A57223Hi | +T*+C*+T*T*G*C*C*T*A*G*T*A*T*A*T*+G* +T*+T | 125919 | 18 |
| 226 | CCAATACTAACTTAA ACC | A57224Hi | +C*+C*+A*A*T*A*C*T*A*A*C*T*T*A*A*+A* +C*+C | 130119 | 18 |
| 227 | TTCAACTCCGAAACT GCC | A57225Hi | +T*+T*+C*A*A*C*T*C*C*G*A*A*A*C*T*+G* +C*+C | 130196 | 18 |
| 228 | GTTGATTGTCTTCCA ATT | A57226Hi | +G*+T*+T*G*A*T*T*G*T*C*T*T*C*C*A*+A* +T*+T | 134758 | 18 |
| 229 | GAATACTTGCTGTCT ATC | A57227Hi | +G*+A*+A*T*A*C*T*T*G*C*T*G*T*C*T*+A* +T*+C | 134850 | 18 |
| 230 | AAGAATACTTGCTGT CTAT | A57228Hi | +A*+A*+G*A*A*T*A*C*T*T*G*C*T*G*T*C*+ T*+A*+T | 134851 | 19 |
| 231 | ACAATCCTCAGGTAA GAG | A57229Hi | +A*+C*+A*A*T*C*C*T*C*A*G*G*T*A*A*+G* +A*+G | 135164 | 18 |
| 232 | ACTGGATGCTCTTGT TAAT | A57230Hi | +A*+C*+T*G*G*A*T*G*C*T*C*T*T*G*T*T*+ A*+A*+T | 135523 | 19 |
| 233 | ATGGATGCTCTCTAG TAA | A57231Hi | +A*+T*+G*G*A*T*G*C*T*C*T*C*T*A*G*+T* +A*+A | 136662 | 18 |
| 234 | TTGAGAGCTTGATCT TTAT | A57232Hi | +T*+T*+G*A*G*A*G*C*T*T*G*A*T*C*T*T*+ T*+A*+T | 136678 | 19 |
| 235 | CATCTTTGAGAGCTT GATC | A57233Hi | +C*+A*+T*C*T*T*T*G*A*G*A*G*C*T*T*G*+ A*+T*+C | 136683 | 19 |
| 236 | CACAAACAGATTGGC TAC | A57234Hi | +C*+A*+C*A*A*A*C*A*G*A*T*T*G*G*C*+T* +A*+C | 137734 | 18 |
| 237 | TCTACGTGTAATACA ACC | A57235Hi | +T*+C*+T*A*C*G*T*G*T*A*A*T*A*C*A*+A* +C*+C | 138335 | 18 |
| 238 | AAAGCTAGCAGAGAC TCCA | A57236Hi | +A*+A*+A*G*C*T*A*G*C*A*G*A*G*A*C*T*+ C*+C*+A | 138834 | 19 |
| 239 | GGACATGTATCTTAA TAGT | A57237Hi | +G*+G*+A*C*A*T*G*T*A*T*C*T*T*A*A*T*+ A*+G*+T | 140893 | 19 |
| 240 | AATCTGTGATCCACT CCTT | A57238Hi | +A*+A*+T*C*T*G*T*G*A*T*C*C*A*C*T*C*+ C*+T*+T | 141809 | 19 |
| 241 | TTCCTGATTATACCAT ATG | A57239Hi | +T*+T*+C*C*T*G*A*T*T*A*T*A*C*C*A*T*+ A*+T*+G | 142174 | 19 |
| 242 | ACATCCTCCTCCACG TAA | A57240Hi | +A*+C*+A*T*C*C*T*C*C*T*C*C*A*C*G*+T* +A*+A | 5111 | 18 |
| 243 | GCCTATTCACAACTT CATC | A57241Hi | +G*+C*+C*T*A*T*T*C*A*C*A*A*C*T*T*C*+ A*+T*+C | 30286 | 19 |
| 244 | AATCTTGCCATTCCTT TCA | A57242Hi | +A*+A*+T*C*T*T*G*C*C*A*T*T*C*C*T*T*+ T*+C*+A | 32561 | 19 |
| 245 | CACAATCTTGCCATT CCTT | A57243Hi | +C*+A*+C*A*A*T*C*T*T*G*C*C*A*T*T*C*+ C*+T*+T | 32564 | 19 |
| 246 | CCTTCAACATGTTTC CACA | A57244Hi | +C*+C*+T*T*C*A*A*C*A*T*G*T*T*T*C*C*+ A*+C*+A | 32579 | 19 |
| 247 | CTTCCAAGCTTCCTC ATTT | A57245Hi | +C*+T*+T*C*C*A*A*G*C*T*T*C*C*T*C*A*+ T*+T*+T | 48546 | 19 |
| 248 | TTATTCAACCTCTCTG TCA | A57246Hi | +T*+T*+A*T*T*C*A*A*C*C*T*C*T*C*T*G*+ T*+C*+A | 93533 | 19 |
| 249 | AGTCCTCATCCATAT CTAT | A57247Hi | +A*+G*+T*C*C*T*C*A*T*C*C*A*T*A*T*C*+ T*+A*+T | 96890 | 19 |
| 250 | ATGCTCTTATCCACA ATCC | A57248Hi | +A*+T*+G*C*T*C*T*T*A*T*C*C*A*C*A*A*+ T*+C*+C | 135068 | 19 |
| 251 | TACATATTTCACAAA CAGA | A57249Hi | +T*+A*+C*A*T*A*T*T*T*C*A*C*A*A*A*C*+ A*+G*+A | 137742 | 19 |
| 252 | TTGGACCAGCGTTTC TATC | A57250H | +T*+T*+G*G*A*C*C*A*G*C*G*T*T*T*C*T*+ A*+T*+C | 228 | 19 |
| 253 | TTGGACCAGCGTTTC TAT | A57251H | +T*+T*+G*G*A*C*C*A*G*C*G*T*T*T*C*+T* +A*+T | 229 | 18 |
| 254 | GACTTCGTTTAATAC CAG | A57252H | +G*+A*+C*T*T*C*G*T*T*T*A*A*T*A*C*+C* +A*+G | 24847 | 18 |
| 255 | GGACTTCGTTTAATA CCAG | A57253H | +G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*A*C*+ C*+A*+G | 24847 | 19 |

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| 256 | ATGGACTTCGTTTAATACC | A57254H | +A*+T*+G*G*A*C*T*T*C*G*T*T*T*A*A*T*+A*+C*+C | 24849 | 19 |
| 257 | TCGAAGCGCCTCCAGCT | A57255H | +T*+C*+G*A*A*G*C*G*C*C*T*C*C*A*+G*+C*+T | 34567 | 17 |
| 258 | TGTTGATCCTTTTGTTCCA | A57256H | +T*+G*+T*T*G*A*T*C*C*T*T*T*T*G*T*T*+C*+C*+A | 53001 | 19 |
| 259 | CTCGCTGCGTCATAAAATG | A57257H | +C*+T*+C*G*C*T*G*C*G*T*C*A*T*A*A*A*+A*+T*+G | 84139 | 19 |
| 260 | CTCGCTGCGTCATAAAAT | A57258H | +C*+T*+C*G*C*T*G*C*G*T*C*A*T*A*A*+A*+A*+T | 84140 | 18 |
| 261 | CTCGCTGCGTCATAAAA | A57259H | +C*+T*+C*G*C*T*G*C*G*T*C*A*T*A*+A*+A*+A | 84141 | 17 |
| 262 | CTCGCTGCGTCATAAA | A57260H | +C*+T*+C*G*C*T*G*C*G*T*C*A*T*+A*+A*+A | 84142 | 16 |
| 263 | GCAGGGGCGCCGGCCACAG | A57261H | +G*+C*+A*G*G*G*G*C*G*C*C*G*G*C*C*A*+C*+A*+G | 56 | 19 |
| 264 | GCAGGGGCGCCGGCCACA | A57262H | +G*+C*+A*G*G*G*G*C*G*C*C*G*G*C*C*+A*+C*+A | 57 | 18 |
| 265 | GGCAGGGGCGCCGGCCACA | A57263H | +G*+G*+C*A*G*G*G*G*C*G*C*C*G*G*C*C*+A*+C*+A | 57 | 19 |
| 266 | CCGGCAGGGGCGCCGGCCA | A57264H | +C*+C*+G*G*C*A*G*G*G*G*C*G*C*C*G*G*+C*+C*+A | 59 | 19 |
| 267 | GAACCGGCAGGGGCGCCGG | A57265H | +G*+A*+A*C*C*G*G*C*A*G*G*G*G*C*G*C*+C*+G*+G | 62 | 19 |
| 268 | GAACCGGCAGGGGCGCCG | A57266H | +G*+A*+A*C*C*G*G*C*A*G*G*G*G*C*G*+C*+C*+G | 63 | 18 |
| 269 | GGAACCGGCAGGGGCGCCG | A57267H | +G*+G*+A*A*C*C*G*G*C*A*G*G*G*G*C*G*+C*+C*+G | 63 | 19 |
| 270 | GGAACCGGCAGGGGCGCC | A57268H | +G*+G*+A*A*C*C*G*G*C*A*G*G*G*G*C*+G*+C*+C | 64 | 18 |
| 271 | GGGAACCGGCAGGGGCGCC | A57269H | +G*+G*+G*A*A*C*C*G*G*C*A*G*G*G*G*C*+G*+C*+C | 64 | 19 |
| 272 | AGGGAACCGGCAGGGGCGC | A57270H | +A*+G*+G*G*A*A*C*C*G*G*C*A*G*G*G*G*+C*+G*+C | 65 | 19 |
| 273 | TCAGGGAACCGGCAGGGGC | A57271H | +T*+C*+A*G*G*G*A*A*C*C*G*G*C*A*G*G*+G*+G*+C | 67 | 19 |
| 274 | TCAGGGAACCGGCAGGGG | A57272H | +T*+C*+A*G*G*G*A*A*C*C*G*G*C*A*G*+G*+G*+G | 68 | 18 |
| 275 | CTCAGGGAACCGGCAGGGG | A57273H | +C*+T*+C*A*G*G*G*A*A*C*C*G*G*C*A*G*+G*+G*+G | 68 | 19 |
| 276 | GCTCAGGGAACCGGCAGGG | A57274H | +G*+C*+T*C*A*G*G*G*A*A*C*C*G*G*C*A*+G*+G*+G | 69 | 19 |
| 277 | TGCTCAGGGAACCGGCAGG | A57275H | +T*+G*+C*T*C*A*G*G*G*A*A*C*C*G*G*C*+A*+G*+G | 70 | 19 |
| 278 | TGCTCAGGGAACCGGCAG | A57276H | +T*+G*+C*T*C*A*G*G*G*A*A*C*C*G*G*+C*+A*+G | 71 | 18 |
| 279 | CTGCTCAGGGAACCGGCAG | A57277H | +C*+T*+G*C*T*C*A*G*G*G*A*A*C*C*G*G*+C*+A*+G | 71 | 19 |
| 280 | CTGCTCAGGGAACCGGCA | A57278H | +C*+T*+G*C*T*C*A*G*G*G*A*A*C*C*G*+G*+C*+A | 72 | 18 |
| 281 | GCTGCTCAGGGAACCGGCA | A57279H | +G*+C*+T*G*C*T*C*A*G*G*G*A*A*C*C*G*+G*+C*+A | 72 | 19 |
| 282 | CGCTGCTCAGGGAACCGGC | A57280H | +C*+G*+C*T*G*C*T*C*A*G*G*G*A*A*C*C*+G*+G*+C | 73 | 19 |
| 283 | CGCTGCTCAGGGAACCGG | A57281H | +C*+G*+C*T*G*C*T*C*A*G*G*G*A*A*C*+C*+G*+G | 74 | 18 |
| 284 | CCGCTGCTCAGGGAACCGG | A57282H | +C*+C*+G*C*T*G*C*T*C*A*G*G*G*A*A*C*+C*+G*+G | 74 | 19 |
| 285 | CGCTGCTCAGGGAACCG | A57283H | +C*+G*+C*T*G*C*T*C*A*G*G*G*A*A*+C*+C*+G | 75 | 17 |
| 286 | CCGCTGCTCAGGGAACCG | A57284H | +C*+C*+G*C*T*G*C*T*C*A*G*G*G*A*A*+C*+C*+G | 75 | 18 |
| 287 | TCCGCTGCTCAGGGAACCG | A57285H | +T*+C*+C*G*C*T*G*C*T*C*A*G*G*G*A*A*+C*+C*+G | 75 | 19 |
| 288 | GTCCGCTGCTCAGGGAACC | A57286H | +G*+T*+C*C*G*C*T*G*C*T*C*A*G*G*G*A*+A*+C*+C | 76 | 19 |
| 289 | CGTCCGCTGCTCAGGGAAC | A57287H | +C*+G*+T*C*C*G*C*T*G*C*T*C*A*G*G*G*+A*+A*+C | 77 | 19 |
| 290 | CGTCCGCTGCTCAGGGAA | A57288H | +C*+G*+T*C*C*G*C*T*G*C*T*C*A*G*G*+G*+A*+A | 78 | 18 |

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| 291 | ACGTCCGCTGCTCAGGGAA | A57289H | +A*+C*+G*T*C*C*G*C*T*G*C*T*C*A*G*G*+G*+A*+A | 78 | 19 |
| 292 | CGTCCGCTGCTCAGGGA | A57290H | +C*+G*+T*C*C*G*C*T*G*C*T*C*A*G*+G*+G*+A | 79 | 17 |
| 293 | ACGTCCGCTGCTCAGGGA | A57291H | +A*+C*+G*T*C*C*G*C*T*G*C*T*C*A*G*+G*+G*+A | 79 | 18 |
| 294 | AACGTCCGCTGCTCAGGGA | A57292H | +A*+A*+C*G*T*C*C*G*C*T*G*C*T*C*A*G*+G*+G*+A | 79 | 19 |
| 295 | ACGTCCGCTGCTCAGGG | A57293H | +A*+C*+G*T*C*C*G*C*T*G*C*T*C*A*+G*+G*+G | 80 | 17 |
| 296 | AACGTCCGCTGCTCAGGG | A57294H | +A*+A*+C*G*T*C*C*G*C*T*G*C*T*C*A*+G*+G*+G | 80 | 18 |
| 297 | GAACGTCCGCTGCTCAGGG | A57295H | +G*+A*+A*C*G*T*C*C*G*C*T*G*C*T*C*A*+G*+G*+G | 80 | 19 |
| 298 | GAACGTCCGCTGCTCAGG | A57296H | +G*+A*+A*C*G*T*C*C*G*C*T*G*C*T*C*+A*+G*+G | 81 | 18 |
| 299 | TTCCAACCCGCCGCCCTCC | A57297H | +T*+T*+C*C*A*A*C*C*C*G*C*C*G*C*C*C*+T*+C*+C | 105 | 19 |
| 300 | TTCCAACCCGCCGCCCTC | A57298H | +T*+T*+C*C*A*A*C*C*C*G*C*C*G*C*C*+C*+T*+C | 106 | 18 |
| 301 | CTTCCAACCCGCCGCCCTC | A57299H | +C*+T*+T*C*C*A*A*C*C*C*G*C*C*G*C*C*+C*+T*+C | 106 | 19 |
| 302 | CTTCCAACCCGCCGCCCT | A57300H | +C*+T*+T*C*C*A*A*C*C*C*G*C*C*G*C*+C*+C*+T | 107 | 18 |
| 303 | GCTTCCAACCCGCCGCCCT | A57301H | +G*+C*+T*T*C*C*A*A*C*C*C*G*C*C*G*C*+C*+C*+T | 107 | 19 |
| 304 | GCTTCCAACCCGCCGCCC | A57302H | +G*+C*+T*T*C*C*A*A*C*C*C*G*C*C*G*+C*+C*+C | 108 | 18 |
| 305 | TGCTTCCAACCCGCCGCCC | A57303H | +T*+G*+C*T*T*C*C*A*A*C*C*C*G*C*C*G*+C*+C*+C | 108 | 19 |
| 306 | CCTGCTTCCAACCCGCCGC | A57304H | +C*+C*+T*G*C*T*T*C*C*A*A*C*C*C*G*C*+C*+G*+C | 110 | 19 |
| 307 | CCTGCTTCCAACCCGCCG | A57305H | +C*+C*+T*G*C*T*T*C*C*A*A*C*C*C*G*+C*+C*+G | 111 | 18 |
| 308 | CTGCCACTAGCCATGGTGG | A57306H | +C*+T*+G*C*C*A*C*T*A*G*C*C*A*T*G*G*+T*+G*+G | 131 | 19 |
| 309 | AGCTGCCACTAGCCATGGT | A57307H | +A*+G*+C*T*G*C*C*A*C*T*A*G*C*C*A*T*+G*+G*+T | 133 | 19 |
| 310 | AGCTGCCACTAGCCATGG | A57308H | +A*+G*+C*T*G*C*C*A*C*T*A*G*C*C*A*+T*+G*+G | 134 | 18 |
| 311 | CAGCTGCCACTAGCCATGG | A57309H | +C*+A*+G*C*T*G*C*C*A*C*T*A*G*C*C*A*+T*+G*+G | 134 | 19 |
| 312 | GACAGCTGCCACTAGCCAT | A57310H | +G*+A*+C*A*G*C*T*G*C*C*A*C*T*A*G*C*+C*+A*+T | 136 | 19 |
| 313 | CTGACAGCTGCCACTAGCC | A57311H | +C*+T*+G*A*C*A*G*C*T*G*C*C*A*C*T*A*+G*+C*+C | 138 | 19 |
| 314 | CCCTGACAGCTGCCACTAG | A57312H | +C*+C*+C*T*G*A*C*A*G*C*T*G*C*C*A*C*+T*+A*+G | 140 | 19 |
| 315 | ACCCCTGACAGCTGCCACT | A57313H | +A*+C*+C*C*C*T*G*A*C*A*G*C*T*G*C*C*+A*+C*+T | 142 | 19 |
| 316 | TCAGAGTTTCCTCGTCCTC | A57314H | +T*+C*+A*G*A*G*T*T*T*C*C*T*C*G*T*C*+C*+T*+C | 166 | 19 |
| 317 | TCAGAGTTTCCTCGTCCT | A57315H | +T*+C*+A*G*A*G*T*T*T*C*C*T*C*G*T*+C*+C*+T | 167 | 18 |
| 318 | TTCAGAGTTTCCTCGTCCT | A57316H | +T*+T*+C*A*G*A*G*T*T*T*C*C*T*C*G*T*+C*+C*+T | 167 | 19 |
| 319 | TCAGAGTTTCCTCGTCC | A57317H | +T*+C*+A*G*A*G*T*T*T*C*C*T*C*G*+T*+C*+C | 168 | 17 |
| 320 | TTCAGAGTTTCCTCGTCC | A57318H | +T*+T*+C*A*G*A*G*T*T*T*C*C*T*C*G*+T*+C*+C | 168 | 18 |
| 321 | CTTCAGAGTTTCCTCGTCC | A57319H | +C*+T*+T*C*A*G*A*G*T*T*T*C*C*T*C*G*+T*+C*+C | 168 | 19 |
| 322 | TCTTCAGAGTTTCCTCGTC | A57320H | +T*+C*+T*T*C*A*G*A*G*T*T*T*C*C*T*C*+G*+T*+C | 169 | 19 |
| 323 | TCTTCAGAGTTTCCTCGT | A57321H | +T*+C*+T*T*C*A*G*A*G*T*T*T*C*C*T*+C*+G*+T | 170 | 18 |
| 324 | TTCTTCAGAGTTTCCTCGT | A57322H | +T*+T*+C*T*T*C*A*G*A*G*T*T*T*C*C*T*+C*+G*+T | 170 | 19 |
| 325 | TTCTTCAGAGTTTCCTCG | A57323H | +T*+T*+C*T*T*C*A*G*A*G*T*T*T*C*C*+T*+C*+G | 171 | 18 |

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| 326 | CTTCTTCAGAGTTTC CTCG | A57324H | +C*+T*+T*C*T*T*C*A*G*A*G*T*T*T*C*C*+ T*+C*+G | 171 | 19 |
| 327 | GACTATCAACTTCTT CAGA | A57325H | +G*+A*+C*T*A*T*C*A*A*C*T*T*C*T*T*C*+ A*+G*+A | 180 | 19 |
| 328 | AGCCTGACTATCAAC TTCT | A57326H | +A*+G*+C*C*T*G*A*C*T*A*T*C*A*A*C*T*+ T*+C*+T | 185 | 19 |
| 329 | AGCCTGACTATCAAC TTC | A57327H | +A*+G*+C*C*T*G*A*C*T*A*T*C*A*A*C*+T* +T*+C | 186 | 18 |
| 330 | CAGCCTGACTATCAA CTTC | A57328H | +C*+A*+G*C*C*T*G*A*C*T*A*T*C*A*A*C*+ T*+T*+C | 186 | 19 |
| 331 | CAGCCTGACTATCAA CTT | A57329H | +C*+A*+G*C*C*T*G*A*C*T*A*T*C*A*A*+C* +T*+T | 187 | 18 |
| 332 | TCAGCCTGACTATCA ACTT | A57330H | +T*+C*+A*G*C*C*T*G*A*C*T*A*T*C*A*A*+ C*+T*+T | 187 | 19 |
| 333 | TCAGCCTGACTATCA ACT | A57331H | +T*+C*+A*G*C*C*T*G*A*C*T*A*T*C*A*+A* +C*+T | 188 | 18 |
| 334 | TTCAGCCTGACTATC AACT | A57332H | +T*+T*+C*A*G*C*C*T*G*A*C*T*A*T*C*A*+ A*+C*+T | 188 | 19 |
| 335 | TCAGCCTGACTATCA AC | A57333H | +T*+C*+A*G*C*C*T*G*A*C*T*A*T*C*+A*+A *+C | 189 | 17 |
| 336 | TTCAGCCTGACTATC AAC | A57334H | +T*+T*+C*A*G*C*C*T*G*A*C*T*A*T*C*+A* +A*+C | 189 | 18 |
| 337 | GTTCAGCCTGACTAT CAAC | A57335H | +G*+T*+T*C*A*G*C*C*T*G*A*C*T*A*T*C*+ A*+A*+C | 189 | 19 |
| 338 | GTTCAGCCTGACTAT CAA | A57336H | +G*+T*+T*C*A*G*C*C*T*G*A*C*T*A*T*+C* +A*+A | 190 | 18 |
| 339 | TGTTCAGCCTGACTA TCAA | A57337H | +T*+G*+T*T*C*A*G*C*C*T*G*A*C*T*A*T*+ C*+A*+A | 190 | 19 |
| 340 | TGTTCAGCCTGACTA TCA | A57338H | +T*+G*+T*T*C*A*G*C*C*T*G*A*C*T*A*+T* +C*+A | 191 | 18 |
| 341 | TTGTTCAGCCTGACT ATCA | A57339H | +T*+T*+G*T*T*C*A*G*C*C*T*G*A*C*T*A*+ T*+C*+A | 191 | 19 |
| 342 | CATTGTTCAGCCTGA CTAT | A57340H | +C*+A*+T*T*G*T*T*C*A*G*C*C*T*G*A*C*+ T*+A*+T | 193 | 19 |
| 343 | ACATTGTTCAGCCTG ACTA | A57341H | +A*+C*+A*T*T*G*T*T*C*A*G*C*C*T*G*A*+ C*+T*+A | 194 | 19 |
| 344 | GACATTGTTCAGCCT GACT | A57342H | +G*+A*+C*A*T*T*G*T*T*C*A*G*C*C*T*G*+ A*+C*+T | 195 | 19 |
| 345 | CCTGGACATTGTTCA GCCT | A57343H | +C*+C*+T*G*G*A*C*A*T*T*G*T*T*C*A*G*+ C*+C*+T | 199 | 19 |
| 346 | TCCTGGACATTGTTC AGCC | A57344H | +T*+C*+C*T*G*G*A*C*A*T*T*G*T*T*C*A*+ G*+C*+C | 200 | 19 |
| 347 | GACCAGCGTTTCTAT CTGT | A57345H | +G*+A*+C*C*A*G*C*G*T*T*T*C*T*A*T*C*+ T*+G*+T | 225 | 19 |
| 348 | GACCAGCGTTTCTAT CTG | A57346H | +G*+A*+C*C*A*G*C*G*T*T*T*C*T*A*T*+C* +T*+G | 226 | 18 |
| 349 | GGACCAGCGTTTCTA TCTG | A57347H | +G*+G*+A*C*C*A*G*C*G*T*T*T*C*T*A*T*+ C*+T*+G | 226 | 19 |
| 350 | TGGACCAGCGTTTCT ATCT | A57348H | +T*+G*+G*A*C*C*A*G*C*G*T*T*T*C*T*A*+ T*+C*+T | 227 | 19 |
| 351 | TGGACCAGCGTTTCT ATC | A57349H | +T*+G*+G*A*C*C*A*G*C*G*T*T*T*C*T*+A* +T*+C | 228 | 18 |
| 352 | TGGACCAGCGTTTCT AT | A57350H | +T*+G*+G*A*C*C*A*G*C*G*T*T*T*C*+T*+A *+T | 229 | 17 |
| 353 | TTTGGACCAGCGTTT CTAT | A57351H | +T*+T*+T*G*G*A*C*C*A*G*C*G*T*T*T*C*+ T*+A*+T | 229 | 19 |
| 354 | TTGGACCAGCGTTTC TA | A57352H | +T*+T*+G*G*A*C*C*A*G*C*G*T*T*T*+C*+T *+A | 230 | 17 |
| 355 | TTTGGACCAGCGTTT CTA | A57353H | +T*+T*+T*G*G*A*C*C*A*G*C*G*T*T*T*+C* +T*+A | 230 | 18 |
| 356 | ATTTGGACCAGCGTT TCTA | A57354H | +A*+T*+T*T*G*G*A*C*C*A*G*C*G*T*T*T*+ C*+T*+A | 230 | 19 |
| 357 | GATTTGGACCAGCGT TTCT | A57355H | +G*+A*+T*T*T*G*G*A*C*C*A*G*C*G*T*T*+ T*+C*+T | 231 | 19 |
| 358 | GATTTGGACCAGCGT TTC | A57356H | +G*+A*+T*T*T*G*G*A*C*C*A*G*C*G*T*+T* +T*+C | 232 | 18 |
| 359 | GGATTTGGACCAGCG TTTC | A57357H | +G*+G*+A*T*T*T*G*G*A*C*C*A*G*C*G*T*+ T*+T*+C | 232 | 19 |
| 360 | GATTTGGACCAGCGT TT | A57358H | +G*+A*+T*T*T*G*G*A*C*C*A*G*C*G*+T*+T *+T | 233 | 17 |

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| 361 | GGATTTGGACCAGCG TTT | A57359H | +G*+G*+A*T*T*T*G*G*A*C*C*A*G*C*G*+T* +T*+T | 233 | 18 |
| 362 | AGGATTTGGACCAGC GTTT | A57360H | +A*+G*+G*A*T*T*T*G*G*A*C*C*A*G*C*G*+ T*+T*+T | 233 | 19 |
| 363 | AGGATTTGGACCAGC GTT | A57361H | +A*+G*+G*A*T*T*T*G*G*A*C*C*A*G*C*+G* +T*+T | 234 | 18 |
| 364 | CAGGATTTGGACCAG CGTT | A57362H | +C*+A*+G*G*A*T*T*T*G*G*A*C*C*A*G*C*+ G*+T*+T | 234 | 19 |
| 365 | CCAGGATTTGGACCA GCGT | A57363H | +C*+C*+A*G*G*A*T*T*T*G*G*A*C*C*A*G*+ C*+G*+T | 235 | 19 |
| 366 | TCCTCCAGGATTTGG ACCA | A57364H | +T*+C*+C*T*C*C*A*G*G*A*T*T*T*G*G*A*+ C*+C*+A | 239 | 19 |
| 367 | TCCTCCAGGATTTGG ACC | A57365H | +T*+C*+C*T*C*C*A*G*G*A*T*T*T*G*G*+A* +C*+C | 240 | 18 |
| 368 | ATCCTCCAGGATTTG GACC | A57366H | +A*+T*+C*C*T*C*C*A*G*G*A*T*T*T*G*G*+ A*+C*+C | 240 | 19 |
| 369 | ATCCTCCAGGATTTG GAC | A57367H | +A*+T*+C*C*T*C*C*A*G*G*A*T*T*T*G*+G* +A*+C | 241 | 18 |
| 370 | GATCCTCCAGGATTT GGAC | A57368H | +G*+A*+T*C*C*T*C*C*A*G*G*A*T*T*T*G*+ G*+A*+C | 241 | 19 |
| 371 | ACCAGCAGATCCTCC AGGA | A57369H | +A*+C*+C*A*G*C*A*G*A*T*C*C*T*C*C*A*+ G*+G*+A | 248 | 19 |
| 372 | AACACCAGCAGATCC TCCA | A57370H | +A*+A*+C*A*C*C*A*G*C*A*G*A*T*C*C*T*+ C*+C*+A | 251 | 19 |
| 373 | TGAACACCAGCAGAT CCTC | A57371H | +T*+G*+A*A*C*A*C*C*A*G*C*A*G*A*T*C*+ C*+T*+C | 253 | 19 |
| 374 | GTGAACACCAGCAGA TCCT | A57372H | +G*+T*+G*A*A*C*A*C*C*A*G*C*A*G*A*T*+ C*+C*+T | 254 | 19 |
| 375 | ACGTGAACACCAGCA GATC | A57373H | +A*+C*+G*T*G*A*A*C*A*C*C*A*G*C*A*G*+ A*+T*+C | 256 | 19 |
| 376 | TACGTGAACACCAGC AGAT | A57374H | +T*+A*+C*G*T*G*A*A*C*A*C*C*A*G*C*A*+ G*+A*+T | 257 | 19 |
| 377 | GTACGTGAACACCAG CAGA | A57375H | +G*+T*+A*C*G*T*G*A*A*C*A*C*C*A*G*C*+ A*+G*+A | 258 | 19 |
| 378 | AGTACGTGAACACCA GCAG | A57376H | +A*+G*+T*A*C*G*T*G*A*A*C*A*C*C*A*G*+ C*+A*+G | 259 | 19 |
| 379 | GAGTACGTGAACACC AGCA | A57377H | +G*+A*+G*T*A*C*G*T*G*A*A*C*A*C*C*A*+ G*+C*+A | 260 | 19 |
| 380 | GGAGTACGTGAACAC CAGC | A57378H | +G*+G*+A*G*T*A*C*G*T*G*A*A*C*A*C*C*+ A*+G*+C | 261 | 19 |
| 381 | CGGAGTACGTGAACA CCAG | A57379H | +C*+G*+G*A*G*T*A*C*G*T*G*A*A*C*A*C*+ C*+A*+G | 262 | 19 |
| 382 | CGGAGTACGTGAACA CCA | A57380H | +C*+G*+G*A*G*T*A*C*G*T*G*A*A*C*A*+C* +C*+A | 263 | 18 |
| 383 | TCGGAGTACGTGAAC ACCA | A57381H | +T*+C*+G*G*A*G*T*A*C*G*T*G*A*A*C*A*+ C*+C*+A | 263 | 19 |
| 384 | CGGAGTACGTGAACA CC | A57382H | +C*+G*+G*A*G*T*A*C*G*T*G*A*A*C*+A*+ C*+C | 264 | 17 |
| 385 | TCGGAGTACGTGAAC ACC | A57383H | +T*+C*+G*G*A*G*T*A*C*G*T*G*A*A*C*+A* +C*+C | 264 | 18 |
| 386 | CTCGGAGTACGTGAA CACC | A57384H | +C*+T*+C*G*G*A*G*T*A*C*G*T*G*A*A*C*+ A*+C*+C | 264 | 19 |
| 387 | TCGGAGTACGTGAAC AC | A57385H | +T*+C*+G*G*A*G*T*A*C*G*T*G*A*A*+C*+ A*+C | 265 | 17 |
| 388 | CTCGGAGTACGTGAA CAC | A57386H | +C*+T*+C*G*G*A*G*T*A*C*G*T*G*A*A*+C* +A*+C | 265 | 18 |
| 389 | GCTCGGAGTACGTGA ACAC | A57387H | +G*+C*+T*C*G*G*A*G*T*A*C*G*T*G*A*A*+ C*+A*+C | 265 | 19 |
| 390 | TCGGAGTACGTGAAC A | A57388H | +T*+C*+G*G*A*G*T*A*C*G*T*G*A*+A*+C*+ A | 266 | 16 |
| 391 | CTCGGAGTACGTGAA CA | A57389H | +C*+T*+C*G*G*A*G*T*A*C*G*T*G*A*+A*+ C*+A | 266 | 17 |
| 392 | GCTCGGAGTACGTGA ACA | A57390H | +G*+C*+T*C*G*G*A*G*T*A*C*G*T*G*A*+A* +C*+A | 266 | 18 |
| 393 | GCTCGGAGTACGTGA AC | A57391H | +G*+C*+T*C*G*G*A*G*T*A*C*G*T*G*+A*+ A*+C | 267 | 17 |
| 394 | AAAGGTGAAGACCTT CCTG | A57392Hi | +A*+A*+A*G*G*T*G*A*A*G*A*C*C*T*T*C*+ C*+T*+G | 451 | 19 |
| 395 | GTCACAATCCACAGC ACC | A57393Hi | +G*+T*+C*A*C*A*A*T*C*C*A*C*A*G*C*+A* +C*+C | 508 | 18 |

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| 396 | AGAAGCAAAGTCACAATCC | A57394Hi | +A*+G*+A*A*G*C*A*A*A*G*T*C*A*C*A*A*+T*+C*+C | 516 | 19 |
| 397 | GCCTTGAAATAACTTGGAG | A57395H | +G*+C*+C*T*T*G*A*A*A*T*A*A*C*T*T*G*+G*+A*+G | 560 | 19 |
| 398 | TTGCCTTGAAATAACTTGG | A57396H | +T*+T*+G*C*C*T*T*G*A*A*A*T*A*A*C*T*+T*+G*+G | 562 | 19 |
| 399 | GCACATGGATATTTTTGCC | A57397H | +G*+C*+A*C*A*T*G*G*A*T*A*T*T*T*T*T*+G*+C*+C | 576 | 19 |
| 400 | GGCACATGGATATTTTTGC | A57398H | +G*+G*+C*A*C*A*T*G*G*A*T*A*T*T*T*T*+T*+G*+C | 577 | 19 |
| 401 | GATCAACAGAGGCACATGG | A57399H | +G*+A*+T*C*A*A*C*A*G*A*G*G*C*A*C*A*+T*+G*+G | 587 | 19 |
| 402 | GATCAACAGAGGCACATG | A57400H | +G*+A*+T*C*A*A*C*A*G*A*G*G*C*A*C*+A*+T*+G | 588 | 18 |
| 403 | CGATCAACAGAGGCACATG | A57401H | +C*+G*+A*T*C*A*A*C*A*G*A*G*G*C*A*C*+A*+T*+G | 588 | 19 |
| 404 | CGATCAACAGAGGCACAT | A57402H | +C*+G*+A*T*C*A*A*C*A*G*A*G*G*C*A*+C*+A*+T | 589 | 18 |
| 405 | ACGATCAACAGAGGCACAT | A57403H | +A*+C*+G*A*T*C*A*A*C*A*G*A*G*G*C*A*+C*+A*+T | 589 | 19 |
| 406 | GACGATCAACAGAGGCACA | A57404H | +G*+A*+C*G*A*T*C*A*A*C*A*G*A*G*G*C*+A*+C*+A | 590 | 19 |
| 407 | GACGATCAACAGAGGCAC | A57405H | +G*+A*+C*G*A*T*C*A*A*C*A*G*A*G*G*+C*+A*+C | 591 | 18 |
| 408 | AGACGATCAACAGAGGCAC | A57406H | +A*+G*+A*C*G*A*T*C*A*A*C*A*G*A*G*G*+C*+A*+C | 591 | 19 |
| 409 | AGACGATCAACAGAGGCA | A57407H | +A*+G*+A*C*G*A*T*C*A*A*C*A*G*A*G*+G*+C*+A | 592 | 18 |
| 410 | AAGACGATCAACAGAGGCA | A57408H | +A*+A*+G*A*C*G*A*T*C*A*A*C*A*G*A*G*+G*+C*+A | 592 | 19 |
| 411 | CAAGACGATCAACAGAGGC | A57409H | +C*+A*+A*G*A*C*G*A*T*C*A*A*C*A*G*A*+G*+G*+C | 593 | 19 |
| 412 | CAAGACGATCAACAGAGG | A57410H | +C*+A*+A*G*A*C*G*A*T*C*A*A*C*A*G*+A*+G*+G | 594 | 18 |
| 413 | CCAAGACGATCAACAGAGG | A57411H | +C*+C*+A*A*G*A*C*G*A*T*C*A*A*C*A*G*+A*+G*+G | 594 | 19 |
| 414 | CCAAGACGATCAACAGAG | A57412H | +C*+C*+A*A*G*A*C*G*A*T*C*A*A*C*A*+G*+A*+G | 595 | 18 |
| 415 | TCCAAGACGATCAACAGAG | A57413H | +T*+C*+C*A*A*G*A*C*G*A*T*C*A*A*C*A*+G*+A*+G | 595 | 19 |
| 416 | GTCCAAGACGATCAACAGA | A57414H | +G*+T*+C*C*A*A*G*A*C*G*A*T*C*A*A*C*+A*+G*+A | 596 | 19 |
| 417 | GTCCAAGACGATCAACAG | A57415H | +G*+T*+C*C*A*A*G*A*C*G*A*T*C*A*A*+C*+A*+G | 597 | 18 |
| 418 | AGTCCAAGACGATCAACAG | A57416H | +A*+G*+T*C*C*A*A*G*A*C*G*A*T*C*A*A*+C*+A*+G | 597 | 19 |
| 419 | GTCCAAGACGATCAACA | A57417H | +G*+T*+C*C*A*A*G*A*C*G*A*T*C*A*+A*+C*+A | 598 | 17 |
| 420 | AGTCCAAGACGATCAACA | A57418H | +A*+G*+T*C*C*A*A*G*A*C*G*A*T*C*A*+A*+C*+A | 598 | 18 |
| 421 | GAGTCCAAGACGATCAACA | A57419H | +G*+A*+G*T*C*C*A*A*G*A*C*G*A*T*C*A*+A*+C*+A | 598 | 19 |
| 422 | GAGTCCAAGACGATCAAC | A57420H | +G*+A*+G*T*C*C*A*A*G*A*C*G*A*T*C*+A*+A*+C | 599 | 18 |
| 423 | TCGCGACTCTCATATA | A57421H | +T*+C*+G*C*G*A*C*T*C*T*C*A*T*+A*+T*+A | 618 | 16 |
| 424 | CTCGCGACTCTCATATA | A57422H | +C*+T*+C*G*C*G*A*C*T*C*T*C*A*T*+A*+T*+A | 618 | 17 |
| 425 | ACTCGCGACTCTCATATA | A57423H | +A*+C*+T*C*G*C*G*A*C*T*C*T*C*A*T*+A*+T*+A | 618 | 18 |
| 426 | CACTCGCGACTCTCATATA | A57424H | +C*+A*+C*T*C*G*C*G*A*C*T*C*T*C*A*T*+A*+T*+A | 618 | 19 |
| 427 | ACTCGCGACTCTCATAT | A57425H | +A*+C*+T*C*G*C*G*A*C*T*C*T*C*A*+T*+A*+T | 619 | 17 |
| 428 | CACTCGCGACTCTCATAT | A57426H | +C*+A*+C*T*C*G*C*G*A*C*T*C*T*C*A*+T*+A*+T | 619 | 18 |
| 429 | ACACTCGCGACTCTCATAT | A57427H | +A*+C*+A*C*T*C*G*C*G*A*C*T*C*T*C*A*+T*+A*+T | 619 | 19 |
| 430 | ACACTCGCGACTCTCATA | A57428H | +A*+C*+A*C*T*C*G*C*G*A*C*T*C*T*C*+A*+T*+A | 620 | 18 |

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| 431 | CACACTCGCGACTCT CATA | A57429H | +C*+A*+C*A*C*T*C*G*C*G*A*C*T*C*T*C*+ A*+T*+A | 620 | 19 |
| 432 | ACACTCGCGACTCTC AT | A57430H | +A*+C*+A*C*T*C*G*C*G*A*C*T*C*T*+C*+A *+T | 621 | 17 |
| 433 | CACACTCGCGACTCT CAT | A57431H | +C*+A*+C*A*C*T*C*G*C*G*A*C*T*C*T*+C* +A*+T | 621 | 18 |
| 434 | GCACACTCGCGACTC TCAT | A57432H | +G*+C*+A*C*A*C*T*C*G*C*G*A*C*T*C*T*+ C*+A*+T | 621 | 19 |
| 435 | CACACTCGCGACTCT CA | A57433H | +C*+A*+C*A*C*T*C*G*C*G*A*C*T*C*+T*+C *+A | 622 | 17 |
| 436 | GCACACTCGCGACTC TCA | A57434H | +G*+C*+A*C*A*C*T*C*G*C*G*A*C*T*C*+T* +C*+A | 622 | 18 |
| 437 | TGCACACTCGCGACT CTCA | A57435H | +T*+G*+C*A*C*A*C*T*C*G*C*G*A*C*T*C*+ T*+C*+A | 622 | 19 |
| 438 | TGCACACTCGCGACT CTC | A57436H | +T*+G*+C*A*C*A*C*T*C*G*C*G*A*C*T*+C* +T*+C | 623 | 18 |
| 439 | CTGCACACTCGCGAC TCTC | A57437H | +C*+T*+G*C*A*C*A*C*T*C*G*C*G*A*C*T*+ C*+T*+C | 623 | 19 |
| 440 | TGCACACTCGCGACT CT | A57438H | +T*+G*+C*A*C*A*C*T*C*G*C*G*A*C*+T*+C *+T | 624 | 17 |
| 441 | CTGCACACTCGCGAC TCT | A57439H | +C*+T*+G*C*A*C*A*C*T*C*G*C*G*A*C*+T* +C*+T | 624 | 18 |
| 442 | GCTGCACACTCGCGA CTCT | A57440H | +G*+C*+T*G*C*A*C*A*C*T*C*G*C*G*A*C*+ T*+C*+T | 624 | 19 |
| 443 | CTGCACACTCGCGAC TC | A57441H | +C*+T*+G*C*A*C*A*C*T*C*G*C*G*A*+C*+T *+C | 625 | 17 |
| 444 | GCTGCACACTCGCGA CTC | A57442H | +G*+C*+T*G*C*A*C*A*C*T*C*G*C*G*A*+C* +T*+C | 625 | 18 |
| 445 | TGCTGCACACTCGCG ACTC | A57443H | +T*+G*+C*T*G*C*A*C*A*C*T*C*G*C*G*A*+ C*+T*+C | 625 | 19 |
| 446 | GCTGCACACTCGCGA CT | A57444H | +G*+C*+T*G*C*A*C*A*C*T*C*G*C*G*+A*+ C*+T | 626 | 17 |
| 447 | TGCTGCACACTCGCG ACT | A57445H | +T*+G*+C*T*G*C*A*C*A*C*T*C*G*C*G*+A* +C*+T | 626 | 18 |
| 448 | CTGCTGCACACTCGC GACT | A57446H | +C*+T*+G*C*T*G*C*A*C*A*C*T*C*G*C*G*+ A*+C*+T | 626 | 19 |
| 449 | TGCTGCACACTCGCG AC | A57447H | +T*+G*+C*T*G*C*A*C*A*C*T*C*G*C*+G*+A *+C | 627 | 17 |
| 450 | CTGCTGCACACTCGC GAC | A57448H | +C*+T*+G*C*T*G*C*A*C*A*C*T*C*G*C*+G* +A*+C | 627 | 18 |
| 451 | CTGCTGCACACTCGC GA | A57449H | +C*+T*+G*C*T*G*C*A*C*A*C*T*C*G*+C*+G *+A | 628 | 17 |
| 452 | AAACGTCTCCTTCCA AACA | A57450Hi | +A*+A*+A*C*G*T*C*T*C*C*T*T*C*C*A*A*+ A*+C*+A | 683 | 19 |
| 453 | AGGTTCCTCAAGCCA AATT | A57451Hi | +A*+G*+G*T*T*C*C*T*C*A*A*G*C*C*A*A*+ A*+T*+T | 746 | 19 |
| 454 | AGGTTCCTCAAGCCA AAT | A57452Hi | +A*+G*+G*T*T*C*C*T*C*A*A*G*C*C*A*+A* +A*+T | 747 | 18 |
| 455 | GAGGTTCCTCAAGCC AAAT | A57453Hi | +G*+A*+G*G*T*T*C*C*T*C*A*A*G*C*C*A*+ A*+A*+T | 747 | 19 |
| 456 | GAACTCTACAAGAGT TTGC | A57454Hi | +G*+A*+A*C*T*C*T*A*C*A*A*G*A*G*T*T*+ T*+G*+C | 1074 | 19 |
| 457 | AACTCTACAAGAGTT TGC | A57455Hi | +A*+A*+C*T*C*T*A*C*A*A*G*A*G*T*T*+T* +G*+C | 1074 | 18 |
| 458 | TGCTGAACTCTACAA GAGT | A57456Hi | +T*+G*+C*T*G*A*A*C*T*C*T*A*C*A*A*G*+ A*+G*+T | 1078 | 19 |
| 459 | TCATTCTTAATTACCA TTT | A57457Hi | +T*+C*+A*T*T*C*T*T*A*A*T*T*A*C*C*A*+ T*+T*+T | 1298 | 19 |
| 460 | GTAAATCATTCTTAAT TAC | A57458Hi | +G*+T*+A*A*A*T*C*A*T*T*C*T*T*A*A*T*+ T*+A*+C | 1303 | 19 |
| 461 | GACTGTAAATCATTC TTAA | A57459Hi | +G*+A*+C*T*G*T*A*A*A*T*C*A*T*T*C*T*+ T*+A*+A | 1307 | 19 |
| 462 | GTTAACATGCAGATG ACAA | A57460Hi | +G*+T*+T*A*A*C*A*T*G*C*A*G*A*T*G*A*+ C*+A*+A | 1397 | 19 |
| 463 | AGTTAACATGCAGAT GACA | A57461Hi | +A*+G*+T*T*A*A*C*A*T*G*C*A*G*A*T*G*+ A*+C*+A | 1398 | 19 |
| 464 | GAGTTAACATGCAGA TGAC | A57462Hi | +G*+A*+G*T*T*A*A*C*A*T*G*C*A*G*A*T*+ G*+A*+C | 1399 | 19 |
| 465 | AGTTAACATGCAGAT GAC | A57463Hi | +A*+G*+T*T*A*A*C*A*T*G*C*A*G*A*T*+G* +A*+C | 1399 | 18 |

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| 466 | TGCATGAGTTAACATGCAG | A57464Hi | +T*+G*+C*A*T*G*A*G*T*T*A*A*C*A*T*G*+C*+A*+G | 1404 | 19 |
| 467 | GCTTTCTGACTGCACCTCC | A57465Hi | +G*+C*+T*T*T*C*T*G*A*C*T*G*C*A*C*C*+T*+C*+C | 1452 | 19 |
| 468 | GCTTTCTGACTGCACCTC | A57466Hi | +G*+C*+T*T*T*C*T*G*A*C*T*G*C*A*C*+C*+T*+C | 1453 | 18 |
| 469 | TGGCTTTCTGACTGCACCT | A57467Hi | +T*+G*+G*C*T*T*T*C*T*G*A*C*T*G*C*A*+C*+C*+T | 1454 | 19 |
| 470 | TGGCTTTCTGACTGCACC | A57468Hi | +T*+G*+G*C*T*T*T*C*T*G*A*C*T*G*C*+A*+C*+C | 1455 | 18 |
| 471 | TTGGCTTTCTGACTGCACC | A57469Hi | +T*+T*+G*G*C*T*T*T*C*T*G*A*C*T*G*C*+A*+C*+C | 1455 | 19 |
| 472 | ATTGGCTTTCTGACTGCAC | A57470Hi | +A*+T*+T*G*G*C*T*T*T*C*T*G*A*C*T*G*+C*+A*+C | 1456 | 19 |
| 473 | TTAAGAAACATTGGCTTTC | A57471Hi | +T*+T*+A*A*G*A*A*A*C*A*T*T*G*G*C*T*+T*+T*+C | 1465 | 19 |
| 474 | ATTAAGAAACATTGGCTTT | A57472Hi | +A*+T*+T*A*A*G*A*A*A*C*A*T*T*G*G*C*+T*+T*+T | 1466 | 19 |
| 475 | CTTTATTATGCCTCCATCT | A57473Hi | +C*+T*+T*T*A*T*T*A*T*G*C*C*T*C*C*A*+T*+C*+T | 1719 | 19 |
| 476 | GCATCTTTATTATGCCTCC | A57474Hi | +G*+C*+A*T*C*T*T*T*A*T*T*A*T*G*C*C*+T*+C*+C | 1723 | 19 |
| 477 | ACAGCATCTTTATTATGCC | A57475Hi | +A*+C*+A*G*C*A*T*C*T*T*T*A*T*T*A*T*+G*+C*+C | 1726 | 19 |
| 478 | TCCGACTTTGAGTCTTAAA | A57476Hi | +T*+C*+C*G*A*C*T*T*T*G*A*G*T*C*T*T*+A*+A*+A | 1748 | 19 |
| 479 | TTCCGACTTTGAGTCTTAA | A57477Hi | +T*+T*+C*C*G*A*C*T*T*T*G*A*G*T*C*T*+T*+A*+A | 1749 | 19 |
| 480 | AAATTCCGACTTTGAGTC | A57478Hi | +A*+A*+A*T*T*C*C*G*A*C*T*T*T*G*A*+G*+T*+C | 1753 | 18 |
| 481 | AAATTCCGACTTTGAGT | A57479Hi | +A*+A*+A*T*T*C*C*G*A*C*T*T*T*G*+A*+G*+T | 1754 | 17 |
| 482 | CAGGAAGCACAATAGGCCA | A57480Hi | +C*+A*+G*G*A*A*G*C*A*C*A*A*T*A*G*G*+C*+C*+A | 1803 | 19 |
| 483 | GAGCAGGAAGCACAATAGG | A57481Hi | +G*+A*+G*C*A*G*G*A*A*G*C*A*C*A*A*T*+A*+G*+G | 1806 | 19 |
| 484 | AGAGCAGGAAGCACAATAG | A57482Hi | +A*+G*+A*G*C*A*G*G*A*A*G*C*A*C*A*A*+T*+A*+G | 1807 | 19 |
| 485 | CAGAGCAGGAAGCACAATA | A57483Hi | +C*+A*+G*A*G*C*A*G*G*A*A*G*C*A*C*A*+A*+T*+A | 1808 | 19 |
| 486 | GGTGCAGAGCAGGAAGCAC | A57484Hi | +G*+G*+T*G*C*A*G*A*G*C*A*G*G*A*A*G*+C*+A*+C | 1812 | 19 |
| 487 | GACAAGTATGCTCAGGCT | A57485Hi | +G*+A*+C*A*A*G*T*A*T*G*C*T*C*A*G*+G*+C*+T | 2065 | 18 |
| 488 | CAAGCTCTTTGATCCTCAG | A57486Hi | +C*+A*+A*G*C*T*C*T*T*T*G*A*T*C*C*T*+C*+A*+G | 3912 | 19 |
| 489 | TGTCACAAGCTCTTTGATC | A57487Hi | +T*+G*+T*C*A*C*A*A*G*C*T*C*T*T*T*G*+A*+T*+C | 3917 | 19 |
| 490 | TGTCACAAGCTCTTTGAT | A57488Hi | +T*+G*+T*C*A*C*A*A*G*C*T*C*T*T*T*+G*+A*+T | 3918 | 18 |
| 491 | GTATGATGGAAAGAGATTT | A57489Hi | +G*+T*+A*T*G*A*T*G*G*A*A*A*G*A*G*A*+T*+T*+T | 3967 | 19 |
| 492 | TAGATTGTATGATGGAAAG | A57490Hi | +T*+A*+G*A*T*T*G*T*A*T*G*A*T*G*G*A*+A*+A*+G | 3973 | 19 |
| 493 | TAGTAGATTGTATGATGG | A57491Hi | +T*+A*+G*T*A*G*A*T*T*G*T*A*T*G*A*+T*+G*+G | 3977 | 18 |
| 494 | CTAGTAGATTGTATGATG | A57492Hi | +C*+T*+A*G*T*A*G*A*T*T*G*T*A*T*G*+A*+T*+G | 3978 | 18 |
| 495 | AGCTAGTAGATTGTATGA | A57493Hi | +A*+G*+C*T*A*G*T*A*G*A*T*T*G*T*A*+T*+G*+A | 3980 | 18 |
| 496 | CAGCTAGTAGATTGTATGA | A57494Hi | +C*+A*+G*C*T*A*G*T*A*G*A*T*T*G*T*A*+T*+G*+A | 3980 | 19 |
| 497 | GCAGCTAGTAGATTGTAT | A57495Hi | +G*+C*+A*G*C*T*A*G*T*A*G*A*T*T*G*+T*+A*+T | 3982 | 18 |
| 498 | AGCAGCTAGTAGATTGTA | A57496Hi | +A*+G*+C*A*G*C*T*A*G*T*A*G*A*T*T*+G*+T*+A | 3983 | 18 |
| 499 | ATTGATGTCATTGTACCT | A57497Hi | +A*+T*+T*G*A*T*G*T*C*A*T*T*G*T*A*+C*+C*+T | 4070 | 18 |
| 500 | CTTACAGTAATTATACTAA | A57498Hi | +C*+T*+T*A*C*A*G*T*A*A*T*T*A*T*A*C*+T*+A*+A | 4193 | 19 |

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| 501 | AAAGGATACTTACAG TAAT | A57499Hi | +A*+A*+A*G*G*A*T*A*C*T*T*A*C*A*G*T*+ A*+A*+T | 4201 | 19 |
| 502 | TAGAAACAAACCTTA ATCT | A57500Hi | +T*+A*+G*A*A*A*C*A*A*A*C*C*T*T*A*A*+ T*+C*+T | 4346 | 19 |
| 503 | AATGGCATCTAGAAA CAAA | A57501Hi | +A*+A*+T*G*G*C*A*T*C*T*A*G*A*A*A*C*+ A*+A*+A | 4355 | 19 |
| 504 | TTAAATGGCATCTAG AAAC | A57502Hi | +T*+T*+A*A*A*T*G*G*C*A*T*C*T*A*G*A*+ A*+A*+C | 4358 | 19 |
| 505 | ATATCATGTTAAATG GCAT | A57503Hi | +A*+T*+A*T*C*A*T*G*T*T*A*A*A*T*G*G*+ C*+A*+T | 4366 | 19 |
| 506 | GAATATCATGTTAAA TGGC | A57504Hi | +G*+A*+A*T*A*T*C*A*T*G*T*T*A*A*A*T*+ G*+G*+C | 4368 | 19 |
| 507 | CTAAAGACTGTCATT TATG | A57505Hi | +C*+T*+A*A*A*G*A*C*T*G*T*C*A*T*T*T*+ A*+T*+G | 4440 | 19 |
| 508 | AAATTTAGGAGCACA GTGA | A57506Hi | +A*+A*+A*T*T*T*A*G*G*A*G*C*A*C*A*G*+ T*+G*+A | 4512 | 19 |
| 509 | AACTCAAGCATGTAA TTAA | A57507Hi | +A*+A*+C*T*C*A*A*G*C*A*T*G*T*A*A*T*+ T*+A*+A | 4636 | 19 |
| 510 | CAATACAATTAAATT GGTA | A57508Hi | +C*+A*+A*T*A*C*A*A*T*T*A*A*A*T*T*G*+ G*+T*+A | 4682 | 19 |
| 511 | ACAATACAATTAAAT TGGT | A57509Hi | +A*+C*+A*A*T*A*C*A*A*T*T*A*A*A*T*T*+ G*+G*+T | 4683 | 19 |
| 512 | TACAATACAATTAAA TTGG | A57510Hi | +T*+A*+C*A*A*T*A*C*A*A*T*T*A*A*A*T*+ T*+G*+G | 4684 | 19 |
| 513 | TAACAATTGATCCAT TAAT | A57511Hi | +T*+A*+A*C*A*A*T*T*G*A*T*C*C*A*T*T*+ A*+A*+T | 4757 | 19 |
| 514 | AGCAAAGCAGAGGTA ACAA | A57512Hi | +A*+G*+C*A*A*A*G*C*A*G*A*G*G*T*A*A* +C*+A*+A | 4770 | 19 |
| 515 | TACATGGAACTTCTG TGAT | A57513Hi | +T*+A*+C*A*T*G*G*A*A*C*T*T*C*T*G*T*+ G*+A*+T | 4806 | 19 |
| 516 | AGGCAACTGAGCTCT CCAG | A57514Hi | +A*+G*+G*C*A*A*C*T*G*A*G*C*T*C*T*C*+ C*+A*+G | 4828 | 19 |
| 517 | CATAGGATGCCAAAC TCAT | A57515Hi | +C*+A*+T*A*G*G*A*T*G*C*C*A*A*A*C*T*+ C*+A*+T | 4937 | 19 |
| 518 | TCACATAGGATGCCA AAC | A57516Hi | +T*+C*+A*C*A*T*A*G*G*A*T*G*C*C*A*+A* +A*+C | 4941 | 18 |
| 519 | TCTGAACAGCTTCTG GTGG | A57517Hi | +T*+C*+T*G*A*A*C*A*G*C*T*T*C*T*G*G*+ T*+G*+G | 4989 | 19 |
| 520 | TTCTGAACAGCTTCT GGTG | A57518Hi | +T*+T*+C*T*G*A*A*C*A*G*C*T*T*C*T*G*+ G*+T*+G | 4990 | 19 |
| 521 | ATTCTGAACAGCTTC TGGT | A57519Hi | +A*+T*+T*C*T*G*A*A*C*A*G*C*T*T*C*T*+ G*+G*+T | 4991 | 19 |
| 522 | AACATTCTGAACAGC TTCT | A57520Hi | +A*+A*+C*A*T*T*C*T*G*A*A*C*A*G*C*T*+ T*+C*+T | 4994 | 19 |
| 523 | AATCCAGCTGTCATA GAAA | A57521Hi | +A*+A*+T*C*C*A*G*C*T*G*T*C*A*T*A*G*+ A*+A*+A | 5075 | 19 |
| 524 | ACAATCCAGCTGTCA TAGA | A57522Hi | +A*+C*+A*A*T*C*C*A*G*C*T*G*T*C*A*T*+ A*+G*+A | 5077 | 19 |
| 525 | ACAATCCAGCTGTCA TAG | A57523Hi | +A*+C*+A*A*T*C*C*A*G*C*T*G*T*C*A*+T* +A*+G | 5078 | 18 |
| 526 | CCACGTAAGCTGAAC AG | A57524Hi | +C*+C*+A*C*G*T*A*A*G*C*T*G*A*A*+C*+A *+G | 5102 | 17 |
| 527 | CCTCCACGTAAGCTG AA | A57525Hi | +C*+C*+T*C*C*A*C*G*T*A*A*G*C*T*+G*+A *+A | 5105 | 17 |
| 528 | CTCCTCCACGTAAGC TGAA | A57526Hi | +C*+T*+C*C*T*C*C*A*C*G*T*A*A*G*C*T*+ G*+A*+A | 5105 | 19 |
| 529 | TCCTCCACGTAAGCT GAA | A57527Hi | +T*+C*+C*T*C*C*A*C*G*T*A*A*G*C*T*+G* +A*+A | 5105 | 18 |
| 530 | CTCCTCCACGTAAGC TGA | A57528Hi | +C*+T*+C*C*T*C*C*A*C*G*T*A*A*G*C*+T* +G*+A | 5106 | 18 |
| 531 | CCTCCTCCACGTAAG CTG | A57529Hi | +C*+C*+T*C*C*T*C*C*A*C*G*T*A*A*G*+C* +T*+G | 5107 | 18 |
| 532 | CTCCTCCACGTAAGC TG | A57530Hi | +C*+T*+C*C*T*C*C*A*C*G*T*A*A*G*+C*+T *+G | 5107 | 17 |
| 533 | TCCTCCTCCACGTAA GCTG | A57531Hi | +T*+C*+C*T*C*C*T*C*C*A*C*G*T*A*A*G*+ C*+T*+G | 5107 | 19 |
| 534 | GACATCCTCCTCCAC GTAA | A57532Hi | +G*+A*+C*A*T*C*C*T*C*C*T*C*C*A*C*G*+ T*+A*+A | 5111 | 19 |
| 535 | TAGGACATCCTCCTC CACG | A57533Hi | +T*+A*+G*G*A*C*A*T*C*C*T*C*C*T*C*C*+ A*+C*+G | 5114 | 19 |

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| 536 | TAGGACATCCTCCTC CAC | A57534Hi | +T*+A*+G*G*A*C*A*T*C*C*T*C*C*T*C*+C* +A*+C | 5115 | 18 |
| 537 | GTAGGACATCCTCCT CCAC | A57535Hi | +G*+T*+A*G*G*A*C*A*T*C*C*T*C*C*T*C*+ C*+A*+C | 5115 | 19 |
| 538 | AGTAGGACATCCTCC TCCA | A57536Hi | +A*+G*+T*A*G*G*A*C*A*T*C*C*T*C*C*T*+ C*+C*+A | 5116 | 19 |
| 539 | AAGTAGGACATCCTC CTCC | A57537Hi | +A*+A*+G*T*A*G*G*A*C*A*T*C*C*T*C*C*+ T*+C*+C | 5117 | 19 |
| 540 | ATAATGGCACAAGTT TCTT | A57538Hi | +A*+T*+A*A*T*G*G*C*A*C*A*A*G*T*T*T*+ C*+T*+T | 5331 | 19 |
| 541 | CCAATAAGGAATAAT GGCA | A57539Hi | +C*+C*+A*A*T*A*A*G*G*A*A*T*A*A*T*G*+ G*+C*+A | 5341 | 19 |
| 542 | GAGTTGAATGACAAG GTGA | A57540Hi | +G*+A*+G*T*T*G*A*A*T*G*A*C*A*A*G*G*+ T*+G*+A | 5375 | 19 |
| 543 | GCAAGGAGTTGAATG ACAA | A57541Hi | +G*+C*+A*A*G*G*A*G*T*T*G*A*A*T*G*A*+ C*+A*+A | 5380 | 19 |
| 544 | GATGCATAAGTAAAG TTGA | A57542Hi | +G*+A*+T*G*C*A*T*A*A*G*T*A*A*A*G*T*+ T*+G*+A | 5404 | 19 |
| 545 | GGATGCATAAGTAAA GTTG | A57543Hi | +G*+G*+A*T*G*C*A*T*A*A*G*T*A*A*A*G*+ T*+T*+G | 5405 | 19 |
| 546 | GATAAGGCTGGATGC ATAA | A57544Hi | +G*+A*+T*A*A*G*G*C*T*G*G*A*T*G*C*A*+ T*+A*+A | 5414 | 19 |
| 547 | GAGAGTAGGCTGCTA CAT | A57545Hi | +G*+A*+G*A*G*T*A*G*G*C*T*G*C*T*A*+C* +A*+T | 5469 | 18 |
| 548 | GAGGAGAGTAGGCTG CTAC | A57546Hi | +G*+A*+G*G*A*G*A*G*T*A*G*G*C*T*G*C* +T*+A*+C | 5471 | 19 |
| 549 | TGAGGAGAGTAGGCT GCTA | A57547Hi | +T*+G*+A*G*G*A*G*A*G*T*A*G*G*C*T*G* +C*+T*+A | 5472 | 19 |
| 550 | GTGAGGAGAGTAGGC TGCT | A57548Hi | +G*+T*+G*A*G*G*A*G*A*G*T*A*G*G*C*T* +G*+C*+T | 5473 | 19 |
| 551 | GTTGAAATTACTCAG AGAA | A57549Hi | +G*+T*+T*G*A*A*A*T*T*A*C*T*C*A*G*A*+ G*+A*+A | 5547 | 19 |
| 552 | TGTGAGTTGAAATTA CTCA | A57550Hi | +T*+G*+T*G*A*G*T*T*G*A*A*A*T*T*A*C*+ T*+C*+A | 5552 | 19 |
| 553 | AGTGTGAGTTGAAAT TACT | A57551Hi | +A*+G*+T*G*T*G*A*G*T*T*G*A*A*A*T*T*+ A*+C*+T | 5554 | 19 |
| 554 | TAGAAATACTGAAAG TAAG | A57552Hi | +T*+A*+G*A*A*A*T*A*C*T*G*A*A*A*G*T*+ A*+A*+G | 5577 | 19 |
| 555 | ATAGAAATACTGAAA GTAA | A57553Hi | +A*+T*+A*G*A*A*A*T*A*C*T*G*A*A*A*G*+ T*+A*+A | 5578 | 19 |
| 556 | AAGTGTGATGTGTAA TAA | A57554Hi | +A*+A*+G*T*G*T*G*A*T*G*T*G*T*A*A*+T* +A*+A | 5608 | 18 |
| 557 | CTAAGTGTGATGTGT AAT | A57555Hi | +C*+T*+A*A*G*T*G*T*G*A*T*G*T*G*T*+A* +A*+T | 5610 | 18 |
| 558 | CTATACTTGACATGG TCA | A57556Hi | +C*+T*+A*T*A*C*T*T*G*A*C*A*T*G*G*+T* +C*+A | 5689 | 18 |
| 559 | AACTATACTTGACAT GGTC | A57557Hi | +A*+A*+C*T*A*T*A*C*T*T*G*A*C*A*T*G*+ G*+T*+C | 5690 | 19 |
| 560 | ACTATACTTGACATG GTC | A57558Hi | +A*+C*+T*A*T*A*C*T*T*G*A*C*A*T*G*+G* +T*+C | 5690 | 18 |
| 561 | GAACTATACTTGACA TGGT | A57559Hi | +G*+A*+A*C*T*A*T*A*C*T*T*G*A*C*A*T*+ G*+G*+T | 5691 | 19 |
| 562 | GAACTATACTTGACA TGG | A57560Hi | +G*+A*+A*C*T*A*T*A*C*T*T*G*A*C*A*+T* +G*+G | 5692 | 18 |
| 563 | TATAGAACTATACTT GACA | A57561Hi | +T*+A*+T*A*G*A*A*C*T*A*T*A*C*T*T*G*+ A*+C*+A | 5695 | 19 |
| 564 | TATAGAACTATACTT GAC | A57562Hi | +T*+A*+T*A*G*A*A*C*T*A*T*A*C*T*T*+G* +A*+C | 5696 | 18 |
| 565 | CTATTATACTATAGA ACTA | A57563Hi | +C*+T*+A*T*T*A*T*A*C*T*A*T*A*G*A*A*+ C*+T*+A | 5704 | 19 |
| 566 | AATTGAAAGTCCTGA TTTC | A57564Hi | +A*+A*+T*T*G*A*A*A*G*T*C*C*T*G*A*T*+ T*+T*+C | 5801 | 19 |
| 567 | TTTACAAGATGCCAA CTTG | A57565Hi | +T*+T*+T*A*C*A*A*G*A*T*G*C*C*A*A*C*+ T*+T*+G | 5849 | 19 |
| 568 | TTACAAGATGCCAAC TTG | A57566Hi | +T*+T*+A*C*A*A*G*A*T*G*C*C*A*A*C*+T* +T*+G | 5849 | 18 |
| 569 | GTTTACAAGATGCCA ACTT | A57567Hi | +G*+T*+T*T*A*C*A*A*G*A*T*G*C*C*A*A*+ C*+T*+T | 5850 | 19 |
| 570 | CTCAGTCTGTTTACA AGAT | A57568Hi | +C*+T*+C*A*G*T*C*T*G*T*T*T*A*C*A*A*+ G*+A*+T | 5858 | 19 |

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| 571 | ACTCAGTCTGTTTAC AAGA | A57569Hi | +A*+C*+T*C*A*G*T*C*T*G*T*T*T*A*C*A*+ A*+G*+A | 5859 | 19 |
| 572 | CTTCACTCAGTCTGT TTAC | A57570Hi | +C*+T*+T*C*A*C*T*C*A*G*T*C*T*G*T*T*+ T*+A*+C | 5863 | 19 |
| 573 | ATCTTCACTCAGTCT GTTT | A57571Hi | +A*+T*+C*T*T*C*A*C*T*C*A*G*T*C*T*G*+ T*+T*+T | 5865 | 19 |
| 574 | TATATCTTCACTCAGT CTG | A57572Hi | +T*+A*+T*A*T*C*T*T*C*A*C*T*C*A*G*T*+ C*+T*+G | 5868 | 19 |
| 575 | CTTTCACATTTCGAA ATAA | A57573Hi | +C*+T*+T*T*C*A*C*A*T*T*T*C*G*A*A*A*+ T*+A*+A | 5914 | 19 |
| 576 | GCTCTTTCACATTTC GAAA | A57574Hi | +G*+C*+T*C*T*T*T*C*A*C*A*T*T*T*C*G*+ A*+A*+A | 5917 | 19 |
| 577 | TAGTAGGCTCTTTCA CATT | A57575Hi | +T*+A*+G*T*A*G*G*C*T*C*T*T*T*C*A*C*+ A*+T*+T | 5923 | 19 |
| 578 | TAGTAGGCTCTTTCA CAT | A57576Hi | +T*+A*+G*T*A*G*G*C*T*C*T*T*T*C*A*+C* +A*+T | 5924 | 18 |
| 579 | CCTAGTAGGCTCTTT CACA | A57577Hi | +C*+C*+T*A*G*T*A*G*G*C*T*C*T*T*T*C*+ A*+C*+A | 5925 | 19 |
| 580 | CTAGTAGGCTCTTTC ACA | A57578Hi | +C*+T*+A*G*T*A*G*G*C*T*C*T*T*T*C*+A* +C*+A | 5925 | 18 |
| 581 | CTAGTAGGCTCTTTC AC | A57579Hi | +C*+T*+A*G*T*A*G*G*C*T*C*T*T*T*+C*+A *+C | 5926 | 17 |
| 582 | CCTAGTAGGCTCTTT CAC | A57580Hi | +C*+C*+T*A*G*T*A*G*G*C*T*C*T*T*T*+C* +A*+C | 5926 | 18 |
| 583 | ATTGATAAGGTCTAG AGAT | A57581Hi | +A*+T*+T*G*A*T*A*A*G*G*T*C*T*A*G*A*+ G*+A*+T | 5954 | 19 |
| 584 | TTCTCTAGAATGAAT TGAT | A57582Hi | +T*+T*+C*T*C*T*A*G*A*A*T*G*A*A*T*T*+ G*+A*+T | 5967 | 19 |
| 585 | GTAGAACTCCTCAAT GGC | A57583Hi | +G*+T*+A*G*A*A*C*T*C*C*T*C*A*A*T*+G* +G*+C | 5997 | 18 |
| 586 | GGTAGAACTCCTCAA TGGC | A57584Hi | +G*+G*+T*A*G*A*A*C*T*C*C*T*C*A*A*T*+ G*+G*+C | 5997 | 19 |
| 587 | GAGGTAGAACTCCTC AATG | A57585Hi | +G*+A*+G*G*T*A*G*A*A*C*T*C*C*T*C*A*+ A*+T*+G | 5999 | 19 |
| 588 | AGGAGGTAGAACTCC TCAA | A57586Hi | +A*+G*+G*A*G*G*T*A*G*A*A*C*T*C*C*T*+ C*+A*+A | 6001 | 19 |
| 589 | ATAGACAGGAGGTAG AACT | A57587Hi | +A*+T*+A*G*A*C*A*G*G*A*G*G*T*A*G*A* +A*+C*+T | 6007 | 19 |
| 590 | AATAGAGGCAAGAAA CGT | A57588Hi | +A*+A*+T*A*G*A*G*G*C*A*A*G*A*A*A*+C* +G*+T | 6085 | 18 |
| 591 | AAGCTAGAATAATAG AGG | A57589Hi | +A*+A*+G*C*T*A*G*A*A*T*A*A*T*A*G*+A* +G*+G | 6095 | 18 |
| 592 | TGAAGCTAGAATAAT AGAG | A57590Hi | +T*+G*+A*A*G*C*T*A*G*A*A*T*A*A*T*A*+ G*+A*+G | 6096 | 19 |
| 593 | TAAGTTATCAGAATG GCTG | A57591Hi | +T*+A*+A*G*T*T*A*T*C*A*G*A*A*T*G*G*+ C*+T*+G | 6127 | 19 |
| 594 | GTAAGTTATCAGAAT GGC | A57592Hi | +G*+T*+A*A*G*T*T*A*T*C*A*G*A*A*T*+G* +G*+C | 6129 | 18 |
| 595 | TGTAAGTTATCAGAA TGG | A57593Hi | +T*+G*+T*A*A*G*T*T*A*T*C*A*G*A*A*+T* +G*+G | 6130 | 18 |
| 596 | GTACCAAGATTATTA AGTG | A57594Hi | +G*+T*+A*C*C*A*A*G*A*T*T*A*T*T*A*A*+ G*+T*+G | 6639 | 19 |
| 597 | GTTGTACCAAGATTA TTA | A57595Hi | +G*+T*+T*G*T*A*C*C*A*A*G*A*T*T*A*+T* +T*+A | 6643 | 18 |
| 598 | AGGTTGTACCAAGAT TATT | A57596Hi | +A*+G*+G*T*T*G*T*A*C*C*A*A*G*A*T*T*+ A*+T*+T | 6644 | 19 |
| 599 | TTTAGAGGTTGTACC AAG | A57597Hi | +T*+T*+T*A*G*A*G*G*T*T*G*T*A*C*C*+A* +A*+G | 6650 | 18 |
| 600 | AGGATACACCTTTCT CCAA | A57598Hi | +A*+G*+G*A*T*A*C*A*C*C*T*T*T*C*T*C*+ C*+A*+A | 7079 | 19 |
| 601 | TAGGATACACCTTTC TCCA | A57599Hi | +T*+A*+G*G*A*T*A*C*A*C*C*T*T*T*C*T*+ C*+C*+A | 7080 | 19 |
| 602 | AGTCAAACATGAATC TCTT | A57600Hi | +A*+G*+T*C*A*A*A*C*A*T*G*A*A*T*C*T*+ C*+T*+T | 7201 | 19 |
| 603 | TTGCACAGAAGTGAC CAAC | A57601H | +T*+T*+G*C*A*C*A*G*A*A*G*T*G*A*C*C*+ A*+A*+C | 7282 | 19 |
| 604 | CTATTAATTTGCACA GAAG | A57602H | +C*+T*+A*T*T*A*A*T*T*T*G*C*A*C*A*G*+ A*+A*+G | 7290 | 19 |
| 605 | TTAAGCTTTGCATTG TACC | A57603H | +T*+T*+A*A*G*C*T*T*T*G*C*A*T*T*G*T*+ A*+C*+C | 7320 | 19 |

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| 606 | ATTAAGCTTTGCATTGTAC | A57604H | +A*+T*+T*A*A*G*C*T*T*T*G*C*A*T*T*G*+T*+A*+C | 7321 | 19 |
| 607 | CCCATTAAGCTTTGCATTG | A57605H | +C*+C*+C*A*T*T*A*A*G*C*T*T*T*G*C*A*+T*+T*+G | 7324 | 19 |
| 608 | TCCCATTAAGCTTTGCATT | A57606H | +T*+C*+C*C*A*T*T*A*A*G*C*T*T*T*G*C*+A*+T*+T | 7325 | 19 |
| 609 | GTCCCATTAAGCTTTGCAT | A57607H | +G*+T*+C*C*C*A*T*T*A*A*G*C*T*T*T*G*+C*+A*+T | 7326 | 19 |
| 610 | GGTCCCATTAAGCTTTGCA | A57608H | +G*+G*+T*C*C*C*A*T*T*A*A*G*C*T*T*T*+G*+C*+A | 7327 | 19 |
| 611 | GGGTCCCATTAAGCTTTGC | A57609H | +G*+G*+G*T*C*C*C*A*T*T*A*A*G*C*T*T*+T*+G*+C | 7328 | 19 |
| 612 | GGGTCCCATTAAGCTTTG | A57610H | +G*+G*+G*T*C*C*C*A*T*T*A*A*G*C*T*+T*+T*+G | 7329 | 18 |
| 613 | GGGGTCCCATTAAGCTTTG | A57611H | +G*+G*+G*G*T*C*C*C*A*T*T*A*A*G*C*T*+T*+T*+G | 7329 | 19 |
| 614 | ATCCTGGGGTCCCATTAAG | A57612H | +A*+T*+C*C*T*G*G*G*G*T*C*C*C*A*T*T*+A*+A*+G | 7334 | 19 |
| 615 | CCAACATCCTGGGGTCCCA | A57613H | +C*+C*+A*A*C*A*T*C*C*T*G*G*G*G*T*C*+C*+C*+A | 7339 | 19 |
| 616 | TCATTTCCAACATCCTGGG | A57614H | +T*+C*+A*T*T*T*C*C*A*A*C*A*T*C*C*T*+G*+G*+G | 7345 | 19 |
| 617 | ATCATTTCCAACATCCTGG | A57615H | +A*+T*+C*A*T*T*T*C*C*A*A*C*A*T*C*C*+T*+G*+G | 7346 | 19 |
| 618 | CCAATCATTTCCAACATCC | A57616H | +C*+C*+A*A*T*C*A*T*T*T*C*C*A*A*C*A*+T*+C*+C | 7349 | 19 |
| 619 | CCCAATCATTTCCAACATC | A57617H | +C*+C*+C*A*A*T*C*A*T*T*T*C*C*A*A*C*+A*+T*+C | 7350 | 19 |
| 620 | TTCCCAATCATTTCCAACA | A57618H | +T*+T*+C*C*C*A*A*T*C*A*T*T*T*C*C*A*+A*+C*+A | 7352 | 19 |
| 621 | CTTCCCAATCATTTCCAAC | A57619H | +C*+T*+T*C*C*C*A*A*T*C*A*T*T*T*C*C*+A*+A*+C | 7353 | 19 |
| 622 | GACTTCCCAATCATTTCCA | A57620H | +G*+A*+C*T*T*C*C*C*A*A*T*C*A*T*T*T*+C*+C*+A | 7355 | 19 |
| 623 | GGACTTCCCAATCATTTCC | A57621H | +G*+G*+A*C*T*T*C*C*C*A*A*T*C*A*T*T*T*+T*+C*+C | 7356 | 19 |
| 624 | AGGACTTCCCAATCATTTC | A57622H | +A*+G*+G*A*C*T*T*C*C*C*A*A*T*C*A*T*+T*+T*+C | 7357 | 19 |
| 625 | AAGGACTTCCCAATCATTT | A57623H | +A*+A*+G*G*A*C*T*T*C*C*C*A*A*T*C*A*+T*+T*+T | 7358 | 19 |
| 626 | GAACACCAAGGACTTCCCA | A57624H | +G*+A*+A*C*A*C*C*A*A*G*G*A*C*T*T*C*+C*+C*+A | 7365 | 19 |
| 627 | TGAACACCAAGGACTTCCC | A57625H | +T*+G*+A*A*C*A*C*C*A*A*G*G*A*C*T*T*+C*+C*+C | 7366 | 19 |
| 628 | TTACATATCTATCATACTT | A57626Hi | +T*+T*+A*C*A*T*A*T*C*T*A*T*C*A*T*A*+C*+T*+T | 7390 | 19 |
| 629 | GTAGCCTTGGATTGCAAA | A57627Hi | +G*+T*+A*G*C*C*T*T*G*G*A*T*T*G*C*+A*+A*+A | 7467 | 18 |
| 630 | AGTAGCCTTGGATTGCAAA | A57628Hi | +A*+G*+T*A*G*C*C*T*T*G*G*A*T*T*G*C*+A*+A*+A | 7467 | 19 |
| 631 | GTAGCCTTGGATTGCAA | A57629Hi | +G*+T*+A*G*C*C*T*T*G*G*A*T*T*G*+C*+A*+A | 7468 | 17 |
| 632 | AGTAGCCTTGGATTGCAA | A57630Hi | +A*+G*+T*A*G*C*C*T*T*G*G*A*T*T*G*+C*+A*+A | 7468 | 18 |
| 633 | AAATCATTGACTCAAGGAA | A57631Hi | +A*+A*+A*T*C*A*T*T*G*A*C*T*C*A*A*G*+G*+A*+A | 7516 | 19 |
| 634 | CTCTATAAATGTAAATCAT | A57632Hi | +C*+T*+C*T*A*T*A*A*A*T*G*T*A*A*A*T*+C*+A*+T | 7528 | 19 |
| 635 | GAGTTTAAAGCTCTCTATA | A57633Hi | +G*+A*+G*T*T*T*A*A*A*G*C*T*C*T*C*T*+A*+T*+A | 7540 | 19 |
| 636 | TCTGAGTTTAAAGCTCTCT | A57634Hi | +T*+C*+T*G*A*G*T*T*T*A*A*A*G*C*T*C*+T*+C*+T | 7543 | 19 |
| 637 | TAAATCAAACTTCTGAGTT | A57635Hi | +T*+A*+A*A*T*C*A*A*A*C*T*T*C*T*G*A*+G*+T*+T | 7554 | 19 |
| 638 | TCTAAATCAAACTTCTGAG | A57636Hi | +T*+C*+T*A*A*A*T*C*A*A*A*C*T*T*C*T*+G*+A*+G | 7556 | 19 |
| 639 | GCTTTCTAAATCAAACTTC | A57637Hi | +G*+C*+T*T*T*C*T*A*A*A*T*C*A*A*A*C*+T*+T*+C | 7560 | 19 |
| 640 | CTGACATGTTACCTTAAAT | A57638Hi | +C*+T*+G*A*C*A*T*G*T*T*A*C*C*T*T*A*+A*+A*+T | 7583 | 19 |

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| 641 | CTGACATGTTACCTTAAA | A57639Hi | +C*+T*+G*A*C*A*T*G*T*T*A*C*C*T*T*+A*+A*+A | 7584 | 18 |
| 642 | ATCAACTTTCAAATTACTA | A57640Hi | +A*+T*+C*A*A*C*T*T*T*C*A*A*A*T*T*A*+C*+T*+A | 7774 | 19 |
| 643 | CATCAACTTTCAAATTACT | A57641Hi | +C*+A*+T*C*A*A*C*T*T*T*C*A*A*A*T*T*+A*+C*+T | 7775 | 19 |
| 644 | CATTATGCTGCAAACTGCA | A57642Hi | +C*+A*+T*T*A*T*G*C*T*G*C*A*A*A*C*T*+G*+C*+A | 7945 | 19 |
| 645 | CATTATGCTGCAAACTGC | A57643Hi | +C*+A*+T*T*A*T*G*C*T*G*C*A*A*A*C*+T*+G*+C | 7946 | 18 |
| 646 | GCTAAGGAAGTAGTCTCA | A57644Hi | +G*+C*+T*A*A*G*G*A*A*G*T*A*G*T*C*+T*+C*+A | 7974 | 18 |
| 647 | TGGCTAAGGAAGTAGTCTC | A57645Hi | +T*+G*+G*C*T*A*A*G*G*A*A*G*T*A*G*T*+C*+T*+C | 7975 | 19 |
| 648 | TGGCTAAGGAAGTAGTCT | A57646Hi | +T*+G*+G*C*T*A*A*G*G*A*A*G*T*A*G*+T*+C*+T | 7976 | 18 |
| 649 | GCAACACATTTGTCAAAGA | A57647Hi | +G*+C*+A*A*C*A*C*A*T*T*T*G*T*C*A*A*+A*+G*+A | 8480 | 19 |
| 650 | AGCAACACATTTGTCAAAG | A57648Hi | +A*+G*+C*A*A*C*A*C*A*T*T*T*G*T*C*A*+A*+A*+G | 8481 | 19 |
| 651 | TAAATATGCTCTTTCCAAA | A57649Hi | +T*+A*+A*A*T*A*T*G*C*T*C*T*T*T*C*C*+A*+A*+A | 8530 | 19 |
| 652 | ATTGTAAATATGCTCTTTC | A57650Hi | +A*+T*+T*G*T*A*A*A*T*A*T*G*C*T*C*T*+T*+T*+C | 8534 | 19 |
| 653 | TGAGTAATTCCTCATCAAA | A57651Hi | +T*+G*+A*G*T*A*A*T*T*C*C*T*C*A*T*C*+A*+A*+A | 8619 | 19 |
| 654 | AGACTGGCTCATCTTTGGA | A57652Hi | +A*+G*+A*C*T*G*G*C*T*C*A*T*C*T*T*T*T*+G*+G*+A | 8705 | 19 |
| 655 | ATAGACTGGCTCATCTTTG | A57653Hi | +A*+T*+A*G*A*C*T*G*G*C*T*C*A*T*C*T*+T*+T*+G | 8707 | 19 |
| 656 | GAGGTTATAGACTGGCTCA | A57654Hi | +G*+A*+G*G*T*T*A*T*A*G*A*C*T*G*G*C*+T*+C*+A | 8713 | 19 |
| 657 | TGAGGTTATAGACTGGCTC | A57655Hi | +T*+G*+A*G*G*T*T*A*T*A*G*A*C*T*G*G*+C*+T*+C | 8714 | 19 |
| 658 | CTGAGGTTATAGACTGGC | A57656Hi | +C*+T*+G*A*G*G*T*T*A*T*A*G*A*C*T*+G*+G*+C | 8716 | 18 |
| 659 | GGAATATGACTAGATGAGT | A57657Hi | +G*+G*+A*A*T*A*T*G*A*C*T*A*G*A*T*G*+A*+G*+T | 8748 | 19 |
| 660 | AGGAATATGACTAGATGAG | A57658Hi | +A*+G*+G*A*A*T*A*T*G*A*C*T*A*G*A*T*+G*+A*+G | 8749 | 19 |
| 661 | GGAATATGACTAGATGAG | A57659Hi | +G*+G*+A*A*T*A*T*G*A*C*T*A*G*A*T*+G*+A*+G | 8749 | 18 |
| 662 | ACAGGAATATGACTAGATG | A57660Hi | +A*+C*+A*G*G*A*A*T*A*T*G*A*C*T*A*G*+A*+T*+G | 8751 | 19 |
| 663 | GGATGAACAAAGTGAGTGA | A57661Hi | +G*+G*+A*T*G*A*A*C*A*A*A*G*T*G*A*G*+T*+G*+A | 8843 | 19 |
| 664 | CTATCTTCTTCACAACTGC | A57662Hi | +C*+T*+A*T*C*T*T*C*T*T*T*C*A*C*A*A*C*+T*+G*+C | 8922 | 19 |
| 665 | TTGCATAATCTCCATTTGG | A57663Hi | +T*+T*+G*C*A*T*A*A*T*C*T*C*C*A*T*T*T*+T*+G*+G | 9181 | 19 |
| 666 | ATCTCTAGTCTATTCCTGC | A57664Hi | +A*+T*+C*T*C*T*A*G*T*C*T*A*T*T*C*C*+T*+G*+C | 9278 | 19 |
| 667 | ATTATTGATTGCTACTGTT | A57665Hi | +A*+T*+T*A*T*T*G*A*T*T*G*C*T*A*C*T*+G*+T*+T | 9718 | 19 |
| 668 | AATTATTGATTGCTACTGT | A57666Hi | +A*+A*+T*T*A*T*T*G*A*T*T*G*C*T*A*C*+T*+G*+T | 9719 | 19 |
| 669 | GTTAGTTTGTGTATATAAA | A57667Hi | +G*+T*+T*A*G*T*T*T*G*T*G*T*A*T*A*T*+A*+A*+A | 9761 | 19 |
| 670 | ATGTTAGTTTGTGTATATA | A57668Hi | +A*+T*+G*T*T*A*G*T*T*T*G*T*G*T*A*T*+A*+T*+A | 9763 | 19 |
| 671 | GATGTTAGTTTGTGTATAT | A57669Hi | +G*+A*+T*G*T*T*A*G*T*T*T*G*T*G*T*A*+T*+A*+T | 9764 | 19 |
| 672 | GATGTTAGTTTGTGTATA | A57670Hi | +G*+A*+T*G*T*T*A*G*T*T*T*G*T*G*T*+A*+T*+A | 9765 | 18 |
| 673 | AGATGTTAGTTTGTGTATA | A57671Hi | +A*+G*+A*T*G*T*T*A*G*T*T*T*G*T*G*T*+A*+T*+A | 9765 | 19 |
| 674 | AAAGATGTTAGTTTGTGTA | A57672Hi | +A*+A*+A*G*A*T*G*T*T*A*G*T*T*T*G*T*+G*+T*+A | 9767 | 19 |
| 675 | TTAGACATGTTGATATATT | A57673Hi | +T*+T*+A*G*A*C*A*T*G*T*T*G*A*T*A*T*+A*+T*+T | 9804 | 19 |

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| 676 | ATCTTAGACATGTTG ATAT | A57674Hi | +A*+T*+C*T*T*A*G*A*C*A*T*G*T*T*G*A*+ T*+A*+T | 9807 | 19 |
| 677 | ATCTTAGACATGTTG ATA | A57675Hi | +A*+T*+C*T*T*A*G*A*C*A*T*G*T*T*G*+A* +T*+A | 9808 | 18 |
| 678 | TATCTTAGACATGTT GATA | A57676Hi | +T*+A*+T*C*T*T*A*G*A*C*A*T*G*T*T*G*+ A*+T*+A | 9808 | 19 |
| 679 | CTCTCATTGTATTTAA TTC | A57677Hi | +C*+T*+C*T*C*A*T*T*G*T*A*T*T*T*A*A*+ T*+T*+C | 10519 | 19 |
| 680 | ATTATGAACTGTTAG CATT | A57678H | +A*+T*+T*A*T*G*A*A*C*T*G*T*T*A*G*C*+ A*+T*+T | 10642 | 19 |
| 681 | CATTATGAACTGTTA GCAT | A57679H | +C*+A*+T*T*A*T*G*A*A*C*T*G*T*T*A*G*+ C*+A*+T | 10643 | 19 |
| 682 | CATTATGAACTGTTA GCA | A57680H | +C*+A*+T*T*A*T*G*A*A*C*T*G*T*T*A*+G* +C*+A | 10644 | 18 |
| 683 | GCATTATGAACTGTT AGCA | A57681H | +G*+C*+A*T*T*A*T*G*A*A*C*T*G*T*T*A*+ G*+C*+A | 10644 | 19 |
| 684 | GCATTATGAACTGTT AGC | A57682H | +G*+C*+A*T*T*A*T*G*A*A*C*T*G*T*T*+A* +G*+C | 10645 | 18 |
| 685 | GGCATTATGAACTGT TAGC | A57683H | +G*+G*+C*A*T*T*A*T*G*A*A*C*T*G*T*T*+ A*+G*+C | 10645 | 19 |
| 686 | GGCATTATGAACTGT TAG | A57684H | +G*+G*+C*A*T*T*A*T*G*A*A*C*T*G*T*+T* +A*+G | 10646 | 18 |
| 687 | TGGCATTATGAACTG TTAG | A57685H | +T*+G*+G*C*A*T*T*A*T*G*A*A*C*T*G*T*+ T*+A*+G | 10646 | 19 |
| 688 | CACTGGCATTATGAA CTGT | A57686H | +C*+A*+C*T*G*G*C*A*T*T*A*T*G*A*A*C*+ T*+G*+T | 10649 | 19 |
| 689 | TACACTGGCATTATG AACT | A57687H | +T*+A*+C*A*C*T*G*G*C*A*T*T*A*T*G*A*+ A*+C*+T | 10651 | 19 |
| 690 | TTACACTGGCATTAT GAAC | A57688H | +T*+T*+A*C*A*C*T*G*G*C*A*T*T*A*T*G*+ A*+A*+C | 10652 | 19 |
| 691 | GACAAGTTTACACTG GCAT | A57689H | +G*+A*+C*A*A*G*T*T*T*A*C*A*C*T*G*G*+ C*+A*+T | 10659 | 19 |
| 692 | GACAAGTTTACACTG GCA | A57690H | +G*+A*+C*A*A*G*T*T*T*A*C*A*C*T*G*+G* +C*+A | 10660 | 18 |
| 693 | TGACAAGTTTACACT GGCA | A57691H | +T*+G*+A*C*A*A*G*T*T*T*A*C*A*C*T*G*+ G*+C*+A | 10660 | 19 |
| 694 | TGACAAGTTTACACT GGC | A57692H | +T*+G*+A*C*A*A*G*T*T*T*A*C*A*C*T*+G* +G*+C | 10661 | 18 |
| 695 | AGGTCTTCAGTCCAA TCA | A57693H | +A*+G*+G*T*C*T*T*C*A*G*T*C*C*A*A*+T* +C*+A | 10680 | 18 |
| 696 | AAGGTCTTCAGTCCA ATCA | A57694H | +A*+A*+G*G*T*C*T*T*C*A*G*T*C*C*A*A*+ T*+C*+A | 10680 | 19 |
| 697 | TAAGGTCTTCAGTCC AATC | A57695H | +T*+A*+A*G*G*T*C*T*T*C*A*G*T*C*C*A*+ A*+T*+C | 10681 | 19 |
| 698 | CTAAGGTCTTCAGTC CAAT | A57696H | +C*+T*+A*A*G*G*T*C*T*T*C*A*G*T*C*C*+ A*+A*+T | 10682 | 19 |
| 699 | GATCTAAGGTCTTCA GTCC | A57697H | +G*+A*+T*C*T*A*A*G*G*T*C*T*T*C*A*G*+ T*+C*+C | 10685 | 19 |
| 700 | GAGATCTAAGGTCTT CAGT | A57698H | +G*+A*+G*A*T*C*T*A*A*G*G*T*C*T*T*C*+ A*+G*+T | 10687 | 19 |
| 701 | GGAGATCTAAGGTCT TCAG | A57699H | +G*+G*+A*G*A*T*C*T*A*A*G*G*T*C*T*T*+ C*+A*+G | 10688 | 19 |
| 702 | AGGAGATCTAAGGTC TTCA | A57700H | +A*+G*+G*A*G*A*T*C*T*A*A*G*G*T*C*T*+ T*+C*+A | 10689 | 19 |
| 703 | GAGGAGATCTAAGGT CTTC | A57701H | +G*+A*+G*G*A*G*A*T*C*T*A*A*G*G*T*C*+ T*+T*+C | 10690 | 19 |
| 704 | GGAGGAGATCTAAGG TCTT | A57702H | +G*+G*+A*G*G*A*G*A*T*C*T*A*A*G*G*T* +C*+T*+T | 10691 | 19 |
| 705 | AGGAGGAGATCTAAG GTCT | A57703H | +A*+G*+G*A*G*G*A*G*A*T*C*T*A*A*G*G* +T*+C*+T | 10692 | 19 |
| 706 | AGGAGGAGATCTAAG GTC | A57704H | +A*+G*+G*A*G*G*A*G*A*T*C*T*A*A*G*+G *+T*+C | 10693 | 18 |
| 707 | TTAGGACATTTAAAT CAAG | A57705Hi | +T*+T*+A*G*G*A*C*A*T*T*T*A*A*A*T*C*+ A*+A*+G | 10837 | 19 |
| 708 | ATGGCATACTCCAGA ACA | A57706Hi | +A*+T*+G*G*C*A*T*A*C*T*C*C*A*G*A*+A* +C*+A | 11171 | 18 |
| 709 | ATTATGGCATACTCC AGAA | A57707Hi | +A*+T*+T*A*T*G*G*C*A*T*A*C*T*C*C*A*+ G*+A*+A | 11173 | 19 |
| 710 | TGAAGCCTGGCATCT AGCA | A57708Hi | +T*+G*+A*A*G*C*C*T*G*G*C*A*T*C*T*T*A*+ G*+C*+A | 11233 | 19 |

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| 711 | GTGAAGCCTGGCATC TAGC | A57709Hi | +G*+T*+G*A*A*G*C*C*T*G*G*C*A*T*C*T*+ A*+G*+C | 11234 | 19 |
| 712 | TGAAGCCTGGCATCT AGC | A57710Hi | +T*+G*+A*A*G*C*C*T*G*G*C*A*T*C*T*+A* +G*+C | 11234 | 18 |
| 713 | CTTGTGAAGCCTGGC ATCT | A57711Hi | +C*+T*+T*G*T*G*A*A*G*C*C*T*G*G*C*A*+ T*+C*+T | 11237 | 19 |
| 714 | ACTTGTGAAGCCTGG CATC | A57712Hi | +A*+C*+T*T*G*T*G*A*A*G*C*C*T*G*G*C*+ A*+T*+C | 11238 | 19 |
| 715 | CTTGTGAAGCCTGGC ATC | A57713Hi | +C*+T*+T*G*T*G*A*A*G*C*C*T*G*G*C*+A* +T*+C | 11238 | 18 |
| 716 | TACTTGTGAAGCCTG GCAT | A57714Hi | +T*+A*+C*T*T*G*T*G*A*A*G*C*C*T*G*G*+ C*+A*+T | 11239 | 19 |
| 717 | ACTTGTGAAGCCTGG CAT | A57715Hi | +A*+C*+T*T*G*T*G*A*A*G*C*C*T*G*G*+C* +A*+T | 11239 | 18 |
| 718 | TACTTGTGAAGCCTG GCA | A57716Hi | +T*+A*+C*T*T*G*T*G*A*A*G*C*C*T*G*+G* +C*+A | 11240 | 18 |
| 719 | TTACTTGTGAAGCCT GGC | A57717Hi | +T*+T*+A*C*T*T*G*T*G*A*A*G*C*C*T*+G* +G*+C | 11241 | 18 |
| 720 | TTTACTTGTGAAGCC TGG | A57718Hi | +T*+T*+T*A*C*T*T*G*T*G*A*A*G*C*C*+T* +G*+G | 11242 | 18 |
| 721 | GAACCTGACATGGAG AATC | A57719Hi | +G*+A*+A*C*C*T*G*A*C*A*T*G*G*A*G*A*+ A*+T*+C | 11393 | 19 |
| 722 | AAGGAACCTGACATG GAGA | A57720Hi | +A*+A*+G*G*A*A*C*C*T*G*A*C*A*T*G*G*+ A*+G*+A | 11396 | 19 |
| 723 | AAGGAACCTGACATG GAG | A57721Hi | +A*+A*+G*G*A*A*C*C*T*G*A*C*A*T*G*+G* +A*+G | 11397 | 18 |
| 724 | GAAGGAACCTGACAT GGAG | A57722Hi | +G*+A*+A*G*G*A*A*C*C*T*G*A*C*A*T*G*+ G*+A*+G | 11397 | 19 |
| 725 | GGAAGGAACCTGACA TGGA | A57723Hi | +G*+G*+A*A*G*G*A*A*C*C*T*G*A*C*A*T*+ G*+G*+A | 11398 | 19 |
| 726 | TTGCATCATTTCAAG ATTT | A57724Hi | +T*+T*+G*C*A*T*C*A*T*T*T*C*A*A*G*A*+ T*+T*+T | 11460 | 19 |
| 727 | AGTGTCCAGCACAGC AATG | A57725Hi | +A*+G*+T*G*T*C*C*A*G*C*A*C*A*G*C*A*+ A*+T*+G | 11489 | 19 |
| 728 | CCTACATGGAAGGAA ACTC | A57726Hi | +C*+C*+T*A*C*A*T*G*G*A*A*G*G*A*A*A*+ C*+T*+C | 11573 | 19 |
| 729 | TCTCTTAGCAGGACT GATG | A57727Hi | +T*+C*+T*C*T*T*A*G*C*A*G*G*A*C*T*G*+ A*+T*+G | 11689 | 19 |
| 730 | CTCTTAGCAGGACTG ATG | A57728Hi | +C*+T*+C*T*T*A*G*C*A*G*G*A*C*T*G*+A* +T*+G | 11689 | 18 |
| 731 | CATCTCTTAGCAGGA CTGA | A57729Hi | +C*+A*+T*C*T*C*T*T*A*G*C*A*G*G*A*C*+ T*+G*+A | 11691 | 19 |
| 732 | CCTCATACTCTCATCT TCC | A57730Hi | +C*+C*+T*C*A*T*A*C*T*C*T*C*A*T*C*T*+ T*+C*+C | 11732 | 19 |
| 733 | CCTCATACTCTCATCT TC | A57731Hi | +C*+C*+T*C*A*T*A*C*T*C*T*C*A*T*C*+T* +T*+C | 11733 | 18 |
| 734 | GTACTGTATGAGGCT AAC | A57732Hi | +G*+T*+A*C*T*G*T*A*T*G*A*G*G*C*T*+A* +A*+C | 11959 | 18 |
| 735 | AGTACTGTATGAGGC TAAC | A57733Hi | +A*+G*+T*A*C*T*G*T*A*T*G*A*G*G*C*T*+ A*+A*+C | 11959 | 19 |
| 736 | AGTACTGTATGAGGC TAA | A57734Hi | +A*+G*+T*A*C*T*G*T*A*T*G*A*G*G*C*+T* +A*+A | 11960 | 18 |
| 737 | GTAGTACTGTATGAG GCT | A57735Hi | +G*+T*+A*G*T*A*C*T*G*T*A*T*G*A*G*+G* +C*+T | 11962 | 18 |
| 738 | ACAAACAGCATCTAT TCTG | A57736Hi | +A*+C*+A*A*A*C*A*G*C*A*T*C*T*A*T*T*+ C*+T*+G | 12012 | 19 |
| 739 | CACTCCAAATATGCT AAAC | A57737Hi | +C*+A*+C*T*C*C*A*A*A*T*A*T*G*C*T*A*+ A*+A*+C | 12146 | 19 |
| 740 | TTCACTCCAAATATG CTAA | A57738Hi | +T*+T*+C*A*C*T*C*C*A*A*A*T*A*T*G*C*+ T*+A*+A | 12148 | 19 |
| 741 | TGTCTTCACTCCAAA TATG | A57739Hi | +T*+G*+T*C*T*T*C*A*C*T*C*C*A*A*A*T*+ A*+T*+G | 12152 | 19 |
| 742 | TTGTCTTCACTCCAA ATAT | A57740Hi | +T*+T*+G*T*C*T*T*C*A*C*T*C*C*A*A*A*+ T*+A*+T | 12153 | 19 |
| 743 | GTACATGTATCTCAT CAGC | A57741Hi | +G*+T*+A*C*A*T*G*T*A*T*C*T*C*A*T*C*+ A*+G*+C | 12189 | 19 |
| 744 | TAGTACATGTATCTC ATCA | A57742Hi | +T*+A*+G*T*A*C*A*T*G*T*A*T*C*T*C*A*+ T*+C*+A | 12191 | 19 |
| 745 | TATAGTACATGTATC TCAT | A57743Hi | +T*+A*+T*A*G*T*A*C*A*T*G*T*A*T*C*T*+ C*+A*+T | 12193 | 19 |

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| 746 | CTATAGTACATGTATCTCA | A57744Hi | +C*+T*+A*T*A*G*T*A*C*A*T*G*T*A*T*C*+T*+C*+A | 12194 | 19 |
| 747 | TTGCATTCTCATCTAGAAT | A57745Hi | +T*+T*+G*C*A*T*T*C*T*C*A*T*C*T*A*G*+A*+A*+T | 12382 | 19 |
| 748 | TTTGCATTCTCATCTAGAA | A57746Hi | +T*+T*+T*G*C*A*T*T*C*T*C*A*T*C*T*A*+G*+A*+A | 12383 | 19 |
| 749 | GCACCTTCATTCCTATTGT | A57747Hi | +G*+C*+A*C*C*T*T*C*A*T*T*C*C*T*A*T*+T*+G*+T | 12404 | 19 |
| 750 | CAAGGCACCTTCATTCCTA | A57748Hi | +C*+A*+A*G*G*C*A*C*C*T*T*C*A*T*T*C*+C*+T*+A | 12408 | 19 |
| 751 | ACAAGGCACCTTCATTCCT | A57749Hi | +A*+C*+A*A*G*G*C*A*C*C*T*T*C*A*T*T*+C*+C*+T | 12409 | 19 |
| 752 | AACAAGGCACCTTCATTCC | A57750Hi | +A*+A*+C*A*A*G*G*C*A*C*C*T*T*C*A*T*+T*+C*+C | 12410 | 19 |
| 753 | AACAAGGCACCTTCATTC | A57751Hi | +A*+A*+C*A*A*G*G*C*A*C*C*T*T*C*A*+T*+T*+C | 12411 | 18 |
| 754 | TTTGAACAAGGCACCTTCA | A57752Hi | +T*+T*+T*G*A*A*C*A*A*G*G*C*A*C*C*T*+T*+C*+A | 12414 | 19 |
| 755 | TATCTCCTACACATCTTGA | A57753Hi | +T*+A*+T*C*T*C*C*T*A*C*A*C*A*T*C*T*+T*+G*+A | 12457 | 19 |
| 756 | CATCAATGATACCATAATC | A57754Hi | +C*+A*+T*C*A*A*T*G*A*T*A*C*C*A*T*A*+A*+T*+C | 12586 | 19 |
| 757 | TCATCAATGATACCATAAT | A57755Hi | +T*+C*+A*T*C*A*A*T*G*A*T*A*C*C*A*T*+A*+A*+T | 12587 | 19 |
| 758 | CTTCATCAATGATACCATA | A57756Hi | +C*+T*+T*C*A*T*C*A*A*T*G*A*T*A*C*C*+A*+T*+A | 12589 | 19 |
| 759 | CCTCTTAGACAACATCTG | A57757Hi | +C*+C*+T*C*T*T*A*G*A*C*A*A*C*A*T*+C*+T*+G | 12653 | 18 |
| 760 | GCCTCTTAGACAACATCT | A57758Hi | +G*+C*+C*T*C*T*T*A*G*A*C*A*A*C*A*+T*+C*+T | 12654 | 18 |
| 761 | TGCCTCTTAGACAACATC | A57759Hi | +T*+G*+C*C*T*C*T*T*A*G*A*C*A*A*C*+A*+T*+C | 12655 | 18 |
| 762 | GCCTCTTAGACAACATC | A57760Hi | +G*+C*+C*T*C*T*T*A*G*A*C*A*A*C*+A*+T*+C | 12655 | 17 |
| 763 | TCTTATGCCTCTTAGACA | A57761Hi | +T*+C*+T*T*A*T*G*C*C*T*C*T*T*A*G*+A*+C*+A | 12660 | 18 |
| 764 | TCTTATGCCTCTTAGAC | A57762Hi | +T*+C*+T*T*A*T*G*C*C*T*C*T*T*A*+G*+A*+C | 12661 | 17 |
| 765 | GAAATACATTCTTATGCC | A57763Hi | +G*+A*+A*A*T*A*C*A*T*T*C*T*T*A*T*+G*+C*+C | 12669 | 18 |
| 766 | GCTCTAGATCTTTATAAAT | A57764Hi | +G*+C*+T*C*T*A*G*A*T*C*T*T*T*A*T*A*+A*+A*+T | 12770 | 19 |
| 767 | AAGCTCTAGATCTTTATA | A57765Hi | +A*+A*+G*C*T*C*T*A*G*A*T*C*T*T*T*+A*+T*+A | 12773 | 18 |
| 768 | TCAAGCTCTAGATCTTTAT | A57766Hi | +T*+C*+A*A*G*C*T*C*T*A*G*A*T*C*T*T*+T*+A*+T | 12774 | 19 |
| 769 | ACTTATCAAGCTCTAGATC | A57767Hi | +A*+C*+T*T*A*T*C*A*A*G*C*T*C*T*A*G*+A*+T*+C | 12779 | 19 |
| 770 | GTTAGACTTATCAAGCTC | A57768Hi | +G*+T*+T*A*G*A*C*T*T*A*T*C*A*A*G*+C*+T*+C | 12785 | 18 |
| 771 | TGGCATCAAAAATTAACAT | A57769H | +T*+G*+G*C*A*T*C*A*A*A*A*A*T*T*A*A*+C*+A*+T | 13017 | 19 |
| 772 | CATGGCATCAAAAATTAAC | A57770H | +C*+A*+T*G*G*C*A*T*C*A*A*A*A*A*T*T*+A*+A*+C | 13019 | 19 |
| 773 | GTGCATGGCATCAAAAATT | A57771H | +G*+T*+G*C*A*T*G*G*C*A*T*C*A*A*A*A*+A*+T*+T | 13022 | 19 |
| 774 | GTGCATGGCATCAAAAAT | A57772H | +G*+T*+G*C*A*T*G*G*C*A*T*C*A*A*A*+A*+A*+T | 13023 | 18 |
| 775 | AGTGCATGGCATCAAAAAT | A57773H | +A*+G*+T*G*C*A*T*G*G*C*A*T*C*A*A*A*+A*+A*+T | 13023 | 19 |
| 776 | AATGAGTGCATGGCATCAA | A57774H | +A*+A*+T*G*A*G*T*G*C*A*T*G*G*C*A*T*+C*+A*+A | 13027 | 19 |
| 777 | GGAAATGAGTGCATGGCAT | A57775H | +G*+G*+A*A*A*T*G*A*G*T*G*C*A*T*G*G*+C*+A*+T | 13030 | 19 |
| 778 | TGGAAATGAGTGCATGGCA | A57776H | +T*+G*+G*A*A*A*T*G*A*G*T*G*C*A*T*G*+G*+C*+A | 13031 | 19 |
| 779 | TGGAAATGAGTGCATGGC | A57777H | +T*+G*+G*A*A*A*T*G*A*G*T*G*C*A*T*+G*+G*+C | 13032 | 18 |
| 780 | CTGGAAATGAGTGCATGGC | A57778H | +C*+T*+G*G*A*A*A*T*G*A*G*T*G*C*A*T*+G*+G*+C | 13032 | 19 |

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| 781 | TTGGCTGGAAATGAG TGCA | A57779H | +T*+T*+G*G*C*T*G*G*A*A*A*T*G*A*G*T*+ G*+C*+A | 13036 | 19 |
| 782 | ATTGGCTGGAAATGA GTGC | A57780H | +A*+T*+T*G*G*C*T*G*G*A*A*A*T*G*A*G*+ T*+G*+C | 13037 | 19 |
| 783 | TCATTGGCTGGAAAT GAGT | A57781H | +T*+C*+A*T*T*G*G*C*T*G*G*A*A*A*T*G*+ A*+G*+T | 13039 | 19 |
| 784 | ATCATTGGCTGGAAA TGAG | A57782H | +A*+T*+C*A*T*T*G*G*C*T*G*G*A*A*A*T*+ G*+A*+G | 13040 | 19 |
| 785 | ATCATTGGCTGGAAA TGA | A57783H | +A*+T*+C*A*T*T*G*G*C*T*G*G*A*A*A*+T* +G*+A | 13041 | 18 |
| 786 | CATCATTGGCTGGAA ATGA | A57784H | +C*+A*+T*C*A*T*T*G*G*C*T*G*G*A*A*A*+ T*+G*+A | 13041 | 19 |
| 787 | TCATCATTGGCTGGA AATG | A57785H | +T*+C*+A*T*C*A*T*T*G*G*C*T*G*G*A*A*+ A*+T*+G | 13042 | 19 |
| 788 | TTCATCATTGGCTGG AAAT | A57786H | +T*+T*+C*A*T*C*A*T*T*G*G*C*T*G*G*A*+ A*+A*+T | 13043 | 19 |
| 789 | TTTGCATCCAAGTTT CTGG | A57787H | +T*+T*+T*G*C*A*T*C*C*A*A*G*T*T*T*C*+ T*+G*+G | 13064 | 19 |
| 790 | AAGCTTTGCATCCAA GTTT | A57788H | +A*+A*+G*C*T*T*T*G*C*A*T*C*C*A*A*G*+ T*+T*+T | 13068 | 19 |
| 791 | GTAAAGCTTTGCATC CAAG | A57789H | +G*+T*+A*A*A*G*C*T*T*T*G*C*A*T*C*C*+ A*+A*+G | 13071 | 19 |
| 792 | GTAAAGCTTTGCATC CAA | A57790H | +G*+T*+A*A*A*G*C*T*T*T*G*C*A*T*C*+C* +A*+A | 13072 | 18 |
| 793 | TGTAAAGCTTTGCAT CCAA | A57791H | +T*+G*+T*A*A*A*G*C*T*T*T*G*C*A*T*C*+ C*+A*+A | 13072 | 19 |
| 794 | TAAACCTTATGCCTT GTT | A57792Hi | +T*+A*+A*A*C*C*T*T*A*T*G*C*C*T*T*+G* +T*+T | 13349 | 18 |
| 795 | GTAAACCTTATGCCT TGT | A57793Hi | +G*+T*+A*A*A*C*C*T*T*A*T*G*C*C*T*+T* +G*+T | 13350 | 18 |
| 796 | AGTAAACCTTATGCC TTGT | A57794Hi | +A*+G*+T*A*A*A*C*C*T*T*A*T*G*C*C*T*+ T*+G*+T | 13350 | 19 |
| 797 | GTAAACCTTATGCCT TG | A57795Hi | +G*+T*+A*A*A*C*C*T*T*A*T*G*C*C*+T*+T *+G | 13351 | 17 |
| 798 | AGTAAACCTTATGCC TTG | A57796Hi | +A*+G*+T*A*A*A*C*C*T*T*A*T*G*C*C*+T* +T*+G | 13351 | 18 |
| 799 | AAGTAAACCTTATGC CTTG | A57797Hi | +A*+A*+G*T*A*A*A*C*C*T*T*A*T*G*C*C*+ T*+T*+G | 13351 | 19 |
| 800 | TAACCTATGCTTGGC TTCA | A57798Hi | +T*+A*+A*C*C*T*A*T*G*C*T*T*G*G*C*T*+ T*+C*+A | 13414 | 19 |
| 801 | AACCTATGCTTGGCT TCA | A57799Hi | +A*+A*+C*C*T*A*T*G*C*T*T*G*G*C*T*+T* +C*+A | 13414 | 18 |
| 802 | TGTAACCTATGCTTG GCT | A57800Hi | +T*+G*+T*A*A*C*C*T*A*T*G*C*T*T*T*G*+G* +C*+T | 13417 | 18 |
| 803 | GTAACCTATGCTTGG CT | A57801Hi | +G*+T*+A*A*C*C*T*A*T*G*C*T*T*T*G*+G*+C *+T | 13417 | 17 |
| 804 | GACTCAACATCATAA TCC | A57802Hi | +G*+A*+C*T*C*A*A*C*A*T*C*A*T*A*A*+T* +C*+C | 13438 | 18 |
| 805 | GACTAAACAAGGACT CCA | A57803Hi | +G*+A*+C*T*A*A*A*C*A*A*G*G*A*C*T*+C* +C*+A | 13591 | 18 |
| 806 | TCAATGGAAAGACTA AAC | A57804Hi | +T*+C*+A*A*T*G*G*A*A*A*G*A*A*C*T*A*+A* +A*+C | 13601 | 18 |
| 807 | GTCAATGGAAAGACT AAA | A57805Hi | +G*+T*+C*A*A*T*G*G*A*A*A*G*A*A*C*T*+A* +A*+A | 13602 | 18 |
| 808 | GCTCACTTCACTGCT GTGA | A57806Hi | +G*+C*+T*C*A*C*T*T*C*A*C*T*G*C*T*G*+ T*+G*+A | 13636 | 19 |
| 809 | AGGATGCTCACTTCA CTGC | A57807Hi | +A*+G*+G*A*T*G*C*T*C*A*C*T*T*C*A*C*+ T*+G*+C | 13641 | 19 |
| 810 | CAGGATGCTCACTTC ACTG | A57808Hi | +C*+A*+G*G*A*T*G*C*T*C*A*C*T*T*C*A*+ C*+T*+G | 13642 | 19 |
| 811 | ACTGTACTGTCACAA GCT | A57809Hi | +A*+C*+T*G*T*A*C*T*G*T*C*A*C*A*A*+G* +C*+T | 13674 | 18 |
| 812 | GAACTGTACTGTCAC AAGC | A57810Hi | +G*+A*+A*C*T*G*T*A*C*T*G*T*C*A*C*A*+ A*+G*+C | 13675 | 19 |
| 813 | TGAACTGTACTGTCA CAA | A57811Hi | +T*+G*+A*A*C*T*G*T*A*C*T*G*T*C*A*+C* +A*+A | 13677 | 18 |
| 814 | AATTGAACTGTACTG TCAC | A57812Hi | +A*+A*+T*T*G*A*A*C*T*G*T*A*C*T*G*T*+ C*+A*+C | 13679 | 19 |
| 815 | TAATTGAACTGTACT GTCA | A57813Hi | +T*+A*+A*T*T*G*A*A*C*T*G*T*A*C*T*G*+ T*+C*+A | 13680 | 19 |

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| 816 | CTAATTGAACTGTAC TGT | A57814Hi | +C*+T*+A*A*T*T*G*A*A*C*T*G*T*A*C*+T* +G*+T | 13682 | 18 |
| 817 | CTGGTAAACTGATAA CTGA | A57815Hi | +C*+T*+G*G*T*A*A*A*C*T*G*A*T*A*A*C*+ T*+G*+A | 13786 | 19 |
| 818 | GCACTCTAAGTGATC AAC | A57816Hi | +G*+C*+A*C*T*C*T*A*A*G*T*G*A*T*C*+A* +A*+C | 14813 | 18 |
| 819 | TAGTTTATCTAGCTT GAG | A57817Hi | +T*+A*+G*T*T*T*A*T*C*T*A*G*C*T*T*+G* +A*+G | 14861 | 18 |
| 820 | GATCAAGCCAGTAAG TTC | A57818Hi | +G*+A*+T*C*A*A*G*C*C*A*G*T*A*A*G*+T* +T*+C | 14931 | 18 |
| 821 | ATTTGATCAAGCCAG TAAG | A57819Hi | +A*+T*+T*T*G*A*T*C*A*A*G*C*C*A*G*T*+ A*+A*+G | 14934 | 19 |
| 822 | CATTTGATCAAGCCA GTAA | A57820Hi | +C*+A*+T*T*T*G*A*T*C*A*A*G*C*C*A*G*+ T*+A*+A | 14935 | 19 |
| 823 | AGTCATTTGATCAAG CCA | A57821Hi | +A*+G*+T*C*A*T*T*T*G*A*T*C*A*A*G*+C* +C*+A | 14939 | 18 |
| 824 | AAGTCATTTGATCAA GCCA | A57822Hi | +A*+A*+G*T*C*A*T*T*T*G*A*T*C*A*A*G*+ C*+C*+A | 14939 | 19 |
| 825 | AAAGTCATTTGATCA AGCC | A57823Hi | +A*+A*+A*G*T*C*A*T*T*T*G*A*T*C*A*A*+ G*+C*+C | 14940 | 19 |
| 826 | AATTAAAGTCATTTG ATCA | A57824Hi | +A*+A*+T*T*A*A*A*G*T*C*A*T*T*T*G*A*+ T*+C*+A | 14944 | 19 |
| 827 | CAATTAAAGTCATTT GATC | A57825Hi | +C*+A*+A*T*T*A*A*A*G*T*C*A*T*T*T*G*+ A*+T*+C | 14945 | 19 |
| 828 | GCAAATGGCAAGTAA TCAG | A57826Hi | +G*+C*+A*A*A*T*G*G*C*A*A*G*T*A*A*T*+ C*+A*+G | 15029 | 19 |
| 829 | GAGCAAATGGCAAGT AATC | A57827Hi | +G*+A*+G*C*A*A*A*T*G*G*C*A*A*G*T*A*+ A*+T*+C | 15031 | 19 |
| 830 | ACTTGAGCAAATGGC AAGT | A57828Hi | +A*+C*+T*T*G*A*G*C*A*A*A*T*G*G*C*A*+ A*+G*+T | 15035 | 19 |
| 831 | CTTGAGCAAATGGCA AGT | A57829Hi | +C*+T*+T*G*A*G*C*A*A*A*T*G*G*C*A*+A* +G*+T | 15035 | 18 |
| 832 | AACTTGAGCAAATGG CAAG | A57830Hi | +A*+A*+C*T*T*G*A*G*C*A*A*A*T*G*G*C*+ A*+A*+G | 15036 | 19 |
| 833 | TGTCAACTTGAGCAA ATGG | A57831Hi | +T*+G*+T*C*A*A*C*T*T*G*A*G*C*A*A*A*+ T*+G*+G | 15040 | 19 |
| 834 | GTCAACTTGAGCAAA TGG | A57832Hi | +G*+T*+C*A*A*C*T*T*G*A*G*C*A*A*A*+T* +G*+G | 15040 | 18 |
| 835 | AGTTGTCAACTTGAG CAAA | A57833Hi | +A*+G*+T*T*G*T*C*A*A*C*T*T*G*A*G*C*+ A*+A*+A | 15043 | 19 |
| 836 | AGAGTTGTCAACTTG AGCA | A57834Hi | +A*+G*+A*G*T*T*G*T*C*A*A*C*T*T*G*A*+ G*+C*+A | 15045 | 19 |
| 837 | TTCAGTTCAAGAGTT GTCA | A57835Hi | +T*+T*+C*A*G*T*T*C*A*A*G*A*G*T*T*G*+ T*+C*+A | 15054 | 19 |
| 838 | GTTTCAGTTCAAGAG TTGT | A57836Hi | +G*+T*+T*T*C*A*G*T*T*C*A*A*G*A*G*T*+ T*+G*+T | 15056 | 19 |
| 839 | CGGCTAAATGTTTCA GTT | A57837Hi | +C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*A*+G* +T*+T | 15066 | 18 |
| 840 | TCGGCTAAATGTTTC AGTT | A57838Hi | +T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*C*A*+ G*+T*+T | 15066 | 19 |
| 841 | CGGCTAAATGTTTCA GT | A57839Hi | +C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*+A*+G *+T | 15067 | 17 |
| 842 | CTCGGCTAAATGTTT CAGT | A57840Hi | +C*+T*+C*G*G*C*T*A*A*A*T*G*T*T*T*C*+ A*+G*+T | 15067 | 19 |
| 843 | CTCGGCTAAATGTTT CAG | A57841Hi | +C*+T*+C*G*G*C*T*A*A*A*T*G*T*T*T*+C* +A*+G | 15068 | 18 |
| 844 | TCGGCTAAATGTTTC AG | A57842Hi | +T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*+C*+A *+G | 15068 | 17 |
| 845 | GCATTAATGGTAGGC TGC | A57843Hi | +G*+C*+A*T*T*A*A*T*G*G*T*A*G*G*C*+T* +G*+C | 15096 | 18 |
| 846 | AGGCATTAATGGTAG GC | A57844Hi | +A*+G*+G*C*A*T*T*A*A*T*G*G*T*A*+G*+ G*+C | 15099 | 17 |
| 847 | CAGTGACTAATAAAG ATGG | A57845Hi | +C*+A*+G*T*G*A*C*T*A*A*T*A*A*A*G*A*+ T*+G*+G | 15153 | 19 |
| 848 | GACAGTGACTAATAA AGA | A57846Hi | +G*+A*+C*A*G*T*G*A*C*T*A*A*T*A*A*+A* +G*+A | 15156 | 18 |
| 849 | ATCTTTGTTCTCAACA AAT | A57847H | +A*+T*+C*T*T*T*G*T*T*C*T*C*A*A*C*A*+ A*+A*+T | 15509 | 19 |
| 850 | AATCTTTGTTCTCAAC AAA | A57848H | +A*+A*+T*C*T*T*T*T*G*T*T*C*T*C*A*A*C*+ A*+A*+A | 15510 | 19 |

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| 851 | AATCTTTGTTCTCAACAA | A57849H | +A*+A*+T*C*T*T*T*G*T*T*C*T*C*A*A*+C*+A*+A | 15511 | 18 |
| 852 | TAATCTTTGTTCTCAACAA | A57850H | +T*+A*+A*T*C*T*T*T*G*T*T*C*T*C*A*A*+C*+A*+A | 15511 | 19 |
| 853 | ATAATCTTTGTTCTCAACA | A57851H | +A*+T*+A*A*T*C*T*T*T*G*T*T*C*T*C*A*+A*+C*+A | 15512 | 19 |
| 854 | TATAATCTTTGTTCTCAAC | A57852H | +T*+A*+T*A*A*T*C*T*T*T*G*T*T*C*T*C*+A*+A*+C | 15513 | 19 |
| 855 | CATATAATCTTTGTTCTCA | A57853H | +C*+A*+T*A*T*A*A*T*C*T*T*T*G*T*T*C*+T*+C*+A | 15515 | 19 |
| 856 | TTAACAATATCATATAATC | A57854H | +T*+T*+A*A*C*A*A*T*A*T*C*A*T*A*T*A*+A*+T*+C | 15525 | 19 |
| 857 | GCACTTAACAATATCATAT | A57855H | +G*+C*+A*C*T*T*A*A*C*A*A*T*A*T*C*A*+T*+A*+T | 15529 | 19 |
| 858 | CGCACTTAACAATATCATA | A57856H | +C*+G*+C*A*C*T*T*A*A*C*A*A*T*A*T*C*+A*+T*+A | 15530 | 19 |
| 859 | CGCACTTAACAATATCAT | A57857H | +C*+G*+C*A*C*T*T*A*A*C*A*A*T*A*T*+C*+A*+T | 15531 | 18 |
| 860 | ACGCACTTAACAATATCAT | A57858H | +A*+C*+G*C*A*C*T*T*A*A*C*A*A*T*A*T*+C*+A*+T | 15531 | 19 |
| 861 | TTAACGCACTTAACAATAT | A57859H | +T*+T*+A*A*C*G*C*A*C*T*T*A*A*C*A*A*+T*+A*+T | 15534 | 19 |
| 862 | TTAACGCACTTAACAATA | A57860H | +T*+T*+A*A*C*G*C*A*C*T*T*A*A*C*A*+A*+T*+A | 15535 | 18 |
| 863 | GTTAACGCACTTAACAATA | A57861H | +G*+T*+T*A*A*C*G*C*A*C*T*T*A*A*C*A*+A*+T*+A | 15535 | 19 |
| 864 | TTAACGCACTTAACAAT | A57862H | +T*+T*+A*A*C*G*C*A*C*T*T*A*A*C*+A*+A*+T | 15536 | 17 |
| 865 | GTTAACGCACTTAACAAT | A57863H | +G*+T*+T*A*A*C*G*C*A*C*T*T*A*A*C*+A*+A*+T | 15536 | 18 |
| 866 | TGTTAACGCACTTAACAAT | A57864H | +T*+G*+T*T*A*A*C*G*C*A*C*T*T*A*A*C*+A*+A*+T | 15536 | 19 |
| 867 | TTTGTTAACGCACTTAACA | A57865H | +T*+T*+T*G*T*T*A*A*C*G*C*A*C*T*T*A*+A*+C*+A | 15538 | 19 |
| 868 | TTTGTTAACGCACTTAAC | A57866H | +T*+T*+T*G*T*T*A*A*C*G*C*A*C*T*T*+A*+A*+C | 15539 | 18 |
| 869 | ATTTGTTAACGCACTTAAC | A57867H | +A*+T*+T*T*G*T*T*A*A*C*G*C*A*C*T*T*+A*+A*+C | 15539 | 19 |
| 870 | AAATTTGTTAACGCACTTA | A57868H | +A*+A*+A*T*T*T*G*T*T*A*A*C*G*C*A*C*+T*+T*+A | 15541 | 19 |
| 871 | TTAAAATTTGTTAACGCAC | A57869H | +T*+T*+A*A*A*A*T*T*T*G*T*T*A*A*C*G*+C*+A*+C | 15544 | 19 |
| 872 | ATGAAGCACAATTTCCTCT | A57870H | +A*+T*+G*A*A*G*C*A*C*A*A*T*T*T*C*C*+T*+C*+T | 15569 | 19 |
| 873 | ACATGAAGCACAATTTCCT | A57871H | +A*+C*+A*T*G*A*A*G*C*A*C*A*A*T*T*T*+C*+C*+T | 15571 | 19 |
| 874 | AGGGAATGTAAACAATGCA | A57872H | +A*+G*+G*G*A*A*T*G*T*A*A*A*C*A*A*T*+G*+C*+A | 15592 | 19 |
| 875 | GCTAGGGAATGTAAACAAT | A57873H | +G*+C*+T*A*G*G*G*A*A*T*G*T*A*A*A*C*+A*+A*+T | 15595 | 19 |
| 876 | CCACAGCCAACTTCAGTAT | A57874Hi | +C*+C*+A*C*A*G*C*C*A*A*C*T*T*C*A*G*+T*+A*+T | 15781 | 19 |
| 877 | TTGTACTACAAGCTCTGAA | A57875Hi | +T*+T*+G*T*A*C*T*A*C*A*A*G*C*T*C*T*+G*+A*+A | 15851 | 19 |
| 878 | TTGTACTACAAGCTCTGA | A57876Hi | +T*+T*+G*T*A*C*T*A*C*A*A*G*C*T*C*+T*+G*+A | 15852 | 18 |
| 879 | GCAGTCTGCTCTCTCTTGC | A57877Hi | +G*+C*+A*G*T*C*T*G*C*T*C*T*C*T*C*T*C*T*+T*+G*+C | 16085 | 19 |
| 880 | GGCAGTCTGCTCTCTCTTG | A57878Hi | +G*+G*+C*A*G*T*C*T*G*C*T*C*T*C*T*C*+T*+T*+G | 16086 | 19 |
| 881 | GCAGTCTGCTCTCTCTTG | A57879Hi | +G*+C*+A*G*T*C*T*G*C*T*C*T*C*T*C*+T*+T*+G | 16086 | 18 |
| 882 | AGGCAGTCTGCTCTCTCTT | A57880Hi | +A*+G*+G*C*A*G*T*C*T*G*C*T*C*T*C*T*+C*+T*+T | 16087 | 19 |
| 883 | TTGAAGGCAGTCTGCTCTC | A57881Hi | +T*+T*+G*A*A*G*G*C*A*G*T*C*T*G*C*T*+C*+T*+C | 16091 | 19 |
| 884 | TTCTTGAAGGCAGTCTGCT | A57882Hi | +T*+T*+C*T*T*G*A*A*G*G*C*A*G*T*C*T*+G*+C*+T | 16094 | 19 |
| 885 | CTTCTTGAAGGCAGTCTGC | A57883Hi | +C*+T*+T*C*T*T*G*A*A*G*G*C*A*G*T*C*+T*+G*+C | 16095 | 19 |

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| 886 | TTCTTGAAGGCAGTC TGC | A57884Hi | +T*+T*+C*T*T*G*A*A*G*G*C*A*G*T*C*+T* +G*+C | 16095 | 18 |
| 887 | GTCTTCTTGAAGGCA GTCT | A57885Hi | +G*+T*+C*T*T*C*T*T*G*A*A*G*G*C*A*G*+ T*+C*+T | 16097 | 19 |
| 888 | TGTCTTCTTGAAGGC AGTC | A57886Hi | +T*+G*+T*C*T*T*C*T*T*G*A*A*G*G*C*A*+ G*+T*+C | 16098 | 19 |
| 889 | GTCTTCTTGAAGGCA GTC | A57887Hi | +G*+T*+C*T*T*C*T*T*G*A*A*G*G*C*A*+G* +T*+C | 16098 | 18 |
| 890 | TTGTCTTCTTGAAGG CAGT | A57888Hi | +T*+T*+G*T*C*T*T*C*T*T*G*A*A*G*G*C*+ A*+G*+T | 16099 | 19 |
| 891 | GCCTCTGTCAATGAA ACAC | A57889Hi | +G*+C*+C*T*C*T*G*T*C*A*A*T*G*A*A*A*+ C*+A*+C | 16211 | 19 |
| 892 | TGCCTCTGTCAATGA AACA | A57890Hi | +T*+G*+C*C*T*C*T*G*T*C*A*A*T*G*A*A*+ A*+C*+A | 16212 | 19 |
| 893 | CCACTCCATGTCTCT GGCC | A57891Hi | +C*+C*+A*C*T*C*C*A*T*G*T*C*T*C*T*G*+ G*+C*+C | 16261 | 19 |
| 894 | TCCACTCCATGTCTC TGGC | A57892Hi | +T*+C*+C*A*C*T*C*C*A*T*G*T*C*T*C*T*+ G*+G*+C | 16262 | 19 |
| 895 | TTCATGCTCTCCACT CCAT | A57893Hi | +T*+T*+C*A*T*G*C*T*C*T*C*C*A*C*T*C*+ C*+A*+T | 16271 | 19 |
| 896 | GTATATCCTGTAGAA ACC | A57894Hi | +G*+T*+A*T*A*T*C*C*T*G*T*A*G*A*A*+A* +C*+C | 16548 | 18 |
| 897 | TAAATGCATATGTAT ATCC | A57895Hi | +T*+A*+A*A*T*G*C*A*T*A*T*G*T*A*T*A*+ T*+C*+C | 16558 | 19 |
| 898 | CACATGTGTGAGGAT GAAA | A57896Hi | +C*+A*+C*A*T*G*T*G*T*G*A*G*G*A*T*G*+ A*+A*+A | 16588 | 19 |
| 899 | AATAATCCTGTCAGT GATT | A57897Hi | +A*+A*+T*A*A*T*C*C*T*G*T*C*A*G*T*G*+ A*+T*+T | 16661 | 19 |
| 900 | TAATAATCCTGTCAG TGA | A57898Hi | +T*+A*+A*T*A*A*T*C*C*T*G*T*C*A*G*+T* +G*+A | 16663 | 18 |
| 901 | GCAATTACATATAGT ATAC | A57899Hi | +G*+C*+A*A*T*T*A*C*A*T*A*T*A*G*T*A*+ T*+A*+C | 16707 | 19 |
| 902 | TGACACAGTGATTTC CATA | A57900Hi | +T*+G*+A*C*A*C*A*G*T*G*A*T*T*T*C*C*+ A*+T*+A | 16741 | 19 |
| 903 | TAATTTCCTGTGGAT AAGA | A57901Hi | +T*+A*+A*T*T*T*C*C*T*G*T*G*G*A*T*A*+ A*+G*+A | 16857 | 19 |
| 904 | TCTCTATTATTGTTCA GCC | A57902Hi | +T*+C*+T*C*T*A*T*T*A*T*T*G*T*T*C*A*+ G*+C*+C | 16895 | 19 |
| 905 | GGCCTTTCTCTATTAT TGT | A57903Hi | +G*+G*+C*C*T*T*T*C*T*C*T*A*T*T*A*T*+ T*+G*+T | 16901 | 19 |
| 906 | TGGCCTTTCTCTATTA TTG | A57904Hi | +T*+G*+G*C*C*T*T*T*C*T*C*T*A*T*T*A*+ T*+T*+G | 16902 | 19 |
| 907 | CAATAGACTTAAAGA CTG | A57905Hi | +C*+A*+A*T*A*G*A*C*T*T*A*A*A*G*A*+C* +T*+G | 17181 | 18 |
| 908 | ACAATAGACTTAAAG ACTG | A57906Hi | +A*+C*+A*A*T*A*G*A*C*T*T*A*A*A*G*A*+ C*+T*+G | 17181 | 19 |
| 909 | GCATCAAATGTTAAC TGTT | A57907Hi | +G*+C*+A*T*C*A*A*A*T*G*T*T*A*A*C*T*+ G*+T*+T | 17355 | 19 |
| 910 | AGCTTCCTGAAGGCT CCAA | A57908Hi | +A*+G*+C*T*T*C*C*T*G*A*A*G*G*C*T*C*+ C*+A*+A | 17548 | 19 |
| 911 | TCTTAACGAGGCTCA ACC | A57909Hi | +T*+C*+T*T*A*A*C*G*A*G*G*C*T*C*A*+A* +C*+C | 17716 | 18 |
| 912 | TTCTTAACGAGGCTC AACC | A57910Hi | +T*+T*+C*T*T*A*A*C*G*A*G*G*C*T*C*A*+ A*+C*+C | 17716 | 19 |
| 913 | TTCTTAACGAGGCTC AAC | A57911Hi | +T*+T*+C*T*T*A*A*C*G*A*G*G*C*T*C*+A* +A*+C | 17717 | 18 |
| 914 | GCTTAAAGCCTTAAG ATC | A57912Hi | +G*+C*+T*T*A*A*A*G*C*C*T*T*A*A*G*+A* +T*+C | 18299 | 18 |
| 915 | GGCTTAAAGCCTTAA GAT | A57913Hi | +G*+G*+C*T*T*A*A*A*G*C*C*T*T*A*A*+G* +A*+T | 18300 | 18 |
| 916 | TGGCTTAAAGCCTTA AGA | A57914Hi | +T*+G*+G*C*T*T*A*A*A*G*C*C*T*T*A*+A* +G*+A | 18301 | 18 |
| 917 | CTGTTTCTTGGCTTA AAGC | A57915Hi | +C*+T*+G*T*T*T*C*T*T*G*G*C*T*T*A*A*+ A*+G*+C | 18308 | 19 |
| 918 | CCAAATTTAAACATC ATGT | A57916Hi | +C*+C*+A*A*A*T*T*T*A*A*A*C*A*T*C*A*+ T*+G*+T | 18421 | 19 |
| 919 | TCCAAATTTAAACAT CATG | A57917Hi | +T*+C*+C*A*A*A*T*T*T*A*A*A*C*A*T*C*+ A*+T*+G | 18422 | 19 |
| 920 | AGATGGCAGCATAAT GAC | A57918Hi | +A*+G*+A*T*G*G*C*A*G*C*A*T*A*A*T*+G* +A*+C | 18447 | 18 |

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| 921 | ATAGATGGCAGCATAATG | A57919Hi | +A*+T*+A*G*A*T*G*G*C*A*G*C*A*T*A*+A*+T*+G | 18449 | 18 |
| 922 | TAAATAGATGGCAGCATAA | A57920Hi | +T*+A*+A*A*T*A*G*A*T*G*G*C*A*G*C*A*+T*+A*+A | 18451 | 19 |
| 923 | ATCATAATTATCAATAAGG | A57921Hi | +A*+T*+C*A*T*A*A*T*T*A*T*C*A*A*T*A*+A*+G*+G | 18521 | 19 |
| 924 | TCATGAGGACTTCCACATT | A57922H | +T*+C*+A*T*G*A*G*G*A*C*T*T*C*C*A*C*+A*+T*+T | 18559 | 19 |
| 925 | CTCATGAGGACTTCCACAT | A57923H | +C*+T*+C*A*T*G*A*G*G*A*C*T*T*C*C*A*+C*+A*+T | 18560 | 19 |
| 926 | CTCATGAGGACTTCCACA | A57924H | +C*+T*+C*A*T*G*A*G*G*A*C*T*T*C*C*+A*+C*+A | 18561 | 18 |
| 927 | ACTCATGAGGACTTCCACA | A57925H | +A*+C*+T*C*A*T*G*A*G*G*A*C*T*T*C*C*+A*+C*+A | 18561 | 19 |
| 928 | GCCACTCATGAGGACTTCC | A57926H | +G*+C*+C*A*C*T*C*A*T*G*A*G*G*A*C*T*+T*+C*+C | 18564 | 19 |
| 929 | ATTGCCACTCATGAGGACT | A57927H | +A*+T*+T*G*C*C*A*C*T*C*A*T*G*A*G*G*+A*+C*+T | 18567 | 19 |
| 930 | CATTGCCACTCATGAGGAC | A57928H | +C*+A*+T*T*G*C*C*A*C*T*C*A*T*G*A*G*+G*+A*+C | 18568 | 19 |
| 931 | TGACATTGCCACTCATGAG | A57929H | +T*+G*+A*C*A*T*T*G*C*C*A*C*T*C*A*T*+G*+A*+G | 18571 | 19 |
| 932 | CTGACATTGCCACTCATGA | A57930H | +C*+T*+G*A*C*A*T*T*G*C*C*A*C*T*C*A*+T*+G*+A | 18572 | 19 |
| 933 | CCTGACATTGCCACTCATG | A57931H | +C*+C*+T*G*A*C*A*T*T*G*C*C*A*C*T*C*+A*+T*+G | 18573 | 19 |
| 934 | ACCTGACATTGCCACTCAT | A57932H | +A*+C*+C*T*G*A*C*A*T*T*G*C*C*A*C*T*+C*+A*+T | 18574 | 19 |
| 935 | ACACCTGACATTGCCACTC | A57933H | +A*+C*+A*C*C*T*G*A*C*A*T*T*G*C*C*A*+C*+T*+C | 18576 | 19 |
| 936 | AACACCTGACATTGCCACT | A57934H | +A*+A*+C*A*C*C*T*G*A*C*A*T*T*G*C*C*+A*+C*+T | 18577 | 19 |
| 937 | TAACACCTGACATTGCCAC | A57935H | +T*+A*+A*C*A*C*C*T*G*A*C*A*T*T*G*C*+C*+A*+C | 18578 | 19 |
| 938 | ATAACACCTGACATTGCCA | A57936H | +A*+T*+A*A*C*A*C*C*T*G*A*C*A*T*T*G*+C*+C*+A | 18579 | 19 |
| 939 | ATTATAACACCTGACATTG | A57937H | +A*+T*+T*A*T*A*A*C*A*C*C*T*G*A*C*A*+T*+T*+G | 18582 | 19 |
| 940 | CACAATATTATAACACCTG | A57938H | +C*+A*+C*A*A*T*A*T*T*A*T*A*A*C*A*C*+C*+T*+G | 18588 | 19 |
| 941 | TCCACCACAATATTATAAC | A57939H | +T*+C*+C*A*C*C*A*C*A*A*T*A*T*T*A*T*+A*+A*+C | 18593 | 19 |
| 942 | CTTCCACCACAATATTATA | A57940H | +C*+T*+T*C*C*A*C*C*A*C*A*A*T*A*T*T*+A*+T*+A | 18595 | 19 |
| 943 | CTTCCACCACAATATTAT | A57941H | +C*+T*+T*C*C*A*C*C*A*C*A*A*T*A*T*+T*+A*+T | 18596 | 18 |
| 944 | GCTTCCACCACAATATTAT | A57942H | +G*+C*+T*T*C*C*A*C*C*A*C*A*A*T*A*T*+T*+A*+T | 18596 | 19 |
| 945 | GCTTCCACCACAATATTA | A57943H | +G*+C*+T*T*C*C*A*C*C*A*C*A*A*T*A*+T*+T*+A | 18597 | 18 |
| 946 | AGCTTCCACCACAATATTA | A57944H | +A*+G*+C*T*T*C*C*A*C*C*A*C*A*A*T*A*+T*+T*+A | 18597 | 19 |
| 947 | CATAGCTTCCACCACAATA | A57945H | +C*+A*+T*A*G*C*T*T*C*C*A*C*C*A*C*A*+A*+T*+A | 18600 | 19 |
| 948 | TCATAGCTTCCACCACAAT | A57946H | +T*+C*+A*T*A*G*C*T*T*C*C*A*C*C*A*C*+A*+A*+T | 18601 | 19 |
| 949 | TTCATAGCTTCCACCACAA | A57947H | +T*+T*+C*A*T*A*G*C*T*T*C*C*A*C*C*A*+C*+A*+A | 18602 | 19 |
| 950 | AATGCTTTCATAGCTTCCA | A57948H | +A*+A*+T*G*C*T*T*T*C*A*T*A*G*C*T*T*+C*+C*+A | 18608 | 19 |
| 951 | GAATGCTTTCATAGCTTCC | A57949H | +G*+A*+A*T*G*C*T*T*T*C*A*T*A*G*C*T*+T*+C*+C | 18609 | 19 |
| 952 | GGAATGCTTTCATAGCTTC | A57950H | +G*+G*+A*A*T*G*C*T*T*T*C*A*T*A*G*C*+T*+T*+C | 18610 | 19 |
| 953 | AGGGAATGCTTTCATAGCT | A57951H | +A*+G*+G*G*A*A*T*G*C*T*T*T*C*A*T*A*+G*+C*+T | 18612 | 19 |
| 954 | GCAAACAGCAACTCACTTC | A57952H | +G*+C*+A*A*A*C*A*G*C*A*A*C*T*C*A*C*+T*+T*+C | 18649 | 19 |
| 955 | GCAAACAGCAACTCACTT | A57953H | +G*+C*+A*A*A*C*A*G*C*A*A*C*T*C*A*+C*+T*+T | 18650 | 18 |

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| 956 | AGCAAACAGCAACTC ACTT | A57954H | +A*+G*+C*A*A*A*C*A*G*C*A*A*C*T*C*A*+ C*+T*+T | 18650 | 19 |
| 957 | GGAGCAAACAGCAAC TCAC | A57955H | +G*+G*+A*G*C*A*A*A*C*A*G*C*A*A*C*T*+ C*+A*+C | 18652 | 19 |
| 958 | CTATGGAGCAAACAG CAAC | A57956H | +C*+T*+A*T*G*G*A*G*C*A*A*A*C*A*G*C*+ A*+A*+C | 18656 | 19 |
| 959 | TAAGCCTATGGAGCA AACA | A57957H | +T*+A*+A*G*C*C*T*A*T*G*G*A*G*C*A*A*+ A*+C*+A | 18661 | 19 |
| 960 | TAAGCCTATGGAGCA AAC | A57958H | +T*+A*+A*G*C*C*T*A*T*G*G*A*G*C*A*+A* +A*+C | 18662 | 18 |
| 961 | GTAAGCCTATGGAGC AAAC | A57959H | +G*+T*+A*A*G*C*C*T*A*T*G*G*A*G*C*A*+ A*+A*+C | 18662 | 19 |
| 962 | TAATGTAAGCCTATG GAGC | A57960H | +T*+A*+A*T*G*T*A*A*G*C*C*T*A*T*G*G*+ A*+G*+C | 18666 | 19 |
| 963 | CTAATGTAAGCCTAT GGAG | A57961H | +C*+T*+A*A*T*G*T*A*A*G*C*C*T*A*T*G*+ G*+A*+G | 18667 | 19 |
| 964 | TATGTCAATATGCTA CTTA | A57962Hi | +T*+A*+T*G*T*C*A*A*T*A*T*G*C*T*A*C*+ T*+T*+A | 18769 | 19 |
| 965 | AGTATGTCAATATGC TACT | A57963Hi | +A*+G*+T*A*T*G*T*C*A*A*T*A*T*G*C*T*+ A*+C*+T | 18771 | 19 |
| 966 | TGTTAACCTCTATAG AGAA | A57964Hi | +T*+G*+T*T*A*A*C*C*T*C*T*A*T*A*G*A*+ G*+A*+A | 19145 | 19 |
| 967 | GTTAACCTCTATAGA GAA | A57965Hi | +G*+T*+T*A*A*C*C*T*C*T*A*T*A*G*A*+G* +A*+A | 19145 | 18 |
| 968 | TGTTAACCTCTATAG AGA | A57966Hi | +T*+G*+T*T*A*A*C*C*T*C*T*A*T*A*G*+A* +G*+A | 19146 | 18 |
| 969 | GTGTTAACCTCTATA GAG | A57967Hi | +G*+T*+G*T*T*A*A*C*C*T*C*T*A*T*A*+G* +A*+G | 19147 | 18 |
| 970 | GATAGTGTTAACCTC TAT | A57968Hi | +G*+A*+T*A*G*T*G*T*T*A*A*C*C*T*C*+T* +A*+T | 19151 | 18 |
| 971 | TGGATAGTGTTAACC TCTA | A57969Hi | +T*+G*+G*A*T*A*G*T*G*T*T*A*A*C*C*T*+ C*+T*+A | 19152 | 19 |
| 972 | ACAGATAGTAGTAGC ATAA | A57970Hi | +A*+C*+A*G*A*T*A*G*T*A*G*T*A*G*C*A*+ T*+A*+A | 19442 | 19 |
| 973 | TCACAAAGGAACTGA TTAT | A57971Hi | +T*+C*+A*C*A*A*A*G*G*A*A*C*T*G*A*T*+ T*+A*+T | 20096 | 19 |
| 974 | AACTAGCTCTCCACA CTG | A57972Hi | +A*+A*+C*T*A*G*C*T*C*T*C*C*A*C*A*+C* +T*+G | 20266 | 18 |
| 975 | ATGGTAACTAGCTCT CCA | A57973Hi | +A*+T*+G*G*T*A*A*C*T*A*G*C*T*C*T*+C* +C*+A | 20271 | 18 |
| 976 | TGATGGTAACTAGCT CTC | A57974Hi | +T*+G*+A*T*G*G*T*A*A*C*T*A*G*C*T*+C* +T*+C | 20273 | 18 |
| 977 | GTGAACCTCTAATAA ATTG | A57975Hi | +G*+T*+G*A*A*C*C*T*C*T*A*A*T*A*A*A*+ T*+T*+G | 20296 | 19 |
| 978 | GAAACAGGTGAACCT CTAA | A57976Hi | +G*+A*+A*A*C*A*G*G*T*G*A*A*C*C*T*C*+ T*+A*+A | 20303 | 19 |
| 979 | AGACAAATCAGATTA ATGC | A57977Hi | +A*+G*+A*C*A*A*A*T*C*A*G*A*T*T*A*A*+ T*+G*+C | 20386 | 19 |
| 980 | CAGACAAATCAGATT AATG | A57978Hi | +C*+A*+G*A*C*A*A*A*T*C*A*G*A*T*T*A*+ A*+T*+G | 20387 | 19 |
| 981 | GATTCAGACAAATCA GATT | A57979Hi | +G*+A*+T*T*C*A*G*A*C*A*A*A*T*C*A*G*+ A*+T*+T | 20391 | 19 |
| 982 | AAGGCAAGCTGTGCC TAAA | A57980Hi | +A*+A*+G*G*C*A*A*G*C*T*G*T*G*C*C*T*+ A*+A*+A | 20509 | 19 |
| 983 | AAAGGCAAGCTGTGC CTAA | A57981Hi | +A*+A*+A*G*G*C*A*A*G*C*T*G*T*G*C*C*+ T*+A*+A | 20510 | 19 |
| 984 | AAGGCAAGCTGTGCC TAA | A57982Hi | +A*+A*+G*G*C*A*A*G*C*T*G*T*G*C*C*+T* +A*+A | 20510 | 18 |
| 985 | AGAGTTTAGAAAGGT AGGT | A57983Hi | +A*+G*+A*G*T*T*T*A*G*A*A*A*G*G*T*A*+ G*+G*+T | 20812 | 19 |
| 986 | GAACTCAGACTGTCA TTAT | A57984Hi | +G*+A*+A*C*T*C*A*G*A*C*T*G*T*C*A*T*+ T*+A*+T | 20899 | 19 |
| 987 | GAACTCAGACTGTCA TTA | A57985Hi | +G*+A*+A*C*T*C*A*G*A*C*T*G*T*C*A*+T* +T*+A | 20900 | 18 |
| 988 | CTGTAGATGTATTTC TTCA | A57986Hi | +C*+T*+G*T*A*G*A*T*G*T*A*T*T*T*C*T*+ T*+C*+A | 21288 | 19 |
| 989 | AAACCTGTAGATGTA TTTC | A57987Hi | +A*+A*+A*C*C*T*G*T*A*G*A*T*G*T*A*T*+ T*+T*+C | 21292 | 19 |
| 990 | TAAATTTATCAGGAA GTGC | A57988Hi | +T*+A*+A*A*T*T*T*A*T*C*A*G*G*A*A*G*+ T*+G*+C | 21330 | 19 |

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| 991 | TTAAATTTATCAGGAAGTG | A57989Hi | +T*+T*+A*A*A*T*T*T*A*T*C*A*G*G*A*A*+G*+T*+G | 21331 | 19 |
| 992 | AAATAGCCATGTATTAATC | A57990Hi | +A*+A*+A*T*A*G*C*C*A*T*G*T*A*T*T*A*+A*+T*+C | 21495 | 19 |
| 993 | GCAGTTGGTTTAGACTCC | A57991Hi | +G*+C*+A*G*T*T*G*G*T*T*T*A*G*A*C*+T*+C*+C | 21551 | 18 |
| 994 | AGCAGTTGGTTTAGACTCC | A57992Hi | +A*+G*+C*A*G*T*T*G*G*T*T*T*A*G*A*C*+T*+C*+C | 21551 | 19 |
| 995 | AGAAGCAGTTGGTTTAGAC | A57993Hi | +A*+G*+A*A*G*C*A*G*T*T*G*G*T*T*T*A*+G*+A*+C | 21554 | 19 |
| 996 | TAGAAGCAGTTGGTTTAGA | A57994Hi | +T*+A*+G*A*A*G*C*A*G*T*T*G*G*T*T*T*+A*+G*+A | 21555 | 19 |
| 997 | TAGAAGCAGTTGGTTTAG | A57995Hi | +T*+A*+G*A*A*G*C*A*G*T*T*G*G*T*T*+T*+A*+G | 21556 | 18 |
| 998 | CTAGAAGCAGTTGGTTTA | A57996Hi | +C*+T*+A*G*A*A*G*C*A*G*T*T*G*G*T*+T*+T*+A | 21557 | 18 |
| 999 | GTCAGCCTAGAAGCAGTTG | A57997Hi | +G*+T*+C*A*G*C*C*T*A*G*A*A*G*C*A*G*+T*+T*+G | 21562 | 19 |
| 1000 | AGTCAGCCTAGAAGCAGTT | A57998Hi | +A*+G*+T*C*A*G*C*C*T*A*G*A*A*G*C*A*+G*+T*+T | 21563 | 19 |
| 1001 | GTCAGCCTAGAAGCAGTT | A57999Hi | +G*+T*+C*A*G*C*C*T*A*G*A*A*G*C*A*+G*+T*+T | 21563 | 18 |
| 1002 | GCAGTCAGCCTAGAAGCA | A571000Hi | +G*+C*+A*G*T*C*A*G*C*C*T*A*G*A*A*+G*+C*+A | 21566 | 18 |
| 1003 | AATTTAAGTCCTCAGGATG | A571001Hi | +A*+A*+T*T*T*A*A*G*T*C*C*T*C*A*G*G*+A*+T*+G | 21640 | 19 |
| 1004 | TAATTTAAGTCCTCAGGAT | A571002Hi | +T*+A*+A*T*T*T*A*A*G*T*C*C*T*C*A*G*+G*+A*+T | 21641 | 19 |
| 1005 | CTTTAATTTAAGTCCTCAG | A571003Hi | +C*+T*+T*T*A*A*T*T*T*A*A*G*T*C*C*T*+C*+A*+G | 21644 | 19 |
| 1006 | CATCTTTAATTTAAGTCCT | A571004Hi | +C*+A*+T*C*T*T*T*A*A*T*T*T*A*A*G*T*+C*+C*+T | 21647 | 19 |
| 1007 | AGCATCTTTAATTTAAGTC | A571005Hi | +A*+G*+C*A*T*C*T*T*T*A*A*T*T*T*A*A*+G*+T*+C | 21649 | 19 |
| 1008 | AGCATCTTTAATTTAAGT | A571006Hi | +A*+G*+C*A*T*C*T*T*T*A*A*T*T*T*A*+A*+G*+T | 21650 | 18 |
| 1009 | CTCTGAAAGAGCATCTTTA | A571007Hi | +C*+T*+C*T*G*A*A*A*G*A*G*C*A*T*C*T*+T*+T*+A | 21658 | 19 |
| 1010 | TCAGTCCTGTGCTCTGACT | A571008Hi | +T*+C*+A*G*T*C*C*T*G*T*G*C*T*C*T*G*+A*+C*+T | 21689 | 19 |
| 1011 | GACTCTCTGCAAGGTAAGG | A571009Hi | +G*+A*+C*T*C*T*C*T*G*C*A*A*G*G*T*A*+A*+G*+G | 21763 | 19 |
| 1012 | TTCAGACTCTCTGCAAGGT | A571010Hi | +T*+T*+C*A*G*A*C*T*C*T*C*T*G*C*A*A*+G*+G*+T | 21767 | 19 |
| 1013 | AGCTGTGAGTTGAACGCC | A571011Hi | +A*+G*+C*T*G*T*G*A*G*T*T*G*A*A*C*+G*+C*+C | 21839 | 18 |
| 1014 | GAGCTGTGAGTTGAACGC | A571012Hi | +G*+A*+G*C*T*G*T*G*A*G*T*T*G*A*A*+C*+G*+C | 21840 | 18 |
| 1015 | AAACAAGAGCTGTGAGTTG | A571013Hi | +A*+A*+A*C*A*A*G*A*G*C*T*G*T*G*A*G*+T*+T*+G | 21845 | 19 |
| 1016 | AACAAGAGCTGTGAGTTG | A571014Hi | +A*+A*+C*A*A*G*A*G*C*T*G*T*G*A*G*+T*+T*+G | 21845 | 18 |
| 1017 | GCATTGTTGTCCTCACAAA | A571015Hi | +G*+C*+A*T*T*G*T*T*G*T*C*C*T*C*A*C*+A*+A*+A | 21924 | 19 |
| 1018 | AAATATTCCTGGTTATCCT | A571016Hi | +A*+A*+A*T*A*T*T*C*C*T*G*G*T*T*A*T*+C*+C*+T | 22024 | 19 |
| 1019 | GCCTATTATAATAATCCTA | A571017Hi | +G*+C*+C*T*A*T*T*A*T*A*A*T*A*A*T*C*+C*+T*+A | 22053 | 19 |
| 1020 | GGATATAATCATGATACTA | A571018Hi | +G*+G*+A*T*A*T*A*A*T*C*A*T*G*A*T*A*+C*+T*+A | 22170 | 19 |
| 1021 | GGATATAATCATGATACT | A571019Hi | +G*+G*+A*T*A*T*A*A*T*C*A*T*G*A*T*+A*+C*+T | 22171 | 18 |
| 1022 | CAAGTTGTAACTTGACTGT | A571020Hi | +C*+A*+A*G*T*T*G*T*A*A*C*T*T*G*A*C*+T*+G*+T | 23204 | 19 |
| 1023 | CAAGTTGTAACTTGACTG | A571021Hi | +C*+A*+A*G*T*T*G*T*A*A*C*T*T*G*A*+C*+T*+G | 23205 | 18 |
| 1024 | GCAAGTTGTAACTTGAC | A571022Hi | +G*+C*+A*A*G*T*T*G*T*A*A*C*T*T*+G*+A*+C | 23207 | 17 |
| 1025 | TGCAAGTTGTAACTTGAC | A571023Hi | +T*+G*+C*A*A*G*T*T*G*T*A*A*C*T*T*+G*+A*+C | 23207 | 18 |

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| 1026 | TAATGTAACATGTGC AAGT | A571024Hi | +T*+A*+A*T*G*T*A*A*C*A*T*G*T*G*C*A*+ A*+G*+T | 23218 | 19 |
| 1027 | TTGGCAGTCAAGTAG CATT | A571025Hi | +T*+T*+G*G*C*A*G*T*C*A*A*G*T*A*G*C*+ A*+T*+T | 23306 | 19 |
| 1028 | ATTTGGCAGTCAAGT AGCA | A571026Hi | +A*+T*+T*T*G*G*C*A*G*T*C*A*A*G*T*A*+ G*+C*+A | 23308 | 19 |
| 1029 | CAATTTGGCAGTCAA GTAG | A571027Hi | +C*+A*+A*T*T*T*G*G*C*A*G*T*C*A*A*G*+ T*+A*+G | 23310 | 19 |
| 1030 | ACCAGCTTGTCTAAA CTTG | A571028Hi | +A*+C*+C*A*G*C*T*T*G*T*C*T*A*A*A*C*+ T*+T*+G | 23833 | 19 |
| 1031 | ACCAGCTTGTCTAAA CTT | A571029Hi | +A*+C*+C*A*G*C*T*T*G*T*C*T*A*A*A*+C* +T*+T | 23834 | 18 |
| 1032 | TTACCAGCTTGTCTA AAC | A571030Hi | +T*+T*+A*C*C*A*G*C*T*T*G*T*C*T*A*+A* +A*+C | 23836 | 18 |
| 1033 | TTTACCAGCTTGTCT AAAC | A571031Hi | +T*+T*+T*A*C*C*A*G*C*T*T*G*T*C*T*A*+ A*+A*+C | 23836 | 19 |
| 1034 | AGCTCCTTTACCAAC ACCT | A571032Hi | +A*+G*+C*T*C*C*T*T*T*A*C*C*A*A*C*A*+ C*+C*+T | 23951 | 19 |
| 1035 | GAGCTCCTTTACCAA CACC | A571033Hi | +G*+A*+G*C*T*C*C*T*T*T*A*C*C*A*A*C*+ A*+C*+C | 23952 | 19 |
| 1036 | AGCTCCTTTACCAAC ACC | A571034Hi | +A*+G*+C*T*C*C*T*T*T*A*C*C*A*A*C*+A* +C*+C | 23952 | 18 |
| 1037 | GGAGCTCCTTTACCA ACAC | A571035Hi | +G*+G*+A*G*C*T*C*C*T*T*T*A*C*C*A*A*+ C*+A*+C | 23953 | 19 |
| 1038 | GAGCTCCTTTACCAA CAC | A571036Hi | +G*+A*+G*C*T*C*C*T*T*T*A*C*C*A*A*+C* +A*+C | 23953 | 18 |
| 1039 | TGGAGCTCCTTTACC AACA | A571037Hi | +T*+G*+G*A*G*C*T*C*C*T*T*T*A*C*C*A*+ A*+C*+A | 23954 | 19 |
| 1040 | ATGGAGCTCCTTTAC CAAC | A571038Hi | +A*+T*+G*G*A*G*C*T*C*C*T*T*T*A*C*C*+ A*+A*+C | 23955 | 19 |
| 1041 | TGGAGCTCCTTTACC AAC | A571039Hi | +T*+G*+G*A*G*C*T*C*C*T*T*T*A*C*C*+A* +A*+C | 23955 | 18 |
| 1042 | TATGGAGCTCCTTTA CCAA | A571040Hi | +T*+A*+T*G*G*A*G*C*T*C*C*T*T*T*A*C*+ C*+A*+A | 23956 | 19 |
| 1043 | ATGGAGCTCCTTTAC CAA | A571041Hi | +A*+T*+G*G*A*G*C*T*C*C*T*T*T*A*C*+C* +A*+A | 23956 | 18 |
| 1044 | AACGGCCTCACAATC AAA | A571042Hi | +A*+A*+C*G*G*C*C*T*C*A*C*A*A*T*C*+A* +A*+A | 23991 | 18 |
| 1045 | TCAACGGCCTCACAA TCA | A571043Hi | +T*+C*+A*A*C*G*G*C*C*T*C*A*C*A*A*+T* +C*+A | 23993 | 18 |
| 1046 | TCAACGGCCTCACAA TC | A571044Hi | +T*+C*+A*A*C*G*G*C*C*T*C*A*C*A*+A*+T *+C | 23994 | 17 |
| 1047 | TCATCAACGGCCTCA CAA | A571045Hi | +T*+C*+A*T*C*A*A*C*G*G*C*C*T*C*A*+C* +A*+A | 23996 | 18 |
| 1048 | TTCATCAACGGCCTC ACA | A571046Hi | +T*+T*+C*A*T*C*A*A*C*G*G*C*C*T*C*+A* +C*+A | 23997 | 18 |
| 1049 | TATTCATCAACGGCC TCA | A571047Hi | +T*+A*+T*T*C*A*T*C*A*A*C*G*G*C*C*+T* +C*+A | 23999 | 18 |
| 1050 | TATTCATCAACGGCC TC | A571048Hi | +T*+A*+T*T*C*A*T*C*A*A*C*G*G*C*+C*+T *+C | 24000 | 17 |
| 1051 | ATATTCATCAACGGC CT | A571049Hi | +A*+T*+A*T*T*C*A*T*C*A*A*C*G*G*+C*+C *+T | 24001 | 17 |
| 1052 | AATATTCATCAACGG CCT | A571050Hi | +A*+A*+T*A*T*T*C*A*T*C*A*A*C*G*G*+C* +C*+T | 24001 | 18 |
| 1053 | AAGTGATCTCTGAGA TACA | A571051Hi | +A*+A*+G*T*G*A*T*C*T*C*T*G*A*G*A*T*+ A*+C*+A | 24071 | 19 |
| 1054 | ACTAAGTGATCTCTG AGAT | A571052Hi | +A*+C*+T*A*A*G*T*G*A*T*C*T*C*T*G*A*+ G*+A*+T | 24074 | 19 |
| 1055 | AGTGTAACTAAGTGA TCTC | A571053Hi | +A*+G*+T*G*T*A*A*C*T*A*A*G*T*G*A*T*+ C*+T*+C | 24080 | 19 |
| 1056 | CTATAAGTGTAACTA AG | A571054Hi | +C*+T*+A*T*A*A*G*T*G*T*A*A*C*T*+A*+A *+G | 24087 | 17 |
| 1057 | TCTATAAGTGTAACT AAG | A571055Hi | +T*+C*+T*A*T*A*A*G*T*G*T*A*A*C*T*+A* +A*+G | 24087 | 18 |
| 1058 | GTCTAAATCCTTATG AGGA | A571056Hi | +G*+T*+C*T*A*A*A*T*C*C*T*T*A*T*G*A*+ G*+G*+A | 24217 | 19 |
| 1059 | CTTCTGAGAATTAAT ATGA | A571057Hi | +C*+T*+T*C*T*G*A*G*A*A*T*T*A*A*T*A*+ T*+G*+A | 24245 | 19 |
| 1060 | TATTTCACCACCTCC AACC | A571058Hi | +T*+A*+T*T*T*C*A*C*C*A*C*C*T*C*C*A*+ A*+C*+C | 24302 | 19 |

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| 1061 | GTCTATGATGATCTC AGAA | A571059Hi | +G*+T*+C*T*A*T*G*A*T*G*A*T*C*T*C*A*+ G*+A*+A | 24336 | 19 |
| 1062 | TGTCTATGATGATCT CAGA | A571060Hi | +T*+G*+T*C*T*A*T*G*A*T*G*A*T*C*T*C*+ A*+G*+A | 24337 | 19 |
| 1063 | GATCTTGTCTATGAT GATC | A571061Hi | +G*+A*+T*C*T*T*G*T*C*T*A*T*G*A*T*G*+ A*+T*+C | 24342 | 19 |
| 1064 | TCACTTAAAGGAATA GTG | A571062Hi | +T*+C*+A*C*T*T*A*A*A*G*G*A*A*T*A*+G* +T*+G | 24395 | 18 |
| 1065 | GTTAAATTACCTTTAA CAT | A571063Hi | +G*+T*+T*A*A*A*T*T*A*C*C*T*T*T*A*A*+ C*+A*+T | 24768 | 19 |
| 1066 | CATCCATGGAAGTTA AATT | A571064Hi | +C*+A*+T*C*C*A*T*G*G*A*A*G*T*T*A*A*+ A*+T*+T | 24779 | 19 |
| 1067 | CGTTTAATACCAGGA TATT | A571065H | +C*+G*+T*T*T*A*A*T*A*C*C*A*G*G*A*T*+ A*+T*+T | 24841 | 19 |
| 1068 | CGTTTAATACCAGGA TAT | A571066H | +C*+G*+T*T*T*A*A*T*A*C*C*A*G*G*A*+T* +A*+T | 24842 | 18 |
| 1069 | TCGTTTAATACCAGG ATAT | A571067H | +T*+C*+G*T*T*T*A*A*T*A*C*C*A*G*G*A*+ T*+A*+T | 24842 | 19 |
| 1070 | CGTTTAATACCAGGA TA | A571068H | +C*+G*+T*T*T*A*A*T*A*C*C*A*G*G*+A*+T *+A | 24843 | 17 |
| 1071 | TCGTTTAATACCAGG ATA | A571069H | +T*+C*+G*T*T*T*A*A*T*A*C*C*A*G*G*+A* +T*+A | 24843 | 18 |
| 1072 | TTCGTTTAATACCAG GATA | A571070H | +T*+T*+C*G*T*T*T*A*A*T*A*C*C*A*G*G*+ A*+T*+A | 24843 | 19 |
| 1073 | CTTCGTTTAATACCA GGAT | A571071H | +C*+T*+T*C*G*T*T*T*A*A*T*A*C*C*A*G*+ G*+A*+T | 24844 | 19 |
| 1074 | GACTTCGTTTAATAC CAGG | A571072H | +G*+A*+C*T*T*C*G*T*T*T*A*A*T*A*C*C*+ A*+G*+G | 24846 | 19 |
| 1075 | GGACTTCGTTTAATA CCA | A571073H | +G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*A*+C* +C*+A | 24848 | 18 |
| 1076 | TGGACTTCGTTTAAT ACCA | A571074H | +T*+G*+G*A*C*T*T*C*G*T*T*T*A*A*T*A*+ C*+C*+A | 24848 | 19 |
| 1077 | GGACTTCGTTTAATA CC | A571075H | +G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*+A*+C *+C | 24849 | 17 |
| 1078 | TGGACTTCGTTTAAT ACC | A571076H | +T*+G*+G*A*C*T*T*C*G*T*T*T*A*A*T*+A* +C*+C | 24849 | 18 |
| 1079 | CATGGACTTCGTTTA ATAC | A571077H | +C*+A*+T*G*G*A*C*T*T*C*G*T*T*T*A*A*+ T*+A*+C | 24850 | 19 |
| 1080 | CATGGACTTCGTTTA ATA | A571078H | +C*+A*+T*G*G*A*C*T*T*C*G*T*T*T*A*+A* +T*+A | 24851 | 18 |
| 1081 | TCATGGACTTCGTTT AATA | A571079H | +T*+C*+A*T*G*G*A*C*T*T*C*G*T*T*T*A*+ A*+T*+A | 24851 | 19 |
| 1082 | TCATGGACTTCGTTT AAT | A571080H | +T*+C*+A*T*G*G*A*C*T*T*C*G*T*T*T*+A* +A*+T | 24852 | 18 |
| 1083 | GCACAGCTTTCACCA CAAA | A571081H | +G*+C*+A*C*A*G*C*T*T*T*C*A*C*C*A*C*+ A*+A*+A | 24871 | 19 |
| 1084 | CCAAACAGCTGAGCG CTGA | A571082H | +C*+C*+A*A*A*C*A*G*C*T*G*A*G*C*G*C*+ T*+G*+A | 24922 | 19 |
| 1085 | CCAAACAGCTGAGCG CTG | A571083H | +C*+C*+A*A*A*C*A*G*C*T*G*A*G*C*G*+C* +T*+G | 24923 | 18 |
| 1086 | GCCAAACAGCTGAGC GCTG | A571084H | +G*+C*+C*A*A*A*C*A*G*C*T*G*A*G*C*G* +C*+T*+G | 24923 | 19 |
| 1087 | GGGCCAAACAGCTGA GCGC | A571085H | +G*+G*+G*C*C*A*A*A*C*A*G*C*T*G*A*G* +C*+G*+C | 24925 | 19 |
| 1088 | GGGCCAAACAGCTGA GCG | A571086H | +G*+G*+G*C*C*A*A*A*C*A*G*C*T*G*A*+G *+C*+G | 24926 | 18 |
| 1089 | AGGGCCAAACAGCTG AGCG | A571087H | +A*+G*+G*G*C*C*A*A*A*C*A*G*C*T*G*A* +G*+C*+G | 24926 | 19 |
| 1090 | TGATTCTCTTGTTACA ATG | A571088Hi | +T*+G*+A*T*T*C*T*C*T*T*G*T*T*A*C*A*+ A*+T*+G | 25007 | 19 |
| 1091 | ATGATTCTCTTGTTAC AAT | A571089Hi | +A*+T*+G*A*T*T*C*T*C*T*T*G*T*T*A*C*+ A*+A*+T | 25008 | 19 |
| 1092 | ATGATTCTCTTGTTAC AA | A571090Hi | +A*+T*+G*A*T*T*C*T*C*T*T*G*T*T*A*+C* +A*+A | 25009 | 18 |
| 1093 | TATGATTCTCTTGTTA CAA | A571091Hi | +T*+A*+T*G*A*T*T*C*T*C*T*T*G*T*T*A*+ C*+A*+A | 25009 | 19 |
| 1094 | ATATGATTCTCTTGTT ACA | A571092Hi | +A*+T*+A*T*G*A*T*T*C*T*C*T*T*G*T*T*+ A*+C*+A | 25010 | 19 |
| 1095 | ACATATGATTCTCTT GTTA | A571093Hi | +A*+C*+A*T*A*T*G*A*T*T*C*T*C*T*T*T*G*+ T*+T*+A | 25012 | 19 |

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| 1096 | GTACATATGATTCTC TTGT | A571094Hi | +G*+T*+A*C*A*T*A*T*G*A*T*T*C*T*C*T*+ T*+G*+T | 25014 | 19 |
| 1097 | CCATCTGTACATATG ATTC | A571095Hi | +C*+C*+A*T*C*T*G*T*A*C*A*T*A*T*G*A*+ T*+T*+C | 25020 | 19 |
| 1098 | CAAGAATGATGTAAA GCAA | A571096Hi | +C*+A*+A*G*A*A*T*G*A*T*G*T*A*A*A*G*+ C*+A*+A | 25143 | 19 |
| 1099 | GACAAAGCTAAATCA AGAA | A571097Hi | +G*+A*+C*A*A*A*G*C*T*A*A*A*T*C*A*A*+ G*+A*+A | 25156 | 19 |
| 1100 | GCTGCTTAATGACAA AGCT | A571098Hi | +G*+C*+T*G*C*T*T*A*A*T*G*A*C*A*A*A*+ G*+C*+T | 25166 | 19 |
| 1101 | CCTTGGTCAATTATA AAGA | A571099Hi | +C*+C*+T*T*G*G*T*C*A*A*T*T*A*T*A*A*+ A*+G*+A | 26097 | 19 |
| 1102 | AGAATGAGGTGTGCT TTAG | A571100Hi | +A*+G*+A*A*T*G*A*G*G*T*G*T*G*C*T*T*+ T*+A*+G | 26122 | 19 |
| 1103 | GAATGAGGTGTGCTT TAG | A571101Hi | +G*+A*+A*T*G*A*G*G*T*G*T*G*C*T*T*+T* +A*+G | 26122 | 18 |
| 1104 | AACAGAATGAGGTGT GCTT | A571102Hi | +A*+A*+C*A*G*A*A*T*G*A*G*G*T*G*T*G*+ C*+T*+T | 26125 | 19 |
| 1105 | CAACAGAATGAGGTG TGCT | A571103Hi | +C*+A*+A*C*A*G*A*A*T*G*A*G*G*T*G*T*+ G*+C*+T | 26126 | 19 |
| 1106 | TACCAACAGAATGAG GTGT | A571104Hi | +T*+A*+C*C*A*A*C*A*G*A*A*T*G*A*G*G*+ T*+G*+T | 26129 | 19 |
| 1107 | ACAGTTTGACCAACT CTAA | A571105Hi | +A*+C*+A*G*T*T*T*G*A*C*C*A*A*C*T*C*+ T*+A*+A | 26166 | 19 |
| 1108 | CTTAACAGTTTGACC AACT | A571106Hi | +C*+T*+T*A*A*C*A*G*T*T*T*G*A*C*C*A*+ A*+C*+T | 26170 | 19 |
| 1109 | CTTAACAGTTTGACC AAC | A571107Hi | +C*+T*+T*A*A*C*A*G*T*T*T*G*A*C*C*+A* +A*+C | 26171 | 18 |
| 1110 | CCTCTAAATCTTGATT TAA | A571108H | +C*+C*+T*C*T*A*A*A*T*C*T*T*G*A*T*T*+ T*+A*+A | 26250 | 19 |
| 1111 | CATCATCATTCTCTTG ATT | A571109H | +C*+A*+T*C*A*T*C*A*T*T*C*T*C*T*T*G*+ A*+T*+T | 26280 | 19 |
| 1112 | CTCATCATCATTCTCT TGA | A571110H | +C*+T*+C*A*T*C*A*T*C*A*T*T*C*T*C*T*+ T*+G*+A | 26282 | 19 |
| 1113 | ACAGGCTTCCAGCCA AAAC | A571111H | +A*+C*+A*G*G*C*T*T*C*C*A*G*C*C*A*A*+ A*+A*+C | 26318 | 19 |
| 1114 | TAACAGGCTTCCAGC CAAA | A571112H | +T*+A*+A*C*A*G*G*C*T*T*C*C*A*G*C*C*+ A*+A*+A | 26320 | 19 |
| 1115 | TTGTAACAGGCTTCC AGCC | A571113H | +T*+T*+G*T*A*A*C*A*G*G*C*T*T*C*C*A*+ G*+C*+C | 26323 | 19 |
| 1116 | CTTTGTAACAGGCTT CCAG | A571114H | +C*+T*+T*T*G*T*A*A*C*A*G*G*C*T*T*C*+ C*+A*+G | 26325 | 19 |
| 1117 | GCTTTGTAACAGGCT TCCA | A571115H | +G*+C*+T*T*T*G*T*A*A*C*A*G*G*C*T*T*+ C*+C*+A | 26326 | 19 |
| 1118 | TCTTTCTATGCCACG TTAA | A571116H | +T*+C*+T*T*T*C*T*A*T*G*C*C*A*C*G*T*+ T*+A*+A | 26346 | 19 |
| 1119 | TCTTTCTATGCCACG TTA | A571117H | +T*+C*+T*T*T*C*T*A*T*G*C*C*A*C*G*+T* +T*+A | 26347 | 18 |
| 1120 | TTCTTTCTATGCCAC GTTA | A571118H | +T*+T*+C*T*T*T*C*T*A*T*G*C*C*A*C*G*+ T*+T*+A | 26347 | 19 |
| 1121 | TTCTTTCTATGCCAC GTT | A571119H | +T*+T*+C*T*T*T*C*T*A*T*G*C*C*A*C*+G* +T*+T | 26348 | 18 |
| 1122 | GTTCTTTCTATGCCA CGTT | A571120H | +G*+T*+T*C*T*T*T*C*T*A*T*G*C*C*A*C*+ G*+T*+T | 26348 | 19 |
| 1123 | TGTTCTTTCTATGCCA CGT | A571121H | +T*+G*+T*T*C*T*T*T*C*T*A*T*G*C*C*A*+ C*+G*+T | 26349 | 19 |
| 1124 | TGTTCTTTCTATGCCA CG | A571122H | +T*+G*+T*T*C*T*T*T*C*T*A*T*G*C*C*+A* +C*+G | 26350 | 18 |
| 1125 | TTGTTCTTTCTATGCC ACG | A571123H | +T*+T*+G*T*T*C*T*T*T*C*T*A*T*G*C*C*+ A*+C*+G | 26350 | 19 |
| 1126 | CGTGCTTGTTCTTTCT ATG | A571124H | +C*+G*+T*G*C*T*T*G*T*T*C*T*T*T*C*T*+ A*+T*+G | 26355 | 19 |
| 1127 | CACGTGCTTGTTCTT TCTA | A571125H | +C*+A*+C*G*T*G*C*T*T*G*T*T*C*T*T*T*+ C*+T*+A | 26357 | 19 |
| 1128 | CACGTGCTTGTTCTT TCT | A571126H | +C*+A*+C*G*T*G*C*T*T*G*T*T*C*T*T*+T* +C*+T | 26358 | 18 |
| 1129 | GCACGTGCTTGTTCT TTCT | A571127H | +G*+C*+A*C*G*T*G*C*T*T*G*T*T*C*T*T*+ T*+C*+T | 26358 | 19 |
| 1130 | CACGTGCTTGTTCTT TC | A571128H | +C*+A*+C*G*T*G*C*T*T*G*T*T*C*T*+T*+T *+C | 26359 | 17 |

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| 1131 | GCACGTGCTTGTTCTTTC | A571129H | +G*+C*+A*C*G*T*G*C*T*T*G*T*T*T*C*T*+T*+T*+C | 26359 | 18 |
| 1132 | TGCACGTGCTTGTTCTTTC | A571130H | +T*+G*+C*A*C*G*T*G*C*T*T*G*T*T*T*C*T*+T*+T*+C | 26359 | 19 |
| 1133 | AACTCTAATATTTATGAGA | A571131Hi | +A*+A*+C*T*C*T*A*A*T*A*T*T*T*A*T*G*+A*+G*+A | 26386 | 19 |
| 1134 | ATTATTTAGTGCCCAGCAT | A571132H | +A*+T*+T*A*T*T*T*A*G*T*G*C*C*C*A*G*+C*+A*+T | 26477 | 19 |
| 1135 | GATTATTTAGTGCCCAGCA | A571133H | +G*+A*+T*T*A*T*T*T*A*G*T*G*C*C*C*A*+G*+C*+A | 26478 | 19 |
| 1136 | GATTATTTAGTGCCCAGC | A571134H | +G*+A*+T*T*A*T*T*T*A*G*T*G*C*C*C*+A*+G*+C | 26479 | 18 |
| 1137 | AGATTATTTAGTGCCCAGC | A571135H | +A*+G*+A*T*T*A*T*T*T*A*G*T*G*C*C*C*+A*+G*+C | 26479 | 19 |
| 1138 | AGGAGATTATTTAGTGCCC | A571136H | +A*+G*+G*A*G*A*T*T*A*T*T*T*A*G*T*G*+C*+C*+C | 26482 | 19 |
| 1139 | AAGGAGATTATTTAGTGCC | A571137H | +A*+A*+G*G*A*G*A*T*T*A*T*T*T*A*G*T*+G*+C*+C | 26483 | 19 |
| 1140 | ACATAAGGAGATTATTTAG | A571138H | +A*+C*+A*T*A*A*G*G*A*G*A*T*T*A*T*T*+T*+A*+G | 26487 | 19 |
| 1141 | GGTACATAAGGAGATTATT | A571139H | +G*+G*+T*A*C*A*T*A*A*G*G*A*G*A*T*T*+A*+T*+T | 26490 | 19 |
| 1142 | TTTGGTACATAAGGAGATT | A571140H | +T*+T*+T*G*G*T*A*C*A*T*A*A*G*G*A*G*+A*+T*+T | 26493 | 19 |
| 1143 | TTTTGGTACATAAGGAGAT | A571141H | +T*+T*+T*T*G*G*T*A*C*A*T*A*A*G*G*A*+G*+A*+T | 26494 | 19 |
| 1144 | GTTTTGGTACATAAGGAGA | A571142H | +G*+T*+T*T*T*G*G*T*A*C*A*T*A*A*G*G*+A*+G*+A | 26495 | 19 |
| 1145 | TGTTTTGGTACATAAGGAG | A571143H | +T*+G*+T*T*T*T*G*G*T*A*C*A*T*A*A*G*+G*+A*+G | 26496 | 19 |
| 1146 | CTGTTTTGGTACATAAGGA | A571144H | +C*+T*+G*T*T*T*T*G*G*T*A*C*A*T*A*A*+G*+G*+A | 26497 | 19 |
| 1147 | AACTGTTTTGGTACATAAG | A571145H | +A*+A*+C*T*G*T*T*T*T*G*G*T*A*C*A*T*+A*+A*+G | 26499 | 19 |
| 1148 | TGTAAACTGTTTTGGTACA | A571146H | +T*+G*+T*A*A*A*C*T*G*T*T*T*T*G*G*T*+A*+C*+A | 26503 | 19 |
| 1149 | CATGTAAACTGTTTTGGTA | A571147H | +C*+A*+T*G*T*A*A*A*C*T*G*T*T*T*T*G*+G*+T*+A | 26505 | 19 |
| 1150 | CAATCTTCTCATGTAAACT | A571148H | +C*+A*+A*T*C*T*T*C*T*C*A*T*G*T*A*A*+A*+C*+T | 26514 | 19 |
| 1151 | CCAATCTTCTCATGTAAAC | A571149H | +C*+C*+A*A*T*C*T*T*C*T*C*A*T*G*T*A*+A*+A*+C | 26515 | 19 |
| 1152 | TCCAATCTTCTCATGTAAA | A571150H | +T*+C*+C*A*A*T*C*T*T*C*T*C*A*T*G*T*+A*+A*+A | 26516 | 19 |
| 1153 | CTCCAATCTTCTCATGTAA | A571151H | +C*+T*+C*C*A*A*T*C*T*T*C*T*C*A*T*G*+T*+A*+A | 26517 | 19 |
| 1154 | CATCTCCAATCTTCTCATG | A571152H | +C*+A*+T*C*T*C*C*A*A*T*C*T*T*C*T*C*+A*+T*+G | 26520 | 19 |
| 1155 | TCATCTCCAATCTTCTCAT | A571153H | +T*+C*+A*T*C*T*C*C*A*A*T*C*T*T*C*T*+C*+A*+T | 26521 | 19 |
| 1156 | TGGCCATCTTCATCTCCAA | A571154H | +T*+G*+G*C*C*A*T*C*T*T*C*A*T*C*T*C*+C*+A*+A | 26530 | 19 |
| 1157 | ATCTCTCAATAATAACTC | A571155Hi | +A*+T*+C*T*C*T*C*A*A*T*A*A*T*A*A*+C*+T*+C | 26746 | 18 |
| 1158 | CCAAATCTCTCAATAATAA | A571156Hi | +C*+C*+A*A*A*T*C*T*C*T*C*A*A*T*A*A*+T*+A*+A | 26749 | 19 |
| 1159 | CTCTGCAATTTCTATCACC | A571157Hi | +C*+T*+C*T*G*C*A*A*T*T*T*C*T*A*T*C*+A*+C*+C | 26861 | 19 |
| 1160 | ATGGCTCTGCAATTTCTAT | A571158Hi | +A*+T*+G*G*C*T*C*T*G*C*A*A*T*T*T*C*+T*+A*+T | 26865 | 19 |
| 1161 | ACCTGCTGGCTAGTCACCA | A571159Hi | +A*+C*+C*T*G*C*T*G*G*C*T*A*G*T*C*A*+C*+C*+A | 26902 | 19 |
| 1162 | ACCTGCTGGCTAGTCACC | A571160Hi | +A*+C*+C*T*G*C*T*G*G*C*T*A*G*T*C*+A*+C*+C | 26903 | 18 |
| 1163 | TTGACAACCTGCTGGCTAG | A571161Hi | +T*+T*+G*A*C*A*A*C*C*T*G*C*T*G*G*C*+T*+A*+G | 26908 | 19 |
| 1164 | TTGACAACCTGCTGGCTA | A571162Hi | +T*+T*+G*A*C*A*A*C*C*T*G*C*T*G*G*+C*+T*+A | 26909 | 18 |
| 1165 | TATTGACAACCTGCTGGCT | A571163Hi | +T*+A*+T*T*G*A*C*A*A*C*C*T*G*C*T*G*+G*+C*+T | 26910 | 19 |

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| 1166 | TATTGACAACCTGCTGGC | A571164Hi | +T*+A*+T*T*G*A*C*A*A*C*C*T*G*C*T*+G*+G*+C | 26911 | 18 |
| 1167 | ATATTGACAACCTGCTGG | A571165Hi | +A*+T*+A*T*T*G*A*C*A*A*C*C*T*G*C*+T*+G*+G | 26912 | 18 |
| 1168 | GATATTGACAACCTGCTGG | A571166Hi | +G*+A*+T*A*T*T*G*A*C*A*A*C*C*T*G*C*+T*+G*+G | 26912 | 19 |
| 1169 | CTGATATTGACAACCTGCT | A571167Hi | +C*+T*+G*A*T*A*T*T*G*A*C*A*A*C*C*T*+G*+C*+T | 26914 | 19 |
| 1170 | GTCAACTCTGTCACATCAG | A571168Hi | +G*+T*+C*A*A*C*T*C*T*G*T*C*A*C*A*T*+C*+A*+G | 26975 | 19 |
| 1171 | GGTCAACTCTGTCACATCA | A571169Hi | +G*+G*+T*C*A*A*C*T*C*T*G*T*C*A*C*A*+T*+C*+A | 26976 | 19 |
| 1172 | CAGGTCAACTCTGTCACAT | A571170Hi | +C*+A*+G*G*T*C*A*A*C*T*C*T*G*T*C*A*+C*+A*+T | 26978 | 19 |
| 1173 | ACAGGTCAACTCTGTCACA | A571171Hi | +A*+C*+A*G*G*T*C*A*A*C*T*C*T*G*T*C*+A*+C*+A | 26979 | 19 |
| 1174 | ACAGGTCAACTCTGTCAC | A571172Hi | +A*+C*+A*G*G*T*C*A*A*C*T*C*T*G*T*+C*+A*+C | 26980 | 18 |
| 1175 | GAAGACAGGTCAACTCTG | A571173Hi | +G*+A*+A*G*A*C*A*G*G*T*C*A*A*C*T*+C*+T*+G | 26984 | 18 |
| 1176 | AGAAGACAGGTCAACTCTG | A571174Hi | +A*+G*+A*A*G*A*C*A*G*G*T*C*A*A*C*T*+C*+T*+G | 26984 | 19 |
| 1177 | AAAGAAGACAGGTCAACTC | A571175Hi | +A*+A*+A*G*A*A*G*A*C*A*G*G*T*C*A*A*+C*+T*+C | 26986 | 19 |
| 1178 | GATGACAGCTTCAAATAAC | A571176Hi | +G*+A*+T*G*A*C*A*G*C*T*T*C*A*A*A*T*+A*+A*+C | 27012 | 19 |
| 1179 | ATGATGTTTGAATGGCACT | A571177Hi | +A*+T*+G*A*T*G*T*T*T*G*A*A*T*G*G*C*+A*+C*+T | 27053 | 19 |
| 1180 | TTATGATGTTTGAATGGCA | A571178Hi | +T*+T*+A*T*G*A*T*G*T*T*T*G*A*A*T*G*+G*+C*+A | 27055 | 19 |
| 1181 | CTTATGATGTTTGAATGG | A571179Hi | +C*+T*+T*A*T*G*A*T*G*T*T*T*G*A*A*+T*+G*+G | 27057 | 18 |
| 1182 | GTCTTATGATGTTTGAATG | A571180Hi | +G*+T*+C*T*T*A*T*G*A*T*G*T*T*T*G*A*+A*+T*+G | 27058 | 19 |
| 1183 | TGAAACAAACCTGATATGC | A571181Hi | +T*+G*+A*A*A*C*A*A*A*C*C*T*G*A*T*A*+T*+G*+C | 27121 | 19 |
| 1184 | ATGAAACAAACCTGATATG | A571182Hi | +A*+T*+G*A*A*A*C*A*A*A*C*C*T*G*A*T*+A*+T*+G | 27122 | 19 |
| 1185 | GAATACTACTATTTGTTTC | A571183Hi | +G*+A*+A*T*A*C*T*A*C*T*A*T*T*T*G*T*+T*+T*+C | 27239 | 19 |
| 1186 | GATGCCAATTTAGCATAG | A571184Hi | +G*+A*+T*G*C*C*A*A*T*T*T*A*G*C*A*+T*+A*+G | 27383 | 18 |
| 1187 | AGATGCCAATTTAGCATAG | A571185Hi | +A*+G*+A*T*G*C*C*A*A*T*T*T*A*G*C*A*+T*+A*+G | 27383 | 19 |
| 1188 | TAAGATGCCAATTTAGCAT | A571186Hi | +T*+A*+A*G*A*T*G*C*C*A*A*T*T*T*A*G*+C*+A*+T | 27385 | 19 |
| 1189 | TTAAGATGCCAATTTAGCA | A571187Hi | +T*+T*+A*A*G*A*T*G*C*C*A*A*T*T*T*A*+G*+C*+A | 27386 | 19 |
| 1190 | TTAAGATGCCAATTTAGC | A571188Hi | +T*+T*+A*A*G*A*T*G*C*C*A*A*T*T*T*+A*+G*+C | 27387 | 18 |
| 1191 | ATTAAGATGCCAATTTAGC | A571189Hi | +A*+T*+T*A*A*G*A*T*G*C*C*A*A*T*T*T*+A*+G*+C | 27387 | 19 |
| 1192 | TATTAAGATGCCAATTTAG | A571190Hi | +T*+A*+T*T*A*A*G*A*T*G*C*C*A*A*T*T*+T*+A*+G | 27388 | 19 |
| 1193 | ATTAAGATGCCAATTTAG | A571191Hi | +A*+T*+T*A*A*G*A*T*G*C*C*A*A*T*T*+T*+A*+G | 27388 | 18 |
| 1194 | ATGAGATTATTAAGATGCC | A571192Hi | +A*+T*+G*A*G*A*T*T*A*T*T*T*A*A*G*A*T*+G*+C*+C | 27395 | 19 |
| 1195 | TTGCTCAACATGAGATTA | A571193Hi | +T*+T*+G*C*T*C*A*A*C*A*T*G*A*G*A*+T*+T*+A | 27405 | 18 |
| 1196 | ATGTAAAGAGATGCTGAGG | A571194Hi | +A*+T*+G*T*A*A*A*G*A*G*A*T*G*C*T*G*+A*+G*+G | 27646 | 19 |
| 1197 | AGATATGTAAAGAGATGCT | A571195Hi | +A*+G*+A*T*A*T*G*T*A*A*A*G*A*G*A*T*+G*+C*+T | 27650 | 19 |
| 1198 | CAGATATGTAAAGAGATGC | A571196Hi | +C*+A*+G*A*T*A*T*G*T*A*A*A*G*A*G*A*+T*+G*+C | 27651 | 19 |
| 1199 | TATCTCTAACAACAATTAA | A571197Hi | +T*+A*+T*C*T*C*T*A*A*C*A*A*C*A*A*T*+T*+A*+A | 27819 | 19 |
| 1200 | CACTTCCCTATGAGCTGGG | A571198H | +C*+A*+C*T*T*C*C*C*T*A*T*G*A*G*C*T*+G*+G*+G | 27917 | 19 |

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| 1201 | TCACTTCCCTATGAG CTGG | A571199H | +T*+C*+A*C*T*T*C*C*C*T*A*T*G*A*G*C*+ T*+G*+G | 27918 | 19 |
| 1202 | TCACTTCCCTATGAG CTG | A571200H | +T*+C*+A*C*T*T*C*C*C*T*A*T*G*A*G*+C* +T*+G | 27919 | 18 |
| 1203 | ATCACTTCCCTATGA GCTG | A571201H | +A*+T*+C*A*C*T*T*C*C*C*T*A*T*G*A*G*+ C*+T*+G | 27919 | 19 |
| 1204 | ATCACTTCCCTATGA GCT | A571202H | +A*+T*+C*A*C*T*T*C*C*C*T*A*T*G*A*+G* +C*+T | 27920 | 18 |
| 1205 | CATCACTTCCCTATG AGCT | A571203H | +C*+A*+T*C*A*C*T*T*C*C*C*T*A*T*G*A*+ G*+C*+T | 27920 | 19 |
| 1206 | GCATCACTTCCCTAT GAGC | A571204H | +G*+C*+A*T*C*A*C*T*T*C*C*C*T*A*T*G*+ A*+G*+C | 27921 | 19 |
| 1207 | GCATCACTTCCCTAT GAG | A571205H | +G*+C*+A*T*C*A*C*T*T*C*C*C*T*A*T*+G* +A*+G | 27922 | 18 |
| 1208 | AGCATCACTTCCCTA TGAG | A571206H | +A*+G*+C*A*T*C*A*C*T*T*C*C*C*T*A*T*+ G*+A*+G | 27922 | 19 |
| 1209 | GGAAAACTTCCTTTG ATGA | A571207H | +G*+G*+A*A*A*A*C*T*T*C*C*T*T*T*G*A*+ T*+G*+A | 27960 | 19 |
| 1210 | GGAAAACTTCCTTTG ATG | A571208H | +G*+G*+A*A*A*A*C*T*T*C*C*T*T*T*G*+A* +T*+G | 27961 | 18 |
| 1211 | TGGAAAACTTCCTTT GATG | A571209H | +T*+G*+G*A*A*A*A*C*T*T*C*C*T*T*T*G*+ A*+T*+G | 27961 | 19 |
| 1212 | TGTGAGTTTACACAT AGAA | A571210Hi | +T*+G*+T*G*A*G*T*T*T*A*C*A*C*A*T*A*+ G*+A*+A | 28236 | 19 |
| 1213 | GTGTGAGTTTACACA TAGA | A571211Hi | +G*+T*+G*T*G*A*G*T*T*T*A*C*A*C*A*T*+ A*+G*+A | 28237 | 19 |
| 1214 | ATTTGAGCAGCCTGA ACC | A571212Hi | +A*+T*+T*T*G*A*G*C*A*G*C*C*T*G*A*+A* +C*+C | 29068 | 18 |
| 1215 | AAATTTGAGCAGCCT GAAC | A571213Hi | +A*+A*+A*T*T*T*G*A*G*C*A*G*C*C*T*G*+ A*+A*+C | 29069 | 19 |
| 1216 | AATTTGAGCAGCCTG AAC | A571214Hi | +A*+A*+T*T*T*G*A*G*C*A*G*C*C*T*G*+A* +A*+C | 29069 | 18 |
| 1217 | GAAGAAATTTGAGCA GCCT | A571215Hi | +G*+A*+A*G*A*A*A*T*T*T*G*A*G*C*A*G*+ C*+C*+T | 29073 | 19 |
| 1218 | TTTCACCTAAGGATT TCTG | A571216Hi | +T*+T*+T*C*A*C*C*T*A*A*G*G*A*T*T*T*+ C*+T*+G | 29113 | 19 |
| 1219 | CCAATGCCTTTATGA TGA | A571217Hi | +C*+C*+A*A*T*G*C*C*T*T*T*A*T*G*A*+T* +G*+A | 29134 | 18 |
| 1220 | TACACTGGTCTCTGT CTCT | A571218Hi | +T*+A*+C*A*C*T*G*G*T*C*T*C*T*G*T*C*+ T*+C*+T | 29214 | 19 |
| 1221 | AGAAACATGCATGAG GTGG | A571219Hi | +A*+G*+A*A*A*C*A*T*G*C*A*T*G*A*G*G*+ T*+G*+G | 29285 | 19 |
| 1222 | AAGAAACATGCATGA GGTG | A571220Hi | +A*+A*+G*A*A*A*C*A*T*G*C*A*T*G*A*G*+ G*+T*+G | 29286 | 19 |
| 1223 | ATTATCCTTGAGAGC AGCC | A571221Hi | +A*+T*+T*A*T*C*C*T*T*G*A*G*A*G*C*A*+ G*+C*+C | 29434 | 19 |
| 1224 | TTATCCTTGAGAGCA GCC | A571222Hi | +T*+T*+A*T*C*C*T*T*G*A*G*A*G*C*A*+G* +C*+C | 29434 | 18 |
| 1225 | CATTATCCTTGAGAG CAGC | A571223Hi | +C*+A*+T*T*A*T*C*C*T*T*G*A*G*A*G*C*+ A*+G*+C | 29435 | 19 |
| 1226 | ATTATCCTTGAGAGC AGC | A571224Hi | +A*+T*+T*A*T*C*C*T*T*G*A*G*A*G*C*+A* +G*+C | 29435 | 18 |
| 1227 | CTCTTTAACTGCACA GTAG | A571225Hi | +C*+T*+C*T*T*T*A*A*C*T*G*C*A*C*A*G*+ T*+A*+G | 29502 | 19 |
| 1228 | TGTTGTCTGTACATA GTAA | A571226Hi | +T*+G*+T*T*G*T*C*T*G*T*A*C*A*T*A*G*+ T*+A*+A | 29604 | 19 |
| 1229 | CAATGTTGTCTGTAC ATAG | A571227Hi | +C*+A*+A*T*G*T*T*G*T*C*T*G*T*A*C*A*+ T*+A*+G | 29607 | 19 |
| 1230 | ATTTCCAGGTGGTTA TGAA | A571228Hi | +A*+T*+T*T*C*C*A*G*G*T*G*G*T*T*A*T*+ G*+A*+A | 29640 | 19 |
| 1231 | GATTTCCAGGTGGTT ATGA | A571229Hi | +G*+A*+T*T*T*C*C*A*G*G*T*G*G*T*T*A*+ T*+G*+A | 29641 | 19 |
| 1232 | AGGAGATTTCCAGGT GGTT | A571230Hi | +A*+G*+G*A*G*A*T*T*T*C*C*A*G*G*T*G*+ G*+T*+T | 29645 | 19 |
| 1233 | TCAAAGGAGATTTCC AGGT | A571231Hi | +T*+C*+A*A*A*G*G*A*G*A*T*T*T*C*C*A*+ G*+G*+T | 29649 | 19 |
| 1234 | GCAGTCGAAATTTCA CAAA | A571232Hi | +G*+C*+A*G*T*C*G*A*A*A*T*T*T*C*A*C*+ A*+A*+A | 29691 | 19 |
| 1235 | CAGTCGAAATTTCAC AAA | A571233Hi | +C*+A*+G*T*C*G*A*A*A*T*T*T*C*A*C*+A* +A*+A | 29691 | 18 |

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| 1236 | GAAGCAGTCGAAATTTCA | A571234Hi | +G*+A*+A*G*C*A*G*T*C*G*A*A*A*T*T*+T*+C*+A | 29695 | 18 |
| 1237 | GGAAGCAGTCGAAATTTC | A571235Hi | +G*+G*+A*A*G*C*A*G*T*C*G*A*A*A*T*+T*+T*+C | 29696 | 18 |
| 1238 | AGGAAGCAGTCGAAATTT | A571236Hi | +A*+G*+G*A*A*G*C*A*G*T*C*G*A*A*A*+T*+T*+T | 29697 | 18 |
| 1239 | TGTAACCAGTCCTCAGACA | A571237Hi | +T*+G*+T*A*A*C*C*A*G*T*C*C*T*C*A*G*+A*+C*+A | 29722 | 19 |
| 1240 | TCTGAATGTAACCAGTCCT | A571238Hi | +T*+C*+T*G*A*A*T*G*T*A*A*C*C*A*G*T*+C*+C*+T | 29728 | 19 |
| 1241 | CTCTGAATGTAACCAGTCC | A571239Hi | +C*+T*+C*T*G*A*A*T*G*T*A*A*C*C*A*G*+T*+C*+C | 29729 | 19 |
| 1242 | AGGCAGAACTCCAAAGACA | A571240Hi | +A*+G*+G*C*A*G*A*A*C*T*C*C*A*A*A*G*+A*+C*+A | 29848 | 19 |
| 1243 | AAGGCAGAACTCCAAAGAC | A571241Hi | +A*+A*+G*G*C*A*G*A*A*C*T*C*C*A*A*A*+G*+A*+C | 29849 | 19 |
| 1244 | CTTTATTAAGGCAGAACTC | A571242Hi | +C*+T*+T*T*A*T*T*A*A*G*G*C*A*G*A*A*+C*+T*+C | 29856 | 19 |
| 1245 | TTCATGCTTTATTAAGGCA | A571243Hi | +T*+T*+C*A*T*G*C*T*T*T*A*T*T*A*A*G*+G*+C*+A | 29862 | 19 |
| 1246 | CTACTCAAGTTCTTCATGC | A571244Hi | +C*+T*+A*C*T*C*A*A*G*T*T*C*T*T*C*A*+T*+G*+C | 29874 | 19 |
| 1247 | GCTACTCAAGTTCTTCATG | A571245Hi | +G*+C*+T*A*C*T*C*A*A*G*T*T*C*T*T*C*+A*+T*+G | 29875 | 19 |
| 1248 | AGCTACTCAAGTTCTTCAT | A571246Hi | +A*+G*+C*T*A*C*T*C*A*A*G*T*T*C*T*T*+C*+A*+T | 29876 | 19 |
| 1249 | GAGCTACTCAAGTTCTTCA | A571247Hi | +G*+A*+G*C*T*A*C*T*C*A*A*G*T*T*C*T*+T*+C*+A | 29877 | 19 |
| 1250 | GAGCTACTCAAGTTCTTC | A571248Hi | +G*+A*+G*C*T*A*C*T*C*A*A*G*T*T*C*+T*+T*+C | 29878 | 18 |
| 1251 | CAAGTGTCTTTCAATGAGA | A571249Hi | +C*+A*+A*G*T*G*T*C*T*T*T*C*A*A*T*G*+A*+G*+A | 29920 | 19 |
| 1252 | CTGCCTATTCACAACTTCA | A571250Hi | +C*+T*+G*C*C*T*A*T*T*C*A*C*A*A*C*T*+T*+C*+A | 30288 | 19 |
| 1253 | GCTGCCTATTCACAACTTC | A571251Hi | +G*+C*+T*G*C*C*T*A*T*T*C*A*C*A*A*C*+T*+T*+C | 30289 | 19 |
| 1254 | GCTGCCTATTCACAACTT | A571252Hi | +G*+C*+T*G*C*C*T*A*T*T*C*A*C*A*A*+C*+T*+T | 30290 | 18 |
| 1255 | GGCTGCCTATTCACAACT | A571253Hi | +G*+G*+C*T*G*C*C*T*A*T*T*C*A*C*A*+A*+C*+T | 30291 | 18 |
| 1256 | TGGCTGCCTATTCACAAC | A571254Hi | +T*+G*+G*C*T*G*C*C*T*A*T*T*C*A*C*+A*+A*+C | 30292 | 18 |
| 1257 | CCTGGCTGCCTATTCACAA | A571255Hi | +C*+C*+T*G*G*C*T*G*C*C*T*A*T*T*C*A*+C*+A*+A | 30293 | 19 |
| 1258 | CCTGGCTGCCTATTCACA | A571256Hi | +C*+C*+T*G*G*C*T*G*C*C*T*A*T*T*C*+A*+C*+A | 30294 | 18 |
| 1259 | TCCTGGCTGCCTATTCACA | A571257Hi | +T*+C*+C*T*G*G*C*T*G*C*C*T*A*T*T*C*+A*+C*+A | 30294 | 19 |
| 1260 | TTCCTGGCTGCCTATTCAC | A571258Hi | +T*+T*+C*C*T*G*G*C*T*G*C*C*T*A*T*T*+C*+A*+C | 30295 | 19 |
| 1261 | TCCTGGCTGCCTATTCAC | A571259Hi | +T*+C*+C*T*G*G*C*T*G*C*C*T*A*T*T*+C*+A*+C | 30295 | 18 |
| 1262 | TTTCCTGGCTGCCTATTCA | A571260Hi | +T*+T*+T*C*C*T*G*G*C*T*G*C*C*T*A*T*+T*+C*+A | 30296 | 19 |
| 1263 | TTCCTGGCTGCCTATTCA | A571261Hi | +T*+T*+C*C*T*G*G*C*T*G*C*C*T*A*T*+T*+C*+A | 30296 | 18 |
| 1264 | TCTTTCCTGGCTGCCTATT | A571262Hi | +T*+C*+T*T*T*C*C*T*G*G*C*T*G*C*C*T*+A*+T*+T | 30298 | 19 |
| 1265 | TCTTTCCTGGCTGCCTAT | A571263Hi | +T*+C*+T*T*T*C*C*T*G*G*C*T*G*C*C*+T*+A*+T | 30299 | 18 |
| 1266 | TTCTTTCCTGGCTGCCTAT | A571264Hi | +T*+T*+C*T*T*T*C*C*T*G*G*C*T*G*C*C*+T*+A*+T | 30299 | 19 |
| 1267 | CTTCTTTCCTGGCTGCCTA | A571265Hi | +C*+T*+T*C*T*T*T*C*C*T*G*G*C*T*G*C*+C*+T*+A | 30300 | 19 |
| 1268 | TGCAGGTCTTACTCAATAG | A571266Hi | +T*+G*+C*A*G*G*T*C*T*T*A*C*T*C*A*A*+T*+A*+G | 30323 | 19 |
| 1269 | TGCAGGTCTTACTCAATA | A571267Hi | +T*+G*+C*A*G*G*T*C*T*T*A*C*T*C*A*+A*+T*+A | 30324 | 18 |
| 1270 | AATTTCATCATAAAGTCAC | A571268Hi | +A*+A*+T*T*T*C*A*T*C*A*T*A*A*A*G*T*+C*+A*+C | 30472 | 19 |

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| 1271 | TGCAAGCAATAAACCTAG | A571269Hi | +T*+G*+C*A*A*G*C*A*A*T*A*A*A*C*C*+T*+A*+G | 30498 | 18 |
| 1272 | TTGCAAGCAATAAACCTAG | A571270Hi | +T*+T*+G*C*A*A*G*C*A*A*T*A*A*A*C*C*+T*+A*+G | 30498 | 19 |
| 1273 | ACTATCCTAGACAGTAAC | A571271Hi | +A*+C*+T*A*T*C*C*T*A*G*A*C*A*G*T*+A*+A*+C | 30536 | 18 |
| 1274 | CTTTAAGAATCACTATCCT | A571272Hi | +C*+T*+T*T*A*A*G*A*A*T*C*A*C*T*A*T*+C*+C*+T | 30546 | 19 |
| 1275 | AGTGGCTAGCTTCTAGCCA | A571273Hi | +A*+G*+T*G*G*C*T*A*G*C*T*T*C*T*A*G*+C*+C*+A | 30770 | 19 |
| 1276 | GTGGCTAGCTTCTAGCCA | A571274Hi | +G*+T*+G*G*C*T*A*G*C*T*T*C*T*A*G*+C*+C*+A | 30770 | 18 |
| 1277 | AAAGTGGCTAGCTTCTAGC | A571275Hi | +A*+A*+A*G*T*G*G*C*T*A*G*C*T*T*C*T*+A*+G*+C | 30772 | 19 |
| 1278 | CAAAGTGGCTAGCTTCTAG | A571276Hi | +C*+A*+A*A*G*T*G*G*C*T*A*G*C*T*T*C*+T*+A*+G | 30773 | 19 |
| 1279 | AACACTTTGAAAGTGGCAG | A571277Hi | +A*+A*+C*A*C*T*T*T*G*A*A*A*G*T*G*G*+C*+A*+G | 31023 | 19 |
| 1280 | GTGATTCAACACTTTGAAA | A571278Hi | +G*+T*+G*A*T*T*C*A*A*C*A*C*T*T*T*G*+A*+A*+A | 31030 | 19 |
| 1281 | CACTGTGATTCAACACTTT | A571279Hi | +C*+A*+C*T*G*T*G*A*T*T*C*A*A*C*A*C*+T*+T*+T | 31034 | 19 |
| 1282 | TACACACTGTGATTCAACA | A571280Hi | +T*+A*+C*A*C*A*C*T*G*T*G*A*T*T*C*A*+A*+C*+A | 31038 | 19 |
| 1283 | CCAACATTACACACTGTG | A571281Hi | +C*+C*+A*A*C*A*T*T*A*C*A*C*A*C*T*+G*+T*+G | 31046 | 18 |
| 1284 | ATCAATTGTCTTGAAGCC | A571282Hi | +A*+T*+C*A*A*T*T*G*T*C*T*T*G*A*A*+G*+C*+C | 31082 | 18 |
| 1285 | GTCTTCAAGTTTCCACATA | A571283Hi | +G*+T*+C*T*T*C*A*A*G*T*T*T*C*C*A*C*+A*+T*+A | 31103 | 19 |
| 1286 | TGTCTTCAAGTTTCCACAT | A571284Hi | +T*+G*+T*C*T*T*C*A*A*G*T*T*T*C*C*A*+C*+A*+T | 31104 | 19 |
| 1287 | AACTTCCTTCACTAAACAT | A571285Hi | +A*+A*+C*T*T*C*C*T*T*C*A*C*T*A*A*A*+C*+A*+T | 31131 | 19 |
| 1288 | ATAAACTTCCTTCACTAAA | A571286Hi | +A*+T*+A*A*A*C*T*T*C*C*T*T*C*A*C*T*+A*+A*+A | 31134 | 19 |
| 1289 | CATTAACTCCAAAACATTC | A571287H | +C*+A*+T*T*A*A*C*T*C*C*A*A*A*A*C*A*+T*+T*+C | 32292 | 19 |
| 1290 | TGCATTAACTCCAAAACAT | A571288H | +T*+G*+C*A*T*T*A*A*C*T*C*C*A*A*A*A*+C*+A*+T | 32294 | 19 |
| 1291 | TCTGCATTAACTCCAAAAC | A571289H | +T*+C*+T*G*C*A*T*T*A*A*C*T*C*C*A*A*+A*+A*+C | 32296 | 19 |
| 1292 | TTCTGCATTAACTCCAAAA | A571290H | +T*+T*+C*T*G*C*A*T*T*A*A*C*T*C*C*A*+A*+A*+A | 32297 | 19 |
| 1293 | ATGCTTCTGCATTAACTCC | A571291H | +A*+T*+G*C*T*T*C*T*G*C*A*T*T*A*A*C*+T*+C*+C | 32301 | 19 |
| 1294 | GTATATGCTTCTGCATTAA | A571292H | +G*+T*+A*T*A*T*G*C*T*T*C*T*G*C*A*T*+T*+A*+A | 32305 | 19 |
| 1295 | ATGTATATGCTTCTGCATT | A571293H | +A*+T*+G*T*A*T*A*T*G*C*T*T*C*T*G*C*+A*+T*+T | 32307 | 19 |
| 1296 | AATGTATATGCTTCTGCAT | A571294H | +A*+A*+T*G*T*A*T*A*T*G*C*T*T*C*T*G*+C*+A*+T | 32308 | 19 |
| 1297 | GGAGAATGTATATGCTTCT | A571295H | +G*+G*+A*G*A*A*T*G*T*A*T*A*T*G*C*T*+T*+C*+T | 32312 | 19 |
| 1298 | CAGCCACTTCAGGAGAATG | A571296H | +C*+A*+G*C*C*A*C*T*T*C*A*G*G*A*G*A*+A*+T*+G | 32323 | 19 |
| 1299 | CACTTTCAGCCACTTCAGG | A571297H | +C*+A*+C*T*T*T*C*A*G*C*C*A*C*T*T*C*+A*+G*+G | 32329 | 19 |
| 1300 | CCACTTTCAGCCACTTCAG | A571298H | +C*+C*+A*C*T*T*T*C*A*G*C*C*A*C*T*T*+C*+A*+G | 32330 | 19 |
| 1301 | GCCACTTTCAGCCACTTCA | A571299H | +G*+C*+C*A*C*T*T*T*C*A*G*C*C*A*C*T*+T*+C*+A | 32331 | 19 |
| 1302 | GATTTAGCATTTTACAGCC | A571300H | +G*+A*+T*T*T*A*G*C*A*T*T*T*T*A*C*A*+G*+C*+C | 32347 | 19 |
| 1303 | AGATGATTTAGCATTTTAC | A571301H | +A*+G*+A*T*G*A*T*T*T*A*G*C*A*T*T*T*+T*+A*+C | 32351 | 19 |
| 1304 | CCTTCAAAAAGATGATTTA | A571302H | +C*+C*+T*T*C*A*A*A*A*A*G*A*T*G*A*T*+T*+T*+A | 32360 | 19 |
| 1305 | CTTCCTTCAAAAAGATGAT | A571303H | +C*+T*+T*C*C*T*T*C*A*A*A*A*A*G*A*T*+G*+A*+T | 32363 | 19 |

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| 1306 | TTCTGTACAAGTTAATGAA | A571304Hi | +T*+T*+C*T*G*T*A*C*A*A*G*T*T*A*A*T*+G*+A*+A | 32392 | 19 |
| 1307 | CCAATATGATATATTCTGT | A571305Hi | +C*+C*+A*A*T*A*T*G*A*T*A*T*A*T*T*C*+T*+G*+T | 32405 | 19 |
| 1308 | TTGATATTCTACCTGGCC | A571306Hi | +T*+T*+G*A*T*A*T*T*C*T*A*C*C*T*G*+G*+C*+C | 32423 | 18 |
| 1309 | TATTGATATTCTACCTGGC | A571307Hi | +T*+A*+T*T*G*A*T*A*T*T*C*T*A*C*C*T*+G*+G*+C | 32424 | 19 |
| 1310 | ATTGATATTCTACCTGGC | A571308Hi | +A*+T*+T*G*A*T*A*T*T*C*T*A*C*C*T*+G*+G*+C | 32424 | 18 |
| 1311 | GTTAGAAATATGCTTGAAA | A571309Hi | +G*+T*+T*A*G*A*A*A*T*A*T*G*C*T*T*G*+A*+A*+A | 32443 | 19 |
| 1312 | ACACGAGATTACATTGCA | A571310Hi | +A*+C*+A*C*G*A*G*A*T*T*A*C*A*T*T*+G*+C*+A | 32510 | 18 |
| 1313 | ACACGAGATTACATTGC | A571311Hi | +A*+C*+A*C*G*A*G*A*T*T*A*C*A*T*+T*+G*+C | 32511 | 17 |
| 1314 | TACTAGTGACACGAGATT | A571312Hi | +T*+A*+C*T*A*G*T*G*A*C*A*C*G*A*G*+A*+T*+T | 32518 | 18 |
| 1315 | ACTAGTGACACGAGATT | A571313Hi | +A*+C*+T*A*G*T*G*A*C*A*C*G*A*G*+A*+T*+T | 32518 | 17 |
| 1316 | TACTAGTGACACGAGAT | A571314Hi | +T*+A*+C*T*A*G*T*G*A*C*A*C*G*A*+G*+A*+T | 32519 | 17 |
| 1317 | GTACTAGTGACACGAGA | A571315Hi | +G*+T*+A*C*T*A*G*T*G*A*C*A*C*G*+A*+G*+A | 32520 | 17 |
| 1318 | GGTACTAGTGACACGAG | A571316Hi | +G*+G*+T*A*C*T*A*G*T*G*A*C*A*C*+G*+A*+G | 32521 | 17 |
| 1319 | TGGTACTAGTGACACGA | A571317Hi | +T*+G*+G*T*A*C*T*A*G*T*G*A*C*A*+C*+G*+A | 32522 | 17 |
| 1320 | AAGTCTATGGTACTAGTG | A571318Hi | +A*+A*+G*T*C*T*A*T*G*G*T*A*C*T*A*+G*+T*+G | 32528 | 18 |
| 1321 | TCAGTGTTCAGATAAAGTA | A571319Hi | +T*+C*+A*G*T*G*T*T*C*A*G*A*T*A*A*A*+G*+T*+A | 32545 | 19 |
| 1322 | ATCTTGCCATTCCTTTCAG | A571320Hi | +A*+T*+C*T*T*G*C*C*A*T*T*C*C*T*T*T*+C*+A*+G | 32560 | 19 |
| 1323 | CCACAATCTTGCCATTCCT | A571321Hi | +C*+C*+A*C*A*A*T*C*T*T*G*C*C*A*T*T*+C*+C*+T | 32565 | 19 |
| 1324 | CACAATCTTGCCATTCCT | A571322Hi | +C*+A*+C*A*A*T*C*T*T*G*C*C*A*T*T*+C*+C*+T | 32565 | 18 |
| 1325 | TCCACAATCTTGCCATTCC | A571323Hi | +T*+C*+C*A*C*A*A*T*C*T*T*G*C*C*A*T*+T*+C*+C | 32566 | 19 |
| 1326 | TGTTTCCACAATCTTGCCA | A571324Hi | +T*+G*+T*T*T*C*C*A*C*A*A*T*C*T*T*G*+C*+C*+A | 32570 | 19 |
| 1327 | ATGTTTCCACAATCTTGCC | A571325Hi | +A*+T*+G*T*T*T*C*C*A*C*A*A*T*C*T*T*+G*+C*+C | 32571 | 19 |
| 1328 | TTCAACATGTTTCCACAAT | A571326Hi | +T*+T*+C*A*A*C*A*T*G*T*T*T*C*C*A*C*+A*+A*+T | 32577 | 19 |
| 1329 | ACCTTCAACATGTTTCCAC | A571327Hi | +A*+C*+C*T*T*C*A*A*C*A*T*G*T*T*T*C*+C*+A*+C | 32580 | 19 |
| 1330 | CAACATCAAGCATCAGGTT | A571328Hi | +C*+A*+A*C*A*T*C*A*A*G*C*A*T*C*A*G*+G*+T*+T | 32608 | 19 |
| 1331 | TGCTATACAATTACCACT | A571329Hi | +T*+G*+C*T*A*T*A*C*A*A*T*T*A*C*C*+A*+C*+T | 32641 | 18 |
| 1332 | ATATTCGTTGTGAAAGA | A571330Hi | +A*+T*+A*T*T*C*G*T*T*G*T*G*A*A*+A*+G*+A | 32738 | 17 |
| 1333 | TATATTCGTTGTGAAAGA | A571331Hi | +T*+A*+T*A*T*T*C*G*T*T*G*T*G*A*A*+A*+G*+A | 32738 | 18 |
| 1334 | GAATAATATATTCGTTGTG | A571332Hi | +G*+A*+A*T*A*A*T*A*T*A*T*T*T*C*G*T*T*+G*+T*+G | 32743 | 19 |
| 1335 | CTTGGACTAGATGTAGTT | A571333Hi | +C*+T*+T*G*G*A*C*T*A*G*A*T*G*T*A*+G*+T*+T | 32823 | 18 |
| 1336 | ACTTGGACTAGATGTAGTT | A571334Hi | +A*+C*+T*T*G*G*A*C*T*A*G*A*T*G*T*A*+G*+T*+T | 32823 | 19 |
| 1337 | ACTTGGACTAGATGTAGT | A571335Hi | +A*+C*+T*T*G*G*A*C*T*A*G*A*T*G*T*+A*+G*+T | 32824 | 18 |
| 1338 | GCACTTGGACTAGATGTA | A571336Hi | +G*+C*+A*C*T*T*G*G*A*C*T*A*G*A*T*+G*+T*+A | 32826 | 18 |
| 1339 | TGGTCTCTGTTGTGCCACT | A571337Hi | +T*+G*+G*T*C*T*C*T*G*T*T*G*T*G*C*C*+A*+C*+T | 32874 | 19 |
| 1340 | TGGTCTCTGTTGTGCCAC | A571338Hi | +T*+G*+G*T*C*T*C*T*G*T*T*G*T*G*C*+C*+A*+C | 32875 | 18 |

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| 1341 | AGTTGGCTCAAATTAGTGG | A571339Hi | +A*+G*+T*T*G*G*C*T*C*A*A*A*T*T*A*G*+T*+G*+G | 33039 | 19 |
| 1342 | GTTGGCTCAAATTAGTGG | A571340Hi | +G*+T*+T*G*G*C*T*C*A*A*A*T*T*A*G*+T*+G*+G | 33039 | 18 |
| 1343 | AGTTGGCTCAAATTAGTG | A571341Hi | +A*+G*+T*T*G*G*C*T*C*A*A*A*T*T*A*+G*+T*+G | 33040 | 18 |
| 1344 | GATGAAACAGTTGGCTCAA | A571342Hi | +G*+A*+T*G*A*A*A*C*A*G*T*T*G*G*C*T*+C*+A*+A | 33047 | 19 |
| 1345 | GAGATGAAACAGTTGGCT | A571343Hi | +G*+A*+G*A*T*G*A*A*A*C*A*G*T*T*G*+G*+C*+T | 33050 | 18 |
| 1346 | TAGAGATGAAACAGTTGGC | A571344Hi | +T*+A*+G*A*G*A*T*G*A*A*A*C*A*G*T*T*+G*+G*+C | 33051 | 19 |
| 1347 | AGAGATGAAACAGTTGGC | A571345Hi | +A*+G*+A*G*A*T*G*A*A*A*C*A*G*T*T*+G*+G*+C | 33051 | 18 |
| 1348 | TACAACTTTCAAAGTTGTT | A571346Hi | +T*+A*+C*A*A*C*T*T*T*C*A*A*A*G*T*T*+G*+T*+T | 33108 | 19 |
| 1349 | TACATTCTAAGCTTACAAC | A571347Hi | +T*+A*+C*A*T*T*C*T*A*A*G*C*T*T*A*C*+A*+A*+C | 33121 | 19 |
| 1350 | TTTAATCCTTACATTCTAA | A571348Hi | +T*+T*+T*A*A*T*C*C*T*T*A*C*A*T*T*C*+T*+A*+A | 33130 | 19 |
| 1351 | GCAGGCATTATCCTAATCC | A571349Hi | +G*+C*+A*G*G*C*A*T*T*A*T*C*C*T*A*A*+T*+C*+C | 33168 | 19 |
| 1352 | ACTTCTTACAAGTCTGCAG | A571350Hi | +A*+C*+T*T*C*T*T*A*C*A*A*G*T*C*T*G*+C*+A*+G | 33281 | 19 |
| 1353 | CTACTTCTTACAAGTCTGC | A571351Hi | +C*+T*+A*C*T*T*C*T*T*A*C*A*A*G*T*C*+T*+G*+C | 33283 | 19 |
| 1354 | CTAGACTGGAGTTTATTCC | A571352Hi | +C*+T*+A*G*A*C*T*G*G*A*G*T*T*T*A*T*+T*+C*+C | 33476 | 19 |
| 1355 | TCCTAGACTGGAGTTTATT | A571353Hi | +T*+C*+C*T*A*G*A*C*T*G*G*A*G*T*T*T*+A*+T*+T | 33478 | 19 |
| 1356 | CCTAGACTGGAGTTTATT | A571354Hi | +C*+C*+T*A*G*A*C*T*G*G*A*G*T*T*T*+A*+T*+T | 33478 | 18 |
| 1357 | ATCCTAGACTGGAGTTTA | A571355Hi | +A*+T*+C*C*T*A*G*A*C*T*G*G*A*G*T*+T*+T*+A | 33480 | 18 |
| 1358 | AATCCTAGACTGGAGTTT | A571356Hi | +A*+A*+T*C*C*T*A*G*A*C*T*G*G*A*G*+T*+T*+T | 33481 | 18 |
| 1359 | GAATCCTAGACTGGAGTTT | A571357Hi | +G*+A*+A*T*C*C*T*A*G*A*C*T*G*G*A*G*+T*+T*+T | 33481 | 19 |
| 1360 | TCTACAGAATCCTAGACTG | A571358Hi | +T*+C*+T*A*C*A*G*A*A*T*C*C*T*A*G*A*+C*+T*+G | 33487 | 19 |
| 1361 | CAGAATCTACAGAATCCTA | A571359Hi | +C*+A*+G*A*A*T*C*T*A*C*A*G*A*A*T*C*+C*+T*+A | 33492 | 19 |
| 1362 | CCAGAATCTACAGAATCCT | A571360Hi | +C*+C*+A*G*A*A*T*C*T*A*C*A*G*A*A*T*+C*+C*+T | 33493 | 19 |
| 1363 | CCAGAATCTACAGAATCC | A571361Hi | +C*+C*+A*G*A*A*T*C*T*A*C*A*G*A*A*+T*+C*+C | 33494 | 18 |
| 1364 | TCTGAGACTGTATTATAAT | A571362Hi | +T*+C*+T*G*A*G*A*C*T*G*T*A*T*T*A*T*+A*+A*+T | 33653 | 19 |
| 1365 | TCTGTGGACACTGAGATAC | A571363Hi | +T*+C*+T*G*T*G*G*A*C*A*C*T*G*A*G*A*+T*+A*+C | 33803 | 19 |
| 1366 | GGTTCTGTGGACACTGAGA | A571364Hi | +G*+G*+T*T*C*T*G*T*G*G*A*C*A*C*T*G*+A*+G*+A | 33806 | 19 |
| 1367 | TGGTTCTGTGGACACTGAG | A571365Hi | +T*+G*+G*T*T*C*T*G*T*G*G*A*C*A*C*T*+G*+A*+G | 33807 | 19 |
| 1368 | TTTGCATGGTTCTGTGGAC | A571366Hi | +T*+T*+T*G*C*A*T*G*G*T*T*C*T*G*T*G*+G*+A*+C | 33813 | 19 |
| 1369 | CTTTGCATGGTTCTGTGGA | A571367Hi | +C*+T*+T*T*G*C*A*T*G*G*T*T*C*T*G*T*+G*+G*+A | 33814 | 19 |
| 1370 | ACTTTGCATGGTTCTGTGG | A571368Hi | +A*+C*+T*T*T*G*C*A*T*G*G*T*T*C*T*G*+T*+G*+G | 33815 | 19 |
| 1371 | GCATATCAGAACCATGTT | A571369Hi | +G*+C*+A*T*A*T*C*A*G*A*A*C*C*A*T*+G*+T*+T | 33837 | 18 |
| 1372 | TGAACTTTAATACAGTCAA | A571370Hi | +T*+G*+A*A*C*T*T*T*A*A*T*A*C*A*G*T*+C*+A*+A | 33885 | 19 |
| 1373 | ATGAACTTTAATACAGTCA | A571371Hi | +A*+T*+G*A*A*C*T*T*T*A*A*T*A*C*A*G*+T*+C*+A | 33886 | 19 |
| 1374 | ATGAACTTTAATACAGTC | A571372Hi | +A*+T*+G*A*A*C*T*T*T*A*A*T*A*C*A*+G*+T*+C | 33887 | 18 |
| 1375 | TACTATGAACTTTAATACA | A571373Hi | +T*+A*+C*T*A*T*G*A*A*C*T*T*T*A*A*T*+A*+C*+A | 33890 | 19 |

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| 1376 | GTACTATGAACTTTA ATAC | A571374Hi | +G*+T*+A*C*T*A*T*G*A*A*C*T*T*T*A*A*+ T*+A*+C | 33891 | 19 |
| 1377 | GTAGGTACTATGAAC TTTA | A571375Hi | +G*+T*+A*G*G*T*A*C*T*A*T*G*A*A*C*T*+ T*+T*+A | 33895 | 19 |
| 1378 | TAGGTACTATGAACT TTA | A571376Hi | +T*+A*+G*G*T*A*C*T*A*T*G*A*A*C*T*+T* +T*+A | 33895 | 18 |
| 1379 | GCAAATGTCACTTGA CTAG | A571377Hi | +G*+C*+A*A*A*T*G*T*C*A*C*T*T*G*A*C*+ T*+A*+G | 33920 | 19 |
| 1380 | AGCAAATGTCACTTG ACTA | A571378Hi | +A*+G*+C*A*A*A*T*G*T*C*A*C*T*T*G*A*+ C*+T*+A | 33921 | 19 |
| 1381 | TGAGCAAATGTCACT TGAC | A571379Hi | +T*+G*+A*G*C*A*A*A*T*G*T*C*A*C*T*T*+ G*+A*+C | 33923 | 19 |
| 1382 | AGGTATTTAAGCTAT TCTT | A571380Hi | +A*+G*+G*T*A*T*T*T*A*A*G*C*T*A*T*T*+ C*+T*+T | 33953 | 19 |
| 1383 | TTAACATCACTGGAC TTCT | A571381Hi | +T*+T*+A*A*C*A*T*C*A*C*T*G*G*A*C*T*+ T*+C*+T | 34024 | 19 |
| 1384 | CAGATTAACATCACT GGA | A571382Hi | +C*+A*+G*A*T*T*A*A*C*A*T*C*A*C*T*+G* +G*+A | 34029 | 18 |
| 1385 | AAAGTGACAGAGACA AGGC | A571383Hi | +A*+A*+A*G*T*G*A*C*A*G*A*G*A*C*A*A*+ G*+G*+C | 34110 | 19 |
| 1386 | TAGAGGTTAAATATT CAGG | A571384Hi | +T*+A*+G*A*G*G*T*T*A*A*A*T*A*T*T*C*+ A*+G*+G | 34141 | 19 |
| 1387 | ATAGAGGTTAAATAT TCAG | A571385Hi | +A*+T*+A*G*A*G*G*T*T*A*A*A*T*A*T*T*+ C*+A*+G | 34142 | 19 |
| 1388 | AAACTTTGAACTCAT AAGA | A571386Hi | +A*+A*+A*C*T*T*T*G*A*A*C*T*C*A*T*A*+ A*+G*+A | 34297 | 19 |
| 1389 | TGGTATAAACACCAA ATTG | A571387Hi | +T*+G*+G*T*A*T*A*A*A*C*A*C*C*A*A*A*+ T*+T*+G | 34417 | 19 |
| 1390 | ATGGTATAAACACCA AATT | A571388Hi | +A*+T*+G*G*T*A*T*A*A*A*C*A*C*C*A*A*+ A*+T*+T | 34418 | 19 |
| 1391 | CTGATTCAATGGTAT AAA | A571389Hi | +C*+T*+G*A*T*T*C*A*A*T*G*G*T*A*T*+A* +A*+A | 34427 | 18 |
| 1392 | GTAATGATGTCTCAT GAC | A571390H | +G*+T*+A*A*T*G*A*T*G*T*C*T*C*A*T*+G* +A*+C | 34543 | 18 |
| 1393 | GGTAATGATGTCTCA TGAC | A571391H | +G*+G*+T*A*A*T*G*A*T*G*T*C*T*C*A*T*+ G*+A*+C | 34543 | 19 |
| 1394 | CTGGTAATGATGTCT CATG | A571392H | +C*+T*+G*G*T*A*A*T*G*A*T*G*T*C*T*C*+ A*+T*+G | 34545 | 19 |
| 1395 | CTGGTAATGATGTCT CAT | A571393H | +C*+T*+G*G*T*A*A*T*G*A*T*G*T*C*T*+C* +A*+T | 34546 | 18 |
| 1396 | ACTGGTAATGATGTC TCAT | A571394H | +A*+C*+T*G*G*T*A*A*T*G*A*T*G*T*C*T*+ C*+A*+T | 34546 | 19 |
| 1397 | GCACTGGTAATGATG TCTC | A571395H | +G*+C*+A*C*T*G*G*T*A*A*T*G*A*T*G*T*+ C*+T*+C | 34548 | 19 |
| 1398 | CTGCACTGGTAATGA TGTC | A571396H | +C*+T*+G*C*A*C*T*G*G*T*A*A*T*G*A*T*+ G*+T*+C | 34550 | 19 |
| 1399 | GCTGCACTGGTAATG ATGT | A571397H | +G*+C*+T*G*C*A*C*T*G*G*T*A*A*T*G*A*+ T*+G*+T | 34551 | 19 |
| 1400 | TCCAGCTGCACTGGT AATG | A571398H | +T*+C*+C*A*G*C*T*G*C*A*C*T*G*G*T*A*+ A*+T*+G | 34555 | 19 |
| 1401 | CCTCCAGCTGCACTG GTAA | A571399H | +C*+C*+T*C*C*A*G*C*T*G*C*A*C*T*G*G*+ T*+A*+A | 34557 | 19 |
| 1402 | GCCTCCAGCTGCACT GGTA | A571400H | +G*+C*+C*T*C*C*A*G*C*T*G*C*A*C*T*G*+ G*+T*+A | 34558 | 19 |
| 1403 | CGCCTCCAGCTGCAC TGGT | A571401H | +C*+G*+C*C*T*C*C*A*G*C*T*G*C*A*C*T*+ G*+G*+T | 34559 | 19 |
| 1404 | GCGCCTCCAGCTGCA CTGG | A571402H | +G*+C*+G*C*C*T*C*C*A*G*C*T*G*C*A*C*+ T*+G*+G | 34560 | 19 |
| 1405 | GAAGCGCCTCCAGCT GCAC | A571403H | +G*+A*+A*G*C*G*C*C*T*C*C*A*G*C*T*G*+ C*+A*+C | 34563 | 19 |
| 1406 | CGAAGCGCCTCCAGC TGCA | A571404H | +C*+G*+A*A*G*C*G*C*C*T*C*C*A*G*C*T*+ G*+C*+A | 34564 | 19 |
| 1407 | TCGAAGCGCCTCCAG CTGC | A571405H | +T*+C*+G*A*A*G*C*G*C*C*T*C*C*A*G*C*+ T*+G*+C | 34565 | 19 |
| 1408 | TCGAAGCGCCTCCAG CTG | A571406H | +T*+C*+G*A*A*G*C*G*C*C*T*C*C*A*G*+C* +T*+G | 34566 | 18 |
| 1409 | CTCGAAGCGCCTCCA GCTG | A571407H | +C*+T*+C*G*A*A*G*C*G*C*C*T*C*C*A*G*+ C*+T*+G | 34566 | 19 |
| 1410 | CTCGAAGCGCCTCCA GCT | A571408H | +C*+T*+C*G*A*A*G*C*G*C*C*T*C*C*A*+G* +C*+T | 34567 | 18 |

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| 1411 | GCTCGAAGCGCCTCCAGCT | A571409H | +G*+C*+T*C*G*A*A*G*C*G*C*C*T*C*C*A*+G*+C*+T | 34567 | 19 |
| 1412 | CTCGAAGCGCCTCCAGC | A571410H | +C*+T*+C*G*A*A*G*C*G*C*C*T*C*C*+A*+G*+C | 34568 | 17 |
| 1413 | GCTCGAAGCGCCTCCAGC | A571411H | +G*+C*+T*C*G*A*A*G*C*G*C*C*T*C*C*+A*+G*+C | 34568 | 18 |
| 1414 | AGCTCGAAGCGCCTCCAGC | A571412H | +A*+G*+C*T*C*G*A*A*G*C*G*C*C*T*C*C*+A*+G*+C | 34568 | 19 |
| 1415 | GCTCGAAGCGCCTCCAG | A571413H | +G*+C*+T*C*G*A*A*G*C*G*C*C*T*C*+C*+A*+G | 34569 | 17 |
| 1416 | AGCTCGAAGCGCCTCCAG | A571414H | +A*+G*+C*T*C*G*A*A*G*C*G*C*C*T*C*+C*+A*+G | 34569 | 18 |
| 1417 | TAGCTCGAAGCGCCTCCAG | A571415H | +T*+A*+G*C*T*C*G*A*A*G*C*G*C*C*T*C*+C*+A*+G | 34569 | 19 |
| 1418 | TAGCTCGAAGCGCCTCCA | A571416H | +T*+A*+G*C*T*C*G*A*A*G*C*G*C*C*T*+C*+C*+A | 34570 | 18 |
| 1419 | AGCTCGAAGCGCCTCCA | A571417H | +A*+G*+C*T*C*G*A*A*G*C*G*C*C*T*+C*+C*+A | 34570 | 17 |
| 1420 | ATAGCTCGAAGCGCCTCCA | A571418H | +A*+T*+A*G*C*T*C*G*A*A*G*C*G*C*C*T*+C*+C*+A | 34570 | 19 |
| 1421 | TAGCTCGAAGCGCCTCC | A571419H | +T*+A*+G*C*T*C*G*A*A*G*C*G*C*C*+T*+C*+C | 34571 | 17 |
| 1422 | ATAGCTCGAAGCGCCTCC | A571420H | +A*+T*+A*G*C*T*C*G*A*A*G*C*G*C*C*+T*+C*+C | 34571 | 18 |
| 1423 | AGCTCGAAGCGCCTCC | A571421H | +A*+G*+C*T*C*G*A*A*G*C*G*C*C*+T*+C*+C | 34571 | 16 |
| 1424 | AATAGCTCGAAGCGCCTCC | A571422H | +A*+A*+T*A*G*C*T*C*G*A*A*G*C*G*C*C*+T*+C*+C | 34571 | 19 |
| 1425 | AATAGCTCGAAGCGCCTC | A571423H | +A*+A*+T*A*G*C*T*C*G*A*A*G*C*G*C*+C*+T*+C | 34572 | 18 |
| 1426 | AAATAGCTCGAAGCGCCTC | A571424H | +A*+A*+A*T*A*G*C*T*C*G*A*A*G*C*G*C*+C*+T*+C | 34572 | 19 |
| 1427 | AATAGCTCGAAGCGCCT | A571425H | +A*+A*+T*A*G*C*T*C*G*A*A*G*C*G*+C*+C*+T | 34573 | 17 |
| 1428 | AAATAGCTCGAAGCGCCT | A571426H | +A*+A*+A*T*A*G*C*T*C*G*A*A*G*C*G*+C*+C*+T | 34573 | 18 |
| 1429 | AAAATAGCTCGAAGCGCCT | A571427H | +A*+A*+A*A*T*A*G*C*T*C*G*A*A*G*C*G*+C*+C*+T | 34573 | 19 |
| 1430 | AATAGCTCGAAGCGCC | A571428H | +A*+A*+T*A*G*C*T*C*G*A*A*G*C*+G*+C*+C | 34574 | 16 |
| 1431 | AAATAGCTCGAAGCGCC | A571429H | +A*+A*+A*T*A*G*C*T*C*G*A*A*G*C*+G*+C*+C | 34574 | 17 |
| 1432 | AAAATAGCTCGAAGCGCC | A571430H | +A*+A*+A*A*T*A*G*C*T*C*G*A*A*G*C*+G*+C*+C | 34574 | 18 |
| 1433 | TAAAATAGCTCGAAGCGCC | A571431H | +T*+A*+A*A*A*T*A*G*C*T*C*G*A*A*G*C*+G*+C*+C | 34574 | 19 |
| 1434 | AAAATAGCTCGAAGCGC | A571432H | +A*+A*+A*A*T*A*G*C*T*C*G*A*A*G*+C*+G*+C | 34575 | 17 |
| 1435 | TAAAATAGCTCGAAGCGC | A571433H | +T*+A*+A*A*A*T*A*G*C*T*C*G*A*A*G*+C*+G*+C | 34575 | 18 |
| 1436 | GTAAAATAGCTCGAAGCGC | A571434H | +G*+T*+A*A*A*A*T*A*G*C*T*C*G*A*A*G*+C*+G*+C | 34575 | 19 |
| 1437 | TAAAATAGCTCGAAGCG | A571435H | +T*+A*+A*A*A*T*A*G*C*T*C*G*A*A*+G*+C*+G | 34576 | 17 |
| 1438 | GTAAAATAGCTCGAAGCG | A571436H | +G*+T*+A*A*A*A*T*A*G*C*T*C*G*A*A*+G*+C*+G | 34576 | 18 |
| 1439 | TGTAAAATAGCTCGAAGCG | A571437H | +T*+G*+T*A*A*A*A*T*A*G*C*T*C*G*A*A*+G*+C*+G | 34576 | 19 |
| 1440 | ATGTAAAATAGCTCGAAGC | A571438H | +A*+T*+G*T*A*A*A*A*T*A*G*C*T*C*G*A*+A*+G*+C | 34577 | 19 |
| 1441 | CAATCAACTATGTAACTTA | A571439Hi | +C*+A*+A*T*C*A*A*C*T*A*T*G*T*A*A*C*+T*+T*+A | 34610 | 19 |
| 1442 | ACAATCAACTATGTAACTT | A571440Hi | +A*+C*+A*A*T*C*A*A*C*T*A*T*G*T*A*A*+C*+T*+T | 34611 | 19 |
| 1443 | TTAGCTAATAGTACAATTC | A571441Hi | +T*+T*+A*G*C*T*A*A*T*A*G*T*A*C*A*A*+T*+T*+C | 34943 | 19 |
| 1444 | TAGCTAATAGTACAATTC | A571442Hi | +T*+A*+G*C*T*A*A*T*A*G*T*A*C*A*A*+T*+T*+C | 34943 | 18 |
| 1445 | AAGAAATTATTTGTGCCTC | A571443Hi | +A*+A*+G*A*A*A*T*T*A*T*T*T*G*T*G*C*+C*+T*+C | 35351 | 19 |

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| 1446 | CCTTCCACCTCAAATATTA | A571444Hi | +C*+C*+T*T*C*C*A*C*C*T*C*A*A*A*T*A*+T*+T*+A | 35392 | 19 |
| 1447 | TCGGTGTGACACTACAA | A571445Hi | +T*+C*+G*G*T*G*T*G*A*C*A*C*T*A*+C*+A*+A | 35637 | 17 |
| 1448 | CAACCATCTGTCCAATCTG | A571446Hi | +C*+A*+A*C*C*A*T*C*T*G*T*C*C*A*A*T*+C*+T*+G | 35800 | 19 |
| 1449 | TGATAGATTTAGGAAGATT | A571447Hi | +T*+G*+A*T*A*G*A*T*T*T*A*G*G*A*A*G*+A*+T*+T | 35928 | 19 |
| 1450 | AATGATAGATTTAGGAAGA | A571448Hi | +A*+A*+T*G*A*T*A*G*A*T*T*T*A*G*G*A*+A*+G*+A | 35930 | 19 |
| 1451 | GACTGAAGAAAGCTCTGTC | A571449Hi | +G*+A*+C*T*G*A*A*G*A*A*A*G*C*T*C*T*+G*+T*+C | 36017 | 19 |
| 1452 | ATGACTGAAGAAAGCTCTG | A571450Hi | +A*+T*+G*A*C*T*G*A*A*G*A*A*A*G*C*T*+C*+T*+G | 36019 | 19 |
| 1453 | CTGAAACTATGAATAGGAC | A571451Hi | +C*+T*+G*A*A*A*C*T*A*T*G*A*A*T*A*G*+G*+A*+C | 36103 | 19 |
| 1454 | AAGGCTGTCAACTTTAAGG | A571452Hi | +A*+A*+G*G*C*T*G*T*C*A*A*C*T*T*T*A*+A*+G*+G | 36238 | 19 |
| 1455 | AAGGCTGTCAACTTTAAG | A571453Hi | +A*+A*+G*G*C*T*G*T*C*A*A*C*T*T*T*+A*+A*+G | 36239 | 18 |
| 1456 | GAATAAGGCTGTCAACTTT | A571454Hi | +G*+A*+A*T*A*A*G*G*C*T*G*T*C*A*A*C*+T*+T*+T | 36242 | 19 |
| 1457 | AGTACAGTCCTCAAGTGAT | A571455Hi | +A*+G*+T*A*C*A*G*T*C*C*T*C*A*A*G*T*+G*+A*+T | 36462 | 19 |
| 1458 | AGTACAGTCCTCAAGTGA | A571456Hi | +A*+G*+T*A*C*A*G*T*C*C*T*C*A*A*G*+T*+G*+A | 36463 | 18 |
| 1459 | TGTACTTACATACTGATAT | A571457Hi | +T*+G*+T*A*C*T*T*A*C*A*T*A*C*T*G*A*+T*+A*+T | 36508 | 19 |
| 1460 | AATGTACTTACATACTGAT | A571458Hi | +A*+A*+T*G*T*A*C*T*T*A*C*A*T*A*C*T*+G*+A*+T | 36510 | 19 |
| 1461 | GAATGTACTTACATACTGA | A571459Hi | +G*+A*+A*T*G*T*A*C*T*T*A*C*A*T*A*C*+T*+G*+A | 36511 | 19 |
| 1462 | AGAATGTACTTACATACTG | A571460Hi | +A*+G*+A*A*T*G*T*A*C*T*T*A*C*A*T*A*+C*+T*+G | 36512 | 19 |
| 1463 | AAGAATGTACTTACATACT | A571461Hi | +A*+A*+G*A*A*T*G*T*A*C*T*T*A*C*A*T*+A*+C*+T | 36513 | 19 |
| 1464 | TAAATGATTAAGCCTTTAC | A571462Hi | +T*+A*+A*A*T*G*A*T*T*A*A*G*C*C*T*T*+T*+A*+C | 36539 | 19 |
| 1465 | AGTAAATGATTAAGCCTTT | A571463Hi | +A*+G*+T*A*A*A*T*G*A*T*T*A*A*G*C*C*+T*+T*+T | 36541 | 19 |
| 1466 | AGTAAATGATTAAGCCTT | A571464Hi | +A*+G*+T*A*A*A*T*G*A*T*T*A*A*G*C*+C*+T*+T | 36542 | 18 |
| 1467 | ACTGCACGGCATGGTACA | A571465Hi | +A*+C*+T*G*C*A*C*G*G*C*A*T*G*G*T*+A*+C*+A | 36616 | 18 |
| 1468 | GGTACTGCACGGCATGG | A571466Hi | +G*+G*+T*A*C*T*G*C*A*C*G*G*C*A*+T*+G*+G | 36620 | 17 |
| 1469 | ATGAATACATGTACACCTA | A571467Hi | +A*+T*+G*A*A*T*A*C*A*T*G*T*A*C*A*C*+C*+T*+A | 36746 | 19 |
| 1470 | TGCAATATGCTATCCTTA | A571468Hi | +T*+G*+C*A*A*T*A*T*G*C*T*A*T*C*C*+T*+T*+A | 36843 | 18 |
| 1471 | TAGATGCAATATGCTATCC | A571469Hi | +T*+A*+G*A*T*G*C*A*A*T*A*T*G*C*T*A*+T*+C*+C | 36846 | 19 |
| 1472 | CACTAGATGCAATATGCT | A571470Hi | +C*+A*+C*T*A*G*A*T*G*C*A*A*T*A*T*+G*+C*+T | 36850 | 18 |
| 1473 | ATATCAGGCCTGACCTTA | A571471Hi | +A*+T*+A*T*C*A*G*G*C*C*T*G*A*C*C*+T*+T*+A | 37398 | 18 |
| 1474 | GTTATATCAGGCCTGACC | A571472Hi | +G*+T*+T*A*T*A*T*C*A*G*G*C*C*T*G*+A*+C*+C | 37401 | 18 |
| 1475 | CTGTTATATCAGGCCTGAC | A571473Hi | +C*+T*+G*T*T*A*T*A*T*C*A*G*G*C*C*T*+G*+A*+C | 37402 | 19 |
| 1476 | GTGCTGTTATATCAGGCCT | A571474Hi | +G*+T*+G*C*T*G*T*T*A*T*A*T*C*A*G*G*+C*+C*+T | 37405 | 19 |
| 1477 | GTGCTGTTATATCAGGCC | A571475Hi | +G*+T*+G*C*T*G*T*T*A*T*A*T*C*A*G*+G*+C*+C | 37406 | 18 |
| 1478 | TGGTGCTGTTATATCAGG | A571476Hi | +T*+G*+G*T*G*C*T*G*T*T*A*T*A*T*C*+A*+G*+G | 37408 | 18 |
| 1479 | CTGGTGCTGTTATATCAGG | A571477Hi | +C*+T*+G*G*T*G*C*T*G*T*T*A*T*A*T*C*+A*+G*+G | 37408 | 19 |
| 1480 | ATCTGGTGCTGTTATATCA | A571478Hi | +A*+T*+C*T*G*G*T*G*C*T*G*T*T*A*T*A*+T*+C*+A | 37410 | 19 |

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| 1481 | AAATCTGGTGCTGTTATAT | A571479Hi | +A*+A*+A*T*C*T*G*G*T*G*C*T*G*T*T*A*+T*+A*+T | 37412 | 19 |
| 1482 | TGCCTACTCTGGAGTCAGC | A571480Hi | +T*+G*+C*C*T*A*C*T*C*T*G*G*A*G*T*C*+A*+G*+C | 37444 | 19 |
| 1483 | AATACAACAGTTGTTCAGG | A571481Hi | +A*+A*+T*A*C*A*A*C*A*G*T*T*G*T*T*C*+A*+G*+G | 37495 | 19 |
| 1484 | AAATACAACAGTTGTTCAG | A571482Hi | +A*+A*+A*T*A*C*A*A*C*A*G*T*T*G*T*T*+C*+A*+G | 37496 | 19 |
| 1485 | TAAATACAACAGTTGTTCA | A571483Hi | +T*+A*+A*A*T*A*C*A*A*C*A*G*T*T*G*T*+T*+C*+A | 37497 | 19 |
| 1486 | TTAAATACAACAGTTGTTC | A571484Hi | +T*+T*+A*A*A*T*A*C*A*A*C*A*G*T*T*G*+T*+T*+C | 37498 | 19 |
| 1487 | GCTTTAAATACAACAGTTG | A571485Hi | +G*+C*+T*T*T*A*A*A*T*A*C*A*A*C*A*G*+T*+T*+G | 37501 | 19 |
| 1488 | AGACATAGTGCTTTAAATA | A571486Hi | +A*+G*+A*C*A*T*A*G*T*G*C*T*T*T*A*A*+A*+T*+A | 37510 | 19 |
| 1489 | GACATAGTGCTTTAAATA | A571487Hi | +G*+A*+C*A*T*A*G*T*G*C*T*T*T*A*A*+A*+T*+A | 37510 | 18 |
| 1490 | CTTAAGGATTCTAGACATA | A571488Hi | +C*+T*+T*A*A*G*G*A*T*T*C*T*A*G*A*C*+A*+T*+A | 37522 | 19 |
| 1491 | TTCTATCACTTGAGGTCCT | A571489Hi | +T*+T*+C*T*A*T*C*A*C*T*T*G*A*G*G*T*+C*+C*+T | 37647 | 19 |
| 1492 | GTTCTATCACTTGAGGTCC | A571490Hi | +G*+T*+T*C*T*A*T*C*A*C*T*T*G*A*G*G*+T*+C*+C | 37648 | 19 |
| 1493 | CTTTGTTCTATCACTTGA | A571491Hi | +C*+T*+T*T*G*T*T*C*T*A*T*C*A*C*T*+T*+G*+A | 37653 | 18 |
| 1494 | CCAAATGAACATTCCTGTA | A571492Hi | +C*+C*+A*A*A*T*G*A*A*C*A*T*T*C*C*T*+G*+T*+A | 37686 | 19 |
| 1495 | ACCAAATGAACATTCCTGT | A571493Hi | +A*+C*+C*A*A*A*T*G*A*A*C*A*T*T*C*C*+T*+G*+T | 37687 | 19 |
| 1496 | TAAGACCAAATGAACATTC | A571494Hi | +T*+A*+A*G*A*C*C*A*A*A*T*G*A*A*C*A*+T*+T*+C | 37691 | 19 |
| 1497 | AACATCATGCTACATGTAA | A571495Hi | +A*+A*+C*A*T*C*A*T*G*C*T*A*C*A*T*G*+T*+A*+A | 37738 | 19 |
| 1498 | AAACATCATGCTACATGTA | A571496Hi | +A*+A*+A*C*A*T*C*A*T*G*C*T*A*C*A*T*+G*+T*+A | 37739 | 19 |
| 1499 | AACTTCTGAGGCTGCCTAT | A571497Hi | +A*+A*+C*T*T*C*T*G*A*G*G*C*T*G*C*C*+T*+A*+T | 37803 | 19 |
| 1500 | AACTTCTGAGGCTGCCTA | A571498Hi | +A*+A*+C*T*T*C*T*G*A*G*G*C*T*G*C*+C*+T*+A | 37804 | 18 |
| 1501 | AGAGGTTCTGACATTCAC | A571499Hi | +A*+G*+A*G*G*T*T*C*T*G*A*C*A*T*T*+C*+A*+C | 37893 | 18 |
| 1502 | CAAAGAGGTTCTGACATT | A571500Hi | +C*+A*+A*A*G*A*G*G*T*T*C*T*G*A*C*+A*+T*+T | 37896 | 18 |
| 1503 | CAACTTTCAGTCCTTATTT | A571501Hi | +C*+A*+A*C*T*T*T*C*A*G*T*C*C*T*T*A*+T*+T*+T | 37925 | 19 |
| 1504 | CTCCAACTTTCAGTCCTTA | A571502Hi | +C*+T*+C*C*A*A*C*T*T*T*C*A*G*T*C*C*+T*+T*+A | 37928 | 19 |
| 1505 | GAAGGCAGCCTTGATAACC | A571503Hi | +G*+A*+A*G*G*C*A*G*C*C*T*T*G*A*T*A*+A*+C*+C | 37953 | 19 |
| 1506 | GAAGGCAGCCTTGATAAC | A571504Hi | +G*+A*+A*G*G*C*A*G*C*C*T*T*G*A*T*+A*+A*+C | 37954 | 18 |
| 1507 | TCCAATTACATGCCAAGGA | A571505Hi | +T*+C*+C*A*A*T*T*A*C*A*T*G*C*C*A*A*+G*+G*+A | 38002 | 19 |
| 1508 | AAGAGTAGCTGGAATAATC | A571506Hi | +A*+A*+G*A*G*T*A*G*C*T*G*G*A*A*T*A*+A*+T*+C | 38365 | 19 |
| 1509 | AGAGTAGCTGGAATAATC | A571507Hi | +A*+G*+A*G*T*A*G*C*T*G*G*A*A*T*A*+A*+T*+C | 38365 | 18 |
| 1510 | GTGCTTTAAGATGCTGGAA | A571508Hi | +G*+T*+G*C*T*T*T*A*A*G*A*T*G*C*T*G*+G*+A*+A | 38472 | 19 |
| 1511 | CTGTGCTTTAAGATGCTGG | A571509Hi | +C*+T*+G*T*G*C*T*T*T*A*A*G*A*T*G*C*+T*+G*+G | 38474 | 19 |
| 1512 | GAGTAGGCTGTGCTTTAAG | A571510Hi | +G*+A*+G*T*A*G*G*C*T*G*T*G*C*T*T*T*+A*+A*+G | 38481 | 19 |
| 1513 | GAGTAGGCTGTGCTTTAA | A571511Hi | +G*+A*+G*T*A*G*G*C*T*G*T*G*C*T*T*+T*+A*+A | 38482 | 18 |
| 1514 | TGTGAGTAGGCTGTGCTTT | A571512Hi | +T*+G*+T*G*A*G*T*A*G*G*C*T*G*T*G*C*+T*+T*+T | 38484 | 19 |
| 1515 | GTGTGAGTAGGCTGTGCTT | A571513Hi | +G*+T*+G*T*G*A*G*T*A*G*G*C*T*G*T*G*+C*+T*+T | 38485 | 19 |

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| 1516 | GTGTGAGTAGGCTGTGCT | A571514Hi | +G*+T*+G*T*G*A*G*T*A*G*G*C*T*G*T*+G*+C*+T | 38486 | 18 |
| 1517 | GTAAGAATGCTTACTGAAT | A571515Hi | +G*+T*+A*A*G*A*A*T*G*C*T*T*A*C*T*G*+A*+A*+T | 38564 | 19 |
| 1518 | GTGTAAGAATGCTTACTGA | A571516Hi | +G*+T*+G*T*A*A*G*A*A*T*G*C*T*T*A*C*+T*+G*+A | 38566 | 19 |
| 1519 | TTGAGTTGAACAGACTGT | A571517Hi | +T*+T*+G*A*G*T*T*G*A*A*C*A*G*A*C*+T*+G*+T | 38728 | 18 |
| 1520 | ATTTGAGTTGAACAGACTG | A571518Hi | +A*+T*+T*T*G*A*G*T*T*G*A*A*C*A*G*A*+C*+T*+G | 38729 | 19 |
| 1521 | TAAACATTTGAGTTGAACA | A571519Hi | +T*+A*+A*A*C*A*T*T*T*G*A*G*T*T*G*A*+A*+C*+A | 38734 | 19 |
| 1522 | ATAAACATTTGAGTTGAAC | A571520Hi | +A*+T*+A*A*A*C*A*T*T*T*G*A*G*T*T*G*+A*+A*+C | 38735 | 19 |
| 1523 | CTGGATTCTTCTGGCATGC | A571521H | +C*+T*+G*G*A*T*T*C*T*T*C*T*G*G*C*A*+T*+G*+C | 38793 | 19 |
| 1524 | CACTGTTTTTTAACCATAT | A571522H | +C*+A*+C*T*G*T*T*T*T*T*T*A*A*C*C*A*+T*+A*+T | 38841 | 19 |
| 1525 | CATTCTTGAAACACTGTTT | A571523H | +C*+A*+T*T*C*T*T*G*A*A*A*C*A*C*T*G*+T*+T*+T | 38852 | 19 |
| 1526 | TATCATTCTTGAAACACTG | A571524H | +T*+A*+T*C*A*T*T*C*T*T*G*A*A*A*C*A*+C*+T*+G | 38855 | 19 |
| 1527 | AATATCATTCTTGAAACAC | A571525H | +A*+A*+T*A*T*C*A*T*T*C*T*T*G*A*A*A*+C*+A*+C | 38857 | 19 |
| 1528 | TGAATATCATTCTTGAAAC | A571526H | +T*+G*+A*A*T*A*T*C*A*T*T*C*T*T*G*A*+A*+A*+C | 38859 | 19 |
| 1529 | TTTGTGAATATCATTCTTG | A571527H | +T*+T*+T*G*T*G*A*A*T*A*T*C*A*T*T*C*+T*+T*+G | 38863 | 19 |
| 1530 | GTTTGTGAATATCATTCTT | A571528H | +G*+T*+T*T*G*T*G*A*A*T*A*T*C*A*T*T*+C*+T*+T | 38864 | 19 |
| 1531 | AGTTTGTGAATATCATTCT | A571529H | +A*+G*+T*T*T*G*T*G*A*A*T*A*T*C*A*T*+T*+C*+T | 38865 | 19 |
| 1532 | CAGTTTGTGAATATCATTC | A571530H | +C*+A*+G*T*T*T*G*T*G*A*A*T*A*T*C*A*+T*+T*+C | 38866 | 19 |
| 1533 | AGGACCAGTTTGTGAATAT | A571531H | +A*+G*+G*A*C*C*A*G*T*T*T*G*T*G*A*A*+T*+A*+T | 38871 | 19 |
| 1534 | TAGGACCAGTTTGTGAATA | A571532H | +T*+A*+G*G*A*C*C*A*G*T*T*T*G*T*G*A*+A*+T*+A | 38872 | 19 |
| 1535 | GCTAGGACCAGTTTGTGAA | A571533H | +G*+C*+T*A*G*G*A*C*C*A*G*T*T*T*G*T*+G*+A*+A | 38874 | 19 |
| 1536 | GCTAGGACCAGTTTGTGA | A571534H | +G*+C*+T*A*G*G*A*C*C*A*G*T*T*T*G*+T*+G*+A | 38875 | 18 |
| 1537 | TGCTAGGACCAGTTTGTGA | A571535H | +T*+G*+C*T*A*G*G*A*C*C*A*G*T*T*T*G*+T*+G*+A | 38875 | 19 |
| 1538 | GCTAGGACCAGTTTGTG | A571536H | +G*+C*+T*A*G*G*A*C*C*A*G*T*T*T*+G*+T*+G | 38876 | 17 |
| 1539 | TGCTAGGACCAGTTTGTG | A571537H | +T*+G*+C*T*A*G*G*A*C*C*A*G*T*T*T*+G*+T*+G | 38876 | 18 |
| 1540 | CTGCTAGGACCAGTTTGTG | A571538H | +C*+T*+G*C*T*A*G*G*A*C*C*A*G*T*T*T*+G*+T*+G | 38876 | 19 |
| 1541 | CTGCTAGGACCAGTTTGT | A571539H | +C*+T*+G*C*T*A*G*G*A*C*C*A*G*T*T*+T*+G*+T | 38877 | 18 |
| 1542 | GCTGCTAGGACCAGTTTGT | A571540H | +G*+C*+T*G*C*T*A*G*G*A*C*C*A*G*T*T*+T*+G*+T | 38877 | 19 |
| 1543 | AGCTGCTAGGACCAGTTTG | A571541H | +A*+G*+C*T*G*C*T*A*G*G*A*C*C*A*G*T*+T*+T*+G | 38878 | 19 |
| 1544 | AAGCTGCTAGGACCAGTTT | A571542H | +A*+A*+G*C*T*G*C*T*A*G*G*A*C*C*A*G*+T*+T*+T | 38879 | 19 |
| 1545 | TCAAAGCTGCTAGGACCAG | A571543H | +T*+C*+A*A*A*G*C*T*G*C*T*A*G*G*A*C*+C*+A*+G | 38882 | 19 |
| 1546 | TCAAAGCTGCTAGGACCA | A571544H | +T*+C*+A*A*A*G*C*T*G*C*T*A*G*G*A*+C*+C*+A | 38883 | 18 |
| 1547 | TTCAAAGCTGCTAGGACCA | A571545H | +T*+T*+C*A*A*A*G*C*T*G*C*T*A*G*G*A*+C*+C*+A | 38883 | 19 |
| 1548 | GTTCAAAGCTGCTAGGACC | A571546H | +G*+T*+T*C*A*A*A*G*C*T*G*C*T*A*G*G*+A*+C*+C | 38884 | 19 |
| 1549 | GTTCAAAGCTGCTAGGAC | A571547H | +G*+T*+T*C*A*A*A*G*C*T*G*C*T*A*G*+G*+A*+C | 38885 | 18 |
| 1550 | TGTTCAAAGCTGCTAGGAC | A571548H | +T*+G*+T*T*C*A*A*A*G*C*T*G*C*T*A*G*+G*+A*+C | 38885 | 19 |

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| 1551 | CCTGTTCAAAGCTGC TAGG | A571549H | +C*+C*+T*G*T*T*C*A*A*A*G*C*T*G*C*T*+ A*+G*+G | 38887 | 19 |
| 1552 | CCTGTTCAAAGCTGC TAG | A571550H | +C*+C*+T*G*T*T*C*A*A*A*G*C*T*G*C*+T* +A*+G | 38888 | 18 |
| 1553 | GCTGGACTTAGCTTA GT | A571551Hi | +G*+C*+T*G*G*A*C*T*T*A*G*C*T*T*+A*+G *+T | 39080 | 17 |
| 1554 | TAGCTGGACTTAGCT TAG | A571552Hi | +T*+A*+G*C*T*G*G*A*C*T*T*A*G*C*T*+T* +A*+G | 39081 | 18 |
| 1555 | GCAAACTAGAGTGGA TTT | A571553Hi | +G*+C*+A*A*A*C*T*A*G*A*G*T*G*G*A*+T* +T*+T | 39152 | 18 |
| 1556 | ACCAAATCATTTCAG AGGT | A571554Hi | +A*+C*+C*A*A*A*T*C*A*T*T*T*C*A*G*A*+ G*+G*+T | 39709 | 19 |
| 1557 | TCTTAACATCTTTAAT AAA | A571555Hi | +T*+C*+T*T*A*A*C*A*T*C*T*T*T*A*A*T*+ A*+A*+A | 39907 | 19 |
| 1558 | CATGGAATCATTTCC ATTA | A571556Hi | +C*+A*+T*G*G*A*A*T*C*A*T*T*T*C*C*A*+ T*+T*+A | 39983 | 19 |
| 1559 | CTTTAATTAATTTATG ACA | A571557Hi | +C*+T*+T*T*A*A*T*T*A*A*T*T*T*A*T*G*+ A*+C*+A | 40024 | 19 |
| 1560 | TTATAGGCAGTGAGT GAC | A571558Hi | +T*+T*+A*T*A*G*G*C*A*G*T*G*A*G*T*+G* +A*+C | 40096 | 18 |
| 1561 | ATATTATAGGCAGTG AGT | A571559Hi | +A*+T*+A*T*T*A*T*A*G*G*C*A*G*T*G*+A* +G*+T | 40099 | 18 |
| 1562 | AAACATATTATAGGC AGTG | A571560Hi | +A*+A*+A*C*A*T*A*T*T*A*T*A*G*G*C*A*+ G*+T*+G | 40102 | 19 |
| 1563 | TTGAGTATAAATGAC TCAA | A571561Hi | +T*+T*+G*A*G*T*A*T*A*A*A*T*G*A*C*T*+ C*+A*+A | 40119 | 19 |
| 1564 | TCTTGCCATACTCAA GGA | A571562Hi | +T*+C*+T*T*G*C*C*A*T*A*C*T*C*A*A*+G* +G*+A | 40150 | 18 |
| 1565 | AAATTCTTGCCATAC TCAA | A571563Hi | +A*+A*+A*T*T*C*T*T*G*C*C*A*T*A*C*T*+ C*+A*+A | 40153 | 19 |
| 1566 | AATTCTTGCCATACT CAA | A571564Hi | +A*+A*+T*T*C*T*T*G*C*C*A*T*A*C*T*+C* +A*+A | 40153 | 18 |
| 1567 | AACATAAATTCTTGC CATA | A571565Hi | +A*+A*+C*A*T*A*A*A*T*T*C*T*T*G*C*C*+ A*+T*+A | 40158 | 19 |
| 1568 | CAACATAAATTCTTG CCAT | A571566Hi | +C*+A*+A*C*A*T*A*A*A*T*T*C*T*T*G*C*+ C*+A*+T | 40159 | 19 |
| 1569 | CGATGCTGCATCTCC TCTG | A571567Hi | +C*+G*+A*T*G*C*T*G*C*A*T*C*T*C*C*T*+ C*+T*+G | 40356 | 19 |
| 1570 | TCGATGCTGCATCTC CTCT | A571568Hi | +T*+C*+G*A*T*G*C*T*G*C*A*T*C*T*C*C*+ T*+C*+T | 40357 | 19 |
| 1571 | CTCGATGCTGCATCT CCTC | A571569Hi | +C*+T*+C*G*A*T*G*C*T*G*C*A*T*C*T*C*+ C*+T*+C | 40358 | 19 |
| 1572 | CTAGAATATGCTTAC TAG | A571570Hi | +C*+T*+A*G*A*A*T*A*T*G*C*T*T*A*C*+T* +A*+G | 40556 | 18 |
| 1573 | GTGGCAATCTTACTG TCAA | A571571Hi | +G*+T*+G*G*C*A*A*T*C*T*T*A*C*T*G*T*+ C*+A*+A | 42238 | 19 |
| 1574 | TGTGGCAATCTTACT GTC | A571572Hi | +T*+G*+T*G*G*C*A*A*T*C*T*T*A*C*T*+G* +T*+C | 42240 | 18 |
| 1575 | CTGTGGCAATCTTAC TGT | A571573Hi | +C*+T*+G*T*G*G*C*A*A*T*C*T*T*A*C*+T* +G*+T | 42241 | 18 |
| 1576 | CTGTGGCAATCTTAC TG | A571574Hi | +C*+T*+G*T*G*G*C*A*A*T*C*T*T*A*+C*+T *+G | 42242 | 17 |
| 1577 | CGGCAACTGTGGCAA TCT | A571575Hi | +C*+G*+G*C*A*A*C*T*G*T*G*G*C*A*A*+T* +C*+T | 42247 | 18 |
| 1578 | GCGGCAACTGTGGCA ATCT | A571576Hi | +G*+C*+G*G*C*A*A*C*T*G*T*G*G*C*A*A* +T*+C*+T | 42247 | 19 |
| 1579 | GCGGCAACTGTGGCA ATC | A571577Hi | +G*+C*+G*G*C*A*A*C*T*G*T*G*G*C*A*+A *+T*+C | 42248 | 18 |
| 1580 | CGCGGCAACTGTGGC AAT | A571578Hi | +C*+G*+C*G*G*C*A*A*C*T*G*T*G*G*C*+A *+A*+T | 42249 | 18 |
| 1581 | ACGCGGCAACTGTGG CAAT | A571579Hi | +A*+C*+G*C*G*G*C*A*A*C*T*G*T*G*G*C* +A*+A*+T | 42249 | 19 |
| 1582 | ACGCGGCAACTGTGG CAA | A571580Hi | +A*+C*+G*C*G*G*C*A*A*C*T*G*T*G*G*+C *+A*+A | 42250 | 18 |
| 1583 | CGCGGCAACTGTGGC AA | A571581Hi | +C*+G*+C*G*G*C*A*A*C*T*G*T*G*G*+C*+ A*+A | 42250 | 17 |
| 1584 | GTTCACAATGCTGGT ATCC | A571582Hi | +G*+T*+T*C*A*C*A*A*T*G*C*T*G*G*T*A*+ T*+C*+C | 42369 | 19 |
| 1585 | TATGTTCACAATGCT GGTA | A571583Hi | +T*+A*+T*G*T*T*C*A*C*A*A*T*G*C*T*G*+ G*+T*+A | 42372 | 19 |

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| 1586 | TTTCACCAACACTCACCAT | A571584Hi | +T*+T*+T*C*A*C*C*A*A*C*A*C*T*C*A*C*+C*+A*+T | 42429 | 19 |
| 1587 | CTTCTCTAATAACTTTAGA | A571585Hi | +C*+T*+T*C*T*C*T*A*A*T*A*A*C*T*T*T*+A*+G*+A | 42505 | 19 |
| 1588 | CGACTGCTGAGGTTACA | A571586Hi | +C*+G*+A*C*T*G*C*T*G*A*G*G*T*T*+A*+C*+A | 42535 | 17 |
| 1589 | CCGACTGCTGAGGTTACA | A571587Hi | +C*+C*+G*A*C*T*G*C*T*G*A*G*G*T*T*T*+A*+C*+A | 42535 | 18 |
| 1590 | CCGACTGCTGAGGTTAC | A571588Hi | +C*+C*+G*A*C*T*G*C*T*G*A*G*G*T*+T*+A*+C | 42536 | 17 |
| 1591 | TCTCCACATCACAGCACTT | A571589Hi | +T*+C*+T*C*C*A*C*A*T*C*A*C*A*G*C*A*+C*+T*+T | 42570 | 19 |
| 1592 | TTCTCCACATCACAGCACT | A571590Hi | +T*+T*+C*T*C*C*A*C*A*T*C*A*C*A*G*C*C*+A*+C*+T | 42571 | 19 |
| 1593 | TGAAAGGCTGTGCGTCA | A571591Hi | +T*+G*+A*A*A*G*G*C*T*G*T*G*C*G*+T*+C*+A | 42650 | 17 |
| 1594 | GTGAAAGGCTGTGCGTCA | A571592Hi | +G*+T*+G*A*A*A*G*G*C*T*G*T*G*C*G*+T*+C*+A | 42650 | 18 |
| 1595 | AGTGAAAGGCTGTGCGTCA | A571593Hi | +A*+G*+T*G*A*A*A*G*G*C*T*G*T*G*C*G*+T*+C*+A | 42650 | 19 |
| 1596 | CAGAGTAAGACATGCAATC | A571594Hi | +C*+A*+G*A*G*T*A*A*G*A*C*A*T*G*C*A*+A*+T*+C | 42833 | 19 |
| 1597 | AGAGTAAGACATGCAATC | A571595Hi | +A*+G*+A*G*T*A*A*G*A*C*A*T*G*C*A*+A*+T*+C | 42833 | 18 |
| 1598 | CTATTCAGAGTAAGACATG | A571596Hi | +C*+T*+A*T*T*C*A*G*A*G*T*A*A*G*A*C*+A*+T*+G | 42838 | 19 |
| 1599 | CTGCAATATTTGGACCTA | A571597Hi | +C*+T*+G*C*A*A*T*A*T*T*T*G*G*A*C*+C*+T*+A | 42880 | 18 |
| 1600 | TCTGCAATATTTGGACCT | A571598Hi | +T*+C*+T*G*C*A*A*T*A*T*T*T*G*G*A*+C*+C*+T | 42881 | 18 |
| 1601 | TGTCTGCAATATTTGGACC | A571599Hi | +T*+G*+T*C*T*G*C*A*A*T*A*T*T*T*G*G*+A*+C*+C | 42882 | 19 |
| 1602 | GCTCTCCAAGTTTAGATGT | A571600Hi | +G*+C*+T*C*T*C*C*A*A*G*T*T*T*A*G*A*+T*+G*+T | 42925 | 19 |
| 1603 | CCTTATTTGGAACTCTGCT | A571601Hi | +C*+C*+T*T*A*T*T*T*G*G*A*A*C*T*C*T*+G*+C*+T | 42941 | 19 |
| 1604 | AATCTCAAGTTCTACCTTA | A571602Hi | +A*+A*+T*C*T*C*A*A*G*T*T*C*T*A*C*C*+T*+T*+A | 42955 | 19 |
| 1605 | GAATCTCAAGTTCTACCTT | A571603Hi | +G*+A*+A*T*C*T*C*A*A*G*T*T*C*T*A*C*+C*+T*+T | 42956 | 19 |
| 1606 | TGAATCTCAAGTTCTACCT | A571604Hi | +T*+G*+A*A*T*C*T*C*A*A*G*T*T*C*T*A*+C*+C*+T | 42957 | 19 |
| 1607 | TGAATCTCAAGTTCTACC | A571605Hi | +T*+G*+A*A*T*C*T*C*A*A*G*T*T*C*T*+A*+C*+C | 42958 | 18 |
| 1608 | TAAATCAGAGTTGAATCTC | A571606Hi | +T*+A*+A*A*T*C*A*G*A*G*T*T*G*A*A*T*+C*+T*+C | 42968 | 19 |
| 1609 | TATGTATCCAAACATGGAT | A571607Hi | +T*+A*+T*G*T*A*T*C*C*A*A*A*C*A*T*G*+G*+A*+T | 43022 | 19 |
| 1610 | TTATGTATCCAAACATGGA | A571608Hi | +T*+T*+A*T*G*T*A*T*C*C*A*A*A*C*A*T*+G*+G*+A | 43023 | 19 |
| 1611 | ACATCGCTGTTCTAGACAG | A571609Hi | +A*+C*+A*T*C*G*C*T*G*T*T*C*T*A*G*A*+C*+A*+G | 43076 | 19 |
| 1612 | ACATCGCTGTTCTAGACA | A571610Hi | +A*+C*+A*T*C*G*C*T*G*T*T*C*T*A*G*+A*+C*+A | 43077 | 18 |
| 1613 | GAACATCGCTGTTCTAGA | A571611Hi | +G*+A*+A*C*A*T*C*G*C*T*G*T*T*C*T*+A*+G*+A | 43079 | 18 |
| 1614 | AATGGAACATCGCTGTTC | A571612Hi | +A*+A*+T*G*G*A*A*C*A*T*C*G*C*T*G*+T*+T*+C | 43083 | 18 |
| 1615 | AATGGAACATCGCTGTT | A571613Hi | +A*+A*+T*G*G*A*A*C*A*T*C*G*C*T*+G*+T*+T | 43084 | 17 |
| 1616 | AAATGGAACATCGCTGTT | A571614Hi | +A*+A*+A*T*G*G*A*A*C*A*T*C*G*C*T*+G*+T*+T | 43084 | 18 |
| 1617 | TAAATGGAACATCGCTGT | A571615Hi | +T*+A*+A*A*T*G*G*A*A*C*A*T*C*G*C*+T*+G*+T | 43085 | 18 |
| 1618 | GCATAAATGGAACATCGC | A571616Hi | +G*+C*+A*T*A*A*A*T*G*G*A*A*C*A*T*+C*+G*+C | 43088 | 18 |
| 1619 | GGCATAAATGGAACATCG | A571617Hi | +G*+G*+C*A*T*A*A*A*T*G*G*A*A*C*A*+T*+C*+G | 43089 | 18 |
| 1620 | AGGCATAAATGGAACATCG | A571618Hi | +A*+G*+G*C*A*T*A*A*A*T*G*G*A*A*C*A*+T*+C*+G | 43089 | 19 |

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| 1621 | AGGTGACAAAGTCTTCATC | A571619Hi | +A*+G*+G*T*G*A*C*A*A*A*G*T*C*T*T*C*+A*+T*+C | 43129 | 19 |
| 1622 | ACAGGTGACAAAGTCTTCA | A571620Hi | +A*+C*+A*G*G*T*G*A*C*A*A*A*G*T*C*T*+T*+C*+A | 43131 | 19 |
| 1623 | TGGAACAGGTGACAAAGTC | A571621Hi | +T*+G*+G*A*A*C*A*G*G*T*G*A*C*A*A*A*+G*+T*+C | 43135 | 19 |
| 1624 | TCTCTCTGGAACAGGTGAC | A571622Hi | +T*+C*+T*C*T*C*T*G*G*A*A*C*A*G*G*T*+G*+A*+C | 43141 | 19 |
| 1625 | ATCTCTCTGGAACAGGTGA | A571623Hi | +A*+T*+C*T*C*T*C*T*G*G*A*A*C*A*G*G*+T*+G*+A | 43142 | 19 |
| 1626 | CTCTCTGGAAACAATAATG | A571624Hi | +C*+T*+C*T*C*T*G*G*A*A*A*C*A*A*T*A*+A*+T*+G | 43170 | 19 |
| 1627 | TACTTTACTGGATTTCCTC | A571625Hi | +T*+A*+C*T*T*T*A*C*T*G*G*A*T*T*T*C*+C*+T*+C | 43265 | 19 |
| 1628 | TTTACTTTACTGGATTTCC | A571626Hi | +T*+T*+T*A*C*T*T*T*A*C*T*G*G*A*T*T*+T*+C*+C | 43267 | 19 |
| 1629 | GGTTCATAAACATAGATCA | A571627Hi | +G*+G*+T*T*C*A*T*A*A*A*C*A*T*A*G*A*+T*+C*+A | 43584 | 19 |
| 1630 | GCTTACTTAGTTCCAGAA | A571628Hi | +G*+C*+T*T*A*C*T*T*A*G*T*T*C*C*A*+G*+A*+A | 43627 | 18 |
| 1631 | TTACACTAGCTTACTTAGT | A571629Hi | +T*+T*+A*C*A*C*T*A*G*C*T*T*A*C*T*T*+A*+G*+T | 43634 | 19 |
| 1632 | TGGAGTTAGGCCATATGAA | A571630Hi | +T*+G*+G*A*G*T*T*A*G*G*C*C*A*T*A*T*+G*+A*+A | 43714 | 19 |
| 1633 | GGAGTTAGGCCATATGAA | A571631Hi | +G*+G*+A*G*T*T*A*G*G*C*C*A*T*A*T*+G*+A*+A | 43714 | 18 |
| 1634 | TTTGGAGTTAGGCCATAT | A571632Hi | +T*+T*+T*G*G*A*G*T*T*A*G*G*C*C*A*+T*+A*+T | 43717 | 18 |
| 1635 | AGTGCCAGTATCACACCAT | A571633Hi | +A*+G*+T*G*C*C*A*G*T*A*T*C*A*C*A*C*+C*+A*+T | 43772 | 19 |
| 1636 | TAGTGCCAGTATCACACCA | A571634Hi | +T*+A*+G*T*G*C*C*A*G*T*A*T*C*A*C*A*+C*+C*+A | 43773 | 19 |
| 1637 | GAATATCATAACATTACAA | A571635Hi | +G*+A*+A*T*A*T*C*A*T*A*A*C*A*T*T*T*A*+C*+A*+A | 43849 | 19 |
| 1638 | GAGGAATATCATAACATTA | A571636Hi | +G*+A*+G*G*A*A*T*A*T*C*A*T*A*A*C*A*+T*+T*+A | 43852 | 19 |
| 1639 | AGTCGAGGAATATCATAA | A571637Hi | +A*+G*+T*C*G*A*G*G*A*A*T*A*T*C*A*+T*+A*+A | 43857 | 18 |
| 1640 | AGTCGAGGAATATCATA | A571638Hi | +A*+G*+T*C*G*A*G*G*A*A*T*A*T*C*+A*+T*+A | 43858 | 17 |
| 1641 | GCAGTCGAGGAATATCAT | A571639Hi | +G*+C*+A*G*T*C*G*A*G*G*A*A*T*A*T*+C*+A*+T | 43859 | 18 |
| 1642 | CAGTCGAGGAATATCAT | A571640Hi | +C*+A*+G*T*C*G*A*G*G*A*A*T*A*T*+C*+A*+T | 43859 | 17 |
| 1643 | GTTCCAACACAAGTAACTG | A571641Hi | +G*+T*+T*C*C*A*A*C*A*C*A*A*G*T*A*A*+C*+T*+G | 43896 | 19 |
| 1644 | TTGTTCCAACACAAGTAAC | A571642Hi | +T*+T*+G*T*T*C*C*A*A*C*A*C*A*A*G*T*+A*+A*+C | 43898 | 19 |
| 1645 | TTAGTTGTTCCAACACAAG | A571643Hi | +T*+T*+A*G*T*T*G*T*T*C*C*A*A*C*A*C*+A*+A*+G | 43902 | 19 |
| 1646 | AGTTAGTTGTTCCAACACA | A571644Hi | +A*+G*+T*T*A*G*T*T*G*T*T*C*C*A*A*C*+A*+C*+A | 43904 | 19 |
| 1647 | GAGTTAGTTGTTCCAACAC | A571645Hi | +G*+A*+G*T*T*A*G*T*T*G*T*T*C*C*A*A*+C*+A*+C | 43905 | 19 |
| 1648 | GAGTTAGTTGTTCCAACA | A571646Hi | +G*+A*+G*T*T*A*G*T*T*G*T*T*C*C*A*+A*+C*+A | 43906 | 18 |
| 1649 | TGAAGAGTTAGTTGTTCCA | A571647Hi | +T*+G*+A*A*G*A*G*T*T*A*G*T*T*G*T*T*+C*+C*+A | 43909 | 19 |
| 1650 | TGAAGAGTTAGTTGTTCC | A571648Hi | +T*+G*+A*A*G*A*G*T*T*A*G*T*T*G*T*+T*+C*+C | 43910 | 18 |
| 1651 | GCTGAAGAGTTAGTTGTTC | A571649Hi | +G*+C*+T*G*A*A*G*A*G*T*T*A*G*T*T*G*+T*+T*+C | 43911 | 19 |
| 1652 | TCTCATCCATCTGTAATTT | A571650Hi | +T*+C*+T*C*A*T*C*C*A*T*C*T*G*T*A*A*+T*+T*+T | 43984 | 19 |
| 1653 | AATCTCATCCATCTGTAAT | A571651Hi | +A*+A*+T*C*T*C*A*T*C*C*A*T*C*T*G*T*+A*+A*+T | 43986 | 19 |
| 1654 | TTACGTTAATAACAATTAT | A571652Hi | +T*+T*+A*C*G*T*T*A*A*T*A*A*C*A*A*T*+T*+A*+T | 44053 | 19 |
| 1655 | TTTACGTTAATAACAATTA | A571653Hi | +T*+T*+T*A*C*G*T*T*A*A*T*A*A*C*A*A*+T*+T*+A | 44054 | 19 |

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| 1656 | TTTACGTTAATAACA ATT | A571654Hi | +T*+T*+T*A*C*G*T*T*A*A*T*A*A*C*A*+A* +T*+T | 44055 | 18 |
| 1657 | TCATTTACGTTAATAA CAA | A571655Hi | +T*+C*+A*T*T*T*A*C*G*T*T*A*A*T*A*A*+ C*+A*+A | 44057 | 19 |
| 1658 | ATGAAATTGCTGATC AGA | A571656Hi | +A*+T*+G*A*A*A*T*T*G*C*T*G*A*T*C*+A* +G*+A | 44138 | 18 |
| 1659 | AATGAAATTGCTGAT CAG | A571657Hi | +A*+A*+T*G*A*A*A*T*T*G*C*T*G*A*T*+C* +A*+G | 44139 | 18 |
| 1660 | GCATGAATGATTACC ATGT | A571658Hi | +G*+C*+A*T*G*A*A*T*G*A*T*T*A*C*C*A*+ T*+G*+T | 44268 | 19 |
| 1661 | CAGCATGAATGATTA CCAT | A571659Hi | +C*+A*+G*C*A*T*G*A*A*T*G*A*T*T*A*C*+ C*+A*+T | 44270 | 19 |
| 1662 | GCTTCAACCTAACTA CTA | A571660Hi | +G*+C*+T*T*C*A*A*C*C*T*A*A*C*T*A*+C* +T*+A | 44340 | 18 |
| 1663 | ACTCTGCTTGTTGTA GTCC | A571661Hi | +A*+C*+T*C*T*G*C*T*T*G*T*T*G*T*A*G*+ T*+C*+C | 44492 | 19 |
| 1664 | GACTCTGCTTGTTGT AGTC | A571662Hi | +G*+A*+C*T*C*T*G*C*T*T*G*T*T*G*T*A*+ G*+T*+C | 44493 | 19 |
| 1665 | GGACTCTGCTTGTTG TAGT | A571663Hi | +G*+G*+A*C*T*C*T*G*C*T*T*G*T*T*G*T*+ A*+G*+T | 44494 | 19 |
| 1666 | GACTCTGCTTGTTGT AGT | A571664Hi | +G*+A*+C*T*C*T*G*C*T*T*G*T*T*G*T*+A* +G*+T | 44494 | 18 |
| 1667 | GGACTCTGCTTGTTG TAG | A571665Hi | +G*+G*+A*C*T*C*T*G*C*T*T*G*T*T*G*+T* +A*+G | 44495 | 18 |
| 1668 | GACTCTGCTTGTTGT AG | A571666Hi | +G*+A*+C*T*C*T*G*C*T*T*G*T*T*G*+T*+A *+G | 44495 | 17 |
| 1669 | TGTGTTGCAGGTCAG GAGG | A571667Hi | +T*+G*+T*G*T*T*G*C*A*G*G*T*C*A*G*G*+ A*+G*+G | 44513 | 19 |
| 1670 | TATGTGTTGCAGGTC AGG | A571668Hi | +T*+A*+T*G*T*G*T*T*G*C*A*G*G*T*C*+A* +G*+G | 44516 | 18 |
| 1671 | GCTACATATGTGTTG CAG | A571669Hi | +G*+C*+T*A*C*A*T*A*T*G*T*G*T*T*G*+C* +A*+G | 44522 | 18 |
| 1672 | TGCTACATATGTGTT GCA | A571670Hi | +T*+G*+C*T*A*C*A*T*A*T*G*T*G*T*T*+G* +C*+A | 44523 | 18 |
| 1673 | ATGCTACATATGTGT TGCA | A571671Hi | +A*+T*+G*C*T*A*C*A*T*A*T*G*T*G*T*T*+ G*+C*+A | 44523 | 19 |
| 1674 | CATGCTACATATGTG TTGC | A571672Hi | +C*+A*+T*G*C*T*A*C*A*T*A*T*G*T*G*T*+ T*+G*+C | 44524 | 19 |
| 1675 | TCATGCTACATATGT GTTG | A571673Hi | +T*+C*+A*T*G*C*T*A*C*A*T*A*T*G*T*G*+ T*+T*+G | 44525 | 19 |
| 1676 | CATGCTACATATGTG TTG | A571674Hi | +C*+A*+T*G*C*T*A*C*A*T*A*T*G*T*G*+T* +T*+G | 44525 | 18 |
| 1677 | CCATTATTGCTCATG CTAC | A571675Hi | +C*+C*+A*T*T*A*T*T*G*C*T*C*A*T*G*C*+ T*+A*+C | 44535 | 19 |
| 1678 | TTAAATTAAGCTGCA GTAA | A571676Hi | +T*+T*+A*A*A*T*T*A*A*G*C*T*G*C*A*G*+ T*+A*+A | 44593 | 19 |
| 1679 | TAATTTATCTGATTAG TCT | A571677Hi | +T*+A*+A*T*T*T*A*T*C*T*G*A*T*T*A*G*+ T*+C*+T | 44643 | 19 |
| 1680 | AATGGTATAATTTAT CTGA | A571678Hi | +A*+A*+T*G*G*T*A*T*A*A*T*T*T*A*T*C*+ T*+G*+A | 44650 | 19 |
| 1681 | TTGGAAATGGTATAA TTTA | A571679Hi | +T*+T*+G*G*A*A*A*T*G*G*T*A*T*A*A*T*+ T*+T*+A | 44655 | 19 |
| 1682 | ATTTGGAAATGGTAT AATT | A571680Hi | +A*+T*+T*T*G*G*A*A*A*T*G*G*T*A*T*A*+ A*+T*+T | 44657 | 19 |
| 1683 | TAGGAATCTCACCTC ATTG | A571681Hi | +T*+A*+G*G*A*A*T*C*T*C*A*C*C*T*C*A*+ T*+T*+G | 44704 | 19 |
| 1684 | ACATTAGGAATCTCA CCTC | A571682Hi | +A*+C*+A*T*T*A*G*G*A*A*T*C*T*C*A*C*+ C*+T*+C | 44708 | 19 |
| 1685 | GCAGCACATTAGGAA TCTC | A571683Hi | +G*+C*+A*G*C*A*C*A*T*T*A*G*G*A*A*T*+ C*+T*+C | 44713 | 19 |
| 1686 | AGCAGCACATTAGGA ATCT | A571684Hi | +A*+G*+C*A*G*C*A*C*A*T*T*A*G*G*A*A*+ T*+C*+T | 44714 | 19 |
| 1687 | CAAACTTAGCTATTA GAAA | A571685Hi | +C*+A*+A*A*C*T*T*A*G*C*T*A*T*T*A*G*+ A*+A*+A | 44930 | 19 |
| 1688 | CCACAAACTTAGCTA TTA | A571686Hi | +C*+C*+A*C*A*A*A*C*T*T*A*G*C*T*A*+T* +T*+A | 44934 | 18 |
| 1689 | CATTAAGTACTTGTC CAGG | A571687Hi | +C*+A*+T*T*A*A*G*T*A*C*T*T*G*T*C*C*+ A*+G*+G | 45010 | 19 |
| 1690 | ACATTAAGTACTTGT CCAG | A571688Hi | +A*+C*+A*T*T*A*A*G*T*A*C*T*T*G*T*C*+ C*+A*+G | 45011 | 19 |

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| 1691 | CATTAAGTACTTGTCCAG | A571689Hi | +C*+A*+T*T*A*A*G*T*A*C*T*T*G*T*C*+C*+A*+G | 45011 | 18 |
| 1692 | GATGAAGACTGCTTCCAAA | A571690Hi | +G*+A*+T*G*A*A*G*A*C*T*G*C*T*T*C*C*+A*+A*+A | 45368 | 19 |
| 1693 | GAGATGAAGACTGCTTCCA | A571691Hi | +G*+A*+G*A*T*G*A*A*G*A*C*T*G*C*T*T*+C*+C*+A | 45370 | 19 |
| 1694 | TGAGATGAAGACTGCTTCC | A571692Hi | +T*+G*+A*G*A*T*G*A*A*G*A*C*T*G*C*T*+T*+C*+C | 45371 | 19 |
| 1695 | AGGACTTGAGATGAAGACT | A571693Hi | +A*+G*+G*A*C*T*T*G*A*G*A*T*G*A*A*G*+A*+C*+T | 45377 | 19 |
| 1696 | AAGGACTTGAGATGAAGAC | A571694Hi | +A*+A*+G*G*A*C*T*T*G*A*G*A*T*G*A*A*+G*+A*+C | 45378 | 19 |
| 1697 | TCAGTACTAGAACACAGTG | A571695Hi | +T*+C*+A*G*T*A*C*T*A*G*A*A*C*A*C*A*+G*+T*+G | 45576 | 19 |
| 1698 | TTCAGTACTAGAACACAGT | A571696Hi | +T*+T*+C*A*G*T*A*C*T*A*G*A*A*C*A*C*+A*+G*+T | 45577 | 19 |
| 1699 | ATGTATAGCTAGAATGAG | A571697Hi | +A*+T*+G*T*A*T*A*G*C*T*A*G*A*A*T*+G*+A*+G | 45732 | 18 |
| 1700 | TTAATATCTTTACCATGTA | A571698Hi | +T*+T*+A*A*T*A*T*C*T*T*T*A*C*C*A*T*+G*+T*+A | 45817 | 19 |
| 1701 | GTATATCCAGTTCTACTTC | A571699Hi | +G*+T*+A*T*A*T*C*C*A*G*T*T*C*T*A*C*+T*+T*+C | 45916 | 19 |
| 1702 | AGTAAGTATATCCAGTTCT | A571700Hi | +A*+G*+T*A*A*G*T*A*T*A*T*C*C*A*G*T*+T*+C*+T | 45921 | 19 |
| 1703 | ATCATATGACTGATAGCC | A571701Hi | +A*+T*+C*A*T*A*T*G*A*C*T*G*A*T*A*+G*+C*+C | 46128 | 18 |
| 1704 | ACATCATATGACTGATAGC | A571702Hi | +A*+C*+A*T*C*A*T*A*T*G*A*C*T*G*A*T*+A*+G*+C | 46129 | 19 |
| 1705 | AACATCATATGACTGATAG | A571703Hi | +A*+A*+C*A*T*C*A*T*A*T*G*A*C*T*G*A*+T*+A*+G | 46130 | 19 |
| 1706 | AGAGATCCAACATCATATG | A571704Hi | +A*+G*+A*G*A*T*C*C*A*A*C*A*T*C*A*T*+A*+T*+G | 46138 | 19 |
| 1707 | TAGGTAAGTAGATTAGCC | A571705Hi | +T*+A*+G*G*T*A*A*G*T*A*G*A*T*T*A*+G*+C*+C | 46358 | 18 |
| 1708 | CTACTAGGTAAGTAGATT | A571706Hi | +C*+T*+A*C*T*A*G*G*T*A*A*G*T*A*G*+A*+T*+T | 46362 | 18 |
| 1709 | GCTACTAGGTAAGTAGATT | A571707Hi | +G*+C*+T*A*C*T*A*G*G*T*A*A*G*T*A*G*+A*+T*+T | 46362 | 19 |
| 1710 | AGCTACTAGGTAAGTAGAT | A571708Hi | +A*+G*+C*T*A*C*T*A*G*G*T*A*A*G*T*A*+G*+A*+T | 46363 | 19 |
| 1711 | AGCTACTAGGTAAGTAGA | A571709Hi | +A*+G*+C*T*A*C*T*A*G*G*T*A*A*G*T*+A*+G*+A | 46364 | 18 |
| 1712 | CTAGCTACTAGGTAAGTAG | A571710Hi | +C*+T*+A*G*C*T*A*C*T*A*G*G*T*A*A*G*+T*+A*+G | 46365 | 19 |
| 1713 | CTAGCTACTAGGTAAGTA | A571711Hi | +C*+T*+A*G*C*T*A*C*T*A*G*G*T*A*A*+G*+T*+A | 46366 | 18 |
| 1714 | TGGCAGCATCCTACCACC | A571712Hi | +T*+G*+G*C*A*G*C*A*T*C*C*T*A*C*C*+A*+C*+C | 46496 | 18 |
| 1715 | GAAGGATGGCAGCATCCTA | A571713Hi | +G*+A*+A*G*G*A*T*G*G*C*A*G*C*A*T*C*+C*+T*+A | 46501 | 19 |
| 1716 | AGAAGGATGGCAGCATCCT | A571714Hi | +A*+G*+A*A*G*G*A*T*G*G*C*A*G*C*A*T*+C*+C*+T | 46502 | 19 |
| 1717 | CAACAGAAGGATGGCAGCA | A571715Hi | +C*+A*+A*C*A*G*A*A*G*G*A*T*G*G*C*A*+G*+C*+A | 46506 | 19 |
| 1718 | CAACAGAAGGATGGCAGC | A571716Hi | +C*+A*+A*C*A*G*A*A*G*G*A*T*G*G*C*+A*+G*+C | 46507 | 18 |
| 1719 | CCAACAGAAGGATGGCAGC | A571717Hi | +C*+C*+A*A*C*A*G*A*A*G*G*A*T*G*G*C*+A*+G*+C | 46507 | 19 |
| 1720 | GGAGATGCCAACAGAAGGA | A571718Hi | +G*+G*+A*G*A*T*G*C*C*A*A*C*A*G*A*A*+G*+G*+A | 46514 | 19 |
| 1721 | TGGAGATGCCAACAGAAGG | A571719Hi | +T*+G*+G*A*G*A*T*G*C*C*A*A*C*A*G*A*+A*+G*+G | 46515 | 19 |
| 1722 | GGAGATGCCAACAGAAGG | A571720Hi | +G*+G*+A*G*A*T*G*C*C*A*A*C*A*G*A*+A*+G*+G | 46515 | 18 |
| 1723 | CTCTGGAGATGCCAACAGA | A571721Hi | +C*+T*+C*T*G*G*A*G*A*T*G*C*C*A*A*C*+A*+G*+A | 46518 | 19 |
| 1724 | ACTCTGGAGATGCCAACAG | A571722Hi | +A*+C*+T*C*T*G*G*A*G*A*T*G*C*C*A*A*+C*+A*+G | 46519 | 19 |
| 1725 | AGTGAAACTCTGGAGATGC | A571723Hi | +A*+G*+T*G*A*A*A*C*T*C*T*G*G*A*G*A*+T*+G*+C | 46525 | 19 |

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| 1726 | TCAAGTGAAACTCTG GAGA | A571724Hi | +T*+C*+A*A*G*T*G*A*A*A*C*T*C*T*G*G*+ A*+G*+A | 46528 | 19 |
| 1727 | GTCTACTTAGGAGGT GTT | A571725Hi | +G*+T*+C*T*A*C*T*T*A*G*G*A*G*G*T*+G* +T*+T | 46549 | 18 |
| 1728 | AGTGTCTACTTAGGA GGT | A571726Hi | +A*+G*+T*G*T*C*T*A*C*T*T*A*G*G*A*+G* +G*+T | 46552 | 18 |
| 1729 | CTAGGCTCTAACCAT TTC | A571727Hi | +C*+T*+A*G*G*C*T*C*T*A*A*C*C*A*T*+T* +T*+C | 46888 | 18 |
| 1730 | ATTATATCAAATTGAT ATT | A571728Hi | +A*+T*+T*A*T*A*T*C*A*A*A*T*T*G*A*T*+ A*+T*+T | 46988 | 19 |
| 1731 | AATTATATCAAATTG ATAT | A571729Hi | +A*+A*+T*T*A*T*A*T*C*A*A*A*T*T*G*A*+ T*+A*+T | 46989 | 19 |
| 1732 | GTCATTCTGAACTTT CTGT | A571730Hi | +G*+T*+C*A*T*T*C*T*G*A*A*C*T*T*T*C*+ T*+G*+T | 47247 | 19 |
| 1733 | AGTCAGATTGTCATT CTGA | A571731Hi | +A*+G*+T*C*A*G*A*T*T*G*T*C*A*T*T*C*+ T*+G*+A | 47256 | 19 |
| 1734 | GTCAAAGCACAAGTT TAAA | A571732Hi | +G*+T*+C*A*A*A*G*C*A*C*A*A*G*T*T*T*+ A*+A*+A | 47371 | 19 |
| 1735 | ACTTCATATGTATTCA CCT | A571733Hi | +A*+C*+T*T*C*A*T*A*T*G*T*A*T*T*C*A*+ C*+C*+T | 47487 | 19 |
| 1736 | ACTTCATATGTATTCA CC | A571734Hi | +A*+C*+T*T*C*A*T*A*T*G*T*A*T*T*C*+A* +C*+C | 47488 | 18 |
| 1737 | AACAATAGCAATGAC CACA | A571735Hi | +A*+A*+C*A*A*T*A*G*C*A*A*T*G*A*C*C*+ A*+C*+A | 47561 | 19 |
| 1738 | TAACAACTTAATTGG TGCT | A571736Hi | +T*+A*+A*C*A*A*C*T*T*A*A*T*T*G*G*T*+ G*+C*+T | 47757 | 19 |
| 1739 | GCGCTGTCCTCAGAG ATGA | A571737Hi | +G*+C*+G*C*T*G*T*C*C*T*C*A*G*A*G*A*+ T*+G*+A | 47973 | 19 |
| 1740 | TAAGCGCTGTCCTCA GAGA | A571738Hi | +T*+A*+A*G*C*G*C*T*G*T*C*C*T*C*A*G*+ A*+G*+A | 47976 | 19 |
| 1741 | AAATTGGAAGGCTGG TTTG | A571739Hi | +A*+A*+A*T*T*G*G*A*A*G*G*C*T*G*G*T*+ T*+T*+G | 48124 | 19 |
| 1742 | TGAATGAAGTAACAA TTAC | A571740Hi | +T*+G*+A*A*T*G*A*A*G*T*A*A*C*A*A*T*+ T*+A*+C | 48233 | 19 |
| 1743 | TCTGAGAACCATTAA ATGA | A571741Hi | +T*+C*+T*G*A*G*A*A*C*C*A*T*T*A*A*A*+ T*+G*+A | 48249 | 19 |
| 1744 | GAATCTGAGAACCAT TAAA | A571742Hi | +G*+A*+A*T*C*T*G*A*G*A*A*C*C*A*T*T*+ A*+A*+A | 48252 | 19 |
| 1745 | CAGCTTGGAGGCCAA TTA | A571743Hi | +C*+A*+G*C*T*T*G*G*A*G*G*C*C*A*A*+T* +T*+A | 48291 | 18 |
| 1746 | TCAGCTTGGAGGCCA ATT | A571744Hi | +T*+C*+A*G*C*T*T*G*G*A*G*G*C*C*A*+A* +T*+T | 48292 | 18 |
| 1747 | ATCAGCTTGGAGGCC AATT | A571745Hi | +A*+T*+C*A*G*C*T*T*G*G*A*G*G*C*C*A*+ A*+T*+T | 48292 | 19 |
| 1748 | ATCAGCTTGGAGGCC AAT | A571746Hi | +A*+T*+C*A*G*C*T*T*G*G*A*G*G*C*C*+A* +A*+T | 48293 | 18 |
| 1749 | ACATCAGCTTGGAGG CCAA | A571747Hi | +A*+C*+A*T*C*A*G*C*T*T*G*G*A*G*G*C*+ C*+A*+A | 48294 | 19 |
| 1750 | GCACATCAGCTTGGA GGCC | A571748Hi | +G*+C*+A*C*A*T*C*A*G*C*T*T*G*G*A*G*+ G*+C*+C | 48296 | 19 |
| 1751 | GCACATCAGCTTGGA GGC | A571749Hi | +G*+C*+A*C*A*T*C*A*G*C*T*T*G*G*A*+G* +G*+C | 48297 | 18 |
| 1752 | AGCACATCAGCTTGG AGGC | A571750Hi | +A*+G*+C*A*C*A*T*C*A*G*C*T*T*G*G*A*+ G*+G*+C | 48297 | 19 |
| 1753 | TAAGCACATCAGCTT GGAG | A571751Hi | +T*+A*+A*G*C*A*C*A*T*C*A*G*C*T*T*G*+ G*+A*+G | 48299 | 19 |
| 1754 | TGTTTCCTGTCACTG TTTC | A571752Hi | +T*+G*+T*T*T*C*C*T*G*T*C*A*C*T*G*T*+ T*+T*+C | 48320 | 19 |
| 1755 | TTGCTCAGCTTGGAC ATCA | A571753Hi | +T*+T*+G*C*T*C*A*G*C*T*T*G*G*A*C*A*+ T*+C*+A | 48383 | 19 |
| 1756 | TTGCTCAGCTTGGAC ATC | A571754Hi | +T*+T*+G*C*T*C*A*G*C*T*T*G*G*A*C*+A* +T*+C | 48384 | 18 |
| 1757 | ATTGCTCAGCTTGGA CATC | A571755Hi | +A*+T*+T*G*C*T*C*A*G*C*T*T*G*G*A*C*+ A*+T*+C | 48384 | 19 |
| 1758 | TAATTGCTCAGCTTG GACA | A571756Hi | +T*+A*+A*T*T*G*C*T*C*A*G*C*T*T*G*G*+ A*+C*+A | 48386 | 19 |
| 1759 | TTAATTGCTCAGCTT GGAC | A571757Hi | +T*+T*+A*A*T*T*G*C*T*C*A*G*C*T*T*G*+ G*+A*+C | 48387 | 19 |
| 1760 | TTTAATTGCTCAGCTT GGA | A571758Hi | +T*+T*+T*A*A*T*T*G*C*T*C*A*G*C*T*T*+ G*+G*+A | 48388 | 19 |

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| 1761 | ACTTCACACTTTAATTGCT | A571759Hi | +A*+C*+T*T*C*A*C*A*C*T*T*T*A*A*T*T*+G*+C*+T | 48397 | 19 |
| 1762 | TAATGCCTCTCAATTATCT | A571760Hi | +T*+A*+A*T*G*C*C*T*C*T*C*A*A*T*T*A*+T*+C*+T | 48479 | 19 |
| 1763 | CTGTACTCTCAGTGAACAG | A571761Hi | +C*+T*+G*T*A*C*T*C*T*C*A*G*T*G*A*A*+C*+A*+G | 48527 | 19 |
| 1764 | TGTACTCTCAGTGAACAG | A571762Hi | +T*+G*+T*A*C*T*C*T*C*A*G*T*G*A*A*+C*+A*+G | 48527 | 18 |
| 1765 | TTCTGTACTCTCAGTGAAC | A571763Hi | +T*+T*+C*T*G*T*A*C*T*C*T*C*A*G*T*G*+A*+A*+C | 48529 | 19 |
| 1766 | TCCTCATTTCTGTACTCTC | A571764Hi | +T*+C*+C*T*C*A*T*T*T*C*T*G*T*A*C*T*+C*+T*+C | 48536 | 19 |
| 1767 | AATCTTCTGCCTTCCAAGC | A571765Hi | +A*+A*+T*C*T*T*C*T*G*C*C*T*T*C*C*A*+A*+G*+C | 48556 | 19 |
| 1768 | CAGATAATCCAAAGAGCTG | A571766Hi | +C*+A*+G*A*T*A*A*T*C*C*A*A*A*G*A*G*+C*+T*+G | 48606 | 19 |
| 1769 | TGGCCTCCACCACAGATA | A571767Hi | +T*+G*+G*C*C*T*C*C*A*C*C*A*C*A*G*+A*+T*+A | 48619 | 18 |
| 1770 | GATGGCCTCCACCACAGAT | A571768Hi | +G*+A*+T*G*G*C*C*T*C*C*A*C*C*A*C*A*+G*+A*+T | 48620 | 19 |
| 1771 | TGATGGCCTCCACCACAGA | A571769Hi | +T*+G*+A*T*G*G*C*C*T*C*C*A*C*C*A*C*+A*+G*+A | 48621 | 19 |
| 1772 | GATGGCCTCCACCACAGA | A571770Hi | +G*+A*+T*G*G*C*C*T*C*C*A*C*C*A*C*+A*+G*+A | 48621 | 18 |
| 1773 | GTGATGGCCTCCACCACAG | A571771Hi | +G*+T*+G*A*T*G*G*C*C*T*C*C*A*C*C*A*+C*+A*+G | 48622 | 19 |
| 1774 | CGTGATGGCCTCCACCACA | A571772Hi | +C*+G*+T*G*A*T*G*G*C*C*T*C*C*A*C*C*+A*+C*+A | 48623 | 19 |
| 1775 | CGTGATGGCCTCCACCAC | A571773Hi | +C*+G*+T*G*A*T*G*G*C*C*T*C*C*A*C*+C*+A*+C | 48624 | 18 |
| 1776 | ACGTGATGGCCTCCACCAC | A571774Hi | +A*+C*+G*T*G*A*T*G*G*C*C*T*C*C*A*C*+C*+A*+C | 48624 | 19 |
| 1777 | GACGTGATGGCCTCCACCA | A571775Hi | +G*+A*+C*G*T*G*A*T*G*G*C*C*T*C*C*A*+C*+C*+A | 48625 | 19 |
| 1778 | AAGACGTGATGGCCTCCA | A571776Hi | +A*+A*+G*A*C*G*T*G*A*T*G*G*C*C*T*+C*+C*+A | 48628 | 18 |
| 1779 | AAGACGTGATGGCCTCC | A571777Hi | +A*+A*+G*A*C*G*T*G*A*T*G*G*C*C*+T*+C*+C | 48629 | 17 |
| 1780 | CAAAGACGTGATGGCCTC | A571778Hi | +C*+A*+A*A*G*A*C*G*T*G*A*T*G*G*C*+C*+T*+C | 48630 | 18 |
| 1781 | CCAAAGACGTGATGGCCTC | A571779Hi | +C*+C*+A*A*A*G*A*C*G*T*G*A*T*G*G*C*+C*+T*+C | 48630 | 19 |
| 1782 | CCACTCCAAAGACGTGATG | A571780Hi | +C*+C*+A*C*T*C*C*A*A*A*G*A*C*G*T*G*+A*+T*+G | 48635 | 19 |
| 1783 | CCACTCCAAAGACGTGAT | A571781Hi | +C*+C*+A*C*T*C*C*A*A*A*G*A*C*G*T*+G*+A*+T | 48636 | 18 |
| 1784 | TCCACTCCAAAGACGTGAT | A571782Hi | +T*+C*+C*A*C*T*C*C*A*A*A*G*A*C*G*T*+G*+A*+T | 48636 | 19 |
| 1785 | CTCCACTCCAAAGACGTGA | A571783Hi | +C*+T*+C*C*A*C*T*C*C*A*A*A*G*A*C*G*+T*+G*+A | 48637 | 19 |
| 1786 | CCTCCACTCCAAAGACGTG | A571784Hi | +C*+C*+T*C*C*A*C*T*C*C*A*A*A*G*A*C*+G*+T*+G | 48638 | 19 |
| 1787 | ACCTCCACTCCAAAGACGT | A571785Hi | +A*+C*+C*T*C*C*A*C*T*C*C*A*A*A*G*A*+C*+G*+T | 48639 | 19 |
| 1788 | TACCTCCACTCCAAAGACG | A571786Hi | +T*+A*+C*C*T*C*C*A*C*T*C*C*A*A*A*G*+A*+C*+G | 48640 | 19 |
| 1789 | ACCTCCACTCCAAAGACG | A571787Hi | +A*+C*+C*T*C*C*A*C*T*C*C*A*A*A*G*+A*+C*+G | 48640 | 18 |
| 1790 | GTACCTCCACTCCAAAGAC | A571788Hi | +G*+T*+A*C*C*T*C*C*A*C*T*C*C*A*A*A*+G*+A*+C | 48641 | 19 |
| 1791 | GGTACCTCCACTCCAAAGA | A571789Hi | +G*+G*+T*A*C*C*T*C*C*A*C*T*C*C*A*A*+A*+G*+A | 48642 | 19 |
| 1792 | CATGGTACCTCCACTCCA | A571790Hi | +C*+A*+T*G*G*T*A*C*C*T*C*C*A*C*T*+C*+C*+A | 48646 | 18 |
| 1793 | CTCTTATTCTGGTCATCTC | A571791Hi | +C*+T*+C*T*T*A*T*T*C*T*G*G*T*C*A*T*+C*+T*+C | 48807 | 19 |
| 1794 | CCTACTCATCAACCAAGA | A571792Hi | +C*+C*+T*A*C*T*C*A*T*C*A*A*C*C*A*+A*+G*+A | 48848 | 18 |
| 1795 | TAATAGGTTTGCCAAACTT | A571793Hi | +T*+A*+A*T*A*G*G*T*T*T*G*C*C*A*A*A*+C*+T*+T | 49060 | 19 |

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| 1796 | CATGTAATAGGTTTG CCAA | A571794Hi | +C*+A*+T*G*T*A*A*T*A*G*G*T*T*T*G*C*+ C*+A*+A | 49064 | 19 |
| 1797 | CATGTAATAGGTTTG CCA | A571795Hi | +C*+A*+T*G*T*A*A*T*A*G*G*T*T*T*G*+C* +C*+A | 49065 | 18 |
| 1798 | CATGTAATAGGTTTG CC | A571796Hi | +C*+A*+T*G*T*A*A*T*A*G*G*T*T*T*+G*+C *+C | 49066 | 17 |
| 1799 | CTTCATGTAATAGGT TTG | A571797Hi | +C*+T*+T*C*A*T*G*T*A*A*T*A*G*G*T*+T* +T*+G | 49068 | 18 |
| 1800 | AGCTTCATGTAATAG GTTT | A571798Hi | +A*+G*+C*T*T*C*A*T*G*T*A*A*T*A*G*G*+ T*+T*+T | 49069 | 19 |
| 1801 | CATGAAATCCATACT GATA | A571799Hi | +C*+A*+T*G*A*A*A*T*C*C*A*T*A*C*T*G*+ A*+T*+A | 49316 | 19 |
| 1802 | TGAAGAATAAGAGTT AGCA | A571800Hi | +T*+G*+A*A*G*A*A*T*A*A*G*A*G*T*T*A*+ G*+C*+A | 49412 | 19 |
| 1803 | TTAAGACCAGTTATA GAC | A571801Hi | +T*+T*+A*A*G*A*C*C*A*G*T*T*A*T*A*+G* +A*+C | 49515 | 18 |
| 1804 | TAGTTAAGACCAGTT ATA | A571802Hi | +T*+A*+G*T*T*A*A*G*A*C*C*A*G*T*T*+A* +T*+A | 49518 | 18 |
| 1805 | TTAGTTAAGACCAGT TAT | A571803Hi | +T*+T*+A*G*T*T*A*A*G*A*C*C*A*G*T*+T* +A*+T | 49519 | 18 |
| 1806 | CCTTAGTTAAGACCA GTTA | A571804Hi | +C*+C*+T*T*A*G*T*T*A*A*G*A*C*C*A*G*+ T*+T*+A | 49520 | 19 |
| 1807 | CTTACCTTAGTTAAG ACCA | A571805Hi | +C*+T*+T*A*C*C*T*T*A*G*T*T*A*A*G*A*+ C*+C*+A | 49524 | 19 |
| 1808 | CTTACCTTAGTTAAG ACC | A571806Hi | +C*+T*+T*A*C*C*T*T*A*G*T*T*A*A*G*+A* +C*+C | 49525 | 18 |
| 1809 | ACTTACCTTAGTTAA GACC | A571807Hi | +A*+C*+T*T*A*C*C*T*T*A*G*T*T*A*A*G*+ A*+C*+C | 49525 | 19 |
| 1810 | TACTTACCTTAGTTAA GAC | A571808Hi | +T*+A*+C*T*T*A*C*C*T*T*A*G*T*T*A*A*+ G*+A*+C | 49526 | 19 |
| 1811 | AATACTTACCTTAGTT AAG | A571809Hi | +A*+A*+T*A*C*T*T*A*C*C*T*T*A*G*T*T*+ A*+A*+G | 49528 | 19 |
| 1812 | ATTTCTGAATCCCAG GATT | A571810H | +A*+T*+T*T*C*T*G*A*A*T*C*C*C*A*G*G*+ A*+T*+T | 49596 | 19 |
| 1813 | TAATCCACATTTCTG AATC | A571811H | +T*+A*+A*T*C*C*A*C*A*T*T*T*C*T*G*A*+ A*+T*+C | 49604 | 19 |
| 1814 | ACTTTTAATCCACATT TCT | A571812H | +A*+C*+T*T*T*T*A*A*T*C*C*A*C*A*T*T*+ T*+C*+T | 49609 | 19 |
| 1815 | TACATCTGCAGTGTG TGAA | A571813H | +T*+A*+C*A*T*C*T*G*C*A*G*T*G*T*G*T*+ G*+A*+A | 49699 | 19 |
| 1816 | ATACATCTGCAGTGT GTGA | A571814H | +A*+T*+A*C*A*T*C*T*G*C*A*G*T*G*T*G*+ T*+G*+A | 49700 | 19 |
| 1817 | GGATACATCTGCAGT GTGT | A571815H | +G*+G*+A*T*A*C*A*T*C*T*G*C*A*G*T*G*+ T*+G*+T | 49702 | 19 |
| 1818 | TCTGGATACATCTGC AGTG | A571816H | +T*+C*+T*G*G*A*T*A*C*A*T*C*T*G*C*A*+ G*+T*+G | 49705 | 19 |
| 1819 | ATCTGGATACATCTG CAGT | A571817H | +A*+T*+C*T*G*G*A*T*A*C*A*T*C*T*G*C*+ A*+G*+T | 49706 | 19 |
| 1820 | TCATCTGGATACATC TGCA | A571818H | +T*+C*+A*T*C*T*G*G*A*T*A*C*A*T*C*T*+ G*+C*+A | 49708 | 19 |
| 1821 | TTGGTCATCTGGATA CATC | A571819H | +T*+T*+G*G*T*C*A*T*C*T*G*G*A*T*A*C*+ A*+T*+C | 49712 | 19 |
| 1822 | CTTGGTCATCTGGAT ACAT | A571820H | +C*+T*+T*G*G*T*C*A*T*C*T*G*G*A*T*A*+ C*+A*+T | 49713 | 19 |
| 1823 | CTTAAACCCAGACAC TGAA | A571821H | +C*+T*+T*A*A*A*C*C*C*A*G*A*C*A*C*T*+ G*+A*+A | 49861 | 19 |
| 1824 | GACTTAAACCCAGAC ACTG | A571822H | +G*+A*+C*T*T*A*A*A*C*C*C*A*G*A*C*A*+ C*+T*+G | 49863 | 19 |
| 1825 | CTATAAGACTTAAAC CCAG | A571823H | +C*+T*+A*T*A*A*G*A*C*T*T*A*A*A*C*C*+ C*+A*+G | 49869 | 19 |
| 1826 | CCTATAAGACTTAAA CCCA | A571824H | +C*+C*+T*A*T*A*A*G*A*C*T*T*A*A*A*C*+ C*+C*+A | 49870 | 19 |
| 1827 | CCTATAAGACTTAAA CCC | A571825H | +C*+C*+T*A*T*A*A*G*A*C*T*T*A*A*A*+C* +C*+C | 49871 | 18 |
| 1828 | TCCTATAAGACTTAA ACCC | A571826H | +T*+C*+C*T*A*T*A*A*G*A*C*T*T*A*A*A*+ C*+C*+C | 49871 | 19 |
| 1829 | TCCTATAAGACTTAA ACC | A571827H | +T*+C*+C*T*A*T*A*A*G*A*C*T*T*A*A*+A* +C*+C | 49872 | 18 |
| 1830 | ATCCTATAAGACTTA AACC | A571828H | +A*+T*+C*C*T*A*T*A*A*G*A*C*T*T*A*A*+ A*+C*+C | 49872 | 19 |

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| 1831 | GATGTCCAGTTCCTATG | A571829H | +G*+A*+T*G*T*C*C*A*G*T*T*C*C*T*+A*+T*+G | 49916 | 17 |
| 1832 | AGATGTCCAGTTCCTATG | A571830H | +A*+G*+A*T*G*T*C*C*A*G*T*T*C*C*T*+A*+T*+G | 49916 | 18 |
| 1833 | CAGATGTCCAGTTCCTATG | A571831H | +C*+A*+G*A*T*G*T*C*C*A*G*T*T*C*C*T*+A*+T*+G | 49916 | 19 |
| 1834 | CAGATGTCCAGTTCCTAT | A571832H | +C*+A*+G*A*T*G*T*C*C*A*G*T*T*C*C*+T*+A*+T | 49917 | 18 |
| 1835 | GCAGATGTCCAGTTCCTAT | A571833H | +G*+C*+A*G*A*T*G*T*C*C*A*G*T*T*C*C*+T*+A*+T | 49917 | 19 |
| 1836 | GCAGATGTCCAGTTCCTA | A571834H | +G*+C*+A*G*A*T*G*T*C*C*A*G*T*T*C*+C*+T*+A | 49918 | 18 |
| 1837 | AGCAGATGTCCAGTTCCTA | A571835H | +A*+G*+C*A*G*A*T*G*T*C*C*A*G*T*T*C*+C*+T*+A | 49918 | 19 |
| 1838 | CAGCAGATGTCCAGTTCCT | A571836H | +C*+A*+G*C*A*G*A*T*G*T*C*C*A*G*T*T*+C*+C*+T | 49919 | 19 |
| 1839 | CCAGCAGATGTCCAGTTCC | A571837H | +C*+C*+A*G*C*A*G*A*T*G*T*C*C*A*G*T*+T*+C*+C | 49920 | 19 |
| 1840 | CCAGCAGATGTCCAGTTC | A571838H | +C*+C*+A*G*C*A*G*A*T*G*T*C*C*A*G*+T*+T*+C | 49921 | 18 |
| 1841 | GCCAGCAGATGTCCAGTTC | A571839H | +G*+C*+C*A*G*C*A*G*A*T*G*T*C*C*A*G*+T*+T*+C | 49921 | 19 |
| 1842 | GCCAGCAGATGTCCAGTT | A571840H | +G*+C*+C*A*G*C*A*G*A*T*G*T*C*C*A*+G*+T*+T | 49922 | 18 |
| 1843 | TGCCAGCAGATGTCCAGTT | A571841H | +T*+G*+C*C*A*G*C*A*G*A*T*G*T*C*C*A*+G*+T*+T | 49922 | 19 |
| 1844 | ATTTTTGCCAGCAGATGTC | A571842H | +A*+T*+T*T*T*T*G*C*C*A*G*C*A*G*A*T*+G*+T*+C | 49927 | 19 |
| 1845 | AGAATTTTTGCCAGCAGAT | A571843H | +A*+G*+A*A*T*T*T*T*T*G*C*C*A*G*C*A*+G*+A*+T | 49930 | 19 |
| 1846 | AAATCGGTATAAGCTGGAA | A571844H | +A*+A*+A*T*C*G*G*T*A*T*A*A*G*C*T*G*+G*+A*+A | 49952 | 19 |
| 1847 | TAAATCGGTATAAGCTGGA | A571845H | +T*+A*+A*A*T*C*G*G*T*A*T*A*A*G*C*T*+G*+G*+A | 49953 | 19 |
| 1848 | TAAATCGGTATAAGCTGG | A571846H | +T*+A*+A*A*T*C*G*G*T*A*T*A*A*G*C*+T*+G*+G | 49954 | 18 |
| 1849 | TTAAATCGGTATAAGCTGG | A571847H | +T*+T*+A*A*A*T*C*G*G*T*A*T*A*A*G*C*+T*+G*+G | 49954 | 19 |
| 1850 | TTAAATCGGTATAAGCTG | A571848H | +T*+T*+A*A*A*T*C*G*G*T*A*T*A*A*G*+C*+T*+G | 49955 | 18 |
| 1851 | CTTAAATCGGTATAAGCTG | A571849H | +C*+T*+T*A*A*A*T*C*G*G*T*A*T*A*A*G*+C*+T*+G | 49955 | 19 |
| 1852 | CTTAAATCGGTATAAGCT | A571850H | +C*+T*+T*A*A*A*T*C*G*G*T*A*T*A*A*+G*+C*+T | 49956 | 18 |
| 1853 | CCTTAAATCGGTATAAGCT | A571851H | +C*+C*+T*T*A*A*A*T*C*G*G*T*A*T*A*A*+G*+C*+T | 49956 | 19 |
| 1854 | CTTAAATCGGTATAAGC | A571852H | +C*+T*+T*A*A*A*T*C*G*G*T*A*T*A*+A*+G*+C | 49957 | 17 |
| 1855 | CCTTAAATCGGTATAAGC | A571853H | +C*+C*+T*T*A*A*A*T*C*G*G*T*A*T*A*+A*+G*+C | 49957 | 18 |
| 1856 | TCCTTAAATCGGTATAAGC | A571854H | +T*+C*+C*T*T*A*A*A*T*C*G*G*T*A*T*A*+A*+G*+C | 49957 | 19 |
| 1857 | TCCTTAAATCGGTATAAG | A571855H | +T*+C*+C*T*T*A*A*A*T*C*G*G*T*A*T*+A*+A*+G | 49958 | 18 |
| 1858 | ATCCTTAAATCGGTATAAG | A571856H | +A*+T*+C*C*T*T*A*A*A*T*C*G*G*T*A*T*+A*+A*+G | 49958 | 19 |
| 1859 | CATCCTTAAATCGGTATAA | A571857H | +C*+A*+T*C*C*T*T*A*A*A*T*C*G*G*T*A*+T*+A*+A | 49959 | 19 |
| 1860 | ACATCCTTAAATCGGTATA | A571858H | +A*+C*+A*T*C*C*T*T*A*A*A*T*C*G*G*T*+A*+T*+A | 49960 | 19 |
| 1861 | ACATCCTTAAATCGGTAT | A571859H | +A*+C*+A*T*C*C*T*T*A*A*A*T*C*G*G*+T*+A*+T | 49961 | 18 |
| 1862 | AACATCCTTAAATCGGTAT | A571860H | +A*+A*+C*A*T*C*C*T*T*A*A*A*T*C*G*G*+T*+A*+T | 49961 | 19 |
| 1863 | AACATCCTTAAATCGGTA | A571861H | +A*+A*+C*A*T*C*C*T*T*A*A*A*T*C*G*+G*+T*+A | 49962 | 18 |
| 1864 | CAACATCCTTAAATCGGTA | A571862H | +C*+A*+A*C*A*T*C*C*T*T*A*A*A*T*C*G*+G*+T*+A | 49962 | 19 |
| 1865 | GCAACATCCTTAAATCGGT | A571863H | +G*+C*+A*A*C*A*T*C*C*T*T*A*A*A*T*C*+G*+G*+T | 49963 | 19 |

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|---|---|---|---|---|---|
| 1866 | GCAACATCCTTAAATCGG | A571864H | +G*+C*+A*A*C*A*T*C*C*T*T*A*A*A*T*+C*+G*+G | 49964 | 18 |
| 1867 | AGCAACATCCTTAAATCGG | A571865H | +A*+G*+C*A*A*C*A*T*C*C*T*T*A*A*A*T*+C*+G*+G | 49964 | 19 |
| 1868 | CAGCAACATCCTTAAATCG | A571866H | +C*+A*+G*C*A*A*C*A*T*C*C*T*T*A*A*A*+T*+C*+G | 49965 | 19 |
| 1869 | TTCAGCAACATCCTTAAAT | A571867H | +T*+T*+C*A*G*C*A*A*C*A*T*C*C*T*T*A*+A*+A*+T | 49967 | 19 |
| 1870 | CCAAGATAATGCACATAC | A571868Hi | +C*+C*+A*A*G*A*T*A*A*T*G*C*A*C*A*+T*+A*+C | 49998 | 18 |
| 1871 | CTTTAGAGATTCAATCCAA | A571869Hi | +C*+T*+T*T*A*G*A*G*A*T*T*C*A*A*T*C*+C*+A*+A | 50151 | 19 |
| 1872 | ACACTGGATCTTTAGAGAT | A571870Hi | +A*+C*+A*C*T*G*G*A*T*C*T*T*T*A*G*A*+G*+A*+T | 50160 | 19 |
| 1873 | ATGCTGACTTTAGAGATTT | A571871Hi | +A*+T*+G*C*T*G*A*C*T*T*T*A*G*A*G*A*+T*+T*+T | 50188 | 19 |
| 1874 | CATGCTGACTTTAGAGATT | A571872Hi | +C*+A*+T*G*C*T*G*A*C*T*T*T*A*G*A*G*+A*+T*+T | 50189 | 19 |
| 1875 | TTTATGAAAGTTGCAAACT | A571873Hi | +T*+T*+T*A*T*G*A*A*A*G*T*T*G*C*A*A*+A*+C*+T | 50587 | 19 |
| 1876 | TAGTTTATGAAAGTTGCAA | A571874Hi | +T*+A*+G*T*T*T*A*T*G*A*A*A*G*T*T*G*+C*+A*+A | 50590 | 19 |
| 1877 | CTGGTCAATGCTGCCAGTT | A571875Hi | +C*+T*+G*G*T*C*A*A*T*G*C*T*G*C*C*A*+G*+T*+T | 50937 | 19 |
| 1878 | CCTGGTCAATGCTGCCAGT | A571876Hi | +C*+C*+T*G*G*T*C*A*A*T*G*C*T*G*C*C*+A*+G*+T | 50938 | 19 |
| 1879 | TTCCTGGTCAATGCTGCCA | A571877Hi | +T*+T*+C*C*T*G*G*T*C*A*A*T*G*C*T*G*+C*+C*+A | 50940 | 19 |
| 1880 | TTCCTGGTCAATGCTGCC | A571878Hi | +T*+T*+C*C*T*G*G*T*C*A*A*T*G*C*T*+G*+C*+C | 50941 | 18 |
| 1881 | TATTCCTGGTCAATGCTGC | A571879Hi | +T*+A*+T*T*C*C*T*G*G*T*C*A*A*T*G*C*+T*+G*+C | 50942 | 19 |
| 1882 | ATTCCTGGTCAATGCTGC | A571880Hi | +A*+T*+T*C*C*T*G*G*T*C*A*A*T*G*C*+T*+G*+C | 50942 | 18 |
| 1883 | CTGTGCAAAGATTAGAGAC | A571881Hi | +C*+T*+G*T*G*C*A*A*A*G*A*T*T*A*G*A*+G*+A*+C | 50971 | 19 |
| 1884 | CCTGAGGCACATTATGAAA | A571882Hi | +C*+C*+T*G*A*G*G*C*A*C*A*T*T*A*T*G*+A*+A*+A | 51097 | 19 |
| 1885 | AATTTATGTATGTCTGAGG | A571883Hi | +A*+A*+T*T*T*A*T*G*T*A*T*G*T*C*T*G*+A*+G*+G | 51727 | 19 |
| 1886 | AATTTATGTATGTCTGAG | A571884Hi | +A*+A*+T*T*T*A*T*G*T*A*T*G*T*C*T*+G*+A*+G | 51728 | 18 |
| 1887 | GATAAGCAAAGTAGCCTTA | A571885Hi | +G*+A*+T*A*A*G*C*A*A*A*G*T*A*G*C*C*+T*+T*+A | 51745 | 19 |
| 1888 | TGATAAGCAAAGTAGCCTT | A571886Hi | +T*+G*+A*T*A*A*G*C*A*A*A*G*T*A*G*C*+C*+T*+T | 51746 | 19 |
| 1889 | TTGATAAGCAAAGTAGCCT | A571887Hi | +T*+T*+G*A*T*A*A*G*C*A*A*A*G*T*A*G*+C*+C*+T | 51747 | 19 |
| 1890 | TTTGATAAGCAAAGTAGCC | A571888Hi | +T*+T*+T*G*A*T*A*A*G*C*A*A*A*G*T*A*+G*+C*+C | 51748 | 19 |
| 1891 | ATACTAATATTTGATAAGC | A571889Hi | +A*+T*+A*C*T*A*A*T*A*T*T*T*G*A*T*A*+A*+G*+C | 51757 | 19 |
| 1892 | AACCACCTTAAGCACATCC | A571890Hi | +A*+A*+C*C*A*C*C*T*T*A*A*G*C*A*C*A*+T*+C*+C | 52275 | 19 |
| 1893 | ACCACCTTAAGCACATCC | A571891Hi | +A*+C*+C*A*C*C*T*T*A*A*G*C*A*C*A*+T*+C*+C | 52275 | 18 |
| 1894 | GGTTCTCTAGAGAGCCTAG | A571892Hi | +G*+G*+T*T*C*T*C*T*A*G*A*G*A*G*C*C*+T*+A*+G | 52461 | 19 |
| 1895 | AGTAGGTTCTCTAGAGAG | A571893Hi | +A*+G*+T*A*G*G*T*T*C*T*C*T*A*G*A*+G*+A*+G | 52466 | 18 |
| 1896 | GATATTAAACAGGATTAAA | A571894Hi | +G*+A*+T*A*T*T*A*A*A*C*A*G*G*A*T*T*+A*+A*+A | 52554 | 19 |
| 1897 | AGATATTAAACAGGATTAA | A571895Hi | +A*+G*+A*T*A*T*T*A*A*A*C*A*G*G*A*T*+T*+A*+A | 52555 | 19 |
| 1898 | GCTTGTCTAAAGCCATAG | A571896Hi | +G*+C*+T*T*G*T*C*T*A*A*A*G*C*C*A*+T*+A*+G | 52590 | 18 |
| 1899 | TTTCAAAGATGCTTGTCTA | A571897Hi | +T*+T*+T*C*A*A*A*G*A*T*G*C*T*T*G*T*+C*+T*+A | 52599 | 19 |
| 1900 | CTCTCTCTCATGACTAAGA | A571898Hi | +C*+T*+C*T*C*T*C*T*C*A*T*G*A*C*T*A*+A*+G*+A | 52705 | 19 |

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|---|---|---|---|---|---|
| 1901 | GTTCATTTAACTATAGATA | A571899Hi | +G*+T*+T*C*A*T*T*T*A*A*C*T*A*T*A*G*+A*+T*+A | 52772 | 19 |
| 1902 | AGGATGTTCATTTAACTAT | A571900Hi | +A*+G*+G*A*T*G*T*T*C*A*T*T*T*A*A*C*+T*+A*+T | 52777 | 19 |
| 1903 | TAGGATGTTCATTTAACTA | A571901Hi | +T*+A*+G*G*A*T*G*T*T*C*A*T*T*T*A*A*+C*+T*+A | 52778 | 19 |
| 1904 | CTAGGATGTTCATTTAAC | A571902Hi | +C*+T*+A*G*G*A*T*G*T*T*C*A*T*T*T*+A*+A*+C | 52780 | 18 |
| 1905 | ATACCTAGGATGTTCATTT | A571903Hi | +A*+T*+A*C*C*T*A*G*G*A*T*G*T*T*C*A*+T*+T*+T | 52783 | 19 |
| 1906 | CAATACCTAGGATGTTCA | A571904Hi | +C*+A*+A*T*A*C*C*T*A*G*G*A*T*G*T*+T*+C*+A | 52786 | 18 |
| 1907 | GAAACAATACCTAGGATG | A571905Hi | +G*+A*+A*A*C*A*A*T*A*C*C*T*A*G*G*+A*+T*+G | 52790 | 18 |
| 1908 | ATGAAACAATACCTAGGAT | A571906Hi | +A*+T*+G*A*A*A*C*A*A*T*A*C*C*T*A*G*+G*+A*+T | 52791 | 19 |
| 1909 | TATATGAAACAATACCTAG | A571907Hi | +T*+A*+T*A*T*G*A*A*A*C*A*A*T*A*C*C*+T*+A*+G | 52794 | 19 |
| 1910 | TGTATATGAAACAATACCT | A571908Hi | +T*+G*+T*A*T*A*T*G*A*A*A*C*A*A*T*A*+C*+C*+T | 52796 | 19 |
| 1911 | TTTGTATATGAAACAATAC | A571909Hi | +T*+T*+T*G*T*A*T*A*T*G*A*A*A*C*A*A*+T*+A*+C | 52798 | 19 |
| 1912 | GAGTTTGTATATGAAACAA | A571910Hi | +G*+A*+G*T*T*T*G*T*A*T*A*T*G*A*A*A*+C*+A*+A | 52801 | 19 |
| 1913 | AACAGTATAAAGCAGAGAG | A571911Hi | +A*+A*+C*A*G*T*A*T*A*A*A*G*C*A*G*A*+G*+A*+G | 52819 | 19 |
| 1914 | CTAAGATTGTCTGAAATCC | A571912H | +C*+T*+A*A*G*A*T*T*G*T*C*T*G*A*A*A*+T*+C*+C | 52892 | 19 |
| 1915 | GCTAAGATTGTCTGAAATC | A571913H | +G*+C*+T*A*A*G*A*T*T*G*T*C*T*G*A*A*+A*+T*+C | 52893 | 19 |
| 1916 | TTGCTAAGATTGTCTGAAA | A571914H | +T*+T*+G*C*T*A*A*G*A*T*T*G*T*C*T*G*+A*+A*+A | 52895 | 19 |
| 1917 | ATTGCTAAGATTGTCTGAA | A571915H | +A*+T*+T*G*C*T*A*A*G*A*T*T*G*T*C*T*+G*+A*+A | 52896 | 19 |
| 1918 | GATTGCTAAGATTGTCTGA | A571916H | +G*+A*+T*T*G*C*T*A*A*G*A*T*T*G*T*C*+T*+G*+A | 52897 | 19 |
| 1919 | AGGATTGCTAAGATTGTCT | A571917H | +A*+G*+G*A*T*T*G*C*T*A*A*G*A*T*T*G*+T*+C*+T | 52899 | 19 |
| 1920 | AGGATTGCTAAGATTGTC | A571918H | +A*+G*+G*A*T*T*G*C*T*A*A*G*A*T*T*+G*+T*+C | 52900 | 18 |
| 1921 | GAGGATTGCTAAGATTGTC | A571919H | +G*+A*+G*G*A*T*T*G*C*T*A*A*G*A*T*T*+G*+T*+C | 52900 | 19 |
| 1922 | TGACAATTTGAGGATTGCT | A571920H | +T*+G*+A*C*A*A*T*T*T*G*A*G*G*A*T*T*+G*+C*+T | 52909 | 19 |
| 1923 | TGACAATTTGAGGATTGC | A571921H | +T*+G*+A*C*A*A*T*T*T*G*A*G*G*A*T*+T*+G*+C | 52910 | 18 |
| 1924 | CTGACAATTTGAGGATTGC | A571922H | +C*+T*+G*A*C*A*A*T*T*T*G*A*G*G*A*T*+T*+G*+C | 52910 | 19 |
| 1925 | GCTGACAATTTGAGGATTG | A571923H | +G*+C*+T*G*A*C*A*A*T*T*T*G*A*G*G*A*+T*+T*+G | 52911 | 19 |
| 1926 | GCTGACAATTTGAGGATT | A571924H | +G*+C*+T*G*A*C*A*A*T*T*T*G*A*G*G*+A*+T*+T | 52912 | 18 |
| 1927 | TGCTGACAATTTGAGGATT | A571925H | +T*+G*+C*T*G*A*C*A*A*T*T*T*G*A*G*G*+A*+T*+T | 52912 | 19 |
| 1928 | ATGCTGACAATTTGAGGAT | A571926H | +A*+T*+G*C*T*G*A*C*A*A*T*T*T*G*A*G*+G*+A*+T | 52913 | 19 |
| 1929 | GATGCTGACAATTTGAGGA | A571927H | +G*+A*+T*G*C*T*G*A*C*A*A*T*T*T*G*A*+G*+G*+A | 52914 | 19 |
| 1930 | GATGCTGACAATTTGAGG | A571928H | +G*+A*+T*G*C*T*G*A*C*A*A*T*T*T*G*+A*+G*+G | 52915 | 18 |
| 1931 | AGATGCTGACAATTTGAGG | A571929H | +A*+G*+A*T*G*C*T*G*A*C*A*A*T*T*T*G*+A*+G*+G | 52915 | 19 |
| 1932 | AGATGCTGACAATTTGAG | A571930H | +A*+G*+A*T*G*C*T*G*A*C*A*A*T*T*T*+G*+A*+G | 52916 | 18 |
| 1933 | AAGATGCTGACAATTTGAG | A571931H | +A*+A*+G*A*T*G*C*T*G*A*C*A*A*T*T*T*+G*+A*+G | 52916 | 19 |
| 1934 | TAGAAAAAGATGCTGACAA | A571932H | +T*+A*+G*A*A*A*A*A*G*A*T*G*C*T*G*A*+C*+A*+A | 52922 | 19 |
| 1935 | TTAGAAAAAGATGCTGACA | A571933H | +T*+T*+A*G*A*A*A*A*A*G*A*T*G*C*T*G*+A*+C*+A | 52923 | 19 |

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|---|---|---|---|---|---|
| 1936 | TTAGAAAAAGATGCTGAC | A571934H | +T*+T*+A*G*A*A*A*A*A*G*A*T*G*C*T*+G*+A*+C | 52924 | 18 |
| 1937 | CTTAGAAAAAGATGCTGAC | A571935H | +C*+T*+T*A*G*A*A*A*A*A*G*A*T*G*C*T*+G*+A*+C | 52924 | 19 |
| 1938 | GCTTAGAAAAAGATGCTGA | A571936H | +G*+C*+T*T*A*G*A*A*A*A*A*G*A*T*G*C*+T*+G*+A | 52925 | 19 |
| 1939 | ACCAGCAGCTTAGAAAAAG | A571937H | +A*+C*+C*A*G*C*A*G*C*T*T*A*G*A*A*A*A*+A*+A*+G | 52932 | 19 |
| 1940 | GCACCAGCAGCTTAGAAAA | A571938H | +G*+C*+A*C*C*A*G*C*A*G*C*T*T*A*G*A*+A*+A*+A | 52934 | 19 |
| 1941 | TGCACCAGCAGCTTAGAAA | A571939H | +T*+G*+C*A*C*C*A*G*C*A*G*C*T*T*A*G*+A*+A*+A | 52935 | 19 |
| 1942 | GATGCACCAGCAGCTTAGA | A571940H | +G*+A*+T*G*C*A*C*C*A*G*C*A*G*C*T*T*+A*+G*+A | 52937 | 19 |
| 1943 | GATCCTTTTGTTCCATGAT | A571941H | +G*+A*+T*C*C*T*T*T*T*G*T*T*C*C*A*T*+G*+A*+T | 52997 | 19 |
| 1944 | CTGTTGATCCTTTTGTTCC | A571942H | +C*+T*+G*T*T*G*A*T*C*C*T*T*T*T*G*T*+T*+C*+C | 53002 | 19 |
| 1945 | CATAACATTTAGGATGCAA | A571943Hi | +C*+A*+T*A*A*C*A*T*T*T*A*G*G*A*T*G*+C*+A*+A | 53037 | 19 |
| 1946 | AGAGTCAGATAAATACATA | A571944Hi | +A*+G*+A*G*T*C*A*G*A*T*A*A*A*T*A*C*+A*+T*+A | 53052 | 19 |
| 1947 | TAGAGTCAGATAAATACAT | A571945Hi | +T*+A*+G*A*G*T*C*A*G*A*T*A*A*A*T*A*+C*+A*+T | 53053 | 19 |
| 1948 | TTGCAACAGAGGTTTAGAA | A571946H | +T*+T*+G*C*A*A*C*A*G*A*G*G*T*T*T*A*+G*+A*+A | 53096 | 19 |
| 1949 | ACTTGCAACAGAGGTTTAG | A571947H | +A*+C*+T*T*G*C*A*A*C*A*G*A*G*G*T*T*+T*+A*+G | 53098 | 19 |
| 1950 | AAACACTTGCAACAGAGGT | A571948H | +A*+A*+A*C*A*C*T*T*G*C*A*A*C*A*G*A*+G*+G*+T | 53102 | 19 |
| 1951 | TTTGCAAAACACTTGCAAC | A571949H | +T*+T*+T*G*C*A*A*A*A*C*A*C*T*T*G*C*+A*+A*+C | 53108 | 19 |
| 1952 | TTTTGCAAAACACTTGCAA | A571950H | +T*+T*+T*T*G*C*A*A*A*A*C*A*C*T*T*G*+C*+A*+A | 53109 | 19 |
| 1953 | CTTTTGCAAAACACTTGCA | A571951H | +C*+T*+T*T*T*G*C*A*A*A*A*C*A*C*T*T*+G*+C*+A | 53110 | 19 |
| 1954 | ATAGCTACTTTTGCAAAAC | A571952H | +A*+T*+A*G*C*T*A*C*T*T*T*T*G*C*A*A*+A*+A*+C | 53117 | 19 |
| 1955 | CCATAGCTACTTTTGCAAA | A571953H | +C*+C*+A*T*A*G*C*T*A*C*T*T*T*T*G*C*+A*+A*+A | 53119 | 19 |
| 1956 | TCCATAGCTACTTTTGCAA | A571954H | +T*+C*+C*A*T*A*G*C*T*A*C*T*T*T*T*G*+C*+A*+A | 53120 | 19 |
| 1957 | ACACGCTCTCTCTAGCATC | A571955H | +A*+C*+A*C*G*C*T*C*T*C*T*C*T*A*G*C*+A*+T*+C | 53157 | 19 |
| 1958 | CACACGCTCTCTCTAGCAT | A571956H | +C*+A*+C*A*C*G*C*T*C*T*C*T*C*T*A*G*+C*+A*+T | 53158 | 19 |
| 1959 | CACACGCTCTCTCTAGCA | A571957H | +C*+A*+C*A*C*G*C*T*C*T*C*T*C*T*A*+G*+C*+A | 53159 | 18 |
| 1960 | TCACACGCTCTCTCTAGCA | A571958H | +T*+C*+A*C*A*C*G*C*T*C*T*C*T*C*T*A*+G*+C*+A | 53159 | 19 |
| 1961 | TCACACGCTCTCTCTAGC | A571959H | +T*+C*+A*C*A*C*G*C*T*C*T*C*T*C*T*+A*+G*+C | 53160 | 18 |
| 1962 | ATCACACGCTCTCTCTAGC | A571960H | +A*+T*+C*A*C*A*C*G*C*T*C*T*C*T*C*T*+A*+G*+C | 53160 | 19 |
| 1963 | GATCACACGCTCTCTCTAG | A571961H | +G*+A*+T*C*A*C*A*C*G*C*T*C*T*C*T*C*+T*+A*+G | 53161 | 19 |
| 1964 | GATCACACGCTCTCTCTA | A571962H | +G*+A*+T*C*A*C*A*C*G*C*T*C*T*C*T*+C*+T*+A | 53162 | 18 |
| 1965 | TGATCACACGCTCTCTCTA | A571963H | +T*+G*+A*T*C*A*C*A*C*G*C*T*C*T*C*T*+C*+T*+A | 53162 | 19 |
| 1966 | CTGATCACACGCTCTCTCT | A571964H | +C*+T*+G*A*T*C*A*C*A*C*G*C*T*C*T*C*+T*+C*+T | 53163 | 19 |
| 1967 | TCTGATCACACGCTCTCTC | A571965H | +T*+C*+T*G*A*T*C*A*C*A*C*G*C*T*C*T*+C*+T*+C | 53164 | 19 |
| 1968 | TCTGATCACACGCTCTCT | A571966H | +T*+C*+T*G*A*T*C*A*C*A*C*G*C*T*C*+T*+C*+T | 53165 | 18 |
| 1969 | TTCTGATCACACGCTCTCT | A571967H | +T*+T*+C*T*G*A*T*C*A*C*A*C*G*C*T*C*+T*+C*+T | 53165 | 19 |
| 1970 | ATTCTGATCACACGCTCTC | A571968H | +A*+T*+T*C*T*G*A*T*C*A*C*A*C*G*C*T*+C*+T*+C | 53166 | 19 |

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|---|---|---|---|---|---|
| 1971 | TATTCTGATCACACG CTCT | A571969H | +T*+A*+T*T*C*T*G*A*T*C*A*C*A*C*G*C*+ T*+C*+T | 53167 | 19 |
| 1972 | TATTCTGATCACACG CTC | A571970H | +T*+A*+T*T*C*T*G*A*T*C*A*C*A*C*G*+C* +T*+C | 53168 | 18 |
| 1973 | TTATTCTGATCACAC GCTC | A571971H | +T*+T*+A*T*T*C*T*G*A*T*C*A*C*A*C*G*+ C*+T*+C | 53168 | 19 |
| 1974 | TTATTCTGATCACAC GCT | A571972H | +T*+T*+A*T*T*C*T*G*A*T*C*A*C*A*C*+G* +C*+T | 53169 | 18 |
| 1975 | GTTATTCTGATCACA CGCT | A571973H | +G*+T*+T*A*T*T*C*T*G*A*T*C*A*C*A*C*+ G*+C*+T | 53169 | 19 |
| 1976 | CTGTTATTCTGATCA CACG | A571974H | +C*+T*+G*T*T*A*T*T*C*T*G*A*T*C*A*C*+ A*+C*+G | 53171 | 19 |
| 1977 | CATGATGCTGTTATT CTGA | A571975H | +C*+A*+T*G*A*T*G*C*T*G*T*T*A*T*T*C*+ T*+G*+A | 53178 | 19 |
| 1978 | CAACCATGATGCTGT TATT | A571976H | +C*+A*+A*C*C*A*T*G*A*T*G*C*T*G*T*T*+ A*+T*+T | 53182 | 19 |
| 1979 | TCAACCATGATGCTG TTAT | A571977H | +T*+C*+A*A*C*C*A*T*G*A*T*G*C*T*G*T*+ T*+A*+T | 53183 | 19 |
| 1980 | TTCAACCATGATGCT GTTA | A571978H | +T*+T*+C*A*A*C*C*A*T*G*A*T*G*C*T*G*+ T*+T*+A | 53184 | 19 |
| 1981 | ATTCAACCATGATGC TGTT | A571979H | +A*+T*+T*C*A*A*C*C*A*T*G*A*T*G*C*T*+ G*+T*+T | 53185 | 19 |
| 1982 | GCATTCAACCATGAT GCTG | A571980H | +G*+C*+A*T*T*C*A*A*C*C*A*T*G*A*T*G*+ C*+T*+G | 53187 | 19 |
| 1983 | AGCATTCAACCATGA TGCT | A571981H | +A*+G*+C*A*T*T*C*A*A*C*C*A*T*G*A*T*+ G*+C*+T | 53188 | 19 |
| 1984 | GCAAGCATTCAACCA TGAT | A571982H | +G*+C*+A*A*G*C*A*T*T*C*A*A*C*C*A*T*+ G*+A*+T | 53191 | 19 |
| 1985 | AGCAAGCATTCAACC ATGA | A571983H | +A*+G*+C*A*A*G*C*A*T*T*C*A*A*C*C*A*+ T*+G*+A | 53192 | 19 |
| 1986 | AAGCAAGCATTCAAC CATG | A571984H | +A*+A*+G*C*A*A*G*C*A*T*T*C*A*A*C*C*+ A*+T*+G | 53193 | 19 |
| 1987 | CTTGATTGGCATCTG CTCC | A571985H | +C*+T*+T*G*A*T*T*G*G*C*A*T*C*T*G*C*+ T*+C*+C | 53218 | 19 |
| 1988 | GCTTGATTGGCATCT GCTC | A571986H | +G*+C*+T*T*G*A*T*T*G*G*C*A*T*C*T*G*+ C*+T*+C | 53219 | 19 |
| 1989 | GCTTGATTGGCATCT GCT | A571987H | +G*+C*+T*T*G*A*T*T*G*G*C*A*T*C*T*+G* +C*+T | 53220 | 18 |
| 1990 | TGCTTGATTGGCATC TGCT | A571988H | +T*+G*+C*T*T*G*A*T*T*G*G*C*A*T*C*T*+ G*+C*+T | 53220 | 19 |
| 1991 | CTTTGCTTGATTGGC ATCT | A571989H | +C*+T*+T*T*G*C*T*T*G*A*T*T*G*G*C*A*+ T*+C*+T | 53223 | 19 |
| 1992 | CTTTGCTTGATTGGC ATC | A571990H | +C*+T*+T*T*G*C*T*T*G*A*T*T*G*G*C*+A* +T*+C | 53224 | 18 |
| 1993 | CCTTTGCTTGATTGG CATC | A571991H | +C*+C*+T*T*T*G*C*T*T*G*A*T*T*G*G*C*+ A*+T*+C | 53224 | 19 |
| 1994 | TCCTTTGCTTGATTG GCAT | A571992H | +T*+C*+C*T*T*T*G*C*T*T*G*A*T*T*G*G*+ C*+A*+T | 53225 | 19 |
| 1995 | TCCTTTGCTTGATTG GCA | A571993H | +T*+C*+C*T*T*T*G*C*T*T*G*A*T*T*G*+G* +C*+A | 53226 | 18 |
| 1996 | CTCCTTTGCTTGATT GGCA | A571994H | +C*+T*+C*C*T*T*T*G*C*T*T*G*A*T*T*G*+ G*+C*+A | 53226 | 19 |
| 1997 | TCCCTCCTTTGCTTG ATTG | A571995H | +T*+C*+C*C*T*C*C*T*T*T*G*C*T*T*G*A*+ T*+T*+G | 53229 | 19 |
| 1998 | TAGTGAAGAATAATA TGAT | A571996Hi | +T*+A*+G*T*G*A*A*G*A*A*T*A*A*T*A*T*+ G*+A*+T | 53350 | 19 |
| 1999 | GTAGTGAAGAATAAT ATGA | A571997Hi | +G*+T*+A*G*T*G*A*A*G*A*A*T*A*A*T*A*+ T*+G*+A | 53351 | 19 |
| 2000 | CTATTACTTCTGGAA TTCT | A571998Hi | +C*+T*+A*T*T*A*C*T*T*C*T*G*G*A*A*T*+ T*+C*+T | 53419 | 19 |
| 2001 | ATGAAATGAAAGATT AGAC | A571999Hi | +A*+T*+G*A*A*A*T*G*A*A*A*G*A*T*T*A*+ G*+A*+C | 53458 | 19 |
| 2002 | TAGAGATGCCTACTA AGG | A572000Hi | +T*+A*+G*A*G*A*T*G*C*C*T*A*C*T*A*+A* +G*+G | 53524 | 18 |
| 2003 | AAGTTGTAGAGATGC CTA | A572001Hi | +A*+A*+G*T*T*G*T*A*G*A*G*A*T*G*C*+C* +T*+A | 53530 | 18 |
| 2004 | GTGGAGTGTATCTGG AGA | A572002Hi | +G*+T*+G*G*A*G*T*G*T*A*T*C*T*G*G*+A* +G*+A | 53550 | 18 |
| 2005 | TGTGGAGTGTATCTG GAG | A572003Hi | +T*+G*+T*G*G*A*G*T*G*T*A*T*C*T*G*+G* +A*+G | 53551 | 18 |

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| 2006 | AACTATGTGTTATGTGGAG | A572004Hi | +A*+A*+C*T*A*T*G*T*G*T*T*A*T*G*T*G*+G*+A*+G | 53562 | 19 |
| 2007 | GAACTATGTGTTATGTGG | A572005Hi | +G*+A*+A*C*T*A*T*G*T*G*T*T*A*T*G*+T*+G*+G | 53564 | 18 |
| 2008 | CTGAATGCTAGTATAAACT | A572006Hi | +C*+T*+G*A*A*T*G*C*T*A*G*T*A*T*A*A*+A*+C*+T | 54093 | 19 |
| 2009 | GCTACCTGAATGCTAGT | A572007Hi | +G*+C*+T*A*C*C*T*G*A*A*T*G*C*T*+A*+G*+T | 54100 | 17 |
| 2010 | TAGTGCTACCTGAATGCT | A572008Hi | +T*+A*+G*T*G*C*T*A*C*C*T*G*A*A*T*+G*+C*+T | 54103 | 18 |
| 2011 | TAGACATAGTGCTACCTG | A572009Hi | +T*+A*+G*A*C*A*T*A*G*T*G*C*T*A*C*+C*+T*+G | 54109 | 18 |
| 2012 | AACTTAATCTTAACAGTCA | A572010Hi | +A*+A*+C*T*T*A*A*T*C*T*T*A*A*C*A*G*+T*+C*+A | 54300 | 19 |
| 2013 | TAACTTAATCTTAACAGTC | A572011Hi | +T*+A*+A*C*T*T*A*A*T*C*T*T*A*A*C*A*+G*+T*+C | 54301 | 19 |
| 2014 | AATTAGATTGTTTATGTGA | A572012Hi | +A*+A*+T*T*A*G*A*T*T*G*T*T*T*A*T*G*+T*+G*+A | 54395 | 19 |
| 2015 | GTATTAAATTATTGATGGA | A572013Hi | +G*+T*+A*T*T*A*A*A*T*T*A*T*T*G*A*T*+G*+G*+A | 54493 | 19 |
| 2016 | ATGCAATAATCTGCATGCA | A572014Hi | +A*+T*+G*C*A*A*T*A*A*T*C*T*G*C*A*T*+G*+C*+A | 54531 | 19 |
| 2017 | TAATGCAATAATCTGCATG | A572015Hi | +T*+A*+A*T*G*C*A*A*T*A*A*T*C*T*G*C*+A*+T*+G | 54533 | 19 |
| 2018 | CTTAATGTGGACTTAGAA | A572016Hi | +C*+T*+T*A*A*T*G*T*G*G*A*C*T*T*A*+G*+A*+A | 54594 | 18 |
| 2019 | TCCTTAATGTGGACTTAG | A572017Hi | +T*+C*+C*T*T*A*A*T*G*T*G*G*A*C*T*+T*+A*+G | 54596 | 18 |
| 2020 | TGTTTCCTTAATGTGGACT | A572018Hi | +T*+G*+T*T*T*C*C*T*T*A*A*T*G*T*G*G*+A*+C*+T | 54599 | 19 |
| 2021 | GTTGTTTCCTTAATGTGGA | A572019Hi | +G*+T*+T*G*T*T*T*C*C*T*T*A*A*T*G*T*+G*+G*+A | 54601 | 19 |
| 2022 | TGTTGTTTCCTTAATGTGG | A572020Hi | +T*+G*+T*T*G*T*T*T*C*C*T*T*A*A*T*G*+T*+G*+G | 54602 | 19 |
| 2023 | GGTATGTTGTTTCCTTAAT | A572021Hi | +G*+G*+T*A*T*G*T*T*G*T*T*T*C*C*T*T*+A*+A*+T | 54606 | 19 |
| 2024 | CTAATACATAATCCTTGG | A572022Hi | +C*+T*+A*A*T*A*C*A*T*A*A*T*C*C*T*+T*+G*+G | 54799 | 18 |
| 2025 | CACAAGATTTAATCAGCAG | A572023Hi | +C*+A*+C*A*A*G*A*T*T*T*A*A*T*C*A*G*+C*+A*+G | 54871 | 19 |
| 2026 | ATCCACAAGATTTAATCA | A572024Hi | +A*+T*+C*C*A*C*A*A*G*A*T*T*T*A*A*+T*+C*+A | 54875 | 18 |
| 2027 | CCACTGTGATTTGATGAGT | A572025Hi | +C*+C*+A*C*T*G*T*G*A*T*T*T*G*A*T*G*+A*+G*+T | 55118 | 19 |
| 2028 | TTCCACTGTGATTTGATGA | A572026Hi | +T*+T*+C*C*A*C*T*G*T*G*A*T*T*T*G*A*+T*+G*+A | 55120 | 19 |
| 2029 | TGTGTGTGCCATCATACAT | A572027Hi | +T*+G*+T*G*T*G*T*G*C*C*A*T*C*A*T*A*+C*+A*+T | 55316 | 19 |
| 2030 | TTGTGTAAAGTATTTGGA | A572028Hi | +T*+T*+G*T*G*T*A*A*A*G*T*A*T*T*T*+G*+G*+A | 56182 | 18 |
| 2031 | ATTGTGTAAAGTATTTGGA | A572029Hi | +A*+T*+T*G*T*G*T*A*A*A*G*T*A*T*T*T*+G*+G*+A | 56182 | 19 |
| 2032 | ATTGTGTAAAGTATTTGG | A572030Hi | +A*+T*+T*G*T*G*T*A*A*A*G*T*A*T*T*+T*+G*+G | 56183 | 18 |
| 2033 | AATTGTGTAAAGTATTTGG | A572031Hi | +A*+A*+T*T*G*T*G*T*A*A*A*G*T*A*T*T*+T*+G*+G | 56183 | 19 |
| 2034 | ATTAGAACCTACTGGACC | A572032Hi | +A*+T*+T*A*G*A*A*C*C*T*A*C*T*G*G*+A*+C*+C | 56227 | 18 |
| 2035 | AGCTTGTTCTTAGGCAAGT | A572033Hi | +A*+G*+C*T*T*G*T*T*C*T*T*A*G*G*C*A*+A*+G*+T | 56294 | 19 |
| 2036 | GGAGCTTGTTCTTAGGCAA | A572034Hi | +G*+G*+A*G*C*T*T*G*T*T*C*T*T*A*G*G*+C*+A*+A | 56296 | 19 |
| 2037 | CCAGGAGCTTGTTCTTAGG | A572035Hi | +C*+C*+A*G*G*A*G*C*T*T*G*T*T*C*T*T*+A*+G*+G | 56299 | 19 |
| 2038 | ACCAGGAGCTTGTTCTTAG | A572036Hi | +A*+C*+C*A*G*G*A*G*C*T*T*G*T*T*C*T*+T*+A*+G | 56300 | 19 |
| 2039 | GCTGTGTAGCCAAGAAAT | A572037Hi | +G*+C*+T*G*T*G*T*A*G*C*C*A*A*G*A*+A*+A*+T | 56355 | 18 |
| 2040 | TGCTGTGTAGCCAAGAAAT | A572038Hi | +T*+G*+C*T*G*T*G*T*A*G*C*C*A*A*G*A*+A*+A*+T | 56355 | 19 |

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| 2041 | TCTGCTGTGTAGCCAAGAA | A572039Hi | +T*+C*+T*G*C*T*G*T*G*T*A*G*C*C*A*A*+G*+A*+A | 56357 | 19 |
| 2042 | ATCTGCTGTGTAGCCAAGA | A572040Hi | +A*+T*+C*T*G*C*T*G*T*G*T*A*G*C*C*A*+A*+G*+A | 56358 | 19 |
| 2043 | TGAATCTGCTGTGTAGCCA | A572041Hi | +T*+G*+A*A*T*C*T*G*C*T*G*T*G*T*A*G*+C*+C*+A | 56361 | 19 |
| 2044 | TGAATCTGCTGTGTAGCC | A572042Hi | +T*+G*+A*A*T*C*T*G*C*T*G*T*G*T*A*+G*+C*+C | 56362 | 18 |
| 2045 | CCATGAATCTGCTGTGTAG | A572043Hi | +C*+C*+A*T*G*A*A*T*C*T*G*C*T*G*T*G*+T*+A*+G | 56364 | 19 |
| 2046 | CTACCATGAATCTGCTGTG | A572044Hi | +C*+T*+A*C*C*A*T*G*A*A*T*C*T*G*C*T*+G*+T*+G | 56367 | 19 |
| 2047 | TACCATGAATCTGCTGTG | A572045Hi | +T*+A*+C*C*A*T*G*A*A*T*C*T*G*C*T*+G*+T*+G | 56367 | 18 |
| 2048 | CACTACCATGAATCTGCT | A572046Hi | +C*+A*+C*T*A*C*C*A*T*G*A*A*T*C*T*+G*+C*+T | 56370 | 18 |
| 2049 | CCACCACTACCATGAATCT | A572047Hi | +C*+C*+A*C*C*A*C*T*A*C*C*A*T*G*A*A*+T*+C*+T | 56373 | 19 |
| 2050 | GCAATCTTTCTCTGATCAT | A572048Hi | +G*+C*+A*A*T*C*T*T*T*C*T*C*T*G*A*T*+C*+A*+T | 56469 | 19 |
| 2051 | CTCTTTAGAATATTCACCAC | A572049Hi | +C*+T*+C*T*T*T*A*G*A*A*T*A*T*T*C*A*+C*+A*+C | 56623 | 19 |
| 2052 | CCTACAGAGTCATTCTCTT | A572050Hi | +C*+C*+T*A*C*A*G*A*G*T*C*A*T*T*C*T*+C*+T*+T | 56637 | 19 |
| 2053 | TCCTACAGAGTCATTCTCT | A572051Hi | +T*+C*+C*T*A*C*A*G*A*G*T*C*A*T*T*C*+T*+C*+T | 56638 | 19 |
| 2054 | TTAAATCCTACAGAGTCAT | A572052Hi | +T*+T*+A*A*A*T*C*C*T*A*C*A*G*A*G*T*+C*+A*+T | 56643 | 19 |
| 2055 | TTTAAATCCTACAGAGTC | A572053Hi | +T*+T*+T*A*A*A*T*C*C*T*A*C*A*G*A*+G*+T*+C | 56645 | 18 |
| 2056 | CTGACTTTAGGCATATGG | A572054Hi | +C*+T*+G*A*C*T*T*T*A*G*G*C*A*T*A*+T*+G*+G | 56740 | 18 |
| 2057 | GCTGACTTTAGGCATATGG | A572055Hi | +G*+C*+T*G*A*C*T*T*T*A*G*G*C*A*T*A*+T*+G*+G | 56740 | 19 |
| 2058 | CTATCCAAGCTGACTTTAG | A572056Hi | +C*+T*+A*T*C*C*A*A*G*C*T*G*A*C*T*T*+T*+A*+G | 56748 | 19 |
| 2059 | AACTATCCAAGCTGACTTT | A572057Hi | +A*+A*+C*T*A*T*C*C*A*A*G*C*T*G*A*C*+T*+T*+T | 56750 | 19 |
| 2060 | AACTATCCAAGCTGACTT | A572058Hi | +A*+A*+C*T*A*T*C*C*A*A*G*C*T*G*A*+C*+T*+T | 56751 | 18 |
| 2061 | GGATCCAAACTATCCAAG | A572059Hi | +G*+G*+A*T*C*C*A*A*A*C*T*A*T*C*C*+A*+A*+G | 56758 | 18 |
| 2062 | TCCTTGGAGGATCCAAACT | A572060Hi | +T*+C*+C*T*T*G*G*A*G*G*A*T*C*C*A*A*+A*+C*+T | 56765 | 19 |
| 2063 | CCTTGGAGGATCCAAACT | A572061Hi | +C*+C*+T*T*G*G*A*G*G*A*T*C*C*A*A*+A*+C*+T | 56765 | 18 |
| 2064 | TCCTTGGAGGATCCAAAC | A572062Hi | +T*+C*+C*T*T*G*G*A*G*G*A*T*C*C*A*+A*+A*+C | 56766 | 18 |
| 2065 | CTGCACATGTTTGTGGAAG | A572063Hi | +C*+T*+G*C*A*C*A*T*G*T*T*T*G*T*G*G*+A*+A*+G | 56790 | 19 |
| 2066 | TATTAATTATCTAGCACTG | A572064Hi | +T*+A*+T*T*A*A*T*T*A*T*C*T*A*G*C*A*+C*+T*+G | 56813 | 19 |
| 2067 | GTACTAAGGTGATTTATGT | A572065Hi | +G*+T*+A*C*T*A*A*G*G*T*G*A*T*T*T*A*+T*+G*+T | 56907 | 19 |
| 2068 | GTACTAAGGTGATTTATG | A572066Hi | +G*+T*+A*C*T*A*A*G*G*T*G*A*T*T*T*+A*+T*+G | 56908 | 18 |
| 2069 | TGTACTAAGGTGATTTATG | A572067Hi | +T*+G*+T*A*C*T*A*A*G*G*T*G*A*T*T*T*+A*+T*+G | 56908 | 19 |
| 2070 | CTTTGTACTAAGGTGATTTT | A572068Hi | +C*+T*+T*T*G*T*A*C*T*A*A*G*G*T*G*A*+T*+T*+T | 56911 | 19 |
| 2071 | CTTTGTACTAAGGTGATT | A572069Hi | +C*+T*+T*T*G*T*A*C*T*A*A*G*G*T*G*+A*+T*+T | 56912 | 18 |
| 2072 | TCACTCCTTACTTTGTACT | A572070Hi | +T*+C*+A*C*T*C*C*T*T*A*C*T*T*T*G*T*+A*+C*+T | 56921 | 19 |
| 2073 | CACTCCTTACTTTGTACT | A572071Hi | +C*+A*+C*T*C*C*T*T*A*C*T*T*T*G*T*+A*+C*+T | 56921 | 18 |
| 2074 | CCTGAAGCCTAGCACAACA | A572072Hi | +C*+C*+T*G*A*A*G*C*C*T*A*G*C*A*C*A*+A*+C*+A | 57305 | 19 |
| 2075 | CCTGAAGCCTAGCACAAC | A572073Hi | +C*+C*+T*G*A*A*G*C*C*T*A*G*C*A*C*+A*+A*+C | 57306 | 18 |

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| 2076 | TCCTGAAGCCTAGCACAAC | A572074Hi | +T*+C*+C*T*G*A*A*G*C*C*T*A*G*C*A*C*+A*+A*+C | 57306 | 19 |
| 2077 | ACTTGTATTCCTGAAGCCT | A572075Hi | +A*+C*+T*T*G*T*A*T*T*C*C*T*G*A*A*G*+C*+C*+T | 57314 | 19 |
| 2078 | TCTTGCTAGAATGCAAAGG | A572076Hi | +T*+C*+T*T*G*C*T*A*G*A*A*T*G*C*A*A*+A*+G*+G | 57354 | 19 |
| 2079 | ATGTAGCACTGAGCAAACA | A572077Hi | +A*+T*+G*T*A*G*C*A*C*T*G*A*G*C*A*A*+A*+C*+A | 57390 | 19 |
| 2080 | TCATTTAATGTAGCACTGA | A572078Hi | +T*+C*+A*T*T*T*A*A*T*G*T*A*G*C*A*C*+T*+G*+A | 57397 | 19 |
| 2081 | TTCATTTAATGTAGCACTG | A572079Hi | +T*+T*+C*A*T*T*T*A*A*T*G*T*A*G*C*A*+C*+T*+G | 57398 | 19 |
| 2082 | CTACTAACCTCTCAGGCC | A572080Hi | +C*+T*+A*C*T*A*A*C*C*T*C*T*C*A*G*+G*+C*+C | 57451 | 18 |
| 2083 | GCTACTAACCTCTCAGGCC | A572081Hi | +G*+C*+T*A*C*T*A*A*C*C*T*C*T*C*A*G*+G*+C*+C | 57451 | 19 |
| 2084 | CCTTGCTACTAACCTCTCA | A572082Hi | +C*+C*+T*T*G*C*T*A*C*T*A*A*C*C*T*C*+T*+C*+A | 57455 | 19 |
| 2085 | GTCCTTGCTACTAACCTC | A572083Hi | +G*+T*+C*C*T*T*G*C*T*A*C*T*A*A*C*+C*+T*+C | 57458 | 18 |
| 2086 | GTTCATTCTTGAAGAATTG | A572084Hi | +G*+T*+T*C*A*T*T*C*T*T*G*A*A*G*A*A*+T*+T*+G | 57499 | 19 |
| 2087 | TGTTCATTCTTGAAGAATT | A572085Hi | +T*+G*+T*T*C*A*T*T*C*T*T*G*A*A*G*A*+A*+T*+T | 57500 | 19 |
| 2088 | TCTTCCAAACACAGCATGT | A572086Hi | +T*+C*+T*T*C*C*A*A*A*C*A*C*A*G*C*A*+T*+G*+T | 57598 | 19 |
| 2089 | TCAAAGCACTACAGAGCTC | A572087Hi | +T*+C*+A*A*A*G*C*A*C*T*A*C*A*G*A*G*+C*+T*+C | 57673 | 19 |
| 2090 | CCACCAGTCTCCAAGTAC | A572088Hi | +C*+C*+A*C*C*A*G*T*C*T*C*C*A*A*G*+T*+A*+C | 57711 | 18 |
| 2091 | ATGTGGTTGGAAGGCACCA | A572089Hi | +A*+T*+G*T*G*G*T*T*G*G*A*A*G*G*C*A*+C*+C*+A | 57738 | 19 |
| 2092 | ATGTGGTTGGAAGGCACC | A572090Hi | +A*+T*+G*T*G*G*T*T*G*G*A*A*G*G*C*+A*+C*+C | 57739 | 18 |
| 2093 | CAAATCTGCTGGCTTCAAA | A572091Hi | +C*+A*+A*A*T*C*T*G*C*T*G*G*C*T*T*C*+A*+A*+A | 57917 | 19 |
| 2094 | TATGCCATAGCAATTATT | A572092Hi | +T*+A*+T*G*C*C*A*T*A*G*C*A*A*T*T*+A*+T*+T | 58021 | 18 |
| 2095 | TGTGCTAAATTCTGTACAC | A572093Hi | +T*+G*+T*G*C*T*A*A*A*T*T*C*T*G*T*A*+C*+A*+C | 58072 | 19 |
| 2096 | ATATCCATCAGTTACTGTG | A572094Hi | +A*+T*+A*T*C*C*A*T*C*A*G*T*T*A*C*T*+G*+T*+G | 58087 | 19 |
| 2097 | TAATATCCATCAGTTACTG | A572095Hi | +T*+A*+A*T*A*T*C*C*A*T*C*A*G*T*T*A*+C*+T*+G | 58089 | 19 |
| 2098 | AATAATATCCATCAGTTAC | A572096Hi | +A*+A*+T*A*A*T*A*T*C*C*A*T*C*A*G*T*+T*+A*+C | 58091 | 19 |
| 2099 | GTAATAGAAATAATATCCA | A572097Hi | +G*+T*+A*A*T*A*G*A*A*A*T*A*A*T*A*T*+C*+C*+A | 58099 | 19 |
| 2100 | GGTAATAGAAATAATATCC | A572098Hi | +G*+G*+T*A*A*T*A*G*A*A*A*T*A*A*T*A*+T*+C*+C | 58100 | 19 |
| 2101 | GGAGCTATCAACTAGAAGA | A572099Hi | +G*+G*+A*G*C*T*A*T*C*A*A*C*T*A*G*A*+A*+G*+A | 58130 | 19 |
| 2102 | GCAAGGAGCTATCAACTAG | A572100Hi | +G*+C*+A*A*G*G*A*G*C*T*A*T*C*A*A*C*+T*+A*+G | 58134 | 19 |
| 2103 | TTCCTCAAAGATATACCTT | A572101Hi | +T*+T*+C*C*T*C*A*A*A*G*A*T*A*T*A*C*+C*+T*+T | 58334 | 19 |
| 2104 | TGTGACATAGAATAACTA | A572102Hi | +T*+G*+T*G*A*C*A*T*A*G*A*A*T*A*A*+C*+T*+A | 58454 | 18 |
| 2105 | AACCAGTACCTTAACACAG | A572103Hi | +A*+A*+C*C*A*G*T*A*C*C*T*T*A*A*C*A*+C*+A*+G | 58497 | 19 |
| 2106 | AACCAGTACCTTAACACA | A572104Hi | +A*+A*+C*C*A*G*T*A*C*C*T*T*A*A*C*+A*+C*+A | 58498 | 18 |
| 2107 | AAACCAGTACCTTAACAC | A572105Hi | +A*+A*+A*C*C*A*G*T*A*C*C*T*T*A*A*+C*+A*+C | 58499 | 18 |
| 2108 | TGTTTACATCCAGACTCCA | A572106Hi | +T*+G*+T*T*T*A*C*A*T*C*C*A*G*A*C*T*+C*+C*+A | 58578 | 19 |
| 2109 | TCTGTTTACATCCAGACTC | A572107Hi | +T*+C*+T*G*T*T*T*A*C*A*T*C*C*A*G*A*+C*+T*+C | 58580 | 19 |
| 2110 | TCTCTGTTTACATCCAGAC | A572108Hi | +T*+C*+T*C*T*G*T*T*T*A*C*A*T*C*C*A*+G*+A*+C | 58582 | 19 |

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| 2111 | ATCTCTGTTTACATCCAGA | A572109Hi | +A*+T*+C*T*C*T*G*T*T*T*A*C*A*T*C*C*+A*+G*+A | 58583 | 19 |
| 2112 | AAGATCTCTGTTTACATCC | A572110Hi | +A*+A*+G*A*T*C*T*C*T*G*T*T*T*A*C*A*+T*+C*+C | 58586 | 19 |
| 2113 | AAGATCTCTGTTTACATC | A572111Hi | +A*+A*+G*A*T*C*T*C*T*G*T*T*T*A*C*+A*+T*+C | 58587 | 18 |
| 2114 | TCAAGATCTCTGTTTACAT | A572112Hi | +T*+C*+A*A*G*A*T*C*T*C*T*G*T*T*T*A*+C*+A*+T | 58588 | 19 |
| 2115 | GGCTTGGCATCAAGATCTC | A572113Hi | +G*+G*+C*T*T*G*G*C*A*T*C*A*A*G*A*T*+C*+T*+C | 58597 | 19 |
| 2116 | TAGCATGAATAATCTGCCA | A572114Hi | +T*+A*+G*C*A*T*G*A*A*T*A*A*T*C*T*G*+C*+C*+A | 58671 | 19 |
| 2117 | GAATAGCATGAATAATCTG | A572115Hi | +G*+A*+A*T*A*G*C*A*T*G*A*A*T*A*A*T*+C*+T*+G | 58674 | 19 |
| 2118 | GATCCTTGAATAGATTGG | A572116Hi | +G*+A*+T*C*C*T*T*G*A*A*T*A*G*A*T*+T*+G*+G | 58726 | 18 |
| 2119 | TACATCTCCAATTTGGAAT | A572117Hi | +T*+A*+C*A*T*C*T*C*C*A*A*T*T*T*G*G*+A*+A*+T | 58770 | 19 |
| 2120 | TGGGACTGCTCTCTTTCTC | A572118H | +T*+G*+G*G*A*C*T*G*C*T*C*T*C*T*T*T*+C*+T*+C | 58885 | 19 |
| 2121 | CAATTTGGGACTGCTCTCT | A572119H | +C*+A*+A*T*T*T*G*G*G*A*C*T*G*C*T*C*+T*+C*+T | 58890 | 19 |
| 2122 | CAATTTGGGACTGCTCTC | A572120H | +C*+A*+A*T*T*T*G*G*G*A*C*T*G*C*T*+C*+T*+C | 58891 | 18 |
| 2123 | CCAATTTGGGACTGCTCTC | A572121H | +C*+C*+A*A*T*T*T*G*G*G*A*C*T*G*C*T*+C*+T*+C | 58891 | 19 |
| 2124 | ACCAATTTGGGACTGCTCT | A572122H | +A*+C*+C*A*A*T*T*T*G*G*G*A*C*T*G*C*+T*+C*+T | 58892 | 19 |
| 2125 | ACCAATTTGGGACTGCTC | A572123H | +A*+C*+C*A*A*T*T*T*G*G*G*A*C*T*G*+C*+T*+C | 58893 | 18 |
| 2126 | CACCAATTTGGGACTGCTC | A572124H | +C*+A*+C*C*A*A*T*T*T*G*G*G*A*C*T*G*+C*+T*+C | 58893 | 19 |
| 2127 | TCCACCAATTTGGGACTGC | A572125H | +T*+C*+C*A*C*C*A*A*T*T*T*G*G*G*A*C*+T*+G*+C | 58895 | 19 |
| 2128 | GTTCCACCAATTTGGGACT | A572126H | +G*+T*+T*C*C*A*C*C*A*A*T*T*T*G*G*G*+A*+C*+T | 58897 | 19 |
| 2129 | AGTTCCACCAATTTGGGAC | A572127H | +A*+G*+T*T*C*C*A*C*C*A*A*T*T*T*G*G*+G*+A*+C | 58898 | 19 |
| 2130 | ACGAGATCCACTATTCA | A572128H | +A*+C*+G*A*G*A*T*C*C*A*C*T*A*T*+T*+C*+A | 58922 | 17 |
| 2131 | CACGAGATCCACTATTCA | A572129H | +C*+A*+C*G*A*G*A*T*C*C*A*C*T*A*T*+T*+C*+A | 58922 | 18 |
| 2132 | TCACGAGATCCACTATTCA | A572130H | +T*+C*+A*C*G*A*G*A*T*C*C*A*C*T*A*T*+T*+C*+A | 58922 | 19 |
| 2133 | TCACGAGATCCACTATTC | A572131H | +T*+C*+A*C*G*A*G*A*T*C*C*A*C*T*A*+T*+T*+C | 58923 | 18 |
| 2134 | TTCACGAGATCCACTATTC | A572132H | +T*+T*+C*A*C*G*A*G*A*T*C*C*A*C*T*A*+T*+T*+C | 58923 | 19 |
| 2135 | GTTCACGAGATCCACTATT | A572133H | +G*+T*+T*C*A*C*G*A*G*A*T*C*C*A*C*T*+A*+T*+T | 58924 | 19 |
| 2136 | GTTCACGAGATCCACTAT | A572134H | +G*+T*+T*C*A*C*G*A*G*A*T*C*C*A*C*+T*+A*+T | 58925 | 18 |
| 2137 | TGTTCACGAGATCCACTAT | A572135H | +T*+G*+T*T*C*A*C*G*A*G*A*T*C*C*A*C*+T*+A*+T | 58925 | 19 |
| 2138 | GTTCACGAGATCCACTA | A572136H | +G*+T*+T*C*A*C*G*A*G*A*T*C*C*A*+C*+T*+A | 58926 | 17 |
| 2139 | TGTTCACGAGATCCACTA | A572137H | +T*+G*+T*T*C*A*C*G*A*G*A*T*C*C*A*+C*+T*+A | 58926 | 18 |
| 2140 | TTGTTCACGAGATCCACTA | A572138H | +T*+T*+G*T*T*C*A*C*G*A*G*A*T*C*C*A*+C*+T*+A | 58926 | 19 |
| 2141 | TTGTTCACGAGATCCACT | A572139H | +T*+T*+G*T*T*C*A*C*G*A*G*A*T*C*C*+A*+C*+T | 58927 | 18 |
| 2142 | CTTGTTCACGAGATCCACT | A572140H | +C*+T*+T*G*T*T*C*A*C*G*A*G*A*T*C*C*+A*+C*+T | 58927 | 19 |
| 2143 | TTGTTCACGAGATCCAC | A572141H | +T*+T*+G*T*T*C*A*C*G*A*G*A*T*C*+C*+A*+C | 58928 | 17 |
| 2144 | CTTGTTCACGAGATCCAC | A572142H | +C*+T*+T*G*T*T*C*A*C*G*A*G*A*T*C*+C*+A*+C | 58928 | 18 |
| 2145 | TCTTGTTCACGAGATCCAC | A572143H | +T*+C*+T*T*G*T*T*C*A*C*G*A*G*A*T*C*+C*+A*+C | 58928 | 19 |

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|---|---|---|---|---|---|
| 2146 | ATCTTGTTCACGAGATCCA | A572144H | +A*+T*+C*T*T*G*T*T*C*A*C*G*A*G*A*T*+C*+C*+A | 58929 | 19 |
| 2147 | ATCTTGTTCACGAGATCC | A572145H | +A*+T*+C*T*T*G*T*T*C*A*C*G*A*G*A*+T*+C*+C | 58930 | 18 |
| 2148 | CATCTTGTTCACGAGATCC | A572146H | +C*+A*+T*C*T*T*G*T*T*C*A*C*G*A*G*A*+T*+C*+C | 58930 | 19 |
| 2149 | CATCTTGTTCACGAGATC | A572147H | +C*+A*+T*C*T*T*G*T*T*C*A*C*G*A*G*+A*+T*+C | 58931 | 18 |
| 2150 | ACATCTTGTTCACGAGATC | A572148H | +A*+C*+A*T*C*T*T*G*T*T*C*A*C*G*A*G*+A*+T*+C | 58931 | 19 |
| 2151 | ACATCTTGTTCACGAGAT | A572149H | +A*+C*+A*T*C*T*T*G*T*T*C*A*C*G*A*+G*+A*+T | 58932 | 18 |
| 2152 | TACATCTTGTTCACGAGAT | A572150H | +T*+A*+C*A*T*C*T*T*G*T*T*C*A*C*G*A*+G*+A*+T | 58932 | 19 |
| 2153 | GTACATCTTGTTCACGAGA | A572151H | +G*+T*+A*C*A*T*C*T*T*G*T*T*C*A*C*G*+A*+G*+A | 58933 | 19 |
| 2154 | GTACATCTTGTTCACGAG | A572152H | +G*+T*+A*C*A*T*C*T*T*G*T*T*C*A*C*+G*+A*+G | 58934 | 18 |
| 2155 | CGTACATCTTGTTCACGAG | A572153H | +C*+G*+T*A*C*A*T*C*T*T*G*T*T*C*A*C*+G*+A*+G | 58934 | 19 |
| 2156 | CGTACATCTTGTTCACGA | A572154H | +C*+G*+T*A*C*A*T*C*T*T*G*T*T*C*A*+C*+G*+A | 58935 | 18 |
| 2157 | TCGTACATCTTGTTCACGA | A572155H | +T*+C*+G*T*A*C*A*T*C*T*T*G*T*T*C*A*+C*+G*+A | 58935 | 19 |
| 2158 | TTCGTACATCTTGTTCACG | A572156H | +T*+T*+C*G*T*A*C*A*T*C*T*T*G*T*T*C*+A*+C*+G | 58936 | 19 |
| 2159 | CTTTTCGTACATCTTGTTC | A572157H | +C*+T*+T*T*T*C*G*T*A*C*A*T*C*T*T*G*+T*+T*+C | 58939 | 19 |
| 2160 | GCTGATGATCTGGCTGTC | A572158H | +G*+C*+T*G*A*T*G*A*T*C*T*G*G*C*T*+G*+T*+C | 58984 | 18 |
| 2161 | AGCTGATGATCTGGCTGTC | A572159H | +A*+G*+C*T*G*A*T*G*A*T*C*T*G*G*C*T*+G*+T*+C | 58984 | 19 |
| 2162 | AGCTGATGATCTGGCTGT | A572160H | +A*+G*+C*T*G*A*T*G*A*T*C*T*G*G*C*+T*+G*+T | 58985 | 18 |
| 2163 | AAGCTGATGATCTGGCTGT | A572161H | +A*+A*+G*C*T*G*A*T*G*A*T*C*T*G*G*C*+T*+G*+T | 58985 | 19 |
| 2164 | CAAGCTGATGATCTGGCTG | A572162H | +C*+A*+A*G*C*T*G*A*T*G*A*T*C*T*G*G*+C*+T*+G | 58986 | 19 |
| 2165 | GCAAGCTGATGATCTGGCT | A572163H | +G*+C*+A*A*G*C*T*G*A*T*G*A*T*C*T*G*+G*+C*+T | 58987 | 19 |
| 2166 | AGCAAGCTGATGATCTGGC | A572164H | +A*+G*+C*A*A*G*C*T*G*A*T*G*A*T*C*T*+G*+G*+C | 58988 | 19 |
| 2167 | TAAGAGCAAGCTGATGATC | A572165H | +T*+A*+A*G*A*G*C*A*A*G*C*T*G*A*T*G*+A*+T*+C | 58992 | 19 |
| 2168 | TTAAGAGCAAGCTGATGAT | A572166H | +T*+T*+A*A*G*A*G*C*A*A*G*C*T*G*A*T*+G*+A*+T | 58993 | 19 |
| 2169 | CCTTAAGAGCAAGCTGATG | A572167H | +C*+C*+T*T*A*A*G*A*G*C*A*A*G*C*T*G*+A*+T*+G | 58995 | 19 |
| 2170 | CCTTAAGAGCAAGCTGAT | A572168H | +C*+C*+T*T*A*A*G*A*G*C*A*A*G*C*T*+G*+A*+T | 58996 | 18 |
| 2171 | TCCTTAAGAGCAAGCTGAT | A572169H | +T*+C*+C*T*T*A*A*G*A*G*C*A*A*G*C*T*+G*+A*+T | 58996 | 19 |
| 2172 | CCTCCTTAAGAGCAAGCTG | A572170H | +C*+C*+T*C*C*T*T*A*A*G*A*G*C*A*A*G*+C*+T*+G | 58998 | 19 |
| 2173 | GGCCAGCCTCCTTAAGAGC | A572171H | +G*+G*+C*C*A*G*C*C*T*C*C*T*T*A*A*G*+A*+G*+C | 59004 | 19 |
| 2174 | GGGCCAGCCTCCTTAAGAG | A572172H | +G*+G*+G*C*C*A*G*C*C*T*C*C*T*T*A*A*+G*+A*+G | 59005 | 19 |
| 2175 | CAGGGCCAGCCTCCTTAAG | A572173H | +C*+A*+G*G*G*C*C*A*G*C*C*T*C*C*T*T*+A*+A*+G | 59007 | 19 |
| 2176 | CAGGGCCAGCCTCCTTAA | A572174H | +C*+A*+G*G*G*C*C*A*G*C*C*T*C*C*T*+T*+A*+A | 59008 | 18 |
| 2177 | CCAGGGCCAGCCTCCTTAA | A572175H | +C*+C*+A*G*G*G*C*C*A*G*C*C*T*C*C*T*+T*+A*+A | 59008 | 19 |
| 2178 | CAAATGCTATTGTTGGCCA | A572176H | +C*+A*+A*A*T*G*C*T*A*T*T*G*T*T*G*G*+C*+C*+A | 59030 | 19 |
| 2179 | GCAAATGCTATTGTTGGCC | A572177H | +G*+C*+A*A*A*T*G*C*T*A*T*T*G*T*T*G*+G*+C*+C | 59031 | 19 |
| 2180 | AGGCAAATGCTATTGTTGG | A572178H | +A*+G*+G*C*A*A*A*T*G*C*T*A*T*T*G*T*+T*+G*+G | 59033 | 19 |

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| 2181 | TCAACTTTTCCTATAC AAA | A572179H | +T*+C*+A*A*C*T*T*T*T*C*C*T*A*T*A*C*+ A*+A*+A | 59060 | 19 |
| 2182 | GTTCAACTTTTCCTAT ACA | A572180H | +G*+T*+T*C*A*A*C*T*T*T*T*C*C*T*A*T*+ A*+C*+A | 59062 | 19 |
| 2183 | GGTTCAACTTTTCCT ATAC | A572181H | +G*+G*+T*T*C*A*A*C*T*T*T*T*C*C*T*A*+ T*+A*+C | 59063 | 19 |
| 2184 | AAGGTTCAACTTTTC CTAT | A572182H | +A*+A*+G*G*T*T*C*A*A*C*T*T*T*T*C*C*+ T*+A*+T | 59065 | 19 |
| 2185 | GAAGGTTCAACTTTT CCTA | A572183H | +G*+A*+A*G*G*T*T*C*A*A*C*T*T*T*T*C*+ C*+T*+A | 59066 | 19 |
| 2186 | AAGAAGGTTCAACTT TTCC | A572184H | +A*+A*+G*A*A*G*G*T*T*C*A*A*C*T*T*T*+ T*+C*+C | 59068 | 19 |
| 2187 | CCAAGAAGGTTCAAC TTTT | A572185H | +C*+C*+A*A*G*A*A*G*G*T*T*C*A*A*C*T*+ T*+T*+T | 59070 | 19 |
| 2188 | GCCAAGAAGGTTCAA CTTT | A572186H | +G*+C*+C*A*A*G*A*A*G*G*T*T*C*A*A*C*+ T*+T*+T | 59071 | 19 |
| 2189 | GGACCAAGCCAAGAA GGTT | A572187H | +G*+G*+A*C*C*A*A*G*C*C*A*A*G*A*A*G* +G*+T*+T | 59078 | 19 |
| 2190 | AGGACCAAGCCAAGA AGGT | A572188H | +A*+G*+G*A*C*C*A*A*G*C*C*A*A*G*A*A* +G*+G*+T | 59079 | 19 |
| 2191 | TGGAAATAAAGGACC AAGC | A572189H | +T*+G*+G*A*A*A*T*A*A*A*G*G*A*C*C*A*+ A*+G*+C | 59088 | 19 |
| 2192 | AAGTCTTATCTGGAA ATAA | A572190H | +A*+A*+G*T*C*T*T*A*T*C*T*G*G*A*A*A*+ T*+A*+A | 59098 | 19 |
| 2193 | GAAGTCTTATCTGGA AATA | A572191H | +G*+A*+A*G*T*C*T*T*A*T*C*T*G*G*A*A*+ A*+T*+A | 59099 | 19 |
| 2194 | TTAGAAGTCTTATCT GGAA | A572192H | +T*+T*+A*G*A*A*G*T*C*T*T*A*T*C*T*G*+ G*+A*+A | 59102 | 19 |
| 2195 | TCCTTAAATTAGAAG TCTT | A572193H | +T*+C*+C*T*T*A*A*A*T*T*A*G*A*A*G*T*+ C*+T*+T | 59110 | 19 |
| 2196 | TTTCCTTAAATTAGAA GTC | A572194H | +T*+T*+T*C*C*T*T*A*A*A*T*T*A*G*A*A*+ G*+T*+C | 59112 | 19 |
| 2197 | AAATATTCTCCTTGTT ACT | A572195Hi | +A*+A*+A*T*A*T*T*C*T*C*C*T*T*G*T*T*+ A*+C*+T | 59141 | 19 |
| 2198 | CTATCTCATAAAGAA CTTA | A572196Hi | +C*+T*+A*T*C*T*C*A*T*A*A*A*G*A*A*C*+ T*+T*+A | 59307 | 19 |
| 2199 | GCTATCTCATAAAGA ACTT | A572197Hi | +G*+C*+T*A*T*C*T*C*A*T*A*A*A*G*A*A*+ C*+T*+T | 59308 | 19 |
| 2200 | TTTGCTATCTCATAAA GAA | A572198Hi | +T*+T*+T*G*C*T*A*T*C*T*C*A*T*A*A*A*+ G*+A*+A | 59311 | 19 |
| 2201 | ATAGGTACATGTAAG CATA | A572199Hi | +A*+T*+A*G*G*T*A*C*A*T*G*T*A*A*G*C*+ A*+T*+A | 59519 | 19 |
| 2202 | GCATAGGTACATGTA AGC | A572200Hi | +G*+C*+A*T*A*G*G*T*A*C*A*T*G*T*A*+A* +G*+C | 59522 | 18 |
| 2203 | TGCATAGGTACATGT AAG | A572201Hi | +T*+G*+C*A*T*A*G*G*T*A*C*A*T*G*T*+A* +A*+G | 59523 | 18 |
| 2204 | GAATGCATAGGTACA TGT | A572202Hi | +G*+A*+A*T*G*C*A*T*A*G*G*T*A*C*A*+T* +G*+T | 59526 | 18 |
| 2205 | ATTTGAATGCATAGG TACA | A572203Hi | +A*+T*+T*T*G*A*A*T*G*C*A*T*A*G*G*T*+ A*+C*+A | 59529 | 19 |
| 2206 | CATTTGAATGCATAG GTAC | A572204Hi | +C*+A*+T*T*T*G*A*A*T*G*C*A*T*A*G*G*+ T*+A*+C | 59530 | 19 |
| 2207 | GCATTATCAATTGAA ATAT | A572205Hi | +G*+C*+A*T*T*A*T*C*A*A*T*T*G*A*A*A*+ T*+A*+T | 59604 | 19 |
| 2208 | TGCATTATCAATTGA AATA | A572206Hi | +T*+G*+C*A*T*T*A*T*C*A*A*T*T*G*A*A*+ A*+T*+A | 59605 | 19 |
| 2209 | ACTTACCATCAATAC ACAT | A572207Hi | +A*+C*+T*T*A*C*C*A*T*C*A*A*T*A*C*A*+ C*+A*+T | 59666 | 19 |
| 2210 | ACATTTAGTGTGAAC AAAT | A572208Hi | +A*+C*+A*T*T*T*A*G*T*G*T*G*A*A*C*A*+ A*+A*+T | 59725 | 19 |
| 2211 | GTAGACTGGTAGACT GACC | A572209Hi | +G*+T*+A*G*A*C*T*G*G*T*A*G*A*C*T*G*+ A*+C*+C | 59913 | 19 |
| 2212 | AAAGTAGACTGGTAG ACTG | A572210Hi | +A*+A*+A*G*T*A*G*A*C*T*G*G*T*A*G*A*+ C*+T*+G | 59916 | 19 |
| 2213 | AGGCACCAAATTGCA TGGA | A572211Hi | +A*+G*+G*C*A*C*C*A*A*A*T*T*G*C*A*T*+ G*+G*+A | 59985 | 19 |
| 2214 | CTTGATGTATAAAGG CACC | A572212Hi | +C*+T*+T*G*A*T*G*T*A*T*A*A*A*G*G*C*+ A*+C*+C | 59997 | 19 |
| 2215 | CCTTGATGTATAAAG GCAC | A572213Hi | +C*+C*+T*T*G*A*T*G*T*A*T*A*A*A*G*G*+ C*+A*+C | 59998 | 19 |

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| 2216 | CTTGATGTATAAAGGCAC | A572214Hi | +C*+T*+T*G*A*T*G*T*A*T*A*A*A*G*G*+C*+A*+C | 59998 | 18 |
| 2217 | ACCTTGATGTATAAAGGCA | A572215Hi | +A*+C*+C*T*T*G*A*T*G*T*A*T*A*A*A*G*+G*+C*+A | 59999 | 19 |
| 2218 | ACCTTGATGTATAAAGGC | A572216Hi | +A*+C*+C*T*T*G*A*T*G*T*A*T*A*A*A*+G*+G*+C | 60000 | 18 |
| 2219 | AACCTTGATGTATAAAGG | A572217Hi | +A*+A*+C*C*T*T*G*A*T*G*T*A*T*A*A*+A*+G*+G | 60001 | 18 |
| 2220 | TGGAAACCTTGATGTATAA | A572218Hi | +T*+G*+G*A*A*A*C*C*T*T*G*A*T*G*T*A*+T*+A*+A | 60004 | 19 |
| 2221 | TGGAAACCTTGATGTATA | A572219Hi | +T*+G*+G*A*A*A*C*C*T*T*G*A*T*G*T*+A*+T*+A | 60005 | 18 |
| 2222 | GTTGGAAACCTTGATGTAT | A572220Hi | +G*+T*+T*G*G*A*A*A*C*C*T*T*G*A*T*G*+T*+A*+T | 60006 | 19 |
| 2223 | GTGTTTGAGAAACCGAGGA | A572221Hi | +G*+T*+G*T*T*T*G*A*G*A*A*A*C*C*G*A*+G*+G*+A | 60064 | 19 |
| 2224 | AAGTGTTTGAGAAACCGAG | A572222Hi | +A*+A*+G*T*G*T*T*T*G*A*G*A*A*A*C*C*+G*+A*+G | 60066 | 19 |
| 2225 | GGTGAAGAGAGAATTTAGA | A572223Hi | +G*+G*+T*G*A*A*G*A*G*A*G*A*A*T*T*T*+A*+G*+A | 60137 | 19 |
| 2226 | AGCCAGGTGAAGAGAGAAT | A572224Hi | +A*+G*+C*C*A*G*G*T*G*A*A*G*A*G*A*G*+A*+A*+T | 60142 | 19 |
| 2227 | ATGTGGTGAATGGTAGTA | A572225Hi | +A*+T*+G*T*G*G*T*G*A*A*T*G*G*T*A*+G*+T*+A | 60245 | 18 |
| 2228 | ATAATGTGGTGAATGGTAG | A572226Hi | +A*+T*+A*A*T*G*T*G*G*T*G*A*A*T*G*G*+T*+A*+G | 60247 | 19 |
| 2229 | ATATAATGTGGTGAATGGT | A572227Hi | +A*+T*+A*T*A*A*T*G*T*G*G*T*G*A*A*T*+G*+G*+T | 60249 | 19 |
| 2230 | GACTTCATGGTACTAACAA | A572228Hi | +G*+A*+C*T*T*C*A*T*G*G*T*A*C*T*A*A*+C*+A*+A | 60307 | 19 |
| 2231 | ATTGACTTCATGGTACTAA | A572229Hi | +A*+T*+T*G*A*C*T*T*C*A*T*G*G*T*A*C*+T*+A*+A | 60310 | 19 |
| 2232 | CATTGACTTCATGGTACTA | A572230Hi | +C*+A*+T*T*G*A*C*T*T*C*A*T*G*G*T*A*+C*+T*+A | 60311 | 19 |
| 2233 | GGTAAGGTTACAACCATG | A572231Hi | +G*+G*+T*A*A*G*G*T*T*A*C*A*A*C*C*+A*+T*+G | 60341 | 18 |
| 2234 | GTATCAATGGTAAGGTTA | A572232Hi | +G*+T*+A*T*C*A*A*T*G*G*T*A*A*G*G*+T*+T*+A | 60349 | 18 |
| 2235 | ATAGATTCCTAACAGTAC | A572233Hi | +A*+T*+A*G*A*T*T*C*C*T*A*A*C*A*G*+T*+A*+C | 60575 | 18 |
| 2236 | TCATAGATTCCTAACAGTA | A572234Hi | +T*+C*+A*T*A*G*A*T*T*C*C*T*A*A*C*A*+G*+T*+A | 60576 | 19 |
| 2237 | TGTGCACATTGAGAATGTC | A572235Hi | +T*+G*+T*G*C*A*C*A*T*T*G*A*G*A*A*T*+G*+T*+C | 60599 | 19 |
| 2238 | TTGTGCACATTGAGAATGT | A572236Hi | +T*+T*+G*T*G*C*A*C*A*T*T*G*A*G*A*A*+T*+G*+T | 60600 | 19 |
| 2239 | TTCCTCAATGATTGCAAAG | A572237Hi | +T*+T*+C*C*T*C*A*A*T*G*A*T*T*G*C*A*+A*+A*+G | 60742 | 19 |
| 2240 | TCCTCAATGATTGCAAAG | A572238Hi | +T*+C*+C*T*C*A*A*T*G*A*T*T*G*C*A*+A*+A*+G | 60742 | 18 |
| 2241 | TTTCCTCAATGATTGCAAA | A572239Hi | +T*+T*+T*C*C*T*C*A*A*T*G*A*T*T*G*C*+A*+A*+A | 60743 | 19 |
| 2242 | ATGTCTCAGTAATTTCCAA | A572240Hi | +A*+T*+G*T*C*T*C*A*G*T*A*A*T*T*T*C*+C*+A*+A | 60947 | 19 |
| 2243 | GACTAGTTTAAGTAATGAA | A572241Hi | +G*+A*+C*T*A*G*T*T*T*A*A*G*T*A*A*T*+G*+A*+A | 60981 | 19 |
| 2244 | AGACTAGTTTAAGTAATGA | A572242Hi | +A*+G*+A*C*T*A*G*T*T*T*A*A*G*T*A*A*+T*+G*+A | 60982 | 19 |
| 2245 | AGACTAGTTTAAGTAATG | A572243Hi | +A*+G*+A*C*T*A*G*T*T*T*A*A*G*T*A*+A*+T*+G | 60983 | 18 |
| 2246 | AGATGTGTCAATGGTAAA | A572244Hi | +A*+G*+A*T*G*T*G*T*C*A*A*T*G*G*T*+A*+A*+A | 61121 | 18 |
| 2247 | CTTTACTCAGACCAGCTG | A572245Hi | +C*+T*+T*T*A*C*T*C*A*G*A*C*C*A*G*+C*+T*+G | 61205 | 18 |
| 2248 | TTCTTTACTCAGACCAGCT | A572246Hi | +T*+T*+C*T*T*T*A*C*T*C*A*G*A*C*C*A*+G*+C*+T | 61206 | 19 |
| 2249 | GTGTTCTTTACTCAGACCA | A572247Hi | +G*+T*+G*T*T*C*T*T*T*A*C*T*C*A*G*A*+C*+C*+A | 61209 | 19 |
| 2250 | AGTGTTCTTTACTCAGACC | A572248Hi | +A*+G*+T*G*T*T*C*T*T*T*A*C*T*C*A*G*+A*+C*+C | 61210 | 19 |

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| 2251 | AGTGTTCTTTACTCAGAC | A572249Hi | +A*+G*+T*G*T*T*C*T*T*T*A*C*T*C*A*+G*+A*+C | 61211 | 18 |
| 2252 | GTATGCTCATGTATCTACA | A572250Hi | +G*+T*+A*T*G*C*T*C*A*T*G*T*A*T*C*T*+A*+C*+A | 61450 | 19 |
| 2253 | GTATGCTCATGTATCTAC | A572251Hi | +G*+T*+A*T*G*C*T*C*A*T*G*T*A*T*C*+T*+A*+C | 61451 | 18 |
| 2254 | AGTATGCTCATGTATCTAC | A572252Hi | +A*+G*+T*A*T*G*C*T*C*A*T*G*T*A*T*C*+T*+A*+C | 61451 | 19 |
| 2255 | GTACAATATCCAGTGATG | A572253Hi | +G*+T*+A*C*A*A*T*A*T*C*C*A*G*T*G*+A*+T*+G | 61638 | 18 |
| 2256 | TGTAGTACAATATCCAGTG | A572254Hi | +T*+G*+T*A*G*T*A*C*A*A*T*A*T*C*C*A*+G*+T*+G | 61641 | 19 |
| 2257 | GTATCATGTAGTACAATAT | A572255Hi | +G*+T*+A*T*C*A*T*G*T*A*G*T*A*C*A*A*+T*+A*+T | 61647 | 19 |
| 2258 | GTATCATGTAGTACAATA | A572256Hi | +G*+T*+A*T*C*A*T*G*T*A*G*T*A*C*A*+A*+T*+A | 61648 | 18 |
| 2259 | CAAATATTACTACATGATA | A572257Hi | +C*+A*+A*A*T*A*T*T*A*C*T*A*C*A*T*G*+A*+T*+A | 61671 | 19 |
| 2260 | GAGTCCTCATTGTTCTACA | A572258Hi | +G*+A*+G*T*C*C*T*C*A*T*T*G*T*T*C*T*+A*+C*+A | 61734 | 19 |
| 2261 | TCTCACAACTTCATTACAT | A572259Hi | +T*+C*+T*C*A*C*A*A*C*T*T*C*A*T*T*A*+C*+A*+T | 61788 | 19 |
| 2262 | TGATTCATTATGACTATTG | A572260Hi | +T*+G*+A*T*T*C*A*T*T*A*T*G*A*C*T*A*+T*+T*+G | 61840 | 19 |
| 2263 | GAGTGATTCATTATGACTA | A572261Hi | +G*+A*+G*T*G*A*T*T*C*A*T*T*A*T*G*A*+C*+T*+A | 61843 | 19 |
| 2264 | TGAGTGATTCATTATGAC | A572262Hi | +T*+G*+A*G*T*G*A*T*T*C*A*T*T*A*T*+G*+A*+C | 61845 | 18 |
| 2265 | GCTGAGTGATTCATTATG | A572263Hi | +G*+C*+T*G*A*G*T*G*A*T*T*C*A*T*T*+A*+T*+G | 61847 | 18 |
| 2266 | TTATAAAGTTTGCTGAGTG | A572264Hi | +T*+T*+A*T*A*A*A*G*T*T*T*G*C*T*G*A*+G*+T*+G | 61857 | 19 |
| 2267 | AGAAATGCCATTTGTGAGT | A572265Hi | +A*+G*+A*A*A*T*G*C*C*A*T*T*T*G*T*G*+A*+G*+T | 62035 | 19 |
| 2268 | TGTTCAAGTCATAGAAATG | A572266Hi | +T*+G*+T*T*C*A*A*G*T*C*A*T*A*G*A*A*+A*+T*+G | 62047 | 19 |
| 2269 | AGAAATCAACAATTATGCA | A572267Hi | +A*+G*+A*A*A*T*C*A*A*C*A*A*T*T*A*T*+G*+C*+A | 62308 | 19 |
| 2270 | TAGAAATCAACAATTATGC | A572268Hi | +T*+A*+G*A*A*A*T*C*A*A*C*A*A*T*T*A*+T*+G*+C | 62309 | 19 |
| 2271 | GCTAGTGTAGATGCTATAT | A572269H | +G*+C*+T*A*G*T*G*T*A*G*A*T*G*C*T*A*+T*+A*+T | 62355 | 19 |
| 2272 | TGCTAGTGTAGATGCTATA | A572270H | +T*+G*+C*T*A*G*T*G*T*A*G*A*T*G*C*T*+A*+T*+A | 62356 | 19 |
| 2273 | TTGCTAGTGTAGATGCTAT | A572271H | +T*+T*+G*C*T*A*G*T*G*T*A*G*A*T*G*C*+T*+A*+T | 62357 | 19 |
| 2274 | CTTGCTAGTGTAGATGCTA | A572272H | +C*+T*+T*G*C*T*A*G*T*G*T*A*G*A*T*G*+C*+T*+A | 62358 | 19 |
| 2275 | TCTTGCTAGTGTAGATGCT | A572273H | +T*+C*+T*T*G*C*T*A*G*T*G*T*A*G*A*T*+G*+C*+T | 62359 | 19 |
| 2276 | TCTTGCTAGTGTAGATGC | A572274H | +T*+C*+T*T*G*C*T*A*G*T*G*T*A*G*A*+T*+G*+C | 62360 | 18 |
| 2277 | TTCTTGCTAGTGTAGATGC | A572275H | +T*+T*+C*T*T*G*C*T*A*G*T*G*T*A*G*A*+T*+G*+C | 62360 | 19 |
| 2278 | TCACCATTCTTGCTAGTGT | A572276H | +T*+C*+A*C*C*A*T*T*C*T*T*G*C*T*A*G*+T*+G*+T | 62366 | 19 |
| 2279 | TCACCATTCTTGCTAGTG | A572277H | +T*+C*+A*C*C*A*T*T*C*T*T*G*C*T*A*+G*+T*+G | 62367 | 18 |
| 2280 | ATCACCATTCTTGCTAGTG | A572278H | +A*+T*+C*A*C*C*A*T*T*C*T*T*G*C*T*A*+G*+T*+G | 62367 | 19 |
| 2281 | GATCACCATTCTTGCTAGT | A572279H | +G*+A*+T*C*A*C*C*A*T*T*C*T*T*G*C*T*+A*+G*+T | 62368 | 19 |
| 2282 | CTGATCACCATTCTTGCTA | A572280H | +C*+T*+G*A*T*C*A*C*C*A*T*T*C*T*T*G*+C*+T*+A | 62370 | 19 |
| 2283 | TCTGATCACCATTCTTGCT | A572281H | +T*+C*+T*G*A*T*C*A*C*C*A*T*T*C*T*T*+G*+C*+T | 62371 | 19 |
| 2284 | TCTGATCACCATTCTTGC | A572282H | +T*+C*+T*G*A*T*C*A*C*C*A*T*T*C*T*+T*+G*+C | 62372 | 18 |
| 2285 | ATCTGATCACCATTCTTGC | A572283H | +A*+T*+C*T*G*A*T*C*A*C*C*A*T*T*C*T*+T*+G*+C | 62372 | 19 |

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| 2286 | GATATCTGATCACCATTCT | A572284H | +G*+A*+T*A*T*C*T*G*A*T*C*A*C*C*A*T*+T*+C*+T | 62375 | 19 |
| 2287 | TGATATCTGATCACCATTC | A572285H | +T*+G*+A*T*A*T*C*T*G*A*T*C*A*C*C*A*+T*+T*+C | 62376 | 19 |
| 2288 | TCTGATATCTGATCACCAT | A572286H | +T*+C*+T*G*A*T*A*T*C*T*G*A*T*C*A*C*+C*+A*+T | 62378 | 19 |
| 2289 | CATCTGATATCTGATCACC | A572287H | +C*+A*+T*C*T*G*A*T*A*T*C*T*G*A*T*C*+A*+C*+C | 62380 | 19 |
| 2290 | TTTCATCTGATATCTGATC | A572288H | +T*+T*+T*C*A*T*C*T*G*A*T*A*T*C*T*G*+A*+T*+C | 62383 | 19 |
| 2291 | ACTTTTCATCTGATATCTG | A572289H | +A*+C*+T*T*T*T*C*A*T*C*T*G*A*T*A*T*+C*+T*+G | 62386 | 19 |
| 2292 | TTAGACAGCACATCTTCAG | A572290H | +T*+T*+A*G*A*C*A*G*C*A*C*A*T*C*T*T*+C*+A*+G | 62448 | 19 |
| 2293 | TTTAGACAGCACATCTTCA | A572291H | +T*+T*+T*A*G*A*C*A*G*C*A*C*A*T*C*T*+T*+C*+A | 62449 | 19 |
| 2294 | AAATTTAGACAGCACATCT | A572292H | +A*+A*+A*T*T*T*A*G*A*C*A*G*C*A*C*A*+T*+C*+T | 62452 | 19 |
| 2295 | AAATTTAGACAGCACATC | A572293H | +A*+A*+A*T*T*T*A*G*A*C*A*G*C*A*C*+A*+T*+C | 62453 | 18 |
| 2296 | CAAATTTAGACAGCACATC | A572294H | +C*+A*+A*A*T*T*T*A*G*A*C*A*G*C*A*C*+A*+T*+C | 62453 | 19 |
| 2297 | ATCAAATTTAGACAGCACA | A572295H | +A*+T*+C*A*A*A*T*T*T*A*G*A*C*A*G*C*+A*+C*+A | 62455 | 19 |
| 2298 | ATCAAATTTAGACAGCAC | A572296H | +A*+T*+C*A*A*A*T*T*T*A*G*A*C*A*G*+C*+A*+C | 62456 | 18 |
| 2299 | CATCAAATTTAGACAGCAC | A572297H | +C*+A*+T*C*A*A*A*T*T*T*A*G*A*C*A*G*+C*+A*+C | 62456 | 19 |
| 2300 | GGTCCATTCATCAAATTTA | A572298H | +G*+G*+T*C*C*A*T*T*C*A*T*C*A*A*A*T*+T*+T*+A | 62464 | 19 |
| 2301 | AGGTCCATTCATCAAATTT | A572299H | +A*+G*+G*T*C*C*A*T*T*C*A*T*C*A*A*A*+T*+T*+T | 62465 | 19 |
| 2302 | CATAGAAGAGTCAGGAATA | A572300H | +C*+A*+T*A*G*A*A*G*A*G*T*C*A*G*G*A*+A*+T*+A | 62485 | 19 |
| 2303 | TCCAGTCTAGTCAGAGTT | A572301Hi | +T*+C*+C*A*G*T*C*T*A*G*T*C*A*G*A*+G*+T*+T | 62778 | 18 |
| 2304 | CGTTCCAGTCTAGTCAGAG | A572302Hi | +C*+G*+T*T*C*C*A*G*T*C*T*A*G*T*C*A*+G*+A*+G | 62780 | 19 |
| 2305 | TCGTTCCAGTCTAGTCAGA | A572303Hi | +T*+C*+G*T*T*C*C*A*G*T*C*T*A*G*T*C*+A*+G*+A | 62781 | 19 |
| 2306 | GAATCTCGTTCCAGTCTA | A572304Hi | +G*+A*+A*T*C*T*C*G*T*T*C*C*A*G*T*+C*+T*+A | 62787 | 18 |
| 2307 | TGGAATCTCGTTCCAGTC | A572305Hi | +T*+G*+G*A*A*T*C*T*C*G*T*T*C*C*A*+G*+T*+C | 62789 | 18 |
| 2308 | GTGGAATCTCGTTCCAG | A572306Hi | +G*+T*+G*G*A*A*T*C*T*C*G*T*T*C*+C*+A*+G | 62791 | 17 |
| 2309 | TTCAATCATACTATATTAA | A572307Hi | +T*+T*+C*A*A*T*C*A*T*A*C*T*A*T*A*T*+T*+A*+A | 63129 | 19 |
| 2310 | CTCAAATATCCTTATTCTA | A572308Hi | +C*+T*+C*A*A*A*T*A*T*C*C*T*T*A*T*T*+C*+T*+A | 63160 | 19 |
| 2311 | TCTCAAATATCCTTATTCT | A572309Hi | +T*+C*+T*C*A*A*A*T*A*T*C*C*T*T*A*T*+T*+C*+T | 63161 | 19 |
| 2312 | GGTTTGACTTGAGACACAA | A572310Hi | +G*+G*+T*T*T*G*A*C*T*T*G*A*G*A*C*A*+C*+A*+A | 63209 | 19 |
| 2313 | TGGTTTGACTTGAGACACA | A572311Hi | +T*+G*+G*T*T*T*G*A*C*T*T*G*A*G*A*C*+A*+C*+A | 63210 | 19 |
| 2314 | GGTTTGACTTGAGACACA | A572312Hi | +G*+G*+T*T*T*G*A*C*T*T*G*A*G*A*C*+A*+C*+A | 63210 | 18 |
| 2315 | TGGTTTGACTTGAGACAC | A572313Hi | +T*+G*+G*T*T*T*G*A*C*T*T*G*A*G*A*+C*+A*+C | 63211 | 18 |
| 2316 | CAGTGAAGAGGCATGAAGA | A572314Hi | +C*+A*+G*T*G*A*A*G*A*G*G*C*A*T*G*A*+A*+G*+A | 63390 | 19 |
| 2317 | GTCAGGAAGCAAATGATTG | A572315Hi | +G*+T*+C*A*G*G*A*A*G*C*A*A*A*T*G*A*+T*+T*+G | 63445 | 19 |
| 2318 | CACAACTTCTATCTAGAAT | A572316Hi | +C*+A*+C*A*A*C*T*T*C*T*A*T*C*T*A*G*+A*+A*+T | 63803 | 19 |
| 2319 | CTGTCACAACTTCTATCTA | A572317Hi | +C*+T*+G*T*C*A*C*A*A*C*T*T*C*T*A*T*+C*+T*+A | 63807 | 19 |
| 2320 | TGTCACAACTTCTATCTA | A572318Hi | +T*+G*+T*C*A*C*A*A*C*T*T*C*T*A*T*+C*+T*+A | 63807 | 18 |

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| 2321 | ACCTGTCACAACTTCTATC | A572319Hi | +A*+C*+C*T*G*T*C*A*C*A*A*C*T*T*C*T*+A*+T*+C | 63809 | 19 |
| 2322 | ACCTGTCACAACTTCTAT | A572320Hi | +A*+C*+C*T*G*T*C*A*C*A*A*C*T*T*C*+T*+A*+T | 63810 | 18 |
| 2323 | AATATTCACAAATTTAGGC | A572321Hi | +A*+A*+T*A*T*T*C*A*C*A*A*A*T*T*T*A*+G*+G*+C | 63990 | 19 |
| 2324 | CCATTAATTCAATGAGGAA | A572322Hi | +C*+C*+A*T*T*A*A*T*T*C*A*A*T*G*A*G*+G*+A*+A | 64177 | 19 |
| 2325 | TTCCATTAATTCAATGAGG | A572323Hi | +T*+T*+C*C*A*T*T*A*A*T*T*C*A*A*T*G*+A*+G*+G | 64179 | 19 |
| 2326 | CATACCTAAATAGTCAATT | A572324Hi | +C*+A*+T*A*C*C*T*A*A*A*T*A*G*T*C*A*+A*+T*+T | 64212 | 19 |
| 2327 | CCATACCTAAATAGTCAAT | A572325Hi | +C*+C*+A*T*A*C*C*T*A*A*A*T*A*G*T*C*+A*+A*+T | 64213 | 19 |
| 2328 | CATACCTAAATAGTCAAT | A572326Hi | +C*+A*+T*A*C*C*T*A*A*A*T*A*G*T*C*+A*+A*+T | 64213 | 18 |
| 2329 | AACCATACCTAAATAGTCA | A572327Hi | +A*+A*+C*C*A*T*A*C*C*T*A*A*A*T*A*G*+T*+C*+A | 64215 | 19 |
| 2330 | AGAACCATACCTAAATAGT | A572328Hi | +A*+G*+A*A*C*C*A*T*A*C*C*T*A*A*A*T*+A*+G*+T | 64217 | 19 |
| 2331 | GAACCATACCTAAATAGT | A572329Hi | +G*+A*+A*C*C*A*T*A*C*C*T*A*A*A*T*+A*+G*+T | 64217 | 18 |
| 2332 | TAAGAATAAGGTATAAATC | A572330Hi | +T*+A*+A*G*A*A*T*A*A*G*G*T*A*T*A*A*+A*+T*+C | 64264 | 19 |
| 2333 | AAAGAACACCAGAGGACTT | A572331Hi | +A*+A*+A*G*A*A*C*A*C*C*A*G*A*G*G*A*+C*+T*+T | 64345 | 19 |
| 2334 | TTGAACTATATATCACATT | A572332Hi | +T*+T*+G*A*A*C*T*A*T*A*T*A*T*C*A*C*+A*+T*+T | 64627 | 19 |
| 2335 | ATACAACACACTGTTAGAA | A572333Hi | +A*+T*+A*C*A*A*C*A*C*A*C*T*G*T*T*A*+G*+A*+A | 64661 | 19 |
| 2336 | ATACAACACACTGTTAGA | A572334Hi | +A*+T*+A*C*A*A*C*A*C*A*C*T*G*T*T*+A*+G*+A | 64662 | 18 |
| 2337 | AATACAACACACTGTTAGA | A572335Hi | +A*+A*+T*A*C*A*A*C*A*C*A*C*T*G*T*T*+A*+G*+A | 64662 | 19 |
| 2338 | ATCCAATACAACACACTGT | A572336Hi | +A*+T*+C*C*A*A*T*A*C*A*A*C*A*C*A*C*+T*+G*+T | 64666 | 19 |
| 2339 | CTATAATAAGGTACTGGA | A572337Hi | +C*+T*+A*T*A*A*T*A*A*G*G*T*A*C*T*+G*+G*+A | 64822 | 18 |
| 2340 | TCTATAATAAGGTACTGGA | A572338Hi | +T*+C*+T*A*T*A*A*T*A*A*G*G*T*A*C*T*+G*+G*+A | 64822 | 19 |
| 2341 | TCTATAATAAGGTACTGG | A572339Hi | +T*+C*+T*A*T*A*A*T*A*A*G*G*T*A*C*+T*+G*+G | 64823 | 18 |
| 2342 | ATCTATAATAAGGTACTG | A572340Hi | +A*+T*+C*T*A*T*A*A*T*A*A*G*G*T*A*+C*+T*+G | 64824 | 18 |
| 2343 | CCTCTAAGTTTGGAAACCA | A572341Hi | +C*+C*+T*C*T*A*A*G*T*T*T*G*G*A*A*A*+C*+C*+A | 65006 | 19 |
| 2344 | TGTCATAATTAGTGATTAG | A572342Hi | +T*+G*+T*C*A*T*A*A*T*T*A*G*T*G*A*T*+T*+A*+G | 65040 | 19 |
| 2345 | AATGTCATAATTAGTGATT | A572343Hi | +A*+A*+T*G*T*C*A*T*A*A*T*T*A*G*T*G*+A*+T*+T | 65042 | 19 |
| 2346 | TAATGTCATAATTAGTGAT | A572344Hi | +T*+A*+A*T*G*T*C*A*T*A*A*T*T*A*G*T*+G*+A*+T | 65043 | 19 |
| 2347 | TACCTCAGCAGATGCTGAA | A572345Hi | +T*+A*+C*C*T*C*A*G*C*A*G*A*T*G*C*T*+G*+A*+A | 65164 | 19 |
| 2348 | TATGAATACCTCAGCAGAT | A572346Hi | +T*+A*+T*G*A*A*T*A*C*C*T*C*A*G*C*A*+G*+A*+T | 65170 | 19 |
| 2349 | GGATAATGTACCATAACC | A572347Hi | +G*+G*+A*T*A*A*T*G*T*A*C*C*A*T*A*+A*+C*+C | 65279 | 18 |
| 2350 | GGATAATGTACCATAAC | A572348Hi | +G*+G*+A*T*A*A*T*G*T*A*C*C*A*T*+A*+A*+C | 65280 | 17 |
| 2351 | AGGATAATGTACCATAAC | A572349Hi | +A*+G*+G*A*T*A*A*T*G*T*A*C*C*A*T*+A*+A*+C | 65280 | 18 |
| 2352 | ACTAATATCTCTCACAGAT | A572350Hi | +A*+C*+T*A*A*T*A*T*C*T*C*T*C*A*C*A*+G*+A*+T | 65347 | 19 |
| 2353 | CCTTTGCTGGTGAAGTCTA | A572351Hi | +C*+C*+T*T*T*G*C*T*G*G*T*G*A*A*G*T*+C*+T*+A | 65494 | 19 |
| 2354 | GGCCTTTGCTGGTGAAGTC | A572352Hi | +G*+G*+C*C*T*T*T*G*C*T*G*G*T*G*A*A*+G*+T*+C | 65496 | 19 |
| 2355 | AGATGGCCTTTGCTGGTGA | A572353Hi | +A*+G*+A*T*G*G*C*C*T*T*T*G*C*T*G*G*+T*+G*+A | 65500 | 19 |

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| 2356 | TAGATGGCCTTTGCTGGTG | A572354Hi | +T*+A*+G*A*T*G*G*C*C*T*T*T*G*C*T*G*+G*+T*+G | 65501 | 19 |
| 2357 | ATCAAAGTTATTAAATTCA | A572355Hi | +A*+T*+C*A*A*A*G*T*T*A*T*T*A*A*A*T*+T*+C*+A | 65556 | 19 |
| 2358 | CATACATCTATCAAAGTTA | A572356Hi | +C*+A*+T*A*C*A*T*C*T*A*T*C*A*A*A*G*+T*+T*+A | 65565 | 19 |
| 2359 | CATACATCTATCAAAGTT | A572357Hi | +C*+A*+T*A*C*A*T*C*T*A*T*C*A*A*A*+G*+T*+T | 65566 | 18 |
| 2360 | CATATTCCTTGAAAGTTAC | A572358Hi | +C*+A*+T*A*T*T*C*C*T*T*G*A*A*A*G*T*+T*+A*+C | 65629 | 19 |
| 2361 | AATCACTAACAGGATAATT | A572359Hi | +A*+A*+T*C*A*C*T*A*A*C*A*G*G*A*T*A*+A*+T*+T | 65705 | 19 |
| 2362 | TAATTAAATCACTAACAGG | A572360Hi | +T*+A*+A*T*T*A*A*A*T*C*A*C*T*A*A*C*+A*+G*+G | 65711 | 19 |
| 2363 | GGATAATTAAATCACTAAC | A572361Hi | +G*+G*+A*T*A*A*T*T*A*A*A*T*C*A*C*T*+A*+A*+C | 65714 | 19 |
| 2364 | GCTTCCAAATTAAGAATCT | A572362Hi | +G*+C*+T*T*C*C*A*A*A*T*T*A*A*G*A*A*+T*+C*+T | 65870 | 19 |
| 2365 | GACAGCCTTCTAAATAAC | A572363Hi | +G*+A*+C*A*G*C*C*T*T*C*T*A*A*A*T*+A*+A*+C | 66490 | 18 |
| 2366 | TAGAAATCATCAGAGTAGG | A572364Hi | +T*+A*+G*A*A*A*T*C*A*T*C*A*G*A*G*T*+A*+G*+G | 66589 | 19 |
| 2367 | TGGCCTATTGATTTGACC | A572365Hi | +T*+G*+G*C*C*T*A*T*T*G*A*T*T*T*G*+A*+C*+C | 66709 | 18 |
| 2368 | TTGGCCTATTGATTTGACC | A572366Hi | +T*+T*+G*G*C*C*T*A*T*T*G*A*T*T*T*T*G*+A*+C*+C | 66709 | 19 |
| 2369 | CCAAACAATTTGGCCTAT | A572367Hi | +C*+C*+A*A*A*C*A*A*T*T*T*G*G*C*C*+T*+A*+T | 66719 | 18 |
| 2370 | CCTCAATTACAACTTCAAT | A572368Hi | +C*+C*+T*C*A*A*T*T*A*C*A*A*C*T*T*C*+A*+A*+T | 66805 | 19 |
| 2371 | TCCTCAATTACAACTTCAA | A572369Hi | +T*+C*+C*T*C*A*A*T*T*A*C*A*A*C*T*T*+C*+A*+A | 66806 | 19 |
| 2372 | ATCCTCAATTACAACTTCA | A572370Hi | +A*+T*+C*C*T*C*A*A*T*T*A*C*A*A*C*T*+T*+C*+A | 66807 | 19 |
| 2373 | ATCCTCAATTACAACTTC | A572371Hi | +A*+T*+C*C*T*C*A*A*T*T*A*C*A*A*C*+T*+T*+C | 66808 | 18 |
| 2374 | CCAACAAATCCTCAATTAC | A572372Hi | +C*+C*+A*A*C*A*A*A*T*C*C*T*C*A*A*T*+T*+A*+C | 66814 | 19 |
| 2375 | TACAAAGCATAAACAGATA | A572373Hi | +T*+A*+C*A*A*A*G*C*A*T*A*A*A*C*A*G*+A*+T*+A | 66848 | 19 |
| 2376 | TACTAACTGCAAACTTAG | A572374Hi | +T*+A*+C*T*A*A*C*T*G*C*A*A*A*C*T*+T*+A*+G | 66970 | 18 |
| 2377 | TTTCCTGAGATGAGGAGAT | A572375Hi | +T*+T*+T*C*C*T*G*A*G*A*T*G*A*G*G*A*+G*+A*+T | 67129 | 19 |
| 2378 | AGCACATTATTTGTACAAG | A572376Hi | +A*+G*+C*A*C*A*T*T*A*T*T*T*G*T*A*C*+A*+A*+G | 67457 | 19 |
| 2379 | GTGAAATGTCTATTAGCAC | A572377Hi | +G*+T*+G*A*A*A*T*G*T*C*T*A*T*T*A*G*+C*+A*+C | 67471 | 19 |
| 2380 | TGAAATGTCTATTAGCAC | A572378Hi | +T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*+C*+A*+C | 67471 | 18 |
| 2381 | TGTGAAATGTCTATTAGCA | A572379Hi | +T*+G*+T*G*A*A*A*T*G*T*C*T*A*T*T*A*+G*+C*+A | 67472 | 19 |
| 2382 | ATATTCAGTATAAATCCTG | A572380Hi | +A*+T*+A*T*T*C*A*G*T*A*T*A*A*A*T*C*+C*+T*+G | 67654 | 19 |
| 2383 | AATATTCAGTATAAATCCT | A572381Hi | +A*+A*+T*A*T*T*C*A*G*T*A*T*A*A*A*T*+C*+C*+T | 67655 | 19 |
| 2384 | ACAATAAATTTGGCTGGCA | A572382Hi | +A*+C*+A*A*T*A*A*A*T*T*T*G*G*C*T*G*+G*+C*+A | 67899 | 19 |
| 2385 | AACACAATAAATTTGGCTG | A572383Hi | +A*+A*+C*A*C*A*A*T*A*A*A*T*T*T*G*G*+C*+T*+G | 67902 | 19 |
| 2386 | TTTATGGAATGGTATTAAA | A572384Hi | +T*+T*+T*A*T*G*G*A*A*T*G*G*T*A*T*T*+A*+A*+A | 67924 | 19 |
| 2387 | AATTTCATGTTTCATGGTT | A572385Hi | +A*+A*+T*T*T*C*A*T*G*T*T*T*C*A*T*G*+G*+T*+T | 67946 | 19 |
| 2388 | GTTGTAATCACACAAATTA | A572386Hi | +G*+T*+T*G*T*A*A*T*C*A*C*A*C*A*A*A*+T*+T*+A | 68001 | 19 |
| 2389 | ATGTTGTAATCACACAAAT | A572387Hi | +A*+T*+G*T*T*G*T*A*A*T*C*A*C*A*C*A*+A*+A*+T | 68003 | 19 |
| 2390 | ACTGCTTTCTGTTTCTCTG | A572388Hi | +A*+C*+T*G*C*T*T*T*C*T*G*T*T*T*C*T*+C*+T*+G | 68125 | 19 |

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| 2391 | TCAGAGGAGCTCATAGTCC | A572389Hi | +T*+C*+A*G*A*G*G*A*G*C*T*C*A*T*A*G*+T*+C*+C | 68234 | 19 |
| 2392 | TTACAGACTAGACACTGG | A572390Hi | +T*+T*+A*C*A*G*A*C*T*A*G*A*C*A*C*+T*+G*+G | 68298 | 18 |
| 2393 | CTCAATCATAAGATCCTT | A572391Hi | +C*+T*+C*A*A*T*C*A*T*A*A*G*A*T*C*+C*+T*+T | 68483 | 18 |
| 2394 | TCACAAGAAATGAGCCTTC | A572392H | +T*+C*+A*C*A*A*G*A*A*A*T*G*A*G*C*C*+T*+T*+C | 68554 | 19 |
| 2395 | TTCACAAGAAATGAGCCTT | A572393H | +T*+T*+C*A*C*A*A*G*A*A*A*T*G*A*G*C*+C*+T*+T | 68555 | 19 |
| 2396 | TTCACAAGAAATGAGCCT | A572394H | +T*+T*+C*A*C*A*A*G*A*A*A*T*G*A*G*+C*+C*+T | 68556 | 18 |
| 2397 | TTTCACAAGAAATGAGCCT | A572395H | +T*+T*+T*C*A*C*A*A*G*A*A*A*T*G*A*G*+C*+C*+T | 68556 | 19 |
| 2398 | TTTTCACAAGAAATGAGCC | A572396H | +T*+T*+T*T*C*A*C*A*A*G*A*A*A*T*G*A*+G*+C*+C | 68557 | 19 |
| 2399 | TTTTTCACAAGAAATGAGC | A572397H | +T*+T*+T*T*T*C*A*C*A*A*G*A*A*A*T*G*+A*+G*+C | 68558 | 19 |
| 2400 | ATTCTCCTACACTAATTGA | A572398H | +A*+T*+T*C*T*C*C*T*A*C*A*C*T*A*A*T*+T*+G*+A | 68587 | 19 |
| 2401 | ATTCTCCTACACTAATTG | A572399H | +A*+T*+T*C*T*C*C*T*A*C*A*C*T*A*A*+T*+T*+G | 68588 | 18 |
| 2402 | AATTCTCCTACACTAATTG | A572400H | +A*+A*+T*T*C*T*C*C*T*A*C*A*C*T*A*A*+T*+T*+G | 68588 | 19 |
| 2403 | CGGTAAAATTCTCCTACAC | A572401H | +C*+G*+G*T*A*A*A*A*T*T*C*T*C*C*T*A*+C*+A*+C | 68594 | 19 |
| 2404 | CGGTAAAATTCTCCTACA | A572402H | +C*+G*+G*T*A*A*A*A*T*T*C*T*C*C*T*+A*+C*+A | 68595 | 18 |
| 2405 | TCGGTAAAATTCTCCTACA | A572403H | +T*+C*+G*G*T*A*A*A*A*T*T*C*T*C*C*T*+A*+C*+A | 68595 | 19 |
| 2406 | TCGGTAAAATTCTCCTAC | A572404H | +T*+C*+G*G*T*A*A*A*A*T*T*C*T*C*C*+T*+A*+C | 68596 | 18 |
| 2407 | CTCGGTAAAATTCTCCTAC | A572405H | +C*+T*+C*G*G*T*A*A*A*A*T*T*C*T*C*C*+T*+A*+C | 68596 | 19 |
| 2408 | CTCGGTAAAATTCTCCTA | A572406H | +C*+T*+C*G*G*T*A*A*A*A*T*T*C*T*C*+C*+T*+A | 68597 | 18 |
| 2409 | TCTCGGTAAAATTCTCCTA | A572407H | +T*+C*+T*C*G*G*T*A*A*A*A*T*T*C*T*C*+C*+T*+A | 68597 | 19 |
| 2410 | ATCTCGGTAAAATTCTCCT | A572408H | +A*+T*+C*T*C*G*G*T*A*A*A*A*T*T*C*T*+C*+C*+T | 68598 | 19 |
| 2411 | CGGCATCTCGGTAAAATTC | A572409H | +C*+G*+G*C*A*T*C*T*C*G*G*T*A*A*A*A*+T*+T*+C | 68602 | 19 |
| 2412 | CGGCATCTCGGTAAAATT | A572410H | +C*+G*+G*C*A*T*C*T*C*G*G*T*A*A*A*+A*+T*+T | 68603 | 18 |
| 2413 | ACGGCATCTCGGTAAAATT | A572411H | +A*+C*+G*G*C*A*T*C*T*C*G*G*T*A*A*A*+A*+T*+T | 68603 | 19 |
| 2414 | ATACGGCATCTCGGTAAAA | A572412H | +A*+T*+A*C*G*G*C*A*T*C*T*C*G*G*T*A*+A*+A*+A | 68605 | 19 |
| 2415 | ATACGGCATCTCGGTAAA | A572413H | +A*+T*+A*C*G*G*C*A*T*C*T*C*G*G*T*+A*+A*+A | 68606 | 18 |
| 2416 | AATACGGCATCTCGGTAAA | A572414H | +A*+A*+T*A*C*G*G*C*A*T*C*T*C*G*G*T*+A*+A*+A | 68606 | 19 |
| 2417 | ATACGGCATCTCGGTAA | A572415H | +A*+T*+A*C*G*G*C*A*T*C*T*C*G*G*+T*+A*+A | 68607 | 17 |
| 2418 | AATACGGCATCTCGGTAA | A572416H | +A*+A*+T*A*C*G*G*C*A*T*C*T*C*G*G*+T*+A*+A | 68607 | 18 |
| 2419 | TAATACGGCATCTCGGTAA | A572417H | +T*+A*+A*T*A*C*G*G*C*A*T*C*T*C*G*G*+T*+A*+A | 68607 | 19 |
| 2420 | ATACGGCATCTCGGTA | A572418H | +A*+T*+A*C*G*G*C*A*T*C*T*C*G*+G*+T*+A | 68608 | 16 |
| 2421 | AATACGGCATCTCGGTA | A572419H | +A*+A*+T*A*C*G*G*C*A*T*C*T*C*G*+G*+T*+A | 68608 | 17 |
| 2422 | TAATACGGCATCTCGGTA | A572420H | +T*+A*+A*T*A*C*G*G*C*A*T*C*T*C*G*+G*+T*+A | 68608 | 18 |
| 2423 | GTAATACGGCATCTCGGTA | A572421H | +G*+T*+A*A*T*A*C*G*G*C*A*T*C*T*C*G*+G*+T*+A | 68608 | 19 |
| 2424 | TAATACGGCATCTCGGT | A572422H | +T*+A*+A*T*A*C*G*G*C*A*T*C*T*C*+G*+G*+T | 68609 | 17 |
| 2425 | GTAATACGGCATCTCGGT | A572423H | +G*+T*+A*A*T*A*C*G*G*C*A*T*C*T*C*+G*+G*+T | 68609 | 18 |

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| 2426 | TGTAATACGGCATCTCGGT | A572424H | +T*+G*+T*A*A*T*A*C*G*G*C*A*T*C*T*C*+G*+G*+T | 68609 | 19 |
| 2427 | TAATACGGCATCTCGG | A572425H | +T*+A*+A*T*A*C*G*G*C*A*T*C*T*+C*+G*+G | 68610 | 16 |
| 2428 | GTAATACGGCATCTCGG | A572426H | +G*+T*+A*A*T*A*C*G*G*C*A*T*C*T*+C*+G*+G | 68610 | 17 |
| 2429 | TGTAATACGGCATCTCGG | A572427H | +T*+G*+T*A*A*T*A*C*G*G*C*A*T*C*T*+C*+G*+G | 68610 | 18 |
| 2430 | CAAATTTGGTGAGCAACG | A572428H | +C*+A*+A*A*T*T*T*G*G*T*G*A*G*C*A*+A*+C*+G | 68629 | 18 |
| 2431 | GCAAATTTGGTGAGCAACG | A572429H | +G*+C*+A*A*A*T*T*T*G*G*T*G*A*G*C*A*+A*+C*+G | 68629 | 19 |
| 2432 | CTTTGCAAATTTGGTGAGC | A572430H | +C*+T*+T*T*G*C*A*A*A*T*T*T*G*G*T*G*+A*+G*+C | 68633 | 19 |
| 2433 | GTTATCAAGAGAATGTCAG | A572431Hi | +G*+T*+T*A*T*C*A*A*G*A*G*A*A*T*G*T*+C*+A*+G | 68710 | 19 |
| 2434 | GTTATCAAGAGAATGTCA | A572432Hi | +G*+T*+T*A*T*C*A*A*G*A*G*A*A*T*G*+T*+C*+A | 68711 | 18 |
| 2435 | AGTTATCAAGAGAATGTC | A572433Hi | +A*+G*+T*T*A*T*C*A*A*G*A*G*A*A*T*+G*+T*+C | 68712 | 18 |
| 2436 | CTAGCTTTGGCATAAATTT | A572434Hi | +C*+T*+A*G*C*T*T*T*G*G*C*A*T*A*A*A*+T*+T*+T | 68731 | 19 |
| 2437 | TTGTTCCTAGCTTTGGCAT | A572435Hi | +T*+T*+G*T*T*C*C*T*A*G*C*T*T*T*T*G*G*+C*+A*+T | 68737 | 19 |
| 2438 | ATTGTTCCTAGCTTTGGCA | A572436Hi | +A*+T*+T*G*T*T*C*C*T*A*G*C*T*T*T*T*G*+G*+C*+A | 68738 | 19 |
| 2439 | AATTGTTCCTAGCTTTGGC | A572437Hi | +A*+A*+T*T*G*T*T*C*C*T*A*G*C*T*T*T*T*+G*+G*+C | 68739 | 19 |
| 2440 | ATTGTTCCTAGCTTTGGC | A572438Hi | +A*+T*+T*G*T*T*C*C*T*A*G*C*T*T*T*T*+G*+G*+C | 68739 | 18 |
| 2441 | ACCAATTGTTCCTAGCTT | A572439Hi | +A*+C*+C*A*A*T*T*G*T*T*C*C*T*A*G*+C*+T*+T | 68743 | 18 |
| 2442 | CCATCTTGAAGTGTACTG | A572440Hi | +C*+C*+A*T*C*T*T*G*A*A*G*T*G*T*A*+C*+T*+G | 68924 | 18 |
| 2443 | ACCATCTTGAAGTGTACTG | A572441Hi | +A*+C*+C*A*T*C*T*T*G*A*A*G*T*G*T*A*+C*+T*+G | 68924 | 19 |
| 2444 | CTAGCTAAAGTGTTCATGG | A572442Hi | +C*+T*+A*G*C*T*A*A*A*G*T*G*T*T*C*A*+T*+G*+G | 69018 | 19 |
| 2445 | GATTTCTAGCTAAAGTGT | A572443Hi | +G*+A*+T*T*T*C*T*A*G*C*T*A*A*A*G*+T*+G*+T | 69024 | 18 |
| 2446 | CTGGTTTCTTAGAAATCAC | A572444Hi | +C*+T*+G*G*T*T*T*C*T*T*A*G*A*A*A*T*+C*+A*+C | 69047 | 19 |
| 2447 | TCTGGTTTCTTAGAAATCA | A572445Hi | +T*+C*+T*G*G*T*T*T*C*T*T*A*G*A*A*A*+T*+C*+A | 69048 | 19 |
| 2448 | CTGTCTGGTTTCTTAGAAA | A572446Hi | +C*+T*+G*T*C*T*G*G*T*T*T*C*T*T*A*G*+A*+A*+A | 69051 | 19 |
| 2449 | ACTTCTGTCTGGTTTCTTA | A572447Hi | +A*+C*+T*T*C*T*G*T*C*T*G*G*T*T*T*C*+T*+T*+A | 69055 | 19 |
| 2450 | TCAGTGTCCTTCAGACTTC | A572448Hi | +T*+C*+A*G*T*G*T*C*C*T*T*C*A*G*A*C*+T*+T*+C | 69069 | 19 |
| 2451 | TACTCCATCTTGTTCAGTG | A572449Hi | +T*+A*+C*T*C*C*A*T*C*T*T*G*T*T*C*A*+G*+T*+G | 69082 | 19 |
| 2452 | CTACTCCATCTTGTTCAGT | A572450Hi | +C*+T*+A*C*T*C*C*A*T*C*T*T*G*T*T*C*+A*+G*+T | 69083 | 19 |
| 2453 | TATGCTACTCCATCTTGTT | A572451Hi | +T*+A*+T*G*C*T*A*C*T*C*C*A*T*C*T*T*+G*+T*+T | 69087 | 19 |
| 2454 | ATGAATTATATTATGCTAC | A572452Hi | +A*+T*+G*A*A*T*T*A*T*A*T*T*A*T*G*C*+T*+A*+C | 69098 | 19 |
| 2455 | CAATGAATTATATTATGCT | A572453Hi | +C*+A*+A*T*G*A*A*T*T*A*T*A*T*T*A*T*+G*+C*+T | 69100 | 19 |
| 2456 | TTCAAAGTGAACCTGAGAA | A572454Hi | +T*+T*+C*A*A*A*G*T*G*A*A*C*C*T*G*A*+G*+A*+A | 69353 | 19 |
| 2457 | CTCATTAACCAAACTACTT | A572455Hi | +C*+T*+C*A*T*T*A*A*C*C*A*A*A*C*T*A*+C*+T*+T | 69551 | 19 |
| 2458 | CTCATTAACCAAACTACT | A572456Hi | +C*+T*+C*A*T*T*A*A*C*C*A*A*A*C*T*+A*+C*+T | 69552 | 18 |
| 2459 | ATGATCAAAAATGGGCCC | A572457H | +A*+T*+G*A*T*C*A*A*A*A*A*T*G*G*G*+C*+C*+C | 69849 | 18 |
| 2460 | CATGATCAAAAATGGGCCC | A572458H | +C*+A*+T*G*A*T*C*A*A*A*A*A*T*G*G*G*+C*+C*+C | 69849 | 19 |

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| 2461 | TCATGATCAAAAATGGGCC | A572459H | +T*+C*+A*T*G*A*T*C*A*A*A*A*A*T*G*G*+G*+C*+C | 69850 | 19 |
| 2462 | GTAAATCTTCATGATCAAA | A572460H | +G*+T*+A*A*A*T*C*T*T*C*A*T*G*A*T*C*+A*+A*+A | 69858 | 19 |
| 2463 | CAGTAAATCTTCATGATCA | A572461H | +C*+A*+G*T*A*A*A*T*C*T*T*C*A*T*G*A*+T*+C*+A | 69860 | 19 |
| 2464 | TCAGTAAATCTTCATGATC | A572462H | +T*+C*+A*G*T*A*A*A*T*C*T*T*C*A*T*G*+A*+T*+C | 69861 | 19 |
| 2465 | AATCATCTGAAGATAATAT | A572463H | +A*+A*+T*C*A*T*C*T*G*A*A*G*A*T*A*A*+T*+A*+T | 69894 | 19 |
| 2466 | GAATCATCTGAAGATAATA | A572464H | +G*+A*+A*T*C*A*T*C*T*G*A*A*G*A*T*A*+A*+T*+A | 69895 | 19 |
| 2467 | TGAATCATCTGAAGATAAT | A572465H | +T*+G*+A*A*T*C*A*T*C*T*G*A*A*G*A*T*+A*+A*+T | 69896 | 19 |
| 2468 | GTGAATCATCTGAAGATAA | A572466H | +G*+T*+G*A*A*T*C*A*T*C*T*G*A*A*G*A*+T*+A*+A | 69897 | 19 |
| 2469 | AGTGAATCATCTGAAGATA | A572467H | +A*+G*+T*G*A*A*T*C*A*T*C*T*G*A*A*G*+A*+T*+A | 69898 | 19 |
| 2470 | GAGTGAATCATCTGAAGAT | A572468H | +G*+A*+G*T*G*A*A*T*C*A*T*C*T*G*A*A*+G*+A*+T | 69899 | 19 |
| 2471 | GAGTGAATCATCTGAAGA | A572469H | +G*+A*+G*T*G*A*A*T*C*A*T*C*T*G*A*+A*+G*+A | 69900 | 18 |
| 2472 | TGAGTGAATCATCTGAAGA | A572470H | +T*+G*+A*G*T*G*A*A*T*C*A*T*C*T*G*A*+A*+G*+A | 69900 | 19 |
| 2473 | TGATTACATCCAAATACTT | A572471Hi | +T*+G*+A*T*T*A*C*A*T*C*C*A*A*A*T*A*+C*+T*+T | 69921 | 19 |
| 2474 | TTATGATTACATCCAAATA | A572472Hi | +T*+T*+A*T*G*A*T*T*A*C*A*T*C*C*A*A*+A*+T*+A | 69924 | 19 |
| 2475 | CTTATGATTACATCCAAAT | A572473Hi | +C*+T*+T*A*T*G*A*T*T*A*C*A*T*C*C*A*+A*+A*+T | 69925 | 19 |
| 2476 | ATTTGAATAATTGGAGGAA | A572474Hi | +A*+T*+T*T*G*A*A*T*A*A*T*T*G*G*A*G*+G*+A*+A | 69984 | 19 |
| 2477 | TCTATAATATTCAAGAAAG | A572475Hi | +T*+C*+T*A*T*A*A*T*A*T*T*C*A*A*G*A*+A*+A*+G | 70104 | 19 |
| 2478 | CCAAACTATGGAGTTTACA | A572476Hi | +C*+C*+A*A*A*C*T*A*T*G*G*A*G*T*T*T*+A*+C*+A | 70288 | 19 |
| 2479 | ACCAAACTATGGAGTTTAC | A572477Hi | +A*+C*+C*A*A*A*C*T*A*T*G*G*A*G*T*T*+T*+A*+C | 70289 | 19 |
| 2480 | CTAGCAATCAGGCTTTCTT | A572478Hi | +C*+T*+A*G*C*A*A*T*C*A*G*G*C*T*T*T*+C*+T*+T | 70333 | 19 |
| 2481 | CTAGCAATCAGGCTTTCT | A572479Hi | +C*+T*+A*G*C*A*A*T*C*A*G*G*C*T*T*+T*+C*+T | 70334 | 18 |
| 2482 | CTCCTAGCAATCAGGCTT | A572480Hi | +C*+T*+C*C*T*A*G*C*A*A*T*C*A*G*G*+C*+T*+T | 70337 | 18 |
| 2483 | CACCTCCTAGCAATCAGGC | A572481Hi | +C*+A*+C*C*T*C*C*T*A*G*C*A*A*T*C*A*+G*+G*+C | 70339 | 19 |
| 2484 | CACCTCCTAGCAATCAGG | A572482Hi | +C*+A*+C*C*T*C*C*T*A*G*C*A*A*T*C*+A*+G*+G | 70340 | 18 |
| 2485 | TGAGCACCTCCTAGCAAT | A572483Hi | +T*+G*+A*G*C*A*C*C*T*C*C*T*A*G*C*+A*+A*+T | 70344 | 18 |
| 2486 | GCAAATAATTTAAATTCAT | A572484Hi | +G*+C*+A*A*A*T*A*A*T*T*T*A*A*A*T*T*+C*+A*+T | 70377 | 19 |
| 2487 | GATTGAAGTTTTGATGACC | A572485H | +G*+A*+T*T*G*A*A*G*T*T*T*T*G*A*T*G*+A*+C*+C | 70431 | 19 |
| 2488 | GATTGAAGTTTTGATGAC | A572486H | +G*+A*+T*T*G*A*A*G*T*T*T*T*G*A*T*+G*+A*+C | 70432 | 18 |
| 2489 | GGATTGAAGTTTTGATGAC | A572487H | +G*+G*+A*T*T*G*A*A*G*T*T*T*T*G*A*T*+G*+A*+C | 70432 | 19 |
| 2490 | GGGATTGAAGTTTTGATGA | A572488H | +G*+G*+G*A*T*T*G*A*A*G*T*T*T*T*G*A*+T*+G*+A | 70433 | 19 |
| 2491 | ATGGGATTGAAGTTTTGAT | A572489H | +A*+T*+G*G*G*A*T*T*G*A*A*G*T*T*T*T*+G*+A*+T | 70435 | 19 |
| 2492 | TATGGGATTGAAGTTTTGA | A572490H | +T*+A*+T*G*G*G*A*T*T*G*A*A*G*T*T*T*+T*+G*+A | 70436 | 19 |
| 2493 | ATATGGGATTGAAGTTTTG | A572491H | +A*+T*+A*T*G*G*G*A*T*T*G*A*A*G*T*T*+T*+T*+G | 70437 | 19 |
| 2494 | CATATGGGATTGAAGTTTTT | A572492H | +C*+A*+T*A*T*G*G*G*A*T*T*G*A*A*G*T*+T*+T*+T | 70438 | 19 |
| 2495 | GCCTCATATGGGATTGAAG | A572493H | +G*+C*+C*T*C*A*T*A*T*G*G*G*A*T*T*T*G*+A*+A*+G | 70442 | 19 |

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| 2496 | GCCTCATATGGGATTGAA | A572494H | +G*+C*+C*T*C*A*T*A*T*G*G*G*A*T*T*+G*+A*+A | 70443 | 18 |
| 2497 | TGCCTCATATGGGATTGAA | A572495H | +T*+G*+C*C*T*C*A*T*A*T*G*G*G*A*T*T*+G*+A*+A | 70443 | 19 |
| 2498 | TGCCTCATATGGGATTGA | A572496H | +T*+G*+C*C*T*C*A*T*A*T*G*G*G*A*T*+T*+G*+A | 70444 | 18 |
| 2499 | ATGCCTCATATGGGATTGA | A572497H | +A*+T*+G*C*C*T*C*A*T*A*T*G*G*G*A*T*+T*+G*+A | 70444 | 19 |
| 2500 | AATGCCTCATATGGGATTG | A572498H | +A*+A*+T*G*C*C*T*C*A*T*A*T*G*G*G*A*+T*+T*+G | 70445 | 19 |
| 2501 | GAATGCCTCATATGGGATT | A572499H | +G*+A*+A*T*G*C*C*T*C*A*T*A*T*G*G*G*+A*+T*+T | 70446 | 19 |
| 2502 | GAATGCCTCATATGGGAT | A572500H | +G*+A*+A*T*G*C*C*T*C*A*T*A*T*G*G*+G*+A*+T | 70447 | 18 |
| 2503 | TGAATGCCTCATATGGGAT | A572501H | +T*+G*+A*A*T*G*C*C*T*C*A*T*A*T*G*G*+G*+A*+T | 70447 | 19 |
| 2504 | TCTGAATGCCTCATATGGG | A572502H | +T*+C*+T*G*A*A*T*G*C*C*T*C*A*T*A*T*+G*+G*+G | 70449 | 19 |
| 2505 | GTCTGAATGCCTCATATGG | A572503H | +G*+T*+C*T*G*A*A*T*G*C*C*T*C*A*T*A*+T*+G*+G | 70450 | 19 |
| 2506 | TGTCTGAATGCCTCATATG | A572504H | +T*+G*+T*C*T*G*A*A*T*G*C*C*T*C*A*T*+A*+T*+G | 70451 | 19 |
| 2507 | TGTCTGAATGCCTCATAT | A572505H | +T*+G*+T*C*T*G*A*A*T*G*C*C*T*C*A*+T*+A*+T | 70452 | 18 |
| 2508 | CTGTCTGAATGCCTCATAT | A572506H | +C*+T*+G*T*C*T*G*A*A*T*G*C*C*T*C*A*+T*+A*+T | 70452 | 19 |
| 2509 | CTGTCTGAATGCCTCATA | A572507H | +C*+T*+G*T*C*T*G*A*A*T*G*C*C*T*C*+A*+T*+A | 70453 | 18 |
| 2510 | GCTGTCTGAATGCCTCATA | A572508H | +G*+C*+T*G*T*C*T*G*A*A*T*G*C*C*T*C*+A*+T*+A | 70453 | 19 |
| 2511 | AATGCTGTCTGAATGCCTC | A572509H | +A*+A*+T*G*C*T*G*T*C*T*G*A*A*T*G*C*+C*+T*+C | 70456 | 19 |
| 2512 | TATTCTCTCTCAGAAGCCA | A572510H | +T*+A*+T*T*C*T*C*T*C*T*C*A*G*A*A*G*+C*+C*+A | 70482 | 19 |
| 2513 | TGATGTAATATATTCTCTC | A572511H | +T*+G*+A*T*G*T*A*A*T*A*T*A*T*T*C*T*+C*+T*+C | 70492 | 19 |
| 2514 | GTGATGTAATATATTCTCT | A572512H | +G*+T*+G*A*T*G*T*A*A*T*A*T*A*T*T*C*+T*+C*+T | 70493 | 19 |
| 2515 | TAGTGATGTAATATATTCT | A572513H | +T*+A*+G*T*G*A*T*G*T*A*A*T*A*T*A*T*+T*+C*+T | 70495 | 19 |
| 2516 | GGTCTAGTGATGTAATATA | A572514H | +G*+G*+T*C*T*A*G*T*G*A*T*G*T*A*A*T*+A*+T*+A | 70499 | 19 |
| 2517 | AAGGTCTAGTGATGTAATA | A572515H | +A*+A*+G*G*T*C*T*A*G*T*G*A*T*G*T*A*+A*+T*+A | 70501 | 19 |
| 2518 | AAAGGTCTAGTGATGTAAT | A572516H | +A*+A*+A*G*G*T*C*T*A*G*T*G*A*T*G*T*+A*+A*+T | 70502 | 19 |
| 2519 | GAAAGGTCTAGTGATGTAA | A572517H | +G*+A*+A*A*G*G*T*C*T*A*G*T*G*A*T*G*+T*+A*+A | 70503 | 19 |
| 2520 | GAAAGGTCTAGTGATGTA | A572518H | +G*+A*+A*A*G*G*T*C*T*A*G*T*G*A*T*+G*+T*+A | 70504 | 18 |
| 2521 | TGAAAGGTCTAGTGATGTA | A572519H | +T*+G*+A*A*A*G*G*T*C*T*A*G*T*G*A*T*+G*+T*+A | 70504 | 19 |
| 2522 | CTGAAAGGTCTAGTGATGT | A572520H | +C*+T*+G*A*A*A*G*G*T*C*T*A*G*T*G*A*+T*+G*+T | 70505 | 19 |
| 2523 | TGCTGAAAGGTCTAGTGAT | A572521H | +T*+G*+C*T*G*A*A*A*G*G*T*C*T*A*G*T*+G*+A*+T | 70507 | 19 |
| 2524 | CATTTGCTGAAAGGTCTAG | A572522H | +C*+A*+T*T*T*G*C*T*G*A*A*A*G*G*T*C*+T*+A*+G | 70511 | 19 |
| 2525 | AGTTCATTTGCTGAAAGGT | A572523H | +A*+G*+T*T*C*A*T*T*T*G*C*T*G*A*A*A*+G*+G*+T | 70515 | 19 |
| 2526 | GCATCAATATCTCTTAGTT | A572524H | +G*+C*+A*T*C*A*A*T*A*T*C*T*C*T*T*A*+G*+T*+T | 70530 | 19 |
| 2527 | GCATCAATATCTCTTAGT | A572525H | +G*+C*+A*T*C*A*A*T*A*T*C*T*C*T*T*+A*+G*+T | 70531 | 18 |
| 2528 | GGCATCAATATCTCTTAGT | A572526H | +G*+G*+C*A*T*C*A*A*T*A*T*C*T*C*T*T*+A*+G*+T | 70531 | 19 |
| 2529 | GGGCATCAATATCTCTTAG | A572527H | +G*+G*+G*C*A*T*C*A*A*T*A*T*C*T*C*T*+T*+A*+G | 70532 | 19 |
| 2530 | AGGGCATCAATATCTCTTA | A572528H | +A*+G*+G*G*C*A*T*C*A*A*T*A*T*C*T*C*+T*+T*+A | 70533 | 19 |

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| 2531 | TAGGGCATCAATATC TCTT | A572529H | +T*+A*+G*G*G*C*A*T*C*A*A*T*A*T*C*T*+ C*+T*+T | 70534 | 19 |
| 2532 | TTAGGGCATCAATAT CTCT | A572530H | +T*+T*+A*G*G*G*C*A*T*C*A*A*T*A*T*C*+ T*+C*+T | 70535 | 19 |
| 2533 | GCTTAGGGCATCAAT ATCT | A572531H | +G*+C*+T*T*A*G*G*G*C*A*T*C*A*A*T*A*+ T*+C*+T | 70537 | 19 |
| 2534 | GCTTAGGGCATCAAT ATC | A572532H | +G*+C*+T*T*A*G*G*G*C*A*T*C*A*A*T*+A* +T*+C | 70538 | 18 |
| 2535 | GGCTTAGGGCATCAA TATC | A572533H | +G*+G*+C*T*T*A*G*G*G*C*A*T*C*A*A*T*+ A*+T*+C | 70538 | 19 |
| 2536 | GGCTTAGGGCATCAA TAT | A572534H | +G*+G*+C*T*T*A*G*G*G*C*A*T*C*A*A*+T* +A*+T | 70539 | 18 |
| 2537 | TGGCTTAGGGCATCA ATAT | A572535H | +T*+G*+G*C*T*T*A*G*G*G*C*A*T*C*A*A*+ T*+A*+T | 70539 | 19 |
| 2538 | TGGCTTAGGGCATCA ATA | A572536H | +T*+G*+G*C*T*T*A*G*G*G*C*A*T*C*A*+A* +T*+A | 70540 | 18 |
| 2539 | CTGGCTTAGGGCATC AATA | A572537H | +C*+T*+G*G*C*T*T*A*G*G*G*C*A*T*C*A*+ A*+T*+A | 70540 | 19 |
| 2540 | CTGGCTTAGGGCATC AAT | A572538H | +C*+T*+G*G*C*T*T*A*G*G*G*C*A*T*C*+A* +A*+T | 70541 | 18 |
| 2541 | TCTGGCTTAGGGCAT CAAT | A572539H | +T*+C*+T*G*G*C*T*T*A*G*G*G*C*A*T*C*+ A*+A*+T | 70541 | 19 |
| 2542 | TTCTGGCTTAGGGCA TCAA | A572540H | +T*+T*+C*T*G*G*C*T*T*A*G*G*G*C*A*T*+ C*+A*+A | 70542 | 19 |
| 2543 | TTTCTGGCTTAGGGC ATCA | A572541H | +T*+T*+T*C*T*G*G*C*T*T*A*G*G*G*C*A*+ T*+C*+A | 70543 | 19 |
| 2544 | ATTTCTGGCTTAGGG CATC | A572542H | +A*+T*+T*T*C*T*G*G*C*T*T*A*G*G*G*C*+ A*+T*+C | 70544 | 19 |
| 2545 | TTTCAAGATGCTCCA AATG | A572543H | +T*+T*+T*C*A*A*G*A*T*G*C*T*C*C*A*A*+ A*+T*+G | 70577 | 19 |
| 2546 | GCTCCAGCTTTTCAA GATG | A572544H | +G*+C*+T*C*C*A*G*C*T*T*T*T*C*A*A*G*+ A*+T*+G | 70586 | 19 |
| 2547 | AGCTCCAGCTTTTCA AGAT | A572545H | +A*+G*+C*T*C*C*A*G*C*T*T*T*T*C*A*A*+ G*+A*+T | 70587 | 19 |
| 2548 | GTGAAGCTCCAGCTT TTCA | A572546H | +G*+T*+G*A*A*G*C*T*C*C*A*G*C*T*T*T*+ T*+C*+A | 70591 | 19 |
| 2549 | GGTGAAGCTCCAGCT TTTC | A572547H | +G*+G*+T*G*A*A*G*C*T*C*C*A*G*C*T*T*+ T*+T*+C | 70592 | 19 |
| 2550 | GGTGAAGCTCCAGCT TTT | A572548H | +G*+G*+T*G*A*A*G*C*T*C*C*A*G*C*T*+T* +T*+T | 70593 | 18 |
| 2551 | TGGTGAAGCTCCAGC TTTT | A572549H | +T*+G*+G*T*G*A*A*G*C*T*C*C*A*G*C*T*+ T*+T*+T | 70593 | 19 |
| 2552 | GCATTCTGGTGAAGC TCCA | A572550H | +G*+C*+A*T*T*C*T*G*G*T*G*A*A*G*C*T*+ C*+C*+A | 70599 | 19 |
| 2553 | GCATTCTGGTGAAGC TCC | A572551H | +G*+C*+A*T*T*C*T*G*G*T*G*A*A*G*C*+T* +C*+C | 70600 | 18 |
| 2554 | TGCATTCTGGTGAAG CTCC | A572552H | +T*+G*+C*A*T*T*C*T*G*G*T*G*A*A*G*C*+ T*+C*+C | 70600 | 19 |
| 2555 | TGCATTCTGGTGAAG CTC | A572553H | +T*+G*+C*A*T*T*C*T*G*G*T*G*A*A*G*+C* +T*+C | 70601 | 18 |
| 2556 | GTGCATTCTGGTGAA GCTC | A572554H | +G*+T*+G*C*A*T*T*C*T*G*G*T*G*A*A*G*+ C*+T*+C | 70601 | 19 |
| 2557 | AGTGCATTCTGGTGA AGCT | A572555H | +A*+G*+T*G*C*A*T*T*C*T*G*G*T*G*A*A*+ G*+C*+T | 70602 | 19 |
| 2558 | AGTGCATTCTGGTGA AGC | A572556H | +A*+G*+T*G*C*A*T*T*C*T*G*G*T*G*A*+A* +G*+C | 70603 | 18 |
| 2559 | GAGTGCATTCTGGTG AAGC | A572557H | +G*+A*+G*T*G*C*A*T*T*C*T*G*G*T*G*A*+ A*+G*+C | 70603 | 19 |
| 2560 | GAGTGCATTCTGGTG AAG | A572558H | +G*+A*+G*T*G*C*A*T*T*C*T*G*G*T*G*+A* +A*+G | 70604 | 18 |
| 2561 | TGAGTGCATTCTGGT GAAG | A572559H | +T*+G*+A*G*T*G*C*A*T*T*C*T*G*G*T*G*+ A*+A*+G | 70604 | 19 |
| 2562 | CGTGAGTGCATTCTG GTGA | A572560H | +C*+G*+T*G*A*G*T*G*C*A*T*T*C*T*G*G*+ T*+G*+A | 70606 | 19 |
| 2563 | CGTGAGTGCATTCTG GTG | A572561H | +C*+G*+T*G*A*G*T*G*C*A*T*T*C*T*G*+G* +T*+G | 70607 | 18 |
| 2564 | TCGTGAGTGCATTCT GGTG | A572562H | +T*+C*+G*T*G*A*G*T*G*C*A*T*T*C*T*G*+ G*+T*+G | 70607 | 19 |
| 2565 | TCGTGAGTGCATTCT GGT | A572563H | +T*+C*+G*T*G*A*G*T*G*C*A*T*T*C*T*+G* +G*+T | 70608 | 18 |

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| 2566 | CTCGTGAGTGCATTCTGGT | A572564H | +C*+T*+C*G*T*G*A*G*T*G*C*A*T*T*C*T*+G*+G*+T | 70608 | 19 |
| 2567 | TCGTGAGTGCATTCTGG | A572565H | +T*+C*+G*T*G*A*G*T*G*C*A*T*T*C*+T*+G*+G | 70609 | 17 |
| 2568 | CTCGTGAGTGCATTCTGG | A572566H | +C*+T*+C*G*T*G*A*G*T*G*C*A*T*T*C*+T*+G*+G | 70609 | 18 |
| 2569 | GCTCGTGAGTGCATTCTGG | A572567H | +G*+C*+T*C*G*T*G*A*G*T*G*C*A*T*T*C*+T*+G*+G | 70609 | 19 |
| 2570 | GCTCGTGAGTGCATTCTG | A572568H | +G*+C*+T*C*G*T*G*A*G*T*G*C*A*T*T*+C*+T*+G | 70610 | 18 |
| 2571 | AGCTCGTGAGTGCATTCTG | A572569H | +A*+G*+C*T*C*G*T*G*A*G*T*G*C*A*T*T*+C*+T*+G | 70610 | 19 |
| 2572 | AGCTCGTGAGTGCATTCT | A572570H | +A*+G*+C*T*C*G*T*G*A*G*T*G*C*A*T*+T*+C*+T | 70611 | 18 |
| 2573 | AAGCTCGTGAGTGCATTCT | A572571H | +A*+A*+G*C*T*C*G*T*G*A*G*T*G*C*A*T*+T*+C*+T | 70611 | 19 |
| 2574 | AAGCTCGTGAGTGCATTC | A572572H | +A*+A*+G*C*T*C*G*T*G*A*G*T*G*C*A*+T*+T*+C | 70612 | 18 |
| 2575 | AAAGCTCGTGAGTGCATTC | A572573H | +A*+A*+A*G*C*T*C*G*T*G*A*G*T*G*C*A*+T*+T*+C | 70612 | 19 |
| 2576 | GAAAGCTCGTGAGTGCATT | A572574H | +G*+A*+A*A*G*C*T*C*G*T*G*A*G*T*G*C*+A*+T*+T | 70613 | 19 |
| 2577 | GAAAGCTCGTGAGTGCAT | A572575H | +G*+A*+A*A*G*C*T*C*G*T*G*A*G*T*G*+C*+A*+T | 70614 | 18 |
| 2578 | GGAAAGCTCGTGAGTGCAT | A572576H | +G*+G*+A*A*A*G*C*T*C*G*T*G*A*G*T*G*+C*+A*+T | 70614 | 19 |
| 2579 | GTGGAAAGCTCGTGAGTGC | A572577H | +G*+T*+G*G*A*A*A*G*C*T*C*G*T*G*A*G*+T*+G*+C | 70616 | 19 |
| 2580 | TGTGGAAAGCTCGTGAGTG | A572578H | +T*+G*+T*G*G*A*A*A*G*C*T*C*G*T*G*A*+G*+T*+G | 70617 | 19 |
| 2581 | TGTGGAAAGCTCGTGAGT | A572579H | +T*+G*+T*G*G*A*A*A*G*C*T*C*G*T*G*+A*+G*+T | 70618 | 18 |
| 2582 | TTGTGGAAAGCTCGTGAGT | A572580H | +T*+T*+G*T*G*G*A*A*A*G*C*T*C*G*T*G*+A*+G*+T | 70618 | 19 |
| 2583 | TTGTGGAAAGCTCGTGAG | A572581H | +T*+T*+G*T*G*G*A*A*A*G*C*T*C*G*T*+G*+A*+G | 70619 | 18 |
| 2584 | GTTGTGGAAAGCTCGTGAG | A572582H | +G*+T*+T*G*T*G*G*A*A*A*G*C*T*C*G*T*+G*+A*+G | 70619 | 19 |
| 2585 | GTTGTGGAAAGCTCGTGA | A572583H | +G*+T*+T*G*T*G*G*A*A*A*G*C*T*C*G*+T*+G*+A | 70620 | 18 |
| 2586 | TGTTGTGGAAAGCTCGTGA | A572584H | +T*+G*+T*T*G*T*G*G*A*A*A*G*C*T*C*G*+T*+G*+A | 70620 | 19 |
| 2587 | TGTTGTGGAAAGCTCGTG | A572585H | +T*+G*+T*T*G*T*G*G*A*A*A*G*C*T*C*+G*+T*+G | 70621 | 18 |
| 2588 | CTGTTGTGGAAAGCTCGTG | A572586H | +C*+T*+G*T*T*G*T*G*G*A*A*A*G*C*T*C*+G*+T*+G | 70621 | 19 |
| 2589 | TGTTGTGGAAAGCTCGT | A572587H | +T*+G*+T*T*G*T*G*G*A*A*A*G*C*T*+C*+G*+T | 70622 | 17 |
| 2590 | CTGTTGTGGAAAGCTCGT | A572588H | +C*+T*+G*T*T*G*T*G*G*A*A*A*G*C*T*+C*+G*+T | 70622 | 18 |
| 2591 | GCTGTTGTGGAAAGCTCGT | A572589H | +G*+C*+T*G*T*T*G*T*G*G*A*A*A*G*C*T*+C*+G*+T | 70622 | 19 |
| 2592 | CTGTTGTGGAAAGCTCG | A572590H | +C*+T*+G*T*T*G*T*G*G*A*A*A*G*C*+T*+C*+G | 70623 | 17 |
| 2593 | GCTGTTGTGGAAAGCTCG | A572591H | +G*+C*+T*G*T*T*G*T*G*G*A*A*A*G*C*+T*+C*+G | 70623 | 18 |
| 2594 | AGCTGTTGTGGAAAGCTCG | A572592H | +A*+G*+C*T*G*T*T*G*T*G*G*A*A*A*G*C*+T*+C*+G | 70623 | 19 |
| 2595 | TAGCTGTTGTGGAAAGCTC | A572593H | +T*+A*+G*C*T*G*T*T*G*T*G*G*A*A*A*G*+C*+T*+C | 70624 | 19 |
| 2596 | ATAGCTGTTGTGGAAAGCT | A572594H | +A*+T*+A*G*C*T*G*T*T*G*T*G*G*A*A*A*+G*+C*+T | 70625 | 19 |
| 2597 | ACATAGCTGTTGTGGAAAG | A572595H | +A*+C*+A*T*A*G*C*T*G*T*T*G*T*G*G*A*+A*+A*+G | 70627 | 19 |
| 2598 | CACATAGCTGTTGTGGAAA | A572596H | +C*+A*+C*A*T*A*G*C*T*G*T*T*G*T*G*G*+A*+A*+A | 70628 | 19 |
| 2599 | AGACTAAGATATGTGTGCA | A572597Hi | +A*+G*+A*C*T*A*A*G*A*T*A*T*G*T*G*T*+G*+C*+A | 70788 | 19 |
| 2600 | ACACAGACTAAGATATGTG | A572598Hi | +A*+C*+A*C*A*G*A*C*T*A*A*G*A*T*A*T*A*T*+G*+T*+G | 70792 | 19 |

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|---|---|---|---|---|---|
| 2601 | CTTTCTAATCAGATCTGTT | A572599Hi | +C*+T*+T*T*C*T*A*A*T*C*A*G*A*T*C*T*+G*+T*+T | 70846 | 19 |
| 2602 | TTCTAGTTTACCTAATCTA | A572600Hi | +T*+T*+C*T*A*G*T*T*T*A*C*C*T*A*A*T*+C*+T*+A | 70967 | 19 |
| 2603 | AATTCTAGTTTACCTAATC | A572601Hi | +A*+A*+T*T*C*T*A*G*T*T*T*A*C*C*T*A*+A*+T*+C | 70969 | 19 |
| 2604 | ACCAAACCAGGTCTAATTC | A572602Hi | +A*+C*+C*A*A*A*C*C*A*G*G*T*C*T*A*A*+T*+T*+C | 70983 | 19 |
| 2605 | CTACCAAACCAGGTCTAAT | A572603Hi | +C*+T*+A*C*C*A*A*A*C*C*A*G*G*T*C*T*+A*+A*+T | 70985 | 19 |
| 2606 | TACCAAACCAGGTCTAAT | A572604Hi | +T*+A*+C*C*A*A*A*C*C*A*G*G*T*C*T*+A*+A*+T | 70985 | 18 |
| 2607 | ACTACCAAACCAGGTCTAA | A572605Hi | +A*+C*+T*A*C*C*A*A*A*C*C*A*G*G*T*C*+T*+A*+A | 70986 | 19 |
| 2608 | ACTACCAAACCAGGTCTA | A572606Hi | +A*+C*+T*A*C*C*A*A*A*C*C*A*G*G*T*+C*+T*+A | 70987 | 18 |
| 2609 | GCCAGTACTACCAAACCA | A572607Hi | +G*+C*+C*A*G*T*A*C*T*A*C*C*A*A*A*+C*+C*+A | 70993 | 18 |
| 2610 | GAGCCAGTACTACCAAACC | A572608Hi | +G*+A*+G*C*C*A*G*T*A*C*T*A*C*C*A*A*+A*+C*+C | 70994 | 19 |
| 2611 | GAGCCAGTACTACCAAAC | A572609Hi | +G*+A*+G*C*C*A*G*T*A*C*T*A*C*C*A*+A*+A*+C | 70995 | 18 |
| 2612 | AGAGCCAGTACTACCAAAC | A572610Hi | +A*+G*+A*G*C*C*A*G*T*A*C*T*A*C*C*A*+A*+A*+C | 70995 | 19 |
| 2613 | TAGCTGAGTCAGAGCCAGT | A572611Hi | +T*+A*+G*C*T*G*A*G*T*C*A*G*A*G*C*C*+A*+G*+T | 71005 | 19 |
| 2614 | TCATTTAGTTGAATCTCTA | A572612Hi | +T*+C*+A*T*T*T*A*G*T*T*G*A*A*T*C*T*+C*+T*+A | 71091 | 19 |
| 2615 | CTATCCTATCAACAAACTA | A572613Hi | +C*+T*+A*T*C*C*T*A*T*C*A*A*C*A*A*A*+C*+T*+A | 71208 | 19 |
| 2616 | GCTATCCTATCAACAAACT | A572614Hi | +G*+C*+T*A*T*C*C*T*A*T*C*A*A*C*A*A*+A*+C*+T | 71209 | 19 |
| 2617 | CTATCCTATCAACAAACT | A572615Hi | +C*+T*+A*T*C*C*T*A*T*C*A*A*C*A*A*+A*+C*+T | 71209 | 18 |
| 2618 | AGCTATCCTATCAACAAAC | A572616Hi | +A*+G*+C*T*A*T*C*C*T*A*T*C*A*A*C*A*+A*+A*+C | 71210 | 19 |
| 2619 | GCTATCCTATCAACAAAC | A572617Hi | +G*+C*+T*A*T*C*C*T*A*T*C*A*A*C*A*+A*+A*+C | 71210 | 18 |
| 2620 | AGAGCTATCCTATCAACAA | A572618Hi | +A*+G*+A*G*C*T*A*T*C*C*T*A*T*C*A*A*+C*+A*+A | 71212 | 19 |
| 2621 | AGAGCTATCCTATCAACA | A572619Hi | +A*+G*+A*G*C*T*A*T*C*C*T*A*T*C*A*+A*+C*+A | 71213 | 18 |
| 2622 | TTCAGAGAGCTATCCTAT | A572620Hi | +T*+T*+C*A*G*A*G*A*G*C*T*A*T*C*C*+T*+A*+T | 71218 | 18 |
| 2623 | ATATCTTCTTTGGCTTTCA | A572621Hi | +A*+T*+A*T*C*T*T*C*T*T*T*G*G*C*T*T*+T*+C*+A | 71283 | 19 |
| 2624 | GCATTTGCAACAAGACTTT | A572622Hi | +G*+C*+A*T*T*T*G*C*A*A*C*A*A*G*A*C*+T*+T*+T | 71645 | 19 |
| 2625 | GCATTTGCAACAAGACTT | A572623Hi | +G*+C*+A*T*T*T*G*C*A*A*C*A*A*G*A*+C*+T*+T | 71646 | 18 |
| 2626 | GAAATGCATTTGCAACAAG | A572624Hi | +G*+A*+A*A*T*G*C*A*T*T*T*G*C*A*A*C*+A*+A*+G | 71650 | 19 |
| 2627 | AAGTATTTAGCAAGGCAAA | A572625Hi | +A*+A*+G*T*A*T*T*T*A*G*C*A*A*G*G*C*+A*+A*+A | 71865 | 19 |
| 2628 | GAAGTATTTAGCAAGGCAA | A572626Hi | +G*+A*+A*G*T*A*T*T*T*A*G*C*A*A*G*G*+C*+A*+A | 71866 | 19 |
| 2629 | GAAGTATTTAGCAAGGCA | A572627Hi | +G*+A*+A*G*T*A*T*T*T*A*G*C*A*A*G*+G*+C*+A | 71867 | 18 |
| 2630 | TGAAGTATTTAGCAAGGC | A572628Hi | +T*+G*+A*A*G*T*A*T*T*T*A*G*C*A*A*+G*+G*+C | 71868 | 18 |
| 2631 | GCAGAGAGTGATGAAGTGA | A572629Hi | +G*+C*+A*G*A*G*A*G*T*G*A*T*G*A*A*G*+T*+G*+A | 71911 | 19 |
| 2632 | TTAAATCAAATTGGATGAC | A572630Hi | +T*+T*+A*A*A*T*C*A*A*A*T*T*G*G*A*T*+G*+A*+C | 72022 | 19 |
| 2633 | AATAGACAGAAACAAGCCT | A572631Hi | +A*+A*+T*A*G*A*C*A*G*A*A*A*C*A*A*G*+C*+C*+T | 72093 | 19 |
| 2634 | GGAATAGACAGAAACAAGC | A572632Hi | +G*+G*+A*A*T*A*G*A*C*A*G*A*A*A*C*A*+A*+G*+C | 72095 | 19 |
| 2635 | CCTCCACAAATCAATTCAG | A572633Hi | +C*+C*+T*C*C*A*C*A*A*A*T*C*A*A*T*T*+C*+A*+G | 72158 | 19 |

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| 2636 | CTCCACAAATCAATTCAG | A572634Hi | +C*+T*+C*C*A*C*A*A*A*T*C*A*A*T*T*+C*+A*+G | 72158 | 18 |
| 2637 | GTCCAGTCATTGAATGCC | A572635Hi | +G*+T*+C*C*A*G*T*C*A*T*T*G*A*A*T*+G*+C*+C | 72304 | 18 |
| 2638 | TGTCCAGTCATTGAATGC | A572636Hi | +T*+G*+T*C*C*A*G*T*C*A*T*T*G*A*A*+T*+G*+C | 72305 | 18 |
| 2639 | AGCTTGTCCAGTCATTGA | A572637Hi | +A*+G*+C*T*T*G*T*C*C*A*G*T*C*A*T*+T*+G*+A | 72309 | 18 |
| 2640 | GGTTCTGAGCTTGTCCAG | A572638Hi | +G*+G*+T*T*C*T*G*A*G*C*T*T*G*T*C*+C*+A*+G | 72316 | 18 |
| 2641 | AAGGTTCTGAGCTTGTCC | A572639Hi | +A*+A*+G*G*T*T*C*T*G*A*G*C*T*T*G*+T*+C*+C | 72318 | 18 |
| 2642 | GAAGGTTCTGAGCTTGTC | A572640Hi | +G*+A*+A*G*G*T*T*C*T*G*A*G*C*T*T*+G*+T*+C | 72319 | 18 |
| 2643 | AGAGAAGGTTCTGAGCTTG | A572641Hi | +A*+G*+A*G*A*A*G*G*T*T*C*T*G*A*G*C*+T*+T*+G | 72321 | 19 |
| 2644 | GAGAAGGTTCTGAGCTTG | A572642Hi | +G*+A*+G*A*A*G*G*T*T*C*T*G*A*G*C*+T*+T*+G | 72321 | 18 |
| 2645 | AAGAGAAGGTTCTGAGCTT | A572643Hi | +A*+A*+G*A*G*A*A*G*G*T*T*C*T*G*A*G*+C*+T*+T | 72322 | 19 |
| 2646 | CCATCTAATGGTGTCATTT | A572644Hi | +C*+C*+A*T*C*T*A*A*T*G*G*T*G*T*C*A*+T*+T*+T | 72353 | 19 |
| 2647 | GTTGAAAGCTTCCTTCAGC | A572645Hi | +G*+T*+T*G*A*A*A*G*C*T*T*C*C*T*T*C*+A*+G*+C | 72988 | 19 |
| 2648 | AGTTGAAAGCTTCCTTCAG | A572646Hi | +A*+G*+T*T*G*A*A*A*G*C*T*T*C*C*T*T*+C*+A*+G | 72989 | 19 |
| 2649 | GAGTTGAAAGCTTCCTTCA | A572647Hi | +G*+A*+G*T*T*G*A*A*A*G*C*T*T*C*C*T*+T*+C*+A | 72990 | 19 |
| 2650 | AGAGTTGAAAGCTTCCTTC | A572648Hi | +A*+G*+A*G*T*T*G*A*A*A*G*C*T*T*C*C*+T*+T*+C | 72991 | 19 |
| 2651 | TAGAGTTGAAAGCTTCCTT | A572649Hi | +T*+A*+G*A*G*T*T*G*A*A*A*G*C*T*T*C*+C*+T*+T | 72992 | 19 |
| 2652 | ATAGAGTTGAAAGCTTCC | A572650Hi | +A*+T*+A*G*A*G*T*T*G*A*A*A*G*C*T*+T*+C*+C | 72994 | 18 |
| 2653 | AATAGAGTTGAAAGCTTCC | A572651Hi | +A*+A*+T*A*G*A*G*T*T*G*A*A*A*G*C*T*+T*+C*+C | 72994 | 19 |
| 2654 | CAACAGAATTTCAGTATAC | A572652Hi | +C*+A*+A*C*A*G*A*A*T*T*T*C*A*G*T*A*+T*+A*+C | 73097 | 19 |
| 2655 | AACTAGAACCATCAAGAAT | A572653Hi | +A*+A*+C*T*A*G*A*A*C*C*A*T*C*A*A*G*+A*+A*+T | 73142 | 19 |
| 2656 | ACTAGAACCATCAAGAAT | A572654Hi | +A*+C*+T*A*G*A*A*C*C*A*T*C*A*A*G*+A*+A*+T | 73142 | 18 |
| 2657 | CTGGTAACTAGAACCATCA | A572655Hi | +C*+T*+G*G*T*A*A*C*T*A*G*A*A*C*C*C*A*+T*+C*+A | 73147 | 19 |
| 2658 | TCTGGTAACTAGAACCATC | A572656Hi | +T*+C*+T*G*G*T*A*A*C*T*A*G*A*A*C*C*+A*+T*+C | 73148 | 19 |
| 2659 | CTGGTAACTAGAACCATC | A572657Hi | +C*+T*+G*G*T*A*A*C*T*A*G*A*A*C*C*+A*+T*+C | 73148 | 18 |
| 2660 | CACCTCTGGTAACTAGAA | A572658Hi | +C*+A*+C*C*T*C*T*G*G*T*A*A*C*T*A*+G*+A*+A | 73153 | 18 |
| 2661 | GCCTTACACACCTCTGGTA | A572659Hi | +G*+C*+C*T*T*A*C*A*C*A*C*C*T*C*T*G*+G*+T*+A | 73160 | 19 |
| 2662 | CCTTACACACCTCTGGTA | A572660Hi | +C*+C*+T*T*A*C*A*C*A*C*C*T*C*T*G*+G*+T*+A | 73160 | 18 |
| 2663 | GCCTTACACACCTCTGGT | A572661Hi | +G*+C*+C*T*T*A*C*A*C*A*C*C*T*C*T*+G*+G*+T | 73161 | 18 |
| 2664 | TAATATTTCTGCCTTACAC | A572662Hi | +T*+A*+A*T*A*T*T*T*C*T*G*C*C*T*T*A*+C*+A*+C | 73170 | 19 |
| 2665 | GTCTAGCTAATATTTCTGC | A572663Hi | +G*+T*+C*T*A*G*C*T*A*A*T*A*T*T*T*C*+T*+G*+C | 73177 | 19 |
| 2666 | AGTCTAGCTAATATTTCT | A572664Hi | +A*+G*+T*C*T*A*G*C*T*A*A*T*A*T*T*+T*+C*+T | 73179 | 18 |
| 2667 | GAGGAACTTAAGTCTAGC | A572665Hi | +G*+A*+G*G*A*A*C*T*T*A*A*G*T*C*T*+A*+G*+C | 73189 | 18 |
| 2668 | GTCCAAATGTGTCAAACTC | A572666H | +G*+T*+C*C*A*A*A*T*G*T*G*T*C*A*A*A*+C*+T*+C | 73255 | 19 |
| 2669 | AGTCCAAATGTGTCAAACT | A572667H | +A*+G*+T*C*C*A*A*A*T*G*T*G*T*C*A*A*+A*+C*+T | 73256 | 19 |
| 2670 | AAGTCCAAATGTGTCAAAC | A572668H | +A*+A*+G*T*C*C*A*A*A*T*G*T*G*T*C*A*+A*+A*+C | 73257 | 19 |

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| 2671 | CTGTGCAAGTCCAAATGTG | A572669H | +C*+T*+G*T*G*C*A*A*G*T*C*C*A*A*A*T*+G*+T*+G | 73263 | 19 |
| 2672 | TATTACTGTGCAAGTCCAA | A572670H | +T*+A*+T*T*A*C*T*G*T*G*C*A*A*G*T*C*+C*+A*+A | 73268 | 19 |
| 2673 | ATTTATTACTGTGCAAGTC | A572671H | +A*+T*+T*T*A*T*T*A*C*T*G*T*G*C*A*A*+G*+T*+C | 73271 | 19 |
| 2674 | AATTTATTACTGTGCAAGT | A572672H | +A*+A*+T*T*T*A*T*T*A*C*T*G*T*G*C*A*+A*+G*+T | 73272 | 19 |
| 2675 | ATGTAAATTTATTACTGTG | A572673H | +A*+T*+G*T*A*A*A*T*T*T*A*T*T*A*C*T*+G*+T*+G | 73277 | 19 |
| 2676 | TGATGTAAATTTATTACTG | A572674H | +T*+G*+A*T*G*T*A*A*A*T*T*T*A*T*T*A*+C*+T*+G | 73279 | 19 |
| 2677 | AATGATGTAAATTTATTAC | A572675H | +A*+A*+T*G*A*T*G*T*A*A*A*T*T*T*A*T*T*+T*+A*+C | 73281 | 19 |
| 2678 | CATTTCGAGAGACATCAAG | A572676H | +C*+A*+T*T*T*C*G*A*G*A*G*A*C*A*T*C*+A*+A*+G | 73337 | 19 |
| 2679 | CATTTCGAGAGACATCAA | A572677H | +C*+A*+T*T*T*C*G*A*G*A*G*A*C*A*T*+C*+A*+A | 73338 | 18 |
| 2680 | TCATTTCGAGAGACATCAA | A572678H | +T*+C*+A*T*T*T*C*G*A*G*A*G*A*C*A*T*+C*+A*+A | 73338 | 19 |
| 2681 | GTCATTTCGAGAGACATCA | A572679H | +G*+T*+C*A*T*T*T*C*G*A*G*A*G*A*C*A*+T*+C*+A | 73339 | 19 |
| 2682 | AATGTCATTTCGAGAGACA | A572680H | +A*+A*+T*G*T*C*A*T*T*T*C*G*A*G*A*G*+A*+C*+A | 73342 | 19 |
| 2683 | AATGTCATTTCGAGAGAC | A572681H | +A*+A*+T*G*T*C*A*T*T*T*C*G*A*G*A*+G*+A*+C | 73343 | 18 |
| 2684 | CAATGTCATTTCGAGAGAC | A572682H | +C*+A*+A*T*G*T*C*A*T*T*T*C*G*A*G*A*+G*+A*+C | 73343 | 19 |
| 2685 | TCCAATGTCATTTCGAGAG | A572683H | +T*+C*+C*A*A*T*G*T*C*A*T*T*T*C*G*A*+G*+A*+G | 73345 | 19 |
| 2686 | TCCAATGTCATTTCGAGA | A572684H | +T*+C*+C*A*A*T*G*T*C*A*T*T*T*C*G*+A*+G*+A | 73346 | 18 |
| 2687 | GTCCAATGTCATTTCGAGA | A572685H | +G*+T*+C*C*A*A*T*G*T*C*A*T*T*T*C*G*+A*+G*+A | 73346 | 19 |
| 2688 | GTCCAATGTCATTTCGAG | A572686H | +G*+T*+C*C*A*A*T*G*T*C*A*T*T*T*C*+G*+A*+G | 73347 | 18 |
| 2689 | GGTCCAATGTCATTTCGAG | A572687H | +G*+G*+T*C*C*A*A*T*G*T*C*A*T*T*T*C*+G*+A*+G | 73347 | 19 |
| 2690 | GGTCCAATGTCATTTCGA | A572688H | +G*+G*+T*C*C*A*A*T*G*T*C*A*T*T*T*+C*+G*+A | 73348 | 18 |
| 2691 | GGGTCCAATGTCATTTCGA | A572689H | +G*+G*+G*T*C*C*A*A*T*G*T*C*A*T*T*T*+C*+G*+A | 73348 | 19 |
| 2692 | AGGGTCCAATGTCATTTCG | A572690H | +A*+G*+G*G*T*C*C*A*A*T*G*T*C*A*T*T*+T*+C*+G | 73349 | 19 |
| 2693 | ACTGAGGGTCCAATGTCAT | A572691H | +A*+C*+T*G*A*G*G*G*T*C*C*A*A*T*G*T*+C*+A*+T | 73353 | 19 |
| 2694 | CACTGAGGGTCCAATGTCA | A572692H | +C*+A*+C*T*G*A*G*G*G*T*C*C*A*A*T*G*+T*+C*+A | 73354 | 19 |
| 2695 | ACCACTGAGGGTCCAATGT | A572693H | +A*+C*+C*A*C*T*G*A*G*G*G*T*C*C*A*A*+T*+G*+T | 73356 | 19 |
| 2696 | AACCACTGAGGGTCCAATG | A572694H | +A*+A*+C*C*A*C*T*G*A*G*G*G*T*C*C*A*+A*+T*+G | 73357 | 19 |
| 2697 | AACCACTGAGGGTCCAAT | A572695H | +A*+A*+C*C*A*C*T*G*A*G*G*G*T*C*C*+A*+A*+T | 73358 | 18 |
| 2698 | AAACCACTGAGGGTCCAAT | A572696H | +A*+A*+A*C*C*A*C*T*G*A*G*G*G*T*C*C*+A*+A*+T | 73358 | 19 |
| 2699 | ATCTAAAACCACTGAGGGT | A572697H | +A*+T*+C*T*A*A*A*A*C*C*A*C*T*G*A*G*+G*+G*+T | 73363 | 19 |
| 2700 | GGATCTAAAACCACTGAGG | A572698H | +G*+G*+A*T*C*T*A*A*A*A*C*C*A*C*T*G*+A*+G*+G | 73365 | 19 |
| 2701 | TCAGAGTTGGACATTTCAC | A572699H | +T*+C*+A*G*A*G*T*T*G*G*A*C*A*T*T*T*+C*+A*+C | 73388 | 19 |
| 2702 | CTGTTTCAGAGTTGGACAT | A572700H | +C*+T*+G*T*T*T*C*A*G*A*G*T*T*G*G*A*+C*+A*+T | 73393 | 19 |
| 2703 | ACTGTTTCAGAGTTGGACA | A572701H | +A*+C*+T*G*T*T*T*C*A*G*A*G*T*T*G*G*+A*+C*+A | 73394 | 19 |
| 2704 | AACTGTTTCAGAGTTGGAC | A572702H | +A*+A*+C*T*G*T*T*T*C*A*G*A*G*T*T*G*+G*+A*+C | 73395 | 19 |
| 2705 | TAAACTGTTTCAGAGTTGG | A572703H | +T*+A*+A*A*C*T*G*T*T*T*C*A*G*A*G*T*+T*+G*+G | 73397 | 19 |

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| 2706 | GGTTAAACTGTTTCAGAGT | A572704H | +G*+G*+T*T*A*A*A*C*T*G*T*T*T*C*A*G*+A*+G*+T | 73400 | 19 |
| 2707 | TGACAGGTTAAACTGTTTC | A572705H | +T*+G*+A*C*A*G*G*T*T*A*A*A*C*T*G*T*+T*+T*+C | 73405 | 19 |
| 2708 | TATGACAGGTTAAACTGTT | A572706H | +T*+A*+T*G*A*C*A*G*G*T*T*A*A*A*C*T*+G*+T*+T | 73407 | 19 |
| 2709 | ATATGACAGGTTAAACTGT | A572707H | +A*+T*+A*T*G*A*C*A*G*G*T*T*A*A*A*C*+T*+G*+T | 73408 | 19 |
| 2710 | TATATGACAGGTTAAACTG | A572708H | +T*+A*+T*A*T*G*A*C*A*G*G*T*T*A*A*A*+C*+T*+G | 73409 | 19 |
| 2711 | TTATATGACAGGTTAAACT | A572709H | +T*+T*+A*T*A*T*G*A*C*A*G*G*T*T*A*A*+A*+C*+T | 73410 | 19 |
| 2712 | GTTATATGACAGGTTAAAC | A572710H | +G*+T*+T*A*T*A*T*G*A*C*A*G*G*T*T*A*+A*+A*+C | 73411 | 19 |
| 2713 | CTGGTTATATGACAGGTTA | A572711H | +C*+T*+G*G*T*T*A*T*A*T*G*A*C*A*G*G*+T*+T*+A | 73414 | 19 |
| 2714 | CTGGTTATATGACAGGTT | A572712H | +C*+T*+G*G*T*T*A*T*A*T*G*A*C*A*G*+G*+T*+T | 73415 | 18 |
| 2715 | GCTGGTTATATGACAGGTT | A572713H | +G*+C*+T*G*G*T*T*A*T*A*T*G*A*C*A*G*+G*+T*+T | 73415 | 19 |
| 2716 | GCTGGTTATATGACAGGT | A572714H | +G*+C*+T*G*G*T*T*A*T*A*T*G*A*C*A*+G*+G*+T | 73416 | 18 |
| 2717 | AGCTGGTTATATGACAGGT | A572715H | +A*+G*+C*T*G*G*T*T*A*T*A*T*G*A*C*A*+G*+G*+T | 73416 | 19 |
| 2718 | CTAAAATGAGCTGCTCCAG | A572716H | +C*+T*+A*A*A*A*T*G*A*G*C*T*G*C*T*C*+C*+A*+G | 73475 | 19 |
| 2719 | TTCTAAAATGAGCTGCTCC | A572717H | +T*+T*+C*T*A*A*A*A*T*G*A*G*C*T*G*C*+T*+C*+C | 73477 | 19 |
| 2720 | CTTCTAAAATGAGCTGCTC | A572718H | +C*+T*+T*C*T*A*A*A*A*T*G*A*G*C*T*G*+C*+T*+C | 73478 | 19 |
| 2721 | CATCAGCATATTTAGGCA | A572719Hi | +C*+A*+T*C*A*G*C*A*T*A*T*T*T*A*G*+G*+C*+A | 73529 | 18 |
| 2722 | GAGGACTCATTAATTTAAA | A572720Hi | +G*+A*+G*G*A*C*T*C*A*T*T*A*A*A*T*T*T*+A*+A*+A | 73996 | 19 |
| 2723 | AAGAGGACTCATTAATTTA | A572721Hi | +A*+A*+G*A*G*G*A*C*T*C*A*T*T*A*A*T*+T*+T*+A | 73998 | 19 |
| 2724 | ACAAGAGACAAGATAATGA | A572722Hi | +A*+C*+A*A*G*A*G*A*C*A*A*G*A*T*A*A*+T*+G*+A | 74088 | 19 |
| 2725 | CACAAGAGACAAGATAATG | A572723Hi | +C*+A*+C*A*A*G*A*G*A*C*A*A*G*A*T*A*+A*+T*+G | 74089 | 19 |
| 2726 | GAGCATATCCCTGATATTT | A572724H | +G*+A*+G*C*A*T*A*T*C*C*C*T*G*A*T*A*+T*+T*+T | 74118 | 19 |
| 2727 | GGAGCATATCCCTGATATT | A572725H | +G*+G*+A*G*C*A*T*A*T*C*C*C*T*G*A*T*+A*+T*+T | 74119 | 19 |
| 2728 | AAGGGGGAGCATATCCCTG | A572726H | +A*+A*+G*G*G*G*G*A*G*C*A*T*A*T*C*C*+C*+T*+G | 74124 | 19 |
| 2729 | AAGGGGGAGCATATCCCT | A572727H | +A*+A*+G*G*G*G*G*A*G*C*A*T*A*T*C*+C*+C*+T | 74125 | 18 |
| 2730 | CAAGGGGGAGCATATCCCT | A572728H | +C*+A*+A*G*G*G*G*G*A*G*C*A*T*A*T*C*+C*+C*+T | 74125 | 19 |
| 2731 | CAAGGGGGAGCATATCCC | A572729H | +C*+A*+A*G*G*G*G*G*A*G*C*A*T*A*T*+C*+C*+C | 74126 | 18 |
| 2732 | TCAAGGGGGAGCATATCCC | A572730H | +T*+C*+A*A*G*G*G*G*A*G*C*A*T*A*T*+C*+C*+C | 74126 | 19 |
| 2733 | TCAAGGGGGAGCATATCC | A572731H | +T*+C*+A*A*G*G*G*G*A*G*C*A*T*A*+T*+C*+C | 74127 | 18 |
| 2734 | CTCAAGGGGGAGCATATCC | A572732H | +C*+T*+C*A*A*G*G*G*G*G*A*G*C*A*T*A*+T*+C*+C | 74127 | 19 |
| 2735 | CTCAAGGGGGAGCATATC | A572733H | +C*+T*+C*A*A*G*G*G*G*G*A*G*C*A*T*+A*+T*+C | 74128 | 18 |
| 2736 | TCTCAAGGGGGAGCATATC | A572734H | +T*+C*+T*C*A*A*G*G*G*G*G*A*G*C*A*T*+A*+T*+C | 74128 | 19 |
| 2737 | TCTCAAGGGGGAGCATAT | A572735H | +T*+C*+T*C*A*A*G*G*G*G*G*A*G*C*A*+T*+A*+T | 74129 | 18 |
| 2738 | GTCTCAAGGGGGAGCATAT | A572736H | +G*+T*+C*T*C*A*A*G*G*G*G*G*A*G*C*A*+T*+A*+T | 74129 | 19 |
| 2739 | AGTCTCAAGGGGGAGCATA | A572737H | +A*+G*+T*C*T*C*A*A*G*G*G*G*G*A*G*C*+A*+T*+A | 74130 | 19 |
| 2740 | AGTCTCAAGGGGGAGCAT | A572738H | +A*+G*+T*C*T*C*A*A*G*G*G*G*G*A*G*+C*+A*+T | 74131 | 18 |

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| 2741 | CAGTCTCAAGGGGGA GCAT | A572739H | +C*+A*+G*T*C*T*C*A*A*G*G*G*G*G*A*G* +C*+A*+T | 74131 | 19 |
| 2742 | CAGTCTCAAGGGGGA GCA | A572740H | +C*+A*+G*T*C*T*C*A*A*G*G*G*G*G*A*+G *+C*+A | 74132 | 18 |
| 2743 | TCAGTCTCAAGGGGG AGCA | A572741H | +T*+C*+A*G*T*C*T*C*A*A*G*G*G*G*G*A*+ G*+C*+A | 74132 | 19 |
| 2744 | TCAGTCTCAAGGGGG AGC | A572742H | +T*+C*+A*G*T*C*T*C*A*A*G*G*G*G*G*+A* +G*+C | 74133 | 18 |
| 2745 | TTCAGTCTCAAGGGG GAGC | A572743H | +T*+T*+C*A*G*T*C*T*C*A*A*G*G*G*G*G*+ A*+G*+C | 74133 | 19 |
| 2746 | CTTCAGTCTCAAGGG GGAG | A572744H | +C*+T*+T*C*A*G*T*C*T*C*A*A*G*G*G*G*+ G*+A*+G | 74134 | 19 |
| 2747 | CCTTCAGTCTCAAGG GGGA | A572745H | +C*+C*+T*T*C*A*G*T*C*T*C*A*A*G*G*G*+ G*+G*+A | 74135 | 19 |
| 2748 | TTCCTTCAGTCTCAA GGGG | A572746H | +T*+T*+C*C*T*T*C*A*G*T*C*T*C*A*A*G*+ G*+G*+G | 74137 | 19 |
| 2749 | GTTCCTTCAGTCTCA AGGG | A572747H | +G*+T*+T*C*C*T*T*C*A*G*T*C*T*C*A*A*+ G*+G*+G | 74138 | 19 |
| 2750 | AGTTCCTTCAGTCTC AAGG | A572748H | +A*+G*+T*T*C*C*T*T*C*A*G*T*C*T*C*A*+ A*+G*+G | 74139 | 19 |
| 2751 | CAGTTCCTTCAGTCT CAAG | A572749H | +C*+A*+G*T*T*C*C*T*T*C*A*G*T*C*T*C*+ A*+A*+G | 74140 | 19 |
| 2752 | TTACTAAGGTTTAAA ATCT | A572750H | +T*+T*+A*C*T*A*A*G*G*T*T*T*A*A*A*A*+ T*+C*+T | 74160 | 19 |
| 2753 | TCTGATAGGGATGAA ATGT | A572751H | +T*+C*+T*G*A*T*A*G*G*G*A*T*G*A*A*A*+ T*+G*+T | 74184 | 19 |
| 2754 | TCTCTGATAGGGATG AAAT | A572752H | +T*+C*+T*C*T*G*A*T*A*G*G*G*A*T*G*A*+ A*+A*+T | 74186 | 19 |
| 2755 | AGAAAGTTCTCTGAT AGGG | A572753H | +A*+G*+A*A*A*G*T*T*C*T*C*T*G*A*T*A*+ G*+G*+G | 74193 | 19 |
| 2756 | AGCCTCAAGAAAGTT CTCT | A572754H | +A*+G*+C*C*T*C*A*A*G*A*A*A*G*T*T*C*+ T*+C*+T | 74200 | 19 |
| 2757 | AAGCCTCAAGAAAGT TCTC | A572755H | +A*+A*+G*C*C*T*C*A*A*G*A*A*A*G*T*T*+ C*+T*+C | 74201 | 19 |
| 2758 | GACAAGCCTCAAGAA AGTT | A572756H | +G*+A*+C*A*A*G*C*C*T*C*A*A*G*A*A*A*+ G*+T*+T | 74204 | 19 |
| 2759 | GGACAAGCCTCAAGA AAGT | A572757H | +G*+G*+A*C*A*A*G*C*C*T*C*A*A*G*A*A*+ A*+G*+T | 74205 | 19 |
| 2760 | AGGACAAGCCTCAAG AAAG | A572758H | +A*+G*+G*A*C*A*A*G*C*C*T*C*A*A*G*A*+ A*+A*+G | 74206 | 19 |
| 2761 | CTTTAGGACAAGCCT CAAG | A572759H | +C*+T*+T*T*A*G*G*A*C*A*A*G*C*C*T*C*+ A*+A*+G | 74210 | 19 |
| 2762 | ACTTTAGGACAAGCC TCAA | A572760H | +A*+C*+T*T*T*A*G*G*A*C*A*A*G*C*C*T*+ C*+A*+A | 74211 | 19 |
| 2763 | ACTTTAGGACAAGCC TCA | A572761H | +A*+C*+T*T*T*A*G*G*A*C*A*A*G*C*C*+T* +C*+A | 74212 | 18 |
| 2764 | CACTTTAGGACAAGC CTCA | A572762H | +C*+A*+C*T*T*T*A*G*G*A*C*A*A*G*C*C*+ T*+C*+A | 74212 | 19 |
| 2765 | CCACTTTAGGACAAG CCTC | A572763H | +C*+C*+A*C*T*T*T*A*G*G*A*C*A*A*G*C*+ C*+T*+C | 74213 | 19 |
| 2766 | TCCACTTTAGGACAA GCCT | A572764H | +T*+C*+C*A*C*T*T*T*A*G*G*A*C*A*A*G*+ C*+C*+T | 74214 | 19 |
| 2767 | CTCCACTTTAGGACA AGCC | A572765H | +C*+T*+C*C*A*C*T*T*T*A*G*G*A*C*A*A*+ G*+C*+C | 74215 | 19 |
| 2768 | CTCTCCACTTTAGGA CAAG | A572766H | +C*+T*+C*T*C*C*A*C*T*T*T*A*G*G*A*C*+ A*+A*+G | 74217 | 19 |
| 2769 | CTCTCCACTTTAGGA CAA | A572767H | +C*+T*+C*T*C*C*A*C*T*T*T*A*G*G*A*+C* +A*+A | 74218 | 18 |
| 2770 | ACTCTCCACTTTAGG ACAA | A572768H | +A*+C*+T*C*T*C*C*A*C*T*T*T*A*G*G*A*+ C*+A*+A | 74218 | 19 |
| 2771 | AACTCTCCACTTTAG GACA | A572769H | +A*+A*+C*T*C*T*C*C*A*C*T*T*T*A*G*G*+ A*+C*+A | 74219 | 19 |
| 2772 | AAACTCTCCACTTTA GGAC | A572770H | +A*+A*+A*C*T*C*T*C*C*A*C*T*T*T*A*G*+ G*+A*+C | 74220 | 19 |
| 2773 | GAAACTCTCCACTTT AGGA | A572771H | +G*+A*+A*A*C*T*C*T*C*C*A*C*T*T*T*A*+ G*+G*+A | 74221 | 19 |
| 2774 | TGAAACTCTCCACTT TAGG | A572772H | +T*+G*+A*A*A*C*T*C*T*C*C*A*C*T*T*T*+ A*+G*+G | 74222 | 19 |
| 2775 | CTGAAACTCTCCACT TTAG | A572773H | +C*+T*+G*A*A*A*C*T*C*T*C*C*A*C*T*T*+ T*+A*+G | 74223 | 19 |

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| 2776 | GCACTGAAACTCTCC ACTT | A572774H | +G*+C*+A*C*T*G*A*A*A*C*T*C*T*C*C*A*+ C*+T*+T | 74226 | 19 |
| 2777 | GGCACTGAAACTCTC CACT | A572775H | +G*+G*+C*A*C*T*G*A*A*A*C*T*C*T*C*C*+ A*+C*+T | 74227 | 19 |
| 2778 | CTGGCACTGAAACTC TCCA | A572776H | +C*+T*+G*G*C*A*C*T*G*A*A*A*C*T*C*T*+ C*+C*+A | 74229 | 19 |
| 2779 | TCTGGCACTGAAACT CTCC | A572777H | +T*+C*+T*G*G*C*A*C*T*G*A*A*A*C*T*C*+ T*+C*+C | 74230 | 19 |
| 2780 | CCTGGTAAGGAGGAG ACC | A572778Hi | +C*+C*+T*G*G*T*A*A*G*G*A*G*G*A*G*+A *+C*+C | 74278 | 18 |
| 2781 | GCCTGGTAAGGAGGA GACC | A572779Hi | +G*+C*+C*T*G*G*T*A*A*G*G*A*A*G*G*A*G* +A*+C*+C | 74278 | 19 |
| 2782 | ATCTTGTACAACTTA GAGG | A572780Hi | +A*+T*+C*T*T*G*T*A*C*A*A*C*T*T*A*G*+ A*+G*+G | 74297 | 19 |
| 2783 | TCTTGTACAACTTAG AGG | A572781Hi | +T*+C*+T*T*G*T*A*C*A*A*C*T*T*A*G*+A* +G*+G | 74297 | 18 |
| 2784 | CATCTTGTACAACTT AGAG | A572782Hi | +C*+A*+T*C*T*T*G*T*A*C*A*A*C*T*T*A*+ G*+A*+G | 74298 | 19 |
| 2785 | ACTCATCTTGTACAA CTT | A572783Hi | +A*+C*+T*C*A*T*C*T*T*G*T*A*C*A*A*+C* +T*+T | 74302 | 18 |
| 2786 | AGCATAATATTTAAA CTGA | A572784Hi | +A*+G*+C*A*T*A*A*T*A*T*T*T*A*A*A*C*+ T*+G*+A | 74360 | 19 |
| 2787 | CAGCATAATATTTAA ACTG | A572785Hi | +C*+A*+G*C*A*T*A*A*T*A*T*T*T*A*A*A*+ C*+T*+G | 74361 | 19 |
| 2788 | TCCAGCATAATATTT AAAC | A572786Hi | +T*+C*+C*A*G*C*A*T*A*A*T*A*T*T*T*A*+ A*+A*+C | 74363 | 19 |
| 2789 | ATGAGCCAATATTTG ACA | A572787Hi | +A*+T*+G*A*G*C*C*A*A*T*A*T*T*T*G*+A* +C*+A | 74753 | 18 |
| 2790 | GTTTGGCACAGTTGT TCC | A572788Hi | +G*+T*+T*T*G*G*C*A*C*A*G*T*T*G*T*+T* +C*+C | 74776 | 18 |
| 2791 | TAGTTTGGCACAGTT GTTC | A572789Hi | +T*+A*+G*T*T*T*G*G*C*A*C*A*G*T*T*G*+ T*+T*+C | 74777 | 19 |
| 2792 | ATTAGTTTGGCACAG TTGT | A572790Hi | +A*+T*+T*A*G*T*T*T*G*G*C*A*C*A*G*T*+ T*+G*+T | 74779 | 19 |
| 2793 | AATTTGCATTAGTTT GGCA | A572791Hi | +A*+A*+T*T*T*G*C*A*T*T*A*G*T*T*T*G*+ G*+C*+A | 74786 | 19 |
| 2794 | GCCAAGTAACTATCA TTT | A572792Hi | +G*+C*+C*A*A*G*T*A*A*C*T*A*T*C*A*+T* +T*+T | 74970 | 18 |
| 2795 | CAGTAGGCCAAGTAA CTA | A572793Hi | +C*+A*+G*T*A*G*G*C*C*A*A*G*T*A*A*+C* +T*+A | 74976 | 18 |
| 2796 | ACAGTAGGCCAAGTA ACT | A572794Hi | +A*+C*+A*G*T*A*G*G*C*C*A*A*G*T*A*+A* +C*+T | 74977 | 18 |
| 2797 | ACAGTAGGCCAAGTA AC | A572795Hi | +A*+C*+A*G*T*A*G*G*C*C*A*A*G*T*+A*+ A*+C | 74978 | 17 |
| 2798 | CACAGTAGGCCAAGT AAC | A572796Hi | +C*+A*+C*A*G*T*A*G*G*C*C*A*A*G*T*+A* +A*+C | 74978 | 18 |
| 2799 | TACACAGTAGGCCAA GTAA | A572797Hi | +T*+A*+C*A*C*A*G*T*A*G*G*C*C*A*A*G*+ T*+A*+A | 74979 | 19 |
| 2800 | ACACAGTAGGCCAAG TAA | A572798Hi | +A*+C*+A*C*A*G*T*A*G*G*C*C*A*A*G*+T* +A*+A | 74979 | 18 |
| 2801 | GCTGAAGAAACTTCA GTAT | A572799Hi | +G*+C*+T*G*A*A*G*A*A*A*C*T*T*C*A*G*+ T*+A*+T | 75088 | 19 |
| 2802 | AATGTCTTGCAAAGC ACAA | A572800Hi | +A*+A*+T*G*T*C*T*T*G*C*A*A*A*G*C*A*+ C*+A*+A | 75212 | 19 |
| 2803 | AACATAATTTCCTCTA TTA | A572801Hi | +A*+A*+C*A*T*A*A*T*T*T*C*C*T*C*T*A*+ T*+T*+A | 75304 | 19 |
| 2804 | TAGGATACAAATGAA CATA | A572802Hi | +T*+A*+G*G*A*T*A*C*A*A*A*T*G*A*A*C*+ A*+T*+A | 75317 | 19 |
| 2805 | TTAGGATACAAATGA ACAT | A572803Hi | +T*+T*+A*G*G*A*T*A*C*A*A*A*T*G*A*A*+ C*+A*+T | 75318 | 19 |
| 2806 | TCTCTATGAAGGAAG ATAA | A572804Hi | +T*+C*+T*C*T*A*T*G*A*A*G*G*A*A*G*A*+ T*+A*+A | 75400 | 19 |
| 2807 | TTCTCTATGAAGGAA GATA | A572805Hi | +T*+T*+C*T*C*T*A*T*G*A*A*G*G*A*A*G*+ A*+T*+A | 75401 | 19 |
| 2808 | ATTCTCTATGAAGGA AGAT | A572806Hi | +A*+T*+T*C*T*C*T*A*T*G*A*A*G*G*A*A*+ G*+A*+T | 75402 | 19 |
| 2809 | GAGTATTCTCTATGA AGG | A572807Hi | +G*+A*+G*T*A*T*T*C*T*C*T*A*T*G*A*+A* +G*+G | 75407 | 18 |
| 2810 | TACTGAGTCAGGTAT AGAA | A572808Hi | +T*+A*+C*T*G*A*G*T*C*A*G*G*T*A*T*A*+ G*+A*+A | 75448 | 19 |

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| 2811 | TGCTATTAAATAGAATTAA | A572809Hi | +T*+G*+C*T*A*T*T*A*A*A*T*A*G*A*A*T*+T*+A*+A | 75476 | 19 |
| 2812 | CTGCTATTAAATAGAATTA | A572810Hi | +C*+T*+G*C*T*A*T*T*A*A*A*T*A*G*A*A*+T*+T*+A | 75477 | 19 |
| 2813 | TTTGATCATTATTAGTTTC | A572811Hi | +T*+T*+T*G*A*T*C*A*T*T*A*T*T*A*G*T*+T*+T*+C | 75546 | 19 |
| 2814 | CTTTGATCATTATTAGTT | A572812Hi | +C*+T*+T*T*G*A*T*C*A*T*T*A*T*T*A*+G*+T*+T | 75548 | 18 |
| 2815 | GCTTTGATCATTATTAGT | A572813Hi | +G*+C*+T*T*T*G*A*T*C*A*T*T*A*T*T*+A*+G*+T | 75549 | 18 |
| 2816 | GATGGCTTTGATCATTAT | A572814Hi | +G*+A*+T*G*G*C*T*T*T*G*A*T*C*A*T*+T*+A*+T | 75553 | 18 |
| 2817 | AAATTAAGATGGCTTTGAT | A572815Hi | +A*+A*+A*T*T*A*A*G*A*T*G*G*C*T*T*T*+G*+A*+T | 75559 | 19 |
| 2818 | CAAATTAAGATGGCTTTGA | A572816Hi | +C*+A*+A*A*T*T*A*A*G*A*T*G*G*C*T*T*+T*+G*+A | 75560 | 19 |
| 2819 | AGTTTGCTTTGCTTACTAG | A572817Hi | +A*+G*+T*T*T*G*C*T*T*T*G*C*T*T*A*C*+T*+A*+G | 75688 | 19 |
| 2820 | GAACTTAATCACAAGTTCC | A572818Hi | +G*+A*+A*C*T*T*A*A*T*C*A*C*A*A*G*T*+T*+C*+C | 75723 | 19 |
| 2821 | TGAACTTAATCACAAGTTC | A572819Hi | +T*+G*+A*A*C*T*T*A*A*T*C*A*C*A*A*G*+T*+T*+C | 75724 | 19 |
| 2822 | TGAACTTAATCACAAGTT | A572820Hi | +T*+G*+A*A*C*T*T*A*A*T*C*A*C*A*A*+G*+T*+T | 75725 | 18 |
| 2823 | TCTGAACTTAATCACAAGT | A572821Hi | +T*+C*+T*G*A*A*C*T*T*A*A*T*C*A*C*A*+A*+G*+T | 75726 | 19 |
| 2824 | TTACTTAATGTTTGTCTGT | A572822Hi | +T*+T*+A*C*T*T*A*A*T*G*T*T*T*G*T*C*+T*+G*+T | 75747 | 19 |
| 2825 | CATCATTACTTAATGTTTG | A572823Hi | +C*+A*+T*C*A*T*T*A*C*T*T*A*A*T*G*T*+T*+T*+G | 75752 | 19 |
| 2826 | GCCATCATTACTTAATGTT | A572824Hi | +G*+C*+C*A*T*C*A*T*T*A*C*T*T*A*A*T*+G*+T*+T | 75754 | 19 |
| 2827 | TACCACAGAGCATCCTGAA | A572825Hi | +T*+A*+C*C*A*C*A*G*A*G*C*A*T*C*C*T*+G*+A*+A | 75818 | 19 |
| 2828 | CTGAGGTACCACAGAGCAT | A572826Hi | +C*+T*+G*A*G*G*T*A*C*C*A*C*A*G*A*G*+C*+A*+T | 75824 | 19 |
| 2829 | ACTCCACAGTCTGAATCAG | A572827Hi | +A*+C*+T*C*C*A*C*A*G*T*C*T*G*A*A*T*+C*+A*+G | 75849 | 19 |
| 2830 | TGACCATACACAAGCTTCA | A572828Hi | +T*+G*+A*C*C*A*T*A*C*A*C*A*A*G*C*T*+T*+C*+A | 75935 | 19 |
| 2831 | CACTGACCATACACAAGCT | A572829Hi | +C*+A*+C*T*G*A*C*C*A*T*A*C*A*C*A*A*+G*+C*+T | 75938 | 19 |
| 2832 | ACACTGACCATACACAAGC | A572830Hi | +A*+C*+A*C*T*G*A*C*C*A*T*A*C*A*C*A*+A*+G*+C | 75939 | 19 |
| 2833 | ACACACTGACCATACACAA | A572831Hi | +A*+C*+A*C*A*C*T*G*A*C*C*A*T*A*C*A*+C*+A*+A | 75941 | 19 |
| 2834 | GACACACTGACCATACACA | A572832Hi | +G*+A*+C*A*C*A*C*T*G*A*C*C*A*T*A*C*+A*+C*+A | 75942 | 19 |
| 2835 | AGATGACACACTGACCATA | A572833Hi | +A*+G*+A*T*G*A*C*A*C*A*C*T*G*A*C*C*+A*+T*+A | 75946 | 19 |
| 2836 | GTGAGATTCAGCTGAGATG | A572834Hi | +G*+T*+G*A*G*A*T*T*C*A*G*C*T*G*A*G*+A*+T*+G | 75960 | 19 |
| 2837 | GGATCATTGTGAGATTCAG | A572835Hi | +G*+G*+A*T*C*A*T*T*G*T*G*A*G*A*T*T*+C*+A*+G | 75968 | 19 |
| 2838 | CATTAGGATCATTGTGAGA | A572836Hi | +C*+A*+T*T*A*G*G*A*T*C*A*T*T*G*T*G*+A*+G*+A | 75973 | 19 |
| 2839 | CCATTAGGATCATTGTGAG | A572837Hi | +C*+C*+A*T*T*A*G*G*A*T*C*A*T*T*G*T*+G*+A*+G | 75974 | 19 |
| 2840 | CCATTAGGATCATTGTGA | A572838Hi | +C*+C*+A*T*T*A*G*G*A*T*C*A*T*T*G*+T*+G*+A | 75975 | 18 |
| 2841 | ACCATTAGGATCATTGTGA | A572839Hi | +A*+C*+C*A*T*T*A*G*G*A*T*C*A*T*T*G*+T*+G*+A | 75975 | 19 |
| 2842 | GTCATACCTGTCCTAGG | A572840Hi | +G*+T*+C*A*T*A*C*C*T*G*T*C*C*T*+A*+G*+G | 75998 | 17 |
| 2843 | GAGGTCATACCTGTCCTAG | A572841Hi | +G*+A*+G*G*T*C*A*T*A*C*C*T*G*T*C*C*+T*+A*+G | 75999 | 19 |
| 2844 | GTAGTGCAAAGCAAACAGA | A572842Hi | +G*+T*+A*G*T*G*C*A*A*A*G*C*A*A*A*C*+A*+G*+A | 76123 | 19 |
| 2845 | TGTAGTGCAAAGCAAACAG | A572843Hi | +T*+G*+T*A*G*T*G*C*A*A*A*G*C*A*A*A*+C*+A*+G | 76124 | 19 |

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| 2846 | TTGTGTAGTGCAAAG CAAA | A572844Hi | +T*+T*+G*T*G*T*A*G*T*G*C*A*A*A*G*C*+ A*+A*+A | 76127 | 19 |
| 2847 | GCATCTTCTCAAATG TAAG | A572845Hi | +G*+C*+A*T*C*T*T*C*T*C*A*A*A*T*G*T*+ A*+A*+G | 76168 | 19 |
| 2848 | GGCATCTTCTCAAAT GTAA | A572846Hi | +G*+G*+C*A*T*C*T*T*C*T*C*A*A*A*T*G*+ T*+A*+A | 76169 | 19 |
| 2849 | GAGTCTTGAGTTTCA TATG | A572847Hi | +G*+A*+G*T*C*T*T*G*A*G*T*T*T*C*A*T*+ A*+T*+G | 76505 | 19 |
| 2850 | TTCAGAGTCTTGAGT TTCA | A572848Hi | +T*+T*+C*A*G*A*G*T*C*T*T*G*A*G*T*T*+ T*+C*+A | 76509 | 19 |
| 2851 | CTTCAGAGTCTTGAG TTTC | A572849Hi | +C*+T*+T*C*A*G*A*G*T*C*T*T*G*A*G*T*+ T*+T*+C | 76510 | 19 |
| 2852 | ACTTCAGAGTCTTGA GTTT | A572850Hi | +A*+C*+T*T*C*A*G*A*G*T*C*T*T*G*A*G*+ T*+T*+T | 76511 | 19 |
| 2853 | AAGACTTCAGAGTCT TGAG | A572851Hi | +A*+A*+G*A*C*T*T*C*A*G*A*G*T*C*T*T*+ G*+A*+G | 76514 | 19 |
| 2854 | TAAGACTTCAGAGTC TTGA | A572852Hi | +T*+A*+A*G*A*C*T*T*C*A*G*A*G*T*C*T*+ T*+G*+A | 76515 | 19 |
| 2855 | TAAGACTTCAGAGTC TTG | A572853Hi | +T*+A*+A*G*A*C*T*T*C*A*G*A*G*T*C*+T* +T*+G | 76516 | 18 |
| 2856 | ACTTAAGACTTCAGA GTCT | A572854Hi | +A*+C*+T*T*A*A*G*A*C*T*T*C*A*G*A*G*+ T*+C*+T | 76518 | 19 |
| 2857 | ATTCTCCACTTAAGA CTTC | A572855Hi | +A*+T*+T*C*T*C*C*A*C*T*T*A*A*G*A*C*+ T*+T*+C | 76525 | 19 |
| 2858 | TGATTCTCCACTTAA GACT | A572856Hi | +T*+G*+A*T*T*C*T*C*C*A*C*T*T*A*A*G*+ A*+C*+T | 76527 | 19 |
| 2859 | ATGATTCTCCACTTA AGAC | A572857Hi | +A*+T*+G*A*T*T*C*T*C*C*A*C*T*T*A*A*+ G*+A*+C | 76528 | 19 |
| 2860 | AATGATTCTCCACTT AAGA | A572858Hi | +A*+A*+T*G*A*T*T*C*T*C*C*A*C*T*T*A*+ A*+G*+A | 76529 | 19 |
| 2861 | AGCTGTCTTCCTGAG AAGC | A572859Hi | +A*+G*+C*T*G*T*C*T*T*C*C*T*G*A*G*A*+ A*+G*+C | 76596 | 19 |
| 2862 | AGCTGTCTTCCTGAG AAG | A572860Hi | +A*+G*+C*T*G*T*C*T*T*C*C*T*G*A*G*+A* +A*+G | 76597 | 18 |
| 2863 | AAGCTGTCTTCCTGA GAAG | A572861Hi | +A*+A*+G*C*T*G*T*C*T*T*C*C*T*G*A*G*+ A*+A*+G | 76597 | 19 |
| 2864 | GAAGCTGTCTTCCTG AGAA | A572862Hi | +G*+A*+A*G*C*T*G*T*C*T*T*C*C*T*G*A*+ G*+A*+A | 76598 | 19 |
| 2865 | AGAAGCTGTCTTCCT GAGA | A572863Hi | +A*+G*+A*A*G*C*T*G*T*C*T*T*C*C*T*G*+ A*+G*+A | 76599 | 19 |
| 2866 | ATCTAGACAATCTTC AAGG | A572864Hi | +A*+T*+C*T*A*G*A*C*A*A*T*C*T*T*C*A*+ A*+G*+G | 76642 | 19 |
| 2867 | TTATCTAGACAATCTT CAA | A572865Hi | +T*+T*+A*T*C*T*A*G*A*C*A*A*T*C*T*T*+ C*+A*+A | 76644 | 19 |
| 2868 | TTTATCTAGACAATCT TC | A572866Hi | +T*+T*+T*A*T*C*T*A*G*A*C*A*A*T*C*+T* +T*+C | 76646 | 18 |
| 2869 | GTATGAGGTACCTCC AAG | A572867Hi | +G*+T*+A*T*G*A*G*G*T*A*C*C*T*C*C*+A* +A*+G | 76853 | 18 |
| 2870 | AGTATGAGGTACCTC CAAG | A572868Hi | +A*+G*+T*A*T*G*A*G*G*T*A*C*C*T*C*C*+ A*+A*+G | 76853 | 19 |
| 2871 | AGTATGAGGTACCTC CAA | A572869Hi | +A*+G*+T*A*T*G*A*G*G*T*A*C*C*T*C*+C* +A*+A | 76854 | 18 |
| 2872 | GGAAATGCAGTATGA GGTA | A572870Hi | +G*+G*+A*A*A*T*G*C*A*G*T*A*T*G*A*G*+ G*+T*+A | 76861 | 19 |
| 2873 | TTAAGAAGGAAATGC AGTA | A572871Hi | +T*+T*+A*A*G*A*A*G*G*A*A*A*T*G*C*A*+ G*+T*+A | 76868 | 19 |
| 2874 | GTTCTATGGAATAAT AATG | A572872Hi | +G*+T*+T*C*T*A*T*G*G*A*A*T*A*A*T*A*+ A*+T*+G | 77334 | 19 |
| 2875 | ATAAAGAGTGTTCTA TGGA | A572873Hi | +A*+T*+A*A*A*G*A*G*T*G*T*T*C*T*A*T*+ G*+G*+A | 77343 | 19 |
| 2876 | CATAAAGAGTGTTCT ATGG | A572874Hi | +C*+A*+T*A*A*A*G*A*G*T*G*T*T*C*T*A*+ T*+G*+G | 77344 | 19 |
| 2877 | TCATAAAGAGTGTTC TATG | A572875Hi | +T*+C*+A*T*A*A*A*G*A*G*T*G*T*T*C*T*+ A*+T*+G | 77345 | 19 |
| 2878 | TCATAAAGAGTGTTC TAT | A572876Hi | +T*+C*+A*T*A*A*A*G*A*G*T*G*T*T*C*+T* +A*+T | 77346 | 18 |
| 2879 | CTCATAAAGAGTGTT CTAT | A572877Hi | +C*+T*+C*A*T*A*A*A*G*A*G*T*G*T*T*C*+ T*+A*+T | 77346 | 19 |
| 2880 | ACTAGCTCATAAAGA GTGT | A572878Hi | +A*+C*+T*A*G*C*T*C*A*T*A*A*A*G*A*G*+ T*+G*+T | 77351 | 19 |

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| 2881 | CAAATTATGTGTGATGTTA | A572879Hi | +C*+A*+A*A*T*T*A*T*G*T*G*T*G*A*T*G*+T*+T*+A | 77479 | 19 |
| 2882 | CCAACATTTGTACAAAGTA | A572880Hi | +C*+C*+A*A*C*A*T*T*T*G*T*A*C*A*A*A*+G*+T*+A | 77520 | 19 |
| 2883 | GAAGCTAAACAGCTATTTA | A572881Hi | +G*+A*+A*G*C*T*A*A*A*C*A*G*C*T*A*T*+T*+T*+A | 77556 | 19 |
| 2884 | ACCTGGAAGCTAAACAGCT | A572882Hi | +A*+C*+C*T*G*G*A*A*G*C*T*A*A*A*C*A*+G*+C*+T | 77561 | 19 |
| 2885 | AATACTTCCACTAAACAAT | A572883Hi | +A*+A*+T*A*C*T*T*C*C*A*C*T*A*A*A*C*+A*+A*+T | 77613 | 19 |
| 2886 | CCATTCTCACACTGACAAT | A572884Hi | +C*+C*+A*T*T*C*T*C*A*C*A*C*T*G*A*C*+A*+A*+T | 77670 | 19 |
| 2887 | GCAAGAAAGGCATAGCAG | A572885H | +G*+C*+A*A*G*A*A*A*G*G*C*A*T*A*G*+C*+A*+G | 77793 | 18 |
| 2888 | GGCAAGAAAGGCATAGCAG | A572886H | +G*+G*+C*A*A*G*A*A*A*G*G*C*A*T*A*G*+C*+A*+G | 77793 | 19 |
| 2889 | GAGGCAAGAAAGGCATAGC | A572887H | +G*+A*+G*G*C*A*A*G*A*A*A*G*G*C*A*T*+A*+G*+C | 77795 | 19 |
| 2890 | AAAATTGCTTCTGGAATAC | A572888H | +A*+A*+A*A*T*T*G*C*T*T*C*T*G*G*A*A*+T*+A*+C | 77856 | 19 |
| 2891 | TCTAAAGGTTCTGTTCCAG | A572889Hi | +T*+C*+T*A*A*A*G*G*T*T*C*T*G*T*T*C*+C*+A*+G | 77925 | 19 |
| 2892 | AATCATGTTTCTAAAGGTT | A572890Hi | +A*+A*+T*C*A*T*G*T*T*T*C*T*A*A*A*G*+G*+T*+T | 77934 | 19 |
| 2893 | ACACAATGATCCACTAAA | A572891Hi | +A*+C*+A*C*A*A*T*G*A*T*C*C*A*C*T*+A*+A*+A | 78078 | 18 |
| 2894 | TACACAATGATCCACTAAA | A572892Hi | +T*+A*+C*A*C*A*A*T*G*A*T*C*C*A*C*T*+A*+A*+A | 78078 | 19 |
| 2895 | ATAGCCAGTATAATCTCAT | A572893Hi | +A*+T*+A*G*C*C*A*G*T*A*T*A*A*T*C*T*+C*+A*+T | 78144 | 19 |
| 2896 | GATAGCCAGTATAATCTCA | A572894Hi | +G*+A*+T*A*G*C*C*A*G*T*A*T*A*A*T*C*+T*+C*+A | 78145 | 19 |
| 2897 | GATAGCCAGTATAATCTC | A572895Hi | +G*+A*+T*A*G*C*C*A*G*T*A*T*A*A*T*+C*+T*+C | 78146 | 18 |
| 2898 | GTGATAGCCAGTATAATC | A572896Hi | +G*+T*+G*A*T*A*G*C*C*A*G*T*A*T*A*+A*+T*+C | 78148 | 18 |
| 2899 | AGTGATAGCCAGTATAATC | A572897Hi | +A*+G*+T*G*A*T*A*G*C*C*A*G*T*A*T*A*+A*+T*+C | 78148 | 19 |
| 2900 | TTAAAGTGATAGCCAGTA | A572898Hi | +T*+T*+A*A*A*G*T*G*A*T*A*G*C*C*A*+G*+T*+A | 78153 | 18 |
| 2901 | GTTAAAGTGATAGCCAGTA | A572899Hi | +G*+T*+T*A*A*A*G*T*G*A*T*A*G*C*C*A*+G*+T*+A | 78153 | 19 |
| 2902 | ACTACATAAACTTGCCTAA | A572900Hi | +A*+C*+T*A*C*A*T*A*A*A*C*T*T*G*C*C*+T*+A*+A | 78273 | 19 |
| 2903 | GAACTACATAAACTTGCCT | A572901Hi | +G*+A*+A*C*T*A*C*A*T*A*A*A*C*T*T*G*+C*+C*+T | 78275 | 19 |
| 2904 | ACCTGGAACTACATAAAC | A572902Hi | +A*+C*+C*T*G*G*A*A*C*T*A*C*A*T*A*+A*+A*+C | 78281 | 18 |
| 2905 | TTTGGTTTATCATGTATGA | A572903Hi | +T*+T*+T*G*G*T*T*T*A*T*C*A*T*G*T*A*+T*+G*+A | 78410 | 19 |
| 2906 | TATGAATTTGGTTTATCAT | A572904Hi | +T*+A*+T*G*A*A*T*T*T*G*G*T*T*T*A*T*+C*+A*+T | 78416 | 19 |
| 2907 | GAATAGCTGACAGCAAGAA | A572905Hi | +G*+A*+A*T*A*G*C*T*G*A*C*A*G*C*A*A*+G*+A*+A | 78469 | 19 |
| 2908 | GCATCATGCAAGCAGCATT | A572906Hi | +G*+C*+A*T*C*A*T*G*C*A*A*G*C*A*G*C*+A*+T*+T | 78523 | 19 |
| 2909 | AGCATCATGCAAGCAGCAT | A572907Hi | +A*+G*+C*A*T*C*A*T*G*C*A*A*G*C*A*G*+C*+A*+T | 78524 | 19 |
| 2910 | AGCTCATTGCAGCATCATG | A572908Hi | +A*+G*+C*T*C*A*T*T*G*C*A*G*C*A*T*C*+A*+T*+G | 78534 | 19 |
| 2911 | GAAGAGCTCATTGCAGCAT | A572909Hi | +G*+A*+A*G*A*G*C*T*C*A*T*T*G*C*A*G*+C*+A*+T | 78538 | 19 |
| 2912 | CACAGAAGAGCTCATTGCA | A572910Hi | +C*+A*+C*A*G*A*A*G*A*G*C*T*C*A*T*T*+G*+C*+A | 78542 | 19 |
| 2913 | TCACAGAAGAGCTCATTGC | A572911Hi | +T*+C*+A*C*A*G*A*A*G*A*G*C*T*C*A*T*+T*+G*+C | 78543 | 19 |
| 2914 | ACACTCTCTATGGCTAAA | A572912Hi | +A*+C*+A*C*T*C*T*C*T*A*T*G*G*C*T*+A*+A*+A | 78591 | 18 |
| 2915 | TAACACTCTCTATGGCTA | A572913Hi | +T*+A*+A*C*A*C*T*C*T*C*T*A*T*G*G*+C*+T*+A | 78593 | 18 |

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| 2916 | GTAACACTCTCTATGGCT | A572914Hi | +G*+T*+A*A*C*A*C*T*C*T*C*T*A*T*G*+G*+C*+T | 78594 | 18 |
| 2917 | TGTAACACTCTCTATGGC | A572915Hi | +T*+G*+T*A*A*C*A*C*T*C*T*C*T*A*T*+G*+G*+C | 78595 | 18 |
| 2918 | GTTTGTGTAACACTCTCTA | A572916Hi | +G*+T*+T*T*G*T*G*T*A*A*C*A*C*T*C*T*+C*+T*+A | 78599 | 19 |
| 2919 | TTATAGGTTTGTGTAACAC | A572917Hi | +T*+T*+A*T*A*G*G*T*T*T*G*T*G*T*A*A*+C*+A*+C | 78605 | 19 |
| 2920 | TTGAGAGCCTGAAGTTGAA | A572918Hi | +T*+T*+G*A*G*A*G*C*C*T*G*A*A*G*T*T*+G*+A*+A | 78792 | 19 |
| 2921 | ATTTGAGAGCCTGAAGTTG | A572919Hi | +A*+T*+T*T*G*A*G*A*G*C*C*T*G*A*A*G*+T*+T*+G | 78794 | 19 |
| 2922 | GATTTGAGAGCCTGAAGTT | A572920Hi | +G*+A*+T*T*T*G*A*G*A*G*C*C*T*G*A*A*+G*+T*+T | 78795 | 19 |
| 2923 | ATGAGTATGCATGTGATTT | A572921Hi | +A*+T*+G*A*G*T*A*T*G*C*A*T*G*T*G*A*+T*+T*+T | 78809 | 19 |
| 2924 | GCATTATTGACATATGAG | A572922Hi | +G*+C*+A*T*T*A*T*T*G*A*C*A*T*A*T*+G*+A*+G | 78823 | 18 |
| 2925 | AGCATTATTGACATATGAG | A572923Hi | +A*+G*+C*A*T*T*A*T*T*G*A*C*A*T*A*T*+G*+A*+G | 78823 | 19 |
| 2926 | CTAGCATTATTGACATAT | A572924Hi | +C*+T*+A*G*C*A*T*T*A*T*T*G*A*C*A*+T*+A*+T | 78826 | 18 |
| 2927 | ATATCTAAAGACCGCAAG | A572925H | +A*+T*+A*T*C*T*A*A*A*G*A*C*C*G*C*+A*+A*+G | 78952 | 18 |
| 2928 | CATATCTAAAGACCGCAAG | A572926H | +C*+A*+T*A*T*C*T*A*A*A*G*A*C*C*G*C*+A*+A*+G | 78952 | 19 |
| 2929 | CATATCTAAAGACCGCAA | A572927H | +C*+A*+T*A*T*C*T*A*A*A*G*A*C*C*G*+C*+A*+A | 78953 | 18 |
| 2930 | TCATATCTAAAGACCGCAA | A572928H | +T*+C*+A*T*A*T*C*T*A*A*A*G*A*C*C*G*+C*+A*+A | 78953 | 19 |
| 2931 | GCTCATATCTAAAGACCGC | A572929H | +G*+C*+T*C*A*T*A*T*C*T*A*A*A*G*A*C*+C*+G*+C | 78955 | 19 |
| 2932 | GCTCATATCTAAAGACCG | A572930H | +G*+C*+T*C*A*T*A*T*C*T*A*A*A*G*A*+C*+C*+G | 78956 | 18 |
| 2933 | TGCTCATATCTAAAGACCG | A572931H | +T*+G*+C*T*C*A*T*A*T*C*T*A*A*A*G*A*+C*+C*+G | 78956 | 19 |
| 2934 | CTGCTCATATCTAAAGACC | A572932H | +C*+T*+G*C*T*C*A*T*A*T*C*T*A*A*A*G*+A*+C*+C | 78957 | 19 |
| 2935 | CTGCTCATATCTAAAGAC | A572933H | +C*+T*+G*C*T*C*A*T*A*T*C*T*A*A*A*+G*+A*+C | 78958 | 18 |
| 2936 | GCTGCTCATATCTAAAGAC | A572934H | +G*+C*+T*G*C*T*C*A*T*A*T*C*T*A*A*A*+G*+A*+C | 78958 | 19 |
| 2937 | TGCTGCTCATATCTAAAGA | A572935H | +T*+G*+C*T*G*C*T*C*A*T*A*T*C*T*A*A*+A*+G*+A | 78959 | 19 |
| 2938 | TTGCTGCTCATATCTAAAG | A572936H | +T*+T*+G*C*T*G*C*T*C*A*T*A*T*C*T*A*+A*+A*+G | 78960 | 19 |
| 2939 | CATTGCTGCTCATATCTAA | A572937H | +C*+A*+T*T*G*C*T*G*C*T*C*A*T*A*T*C*+T*+A*+A | 78962 | 19 |
| 2940 | ATCATTGCTGCTCATATCT | A572938H | +A*+T*+C*A*T*T*G*C*T*G*C*T*C*A*T*A*+T*+C*+T | 78964 | 19 |
| 2941 | TTCAAAGATTTCCAGTGTG | A572939H | +T*+T*+C*A*A*A*G*A*T*T*T*C*C*A*G*T*+G*+T*+G | 79005 | 19 |
| 2942 | GTTCAAAGATTTCCAGTGT | A572940H | +G*+T*+T*C*A*A*A*G*A*T*T*T*C*C*A*G*+T*+G*+T | 79006 | 19 |
| 2943 | TAAGTTCAAAGATTTCCAG | A572941H | +T*+A*+A*G*T*T*C*A*A*A*G*A*T*T*T*C*+C*+A*+G | 79009 | 19 |
| 2944 | TTAAGTTCAAAGATTTCCA | A572942H | +T*+T*+A*A*G*T*T*C*A*A*A*G*A*T*T*T*+C*+C*+A | 79010 | 19 |
| 2945 | CTTAAGTTCAAAGATTTCC | A572943H | +C*+T*+T*A*A*G*T*T*C*A*A*A*G*A*T*T*+T*+C*+C | 79011 | 19 |
| 2946 | CCTTAAGTTCAAAGATTTC | A572944H | +C*+C*+T*T*A*A*G*T*T*C*A*A*A*G*A*T*+T*+T*+C | 79012 | 19 |
| 2947 | CCCTTAAGTTCAAAGATTT | A572945H | +C*+C*+C*T*T*A*A*G*T*T*C*A*A*A*G*A*+T*+T*+T | 79013 | 19 |
| 2948 | TTCCCTTAAGTTCAAAGAT | A572946H | +T*+T*+C*C*C*T*T*A*A*G*T*T*C*A*A*A*+G*+A*+T | 79015 | 19 |
| 2949 | AGTTCCCTTAAGTTCAAAG | A572947H | +A*+G*+T*T*C*C*C*T*T*A*A*G*T*T*C*A*+A*+A*+G | 79017 | 19 |
| 2950 | GAGTTCCCTTAAGTTCAAA | A572948H | +G*+A*+G*T*T*C*C*C*T*T*A*A*G*T*T*C*+A*+A*+A | 79018 | 19 |

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| 2951 | AGAGTTCCCTTAAGTTCAA | A572949H | +A*+G*+A*G*T*T*C*C*C*T*T*A*A*G*T*T*+C*+A*+A | 79019 | 19 |
| 2952 | AGAGTTCCCTTAAGTTCA | A572950H | +A*+G*+A*G*T*T*C*C*C*T*T*A*A*G*T*+T*+C*+A | 79020 | 18 |
| 2953 | AAGAGTTCCCTTAAGTTCA | A572951H | +A*+A*+G*A*G*T*T*C*C*C*T*T*A*A*G*T*+T*+C*+A | 79020 | 19 |
| 2954 | TAAGAGTTCCCTTAAGTTC | A572952H | +T*+A*+A*G*A*G*T*T*C*C*C*T*T*A*A*G*+T*+T*+C | 79021 | 19 |
| 2955 | CTAAATAAGAGTTCCCTTA | A572953H | +C*+T*+A*A*A*T*A*A*G*A*G*T*T*C*C*C*+T*+T*+A | 79026 | 19 |
| 2956 | TGATTATGGCTAAATAAGA | A572954H | +T*+G*+A*T*T*A*T*G*G*C*T*A*A*A*T*A*+A*+G*+A | 79035 | 19 |
| 2957 | CTGATTATGGCTAAATAAG | A572955H | +C*+T*+G*A*T*T*A*T*G*G*C*T*A*A*A*T*+A*+A*+G | 79036 | 19 |
| 2958 | TCTGATTATGGCTAAATAA | A572956H | +T*+C*+T*G*A*T*T*A*T*G*G*C*T*A*A*A*+T*+A*+A | 79037 | 19 |
| 2959 | TCTGATTATGGCTAAATA | A572957H | +T*+C*+T*G*A*T*T*A*T*G*G*C*T*A*A*+A*+T*+A | 79038 | 18 |
| 2960 | ATCTGATTATGGCTAAATA | A572958H | +A*+T*+C*T*G*A*T*T*A*T*G*G*C*T*A*A*+A*+T*+A | 79038 | 19 |
| 2961 | GATCTGATTATGGCTAAAT | A572959H | +G*+A*+T*C*T*G*A*T*T*A*T*G*G*C*T*A*+A*+A*+T | 79039 | 19 |
| 2962 | TGATCTGATTATGGCTAAA | A572960H | +T*+G*+A*T*C*T*G*A*T*T*A*T*G*G*C*T*+A*+A*+A | 79040 | 19 |
| 2963 | CTGATCTGATTATGGCTAA | A572961H | +C*+T*+G*A*T*C*T*G*A*T*T*A*T*G*G*C*+T*+A*+A | 79041 | 19 |
| 2964 | CTGATCTGATTATGGCTA | A572962H | +C*+T*+G*A*T*C*T*G*A*T*T*A*T*G*G*+C*+T*+A | 79042 | 18 |
| 2965 | GCTGATCTGATTATGGCTA | A572963H | +G*+C*+T*G*A*T*C*T*G*A*T*T*A*T*G*G*+C*+T*+A | 79042 | 19 |
| 2966 | GCTGATCTGATTATGGCT | A572964H | +G*+C*+T*G*A*T*C*T*G*A*T*T*A*T*G*+G*+C*+T | 79043 | 18 |
| 2967 | TGCTGATCTGATTATGGCT | A572965H | +T*+G*+C*T*G*A*T*C*T*G*A*T*T*A*T*G*+G*+C*+T | 79043 | 19 |
| 2968 | TGCTGATCTGATTATGGC | A572966H | +T*+G*+C*T*G*A*T*C*T*G*A*T*T*A*T*+G*+G*+C | 79044 | 18 |
| 2969 | ATGCTGATCTGATTATGGC | A572967H | +A*+T*+G*C*T*G*A*T*C*T*G*A*T*T*A*T*+G*+G*+C | 79044 | 19 |
| 2970 | GATGCTGATCTGATTATGG | A572968H | +G*+A*+T*G*C*T*G*A*T*C*T*G*A*T*T*A*+T*+G*+G | 79045 | 19 |
| 2971 | CAAGATGCTGATCTGATTA | A572969H | +C*+A*+A*G*A*T*G*C*T*G*A*T*C*T*G*A*+T*+T*+A | 79048 | 19 |
| 2972 | CCAAGATGCTGATCTGATT | A572970H | +C*+C*+A*A*G*A*T*G*C*T*G*A*T*C*T*G*+A*+T*+T | 79049 | 19 |
| 2973 | TCCAAGATGCTGATCTGAT | A572971H | +T*+C*+C*A*A*G*A*T*G*C*T*G*A*T*C*T*+G*+A*+T | 79050 | 19 |
| 2974 | GTCCAAGATGCTGATCTGA | A572972H | +G*+T*+C*C*A*A*G*A*T*G*C*T*G*A*T*C*+T*+G*+A | 79051 | 19 |
| 2975 | AGTCCAAGATGCTGATCTG | A572973H | +A*+G*+T*C*C*A*A*G*A*T*G*C*T*G*A*T*+C*+T*+G | 79052 | 19 |
| 2976 | AAGTCCAAGATGCTGATCT | A572974H | +A*+A*+G*T*C*C*A*A*G*A*T*G*C*T*G*A*+T*+C*+T | 79053 | 19 |
| 2977 | AAGTCCAAGATGCTGATC | A572975H | +A*+A*+G*T*C*C*A*A*G*A*T*G*C*T*G*+A*+T*+C | 79054 | 18 |
| 2978 | CAAGTCCAAGATGCTGATC | A572976H | +C*+A*+A*G*T*C*C*A*A*G*A*T*G*C*T*G*+A*+T*+C | 79054 | 19 |
| 2979 | TCAAGTCCAAGATGCTGAT | A572977H | +T*+C*+A*A*G*T*C*C*A*A*G*A*T*G*C*T*+G*+A*+T | 79055 | 19 |
| 2980 | CTCAAGTCCAAGATGCTGA | A572978H | +C*+T*+C*A*A*G*T*C*C*A*A*G*A*T*G*C*+T*+G*+A | 79056 | 19 |
| 2981 | TTCACTCAAGTCCAAGATG | A572979H | +T*+T*+C*A*C*T*C*A*A*G*T*C*C*A*A*G*+A*+T*+G | 79060 | 19 |
| 2982 | TTCACTCAAGTCCAAGAT | A572980H | +T*+T*+C*A*C*T*C*A*A*G*T*C*C*A*A*+G*+A*+T | 79061 | 18 |
| 2983 | TTTCACTCAAGTCCAAGAT | A572981H | +T*+T*+T*C*A*C*T*C*A*A*G*T*C*C*A*A*+G*+A*+T | 79061 | 19 |
| 2984 | TTTTCACTCAAGTCCAAGA | A572982H | +T*+T*+T*T*C*A*C*T*C*A*A*G*T*C*C*A*+A*+G*+A | 79062 | 19 |
| 2985 | GCTTTTTCACTCAAGTCCA | A572983H | +G*+C*+T*T*T*T*T*C*A*C*T*C*A*A*G*T*+C*+C*+A | 79065 | 19 |

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| 2986 | CTACTCTAGACCATAAATA | A572984H | +C*+T*+A*C*T*C*T*A*G*A*C*C*A*T*A*A*+A*+T*+A | 79085 | 19 |
| 2987 | CAGTTTCTCTACTCTAGAC | A572985H | +C*+A*+G*T*T*T*C*T*C*T*A*C*T*C*T*A*+G*+A*+C | 79093 | 19 |
| 2988 | TGCAGTTTCTCTACTCTAG | A572986H | +T*+G*+C*A*G*T*T*T*C*T*C*T*A*C*T*C*+T*+A*+G | 79095 | 19 |
| 2989 | ATGCAGTTTCTCTACTCTA | A572987H | +A*+T*+G*C*A*G*T*T*T*C*T*C*T*A*C*T*+C*+T*+A | 79096 | 19 |
| 2990 | GATGCAGTTTCTCTACTCT | A572988H | +G*+A*+T*G*C*A*G*T*T*T*C*T*C*T*A*C*+T*+C*+T | 79097 | 19 |
| 2991 | AGATGCAGTTTCTCTACTC | A572989H | +A*+G*+A*T*G*C*A*G*T*T*T*C*T*C*T*A*+C*+T*+C | 79098 | 19 |
| 2992 | TGTGAGAAAGATGCAGTTT | A572990H | +T*+G*+T*G*A*G*A*A*A*G*A*T*G*C*A*G*+T*+T*+T | 79106 | 19 |
| 2993 | TTGTGAGAAAGATGCAGTT | A572991H | +T*+T*+G*T*G*A*G*A*A*A*G*A*T*G*C*A*+G*+T*+T | 79107 | 19 |
| 2994 | TATTGTGAGAAAGATGCAG | A572992H | +T*+A*+T*T*G*T*G*A*G*A*A*A*G*A*T*G*+C*+A*+G | 79109 | 19 |
| 2995 | TCAGTTTATTGTGAGAAAG | A572993H | +T*+C*+A*G*T*T*T*A*T*T*G*T*G*A*G*A*+A*+A*+G | 79115 | 19 |
| 2996 | TCTTTCAGTTTATTGTGAG | A572994H | +T*+C*+T*T*T*C*A*G*T*T*T*A*T*T*G*T*+G*+A*+G | 79119 | 19 |
| 2997 | ATGCAAATCATAAAGTATA | A572995Hi | +A*+T*+G*C*A*A*A*T*C*A*T*A*A*A*G*T*+A*+T*+A | 79166 | 19 |
| 2998 | GATGCAAATCATAAAGTAT | A572996Hi | +G*+A*+T*G*C*A*A*A*T*C*A*T*A*A*A*G*+T*+A*+T | 79167 | 19 |
| 2999 | TGATGCAAATCATAAAGTA | A572997Hi | +T*+G*+A*T*G*C*A*A*A*T*C*A*T*A*A*A*+G*+T*+A | 79168 | 19 |
| 3000 | GAAGCTTCTAGTTTCATGA | A572998Hi | +G*+A*+A*G*C*T*T*C*T*A*G*T*T*T*C*A*+T*+G*+A | 79233 | 19 |
| 3001 | TAGTTAACAGGAAGCTTCT | A572999Hi | +T*+A*+G*T*T*A*A*C*A*G*G*A*A*G*C*T*+T*+C*+T | 79243 | 19 |
| 3002 | TTTATAGTTAACAGGAAGC | A573000Hi | +T*+T*+T*A*T*A*G*T*T*A*A*C*A*G*G*A*+A*+G*+C | 79247 | 19 |
| 3003 | AATTTATAGTTAACAGGAA | A573001Hi | +A*+A*+T*T*T*A*T*A*G*T*T*A*A*C*A*G*+G*+A*+A | 79249 | 19 |
| 3004 | GCTGTTTAGCTTTCAGATT | A573002Hi | +G*+C*+T*G*T*T*T*A*G*C*T*T*T*C*A*G*+A*+T*+T | 79455 | 19 |
| 3005 | AGCTGTTTAGCTTTCAGAT | A573003Hi | +A*+G*+C*T*G*T*T*T*A*G*C*T*T*T*C*A*+G*+A*+T | 79456 | 19 |
| 3006 | TAGCTGTTTAGCTTTCAGA | A573004Hi | +T*+A*+G*C*T*G*T*T*T*A*G*C*T*T*T*C*+A*+G*+A | 79457 | 19 |
| 3007 | TCTAGCTGTTTAGCTTTCA | A573005Hi | +T*+C*+T*A*G*C*T*G*T*T*T*A*G*C*T*T*+T*+C*+A | 79459 | 19 |
| 3008 | ATCTAGCTGTTTAGCTTTC | A573006Hi | +A*+T*+C*T*A*G*C*T*G*T*T*T*A*G*C*T*+T*+T*+C | 79460 | 19 |
| 3009 | TTATATCTAGCTGTTTAGC | A573007Hi | +T*+T*+A*T*A*T*C*T*A*G*C*T*G*T*T*T*+A*+G*+C | 79464 | 19 |
| 3010 | TATATCTAGCTGTTTAGC | A573008Hi | +T*+A*+T*A*T*C*T*A*G*C*T*G*T*T*T*+A*+G*+C | 79464 | 18 |
| 3011 | ATTTATATCTAGCTGTTTA | A573009Hi | +A*+T*+T*T*A*T*A*T*C*T*A*G*C*T*G*T*+T*+T*+A | 79466 | 19 |
| 3012 | TACTTTGTACAAATGTTGG | A573010Hi | +T*+A*+C*T*T*T*G*T*A*C*A*A*A*T*G*T*+T*+G*+G | 79493 | 19 |
| 3013 | TTACTTTGTACAAATGTTG | A573011Hi | +T*+T*+A*C*T*T*T*G*T*A*C*A*A*A*T*G*+T*+T*+G | 79494 | 19 |
| 3014 | TATGTTATATGATAACATC | A573012Hi | +T*+A*+T*G*T*T*A*T*A*T*G*A*T*A*A*C*+A*+T*+C | 79546 | 19 |
| 3015 | CATAGTTAAGTAACAGTTA | A573013Hi | +C*+A*+T*A*G*T*T*A*A*G*T*A*A*C*A*G*+T*+T*+A | 79589 | 19 |
| 3016 | TTTGTCATAGTTAAGTAAC | A573014Hi | +T*+T*+T*G*T*C*A*T*A*G*T*T*A*A*G*T*+A*+A*+C | 79594 | 19 |
| 3017 | TGAGCTAGTACTATAAAG | A573015Hi | +T*+G*+A*G*C*T*A*G*T*A*C*T*A*T*A*+A*+A*+G | 79663 | 18 |
| 3018 | TTATGAGCTAGTACTATAA | A573016Hi | +T*+T*+A*T*G*A*G*C*T*A*G*T*A*C*T*A*+T*+A*+A | 79665 | 19 |
| 3019 | TTTATGAGCTAGTACTATA | A573017Hi | +T*+T*+T*A*T*G*A*G*C*T*A*G*T*A*C*T*+A*+T*+A | 79666 | 19 |
| 3020 | TCTTTATGAGCTAGTACTA | A573018Hi | +T*+C*+T*T*T*A*T*G*A*G*C*T*A*G*T*A*+C*+T*+A | 79668 | 19 |

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| 3021 | CACTCTTTATGAGCTAGTA | A573019Hi | +C*+A*+C*T*C*T*T*T*A*T*G*A*G*C*T*A*+G*+T*+A | 79671 | 19 |
| 3022 | CACTCTTTATGAGCTAGT | A573020Hi | +C*+A*+C*T*C*T*T*T*A*T*G*A*G*C*T*+A*+G*+T | 79672 | 18 |
| 3023 | ACTATTCCATAGAACACTC | A573021Hi | +A*+C*+T*A*T*T*C*C*A*T*A*G*A*A*C*A*+C*+T*+C | 79685 | 19 |
| 3024 | GATATTTACAATGCTTATT | A573022Hi | +G*+A*+T*A*T*T*T*A*C*A*A*T*G*C*T*T*+A*+T*+T | 79735 | 19 |
| 3025 | GATACAATGACACACAGCA | A573023Hi | +G*+A*+T*A*C*A*A*T*G*A*C*A*C*A*C*A*+G*+C*+A | 79910 | 19 |
| 3026 | TGATACAATGACACACAGC | A573024Hi | +T*+G*+A*T*A*C*A*A*T*G*A*C*A*C*A*C*+A*+G*+C | 79911 | 19 |
| 3027 | GTTAACAGATTGGACAGAG | A573025Hi | +G*+T*+T*A*A*C*A*G*A*T*T*G*G*A*C*A*+G*+A*+G | 79936 | 19 |
| 3028 | CTGTTAACAGATTGGACAG | A573026Hi | +C*+T*+G*T*T*A*A*C*A*G*A*T*T*G*G*A*+C*+A*+G | 79938 | 19 |
| 3029 | TCTGTTAACAGATTGGACA | A573027Hi | +T*+C*+T*G*T*T*A*A*C*A*G*A*T*T*G*G*+A*+C*+A | 79939 | 19 |
| 3030 | GAGTCTGTTAACAGATTGG | A573028Hi | +G*+A*+G*T*C*T*G*T*T*A*A*C*A*G*A*T*+T*+G*+G | 79942 | 19 |
| 3031 | AGAGTCTGTTAACAGATTG | A573029Hi | +A*+G*+A*G*T*C*T*G*T*T*A*A*C*A*G*A*+T*+T*+G | 79943 | 19 |
| 3032 | GAGTCTGTTAACAGATTG | A573030Hi | +G*+A*+G*T*C*T*G*T*T*A*A*C*A*G*A*+T*+T*+G | 79943 | 18 |
| 3033 | AAGAGTCTGTTAACAGATT | A573031Hi | +A*+A*+G*A*G*T*C*T*G*T*T*A*A*C*A*G*+A*+T*+T | 79944 | 19 |
| 3034 | AGAAATTTAAGAATGTACC | A573032Hi | +A*+G*+A*A*A*T*T*T*A*A*G*A*A*T*G*T*+A*+C*+C | 80030 | 19 |
| 3035 | CTCACAGTGTCAGACACTT | A573033Hi | +C*+T*+C*A*C*A*G*T*G*T*C*A*G*A*C*A*+C*+T*+T | 80200 | 19 |
| 3036 | AAACCTGCATGCAATTTAG | A573034Hi | +A*+A*+A*C*C*T*G*C*A*T*G*C*A*A*T*T*+T*+A*+G | 80385 | 19 |
| 3037 | ACTACAAACCTGCATGCAA | A573035Hi | +A*+C*+T*A*C*A*A*A*C*C*T*G*C*A*T*G*+C*+A*+A | 80390 | 19 |
| 3038 | CTGCTCCTTCAGTAAAGG | A573036Hi | +C*+T*+G*C*T*C*C*T*T*C*A*G*T*A*A*+A*+G*+G | 80424 | 18 |
| 3039 | CATTCTGCTCCTTCAGTAA | A573037Hi | +C*+A*+T*T*C*T*G*C*T*C*C*T*T*C*A*G*+T*+A*+A | 80427 | 19 |
| 3040 | TCATTCTGCTCCTTCAGTA | A573038Hi | +T*+C*+A*T*T*C*T*G*C*T*C*C*T*T*C*A*+G*+T*+A | 80428 | 19 |
| 3041 | CATTGAAAGTAAGGAAGTT | A573039Hi | +C*+A*+T*T*G*A*A*A*G*T*A*A*G*G*A*A*+G*+T*+T | 80487 | 19 |
| 3042 | CATTGAAAGTAAGGAAGT | A573040Hi | +C*+A*+T*T*G*A*A*A*G*T*A*A*G*G*A*+A*+G*+T | 80488 | 18 |
| 3043 | CTTCATCTCTTCAAGACAT | A573041Hi | +C*+T*+T*C*A*T*C*T*C*T*T*C*A*A*G*A*+C*+A*+T | 80503 | 19 |
| 3044 | ACATACTTCATCTCTTCAA | A573042Hi | +A*+C*+A*T*A*C*T*T*C*A*T*C*T*C*T*T*+C*+A*+A | 80508 | 19 |
| 3045 | ACATACTTCATCTCTTCA | A573043Hi | +A*+C*+A*T*A*C*T*T*C*A*T*C*T*C*T*+T*+C*+A | 80509 | 18 |
| 3046 | AGTTGTCAGTATGTGTTT | A573044Hi | +A*+G*+T*T*G*T*C*A*G*T*A*T*G*T*G*+T*+T*+T | 80616 | 18 |
| 3047 | TGTCATAAGTTGTCAGTA | A573045Hi | +T*+G*+T*C*A*T*A*A*G*T*T*G*T*C*A*+G*+T*+A | 80623 | 18 |
| 3048 | TTTGTCATAAGTTGTCAGT | A573046Hi | +T*+T*+T*G*T*C*A*T*A*A*G*T*T*G*T*C*+A*+G*+T | 80624 | 19 |
| 3049 | TTTGTCATAAGTTGTCAG | A573047Hi | +T*+T*+T*G*T*C*A*T*A*A*G*T*T*G*T*+C*+A*+G | 80625 | 18 |
| 3050 | GGTTTGTCATAAGTTGTC | A573048Hi | +G*+G*+T*T*T*G*T*C*A*T*A*A*G*T*T*+G*+T*+C | 80627 | 18 |
| 3051 | AAGGTTTGTCATAAGTTG | A573049Hi | +A*+A*+G*G*T*T*T*G*T*C*A*T*A*A*G*+T*+T*+G | 80629 | 18 |
| 3052 | TTTCCAAAGGTTTGTCATA | A573050Hi | +T*+T*+T*C*C*A*A*A*G*G*T*T*T*G*T*C*+A*+T*+A | 80634 | 19 |
| 3053 | GATTCCATCAGCAGCTTGC | A573051Hi | +G*+A*+T*T*C*C*A*T*C*A*G*C*A*G*C*T*+T*+G*+C | 80679 | 19 |
| 3054 | GATTCCATCAGCAGCTTG | A573052Hi | +G*+A*+T*T*C*C*A*T*C*A*G*C*A*G*C*+T*+T*+G | 80680 | 18 |
| 3055 | AGATTCCATCAGCAGCTTG | A573053Hi | +A*+G*+A*T*T*C*C*A*T*C*A*G*C*A*G*C*+T*+T*+G | 80680 | 19 |

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| 3056 | CAGATTCCATCAGCA GCTT | A573054Hi | +C*+A*+G*A*T*T*C*C*A*T*C*A*G*C*A*G*+ C*+T*+T | 80681 | 19 |
| 3057 | AGATTCCATCAGCAG CTT | A573055Hi | +A*+G*+A*T*T*C*C*A*T*C*A*G*C*A*G*+C* +T*+T | 80681 | 18 |
| 3058 | CACAGATTCCATCAG CAGC | A573056Hi | +C*+A*+C*A*G*A*T*T*C*C*A*T*C*A*G*C*+ A*+G*+C | 80683 | 19 |
| 3059 | GCTCACAGATTCCAT CAGC | A573057Hi | +G*+C*+T*C*A*C*A*G*A*T*T*C*C*A*T*C*+ A*+G*+C | 80686 | 19 |
| 3060 | GGCTCACAGATTCCA TCAG | A573058Hi | +G*+G*+C*T*C*A*C*A*G*A*T*T*C*C*A*T*+ C*+A*+G | 80687 | 19 |
| 3061 | GCTCACAGATTCCAT CAG | A573059Hi | +G*+C*+T*C*A*C*A*G*A*T*T*C*C*A*T*+C* +A*+G | 80687 | 18 |
| 3062 | AGAAAGGCTCACAGA TTCC | A573060Hi | +A*+G*+A*A*A*G*G*C*T*C*A*C*A*G*A*T*+ T*+C*+C | 80692 | 19 |
| 3063 | AAACAAGAAAGGCTC ACAG | A573061Hi | +A*+A*+A*C*A*A*G*A*A*A*G*G*C*T*C*A*+ C*+A*+G | 80697 | 19 |
| 3064 | GAAACAAGAAAGGCT CACA | A573062Hi | +G*+A*+A*A*C*A*A*G*A*A*A*G*G*C*T*C*+ A*+C*+A | 80698 | 19 |
| 3065 | AGCCAATCTCAGGAG GAAT | A573063H | +A*+G*+C*C*A*A*T*C*T*C*A*G*G*A*G*G*+ A*+A*+T | 80789 | 19 |
| 3066 | CAGCCAATCTCAGGA GGAA | A573064H | +C*+A*+G*C*C*A*A*T*C*T*C*A*G*G*A*G*+ G*+A*+A | 80790 | 19 |
| 3067 | AAGACAGCCAATCTC AGGA | A573065H | +A*+A*+G*A*C*A*G*C*C*A*A*T*C*T*C*A*+ G*+G*+A | 80794 | 19 |
| 3068 | CAAGACAGCCAATCT CAGG | A573066H | +C*+A*+A*G*A*C*A*G*C*C*A*A*T*C*T*C*+ A*+G*+G | 80795 | 19 |
| 3069 | TCAAGACAGCCAATC TCAG | A573067H | +T*+C*+A*A*G*A*C*A*G*C*C*A*A*T*C*T*+ C*+A*+G | 80796 | 19 |
| 3070 | TTTCAAGACAGCCAA TCTC | A573068H | +T*+T*+T*C*A*A*G*A*C*A*G*C*C*A*A*T*+ C*+T*+C | 80798 | 19 |
| 3071 | GATTTTCAAGACAGC CAAT | A573069H | +G*+A*+T*T*T*T*C*A*A*G*A*C*A*G*C*C*+ A*+A*+T | 80801 | 19 |
| 3072 | AGATTTTCAAGACAG CCAA | A573070H | +A*+G*+A*T*T*T*T*C*A*A*G*A*C*A*G*C*+ C*+A*+A | 80802 | 19 |
| 3073 | ATGTCAGATTTTCAA GACA | A573071H | +A*+T*+G*T*C*A*G*A*T*T*T*T*C*A*A*G*+ A*+C*+A | 80807 | 19 |
| 3074 | GATGTCAGATTTTCA AGAC | A573072H | +G*+A*+T*G*T*C*A*G*A*T*T*T*T*C*A*A*+ G*+A*+C | 80808 | 19 |
| 3075 | GAGATGTCAGATTTT CAAG | A573073H | +G*+A*+G*A*T*G*T*C*A*G*A*T*T*T*T*C*+ A*+A*+G | 80810 | 19 |
| 3076 | CTGACATCCAGAGAT GTCA | A573074H | +C*+T*+G*A*C*A*T*C*C*A*G*A*G*A*T*G*+ T*+C*+A | 80820 | 19 |
| 3077 | ACTGACATCCAGAGA TGTC | A573075H | +A*+C*+T*G*A*C*A*T*C*C*A*G*A*G*A*T*+ G*+T*+C | 80821 | 19 |
| 3078 | TTGTAACTGACATCC AGAG | A573076H | +T*+T*+G*T*A*A*C*T*G*A*C*A*T*C*C*A*+ G*+A*+G | 80826 | 19 |
| 3079 | GTTGTAACTGACATC CAGA | A573077H | +G*+T*+T*G*T*A*A*C*T*G*A*C*A*T*C*C*+ A*+G*+A | 80827 | 19 |
| 3080 | CAAGTTGTAACTGAC ATCC | A573078H | +C*+A*+A*G*T*T*G*T*A*A*C*T*G*A*C*A*+ T*+C*+C | 80830 | 19 |
| 3081 | CAAGTTGTAACTGAC ATC | A573079H | +C*+A*+A*G*T*T*G*T*A*A*C*T*G*A*C*+A* +T*+C | 80831 | 18 |
| 3082 | CCAAGTTGTAACTGA CATC | A573080H | +C*+C*+A*A*G*T*T*G*T*A*A*C*T*G*A*C*+ A*+T*+C | 80831 | 19 |
| 3083 | CCAAGTTGTAACTGA CAT | A573081H | +C*+C*+A*A*G*T*T*G*T*A*A*C*T*G*A*+C* +A*+T | 80832 | 18 |
| 3084 | TCCAAGTTGTAACTG ACAT | A573082H | +T*+C*+C*A*A*G*T*T*G*T*A*A*C*T*G*A*+ C*+A*+T | 80832 | 19 |
| 3085 | TTCCAAGTTGTAACT GACA | A573083H | +T*+T*+C*C*A*A*G*T*T*G*T*A*A*C*T*G*+ A*+C*+A | 80833 | 19 |
| 3086 | GTTCCAAGTTGTAAC TGAC | A573084H | +G*+T*+T*C*C*A*A*G*T*T*G*T*A*A*C*T*+ G*+A*+C | 80834 | 19 |
| 3087 | TTAGTTCCAAGTTGT AACT | A573085H | +T*+T*+A*G*T*T*C*C*A*A*G*T*T*G*T*A*+ A*+C*+T | 80837 | 19 |
| 3088 | GATCTTAGTTCCAAG TTGT | A573086H | +G*+A*+T*C*T*T*A*G*T*T*C*C*A*A*G*T*+ T*+G*+T | 80841 | 19 |
| 3089 | GGATCTTAGTTCCAA GTTG | A573087H | +G*+G*+A*T*C*T*T*A*G*T*T*C*C*A*A*G*+ T*+T*+G | 80842 | 19 |
| 3090 | AAGGATCTTAGTTCC AAGT | A573088H | +A*+A*+G*G*A*T*C*T*T*A*G*T*T*C*C*A*+ A*+G*+T | 80844 | 19 |

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| 3091 | GGGAAAGGATCTTAGTTCC | A573089H | +G*+G*+G*A*A*A*G*G*A*T*C*T*T*A*G*T*+T*+C*+C | 80848 | 19 |
| 3092 | CATTGGGAAAGGATCTTAG | A573090H | +C*+A*+T*T*G*G*G*A*A*A*G*G*A*T*C*T*+T*+A*+G | 80852 | 19 |
| 3093 | TTCATTGGGAAAGGATCTT | A573091H | +T*+T*+C*A*T*T*G*G*G*A*A*A*G*G*A*T*+C*+T*+T | 80854 | 19 |
| 3094 | TTTCATTGGGAAAGGATCT | A573092H | +T*+T*+T*C*A*T*T*G*G*G*A*A*A*G*G*A*+T*+C*+T | 80855 | 19 |
| 3095 | TTTCATTGGGAAAGGATC | A573093H | +T*+T*+T*C*A*T*T*G*G*G*A*A*A*G*G*+A*+T*+C | 80856 | 18 |
| 3096 | ATTTCATTGGGAAAGGATC | A573094H | +A*+T*+T*T*C*A*T*T*G*G*G*A*A*A*G*G*+A*+T*+C | 80856 | 19 |
| 3097 | ATATTTTGCTTAATTTCCC | A573095H | +A*+T*+A*T*T*T*T*G*C*T*T*A*A*T*T*T*+C*+C*+C | 80876 | 19 |
| 3098 | ATCCCATATTTTGCTTAAT | A573096H | +A*+T*+C*C*C*A*T*A*T*T*T*T*G*C*T*T*+A*+A*+T | 80881 | 19 |
| 3099 | GGAAGATCCCATATTTTGC | A573097H | +G*+G*+A*A*G*A*T*C*C*C*A*T*A*T*T*T*+T*+G*+C | 80886 | 19 |
| 3100 | CATCCAAAGGAAGATCCCA | A573098H | +C*+A*+T*C*C*A*A*A*G*G*A*A*G*A*T*C*+C*+C*+A | 80894 | 19 |
| 3101 | TTCATCCAAAGGAAGATCC | A573099H | +T*+T*+C*A*T*C*C*A*A*A*G*G*A*A*G*A*+T*+C*+C | 80896 | 19 |
| 3102 | GTTCATCCAAAGGAAGATC | A573100H | +G*+T*+T*C*A*T*C*C*A*A*A*G*G*A*A*G*+A*+T*+C | 80897 | 19 |
| 3103 | GCAGTTCATCCAAAGGAAG | A573101H | +G*+C*+A*G*T*T*C*A*T*C*C*A*A*A*G*G*+A*+A*+G | 80900 | 19 |
| 3104 | TACATCCTATATGTTTAAA | A573102H | +T*+A*+C*A*T*C*C*T*A*T*A*T*G*T*T*T*+A*+A*+A | 80933 | 19 |
| 3105 | CTTTGGCTTTACATCCTAT | A573103H | +C*+T*+T*T*G*G*C*T*T*T*A*C*A*T*C*C*+T*+A*+T | 80942 | 19 |
| 3106 | TCTTTGGCTTTACATCCTA | A573104H | +T*+C*+T*T*T*G*G*C*T*T*T*A*C*A*T*C*+C*+T*+A | 80943 | 19 |
| 3107 | ATGTCTTTGGCTTTACATC | A573105H | +A*+T*+G*T*C*T*T*T*G*G*C*T*T*T*A*C*+A*+T*+C | 80946 | 19 |
| 3108 | TGATGTCTTTGGCTTTACA | A573106H | +T*+G*+A*T*G*T*C*T*T*T*G*G*C*T*T*T*+A*+C*+A | 80948 | 19 |
| 3109 | ATGATGTCTTTGGCTTTAC | A573107H | +A*+T*+G*A*T*G*T*C*T*T*T*G*G*C*T*T*+T*+A*+C | 80949 | 19 |
| 3110 | GTCCATCAAAGTCACAGA | A573108Hi | +G*+T*+C*C*A*T*C*A*A*A*G*T*C*A*C*+A*+G*+A | 81026 | 18 |
| 3111 | CTCTACAGTGGCACCACAG | A573109Hi | +C*+T*+C*T*A*C*A*G*T*G*G*C*A*C*C*A*+C*+A*+G | 81134 | 19 |
| 3112 | TCTCTACAGTGGCACCACA | A573110Hi | +T*+C*+T*C*T*A*C*A*G*T*G*G*C*A*C*C*+A*+C*+A | 81135 | 19 |
| 3113 | TTTAAGATGTAAGAGGCAT | A573111Hi | +T*+T*+T*A*A*G*A*T*G*T*A*A*G*A*G*G*+C*+A*+T | 81345 | 19 |
| 3114 | GAGTAGATTACTCATCCT | A573112Hi | +G*+A*+G*T*A*G*A*T*T*A*C*T*C*A*T*+C*+C*+T | 81416 | 18 |
| 3115 | ACTGATCAAGGTGAGTAGA | A573113Hi | +A*+C*+T*G*A*T*C*A*A*G*G*T*G*A*G*T*+A*+G*+A | 81427 | 19 |
| 3116 | ACTGATCAAGGTGAGTAG | A573114Hi | +A*+C*+T*G*A*T*C*A*A*G*G*T*G*A*G*+T*+A*+G | 81428 | 18 |
| 3117 | ACAGTGATACTTGAGAAGT | A573115Hi | +A*+C*+A*G*T*G*A*T*A*C*T*T*G*A*G*A*+A*+G*+T | 81461 | 19 |
| 3118 | CAGTGATACTTGAGAAGT | A573116Hi | +C*+A*+G*T*G*A*T*A*C*T*T*G*A*G*A*+A*+G*+T | 81461 | 18 |
| 3119 | AACAGTGATACTTGAGAAG | A573117Hi | +A*+A*+C*A*G*T*G*A*T*A*C*T*T*G*A*G*+A*+A*+G | 81462 | 19 |
| 3120 | AGACCAGAAACAGTGATAC | A573118Hi | +A*+G*+A*C*C*A*G*A*A*A*C*A*G*T*G*A*+T*+A*+C | 81470 | 19 |
| 3121 | AAGACCAGAAACAGTGATA | A573119Hi | +A*+A*+G*A*C*C*A*G*A*A*A*C*A*G*T*G*+A*+T*+A | 81471 | 19 |
| 3122 | AAAGACCAGAAACAGTGAT | A573120Hi | +A*+A*+A*G*A*C*C*A*G*A*A*A*C*A*G*T*+G*+A*+T | 81472 | 19 |
| 3123 | GTAAAGACCAGAAACAGTG | A573121Hi | +G*+T*+A*A*A*G*A*C*C*A*G*A*A*A*C*A*+G*+T*+G | 81474 | 19 |
| 3124 | TGAGAAAGTAATAAGACC | A573122Hi | +T*+G*+A*G*A*A*A*G*T*A*A*T*A*A*G*+A*+C*+C | 81560 | 18 |
| 3125 | ATGAGAAAGTAATAAGACC | A573123Hi | +A*+T*+G*A*G*A*A*A*G*T*A*A*T*A*A*G*+A*+C*+C | 81560 | 19 |

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| 3126 | TTTATGAGAAAGTAATAAG | A573124Hi | +T*+T*+T*A*T*G*A*G*A*A*A*G*T*A*A*T*+A*+A*+G | 81563 | 19 |
| 3127 | TTACAGTCAAGTTGAGAGG | A573125Hi | +T*+T*+A*C*A*G*T*C*A*A*G*T*T*G*A*G*+A*+G*+G | 81643 | 19 |
| 3128 | GATATTACAGTCAAGTTGA | A573126Hi | +G*+A*+T*A*T*T*A*C*A*G*T*C*A*A*G*T*+T*+G*+A | 81647 | 19 |
| 3129 | AATCACTGGTAATTAAACA | A573127Hi | +A*+A*+T*C*A*C*T*G*G*T*A*A*T*T*A*A*+A*+C*+A | 81748 | 19 |
| 3130 | CTACTAAATGTTTAGTAAG | A573128Hi | +C*+T*+A*C*T*A*A*A*T*G*T*T*T*A*G*T*+A*+A*+G | 81984 | 19 |
| 3131 | CTAGTTCTACTAAATGTTT | A573129Hi | +C*+T*+A*G*T*T*C*T*A*C*T*A*A*A*T*G*+T*+T*+T | 81990 | 19 |
| 3132 | GCTAGTTCTACTAAATGTT | A573130Hi | +G*+C*+T*A*G*T*T*C*T*A*C*T*A*A*A*T*+G*+T*+T | 81991 | 19 |
| 3133 | ATAAACTATTATACTATCA | A573131Hi | +A*+T*+A*A*A*C*T*A*T*T*A*T*A*C*T*A*+T*+C*+A | 82514 | 19 |
| 3134 | CAAAGTCCATATGACATAG | A573132Hi | +C*+A*+A*A*G*T*C*C*A*T*A*T*G*A*C*A*+T*+A*+G | 82717 | 19 |
| 3135 | CACAAAGTCCATATGACA | A573133Hi | +C*+A*+C*A*A*A*G*T*C*C*A*T*A*T*G*+A*+C*+A | 82720 | 18 |
| 3136 | TCACAAAGTCCATATGACA | A573134Hi | +T*+C*+A*C*A*A*A*G*T*C*C*A*T*A*T*G*+A*+C*+A | 82720 | 19 |
| 3137 | TAGAATACGATATGCAATA | A573135Hi | +T*+A*+G*A*A*T*A*C*G*A*T*A*T*G*C*A*+A*+T*+A | 83172 | 19 |
| 3138 | TAGAATACGATATGCAAT | A573136Hi | +T*+A*+G*A*A*T*A*C*G*A*T*A*T*G*C*+A*+A*+T | 83173 | 18 |
| 3139 | TTAGAATACGATATGCAA | A573137Hi | +T*+T*+A*G*A*A*T*A*C*G*A*T*A*T*G*+C*+A*+A | 83174 | 18 |
| 3140 | TAATTAGAATACGATATG | A573138Hi | +T*+A*+A*T*T*A*G*A*A*T*A*C*G*A*T*+A*+T*+G | 83177 | 18 |
| 3141 | CTAATTAGAATACGATATG | A573139Hi | +C*+T*+A*A*T*T*A*G*A*A*T*A*C*G*A*T*+A*+T*+G | 83177 | 19 |
| 3142 | CTAATTAGAATACGATAT | A573140Hi | +C*+T*+A*A*T*T*A*G*A*A*T*A*C*G*A*+T*+A*+T | 83178 | 18 |
| 3143 | ACTAATTAGAATACGATAT | A573141Hi | +A*+C*+T*A*A*T*T*A*G*A*A*T*A*C*G*A*+T*+A*+T | 83178 | 19 |
| 3144 | GTACTGTTAATGCATATAT | A573142Hi | +G*+T*+A*C*T*G*T*T*A*A*T*G*C*A*T*A*+T*+A*+T | 83302 | 19 |
| 3145 | TGTACATGTCTTTCAGAGT | A573143Hi | +T*+G*+T*A*C*A*T*G*T*C*T*T*T*T*C*A*G*+A*+G*+T | 83319 | 19 |
| 3146 | ATGTACATGTCTTTCAGAG | A573144Hi | +A*+T*+G*T*A*C*A*T*G*T*C*T*T*T*T*C*A*+G*+A*+G | 83320 | 19 |
| 3147 | AATAATGTACATGTCTTTC | A573145Hi | +A*+A*+T*A*A*T*G*T*A*C*A*T*G*T*C*T*+T*+T*+C | 83324 | 19 |
| 3148 | AGATTTAGGTGAGTTCTTT | A573146Hi | +A*+G*+A*T*T*T*A*G*G*T*G*A*G*T*T*C*+T*+T*+T | 83400 | 19 |
| 3149 | AAGTTTCATTCGGTTATA | A573147H | +A*+A*+G*T*T*T*C*A*T*T*C*G*G*T*T*T*+A*+T*+A | 83505 | 18 |
| 3150 | TAAGTTTCATTCGGTTATA | A573148H | +T*+A*+A*G*T*T*T*C*A*T*T*C*G*G*T*T*T*+A*+T*+A | 83505 | 19 |
| 3151 | ATAAGTTTCATTCGGTTAT | A573149H | +A*+T*+A*A*G*T*T*T*C*A*T*T*C*G*G*T*T*+T*+A*+T | 83506 | 19 |
| 3152 | ATAAGTTTCATTCGGTTA | A573150H | +A*+T*+A*A*G*T*T*T*C*A*T*T*C*G*G*+T*+T*+A | 83507 | 18 |
| 3153 | CATAAGTTTCATTCGGTTA | A573151H | +C*+A*+T*A*A*G*T*T*T*C*A*T*T*C*G*G*+T*+T*+A | 83507 | 19 |
| 3154 | TTTACCACTCCCAGTATTT | A573152H | +T*+T*+T*A*C*C*A*C*T*C*C*C*A*G*T*A*+T*+T*+T | 83534 | 19 |
| 3155 | TTTACCACTCCCAGTATT | A573153H | +T*+T*+T*A*C*C*A*C*T*C*C*C*A*G*T*+A*+T*+T | 83535 | 18 |
| 3156 | TTTTACCACTCCCAGTATT | A573154H | +T*+T*+T*T*A*C*C*A*C*T*C*C*C*A*G*T*+A*+T*+T | 83535 | 19 |
| 3157 | GTTTTACCACTCCCAGTAT | A573155H | +G*+T*+T*T*T*A*C*C*A*C*T*C*C*C*A*G*+T*+A*+T | 83536 | 19 |
| 3158 | GTTTTACCACTCCCAGTA | A573156H | +G*+T*+T*T*T*A*C*C*A*C*T*C*C*C*A*+G*+T*+A | 83537 | 18 |
| 3159 | GGTTTTACCACTCCCAGTA | A573157H | +G*+G*+T*T*T*T*A*C*C*A*C*T*C*C*C*A*+G*+T*+A | 83537 | 19 |
| 3160 | TGGTTTTACCACTCCCAGT | A573158H | +T*+G*+G*T*T*T*T*A*C*C*A*C*T*C*C*C*+A*+G*+T | 83538 | 19 |

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| 3161 | GTGGTTTTACCACTCCCAG | A573159H | +G*+T*+G*G*T*T*T*T*A*C*C*A*C*T*C*C*+C*+A*+G | 83539 | 19 |
| 3162 | GGTGGTTTTACCACTCCCA | A573160H | +G*+G*+T*G*G*T*T*T*T*A*C*C*A*C*T*C*+C*+C*+A | 83540 | 19 |
| 3163 | GGTGGTTTTACCACTCCC | A573161H | +G*+G*+T*G*G*T*T*T*T*A*C*C*A*C*T*+C*+C*+C | 83541 | 18 |
| 3164 | AGGTGGTTTTACCACTCCC | A573162H | +A*+G*+G*T*G*G*T*T*T*T*A*C*C*A*C*T*+C*+C*+C | 83541 | 19 |
| 3165 | AGGTGGTTTTACCACTCC | A573163H | +A*+G*+G*T*G*G*T*T*T*T*A*C*C*A*C*+T*+C*+C | 83542 | 18 |
| 3166 | AAGGTGGTTTTACCACTCC | A573164H | +A*+A*+G*G*T*G*G*T*T*T*T*A*C*C*A*C*+T*+C*+C | 83542 | 19 |
| 3167 | CTTGGTTTTCATTAATTGC | A573165H | +C*+T*+T*G*G*T*T*T*T*C*A*T*T*A*A*T*+T*+G*+C | 83567 | 19 |
| 3168 | TCTTGGTTTTCATTAATTG | A573166H | +T*+C*+T*T*G*G*T*T*T*T*C*A*T*T*A*A*+T*+T*+G | 83568 | 19 |
| 3169 | CAAGATCTGATTTCTTGGT | A573167H | +C*+A*+A*G*A*T*C*T*G*A*T*T*T*C*T*T*+G*+G*+T | 83580 | 19 |
| 3170 | TGCATTCCAAGATCTGATT | A573168H | +T*+G*+C*A*T*T*C*C*A*A*G*A*T*C*T*G*+A*+T*+T | 83587 | 19 |
| 3171 | ACTTTGCATTCCAAGATCT | A573169H | +A*+C*+T*T*T*G*C*A*T*T*C*C*A*A*G*A*+T*+C*+T | 83591 | 19 |
| 3172 | GCACTTTGCATTCCAAGAT | A573170H | +G*+C*+A*C*T*T*T*G*C*A*T*T*C*C*A*A*+G*+A*+T | 83593 | 19 |
| 3173 | GGCACTTTGCATTCCAAGA | A573171H | +G*+G*+C*A*C*T*T*T*G*C*A*T*T*C*C*A*+A*+G*+A | 83594 | 19 |
| 3174 | GGCACTTTGCATTCCAAG | A573172H | +G*+G*+C*A*C*T*T*T*G*C*A*T*T*C*C*+A*+A*+G | 83595 | 18 |
| 3175 | TGGCACTTTGCATTCCAAG | A573173H | +T*+G*+G*C*A*C*T*T*T*G*C*A*T*T*C*C*+A*+A*+G | 83595 | 19 |
| 3176 | TGCCAACTGTGGCACTTTG | A573174H | +T*+G*+C*C*A*A*C*T*G*T*G*G*C*A*C*T*+T*+T*+G | 83604 | 19 |
| 3177 | ATGCCAACTGTGGCACTTT | A573175H | +A*+T*+G*C*C*A*A*C*T*G*T*G*G*C*A*C*+T*+T*+T | 83605 | 19 |
| 3178 | TATGCCAACTGTGGCACTT | A573176H | +T*+A*+T*G*C*C*A*A*C*T*G*T*G*G*C*A*+C*+T*+T | 83606 | 19 |
| 3179 | CTATGCCAACTGTGGCACT | A573177H | +C*+T*+A*T*G*C*C*A*A*C*T*G*T*G*G*C*+A*+C*+T | 83607 | 19 |
| 3180 | CTATGCCAACTGTGGCAC | A573178H | +C*+T*+A*T*G*C*C*A*A*C*T*G*T*G*G*+C*+A*+C | 83608 | 18 |
| 3181 | TCTATGCCAACTGTGGCAC | A573179H | +T*+C*+T*A*T*G*C*C*A*A*C*T*G*T*G*G*+C*+A*+C | 83608 | 19 |
| 3182 | ATCTATGCCAACTGTGGCA | A573180H | +A*+T*+C*T*A*T*G*C*C*A*A*C*T*G*T*G*+G*+C*+A | 83609 | 19 |
| 3183 | CATCTATGCCAACTGTGGC | A573181H | +C*+A*+T*C*T*A*T*G*C*C*A*A*C*T*G*T*+G*+G*+C | 83610 | 19 |
| 3184 | CATCTATGCCAACTGTGG | A573182H | +C*+A*+T*C*T*A*T*G*C*C*A*A*C*T*G*+T*+G*+G | 83611 | 18 |
| 3185 | ACATCTATGCCAACTGTGG | A573183H | +A*+C*+A*T*C*T*A*T*G*C*C*A*A*C*T*G*+T*+G*+G | 83611 | 19 |
| 3186 | CACATCTATGCCAACTGTG | A573184H | +C*+A*+C*A*T*C*T*A*T*G*C*C*A*A*C*T*+G*+T*+G | 83612 | 19 |
| 3187 | CACATCTATGCCAACTGT | A573185H | +C*+A*+C*A*T*C*T*A*T*G*C*C*A*A*C*+T*+G*+T | 83613 | 18 |
| 3188 | TCACATCTATGCCAACTGT | A573186H | +T*+C*+A*C*A*T*C*T*A*T*G*C*C*A*A*C*+T*+G*+T | 83613 | 19 |
| 3189 | TTCACATCTATGCCAACTG | A573187H | +T*+T*+C*A*C*A*T*C*T*A*T*G*C*C*A*A*+C*+T*+G | 83614 | 19 |
| 3190 | CCAGTCTTTCACATCTATG | A573188H | +C*+C*+A*G*T*C*T*T*T*C*A*C*A*T*C*T*+A*+T*+G | 83621 | 19 |
| 3191 | CCAGTCTTTCACATCTAT | A573189H | +C*+C*+A*G*T*C*T*T*T*C*A*C*A*T*C*+T*+A*+T | 83622 | 18 |
| 3192 | GCCAGTCTTTCACATCTAT | A573190H | +G*+C*+C*A*G*T*C*T*T*T*C*A*C*A*T*T*C*+T*+A*+T | 83622 | 19 |
| 3193 | GGCCAGTCTTTCACATCTA | A573191H | +G*+G*+C*C*A*G*T*C*T*T*T*C*A*C*A*T*+C*+T*+A | 83623 | 19 |
| 3194 | AGGCCAGTCTTTCACATCT | A573192H | +A*+G*+G*C*C*A*G*T*C*T*T*T*C*A*C*A*+T*+C*+T | 83624 | 19 |
| 3195 | TGGATAGGCCAGTCTTTCA | A573193H | +T*+G*+G*A*T*A*G*G*C*C*A*G*T*C*T*T*+T*+C*+A | 83629 | 19 |

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| 3196 | TTGGATAGGCCAGTC TTTC | A573194H | +T*+T*+G*G*A*T*A*G*G*C*C*A*G*T*C*T*+ T*+T*+C | 83630 | 19 |
| 3197 | TTGGATAGGCCAGTC TTT | A573195H | +T*+T*+G*G*A*T*A*G*G*C*C*A*G*T*C*+T* +T*+T | 83631 | 18 |
| 3198 | TTTGGATAGGCCAGT CTTT | A573196H | +T*+T*+T*G*G*A*T*A*G*G*C*C*A*G*T*C*+ T*+T*+T | 83631 | 19 |
| 3199 | ATTTGGATAGGCCAG TCTT | A573197H | +A*+T*+T*T*G*G*A*T*A*G*G*C*C*A*G*T*+ C*+T*+T | 83632 | 19 |
| 3200 | ATTTGGATAGGCCAG TCT | A573198H | +A*+T*+T*T*G*G*A*T*A*G*G*C*C*A*G*+T* +C*+T | 83633 | 18 |
| 3201 | TATTTGGATAGGCCA GTCT | A573199H | +T*+A*+T*T*T*G*G*A*T*A*G*G*C*C*A*G*+ T*+C*+T | 83633 | 19 |
| 3202 | TTATTTGGATAGGCC AGTC | A573200H | +T*+T*+A*T*T*T*G*G*A*T*A*G*G*C*C*A*+ G*+T*+C | 83634 | 19 |
| 3203 | TTATTTGGATAGGCC AGT | A573201H | +T*+T*+A*T*T*T*G*G*A*T*A*G*G*C*C*+A* +G*+T | 83635 | 18 |
| 3204 | CTTATTTGGATAGGC CAGT | A573202H | +C*+T*+T*A*T*T*T*G*G*A*T*A*G*G*C*C*+ A*+G*+T | 83635 | 19 |
| 3205 | CTTATTTGGATAGGC CAG | A573203H | +C*+T*+T*A*T*T*T*G*G*A*T*A*G*G*C*+C* +A*+G | 83636 | 18 |
| 3206 | TCTTATTTGGATAGG CCAG | A573204H | +T*+C*+T*T*A*T*T*T*G*G*A*T*A*G*G*C*+ C*+A*+G | 83636 | 19 |
| 3207 | TCTTATTTGGATAGG CCA | A573205H | +T*+C*+T*T*A*T*T*T*G*G*A*T*A*G*G*+C* +C*+A | 83637 | 18 |
| 3208 | CTCTTATTTGGATAG GCCA | A573206H | +C*+T*+C*T*T*A*T*T*T*G*G*A*T*A*G*G*+ C*+C*+A | 83637 | 19 |
| 3209 | CTCTTATTTGGATAG GCC | A573207H | +C*+T*+C*T*T*A*T*T*T*G*G*A*T*A*G*+G* +C*+C | 83638 | 18 |
| 3210 | ACGAGATCTCTCTTT CTTT | A573208H | +A*+C*+G*A*G*A*T*C*T*C*T*C*T*T*T*C*+ T*+T*+T | 83659 | 19 |
| 3211 | CTGCAAAATCCCACA CATT | A573209H | +C*+T*+G*C*A*A*A*A*T*C*C*C*A*C*A*C*+ A*+T*+T | 83682 | 19 |
| 3212 | GTTTCTGGATATTAG AACA | A573210Hi | +G*+T*+T*T*C*T*G*G*A*T*A*T*T*A*G*A*+ A*+C*+A | 83775 | 19 |
| 3213 | CAGGTTTCTGGATAT TAGA | A573211Hi | +C*+A*+G*G*T*T*T*C*T*G*G*A*T*A*T*T*+ A*+G*+A | 83778 | 19 |
| 3214 | CAGGTTTCTGGATAT TAG | A573212Hi | +C*+A*+G*G*T*T*T*C*T*G*G*A*T*A*T*+T* +A*+G | 83779 | 18 |
| 3215 | TATTTAGCATACTAAT AAG | A573213Hi | +T*+A*+T*T*T*A*G*C*A*T*A*C*T*A*A*T*+ A*+A*+G | 83997 | 19 |
| 3216 | CGCTGCGTCATAAAA TG | A573214H | +C*+G*+C*T*G*C*G*T*C*A*T*A*A*A*+A*+T *+G | 84139 | 17 |
| 3217 | TCGCTGCGTCATAAA ATG | A573215H | +T*+C*+G*C*T*G*C*G*T*C*A*T*A*A*A*+A* +T*+G | 84139 | 18 |
| 3218 | TCGCTGCGTCATAAA AT | A573216H | +T*+C*+G*C*T*G*C*G*T*C*A*T*A*A*+A*+A *+T | 84140 | 17 |
| 3219 | GCTCGCTGCGTCATA AAAT | A573217H | +G*+C*+T*C*G*C*T*G*C*G*T*C*A*T*A*A*+ A*+A*+T | 84140 | 19 |
| 3220 | TCGCTGCGTCATAAA A | A573218H | +T*+C*+G*C*T*G*C*G*T*C*A*T*A*+A*+A*+ A | 84141 | 16 |
| 3221 | GCTCGCTGCGTCATA AAA | A573219H | +G*+C*+T*C*G*C*T*G*C*G*T*C*A*T*A*+A* +A*+A | 84141 | 18 |
| 3222 | TGCTCGCTGCGTCAT AAAA | A573220H | +T*+G*+C*T*C*G*C*T*G*C*G*T*C*A*T*A*+ A*+A*+A | 84141 | 19 |
| 3223 | GCTCGCTGCGTCATA AA | A573221H | +G*+C*+T*C*G*C*T*G*C*G*T*C*A*T*+A*+A *+A | 84142 | 17 |
| 3224 | TGCTCGCTGCGTCAT AAA | A573222H | +T*+G*+C*T*C*G*C*T*G*C*G*T*C*A*T*+A* +A*+A | 84142 | 18 |
| 3225 | ATGCTCGCTGCGTCA TAAA | A573223H | +A*+T*+G*C*T*C*G*C*T*G*C*G*T*C*A*T*+ A*+A*+A | 84142 | 19 |
| 3226 | GCTCGCTGCGTCATA A | A573224H | +G*+C*+T*C*G*C*T*G*C*G*T*C*A*+T*+A*+ A | 84143 | 16 |
| 3227 | TGCTCGCTGCGTCAT AA | A573225H | +T*+G*+C*T*C*G*C*T*G*C*G*T*C*A*+T*+A *+A | 84143 | 17 |
| 3228 | ATGCTCGCTGCGTCA TAA | A573226H | +A*+T*+G*C*T*C*G*C*T*G*C*G*T*C*A*+T* +A*+A | 84143 | 18 |
| 3229 | AATGCTCGCTGCGTC ATAA | A573227H | +A*+A*+T*G*C*T*C*G*C*T*G*C*G*T*C*A*+ T*+A*+A | 84143 | 19 |
| 3230 | AATGCTCGCTGCGTC ATA | A573228H | +A*+A*+T*G*C*T*C*G*C*T*G*C*G*T*C*+A* +T*+A | 84144 | 18 |

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| 3231 | CAATGCTCGCTGCGTCATA | A573229H | +C*+A*+A*T*G*C*T*C*G*C*T*G*C*G*T*C*+A*+T*+A | 84144 | 19 |
| 3232 | AATGCTCGCTGCGTCAT | A573230H | +A*+A*+T*G*C*T*C*G*C*T*G*C*G*T*+C*+A*+T | 84145 | 17 |
| 3233 | CAATGCTCGCTGCGTCAT | A573231H | +C*+A*+A*T*G*C*T*C*G*C*T*G*C*G*T*+C*+A*+T | 84145 | 18 |
| 3234 | ACAATGCTCGCTGCGTCAT | A573232H | +A*+C*+A*A*T*G*C*T*C*G*C*T*G*C*G*T*+C*+A*+T | 84145 | 19 |
| 3235 | CAATGCTCGCTGCGTCA | A573233H | +C*+A*+A*T*G*C*T*C*G*C*T*G*C*G*+T*+C*+A | 84146 | 17 |
| 3236 | ACAATGCTCGCTGCGTCA | A573234H | +A*+C*+A*A*T*G*C*T*C*G*C*T*G*C*G*+T*+C*+A | 84146 | 18 |
| 3237 | TACAATGCTCGCTGCGTCA | A573235H | +T*+A*+C*A*A*T*G*C*T*C*G*C*T*G*C*G*+T*+C*+A | 84146 | 19 |
| 3238 | TACAATGCTCGCTGCGTC | A573236H | +T*+A*+C*A*A*T*G*C*T*C*G*C*T*G*C*+G*+T*+C | 84147 | 18 |
| 3239 | GTACAATGCTCGCTGCGTC | A573237H | +G*+T*+A*C*A*A*T*G*C*T*C*G*C*T*G*C*+G*+T*+C | 84147 | 19 |
| 3240 | TACAATGCTCGCTGCGT | A573238H | +T*+A*+C*A*A*T*G*C*T*C*G*C*T*G*+C*+G*+T | 84148 | 17 |
| 3241 | GTACAATGCTCGCTGCGT | A573239H | +G*+T*+A*C*A*A*T*G*C*T*C*G*C*T*G*+C*+G*+T | 84148 | 18 |
| 3242 | GGTACAATGCTCGCTGCGT | A573240H | +G*+G*+T*A*C*A*A*T*G*C*T*C*G*C*T*G*+C*+G*+T | 84148 | 19 |
| 3243 | TACAATGCTCGCTGCG | A573241H | +T*+A*+C*A*A*T*G*C*T*C*G*C*T*+G*+C*+G | 84149 | 16 |
| 3244 | GTACAATGCTCGCTGCG | A573242H | +G*+T*+A*C*A*A*T*G*C*T*C*G*C*T*+G*+C*+G | 84149 | 17 |
| 3245 | GGTACAATGCTCGCTGCG | A573243H | +G*+G*+T*A*C*A*A*T*G*C*T*C*G*C*T*+G*+C*+G | 84149 | 18 |
| 3246 | AGGTACAATGCTCGCTGCG | A573244H | +A*+G*+G*T*A*C*A*A*T*G*C*T*C*G*C*T*+G*+C*+G | 84149 | 19 |
| 3247 | AGGTACAATGCTCGCTGC | A573245H | +A*+G*+G*T*A*C*A*A*T*G*C*T*C*G*C*+T*+G*+C | 84150 | 18 |
| 3248 | AAGGTACAATGCTCGCTGC | A573246H | +A*+A*+G*G*T*A*C*A*A*T*G*C*T*C*G*C*+T*+G*+C | 84150 | 19 |
| 3249 | AGGTACAATGCTCGCTG | A573247H | +A*+G*+G*T*A*C*A*A*T*G*C*T*C*G*+C*+T*+G | 84151 | 17 |
| 3250 | AAGGTACAATGCTCGCTG | A573248H | +A*+A*+G*G*T*A*C*A*A*T*G*C*T*C*G*+C*+T*+G | 84151 | 18 |
| 3251 | CAAGGTACAATGCTCGCTG | A573249H | +C*+A*+A*G*G*T*A*C*A*A*T*G*C*T*C*G*+C*+T*+G | 84151 | 19 |
| 3252 | AAGGTACAATGCTCGCT | A573250H | +A*+A*+G*G*T*A*C*A*A*T*G*C*T*C*+G*+C*+T | 84152 | 17 |
| 3253 | CAAGGTACAATGCTCGCT | A573251H | +C*+A*+A*G*G*T*A*C*A*A*T*G*C*T*C*+G*+C*+T | 84152 | 18 |
| 3254 | GCAAGGTACAATGCTCGCT | A573252H | +G*+C*+A*A*G*G*T*A*C*A*A*T*G*C*T*C*+G*+C*+T | 84152 | 19 |
| 3255 | AGCAAGGTACAATGCTCGC | A573253H | +A*+G*+C*A*A*G*G*T*A*C*A*A*T*G*C*T*+C*+G*+C | 84153 | 19 |
| 3256 | AGCAAGGTACAATGCTCG | A573254H | +A*+G*+C*A*A*G*G*T*A*C*A*A*T*G*C*+T*+C*+G | 84154 | 18 |
| 3257 | CAGCAAGGTACAATGCTCG | A573255H | +C*+A*+G*C*A*A*G*G*T*A*C*A*A*T*G*C*+T*+C*+G | 84154 | 19 |
| 3258 | ACAGCAAGGTACAATGCTC | A573256H | +A*+C*+A*G*C*A*A*G*G*T*A*C*A*A*T*G*+C*+T*+C | 84155 | 19 |
| 3259 | GACAGCAAGGTACAATGCT | A573257H | +G*+A*+C*A*G*C*A*A*G*G*T*A*C*A*A*T*+G*+C*+T | 84156 | 19 |
| 3260 | AGACAGCAAGGTACAATGC | A573258H | +A*+G*+A*C*A*G*C*A*A*G*G*T*A*C*A*A*+T*+G*+C | 84157 | 19 |
| 3261 | TAGACAGCAAGGTACAATG | A573259H | +T*+A*+G*A*C*A*G*C*A*A*G*G*T*A*C*A*+A*+T*+G | 84158 | 19 |
| 3262 | GTCATAGACAGCAAGGTAC | A573260H | +G*+T*+C*A*T*A*G*A*C*A*G*C*A*A*G*G*+T*+A*+C | 84162 | 19 |
| 3263 | GGTCATAGACAGCAAGGTA | A573261H | +G*+G*+T*C*A*T*A*G*A*C*A*G*C*A*A*G*+G*+T*+A | 84163 | 19 |
| 3264 | GGTCATAGACAGCAAGGT | A573262H | +G*+G*+T*C*A*T*A*G*A*C*A*G*C*A*A*+G*+G*+T | 84164 | 18 |
| 3265 | AGGTCATAGACAGCAAGGT | A573263H | +A*+G*+G*T*C*A*T*A*G*A*C*A*G*C*A*A*+G*+G*+T | 84164 | 19 |

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| 3266 | AGGTCATAGACAGCAAGG | A573264H | +A*+G*+G*T*C*A*T*A*G*A*C*A*G*C*A*+A*+G*+G | 84165 | 18 |
| 3267 | ATCAACTTCAGCCTGTCC | A573265H | +A*+T*+C*A*A*C*T*T*C*A*G*C*C*T*G*+T*+C*+C | 84190 | 18 |
| 3268 | CATCAACTTCAGCCTGTCC | A573266H | +C*+A*+T*C*A*A*C*T*T*C*A*G*C*C*T*G*+T*+C*+C | 84190 | 19 |
| 3269 | GCATCAACTTCAGCCTGTC | A573267H | +G*+C*+A*T*C*A*A*C*T*T*C*A*G*C*C*T*+G*+T*+C | 84191 | 19 |
| 3270 | GCATCAACTTCAGCCTGT | A573268H | +G*+C*+A*T*C*A*A*C*T*T*C*A*G*C*C*+T*+G*+T | 84192 | 18 |
| 3271 | GGCATCAACTTCAGCCTGT | A573269H | +G*+G*+C*A*T*C*A*A*C*T*T*C*A*G*C*C*+T*+G*+T | 84192 | 19 |
| 3272 | GGCATCAACTTCAGCCTG | A573270H | +G*+G*+C*A*T*C*A*A*C*T*T*C*A*G*C*+C*+T*+G | 84193 | 18 |
| 3273 | TGGCATCAACTTCAGCCTG | A573271H | +T*+G*+G*C*A*T*C*A*A*C*T*T*C*A*G*C*+C*+T*+G | 84193 | 19 |
| 3274 | TGGCATCAACTTCAGCCT | A573272H | +T*+G*+G*C*A*T*C*A*A*C*T*T*C*A*G*+C*+C*+T | 84194 | 18 |
| 3275 | ATGGCATCAACTTCAGCCT | A573273H | +A*+T*+G*G*C*A*T*C*A*A*C*T*T*C*A*G*+C*+C*+T | 84194 | 19 |
| 3276 | CATGGCATCAACTTCAGCC | A573274H | +C*+A*+T*G*G*C*A*T*C*A*A*C*T*T*C*A*+G*+C*+C | 84195 | 19 |
| 3277 | TCATGGCATCAACTTCAGC | A573275H | +T*+C*+A*T*G*G*C*A*T*C*A*A*C*T*T*C*+A*+G*+C | 84196 | 19 |
| 3278 | TTCATGGCATCAACTTCAG | A573276H | +T*+T*+C*A*T*G*G*C*A*T*C*A*A*C*T*T*+C*+A*+G | 84197 | 19 |
| 3279 | AGGCTTCATGGCATCAACT | A573277H | +A*+G*+G*C*T*T*C*A*T*G*G*C*A*T*C*A*+A*+C*+T | 84201 | 19 |
| 3280 | AAGGCTTCATGGCATCAAC | A573278H | +A*+A*+G*G*C*T*T*C*A*T*G*G*C*A*T*C*+A*+A*+C | 84202 | 19 |
| 3281 | AGCCAAGGCTTCATGGCAT | A573279H | +A*+G*+C*C*A*A*G*G*C*T*T*C*A*T*G*G*+C*+A*+T | 84206 | 19 |
| 3282 | AGCCAAGGCTTCATGGCA | A573280H | +A*+G*+C*C*A*A*G*G*C*T*T*C*A*T*G*+G*+C*+A | 84207 | 18 |
| 3283 | GAGCCAAGGCTTCATGGCA | A573281H | +G*+A*+G*C*C*A*A*G*G*C*T*T*C*A*T*G*+G*+C*+A | 84207 | 19 |
| 3284 | AGAGCCAAGGCTTCATGGC | A573282H | +A*+G*+A*G*C*C*A*A*G*G*C*T*T*C*A*T*+G*+G*+C | 84208 | 19 |
| 3285 | AAGAGCCAAGGCTTCATGG | A573283H | +A*+A*+G*A*G*C*C*A*A*G*G*C*T*T*C*A*+T*+G*+G | 84209 | 19 |
| 3286 | GAAGAGCCAAGGCTTCATG | A573284H | +G*+A*+A*G*A*G*C*C*A*A*G*G*C*T*T*C*+A*+T*+G | 84210 | 19 |
| 3287 | GAAGAGCCAAGGCTTCAT | A573285H | +G*+A*+A*G*A*G*C*C*A*A*G*G*C*T*T*+C*+A*+T | 84211 | 18 |
| 3288 | TGAAGAGCCAAGGCTTCAT | A573286H | +T*+G*+A*A*G*A*G*C*C*A*A*G*G*C*T*T*+C*+A*+T | 84211 | 19 |
| 3289 | TATTGAAGAGCCAAGGCTT | A573287H | +T*+A*+T*T*G*A*A*G*A*G*C*C*A*A*G*G*+C*+T*+T | 84214 | 19 |
| 3290 | TTATATTGAAGAGCCAAGG | A573288H | +T*+T*+A*T*A*T*T*G*A*A*G*A*G*C*C*A*+A*+G*+G | 84217 | 19 |
| 3291 | TTATATTGAAGAGCCAAG | A573289H | +T*+T*+A*T*A*T*T*G*A*A*G*A*G*C*C*+A*+A*+G | 84218 | 18 |
| 3292 | TTTATATTGAAGAGCCAAG | A573290H | +T*+T*+T*A*T*A*T*T*G*A*A*G*A*G*C*C*+A*+A*+G | 84218 | 19 |
| 3293 | CTTTATATTGAAGAGCCAA | A573291H | +C*+T*+T*T*A*T*A*T*T*G*A*A*G*A*G*C*+C*+A*+A | 84219 | 19 |
| 3294 | GACCACTTAAAGGATACAA | A573292Hi | +G*+A*+C*C*A*C*T*T*A*A*A*G*G*A*T*A*+C*+A*+A | 84643 | 19 |
| 3295 | ATAGCTGACAACAAGACAA | A573293Hi | +A*+T*+A*G*C*T*G*A*C*A*A*C*A*A*G*A*+C*+A*+A | 84724 | 19 |
| 3296 | GAAGAGTTCATTGCAGCAT | A573294Hi | +G*+A*+A*G*A*G*T*T*C*A*T*T*G*C*A*G*+C*+A*+T | 84795 | 19 |
| 3297 | AGAAGAGTTCATTGCAGCA | A573295Hi | +A*+G*+A*A*G*A*G*T*T*C*A*T*T*G*C*A*+G*+C*+A | 84796 | 19 |
| 3298 | CAGAAGAGTTCATTGCAGC | A573296Hi | +C*+A*+G*A*A*G*A*G*T*T*C*A*T*T*G*C*+A*+G*+C | 84797 | 19 |
| 3299 | GAGTCTACAATGAAAGAAT | A573297Hi | +G*+A*+G*T*C*T*A*C*A*A*T*G*A*A*A*G*+A*+A*+T | 84987 | 19 |
| 3300 | TATATCAAATTAACGTCAT | A573298Hi | +T*+A*+T*A*T*C*A*A*A*T*T*A*A*C*G*T*+C*+A*+T | 85076 | 19 |

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| 3301 | TTATATCAAATTAACGTCA | A573299Hi | +T*+T*+A*T*A*T*C*A*A*A*T*T*A*A*C*G*+T*+C*+A | 85077 | 19 |
| 3302 | TATATCAAATTAACGTCA | A573300Hi | +T*+A*+T*A*T*C*A*A*A*T*T*A*A*C*G*+T*+C*+A | 85077 | 18 |
| 3303 | AAATTATATCAAATTAACG | A573301Hi | +A*+A*+A*T*T*A*T*A*T*C*A*A*A*T*T*A*+A*+C*+G | 85080 | 19 |
| 3304 | GCTTTCCGTGACATTCAC | A573302Hi | +G*+C*+T*T*T*C*C*G*T*G*A*C*A*T*T*+C*+A*+C | 85345 | 18 |
| 3305 | TTGCTTTCCGTGACATTCA | A573303Hi | +T*+T*+G*C*T*T*T*C*C*G*T*G*A*C*A*T*+T*+C*+A | 85346 | 19 |
| 3306 | TGCTTTCCGTGACATTCA | A573304Hi | +T*+G*+C*T*T*T*C*C*G*T*G*A*C*A*T*+T*+C*+A | 85346 | 18 |
| 3307 | TTGCTTTCCGTGACATTC | A573305Hi | +T*+T*+G*C*T*T*T*C*C*G*T*G*A*C*A*+T*+T*+C | 85347 | 18 |
| 3308 | ATTTGCTTTCCGTGACATT | A573306Hi | +A*+T*+T*T*G*C*T*T*T*C*C*G*T*G*A*C*+A*+T*+T | 85348 | 19 |
| 3309 | GTTGATATTTGCTTTCCGT | A573307Hi | +G*+T*+T*G*A*T*A*T*T*T*G*C*T*T*T*C*+C*+G*+T | 85354 | 19 |
| 3310 | CTCACATTCCTGTTGATAT | A573308Hi | +C*+T*+C*A*C*A*T*T*C*C*T*G*T*T*G*A*+T*+A*+T | 85365 | 19 |
| 3311 | CTCACATTCCTGTTGATA | A573309Hi | +C*+T*+C*A*C*A*T*T*C*C*T*G*T*T*G*+A*+T*+A | 85366 | 18 |
| 3312 | GCTCACATTCCTGTTGAT | A573310Hi | +G*+C*+T*C*A*C*A*T*T*C*C*T*G*T*T*+G*+A*+T | 85367 | 18 |
| 3313 | GGCCTGCTCACATTCCTGT | A573311Hi | +G*+G*+C*C*T*G*C*T*C*A*C*A*T*T*C*C*+T*+G*+T | 85371 | 19 |
| 3314 | GGAAGAAGAAGCGCGAGC | A573312H | +G*+G*+A*A*G*A*A*G*A*A*G*C*G*C*G*+A*+G*+C | 85435 | 18 |
| 3315 | GGGAAGAAGAAGCGCGAGC | A573313H | +G*+G*+G*A*A*G*A*A*G*A*A*G*C*G*C*G*+A*+G*+C | 85435 | 19 |
| 3316 | GGGAAGAAGAAGCGCGAG | A573314H | +G*+G*+G*A*A*G*A*A*G*A*A*G*C*G*C*+G*+A*+G | 85436 | 18 |
| 3317 | GGGGAAGAAGAAGCGCGAG | A573315H | +G*+G*+G*G*A*A*G*A*A*G*A*A*G*C*G*C*+G*+A*+G | 85436 | 19 |
| 3318 | GGGAAGAAGAAGCGCGA | A573316H | +G*+G*+G*A*A*G*A*A*G*A*A*G*C*G*+C*+G*+A | 85437 | 17 |
| 3319 | GGGGAAGAAGAAGCGCGA | A573317H | +G*+G*+G*G*A*A*G*A*A*G*A*A*G*C*G*+C*+G*+A | 85437 | 18 |
| 3320 | AGGGGAAGAAGAAGCGCGA | A573318H | +A*+G*+G*G*G*A*A*G*A*A*G*A*A*G*C*G*+C*+G*+A | 85437 | 19 |
| 3321 | ACAGGGGAAGAAGAAGCGC | A573319H | +A*+C*+A*G*G*G*G*A*A*G*A*A*G*A*A*G*+C*+G*+C | 85439 | 19 |
| 3322 | TCACAGGGGAAGAAGAAGC | A573320H | +T*+C*+A*C*A*G*G*G*G*A*A*G*A*A*G*A*+A*+G*+C | 85441 | 19 |
| 3323 | AATCACAGGGGAAGAAGAA | A573321H | +A*+A*+T*C*A*C*A*G*G*G*G*A*A*G*A*A*+G*+A*+A | 85443 | 19 |
| 3324 | AACGAGAATCACAGGGGAA | A573322H | +A*+A*+C*G*A*G*A*A*T*C*A*C*A*G*G*G*+G*+A*+A | 85449 | 19 |
| 3325 | GTGCCAACGAGAATCACAG | A573323H | +G*+T*+G*C*C*A*A*C*G*A*G*A*A*T*C*A*+C*+A*+G | 85454 | 19 |
| 3326 | GTGCCAACGAGAATCACA | A573324H | +G*+T*+G*C*C*A*A*C*G*A*G*A*A*T*C*+A*+C*+A | 85455 | 18 |
| 3327 | TGTGCCAACGAGAATCACA | A573325H | +T*+G*+T*G*C*C*A*A*C*G*A*G*A*A*T*C*+A*+C*+A | 85455 | 19 |
| 3328 | GTGTGCCAACGAGAATCAC | A573326H | +G*+T*+G*T*G*C*C*A*A*C*G*A*G*A*A*T*+C*+A*+C | 85456 | 19 |
| 3329 | GTGTGCCAACGAGAATCA | A573327H | +G*+T*+G*T*G*C*C*A*A*C*G*A*G*A*A*+T*+C*+A | 85457 | 18 |
| 3330 | TGTGTGCCAACGAGAATCA | A573328H | +T*+G*+T*G*T*G*C*C*A*A*C*G*A*G*A*A*+T*+C*+A | 85457 | 19 |
| 3331 | AATGTGTGCCAACGAGAAT | A573329H | +A*+A*+T*G*T*G*T*G*C*C*A*A*C*G*A*G*+A*+A*+T | 85459 | 19 |
| 3332 | AAATGTGTGCCAACGAGAA | A573330H | +A*+A*+A*T*G*T*G*T*G*C*C*A*A*C*G*A*+G*+A*+A | 85460 | 19 |
| 3333 | AAATGTGTGCCAACGAGA | A573331H | +A*+A*+A*T*G*T*G*T*G*C*C*A*A*C*G*+A*+G*+A | 85461 | 18 |
| 3334 | CAAATGTGTGCCAACGAGA | A573332H | +C*+A*+A*A*T*G*T*G*T*G*C*C*A*A*C*G*+A*+G*+A | 85461 | 19 |
| 3335 | CAAATGTGTGCCAACGAG | A573333H | +C*+A*+A*A*T*G*T*G*T*G*C*C*A*A*C*+G*+A*+G | 85462 | 18 |

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| 3336 | CCAAATGTGTGCCAACGAG | A573334H | +C*+C*+A*A*A*T*G*T*G*T*G*C*C*A*A*C*+G*+A*+G | 85462 | 19 |
| 3337 | CCAAATGTGTGCCAACGA | A573335H | +C*+C*+A*A*A*T*G*T*G*T*G*C*C*A*A*+C*+G*+A | 85463 | 18 |
| 3338 | TCCAAATGTGTGCCAACGA | A573336H | +T*+C*+C*A*A*A*T*G*T*G*T*G*C*C*A*A*+C*+G*+A | 85463 | 19 |
| 3339 | TCCAAATGTGTGCCAACG | A573337H | +T*+C*+C*A*A*A*T*G*T*G*T*G*C*C*A*+A*+C*+G | 85464 | 18 |
| 3340 | ATCCAAATGTGTGCCAACG | A573338H | +A*+T*+C*C*A*A*A*T*G*T*G*T*G*C*C*A*+A*+C*+G | 85464 | 19 |
| 3341 | AGTTCCTTGGTGATTTTAC | A573339H | +A*+G*+T*T*C*C*T*T*G*G*T*G*A*T*T*T*+T*+A*+C | 85517 | 19 |
| 3342 | GGAGTTCCTTGGTGATTTT | A573340H | +G*+G*+A*G*T*T*C*C*T*T*G*G*T*G*A*T*+T*+T*+T | 85519 | 19 |
| 3343 | TCAGGAGTTCCTTGGTGAT | A573341H | +T*+C*+A*G*G*A*G*T*T*C*C*T*T*G*G*T*+G*+A*+T | 85522 | 19 |
| 3344 | ATTCAGGAGTTCCTTGGTG | A573342H | +A*+T*+T*C*A*G*G*A*G*T*T*C*C*T*T*G*+G*+T*+G | 85524 | 19 |
| 3345 | GCTTATTCAGGAGTTCCTT | A573343H | +G*+C*+T*T*A*T*T*C*A*G*G*A*G*T*T*C*+C*+T*+T | 85528 | 19 |
| 3346 | CGCTTATTCAGGAGTTCCT | A573344H | +C*+G*+C*T*T*A*T*T*C*A*G*G*A*G*T*T*+C*+C*+T | 85529 | 19 |
| 3347 | CGCTTATTCAGGAGTTCC | A573345H | +C*+G*+C*T*T*A*T*T*C*A*G*G*A*G*T*+T*+C*+C | 85530 | 18 |
| 3348 | TCGCTTATTCAGGAGTTCC | A573346H | +T*+C*+G*C*T*T*A*T*T*C*A*G*G*A*G*T*+T*+C*+C | 85530 | 19 |
| 3349 | CCTCGCTTATTCAGGAGTT | A573347H | +C*+C*+T*C*G*C*T*T*A*T*T*C*A*G*G*A*+G*+T*+T | 85532 | 19 |
| 3350 | CCTCGCTTATTCAGGAGT | A573348H | +C*+C*+T*C*G*C*T*T*A*T*T*C*A*G*G*+A*+G*+T | 85533 | 18 |
| 3351 | CCCTCGCTTATTCAGGAGT | A573349H | +C*+C*+C*T*C*G*C*T*T*A*T*T*C*A*G*G*+A*+G*+T | 85533 | 19 |
| 3352 | ACCCTCGCTTATTCAGGAG | A573350H | +A*+C*+C*C*T*C*G*C*T*T*A*T*T*C*A*G*+G*+A*+G | 85534 | 19 |
| 3353 | AACCCTCGCTTATTCAGGA | A573351H | +A*+A*+C*C*C*T*C*G*C*T*T*A*T*T*C*A*+G*+G*+A | 85535 | 19 |
| 3354 | AACCCTCGCTTATTCAGG | A573352H | +A*+A*+C*C*C*T*C*G*C*T*T*A*T*T*C*+A*+G*+G | 85536 | 18 |
| 3355 | GAACCCTCGCTTATTCAGG | A573353H | +G*+A*+A*C*C*C*T*C*G*C*T*T*A*T*T*C*+A*+G*+G | 85536 | 19 |
| 3356 | GAACCCTCGCTTATTCAG | A573354H | +G*+A*+A*C*C*C*T*C*G*C*T*T*A*T*T*+C*+A*+G | 85537 | 18 |
| 3357 | GGAACCCTCGCTTATTCAG | A573355H | +G*+G*+A*A*C*C*C*T*C*G*C*T*T*A*T*T*+C*+A*+G | 85537 | 19 |
| 3358 | GGAACCCTCGCTTATTCA | A573356H | +G*+G*+A*A*C*C*C*T*C*G*C*T*T*A*T*+T*+C*+A | 85538 | 18 |
| 3359 | GGGAACCCTCGCTTATTCA | A573357H | +G*+G*+G*A*A*C*C*C*T*C*G*C*T*T*A*T*+T*+C*+A | 85538 | 19 |
| 3360 | GGAACCCTCGCTTATTC | A573358H | +G*+G*+A*A*C*C*C*T*C*G*C*T*T*A*+T*+T*+C | 85539 | 17 |
| 3361 | GGGAACCCTCGCTTATTC | A573359H | +G*+G*+G*A*A*C*C*C*T*C*G*C*T*T*A*+T*+T*+C | 85539 | 18 |
| 3362 | AGGGAACCCTCGCTTATTC | A573360H | +A*+G*+G*G*A*A*C*C*C*T*C*G*C*T*T*T*A*+T*+T*+C | 85539 | 19 |
| 3363 | GGGAACCCTCGCTTATT | A573361H | +G*+G*+G*A*A*C*C*C*T*C*G*C*T*T*+A*+T*+T | 85540 | 17 |
| 3364 | AGGGAACCCTCGCTTATT | A573362H | +A*+G*+G*G*A*A*C*C*C*T*C*G*C*T*T*T*+A*+T*+T | 85540 | 18 |
| 3365 | CAGGGAACCCTCGCTTATT | A573363H | +C*+A*+G*G*G*A*A*C*C*C*T*C*G*C*T*T*T*+A*+T*+T | 85540 | 19 |
| 3366 | GGGAACCCTCGCTTAT | A573364H | +G*+G*+G*A*A*C*C*C*T*C*G*C*T*+T*+A*+T | 85541 | 16 |
| 3367 | AGGGAACCCTCGCTTAT | A573365H | +A*+G*+G*G*A*A*C*C*C*T*C*G*C*T*+T*+A*+T | 85541 | 17 |
| 3368 | CAGGGAACCCTCGCTTAT | A573366H | +C*+A*+G*G*G*A*A*C*C*C*T*C*G*C*T*+T*+A*+T | 85541 | 18 |
| 3369 | GCAGGGAACCCTCGCTTAT | A573367H | +G*+C*+A*G*G*G*A*A*C*C*C*T*C*G*C*T*+T*+A*+T | 85541 | 19 |
| 3370 | GCAGGGAACCCTCGCTTA | A573368H | +G*+C*+A*G*G*G*A*A*C*C*C*T*C*G*C*+T*+T*+A | 85542 | 18 |

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| 3371 | AAAGTGGTAATCTCG TAT | A573369H | +A*+A*+A*G*T*G*G*T*A*A*T*C*T*C*G*+T* +A*+T | 85561 | 18 |
| 3372 | CAAAGTGGTAATCTC GTAT | A573370H | +C*+A*+A*A*G*T*G*G*T*A*A*T*C*T*C*G*+ T*+A*+T | 85561 | 19 |
| 3373 | CAAAGTGGTAATCTC GTA | A573371H | +C*+A*+A*A*G*T*G*G*T*A*A*T*C*T*C*+G* +T*+A | 85562 | 18 |
| 3374 | ACAAAGTGGTAATCT CGTA | A573372H | +A*+C*+A*A*A*G*T*G*G*T*A*A*T*C*T*C*+ G*+T*+A | 85562 | 19 |
| 3375 | ACAAAGTGGTAATCT CGT | A573373H | +A*+C*+A*A*A*G*T*G*G*T*A*A*T*C*T*+C* +G*+T | 85563 | 18 |
| 3376 | CACAAAGTGGTAATC TCGT | A573374H | +C*+A*+C*A*A*A*G*T*G*G*T*A*A*T*C*T*+ C*+G*+T | 85563 | 19 |
| 3377 | TCACAAAGTGGTAAT CTCG | A573375H | +T*+C*+A*C*A*A*A*G*T*G*G*T*A*A*T*C*+ T*+C*+G | 85564 | 19 |
| 3378 | TTCACAAAGTGGTAA TCTC | A573376H | +T*+T*+C*A*C*A*A*A*G*T*G*G*T*A*A*T*+ C*+T*+C | 85565 | 19 |
| 3379 | CATTCACAAAGTGGT AATC | A573377H | +C*+A*+T*T*C*A*C*A*A*A*G*T*G*G*T*A*+ A*+T*+C | 85567 | 19 |
| 3380 | GGCATTCACAAAGTG GTAA | A573378H | +G*+G*+C*A*T*T*C*A*C*A*A*A*G*T*G*G*+ T*+A*+A | 85569 | 19 |
| 3381 | TGGCATTCACAAAGT GGTA | A573379H | +T*+G*+G*C*A*T*T*C*A*C*A*A*A*G*T*G*+ G*+T*+A | 85570 | 19 |
| 3382 | GGTGGCATTCACAAA GTGG | A573380H | +G*+G*+T*G*G*C*A*T*T*C*A*C*A*A*A*G*+ T*+G*+G | 85572 | 19 |
| 3383 | CGGTGGCATTCACAA AGTG | A573381H | +C*+G*+G*T*G*G*C*A*T*T*C*A*C*A*A*A*+ G*+T*+G | 85573 | 19 |
| 3384 | CTCGGTGGCATTCAC AAAG | A573382H | +C*+T*+C*G*G*T*G*G*C*A*T*T*C*A*C*A*+ A*+A*+G | 85575 | 19 |
| 3385 | CTCGGTGGCATTCAC AAA | A573383H | +C*+T*+C*G*G*T*G*G*C*A*T*T*C*A*C*+A* +A*+A | 85576 | 18 |
| 3386 | CCTCGGTGGCATTCA CAAA | A573384H | +C*+C*+T*C*G*G*T*G*G*C*A*T*T*C*A*C*+ A*+A*+A | 85576 | 19 |
| 3387 | TCCTCGGTGGCATTC ACAA | A573385H | +T*+C*+C*T*C*G*G*T*G*G*C*A*T*T*C*A*+ C*+A*+A | 85577 | 19 |
| 3388 | ATTCCTCGGTGGCAT TCAC | A573386H | +A*+T*+T*C*C*T*C*G*G*T*G*G*C*A*T*T*+ C*+A*+C | 85579 | 19 |
| 3389 | AGATTCCTCGGTGGC ATTC | A573387H | +A*+G*+A*T*T*C*C*T*C*G*G*T*G*G*C*A*+ T*+T*+C | 85581 | 19 |
| 3390 | CAGATTCCTCGGTGG CATT | A573388H | +C*+A*+G*A*T*T*C*C*T*C*G*G*T*G*G*C*+ A*+T*+T | 85582 | 19 |
| 3391 | CATCAGATTCCTCGG TGGC | A573389H | +C*+A*+T*C*A*G*A*T*T*C*C*T*C*G*G*T*+ G*+G*+C | 85585 | 19 |
| 3392 | CATCAGATTCCTCGG TGG | A573390H | +C*+A*+T*C*A*G*A*T*T*C*C*T*C*G*G*+T* +G*+G | 85586 | 18 |
| 3393 | GCATCAGATTCCTCG GTGG | A573391H | +G*+C*+A*T*C*A*G*A*T*T*C*C*T*C*G*G*+ T*+G*+G | 85586 | 19 |
| 3394 | GCATCAGATTCCTCG GTG | A573392H | +G*+C*+A*T*C*A*G*A*T*T*C*C*T*C*G*+G* +T*+G | 85587 | 18 |
| 3395 | AGCATCAGATTCCTC GGTG | A573393H | +A*+G*+C*A*T*C*A*G*A*T*T*C*C*T*C*G*+ G*+T*+G | 85587 | 19 |
| 3396 | AAGCATCAGATTCCT CGGT | A573394H | +A*+A*+G*C*A*T*C*A*G*A*T*T*C*C*T*C*+ G*+G*+T | 85588 | 19 |
| 3397 | AAAGCATCAGATTCC TCGG | A573395H | +A*+A*+A*G*C*A*T*C*A*G*A*T*T*C*C*T*+ C*+G*+G | 85589 | 19 |
| 3398 | GCCAAAGCATCAGAT TCCT | A573396H | +G*+C*+C*A*A*A*G*C*A*T*C*A*G*A*T*T*+ C*+C*+T | 85592 | 19 |
| 3399 | TGCCAAAGCATCAGA TTCC | A573397H | +T*+G*+C*C*A*A*A*G*C*A*T*C*A*G*A*T*+ T*+C*+C | 85593 | 19 |
| 3400 | GTTTTGCCAAAGCAT CAGA | A573398H | +G*+T*+T*T*T*G*C*C*A*A*A*G*C*A*T*C*+ A*+G*+A | 85597 | 19 |
| 3401 | GTTTTGCCAAAGCAT CAG | A573399H | +G*+T*+T*T*T*G*C*C*A*A*A*G*C*A*T*+C* +A*+G | 85598 | 18 |
| 3402 | AGTTTTGCCAAAGCA TCAG | A573400H | +A*+G*+T*T*T*T*G*C*C*A*A*A*G*C*A*T*+ C*+A*+G | 85598 | 19 |
| 3403 | GAAGTTTTGCCAAAG CATC | A573401H | +G*+A*+A*G*T*T*T*T*G*C*C*A*A*A*G*C*+ A*+T*+C | 85600 | 19 |
| 3404 | CGAAGTTTTGCCAAA GCAT | A573402H | +C*+G*+A*A*G*T*T*T*T*G*C*C*A*A*A*G*+ C*+A*+T | 85601 | 19 |
| 3405 | CCGAAGTTTTGCCAA AGCA | A573403H | +C*+C*+G*A*A*G*T*T*T*T*G*C*C*A*A*A*+ G*+C*+A | 85602 | 19 |

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| 3406 | CCGAAGTTTTGCCAAAGC | A573404H | +C*+C*+G*A*A*G*T*T*T*T*G*C*C*A*A*+A*+G*+C | 85603 | 18 |
| 3407 | TCCGAAGTTTTGCCAAAGC | A573405H | +T*+C*+C*G*A*A*G*T*T*T*T*G*C*C*A*A*+A*+G*+C | 85603 | 19 |
| 3408 | TTCCGAAGTTTTGCCAAAG | A573406H | +T*+T*+C*C*G*A*A*G*T*T*T*T*G*C*C*A*+A*+A*+G | 85604 | 19 |
| 3409 | TTTCCGAAGTTTTGCCAAA | A573407H | +T*+T*+T*C*C*G*A*A*G*T*T*T*T*G*C*C*+A*+A*+A | 85605 | 19 |
| 3410 | TTTTCCGAAGTTTTGCCAA | A573408H | +T*+T*+T*T*C*C*G*A*A*G*T*T*T*T*G*C*+C*+A*+A | 85606 | 19 |
| 3411 | TTTTCCGAAGTTTTGCCA | A573409H | +T*+T*+T*T*C*C*G*A*A*G*T*T*T*T*G*+C*+C*+A | 85607 | 18 |
| 3412 | GTTTTCCGAAGTTTTGCCA | A573410H | +G*+T*+T*T*T*C*C*G*A*A*G*T*T*T*T*G*+C*+C*+A | 85607 | 19 |
| 3413 | GGTTTTCCGAAGTTTTGCC | A573411H | +G*+G*+T*T*T*T*C*C*G*A*A*G*T*T*T*T*+G*+C*+C | 85608 | 19 |
| 3414 | ATGGTTTTCCGAAGTTTTG | A573412H | +A*+T*+G*G*T*T*T*T*C*C*G*A*A*G*T*T*+T*+T*+G | 85610 | 19 |
| 3415 | GATGGTTTTCCGAAGTTTT | A573413H | +G*+A*+T*G*G*T*T*T*T*C*C*G*A*A*G*T*+T*+T*+T | 85611 | 19 |
| 3416 | TGATGGTTTTCCGAAGTTT | A573414H | +T*+G*+A*T*G*G*T*T*T*T*C*C*G*A*A*G*+T*+T*+T | 85612 | 19 |
| 3417 | ATGATGGTTTTCCGAAGTT | A573415H | +A*+T*+G*A*T*G*G*T*T*T*T*C*C*G*A*A*+G*+T*+T | 85613 | 19 |
| 3418 | ATGATGGTTTTCCGAAGT | A573416H | +A*+T*+G*A*T*G*G*T*T*T*T*C*C*G*A*+A*+G*+T | 85614 | 18 |
| 3419 | TATGATGGTTTTCCGAAGT | A573417H | +T*+A*+T*G*A*T*G*G*T*T*T*T*C*C*G*A*+A*+G*+T | 85614 | 19 |
| 3420 | TGAAATTAAGGCTCTCGT | A573418H | +T*+G*+A*A*A*T*T*A*A*G*G*C*T*C*T*+C*+G*+T | 85634 | 18 |
| 3421 | TTGAAATTAAGGCTCTCGT | A573419H | +T*+T*+G*A*A*A*T*T*A*A*G*G*C*T*C*T*+C*+G*+T | 85634 | 19 |
| 3422 | CTCTACCAGCCTACCATG | A573420Hi | +C*+T*+C*T*A*C*C*A*G*C*C*T*A*C*C*+A*+T*+G | 85658 | 18 |
| 3423 | GAGTTGCTCACTTCTCAAA | A573421Hi | +G*+A*+G*T*T*G*C*T*C*A*C*T*T*C*T*C*+A*+A*+A | 85720 | 19 |
| 3424 | GAGTTGCTCACTTCTCAA | A573422Hi | +G*+A*+G*T*T*G*C*T*C*A*C*T*T*C*T*+C*+A*+A | 85721 | 18 |
| 3425 | AGACCTCAGTATTCACCTT | A573423Hi | +A*+G*+A*C*C*T*C*A*G*T*A*T*T*C*A*C*+C*+T*+T | 85992 | 19 |
| 3426 | GTCTTCATGACTAAATAAA | A573424Hi | +G*+T*+C*T*T*C*A*T*G*A*C*T*A*A*A*T*+A*+A*+A | 86179 | 19 |
| 3427 | AGTGGTCTTCATGACTAAA | A573425Hi | +A*+G*+T*G*G*T*C*T*T*C*A*T*G*A*C*T*+A*+A*+A | 86183 | 19 |
| 3428 | AGTGGTCTTCATGACTAA | A573426Hi | +A*+G*+T*G*G*T*C*T*T*C*A*T*G*A*C*+T*+A*+A | 86184 | 18 |
| 3429 | TGAACTAAGTAATTAGTGA | A573427Hi | +T*+G*+A*A*C*T*A*A*G*T*A*A*T*T*A*G*+T*+G*+A | 86223 | 19 |
| 3430 | GAACTAAGTAATTAGTGA | A573428Hi | +G*+A*+A*C*T*A*A*G*T*A*A*T*T*A*G*+T*+G*+A | 86223 | 18 |
| 3431 | GTACAGTTTACACCACACT | A573429Hi | +G*+T*+A*C*A*G*T*T*T*A*C*A*C*C*A*C*+A*+C*+T | 86405 | 19 |
| 3432 | GTACAGTTTACACCACAC | A573430Hi | +G*+T*+A*C*A*G*T*T*T*A*C*A*C*C*A*+C*+A*+C | 86406 | 18 |
| 3433 | CAGTACAGTTTACACCACA | A573431Hi | +C*+A*+G*T*A*C*A*G*T*T*T*A*C*A*C*C*+A*+C*+A | 86407 | 19 |
| 3434 | AGTACAGTTTACACCACA | A573432Hi | +A*+G*+T*A*C*A*G*T*T*T*A*C*A*C*C*+A*+C*+A | 86407 | 18 |
| 3435 | TCAGTACAGTTTACACCAC | A573433Hi | +T*+C*+A*G*T*A*C*A*G*T*T*T*A*C*A*C*+C*+A*+C | 86408 | 19 |
| 3436 | TTTCAGTACAGTTTACACC | A573434Hi | +T*+T*+T*C*A*G*T*A*C*A*G*T*T*T*A*C*+A*+C*+C | 86410 | 19 |
| 3437 | GTCATATGGAACTATCAAG | A573435Hi | +G*+T*+C*A*T*A*T*G*G*A*A*C*T*A*T*C*+A*+A*+G | 86435 | 19 |
| 3438 | ACTAAGTGAAATTCATCAT | A573436Hi | +A*+C*+T*A*A*G*T*G*A*A*A*T*T*C*A*T*+C*+A*+T | 86461 | 19 |
| 3439 | AATAGGACTCTATTTATC | A573437Hi | +A*+A*+T*A*G*G*A*C*T*C*T*A*T*T*T*+A*+T*+C | 86525 | 18 |
| 3440 | GGAGTTATAACCAAGGTG | A573438Hi | +G*+G*+A*G*T*T*A*T*A*A*C*C*A*A*G*+G*+T*+G | 86629 | 18 |

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| 3441 | AGCACACATAATCTATATA | A573439Hi | +A*+G*+C*A*C*A*C*A*T*A*A*T*C*T*A*T*+A*+T*+A | 86679 | 19 |
| 3442 | TACAAATGGCTCATTAGGT | A573440Hi | +T*+A*+C*A*A*A*T*G*G*C*T*C*A*T*T*A*+G*+G*+T | 86708 | 19 |
| 3443 | ATTACATGTCCAACAAGA | A573441Hi | +A*+T*+T*A*C*A*T*G*T*C*C*A*A*C*A*+A*+G*+A | 86878 | 18 |
| 3444 | AATTACATGTCCAACAAGA | A573442Hi | +A*+A*+T*T*A*C*A*T*G*T*C*C*A*A*C*A*+A*+G*+A | 86878 | 19 |
| 3445 | TAATTACATGTCCAACAAG | A573443Hi | +T*+A*+A*T*T*A*C*A*T*G*T*C*C*A*A*C*+A*+A*+G | 86879 | 19 |
| 3446 | ATCAACTAAATTCAGGCCT | A573444Hi | +A*+T*+C*A*A*C*T*A*A*A*T*T*C*A*G*G*+C*+C*+T | 87110 | 19 |
| 3447 | ATCAACTAAATTCAGGCC | A573445Hi | +A*+T*+C*A*A*C*T*A*A*A*T*T*C*A*G*+G*+C*+C | 87111 | 18 |
| 3448 | CATCAACTAAATTCAGGC | A573446Hi | +C*+A*+T*C*A*A*C*T*A*A*A*T*T*C*A*+G*+G*+C | 87112 | 18 |
| 3449 | GCATCAACTAAATTCAGG | A573447Hi | +G*+C*+A*T*C*A*A*C*T*A*A*A*T*T*C*+A*+G*+G | 87113 | 18 |
| 3450 | TGCATCAACTAAATTCAGG | A573448Hi | +T*+G*+C*A*T*C*A*A*C*T*A*A*A*T*T*C*+A*+G*+G | 87113 | 19 |
| 3451 | TGCATCAACTAAATTCAG | A573449Hi | +T*+G*+C*A*T*C*A*A*C*T*A*A*A*T*T*+C*+A*+G | 87114 | 18 |
| 3452 | TTTGCATCAACTAAATTCA | A573450Hi | +T*+T*+T*G*C*A*T*C*A*A*C*T*A*A*A*T*+T*+C*+A | 87115 | 19 |
| 3453 | TCTGTGACTTTGCATCAAC | A573451Hi | +T*+C*+T*G*T*G*A*C*T*T*T*G*C*A*T*C*+A*+A*+C | 87123 | 19 |
| 3454 | CAGTATTAATACAGCTTAA | A573452Hi | +C*+A*+G*T*A*T*T*A*A*T*A*C*A*G*C*T*+T*+A*+A | 87154 | 19 |
| 3455 | GGTAATGATATCTATTAG | A573453Hi | +G*+G*+T*A*A*T*G*A*T*A*T*C*T*A*T*+T*+A*+G | 87180 | 18 |
| 3456 | TTGGTAATGATATCTATTA | A573454Hi | +T*+T*+G*G*T*A*A*T*G*A*T*A*T*C*T*A*+T*+T*+A | 87181 | 19 |
| 3457 | ATTGGTAATGATATCTATT | A573455Hi | +A*+T*+T*G*G*T*A*A*T*G*A*T*A*T*C*T*+A*+T*+T | 87182 | 19 |
| 3458 | ATTGGTAATGATATCTAT | A573456Hi | +A*+T*+T*G*G*T*A*A*T*G*A*T*A*T*C*+T*+A*+T | 87183 | 18 |
| 3459 | TGCATCCATTAGCAATATA | A573457Hi | +T*+G*+C*A*T*C*C*A*T*T*A*G*C*A*A*T*+A*+T*+A | 87312 | 19 |
| 3460 | CAGAATGCTGCATCCATTA | A573458Hi | +C*+A*+G*A*A*T*G*C*T*G*C*A*T*C*C*A*+T*+T*+A | 87320 | 19 |
| 3461 | ACCATTATGCCAGAATGCT | A573459Hi | +A*+C*+C*A*T*T*A*T*G*C*C*A*G*A*A*T*+G*+C*+T | 87330 | 19 |
| 3462 | AACCATTATGCCAGAATGC | A573460Hi | +A*+A*+C*C*A*T*T*A*T*G*C*C*A*G*A*A*+T*+G*+C | 87331 | 19 |
| 3463 | AAACCATTATGCCAGAATG | A573461Hi | +A*+A*+A*C*C*A*T*T*A*T*G*C*C*A*G*A*+A*+T*+G | 87332 | 19 |
| 3464 | CAAACCATTATGCCAGAAT | A573462Hi | +C*+A*+A*A*C*C*A*T*T*A*T*G*C*C*A*G*+A*+A*+T | 87333 | 19 |
| 3465 | TCTACAAAGCAATCAAATG | A573463Hi | +T*+C*+T*A*C*A*A*A*G*C*A*A*T*C*A*A*+A*+T*+G | 87358 | 19 |
| 3466 | CAGGTTGAAGCACCTCAGG | A573464Hi | +C*+A*+G*G*T*T*G*A*A*G*C*A*C*C*T*C*+A*+G*+G | 87440 | 19 |
| 3467 | ATTCAGGTTGAAGCACCTC | A573465Hi | +A*+T*+T*C*A*G*G*T*T*G*A*A*G*C*A*C*+C*+T*+C | 87443 | 19 |
| 3468 | CTGCTCTTTGAATTCAGGT | A573466Hi | +C*+T*+G*C*T*C*T*T*T*G*A*A*T*T*C*A*+G*+G*+T | 87454 | 19 |
| 3469 | AGCTGCTCTTTGAATTCAG | A573467Hi | +A*+G*+C*T*G*C*T*C*T*T*T*G*A*A*T*T*+C*+A*+G | 87456 | 19 |
| 3470 | AGATTAGAGAAGAGCTAAG | A573468Hi | +A*+G*+A*T*T*A*G*A*G*A*A*G*A*G*C*T*+A*+A*+G | 87534 | 19 |
| 3471 | TTAATAAGGTTGAGACAGA | A573469Hi | +T*+T*+A*A*T*A*A*G*G*T*T*G*A*G*A*C*+A*+G*+A | 87556 | 19 |
| 3472 | AAAGTGTCTGCACAGACAC | A573470Hi | +A*+A*+A*G*T*G*T*C*T*G*C*A*C*A*G*A*+C*+A*+C | 87578 | 19 |
| 3473 | ATGCCTGCTCTGCTAATGG | A573471Hi | +A*+T*+G*C*C*T*G*C*T*C*T*G*C*T*A*A*+T*+G*+G | 87708 | 19 |
| 3474 | TTACTCAAGAGACTGTTT | A573472Hi | +T*+T*+A*C*T*C*A*A*G*A*G*A*C*T*G*+T*+T*+T | 87957 | 18 |
| 3475 | AATGGTTACTCAAGAGACT | A573473Hi | +A*+A*+T*G*G*T*T*A*C*T*C*A*A*G*A*G*+A*+C*+T | 87961 | 19 |

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| 3476 | GACAACCATAACCATTAC | A573474Hi | +G*+A*+C*A*A*C*C*A*T*A*A*C*C*A*T*+T*+A*+C | 87997 | 18 |
| 3477 | AGACAACCATAACCATTA | A573475Hi | +A*+G*+A*C*A*A*C*C*A*T*A*A*C*C*A*+T*+T*+A | 87998 | 18 |
| 3478 | TATGGAAATTACATATTCT | A573476Hi | +T*+A*+T*G*G*A*A*A*T*T*A*C*A*T*A*T*+T*+C*+T | 88139 | 19 |
| 3479 | ACCAGATGGCAAACTCTCC | A573477Hi | +A*+C*+C*A*G*A*T*G*G*C*A*A*A*C*T*C*+T*+C*+C | 88171 | 19 |
| 3480 | CACCAGATGGCAAACTCTC | A573478Hi | +C*+A*+C*C*A*G*A*T*G*G*C*A*A*A*C*T*+C*+T*+C | 88172 | 19 |
| 3481 | GGATGATCATTGTTCTGT | A573479Hi | +G*+G*+A*T*G*A*T*C*A*T*T*G*T*T*C*+T*+G*+T | 88366 | 18 |
| 3482 | GAGGATGATCATTGTTCTG | A573480Hi | +G*+A*+G*G*A*T*G*A*T*C*A*T*T*G*T*T*+C*+T*+G | 88367 | 19 |
| 3483 | GGAGAGGATGATCATTGTT | A573481Hi | +G*+G*+A*G*A*G*G*A*T*G*A*T*C*A*T*T*+G*+T*+T | 88370 | 19 |
| 3484 | GAGAGGATGATCATTGTT | A573482Hi | +G*+A*+G*A*G*G*A*T*G*A*T*C*A*T*T*+G*+T*+T | 88370 | 18 |
| 3485 | AGGAGAGGATGATCATTGT | A573483Hi | +A*+G*+G*A*G*A*G*G*A*T*G*A*T*C*A*T*+T*+G*+T | 88371 | 19 |
| 3486 | AGGAGAGGATGATCATTG | A573484Hi | +A*+G*+G*A*G*A*G*G*A*T*G*A*T*C*A*+T*+T*+G | 88372 | 18 |
| 3487 | TAGGAGAGGATGATCATTG | A573485Hi | +T*+A*+G*G*A*G*A*G*G*A*T*G*A*T*C*A*+T*+T*+G | 88372 | 19 |
| 3488 | TACAAATTACAAGAGCTTT | A573486Hi | +T*+A*+C*A*A*A*T*T*A*C*A*A*G*A*G*C*+T*+T*+T | 88584 | 19 |
| 3489 | GTACAAATTACAAGAGCTT | A573487Hi | +G*+T*+A*C*A*A*A*T*T*A*C*A*A*G*A*G*+C*+T*+T | 88585 | 19 |
| 3490 | AGTACAAATTACAAGAGCT | A573488Hi | +A*+G*+T*A*C*A*A*A*T*T*A*C*A*A*G*A*+G*+C*+T | 88586 | 19 |
| 3491 | CAGTACAAATTACAAGAGC | A573489Hi | +C*+A*+G*T*A*C*A*A*A*T*T*A*C*A*A*G*+A*+G*+C | 88587 | 19 |
| 3492 | GATATCAGTACAAATTAC | A573490Hi | +G*+A*+T*A*T*C*A*G*T*A*C*A*A*A*T*+T*+A*+C | 88593 | 18 |
| 3493 | ATGTGAAACAGACACGCTA | A573491Hi | +A*+T*+G*T*G*A*A*A*C*A*G*A*C*A*C*G*+C*+T*+A | 88617 | 19 |
| 3494 | TGTGAAACAGACACGCTA | A573492Hi | +T*+G*+T*G*A*A*A*C*A*G*A*C*A*C*G*+C*+T*+A | 88617 | 18 |
| 3495 | TAATGTGAAACAGACACGC | A573493Hi | +T*+A*+A*T*G*T*G*A*A*A*C*A*G*A*C*A*+C*+G*+C | 88619 | 19 |
| 3496 | ACTTAATGTGAAACAGACA | A573494Hi | +A*+C*+T*T*A*A*T*G*T*G*A*A*A*C*A*G*+A*+C*+A | 88622 | 19 |
| 3497 | TAAACTTAATGTGAAACAG | A573495Hi | +T*+A*+A*A*C*T*T*A*A*T*G*T*G*A*A*A*+C*+A*+G | 88625 | 19 |
| 3498 | ATTAAACTTAATGTGAAAC | A573496Hi | +A*+T*+T*A*A*A*C*T*T*A*A*T*G*T*G*A*+A*+A*+C | 88627 | 19 |
| 3499 | CATTAAACTTAATGTGAAA | A573497Hi | +C*+A*+T*T*A*A*A*C*T*T*A*A*T*G*T*G*+A*+A*+A | 88628 | 19 |
| 3500 | CAAATTCAGTGCTAACAGT | A573498Hi | +C*+A*+A*A*T*T*C*A*G*T*G*C*T*A*A*C*+A*+G*+T | 88893 | 19 |
| 3501 | TGGCAAATTCAGTGCTAA | A573499Hi | +T*+G*+G*C*A*A*A*T*T*C*A*G*T*G*C*+T*+A*+A | 88897 | 18 |
| 3502 | TTGGCAAATTCAGTGCTAA | A573500Hi | +T*+T*+G*G*C*A*A*A*T*T*C*A*G*T*G*C*+T*+A*+A | 88897 | 19 |
| 3503 | GTTGGCAAATTCAGTGCTA | A573501Hi | +G*+T*+T*G*G*C*A*A*A*T*T*C*A*G*T*G*+C*+T*+A | 88898 | 19 |
| 3504 | TGGTTGGCAAATTCAGTGC | A573502Hi | +T*+G*+G*T*T*G*G*C*A*A*A*T*T*C*A*G*+T*+G*+C | 88900 | 19 |
| 3505 | GGTTGGCAAATTCAGTGC | A573503Hi | +G*+G*+T*T*G*G*C*A*A*A*T*T*C*A*G*+T*+G*+C | 88900 | 18 |
| 3506 | ATGGTTGGCAAATTCAGT | A573504Hi | +A*+T*+G*G*T*T*G*G*C*A*A*A*T*T*C*+A*+G*+T | 88902 | 18 |
| 3507 | CAAATGACAAGCCGTAAA | A573505Hi | +C*+A*+A*A*T*G*A*C*A*A*G*C*C*G*T*+A*+A*+A | 88947 | 18 |
| 3508 | ACAAATGACAAGCCGTAAA | A573506Hi | +A*+C*+A*A*A*T*G*A*C*A*A*G*C*C*G*T*+A*+A*+A | 88947 | 19 |
| 3509 | ACAAATGACAAGCCGTAA | A573507Hi | +A*+C*+A*A*A*T*G*A*C*A*A*G*C*C*G*+T*+A*+A | 88948 | 18 |
| 3510 | TACAAATGACAAGCCGTAA | A573508Hi | +T*+A*+C*A*A*A*T*G*A*C*A*A*G*C*C*G*+T*+A*+A | 88948 | 19 |

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| 3511 | TTACAAATGACAAGC CGTA | A573509Hi | +T*+T*+A*C*A*A*A*T*G*A*C*A*A*G*C*C*+ G*+T*+A | 88949 | 19 |
| 3512 | ATTACAAATGACAAG CCGT | A573510Hi | +A*+T*+T*A*C*A*A*A*T*G*A*C*A*A*G*C*+ C*+G*+T | 88950 | 19 |
| 3513 | AATTACAAATGACAA GCCG | A573511Hi | +A*+A*+T*T*A*C*A*A*A*T*G*A*C*A*A*G*+ C*+C*+G | 88951 | 19 |
| 3514 | ATTACAAATGACAAG CCG | A573512Hi | +A*+T*+T*A*C*A*A*A*T*G*A*C*A*A*G*+C* +C*+G | 88951 | 18 |
| 3515 | AAATTACAAATGACA AGCC | A573513Hi | +A*+A*+A*T*T*A*C*A*A*A*T*G*A*C*A*A*+ G*+C*+C | 88952 | 19 |
| 3516 | GAATCAGCTGTCCAA CAAC | A573514H | +G*+A*+A*T*C*A*G*C*T*G*T*C*C*A*A*C*+ A*+A*+C | 88991 | 19 |
| 3517 | GGAATCAGCTGTCCA ACAA | A573515H | +G*+G*+A*A*T*C*A*G*C*T*G*T*C*C*A*A*+ C*+A*+A | 88992 | 19 |
| 3518 | GGAATCAGCTGTCCA ACA | A573516H | +G*+G*+A*A*T*C*A*G*C*T*G*T*C*C*A*+A* +C*+A | 88993 | 18 |
| 3519 | TGGAATCAGCTGTCC AACA | A573517H | +T*+G*+G*A*A*T*C*A*G*C*T*G*T*C*C*A*+ A*+C*+A | 88993 | 19 |
| 3520 | AGTCTGGAATCAGCT GTCC | A573518H | +A*+G*+T*C*T*G*G*A*A*T*C*A*G*C*T*G*+ T*+C*+C | 88997 | 19 |
| 3521 | CAGTCTGGAATCAGC TGTC | A573519H | +C*+A*+G*T*C*T*G*G*A*A*T*C*A*G*C*T*+ G*+T*+C | 88998 | 19 |
| 3522 | CAGTCTGGAATCAGC TGT | A573520H | +C*+A*+G*T*C*T*G*G*A*A*T*C*A*G*C*+T* +G*+T | 88999 | 18 |
| 3523 | GCAGTCTGGAATCAG CTGT | A573521H | +G*+C*+A*G*T*C*T*G*G*A*A*T*C*A*G*C*+ T*+G*+T | 88999 | 19 |
| 3524 | GCAGTCTGGAATCAG CTG | A573522H | +G*+C*+A*G*T*C*T*G*G*A*A*T*C*A*G*+C* +T*+G | 89000 | 18 |
| 3525 | AGCAGTCTGGAATCA GCTG | A573523H | +A*+G*+C*A*G*T*C*T*G*G*A*A*T*C*A*G*+ C*+T*+G | 89000 | 19 |
| 3526 | TAGCAGTCTGGAATC AGCT | A573524H | +T*+A*+G*C*A*G*T*C*T*G*G*A*A*T*C*A*+ G*+C*+T | 89001 | 19 |
| 3527 | CATAGCAGTCTGGAA TCAG | A573525H | +C*+A*+T*A*G*C*A*G*T*C*T*G*G*A*A*T*+ C*+A*+G | 89003 | 19 |
| 3528 | ACATAGCAGTCTGGA ATCA | A573526H | +A*+C*+A*T*A*G*C*A*G*T*C*T*G*G*A*A*+ T*+C*+A | 89004 | 19 |
| 3529 | GTTCTACATAGCAGT CTGG | A573527H | +G*+T*+T*C*T*A*C*A*T*A*G*C*A*G*T*C*+ T*+G*+G | 89009 | 19 |
| 3530 | AAGTTCTACATAGCA GTCT | A573528H | +A*+A*+G*T*T*C*T*A*C*A*T*A*G*C*A*G*+ T*+C*+T | 89011 | 19 |
| 3531 | CAAGTTCTACATAGC AGTC | A573529H | +C*+A*+A*G*T*T*C*T*A*C*A*T*A*G*C*A*+ G*+T*+C | 89012 | 19 |
| 3532 | TCAAGTTCTACATAG CAGT | A573530H | +T*+C*+A*A*G*T*T*C*T*A*C*A*T*A*G*C*+ A*+G*+T | 89013 | 19 |
| 3533 | CGCTCCGATAAAATG ATTT | A573531H | +C*+G*+C*T*C*C*G*A*T*A*A*A*A*T*G*A*+ T*+T*+T | 89034 | 19 |
| 3534 | CGCTCCGATAAAATG ATT | A573532H | +C*+G*+C*T*C*C*G*A*T*A*A*A*A*T*G*+A* +T*+T | 89035 | 18 |
| 3535 | ACGCTCCGATAAAAT GATT | A573533H | +A*+C*+G*C*T*C*C*G*A*T*A*A*A*A*T*G*+ A*+T*+T | 89035 | 19 |
| 3536 | CGCTCCGATAAAATG AT | A573534H | +C*+G*+C*T*C*C*G*A*T*A*A*A*A*T*+G*+A *+T | 89036 | 17 |
| 3537 | ACGCTCCGATAAAAT GAT | A573535H | +A*+C*+G*C*T*C*C*G*A*T*A*A*A*A*T*+G* +A*+T | 89036 | 18 |
| 3538 | TACGCTCCGATAAAA TGAT | A573536H | +T*+A*+C*G*C*T*C*C*G*A*T*A*A*A*A*T*+ G*+A*+T | 89036 | 19 |
| 3539 | ACGCTCCGATAAAAT GA | A573537H | +A*+C*+G*C*T*C*C*G*A*T*A*A*A*A*+T*+G *+A | 89037 | 17 |
| 3540 | TACGCTCCGATAAAA TGA | A573538H | +T*+A*+C*G*C*T*C*C*G*A*T*A*A*A*A*+T* +G*+A | 89037 | 18 |
| 3541 | TTACGCTCCGATAAA ATGA | A573539H | +T*+T*+A*C*G*C*T*C*C*G*A*T*A*A*A*A*+ T*+G*+A | 89037 | 19 |
| 3542 | TACGCTCCGATAAAA TG | A573540H | +T*+A*+C*G*C*T*C*C*G*A*T*A*A*A*+A*+T *+G | 89038 | 17 |
| 3543 | TTACGCTCCGATAAA ATG | A573541H | +T*+T*+A*C*G*C*T*C*C*G*A*T*A*A*A*+A* +T*+G | 89038 | 18 |
| 3544 | TTTACGCTCCGATAA AATG | A573542H | +T*+T*+T*A*C*G*C*T*C*C*G*A*T*A*A*A*+ A*+T*+G | 89038 | 19 |
| 3545 | TTTTTACGCTCCGAT AAAA | A573543H | +T*+T*+T*T*T*A*C*G*C*T*C*C*G*A*T*A*+ A*+A*+A | 89040 | 19 |

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| 3546 | TTTTTACGCTCCGATAAA | A573544H | +T*+T*+T*T*T*A*C*G*C*T*C*C*G*A*T*+A*+A*+A | 89041 | 18 |
| 3547 | ATTTTTACGCTCCGATAAA | A573545H | +A*+T*+T*T*T*T*A*C*G*C*T*C*C*G*A*T*+A*+A*+A | 89041 | 19 |
| 3548 | TTTTTACGCTCCGATAA | A573546H | +T*+T*+T*T*T*A*C*G*C*T*C*C*G*A*+T*+A*+A | 89042 | 17 |
| 3549 | ATTTTTACGCTCCGATAA | A573547H | +A*+T*+T*T*T*T*A*C*G*C*T*C*C*G*A*+T*+A*+A | 89042 | 18 |
| 3550 | CATTTTTACGCTCCGATAA | A573548H | +C*+A*+T*T*T*T*T*A*C*G*C*T*C*C*G*A*+T*+A*+A | 89042 | 19 |
| 3551 | TTTTTACGCTCCGATA | A573549H | +T*+T*+T*T*T*A*C*G*C*T*C*C*G*+A*+T*+A | 89043 | 16 |
| 3552 | ATTTTTACGCTCCGATA | A573550H | +A*+T*+T*T*T*T*A*C*G*C*T*C*C*G*+A*+T*+A | 89043 | 17 |
| 3553 | CATTTTTACGCTCCGATA | A573551H | +C*+A*+T*T*T*T*T*A*C*G*C*T*C*C*G*+A*+T*+A | 89043 | 18 |
| 3554 | ACATTTTTACGCTCCGATA | A573552H | +A*+C*+A*T*T*T*T*T*A*C*G*C*T*C*C*G*+A*+T*+A | 89043 | 19 |
| 3555 | ATTTTTACGCTCCGATT | A573553H | +A*+T*+T*T*T*T*A*C*G*C*T*C*C*+G*+A*+T | 89044 | 16 |
| 3556 | CATTTTTACGCTCCGAT | A573554H | +C*+A*+T*T*T*T*T*A*C*G*C*T*C*C*+G*+A*+T | 89044 | 17 |
| 3557 | ACATTTTTACGCTCCGAT | A573555H | +A*+C*+A*T*T*T*T*T*A*C*G*C*T*C*C*+G*+A*+T | 89044 | 18 |
| 3558 | CACATTTTTACGCTCCGAT | A573556H | +C*+A*+C*A*T*T*T*T*T*A*C*G*C*T*C*C*+G*+A*+T | 89044 | 19 |
| 3559 | ACATTTTTACGCTCCGA | A573557H | +A*+C*+A*T*T*T*T*T*A*C*G*C*T*C*+C*+G*+A | 89045 | 17 |
| 3560 | CACATTTTTACGCTCCGA | A573558H | +C*+A*+C*A*T*T*T*T*T*A*C*G*C*T*C*+C*+G*+A | 89045 | 18 |
| 3561 | GCACATTTTTACGCTCCGA | A573559H | +G*+C*+A*C*A*T*T*T*T*T*A*C*G*C*T*C*+C*+G*+A | 89045 | 19 |
| 3562 | GCACATTTTTACGCTCCG | A573560H | +G*+C*+A*C*A*T*T*T*T*T*A*C*G*C*T*+C*+C*+G | 89046 | 18 |
| 3563 | GGCACATTTTTACGCTCCG | A573561H | +G*+G*+C*A*C*A*T*T*T*T*T*A*C*G*C*T*+C*+C*+G | 89046 | 19 |
| 3564 | GCACATTTTTACGCTCC | A573562H | +G*+C*+A*C*A*T*T*T*T*T*A*C*G*C*+T*+C*+C | 89047 | 17 |
| 3565 | GGCACATTTTTACGCTCC | A573563H | +G*+G*+C*A*C*A*T*T*T*T*T*A*C*G*C*+T*+C*+C | 89047 | 18 |
| 3566 | TGGCACATTTTTACGCTCC | A573564H | +T*+G*+G*C*A*C*A*T*T*T*T*T*A*C*G*C*+T*+C*+C | 89047 | 19 |
| 3567 | TTGGCACATTTTTACGCTC | A573565H | +T*+T*+G*G*C*A*C*A*T*T*T*T*T*A*C*G*+C*+T*+C | 89048 | 19 |
| 3568 | TTGGCACATTTTTACGCT | A573566H | +T*+T*+G*G*C*A*C*A*T*T*T*T*T*A*C*+G*+C*+T | 89049 | 18 |
| 3569 | ATTGGCACATTTTTACGCT | A573567H | +A*+T*+T*G*G*C*A*C*A*T*T*T*T*T*A*C*+G*+C*+T | 89049 | 19 |
| 3570 | TTGGCACATTTTTACGC | A573568H | +T*+T*+G*G*C*A*C*A*T*T*T*T*T*A*+C*+G*+C | 89050 | 17 |
| 3571 | ATTGGCACATTTTTACGC | A573569H | +A*+T*+T*G*G*C*A*C*A*T*T*T*T*T*A*+C*+G*+C | 89050 | 18 |
| 3572 | AATTGGCACATTTTTACGC | A573570H | +A*+A*+T*T*G*G*C*A*C*A*T*T*T*T*T*T*A*+C*+G*+C | 89050 | 19 |
| 3573 | CAATTGGCACATTTTTACG | A573571H | +C*+A*+A*T*T*G*G*C*A*C*A*T*T*T*T*T*+A*+C*+G | 89051 | 19 |
| 3574 | GGAAATTCAATTGGCACAT | A573572H | +G*+G*+A*A*A*T*T*C*A*A*T*T*G*G*C*A*+C*+A*+T | 89058 | 19 |
| 3575 | TAGTTGTAATAATCGTTTC | A573573H | +T*+A*+G*T*T*G*T*A*A*T*A*A*T*C*G*T*+T*+T*+C | 89089 | 19 |
| 3576 | CTAGTTGTAATAATCGTTT | A573574H | +C*+T*+A*G*T*T*G*T*A*A*T*A*A*T*C*G*+T*+T*+T | 89090 | 19 |
| 3577 | ACTAGTTGTAATAATCGTT | A573575H | +A*+C*+T*A*G*T*T*G*T*A*A*T*A*A*T*C*+G*+T*+T | 89091 | 19 |
| 3578 | ACTAGTTGTAATAATCGT | A573576H | +A*+C*+T*A*G*T*T*G*T*A*A*T*A*A*T*+C*+G*+T | 89092 | 18 |
| 3579 | CACTAGTTGTAATAATCGT | A573577H | +C*+A*+C*T*A*G*T*T*G*T*A*A*T*A*A*T*+C*+G*+T | 89092 | 19 |
| 3580 | CACTAGTTGTAATAATCG | A573578H | +C*+A*+C*T*A*G*T*T*G*T*A*A*T*A*A*+T*+C*+G | 89093 | 18 |

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| 3581 | TCACTAGTTGTAATA ATCG | A573579H | +T*+C*+A*C*T*A*G*T*T*G*T*A*A*T*A*A*+ T*+C*+G | 89093 | 19 |
| 3582 | CTCACTAGTTGTAAT AATC | A573580H | +C*+T*+C*A*C*T*A*G*T*T*G*T*A*A*T*A*+ A*+T*+C | 89094 | 19 |
| 3583 | TCTCTCACTAGTTGT AATA | A573581H | +T*+C*+T*C*T*C*A*C*T*A*G*T*T*G*T*A*+ A*+T*+A | 89097 | 19 |
| 3584 | TTCTCTCACTAGTTGT AAT | A573582H | +T*+T*+C*T*C*T*C*A*C*T*A*G*T*T*G*T*+ A*+A*+T | 89098 | 19 |
| 3585 | TTTTCTCTCACTAGTT GTA | A573583H | +T*+T*+T*T*C*T*C*T*C*A*C*T*A*G*T*T*+ G*+T*+A | 89100 | 19 |
| 3586 | CTCATTTTCATCTAAC TGC | A573584H | +C*+T*+C*A*T*T*T*T*C*A*T*C*T*A*A*C*+ T*+G*+C | 89125 | 19 |
| 3587 | GCTCATTTTCATCTAA CTG | A573585H | +G*+C*+T*C*A*T*T*T*T*C*A*T*C*T*A*A*+ C*+T*+G | 89126 | 19 |
| 3588 | GAGGAAGCTCATTTT CATC | A573586H | +G*+A*+G*G*A*A*G*C*T*C*A*T*T*T*T*C*+ A*+T*+C | 89132 | 19 |
| 3589 | GTGAGGAAGCTCATT TTCA | A573587H | +G*+T*+G*A*G*G*A*A*G*C*T*C*A*T*T*T*+ T*+C*+A | 89134 | 19 |
| 3590 | CGTGAGGAAGCTCAT TTTC | A573588H | +C*+G*+T*G*A*G*G*A*A*G*C*T*C*A*T*T*+ T*+T*+C | 89135 | 19 |
| 3591 | GCGTGAGGAAGCTCA TTTT | A573589H | +G*+C*+G*T*G*A*G*G*A*A*G*C*T*C*A*T*+ T*+T*+T | 89136 | 19 |
| 3592 | TGCGTGAGGAAGCTC ATTT | A573590H | +T*+G*+C*G*T*G*A*G*G*A*A*G*C*T*C*A*+ T*+T*+T | 89137 | 19 |
| 3593 | TGCGTGAGGAAGCTC ATT | A573591H | +T*+G*+C*G*T*G*A*G*G*A*A*G*C*T*C*+A* +T*+T | 89138 | 18 |
| 3594 | CTGCGTGAGGAAGCT CATT | A573592H | +C*+T*+G*C*G*T*G*A*G*G*A*A*G*C*T*C*+ A*+T*+T | 89138 | 19 |
| 3595 | ACTGCGTGAGGAAGC TCAT | A573593H | +A*+C*+T*G*C*G*T*G*A*G*G*A*A*G*C*T*+ C*+A*+T | 89139 | 19 |
| 3596 | AACTGCGTGAGGAAG CTCA | A573594H | +A*+A*+C*T*G*C*G*T*G*A*G*G*A*A*G*C* +T*+C*+A | 89140 | 19 |
| 3597 | AACTGCGTGAGGAAG CTC | A573595H | +A*+A*+C*T*G*C*G*T*G*A*G*G*A*A*G*+C *+T*+C | 89141 | 18 |
| 3598 | GAACTGCGTGAGGAA GCTC | A573596H | +G*+A*+A*C*T*G*C*G*T*G*A*G*G*A*A*G* +C*+T*+C | 89141 | 19 |
| 3599 | TGAACTGCGTGAGGA AGCT | A573597H | +T*+G*+A*A*C*T*G*C*G*T*G*A*G*G*A*A*+ G*+C*+T | 89142 | 19 |
| 3600 | GTGAACTGCGTGAGG AAGC | A573598H | +G*+T*+G*A*A*C*T*G*C*G*T*G*A*G*G*A* +A*+G*+C | 89143 | 19 |
| 3601 | AAGTGAACTGCGTGA GGAA | A573599H | +A*+A*+G*T*G*A*A*C*T*G*C*G*T*G*A*G*+ G*+A*+A | 89145 | 19 |
| 3602 | TTAGAAAGTGAACTG CGTG | A573600H | +T*+T*+A*G*A*A*A*G*T*G*A*A*C*T*G*C*+ G*+T*+G | 89150 | 19 |
| 3603 | ATTTAGAAAGTGAAC TGCG | A573601H | +A*+T*+T*T*A*G*A*A*A*G*T*G*A*A*C*T*+ G*+C*+G | 89152 | 19 |
| 3604 | CATTTAGAAAGTGAA CTGC | A573602H | +C*+A*+T*T*T*A*G*A*A*A*G*T*G*A*A*C*+ T*+G*+C | 89153 | 19 |
| 3605 | TTACTCCTAGGTGAT TTCT | A573603Hi | +T*+T*+A*C*T*C*C*T*A*G*G*T*G*A*T*T*+ T*+C*+T | 89378 | 19 |
| 3606 | TTTACTCCTAGGTGA TTTC | A573604Hi | +T*+T*+T*A*C*T*C*C*T*A*G*G*T*G*A*T*+ T*+T*+C | 89379 | 19 |
| 3607 | GTTCCACAGCTCCTG AATA | A573605Hi | +G*+T*+T*C*C*A*C*A*G*C*T*C*C*T*G*A*+ A*+T*+A | 89458 | 19 |
| 3608 | AGCTAGATCTTCCAC TCA | A573606Hi | +A*+G*+C*T*A*G*A*T*C*T*T*C*C*A*C*+T* +C*+A | 89621 | 18 |
| 3609 | GAGCTAGATCTTCCA CTC | A573607Hi | +G*+A*+G*C*T*A*G*A*T*C*T*T*C*C*A*+C* +T*+C | 89622 | 18 |
| 3610 | AGAGCTAGATCTTCC ACT | A573608Hi | +A*+G*+A*G*C*T*A*G*A*T*C*T*T*C*C*+A* +C*+T | 89623 | 18 |
| 3611 | GAGAGCTAGATCTTC CACT | A573609Hi | +G*+A*+G*A*G*C*T*A*G*A*T*C*T*T*C*C*+ A*+C*+T | 89623 | 19 |
| 3612 | GAGAGCTAGATCTTC CAC | A573610Hi | +G*+A*+G*A*G*C*T*A*G*A*T*C*T*T*C*+C* +A*+C | 89624 | 18 |
| 3613 | ACAATTAGCACTGAA GTTG | A573611Hi | +A*+C*+A*A*T*T*A*G*C*A*C*T*G*A*A*G*+ T*+T*+G | 89682 | 19 |
| 3614 | CAATTAGCACTGAAG TTG | A573612Hi | +C*+A*+A*T*T*A*G*C*A*C*T*G*A*A*G*+T* +T*+G | 89682 | 18 |
| 3615 | TCAAGTACACAATTA GCAC | A573613Hi | +T*+C*+A*A*G*T*A*C*A*C*A*A*T*T*A*G*+ C*+A*+C | 89690 | 19 |

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| 3616 | ATCAAGTACACAATTAGCA | A573614Hi | +A*+T*+C*A*A*G*T*A*C*A*C*A*A*T*T*A*+G*+C*+A | 89691 | 19 |
| 3617 | GATCAAGTACACAATTAGC | A573615Hi | +G*+A*+T*C*A*A*G*T*A*C*A*C*A*A*T*T*+A*+G*+C | 89692 | 19 |
| 3618 | ATCAAGTACACAATTAGC | A573616Hi | +A*+T*+C*A*A*G*T*A*C*A*C*A*A*T*T*+A*+G*+C | 89692 | 18 |
| 3619 | ATGATCAAGTACACAATTA | A573617Hi | +A*+T*+G*A*T*C*A*A*G*T*A*C*A*C*A*A*+T*+T*+A | 89694 | 19 |
| 3620 | GTAATATGATCAAGTACAC | A573618Hi | +G*+T*+A*A*T*A*T*G*A*T*C*A*A*G*T*A*+C*+A*+C | 89699 | 19 |
| 3621 | CTATCAAACAACTCACACA | A573619Hi | +C*+T*+A*T*C*A*A*A*C*A*A*C*T*C*A*C*+A*+C*+A | 89729 | 19 |
| 3622 | TACTATCAAACAACTCACA | A573620Hi | +T*+A*+C*T*A*T*C*A*A*A*C*A*A*C*T*C*+A*+C*+A | 89731 | 19 |
| 3623 | CTAGTACTATCAAACAAC | A573621Hi | +C*+T*+A*G*T*A*C*T*A*T*C*A*A*A*C*+A*+A*+C | 89736 | 18 |
| 3624 | TACTCTAGTACTATCAAAC | A573622Hi | +T*+A*+C*T*C*T*A*G*T*A*C*T*A*T*C*A*+A*+A*+C | 89739 | 19 |
| 3625 | TTACTCTAGTACTATCAAA | A573623Hi | +T*+T*+A*C*T*C*T*A*G*T*A*C*T*A*T*C*+A*+A*+A | 89740 | 19 |
| 3626 | CCAGTCACTTACTCTAGTA | A573624Hi | +C*+C*+A*G*T*C*A*C*T*T*A*C*T*C*T*A*+G*+T*+A | 89748 | 19 |
| 3627 | AGGAACAGATCATAAACCA | A573625Hi | +A*+G*+G*A*A*C*A*G*A*T*C*A*T*A*A*A*+C*+C*+A | 89816 | 19 |
| 3628 | CAGATAAGAAACACAGCAT | A573626Hi | +C*+A*+G*A*T*A*A*G*A*A*A*C*A*C*A*G*+C*+A*+T | 89866 | 19 |
| 3629 | CAATATTATAATGGAGTAT | A573627Hi | +C*+A*+A*T*A*T*T*A*T*A*A*T*G*G*A*G*+T*+A*+T | 90032 | 19 |
| 3630 | CCAATATTATAATGGAGTA | A573628Hi | +C*+C*+A*A*T*A*T*T*A*T*A*A*T*G*G*A*+G*+T*+A | 90033 | 19 |
| 3631 | CCAATATTATAATGGAGT | A573629Hi | +C*+C*+A*A*T*A*T*T*A*T*A*A*T*G*G*+A*+G*+T | 90034 | 18 |
| 3632 | AGCTGTGCATCCTATGGTC | A573630Hi | +A*+G*+C*T*G*T*G*C*A*T*C*C*T*A*T*G*+G*+T*+C | 90059 | 19 |
| 3633 | GCTGTGCATCCTATGGTC | A573631Hi | +G*+C*+T*G*T*G*C*A*T*C*C*T*A*T*G*+G*+T*+C | 90059 | 18 |
| 3634 | TAGAAGCTGTGCATCCTA | A573632Hi | +T*+A*+G*A*A*G*C*T*G*T*G*C*A*T*C*+C*+T*+A | 90064 | 18 |
| 3635 | GACTAGAAGCTGTGCATC | A573633Hi | +G*+A*+C*T*A*G*A*A*G*C*T*G*T*G*C*+A*+T*+C | 90067 | 18 |
| 3636 | ATCAAACAGTGAAACATGG | A573634Hi | +A*+T*+C*A*A*A*C*A*G*T*G*A*A*A*C*A*+T*+G*+G | 90182 | 19 |
| 3637 | TGGGTCTTGAAAATGAAGA | A573635H | +T*+G*+G*G*T*C*T*T*G*A*A*A*A*T*G*A*+A*+G*+A | 90223 | 19 |
| 3638 | GTGCTGGGTCTTGAAAATG | A573636H | +G*+T*+G*C*T*G*G*G*T*C*T*T*G*A*A*A*+A*+T*+G | 90227 | 19 |
| 3639 | AGTGCTGGGTCTTGAAAAT | A573637H | +A*+G*+T*G*C*T*G*G*G*T*C*T*T*G*A*A*+A*+A*+T | 90228 | 19 |
| 3640 | CAGTGCTGGGTCTTGAAAA | A573638H | +C*+A*+G*T*G*C*T*G*G*G*T*C*T*T*G*A*+A*+A*+A | 90229 | 19 |
| 3641 | GCAGTGCTGGGTCTTGAAA | A573639H | +G*+C*+A*G*T*G*C*T*G*G*G*T*C*T*T*G*+A*+A*+A | 90230 | 19 |
| 3642 | CTGCAGTGCTGGGTCTTGA | A573640H | +C*+T*+G*C*A*G*T*G*C*T*G*G*G*T*C*T*+T*+G*+A | 90232 | 19 |
| 3643 | TCACTTAACTGCAGTGCTG | A573641H | +T*+C*+A*C*T*T*A*A*C*T*G*C*A*G*T*G*+C*+T*+G | 90240 | 19 |
| 3644 | AGTCACTTAACTGCAGTGC | A573642H | +A*+G*+T*C*A*C*T*T*A*A*C*T*G*C*A*G*+T*+G*+C | 90242 | 19 |
| 3645 | GCCACTTGGGTTCCACAAA | A573643H | +G*+C*+C*A*C*T*T*G*G*G*T*T*C*C*A*C*+A*+A*+A | 90266 | 19 |
| 3646 | GCCACTTGGGTTCCACAA | A573644H | +G*+C*+C*A*C*T*T*G*G*G*T*T*C*C*A*+C*+A*+A | 90267 | 18 |
| 3647 | AGCCACTTGGGTTCCACAA | A573645H | +A*+G*+C*C*A*C*T*T*G*G*G*T*T*C*C*A*+C*+A*+A | 90267 | 19 |
| 3648 | AAAGCCACTTGGGTTCCAC | A573646H | +A*+A*+A*G*C*C*A*C*T*T*G*G*G*T*T*C*+C*+A*+C | 90269 | 19 |
| 3649 | CAAAGCCACTTGGGTTCCA | A573647H | +C*+A*+A*A*G*C*C*A*C*T*T*G*G*G*T*T*+C*+C*+A | 90270 | 19 |
| 3650 | TTACAAAGCCACTTGGGTT | A573648H | +T*+T*+A*C*A*A*A*G*C*C*A*C*T*T*G*G*+G*+T*+T | 90273 | 19 |

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| 3651 | CCATGATTTTACAAAGCCA | A573649H | +C*+C*+A*T*G*A*T*T*T*T*A*C*A*A*A*G*+C*+C*+A | 90281 | 19 |
| 3652 | GCCATGATTTTACAAAGCC | A573650H | +G*+C*+C*A*T*G*A*T*T*T*T*A*C*A*A*A*+G*+C*+C | 90282 | 19 |
| 3653 | ATCTGTTCTATGCTTTGAC | A573651Hi | +A*+T*+C*T*G*T*T*C*T*A*T*G*C*T*T*T*+G*+A*+C | 90341 | 19 |
| 3654 | CATCTGTTCTATGCTTTGA | A573652Hi | +C*+A*+T*C*T*G*T*T*C*T*A*T*G*C*T*T*+T*+G*+A | 90342 | 19 |
| 3655 | CCATCTGTTCTATGCTTTG | A573653Hi | +C*+C*+A*T*C*T*G*T*T*C*T*A*T*G*C*T*+T*+T*+G | 90343 | 19 |
| 3656 | GTTTCTGCCTTAACTAAAC | A573654Hi | +G*+T*+T*T*C*T*G*C*C*T*T*A*A*C*T*A*+A*+A*+C | 90393 | 19 |
| 3657 | ATGTGAAATGTTCCACAGT | A573655Hi | +A*+T*+G*T*G*A*A*A*T*G*T*T*C*C*A*C*+A*+G*+T | 90429 | 19 |
| 3658 | CTATGTGAAATGTTCCACA | A573656Hi | +C*+T*+A*T*G*T*G*A*A*A*T*G*T*T*C*C*+A*+C*+A | 90431 | 19 |
| 3659 | TAGTCTTCTATGTGAAATG | A573657Hi | +T*+A*+G*T*C*T*T*C*T*A*T*G*T*G*A*A*+A*+T*+G | 90438 | 19 |
| 3660 | CTTTCCTTCTTCCATGAAG | A573658Hi | +C*+T*+T*T*C*C*T*T*C*T*T*C*C*A*T*G*+A*+A*+G | 90466 | 19 |
| 3661 | CATGGAAGTGAACTCAAGA | A573659Hi | +C*+A*+T*G*G*A*A*G*T*G*A*A*C*T*C*A*+A*+G*+A | 90488 | 19 |
| 3662 | GTCATGGAAGTGAACTCA | A573660Hi | +G*+T*+C*A*T*G*G*A*A*G*T*G*A*A*C*+T*+C*+A | 90491 | 18 |
| 3663 | AAGTCATGGAAGTGAACTC | A573661Hi | +A*+A*+G*T*C*A*T*G*G*A*A*G*T*G*A*A*+C*+T*+C | 90492 | 19 |
| 3664 | TACAAACATCTGTATGTGG | A573662Hi | +T*+A*+C*A*A*A*C*A*T*C*T*G*T*A*T*G*+T*+G*+G | 90521 | 19 |
| 3665 | TCTAGTAAAGCAGCATGG | A573663Hi | +T*+C*+T*A*G*T*A*A*A*G*C*A*G*C*A*+T*+G*+G | 90550 | 18 |
| 3666 | AGGATCTAGTAAAGCAGCA | A573664Hi | +A*+G*+G*A*T*C*T*A*G*T*A*A*A*G*C*A*+G*+C*+A | 90553 | 19 |
| 3667 | CATCAGGATCTAGTAAAGC | A573665Hi | +C*+A*+T*C*A*G*G*A*T*C*T*A*G*T*A*A*+A*+G*+C | 90557 | 19 |
| 3668 | TCATCAGGATCTAGTAAAG | A573666Hi | +T*+C*+A*T*C*A*G*G*A*T*C*T*A*G*T*A*+A*+A*+G | 90558 | 19 |
| 3669 | ACATCATCAGGATCTAGTA | A573667Hi | +A*+C*+A*T*C*A*T*C*A*G*G*A*T*C*T*A*+G*+T*+A | 90561 | 19 |
| 3670 | TGACATCATCAGGATCTAG | A573668Hi | +T*+G*+A*C*A*T*C*A*T*C*A*G*G*A*T*C*+T*+A*+G | 90563 | 19 |
| 3671 | GTTTCACAGGCTCAGCAAC | A573669Hi | +G*+T*+T*T*C*A*C*A*G*G*C*T*C*A*G*C*+A*+A*+C | 90660 | 19 |
| 3672 | AGGTTTCACAGGCTCAGCA | A573670Hi | +A*+G*+G*T*T*T*C*A*C*A*G*G*C*T*C*A*+G*+C*+A | 90662 | 19 |
| 3673 | GATAGAGGTTTCACAGGCT | A573671Hi | +G*+A*+T*A*G*A*G*G*T*T*T*C*A*C*A*G*+G*+C*+T | 90667 | 19 |
| 3674 | CTAGATAGAGGTTTCACAG | A573672Hi | +C*+T*+A*G*A*T*A*G*A*G*G*T*T*T*C*A*+C*+A*+G | 90670 | 19 |
| 3675 | CTAGATAGAGGTTTCACA | A573673Hi | +C*+T*+A*G*A*T*A*G*A*G*G*T*T*T*C*+A*+C*+A | 90671 | 18 |
| 3676 | TCTAGATAGAGGTTTCACA | A573674Hi | +T*+C*+T*A*G*A*T*A*G*A*G*G*T*T*T*C*+A*+C*+A | 90671 | 19 |
| 3677 | ATCTAGATAGAGGTTTCAC | A573675Hi | +A*+T*+C*T*A*G*A*T*A*G*A*G*G*T*T*T*+C*+A*+C | 90672 | 19 |
| 3678 | TATCTAGATAGAGGTTTCA | A573676Hi | +T*+A*+T*C*T*A*G*A*T*A*G*A*G*G*T*T*+T*+C*+A | 90673 | 19 |
| 3679 | ATGTTATCTAGATAGAGGT | A573677Hi | +A*+T*+G*T*T*A*T*C*T*A*G*A*T*A*G*A*+G*+G*+T | 90677 | 19 |
| 3680 | ATGTTATCTAGATAGAGG | A573678Hi | +A*+T*+G*T*T*A*T*C*T*A*G*A*T*A*G*+A*+G*+G | 90678 | 18 |
| 3681 | CATGTTATCTAGATAGAGG | A573679Hi | +C*+A*+T*G*T*T*A*T*C*T*A*G*A*T*A*G*+A*+G*+G | 90678 | 19 |
| 3682 | CATGTTATCTAGATAGAG | A573680Hi | +C*+A*+T*G*T*T*A*T*C*T*A*G*A*T*A*+G*+A*+G | 90679 | 18 |
| 3683 | CCATGTTATCTAGATAGAG | A573681Hi | +C*+C*+A*T*G*T*T*A*T*C*T*A*G*A*T*A*+G*+A*+G | 90679 | 19 |
| 3684 | TTATGTCAAAGCTACAGAG | A573682Hi | +T*+T*+A*T*G*T*C*A*A*A*G*C*T*A*C*A*+G*+A*+G | 90869 | 19 |
| 3685 | CAATGTGCAACAAAGAATT | A573683Hi | +C*+A*+A*T*G*T*G*C*A*A*C*A*A*A*G*A*+A*+T*+T | 90958 | 19 |

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| 3686 | ACAATGTGCAACAAA GAAT | A573684Hi | +A*+C*+A*A*T*G*T*G*C*A*A*C*A*A*A*G*+ A*+A*+T | 90959 | 19 |
| 3687 | TCACATTCTCCAAGC AATA | A573685Hi | +T*+C*+A*C*A*T*T*C*T*C*C*A*A*G*C*A*+ A*+T*+A | 91070 | 19 |
| 3688 | TATGGTTTAATTGGA AGAG | A573686Hi | +T*+A*+T*G*G*T*T*T*A*A*T*T*G*G*A*A*+ G*+A*+G | 91206 | 19 |
| 3689 | TATGGTTTAATTGGA AGA | A573687Hi | +T*+A*+T*G*G*T*T*T*A*A*T*T*G*G*A*+A* +G*+A | 91207 | 18 |
| 3690 | CTTTATGGTTTAATTG GAA | A573688Hi | +C*+T*+T*T*A*T*G*G*T*T*T*A*A*T*T*G*+ G*+A*+A | 91209 | 19 |
| 3691 | TAATTACCTTTATGGT TTA | A573689Hi | +T*+A*+A*T*T*A*C*C*T*T*T*A*T*G*G*T*+ T*+T*+A | 91216 | 19 |
| 3692 | TGAGTGAATTTAATT ACC | A573690Hi | +T*+G*+A*G*T*G*A*A*T*T*T*A*A*T*T*+A* +C*+C | 91227 | 18 |
| 3693 | TAGATGGAATTTAGG AACA | A573691Hi | +T*+A*+G*A*T*G*G*A*A*T*T*T*A*G*G*A*+ A*+C*+A | 91261 | 19 |
| 3694 | GCATTAAGAAATTTC ACAG | A573692Hi | +G*+C*+A*T*T*A*A*G*A*A*A*T*T*T*C*A*+ C*+A*+G | 91570 | 19 |
| 3695 | TAATGCATTAAGAAA TTTC | A573693Hi | +T*+A*+A*T*G*C*A*T*T*A*A*G*A*A*A*T*+ T*+T*+C | 91574 | 19 |
| 3696 | GCAGCTACCTACACA TCTT | A573694Hi | +G*+C*+A*G*C*T*A*C*C*T*A*C*A*C*A*T*+ C*+T*+T | 91811 | 19 |
| 3697 | CAGGATGCAGCTACC TACA | A573695Hi | +C*+A*+G*G*A*T*G*C*A*G*C*T*A*C*C*T*+ A*+C*+A | 91817 | 19 |
| 3698 | AGGATGCAGCTACCT ACA | A573696Hi | +A*+G*+G*A*T*G*C*A*G*C*T*A*C*C*T*+A* +C*+A | 91817 | 18 |
| 3699 | GTACAGGATGCAGCT ACCT | A573697Hi | +G*+T*+A*C*A*G*G*A*T*G*C*A*G*C*T*A*+ C*+C*+T | 91820 | 19 |
| 3700 | TACAGGATGCAGCTA CCT | A573698Hi | +T*+A*+C*A*G*G*A*T*G*C*A*G*C*T*A*+C* +C*+T | 91820 | 18 |
| 3701 | TGTACAGGATGCAGC TACC | A573699Hi | +T*+G*+T*A*C*A*G*G*A*T*G*C*A*G*C*T*+ A*+C*+C | 91821 | 19 |
| 3702 | GTACAGGATGCAGCT ACC | A573700Hi | +G*+T*+A*C*A*G*G*A*T*G*C*A*G*C*T*+A* +C*+C | 91821 | 18 |
| 3703 | CTTTGCTGTACAGGA TGCA | A573701Hi | +C*+T*+T*T*G*C*T*G*T*A*C*A*G*G*A*T*+ G*+C*+A | 91827 | 19 |
| 3704 | TCCTTTGCTGTACAG GATG | A573702Hi | +T*+C*+C*T*T*T*G*C*T*G*T*A*C*A*G*G*+ A*+T*+G | 91829 | 19 |
| 3705 | TGGAGTTGAGTTACC TCCT | A573703Hi | +T*+G*+G*A*G*T*T*G*A*G*T*T*A*C*C*T*+ C*+C*+T | 91902 | 19 |
| 3706 | GCAAACCTCTTCCTT ATTC | A573704Hi | +G*+C*+A*A*A*C*C*T*C*T*T*C*C*T*T*A*+ T*+T*+C | 92034 | 19 |
| 3707 | TGATGCAAACCTCTT CCTT | A573705Hi | +T*+G*+A*T*G*C*A*A*A*C*C*T*C*T*T*C*+ C*+T*+T | 92038 | 19 |
| 3708 | TATTGCAGTCATAGT GAAA | A573706Hi | +T*+A*+T*T*G*C*A*G*T*C*A*T*A*G*T*G*+ A*+A*+A | 92084 | 19 |
| 3709 | TATTGCAGTCATAGT GAA | A573707Hi | +T*+A*+T*T*G*C*A*G*T*C*A*T*A*G*T*+G* +A*+A | 92085 | 18 |
| 3710 | TTATTGCAGTCATAG TGAA | A573708Hi | +T*+T*+A*T*T*G*C*A*G*T*C*A*T*A*G*T*+ G*+A*+A | 92085 | 19 |
| 3711 | TTATTGCAGTCATAG TGA | A573709Hi | +T*+T*+A*T*T*G*C*A*G*T*C*A*T*A*G*+T* +G*+A | 92086 | 18 |
| 3712 | TTTATTGCAGTCATA GTG | A573710Hi | +T*+T*+T*A*T*T*G*C*A*G*T*C*A*T*A*+G* +T*+G | 92087 | 18 |
| 3713 | TTCAACTTAATTACTC CA | A573711Hi | +T*+T*+C*A*A*C*T*T*A*A*T*T*A*C*T*+C* +C*+A | 92121 | 18 |
| 3714 | TTTCAACTTAATTACT CCA | A573712Hi | +T*+T*+T*C*A*A*C*T*T*A*A*T*T*A*C*T*+ C*+C*+A | 92121 | 19 |
| 3715 | AGTGGCTCAAATTAA CTTA | A573713Hi | +A*+G*+T*G*G*C*T*C*A*A*A*T*T*A*A*C*+ T*+T*+A | 92197 | 19 |
| 3716 | TTGAGTGGCTCAAAT TAAC | A573714Hi | +T*+T*+G*A*G*T*G*G*C*T*C*A*A*A*T*T*+ A*+A*+C | 92200 | 19 |
| 3717 | AGTAACTTTGAGTGG CTC | A573715Hi | +A*+G*+T*A*A*C*T*T*T*G*A*G*T*G*G*+C* +T*+C | 92208 | 18 |
| 3718 | AAGTAACTTTGAGTG GCT | A573716Hi | +A*+A*+G*T*A*A*C*T*T*T*G*A*G*T*G*+G* +C*+T | 92209 | 18 |
| 3719 | GCTCTTGGTTTCACT TGAT | A573717Hi | +G*+C*+T*C*T*T*G*G*T*T*T*C*A*C*T*T*+ G*+A*+T | 92376 | 19 |
| 3720 | TGCTCTTGGTTTCAC TTGA | A573718Hi | +T*+G*+C*T*C*T*T*G*G*T*T*T*C*A*C*T*+ T*+G*+A | 92377 | 19 |

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| 3721 | AGTTGCTCTTGGTTTCACT | A573719Hi | +A*+G*+T*T*G*C*T*C*T*T*G*G*T*T*T*C*+A*+C*+T | 92380 | 19 |
| 3722 | CAAGTTGCTCTTGGTTTCA | A573720Hi | +C*+A*+A*G*T*T*G*C*T*C*T*T*G*G*T*T*+T*+C*+A | 92382 | 19 |
| 3723 | TGTCAGACAAGTTGCTCTT | A573721Hi | +T*+G*+T*C*A*G*A*C*A*A*G*T*T*G*C*T*+C*+T*+T | 92389 | 19 |
| 3724 | CTGTCAGACAAGTTGCTCT | A573722Hi | +C*+T*+G*T*C*A*G*A*C*A*A*G*T*T*G*C*+T*+C*+T | 92390 | 19 |
| 3725 | CTGTCAGACAAGTTGCTC | A573723Hi | +C*+T*+G*T*C*A*G*A*C*A*A*G*T*T*G*+C*+T*+C | 92391 | 18 |
| 3726 | GCTGTCAGACAAGTTGCTC | A573724Hi | +G*+C*+T*G*T*C*A*G*A*C*A*A*G*T*T*G*+C*+T*+C | 92391 | 19 |
| 3727 | ATTCATGAAGGTGAATACT | A573725Hi | +A*+T*+T*C*A*T*G*A*A*G*G*T*G*A*A*T*+A*+C*+T | 92430 | 19 |
| 3728 | TGATTCATGAAGGTGAATA | A573726Hi | +T*+G*+A*T*T*C*A*T*G*A*A*G*G*T*G*A*+A*+T*+A | 92432 | 19 |
| 3729 | CTTGATTCATGAAGGTGAA | A573727Hi | +C*+T*+T*G*A*T*T*C*A*T*G*A*A*G*G*T*+G*+A*+A | 92434 | 19 |
| 3730 | GCCTTGATTCATGAAGGTG | A573728Hi | +G*+C*+C*T*T*G*A*T*T*C*A*T*G*A*A*G*+G*+T*+G | 92436 | 19 |
| 3731 | GCCTTGATTCATGAAGGT | A573729Hi | +G*+C*+C*T*T*G*A*T*T*C*A*T*G*A*A*+G*+G*+T | 92437 | 18 |
| 3732 | TTGCCTTGATTCATGAAGG | A573730Hi | +T*+T*+G*C*C*T*T*G*A*T*T*C*A*T*G*A*+A*+G*+G | 92438 | 19 |
| 3733 | TTCTGCACCATGAAATTAT | A573731Hi | +T*+T*+C*T*G*C*A*C*C*A*T*G*A*A*A*T*+T*+A*+T | 92465 | 19 |
| 3734 | CTTCTGCACCATGAAATTA | A573732Hi | +C*+T*+T*C*T*G*C*A*C*C*A*T*G*A*A*A*+T*+T*+A | 92466 | 19 |
| 3735 | TAGAGCTTCTGCACCATGA | A573733Hi | +T*+A*+G*A*G*C*T*T*C*T*G*C*A*C*C*A*+T*+G*+A | 92471 | 19 |
| 3736 | TTAGAGCTTCTGCACCATG | A573734Hi | +T*+T*+A*G*A*G*C*T*T*C*T*G*C*A*C*C*+A*+T*+G | 92472 | 19 |
| 3737 | CATTAGAGCTTCTGCACCA | A573735Hi | +C*+A*+T*T*A*G*A*G*C*T*T*C*T*G*C*A*+C*+C*+A | 92474 | 19 |
| 3738 | CATTAGAGCTTCTGCACC | A573736Hi | +C*+A*+T*T*A*G*A*G*C*T*T*C*T*G*C*+A*+C*+C | 92475 | 18 |
| 3739 | CTCATTAGAGCTTCTGCAC | A573737Hi | +C*+T*+C*A*T*T*A*G*A*G*C*T*T*C*T*G*+C*+A*+C | 92476 | 19 |
| 3740 | CCTGCCTTAATGGTACCT | A573738Hi | +C*+C*+T*G*C*C*T*T*A*A*T*G*G*T*A*+C*+C*+T | 92547 | 18 |
| 3741 | AGTTAAATGAGTCTTGTAA | A573739Hi | +A*+G*+T*T*A*A*A*T*G*A*G*T*C*T*T*G*+T*+A*+A | 92572 | 19 |
| 3742 | TTTATCATACAGTTAAATG | A573740Hi | +T*+T*+T*A*T*C*A*T*A*C*A*G*T*T*A*A*+A*+T*+G | 92582 | 19 |
| 3743 | ATGTTCCACCTGATTAATT | A573741Hi | +A*+T*+G*T*T*C*C*A*C*C*T*G*A*T*T*A*+A*+T*+T | 92624 | 19 |
| 3744 | CTTATTCAAGGAAAGAGAA | A573742Hi | +C*+T*+T*A*T*T*C*A*A*G*G*A*A*A*G*A*+G*+A*+A | 92711 | 19 |
| 3745 | GCCTTATTCAAGGAAAGAG | A573743Hi | +G*+C*+C*T*T*A*T*T*C*A*A*G*G*A*A*A*+G*+A*+G | 92713 | 19 |
| 3746 | AACTGATGCCTTATTCAAG | A573744Hi | +A*+A*+C*T*G*A*T*G*C*C*T*T*A*T*T*C*+A*+A*+G | 92720 | 19 |
| 3747 | ACCTGAATAGCTAACTGAT | A573745Hi | +A*+C*+C*T*G*A*A*T*A*G*C*T*A*A*C*T*+G*+A*+T | 92732 | 19 |
| 3748 | ACCTGAATAGCTAACTGA | A573746Hi | +A*+C*+C*T*G*A*A*T*A*G*C*T*A*A*C*+T*+G*+A | 92733 | 18 |
| 3749 | TAACCTGAATAGCTAACTG | A573747Hi | +T*+A*+A*C*C*T*G*A*A*T*A*G*C*T*A*A*+C*+T*+G | 92734 | 19 |
| 3750 | TGACTTTATCACCTTTAAA | A573748Hi | +T*+G*+A*C*T*T*T*A*T*C*A*C*C*T*T*T*+A*+A*+A | 92780 | 19 |
| 3751 | TATCTTGACTTTATCACC | A573749Hi | +T*+A*+T*C*T*T*G*A*C*T*T*T*A*T*C*+A*+C*+C | 92786 | 18 |
| 3752 | CAACATTATCTTGACTTTA | A573750Hi | +C*+A*+A*C*A*T*T*A*T*C*T*T*G*A*C*T*+T*+T*+A | 92791 | 19 |
| 3753 | TCTGCAACATTATCTTGAC | A573751Hi | +T*+C*+T*G*C*A*A*C*A*T*T*A*T*C*T*T*+G*+A*+C | 92795 | 19 |
| 3754 | AATCTGCAACATTATCTTG | A573752Hi | +A*+A*+T*C*T*G*C*A*A*C*A*T*T*A*T*C*+T*+T*+G | 92797 | 19 |
| 3755 | AATGATAAATTGTTCACAT | A573753Hi | +A*+A*+T*G*A*T*A*A*A*T*T*G*T*T*C*A*+C*+A*+T | 92859 | 19 |

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| 3756 | GTGGAGCAGAACCAC GCAG | A573754Hi | +G*+T*+G*G*A*G*C*A*G*A*A*C*C*A*C*G* +C*+A*+G | 92909 | 19 |
| 3757 | CATGTGGAGCAGAAC CACG | A573755Hi | +C*+A*+T*G*T*G*G*A*G*C*A*G*A*A*C*C*+ A*+C*+G | 92912 | 19 |
| 3758 | GTACCTTTCTTGCAC TTTC | A573756Hi | +G*+T*+A*C*C*T*T*T*C*T*T*G*C*A*C*T*+ T*+T*+C | 92978 | 19 |
| 3759 | ATGGAGAAGCACCAA TACT | A573757Hi | +A*+T*+G*G*A*G*A*A*G*C*A*C*C*A*A*T*+ A*+C*+T | 93011 | 19 |
| 3760 | GGAGAAGCACCAATA CT | A573758Hi | +G*+G*+A*G*A*A*G*C*A*C*C*A*A*T*+A*+ C*+T | 93011 | 17 |
| 3761 | TGGAGAAGCACCAAT ACT | A573759Hi | +T*+G*+G*A*G*A*A*G*C*A*C*C*A*A*T*+A* +C*+T | 93011 | 18 |
| 3762 | CATGGAGAAGCACCA ATAC | A573760Hi | +C*+A*+T*G*G*A*G*A*A*G*C*A*C*C*A*A*+ T*+A*+C | 93012 | 19 |
| 3763 | ATGGAGAAGCACCAA TAC | A573761Hi | +A*+T*+G*G*A*G*A*A*G*C*A*C*C*A*A*+T* +A*+C | 93012 | 18 |
| 3764 | AACCAGCCACCATGA AAG | A573762Hi | +A*+A*+C*C*A*G*C*C*A*C*C*A*T*G*A*+A* +A*+G | 93094 | 18 |
| 3765 | TTCTCTTGGTAACCA GCCA | A573763Hi | +T*+T*+C*T*C*T*T*G*G*T*A*A*C*C*A*G*+ C*+C*+A | 93103 | 19 |
| 3766 | TTTCTCTTGGTAACC AGCC | A573764Hi | +T*+T*+T*C*T*C*T*T*G*G*T*A*A*C*C*A*+ G*+C*+C | 93104 | 19 |
| 3767 | ATTTCTCTTGGTAAC CAGC | A573765Hi | +A*+T*+T*T*C*T*C*T*T*G*G*T*A*A*C*C*+ A*+G*+C | 93105 | 19 |
| 3768 | TTCATTTCTCTTGGTA ACC | A573766Hi | +T*+T*+C*A*T*T*T*C*T*C*T*T*G*G*T*A*+ A*+C*+C | 93108 | 19 |
| 3769 | CAAAGATGGACACAT CATT | A573767Hi | +C*+A*+A*A*G*A*T*G*G*A*C*A*C*A*T*C*+ A*+T*+T | 93282 | 19 |
| 3770 | GAAGTTTCCAAAGAT GGAC | A573768Hi | +G*+A*+A*G*T*T*T*C*C*A*A*A*G*A*T*G*+ G*+A*+C | 93290 | 19 |
| 3771 | ATTATTATCTAGTTAT TCT | A573769Hi | +A*+T*+T*A*T*T*A*T*C*T*A*G*T*T*A*T*+ T*+C*+T | 93399 | 19 |
| 3772 | CATTATTATCTAGTTA TTC | A573770Hi | +C*+A*+T*T*A*T*T*A*T*C*T*A*G*T*T*A*+ T*+T*+C | 93400 | 19 |
| 3773 | GTTAGCCATTATTAT CTA | A573771Hi | +G*+T*+T*A*G*C*C*A*T*T*A*T*T*A*T*+C* +T*+A | 93407 | 18 |
| 3774 | TGTTAGCCATTATTAT CTA | A573772Hi | +T*+G*+T*T*A*G*C*C*A*T*T*A*T*T*A*T*+ C*+T*+A | 93407 | 19 |
| 3775 | ATTCAACCTCTCTGT CAAT | A573773Hi | +A*+T*+T*C*A*A*C*C*T*C*T*C*T*G*T*C*+ A*+A*+T | 93531 | 19 |
| 3776 | CTCTTCCTGAATGTG TACC | A573774Hi | +C*+T*+C*T*T*C*C*T*G*A*A*T*G*T*G*T*+ A*+C*+C | 93562 | 19 |
| 3777 | CCTCTTCCTGAATGT GTAC | A573775Hi | +C*+C*+T*C*T*T*C*C*T*G*A*A*T*G*T*G*+ T*+A*+C | 93563 | 19 |
| 3778 | AACTCTACCTCTTCCT GAA | A573776Hi | +A*+A*+C*T*C*T*A*C*C*T*C*T*T*C*C*T*+ G*+A*+A | 93570 | 19 |
| 3779 | TTTAAGTGCTAAGAC CTTT | A573777Hi | +T*+T*+T*A*A*G*T*G*C*T*A*A*G*A*C*C*+ T*+T*+T | 93754 | 19 |
| 3780 | GTACTTTATAGCAAT TCCA | A573778Hi | +G*+T*+A*C*T*T*T*A*T*A*G*C*A*A*T*T*+ C*+C*+A | 93826 | 19 |
| 3781 | TGTACTTTATAGCAA TTCC | A573779Hi | +T*+G*+T*A*C*T*T*T*A*T*A*G*C*A*A*T*+ T*+C*+C | 93827 | 19 |
| 3782 | GTGTACTTTATAGCA ATTC | A573780Hi | +G*+T*+G*T*A*C*T*T*T*A*T*A*G*C*A*A*+ T*+T*+C | 93828 | 19 |
| 3783 | CATATTGGTATTTAAT GAC | A573781Hi | +C*+A*+T*A*T*T*G*G*T*A*T*T*T*A*A*T*+ G*+A*+C | 93903 | 19 |
| 3784 | GTTATAAAGTCCTTA GGCC | A573782Hi | +G*+T*+T*A*T*A*A*A*G*T*C*C*T*T*A*G*+ G*+C*+C | 94004 | 19 |
| 3785 | GTTATAAAGTCCTTA GGC | A573783Hi | +G*+T*+T*A*T*A*A*A*G*T*C*C*T*T*A*+G* +G*+C | 94005 | 18 |
| 3786 | GAAATACCAGGTTAT AAAG | A573784Hi | +G*+A*+A*A*T*A*C*C*A*G*G*T*T*A*T*A*+ A*+A*+G | 94014 | 19 |
| 3787 | GTGAAATACCAGGTT ATA | A573785Hi | +G*+T*+G*A*A*A*T*A*C*C*A*G*G*T*T*+A* +T*+A | 94017 | 18 |
| 3788 | TTCTACTTGCAGTGT CTGG | A573786Hi | +T*+T*+C*T*A*C*T*T*G*C*A*G*T*G*T*C*+ T*+G*+G | 94478 | 19 |
| 3789 | GGATTCTACTTGCAG TGT | A573787Hi | +G*+G*+A*T*T*C*T*A*C*T*T*G*C*A*G*+T* +G*+T | 94482 | 18 |
| 3790 | GATGGATTCTACTTG CAGT | A573788Hi | +G*+A*+T*G*G*A*T*T*C*T*A*C*T*T*G*C*+ A*+G*+T | 94484 | 19 |

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| 3791 | ATGGATTCTACTTGCAGT | A573789Hi | +A*+T*+G*G*A*T*T*C*T*A*C*T*T*G*C*+A*+G*+T | 94484 | 18 |
| 3792 | TGATGGATTCTACTTGCAG | A573790Hi | +T*+G*+A*T*G*G*A*T*T*C*T*A*C*T*T*G*+C*+A*+G | 94485 | 19 |
| 3793 | GATGGATTCTACTTGCAG | A573791Hi | +G*+A*+T*G*G*A*T*T*C*T*A*C*T*T*G*+C*+A*+G | 94485 | 18 |
| 3794 | GATTCTCAAAGTAACTAC | A573792Hi | +G*+A*+T*T*C*T*C*A*A*A*G*T*A*A*C*+T*+A*+C | 94511 | 18 |
| 3795 | TCATGATTCTCAAAGTAAC | A573793Hi | +T*+C*+A*T*G*A*T*T*C*T*C*A*A*A*G*T*+A*+A*+C | 94514 | 19 |
| 3796 | TTTCATGATTCTCAAAGTA | A573794Hi | +T*+T*+T*C*A*T*G*A*T*T*C*T*C*A*A*A*+G*+T*+A | 94516 | 19 |
| 3797 | GAGTTTCATGATTCTCAAA | A573795Hi | +G*+A*+G*T*T*T*C*A*T*G*A*T*T*C*T*C*+A*+A*+A | 94519 | 19 |
| 3798 | AGAGTTTCATGATTCTCAA | A573796Hi | +A*+G*+A*G*T*T*T*C*A*T*G*A*T*T*C*T*+C*+A*+A | 94520 | 19 |
| 3799 | ATTTATATACTAGGAGAGG | A573797Hi | +A*+T*+T*T*A*T*A*T*A*C*T*A*G*G*A*G*+A*+G*+G | 94571 | 19 |
| 3800 | CATTTATATACTAGGAGAG | A573798Hi | +C*+A*+T*T*T*A*T*A*T*A*C*T*A*G*G*A*+G*+A*+G | 94572 | 19 |
| 3801 | ACAGGTTTGAAATAGAAAT | A573799Hi | +A*+C*+A*G*G*T*T*T*G*A*A*A*T*A*G*A*+A*+A*+T | 94600 | 19 |
| 3802 | CAGTCTCATCAATAATATA | A573800Hi | +C*+A*+G*T*C*T*C*A*T*C*A*A*T*A*A*T*+A*+T*+A | 94654 | 19 |
| 3803 | GCAGTCTCATCAATAATAT | A573801Hi | +G*+C*+A*G*T*C*T*C*A*T*C*A*A*T*A*A*+T*+A*+T | 94655 | 19 |
| 3804 | GCAGTCTCATCAATAATA | A573802Hi | +G*+C*+A*G*T*C*T*C*A*T*C*A*A*T*A*+A*+T*+A | 94656 | 18 |
| 3805 | GTCTCTTTGCTCAGTGAAA | A573803Hi | +G*+T*+C*T*C*T*T*T*G*C*T*C*A*G*T*G*+A*+A*+A | 94902 | 19 |
| 3806 | GTCTCTTTGCTCAGTGAA | A573804Hi | +G*+T*+C*T*C*T*T*T*G*C*T*C*A*G*T*+G*+A*+A | 94903 | 18 |
| 3807 | GTTGCAAATTTAAAGCATT | A573805Hi | +G*+T*+T*G*C*A*A*A*T*T*T*A*A*A*G*C*+A*+T*+T | 94925 | 19 |
| 3808 | CCACTTTCACTGTCAAAT | A573806H | +C*+C*+A*C*T*T*T*C*A*C*T*G*T*C*A*A*+A*+A*+T | 94992 | 19 |
| 3809 | CTTCCACTTTCACTGTCAA | A573807H | +C*+T*+T*C*C*A*C*T*T*T*C*A*C*T*G*T*+C*+A*+A | 94995 | 19 |
| 3810 | CAACCTTCCACTTTCACTG | A573808H | +C*+A*+A*C*C*T*T*C*C*A*C*T*T*T*C*A*+C*+T*+G | 94999 | 19 |
| 3811 | GACAACCTTCCACTTTCAC | A573809H | +G*+A*+C*A*A*C*C*T*T*C*C*A*C*T*T*T*+C*+A*+C | 95001 | 19 |
| 3812 | GGACAACCTTCCACTTTCA | A573810H | +G*+G*+A*C*A*A*C*C*T*T*C*C*A*C*T*T*+T*+C*+A | 95002 | 19 |
| 3813 | TTGGACAACCTTCCACTTT | A573811H | +T*+T*+G*G*A*C*A*A*C*C*T*T*C*C*A*C*+T*+T*+T | 95004 | 19 |
| 3814 | TTGGACAACCTTCCACTT | A573812H | +T*+T*+G*G*A*C*A*A*C*C*T*T*C*C*A*+C*+T*+T | 95005 | 18 |
| 3815 | TTTGGACAACCTTCCACTT | A573813H | +T*+T*+T*G*G*A*C*A*A*C*C*T*T*C*C*A*+C*+T*+T | 95005 | 19 |
| 3816 | TTTTGGACAACCTTCCACT | A573814H | +T*+T*+T*T*G*G*A*C*A*A*C*C*T*T*C*C*+A*+C*+T | 95006 | 19 |
| 3817 | GTTTTGGACAACCTTCCAC | A573815H | +G*+T*+T*T*T*G*G*A*C*A*A*C*C*T*T*C*+C*+A*+C | 95007 | 19 |
| 3818 | TGTTTTGGACAACCTTCCA | A573816H | +T*+G*+T*T*T*T*G*G*A*C*A*A*C*C*T*T*+C*+C*+A | 95008 | 19 |
| 3819 | TGTTTTGGACAACCTTCC | A573817H | +T*+G*+T*T*T*T*G*G*A*C*A*A*C*C*T*+T*+C*+C | 95009 | 18 |
| 3820 | GTGTTTTGGACAACCTTCC | A573818H | +G*+T*+G*T*T*T*T*G*G*A*C*A*A*C*C*T*+T*+C*+C | 95009 | 19 |
| 3821 | AGGGTGTTTTGGACAACCT | A573819H | +A*+G*+G*G*T*G*T*T*T*T*G*G*A*C*A*A*+C*+C*+T | 95012 | 19 |
| 3822 | AGGGTGTTTTGGACAACC | A573820H | +A*+G*+G*G*T*G*T*T*T*T*G*G*A*C*A*+A*+C*+C | 95013 | 18 |
| 3823 | TAGGGTGTTTTGGACAACC | A573821H | +T*+A*+G*G*G*T*G*T*T*T*T*G*G*A*C*A*+A*+C*+C | 95013 | 19 |
| 3824 | CTTAGGGTGTTTTGGACAA | A573822H | +C*+T*+T*A*G*G*G*T*G*T*T*T*T*G*G*A*+C*+A*+A | 95015 | 19 |
| 3825 | CCTTAGGGTGTTTTGGACA | A573823H | +C*+C*+T*T*A*G*G*G*T*G*T*T*T*T*T*G*G*+A*+C*+A | 95016 | 19 |

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| 3826 | CCCTTAGGGTGTTTTGGAC | A573824H | +C*+C*+C*T*T*A*G*G*G*T*G*T*T*T*T*G*+G*+A*+C | 95017 | 19 |
| 3827 | AATTTTTCCACATCTCTAC | A573825H | +A*+A*+T*T*T*T*T*C*C*A*C*A*T*C*T*C*+T*+A*+C | 95047 | 19 |
| 3828 | GTGACATGTAGTTCTTTGG | A573826H | +G*+T*+G*A*C*A*T*G*T*A*G*T*T*C*T*T*+T*+G*+G | 95088 | 19 |
| 3829 | ATACTGTGACATGTAGTTC | A573827H | +A*+T*+A*C*T*G*T*G*A*C*A*T*G*T*A*G*+T*+T*+C | 95093 | 19 |
| 3830 | CTTAAAATACTGTGACATG | A573828H | +C*+T*+T*A*A*A*A*T*A*C*T*G*T*G*A*C*+A*+T*+G | 95099 | 19 |
| 3831 | GAGCTTAAAATACTGTGAC | A573829H | +G*+A*+G*C*T*T*A*A*A*A*T*A*C*T*G*T*+G*+A*+C | 95102 | 19 |
| 3832 | CTAGGAGCTTAAAATACTG | A573830H | +C*+T*+A*G*G*A*G*C*T*T*A*A*A*A*T*A*+C*+T*+G | 95106 | 19 |
| 3833 | TCTAGGAGCTTAAAATACT | A573831H | +T*+C*+T*A*G*G*A*G*C*T*T*A*A*A*A*T*+A*+C*+T | 95107 | 19 |
| 3834 | AATTTTTCTAGGAGCTTAA | A573832H | +A*+A*+T*T*T*T*T*C*T*A*G*G*A*G*C*T*+T*+A*+A | 95113 | 19 |
| 3835 | CTGGAATTTTTCTAGGAGC | A573833H | +C*+T*+G*G*A*A*T*T*T*T*T*C*T*A*G*G*+A*+G*+C | 95117 | 19 |
| 3836 | TCTGGAATTTTTCTAGGAG | A573834H | +T*+C*+T*G*G*A*A*T*T*T*T*T*C*T*A*G*+G*+A*+G | 95118 | 19 |
| 3837 | ATCTGGAATTTTTCTAGGA | A573835H | +A*+T*+C*T*G*G*A*A*T*T*T*T*T*C*T*A*+G*+G*+A | 95119 | 19 |
| 3838 | AATCTGGAATTTTTCTAGG | A573836H | +A*+A*+T*C*T*G*G*A*A*T*T*T*T*T*C*T*+A*+G*+G | 95120 | 19 |
| 3839 | CAATCTGGAATTTTTCTAG | A573837H | +C*+A*+A*T*C*T*G*G*A*A*T*T*T*T*T*C*+T*+A*+G | 95121 | 19 |
| 3840 | TGGCAAAGCAATCTGGAAT | A573838H | +T*+G*+G*C*A*A*A*G*C*A*A*T*C*T*G*G*+A*+A*+T | 95129 | 19 |
| 3841 | TATTGGCAAAGCAATCTGG | A573839H | +T*+A*+T*T*G*G*C*A*A*A*G*C*A*A*T*C*+T*+G*+G | 95132 | 19 |
| 3842 | CTATTGGCAAAGCAATCTG | A573840H | +C*+T*+A*T*T*G*G*C*A*A*A*G*C*A*A*T*+C*+T*+G | 95133 | 19 |
| 3843 | CCTATTGGCAAAGCAATCT | A573841H | +C*+C*+T*A*T*T*G*G*C*A*A*A*G*C*A*A*+T*+C*+T | 95134 | 19 |
| 3844 | TCCTATTGGCAAAGCAATC | A573842H | +T*+C*+C*T*A*T*T*G*G*C*A*A*A*G*C*A*+A*+T*+C | 95135 | 19 |
| 3845 | CTCCTATTGGCAAAGCAAT | A573843H | +C*+T*+C*C*T*A*T*T*G*G*C*A*A*A*G*C*+A*+A*+T | 95136 | 19 |
| 3846 | TTCTCCTATTGGCAAAGCA | A573844H | +T*+T*+C*T*C*C*T*A*T*T*G*G*C*A*A*A*+G*+C*+A | 95138 | 19 |
| 3847 | TCTTCTCCTATTGGCAAAG | A573845H | +T*+C*+T*T*C*T*C*C*T*A*T*T*G*G*C*A*+A*+A*+G | 95140 | 19 |
| 3848 | ATTCTTCTCCTATTGGCAA | A573846H | +A*+T*+T*C*T*T*C*T*C*C*T*A*T*T*G*G*+C*+A*+A | 95142 | 19 |
| 3849 | ATATTCTTCTCCTATTGGC | A573847H | +A*+T*+A*T*T*C*T*T*C*T*C*C*T*A*T*T*+G*+G*+C | 95144 | 19 |
| 3850 | TGGAACCAGCAAATATTCT | A573848H | +T*+G*+G*A*A*C*C*A*G*C*A*A*A*T*A*T*+T*+C*+T | 95156 | 19 |
| 3851 | TTGGAACCAGCAAATATTC | A573849H | +T*+T*+G*G*A*A*C*C*A*G*C*A*A*A*T*A*+T*+T*+C | 95157 | 19 |
| 3852 | CTTGGAACCAGCAAATATT | A573850H | +C*+T*+T*G*G*A*A*C*C*A*G*C*A*A*A*T*+A*+T*+T | 95158 | 19 |
| 3853 | CTGCTTGGAACCAGCAAAT | A573851H | +C*+T*+G*C*T*T*G*G*A*A*C*C*A*G*C*A*+A*+A*+T | 95161 | 19 |
| 3854 | ATAGTGAATTTCCATGTAG | A573852Hi | +A*+T*+A*G*T*G*A*A*T*T*T*C*C*A*T*G*+T*+A*+G | 95207 | 19 |
| 3855 | CTATTATAGACTACAGTTA | A573853Hi | +C*+T*+A*T*T*A*T*A*G*A*C*T*A*C*A*G*+T*+T*+A | 95247 | 19 |
| 3856 | CTATTATAGACTACAGTT | A573854Hi | +C*+T*+A*T*T*A*T*A*G*A*C*T*A*C*A*+G*+T*+T | 95248 | 18 |
| 3857 | AGTGTCAGATGCAATGTTT | A573855Hi | +A*+G*+T*G*T*C*A*G*A*T*G*C*A*A*T*G*+T*+T*+T | 95340 | 19 |
| 3858 | CTCTCAGTGTTGTTTAAGA | A573856Hi | +C*+T*+C*T*C*A*G*T*G*T*T*G*T*T*T*T*A*+A*+G*+A | 95489 | 19 |
| 3859 | CTCTCTCAGTGTTGTTTAA | A573857Hi | +C*+T*+C*T*C*T*C*A*G*T*G*T*T*G*T*T*T*+T*+A*+A | 95491 | 19 |
| 3860 | ACTCTCTCAGTGTTGTTTA | A573858Hi | +A*+C*+T*C*T*C*T*C*A*G*T*G*T*T*G*T*+T*+T*+A | 95492 | 19 |

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| 3861 | ATTTGCACATTTCAACATC | A573859Hi | +A*+T*+T*T*G*C*A*C*A*T*T*T*C*A*A*C*+A*+T*+C | 95657 | 19 |
| 3862 | ATTGGCTGCATCCATCAAT | A573860Hi | +A*+T*+T*G*G*C*T*G*C*A*T*C*C*A*T*C*+A*+A*+T | 95683 | 19 |
| 3863 | AGATGTAGATGCATGAAAT | A573861Hi | +A*+G*+A*T*G*T*A*G*A*T*G*C*A*T*G*A*+A*+A*+T | 95827 | 19 |
| 3864 | TCAGATGTAGATGCATGAA | A573862Hi | +T*+C*+A*G*A*T*G*T*A*G*A*T*G*C*A*T*+G*+A*+A | 95829 | 19 |
| 3865 | CTCAGATGTAGATGCATGA | A573863Hi | +C*+T*+C*A*G*A*T*G*T*A*G*A*T*G*C*A*+T*+G*+A | 95830 | 19 |
| 3866 | CTCAGATGTAGATGCATG | A573864Hi | +C*+T*+C*A*G*A*T*G*T*A*G*A*T*G*C*+A*+T*+G | 95831 | 18 |
| 3867 | TGCTCAGATGTAGATGCAT | A573865Hi | +T*+G*+C*T*C*A*G*A*T*G*T*A*G*A*T*G*+C*+A*+T | 95832 | 19 |
| 3868 | GCTCAGATGTAGATGCAT | A573866Hi | +G*+C*+T*C*A*G*A*T*G*T*A*G*A*T*G*+C*+A*+T | 95832 | 18 |
| 3869 | TGCTCAGATGTAGATGCA | A573867Hi | +T*+G*+C*T*C*A*G*A*T*G*T*A*G*A*T*+G*+C*+A | 95833 | 18 |
| 3870 | GCATGCTCAGATGTAGATG | A573868Hi | +G*+C*+A*T*G*C*T*C*A*G*A*T*G*T*A*G*+A*+T*+G | 95835 | 19 |
| 3871 | CATGCTCAGATGTAGATG | A573869Hi | +C*+A*+T*G*C*T*C*A*G*A*T*G*T*A*G*+A*+T*+G | 95835 | 18 |
| 3872 | TGCATGCTCAGATGTAGAT | A573870Hi | +T*+G*+C*A*T*G*C*T*C*A*G*A*T*G*T*A*+G*+A*+T | 95836 | 19 |
| 3873 | GCATGCTCAGATGTAGAT | A573871Hi | +G*+C*+A*T*G*C*T*C*A*G*A*T*G*T*A*+G*+A*+T | 95836 | 18 |
| 3874 | TCAAATGCATGCTCAGATG | A573872Hi | +T*+C*+A*A*A*T*G*C*A*T*G*C*T*C*A*G*+A*+T*+G | 95841 | 19 |
| 3875 | TGGTTATACAGCCTCACA | A573873Hi | +T*+G*+G*T*T*A*T*A*C*A*G*C*C*T*C*+A*+C*+A | 96000 | 18 |
| 3876 | TATGGTTATACAGCCTCAC | A573874Hi | +T*+A*+T*G*G*T*T*A*T*A*C*A*G*C*C*T*+C*+A*+C | 96001 | 19 |
| 3877 | ACTATGGTTATACAGCCT | A573875Hi | +A*+C*+T*A*T*G*G*T*T*A*T*A*C*A*G*+C*+C*+T | 96004 | 18 |
| 3878 | ACTATGGTTATACAGCC | A573876Hi | +A*+C*+T*A*T*G*G*T*T*A*T*A*C*A*+G*+C*+C | 96005 | 17 |
| 3879 | AGGACACTATGGTTATAC | A573877Hi | +A*+G*+G*A*C*A*C*T*A*T*G*G*T*T*A*+T*+A*+C | 96009 | 18 |
| 3880 | CTATCACAGGCCTGTGGTC | A573878H | +C*+T*+A*T*C*A*C*A*G*G*C*C*T*G*T*G*+G*+T*+C | 96045 | 19 |
| 3881 | GGAAGCTCTATCACAGGCC | A573879H | +G*+G*+A*A*G*C*T*C*T*A*T*C*A*C*A*G*+G*+C*+C | 96052 | 19 |
| 3882 | GGGAAGCTCTATCACAGGC | A573880H | +G*+G*+G*A*A*G*C*T*C*T*A*T*C*A*C*A*+G*+G*+C | 96053 | 19 |
| 3883 | TGGGGAAGCTCTATCACAG | A573881H | +T*+G*+G*G*G*A*A*G*C*T*C*T*A*T*C*A*+C*+A*+G | 96055 | 19 |
| 3884 | AATGGGGAAGCTCTATCAC | A573882H | +A*+A*+T*G*G*G*G*A*A*G*C*T*C*T*A*T*+C*+A*+C | 96057 | 19 |
| 3885 | TCACAATGGGGAAGCTCTA | A573883H | +T*+C*+A*C*A*A*T*G*G*G*G*A*A*G*C*T*+C*+T*+A | 96061 | 19 |
| 3886 | TCTCACAATGGGGAAGCTC | A573884H | +T*+C*+T*C*A*C*A*A*T*G*G*G*G*A*A*G*+C*+T*+C | 96063 | 19 |
| 3887 | TCTCACAATGGGGAAGCT | A573885H | +T*+C*+T*C*A*C*A*A*T*G*G*G*G*A*A*+G*+C*+T | 96064 | 18 |
| 3888 | TTCTCACAATGGGGAAGCT | A573886H | +T*+T*+C*T*C*A*C*A*A*T*G*G*G*G*A*A*+G*+C*+T | 96064 | 19 |
| 3889 | CAGAGTTCTCACAATGGGG | A573887H | +C*+A*+G*A*G*T*T*C*T*C*A*C*A*A*T*G*+G*+G*+G | 96069 | 19 |
| 3890 | GATAATTTCAGAGTTCTCA | A573888H | +G*+A*+T*A*A*T*T*T*C*A*G*A*G*T*T*C*+T*+C*+A | 96077 | 19 |
| 3891 | TGATAATTTCAGAGTTCTC | A573889H | +T*+G*+A*T*A*A*T*T*T*C*A*G*A*G*T*T*+C*+T*+C | 96078 | 19 |
| 3892 | ATGATAATTTCAGAGTTCT | A573890H | +A*+T*+G*A*T*A*A*T*T*T*C*A*G*A*G*T*+T*+C*+T | 96079 | 19 |
| 3893 | CGGATGATAATTTCAGAGT | A573891H | +C*+G*+G*A*T*G*A*T*A*A*T*T*T*C*A*G*+A*+G*+T | 96082 | 19 |
| 3894 | CGGATGATAATTTCAGAG | A573892H | +C*+G*+G*A*T*G*A*T*A*A*T*T*T*C*A*+G*+A*+G | 96083 | 18 |
| 3895 | TCGGATGATAATTTCAGAG | A573893H | +T*+C*+G*G*A*T*G*A*T*A*A*T*T*T*C*A*+G*+A*+G | 96083 | 19 |

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| 3896 | TCGGATGATAATTTCAGA | A573894H | +T*+C*+G*G*A*T*G*A*T*A*A*T*T*T*C*+A*+G*+A | 96084 | 18 |
| 3897 | GTCGGATGATAATTTCAGA | A573895H | +G*+T*+C*G*G*A*T*G*A*T*A*A*T*T*T*C*+A*+G*+A | 96084 | 19 |
| 3898 | GTCGGATGATAATTTCAG | A573896H | +G*+T*+C*G*G*A*T*G*A*T*A*A*T*T*T*+C*+A*+G | 96085 | 18 |
| 3899 | AGTCGGATGATAATTTCAG | A573897H | +A*+G*+T*C*G*G*A*T*G*A*T*A*A*T*T*T*+C*+A*+G | 96085 | 19 |
| 3900 | TAGTCGGATGATAATTTCA | A573898H | +T*+A*+G*T*C*G*G*A*T*G*A*T*A*A*T*T*+T*+C*+A | 96086 | 19 |
| 3901 | TAGTCGGATGATAATTTC | A573899H | +T*+A*+G*T*C*G*G*A*T*G*A*T*A*A*T*+T*+T*+C | 96087 | 18 |
| 3902 | ATAGTCGGATGATAATTTC | A573900H | +A*+T*+A*G*T*C*G*G*A*T*G*A*T*A*A*T*+T*+T*+C | 96087 | 19 |
| 3903 | TATAGTCGGATGATAATTT | A573901H | +T*+A*+T*A*G*T*C*G*G*A*T*G*A*T*A*A*+T*+T*+T | 96088 | 19 |
| 3904 | CATATAGTCGGATGATAAT | A573902H | +C*+A*+T*A*T*A*G*T*C*G*G*A*T*G*A*T*+A*+A*+T | 96090 | 19 |
| 3905 | TCATATAGTCGGATGATAA | A573903H | +T*+C*+A*T*A*T*A*G*T*C*G*G*A*T*G*A*+T*+A*+A | 96091 | 19 |
| 3906 | TCATATAGTCGGATGATA | A573904H | +T*+C*+A*T*A*T*A*G*T*C*G*G*A*T*G*+A*+T*+A | 96092 | 18 |
| 3907 | TTCATATAGTCGGATGATA | A573905H | +T*+T*+C*A*T*A*T*A*G*T*C*G*G*A*T*G*+A*+T*+A | 96092 | 19 |
| 3908 | TTTCATATAGTCGGATGAT | A573906H | +T*+T*+T*C*A*T*A*T*A*G*T*C*G*G*A*T*+G*+A*+T | 96093 | 19 |
| 3909 | TTTCATATAGTCGGATGA | A573907H | +T*+T*+T*C*A*T*A*T*A*G*T*C*G*G*A*+T*+G*+A | 96094 | 18 |
| 3910 | ATTTCATATAGTCGGATGA | A573908H | +A*+T*+T*T*C*A*T*A*T*A*G*T*C*G*G*A*+T*+G*+A | 96094 | 19 |
| 3911 | TTTCATATAGTCGGATG | A573909H | +T*+T*+T*C*A*T*A*T*A*G*T*C*G*G*+A*+T*+G | 96095 | 17 |
| 3912 | ATTTCATATAGTCGGATG | A573910H | +A*+T*+T*T*C*A*T*A*T*A*G*T*C*G*G*+A*+T*+G | 96095 | 18 |
| 3913 | CATTTCATATAGTCGGATG | A573911H | +C*+A*+T*T*T*C*A*T*A*T*A*G*T*C*G*G*+A*+T*+G | 96095 | 19 |
| 3914 | ATTTCATATAGTCGGAT | A573912H | +A*+T*+T*T*C*A*T*A*T*A*G*T*C*G*+G*+A*+T | 96096 | 17 |
| 3915 | CATTTCATATAGTCGGAT | A573913H | +C*+A*+T*T*T*C*A*T*A*T*A*G*T*C*G*+G*+A*+T | 96096 | 18 |
| 3916 | GCATTTCATATAGTCGGAT | A573914H | +G*+C*+A*T*T*T*C*A*T*A*T*A*G*T*C*G*+G*+A*+T | 96096 | 19 |
| 3917 | GGCATTTCATATAGTCGGA | A573915H | +G*+G*+C*A*T*T*T*C*A*T*A*T*A*G*T*C*+G*+G*+A | 96097 | 19 |
| 3918 | GGCATTTCATATAGTCGG | A573916H | +G*+G*+C*A*T*T*T*C*A*T*A*T*A*G*T*+C*+G*+G | 96098 | 18 |
| 3919 | AGGCATTTCATATAGTCGG | A573917H | +A*+G*+G*C*A*T*T*T*C*A*T*A*T*A*G*T*+C*+G*+G | 96098 | 19 |
| 3920 | GGCATTTCATATAGTCG | A573918H | +G*+G*+C*A*T*T*T*C*A*T*A*T*A*G*+T*+C*+G | 96099 | 17 |
| 3921 | AGGCATTTCATATAGTCG | A573919H | +A*+G*+G*C*A*T*T*T*C*A*T*A*T*A*G*+T*+C*+G | 96099 | 18 |
| 3922 | AAGGCATTTCATATAGTCG | A573920H | +A*+A*+G*G*C*A*T*T*T*C*A*T*A*T*A*G*+T*+C*+G | 96099 | 19 |
| 3923 | AAGTAATCGATTGATTAA | A573921H | +A*+A*+G*T*A*A*T*C*G*A*T*T*G*A*T*+T*+A*+A | 96144 | 18 |
| 3924 | CAAGTAATCGATTGATTAA | A573922H | +C*+A*+A*G*T*A*A*T*C*G*A*T*T*G*A*T*+T*+A*+A | 96144 | 19 |
| 3925 | CAAGTAATCGATTGATTA | A573923H | +C*+A*+A*G*T*A*A*T*C*G*A*T*T*G*A*+T*+T*+A | 96145 | 18 |
| 3926 | TCAAGTAATCGATTGATTA | A573924H | +T*+C*+A*A*G*T*A*A*T*C*G*A*T*T*G*A*+T*+T*+A | 96145 | 19 |
| 3927 | TCAAGTAATCGATTGATT | A573925H | +T*+C*+A*A*G*T*A*A*T*C*G*A*T*T*G*+A*+T*+T | 96146 | 18 |
| 3928 | CTCAAGTAATCGATTGATT | A573926H | +C*+T*+C*A*A*G*T*A*A*T*C*G*A*T*T*G*+A*+T*+T | 96146 | 19 |
| 3929 | TCAAGTAATCGATTGAT | A573927H | +T*+C*+A*A*G*T*A*A*T*C*G*A*T*T*+G*+A*+T | 96147 | 17 |
| 3930 | CTCAAGTAATCGATTGAT | A573928H | +C*+T*+C*A*A*G*T*A*A*T*C*G*A*T*T*+G*+A*+T | 96147 | 18 |

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| 3931 | TCTCAAGTAATCGATTGAT | A573929H | +T*+C*+T*C*A*A*G*T*A*A*T*C*G*A*T*T*+G*+A*+T | 96147 | 19 |
| 3932 | CTCAAGTAATCGATTGA | A573930H | +C*+T*+C*A*A*G*T*A*A*T*C*G*A*T*+T*+G*+A | 96148 | 17 |
| 3933 | TCTCAAGTAATCGATTGA | A573931H | +T*+C*+T*C*A*A*G*T*A*A*T*C*G*A*T*+T*+G*+A | 96148 | 18 |
| 3934 | ATCTCAAGTAATCGATTGA | A573932H | +A*+T*+C*T*C*A*A*G*T*A*A*T*C*G*A*T*+T*+G*+A | 96148 | 19 |
| 3935 | AATCTCAAGTAATCGATTG | A573933H | +A*+A*+T*C*T*C*A*A*G*T*A*A*T*C*G*A*+T*+T*+G | 96149 | 19 |
| 3936 | AATCTCAAGTAATCGATT | A573934H | +A*+A*+T*C*T*C*A*A*G*T*A*A*T*C*G*+A*+T*+T | 96150 | 18 |
| 3937 | AAATCTCAAGTAATCGATT | A573935H | +A*+A*+A*T*C*T*C*A*A*G*T*A*A*T*C*G*+A*+T*+T | 96150 | 19 |
| 3938 | GAAATCTCAAGTAATCGAT | A573936H | +G*+A*+A*A*T*C*T*C*A*A*G*T*A*A*T*C*+G*+A*+T | 96151 | 19 |
| 3939 | GAAATCTCAAGTAATCGA | A573937H | +G*+A*+A*A*T*C*T*C*A*A*G*T*A*A*T*+C*+G*+A | 96152 | 18 |
| 3940 | TGAAATCTCAAGTAATCGA | A573938H | +T*+G*+A*A*A*T*C*T*C*A*A*G*T*A*A*T*+C*+G*+A | 96152 | 19 |
| 3941 | GAAATCTCAAGTAATCG | A573939H | +G*+A*+A*A*T*C*T*C*A*A*G*T*A*A*+T*+C*+G | 96153 | 17 |
| 3942 | TGAAATCTCAAGTAATCG | A573940H | +T*+G*+A*A*A*T*C*T*C*A*A*G*T*A*A*+T*+C*+G | 96153 | 18 |
| 3943 | GTGAAATCTCAAGTAATCG | A573941H | +G*+T*+G*A*A*A*T*C*T*C*A*A*G*T*A*A*+T*+C*+G | 96153 | 19 |
| 3944 | AAGGTGAAATCTCAAGTAA | A573942H | +A*+A*+G*G*T*G*A*A*A*T*C*T*C*A*A*G*+T*+A*+A | 96156 | 19 |
| 3945 | TAAGGTGAAATCTCAAGTA | A573943H | +T*+A*+A*G*G*T*G*A*A*A*T*C*T*C*A*A*+G*+T*+A | 96157 | 19 |
| 3946 | TAAGGTGAAATCTCAAGT | A573944H | +T*+A*+A*G*G*T*G*A*A*A*T*C*T*C*A*+A*+G*+T | 96158 | 18 |
| 3947 | GTAAGGTGAAATCTCAAGT | A573945H | +G*+T*+A*A*G*G*T*G*A*A*A*T*C*T*C*A*+A*+G*+T | 96158 | 19 |
| 3948 | TGTAAGGTGAAATCTCAAG | A573946H | +T*+G*+T*A*A*G*G*T*G*A*A*A*T*C*T*C*+A*+A*+G | 96159 | 19 |
| 3949 | GCATGTAAGGTGAAATCTC | A573947H | +G*+C*+A*T*G*T*A*A*G*G*T*G*A*A*A*T*+C*+T*+C | 96162 | 19 |
| 3950 | AAGCATGTAAGGTGAAATC | A573948H | +A*+A*+G*C*A*T*G*T*A*A*G*G*T*G*A*A*+A*+T*+C | 96164 | 19 |
| 3951 | AAAGCATGTAAGGTGAAAT | A573949H | +A*+A*+A*G*C*A*T*G*T*A*A*G*G*T*G*A*+A*+A*+T | 96165 | 19 |
| 3952 | GAAAGCATGTAAGGTGAAA | A573950H | +G*+A*+A*A*G*C*A*T*G*T*A*A*G*G*T*G*+A*+A*+A | 96166 | 19 |
| 3953 | CCTGAAAGCATGTAAGGTG | A573951H | +C*+C*+T*G*A*A*A*G*C*A*T*G*T*A*A*G*+G*+T*+G | 96169 | 19 |
| 3954 | CCCTGAAAGCATGTAAGGT | A573952H | +C*+C*+C*T*G*A*A*A*G*C*A*T*G*T*A*A*+G*+G*+T | 96170 | 19 |
| 3955 | CCCTGAAAGCATGTAAGG | A573953H | +C*+C*+C*T*G*A*A*A*G*C*A*T*G*T*A*+A*+G*+G | 96171 | 18 |
| 3956 | TCCCTGAAAGCATGTAAGG | A573954H | +T*+C*+C*C*T*G*A*A*A*G*C*A*T*G*T*A*+A*+G*+G | 96171 | 19 |
| 3957 | TCTCCCTGAAAGCATGTAA | A573955H | +T*+C*+T*C*C*C*T*G*A*A*A*G*C*A*T*G*+T*+A*+A | 96173 | 19 |
| 3958 | ATTCTTCAGCTGCCTTCCA | A573956Hi | +A*+T*+T*C*T*T*C*A*G*C*T*G*C*C*T*T*+C*+C*+A | 96317 | 19 |
| 3959 | TCTAATTCTTCAGCTGCCT | A573957Hi | +T*+C*+T*A*A*T*T*C*T*T*C*A*G*C*T*G*+C*+C*+T | 96321 | 19 |
| 3960 | TGAGGTTATATGTGCTTG | A573958Hi | +T*+G*+A*G*G*T*T*A*T*A*T*G*T*G*C*+T*+T*+G | 96383 | 18 |
| 3961 | GAGGTTATATGTGCTTG | A573959Hi | +G*+A*+G*G*T*T*A*T*A*T*G*T*G*C*+T*+T*+G | 96383 | 17 |
| 3962 | AGTGGCTGTGCAACAGAAA | A573960Hi | +A*+G*+T*G*G*C*T*G*T*G*C*A*A*C*A*G*+A*+A*+A | 96483 | 19 |
| 3963 | AAACACCGGATTTGCTCTT | A573961Hi | +A*+A*+A*C*A*C*C*G*G*A*T*T*T*G*C*T*+C*+T*+T | 96518 | 19 |
| 3964 | AAACACCGGATTTGCTCT | A573962Hi | +A*+A*+A*C*A*C*C*G*G*A*T*T*T*G*C*+T*+C*+T | 96519 | 18 |
| 3965 | ACACCTGTGTAAAGCTAAT | A573963Hi | +A*+C*+A*C*C*T*G*T*G*T*A*A*A*G*C*T*+A*+A*+T | 96615 | 19 |

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| 3966 | TATGTTGATTAATTCCAAT | A573964Hi | +T*+A*+T*G*T*T*G*A*T*T*A*A*T*T*C*C*+A*+A*+T | 96663 | 19 |
| 3967 | ACCTATATGTTGATTAATT | A573965Hi | +A*+C*+C*T*A*T*A*T*G*T*T*G*A*T*T*A*+A*+T*+T | 96668 | 19 |
| 3968 | AACTACCTATATGTTGATT | A573966Hi | +A*+A*+C*T*A*C*C*T*A*T*A*T*G*T*T*G*+A*+T*+T | 96672 | 19 |
| 3969 | ATGCTGTTAAGCAGTTTAA | A573967Hi | +A*+T*+G*C*T*G*T*T*A*A*G*C*A*G*T*T*+T*+A*+A | 96800 | 19 |
| 3970 | GATGCTGTTAAGCAGTTTA | A573968Hi | +G*+A*+T*G*C*T*G*T*T*A*A*G*C*A*G*T*+T*+T*+A | 96801 | 19 |
| 3971 | GTTGATGCTGTTAAGCAG | A573969Hi | +G*+T*+T*G*A*T*G*C*T*G*T*T*A*A*G*+C*+A*+G | 96805 | 18 |
| 3972 | AGGTTGATGCTGTTAAGCA | A573970Hi | +A*+G*+G*T*T*G*A*T*G*C*T*G*T*T*A*A*+G*+C*+A | 96806 | 19 |
| 3973 | CAGGTTGATGCTGTTAAGC | A573971Hi | +C*+A*+G*G*T*T*G*A*T*G*C*T*G*T*T*A*+A*+G*+C | 96807 | 19 |
| 3974 | AGGTTGATGCTGTTAAGC | A573972Hi | +A*+G*+G*T*T*G*A*T*G*C*T*G*T*T*A*+A*+G*+C | 96807 | 18 |
| 3975 | TCAGGTTGATGCTGTTAAG | A573973Hi | +T*+C*+A*G*G*T*T*G*A*T*G*C*T*G*T*T*+A*+A*+G | 96808 | 19 |
| 3976 | TCCATTTCAGGTTGATGCT | A573974Hi | +T*+C*+C*A*T*T*T*C*A*G*G*T*T*G*A*T*+G*+C*+T | 96814 | 19 |
| 3977 | ATCCATTTCAGGTTGATGC | A573975Hi | +A*+T*+C*C*A*T*T*T*C*A*G*G*T*T*G*A*+T*+G*+C | 96815 | 19 |
| 3978 | TCCATTTCAGGTTGATGC | A573976Hi | +T*+C*+C*A*T*T*T*C*A*G*G*T*T*G*A*+T*+G*+C | 96815 | 18 |
| 3979 | AAGATCCATTTCAGGTTGA | A573977Hi | +A*+A*+G*A*T*C*C*A*T*T*T*C*A*G*G*T*+T*+G*+A | 96818 | 19 |
| 3980 | CTCATCCATATCTATTAAA | A573978Hi | +C*+T*+C*A*T*C*C*A*T*A*T*C*T*A*T*T*+A*+A*+A | 96886 | 19 |
| 3981 | GTCCTCATCCATATCTATT | A573979Hi | +G*+T*+C*C*T*C*A*T*C*C*A*T*A*T*C*T*+A*+T*+T | 96889 | 19 |
| 3982 | TATGAGTCCTCATCCATAT | A573980Hi | +T*+A*+T*G*A*G*T*C*C*T*C*A*T*C*C*A*+T*+A*+T | 96894 | 19 |
| 3983 | TATGAGTCCTCATCCATA | A573981Hi | +T*+A*+T*G*A*G*T*C*C*T*C*A*T*C*C*+A*+T*+A | 96895 | 18 |
| 3984 | ATATGAGTCCTCATCCATA | A573982Hi | +A*+T*+A*T*G*A*G*T*C*C*T*C*A*T*C*C*+A*+T*+A | 96895 | 19 |
| 3985 | TGGGCGAAGTGCTCGTT | A573983H | +T*+G*+G*G*C*G*A*A*G*T*G*C*T*C*+G*+T*+T | 97039 | 17 |
| 3986 | TTGGGCGAAGTGCTCGTT | A573984H | +T*+T*+G*G*G*C*G*A*A*G*T*G*C*T*C*+G*+T*+T | 97039 | 18 |
| 3987 | TTTGGGCGAAGTGCTCGTT | A573985H | +T*+T*+T*G*G*G*C*G*A*A*G*T*G*C*T*C*+G*+T*+T | 97039 | 19 |
| 3988 | TTGGGCGAAGTGCTCGT | A573986H | +T*+T*+G*G*G*C*G*A*A*G*T*G*C*T*+C*+G*+T | 97040 | 17 |
| 3989 | TTTGGGCGAAGTGCTCGT | A573987H | +T*+T*+T*G*G*G*C*G*A*A*G*T*G*C*T*+C*+G*+T | 97040 | 18 |
| 3990 | GTTTGGGCGAAGTGCTCGT | A573988H | +G*+T*+T*T*G*G*G*C*G*A*A*G*T*G*C*T*+C*+G*+T | 97040 | 19 |
| 3991 | TTTGGGCGAAGTGCTCG | A573989H | +T*+T*+T*G*G*G*C*G*A*A*G*T*G*C*+T*+C*+G | 97041 | 17 |
| 3992 | GTTTGGGCGAAGTGCTCG | A573990H | +G*+T*+T*T*G*G*G*C*G*A*A*G*T*G*C*+T*+C*+G | 97041 | 18 |
| 3993 | TGTTTGGGCGAAGTGCTCG | A573991H | +T*+G*+T*T*T*G*G*G*C*G*A*A*G*T*G*C*+T*+C*+G | 97041 | 19 |
| 3994 | TGTTTGGGCGAAGTGCTC | A573992H | +T*+G*+T*T*T*G*G*G*C*G*A*A*G*T*G*+C*+T*+C | 97042 | 18 |
| 3995 | CTGTTTGGGCGAAGTGCTC | A573993H | +C*+T*+G*T*T*T*G*G*G*C*G*A*A*G*T*G*+C*+T*+C | 97042 | 19 |
| 3996 | TGTTTGGGCGAAGTGCT | A573994H | +T*+G*+T*T*T*G*G*G*C*G*A*A*G*T*+G*+C*+T | 97043 | 17 |
| 3997 | CTGTTTGGGCGAAGTGCT | A573995H | +C*+T*+G*T*T*T*G*G*G*C*G*A*A*G*T*+G*+C*+T | 97043 | 18 |
| 3998 | TCTGTTTGGGCGAAGTGCT | A573996H | +T*+C*+T*G*T*T*T*G*G*G*C*G*A*A*G*T*+G*+C*+T | 97043 | 19 |
| 3999 | TCTGTTTGGGCGAAGTGC | A573997H | +T*+C*+T*G*T*T*T*G*G*G*C*G*A*A*G*+T*+G*+C | 97044 | 18 |
| 4000 | TTCTGTTTGGGCGAAGTGC | A573998H | +T*+T*+C*T*G*T*T*T*G*G*G*C*G*A*A*G*+T*+G*+C | 97044 | 19 |

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| 4001 | TTCTGTTTGGGCGAAGTG | A573999H | +T*+T*+C*T*G*T*T*T*G*G*G*C*G*A*A*+G*+T*+G | 97045 | 18 |
| 4002 | ATTCTGTTTGGGCGAAGTG | A574000H | +A*+T*+T*C*T*G*T*T*T*G*G*G*C*G*A*A*+G*+T*+G | 97045 | 19 |
| 4003 | CATTCTGTTTGGGCGAAGT | A574001H | +C*+A*+T*T*C*T*G*T*T*T*G*G*G*C*G*A*+A*+G*+T | 97046 | 19 |
| 4004 | ACATTCTGTTTGGGCGAAG | A574002H | +A*+C*+A*T*T*C*T*G*T*T*T*G*G*G*C*G*+A*+A*+G | 97047 | 19 |
| 4005 | CAATACATTCTGTTTGGGC | A574003H | +C*+A*+A*T*A*C*A*T*T*C*T*G*T*T*T*G*+G*+G*+C | 97051 | 19 |
| 4006 | CGCCAATACATTCTGTTTG | A574004H | +C*+G*+C*C*A*A*T*A*C*A*T*T*C*T*G*T*+T*+T*+G | 97054 | 19 |
| 4007 | CGCCAATACATTCTGTTT | A574005H | +C*+G*+C*C*A*A*T*A*C*A*T*T*C*T*G*+T*+T*+T | 97055 | 18 |
| 4008 | TCGCCAATACATTCTGTTT | A574006H | +T*+C*+G*C*C*A*A*T*A*C*A*T*T*C*T*G*+T*+T*+T | 97055 | 19 |
| 4009 | TCGCCAATACATTCTGTT | A574007H | +T*+C*+G*C*C*A*A*T*A*C*A*T*T*C*T*+G*+T*+T | 97056 | 18 |
| 4010 | GTCGCCAATACATTCTGTT | A574008H | +G*+T*+C*G*C*C*A*A*T*A*C*A*T*T*C*T*+G*+T*+T | 97056 | 19 |
| 4011 | TCGCCAATACATTCTGT | A574009H | +T*+C*+G*C*C*A*A*T*A*C*A*T*T*C*+T*+G*+T | 97057 | 17 |
| 4012 | GTCGCCAATACATTCTGT | A574010H | +G*+T*+C*G*C*C*A*A*T*A*C*A*T*T*C*+T*+G*+T | 97057 | 18 |
| 4013 | TGTCGCCAATACATTCTGT | A574011H | +T*+G*+T*C*G*C*C*A*A*T*A*C*A*T*T*C*+T*+G*+T | 97057 | 19 |
| 4014 | GTCGCCAATACATTCTG | A574012H | +G*+T*+C*G*C*C*A*A*T*A*C*A*T*T*+C*+T*+G | 97058 | 17 |
| 4015 | TGTCGCCAATACATTCTG | A574013H | +T*+G*+T*C*G*C*C*A*A*T*A*C*A*T*T*+C*+T*+G | 97058 | 18 |
| 4016 | TTGTCGCCAATACATTCTG | A574014H | +T*+T*+G*T*C*G*C*C*A*A*T*A*C*A*T*T*+C*+T*+G | 97058 | 19 |
| 4017 | TGTCGCCAATACATTCT | A574015H | +T*+G*+T*C*G*C*C*A*A*T*A*C*A*T*+T*+C*+T | 97059 | 17 |
| 4018 | TTGTCGCCAATACATTCT | A574016H | +T*+T*+G*T*C*G*C*C*A*A*T*A*C*A*T*+T*+C*+T | 97059 | 18 |
| 4019 | CTTGTCGCCAATACATTCT | A574017H | +C*+T*+T*G*T*C*G*C*C*A*A*T*A*C*A*T*+T*+C*+T | 97059 | 19 |
| 4020 | TTGTCGCCAATACATTC | A574018H | +T*+T*+G*T*C*G*C*C*A*A*T*A*C*A*+T*+T*+C | 97060 | 17 |
| 4021 | CTTGTCGCCAATACATTC | A574019H | +C*+T*+T*G*T*C*G*C*C*A*A*T*A*C*A*+T*+T*+C | 97060 | 18 |
| 4022 | CCTTGTCGCCAATACATTC | A574020H | +C*+C*+T*T*G*T*C*G*C*C*A*A*T*A*C*A*+T*+T*+C | 97060 | 19 |
| 4023 | CTTGTCGCCAATACATT | A574021H | +C*+T*+T*G*T*C*G*C*C*A*A*T*A*C*+A*+T*+T | 97061 | 17 |
| 4024 | CCTTGTCGCCAATACATT | A574022H | +C*+C*+T*T*G*T*C*G*C*C*A*A*T*A*C*+A*+T*+T | 97061 | 18 |
| 4025 | GCCTTGTCGCCAATACATT | A574023H | +G*+C*+C*T*T*G*T*C*G*C*C*A*A*T*A*C*+A*+T*+T | 97061 | 19 |
| 4026 | CCTTGTCGCCAATACAT | A574024H | +C*+C*+T*T*G*T*C*G*C*C*A*A*T*A*+C*+A*+T | 97062 | 17 |
| 4027 | GCCTTGTCGCCAATACAT | A574025H | +G*+C*+C*T*T*G*T*C*G*C*C*A*A*T*A*+C*+A*+T | 97062 | 18 |
| 4028 | TGCCTTGTCGCCAATACAT | A574026H | +T*+G*+C*C*T*T*G*T*C*G*C*C*A*A*T*A*+C*+A*+T | 97062 | 19 |
| 4029 | TCAGGAGACCAATTTAAGT | A574027H | +T*+C*+A*G*G*A*G*A*C*C*A*A*T*T*T*A*+A*+G*+T | 97084 | 19 |
| 4030 | CTTCAGGAGACCAATTTAA | A574028H | +C*+T*+T*C*A*G*G*A*G*A*C*C*A*A*T*T*+T*+A*+A | 97086 | 19 |
| 4031 | GCTTCAGGAGACCAATTTA | A574029H | +G*+C*+T*T*C*A*G*G*A*G*A*C*C*A*A*T*+T*+T*+A | 97087 | 19 |
| 4032 | GCTTCAGGAGACCAATTT | A574030H | +G*+C*+T*T*C*A*G*G*A*G*A*C*C*A*A*+T*+T*+T | 97088 | 18 |
| 4033 | AGCTTCAGGAGACCAATTT | A574031H | +A*+G*+C*T*T*C*A*G*G*A*G*A*C*C*A*A*+T*+T*+T | 97088 | 19 |
| 4034 | GCTTCAGGAGACCAATT | A574032H | +G*+C*+T*T*C*A*G*G*A*G*A*C*C*A*+A*+T*+T | 97089 | 17 |
| 4035 | AGCTTCAGGAGACCAATT | A574033H | +A*+G*+C*T*T*C*A*G*G*A*G*A*C*C*A*+A*+T*+T | 97089 | 18 |

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| 4036 | AAGCTTCAGGAGACC AATT | A574034H | +A*+A*+G*C*T*T*C*A*G*G*A*G*A*C*C*A*+ A*+T*+T | 97089 | 19 |
| 4037 | GACAATAAGCTTCAG GAGA | A574035H | +G*+A*+C*A*A*T*A*A*G*C*T*T*C*A*G*G*+ A*+G*+A | 97095 | 19 |
| 4038 | GACAATAAGCTTCAG GAG | A574036H | +G*+A*+C*A*A*T*A*A*G*C*T*T*C*A*G*+G* +A*+G | 97096 | 18 |
| 4039 | AGACAATAAGCTTCA GGAG | A574037H | +A*+G*+A*C*A*A*T*A*A*G*C*T*T*C*A*G*+ G*+A*+G | 97096 | 19 |
| 4040 | CAGACAATAAGCTTC AGGA | A574038H | +C*+A*+G*A*C*A*A*T*A*A*G*C*T*T*C*A*+ G*+G*+A | 97097 | 19 |
| 4041 | CAGACAATAAGCTTC AGG | A574039H | +C*+A*+G*A*C*A*A*T*A*A*G*C*T*T*C*+A* +G*+G | 97098 | 18 |
| 4042 | CCAGACAATAAGCTT CAGG | A574040H | +C*+C*+A*G*A*C*A*A*T*A*A*G*C*T*T*C*+ A*+G*+G | 97098 | 19 |
| 4043 | CCAGACAATAAGCTT CAG | A574041H | +C*+C*+A*G*A*C*A*A*T*A*A*G*C*T*T*+C* +A*+G | 97099 | 18 |
| 4044 | ACCAGACAATAAGCT TCAG | A574042H | +A*+C*+C*A*G*A*C*A*A*T*A*A*G*C*T*T*+ C*+A*+G | 97099 | 19 |
| 4045 | ATCCTACCAGACAAT AAGC | A574043H | +A*+T*+C*C*T*A*C*C*A*G*A*C*A*A*T*A*+ A*+G*+C | 97104 | 19 |
| 4046 | CAGATCCTACCAGAC AATA | A574044H | +C*+A*+G*A*T*C*C*T*A*C*C*A*G*A*C*A*+ A*+T*+A | 97107 | 19 |
| 4047 | GACTTCAGATCCTAC CAGA | A574045H | +G*+A*+C*T*T*C*A*G*A*T*C*C*T*A*C*C*+ A*+G*+A | 97112 | 19 |
| 4048 | AAGACTTCAGATCCT ACCA | A574046H | +A*+A*+G*A*C*T*T*C*A*G*A*T*C*C*T*A*+ C*+C*+A | 97114 | 19 |
| 4049 | CTAAGACTTCAGATC CTAC | A574047H | +C*+T*+A*A*G*A*C*T*T*C*A*G*A*T*C*C*+ T*+A*+C | 97116 | 19 |
| 4050 | GTCTAAGACTTCAGA TCCT | A574048H | +G*+T*+C*T*A*A*G*A*C*T*T*C*A*G*A*T*+ C*+C*+T | 97118 | 19 |
| 4051 | TGTCTAAGACTTCAG ATCC | A574049H | +T*+G*+T*C*T*A*A*G*A*C*T*T*C*A*G*A*+ T*+C*+C | 97119 | 19 |
| 4052 | TGTCTAAGACTTCAG ATC | A574050H | +T*+G*+T*C*T*A*A*G*A*C*T*T*C*A*G*+A* +T*+C | 97120 | 18 |
| 4053 | TTGTCTAAGACTTCA GATC | A574051H | +T*+T*+G*T*C*T*A*A*G*A*C*T*T*C*A*G*+ A*+T*+C | 97120 | 19 |
| 4054 | TGATTGTCTAAGACT TCAG | A574052H | +T*+G*+A*T*T*G*T*C*T*A*A*G*A*C*T*T*+ C*+A*+G | 97123 | 19 |
| 4055 | TACAAGAAGGAACTG TAAT | A574053H | +T*+A*+C*A*A*G*A*A*G*G*A*A*C*T*G*T*+ A*+A*+T | 97161 | 19 |
| 4056 | TCTACAAGAAGGAAC TGTA | A574054H | +T*+C*+T*A*C*A*A*G*A*A*G*G*A*A*C*T*+ G*+T*+A | 97163 | 19 |
| 4057 | TTGGCCCAAAAGAAT ACAG | A574055H | +T*+T*+G*G*C*C*C*A*A*A*A*G*A*A*T*A*+ C*+A*+G | 97324 | 19 |
| 4058 | CTTGGCCCAAAAGAA TACA | A574056H | +C*+T*+T*G*G*C*C*C*A*A*A*A*G*A*A*T*+ A*+C*+A | 97325 | 19 |
| 4059 | CTTGGCCCAAAAGAA TAC | A574057H | +C*+T*+T*G*G*C*C*C*A*A*A*A*G*A*A*+T* +A*+C | 97326 | 18 |
| 4060 | ACTTGGCCCAAAAGA ATAC | A574058H | +A*+C*+T*T*G*G*C*C*C*A*A*A*A*G*A*A*+ T*+A*+C | 97326 | 19 |
| 4061 | AACTTGGCCCAAAAG AATA | A574059H | +A*+A*+C*T*T*G*G*C*C*C*A*A*A*A*G*A*+ A*+T*+A | 97327 | 19 |
| 4062 | CAACTTGGCCCAAAA GAAT | A574060H | +C*+A*+A*C*T*T*G*G*C*C*C*A*A*A*A*G*+ A*+A*+T | 97328 | 19 |
| 4063 | ACAACTTGGCCCAAA AGAA | A574061H | +A*+C*+A*A*C*T*T*G*G*C*C*C*A*A*A*A*+ G*+A*+A | 97329 | 19 |
| 4064 | GTCCACAACTTGGCC CAAA | A574062H | +G*+T*+C*C*A*C*A*A*C*T*T*G*G*C*C*C*+ A*+A*+A | 97333 | 19 |
| 4065 | GTGGTCCACAACTTG GCCC | A574063H | +G*+T*+G*G*T*C*C*A*C*A*A*C*T*T*G*G*+ C*+C*+C | 97336 | 19 |
| 4066 | CAATGTGGTCCACAA CTTG | A574064H | +C*+A*+A*T*G*T*G*G*T*C*C*A*C*A*A*C*+ T*+T*+G | 97340 | 19 |
| 4067 | ATCAATGTGGTCCAC AACT | A574065H | +A*+T*+C*A*A*T*G*T*G*G*T*C*C*A*C*A*+ A*+C*+T | 97342 | 19 |
| 4068 | ATCAATGTGGTCCAC AAC | A574066H | +A*+T*+C*A*A*T*G*T*G*G*T*C*C*A*C*+A* +A*+C | 97343 | 18 |
| 4069 | AATCAATGTGGTCCA CAAC | A574067H | +A*+A*+T*C*A*A*T*G*T*G*G*T*C*C*A*C*+ A*+A*+C | 97343 | 19 |
| 4070 | AGAGAATCAATGTGG TCCA | A574068H | +A*+G*+A*G*A*A*T*C*A*A*T*G*T*G*G*T*+ C*+C*+A | 97347 | 19 |

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| 4071 | TGAGAGAATCAATGTGGTC | A574069H | +T*+G*+A*G*A*G*A*A*T*C*A*A*T*G*T*G*+G*+T*+C | 97349 | 19 |
| 4072 | TCCAGCAACCCAGGAAACC | A574070H | +T*+C*+C*A*G*C*A*A*C*C*C*A*G*G*A*A*+A*+C*+C | 97377 | 19 |
| 4073 | TCCAGCAACCCAGGAAAC | A574071H | +T*+C*+C*A*G*C*A*A*C*C*C*A*G*G*A*+A*+A*+C | 97378 | 18 |
| 4074 | CTCCAGCAACCCAGGAAAC | A574072H | +C*+T*+C*C*A*G*C*A*A*C*C*C*A*G*G*A*+A*+A*+C | 97378 | 19 |
| 4075 | ATCTCCAGCAACCCAGGAA | A574073H | +A*+T*+C*T*C*C*A*G*C*A*A*C*C*C*A*G*+G*+A*+A | 97380 | 19 |
| 4076 | ATCAATCTCCAGCAACCCA | A574074H | +A*+T*+C*A*A*T*C*T*C*C*A*G*C*A*A*C*+C*+C*+A | 97384 | 19 |
| 4077 | TATCAATCTCCAGCAACCC | A574075H | +T*+A*+T*C*A*A*T*C*T*C*C*A*G*C*A*A*+C*+C*+C | 97385 | 19 |
| 4078 | TATCAATCTCCAGCAACC | A574076H | +T*+A*+T*C*A*A*T*C*T*C*C*A*G*C*A*+A*+C*+C | 97386 | 18 |
| 4079 | ATATCAATCTCCAGCAACC | A574077H | +A*+T*+A*T*C*A*A*T*C*T*C*C*A*G*C*A*+A*+C*+C | 97386 | 19 |
| 4080 | TCACCACAAATATCAATCT | A574078H | +T*+C*+A*C*C*A*C*A*A*A*T*A*T*C*A*A*+T*+C*+T | 97395 | 19 |
| 4081 | TCACCACAAATATCAATC | A574079H | +T*+C*+A*C*C*A*C*A*A*A*T*A*T*C*A*+A*+T*+C | 97396 | 18 |
| 4082 | TTCACCACAAATATCAATC | A574080H | +T*+T*+C*A*C*C*A*C*A*A*A*T*A*T*C*A*+A*+T*+C | 97396 | 19 |
| 4083 | CTCCTTCACCACAAATATC | A574081H | +C*+T*+C*C*T*T*C*A*C*C*A*C*A*A*A*T*+A*+T*+C | 97400 | 19 |
| 4084 | TTCTCCTTCACCACAAATA | A574082H | +T*+T*+C*T*C*C*T*T*C*A*C*C*A*C*A*A*+A*+T*+A | 97402 | 19 |
| 4085 | TTCTCCTTCACCACAAAT | A574083H | +T*+T*+C*T*C*C*T*T*C*A*C*C*A*C*A*+A*+A*+T | 97403 | 18 |
| 4086 | TTTCTCCTTCACCACAAAT | A574084H | +T*+T*+T*C*T*C*C*T*T*C*A*C*C*A*C*A*+A*+A*+T | 97403 | 19 |
| 4087 | ACAGAGTTTCTCCTTCACC | A574085H | +A*+C*+A*G*A*G*T*T*T*C*T*C*C*T*T*T*C*+A*+C*+C | 97409 | 19 |
| 4088 | AACAGAGTTTCTCCTTCAC | A574086H | +A*+A*+C*A*G*A*G*T*T*T*C*T*C*C*T*T*+C*+A*+C | 97410 | 19 |
| 4089 | CAACAGAGTTTCTCCTTCA | A574087H | +C*+A*+A*C*A*G*A*G*T*T*T*C*T*C*C*T*+T*+C*+A | 97411 | 19 |
| 4090 | TCAACAGAGTTTCTCCTTC | A574088H | +T*+C*+A*A*C*A*G*A*G*T*T*T*C*T*C*C*+T*+T*+C | 97412 | 19 |
| 4091 | CCATTTCTTCAACAGAGTT | A574089H | +C*+C*+A*T*T*T*C*T*T*C*A*A*C*A*G*A*+G*+T*+T | 97420 | 19 |
| 4092 | TAATGCCCATTTCTTCAAC | A574090H | +T*+A*+A*T*G*C*C*C*A*T*T*T*C*T*T*C*+A*+A*+C | 97426 | 19 |
| 4093 | ATATAATGCCCATTTCTTC | A574091H | +A*+T*+A*T*A*A*T*G*C*C*C*A*T*T*T*C*+T*+T*+C | 97429 | 19 |
| 4094 | CTTCACCATCATTAAAACT | A574092H | +C*+T*+T*C*A*C*C*A*T*C*A*T*T*A*A*A*+A*+C*+T | 97448 | 19 |
| 4095 | ATCAAGTAAGATTTTTTGA | A574093H | +A*+T*+C*A*A*G*T*A*A*G*A*T*T*T*T*T*+T*+G*+A | 97471 | 19 |
| 4096 | CATCAAGTAAGATTTTTTG | A574094H | +C*+A*+T*C*A*A*G*T*A*A*G*A*T*T*T*T*+T*+T*+G | 97472 | 19 |
| 4097 | TCAAGTCATCAAGTAAGAT | A574095H | +T*+C*+A*A*G*T*C*A*T*C*A*A*G*T*A*A*+G*+A*+T | 97478 | 19 |
| 4098 | ATCAAGTCATCAAGTAAGA | A574096H | +A*+T*+C*A*A*G*T*C*A*T*C*A*A*G*T*A*+A*+G*+A | 97479 | 19 |
| 4099 | ATCAAGTCATCAAGTAAG | A574097H | +A*+T*+C*A*A*G*T*C*A*T*C*A*A*G*T*+A*+A*+G | 97480 | 18 |
| 4100 | CATCAAGTCATCAAGTAAG | A574098H | +C*+A*+T*C*A*A*G*T*C*A*T*C*A*A*G*T*+A*+A*+G | 97480 | 19 |
| 4101 | TCATCAAGTCATCAAGTAA | A574099H | +T*+C*+A*T*C*A*A*G*T*C*A*T*C*A*A*G*+T*+A*+A | 97481 | 19 |
| 4102 | GCTTTCTTCATCAAGTCAT | A574100H | +G*+C*+T*T*T*C*T*T*C*A*T*C*A*A*G*T*+C*+A*+T | 97488 | 19 |
| 4103 | TCTGAATCTAGAATACAAG | A574101Hi | +T*+C*+T*G*A*A*T*C*T*A*G*A*A*T*A*C*+A*+A*+G | 97682 | 19 |
| 4104 | GCTGTTATTATATGGCAGA | A574102Hi | +G*+C*+T*G*T*T*A*T*T*A*T*A*T*G*G*C*+A*+G*+A | 97842 | 19 |
| 4105 | TTGCCACATTCATGAAGCT | A574103Hi | +T*+T*+G*C*C*A*C*A*T*T*C*A*T*G*A*A*+G*+C*+T | 97864 | 19 |

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| 4106 | CATCTGACTAGAAAG TTAT | A574104Hi | +C*+A*+T*C*T*G*A*C*T*A*G*A*A*A*G*T*+ T*+A*+T | 97896 | 19 |
| 4107 | GACATCTGACTAGAA AGTT | A574105Hi | +G*+A*+C*A*T*C*T*G*A*C*T*A*G*A*A*A*+ G*+T*+T | 97898 | 19 |
| 4108 | CTACCAGACATCTGA CTA | A574106Hi | +C*+T*+A*C*C*A*G*A*C*A*T*C*T*G*A*+C* +T*+A | 97905 | 18 |
| 4109 | CAGACTACCAGACAT CTGA | A574107Hi | +C*+A*+G*A*C*T*A*C*C*A*G*A*C*A*T*C*+ T*+G*+A | 97908 | 19 |
| 4110 | GCAGACTACCAGACA TCTG | A574108Hi | +G*+C*+A*G*A*C*T*A*C*C*A*G*A*C*A*T*+ C*+T*+G | 97909 | 19 |
| 4111 | ACTGCTGCAGACTAC CAGA | A574109Hi | +A*+C*+T*G*C*T*G*C*A*G*A*C*T*A*C*C*+ A*+G*+A | 97915 | 19 |
| 4112 | GAACTGCTGCAGACT ACCA | A574110Hi | +G*+A*+A*C*T*G*C*T*G*C*A*G*A*C*T*A*+ C*+C*+A | 97917 | 19 |
| 4113 | TGAACTGCTGCAGAC TACC | A574111Hi | +T*+G*+A*A*C*T*G*C*T*G*C*A*G*A*C*T*+ A*+C*+C | 97918 | 19 |
| 4114 | TCTGAACTGCTGCAG ACTA | A574112Hi | +T*+C*+T*G*A*A*C*T*G*C*T*G*C*A*G*A*+ C*+T*+A | 97920 | 19 |
| 4115 | CTGAACTGCTGCAGA CTA | A574113Hi | +C*+T*+G*A*A*C*T*G*C*T*G*C*A*G*A*+C* +T*+A | 97920 | 18 |
| 4116 | ACGTTCACTTGTAGA ATT | A574114Hi | +A*+C*+G*T*T*C*A*C*T*T*G*T*A*G*A*+A* +T*+T | 97938 | 18 |
| 4117 | CTACGTTCACTTGTA GAA | A574115Hi | +C*+T*+A*C*G*T*T*C*A*C*T*T*G*T*A*+G* +A*+A | 97940 | 18 |
| 4118 | CCTACGTTCACTTGT AG | A574116Hi | +C*+C*+T*A*C*G*T*T*C*A*C*T*T*G*+T*+A *+G | 97942 | 17 |
| 4119 | TCCTACGTTCACTTG TAG | A574117Hi | +T*+C*+C*T*A*C*G*T*T*C*A*C*T*T*G*+T* +A*+G | 97942 | 18 |
| 4120 | TATTCCTACGTTCACT TGT | A574118Hi | +T*+A*+T*T*C*C*T*A*C*G*T*T*C*A*C*T*+ T*+G*+T | 97944 | 19 |
| 4121 | TATTCCTACGTTCACT TG | A574119Hi | +T*+A*+T*T*C*C*T*A*C*G*T*T*C*A*C*+T* +T*+G | 97945 | 18 |
| 4122 | AACAACATTTAAGGA GATA | A574120Hi | +A*+A*+C*A*A*C*A*T*T*T*A*A*G*G*A*G*+ A*+T*+A | 98114 | 19 |
| 4123 | GATTTACTAAGAGAT CTC | A574121H | +G*+A*+T*T*T*A*C*T*A*A*G*A*G*A*T*+C* +T*+C | 98164 | 18 |
| 4124 | GGATTTACTAAGAGA TCTC | A574122H | +G*+G*+A*T*T*T*A*C*T*A*A*G*A*G*A*T*+ C*+T*+C | 98164 | 19 |
| 4125 | GGTTGATCTGGATTT ACTA | A574123H | +G*+G*+T*T*G*A*T*C*T*G*G*A*T*T*T*T*A*+ C*+T*+A | 98173 | 19 |
| 4126 | TGGTTGATCTGGATT TACT | A574124H | +T*+G*+G*T*T*G*A*T*C*T*G*G*A*T*T*T*+ A*+C*+T | 98174 | 19 |
| 4127 | TGGTTGATCTGGATT TAC | A574125H | +T*+G*+G*T*T*G*A*T*C*T*G*G*A*T*T*+T* +A*+C | 98175 | 18 |
| 4128 | TTGGTTGATCTGGAT TTAC | A574126H | +T*+T*+G*G*T*T*G*A*T*C*T*G*G*A*T*T*+ T*+A*+C | 98175 | 19 |
| 4129 | CCTTGGTTGATCTGG ATTT | A574127H | +C*+C*+T*T*G*G*T*T*G*A*T*C*T*G*G*A*+ T*+T*+T | 98177 | 19 |
| 4130 | GCCTTGGTTGATCTG GATT | A574128H | +G*+C*+C*T*T*G*G*T*T*G*A*T*C*T*G*G*+ A*+T*+T | 98178 | 19 |
| 4131 | GCCTTGGTTGATCTG GAT | A574129H | +G*+C*+C*T*T*G*G*T*T*G*A*T*C*T*G*+G* +A*+T | 98179 | 18 |
| 4132 | AGCCTTGGTTGATCT GGAT | A574130H | +A*+G*+C*C*T*T*G*G*T*T*G*A*T*C*T*G*+ G*+A*+T | 98179 | 19 |
| 4133 | GAGCCTTGGTTGATC TGGA | A574131H | +G*+A*+G*C*C*T*T*G*G*T*T*G*A*T*C*T*+ G*+G*+A | 98180 | 19 |
| 4134 | GAGCCTTGGTTGATC TGG | A574132H | +G*+A*+G*C*C*T*T*G*G*T*T*G*A*T*C*+T* +G*+G | 98181 | 18 |
| 4135 | TGAGCCTTGGTTGAT CTGG | A574133H | +T*+G*+A*G*C*C*T*T*G*G*T*T*G*A*T*C*+ T*+G*+G | 98181 | 19 |
| 4136 | GTGAGCCTTGGTTGA TCTG | A574134H | +G*+T*+G*A*G*C*C*T*T*G*G*T*T*G*A*T*+ C*+T*+G | 98182 | 19 |
| 4137 | GTGAGCCTTGGTTGA TCT | A574135H | +G*+T*+G*A*G*C*C*T*T*G*G*T*T*G*A*+T* +C*+T | 98183 | 18 |
| 4138 | GGTGAGCCTTGGTTG ATCT | A574136H | +G*+G*+T*G*A*G*C*C*T*T*G*G*T*T*G*A*+ T*+C*+T | 98183 | 19 |
| 4139 | GGTGAGCCTTGGTTG ATC | A574137H | +G*+G*+T*G*A*G*C*C*T*T*G*G*T*T*G*+A* +T*+C | 98184 | 18 |
| 4140 | TGGTGAGCCTTGGTT GATC | A574138H | +T*+G*+G*T*G*A*G*C*C*T*T*G*G*T*T*G*+ A*+T*+C | 98184 | 19 |

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| 4141 | AATGGTGAGCCTTGGTTGA | A574139H | +A*+A*+T*G*G*T*G*A*G*C*C*T*T*G*G*T*+T*+G*+A | 98186 | 19 |
| 4142 | AATGGTGAGCCTTGGTTG | A574140H | +A*+A*+T*G*G*T*G*A*G*C*C*T*T*G*G*+T*+T*+G | 98187 | 18 |
| 4143 | GAATGGTGAGCCTTGGTTG | A574141H | +G*+A*+A*T*G*G*T*G*A*G*C*C*T*T*G*G*+T*+T*+G | 98187 | 19 |
| 4144 | GAATGGTGAGCCTTGGTT | A574142H | +G*+A*+A*T*G*G*T*G*A*G*C*C*T*T*G*+G*+T*+T | 98188 | 18 |
| 4145 | GGAATGGTGAGCCTTGGTT | A574143H | +G*+G*+A*A*T*G*G*T*G*A*G*C*C*T*T*G*+G*+T*+T | 98188 | 19 |
| 4146 | TGGAATGGTGAGCCTTGGT | A574144H | +T*+G*+G*A*A*T*G*G*T*G*A*G*C*C*T*T*+G*+G*+T | 98189 | 19 |
| 4147 | TATTGGAATGGTGAGCCTT | A574145H | +T*+A*+T*T*G*G*A*A*T*G*G*T*G*A*G*C*+C*+T*+T | 98192 | 19 |
| 4148 | TATTGGAATGGTGAGCCT | A574146H | +T*+A*+T*T*G*G*A*A*T*G*G*T*G*A*G*+C*+C*+T | 98193 | 18 |
| 4149 | ATATTGGAATGGTGAGCCT | A574147H | +A*+T*+A*T*T*G*G*A*A*T*G*G*T*G*A*G*+C*+C*+T | 98193 | 19 |
| 4150 | CAATCTGAGATATTGGAAT | A574148H | +C*+A*+A*T*C*T*G*A*G*A*T*A*T*T*G*G*+A*+A*+T | 98202 | 19 |
| 4151 | GGCAATCTGAGATATTGGA | A574149H | +G*+G*+C*A*A*T*C*T*G*A*G*A*T*A*T*T*+G*+G*+A | 98204 | 19 |
| 4152 | GGCAATCTGAGATATTGG | A574150H | +G*+G*+C*A*A*T*C*T*G*A*G*A*T*A*T*+T*+G*+G | 98205 | 18 |
| 4153 | GGGCAATCTGAGATATTGG | A574151H | +G*+G*+G*C*A*A*T*C*T*G*A*G*A*T*A*T*+T*+G*+G | 98205 | 19 |
| 4154 | GGGCAATCTGAGATATTG | A574152H | +G*+G*+G*C*A*A*T*C*T*G*A*G*A*T*A*+T*+T*+G | 98206 | 18 |
| 4155 | GGGGCAATCTGAGATATTG | A574153H | +G*+G*+G*G*C*A*A*T*C*T*G*A*G*A*T*A*+T*+T*+G | 98206 | 19 |
| 4156 | GGGGCAATCTGAGATATT | A574154H | +G*+G*+G*G*C*A*A*T*C*T*G*A*G*A*T*+A*+T*+T | 98207 | 18 |
| 4157 | AGGGGCAATCTGAGATATT | A574155H | +A*+G*+G*G*G*C*A*A*T*C*T*G*A*G*A*T*+A*+T*+T | 98207 | 19 |
| 4158 | AGGGGCAATCTGAGATAT | A574156H | +A*+G*+G*G*G*C*A*A*T*C*T*G*A*G*A*+T*+A*+T | 98208 | 18 |
| 4159 | CAGGGGCAATCTGAGATAT | A574157H | +C*+A*+G*G*G*G*C*A*A*T*C*T*G*A*G*A*+T*+A*+T | 98208 | 19 |
| 4160 | GTCAGGGGCAATCTGAGAT | A574158H | +G*+T*+C*A*G*G*G*G*C*A*A*T*C*T*G*A*+G*+A*+T | 98210 | 19 |
| 4161 | CAAGTCAGGGGCAATCTGA | A574159H | +C*+A*+A*G*T*C*A*G*G*G*G*C*A*A*T*C*+T*+G*+A | 98213 | 19 |
| 4162 | TCAAGTCAGGGGCAATCTG | A574160H | +T*+C*+A*A*G*T*C*A*G*G*G*G*C*A*A*T*+C*+T*+G | 98214 | 19 |
| 4163 | ATCAAGTCAGGGGCAATCT | A574161H | +A*+T*+C*A*A*G*T*C*A*G*G*G*G*C*A*A*+T*+C*+T | 98215 | 19 |
| 4164 | ATCAAGTCAGGGGCAATC | A574162H | +A*+T*+C*A*A*G*T*C*A*G*G*G*G*C*A*+A*+T*+C | 98216 | 18 |
| 4165 | AATCAAGTCAGGGGCAATC | A574163H | +A*+A*+T*C*A*A*G*T*C*A*G*G*G*G*C*A*+A*+T*+C | 98216 | 19 |
| 4166 | AATCAAGTCAGGGGCAAT | A574164H | +A*+A*+T*C*A*A*G*T*C*A*G*G*G*G*C*+A*+A*+T | 98217 | 18 |
| 4167 | AAATCAAGTCAGGGGCAAT | A574165H | +A*+A*+A*T*C*A*A*G*T*C*A*G*G*G*G*C*+A*+A*+T | 98217 | 19 |
| 4168 | CAAAATCAAGTCAGGGGCA | A574166H | +C*+A*+A*A*A*T*C*A*A*G*T*C*A*G*G*G*+G*+C*+A | 98219 | 19 |
| 4169 | CCAAAATCAAGTCAGGGGC | A574167H | +C*+C*+A*A*A*A*T*C*A*A*G*T*C*A*G*G*+G*+G*+C | 98220 | 19 |
| 4170 | CAGCCAAAATCAAGTCAGG | A574168H | +C*+A*+G*C*C*A*A*A*A*T*C*A*A*G*T*C*+A*+G*+G | 98223 | 19 |
| 4171 | GTCAGCCAAAATCAAGTCA | A574169H | +G*+T*+C*A*G*C*C*A*A*A*A*T*C*A*A*G*+T*+C*+A | 98225 | 19 |
| 4172 | GGTCAGCCAAAATCAAGTC | A574170H | +G*+G*+T*C*A*G*C*C*A*A*A*A*T*C*A*A*+G*+T*+C | 98226 | 19 |
| 4173 | GGTCAGCCAAAATCAAGT | A574171H | +G*+G*+T*C*A*G*C*C*A*A*A*A*T*C*A*+A*+G*+T | 98227 | 18 |
| 4174 | AGGTCAGCCAAAATCAAGT | A574172H | +A*+G*+G*T*C*A*G*C*C*A*A*A*A*T*C*A*+A*+G*+T | 98227 | 19 |
| 4175 | CAGGTCAGCCAAAATCAAG | A574173H | +C*+A*+G*G*T*C*A*G*C*C*A*A*A*A*T*C*+A*+A*+G | 98228 | 19 |

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| 4176 | GCAGGTCAGCCAAAA TCAA | A574174H | +G*+C*+A*G*G*T*C*A*G*C*C*A*A*A*A*T*+ C*+A*+A | 98229 | 19 |
| 4177 | GGCAGGTCAGCCAAA ATCA | A574175H | +G*+G*+C*A*G*G*T*C*A*G*C*C*A*A*A*A* +T*+C*+A | 98230 | 19 |
| 4178 | GGCAGGTCAGCCAAA ATC | A574176H | +G*+G*+C*A*G*G*T*C*A*G*C*C*A*A*A*+A *+T*+C | 98231 | 18 |
| 4179 | AGGCAGGTCAGCCAA AATC | A574177H | +A*+G*+G*C*A*G*G*T*C*A*G*C*C*A*A*A* +A*+T*+C | 98231 | 19 |
| 4180 | TAGGCAGGTCAGCCA AAAT | A574178H | +T*+A*+G*G*C*A*G*G*T*C*A*G*C*C*A*A*+ A*+A*+T | 98232 | 19 |
| 4181 | CTAGGCAGGTCAGCC AAAA | A574179H | +C*+T*+A*G*G*C*A*G*G*T*C*A*G*C*C*A*+ A*+A*+A | 98233 | 19 |
| 4182 | CTAGGCAGGTCAGCC AAA | A574180H | +C*+T*+A*G*G*C*A*G*G*T*C*A*G*C*C*+A* +A*+A | 98234 | 18 |
| 4183 | TCTAGGCAGGTCAGC CAAA | A574181H | +T*+C*+T*A*G*G*C*A*G*G*T*C*A*G*C*C*+ A*+A*+A | 98234 | 19 |
| 4184 | TTCTAGGCAGGTCAG CCAA | A574182H | +T*+T*+C*T*A*G*G*C*A*G*G*T*C*A*G*C*+ C*+A*+A | 98235 | 19 |
| 4185 | TTTCTAGGCAGGTCA GCCA | A574183H | +T*+T*+T*C*T*A*G*G*C*A*G*G*T*C*A*G*+ C*+C*+A | 98236 | 19 |
| 4186 | ATTTCTAGGCAGGTC AGCC | A574184H | +A*+T*+T*T*C*T*A*G*G*C*A*G*G*T*C*A*+ G*+C*+C | 98237 | 19 |
| 4187 | ATATTTCTAGGCAGG TCAG | A574185H | +A*+T*+A*T*T*T*C*T*A*G*G*C*A*G*G*T*+ C*+A*+G | 98239 | 19 |
| 4188 | ATAATATTTCTAGGC AGGT | A574186H | +A*+T*+A*A*T*A*T*T*T*C*T*A*G*G*C*A*+ G*+G*+T | 98242 | 19 |
| 4189 | CAACATAATATTTCTA GGC | A574187H | +C*+A*+A*C*A*T*A*A*T*A*T*T*T*C*T*A*+ G*+G*+C | 98246 | 19 |
| 4190 | GGAGCTTGTTCAAAT TCCA | A574188H | +G*+G*+A*G*C*T*T*G*T*T*C*A*A*A*T*T*+ C*+C*+A | 98278 | 19 |
| 4191 | ACTCTGGAGCTTGTT CAAA | A574189H | +A*+C*+T*C*T*G*G*A*G*C*T*T*G*T*T*C*+ A*+A*+A | 98283 | 19 |
| 4192 | AACTCTGGAGCTTGT TCAA | A574190H | +A*+A*+C*T*C*T*G*G*A*G*C*T*T*G*T*T*+ C*+A*+A | 98284 | 19 |
| 4193 | AAACTCTGGAGCTTG TTCA | A574191H | +A*+A*+A*C*T*C*T*G*G*A*G*C*T*T*G*T*+ T*+C*+A | 98285 | 19 |
| 4194 | AAACTCTGGAGCTTG TTC | A574192H | +A*+A*+A*C*T*C*T*G*G*A*G*C*T*T*G*+T* +T*+C | 98286 | 18 |
| 4195 | GAAACTCTGGAGCTT GTTC | A574193H | +G*+A*+A*A*C*T*C*T*G*G*A*G*C*T*T*G*+ T*+T*+C | 98286 | 19 |
| 4196 | TAGGAGAAACTCTGG AGCT | A574194H | +T*+A*+G*G*A*G*A*A*A*C*T*C*T*G*G*A*+ G*+C*+T | 98291 | 19 |
| 4197 | TAGGAGAAACTCTGG AGC | A574195H | +T*+A*+G*G*A*G*A*A*A*C*T*C*T*G*G*+A* +G*+C | 98292 | 18 |
| 4198 | CTAGGAGAAACTCTG GAGC | A574196H | +C*+T*+A*G*G*A*G*A*A*A*C*T*C*T*G*G*+ A*+G*+C | 98292 | 19 |
| 4199 | TTCTAAATTATAAGG AGAA | A574197Hi | +T*+T*+C*T*A*A*A*T*T*A*T*A*A*G*G*A*+ G*+A*+A | 98355 | 19 |
| 4200 | GATCCTAGTCTACAT GAT | A574198Hi | +G*+A*+T*C*C*T*A*G*T*C*T*A*C*A*T*+G* +A*+T | 98500 | 18 |
| 4201 | TGATCCTAGTCTACA TGA | A574199Hi | +T*+G*+A*T*C*C*T*A*G*T*C*T*A*C*A*+T* +G*+A | 98501 | 18 |
| 4202 | TTGATCCTAGTCTAC ATG | A574200Hi | +T*+T*+G*A*T*C*C*T*A*G*T*C*T*A*C*+A* +T*+G | 98502 | 18 |
| 4203 | TCCTCATCTTGATCCT AGT | A574201Hi | +T*+C*+C*T*C*A*T*C*T*T*G*A*T*C*C*T*+ A*+G*+T | 98509 | 19 |
| 4204 | TGGCAATTAAGGCAA ATAC | A574202Hi | +T*+G*+G*C*A*A*T*T*A*A*G*G*C*A*A*A*+ T*+A*+C | 98571 | 19 |
| 4205 | GGCAATTAAGGCAAA TAC | A574203Hi | +G*+G*+C*A*A*T*T*A*A*G*G*C*A*A*A*+T* +A*+C | 98571 | 18 |
| 4206 | CTGGCAATTAAGGCA AATA | A574204Hi | +C*+T*+G*G*C*A*A*T*T*A*A*G*G*C*A*A*+ A*+T*+A | 98572 | 19 |
| 4207 | ATGGCTGCTTCACTT AAC | A574205Hi | +A*+T*+G*G*C*T*G*C*T*T*C*A*C*T*T*+A* +A*+C | 98626 | 18 |
| 4208 | TGAGGTGTGCTTCCT TTAC | A574206Hi | +T*+G*+A*G*G*T*G*T*G*C*T*T*C*C*T*T*+ T*+A*+C | 98666 | 19 |
| 4209 | GAGGTGTGCTTCCTT TAC | A574207Hi | +G*+A*+G*G*T*G*T*G*C*T*T*C*C*T*T*+T* +A*+C | 98666 | 18 |
| 4210 | ACTGAGGTGTGCTTC CTTT | A574208Hi | +A*+C*+T*G*A*G*G*T*G*T*G*C*T*T*C*C*+ T*+T*+T | 98668 | 19 |

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| 4211 | CACTGAGGTGTGCTTCCTT | A574209Hi | +C*+A*+C*T*G*A*G*G*T*G*T*G*C*T*T*C*+C*+T*+T | 98669 | 19 |
| 4212 | ACTGAGGTGTGCTTCCTT | A574210Hi | +A*+C*+T*G*A*G*G*T*G*T*G*C*T*T*C*+C*+T*+T | 98669 | 18 |
| 4213 | ACACTGAGGTGTGCTTCCT | A574211Hi | +A*+C*+A*C*T*G*A*G*G*T*G*T*G*C*T*T*+C*+C*+T | 98670 | 19 |
| 4214 | CTACACTGAGGTGTGCTTC | A574212Hi | +C*+T*+A*C*A*C*T*G*A*G*G*T*G*T*G*C*+T*+T*+C | 98672 | 19 |
| 4215 | CTACACTGAGGTGTGCTT | A574213Hi | +C*+T*+A*C*A*C*T*G*A*G*G*T*G*T*G*+C*+T*+T | 98673 | 18 |
| 4216 | AATTCAGCATTGTCACACT | A574214Hi | +A*+A*+T*T*C*A*G*C*A*T*T*G*T*C*A*C*+A*+C*+T | 98714 | 19 |
| 4217 | CTATGAGAATTCAGCATTG | A574215Hi | +C*+T*+A*T*G*A*G*A*A*T*T*C*A*G*C*A*+T*+T*+G | 98721 | 19 |
| 4218 | ATGAATATTTCTATGAGAA | A574216Hi | +A*+T*+G*A*A*T*A*T*T*T*C*T*A*T*G*A*+G*+A*+A | 98731 | 19 |
| 4219 | CTACATGAATTCAATGATT | A574217Hi | +C*+T*+A*C*A*T*G*A*A*T*T*C*A*A*T*G*+A*+T*+T | 98889 | 19 |
| 4220 | GTTACCATGACTTCACCTT | A574218Hi | +G*+T*+T*A*C*C*A*T*G*A*C*T*T*C*A*C*+C*+T*+T | 98931 | 19 |
| 4221 | CAGGAAGTCAAGATACAAA | A574219Hi | +C*+A*+G*G*A*A*G*T*C*A*A*G*A*T*A*C*+A*+A*+A | 98968 | 19 |
| 4222 | TAAATAGCTAAACTTCTCC | A574220Hi | +T*+A*+A*A*T*A*G*C*T*A*A*A*C*T*T*C*+T*+C*+C | 99319 | 19 |
| 4223 | TTATGTCCTGACTGACAG | A574221Hi | +T*+T*+A*T*G*T*C*C*T*G*A*C*T*G*A*+C*+A*+G | 99613 | 18 |
| 4224 | ATTATGTCCTGACTGACAG | A574222Hi | +A*+T*+T*A*T*G*T*C*C*T*G*A*C*T*G*A*+C*+A*+G | 99613 | 19 |
| 4225 | TTCCTGTATACCTTGAAGT | A574223Hi | +T*+T*+C*C*T*G*T*A*T*A*C*C*T*T*G*A*+A*+G*+T | 99833 | 19 |
| 4226 | TCCTGTATACCTTGAAGT | A574224Hi | +T*+C*+C*T*G*T*A*T*A*C*C*T*T*G*A*+A*+G*+T | 99833 | 18 |
| 4227 | CTGGTACTTTCCTGTATAC | A574225Hi | +C*+T*+G*G*T*A*C*T*T*T*C*C*T*G*T*A*+T*+A*+C | 99841 | 19 |
| 4228 | GACGTTTCCACATACACTA | A574226Hi | +G*+A*+C*G*T*T*T*C*C*A*C*A*T*A*C*A*+C*+T*+A | 99970 | 19 |
| 4229 | TGACGTTTCCACATACACT | A574227Hi | +T*+G*+A*C*G*T*T*T*C*C*A*C*A*T*A*C*+A*+C*+T | 99971 | 19 |
| 4230 | ATGACGTTTCCACATACAC | A574228Hi | +A*+T*+G*A*C*G*T*T*T*C*C*A*C*A*T*A*+C*+A*+C | 99972 | 19 |
| 4231 | TGACGTTTCCACATACAC | A574229Hi | +T*+G*+A*C*G*T*T*T*C*C*A*C*A*T*A*+C*+A*+C | 99972 | 18 |
| 4232 | AATGACGTTTCCACATACA | A574230Hi | +A*+A*+T*G*A*C*G*T*T*T*C*C*A*C*A*T*+A*+C*+A | 99973 | 19 |
| 4233 | AATGACGTTTCCACATAC | A574231Hi | +A*+A*+T*G*A*C*G*T*T*T*C*C*A*C*A*+T*+A*+C | 99974 | 18 |
| 4234 | TTTGTAAATGACGTTTCCA | A574232Hi | +T*+T*+T*G*T*A*A*A*T*G*A*C*G*T*T*T*+C*+C*+A | 99979 | 19 |
| 4235 | CTTTGTAAATGACGTTTC | A574233Hi | +C*+T*+T*T*G*T*A*A*A*T*G*A*C*G*T*+T*+T*+C | 99981 | 18 |
| 4236 | ACTTTGTAAATGACGTTTC | A574234Hi | +A*+C*+T*T*T*G*T*A*A*A*T*G*A*C*G*T*+T*+T*+C | 99981 | 19 |
| 4237 | AGACTTTGTAAATGACGT | A574235Hi | +A*+G*+A*C*T*T*T*G*T*A*A*A*T*G*A*+C*+G*+T | 99984 | 18 |
| 4238 | CAGACTTTGTAAATGACG | A574236Hi | +C*+A*+G*A*C*T*T*T*G*T*A*A*A*T*G*+A*+C*+G | 99985 | 18 |
| 4239 | ACAGACTTTGTAAATGACG | A574237Hi | +A*+C*+A*G*A*C*T*T*T*G*T*A*A*A*T*G*+A*+C*+G | 99985 | 19 |
| 4240 | AACAGACTTTGTAAATGAC | A574238Hi | +A*+A*+C*A*G*A*C*T*T*T*G*T*A*A*A*T*+G*+A*+C | 99986 | 19 |
| 4241 | GCCAACTAAACAGACTTTG | A574239Hi | +G*+C*+C*A*A*C*T*A*A*A*C*A*G*A*C*T*+T*+T*+G | 99994 | 19 |
| 4242 | GGCCAACTAAACAGACTTT | A574240Hi | +G*+G*+C*C*A*A*C*T*A*A*A*C*A*G*A*C*+T*+T*+T | 99995 | 19 |
| 4243 | GGCCAACTAAACAGACTT | A574241Hi | +G*+G*+C*C*A*A*C*T*A*A*A*C*A*G*A*+C*+T*+T | 99996 | 18 |
| 4244 | TCTAGACTGCTTTCTGTAA | A574242Hi | +T*+C*+T*A*G*A*C*T*G*C*T*T*T*C*T*G*+T*+A*+A | 100406 | 19 |
| 4245 | TATCTAGACTGCTTTCTGT | A574243Hi | +T*+A*+T*C*T*A*G*A*C*T*G*C*T*T*T*C*+T*+G*+T | 100408 | 19 |

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| 4246 | ACTCCTATCTAGACTGCT | A574244Hi | +A*+C*+T*C*C*T*A*T*C*T*A*G*A*C*T*+G*+C*+T | 100414 | 18 |
| 4247 | TCTTTGGCAACATCCGGA | A574245Hi | +T*+C*+T*T*T*G*G*C*A*A*C*A*T*C*C*+G*+G*+A | 100590 | 18 |
| 4248 | ATCTTTGGCAACATCCG | A574246Hi | +A*+T*+C*T*T*T*G*G*C*A*A*C*A*T*+C*+C*+G | 100592 | 17 |
| 4249 | TATCTTTGGCAACATCCG | A574247Hi | +T*+A*+T*C*T*T*T*G*G*C*A*A*C*A*T*+C*+C*+G | 100592 | 18 |
| 4250 | GAAGGATACACCTAATTT | A574248Hi | +G*+A*+A*G*G*A*T*A*C*A*C*C*T*A*A*+T*+T*+T | 100641 | 18 |
| 4251 | ATATAAAGATGCTGGAGTC | A574249Hi | +A*+T*+A*T*A*A*A*G*A*T*G*C*T*G*G*A*+G*+T*+C | 100680 | 19 |
| 4252 | TATAAAGATGCTGGAGTC | A574250Hi | +T*+A*+T*A*A*A*G*A*T*G*C*T*G*G*A*+G*+T*+C | 100680 | 18 |
| 4253 | AATATAAAGATGCTGGAGT | A574251Hi | +A*+A*+T*A*T*A*A*A*G*A*T*G*C*T*G*G*+A*+G*+T | 100681 | 19 |
| 4254 | CTATTCATATCTATTAAGG | A574252Hi | +C*+T*+A*T*T*C*A*T*A*T*C*T*A*T*T*A*+A*+G*+G | 100840 | 19 |
| 4255 | GTCTATTCATATCTATTAA | A574253Hi | +G*+T*+C*T*A*T*T*C*A*T*A*T*C*T*A*T*+T*+A*+A | 100842 | 19 |
| 4256 | AAGTCTATTCATATCTATT | A574254Hi | +A*+A*+G*T*C*T*A*T*T*C*A*T*A*T*C*T*+A*+T*+T | 100844 | 19 |
| 4257 | ATTGAAGGCAAGGAAATTT | A574255Hi | +A*+T*+T*G*A*A*G*G*C*A*A*G*G*A*A*A*+T*+T*+T | 101017 | 19 |
| 4258 | AATTGAAGGCAAGGAAATT | A574256Hi | +A*+A*+T*T*G*A*A*G*G*C*A*A*G*G*A*A*+A*+T*+T | 101018 | 19 |
| 4259 | GATTGTCATGTCTTTCAGG | A574257Hi | +G*+A*+T*T*G*T*C*A*T*G*T*C*T*T*T*T*C*+A*+G*+G | 101103 | 19 |
| 4260 | GGATTGTCATGTCTTTCAG | A574258Hi | +G*+G*+A*T*T*G*T*C*A*T*G*T*C*T*T*T*T*+C*+A*+G | 101104 | 19 |
| 4261 | TGGATTGTCATGTCTTTCA | A574259Hi | +T*+G*+G*A*T*T*G*T*C*A*T*G*T*C*T*T*T*+T*+C*+A | 101105 | 19 |
| 4262 | AGTATGGATTGTCATGTC | A574260Hi | +A*+G*+T*A*T*G*G*A*T*T*G*T*C*A*T*+G*+T*+C | 101110 | 18 |
| 4263 | GGTCGGAGAGATGGAAAC | A574261Hi | +G*+G*+T*C*G*G*A*G*A*G*A*T*G*G*A*+A*+A*+C | 101643 | 18 |
| 4264 | GTCGGAGAGATGGAAAC | A574262Hi | +G*+T*+C*G*G*A*G*A*G*A*T*G*G*A*+A*+A*+C | 101643 | 17 |
| 4265 | AGGATTGTTGGTATTGAG | A574263Hi | +A*+G*+G*A*T*T*G*T*T*G*G*T*A*T*T*+G*+A*+G | 101765 | 18 |
| 4266 | ACCATTAGTTAGGATTGT | A574264Hi | +A*+C*+C*A*T*T*A*G*T*T*A*G*G*A*T*+T*+G*+T | 101775 | 18 |
| 4267 | TGGTATTCTCTCATTCTAT | A574265Hi | +T*+G*+G*T*A*T*T*C*T*C*T*C*A*T*T*C*+T*+A*+T | 101824 | 19 |
| 4268 | TTGGTATTCTCTCATTCTA | A574266Hi | +T*+T*+G*G*T*A*T*T*C*T*C*T*C*A*T*T*+C*+T*+A | 101825 | 19 |
| 4269 | ATCTTATCAGTCTTGGTAT | A574267Hi | +A*+T*+C*T*T*A*T*C*A*G*T*C*T*T*T*G*G*+T*+A*+T | 101837 | 19 |
| 4270 | GCATCTTATCAGTCTTGGT | A574268Hi | +G*+C*+A*T*C*T*T*A*T*C*A*G*T*C*T*T*+G*+G*+T | 101839 | 19 |
| 4271 | TATTTGCATCTTATCAGTC | A574269Hi | +T*+A*+T*T*T*G*C*A*T*C*T*T*A*T*C*A*+G*+T*+C | 101844 | 19 |
| 4272 | GAAATTACACATCTATGGA | A574270Hi | +G*+A*+A*A*T*T*A*C*A*C*A*T*C*T*A*T*+G*+G*+A | 102004 | 19 |
| 4273 | GGTGAAATTACACATCTAT | A574271Hi | +G*+G*+T*G*A*A*A*T*T*A*C*A*C*A*T*C*+T*+A*+T | 102007 | 19 |
| 4274 | TGGATATAAGTGAATACAC | A574272Hi | +T*+G*+G*A*T*A*T*A*A*G*T*G*A*A*T*A*+C*+A*+C | 102064 | 19 |
| 4275 | CTTGATGGATATAAGTGAA | A574273Hi | +C*+T*+T*G*A*T*G*G*A*T*A*T*A*A*G*T*+G*+A*+A | 102069 | 19 |
| 4276 | GTCACTTGATGGATATAAG | A574274Hi | +G*+T*+C*A*C*T*T*G*A*T*G*G*A*T*A*T*+A*+A*+G | 102073 | 19 |
| 4277 | GAAATGTAGTCACTTGATG | A574275Hi | +G*+A*+A*A*T*G*T*A*G*T*C*A*C*T*T*G*+A*+T*+G | 102081 | 19 |
| 4278 | TGCCTTGAAATGTAGTCAC | A574276Hi | +T*+G*+C*C*T*T*G*A*A*A*T*G*T*A*G*T*+C*+A*+C | 102087 | 19 |
| 4279 | GTGCCTTGAAATGTAGTCA | A574277Hi | +G*+T*+G*C*C*T*T*G*A*A*A*T*G*T*A*G*+T*+C*+A | 102088 | 19 |
| 4280 | GTACAATATTTATGGTTCT | A574278Hi | +G*+T*+A*C*A*A*T*A*T*T*T*A*T*G*G*T*+T*+C*+T | 102113 | 19 |

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| 4281 | GCAAATCCTGTTTGTACAA | A574279Hi | +G*+C*+A*A*A*T*C*C*T*G*T*T*T*G*T*A*+C*+A*+A | 102126 | 19 |
| 4282 | CTGAGCATGCTTTGTACCT | A574280Hi | +C*+T*+G*A*G*C*A*T*G*C*T*T*T*G*T*A*+C*+C*+T | 102269 | 19 |
| 4283 | CTGAGCATGCTTTGTACC | A574281Hi | +C*+T*+G*A*G*C*A*T*G*C*T*T*T*G*T*+A*+C*+C | 102270 | 18 |
| 4284 | ATTTCCTGAGCATGCTTTG | A574282Hi | +A*+T*+T*T*C*C*T*G*A*G*C*A*T*G*C*T*+T*+T*+G | 102274 | 19 |
| 4285 | AAGTGCTCTAGACAAACCG | A574283Hi | +A*+A*+G*T*G*C*T*C*T*A*G*A*C*A*A*A*+C*+C*+G | 102304 | 19 |
| 4286 | AGTGCTCTAGACAACCG | A574284Hi | +A*+G*+T*G*C*T*C*T*A*G*A*C*A*A*A*+C*+C*+G | 102304 | 18 |
| 4287 | ACAAGTGCTCTAGACAAAC | A574285Hi | +A*+C*+A*A*G*T*G*C*T*C*T*A*G*A*C*A*+A*+A*+C | 102306 | 19 |
| 4288 | AATTCAGCTCCATAGTCAT | A574286Hi | +A*+A*+T*T*C*A*G*C*T*C*C*A*T*A*G*T*+C*+A*+T | 102570 | 19 |
| 4289 | CTAAATTCAGCTCCATAGT | A574287Hi | +C*+T*+A*A*A*T*T*C*A*G*C*T*C*C*A*T*+A*+G*+T | 102573 | 19 |
| 4290 | TCTAAATTCAGCTCCATAG | A574288Hi | +T*+C*+T*A*A*A*T*T*C*A*G*C*T*C*C*A*+T*+A*+G | 102574 | 19 |
| 4291 | TCATTCCACTTTGATTGTG | A574289Hi | +T*+C*+A*T*T*C*C*A*C*T*T*T*G*A*T*T*+G*+T*+G | 102643 | 19 |
| 4292 | ATCATTCCACTTTGATTGT | A574290Hi | +A*+T*+C*A*T*T*C*C*A*C*T*T*T*G*A*T*+T*+G*+T | 102644 | 19 |
| 4293 | TCCTATCATTCCACTTTGA | A574291Hi | +T*+C*+C*T*A*T*C*A*T*T*C*C*A*C*T*T*+T*+G*+A | 102648 | 19 |
| 4294 | GTTCCTTACTTCCAACTCA | A574292Hi | +G*+T*+T*C*C*T*T*A*C*T*T*C*C*A*A*C*+T*+C*+A | 102693 | 19 |
| 4295 | CTGAGTTCCTTACTTCCAA | A574293Hi | +C*+T*+G*A*G*T*T*C*C*T*T*A*C*T*T*C*+C*+A*+A | 102697 | 19 |
| 4296 | TGAGTTCCTTACTTCCAA | A574294Hi | +T*+G*+A*G*T*T*C*C*T*T*A*C*T*T*C*+C*+A*+A | 102697 | 18 |
| 4297 | TTTCCACTACCACCACACC | A574295Hi | +T*+T*+T*C*C*A*C*T*A*C*C*A*C*C*A*C*+A*+C*+C | 102760 | 19 |
| 4298 | TCCATATAGCTGATGATAA | A574296Hi | +T*+C*+C*A*T*A*T*A*G*C*T*G*A*T*G*A*+T*+A*+A | 102912 | 19 |
| 4299 | TTCTACCTTCCATATAGCT | A574297Hi | +T*+T*+C*T*A*C*C*T*T*C*C*A*T*A*T*A*+G*+C*+T | 102920 | 19 |
| 4300 | CAACTCAATCACAGCCTAT | A574298Hi | +C*+A*+A*C*T*C*A*A*T*C*A*C*A*G*C*C*+T*+A*+T | 102980 | 19 |
| 4301 | CTTCCAACTCAATCACAGC | A574299Hi | +C*+T*+T*C*C*A*A*C*T*C*A*A*T*C*A*C*+A*+G*+C | 102984 | 19 |
| 4302 | TAGCCACCTCCTAAGTGCT | A574300Hi | +T*+A*+G*C*C*A*C*C*T*C*C*T*A*A*G*T*+G*+C*+T | 103047 | 19 |
| 4303 | TCACTTATAGCCACCTCCT | A574301Hi | +T*+C*+A*C*T*T*A*T*A*G*C*C*A*C*C*T*+C*+C*+T | 103054 | 19 |
| 4304 | TTCACTTATAGCCACCTCC | A574302Hi | +T*+T*+C*A*C*T*T*A*T*A*G*C*C*A*C*C*+T*+C*+C | 103055 | 19 |
| 4305 | TCACTTATAGCCACCTCC | A574303Hi | +T*+C*+A*C*T*T*A*T*A*G*C*C*A*C*C*+T*+C*+C | 103055 | 18 |
| 4306 | TATGTCATCCACTTCTGTG | A574304Hi | +T*+A*+T*G*T*C*A*T*C*C*A*C*T*T*C*T*+G*+T*+G | 103112 | 19 |
| 4307 | TTATGTCATCCACTTCTGT | A574305Hi | +T*+T*+A*T*G*T*C*A*T*C*C*A*C*T*T*C*+T*+G*+T | 103113 | 19 |
| 4308 | CCTGCTCAATTATGTCATC | A574306Hi | +C*+C*+T*G*C*T*C*A*A*T*T*A*T*G*T*C*+A*+T*+C | 103122 | 19 |
| 4309 | ATCAAATCTCCTTTAACAT | A574307Hi | +A*+T*+C*A*A*A*T*C*T*C*C*T*T*T*A*A*+C*+A*+T | 103218 | 19 |
| 4310 | AATCAAATCTCCTTTAACA | A574308Hi | +A*+A*+T*C*A*A*A*T*C*T*C*C*T*T*T*A*+A*+C*+A | 103219 | 19 |
| 4311 | TTCATTGAATCAAATCTCC | A574309Hi | +T*+T*+C*A*T*T*G*A*A*T*C*A*A*A*T*C*+T*+C*+C | 103226 | 19 |
| 4312 | GTTTCATTGAATCAAATCT | A574310Hi | +G*+T*+T*T*C*A*T*T*G*A*A*T*C*A*A*A*+T*+C*+T | 103228 | 19 |
| 4313 | TGTTTCATTGAATCAAATC | A574311Hi | +T*+G*+T*T*T*C*A*T*T*G*A*A*T*C*A*A*+A*+T*+C | 103229 | 19 |
| 4314 | GTTTCATTGAATCAAATC | A574312Hi | +G*+T*+T*T*C*A*T*T*G*A*A*T*C*A*A*+A*+T*+C | 103229 | 18 |
| 4315 | AATACAAAGCACTTAAATT | A574313Hi | +A*+A*+T*A*C*A*A*A*G*C*A*C*T*T*A*A*+A*+T*+T | 103332 | 19 |

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| 4316 | AACTGATCCAAAACT GCCA | A574314H | +A*+A*+C*T*G*A*T*C*C*A*A*A*A*C*T*G*+ C*+C*+A | 103368 | 19 |
| 4317 | AAACTGATCCAAAAC TGCC | A574315H | +A*+A*+A*C*T*G*A*T*C*C*A*A*A*A*C*T*+ G*+C*+C | 103369 | 19 |
| 4318 | TCCTTCATAGGCTGC TCG | A574316H | +T*+C*+C*T*T*C*A*T*A*G*G*C*T*G*C*+T* +C*+G | 103390 | 18 |
| 4319 | CTCCTTCATAGGCTG CTCG | A574317H | +C*+T*+C*C*T*T*C*A*T*A*G*G*C*T*G*C*+ T*+C*+G | 103390 | 19 |
| 4320 | TCACAGCCACTTCTT CTCC | A574318H | +T*+C*+A*C*A*G*C*C*A*C*T*T*C*T*T*C*+ T*+C*+C | 103405 | 19 |
| 4321 | AATCTTCACAGCCAC TTCT | A574319H | +A*+A*+T*C*T*T*C*A*C*A*G*C*C*A*C*T*+ T*+C*+T | 103410 | 19 |
| 4322 | GCAGCTAGGAGTCTG ACT | A574320Hi | +G*+C*+A*G*C*T*A*G*G*A*G*T*C*T*G*+A* +C*+T | 103864 | 18 |
| 4323 | GCTAGGCTTCAAGGT CTG | A574321Hi | +G*+C*+T*A*G*G*C*T*T*C*A*A*G*G*T*+C* +T*+G | 103895 | 18 |
| 4324 | CTTGCTAGGCTTCAA GGT | A574322Hi | +C*+T*+T*G*C*T*A*G*G*C*T*T*C*A*A*+G* +G*+T | 103898 | 18 |
| 4325 | AAGTCAGGAGCTTGC TAG | A574323Hi | +A*+A*+G*T*C*A*G*G*A*G*C*T*T*G*C*+T* +A*+G | 103908 | 18 |
| 4326 | AGGTGCAAGCTTATC AG | A574324Hi | +A*+G*+G*T*G*C*A*A*G*C*T*T*A*T*+C*+A *+G | 104100 | 17 |
| 4327 | TCCATCTTTGTAGCA AGT | A574325Hi | +T*+C*+C*A*T*C*T*T*T*G*T*A*G*C*A*+A* +G*+T | 104161 | 18 |
| 4328 | GTAGGAAATAGGATA AGC | A574326Hi | +G*+T*+A*G*G*A*A*A*T*A*G*G*A*T*A*+A* +G*+C | 104191 | 18 |
| 4329 | AGTCAGTCCATGCTG TCT | A574327Hi | +A*+G*+T*C*A*G*T*C*C*A*T*G*C*T*G*+T* +C*+T | 104327 | 18 |
| 4330 | ATAGCAAGGAGTCAG TCC | A574328Hi | +A*+T*+A*G*C*A*A*G*G*A*G*T*C*A*G*+T* +C*+C | 104336 | 18 |
| 4331 | CTCATCTCACATAGC AAG | A574329Hi | +C*+T*+C*A*T*C*T*C*A*C*A*T*A*G*C*+A* +A*+G | 104346 | 18 |
| 4332 | GCAGTAAGTCATGTG CTG | A574330Hi | +G*+C*+A*G*T*A*A*G*T*C*A*T*G*T*G*+C* +T*+G | 105020 | 18 |
| 4333 | CTCTCCTGTTTAGAG CAG | A574331Hi | +C*+T*+C*T*C*C*T*G*T*T*T*A*G*A*G*+C* +A*+G | 105034 | 18 |
| 4334 | TCCATCTCTCCTGTTT AG | A574332Hi | +T*+C*+C*A*T*C*T*C*T*C*C*T*G*T*T*+T* +A*+G | 105039 | 18 |
| 4335 | ATCCATCTCTCCTGTT TA | A574333Hi | +A*+T*+C*C*A*T*C*T*C*T*C*C*T*G*T*+T* +T*+A | 105040 | 18 |
| 4336 | TAACTCATAGATTAA TCA | A574334Hi | +T*+A*+A*C*T*C*A*T*A*G*A*T*T*A*A*+T* +C*+A | 105077 | 18 |
| 4337 | CTAACTCATAGATTA ATC | A574335Hi | +C*+T*+A*A*C*T*C*A*T*A*G*A*T*T*A*+A* +T*+C | 105078 | 18 |
| 4338 | GTGGTAACTTGAACA AGC | A574336Hi | +G*+T*+G*G*T*A*A*C*T*T*G*A*A*C*A*+A* +G*+C | 106255 | 18 |
| 4339 | AGTGGTAACTTGAAC AAG | A574337Hi | +A*+G*+T*G*G*T*A*A*C*T*T*G*A*A*C*+A* +A*+G | 106256 | 18 |
| 4340 | GAAAGTGGTAACTTG AAC | A574338Hi | +G*+A*+A*A*G*T*G*G*T*A*A*C*T*T*G*+A* +A*+C | 106259 | 18 |
| 4341 | GCAAGTTATTGATCT ATG | A574339Hi | +G*+C*+A*A*G*T*T*A*T*T*G*A*T*C*T*+A* +T*+G | 106746 | 18 |
| 4342 | TGTAGGCCATTTGAT TCC | A574340Hi | +T*+G*+T*A*G*G*C*C*A*T*T*T*G*A*T*+T* +C*+C | 107017 | 18 |
| 4343 | GGTTATTATGTAGGC CAT | A574341Hi | +G*+G*+T*T*A*T*T*A*T*G*T*A*G*G*C*+C* +A*+T | 107025 | 18 |
| 4344 | ACTGTTAACTAACAG TGT | A574342Hi | +A*+C*+T*G*T*T*A*A*C*T*A*A*C*A*G*+T* +G*+T | 107313 | 18 |
| 4345 | GTTGAGTTCTGGTAT AAG | A574343Hi | +G*+T*+T*G*A*G*T*T*C*T*G*G*T*A*T*+A* +A*+G | 107464 | 18 |
| 4346 | AGTTGAGTTCTGGTA TAA | A574344Hi | +A*+G*+T*T*G*A*G*T*T*C*T*G*G*T*A*+T* +A*+A | 107465 | 18 |
| 4347 | GATCATATTTGCTTA GTA | A574345Hi | +G*+A*+T*C*A*T*A*T*T*T*G*C*T*T*A*+G* +T*+A | 108224 | 18 |
| 4348 | GACTGTGATCATATT TGC | A574346Hi | +G*+A*+C*T*G*T*G*A*T*C*A*T*A*T*T*+T* +G*+C | 108230 | 18 |
| 4349 | CAACCAGCTTCAAAG ATG | A574347Hi | +C*+A*+A*C*C*A*G*C*T*T*C*A*A*A*G*+A* +T*+G | 108360 | 18 |
| 4350 | TGCTTCTTAACAACC AGC | A574348Hi | +T*+G*+C*T*T*C*T*T*A*A*C*A*A*C*C*+A* +G*+C | 108370 | 18 |

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| 4351 | CCTGGCTGCAACAATCTC | A574349Hi | +C*+C*+T*G*G*C*T*G*C*A*A*C*A*A*T*+C*+T*+C | 108700 | 18 |
| 4352 | AATCAGCTGCAACTGGCA | A574350Hi | +A*+A*+T*C*A*G*C*T*G*C*A*A*C*T*G*+G*+C*+A | 109144 | 18 |
| 4353 | ACTAATCAGCTGCAACTG | A574351Hi | +A*+C*+T*A*A*T*C*A*G*C*T*G*C*A*A*+C*+T*+G | 109147 | 18 |
| 4354 | ACTACTAATCAGCTGCAA | A574352Hi | +A*+C*+T*A*C*T*A*A*T*C*A*G*C*T*G*+C*+A*+A | 109150 | 18 |
| 4355 | AGCCACTACTAATCAGCT | A574353Hi | +A*+G*+C*C*A*C*T*A*C*T*A*A*T*C*A*+G*+C*+T | 109154 | 18 |
| 4356 | TATAGCCACTACTAATCA | A574354Hi | +T*+A*+T*A*G*C*C*A*C*T*A*C*T*A*A*+T*+C*+A | 109157 | 18 |
| 4357 | TCTCTATAGCCACTACTA | A574355Hi | +T*+C*+T*C*T*A*T*A*G*C*C*A*C*T*A*+C*+T*+A | 109161 | 18 |
| 4358 | GACTGGATCATAGCAAAC | A574356Hi | +G*+A*+C*T*G*G*A*T*C*A*T*A*G*C*A*+A*+A*+C | 109849 | 18 |
| 4359 | GGAGGTGGCAAAGCACCAC | A574357H | +G*+G*+A*G*G*T*G*G*C*A*A*A*G*C*A*C*+C*+A*+C | 109977 | 19 |
| 4360 | GGGTGGTGGAGGTGGCAAA | A574358H | +G*+G*+G*T*G*G*T*G*G*A*G*G*T*G*G*C*+A*+A*+A | 109984 | 19 |
| 4361 | TCAAACTGGGGTGGTGGAG | A574359H | +T*+C*+A*A*A*C*T*G*G*G*G*T*G*G*T*G*+G*+A*+G | 109992 | 19 |
| 4362 | ATCAAACTGGGGTGGTGGA | A574360H | +A*+T*+C*A*A*A*C*T*G*G*G*G*T*G*G*T*+G*+G*+A | 109993 | 19 |
| 4363 | TATCAAACTGGGGTGGTGG | A574361H | +T*+A*+T*C*A*A*A*C*T*G*G*G*G*T*G*G*+T*+G*+G | 109994 | 19 |
| 4364 | GATATCAAACTGGGGTGGT | A574362H | +G*+A*+T*A*T*C*A*A*A*C*T*G*G*G*G*T*+G*+G*+T | 109996 | 19 |
| 4365 | CCAGCAAAGATATCAAACT | A574363H | +C*+C*+A*G*C*A*A*A*G*A*T*A*T*C*A*A*+A*+C*+T | 110004 | 19 |
| 4366 | GCTGCCAGCAAAGATATCA | A574364H | +G*+C*+T*G*C*C*A*G*C*A*A*A*G*A*T*A*+T*+C*+A | 110008 | 19 |
| 4367 | GCTGCCAGCAAAGATATC | A574365H | +G*+C*+T*G*C*C*A*G*C*A*A*A*G*A*T*+A*+T*+C | 110009 | 18 |
| 4368 | AGCTGCCAGCAAAGATATC | A574366H | +A*+G*+C*T*G*C*C*A*G*C*A*A*A*G*A*T*+A*+T*+C | 110009 | 19 |
| 4369 | CAGCTGCCAGCAAAGATAT | A574367H | +C*+A*+G*C*T*G*C*C*A*G*C*A*A*A*G*A*+T*+A*+T | 110010 | 19 |
| 4370 | ACCAACATCCGGGGACGAA | A574368H | +A*+C*+C*A*A*C*A*T*C*C*G*G*G*G*A*C*+G*+A*+A | 110032 | 19 |
| 4371 | ACCAACATCCGGGGACGA | A574369H | +A*+C*+C*A*A*C*A*T*C*C*G*G*G*G*A*+C*+G*+A | 110033 | 18 |
| 4372 | CACCAACATCCGGGGACGA | A574370H | +C*+A*+C*C*A*A*C*A*T*C*C*G*G*G*G*A*+C*+G*+A | 110033 | 19 |
| 4373 | ACCAACATCCGGGGACG | A574371H | +A*+C*+C*A*A*C*A*T*C*C*G*G*G*G*+A*+C*+G | 110034 | 17 |
| 4374 | CACCAACATCCGGGGACG | A574372H | +C*+A*+C*C*A*A*C*A*T*C*C*G*G*G*G*+A*+C*+G | 110034 | 18 |
| 4375 | TCACCAACATCCGGGGACG | A574373H | +T*+C*+A*C*C*A*A*C*A*T*C*C*G*G*G*G*+A*+C*+G | 110034 | 19 |
| 4376 | ATCACCAACATCCGGGGAC | A574374H | +A*+T*+C*A*C*C*A*A*C*A*T*C*C*G*G*G*+G*+A*+C | 110035 | 19 |
| 4377 | CTCCATCACCAACATCCGG | A574375H | +C*+T*+C*C*A*T*C*A*C*C*A*A*C*A*T*C*+C*+G*+G | 110039 | 19 |
| 4378 | CTCCATCACCAACATCCG | A574376H | +C*+T*+C*C*A*T*C*A*C*C*A*A*C*A*T*+C*+C*+G | 110040 | 18 |
| 4379 | ACTCCATCACCAACATCCG | A574377H | +A*+C*+T*C*C*A*T*C*A*C*C*A*A*C*A*T*+C*+C*+G | 110040 | 19 |
| 4380 | GGCTAACTCCATCACCAAC | A574378H | +G*+G*+C*T*A*A*C*T*C*C*A*T*C*A*C*C*+A*+A*+C | 110045 | 19 |
| 4381 | GAGGCTAACTCCATCACCA | A574379H | +G*+A*+G*G*C*T*A*A*C*T*C*C*A*T*C*A*+C*+C*+A | 110047 | 19 |
| 4382 | GGAGGCTAACTCCATCACC | A574380H | +G*+G*+A*G*G*C*T*A*A*C*T*C*C*A*T*C*+A*+C*+C | 110048 | 19 |
| 4383 | TGGAGGCTAACTCCATCAC | A574381H | +T*+G*+G*A*G*G*C*T*A*A*C*T*C*C*A*T*+C*+A*+C | 110049 | 19 |
| 4384 | TTGGAGGCTAACTCCATCA | A574382H | +T*+T*+G*G*A*G*G*C*T*A*A*C*T*C*C*A*+T*+C*+A | 110050 | 19 |
| 4385 | CCTTGGAGGCTAACTCCAT | A574383H | +C*+C*+T*T*G*G*A*G*G*C*T*A*A*C*T*C*+C*+A*+T | 110052 | 19 |

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| 4386 | AACCCTTGGAGGCTAACTC | A574384H | +A*+A*+C*C*C*T*T*G*G*A*G*G*C*T*A*A*+C*+T*+C | 110055 | 19 |
| 4387 | GAACCCTTGGAGGCTAACT | A574385H | +G*+A*+A*C*C*C*T*T*G*G*A*G*G*C*T*A*+A*+C*+T | 110056 | 19 |
| 4388 | GAACCCTTGGAGGCTAAC | A574386H | +G*+A*+A*C*C*C*T*T*G*G*A*G*G*C*T*+A*+A*+C | 110057 | 18 |
| 4389 | GGAACCCTTGGAGGCTAAC | A574387H | +G*+G*+A*A*C*C*C*T*T*G*G*A*G*G*C*T*+A*+A*+C | 110057 | 19 |
| 4390 | GGAACCCTTGGAGGCTAA | A574388H | +G*+G*+A*A*C*C*C*T*T*G*G*A*G*G*C*+T*+A*+A | 110058 | 18 |
| 4391 | AGGAACCCTTGGAGGCTAA | A574389H | +A*+G*+G*A*A*C*C*C*T*T*G*G*A*G*G*C*+T*+A*+A | 110058 | 19 |
| 4392 | AGGAACCCTTGGAGGCTA | A574390H | +A*+G*+G*A*A*C*C*C*T*T*G*G*A*G*G*+C*+T*+A | 110059 | 18 |
| 4393 | AAGGAACCCTTGGAGGCTA | A574391H | +A*+A*+G*G*A*A*C*C*C*T*T*G*G*A*G*G*+C*+T*+A | 110059 | 19 |
| 4394 | CAAGGAACCCTTGGAGGCT | A574392H | +C*+A*+A*G*G*A*A*C*C*C*T*T*G*G*A*G*+G*+C*+T | 110060 | 19 |
| 4395 | CCAAGGAACCCTTGGAGGC | A574393H | +C*+C*+A*A*G*G*A*A*C*C*C*T*T*G*G*A*+G*+G*+C | 110061 | 19 |
| 4396 | GATCCAAGGAACCCTTGGA | A574394H | +G*+A*+T*C*C*A*A*G*G*A*A*C*C*C*T*T*+G*+G*+A | 110064 | 19 |
| 4397 | CGATCCAAGGAACCCTTGG | A574395H | +C*+G*+A*T*C*C*A*A*G*G*A*A*C*C*C*T*+T*+G*+G | 110065 | 19 |
| 4398 | CGATCCAAGGAACCCTTG | A574396H | +C*+G*+A*T*C*C*A*A*G*G*A*A*C*C*C*+T*+T*+G | 110066 | 18 |
| 4399 | GCGATCCAAGGAACCCTTG | A574397H | +G*+C*+G*A*T*C*C*A*A*G*G*A*A*C*C*C*+T*+T*+G | 110066 | 19 |
| 4400 | GCGATCCAAGGAACCCTT | A574398H | +G*+C*+G*A*T*C*C*A*A*G*G*A*A*C*C*+C*+T*+T | 110067 | 18 |
| 4401 | GGCGATCCAAGGAACCCTT | A574399H | +G*+G*+C*G*A*T*C*C*A*A*G*G*A*A*C*C*+C*+T*+T | 110067 | 19 |
| 4402 | AGGCGATCCAAGGAACCCT | A574400H | +A*+G*+G*C*G*A*T*C*C*A*A*G*G*A*A*C*+C*+C*+T | 110068 | 19 |
| 4403 | CAGGCGATCCAAGGAACCC | A574401H | +C*+A*+G*G*C*G*A*T*C*C*A*A*G*G*A*A*+C*+C*+C | 110069 | 19 |
| 4404 | CAGGCGATCCAAGGAACC | A574402H | +C*+A*+G*G*C*G*A*T*C*C*A*A*G*G*A*+A*+C*+C | 110070 | 18 |
| 4405 | GCAGGCGATCCAAGGAACC | A574403H | +G*+C*+A*G*G*C*G*A*T*C*C*A*A*G*G*A*+A*+C*+C | 110070 | 19 |
| 4406 | GCAGGCGATCCAAGGAAC | A574404H | +G*+C*+A*G*G*C*G*A*T*C*C*A*A*G*G*+A*+A*+C | 110071 | 18 |
| 4407 | AGCAGGCGATCCAAGGAAC | A574405H | +A*+G*+C*A*G*G*C*G*A*T*C*C*A*A*G*G*+A*+A*+C | 110071 | 19 |
| 4408 | GCAGGCGATCCAAGGAA | A574406H | +G*+C*+A*G*G*C*G*A*T*C*C*A*A*G*+G*+A*+A | 110072 | 17 |
| 4409 | AGCAGGCGATCCAAGGAA | A574407H | +A*+G*+C*A*G*G*C*G*A*T*C*C*A*A*G*+G*+A*+A | 110072 | 18 |
| 4410 | AAGCAGGCGATCCAAGGAA | A574408H | +A*+A*+G*C*A*G*G*C*G*A*T*C*C*A*A*G*+G*+A*+A | 110072 | 19 |
| 4411 | GAAGCAGGCGATCCAAGGA | A574409H | +G*+A*+A*G*C*A*G*G*C*G*A*T*C*C*A*A*+G*+G*+A | 110073 | 19 |
| 4412 | GAAGCAGGCGATCCAAGG | A574410H | +G*+A*+A*G*C*A*G*G*C*G*A*T*C*C*A*+A*+G*+G | 110074 | 18 |
| 4413 | TGAAGCAGGCGATCCAAGG | A574411H | +T*+G*+A*A*G*C*A*G*G*C*G*A*T*C*C*A*+A*+G*+G | 110074 | 19 |
| 4414 | TGAAGCAGGCGATCCAAG | A574412H | +T*+G*+A*A*G*C*A*G*G*C*G*A*T*C*C*+A*+A*+G | 110075 | 18 |
| 4415 | CTGAAGCAGGCGATCCAAG | A574413H | +C*+T*+G*A*A*G*C*A*G*G*C*G*A*T*C*C*+A*+A*+G | 110075 | 19 |
| 4416 | TGAAGCAGGCGATCCAA | A574414H | +T*+G*+A*A*G*C*A*G*G*C*G*A*T*C*+C*+A*+A | 110076 | 17 |
| 4417 | CTGAAGCAGGCGATCCAA | A574415H | +C*+T*+G*A*A*G*C*A*G*G*C*G*A*T*C*+C*+A*+A | 110076 | 18 |
| 4418 | GCTGAAGCAGGCGATCCAA | A574416H | +G*+C*+T*G*A*A*G*C*A*G*G*C*G*A*T*C*+C*+A*+A | 110076 | 19 |
| 4419 | GCTGAAGCAGGCGATCCA | A574417H | +G*+C*+T*G*A*A*G*C*A*G*G*C*G*A*T*+C*+C*+A | 110077 | 18 |
| 4420 | TGCTGAAGCAGGCGATCCA | A574418H | +T*+G*+C*T*G*A*A*G*C*A*G*G*C*G*A*T*+C*+C*+A | 110077 | 19 |

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| 4421 | CCTGCTGAAGCAGGC GATC | A574419H | +C*+C*+T*G*C*T*G*A*A*G*C*A*G*G*C*G* +A*+T*+C | 110079 | 19 |
| 4422 | TCCTGCTGAAGCAGG CGAT | A574420H | +T*+C*+C*T*G*C*T*G*A*A*G*C*A*G*G*C*+ G*+A*+T | 110080 | 19 |
| 4423 | TCCTGCTGAAGCAGG CGA | A574421H | +T*+C*+C*T*G*C*T*G*A*A*G*C*A*G*G*+C* +G*+A | 110081 | 18 |
| 4424 | GTCCTGCTGAAGCAG GCGA | A574422H | +G*+T*+C*C*T*G*C*T*G*A*A*G*C*A*G*G*+ C*+G*+A | 110081 | 19 |
| 4425 | GTCCTGCTGAAGCAG GCG | A574423H | +G*+T*+C*C*T*G*C*T*G*A*A*G*C*A*G*+G* +C*+G | 110082 | 18 |
| 4426 | TGTCCTGCTGAAGCA GGCG | A574424H | +T*+G*+T*C*C*T*G*C*T*G*A*A*G*C*A*G*+ G*+C*+G | 110082 | 19 |
| 4427 | TTGTCCTGCTGAAGC AGGC | A574425H | +T*+T*+G*T*C*C*T*G*C*T*G*A*A*G*C*A*+ G*+G*+C | 110083 | 19 |
| 4428 | TTGTCCTGCTGAAGC AGG | A574426H | +T*+T*+G*T*C*C*T*G*C*T*G*A*A*G*C*+A* +G*+G | 110084 | 18 |
| 4429 | TTTGTCCTGCTGAAG CAGG | A574427H | +T*+T*+T*G*T*C*C*T*G*C*T*G*A*A*G*C*+ A*+G*+G | 110084 | 19 |
| 4430 | TGGCTTTGTCCTGCT GAAG | A574428H | +T*+G*+G*C*T*T*T*G*T*C*C*T*G*C*T*G*+ A*+A*+G | 110088 | 19 |
| 4431 | CTGGCTTTGTCCTGC TGAA | A574429H | +C*+T*+G*G*C*T*T*T*G*T*C*C*T*G*C*T*+ G*+A*+A | 110089 | 19 |
| 4432 | TAGTGAGGCTGGCTT TGTC | A574430H | +T*+A*+G*T*G*A*G*G*C*T*G*G*C*T*T*T*+ G*+T*+C | 110097 | 19 |
| 4433 | CTAGTGAGGCTGGCT TTGT | A574431H | +C*+T*+A*G*T*G*A*G*G*C*T*G*G*C*T*T*+ T*+G*+T | 110098 | 19 |
| 4434 | TCTAGTGAGGCTGGC TTTG | A574432H | +T*+C*+T*A*G*T*G*A*G*G*C*T*G*G*C*T*+ T*+T*+G | 110099 | 19 |
| 4435 | TTCTAGTGAGGCTGG CTTT | A574433H | +T*+T*+C*T*A*G*T*G*A*G*G*C*T*G*G*C*+ T*+T*+T | 110100 | 19 |
| 4436 | GTTCTAGTGAGGCTG GCTT | A574434H | +G*+T*+T*C*T*A*G*T*G*A*G*G*C*T*G*G*+ C*+T*+T | 110101 | 19 |
| 4437 | GGTTCTAGTGAGGCT GGCT | A574435H | +G*+G*+T*T*C*T*A*G*T*G*A*G*G*C*T*G*+ G*+C*+T | 110102 | 19 |
| 4438 | GGTTCTAGTGAGGCT GGC | A574436H | +G*+G*+T*T*C*T*A*G*T*G*A*G*G*C*T*+G* +G*+C | 110103 | 18 |
| 4439 | GGGTTCTAGTGAGGC TGGC | A574437H | +G*+G*+G*T*T*C*T*A*G*T*G*A*G*G*C*T*+ G*+G*+C | 110103 | 19 |
| 4440 | GGGTTCTAGTGAGGC TGG | A574438H | +G*+G*+G*T*T*C*T*A*G*T*G*A*G*G*C*+T* +G*+G | 110104 | 18 |
| 4441 | AGGGTTCTAGTGAGG CTGG | A574439H | +A*+G*+G*G*T*T*C*T*A*G*T*G*A*G*G*C*+ T*+G*+G | 110104 | 19 |
| 4442 | TAGGGTTCTAGTGAG GCTG | A574440H | +T*+A*+G*G*G*T*T*C*T*A*G*T*G*A*G*G*+ C*+T*+G | 110105 | 19 |
| 4443 | GCTGTAGGGTTCTAG TGAG | A574441H | +G*+C*+T*G*T*A*G*G*G*T*T*C*T*A*G*T*+ G*+A*+G | 110109 | 19 |
| 4444 | GCTGTAGGGTTCTAG TGA | A574442H | +G*+C*+T*G*T*A*G*G*G*T*T*C*T*A*G*+T* +G*+A | 110110 | 18 |
| 4445 | TGCTGTAGGGTTCTA GTGA | A574443H | +T*+G*+C*T*G*T*A*G*G*G*T*T*C*T*A*G*+ T*+G*+A | 110110 | 19 |
| 4446 | GTGCTGTAGGGTTCT AGTG | A574444H | +G*+T*+G*C*T*G*T*A*G*G*G*T*T*C*T*A*+ G*+T*+G | 110111 | 19 |
| 4447 | CCTGTGCTGTAGGGT TCTA | A574445H | +C*+C*+T*G*T*G*C*T*G*T*A*G*G*G*T*T*+ C*+T*+A | 110114 | 19 |
| 4448 | CCTGTGCTGTAGGGT TCT | A574446H | +C*+C*+T*G*T*G*C*T*G*T*A*G*G*G*T*+T* +C*+T | 110115 | 18 |
| 4449 | TCCTGTGCTGTAGGG TTCT | A574447H | +T*+C*+C*T*G*T*G*C*T*G*T*A*G*G*G*T*+ T*+C*+T | 110115 | 19 |
| 4450 | TCCTGTGCTGTAGGG TTC | A574448H | +T*+C*+C*T*G*T*G*C*T*G*T*A*G*G*G*+T* +T*+C | 110116 | 18 |
| 4451 | ATCCTGTGCTGTAGG GTTC | A574449H | +A*+T*+C*C*T*G*T*G*C*T*G*T*A*G*G*G*+ T*+T*+C | 110116 | 19 |
| 4452 | CAATCCTGTGCTGTA GGGT | A574450H | +C*+A*+A*T*C*C*T*G*T*G*C*T*G*T*A*G*+ G*+G*+T | 110118 | 19 |
| 4453 | GCAATCCTGTGCTGT AGGG | A574451H | +G*+C*+A*A*T*C*C*T*G*T*G*C*T*G*T*A*+ G*+G*+G | 110119 | 19 |
| 4454 | TGCAATCCTGTGCTG TAGG | A574452H | +T*+G*+C*A*A*T*C*C*T*G*T*G*C*T*G*T*+ A*+G*+G | 110120 | 19 |
| 4455 | TGCAATCCTGTGCTG TAG | A574453H | +T*+G*+C*A*A*T*C*C*T*G*T*G*C*T*G*+T* +A*+G | 110121 | 18 |

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| 4456 | GTGCAATCCTGTGCTGTAG | A574454H | +G*+T*+G*C*A*A*T*C*C*T*G*T*G*C*T*G*+T*+A*+G | 110121 | 19 |
| 4457 | GTGCAATCCTGTGCTGTA | A574455H | +G*+T*+G*C*A*A*T*C*C*T*G*T*G*C*T*+G*+T*+A | 110122 | 18 |
| 4458 | AGTGCAATCCTGTGCTGTA | A574456H | +A*+G*+T*G*C*A*A*T*C*C*T*G*T*G*C*T*+G*+T*+A | 110122 | 19 |
| 4459 | GGAGTGCAATCCTGTGCTG | A574457H | +G*+G*+A*G*T*G*C*A*A*T*C*C*T*G*T*G*+C*+T*+G | 110124 | 19 |
| 4460 | GGAGTGCAATCCTGTGCT | A574458H | +G*+G*+A*G*T*G*C*A*A*T*C*C*T*G*T*+G*+C*+T | 110125 | 18 |
| 4461 | TGGAGTGCAATCCTGTGCT | A574459H | +T*+G*+G*A*G*T*G*C*A*A*T*C*C*T*G*T*+G*+C*+T | 110125 | 19 |
| 4462 | TTACTACTTGCTATGAGG | A574460Hi | +T*+T*+A*C*T*A*C*T*T*G*C*T*A*T*G*+A*+G*+G | 110351 | 18 |
| 4463 | GAAGGCAGATCAGTACAG | A574461Hi | +G*+A*+A*G*G*C*A*G*A*T*C*A*G*T*A*+C*+A*+G | 110416 | 18 |
| 4464 | GGAATCATGTAATTGACA | A574462Hi | +G*+G*+A*A*T*C*A*T*G*T*A*A*T*T*G*+A*+C*+A | 110475 | 18 |
| 4465 | TATGGACTCATCTTTCCT | A574463Hi | +T*+A*+T*G*G*A*C*T*C*A*T*C*T*T*T*+C*+C*+T | 110497 | 18 |
| 4466 | GAGAAGTATGGACTCATC | A574464Hi | +G*+A*+G*A*A*G*T*A*T*G*G*A*C*T*C*+A*+T*+C | 110503 | 18 |
| 4467 | TGAGAAGTATGGACTCAT | A574465Hi | +T*+G*+A*G*A*A*G*T*A*T*G*G*A*C*T*+C*+A*+T | 110504 | 18 |
| 4468 | CCTTGAGAAGTATGGACT | A574466Hi | +C*+C*+T*T*G*A*G*A*A*G*T*A*T*G*G*+A*+C*+T | 110507 | 18 |
| 4469 | TTAGATTCTGATGGCAAG | A574467Hi | +T*+T*+A*G*A*T*T*C*T*G*A*T*G*G*C*+A*+A*+G | 111419 | 18 |
| 4470 | TACTTAGATTCTGATGGC | A574468Hi | +T*+A*+C*T*T*A*G*A*T*T*C*T*G*A*T*+G*+G*+C | 111422 | 18 |
| 4471 | GTACTTAGATTCTGATGG | A574469Hi | +G*+T*+A*C*T*T*A*G*A*T*T*C*T*G*A*+T*+G*+G | 111423 | 18 |
| 4472 | AAGGCATATTCATAGCAT | A574470Hi | +A*+A*+G*G*C*A*T*A*T*T*C*A*T*A*G*+C*+A*+T | 111625 | 18 |
| 4473 | GAGTTAGTTAAATGAAGG | A574471Hi | +G*+A*+G*T*T*A*G*T*T*A*A*A*T*G*A*+A*+G*+G | 111838 | 18 |
| 4474 | GGTGTTTCGAACAGTGTT | A574472Hi | +G*+G*+T*G*T*T*T*C*G*A*A*C*A*G*T*+G*+T*+T | 111932 | 18 |
| 4475 | GGTGTTTCGAACAGTGT | A574473Hi | +G*+G*+T*G*T*T*T*C*G*A*A*C*A*G*+T*+G*+T | 111933 | 17 |
| 4476 | TGCTGGTAGAAGATTGAT | A574474Hi | +T*+G*+C*T*G*G*T*A*G*A*A*G*A*T*T*+G*+A*+T | 112135 | 18 |
| 4477 | GTGCTGGTAGAAGATTGA | A574475Hi | +G*+T*+G*C*T*G*G*T*A*G*A*A*G*A*T*+T*+G*+A | 112136 | 18 |
| 4478 | TGCTGGTAGAAGATTGA | A574476Hi | +T*+G*+C*T*G*G*T*A*G*A*A*G*A*T*+T*+G*+A | 112136 | 17 |
| 4479 | AGTGCTGGTAGAAGATTG | A574477Hi | +A*+G*+T*G*C*T*G*G*T*A*G*A*A*G*A*+T*+T*+G | 112137 | 18 |
| 4480 | TAGTGCTGGTAGAAGATT | A574478Hi | +T*+A*+G*T*G*C*T*G*G*T*A*G*A*A*G*+A*+T*+T | 112138 | 18 |
| 4481 | TTAGTGCTGGTAGAAGAT | A574479Hi | +T*+T*+A*G*T*G*C*T*G*G*T*A*G*A*A*+G*+A*+T | 112139 | 18 |
| 4482 | TCACTCTAAACAGCTCCA | A574480Hi | +T*+C*+A*C*T*C*T*A*A*A*C*A*G*C*T*+C*+C*+A | 112250 | 18 |
| 4483 | GTCACTCTAAACAGCTCC | A574481Hi | +G*+T*+C*A*C*T*C*T*A*A*A*C*A*G*C*+T*+C*+C | 112251 | 18 |
| 4484 | GAGCATGTAACGTGAAG | A574482Hi | +G*+A*+G*C*A*T*G*T*A*A*C*G*T*G*+A*+A*+G | 112282 | 17 |
| 4485 | TACCAAGGCAGTACATTC | A574483Hi | +T*+A*+C*C*A*A*G*G*C*A*G*T*A*C*A*+T*+T*+C | 112448 | 18 |
| 4486 | TGATGTACCAAGGCAGTA | A574484Hi | +T*+G*+A*T*G*T*A*C*C*A*A*G*G*C*A*+G*+T*+A | 112453 | 18 |
| 4487 | GTGATGTACCAAGGCAGT | A574485Hi | +G*+T*+G*A*T*G*T*A*C*C*A*A*G*G*C*+A*+G*+T | 112454 | 18 |
| 4488 | GGTGATGTACCAAGGCAG | A574486Hi | +G*+G*+T*G*A*T*G*T*A*C*C*A*A*G*G*+C*+A*+G | 112455 | 18 |
| 4489 | AGCTAACACTTCATGACA | A574487Hi | +A*+G*+C*T*A*A*C*A*C*T*T*C*A*T*G*+A*+C*+A | 112993 | 18 |
| 4490 | GTGTCACAATCCAGAAGG | A574488Hi | +G*+T*+G*T*C*A*C*A*A*T*C*C*A*G*A*+A*+G*+G | 113245 | 18 |

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| 4491 | GCCAGTCATTTAGTATAC | A574489Hi | +G*+C*+C*A*G*T*C*A*T*T*T*A*G*T*A*+T*+A*+C | 113295 | 18 |
| 4492 | GGCCAGTCATTTAGTATA | A574490Hi | +G*+G*+C*C*A*G*T*C*A*T*T*T*A*G*T*+A*+T*+A | 113296 | 18 |
| 4493 | ATGTACTAGGTATCTATG | A574491Hi | +A*+T*+G*T*A*C*T*A*G*G*T*A*T*C*T*+A*+T*+G | 113316 | 18 |
| 4494 | GCTTAAAGTAAACTTTAT | A574492Hi | +G*+C*+T*T*A*A*A*G*T*A*A*A*C*T*T*+T*+A*+T | 113389 | 18 |
| 4495 | TCATAGCTTAAAGTAAAC | A574493Hi | +T*+C*+A*T*A*G*C*T*T*A*A*A*G*T*A*+A*+A*+C | 113394 | 18 |
| 4496 | AACCATGACTATTGTCAA | A574494Hi | +A*+A*+C*C*A*T*G*A*C*T*A*T*T*G*T*+C*+A*+A | 113502 | 18 |
| 4497 | TAATCTTAAGAAGTGCAG | A574495Hi | +T*+A*+A*T*C*T*T*A*A*G*A*A*G*T*G*+C*+A*+G | 113619 | 18 |
| 4498 | AGATAATATCTTGGTTAG | A574496Hi | +A*+G*+A*T*A*A*T*A*T*C*T*T*G*G*T*+T*+A*+G | 113660 | 18 |
| 4499 | ATACTTTCCAAAGGCTAA | A574497Hi | +A*+T*+A*C*T*T*T*C*C*A*A*A*G*G*C*+T*+A*+A | 113722 | 18 |
| 4500 | CCAAATCCTTTATAAGAC | A574498Hi | +C*+C*+A*A*A*T*C*C*T*T*T*A*T*A*A*+G*+A*+C | 113782 | 18 |
| 4501 | CCTTCACAGTAAGTAATG | A574499Hi | +C*+C*+T*T*C*A*C*A*G*T*A*A*G*T*A*+A*+T*+G | 113927 | 18 |
| 4502 | TGCTTATTCGTGACTGTT | A574500Hi | +T*+G*+C*T*T*A*T*T*C*G*T*G*A*C*T*+G*+T*+T | 114215 | 18 |
| 4503 | TTGCTTATTCGTGACTGT | A574501Hi | +T*+T*+G*C*T*T*A*T*T*C*G*T*G*A*C*+T*+G*+T | 114216 | 18 |
| 4504 | TGCTTATTCGTGACTGT | A574502Hi | +T*+G*+C*T*T*A*T*T*C*G*T*G*A*C*+T*+G*+T | 114216 | 17 |
| 4505 | TTTGCTTATTCGTGACTG | A574503Hi | +T*+T*+T*G*C*T*T*A*T*T*C*G*T*G*A*+C*+T*+G | 114217 | 18 |
| 4506 | CTTTGCTTATTCGTGAC | A574504Hi | +C*+T*+T*T*G*C*T*T*A*T*T*C*G*T*+G*+A*+C | 114219 | 17 |
| 4507 | ATGATGTCAAATTGACTA | A574505Hi | +A*+T*+G*A*T*G*T*C*A*A*A*T*T*G*A*+C*+T*+A | 114321 | 18 |
| 4508 | GTCTTATCCATTCTGGAA | A574506Hi | +G*+T*+C*T*T*A*T*C*C*A*T*T*C*T*G*+G*+A*+A | 114435 | 18 |
| 4509 | GGTCTTATCCATTCTGGA | A574507Hi | +G*+G*+T*C*T*T*A*T*C*C*A*T*T*C*T*+G*+G*+A | 114436 | 18 |
| 4510 | CTGTTTGAGTATATAATT | A574508Hi | +C*+T*+G*T*T*T*G*A*G*T*A*T*A*T*A*+A*+T*+T | 114678 | 18 |
| 4511 | GGTATATAATCATGGCTGA | A574509H | +G*+G*+T*A*T*A*T*A*A*T*C*A*T*G*G*C*+T*+G*+A | 115308 | 19 |
| 4512 | GGTATATAATCATGGCTG | A574510H | +G*+G*+T*A*T*A*T*A*A*T*C*A*T*G*G*+C*+T*+G | 115309 | 18 |
| 4513 | CGGTATATAATCATGGCTG | A574511H | +C*+G*+G*T*A*T*A*T*A*A*T*C*A*T*G*G*+C*+T*+G | 115309 | 19 |
| 4514 | CGGTATATAATCATGGCT | A574512H | +C*+G*+G*T*A*T*A*T*A*A*T*C*A*T*G*+G*+C*+T | 115310 | 18 |
| 4515 | TCGGTATATAATCATGGCT | A574513H | +T*+C*+G*G*T*A*T*A*T*A*A*T*C*A*T*G*+G*+C*+T | 115310 | 19 |
| 4516 | TCGGTATATAATCATGGC | A574514H | +T*+C*+G*G*T*A*T*A*T*A*A*T*C*A*T*+G*+G*+C | 115311 | 18 |
| 4517 | CTCGGTATATAATCATGGC | A574515H | +C*+T*+C*G*G*T*A*T*A*T*A*A*T*C*A*T*+G*+G*+C | 115311 | 19 |
| 4518 | TCTCGGTATATAATCATGG | A574516H | +T*+C*+T*C*G*G*T*A*T*A*T*A*A*T*C*A*+T*+G*+G | 115312 | 19 |
| 4519 | TCTCGGTATATAATCATG | A574517H | +T*+C*+T*C*G*G*T*A*T*A*T*A*A*T*C*+A*+T*+G | 115313 | 18 |
| 4520 | GTCTCGGTATATAATCATG | A574518H | +G*+T*+C*T*C*G*G*T*A*T*A*T*A*A*T*C*+A*+T*+G | 115313 | 19 |
| 4521 | AAAAGCAGCACATTGTGGG | A574519H | +A*+A*+A*A*G*C*A*G*C*A*C*A*T*T*G*T*+G*+G*+G | 115339 | 19 |
| 4522 | GAAAAGCAGCACATTGTGG | A574520H | +G*+A*+A*A*A*G*C*A*G*C*A*C*A*T*T*G*+T*+G*+G | 115340 | 19 |
| 4523 | GTGAAAAGCAGCACATTGT | A574521H | +G*+T*+G*A*A*A*A*G*C*A*G*C*A*C*A*T*+T*+G*+T | 115342 | 19 |
| 4524 | GATACAGTGTGAAAAGCAG | A574522H | +G*+A*+T*A*C*A*G*T*G*T*G*A*A*A*A*G*+C*+A*+G | 115350 | 19 |
| 4525 | TGGGATACAGTGTGAAAAG | A574523H | +T*+G*+G*G*A*T*A*C*A*G*T*G*T*G*A*A*+A*+A*+G | 115353 | 19 |

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| 4526 | CATTGGGATACAGTG TGAA | A574524H | +C*+A*+T*T*G*G*G*A*T*A*C*A*G*T*G*T*+ G*+A*+A | 115356 | 19 |
| 4527 | GCATTGGGATACAGT GTGA | A574525H | +G*+C*+A*T*T*G*G*G*A*T*A*C*A*G*T*G*+ T*+G*+A | 115357 | 19 |
| 4528 | GCATTGGGATACAGT GTG | A574526H | +G*+C*+A*T*T*G*G*G*A*T*A*C*A*G*T*+G* +T*+G | 115358 | 18 |
| 4529 | AGCATTGGGATACAG TGTG | A574527H | +A*+G*+C*A*T*T*G*G*G*A*T*A*C*A*G*T*+ G*+T*+G | 115358 | 19 |
| 4530 | AGCATTGGGATACAG TGT | A574528H | +A*+G*+C*A*T*T*G*G*G*A*T*A*C*A*G*+T* +G*+T | 115359 | 18 |
| 4531 | CAGCATTGGGATACA GTGT | A574529H | +C*+A*+G*C*A*T*T*G*G*G*A*T*A*C*A*G*+ T*+G*+T | 115359 | 19 |
| 4532 | GCAGCATTGGGATAC AGTG | A574530H | +G*+C*+A*G*C*A*T*T*G*G*G*A*T*A*C*A*+ G*+T*+G | 115360 | 19 |
| 4533 | GCAGCATTGGGATAC AGT | A574531H | +G*+C*+A*G*C*A*T*T*G*G*G*A*T*A*C*+A* +G*+T | 115361 | 18 |
| 4534 | GGCAGCATTGGGATA CAGT | A574532H | +G*+G*+C*A*G*C*A*T*T*G*G*G*A*T*A*C*+ A*+G*+T | 115361 | 19 |
| 4535 | GGCAGCATTGGGATA CAG | A574533H | +G*+G*+C*A*G*C*A*T*T*G*G*G*A*T*A*+C* +A*+G | 115362 | 18 |
| 4536 | TGGCAGCATTGGGAT ACAG | A574534H | +T*+G*+G*C*A*G*C*A*T*T*G*G*G*A*T*A*+ C*+A*+G | 115362 | 19 |
| 4537 | TGGCAGCATTGGGAT ACA | A574535H | +T*+G*+G*C*A*G*C*A*T*T*G*G*G*A*T*+A* +C*+A | 115363 | 18 |
| 4538 | ATGGCAGCATTGGGA TACA | A574536H | +A*+T*+G*G*C*A*G*C*A*T*T*G*G*G*A*T*+ A*+C*+A | 115363 | 19 |
| 4539 | TGGCAGCATTGGGAT AC | A574537H | +T*+G*+G*C*A*G*C*A*T*T*G*G*G*A*+T*+ A*+C | 115364 | 17 |
| 4540 | ATGGCAGCATTGGGA TAC | A574538H | +A*+T*+G*G*C*A*G*C*A*T*T*G*G*G*A*+T* +A*+C | 115364 | 18 |
| 4541 | GATGGCAGCATTGGG ATAC | A574539H | +G*+A*+T*G*G*C*A*G*C*A*T*T*G*G*G*A* +T*+A*+C | 115364 | 19 |
| 4542 | TGATGGCAGCATTGG GATA | A574540H | +T*+G*+A*T*G*G*C*A*G*C*A*T*T*G*G*G*+ A*+T*+A | 115365 | 19 |
| 4543 | TGATGGCAGCATTGG GAT | A574541H | +T*+G*+A*T*G*G*C*A*G*C*A*T*T*G*G*+G* +A*+T | 115366 | 18 |
| 4544 | ATGATGGCAGCATTG GGAT | A574542H | +A*+T*+G*A*T*G*G*C*A*G*C*A*T*T*G*G*+ G*+A*+T | 115366 | 19 |
| 4545 | AATGATGGCAGCATT GGGA | A574543H | +A*+A*+T*G*A*T*G*G*C*A*G*C*A*T*T*G*+ G*+G*+A | 115367 | 19 |
| 4546 | CTTTGCAATGATGGC AGCA | A574544H | +C*+T*+T*T*G*C*A*A*T*G*A*T*G*G*C*A*+ G*+C*+A | 115373 | 19 |
| 4547 | CTTTGCAATGATGGC AGC | A574545H | +C*+T*+T*T*G*C*A*A*T*G*A*T*G*G*C*+A* +G*+C | 115374 | 18 |
| 4548 | TCTTTGCAATGATGG CAGC | A574546H | +T*+C*+T*T*T*G*C*A*A*T*G*A*T*G*G*C*+ A*+G*+C | 115374 | 19 |
| 4549 | CAATCTTTGCAATGA TGGC | A574547H | +C*+A*+A*T*C*T*T*T*G*C*A*A*T*G*A*T*+ G*+G*+C | 115377 | 19 |
| 4550 | GTCAGCAATCTTTGC AATG | A574548H | +G*+T*+C*A*G*C*A*A*T*C*T*T*T*G*C*A*+ A*+T*+G | 115382 | 19 |
| 4551 | GTAGTCAGCAATCTT TGCA | A574549H | +G*+T*+A*G*T*C*A*G*C*A*A*T*C*T*T*T*+ G*+C*+A | 115385 | 19 |
| 4552 | CGTAGTCAGCAATCT TTGC | A574550H | +C*+G*+T*A*G*T*C*A*G*C*A*A*T*C*T*T*+ T*+G*+C | 115386 | 19 |
| 4553 | CCGTAGTCAGCAATC TTTG | A574551H | +C*+C*+G*T*A*G*T*C*A*G*C*A*A*T*C*T*+ T*+T*+G | 115387 | 19 |
| 4554 | CCGTAGTCAGCAATC TTT | A574552H | +C*+C*+G*T*A*G*T*C*A*G*C*A*A*T*C*+T* +T*+T | 115388 | 18 |
| 4555 | GCCGTAGTCAGCAAT CTTT | A574553H | +G*+C*+C*G*T*A*G*T*C*A*G*C*A*A*T*C*+ T*+T*+T | 115388 | 19 |
| 4556 | TGCCGTAGTCAGCAA TCTT | A574554H | +T*+G*+C*C*G*T*A*G*T*C*A*G*C*A*A*T*+ C*+T*+T | 115389 | 19 |
| 4557 | TGCCGTAGTCAGCAA TCT | A574555H | +T*+G*+C*C*G*T*A*G*T*C*A*G*C*A*A*+T* +C*+T | 115390 | 18 |
| 4558 | ATGCCGTAGTCAGCA ATCT | A574556H | +A*+T*+G*C*C*G*T*A*G*T*C*A*G*C*A*A*+ T*+C*+T | 115390 | 19 |
| 4559 | GCAATGCCGTAGTCA GCAA | A574557H | +G*+C*+A*A*T*G*C*C*G*T*A*G*T*C*A*G*+ C*+A*+A | 115393 | 19 |
| 4560 | GAGCAATGCCGTAGT CAGC | A574558H | +G*+A*+G*C*A*A*T*G*C*C*G*T*A*G*T*C*+ A*+G*+C | 115395 | 19 |

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| 4561 | GAGCAATGCCGTAGTCAG | A574559H | +G*+A*+G*C*A*A*T*G*C*C*G*T*A*G*T*+C*+A*+G | 115396 | 18 |
| 4562 | TGAGCAATGCCGTAGTCAG | A574560H | +T*+G*+A*G*C*A*A*T*G*C*C*G*T*A*G*T*+C*+A*+G | 115396 | 19 |
| 4563 | GAGCAATGCCGTAGTCA | A574561H | +G*+A*+G*C*A*A*T*G*C*C*G*T*A*G*+T*+C*+A | 115397 | 17 |
| 4564 | TGAGCAATGCCGTAGTCA | A574562H | +T*+G*+A*G*C*A*A*T*G*C*C*G*T*A*G*+T*+C*+A | 115397 | 18 |
| 4565 | CTGAGCAATGCCGTAGTCA | A574563H | +C*+T*+G*A*G*C*A*A*T*G*C*C*G*T*A*G*+T*+C*+A | 115397 | 19 |
| 4566 | TGAGCAATGCCGTAGTC | A574564H | +T*+G*+A*G*C*A*A*T*G*C*C*G*T*A*+G*+T*+C | 115398 | 17 |
| 4567 | CTGAGCAATGCCGTAGTC | A574565H | +C*+T*+G*A*G*C*A*A*T*G*C*C*G*T*A*+G*+T*+C | 115398 | 18 |
| 4568 | ACTGAGCAATGCCGTAGTC | A574566H | +A*+C*+T*G*A*G*C*A*A*T*G*C*C*G*T*A*+G*+T*+C | 115398 | 19 |
| 4569 | AGTACTGAGCAATGCCGTA | A574567H | +A*+G*+T*A*C*T*G*A*G*C*A*A*T*G*C*C*+G*+T*+A | 115401 | 19 |
| 4570 | AGTACTGAGCAATGCCGT | A574568H | +A*+G*+T*A*C*T*G*A*G*C*A*A*T*G*C*+C*+G*+T | 115402 | 18 |
| 4571 | CAGTACTGAGCAATGCCGT | A574569H | +C*+A*+G*T*A*C*T*G*A*G*C*A*A*T*G*C*+C*+G*+T | 115402 | 19 |
| 4572 | AGTACTGAGCAATGCCG | A574570H | +A*+G*+T*A*C*T*G*A*G*C*A*A*T*G*+C*+C*+G | 115403 | 17 |
| 4573 | CAGTACTGAGCAATGCCG | A574571H | +C*+A*+G*T*A*C*T*G*A*G*C*A*A*T*G*+C*+C*+G | 115403 | 18 |
| 4574 | GCAGTACTGAGCAATGCCG | A574572H | +G*+C*+A*G*T*A*C*T*G*A*G*C*A*A*T*G*+C*+C*+G | 115403 | 19 |
| 4575 | AGCAGTACTGAGCAATGCC | A574573H | +A*+G*+C*A*G*T*A*C*T*G*A*G*C*A*A*T*+G*+C*+C | 115404 | 19 |
| 4576 | CCCCATTCTACAGCAGTAC | A574574H | +C*+C*+C*C*A*T*T*C*T*A*C*A*G*C*A*G*+T*+A*+C | 115415 | 19 |
| 4577 | TCCCCATTCTACAGCAGTA | A574575H | +T*+C*+C*C*C*A*T*T*C*T*A*C*A*G*C*A*+G*+T*+A | 115416 | 19 |
| 4578 | GGTTATCCATCCTGAAGA | A574576Hi | +G*+G*+T*T*A*T*C*C*A*T*C*C*T*G*A*+A*+G*+A | 115489 | 18 |
| 4579 | GGTCAGTGGTTATCCATC | A574577Hi | +G*+G*+T*C*A*G*T*G*G*T*T*A*T*C*C*+A*+T*+C | 115496 | 18 |
| 4580 | AGGTCAGTGGTTATCCAT | A574578Hi | +A*+G*+G*T*C*A*G*T*G*G*T*T*A*T*C*+C*+A*+T | 115497 | 18 |
| 4581 | TGAGGTCAGTGGTTATCC | A574579Hi | +T*+G*+A*G*G*T*C*A*G*T*G*G*T*T*A*+T*+C*+C | 115499 | 18 |
| 4582 | CTTCTGAACTCACATCTG | A574580Hi | +C*+T*+T*C*T*G*A*A*C*T*C*A*C*A*T*+C*+T*+G | 115515 | 18 |
| 4583 | GAATTTGATTTGCCTCAC | A574581Hi | +G*+A*+A*T*T*T*G*A*T*T*T*G*C*C*T*+C*+A*+C | 115797 | 18 |
| 4584 | GAGACAACATGTCTGTAC | A574582Hi | +G*+A*+G*A*C*A*A*C*A*T*G*T*C*T*G*+T*+A*+C | 116122 | 18 |
| 4585 | TTAATTGAGTTGCAATCA | A574583Hi | +T*+T*+A*A*T*T*G*A*G*T*T*G*C*A*A*+T*+C*+A | 116278 | 18 |
| 4586 | GGTGATTTAATTGAGTTG | A574584Hi | +G*+G*+T*G*A*T*T*T*A*A*T*T*G*A*G*+T*+T*+G | 116284 | 18 |
| 4587 | TCAGCCAGAACATACACT | A574585Hi | +T*+C*+A*G*C*C*A*G*A*A*C*A*T*A*C*+A*+C*+T | 116513 | 18 |
| 4588 | GGCCAATTACTGAGTGAT | A574586Hi | +G*+G*+C*C*A*A*T*T*A*C*T*G*A*G*T*+G*+A*+T | 116725 | 18 |
| 4589 | GCCAAATATCTCTGGATC | A574587Hi | +G*+C*+C*A*A*A*T*A*T*C*T*C*T*G*G*+A*+T*+C | 116773 | 18 |
| 4590 | GTCCAGTCCACCTTCATG | A574588Hi | +G*+T*+C*C*A*G*T*C*C*A*C*C*T*T*C*+A*+T*+G | 117035 | 18 |
| 4591 | GAAACTGAGTGGTCCAGT | A574589Hi | +G*+A*+A*A*C*T*G*A*G*T*G*G*T*C*C*+A*+G*+T | 117046 | 18 |
| 4592 | ATGAGTCTGAACCAAGGT | A574590Hi | +A*+T*+G*A*G*T*C*T*G*A*A*C*C*A*A*+G*+G*+T | 117238 | 18 |
| 4593 | GCTTGGTATGAAGAATCA | A574591Hi | +G*+C*+T*T*G*G*T*A*T*G*A*A*G*A*A*+T*+C*+A | 117323 | 18 |
| 4594 | CATCGCTCATGCTCTGGA | A574592Hi | +C*+A*+T*C*G*C*T*C*A*T*G*C*T*C*T*+G*+G*+A | 117897 | 18 |
| 4595 | GCACATCGCTCATGCTCT | A574593Hi | +G*+C*+A*C*A*T*C*G*C*T*C*A*T*G*C*+T*+C*+T | 117900 | 18 |

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| 4596 | GCTATCACAGTGCTG GAC | A574594Hi | +G*+C*+T*A*T*C*A*C*A*G*T*G*C*T*G*+G* +A*+C | 118115 | 18 |
| 4597 | CCAAGTTATTTAAAG GTG | A574595Hi | +C*+C*+A*A*G*T*T*A*T*T*T*A*A*A*G*+G* +T*+G | 118227 | 18 |
| 4598 | GTAGAGTATGTTCCA TAA | A574596Hi | +G*+T*+A*G*A*G*T*A*T*G*T*T*C*C*A*+T* +A*+A | 118473 | 18 |
| 4599 | AGTAGAGTATGTTCC ATA | A574597Hi | +A*+G*+T*A*G*A*G*T*A*T*G*T*T*C*C*+A* +T*+A | 118474 | 18 |
| 4600 | ATGAGTAGAGTATGT TCC | A574598Hi | +A*+T*+G*A*G*T*A*G*A*G*T*A*T*G*T*+T* +C*+C | 118477 | 18 |
| 4601 | GTTCTTGATTGCACT AAC | A574599Hi | +G*+T*+T*C*T*T*G*A*T*T*G*C*A*C*T*+A* +A*+C | 118849 | 18 |
| 4602 | CTAGTGTTCTTGATT GCA | A574600Hi | +C*+T*+A*G*T*G*T*T*C*T*T*G*A*T*T*+G* +C*+A | 118854 | 18 |
| 4603 | CTAGTGTTCTTGATT GC | A574601Hi | +C*+T*+A*G*T*G*T*T*C*T*T*G*A*T*+T*+G *+C | 118855 | 17 |
| 4604 | GCAAAGTCAAGAGTA CTT | A574602Hi | +G*+C*+A*A*A*G*T*C*A*A*G*A*G*T*A*+C* +T*+T | 119475 | 18 |
| 4605 | AGCTCAGCAGTCCTC ACC | A574603Hi | +A*+G*+C*T*C*A*G*C*A*G*T*C*C*T*C*+A* +C*+C | 120017 | 18 |
| 4606 | AATTCATAGCCTTCA AGG | A574604Hi | +A*+A*+T*T*C*A*T*A*G*C*C*T*T*C*A*+A* +G*+G | 120095 | 18 |
| 4607 | CTTTCTAAGATGATA TGC | A574605Hi | +C*+T*+T*T*C*T*A*A*G*A*T*G*A*T*A*+T* +G*+C | 120966 | 18 |
| 4608 | GATCACTTTCTAAGA TGA | A574606Hi | +G*+A*+T*C*A*C*T*T*T*C*T*A*A*G*A*+T* +G*+A | 120971 | 18 |
| 4609 | TTCTAACACTCTCATT AT | A574607Hi | +T*+T*+C*T*A*A*C*A*C*T*C*T*C*A*T*+T* +A*+T | 121272 | 18 |
| 4610 | TATTTCCAGGACAGT GTT | A574608Hi | +T*+A*+T*T*T*C*C*A*G*G*A*C*A*G*T*+G* +T*+T | 121361 | 18 |
| 4611 | GGATAAACATTCAAT GGT | A574609Hi | +G*+G*+A*T*A*A*A*C*A*T*T*C*A*A*T*+G* +G*+T | 121461 | 18 |
| 4612 | GTGGAGTTCTAACAG CAA | A574610Hi | +G*+T*+G*G*A*G*T*T*C*T*A*A*C*A*G*+C* +A*+A | 122179 | 18 |
| 4613 | CATTCCAGGATAATG AGT | A574611Hi | +C*+A*+T*T*C*C*A*G*G*A*T*A*A*T*G*+A* +G*+T | 122235 | 18 |
| 4614 | AGGTTTATCCAATTA ATA | A574612Hi | +A*+G*+G*T*T*T*A*T*C*C*A*A*T*T*A*+A* +T*+A | 122605 | 18 |
| 4615 | TGGTTTGTGCACATT TGT | A574613Hi | +T*+G*+G*T*T*T*G*T*G*C*A*C*A*T*T*+T* +G*+T | 123023 | 18 |
| 4616 | CACAGATGGTTTGTG CAC | A574614Hi | +C*+A*+C*A*G*A*T*G*G*T*T*T*G*T*G*+C* +A*+C | 123029 | 18 |
| 4617 | ATGTCCTCACAGATG GTT | A574615Hi | +A*+T*+G*T*C*C*T*C*A*C*A*G*A*T*G*+G* +T*+T | 123036 | 18 |
| 4618 | TATGTCCTCACAGAT GGT | A574616Hi | +T*+A*+T*G*T*C*C*T*C*A*C*A*G*A*T*+G* +G*+T | 123037 | 18 |
| 4619 | TTGATCTCCACTAAG AG | A574617Hi | +T*+T*+G*A*T*C*T*C*C*A*C*T*A*A*+G*+A *+G | 123230 | 17 |
| 4620 | TAAGCCTAAGACTGG TTA | A574618Hi | +T*+A*+A*G*C*C*T*A*A*G*A*C*T*G*G*+T* +T*+A | 124361 | 18 |
| 4621 | GCTAAGCCTAAGACT GGT | A574619Hi | +G*+C*+T*A*A*G*C*C*T*A*A*G*A*C*T*+G* +G*+T | 124363 | 18 |
| 4622 | TGGCACACAATTGGC TGA | A574620Hi | +T*+G*+G*C*A*C*A*C*A*A*T*T*G*G*C*+T* +G*+A | 124651 | 18 |
| 4623 | GTGGCACACAATTGG CTG | A574621Hi | +G*+T*+G*G*C*A*C*A*C*A*A*T*T*G*G*+C* +T*+G | 124652 | 18 |
| 4624 | AGACAGTCTTAGTAA AGG | A574622Hi | +A*+G*+A*C*A*G*T*C*T*T*A*G*T*A*A*+A* +G*+G | 125199 | 18 |
| 4625 | TACTCTTGGATGCTT TGT | A574623Hi | +T*+A*+C*T*C*T*T*G*G*A*T*G*C*T*T*+T* +G*+T | 125261 | 18 |
| 4626 | GTATACTCTTGGATG CTT | A574624Hi | +G*+T*+A*T*A*C*T*C*T*T*G*G*A*T*G*+C* +T*+T | 125264 | 18 |
| 4627 | GACATTTGTCTGCCA AGA | A574625Hi | +G*+A*+C*A*T*T*T*G*T*C*T*G*C*C*A*+A* +G*+A | 125302 | 18 |
| 4628 | GCAAATCTTCCAACT AAA | A574626Hi | +G*+C*+A*A*A*T*C*T*T*C*C*A*A*C*T*+A* +A*+A | 125469 | 18 |
| 4629 | CTTTCAGATAATATG GTG | A574627Hi | +C*+T*+T*T*C*A*G*A*T*A*A*T*A*T*G*+G* +T*+G | 125502 | 18 |
| 4630 | TAGTTGTACTTGACT ATT | A574628Hi | +T*+A*+G*T*T*G*T*A*C*T*T*G*A*C*T*+A* +T*+T | 125644 | 18 |

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| 4631 | TCCTGTCTTGCCTAGTAT | A574629Hi | +T*+C*+C*T*G*T*C*T*T*G*C*C*T*A*G*+T*+A*+T | 125924 | 18 |
| 4632 | GTAGTTGAAAGGAACAGG | A574630Hi | +G*+T*+A*G*T*T*G*A*A*A*G*G*A*A*C*+A*+G*+G | 126151 | 18 |
| 4633 | TCTAGTAGTTGAAAGGAA | A574631Hi | +T*+C*+T*A*G*T*A*G*T*T*G*A*A*A*G*+G*+A*+A | 126155 | 18 |
| 4634 | GAGCTTCTAGTAGTTGAA | A574632Hi | +G*+A*+G*C*T*T*C*T*A*G*T*A*G*T*T*+G*+A*+A | 126160 | 18 |
| 4635 | GTTGAGCTTCTAGTAGTT | A574633Hi | +G*+T*+T*G*A*G*C*T*T*C*T*A*G*T*A*+G*+T*+T | 126163 | 18 |
| 4636 | GTTGAGCTTCTAGTAGT | A574634Hi | +G*+T*+T*G*A*G*C*T*T*C*T*A*G*T*+A*+G*+T | 126164 | 17 |
| 4637 | AGTTGAGCTTCTAGTAGT | A574635Hi | +A*+G*+T*T*G*A*G*C*T*T*C*T*A*G*T*+A*+G*+T | 126164 | 18 |
| 4638 | TGTTATAGCTCTGTCAAG | A574636Hi | +T*+G*+T*T*A*T*A*G*C*T*C*T*G*T*C*+A*+A*+G | 126447 | 18 |
| 4639 | GCAGATTGCAGCCAATGA | A574637Hi | +G*+C*+A*G*A*T*T*G*C*A*G*C*C*A*A*+T*+G*+A | 127160 | 18 |
| 4640 | AGCAGATTGCAGCCAATG | A574638Hi | +A*+G*+C*A*G*A*T*T*G*C*A*G*C*C*A*+A*+T*+G | 127161 | 18 |
| 4641 | CAGCAGATTGCAGCCAAT | A574639Hi | +C*+A*+G*C*A*G*A*T*T*G*C*A*G*C*C*+A*+A*+T | 127162 | 18 |
| 4642 | TTGGCTACTATAGTTCAG | A574640Hi | +T*+T*+G*G*C*T*A*C*T*A*T*A*G*T*T*+C*+A*+G | 127267 | 18 |
| 4643 | GTTGGCTACTATAGTTCA | A574641Hi | +G*+T*+T*G*G*C*T*A*C*T*A*T*A*G*T*+T*+C*+A | 127268 | 18 |
| 4644 | ATATTCTACTATCAGCAAC | A574642H | +A*+T*+A*T*T*C*T*A*C*T*A*T*C*A*G*C*+A*+A*+C | 129306 | 19 |
| 4645 | GCACAATATTCTACTATCA | A574643H | +G*+C*+A*C*A*A*T*A*T*T*C*T*A*C*T*A*+T*+C*+A | 129311 | 19 |
| 4646 | GCACAATATTCTACTATC | A574644H | +G*+C*+A*C*A*A*T*A*T*T*C*T*A*C*T*+A*+T*+C | 129312 | 18 |
| 4647 | AGCACAATATTCTACTATC | A574645H | +A*+G*+C*A*C*A*A*T*A*T*T*C*T*A*C*T*+A*+T*+C | 129312 | 19 |
| 4648 | AAGCACAATATTCTACTAT | A574646H | +A*+A*+G*C*A*C*A*A*T*A*T*T*C*T*A*C*+T*+A*+T | 129313 | 19 |
| 4649 | TAAGCACAATATTCTACTA | A574647H | +T*+A*+A*G*C*A*C*A*A*T*A*T*T*C*T*A*+C*+T*+A | 129314 | 19 |
| 4650 | CTAAGCACAATATTCTACT | A574648H | +C*+T*+A*A*G*C*A*C*A*A*T*A*T*T*C*T*+A*+C*+T | 129315 | 19 |
| 4651 | CTAAGCACAATATTCTAC | A574649H | +C*+T*+A*A*G*C*A*C*A*A*T*A*T*T*C*+T*+A*+C | 129316 | 18 |
| 4652 | GCTAAGCACAATATTCTAC | A574650H | +G*+C*+T*A*A*G*C*A*C*A*A*T*A*T*T*C*+T*+A*+C | 129316 | 19 |
| 4653 | AGGCTAAGCACAATATTCT | A574651H | +A*+G*+G*C*T*A*A*G*C*A*C*A*A*T*A*T*+T*+C*+T | 129318 | 19 |
| 4654 | AGGCTAAGCACAATATTC | A574652H | +A*+G*+G*C*T*A*A*G*C*A*C*A*A*T*A*+T*+T*+C | 129319 | 18 |
| 4655 | AAGGCTAAGCACAATATTC | A574653H | +A*+A*+G*G*C*T*A*A*G*C*A*C*A*A*T*A*+T*+T*+C | 129319 | 19 |
| 4656 | CAAGGCTAAGCACAATATT | A574654H | +C*+A*+A*G*G*C*T*A*A*G*C*A*C*A*A*T*+A*+T*+T | 129320 | 19 |
| 4657 | CCAAGGCTAAGCACAATAT | A574655H | +C*+C*+A*A*G*G*C*T*A*A*G*C*A*C*A*A*+T*+A*+T | 129321 | 19 |
| 4658 | ACCAAGGCTAAGCACAATA | A574656H | +A*+C*+C*A*A*G*G*C*T*A*A*G*C*A*C*A*+A*+T*+A | 129322 | 19 |
| 4659 | ACCAAGGCTAAGCACAAT | A574657H | +A*+C*+C*A*A*G*G*C*T*A*A*G*C*A*C*+A*+A*+T | 129323 | 18 |
| 4660 | CACCAAGGCTAAGCACAAT | A574658H | +C*+A*+C*C*A*A*G*G*C*T*A*A*G*C*A*C*+A*+A*+T | 129323 | 19 |
| 4661 | CACCAAGGCTAAGCACAA | A574659H | +C*+A*+C*C*A*A*G*G*C*T*A*A*G*C*A*+C*+A*+A | 129324 | 18 |
| 4662 | GCACCAAGGCTAAGCACAA | A574660H | +G*+C*+A*C*C*A*A*G*G*C*T*A*A*G*C*A*+C*+A*+A | 129324 | 19 |
| 4663 | GCACCAAGGCTAAGCACA | A574661H | +G*+C*+A*C*C*A*A*G*G*C*T*A*A*G*C*+A*+C*+A | 129325 | 18 |
| 4664 | TGCACCAAGGCTAAGCACA | A574662H | +T*+G*+C*A*C*C*A*A*G*G*C*T*A*A*G*C*+A*+C*+A | 129325 | 19 |
| 4665 | TGCACCAAGGCTAAGCAC | A574663H | +T*+G*+C*A*C*C*A*A*G*G*C*T*A*A*G*+C*+A*+C | 129326 | 18 |

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| 4666 | ATGCACCAAGGCTAAGCAC | A574664H | +A*+T*+G*C*A*C*C*A*A*G*G*C*T*A*A*G*+C*+A*+C | 129326 | 19 |
| 4667 | GATGCACCAAGGCTAAGCA | A574665H | +G*+A*+T*G*C*A*C*C*A*A*G*G*C*T*A*A*+G*+C*+A | 129327 | 19 |
| 4668 | GATGCACCAAGGCTAAGC | A574666H | +G*+A*+T*G*C*A*C*C*A*A*G*G*C*T*A*+A*+G*+C | 129328 | 18 |
| 4669 | AGATGCACCAAGGCTAAGC | A574667H | +A*+G*+A*T*G*C*A*C*C*A*A*G*G*C*T*A*+A*+G*+C | 129328 | 19 |
| 4670 | AGATGCACCAAGGCTAAG | A574668H | +A*+G*+A*T*G*C*A*C*C*A*A*G*G*C*T*+A*+A*+G | 129329 | 18 |
| 4671 | AAGATGCACCAAGGCTAAG | A574669H | +A*+A*+G*A*T*G*C*A*C*C*A*A*G*G*C*T*+A*+A*+G | 129329 | 19 |
| 4672 | AAGATGCACCAAGGCTAA | A574670H | +A*+A*+G*A*T*G*C*A*C*C*A*A*G*G*C*+T*+A*+A | 129330 | 18 |
| 4673 | GAAGATGCACCAAGGCTAA | A574671H | +G*+A*+A*G*A*T*G*C*A*C*C*A*A*G*G*C*+T*+A*+A | 129330 | 19 |
| 4674 | GGAAGATGCACCAAGGCTA | A574672H | +G*+G*+A*A*G*A*T*G*C*A*C*C*A*A*G*G*+C*+T*+A | 129331 | 19 |
| 4675 | CAGGAAGATGCACCAAGGC | A574673H | +C*+A*+G*G*A*A*G*A*T*G*C*A*C*C*A*A*+G*+G*+C | 129333 | 19 |
| 4676 | AACAGGAAGATGCACCAAG | A574674H | +A*+A*+C*A*G*G*A*A*G*A*T*G*C*A*C*C*+A*+A*+G | 129335 | 19 |
| 4677 | GAGTACCAGACTGTGTCCC | A574675H | +G*+A*+G*T*A*C*C*A*G*A*C*T*G*T*G*T*+C*+C*+C | 129378 | 19 |
| 4678 | AGAGTACCAGACTGTGTCC | A574676H | +A*+G*+A*G*T*A*C*C*A*G*A*C*T*G*T*G*+T*+C*+C | 129379 | 19 |
| 4679 | AGAGTACCAGACTGTGTC | A574677H | +A*+G*+A*G*T*A*C*C*A*G*A*C*T*G*T*+G*+T*+C | 129380 | 18 |
| 4680 | GAGAGTACCAGACTGTGTC | A574678H | +G*+A*+G*A*G*T*A*C*C*A*G*A*C*T*G*T*+G*+T*+C | 129380 | 19 |
| 4681 | GGAGAGTACCAGACTGTGT | A574679H | +G*+G*+A*G*A*G*T*A*C*C*A*G*A*C*T*G*+T*+G*+T | 129381 | 19 |
| 4682 | CAGGAGAGTACCAGACTGT | A574680H | +C*+A*+G*G*A*G*A*G*T*A*C*C*A*G*A*C*+T*+G*+T | 129383 | 19 |
| 4683 | CAGGAGAGTACCAGACTG | A574681H | +C*+A*+G*G*A*G*A*G*T*A*C*C*A*G*A*+C*+T*+G | 129384 | 18 |
| 4684 | CCAGGAGAGTACCAGACTG | A574682H | +C*+C*+A*G*G*A*G*A*G*T*A*C*C*A*G*A*+C*+T*+G | 129384 | 19 |
| 4685 | TGACCAGGAGAGTACCAGA | A574683H | +T*+G*+A*C*C*A*G*G*A*G*A*G*T*A*C*C*+A*+G*+A | 129387 | 19 |
| 4686 | TTGATGACCAGGAGAGTAC | A574684H | +T*+T*+G*A*T*G*A*C*C*A*G*G*A*G*A*G*+T*+A*+C | 129391 | 19 |
| 4687 | TATTGATGACCAGGAGAGT | A574685H | +T*+A*+T*T*G*A*T*G*A*C*C*A*G*G*A*A*G*+A*+G*+T | 129393 | 19 |
| 4688 | GGTATTGATGACCAGGAGA | A574686H | +G*+G*+T*A*T*T*G*A*T*G*A*C*C*A*G*G*+A*+G*+A | 129395 | 19 |
| 4689 | GGTATTGATGACCAGGAG | A574687H | +G*+G*+T*A*T*T*G*A*T*G*A*C*C*A*G*+G*+A*+G | 129396 | 18 |
| 4690 | CGGTATTGATGACCAGGAG | A574688H | +C*+G*+G*T*A*T*T*G*A*T*G*A*C*C*A*G*+G*+A*+G | 129396 | 19 |
| 4691 | TCGGTATTGATGACCAGGA | A574689H | +T*+C*+G*G*T*A*T*T*G*A*T*G*A*C*C*C*A*+G*+G*+A | 129397 | 19 |
| 4692 | TTCGGTATTGATGACCAGG | A574690H | +T*+T*+C*G*G*T*A*T*T*G*A*T*G*A*C*C*C*+A*+G*+G | 129398 | 19 |
| 4693 | TCTTCGGTATTGATGACCA | A574691H | +T*+C*+T*T*C*G*G*T*A*T*T*G*A*T*G*A*+C*+C*+A | 129400 | 19 |
| 4694 | TCTTCGGTATTGATGACC | A574692H | +T*+C*+T*T*C*G*G*T*A*T*T*G*A*T*G*+A*+C*+C | 129401 | 18 |
| 4695 | ATCTTCGGTATTGATGACC | A574693H | +A*+T*+C*T*T*C*G*G*T*A*T*T*G*A*T*G*+A*+C*+C | 129401 | 19 |
| 4696 | ATCTTCGGTATTGATGAC | A574694H | +A*+T*+C*T*T*C*G*G*T*A*T*T*G*A*T*+G*+A*+C | 129402 | 18 |
| 4697 | CATCTTCGGTATTGATGAC | A574695H | +C*+A*+T*C*T*T*C*G*G*T*A*T*T*G*A*T*+G*+A*+C | 129402 | 19 |
| 4698 | CATCTTCGGTATTGATGA | A574696H | +C*+A*+T*C*T*T*C*G*G*T*A*T*T*G*A*+T*+G*+A | 129403 | 18 |
| 4699 | CCATCTTCGGTATTGATGA | A574697H | +C*+C*+A*T*C*T*T*C*G*G*T*A*T*T*G*A*+T*+G*+A | 129403 | 19 |
| 4700 | CCATCTTCGGTATTGATG | A574698H | +C*+C*+A*T*C*T*T*C*G*G*T*A*T*T*G*+A*+T*+G | 129404 | 18 |

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| 4701 | CCCATCTTCGGTATTGATG | A574699H | +C*+C*+C*A*T*C*T*T*C*G*G*T*A*T*T*G*+A*+T*+G | 129404 | 19 |
| 4702 | CCCATCTTCGGTATTGAT | A574700H | +C*+C*+C*A*T*C*T*T*C*G*G*T*A*T*T*+G*+A*+T | 129405 | 18 |
| 4703 | TCCCATCTTCGGTATTGAT | A574701H | +T*+C*+C*C*A*T*C*T*T*C*G*G*T*A*T*T*+G*+A*+T | 129405 | 19 |
| 4704 | CCCATCTTCGGTATTGA | A574702H | +C*+C*+C*A*T*C*T*T*C*G*G*T*A*T*+T*+G*+A | 129406 | 17 |
| 4705 | TCCCATCTTCGGTATTGA | A574703H | +T*+C*+C*C*A*T*C*T*T*C*G*G*T*A*T*+T*+G*+A | 129406 | 18 |
| 4706 | TTCCCATCTTCGGTATTGA | A574704H | +T*+T*+C*C*C*A*T*C*T*T*C*G*G*T*A*T*+T*+G*+A | 129406 | 19 |
| 4707 | TTTCCCATCTTCGGTATTG | A574705H | +T*+T*+T*C*C*C*A*T*C*T*T*C*G*G*T*A*+T*+T*+G | 129407 | 19 |
| 4708 | TTTTCCCATCTTCGGTATT | A574706H | +T*+T*+T*T*C*C*C*A*T*C*T*T*C*G*G*T*+A*+T*+T | 129408 | 19 |
| 4709 | TTTTCCCATCTTCGGTAT | A574707H | +T*+T*+T*T*C*C*C*A*T*C*T*T*C*G*G*+T*+A*+T | 129409 | 18 |
| 4710 | TTTTTCCCATCTTCGGTAT | A574708H | +T*+T*+T*T*T*C*C*C*A*T*C*T*T*C*G*G*+T*+A*+T | 129409 | 19 |
| 4711 | CTTTTTCCCATCTTCGGTA | A574709H | +C*+T*+T*T*T*T*C*C*C*A*T*C*T*T*C*G*+G*+T*+A | 129410 | 19 |
| 4712 | TCTTTTTCCCATCTTCGGT | A574710H | +T*+C*+T*T*T*T*T*C*C*C*A*T*C*T*T*C*+G*+G*+T | 129411 | 19 |
| 4713 | TTCTAGGGTATGTCTCTTT | A574711H | +T*+T*+C*T*A*G*G*G*T*A*T*G*T*C*T*C*+T*+T*+T | 129425 | 19 |
| 4714 | TTTCTAGGGTATGTCTCTT | A574712H | +T*+T*+T*C*T*A*G*G*G*T*A*T*G*T*C*T*+C*+T*+T | 129426 | 19 |
| 4715 | CATCTTTTCTAGGGTATGT | A574713H | +C*+A*+T*C*T*T*T*T*C*T*A*G*G*G*T*A*+T*+G*+T | 129431 | 19 |
| 4716 | TCATCTTTTCTAGGGTATG | A574714H | +T*+C*+A*T*C*T*T*T*T*C*T*A*G*G*G*T*+A*+T*+G | 129432 | 19 |
| 4717 | GTCATCTTTTCTAGGGTAT | A574715H | +G*+T*+C*A*T*C*T*T*T*T*C*T*A*G*G*G*+T*+A*+T | 129433 | 19 |
| 4718 | TTGCTTGGAAAAGGAATTG | A574716H | +T*+T*+G*C*T*T*G*G*A*A*A*A*G*G*A*A*+T*+T*+G | 129476 | 19 |
| 4719 | GTGACCTTCCACAATTCC | A574717Hi | +G*+T*+G*A*C*C*T*T*C*C*A*C*A*A*T*+T*+C*+C | 129628 | 18 |
| 4720 | GAGGTAATACCAGGAGCA | A574718Hi | +G*+A*+G*G*T*A*A*T*A*C*C*A*G*G*A*+G*+C*+A | 129730 | 18 |
| 4721 | GTTGAGGTAATACCAGGA | A574719Hi | +G*+T*+T*G*A*G*G*T*A*A*T*A*C*C*A*+G*+G*+A | 129733 | 18 |
| 4722 | CACAGTTGAGGTAATACC | A574720Hi | +C*+A*+C*A*G*T*T*G*A*G*G*T*A*A*T*+A*+C*+C | 129737 | 18 |
| 4723 | TGTTTAAGCCTGGCACAC | A574721Hi | +T*+G*+T*T*T*A*A*G*C*C*T*G*G*C*A*+C*+A*+C | 129878 | 18 |
| 4724 | TCCGAAACTGCCAGTGGA | A574722Hi | +T*+C*+C*G*A*A*A*C*T*G*C*C*A*G*T*+G*+G*+A | 130190 | 18 |
| 4725 | TCAACTCCGAAACTGCCA | A574723Hi | +T*+C*+A*A*C*T*C*C*G*A*A*A*C*T*G*+C*+C*+A | 130195 | 18 |
| 4726 | CACATTGACAACTGCTCC | A574724Hi | +C*+A*+C*A*T*T*G*A*C*A*A*C*T*G*C*+T*+C*+C | 130403 | 18 |
| 4727 | CACATTGACAACTGCTC | A574725Hi | +C*+A*+C*A*T*T*G*A*C*A*A*C*T*G*+C*+T*+C | 130404 | 17 |
| 4728 | TCACATTGACAACTGCTC | A574726Hi | +T*+C*+A*C*A*T*T*G*A*C*A*A*C*T*G*+C*+T*+C | 130404 | 18 |
| 4729 | CGGTTCCAACCAAAAGAAA | A574727H | +C*+G*+G*T*T*C*C*A*A*C*C*A*A*A*A*G*+A*+A*+A | 131132 | 19 |
| 4730 | CGGTTCCAACCAAAAGAA | A574728H | +C*+G*+G*T*T*C*C*A*A*C*C*A*A*A*A*+G*+A*+A | 131133 | 18 |
| 4731 | GCGGTTCCAACCAAAAGAA | A574729H | +G*+C*+G*G*T*T*C*C*A*A*C*C*A*A*A*A*+G*+A*+A | 131133 | 19 |
| 4732 | GCGGTTCCAACCAAAAGA | A574730H | +G*+C*+G*G*T*T*C*C*A*A*C*C*A*A*A*+A*+G*+A | 131134 | 18 |
| 4733 | AGCGGTTCCAACCAAAAGA | A574731H | +A*+G*+C*G*G*T*T*C*C*A*A*C*C*A*A*A*+A*+G*+A | 131134 | 19 |
| 4734 | AGCGGTTCCAACCAAAAG | A574732H | +A*+G*+C*G*G*T*T*C*C*A*A*C*C*A*A*+A*+A*+G | 131135 | 18 |
| 4735 | CAGCGGTTCCAACCAAAAG | A574733H | +C*+A*+G*C*G*G*T*T*C*C*A*A*C*C*A*A*+A*+A*+G | 131135 | 19 |

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| 4736 | TCAGCGGTTCCAACCAAAA | A574734H | +T*+C*+A*G*C*G*G*T*T*C*C*A*A*C*C*A*+A*+A*+A | 131136 | 19 |
| 4737 | TCAGCGGTTCCAACCAAA | A574735H | +T*+C*+A*G*C*G*G*T*T*C*C*A*A*C*C*+A*+A*+A | 131137 | 18 |
| 4738 | ATCAGCGGTTCCAACCAAA | A574736H | +A*+T*+C*A*G*C*G*G*T*T*C*C*A*A*C*C*+A*+A*+A | 131137 | 19 |
| 4739 | TCAGCGGTTCCAACCAA | A574737H | +T*+C*+A*G*C*G*G*T*T*C*C*A*A*C*+C*+A*+A | 131138 | 17 |
| 4740 | ATCAGCGGTTCCAACCAA | A574738H | +A*+T*+C*A*G*C*G*G*T*T*C*C*A*A*C*+C*+A*+A | 131138 | 18 |
| 4741 | CATCAGCGGTTCCAACCAA | A574739H | +C*+A*+T*C*A*G*C*G*G*T*T*C*C*A*A*C*+C*+A*+A | 131138 | 19 |
| 4742 | CATCAGCGGTTCCAACCA | A574740H | +C*+A*+T*C*A*G*C*G*G*T*T*C*C*A*A*+C*+C*+A | 131139 | 18 |
| 4743 | CCATCAGCGGTTCCAACCA | A574741H | +C*+C*+A*T*C*A*G*C*G*G*T*T*C*C*A*A*+C*+C*+A | 131139 | 19 |
| 4744 | GCCATCAGCGGTTCCAACC | A574742H | +G*+C*+C*A*T*C*A*G*C*G*G*T*T*C*C*A*+A*+C*+C | 131140 | 19 |
| 4745 | GCCATCAGCGGTTCCAAC | A574743H | +G*+C*+C*A*T*C*A*G*C*G*G*T*T*C*C*+A*+A*+C | 131141 | 18 |
| 4746 | TGCCATCAGCGGTTCCAAC | A574744H | +T*+G*+C*C*A*T*C*A*G*C*G*G*T*T*C*C*+A*+A*+C | 131141 | 19 |
| 4747 | GCCATCAGCGGTTCCAA | A574745H | +G*+C*+C*A*T*C*A*G*C*G*G*T*T*C*+C*+A*+A | 131142 | 17 |
| 4748 | TGCCATCAGCGGTTCCAA | A574746H | +T*+G*+C*C*A*T*C*A*G*C*G*G*T*T*C*+C*+A*+A | 131142 | 18 |
| 4749 | TTGCCATCAGCGGTTCCAA | A574747H | +T*+T*+G*C*C*A*T*C*A*G*C*G*G*T*T*C*+C*+A*+A | 131142 | 19 |
| 4750 | TGCCATCAGCGGTTCCA | A574748H | +T*+G*+C*C*A*T*C*A*G*C*G*G*T*T*+C*+C*+A | 131143 | 17 |
| 4751 | TTGCCATCAGCGGTTCCA | A574749H | +T*+T*+G*C*C*A*T*C*A*G*C*G*G*T*T*+C*+C*+A | 131143 | 18 |
| 4752 | AATTTAGATGTAGAATGCA | A574750Hi | +A*+A*+T*T*T*A*G*A*T*G*T*A*G*A*A*T*+G*+C*+A | 131204 | 19 |
| 4753 | AATTTATGATTCTTGCTCT | A574751Hi | +A*+A*+T*T*T*A*T*G*A*T*T*C*T*T*G*C*+T*+C*+T | 131285 | 19 |
| 4754 | CATAATTTATGATTCTTGC | A574752Hi | +C*+A*+T*A*A*T*T*T*A*T*G*A*T*T*C*T*+T*+G*+C | 131288 | 19 |
| 4755 | ATACAGTCAATCAGCAAGT | A574753Hi | +A*+T*+A*C*A*G*T*C*A*A*T*C*A*G*C*A*+A*+G*+T | 131359 | 19 |
| 4756 | AATATACAGTCAATCAGCA | A574754Hi | +A*+A*+T*A*T*A*C*A*G*T*C*A*A*T*C*A*+G*+C*+A | 131362 | 19 |
| 4757 | AAATATACAGTCAATCAGC | A574755Hi | +A*+A*+A*T*A*T*A*C*A*G*T*C*A*A*T*C*+A*+G*+C | 131363 | 19 |
| 4758 | AATATACAGTCAATCAGC | A574756Hi | +A*+A*+T*A*T*A*C*A*G*T*C*A*A*T*C*+A*+G*+C | 131363 | 18 |
| 4759 | AAATATACAGTCAATCAG | A574757Hi | +A*+A*+A*T*A*T*A*C*A*G*T*C*A*A*T*+C*+A*+G | 131364 | 18 |
| 4760 | TCTTAGTTCATTCATATAA | A574758Hi | +T*+C*+T*T*A*G*T*T*C*A*T*T*C*A*T*A*+T*+A*+A | 131381 | 19 |
| 4761 | ATCAGATGTCATTTATCAT | A574759Hi | +A*+T*+C*A*G*A*T*G*T*C*A*T*T*T*A*T*+C*+A*+T | 131405 | 19 |
| 4762 | ATTATCAATCAGATGTCAT | A574760Hi | +A*+T*+T*A*T*C*A*A*T*C*A*G*A*T*G*T*+C*+A*+T | 131412 | 19 |
| 4763 | ATATTTATAAGGAATTATC | A574761Hi | +A*+T*+A*T*T*T*A*T*A*A*G*G*A*A*T*T*+A*+T*+C | 131472 | 19 |
| 4764 | GATTTCTTCAATGCTTAAG | A574762Hi | +G*+A*+T*T*T*C*T*T*C*A*A*T*G*C*T*T*+A*+A*+G | 131551 | 19 |
| 4765 | ATGATTTCTTCAATGCTTA | A574763Hi | +A*+T*+G*A*T*T*T*C*T*T*C*A*A*T*G*C*+T*+T*+A | 131553 | 19 |
| 4766 | GTGAATAGATGGAACCAA | A574764Hi | +G*+T*+G*A*A*T*A*G*A*T*G*G*A*A*C*+C*+A*+A | 131641 | 18 |
| 4767 | AGTGAATAGATGGAACCA | A574765Hi | +A*+G*+T*G*A*A*T*A*G*A*T*G*G*A*A*+C*+C*+A | 131642 | 18 |
| 4768 | GAGTGAATAGATGGAACC | A574766Hi | +G*+A*+G*T*G*A*A*T*A*G*A*T*G*G*A*+A*+C*+C | 131643 | 18 |
| 4769 | TTATTGTTACATTCAATCT | A574767Hi | +T*+T*+A*T*T*G*T*T*A*C*A*T*T*C*A*A*+T*+C*+T | 131778 | 19 |
| 4770 | TACTCGTGAAGCTGATGTT | A574768Hi | +T*+A*+C*T*C*G*T*G*A*A*G*C*T*G*A*T*+G*+T*+T | 132888 | 19 |

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| 4771 | ACTCGTGAAGCTGATGTT | A574769Hi | +A*+C*+T*C*G*T*G*A*A*G*C*T*G*A*T*+G*+T*+T | 132888 | 18 |
| 4772 | CCATCTTAAATGATTAGAG | A574770Hi | +C*+C*+A*T*C*T*T*A*A*A*T*G*A*T*T*A*+G*+A*+G | 134155 | 19 |
| 4773 | CAAATTGAGTATCCACAGA | A574771Hi | +C*+A*+A*A*T*T*G*A*G*T*A*T*C*C*A*C*+A*+G*+A | 134214 | 19 |
| 4774 | CAAATTGAGTATCCACAG | A574772Hi | +C*+A*+A*A*T*T*G*A*G*T*A*T*C*C*A*+C*+A*+G | 134215 | 18 |
| 4775 | AGTATCTTCAAAGGAGCAG | A574773H | +A*+G*+T*A*T*C*T*T*C*A*A*A*G*G*A*G*+C*+A*+G | 134274 | 19 |
| 4776 | TATTTAGTATCTTCAAAGG | A574774H | +T*+A*+T*T*T*A*G*T*A*T*C*T*T*C*A*A*+A*+G*+G | 134279 | 19 |
| 4777 | TCCTATATTTAGTATCTTC | A574775H | +T*+C*+C*T*A*T*A*T*T*T*A*G*T*A*T*C*+T*+T*+C | 134284 | 19 |
| 4778 | ATGGAGTACTGACATTTCC | A574776H | +A*+T*+G*G*A*G*T*A*C*T*G*A*C*A*T*T*+T*+C*+C | 134300 | 19 |
| 4779 | AATGGAGTACTGACATTTC | A574777H | +A*+A*+T*G*G*A*G*T*A*C*T*G*A*C*A*T*+T*+T*+C | 134301 | 19 |
| 4780 | ACACATCAATGGAGTACTG | A574778H | +A*+C*+A*C*A*T*C*A*A*T*G*G*A*G*T*A*+C*+T*+G | 134308 | 19 |
| 4781 | AACACATCAATGGAGTACT | A574779H | +A*+A*+C*A*C*A*T*C*A*A*T*G*G*A*G*T*+A*+C*+T | 134309 | 19 |
| 4782 | CTCAAACACATCAATGGAG | A574780H | +C*+T*+C*A*A*A*C*A*C*A*T*C*A*A*T*G*+G*+A*+G | 134313 | 19 |
| 4783 | TCACTCAAACACATCAATG | A574781H | +T*+C*+A*C*T*C*A*A*A*C*A*C*A*T*C*A*+A*+T*+G | 134316 | 19 |
| 4784 | TGGATTCACTCAAACACAT | A574782H | +T*+G*+G*A*T*T*C*A*C*T*C*A*A*A*C*A*+C*+A*+T | 134321 | 19 |
| 4785 | GTGGATTCACTCAAACACA | A574783H | +G*+T*+G*G*A*T*T*C*A*C*T*C*A*A*A*C*+A*+C*+A | 134322 | 19 |
| 4786 | TGTGGATTCACTCAAACAC | A574784H | +T*+G*+T*G*G*A*T*T*C*A*C*T*C*A*A*A*+C*+A*+C | 134323 | 19 |
| 4787 | TTGTGGATTCACTCAAACA | A574785H | +T*+T*+G*T*G*G*A*T*T*C*A*C*T*C*A*A*+A*+C*+A | 134324 | 19 |
| 4788 | TTGTGGATTCACTCAAAC | A574786H | +T*+T*+G*T*G*G*A*T*T*C*A*C*T*C*A*+A*+A*+C | 134325 | 18 |
| 4789 | TTTGTGGATTCACTCAAAC | A574787H | +T*+T*+T*G*T*G*G*A*T*T*C*A*C*T*C*A*+A*+A*+C | 134325 | 19 |
| 4790 | GTTGAATTTGTGGATTCAC | A574788H | +G*+T*+T*G*A*A*T*T*T*G*T*G*G*A*T*T*+C*+A*+C | 134331 | 19 |
| 4791 | CTCCCCACATTACATTTCT | A574789H | +C*+T*+C*C*C*C*A*C*A*T*T*A*C*A*T*T*+T*+C*+T | 134354 | 19 |
| 4792 | TCCTCCCCACATTACATTT | A574790H | +T*+C*+C*T*C*C*C*C*A*C*A*T*T*A*C*A*+T*+T*+T | 134356 | 19 |
| 4793 | ATCCTCCCCACATTACATT | A574791H | +A*+T*+C*C*T*C*C*C*C*A*C*A*T*T*A*C*+A*+T*+T | 134357 | 19 |
| 4794 | ATCCTCCCCACATTACAT | A574792H | +A*+T*+C*C*T*C*C*C*C*A*C*A*T*T*A*+C*+A*+T | 134358 | 18 |
| 4795 | CATCCTCCCCACATTACAT | A574793H | +C*+A*+T*C*C*T*C*C*C*C*A*C*A*T*T*A*+C*+A*+T | 134358 | 19 |
| 4796 | ACATCCTCCCCACATTACA | A574794H | +A*+C*+A*T*C*C*T*C*C*C*C*A*C*A*T*T*+A*+C*+A | 134359 | 19 |
| 4797 | ACATCCTCCCCACATTAC | A574795H | +A*+C*+A*T*C*C*T*C*C*C*C*A*C*A*T*+T*+A*+C | 134360 | 18 |
| 4798 | CACATCCTCCCCACATTAC | A574796H | +C*+A*+C*A*T*C*C*T*C*C*C*C*A*C*A*T*+T*+A*+C | 134360 | 19 |
| 4799 | TTTGTGCCACATCCTCCCC | A574797H | +T*+T*+T*G*T*G*C*C*A*C*A*T*C*C*T*C*+C*+C*+C | 134367 | 19 |
| 4800 | AAATCTTTGTGCCACATCC | A574798H | +A*+A*+A*T*C*T*T*T*G*T*G*C*C*A*C*A*+T*+C*+C | 134372 | 19 |
| 4801 | AAAATCTTTGTGCCACATC | A574799H | +A*+A*+A*A*T*C*T*T*T*G*T*G*C*C*A*C*+A*+T*+C | 134373 | 19 |
| 4802 | GAAATCATTAGAAAAGGAG | A574800H | +G*+A*+A*A*T*C*A*T*T*A*G*A*A*A*A*G*+G*+A*+G | 134392 | 19 |
| 4803 | GGTGAAATCATTAGAAAAG | A574801H | +G*+G*+T*G*A*A*A*T*C*A*T*T*A*G*A*A*+A*+A*+G | 134395 | 19 |
| 4804 | AATGGTGAAATCATTAGAA | A574802H | +A*+A*+T*G*G*T*G*A*A*A*T*C*A*T*T*A*+G*+A*+A | 134398 | 19 |
| 4805 | AATGGTGAAATCATTAGA | A574803H | +A*+A*+T*G*G*T*G*A*A*A*T*C*A*T*T*+A*+G*+A | 134399 | 18 |

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| 4806 | GAATGGTGAAATCAT TAGA | A574804H | +G*+A*+A*T*G*G*T*G*A*A*A*T*C*A*T*T*+ A*+G*+A | 134399 | 19 |
| 4807 | TCTGAATGGTGAAAT CATT | A574805H | +T*+C*+T*G*A*A*T*G*G*T*G*A*A*A*T*C*+ A*+T*+T | 134402 | 19 |
| 4808 | TCTCAATGAGTTTCT GAAT | A574806H | +T*+C*+T*C*A*A*T*G*A*G*T*T*T*C*T*G*+ A*+A*+T | 134414 | 19 |
| 4809 | GTCTCAATGAGTTTC TGAA | A574807H | +G*+T*+C*T*C*A*A*T*G*A*G*T*T*T*C*T*+ G*+A*+A | 134415 | 19 |
| 4810 | CTTGTCTCAATGAGT TTCT | A574808H | +C*+T*+T*G*T*C*T*C*A*A*T*G*A*G*T*T*+ T*+C*+T | 134418 | 19 |
| 4811 | CTTGTCTCAATGAGT TTC | A574809H | +C*+T*+T*G*T*C*T*C*A*A*T*G*A*G*T*+T* +T*+C | 134419 | 18 |
| 4812 | TCTTGTCTCAATGAG TTTC | A574810H | +T*+C*+T*T*G*T*C*T*C*A*A*T*G*A*G*T*+ T*+T*+C | 134419 | 19 |
| 4813 | TTCTTGTCTCAATGA GTTT | A574811H | +T*+T*+C*T*T*G*T*C*T*C*A*A*T*G*A*G*+ T*+T*+T | 134420 | 19 |
| 4814 | TTCTTGTCTCAATGA GTT | A574812H | +T*+T*+C*T*T*G*T*C*T*C*A*A*T*G*A*+G* +T*+T | 134421 | 18 |
| 4815 | GTTCTTGTCTCAATG AGTT | A574813H | +G*+T*+T*C*T*T*G*T*C*T*C*A*A*T*G*A*+ G*+T*+T | 134421 | 19 |
| 4816 | GTTCTTGTCTCAATG AGT | A574814H | +G*+T*+T*C*T*T*G*T*C*T*C*A*A*T*G*+A* +G*+T | 134422 | 18 |
| 4817 | TGTTCTTGTCTCAAT GAGT | A574815H | +T*+G*+T*T*C*T*T*G*T*C*T*C*A*A*T*G*+ A*+G*+T | 134422 | 19 |
| 4818 | TTGTTCTTGTCTCAAT GAG | A574816H | +T*+T*+G*T*T*C*T*T*G*T*C*T*C*A*A*T*+ G*+A*+G | 134423 | 19 |
| 4819 | GCTTGTTCTTGTCTC AATG | A574817H | +G*+C*+T*T*G*T*T*C*T*T*G*T*C*T*C*A*+ A*+T*+G | 134425 | 19 |
| 4820 | GGCTTGTTCTTGTCT CAAT | A574818H | +G*+G*+C*T*T*G*T*T*C*T*T*G*T*C*T*C*+ A*+A*+T | 134426 | 19 |
| 4821 | GTTGGCTTGTTCTTG TCTC | A574819H | +G*+T*+T*G*G*C*T*T*G*T*T*C*T*T*G*T*+ C*+T*+C | 134429 | 19 |
| 4822 | GTTGGCTTGTTCTTG TCT | A574820H | +G*+T*+T*G*G*C*T*T*G*T*T*C*T*T*G*+T* +C*+T | 134430 | 18 |
| 4823 | AGTTGGCTTGTTCTT GTCT | A574821H | +A*+G*+T*T*G*G*C*T*T*G*T*T*C*T*T*G*+ T*+C*+T | 134430 | 19 |
| 4824 | AGTTGGCTTGTTCTT GTC | A574822H | +A*+G*+T*T*G*G*C*T*T*G*T*T*C*T*T*+G* +T*+C | 134431 | 18 |
| 4825 | TTATGAATTATCAAC AGTA | A574823Hi | +T*+T*+A*T*G*A*A*T*T*A*T*C*A*A*C*A*+ G*+T*+A | 134519 | 19 |
| 4826 | TTCCTTATGAATTATC AAC | A574824Hi | +T*+T*+C*C*T*T*A*T*G*A*A*T*T*A*T*C*+ A*+A*+C | 134523 | 19 |
| 4827 | AAGATCTTCCTTATG AATT | A574825Hi | +A*+A*+G*A*T*C*T*T*C*C*T*T*A*T*G*A*+ A*+T*+T | 134529 | 19 |
| 4828 | ATACTACTAAGATTA CAAT | A574826Hi | +A*+T*+A*C*T*A*C*T*A*A*G*A*T*T*A*C*+ A*+A*+T | 134683 | 19 |
| 4829 | AATACTACTAAGATT ACAA | A574827Hi | +A*+A*+T*A*C*T*A*C*T*A*A*G*A*T*T*A*+ C*+A*+A | 134684 | 19 |
| 4830 | GTCTTCCAATTTCAT GTCT | A574828Hi | +G*+T*+C*T*T*C*C*A*A*T*T*T*C*A*T*G*+ T*+C*+T | 134750 | 19 |
| 4831 | TGTCTTCCAATTTCAT GTC | A574829Hi | +T*+G*+T*C*T*T*C*C*A*A*T*T*T*C*A*T*+ G*+T*+C | 134751 | 19 |
| 4832 | TATCTTTCCTACAATC AAT | A574830Hi | +T*+A*+T*C*T*T*T*C*C*T*A*C*A*A*T*C*+ A*+A*+T | 134835 | 19 |
| 4833 | CTATCTTTCCTACAAT CAA | A574831Hi | +C*+T*+A*T*C*T*T*T*C*C*T*A*C*A*A*T*+ C*+A*+A | 134836 | 19 |
| 4834 | AATACTTGCTGTCTA TCT | A574832Hi | +A*+A*+T*A*C*T*T*G*C*T*G*T*C*T*A*+T* +C*+T | 134849 | 18 |
| 4835 | AGAATACTTGCTGTC TATC | A574833Hi | +A*+G*+A*A*T*A*C*T*T*G*C*T*G*T*C*T*+ A*+T*+C | 134850 | 19 |
| 4836 | CAAGAATACTTGCTG TCTA | A574834Hi | +C*+A*+A*G*A*A*T*A*C*T*T*G*C*T*G*T*+ C*+T*+A | 134852 | 19 |
| 4837 | GCAAGAATACTTGCT GTCT | A574835Hi | +G*+C*+A*A*G*A*A*T*A*C*T*T*G*C*T*G*+ T*+C*+T | 134853 | 19 |
| 4838 | GACAAGCAAGAATAC TTGC | A574836Hi | +G*+A*+C*A*A*G*C*A*A*G*A*A*T*A*C*T*+ T*+G*+C | 134858 | 19 |
| 4839 | GAAACTGGTATCACT AACT | A574837Hi | +G*+A*+A*A*C*T*G*G*T*A*T*C*A*C*T*A*+ A*+C*+T | 134926 | 19 |
| 4840 | TTGAAACTGGTATCA CTAA | A574838Hi | +T*+T*+G*A*A*A*C*T*G*G*T*A*T*C*A*C*+ T*+A*+A | 134928 | 19 |

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| 4841 | TGAAACTGGTATCAC TAA | A574839Hi | +T*+G*+A*A*A*C*T*G*G*T*A*T*C*A*C*+T* +A*+A | 134928 | 18 |
| 4842 | GTTTGAAACTGGTAT CACT | A574840Hi | +G*+T*+T*T*G*A*A*A*C*T*G*G*T*A*T*C*+ A*+C*+T | 134930 | 19 |
| 4843 | TGTTTGAAACTGGTA TCAC | A574841Hi | +T*+G*+T*T*T*G*A*A*A*C*T*G*G*T*A*T*+ C*+A*+C | 134931 | 19 |
| 4844 | GTTTGAAACTGGTAT CAC | A574842Hi | +G*+T*+T*T*G*A*A*A*C*T*G*G*T*A*T*+C* +A*+C | 134931 | 18 |
| 4845 | CAAACTTGAAAGAGG TTTA | A574843Hi | +C*+A*+A*A*C*T*T*G*A*A*A*G*A*G*G*T*+ T*+T*+A | 134972 | 19 |
| 4846 | CAATAGATGGCAAAG CAAT | A574844Hi | +C*+A*+A*T*A*G*A*T*G*G*C*A*A*A*G*C*+ A*+A*+T | 135103 | 19 |
| 4847 | TGACTGAAGATGTGA AAGG | A574845Hi | +T*+G*+A*C*T*G*A*A*G*A*T*G*T*G*A*A*+ A*+G*+G | 135144 | 19 |
| 4848 | AGATGACTGAAGATG TGAA | A574846Hi | +A*+G*+A*T*G*A*C*T*G*A*A*G*A*T*G*T*+ G*+A*+A | 135147 | 19 |
| 4849 | CCTCAGGTAAGAGAT GACT | A574847Hi | +C*+C*+T*C*A*G*G*T*A*A*G*A*G*A*A*T*G*+ A*+C*+T | 135158 | 19 |
| 4850 | ATCCTCAGGTAAGAG ATGA | A574848Hi | +A*+T*+C*C*T*C*A*G*G*T*A*A*G*A*G*A*A*+ T*+G*+A | 135160 | 19 |
| 4851 | AATCCTCAGGTAAGA GATG | A574849Hi | +A*+A*+T*C*C*T*C*A*G*G*T*A*A*G*A*G*+ A*+T*+G | 135161 | 19 |
| 4852 | ACAATCCTCAGGTAA GAGA | A574850Hi | +A*+C*+A*A*T*C*C*T*C*A*G*G*T*A*A*G*+ A*+G*+A | 135163 | 19 |
| 4853 | AGAATATTACAATCC TCAG | A574851Hi | +A*+G*+A*A*T*A*T*T*A*C*A*A*T*C*C*T*+ C*+A*+G | 135171 | 19 |
| 4854 | GGATTTGTGACTCAA AGCT | A574852Hi | +G*+G*+A*T*T*T*G*T*G*A*C*T*C*A*A*A*+ G*+C*+T | 135307 | 19 |
| 4855 | ACTGAGAACAGTGAG AAGT | A574853Hi | +A*+C*+T*G*A*G*A*A*C*A*G*T*G*A*G*A*+ A*+G*+T | 135461 | 19 |
| 4856 | TGTTAATGTGGCCAC AGAT | A574854Hi | +T*+G*+T*T*A*A*T*G*T*G*G*C*C*A*C*A*+ G*+A*+T | 135511 | 19 |
| 4857 | AACTGGATGCTCTTG TTAA | A574855Hi | +A*+A*+C*T*G*G*A*T*G*C*T*C*T*T*G*T*+ T*+A*+A | 135524 | 19 |
| 4858 | GAACTGGATGCTCTT GTTA | A574856Hi | +G*+A*+A*C*T*G*G*A*T*G*C*T*C*T*T*G*+ T*+T*+A | 135525 | 19 |
| 4859 | GAGAACTGGATGCTC TTGT | A574857Hi | +G*+A*+G*A*A*C*T*G*G*A*T*G*C*T*C*T*+ T*+G*+T | 135527 | 19 |
| 4860 | TGAGAACTGGATGCT CTTG | A574858Hi | +T*+G*+A*G*A*A*C*T*G*G*A*T*G*C*T*C*+ T*+T*+G | 135528 | 19 |
| 4861 | GCATCAGATTGATGT ACA | A574859Hi | +G*+C*+A*T*C*A*G*A*T*T*G*A*T*G*T*+A* +C*+A | 135609 | 18 |
| 4862 | TGCATCAGATTGATG TAC | A574860Hi | +T*+G*+C*A*T*C*A*G*A*T*T*G*A*T*G*+T* +A*+C | 135610 | 18 |
| 4863 | ATTGCATCAGATTGA TGT | A574861Hi | +A*+T*+T*G*C*A*T*C*A*G*A*T*T*G*A*+T* +G*+T | 135612 | 18 |
| 4864 | GCAAGCACTGAATTA TGAA | A574862Hi | +G*+C*+A*A*G*C*A*C*T*G*A*A*T*T*A*T*+ G*+A*+A | 135710 | 19 |
| 4865 | GCAAGCACTGAATTA TGA | A574863Hi | +G*+C*+A*A*G*C*A*C*T*G*A*A*T*T*A*+T* +G*+A | 135711 | 18 |
| 4866 | CTGAGTCAATTTCAG TTTG | A574864Hi | +C*+T*+G*A*G*T*C*A*A*T*T*T*C*A*G*T*+ T*+T*+G | 135780 | 19 |
| 4867 | GATCTGAGTCAATTT CAGT | A574865Hi | +G*+A*+T*C*T*G*A*G*T*C*A*A*T*T*T*C*+ A*+G*+T | 135783 | 19 |
| 4868 | AGATCTGAGTCAATT TCAG | A574866Hi | +A*+G*+A*T*C*T*G*A*G*T*C*A*A*T*T*T*+ C*+A*+G | 135784 | 19 |
| 4869 | GAGATCTGAGTCAAT TTCA | A574867Hi | +G*+A*+G*A*T*C*T*G*A*G*T*C*A*A*T*T*+ T*+C*+A | 135785 | 19 |
| 4870 | CTTAGAGATCTGAGT CAAT | A574868Hi | +C*+T*+T*A*G*A*G*A*T*C*T*G*A*G*T*C*+ A*+A*+T | 135789 | 19 |
| 4871 | CTGCCACTCAGAGCA AGTG | A574869Hi | +C*+T*+G*C*C*A*C*T*C*A*G*A*G*C*A*A*+ G*+T*+G | 135903 | 19 |
| 4872 | CTAACCTGCCACTCA GAGC | A574870Hi | +C*+T*+A*A*C*C*T*G*C*C*A*C*T*C*A*G*+ A*+G*+C | 135908 | 19 |
| 4873 | CTAACCTGCCACTCA GAG | A574871Hi | +C*+T*+A*A*C*C*T*G*C*C*A*C*T*C*A*+G* +A*+G | 135909 | 18 |
| 4874 | CCTAACCTGCCACTC AGAG | A574872Hi | +C*+C*+T*A*A*C*C*T*G*C*C*A*C*T*C*A*+ G*+A*+G | 135909 | 19 |
| 4875 | AGCTACCTAGTGGTT TCTA | A574873Hi | +A*+G*+C*T*A*C*C*T*A*G*T*G*G*T*T*T*+ C*+T*+A | 136044 | 19 |

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| 4876 | GCTACCTAGTGGTTTCTA | A574874Hi | +G*+C*+T*A*C*C*T*A*G*T*G*G*T*T*T*+C*+T*+A | 136044 | 18 |
| 4877 | GCAGTATATCTTAACCTC | A574875Hi | +G*+C*+A*G*T*A*T*A*T*C*T*T*A*A*C*+C*+T*+C | 136177 | 18 |
| 4878 | GCAGTATATCTTAACCT | A574876Hi | +G*+C*+A*G*T*A*T*A*T*C*T*T*A*A*+C*+C*+T | 136178 | 17 |
| 4879 | ATGTTAACCACATACTAGT | A574877Hi | +A*+T*+G*T*T*A*A*C*C*A*C*A*T*A*C*T*+A*+G*+T | 136260 | 19 |
| 4880 | TGTTAACCACATACTAGT | A574878Hi | +T*+G*+T*T*A*A*C*C*A*C*A*T*A*C*T*+A*+G*+T | 136260 | 18 |
| 4881 | AATGTTAACCACATACTAG | A574879Hi | +A*+A*+T*G*T*T*A*A*C*C*A*C*A*T*A*C*+T*+A*+G | 136261 | 19 |
| 4882 | CTCTCTAGTAAAGCATCT | A574880Hi | +C*+T*+C*T*C*T*A*G*T*A*A*A*G*C*A*+T*+C*+T | 136655 | 18 |
| 4883 | GCTCTCTAGTAAAGCATC | A574881Hi | +G*+C*+T*C*T*C*T*A*G*T*A*A*A*G*C*+A*+T*+C | 136656 | 18 |
| 4884 | GATGCTCTCTAGTAAAGC | A574882Hi | +G*+A*+T*G*C*T*C*T*C*T*A*G*T*A*A*+A*+G*+C | 136659 | 18 |
| 4885 | TATGGATGCTCTCTAGTA | A574883Hi | +T*+A*+T*G*G*A*T*G*C*T*C*T*C*T*A*+G*+T*+A | 136663 | 18 |
| 4886 | ATCTTTATGGATGCTCTCT | A574884Hi | +A*+T*+C*T*T*T*A*T*G*G*A*T*G*C*T*C*+T*+C*+T | 136667 | 19 |
| 4887 | CTTGATCTTTATGGATGC | A574885Hi | +C*+T*+T*G*A*T*C*T*T*T*A*T*G*G*A*+T*+G*+C | 136672 | 18 |
| 4888 | GAGAGCTTGATCTTTATGG | A574886Hi | +G*+A*+G*A*G*C*T*T*G*A*T*C*T*T*T*A*+T*+G*+G | 136676 | 19 |
| 4889 | TGAGAGCTTGATCTTTAT | A574887Hi | +T*+G*+A*G*A*G*C*T*T*G*A*T*C*T*T*+T*+A*+T | 136678 | 18 |
| 4890 | ATCTTTGAGAGCTTGATCT | A574888Hi | +A*+T*+C*T*T*T*G*A*G*A*G*C*T*T*G*A*+T*+C*+T | 136682 | 19 |
| 4891 | ATCTTTGAGAGCTTGATC | A574889Hi | +A*+T*+C*T*T*T*G*A*G*A*G*C*T*T*G*+A*+T*+C | 136683 | 18 |
| 4892 | TCAGAAGAGAGCAAATATT | A574890Hi | +T*+C*+A*G*A*A*G*A*G*A*G*C*A*A*A*T*+A*+T*+T | 136752 | 19 |
| 4893 | ACTTGTTCAGAAGAGAGC | A574891Hi | +A*+C*+T*T*G*T*T*C*A*G*A*A*G*A*G*+A*+G*+C | 136759 | 18 |
| 4894 | GATACTTGTTCAGAAGAGA | A574892Hi | +G*+A*+T*A*C*T*T*G*T*T*C*A*G*A*A*G*+A*+G*+A | 136761 | 19 |
| 4895 | CACAGGAGATACTTGTTCA | A574893Hi | +C*+A*+C*A*G*G*A*G*A*T*A*C*T*T*G*T*+T*+C*+A | 136768 | 19 |
| 4896 | AGGCCACAGGAGATACTTG | A574894Hi | +A*+G*+G*C*C*A*C*A*G*G*A*G*A*T*A*C*+T*+T*+G | 136772 | 19 |
| 4897 | TGCCTCTCAGTCGGTGTGT | A574895Hi | +T*+G*+C*C*T*C*T*C*A*G*T*C*G*G*T*G*+T*+G*+T | 136869 | 19 |
| 4898 | GCCTCTCAGTCGGTGTGT | A574896Hi | +G*+C*+C*T*C*T*C*A*G*T*C*G*G*T*G*+T*+G*+T | 136869 | 18 |
| 4899 | TGCCTCTCAGTCGGTGTG | A574897Hi | +T*+G*+C*C*T*C*T*C*A*G*T*C*G*G*T*+G*+T*+G | 136870 | 18 |
| 4900 | GCCTCTCAGTCGGTGTG | A574898Hi | +G*+C*+C*T*C*T*C*A*G*T*C*G*G*T*+G*+T*+G | 136870 | 17 |
| 4901 | ATGCCTCTCAGTCGGTGT | A574899Hi | +A*+T*+G*C*C*T*C*T*C*A*G*T*C*G*G*+T*+G*+T | 136871 | 18 |
| 4902 | GCAGTCATCTTTCATTAC | A574900Hi | +G*+C*+A*G*T*C*A*T*C*T*T*T*C*A*T*+T*+A*+C | 136894 | 18 |
| 4903 | GGCAGTCATCTTTCATTAC | A574901Hi | +G*+G*+C*A*G*T*C*A*T*C*T*T*T*C*A*T*+T*+A*+C | 136894 | 19 |
| 4904 | TGCAGACCTAGAACTCCA | A574902Hi | +T*+G*+C*A*G*A*C*C*T*A*G*A*A*C*T*+C*+C*+A | 136942 | 18 |
| 4905 | TGTTGCAGACCTAGAACTC | A574903Hi | +T*+G*+T*T*G*C*A*G*A*C*C*T*A*G*A*A*+C*+T*+C | 136944 | 19 |
| 4906 | AACATGTTGCAGACCTAG | A574904Hi | +A*+A*+C*A*T*G*T*T*G*C*A*G*A*C*C*+T*+A*+G | 136949 | 18 |
| 4907 | ATGATGTGTTGTCAGAGAG | A574905Hi | +A*+T*+G*A*T*G*T*G*T*T*G*T*C*A*G*A*+G*+A*+G | 137224 | 19 |
| 4908 | ATATGATGTGTTGTCAGAG | A574906Hi | +A*+T*+A*T*G*A*T*G*T*G*T*T*G*T*C*A*+G*+A*+G | 137226 | 19 |
| 4909 | TATGATGTGTTGTCAGAG | A574907Hi | +T*+A*+T*G*A*T*G*T*G*T*T*G*T*C*A*+G*+A*+G | 137226 | 18 |
| 4910 | AATATGATGTGTTGTCAGA | A574908Hi | +A*+A*+T*A*T*G*A*T*G*T*G*T*T*G*T*C*+A*+G*+A | 137227 | 19 |

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| 4911 | TAAATCAGATAGATA ACAT | A574909Hi | +T*+A*+A*A*T*C*A*G*A*T*A*G*A*T*A*A*+ C*+A*+T | 137343 | 19 |
| 4912 | TAAATCAGATAGATA ACA | A574910Hi | +T*+A*+A*A*T*C*A*G*A*T*A*G*A*T*A*+A* +C*+A | 137344 | 18 |
| 4913 | TTAAATCAGATAGAT AACA | A574911Hi | +T*+T*+A*A*A*T*C*A*G*A*T*A*G*A*T*A*+ A*+C*+A | 137344 | 19 |
| 4914 | TTTAAATCAGATAGA TAAC | A574912Hi | +T*+T*+T*A*A*A*T*C*A*G*A*T*A*G*A*T*+ A*+A*+C | 137345 | 19 |
| 4915 | GCATTTAAATCAGAT AGAT | A574913Hi | +G*+C*+A*T*T*T*A*A*A*T*C*A*G*A*T*A*+ G*+A*+T | 137348 | 19 |
| 4916 | GTCACTGTCATATTA TAGA | A574914Hi | +G*+T*+C*A*C*T*G*T*C*A*T*A*T*T*A*T*+ A*+G*+A | 137592 | 19 |
| 4917 | TGTCACTGTCATATT ATAG | A574915Hi | +T*+G*+T*C*A*C*T*G*T*C*A*T*A*T*T*A*+ T*+A*+G | 137593 | 19 |
| 4918 | TGGTGTCACTGTCAT ATTA | A574916Hi | +T*+G*+G*T*G*T*C*A*C*T*G*T*C*A*T*A*+ T*+T*+A | 137596 | 19 |
| 4919 | TCACAAACAGATTGG CTAC | A574917Hi | +T*+C*+A*C*A*A*A*C*A*G*A*T*T*G*G*C*+ T*+A*+C | 137734 | 19 |
| 4920 | TTTCACAAACAGATT GGCT | A574918Hi | +T*+T*+T*C*A*C*A*A*A*C*A*G*A*T*T*G*+ G*+C*+T | 137736 | 19 |
| 4921 | GTACATATTTCACAA ACAG | A574919Hi | +G*+T*+A*C*A*T*A*T*T*T*C*A*C*A*A*A*+ C*+A*+G | 137743 | 19 |
| 4922 | TAGTTGCAGTGTCTT CAAA | A574920Hi | +T*+A*+G*T*T*G*C*A*G*T*G*T*C*T*T*C*+ A*+A*+A | 137936 | 19 |
| 4923 | TTAGTTGCAGTGTCT TCAA | A574921Hi | +T*+T*+A*G*T*T*G*C*A*G*T*G*T*C*T*T*+ C*+A*+A | 137937 | 19 |
| 4924 | TTTAGTTGCAGTGTC TTCA | A574922Hi | +T*+T*+T*A*G*T*T*G*C*A*G*T*G*T*C*T*+ T*+C*+A | 137938 | 19 |
| 4925 | ATTTAGTTGCAGTGT CTTC | A574923Hi | +A*+T*+T*T*A*G*T*T*G*C*A*G*T*G*T*C*+ T*+T*+C | 137939 | 19 |
| 4926 | AAAGATTATGTCCAA TGTT | A574924Hi | +A*+A*+A*G*A*T*T*A*T*G*T*C*C*A*A*T*+ G*+T*+T | 138151 | 19 |
| 4927 | TATATAACATGCTTT GGTA | A574925Hi | +T*+A*+T*A*T*A*A*C*A*T*G*C*T*T*T*G*+ G*+T*+A | 138219 | 19 |
| 4928 | ATATATAACATGCTTT GGT | A574926Hi | +A*+T*+A*T*A*T*A*A*C*A*T*G*C*T*T*T*+ G*+G*+T | 138220 | 19 |
| 4929 | TATATAACATGCTTT GGT | A574927Hi | +T*+A*+T*A*T*A*A*C*A*T*G*C*T*T*T*T*+G* +G*+T | 138220 | 18 |
| 4930 | GCTAGACTATTGCAA TTAT | A574928Hi | +G*+C*+T*A*G*A*C*T*A*T*T*G*C*A*A*T*+ T*+A*+T | 138270 | 19 |
| 4931 | CTAGACTATTGCAAT TAT | A574929Hi | +C*+T*+A*G*A*C*T*A*T*T*G*C*A*A*T*+T* +A*+T | 138270 | 18 |
| 4932 | AGCTAGACTATTGCA ATTA | A574930Hi | +A*+G*+C*T*A*G*A*C*T*A*T*T*G*C*A*A*+ T*+T*+A | 138271 | 19 |
| 4933 | GCTAGACTATTGCAA TTA | A574931Hi | +G*+C*+T*A*G*A*C*T*A*T*T*G*C*A*A*+T* +T*+A | 138271 | 18 |
| 4934 | AAACAAGCTAGACTA TTGC | A574932Hi | +A*+A*+A*C*A*A*G*C*T*A*G*A*C*T*A*T*+ T*+G*+C | 138276 | 19 |
| 4935 | TAAACAAGCTAGACT ATTG | A574933Hi | +T*+A*+A*A*C*A*A*G*C*T*A*G*A*C*T*A*+ T*+T*+G | 138277 | 19 |
| 4936 | CTAAACAAGCTAGAC TATT | A574934Hi | +C*+T*+A*A*A*C*A*A*G*C*T*A*G*A*C*T*+ A*+T*+T | 138278 | 19 |
| 4937 | CTAAACAAGCTAGAC TAT | A574935Hi | +C*+T*+A*A*A*C*A*A*G*C*T*A*G*A*C*+T* +A*+T | 138279 | 18 |
| 4938 | CTAAACAAGCTAGAC TA | A574936Hi | +C*+T*+A*A*A*C*A*A*G*C*T*A*G*A*+C*+T *+A | 138280 | 17 |
| 4939 | ACTAAACAAGCTAGA CTA | A574937Hi | +A*+C*+T*A*A*A*C*A*A*G*C*T*A*G*A*+C* +T*+A | 138280 | 18 |
| 4940 | AACTAAACAAGCTAG ACT | A574938Hi | +A*+A*+C*T*A*A*A*C*A*A*G*C*T*A*G*+A* +C*+T | 138281 | 18 |
| 4941 | AAATTTCTACGTGTA ATAC | A574939Hi | +A*+A*+A*T*T*T*C*T*A*C*G*T*G*T*A*A*+ T*+A*+C | 138339 | 19 |
| 4942 | AATTTCTACGTGTAA TAC | A574940Hi | +A*+A*+T*T*T*C*T*A*C*G*T*G*T*A*A*+T* +A*+C | 138339 | 18 |
| 4943 | AGTCATCACTATTTG TTT | A574941Hi | +A*+G*+T*C*A*T*C*A*C*T*A*T*T*T*G*+T* +T*+T | 138366 | 18 |
| 4944 | AAGTCATCACTATTT GTTT | A574942Hi | +A*+A*+G*T*C*A*T*C*A*C*T*A*T*T*T*G*+ T*+T*+T | 138366 | 19 |
| 4945 | GTTGGAATCACTGAA AGCT | A574943H | +G*+T*+T*G*G*A*A*T*C*A*C*T*G*A*A*A*+ G*+C*+T | 138418 | 19 |

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| 4946 | TGTTGGAATCACTGAAAGC | A574944H | +T*+G*+T*T*G*G*A*A*T*C*A*C*T*G*A*A*+A*+G*+C | 138419 | 19 |
| 4947 | GTGTCTACCACCACTGTTA | A574945H | +G*+T*+G*T*C*T*A*C*C*A*C*C*A*C*T*G*+T*+T*+A | 138441 | 19 |
| 4948 | GTGTCTACCACCACTGTT | A574946H | +G*+T*+G*T*C*T*A*C*C*A*C*C*A*C*T*+G*+T*+T | 138442 | 18 |
| 4949 | AGTGTCTACCACCACTGTT | A574947H | +A*+G*+T*G*T*C*T*A*C*C*A*C*C*A*C*T*+G*+T*+T | 138442 | 19 |
| 4950 | TCCACAACAGGGCTATTTT | A574948H | +T*+C*+C*A*C*A*A*C*A*G*G*G*C*T*A*T*+T*+T*+T | 138480 | 19 |
| 4951 | CTTCCACAACAGGGCTATT | A574949H | +C*+T*+T*C*C*A*C*A*A*C*A*G*G*G*C*T*+A*+T*+T | 138482 | 19 |
| 4952 | ACTTCCACAACAGGGCTAT | A574950H | +A*+C*+T*T*C*C*A*C*A*A*C*A*G*G*G*C*+T*+A*+T | 138483 | 19 |
| 4953 | ACTTCCACAACAGGGCTA | A574951H | +A*+C*+T*T*C*C*A*C*A*A*C*A*G*G*G*+C*+T*+A | 138484 | 18 |
| 4954 | CACTTCCACAACAGGGCTA | A574952H | +C*+A*+C*T*T*C*C*A*C*A*A*C*A*G*G*G*+C*+T*+A | 138484 | 19 |
| 4955 | CCCACACTTCCACAACAGG | A574953H | +C*+C*+C*A*C*A*C*T*T*C*C*A*C*A*A*C*+A*+G*+G | 138488 | 19 |
| 4956 | TCCCACACTTCCACAACAG | A574954H | +T*+C*+C*C*A*C*A*C*T*T*C*C*A*C*A*A*+C*+A*+G | 138489 | 19 |
| 4957 | TATCCCACACTTCCACAAC | A574955H | +T*+A*+T*C*C*C*A*C*A*C*T*T*C*C*A*C*+A*+A*+C | 138491 | 19 |
| 4958 | TATCCCACACTTCCACAA | A574956H | +T*+A*+T*C*C*C*A*C*A*C*T*T*C*C*A*+C*+A*+A | 138492 | 18 |
| 4959 | TTATCCCACACTTCCACAA | A574957H | +T*+T*+A*T*C*C*C*A*C*A*C*T*T*C*C*A*+C*+A*+A | 138492 | 19 |
| 4960 | TCTTATCCCACACTTCCAC | A574958H | +T*+C*+T*T*A*T*C*C*C*A*C*A*C*T*T*C*+C*+A*+C | 138494 | 19 |
| 4961 | GTTTTCTTATCCCACACTT | A574959H | +G*+T*+T*T*T*C*T*T*A*T*C*C*C*A*C*A*+C*+T*+T | 138498 | 19 |
| 4962 | AGTTTTCTTATCCCACACT | A574960H | +A*+G*+T*T*T*T*C*T*T*A*T*C*C*C*A*C*+A*+C*+T | 138499 | 19 |
| 4963 | CATGAAGTGCAAAGATAAT | A574961Hi | +C*+A*+T*G*A*A*G*T*G*C*A*A*A*G*A*T*+A*+A*+T | 138595 | 19 |
| 4964 | CACATGAAGTGCAAAGATA | A574962Hi | +C*+A*+C*A*T*G*A*A*G*T*G*C*A*A*A*G*+A*+T*+A | 138597 | 19 |
| 4965 | GGTGCTGAGAAGCATTACA | A574963Hi | +G*+G*+T*G*C*T*G*A*G*A*A*G*C*A*T*T*+A*+C*+A | 138686 | 19 |
| 4966 | TGGTGCTGAGAAGCATTAC | A574964Hi | +T*+G*+G*T*G*C*T*G*A*G*A*A*A*G*C*A*T*+T*+A*+C | 138687 | 19 |
| 4967 | TGGTGCTGAGAAGCATTA | A574965Hi | +T*+G*+G*T*G*C*T*G*A*G*A*A*A*G*C*A*+T*+T*+A | 138688 | 18 |
| 4968 | TATATTTGACACTGTGAC | A574966Hi | +T*+A*+T*A*T*T*T*G*A*C*A*C*T*G*T*+G*+A*+C | 138864 | 18 |
| 4969 | GACTAAGCACTATGCTCT | A574967Hi | +G*+A*+C*T*A*A*G*C*A*C*T*A*T*G*C*+T*+C*+T | 139017 | 18 |
| 4970 | GACTAAGCACTATGCTC | A574968Hi | +G*+A*+C*T*A*A*G*C*A*C*T*A*T*G*+C*+T*+C | 139018 | 17 |
| 4971 | TCAGACTAAGCACTATGCT | A574969Hi | +T*+C*+A*G*A*C*T*A*A*G*C*A*C*T*A*T*+G*+C*+T | 139019 | 19 |
| 4972 | CATCAGACTAAGCACTATG | A574970Hi | +C*+A*+T*C*A*G*A*C*T*A*A*G*C*A*C*T*+A*+T*+G | 139021 | 19 |
| 4973 | GCATCAGACTAAGCACTA | A574971Hi | +G*+C*+A*T*C*A*G*A*C*T*A*A*G*C*A*+C*+T*+A | 139023 | 18 |
| 4974 | GGCTGCATCAGACTAAGCA | A574972Hi | +G*+G*+C*T*G*C*A*T*C*A*G*A*C*T*A*A*+G*+C*+A | 139026 | 19 |
| 4975 | TGTGCTTGCTATGGATTTG | A574973Hi | +T*+G*+T*G*C*T*T*G*C*T*A*T*G*G*A*T*+T*+T*+G | 139054 | 19 |
| 4976 | AATGTGCTTGCTATGGAT | A574974Hi | +A*+A*+T*G*T*G*C*T*T*G*C*T*A*T*G*+G*+A*+T | 139057 | 18 |
| 4977 | GAATGTGCTTGCTATGGA | A574975Hi | +G*+A*+A*T*G*T*G*C*T*T*G*C*T*A*T*+G*+G*+A | 139058 | 18 |
| 4978 | GCACAGAAAGAATGTGCTT | A574976Hi | +G*+C*+A*C*A*G*A*A*A*G*A*A*T*G*T*G*+C*+T*+T | 139066 | 19 |
| 4979 | ACCAGCACAGAAAGAATGT | A574977Hi | +A*+C*+C*A*G*C*A*C*A*G*A*A*A*G*A*A*+T*+G*+T | 139070 | 19 |
| 4980 | GCTAGCAAATAAGCTTGAA | A574978Hi | +G*+C*+T*A*G*C*A*A*A*T*A*A*G*C*T*T*+G*+A*+A | 139108 | 19 |

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| 4981 | TGGCTAGCAAATAAG CTT | A574979Hi | +T*+G*+G*C*T*A*G*C*A*A*A*T*A*A*G*+C* +T*+T | 139111 | 18 |
| 4982 | AAGTGGCTAGCAAAT AAGC | A574980Hi | +A*+A*+G*T*G*G*C*T*A*G*C*A*A*A*T*A*+ A*+G*+C | 139113 | 19 |
| 4983 | ATCAAGGAGACCTGT TGG | A574981Hi | +A*+T*+C*A*A*G*G*A*G*A*C*C*T*G*T*+T* +G*+G | 139302 | 18 |
| 4984 | CCTTTATCAAGGAGA CCTG | A574982Hi | +C*+C*+T*T*T*A*T*C*A*A*G*G*A*G*A*C*+ C*+T*+G | 139306 | 19 |
| 4985 | AAAGAATCCTAATCG TTT | A574983Hi | +A*+A*+A*G*A*A*T*C*C*T*A*A*T*C*G*+T* +T*+T | 139348 | 18 |
| 4986 | CAGAACCAGTGAATA GTCT | A574984Hi | +C*+A*+G*A*A*C*C*A*G*T*G*A*A*T*A*G*+ T*+C*+T | 139398 | 19 |
| 4987 | CAGAACCAGTGAATA GTC | A574985Hi | +C*+A*+G*A*A*C*C*A*G*T*G*A*A*T*A*+G* +T*+C | 139399 | 18 |
| 4988 | CCAGAACCAGTGAAT AGT | A574986Hi | +C*+C*+A*G*A*A*C*C*A*G*T*G*A*A*T*+A* +G*+T | 139400 | 18 |
| 4989 | GGAAATTATGAATAA GAGG | A574987Hi | +G*+G*+A*A*A*T*T*A*T*G*A*A*T*A*A*G*+ A*+G*+G | 139600 | 19 |
| 4990 | CTTTACTTGAAGCAT AAAT | A574988Hi | +C*+T*+T*T*A*C*T*T*G*A*A*G*C*A*T*A*+ A*+A*+T | 139650 | 19 |
| 4991 | TTTGTGTTTTGATTCC TTG | A574989H | +T*+T*+T*G*T*G*T*T*T*T*G*A*T*T*C*C*+ T*+T*+G | 139867 | 19 |
| 4992 | AGACATTTTGTGTTTT GAT | A574990H | +A*+G*+A*C*A*T*T*T*T*G*T*G*T*T*T*T*+ G*+A*+T | 139873 | 19 |
| 4993 | GAATAAGACATTTTG TGTT | A574991H | +G*+A*+A*T*A*A*G*A*C*A*T*T*T*T*G*T*+ G*+T*+T | 139878 | 19 |
| 4994 | AGAATAAGACATTTT GTGT | A574992H | +A*+G*+A*A*T*A*A*G*A*C*A*T*T*T*T*G*+ T*+G*+T | 139879 | 19 |
| 4995 | CCAGAATAAGACATT TTGT | A574993H | +C*+C*+A*G*A*A*T*A*A*G*A*C*A*T*T*T*+ T*+G*+T | 139881 | 19 |
| 4996 | CTCTCCCAGAATAAG ACAT | A574994H | +C*+T*+C*T*C*C*C*A*G*A*A*T*A*A*G*A*+ C*+A*+T | 139886 | 19 |
| 4997 | TTTCACTCTCCCAGA ATAA | A574995H | +T*+T*+T*C*A*C*T*C*T*C*C*C*A*G*A*A*+ T*+A*+A | 139891 | 19 |
| 4998 | GTGTTCTTCTGAAGG CAGA | A574996H | +G*+T*+G*T*T*C*T*T*C*T*G*A*A*G*G*C*+ A*+G*+A | 139914 | 19 |
| 4999 | GTGTTCTTCTGAAGG CAG | A574997H | +G*+T*+G*T*T*C*T*T*C*T*G*A*A*G*G*+C* +A*+G | 139915 | 18 |
| 5000 | AGTGTTCTTCTGAAG GCAG | A574998H | +A*+G*+T*G*T*T*C*T*T*C*T*G*A*A*G*G*+ C*+A*+G | 139915 | 19 |
| 5001 | AGAGCAGTGTTCTTC TGAA | A574999H | +A*+G*+A*G*C*A*G*T*G*T*T*C*T*T*C*T*+ G*+A*+A | 139920 | 19 |
| 5002 | AAGAGCAGTGTTCTT CTGA | A575000H | +A*+A*+G*A*G*C*A*G*T*G*T*T*C*T*T*C*+ T*+G*+A | 139921 | 19 |
| 5003 | AAAGAGCAGTGTTCT TCTG | A575001H | +A*+A*+A*G*A*G*C*A*G*T*G*T*T*C*T*T*+ C*+T*+G | 139922 | 19 |
| 5004 | CCAAAGAGCAGTGTT CTTC | A575002H | +C*+C*+A*A*A*G*A*G*C*A*G*T*G*T*T*C*+ T*+T*+C | 139924 | 19 |
| 5005 | TATCCAAAGAGCAGT GTTC | A575003H | +T*+A*+T*C*C*A*A*A*G*A*G*C*A*G*T*G*+ T*+T*+C | 139927 | 19 |
| 5006 | CTATCCAAAGAGCAG TGTT | A575004H | +C*+T*+A*T*C*C*A*A*A*G*A*G*C*A*G*T*+ G*+T*+T | 139928 | 19 |
| 5007 | TTCCTATCCAAAGAG CAGT | A575005H | +T*+T*+C*C*T*A*T*C*C*A*A*A*G*A*G*C*+ A*+G*+T | 139931 | 19 |
| 5008 | GTTCCTATCCAAAGA GCAG | A575006H | +G*+T*+T*C*C*T*A*T*C*C*A*A*A*G*A*G*+ C*+A*+G | 139932 | 19 |
| 5009 | TCCAGTTCCTATCCA AAGA | A575007H | +T*+C*+C*A*G*T*T*C*C*T*A*T*C*C*A*A*+ A*+G*+A | 139936 | 19 |
| 5010 | CTCCAGTTCCTATCC AAAG | A575008H | +C*+T*+C*C*A*G*T*T*C*C*T*A*T*C*C*A*+ A*+A*+G | 139937 | 19 |
| 5011 | TCCTCCAGTTCCTAT CCAA | A575009H | +T*+C*+C*T*C*C*A*G*T*T*C*C*T*A*T*C*+ C*+A*+A | 139939 | 19 |
| 5012 | GCCTCCTCCAGTTCC TATC | A575010H | +G*+C*+C*T*C*C*T*C*C*A*G*T*T*C*C*T*+ A*+T*+C | 139942 | 19 |
| 5013 | GGCCTCCTCCAGTTC CTAT | A575011H | +G*+G*+C*C*T*C*C*T*C*C*A*G*T*T*C*C*+ T*+A*+T | 139943 | 19 |
| 5014 | GGCCTCCTCCAGTTC CTA | A575012H | +G*+G*+C*C*T*C*C*T*C*C*A*G*T*T*C*+C* +T*+A | 139944 | 18 |
| 5015 | TGGCCTCCTCCAGTT CCTA | A575013H | +T*+G*+G*C*C*T*C*C*T*C*C*A*G*T*T*C*+ C*+T*+A | 139944 | 19 |

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| 5016 | AATATGGCCTCCTCC AGTT | A575014H | +A*+A*+T*A*T*G*G*C*C*T*C*C*T*C*C*A*+ G*+T*+T | 139948 | 19 |
| 5017 | AAATATGGCCTCCTC CAGT | A575015H | +A*+A*+A*T*A*T*G*G*C*C*T*C*C*T*C*C*+ A*+G*+T | 139949 | 19 |
| 5018 | TAAAATATGGCCTCC TCCA | A575016H | +T*+A*+A*A*A*T*A*T*G*G*C*C*T*C*C*T*+ C*+C*+A | 139951 | 19 |
| 5019 | GTAAAATATGGCCTC CTCC | A575017H | +G*+T*+A*A*A*A*T*A*T*G*G*C*C*T*C*C*+ T*+C*+C | 139952 | 19 |
| 5020 | GTAAAATATGGCCTC CTC | A575018H | +G*+T*+A*A*A*A*T*A*T*G*G*C*C*T*C*+C* +T*+C | 139953 | 18 |
| 5021 | AGTAAAATATGGCCT CCTC | A575019H | +A*+G*+T*A*A*A*A*T*A*T*G*G*C*C*T*C*+ C*+T*+C | 139953 | 19 |
| 5022 | GAGTAAAATATGGCC TCCT | A575020H | +G*+A*+G*T*A*A*A*A*T*A*T*G*G*C*C*T*+ C*+C*+T | 139954 | 19 |
| 5023 | GACGAGTTGAAAGAT CCA | A575021H | +G*+A*+C*G*A*G*T*T*G*A*A*A*G*A*T*+C* +C*+A | 139974 | 18 |
| 5024 | CGACGAGTTGAAAGA TCCA | A575022H | +C*+G*+A*C*G*A*G*T*T*G*A*A*A*G*A*T*+ C*+C*+A | 139974 | 19 |
| 5025 | GACGAGTTGAAAGAT CC | A575023H | +G*+A*+C*G*A*G*T*T*G*A*A*A*G*A*+T*+ C*+C | 139975 | 17 |
| 5026 | CGACGAGTTGAAAGA TCC | A575024H | +C*+G*+A*C*G*A*G*T*T*G*A*A*A*G*A*+T* +C*+C | 139975 | 18 |
| 5027 | TCGACGAGTTGAAAG ATCC | A575025H | +T*+C*+G*A*C*G*A*G*T*T*G*A*A*A*G*A*+ T*+C*+C | 139975 | 19 |
| 5028 | CGACGAGTTGAAAGA TC | A575026H | +C*+G*+A*C*G*A*G*T*T*G*A*A*A*G*+A*+ T*+C | 139976 | 17 |
| 5029 | TCGACGAGTTGAAAG ATC | A575027H | +T*+C*+G*A*C*G*A*G*T*T*G*A*A*A*G*+A* +T*+C | 139976 | 18 |
| 5030 | TCATGACTCTGACCG AAT | A575028H | +T*+C*+A*T*G*A*C*T*C*T*G*A*C*C*G*+A* +A*+T | 140022 | 18 |
| 5031 | ATCATGACTCTGACC GAAT | A575029H | +A*+T*+C*A*T*G*A*C*T*C*T*G*A*C*C*G*+ A*+A*+T | 140022 | 19 |
| 5032 | TCATGACTCTGACCG AA | A575030H | +T*+C*+A*T*G*A*C*T*C*T*G*A*C*C*+G*+A *+A | 140023 | 17 |
| 5033 | ATCATGACTCTGACC GAA | A575031H | +A*+T*+C*A*T*G*A*C*T*C*T*G*A*C*C*+G* +A*+A | 140023 | 18 |
| 5034 | CATCATGACTCTGAC CGAA | A575032H | +C*+A*+T*C*A*T*G*A*C*T*C*T*G*A*C*C*+ G*+A*+A | 140023 | 19 |
| 5035 | CATCATGACTCTGAC CGA | A575033H | +C*+A*+T*C*A*T*G*A*C*T*C*T*G*A*C*+C* +G*+A | 140024 | 18 |
| 5036 | TCATCATGACTCTGA CCGA | A575034H | +T*+C*+A*T*C*A*T*G*A*C*T*C*T*G*A*C*+ C*+G*+A | 140024 | 19 |
| 5037 | TCATCATGACTCTGA CCG | A575035H | +T*+C*+A*T*C*A*T*G*A*C*T*C*T*G*A*+C* +C*+G | 140025 | 18 |
| 5038 | GTCATCATGACTCTG ACCG | A575036H | +G*+T*+C*A*T*C*A*T*G*A*C*T*C*T*G*A*+ C*+C*+G | 140025 | 19 |
| 5039 | TGTCATCATGACTCT GACC | A575037H | +T*+G*+T*C*A*T*C*A*T*G*A*C*T*C*T*G*+ A*+C*+C | 140026 | 19 |
| 5040 | GCTGTCATCATGACT CTGA | A575038H | +G*+C*+T*G*T*C*A*T*C*A*T*G*A*C*T*C*+ T*+G*+A | 140028 | 19 |
| 5041 | AGCTGTGCTGTCATC ATGA | A575039H | +A*+G*+C*T*G*T*G*C*T*G*T*C*A*T*C*A*+ T*+G*+A | 140034 | 19 |
| 5042 | CTAAAGGAAAGAAAC TTGC | A575040Hi | +C*+T*+A*A*A*G*G*A*A*A*G*A*A*A*C*T*+ T*+G*+C | 140055 | 19 |
| 5043 | TATAAGACTTAGAGA ATAT | A575041Hi | +T*+A*+T*A*A*G*A*C*T*T*A*G*A*G*A*A*+ T*+A*+T | 140083 | 19 |
| 5044 | TTATAAGACTTAGAG AATA | A575042Hi | +T*+T*+A*T*A*A*G*A*C*T*T*A*G*A*G*A*+ A*+T*+A | 140084 | 19 |
| 5045 | TTTATAAGACTTAGA GAAT | A575043Hi | +T*+T*+T*A*T*A*A*G*A*C*T*T*A*G*A*G*+ A*+A*+T | 140085 | 19 |
| 5046 | TGCAGTAATCTGCTT CTCT | A575044Hi | +T*+G*+C*A*G*T*A*A*T*C*T*G*C*T*T*C*+ T*+C*+T | 140254 | 19 |
| 5047 | GCAGTAATCTGCTTC TCT | A575045Hi | +G*+C*+A*G*T*A*A*T*C*T*G*C*T*T*C*+T* +C*+T | 140254 | 18 |
| 5048 | TGCAGTAATCTGCTT CTC | A575046Hi | +T*+G*+C*A*G*T*A*A*T*C*T*G*C*T*T*+C* +T*+C | 140255 | 18 |
| 5049 | AGCTGCAGTAATCTG CTTC | A575047Hi | +A*+G*+C*T*G*C*A*G*T*A*A*T*C*T*G*C*+ T*+T*+C | 140257 | 19 |
| 5050 | GCTGCAGTAATCTGC TTC | A575048Hi | +G*+C*+T*G*C*A*G*T*A*A*T*C*T*G*C*+T* +T*+C | 140257 | 18 |

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| 5051 | TCAGCTGCAGTAATC TGCT | A575049Hi | +T*+C*+A*G*C*T*G*C*A*G*T*A*A*T*C*T*+ G*+C*+T | 140259 | 19 |
| 5052 | GTTCAGCTGCAGTAA TCTG | A575050Hi | +G*+T*+T*C*A*G*C*T*G*C*A*G*T*A*A*T*+ C*+T*+G | 140261 | 19 |
| 5053 | TGTTCAGCTGCAGTA ATCT | A575051Hi | +T*+G*+T*T*C*A*G*C*T*G*C*A*G*T*A*A*+ T*+C*+T | 140262 | 19 |
| 5054 | GTGTTCAGCTGCAGT AAT | A575052Hi | +G*+T*+G*T*T*C*A*G*C*T*G*C*A*G*T*+A* +A*+T | 140264 | 18 |
| 5055 | GGCTAGACTATGATT AAA | A575053Hi | +G*+G*+C*T*A*G*A*C*T*A*T*G*A*T*T*+A* +A*+A | 140393 | 18 |
| 5056 | GAGGCTAGACTATGA TTAA | A575054Hi | +G*+A*+G*G*C*T*A*G*A*C*T*A*T*G*A*T*+ T*+A*+A | 140394 | 19 |
| 5057 | GAGGCTAGACTATGA TTA | A575055Hi | +G*+A*+G*G*C*T*A*G*A*C*T*A*T*G*A*+T* +T*+A | 140395 | 18 |
| 5058 | ATGAGATTCTTTAAC AAGC | A575056Hi | +A*+T*+G*A*G*A*T*T*C*T*T*T*A*A*C*A*+ A*+G*+C | 140416 | 19 |
| 5059 | GCTTGTGTGGACATG TATC | A575057Hi | +G*+C*+T*T*G*T*G*T*G*G*A*C*A*T*G*T*+ A*+T*+C | 140901 | 19 |
| 5060 | CTGCTTGTGTGGACA TGTA | A575058Hi | +C*+T*+G*C*T*T*G*T*G*T*G*G*A*C*A*T*+ G*+T*+A | 140903 | 19 |
| 5061 | TCTGCTTGTGTGGAC ATGT | A575059Hi | +T*+C*+T*G*C*T*T*G*T*G*T*G*G*A*C*A*+ T*+G*+T | 140904 | 19 |
| 5062 | TTTGGTAGAATAAGA CTAC | A575060Hi | +T*+T*+T*G*G*T*A*G*A*A*T*A*A*G*A*C*+ T*+A*+C | 140951 | 19 |
| 5063 | CTTTGGTAGAATAAG ACTA | A575061Hi | +C*+T*+T*T*G*G*T*A*G*A*A*T*A*A*G*A*+ C*+T*+A | 140952 | 19 |
| 5064 | ACAACTTTGGTAGAA TAAG | A575062Hi | +A*+C*+A*A*C*T*T*T*G*G*T*A*G*A*A*T*+ A*+A*+G | 140956 | 19 |
| 5065 | CAACAACTTTGGTAG AAT | A575063Hi | +C*+A*+A*C*A*A*C*T*T*T*G*G*T*A*G*+A* +A*+T | 140959 | 18 |
| 5066 | TGCAACAACTTTGGT AGAA | A575064Hi | +T*+G*+C*A*A*C*A*A*C*T*T*T*G*G*T*A*+ G*+A*+A | 140960 | 19 |
| 5067 | AGAGAATGCAACAAC TTTG | A575065Hi | +A*+G*+A*G*A*A*T*G*C*A*A*C*A*A*C*T*+ T*+T*+G | 140966 | 19 |
| 5068 | CAACTAGAGAATGCA ACAA | A575066Hi | +C*+A*+A*C*T*A*G*A*G*A*A*T*G*C*A*A*+ C*+A*+A | 140971 | 19 |
| 5069 | CAACTAGAGAATGCA ACA | A575067Hi | +C*+A*+A*C*T*A*G*A*G*A*A*T*G*C*A*+A* +C*+A | 140972 | 18 |
| 5070 | AATTCAACTAGAGAA TGCA | A575068Hi | +A*+A*+T*T*C*A*A*C*T*A*G*A*G*A*A*T*+ G*+C*+A | 140975 | 19 |
| 5071 | CATACAATTCAACTA GAGA | A575069Hi | +C*+A*+T*A*C*A*A*T*T*C*A*A*C*T*A*G*+ A*+G*+A | 140980 | 19 |
| 5072 | TACATACAATTCAAC TAGA | A575070Hi | +T*+A*+C*A*T*A*C*A*A*T*T*C*A*A*C*T*+ A*+G*+A | 140982 | 19 |
| 5073 | GTACATACAATTCAA CTAG | A575071Hi | +G*+T*+A*C*A*T*A*C*A*A*T*T*C*A*A*C*+ T*+A*+G | 140983 | 19 |
| 5074 | CCAAAGTACATACAA TTCA | A575072Hi | +C*+C*+A*A*A*G*T*A*C*A*T*A*C*A*A*T*+ T*+C*+A | 140988 | 19 |
| 5075 | CTTCAGTTATAAGCA AGCT | A575073Hi | +C*+T*+T*C*A*G*T*T*A*T*A*A*G*C*A*A*+ G*+C*+T | 141016 | 19 |
| 5076 | TTCAGTTATAAGCAA GCT | A575074Hi | +T*+T*+C*A*G*T*T*A*T*A*A*G*C*A*A*+G* +C*+T | 141016 | 18 |
| 5077 | ACTTCAGTTATAAGC AAGC | A575075Hi | +A*+C*+T*T*C*A*G*T*T*A*T*A*A*G*C*A*+ A*+G*+C | 141017 | 19 |
| 5078 | CTTCAGTTATAAGCA AGC | A575076Hi | +C*+T*+T*C*A*G*T*T*A*T*A*A*G*C*A*+A* +G*+C | 141017 | 18 |
| 5079 | AACTTCAGTTATAAG CAAG | A575077Hi | +A*+A*+C*T*T*C*A*G*T*T*A*T*A*A*G*C*+ A*+A*+G | 141018 | 19 |
| 5080 | TAACTTCAGTTATAA GCAA | A575078Hi | +T*+A*+A*C*T*T*C*A*G*T*T*A*T*A*A*G*+ C*+A*+A | 141019 | 19 |
| 5081 | CCACTATAACTTCAG TTAT | A575079Hi | +C*+C*+A*C*T*A*T*A*A*C*T*T*C*A*G*T*+ T*+A*+T | 141025 | 19 |
| 5082 | TGGAGGCAGGAGAG GTACA | A575080Hi | +T*+G*+G*A*G*G*C*A*G*G*A*G*A*G*G*T* +A*+C*+A | 141126 | 19 |
| 5083 | AATGTGGTAGATGAT GGAG | A575081Hi | +A*+A*+T*G*T*G*G*T*A*G*A*T*G*A*T*G*+ G*+A*+G | 141140 | 19 |
| 5084 | GATCTGGTAGGAATG TGGT | A575082Hi | +G*+A*+T*C*T*G*G*T*A*G*G*A*A*T*G*T*+ G*+G*+T | 141151 | 19 |
| 5085 | GAAGAACTGGATGTT CATC | A575083Hi | +G*+A*+A*G*A*A*C*T*G*G*A*T*G*T*T*C*+ A*+T*+C | 141181 | 19 |

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| 5086 | AGAAGAACTGGATGTTCAT | A575084Hi | +A*+G*+A*A*G*A*A*C*T*G*G*A*T*G*T*T*+C*+A*+T | 141182 | 19 |
| 5087 | CTTAGATGGATGGATATAC | A575085Hi | +C*+T*+T*A*G*A*T*G*G*A*T*G*G*A*T*A*+T*+A*+C | 141604 | 19 |
| 5088 | GGACACTTAGATGGATGGA | A575086Hi | +G*+G*+A*C*A*C*T*T*A*G*A*T*G*G*A*T*+G*+G*+A | 141609 | 19 |
| 5089 | AGTATTTAGATGGACACTT | A575087Hi | +A*+G*+T*A*T*T*T*A*G*A*T*G*G*A*C*A*+C*+T*+T | 141620 | 19 |
| 5090 | ATGAGTATTTAGATGGACA | A575088Hi | +A*+T*+G*A*G*T*A*T*T*T*A*G*A*T*G*G*+A*+C*+A | 141623 | 19 |
| 5091 | ATGAGTATTTAGATGGAC | A575089Hi | +A*+T*+G*A*G*T*A*T*T*T*A*G*A*T*G*+G*+A*+C | 141624 | 18 |
| 5092 | TATGAGTATTTAGATGGA | A575090Hi | +T*+A*+T*G*A*G*T*A*T*T*T*A*G*A*T*+G*+G*+A | 141625 | 18 |
| 5093 | TAAGGTACAAATATGAGTA | A575091Hi | +T*+A*+A*G*G*T*A*C*A*A*A*T*A*T*G*A*+G*+T*+A | 141654 | 19 |
| 5094 | AGTTCTTTGGATATGGTAA | A575092Hi | +A*+G*+T*T*C*T*T*T*G*G*A*T*A*T*G*G*+T*+A*+A | 141670 | 19 |
| 5095 | AATTATGTGAGTCTGAGAA | A575093Hi | +A*+A*+T*T*A*T*G*T*G*A*G*T*C*T*G*A*+G*+A*+A | 141778 | 19 |
| 5096 | AATTATGTGAGTCTGAGA | A575094Hi | +A*+A*+T*T*A*T*G*T*G*A*G*T*C*T*G*+A*+G*+A | 141779 | 18 |
| 5097 | GATCCACTCCTTGCTGCAA | A575095Hi | +G*+A*+T*C*C*A*C*T*C*C*T*T*G*C*T*G*+C*+A*+A | 141802 | 19 |
| 5098 | ATCCACTCCTTGCTGCAA | A575096Hi | +A*+T*+C*C*A*C*T*C*C*T*T*G*C*T*G*+C*+A*+A | 141802 | 18 |
| 5099 | TGATCCACTCCTTGCTGCA | A575097Hi | +T*+G*+A*T*C*C*A*C*T*C*C*T*T*G*C*T*+G*+C*+A | 141803 | 19 |
| 5100 | TGTGATCCACTCCTTGCTG | A575098Hi | +T*+G*+T*G*A*T*C*C*A*C*T*C*C*T*T*G*+C*+T*+G | 141805 | 19 |
| 5101 | TCTGTGATCCACTCCTTGC | A575099Hi | +T*+C*+T*G*T*G*A*T*C*C*A*C*T*C*C*T*+T*+G*+C | 141807 | 19 |
| 5102 | AATCTGTGATCCACTCCT | A575100Hi | +A*+A*+T*C*T*G*T*G*A*T*C*C*A*C*T*+C*+C*+T | 141810 | 18 |
| 5103 | ATACCTTGGAACTGAATTC | A575101Hi | +A*+T*+A*C*C*T*T*G*G*A*A*C*T*G*A*A*+T*+T*+C | 141898 | 19 |
| 5104 | CACAAATACCTTGGAACTG | A575102Hi | +C*+A*+C*A*A*A*T*A*C*C*T*T*G*G*A*A*+C*+T*+G | 141903 | 19 |
| 5105 | ACACAAATACCTTGGAACT | A575103Hi | +A*+C*+A*C*A*A*A*T*A*C*C*T*T*G*G*A*+A*+C*+T | 141904 | 19 |
| 5106 | GACACAAATACCTTGGAAC | A575104Hi | +G*+A*+C*A*C*A*A*A*T*A*C*C*T*T*G*G*+A*+A*+C | 141905 | 19 |
| 5107 | CCAATACCAGCATGACATT | A575105H | +C*+C*+A*A*T*A*C*C*A*G*C*A*T*G*A*C*+A*+T*+T | 142021 | 19 |
| 5108 | CCCAATACCAGCATGACAT | A575106H | +C*+C*+C*A*A*T*A*C*C*A*G*C*A*T*G*A*+C*+A*+T | 142022 | 19 |
| 5109 | CCCAATACCAGCATGACA | A575107H | +C*+C*+C*A*A*T*A*C*C*A*G*C*A*T*G*+A*+C*+A | 142023 | 18 |
| 5110 | GCCCAATACCAGCATGACA | A575108H | +G*+C*+C*C*A*A*T*A*C*C*A*G*C*A*T*G*+A*+C*+A | 142023 | 19 |
| 5111 | TAGCCCAATACCAGCATGA | A575109H | +T*+A*+G*C*C*C*A*A*T*A*C*C*A*G*C*A*+T*+G*+A | 142025 | 19 |
| 5112 | CTGATTATACCATATGTAA | A575110Hi | +C*+T*+G*A*T*T*A*T*A*C*C*A*T*A*T*G*+T*+A*+A | 142171 | 19 |
| 5113 | CACTTCATATCACTTGTAA | A575111Hi | +C*+A*+C*T*T*C*A*T*A*T*C*A*C*T*T*G*+T*+A*+A | 142243 | 19 |
| 5114 | TAACACTTCATATCACTTG | A575112Hi | +T*+A*+A*C*A*C*T*T*C*A*T*A*T*C*A*C*+T*+T*+G | 142246 | 19 |
| 5115 | GATTGACACCTCTACTTCA | A575113Hi | +G*+A*+T*T*G*A*C*A*C*C*T*C*T*A*C*T*+T*+C*+A | 142283 | 19 |
| 5116 | GCTAGTGATTGACACCTC | A575114Hi | +G*+C*+T*A*G*T*G*A*T*T*G*A*C*A*C*+C*+T*+C | 142290 | 18 |
| 5117 | TGAGCTAGTGATTGACACC | A575115Hi | +T*+G*+A*G*C*T*A*G*T*G*A*T*T*G*A*C*+A*+C*+C | 142292 | 19 |
| 5118 | GAGCTAGTGATTGACACC | A575116Hi | +G*+A*+G*C*T*A*G*T*G*A*T*T*G*A*C*+A*+C*+C | 142292 | 18 |
| 5119 | TTGAGCTAGTGATTGACAC | A575117Hi | +T*+T*+G*A*G*C*T*A*G*T*G*A*T*T*G*A*+C*+A*+C | 142293 | 19 |
| 5120 | TAAGGTTGAGCTAGTGATT | A575118Hi | +T*+A*+A*G*G*T*T*G*A*G*C*T*A*G*T*G*+A*+T*+T | 142298 | 19 |

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| 5121 | TAAGGTTGAGCTAGTGAT | A575119Hi | +T*+A*+A*G*G*T*T*G*A*G*C*T*A*G*T*+G*+A*+T | 142299 | 18 |
| 5122 | TAAGGTTGAGCTAGTGA | A575120Hi | +T*+A*+A*G*G*T*T*G*A*G*C*T*A*G*+T*+G*+A | 142300 | 17 |
| 5123 | TTAAGGTTGAGCTAGTGA | A575121Hi | +T*+T*+A*A*G*G*T*T*G*A*G*C*T*A*G*+T*+G*+A | 142300 | 18 |
| 5124 | GTCAAGCAAGATTGTATCT | A575122H | +G*+T*+C*A*A*G*C*A*A*G*A*T*T*G*T*A*+T*+C*+T | 142648 | 19 |
| 5125 | GTCAAGCAAGATTGTATC | A575123H | +G*+T*+C*A*A*G*C*A*A*G*A*T*T*G*T*+A*+T*+C | 142649 | 18 |
| 5126 | TGTGGAAGATTGATGTCCC | A575124H | +T*+G*+T*G*G*A*A*G*A*T*T*G*A*T*G*T*+C*+C*+C | 142672 | 19 |
| 5127 | TGTGGAAGATTGATGTCC | A575125H | +T*+G*+T*G*G*A*A*G*A*T*T*G*A*T*G*+T*+C*+C | 142673 | 18 |
| 5128 | ATGTGGAAGATTGATGTCC | A575126H | +A*+T*+G*T*G*G*A*A*G*A*T*T*G*A*T*G*+T*+C*+C | 142673 | 19 |
| 5129 | TCATGTGGAAGATTGATGT | A575127H | +T*+C*+A*T*G*T*G*G*A*A*G*A*T*T*G*A*+T*+G*+T | 142675 | 19 |
| 5130 | TCATGTGGAAGATTGATG | A575128H | +T*+C*+A*T*G*T*G*G*A*A*G*A*T*T*G*+A*+T*+G | 142676 | 18 |
| 5131 | TTCATGTGGAAGATTGATG | A575129H | +T*+T*+C*A*T*G*T*G*G*A*A*G*A*T*T*G*+A*+T*+G | 142676 | 19 |
| 5132 | CTTCATGTGGAAGATTGAT | A575130H | +C*+T*+T*C*A*T*G*T*G*G*A*A*G*A*T*T*+G*+A*+T | 142677 | 19 |
| 5133 | GCACTTCATGTGGAAGATT | A575131H | +G*+C*+A*C*T*T*C*A*T*G*T*G*G*A*A*G*+A*+T*+T | 142680 | 19 |
| 5134 | GCACTTCATGTGGAAGAT | A575132H | +G*+C*+A*C*T*T*C*A*T*G*T*G*G*A*A*+G*+A*+T | 142681 | 18 |
| 5135 | TGCACTTCATGTGGAAGAT | A575133H | +T*+G*+C*A*C*T*T*C*A*T*G*T*G*G*A*A*+G*+A*+T | 142681 | 19 |
| 5136 | TGCACTTCATGTGGAAGA | A575134H | +T*+G*+C*A*C*T*T*C*A*T*G*T*G*G*A*+A*+G*+A | 142682 | 18 |
| 5137 | TTGCACTTCATGTGGAAGA | A575135H | +T*+T*+G*C*A*C*T*T*C*A*T*G*T*G*G*A*+A*+G*+A | 142682 | 19 |
| 5138 | AAATTTTGCACTTCATGTG | A575136H | +A*+A*+A*T*T*T*T*G*C*A*C*T*T*C*A*T*+G*+T*+G | 142687 | 19 |
| 5139 | CTAAATTTTGCACTTCATG | A575137H | +C*+T*+A*A*A*T*T*T*T*G*C*A*C*T*T*C*+A*+T*+G | 142689 | 19 |
| 5140 | TTCAGCTAATTCTTTTCTC | A575138H | +T*+T*+C*A*G*C*T*A*A*T*T*C*T*T*T*T*+C*+T*+C | 142724 | 19 |
| 5141 | TTCCTATCCAAAGACAATT | A575139H | +T*+T*+C*C*T*A*T*C*C*A*A*A*G*A*C*A*+A*+T*+T | 142782 | 19 |
| 5142 | CAAAAAATGTGAGTACCCT | A575140H | +C*+A*+A*A*A*A*A*T*G*T*G*A*G*T*A*C*+C*+C*+T | 142851 | 19 |
| 5143 | TGAGTACTTAAATTAGGTA | A575141H | +T*+G*+A*G*T*A*C*T*T*A*A*A*T*T*A*G*+G*+T*+A | 143036 | 19 |
| 5144 | TGAGTACTTAAATTAGGT | A575142H | +T*+G*+A*G*T*A*C*T*T*A*A*A*T*T*A*+G*+G*+T | 143037 | 18 |
| 5145 | ATGAGTACTTAAATTAGGT | A575143H | +A*+T*+G*A*G*T*A*C*T*T*A*A*A*T*T*A*+G*+G*+T | 143037 | 19 |
| 5146 | GTATGAGTACTTAAATTAG | A575144H | +G*+T*+A*T*G*A*G*T*A*C*T*T*A*A*A*T*+T*+A*+G | 143039 | 19 |
| 5147 | GTATGAGTACTTAAATTA | A575145H | +G*+T*+A*T*G*A*G*T*A*C*T*T*A*A*A*+T*+T*+A | 143040 | 18 |
| 5148 | AGTATGAGTACTTAAATTA | A575146H | +A*+G*+T*A*T*G*A*G*T*A*C*T*T*A*A*A*+T*+T*+A | 143040 | 19 |
| 5149 | TTAGTATGAGTACTTAAAT | A575147H | +T*+T*+A*G*T*A*T*G*A*G*T*A*C*T*T*A*+A*+A*+T | 143042 | 19 |
| 5150 | TTTAGTATGAGTACTTAAA | A575148H | +T*+T*+T*A*G*T*A*T*G*A*G*T*A*C*T*T*+A*+A*+A | 143043 | 19 |
| 5151 | TTTAGTATGAGTACTTAA | A575149H | +T*+T*+T*A*G*T*A*T*G*A*G*T*A*C*T*+T*+A*+A | 143044 | 18 |
| 5152 | TTTTAGTATGAGTACTTAA | A575150H | +T*+T*+T*T*A*G*T*A*T*G*A*G*T*A*C*T*+T*+A*+A | 143044 | 19 |
| 5153 | TTTTAGTATGAGTACTTA | A575151H | +T*+T*+T*T*A*G*T*A*T*G*A*G*T*A*C*+T*+T*+A | 143045 | 18 |
| 5154 | ATTTTAGTATGAGTACTTA | A575152H | +A*+T*+T*T*T*A*G*T*A*T*G*A*G*T*A*C*+T*+T*+A | 143045 | 19 |
| 5155 | AATTTTAGTATGAGTACTT | A575153H | +A*+A*+T*T*T*T*A*G*T*A*T*G*A*G*T*A*+C*+T*+T | 143046 | 19 |

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| 5156 | TAAATTTTAGTATGAGTAC | A575154H | +T*+A*+A*A*T*T*T*T*A*G*T*A*T*G*A*G*+T*+A*+C | 143048 | 19 |
| 5157 | CGGCCTTATAAATTTTAGT | A575155H | +C*+G*+G*C*C*T*T*A*T*A*A*A*T*T*T*T*+A*+G*+T | 143056 | 19 |
| 5158 | TATCGGCCTTATAAATTTT | A575156H | +T*+A*+T*C*G*G*C*C*T*T*A*T*A*A*A*T*+T*+T*+T | 143059 | 19 |
| 5159 | TATCGGCCTTATAAATTT | A575157H | +T*+A*+T*C*G*G*C*C*T*T*A*T*A*A*A*+T*+T*+T | 143060 | 18 |
| 5160 | TTATCGGCCTTATAAATTT | A575158H | +T*+T*+A*T*C*G*G*C*C*T*T*A*T*A*A*A*+T*+T*+T | 143060 | 19 |
| 5161 | ATTATCGGCCTTATAAATT | A575159H | +A*+T*+T*A*T*C*G*G*C*C*T*T*A*T*A*A*+A*+T*+T | 143061 | 19 |
| 5162 | ATTATCGGCCTTATAAAT | A575160H | +A*+T*+T*A*T*C*G*G*C*C*T*T*A*T*A*A*+A*+A*+T | 143062 | 18 |
| 5163 | AATTATCGGCCTTATAAAT | A575161H | +A*+A*+T*T*A*T*C*G*G*C*C*T*T*A*T*A*A*+A*+A*+T | 143062 | 19 |
| 5164 | AATTATCGGCCTTATAAA | A575162H | +A*+A*+T*T*A*T*C*G*G*C*C*T*T*A*T*A*+A*+A*+A | 143063 | 18 |
| 5165 | AAATTATCGGCCTTATAAA | A575163H | +A*+A*+A*T*T*A*T*C*G*G*C*C*T*T*A*T*A*+A*+A*+A | 143063 | 19 |
| 5166 | AATTATCGGCCTTATAA | A575164H | +A*+A*+T*T*A*T*C*G*G*C*C*T*T*A*+T*+A*+A | 143064 | 17 |
| 5167 | AAATTATCGGCCTTATAA | A575165H | +A*+A*+A*T*T*A*T*C*G*G*C*C*T*T*A*+T*+A*+A | 143064 | 18 |
| 5168 | AAAATTATCGGCCTTATAA | A575166H | +A*+A*+A*A*T*T*A*T*C*G*G*C*C*T*T*A*+T*+A*+A | 143064 | 19 |
| 5169 | CAAAAAATTATCGGCCTTA | A575167H | +C*+A*+A*A*A*A*A*T*T*A*T*C*G*G*C*C*+T*+T*+A | 143067 | 19 |
| 5170 | GGAAACTGTCTTAATATTT | A575168H | +G*+G*+A*A*A*C*T*G*T*C*T*T*T*A*A*T*A*+T*+T*+T | 143185 | 19 |
| 5171 | GGGAAACTGTCTTAATATT | A575169H | +G*+G*+G*A*A*A*C*T*G*T*C*T*T*T*A*A*T*+A*+T*+T | 143186 | 19 |
| 5172 | CATATATGATAGTGCATTT | A575170H | +C*+A*+T*A*T*A*T*G*A*T*A*G*T*G*C*A*+T*+T*+T | 143235 | 19 |
| 5173 | AAGCATATATGATAGTGCA | A575171H | +A*+A*+G*C*A*T*A*T*A*T*G*A*T*A*G*T*+G*+C*+A | 143238 | 19 |
| 5174 | CAAGCATATATGATAGTGC | A575172H | +C*+A*+A*G*C*A*T*A*T*A*T*G*A*T*A*G*+T*+G*+C | 143239 | 19 |
| 5175 | TTCACATACCAACAAAGGA | A575173H | +T*+T*+C*A*C*A*T*A*C*C*A*A*C*A*A*A*+G*+G*+A | 143289 | 19 |
| 5176 | TTCACATACCAACAAAGG | A575174H | +T*+T*+C*A*C*A*T*A*C*C*A*A*C*A*A*+A*+G*+G | 143290 | 18 |
| 5177 | ATTCACATACCAACAAAGG | A575175H | +A*+T*+T*C*A*C*A*T*A*C*C*A*A*C*A*A*+A*+G*+G | 143290 | 19 |
| 5178 | GTTGTGTAAGATGCACTGT | A575176H | +G*+T*+T*G*T*G*T*A*A*G*A*T*G*C*A*C*+T*+G*+T | 143329 | 19 |
| 5179 | GAAGTTGTGTAAGATGCAC | A575177H | +G*+A*+A*G*T*T*G*T*G*T*A*A*G*A*T*G*+C*+A*+C | 143332 | 19 |
| 5180 | AGTGAAGTTGTGTAAGATG | A575178H | +A*+G*+T*G*A*A*G*T*T*G*T*G*T*A*A*G*+A*+T*+G | 143335 | 19 |
| 5181 | AGTACTTTTAATGGAGTTT | A575179H | +A*+G*+T*A*C*T*T*T*T*A*A*T*G*G*A*G*+T*+T*+T | 143366 | 19 |
| 5182 | GACAGTATGTCATGTTTTT | A575180H | +G*+A*+C*A*G*T*A*T*G*T*C*A*T*G*T*T*+T*+T*+T | 143390 | 19 |
| 5183 | TTTGACAGTATGTCATGTT | A575181H | +T*+T*+T*G*A*C*A*G*T*A*T*G*T*C*A*T*+G*+T*+T | 143393 | 19 |
| 5184 | ACTTTGACAGTATGTCATG | A575182H | +A*+C*+T*T*T*G*A*C*A*G*T*A*T*G*T*C*+A*+T*+G | 143395 | 19 |
| 5185 | GACTTTGACAGTATGTCAT | A575183H | +G*+A*+C*T*T*T*G*A*C*A*G*T*A*T*G*T*+C*+A*+T | 143396 | 19 |
| 5186 | GGACTTTGACAGTATGTCA | A575184H | +G*+G*+A*C*T*T*T*G*A*C*A*G*T*A*T*G*+T*+C*+A | 143397 | 19 |
| 5187 | GGACTTTGACAGTATGTC | A575185H | +G*+G*+A*C*T*T*T*G*A*C*A*G*T*A*T*+G*+T*+C | 143398 | 18 |
| 5188 | GAGGACTTTGACAGTATGT | A575186H | +G*+A*+G*G*A*C*T*T*T*G*A*C*A*G*T*A*+T*+G*+T | 143399 | 19 |
| 5189 | ATGAGGACTTTGACAGTAT | A575187H | +A*+T*+G*A*G*G*A*C*T*T*T*G*A*C*A*G*+T*+A*+T | 143401 | 19 |
| 5190 | ATATGAGGACTTTGACAGT | A575188H | +A*+T*+A*T*G*A*G*G*A*C*T*T*T*G*A*C*+A*+G*+T | 143403 | 19 |

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| 5191 | GATATGAGGACTTTG ACAG | A575189H | +G*+A*+T*A*T*G*A*G*G*A*C*T*T*T*G*A*+ C*+A*+G | 143404 | 19 |
| 5192 | CCTAGATATGAGGAC TTTG | A575190H | +C*+C*+T*A*G*A*T*A*T*G*A*G*G*A*C*T*+ T*+T*+G | 143408 | 19 |
| 5193 | TCCTAGATATGAGGA CTTT | A575191H | +T*+C*+C*T*A*G*A*T*A*T*G*A*G*G*A*C*+ T*+T*+T | 143409 | 19 |
| 5194 | TCCTAGATATGAGGA CTT | A575192H | +T*+C*+C*T*A*G*A*T*A*T*G*A*G*G*A*+C* +T*+T | 143410 | 18 |
| 5195 | GTATTTACACTAATTA TAC | A575193H | +G*+T*+A*T*T*T*A*C*A*C*T*A*A*T*T*A*+ T*+A*+C | 143531 | 19 |
| 5196 | ACACTGTATTTACAC TAAT | A575194H | +A*+C*+A*C*T*G*T*A*T*T*T*A*C*A*C*T*+ A*+A*+T | 143536 | 19 |
| 5197 | GAAGGACTGAACACT GTAT | A575195H | +G*+A*+A*G*G*A*C*T*G*A*A*C*A*C*T*G*+ T*+A*+T | 143546 | 19 |
| 5198 | GAAGGACTGAACACT GTA | A575196H | +G*+A*+A*G*G*A*C*T*G*A*A*C*A*C*T*+G* +T*+A | 143547 | 18 |
| 5199 | TGAAGGACTGAACAC TGTA | A575197H | +T*+G*+A*A*G*G*A*C*T*G*A*A*C*A*C*T*+ G*+T*+A | 143547 | 19 |
| 5200 | TTGAAGGACTGAACA CTGT | A575198H | +T*+T*+G*A*A*G*G*A*C*T*G*A*A*C*A*C*+ T*+G*+T | 143548 | 19 |
| 5201 | TTGAAGGACTGAACA CTG | A575199H | +T*+T*+G*A*A*G*G*A*C*T*G*A*A*C*A*+C* +T*+G | 143549 | 18 |
| 5202 | CTTGAAGGACTGAAC ACTG | A575200H | +C*+T*+T*G*A*A*G*G*A*C*T*G*A*A*C*A*+ C*+T*+G | 143549 | 19 |
| 5203 | TCACTTGAAGGACTG AACA | A575201H | +T*+C*+A*C*T*T*G*A*A*G*G*A*C*T*G*A*+ A*+C*+A | 143552 | 19 |
| 5204 | TCACTTGAAGGACTG AAC | A575202H | +T*+C*+A*C*T*T*G*A*A*G*G*A*C*T*G*+A* +A*+C | 143553 | 18 |
| 5205 | ATCACTTGAAGGACT GAAC | A575203H | +A*+T*+C*A*C*T*T*G*A*A*G*G*A*C*T*G*+ A*+A*+C | 143553 | 19 |
| 5206 | ATATCACTTGAAGGA CTGA | A575204H | +A*+T*+A*T*C*A*C*T*T*G*A*A*G*G*A*C*+ T*+G*+A | 143555 | 19 |
| 5207 | AATATCACTTGAAGG ACTG | A575205H | +A*+A*+T*A*T*C*A*C*T*T*G*A*A*G*G*A*+ C*+T*+G | 143556 | 19 |
| 5208 | AAATATCACTTGAAG GACT | A575206H | +A*+A*+A*T*A*T*C*A*C*T*T*G*A*A*G*G*+ A*+C*+T | 143557 | 19 |
| 5209 | AGATGAATATAAGCA TTAG | A575207H | +A*+G*+A*T*G*A*A*T*A*T*A*A*G*C*A*T*+ T*+A*+G | 143626 | 19 |
| 5210 | AAGATGAATATAAGC ATTA | A575208H | +A*+A*+G*A*T*G*A*A*T*A*T*A*A*G*C*A*+ T*+T*+A | 143627 | 19 |
| 5211 | GGAAAAGATGAATAT AAGC | A575209H | +G*+G*+A*A*A*A*G*A*T*G*A*A*T*A*T*A*+ A*+G*+C | 143631 | 19 |
| 5212 | CATCACAAATTTAGG GAAA | A575210H | +C*+A*+T*C*A*C*A*A*A*T*T*T*A*G*G*G*+ A*+A*+A | 143645 | 19 |
| 5213 | GCATCACAAATTTAG GGAA | A575211H | +G*+C*+A*T*C*A*C*A*A*A*T*T*T*A*G*G*+ G*+A*+A | 143646 | 19 |
| 5214 | CAGCATCACAAATTT AGGG | A575212H | +C*+A*+G*C*A*T*C*A*C*A*A*A*T*T*T*A*+ G*+G*+G | 143648 | 19 |
| 5215 | GCAGCATCACAAATT TAGG | A575213H | +G*+C*+A*G*C*A*T*C*A*C*A*A*A*T*T*T*+ A*+G*+G | 143649 | 19 |
| 5216 | TGCAGCATCACAAAT TTAG | A575214H | +T*+G*+C*A*G*C*A*T*C*A*C*A*A*A*T*T*+ T*+A*+G | 143650 | 19 |
| 5217 | CTGCAGCATCACAAA TTTA | A575215H | +C*+T*+G*C*A*G*C*A*T*C*A*C*A*A*A*T*+ T*+T*+A | 143651 | 19 |
| 5218 | GATCTGCAGCATCAC AAAT | A575216H | +G*+A*+T*C*T*G*C*A*G*C*A*T*C*A*C*A*+ A*+A*+T | 143654 | 19 |
| 5219 | AGGATCTGCAGCATC ACAA | A575217H | +A*+G*+G*A*T*C*T*G*C*A*G*C*A*T*C*A*+ C*+A*+A | 143656 | 19 |
| 5220 | AGGATCTGCAGCATC ACA | A575218H | +A*+G*+G*A*T*C*T*G*C*A*G*C*A*T*C*+A* +C*+A | 143657 | 18 |
| 5221 | TAGGATCTGCAGCAT CACA | A575219H | +T*+A*+G*G*A*T*C*T*G*C*A*G*C*A*T*C*+ A*+C*+A | 143657 | 19 |
| 5222 | TAGGATCTGCAGCAT CAC | A575220H | +T*+A*+G*G*A*T*C*T*G*C*A*G*C*A*T*+C* +A*+C | 143658 | 18 |
| 5223 | GTAGGATCTGCAGCA TCAC | A575221H | +G*+T*+A*G*G*A*T*C*T*G*C*A*G*C*A*T*+ C*+A*+C | 143658 | 19 |
| 5224 | ATGTAGGATCTGCAG CATC | A575222H | +A*+T*+G*T*A*G*G*A*T*C*T*G*C*A*G*C*+ A*+T*+C | 143660 | 19 |
| 5225 | ATGATGTAGGATCTG CAGC | A575223H | +A*+T*+G*A*T*G*T*A*G*G*A*T*C*T*G*C*+ A*+G*+C | 143663 | 19 |

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| 5226 | GCTGTGGAATTCTATAATT | A575224H | +G*+C*+T*G*T*G*G*A*A*T*T*C*T*A*T*A*+A*+T*+T | 143709 | 19 |
| 5227 | GGAGCTGTGGAATTCTATA | A575225H | +G*+G*+A*G*C*T*G*T*G*G*A*A*T*T*C*T*+A*+T*+A | 143712 | 19 |
| 5228 | GGTAGGAGCTGTGGAATTC | A575226H | +G*+G*+T*A*G*G*A*G*C*T*G*T*G*G*A*A*+T*+T*+C | 143716 | 19 |
| 5229 | TGGTAGGAGCTGTGGAATT | A575227H | +T*+G*+G*T*A*G*G*A*G*C*T*G*T*G*G*A*+A*+T*+T | 143717 | 19 |
| 5230 | CTTGGTAGGAGCTGTGGAA | A575228H | +C*+T*+T*G*G*T*A*G*G*A*G*C*T*G*T*G*+G*+A*+A | 143719 | 19 |
| 5231 | TCTTGGTAGGAGCTGTGGA | A575229H | +T*+C*+T*T*G*G*T*A*G*G*A*G*C*T*G*T*+G*+G*+A | 143720 | 19 |
| 5232 | GTCTTGGTAGGAGCTGTGG | A575230H | +G*+T*+C*T*T*G*G*T*A*G*G*A*G*C*T*G*+T*+G*+G | 143721 | 19 |
| 5233 | TGGTCTTGGTAGGAGCTGT | A575231H | +T*+G*+G*T*C*T*T*G*G*T*A*G*G*A*G*C*+T*+G*+T | 143723 | 19 |
| 5234 | ATGGTCTTGGTAGGAGCTG | A575232H | +A*+T*+G*G*T*C*T*T*G*G*T*A*G*G*A*G*+C*+T*+G | 143724 | 19 |
| 5235 | CATGGTCTTGGTAGGAGCT | A575233H | +C*+A*+T*G*G*T*C*T*T*G*G*T*A*G*G*A*+G*+C*+T | 143725 | 19 |
| 5236 | TCATGGTCTTGGTAGGAGC | A575234H | +T*+C*+A*T*G*G*T*C*T*T*G*G*T*A*G*G*+A*+G*+C | 143726 | 19 |
| 5237 | CTCATGGTCTTGGTAGGAG | A575235H | +C*+T*+C*A*T*G*G*T*C*T*T*G*G*T*A*G*+G*+A*+G | 143727 | 19 |
| 5238 | CTCATGGTCTTGGTAGGA | A575236H | +C*+T*+C*A*T*G*G*T*C*T*T*G*G*T*A*+G*+G*+A | 143728 | 18 |
| 5239 | CCTCATGGTCTTGGTAGGA | A575237H | +C*+C*+T*C*A*T*G*G*T*C*T*T*G*G*T*A*+G*+G*+A | 143728 | 19 |
| 5240 | TCCTCATGGTCTTGGTAGG | A575238H | +T*+C*+C*T*C*A*T*G*G*T*C*T*T*G*G*T*+A*+G*+G | 143729 | 19 |
| 5241 | CAGCAACTGAAAAGTGTTA | A575239H | +C*+A*+G*C*A*A*C*T*G*A*A*A*A*G*T*G*+T*+T*+A | 143756 | 19 |
| 5242 | TCTCCTTCAGCAACTGAAA | A575240H | +T*+C*+T*C*C*T*T*C*A*G*C*A*A*C*T*G*+A*+A*+A | 143763 | 19 |
| 5243 | CCATCATAACTAAAGCTC | A575241H | +C*+C*+A*T*C*A*T*A*A*C*T*A*A*A*G*+C*+T*+C | 143785 | 18 |
| 5244 | TCCATCATAACTAAGCTC | A575242H | +T*+C*+C*A*T*C*A*T*A*A*C*T*A*A*A*G*+C*+T*+C | 143785 | 19 |
| 5245 | ATCCATCATAACTAAAGCT | A575243H | +A*+T*+C*C*A*T*C*A*T*A*A*C*T*A*A*A*+G*+C*+T | 143786 | 19 |
| 5246 | TATCCATCATAACTAAAGC | A575244H | +T*+A*+T*C*C*A*T*C*A*T*A*A*C*T*A*A*+A*+G*+C | 143787 | 19 |
| 5247 | TTATCCATCATAACTAAAG | A575245H | +T*+T*+A*T*C*C*A*T*C*A*T*A*A*C*T*A*+A*+A*+G | 143788 | 19 |
| 5248 | TATTTTTATCCATCATAAC | A575246H | +T*+A*+T*T*T*T*T*A*T*C*C*A*T*C*A*T*+A*+A*+C | 143793 | 19 |
| 5249 | CCTAGGGTGGCAGATATTT | A575247H | +C*+C*+T*A*G*G*G*T*G*G*C*A*G*A*T*A*+T*+T*+T | 143807 | 19 |
| 5250 | TGGAAGCCTAGGGTGGCAG | A575248H | +T*+G*+G*A*A*G*C*C*T*A*G*G*G*T*G*G*+C*+A*+G | 143813 | 19 |
| 5251 | GCTATGTAAACAATTTAAG | A575249H | +G*+C*+T*A*T*G*T*A*A*A*C*A*A*T*T*T*+A*+A*+G | 143839 | 19 |
| 5252 | AGCTATGTAAACAATTTAA | A575250H | +A*+G*+C*T*A*T*G*T*A*A*A*C*A*A*T*T*+T*+A*+A | 143840 | 19 |
| 5253 | AAGCTATGTAAACAATTTA | A575251H | +A*+A*+G*C*T*A*T*G*T*A*A*A*C*A*A*T*+T*+T*+A | 143841 | 19 |
| 5254 | GTAAGCTATGTAAACAATT | A575252H | +G*+T*+A*A*G*C*T*A*T*G*T*A*A*A*C*A*+A*+T*+T | 143843 | 19 |
| 5255 | GGTAAGCTATGTAAACAAT | A575253H | +G*+G*+T*A*A*G*C*T*A*T*G*T*A*A*A*C*+A*+A*+T | 143844 | 19 |
| 5256 | TGGTAAGCTATGTAAACAA | A575254H | +T*+G*+G*T*A*A*G*C*T*A*T*G*T*A*A*A*+C*+A*+A | 143845 | 19 |
| 5257 | TGTGGTAAGCTATGTAAAC | A575255H | +T*+G*+T*G*G*T*A*A*G*C*T*A*T*G*T*A*+A*+A*+C | 143847 | 19 |
| 5258 | TATTTGGCCCTGATACTCC | A575256H | +T*+A*+T*T*T*G*G*C*C*C*T*G*A*T*A*C*+T*+C*+C | 143869 | 19 |
| 5259 | TAGGTATTTGGCCCTGATA | A575257H | +T*+A*+G*G*T*A*T*T*T*G*G*C*C*C*T*G*+A*+T*+A | 143873 | 19 |
| 5260 | ACATAGGTATTTGGCCCTG | A575258H | +A*+C*+A*T*A*G*G*T*A*T*T*T*G*G*C*C*+C*+T*+G | 143876 | 19 |

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| 5261 | ACATAGGTATTTGGCCCT | A575259H | +A*+C*+A*T*A*G*G*T*A*T*T*T*G*G*C*+C*+C*+T | 143877 | 18 |
| 5262 | TACATAGGTATTTGGCCCT | A575260H | +T*+A*+C*A*T*A*G*G*T*A*T*T*T*G*G*C*+C*+C*+T | 143877 | 19 |
| 5263 | TACATAGGTATTTGGCCC | A575261H | +T*+A*+C*A*T*A*G*G*T*A*T*T*T*G*G*+C*+C*+C | 143878 | 18 |
| 5264 | TTACATAGGTATTTGGCCC | A575262H | +T*+T*+A*C*A*T*A*G*G*T*A*T*T*T*G*G*+C*+C*+C | 143878 | 19 |
| 5265 | TTACATAGGTATTTGGCC | A575263H | +T*+T*+A*C*A*T*A*G*G*T*A*T*T*T*G*+G*+C*+C | 143879 | 18 |
| 5266 | ATTACATAGGTATTTGGCC | A575264H | +A*+T*+T*A*C*A*T*A*G*G*T*A*T*T*T*G*+G*+C*+C | 143879 | 19 |
| 5267 | ATTACATAGGTATTTGGC | A575265H | +A*+T*+T*A*C*A*T*A*G*G*T*A*T*T*T*+G*+G*+C | 143880 | 18 |
| 5268 | TATTACATAGGTATTTGGC | A575266H | +T*+A*+T*T*A*C*A*T*A*G*G*T*A*T*T*T*+G*+G*+C | 143880 | 19 |
| 5269 | CTCAAATTATTACATAGGT | A575267H | +C*+T*+C*A*A*A*T*T*A*T*T*A*C*A*T*A*+G*+G*+T | 143887 | 19 |
| 5270 | CCTCAAATTATTACATAGG | A575268H | +C*+C*+T*C*A*A*A*T*T*A*T*T*A*C*A*T*+A*+G*+G | 143888 | 19 |
| 5271 | CAGGGCCAAAGAATTTACC | A575269H | +C*+A*+G*G*G*C*C*A*A*A*G*A*A*T*T*T*+A*+C*+C | 143935 | 19 |
| 5272 | TCAGGGCCAAAGAATTTAC | A575270H | +T*+C*+A*G*G*G*C*C*A*A*A*G*A*A*T*T*+T*+A*+C | 143936 | 19 |
| 5273 | GGTCAGGGCCAAAGAATTT | A575271H | +G*+G*+T*C*A*G*G*G*C*C*A*A*A*G*A*A*+T*+T*+T | 143938 | 19 |
| 5274 | TGGTCAGGGCCAAAGAATT | A575272H | +T*+G*+G*T*C*A*G*G*G*C*C*A*A*A*G*A*+A*+T*+T | 143939 | 19 |
| 5275 | CTGGTCAGGGCCAAAGAAT | A575273H | +C*+T*+G*G*T*C*A*G*G*G*C*C*A*A*A*G*+A*+A*+T | 143940 | 19 |
| 5276 | TACTGGTCAGGGCCAAAGA | A575274H | +T*+A*+C*T*G*G*T*C*A*G*G*G*C*C*A*A*+A*+G*+A | 143942 | 19 |
| 5277 | ATGAATACTGGTCAGGGC | A575275H | +A*+T*+G*A*A*T*A*C*T*G*G*T*C*A*G*+G*+G*+C | 143948 | 18 |
| 5278 | AATGAATACTGGTCAGGGC | A575276H | +A*+A*+T*G*A*A*T*A*C*T*G*G*T*C*A*G*+G*+G*+C | 143948 | 19 |
| 5279 | GTCCTATCACAGGGAATT | A575277H | +G*+T*+C*C*T*A*T*C*A*C*A*G*G*G*A*+A*+T*+T | 143976 | 18 |
| 5280 | TGTCCTATCACAGGGAATT | A575278H | +T*+G*+T*C*C*T*A*T*C*A*C*A*G*G*G*A*+A*+T*+T | 143976 | 19 |
| 5281 | TTGTCCTATCACAGGGAAT | A575279H | +T*+T*+G*T*C*C*T*A*T*C*A*C*A*G*G*G*+A*+A*+T | 143977 | 19 |
| 5282 | GTTGTCCTATCACAGGGAA | A575280H | +G*+T*+T*G*T*C*C*T*A*T*C*A*C*A*G*G*+G*+A*+A | 143978 | 19 |
| 5283 | GTTGTCCTATCACAGGGA | A575281H | +G*+T*+T*G*T*C*C*T*A*T*C*A*C*A*G*+G*+G*+A | 143979 | 18 |
| 5284 | AGTTGTCCTATCACAGGGA | A575282H | +A*+G*+T*T*G*T*C*C*T*A*T*C*A*C*A*G*+G*+G*+A | 143979 | 19 |
| 5285 | AGTTGTCCTATCACAGGG | A575283H | +A*+G*+T*T*G*T*C*C*T*A*T*C*A*C*A*+G*+G*+G | 143980 | 18 |
| 5286 | TAGTTGTCCTATCACAGGG | A575284H | +T*+A*+G*T*T*G*T*C*C*T*A*T*C*A*C*A*+G*+G*+G | 143980 | 19 |
| 5287 | ACTAGTTGTCCTATCACAG | A575285H | +A*+C*+T*A*G*T*T*G*T*C*C*T*A*T*C*A*+C*+A*+G | 143982 | 19 |
| 5288 | ACTAGTTGTCCTATCACA | A575286H | +A*+C*+T*A*G*T*T*G*T*C*C*T*A*T*C*+A*+C*+A | 143983 | 18 |
| 5289 | AAATGCCATAAGTTCTGAG | A575287H | +A*+A*+A*T*G*C*C*A*T*A*A*G*T*T*C*T*+G*+A*+G | 144013 | 19 |
| 5290 | CACTGGAACAAAGAGCTCT | A575288H | +C*+A*+C*T*G*G*A*A*C*A*A*A*G*A*G*C*+T*+C*+T | 144161 | 19 |
| 5291 | AACACTGGAACAAAGAGCT | A575289H | +A*+A*+C*A*C*T*G*G*A*A*C*A*A*A*G*A*+G*+C*+T | 144163 | 19 |
| 5292 | TAACACTGGAACAAAGAGC | A575290H | +T*+A*+A*C*A*C*T*G*G*A*A*C*A*A*A*G*+A*+G*+C | 144164 | 19 |
| 5293 | ATAACACTGGAACAAAGAG | A575291H | +A*+T*+A*A*C*A*C*T*G*G*A*A*C*A*A*A*+G*+A*+G | 144165 | 19 |
| 5294 | AAAGAGATAACACTGGAAC | A575292H | +A*+A*+A*G*A*G*A*T*A*A*C*A*C*T*G*G*+A*+A*+C | 144171 | 19 |
| 5295 | TGAAAGAGATAACACTGGA | A575293H | +T*+G*+A*A*A*G*A*G*A*T*A*A*C*A*C*T*+G*+G*+A | 144173 | 19 |

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|---|---|---|---|---|---|
| 5296 | CAGCATCATGCAAGCAGCA | A575294Hi | +C*+A*+G*C*A*T*C*A*T*G*C*A*A*G*C*A*+G*+C*+A | 78525<br>84782 | 19 |
| 5297 | GTTTGAAGGAATAGCTGA | A575295Hi | +G*+T*+T*T*G*A*A*G*G*A*A*T*A*G*C*+T*+G*+A | 78478<br>84735 | 18 |
| 5298 | CAGCATCATGCAAGCAGC | A575296Hi | +C*+A*+G*C*A*T*C*A*T*G*C*A*A*G*C*+A*+G*+C | 78526<br>84783 | 18 |
| 5299 | GCAGCATCATGCAAGCAG | A575297Hi | +G*+C*+A*G*C*A*T*C*A*T*G*C*A*A*G*+C*+A*+G | 78527<br>84784 | 18 |
| 5300 | TGCAGCATCATGCAAGCAG | A575298Hi | +T*+G*+C*A*G*C*A*T*C*A*T*G*C*A*A*G*+C*+A*+G | 78527<br>84784 | 19 |
| 5301 | TTGCAGCATCATGCAAGCA | A575299Hi | +T*+T*+G*C*A*G*C*A*T*C*A*T*G*C*A*A*+G*+C*+A | 78528<br>84785 | 19 |
| 5302 | | Neg1 | +C*+G*+T*T*T*A*G*G*C*T*A*T*G*T*A*+C*+T*+T | | 18 |
| 5303 | | R01002 | +T*+A*+C*G*C*G*C*G*G*T*T*G*T*+T*+T*+T*+A | | 16 |
| 5304 | | R01011 | +G*+A*+T*C*A*T*T*C*G*C*G*G*A*C*+A*+A*+C | | 17 |
| 5305 | | R01025 | +A*+T*+A*T*G*T*G*T*C*G*C*G*A*T*T*G*+G*+A*+G | | 19 |

**Table 1**: List of human LRRK2-specific ASOs and Control oligonucleotides. An "H" after the ASO name indicates a human LRRK2-specific sequence that binds to an exonic region of the pre-mRNA and a "Hi" after the ASO name indicates a human LRRK2-specific sequence that binds to an intronic region of the pre-mRNA. 16, 17, 18 and 19 mers were designed according to in house criteria, Neg1 (described in WO2014154843 A1), R01002, R01011 and R01025 were used as non-targeting control oligonucleotides in some experiments.

The ASOs of the present invention hybridize, for example, with hybridizing active regions. Such regions comprise or consist, for example, of positions 1 to 500, 501 to 1000, 1001 to 1500, 1501 to 2000, 2001 to 2500, 3501 to 4000, 4001 to 4500, 4501 to 5000, 5001 to 5500, 5001 to 6000, 6001 to 6500, 6501 to 7000, 7001 to 7500, 7501 to 8000, 8001 to 8500, 8501 to 9000, 9001 to 10000, 10501 to 11000, 11001 to 11500, 11501 to 12000, 12001 to 12500, 12501 to 13000, 13001 to 13500, 13501 to 1400, 14501 to 15000, 15001 to 15500, 15501 to 16000, 16001 to 16500, 16501 to 17000, 17001 to 17500, 17501 to 18000, 18001 to 18500, 18501 to 19000, 19001 to 19500, 20001 to 20500, 20501 to 21000, 21001 to 21500, 21501 to 22000, 22001 to 22500, 23001 to 23500, 23501 to 24000, 24001 to 24500, 24501 to 25000, 25001 to 25500, 26001 to 26500, 26501 to 27000, 27001 to 27500, 27501 to 28000, 28001 to 28500, 29001 to 29500, 29501 to 30000, 30001 to 30500, 30501 to 31000, 31001 to 31500, 32001 to 32500, 33001 to 33500, 33501 to 34000, 34001 to 34500, 34501 to 35000, 35001 to 35500, 35501 to 36000, 36001 to 36500, 36501 to 37000,

37001 to 37500, 37501 to 38000, 38001 to 38500, 38501 to 39000, 39001 to 39500, 39501 to 40000, 40001 to 40500, 40501 to 41000, 42001 to 42500, 42501 to 43000, 43001 to 43500, 43501 to 44000, 44001 to 44500, 44501 to 45000, 45001 to 45500, 45501 to 46000, 46001 to 46500, 46501 to 47000, 47001 to 47500, 47501 to 48000, 48001 to 48500, 48501 to 49000, 49001 to 49500, 49501 to 50000, 50001 to 50500, 50501 to 51000, 51001 to 51500, 51501 to 52000, 52001 to 52500, 52501 to 53000, 53001 to 53500, 53501 to 54000, 54001 to 54500, 54501 to 55000, 55001 to 55500, 56001 to 56500, 56501 to 57000, 57001 to 57500, 57501 to 58000, 58001 to 58500, 58501 to 59000, 59001 to 59500, 59501 to 60000, 60001 to 60500, 60501 to 61000, 61001 to 61500, 61501 to 62000, 62001 to 62500, 62501 to 63000, 63001 to 63500, 63501 to 64000, 64001 to 64500, 64501 to 65000, 65001 to 65500, 65501 to 66000, 66001 to 66500, 66501 to 67000, 67001 to 67500, 67501 to 68000, 68001 to 68500, 68501 to 69000, 69001 to 69500, 69501 to 70000, 70001 to 70500, 70501 to 71000, 71001 to 71500, 71501 to 72000, 72001 to 72500, 72501 to 73000, 73001 to 73500, 73501 to 74000, 74001 to 74500, 74501 to 75000, 75001 to 75500, 75501 to 76000, 76001 to 76500, 76501 to 77000, 77001 to 77500, 77501 to 78000, 78001 to 78500, 78501 to 79000, 79001 to 79500, 79501 to 80000, 80001 to 80500, 80501 to 81000, 81001 to 81500, 81501 to 82000, 82001 to 82500, 82501 to 83000, 83001 to 83500, 83501 to 84000, 84001 to 84500, 84501 to 85000, 85001 to 85500, 85501 to 86000, 86001 to 86500, 86501 to 87000, 87001 to 87500, 87501 to 88000, 88001 to 88500, 88501 to 89000, 89001 to 89500, 89501 to 90000, 90001 to 90500, 90501 to 91000, 91001 to 91500, 91501 to 92000, 92001 to 92500, 92501 to 93000, 93001 to 93500, 93501 to 94000, 94001 to 94500, 94501 to 95000, 95001 to 95500, 95501 to 96000, 96001 to 96500, 96501 to 97000, 97001 to 97500, 97501 to 98000, 98001 to 98500, 98501 to 99000, 99001 to 99500, 99501 to 100000, 100001 to 100500, 100501 to 101000, 101001 to 101500, 101501 to 102000, 102001 to 102500, 102501 to 103000, 103001 to 103500, 103501 to 104000, 104001 to 104500, 105001 to 105500, 105501 to 106000, 106001 to 106500, 106501 to 107000, 107001 to 107500, 108001 to 108500, 108501 to 109000, 109001 to 109500, 109501 to 110000, 110001 to 110500, 110501 to 111000, 111001 to 111500, 111501 to 112000, 112001 to 112500, 112501 to 113000, 113001 to 113500, 113501 to 114000, 114001 to 114500, 114501 to 115000, 115001 to 115500, 115501 to 116000, 116001 to 116500, 116501 to 117000, 117001 to 117500, 117501 to 118000, 118001 to 118500, 118501 to 119000, 119001 to 119500, 119501 to 120000, 120001 to 120500, 120501 to 121000, 121001 to 121500, 122001 to 122500, 122501 to 123000, 123001 to 123500, 124001 to 124500, 124501 to 125000, 125001 to 126000, 126001 to 126500, 127001 to 127500, 129001 to 129500, 129501 to 130000, 130001 to 130500, 131001 to 131500, 131501 to

132000, 132501 to 133000, 134001 to 134500, 134501 to 135000, 135001 to 135500, 135501 to 136000, 136001 to 136500, 136501 to 137000, 137001 to 137500, 137501 to 138000, 138001 to 138500, 138501 to 139000, 139001 to 139500, 139501 to 140000, 140001 to 140500, 140501 to 141000, 141001 to 141500, 141501 to 142000, 142001 to 142500, 142501 to 143000, 143001 to 143500, 143501 to 144000, or 144001 to 144173 of SEQ ID NO.2. ASOs hybridizing in these regions are shown in the following **Table 2**:

| Region on Seq ID No.2 / ASO name | Position on Seq ID No 2 | SEQ ID NO. |
|---|---|---|
| 1-500 | | |
| A57250H | 228 | 252 |
| A57251H | 229 | 253 |
| A57261H | 56 | 263 |
| A57262H | 57 | 264 |
| A57263H | 57 | 265 |
| A57264H | 59 | 266 |
| A57265H | 62 | 267 |
| A57266H | 63 | 268 |
| A57267H | 63 | 269 |
| A57268H | 64 | 270 |
| A57269H | 64 | 271 |
| A57270H | 65 | 272 |
| A57271H | 67 | 273 |
| A57272H | 68 | 274 |
| A57273H | 68 | 275 |
| A57274H | 69 | 276 |
| A57275H | 70 | 277 |
| A57276H | 71 | 278 |
| A57277H | 71 | 279 |
| A57278H | 72 | 280 |
| A57279H | 72 | 281 |
| A57280H | 73 | 282 |
| A57281H | 74 | 283 |
| A57282H | 74 | 284 |
| A57283H | 75 | 285 |
| A57284H | 75 | 286 |
| A57285H | 75 | 287 |
| A57286H | 76 | 288 |
| A57287H | 77 | 289 |
| A57288H | 78 | 290 |
| A57289H | 78 | 291 |
| A57290H | 79 | 292 |
| A57291H | 79 | 293 |

| | | |
|---|---|---|
| A57292H | 79 | 294 |
| A57293H | 80 | 295 |
| A57294H | 80 | 296 |
| A57295H | 80 | 297 |
| A57296H | 81 | 298 |
| A57297H | 105 | 299 |
| A57298H | 106 | 300 |
| A57299H | 106 | 301 |
| A57300H | 107 | 302 |
| A57301H | 107 | 303 |
| A57302H | 108 | 304 |
| A57303H | 108 | 305 |
| A57304H | 110 | 306 |
| A57305H | 111 | 307 |
| A57306H | 131 | 308 |
| A57307H | 133 | 309 |
| A57308H | 134 | 310 |
| A57309H | 134 | 311 |
| A57310H | 136 | 312 |
| A57311H | 138 | 313 |
| A57312H | 140 | 314 |
| A57313H | 142 | 315 |
| A57314H | 166 | 316 |
| A57315H | 167 | 317 |
| A57316H | 167 | 318 |
| A57317H | 168 | 319 |
| A57318H | 168 | 320 |
| A57319H | 168 | 321 |
| A57320H | 169 | 322 |
| A57321H | 170 | 323 |
| A57322H | 170 | 324 |
| A57323H | 171 | 325 |
| A57324H | 171 | 326 |
| A57325H | 180 | 327 |
| A57326H | 185 | 328 |
| A57327H | 186 | 329 |
| A57328H | 186 | 330 |
| A57329H | 187 | 331 |
| A57330H | 187 | 332 |
| A57331H | 188 | 333 |
| A57332H | 188 | 334 |
| A57333H | 189 | 335 |
| A57334H | 189 | 336 |
| A57335H | 189 | 337 |
| A57336H | 190 | 338 |

| | | |
|---|---|---|
| A57337H | 190 | 339 |
| A57338H | 191 | 340 |
| A57339H | 191 | 341 |
| A57340H | 193 | 342 |
| A57341H | 194 | 343 |
| A57342H | 195 | 344 |
| A57343H | 199 | 345 |
| A57344H | 200 | 346 |
| A57345H | 225 | 347 |
| A57346H | 226 | 348 |
| A57347H | 226 | 349 |
| A57348H | 227 | 350 |
| A57349H | 228 | 351 |
| A57350H | 229 | 352 |
| A57351H | 229 | 353 |
| A57352H | 230 | 354 |
| A57353H | 230 | 355 |
| A57354H | 230 | 356 |
| A57355H | 231 | 357 |
| A57356H | 232 | 358 |
| A57357H | 232 | 359 |
| A57358H | 233 | 360 |
| A57359H | 233 | 361 |
| A57360H | 233 | 362 |
| A57361H | 234 | 363 |
| A57362H | 234 | 364 |
| A57363H | 235 | 365 |
| A57364H | 239 | 366 |
| A57365H | 240 | 367 |
| A57366H | 240 | 368 |
| A57367H | 241 | 369 |
| A57368H | 241 | 370 |
| A57369H | 248 | 371 |
| A57370H | 251 | 372 |
| A57371H | 253 | 373 |
| A57372H | 254 | 374 |
| A57373H | 256 | 375 |
| A57374H | 257 | 376 |
| A57375H | 258 | 377 |
| A57376H | 259 | 378 |
| A57377H | 260 | 379 |
| A57378H | 261 | 380 |
| A57379H | 262 | 381 |
| A57380H | 263 | 382 |
| A57381H | 263 | 383 |

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|---|---|---|
| A57382H | 264 | 384 |
| A57383H | 264 | 385 |
| A57384H | 264 | 386 |
| A57385H | 265 | 387 |
| A57386H | 265 | 388 |
| A57387H | 265 | 389 |
| A57388H | 266 | 390 |
| A57389H | 266 | 391 |
| A57390H | 266 | 392 |
| A57391H | 267 | 393 |
| A57392Hi | 451 | 394 |
| 501-1000 | | |
| A57001Hi | 509 | 3 |
| A57002Hi | 681 | 4 |
| A57393Hi | 508 | 395 |
| A57394Hi | 516 | 396 |
| A57395H | 560 | 397 |
| A57396H | 562 | 398 |
| A57397H | 576 | 399 |
| A57398H | 577 | 400 |
| A57399H | 587 | 401 |
| A57400H | 588 | 402 |
| A57401H | 588 | 403 |
| A57402H | 589 | 404 |
| A57403H | 589 | 405 |
| A57404H | 590 | 406 |
| A57405H | 591 | 407 |
| A57406H | 591 | 408 |
| A57407H | 592 | 409 |
| A57408H | 592 | 410 |
| A57409H | 593 | 411 |
| A57410H | 594 | 412 |
| A57411H | 594 | 413 |
| A57412H | 595 | 414 |
| A57413H | 595 | 415 |
| A57414H | 596 | 416 |
| A57415H | 597 | 417 |
| A57416H | 597 | 418 |
| A57417H | 598 | 419 |
| A57418H | 598 | 420 |
| A57419H | 598 | 421 |
| A57420H | 599 | 422 |
| A57421H | 618 | 423 |
| A57422H | 618 | 424 |
| A57423H | 618 | 425 |

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|---|---|---|
| A57424H | 618 | 426 |
| A57425H | 619 | 427 |
| A57426H | 619 | 428 |
| A57427H | 619 | 429 |
| A57428H | 620 | 430 |
| A57429H | 620 | 431 |
| A57430H | 621 | 432 |
| A57431H | 621 | 433 |
| A57432H | 621 | 434 |
| A57433H | 622 | 435 |
| A57434H | 622 | 436 |
| A57435H | 622 | 437 |
| A57436H | 623 | 438 |
| A57437H | 623 | 439 |
| A57438H | 624 | 440 |
| A57439H | 624 | 441 |
| A57440H | 624 | 442 |
| A57441H | 625 | 443 |
| A57442H | 625 | 444 |
| A57443H | 625 | 445 |
| A57444H | 626 | 446 |
| A57445H | 626 | 447 |
| A57446H | 626 | 448 |
| A57447H | 627 | 449 |
| A57448H | 627 | 450 |
| A57449H | 628 | 451 |
| A57450Hi | 683 | 452 |
| A57451Hi | 746 | 453 |
| A57452Hi | 747 | 454 |
| A57453Hi | 747 | 455 |
| 1001-1500 | | |
| A57003Hi | 1112 | 5 |
| A57004Hi | 1142 | 6 |
| A57005Hi | 1299 | 7 |
| A57006Hi | 1459 | 8 |
| A57454Hi | 1074 | 456 |
| A57455Hi | 1074 | 457 |
| A57456Hi | 1078 | 458 |
| A57457Hi | 1298 | 459 |
| A57458Hi | 1303 | 460 |
| A57459Hi | 1307 | 461 |
| A57460Hi | 1397 | 462 |
| A57461Hi | 1398 | 463 |
| A57462Hi | 1399 | 464 |
| A57463Hi | 1399 | 465 |

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|---|---|---|
| A57464Hi | 1404 | 466 |
| A57465Hi | 1452 | 467 |
| A57466Hi | 1453 | 468 |
| A57467Hi | 1454 | 469 |
| A57468Hi | 1455 | 470 |
| A57469Hi | 1455 | 471 |
| A57470Hi | 1456 | 472 |
| A57471Hi | 1465 | 473 |
| A57472Hi | 1466 | 474 |
| 1501-2000 | | |
| A57007Hi | 1718 | 9 |
| A57008Hi | 1720 | 10 |
| A57009Hi | 1749 | 11 |
| A57010Hi | 1773 | 12 |
| A57473Hi | 1719 | 475 |
| A57474Hi | 1723 | 476 |
| A57475Hi | 1726 | 477 |
| A57476Hi | 1748 | 478 |
| A57477Hi | 1749 | 479 |
| A57478Hi | 1753 | 480 |
| A57479Hi | 1754 | 481 |
| A57480Hi | 1803 | 482 |
| A57481Hi | 1806 | 483 |
| A57482Hi | 1807 | 484 |
| A57483Hi | 1808 | 485 |
| A57484Hi | 1812 | 486 |
| 4862001-2500 | | |
| A57485Hi | 2065 | 487 |
| 3501-4000 | | |
| A57486Hi | 3912 | 488 |
| A57487Hi | 3917 | 489 |
| A57488Hi | 3918 | 490 |
| A57489Hi | 3967 | 491 |
| A57490Hi | 3973 | 492 |
| A57491Hi | 3977 | 493 |
| A57492Hi | 3978 | 494 |
| A57493Hi | 3980 | 495 |
| A57494Hi | 3980 | 496 |
| A57495Hi | 3982 | 497 |
| A57496Hi | 3983 | 498 |
| 4001-4500 | | |
| A57011Hi | 4070 | 13 |
| A57012Hi | 4195 | 14 |
| A57497Hi | 4070 | 499 |
| A57498Hi | 4193 | 500 |

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|---|---|---|
| A57499Hi | 4201 | 501 |
| A57500Hi | 4346 | 502 |
| A57501Hi | 4355 | 503 |
| A57502Hi | 4358 | 504 |
| A57503Hi | 4366 | 505 |
| A57504Hi | 4368 | 506 |
| A57505Hi | 4440 | 507 |
| 4501-5000 | | |
| A57013Hi | 4829 | 15 |
| A57014Hi | 4939 | 16 |
| A57015Hi | 4940 | 17 |
| A57506Hi | 4512 | 508 |
| A57507Hi | 4636 | 509 |
| A57508Hi | 4682 | 510 |
| A57509Hi | 4683 | 511 |
| A57510Hi | 4684 | 512 |
| A57511Hi | 4757 | 513 |
| A57512Hi | 4770 | 514 |
| A57513Hi | 4806 | 515 |
| A57514Hi | 4828 | 516 |
| A57515Hi | 4937 | 517 |
| A57516Hi | 4941 | 518 |
| A57517Hi | 4989 | 519 |
| A57518Hi | 4990 | 520 |
| A57519Hi | 4991 | 521 |
| A57520Hi | 4994 | 522 |
| 5001-5500 | | |
| A57016Hi | 5077 | 18 |
| A57017Hi | 5101 | 19 |
| A57018Hi | 5104 | 20 |
| A57019Hi | 5110 | 21 |
| A57020Hi | 5140 | 22 |
| A57240Hi | 5111 | 242 |
| A57521Hi | 5075 | 523 |
| A57522Hi | 5077 | 524 |
| A57523Hi | 5078 | 525 |
| A57524Hi | 5102 | 526 |
| A57525Hi | 5105 | 527 |
| A57526Hi | 5105 | 528 |
| A57527Hi | 5105 | 529 |
| A57528Hi | 5106 | 530 |
| A57529Hi | 5107 | 531 |
| A57530Hi | 5107 | 532 |
| A57531Hi | 5107 | 533 |
| A57532Hi | 5111 | 534 |

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|---|---|---|
| A57533Hi | 5114 | 535 |
| A57534Hi | 5115 | 536 |
| A57535Hi | 5115 | 537 |
| A57536Hi | 5116 | 538 |
| A57537Hi | 5117 | 539 |
| A57538Hi | 5331 | 540 |
| A57539Hi | 5341 | 541 |
| A57540Hi | 5375 | 542 |
| A57541Hi | 5380 | 543 |
| A57542Hi | 5404 | 544 |
| A57543Hi | 5405 | 545 |
| A57544Hi | 5414 | 546 |
| A57545Hi | 5469 | 547 |
| A57546Hi | 5471 | 548 |
| A57547Hi | 5472 | 549 |
| A57548Hi | 5473 | 550 |
| 5501-6000 | | |
| A57021Hi | 5827 | 23 |
| A57022Hi | 5870 | 24 |
| A57023Hi | 5996 | 25 |
| A57549Hi | 5547 | 551 |
| A57550Hi | 5552 | 552 |
| A57551Hi | 5554 | 553 |
| A57552Hi | 5577 | 554 |
| A57553Hi | 5578 | 555 |
| A57554Hi | 5608 | 556 |
| A57555Hi | 5610 | 557 |
| A57556Hi | 5689 | 558 |
| A57557Hi | 5690 | 559 |
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| A57890Hi | 16212 | 892 |
| A57891Hi | 16261 | 893 |

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| A57906Hi | 17181 | 908 |
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| A57915Hi | 18308 | 917 |
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| A57918Hi | 18447 | 920 |
| A57919Hi | 18449 | 921 |
| A57920Hi | 18451 | 922 |
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| A57961H | 18667 | 963 |
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| A57963Hi | 18771 | 965 |
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| A57984Hi | 20899 | 986 |
| A57985Hi | 20900 | 987 |
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| A571125H | 26357 | 1127 |

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| A571165Hi | 26912 | 1167 |
| A571166Hi | 26912 | 1168 |

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| A571309Hi | 32443 | 1311 |
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| A57244Hi | 32579 | 246 |
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| A571393H | 34546 | 1395 |

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| A571437H | 34576 | 1439 |
| A571438H | 34577 | 1440 |

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| A57255H | 34567 | 257 |
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| A571446Hi | 35800 | 1448 |
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| A571448Hi | 35930 | 1450 |
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| A571453Hi | 36239 | 1455 |
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| A571456Hi | 36463 | 1458 |
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| A571470Hi | 36850 | 1472 |
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| A571473Hi | 37402 | 1475 |

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| A571483Hi | 37497 | 1485 |
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| A571512Hi | 38484 | 1514 |
| A571513Hi | 38485 | 1515 |

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| A57091Hi | 42242 | 93 |
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| A571576Hi | 42247 | 1578 |
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| A571582Hi | 42369 | 1584 |
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| A571584Hi | 42429 | 1586 |
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| A571650Hi | 43984 | 1652 |
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| A571738Hi | 47976 | 1740 |
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| A57107Hi | 48387 | 109 |
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| A571746Hi | 48293 | 1748 |

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| A571792Hi | 48848 | 1794 |
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| A571828H | 49872 | 1830 |
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| A571856H | 49958 | 1858 |
| A571857H | 49959 | 1859 |
| A571858H | 49960 | 1860 |
| A571859H | 49961 | 1861 |
| A571860H | 49961 | 1862 |
| A571861H | 49962 | 1863 |
| A571862H | 49962 | 1864 |
| A571863H | 49963 | 1865 |
| A571864H | 49964 | 1866 |
| A571865H | 49964 | 1867 |

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| A571867H | 49967 | 1869 |
| A571868Hi | 49998 | 1870 |
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| A571872Hi | 50189 | 1874 |
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| A571874Hi | 50590 | 1876 |
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| A571877Hi | 50940 | 1879 |
| A571878Hi | 50941 | 1880 |
| A571879Hi | 50942 | 1881 |
| A571880Hi | 50942 | 1882 |
| A571881Hi | 50971 | 1883 |
| 51001-51500 | | |
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| A571882Hi | 51097 | 1884 |
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| A571883Hi | 51727 | 1885 |
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| A571885Hi | 51745 | 1887 |
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| A571888Hi | 51748 | 1890 |
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| A571890Hi | 52275 | 1892 |
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| A571892Hi | 52461 | 1894 |
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| A571902Hi | 52780 | 1904 |

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| A571949H | 53108 | 1951 |
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| A571951H | 53110 | 1953 |
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| A571953H | 53119 | 1955 |
| A571954H | 53120 | 1956 |
| A571955H | 53157 | 1957 |
| A571956H | 53158 | 1958 |
| A571957H | 53159 | 1959 |
| A571958H | 53159 | 1960 |
| A571959H | 53160 | 1961 |
| A571960H | 53160 | 1962 |
| A571961H | 53161 | 1963 |
| A571962H | 53162 | 1964 |
| A571963H | 53162 | 1965 |
| A571964H | 53163 | 1966 |
| A571965H | 53164 | 1967 |
| A571966H | 53165 | 1968 |
| A571967H | 53165 | 1969 |
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| A571971H | 53168 | 1973 |
| A571972H | 53169 | 1974 |
| A571973H | 53169 | 1975 |
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| A571975H | 53178 | 1977 |
| A571976H | 53182 | 1978 |
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| A571990H | 53224 | 1992 |
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| A574955H | 138491 | 4957 |
| A574956H | 138492 | 4958 |
| A574957H | 138492 | 4959 |
| A574958H | 138494 | 4960 |
| A574959H | 138498 | 4961 |
| A574960H | 138499 | 4962 |
| 138501-139000 | | |
| A57236Hi | 138834 | 238 |
| A574961Hi | 138595 | 4963 |
| A574962Hi | 138597 | 4964 |
| A574963Hi | 138686 | 4965 |
| A574964Hi | 138687 | 4966 |
| A574965Hi | 138688 | 4967 |
| A574966Hi | 138864 | 4968 |
| 139001-139500 | | |

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|---|---|---|
| A574967Hi | 139017 | 4969 |
| A574968Hi | 139018 | 4970 |
| A574969Hi | 139019 | 4971 |
| A574970Hi | 139021 | 4972 |
| A574971Hi | 139023 | 4973 |
| A574972Hi | 139026 | 4974 |
| A574973Hi | 139054 | 4975 |
| A574974Hi | 139057 | 4976 |
| A574975Hi | 139058 | 4977 |
| A574976Hi | 139066 | 4978 |
| A574977Hi | 139070 | 4979 |
| A574978Hi | 139108 | 4980 |
| A574979Hi | 139111 | 4981 |
| A574980Hi | 139113 | 4982 |
| A574981Hi | 139302 | 4983 |
| A574982Hi | 139306 | 4984 |
| A574983Hi | 139348 | 4985 |
| A574984Hi | 139398 | 4986 |
| A574985Hi | 139399 | 4987 |
| A574986Hi | 139400 | 4988 |
| 139501-140000 | | |
| A574987Hi | 139600 | 4989 |
| A574988Hi | 139650 | 4990 |
| A574989H | 139867 | 4991 |
| A574990H | 139873 | 4992 |
| A574991H | 139878 | 4993 |
| A574992H | 139879 | 4994 |
| A574993H | 139881 | 4995 |
| A574994H | 139886 | 4996 |
| A574995H | 139891 | 4997 |
| A574996H | 139914 | 4998 |
| A574997H | 139915 | 4999 |
| A574998H | 139915 | 5000 |
| A574999H | 139920 | 5001 |
| A575000H | 139921 | 5002 |
| A575001H | 139922 | 5003 |
| A575002H | 139924 | 5004 |
| A575003H | 139927 | 5005 |
| A575004H | 139928 | 5006 |
| A575005H | 139931 | 5007 |
| A575006H | 139932 | 5008 |
| A575007H | 139936 | 5009 |
| A575008H | 139937 | 5010 |
| A575009H | 139939 | 5011 |
| A575010H | 139942 | 5012 |

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|---|---|---|
| A575011H | 139943 | 5013 |
| A575012H | 139944 | 5014 |
| A575013H | 139944 | 5015 |
| A575014H | 139948 | 5016 |
| A575015H | 139949 | 5017 |
| A575016H | 139951 | 5018 |
| A575017H | 139952 | 5019 |
| A575018H | 139953 | 5020 |
| A575019H | 139953 | 5021 |
| A575020H | 139954 | 5022 |
| A575021H | 139974 | 5023 |
| A575022H | 139974 | 5024 |
| A575023H | 139975 | 5025 |
| A575024H | 139975 | 5026 |
| A575025H | 139975 | 5027 |
| A575026H | 139976 | 5028 |
| A575027H | 139976 | 5029 |
| 140001-140500 | | |
| A575028H | 140022 | 5030 |
| A575029H | 140022 | 5031 |
| A575030H | 140023 | 5032 |
| A575031H | 140023 | 5033 |
| A575032H | 140023 | 5034 |
| A575033H | 140024 | 5035 |
| A575034H | 140024 | 5036 |
| A575035H | 140025 | 5037 |
| A575036H | 140025 | 5038 |
| A575037H | 140026 | 5039 |
| A575038H | 140028 | 5040 |
| A575039H | 140034 | 5041 |
| A575040Hi | 140055 | 5042 |
| A575041Hi | 140083 | 5043 |
| A575042Hi | 140084 | 5044 |
| A575043Hi | 140085 | 5045 |
| A575044Hi | 140254 | 5046 |
| A575045Hi | 140254 | 5047 |
| A575046Hi | 140255 | 5048 |
| A575047Hi | 140257 | 5049 |
| A575048Hi | 140257 | 5050 |
| A575049Hi | 140259 | 5051 |
| A575050Hi | 140261 | 5052 |
| A575051Hi | 140262 | 5053 |
| A575052Hi | 140264 | 5054 |
| A575053Hi | 140393 | 5055 |
| A575054Hi | 140394 | 5056 |

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|---|---|---|
| A575055Hi | 140395 | 5057 |
| A575056Hi | 140416 | 5058 |
| 140501-141000 | | |
| A57237Hi | 140893 | 239 |
| A575057Hi | 140901 | 5059 |
| A575058Hi | 140903 | 5060 |
| A575059Hi | 140904 | 5061 |
| A575060Hi | 140951 | 5062 |
| A575061Hi | 140952 | 5063 |
| A575062Hi | 140956 | 5064 |
| A575063Hi | 140959 | 5065 |
| A575064Hi | 140960 | 5066 |
| A575065Hi | 140966 | 5067 |
| A575066Hi | 140971 | 5068 |
| A575067Hi | 140972 | 5069 |
| A575068Hi | 140975 | 5070 |
| A575069Hi | 140980 | 5071 |
| A575070Hi | 140982 | 5072 |
| A575071Hi | 140983 | 5073 |
| A575072Hi | 140988 | 5074 |
| 141001-141500 | | |
| A575073Hi | 141016 | 5075 |
| A575074Hi | 141016 | 5076 |
| A575075Hi | 141017 | 5077 |
| A575076Hi | 141017 | 5078 |
| A575077Hi | 141018 | 5079 |
| A575078Hi | 141019 | 5080 |
| A575079Hi | 141025 | 5081 |
| A575080Hi | 141126 | 5082 |
| A575081Hi | 141140 | 5083 |
| A575082Hi | 141151 | 5084 |
| A575083Hi | 141181 | 5085 |
| A575084Hi | 141182 | 5086 |
| 141501-142000 | | |
| A57238Hi | 141809 | 240 |
| A575085Hi | 141604 | 5087 |
| A575086Hi | 141609 | 5088 |
| A575087Hi | 141620 | 5089 |
| A575088Hi | 141623 | 5090 |
| A575089Hi | 141624 | 5091 |
| A575090Hi | 141625 | 5092 |
| A575091Hi | 141654 | 5093 |
| A575092Hi | 141670 | 5094 |
| A575093Hi | 141778 | 5095 |
| A575094Hi | 141779 | 5096 |

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|---|---|---|
| A575095Hi | 141802 | 5097 |
| A575096Hi | 141802 | 5098 |
| A575097Hi | 141803 | 5099 |
| A575098Hi | 141805 | 5100 |
| A575099Hi | 141807 | 5101 |
| A575100Hi | 141810 | 5102 |
| A575101Hi | 141898 | 5103 |
| A575102Hi | 141903 | 5104 |
| A575103Hi | 141904 | 5105 |
| A575104Hi | 141905 | 5106 |
| 142001-142500 | | |
| A57239Hi | 142174 | 241 |
| A575105H | 142021 | 5107 |
| A575106H | 142022 | 5108 |
| A575107H | 142023 | 5109 |
| A575108H | 142023 | 5110 |
| A575109H | 142025 | 5111 |
| A575110Hi | 142171 | 5112 |
| A575111Hi | 142243 | 5113 |
| A575112Hi | 142246 | 5114 |
| A575113Hi | 142283 | 5115 |
| A575114Hi | 142290 | 5116 |
| A575115Hi | 142292 | 5117 |
| A575116Hi | 142292 | 5118 |
| A575117Hi | 142293 | 5119 |
| A575118Hi | 142298 | 5120 |
| A575119Hi | 142299 | 5121 |
| A575120Hi | 142300 | 5122 |
| A575121Hi | 142300 | 5123 |
| 142501-143000 | | |
| A575122H | 142648 | 5124 |
| A575123H | 142649 | 5125 |
| A575124H | 142672 | 5126 |
| A575125H | 142673 | 5127 |
| A575126H | 142673 | 5128 |
| A575127H | 142675 | 5129 |
| A575128H | 142676 | 5130 |
| A575129H | 142676 | 5131 |
| A575130H | 142677 | 5132 |
| A575131H | 142680 | 5133 |
| A575132H | 142681 | 5134 |
| A575133H | 142681 | 5135 |
| A575134H | 142682 | 5136 |
| A575135H | 142682 | 5137 |
| A575136H | 142687 | 5138 |

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|---|---|---|
| A575137H | 142689 | 5139 |
| A575138H | 142724 | 5140 |
| A575139H | 142782 | 5141 |
| A575140H | 142851 | 5142 |
| 143001-143500 | | |
| A575141H | 143036 | 5143 |
| A575142H | 143037 | 5144 |
| A575143H | 143037 | 5145 |
| A575144H | 143039 | 5146 |
| A575145H | 143040 | 5147 |
| A575146H | 143040 | 5148 |
| A575147H | 143042 | 5149 |
| A575148H | 143043 | 5150 |
| A575149H | 143044 | 5151 |
| A575150H | 143044 | 5152 |
| A575151H | 143045 | 5153 |
| A575152H | 143045 | 5154 |
| A575153H | 143046 | 5155 |
| A575154H | 143048 | 5156 |
| A575155H | 143056 | 5157 |
| A575156H | 143059 | 5158 |
| A575157H | 143060 | 5159 |
| A575158H | 143060 | 5160 |
| A575159H | 143061 | 5161 |
| A575160H | 143062 | 5162 |
| A575161H | 143062 | 5163 |
| A575162H | 143063 | 5164 |
| A575163H | 143063 | 5165 |
| A575164H | 143064 | 5166 |
| A575165H | 143064 | 5167 |
| A575166H | 143064 | 5168 |
| A575167H | 143067 | 5169 |
| A575168H | 143185 | 5170 |
| A575169H | 143186 | 5171 |
| A575170H | 143235 | 5172 |
| A575171H | 143238 | 5173 |
| A575172H | 143239 | 5174 |
| A575173H | 143289 | 5175 |
| A575174H | 143290 | 5176 |
| A575175H | 143290 | 5177 |
| A575176H | 143329 | 5178 |
| A575177H | 143332 | 5179 |
| A575178H | 143335 | 5180 |
| A575179H | 143366 | 5181 |
| A575180H | 143390 | 5182 |

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|---|---|---|
| A575181H | 143393 | 5183 |
| A575182H | 143395 | 5184 |
| A575183H | 143396 | 5185 |
| A575184H | 143397 | 5186 |
| A575185H | 143398 | 5187 |
| A575186H | 143399 | 5188 |
| A575187H | 143401 | 5189 |
| A575188H | 143403 | 5190 |
| A575189H | 143404 | 5191 |
| A575190H | 143408 | 5192 |
| A575191H | 143409 | 5193 |
| A575192H | 143410 | 5194 |
| 143501-144000 | | |
| A575193H | 143531 | 5195 |
| A575194H | 143536 | 5196 |
| A575195H | 143546 | 5197 |
| A575196H | 143547 | 5198 |
| A575197H | 143547 | 5199 |
| A575198H | 143548 | 5200 |
| A575199H | 143549 | 5201 |
| A575200H | 143549 | 5202 |
| A575201H | 143552 | 5203 |
| A575202H | 143553 | 5204 |
| A575203H | 143553 | 5205 |
| A575204H | 143555 | 5206 |
| A575205H | 143556 | 5207 |
| A575206H | 143557 | 5208 |
| A575207H | 143626 | 5209 |
| A575208H | 143627 | 5210 |
| A575209H | 143631 | 5211 |
| A575210H | 143645 | 5212 |
| A575211H | 143646 | 5213 |
| A575212H | 143648 | 5214 |
| A575213H | 143649 | 5215 |
| A575214H | 143650 | 5216 |
| A575215H | 143651 | 5217 |
| A575216H | 143654 | 5218 |
| A575217H | 143656 | 5219 |
| A575218H | 143657 | 5220 |
| A575219H | 143657 | 5221 |
| A575220H | 143658 | 5222 |
| A575221H | 143658 | 5223 |
| A575222H | 143660 | 5224 |
| A575223H | 143663 | 5225 |
| A575224H | 143709 | 5226 |

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|---|---|---|
| A575225H | 143712 | 5227 |
| A575226H | 143716 | 5228 |
| A575227H | 143717 | 5229 |
| A575228H | 143719 | 5230 |
| A575229H | 143720 | 5231 |
| A575230H | 143721 | 5232 |
| A575231H | 143723 | 5233 |
| A575232H | 143724 | 5234 |
| A575233H | 143725 | 5235 |
| A575234H | 143726 | 5236 |
| A575235H | 143727 | 5237 |
| A575236H | 143728 | 5238 |
| A575237H | 143728 | 5239 |
| A575238H | 143729 | 5240 |
| A575239H | 143756 | 5241 |
| A575240H | 143763 | 5242 |
| A575241H | 143785 | 5243 |
| A575242H | 143785 | 5244 |
| A575243H | 143786 | 5245 |
| A575244H | 143787 | 5246 |
| A575245H | 143788 | 5247 |
| A575246H | 143793 | 5248 |
| A575247H | 143807 | 5249 |
| A575248H | 143813 | 5250 |
| A575249H | 143839 | 5251 |
| A575250H | 143840 | 5252 |
| A575251H | 143841 | 5253 |
| A575252H | 143843 | 5254 |
| A575253H | 143844 | 5255 |
| A575254H | 143845 | 5256 |
| A575255H | 143847 | 5257 |
| A575256H | 143869 | 5258 |
| A575257H | 143873 | 5259 |
| A575258H | 143876 | 5260 |
| A575259H | 143877 | 5261 |
| A575260H | 143877 | 5262 |
| A575261H | 143878 | 5263 |
| A575262H | 143878 | 5264 |
| A575263H | 143879 | 5265 |
| A575264H | 143879 | 5266 |
| A575265H | 143880 | 5267 |
| A575266H | 143880 | 5268 |
| A575267H | 143887 | 5269 |
| A575268H | 143888 | 5270 |
| A575269H | 143935 | 5271 |

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|---|---|---|
| A575270H | 143936 | 5272 |
| A575271H | 143938 | 5273 |
| A575272H | 143939 | 5274 |
| A575273H | 143940 | 5275 |
| A575274H | 143942 | 5276 |
| A575275H | 143948 | 5277 |
| A575276H | 143948 | 5278 |
| A575277H | 143976 | 5279 |
| A575278H | 143976 | 5280 |
| A575279H | 143977 | 5281 |
| A575280H | 143978 | 5282 |
| A575281H | 143979 | 5283 |
| A575282H | 143979 | 5284 |
| A575283H | 143980 | 5285 |
| A575284H | 143980 | 5286 |
| A575285H | 143982 | 5287 |
| A575286H | 143983 | 5288 |
| 144001-144173 | | |
| A575287H | 144013 | 5289 |
| A575288H | 144161 | 5290 |
| A575289H | 144163 | 5291 |
| A575290H | 144164 | 5292 |
| A575291H | 144165 | 5293 |
| A575292H | 144171 | 5294 |
| A575293H | 144173 | 5295 |

The oligonucleotides of the present invention hybridize, for example, with mRNA and/or pre-mRNA of human LRRK2 of SEQ ID NO. 1 and/or SEQ ID NO.2. Such oligonucleotides are called LRRK2 antisense oligonucleotides. Oligonucleotides of the present invention, which are for example antisense oligonucleotides, are shown in Table 1. The present invention further refers to oligonucleotides such as antisense oligonucleotides having about 80 % to 99 %, about 85 % to 98 %, about 90 % to 95 %, about 90 % to 99%, about 93% to about 99%, about 94% to about 99%, about 95% to about 99%, at least about 85 %, 86 %, 87 %, 88 %, 89 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, or 99 % sequence homology to an oligonucleotide of Table 1.

Moreover, the present invention refers to oligonucleotides such as antisense oligonucleotides comprising or consisting of at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21 or at least 22 nucleotides of any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301.

Each nucleotide of the sequence can be modified, wherein ASOs of the present invention preferably comprise a core of 6 to 8 unmodified nucleotides. ASOs of the present invention comprise, for example, one or more modified nucleotides, e.g., 1, 2, 3, 4 or 5 nucleotides at the 5´- and/or 3´-end of the oligonucleotide, i.e., on the 5´- and/or 3´-side of the core. The 5´- and 3´-end can be modified identically or differently. If the 5´- and 3´-ends are modified identically the nucleotides are modified at the same positions counted from the 5´- and 3´-end (in each case starting the counting with 1 from the end), respectively, having the same modification for example LNA-modification. If the 5´- and 3´-ends are modified differently the position of the modified nucleotide and/or the type of modification at the 5´- and 3´-ends differ; the type of nucleotide modification is the same (e.g., LNA) or different. Modified nucleotides such as LNA-modified nucleotides need not to follow in a row, but may be separated by one or more unmodified nucleotides. In the following table exemplary modification patterns at the 5´- and 3´-end of the ASOs of the present invention are described, wherein an unmodified nucleotide is indicated by "_" and the number on either side of the "_" refers to the number of modified nucleotides such as LNA-modified nucleotides in a row. The modified nucleotide(s) is/are at any position of the 5´- and/or 3´-end of the ASO as shown in the following **Table 3:**

| **LNA modification at the 5´-side of the core** | **LNA modification at the 3´-side of the core** | **Abbreviation** |
|---|---|---|
| 3 | 3 | 3+3 |
| 3 | 2 | 3+2 |
| 2 | 3 | 2+3 |
| 1_1 | 3 | 1_1+3 |
| 1_1 | 2 | 1_1+2 |
| 1_1 | 1_1 | 1_1+1_1 |
| 3 | 1_1 | 3+1_1 |
| 2 | 1_1 | 2+1_1 |
| 2 | 2 | 2+2 |
| 4 | 3 | 4+3 |
| 4 | 2 | 4+2 |
| 4 | 1_1 | 4+1_1 |

| | | |
|---|---|---|
| 2_1 | 3 | 2_1+3 |
| 2_1 | 1_1 | 2_1+1_1 |
| 2_1 | 2 | 2_1+2 |
| 3 | 4 | 3+4 |
| 2 | 4 | 2+4 |
| 1_1 | 4 | 1_1+4 |
| 3 | 1_2 | 3+1_2 |
| 1_1 | 1_2 | 1_1+1_2 |
| 2 | 1_2 | 2+1_2 |

**Table 3**

which indicates specific positions of the LNA modifications at the 5´- and 3´-end of each ASO in **Table 4**:

| **Position of the modification at the 5´-end (counted from the 5´-end starting with 1)** | **Position of the modification at the 3´-end (counted from the 3´-end starting with 1)** | **Abbreviation** |
|---|---|---|
| nucleotides 1 to 5 | nucleotides 1 to 5 | 5+5 |
| nucleotides 1 to 4 | nucleotides 1 to 4 | 4+4 |
| nucleotides 1 to 3 | nucleotides 1 to 3 | 3+3 |
| nucleotides 1 and 2 | nucleotides 1 and 2 | 2+2 |
| nucleotide 1 | nucleotide 1 | 1+1 |
| nucleotides 1 to 5 | nucleotides 1 to 4 | 5+4 |
| nucleotides 1 to 4 | nucleotides 1 to 3 | 4+3 |
| nucleotides 1 to 3 | nucleotides 1 and 2 | 3+2 |
| nucleotides 1 and 2 | nucleotide 1 | 2+1 |
| nucleotide 1 | nucleotides 1 to 5 | 1+5 |
| nucleotides 1 to 5 | nucleotides 1 to 3 | 5+3 |
| nucleotides 1 to 4 | nucleotides 1 and 2 | 4+2 |
| nucleotides 1 to 3 | nucleotide 1 | 3+1 |
| nucleotides 1 and 2 | nucleotides 1 to 5 | 2+5 |
| nucleotide 1 | nucleotides 1 to 4 | 1+4 |
| nucleotides 1 to 5 | nucleotides 1 and 2 | 5+2 |
| nucleotides 1 to 4 | nucleotide 1 | 4+1 |
| nucleotides 1 to 3 | nucleotides 1 to 5 | 3+5 |
| nucleotides 1 and 2 | nucleotides 1 to 4 | 2+4 |
| nucleotide 1 | nucleotides 1 to 3 | 1+3 |
| nucleotides 1 to 5 | nucleotide 1 | 5+1 |
| nucleotides 1 to 4 | nucleotides 1 to 5 | 4+5 |
| nucleotides 1 to 3 | nucleotides 1 to 4 | 3+4 |
| nucleotides 1 and 2 | nucleotides 1 to 3 | 2+3 |
| nucleotide 1 | nucleotides 1 and 2 | 1+2 |
| nucleotides 1 and 2 | nucleotides 1 and 3 | 2+1_1 |

| | | |
|---|---|---|
| nucleotides 1 and 3 | nucleotides 1 to 3 | 1_1+3 |
| nucleotides 1 and 3 | nucleotides 1 and 3 | 1_1+1_1 |
| nucleotides 1 to 3 | nucleotides 1 and 3 | 3+1_1 |
| nucleotides 1 to 4 | nucleotides 1 and 3 | 4+1_1 |
| nucleotides 1, 2 and 4 | nucleotides 1 to 3 | 2_1+3 |
| nucleotides 1, 2 and 4 | nucleotides 1 and 3 | 2_1+1_1 |
| nucleotides 1, 2 and 4 | nucleotides 1 and 2 | 2_1+2 |
| nucleotides 1 and 3 | nucleotides 1 to 4 | 1_1+4 |
| nucleotides 1 to 3 | nucleotides 1,2 and 4 | 3+1_2 |
| nucleotides 1 and 3 | nucleotides 1, 2 and 4 | 1_1+1_2 |
| nucleotides 1 and 2 | nucleotides 1, 2 and 4 | 2+1_2 |

**Table 4**

In some embodiments, the oligonucleotide of the present invention can reduce the amount of LRRK2 mRNA and/or the LRRK2 protein expression for example by about 30 % - 100 %, 35 % - 99 %, 40 % - 98 %, 45 % - 97 %, 50 % - 96 %, 55 % - 95 %, 60 % - 90 %, 65 % - 85 %, 70 % - 80 % or at least about 30 %, 35 %, 40 %, 45 %, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or 100%. The reduction of the amount of the LRRK2 mRNA and/or LRRK2 protein expression can be determined by the comparison of the amount of the LRRK2 mRNA and/or LRRK2 protein expression in a sample treated with an oligonucleotide of the present invention and a corresponding untreated control. The untreated control is, for example, LRRK2, LRRK2 mRNA, LRRK2 pre-mRNA expression, or a combination thereof in a subject prior to administration of an oligonucleotide of the present invention is administered or an untreated sample such as a cell, blood, urine, saliva etc.. The untreated sample is, for example, taken from a subject before an oligonucleotide of the present invention is administered.

The oligonucleotide of the present invention reduces the amount of LRRK2 mRNA and/or the expression of LRRK2 protein expression at a nanomolar or micromolar concentration for example at a concentration of about 0.1, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900 or 950 nM, or 1, 10 or 100 µM.

The oligonucleotide of the present invention is, for example, used in a concentration of about 1, 3, 5, 9, 10, 15, 27, 30, 40, 50, 75, 82, 100, 250, 300, 500, or 740 nM, or about 1, 2.2, 3, 5, 6.6 or 10 µM.

The present invention also refers to a pharmaceutical composition comprising an oligonucleotide described herein and a pharmaceutically acceptable carrier, excipient, stimulant, adjuvant, and/or dilutant. Optionally, the pharmaceutical composition further comprises another oligonucleotide which is different from the present invention, an antibody and/or a small molecule such as a therapeutically active agent for use in preventing and/or treating a human disease, for example PD – a prevalent and severe neurodegenerative disease.

The oligonucleotide or the pharmaceutical composition of the present invention is, for example, for use in a method of preventing and/or treating a disorder such as a neurodegenerative disorder. The neurodegenerative disorder is, for example, Parkinson´s disease, Alzheimer´s disease, Huntington's disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia or prion diseases.

The disorder is, for example, characterized by activity of LRRK2, such as overactivity or a LRRK2 mRNA and/or protein imbalance, i.e., the LRRK2 mRNA and/or protein level is abnormal (e.g., increased) in comparison to the level in a normal, healthy cell, tissue, organ or subject, or LRRK2 activity is abnormal. The LRRK2 level is, for example, increased by an increased amount of LRRK2 mRNA and/or LRRK2 protein expression. Overactivity of LRRK2 function is, for example, caused by activating mutations or by unknown genetic, epigenetic or environmental mechanisms.

The LRRK2 mRNA and protein level, respectively, can be measured by any standard method known to a person skilled in the art, such as immunohistochemistry, western blot, quantitative real time PCR or QUANTIGENE assay known to a person skilled in the art.

An oligonucleotide or a pharmaceutical composition described herein can be administered locally or systemically for example orally, sublingually, nasally, subcutaneously, intravenously, intraperitoneally, intramuscularly, intratumorally, intrathecally, intraventricularly, transdermal and/or rectally. The oligonucleotide is, for example, administered alone or in combination with another oligonucleotide of the present invention, and optionally in combination with another compound such as

another oligonucleotide different from the present invention, an antibody, and/or a small molecule.

Further, two or more oligonucleotides of the present invention are, for example, administered together, at the same time point, e.g., in a pharmaceutical composition or separately, or on staggered intervals. Alternatively or in addition, one or more oligonucleotides described herein can be administered together with another compound such as another oligonucleotide (i.e., different from the present invention), an antibody, and/or a small molecule, at the same time point for example in a pharmaceutical composition or separately, or on staggered intervals. In some of these combinations, the oligonucleotide of the present invention reduces, for example, the amount of LRRK2 mRNA and/or LRRK2 protein expression and the other oligonucleotide (i.e., different from the present invention), the antibody and/or small molecule inhibits (antagonist) or stimulates (agonist) a further factor involved in formation or progression of neurodegenerative diseases. This factor is, for example, α-synuclein, Tau, TDO, NLRP3, PFKB3 or a combination thereof. The factor can be a factor whose level or activity is increased or decreased in a cell, tissue, organ or subject depending on the cell, tissue, organ or subject and its individual conditions.

The oligonucleotide of the present invention is, for example, combined with another therapeutically active agent. Suitable therapeutically active agents include, but are not limited to L-dopa, a dopamine agonist, monoamine oxidase inhibitor, etc. known to those skilled in the art.

An antibody in combination with the oligonucleotide or the pharmaceutical composition of the present invention is, for example, an anti-α-synuclein such as Prasinezumab (RO7046015/PRX002), Cinpanemab, ABBV-805, MEDI1341 or LU AF82422 antibody.

A subject of the present invention is for example a mammalian (e.g., a human, dog, cat horse, cow, pig), bird, or fish.

**Examples**

The following examples illustrate non-limiting embodiments of the present invention, but the invention is not limited to these examples. The following experiments were

performed on cells endogenously expressing LRRK2, i.e., the cells do not represent an artificial system comprising transfected reporter constructs. Such artificial systems generally show a higher degree of inhibition and lower $IC_{50}$ values than endogenous systems which are closer to therapeutically relevant *in vivo* systems. Further, in the following experiments no transfecting agent were used, i.e., gymnotic delivery was performed. Transfecting agents are known to increase the activity of an oligonucleotide which influences artificially the $IC_{50}$ value (see for example Zhang et al., Gene Therapy, 2011, 18, 326-333; Stanton et al., Nucleic Acid Therapeutics, Vol. 22, No. 5, 2012). Since artificial systems using a transfecting agent are hard or impossible to translate into therapeutic approaches and no transfection formulation has been approved so far for oligonucleotides, the following experiments were performed without any transfecting agent.

**Example 1**: Target knockdown efficacy screens of human LRRK2-specific ASOs in A549 and MDA-MB-231 cells

Knockdown efficacy of the LRRK2-specific ASOs was tested in human A549 cells and MDA-MB-231 cells. The cells were treated with the respective LRRK2-specific ASO or control oligonucleotide at a concentration of 5 µM without the use of a transfection reagent. After three days of treatment, cells were lyzed. LRRK2 and HPRT1 mRNA expression was analyzed using the QUANTIGENE SINGLEPLEX assay (THERMOFISHER) and the LRRK2 expression values were normalized to HPRT1 values. The results of ASOs in A549 cells and in MDA-MB-231 cells are shown as residual LRRK2 mRNA expression relative to mock-treated cells (set as 1) in FIGs. 3A to 3D, Table 5 and FIGs. 4A to 4D. Treatment of A549 cells with the ASOs A57162Hi (SEQ ID NO.164), A57147Hi (SEQ ID NO.149), A57208Hi (SEQ ID NO.210), A57187Hi (SEQ ID NO.189), A57146Hi (SEQ ID NO.148), A575302Hi (SEQ ID NO. 69), A575307Hi (SEQ ID NO. 69), A575308Hi (SEQ ID NO. 69), A575309Hi (SEQ ID NO. 69), A575310Hi (SEQ ID NO. 69), A575313Hi (SEQ ID NO. 69), A575321Hi (SEQ ID NO. 142), A575323Hi (SEQ ID NO. 142), A575326Hi (SEQ ID NO. 142), A575327Hi (SEQ ID NO. 142), A575335Hi (SEQ ID NO. 209), A575337Hi (SEQ ID NO. 209), A575338Hi (SEQ ID NO. 209), A575341Hi (SEQ ID NO. 209), A575349Hi, A575351Hi (SEQ ID NO. 210), A575354Hi (SEQ ID NO. 210), and A575355Hi (SEQ ID NO. 209), respectively, resulted in a target inhibition of >85 % (represented by a residual LRRK2 mRNA expression of <0.15 as compared to mock-treated cells) (FIGs. 3A to 3D). As shown in FIGs. 4A to 4D, treatment with the ASOs A57252H (SEQ ID NO.254),

A57253H (SEQ ID NO.255) and A57024Hi (SEQ ID NO.26) resulted in a target inhibition of ≥75% (represented by a residual LRRK2 mRNA expression of ≤0.25 as compared to mock treated cells). **Table 5** shows mean residual expression of human LRRK2 (normalized to HPRT1 and compared to mock-treated cells) in A549 cells after ASO treatment:

| **Name** | **Mean residual expression of human LRRK2 (normalized to HPRT1 and compared to mock-treated cells)** |
|---|---|
| A57001Hi | 1.04 |
| A57002Hi | 0.97 |
| A57003Hi | 0.95 |
| A57004Hi | 0.58 |
| A57005Hi | 0.57 |
| A57006Hi | 0.59 |
| A57007Hi | 0.66 |
| A57008Hi | 0.48 |
| A57009Hi | 0.42 |
| A57010Hi | 0.44 |
| A57011Hi | 0.82 |
| A57012Hi | 0.99 |
| A57013Hi | 0.63 |
| A57014Hi | 0.94 |
| A57015Hi | 0.94 |
| A57016Hi | 0.79 |
| A57017Hi | 0.98 |
| A57018Hi | 0.86 |
| A57019Hi | 0.91 |
| A57020Hi | 0.94 |
| A57021Hi | 0.56 |
| A57022Hi | 0.79 |
| A57023Hi | 0.91 |
| A57024Hi | 0.51 |

| | |
|---|---|
| A57025Hi | 0.86 |
| A57026Hi | 0.86 |
| A57027Hi | 0.41 |
| A57028Hi | 0.63 |
| A57029Hi | 0.46 |
| A57030Hi | 0.61 |
| A57031Hi | 0.52 |
| A57032Hi | 0.67 |
| A57033Hi | 0.64 |
| A57034Hi | 0.89 |
| A57035Hi | 0.75 |
| A57036Hi | 1.01 |
| A57037Hi | 0.93 |
| A57038Hi | 0.73 |
| A57039Hi | 0.86 |
| A57040Hi | 0.82 |
| A57041Hi | 0.67 |
| A57042Hi | 0.38 |
| A57043Hi | 0.34 |
| A57044Hi | 0.35 |
| A57045Hi | 0.42 |
| A57046Hi | 0.79 |
| A57047Hi | 1.24 |
| A57048Hi | 0.38 |
| A57049Hi | 0.48 |
| A57050Hi | 0.84 |
| A57051Hi | 0.69 |
| A57052Hi | 0.60 |
| A57053Hi | 0.67 |
| A57054Hi | 0.60 |

| | |
|---|---|
| A57055Hi | 0.83 |
| A57056Hi | 0.67 |
| A57057Hi | 0.67 |
| A57058Hi | 0.27 |
| A57059Hi | 0.68 |
| A57060Hi | 0.51 |
| A57061Hi | 0.52 |
| A57062Hi | 0.33 |
| A57063Hi | 0.51 |
| A57064Hi | 0.25 |
| A57065Hi | 0.57 |
| A57066Hi | 0.90 |
| A57067Hi | 0.16 |
| A57068Hi | 0.34 |
| A57069Hi | 0.81 |
| A57070Hi | 0.93 |
| A57071Hi | 0.53 |
| A57072Hi | 0.66 |
| A57073Hi | 0.57 |
| A57074Hi | 0.60 |
| A57075Hi | 0.39 |
| A57076Hi | 0.68 |
| A57077Hi | 0.98 |
| A57078Hi | 0.86 |
| A57079Hi | 0.75 |
| A57080Hi | 0.95 |
| A57081Hi | 1.03 |
| A57082Hi | 0.76 |
| A57083Hi | 0.82 |
| A57084Hi | 0.84 |

| | |
|---|---|
| A57085Hi | 1.09 |
| A57086Hi | 0.54 |
| A57087Hi | 0.95 |
| A57088Hi | 0.59 |
| A57089Hi | 0.43 |
| A57090Hi | 0.25 |
| A57091Hi | 0.54 |
| A57092Hi | 0.66 |
| A57093Hi | 0.34 |
| A57094Hi | 0.46 |
| A57095Hi | 0.34 |
| A57096Hi | 0.75 |
| A57097Hi | 0.62 |
| A57098Hi | 0.54 |
| A57099Hi | 0.70 |
| A57100Hi | 0.89 |
| A57101Hi | 0.42 |
| A57102Hi | 0.35 |
| A57103Hi | 0.99 |
| A57104Hi | 0.42 |
| A57105Hi | 0.36 |
| A57106Hi | 0.41 |
| A57107Hi | 0.38 |
| A57108Hi | 0.75 |
| A57109Hi | 0.86 |
| A57110Hi | 0.85 |
| A57111Hi | 1.02 |
| A57112Hi | 0.44 |
| A57113Hi | 0.77 |
| A57114Hi | 0.61 |

| | |
|---|---|
| A57115Hi | 0.72 |
| A57116Hi | 0.51 |
| A57117Hi | 0.70 |
| A57118Hi | 1.11 |
| A57119Hi | 0.63 |
| A57120Hi | 0.49 |
| A57121Hi | 0.44 |
| A57122Hi | 0.64 |
| A57123Hi | 0.80 |
| A57124Hi | 0.52 |
| A57125Hi | 0.68 |
| A57126Hi | 0.79 |
| A57127Hi | 0.85 |
| A57128Hi | 0.67 |
| A57129Hi | 0.80 |
| A57130Hi | 0.76 |
| A57131Hi | 0.70 |
| A57132Hi | 0.52 |
| A57133Hi | 0.71 |
| A57134Hi | 0.76 |
| A57135Hi | 0.61 |
| A57136Hi | 0.53 |
| A57137Hi | 0.84 |
| A57138Hi | 0.48 |
| A57139Hi | 0.68 |
| A57140Hi | 0.21 |
| A57141Hi | 0.80 |
| A57142Hi | 1.03 |
| A57143Hi | 0.76 |
| A57144Hi | 0.68 |

| | |
|---|---|
| A57145Hi | 0.76 |
| A57146Hi | 0.14 |
| A57147Hi | 0.12 |
| A57148Hi | 0.63 |
| A57149Hi | 0.46 |
| A57150Hi | 0.31 |
| A57151Hi | 0.53 |
| A57152Hi | 0.56 |
| A57153Hi | 0.58 |
| A57154Hi | 0.66 |
| A57155Hi | 0.63 |
| A57156Hi | 0.58 |
| A57157Hi | 0.39 |
| A57158Hi | 0.53 |
| A57159Hi | 0.36 |
| A57160Hi | 0.26 |
| A57161Hi | 0.39 |
| A57162Hi | 0.11 |
| A57163Hi | 0.30 |
| A57164Hi | 0.46 |
| A57165Hi | 0.63 |
| A57166Hi | 0.76 |
| A57167Hi | 0.47 |
| A57168Hi | 0.73 |
| A57169Hi | 0.25 |
| A57170Hi | 1.03 |
| A57171Hi | 0.50 |
| A57172Hi | 0.43 |
| A57173Hi | 0.48 |
| A57174Hi | 0.55 |

| | |
|---|---|
| A57175Hi | 0.43 |
| A57176Hi | 0.39 |
| A57177Hi | 0.82 |
| A57178Hi | 0.58 |
| A57179Hi | 0.46 |
| A57180Hi | 0.27 |
| A57181Hi | 0.66 |
| A57182Hi | 0.52 |
| A57183Hi | 0.51 |
| A57184Hi | 0.18 |
| A57185Hi | 0.67 |
| A57186Hi | 0.69 |
| A57187Hi | 0.14 |
| A57188Hi | 0.45 |
| A57189Hi | 0.89 |
| A57190Hi | 0.53 |
| A57191Hi | 0.89 |
| A57192Hi | 0.82 |
| A57193Hi | 0.94 |
| A57194Hi | 1.02 |
| A57195Hi | 0.73 |
| A57196Hi | 0.94 |
| A57197Hi | 0.72 |
| A57198Hi | 0.59 |
| A57199Hi | 0.51 |
| A57200Hi | 0.39 |
| A57201Hi | 0.53 |
| A57202Hi | 0.15 |
| A57203Hi | 0.84 |
| A57204Hi | 0.66 |

| | |
|---|---|
| A57205Hi | 0.61 |
| A57206Hi | 0.95 |
| A57207Hi | 0.25 |
| A57208Hi | 0.14 |
| A57209Hi | 0.30 |
| A57210Hi | 0.43 |
| A57211Hi | 0.70 |
| A57212Hi | 0.62 |
| A57213Hi | 0.86 |
| A57214Hi | 0.73 |
| A57215Hi | 0.87 |
| A57216Hi | 0.76 |
| A57217Hi | 0.79 |
| A57218Hi | 0.54 |
| A57219Hi | 0.86 |
| A57220Hi | 0.18 |
| A57221Hi | 0.51 |
| A57222Hi | 0.17 |
| A57223Hi | 0.69 |
| A57224Hi | 0.64 |
| A57225Hi | 0.63 |
| A57226Hi | 0.33 |
| A57227Hi | 0.91 |
| A57228Hi | 1.07 |
| A57229Hi | 0.77 |
| A57230Hi | 0.46 |
| A57231Hi | 0.75 |
| A57232Hi | 0.56 |
| A57233Hi | 0.72 |
| A57234Hi | 0.70 |

| | |
|---|---|
| A57235Hi | 0.64 |
| A57236Hi | 0.68 |
| A57237Hi | 0.15 |
| A57238Hi | 0.46 |
| A57239Hi | 0.19 |
| A57240Hi | 0.72 |
| A57241Hi | 0.96 |
| A57242Hi | 0.36 |
| A57243Hi | 0.33 |
| A57244Hi | 0.53 |
| A57245Hi | 0.78 |
| A57246Hi | 0.53 |
| A57247Hi | 0.49 |
| A57248Hi | 0.32 |
| A57249Hi | 0.37 |
| A57250H | 0.55 |
| A57251H | 0.43 |
| A57252H | 0.15 |
| A57253H | 0.20 |
| A57254H | 0.25 |
| A57255H | 0.95 |
| A57256H | 0.29 |
| A57257H | 0.69 |
| A57258H | 0.63 |
| A57259H | 0.47 |
| A57260H | 0.46 |
| A575301Hi | 0.29 |
| A575302Hi | 0.14 |
| A575304Hi | 0.38 |
| A575307Hi | 0.06 |

| | |
|---|---|
| A575308Hi | 0.11 |
| A575309Hi | 0.07 |
| A575310Hi | 0.07 |
| A575312Hi | 0.17 |
| A575313Hi | 0.08 |
| A575315Hi | 0.24 |
| A575316Hi | 0.22 |
| A575318Hi | 0.31 |
| A575321Hi | 0.12 |
| A575322Hi | 0.20 |
| A575323Hi | 0.09 |
| A575324Hi | 0.18 |
| A575326Hi | 0.11 |
| A575327Hi | 0.10 |
| A575329Hi | 0.27 |
| A575330Hi | 0.28 |
| A575332Hi | 0.25 |
| A575335Hi | 0.07 |
| A575336Hi | 0.21 |
| A575337Hi | 0.09 |
| A575338Hi | 0.07 |
| A575340Hi | 0.17 |
| A575341Hi | 0.04 |
| A575343Hi | 0.33 |
| A575344Hi | 0.15 |
| A575346Hi | 0.22 |
| A575349Hi | 0.05 |
| A575350Hi | 0.16 |
| A575351Hi | 0.10 |
| A575352Hi | 0.19 |

| | |
|---|---|
| A575354Hi | 0.14 |
| A575355Hi | 0.11 |
| Neg1 | 1.00 |
| R01002 | 1.09 |
| R01011 | 1.18 |
| R01025 | 0.83 |

**Example 2**: Concentration-response curves and determination of $IC_{50}$ values of selected human LRRK2-specific ASOs in A549 cells

Knockdown efficacy of selected ASO was tested in human A549 cells at different concentrations. Therefore, cells were treated with the respective LRRK2 ASO at the following concentrations: 10000 nM, 3333 nM, 1111 nM, 370 nM, 123 nM, 41 nM, 14 nM without the use of a transfection reagent. After three days of treatment, cells were lyzed. LRRK2 and HPRT1 mRNA expression was analyzed using the QUANTIGENE SINGLEPLEX assay (THERMOFISHER) and the LRRK2 expression values were normalized to HPRT1 values. Concentration-dependent knockdown of LRRK2 mRNA expression is shown as residual LRRK2 mRNA expression normalized to HPRT1 mRNA expression relative to mock-treated cells (set as 1) in the following **Table 6**:

| | **ASO concentration** | | | | | | | **$IC_{50}$ value** | **SEQ ID NO.** |
|---|---|---|---|---|---|---|---|---|---|
| **ASO ID** | **14 nM** | **41 nM** | **123 nM** | **370 nM** | **1111 nM** | **3333 nM** | **10000 nM** | **(nM)** | |
| A57043Hi | 1.11 | 0.98 | 1.05 | 0.82 | 0.56 | 0.37 | 0.25 | 883 | 45 |
| A57044Hi | 1.07 | 0.99 | 0.79 | 0.92 | 0.57 | 0.49 | 0.30 | 1530 | 46 |
| A57058Hi | 1.01 | 0.71 | 0.79 | 0.71 | 0.52 | 0.36 | 0.28 | 1438 | 60 |
| A57064Hi | 0.95 | 0.72 | 0.85 | 0.74 | 0.44 | 0.31 | 0.19 | 1586 | 66 |
| A57067Hi | 1.01 | 0.95 | 0.77 | 0.68 | 0.39 | 0.20 | 0.12 | 622 | 69 |
| A57140Hi | 0.89 | 0.85 | 0.84 | 0.67 | 0.49 | 0.29 | 0.15 | 2207 | 142 |
| A57160Hi | 0.87 | 0.80 | 0.93 | 0.80 | 0.48 | 0.30 | 0.21 | 847 | 162 |
| A57162Hi | 0.96 | 0.86 | 0.67 | 0.61 | 0.40 | 0.15 | 0.11 | 646 | 164 |
| A57169Hi | 1.00 | 0.87 | 0.83 | 0.75 | 0.62 | 0.38 | 0.19 | 888 | 171 |
| A57184Hi | n.d. | 0.93 | 0.89 | 0.79 | 0.53 | 0.26 | 0.14 | 1169 | 186 |
| A57202Hi | 0.98 | 0.94 | 0.86 | 0.73 | 0.43 | 0.27 | 0.15 | 759 | 204 |
| A57207Hi | 0.84 | 0.90 | 0.87 | 0.62 | 0.41 | 0.21 | 0.16 | 640 | 209 |
| A57208Hi | 1.04 | 0.87 | 0.71 | 0.48 | 0.27 | 0.13 | 0.10 | 284 | 210 |
| A57220Hi | n.d. | 1.02 | 0.62 | 0.60 | 0.45 | 0.24 | 0.14 | 514 | 222 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| A57222Hi | 1.06 | 0.68 | 0.81 | 0.59 | 0.45 | 0.26 | 0.24 | 429 | 224 |
| A57239Hi | 0.99 | 0.99 | 0.83 | 0.80 | 0.49 | 0.24 | 0.16 | 920 | 241 |
| A57248Hi | 1.11 | 0.77 | 0.74 | 0.48 | 0.55 | 0.38 | 0.40 | 113 | 250 |
| A57147Hi | n.d. | 0.68 | 0.76 | 0.50 | 0.36 | 0.23 | 0.26 | 238 | 149 |
| A57252H | 0.81 | 0.77 | 0.71 | 0.59 | 0.38 | 0.23 | 0.13 | 1852 | 254 |
| A57253H | 0.76 | 0.79 | 0.83 | 0.62 | 0.47 | 0.28 | 0.18 | 347 | 255 |
| A57254H | 0.81 | 1.03 | 0.68 | 0.89 | 0.55 | 0.33 | 0.19 | 6144 | 256 |
| A57237Hi | n.d. | 0.89 | 0.85 | 0.72 | 0.54 | 0.30 | 0.18 | 1462 | 239 |

**Example 3**: Knockdown of human LRRK2 mRNA in transgenic mice:

The bioactivity of human LRRK2-targeting ASOs was tested in mice expressing human LRRK2 (The Jackson Laboratory: C57BL/6J-Tg(LRRK2*G2019S)2AMjff/J, Stain #: 018785). These mice express endogenous mouse LRRK2 as well as human LRRK2 which is under the control of the human promoter/enhancer regions within the bacterial artificial chromosome (BAC) transgene. The human LRRK2 expression can be detected in the central nervous system and periphery (Bieri et al., 2019; Sitzia et al., 2022).

Human LRRK2 transgenic mice were either treated with a single intracerebroventricular (ICV, n=11 mice) bolus dose of 100 μg of LRRK2 antisense oligonucleotide or received PBS as the vehicle control group (n= 4 mice). Fourteen days after ICV injections, mice were sacrificed, tissues were harvested, and total RNA was extracted and processed for detection of LRRK2 mRNA using real-time PCR analysis. Treatment with selected ASOs resulted in statistically significant reductions of human LRRK2 mRNA ranging from ~40% to ~90% in the CNS regions, compared to vehicle control.

**Table 7** shows the treatment with an ASO (SEQ ID NO.209) resulted in statistically significant reduction (~45-50%) of human LRRK2 mRNA in the striatum and cortex areas of the central nervous system, compared to vehicle control and normalized to the expression of HPRT1, a house keeping gene (**Table 7**). In the study cohort no statistically significant changes of human LRRK2 mRNA levels were detected in peripheral tissues lung, liver, blood, and kidney.

**Table 7** shows human LRRK2 mRNA knockdown in transgenic mice treated with SEQ ID NO.209 ASO:

| Tissue | LRKK2 mRNA reduction [%] | SEM | p value |
|---|---|---|---|
| Striatum | 50.19 | 0.06 | 0.0010 |
| Cortex | 44.40 | 0.05 | 0.0101 |
| Lung | no reduction | 0.34 | 0.1288 |
| Kidney | no reduction | 0.22 | 0.9973 |
| Liver | no reduction | 0.19 | 0.5134 |
| Blood | no reduction | 0.15 | 0.8556 |

**Table 7** shows reduction of human LRRK2 mRNA levels in different regions of the central nervous system and in peripheral tissues detected by real-time PCR 14 days after ICV injection of either 100 µg of LRRK2 ASO1 (n=12-13) or PBS vehicle (n=4).

Gene expression was normalized to HPRT1, a house keeping gene, and compared to human LRRK2 mRNA levels detected in PBS vehicle-treated animals (n=4). Variance is displayed as standard error of the mean (SEM). One way ANOVA was used to determine statistical significance.

**Embodiments of the invention**

1. An oligonucleotide comprising 10 to 25 nucleotides, wherein the sequence of nucleotides of the oligonucleotide is at least 80 to 90 % complementary to a corresponding region of a LRRK2 nucleic acid sequence and wherein at least one nucleotide is modified and the modification selected from a modified sugar and optionally a modified internucleoside linkage.

2. The oligonucleotide according to embodiment 1, wherein the LRRK2 nucleic acid is mRNA of leucine-rich repeat kinase 2 (LRRK2) of SEQ ID NO.1 and/or pre-mRNA of LRRK2 of SEQ ID NO.2 and/or a fragment thereof.

3. The oligonucleotide according to embodiment 1 or 2, wherein the modification is selected from the group consisting of LNA, ENA, cET, a 2'Fluoro modified nucleotide, a

2´O-Methyl modified nucleotide, a 2´O-Methoxy modified nucleotide, a FANA and a combination thereof.

4. The oligonucleotide according to any one of embodiments 1 to 3, wherein the modification is located in a sequence of at least 3 nucleotides or at least 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide.

5. The oligonucleotide according to any one of embodiments 1 to 4, wherein the modification is located in a sequence of 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide.

6. The oligonucleotide according to any one of embodiments 1 to 5, wherein the internucleoside linkage is selected from the group consisting of phosphodiester, phosphorothioate, methylphosphonate, methyl phosphorothioate, phosphoramidate, phosphorodiamidate, thiophosphoramidate, mesyl phosphoramidate or a combination thereof

7. An oligonucleotide comprising 10 to 25 nucleotides, at least one nucleotide having a bridged nucleic acid modification selected from the group consisting of LNA, ENA, cET, a 2'Fluoro modified nucleotide, a 2´O-Methyl modified nucleotide, a 2´O-Methoxy modified nucleotide, a FANA and a combination thereof, wherein said modification is located in a sequence of 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide and wherein the oligonucleotide hybridizes with a transcript or an mRNA of leucine-rich repeat kinase 2 (LRRK2) of SEQ ID NO.1 and/or with pre-mRNA of LRRK2 of SEQ ID NO.2 and/or a fragment thereof.

8. The oligonucleotide according to any one of embodiments 1 to 7, wherein the oligonucleotide hybridizes outside a hybridizing active region or within a hybridizing active region of position 27001 to 27500, position 102001 to 102500, position 80501 to 81000, position 24501 to 25000, position 114001 to 114500, position 92001 to 92500, position 99501 to 100000, position 67001 to 67500, position 15001 to 15500, position 24001 to 24500, position 26501 to 27000, position 79501 to 80000, position 87001 to 87500, position 120501 to 121000, position 142001 to 142500, position 135001 to 135500, position 71001 to 71500, position 140501 to 141000 or a combination thereof.

9. The oligonucleotide according to and one of embodiments 1 to 8, wherein the oligonucleotide comprises SEQ ID NO.69, SEQ ID NO.210, SEQ ID NO.164, SEQ ID NO.254, SEQ ID NO.222, SEQ ID NO.186, SEQ ID NO.204, SEQ ID NO.142, SEQ ID NO.209, SEQ ID NO.255, SEQ ID NO.45, SEQ ID NO.46, SEQ ID NO.60, SEQ ID NO.66, SEQ ID NO.162, SEQ ID NO.171, SEQ ID NO.224, SEQ ID NO.241, SEQ ID NO.250, SEQ ID NO.149, SEQ ID NO.256, SEQ ID NO.239, or a combination thereof.

10. The oligonucleotide according to any one of embodiments 1 to 9, wherein the oligonucleotide is selected from the group consisting of

+A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C (A57067Hi; SEQ ID NO.69),
+T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C (A57208Hi; SEQ ID NO.210),
+G*+T*+C*A*T*A*A*G*T*T*G*T*C*A*G*+T*+A*+T (A57162Hi; SEQ ID NO.164),
+G*+A*+C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57252H; SEQ ID NO.254),
+C*+T*+T*T*G*C*T*T*A*T*T*C*G*T*G*+A*+C*+T (A57220Hi; SEQ ID NO.222),
+T*+T*+T*A*T*T*G*C*A*G*T*C*A*T*A*G*+T*+G*+A (A57184Hi; SEQ ID NO.186),
+C*+T*+T*T*G*T*A*A*A*T*G*A*C*G*T*T*+T*+C*+C (A57202Hi; SEQ ID NO.204),
+T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A*+C*+A (A57140Hi, SEQ ID NO.142),
+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*C*+T*+C*+A (A57207Hi; SEQ ID NO.209),
+G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57253H; SEQ ID NO.255),
+C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*A*G*+T*+T*+C (A57043Hi; SEQ ID NO.45),
+T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*C*+A*+G*+T (A57044Hi; SEQ ID NO.46),
+G*+T*+G*T*A*A*C*T*A*A*G*T*G*A*T*+C*+T*+C (A57058Hi; SEQ ID NO.60),
+G*+A*+T*A*T*T*G*A*C*A*A*C*C*T*G*+C*+T*+G (A57064Hi; SEQ ID NO.66),
+T*+G*+T*G*T*T*A*C*C*A*T*A*T*C*C*A*+T*+T*+T (A57160Hi; SEQ ID NO.162),
+C*+T*+G*T*G*A*C*T*T*T*G*C*A*T*C*A*+A*+C*+T (A57169Hi; SEQ ID NO.171),
+C*+A*+A*T*G*T*A*T*A*C*C*A*T*G*C*+A*+G*+T (A57222Hi; SEQ ID NO.224),
+T*+T*+C*C*T*G*A*T*T*A*T*A*C*C*A*T*+A*+T*+G (A57239Hi; SEQ ID NO.241),
+A*+T*+G*C*T*C*T*T*A*T*C*C*A*C*A*A*+T*+C*+C (A57248Hi; SEQ ID NO.250),
+T*+T*+T*G*A*T*C*T*G*T*A*G*T*A*C*A*+T*+A*+C (A57147Hi; SEQ ID NO.149),
+A*+T*+G*G*A*C*T*T*C*G*T*T*T*A*A*T*+A*+C*+C (A57254H; SEQ ID NO.256),
+G*+G*+A*C*A*T*G*T*A*T*C*T*T*A*A*T*+A*+G*+T (A57237Hi; SEQ ID NO.239),

and a combination thereof, wherein + indicates an LNA nucleotide and * indicates a phosphorothioate (PTO) linkage between the nucleotides.

11. The oligonucleotide according to any one of embodiments 1 to 10, wherein the oligonucleotide has 80 to 99 %, 85 to 98 %, 90 to 95 or 93 % sequence identity to any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301.

12. The oligonucleotide according to any one of embodiments 1 to 11, wherein said oligonucleotide comprises at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21 or at least 22 contiguous nucleotides of any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301.

13. The oligonucleotide according to any one of embodiments 1 to 12, wherein the oligonucleotide inhibits the expression of LRRK2, a LRRK2 mRNA, a LRRK2 pre-mRNA or a combination thereof at a nanomolar or micromolar concentration.

14. A pharmaceutical composition comprising an oligonucleotide according to any one of embodiments 1 to 13 and a pharmaceutically acceptable carrier, excipient, adjuvant, or a combination thereof.

15. The pharmaceutical composition according to embodiment 14, further comprising a therapeutically active agent.

16. The oligonucleotide according to any one of embodiments 1 to 13, or the pharmaceutical composition according to embodiment 14 or 15 for use in a method of preventing and/or treating a human disease such as a neurodegenerative disease.

17. The oligonucleotide or the pharmaceutical composition according to embodiment 16, wherein the pharmaceutically acceptable carrier, excipient, adjuvant, or a combination thereof, or the therapeutically active agent is administrated separately before or after delivery of the oligonucleotide, or is administered simultaneously via different delivery methods.

18. The oligonucleotide according to embodiment 16 or 17, wherein the disease is selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system

atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease.

19. The oligonucleotide or pharmaceutical composition for use according to any one of embodiments 16 to 18, wherein the oligonucleotide and/or the pharmaceutical composition is for local or systemic administration.

20. A method of preventing and/or treating a human disease comprising administering a therapeutically effective amount of an oligonucleotide according to any one of claims 1 to 13 or a pharmaceutical composition according to any one of embodiments 14 or 15.

21. The method of embodiment 20, wherein said human disease is selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease.

22. The method of embodiment 20 or 21, wherein said oligonucleotide or pharmaceutical composition is administered locally or systemically.

## Claims

1. An oligonucleotide comprising 10 to 25 nucleotides, wherein the sequence of nucleotides of the oligonucleotide is at least 80 to 90 % complementary to a corresponding region of a LRRK2 nucleic acid sequence and wherein at least one nucleotide is modified and the modification selected from a modified sugar and optionally a modified internucleoside linkage.

2. The oligonucleotide according to claim 1, wherein the LRRK2 nucleic acid is mRNA of leucine-rich repeat kinase 2 (LRRK2) of SEQ ID NO.1 and/or pre-mRNA of LRRK2 of SEQ ID NO.2 and/or a fragment thereof.

3. The oligonucleotide according to claim 1 or 2, wherein the modification is selected from the group consisting of LNA, ENA, cET, a 2'Fluoro modified nucleotide, a 2´O-Methyl modified nucleotide, a 2´O-Methoxy modified nucleotide, a FANA and a combination thereof.

4. The oligonucleotide according to any one of claims 1 to 3, wherein the modification is located in a sequence of at least 3 nucleotides or at least 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide.

5. The oligonucleotide according to any one of claims 1 to 4, wherein the modification is located in a sequence of 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide.

6. The oligonucleotide comprising 10 to 25 nucleotides according to claim 1, at least one nucleotide having a bridged nucleic acid modification selected from the group consisting of LNA, ENA, cET, a 2'Fluoro modified nucleotide, a 2´O-Methyl modified nucleotide, a 2´O-Methoxy modified nucleotide, a FANA and a combination thereof, wherein said modification is located in a sequence of 5 nucleotides of the 5´-end and/or 3´-end of the oligonucleotide and wherein the oligonucleotide hybridizes with a transcript or an mRNA of leucine-rich repeat kinase 2 (LRRK2) of SEQ ID NO.1 and/or with pre-mRNA of LRRK2 of SEQ ID NO.2 and/or a fragment thereof.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the oligonucleotide hybridizes outside a hybridizing active region or within a hybridizing active region of

position 27001 to 27500, position 102001 to 102500, position 80501 to 81000, position 24501 to 25000, position 114001 to 114500, position 92001 to 92500, position 99501 to 100000, position 67001 to 67500, position 15001 to 15500, position 24001 to 24500, position 26501 to 27000, position 79501 to 80000, position 87001 to 87500, position 120501 to 121000, position 142001 to 142500, position 135001 to 135500, position 71001 to 71500, position 140501 to 141000 or a combination thereof.

8. The oligonucleotide according to and one of claims 1 to 7, wherein the oligonucleotide comprises SEQ ID NO.69, SEQ ID NO.210, SEQ ID NO.164, SEQ ID NO.254, SEQ ID NO.222, SEQ ID NO.186, SEQ ID NO.204, SEQ ID NO.142, SEQ ID NO.209, SEQ ID NO.255, SEQ ID NO.45, SEQ ID NO.46, SEQ ID NO.60, SEQ ID NO.66, SEQ ID NO.162, SEQ ID NO.171, SEQ ID NO.224, SEQ ID NO.241, SEQ ID NO.250, SEQ ID NO.149, SEQ ID NO.256, SEQ ID NO.239, or a combination thereof.

9. The oligonucleotide according to any one of claims 1 to 8, wherein the oligonucleotide is selected from the group consisting of

+A*+A*+T*A*C*T*A*C*T*A*T*T*T*G*T*T*+T*+C*+C (A57067Hi; SEQ ID NO.69),

+T*+A*+C*A*A*T*A*T*T*T*A*T*G*G*T*T*+C*+T*+C (A57208Hi; SEQ ID NO.210),

+G*+T*+C*A*T*A*A*G*T*T*G*T*C*A*G*+T*+A*+T (A57162Hi; SEQ ID NO.164),

+G*+A*+C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57252H; SEQ ID NO.254),

+C*+T*+T*T*G*C*T*T*A*T*T*C*G*T*G*+A*+C*+T (A57220Hi; SEQ ID NO.222),

+T*+T*+T*A*T*T*G*C*A*G*T*C*A*T*A*G*+T*+G*+A (A57184Hi; SEQ ID NO.186),

+C*+T*+T*T*G*T*A*A*A*T*G*A*C*G*T*T*+T*+C*+C (A57202Hi; SEQ ID NO.204),

+T*+G*+A*A*A*T*G*T*C*T*A*T*T*A*G*C*+A*+C*+A (A57140Hi, SEQ ID NO.142),

+A*+C*+A*A*T*A*T*T*T*A*T*G*G*T*T*T*C*+T*+C*+A (A57207Hi; SEQ ID NO.209),

+G*+G*+A*C*T*T*C*G*T*T*T*A*A*T*A*C*+C*+A*+G (A57253H; SEQ ID NO.255),

+C*+G*+G*C*T*A*A*A*T*G*T*T*T*C*A*G*+T*+T*+C (A57043Hi; SEQ ID NO.45),

+T*+C*+G*G*C*T*A*A*A*T*G*T*T*T*T*C*+A*+G*+T (A57044Hi; SEQ ID NO.46),

+G*+T*+G*T*A*A*C*T*A*A*G*T*G*A*T*+C*+T*+C (A57058Hi; SEQ ID NO.60),

+G*+A*+T*A*T*T*G*A*C*A*A*C*C*T*G*+C*+T*+G (A57064Hi; SEQ ID NO.66),

+T*+G*+T*G*T*T*A*C*C*A*T*A*T*C*C*A*+T*+T*+T (A57160Hi; SEQ ID NO.162),

+C*+T*+G*T*G*A*C*T*T*T*G*C*A*T*C*A*+A*+C*+T (A57169Hi; SEQ ID NO.171),

+C*+A*+A*T*G*T*A*T*A*C*C*A*T*G*C*+A*+G*+T (A57222Hi; SEQ ID NO.224),

+T*+T*+C*C*T*G*A*T*T*A*T*A*C*C*A*T*+A*+T*+G (A57239Hi; SEQ ID NO.241),

+A*+T*+G*C*T*C*T*T*A*T*C*C*A*C*A*A*+T*+C*+C (A57248Hi; SEQ ID NO.250),

+T*+T*+T*G*A*T*C*T*G*T*A*G*T*A*C*A*+T*+A*+C (A57147Hi; SEQ ID NO.149), +A*+T*+G*G*A*C*T*T*C*G*T*T*T*A*A*T*+A*+C*+C (A57254H; SEQ ID NO.256), +G*+G*+A*C*A*T*G*T*A*T*C*T*T*A*A*T*+A*+G*+T (A57237Hi; SEQ ID NO.239), and a combination thereof, wherein + indicates an LNA nucleotide and * indicates a phosphorothioate (PTO) linkage between the nucleotides.

10. The oligonucleotide according to any one of claims 1 to 9, wherein the oligonucleotide has 80 to 99 %, 85 to 98 %, 90 to 95 or 93 % sequence identity to any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301.

11. The oligonucleotide according to any one of claims 1 to 10, wherein said oligonucleotide comprises at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21 or at least 22 contiguous nucleotides of any one of the oligonucleotides of SEQ ID NO.3 – SEQ ID NO.5301.

12. The oligonucleotide according to any one of claims 1 to 11, wherein the oligonucleotide inhibits the expression of LRRK2, a LRRK2 mRNA, a LRRK2 pre-mRNA or a combination thereof at a nanomolar or micromolar concentration.

13. A pharmaceutical composition comprising an oligonucleotide according to any one of claims 1 to 12 and a pharmaceutically acceptable carrier, excipient, adjuvant, or a combination thereof.

14. The pharmaceutical composition according to claim 13, further comprising a therapeutically active agent.

15. The oligonucleotide according to any one of claims 1 to 12, or the pharmaceutical composition according to claim 13 or 14 for use in a method of preventing and/or treating a human disease such as a neurodegenerative disease.

16. The oligonucleotide or the pharmaceutical composition according to claim 15, wherein the pharmaceutically acceptable carrier, excipient, adjuvant, or a combination thereof, or the therapeutically active agent is administrated separately before or after

delivery of the oligonucleotide, or is administered simultaneously via different delivery methods.

17. The oligonucleotide according to claim 15 or 16, wherein the disease is selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease.

18. The oligonucleotide or pharmaceutical composition for use according to any one of claims 15 to 17, wherein the oligonucleotide and/or the pharmaceutical composition is for local or systemic administration.

19. A method of preventing and/or treating a human disease comprising administering a therapeutically effective amount of an oligonucleotide according to any one of claims 1 to 12 or a pharmaceutical composition according to any one of claims 13 or 14.

20. The method of claim 19, wherein said human disease is selected from the group consisting of Parkinson´s disease (PD), Alzheimer´s disease, Huntington´s disease, amyotrophic lateral sclerosis, multiple sclerosis, multiple system atrophy, dementia with Lewy bodies (DLB), pure autonomic failure (PAF), frontotemporal dementia and prion disease.

21. The method of claim 19 or 20, wherein said oligonucleotide or pharmaceutical composition is administered locally or systemically.