VERIFICATION OF FOOD ORIGIN BASED ON NUCLEIC ACID PATTERN RECOGNITION

BACKGROUND OF THE INVENTION

This invention relates generally to applied genomics methods and, more specifically, to methods for determining the source of a fish sample.

Increased focus has been placed on healthy food, and consumers are increasingly concerned with core issues such as sustainable and environmentally safe harvest and production processes, the use of drugs and feed additives as well as the welfare of the production animals. Governmental authorities, seafood retail traders and consumers presently have no available system to verify whether the production process is in accordance with information provided, whether the product has the origin as claimed or whether, for example, a fillet in the supermarket has the correct brand name.

Seafood operators are becoming increasingly aware of the importance of implementing quality control mechanisms together with traceability systems for the purpose of establishing verifiable substance in order to protect their products and brand names. Similarly, retailers and consumers want to be able to check whether they have received the desired product or brand in accord with the claimed quality.

Presently existing traceability systems are unreliable as they depend on "paper flow" along the value chain to provide information regarding origin; production parameters; processing time, date and environment; and transport. Consequently, there is a need for an authenticity system verifying the origin of products at high speed and low cost.

Several reasons support the need of a genetic online traceability system. First, consumers growing concern with regard to core issues like the health risk of consuming a particular product. Furthermore, consumers are increasingly concerned with whether a product has been subjected to resource and environmentally friendly harvest and production as well as with animal welfare issues. In addition to these consumer demands, recent regulations passed in the United States and the European Union focus on environmentally friendly harvest and production. Significantly, each of the foregoing issues is related to product origin.

Thus, there exists a need for genetic markers that can be used to unambiguously and reliably identify the origin of a fish sample and for methods to efficiently determine the origin of a fish sample using such markers. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF THE INVENTION

According to a first aspect of the present invention, there is provided a method for determining the origin of a sample from any plant and animal species which has a reproduction involving the mating of two parents to produce a set of offspring, comprising:

(a) providing a parent genotype database which contains a collection of candidate parent genotypes each representing a distinct parentage origin by using any type of genetic marker and genotyping technology, and comparing a sample genotype to the parentage genotype database, such that a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample and

(b) providing an origin genotype database encompassing a collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin by using any type of genetic marker and genotyping technology, and comparing a sample genotype to the candidate genotype profiles, wherein a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample; and

(c) providing genetic logistics, which is predicated on the fact that a member of the food value chain receives distinct and identifiable batches of genetic material from the broodstock of origin or from the last multiplier such that a member of the food value chain giving rise to the sample can be identified; and

wherein the parentage of origin and population of origin of the sample together with the logistics information allows tracing a sample back to any stage of the food value chain.

According to a second aspect of the invention, there is provided the method of the first aspect, further comprising sample and candidate parent genotypes belonging to a species selected from the group consisting of rainbow trout, halibut, seabass and Atlantic cod.

According to a third aspect of the invention, there is provided the method of the first aspect, further comprising the initial steps of:

(a) extracting nucleic acid corresponding to each of said distinct populations of origin; and

(b) genotyping the extracted nucleic acid with selected genetic markers to obtain said collection of candidate parent genotypes.

According to a fourth aspect of the invention, there is provided the method as defined above, further comprising identifying said SNPs by performing an oligonucleotide ligation assay (OLA).

According to a fifth aspect of the invention, there is provided the method as defined above, further comprising identifying said SNPS by performing a hubridization assay.

According to a sixth aspect of the invention, there is provided the method of the first aspect, further comprising generating a central database capable of storing said population of candidate parent genotypes.

According to a seventh aspect of the invention, there is provided an apparatus for determining the origin of a sample from any plant and animal species which has a reproduction method involving the mating of two parents to produce a set of offspring, comprising:

(a) a computer readable medium encompassing a parent genotype database that contains a collection of candidate parent genotypes that each represent a distinct parentage origin; and

(b) a computer readable medium encompassing an origin genotype database encompassing a collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin; and

(c) a computer readable medium encompassing genetic logistics, which is predicated on the fact that a member of the food value chain receives distinct and identifiable batches of genetic material from the broodstock of origin or from the last multiplier such that a member of the production system giving rise to the sample can be identified; and

wherein the computer apparatus comprises appropriate hardware, software and/or networking in order to perform the steps of comparing a sample genotype to the parentage genotype database and comparing a sample genotype to the candidate genotype profiles, and the step of verifying the origin of a particular sample or of excluding a particular producer as a potential source of the sample;

wherein, when comparing a sample genotype to the parentage genotype database, a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample; and

wherein, when comparing a sample genotype to the candidate genotype profiles, a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample; and

wherein the parentage of origin and population of origin of the sample together with the logistics information allows tracing a sample back to any stage of the food value chain.

According to an eighth aspect of the invention, there is provided the apparatus as defined above, further comprising sample and candidate parent genotypes belonging to a species selected from the group consisting of rainbow trout, halibut, seabass and Atlantic cod.

Disclosed herein are isolated nucleic acid molecules that encompass a single nucleotide polymorphism (SNP) associated with fish. Disclosed further are isolated nucleic acid molecules that encompass a microsatellite sequence and corresponding primers associated with fish. Disclosed yet further are nucleotide sequences corresponding to Polymerase Chain Reaction (PCR) primers, Oligonucleotide Ligation Assay (OLA) primers. The polymorphism nucleotide sequences and corresponding primers provided by the present invention are described below, designated SEQ ID NOS:1-1377, and set forth in Figures 1 through 9 and 11.

Disclosed further herein is a method of determining the parentage origin of a fish sample by providing a parentage genotype database that contains a collection of candidate parent genotypes that each represent a distinct parentage origin and comparing a sample genotype to the parentage genotype database, such that a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample. Disclosed is also a method of determining the origin of a fish sample by providing an origin genotype database encompassing a

collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin; and comparing a sample genotype to the candidate genotype profiles, wherein a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide sequences of Salmo salar Single Nucleotide Polymorphisms (SNPs) and corresponding OLA primers (SEQ ID NOS: 1-112).

Figure 2 shows the nucleotide sequences of Polymerase Chain Reaction (PCR) primers corresponding to Salmo salar Single Nucleotide Polymorphisms (SNPs) (SEQ ID NOS: 113-154).

Figure 3 shows the nucleotide sequences of Salmo salar microsatellites (SEQ ID NOS: 155-164).

Figure 4 shows the nucleotide sequences of Orechromis niloticus Single Nucleotide Polymorphisms (SNPs) and corresponding OLA and SNP primers (SEQ ID NOS: 165-308).

Figure 5 shows the nucleotide sequences of Orechromis niloticus microsatellites (SEQ ID NOS: 309-367).

Figure 6 shows the nucleotide sequences of Orechromis niloticus polymorphic sites (SEQ ID NOS: 368-373).

Figure 7 shows the nucleotide sequences of Atlantic halibut Single Nucleotide Polymorphism (SNPs) (SEQ ID NOS: 374-409).

Figure 8 shows the nucleotide sequences of cod polymorphic sites (SEQ ID NOS: 410-414).

Figure 9 shows the nucleotide sequences of seabass polymorphic sites (SEQ ID NOS: 415-472).

Figure 10 shows a schematic illustration of the invention method for determining the parentage origin of a fish sample.

Figure 11 shows nucleotide sequences of *Oreochromis niloticus* microsatellites and corresponding primers (SEQ ID NOS: 473-1377).

DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to isolated nucleic acid molecules that encompass a single nucleotide polymorphism (SNP) associated with several distinct species of fish. The present invention further is directed to isolated nucleic acid molecules that encompass a microsatellite sequence associated with several distinct species of fish. Also provided are methods for determining the parentage origin or population of origin of a sample based on matching of genetic markers.

As used herein, the term "fish," refers to organisms falling into one of two groups, "cartilagenous fish" or class *Chondrichthyes* and "bony fish" or class *Osteichthyes* (formerly class name, but still widely used). Most of the modern *Osteichthyes* belong the order *Teleostei*.

In one embodiment, the invention provides an isolated nucleic acid molecule encompassing a single nucleotide polymorphism (SNP), where the isolated nucleic acid molecule is selected from the group set forth in Figure 1, which correspond to the order *Salmoniformes*, family *Salmonidae*, genus *Salmo* and species *Salmo salar*. Also provided are nucleic acid molecules that hybridize to the nucleic acid molecule selected from the group set forth in Figure 1 or its complement under highly stringent hybridization conditions. Figure 1 shows isolated nucleic acid molecules encompassing a single nucleotide polymorphism (SNP) and corresponding OLA primers consecutively designated as SEQ ID NOS: 1-112, which correspond to the order *Salmoniformes*, family *Salmonidae*, genus *Salmo* and species *Salmo salar*. Figure 2 shows isolated nucleic acid molecules that represent PCR primers corresponding to *Salmo salar* single nucleotide polymorphism (SNP) (SEQ ID NOS: 113-154).

As used herein, the term "salmon," refers to organisms belonging to the order *Salmoniformes*, family *Salmonidae*, genus *Salmo* and species *Salmo salar*. All salmonids live in freshwater or migrate into freshwater to spawn in the streams of their origins. Salmo salar is the main species in northern Europe and North America and also the main species of farmed salmon. Worldwide production of farmed salmon has exceeded 800 000 tons per year.

In a further embodiment, the invention provides an isolated nucleic acid molecule encompassing a single nucleotide polymorphism (SNP), where the isolated nucleic acid molecule is selected from the

group set forth in Figure 4, which correspond to the order *Perciformes*, family *Cichlidae*, genus *Oreochromis* and species *Oreochromis niloticus*. Also provided are nucleic acid molecules that hybridize to the nucleic acid molecule selected from the group set forth in Figure 4 or its complement under highly stringent hybridization conditions. Figure 4 shows isolated nucleic acid molecules of the invention encompassing a single nucleotide polymorphism (SNP) as well as corresponding OLA and SNP primer sequences consecutively designated as SEQ ID NOS: 165-308, which correspond to the order *Perciformes*, family *Cichlidae*, genus *Oreochromis* and species *Oreochromis niloticus*. Figure 6 shows further isolated nucleic acid molecules of the invention encompassing a polymorhic nucleotide sequence designated as SEQ ID NOS: 368-373, which also correspond to *Oreochromis niloticus*.

As used herein, the term "tilapia," refers to organisms belonging to the order *Perciformes*, family *Cichlidae*, genus *Oreochromis*. The species *Oreochromis niloticus* is the most common tilapia species in modern aquaculture and the majority of isolated nucleotide sequences set forth herein correspond to this species. Most tilapia species belonging to the genus *Oreochromis* are closely genetically related. Individuals from different tilapia species freely mate with each other, thus making species hybrids that are fertile and often with good production qualities. Furthermore, genetic markers isolated from one tilapia species be used with distinct tilapia species or tilapia hybrids. Therefore, the term "tilapia" refers to organisms belonging to the genus *Oreochromis* in general.

Tilapia are a group of perch-like fishes of the *Cichlidae* family that are native to the freshwaters of tropical Africa and represent one of the most important aquatic species in culture today. World-wide production of tilapia exceeds 1 billion pounds per year and production of tilapia in the United States is increasing rapidly.

The invention provides isolated nucleic acid molecules that encompass a microsatellite sequence associated with several distinct species of fish. In such an embodiment, the invention provides an isolated nucleic acid molecule encompassing a microsatellite sequence, where the isolated nucleic acid molecule is selected from the group set forth in Figure 3 and designated SEQ ID NOS: 155-164, which correspond to the salmon. Also provided are nucleic acid molecules that hybridize to the nucleic acid molecule selected from the group designated SEQ ID NOS: 155-164 or its complement under highly stringent hybridization conditions.

In yet another embodiment, the invention provides an isolated nucleic acid molecule encompassing a microsatellite sequence, where the isolated nucleic acid molecule is selected from the sequences set forth in Figures 5 (SEQ ID NOS: 309-367) and 11, which correspond to the tilapia. Also provided are nucleic acid molecules that hybridize to a microsatellite nucleic acid molecule set forth in Figures 5 and 11, or its complement under highly stringent hybridization conditions. Figure 11 shows isolated nucleic acid molecule encompassing tilapia microsatellite nucleotide

sequences and corresponding primers consecutively designated SEQ ID NOS: 473-1377.

In yet another embodiment, the invention provides an isolated nucleic acid molecule encompassing encompassing a single nucleotide polymorphism (SNP), where the isolated nucleic acid molecule has a nucleotide sequence selected from the group designated SEQ ID NOS: 374-409 and set forth in Figure 7, which correspond to halibut.

As used herein, the term "halibut" refers to organisms that belong the order *Pleuronectiformes*, family *Pleuronectidae*, and genus *Hippoglossus* and species *Hippoglossus hippoglossus*, a large saltwater flatfish that can be up to 4 meters in length and is found in the North Atlantic and North Eastern Pacific.

Also provided are nucleic acid molecules that hybridize to the nucleic acid molecule selected from the group designated SEQ ID NOS: 374-409 or its complement under highly stringent hybridization conditions.

In a further embodiment, the invention provides an isolated nucleic acid molecule encompassing a polymorphic sequence, where the isolated nucleic acid molecule has a nucleotide sequence selected from the group designated SEQ ID NOS: 415-472 and shown in Figure 9, which correspond to the seabass. Also provided are a nucleic acid molecules that hybridize to the nucleic acid molecule of selected from the group designated SEQ ID NOS: 415-472, or its complement under highly stringent hybridization conditions.

As used herein, the term "seabass" refers to organisms that belong the order *Perciformes*, the family *Serranidae*, and include the black sea bass *Centropristis*, as well as organisms belonging to the family *Moronidae*, in particular, the European sea bass *Dicentrarchus laborax*.

In another embodiment, the invention provides an isolated nucleic acid molecule encompassing a polymorphic sequence, where the isolated nucleic acid molecule has a nucleotide sequence selected from the group designated SEQ ID NOS: 410-414 and shown in Figure 8, which correspond to cod. Also provided are a nucleic acid molecules that hybridize to the nucleic acid molecule having a nucleotide sequence selected from the group designated SEQ ID NOS: 410-414, or its complement under highly stringent hybridization conditions.

As used herein, the term "cod" refers to the Atlantic cod, which belongs to the order *Gadiformes*, family *Gadidae*, species *Gadus morhua*, and is a saltwater fish found in the North Atlantic above 45° N.

The isolated nucleic acid molecules of the invention encompassing polymorphic nucleotide sequences, including SNPs and microsatellite sequences, as set forth above represent genetic markers that can be used, for example, to genotype fish and are useful as components of a parentage genotype database in the methods of the invention to determine the origin of a fish sample. Furthermore, the invention provides isolated nucleic acid molecules that can be used, for example, as probes to detect the presence of one or more genetic markers in fish samples and in other screening applications known to those skilled in the art.

The invention further is directed to a method of determining the parentage origin of a fish sample by providing a parentage genotype database that contains a collection of candidate parent genotypes, also referred to as candidate origin genotypes, that each represent a distinct parentage origin and comparing a sample genotype to the parentage genotype database, such that a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample.

The ability to identify the parentage origin of a fish sample via the methods provided by the present invention allows for improved quality control mechanisms in commercial aquaculture. Genetic markers, for example, an insertion, deletion, rearrangement, single nucleotide polymorphism (SNP), a microsatellite (MS) or a variable number tandem repeat (VNTR) polymorphism, are important tools that allow identification of the parentage origin using the

methods provided by the invention. The present invention provides the benefit of allowing direct identification of the parentage individuals or origin population rather than indirect identification merely based on the assignment of a sample to a population based on the matching of genetic profiles based on gene frequencies, a traditionally used method based on the statistical guess that an individual with a specific genetic makeup or genotype belongs to a specific population with a specific gene frequency at those loci. In contrast, the invention method establishes parentage by matching offspring or sample genotype with a set of pre-typed panels corresponding to potential parent or origin genotypes. Thus, the present invention represents a significant improvement over traditional identification methods based on population genetics.

The methods of the invention exemplified herein for an origin or parentage determination of a fish sample are equally applicable to a variety of other organisms and biomaterials. A unique aspect of the invention method, in addition to the particular compositions provided by the invention, is the employment of large-scale parentage or origin analysis based on checking a sample genotype against a parentage or origin genotype database and by that be able to determine which parent pair the particular individual originates from. The invention methods distinguish from traditional tracing systems of livestock, for example, cattle, which is based on individually comparing samples with origin candidates rather than by comparison against an exhaustive origin database.

Due to their high biological capacity for reproduction (fecundity), fish provide an especially appropriate target for practicing the methods of the invention. For example, a female salmon breeder can produce up to 10,000 offspring and some shellfishes have millions of offspring. In particular, genotyping a female salmon breeder and its male partner provides the ability to verify the origin of 40 metric tons of seafood. Regardless of the additional benefits conferred upon the methods of the invention by virtue of the fecundity of fish, the methods are nevertheless also applicable to other biomaterials containing nucleic acid based on the genotyping and subsequent establishment of parentage/origin genotype databases and comparison of a sample genotype against such a database.

The invention further provides an isolated nucleic acid molecule having a nucleotide sequence that hybridizes to a nucleic acid molecule encompassing a polymorphic nucleotide sequence, for example, a SNP and microsatellite sequences of the invention, as set forth in Figures 1-9 and 11, or its complement under stringent conditions. In one embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of a salmon SNP set forth in Figure 1, or the complement thereof. Such an oligonucleotide is able to specifically hybridize to a complementary nucleic acid molecule under highly stringent hybridization conditions.

Further provided are isolated oligonucleotides containing at least 17 contiguous nucleotides of a SNP-containing nucleic acid molecule

or of its complement. Also provided are isolated oligonucleotides containing at least 17 contiguous nucleotides of a microsatellite sequence-containing nucleic acid molecule or of its complement. An isolated oligonucleotide can thus contain at least 18, 19, 20, 22, or at least 25 contiguous nucleotides, such as at least 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 350, 400, 500, 600, 700, 800 or more contiguous nucleotides from the reference nucleotide sequence, up to the full length sequence. An invention oligonucleotide can be single or double stranded, and represent the sense or antisense strand.

In one embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of an isolated nucleic acid molecule encompassing a salmon single nucleotide polymorphism (SNP) as described above and set forth in Figure 1, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides an isolated nucleic acid molecule encompassing a tilapia single nucleotide polymorphism (SNP) as described above and set forth in Figures 4 and 6, or the complement thereof. Such oligonucleotides are able to specifically hybridize to a polymorphic nucleic acid molecule of the invention under highly stringent hybridization conditions.

In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the microsatellite sequence-containing nucleic acid molecule designated SEQ ID 155-164, or the complement thereof. The invention also provides an isolated oligonucleotide containing at least 17

contiguous nucleotides of the microsatellite sequence-containing nucleic acid molecule designated SEQ ID 309-367, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the microsatellite sequence-containing nucleic acid molecules set forth in Figure 11 (along with corresponding primers) and consecutively designated SEQ ID NOS: 473-1377, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the polymorphic sequence-containing nucleic acid molecule designated SEQ ID NOS: 368-373, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the polymorphic sequence-containing nucleic acid molecule designated SEQ ID NOS: 374-409, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the polymorphic sequence-containing nucleic acid molecule designated SEQ ID NOS: 410-414, or the complement thereof. In a further embodiment, the isolated oligonucleotide comprises at least 17 contiguous nucleotides of the polymorphic sequence-containing nucleic acid molecule designated SEQ ID NOS: 415-472, or the complement thereof. Such oligonucleotides are able to specifically hybridize to a microsatellite sequence-containing nucleic acid molecule under highly stringent hybridization conditions.

The invention oligonucleotides can be advantageously used, for example, as probes to detect polymorphic nucleotide sequence-containing nucleic acid molecules, for example SNP-containing and

microsatellite sequence-containing nucleic acid molecules in a sample; as sequencing or PCR primers; or in other applications known to those skilled in the art in which hybridization to a SNP-containing nucleic acid molecule and a microsatellite sequence-containing nucleic acid molecule is desirable.

In one embodiment, the invention provides a primer pair containing an isolated oligonucleotide containing at least 17 contiguous nucleotides of a SNP-containing nucleic acid molecule and an isolated nucleic acid molecule containing at least 17 contiguous nucleotides of the complement of a SNP-containing nucleic acid molecule of the invention. In a further embodiment, the invention provides a primer pair containing an isolated oligonucleotide containing at least 17 contiguous nucleotides of a microsatellite sequence-containing nucleic acid molecule and an isolated nucleic acid molecule containing at least 17 contiguous nucleotides of the complement of a microsatellite sequence-containing nucleic acid molecule of the invention. The primer pairs provided by the invention can be used, for example, to amplify a nucleic acid molecule by the polymerase chain reaction (PCR). The skilled person can determine an appropriate primer length and sequence composition for the intended application.

The present invention further provides isolated nucleic acid molecules encompassing a microsatellite sequence associated with tilapia and set forth as SEQ ID NOS: 309-367 and, set forth along with corresponding primers and consecutively designated as SEQ ID NOS: 473-1377; isolated nucleic acid molecules

encompassing a microsatellite sequence associated with Atlantic salmon and set forth as SEQ ID NOS: 155-164; isolated nucleic acid molecules encompassing a polymorphic nucleotide sequence associated with halibut and set forth as SEQ ID NOS: 374-409; isolated nucleic acid molecules encompassing a polymorphic nucleotide sequence associated with cod and set forth as SEQ ID NOS: 410-414; and isolated nucleic acid molecules encompassing a polymorphic nucleotide sequence associated with seabass and set forth as SEQ ID NOS: 415-472. The isolated nucleic acid molecules designated SEQ ID NOS: 155-164, 309-367, 374-472 and those shown in Figure 11 along with corresponding primers (SEQ ID NOS: 473-1377) encompass polymorphic nucleotide sequences of the above-named species. The invention further provides oligonucleotides that hybridize to the nucleotide sequences of the nucleic acid molecules designated SEQ ID NOS: 155-164, 309-367, 374-472 and those nucleic acid molecules shown in Figure 11 that correspond to microsatellite sequences, which are consecutively designated with their corresponding primers as SEQ ID NOS: 473-1377.

The term "isolated," in reference to an invention nucleic acid molecule is intended to mean that the molecule is substantially removed or separated from components with which it is naturally associated, or is otherwise modified by the hand of man, thereby excluding nucleic acid molecules as they exist in nature.

The term "nucleic acid molecule," as used herein, refers to an oligonucleotide or polynucleotide of natural or synthetic origin. A nucleic acid

molecule can be single- or double-stranded genomic DNA, cDNA or RNA, and can represent the sense strand, the antisense strand, or both. A nucleic acid molecule can include one or more non-native nucleotides, having, for example, modifications to the base, the sugar, or the phosphate portion, or having a modified phosphodiester linkage. Such modifications can be advantageous in increasing the stability of the nucleic acid molecule. Furthermore, a nucleic acid molecule can include, for example, a detectable moiety, such as a radiolabel, a fluorochrome, a ferromagnetic substance, a luminescent tag or a detectable binding agent such as biotin. Such modifications can be advantageous in applications where detection of a hybridizing nucleic acid molecule is desired.

As used herein, a "probe" or "oligonucleotide" is single-stranded or double-stranded DNA or RNA, or analogs thereof, that has a sequence of nucleotides that includes at least 15, at least 20, at least 50, at least 100, at least 200, at least 300, at least 400, or at least 500 contiguous bases that are the same as, or the complement of, any contiguous bases set forth in any of SEQ ID NOS: 1-1377. Oligonucleotides are useful, for example, as probes or as primers for amplification reactions such as the polymerase chain reaction (PCR). In addition, oligonucleotides can bind to the sense or anti-sense strands of other nucleic acids. Preferred regions from which to construct a probe include those nucleic acid sequences that contain the SNP or a microsatellite. Probes can be labeled by methods well-known in the art, as described hereinafter, and used in various diagnostic kits.

As used herein, the term "single nucleotide polymorphism" or "SNP" is intended to mean a difference in nucleotide sequence between two related nucleic acid molecules of one nucleotide at a specified position. The term refers to a nucleotide substitution at a particular position compared to an otherwise identical nucleic acid sequence at adjacent nucleotide positions. Therefore, the term refers to a relative difference in primary structure between two compared nucleic acid molecules that are substantially related.

As used herein, the term "microsatellite" or "microsatellite sequence" is intended to refer to a tandem repeat sequence that is either present or varies in length at a particular position compared to an otherwise identical nucleic acid sequence at the same nucleotide positions.

The term "polymorphic" as used herein to a nucleotide sequence of the invention is intended to refer any variation in nucleotide sequence between two related nuclear acid molecules and is meant to encompass both SNPs and microsatellites.

Eucaryotic genomes contain a large number of single nucleotide polymorphisms, which make it easy to look for allelic versions of a gene by sequencing samples of the gene taken from different members of a population or from a heterozygous individual. Similarly, eucaryotic genomes contain a large number of interspersed simple tandem repeat sequences, designated microsatellites, which vary in length among individuals. SNPs and microsatellites represent

highly informative polymorphic markers that can be typed, for example, using the polymerase chain reaction (PCR). Such polymorphic sequence variants further can be detected using the oligonucleotide ligation assay (OLA) as described in Example 2, or other appropriate detection method known in the art.

The invention nucleic acid molecules and oligonucleotides can be advantageously used, for example, as probes to detect nucleic acid molecules encompassing a particular single nucleotide polymorphism in a sample; as probes to detect nucleic acid molecules encompassing a particular microsatellite sequence in a sample; as sequencing or PCR primers; or in other applications known to those skilled in the art in which hybridization to an invention nucleic acid molecule is desirable.

Hybridization refers to the binding of complementary strands of nucleic acid, for example, sense:antisense strands or probe:target-DNA, to each other through hydrogen bonds, similar to the bonds that naturally occur in chromosomal DNA. Stringency levels used to hybridize a given probe with target-DNA can be readily varied by those of skill in the art.

Stringent hybridization are conditions under which polynucleic acid hybrids are stable. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_m) of the hybrids. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the hybridization reaction is performed under conditions of lower stringency, followed by

washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions.

Specific hybridization refers to the ability of a nucleic acid molecule to hybridize to the reference nucleic acid molecule without hybridization under the same conditions with nucleic acid molecules that are not the reference molecule. Under moderately stringent hybridization conditions the hybridized nucleic acids will generally have at least about 60% identity, at least about 75% identity, more at least about 85% identity; or at least about 90% identity. Moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.2X SSPE, 0.2% SDS, at 42°C. In contrast, high stringency hybridization conditions can be provided, for example, by hybridization in 50% formamide, 5X Denhart's solution, 5X SSPE, 0.2% SDS at 42°C, followed by washing in 0.1X SSPE, and 0.1% SDS at 65°C. Low stringency hybridization conditions include hybridization in 10% formamide, 5X Denhart's solution, 6X SSPE, 0.2% SDS at 22°C, followed by washing in 1X SSPE, 0.2% SDS, at 37°C. Denhart's solution contains 1% Ficoll, 1% polyvinylpyrolidone, and 1% bovine serum albumin (BSA). 20X SSPE (sodium chloride, sodium phosphate, ethylene diamide tetraacetic acid (EDTA)) contains 3M sodium chloride, 0.2M sodium phosphate, and 0.025 M (EDTA). Other suitable moderately stringent and highly stringent hybridization buffers and conditions are well known to those of skill in the art and are described, for example, in Sambrook et al.,

Molecular Cloning: A Laboratory Manual, 3rd ed., Cold Spring Harbor Press, Plainview, New York (2001) and in Ausubel et al. (Current Protocols in Molecular Biology (Supplement 47), John Wiley & Sons, New York (1999)).

Nucleic acid molecules of the invention hybridize under moderately stringent or highly stringent conditions to substantially the entire sequence, or substantial portions, for example, typically at least 15, 17, 21, 25, 30, 40, 50 or more nucleotides of the nucleic acid sequence set forth in SEQ ID NOS: 1-1377.

An invention nucleic acid molecule or oligonucleotide containing a single nucleotide polymorphism or a microsatellite sequence can further contain nucleotide additions or additional nucleotide sequences including, for example, sequences that facilitate identification of the oligonucleotide.

The invention also provides an isolated nucleic acid probe that specifically hybridizes to and detects a polymorphic nucleic acid sequence of the invention, wherein the polymorphic nucleic acid sequence is selected from nucleic acid molecules set forth, along with corresponding primers, in Figures 1-9 and 11 and designated SEQ ID NOS: 1-1377. Therefore, the invention provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a SNP or microsatellite sequence as described herein. An isolated nucleic acid probe of the invention contains at least approximately 17 contiguous nucleotides of the complement of a polymorphic nucleic acid molecule of the invention.

The probe can be used, for example, to detect the presence of a SNP-containing nucleic acid molecule in a sample. The skilled person can determine an appropriate probe length and sequence composition for the intended application.

The invention provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a SNP, wherein the nucleic acid sequence is selected from the group shown in Figure 1 along with primer sequences as SEQ ID NOS: 1-112. The invention further provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a SNP, wherein the nucleic acid sequence is selected the group shown in Figure 4 along with primer sequences as SEQ ID NOS: 165-308. The invention further provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a SNP, wherein the nucleic acid sequence is selected the group shown in Figure 7 and designated SEQ ID NOS: 374-409.

The invention further provides an isolated nucleic acid probe that specifically hybridizes to and detects a polymorphic nucleic acid sequence, wherein the nucleic acid sequence is selected the group shown in Figures 6, 8 and 9; set forth as SEQ ID NOS: 368-373 and 410-472. The invention also provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a microsatellite sequence, wherein the nucleic acid sequence is selected from the group shown in Figures 3 and 5; set forth as SEQ ID NOS:155-164 and 309-367.

The invention further provides an isolated nucleic acid probe that specifically hybridizes to and detects nucleic acid sequence encompassing a microsatellite sequence, wherein the nucleic acid sequence is selected the group shown in Figure 11 along with primer sequences as SEQ ID NOS: 473-1377. As described herein, an isolated nucleic acid probe of the invention contains at least approximately 17 contiguous nucleotides of the complement of a SNP-containing nucleic acid molecule of the invention or a microsatellite-containing nucleic acid molecule of the invention. The probe can be used, for example, to detect the presence of a SNP-containing nucleic acid molecule or a microsatellite-containing nucleic acid molecule in a sample. The skilled person can determine an appropriate probe length and sequence composition for the intended application.

An isolated nucleic acid molecule or oligonucleotide of the invention can be produced or isolated by methods known in the art. The method chosen will depend, for example, on the type of nucleic acid molecule one intends to isolate. Those skilled in the art, based on knowledge of the nucleotide sequences disclosed herein, can readily isolate the isolated nucleic acid molecules as genomic DNA; as full-length cDNA or desired fragments therefrom; or as full-length mRNA or desired fragments therefrom, by methods known in the art.

An invention nucleic acid molecule does not consist of the exact sequence of a nucleotide sequence set forth in publically available databases, such as Expressed Sequence Tags (ESTs), Sequence Tagged Sites

(STSs) and genomic fragments, deposited in public databases such as the nr, dbest, dbsts and gss databases, and TIGR, SANGER center, WUST1 and DOE databases.

One useful method for producing an isolated nucleic acid molecule of the invention involves amplification of the nucleic acid molecule using the polymerase chain reaction (PCR) and specific primers and, optionally, purification of the resulting product by gel electrophoresis. Either PCR or reverse-transcription PCR (RT-PCR) can be used to produce a nucleic acid molecule having any desired nucleotide boundaries. Desired modifications to the nucleic acid sequence can also be introduced by choosing an appropriate primer with one or more additions, deletions or substitutions. Such nucleic acid molecules can be amplified exponentially starting from as little as a single gene or mRNA copy, from any cell, tissue or species of interest.

Furthermore, an isolated nucleic acid molecule or oligonucleotide of the invention can be produced by synthetic means. For example, a single strand of a nucleic acid molecule can be chemically synthesized in one piece, or in several pieces, by automated synthesis methods known in the art. The complementary strand can likewise be synthesized in one or more pieces, and a double-stranded molecule made by annealing the complementary strands. Direct synthesis is particularly advantageous for producing relatively short molecules, such as oligonucleotide probes and primers, and nucleic acid molecules containing modified nucleotides or linkages.

Genetic markers, for example, an insertion, deletion, rearrangement, SNP, microsatellite or variable number tandem repeat (VNTR) polymorphism, are important tools that allow identification of the parentage origin using the methods provided by the invention. For example, the presence in a fish sample of a nucleic acid molecule of the invention containing a polymorphic nucleotide sequence, for example, a SNP or a microsatellite sequence is indicative of the origin of the sample. Thus, the invention provides methods for detecting a nucleic acid molecule containing a SNP or a microsatellite in a fish sample. This information can be useful, for example, to determine the origin of the fish sample.

In one embodiment, the method is practiced by contacting a sample containing nucleic acids with one or more oligonucleotides containing contiguous sequences from a SNP-containing nucleic acid molecule of the invention, under high stringency hybridization conditions, and detecting a nucleic acid molecule that hybridizes to the oligonucleotide. In an alternative embodiment the method is practiced by contacting a fish sample with a primer pair suitable for amplifying a SNP-containing nucleic acid molecule of the invention, amplifying a nucleic acid molecule using polymerase chain reaction, and detecting the amplification.

As used herein, the term "sample" is intended to mean any biological fluid, cell, tissue, organ or portion thereof, or any environmental sample (e.g. soil, food, water, effluent and the like) that contains or potentially contains a SNP-containing nucleic acid

molecule of the invention. For example, a sample can be an egg, a section obtained from a commercially sold fish filet, breeder, smelt, slaughtered fish, or can be a subcellular fraction or extract, or a crude or substantially pure nucleic acid preparation. A sample can be prepared by methods known in the art suitable for the particular format of the detection method employed. A sample can correspond to an individual fish or can correspond to more than one individual.

The methods of detecting a nucleic acid molecule in a sample can be either qualitative or quantitative, and can detect the presence, abundance, integrity or structure of the nucleic acid molecule as desired for a particular application. Suitable hybridization-based assay methods include, for example, *in situ* hybridization, which can be used to detect altered chromosomal location of the nucleic acid molecule, altered gene copy number, and RNA abundance, depending on the assay format used. Other hybridization methods include, for example, Northern blots and RNase protection assays, which can be used to determine the abundance and integrity of different RNA splice variants, and Southern blots, which can be used to determine the copy number and integrity of DNA. A hybridization probe can be labeled with any suitable detectable moiety, such as a radioisotope, fluorochrome, chemiluminescent marker, biotin, or other detectable moiety known in the art that is detectable by analytical methods.

Suitable amplification-based detection methods are also well known in the art, and include, for example, qualitative or quantitative polymerase

chain reaction (PCR); reverse-transcription PCR (RT-PCR); single strand conformational polymorphism (SSCP) analysis, which can readily identify a single point mutation in DNA based on differences in the secondary structure of single-strand DNA that produce an altered electrophoretic mobility upon non-denaturing gel electrophoresis.

The invention also provides a method of determining the origin of a fish sample by providing a parentage genotype database encompassing a collection of candidate parent genotypes, wherein each of the candidate parent genotypes represents a distinct parent; and comparing a sample genotype to the parentage genotype database, wherein a match between the sample genotype and one of the candidate parent genotypes or the genotype of each of the two individuals in a parent pair identifies the origin of the sample.

In a related but distinct embodiment, the invention provides a method of determining the origin of a fish sample by providing an origin genotype database encompassing a collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin; and comparing a sample genotype to the candidate genotype profiles, wherein a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample.

The terms "parentage genotype database" and "origin genotype database" as used herein, refer to a

compilation of a collection of nucleotide sequences corresponding to candidate parent genotypes or candidate genotype profiles, respectively, in a centralized location that is capable of being searched with a sample gentoype to determine a match.

As used herein, the terms "candidate parent genotype" and "candidate origin genotype," refer to the individual components of the collection that make up the "parentage genotype database" or "origin genotype database," respectively. The concept of an origin versus a parent can be used to include the situation where the database includes individuals removed by more than one generation as well as to include other databases encompassing genotypes that do not correspond to parent components, for example, those comprised of biomaterials not capable of sexual reproduction. In addition, an origin genotype consist of a profile or panel that reflects a genetically unique set of markers corresponding to a specific population or batch rather than an individual parent as is desired in those embodiments where the method is practiced to identify, for example, a sample, for example, a fingerling, with regard to a distinct genetic combination of potential parents. The unique spectrum of genetic profiles created by a particular parent population or population of origin can thus be used to trace a sample to a specific producer.

As used herein, the term "origin" refers to the source that is identified by matching the genotype of a sample to a collection of candidate genotypes consisting of, for example, individual candidate parent genotypes or candidate genotype profiles/panels. As

described herein, in certain embodiments of the invention it is desirable to identify the originating broodstock in a strict parentage test, while in other embodiments the invention methods can be utilized to match a candidate to a population of origin or batch of origin that is represented by a genotype profile or panel that collectively reflects a group of individual parents.

The parentage or origin genotype database encompasses a collection of candidate parent or origin genotypes, which can be established through genetic markers known in the art and described herein, for example, those represented by the SNPs and microsatellite sequences encompassed in the nucleic acid molecules provided by the invention. The genetic markers are sufficient to distinguish one of the candidate parent genotypes from other candidate parent genotypes in the database. The parentage genotype database can comprise genotypes of 2 or more, 3 or more, 5 or more, 10 or more, 20 or more, 50 or more, 100 or more, 200 or more, 500 or more, 1000 or more, 2000 or more, 5000 or more, or 10,000 or more, 15,000 or more, 30,00 or more, or 60,000 or more candidate parents. In addition, the number of genetic markers required to obtain the required statistical power to practice the methods of the invention depends on a variety of factors, including, the desired application of the method, the allele frequency of the marker, and the size of the collection encompassing the database. It is contemplated that at least 30 or more, at least 40 or more, at least 50 or more, at least 60 or more, at least 70 or more, at least 80 or more, at least 90 or more, at least 100 or more, at least 120 or more

SNPs must be typed in methods for assigning a parent pair via the invention methods. In addition, it is estimated that at least 5 or more, at least 10 or more, at least 20 or more, at least 40 or more microsatellite markers can be typed in methods for assigning an individual to a parent pair via the invention methods. It is understood that the number of markers necessary can based on the particular parameters provided by the breeding and production organization, for example, different numbers of families in the production units.

In a preferred embodiment, the parentage genotype database is exhaustive, which means it can include all of the candidate parent or origin genotypes that potentially could represent the parental origin of a sample. For example, a parentage genotype database can include genotypes of substantially all of the parents from each hatchery that provides fingerlings. The number of candidate parent or origin genotypes in a parentage genotype database will depend on the needs of the user and will vary depending on the source of the sample to be identified, the availability of access to candidate parent or origin genotypes and the complexity of genetic markers expressed in the sample.

The parentage or origin genotype database can be directed to a candidate parent or origin genotypes of a single species or can contain representative genotypes corresponding to a variety of potential origin species, for example, cod and tilapia, as desired. Species specific markers may be used in order to verify or test whether a food sample or individual sample represents the species that the sample is sold or marketed as.

In one embodiment, the invention can be practiced to verify species origin. In this regard, the total result of genotyping of a sample with a high number of markers can be used to verify that the sample belongs to a species based on predetermined information regarding markers, which can be supplied, for example, by the producer. Although a proportion markers may correspond more than one species, differences in the number of alleles, allele sizes and allele frequencies can be used to distinguish between species.

Furthermore, if desired by the user, the candidate parent or origin genotypes can represent, for example, two populations such as farm raised salmon and wild salmon and the invention used to assign a sample to one of these candidate populations of origin rather than to a particular parent pair.

Thus, the invention provides a parentage or origin genotype database encompassing a collection of candidate parent or origin genotypes. The candidate parent or origin genotypes can be constructed by a variety of genotyping methods known those skilled in the art and described herein, for example, using genetic markers provided by the present invention.

It is contemplated that the parentage genotype database can encompass genotypes of existing broodstock and can be a complete collection of all broodstock genotypes. It is contemplated that the highest possible number of breeders from the hatcheries supplying samples is genotyped for inclusion in the parentage genotype database. In addition to genotyping

broodstock and for optional inclusion into the parentage genotype database, it is further contemplated that genotyping can also be performed for a representative number of individuals from a farm when smelt are introduced or fish are harvested for slaughter. Thus, in the methods of the invention a parentage genotype database can be a partial or complete collection of candidate parent or origin genotypes corresponding to a desired population of potential parents. Once determined, the sample genotype can be compared to the parentage origin database.

It is understood that the methods provided by the invention enable the user to trace back not only to the individual genetic origin, for example, as defined by broodstock, breeding nucleus or hatchery, but also can be used to trace a sample back to any level desired throughout the food value chain by selecting the appropriate markers. This embodiment of the invention, which also can be described as optimized genetic logistics or genetic flow control, is predicated on the fact that a member of the production system, for example, a farmer receives distinct and identifiable batches of genetic material from the broodstock of origin or from the last multiplier providing seeds to the farmer such that the parents giving rise to the sample can be identified, typed and used to establish a genotype profile or panel. In particular, although a farmer may share genetic material with other farmers, each farmer receives a unique set of fingerlings originating from a distinct combination of parents that do not give rise to offspring in other farms - if the distribution from the hatcheries is organized optimally

. Therefore, the provider of fingerlings, generally the hatchery, can collect and type DNA corresponding to different sets of parents that will give rise to specific batches of offspring targeting different farmers. In this embodiment of the invention methods, not only the brood stock profile as defined by its parentage genotype collection will be unique, but every farmed fish population or batch will be assigned a unique genetic origin genotype profile or panel that allows tracing the population of origin.

The methods of the invention for determining the origin of a fish sample by providing an origin genotype database encompassing a collection of candidate genotype profiles or panels further enable an individual producer or entity within the commercial chain, for example, a farmer, to collect tissue from a representative number of the fish traded, for example, to be traded at the wholesale level, and establish a "biobank," which is another term for an origin genotype database that encompasses a collection of candidate genotype profiles. Once established, the biobank can be accessed to either verify the origin of a particular sample or exclude the corresponding producer as a potential source of the sample, for example, in situations of pathogen contamination, irregular or illegal acts.

Thus, as described herein, the invention methods allow for tracing a food sample back virtually to any level of the commercial chain by utilizing unique genetic markers and instant verification technology against a comprehensive or exhaustive database. The methods involve parentage or origin

tests at different levels and can further be combined with other methods known in the art, for example, matching of genetic profiles based on gene frequencies, a method that relies on the statistical likelihood that an individual with a specific genetic makeup or genotype belongs to a specific population with a specific gene frequency at those loci. By comparison, the invention methods identify origin or parentage on the basis of direct matching of the offspring or sample genotype with a collection of genotypes that represent individual parentage or genotype profiles or panel reflecting a unique population of origin. A biobank further can encompass mitochondrial genetic markers that are useful in the methods for identifying parentage or origin based on their maternal inheritance pattern.

The determination of the genotypes corresponding to the sample as well as to the collection of candidate parent or origin genotypes that make up the origin database can be accomplished by a variety of genotyping methods known in the art and described herein and can utilize a variety of genetic markers, including, for example, the particular SNP and microsatellite markers provided by the invention. Thus, a parentage genotype database, which can be constructed to contain a collection of candidate parent or origin genotypes can be accessed by a variety of means to compare a sample genotype and determine its origin/parentage. The determination of the sample genotype can be performed instantaneously, for example, using array or chip technology known in the art and the results can be advantageously transmitted via satellite or via a computer, allowing direct or remote linking to

a central repository containing the origin genotype database by methods disclosed herein.

In a preferred embodiment of the invention method, the genotype determination of the candidate parent or origin genotypes that make up the parentage genotype database is performed via an accurate and fast high-throughput method, for example, a chip-based or gel-based method for detecting poymorphic markers, such as, for example, the SNPs or microsatellite sequences provided by the invention set forth in Figures 1-9 and 11 along with corresponding primer sequences (SEQ ID NOS: 1-1377). Because of the large number of individuals that will be genotyped for inclusion in the parentage genotype database, it is important that the genotyping system employed is appropriate for high-throughput conditions. In particular, genotyping methods that avoid multiple steps and do not require, for example, performance of PCR or electrophoresis are particularly useful for genotyping candidate origin or parent individuals. For example , the Invader™ detection platform, which involves direct hybridization of genomic DNA with differentially labelled SNP-containing probes allows sensitive and accurate detection of SNPs without sample amplification by PCR, as well as other technologies known in the art for fast and accurate high-throughput genotyping are useful in the methods of the invention.

The methods of the invention thus can employ a variety of genotyping methods available for characterization of genetic variation including, for example, techniques based arrays, solution-based, bead-based and gel-based systems, and MALDI-TOF mass

spectrometry. Arrays, which involve binding of the sample molecules to a target on a substrate, can comprise a glass slide, or a semi-solid substrate, such as nitrocellulose membrane and the sample nucleotide sequence can be DNA, RNA, or any permutation thereof. One convenient method for determining the sample genotype involves use of a micoarray.

In contrast to the genotyping of the candidate parent genotypes that make up the parentage genotype database, different criteria are of importance in the selection of a genotyping method for the sample. As described herein, the methods of the invention can involve remote methods in which the step of determining the sample genotype is physically separated from the step of comparing the sample genotype to the parentage genotype database. For example, the sample genotyping can be performed by an individual with a low level expertise at a remote location, such as a warehouse, store, or anywhere along the commercial chain. Therefore, it is understood that the sample genotyping is approriately performed via a reliable, robust and relatively simple methodology, for example, a chip technology such as the Motorola eSensor™ DNA chip system. It is contemplated that capturing probes for the SNPs, for example, nucleic acid molecules of the invention as described herein, are placed at the surface of the chip and hybridized to a pool of PCR products representing the profiling nucleic acid molecules. Subsequently, a second hybridization can be performed using differentially labelled probes, for example, oligonucleotide probes provided by the present invention and described herein. Upon application of a slight voltage to the chip, electronic signals will

communicate the particular SNPs detected in the sample and, thereby, the sample genotype.

As described herein, the methods of the invention can be used in direct methods performed at any point along the production line between hatchery and consumer. Therefore, the sample can be an egg as well as a filet sample corresponding to a findling or any other sample appropriate for gentoyping. The nucleic acid material to be genotyped can be extracted by any method desired by the user including, for example, automated extraction using a commercially available isolation robot. In a preferred embodiment, the methods of the invention can be used in remote methods in which the step of determining the sample genotype is physically separated from the step of comparing the sample genotype to the parentage genotype database. For example, the sample genotyping can be performed by a sales employee at a remote location, such as a warehouse, store, or anywhere along the commercial chain, and the comparison step performed instantaneously at a different location by conveniently interfacing the remote locations via a network such as the internet.

Once a sample genotype has been determined it is contemplated that origin determination can be performed instantenously. If desired, a parentage genotype database can be conveniently stored on a computer readable medium. Accordingly, the invention provides a computer readable medium encompassing an parentage genotype database, for example, an exhaustive collection of candidate parent or origin genotypes. Such a computer readable medium encompassing a

parentage genotype database is useful for comparing the sample gentype with the candidate parent or origin genotypes, which can be conveniently performed on a computer apparatus. The use of a computer apparatus is convenient since a parentage genotype database can be conveniently stored and accessed for comparison to the genotype of a sample. A parentage genotype database can be conveniently accessed using appropriate hardware, software, and/or networking, for example, using hardware interfaced with networks, including the internet. By using various hardware, software and network combinations, the methods of the invention including the step of comparing the genotype of a sample to a parentage genotype database can be conveniently performed in a variety of configurations. Accordingly, the invention additionally provides a computer apparatus for carrying out computer executable steps corresponding to steps of invention methods. For example, a single computer apparatus can contain instructions for carrying out the computer executable step(s) of comparing the genotype determined for a sample to a parentage genotype database, and instructions for determining whether the sample genotype corresponds to one or more of the candidate parent or origin genotypes in the parentage genotype database.

Alternatively, the computer apparatus can contain instructions for carrying out the steps of an invention method while the parentage genotype database is stored on a separate medium. In addition, instructions for determining whether a sample genotype corresponds to candidate parent or origin genotypes in the parentage genotype database can be contained on a

separate computer apparatus or separate medium, or combined with the computer apparatus containing the computer executable steps of the method and/or the database on a separate medium. Such a separate computer readable medium can be another computer apparatus, a storage medium such as a floppy disk, Zip disk or a server such as a file-server, which can be accessed by a carrier wave such as an electromagnetic carrier wave. Thus, a computer apparatus containing a parentage genotype database or a file-server on which the parentage genotype database is stored can be remotely accessed, for example, via a satellite or via a network such as the internet. One skilled in the art will know or can readily determine appropriate hardware, software or network interfaces that allow interconnection of an invention computer apparatus.

A parentage genotype database useful in the methods of the invention is interactive and capable of being updated with additional candidate parent or origin genotypes. It further is contemplated that the database includes the appropriate software providing statistical algorithms that can be implemented directly to compare the sample genotype to the collection of candidate parent gentoypes without having to resort to transferring data to a further location. Routines for the estimation of likelihood of origin of a sample are well known in the art and include, for example, Maximum Likelihood, Quasi-Maximum Likelihood and Generalized Method of Moments.

While the invention method is exemplified for fish species and fish/seafood products, those skilled in the art will appreciate that the methods provided by

the invention are applicable to identify other species by genotyping samples and comparison of the sample genotypes with genotypes of potential parents. Thus, the invention method is applicable to plant and animal species that have a reproduction method similar to, for example, tilapia, salmon and other fish species, in particular, involving the mating of two parents in order to produce a set of offspring.

It is understood that modifications which do not substantially affect the activity of the various embodiments of this invention are also included within the definition of the invention provided herein. Accordingly, the following examples are intended to illustrate but not limit the present invention.

Example I

Isolation of SNP markers from Salmon and Tilapia

This example describes isolation of genomic DNA containing SNP markers from an Atlantic salmon (*Salmo salar*) individual and a Nile tilapia (*Oreochromis niloticus*) individual.

Two genomic libraries, one for tilapia and one for salmon were constructed using the following procedure. The genomic DNA was digested with restriction enzyme Sau 3A (Gibco BRL) followed by electrophoresis in a 1% TBE agarose gel. Using 1Kb DNA size ladder (Amersham Pharmacia), DNA fragments of the size range 900 - 1100 bp were excised from the gel and isolated using QIAquick Gel extraction kit (Qiagen). The isolated DNA fragments were then ligated to Ready-

to-Go pUC18 (Amersham Pharmacia), linearized with BamHI, BAP treated and formulated with T4 DNA ligase, followed by transformation into *E. coli* Pack Gold supercompetent cells (Stratagene). Cells from the libraries were grown on LA amp agar plates and clones were picked at random and cultured over night in LB medium. Plasmids were then isolated using QIAprep Spin Miniprep kit (Qiagen) followed by sequencing of the clone insert using standard M13 forward and reverse sequencing primers and Big Dye Terminator Sequencing kit (ABI).

Primers for PCR were designed from the insert sequences seeking to obtain as large amplicons as possible and with a minimum length of 400 bp using the *Primer3* software (http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi). Primers were ordered from and synthesized at MWG, Germany, and an additional M13 forward (5'- TGT AAA ACG ACG GCC AGT -3') or reverse (5'- CAG GAA ACA GCT ATG ACC - 3') sequence was added to the 5'end of each forward and reverse prime respectively in each PCR primer pair in order to simplify subsequent sequencing efforts.

Using the PCR primers described above amplicons were produced from six DNA samples: individually genomic DNA samples from five unrelated fishes as well as a sample of pooled DNA from 20 fish. The PCR reaction took place in a total volume of 20 µl, consisting of 100 ng DNA, 5 pmol of each primer, 2 µl dNTP (2mM), 2 µl 10xPCR buffer (supplied by ABI optimized for the enzyme), 0.2 µl Ampli-taq polymerase (ABI). Temperature cycling was performed with an

initial denaturation step of 95 °C for 3 minutes, then 12 cycles of 95 °C for 30 seconds each, 58 °C for 30 seconds and 72°C for 30 seconds, then 25 cycles at 95°C for 30 seconds each and 68°C for 1 minute. Amplification was performed on a GeneAmp 9600 from ABI.

Subsequent to performance of the PCR, 3.6 µl PCR-product was mixed with 0.7 µl Exonuclease I (10U/µl Amersham) and 0.7 µl Shrimp Alkaline Phosphatase (2U/µl Amersham) and incubated at 37°C for 15 min followed by 80°C for 15 minutes.

The purified PCR segments were sequenced with the Big Dye Terminator-kit from ABI following the supplied recommended protocol, with standard M13 forward and reverse primers matching the respective sequences at the primer ends of the amplicon and analysed on an ABI 377 Automated Sequencer from ABI. The DNA sequences from the 5 individuals and the DNA pool were aligned using Sequencher™ 4.1 software (Gene Codes Corporation, USA) and SNPs were identified as irregular point variations.

Example 2

Determination of SNP variation in Tilapia and Salmon

This example describes the analysis of tilapia and salmon SNPs by oligonucleotide ligation assay (OLA). The three primers of a OLA analysis were designed as follows:

1) Allele-specific oligonucleotide-1: 5'ABI_colour-(*PRIMER SEQUENCE*)-X-3'

2) Allele-specific oligonucleotide-2: 5'ABI_colour-AAAAA- (*PRIMER SEQUENCE*) -Y-3'

3) Joining-oligonucleotide: 5'-P-PRIMER-3'

The allele discriminating primer were selected from the upstream flanking sequence of the SNP, including the SNP point, and end labeled with a fluorescent dye compatible with the ABI 377 Automated Sequencer machine (tamra, fam or tet). Both allele specific oligonucleotide 1 (AS1) and AS2 were labeled with the same dye. The X and Y at the 3' end of AS1 and AS2, respectively, indicate the nucleotide discriminating the SNP. The AS2 oligonucleotide has a five adenine nucleotide extension in order to allow discrimination of the OLA products and, thereby, the two genotypes. The joining oligonucleotide is labeled with a phosphate group in its 5' end in order to make a subsequent ligation possible.

Amplicons containing the SNP were produced using the PCR primers designed at the initial, SNP isolation, step as described in Example 1 above, followed by an Exo-sap purification also as described in Example 1.

The OLA reactions took place in a total volume of 10 µl with the following reagents: 0.25 µl ligase (Pfu DNA ligase, Stratagene, 4 U/µl), 1 µl 10x ligase buffer (Stratagene), 2.5 µl PCR product (purified by exo-sap), 0.5 µl allele-specific oligonucleotide 1 (150 fmol/µl), 0.5 µl allele-specific oligonucleotide 2 (150 fmol/µl) and 0.5 µl joining oligonucleotide (150 fmol/µl) with the following

temperature profile: an initial denaturation step of 94_C (10 seconds) then 25 cycles of 95_C (30 seconds) and 55_C (1 min) on a GeneAmp 9600 from ABI. Equal amount of OLA products and formamide gel loading buffer was mixed and loaded onto 6 % SequaGel® (National Diagnostics) and ran on ABI 377 Automated Sequencer (ABI) and analysed using GenScan software (ABI).

Example 3

Isolation of microsatellite markers from Atlantic salmon, Tilapia, Cod, Atlantic halibut, Seabass

This example describes isolation of genomic DNA containing microsatellite markers from an Atlantic salmon individual, a Nile tilapia individual, a Cod individual, an Atlantic halibut individual, a Seabass individual.

The procedure for isolation of microsatellite containing DNA was identical for each species. The procedure set forth below describes the isolation from one species.

A genomic library was constructed using the following procedure. Genomic DNA was digested with restriction enzyme Sau 3A (Gibco BRL) followed by electrophoresis in a 1% TBE agarose gel. Using 1Kb DNA size ladder (Amersham Pharmacia), DNA fragments of the size range 900 - 1100 bp were excised from the gel and isolated using QIAquick Gel extraction kit (Qiagen). The isolated DNA fragments were then ligated to Ready-to-Go pUC18 (Amersham Pharmacia), linearized with BamHI, BAP treated and formulated with T4 DNA ligase, followed by transformation into *E. coli* Pack Gold

supercompetent cells (Stratagene). Cells from the libraries were grown on LA amp agar plates in 37 °C for 12 hours. A colony replica of each plate were done using *Colony/Plaque Screen NEF 990A* filters (DuPont, Laborel) using the following procedure:

Each filter was uniquely marked with pencil and placed on top of the colony plate. The filters were subsequently stabbed with needle at three locations in order to optimize later orientation of autoradiograms/LA plates.

The filters were lifted from the colony plates and placed on 3 ml 0.5 M NaOH pools for denaturation of colony/DNA for 2 min before placed for 1 min on 3MM filter paper for short drying. The denaturation step was then repeated once before neutralization of filter on 3 ml 1 M Tris (pH 7.5) for 2 min, 1 min of short drying on 3MM filter before one repetition of neutralization step. Filters were air dried in 65 °C for 30 min. for fixation of DNA before washing in 2x SSC, 0.5% SDS, 50°C. Filters were pre hybridized in 120 ml 20x SSC,24 ml 10%SDS, 24 ml Denhards, 6 ml tRNA 10mg/ml, 306 ml H_2O for 30 min. in 50°C before P^{32} (Amersham) end labeled probe was added and this hybridization step continued in 50°C for 12 hours. The probe was a $(GT)_{10}$ oligonucleotide (synthesized at MWG, Germany). Filters were washed twice in 2x SSC, 0.5%SDS, 15 min. room temp. and twice in 0.5x SSC, 0.5% SDS, 50°C, briefly dried at 3MM filter paper, wrapped in plastic film before placing film (Hyperfilm ™ MP, Amersham) on top of the filters and placed in -70°C for about 5 hours. The film was developed using Curix60 developer machine (AGFA)

following the supplied recommended protocol and colonies at the original plates containing GT microsatellites were identified. Colonies were picked and transferred to new LA amp agar plates from which over night cultures were produced in LB amp media. Plasmids were isolated using QIAprep Spin Miniprep kit (Qiagen) followed by sequencing of the clone insert using standard M13 forward and reverse sequencing primers, Big Dye Terminator Sequencing kit (ABI) following the supplied recommended protocol and detecting/analyzing the sequence on a 377 Automated Sequencer from ABI.

PCR primers flanking the $(GT)_n$ repeat were designed using the *Primer3* software(http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi). Primers were ordered from and synthesized at MWG, Germany. One of the primers in each PCR set was labeled at its 5′ end by the primer synthesizing company with dyes that enables subsequent analysis using Automated sequencing machinery (ABI 377).

Example 4

Determination of microsatellite variation in Atlantic salmon, Tilapia, Cod, Atlantic halibut, Seabass

This example describes the analysis of microsatellite variation in Atlantic, Nile tilapia, Cod, Atlantic halibut and Seabass by PCR followed by analysis on automated DNA sequencing/analyzing machine (ABI 377).

The procedure was identical for each species. The procedure set forth below describes such variation determination from one species.

Genomic DNA from 20 unrelated fishes was genotyped for a given microsatellite marker in order to detect the level of polymorphism as well as study how efficient (and the quality) each microsatellite marker was amplified by PCR. The PCR reaction took place in a total volume of 20 µl, consisting of 100 ng DNA, 5 pmol of each primer, 2 µl dNTP (2mM), 2 µl 10xPCR buffer (supplied by ABI optimized for the enzyme), 0.2 µl Ampli-taq polymerase (ABI). Temperature cycling was performed with an initial denaturation step of 95 °C for 3 minutes, then 12 cycles of 95 °C for 30 seconds, 58 °C for 30 seconds and 72°C for 30 seconds, then 25 cycles at 95°C for 30 seconds each and 68°C for 1 minute. Amplification was performed on a GeneAmp 9600 from ABI.

Example 5

Parentage testing of fish

This example describes the usage of microsatellite markers for assignment of individuals to the correct parent pair. The procedure for such typing and assignment is identical for all species. Thus, for exemplification, the procedure given below describes such analysis for Atlantic salmon.

Genomic DNA from 6 female and 4 male breeders were genotyped for a total of 8 microsatellites (SEQ ID NOS:) according to the procedure set forth in Example 4. It was known which male that was crossed to which females. Furthermore, genomic DNA was isolated from a total of 13 offspring and these individuals were subsequently genotyped for the same set of markers as the group of potential parents. The genotyping results are presented in table 1.

Table 1. Genotypes of 13 Atlantic salmon offspring, 4 male parents and 6 female partners for 8 microsatellite markers.

Marker:	104	104	106	106	109	109	115	115	125	125	131	131	135	135	173	173
Offspring																
B001F06	193	201	244	246	149	157	119	119	152	160	196	200	382	398	229	278
B002A03	193	221	246	246	149	153	0	0	152	160	200	200	380	380	239	278
B001F10	207	221	246	246	149	151	119	119	160	162	196	196	380	380	229	229
B002C03	201	221	246	246	151	153	125	125	160	160	196	196	380	380	229	229
B004B01	201	201	246	246	149	151	125	125	152	160	196	196	380	380	229	239
B002E08	201	201	246	246	153	153	119	119	152	160	196	204	380	380	229	278
B003C07	201	201	246	248	151	153	119	119	152	160	196	204	380	380	229	278
B007B07	201	201	248	246	149	153	119	121	152	160	196	204	380	380	229	278
B003H09	201	201	246	246	149	151	123	125	152	162	196	204	380	398	237	251
B003B08	201	213	246	246	149	157	119	119	152	162	196	196	380	380	278	278
B006B05	201	207	246	246	149	157	121	121	152	162	196	204	380	380	237	249
B007G05	207	213	246	246	149	149	121	121	152	162	196	196	380	380	237	249
B008C02	203	213	246	246	149	153	119	123	152	154	196	204	380	380	229	245
Males																
P01-E09	181	193	246	246	149	153	0	0	152	160	200	202	380	382	229	239
P01-E10	201	207	246	246	149	153	119	125	160	162	196	196	380	380	229	239
P01-E11	201	207	246	246	149	149	119	121	160	162	196	196	380	380	237	278
P01-E12	189	203	246	246	149	153	123	125	152	162	200	204	380	380	237	245
Females																
P01-A07	201	221	244	246	149	157	119	119	152	162	196	200	380	398	237	278
P02-A03	201	221	246	246	151	153	0	0	152	160	196	204	380	380	229	229
P02-D10	201	221	246	248	151	153	125	125	152	152	204	204	380	380	237	278
P02-A05	173	201	246	246	151	153	121	125	152	152	204	204	380	398	251	278
P01-B06	201	213	246	246	153	155	121	125	154	160	196	196	380	380	229	278
P02-E08	201	213	246	246	149	157	0	0	152	152	196	204	380	380	249	278

A comparison analysis was performed between the genotypes of the offspring and the potential parent pairs and the correct parent pair was identified based on their ability to produce an offspring with the same genotype as found in a particular offspring. The result of such parent pair assignment of the offspring genotyped is presented in table 2.

Table 2. Assignment of offspring to parent pair

ID	SIRE	DAM
B001F06	P01-E09	P01-A07
B002A03	P01-E09	P01-A07
B001F10	P01-E10	P02-A03
B002C03	P01-E10	P02-A03
B004B01	P01-E10	P02-A03
B002E08	P01-E10	P02-D10
B003C07	P01-E10	P02-D10
B007B07	P01-E10	P02-D10
B001C12	P01-E11	P02-A05
B003H09	P01-E11	P02-A05
B004D04	P01-E11	P02-A05
B003B08	P01-E11	P02-E08
B006B05	P01-E11	P02-E08
B007G05	P01-E11	P02-E08
B008C02	P01-E12	P01-B06

This example demonstrates an assignment analysis of a small number of offspring/families. The same procedure is used for identify the correct parent pair in a situation where any number of offspring/samples are to be assigned to correct parent pair identified from any size of potential male and female parent individual group available.

This example is shown for microsatellite markers. Identical tests can be performed by using other genetic markers as for example SNPs.

Throughout this application various publications have been referenced within parentheses. The disclosures of these publications in their entireties are hereby incorporated by reference in this application in order to more fully describe the state of the art to which this invention pertains.

Although the invention has been described with reference to the disclosed embodiments, those skilled in the art will readily appreciate that the

specific experiments detailed are only illustrative of the invention. It should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

Claims:

1. A method for determining the origin of a sample from any plant and animal species which has a reproduction involving the mating of two parents to produce a set of offspring, comprising:

(a) providing a parent genotype database which contains a collection of candidate parent genotypes each representing a distinct parentage origin by using any type of genetic marker and genotyping technology, and comparing a sample genotype to the parentage genotype database, such that a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample and

(b) providing an origin genotype database encompassing a collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin by using any type of genetic marker and genotyping technology, and comparing a sample genotype to the candidate genotype profiles, wherein a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample; and

(c) providing genetic logistics, which is predicated on the fact that a member of the food value chain receives distinct and identifiable batches of genetic material from the broodstock of origin or from the last multiplier such that a member of the food value chain giving rise to the sample can be identified; and

wherein the parentage of origin and population of origin of the sample together with the logistics information allows tracing a sample back to any stage of the food value chain.

2. The method of claim 1, wherein said animal species is an aquaculture species.

3. The method of claim 1 or 2, wherein said species is fish.

4. The method of claim 3, wherein said fish is Atlantic salmon, tilapia, cod, Atlantic halibut or seabass.

5. The method of claim 1, wherein said parentage genotype database comprises every potential origin genotype.

6. The method of claim 1, wherein said candidate parent genotypes comprise two or more distinct species.

7. The method of claim 1, wherein said sample and candidate parent genotypes belong to the family Salmonidae.

8. The method of claim 1, wherein said sample and candidate parent genotypes belong to the species *Salmo salar*.

9. The method of claim 1, wherein said sample and candidate parent genotypes belong to the genus tilapia.

10. The method of claim 1, wherein said sample and candidate parent genotypes belong to the species *Oreochromis niloticus*.

11. The method of claim 1, further comprising sample and candidate parent genotypes belonging to a species selected from the group consisting of rainbow trout, halibut, seabass and Atlantic cod.

12. The method of claim 1, further comprising the initial steps of:

(a) extracting nucleic acid corresponding to each of said distinct populations of origin ; and

(b) genotyping the extracted nucleic acid with selected genetic markers to obtain said collection of candidate parent genotypes.

13. The method of claim 12, wherein said nucleic acid is extracted from broodstock individuals.

14. The method of claim 12, wherein said genetic markers are selected from the group consisting of single nucleotide polymorphisms (SNPs), microsatellites, restriction length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLP), random amplified polymorphic DNA (RAPD), mitochondrial DNA.

15. The method of claim 14, wherein said genetic markers comprise SNPs.

16. The method of claim 15, further comprising identifying said SNPs by performing an oligonucleotide ligation assay (OLA).

17. The method of claim 15, further comprising identifying said SNPs by performing a hybridization assay.

18. The method of claim 17, wherein said hybridization assay is performed on a DNA chip.

19. The method of claim 1, wherein the absence of said match excludes said candidate genotypes as the origin of said sample.

20. The method of claim 1, further comprising generating a central database capable of storing said population of candidate parent genotypes.

21. The method of claim 1, wherein said central database is capable of instantaneously comparing said sample genotype to said collection of candidate parent genotypes.

22. The method of claim 21, wherein said central database of candidate parent genotypes is on the accessible through the internet.

23. An apparatus for determining the origin of a sample from any plant and animal species which has a reproduction method involving the mating of two parents to produce a set of offspring, comprising:

(a) a computer readable medium encompassing a parent genotype database that contains a collection of candidate parent genotypes that each represent a distinct parentage origin; and

(b) a computer readable medium encompassing an origin genotype database encompassing a collection of candidate genotype profiles, wherein each of the candidate genotype profiles represents a distinct population of origin; and

(c) a computer readable medium encompassing genetic logistics, which is predicated on the fact that a member of the food value chain receives distinct and identifiable batches of genetic material from the broodstock of origin or from the last multiplier such that a member of the production system giving rise to the sample can be identified; and

wherein the computer apparatus comprises appropriate hardware, software and/or networking in order to perform the steps of

comparing a sample genotype to the parentage genotype database and comparing a sample genotype to the candidate genotype profiles, and the step of verifying the origin of a particular sample or of excluding a particular producer as a potential source of the sample;

wherein, when comparing a sample genotype to the parentage genotype database, a match between a sample genotype and one of the candidate parent genotypes identifies the parentage origin of the sample; and

wherein, when comparing a sample genotype to the candidate genotype profiles, a match between the sample genotype and one of the candidate genotype profiles identifies the population of origin of the sample; and

wherein the parentage of origin and population of origin of the sample together with the logistics information allows tracing a sample back to any stage of the food value chain.

24. The apparatus of claim 23, wherein said animal species is an aquaculture species.

25. The apparatus of claim 22 or 23, wherein said species is fish.

26. The apparatus of claim 24, wherein said fish is Atlantic salmon, tilapia, cod, Atlantic halibut or seabass.

27. The apparatus of claim 23, wherein said parentage genotype database comprises every potential origin genotype.

28. The apparatus of claim 23, wherein said candidate parent genotypes comprise two or more distinct species.

29. The apparatus of claim 23, wherein said sample and candidate parent genotypes belong to the family Salmonidae.

30. The apparatus of claim 23, wherein said sample and candidate parent genotypes belong to the species *Salmo salar*.

31. The apparatus of claim 23, wherein said sample and candidate parent genotypes belong to the genus tilapia.

32. The apparatus of claim 23, wherein said sample and candidate parent genotypes belong to the species *Oreochromis niloticus*.

33. The apparatus of claim 23, further comprising sample and candidate parent genotypes belonging to a species selected from the group consisting of rainbow trout, halibut, seabass and Atlantic cod.

34. The apparatus of claim 23, wherein said collection of candidate parent genotypes is obtained by the initial steps of:
(a) extracting nucleic acid corresponding to each of said distinct populations of origin; and
(b) genotyping the extracted nucleic acid with selected genetic markers.

35. The apparatus of claim 34, wherein said nucleic acid is extracted from broodstock individuals.

36. The apparatus of claim 34, wherein said genetic markers are selected from the group consisting of single nucleotide polymorphisms (SNPs), microsatellites, restriction length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLP), random amplified polymorphic DNA (RAPD), mitochondrial DNA.

37. The apparatus of claim 36, wherein said genetic markers comprise SNPs.

38. The apparatus of claim 37, wherein said SNPs are identified by performing an oligonucleotide ligation assay (OLA).

39. The apparatus of claim 37, wherein said SNPs are identified by performing a hybridization assay.

40. The apparatus of claim 39, wherein said hybridization assay is performed on a DNA chip.

41. The apparatus of claim 23, wherein the absence of said match excludes said candidate genotypes as the origin of said sample.

42. The apparatus of claim 23, wherein said computer readable medium encompassing a parent genotype database is a central database capable of storing said population of candidate parent genotypes.

43. The apparatus of claim 23, wherein said central database is capable of instantaneously comparing said sample genotype to said collection of candidate parent genotypes.

44. The apparatus of claim 43, wherein said central database of candidate parent genotypes is accessible through the internet.

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SNP-primers (OLA) and the corresponding sequence

ALLEL specified OLIGO-1: **5'ABI_colour-PRIMER-N-3'**

ALLEL specified OLIGO-2: **5'ABI_colour-n(A)-PRIMER-N-3'**

JOINING-OLIGO: **5'-P-PRIMER-3'**

tamra=red, fam=blue, tet=green, hex=yellow (ladder)

SAL146A

AACCAAAAGCACAGAGACCCAAATAATGGTGAATTACATACACTCAGAATCAACAA
AAGCACAGTNCCACAGCAAGCAGCTGACATTAATTGAGGAGTCCATAAACACAAAC
AACTTCTGGCA/TAAATTGGAAAAAACAAAAAAATGGTGACATATGGACAACCCATT
TTAAAACACTCTACAACACCATTCAAATTGATGCAAACACAGAACAATTGT

SAL146a2-A **tet-TAAACACAAACAACTTCTGGCA**
SAL146a2-T **tet-AAAAAATAAACACAAACAACTTCTGGCT**
SAL146a2 **P-AAATTGGAAAAAACAAAAAAATGG**

SAL96A

GGATGGAGTTTTGGTGACATCACCAGGCAATAAATTAGTTAATAAACCAATAAGAA
AGAGAGTTCCTAAACCTCTCTGCCAATACAAGCAAGTTTTCAGTTTCCCCTCCCCACT
TCCAGACACTCCCAGACTGTCCTAGCAAAATGTATCTTTCCTAAGAAGCTTTTTTAGT
TTATTTTTGACAATTTCAATTGAAAA/TCAATCACATTAATGTACTTCATTAATACCCA
GAAACTATATGATATTGAGATAAAAACGCCTGCATTGGACATTTAAAGAAAGCATA
ACAGAA

SAL96a2-A **tet-ATTTTTGACAATTTCAATTGAAAA**
SAL96a2-T **tet-AAAAAATTTTTGACAATTTCAATTGAAAT**
SAL96a2 **P-CAATCACATTAATGTACTTCATTA**

SAL78A

GTGCTGAGTGATTAGTGCTTTTTGAGGTCAGTTCGGTTTCGGTTTTATAATAAA
AAAAATAATAATGTTTTTTCAATTTCGGATTCAATACTAATTTTTTTTACATTAAA
TGCACTATGCATTACGTGGGTTGAATGCTGTAACAACACYGAATAAAACAATGA
ATCCAATCCCAC/TGATGGTAGAGACTGCCCATTACTGCTTATTAACCATAATTT
ATTCACATGACTAATTCTGTTGTTGTGTATATTACATTTGATTTATTTG

SAL78a-C **fam-ACAATGAATCCAATCCCAC**
SAL78a-T **fam-AAAAAACAATGAATCCAATCCCAT**
SAL78a **P-GATGGTAGAGACTGCCCAT**

SAL87A

CAGGAAGAGAGTTGAAGATAGTTATTAGGAAGTGCAGTCATTCTCTTTGGTTCC
TTGGTCCTTGACACACACATTGTGCATTGGTTCCCTATAACATACGGAGACACA
GACCCAGAAATGGCTTCTCATCTCTCC/ACTCTCCATCCTCCTACTCATCTTCAG

Figure 1A

ACTCTCAGGTAAGGGTAACATGTTTCTATGAAGTGCTGAAGTTGAGGTCAGGGA
CTGGGACAAATGTTGGAACTCTGAAGACAGAAGCAGCAGCAGTTTGTCTTATCA
ATAACACTTCCTGTATTATG

SAL87a-C	tamra-AAATGGCTTCTCATCTCTCC
SAL87a-A	tamra-AAAAAAAATGGCTTCTCATCTCTCA
SAL87a	P-CTCTCCATCCTCCTACTCATC

SAL46A

CCACTCGTTTCCTTCCCGTATCCAAACCACATGGTCGGCGTTCCGAAGGTCCAA
CTAGGAGAACATGACCGCCCCCTGGAGAGGCTCGGAAGCCGAGGAGATGAT/G
ATGTAGCAGGTAATATTTTTTTAACAGTAATGTCATTAAAACCCAGGTAGTTGAT
ACATGGATGCAGGGTCTTGTCCTTCTTCTCCACAAAGAAGAACCCTGCGCTGGC
GGGGGA

SAL46a-T	tet-GGAAGCCGAGGAGATGAT
SAL46a-G	tet-AAAAAAGGAAGCCGAGGAGATGAG
SAL46a	P-ATGTAGCAGGTAATATTTTTTTAA

SAL15A

AACATGACATCACAATACACATACACACACTCACATGCAGACACACACACACGC
AAATACATACACACACTTTGATGTATTGCCTTTTATGTTGCAGTGACAGGGTTG
GCACTGGGCCTAGAGCAGAGTGTAGTTTATGATGGTGGGTATAATAGGACCAG
TTAAAAATAACTTTATTTTCAAATACACACTCAAACAGACAGAGGTGACA/GTAA
TGAGAGGACGGAAGGAGAAGACGTAAGGAGAGAACGGAGAAAGAGAGTAGAG
AGACAGAAAGAAGGGGAGAGACAGTGAA

SAL15a2-A	tamra-ACACTCAAACAGACAGAGGTGACA
SAL15a2-G	tamra-AAAAACACTCAAACAGACAGAGGTGACG
SAL15a2	P-TAATGAGAGGACGGAAGGAGAAG

SAL147a

CCAACACAAAGAAATACACAACCTAGAAAATCATAGAGATACAAAACCAGAACA
ATGCCCAAAAACCCC/TGGAACACATAAAACAAACACCCCTCTTACATAAGAACA
TATCCCAACAAACCCCAAACCACATAAAACAAACACCCCCTGCCACGTCCTGAC
CAAACTACAATAACAAATAACCCCTTTACTGGTCAGGACGTGACAGCTAAAC

SAL147a-2 C	tet-GAACAATGCCCAAAAACCCC
SAL147a-2 T	tet-AAAAAGAACAATGCCCAAAAACCCT
SAL147a-2	P-GGAACACATAAAACAAACACCCC

SAL126B1

GGACCTGAAGAACTGTAATATCCTATGTTTCTCAGAGTCGTGGCTGAACAAGGA
CATGGATAATACTGTATATGTACATCTAG/ACTGTTTTTTCTATACATTATCAAGA

Figure 1B

CTGAACGGCAGCTTCAGGTAAAGTAAAGGGGGGAGGTGTATGTATGTCTCTTT
GTTAGCAACAGCTGGCACGCAATCTCTAATATTAAGGAAATCTCAAGGTTTTGC
TCACCTGAGCTAGAATACTCAATGATAAACTGCAGACAATACTATTTACCGAGA
GAGTTTTCTTATATTGTTTTCCATAGCTCTCTATTTACCACCAC

SAL126B1-G	**fam-GATAATACTGTATATGTACATCTAG**
SAL126B1-A	**fam-AAAAGATAATACTGTATATGTACATCTAA**
SAL126B1	**P-CTGTTTTTTCTATACATTATCA**

SAL126B2
TTTTTTCTATACATTATCAAGACTGAACGGCAGCTTCAGGTAAAGTAAAGGGGG
GAGGTGTATGTATGTCTCTTTGTTAGCAACAGCTGGCACGCAATCTCTAATATT
AAGGAAATCTCAAGGTTTTGCTCACCTGAGCTAGAATACTCAATGATAAACTGC
AGACAATACTATTTACCGAGAGAGTTTTCTTATATTGTTTTCCATAGCTCTCTAT
TTACCACCACAAACCGATGCTGGCGCTAAGACCACACTCAACGAGCTGTATAGA
GCCATAAGC/AAAACAAGAAAAGCCACATCCAGAGGCAGCGCTACTAGTGGGGA
AACTGAAATCTGTCTTACCTCATTTTTACCAGAATGT

SAL126B2-C	**tet-CGAGCTGTATAGAGCCATAAGC**
SAL126B2-A	**tet-AAAAACGAGCTGTATAGAGCCATAAGA**
SAL126B2	**P-AAACAAGAAAAGCCACATCC**

SAL19B
AAGCATTTGTCCATTTATACATGTTTCATTCCAGACTAGAAGTGTGTGCAGAAAGGAGGCCAT
CTAGTGGTGAAAATGGCATCTACCAAAAC/TCACACGCGACCAAAATCTCTGTCCTGCTACTTA
GTAGACATGAAGCTAGGGTTTGGGTTGTGTTTGAGGCTAGGTTCAACCCTAACCCTAGCCTCA
ACCAGAACCCTAACTCTTGCCTTA

SAL19B-C	**tamra-TGAAAATGGCATCTACCAAAAC**
SAL19B-T	tamra-AAAATGAAAATGGCATCTACCAAAAT
SAL19B	**P-CACACGCGACCAAAATCTCT**

SAL23B
CACAGAATCTGATTACCCTGTGGCTTTAGCTACGTGTGGGATTTGTAGAAATTA
ATAGTGCAGCTAGGGCCCTTCTGTTCTGCTGCAGATTCCACAATATAGCCTGGT
TAACGCC/TGCAGCGTTTAATCTGGTTTAACCAGGGTATCCAGAAAAAACAGAC
AACACATCAAGCTCTGACTGACTAATAACATGACCAAGAGTATCCATCCATTAC
TCTACAGCTGTGCAGAAGGTCTGATAAAAATGAAACCAGCAGTTCTAATCTACA
ATATTGCATAGATGACAGGAATTGGCTCAGTGGAATTTTGCACCTCTGATAAGA
CCGCTTCC

SAL23B-C	**fam-CAATATAGCCTGGTTAACGCC**
SAL23B-T	**fam-AAAAAACAATATAGCCTGGTTAACGCT**
SAL23B	**P-GCAGCGTTTAATCTGGTTTAAC**

Figure 1C

SAL62B
TCCTCCGAGCCCATTGGACGGGAGCCTCGGCCTCTCCGTGCCGCCCCA/GAAAT CCAACCCCACCCCCCCACCTTCGCCGAGGCGCGCTTGGTGTCTTTTGTTAGGGCC GACACTTTACGCGCAATAATAGTCACCGGCCGAATTCTAGCCTGCTATGACAAA C

SAL62B-A	**tamra-CTCTCCGTGCCGCCCCA**
SAL62B-G	**tamra-AAAACTCTCCGTGCCGCCCCG**
SAL62B	**P-AAATCCAACCCCACCCCCC**

SAL122B
TGTACAGTATAAAGCAAGGGTGCAACTTTGTTTTTCGAAGTGGGGGGGGACATAACTA TTATTATAATTTTTTTCCCCCAGTTGGATAAACACTCCAAACAG/TCCTACCCGACTG CTTGGAGGTGTCCGCATGGTCCTAAAGCACCCCGTAGCNTCGTTTTGTATCACATTCC AATGATAAAACTAAGGGGGACAAAAATGTAATTTCAGAATTTGGGGGGAGACATGT ACTCATCTGGTTTAAAGAATCAATGTCTTTTGGGGTCTTTTGCATTTTATTATATTTTA TATACAAGTCTACATCTTATTATTTATTTTTTT

SAL122B-G	**fam-GGATAAACACTCCAAACAG**
SAL122B-T	**fam-AAAAAGGATAAACACTCCAAACAT**
SAL122B	**P-CCTACCCGACTGCTTGGAG**

SAL162B-1
GTGACATCGGCGGATTTGGTGGATTAAGAGGCATCCAATGCAAGCTGATATCTCTAT CTTAAATTGACAGATTTTTATTGGGATTTTTTA/TATTATGCTAATTAGATTCCCGCGG GGCACGGACATTGACTCTAGGGGATTTAAACTGTGTAGTACTACGGCTCTATTCAAT CTGTATCAATGAAGCATTAACATTGAAGTGTTGACACACCAGGGAATATTGCCCCTA ATTAGTACAAGGAAGCTATGTAGAAATACAGACGGTCTAAAGGGCCCTTCCC

SAL162B1-A	**fam-CAGATTTTTATTGGGATTTTTTA**
SAL162B1-T	**fam-AAAAACAGATTTTTATTGGGATTTTTTT**
SAL162B1	**P-ATTATGCTAATTAGATTCCCGC**

SAL162B2
ATTATGCTAATTAGATTCCCGCGGGGCACGGACATTGACTCTAGGGGATTTAAACTG TGTAGTACTACGGCTCTATTCAATCTGTATCAATGAAGCATTAACATTGAAGTGTTGA CACACCAGGGAATATTGCCCCTAATTAGTACAAGGAAGCTATGTAGAAATACAGAC GGTCTAAAGGGCCCTTCCCTCTTTGTTCCCTTCATCTGTACTGGTCTTAAAACAAAGG CTATGGTAAAACAATCAATCATTTATCTGTGCTTTTACTCG/ATCCAGTTTGATGCCA ATGCAGTTGGAGGAAAGGAGATGAGGAGAGGAAAAGCCACTTTACACTATTGAGAT ACACCCAGATGAGTCATCTCTACCATT

SAL162B2-G	**tet-ATCATTTATCTGTGCTTTTACTCG**
SAL162B2-A	**tet-AAAAATCATTTATCTGTGCTTTTACTCA**
SAL162B2	**P-TCCAGTTTGATGCCAATGCAG**

Figure 1D

SAL23M
GAGTCACAATGTATACACATAATATTATAGTGACTATTCAGTTTACAATTGATAT
TTAAAGATAGAATCCTTAGTTGCTGTATCCATTTTTGGG/ACTTGAATGATAAAG
ACCCATTTTGTTTCTTGAAGAATATAATTTATAAATGCCTAATGAGCTTAGTTCA
ACTATTACAAAACTTGTTTCAATTAGGA

SAL23M-G	**tamra-TTAGTTGCTGTATCCATTTTTGGG**
SAL23M-A	**tamra-AAAATTAGTTGCTGTATCCATTTTTGGA**
SAL23M	**P-CTTGAATGATAAAGACCCATTTTG**

SAL93M
TTGAACACCAAAACAGAGTGTCAAGAGAATATGGAAACACATGGAAACCATATAAG
AACAGAC/GATTATTATTATATTAATTATATAACAAATATAATCTATAGTTAATATCT
TTTGTAGAACACGTTACATTGAACTAATGAAATATTACACTGA

SAL93M-C	**fam-ACATGGAAACCATATAAGAACAGAC**
SAL93M-G	fam-AAAACATGGAAACCATATAAGAACAGAG
SAL93M	**P-ATTATTATTATATTAATTATATAACAAATA**

SAL78i
AACTGGTGATGGAGCAAAGGAGAGAGAGAAGAAAGAAGAGTTTAAGGCAGGAA
AAGGCACTTTTGGCATCATTGGGATTCAATCTGGAAATCCTGTTCCAACGATGC/
GAACAGACATATGAAGATTCACTCTAAAGTTCCTCAGAGTAAAAATACACCACA
GAAATACACCACAAGTGGAAAAGTCCACTTGGTGACATCACAGGCTCTA

SAL78i-C	**tet-GGAAATCCTGTTCCAACGATGC**
SAL78i-G	**tet-AAAAAAAGGAAATCCTGTTCCAACGATGG**
SAL78i-ola	**P-AACAGACATATGAAGATTCACTCTA**

SAL84i
AAAACTCCCTAGAAAGGACAAAAACCTAGGAAGAAACCTAGAGAGGAACCAGG
CTATGAGGGGTGGCCAGTCCTCTTCTGGCTGTGCAGGGTGGATATTATAACAGA
ACAC/TGGTCAAGATGTTAAAATGTTAAAATGTTCATAAATGACCAGCATGGTCA
AATAATAATAATCATAGTAGTTGTCGAGGGTGCAACAAGCACGTCCGGTGAAC

SAL84i-C	**tet-CAGGGTGGATATTATAACAGAACAC**
SAL84i-T	**tet-AAAAACAGGGTGGATATTATAACAGAACAT**
SAL84i-ola	**P-GGTCAAGATGTTAAAATGTTAAAATGT**

Figure 1E

SALU4i

TTATGGACTATTAGGGTTAGACCAGGGACAGGGGTGGTGGGTTAGTTAGTGGC
TAGTTAACAGTGATAGTTAGTTGAACATCATAAACCTCCTGTAGTGGTTTAA/TA
CAAATATAGTATTACCACATTATTCTGTCACTAMTACAAACATTGAAGGGTTAA
AGGATGTGTTCATGCTGGTAAAGAATGA

SALU4i-A	tamra-AACCTCCTGTAGTGGTTTAA
SALU4i-T	tamra-AAAAAAAAACCTCCTGTAGTGGTTTAT
SALU4i-ola	P-ACAAATATAGTATTACCACATTATTCT

SAL70i

ACAAAAAAAGAAAGTGGCACAGCAATTCATTTTTTGTTCTGAAAACAAAATGTT
ACGGTTGGGGCAAATCCAATACATTACTCAGTACCACTCTCCGTATTTTCAAGC
ACAATGGTGGCC/TGCATCATGTTATGGGTTAACTTGTAATCATTAAGGACTGGG
GAGTTTTTCCAGGACAAAAAAAGATACGGAATGGAGCTAAGCACAGGTAAAATC
CTAGAAGAAAACCTA

SAL70i-C	fam-TATTTTCAAGCACAATGGTGGCC
SAL70i-T	fam-AAAAAATATTTTCAAGCACAATGGTGGCT
SAL70i-ola	P-GCATCATGTTATGGGTTAACTTG

SAL59i

GGAAGGAGTTCTGGAATGAGCTGGTCTGCTGAAGCGGTGCCCCCAGTTGTATA
AAGTGAGCTGAAGAACTGGCCATAGAGGGGCCAGAGTGAAGAATAATA/GTTCC
TCAGCCTTTGGAACACCCATTGGGCAACAGCTGGCCATGGTGTCTAGTTACCCC
CTCACACTCAACAGGCTAGTGGTATCAGCTATGCACAGACAGATGTTCTTGTCA
AAGTCAG

SAL59i-A	fam-AGAGGGGCCAGAGTGAAGAATAATA
SAL59i-G	fam-AAAAAAGAGGGGCCAGAGTGAAGAATAATG
SAL59i-ola	P-TTCCTCAGCCTTTGGAACACCCA

SAL46ii

TCAGTCTCCTGAGGAGGAATAGGTTTTGTCGTGCTCTCTTCACGACTGTATTGG
TGTGCTTGGCCCATGTTAATTTGTTTTTAATTATTATTATTTCTTTACCCCTTTTT
CTCCCCAATTTCATGGTATCCAATTGGTA/TGTAGTTACTGTCTTGTCTCATCAC
TGCAACTCCCGTACGGACTCGGGAGAGGCGAAGGTCGAGAGCCATGCGTCCTC
CGAAACACAACCCAACCAAGCCACACTGCTTTTTGACACAACACACATCCAACC
CGGAAGCCAGCCGCACCAATGTGTCGGAGGAAACACCGTACACCTAGCGACCT
GGTCAGCGTGCACTGTGCCCGGCCCGCCACAGGAGTCACTAGCGCGCGATGAG
ACAAGGAAATCCCTGCCGGCCAAA

SAL46ii-A	tamra-TTTCATGGTATCCAATTGGTA
SAL46ii-T	tamra-AAAAATTTCATGGTATCCAATTGGTT
SAL46ii-ola	P-GTAGTTACTGTCTTGTCTCATCA

Figure 1F

SAL43ii

CAGCACACCAACACATCACATCAGTTATGTGCCATCTACCTCACGTTGTTTCTCT
CCCCCATTGCAAAATTAAAATGAGGCACGCTGTCAATATCACAACAAGGTGAGC
GTGGAATAAACCAGCCTCATTTAAAACCCAGCTCTGAGCATACCGCTGTCATCA
ATACCAGTTGTGATGAGGGTAGCTCATAAAATCCAGACATTGTTACTGATAGCC
TTTAGATTGTCTGAGCCTTCAGTCTTTATAGC/TACCCAGCTGTCTTCTCCGGTC
TGTCACTCCTCAGCTGAAAATGTCTTCATCTTAGTGACAGGTGACTCCCTCCCA
CACTTTTGACCTGACCCACATTCCTCCACGGTGCTC

SAL43ii-C	**tamra-CTGAGCCTTCAGTCTTTATAGC**
SAL43ii-T	**tamra-AAAAAACTGAGCCTTCAGTCTTTATAGT**
SAL43ii-ola	**P-ACCCAGCTGTCTTCTCCGGTC**

SAL48ii

GAATTTTTTGTTTTGATATCATTGTGTATGATGTTGTTTTTGGGCAGTTGTGTTACTTG
TTCGTTTTGCTAAAAGTAATGCCGGCATTGTTGGGTCTGGTTTTAGCATC/AATGTGG
TGGACTTCCCTTTGACTTTCATTCCAAATACCTCAGGACTTCATCTGCATAATCCCAC
TCCTCTAGCGGAAGGACAGCCAGTCAATTCCTTCGCTCCACCTTTTCCTTTCCAGTGT
AAGTACAGTAGCCTACGCAAAATAACCTTGGAGATGTTTTCCTTATGAGGTAGCTCC
AGATGTAGGGACCTTAGAATCACATGTAGCCGGCCTACATTAGCCTAGATACCATGT
GTTCTATAATGTCAACAATATTAGGCAGACCCTTCTAATTACTTACGTAATTCTC

SAL48 C	fam-TGTTGGGTCTGGTTTTAGCATC
SAL48 A	fam-AAAAAATGTTGGGTCTGGTTTTAGCATA
SAL48-ola	P-ATGTGGTGGACTTCCCTTTGA

SAL83ii

AAGTTTGAATTGATTCTTGGTACTTAGAGCTGGGAACCACTGGATGTAACTCTAAGA
CTACAAGTGAATGGTTTTAGCTTCCCTCTGAATCAACCTCGGCAGTGTTGCTTGGCAT
CACACTTTTTAGCTCAACACAACAACACCTGATTCAAATGAACTAATAACTC/AATCT
TAATTTTAGCCCACAATTGGTTTCATCAGGTGTGCTGCTGTGGGGCTGGAGAAAAGT
GTGACATCAACACGGCTCTTGAGGACTGCAGCTGCA

SAL83 C	tamra-CCTGATTCAAATGAACTAATAACTC
SAL83A	tamra-AAAAAGATTCAAATGAACTAATAACTA
SAL83-ola	P-ATCTTAATTTTAGCCCACAATT

SAL19D

CTTTGTCTTGATGAACGGTTGAAATGTAGCCCCAACAGCCCTCAAACTCAACTCTGC
ATGTTTTCATTGTTCCCCTCTAGTCAGTGACTGATTTAAACCTGTGACACCAGGTGTG
TGCAATTCATTACCAGGTAGAAGAGAAAACCAGCAGGCTCCAAACCTCTAGGGTAA

Figure 1G

GAGTTGAGTATCCTTGCCCAACAGGTTTGCCTTCATGTAACTTGTAATATACATGTAA
CTCAAGTATACAAGGTCTGTGTTGTTATGGTTTTATAAACTAGTGTAAGGGTTTAAAA
AAAATACTGTCCTATGTTGACCATAACCTACTACTCAAATGCATCATGAATTTGCATG
CTCCAAAAGAGACTCATCTGTGCTAGATTAAAAGTGGCTAAATCAGTTGTGATGTAA
ATCATGTGCATAGTCACACGTGGTTTATGTTTCTGGGTGACTGGGTGGAACATTACTT
TGCCATAAGGAACGTGCTGCATTATTAAGGCATGCCTCAAATAAAACAGGGGTTCTT
GGAATTAATCGAATACGTTTAGGCAAACAGTTACAGCACATAATAGTC

SAL13D

TGAGAGCATAGTAATTCTGAAGTAATTCTGAAAAAAATCTGAAAAAAATTATGCTTT
TATTTTTCTTCACAAAAATAGTGCACTGGGCTTTTTAATAGTCCTGTATTAGCAGCAA
CATTAGTCCAGCATTTTATGTCACTTCGAGGAATACAACACTGAGTCTTGCATGAATC
CCCTGTTGTTCTGGAAGACTGTGTGATCTTGCTCCCCTTGGCCAGATGTAATAGCAGG
ACGCGTTCTCAAAGCATGCGCACAGCAGCTGGCAGGTGTCTTCACAGACATTTTCAA
TCTCTCCTTGTCGTTGTCTGTAATCCCAAAATGTTTCAAGCTGACCACCATTGTCCCT
GTTCCCAAGAACTCAAAGATAACCTGCCTAAATGACTATCGTCCTGTAGCAGCCACA
TCTGTAATTATGAAGTGCTTTGAAAGGCTGAACATGACACACATCAACACCATCATC
CCAATACGCATACTGCCCCAAA

SAL42D

TGAGGGTTGCCCCTCTCTCTTACTCTCTCTCTCTCCCTGTCCTCCGCCCTGACG
AATCTCCCCATACAAAACCATCTGTGTCATTTCATTAACCGCACTTCCCTCGT
TCTCTCTCTCTCTCTCCCTCCTTCCCTCTCTCCCCCTGGCCGGGGTTCACCATG
TTAGTGTGTCCGTATTCATGGAGCCGTCCCCTCCTGCATAGCGTAATGAAGTC
AGGACCTCTCAGCACCACTGTAATTCCAGCGACTAGTTTGTGCAACGCAACA
ATTTATCACTTGTCACGAAGACACTTAGTGTTGTACTGCTTAACAAGGACATC
CTGTGAGCCTGGGCTACTAGCAGGGAGCCGTTTGCATATTTACTAAATGCGG
AGTGTCATTGCCACCACGGCCTGTTGCCTGCATGAATTATTTCTCTATCTGCA
ATAAACAGATGGGTAATTATTACTGCCATAATCAGATAAATTCTCTCTGTAAT
GTTCTAACGTGGCAAAATCTTTTAACTCATTGCAGGCTGAGGGATATTTATAG
ACTCAGAATGGTGAGGCTGAAG

SAL53D-B

TCTCTGTACTTTGCTCAGTTCATCTTTCCCTCAATCCTGACTAGTCTCCCAGTC
CCTGCCGCTGAAAAACATCCAAACAGCATGATGATGCCTCCACCATGCTTCA
CCGTAGGGATGGTATTGGCGATGAGAGGTGCCAGCTTTCTTCCAGACATGAC
GCTTGGCATTCAGGCCAGAGTTCAATCTTGGTTTCATCAGACCAGAGAATCTT
GCTTCTCATGGTCTGAGTGTCCTTTAGGTACCTTTTGGCAAACACCAAGCAAG

Figure 1H

TTGTCATGTGCCTTGCATGTGTCATGTGCCGAATTCACTGCACTTCCATTCAG
TTTTTCAACTTGTACTGGGGGACTTTCAGACCTTCTTGTGAGGCCTGTGGGCA
TCAGAGCAAAACGTGTACATAAGAGTCTCACCTTTCCACAGAGGGGTCATAT
TAGGTTGTAACTCAA

SAL57D

TAGCATGAGTTCCAGTCTGTTTGTGCTATTATGACAACTCCCAGTCAGCAGCG
ATGGAATAGACACGCGCACAAACAGATATGTGACAAGGCTACTGTCTGTATA
CATGGCCTATTTTTCATTGTTTGTTGAGAACCTGTCCTATACCGTACAGTTAA
AGTCATCATTACCATGTTTTGCTGTAATGGAGGTTCTCAGTGATACATATAGA
CAATGCCCTTTATTATCTAGTATAAACAGTAGCTTTCCATTCCACTGTCCCAC
TTTGATTGCAATATAAGTGCTTTGAATTAATTGATACCCAACATGTTCACACG
TTACATACACTAGTGGTTCTGGGGGGGGGGGGACAGTGCCCCTGTGACAACA
ATTTTGGAACCCCTTGTGGCCCCCCTAAATGTGGAGAATGAACTAATTTTTAC
ATAACTAATTTTTGCTATCGTTCTTTTTTTACATCCGTTATTAGACAGTGGCGA
CGATGATGATTATGAGCATGGTCTTTTGCCTGCTAATGCCTGCAATGCAGTGA
AGAAAACGATATGACAACAATAACGTCTAATGTAACTGGCCCCTCTAACAGT
GCAACTGGCCCCAGCTTGGCCACCCCAGTTGAAATGGTCTAGAACCGCCACT
AGTTAC

SAL61D

TTTTACAGTGGATATAGATACTTTTGTACCTGTTTCCTCCANCATCTTCACAA
GGTCTTTTGCTGTTGTTCTGGGATTGATTTGCACTTTTCACACCAAANTACGTT
CATCTATTGGAGACAAAACACGTCTCCTTCCTGAGCGGTATGAAAGCTGCGT
GGTCCCATGGTGTTTATACTTGCATACTATTATTTGTACAGATGAACGTGGTA
CCTTCANNTNTTTGGAAATTGCTCCTAAGGATGAACCANACTTGTGGAGGTC
TACAATTTTTTTTCTGAGGTCTTGGCTGATTTCTTTTGATTTTCCCATGATGTC
AAACAAAGAGGCACTGAGATTGAAGGTAGGCCTTGAAACACATACACAGAC
TCAAATGATGTCAATWAGCCYMTCAGAAGCNTTCTAAAASCCATGACATMW
YATTTTGTGCATTTTCCAASCTGTTTWWARGSRCAGTCAACTTAGTGGTATGT
AATCTTCTGACCCAATGGAATTGTGATACAGKGAATTATAAGTGAAATAATC
TCTCTGTATTAATTGTTGGAAAAATGACTTGTGTCATGCACAAAGTAGATGTC
CTAACCGTCTTGCCAAAACTATAGTTTGTTAACAAGAAATTTGTGGAGTGGTT
GAAAAACGAGTTTTAATGACTCCAACCTAAGTGTATGTAAACTTCCGACTTC
AACTGTACATGTCATTTCAGGTCAATAACCACAGTCACGTGTTAGGTCCAAG
GTGTCATAATATGCGACTGTGGTCGTTTGTTCCTGCTGTATCTAAGAGACTTT

Figure 1I

GGACTGACCCAATAACAACAGTGAAGTTAGTTTGACATTGTTTTCCCCGTTGT
ATGAAACCCTGCACCGCAGCCCCCTACTAAAAGCCTGCAGTTCCCTCTTTCCC
TCCTTTTATGAGATGTACAGTATGTCCTGTAACCTCTGGT

SAL73D-A

TTCTTTAGCCATCTCAGTGATTTGGTTTCACAAGGCTCTCTGGGACTTTGTTGT
TTTGGTTGTTACTTCTGTAAAAGTTGTTAGCCTAAAGCTGTTATCAAAAACTA
TTATACTGAACACAAATATAAACGCAACATGCAACAATTTTAAAGATTTTGT
TGAGTTACAGTTCATATAAGGAAATCAGTCAATCTAAATAAATAAATTGGGC
CCTAATCTATGGATTTCACATGAATGGGCATGGGCCAGGCCATGGGTAGGCC
TGGGAGGGCATAGGACAACCCACTGGGGAGCTAGGCCCAGCCAATCAGAAT
TAGTTTCCCCTACAAAAGGGTTTATTACAGACATAAATACTCCTGTATACATC
TGTATTCATTTCTAGCTGAAGGGACTTAAGAGGGGACCTGGGGACTTATGAC
ATAGCGTTTGGCAGTGGTTCCAGGTCTGGTGACACGAGCAGTATTGGACTGT
GATGAATGACATGTATCTAAATATAGTGAGGAGCCCCACTTCACCCGGGACT
CCAGTTCACAGACAGAAACACACAGCCCAGGCCAA

SAL249D

CGCATCTACTTGCGACCCTTATGCTGTAAACACAGTCCAGTTCAGTCTGTCAA
TGCAATTGAATCCTACCCCAATGCGCTCTGCCTACAAGAAAATATCTTGCATA
GTTTGTTTTGTTTTGGTATGTTGCATTGAAAGTGGCTAATATTGCATTGATTCG
ATCACAATTCACACAGTAGAGGGAAATGTTGATAGTATTAACTAAAGCGGAA
AACTAGAAAGTTGTGTGAAGTTCAGTCCAGGGAGAGCTGCTTAGAGAGAATA
TTGGTTACAGATGGTTAGAGGTAGCCTGAGAATCTTCCAGAACATGTAATTC
CTGTAGTCTACCCCTCTTCTCTTTTTACCTTTTGTCTTTGTAAAACTCAGGTTA
TCTGGAGTCATTATACAGTGCCCTGCTGAAAAATACCTCAAAGCGGTGGCAT
TTGTG

Figure 1J

PCR primers for the respective salmon SNPs

M13-primer attachment:

SAL59U TGTAAAACGACGGCCAGTCCCCAGGAATGTTCTCAC
SAL59R CAGGAAACAGCTATGACCTTTCCCCTCAAGCATAATCTA

SAL70U TGTAAAACGACGGCCAGTCGTCGGGCTCGTCAGA
SAL70R CAGGAAACAGCTATGACCATTTTCAGGTCTTGCCGTAG

SAL78U TGTAAAACGACGGCCAGTTAGGTGGGGTGTAAAAGTCC
SAL78R CAGGAAACAGCTATGACCACTCAAATTTGGGTCTGAATG

SAL84U TGTAAAACGACGGCCAGTGACCCTTGGGTAAATCAAATC
SAL84R CAGGAAACAGCTATGACCGCGACTGCTGTCATGTCTAC

SAL43U-ii TGTAAAACGACGGCCAGTCACAACCCCATACATTATTCA
SAL43R-ii CAGGAAACAGCTATGACCGGGTAGAGGAGAGGAAAGG

SAL46U-ii TGTAAAACGACGGCCAGTGACCCATGGCAAATCTTTTCA
SAL46R-ii CAGGAAACAGCTATGACCCGTGACCGGGAGGCTC

SAL48U-ii TGTAAAACGACGGCCAGTGGAAACAGAGTTCGGGACAGG
SAL48R-ii CAGGAAACAGCTATGACCGCAGAAGAATGATGGGCACC

SAL83U-ii TGTAAAACGACGGCCAGTTGTCCAAATCCTCTTTCCCTC
SAL83R-ii CAGGAAACAGCTATGACCCATGTCACCTGGAGCTGATG

SAL19BNYM13U TGTAAAACGACGGCCAGTTGTAGTGCCCTTGGGTTCAT
SAL19BNYM13R CAGGAAACAGCTATGACCTGCCCAGCATTAGGTTAAGG

SAL23BM13U TGTAAAACGACGGCCAGTTTGTTGGCCAAATATGAACG
SAL23BM13R CAGGAAACAGCTATGACCTGCAACATTACCTTCAGCACA

SAL162BM13U TGTAAAACGACGGCCAGTTGGGGGTCATAGAGCAAAAC
SAL162BM13R CAGGAAACAGCTATGACCCAGGGCACAGACTACAGTGG
(Works with both SNP 162 b1 and b2)

SAL23MU TGTAAAACGACGGCCAGTCTGTCGGGAGAAACACGATT
SAL23MR CAGGAAACAGCTATGACCAGCCATCCCAAGGTTCTTTT

SAL93MU TGTAAAACGACGGCCAGTCATTCAAATTGACATCGCAAA
SAL93MR CAGGAAACAGCTATGACCGTCCTACAAGCCCTGGTCAA

Figure 2A

Without M13-primer attachment:

SAL15A-U	GCCACAACAACAGTTGAACG
SAL15A-R	TCCTCCCTCTCAGTCTGTCC
SAL46A-U	GAGTATGCCTCGACCCAAGA
SAL46A-R	GCTATTCCCACGGAGTACCA
SAL78A-L	TGACAGGATAACAACCCCATT
SAL78A-R	AGCCAGGCAGCAGCTCTAT
SAL87A-L	TTCTGTTCACGGGTGATTGA
SAL87A-R	TGGTGGAGCTTCCTGTCTTC
SAL96A-L	TGTGCGCTATCTTGGATGTT
SAL96A-R	CAAGGTGATTTGGTGGGTTC
SAL146A-L	TGGAAACTGGAAAAGAAGCA
SAL146A-R	CTGCTTTGTTTGGTTGAGCA
SAL147A-L	AACTTCCCACAAACCACAGG
SAL147A-R	TGGGGTAATGGGACATTGTT
SAL126B-L	ATGGCTGGTAAACTGCCAAG
SAL126B-R	TGCACAGGTGACATTCTGGT

(works for both SNP 162b1 and b2)

Figure 2B

L-104

GAGTGTTCCTGTCGTGtGTTCCAGAGAGACAAAGACACAGCGATCTGCTGACAATAGGAGCAC
AGAGCTCAGGGAAGTGGTCCTTTTCACCTCCACACAGTCTCCATAGAACACACACACACACAC
ACACATACACACACACACACACACACACACACACACACACACACACACACACACACACACAG
CCCCAAATGACACGTCTTGCCAATAATGTCTGACCTACTGGCAAATAACATTCTCACTCCAAT
GGTCATTGCCAGCACTGCAGACATGTTGACTTTGGGGGGGATCCACTAGTTCTAGAGCGGCCG
CCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGC

L-106

CTGGAAACTCAAAGAGTGCGAGGATGAGAACGCGAAGCCGGGTAAAAAGTGAGTTTCACAC
GCACGAGCGCACCCGAGCTCGCATGCACACACACACACACACACACACACACATACACACACAC
ACTCCAACAGAGAAATCCCCTGCCTCCCAGATACTCCCCCAGCATCCACAAGACACTACTATG
TTATCTGTATAACCAGGGAGTATGTGTGTAACATGTGATGTCCCCTCTGATAGAGATCTTACC
CAGCCCAAGCGTCGTGACAGACAGATCCAGAAAATCACCAACGCCACACGGGGGGGGATCCA
CTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTG

L-109

GTATTGTAGCTCGACTCCCATTTAGACAGGCACACCCCTTAGAGGACAGATAGTCACACGGTG
GATGTCAACATTATCCTCAGTGTAAGGTTAGCTATGGTAACATATTTTTGGAGGTCAGAAACA
TACAACGATATGCACACACACACACACACACACACACACACACACACACACACACACACACATC
CTCAAAGACCACGATCAAGAATATTATCACTCACAGTTGGGCAGGCTGTTTCCAGCGTAGCCA
TCCATTCCGTATGCCTTCAGCGCTCTGGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACC.

L-114

AAAAGTCCCTGATGGTCAAACATCAGGATTAGCTTTAGATTAGCATTAGGCGCTAACTCGCTA
AGCTTCGCTTAACTTGCTGAGCAGGTCCTAAAGAACAAATAGCTCAGCTCTACCCAATCACTT
CCCCTGATACTGACTGACTGACTGAACACACACACACACACACACACACACACACACACACA
CACACACACACACACACACACACACACGCTATAGTATAGTGTTTGACTGTGCAGTGCAGTCAGCA
CATGGATCATTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATT

L-115

GCTTTCCCTTATCTTACTACACCCTCACACAGAAACAAAACACTTGCACATTCGCATGCACAC
ACACACACACACACACACACACACACACACACACACACACAC

Figure 3A

ACACACACCTCCCAGCTTGCTTTGCTTGATAAATATGATGACCCAGACAG
GCTCCATCTCCTGTTGTGACCTCCCTCACCCCCATTACCCCCTCACCCCCCTGCCAAGCCTGGG
GGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAG
TCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
ACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCC
CGCACCGATCGCCCT

L-184

CTTTGTCATCTTATTTTGGTGTCCATTAAGGAACTCCAATACTGGAGTGGAAAAAGATGGTTT
GTTTCTAGAAAAGCCACCGACGTTGTAGTATTGTTCCCTACTGCCTCTGATGCACCACTCTGCC
TCTCACAACCCACAGAACCCAGAGTCAGCCATATCTAATCTGAGGTCCAACATCACACGACTC
CTCTCCAGCTTCAGGGCTACACACACACACACACACACACACGTGAATATTAACAGAGCAGTTCC
AAATGATGTCAGACCTCAGGCTAGTAACTATGCTATTCAATATATGTATGACTTCCAACTATA
GTAACTGTATTTCTCTGAAATGGTATTCATAGAAATGTTAGCTAACAATGGCTGGACTAGATG
GCTGGAGTGCTGTAGAGGCCTAAACGTTCTGCTTTTTCTATTAGCTAGCCTAAACCCCATCCA
GCCATTAAAAGCCATTCAAACTTCTATAGCAGCATCATAAATTAACCAAACCCATTACGGGCC
AAAGAGTGG

L-125

GAGGATGAACAGCAGCATAGCACACAGAGCACTCCGAGTCAGATCGCTGGGTTGGAACTGGG
CTGCTGCCTTAAATAGAACTGTAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGC
GCGCGTGTGTGTGTGATCTACTATGTATTCTAAGAGGCTCTGAGATAGTGTGGTGTGATGCCA
CAGCACTCTGAATCATTGGGATAACAGGGAGGCTCGGTCAAGGCACAGTGGGCTGCAGGAAT
TCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGT

L-135

GTTCCCAGCCTGAGTAGAGCACCTCTCTGGTGGACGGGATCCTCCGAGCGATCAGAACCCACA
GAGGGGTCAGCGCCACAAACACAGCACACACCAACGGGTTGGCATAGTCGTTAAACTCTATA
AGAGAACACACACACACACACACACACACACACACACACACACAGGGGTTAACATCATCGTTAT
GCTATATAACACACACTTCATCAGCTCAATATAGAAACTCAGACTGGGTGTGAATGGGAAATC
GTCAGTGTTTCCATGTATTTATGTGTGGTC

Figure 3B

L-173

CAGTAGTAATGGTATGGAGGTTAGAGTAGGAAGGAGTTTCTGTGTTACCCCCCCTCATTAATG
ACAGAACAGAATTAAGAGGGTTCCACCCACCAGAAGGTGTCTAGGAGTATGAACTAGGGGTT
GATTTGGGCATGTCTAACTGTTAACTTCTCTCTCTCTCTCCTCTCTCCTCTCTCCTCTCTCCTCTC
TCCTCTCCTCTCTCAGGAACGATGGGACAGAATTTGGGGGTTCTATCTACCAGAAGGTGGATG
ACCAGTTGGAGACGGCGGTCACTCTGGCCTGGACGGCCGGCAGCAACAACACACGCTTCGGC
ATCGCAGCCAAATACGCTCTGGACAAAGATGCTTCCCTGTCTGTGAGTAACACACACTTACGT
TTACACACACGTTCCATTTACACGCTTTACCCTGGCGGGACTTCAGCCAGCTTTACACACTAAC
ACACGTTCTCTGGCTGTCTCTAACTGTGTGTCCCCCTGCAGGCCAAAGTGAATAACGC

L-154

CTCTGAAATTCCTGTGCGGTTTGGAAGAATAAGACATCCCGCCTACTTTAAAGGCAGTCTTTA
AAGCATGTGTTACAGCACATAGAAATGCTCTTGTCATCATCTTGGGTTAGTTTGAAATGCCAT
GNTGACATTTTCCAAGGTCACATAGGCTAGCGCTTCTGAGTCAATGTCTAGGGAAAGTAAGAC
GGATGAGAGCTGTCTTCAGTAGGTCTGGATAAGGACTGTTAAATGAGATGAGAGAAANCTCA
TCAGAAGGCTCCATCTCTGTACTGTATGTGTGTGTGTGTGTGTGTGTGCGTCTGTGTCTGAATC
TGTTCCAGTACTGCTGAGAAGCATCTCATGGCACCTCATTTAATTCAACATCCACAGCACGGT
AAACACAGACACACATTTCCAGTCTCACTACTCTAAAGCCCTCCCAATGGCTCGCAATTCAAT
CATATCCTGTCTCCTTCTATGGACTGTTTCGAAATTGACGTGTCAGTCAGAACATCTGTGTGTG
TGGTATGTCCACGGACTCCACATAATTCACAAAGAATATCAGAGT AGGTGGTGATGTAG

Figure 3C

SNP311: 377BP

GAAATGTTTCAGGGTTCTTGAGAAGTTTCCAGGAGTCAGCAAATAGGTTCAAGTGGGATTTG
AACATGTTCTAAAATTCCTGACAGAAGACAGAATGGTCCATGAGGAGGCTGAGCAGTCCTTC
ATCATGTTTAAATAGGGTTCCTATGATTTTTTTAAGGGGCTTCTTTCTTCTCTAGTTTCAAGTG
TCTATTATTGGTCATTGAGAAAGTTCCAGGAGCACTTTCAGAGGTTCTGCAAACAGATGTTGT
TAAAGAAGCTATTGCAGTAGGGCTAATTTGAAATAGGTTGTCTGATTTTGTCACTGAAGTACT
AAAAGT**A**TAGTAAAGAAGTATAGTCTTTGAAATGTTTCAGGGCTCTTGAAGATTCTGAAGGTC

SNP 311U	TGTAAAACGACGGCCAGT	TGTTCTAAAATTCCTGACAGAA
SNP311L	CAGGAAACAGCTATGACC	CTTCAAGAGCCCTGAAACA

OLA311-1	Tamra	AAAAATCTGATTTTGTCACTGAAGTACTAAAAGTA
OLA311-2	Tamra	TCTGATTTTGTCACTGAAGTACTAAAAGTG
OLA311-3	Phosphate	TAGTAAAGAAGTATAGTCTTTGAAATGTTT

SNP107:

AACTCGAGTTTTATGGTCAGCGATCAACAACCTGCGAAAAAAGATAATCTTTACTGTTTTTTT
CCATCACTATTTATTGTCATGACCTTTCATGGACCTTTCTTTCATCTGAGAAAAATGTGCTAAA
ATGCACATGATGTGGTACAAAGCCACTGTGTGCTTTTTACACATATTCCATCTTTTGTAGGAT
GTGTGTATTCTGAATACAAAGATTCTTCAAAGAGTCATAATCTAAATAGAAACAACATTAGAG
AGAATCAATGTAACTGCAAAGTGTGTCTCATAAGACCCCAGGAGTTCCAGTGTAGTAGGTGT
GCTGGGTCTATAAATGCTTAAGAAGGAT**G**TAATACTTAAGCATTATGAATGCCCTTGCAGAA
GTAACTCATAATAAATAACACCAACCCAAATACTAAGACTAATTAAAAAGGTGAACATAATATT
GTGGCTATCTGTCCACTTTCATCCCAACCTTAGTACGGCAATGCTACATGAATAT

T-107U	TGTAAAACGACGGCCAGT	TATGGTCACCGATCAACAA
T-107L	CAGGAAACAGCTATGACC	TAGCATTGCCGTACTAAGGT

OLA107-1	Tamra	AAAAACATTCATAATGCTTAAGTATTAC
OLA107-2	Tamra	CATTCATAATGCTTAAGTATTAT
OLA107-3	Phosphate	ATCCTTCTTAAGCATTTATAGA

Figure 4A

17/169

SNP111:

AGTAGTGCACATGACACAGTTATTCACATGAAAACATTGCACGAAACTCAATGTGACTGGAT
TACCTGATCATCTTTAGTTTGCAAATAAACTTACTGGTGAACAAAAACCTGAACCTTGGTGAC
TCCTGCCCCTAGTTTGCTTCAACAACCCAATCCACCATTTTTACATATCTTTAGTCCTTTAGAA
CAAGTTCATGCATCAAAATATTAAGTATACAAAAAAACACTATCCTCGTTCTTGTTCTGCGTTT
TAATAGCAGAACATGACGACTTTGAAAACAGGCTGAAAACACAGCACGGTGCTGCTGGAGA
AAAGTTGTGCGCCTCAGCACAGTTAAAATCTATCAAACCCGCATTGCTGTAAATGTAATCAAA
AGCCCATCCCGGTGCTCTGCCACATCGCCGCTTAATTAAACGGTGAGAATATTAATAGAAAA
CTGCTTTATGTTGAAGCAGAAAATAAATAG

T-111U	TGTAAAACGACGGCCAGT	GTGCACATGACACAGTTATTC
T-111L	CAGGAAACAGCTATGACC	CTATTTATTTTCTGCTTCAACAT

OLA111-1		TCTTGTTCTGCGTTTTAATAA
OLA111-2		AAAATCTTGTTCTGCGTTTTAATAG
OLA111-3	PHOSPHAT/TET	CAGAACATGACGACTTTGAAA

snp 81: 717bp

AGTCTCTTCATTTGCAAGCCACCCTTTGGAGAAAACTCATTTCTGCCACTTTTATCTGCGATC
TTGTTCATTCTGTCACTACCCAGAGCTNATGCAACAAAGATCAACTCGACAGCTTTGCTTTCA
CGCTCAGCTCTTTCTTTGCCACAAGAGACCACAACAGTCTGTATCACTGCTGATGCTGCACC
AATCTATCTGATAGTCTCCCGCTCAACTCTTCCTTCACTCGTGGATAAGACCCCAGGGATTC
CTTTACTTGGGGCAGTAACTCATTCCTGACCCTAAGTAGTCACTCTATCCTTCACCAACTGAG
GACTCTGACCTTGGACTTTGAGGTGCAGTATGGCTACTGAACCAGATACTTTGGTTGTGCCT
GGTTGAACAAACTCCCACGCAACCTAAAATAAAAGGAACAAACTCTCTGGTCCCCCTTATCA
AAGTGGGGAACCACAATTCCGAGTTCCAATCCAGATAGATTTTCTTAGTTTTTTGTGCCCACC
ACAAAGTCCTGCCCTCAACCCAATAGAACATCTTTGGAATGAATTACAGCAGAAACTGCGAG
CCAGAGCAGCTCATGCAACATGAGTGTCTGACCTCATAAATACACTTCTGGAAGAACGGTTA
AAAATTCCCATAAACACACCTTATGGAAGTCTTGAAGTGTTGAGGCTCTTTGAGCAGCAAAG
GGTGGGACAACATCATTTTAACCCTATCGAT

Figure 4B

SNP81U	TGTAAAACGACGGCCAGT	GCCACCCTTTGGAGAAAACT
SNP81L	CAGGAAACAGCTATGACC	AAAATGATGTTGTCCCACCC

OLA81-1	TET	AAAAAGAGGGCAGGACTTTGTGC
OLA81-2	TET	GAGGGCAGGACTTTGTGG
OLA-81-3	PHOSPHATE	TGGGCACAAAAAACTAAGA

snp 64

ATACATGG CTTAAATAAA CAAAGTCACT TCTATTATCC ATCCATTCAT
CCATGGATGT GGAGCAGTAG CGACTACCTC ACAGTCCACT AGTCCCCAGT
TGTGTTACAG AAGTTCTTCA GTTATCTGCA CGCCACCTGG ATAGAAAGAA
AAAAGCAATC TATCAAATAT GTTTTTTGTC TTCTTCCTGT GCACTTGTGC
TCTAATCAGG TGATTTCGGT TAATGTGGAA AATAGTGGAG CGGAACAGCA
AAACAGGTTT TGAGGAGTGA AAATACACAT GGACATTGCT TTTATTTTTA
TTGCACAAAA GGAGCATGAT GGTAAAGGGG AAGCTGCATC CAGGACAGAA
ACAGCTGCAT TTTACTGCAT TTTTCAGCTT CTTTCAAGCA CCTGCACAAA
CAGCATCCTA ATGCTAAGCT AACCAGGAGC CCAGAGTCA TGACAAAGC
TGAGTGAAT GCCCAACCCC ATT

SNP64U	TGTAAAACGACGGCCAGT	CATGGCTTAAATAAACAAAGTCA
SNP64L	CAGGAAACAGCTATGACC	GTTGGGCATTCACTCAGCTT

OLA64-1	FAM	AAAAACACTATTTTCCACATTAACCA
OLA64-2	FAM	CACTATTTTCCACATTAACCG
OLA64-3	PHOSPHATE	AAATCACCTGATTAGAGCAC

Figure 4C

snp99; 528bp

ATCCCTGCCACACTGCTTTGGCTATTTGCACCGAAACCCCCCACTTCCAGCTTCCAGTAATG
GAGGACAACTAATCAGAATAGAGCTGGTTTAAAAGGGGGAAGAGTTAAAACAGTTTGCCCCT
CAATTCATTGTCAGTCTGAAATAATGTCACGGGTATACAGCGAATGAATACATTTAAAAGAGT
TTCCACCATGTTGTTACAACAGCACTTTGTCTTTTGTGTTATAATTATATATCATTTTAAATAAG
AGTTCTTTGGTTTTATTGGGCAAAACACAGTATTTGCAGGGGAGAGTAAAAAGACTGCTCTT
ATCCATATATATAAGCATATGAGCGCAGTCTTACTTGGTTCGTAGTAATCATAGATGACAACC
GTAGCTTCCTGGACTTTGGCAACTTTATACTCAATAATCAGAGGAATCTGGACACACATCTCC
GCGTTGTCACCTGGAAATAAATGTACAACTTAAGCTTCAGTATTTACACTCAGACACATCAGT
GTTTGTGAGCCGCTCACTGAGTCCA

SNP99U	TGTAAAACGACGGCCAGT	GCCACACTGCTTTGGCTATT
SNP99L	CAGGAAACAGCTATGACC	CGGCTCACAAACACTGATGT

OLA99-1	FAM	AAAAATCCAGGAAGCTACGGTT
OLA99-2	FAM	TCCAGGAAGCTACGGTC
OLA99-3	PHOSPHATE	GTCATCTATGATTACTACGAACC

SNP38:

TACACAGACCTGGGCAATTTAAAGTTGCATTGTGGATCACGATTGGTTAAAAACCAACGAACT
GCAAATTCACGCTTGATATTTCATATTTTAGTGAACACAGAGAAAATTTCTTTCTTTAGAATGA
AAATGAGTTGTTTTCTGAGAACAAACTGGTTTGGGATTGTAAAAGACATCTATATACATTTTT
ATTGCACTTTAAATGTCTGGTGAAGTCTGACACTCTTTAAATGAAACCAAGACTTTTGTGAATT
GCTGGATTGATGGCGGTCATAAAATATGACAAAATGCTGGTGATGTCGACAGACTGCTGTGG
CAGCCGCGAGGAGAGGGCGGCTTCTCGTGAGGTCATATCCAGAGACAATACTTTAAGACTTG
TTTGCTCTATTAAAAAGTTGGATGAAGTTCTACTTTTGTAAATGCGCGGTAGATCATTTTGTTC
CCGGCTCTCAATCACTCGCCAATTCTTCATTCACCTCAATTAGATTTCTCACATCATTACCAAT
GTTTAGTGACAGCTGTAGATTATGCAGAATGTCTTGCTGATTTAATCACCCTTAATGACTGGG
CTAGTCCTGTGAAGATTGATACAAACATCTTTCCCAGAGGCAGAATGGA

T-38 U	TGTAAAACGACGGCCAGT	CAACGAACTGCAAATTCACG
T-38 L	CAGGAAACAGCTATGACC	TCTGCCTCTGGGAAAGATGT

OLA38-1		GGGAACAAAATGATCTACCG
OLA38-2		AAAA GGGAACAAAATGATCTACCA
OLA38-3	PHOSPHATE/FAM	CGCATTTACAAAAGTAGAACTT

Figure 4D

SNP69:

TTTCACAGCATAGTCAGAGATGCTGCTGCACTCAATCTATGGAGATCAAATACAACAAACAG
ACACATCAACTATATCAAGGGACCATCGCTAGCTGTGAGTGATGTCATTACCATTGATTGGTG
AATAAAACACCTACCCCTATAACCTTCTTGGCTCCAGCTTTGGCGGCAAACATGCAAAGGATA
CCCGTCCCACTGCCCACATCAAGCACCACCTTGTCCTTAAAAAGGTGCTTGTTGTGGAACATG
GAATTGCGGTACGTGAGAGTGCGAACTTCATCCTTCAGCATCTCCTACAGCACAAAAGCAGG
ATTCATGAATACACACACAAGTTTCCTTGAGTTACTGCTCTAAACACACAGATTACAAACCAG
AAAAATACCTCATGAATTCCAAAGTGGGCGTATGAGTCAAAGTAGTAGTCCTTAGATGTCATG
TCCTCAGCTGCAGGCTTGGCTGAGCTCTCCCCCTGGGAAACCTCACAGAAGACCAAGATCGTC
TCAATTAAACATCATCTTTGCTAAACTCAGACANCCAGCAGCTTTGCTGGCTTCAAACCATTA
AATGTATTAATATAGCAACTCTGTTCC

SNP-69U	TGTAAAACGACGGCCAGT	GATGCTGCTGCACTCAATCT
SNP-69L	CAGGAAACAGCTATGACC	ATGGTTTGAAGCCAGCAAAG

OLA69-1	Tamra	AAAAAGATACCCGTCCCACTGCCT
OLA69-2	Tamra	GATACCCGTCCCACTGCCC
OLA69-3	Phosphate	ACATCAAGCACCACCTTGTCCT

snp 120 543 bp

GCTTAAGCACCCAGACTCTACTCCAGAGGCATGTTCATGTAATATGTGCAGAATGTGGTTTG
TGCTTGTTTTTAAGCAAGAATTCTGTGAGAAAGCAATCTGCTGGATTTTGCCCATGTTGCTCC
CAAACTTAGTTAAAGGTTTAATTTGATAGGCTATTAAACAGTTTTCAATCAAACACAAGATTTA
TGTGATTTGCAAACTTAATTCTGCTTTTATGTATTTGTTTTTTGTTTTTTTTTTAAACAGTGTCCC
CTCTTTTAAATAAAGGGCTCGAAAGGACCACAGTACTGTAATTTGGGAATTAAAAAATAAAGC
AAACCAACCTTGCAAATGTGCCGTAAACTGCCCATTTATTGAGCTGCTTTGTAGTCATGCCA
CACCCATTGTCCAGGACAATGACTGCAGGCTTCCCGAGACTTTCATCAAACAGCTGTTAAAC
AGATACTAATACTGAGTTACCGGTCTTCTGGATGCATGAGATTAAGCCAGTATTCAATAAACA
TACAGTGGGGGAAAAAAGTATTTAGTCAGCCACCAATTG

SNP 120 U	TGTAAAACGACGGCCAGT	TCTACTCCAGAGGCATGTTC
SNP 120 L	CAGGAAACAGCTATGACC	TTTCCCCCACTGTATGTTT

Figure 4E

HEX	120-1	25	AAAAAAGTACTGTGGTCCTTTCGAT
HEX		20	AGTACTGTGGTCCTTTCGAG
P		20	CCCTTTATTTAAAAGAGGGG

SNP´EN KAN VÆRE EN **G** ELLER **T**.

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snp 126 472 bp

ATGTTTAAGTGAACATCACATACACACCATCACACGTGCCCGCATGGGAGTGGACTGAATGC
AGCATGGACAGCAGGGGAGGAGGAGAAAGCTATTCAATACCTTGTCTGTCAGGCACCTTCC
CAGCCCTCGTTCATGTTTTATAACTCGAAGAGGCACGTATCTTACTGTAGCTACTTTTGTGCA
TGCCCCGTCCCAGGAGCAGGAGAATGTGCCTCCGCCTAAGCTTGTGTCATCTCACACAGCA
GCTCACCATCTCACTCAAACTGATAGTTTGATCAAAAGAGACATAGATATTGAAAAGAGCTTT
CCCCTGGTGGCAGGGCTGTGACAATACGACGACAAAATTAAATCACTTTTCTTTCTCTCTGT
CTGCCAGCCCGCTGCCTGCCAATGTGTTATTCACAATTCGAGTCCTAATCTCGTTAGCCCAA
AATTGTCCAATTTGATTTAATGTGCATTCTGTCCTTGA

SNP 126 U	TGTAAAACGACGGCCAGT	GTGAACATCACATACACACCA
SNP 126 L	CAGGAAACAGCTATGACC	AAGGACAGAATGCACATTAAA

	126-1	24	AAAAATTCTCCTGCTCCTGGGACG
	126-2	19	TTCTCCTGCTCCTGGGACA
P	126-3	19	GGGCATGCACAAAAGTAGC

SNP = G/A

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snp 135 770 bp

TGCCAGGCTGCCTGTGTAGAATGTAGACTAGCATTCCAGTGTTCACACCATGGAGGGATCC
GCAGCTTGTATTTGTGGAGAAGCCGGCTCACCGTAAGTCTTCTTGTTAATTCAAGGGTTTCA
CTTTTTAAAAGCAACTATTACATCAATCACACAAGAGATGCTGTATACCGAGGAAAAAACTCA
CCACAACTGATGTCTACAGTACCCTCCCTAGAGAAATTCACACCAAGATCCATACAGGAGAG
GTGTCACTTTAATTATCACGGTGTGAATGAGAGGCGATCCCTGATAAGTGCAGCACAAATAC
AGCAGTCAAACTTTTCTTAAAAGCCATAAGCAATGACATGGTTTTCTTTTTGCAGGACGTACA
AAGTAAAGGTTGGGGTCCGGGTCCATTTTATTGTTATTAACAACTGATCAAACAAATAAATAA
ATAAAACTAATCCCGTTTTACCACCTCTCACATCTCATTGATCCACTGAGACGGTGTGACTGC
TTT

Figure 4F

CTTTCTTTGATCTCATATGAATAGCCCCACACCGAAGTAGCCATTCACCCATAATTATATGTT
ATTATTATTCTCCTGACTCCACCATTTGACTAATTCTGTTTTCCACATCGCTAACACCAGCAGT
TACAGGCATTAGAAACATTTTCTTTTTTTGTATTGTCTTTTATTTCTGCATTGCGACATTCAGG
GTGTGATTGTGTAATCATCATCATGCTCCTGTGGAAATCAATGGCAGGTCTGTGTTCTATTCC
TGGCTACTACAAAT

SNP 135 U	TGTAAAACGACGGCCAGT	GGCTGCCTGTGTAGAATGTAGA
SNP 135 L	CAGGAAACAGCTATGACC	GAACACAGACCTGCCATTGA

[redacted]	135-1	25	AAAAATGCTGCACTTATCAGGGATC
[redacted]	135-2	20	TGCTGCACTTATCAGGGATT
P	135-3	19	GCCTCTCATTCACACCGTG

SNP C/T

---

snp 164 401bp

**ACCTGCAGTTGGTAAGGGACTACATGTTGCAGAAACATGTCATATTGGG
CTTTACTGTCATAGACTGTGAAGATGGAGATGGAGATGGAATGAACCAT
TTATACCCATCTTGAAACCTAAGCTTTAGCTATATGTACTGCTTAGTTTT
TTTAAATAAGTGATCATATTTCAATTAAAGGTTGGAGCAGTAAGCTAATG
CTAGCACTAATAAGGAACATCCAAAGACTTGTCTGTCACACAGAAACCTT
CTAATAAATGCTCAGTACATTCCAATAAAATCCCAGAATTTTACTACTCA
AACTGGAGCACAGACTTCTTGGACAGTCTGTCAGTACAGTTAACTACAC
AACAGCCGTATTATGTGTTCCAAAAGTGATGGTGAGTTTAACCAGGTGA
GGTAA**

SNP164U	TGTAAAACGACGGCCAGT	CCTGCAGTTGGTAAGGGACT
SNP164L	CAGGAAACAGCTATGACC	CACCATCACTTTTGGAACACA

[redacted]	164-1	26	AAAAATGAAATATGATCACTTATTTT
[redacted]	164-2	21	TGAAATATGATCACTTATTTA
P	164-3	22	AAAAAACTAAGCAGTACATATA

SNP= A eller T

Figure 4G

snp 165 536bp

GTATACTCCTGCTGCGTAAGGCAAACAGCAGTGGTGACTAATACAGCCACACTCCTGACTTT
GAACCTAAAAAAACATCCAGTCCAATGCATCTGACATAGAAACCGCCTGCCTGTACTTTGCT
ATTTCTGGCAATGGGATACAACACCTCTGACTAACCAGTGTTTGCTGGGTGTTAATTACAAAT
ACTCTAATTATACACTTTGGAAATTTCAGCAAATACACATTACTGTGCAAAGGTCTTGAGGCA
ATCCTCATGCCTTGATATGTTTCTAGGAAAATGGGAAGTAGGTGCAGCGATTTGCATGGACA
CGTGCACGAAAAGGACAACAGAGTTTTTACAATTCCAACAAACTTCAAAGTCAATATTTGCTG
TGACCACCTTTATTCTTCAACACAGCCTGAACTCTCTTAGGAAGGTTTCTTTACGTAGTCTTC
AGGAATAGTTCTCCAGGCTTCTTGCCGGACATTTAAAGCTCTTTTCTGTGAAGATGATCCCA
CACTCTGTCAGTAACGTTGAGGTCTGGGCTTTGGGA

SNP165U	TGTAAAACGACGGCCAGT	ATACTCCTGCTGCGTAAGGC
SNP165L	CAGGAAACAGCTATGACC	GCCCAGACCTCAACGTTACT

[redacted]	165-1	23	AAAAATTGAGGCAATCCTCATGC
[redacted]	165-2	18	TTGAGGCAATCCTCATGT
P	165-3	23	CTTGATATGTTTCTAGGAAAATG

Snp= C eller T

SNP178: 712BP

AGCAGTGGAAGCAGGGCGTTTGGACTGAAACATGCGGCGGTAAGACTGGCTGATGTCGCT
GTTCCTCGGGATGGTGGAGGATTTGTCAAAGTCTGAGGACTGCTGCTCCACTTCCTGATCT
GCTCCCACAGTGTAGTAGTCACAGTCCGATACTACAGAGACCAGGAGGGGGGAGAATTTAG
CATGATAATTTAATTTGTTTGAATAGAGCTGTCTGCAGAGTCAGTGTAACTGCTGATGATCTC
AAGCATTTCTCTGATATTATATAATTAAAGTCTTCTTAATTCAAGTTAACTTTAATTAGATTTTT
TCTGTTTTATATCTATGAGTATAGCTCAGAGCGAGATTTGACAAGTTTAGAAGAGACACAATG
AAAGTTTGTTTTTCAGTAATATACAATTCAGGTTTGTTTCTGGGTCCATATTTAGGTAAAAGAA
CATTTGTTATTCACAGCTGTCTTTCTGATTTCCCGAATATTGTTGGTGCTGATAATGGTAGGT
AATATTGGAGCTGCCTCTTAGCAGCCAGGCATCCTTTGCTGGAGATAAACTGTGAAATAGTT
TGTACTTAATTAATCTGGTGGGAGTAAGTTAAGTAAGTTTACCCTGTGAGGGGATGGTGTCC
TCTGAGCAGCAGGGTGTGTTGGTCTGGCTGCTGTAGCCGCTGGAGCCCTGCAGGGAATCT
CTGCTGGAGCCGTGGATGTCCAGCTGGA

Figure 4H

SNP 178 U	AGGGCGTTTGGACTGAAAC
SNP 178 L	ACGGCTCCAGCAGAGATTC

	178-1	31	AAAAACAATATTACCTACCATTATCAGCACT
	178-2	26	CAATATTACCTACCATTATCAGCACC
P	178-3	22	AACAATATTCGGGAAATCAGAA

Tot.lengde 48

SNP= C eller T

SNP 184 :442BP

GTGGTAGCTCCTGCAGTGATTTGAGCACCAAGTGAACAGATGTTATGTTGTCGTCAGCTCCT
TTTCCCAGTGCCTGGGACAGCTGTTCAAGATCCTTTATTATATGCAGCCTGAGAAACAAACT
GACGTCCTTCACGGGTGGCTGGATTATCTGTTGGACAACCTGAACAAAGAATGAGTGACAG
CATCATTGTTAGACGTAATAAAACAAGCGACATCATTCATTGAGTTTTGCGGATTGTTAATGA
ACTCGATGGAATGATTTGAGAGCTTGGCTACACATAAACTAAAAATATGCTAGGAGTTAAGC
TGCTTAGATATTGCCACTACTGTACAAAGTAACTCTCACTTCAGATACTTCATTTACAAATGAT
TAGGATCCACAAAAATAGAGTAATTATGATCTGCTCACCTCAGGTTTCTCTGAGGCTCCCAG
CATCAT

SNP 184 U	TCCTGCAGTGATTTGAGCAC
SNP 184 L	GGAGCCTCAGAGAAACCTGA

	184-1	28	AAAAACTAACAATGATGCTGTCACTCAC
	184-2	23	CTAACAATGATGCTGTCACTCAT
P	184-3	21	TCTTTGTTCAGGTTGTCCAAC

Tot. lengde 44

Snp= C eller T

SNP 517 562 bp

AATTTAGTTAGACTCTCGAGATTTTAAATACAATAAAAACAGTATAACCTGGTAGTAACACAT
GTCGTACTCCAACTGGTGGTTTGTTAGTTAAGCCACATGTGGATTTAAGCCACCAGCTGACA
AAACTATTCACTAGCAGCATTTAACCTATGAATGCTAAAGCGAGCTAGCAGAGGTTGGTTAG
CTAACTGGCTGGC

Figure 4I

TAGGTAGCCATGTGGAATCGACCACGAGATCTATTCGCCCATATGTGAATGGAGCGGTAAAT
AGATTTACGACGCAAGACAGAGTAACGCCATGAAATACCCCCCTGTTCCCAAACGACAAAAA
CACCCCCTTCCTTTCTGCAGTTTACCTACTTACGGTGACGGTTTGGGTCCAGGGGTAGAATA
ACACCGGTAAAGTTCACGACAACGTCAGTGACCGTAGTTGACAAGGGTCCGCCCACTACCA
GACTCATCTGTGCATTGGCTCATGTGCATCTCATGCCGGCAGCAATTGGCTGAAGCTAGGA
CAACCCTTTTGTAGTGACGTATCATTAGATTAATTTACTGAACATTCGCTGAAT

SNP 517 U	TGTAAAACGACGGCCAGT	TGTCGTACTCCAACTGGTGGT
SNP 517 L	CAGGAAACAGCTATGACC	TTGTCCTAGCTTCAGCCAAT

FAM	517-1	27	AAAAAATCTATTTACCGCTCCATTCAC
FAM	517-2	22	ATCTATTTACCGCTCCATTCAT
P	517-3	20	ATATGGGCGAATAGATCTCG

Tot. lengde 42

Snp= C eller T

SNP 560 730 bp

ATGAGACAGGGTTAAGCTGTGAGCATAAAAGATGCTCAAATGACAGGAAGAACTGCAGAGA
TCGAGAACATTTTGGAAAGCAAAGTTGAAACACAGCTGACTGATGACACAGATGGACCAGG
ATCAAGTACACGATTTGACTGTGTGCGCCAAGCTGTGCTGTGGCATGCCTTCGACTAATCAG
CTCTGTGTCTCTGCCACCTGCACTGAGCTCTCATGAAGCAGAGGGGCATTTGAGGACTTGA
AATAAAGACTTGTGTATTCCTTGTCATGTGCTTTCCTTTTCAACACATTAAGTTTCAATTTTCA
TATATACTAAATCATGATCGGCAAGTACTGCAGCTAGATAAAGATAGCCAGGGCTTATCCCA
CAAACTAAAGAATTTGCAAAGATATGAGAAAAAGAGCTTCGATAGAAAACTTTGTGGTCCAG
AGTGATTAGCATAGCAATTTTTCTGCTTTTCTGCTTGCCTTGCAACTAATTTACCCAAAAGCA
CAATAGTTTTATATAATAAAGGCTTAATAAGGCTCCAATAGGTTCTCTCAAATCTGCTCAAAA
GAAAAAGTCAACAACAGAAAACCTCAAAAATTACCCCAATGTAACTCCACCACAGATTTCTTT
CATGACCCCAAAAGAATGAGGTTACAGGCTGTCCATTCACTTGGACACAAAGACAAAGTCCC
CATTATGGTTGCCTTGCTCTTTTATAGAATCCTAACCTATACAGTT

Figure 4J

SNP 560 U	TGTAAAACGACGGCCAGT	ACAGGGTTAAGCTGTGAGCA
SNP 560 L	CAGGAAACAGCTATGACC	TAAAAGAGCAAGGCAACCAT

FAM	560-1	26	AAAAAGGCATTTGAGGACTTGAAATG
FAM	560-2	21	GGCATTTGAGGACTTGAAATA
P	560-3	24	AAGACTTGTGTATTCCTTGTCATG

Tot. lengde 45

Snp=A eller G

443

TTATTCATTTGTGTCTTGTCAAGATTGTCCTTTTTCAGTATAGGTTTTATTACAGCAGTTTTTAG
TGATTCTGGAAACACACCTGATATTAAAGAAAAGTTGACGATCTGTAACAGGTCATAGATACT
GAAACTACATGTTTSGTCAATCTCCGACCAAAATTCACTGAGCCAGCAGCAAAAGAAGACCA
AATTTATGCTTCATGTTAGAAAAACATTGTCATGAATTCCAAAAATGTCATCCAAAAATGTTA
AGGGAAAAGCTATAACTCACCTAGAGCTGTCCATGATACTGTGCAGGCGGTGGGCGATGGTA
AGGACTGTGCAGTCTGAGAACTCTTTGCGGATGGTGTTCTGAATCAGGTTGTCTGTCTCCAGG
TCAACAGCTGCCGTGGCTTCATCCAGAATTAGGATACGTGACTTTCTCAGGAGTGCTCGAGCC
AGACACAGCAGCTGCCTCTGCCCAACACTGGGAAGATCGTAGGTCATAGCTGTTTCCTGG

SNP-primer sekvens:

snp443u	TGTAAAACGACGGCCAGT CCTGTAGTTATTCATTTGTGTC
snp443l	CAGGAAACAGCTATGACC TACGATCTTCCCAGTGTTGG

OLA-primer sekvens:

OLA-443-1	AAAAAGGTCATAGATACTGAAACTACATGTTTC	
OLA-443-2	GGTCATAGATACTGAAACTACATGTTTT	
OLA-443-3	GTCAATCTCCGACCAAAATTCA	PHOSPHAT

484

GCTCAGCCTTAATCTTTGGAATTAAGGATCCATGAATCTGATTTAACTGAACAACTATAGACA
ATGCACTTTTCATTTCATTTCTCTGAATCTATACTTTGAGTTTCAGTTTGTTTGTGTTTATTCAA
CCATAAAAAAGCTGCTGCTTCTAATCAAAGGCGCTATGAAATCTTAGCTATCGCTGGAACAAAT
CTTTGAGGTGTCTG

Figure 4K

ATGAACAAGATTTGCTACAAGGTGCCCAAAATCTAATCTGATCATCTACTGCCTAGATGTCST
ACGCAACAGACAGTTCCTTCTGCAGATGCATTTCTTTAACTTTGGTTTACCTGCTCCTCTACTT
TCACAGAGTAATCCTATAGCATCTTGGCACACAATGGCAGAAAAAACCTTGGTGGACTGGGA
CTGGCCCGTC

SNP-primer sekvens:

snp484u	TGTAAAACGACGGCCAGT	CCCAGTCCACCAAGGTTTTT
snp484l	CAGGAAACAGCTATGACC	CGCTGAGCCTTAATGTTTGG

OLA-primer sekvens

OLA-484-1	AAAAATCTGATCATCTACTGCCTAGATGTCA	[redacted]
OLA-484-2	TCTGATCATCTACTGCCTAGATGTCC	
OLA-484-3	TACGCAACAGACAGTTCCTTCT	PHOSPHAT

573

CTTACAAATGGGAAAGTGAGGACACGTCATTAAAGATGCCATCGGGAAGCTCTGAGATTTCA
TTGCCATGAAGAGACCTTAAGGGTGAAGGGGAAGGAGAGGACAAAAAGAGAAAATTCATGA
AGACATCTGAGCACAGAAAGAAAATCATACTATTAGAACAAAGTTCAATAGAAGATTTACTGA
TTGGTCAACTGCCAGAAAATCAACTAGTTTTTGATTTGTTAAAACACACTAGTATCAATTTTTT
TTTAAAAAGACAAGTATTTGAACATTGTCCATGAAATGTCCCATTTCAGTATTTATAGCAGTG
CTCCTGTGTCCAAATGGTAAAGCTATATTTTTTTGAAAGTAAACCAAAGAGTCGATATATTAAT
TGTCAGTGCTGGGTTGATTGCTTTCCAACAAACCAAAACCAGAAATATCAGGAACAATGGCG
CAATGTTGTCTTGGCATTCTAAATGAGCGGGAGGTGGTT

SNP-primer sekvens:

snp573u	TGTAAAACGACGGCCAGT	AATGGGAAAGTGAGGACACG
snp573l	CAGGAAACAGCTATGACC	GAATGCCAACAACATTGC

OLA-primer sekvens:

OLA-573-1	AAAAACCATTTGGACACAGGAGCACT	[redacted]
OLA-573-2	CCATTTGGACACAGGAGCACC	
OLA-573-3	GCTATAAATACTGAAATGGGACATTT	PHOSPHAT

638

ACATTTAGATTCCCAAAGCTTCATTATTTTATTTGAACTTATACTATATCC
ATTTACAGATGCACACAAGTATGGTTTTAAGACACAATTGGAAGTATGAC
TGTGCTGGTTTGGGTCAAAAATGTCATCTACCTACCAACAAGCAGAGGG
TLAAACAGAAATCCTGTCCATAGGCTTGATTTCTTGCATTTGCGTAATAT

Figure 4L

CTCTGTTTTAGAAATCACATGACTATCCAGCGTTGCAACCAGGAAAGAG
TTGCAGTCTTACGCACCTCTCTGCAGTTTCTCTCCTCCTTCTATGACCCC
AAACCCCATCACCATAGAAACTGTGTCTGCTCACAGACCAACGAACCAA
CCAAAACTGAATTAAGCATAAAACAATCACAAAGAAAGAACAATACAGT
TTCCTCAGCTCCATCAGCATGTCTGTTATACCCCATTCCTAAAAGAATGC
TTAAAGACTTCCTACCGTTGGTTAAATGATTCACTATAAAATGTTGTGGA
G□

SNP-primere:

snp638u	TGTAAAACGACGGCCAGT	CATTTAGATTCCCAAAGCTTCA
snp638l	CAGGAAACAGCTATGACC	TCAATCATTTAACCAACGCTAG

OLA-primere:

OLA-638-1	AAAAATTTTAAGACACAATTGGAAGTATGAC	[redacted]
OLA-638-2	TTTTAAGACACAATTGGAAGTATGAG	PHO
OLA-638-3	TGTGCTGGTTTGGGTCAAA	SPHA
		T

454

ATGTTGCTTGTCATCCCACAGTTTGTGATATAAAAAAGCACAGCTTCTGTGCATTCCTCCAGCT
TGGTTGAATTAATCCCAGGTTGTGTGATCAAAGCAGTCCTGTAGCTGTGATTGAGCCTCTTCA
GGCTGTGATCGTCTTCATTCSTGACTTTGTACTTCTAGCAGAAAATGTTGCAAATGTCACATGC
TGGTAGAAGTTGGGGAGTACTGTTTTAAGACACCAGTGGTTAAAGTCGCCCACATGTGGGTGA
CTGAATGGATGCGCTGCTGTTTGATAATGATGGCATTAGCATCTGGTGGGATGAAGACAACAG
TGACTATCACCACTGAAAACTAAATATTATATTTACCTAATGTTAATTTTCCTCTAATTATTGG
AGTTAGAAGTGTAGTTTAAAAGTTCTGAAACACTCTTAAGCTGCAAATATTCACAAGATGTTG
TAAA

SNP-primere:

snp454u	TGTAAAACGACGGCCAGT	CATTTATCAGTTGCCATGTAGG
snp454l	CAGGAAACAGCTATGACC	TTGGATGTTGCTTGTCATCC

OLA-primere

OLA-454-1	AAAAAAGGCTGTGATCGTCTTCATTCC	[redacted]
OLA-454-2	AGGCTGTGATCGTCTTCATTCT	PHOSPHA
OLA-454-3	TGACTTTGTACTTCTAGCAGAAAATG	T

Figure 4M

491

ACGGCCAGTCACACAGCCCCTTTCTCAATTTGATGACACATGTATCGGTCCCGCTGCTAGCTG
TTTAATAAAGTCATTGACAAAGAGCCAGCATGAGACAGTGTCTGAAAGCAGTTTCAAGAGTT
GTGTGAGAGTTGGCAACAGTCTGATACSGAAGGAGATAGAGATGCTCTCCCGCAGGGTGTGA
TTTAGACAGGAGGCGGAACTGAGCTCTGGTGGGCTGCGACCCATTTAACCCCTGGAAGTGAC
GCTGCTGTTCTTTCACAGTTAATATCAGTGTTCTATTTAATAGCCATAATTTATACAGGTTTAT
TGTTTGAAACCTTTTGCATACACTATATTGCCAAAAGAATTCACTCACTCATCCAAACAATCA
AATTCAGGTGGGTCATAGCTG

SNP-primer sekvenser:

snp491u	TGTAAAACGACGGCCAGT	CACACAGCCCCTTTCTCAAT
snp491l	CAGGAAACAGCTATGACC	CACCTGAATTTGATTGTTTGGA

OLA-primer sekvenser:

OLA-491-1	AAAAAGAGAGTTGGCAACAGTCTGATACC	[redacted]
OLA-491-2	GAGAGTTGGCAACAGTCTGATACT	PHOS
OLA-491-3	GAAGGAGATAGAGATGCTCTCCC	PHAT

SNP 528

TTTCTTTTATAATGCAATATAATCTGCATATAAACATTTGAGATTATAAAAAGCATTCAAAAGC
ATTTAAGATTATAAATTCAACTCAACAGTTTAAAGTGGTTATCACTACACCTGCAACAAAGGTT
AATATGATTATGTTATTAATGCAATGGTAATGATGATGATTATGCACAATAGCAGCAAAATATT
TCCCTCATATCAACAGTAATAATATTCAACATTGCTGTCAATACATTTTTCAAAAAATGCCTCT
CTGTGCAAAATGGGTTTAAAAACATAAACAACTGTCAGATGCTGTTTGTCTGTGATTTGAAAA
GGGGGAACAAATTGTGGCAGGATCAGCCTGATATTATTTGTATCCCACTGTAACTTTACTGT
ATAAAGAGCTAACATGTCCAAAATGTCAGGAGTAGTCATTACAAGAAGTGTTTGTGAACTAAA
AATCAAGAATGTGGGATCCTGTTTGTCCGTGATTTGGAGAGCCCAGCGCGTGCTCCCGACG
CAGGGGAGACCTCACCTTGGCACTTGTGCAGGTGAAGCCAAATGGAAGATATGCCCCGTCA
AAAACCTGTCCATTATGCTAGCAGTGTCCGAGCGTTTTT

SNP528U	TGTAAAACGACGGCCAGT	CATTTGAGATTATAAAAAGCA AT TTCAA
SNP528L	CAGGAAACAGCTATGACC	TCTTCCATTTGGCTTCACCT

Figure 4N

OLA-primere:

OLA-528-1 AAAAAACATTCTTGATTTTTAGTTCACAAACA

OLA-528-2 ACATTCTTGATTTTTAGTTCACAAACG

OLA-528-3 CTTCTTGTAATGACTACTCCTGACATT



PHOSPHAT

Figure 4O

TN299
TGNGTTNTTCCNANNGANCTCTTTGAAGCCCCCCTCGAGGTTNACGGTATCGATAAGCTTGAT
ATCGAATTCCTGCAGCCCCCTGAGGGACGGGCGCGNACACACACACACACACACGCACACAC
ACGCACANACACACACACACACACACACACACACACACACACACACTTACTCTTACTCTTACTGTAG
TGGCGAGGGTGTATTTGATGCTGATGACGGGCAACCGAGCATCGATCTGCACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGA
GGGCGAGGGGGCGACGGTTGCAACAGTCCAGTTGCGGTCGAGGCATTGTGGTGGGTGGTTGG
CGGGCGTCCGAGTCGTTTTGTGCCTCCTCTAACTCGTCTTCTCCTGGCAGGACTGACAGACCG
ACACAAAGTCACGCAGGAAAGAAGCACGGCTTAGGATGGCGAGTGCGGCGCCAGCCAGGAA
GCCGTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCNCTAT
AGTGAGTCGTATTACGCGCGCTCACTGGCCGTTGTTTTACAACGGTCGTGACTGGGAAAACCC
TGGCGTTACCCAACTTAATCGCCTTTGGAGCAAAATTCCCCCTTTTNGCCAGGNTGGCGTTAA
ATAAGCGAAAGAAGGCCCCGAACCGGATTCGNCCCTTTCCNAAAAGGTTGGCCNCAATCCTT
GAATNGNCGAAATGGGAAATTTNTAAGCGTTTAAATATTTTTGGTNAAAAATTCGCN

TN641
ATCTGACTGTAGCAAATTTGCTAACCAGTCAGTGTCATTGCAATTCTTCAGATACATGAAACA
TTTCTGTGGCACTGGTACATGAGACATACTTACCAAATTCCACAGCATATTTCTCTCCGAGGCT
CTTGCCATCTTTTTTTTTTTTTTTTAAGCTATGCAGAAGGTTGCAGTGTTTCTACTGGAAACTGTT
TATCCTCCAAACAGCCTGCTTAAAATCAATATTTTACCTCCAATCTCCAGTTACTATTCCACTG
CTCTTCTTTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTGTGTGCGCAAAGTGTGTG
TACAGCTGTGCACAAATGCAAATGATTACAAAGAGCCCCGACACAGACATTGAAATACCTGC
TGATATGCTTAAAGTTGATATGATAGTAGAT

TN203
TNNNNCTCTGAACANTCTTTGGCCTTTCCNGCCCCTTCTCGAGGTCGACGGTATCGATAAGCTT
GATATCGAATTCCTGCAGCCCTTTAGCACTGATGTGAGTTAGCAGAAGATCTGGCAGAGGTCT
GTTGTGAATGCTGGTCTTATATGCTGGTGGCTTGATTGGAACCAGGCGTGGAGACTGATTGGA
GGCTCTGCCTGAAGGTGGAGCCCAGTGGAGTGGAAAAACCCCACACTCACCCAGACCATAAC
ATATAGTTGGTTTACACAGCTTTGTGTATGTATGTGTATGCATGTGTAATGTATGTATAGACAC
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGATTTACATTGCTG
TGCTTGAGAGCCANCATCTACCGGAACCAAATTCCTTGTNTTTGTCTGCACATATACTTGGGG
GGGATCCANTTGTTCTAGAGCGGNCGNCACCGNGGTGGANCTCCANTTCGCCCTATAGNGAN
TCNTATTACNCNCNCTTCANTTGGCCGTNNTTTTTNCNAACTNTCNNNNACTTGNGAAAAACC
CNTGNCNGNTTACCCANCTTTAANNNNCTTNCTANNC

TN307
AAATCACACA TATGTGCACA CATACCACAC GCGCGCANAC ACACACACAG
GCGGGTATCC CCGACCCTGG GGGAGCTGCT TGGTTCTCCC ACACTCGCTG
TCATTTTTTT TTTTTTTTTT TCTTACTGCA GTGTTTTAGA ACATTTTATC
TAAACTCTGG AGGATCGGGC TGGGGTTTCC CCTAGTAACA CACACACACA

Figure 5A

CACACACGCA CACACACACA CACAGTGCTT NTCCAAAGGC TCTCCCTGTC
CTTGGCAAGG ACACATTGAA CTGCGGGACT CCTGCCATAC ATAGAAACAC
ACACACACAC ACACACACAC ACACGGACAC TCATTCACAA AATGA

TN210
CTCTCCTTTGGTNGGAGATCTACNGGAANGCCCTTCGTTTGGGGAAAGTACCCATAAGCTTGA
TATCGAATTCCTGCAGCCCACTCTGGGNTAGTAGAAAAGCGCTATATAAGAATGNGGGGATTT
ACAAGTCCAATGTGTAAACACATCTTCCTCATTCATTATTCTTTGTCAAACCAACAAAGTGCA
GCCAAATATTTTTAATTAAGCAATTGTGTGTTCCTTGAACAGCCTAGATTCAAACAGATCTAA
TTTAGCATGTCATGTAAACCTATTGCTTATTATCTTTTATTGACAACAGTGGGATGAACCTGGG
CACGTGCACGCACACACACACACACACACACACACACACACAGTTGTGCAAAGAAATTTGGAAA
AACACCATCATCAGCACGTNCGCCGTGGCTGACGACGCAAATAGCAGCTGAGCTTGAGTTGG
AGATCAGTGAAGCCAGTCTCTTTGAAGATGTATTGCCACCAGGAAAAAAAAATTTTTGCAGCTT
CTTCCTTAAAGCANGGGGGGATCCACTAGTTCTAANANNCGGGNCGTCNACCGGGGGTGGGA
NNCNTCCNAANTNNNCCCCTATAGTNNAGTCNGTANTACGCCGCCGCTTCACC

TN537
CCTGACTCGTGCTCAGATTAATATCACCATTGATCAGATTGGATGGGAGGTGTCCTCACACCC
GCTCCAAACACCCCCCACCCCCAAACACCACACACACACACACACACACACACACACTCCCT
CACTCTTTCATTGCAGGGAATAGGGCTTTGCACTCTGAGAATTCCAGTAATGCGCCTTTCCGCC
ATGCAGCTGTGATTTGAAGCACACATGCGCATTTCATATTTATGTGTGTGTGTATGTGTTGGCT
TTCNTGTATTTTGGCATGTGCAAAAGTGCCTGCAAGCTCACCTGCGTGTCTCACCTCTTTGGTT
TTATTCATGAACACTTCTTCTTCATGGTTGTTTTTTTGGTGCTGCTCTTTTGAAAATGGTACTGC
AAAAGGGCCTGCAAATGTGCTGTGGGG

TN655
ACACCATTATGCTATAATGGTAGTGTTATTGGAGGAGGGGATGATGAGGAAGATTAAGATGT
CCATCTGTTGCCCGACAGTCAGCTCAGATCAGCATGTGGACGTACTGACTGCTACGAAGCCAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
GTGTGAGACAGCCAACAGGGTTCGGCAGAATCCAACAGGGA

TN380
TGTGTNTTGTCNGAACCTTGGGTACCGNGCCCCCCNTCGAGGTCGACGGTATCGATAAGCTTG
ATATCGAATTCCTGCAGCCCCCCCCGCCCCACGCCCTCTGCCCAAACTGTCGACACCGCCGTAA
ACGGGGACGCTCAGCTGGGTTGTCTCCCACGGTGACATGGTCACGTGGTTGCAGGGCAGTCA
AATGAGACTGCTGTCTGCTAGCGCTCGTTACAGTCAAAACCACCTCATACTTGAATCAGTAAG
TCACACACACTCACACTCACACACACACACACACACACACACACTCTCACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
TTGCGGTTTCTGTTTTGGTCTTAAAGTTAGAGGAGGAGAATATGTTGAGAAGTTTTACTGGAA
TGCGTCTCCTTCCTGTATGGAGCGTAACCATCTGTGGGGGGGATCCACTTNGTTTCTAGAGCG
GNCGCCANCGGGGTGGGAG

Figure 5B

CTTTCAATTTGGCCTTATAGTGGAGTNGGNATTTACGCGCCGCCTTANTTGNCCNNTTNGTTTT
AAAAACGTTTGTTNAATTTGGGAAAAAACCNTTGGNNNGTTTNNCCC

TN188

GNNNNNNGGNGANGTTGTNTTGTNACTNGNNGNGTNTNANGGAACTTTC
NCAAGTGCCTTTCCGCTTTAGANCTAGTGNATNCGNCAAACGGAATTCT
GCCACAAACACAGGTCAAACCACAGTGTTCAGCATCTATATGGGGTANG
NGANTGTCATGTTCCGCAGCCNGTTGANGTNAAGCCAAAACATACCGAT
CATTTCAGCTACTGCCTGACTCGACTCTCCCATGTGGTCCAAATGGCTGA
CCAATTAACAGCAGCTTAACTCTTGAGTCCAAACAGCTATCTCTCTTTCT
CACACACACACACACACACACACACACACACACACACACACACACACAC
ACACCTGCATGAACACATAAGCAGAAAAGCGGATGCACACAAGCATACA
AAGTAATGGACATGCTGATCCACAAGCACTTAGACCCAGTGGGCTGCAG
GAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCG
GTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTA
ATCATGGTCATAGCTGNTTCCTGTGTGAAATTGTTATCCGCTACAATTCC
ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAA
TGAGTGAGCTAAT

TN371

TTTACCTCCCTTTGAAAGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCC
TGCAGCCCATCGCAGCTGCCTTTATAAGCGATATTGCAATGGGACATTTGCTTCTCGCACGAA
CATTATCCAACGATTTCCCCCTGAAGGCTTGGCATGTTCAATTTGAGACGCAGCCTAAAATAC
CAGGCAGCGCATCTCACACCCTGGCATGTGGTGGTGTCACTCCTGTTCATCACTCAGTTCCCGT
TAGACTCCCACTGGAGCGAGATGGGTTTGATGCTGTGTGTGTGAGTGTGTGTGTGCAAGCCAG
TTCTTTCTTAATGCTTGTTTGATGGTGCATTTGTGCACTTTGTTGTGTATCTCTATTTACTTTTGT
AGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGAATGCTGTCTGTGTAGTAAACAGACGC
AGCGCAAGTCGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGNGGTGGAGCTCCAATT
CGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCCGNCGTTTAACAACGTCGTGACTGG
GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATNCCCTTTCNCCAGNTGGNNTA
ATAGCGAANAAGGCCCGCACCGAACGCCCTTTCCCAACAGGTTGCGCANCCNAATGGCGAAT
GGGAAATTGNAAGCCNTAAATANTTTTGTTAAAATTCNCCNTANAATTTTTGGTAAAATCNNN
TTANTTTTTTAACCCAATAGGCCGANATNGGCC

TN320

CTGCACACAC AGCATGTCTT AAAAACTAAT GCTGAGCTCC ATCAGGGCTG
GATGCCATGA GTCTTAATTA AGACAGCCAT GCCAAGTCAA GAAGTGAATA
ATTCTACTCC CCACCAACCA CCACCATCTC CCTATTACAC ACACACACAC
ACACACACAC ACAGAAGCCT AAACTCTCAT TTGCAGATGG ATGAGCGTGT
AGATGCAGAC AAACCACAAA GAGAGACTCA GATTATCAGT TTTAATGGGT
CAGAAAAAGC TTGCTCAGTG AGTAGTGTGT GGATGCCTGT GTGGGCGCTG
AGATAGAAAA ACCATTTAGT CACACCTACA TGAGATACCT GTTGTGT

TN124

TTNGANCTNTTGGACCTTCNGACCCCNTCTGGAGNTCGACGGTATCGATAAG

Figure 5C

CTTGATATCGAATTCCTGCAGCCCNTCAGATTTACAGTCTATACTTCATATTNNGATGGAGTG
GGAAAGAAAAGCAGGACAGGCGCAGGACACACACACACGCACACACACGCACGCACACACA
CACACACACACACACCTTATGGAAGCTATTAGTTCTGATAACTATTATTACTTCCTAATCATCC
TAGTGTCATGTTGAACACTTCACAGGAGTGAGAAGCTTGCAAATCTAAGCAGGCAGGTGTCA
AAGCAAAAAAAAAAAAGAAGAAGAAGAAAAAAAAGGAAGAAAAAAATGCTGTAATGTTGCAAT
AATGTGCAGGCAGCTGAGGAGAAAATGACTGCCCAGATACAGACTGCAGCTAAGTGATTCAG
AAGAAGAGGCTAGCGAGCTTTGACTGAAGCAGATGGCCTCTGTTATAAAAAAAGTGCATTAAA
CACAAAGATCTTCTTACTTTACCCACAGAAAGATAAAGTTGATGCCGTTTTATGAACCCTGNG
NGGATATAAAGAGCCCACTATTGGGAANTATGGACAGNGCTNCTNTCCATGG

TN223
TTNACTTTTAATTCCCTTTTGAACGCGGCCGCNGCCGTTCTAGAACTAGTGGNTCCCCCACAA
AATCTCTCCAGCCTGTAAGAACAAAACAATGCAGTCTTATCAGGGATCTCTTATTTGTTTACA
CAacaaATCAgAGCCGACTGGTGGAAAGTTCCTGCGCTTTTGTTTATCTCGGCTAACTGAGGGCA
GAAGAACAGGACGGTCCAGTTGATTACTTGAGGTGTTTTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGCGCGTATGTGTGTGCTGAACTCTTTACATTTCTTTTCTTTTTCAGGAAGAC
TTGCAGCAGTTGATACTCATGCCTCTCCCAAATGTTGCCATTCTGGGACCTGTGTAAAAGCAG
CAGGATTTACGCTGGAATTTTAGTTCTGCTGAGCCAAATAAGACAGGTCAGGGTGAAGAAGG
CACAGCCAAATAAAAGCCTACCACAAAACGGAAANGTTATGACAAATCANACTATGAGGCAA
AAAAGAAAGCTCAGCTTTTTTGGTTTCATGGACAAAAGAATTTATGTGGCTGGAATATGACGA
GCTAAATAACATAATGTTCTGCCGGGTGTGTNGTGAGTTTCNTTTNATTTGAGTCGACAAGCG
CCTTTTGTNACTGGGACCAGTTATTTNGNAGAAANACCCCATTAGAACCCATGAGNANATCAA
GAAAGCATTATTTGCCCANNTCTGCNATATCTTTTCCCAGAACAANACANGCATTTGCAAAAA
NATTAACCNNGCNGNAACCCNAAGTCCCTGAAAAAATNTTTTAAAAGCGGGGGCTNC

TN369
TTGATTTNATTCCCTTGGAAACCCNGTNCCNTTTGGAGGTCGACCGTATCGATAAGCTTGATA
TCGAATTCCTGCAGCCCCNTTATATGCATTCATCCCATCACCTGGAACaCACACAGAAAGCTG
AGTCACACTAAAATAATTACTCTAATTACTcCATTTCATCACTAGTATTTACACAAACCAGTGA
AACACACACACACACACACACACACACACACACACACACACACACACACACACACACATTGTGTCACT
CTTAAAGAAGTAATAATACACCAAGAAAAATACCTGACTGATGTAACAGGAATACACTCTGA
TCAGATGCCAGACTCGTTAAACTGGTTTCATGTGTTTCCTTGCGGTGACAGACGAGCATTAGC
AATTTACAATTTACTGTTCCTTGTTTGACCTTTATATTTATTTGGGGGATCCACTAGTTCTAGA
GCGGCCGCCACCGNGGTGGAGCTTCAATTNGCCCTATAGTGAGTCGTATTACGCGCGCTCACT
GGCCCGTNGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAANTTTAATNGCCTT
GNAGCACATTCCCCTTTCGCCACTGGGGNTAATTAGCGAANAGGCCCNCCCNNTC

TN346
TNNNNTNTTGGNCTTTGAAGCCCNTTCCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCCCGAGTGTGTGTGTGTGTCTGTTTGTGGAGTGTGGTAGCT
TTTCATCTCCAGAGGGGAAAACACAGGCAT

Figure 5D

GTATTTGCTTGTTTTTGTTTTCCCCTGCCTCCCTCTCGTTCAAGCCCTCGTCTCTATGCCTCCCT
CATCCCCGAGCTTCTATTGTGTGGCTGAGATGAAAACTAAACAGAGCCGAACCTGATCTCTCC
TGTCTGATGCACACACACACACACACACCCACACAGACACACACAAAGATGTGCATGCCTGC
AGACGCTCTCTGTGTGGTCCTGCACGTCTTTAGATCTTCACACAGTTGCCGCCAAAGTCTTCTA
GAGTTGTGTGCTTATCACTGTTCTCTTTCTGCGCATTATACTACGAGTTTTCAGCAGCAGTGAT
TTCACCAAGTCGTTTTGTTCTTTTCGCTTTTTCCTCCGTTACTTCAAACAGAAGTAGACAGGAC
AGAAATGTCTCACAATGAAATAAACACTGAAATACTGGTAGAGCAAGAGCGAAGATGAGTCT
GAAAGATCTCGATCGATTCATGTGAAGTAGGACTGCTGATGAGCCTAGTAGAAGGACCNTGG
ATATTGGGCCTGATGAAACGGGAGGTGATAGCGGGAGGAAGGGTGCATTGATCTGCCCANCA
NTGACAACTGACAGACAAACGCAGGGNNTTTTGANACGCAN

TN689

ACTGACAAACACACTTGCAGTGAGACACAGTGAAAGTCAATACTCTTCGCCTTCTTCCCTTCT
CTTCCTTTGACTCCCCGTCTCCTTCACTCCTCTCACCAAACATCCGCATCTATTCCTGTCGGACC
TCCTCTCAAAACCACAGAATACACTCCTCCTCACACAGACACACAGACACACAGACACACAC
ACACATACACACACTGACTAACCACAGAGGCAGAGGCATGATGGAGCCACACTAACAAAGCA
GCCACCGGGAACACATGATGCTGTGACTCAACATCATCCGTGCCTGCAGAGGACATCAAAAA
T

TN377

AANTTTGANTGCCCTTTNANCGCGGCCGTGGNCGNTCTAGAACTAGTGGATCCCCCACGCACC
AGCAGCAATACTCAAACGTCCCGTATCTTCCGAGGAAAGGGGTGTGCATGTGGGAGTGTGTG
TGTGTGTGTGTGTATGTGTGTGTGTGCTTGGCAGTGACGAAAGCGCAGTGATAAGAACACG
TCCCTTTCACCTAAGTCACAAAATATTACCATGTGTTGCAACTCCATATATACTCTTTTCTTCTT
TTATCATTCATTTGTTACACAAATCTGCTATCTGTGTCCCTGTGTGCAGCCTACAAAAAACATG
TTTCAGCTCCTTTTTTTTTAATTCTGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG
TCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGC
TTGGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAC
AACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAAGTGAGCTAACTCA
CATTAATTGCGTTGCGCTCACTGGCCGCTTTCCAGTCGGGAAACCTGTNGTGCCAGCTTGCATT
AATGGAATCGGGCAACGCCCCGGNGAGAAGGCCGGTTTGCCGTATTTGGGCCGCTTTTTCCGC
TTTCTTNGNTTACTGACTTCGGTTGNGCTTCGGGTCGTTCGGNTGCCGGNAACCGGTNTTNGG
NTTAACTTCAAAGGGCGGGAAATTCCGGTTNTCCNCAGAATTCAGGGGGN

TN284

GAGAGGNNNNNGGNGNNNNNNANNTTATCTNTGACATATGATCTNNNTGAAACCCCCCTCGA
GTTTANGGAATCGATCNCTTGNNNCGAATTCCTGCAGCCCACAGTTGCTCCTCTGCATTGTCC
CGAATGGAAACCAAGACAGTAGCAGtctttAGTTTATAggATtttcCTGACGTTCAAGGTGTCAATAT
GACAGACTGATGATAAACAGAAAAATATGTAGCATTTTCTTGTCCGCAGCCGGTTTCCAGTGA
GAAGACAATGACAACATGACGAGCTGATTGTAAGAGGTTAGCTCAGCAAGCCTCCACCTGA

Figure 5E

GAGAGCTTAGTTGTTTCAGCACCAGATGCCCCCCCCCCCCCCCCCCACACACACACACAC
ACACACACACACACACCGGCACTGTGAGTGACCAAATGAAAAAGGGTATGAATCAAAGCTGC
GGCGTCCTCGNGGGGGATCCACTANTTNTANAGCGGNCGCCACCGCNGTGGAGCTCCAATTC
NCCCTATANNGANNNNNNATNACNCNCNCTCACTGGCCCNNNNTTTACAANNNNNNGACTGG
GAAAAACCTTGGNGTACCCCAACTTNAACNCCCTTNCANAANAATCCCCTTTTCCCAANTTGG
NNNANTANCCAAAAAGGCCCCAACCCNATCGCCCTTTCCAAANAANNTNNCNCAACCNTNAA
NTGNNAAANNGGAAAANTNTNAACCNNNAAAAATTTNNNNNTAAAAANNNCNNNNANAAAA
TTNNNNNTAAAANNANNNNNNATTTTTTAACCCAANNNNNCCAAATNNGNNAAAAACCCTNN
NAAANCAAAANAAANNNCCC

TN180
TTGAATNCNTTGNGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAA
TTCCTGCAGCCCCCGTTCACTATCTAGGACACCAGCGGCGGCGACTTGTAGTGTAACTTTGCA
CACAAACAGTGTTTTCTCACTCCCCCCAGATCTCTTTCCATCTCTCACACACACACACACACAC
ACACACACACACACACAGGAAAGGGAAAGCAGCGTGTCCTGCAACCATCAGCACTTTCACCG
GTGTCCTCGCCAGACCGTCCCCGTCTCCTCTCATGTCCTTAATGACTCTCCCACTTGGCGTCCT
CTCTCCCTCACCTCCCTACCGCCTTTCCTCCTGCACCGTCAATGCCCTCCATCCTACTCCAGCA
CCCAGTTTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACGCGGTGGAGCTCCAATTCGCCT
ATAGTGAGTCCGTATTACGCGCGCTCACTGGCCCGTCGTTTTACAACGGTCGTGACTGGGAAA
ACCCTGGGCGTTACCCAACTTAATCGCCTTGCAGCACATTCCCCTTTCGCAGCTTGGGCGTAAT
AGCGAAAGAGCCCGANCCCGATCGGCCTTTCCAAACAAGTGCGCAAGCN

TN293
TGNTTTGANTGCNTTTGACCGCGGNGGCGGCCGNTCTAGAACTAGTGGATCCCCCAAAGCTTT
GGAGGTTCCTCAAGCCTTAAAAAAAGCCACCAGTTTTCACTCTAAAGATGCTTCTCCTACTAC
CGCTGTTCTGTCCAGGTCAAGGAAGTTTGAGTCCCACCTCTCCCATCGTCCTGGAGAAGCCAG
AGAGCCTCAACACTGTCACCTTCAGCGAGGACTCTGTGTAAGCGCGCACATGAGTAAACACA
CACACACACACACACACACACACACACACACATACACACAAAAATCAGCTATTAATAAACCGTC
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GGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGT
ACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGGCGTAATCATGGTCATAGCT
GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAA
GTGTAAAGCCTGGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGGCGTTGCGCTCACT
GGNCCGCTTTTCANGTCNGGGAAACCCTGGTCGTGCCCAGCTGGCANTTAAANGNAATTNGG
CCAACGCCCGGGGAGAAGGCCNGTTTGGCGTATTTGGGCGCTNTTTCCGCTTTCTTGGGTTAA
CTGACTTGGNTGGCTTGGGGCCGTTCGGNTTGNGGGNANCC

TN505
GTTTGTGAGTCTGTGCAGAAATGGCAGAGCAAGCGTGTCAGATGAAGAAAAATGCTGTTGTA
GAAGTAAATGAGCCAAAGTCCTGAAAGACAGGAGGTGTGGAGAGTTATTTTCAGAAAGGTCA
TAGACTCTGTGATCCATTAATGTTGACACC

Figure 5F

GATAAAGTTCCCTACTGAAGCATGCATATAGTCCACACACTGCTACATCTGGCTCCAGTAACT
TTCTGCTCCACTGACTGTATGTCCACACACACACACACACACACACACACACACACACACACA
CACACACACACACACACGCAGTATCATACTCAGGTGTGGGCGGAGGACCTGTCCTCTTGG

TN387
TGATTGCACT GCTGGATGTT GGTATCCTTG CTGTGATACT GTAAGTCATA
TGAGGGTGGT CTCTCTCTCT CTGATATTTG CTATAACAGA CAAACTATGA
CCCCCCTTGT TTGTGTTTTT GAAGCCAGTG ATTTAATGAC CTCCTGCTAT
CTAGACTGAA AAGAGTGAAA GTTATTCTGG ACAAAAGTGT AAACTTGATT
AGAAATTTTT TTCAACTGTC TTATAATTAT TGGCTCACTC AATTTGTATT
TTATTTTATT TGTATTATTT GTTGCAGACA TAAAACACAC ACACACACAC
ACACACACAC ACACACACAC ACACACACAC ACACACACAC TATTGTTTCT
CTAATGGCAA TTAGGCAAAG GTTCATCTGG TAGGGTAGGT TGAAATTAAN
AAGTGGGGGG ATCCACTNNG TCTAGAGCGG CCGCCACCGC GGTGGGAGCT
CCAATTCGCC CTATAGTGAG TCGTATTACG CGCGCTCACT GGCCGTCGTT
TACAACGTCG NGACTGGGGA AAN

TN462
TGNNNTTTGAANNNCTNTGAATGGCCCTTNCCGCGGTGNCGGCCGCTCTAGAACTAGTGGATC
CCCCACATGTAGTTAGTTTCCTTTTACACTGCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
CGTGTGCAGTGATGTGTAGTGCTTTTGTCCTGTCCATGGTCCTACTGTGAAACAGACTCTTTAA
CTTTTCAAGCAGTGAATGTTTTTTTGACTCAAGGTTGTGTGACTTTCACCTGATGTATGCTGTT
AGATTTCCCACTCTTCAGTAACCCGTGGACTTGAAGCATTATCAATGATAAGGAATAATTCAA
GTTATTCCAGGTGTCCCCAACCTCAAAGGGTCACTATAGTTAATCAACAGTATAGAAAAAAAA
CACATCAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGG
GCCCGGTACCCAGCTTTTGNTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTC
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ATAAAGTGTAAAACCTGGGGTGCCTAAAGAGGGAGCTAACTCACANTAAATGCCGTTGCGCT
CACTGGCCCNTTTTCANNCGGGAAANCTGTNGNGCCACTGCATTAATNAATCGGCCAACGCN
CCGGGAAAAGCCGTTGCNTATTTGGGCGCTNTTCCNTTNCTTGGTAATGACTCNNTTNGCTTN
GGCNGTTCGGNTTNGGNNAACCGGNATNAGNTTACTCAAAGGGG
GGNAN

TN201
TNTATTTGNCTCNCNGAACTNCTTGGAAACCCCGCCCCNTTTNGAGGTCGACCGTATCGATAA
GCTTGATATCGAATTCCTGCAGCCCACNCTTGCCTATTCAGGCTCTTCTTTNGCTGTAACACCA
CCAACCCCCTCACACTGACACACACACACACACACACACACTCCCTTCCTCGCTATCTGGCAG
TCTTGTTGCCTGGAGGGAGTTCATTCTGCCCTCCTTCTCTCCTCCTCTCCTCCACCTCTTTCCTT
GTGTATCGGCAGTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGGGGAGGGTGAGAAAATGA
GAGAGCGAGAGAGAGAGTGGCAGCAGTAGCGGAGGAAGCAGAGCTGTCTCTCTTCTGATCAT
CTTTCTTGGATAGAGGGATAAAAGGCAGTCCTAGGAATCAGTCGTTGCTCTTGTCTGCAGGAT
TTACCCAGCCTGAGTTTATTCTCCCTCCTT

Figure 5G

CCTCTTTTCACCTCTTCTTGACACTGGACCGCTAGCTTTTACATCTCTCTCTCCGGGGGGGGAT
CCACTAGTTCTAGAGCNGCCGCCACCGNGGGGGGNGCTCCAATTCGCCTATAGGGNGTCCGN
ATTANCNCCCNC

TN658
TGTGCCATCCTCTACAGCGAGACAATTTCACAGTGTCCAAAGCCGATTCTCTGCGCTTGTTAAT
TGAATCGGATTTCTTATAGTTTAAAATCCACACACACACACACACACACACACACACACACAC
ACACACACACACAGACTCATGTAGCTACAGCCCAAACTGTATAAGGGGTTTATCTAGCTCTGT
AAAGCCAAAGCAGGAGATATAAAGACACACACAGAGCCACAGAGAGTATTTTACCGGCGTGT
TTGAACGTTTCCAAATCTCAGAATAAAATGTCTTCACCTGCTGAGGTGTGTGTGGCTGTCTCA
GTGTGTGGGA

TN366
TGNGTTNNNCTCNNGATTCCTTGNGTACCGCGCCCCCCNTCGAGGTCGACGGTATCGATAAGC
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TTACTGCAAGATGTCAAATGCTAAAGTTCCTCCTTAAACAGATATTACAGGAAAAAGAGTTTG
TATTTTGTTGTAAGTTAACGGTTGTCACACAATCAGCTTATAAAAGTGAACACTATTCCTCACT
CTCACACGCACACACAGGGCAGCACAAATGAACAACTGTACGGTGCAGGATTATTACAGTAT
AAGTTTTAGAAGCGATGACTGTGACATTCCTCCTCACTGCTGAGTTCATGACTAAGACGGATT
AACTGGACTTCCATTTCTGCTTATCATATGGATGGGATTAACCTGTGCTATGGATCTCACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACATATATACAGGAACAGCTCA
GCACAGAACACACACTCACACTCCCTGTAGTAGGGGGGGATCCACTAGTTCTAGAGCGGCCG
CCACCGcGGTGGAGCTTCAATTCGCCCTATAGTGAGGTCGTATTACGCGCGCTCN

TN273
GTTTGAACCTTGGGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAA
TTCCTGCAGCCCTACTGCGATCGACTACAGGCGGCAGTGCGACTTCAGCACCACGGACAGTGC
CATGAACACAGCAAGGCAAGGCACTGACTGCGATACCTGACTGTATCAAATTACTAACCAGC
AGGGCATAAAAGAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTCCTAAAGGCAGTGACAGGAACAGGGAGAGAGAAAGTAG
TCCAGTATCACAGGCTGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCT
CCAATTCNCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCNNG
ACTGGGAAAACCCTGGCGTTACCCAACTTAATTCGCCTTGCAGCACATCCCCCTTTCNNCAGC
TGGCGTNATANNGAANAGGCCCGCACCGATCGCCCTTTCCAACAGTTGCNCAACCTNAATGG
CCGAANGGAAATTTGTAAGCCTTNATATTTTGGTTAAAATTNN

TN608
GAACAGAAGAACACACCCTGCCAGCAGAGAGCTCANGTTCCTACAGACTGACGCAGTGTCAC
TCATCCACTGTGCACACACACACACACCGACACACACCCAGCCTCCTTTTGCATGCCGTGTTT
CTAGAGATATGCATTCAACATTTCATGTACACACATAAACAAGTCGTTGACACACACACACAC
ACACACACACACTCTCATGT

Figure 5H

ATACAGTGAGATACACTCTTTCTCTTTTGAATTAGTGATGAGGGACTGAGCTGCTGAATTATG
CAGGAGACACAAAGAGAGAAAGTTGCTGAAACTACACATGGTTTT

TN237
TTTGAATGCCCTTCCANGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTC
CTGCAGCCCACATTATCCAATGCACAGGTGTGGAAAAAGAGCAGCAATGTGCACAGACacTGA
TGATGTTACACTGTCAGTAAAAACATCAGTAGGCTTAACTCTGAAGGAACACTGACACAGCA
AAATTGCATCAGTGTTAATCCCATCTTAATCACAACATAATACTAATGATGGTGCAGGCTTAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACTCTTTTAATGCCATCAGTGGTTGCTGCACATCTTCTGCAGGTAAAATTTCTTGTTCTT
CTCTGAAACGGCTGTAGCAGAATTTATTTATTTGTAGCTGCTGTGATAGCTTTACAGCAATCAC
AGCAGCAGACAGTGACTCCACTGCTGTTCGTGCAGATATGCAAAACTAAAGCCTCGGTCAAC
AGGCACATGTGAACACCTGCTCTTAGCTCAGCTCTGCTCTCTGCTGCATGTGAAGGGTCAGTN
GGTGTGAACATGTGGTGCTTGTGGGGGGGGGGGGATCCACTATTTTCTAGAAGCGGGNCGNC
CCCGGGGGTGGAGCTCCAATTCGCCCTNTAGGGGAGTTCGTATTACGCGCGCTNACTGGGCGG
GNGTTTACAACGGTCGTGACTGGGAAAACCTTGGCGTTACCCCAANTTAANTCGCCTTTNAGC
AAANTCCCCCTTTTTGCCAGNNTGGGGTAATNGCGNAANAGGCCCCCT

TN321
ACCTGGCAAA CAACACACTA AGGTTGGACA ACTGGNCGAA TTTATCGACC ATCGATCATA
GACTGAGCCT TTCACCGATT GTTTTTACAA GAGCGATTTA TTCATTTTCC CATTAGTAAG
TCTGCTAATA ATGTTGGTTG AAGCTAAGAG AAGCAGTCCA CACACACACA CACACACACA
CACACACACA CACACACACA CACACACACC CCCTTTTCCA GCTGTGAGCA AATGCATGCT
CTTCAGAGTG CGACAAATGA CTCCTTTTCC ATGGTATGAA ACAACATCAT TTCCTTGACA
GATATTTAGA ATAGCCAGA GTGCACAGTG TCCACCTGGG GCTGTCTTTT TCATATTTAA
CCATTTTAGT CAAATCACTT TGGATATTCT GCTGGTGAAA AGCTTTTCCG GAGCTTGTCA
ATCAAAAAGT CACCAAAAGT CACCTGCATG AATATATTGC TATCGTCAT TTATTGGGAC
TGATGAATGT CNGTTTGGAA AAAATTTTTA GTTTTTCACC CCAACCTTTN CTACCGCACC
CAAAGTTNTG GTATTTAGTA ATTNTAAAAC CTCTTTACCN AGGANN

TN390
ATCCATTGTA AACTTTCTAT AAACTCTGTA AACATTGATT CAAATATAGG CTGTAATGGT
AAGCTGCGTT GTCTGTAGCA GCGGCATTCA CAGCATCTCT AGCATAAGCA TGAAGCTTAG
TCACATACCA GTAATGCAT GTAGGCTGCA TAATGGCGTC AGCATATGTT ATGCTTCCAC
ATCCTTGAAC ATCCTATACA CACACACACA CACACACACA CACACACACA ACACACACA
CACACACACA CACACACCCC AACACACACA CACACACACA AGACTACTC AGCAGCACAT

Figure 5I

GTGCTGCCAC TTTTCCCACA GGGCTCTGTA GAAATAACTA CAAACACATA TTGT

TN472

GTTTNNNNNTNTGTNAATCTTTTGNCCGTGGCCNCGGCCCGCTCTAGAACTAGTGGATCCCCC
CCCTGCTGGACACATAGATGAAGTCTCAAACATTTATTTGCAAGGGTGGGAAGTTGAGTGCTG
AATTATGGGTAATGAGTTTGGTCCAAAATGGATGCACAGTGTGGTGTAACATCTAAATCTCCA
CGCAGTCCCTGGCTCTCTCTCTCTCATTTAGCTGTGGTGTAGAACACAGCTTTGAATTTCATTT
CAGGCTGTGGAATTATTTACAGACAACACACTTCCTCATAGTTGTGATTGACATTAAAGAAAA
TCAATCAGTGTAATGACGGGGAGTTTTAATCTACTGAGGGCAGCGATGGATCTGAAGCAGCT
GCTCACACACACACACACACACACACACACACACACACACACACACACACACACAGTCAGTAAATGGTTA
TTTTAATACCTGTTGATCTGTAATTTTGAACCTGCTCCGGAGCAGATTTGTGGAGCAATTACAC
CGTCCATGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGG
CCCGGTACCCAGCTTTTGGTCCCTTTAGTGANGGTTAATTGCGCGCTTGGCGTAATCATGGTCA
TAGCTGGTTCCTGGGTGAAATTGGTATNCGTCACAATTNCCCACAACATCGAAGCCGGAAGCA
TAAAGTGTAAAGCCTGGGGTGCCTAATGAGGTGAGCTAACTTACATTAATTGCGTTGCGCTAC
TGGCCCGTTTTCCAATCGGNAACCTGTCGNGCCACTTN

TN294

TNNNNTTTTTGACTANGTNATTGCNCTTTGAANGCGGCCNCGGCCGCTCTAGAACTAGTGGAT
CCCCCATCGCGTCAGCAGGACAGGCAGCCATTTCTGGAGCTCGTCCTATCTTTAGAACAGAAA
CTGTGCTGATAACAGAGCTTCCACAGCAGCTAAATACACAGCTTATCCCACAACACACACACA
CACACACACACACACACACACACACACTAGTGTTACATGTGTAGGCTGTTTTTTCCCCACATGCAAA
TAGCGGGCTGGTTTCGGGAGGCGATTCACTTTCAACATCATTTAGCTGCCTGACTGACCAGTG
AGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGG
TACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCT
GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAA
GTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC
CGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG
AGGCGGTTTGCGTATTGGGCGCTNTTTCGCTTNCTNGNTTAATTGACTCGCTGNGCTCGGCCGT
TCGGCTGCGGCNAGCGGTNTAGCTTACTCAAAGGCGGGAAACNGTTNTTCACAGAATCAGGG
GATACCCCAGGAAAGACNTTTTGAGCCAAAGGCC

TN552

TATTTACACAGCCAGGAGACAAATAGAAACATCATCATTTATCAGTTTTCTGGTCTAATAAGA
AACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACAGAGTAATGGCTTTAAAAAAAGTTCTTAAATCTGAATAGTATGTTGGAGATGTATGTA
AATGAGGCAACTTGGACTAACAGTGCAAAACAGGACAGTCATTTCTGTGGAAATAAGCTTCA
GGGATTTCCT

Figure 5J

TGCTGGTCCTCGGATGGGCTAAAAATCAGCTTGCGTGTGACTTTAATGGAGT
GCAGCTCTCACACAGTAAAGCCCCGAAGCAGTAA

TN520
GCCATCCCGCCTCCACACACACACACACACACATACACACACACACACACACACAC
ACACACACACACATGCTGCGAGGTAACGGCAGACAGGCGCGTGACTCATTAGGCATTCGTCC
CCCAGGGAGATCGCTGGGGGGGCGCGTGCGAGGGAGAGAGAGCGCCGCAGCTGCAGGAATG
TCACGGGCGGCTTCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCTTGCTAATGC
TGGTTGGAGCCAACGGCGGGGCACTGCACCTTTCANGAAATAACGCATGGAGAAAGGGGAGG
AAAAAAAGGGAAAAAAACATACTTATTAGTTCTCTTTTCCACCAAGTGCTTATTTAAAAGTCT
AAAATGAATTTAGAGAGAAAACATTAGATTGCCTTATAATTTCTGCTTTAATTAGAATGCTTTT
GCT

TN197
TTTGATGCCTTTGGAACCACCGCGGTGGTTTGNCGCTCTAGACCTAGTGGATCCCCCCCATGG
ACACCAGAACAGGAAAGTNATGAACACACACACACATCTACACACACNCTGACTCAGCATGA
AGTGATACACACACATGAACACATGTGAACTCGTTGACTGAGTGAGAAATGACACACACACC
TACACCGAAATGGTGATTCATTGAGAAGTGATCCACACACAAAATACACATGCAGACGCTCG
TGCAATGAAGAGTAATGCACACACACATGCTCGTGCAATGAAGAATGCTTTGCTAACAAATG
CTTATGCTGATATGCAAAATGCTGCATACACACACACACACACACACACACACACACAGA
CTCTGTTACAAGAAGCCATTGATTACACAGAACGCATTTTATGTCATCCAGAGGGCACATTAT
GTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCCGG
TACCCAGCTTTTTGTTCCCTTTTAGTGGAGGGGTTAATTGCGCGCTTGGGCGTAATCATGGTCA
TAAGCTGTTTCCCTTGGGTGAAAATTGGTTATTNCCGCTTCACAATTTCCACACAACATACNG
AGCCCGGAAGCATTTAAAAGGTGTAAAA

TN538
ATCTGGACCAACAACCATATTCAAAGTCAATGAAATCAACTTTCTTCCTCATTCTGATGCAAC
TCTCAGTTTGAAGTTCAGCATGTTGTCTGGATCTTGTCTAGATGACTACGGAAAGTGTGAAAA
GTATACCTAATAAAGTGTCTGGTGATGATTTGCACACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACAAGTG
ATCAGTGGACCTAAGAACAGACCACAGCAACAAA

TN211
ATNTTGTAAC ATGAAAAGAT TTANAANGAA CTNCCCCGCG TACTTGGGNA
AAAACCCCCA GGGGATCCCC CCNGGAGTCA GTTACTGCAC AGTTTTTTGG
CAAGTTGAGA GGCTACTGTT AAACCTAACC ACACACACAC CACACACAC ACACACACGC
ACACGCACAC ACACACACAC ACACACACAC CACACACAA TAAGAGCAGA AGCATGTGTT
CCTGAGCATT GCAGATATGT ACTGGTAAA CATGCCAACT AAGGTTGTGG GTTGTTTTCA
CATTGGCTCT GTGTGCATGA

Figure 5K

AGGCGTTTTA ATGACAGCTT TTGGGCTGCA GGAATTCGAT ATCAAGCTTA TCGATACCGN
CGACCTCGAG GGGGGGCCCG GTACCCAGCT TTTGTTCCCT TTAGTGAGGG TTAATTGCGC
GCTTGGCGTA ATCATGGTCA TAGCTGTTTC CTGTGTGAAA TTGTTATCCG CTCACAATTC
CACACAACAT ACGAGCCGGA AGCATAAAGT TAAAGCCTG GGGTGCCTAA TGAGTGAGCT
AACTCACATT AATTGCGTTG CGCTCACTGC CCGNTTTCCA GTCGGGAAAC CTGGCGNGCC
AGCTGCATTA ANA

TN412
AGGGTNNTNANNTTATNTTNTANTTGNNNTNNAATNTGATGCCNCCCCCTTTCGAGGTCGACG
GTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCGaCATTGTCGGTGGACATTAACGCCA
CActGTGCAGTAGTGACCTTGAATTAATTTACAGCACGATGCTGCTGAGCCAAGACCTCATTCA
CACACACACACACACACACACACACACACACACACAAAAACGCAAAACATCGGCAGCATTGTTT
CCTTCAGAAAATGAGGTCACGTTAAACTACTTCCAGTGCCATATATGGGCAAAAACATCATCC
AATACACACACAGCAGAGTTTACAGAACACACCAGTTTGTTATTCAAATAAAAGATCAACTGT
GATAAGTCCTAAGTGTCTAATTTATTAGAAATGTTCAAAACGGAGACAATTAAATCGCATCTT
TTGTGTTTACAATGTGACAACACAAACACCACTTTTGTCTGCGTTTGCCTGGTCCTTTAGGCTC
AGGCAGCAGCATTATGTTGGTCTTGTTTGCTTCTTTCAGCTTTGCTTCCCCAGTCTTATCCAGTC
CATCATCCTTTTTCCAACACGAGCCATCTCCCTAGCAGCCAAGCCAG

TN348
TTGATCCCTTGCTCCCGGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCCCACCTCGGCTC
AGCTTAGCCCGGCGCACTGCTTTTAGCACACGGCATTTNCACGTGCATGTCCCTGCCACATAC
CATGGCGTGCACGTCAACACACCAGCGCACACACACACTCTACATGGCAGTGTTATTTACTGA
GATGTATATATACATTCACAGGACTGATTACAGCCGCTAAGAAGTGTATCTCAAACTGTAAAT
AATTCAACATAGACAAGCAGCTTGGCTCTGACCTCACACTTGACTCAGCAGAAACACACACA
CACACACACACACAAGCAAACTGTAGGTTCAGCTAATGGATGTTTACAACTGTTCATTTGTGG
ATTAGCTGCTTGTGCATGCAGCATTTTCGTCTGCAAGAAGGAGAAAAGTGGGCTGCAGGAATT
CGATATCAAAGCTTATCGATACCGTCGANCTNGAAAGGGGGGGCCCGGGTANCCCAGNTTTT
TGGTNCCCTTTAAGNGAGGGGTTNAATTNCCCCGCTTTGGCCGTNATTCAATGGGNCANTAGG
CTTGGTTTCCCTGGGGNGGNAAG

TN207
TTNTNTTTNTNTCNNGTAGNTTCTCACNCGATTGGCCCNTCCTTTTTGGGTTAAGGTANCCNAT
AAGCTTGATATCGAATTCCTGCAGCCCAAATCTTACNNTGAGATCATCCCATAAAAAGGCTTT
CTNTCTCTCTCTCTCTCTCCCTCTCTCTCTGTCACACACACACACACACACACACACACACACA
CACACACACACACAAGATCCAATAGTTGGGTTGCAGTCACGTGGTTCTGATGACGTGCGGAG
GCAGCGCGATTTTTGAGTGGAGGGCGGAAGTAAACATGGAGGACACTGTGGAGAGTCAGGAG
AGCAGCTATTGTGCAACTTTAGACCCCGTTTCTCGGGAGAGATATAAACAGATAGTTAAAAAA
TATATCGGACGTGATCCGTATTCTTTGAAAATGTCCGAATACACCACAGCAGTAAAGGATTTG
CCTACTATCGAGGCTGTGGATGGGGGAT

Figure 5L

CCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTAT
TACGCGCGCTCACTGGCCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCA
ACTTAATCGCCTTGC

TN134
TTNTATNTTCATGTGANTCNNNNTCTCCCCCGCGNTGGCNGCCGCTCTAGAACTAGTGGATCC
CCCACCAGCAGAATAAGGTNGGNTCACCATACAGTCTTAGTGACAGCTGAGTATTGAAAAGG
CTGCTTGCAGAAGAGAGGTGCCTCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTTTGTGTT
TGTGTGCCTATGAGAAGAAGAGAGAGACAAGACACAACAAAAAAGAATAGGAGATAGTCTG
TTGCCCTCAGACACATCTTTGCACTCCAAGGCATCACACTGGGTGTGTGCGTTTGTGAGGTTCT
GCATATTTTGAGCACTTTTTGAGCAAGATTTAATTAAATTAAATTAAATTTAATTCAATTTTAT
TTATATAGCGCCAAATCCCAACAACAGTCACTTCAAGGCGCGTTATATTGTAAGGTAGACCCT
ACAGTAATACATACNAAGAAANACCCAACNATCATATGACCCTGAGCNGGCACTTTGGTTGA
CAGTGGNAAGGAAAAACTCTCCTTCAACANGAAA

TN221
TTGTNNNNCCTCGTNAATGCNCTTTTGAANGCGGCCNCGGCCGNTNTAGAACTAGTGGAtCCC
CCCCAATTGATGAAGAGGTAACACCAGAGTAGAGGCTATTaCAGAAGTCGAGGCGAGATGAG
ATGAAGCCATGGGTCGCTGTGATATATGCCACACACACACACACACAAACACACACACACAC
ACACACACACACACACACACACACACACACACACCGTTATTGCTCACGATCACGTTTTTTATTTA
TAATAACAATGCACCGTGACAGCTCGTCCCGGTCCAGCCAGCCTCCCACTCGACTCTGCCGTC
ACTATATAGACACACAGAAGGAAGACACTCATGACACAATCGCCACCACCTGTGGCTCACCT
GCCTCCCGGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGG
GCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTC
ATAGCTGGTTNCTGTGTGAAATTGTTATCCGCTCACAATTTCACACAACATACGAGCCGGAAG
CATAAAGTGTAAAGNCTGGGGTGGCCTAATGAGTGAGCTTACTACATTAATTGGCGTTGCGCT
CACTGGCCGCTTTTCANGTCGGGGAAACTTNNTCGTNNCNANGTTGCANTTATTGAATTCGGC
CAACNCCCCGGGANAGGCCGGTTTCCGTTTTGGGCGCTTTTTCCGCTTCTTGGTTAATTGACTT
GCTTGCGCTTGGNNCCTTNCGGTTGGGGCGANCNGGTATNAAGCTTANTTNAANGGCGGNAA
TACCGGGTTNTCACANAAT

TN470
ATATTGTGTG AGGGGGTGTC TTCCTGGTGT CATGCTGTGC TGGCAATATT
GCAAAAGACA TGCTCAGGTG TGCGTTCAAG TGTGTGTGTG TGTGTGTGTG
CGTGTGTGTG TGTAAGACAG AGAGAGATAA GGATCTTTGT CTATTTCCGC
ACCTGCTTAA AGAGTTGTGG GACCGTGATC TGATTGGCGT CTCCTGAACA
GGGACTTCTG GTATGGACGG AGGCTCAGTG ACCGGCGTCT GTTCCTGTGA
TAACAGGGGA GGGGAAATGT GAAACACCAG CATACTGAAT GACAAGAGAG
TGGGGGATCC ACTAGTTCTA GAGCGGCCGC CACCGCGGTG GAGCTCCAAT
TCGCCCTATA GTGAGTCGTA TTACGCGCGC TCACTGGCCG TCGTTTTACA
ACGTNCGTGA CTGGGAAAAC CCTGGCGTTA CCCANCTTAA TCGCCTTGCA

Figure 5M

GCACATTCCC CTTTNGCCAG CTGGCGTTAA TAGCNAAAAA GCCCCGCACC
GGNTCGCCCT TTCCAACAGT TTCTCCATCC TNAAATGGCC GAATGGAAAT
TTGTAAGCCG TT

TN206
GGNNNNGNNNNNTANNTTTNTNTTCCTANTNTNGAAGATNTANAGGGANCCCTCGTTTCTTTN
GGGNAACNACCCTATCGATAAGCTGGANGTCGAATTCCTGCAGCNNCTTTGTGTGTGGTCTGA
GTGGTTCCNGGGGGGGGAGGAGTGAACCAGTCTCAGACACTTCAGACTGCAGTCTCTCTCTCTC
TCTCACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
AAGCAGGGATGGACGCACGCACACACATGCACACACACGCACACACACACACACACACACACA
CATGCACACAGTGATGAGTGCAAAGAGGGAGAGGNCCAATAAACAAGGGGGGGATCCACTA
GTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCG
CGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAAT
CGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCNGTAATAGCGAANAGGCCCGNACCGATCG
GCCTTTCCAAACAAGNTGCNCAACCTGAATGGNCAATGGAAAATGNAAN

TN553
TGGATGTACTGTCCTATGTCAGTGAAGGACTCTGGCAACCCACTAATGCAGCTGGATTTGCAT
TGAGTGAAATGAAGCGAAAGTTTTAAATGGCATCAGTCTTGCTATTAAAGCAAAGCAAAACA
TCAGACAAACAGGGAGGAGCAGCTCTCTCCTCTATCCGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTATGTGTGTGTAGTAACTGGGGGAGTGCTGTCCCTTGCC
TCTGCTCAGTGTGTGCAGCAGCTGCAGCTTTCAGCCTCGGTCTATACTGTAN

TN530
AGGCTTGAATGATGGTCTTAAAGGGGGCAGTATATAACCTGTGTGTCTTTATCATTATATGTG
TGTGTGTGTGTGTGTGTGTGTGTGTTTCCTGGAGAGCAAAGGCTGTGAATGAACTCCTAAATCAC
ACTATTGATCAGCCCTTCCTCCCAGACACACGCTGGGATCGAGGGCAGTTAAAT

TN285
GNNNNTNNTNNNTTNNTTGNNNNNNTCCGTTGGGAGCNCCCCGCGGTGGCGGCCGCTCTAGA
ACTAGTGGATCCCCCACAATGATAGCAGTGGAATTATCTAACACACAGATACACACGTAACA
GCCACAGACCCCTAACATGCTTATCTAAGTGGCGATATTACAGTAATACATTATAATCACACT
CTTTGATCACTCTATCTGGGACACCTGCTGCACTTTGGGGGATGCAGAACTGCTTTGTCTGCAG
ATATATACACATAACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACACTCTATATGACAACCAAATTTTCCCCTCACAACCGTAATGGAACAAACGGC
AGAGCTATTAGATTAGCAGGACATGTAACAACACAATAAACTGGGAGCACACCTGAGGCTGG
ATGCAGTGTAAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGG
GGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGGTTAATTGCGCCCTTTGGGCGTAATC
ATGGCATAGCTGTTTCCTGTGTGAAAATTGTTATCCGCTCACAATTTCACACAACATACGAGC
CGGAAGCTTAAAGTGTAAAGCCTNGGGTGNCT

Figure 5N

TN202

TNTTTGACTC CTTGGAACTC CCCGCGGTGG CGGCCGCTCT AGAACTAGTG GATCCCCCAC
TTGAGTCAAT TCCCTGTGAA TTAACATAAA TGTGGTGATT CGCCAACATA
AGCAGCTGTG TTATGACTGA TGTGAATACA GTGGAAGGGT CTGGAAAAGC
AGATGCACAG CTATGAGCTG CTGCATTGCT GCTAGTCAGG
AGCTGTCAGG AAAAGACTAG AAGCAGGTCC CAGATGGGAA CGCATGTGAA
CACAAAGTAG AGCTTTGCAT GCTCAGCAAA CCTTCTTAAG ATAAATACAA
TTGTGTGTGT GTGTGTGTGT GTGTGTTTGA GTGCTGGAGG GGTCTTTCAC AGTTCCTTGG
AATAAGCCTG TTCTTGCGTT GTGAGGGTGC AGCTAAACAT
AAATCATGCA TTAGGCTTTC TTAGAGGAGA ACTTGGTTTC GAACATATCA GCTTGAATTT
CGGACCCGCG TGGGCTGCAG GGAATTCGAT ATCAAGCTTA TCGATACCCG
TCGACCTCGA GGGGGGGCCC CGGGTCCCAG CTTTT

TN168

TGNNTTTGACAACCTTGGGTACCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATA
TCGAATTCCTGCAGCCCAAAGCGACAGGTGCACGCTCAGCCTCACGCCCACACACTCCATATA
AGGACACAGGCGCACCGGGCTGTCACAGCAGGAAATCAGGAGGGTTTGAACTGTCAGAGGG
GAAAGTGGAAAAGCTTAAACAGTGGAGCTGGAATAGGCTCTGCCCCCATCACCCTGATTACC
TGTTGGACTTTGCTCAGGTGTATTAAAGCAGCTGGACAGATGTTAGAGATTATTTCTGTTTTGA
CTGAAAGCTGCTCGTCAGACACACACAGACCGTAACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACAGTGTGTATCAAATTCACTGTTTACAAACCATGAATGAC
TCATACCAAAATCATCAATATGATCAATAACACTGATGATTATTATCACTGTGATCATTACTG
CTACGCGTGTTGTGACGCACCAGCACCAGTGGGGGATCCACTAGTTCTAGAGCGGGCCGNCA
CCGGGGGTGGAGCTCCAATTCGCCCCTATAGGGAGTCGTATTACGCGCGCTNAATGGCCGTCG
TTTA

TN263

TTTGANANCGTTGGGTACCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGA
ATTCCTGCAGCCCCCATGTTGACAAACCAGGATTCATGCTTTTCAAGACTGTCTGTCCATCCGT
GCCAAGGACCCCCCCCATAGAGGCATAGAGCTACAGCCACCATGACCCTGTTCCACACACACG
CACGCATACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACGCCTCTCTCATCTGTCCTTTCACATGTAACCCAGCAGAACAAAAGCAAAGGACT
GGAAACACATTTTCCCGTCCTTATGAGCACTTCACTTCCTGTGTGCATATGTCTGTTTACATAT
CACTCCTGCCCTTCATCCAACACGCTTACACAAAAATGCATCACCCATTTGTCCCCTACTTTTT
AGCCCATGCTTGTCTGTAAATATATATGTATGCAGCTTCTTTTTTCATTAGGATCAGAGTGCAG
GAGCCCAGGAACAGGTCCAAGAACTGAAACATAAGGAGATTGGAAAGAAAGCGTTGTGAAA
TTTGGAGGGAACCTTCAGCTTTTCACGCTGCTGNGATGGA

Figure 50

TN399
TTTGTGCCAG TGAAGCATGT AGGTGCATGC TTGTGTGTGT CTGTGTGTAT
ATCGATGTCT TAGGAGAGAC GTTAATGTCC TGGGAGCAGA CCGTCACTTT
GGTGAGAGTA AATATACCTA AAAGCGCCCT GAGAGCAACA GGACTCTTCT
CTCACTGACA CAATATTATT CTGCTGTTCT TCACAAGCTC TGGGGAACTC
GTACACACAC ACACACACAC ACACACACAC ACACACACAC ACTTTCTCTC
TCTCTATCCC ACCAGGCTTG TTTATGAGTG TGATTACACA GAGAGAGGTC
CGGTTGTCCA GCTCACCTGA GAGCGCATCA GGTGCAGTGC CCTGGGGCTT
TGTGCCTGTT TGTGTTTGGA CAGTGCTGTG TATTTTTGGA ACGGCACACT
TTTTGTGCCT GACAGTGAGT TTTTTGGTTT TGTTTCCTGN TTTATTCCTT
CTGTTACTGT GTGAAAAAGA GATATAGTGT TTGTTTAAGG NGTCCCATGT
TGGGTTAGAT GCCCCAAACT TCTGGGGTCC TAAAATTCAA CC

TN662
TGCAGCTGACCTTCACTCTTATCTCACTTATGGCTGCTAACATGCCTGATGGATGTTTCCTTAT
TGTTTGTACAGACTGACCCGTGTGGAATCTGTTTACAAGACTTGTGTGTATATATGTGTGTGTG
TGTGTGTGTGTGTTAGGGGGGGTCTGGGCTTTCATGCTGTCTGCTCAGTTGTATCCCACACTAC
TGAAAAAAAACCACACACACGATACTGAAATGTTCCTATAACTGGGATTTTAGAGAAATTGA
AACAGCATATTAGTCT

TN215
AGGNNGNNNN NAGNTTATCT TNNATNNGGG GNTTNAAGGN ANCCTTCCCN
CTANTGGGNA ACGACCCTAT CGATAAGCTN GANNTCGAAT TCCTGCAGCC
CATTNACCAT CAAACAGACA CTTCATTNGG GGNGCAGTGA TAACAAATAC
ATTGTGTAGG ATAATGATGG CAGTGGTTCA TATTGTTCAT TATACGTCTG
GGTGTCATAC GGCACTTGCA AATTTATACG TCTGTGGGTG CTTGTGTGTG
TGTGTGTGTG TGTGTGTGTG TGCGTGTGTG TGTGTGTGTG TGCGCGTGTG
TCTTTGTTTT TGTCATTTTC ATGTTTCAGC AAATTAACGT CTGAACCATT
GGGAAGAAAA ATATACCATC ATTTGCCATT GGNGACAAAC AATATATTTT
GGATAATGAT TGCATCTATT GGCTTCTGCA TTTGNAAATG TGAGGTAATG
AATTTCCTTT GNGAGCAATG AAAGCAAACA GACATATTAT GTCACTTTGC
TTGAACAGGG GGGGATCCAC TAGTTCTAGA GCGGCCGNCA CCCGNGGNGG
ACTCCAATTC CCCTATAGNG ANNNCNTANT ACGCCGCTCA CTGGCCCNCN
N

TN171
TNNTTTGATCCGTNAATCNCTTTGAACCGGCCCCTCCCTTTAGGTCGACGGTCTCGATAAGCTT
GATATCGAATTCCTGCAGCCCACTGCTATcCATTGACAGATATTGAGTTTTCCCTTCAtGTTGCT
GCCATCACCTCTTGCTTATCATGCTCACTCTTTTGCAGCTATAATAGCAGTATGTCACTGGCTA
CCATGTATGCACACACACATTATACAGTGACATATACACATTAATCCATAAGATATGCTAATT
GATTATATAAAAGACATAGTCTTTCCTTCGTGTGTGCACACATGCACACACACACACACACAC
ACACACACACACACACACACACACACACTAAAACATGCACACATAACCTCTGCCCTAACTCACA
GTGTTCTTTGTCTCTAATAGCTGCTAACTCATTTAGCACT

Figure 5P

TCATGTTAGAGAGAGAGTGGAGTCTGAGTAGGAGGGGGNGGATCCACTAGTTCTAGAGCGGC
CGCCACCGCGGTGGAGCTCCAATTCGCCCTTATAGTGAGTCGGTATTACGCGCGCTCACTGGG
CCGTCTGTTTTACAACGTNGTGACTGGGGAAAACCNTGGGCCGTTNCCCCAACTTAAATTGCC
TTTGGAANCACATTCCCCTTTTGCCAGNTTGGGCGNTAATAGCCNNAAAAGGCCN

TN145
GGNNNNNNNNNANCTTNTNTTNTTCNANAANACTTNANTGAACNCCNCCCCCTTTNGAGGTC
GACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCcTcAGATCAAGTTTCAAACAGCC
ATCCCcgtCTTTCTCCACACTCAAACACACACACACACACCCTTGTATATATATACACACACAC
ACACACACACACACACACCCTTGTATATATATACACACACACACACACACACACACACCC
TTGTATATACACACACACATTTCCCTTCAAGATGCACAATCAAACGGGCTCACAGAAAATA
TACTCCACTGAACACCCTGTAAAATGTCTTTAGGCTGGAGACATGTGGGGGATCCACTAGTTC
TAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCT
CACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATCGC
CTTGCAGCACATCCCCCTTTCGCCAGCTGGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC
TTCCAAACAGTTGCGCAGCCTGAATGGCGAATGGAAAATGGTAAGCGTTNATN

TN540
AAATTAGTACTGTTACATGAAGAAAACTcTGGGTTAAGCACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACTACCAGGGGAGTTGAGAGTCCTGCGCAGCATC
TTTGCTGTTCCTACGAT

TN128
TTGCTTCATT CCTTGCNTCC CCGNGGTGGT CGGCCGCTCT ACNACTAGTG GATCCCCCCC
GGGGTGAAAG AGATGAGTGT NTGAGCAAGA GGAATAAAAG ACAAAGAGAG
CAGGGGAAAT AGCTAATGAT GAGAGAAAGG GAAAGAGGTG AGCATTTGAT
GAGACTGTAT TTCTATTAAA CTGTCAGAGA ATTTGCTCTT
TTTCTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG CGCGCGAGCG CCCTTCACAG
AGGCACAGTA ATGTGGCTGA CCCAAATGAC TAGGAAAATA TTGGGAGAGT
GAAAGACGGA AGCCTCTGTT GAATACTGAT GAAGCTCAGC ACAAAGCTTC
CTCCTGGGGG CTGCAGGAAT TCNATATCAA GCTTATCGAT
ACCGTCNACC TCGAGGGGGG GCCCGGNACC CAGCTTTTGN TCCCTTTAGT
GAGGGTTAAT TGCGCGCTTG GCGTAATCAT GGTCATAGCT GTTTCCTGTG TGAAATTGTT
ATCCCGCTCA CAATTCCACA CAACATACGA GCCCGGAAGC ATAAAGTGTA
AAGCCTGGGG TGCCTAATGA GTGN

Figure 5Q

TN526

CCCTCATTTTTTGTTGTCTCCAGACCTCTGCCCATATTTCCACCAGCTTTTTCCTTTTCTTGCTTC
GTTGGTGTGTGTGTGTGAGTCTCTTCCTCAGCCCATCTGTTTGTAACTGTGCACGTCTGTCTGC
CTTACACCAGACTAAACACATACAGACACACAGACACACACACACACACGTACATTCAGCTT
TTCATTAAATATACCAGTGACAGGATATGACAAGCTCTCCCAGCTTTTTAATTTAGCGCCGGT
GTCCGCCCACCTCCTCAGAGAGCTGGTCTAAAACCTGTCACTGCCAACAGTTGAGGGATGACA
AGGTAATTAATAGTTTCACTACAATGCAGCCAACTCTTTTAGGAGCTGGACAGACAGGATGAG
CAGAAAAACAAGGAAGCATGTGGAGAGAGGAGAGATTAGGAGGCAGGGGATGAGCAAAAA
ATATTGACAGACAGAGCAGGAAGATGAACAGAAATAGTCTGGTAAACCAGACGGGG

Figure 5R

TN150

TTNNAAGCCCTTGGNAGNCCCCCTCGAGGTTGACGGTATCGATNNGCTTGATATCGAAT
TCCTGCAGCCCCCTTCCACTGTTGAAGCTGTCACAGGATTTGATAGAAGAGCATATGAT
TGCTACACCTGCACTTGCTTGCTTTTCACTTTTCACCTCTTTAGTTACATTAAAAAGTC
TCAGTTTGTTTGGCTTACACACATGCTTGAAAAGACACACTTATCTCACTCACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACAGACGTcTC
ACCTgTTTTACTAGGTAAGGCTCAAAACGGATCATCTAAGCCAAtCACCTTTCAGGAAG
CAGGGATCAGCCAAAATCTCCTCAATTAATAGCTAAAGTAACCTTCAGTGACCTGACTG
TGGTCTACCACAAACACACCCACACTTACACACAGACATGCGCGCACTTACACACACAC
TCTCTCTCTATTGTCGGTCCATTTACCATTAGTCTGGGATTTTTTTTNTATTCATTTGAG
TATAGCTTAGTATTAGTAAACATGTGAGGAACAGGATCAAGNATGTGAGGCACATCTAT
CTATCTAAACTGTAAGGGTGGACTGACCTTTTCCCTACCTNTAGGNGCTTAGATGAAAA
GATGAATGCCTGTCNGGNGTNAACACCGGATTTTTNTTTNGGNAACAAAAACTGNTGGA
CNTTNTNGCTGGCAGCAACCCNTCCTTNGATAGGACTGAANAGNCCCCTGTCTNNAACT
GGGTTTTTATTTG

TN209

GNGNNNAGNT ATTTGTCNCA AANACNAAAA ANNNCNCCCC ANCTGNGAAA
CNCNCTANCN ATAAGCNGGN GATCGAATTC CTGCAGCCCA CAAAAGCACC
CAGATGTTCA AACACCGGGG GGACNCAAAA ANANTNCACN CACACACACA
CACACACACA CACACACACA CACACACTGA CACACAAAAG GTTTCATTTG
AATTCAAACC AAATTGACTT CAGGCAAACA AAACGTTGCT GAAATGATAT
TTTGTGTTAG AATCTAAGAA TTCAGGAAAT ATGTTATAAT GAATGAATTA
TCAGCAGCTT TGATACTTTC AGACGNNGTA TTTGACTCGC TCTGGTAACT
GAAGCTAACC TGTGATGCAG TTTGGTTTGT TCGCGTGTTG TNAGTTGCTT
GTGTNGTTTC TGTTTGCCTT CCTCCTTGNC TTGTGTGGGG GATCCACTAG
TTCTAGAGCG GCCGCCACCG CGGNGGAGCT CCAATTCGCC CTATAGNGAA
NNCNNANTAC NCNCGCTCAN TGGCCCCNCN NTTTACAANN NNCNNNACNG
GGAAAANCCC NNNNNNNAAC CCCAAACTNA AANACCNTGC

TN531

ACTGACACACAAAAAAAAGCCAACGGTCTGAATTGAGATGAAAATACTGCTGTGGAGGGAGCGACGCTNAA
AATACCAGGCAGGGCTGCAATTAGTGGTGTGTGCGCGGAGCAGCTGCTGCGGTTCAGAGCACTAAGTGTCT
CTAATTACTGCTGCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTATGCTGATATGTGCACGCCCAACCCA
TGAGGGGTGTCCTCTGCTGAGTATCTCTATTTAACATGCTCTGTGTGTGTGTGAGTGTGTGTGTA

TN535

CCATCCATGAAACCATTTGACTCCTAAAGCACACTGTTAAGTGAGAGGATGCACTTCTC
CTTGATTTAAATGAGCAGCGGGTATCAGCAGTTTAGCTCCTGCAGAGCATGAGCTCCAC
ACACACACACACACACACACACACGCTTACACATTGTCACATAAGAGAAGTTATCTACT
TGTTGCTGTATGGAGAGCTAAAGCTTCTGTTATGAAAAATGGGCTATTATCTTCTTATT
GATCACATTGTTGATGAGACAAATGGCGGAACTGATAGATGGGGTTTTATCACCTTAAC
TGTTGTCAGTATGAATATGGAT

TN666

ATATGTTCTGGACACTCAGGTGAAGAGAGGTGCTGAGCTGTCAACTGATTACCAGGTGT
TGGTGAGATGGATCAGCTGGTGGAGAAGAATGCTGGACAGACAGACCTGATAGTA

Figure 6A

ATGGTGCGCTAGGAATAGCAATAGTATGCTGCTTTTAATTAGAAATCAATATCACATGC
CCCCCAGAAAAGGAAACAATAATTTTTTTCCACATCTTAAAGGCAGGAATAAATTACCC
TCAAAAGAATTACACTCAGTGAAAATGTTGCCTTGCGTGCCAATTGCTCTTCTTCTTTT
TTCTTACATTCTTACATGCATGAATTCTCTCTCTCTCTCTCTCACACACACACACACAC
ACACACACAAGCTGGAGATGAAAGCCTCATTCAAGGTGTAACTGTGTTATAAAAAGAAA
TTANTTGGAGAT

TN685
GACGTCTNCACTCTACATGGAAAAACACACACTTACTCTACTCATCACGCTCTGTTATCTGTCAGCAATTA
CTCACTGCCTCCTACCCACCAAACCCCTCGAGAAGCATTACTTTGAAATGCCCAGAAACACACACACACAC
ACACACACACACACACACACACAGNTTTACACATTCACACTTTCACATTTCCACACCTGtGGAGAAAACCA
GTTTCTCTGGCATTTTATCAGCTTATTTGCTGNTGCTATGGAAACAAGCCTTGCANAGAGAGATGGGATTT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCCC

Figure 6B

SNPHAL-23:
TGACCTCATCTTACAGTTTCAGTTGTCGAGGTTACAGTGACATTTATATGAGAAAAAGTATGTAGAGATA
TGTACACAGAAACTGCACTGGTTAGCGGAGTCATACAACCGCAGTGCGGTAATTCTAGTTTTGTTTTTTTT
ATAAATGGGTTAGCTATTTTTACAATCTACAAATAGTAATCAATACATTTTGTCACAGTATGTTACACAA
AGAAATTGGCATTAAAGTTGGCATCTTGTTGTCTCACCAGCCTGACGATACAGCTGAAATCTTTGCTGCTT
AATGCTCAAATAGAGTCCTCAATGGCGTTCTGCAAGTCATTTTGATTGGTTGGTCCTTGTGAAGAGGAGA
ATAAAATGAATTAGTGCCAATATCAGTTTACAATCAAACCTTTTTGTGTAGACCTTGTGTAAACAGAGTC
AAAGGACATTGTGCAACAATGACATACATTTTTTCCACAGTACCTGTCGTCCACTGCTGAACATCTGACA
CCCATTACTGGACTGTGTCTTCCTGTAGAGTGGTGATGTTCTCAAGGTCCTTTGCACAGTCTGTCAAAACA
AAAT

SNPHAL-41:
TTGGCTTCATTGTGTTGTCTCTATATAGAGTTTATGGTCCAGATATTTTTATAGCTTTGGTTTTTTACTGTC
TTTAACAGTTCTGCTGCAGCCCGTTATCCCTCCGATCAATTTTTGTTACTGGCTTTATCAGGAATGTGACC
TCACATCCTTTTTTCGAGGCTGAATGGTGATACATTTAATTGAGAAGAAATGTAATGCCGCCATGTCTGTT
TAAAATACATGTAGAATATATACGGTGTGATAAAACATGTGTAACAACACCCAGAGGAGACACAGGGAG
ATGTCCATCAAATCCAGTTTCTAAAGGTCCACATTATCCGTGGAGGGGTCTAACAAGGCAGCAAGTGAA
ATAACGTGTGGGTGGTTGTTAGCAGCTTAAAAGACGAACTGGAAACTTTGTGCTTCTTCATCTCTGTTCA
GAAAGGAGCAGGAAAAAAAATCAATTTAAAAAAAGAAAAGAAAGCTTTGAAATACAAACTGTAAAATT
TGATTTCAAATAGAAAATATTCAATAATGGCTCAGAGTCAAATTGTTCTTTAAAAACACATTTGGTCACA
GCGTCGTTCTTGTTTAATGTTTCCATCAACAACACTGACTGATTTAAGATTCCACTTCAATCCACGTCACC
AGATTCCTGCTCACATGTATGAAGTCTGACACCAACATGTGTACATACATAAACAATGACATTC

SNPHAL-45:
TTATTGTTGGAGGCATTCATTGTATGTTTTGTTTCTATGCTTAAATTTCCATCGCTTTACAATTAACCCTTG
GTCTTCAAACTTGCTTGGGAAGGTGGCAGGAAATGTACCACTCTCCACAGGTCAAATTCCTTCATGGGCA
GCCGCTGCGCTACTTGGACCGACACAGATGGAAAGGAGCACACCTATGGAATATACTGATGATGACAAC
ACATGCGCAACATGTTTCCTTCCAAATGTGGAGTTATGTTTGGTATATTTATGTAAAATAATAAAGCATTT
TTCAACTGTCATGAGGTTCTAGGATTTCTGTCAAGAACGTTGTGTTTGTGGTCCTGTTTAATACAAATCAA
TATAGTGATGGGCGGCGTGGTGGTTAGCAGTGTCGCCTTACAGAATGAAGGTTCCCAGTTAAATCTTGAT
TTTCTAGTTTTTATCTGGTACTCCTCTGACAGTCCAAAGACATGCACTCTGTGACCGTTGGTGAGAATAGT
TTTGTTTCATTGTCAGCTGGGTGGGATTGGCTCCAGCTCCCCCCGTGACTCTCATTGATGGATCGACATTT
CCAAAAATGATATAACATATGTATTGCAGCACT

SNPHAL-50:
CCCACCTTGGGCGTCACGTTCTTTATACTGCAGGGAGAAGAGGATGGAGAAGTTATTCTGGTCCAACACT
ACCCCATCCAGTGGGATCTGAATTTAGTTTTCTCCTTTTACCACCAGGATAACGTGACTTGTACACTGAAG
ATATGTTAGTTCTAACTCCCATAACTGTACACACTGGCTGAAAAGGGCAATACTGCTGCATGCCAATCTA
CAACCTCACACCGCGCCAGAAAGAAAGAAAGTTTGTCACGATCACTGTTTTCTCTCCACACTGCCATTTC
ACGCTCAGCCTGTTTGCCAGCTGAGAGCTAAATGGAGCGATTTGTGAGAGAAAAACAGCTGAGTCCTTCC
CCGCCGGTCGACTTGCTGCAGGTGTGGGGAGGAATTTGCCTCTGGAATGTATTTTCTAATTAAGGATTAT
CAACAGCCCAGCGCCTGCTGAGAGCCCCAGTCTGGTTTTGGGCAATCAGGAAAGCCTCTCTCCATTTTAT
TCACTCCAAAAATATCTCAGTGTCACGCTCTCGCGTTCTCTACGGGATAGAGGTAGAGGTCTAGTTTACA
TCCTGCAGCTCAGACACTCGCAAATTCACAATTTGCTGCGTGTTGTTGTGCTGGTAGCTCAGAGTCTGACC
TTGGAGGAGAGTTGGTTGGCTGATGTTTGGTTCATAAGTGCAGTGTGTGAAATCTGACTT

SNPHAL-53:
TATATTATGGGACATCCTGTGTGAATCAATCAATCATCAATCAATTTGTGCTGCCACAAATCTGCACAAC
TTTTGTGGGGCACAAAGTCAGCTGCCGCTAAACATCTGTAACACCAAAGGCAGCTGCCTCCAAACTGTGT
GGCATCAAAGCCAACTACCGTTACATGTCAGTGTCACTTTCTGTTGACACCAGAAGTACGAGCTACCGCT
GCCACGATTTGAGTTTGCCCTTACTAGTAAAACGAACGTAGCAGCCTGAGCTGCCATTGACTTCAACGTT

Figure 7A

TGAGAAGCAACAGGAAAGTTGAGCATACTGATGTTTGTCAACGAAAACGAGTTAATATTCACTTCACTG
GCAGGAAATATTATTATACTGACATTTTACGTGTCCAAGTGAATCGTAGATGTTAAATTGTACAATGTCT
GGAGGCAGTGTTCGAGTTGAGCCGCCTTTTGTTGACTTCAGTGATGTTTGCGTCGG

SNPHAL-55:
ACATCAAGTCTTTACCAAATGCCTAATTTTTAACCATAACTTTATAGCAAAACATATACAATAGCCACAA
ACTTCCAGGCAAAATGTTTGTGGTAATGATACATATTACGCAAGCGCAATTTTTGCTCTTCTATATGCTAA
CTTTTGTCTCTCAAATTTTTTTTTTACTGCTGCTAATTAAAGGCTAATGAAAGTGGTGAGACAGACTGCAA
TGTTACTGTAAAATGCTAAAAGAAAATTGTGTATGGTTGCAGGTGATAACTGTGTGGGTTTGTCCCCACA
AGCTACAATTTTAACATGACTTCCACGAGCATGGACCACACCACGACTGTGTATCATTTGAATGGAAATT
CAGGCTGTATAGGATTTTGCGGATGGATGAATGGATGTGGAAGGAAAGGATGAAGATGGATGAAGAATG
TCTCTATCAGGCTGGTCTGTGAGGATATGCCGTGGACTGGGCAGATATAGACTCCGTCTCAGTAACATTT
CTGCCCAATCTGATGTCGGACCCCCAAAAAGTCAGATTTTATTTGAGCTGGGTTGACTTTGGGCTTGAAG
AATATCGTTGAGGTTGTTGCGGATGTAGGAAAGCATTGTTGTGA

SNPHAL-69:
GTGAAAAACTAATAACTTGAGTGTAATATGAAAACGTATTCGAGGTTATTGGTCTGATCTGTGTTCAAAT
GTTCAAGTTCAATAAGTCTCTCTGGATGAATCGTGTTTCTTCCAGCCTGTGTGAAGTTGCATAACGGTCTG
TGTGCCCTCATTAACTGAGCATGCTGAGAATGAAGCAAGTGGTGATTTAATTTCTTATCTTATTAAACTTA
TACCTACAGAAGTTTCATTCCACCAAATATTTGTCCTTACTTGGGTCAATAAAGGCAAAAGGGGAGAATG
GATTTATAATATAAACGTGCATCTGGACTTGTGTCTACTTGAAAAGAAGATGAAGCAGGAAATGACCTCT
CTAATTTATATGCACATTATAAGTGTGATCACATGATCTCTGGATATGGGAATGAGAGTATATTACTATG
CAAAGTAAATAAAACACCAGCATAGTCTGCAATCAGCTAAATTAAAAGCTGAATCAATCACATAATACA
ATATATTATATTCTCTTGATTTTATTAGAAATTGGTTTTATTTAATTTATTGGATTATTTTTATATTTTAATT
ATTTTCAACTTTTGTGTATAAGTAAATCATTTTACATGCAATCAGAAGACTTGGAGACGTATTAAAAAAG
GCAGACATAACTCATGTCTTTTAGCATCATCAAGTCTATTCTTAGTGTCTTTATCTAAAGATAAAATCTCA
AAATGTGCCAGAGGACTGAGTGAGTTTTAGGGACAAAAGGAAAACCACAACACGCGGACGACGTCAGT
AAGTTCACTTTGGACTGCAGAGAAGAGAGAATTTCATTTACAGTGCAGCATTTAACAATTAATGCAAAAT
ATAACTAGAAACACATGTTGACCGTTA

SNPHAL-70:
ATTACTATTTCTCTTTGTAACAAATACAGAAGTGTTCAATTAGTCACACATACATAACTGAAGAAATACT
ATAAACTTTGCAAAGACAGTATATATTGCAGTATAGAACACTCAAAACAGCAACACACACAAGTATTTA
AAAGTGAAATCTTATTCAATAAAAGACACCAAAGAAATATATTTAAATTATCAATGTTGTTACTGTTGTA
CAGAAAACCCTACATACTGCACTACAGAACAGGCATTTTCAGCAGTTGCTGGAAGCTCTATTTGCATTTT
GTCACCAGAGCACAATGAATCCTGGGATCACTGCTGTAGTGGTAAAAACTATCATTTTCGAGCAGCTCTC
CCACGCTGTTATTAAAAAGGTGGATGAACTTCAGTCACCCATATACGAGACTATATATAGACTAGGAGA
GCTAGAGACAACTGGAAATCTAATCATATAGACCAATACATTAGCATTTTATTACTATTATCCTTATTGTA
TATATGTACTGGCGTGGGATAAAACAATAGTAGAATGTAACTAAGTACATTTACTCAATTACTGTTTACA
AATTTGAGGGACTACATTACTTGAGTGTTGCAATTTCTTTTTACTTGATACA

SNPHAL-73:
AAATGGCACCAAACGGTGTGTGACCGGGCTGTGTGCATTCGTGATTATTTTCGTCAAGTGGTTTGGACGG
TGACCTTGTGTCCGCAGTGTTGTGCAGCCACGGGCGTTTTAATGTCTCTAATGTGGCGAGCAGCTGCAGT
CTGAGGCAGCACGGTGCGTCTGCACATGAGTGATTGACATGTCAGACAAGCAGCGTGACTGAAGCGTGT
GTGACCTTCGAGTTGCTTCAACCGCTTTGTCTCGACTTTTGCTCCAGATCTATCTGTGCATTGATCGATCT
GGATCAAACGAACTCACTGCTCTTTCTCTGCAGTCCACTGATAAGTTTACCACCTGCTCAAGTGTGCTTGT
GCATTTAGT

Figure 7B

SNPHAL-101:
GGTCTCTTGCAAGTGATATATCAAGTCTGCATTTAAGGAATTTCTTCAGATTTTGACAAAAGATTAACTG
ATGAGATTTCAGTGGTCGAAGGTAAAAGTCATGGTGACACTATATCATTGTGAATGTGATATGTCAGGAA
CACCTGGAGGGACTGAAACTGGCATAAAACCACTGGACTCTATCTAACCTAGTTTAACATTGTGTACATT
TGAAGTAAATCAATCAACATGTCTTTCTGTCTCCTCCAGTTGTCAGATCTGATCAGTGTGAAGCTCCTCAA
TGGTACGTCTGCCACTCTCAGCTTCAGGTGCAATGATGAGAGTGTTCAACTTCCTCTTCCTGTCCTGTCTC
ACATCAACCAACCGAAGGAAATAGTGAGATTATGATTATTTAGTAGATTTTAGATTTATGATTAAATAAA
GGTCATATGATTCATATCATTTACTCTGTTTTAACAGCTCTGCTTGCAGACAGATGGAAAGTTTACCTCTA
ATTTTGCTCAAGACCTGCCGCTGGCGAGGAAGACAAAATCCCCTGTTGTGGTCCTGGAGAACAAGAGGA
CCCTGACTCCTGTAAAACACATTTTATGCCAGTGTGATGTTTGAGTGCTAAAGCTTGTCTTATGCTGAAGT
TAAGGTTAGGTTAAGATAGGTTAGGTTAAGGTAAGGGCAAACACAAATCAATTGGGAAAGAGACTGTAA
CGCGATGTCTGTATAAGAGATTGTGATTATAATCAGCCGTAACTGTGTTGACCATAGAAATGTAGATCAT
TCTTTAGATAATCAGGTGTTTTCTTTTCTCGTATAGAAATAATGAAAACCTTTGATTCCTTCCTGAACTTCT
ACAGGTTCTGCAGACACCTTCACTGAGTCACTTTGTATAGAAGATCTTGCTAAATGCCTCCTGTTGTTCTG
CCTCATATATTCTACCATGCAAGTAATGATGTATGGCAGGTGTCGGTGGGCACCCAGGAGATGCTCCAGA
TGGTCAGAGAGGTGG

SNPHAL-106:
CAGCGTGTGGGTCTATTTCAGAATCAAGATGAAGACATTAGAACAGCTGCACCCTTCAGTGGGTGGTAAC
ATGCAAGGCGTCCCATACGCTCTATTGTTGCCCCAGGCTTACCCTGTACTTGCTGCTAGCATGTACACATA
AACTAATCATAACACTAATCTCACCATGCTACTGTACACTTGTGAAAGCAGACCATCTGTGCGGGCTTCC
CAATTAGCTGCCGTCATATGGCACAGGATGGGAAAAAGATCGGAGTCCTCGCTACACCACTGTACAGGA
GAAAATAATAAACAGCACGCTTGACTAATCCGCCGTTAAGCTGCAGGATTTCATCTGTAAAGCCCCGAA
GATAAAGTTGCGGGTCTTCCTGCACAGAACACGACCATTGTGCATCCTGTGAATAGGTGGATTGTCCTGT
ATATTATCTCCAGGATGGCACTCGTTAGACAAATAGCTTACATTGTCTTCCAACAAAAAAAACCCGGTCA
GGAGCATCGATCAGGGAGACACGCCTTATCAAATTACAACAGCCAAACAACAGGCAACACAATCGTGAC
GAGCACCAGGGCAATAGGAGCAATATCTTAGAAACCAGCAACACAAAGAGGCTCATAAGAGATCCCAA
TCTATCAAGCAGACAGCGGAGAGTATGCACGTGTTTGCATTTGTGTGTCTTTACCT

SNPHAL-113:
CTTGACAATGCATCACATATAATATAAACTAATGAAAAGCTCAGGGCTCCACACTAACTTTTCCCATTAG
TAGCACTGGTGCTGCCTACTGAAAATTTTAGGAGCCCCAGCATAACATTTAGAGCACTGCGTATTGTAAA
TTGACATGTAGATAATACACATTACATGGTATTTTGCCATCAAATCTGAGCAGCATCAGTGTGGCTGCAC
CACGTGTCTGAAAAAGACATTCGATTTCTAGTCTTGCAAGGTGCGTTCCAAGGAAATCCCTGGAGTAACA
AGGCAACCAAAAACATTTCAACACCCAAGAACCTCATCACTCATTTGATGGTTATGACAAGTTTTCAATG
CAAGCTAAAATTTAAGCAACTCACCAACTGCATTTATACAAAATGTAAAAAAAGTTTCTTGTCATAATAT
GATAGATTCGTATCGCACAATAATGTGAAAAACATCTTGATATAATAATAAAGTGTTCACATTACAACAG
GATACTCATCTGTTTTTCTTTTTCTGGCATGGCAGCAACATGCTCCTGCACAGTTCAGTACATGTGCTTTC
CTAGAAATAGTTCACAGAAATAACTTTGTTTTAAAAGGAAGGGGTCATAAAGTAGTGCGTCAAGGTTTTT
ATAGGTTTATCAAATGAAGACATCAAATAACAGTATAAGATTATTACTATCATTACAGCACAACAACATA
CCCCTCCTTCTCCTCCCTTCAGAGCACATCCCTCTGAACCAACTCCTCTCTCCTGGTAAAGGTTTGCAGAC
GGGACGACACATTTAGATTCGGTAT

SNPHAL-132:
GGCCAGGGCTAGACAATCAAGCATTCTCTGCAACAAGGAGGACTTTCAGTTAGCACATTAATCCAGATGT
TCTTGGATTAAATTGATTTGGGTTGCAAGTAAAGACTTTAGACGTTTTGGTCATTTTAGTCTCGACTAATT
CCAAGAAACAAGAAATTTTAGTCAAAGCCAAAAATTTAGATTTTTGGCAAACTTCAGCAAACTGCTTTCC
AATTAGATTAGAAAAAACATTGGCAAACCCAGTGCGATTGAATTACTGGAATGAAAGTCAATCACAGAG
TAAATAACAAAAACAATCAGAGAGTACGTTGAACTAAAGCCCGGTCATGAATCCTATTTTTATAATGTCT
TTGTCAGGTCTGTGCCAAGAGGTTGTTGATTTCATTCTATAGTTGTGTAGGTTTGTTGGTGGTAAGTGTTG
AACTAGATTGTGTTACACAATAAGCAGTAGGCAGATAGTCGAGCTGAGACAATTAACACATATGTTAAA
GTTAATAACGGCGTAAAGCATCGTGATGTGTCGAGCTGCTGTCAGACATTTCTTACCCGTTTCTGCAAAT
GAGCAAGAAGACATCATGGTCATAGCT

Figure 7C

SNPHAL-133:
GTATTATTATTAATCTAAAGCACATTGACATTGTCGTCTAAATCCCAGGAGAAGTATTTCACTAAAATAA
AGAACTCTCTAAAGACTCGTCATCTAAATACAAAGATCAATCAGTTTGAGAGATAAAGAATTACAAGTC
GACAGATGAAACAATTTGCTCATTTAGGGGGAAAACAAGTGTTTTTATCCACTTTTCCTTCGTCGAACGT
GTTCATAAAAAGGGGAGAAAACTGTCAGCAAAGCACAAAACGTCACTTAGCAGACTTGAAGCCAATTTC
TACCGGCTATAATAGCAGTACAAATGCAGTGTCTTGTATTTTCTTTCTTTGAGAATGCTTTAATTGCATAT
GTAGCTGCAGCGTTATGCTTGAGACTGAAAGAAAGGTTATGATTCCCAATTAGGATGAGGATTAGTTGCC
ATGGAGACAGCTGCCTCCAGATTCCACAGTAACACAAAACTAATTTACGGAGCCGGAGCTTGATATAAA
AACCAAATTTCATTTTCAAAATGAGGCATCACTTCCCACTCACATTGGTACACACGTGTATCGCAAAGTT
CACTCGAGATCTGGCAAGTGTTACAT

SNPHAL-47:
CTACAACTTTAATCTTACCAGACTTAGTTCTTGCTACTGAAACTGAGGAATACATGAGCAAAAATAAAAT
CTACTTTTGATATTCTTTCCTAAATTGGCAAAATCAGTACAAGAAGCTAAATCTTTAAAACACGAGTTCGA
AATGGCAAATAATTTTTAACATGTATCAGATCCAATTCAACTTTAAAAAAAATCCTGGTTAAATGGTAATG
ATATGGAACCAGGAATGTCTCTCGAAGTATCTGCAAAATGCACAAAATAAACCACAATCAGCTGTAAATA
TTTGGTCGTTAACCTTCTGAGAGGTTTCCCTTTTCTTCTTATCTTCTTTCTTCTTTTTCTTGTCTTCCATGA
ACTACTGTTCCCTTTCTGGATTCTCCTGTCTGGGGTAGAGAAAAGTACACGTTCAGTTATTGCAACACCT
CAAGTCGTACGGAAAAGCAACGCAATGCACGCACACAAATAGATAATGTGCACTTCATCCGACCAGTG
CCAAGTTTTACTCCTACACAGTCAGAGTTGTAA

SNPHAL-1:
CCACGCCCCCAAATATTGACTGTTGCTGTAGCAGCGGTAGCTACCATGG
GTTCTTTTGACTTAATGTGACTCTGCACCGCACTGATTTAACGTGATGCA
TGCTGGTTAGAAATTTTGTCTGACTTTTACCAGCGCTGCAAAACATCACC
ATGTCACATGACCTTAAAATATTGTGGGAGCGAGTCAGCTGCAATCAGA
CCGTGCAGTTGTTCTCCTTCAGCTGCAGAACCTGGGAACCACAGTCTAT
GGAACCAGCCCTGTGACAACATAACTTTGTCCTGATTGGCTGAACACAT
GAAGAATCTTACGTTATATTCTTACACATTCAGAACAACTACCTGCTGCC
TATTTTTCTCCAAAGAGGATGAGATGTCTTTAATCTCTACCTGACAATTT
TCTATTTACACTTTACAGTTTGAATTTTCAGTCGTTAAAACAGTTTTGTTC
AGGAGATTGTTCGTGTGA

SNPHAL-2:
AAACATTCCAGCATCCACTTTTCTGTCCCAATTATGGTCAAAGGCGTGAGAGGAGAAAGTTGAACTCCT
CTCGCCAAACTCCATCTGGAGGCGCTGTGGCGGCACGATCCGCCAAGTGCTGGCGGGGCTCACTAGC
ATTCTGCTCTTGAAAATAATGAACATTCAGTTTTGCCATCTACCGCATATCCTGCCATCTTGTGAATTAA
GGGAGGGAAGAGGGAGTGATGGACAGACAGAGGAAGAGACGGAGGTGAAACAGTGGAGGCAAAGAA
AGTTGGACAGAAAGTTGATTTTCATCTGAACAGACAGGATTTTGTAGCAATTATTGAAATTTGTCAAAAA
TGACAAATATATGTGGAAAGACAGAAACTCTCATAGCTCGATAGACAGAACAGGTGACAAATGAGAAAT
GAACATAAAGCACATTAGCATGGTGTTGTGTTGCCATGTGTTCCGATCAGGATCCACGTTTTTTTTCATC
AAACGATAAAGGTGATCACTTTGAATTCATTTGCAGTGACTCCTTCCCTCTAAAAGAACAAGTGGACCAA
CA

SNPHAL-3:
CGAGGGCTAGTGCTTTATACCCTTCGGATTTTTCAGATCCTCACTTCCAACGGAGGGGTACCCAGAATT
CCTTTCAAATCACCAGCAAACTGGGAGAGAGACCCACAAATGTAGTATTTTCTCCATGAATAAGATAAAA
AAATTATGAGTATTATGGTCACCTTTTTCTCAACAACCTTAAAGAACAAGATTGCGAGCGCGCTAGCATG
CTAGGGATCTTTTTTCTGCATGATATTCCTGTATTTTCACATAATGTCATGTCGCATCCCCCTTGAAGGG
CTGTCCCAATTCGTAGGGAAATGTTTCAACCACTACCCCTTGTGACTCCGTTTCAAGGGGCAGGATAAC
CCTCAAAAACAAGGGGTGAAATGAGATT

Figure 7D

SNPHAL-11:
ATCGGAGTAAATGGTCTTCAGAGATACACTCTAAAGCCGAGTGAGAATTTTTGCGCTTAAACTGCATTCT
CAGTTCGATGGAAGCAATAAGGTAGAAATGGTTTTACAGAAGCCTTTGGACCGAGAGAAACAAGAGCA
CATATCGTTAGTGTTGACTGCGGAGGACGGAGGAGAACCACAGAGGACAGGAACAATGCAGATTCACG
TG**ACTG**TGTTGGATGTAAACGACAATGCCCCTGTCTTCGGTAAACAGGTTTACAAAGCAAGTATTACAG
AAAACTCCGCAATAGGAACCCTCGTTACTAAAGTCAGTGCTTCAGATGCAGACAAAGGCTCAAACGGC
GAGGTTACATACGCCATAGGGAATAGCATGGATACCGTTTCAAAATTATTTCACATTAATAGTCACGGTG
AGGTGATACTAGATGGTGCAATAGACTATGAAAAAGAAAAACATTATCACATCGACATAGAAGCGGTCG
ATCAGGGCGGACTCTCAGATTCAAGTAAGATAA

SNPHAL-25:
AGCACTAAAAATCAATTACCCTGATCGCAGCAATTAACAGTCAAATGATCGAGCAAAGGAAATAAA**TTG**
ATATTTACAATAATGCAATTGGAAAGCAAGTAAAACTTAGAGCTATTCTAGATTAGGGCTTAAAGTCAAA
ATGATTCGAGAATAAAAAGCATTTGACTAAAGTTGCAAATTATAGTATTCACCCAACAAATGACTGCCTG
TTTCAGTCACATGAACTCTGCTTCTCCTTTTCCGTTTGATCCACAGAATATACCGGGCTTTATAAATATG
AGTGGGAGTTTAACCGTGGGAATTGAACCTCAGGAGGCAGCATTTGTTTATCTTCTCCCCGTGAAATAT
CTCCAAAAATGCAAGAGAGGGCAAC

SNPHAL-76:
ATAAAAGCAACAATAGTGTTTTCTATCAGAAGATCCGAACTGTAGTCATTCCATTTCATAAGCAATAACA
CAAATGTTTATTACAGTTTCCCCTTAACCTGTGAAATACTTCAACCATATACTGAAAAACATTATCAAAGA
CTTTACGTTTTGGAATAGCAGGTGTTGTTTCATGTAGCTTTACAGTATCATTACTCAGCGTCATGCTTCA
GAGCATAGAGACAAAGTGTAAACATGAATTCAAATAAATTATTAAATCGCAAAAAAAAGGAAGCTTGGAA
TTTTCTTGTTCTTGCAGGTTAAGTTACAAACTGGAAGGCAAAGACAATCATCGAGTTTTACATCCAGTCG
TCTCAGCTTGGAGCGTTTGAGTCCTGAGGGTCACCGAGCCGCAGCAACTTTGAGATCAAGGTCGGGCA
GCGACGAACAGTCAAGGTCAACGATCCCGTCCCGCGCACGCGAGAGCATCTCTGTTCGCAAAAGTTCC
CTGAGAGAGTCC

SNPHAL-77:
TATCGTTTTCATCAAAGTTTTCATTCAGGATTTCTTTCTCATAATCAATATGACTCAATAATTACAAACTAT
AAGAACTATTTCCAGCGTGATGCTACTTAAATACGGCGAATTGATCCAATGCAGAGGGGCGGGATTTAG
AGATGTCAAAAATACACCTCAGTTTTCCAAAGAAATGATTGATTACACCGTGGACTAATGTCACGCTTAA
TAGCAACAATAATAATGGTCTCATTCTAAATACACATAATTGTGTACTGTGAGCGTATGCAGGTTTATTTT
TATTCCTATGTTTGACAGTTTCACCATATTCTATACAAAGATGCATCAATCTTATTTTTTCAGATCTGATTC
TAATACCTGAATTTGGAACACTACCTATACCAGT

SNPHAL-81:
ACTTCCTCATGGCTATTTTGACAGGCTCTATAAATAAAGTTACGAAAGTTATTAACCAACATTGTTACAGT
TAATTCTGCTTCTATCCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAGCATCATTAAG
TTAAGTATGCGTGAGGAAGTGAGAGCAGGGGAAATACAGATGACTTCATCGCCACACCACTGATGGAA
AGTCCAATGTGTCAGTAGTAACAATCTCGGTGTTGTGTATTTGTCCTCACAGCCAATCAAAGGGCATTT
GTGCTTTTATGTGTGTGTGTATATATGTGACACCTTTGTTTTGTCTGTGTGTAACTTCACCCACCGTAAA
TAACTGACCTGGTGGATGGGATGGTGGACAGCCTCATTAAGGACAATCCCAAGAGCATCAATTGATGG
CTGACAGGTGGAGTCGTGGGTTCAGCAAATGTCAAAATG

SNPHAL-82:
CTGTGGCGCTCTCTCTCTCTCTCTCCTCGCTGTGCTCCAGCTGACTACAAACACAGATTCAGTGGGAGA
CAGTTCGATGCCCGTCGTCCATCTTCACTGGCAGCGTCTCCTCTCCGTGGTTCACCCAGGGAGCGCCG
TCCACCGGGGATCCACCGAGCTAAATAACCCACCGGACCCAGATACCTTATGGAGTGTGAAGAAATAT
TTTTTGTTTATAAATCTTCTGGATTAGAATGTTTTATTTCGTAAGATATGATGGAAAACCCATGTCCGATT

Figure 7E

GTAGGATGTGTTTAGTTAAAACAACATTTCAGTACTTTTATCATTTATTATGCTTCATTGACTAACAAAAC
CTTTTAGCTTGTGTTGTGGAGAGTTCAGTGAACCGCAGAAACTCAGAGAAGATACCGAAGTAGACGCT
GCGGGAGCGGTTCTATCACAGAGTTTCTGGGATAAACAGCCGGAATGCGTCCAGGAACAAACTTGGAT
TATTTTT

SNPHAL-84:
GAGAAACGAGCTGAGTAAGAATGAGTCATGCTTTCAATTATGCATCAGCCTGACGGACAGGCAGTGTTT
GCTTTCAGATAGCAGTCAAGAGAGGCTAGACTTACAGGTGACCCTGTAATCTGTTGCCATGCTGTCTTT
ACTTGAAAAACCAGAAAATGGTGAGAAAACCAATCGAAAAACTGAACACTCTCGAATAAACAAACAGTTA
TAACTAATCTGAATTAATTAAAACCAATCAATCTGACTTTCTACTCCTACTATTACGCTCCACGTATATGC
CCACAGTTCCATTCGTACTAAAATGACGGTCTGCGTCGGTCTGGCATTGCTCGCATGCGTACGTGATC
CCACATTCCATTCCATTCCAGTAGGTGGGGTAATGCGCAATAAGGTTGTTTGTCAACCTCCGTTTAAAT
CAAGAACTTCCATCAGGAAGTACTCATCCCGACCAAGCGTATAGCTGTGACTTCTCTCCAGGAGTTCAC
CCCGTGTGCGTGTTCTTATACTCCTTCATAGATTGGTTGTTCAATCATGGGTATCGGAGGATCTCCTCAT
GCAGCTTCTTTTTAAAACCAGTGTCCATGTTGTTCATCTTCTTCTTTTATTTGCAAACAAACAAACATATG
TTGCACTTGGAGCATGCACAGTCAATGCATACTGTCAGCGTGGTTACAAATACAAAACATTTATGTCAC
GAGGACCATAGCGGACCCTAGTGGACTGACGGATGTGGAAATCACACTGAAAAAAGATTTGTTTACCA
ACTTAAAAAAACGACTTTAATTGATGACACAGAAATTAATACGTTTTATTAAAATCAAAGTTATCAAGCGT
AAAATAACATGTTAACATTCATCTGAACCAATTCATTCATTTGTGTGTTACCGGTTAAATATATTTTCTAC
GTTGGTAAACAATTTTCTTTTTCCAGTGTATGAATTTGCCTTTCATGTTCCCATCTCTATCCCTCTGGTGT
GA

SNPHAL-89:
CTACCCCTGACATCAGAAACCAGGAACGTACAGCTTCTGGAGGAGATACTGATCATAGTTGCTGATATT
CACACATGAGGTGAAAGTAACATATTGAGGGCAAATTTAGTTTCACAAAGAAAAAGCTGTCATTTATATA
CATCTACCACATAAAACATTTTTAATCCTTCTTTAAATTTATCTTATAAAATCCCTGACACCCAAGATAAGT
ATAGATGAGTTATTGATCCTCGTAGAGAAAATTCGAATTTGACACAGCAGCACAAAAGAGCAGCTGCCA
AGGGGATGTAGTAAGAATTAAAACTAAGAAAAGAAACAGAAGATAAGATAAAAATAGAAATACTATATAC
AGTATTGGACTGTTCTATAAATATTAAAGTTATGCGATATACATGTACAATATATAGCCTACCTGAAATTA
CAATACCACAGTTGCAATGCTTTCTTTTGTGTCAAATTAATTATCTACTTAACTGAGCTGCAATTTTCTTT
GCAGCATTAACAGGTTGTTAGCTGAGATATATAAAACAAATATGGCATGAGATGAAAAATACTATCCACA
GGTAGACTGCAGTACCATGAAGTCATGGAGGAAGACAACTTGCCATCTAGATGAGTTTCAAGTTATACA
ACTTGATAAACACACATGATTCACCTTTATAGTGGAGTCTCCATCTGTCGT

SNPHAL-104:
GCGGGATGCAGGAACTCCACAAGCTGTTGCCGGCAACTGCAGGTGCGAGTCACTCTCAGCTTATTTGT
ATTTGCCGGATCAGCCATATTACCAATAACATGTATGAAATGTTCAAGAAATAAAATGGGCAAAGTGTGA
AATCCTTGTGGTACATCTTGGATTACTTTTTCTGTTTTTGTATTATTTTTAAGCTTTTTAATTGTGACAAAT
CATTAGTTGTGTAGGGGACAATCAAGAATATTTTCCCTTTATATTTGTTTTTAGTAATTGTACAAAATCCT
GTATAATCTTCGTTGTTTAAAAAATTCATTTATGTTTAATTCTTCTAGACGTGTTTGTTCATATTGACACCT
ACACTGCTGAAACTGGAGTGTCACGGTTCTTGGAGCAAAACAGAAACTGGAGGTCAGTGTTTATTATGT
TGATCTCACGTCTGTCAGTTAATCTAATGTGAACAATACTGACATTTAAAGCTTAATAATAATGACTTACT
GTTTTTAAACAGATATGACAAACGTGAGGACATGAATCCCTCAAACCCTGAAATCAAGATGTACTCTCAT
CTGCTAATGGAGGCTGATGTTACCAAAATACATCTACTCCAGGACACTCACCAGCCTCT

SNPHAL-117:
ATGAATATAAATAGTTATCCGTGTTAATAACCTAAGAGCAAGTTGGCAAACAGCGTGATTTGGCAGCTGT
CCATCTGTCTCTGGGTGTCAAGGAAAGGCTGCTTGTGTAAGAGCAGAGAGATAAACATGCTGCAATAG
AGCATCTTTCAAATGACTGAACATAAACACTGGAATAGTATTAAATGTAAAATTGATAAATCAAATGTCAG
AAATGAAAAGTCTCAAATCCTTGTAACTCATGGGAGAAGAGACAAATGTGGATTTTGACTATGACCTTGA
ATCAGTGAGACGGTTGGTCATGATTAGATTTACAATGACAAAGCACTTTGTCGTCCCTGGAGCTTGATC
ATGGAGTACATGCCATTAGGAGTTATGGATATTGTATGTTAGGCAGTTACATAAAATTAATTGAGATTAA
TCACCTGCAATTTAAACGCTACAGCTGGTTAAAAATAGGTAGCTGCTGTCCATGTACAGTATGAGACAC
TTGTGTTCAATGTCTCTATATAATCTACCTACTAATTCCACAAACGTCTGTATTTCCATGTGTCTTTATG

Figure 7F

SNPHAL-116:
TCTGGTTATGGAAAGACATGATCAAGTTCATCAGTTTGAATTGAAATGCTGCATGTTTTTAAGAAACCTA
TCTACAGTCATGTCAGAAATCAGTGAATTCTCTGTCATTCATCTATAAAACTGAATGAGGACGTGGATAA
AAACGAAGGTTTCTTTGCTGAGTGGCTGATTTGACCTCTTTGTCATTGGGAGAGGAGGAGGTGAGTTG
CAGCTTGATGCCCCCGATGTCTCTCGGAAAATGACTGGGCACAATGAAGAGGCTCTGGGAAGCATCCG
ATGTGGGAGAACTGGAGGAATTTTCTTGAAAGAAAAAAAAATCTTGGATGGTTTTCTCTGCTTTCCTGGCT
GGCAGTGCAGGAAAGCTTCATACTGCACATGCAAATACAGCCGGAACGGGGATGAATCATTGGAGCGA
TGAAGAAATTGAATTNATTNANTTTTATTTTACAAAAATACTCTGAAATGATTGGTGTAAATTGTTTCCAG
TTTAGGAAGACAGAGCTTCTCTATATATATAAAACTATTTTCTCAGAGTTTGGGATTAT

SNPHAL-121:
ATCCGATAATAATTCACGTTTCTTAAAATAAGTTTATAGCCTTTAGTTAATGCACACCTGAGGGTAAAATT
GCAAAACATGGTAAGCAAATATGGAGTGTTTGTTTAGTTTTTTAGTGATGTACATCANAAAACTTCAAAC
AACTTTAGGTGGAGGAGGAAAATTTCTCCTTCAAAAGAATTTTAATTAAATATTTCCACATCTCAAATAAT
ACGGAGCCCCCCCTGGTATCAGGTGAAGAAAAAAAAAAGATCCATTCCCTCAGTTTAACAAACCACTTT
ACGCATGTAAGCATATAAATCAATCAATCAATCAAATTTTATTTGCATAGTCCATATTCACAAATCACAAG
TTGTGACATCCTCTGCTCTTAACCCTCAACAAGAGTAAGGGAAAAACTACTAAAAAAAAACTGTTAACAA
GGTAAAAAGAAGGTAGAAACCTCAGAGAGAGCCACATGTGAGGGATCCCTCTCCCAGGACGGACAGA
AGTGCAATAGATGCCCACGTGT

SNPHAL-126:
CTTCTCAATTCCGGGAATACCATTAAGGCAGACTTTGTACCTTTAATGGAACTGAAACCAGGCTCCCTC
TCTCCATTTGTTCTCCGAATTCTAGGATCACTCATTTTGTTTTCGCTCATTTTGTGTTGTTCACTGTCACT
AACATCGGCGCCGCTGTATTCTGTCGTCAGGTTCAACCCAGCACCCACTCATGGTTTGAAGGAATTAAA
TCAGAAGCAGGCTGAATGGAGGAGATGCTTTCATGGTGCGGAGCATGAATCAGAGTTCAGTGTATAGA
TGTAACTCAAAGTTGTTATTCTGTTGTTAACACTGTAAGTTTGATCACTTTTTGATTTTTAATAATTGACGT
GTTTTATATTTTCAGAGACTAAACGAGGAGAGAGCGGAGAGAAAGAAACTCAGGATGCAGCAGTGGAG
ACAGAAACAGGAAGAAGGTACAAATGATTCAGGGTTTTTTGAGAAGATGTAGATGAAATGACAATAATA
AAGGAGGATAAGGGGAACATAATCAACATTGAAACATCCCTGACATTATTTAATAACAAATTTGTAAATA
AATTCAATTAAATATTGAT

SNPHAL-135:
TGTTGCTCTTGTTTTCCCAAAATATATTCTTATATTCGATGCCCACATTGTGTCTAGAAAATGAACTGCAG
CAAATACTGAGGAGTTTTTAGCCTTTATCCCAAACCCCTAAACACTAATGTGTCCTATTTTACATCCTCC
GTTCTACTTGGCAGGAGATTTTGGCAGTAAAACCAGTTTTTCTGTTAAATATTGAAACTATCAGCTTTTG
GCTGTGCTGGTGTCAGCTAAGACAGTCCCTTGGGGAAATAATAAGGAAGAGATGGACAAACTTCCTCC
TGCTAAAGTTCACAGACACAGTTTTAATGAGGGTGCATAAAGTGTAAATGTAATCACTTTAAACTCGAGC
TGGTTGGTTTGGACTTCACTTCTGTGTCGTGCTTTTTATAACAACTGCAAAAGGACAACACAGAAGATAT
TGGTTAAAGTAAAAGTTTCAGTCTGTCATAACTAATTTACCTGACGACTGAGTTTACATTTTCTACAATTT
GACAGGTGTGTTTAACAAACTTATAGCAGTTCAACTTTAGTTAGAGCTGTAAGAGAAGGTGCAATGATAA
GTTCAACTAACAAGAATAAGTCAATGGACTCTTTTTGAATAACCTAAGCATCTAAAGTGAACTCGAGTAA
ACTCTCCCTCTTACTTTAGATCCCCAGGTTATTCCAATGAT

SNPHAL-137:
TCCTGCTTCTCAGTTGCTTCATTCATAACACATCCTTGACAATTTTAGGATGGTAATCTATGTGTCGCTT
GTGTTCAGGGAAGTAGGTTGTCTGATAACGGCTGCGTTATGTTCCAGACTAACCCATAATGGTCTCTCT
TCGACTTTCCCTACTGCAGAGCCAGGTATACAGGAGCCAGCCTGACTTAGTGTCAGCTGTCTATGACA
CCACAGCCTCCACTCTGGCTGTGGACTACTCCTATGCACAGTACCCAAACCAAACTGATGCCACACAG
AACTACAGCCAGTACCTCTATCCTTCTGAGTACACTGCAGACAGCACATGGATCAGCCCTGAGCAACGT
AAGGAGAACATTCTCACGCTCTCAGCCTTTTTAAGCTTAACCAATCTCTAAATGTTAACAGGATCTTTAT

Figure 7G

CAGAGATCAGTCAAACACTCACAGTCTGACTCTTGTTTTCCCCGTAGCACCCCCTCGTCCTGCAACCCC
AGAGAAGTTTAGCATACCCCACCGCTGTGCCCGCTTTGGACCTGGTGGTCACCTGGTTCAAGTTCTGC
CCAATCTCCCC

SNPHAL-138:
ACTTATAATCACTAATTCAAATAATGAACCACTTCATTCATCTCTGTTAGTAAAACTGAAAAAGCTCATGA
GAAAAGACACTAAACACACCAGGTTTTCAAAGCTGAATTCTTTAAAGCCTGCAAACTTAAAGTAACACAG
AGATTAGTCTGATATGTACTAGATTGTGTTATTGTTATTATAACTGTCATCCTAAATTTGAGATATTCAATT
ATGGGACAAAATTTGTTTGAGATGAACTCATTTTTGAACAGATTCTTTTTGTTTGTTTGAATTATCACTGT
AGGCTGATTTATAAATCAGTTTAAGTAAGATTTTGTTGTTTTTGCAAGTGTCCACATTGTTGTTATGTTGC
ATTAAAACTAATTCAACCCACATTTTTAATGAAAACATAACTGAAGTATTAACTCTAGTTTTTGGTTCTATC
TGCAGGTGGTCAGAAGAGTGACCGCAGATCGGTGGTCTCCAGTCTCGACTGTCTCTCCAGCATTGTGG
AGCGAATCTCCACTGACAACAGCAGCTTGATGCCGG

SNPHAL-144:
GGCACTACCCCGCACTACC:CTTCCTGGATAAAAAACACATGTGGGAGCCCACAACCCCCACTGCATAA
GCAAATAATGCCTGGGGATTGGCTAGTGCGATTCATTTCACTATTATTCCATAGGCACGCTAACAGGAA
TAATATGCCATTGTCCTTTTATTTCTTTTACTTCTCATCACCTTTGTGTAAAATCACATCCATCCACGAGC
CAACCAACCAAAAAACTGTAAGTGCACCTTTTTTAAAAAAAAAACAGTTTGCACATTCAAGACACATAAA
AAGGTCAAAATGTCACTGTGCAGTTTAACTCCCTCTCCCCAAAAGTCCTTGACCATAAGCACAGTCTGG
GTTGTCGAAAATAAAATATAAAAAACTGCACAATTTATGAAGGAGTGTACATTTTGACACGCATAAACAG
TACCTTGAAGATATACATAAAATTAAAAAGTCAGCATAGAGAGCCAACTTCAGTTTCTCCCATAAGCCCA
ACAGTTAGTGAACTTGGCATCCCTCGCCGCAAACGTGTATACCATATGCACCGTACATAAGTACTTTCT
ATAAAAAATAAAAAAGATTCTTTCCATCAGATGACAAAACAGATCTGATTGCTATATCGTTAAGAAAAAGT
ACAAAGTTTGATCGAAAACAAAAATGACCACACATATACAGACAGAAGAAATACTTTGCACACTTGCCTG
GGCGACAAAGATAATACTGATGTGTATTTTTGACAAAAAAAAGAAAAGCGAGGGGGAGAAAGTCAAACT
TTTAAGTCCTCAGGCTTCTTGTAAACTGCAATTTGAATGTAATGCTTAACAG

SNPHAL-119:
TCCTCTACATTAGCGGTCGAAGACGCCGCTTCAGAAGGAGGAGGATCCGAGCTGTGAGCGGTTATCTC
TGTAAAAACAGATGTACAGGTCTCTGTGACCTGCTCGATCTCTTCCTGTGATTCTGGTTTTAGGTTGGA
GAAGAACCATTCTGGATCTTAAATTTAAACGGTGCTCTGATCTAGGAAGGTCTCTGCCTCAGGTGTTAA
ATCAGGTTTTAACTCGGAGGCAGTCTGCTGACATGTCCCTTCTTTACGGTGTTGTTGCCAAAATTCCAG
GCTATTGAAAAGCTCATCACAGTCCCCACATTGGTAGAGGATCCTAGGCTGGTCTGCTGTCACTGTTGC
ATCAGCTGCAGTCTGGCTGAGTTCACTTTTATCAATTTGAACAGAGGATGGTCCTTCTTGGACTTGAATC
TGTTGAAGTGAAACTGTCCTTGATACATTTAATAGCTTTTGCTGCAAAGAGAAGGGAGGAAAGAGGAAA
AACAGGGATTAGCTTCAATTTCTCTATGCAAAAATAAAACAACTCGGTAATATTAATCAAATACCTGTTAA
GTCACTTCCACCTGCTGTGTTTTTCTTTAATTTTATCCTATCTGGCAGATAGGGAATGAGAATTGAGTGC
CGGGGTACTGAGGTCAATTAGAGCAGCGTGTGTTTAGAGCCAAGGTTCC

Figure 7H

COD-2:

TTTTTAACAGTAGGTAACGTGTTTACGTGGGTGAATAATTTAACTGTTTTTCACCACTTTACTATCTCTCT
TGTAAACCAATCCTTGCAGACATTTGGAAATAAACATGTCCTCTGCCGTTGTCCCATGTCCATTGTGACAA
CATTGGGCAATGTTGCCGTGTCATGTTTTTGCTGGTTTTGTTTGGGTATTGTGTATCATTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCACT
GAGCTGAGCCAAATGCCTGGGGGGATCCTCTAGAGTCNACCTGCANGCATGCAAGCTTGGCACTGGCCGTC
T

COD-3:
TCTCTCTCTCGTTCTCTCTGACATGCTTGGAGGGTACATTGCAGAGATCCGTCTGCTGGATCAAACAAGGT
CTAATCCATAAATGTGTTAGGTTAATAACTTAAAGAGTTGATTTNCAGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTG
CGTGCGTGCGTGCGTGCGTGCGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGAGTGTGTGTGTGTGTGTGTTCGT
ATGCGCGCATGTGTTTGTGTGTGTGGAACTAAGGGAACGGTGAGAGGAAAGGAGGACAGGATGATGACAGG
CTAGCGATGCAGAAGATCATATCCGTGTC

COD-8:
AGACATCGCTTTCTCACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACAATGAAGAAAAAAACATTTACCTGGCAGGAACCAGTGTTGCTCAACTGGAATATCCCTGTTTCTTTATA
TATCCTATCTGCTATGCATTTCAAAATACATTTGTTGCATTGGCAGACCTTATCAAACGTTTTGCTAGCTA
TAAGATTTGTTTATATATGTAAGGGGGGGGGGTCCTGTTTAAATATAGGTGTGAAATCTGGACAGATGGTT
CAGTCGAGTTTTTTTTTCTGATATTCATTAAAAGTGGGATAAATGTGGTCGCCT

COD-41:
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACGTTGATCTTTCTATTCATCTTTCCCACTGGGCTCTTATTCACAGGGAGTCACG
GCGCGACAGAGCGACACAGTGAACATTCGAGAGAGGGAAGGAAACCCAAGAGGTCCTTTGGCTGACGGATT
AACTCCAACCGCGGCTTTTCCACCTGCTGAACAAGAACTGAAGACAATGAGCGGCGGCTAACCACGTTAGT
CGCTCACAATGAGAT

cod-65:
GCCCTGATCGCCATGACGACAAACCAGACACAATTACCTTGTCACAGCTGCCTGGGAAAAATATTGTTTAT
AGATAAATAAGAATTGAACCACAAGGGCGTTTATCAAAGTCGGGCTTGAGTGAGGAGGGGGGGTGAGAGAG
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGTATATGAGAAATACACAAATCTATAT
ATTTATTATACTTTTGGACTGAATGCCCGTTCCACAATGTGACTTTACCTGTTTACTGCCGGCAGTAGAGG
GGAGAAGAAACCATTTTTATTCATGCGCAGATGACAAACGAGCAGGTCAAGCGAATCAGAGGTCAAGTGAA
GTGGATTACTTTGTTGTTTTTTTTTGCCGTATGAGTTTGATATTCATATTTCGTATTCGCCGTATTAACTGC
CCGGTTCAAGGACAGAGACGTAGGGGAGGGGCGAATACGATTGCA

Figure 8

SB1
AGCAACCAAGCCAGAACCAAACCTGGGAAGTTCAATAGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTAACCCCCCTAgCAAGCAGGACGA
AACCAGNATCC

SB2
ATCTGCAAATAAGTTAATATTCACGCTTACCTACAATGATATCTGTAGCATTTATATCAGATTA
TATCTACAAACAGTTTTATTGTTAATGCAAAAGGGAGCAGGGATTTTGGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTACCTGTGCTGGAGGCATGATGTACTGCTGGATGTGTTCTCCAGTAAT
GTGCTCTGGTTCAAAGCTGTCATCTGCAATAATGACTTCTATGTTGCTATANAAACTCCGGAT
GCTATTCAACAACACCTTGAGTTGTCTGTAGCGCANGAATGTCTTTGTCGTGATGGTGACTTG
CGAGCTGATATCTGATTGAGTTATTAAAACAAAAAGACAAGGTGATAAGACACAGTGTAAGC
AGAACTGTCATGTCATGGGGAAAAGAATTCCATTGTCAAATATCTACCTGTTCCCATGTCGTA
TAGGACTGGCACCTGAGGCTGTTTGATGGTAATGGGAAACACAGCTTCATGCTTGTCAAAACT
GGAAGGAGGCTGAGTCAGAANAAGACAGTCAAGGGGTGGTTTACCAGTAATACATTACTTAA
TTCTGACATTTAAAAAACAANGNGGGCTAAGACCCCCAGTGAATCTTGCCTGTCTGAAACACA
CAAAN

SB3
TGGNTCTGGNTCTTCATCCTCTGGGACTCTGTTTCCCTCCAGCTGTGGACCAGCAGTGTTAGCA
TGTTAGCTCCACTTCACTAATTAGCACTCCTGGCTAATCAGCTCCATGTTACTGTTCACCTGCC
ACACACACACACACACACACACACACACACACACACACACACACACACACAGAGTCACTTCAAAGACT
CTCCTCCTCTTCATCATCCGTTTTCCTCTTCGCTCCAGTTTTTCTTTTCATCTCGTCTTCAACTGC
TCCCAGCAGGTGTTCACACTCAGAAAAGACTTTAAATGAGATTACTGTACACACTGTACGTGT
GTGTGTGTGTGTGTGTGTGTGCGTGCGTGCGTGCGTGCGTGTGTGTGTGTGTGTGCGTGTGT
GTGTGAGCCCANCCTTAAGCTCTNTGTCTNCATGGTAACACAACCCAAAGGAGAGGGGAAGN
GAGTNNTGTGGTTAAAAAGAGAAAACAGGGATTTAANAGCTGATGAAAANATCTGTCTGTGN
TGNCCCCTGGGGGGGGAGGGNCAACTACCCCACNTTTNTTTACAGNGCCCNTAATCAATAAT
GGGTTGGTGAAAAAGAACNCNGATANNTCNCTTGGGCAAAAGTTNTGNTTTNNGGGGGTT

SB4
CTGGTTAGTCCTGTACGTGTTTGTCTCCTCTAAAAGTAACCAAATACCAGTCTACTTGCCACTC
TTGAATAACTCTCTGACCGACTGGACTGCTGAGAAGGTTGTGCGAGTGTGTCCAGATTCATAT
GTGTGTGTGTGTGTGTGTGTGTGTGTATCAAACAGAAGAGAAAATGCTAAAAGTCATGCAAG
ACAGCGGAATAAAGCTGGAATAGCAACAAGGGAGAAACTGGATGGCAATGAAGTGAGTGAA
CAGACAGGTTATTGGCAGCAGAGGGAAAGTAAAAGGCTGGATGTCCATTGAAGACGTAGATG
AAGGAAAGAGAAGGTGCTTTTAGTAGCTAAAAGGAGAGGAAGAGTGCCAGAAATATATAAA
CTACACAGTTTAAATGTTGGTAACAGGGGAACCACAGTTAGAGAGGNTTATGTTCATCCTTAA
TGGCTCTTTCCCTGTAACCCATAGTGGACCAATCTTGAACTTGGCTTCTTATAAATCATCATCA
T

Figure 9A

CTGAATCANAAGTTAGTGATAAGTGTCTTTCCNGGGGGGTGGTCTCTCCAAAAAAGGCTTTAT
TTTGTCACATGGGCCATTACGGCATTTAACGTGCATGGCCGGTCCTTAAGCAAGCTACTTGGC
TGN

SB5
TGAATAAATACTTCGTCCACCACTGGAACCGCGCTCATTCACATTAACATTCATACAGTAGCT
GCAGGAGACATATGGCCAATTACACTCAACCATTTCCTGCTCTCTCACTCACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACAAAAAGAGCTCTCATGTAA
ACAGTGGCCTACATAATACACACTGTCTTTCTTGACTGCTTTCTCTCTCTCTCCCTCTCTGTCTG
TAAATGGGTCAGTTGAGACAGACCACTGGTCANACAGACTTGGCACGGGTCCGTGTGTGTGT
GTGAAGTTGTTAAATTCTTTGAGAGCTTTGTAATGGGGTGTGTTTGTGAACNAAGCTTTCTTGT
TGACACNGGTTTGCTGTAACTGCTTACTAGTATGAAAATAAAGTGGAGGAAGCCCAACGGGG
GACAAACTCATCACAACTTTTAAAATGTATAATACTGGGGTAGAAATGTGGCATCAAATCTAG
GANGGNCACANGAAAACACTCTGAAAAGAAAACAGCTAAGGCAATGGNTATTAATTCTGAG
ACCAGAATATCATACATACTGGGTGTGGGNGTGGGGGGGGNCTGTGGCTGGGCTCTGTCTNTT
AAAACC

SB6
CAGTTTCTCACTTAAGGACATCTGAGTGTGTGGCAGAAGCTGCAGCACGGATTGAATGCTGCC
CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGNGCACACATGCACAA
ACTGAACATAGAAGTGAAAGTGATGTGNGAGCAGCTCTTCAATATCTGACTCTGCCTTGTTTC
CAACAGAGATANACCTCTGCANAAACACANGATTCTCTAGTGCAGTTTGCACAACACCAGGG
CATGTATTAATTCACTCTGCACAATAAACACTATCACAGGTCCTGAATGTTTGGGTGGATGGN
TCCTGAAATAAAACACACACCCCCTCNGNGAGTGTTACACAAGCTGTTNTTGAAGCATGGAA
GAAAGTCAAAGTGTNNGAGGAGGAGCGAAACGCAGGACAGAGAGACAGAGAGAAATGCGTG
ACATACTGTAGCTCACTGCCCCACTCTTTTTATGGCTCTTATGAAACANACTGNGTATATCNTG
GTGGNATTTTTCACATTTATACCCACCNCACANAANAGAATTTATCCNTCCCCTTGANNCCCA
TAAAATATTTAAGGNGGGGTCCNGGGGAATGGGACCTAAACCACCAAAAAAACCCNTTCAAG
GAAATAACCATCAATTTTCAAAAANNCTGNCATTCAAGTTCN

SB7
AAAGACAAGACACAGCCTGGCCAACTAACTGGAACTGTGAGCCTGGAAGCTTTATGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAGAGAGAGAGAGAGAGAG
AGAGAGAGTGTGTCTGCATGCACACAAAGAGTGAGAATATTCACTATGAGAGGAGATATTTG
TTCAGCCGGGGAATTTACTGATGAGATTAGCTCTGGTTAGGGGGTTTGGGGGTGTGGAATGTA
AACAAAAGGCAAGCGGAGAGAAAGACTTTANGAGAAGATTNGGCACCCCCNCNCCCCCNTTC
NTGNGCANCNNNTNACAGNNNNNTTTTNAGNTTNCTNNGNGTNTNCNTAACAANNNCCTTNN
ANGGCCANNCNNNNNNGNCTNGTNAACCNTNTTAAAGTGNATTTNTGAAACATTNNGNNTNN
NNTNNTNAANNTNCN

Figure 9B

SB8
TTGCCAGAGCAGCTTTGCACTCTGAATGTACAACTGATAATATTGGATTTGTATGTTTAGCATT
AGAAAATAGTTGCTTTCAAATTATGCATTTGCTCCATAAGACCGCATTAATAATGGAGCAGGC
TGGTATCTGCCATTTGTTCTTCTTTGTTCCTCTTGAAACGTGACATCAATTATGTATCACCAAA
AAATTGTGAATTAAATACAATGCATATTTTTCTTTGCAGTCAAAAGAGAATGTCCGATGAGAA
AATTCTTTACGGATATCAGAAGAAATACTAAATGATTCTGTTACTTGAAAATAAAAGTTGAAA
GTCCAGTTGGGTTGGACAGTCGAGACAAGCTTGGCTTCAGTATAAATATCATCCAGTGTGACC
TCGGCTGTAGAGCTGGCTCTGGCCCTTTGTTGAACTAAAGCTTTTAGCAACACAGTAGGCATG
TGCACACACAAAACACACACACACACACACACACACACACACACACACACACAAGATACACGTGTG
CAGGTAGACACGTTGCTTGAATGTCCATTACTGACTTACTATGCCATTACTGtGAGAACTGATA
GCACGGAATACTGGTTTATTGCTCTGNCTGNAATTTATCCTCAAATCAGAGAANAGCTTNTGG
AAG

SB9
CCATAGCTTGGCAACTTACATAAAATGTTTAAGTAGTTTAGTGAAGAGAAGAAAATATGATTA
GTTAGAGTACCATAGNAATATAGTAACCATGGGCATACACACACACACACACACACACACAC
AGAGAACTACACGCACACACACATACACAAATATAAACATTTACACAGGCCCACACACCCAT
ACACATATGTATACCCATATATCCAATATGTATAGCTTCCTCACTATTCGTTACAACGTTGTGT
GTCTGTCCGTCTGGTTTTTGTGCTGGTTTTTGCCCCTTTTTTATTAGAAATCGATCCATTTTGTG
CCTGCATCTCACGCTGACTAGCGGAGCTGACGTAACCTGGCTGCCAGCGTGCACTGCAGTCAA
ATGTAAACAATGCCATAAGCAGGCTGCATTTGCCAGGNTTCACAGTGCCCCCTTTAGGAAACA
CCATTAATGAAAGGNTAAAAGGAGAAAGTGTAAATGCAGTGCAGTGGTCACTGGTATATTTT
ATGTTAGCCGGCATTTTGGAAAAAAAAATGTTANTTNGGCTTGGNGGNTTAACCCATTATTTG
GGGTTATTAAAGCCTTNACCCCATTGGCGGGAGGCCCCACCCCAATTTTTNAAAAGGCCTTTT
NGANCCCAAAGGNCCCCCCCAATTGGTTNNGGGCTTTTCGGCCGGAAAGGCCCCCACCCNCC
CAAATTTGGGAAGGTTTNTTTTTTTTTTGNGGGGNGGGGNTAAAAAAGGGGGGGAGAGNTTTT
TTTTTTTANAAAAACGCGG

SB10
TTTTGCCCTTCATAATAGTCGCAGCACTTGTCATTCCCAGTGAACTCTGCCCCCTGTACTCCTT
CCAACATATCCCAATACACACACACACACACACACACACACACACACACACACACACACACACA
CACAAACACACTGGTGAGCGAGTTGACTGCGGAGCAAAAAGTGGCAGGAGAGAGTGGCATT
GGGAACGTCTGTGCCAGTTGCCTGCCGACGGCACCTTTGGGATTGGTAAAGTTTGATTTGATG
GCTTTCCCTGTTAATTAGGGTTTGGAGGTGACTCCTGAAATGGAAATGGGCAAAATGTTCAAA
AAAAGATGTGCCAATTCCCACACCCCCTCCATCTCCACCTTCCAAAACATGTGACCCATATAC
TGGAGTACCTAGTGAAGAAAGTAGAACAATCAAGTCATTTGAAGTTATAGGCCACTCTGTATT
TGTGTTTTTCTGCCAACGTAGGCAGGGCAGTTCAGTCAAACTAATAATGTGAAATAGGCTAAA
ACTTGTATGTGAACAAAAGTCAACCAACAAAATNTNGGGAACCAAAGAANAANAATGGTTTG
GTTCTTTTAATTAATTNGGGCCATACATNTTTTGNTTC

Figure 9C

AAGCCTTTTNAAAATTTACATTGTCNAAGGTAACAACTGGTNCCCCTTGTTNNTTNTNGAAAA
AAATNC

SB12
ATTTAGTTGGTTGAACAGATGCAGATAATGGTGCACTCGCTACATCCCTATATTGTACAGATT
GTAAGCCCTTTGATGCAAATTTGATGCAAATTTATTTTTTTAATTTGGGTAATAAAATTGACTT
GGTACTTAAGAGAATGTATTTGGATGCTCTCCACCACTGTGTTTCAGGAGCTATATTATTCTGA
AGTTAAGTAACCAATGTAATAAAAGGTTGAGAGAACAGAGACAAGCCATAGAGACAGGTCC
ACCTGCAATGACCTCAGTCCTCCCACTCACCTCTGAACCTTCTCCTGAGGATTTGTCAAACATC
TCCAGCGCAGTAATCACATGACATTTACAACTGAACTTCTTTCACCAGTATGAATAACACCCC
ACACACACACACACACACACACACACACACACACACAGTGAGACACGTAATTAATTACAGTAACAT
ATCGTCCAGTAGAAAGGAGTGACTTTTAAGGTTGACTGTTTCAGTTACGTTGTCATGCTGTGCT
GTGGACTTTTCACATTCTTCAGACCTTTCTGTGGAGAGAACCCCCCCCTTCGCAAAGGTGTCA
AAAAGATTTTCCCAGCCCGAGGCACATTAAAAATGAAACCAAAGGNGCTCACCCAACTTNCC
AATTAGCTGAAAGAAATTTCTTTTGGAAT

SB13
ATTCGGGGCAACCTGGAAAAAATTTAAGATGCACTGTTTGCAAATGACCTCGTGACAACATAT
GTTGACACGACTTGTCACATATGTTCCTTAAAAGGTGTTGCGTGTGTGTACTGCACATAACAC
ACACACACACACACAAACAATGAAAGCCATGTCATTCCATGGAAACTGTTGCTGTTGGTTCCA
GGAAGTGAGACAAACCAGATACAGGAAGTGAACGGCCACCCAGTCATGGTGGAAACTGGGG
GTGGAAGCTAAGAATACTGCAGACCTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGATTTGTGAACCTGTGGTCTGCAAGAAAAGAATCACATCAGGAA
GTGATAAAAAGTCTGAAAGGACAATTTTATTTTTCTGTTTTTNAAAAACATGTTTAACTTGAA
GCTGTTTGTTGGTCTCCCGCTCTTATTGGTATTTTATATTTCATTGGNACATGAAACCCATGCC
TGCTGTAAATCACCACAACATCCCAGANGAATTGTTNTTAGGTGNCAGGTTGGNCCTCGNCTG
CTCANTTTGGAGCCCNCTCANAGAGNGACTGTTTTATTTAAAACTTTCCCNAAATAACTGT

SB14
TGCTGTAGCGCGGTAACACTCATTGTGTGTCTCACACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACTGACCACCTAATTTTGGAAACTCTTTTGGAA
ACGCTGTCATCCACGTGCACGCGCACACAGACCTGTCCCACATAATGAGCTGCATTATCTCCC
CATCTGTGTTTATGCTTTATTTGAGCTCATTTGGAATCAGCCAGCTTTTTATTTAGGGCTTGGCT
TATTAGTGGCAGTGTCGAGATAGAAGTGGTTGGATGGTATTTGAGTCACCTGGGAAATTATGG
ATAAGATAAAGCTACCTGCTTATTCCTTCGGGGGGAAAACACACAACACATTACAGACTGTAT
TAACTGGCTGGATGACGGACTAGGACGCAGAGAAAGGCAGACAGGAAAAGATACAGATGTA
GTAGTAGGGCTACACATTAAAAGCATTAATTACACTACACAACATTAAAAACTTTATTATTGG
GGAGTCCCCCTATTCCAGGGAAATATTTTGNGGAGGTCTTATGGTTAAAA

Figure 9D

AAAGGCCTCCTCTTCTTTAATAAGGCCCCCACCACCACCAATGGCCNGGCNANGAAAACCAA
AAACCCCCCCNCCCCCCAAAAAAAACCAAGGTTTTTAAAAAAAATTNGGGGGGTNAAAATTNG
GGNCCTTACCTTAAAATAANGGGAAGGCCTTTTTCCCGGGNNCTTTTTTAATTT

SB15
GGGGATCATTAAAATAAACCAGGTACTGATTTCTGAATCANTCTGATGTCCTGATGGTTCAGA
GGGATGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGNTGACACCTGTC
ATGCATGCACTGGTAATCTTGCTTTGCTGTATACTGACACACTCAGATCCTNTAGAGTCGACCT
GCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG
TTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTNATAGCNAAGAGG
CCCGCACCGATCGCNCTTNCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGT
ATTTTNTCCTTACGCATNTGTGCGGTNTTTCACACCGCATATGGTGCACTCTTCATTACAATCT
GCTCTGATGCCGGCATANTTAAGCNAGNCCCGNACACCCNCCAANNACCCGCTTGACGCGCC
CTGATNGGCTTGNATNGCTCCCGGNCATCCGCTTTACAGANAAGTCTGTGANCCGTCTCCNGG
AAGCTTTNNTNTGTNANNAAAGTTTTGTNCNNGTCNNTCACCNNNAACTNGCGCCGGANAAN
NAAAAGGGCCTTNGCTGAAAACNTCNTTATTTTTT

SB16
TTTGAAACCGGGCACCCAACTGCTCTCTTTCTTTCACTCTCCCTCTCTCTGAATTGTCAACCTAT
TAAATGTCTCTTTGTATCTCGCCCATTCACACACAAACTGACCAATGGAAAGCTTTGGACCCTT
TCAGTGACAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGATTGTCATAACGGAGCTGTCC
CAGTTCTTTTTGTACATTGATTGCACCAATGTTATTTTACTAGTTTAGAAAGCAGATGTCACTG
CATGTGTGCGTGTGTGAGAGAGTGTTTGTGAATGAGACTGACAGAGACTGTGAGGGTGGTGT
GTATGTGGTAGAGTTACATGAAGAACAATAGCCTTATTGTACCTGTCTGCTGCTACTGTCTGTC
TTGTGTCGATGCTCTGCACTGAGCCTATTTGCCTCATTCTTTGTGTAACCGATCACACATTTGT
GAATAAAGTTCGACATTTCTGAGTTATATCATACACTTGTAAGCTCTCTGGTGGCTTAAGTGGT
GCANGGTTCCCCANTGTATTGGAACTAANTATCACCAGNGGATGTTTTCTACCAACACTGGCT
TCGACTATTATTCAGTATTGCTCTTGCATTTAACACTACATGGGCGAACAT

SB17
CAAATCTAATAACGGCTCCACTCTGGTTATTGGAATGCTCGCCACACTTACCTTTGCACACTTT
GTGTCACACACACACACACACACACACACACACACACACACACACACACACACACACACACACGTA
GACTGAGGTATATACTTACTCTTTATTCAGAAAAACCTTACTTAGCACTCTCTTTCAAATTATA
TTACACTTACTGTACATCACATGTGAACACATACAGTAGTGCTGTAAATTGATTTCAGTTAAC
CATCATGACAGTGTTTTTTAATAGAGAATAGTGGGAAACTGTAGGTTAAACATACTTTAGGGT
TGAGAATGTTGTATGTCTGACGTCTCACATCCTAATACCAGTCAACATTAGTGGTCAAAAAGA
GTGTTACTCATTACTCTGAAGAGACACAGAGTAAAATGAGAAGTAGAGCACTAGGCATGAAG
TGAACAGCAGGGAGCAGCAATAGAATTGTGCAAACATTACATTGCCTGTGTTTGGTCAGAGA
GCTTCTGGTTTCATATATGTTGGTGTAACCCGGATGCTATCAACGGCAGTCCAAGCTACCAGG
TGTATCTACCCANGTACATTTACTTATTGCTGNCATCTCTTCAGTCTGTCCCTATGCTAATATG
GTCTATTGTGTAAACCGGGGCCTTTNGGCTTAATCTAAGTCN

SB18
AGGCGTTGTAAATCAGTCACACAGCTCCCATGTCACTGGAGATACTGGAAATGACTCCACTTC
CAGTCCTCAGCGTCCTGCCCATGTGATTGCCACTTTAAAAGACATTTGCTTTATAATACACTTA
CATTTTTTTAAAGATTCATTTTCAGACTGCGAACTGTACACTGGCGGCAAAGGGGGGGCTTTG
TACTGACCTTGACAAAAAACGCCCAACTAATTCATCTTTTGCTCTCGAACATCAAGGCCGATG
AACTGATAGCGTTTTATTGCTGGCAATAACAATATCACACCGATGGCACAAGGTCCCATTACA
TCACCGAATTCATTCACAGCTTAACTGACTCTGTGTATTCCAGTTACACACACACACACACAC

Figure 9E

ACACACACACACACACACACACACACACACACACACACACACACCTGTAGTTGCCCTTCTTGC
GGAGCTGCTCCTTGAAAGTGGCCCAGGGTGAGACTGTGGCTCTTCATGGCCTCCGGTA

SB19
AATTAACTATTAATATAGTTACAGCGGTTGTGCATGGGAGTTTCATACCTAGTGGAAATTAAG
AGCTTATCACACTGCACAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGT
TTGTTTGTTTGTTTGTTTGTTTAACAGCTGTTCAGGATTTTATTTTGGGTGAAATGCATGAGTCT
GTTTTTTATGTACCATGTACCCTGTGTTTTCACTGTCCTACCACAACTGACTTGTCTTATCATTA
GGACAGGGACTCGGGCAACAAAGTCTGCATTGTGGTTTTTCTCTTTACACCAGTGCTAGCGCT
ACTTGTGTCAAAGCCGGGGCAGATTTTCAAACATTCCTCATACTTGCTGACATATTTCTTCATG
GTTTGCTCCTGTCTNCATTGCGCTGTCTGACTCAATTTCTTCACCCGCCCTTTTCTTAGCATGCA
AATGTGTGTTTTGTTTTAGTGTAAAANGAAAGCGTATGCTCACTGGTTAACACGCACAAGCTG
AAGGTTGCAGTGCACTTTGACATGACATTTAAAAATCATTCTNTACAGGAACCAGTTGGTGTA
GCCCAAATCCATCAGGGCCACATACTTCAACCCGGGGTAGAAGTTATTCTGGGTTATACTGCA
CCATNTNTANCCCCGGGCCATTGTTTTATNTNT

SB20
TAAATCCTCTTCACAGCGTTGTCTAATTACTCCCAACAACATGGTAGCTGATTAACTTGTAATT
GCTGCTCTGAACGCAGCCTGTCCCTCTCTTCTCGTTAGGGTTATTACTGACTATAATTACCGCT
AATGTGCATTGAGGAACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACTCACACACACATACACACACACACACACATACACACACACACACACAACCT
CACATGTACACAAACAGACGTGCAGGTGGAAGCTCATGCACAAGCACCTGAACACACATATT
CTTCTTCACAATACACTCGTGCACACACCTCGCCAGGAGAATACTTATATTCTTGGAAACTGT
GACTGGTGCACAAAGCAATAACAGTGAAATTTAGGCAACTAAATTCATTTTCCGTACGTTCCC
TCATTTAAGTGGNGGGATTCACAGCAGCCAAAAACCCTTTAATGGTCTTCATATGTCACCTCA
TGTCTTTNCTGGNCCTTTAAAGCCCCATCATTTACCCCAAATCGGACATTGATGTCCCTTGAGC
AGTGCTGAAAGTGAAGCCTATGACATTCTNCCTACCATTTGAGATTTGGTAAATTGNGGATGA
TGTGAACGTACCAGCGTAGGCTATTTTCTNTTGGTAA

SB21
GNTANGAATGAGANGANTNCGAGCTCGGTACCCGGGGATCAATTTCAATGCATTCTAAAGAC
CATCATCATTAAACGTTGTGCTTGGGTCGTCACTGCCCGGGCCCTAATTAAATATATATCTTTT
ATTCAATATTTATCACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACAAACGCACAAACACCTTGTGTTCTTTAGTTTAGTGCATTTAGTTAGATT
ATATATATATATTTTATGAA

SB22
GCTGCCTGCANGTCGACTCTAGAGGATCGGCACATGTCTACAATATCAGGTAACTGACTTTGT
ACTTAAGGGGGGCAACTGTTAAAAATAGACTCACACCCCGAGACTGCCAGCTCTGCCTGAGC
TCATACTGAAGTCCTACATCATAGGTCTATATCTTCAACCACACGGCTATGAAAAGGGTACGT
ACTACATGCATGGCTGAAAATCCCCTTCAAAGGCTATGACATCTGTACTAATACCTCAAGTAA
TAATACTACTTTTATTATGTGTGATTCAGCTGTGAGCTAACTTGTTTGACATATGTTGGTGGTT
TTTTCTTTGGGCATGGTAAATGTTGTCAATCACACTGCTTTGACGCTTACAACACTGATGATGG
GTTGACATGCACACACACACACCACACACACACACACACACACACACACACACACACACACACT
CTGCTGTGCTGCTTGACACTCATGATTCACTCTGTAAAGGCATCAGAATTAATTCCACATGATT
TACACCGTGTAATGAATTTTGACAAAATACTTGNTTGTGGTTTTCACCCCTGGTCATTTGCAGC
AGTGAGTGGTTGAAGAAAAATNTTTCAATTTTGANGGCAGGAATNGTTNTTTATTTTTTCAAA
AAACAAGTTTTAAAAATGNTACCTGGNAATTTTGGGNAATTTCCAAAGCCGAAGTTTNGTNTC
CACAATNACANGNAAAGCNTTTTAAAANAATGCNCCCNTGGGT

Figure 9F

SB23

GAACTTTAACCTTTCCCGGGGATCTTGATCACACTCGGAGAGATGACACATGGTTACTGTAAA
CATACAAGCTACAGTAaacTACAATTCCTGCACACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACTTATTGTGCAGCCTGCAGCGATGCACAAAATCAT
GCACTGACCTTCACATAAAGACTCCAGGGGTGTGCTTTTATGTGCACTTTAAAGTGTGTATATT
AAGGCTGCATTGCATTAATAAGATGTTGTGTATATATATGTATGGAGAGAGAGAGAGAGAAA
GAGAGAGGGGGTGAATNAGAGGAATGTTTTCCGTCTGCCATTATTACNCCATGTNTGACNGCC
AGCCTGNCTNTTTCTCTNTCTCTCTNANANCANCCAGGNNTTCTGCTCCCCTTTTTNTNCTNCA
NCAATNTGTNTNTCTNCNTNCCTNNANNCTNCCTNTTNTTTTTTNTGGGAACTATNNCCACATT
CTNTNTGANNNGNNCTTCGTNTGCNNCCGNATTNCCTNTTTTATNNATNCATTNNTCCNTNCC
CNNNNTNTTTTTTTTTTNTGGNNNTNCNTTTATTTNNCNNGCTNNCCTTTCAGANTTTGNNNGNN
NAANTTNTTNCCCCNNTNNNNNCTNTNNCNTNNNTNNTTNNNTNCNNNCANNNTNGNNNNNT
TTNNTTTCTTTNNNNANN

SB24

GNTACGAATTNGAGCTCGGTACCCGGGGATCCCTGTGCCAGCTCTCTGTTCTGTGTCACTATT
AGAGAGCCCGCTCANAGTGAACACATCATTAAACCTCAATAAAAAGCCTTTATTCACCCCCAA
ATTATTACAGGAACATGTGTGAACCAAGCGGGCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTTGAGAGAGGCAAGTTGTAAATGAGTGTGTGTTAGTAATGCACGGGGAAAGAC
GGACAGAGAGTTCACAAAGAGTACTGTATTGCTCATATAAAAGCCTTTGTATTTTGTAATATT
CTTGGAAGAAGCATGTGGGTATGTGTGTGTGTGTGCACAGTGGTTGGTCCAGTCATGTCAATG
TAATGGAGCATGATGACTTGTTACTGTAGGTGCCAGGGAAAGAGAGAAAGACGGAGTATGAT
GGGAAGAGAAACCTAGAGAGACACAGTAACACCAGAAAATGCTACAGCAAAACTCATCCAT
GTGTGAAATACTTTGNTTTAAGATGCTTCGGTGGGATGGTTGCTACACACTGGGCTAGTTTTG
NGGCTAACTACTAAAATGCCATANAAATACAAAGCTTGNCGCATTTCAAGGGTCTTGACCTGT
ACAAAATACTANAAAATGCCNATTTTCTGTGCTGGCTTTTGGGATGTNCTATTGAAAGAAATG
TNAAAAAAAAAAAAAAAAAGCC

SB25

ATANGAATGAGAGCTNGGNCCCGGGGATCAAAGCANAAAGTCTGACAAGAACCGAGAAACC
TCTGAGAAATATATGCAAGCAAGCATGCGCGCACACACACTTTGGCAGAGGACTGCCTGTCA
GAATGCCAAAGAAACTACTCTTTGAGCTCTCCATAAATTTACTTTGAAGGAGTTCTGACTGGG
TAATAGCTTGTATGGAAAATACTGTCACAAGAGAAAATACACACACACACACACACACACAC
ACACAAAACACACACACACAATCTCAAAGCCCCTTATTTATAATCGCATTCGTGACAAAAGA
ATTGGAAGGAAACACAGCACCACTGGCATTAATTAAAGAGAATCATATTTTATGAAGCAATT
CTCAGGAAGTAAGTGCAGCACTGACCCTCCAGCCCCACCCCAGACAGACAATGTCAAATAAA
TTAACATTTAAATTAGGGCATAGACCAGACCAGTCTGGGCTAGGAGCAACATCACCCTACTAG
CAACCCGCCTTAGCAACCCGTAAGTAGGCCTATAGTGNTGGCGANGGTACTAGAGCAGAACT
GGGCCTTGTACAATGCTGAAAACACACACACNCACCCNCTGGTTTCTGNGGGTATACCGTGCC
CTGTCCTGGNGGGTANGGATAAACTTTTTNATNGGGGGCAAACATNGCAGACCCCTANACCTT
GGGGGGNGTACCAACGGNGNGGNCCTT

SB26

ATCTTTTTTATATTTGAGTCAAATTTCTGCAATGTCAGGTTTCTGAGGAAATGCGGTATACAAG
TTTCAGGGCATGCTAGGAGACTAAATACAGAGAGGGGATGCAAGTGTGAAGGGGAAGAATTG
ATATTTACCACAGGCAATATTATCAGCAATTGTGCTGTATGTAGTCACACATTTTCTCAACACA
CACACACACACACACACACACACACACACACACACTGCGCTCAAACACCATATATTCAAATCTG
TCATGTGCCAATTCTTGTTTCTATGCTATGTTTTCATCCGTGTCTGTGCATCTGTATAAAGCACT
TTGTAACACTAGTTAACAAAAAGCGATCTGTAGATAAATCTGCCTTGACCCACTTTGTTTTGCT
ATTTTCATTTACACTGTGCAAGTGGAAGCATGGTGGAGCACGCAGGAGTGTATCAATATCAGG

Figure 9G

ACAAATGCAATGCAATGAAAGCAGCTTGTAGGGTCAAATAGCTCTGGTAACANGTCTAATT
GAATCTGTGTCANGTTCTCAGTGCAGGTCATNCACCACTGTATGCACAAGATGGAAATCAATA
TGTNCTCTCTGAATCATGGGACACAGTCTAATTTCATTGAAGGCTTNTNTTTTTTTNTTTTGTA
CATGTGCAGGTTAATGAAAGGCATTGTT

SB27
NCAGNANCNACNCNNCNCGGNNCCCGGGGACNGCTCTTNAAGACACANNNNAGAATNNCAG
ANGACACGGGGGCAACACNGAATATTANAGGACTAACATATTTATCCTGCCTCCAACAACCA
AAAACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACAAGCAGAAACACATGCATACACCAGCCGCCCTCTCATCCCTCATCTGCCCAGTGCAGATCC
TCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTG
GGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCG
TAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAAT
GGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCCGCATATGGNGC
ACTCTCAAGTACAATCTGCTCTTGATGCCGCATANTTAAGCCAGCCCCGACACCCGCCAACAC
CCGCTGACGCGCCCTGACGGGCTTGTTTGCTTCCCGGCATTCGNTTACAGACAAGCTGTGACC
GGTTCCCGGGAAGCTGCATGTGTTCAAAAGGTTTTCACCCGNNTTCACCNAAACCCNCGAAAN
NAAAAGGGGCCTTNGTGANACNCCNT

SB28
TCAGTTCAGCCACAGACTGACTGGCTTTTACAGTTTTACGTGTGGTTTAAGTGTTGTGTTATTT
GTGGTCACTGGCATTTTCTAATTCACATTAAAGAAAATAAAAAAAGTTTTTTTTGTATCCTTTA
TGAAGAAAACTTCCTATAAATAACATTTCAGACCCTATTCCAGGACTCACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACTTTTGATTAATGCTGTGATGCATCAGAGGTTACTTACTTCTAACTCTACTCAAGGTAAGAT
TGAAGTAAACAACCTCTTATTTGTTTTTGTTTCATTATTCAAGCTGTTCCCTATTTTCCCCAGAT
AAAATCGATTAAAAAAAGCAAAAGGACTCAAGGCTGCCGAGCTCTTTCTGGGAAAATCAGTC
AGTGTTTCCGTTCAGTGGGAAGTCAGAGAAATCAAAATCAATTCAGCAACAGAGAATGCCCT
TTATAATCGCATTGATTGGTTCCTGTTATTCTCACTTGAATTGGACTTCTCTCTCTCTCTTTGGC
TCCCGCTCTGGTTGGNGACTTACACACCTTTCCACACACCCCAAACCCCCGGCCAGACTGTTA
CCGTANCCAAACATGGGTATCTTCATTAAG

SB29
TCAGTTCAGCCACAGACTGACTGGCTTTTACAGTTTTACGTGTGGTTTAAGTGTTGTGTTATTT
GTGGTCACTGGCATTTTCTAATTCACATTAAAGAAAATAAAAAAAGTTTTTTTTGTATCCTTTA
TGAAGAAAACTTCCTATAAATAACATTTCAGACCCTATTCCAGGACTCACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACTTTTGATTAATGCTGTGATGCATCAGAGGTTACTTACTTCTAACTCTACTCAAGGTAAGAT
TGAAGTAAACAACCTCTTATTTGTTTTTGTTTCATTATTCAAGCTGTTCCCTATTTTCCCCAGAT
AAAATCGATTAAAAAAAGCAAAAGGACTCAAGGCTGCCGAGCTCTTTCTGGGAAAATCAGTC
AGTGTTTCCGTTCAGTGGGAAGTCAGAGAAATCAAAATCAATTCAGCAACAGAGAATGCCCT
TTATAATCGCATTGATTGGTTCCTGTTATTCTCACTTGAATTGGACTTCTCTCTCTCTCTTTGGC
TCCCGCTCTGGTTGGNGACTTACACACCTTTCCACACACCCCAAACCCCCGGCCAGACTGTTA
CCGTANCCAAACATGGGTATCTTCATTAAG

SB30
TATCACGCCTGAGTTATGCAATATCACACACATCCACACGTACACACACACAGGCAGAAATC
ATAACAGTGATGGTGACGGTGATGCAAGAGATAAAGGAGCAGTCCGCATATTACAGCATGGC
AGCAGGTCGACAGGCGGTGACAGCCAGGAGAGAGAGAGATTACTGGAACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACAATCTCTCTCTCTCACACACACAT
ACAGGCACTCAGAAGGTGAGATATGTCTCCCAGCATAGAGATGTACTCTGCTGTAATCTCTTT

Figure 9H

GTCTACAAGATACACTTAGATGGATGGNTACAGGACACAGAGAGGGTGTGTGTTGCTGCGTA
TGCCGTACGTCCANTCTTCAGTCTGATAAACCCANAGCCACATTTTGAAACCATTTTAATATAT
AAGTTATAAGTTAATATGNTGGNTTANTTCTATATTTGCTGGGTTTAATATTTTTAATAAATCT
TGGGGATTTCCTTCAAGTTTCTCTTNTACAATACTCACCTGNCATATGGCATAGTANTGGGTTT
TACAATATACAAAATATGCTCTTTGCGGGCGGGAAATNGTTGTTNAAAGCTGTGTTTGATCCC
CGGGTNCCCAGCTCGAATTCNTAATCATGGGN

SB31
AATGGTGTCCTCGGAGAGGGAATTACACAGCTGAATTTCGATGAGAACAGAAGAAAGGAAGA
GGAAGGGAGAACAAGCAGAGGCGGGGAAGGCATGTGAAAAGGGAGAGAGGGAAGGAGGAT
AGTATATCCTTCAAGAAAGAAAAAAAAAAAGGAGAAATGGGAGGAATGTGGAAAAGTATGT
AGAAGACTGGACTGGAGTGTGAGTGAGCCTCGCAAGACTTGATGCTAAAAACACGCAAAAGA
ATTTCAAATGAAAATCCTTGAAAATGAATCCTCACGAGTGCAGTTTGGGGTGTGTGTGTGTGT
GTGTGTGTGTGCGTGTGTGTTGCTGGACTGAGATAACATCNATATCTGTGAGCNTTTGGCCCA
TAATTTGTGCTGACAAGTGAATGTCTGTGCCTGTGTCTTATTTGGTTGGGAT

SB32
CCTCCCCAAAGCACAGTGATTAAAACCCACTAGAGAAACTGAGACATACCCAGAGCGGTTGT
AGTCAGGCTCTATTTACACCCAGTGGATTACTTAAGTGCGTGCGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGNGCGCNCATATGTGTNTGCNTGCTTGCGTGTCTTTCTC
CTGGCNCTGNAAGACCCTTGNGCCCTCTCCACCATGTCGCAGCTGTCATCCAATCACAGAGGG
CAAAGAGCTAATCACATGACCCCAGAGTAGAGTTGGCCGTGTCACTCGATGCCGNCTGTATTT
GTGTTGCTATTGCCANGACATGGGTATGCANACACATAAAAGNGAGACGTTCTCA

SB33
TAGTATGTAGCATCTGAATTAGTGCTCACTCACACACACACACACACACACACACACACAC
ACACACACACTCGTAATGCTGAACTNGGGTCCATCGCTGCCCTTCATGGTGCATTGCATTGCA
GAGAGGAAGGGAGGTGTGTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
ANACAGTGCCCTCATAAATAATTTCACTCNATATTGCTTTTAAACGATAGCATCCCACGGNTG
GCCCGCCGCGGNGTGCAACTCGNCCATAAATGATACTGTCAGGGCTAATACACGGCTTCCATT
ATTAAGGAGGCACNGAGCGGGTGCTGCTGCAACGCTGCACCCTTCGCATTCACTCCGACAGN
CGGGGCANCAGCGCAACGGC

SB34
ATTGACATCTCTTTTATGTTTCTCTCTTTTCCGATCGCAGTCAGCCACCTTTCGCTTCTTACAAA
AAGAGCTCACAGTGCAGTGATGAACCCTAGTGCTTGTTTGTCCAAATGTCAGCAGTTTTGTAA
ACTGCGTGTGTATGTGTGTGTGTGTGCGAACTTGTGAAAAAAGAAATCTCTGGTGCTTGTAAC
TTTTTGTGTGTATGCTTGCACCTTTTTGTGTTCATCACATAGTTGTGGGTGGGTGTTTTTGGAGC
AGTCACACACACACACACACACACACACACACACACACACACACACATATGCACAGTGTAATGTCATG
TGCATTTCCTGTACACTTAGTCTCTAATGCAGAATGTGGTGGTAGGGGAAGTCTAAATGATTA
ATGATTGCCTCTGTGGTCTGTCTGCCAAGGCTGCAGCTATAACCAGTGTCATTCTCTCTTACTG
CTGTCACTCCATGAATATTGTATAGGTTATGGACTTGCTTGGCGCTGNCATCTACCACTACTTG
GGCATGTTTTAATCCT

SB35
CTCTTACTCCCCATGTCAGTGGGCTAATGAGACTGACAGAATGCAAAAGAGAAGAGCTTATGT
ACAATGTGTGTGTGTGTGTGTTCCTGTGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGCGTGT
GTGACTGTGCGAAGGTGGAGGTTGCAGAAAAGTAGCCTGAAGGAGGGCTTAGGAATATTTCA
GTATTGGAGGACCTCTTTGACTCTCACTCTGCCTACACACAGACATACACACACCGGTCAAAC
AAATCTCTATTATCAAAGTGACTCTGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG

Figure 9I

TGTGTGGNTGTCATTCATGCTCATATGACCCATACATCCCAATCCTCACAGGAATTCATGAAG
AATTGTTGGTGAGTATGGTGCCTTTATGATGATTTTGATAATCTCCTGTTTTATAAATCTGATT
A

SB36
ATTCTGTAGTTTTGGGAAGATGAGGCTTTGGCTCACAGGTATATACACACACACACACACACA
CACACACACACATACACACATATATCCACTGTTCACACCCTTCACGTCAAACGAAGTGAGATG
GCCTAGATAGTTAGACGGGGAGACAAGCAGGGTGTTAGAGGGAGCAGAAAGGAG

SB37
GCACTGCTTTTTTAACACTGGTTTATAGCCTGCAGGAACCATGACNTNCCCAGATGTCTGTCTG
TGTATTCCCACACCCATGCAGCAAGCACACACACACACACACACACACACACACACACGCAC
ACACACATCTTAGTGAAACACCTAGTGAATTTATGTTCACCCTGTTCTCACTTCCTCTTCTTCC
TCTCTTCCAACAGTTCAGGGCTTATTTCTTTCACCTCCTGGGAGTGTGGCAATGGAGTAAAAG
AAAAGTGAGAGGAAGAAACAGGGAGTTGAAGGGAAAGTGAGAACGACTTGAAGGTGTCCTG
AGAGCGCTTTTGCTTTATGGAAAACGCTGCGGCTAATCCTCTGAGTGTCACTGCGCCCTCCGC
ATCCTAAATAAGAACCTTTGTGCACGGTAAGTACAGACACATCTCAATACGTGACTATCTCAG
CCCCCCCCCCCCCCCCTTCCCGTTGCTCACGCAGCCTTGGAAAAACAAAAAAACACTAACAATC
AACTGCATGAGCTTTGC

SB38
CTGCTGTGACTGACAGCCTTATTACCACACACTCCTCTCTTACTATAACACCGTGCTGCCTACA
CACACACACACACACACACACACACACACACACACACACACACACACCACCCACTCCCTCTTTTTAACC
TATCCACCGGCACTCTTCTTTGCTCACACACACAGAGCAGTCTGTCAAACACTCTTTTCTTCAT
CACTGTATTTCCAGAAGAATTAATTATTACTGAAACAGAAACAAATATGAATTGTCTAGCAAA
GGTTCAACTACAGTTTTTTCCTACAGTCTGCAAACAACAGGCATTTAGGCACAAACATACTGT
ACAGCAGCCTGATAATGAGACTTTCTTTTTGGTTTCACTGCATTATTCAGATGTTGTGACAGTC
TTATGTGCAACTGTTTCCTGTTTAGGGAGTTACTGTTATTTTGTCCGTTTTTAAAGTAGTTATTT
CTGGTCAGTTGACTTAAAACAACTT

SB39
GAGAGGTTGCAGTCGTGCTACAAGGGTGAGGGCACACTGGACCTGGCCTGGCTCAAAGTCAA
AGATATTCCCTGCAGCAGTGCGGTGAGTACTACTAAAATACACACAGACACACACACACACA
CACACACACACACACACACACAGACACACAGTTTACACAGTTTAATGACAGTACTGGGGAGA
TATTTACTATATTGGTGGTTCTCTTTTCTTCCACACATACTTTGCGCGCAGCATGTAACATGTA
GTGCTCTAATCTACCAGAACAGCAGGTGTCTTGCAGTTATGTTTATTAAACCCACTCATTTAGG
AAAAGGGTGTTTCATAGGACTGTATTGAAAGAAAAGCCAATCAGTGATGATTTCCTATTGTTT
TAATCATTTCTAACTAAGGGACGCTACAGGTGAGTATCTCTGAGGGAAAATCAGNTTGTGAAA
GCTCTCCCACATGTTACTGTAATGAGCTTGTGTGCACTGTGGGAGGCCTTCATGAACACTATA
TTC

SB40
ATCTTGAGAAAAGTAACGATTGCCTGTAATTCAGGTCTGTGTTATAAATGAACCAAACATGCC
TGCCCTGTGCAGCTCAAAGAATACACGCACGCACGCACGCACGCAACCACGAACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ATACTGTTAGATGGTAGAATGTGAAGCCCCTTGAATTACTCATGCTCAGTGTGGAGCTCAATA
CACATTTGCACATAGACACATGGGTACACACACTCACATACACGCATACAAGTACAGCATTTA
AATCAGCAACGGCAGAGTGGGCAAACCTGGGGTACGGAGGGGTGGGAGGGCAGAACTTTTTG
CAGGTTATAGCCACACAAAAAGACACGGAGGACAGGAAGAAAGAAGGAACTGT

Figure 9J

SB41
TAAAGCTCTCTGGTGGAACTATAACAGCATACCCTTCCTCCAATACACACACATACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACATCTCAATACACAACACATAAGATTCAATTCAATAAAGATGAATGGAACTTCGTATGTGA
ACCTTGTAGTATTAATACCTCAGAGTGAACAGTTCCTATGAAAACTGCAGACACTGGAGAAA
GATGTTGCTGCTGATTTGTTTTATTTTATTTAAACACCACAAACCAAATTCCATTCTCCACCCC
AATAATTGTATTTGGGTGGAGCAATAAATCTCAGAATCTGAAAACCTTGAAACAGAAAAACC
AAAGCAATCTGAATGGATGGATTTCACTTTGTGTGTGTTTTTTTTTTGTAACTGGATGAACGG
ATGGTAGAGTTTTAAAAATGATAGCTATACCTTCTTTGGAGAGGCGTAAGATGTGCTCTCCCA
GCTCCTGGAAGC

SB42
AGTATTGCCCACCCAGGCTGATGAAACCCTGTGGTGTGTGGGCAGATTGTTCACACCGCATCT
TTCAGTTGTGCTTCCTGAACAAAACCACCCTCTGCACTCCCACTCGGATTGCTAAGAGGTCAA
GTACATGCACACACACACACACACACACACACACACACACACACACACACACACACACTGTGGAGAAAGA
AGTCACGGTTATTCTCAAGTTCTCTTTTCTCTTTTCACTGAGATTGGGGTTGCACACAAACACA
TTGCAACAGTCTCTCAGGTCACATCAATTCATATGCGCACCTTTTCTAGGGTCAGGGTTACAC
ACACACATAGGCACAAACACACACACACACACACAAAGACTTTCCCAAGTGAGATTGCAGCT
CTACCAATAAGGCCTCAGGTCTGCAGCAACAGCAAACTCCCCCATAGAGACCAAAGCCAATT
TATTTCAGTCAGGCTGCTGGTGACAGAAACGGAAGCTTTAACAGAGG

SB43
TGTTTAGCTATCTTTTGTTTTTATGTTATTGTGTAGTCGATGCTGTCTGCCACTTGAGGGAAAA
CATTTTAGATAACACATATTAATCATTTATGAGTTGATAAAGTCAGAAATACTGCTGAAAACT
TTCTTGATGAATAAAAGCAGCAGGGTGCCTTTTCCCTACCTGTATCACTCACACCAACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
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CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACACACACACACACCTACCTAGGGGCACTATAGTTATATTAGGGTTTTATGCTC
CAAACTGTGATGTGTTGAAGTGCAACGAGTGACCTTCTGACAAGGACGG

SB44
GGGGCAGCGGCAGGCCACAGCGCGGGCCCCTTTGTGCTGTTCACCAGCTAGAGACGCACGGA
CAGGAGACACAGTCTAAGGCGAGAGACAGGCCTGGTGCTAATGTCTGCTCTAACTCAATAGA
GAGGCTGCCTCGCTGCTTTGGCTGGCTGCTCTCACTCTCTCTGATTGACCACTCCATTAAAACT
GCACTGACATGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGGAGGGAGGGTTATC
CTTTAGAGATCCCCGGGTAC

SB45
ATTCCCACCAGCTTCCCTCCCAGCACGGCGCAGATGAAGAGGATGACTTATGCCAAACAGGTT
CCCTCCAGGTAAACACTGACTTCCTGTGATGGACCAAACGACTCCGAACAGCAGAGCGAACA
GACACACTGCGCGCGCGCACACACACACACACACACACACACACACACACACACACACACACAC
ACACACAGGTTAATACACACAGTCTCTCAGTCTCTACAGTGTTCCCCTGTTGGAGCTGACCAA
CGGTGGCCATTTTATTTGACATTTTGCAAATTATGTTTTTATGTTAGTACTTCAACTGATGGAC
TGTGTGTGTATTAATGTATTAACACACACACAGACACACACACACACACACACACACACACACA
CACAGACACACTCAGGTACCTTTAGTAATGACCAGGCTGAAGAGTCCATGAGGTCGAGGACA
TCTGTCCTTCAGGCTGATACAAGACGAACAGCAGGAGGACGAGTCAGATGCTGCCATNTTNA
TTCAAACACACACN

SB46
CAGATATTGCCCCCTGTGTGTTGTGATTGTAAAAAGGCAACTGCTTGCTAATGTTCACTATATC
CACAGTGTTTCCAGTTTGTTTTGCCGCCCTCCAGTGGCCAAAAAAGTTATTAATGTTGTTGTAA

Figure 9K

CTAAAGAGCTTGAACCTAGTATTATTTGTGTAAAGACAACCTGTTACAACATATATAGCACAA
TGTGTATAGCATGTGCAGTAATAGCCACTGTGACTGACTGACTGTGTGTGTGTGTGTGTGTGT
GTGTTATGTTTTCGGAGCAGTACTGCATCTGGACTGACGGGCTGTGTGCGCTGCTGGGCAGAG
AGATGGGCAGTGACCTGACACGCAGTGACCTAGATACTCTCATCAGCATGGAGATGAAGCTC
CGCCTCCTAGACCTTGANAACATCACAATCCCAGAAGCCCCGCCCCCCGTGCCGAANGAGCC
TAGCTCGTATAACTTCACTTACAACTACAGCTGAGTGTGTGTGTGTGTGTGTGT

SB47
AATTCGAGCTCCGTACCCGGGGATCTGGAATGATGGAAATGGCTGGAAATGGCTGCACAATC
ATAAGGATGCGGTGGTGGTGTCACAGTACAATCAGGTAACATCTCGGTGATATGGACACTTG
AAGTGGTTAGTGCTTGAGACAGGTAAATAGTCTCTCAGTGCTAACAGCGCTTCCAGCTCTTTC
CCTGCCTGTGTGTATATACTCAAGTTTCCCTGGGCGTATGCATGCTCCTGTACTGTAAACACCT
ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCCTCCCCCCTCCTCCTGCTNCTGTGTGTCGG
CATGCGGNAACCAGCAGCACTGTAATCAAACTATCACTGCGCAGGGGAATAGCGCTCTCTTC
AAGCGGCTCCTGTTTCCCCCTTACACCAAAAACAAATAATTACTCCACCATTTTTGGGTAAAC
CATAAACCGAACGTGTCGCCTGCGCTGC

SB48
GGTTCTCATTTATGACTCACACATTGATAGTCNGTGCTGAAATAGTGTAAATACAAACACACA
GAGACAATGTGGACCATGAGTCAGTGACTATCATAAGTGCTCAACATTTAAACCATCTAGCTC
TGAGAAAACCTTTGCTTCTTTGTTTTTGCCTTTATCGTTCTGGATGTCAGCCAAAACAGACAAA
CACAGTCTTGGATACACACACACAGACACACAGACAGACACACAGACACACAGACACACAG
ACAGACACACAGACACACACACAGACACACAGACACACAGACACACAGACACACACACAGA
CACACACACACACACACACACACACACACACACACCTGAATGGCCCAGGAAACAGTNGGGCTGCAG
GGCAATTCTAAAGACATGACTAAAACCTGTTAAGTTTCCACTACACATnCTGTTGTCCTAAAC
ATCTCCTGCACCTCTGCATGTATGTGGATTGTGTGCTCTGT

SB49
CATGTTNGTAGCTTTTTTTTTTTTTTTTTTTTTTTAGCTAAACCAACATCGTG
TTAGCAAAGAGCCACAGAAGAACAAACCACCAGGCTTGTTTGGCTAACAGTGACCTTTCCAC
ATCCTCATTAACTGCACGTAACAACACACACACACACACACACACACACACACACACTAGGCTA
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CAACGTGTGATAAAGCGAAAGAACGTCAGCTTGGCCCTTCGTGTCCACTTGTCAACACAAACA
AGTCTGGGAGGCAACTTTTCAAACGTTGAAGGAGCTAGCTAAAAAGCTACTTAGCAAGCATG
CTAACCTTCGCTAGCTGAGCATTTATAAAAGTAGCACACTGAAATGGCTGCGTTCAAGGATCC
CCGGGTAC

SB50
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CCACGCCGGTGGTGTGGGCCTGAAGAAAACCTTCTTGGAAAAGAGTCCAGACTTGCAGTCTCT
GCGCTACGCCTTGTCTCTGTACACCCAGGCCACAGACAAGCTCATCAGGAAGTTTGTCCTCTC
ACAGAGCGCTCAGGGTGCGACTTCAAACAGCAACAACACACACACACACACACACACACACACA
CACACACACACACACACACACACACACACACACTGTCACACAGCAGGTTCAAATGATTTCACACAAAA
TGTTTCACTTACTCTCAAAGAGCTCCACTGCTTATTCTTACTAAAAGTAAGGCTTATGGAATTA
AATGGGATTATGAGATTAAATAGAATAACTTGGTTACCGNGTTGNAATGTTTAATTCATTGCT
ACAGTGAATTACAATNACCATACCAAGCAGATTCAAAA

SB51
CTATCTGTGTCCTGCCATAACTTTATCAACACTTAAATCAGAGCTTTAATCTTATCTGACCCCC
CCCCCCCCATCGTCTGTGTCTGCTAGGTCAGCTGACTTCCTGCTCAGAGACTGGCTCACTTCCT

Figure 9L

GGCTGCGTCATTTTCCTCTCTTACCGCCACTGTGATGACGTGTTGTGTTCAAATCTCTGATACC
TGATCTGACATAATCGCACGGTCTCTTATTGGGCTGCTGATGGCTGCTTATTGGCCTCTGGGCT
GTGTTTTACAGGAAGATATTGATGGTTTGATATTAGCTTCTTACTGGCAAATACACACACACA
CACACACACACACACACACACACACAGACACAAATCTGCCTCTTAGTTATTGATGAGCTAATATC
TGTGATTATTTGTAGTGCACAAAGAAAGACAACTGTCCAAATTATCATCATGTAGAGTACAGT
ANTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTTTTGAAAACCGTTATCTGT
TACACNCCCCNATCCGATAAGGAAAA

SB52
GTAGGAATGAGCAGCCCGTGACATGGGTTAATTTACTGGACCTAGGAAGGTTCATTGTTTCCT
GTCATTCCTGAACTCATCGCACTGACCTTTACCGCCCTGTCCTGCGCTGTGCGTGTGTACACAT
GGACATGTGCATGCACACACACACACACGCACGCACACACACACACACACACACACCA
ACTACAAATGTATACTGCTCAAATGACTACACTGCTCACTGCCTAACCACAGAAAGAGAAAA
AGTGAGAGCGACACATTGACAAACAGATGGACAGATAAAGACAAAGAGCAACCACCCTTTCA
ACTGTCCAAAAGTATCCTTGAATTCCAGAAAGTTTCACATTATTTTCTACAATAATAAAAAAA
ACACACCAGAATACCCCAAGGGGAAAAGAAAACCAGTATACAGAAGGTTAGCTGTCTATCTG
CTAGTAACCTATTAAGGACAATTATAGAGGCCTATGATTGATAAATAGATGACCTCAAGGCCA
AATTTNAACTATATT

SB53
AACAATGCAGCTGGCTGGTGCTTCATTTCATCCGAGATACTGTGGTGTTAATGAGGGCCCCAG
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CACACACACATGTTTACACAGATACTGTACATGTAGGTGTTTGTACAGGTGTTTGCAGTGAGT
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CAAACAAAAGGGTACAGATTTAATCCGACATGAAGCACAAAGAAACAGCAGATAAAACTGC
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TCAGTAAGGCTGAGTCAGCAAAAAAACATACTAAATCCATAATTTAATGATTTAATTTTTGTC
CTTAAAGATGAGAACTAAACACATAAAAAGTTGTAAGGTAATGTAATACTTATTT

SB54
AGATTAGAGAGATACTGGAGGATACAGGAGTTAGTTTATATATGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTTCACTGCAAAGCATCATTTCTTGTCTAAAAAGAAA
AATAATCTTGTCAAGCATTATTGCATTAGACATTTTTGTTTTAAGAAAATATTTTAGTTTTGTC
TTAATAAAATATTCCAGCTAATATTGAGCTAGATTTAACAATAAGTTAAGACAATGGTTTGCA
TAATATTCCAGCAGAGGAACACAAGTATTTTCCTTATTTTAAGAATAAGACTAGAGAAAGTAG
TCTAGTGACCAAAATACTTAAGTCTATCTTAAATAACTGAGTTTTCATTGTTTGTAAGCACAAC
TTTTTTACTTTTTTCTAGTTTTAAGACCCATTACAGTGTGTCAGTGGTTAGA

SB55
CCCGGGTATATTCTATCAACCATTAATTACTCAAAATAATGTTTAGTTCAATAAATATATGTAT
TGATAGGTAATATCATTATAGTTCAATGCATTTCATGTCTAAGTTAGGCCATTTAATCATGCAA
ATTGTTTTGTTTTTGAGAATTAAAGAAAAACAATGTTTACAAAATGCAACATATTAATCATAA
GAAGTGTTTTTAAAAATGAGACACGCTGCGAATACCGACAGTAAAAGCTGCATTGCAATAAA
TAAATAAAAAAAAACATCGCCATATATCTTAAAATCTGACTTTGTTACTAATGAATTGCCCTAA
AAAGACACGCAGATAACCGGCACGGATTGTCTCCCACTCATCCCAAATAAATATATAAAGGA
TGGGTGGACAAAAACCACGCCTTTCAAGAGATGATGACGAGCACCTGTGACCCCCGCAACAT
TTTTCACACACACGCACACACACACACACACACACACACACACACACATACACACACACACACA
CACATACACTCGCCACATTGTTAACGCTGGAGACAAGAGTACAGCAA

Figure 9M

SB56
TTAAAACTGATGAGAAAACTAAGAAACATGCAGGGGTGCGACCCTCCCCTTGGCATTGACCG
CCCTCTCCCTTCCCATGGACACTCTTGTGTGAATTTGGAGCAAAGCCCCCTGGATAAATGGAA
GGTTTAATGTAATCCCTATAAAATCCTGTTCATGCTGCTACTCTTTCTCTCTTTCTGCCTCTCCC
TCTCCTCTTTCATTCATTCCTGCTCTCCCAGGGAGCACGTTAAATGGTTAACGGCGGGGCCAA
GCGCGAGGTGTAAACCGCAAAGAGATGGGGCTAAGTGTTGGGAGCGTGGGACCACAAGCTCC
ACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGNGCGANGAGAGATTANCCCCCTTTTAAAGAGC
CCGCTTTTAATCTGGTCTACCCCTCGTCTCTCCCGCTTTCCCAGTCTATCTTTCTCGGTGACAGT
GAAACTTTT

SB57
TCCTCGGAGCGGATGCCACCCTCCGTGTTTTGCAGGTCGCCGCTCTCTGATGGAAAGCTCTGA
ATAACAAAGACATGTTTGAGAGCAGCAGCGGCATCAGCAGCAGCAGCAGCAGCAGCAGCAG
TCTGGGCTGAGCGCTGACGTCAAGGAGCCATGACTGTGCCAAGCAGCATCCAGACTCCAGTC
CACCACAAACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACAAACACATTGACCTGCTGCTGCCACTGTGGCCTGTTTGGAAGCACCCCATGTCAAAAGT
TAGAAACACACCACCCTGCGTGCTGTGATTGACTCTTCAAAGTTGGCCTGTGATTAGGGTCAG
AGTGGTGTTTTCGCTCTCAGAATACTCTTATTGCAGAAGTCACCGCACAAGTGATACACTCTG
GTGGTGTGTTTGGAGTCCCCTTGCTTTTTTCTGGTCTGTGTGTCTATCCCCAGCTGTCTAAGTTA
GGGGGGAGGGATAGGCTGGAACAATANGCGCCATTTGTCCTGCTAAAAGGGGACAGGAAGC
ATTTGATTTTCAGCCTGTTCCAAGCTTNTAAGCCATNCCTTGAATTGGCTAAATGGGAACATTT
TCCTTCTAACGG

SB58
TTTGAAACCGGGCACCCAACTGCTCTCTTTCTTTCACTCTCCCTCTCTCTGAATTGTCAACCTAT
TAAATGTCTCTTTGTATCTCGCCCATTCACACACAAACTGACCAATGGAAAGCTTTGGACCCTT
TCAGTGACAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGATTGTCATAACGGAGCTGTCC
CAGTTCTTTTTGTACATTGATTGCACCAATGTTATTTTACTAGTTTAGAAAGCAGATGTCACTG
CATGTGTGCGTGTGTGAGAGAGTGTTTGTGAATGAGACTGACAGAGACTGTGAGGGTGGTGT
GTATGTGGTAGAGTTACATGAAGAACAATAGCCTTATTGTACCTGTCTGCTGCTACTGTCTGTC
TTGTGTCGATGCTCTGCACTGAGCCTATTTGCCTCATTCTTTGTGTAACCGATCACACATTTGT
GAATAAAGTTCGACATTTCTGAGTTATATCATACACTTGTAAGCTCTCTGGTGGCTTAAGTGGT
GCANGGTTCCCCANTGTATTGGAACTAANTATCACCAGNGGATGTTTTCTACCAACACTGGCT
TCGACTATTATTCAGTATTGCTCTTGCATTTAACACTACATGGGCGAACAT

SB59
CTGGTTAGTCCTGTACGTGTTTGTCTCCTCTAAAAGTAACCAAATACCAGTCTACTTGCCACTC
TTGAATAACTCTCTGACCGACTGGACTGCTGAGAAGGTTGTGCGAGTGTGTCCAGATTCATAT
GTGTGTGTGTGTGTGTGTGTGTGTGTATCAAACAGAAGAGAAAATGCTAAAAGTCATGCAAG
ACAGCGGAATAAAGCTGGAATAGCAACAAGGGAGAAACTGGATGGCAATGAAGTGAGTGAA
CAGACAGGTTATTGGCAGCAGAGGGAAAGTAAAAGGCTGGATGTCCATTGAAGACGTAGATG
AAGGAAAGAGAAGGTGCTTTTAGTAGCTAAAAGGAGAGGAAGAGTGCCAGAAATATATAAA
CTACACAGTTTAAATGTTGGTAACAGGGGAACCACAGTTAGAGAGGNTTATGTTCATCCTTAA
TGGCTCTTTCCCTGTAACCCATAGTGGACCAATCTTGAACTTGGCTTCTTATAAATCATCATCA
TCTGAATCANAAGTTAGTGATAAGTGTCTTTCCNGGGGGGTGGTCTCTCCAAAAAAGGCTTTA
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CTGN

Figure 9N

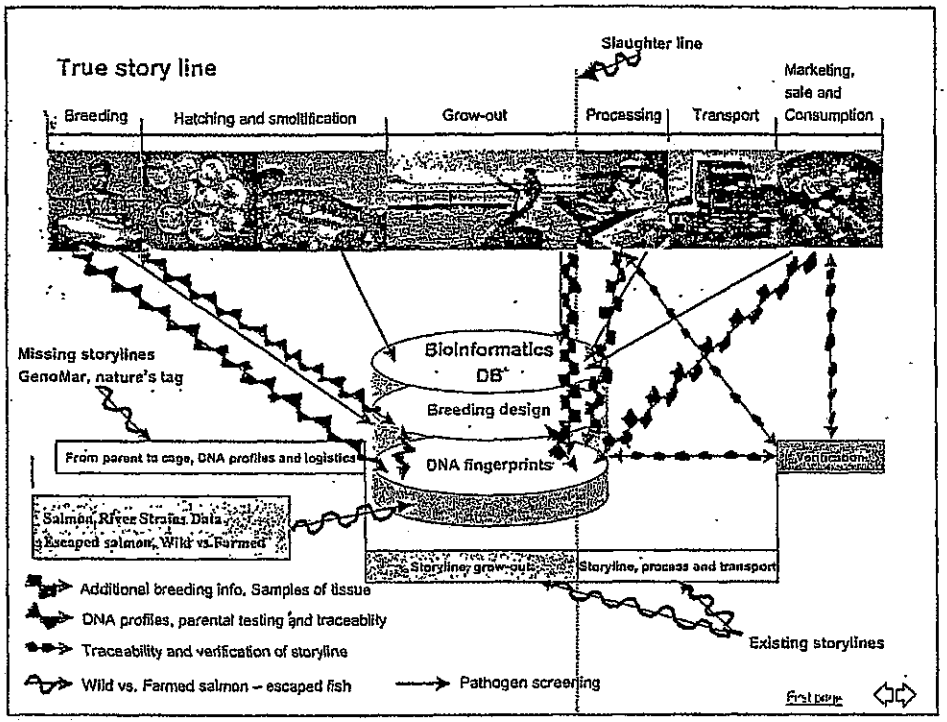

True story line
Slaughter line
Marketing, sale and Consumption
Breeding
Hatching and smoltification
Grow-out
Processing
Transport
Missing storylines
GenoMar, nature's tag
BioInformatics DB
Breeding design
DNA fingerprints
From parent to cage, DNA profiles and logistics
Verification
Salmon, River Strains Data
Escaped salmon, Wild vs Farmed
Storyline, grow-out
Storyline, process and transport
Additional breeding info, Samples of tissue
DNA profiles, parental testing and traceability
Traceability and verification of storyline
Wild vs. Farmed salmon – escaped fish
Pathogen screening
Existing storylines
First page

Figure 10

LG1

GM299

TGNGTTNTTCCNANNGANCTCTTTGAAGCCCCCCTCGAGGTTNACGGTATCGATAAGCTTGA
TATCGAATTCCTGCAGCCCCCTGAGGGACGGGCGCGNACACACACACACACACACGCACA
CACACGCACANACACACACACACACACACACACACACACACACACACACACTTACTCTTACTCTTACT
GTAGTGGCGAGGGTGTATTTGATGCTGATGACGGGCAACCGAGCATCGATCTGCACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CAGAGGGCGAGGGGGGCGACGGTTGCAACAGTCCAGTTGCGGTCGAGGCATTGTGGTGGG
TGGTTGGCGGGCGTCCGAGTCGTTTTGTGCCTCCTCTAACTCGTCTTCTCCTGGCAGGACT
GACAGACCGACACAAAGTCACGCAGGAAAGAAGCACGGCTTAGGATGGCGAGTGCGGCGC
CAGCCAGGAAGCCGTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTC
CAATTCGCNCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTTGTTTTACAACGGTCGT
GACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTTGGAGCAAAATTCCCCCTTTTNG
CCAGGNTGGCGTTAAATAAGCGAAAGAAGGCCCCGAACCGGATTCGNCCCTTTCCNAAAAG
GTTGGCCNCAATCCTTGAATNGNCGAAATGGGAAATTTNTAAGCGTTTAAATATTTTTGGTNA
AAAATTCGCN

299U = TAGTGGCGAGGGTGTATTTGA
299L= CGACCGCAACTGGACTG

GM494

GM507

TGCCCCACAGCTCTCTGACCCGCCTCGTTCCCTTCCTGCACACACACAATGCATTAAATAAA
CACACACACACACACACACACACACACACACACAGCACTGGAGACGCACATGGAGTCCCAGTGAG
GCAGGATCTCAGTGTTCCAGGTGACCATGGCGTTGGAGATGCTGTCCTCCTGCCGGTGTCT
CTCCTTCATCTGACGCTTCTTCCTCTGGGCTTCTTTCAGCTCTGAAGGAGACGCAACAGCAC
GAGCCAATCAAATCCAAGAACAGCACCAGCCAGTGACCTCAATACGTGTGTGTGTGTGTGT
GTGTGTGTGTACCTCTCCTCTTGGCTCCTGCCACCATCTCCTCGTACTCCAGCTTGTGTCTC
TTGAGTTTCCTCTGTAGATTT

507U= CCTTCCTGCACACACACAAT
507L= GCTGGTGCTGTTCTTGGATT

GM630

AGTGTCCGGATGGCTAAGAGTCTCTGTCAGCAACTACTGCAAGACACATGTAGCGCTCTAG
ATAAGGTGTGTGCACATGTGCGTGAATTTAACTCTGTCCCTGTTTTGCAGCACATCACCTGA
TTCCTTTTTCTCCTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGT

Figure 11 A

GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGGTCTCACACCTCCTCCATCAAT
GTGAGCAGCCAATTAGGGAGCAGCTAAATGTGGTCAAGTCACTGTGGCAGGAAGAGAGGT
GCATCCTGGGAAGCTGCC

T630U= GTTTTGCAGCACATCACCTG
T630L= GCCACAGTGACTTGACCACA

GM452
TTNTTTCTNCCNANAAGATCCNTTGGAACCCCGCCCCTTTTNGAGGTCGACCCGTATCGATA
AGCTTGATATCGAATTCCTGCAGCCCCccTCAAAAGTGCAACTACAGTAACAATGaTTTGATG
TCATTAAGAGGAATGTGCTAGAAGATTTACATAGCATGGATCAGATTACTGGATCACAGATC
ACAGAATTATGGATTTATAGCTCCTGTGGTGACTTAACTCAATCGGATGTCCTCATAACTATA
GAAAAACACTATTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGAGACTTTGTAATGGTGGCTTTCAAAGACAAGTGGACATGAACCAATGGT

452U= CCCTCAAAAGTGCAACTACAG
452L= TGAAAGCCACCATTACAAAGT

GM686
CCATAATACACACACAAACAACTAAGCACACACACACACACACACCTTTCCTTGCTTACAGTG
GGTCTTCCTGTAGTTGNGGCGCCTCGCCGAACAAACACAGAGCAACAATACAGTACTGGCT
AATCTGTGATCCTAAGGAACATCAAGTTCTGGAAACACAGCCAAACGCCTGCGCGCACACG
CACACACAGACACACACACACACACACGGGTGAACAAACAGCTATCCCAGACAT

686U= TGCTTACAGTGGGTCTTCCTG
686L= TGGGATAGCTGTTTGTTCACC

GM262
TTGNTTTNATGACCGTNAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCC
CCAAGAGCAGATGCTGCTGCTATGAAGATAGATCACAGTGGGCGCACCGTTTCCTTCCTGc
GTGCTGTGATGCTGGGGTATCCAGACACCGCGCGCGCGTGTGTGTGTGTGTGTGTGTGCG
TGTGTGTGTGTGTGTGTGTGTGAGAAAGAGGAAGTAAAAAGAAAGCCCAAAATGTTGAGTGT
CTTCTTTTGCAGCTATATACATGTGCATTGTAGAGTATTTGGATTTGTTTTTGGTTTATTTCTTT
TTTCTTTCTCATGCACAGCTATATGACAATTTACTAATAAATTATAGCTGCATGTGAATGTCCT
ACAAATGTGTCTGCCTGGCTGTGCCCTATTGATCAGCCAGATTGCACCTGGGGCTCCGGAT
GGATGACCCTCTATTAGGCTGTCGGAATCCCAGTAAAGAACATCTCAGCAGCTGGGGGGCT
GCAGGAATTCGATATCAAGCTTATCGATACCCGTCGACCTCGAGGGGGGGCCCCGGTACCC
AGCTTTTTGGTCCCTTTAGTGGAAGGGTTAAATTGCCCNCTTTGGCGTAATCATGGN

Figure 11 B

262U= AGATGCTGCTGCTATGAAGAT
262L= GCTGCAAAAGAAGACACTCA

GM641
ATCTGACTGTAGCAAATTTGCTAACCAGTCAGTGTCATTGCAATTCTTCAGATACATGAAACA
TTTCTGTGGCACTGGTACATGAGACATACTTACCAAATTCCACAGCATATTTCTCTCCGAGGC
TCTTGCCATCTTTTTTTTTTTTTTTTAAGCTATGCAGAAGGTTGCAGTGTTTCTACTGGAAACTG
TTTATCCTCCAAACAGCCTGCTTAAAATCAATATTTTACCTCCAATCTCCAGTTACTATTCCAC
TGCTCTTCTTTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTGTGTGCGCAAAGTG
TGTGTACAGCTGTGCACAAATGCAAATGATTACAAAGAGCCCCGACACAGACATTGAAATAC
CTGCTGATATGCTTAAAGTTGATATGATAGTAGAT

641U= TGCAGAAGGTTGCAGTGTTT
641L= GTCGGGGCTCTTTGTAATCA

GM373
TTGTNNNCCCTTTGATGCCTTTGNACGCGGCNCGGCCGNTCTAGAACTAGTGGATCCCCCCCCC
AATCAAATTAACCAGAGCAACATGCTGCCACTCAGTTTTTCATTGACATGCTGCCGTGTCATC
GCCTcCTGGAGGGCACCATCTCTAAGGAAACAGCTTTTTTCACCTAGAAAGCACACACACACA
CACACACACACACACACACACACACACACACTCATTATTTCTAATGAGATTGTAAAAGTTGAAGG
AGAGAAGTTATATTAACTCTTCTAGTAGACAAAGACCTCTGTATCTCACGTCATCTCCAGCTA
GAAGCCAAGACATTACCTTCTTCAAATAGAAGCTTCTCTATTAAATTTACTCTGTTGTGCATGC
CCTCTGTAAACACATCTGTGGAATAATATTTCACATTTGTCCCCTTTAACATGGAAGTCTAAAT
GGACTGACGTAGCTCTGGAGCAGGTGCCAAGTGGGGGCTGCAGGAATTCGATATCAAGCTTA
TCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGNTCCCTTTAGTGAGGGTTA
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AATTTCACACAACATACCGAGCCCGGAAGCNTAAAAGGGGTAAANNCTTGGGGGTGCCCTAA
NGNGGGGNGCTAACTCACANTAATTGGGGGTTGCGCTCACTTGNCCCGTTTTCCAATCGGGAA
AACCTNTTGGGGCCAACTTGGATTTAAANGAATTGGCCAACCCCCGGGGAGAAGNNTTTCNG
ANTTGGGCNCTCTTCCT

373U= GGCACCATCTCTAAGGAAA
373L= TAAAGGGGACAAATGTGAAAT

GM619

GM535
CCATCCATGAAACCATTTGACTCCTAAAGCACACTGTTAAGTGAGAGGATGCACTTCTCCTT
GATTTAAATGAGCAGCGGGTATCAGCAGTTTAGCTCCTGCAGAGCATGAGCTCCACACACA
CACACACACACACACACACGCTTACACATTGTCACATAAGAGAAGTTATCTACTTGTTGCTGT
ATGGAGAGCTAAA

Figure 11 C

GCTTCTGTTATGAAAAATGGGCTATTATCTTCTTATTGATCACATTGTTGATGAGACAAATGG
CGGAACTGATAGATGGGGTTTTATCACCTTAACTGTTGTCAGTATGAATATGGAT

535U= AAATGAGCAGCGGGTATCAG
535L= GTTCCGCCATTTGTCTCATC

GM479

LG 2

GM203
TNNNNCTCTGAACANTCTTTGGCCTTTCCNGCCCCTTCTCGAGGTCGACGGTATCGATAAGC
TTGATATCGAATTCCTGCAGCCCTTTAGCACTGATGTGAGTTAGCAGAAGATCTGGCAGAGG
TCTGTTGTGAATGCTGGTCTTATATGCTGGTGGCTTGATTGGAACCAGGCGTGGAGACTGAT
TGGAGGCTCTGCCTGAAGGTGGAGCCCAGTGGAGTGGAAAAACCCCACACTCACCCAGAC
CATAACATATAGTTGGTTTACACAGCTTTGTGTATGTATGTGTATGCATGTGTAATGTATGTAT
AGACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGATTTA
CATTGCTGTGCTTGAGAGCCANCATCTACCGGAACCAAATTCCTTGTNTTTGTCTGCACATAT
ACTTGGGGGGGATCCANTTGTTCTAGAGCGGNCGNCACCGNGGTGGANCTCCANTTCGCC
CTATAGNGANTCNTATTACNCNCNCTTCANTTGGCCGTNNTTTTTNCNAACTNTCNNNNACTT
GNGAAAAACCCNTGNCNGNTTACCCANCTTTAANNNNCTTNCTANNC

203U= GTGGAGCCCAGTGGAGTG
203L= ATTTGGTTCCGGTAGATGGTG

GM551

GM443
TGGACTCCNGAGCCCTTGNAACCCCCCTCGAGGTCGACGNTATCGNTAAGCTTGATATCGA
ATTCCTGCAGCCCCCTATTCATTCCTTAATCATCTGTTCATCCATATATNGNGGGTATCCATA
CATCATCGATCCATCCTCTCTTGTTATCATCTGCTCTTCCCCTCCTGCCCCAACTCATCTCTC
TCTCTGCCCTCTCTACATCCATTCATTCATCCAAATCTCAATCCCTCCATCCCAATATCGATC
CATGCACACAAACATTCATCTATCCACTATGAATATATCTATCCAACCATCCTTCCTTCCTGCT
CTCCCTCCTTCCTCCCTTGGCTCCTTATCCCAGTCGAAAGGCTTCTACAGCAAGACTTAACA
CGCTCCACTACCTCCCCGTCCCTGCATGTGAACACACGCACGCACGCACACACACACACAC
ACACACACACACACAAAGGCAGTCCCTACAGGATGCAAGACTCAAAGACACACAGGACATC
GTTTTCACAGCTNCCTGAGCAACTCAAATGGGGGGGGAACCACTAGTTCTAAGAGCGGCCG
CCACCGCGGGN

443U= CTGCATCCTGTAGGGACTG
443L= CAAGACTTAACACGCTCCACT

GM307
AAATCACACATATGTGCACACATACCACACGCGCGCANACACACACACAG
GCGGGTATCCCCGACCCTGGGGGAGCTGCTTGGTTCTCCCACACTCGCTG
TCATTTTTTTTTTTTTTTTTTCTTACTGCAGTGTTTTAGAACATTTTATC

Figure 11 D

TAAACTCTGGAGGATCGGGCTGGGGTTTCCCCTAGTAACACACACACACA
CACACACGCACACACACACACACACAGTGCTTNTCCAAAGGCTCTCCCTGTC
CTTGGCAAGGACACATTGAACTGCGGGACTCCTGCCATACATAGAAACAC
ACACACACACACACACACACACACACGGACACTCATTCACAAAATGA

307U= GATCGGGCTGGGGTTTC
307L= AGTCCCGCAGTTCAATGTGTC

GM664
GGGATCAAACAGGCAGATTTGCCACGCCTGACACCCCTGCTGCTGCAAGTGTGTGTTTTGT
GTATGTGTGTGTGTGTGTGTGTGAACTCAGCTCGGACTCAGTAATGACAGGATTTGTTAAAC
AGTNAATTAATGAATAATGAAATATCCAGCACGCGCCTGCCTTGCCTGGAGCACAGCGCCC
CGAGCAGGAATTACTCCCGACCGGCACTCGGCTGTCTGCATGCTGGATAACCTGAGCGTGC
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGGATAANCATTTTTACAGCCCATTGCG
TGACAGAACGCCGANGGGCTTTGCTGAT

664U= GTGAACTCAGCTCGGACTCA
664L= ACGCAATGGGCTGTAAAAAT

GM650
TGCCCTGTATGATTTATAACTGTGGGTCTGTCAGTGTTTACTGCCAAAAATTGGCTTGTTTCA
GCAATAACATGCATACACACACACACACACACACACACACACACACACACAAACACACCCTCACTC
ACATGAAAACATCAGACCAACCACAATGGACCTTTCTCCCACATTTTTACCTCACTCTCAGTG
GAATTTCAGCTTCACGGCTGCTTTCAAATCCAAAAACTTTGTACCTCCCAGGTTTCCTCGTCA
TTGCTTCGGAGCCAGCAGAAGACATGGAGCGGCAAGCTGGAAAAGAATACACGCAGAAACC
TGAACACACCCATGTTTTATATTTGAAGTTTGGAAAGTTTTTTTATGCACCTTAAAAATCTGGC
AATCTCACAAACCTCAAAAGACTGAAGTTAAATTCTCTCC

650U= CTGCCAAAAATTGGCTTGTT
650L= GAAGCAATGACGAGGAAACC

GM578
CCGAGCTGGGGGACATGGGGCAGGGGGTGGGGGGCTTGGACACACACTGTGAGCTGTAG
TTGTCCTGTGATACAACACACACACACACACACACACACACACACACACACACACACACACACA
CATATATCAGAAGGAGCTGTTTCTTCTTCAGGTTTTCATTCTCACAGCCAGCACCAGTCTAGG
TTGGAGCGCCTGCAGTCAGCTGACAGTAGAAACAACATGTCTGCCAGCAGCTGGTTAACTG
CAGAGAACCAGCCGCTGCTCTCTGGTTAATTGCAGCGAACACTGAAGTGTGTGTATGTGTGT
GTCTTTGTTAGAGACGACAGGAAAGGAGTGAAGACACACACTCGTGTGGCTGGTTCTACTT
GGTTTTCGGTGTGTGCTGCTCTGGATGTGAAGCCTTTGCTAAACTAACCACACAGCCTGGTA
CGGTGGG

578U= GGGGCTTGGACACACACT
578L= CTGCTGGCAGACATGTTGTT

GM638
CCGTTTTCCCCTCTACTGCCTCCACACCCAGCCTGCATGTTTGTTATGCTGCCTTCAGGCTT
GGTTTGGAAATGTGGGCGTTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCCTGTGTGTG
GGAGAATTGCTGCACATTAACAACCCGACAAAATGGAAAGTAGTGCCGGGACTTTTTGCTTG
ATAAGCA

Figure 11 E

638U= CCGTTTTCCCCTCTACTGC
638L= AAGTCCCGGCACTACTTTCC

GM11
TTGAANCCTTGGAACCCNNGGTGGCNGCCGCTCTAGAACTAGTGGATCCC
CCCTGATTGTGTGATTCAAACCAGCTGAATGTGGCAGCCATGCCCCAGAG
CATCATGGGAACTGAAGTCTCTAGATTCAGTCTGCCGAGTAGTTCTTATA
GATTATTATTGATCCCAGCAGCAGGAGAGGTGTGTGTGTGTGTGTGTGTG
TGTCAGACTCGAACATGATCTCAAGTCACGTGCCTCTTAATCACTATAGG
AACCAGCTGATGTGTTGCATAAGACAGGTGGTGGGGTTATCGAGATGACA
TCATCATACTGCTTAGTTTACAGAAAAATGTGTGACAACCATCCGTTCTG
CTTTGCGTATGCCAATGTGGACCCAGACCCCTGCCCCACTGTTTCCAAAT
ATCTTGAGCTCATCTACAGCTGTGAACAAAAAGGTAACTTCTCCATCGGT
TTTTCTAAACATTTTCATGTAGTATTACATATTTATCNTGAGTTAGTGCA
ATTCCGGCTTTCATGCTTTTGTGCTTTGAATGCTCAGTGTGCCTGCATGG
CTTGGGTCTTGAACATGGGCNACATCTTANAATGCCATGCTCTNTGCTTT
CCTTCTC

11U=GATTCAGTCTGCCGAGTAGT
11L=GAGGCACGTGACTTGAGA

GM419
AGGAGGNGTNACNTATTTNTATATCNNGGNNGTGAANAGGTTCTCCNTTTGGTTAAGGGCC
CACCGTATCGANNNGCNGGATATCGAATTCCTGCAGCccaCTgTGGGCTGGTTGCGTGTGCT
GCaGaGttcGGAGCAGAAACTAGGACACCCTGAGATCAACAGGAAACCAAAACCCTCCGTCTA
CTGACATCATGACCCAGAAACACCCACCCCCACACACATACACACACAGAGTGAAGGAGAA
GTTGGCTCACCTTGGGAAGGCTCCCTCCTCGGTCTCCCTGCTCTCTCTCTCTCACACACACA
CACACACACACAAACTCCATCCATAACTCTTCATCACTTTGCTGACCATCATCATCCTAAGGA
GGTTCGTCTCACCTCAGCCAAGGAGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCG
CGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTNT
TACAACGTCGGGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCC
CCCTTTCGCCAGCTGGCCGTAATAGCGAAGAGGCCCCGCACCGATCGCCCTTNCNAACAGT
C

419U= CTGGTTGCGTGTGCTG
419L= CCTCCTTAGGATGATGATGGT

GM683
TCTTTGATAATTAAGGTGTGATTCTCAGAGAAATAGAATCTTGCATAACCAGACTTTTCTCTAC
AACACTTTAAAAGCTTTTTCGGCAGAATTTGTGAACAGAAATGCAAGGATGCCCCTGTTAGAT
CACATATTATTTTTCGCTCTTTAAAACCATTCAGCAAAAGAACCAAACCCTTACACGTTTCTGC
ACGATCCAAATCTTCATCAAAACTTGCCATTTGGAGTGTACAGGTTACTAGCTTAAGACAGTC
TTATGCCAACAGTCTACAACTTATCAGTTAGACAAGGTTATTTATATACCCAACAGTTGGCAA
GTCAATTATCTGGCAACACCTGCAACACGAAGATGAAACAGTGTTTCAAACAAATCTGCAAA
AATGTCAGTGAAAATTACAGATTACTAAAGGGGTGCGCGCACGTCACGCACATGCATGCAC
ACACACACACACACACACACACACACACAAAATCAAAGGCAGTGAAGATCCAAAATGGAAAGCA
TCACAGCTATAGG

683U=TTATCTGGCAACACCTGCAA
683L= TGTGATGCTTTCCATTTTGG

Figure 11 F

GM143
TTNNNTNTTTGATANGATANACCTNNNTAAACGCCCCGGCGTTTTNTCTAGAACTAGtGGATCC
CCCCCAAAGGTCAGAAAGAGAAACACCTTTcTTTGCCGGCTCTTCACGCTTCACTGATGACATT
TCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAGAGAGAGAGA
GAGTCAGAGAGAGTGTGTGTGTTTGTGTGCATACCTGTATTAATCATGCTGTGAGTGAACTGC
TCTGTTTGTTCATACTGTTAAAATAACTCATTAAATTACTTGCATCCTTACTTTACTTTCTCAAC
CATCTATTCTCTTCTGCTCATCCTTATCAGGGCTGCAGGGGGGCTGGAGCCAATCCCAGCTAC
CATAGAGCAACAGGCAGAATGCACCCTGGACAGGTCGCCAGTCTGTCACANAGAGACAGACA
GTCATTTTTCACCAGTTTAAAATCCNAATTANCCTAACCCCACTNACCCCGNTNAAGGGCTTTT
GACCATGGGANGAAACCCCAGTNCCCCAAGGGTCCCNCACCNACNTGTGNAAAAACNTNTAA
ACTNTTCACNCCAAAAGGGCNCCCCGNAANTNCCCCCCNCCT

143U=ACGCTTCACTGATGACATTTC
143L=CCCTGATAAGGATGAGCAGA

GM210
CTCTCCTTTGGTNGGAGATCTACNGGAANGCCCTTCGTTTGGGGAAAGTACCCATAAGCTTG
ATATCGAATTCCTGCAGCCCACTCTGGGNTAGTAGAAAAGCGCTATATAAGAATGNGGGGAT
TTACAAGTCCAATGTGTAAACACATCTTCCTCATTCATTATTCTTTGTCAAACCAACAAAGTGC
AGCCAAATATTTTTAATTAAGCAATTGTGTGTTCCTTGAACAGCCTAGATTCAAACAGATCTA
ATTTAGCATGTCATGTAAACCTATTGCTTATTATCTTTTATTGACAACAGTGGGATGAACCTG
GGCACGTGCACGCACACACACACACACACACACACACACACACAGTTGTGCAAAGAAATTTGG
AAAAACACCATCATCAGCACGTNCGCCGTGGCTGACGACGCAAATAGCAGCTGAGCTTGAG
TTGGAGATCAGTGAAGCCAGTCTCTTTGAAGATGTATTGCCACCAGGAAAAAAAATTTTTGC
AGCTTCTTCCTTAAAGCANGGGGGGATCCACTAGTTCTAANANNCGGGNCGTCNACCGGGG
GTGGGANNCNTCCNAANTNNNCCCCTATAGTNNAGTCNGTANTACGCCGCCGCTTCACC

210U= GAACAGCCTAGATTCAAACAG
210L= CGTGCTGATGATGGTGT

LG 3

GM21
NTNTTNTTTGATANGTNATGCNCTNTGAGNTCCCCGCGGTGNTCGGCCGCTCTAGAACTAGTG
GATCCCCCCCCCCTGAAGCTGGCTGTGCACAACAGCTGCAGGCTGCATGCCCCCCCCGTCCACA
CACACACACACACACACACACACACACCCTCTCAGTAGCTGAAAGTGCCAGGAATGTGTTGACT
GCTTACAAACAGAACCCAAACCCAGGTTTCACTGCGATCCTGCAGCACAGACACTGCAGTGCT
CCTTATGTGACTGCATGCAGGGATAGTTACGCTGTAGTAGATTTAGTGTGTAAATGTTTATCA
ACTGTAGTCAGAACTACATCTGATGGGTGCCCACAATCAAGTTCGGACTATAGTTACATTAAC
ATTTGGTTATTAGCATGAAAAAGAAGAGACGGTGATTTTTGTGTGTTTCTGCAACATCTGATG
CTCGTCATATTTGCTGGTAGTTAATAATTAATGAAATATTGTAAGGTGAATGTGGTGGTGCTCT
ATATAACTAGCGTTAAGAAAACCCCNCCGTTAAGCTTATTGCGCCCACTAACGGGGGCTGCAG
GAATTCGATATCAAAGCTTATCGATCCCGTTNACCTT

21U=CTGGCTGTGCACAACA
21L=TTTGTAAGCAGTCAACACATT

GM6
TNNNTTNNNNCTANNGAANCNCTTTGGANACCCNGCCCCCNCTCGAGGTCGACGGTATCGA
TAAGCTTGATATCGAATTCCTGCAGCCCACAGAGCTTCCATATGAAACAAGTAGGAGCTGTT

Figure 11 G

TACATGAGAAACAGTGTCGGGTTGTGCTCCTTAGCCGCCTACCCACACACACACACACACA
CACACACACACACATAGCCACAGCAGAATAGTTGTTGGCTGGGGCATTGCTGCACTCACAA
AGAGCGTCTGCAGACTTTTATTCTTTTAATAGACCAAATGTGTAGCACAATGGGGGGGATCC
ACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTAT
TACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCC
AACTTAATCGCCTTGCAGAAAATCCCCNTTTNGCNAGNTGGGCGTAATAGCGAAAAGGCCC
GAACCGATCGCCCTTCCAACAGTTGCGCAACCTGANTGGCAANTGGAAATTGTAAAGCGTA
AATTTTTTGGTNAAAATTCCGNGTTAAATTTTTTTGGTAAAAANANCNCATTTTT

6U= TCGGGTTGTGCTCCTTAG
6L= AGCCAACAACTATTCTGCTGT

Opsin-Blue

GM636
CACGNACTCNGTCAACTCTGAGCCTGTCGCTTCCCATCCATCCCCACATGCAACGCCCCCT
TTGNTTNTCCAAGCACAGTCCAGCCCAACTCACTCCTCCCTTAGTGCTGCTGCTGTGTGTGT
GTGTGTGTGTGTGTGTGAGTCTGCCTGTCACACCGAGTTAGCTTTTCAGTAACTCGGTGAAC
CCGGAGGTGAAACAAACTGCTGCCGGGATGATCAGGCACGCTTTACCATTGGACCACCTCT
CCGCATGTAATCAGGTCTCACATNCTTTTTTGTGAATGACAAATA

636U= AACTCTGAGCCTGTCGCTTC
636L= GGCAGCAGTTTGTTTCACCT

GM264
AGNNNNNNTNNANTTTNTNTTTTGACANGNNAGCTTATGGAACACTCGGTGGNTTCCGCTCT
AGAACTAGTGGATCCCCCATCGAGAAAACACGGCTCGGGCAAagCCAGAGCAGACAGAAGA
TTTAATAAGAaGtGGTAGCTTTAGGCGTGTATAAATTGCAGCGGGAAGATCTGACAACATGTA
TCATAATGGAAATGTGAAATGTGGTGGCTTTCTATAAACAGACATGCAGATGGCTAAGAACC
TCTTCACCAGCTCTTTTTTTTCTCTTTTTTTTTCTATAACGAGGAAAAAGGAGGCGGTGGGAC
GGGGGGTTGATAATGCACACTCACTCACAGCATCAATAATAAAACCACTGAGTTTAACATTG
CTCTCCCACTTAATTAACCACAGTATGGACTACGCACTTAGTGTATATCTGCAAATCAGGCAC
TATTACACACACACACACACACACACACACACACACACACACAGAACAGTCAACCAACATATCACTT
ACTGGAGCATTAAATTTCATATTCCCATGGcAATAGTGGGCTGCAAGGAATTCNATATCAAGC
TTATCGATACCCGNCGACCTCAAGGGGGGCCCCGGACCCACTTTTGGTCCTTTANTGANGG
GTNAATGCCCCTTGC

264U= GCAGATGGCTAAGAACCTC
264L= TTTAATGCTCCAGTGAGTGAT

GM17
TTGAANNCCTTTGAAANNCCCGCGGTGNTGGGCGNTCTAGNACTAGTGGATCCCCCCCTCA
TCTCTGTCTCTCTCTCTCTcTCCCTCTGTTTCCATCTCATATACTCTCCAGCTTTGGCAGGCACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACATATATATATGCACT
CTCCACAGGGATCCAAACTATTACAGTATAGAGCTCTATGCCATCTGGCTGAGGAGGTATGG
ACAGGTATCAGACAAAAACCCACACACGCACGCATATCATATCACCCTGAGCCAACAGCAAT
ATTAAGCTGAGCTCTCCCACTGTGCATGTGTGTCCACACCCTTTTCAGTGTTTCAAAATGGG
GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTNGAGGGGGGGCCCGGTAC
CCAGCTTTTGTTCCCTTTAGTGAGGGGTTAATTGCGCGCTTGGCGTAATCATGGTCTTAGCT

Figure 11 H

GGTTTCCTTGGGTGGAAAAATTTGTTANTCCCGTTTCACAAATTTNCACANCTAACCATTACC
GAANCCCTNTAAGCNTTTAAANANGNTNGTAAAAGCNCCTGGGGGNGTTGCNCTAAAAGGA
ATNGNGGACGCTTTAANTTCATANTTNAANTNGNGGGGGTC

17U= CCCTCTGTTTCCATCTCA
17L= GATACCTGTCCATACCTCCTC

GM537
CCTGACTCGTGCTCAGATTAATATCACCATTGATCAGATTGGATGGGAGGTGTCCTCACACC
CGCTCCAAACACCCCCCACCCCCAAACACCACACACACACACACACACACACACACTCC
CTCACTCTTTCATTGCAGGGAATAGGGCTTTGCACTCTGAGAATTCCAGTAATGCGCCTTTC
CGCCATGCAGCTGTGATTTGAAGCACACATGCGCATTTCATATTTATGTGTGTGTGTATGTGT
TGGCTTTCNTGTATTTTGGCATGTGCAAAAGTGCCTGCAAGCTCACCTGCGTGTCTCACCTC
TTTGGTTTTATTCATGAACACTTCTTCTTCATGGTTGTTTTTTTGGTGCTGCTCTTTTGAAAAT
GGTACTGCAAAAGGGCCTGCAAATGTGCTGTGGGG

537U= ATCAGATTGGATGGGAGGTG
537L= AATATGAAATGCGCATGTGTG

CSki

GM544

GM12
TTGAGATCNCTNNNAAGCCCNTCCTTTGGGTAACGTCCCACNACTAGTGG
ATCCCCCAAAAAGTCTCTTTCGTNCCATTGGGTGTTCAAATAAAGAAGGG
CTAATTTTATTCAAATCAAGGCTTCCTGCTTCTCACTGTGTGTTTCTCTT
ATTCTCTTTCTTATTGTTGCGCAGGCACACACACACACACACACACACAC
ACACACACACACGGACATTAGCATACACATTGCCACCACCGAGTCAGGCT
TAATTGAAAAGCATCTTTTAAGAATGTTAAGAAGTGCCCTGTTAGCCGGG
GGAGAGGATAAAGGCTGTTACATTATTCAGGGCACTTGAATTGGGTTTCA
CCAGCGTCGGTTTCCTTCTGCTTTGATTGGGTTTTGTCTTGTGGTTTTTT
GGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTNGAG
GGGGGGCCCGGTACCCAGCTTTTTGTTCCCTTTAGTGAGGGTTAATTGCG
CGCTTGGCCGTAATCATGGTCATAGC

12U= CCATTGGGTGTTCAAATAAA
12L= GGCTAACAGGGCACTTCTTA

LG 4

GM655
ACACCATTATGCTATAATGGTAGTGTTATTGGAGGAGGGGATGATGAGGAAGATTAAGATGT
CCATCTGTTGCCCGACAGTCAGCTCAGATCAGCATGTGGACGTACTGACTGCTACGAAGCC

Figure 11 I

ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
AGTGTGAGACAGCCAACAGGGTTCGGCAGAATCCAACAGGGA

655U= CCGACAGTCAGCTCAGATCA
655L= AACCCTGTTGGCTGTCTCAC

GM52
TTGAANCCCTTGGATTCCCGCGGNGGTTGCCGNTCTAGANCTAGTGGATCCCCCCCACTCA
AAGCCGAGAACTGGATTTATATGGATGTGTGTGCGTGAGAACGATGNTACTGCCGAGTCCC
TGGACTTTCTCACTGAAGGGTGCTGTGTTTACTGCAGTTAGCCGAGTCCCTTCAGCATGTCG
TCACAGGGGAGAAGTGTTTAATAGGGATGTTTGTATTCCTGCACTGCTGCTGATTTGAGATT
AGAGCTGAACTGTTGAGCGGGGGATATGCGCACACACACACACACACACACGCACCATCCT
GAGGGGCTTTGTTGCAATATTAAGGCGGGTAAGTATCAGCCGCATATAGTATTTAGGGGGT
CTCATCCAGCCCCTTGACCCTGTGCCTGTCTGTGTGGGCTGCAGGAATTCNATATCAAGCTT
ATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGG
TTAATTGCGCGCTTGGCGTAATCATGGTCATAAGCTGTTTCCTGTGTGAAAATTGGTATCCC
GTNACAATTCCCACAACATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGGTGCCTAATG
ANTTGAGCTACTTNC

52U=CAAAGCCGAGAACTGGATT
52L=TGGATGAGACCCCCTAAATAC

GM546

GM167
TNTTTGACGCCTTNGATCCCCGCGGTGGTNGCCGNTCTAGAACTAGTGGATCCCCCACCCG
TTGAGTGCCGTGCTCTCCCCTGGGAACACAAGCACAGCTGAGAGtaaATGGCAATTACTGTG
TTTAACTGTTTTATCCGCGCTCAGAGGCAACCATACATCGCAGATTCCACAGAACATCATTAA
AACACACTTAGATACACGCACACGAGCACTGCGCTCGTACGCACACACACACACACACACA
CTCACTGTCACATCACGTCTGGTGGCTTATTCATGCCTGTCACATCGTCATTTACTCAACCAT
GATGGAGTGATACAAATACCGGCAGACATATTTCAATATTCTGCTGGAGCAAATTATGATGG
GCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCgAGGGGGGGCCCGGTACC
CAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGT
TTCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT
GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTTAN

167U=CGCAGATTCCACAGAACA
167L=CCGGTATTTGTATCACTCCAT

GM380
TGTGTNTTGTCNGAACCTTGGGTACCGNGCCCCCCNTCGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCCCCCCGCCCCACGCCCTCTGCCCAAACTGTCGACACCGCC
GTAAACGGGGACGCTCAGCTGGGTTGTCTCCCACGGTGACATGGTCACGTGGTTGCAGGG
CAGTCAAATGAGACTGCTGTCTGCTAGCGCTCGTTACAGTCAAAACCACCTCATACTTGAAT
CAGTAAGTCACACACACTCACACTCACACACACACACACACACACACTCTCACACACACA
CACACACACACACACACACACACACACACACACACACACACGCTCACTGTGGGTCGCCTGCTCGC
ATAGATCTCTTGCGGTTTCTGTTTTGGTCTTAAAGTTAGAGGAGGAGAATATGTTGAGAAGTT
TTACTGGAATGCGTCTCCTTCCTGTATGGAGCGTAACCATCTGTGGGGGGGATCCACTTNGT
TTCTAGAGCGGNCGCCANCGGGGTGGGAGCTTTCAATTTGGCCTTATAGTGGAGTNGGNAT
TTACGCGCCGCCTTANTTGNCCNNTTNGTTTTAAAAACGTTTGTTNAATTTGGGAAAAAACCN
TTGGNNNGTTTNNCCC

Figure 11 J

380U=CGCTCGTTACAGTCAAAACC
380L=ATACAGGAAGGAGACGCATTC

GM342
GGNNNTNNGNNNANNTTNTNTTNTTACATGGNNGATCTTATNNAAATNCCCCGGCCCNTTCT
GGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCANcTCTGTTCCTCGGT
CAAGCTCTCTGGCaCTTCTCACCTTCAGGTAAAAAAAAAAAGAAAAAAAAAAGTCAGGCATAC
TCTGTCCATCCATCTATCTATCCATCAATCCATCCATCATTCATCCAGCCATCAATCCTCTGT
CACCCATAGTCGACTTCAGGCTCTTGGCTGTGTTTAATGGTTGTATTTTATTGCCGGGCTGT
GTCTCCTGCCTTCCCCGTTGGTCGTCCCACTGTGTAACCGTTCAGCCTTGGTCTGCGGGCT
CTGTTAATCTGCTGCTTAATTAGTGTTGATGAATGGCTCAGTGTGTATGGATGTGTGTGTGTG
TGTGTGTGTGTGTGTCTGTGTGCATGCGTACAAGTGAGCACGTGTGTGCTGGTTTTGGCTTT
GTGTGTGTGTGTGTTTGAATGAATTCGTGTGTGNGTGGNGCATNANCCCCCNGGGGNGTTN
TTTNTGTTNNTTGGGTGGGGGGANCCNTTNNTTTTNNNANGGGGCCCCACCCGGGGGGGG
GGGACTGCAANTTNCCCTTNTAANGGGGGNNNNNTN

342U=TCAATCCTCTGTCACCCATAG
342L=AAAGCCAAAACCAGCACA

GM188
GNNNNNNGGNGANGTTGTNTTGTNACTNGNNGNGTNTNANGGAACTTTCNCAAGTGCCTTT
CCGCTTTAGANCTAGTGNATNCGNCAAACGGAATTCTGCCACAAACACAGGTCAAACCACA
GTGTTCAGCATCTATATGGGGTANGNGANTGTCATGTTCCGCAGCCNGTTGANGTNAAGCC
AAAACATACCGATCATTTCAGCTACTGCCTGACTCGACTCTCCCATGTGGTCCAAATGGCTG
ACCAATTAACAGCAGCTTAACTCTTGAGTCCAAACAGCTATCTCTCTTTCTCACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACCTGCATGAACACATAAGCAGA
AAAGCGGATGCACACAAGCATACAAAGTAATGGACATGCTGATCCACAAGCACTTAGACCCA
GTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCG
GTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATA
GCTGNTTCCTGTGTGAAATTGTTATCCGCTACAATTCCACACAACATACGAGCCGGAAGCAT
AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAAT

188U=GTGGTCCAAATGGCTGAC
188L=CGCTTTTCTGCTTATGTGTTC

GM53
TTGATNCCCTTGNAACCCNCGGTGGCGGCCGCTCTAGAACTAGTGGATCC
CCCATCTAATCTCACATGGCAATATTTTATCAATAGTGTATCACCTGATA
TTACATATTAACTGACAGGATCAAGTGCTGACAGTGCCTAAGAACTGCTT
TACAGTGCTACTAACAGTATGTGAGATGGGTGTAGGTGAGATTTTAATAT
TCACCAAGCCAAATTACTTTCAGAAAAAGACTCTAAAACAATCCTTCGGG
CTAAACAAAAGCCTCTCAGTTTGTCCTTGTGCAGAAAAAGCGATAAATCG
GTATATAAAAGCAGCACAGAATAATGCATTTCCACCATAGCCACAAGCTG
CTATACAATTCTCCAGAACATTACAAGCCCAGCAGGATGTTCACAATCAA
AAAATACCACACACACAAACACACACACACACACACACACACACACAC
ACACACACAAACACACTCAGAAGTGAATGGAAAAGCCAACATCTTAGAAA
TAAACACAATACAAATGGGGGCTGCAGGAATTCGATATCAAGCTTATCGA
TACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCTTTAGT
GAGGGC

Figure 11 K

53U=CAATCCTTCGGGCTAAAC
53L=TTCTAAGATGTTGGCTTTTCC

GM37
GAAGCCCGTTGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCTCTTCA
GGGGCAGAGGACATCAAGTGTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGC
AGAGAGAGAGAGATACAGACAGACCCACACATGTCATGTCGAGACCACCGGTGCAGACATT
AGTGTGTGAGGGTCAGTGAACAGGTCAGGAGGTATTTGCTCGACAGTGTTGGACTTGATCA
CGATGTCCTGTAATGTGGAATTTGTGTGTGTAGTCTACGTGTGCATGTGACTCTAGAGGTCA
GAAGCACATGTTGTTATTTTTCCACTTTGAACAAGTTAAAAATTATACTCATCCTTCTCTTCCA
AACTAGAACGGACAGACATCAAGCGCACTTAACTCTTTACAGTAAATACTTCGGCTCACATG
TCCGTCTTGGATCATTGCCCATTTATTCATTTTGCACTTTAAGATCTCACCCGATACTTTATCT
AAATTAAGACCTTTTTCTTANNTTGGGCCTTGCAGGAAATTCCATTNTAAGCCTTATTCGAAT
NCCGNCGANCTN

37U=GGGGCAGAGGACATCAA
37L=CAACACTGTCGAGCAAATACC

UVOPS

GM241
ANGTGGTTTTTTTTTNNNNNTTNNNNNTTTGANGGCCTTTNANGCGGCCCGGCCGCTCTAGAA
CTAGTGGATCCCCCACAATAAACATTATCCACACACCTTAAAACTAACTAAACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGGCTCTGAA
ACCATCAGTCCAACCCAGAAGTTTTTCTTTGTTGATTTATATGTTTTATACTGGAAAAAACTAT
CAGAGAAGTATGCATGTCCCTAGGGAGACCTCCAGAGACAGGCTGTTTTTCATGACACTTTTT
CCCACCCATCGGAGCAGTAACAGACAAACAACCTTTTCTTGGAAAAAAGGTTGATACTGTTCC
TTGCCAGGTTAGTCAATTTCAACCCTAGTCAGCTATGTGTGTGTAAAGGTGGATGCACAACAA
CCAATTACAGAGGAAAGAATTTAGTCTCTGTGCTCAAAGTTATTTGGGCTGCAGGAATTCGAT
ATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGTTTTGGTTCCTTTTA
GTGANGGGTNAATGCGCCCTTNGCGTAATCATGGGCATAGCTGGTTNCCTGNGGGAAAATGG
TATNCGGTTACAATTCCACAACATTTCGNGCCCGGAAGCNNAAAGNNGNAAACCTGGGGGGTG
NTAAATGAGGGANCTTACCNACATAAATNGGGTTGGGCTNACTGGGCCGNTTTTCAGTGGGA
ACCTNTCGTGCCACTTGATTAATGAATCGGCCAACNCNCGGGANAGGGCGTTTGCCCTATGGN
GGCTTTTCGCTTCTGCT

241U= ACAATAAACATTATCCACACA
241L= GACTAGGGTTGAAATTGACT

GM317
ACATTCAGGACTATAATATGTGTTTTTAGGATTCACCCCCCTTCTCTCTC
ACGTGTCCTCTTTGCAGGAAAAGTCTGTTTATTTCCTTCTTGGCTGTAGG
AAGTGTGTGTCCTCCCTGCAAGTGGATCAGCTTCCCTGTGGGTGGAGGTG
ACTCGTGTTCTCACTGCTGTGGCAGGCAAAGGTGCCAAATGCACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACAGGATCAAGACCTGGACAGTGTGGAGGGCTAAGC
TCTGCTGCTTCTATGCAGCCTTCAGGGCTACATTACAGGTTGTCCCAAACTTAACCCTGTGCCT
GTTAGCTAACTAT

Figure 11 L

317U= TTATTTCCTTCTTGGCTGTAG
317L= TAAGTTTGGGACAACCTGTA

GM111
GNGNNGNANNTNATTTGNTNGANNAAGGAACATGGAGGAACCCNCGCTTCTTTANGAGNAC
CACCGTATCGATAAGCNGGANATCGAATTCCTGCAGCCCCTTGGCAAAGCTTCCAGTGGGG
AGGGGGGGGATACAGACTCGATGAGGCATTTTTTTCCCCAGGTAAGAAAAATAGAAGGCTG
ACTCTAAACAGACTGTGAGCAGATGGTGGATTACTGTGTCAAGAATTATAACTGGTAAATATT
ACAAATGAGATACAACACACACACACACACACACACACACACACACACATACACACACACACAC
ACACACACACACACACACACACACACACACACACAAATAGGCTACTGAGAAAGATGCTAGCTATTG
ATCAGCTGGGATTTGAGTCTTCCTTTATGATTACTGTGACAGCAGTGCTTATCATTGTGCAAT
AACACCAGTCTGTGCTTCCCACAGTAATCACTCTGGAGCCAAGTGTTATGTCTACTAGCTGA
ATGGAAAATTGCAGAGGNGGAATATTCACCCCCACACACTTTGAAANCAAAANCTTTGCCTG
GGGGGCCNCAANAACTCACAACTAAAGGCCCATTTGCAT

111U=GTGAGCAGATGGTGGATTACT
111L=GGAAGCACAGACTGGTGTT

GM637
TCAGGTATGGACTTATGCACCTTCTTTGTCACACCTTTCTGCAACTCTGTTAGTTGGCTAACC
TCCCTTCGTGCTACTTTGATCTTGCCCTCTAGCCTCCTTCTCCATGGAGGGTACTGCCCCTT
GTGGCTGTTCAACTTGTAGCCAAGCAGCTCACTGATCACTGCTGCCGTAGTGTAGATCAGCT
TGTTAGTGTCGGTAATCGTGGTTGTAGGTATCTGCTTTTGTCTTGCACTGTCCACTTTTTTGC
AATGACAATGCAGATTTTCCACTTTTGGGACAAATACATGCAGATTTACTGTATGTGTGTGTG
TGTGTGTGTGTGTGTGCAACATTGGCATTTGTTTACTCAGATCCAAGGCA

637U= GCTGCCGTAGTGTAGATCAG
637L= TGCCTTGGATCTGAGTAAACA

LG 5

GM371
TTTACCTCCCTTTGAAAGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATT
CCTGCAGCCCATCGCAGCTGCCTTTATAAGCGATATTGCAATGGGACATTTGCTTCTCGCAC
GAACATTATCCAACGATTTCCCCCTGAAGGCTTGGCATGTTCAATTTGAGACGCAGCCTAAA
ATACCAGGCAGCGCATCTCACACCCTGGCATGTGGTGGTGTCACTCCTGTTCATCACTCAGT
TCCCGTTAGACTCCCACTGGAGCGAGATGGGTTTGATGCTGTGTGTGTGAGTGTGTGTGTG
CAAGCCAGTTCTTTCTTAATGCTTGTTTGATGGTGCATTTGTGCACTTTGTTGTGTATCTCTAT
TTACTTTTGTAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGAATGCTGTCTGTGTAG
TAAACAGACGCAGCGCAAGTCGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGNGG
TGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCCGNCGTTTAA
CAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATNCCC
TTTCNCCAGNTGGNNTAATAGCGAANAAGGCCCGCACCGAACGCCCTTTCCCAACAGGTTG
CGCANCCNAATGGCGAATGGGAAATTGNAAGCCNTAAATANTTTTGTTAAAATTCNCCNTAN
AATTTTTGGTAAAATCNNNTTANTTTTTTAACCCAATAGGCCGANATNGGCC

371U=GGAGCGAGATGGGTTTG
371L=GCTGCGTCTGTTTACTACACA

Figure 11 M

GM489

GM462
TGNNNTTTGAANNNCTNTGAATGGCCCTTNCCGCGGTGNCGGCCGCTCTAGAACTAGTGGA
TCCCCCACATGTAGTTAGTTTCCTTTTACACTGCTCCGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGCGTGTGCAGTGATGTGTAGTGCTTTTGTCCTGTCCATGGTCCTACTGTGAAACAGACTC
TTTAACTTTTCAAGCAGTGAATGTTTTTTTGACTCAAGGTTGTGTGACTTTCACCTGATGTATG
CTGTTAGATTTCCCACTCTTCAGTAACCCGTGGACTTGAAGCATTATCAATGATAAGGAATAA
TTCAAGTTATTCCAGGTGTCCCCAACCTCAAAGGGTCACTATAGTTAATCAACAGTATAGAAA
AAAAACACATCAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG
GGGGGGCCCGGTACCCAGCTTTTGNTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAA
TCATGGTCATAGCTGNTTCCTGTGTGAAAATGNTATCCGCTCACAATTNCACACACATACGA
ACCGGAAGCATAAAGTGTAAAACCTGGGGTGCCTAAAGAGGGAGCTAACTCACANTAAATG
CCGTTGCGCTCACTGGCCCNTTTTCANNCGGGAAANCTGTNGNGCCACTGCATTAATNAAT
CGGCCAACGCNCCGGGAAAAGCCGTTGCNTATTTGGGCGCTNTTCCNTTNCTTGGTAATGA
CTCNNTTNGCTTNGGCNGTTCGGNTTNGGNNAACCGGNATNAGNTTACTCAAAGGGGGGNA
N

462U=AGTTTCCTTTTACACTGCTCC
462L=TCCACGGGTTACTGAAGA

GM287
TGTGTCTNCCNCCNGATTTTTTGCATCCCGCCCCCTTTCGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCCCACGCCCCTGATATGGAACCTTTAAGCCTTGACAGAGTT
TACACAGGTGAGTTATGAAAATATGCACCACACTGGTGCATTCTGGGAATATTGTGGTTTTTC
AGTTATCAGCAGTGGGTGGCGGCTTTGGCTTAGTGCCATCTCCATAAACACACAAAAGCATC
GGCGTGCCTCTCATGGATACTGCTGGCGTTGCCATGGAAACATGTGAGGAGAAACTGCAGA
ATATAGGATCAACTGTAGCTCCCCCCACCACCACCACACACACACACACACACACACACACA
CACACACACACACACTATGAATGATTATGCAAATGAAGCGACGGAGACCTGCTGTAGCGTTC
AGACGCTCCGAGGCTCCTTTATGTCTCCACCTGCTCCAGCCTTCACACAGCACTNCGACTG
ACCGAGCAGACCAATCAGCACCTNCACATACTCTCACATGACCTTTCATCGCTTTAGCTGAA
GCCNNCAGTGCACAGGCACTAATCTACCTTTGCCTCTAAAACACACGAGGGCTN

287U=TAGTGCCATCTCCATAAACAC
287L=GTCTCCGTCGCTTCATT

GM634
CAGCTACACTATTAGAGAGTGAACATTTGACTGAAACATGACTGCAGGAGACATGATATAAT
CAATGAATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GACATTATTACAGAATAATTTAACTGAAATATGTCTGGAGGAGAGCTCGAACAGAACAACATT
AAACTGAATCACTGCCGAAGTGTTTTCTCTCCTCTGCTGAAAGTTTAATGTCGGGTTTGTCCT
TGCTGACTTTTGTCAGCAGCTTCTTAGATAACATCCGG

634U= CTGAAACATGACTGCAGGAG
634L= CCCGACATTAAACTTTCAGCA

YPAX9

GM112
ATNTTNTTACTATTTATCTTNNNANTTCTCTTNCTTANTGGGNAAAGGCTTCTGANCTNGTGGA
TCCCCNNCAACAAACAGACANTTTGACAGATGCACACACGCACAGTNGGNCAGACTCCGATA

Figure 11 N

TTCATCACGTTTAACTCATACAAATTTAATGCATGCATGAACACACATGTAAATGCACACATG
TATGAACATCTGGACATGTAAGAAAGCCTAGGTGTGCATAACACACACGCACACACACACAC
ACACACACACACACACACACAAACATGCACACACATGCACGTATGCCGGTCCATTTACACTGTG
GCGACAGTGAGTCTGTTAGCGGGATGCCATAGTGGGCTGCAGGAATTCGATATCAAGCTTATC
GATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAAT
TGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGNTCACAATT
NCACACAACATACGAGCCGGAACATAAAGTGTAAANT

112U= CCGATATTCATCACGTTTAAC
112L= ATCCCGCTAACAGACTCA

GM222
NTTTGACAANCNTTGGGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATA
TCGAATTCCTGCAGCCCCCATNTTCACAGTTAACCAGCGCCTGCTGACAAACGACAGTAGC
GGTTTTGCAGCTGGGAGATGAATCAGACCGTCATAACTTAACATGTGGTCGCCTGCAAACG
GTGACATCTTCGCAACTTCGATGCCAAATGAGCCTGTTGTCTGCACGCCAATGCAAAAGCCA
CTCACTCACACACACACACACACACACACACACACACACGAATAAAGAGACGGATCCGCTGGTT
AGGCATGCCATGCAGATTCGCACCTGCACACGCCAGATAGCCAAATCCAACGCAAGTTGCA
AAAACAAGCCCCGCATTTCGGAAAATCATGCCATAACGTTTACTCATAATCACACCGGGCTT
NCAGCTAGCAACCTTAACTAGCAGCATATCTGCTAGCATCGCCAAGAAGGGGGGGGATCCAC
TAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCTATAGGGAGTCGTATTAC
GCGCGCTCACTGGGCCGTNTTTTACAACGTCGTGACTGGGAAAACC

222U=AACGGTGACATCTTCGCAACT
222L=GATTTGGCTATCTGGCGTGTG

GM469
ATCTTNACAGTTAACCAGCGCCTGCTGACAAACGACAGTAGCGGTTTTGC
AGCTGGGAGATGAATCAGACCGTCATAACTTAACATGTGGTCGCCTGCAA
ACGGTGACATCTTCGCAACTTCGATGCCAAATGAGCCTGTTGTCTGCACG
CCAATGCAAAAGCCACTCACTCACACACACACACACACACACACACACAC
ACGAATAAAGAGACGGATCCGCTGGTTAGGCATGCCATGCAGATTCGCAC
CTGCACACGCCAGATAGCCAAATCCAACGCAAGTTGCAAAAACAAGCCCC
GCATTTCGGAAAATCATGCCATAACGTTTACTCATAATCACACCGGGCTT
CCAGCTAGCAACCTTAACTAGCAGCATATCTGCTAGCATCGCCAAGAAGG
GGGGGGATCCACTAGTTCTAGAGCGGCCGCACCGCGGTGGGAGCTCCAAT
TCGCCTATAGTGGGTTCGTATTACGCGCGCTNNTGGCCCGGCGGTTTACA
ACGGTCGTGACTGGGAAAACCTTGGGCGTTACCCAACTTAAATCGNCTTG
CAGCACATCT

469U=ATGCCAAATGAGCCTGTT
469L=CCCGGTGTGATTATGAGTAAA

GM320
CTGCACACACAGCATGTCTTAAAAACTAATGCTGAGCTCCATCAGGGCTG
GATGCCATGAGTCTTAATTAAGACAGCCATGCCAAGTCAAGAAGTGAATA
ATTCTACTCCCCACCAACCACCACCATCTCCCTATTACACACACACACAC
ACACACACACACAGAAGCCTAAACTCTCATTTGCAGATGGATGAGCGTGT

Figure 11 O

AGATGCAGACAAACCACAAAGAGAGACTCAGATTATCAGTTTTAATGGGT
CAGAAAAAGCTTGCTCAGTGAGTAGTGTGTGGATGCCTGTGTGGGCGCTG
AGATAGAAAAACCATTTAGTCACACCTACATGAGATACCTGTTGTGT

320U=AGACAGCCATGCCAAGT
320L=TTTCTGACCCATTAAAACTGA

GM124
TTNGANCTNTTGGACCTTCNGACCCCNTCTGGAGNTCGACGGTATCGATAAGCTTGATATCG
AATTCCTGCAGCCCNTCAGATTTACAGTCTATACTTCATATTCTGATGGAGTGGGAAAGAAAA
GCAGGACAGGCGCAGGACACACACACACGCACACACACGCACGCACACACACACACACAC
ACACACCTTATGGAAGCTATTAGTTCTGATAACTATTATTACTTCCTAATCATCCTAGTGTCAT
GTTGAACACTTCACAGGAGTGAGAAGCTTGCAAATCTAAGCAGGCAGGTGTCAAAGCAAAA
AAAAAAAGAAGAAGAAGAAAAAAAGGAAGAAAAAAATGCTGTAATGTTGCAATAATGTGCAG
GCAGCTGAGGAGAAAATGACTGCCCAGATACAGACTGCAGCTAAGTGATTCAGAAGAAGAG
GCTAGCGAGCTTTGACTGAAGCAGATGGCCTCTGTTATAAAAAAGTGCATTAAACACAAAGA
TCTTCTTACTTTACCCACAGAAAGATAAAGTTGATGCCGTTTTATGAACCCTGNGNGGATATA
AAGAGCCCACTATTGGGAANTATGGACAGNGCTNCTNTCCATGG

124U=TCATATTCTGATGGAGTGGG
124L=GTATCTGGGCAGTCATTTTCT

LG 6

GM420

GM223
TTNACTTTTAATTCCCTTTTGAACGCGGCCGCNGCCGTTCTAGAACTAGTGGNTCCCCCACA
AAATCTCTCCAGCCTGTAAGAACAAAACAATGCAGTCTTATCAGGGATCTCTTATTTGTTTAC
ACAacaaATCAgAGCCGACTGGTGGAAAGTTCCTGCGCTTTTGTTTATCTCGGCTAACTGAGG
GCAGAAGAACAGGACGGTCCAGTTGATTACTTGAGGTGTTTTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGCGCGTATGTGTGTGCTGAACTCTTTACATTTCTTTTCTTTTTCAGG
AAGACTTGCAGCAGTTGATACTCATGCCTCTCCCAAATGTTGCCATTCTGGGACCTGTGTAA
AAGCAGCAGGATTTACGCTGGAATTTTAGTTCTGCTGAGCCAAATAAGACAGGTCAGGGTGA
AGAAGGCACAGCCAAATAAAAGCCTACCACAAAACGGAAANGTTATGACAAATCANACTATG
AGGCAAAAAAGAAAGCTCAGCTTTTTTGGTTTCATGGACAAAAGAATTTATGTGGCTGGAATA
TGACGAGCTAAATAACATAATGTTCTGCCGGGTGTGTNGTGAGTTTCNTTTNATTTGAGTCG
ACAAGCGCCTTTTGTNACTGGGACCAGTTATTTNGNAGAAANACCCCATTAGAACCCATGAG
NANATCAAGAAAGCATTATTTGCCCANNTCTGCNATATCTTTTCCCAGAACAANACANGCATT
TGCAAAAANATTAACCNNGCNGNAACCCNAAGTCCCTGAAAAAATNTTTTAAAAGCGGGGGC
TNC

223U=GTTTATCTCGGCTAACTGAGG
223L=GTCCCAGAATGGCAACA

GM16
GNNNGGNNNNNNNNTTNANTTTNTNTAAGTGATAGNAGATCTTNAGGGAAACNCCGTTCNNT
TTNGAGGCCGACNGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCACATTCTTAGTTCA
AGCAGTATTATNNAAGCCATTCCTTTGATCCTGAGCACCTCTAACCACTTTGTGTTGGGGGA

Figure 11 P

GGCTTTATTGTAGATACATCCTATCTAGAAGATCTGTTTCTTGTGTTGTAAGCTTCCTGCTTTT
ATGACCCTTTTGGTCAGCAGGAGGTCACACAAACGCACACACACACACACACACACACACA
CACACACACACACACACATTCTTACTTACATACAGAAGTTCACACATACACATACAAAGCCTT
GTCTTAGAACCATGTGGGCGTTGCTTTGCTGTGTGAACTGTCTCTCAATAAAAGGCAGCAGG
AGGAGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCC
CTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAA
ACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGGCAG

16U=TTGGGGGAGGCTTTATTGTA
16L=GCCCACATGGTTCTAAGACA

GM198
NNNNNNGGNNNNNNNNNNNNTTANNTTNTNTNTTTGNAGNGGATCTTAANGNGAACNCTCC
NCCCTTTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCTGAAAAT
CTTCCTTGATGAACTGCACTAaGAATAGGGTCCTTTATGAGTCTCATTACCAAACCCAAACTG
TTTCAGGCAGAGCTGTGCGAGACACCCCGACAAGTCCTGGTAATTATCTTTAGTGAGCGGA
GCGCGACACACTGCTGTCGCTTCATGAACACATAGCACAGAGCTAACCGCTCAGAGAGATT
ACAGGCTCATGTGCATCAAAGACGAGCACGCACTCACACACACACACACACACACACACAC
ACACACACACACACACACACCGTTTAATACACATGTCCACTTTGCTGATGTAAACCAATTTTT
TTCTTTTTTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTC
GCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGGTCGTTTTACAACNGTCGTGACT
GGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCAGCTN
GGCGTAATAGCGAA

198U=TCGGGTCAAGCCAAAAC
198L=ACTGCTCCCCACTGTAATCAT

GM435
TNTNTTNNNCNNCTAGANNNTTTTGGNCTTCCCNCCCCCTTTCGAGGTCGACNGTATCGATA
AGCTTGATATCGAATTCCTGCAGCCCCTTTTGTTTCGCGGTGTCTGAAGTGAATGNGACANT
GAATAAACAGCCCTCAACCCTGAGCTCCTCGCTCAACTTAGGGAACGAGCGTGCGCTTTGA
AACAAATGCAGAGAGGCTGACACGCACCAATATATAAATGGACACACACACACACTGAGGG
AGGCATTTAGCTCGATGCACTACCAGCAAGTAGTGACACATGTGGCTCAGAGGGAGTAAGC
TGCTGGAGGAGTTGGCAAGCAGCTGGAAGTCTTGCTGGCATGCCTCACTGCTAAACTATGC
ACAAGTAGAAACGCACACACACACGCACGCACACACACACACACACACACACACACACACA
CACACACACACACACAGGTTCGACCATGTTTCTTCTCTTCACCTTAGCACCCACCTCNTCAG
TGGGGGATCCACTAGTTCTAGAGCGGCCGNCACCGCNGTGGAGCTCCAATTTCNCCCTATA
GTGAGGTTCGTATTACGCNCCGCNTCANTTGGCCGNNTGTTTTANAACNNTTGGNGGACN

435U=GAGGTGGGTGCTGAGGT
435L=GAGTAAGCTGCTGGAGGAGTT

GM558
ATGCTTCCCAAAGGCTTCTTGAAGCTTAAATGATTGTAGCACATGGAATTACAATCACATTAA
GATTATCTTAGCCTTGAAGGAATAGTTTGACATTTTGGCAGATTTTGCTTATTGGATTTTCTTG
CTAAAAGTTAAAGCCCTTTTACAGAGAGAGTATTTCACAATATTTAAACAGGCGGGTGACGA
ATTAAAGTTTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTG
CAGTCTTATAAAGCCTTTGCCAAATCAAACATGCAGATCATCAAAAATGAGAT

Figure 11 O

558U=TTGGCAGATTTTGCTTATTGG
558L=CATGTTTGATTTGGCAAAGG

GM166
GNNTNNNACTTCNTCTTTNACTNANGATCTTTNTGAAAGCCCNNCCGCTTTGGCGGCCGCNCT
AGAACTAGTGGATCCCCCACAGAGCGCAgAGGAagGCTGTGTGAGGCGTGTAATGCTAAAttAT
TTGATCACTGAAACTAGAAATGTATGGTATGTTTGAACATGCTTATACACACAAAGCGTGCAC
ATACACACACACACACACACACACACACACACACACACACACACACACACACACACACACGGTA
AACCATAAACTTCCACATTACAGATTCATTTGCTCATTTGAGCAAATCTGCGTTTGGTCCACCC
ACCGCTCTTGAAGGGTCAGTCTTATGAAACAATTGCGTATTTAATGAGGCTCTGCATACAAGC
AACTCTGTGCACGAGCTCAAACACACACATACACATTCCCATACACACTCATTATGTACGCAG
TGCTCCCACTCAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG
GGGGGCCCGGTACCCAGCTTTTGCCCCCTTTANGGGANGGGGTTAAATNTGCCCCNCTTGGGC
CGTAAATTCATGGGGNAATAAGCNTGGTNTTCCCTGNGNTGNAAAANCTNGGTTTTCCCCNNT
TCACNATTTTNNCCCCCNANCTTNNGGGAANNCCGGAAAACCTTTTAAANTTTTNAAANCCCC
NNGCT

166U=TGTGAGGCGTGTAATGCTAAA
166L=AAGAGCGGTGGGTGGAC

LG 7

JTSRAS

GM65
TTGATTCCTTGGANTACCNCGGTGGCNGCCGCTCTAGAACTAGTGGATCCCCCACAATTACAT
GTAAATACTTTATTCTGTCCTCTCCACACCCTCCATCAGGATAAAGAGAAGGTGAGTCTCCCA
TAGTGCATTTCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAACGG
TCAGCGTGTGCAGGTGGAGGTCGAGGAGTCGAGCGGCGACGGGCAGATCCACAGTCTGGACC
CTCAGCTGGAGCGGCAGGTGGAGATAGTCAGGAACCTGGTGGACTCGTACCTTGCCATTATCC
ACCGTACCATCAGGGACCTGATCCCCAAGACCATCATGCACCTGATGGTCAACAATGTACGAC
ACACACACATACACAAGGGGGCTGCAGGAATTCNATATCAAGCTTATCGATACCGTCGACCT
CGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGT
AATCATGGTCATAGCTGTTTNCTGTGTGAAATTGTNATCCGCTNACAATTCCACACAACATAC
GANCCGGAAGCATAAAGTGTAAAGCNTGAGGTGCCCTAATGAGTGAGCTAACTC

65U=CCTCCATCAGGATAAAGAGAA
65L=ACTCCTCGACCTCCACC

GM685
GACGTCTNCACTCTACATGGAAAAACACACACTTACTCTACTCATCACGCTCTGTTATCTGTC
AGCAATTACTCACTGCCTCCTACCCACCAAACCCCTCGAGAAGCATTACTTTGAAATGCCCA
GAAACACACACACACACACACACACACACACACACACACACAGNTTTACACATTCACACTTTCA
CATTTCCACACCTGtGGAGAAAACCAGTTTCTCTGGCATTTTATCAGCTTATTTGCTGNTGCT
ATGGAAACAAGCCTTGCANAGAGAGATGGGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGCCC

685U=ACTGCCTCCTACCCACCAA
685L=GCAAGGCTTGTTTCCATAGC

Figure 11 R

GM25
TTNNANACCTTNGANCCNGGCCCCTTCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAA
TTCCTGCAGCCCNTAGGGGAGGCGGGTGTCAGCTGAGACCATCAGTCATGCATGGACGCT
GCTGTGTGGCTCTGTGGATGTGATAAAAACCAAAGCAGAGCACTGCAAACAACTGCTGCTG
TGCACGCACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACGGATACACATAAACAGTCAATTATCAGTGAAATAGCACAACACTCTCTTTC
TTCTGTATACTGTTTCCCTTTCAGTCTCTTCCACATCACGTCGTGTTCCCGACTCTCTCCCCG
TCACTCTCTGTTCCCCTCCCCTCTCCCTTTCTCTCTGCAATCTCTCATCATCGCTTTAGCACA
TTAATTGACTCATTATTCCAATTCGTGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGN
GGTGGAGCTCCAATTCGCCCTATAGTGAAGTCGTATTACGCGCGCTCACTGGGCCCGGTCG
TTTTACAACGGTCGTGGACTGGGAAAACCCTTGGCGNTACCT

25U=GCTGCTGTGTGGCTCTGTG
25L=AACACGACGTGATGTGGAAGA

GM407
ACATCAGCGGCTGAGTGAACATCGGCTCGTCCATCTCGTTATGACCCATC
CGACGGTAACACACCTGCGCACACACACACACACACACACACACACACACAC
ACACACACACAGTAAGGACTGTTTCCAGGTGTGTGAACAGGTAGGAGCAG
ACTCCAGATGATGGATGTGTGTCAGAGAGGAGAGACGCAGGGAAACAGTC
GCCTCTGAGGTCTGCTGTGACTTCACACAGTGAAATAAAATATATAATGT
CATAAATAATAACGTGTCTGCTCATAGCTTTACCTGCTGAGCATAGCAAC
ATGTAGGGAGGAGCAAATGTGCTAAAAAAAAAATTAAATAACCAACAAAG
AGCCAAGACAGGAAGAGGGAGGAAACATGATGACATCATTGAAAACAAAA
ATGAAAAAAGGAAACAAAAATTAATTTAACATCAGAAACAAACGTTCTAT
AAACGTGTGTGNGTTTTTACTGGACCAGGTTGACCCACCAACGTCTTTTG
TGGNAANGGNGGCTTTTCCACTCGGGGGGCTTGCAAGGAAATTCCGAATT
TCAAAGCTTTATCGGATAACCCGTNG

407U=GGCTCGTCCATCTCGT
407L=CTTGGCTCTTTGTTGGTTATT

GM369
TTGATTTNATTCCCTTGGAAACCCNGTNCCNTTTGGAGGTCGACCGTATCGATAAGCTTGAT
ATCGAATTCCTGCAGCCCCNTTATATGCATTCATCCCATCACCTGGAACaCACACAGAAAGC
TGAGTCACACTAAAATAATTACTCTAATTACTcCATTTCATCACTAGTATTTACACAAACCAGT
GAAACACACACACACACACACACACACACACACACACACACACACACACACACACACACATTGTGTCA
CTCTTAAAGAAGTAATAATACACCAAGAAAAATACCTGACTGATGTAACAGGAATACACTCTG
ATCAGATGCCAGACTCGTTAAACTGGTTTCATGTGTTTCCTTGCGGTGACAGACGAGCATTA
GCAATTTACAATTTACTGTTCCTTGTTTGACCTTTATATTTATTTGGGGGATCCACTAGTTCTA
GAGCGGCCGCCACCGNGGTGGAGCTTCAATTNGCCCTATAGTGAGTCGTATTACGCGCGCT
CACTGGCCCGTNGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAANTTTAATN
GCCTTGNAGCACATTCCCCTTTCGCCACTGGGGNTAATTAGCGAANAGGCCCNCCCNNTC

369U=TGCATTCATCCCATCACC
369L=TTTAACGAGTCTGGCATCTGA

GM235
TTNNAATCCCTTTGCAATNGCCCTTNCGGTCNACGGTATCGATCNGCTTGATATCGAATTNC
TGCAGCCCACTAGGAAATCATTTGTGCCCTTTGTATTGTTTATTTATGCACTCTAGTtGGCGta

Figure 11 S

GGCAAACAGAAATGGTCCGCAATATATGCTCCCACAAATAGGCACAGGCACGCGCACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACAGGGGGGTTTATGGAAG
CAAGTGGTGACACGCTGTGGACAGGTTTCGAGAGGTTTAGCGACATGTGTGGTCTAAAGTT
AGCGCAGTTGGAGAATGCCTTCCATCTTTGCGTCCATCCATCCCTGAGCGTACCCTCCTCTC
CAGCTGTCTCCATCTCATCCCCTGACCTGAGCTGCTGTCAGGGGGGGGGATCCACTAGTTCT
AGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCG
CTCACTGGCCGTNGTTTTACAACNTCGTGACTGGGNAAAACCCTGGCGTTACCCAACTTAAT
CNCCTTGCAGCACATCCCCCTTTNGNCAGNTTGGCGTNATANCGAAGAGGCCCNGCACCGA
TCGCCCTTCCAAAANGTTGCNCAANCTGAANGGCGAAATGGGAANTTGTTAGCNGTTAAANA
TTTTNGTNNAAAATTCCCNGTTAAAATTTTTNGTTANAANNANCCTCAATTTTTTTTAACCAATT
TGGGCTAAAAATCCGGCAAAAANTNCCTTTTTTAAATNNAANANGAATTTNTACCCAGAATNG
GGGGTTNNANNGGTTTTCNTCCG

235U=TGCCCTTTGT ATTGTTTATTT
235L=CACAGCGTGTCACCACT

GM346
TNNNNTNTTGGNCTTTGAAGCCCNTTCCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCCCGAGTGTGTGTGTGTGTCTGTTTGTGGAGTGTGGT
AGCTTTTCATCTCCAGAGGGGAAAACACAGGCATGTATTTGCTTGTTTTTGTTTTCCCCTGCC
TCCCTCTCGTTCAAGCCCTCGTCTCTATGCCTCCCTCATCCCCGAGCTTCTATTGTGTGGCT
GAGATGAAAACTAAACAGAGCCGAACCTGATCTCTCCTGTCTGATGCACACACACACACACA
CACCCACACAGACACACACAAAGATGTGCATGCCTGCAGACGCTCTCTGTGTGGTCCTGCA
CGTCTTTAGATCTTCACACAGTTGCCGCCAAAGTCTTCTAGAGTTGTGTGCTTATCACTGTTC
TCTTTCTGCGCATTATACTACGAGTTTTCAGCAGCAGTGATTTCACCAAGTCGTTTTGTTCTT
TTCGCTTTTTCCTCCGTTACTTCAAACAGAAGTAGACAGGACAGAAATGTCTCACAATGAAAT
AAACACTGAAATACTGGTAGAGCAAGAGCGAAGATGAGTCTGAAAGATCTCGATCGATTCAT
GTGAAGTAGGACTGCTGATGAGCCTAGTAGAAGGACCNTGGATATTGGGCCTGATGAAACG
GGAGGTGATAGCGGGAGGAAGGGTGCATTGATCTGCCCANCANTGACAACTGACAGACAA
ACGCAGGGNNTTTTGANACGCAN

346U=ATCCCCGAGCTTCTATTGTGT
346L=GGCGGCAACTGTGTGA

GM504
TATCGCAGACACCTATATGCAATTACTGTAATGACCAGGAAATATCAAGATTGAGATTTTTCT
CTGAAATATTTATCTCAGCTTTGACGTGCATCAGCAAGCTCAGACAATTATGTACATTACCCT
GTTACATTATTCCTGAAGACACACACACACACACACACACACACACACACACACACAGTCTTTAT
CTGCTGATGAAAAATATGCTTGAGGGCAGCTACTAAAT

504U=TCTCAGCTTTGACGTGCATC
504L=GCTGCCCTCAAGCATATTTT

GM689
ACTGACAAACACACTTGCAGTGAGACACAGTGAAAGTCAATACTCTTCGCCTTCTTCCCTTCT
CTTCCTTTGACTCCCCGTCTCCTTCACTCCTCTCACCAAACATCCGCATCTATTCCTGTCGGA
CCTCCTCTCAAAACCACAGAATACACTCCTCCTCACACAGACACACAGACACACAGACACAC
ACACACATACACACACTGACTAACCACAGAGGCAGAGGCATGATGGAGCCACACTAACAAA
GCAGCCACCGGGAACACATGATGCTGTGACTCAACATCATCCGTGCCTGCAGAGGACATCA
AAAAT

Figure 11 T

689U=TTCGCCTTCTTCCCTTCTCT
689L=TTAGTGTGGCTCCATCATGC

GM45
TNNNNTNTTNTCTTNGAANANGNTNATCTTNNNGAATACCCGGCCCCNTTTCGAGGTCGACG
GTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCNGTGTTGCTCAGTCGCAGGAATGG
GGGTTCCTCTCTATTTCAACAGCATTAAACAAGGCAAGAAAGATCTAACAGTGCATTTATCCC
AGATTAAAGCCATTAAGGAAAAAAATAAGTCATCCCCTGCAGTTTCACTAATTTCACATGAGT
ATTCCTGATTGATTCCACGAGCCAGGCTATGCAAACCTTTGCCACCCAATGAAAAGAGCAGG
AGACTCCAGTCAGTGGAAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAGAGAAA
GAGGTCTTAAGGCGCTCCACTCTAAACCTGCCAAGCATCCATCAAGCTCACTCTGGCTCCTC
TCAGCTCACTTAACATGTTTCCCCCTGCAGTATTCTGGGGCTCTGACCTTGTTNCACAACAA
CACAATNTTTTCTGGCGAAAAAATGAAATATATNTGTATGAAAATGGGAAAAATGGTTGCTCT
TTGGGGTGCTTGGCTGGAACCTTAACTTTTNTGTNCAAACGACTGGCCATTGCCTTAGACN

45U=CCAATGAAAAGAGCAGGAGA
45L=CTTGGCAGGTTTAGAGTGGAG

GM377
AANTTTGANTGCCCTTTNANCGCGGCCGTGGNCGNTCTAGAACTAGTGGATCCCCCACGCACC
AGCAGCAATACTCAAACGTCCCGTATCTTCCGAGGAAAGGGGTGTGCATGTGGGAGTGTGTG
TGTGTGTGTGTGTATGTGTGTGTGTGCTTGGCAGTGACGAAAGCGCAGTGATAAGAACACG
TCCCTTTCACCTAAGTCACAAAATATTACCATGTGTTGCAACTCCATATATACTCTTTTCTTCTT
TTATCATTCATTTGTTACACAAATCTGCTATCTGTGTCCCTGTGTGCAGCCTACAAAAAACATG
TTTCAGCTCCTTTTTTTTTAATTCTGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG
TCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGC
TTGGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAC
AACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAAGTGAGCTAACTCA
CATTAATTGCGTTGCGCTCACTGGCCGCTTTCCAGTCGGGAAACCTGTNGTGCCAGCTTGCATT
AATGGAATCGGGCAACGCCCCGGNGAGAAGGCCGGTTTGCCGTATTTGGGCCGCTTTTTCCGC
TTTCTTNGNTTACTGACTTCGGTTGNGCTTCGGGTCGTTCGGNTGCCGGNAACCGGTNTTNGG
NTTAACTTCAAAGGGCGGGAAATTCCGGTTNTCCNCAGAATTCAGGGGGN

377U=ACCAGCAGCAATACTCAAAC
377L=ACAGGGACACAGATAGCAGAT

GM284
GAGAGGNNNNNGGNGNNNNNNANNTTATCTNTGACATATGATCTNNNTGAAACCCCCCTCG
AGTTTANGGAATCGATCNCTTGNNNCGAATTCCTGCAGCCCACAGTTGCTCCTCTGCATTGT
CCCGAATGGAAACCAAGACAGTAGCAGtctttAGTTTATAggATtttcCTGACGTTCAAGGTGTCAA
TATGACAGACTGATGATAAACAGAAAAATATGTAGCATTTTCTTGTCCGCAGCCGGTTTCCA
GTGAGAAGACAATGACAACATGACGAGCTGATTGTAAGAGGTTAGCTCAGCAAGCCTCCAC
CTGAGAGAGCTTAGTTGTTTCAGCACCAGATGCCCCCCCCCCCCCCCCCCACACACACAC
ACACACACACACACACACACACACCGGCACTGTGAGTGACCAAATGAAAAAGGGTATGAATCA
AAGCTGCGGCGTCCTCGNGGGGGATCCACTANTTNTANAGCGGNCGCCACCGCNGTGGAG
CTCCAATTCNCCCTATANNGANNNNNNATNACNCNCNCTCACTGGCCCNNNNTTTACAANNN
NNNGACTGGGAAAAACCTTGGNGTACCCCAACTTNAACNCCCTTNCANAANAATCCCCTTTT

Figure 11 U

CCCAANTTGGNNNANTANCCAAAAAGGCCCCAACCCNATCGCCCTTTCCAAANAANNTNNC
NCAACCNTNAANTGNNAAANNGGAAAANTNTNAACCNNNAAAAATTTNNNNNTAAAAANNNC
NNNNANAAAATTNNNNNTAAAANNANNNNNNATTTTTTAACCCAANNNNNCCAAATNNGNNA
AAAACCCTNNNAAANCAAAANAAANNNCCC

284U=AGCCGGTTTCCAGTGAGAA
284L=CGCAGCTTTGATTCATACCCT

GM404
ACCTGTACGGATGGGTGTGAATGGGTGAATGAGGCATGTTGGATAAATCA
CTTTGAGTGTTCCAGTAGAGCAGATAAGCCCTATATTAGAACCCGCCCAT
TCACCATATTCACAATGAAAATGTATCTGTAATATCTCATATGACTCACC
CTACAGTCCTCAGACACACAGACATATGTCAGGTTAACAGGCAGTTCTGC
CATGAAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAG
AGAGAGAGAGAGAGAGAGACGTGCTATAATGTATGATTGAGACATGGCAC
TGAGAAAAATACACCAAACTGGAGTTGGCAGAGCCTAAGATTTTCAATAT
ATGCAATTTTATTNGCACCAAATCACAGCATCAGTTGCCTCAAGGTGATT
TATACTGTAAGGTAAAGATCCTACAGTAATACAGACAAAACCAGAACAAT
CAGATGACCTCCTATCAGCNACCACTTGGTGACAGTGGGAAGGAAAAACA
CTCTTTTAACACAAAGACATGGTTAGACAGCNTGTTCTAATAATTATNAG
GGTGAATACNNTACCACANTTTATCTGAATTAGAACCNGAAATTAGAGAT
ATGCAGCTTTGGCTTTTAGGCCTTCTGCCNTTAACTNGGTTANCTCCTNT
GGNTTAANTAATAAAGTTGGTTGGCTGCAGGAATTCGNTTTCAGCTTNTT
GTTCCTNNACCTNGNGGGG

404U= AGTAGAGCAGATAAGCCCTAT
404L= GCCATGTCTCAATCATACA

GM629
CCCACCAGGCTGTCAACTAACAAAGTCACCACAAACAAGCACATCANNGTCAAGGGTGCTT
CAGGTGTGTGGAAGCAGAAGACAAGCCCCATTTCTACCAGAACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACCTATATAAGA
AAGACAGAGGAGAGGGCTTACGAGAGAGACAGAAAGTGTTGAGTCATGTGGCGAGCACAG
AGGGATCGTGACACATACATGGTTACATTTGTGAAGCGGACCCTTTGGTTTCCAGGCTGTGA
CTGATTGTAGAGGCAGAGGTGACCATAATAAACAACAACAGGAAAGTAAAATTGTTTAAAAA
AAAATTCCCAACCAAATGTGAAGCACATGACCACCACAACATACAGTACGCCATACTATTTAT
TAAATAATTACATTTCAGATGCTTCCACCGTGGCACCAAAAT

629U= TCAGGTGTGTGGAAGCAGAA
629L= ACGGTGGAGGCATCTGAAAT

GM18
TTNNNNTTNNNNNCTNTGTNAAGCTCCCTTTNGGAGTCCCCCCTCGAGGTTNGACGGTATC
GATAAGCTTGATATCGAATTCCTGCAGCCCACATGGCACACACACTCACACAAATACACAAA
TCGATAGACAGACACAGATGCCAACACACTTATACATAGATCCACAACGCACATATACACCC
GGCTTTTGATTACCTCCCACCTTTATTTCTTCTTAGCATCCTTTCCCTTGTGCCCCCCTCCAA
TCCGACCCTATCCATATCCCGTTGTTTGTCCTCCTCCCTCCCCCTCTACCTTACCCCTCATTG
CAGAACGCATGTAACACACACACACACACACACACACACACACACACACACACACACCCTAACCTG
TCAGGTAACATCAGAGAAGGGGAGAGTTGAAGAGACGTGACAGCATGCTGAAGGAATCGAG
TGCCAGGAACACAGACCTCTCTCTGTTCACCTCTGCTGTGCTGGAACACAACGAGCTCCAG

Figure 11 V

CCCCTCACCTTTGTTAAGGATCAGACCTGTTTGGAGAGTGCTGGAGAACCTCCAACAGTCAG
AGGGAGTGAAGACACGCTGAGGAAAGGAGATATTAGAGAANAAGTTNTCGAGAGGGAAGTT
CTGATAATCAATAGGCGCCGGAGAGTTGAAGTTGGAAGAAGAAGAAAACAAAGGCAGGAAA
AAANGGAAAGAAAGGCGTTAAATAGGGANGGGGGGGGGGATNCCACTTANGTTTNTAGAAG
CCGGGCGACANCNGNNGGNGGANCTTNCAAATTCGNCCTTANANGGGGAGNCCGTTTTAC
CNCGCCCCTCCTNGG

18U=ACAGCGTAGGTTGAGGTAAA
18L=TCTTCGCTCTGGTCCAA

LG8

GM139
ANGCCGTTGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCCTATGACTC
GATGCCGCACACACATGGAGCCTGGAACACCTAAAACTGTATAAGATCAACAGGAACCTAAA
AGCCTTCATCAGGAACTCAGTGTGGATGGCAAACAACAGTAGAGGTCAACTTCAAGCCCATA
GCACAAGTCAGCATCAAGTGTGGGATCTACCAAGAAGAGGCTCTGTCCCCACTGCTGTTCT
ACAGCAATGAATAATAAATAAAAGACCTCATAGTCAGTCAGATCTGAATGATTAAACTGCAGC
TTCTTCACTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTCACTCCAGAAAAATG
CAGTCTGACTGCTCCGACTGAGTCTAAGTCAGAGTAAAGTTCACATGCTGTGTTAGGGTGGT
TACTCAAAACGAAAACAAAATATTATGCATTACTGGNTCCTTTTCTTAAAAGTTATGCAGAACA
TTACTTAGTTACCTCCTGGGAGTAAGTCCTCTTTNANGAGGATAAATCTTTCCTGGCACAAAA
NAAAA

139U=GTGGGATCTACCAAGAAGAG
139L=TTTGAGTAACCACCCTAACAC

GM354
GGGTTNGGNTANATTGTGTTCNNNANGCTNGTCNCNCNGGAAACGCCCCCCCCTTTCGAGGTC
GACGgTATCGATAAGCTTGATATCGAATTCCTGCAGCCCAAAgGGAGTTTTTCCTCCCCACTGT
CCCACCGtATGAAGCACTCGGAGGCGACTGTTGTGATTTGTGCTGCAAAGTAATCGTCCAAGG
TGTCCCAATGATGTGTTTCAGTGTGGCTGCTGAGGAAGAGGAGTTGCTTCATCAATTTGAACT
GTAGCTCAGGATCAGCAGACTCGGTCCTCACCATGGATACAGGCAGCAGCCATGACAGCTGA
CGCTGCAGTGTGACAGATCCGGGAGAGCAGGTCAGGCTGGACCCACTGTGACCCCTGTGTTC
ACACACACACACACACACACACACACACACACACACACACACACACACATGCAGCCTGTAACACAGTA
ACCCTGAACGTGCCTTACTGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGNGGTGGA
GCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTAGTTTTACAACAGT
CGTGACTGGGAAAACCNTGGCGTNACCCCAACTTAATCGCCTTGCAGCACATTCCCCTTTTGG
CAGNN

354U=CGGGAGAGCAGGTCAG
354L=CACGTTCAGGGTTACTGTGTT

GM271
TNNNNTNNTTGGTTTGACNACCTTGGGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGAT
AAGCTTGATATCGAATTCCTGCAGCCCACCTCTGCTCTTCTTTGGTTTGATGACTATTTGTCC
ATAAGTGACGTCAGTTCTCACTGCTGAGTCGACTGCAGCTGGATCAGTCTCTGCACAGTAAA

Figure 11 W

ACACACACACACACACACACACACACACACACACACACACACACACACACAGGTGTA
GAAACTACTTTGTATGAACGACTTCCCATCAGGATGCACTCAGAGGGTTAGAGTATCCCCTC
AGATGTCTACAGCTCTGTGCTGAGCCCCCTGCTCCATACTTTCTACTCATACGACTGCAGCC
AGCTACACATTCATAAAATCTGAATGGGCAGAGTTTCAGGCTGAGAGCAGCCAACAACAGG
AAGTTTCTGCTGTGGTTTTACTCAATTCTGTTTGCAGAAATTAAAATAAAAGGTTTTGGGGGG
ATCCACTTAGTTCTAGAGCGGCCGCCACCGGNGGNGNANCTCCANTTCNCCTATAGNGAGN
TCCGTATTACGCGCGCTCCTGGCCCGNTCGTTTACAAACGTTCGTGACTGGGAAAACCCTG
GGGCGTTN

271U=GCAGCTGGATCAGTCTCTG
271L=TGGGAAGTCGTTCATACAAAG

GM180
TTGAATNCNTTGNGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCG
AATTCCTGCAGCCCCCGTTCACTATCTAGGACACCAGCGGCGGCGACTTGTAGTGTAACTTT
GCACACAAACAGTGTTTTCTCACTCCCCCCAGATCTCTTTCCATCTCTCACACACACACACAC
ACACACACACACACACACACACAGGAAAGGGAAAGCAGCGTGTCCTGCAACCATCAGCACTTT
CACCGGTGTCCTCGCCAGACCGTCCCCGTCTCCTCTCATGTCCTTAATGACTCTCCCACTTG
GCGTCCTCTCTCCCTCACCTCCCTACCGCCTTTCCTCCTGCACCGTCAATGCCCTCCATCCT
ACTCCAGCACCCAGTTTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACGCGGTGGAGC
TCCAATTCGCCTATAGTGAGTCCGTATTACGCGCGCTCACTGGCCCGTCGTTTTACAACGGT
CGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTTGCAGCACATTCCCCTTTCG
CAGCTTGGGCGTAATAGCGAAAGAGCCCGANCCCGATCGGCCTTTCCAAACAAGTGCGCAA
GCN

180U=CGGCGGCGACTTGTAGTGTAA
180L=GGACGGTCTGGCGAGGAC

GM293
TGNTTTGANTGCNTTTGACCGCGGNGGCGGCCGNTCTAGAACTAGTGGATCCCCCAAAGCT
TTGGAGGTTCCTCAAGCCTTAAAAAAAGCCACCAGTTTTCACTCTAAAGATGCTTCTCCTACT
ACCGCTGTTCTGTCCAGGTCAAGGAAGTTTGAGTCCCACCTCTCCCATCGTCCTGGAGAAG
CCAGAGAGCCTCAACACTGTCACCTTCAGCGAGGACTCTGTGTAAGCGCGCACATGAGTAA
ACACACACACACACACACACACACACACACACACACACATACACACAAAAATCAGCTATTAATAAAC
CGTCTGCATGCTTCATAATTACAGACAATGCTCAGAGAAGTGTGTGATGAACAACTACTTCG
GCATCGGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGG
GCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGGCGTAATCATG
GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCG
GAAGCATAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGGCG
TTGCGCTCACTGGNCCGCTTTTCANGTCNGGGAAACCCTGGTCGTGCCCAGCTGGCANTTA
AANGNAATTNGGCCAACGCCCGGGGAGAAGGCCNGTTTGGCGTATTTGGGCGCTNTTTCC
GCTTTCTTGGGTTAACTGACTTGGNTGGCTTGGGGCCGTTCGGNTTGNGGGNANCC

293U=CGCTGTTCTGTCCAGGTC
293L=GCCGAAGTAGTTGTTCATCAC

CLC5

GM213
TTGANTCCTTGCATTACCGCGGCNGTTGCCGTTCTAGACCTAGTGGATCCCCCACTCGTTGA
TTAGAGCAAGCTGACCTGAAGTTGTTTACATATATTCAATAACAAAGCAAACTAAAACCCTTT

Figure 11 X

TTATTCTGACAGGCACACCTAATAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTAGGGATGTTAAACTTTGATTTTATTTATCTGTGAAGCTTTATTGTGTAA
CCCTACATATGTCTTTATATTTNTATCACCTATGTTGAGCACACGGAGTTTATGTGTNATGAA
ATGTGGTATATAANTAAAATTGCCAATGTCAATGTGGTATCGTANTGATCTGNTAAAATCAGN
TNCTGCTTGAGAAAATGNTTCACAACACACTGTTACCTGGNAACAACTGCTTCTGTAAAAATG
ACCGNNNGCNACCNGTTNTNCTTTNNNCCTCANAGAATTCCNATTTCTAANCTTTATCCATAC
CNNTCCTNNNTTCNAAGGNNNGGGGNCCCNGGNNNCCCAAACTTCNTTGTTCCNCTTTNNN
CNTAANGGNTTNAAACTTNCCTATCTCNTNTNNCCNNTAANTTNNATATCNCNNTTANCCTTG
NTTTTCCTTGGNGGANNAAAAAATTNTNTNATNTCCCNTTTTCCATAANTCTNNCCTCCTNCC
G

213U=TTTTATTCTGACAGGCACA
213L=AAAATCAAAGTTTAACATCCC

GM505
GTTTGTGAGTCTGTGCAGAAATGGCAGAGCAAGCGTGTCAGATGAAGAAAAATGCTGTTGTA
GAAGTAAATGAGCCAAAGTCCTGAAAGACAGGAGGTGTGGAGAGTTATTTTCAGAAAGGTC
ATAGACTCTGTGATCCATTAATGTTGACACCGATAAAGTTCCCTACTGAAGCATGCATATAGT
CCACACACTGCTACATCTGGCTCCAGTAACTTTCTGCTCCACTGACTGTATGTCCACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACGCAGTATCATACT
CAGGTGTGGGCGGAGGACCTGTCCTCTTGG

505U=TGAAAGACAGGAGGTGTGGA
505L=CGCCCACACCTGAGTATGAT

GM635
CTCAGTGCTAAAGATATTGTAAAATGTGTGAGTGTGAGTGCACTCTGGTCTCTGGTGGACAA
ATGATGTGATAAAAAAACCACACACACACACACACACACACACACACACAGAGTGTAGCTGTAG
TGACAGTAAATGTTGTTAAATACAGTGCTGTAATAAACTTCACTTCACACTTAGAGTTTCCTCA
TTCTGTGTTATTCCCTCTGTTTCAGGCATGGACAGCAGACTAGTCCTCACTCTCCTGTTTGTG
ATGCTGACTGGGTGTTTCATGGGCACTTATGCTCAAAATAATACAACCAGTGTGACTCCAGC
AACCAGCACAAACACTACCAGCAGCAACACCAACACCACCTNCAACACCAACACCACAGCA
CCATCCAGCAACACCAGCACATCAGCAACAACCAGTACGAACTCATT

635U= GTGCACTCTGGTCTCTGGTG
635L= CTGTCCATGCCTGAAACAGA

GM24
TTGANTCCATTGCATTTCCGCGGCNGTTGCCGTTCTAGANCTAGNGGATCCCCCACACCGC
ATGGGTAATACTGTATGCATTACATGCATGAGCAGCTAAGTGTGCCCCTCGGTGAGTTTTCT
GTTGCTCTGACTCATATTTATTCTGAAAGCAGAACACAAGTGATTCCTCCCCAACAGTAAAAT
GTATATATACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
NGGACCAGAGTGCTCATCAAAATCCTGTCATGGCTCTAGAGCGTGTGTTTTTACCCACAGCA
GGGGAGTTATTTGAGTGTGTGACTGCATGTANGTGGNCAGACCTTTCGGGTGTTTTTGATGT
TTTATACTGGGGGGCTGCAGGAATTTCNATATCAAGCTTATCGATACCGTCNNCCTTGAGGG
GGGGCCCGGCACCCAGCTTTTGTTCCCTTTAGTGAGGGNTTAATTGCCNCTTGGCGTTNTC

Figure 11 Y

ATGGNCATAGCTGNNTCCCTGTGNGAAATTGTTATCCGCTCNCANTTTNCACACATATNCNA
NCCNGGAAGCATANANNGGTAAANCCTNGGGGTGCCNAANNGAGNTGAACTAACTNACNNT
TNTCNNGCNNNNCCCNCC

24U=GTGATTCCTCCCCAACAGTAA
24L=AGCCATGACAGGATTTTGA

GM150
TTNNAAGCCCTTGGNAGNCCCCCTCGAGGTTGACGGTATCGATNNGCTTGATATCGAATTC
CTGCAGCCCCCTTCCACTGTTGAAGCTGTCACAGGATTTGATAGAAGAGCATATGATTGCTA
CACCTGCACTTGCTTGCTTTTCACTTTTCACCTCTTTAGTTACATTAAAAAGTCTCAGTTTGTT
TGGCTTACACACATGCTTGAAAAGACACACTTATCTCACTCACACACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACAGACGTcTCACCTgTTTTACTAGGTA
AGGCTCAAAACGGATCATCTAAGCCAAtCACCTTTCAGGAAGCAGGGATCAGCCAAAATCTC
CTCAATTAATAGCTAAAGTAACCTTCAGTGACCTGACTGTGGTCTACCACAAACACACCCAC
ACTTACACACAGACATGCGCGCACTTACACACACACTCTCTCTCTATTGTCGGTCCATTTACC
ATTAGTCTGGGATTTTTTTNTATTCATTTGAGTATAGCTTAGTATTAGTAAACATGTGAGGAAC
AGGATCAAGNATGTGAGGCACATCTATCTATCTAAACTGTAAGGGTGGACTGACCTTTTCCC
TACCTNTAGGNGCTTAGATGAAAAGATGAATGCCTGTCNGGNGTNAACACCGGATTTTTNTT
TNGGNAACAAAAACTGNTGGACNTTNTNGCTGGCAGCAACCCNTCCTTNGATAGGACTGAA
NAGNCCCCTGTCTNNAACTGGGTTTTTATTTG

150U=GTCTCAGTTTGTTTGGCTTAC
150L=AGGTGATTGGCTTAGATGAT

LG 9

GM31
GCCTTTGCTCCCCGCGGTGGCNGCCGCTCTAGAACTAGTGGATCCCCCACATACTGATAGC
CGTGGGAGCTGTTATGATGCTTGTGGGCTTCCTTGGATGGTATGGTGCCATTCAGGAATCTC
AGTGCCTTCTGGGCACAGTGAGTATACCGTTTTATCCACAAGTGACACTTTTTTTCAAATAAA
GTATTTTAATCTTTGGAGTCACTGAAGTTAAAATAAATATCTTTGATTTCTAGTTCTTCTTCTTT
TTGGTGATCCTGTTTGCCTGTGAAGTGGCTGCAGCAATCTGGGGTTTCATGAACAGGGACA
CTGTAAGCGCACGCACACACGCACACACAGACACACACACACACACACACACTGTCACGGC
TCACAGCTTGTTTGATGTCTGCATTGATGTTCCTTCTCTGCTCCTGTAGTGAATCATCTCTGT
TTGTTGCTGTGTCTTTTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCT
CGAGGGGGGGCCCCGGTACCCAGCTTTTTGTTCCCTTTAGTGGAAGGGGTTAAATTGCGCC
TTTGGGCGTAATCATGGNCATTAGCTGTTTCCCTGGGGNGAAAATTGGTATNCGCTTACAAT
TTCCCACAACATACGA

31U=ACCGTTTTATCCACAAGTGAC
31L=CAGGAGCAGAGAAGGAACA

IGF2

GM601
CTGACAAnACAATGAGCTCTGCTTCTCCAGTGTGAGCGCGACnAACCTTGGACAACTAACAC
ACACACACACTCACACACACACACACACACACACACACACACACACACACACACACACGCAGACACTC
CACGCTGACTGTCTTGGCAAAAGAGTTATGT

Figure 11 Z

601U=TGAGCTCTGCTTCTCCAGTG
601L=CAGTCAGCGTGGAGTGTCTG

GM119
GNGNTNATNTTATTTGTTNTAGTAATCTANNTTNNGCTCCGCCCTTTGTTA
NATCGACCGTCTCGATAAGCTTGANATCGAATTCCTGCAGCCCATTCNNAGAAATTTCTCGT
ATTTCATGCGGGGGNCAAACCACACCTGATTAAATCCTACTGGCAAAGACACACACATACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACTACTACACTGAGTAAAATGGGTAAGATCTGTTGTGACGGTCAGAGGAATGTAAGGAGA
GCTGAGGTGAAGTGGTGCTGCTGCACCAGAGAGGTTGTCATGGAGAACGAAACCCAAAAAG
AGACGTGGTGATCGATAATGCTTCCTTATTCTCACAAGAGGTCATACAGGTTACAGAGGAGT
GGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAG
TGAGTCGTATTACGCGCGCTCACTGGCCCGTCGTTTTACAAACGTNGTGACTGGGAAAACC
CTTNGCGTTACCCAACTTAATCGCCTTGGNAACACATTCCCCTTTTNGCAN

119U=AATTTCTCGTATTTCATGCTA
119L=TCCTTACATTCCTCTGACC

GM431
TCTTGTTNNATCNCTTGGACACCCGCCCCTTTNGAGGNCGACNGTATCGATAAGCTTGATAT
CGAATTCCTGCAGCCcAGagGGAGGGAGGGACGAGGTCAGTGGGGttcATTTcCATCCGGcAA
ACCTCAAACAGACACATGCACACACACACACACACACACACACACACACACACACACACACACA
CAAACAAGAACTTGTATGGAGCAGAGTTTTCCAGCAGGAGCTCAATTTGTGTTTGGGCTCAC
TTACACTATTATATTGGTCCAGTATGATCTCAGCTCAGACTGAGTCTAAATGTCTCTGTCTGC
CTATTTGTAGGTGGGATTGTGTGTATGTGTGTGTCTGTGTGCAAGCGAAATGTGGGGGATC
CACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTA
TTACGCGCGCTCACTGGCCGTNGTTTTACAACGTNGTGACTGGNAAAACCCTGGCGTTACC
CAACTTNATCGCCTTGNAGNACATTCCCCTTTTNNGCAGCTTGGCGTTAATAGNCGAANAGG
CCCCGGACCGAATCGGCCCTTTCCAAACANTTTGCNCAAGCCTTGAAN

431U=GTCAGTGGGGTTCATTTC
431L=AGGCAGACAGAGACATTTAGA

GM672
ATATGTACCTTGCTTTCNAATACGCTCTCTAGATAAAGCCTGACCTTCAGTTTTCTCTGCAGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGNGCGTGCGTGCGTGTGTGTGTGTGCAGTTGTT
CTTCCCTTTTGCTCTTATGAAGCTGTTATGCAGAGAAAACTCTTGTCATGTAAATCTCATCTTT
AGCTGTCTGTCCTTTCCTTTGGGTGGCTAGCTGTTCGGGTAGATATAGTATTTGCTCTTATTG
CTTGAAGCTGNGGGGACGGAGGTTTTCTATATGAAGAATGATTTTAAATAAATTCATTATTCA
GCTCAGTAAAGTTTTATTAAACCCTTGGGGCATGTTGGAGGGCGTCGCGTGAACTGAAGGG
CANACCCACATATCTCAACCATGTATACTTATTAANAAATTGATGTGCCTTGCTGCTTAAACT
GCTGTGCANGCAGGTGCCAAAATGTAACCGATCACTTTAATGTTTTATGA

672U= GCCTGACCTTCAGTTTTCTC
672L= GAACAGCTAGCCACCCAAAG

GM227
TTTGAANTCCCTTTGAACGNGGCNGCGGCCGNTCTAGAACTAGTGGATCCCCCCCCATTTAAG
ATCAGTGTCCTTAATAACCACACCCAAGACCTCACACCCAATGAGATGATGAGGGGAGGtcAC

Figure 11 AA

AGATCACATCAGATTAGTGCAGCTTGTTTTGCTTTGGCGGTTGAAGCCCCCATGCCTCACATG
CGCAAACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACGTGCACAGACACTACCAGcTTGTCACTGcTGCCCTCTTAATGTGA
AAGCAAGTATATTTTGACAGATAACAAATGAGTGGCAGGAGAACACAGTGGGCTGCAGGAAT
TCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTCCCAGCTTTTGTTCCC
TTTAGTGAGGGGTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGNTTCCTGTGGGAAATT
GGTATCCGNTNACAATTCACACAACATACNAGCCGGAAGCATAAAGTGTAAAGNCTGGGGTG
CCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTACTGGCCGNTTTCCAGTCGGGAAA
CTGTCGTGCCAGCTGCATTAATGAATCGGGCAACNCGCGGTGAGAGGCCGTTTGCGTATTGGG
CGCTNTTTCGCTTTCTTCGGTTANTGGCTTGATTGNCTNGNAAGTTCGGGTNCGGGAGNGGTN
TANNTTACTNAAAGGCGNAATCGGTTTTNT

227U=ATGAGATGATGAGGGGAGG
227L=GCAGTGACAAGCTGGTAGTGT

GM76
TTGANNTNTGAAGCCTTTNGAATACCCCTTCCCNTTNTGGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCNTTCACACACACATACAGAGACAGTGTGNTAGCGGAAGTC
CAAAGTGACCAAAGTGTTCAGGGAGAGACGGTGATGAAGCACACACAGCTAAGCTGCTACA
GTTATAGTTGGATGCTCTGACCACATACTGACTAGATAGACTGACCACAGTTCACCACATCA
CTGCTAAAAAGAAAGACTATGAGGTCAGGTGATAATCACTACGAACAGTTACACACACTTCA
TCACTTCATCCACACACGCGCGCACACACACACACACACACACACACACACACAGGTTGGCATT
ACCTTAAGTTTAGCTGTGTTAGGCTGTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCG
CGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTT
TACAACGTCGTGACTGGGAAAACCCTTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCC
CCCTTTCGCCAGCTNGGCGTAATAGCGAAGANGCCCCACCCNN

76U=CGGTGATGAAGCACAAC
76L=AGCTAAACTTAAGGTAATGCC

GM336
ACGCTCGCACCAGGAAGCAACTCAATGGCTCCTTTTGATGCTCTTTAATG
ATATACAGTATTTCATTACCACTCTCACCACACACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACAACTA
TTATAAGAAAGACCATCACAAATGGTATACACATCCATGTAACGTCAATA
AAAAACACATTTTGTTATTTATAGCCACAGCCGTTTCACACACAAGCACA
TAGTGT

336U=GCACCAGGAAGCAACTCA
336L=CGGCTGTGGCTATAAATAACA

GM141
TNNTNTTTTGGACAACTNANCTCTTGGANACCCNGCCCCNTNTCGAGGTCGACGGTATCGAT
AAGCTTGATATCGAATTCCTGCAGCCCACcTCTTAAGTTGCACTAGCTCAGGGTTCTTCTCTG
CCACAGAGATGACATTCCATTGTTCTGTCCACTGAGACAAAGTTAAAATTACCGGTAATAATT
AGTGTAAATGCTGATTAAGCAGTCACAGTATTGAGATCCAAATCACAAACACACAGGCACAC
ACGTGCACACATGCGAACACACACACACACACACACACACACACACACACACACACATACACATAC
ACATACACACACATACAGCAGATTTTCTGCAAATATTCTGGTTCTTCATTGGAGATTCTTGAG
ATTAGAAATGTAAAATACATAATTTAACTCTTCAAGTTATTTAAAGAGGCTTTCTTTTTCCCCA

Figure 11 BB

CAGCTTTCAGTTTGATCTCTTGCGTTTTAGACATGAAGGCGCCCGTTGTCACCCTGTTGCAA
CTGTTTAGGTTCCTCCCGGCTTTCACACACGCCCTCTCTCTTTGGTTGGTCTGAACTGTGCC
CCTGTGGGCTGCATTGGCAGAAAGGAGTTTTCTGGGGGCATTTGCTN

141U=TCTGCCACAGAGATGACATTC
141L=AGCTGTGGGGAAAAAGAAAG

GM570

GM389
AAATTAACTCTCCCAATTCTGCCAAGCAGAGTGGTCAAATATCAGACTCA
GTTTTATTGTCATTCAACAATTTGACATGATATGAATGAAACACAGTTAC
TTAGGTCTTGGCATTGCATCATGCTACCAAACAACAAGTGAAACAGTAGG
AAGAATAAATAATTACCAAAAGAAAGTAAGAAAATATGCAGGTGTAATAG
GTGCAACTTGATAAGCAAATATCAAATATCAAAAAAAGTTGCTCACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACGGCTCACAAAATTTCAAAATCCCTGGTAGCCCTTTG
GGCAGGCACGCTTCAGTTTTTGGTAGCCCGAATTAAAAAGAGAACAATTT
TTTTACTGATGTCTTGTTTCCTTTACAATATTGN

389U=GTTACTTAGGTCTTGGCATTG
389L=GCTACCAGGGATTTTGAA

GM318
TTTTTGGGCAGCAACAGGACGTGAACAGACGTATATCAGTCAACTGGAGG
CTACCAGTCCAAAGCTGTGGAACAATAAACATAACAGAGCGAATGCACTC
ACACACACACACACACACACACACACACACACACACACACACACACACAGAAGGGG
AGACAATGTTGTTTTCCATGGAAACATCTCTTTGCTGTTGCAAGGACTGC
TGCATACTTTATGTCACACATGACACAGACCCTGACCACTCTTACAGTGT
TAGTAAACATACAGAAATACCATATTTGTGCTTCATGTTGTCTCTGCTTT
ACACCTGTAACCACATGCACATGGTGCATTAATTGTGCTACACTAAAGAT
GCAAATTTGACCTTTTTCCACCAACGCTGCACCACTGCTGGTCCCGTGTG
GAAAAGGTATTGAATGAAGGCAGAGGGGGAAATTATAATTCTGGCAGAGC
CCTCTTCTGCTTATAGCATCTCTGNCATTCATTCCTCCTCATTCTTCCTT
CTNCAGCTTAAATGCCTTTCTTCTTCTGCTATGGCTTTTNCAACACCCAC
CCAACACT

318U=TAAACATAACAGAGCGAATGCTA
318L=CGTTGGTGGAAAAAGGTC

GM387
TGATTGCACTGCTGGATGTTGGTATCCTTGCTGTGATACTGTAAGTCATA
TGAGGGTGGTCTCTCTCTCTCTGATATTTGCTATAACAGACAAACTATGA
CCCCCCTTGTTTGTGTTTTTGAAGCCAGTGATTTAATGACCTCCTGCTAT
CTAGACTGAAAAGAGTGAAAGTTATTCTGGACAAAAGTGTAAACTTGATT
AGAAATTTTTTTCAACTGTCTTATAATTATTGGCTCACTCAATTTGTATT
TTATTTTATTTGTATTATTTGTTGCAGACATAAAACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACTATTGTTTCT
CTAATGGCAATTAGGCAAAGGTTCATCTGGTAGGGTAGGTTGAAATTAAN

Figure 11 CC

AAGTGGGGGGATCCACTNNGTCTAGAGCGGCCGCCACCGCGGTGGGAGCTCCAATTCGCC
CTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTT
TACAACGTCGNGACTGGGGAAAN

387U=CCCCTTGTTTGTGTTTTTGA
387L=CCAGATGAACCTTTGCCTAAT

GM75
NNTTTGAAGCCTTTGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCACAAC
AGCTGGTAACAGACACAGAACAGAACTGAGCTGTCACATCTACACTGCAGAGCTGACACAC
ACACACACACACACACGATAGTGCTGAAACTTTAATACAAACACATACACACACATGCTGAC
ATACATATACCAGCAACTGCACTAATTCTCTCTCTCTCACGCACACACACACACACACACCA
GTATACATATGAGCAATCCAGTCTTGATCTATGAGCTGTGGAAAAGCCAGCTGATATTTTTCA
TGTGTGTTCCCTTTATCAGAGCTCAGTTCTGCAGGTCTTCTCTCTGATTCTTATCTGTGGCAG
ATGAAGCAAGAACTTCCTGGATCCCACAGGGGGCTGCAGGAATTCGATATCAAGCTTATCG
ATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGNTCCCTTTAGTGAGGGTTAA
TTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGGTATCCGCTCACA
ATTCCACACAAT

75U=ACCAGCAACTGCACTAATTCT
75L=CAGCTGGCTTTTCCACA

GM281
TNTNTNNTTGATTNGAATCCTTGGANCTCCCCGCGGTNGCGGCCGCTCTAGAACTAGTGGATC
CCCCCCCTCACTGCTTCCCCCAAGCCATCAGACTCCTGAACACTCGGTGACTGGACTGACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACCTTCA
TACATCAAGTAACTTTTTGCACAATGCTCAGTCTTTTGCACAACCCACCGTCATTGTTGCACTT
TTCTATTGCACTGTTGTGTCTTGTGTCTGTATCGTTCTGTTCTGTGGTGTCTTTGTTTCGTTTTTT
TGCAATTTTTGCACACTTGCACTTTATGTAGTCCTGTGATGATTGTCTGTTATATGTCATAAGT
AGCACCATGGTCTTGGAGCAACGTTGTCTCGATTCACTGTGTGCTGTGGGCTGCAGGAATTCG
ATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTT
TAGTGAGGGTTAATTGCGCGCTTNGGCGTAATCATGGTCATAGCTGGTTTCCTGTGTGAAATT
GNTATCCCGCTCACAATTCCNT

281U=CCCCAAGCCATCAGACT
281L=AAAACGAAACAAAGACACCAC

GM161
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TGACAAAAGACAGGATCAGTCATTCTCACACACACACACACACACACACACACACACACACACA
AACCTGTAATTGCCACTAATATTAACACTCGGCTCAATTTTAATTGTATTAGAAGAGACAGCA
TGTGCATGGAGCTGTTTGCTTCTCGTTTCCATGTTAATGAGCTGATGGCTGCAATTAAACTGT
GATCCTGTTAGACTTCGATTCCAAGGGAGGAGACAGGAGGAGGGGAAAGTGAGGGAGGAG
GAGGTGATTAAGAGAGGAATGAAGAGGGGAAATAAAGAGGAAAGAAAAGGGGGCTGCAGG
AATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTT
GTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGNTTCCTGTG
TGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAAGTGTAAAC
NTNGGGTGCTAATGAGTGAGCTACTCCATTANTTGCGTTCGCTCCN

Figure 11 DD

161U=ATGACAAAAGACAGGATCAGT
161L=TCCCCTCTTCATTCCTCT

GM26
TTGTTCCTTCCTTGCCNCCNTTTGTTGNGGACCTNCTAGAACTAGTGGAT
CCCCCCAGATGACATATTTTTNAGCTGCCAATCACTCATATNGGNGGNAC
AGAAACTCCAGTGCANGGGCACAAACACACAATCTCTCAATCATATCTTT
GCATGCAAACTTTCAGTCACTGTCTTAATCTTTGGCTGGCACACACACAG
ACACACACACACACACACACACACGCACGTACATAACCAAAAAAAATAAA
TGCAAAGTCGATACTGTCAAGTAAAAAATTGCAGTGCAGNGCAGCATTCA
ACAGGTGACTCAACAGAAGGTGGTCAAAATCTTAAAACCAAACATGCAGT
CATCACAGATAAAATGAAAATAACTATACAGAACAGACTTTCTTCCATTT
TACTGTGGGCTGCAGGAATTTCNATATCAAGCTTATTGATACCGTCGANC
TNTAGGGGGGGCCCCGGTNCCCAGTTTTNTGNTCCCTTTTAGTGANGGTT
AATTGCGCGCTTTGGCGNTATTCATTG

26U=TGCAAACTTTCAGTCACTGTC
26L=GATTTTGACCACCTTCTGTTG

GM607
AGCCGATGCCACATCTGTTTGTCATGTTAGCACTTAAGCGCCTGCAGGAGCCATGATGCTAA
GTGGAGACAGAGTCCTCTCTCCCACTCTCTCCATCCACCCTTTCTCCTAATTACATTTGTTCA
TTAATCCATTTTCTGCCCACTTCTCTTTCTTGTTTATGTTCTTGCATCAGTGGGCTTTTGCCTC
CTCCGACCAGCAGACAGTGACCTTTAAGGAGATGCCAGAAGACTCTGTAAGACAATGTTAC
CCCTTCACCCTCTCGCTAAATGCACACATACACACACACACACACACACACACACACACACA
CACACACACACACACACACCCTTACCCAGTCCCATCCTT

607U=CCGACCAGCAGACAGTGAC
607L=AAGGATGGGACTGGGTAAGG

GM565
GGCATAGAAAATGTGGACAGACAGAGTGTTGTTTNTCCACGGAGCTGGAGAAGTGTAACAA
TCATAAAGAGTGTGCAGTTCATAAAAGCACAGTGCAGAGAATCGCCTTTCATAGAGTTTGGT
AGACAAAAAAATATGTGAACGAATAAAAATATTAGTGTAATACAACTTAAGAGACACCTTAGT
TAGTGGTTGGATGCCTATGATGTGTATACATTATATATACTTTAACACCATCCCTCACCACCA
CCACCACCACACACACACACACACACACACAACAAAATAAAATAAAAAAACAGAAAAAGATATTT
TTAACTAGCTAACAGCCTTAGAGTATCCCCAAGCTGAACACAGAGGCTACTTCGTCCTGTAT
GTGTTTTCCTGGAACCAAAATAATAAAAAAGGAGGAAGTGATTCATGCTGAATAAGACAAAT
GGCAAAGCAGCTACTGTGCATCACTATTTCACTGGTCAGTTCCTGCT

565U=GGTTGGATGCCTATGATGTG
565L=AGCCTCTGTGTTCAGCTTGG

GM643
ACTTGGACAACAATGGGATGAAATGCTGGTGTTGTTTAAAGTTTACAGAGCATTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTACAGTGGTTTGGCTGGAGGAGAGAGAAGAAGCA
GGGGGTGTAAAGAAGTGAGTCAGGAAATGGTGAAATGTGAGGAGATGGAAGACTTGAGGG
GGGACAGAAAAAGAAAGAGGAGCGCATACTGTAAACAGAAACGTGTCAGGGCTGATCTTCA
TCAGCAGATCCCACTCTGACTGAGGACTTCAGGTGATTGTCTCAGAGGAAACCCTTCATGCA
GTCTGATTGAGGAGTTGCATAATTAGGCTTGAGGGTTTCTTTAAAGATGAATTA

Figure 11 EE

643U=TTGGACAACAATGGGATGAA
643L=AAGATCAGCCCTGACACGTT

GM361
TTNGTTTGACAACCGNTGGGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTG
ATATCGAATTCCTGCAGCCCACTCAATGAATTAAATCTGAGCTACTTTCAATGTATCATTGAA
TCTGAATAATCTTTATTATCACTATACACACAGAGCAATGCAACATCACAAAACCGGTTTCTT
GGAGTTTTCCTTTTTTTTAACTTCTTTCTCGTAACAGTGTGTATATGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGtGCGTGTGtGCGTGTGCATTTACaCGGAAATGTCTGGAAAG
GTCATAGCATCCAGTGAAAATTCTAGGGGAACGAGGCAGCACAGAGGTTACACTGTCACCT
CACAGCATGAAGTTCCTGATTCAAAACCCAGCTGGGAACTTTCCATGTTCTTCCTGTGGGGG
ATCCACTAGTTCTAGAGCGGNCGCCACCGCGGNGGAGCTCCAATTCGCCCTATAGTGAGTC
GTATTACGCGCGCTCACTGGCCCGNGCGNTTNAACAACCTTCGTNGACNTGGGGAAAAACC
CCNGGGCGGGTTCCCCCCNACCTTAAAANCCCCNNTTNGCAGCNAAAATTCCCCCCTTTTTT
CCCCCCAGTNTTGGCGTNTATNAACCAAAANANG

361U=CCGGTTTCTTGGAGTTTTC
361L=CCCCTAGAATTTTCACTGGAT

GM442
TTTAAANCCCTTGGACCGTCCCCACCCTNNAGGTCGACGGTATCGATAAGCTTGATATCGAA
TTCCTGCAGCCCACTGATGTNTTNTTTTTCTATACTGTTGATTAACTATGGTGACCCTTTGAG
GTTGGGGACACCTGGAATAACTTGAATTATTCCTTATCATTGATAATGCTTCAAGTNCACGGG
TTACTGAAGAGNGGGAAATCTAACAGCATACATCAGGTGAAAGTCACACAACCTTGAGTCAA
AAAAACATTCACTGCTTGAAAAGTTAAAGAGTCTGTTTCACAGTAGGACCATGGACAGGACA
AAAGCACTACACATCACTGCACACGCACACACACACACACACACACACACACACGGAGCAN
NGTAAAAGGAAACTAACTACATGTGGGGGATCCACTAGTTCTAGAGCGGNCGCCACCGCGG
TGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTNACTGGCCGTCGTTTTACA
ACGTCNTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGNCTTGCAGNACATCCCCCTT
TCGCCAGCTTGGGCGTAATAGCCGAANAGGCCCCGNANCGATTCGGNCTTTCCAAACAGTT
GCGCCACCTGGATGNCCNATGGGAATTGTAAGCCNTAATATTTTTGNTAAATTC

442U=AGTTTCCTTTTACACTGCTCC
442L=CAGCATACATCAGGTGAAAGT

GM114
GGNNGNNGNANNTTATNTCTNCTAGNAANTTNAGNNATNCTCCCCCCTTTTGAGGNCGACC
NTATCGATAAGCTTGATATCGAATTCCTGCAGCCCACATTAACAGAACAGGACACACAAGGG
TGCAGGATCTTTTCATCTCCACATTATCAGTGAGATTACTAATGAGAGCAGTTGTATGTGCTT
ATAACACCATCACTTTCAGCCTATTGAGCCTTGTGAGCACACAGCCAGTTCTCTGCAACTGT
GGGAGTTATCAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAATTAGTGTTGAGGAAGAG
GGATAGTGGGGTTAAACTAAACACTATGGAGAACCATGACATCTGGGAGAAAGGATGAGGG
AAGGCTTTTCTCTCTGCACAGTCATGCACAGAAACAGAGACTTGGCTCTTATTCTTTGCCCCT
TTCTTTCCCATTTCATCACCTTTTTAGAGCTATAGTGCACAGAGGGTGGAGAGGACCCCTCT
GCTGGGACAAAAGGCATCTCATCTTAAGGATGAGGGGGGTGGAATGAATATGCATTGGAAA
TGGGGGGGAATTGAAATGGAAATACNGGGAAGTAANTNNCCATGN

114U=GCCTATTGAGCCTTGTGAGA
114L=GTTTAACCCCACTATCCCTTC

Figure 11 FF

GM165
TTGNTNTCCNNTGTGATCTTCNNTGGAAACNCCCGCCCCCTTTCGAGGTCGACNGTATCGAT
AAGCTTGATATCGAATTCCTGCAGCCCCCTcTGGGAAGTTTCTCCGCATTCCTGCAATaGATT
CAGACATACACACCTAAAAATTAATAGACAGGAAGCTGGAAGGAACCTGAAGCTGAGGCTG
GGTAAGTGTGTGCAGGCTGAGAGTGTGCTGCTCTTTTTCACAACAGCTCATCAGTTGTTGCC
TTCATGTCCACTGTTGTGTGTGTGTGTGTGTGTGTGCTGAAACAGGAGTTTGGAGGGGCTAC
TGCTGTAGGACTGGAGACCAGAACCTCATCATCCCCGCCCTGCCAGGTGCTGTATTTTCCT
GACTCATCCTCTGTTTCATCGCTGAATGCTTCTCTGTCACTTTCCCCGCCTGCACAAACATAA
CTCAGTCACAGGAAGTGCTCTACCGCTTTCAGTTACGTCCTCACTAAAGCGTATCTCTTGGT
CATTGTGTCTTCAAGTGCAGATACAGTGAAAACAGAGGAAGCTATTTTTCTTTAAGTGTTGTT
AGAGCTGAAATAACCACAGCTTCCACCCAAGAAAATGCAGCATTTGTAGGGAAGGTTCGTAT
TTTAAAGTGTTCA

165U=CTCATCAGTTGTTGCCTTCAT
165L=CGGTAGAGCACTTCCTGTG

GM189
TTTGAAACCCTTGGACCGGCCCCCCCCTCNAGGTCGACGGTATCGATAAGCTTGATATCGA
ATTCCTGCAGCCCACACACAACAAGGGATTTTCTGAGGTTTGAATTCAATTGTAAACAGTAAA
ACAAGCTTCACAGGATCATAAGGAGCAACATAACAGAAGGAGCAGGTGTGCATAAAACACA
AAGGATCACTCTCACCATGTTCCCACTGTGGAGGCTTGCTTTCTTAATGATATAATAATATAT
CATTAAGAATGCATATATATATATATACATATATATGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTAGAGAGAGAGAGAGAGAGATGCATTTAATACATATCTTAATATAGGAAAAGGAA
GTGAAATTTCAAGAGCACATCTGAGTTTTTCCACATGATAAAGAAATCTTTCAGCGTGACTTG
GGCTTAAAGTCTAAGAAATAAATGTGTAAAATTACAGAAAAAATTCTGGTAGCTCATTGTCTC
ATGGTCCTGtAATTTTCTGTTAATTTAGAAAATGGGGGGGATCCACTAGTTCTAGAGCGGCC
GNCACCGCGGTGGAGCTCAATTCGCCCCTATAGNGAGTCCGTATTACGCNCGCTNACTGGC
CCGNCGTTTTACAACCNTNNNNGACTGGGAAAACCCC

189U=GCAACATAACAGAAGGAGCAG
189L=CCCAAGTCACGCTGAAAG

GM488

GM513
CCTCCTACAATCCTAATCCCTGTTAATTACACTTCCTGCCCACCACAGACCTGAATAATAACC
CACCGCTCCTTATCAATATGGNAGCACTGGCTGCTATTACACTTTCTGCTCTGCATGATACTA
CCCCACATTGTAGTCCACACACACACGCACACACTCACACACACACACACACACACACACAC
ACACACACTTTTTTTGTTGGATGACCAATTCCAAAAAACACAGG

513U=ATTACACTTCCTGCCCACCA
513L=TTGGAATTGGTCATCCAACA

GM572

GM178
GNGNNTNGNNGANNTTNTATTGGATNATNNAAGATCTTTAATGNNTNACTCCGGNGGTTCNN
CNCTAGANCTAGTGGATCCCCCCCTGAGCCCTTGAGGCAATTTGCACTAAAACCCTGAAAG
AGTGGATATGCCtatCATGATAATCTTGAATGTGGGGCACCTGGAACTGTTGGCTGTGTGTGT

Figure 11 GG

GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTAGGGTGGTGGTTTTC
CAGTATGTTTAGCCTTTGGTTCCAGCTGGAAAGCATTAAAAAAATCTGACCCTNCATTGCACT
TACTTTGAAATTTGGTCCTCTATCTGTGTCAAGTTAAAATAAAAGCTTGGCAATAAATTGTCTC
AGACACTTCANAAGTAAATGTATGCAGACTGATGTTTTGACATGCAAATCCCCCTATTGTCCC
CAATGTTGNGTCAAAGCCCTTTTAACTTATAAGACCTGGGGGCTGCANGAATTCGATATCAA
GCTTATCGAAACCCGNNNACCTNAAGGGGGGCCCCGGTACCCAACTTTTGNTCCCTTTAAN
GNANGGGTTAAATTGCCCCCCTTNNNNTAAACANTGGNCAAAAAANNTNNTNCCNNNNNNA
AAAAAN

178U=TGGGGCACCTGGAACTG
178L=GCTGGAACCAAAGGCTAAACA

GM208
TTNTTTTNNTNCCTCGGNTTGCCCTTCGTNTACCCGGCCCCCNCTCGAGGTCGACGGTATC
GATAAGCTTGATATCGAATTCCTGCAGCCCCCACTCTAACTCAATTATTGCATCTTAGCTAGT
GTCCCAGTGAAACAGTGATTAATATTCATGCAGATTAACCAGGAAACAATTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTGTGTGTCTGTGTGTGTGTA
ATTCATAGGCATTTTGAGAGTGTATAGGGACTAGCTCACATTTGGAGCCAGCCTCAAGTGCT
GATTTGAAGATCTTCTGTTTGTGGCAGTTGCACATCGACTTTAATTTTCACCACTGGAGTCGC
TTGACCCAATGCAGAAGTGCTTTTGATCTGCCTTTCTAATGACTGGCAGTAGGTGAATCCTTT
TTTTTTTTTTATTTTGTTAACAAACTCAAATTGCATAGAAGTCTATGTAAAAACAACCGTTCTTT
GGTCTCACTAGTTTTATGNTATAACCCAAATAATGGTCATTTANNTAAGTTNTGATCNNAAAA
GNACATAAGATANTTNGGGNTTTTTAAN

208U=AGCTAGTGTCCCAGTGAAA
208L=ATTAGAAAGGCAGATCAAAAG

GM462
TGNNNTTTGAANNNCTNTGAATGGCCCTTNCCGCGGTGNCGGCCGCTCTAGAACTAGTGGA
TCCCCCACATGTAGTTAGTTTCCTTTTACACTGCTCCGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGCGTGTGCAGTGATGTGTAGTGCTTTTGTCCTGTCCATGGTCCTACTGTGAAACAGACTC
TTTAACTTTTCAAGCAGTGAATGTTTTTTTGACTCAAGGTTGTGTGACTTTCACCTGATGTATG
CTGTTAGATTTCCCACTCTTCAGTAACCCGTGGACTTGAAGCATTATCAATGATAAGGAATAA
TTCAAGTTATTCCAGGTGTCCCCAACCTCAAAGGGTCACTATAGTTAATCAACAGTATAGAAA
AAAAACACATCAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG
GGGGGGCCCGGTACCCAGCTTTTGNTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAA
TCATGGTCATAGCTGNTTCCTGTGTGAAAATGNTATCCGCTCACAATTNCACACACATACGA
ACCGGAAGCATAAAGTGTAAAACCTGGGGTGCCTAAAGAGGGAGCTAACTCACANTAAATG
CCGTTGCGCTCACTGGCCCNTTTTCANNCGGGAAANCTGTNGNGCCACTGCATTAATNAAT
CGGCCAACGCNCCGGGAAAAGCCGTTGCNTATTTGGGCGCTNTTCCNTTNCTTGGTAATGA
CTCNNTTNGCTTNGGCNGTTCGGNTTNGGNNAACCGGNATNAGNTTACTCAAAGGGGGGNA
N

462U=AGTTTCCTTTTACACTGCTCC
462L=TCCACGGGTTACTGAAGA

GM2
TNNNNCTNCGTNACCCCTTTGGAATACCCCGCCCCTTCTNGAGGTCGACGGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCCNATGACCACAGCGTGTGGATGAATTACCTCTAAATAT
TGCGGCTTATCCCTCTGTAAGTGACACTGGTGTTAGATTGCAAACTGACAGTCAGCTGCCAT

Figure 11 HH

AACTAAAGAGATTTTCTAAATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTTCTCGTGTGTGTGTGTGTGTGTGTGGCTGCTGAGCTGGAGTGATTATGG
GGTTTAGNTGNCCGTTTGCGTGGCTGNGGTGNTGACACACNTTGTNTACTATGTGATGTTCC
CGTTTAGGCAGNGTGGTAAAAGCGAGGTANCAAGAAATTCCTTGTCTGACATTTAATGGACT
GTAACCTACTCTATTTGACCGCTCACANGTTATTGAATCTCTGTCTTAAACATANGTTANTNG
GGNGGATCCACCTATNTCTANAAGCGGCCNCCACCTCNGTGGANCNCCNNTCCCCCTNTAG
TGAGTNGNATACNCCCNGCTNACTTGNCCCCTNNNTNC

2U=GCGGCTTATCCCTCTGTA
2L=TAAACCCCATAATCACTCCAG

YWT1_1

LG 10

GM459
GNAGNGNTGTGNNACTTATTNTNNNANAANAANTNANACTNAAGNCTCGCGGAGTTTGGCN
ATCTACCNCTAGTGGATCCCCCCCNGCCTTGGATCTGAgTAAACaaATGCCAATGTTGCACA
AACACACACAGNCACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACANNAAATCTGCATTTATTTGTCCCACAAGTGGAAACTCTGCATTGTCATTGCAAAA
AAGTGGACAGAGCACGGTATANAAAGTGCACTATACAAACAATNTGGAAACATATATATGGA
CATGAGTATNCAAAAATATNGGTGTATGTATACACACACACACACATATNTATCTATCTATCTA
TCTATCTATCTATNTGNGAGNATAACTAGANTTTATGCATANTATATAANGGGTGGNTATATA
AATATATAAATATATGANGGCTGTANGAATTCNATATAAACCNTATAGATACNGGGGAGNTCC
AGGGNNNANCTNNTGCNCNCTTTAGTGATGGTTAANTGAGCNGCTAACGAAATCNTGGNCA
TAATNGGGNGNCNTGNNTAAAAANNTNTATTCGGATTANCAATTNCACACAAANATNCCAAG
NCGGAATNTTAAAAGNGTNAAACCTTNGGG

459U=CGGCACATACATCTACTACCT
459L=TCACCATCAACGCTGAA

GM549

GM614
GAGAGAACAAGAGGCAGGTTAGCACCACGGACCCACACACACACACACACACACACACACA
CACACACACAGNGTTTTCATGTTTGTGGGGACATCTCATTGGCATAATGCTTTCCCT

614U=AAGAGGCAGGTTAGCACCAC
614L=AGGGAAAGCATTATGCCAAT

GM10
NNTTNNTTGNAGTNANCTCTTTGGATACCCGGCCCCCTCTCGAGGTCGACGGTATCGATAA
GCTTGATATCGAATTCCTGCAGCCCCNTCGAGGCTCGGAAACCTTTACTTCATTATACACGT
CCTTAGATGTGTTCATTTTAGACACACTGCATGTGGTGATTACGTGGTGATCAGGTGGAGCT
CGAAACAAGGAAAAAGATGTTATTTTGCTTAAATCTGAGAAAAAATGCATGGACCTTGGTTG
GGAATTATCTCCCAGATTGTTCTTGTTTCTTTCTTGGCTCTGCTTGCACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACAGGAAGTATCACATGTCTGGGT
GATAAATGTCACCCCTGAGGTGTCTGGCAGACGTATATCTGATAATATTTAATTGACGTATAG
AGTGCATGTCTCCACAACTGCAGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCG

Figure 11 II

GTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCCGTCGTTTTA
CAACGGTCGTNGACTGGGAAAACCCTG

10U=CTTGTTTCTTTCTTGGCTCT
10L=CTCAGGGGTGACATTTATCA

GM573

GM105
GNNNNGNNNNNTNNTTNNNTTNNNTTNAGNANATTTAANGNAACNCTCGCCTATTTTGGAAA
ACCGACCCGTATCGATAAGCTTGANATCGAATTCCTGCAGCCCNTTTGGCAGAGACACCAG
CACCAGTGGGGGGGTGTTCCTCAAGCTGCCCATGCCACCCAAACACACACACACACACACA
CACACACCCTCCTCTCACTTTTCATTTCTCTACATCTGTTTTTCCCCCAAATTTACTTCAAATA
AGAGCAAACGCCGGCTCTGGAACGCCTCCTATAAATCCGAGGAGCGTTACGAAGACGGGG
TTTAGGGGTCTGAGTTAAAATAACTGGCTGTCTAATCATCTGCACAACAATATTTGCTGTGAG
GCATTCTAAATAGATTATCGCTAGTCCATCTGTGTCATCATTGATTTATAAGGCATTAAGCTG
CTCGGGGAAGAGATAGGGGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGGCGGT
GGAGCTCCAATTCGCCCTATAGTGAGGTCCGTATTACGCGCGCTNACTGGCCCCGTCGTTT
TACAACGGTNNNGGACTGGGAAAACCCNGGGNGGTTACCCAACTTAATCGNCTTG

105U=GCAGAGACACCAGCACCAG
105L=TTATAGGAGGCGTTCCAGAGC

GM258
TTGGTTGTNANANCCCTTTGGAAAGCCCCCCCTCGAGGTCGACGGTATCGATNAGCTTGAT
ATCGAATTCCTGCAGCCCCCGAGCGGTTGATGGCGggGATCTCAGAGTAGACGTcAGAGGA
TTCTGGGtAATTTTNCAcCACCAGGTTACAGGTGTGATGAAGCAGAGACTGACGGTGGACCG
TGTCCTTCACCTCCACCACTTTCTCCAGGTAACTCAGCTCAAAGCCTTTAGCCTGCGCACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACTCACTCAGAGGACGACGTTCGATCTCCGCCTGAAATCTCTAATC
TTGACTCCTTATTTAGAGGAATAACAAACTGGGGGGGATCCACTAGTTCTAGAGCGGNCGC
CACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGT
CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCANCTTAATCGCCTTGCAGCAC
ATTCCCCTTTNGCCAGCTGGGCGTAAATNNCGAAGAAGGCCNNCACCGGATCGCCCTTTCN
AACAGTTTGCNCACNCTGAATGGCGAATGGGAAATTGTAAGCCGTTAATATTTTNNTAAAAAT
TCNCGTTTAAANTTTTTTGNTANAANCNGCTTCATTTTTTAACCCATTAGGCCNAAAATCGGG
NAAATTCCCTTTATAAATNAAAAAGGAATAGANCCGANATAANGGNTTGANGTGGTTGGTTC
NNNTTTGGANG

258U=CCTTCACCTCCACCACTTTCT
258L=AGATCGAACGTCGTCCTCTG

GM201
TNTATTTGNCTCNCNGAACTNCTTGGAAACCCCGCCCCNTTTNGAGGTCGACCGTATCGATA
AGCTTGATATCGAATTCCTGCAGCCCACNCTTGCCTATTCAGGCTCTTCTTTNGCTGTAACA
CCACCAACCCCCTCACACTGACACACACACACACACACACACACACTCCCTTCCTCGCTATCTG
GCAGTCTTGTTGCCTGGAGGGAGTTCATTCTGCCCTCCTTCTCTCCTCCTCTCCTCCACCTC
TTTCCTTGTGTATCGGCAGTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGGGGAGGGTGAG
AAAATGAGAGAGCGAGAGAGAGAGTGGCAGCAGTAGCGGAGGAAGCAGAGCTGTCTCTCT

Figure 11 JJ

TCTGATCATCTTTCTTGGATAGAGGGATAAAAGGCAGTCCTAGGAATCAGTCGTTGCTCTTG
TCTGCAGGATTTACCCAGCCTGAGTTTATTCTCCCTCCTTCCTCTTTTCACCTCTTCTTGACA
CTGGACCGCTAGCTTTTACATCTCTCTCTCCGGGGGGGGATCCACTAGTTCTAGAGCNGCC
GCCACCGNGGGGGGNGCTCCAATTCGCCTATAGGGNGTCCGNATTANCNCCCNC

201U=TATTCAGGCTCTTCTTTTGCT
201L=CAGAATGAACTCCCTCCAG

GM148
GNNNNNNGNNANGTATATTGTTATANGAGATCANANGNATACNCCCCGGTTTTGNGAAATAG
ACCTAGTGGATCCCCCCCAAGCTGGTGTCAGGCTGTGTGTTAATACTGAAGCCTGTCTGCC
CTTAGGaaGAATGGATAAGGAATAAAGGCAGACACATATTACTCTGCGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAGAGA
CAGAGTGTGTGTCCTGTGCACTGCAGTTCCTGATTTACATTAAATGATCATCACCCGAGCAG
AGAGAAGTTCTAGCACATTTTAAGCCCTCGACCGCACCCTGTTCTCANTAAATGCCTNCTTTA
CTGTCAGGTCTGCTCCTACATACCAAATAGAGCANAGAGATGAAGGGGGGCTGCANGAATT
CGATATCAAGCTTATCGATACCCGANCACCTNNANGGGGGGCNCCCNGNACCCAAATTTTT
TGGNNCCNTTTAANGNAAAGGGGNNNNAAATTNGNNNCCNCCNT

148U=TAAGGAATAAAGGCAGACACA
148L=GGTCGAGGGCTTAAAATG

GM41
GATNCCTTTGAATNCCCGNGGTGGCGGCCGCTCTAGAACTAGTGGATCCC
CCACAGCCAGGACCGATGTGAACTTTGCAATTCACTTTGACAATGTGTAT
GAAATTCTGAAATTAAGAAATATGATTTTTCACACACACACACACACACA
CACACACACACACACACACACACACACACACACACACAAAGAAAAAAAAACGTA
ATTTATGTTTGAAACCAGGAACTTTTTTTTAATGACTGGGAAAAATACTT
GTGGAAACCTGTAAAGTTCTGTAACTGTATCTCGTGTAGCTGCAACACCA
TCATGTGGACAAATCTGCCAAAGTTCTTGAACATGCTTTTTGTGCTAGTT
CTCAACATTTTAGATGTCTGACTGTGGGCTGCAGGAATTCGATATCAAGC
TTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTC
CCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGT
TTCCTGTGTGAAATTGTTATCCGCTCACAATTCACACAACATACGAGCCC
GGAAGCATAAAGTGTAAAGCCTGG

41U=CCAGGACCGATGTGAACTTTG
41L=TGGTGTTGCAGCTACACGAGA

GM314
ACCAGTGATAAAATGTTATTTTCCAAAGAGACAAGTAAGCCAAATTAATG
ATAATTTATTTATAAAACATCTCTAAGGTGGAAGTCATGTTAGAAGAAAG
GAATGGAGCACTGCTTCAGTGTAATACTGAGTGTGAATGTGCGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGCACAG
CATGAGTCACCCAGCCTGCCTGTGATTGGATGGTAGTTTATGGGTGAGGG
AGGAGAAAGAGAGCCTT

314U= TAAGGTGGAAGTCATGTTAGA
314L= CTCACCCATAAACTACCATC

Figure 11 KK

GM231
GNNNNNNNAGGGTNTNTTGNTNTTGGGNTAAANGGAATGCTCGCCGGTTCTNNNCTAGACC
TANTGGATCCCCCATctGTGTTTTAACCATAGATTATaCAAcACACATATACGCACACACACAca
cacaCACACACACACACACACACACACACACACACATATATATGTATATATATTCTTATTAGCGCC
AAAGTTGAGCATTTTAACAATGGAGTGCATGAGGATTGACTAAACTGCAGTTTTTGACATGAT
GGTTGATGAATCTGGACATGTTATGGTTAAATGTTCCATTCCCTACACTTTATAAGCAGAATG
TAAGGAGAGATGAGGTCTGAGTTTTTAACCAAACCTTTGAAAAATGCATGTGCTATATTTACT
GcTTCAGTTTTAGGCGATAAGTCAGAGATGGTGCTCTTGAATTTATGGGGGTAAGGAATAAC
CAACATGGTTGGTGCACCCGGGTNGGTCAAACCTTTTNTTTTGAAAACTGGGCANCCAATTT
TTTTNAAAGGGCCCNGNNAAAANTTGCCCCAAGGGNAAANTTTNGGGGTTCNAAANGNGNN
NTTTNGCTCCNCCCANNNGNNGNGNAAAAANNNNNNTGNAAAAAAANGGNNNNNNNAAANN
NNNNNNNNNNNNNNNNAAAAANAANNCNTTTNNNNGGGGGGNCA

231U=CATCTGTGTTTTAACCATAGA
231L=TTGGCGCTAATAAGAATA

GM575

GM633
TGGTGTCCCAAGAAAACCAGGACACCGCCACACACACACACACACACACACACACACACAC
ACACACACACACACACACACACAAACCTAAAAGGGAAACAAGGGACACAAGCACAATGCATAA
CCCTGGCTGGGGACTGCCAGCACAAGATAACCCCAGAAAATGTTTATCAAGCACATGAGTC
CTGGGTCCC

633U=GTGTCCCAAGAAAACCAGGA
633L=GACCCAGGACTCATGTGCTT

LG 11

GM70
CTNTGANTNCTTTGGCCTTTCCANACNCCTTTCGGGGTTTTGGAGNCCGACNGTATCGATAA
GCTTGATATCGAATTCCTGCAGNCCCTTTTTCTCCCCGAGAGACTGCACACAACATTAAAGC
CTAGTGTTGTGTGTAAATGTGGTTTGCACAAATCACATCCCTGTGCCAGAATCCATACGTCC
AGTCAAGCACAGTCAGAACGAACACACACACACACACACACACACACACACACACACACAC
ACACACACACTCCCAGACAATGCTCTCTGTCATCCTACCTCAGGGCTCCATCTCTCATTTAC
CCTGTTTGCCATGGCAACATGGTTTGGGGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCAC
CGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGGTCG
TTTTACAACGTCGTGACTGGGAAAACCCTNGGCGTTACCCAACTTAATCGCCTTGCAGCACA
TCCCCCTTTCGCCAGCTGGCGTAATAGCCGAAGAGGCCCGCACCGATCGGCCTTTCCAAAC
AAGTTGCGCAACCTGGAATGGCNAATGGGAAATTGTNAAGCGTTAATTATTTTTGNTNAA

70U=CCCTGTGCCAGAATCCAT
70L=GGCAAACAGGGTAAATGAGAG

GM367
CTTTGANACCGTTGGGTACCGCGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATAT
CGAATTCCTGCAGCCCCCAGCTTACCTCCCCATTGACTGGAGCTGAGAGACATTTTCAAAAG
TTAAAAGACAGAGAAGGAAATGCAGGGTCACCGGGCTGAGGAGGGTCGCTCCCCCCTAAC
GCTACACAGGAAACGGGGTTAGAAACACATTTAGCCATAAATGACAGGTAACCACTTCCTGA

Figure 11 LL

TCCCCCCCTTGACATCCACAACAGCTCCCGTAAGTGTTGACTGACAGCATCCCCCTTTATTC
CATTTTTCTGCTCATAACAAGGCAGTGATTGATGACTGTTTGTCCTCGTGTGCCATTTTTCTG
TATATTCACATTTTAGCCAACACACACACACACACGCACACACACACACACACACACACACA
CACACACACAGCTCTGGCTCATTTACAGGGCATCTGTGAAGGTTGAAACCTCCTCTTAGCAA
GTCAAGTGAGATCATTCTCCTACCACCCCTCCCTCTTGCCTACCCACATACAAAAAATACACA
CATGCACACACGCACAGTTTTGCTCAACCCATCAAAAAGAGTCGCA

367U=ATCCCCCTTTATTCCATTTTT
367L=GGAGGGGTGGTAGGAGAA

GM85
GGNNNGNNGNANTTATTTTTNTNANNNATNTNAANCNNAGCNCCCNCGTTGGNNGCCGCTC
TAGAACTAGTGGATCCCCCAAACACCTAAATGCATTATCACTATTAATAAATGCGTCAANGCA
GATGCTTGTTATATGATTATGATGCAATAGCAATAACAAAATAATGAAACTAGAAATAGTAAAA
TGAAATAATAAAAATGGCAGAAAAATAACACCTCAATTCCTCACACTTTCTAAATCCATGTCC
AGTTGACTGAATTAATACCTTTATGCCAGGTGGATTGCAGTCAAGTTGCAGATGATCTGATT
GCATCTGACAGATGATCCATGAAAACGATGCACCTGAGATCAGTTTTAAGTGTCATTGCAAA
ATGTGTCTATACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACGGGTGCTAGGCTAGACCCCTCATGCTAACCAAGCCTACCACAG
CCATGAGCGACAGANATAAATATGAAGACATACCGGCTTGGACATCGTCTGG

85U=CATGAAAACGATGCACCTG
85L=TAGCATGAGGGGTCTAGCCTA

GM276
GNNNNNNGNNANNTNTNTTGNNCNANGGGAGTTTGATGCACTTCNCGGTGNCTNCCGCTCT
AGAACTAGTGGATCCCCCATCGCAGGAGGCTTTACCACATGTTTAGATCTGAACAGTGCACT
GTGAGATCAaaCACACACCAGGTGCTCTCATGTAATCACATCTGTTTCAAATGTAGTCTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTCCAGGACACCATGTTCAAGAGCATCATATCGTAT
GTCACTACATCAACACATAATTAGACACAGATCTTAGTCGCCCTGAAGAGTCGGGGTGACAG
AGACGCAACTTGACCAAAATCACCCACTCACACTCTCAGTGCAGAACATGATATTAGAAGCA
GCCCTGCTGTCACACTGCTGGGAGTTGTAGATGAGACAAGCTAAGATGATGGAAGGTGGGT
TTACATGCATCTCCTCATGCCAGTAGCTTCTCTGGGTTCTTGCAGAGGGTTTGCAGCANGCT
TCTTTGGAAGTTTTCTTCAGGTATTTCANGAACCAGGAACTCNGCAGTAGATCAAATTTGCNG
TAAACAATTAAACATAACTGCACAGGTGGCTGGACCCCANTGGATGCTGCACATACTGTNAA
ACTCTACTTTTT

276U=CGCAGGAGGCTTTACCACA
276L=TCAAGTTGCGTCTCTGTCACC

GM40
TNTNTCTTTTGATAAGTAGATCCNNTTGGNACCGCCCTNGCGGTTCGCTCTAGAACTNGTGGA
TCCCCCAAAGCAGCTTAAAGCAACACGGGCTCGCNGTCAGAGCATAACTAGTGTCATAAAAT
TCAAGTAACTGCTAATTGCTGCTCTCTATACAAAAGTGGATTCAGTTAACAGCCACAACTGAA
AAACTGAAATAGCGTCCAGGAAAATGAAAAATCTCACTAAACTCATCTTTAATATTTCAATTT
ATTTTCTCATAGTCGGGAAGACATGCTGTAATACGCACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACGTATAGAATTTCCTGTCATGTTGCC
CAATTCACTGCTTTTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG
GGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATC
ATGGGCATAGCTGNTTCCTGTGTGAAATTGGTATCCGNTCACAATTTCACACAACATACGAGC
CGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTNGAGCTAN

Figure 11 MM

40U=GCCACAACTGAAAAACTGAAA
40L=GGGCAACATGACAGGAAA

GM30
TTTTGACTCNNAGCCCTTTGGAATACCCGGCCCCTTCTNGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCATTTTATATCAAGATCTAAAGTATCACATNTAGTGGAATTTT
CATTAACTCACCAGAATAAACAAAGTTCAAAAGTAGCAGAGGAAGGAGACAGCGCAATGTTA
AGAAATTCATCTTAAAATCTATATCCACTCTGTAACACACAAGACGTCACTCTATGGGTCCCA
TATATAGTCCCTGAAGGGCTCCTGTGTGTGTGACTGCGTGTGTGTGTGTGTGTGTGTGTGTG
TGCGCGCTAATAAAAACTGCTCAGCAGAAATGAGCATCAGCCTCATCCTGTAATTAGACCTC
TCTGCTTTGTAACAGCTTTTTTTTGAATGGTTGAGTTAGAAGGGCAGTTTTTGCGGCTTCCTG
ATTGGAAGTAGTGATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATAATATA
TTAAATATTAATATACTGTATATTATATTAAAGATGTCATTAAAAAATACAATCCAAACATTATG
GAACGACCCCATTACATTCAGGGGG

30U=AGACAGCGCAATGTTAAGAAA
30L=AGGATGAGGCTGATGCTC

GM658
TGTGCCATCCTCTACAGCGAGACAATTTCACAGTGTCCAAAGCCGATTCTCTGCGCTTGTTA
ATTGAATCGGATTTCTTATAGTTTAAAATCCACACACACACACACACACACACACACACACAC
ACACACACACACACAGACTCATGTAGCTACAGCCCAAACTGTATAAGGGGTTTATCTAGCTC
TGTAAAGCCAAAGCAGGAGATATAAAGACACACACAGAGCCACAGAGAGTATTTTACCGGC
GTGTTTGAACGTTTCCAAATCTCAGAATAAAATGTCTTCACCTGCTGAGGTGTGTGTGGCTG
TCTCAGTGTGTGGGA

658U=TGCGCTTGTTAATTGAATCG
658L=TCCTGCTTTGGCTTTACAGA

GM665
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AAGGGATTCAAGGAAAGAAGGAAAAGTGAAAAGGGGGGGTTATGACTGAAGGAGATACACAG
AACCCATATATCCTGCTGTGTTTGTGTGCACAGAGATGCGTGTGTGTGTGTGTGTGTGTGTG
CGTGCACAAGTGTGTGTGTGTGAGTGAGAAGTCAAGCAGAACCTAACAAACACTGAATATG
GATGAGGA

665U=TAGTTGGTCCCTGGTTGCTT
665L=CAGTGTTTGTTAGGTTCTGCTTG

GM366
TGNGTTNNNCTCNNGATTCCTTGNGTACCGCGCCCCCCNTCGAGGTCGACGGTATCGATAA
GCTTGATATCGAATTCCTGCAGCCCCCTGTCTTCATGGCACACACACACACAGATAATGTGC
CCTTTACTGCAAGATGTCAAATGCTAAAGTTCCTCCTTAAACAGATATTACAGGAAAAAGAGT
TTGTATTTTGTTGTAAGTTAACGGTTGTCACACAATCAGCTTATAAAAGTGAACACTATTCCTC
ACTCTCACACGCACACACAGGGCAGCACAAATGAACAACTGTACGGTGCAGGATTATTACA
GTATAAGTTTTAGAAGCGATGACTGTGACATTCCTCCTCACTGCTGAGTTCATGACTAAGAC
GGATTAACTGGACTTCCATTTCTGCTTATCATATGGATGGGATTAACCTGTGCTATGGATCTC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACATATATACAGGAAC
AGCTCAGCACAGAACACACACTCACACTCCCTGTAGTAGGGGGGGATCCACTAGTTCTAGA

Figure 11 NN

GCGGCCGCCACCGcGGTGGAGCTTCAATTCGCCCTATAGTGAGGTCGTATTACGCGCGCTC
N

366U=GGATTAACCTGTGCTATGGA
366L=ACTACAGGGAGTGTGAGTGTG

GM339
GTTTGACAACNTTGGGNACCGCGCCCCCCNTCGAGGTCGACGGTATCGATAAGCTTGATAT
CGAATTCCTGCAGCCCAAATcAGTATGTGCATGTTGTATTGCACATGtGTATTAGCTCAGTCG
TGTCCTTGCCTCAGCCTCACCTCTTGGGGACAAAGGCTCTTTTCACCACACACTCTCTCTCT
TTCACTCCTCTTTTTCTGTCTCTCTCTCTCTCTCTTTCTCTCTCACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
GCACGTGCAGACCCATAAGGGCGTATTTGGAGAGCAAGTAGATCTTGTTACCTGTGATCTCT
CTCTCCCTCACACACATGCTCGCTAAGGGGGGGATCCACTAGTTCTAGAGCGGNCGCCACC
GCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTT
TTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCC
CCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC

339U=GCCTCAGCCTCACCTCTT
339L=CTCTCCAAATACGCCCTTATG

GM273
GTTTGAACCTTGGGTACCGNGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCG
AATTCCTGCAGCCCTACTGCGATCGACTACAGGCGGCAGTGCGACTTCAGCACCACGGACA
GTGCCATGAACACAGCAAGGCAAGGCACTGACTGCGATACCTGACTGTATCAAATTACTAAC
CAGCAGGGCATAAAAGAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTCCTAAAGGCAGTGACAGGAACAGGGAGAGAG
AAAGTAGTCCAGTATCACAGGCTGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGC
GGTGGAGCTCCAATTCNCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTA
CAACGTCNNGACTGGGAAAACCCTGGCGTTACCCAACTTAATTCGCCTTGCAGCACATCCC
CCTTTCNNCAGCTGGCGTNATANNGAANAGGCCCGCACCGATCGCCCTTTCCAACAGTTGC
NCAACCTNAATGGCCGAANGGAAATTTGTAAGCCTTNATATTTTGGTTAAAATTNN

273U=TACTAACCAGCAGGGCATAAA
273L=CTCTCCCTGTTCCTGTCACT

GM608
GAACAGAAGAACACACCCTGCCAGCAGAGAGCTCANGTTCCTACAGACTGACGCAGTGTCA
CTCATCCACTGTGCACACACACACACACCGACACACACCCAGCCTCCTTTTGCATGCCGTGT
TTCTAGAGATATGCATTCAACATTTCATGTACACACATAAACAAGTCGTTGACACACACACAC
ACACACACACACACTCTCATGTATACAGTGAGATACACTCTTTCTCTTTTGAATTAGTGATGA
GGGACTGAGCTGCTGAATTATGCAGGAGACACAAAGAGAGAAAGTTGCTGAAACTACACAT
GGTTTT

608U=TTTTGCATGCCGTGTTTCTA
608L=GCAGCTCAGTCCCTCATCAC

GM72
GNAGGGNNNNNTTNNAGCTTATCTNTGACTTGNNNAACNAAGNGAAAACCNCGCCCCTTTT
GGAGNATCGACCCGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCTTTATCTGAGGTT
GTTTGATGAAAATTGGGGAATATTGCTGGATTATTTGCTGATGCTTATCAAGAGAGGGTCAG

Figure 11 OO

GTTTTATGGAACAAAGAATATTGAAAATCTTAAAAGCTGTAACACTGCACCGAGTGTTTTTGG
TTCATTTCACCGTCTATAATTATAACACACCTCTTTCTGTATTCTTCCATCCTTGTCCGTAAGT
CTGTCTGCATTCTTACGTGTGTGTGTTTGTGTGTTTGTGTGTGTGTGTGTGTGTGTGNGC
AAATCTTTTTGTCTAGTGTTTGCAGTAATCTGAGTGTTTCAGAAGGTGGACCCAAGACTACAC
TCTATAAACATTCATAGCATCTATATCCTGTAAAAATATGCATATANACAAGTTACATATTAAC
ACCTGCAGTCACAATAGCTANCGATGGCTTTCGCTTTATTCCGGAATTTTCTGGAAATCTCTT
TTCCCCCCTACGGNGTAAAAAAATATTTGNCCNTAAGGNAAAANATNGGCCCCTNTTTTNTTA
CAAAAACCN

72U=CCGAGTGTTTTTGGTTCATT
72L=GTAGTCTTGGGTCCACCTTCT

GM90
GAATTCATTTGCATTCCCGCGGCGGTGGCCGNTCTAGAACTAGTGGATCC
CCCATCCAGATTGTGGCTGCAATGATCATTTTCACGCTCCCTTGCCTCAC
CTTGTCACCTGTTTCAATTAACATACATTTTGTGGATCAGGAAAGGTAAG
TCTACCAAATGCTGAGACCAGAAATGTAATCAGTGCCACAATAGTATATT
ACAGCATTTGTCACTGATAGTAACACATTCAAATACACACACACACACAC
ACACACACAAAATATTTGTTTGGTGAAATTTCACAGATGTATGCAATCAG
ATACATTCTCCAGTCCTGCAAAAAGCACAGTGTGTAACTTGTCATCTTAC
TCTCAGAGTCTGTCAACACGCTGAGTAAATAAAGTAATAAAACAACTGGG
CAACATGGTGTTGGATCTTTTGTGGGCTGCAGGAATTCGATATCAAGCTT
ATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCC
TTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTT
CCTGTGTGAAATTGGTATCCGCTCACAATTC

90U=ATGTAATCAGTGCCACAATAG
90L=TTACTCAGCGTGTTGACAG

GM353
GTNANTTNTTTCTNCNATGTCTCTTTGAAAGCCCCCCGCNTTGGCGGCCGCTCTAGAACTAG
TGGATCCCCCAAACAACACTAACAATGCAGCACACCAGGCTGGAAGGAAGCACaCAaTGAAT
ACCTCTGACTCCGGTCTGTGTTGGGCTCATAGGTCCGTTTGAGTTATCTGTAGGAGACATCC
CTGTCTTACACTGAACTTTACTAAGCTGCAGCTCTTTCCTCTCCACTCACTTTCCTTTTCCTCA
AGTCTCTCCTGACCCCACTGTCATTGTCGCCATTGATTTCCATCTACTTTGCTTTTGCTGAAT
CCCGCTGATGTCGCCAACGTCACTTCCATCTGCCTGTCTGTCCGTCAGGCTGCTGTCCCAC
GACACTGAAGCAGCTCGTGAGGGCGAGGAGGAAGAGAAGCAGAAAGACCGGGGGTTGGG
GTGAAAAGAGCTAGATTCATTTAGCACACACACACACACACACACACACACACACACACACA
CACACACACACACACTGACGTAATGAGTCTAATGATTTGCATCCAGTTGGAAGATCACAAAA
TTGCANGGGGCTTGCAGGAATTCGATATCAAGCTTTATCGATACCGNCGACCTNNAGGGGG
GGCCCCGGTACCCAAGCTTTTGNTCCCTTTTAGNGAGGGGC

353U=GGCGAGGAGGAAGAGA
353L=ACTGGATGCAAATCATTAGAC

GM237
TTTGAATGCCCTTCCANGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATT
CCTGCAGCCCACATTATCCAATGCACAGGTGTGGAAAAAGAGCAGCAATGTGCACAGACacT
GATGATGTTACACTGTCAGTAAAAACATCAGTAGGCTTAACTCTGAAGGAACACTGACACAG
CAAAATTGCATCAGTGTTAATCCCATCTTAATCACAACATAATACTAATGATGGTGCAGGCTT
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC

Figure 11 PP

ACACACACTCTTTTAATGCCATCAGTGGTTGCTGCACATCTTCTGCAGGTAAAATTTCTTGTT
CTTCTCTGAAACGGCTGTAGCAGAATTTATTTATTTGTAGCTGCTGTGATAGCTTTACAGCAA
TCACAGCAGCAGACAGTGACTCCACTGCTGTTCGTGCAGATATGCAAAACTAAAGCCTCGGT
CAACAGGCACATGTGAACACCTGCTCTTAGCTCAGCTCTGCTCTCTGCTGCATGTGAAGGGT
CAGTNGGTGTGAACATGTGGTGCTTGTGGGGGGGGGGGGATCCACTATTTTCTAGAAGCG
GGNCGNCCCCGGGGGTGGAGCTCCAATTCGCCCTNTAGGGGAGTTCGTATTACGCGCGCT
NACTGGGCGGGNGTTTACAACGGTCGTGACTGGGAAAACCTTGGCGTTACCCCAANTTAAN
TCGCCTTTNAGCAAANTCCCCCTTTTTGCCAGNNTGGGGTAATNGCGNAANAGGCCCCCT

237U=TTAATCCCATCTTAATCACAA
237L=CTGAGCTAAGAGCAGGTG

GM103
TCNCTTTGACTCTNATCCCTTTGGANACCCCNCCCCCTNTCGAGGTCGACGGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCACaTTTATACATCAAGTCCTTAGTGCACCTGTTGCAAAC
GATTGAAACATGTTTTACTGTGTTTCTCAGTCATAAAAAGCTTGAAATTCTTAAAAAGGTTGTT
GAACGCTCTTCTTCAATCCCAGAGCTTTCATTACCAATTAAACTAGAGCTAGACACAGCCTC
GCCTATTGGTGTGTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGGGAAACCCCACTA
AACTCAAGATGGGGGTGGGGTATTTAATGGTGTTCAAAATAAAGGGGGGTCCACTTGTCCA
CAGTTGCTATAGAAACACCAAATGTGAAATACAAAGCGACTCCAAGGCTAAACTCTATATTG
GTGGCCACATGCGAAATACATATAATGAAGTAAAACTAGGTTACTTTACTCTACTTAAACTAC
CTGTCTGGGATTTTGTATCAAATAAAATCCCAACACTGTGATGCATTTATGATCCACNAACAT
TGTGTCCNGTATAACTAAACTNCCCCCTTTNGGGGC

103U=CCCAGAGCTTTCATTACC
103L=CCACCAATATAGAGTTTAGCC

LG 12

GM440
ANNTTNGAAGCCCTTGGANCGGCCCCCCCCTTTAGGTCGACGGTANCGATAAGCTTGATAT
CGAATTCCTGCAGCCCACAACAACACGCAGCTGCTTCCGTGCTGCACTTTTACTGNGGGCG
GGGCTTCGCTCACACACACACACACACACACACACACACACACACACACACACACACGAAAGCAG
GTGAGGCAAGATAAGGTGTTGCTCAGGACTAACAGGTGTTTTTACCTGCAGACGCTTTACTG
ACACAGTTTGGAAGAACGAGTCTGAACAGACTTTGTTCAATTAATGATAACGAGTCAGATGTT
GACTTTGATTAAAAACAAGCAGTGACATCATAATCATAATCAGTCATCAACACTAATACTCAT
GTTATTCTGTTAATCTCCCATTATTACTACATTACCTGCTGTAACACAGAATACTTCATTGTTC
TGTTTTGACTTTATTTGTTACTCAAATATTTGATATGCTGACAGCAGAAGTCTGTTATTAAGTT
ATAAGCTCGTATAAATACTCAGAAGCAACAATGATGATGATGTTTCAAGCTGCTGTAACACAG
GATGAATGAAGCCTGTGTGTGTGNCGTCCTGNGGGGGGATCCACTAGTTTCTAGAGCGGCC
GCCACCCGGCGGTGGGAGCTTCCAATTCGGCCTATAGNGGGG

440U=TGGGAGATTAACAGAATAACA
440L=CTGCACTTTTACTGAGGG

GM651
TCATAAGAAAGTTGATGTTCTGTATATCTGCAGTTTTCGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGCATCAAATCTGTTAGGCATTGCAAACATTGNGGAGGGATGTTCAGAAATTTG

Figure 11 QQ

AACACATACAGTGATACAGAGGGAGATTAAAAGGTATGTCTGTGATTTGAATGGCTCTTTCT
CCTCACATTTTCATTTCTAACATTTACATACGTTAATCTTCACATATACATTTCCGATGTGTTT
GGTGTCACAACCTTTTCCAGTCTATCGCTGTTCCAGCTTCCGTTGTTGCTAATGTGACTGTG
AGTGGTAAGAAGGCAAAAACTGTGAAGTGACTCACACATAAGTATCTTTAACAATTTTCAGCC
TAGCGGGTAGGTCTGCCAATATGTCAGTGGGGCTGGCACCCCTGATGGGCACACATCATTG
ATAT

651U= AAGAAAGTTGATGTTCTGTATATCTGC
651L= TGAGGAGAAAGAGCCATTCAA

GM668
AGCCTTTTCAGTCTTTGTATATGTGTACAGTACGTATATGTGTGTGTGCGTGCCTGTGTGTGT
ATACGTATATATGTGTGTGTGTGTGTGTGTGTGTGTGATGAATGGGCAAGTGCCAAGCAGC
GTTCCCTTGGT

668U= GCCTTTTCAGTCTTTGTATA
668L= GAACGCTGCTTGGCACTT

GM182
GTTNNAATCCTTGGGAAGCCCCACCGCGNTGGCGGCCGCTCTAGAACTAGTGGATCCCCCA
CATGGGTCAGCACANTTACACCATTAACATGTCACCCTGGCTGCCTGCATGGACTTAGCCTC
TGCCAATAGCAAGTTGGCTCCTGGGCACTAATGAGTAGCTAGGTAATTAGAGGTTGGCTTGA
TTCTACCTTACTCACAAGCAAACAAGCACACATAAACACTCTCTCTCTCTCTCTCACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACATTT
ACAAATGCAACACATATCTGGATGTTGGTATGTGGCTCTTTCTCTCTGCCTAAATGGGTGGG
CTAGCCATATGTCACAGCAGTTGTGCTGCATTAGTGCACTGGGTGATATACTTTAATGAACC
TGCTTCTGAGAAGGAAAGGGAAGGAGGCGTGTTTNCTAAATTTTTTGGGCTGCANGAATTCG
ATNTCAAAGCTTATCGATACCGTNGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCC
CTTTTAGTGAGGGTTAATTGCCCGCTTTGGCGTAATCATGGTCATAGATGTTNCTGGGGTGA
AAATGGTATTCCGCTCACAAN

182U=GACTTAGCCTCTGCCAATAGC
182L= AGCCACATACCAACATCCAG

GM562
TGAAAGATGAAGCTACTCACCTCTGAGAAGTGAGTGGTTTGTCTTTGTGTTTTGATAAATTAT
AATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGGCACAT
GTCTGGAAATGACTGTTAGATGAGGAATTCCATAAACGAGTGTGCTTGTTTGGTGCTGTGAT
GTCATGGAGTCAGTCTGTCA

562U= GTGGTTTGTCTTTGTGTTTTGA
562L= CAGCACCAAACAAGCACACT

GM402
TCTTATCTTTGTGACATCTCACTGTGTTTTTCATGCTTTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTAATTTCCACTGCAGGAAATATCGGA
GCAGAGCTCTCTTACAACAATGTTGGCATGTTCATATCATCTGATGCTGG
CAATACCTGGAGACCGGTGAGCCTCACACCTACATTTACACCCACAGCCA

Figure 11 RR

GCAGACCTGCAGCAGTTTCAAACTTTGACAGATGATGTAAAAAATTAAAC
ACTTTTACAAATATTGTATTTTCTGGCTTCTTGTTATGTAACACCTTTAG
TTTCCACTCCAGCTTACTGCAGGTTACAACAGGCTTTTTTATANNACACT
TCAGACACGCTACACGGNAAAGCAAGAGTGCAGACAATGAT

402U= ACTGTGTTTTTCATGCTTTG
402L= GGTGTAAATGTAGGTGTGAGG

GM584
CCCTCAGTTCCTGTGACAATGACGTGCAGCAGTTTGTTCTGGTTCTGGTGGCGTAACGTTTG
TTTTCTGGGGCTGCTNTAATGTTTCTGTTTGACATCGTAAATCTTTGGGGTCGTCTTATTGGT
CCCATCATGGTCACATGGTCTCAGATGTTTCTGTATAATCCCGCTCCCACCTGCACACCCTC
TGTAGTGCAACCGCATATTTTTATTTGACTGTGTGTGTGTGTGTGTGTGTGTGTGAGAACT
GCAGCGTCCTGACTATAAAATGATTTAGAAGGAAAATAATTTTTCTTTGTTGGAACCAGTTTT
TGACCACCAGGTGGAGCTGTGGTTGCTGTGCAGGGAGGCAAGCACCTGCAGCCAATCATA
GCCGGTTGTGGNTGTTTGAGCTGAANGGAACTCGTGGATGTTTNCACCTTCATGTTTTAAGG
NTTTGGG

584U= GTATAATCCCGCTCCCACCT
584L= ATAGTCAGGACGCTGCAGTT

GM101
ATTTNAAANTGNANACTTAGANGATCCTCCNCTANCTGGGAAAACCNCCT
AGGGGATCCCCCCANNCACACGCACATATGTCATTTTTTNCATATCTCAGT
GAGAACATCTANGGGGCATAACCCTAACCATGACCTGTAACTGTAACCCT
GACACTAAACCACATTTAGAGTCTAAAAGATGCCTTCAAACTTGTGGGGA
CCATGGATATAAATACACACACACACACACACACACACACACACACACAC
ACACACACACTCAGGTGCAGGTCTCGAGAGCAGAGCAGGACTTGGTCCTG
TGCAGCTTCTCCCAGAAGTTGGAGTCAAGCGGGGGGCTGCAGGAATTCGA
TATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGC
TTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTC
ATAGCTGNTTCCTGTGTGAAATTGNTATCCGCTCACAATTCCACACAACA
TACGAGCCGGAAGCATAAAGNGTAAAGCCTGGGGTGCCTAATGAGTGAGC
TAACTCACATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAAC
CN

101U= ACCTGTAACTGTAACCCTGAC
101L= AAGTCCTGCTCTGCTCTC

GM4
TNNAAGCNCTTTGGAAGACCCGCNGNGTTTGGCGATCTAGCNCTAGTGGATCCCCCCCTGG
GGAATCATTATTTTAACAAGTGTCCTCACAACAATAGTTAAACAAACGTGTGTGTGTGAAAGG
GGAACATTCCATCCATTCTTGGTCTTCCTGAGGAAAAAGCAAAAACATCACACACACAAACT
GACACACACACACACACACACACAGACTGTTGACAGCAGGCAGCAGGAAAGGTGCACATAC
ACGCCTCTAAGGTCATTCACACATCCGCCTCGTCTTTCAGCTCTCCGCCCATCAAGTCCTAG
TAGTTTTAGCCATCAATCCATCTGGCAGTCCATTTTTATTTTGGCAGACATGCTTCTCCTGCC
ATTAGTCTACAATTCAAAACTACTCCTACATTAAGTATACAATGAATATCCTGTGGGCTGCAG

Figure 11 SS

GAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTT
TGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGT
GTGAAATTGTTATCCGCTCACAATTCCACACAACATAC

4U= CATTCTTGGTCTTCCTGA
4L= AAACTACTAGGACTTGATGGG

GM321
ACCTGGCAAACAACACACTAAGGTTGGACAACTGGNCGAATTTATCGACC
ATCGATCATAGACTGAGCCTTTCACCGATTGTTTTTACAAGAGCGATTTA
TTCATTTTCCCATTAGTAAGTCTGCTAATAATGTTGGTTGAAGCTAAGAG
AAGCAGTCCACACACACACACACACACACACACACACACACACACACACA
CACACACACCCCCTTTTCCAGCTGTGAGCAAATGCATGCTCTTCAGAGTG
CGACAAATGACTCCTTTTCCATGGTATGAAACAACATCATTTCCTTGACA
GATATTTAGATATAGCCAGAGTGCACAGTGTCCACCTGGGGCTGTCTTTT
TCATATTTAACCATTTTAGTCAAATCACTTTGGATATTCTGCTGGTGAAA
AGCTTTTCCGGAGCTTGTCAATCAAAAAGTCACCAAAAGTCACCTGCATG
AATATATTGCCTATCGTCATTTATTGGGACTGATGAATGTCNGTTTGGAA
AAAATTTTTAGTTTTTCACCCCAACCTTTNCTACCGCACCCAAAGTTNTG
GTATTTAGTAATTNTAAAACCTCTTTACCNAGGANN

321U= TGGCAAACAACACACTAAGGT
321L= GTCATTTGTCGCACTCTGAAG

GM514
TGAGACTTCGTCATCAGTGGTCCACAGTTTTCCATTCTTGTTTCCCACCGACTGAAGAAACAA
AGGCAGAAGCCAATCAGATTTTCACTTTTTCTTTTTGTGCGCGTGTGTGTACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACTTCTTGCCTACATGTAGGG
GTCTCCACTTACCCGGTCATTCATGAGCAAGTCCTTCACAATGAAGTTGGCAACAATGGATT
TCATTGGGGAAGCAAACTGATCTGGAGCCAGCATGGAAATATGGGG

514U= AAAGGCAGAAGCCAATCAGA
514L= TTTGCTTCCCCAATGAAATC

GM108
TNNTNTTTTGACTAANANATCTCTTGGATACCCNGCCCCCTNTCGAGGTCGACGGTATCGAT
AAGCTTGATATCGAATTCCTGCAGCCCCcTATCAGCAGGTGGGCTTTTGGTTTAGTAAAACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACGTGCATGTAAG
CGCACACACATACATACCACAATGTATACATACAGCAACTTGTGCACAAGCCCCTTTAGGTA
AAATACCTTCGAGCCAACAACTCCAAATCAAGCCACCCACCCCCAATGCACACACTCACGCT
CTCACATACCTTGGAGTAAAGCGAGCGTAGCTGAGCGCTCGCAGCTCAATCCCCCCAACCC
CTCTCCCCACCTTTAATCTGATTTGACGTTCAGCAATACAGGGACACACATACGCCACACAT
GCATAACATACTCCTTAAATACACACACACAGAAGGAGGAAGGCCGTGTNAACGTTTCTGAA
CTGCAGTCTTGTGTAAACACCTGCCAGTAATCTAGCAGCTGAGATGAATCCAGATGAAGCAG
AGCCTGGTTTACAGGTNCTTTACAGGTTGGGGTTACTTGGGGGNNGAAT

Figure 11 TT

108U= TATCAGCAGGTGGGCTTTTG
108L= GGTGGCTTGATTTGGAGTTG

GM583
CCATATTTCCATGCTGGCTCCAGATCAGTTTGCTTCCCCAATGAAATCCATTGTTGCCAACTT
CATTGTGAAGGACTTGGTCATGAATGACCGGGTAAGTGGAGACCCCTACATGTAGGCAAGA
AGTGTGTGNGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTACACACATGCGCAC
AAAAAGAAAAAGTGAAAATCTGATTGGCTTCTGCCTTTGTTTCTTCAGTCGGTGGGAAACAA
GAATGGAAAACTGTGGACCACTGATGACGAAGTCTCACCTGAAGTTCTTGCTAAGGTAAGAG
GTGAT

583U= AAAGGCAGAAGCCAATCAGA
583L= AAAGGCAGAAGCCAATCAGA

GM427
TTNACTTNNTGATTCCCTTTGAAAGNGGCCCGCGGCCGTTTTAGAACTAGTGGNTCCCCCCC
AGGTGCAGGCAGACANCAgATACACTCATGGAAGATaAACGGACCCAACACACACACAAGC
ACGcaCAGGCACACAGcGAAGGATAAATGGACCCANTANCAGGGAGGTCTGACAGAATGCC
TTTTNACACCTGGCTGAGCCCAGCGGAAGGTGACAGAGTcACATcTCCCAAAGCGAACACAC
ACACACACACACACACACACACACACACACACACACACACACACACCTTcTcACATTGGGGAGT
TCAGGGTCATAAGCAGCATCATGAATAAAATGAGGCTGTCTTAAACAGAAGGAGCTCTGTGT
ATGCATGTGTGTGGGTGNGTTTGTATGNGNGAGACTGNGTTTGTGTTTGTNCAAGGGGCTG
CNGGAATTCGATATNAAGCTTATNGATACCGTCGACCTTNANGGGGGGCCCGGTACCCAGC
TTTTGGTTCCCTTTATGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATNGCTGTTTNCT
TGTGTGAAAATGATATTCGNTCACAATTTCACNCAACATACCNANCCCGGAAGCATAAAGTG
TANAAGNCTGNGGTGCCTAANGAAGNGAGCTTACTTACNATTAATTTGGTNTGCGCTTACTT
GCCCNGNTTTCAAGTTGGGGAAACCTGTCNATGCCAGCTGCTTTAAANAAATCGGTCAANNC
CCGGGGGAANAAGCCGGTTTGCTAATTGGNCCNCTTTTCCCTTACTTGNTTANTTGACTTTN
TGGGTTGGNATGNN

427U= CCAGCGGAAGGTGACAGAG
427L= CCTGAACTCCCCAATGTGAGA

GM240
TNTTGNACTCNNNAAGCCCCTTCCNAGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTG
ATATCGAATTCCTGCAGCCCCCAGTATAAATGGGAGGATTTCTTGTTGTTATAGTGTAATAAG
GGTGACGATCAACAGGTGGAGATAATGGAGCTTAGTTTCATTGAGCCAAAAAAATCACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGTC
TCTGTGCAACCTCAACACATCAATAAATTACATCAGATGCATAGATTACCATTACAAATCCTTT
CCACAGTATCAGACACTGTACGTCTTCCTCCTGTGGATTAATGTCTCGTTTCATCAGCATCCA
AAAAAATGCTCTTTGAGCTTTGGATTGTTGAAAGTAAGAAAGTGAAGAGGAAAGTAGTAGTT
GCAGTTGAAACATAGAGAGGTTTGGGCTTTTTTTGCGTGGGGGGAGTTAGACTGAAGAAGA
TGCAGGTGGGCTGCCGGCGTATGTGTAAAAACCTACTTGTGAACTTGGTTGTGGGGGGATC
CACTAGTTCTAGAGCGGNCGCCACCGGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGT
ATTACGCGCGCTCACTGGCCGTCGTTTACAACGGTNGTGACTGGGGAAAACCCTTGGCGGT
TACCCCAACTTAATCGGCTTGGCAGCACAATNCCCCTTTNGCCAGCTTGGCGGTAATAGCC
GAANAGGCCCCGACCCGAATCGGNCCTTTCCAAACAGGTTGGGCAAGCC

Figure 11 UU

240U= GGGAGGATTTCTTGTTGTTAT
240L= GGAGGAAGACGTACAGTGTC

GM539
AAAAGGGGTTTGCTGGCACACAATAAAAAAATCTACACACACACACACTCAGGCACAGACAC
ACGCAGACACACACACATCGCACAGGTACAAAGAACAAAAAAAACAAGCTCATAAAGGCACA
AACAGACACATCTATACACACACACACACACACACACACACACACTCTCACACACATGTGCAGC
CCTCCGGTCCTGATCAATACATGACAAGAGTAAATCTCCTCCGGACGTCAGGCAGTCCAATC
AAAGGGCTTGGTGTTCTTATAGGGGATCACAAGAGCCAGGGGGAGACAAACAATGATGTGA
ATCCTCAACAACACCACAAT

539U= GGTTTGCTGGCACACAATAA
539L= CTGGCTCTTGTGATCCCCTA

GM28
TTNTTTTNNTCNNGNNATTCCTNNATCCCCGGCGGTTCCGTTCTAGAACTAGTGGATCCCCC
ACTCaGAATCTCTTTCACATACCAAgcATgCACACAGAAACAGATACACACACaaactcTCTCGC
AATCCATCACACACACACACACACACACACACAGCGAACAAAGTGTCAGGTGGCAGTGGAAAC
GTGGTGATTTGTTCCTCCTGACAGACAGGAAATAAGGGAGTCGACCAGGGACCTCACTTCC
TCTAAGATCTGACTAACCTGACATCTATCAGACAACCCCCCCCACACACATGCATTCACACT
GTCCTCCAATGTTTGGTCTACTCTAAAACACATGCACACACACACACACACACATAAATTCAC
CATCCATCAGGCTCCTAAGTCCCCGCAGGGGGGGGCTGCAGGAATTCGATATCAAGCTTATC
GATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTA
ATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAAATTGTTATCCGCTTAC
AANTTCCACACAACATNCGAGCCCGGN

28U= GACAGACAGGAAATAAGGGAG
28L= AGCCTGATGGATGGTGA

GM251
TTGATNNAAGTGATCTCANNGAACNCNCCTCAGGTTTANGGAATCGATCNCTTGATATCGAAT
TCCTGcAGCCCATCCATTGTAAACTTTCTATAAACTCTGTAAACATTGATTCAAATATAGGctgtA
ATGGTAAGCTGCGTTGTCTGTAGCAGCGGCATTCACAGCATCTCTAGCATAAGCATGAAGCTT
AGTCACATACCATGTAATGCATGTAGGCTGCATAATGGCGTCAGCATATGTTATGCTTCCACA
TCCTTGAACATCCTATACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACCCCAACACACACACACACACACACAAAGACTACTCAGCAGCACATGTGCT
GCCACTTTTCCCACAGGGCTCTGTAGAAATAACTACAAACACATATTGTGGGGGATCCACTAG
TTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGC
GCTCACTGGCCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTNGGCGTTACCCAACTTAA
TTCGCCTTGAAGNNATTCCCTTTTTTGCCAANGTGGGGGNNATNANCAAAAAAGGGCCCCGA
CCCNGAATGGGCCTTTTCCAAAAAAATTTGGCNCAAACCNTTNAATNGNGCNAAAATGGGAA
AATTTGTAAAGCCGTTNAAATAATTTTNGGTTAAAAAATTCCGGGGTTAAAAATTTTTTTGGT
NAAAAATCNAGNNTTNATTTTTTTTTAAACCCAATTAGGGCCCNNAAAATCGGGCAAAAAATT
CCCCNTTTTTTAAAATTCAAAANGGAATTTGNANCCCGAGNATTNGGGGGNNG

Figure 11 VV

251U= GGCATTCACAGCATCTC
251L= ATGTGCTGCTGAGTAGTCTT

GM677
CCCCATTATTTATTGGGGGTNCCAAATTAAGGTAAATTTAGGGAAGGAAGGGGGNAGNAGG
TTAGGGNAGNAGNAGTCATTTCCTCTCCCTTCTGGTTGGCATGGTGCTTAAGCCTTCAAAAT
GCTGACATCAGCACTCAGCTCTGACTACAACGACCGAAAACACGCACGCACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACAGTTCAGTTCAGTAAC
AGGTTTGAGCTAAATGCTCTATTCAAGATGCATCTTAATCAGCAGCAGCATCAACATGATTGC
GACTGCGGTGTATGACAACCGCATCATATAACATCATCTTTCATTCATCAGTGGCTCAGATAN
CTGC

677U= AAGCCTTCAAAATGCTGACA
677L= GCAATCATGTTGATGCTGCT

GM673
TGGACATTGTTCNAACCNTTTTGTGTATACCCNCANCTCGTGTCTATGGAGACCGCAGCAAC
ATTGAGAGCAAACACCGGGAGCTCGTTTACTCGAGCGTTCACACCGAACCTCACTTGTGCG
TTACTGTGTGAAAGTGCGGCACGGGTTCAGTGACTCAGTAATATCTAAACTTCGAAATAAGT
TGAGCTTACTTTATGTNCACACACACACACACACACACACACACACACACACACACACACACAC
ACACCGGGTACTGAATTTAATTAAAATCTGGGTAACTGTCTAAAGTAATGGCTGCGTTAATAA
GAACACAGCCAATATCAGTATAATTATCGGTGGTGGTGATCGGtGCGTCTCTCACGCTTCTTT
CCTGCCAGACTGTCGCTCTGTGCTCAGAATGAGATCTGTCCCGTCTGAGCTGTTAACCAGC
CCATCTTCTGTTTTGGGGACAAAAACAAACATTAAGA

673U= CGAACCTCACTTGTGCGTTA
673L= CGATCACCACCACCGATAAT

GM390
ATCCATTGTAAACTTTCTATAAACTCTGTAAACATTGATTCAAATATAGG
CTGTAATGGTAAGCTGCGTTGTCTGTAGCAGCGGCATTCACAGCATCTCT
AGCATAAGCATGAAGCTTAGTCACATACCATGTAATGCATGTAGGCTGCA
TAATGGCGTCAGCATATGTTATGCTTCCACATCCTTGAACATCCTATACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACCCCAACACACACACACACACACAAAGACTACTCAGCAGCACAT
GTGCTGCCACTTTTCCCACAGGGCTCTGTAGAAATAACTACAAACACATA
TTGT

390U= TCTGTAGCAGCGGCATTCAC
390L= ACAGAGCCCTGTGGGAAAAGT

GM38
GACCTTNTNTATTNCANACAGATCTTCTTGGAAACCCGCCCCNTNTCGAGGTCGACNGTATC
GATAAGCTTGATATCGAATTCCTGCAGCCCCCTTAGTGATAGACTTAGCAATACCGATTGGC
AGTAGAAGGAACACACACACACACACACACACAAATATATATGACTGAAGAAGTCAGTTGGATG
ACTGGCAAAATGTTTCTCCTCCTGAAAACACTATGTCCAGATGAACAGAATCAACCTTTGGG
GACATATGTATGTATATATATACACATAAAATAACCTGCAATAGGTGAAGTAGTAGCCAGCTT

Figure 11 XX

TATTTTTTAATTTTTTATTAAGGCTGTAAAACCCCTCACTAAACACTTTATAGACTTTTTCTCAG
ATAGGCATGAACATTTTCAGACTTTTCTCTCTTGTTTGGGGGATCCACTAGTTCTAGAGCGG
CCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGG
CCGTCGTTTTACAACTGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATNCGCCTT
GCAGCACATCCCCCTTTNGCCAGCTTGGCGTAATAGNCGAANAGGCCCGCACCCATC

38U= GCATACCGAACCGAAAG
38L= TGTAGAAATGATGAGCCAAAA

GM472

GTTTNNNNNTNTGTNAATCTTTTGNCCGTGGCCNCGGCCCGCTCTAGAACTAGTGGATCCC
CCCCCTGCTGGACACATAGATGAAGTCTCAAACATTTATTTGCAAGGGTGGGAAGTTGAGTG
CTGAATTATGGGTAATGAGTTTGGTCCAAAATGGATGCACAGTGTGGTGTAACATCTAAATC
TCCACGCAGTCCCTGGCTCTCTCTCTCTCATTTAGCTGTGGTGTAGAACACAGCTTTGAATTT
CATTTCAGGCTGTGGAATTATTTACAGACAACACACTTCCTCATAGTTGTGATTGACATTAAA
GAAAATCAATCAGTGTAATGACGGGGAGTTTTAATCTACTGAGGGCAGCGATGGATCTGAAG
CAGCTGCTCACACACACACACACACACACACACACACACACACACACACACACACACAGTCAGTAAAT
GGTTATTTTAATACCTGTTGATCTGTAATTTTGAACCTGCTCCGGAGCAGATTTGTGGAGCAA
TTACACCGTCCATGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG
GGGGGGCCCGGTACCCAGCTTTTGGTCCCTTTAGTGANGGTTAATTGCGCGCTTGGCGTAA
TCATGGTCATAGCTGGTTCCTGGGTGAAATTGGTATNCGTCACAATTNCCCACAACATCGAA
GCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGGTGAGCTAACTTACATTAATTG
CGTTGCGCTACTGGCCCGTTTTCCAATCGGNAACCTGTCGNGCCACTTN

472U= CTAAATCTCCACGCAGTCC
472L= TGTAATTGCTCCACAAATCTG

INSULIN

GM561

GCCGTCTCCTTCGACTGACAGTACAGACGGCAGCGCTCGTCAGCTGAGACACACAAACGG
GTCAGTGCAGGAGTTTCACATCATTCTGAAAACATCTGCTGACATCTGCTAACGTCTGCTAA
CATCTGCTAACATCTGCTAACATCTGCTCGACACTAAAGAGTTAAAGGAGGAGAGTTTTCCT
CCAGCAGCAGATTCCTCACTGATGACTTTTACATGTGCGCACACACACACACACACACACAC
ACACACACACACACACACACACACACGTTTCTATGTCTCTGTGAGGACCCTCAGTTACATAACG
TATTTCCGAGACTATAAATCTGAAGCTGGAAACCTCGCCTGAATCTCCGAACA

561U= AGAGTTTTCCTCCAGCAGCA
561L= GGAGATTCAGGCGAGGTTTC

GM280

TTGTTTNCNTCCGTTGGAAGCCCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCC
ACGCACCAGCATAAAGCCATCCACATACATTTCAAATCAAACTGtGTTTAGAGAAACCGCAAC
CTcTTCTTTTCAGATGTGACTCCCAGCTGCCTGGAGGAAAATGGATTAACACACACACACAC
ACACACACACACACACACACACACACACACACACACACAAGCTCTGTCCACACCTCCAATCACGTT
CTAGCACACCAAGTGCTTCACCCACCCCCTATTAACGCACACATTCACACGCAGAGGGGAT

Figure 11 YY

CTCTCTCTTTTTGCACAAGTCTATTATTAGCTGTTCAACCCAGAGACAAACTAATGACACGTT
GGGATGAATCACCAGAGCTGCTGCCTTCGACTATCATTACACTCACAGCAGAGCTACTGTAG
AGACATCCATGTAGGATGCTGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTN
GACCTNGAGGGGGGGCCCGGTACCCAGCTTTTTGGTTCCCTTTAGTGAGGGNTTAANTTGG
CGCCGCTTGGCGTAATNATGGGCATAGCTGTTTNCCTGGGTNGNAATTNGTTANTCCGNTC
ACAAATTTNCCCNCAANCATTACGGAGGCCCGGGAAGC

280U= AAACCGCAACCTCTTCTTTTC
280L= GTTAATAGGGGGTGGGTGAA

GM80

GNGNNNNNNGNNTANTTNTNTTNTNTNTNTAGATCNAANNGAACTCTCCNGCGTTNGNGGC
CGCTCTAGAACTAGTGGATCCCCCACGTGCGTGCAGCTGNNGAGCACCTTGCTCATTTGCA
CTGTGTAACTATTCATTTTTATATGCTTGTTTCTCTTTATGAATAATAAACCAGCGTGTATCCC
AGCCTCTCTCTTAGGTCGTGCATATGTGCCCAGATGTTCCAGCAGTCACTTAATGTGTTTTTA
TTGTTGATGGATCTGTTTTCTTCTGACAGCCAGACTGCATGCTCATCTCAAGAGAGGGCTGT
ATCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGCTCACTGGGCTTCTACAG
CTACAGTCTCTTAATAATAGATCGCCATCATGGTAACCGTTGTTGTGCTGACCTTAAGTGCTG
CACAGTGCTAAAACAGACACCAGCCTCGACTAGTGTTTTCCTGCTGAAGTAAGTGCACCGTC
ATCCACAGTCTGTCTCTCTCTGACTGAGGACAGACAGACAGCCAAGCAGAGGAGN

80U= TGAATAATAAACCAGCGTGTA
80L= TAGAAGCCCAGTGAGCA

GM524

AAGCNACCACCCCAGTGTTACACAGATGGGATAAGTTTCTGTATGCTAAAATGCAATGATTG
TCTTTTTTTGAACATAATGATTCAAAGTAACACACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACAAAAGTAGCTCTATTTCCACCTCA
ACCATTCACAAAACAGTAGCTACCTGGCTTGTCTATATGATCACCTTACAACAAACCTATGCA
CACTATTTTTGTTCAGTGTTCATGCCATTCACCTAATGGATATAGACATTAGTCCATGTCCTT
GATAGTCCTGATGGTTTCCAACGTTACTGGCATGACGAGCAGAACCCACCTGTGATGCTTTC
TACATGCCACAGTGGAGGGGGCGCCATAATGGTCTGGGGAACTTTTTCCTTCAGTGGAACA
ACGGAGCTTCAGGAGGTGCAGGAGCATCAAACGGGGGGATCCTCTAGAGTCGACCTGCAN
GCATGCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
ACCCAACTTAATCGCCTTGCAGCACATNCCCCTTTTCGCCAGCTNGGGGTAATANCGAAANA
GGCCCCGCACCGATCGCCT

524U= CCACCCCAGTGTTACACAGAT
524L= CCATTAGGTGAATGGCATGA

GM684

AAGAGCATCTGGCAATGAGAACGAATACAACTGGGCTTTAGACTGCAGCCAGTCTCCATTTA
TCAGAACCAATATGTGAGCTGCTAAAGCCTGAGAGAACCGGAGAACGGCTGAAGAAGTCAC
AGAGCATAATGCATAGAGTGAGATGGAGTGCTATGCACCCTGCTGCGTACTGAGACAATCA
CACTGTAATTACACTTATGGCGCGTGTGAGATGGACCTATAATCACCTAATCATATCGATCAA
ACCCACACAGCGCTCTGACTCGCGCAAACAGCTGAAAGACTGAAAGATTTTAAGAGATGAAA
GACATTTTCAGATATGCACACACACACACACACACACACACACACACACACACACACACACA

Figure 11 ZZ

TCGCGCTGTTTTGTCAGTTTGGTCACCCATTAACAAAAAAAGCCCAGCTCACAGCTCGTCAA
CGCATACTGAGGGCTaTATGTGCTTCCGNACGCGCATACCGCCCACGCGCACACAAGCCCT
ACACATTCACACCGGACGAGATTACAACANGNGCCAGGTCGCCTGTGCGTCTCCAC

684U= ACTTATGGCGCGTGTGAGAT
684L= TGGGTGACCAAACTGACAAA

GM269

NGGGNNNNNGNNNAANTTCTNTTNNTTGAAGNNGATCTTNTTGGAATACCCGGCCCCTTCT
NGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCcAAGACTGGAGATG
CTGTCAGTCAGAGtaACAGCGCATGAATAATTGCTTTCATAAAACTGTTGCGCTCCAGTTGGT
TCGCTGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAAGTGGAAAAAAAAAC
TCTCTAAAGATCAATAGGGACATGGCGTTAAACTAGTTTGTCATTAAAACGGGACAGTCCCC
AGAACTTAAAATCAAATTTGGCATAAGTTTGGCTTGAAGTCTGAACTAGCTTGACTGAAGGTT
TCTCATGCAGCCGTCATGTTTGTGCGGTTTGTTAGGGGGGGATCCACTAGTTCTAGAGCGG
CCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGG
CCGNCGTTTANAACGTCGNGACTGGGAAAACCCTGGGCGTTACCCAACTTAANCGCCTTGC
AGCANATCCCCCTTTTCGCCAGNTNGGCGNNAATAGCGAAAAAGGCCCCGCACCGATCGG
CCTTCCCAAACAGTTGCGCANCCTTGAAN

269U= TGCGCTCCAGTTGGTTC
269L= TAACGCCATGTCCCTATTGAT

GM543

TGGATAAGCTTTGTTCAAATAAGATATATCTTCTGTCACATTAGACAAAATCTAATCTGACAGA
TGATACGTGTCGGTCCGGCTCTTCAAGCAACTAAAAGCATGAAGCTGGAATCCAATCTTTCA
AATGCAGATTCATTTGAGGCGGATTAGAGAACGAGTGACTCAGGAAGTGTGCGTGTGTGCG
TGCATGCCCCGTGTGTGTGTGTACATGTGATAAAGTTGTGGTGTGACTAAGTTCTGACAGTC
TGCCAGGGCTGGAAACGTCTGCCATCGATCCTAATTTGGCAGCAGATCCTCTGACTACAATA
GGCTCTCCAATCTGCTACAGTCACTCTTACTGGGTGGGACCAAGACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACAGAGACTTGGCTTACCAAACCAG
AAAGGAAACAGACgGGaCAGAGAGACCAGCCTTGACAAAACAACCTTTACAC

543U= CGTCTGCCATCGATCCTAAT
543L= CAAGGCTGGTCTCTCTGtCC

GM46

TTGAATCCCTTGCATCCCNCGGNGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCCCCTTGAGG
AAAATTATTTGCCCACAACTGCTCTAATGGATTCAGACGTCATCCTCAGCTTTCATCTGTTACG
TTGACTTTTGTCGTGTGGCATTTTCTATATATATTTCCACTTCATAAAATTCTGCGTTACTACCC
CTGTCCACCAGGCTGTGCTGTTTCACTTTGTCGTCACAACAACAACAACCTGCTGATTGCTGTG
CTCAACAGTCATGCGCACCTTAATGGATGTATCGAACAAGCGTTTAATACCCAACTGTTTGTG
TGTGTGTGTGTGTGTGTGTCAGGGGGATGTGTAAGCAGCTCCGTTTCAGAGTGAAAGGAAAAT
GGATGGAAATGATATACTCTGTTCTTAATTCTGTCTTTTTAATGATAAAGCTGGTTTCTTTGAT
TTTAGCCAACTGGTTCAGAATGGTCAGTACGGACTTGAGACTGAGGTGGGCTGCAGGAATTCG

Figure 11 AAA

ATATCAAGCTTATCGATACCGTCGACCTCNAGGGGGGGCCCGGTACCCAGCTTTTTGNTCCCT
TTTGTGAGGGTTAATTGCCCCCTTGGCGTAATCATGGCCATAGCTGNTTCCC

46U= GCGTTACTACCCCTGTCC
46L= TTGGCTAAAATCAAAGAAACC

GM543
TGGATAAGCTTTGTTCAAATAAGATATATCTTCTGTCACATTAGACAAAATCTAATCTGACAGA
TGATACGTGTCGGTCCGGCTCTTCAAGCAACTAAAAGCATGAAGCTGGAATCCAATCTTTCA
AATGCAGATTCATTTGAGGCGGATTAGAGAACGAGTGACTCAGGAAGTGTGCGTGTGTGCG
TGCATGCCCCGTGTGTGTGTGTACATGTGATAAAGTTGTGGTGTGACTAAGTTCTGACAGTC
TGCCAGGGCTGGAAACGTCTGCCATCGATCCTAATTTGGCAGCAGATCCTCTGACTACAATA
GGCTCTCCAATCTGCTACAGTCACTCTTACTGGGTGGGACCAAGACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACAGAGACTTGGCTTACCAAACCAG
AAAGGAAACAGACgGGaCAGAGAGACCAGCCTTGACAAAACAACCTTTACAC

543U= CGTCTGCCATCGATCCTAAT
543L= CAAGGCTGGTCTCTCTGtCC

GM527
NTNGCNNANCTNACGNAANCACCCCACTNTTTAGGAACCCCANCNGACTTCACCGTGTGCT
GGTGTTTGTGTGCACATGATCTTCCACAATTGAAATGCTTGCACGTATGTGTATAAATAGAAA
ATGTCGAAATGTGATGTCTCTGTGAGTGTGTGCTTCTGATGCGGCAGTGTGCATGTGTGAGC
TTGTTCTCTGGCTCATTTGCATATCTACGTCTCATCACGTTGCCAAGACAACCTCATCTGTTC
ATCTGGGAGGGCAGGAAATAAAGCGATGGTGCAAACACAGTGAAAGAGAGACATGCGCAAC
ACACACACACACACACACACACACACACATAAATACAGACACACACACAAATGCATGCATACAG
GTTCATTTAATAACAGCGCTTACAAATGAATTATTTCCATTGGTAGAGATTTAATAAGTTACTT
GGTTTTCACGGACCTCAGAGATAAATTGG

527U= ATCTGGGAGGGCAGGAAATA
527L= CTCTGAGGTCCGTGAAAACC

GM454
TNNNTNTTGNCTTTGAAGCCCTTCCNGGCCCCCTCGAGGTCGACGGTATCGATAAGCTTGA
TATCGAATTCCTGCAGCCCCCACGTGGCTAATCGAAGAACAGTCCTATTTGATATTGGAAAG
AATAGACTGATCTAAAACTGGGACAAACACTAGCACAGAAAAAAATGAGCACCTATACATCA
GTGTGTCAATGGAACAGAGTTTCGACTGCACAAAAACAAAACAACTGAAGCAACAAAGAAAT
AACCAGTGATCACCAGTGTGATCTGCAATAGTGGGCTAACTGACGGAGTAAAGGGGGCGTT
AAAGACAGAAAATGGACACAGCAGCAGCAACAAAACGCTTCTAAAATCAGATCAGAGGTAGA
AGAAAAACCCTTTTACTCTGCTGATGATTACATCAAAGTGATTATGAGAATATGTGAGGAGCA
CATTTGAGACGGTCCTAATCAACCGCGCAGATTAGGACGATAATAGGAAAAACAAGTAAAGA
GGTGGAAAGGGTGAGAGGAAAATTAGAGTTTTGTTAAAGTAATACACACACACACaCACACA
CACACACACACACACACACACACACACACGCACACACACACACACACACACACACACTTTTCAACC

Figure 11 BBB

ACCGCCGTTGGGGAGTCTACCACTTTATCTGGTTGNCAAACAAATNGGTTGACTTATGGANA
ANTTCTGAGCCTGGGGAATTTTGTTCGNGCCCCTTAATTTGATGGGGGNCNCCNAAAANTTT
TTGGCAGCTTTTATTAACATTTCGCTTGCTTAANGGGGCCNCG

454U= CAAGTAAAGAGGTGGAAAGG
454L= AGCAAGCGAAATGTAATAAAA

GM547

GM135
TTNNNTTNNNTNCTNAGTAGATTCTCTTGGANGGGCCCCNTCCTTTTNGGNTNACGGTANCC
GATAAGCTTGATATCGAATTCCTGCAGCCCACTGTAGGNTGCATTAACAGCCACAGATGTCA
GGTATCCCGGTCCAGACACGGTCGTCAGCAGTTCAGCTATAAACCAGCCATACACATTCCTT
CCTTCCCTGTCTCCCACCAGCTGAGCATTTCTCTCACACACACACACACACACACACACACA
CACACACACACACACACACACACACACACGGGGACAGGCTAGAATTAAAACTCCAGGGTTGTC
CAATGAGAAACCTTCATGATTGGACATCAGTAGAGGCAGAAATTCAAACTGTGAACCAATCA
GATTGTGTGTCCCGTTTGCTTCCCCCTTCAACACCTTATTAGGGCGACCTTCCATGTCTCTC
ANATTTTCCGGTCTTGTTGGGGTTGGCACCCCGGGTAAAAGGAATGGTCAATCAAGCCACTT
NTNGGGGGGGAATCCCANCNTTGGTTTCTTAAGGANACCGGGGNCCGGGCCAAAACCGGG
NNGGGGNTNGGGGAANNCNTNTCCAAAAATTTTCGGGNCCCCTTTATTTAAGGNNGGGAAN
NTTTCCNNNAATTTTTAACCCGCNNGGCNGGCCTTTTAAACNTGGGGGCCCCGNNNTNNGG
NTTTTTTTAACCAAAACCGGTTTCNNTTGGAACCTTTGGGGGGAAAAAAAAACCCCCCTTGN
GGNCGGTTTTAACCC

135U= GGTCCAGACACGGTCGTC
135L= ATGGAAGGTCGCCCTAATAAG

GM563
AGGGTGGCTATTAACAAGGCAATCTAAGCTTGAACTTCAACTAAACACATGCATTTTTCTGCT
ATACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA
GGCTGAAGAGCTTTTTTTTAACCCACATAGCTGCTCTCTTTCAGATCCTGTACTGATTACACG
TCACCATTCTGTGACCTAACACTGATTGCCTTAATCTTGCTTTAACATCAGATTTAACAGTATA
ACCATAGAAAATAGGACTAGGACATAGGACTAACTGTTCAAACCCTTATTTTTCCCCCTCCTC
CAGCGCTCGGAAGC

563U= GGTGGCTATTAACAAGGCAATC
563L= GGTCACAGAATGGTGACGTG

GM274
NTTCTTCCTNANNGAGCTNCTTNGAAANTTCCCCTCGAGGTTTNGGGTATCGATCCGCTTGA
TATCGAATTCCTGCAGCCCAAAAATAGGATTTAGAATagCAAACTTTATAAACTTTCTGTAATA
ATATGTATATTTTTTTTAAGTAAAATACACTGTGGCTTCTAATTTGGCACAAATAGAATGTTTGC
TTTGTTGAGAAAGGTCAAACACACAGACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACGTACAAAAGACATTGTGATTTGTGTATCAACTGCAAGGCAACCT
GCTGCTGCCCCCAAATTACTCTGTGGCAGGTGTAAAAAATTTGCCCTGTGAGAGCACTACAC

Figure 11 CCC

ACAGGTTGATTGCACACCTGCTTTGCTATTTTACAGGTGCTGTTTGTGCTAGCGAAGACTGC
GGCTCCCTCCCGAGGCACCCCCACACCCACCCAGTTTCACGCCAATAAGTCCTGTGCCTGC
CAGCATGACAGAAACCTNATCATGCTAATCCAAATGCTAACTGAATCAGCCATAGAACTGCA
TTGGTTTCTGCTGTTTTGCTTGCACTGACAANGGTTCTAGCTTATCATTTTGCCCTTGCCTGA
AATGGGANTGAATAATTAAAGCAGTTGGGTTAAAATATTGAANTTNGGGGGGGGATCCACTT
AGNTTTTAGANCGGCCGCCACNGGNNNTGGAGCTCCAATTTCGCCCTNNAGGGGAGTTCGT
TTTANGCGCGCTAATGNTCGTCGTTTNACAACGTTGTGACCTGG

274U= GTAAAATACACTGTGGCTTCT
274L= AGCACCTGTAAAATAGCAA

GM117
TGCATTCNNTTGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCCCTCTCT
CTCTGGGGCAAGAGTCCCTCACATGAAAGCAGAAAAGCCACACGTGCGCGCGCGCACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACCACCCTTTAACCC
TCTCATTAGTGTAATCCTGCATGAGAACAGTAAATTGTCATGAATAAATCCACTTAGAAGTCA
GCGAATGAAAGACTTTCACTTTGAGTTGGTTGCATTACCATTTCAATAAGCGTGCCACGCTG
CAAAACGTTGGCAGTGTTTGACAGAGTAATTGGGAACATTAACGAGTAGATAAAATGTGGTA
AGCGGAGGGAGGCGTCCGTGTAAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACC
GTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGGTTCCTTTAGTGAGGGGTTAATTGC
CCGCTTGGCGGTAATCATTGGCATAGCTGGTTTCCTGGGGNNAAATGGTANTCCGGTNANN
AATTCCCCACAAAANN

117U= GTCCCTCACATGAAAGCAGAA
117L= CCTCCCTCCGCTTACCAC

GM632
CAAGCAGCTACTCATGTGAGACCACACTGACTCAATGGTTGCTTATGTCTTCTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTGTTGAAAGTCTCCCACACACT
CCCTTGTCTTTGCATAGACCAGAGGTTCCCAAAGTGTGG

632U= GCAGCTACTCATGTGAGACC
632L= TGGGAACCTCTGGTCTATGC

GM294
TNNNNTTTTTGACTANGTNATTGCNCTTTGAANGCGGCCNCGGCCGCTCTAGAACTAGTGGA
TCCCCCATCGCGTCAGCAGGACAGGCAGCCATTTCTGGAGCTCGTCCTATCTTTAGAACAG
AAACTGTGCTGATAACAGAGCTTCCACAGCAGCTAAATACACAGCTTATCCCACAACACACA
CACACACACACACACACACACACACACACTAGTGTTACATGTGTAGGCTGTTTTTTCCCCACAT
GCAAATAGCGGGCTGGTTTCGGGAGGCGATTCACTTTCAACATCATTTAGCTGCCTGACTGA
CCAGTGAGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGG
GGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCAT
GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCC
GGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCC
AACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTNTTTCGCTTNCTNGNTTAATTGACT

Figure 11 DDD

CGCTGNGCTCGGCCGTTCGGCTGCGGCNAGCGGTNTAGCTTACTCAAAGGCGGGAAACNG
TTNTTCACAGAATCAGGGGATACCCCAGGAAAGACNTTTTGAGCCAAAGGCC

294U= GCTCGTCCTATCTTTAGAACA
294L= AAACCAGCCCGCTATT

LG 13

GM486

GM628
CACAGCAACCTGAGACGAGCGGGTCTCATCAGCCAAATCCCACTGAGCAAACAAGACACGA
TCTCGCTTTTCTGCTGAGAACAATCTGACCTGCATGAAATGTGATCAGCTGGAGATTCACCG
CAGTACTGCAGTGCTGCAACACACACACACACACACACACACACACACACACACACACACTAAC
CCTGACATTTTTAACACTTAGTGCGTTACTTCAAGCTCATTTTAAATCATGAACTTAACGAGTT
ACCTTACGGCGGGCGGGG

628U= ACACGATCTCGCTTTTCTGC
628L= CCGCCGTAAGGTAACTCGT

GM627
GTGATGGAGATGTTGGTGTTTTGTACGGAGCAGATGTACTCGCCGCTGTCGTTGTGGCTGA
CATCGGACAGCTTGAGGGTCCCGTTGGTCAGAATGGAGATACGAGGATACAGCAgAGGGTC
CGACAGCAGAGCACCTGTGTCCTCCCGGTCCCTGCAGGCAACACACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
GAGCAGAGATATTGATCGTTACATATGCCAATCGGCTCTGTGTCTCCANAATCATTGCAGAC
TTATTCTAACATCAGATTGCAGAATAAGATCCCAGGAACTGGATCAATGGAAGTGTGTATCCT
CGCCGATCGGTGACTTGATAACAGACACAAAGGGATCAATAAATGATGAGAGAGCAGAAAG
AACAGCTGTAATTTCTAAGGGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGC
ACTGGCCCGTCGTTTTAC

627U= CCGTTGGTCAGAATGGAGAT
627L= CCGATTGGCATATGTAACGA

GM122
TNNTNTTTTGACAANTNANCTCTTGGANACCCNGCCCCCTCTCGAGGTCGACGGTATCGATA
AGCTTGATATCGAATTCCTGCAGCCCCCTCATCCCATTCCTTGCTTTGTGATTCTAAGCCCC
GCCCACAATAGTTTTTACCTGTGTTTAACTATTTTTAGACGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTCAGATTGTCTCCTTTAGTGTTTCTTAGGTTTGAATTGT
CCAATAATCTCAGCTTTTGCTGCCTTTGTGACCTTTTTTTGTTTCCTCTCTTCAGCTTGATGTA
ACAATTTTAGTTAACTGAAAATGATCTGGTTTTCTGATGTGCTTACAAAATAAAAATTAAAAAT
ATACATTACTTAAAACTAAAAGTAGGGAATATCTTTTTTTTAATTAGGTAAAATTTGTCAAAATA
TCCAGCCTGAAGAGACTTTGATGCAAATGTTTATTGGAAAGTGGGATGCCTGCATCACTGTA
AGTCAGGTGGGGGGGATCCACCTAGTTCTAGAGCGGCCGCCACCCGCGGTGGAGCTCCAA
TTCGCCTATAGGNGAGTCGTATTACCCCGCTCACTGGCCCC

Figure 11 EEE

122U= AGCCCCGCCCACAATAG
122L= AAAGGTCACAAAGGCAGCAAA

GM552
TATTTACACAGCCAGGAGACAAATAGAAACATCATCATTTATCAGTTTTCTGGTCTAATAAGA
AACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACAGAGTAATGGCTTTAAAAAAGTTCTTAAATCTGAATAGTATGTTGGAGATGTATGTAA
ATGAGGCAACTTGGACTAACAGTGCAAAACAGGACAGTCATTTCTGTGGAAATAAGCTTCAG
GGATTTCCTTGCTGGTCCTCGGATGGGCTAAAAATCAGCTTGCGTGTGACTTTAATGGAGTG
CAGCTCTCACACAGTAAAGCCCCGAAGCAGTAA

552U= CACAGCCAGGAGACAAATAGAA
552L= TGACTGTCCTGTTTTGCACTG

GM501

501U= CAACAGGATTATGGAACAGG
501L= GTATGCGGATTGCATGTTTG

GM602
ATCTGTTGTCTGTGACATCCATTTTGCAATGTGGCGCCAGCCAAAATGCTAAACTGTTTCCTA
ATAATTCTTATCCTGACACTGATTTCTTTTTTTAAATATTGCTTAATAATATAAAAAAAATACAC
CCACACACACACACACACACACACACACACTGTCCTCAGCACATATGTTATCTGACATGGACTG
CTGTCCCGGCATGGGACAGCAGTCTAGTTAATAAGTATAAACCCCATCCATCCAACAAACAT
AATTCAGATCCCATGATGTATTTATTACACACAGCCATAGACCTTTCCCCTGAATTATTTCCA
CCAGTCACTGAATTAAAGATCATATAGGCATGAGGA

602U= TGTCTGTGACATCCATTTTGC
602L= GGACAGCAGTCCATGTCAGA

GM596
CCCATTAATAGCTCTTTGTGTATTGGTGTGTACTTGTATGTTGTGCATGTGTTTGCGTGTGCA
TGCATGTGGGTTCTGACATGGATTGGAGCAGCTAATCACACCATTAATCACAGCGCAGGAC
CAAAGTGACACTTTTCGTCTCCCCACACCTCCAGTGTTTTTCCTTTTAATGCTCACTGTAATG
GGAACACACACACACACACACACACACACACACACACACACACCTACATAAGACTTGTACCAGAGC
AAGTGCCTTAGACTGCAGGCTTATTTTTCTTGAGTTGG

596U= TTCTGACATGGATTGGAGCA
596L= AGCCTGCAGTCTAAGGCACT

GM125
NTNTTGNTCCTNNNGANNNNTTTGGNATNCCNGCCCCCTTTCGAGGTCGACGGTATCGATA
AGCTTGATATCGAATTCCTGCAGCCCCCNGCAGACAGCAGCAGCTGGAGTGGGACGACTCC
ACCCTCACCTACTAAACACACACAAGACACCCAAACAAGAGCTCCCGACACACACATCAGAA

Figure 11 FFF

ACTCACTCATACTCCCTCCCTCACACACACACACACACACACACACACACACACACAC
ACACTCTCTCTCTCACACATGCAGCACTCCCTGCAGTTTCATGTCTAGGAGCCATGATGTAA
AAACTTAACAAAAATAAAATAAAAAAAATCAAGAAAAGGAGAAACATAAAGTCCCTTCAGCGT
ATATATGGTCAAGGTTTTCCTGTTGTTATCTTAAGTGGTGGTCCATATAGAATTCAGCATTTC
CATGCTGGGGAAATAGGTTTTGCAGCTGTTTGAGCTAAGATTTTCAAGTTATTCACAAAATGA
AGANCCATAATGTGTGTCAGGCGAAGAACTCCATTCAAATGGCATGTAATAGCCAGAAACCG
CACTGTTTCGCCGAAATATNGCGATTTTACCCAGGTCCTTAAGGCCGGT

125U= ACTCCACCCTCACCTACTAA
125L= AGGGACTTTATGTTTCTCCTT

GM520
GCCATCCCGCCTCCACACACACACACACACACATACACACACACACACACACACACACA
CACACACACACACATGCTGCGAGGTAACGGCAGACAGGCGCGTGACTCATTAGGCATTCGT
CCCCCAGGGAGATCGCTGGGGGGGCGCGTGCGAGGGAGAGAGAGCGCCGCAGCTGCAG
GAATGTCACGGGCGGCTTCTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCTT
GCTAATGCTGGTTGGAGCCAACGGCGGGGCACTGCACCTTTCANGAAATAACGCATGGAGA
AAGGGGAGGAAAAAAAGGGAAAAAAACATACTTATTAGTTCTCTTTTCCACCAAGTGCTTATT
TAAAAGTCTAAAATGAATTTAGAGAGAAAACATTAGATTGCCTTATAATTTCTGCTTTAATTAG
AATGCTTTTGCT

520U= CGTGACTCATTAGGCATTCG
520L= TTTTCCTCCCCTTTCTCCAT

GM363
GACTTTGATTGCCTTTGACCGCGGCNGCGGCCGNTCTAGAACTAGTGGATCCCCCACAAGAGA
GGAGTCCAGTGGGCGTGGCTGAGCTGGTTTGCTCTGTGGTGGAGATGAACCTTCATGACAAAG
CATGCCAGTCCCAGTCATCCTCCACAGCTGGGAGCGCTTCCCTGGCTCCTGCACAATAATCCA
TGTATACAGAATGATTATACTTTTTATCATTTTCCTTTCTTTTTTTTCCCCTCTCTCTCTCTCT
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGAGGAAAAG
ATAATGGCAACAGGTTTTCTGATCAGCCTGACACATGCCCAAAAAAACCTTTTTTGTTTCAAAA
TAAAACTTGAGTTGATGGCAAGTTTTGCTGCTGGGTTGCTACTTTCATCTGCACACAGATGAA
TGCGTTAACAAAATTCCAGGTAGTATTCAAAGTGTGGTATTAGCAAATTGACCATTTTTGGGC
TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCGGTACCCAGCT
TTTGGTCCTTTAGTGAGGGTTAATTGCGCCCTTGGCCGTAATCATGGGCATAGCTGGTTNCTGN
GTGAAATTGNTATTCCGTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGGGGTAAA
GCCTGGGGTGGCTAAAGAGGGGGCTTACCTAACATAATTTGCGGTGGCGCTTNATGGGCCGG
TTTNCAGTCGGGAAACCTGNCGNGGCC

363U= CCAGTCCCAGTCATCCT
363L= AGAAAACCTGTTGCCATTATC

GM1
TNNAGANCCTCTTNGNAAANCCCGNGGTGTTTNGGCGATCTACNCCTAGTGGATCCCCCAA
AAATCTAGGGCACCCCATTTNACACTCTGTGCTTTTATCAAGTGCATAANGGGATAAACAACA
ACAGCAAGTTTGCCAACTCTCCATTAAAGTTGTGATTTTAGTGTGCTTTTGGGTTTGCTCTCT
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACACACACACACACACACACACACAC

Figure 11 GGG

ACACACACACACACACACAGAGTGTAGAAATGAGTGACTGCTGCACTGTTTTTGTTGTTTT
TTACCATAAGCCTTTTAGCTTTGACTTTATCCTGCCACTTGTAGAGCTGTGAAAGTGGCTGAA
GAGACAAAAATCTATCTCTCAGGTCTGAGGGATCTTACGGTCTTTGGAAAATATTGATCAGC
AGAACTGACTTGGAGTTAAAAAACTGCTCTGTANGAAAGCANCAAGGACATTTGTATCCAGT
GGGCTGCANGNAATTCGGANNTCAAGCTTTATCGATACCGNCGACCTNGAGGGGGGGCCC
GGNACCCAACTTTGTNCCCTTTAGAGANGGTTAATTGCGCGCTNN

1U= ATTTTAGTGTGCTTTTGGGT
1L= AAAAACAGTGCAGCAGTCA

LG 14

GM163
TTTGACTNCCTTGGGNACCGCGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATC
GAATTCCTGCAGCCCCCCTTGGGGCTAGCTAGATTGCTTGACTGCTAGCTAGCACAAAGCA
GTGCTAGCTTAGTGAGGATGTTTTACTTCCTGCTCTTTATCTCCTCACCTGTGTTCATATATG
GTAAAAGCTAATCCATATAGAGGGGTGAGGGGAGATGACCCTTTGTGATCAGCAGGAAGTC
ACACAAACGCACCCCCATTCACACACACTCACTCACTCACGTGCACGCACACACACACACAC
ACACACACACACACACACACACAGTGTTTTAACCTTTTGTGACCATATGGGTGTTACAATGTGTG
GCGCTTGTATTCTTAGAATAAAAGGCTGTTTATTGGAAGGTGGCTAGGAGACAGGTGAGGA
GCATTCAGCTCCAGTAGCTTTGGTTCCGGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCA
CCGGCGGTGGAGCTCCAATTCGCCCTATAGTGAGGTCGTATTACGCGCGCTCNTGGGNCC
GTCGTTTACAACCGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTTGCAC
ACN

163U= TATAGAGGGGTGAGGGGAGAT
163L= AGAATACAAGCGCCACACAT

GM384
GACGTGATTTCCATACAAATTACTGTTGTCATGGTAACTGGTTGAAAGAGGTCATTACCTAG
GTGATATTGGTGACAAATGATGAAAGGCTGGCACTGGACCAAGTGCTCTTCAACAAAGGAC
AAGTGGCTTTCACAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTTACACATGCAGAGAGT
GTCAATCAGCTAGACAGGAGCATGCACAGCCACAAGCAAGTAATCTGCTGTAGACTTCCATC
ATAGGCGAGTTTAGGCGAGTGCTCAAGCGCCTCTAAATTTCATCACAGCACCTCTAAAAACA
ACTGTAGTGATGGTAATAATGATGATGTATTTCAGTATTATCTTCTGATATTGTCCTCTAATGT
TCTATTTTGGAGGATGAAAACTGCCCAGTGTTGTTGATGTGGTGATGTTGCAGTGCGC

384U= AAAGGCTGGCACTGGA
384L= CTAAACTCGCCTATGATGGAA

GM659
GCTGTCCAGCTGTGTTTCCCTTGTGAGATTAATTGCCGAGATAGTGTGTGTGTTTTGCCTGT
GTGTGTGTGTGTGTGTGTGTGTGTTTTGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG

Figure 11 HHH

TGTGTGTGTGTGTNCCTTGCAGGTGAGTTTCCAGGTTAGNGCACACACTGTGCTTGTGTANG
ATATGNGATATTGCTGANGAAGCANTAAAAAGAGTGC

659U= AGCTGTGTTTCCCTTGTGAGA
659L= ACCTGGAAACTCACCTGCAA

GM378
TGGTANNNCCCTCTNGAATGCTCTTTGGANGCGGCCNCGGCCGNTCTAGAACTAGTGGATCCC
CCCCAGGACGGACGAGGTGCTGGCGAAGTCCTGCCTTAgACCTGGGGGAGCGAGATATGAGG
ACCAGCGTGCaAAACACCCACCACACACACACACACACACACACACACACACACACACAC
AGACAGTCATCACCTCCTGGGGTTAATGAAGCTGAAGTAGCGATGGGCTCTGAGATCTGGTGC
CATATGTTAAATTATTAGGACGGGGGGGACAGTAGGGACAGACAGACGGACAGCAAGAGAA
GTCAGTTGGCTCAAATGACAGAGATAACCATAAAAAAAAAGTGACTAAACAGCAAGAATGATT
TCCACTGTCCTGAAATCATTTCAGAAACATCTCTCTCTGTATAAAGATTCAGATTTATAGTGCA
TTCTAAGCACTCTGGCAGGAGGAGCAAACAACTAACCAACAGTCTACAACTCAAATCAAAAA
TCATGAAGTGCAGTCAGGGTGCAGATGGAGGTCCTGCTACTTACTCTCCTCCTGCAGCCGGGG
GGCTGCAGGAATTCGATATCAAGCTTATCGGTTCCGNCGACCTTGAAGGGGGGCCCGGTCCCA
NNTTTGGTCCTTTAGGGAGGGTTAAATGCNCCTTGGNGTAANCATGGCATAGCTGTTTCCGNG
NGAAAATGTTTTCCNGCTCATTTCCCCCAAAATNNTANCCGGAGCTTTTNTAAAGNCGGGGGG
GCCTAAAGGNGGGNGCTTACCCCCANTTAATTGGNGGTGNGCCNNTGNCCCNTTTNACCT

378U= GGGGAGCGAGATATGAGGA
378L= CTGCCAGAGTGCTTAGAATGC

GM576
CCCCAGGGTGCCGAGCGCTAACACTGCTGACCTCTAGAGCAGGTCACCATGACAGCGTGT
GTGTGTATGTGCATTTGATCTTGTTGTTTGGAGCACAACTGTACACGCGCCTTCACGCAATA
ACTCATCTGCCTGCCCTGGAGAACAGAGTGGTCCTGCTATTTCTGCTCAGAGTCATTATCAT
CACCGTTACCTCCTCTGTGACTGCCCCCTTTAACTCCACACCGCCCAAGAATCTCTCTCTCT
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CTGTCCTGCAGGTCAGAGCCAAGTCCAAGAGGCATGGGCTTCATTGGCAGGCAGTGTGAAT
AACAGGAATTGCAGGGAATACTAAGTCCAAAACGGGCTGCACTTTTACACTATTGATAGAAC
ATGGG

576U= CCCTGGAGAACAGAGTGGTC
576L= CTTGGACTTGGCTCTGACCT

GM460
GGNGNTNGGTTNNNTTGTGTTNNGATAGTGATCTNTTGGAACCCCCCCCCTTCGAGGTCGA
CGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCAaTCCATGACTGACAGTGACAGA
CTGACTCTGTCTTCTCTGCCTGTGTCTGTTGTTTTTGTCCTCTGCAACAGGACAAACTCTCTC
TCTCCATCACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACACACACACGCACAATTCTGCCACTCATGTCTCACAACTTCAAAAGAAG
CAAATGAGACAACAAATTATTCAGAAAAGCGTTTGCTCTGGTGATAATTTTCTATCAAACCAG

Figure 11 III

GCTTGTTTTTGCAAATAGATTGCAAACAGAGTCTGCTGGGGGGGATCCACTAGTTCTAGAGC
GGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACT
GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTT
GCAGCACATCCCCCTTTCGCCAGCTGGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCC
TTCCAACAGTTGCGCN

460U= TCTCTGCCTGTGTCTGTTGT
460L= GAGCAAACGCTTTTCTGAATA

GM631
CTGTGGTGCATTTGTGTTTGGGTGAGTCTGAGGGGTGACTGCTTAAGTAAAATATGGTCCAC
CCTTTCTCTCGAATTTAACGTGCTCCACCTGTGGAATGATGAGGAAATTTCTCAAATTATTAC
CAAACCTTTTCTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTTAATTTATGAGAATGTAAAAAAACCCAACCAGGGGGAGCACAAGCCAACAT
GCTCCTGATGCTGATCCCAAACATGGATAAGATGGGGAAGGTTACATCAGGAAGGGCATCC
GGCACAAAACCTTTGCCAAATCAAACATGCGGGTCATCAAGAATGAGATTTTTCAGAACTAA
TCAGTCAG

631U= TCCACCTGTGGAATGATGAG
631L= CATGTTTGGGATCAGCATCA

GM212
TNATNTTNAACANGAAAAGCNNAAAANGACTNCCCNCGAACTGNGGAAAA
CCCCCAGGGGATCCCCCCCNGNGAGTGATGGCGTCCCCTTTTNCCACTT
CCTCCCACAGCATCCTGGGGGNTCCTCCCTCCCTGCTGGNGCCCCCCACG
GNGGCCATCACTCTCCTCCACGCTGAGGTCACACACCTCTGATCCCACTC
ACACTCACGCAGATTCACACACAGNCTCTCACACACACACACACACACAC
ACACACACACACACACACACACACACACACACTTTTATTCACACACACTCAC
TCACACACACTCCTATTCACACACACACTGGTCATGAAAGGAAGTCTCTC
AGTAAATTTAGATAAAAAACGATTTGAGCTTTGAGTTTGTGGTAAAAAGA
GAAACTCTGAGGATGTGCAGAGACCCAGTGAGCTGAAGGCTCGNATGGNC
GNGATGTCGCGGNGCGACNCCGTCACCCTGTAAGGGGGCTGCAGGAATTC
GATATCAAGCTTATCGATACCGNCGACCTCNAGGGGGGGCCCGGNACCCA
GCTTTNGGTCCCTTTANTGAGGGGNAATNGCGCGCTTGGCGNAANCATGG
CATAGCTGNN

212U= CATCCTTCATCATCCTCCCTC
212L= CCTTCAGCTCACTGGGTCTC

GM597
CCCCACTTGGGTTTGAGCTTGGAGTAGTGCACACACACCACACACACACACACACACACAC
ACACACACACACACACACACAGTCAGCTGAATGCACTTTATCTTTTCTGATCAATGGTGCGGGA
TTACAGAGG

Figure 11 JJJ

597U= ACTTGGGTTTGAGCTTGGAG
597L= CTCTGTAATCCCGCACCATT

GM338
TTGCTTGTNAANCCCTTTGGAAGCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCG
AATTCCTGCAGCCCCCTGCTGTGCCCACGTGGAGCCTCAACGCTCATTTCACAACACGGAC
TCAGcGGGGATGCAAATGTGACGTCGTGCAGCCAAACTTTCATCATGTGACGTTTTCACACC
CGAAATCTGCTACACACACACACACACACACACACACACACACACACTCACAGACTCACTCACTCA
CACACACACACACACACACACTCACAGACTCACTCACTCACACACACACACACACACTGCTG
GCACGCTGCTCGGCTGCGTCGGGGGAGAAGCGGCGGACGGACGGGTCACCCAGCTCGGT
TGGCAGCTCAGCTCCGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGC
TCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCG
TGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCA
GCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGGCCTTNCAACAGTTTGCGCAGNCTGA
ATGGCGAATGGAAATTGTAAGCGTTAATATTTTGGTAAAATTCGGCGTTAAATTTTTGGTNAA
ATCAGCTCATTTTTTAAACCAATAGGCCGAAAATTGGGNAAAATCCCTTTTTNAATTCAAAGN
AATTGACCGAGATAGGGTTGNANTNGTTGTTCCAAGTTTTGGAACAAAGAGNTCCCTNTTTA
AGGAACGGNGGCN

338U= TCGTGCAGCCAAACTTTCATC
338L= CGACGCAGCCGAGCAG

GM283
TTTNATCCCTTNNATTGGCCCCNCCCTTNAGGTCGACGGTCTCGATAAGCTTGATATCGAAT
TCCTGCAGCCCCCGGATTGTGACAAGGAGCCAGAACTCACAGGATCGacATaGATCCAGCCT
GCTCTGTCCATCTGCTCCAAGCTTCATTCCCAGCATATCAATACCCCATGTCACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGAGCACTCTGTCA
CCTGCGACTTCTCCTGGTCCCATCACTCTCCCACCACTCCAGCCCTTGGCTGCAAAGCCTG
CTTATGTTTCATCCTGACACTTAGAGAAAATCCTTGCTTGTCTATAAGCGCATTCAGCACCAC
ACAAAGGGAACGGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTC
CAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTNACTGGCCGTNNGTTTACAACCGTNGT
GACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATNCCCCCTTTTCGCC
AGCTTGGCNTAAATAANCCGAAAGAGGCCNGCAACCNGATCGGCCCNTTNCCAAACAGTTG
CGCANCCCTGAATGGCGAATNGGAAATTGNTAGGNGTT

283U= ATTGTGACAAGGAGCCAGAAC
283L= AAGTCGCAGGTGACAGAGTG

GM47
GGAGGNGGNTNTTNGTTCAAGGAGGGAATTANANTNNACACTCNTTNGTT
TNGNATAGANCTAGTGGATCCCCCGCTCGGCATCTCCCAGCCTCGTGCAC
AGAAAAACACACATGCATGTTTCAGTAAATAAGGGACCTCTATCGTCGCA
GGTAGACTGAAGGCGCACGCACACCTGCTCATCTAATGAGAGCACTATCA
CCTGGACTCTCCTGCCTCAATTAGCCTCTGTTCCTCCTTCAGCGAGAAAC
ACACACACACACACACACACACACACACACACACACACACACACACACAGAAAG
ACCGAGTCACTCAGGTTTATAGTATACACACAATACACTTCTGTCCCCAA

Figure 11 KKK

GAGGACTTCGCCACTCTACGCTCTCCTGCACAGTGCAGCACTCAGCTCTT
TAGCAGCATTAAATCAACAGGGGGCTGCAGGAATTCGATATCAAGCTTAT
CGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTT
TAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAAGCTGGTTC
CTGNGTGAAAATTGTTATCCGCTCACAATTNCACACAACATACGAGCC

47U= GTCGCAGGTAGACTGAAGG
47L= TCTTGGGGACAGAAGTGTATT

LG 15

GM197
TTTGATGCCTTTGGAACCACCGCGGTGGTTTGNCGCTCTAGACCTAGTGGATCCCCCCCAT
GGACACCAGAACAGGAAAGTGATGAACACACACACACATCTACACACACACTGACTCAGCA
TGAAGTGATACACACACATGAACACATGTGAACTCGTTGACTGAGTGAGAAATGACACACAC
ACCTACACCGAAATGGTGATTCATTGAGAAGTGATCCACACACAAAATACACATGCAGACGC
TCGTGCAATGAAGAGTAATGCACACACACATGCTCGTGCAATGAAGAATGCTTTGCTAACAA
ATGCTTATGCTGATATGCAAAATGCTGCATACACACACACACACACACACACACACACACAC
AGACTCTGTTACAAGAAGCCATTGATTACACAGAACGCATTTTATGTCATCCAGAGGGCACA
TTATGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGC
CCCGGTACCCAGCTTTTTGTTCCCTTTTAGTGGAGGGGTTAATTGCGCGCTTGGGCGTAATC
ATGGTCATAAGCTGTTTCCCTTGGGTGAAAATTGGTTATTNCCGCTTCACAATTTCCACACAA
CATACNGAGCCCGGAAGCATTTAAAAGGTGTAAAA

197U= CTCGTGCAATGAAGAGTAATG
197L= GCGTTCTGTGTAATCAATGG

GM538
ATCTGGACCAACAACCATATTCAAAGTCAATGAAATCAACTTTCTTCCTCATTCTGATGCAAC
TCTCAGTTTGAAGTTCAGCATGTTGTCTGGATCTTGTCTAGATGACTACGGAAAGTGTGAAA
AGTATACCTAATAAAGTGTCTGGTGATGATTTGCACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAAGT
GATCAGTGGACCTAAGAACAGACCACAGCAACAAA

538U= CAGCATGTTGTCTGGATCTTG
538L= TTTGTTGCTGTGGTCTGTTCTT

GM531
ACTGACACACAAAAAAAAGCCAACGGTCTGAATTGAGATGAAAATACTGCTGTGGAGGGAG
CGACGCTNAAAATACCAGGCAGGGCTGCAATTAGTGGTGTGTGCGCGGAGCAGCTGCTGC
GGTTCAGAGCACTAAGTGTCTCTAATTACTGCTGCAGAGAGTGTGTGTGTGTGTGTGTGT
GTGTATGCTGATATGTGCACGCCCAACCCATGAGGGGTGTCCTCTGCTGAGTATCTCTATTT
AACATGCTCTGTGTGTGTGTGAGTGTGTGTGTA

Figure 11.LLL

531U= AAAGCCAACGGTCTGAATTG
531L= AGCAGAGGACACCCCTCAT

GM211
ATNTTGTAACATGAAAAGATTTANAANGAACTNCCCCGCGTACTTGGGNA
AAAACCCCCAGGGGATCCCCCCNGGAGTCAGTTACTGCACAGTTTTTTGG
CAAGTTGAGAGGCTACTGTTAAACCTAACCACACACACACACACACACAC
ACACACACGCACACGCACACACACACACACACACACACACACACACACAA
TAAGAGCAGAAGCATGTGTTCCTGAGCATTGCAGATATGTAACTGGTAAA
CATGCCAACTAAGGTTGTGGGTTGTTTTCACATTGGCTCTGTGTGCATGA
AGGCGTTTTAATGACAGCTTTTGGGCTGCAGGAATTCGATATCAAGCTTA
TCGATACCGNCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCT
TTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTC
CTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA
AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATT
AATTGCGTTGCGCTCACTGCCCGNTTTCCAGTCGGGAAACCTGGCGNGCC
AGCTGCATTAANA

211U= GCAAGTTGAGAGGCTACTGT
211L= AAACAACCCACAACCTTAGTT

GM412
AGGGTNNTNANNTTATNTTNTANTTGNNNTNNAATNTGATGCCNCCCCCTTTCGAGGTCGAC
GGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCGaCATTGTCGGTGGACATTAACGC
CACActGTGCAGTAGTGACCTTGAATTAATTTACAGCACGATGCTGCTGAGCCAAGACCTCAT
TCACACACACACACACACACACACACACACACACACACACACAAAAACGCAAAACATCGGCAGCATTG
TTTCCTTCAGAAAATGAGGTCACGTTAAACTACTTCCAGTGCCATATATGGGCAAAAACATCA
TCCAATACACACACAGCAGAGTTTACAGAACACACCAGTTTGTTATTCAAATAAAAGATCAAC
TGTGATAAGTCCTAAGTGTCTAATTTATTAGAAATGTTCAAAACGGAGACAATTAAATCGCAT
CTTTTGTGTTTACAATGTGACAACACAAACACCACTTTTGTCTGCGTTTGCCTGGTCCTTTAG
GCTCAGGCAGCAGCATTATGTTGGTCTTGTTTGCTTCTTTCAGCTTTGCTTCCCCAGTCTTAT
CCAGTCCATCATCCTTTTTCCAACACGAGCCATCTCCCTAGCAGCCAAGCCAG

412U= TGCTGCTGAGCCAAGA
412L= GTCTCCGTTTTGAACATTTCT

GM348
TTGATCCCTTGCTCCCGGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCCACCTCGGC
TCAGCTTAGCCCGGCGCACTGCTTTTAGCACACGGCATTTNCACGTGCATGTCCCTGCCAC
ATACCATGGCGTGCACGTCAACACACCAGCGCACACACACACTCTACATGGCAGTGTTATTT
ACTGAGATGTATATATACATTCACAGGACTGATTACAGCCGCTAAGAAGTGTATCTCAAACTG
TAAATAATTCAACATAGACAAGCAGCTTGGCTCTGACCTCACACTTGACTCAGCAGAAACAC
ACACACACACACACACACACAAGCAAACTGTAGGTTCAGCTAATGGATGTTTACAACTGTTCATT
TGTGGATTAGCTGCTTGTGCATGCAGCATTTTCGTCTGCAAGAAGGAGAAAAGTGGGCTGC
AGGAATTCGATATCAAAGCTTATCGATACCGTCGANCTNGAAAGGGGGGGCCCGGGTANCC
CAGNTTTTTGGTNCCCTTTAAGNGAGGGGTTNAATTNCCCCGCTTTGGCCGTNATTCAATGG
GNCANTAGGCTTGGTTTCCCTGGGGNGGNAAG

Figure 11 MMM

348U= CCACCATGCCATCCACA
348L= TGTCGGTAGGAGCCAAATACA

GM20
TNNNTTNTNTCTTNGATAGNNATCTNTTGGAAACCCCGNCCCNTTTCGAGGTCGACNGTATC
GATAAGCTTGATATCGAATTCCTGCAGCCCCcTGAGGGTTTCTTAAGCCACATTTATCTGCTC
GTTTGTCAAGCGAACTCATATATCTAAGTGCAAATAATTGTTTTAACCCCCTCCCCACACACA
CACACACACACACACACACACACCCAAACAAACAAACAAACACGTGTGTGCCTGTTTACATC
TGTGATCTAATTTCTTCTCGTCTCTGTGTGCACACTCTCTGTCCCAGCGGTGTAGTGTGTAGT
AAGAGGGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCC
CTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAA
ACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAAT
AGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGG
AAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGGTAAATCAC

20U= TAAAGCCACATTTATCTGCTC
20L= CTACACCGCTGGGACA

GM567
TCTAAATGCTCTAACTGATCTGTACACAAGAGTACGTTAATGTACACACACACACACACACAC
ACACACACAAATTACAGGGCAACAATTTGCATAGCAGTCAAATGTGAGCGCACACCGAGAC
GTTTCCCCTTACCTGTGCTGTAGAGCGTCCGTGTTTTCTTCTTCGGTGCAGGTGGCAGCAG
GCAGCTGTCCACAGACTCTATCCCTGGCAGCAGTGGGAAGCTGAGGGCTCGACCTC

567U= AAATGCTCTAACTGATCTGTACACAAG
567L= GGACGCTCTACAGCACAGGT

GM437
GNNNNTTNNNTNNNNCTANNGATCCTTTGGAAGCNCCCCGCGNTGGCGGCCGCTCTAGAA
CTAGTGGATCCCCCCCCTGATGTGTCACAAGGGTTTGTCAAGATCACAGCAGGGTCCCCAAG
AGATAATCTCAGTTTTGGGTTTTGGAGGCAGGGCGTAAAAGAGGGTGTGTGTTGTTAGG
CTGCTGGCAGCTGACAGAGATACACAGCATGCACAAATAGAAAGTACGAGAAAGATGACAA
TACGCTGAGGTCACACAAACACGCGCGCTCGCACACTGCTCATGCAAATGCACACGCATTC
ATTCACGCCTTGATGGCACCATCTGCCCTCTCCTGCAGCCTCTCTGTAAGCCTGGATGCAAA
CTGTTGCTTATAATATCATACCTGCTGAGTAATATGCACACGCACACACACACACGCATGCAT
ATGGACACACACACTTACATATGCTCAAACAGCAGTGAAAAAGTTGTAAGTAGTTTGACAGA
AAAAGATCAGGAATATGAAAAACGCACGCACACACACACTNACACACACACACACACACACA
CACACACACTTACACACACACACACGCACACACACACTTACACACACACACACACACACACA
CACACACACACACACACACACACACACACNACGTGTTCTTGATCCT

437U= AGCCCCTTAATGAGATCAAAG
437L= CCTCTCTGTAAGCCTGGATG

Figure 11 NNN

GM234
TTNGATCCCTTGAACGCCNNTCCTTTAGGTCNACGGTCNCGATAAGCTTGATATCGAATTCC
TGCAGCCCATCGCTGTGTATTTCTATCACAGAGGACAGTGTTTACcaTCACTCTCTGTTTCCC
TTAATCTGAAACGTTATTTGCATCTTTCCTCAAGGGATGACTCGGTCGTGTCTCCCTCTGCTT
CAGTGAGTTAGAGAAGTGTGTGTGTGTGTGTGTGTGTGTGCGTGCGTGTGTGTGTGTGC
ATTTCTGCATGTGTGTCTGCCGCTCCTCTTTAATTACCGTCTcTTTTTCTCTGCACCATTGCTA
AACTTCCTCCACAGGTTCCTGCTGGTGTCTGAGTGTGTGGGCAACATGCCAATGACAGTCTT
TTCATTTCACAGAATAGGGTGGCATGGTAGTGCAGTGGTTACCCCTGTcTCCTCACAGcAAG
TCGGTCCCACGTTTGAATCCTGGACGGCGCATcTCTGCGTGGACTTTGCTCCGGGTTCTTNC
TGCAGTCCAAACACATGCAGTTAGCTGAGAATTCGAACTGACTGTGCGTGTNNCACGATCTT
ATAGCCCCGNGTTGGTGTCTTACTGCATATCTTAATAATGTTAGTGCTNAGGTGCTTTTTACC
CTAACAATTCACATCTCGCCTTCTTTTCCGNNCATCAAGAN

234U= ATCGCTGTGTATTTCTATCAC
234L= ATGCCACCCTATTCTGT

GM599
CCCAGTTCATATTACCATCAAGTTGGTGCTCCACAAACACTTTCACAGAAGCACATACAGAAT
AGCGCACTGTTGCATTTGCATGAAGACAAGTTCATCAGTTCCTCAACCTCTCCCGACCCCCT
CTGATTTCCTGCCCAGCCACTCCTATTACCTGCAGAAACAGGAAAATGGTTATACATCCTCC
ATACATCTACAGTGGTGGGTGTTTGCCATGCAGTAAATGGCTGGAATATTAAATGAGTTTATT
GGATGCTTCTATACAGGCGCCGCTGCAGAAATAGGACTGAATTATACATAGATTTAGAGATG
TGTGTGTGTGTGTGTGTGTGTGTGGAGTGGGAAAATAGGGGGAGAGAAAAACAAAGCAGCA
AAGGTCTATGTAGAATCAGCTGTCAATTATGCTGG

599U= CATGCAGTAAATGGCTGGAA
599L= CCAGCATAATTGACAGCTGATT

GM502

502U=
502L=

GM515
CCCAAGGACAAATAAATATATCCCGTGTATTTAGTTATTTATAGACACGCGTGCGTGTGCGT
GTGTTCTGTCTGTCATGAGTAAGAGACTATTACACCTCTCGGAAAACTGGGACGCGGTACAT
GCGAGTGCCTGTGGAGATGTACAAAAGAGGAGAAGAGCCACACACACACACACACACACAC
ACACTCACAGGAATAATTAATCAATATTGTTTCCATTAGCAAGCCGGAGAAGGAAGACACTG
CACCATAATTAGGAGACACTGCAGAGCTGCAACCTCCTCTCATCAAGCAGTAAATCAAGATG
TACACACACACACTCACACACACACACACACTGCAGGCTTTTTTTTTTTTTTTTTTGCATGACC
TCTCTTCATGACAGATTCTAAATGACCACAAATGACTCAGGAATGGACGTTTTGTTATGTCAT
CAAAGGCAAAAAAAGACACTAAGGGTAGGGCAGGG

515U= CGAGTGCCTGTGGAGATGTA
515L= CTGTCATGAAGAGAGGTCATGC

Figure 11 OOO

GM358
TTTGANATTCCNTNGGCACTGGCCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATAT
CGAATTCCTGCAGCCCCCATAATAAACCTTCCACATAGTTACCTGTTCTGTTTCCACCATATC
CCTGTCTCACACACACACACACACACACACACACACACACACACACACACACACACACACACTACTTA
ACACACTGGAACTTCCAGACCCGCCCAGTCATGTTTTATTGAAGTCTCCTTTATTTGTTTGCT
TGGATCAGCGACTTTTAGGTATTTTGTTTTTTTACTTAGTCATTTTTATTACTTTTTTTTTTTTT
TTTTTTTGCTTTGGTCAGCCATCTTGGCAGTAATGGCTGGCATGGCACATGATGATGACTGC
ATTGCGTTACCTTTGGtGCATGCAACACATGCTTGAAGCCCAGAGAGCGACACACCCATCCA
AACATCTGCTGCTTGGCAGGGCTCCAGCAGGGGGGGGATCCACTAGTTCTAGAGCGGCCGC
AACCGGNGGTGGAGCTCCCATTCGCCTATAAGGGNGTCNNTTTANCCGCGCTTACTGGGCC
CGTNNGTTTACAAACGNTCNCGGACTNGGGAAAACCCTTGGGGGTTACCCAACTTAATTCN
CCTTTGNAAGAANAATCCCCCTTTTTTGGCAAGGTTNGGGGNGTNANN

358U= ACCTGTTCTGTTTCCACC
358L= AAATACCTAAAAGTCGCTGAT

GM517
TGACAAANCCCTTTTTTTTCTTTNTTTTNTTTTTTTTGCTTAACTCTAAGCAACTACAGCAGTAA
TAAATAAGATTCTTCACTTATAAATCTCACATATGTATTATGTAGCACTGACATGTGCAAGGAT
GTGTACACACACACACACACACACACACACACACACACTTTTATGTGTTGATGAGGGTGACAGTAT
TCTAGGTAGTCATGCAGTAGGAGACCCTCTGTTG

517U= GCACTGACATGTGCAAGGAT
517L= CAACAGAGGGTCTCCTACTGC

GM193
TTTGAAATCCTTGGACCGGCCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATCGA
ATTCCTGCAGCCCACAACGTTGGTGTAACTCCAACACACACTAACCTTTGAAACAACACCAA
ACCAATTAGACTTCTCCACTGTCTTGAACATGTTACCTAGCAACATTGTATCCCTGCAGTGAC
TTTGTGCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGATTTTGTGCTGCAAGA
GGAATCTCCATGGAAACAACAACAGGCAGACACAACAGCACAGCTTGACTCACCTGAAAAT
CATCTGTCCTACAGATAAAACACAGGCGAACGAACCGAGTCTTTGTTTGTGGCTCGTAGTGT
CTAAATAGGACCTTTAGCCAATAAGATCCGAGAAAAATCCAAAGACGGATTACATNCTAAAT
GTTAATCACAACTCATGGGATGTGTGTAGACAACTCTAACACACTTCCTGNCACACCTGTTTT
ANTGGCAACTTAATTAANAATNGGAAGNNTTGCATTNAATATNGGACCATNATTTTGGGGGG
GATCCCNCTTNNTTTNTTANAAGCNGGCCCNGCNNTCNTNNGGGGGGGGAGCCTCCNAAAT
TNGGCCCTTTTATAGNNGGAATTTTCGCTATTTTNCNGTNGNNGANNTTANATGGGGCTCCC
TTNCC

193U= ACCTAGCAACATTGTATCCCT
193L= TCGCCTGTGTTTTATCTGTAG

GM676
GCAATCCTNCTCGGNACCCCCTTGTGGTTCTTACCCGAGTGACTC
CCTGCAGGTTCAGGGAGAAGAGGTGAGGATTCACGGCGATGAAGTCTCCG

Figure 11 PPP

TAGAACTCCTGCAGACACACACACACACACACACACACACACACACAC
ACACACACACACACACACAGACAGTAAGCTATACTTCTGCTATTTTGGTT
TTGATGATGTCACTCAGGTGTATGAACTGTGTTCACACCAAACATGAAGC
AGAGTGATGGTGATGCTCACGCAGGGAGGAGGACAGCTTTCCAAGACATC
CTATGAATTCTCGGCACAGTTTTGTTCTGTGTCTGCATTAAAATTAAATT
TGATCAAACAGCTCGG

676U= GATTCACGGCGATGAAGTCT
676L= CGTGAGCATCACCATCACTC

GM94
NNNNGNNGGNNNNGNNNNNNTANNTTTNTNTTCNATNGGAACGNGGATCNAANGGGAACG
GCTCNTTCGTANTGGGGAAACNTACCNATAAGCTTGATATCGAATTCCTGCAGCCCAAATTN
TGNTNTCTGCTGCCTTGATTGATGATNGGCNNGGTTTTTTCTTGCTCACTTTCTCTTTACTCT
ATCCAGATTGTTTCTCGACCAGCTAAGTCTATAATATTGGGAAAGATGTTTTGATTGTCAACA
ATCCAAACACACACATAAACACACACACACACACACACACACACACACACACACACACACAA
ATGCACCCCCAAACTCATACGTTCATACTCAAACGCATATTTCTATACCTTGAGCAACCCCAC
CCTGAAGTGGACTCCACTTTATGAACTGTTTAGAGAGACACTGGTAAGTGGAATATAAATATA
CATTNGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGNGGAGCTCCAATTCGCCC
TATAGNGAGTCGNATTACGCGCGCTCACTGGCCGNCGNTTTACAACGNCGNGACTGGGAAA
ACCCTGGCGNTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGNAA
TAGCGAANAGGCC

94U= TTGGGAAAGATGTTTTGAT
94L= GAAATATGCGTTTGAGTATGA

LG 16

GM207
TTNTNTTTNTNTCNNGTAGNTTCTCACNCGATTGGCCCNTCCTTTTTGGGTTAAGGTANCCNA
TAAGCTTGATATCGAATTCCTGCAGCCCAAATCTTACNNTGAGATCATCCCATAAAAAGGCTT
TCTNTCTCTCTCTCTCTCTCCCTCTCTCTCTGTCACACACACACACACACACACACACACACA
CACACACACACACACAAGATCCAATAGTTGGGTTGCAGTCACGTGGTTCTGATGACGTGCG
GAGGCAGCGCGATTTTTGAGTGGAGGGCGGAAGTAAACATGGAGGACACTGTGGAGAGTC
AGGAGAGCAGCTATTGTGCAACTTTAGACCCCGTTTCTCGGGAGAGATATAAACAGATAGTT
AAAAAATATATCGGACGTGATCCGTATTCTTTGAAAATGTCCGAATACACCACAGCAGTAAAG
GATTTGCCTACTATCGAGGCTGTGGATGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCG
CGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCCGTCGTT
TTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGC

207U= CAATGAGATCATCCCATAAAA
207L= GTGACTGCAACCCAACTATT

GM134
TTNTATNTTCATGTGANTCNNNNTCTCCCCCGCGNTGGCNGCCGCTCTAGAACTAGTGGATC
CCCCACCAGCAGAATAAGGTNGGNTCACCATACAGTCTTAGTGACAGCTGAGTATTGAAAA
GGCTGCTTGCAGAAGAGAGGTGCCTCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTTT

Figure 11 QQQ

GTGTTTGTGTGCCTATGAGAAGAAGAGAGAGACAAGACACAACAAAAAAGAATAGGAGATA
GTCTGTTGCCCTCAGACACATCTTTGCACTCCAAGGCATCACACTGGGTGTGTGCGTTTGTG
AGGTTCTGCATATTTTGAGCACTTTTTGAGCAAGATTTAATTAAATTAAATTTAAATTTAATTCAA
TTTTATTTATATAGCGCCAAATCCCAACAACAGTCACTTCAAGGCGCGTTATATTGTAAGGTA
GACCCTACAGTAATACATACNAAGAAANACCCAACNATCATATGACCCTGAGCNGGCACTTT
GGTTGACAGTGGNAAGGAAAAACTCTCCTTCAACANGAAA

134U= ATAAGGTCGGGTCACCAT
134L= AGGGCAACAGACTATCTCT

GM221
TTGTNNNNCCTCGTNAATGCNCTTTTGAANGCGGCCNCGGCCGNTNTAGAACTAGTGGAtCCC
CCCCAATTGATGAAGAGGTAACACCAGAGTAGAGGCTATTaCAGAAGTCGAGGCGAGATGAG
ATGAAGCCATGGGTCGCTGTGATATATGCCACACACACACACACACAAACACACACACACAC
ACACACACACACACACACACACACACACACACACCGTTATTGCTCACGATCACGTTTTTTATTTA
TAATAACAATGCACCGTGACAGCTCGTCCCGGTCCAGCCAGCCTCCCACTCGACTCTGCCGTC
ACTATATAGACACACAGAAGGAAGACACTCATGACACAATCGCCACCACCTGTGGCTCACCT
GCCTCCCGGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGG
GCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTC
ATAGCTGGTTNCTGTGTGAAATTGTTATCCGCTCACAATTTCACACAACATACGAGCCGGAAG
CATAAAGTGTAAAGNCTGGGGTGGCCTAATGAGTGAGCTTACTACATTAATTGGCGTTGCGCT
CACTGGCCGCTTTTCANGTCGGGGAAACTTNNTCGTNNCNANGTTGCANTTATTGAATTCGGC
CAACNCCCCGGGANAGGCCGGTTTCCGTTTTGGGCGCTTTTTCCGCTTCTTGGTTAATTGACTT
GCTTGCGCTTGGNNCCTTNCGGTTGGGGCGANCNGGTATNAAGCTTANTTNAANGGCGGNAA
TACCGGGTTNTCACANAAT

221U= TACAGAAGTCGAGGCGAGATG
221L= GTGGTGGCGATTGTGTCAT

GM183
GGGTNGANTCTCTTTGACATAAGACTCTTGGAAAGCCCCCGCTTTGGCNGCCGCNCTAGAACT
AGTGGATCCCCCCCCTGCATTTTGTCTGcCTCAGTCTCCTGGGGGCAGTTATTGCaGCTTCCTGTG
CTCATTATCATTATCTATCACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACCACAAGAAAATTGCTGATTTATGTGTCATGGCATGTTTTTTTCCCTTTGGGTTTCC
TTACAGATACAGTTTGTGATACATCATGCTTTTCTATTTGTGTTCAATCCTTTTATTATATTTTC
TTCTATTTTCTCCCCCATGTTTTGTTTTTTCTGCCGGTCAGCTTAGACATCAGGCAGCAGTGGT
GGGACGCCATCACATGTAGACAAACTGGAATCTAACCATTGTGTGAAAGAATGTAGGGGGAC
AGACGTTTCAAACACAGCAAGTGTGGGCTGCAGGAATTCNATATCAAGCTTATCGATACCGTC
GACCTTCAGGGGGNGGGCCCGGTACCCCCAGCNTTTTGGTCCCCTTTNAAGTGGATGGGTTTN
AATTGCCCCCCCTTTTGCCGNTAAATNCGNGGGNCCANAANNTTNGTTTTNCTGGGNGGTGNA
ANNCCGGNNCNCCCCNTTNAAAAATTNCCCNCAAANNATTTATCCTTCCCCCCCCCCT

183U= AGTTATTGCGGCTTCCTGTG
183L= AAACAAAACATGGGGGAGAAA

GM138
TNCGTTNCCCGCGGNGGCGGCCGCTCTAGAACTAGTGGATCCCCCACGAT
GACCTTAAGCAGAGCTAGATAAAAATGAAACCCATCGTGTCTCCGTTTAT

Figure 11 RRR

GGNTTACCAAATGAAGAANGAGTGCCCCGCCAAAGTAAAACAACACAGTC
CAAGTTCCAGATCTGCTCACAGCATTTGCTGCTGGCGGCATATTTTTTTT
GGCTATTACACGAGTTTTAGTCTTTTAGTGACATGATGAGGATGTCAGGG
GGTCAGAGGTCACAGAGAGATGGATGAACCCTNATTTGTCTCAGACTTAA
AGTGACCTGTGTGGGCTATTATGAAACAACTGCACTTGTAGAATCATGAT
CAAGGAGATAAGATGAGAGGAGCGGGACTGTTGCTCACAGAAGGGTTATT
AGAAAATGCTGTGTGTGCGTGCGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGCAATTCCAGCGCCTNATTATTGCTCAGTTGCTTGGAGACTGCCACAG
GGCAGCGTTCACACGGGGGCTGCANGAATTCGATATCAAGCTTATCC

138U= CTGTGTGGGCTATTATGAAAC
138L= GGCAGTCTCCAAGCAA

GM528
GCAGCACACTGTTCAAATGTAAAATGCTTCCACGCACCTTTGGTGAAACGTACAGCGCTGTG
ATCTCCAAACACATCGTCTGTATCCTTGAAGCCTGCAGATATGCTGAATGCATCCCCTCTTG
GTGGCTCAGGGTCTTTTTTCTCCTGCCTTTGTGGCACACTTTGTGTTTCTGTGCACTCTGCT
GCTCCCAGCTGTCAATGAATGGTTTTCAAGGAAACCACAGAGAGCAGCGAGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCACATTACAGGCAAAAA
CACCCATCAGCTCTGCACGGGTGGTTCTGTGATGTCAGTGTTTTCTACATACAGGCTTTACC
TCAGCGGGCT

528U= TTTTTCTCCTGCCTTTGTGG
528L= CGCTGAGGTAAAGCCTGTATG

GM497

497U=
497L=

GM609
AACCCACCCTAGTTTAAATACTCAGACACACACACTCACACGTCACCTCAATCCTTCCCAGA
GTGCCTTTGTTCTGTCGATTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTTATAAGGAGAGAGAATCATGCCATACGAAAAATGACAACCAGTAAGGACCGTGCC
TGCCAAAAACCTAAGACATACAAAGCATGAGGTGT

609U= TCCCAGAGTGCCTTTGTTCT
609L= GCACGGTCCTTACTGGTTGT

GM71
ANNTCCNNAAGCNCTTTGGAATACCCCGGCCCTTTCTGGAGGTCGACGGTATCGATAAGCT
TGATATCGAATTCCTGCAGCCCTTAAAAAACAAAACAAAAACAAAAGCAGNTCTCTTGGCAAT
TTGCTTAGGTGGCGGGCTGTTGCCTGCATGGTGCCTTTCGTGACTGTTATTCCCACAGGAA
GTGAAGGTTGTGGAATGCCCCTGCAGTCTCTCTCCATATGCCCAGAAAAAGGAACACACAC
ACACACACACACACGCACACACACACACACACACACACACACACACACACAAGCAAGGACAGG
AGAGGCTTTGCTTTATTGTGTGGAACACTATATTTATGGATAATGTTTGATTCTTGGGGGGG

Figure 11 SSS

GATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGT
CGTATTACGCGCGCTCACTGGCCCGTCGTTTTACAACGGTCGTGACTGGGAAAACCCTTGG
CGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTNGGCGTAATAGCGAA
GAGGCCCGCACCGATCGCNCTTCCNAACAGTTGCGCANCTGAAT

71U= ATGCCCCTGCAGTCTCT
71L= ATAAAGCAAAGCCTCTCCTGT

GM304
TGCAGGGCTGGAGGTAGCAGGAGTCCACTGTTACTGCACAACGCTCGCGC
ACAGACACATGCACACACAAAACCTCTCATCCCTCTGGAGAAAATGAATT
CTCTTTCTCTTTTTCCTCTTTTCCCCCCCTTTACCTTTTTGCCTCTGTCA
GCGCAACTACCATAACTTCAACCTGAACACAAATCCCATCTCTCACACAC
AAACATGCACACACACATATATGCACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACAAAGAGTCACTCAC
CTGGTCACCTGCCCGAGGGGTTGTGATGCTGTTTCACTCTTTGCAGGGGT
CTCTGTTTCGTGTCCGCCT

304U= AGCGCAACTACCATAACTTCA
304L= GCAGGTGACCAGGTGAGT

LG 17

GM470
ATATTGTGTGAGGGGGTGTCTTCCTGGTGTCATGCTGTGCTGGCAATATT
GCAAAAGACATGCTCAGGTGTGCGTTCAAGTGTGTGTGTGTGTGTGTGTG
CGTGTGTGTGTGTAAGACAGAGAGAGATAAGGATCTTTGTCTATTTCCGC
ACCTGCTTAAAGAGTTGTGGGACCGTGATCTGATTGGCGTCTCCTGAACA
GGGACTTCTGGTATGGACGGAGGCTCAGTGACCGGCGTCTGTTCCTGTGA
TAACAGGGGAGGGGAAATGTGAAACACCAGCATACTGAATGACAAGAGAG
TGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAAT
TCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACA
ACGTNCGTGACTGGGAAAACCCTGGCGTTACCCANCTTAATCGCCTTGCA
GCACATTCCCCTTTNGCCAGCTGGCGTTAATAGCNAAAAAGCCCCGCACC
GGNTCGCCCTTTCCAACAGTTTCTCCATCCTNAAATGGCCGAATGGAAAT
TTGTAAGCCGTT

470U= GGGTGTCTTCCTGGTGTCA
470L= ATCCCCCACTCTCTTGTCATT

GM403
ATATTGTGTGAGGGGGTGTCTTCCTGGTGTCATGCTGTGCTGGCAATATT
GCAAAAGACATGCTCAGGTGTGCGTTCAAGTGTGTGTGTGTGTGTGTGTG
CGTGTGTGTGTGTAAGACAGAGAGAGATAAGGATCTTTGTCTATTTCCGC
ACCTGCTTAAAGAGTTGTGGGACCGTGATCTGATTGGCGTCTCCTGAACA
GGGACTTCTGGTATGGACGGAGGCTCAGTGACCGGCGTCTGTTCCTGTGA
TAACAGGGGAGGGGAAATGTGAAACACCAGCATACTGAATGACAAGAGAG
TGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAAT

Figure 11 TTT

TCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACA
ACGTNCGTGACTGGGAAAACCCTGGCGTTACCCANCTTAATCGCCTTGCA
GCACATTCCCCTTTNGCCAGCTGGCGTTAATAGCNAAAAAGCCCCGCACC
GGNTCGCCCTTTCCAACAGTTTCTCCATCCTNAAATGGCCGAATGGAAAT
TTGTAAGCCGTT

403U= GGGTGTCTTCCTGGTGTCA
403L= ATCCCCCACTCTCTTGTCATT

GM569

PROLACTIN

GM159
TTGAAGACCGTAGCTCCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCACAGT
GAGATCAAGACCTGGAAACATTTTGGGGTATGTAGGAATTTTGAAGTGTGTGTGTGTGTGTG
TGTGGTGTTTTTCACCACAATATGCCAACTAATTGAAAATGTTTAGACAGATCCTAACATCAC
TACTAAAAAAACCTGTGATGGTAATGTAGTCTTTCTTCTAGGGTTTCTAAGGGGTTGTTGCAC
ATTTATCAGCTAATGAGAAGTGTTATCAGACATTAGATGGGTTGCTATGCAGCTTGTTTATCT
CANTGATTGNCCACAGATAATGCCTTAGTAAGCATTCAGTGCATTATCAGTTAAATTGCCTAT
TTCCCCTCATGTATATTAAACTACTCCTGATGTGGTGGGCTGCAGGAATTCGATATCAAGCTT
ATCGATACCGTCGACCTCNAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGG
TTAATTGCNCGCTTGGCCGTAATCATGGGCATAGCTGTTTCCTGTGTGAAAATTGTTATCCC
GCTCACCAATTTCCACCACCAACATNCGAGCCCGGAAGCATANAAGTGGTTAAAC

159U= CAAGACCTGGAAACATTTTGG
159L= CAACAACCCCTTAGAAACCCT

GM351
TTNNATCCCTTTGGAANANCCCNCCCCTTTTGGAGNTCGACCCGTATCGATAAGCTTGATAT
CGAATTCCTGCAGCCCCcTCATATCTGGGGCAGACTGTGCTTTcAatTCAATGCCAGCATGAG
CTGTGCAACTACATATAGCTGCAGACGAGCATGCCAAAACATACATCAATGGATCCTCTGAT
GTAGTGCCCTTCTGCATATCTGACTGTCAGGTATTTTATGTTACTGACTTATAGTATTTCATAA
AGACGTGCTTGAACTTATATATACACACACACACAGACGCGCACACACACACACACACAC
ACACACACACGCACACACAAGCTGTTCAGGCTGGGTGGTAAGCACCGGGCGAACTGCCAG
TAAAGGCTAGATGGGAGAGCTGTAGAAAGATGGAAGAAGTTAAGCAGGAGAGGAGCGGTG
ACGGCATGGGGGGGATCCACTAGTTNTAGAGCGGNCGCCACCGCGGTGGGAGCTCCAATT
CGCCCTATAGGTGAGTCCTATTACGCGCGGCTCACTGGCCGTCGTTTTACAACCGTCCTGA
ACTGGGNAAAACCCTGNGCGNTTCCCAACCTTNNATNGGGCTTGGAGGNNNNNGCN

351U= CTCTGATGTAGTGCCCTTCTG
351L= GTCACCGCTCCTCTCCT

GM506
TNANCCTTTAAGCCTTGAAGNCCCNCGAGTTAGCGNTNGCCCAGCTNGGCGGCACGGAGC
AGCTTCCCCTGCTGGCTNATTTGGTGCTTTATTACTGNGGACATGCagACCAGCCTGTTCTG

Figure 11 UUU

GTGCAGCTCTACCAGGTTGAGGTCAGAGCAGATTCATGTGCACACACACACACACACACAC
ACACAGACACACACACAGACATGCACAGGACACAATAACCATGAATACTTCCTTCCTCTGCA
CAGCTCACCCTGGTTGGAGGAGAGCGGAGAAGAGNNGTGTTTATTCAGTCTCTGGAGCTCG
GACACACGGCTGGAACTAGAGCTGTGAA

506U= CCTGTTCTGGTGCAGCTCTA
506L= AGCTGTGCAGAGGAAGGAAG

GM34
ATTCCCGTAGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCCTGGCATCA
GCATCCAAGCTAGCAAAACTGAAAGTGTGCAGAGCTTGAGGTTGCAAGTTGAAGCAATGGT
TTTCTAGAGTGGGTGGGGTAGGGTGTGTGTGTGTGTGTGTGTGTGTCGGTAGGAGGGAT
ATGAGCGAGGAAAGGTAAATCATGAAGCCGAGGTTCTCAGGGACAGATTGAGATCATAATT
CAAATCAGCCATATTACAGATTGTGAAGTGGAGGAGAGTGATTGCCTCAATTAAGCCAGTTT
GTCTTGAGGGTCCTCTTTGCTTAGTCTGCACAGCTCACAGTCCCTCCTCTTTCAGCATCTCC
TCCCGACTCCTCTTCTTCTACTCTCACCCACCTTCTCCCGTAGCCCATTAAATTTGATGGTGC
CATCATCATCTGTGTTCTGNCCTTGNNAAGTCCCGGNGGCTGCAANNAATTCNATNTCAAGC
CTTATCCATCCCGTCANCCNTNAAGNGGGNGGCCCCNNTNCCCCAATTTTTTNGTTNCCCTT
TTAACNNNAGGGNTTNAANTCCG

34U= AATGGTTTTCTAGAGTGGGTG
34L= CCTCGGCTTCATGATTTAC

GM532
CCCTCACTCAGACACACACAGATGCATAGTCCTCACGCACGCNCGCACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACGCGCGCGCGCACAGGTAA
CCCTTTAATCACCTGTACTGTACGTCAACTTTTAAGATTTTAATGCACACACACCTCAAATTTC
TGCCGTAGCTCCTCGTTGCCCTCCTCCCCCTCCGGAGGGACAGGTACATTGAAGTACTCGC
CTTCTTCTTGGGAGAGCAGCTTAAACCTAAAGTGAGAGAATATTTCCAGTCAAATCAATTCCC
AATTAGTTTATACAATTGGGGTGTTTAACTGCTGCCATTAGCTGAAGCTGCTGACAGTTACTG
CACCAATTTAAGGGTCTAAAGAATAATCAGG

532U= CACAGATGCATAGTCCTCACG
532L= TCCCAAGAAGAAGGCGAGTA

GM574

GM206
GGNNNNGNNNNNTANNTTTNTNTTCCTANTNTNGAAGATNTANAGGGANCCCTCGTTTCTTT
NGGGNAACNACCCTATCGATAAGCTGGANGTCGAATTCCTGCAGCNNCTTTGTGTGTGGTC
TGAGTGGTTCCNGGGGGGGAGGAGTGAACCAGTCTCAGACACTTCAGACTGCAGTCTCTCT
CTCTCTCTCACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACAAGCAGGGATGGACGCACGCACACACATGCACACACACGCACACACACACACACAC
ACACACATGCACACAGTGATGAGTGCAAAGAGGGAGAGGNCCAATAAACAAGGGGGGGAT
CCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGT

Figure 11 VVV

ATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTAC
CCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCNGTAATAGCGAANAGGC
CCGNACCGATCGGCCTTTCCAAACAAGNTGCNCAACCTGAATGGNCAATGGAAAATGNAAN

206U= GGAGTGAACCAGTCTCAGACA
206L= TCCCTCTTTGCACTCATCA

GM553
TGGATGTACTGTCCTATGTCAGTGAAGGACTCTGGCAACCCACTAATGCAGCTGGATTTGCA
TTGAGTGAAATGAAGCGAAAGTTTTAAATGGCATCAGTCTTGCTATTAAAGCAAAGCAAAACA
TCAGACAAACAGGGAGGAGCAGCTCTCTCCTCTATCCGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTATGTGTGTGTAGTAACTGGGGGAGTGCTGTCCC
TTGCCTCTGCTCAGTGTGTGCAGCAGCTGCAGCTTTCAGCCTCGGTCTATACTGTAN

553U= GCTGGATTTGCATTGAGTGA
553L= TAGACCGAGGCTGAAAGCTG

GM509
TGAATTATTAAAAGNGTTGTTTTCCCTTATTGCATTGCAGCAATGTGCCTCTTTGCTAGAAAT
GAGCTGCACATTGTGGAGTTTGAATGCTTAAAGCGACCCACCTCCAACAGCAAAGCCAGGA
GAGGAGCGCCCCCCACCCCCGACACACACACACACACACACACACACACACACACACACAC
ACACACATCTGAATATCTGAATGACCACAACGTTATGCTCAGATGGCTCTCTTACGTTTCTCT
TATATAATGCACGTTGTGAACTAACTAGTTTGTTTTGCTAAACTGTGCAGGGCTGCAACTAAT
GATTATCTCCATTATTGCCTAATGGACATTACACTATAAAGTGTTGGAGAATGGTGAAAATGC
CCATCACAATTTTCTAAAGCCCAAGGTGATT

509U= CAACAGCAAAGCCAGGAGAG
509L= AGCCCTGCACAGTTTAGCAA

GM414
AGAACTAGTGGATCCCCCCCCACACAGGGTAAGTCTGGCAGCTGTGTGAAGGTCAGCTGATGC
TGGACTGCTGAGAGGAAAGTAGCTGCACGCGCCCTCTGCAGTCTGTGTGTGTGTTTATCTGTC
TGCATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGTGCGTCTGTGTGTGTGTCCCTG
TGTTTGTGTGTGTGTGTGTGTTGTCCTGTGATGTTTATCTACACACTGTGTTGACCTCATTTATT
ATTTACAGCCACCAAACTGAAGACTGAAACACCAACAGCTGCAGTTCCTGAGACGTCCAGCA
GAGGCAGCAGTGAGCCAGCCCCACACAGACAGATGTGGGTTCAAACAGCAGCAGCTGCAGCT
CTGATGTTTAGACTGTCATTATCTTCCATCCACAGGTTTGNGCTGCATTTGCCTTTCTAGTCTC
ACTGACCACTCAAAGCTTTATCACACCTACAGCCAGTTGAAT

414U=GCTGGACTGCTGAGAGGAA
414L=CTGCTGTTTGAACCCACATCT

GM545

Figure 11 WWW

LG 18

GM530
AGGCTTGAATGATGGTCTTAAAGGGGGCAGTATATAACCTGTGTGTCTTTATCATTATATGTG
TGTGTGTGTGTGTGTGTGTGTGTTTCCTGGAGAGCAAAGGCTGTGAATGAACTCCTAAATCA
CACTATTGATCAGCCCTTCCTCCCAGACACACGCTGGGATCGAGGGCAGTTAAAT

530U= ATGGTCTTAAAGGGGGCAGT
530L= GGAGGAAGGGCTGATCAATA

GM397
AGGTCTTGTTTTTTTTTGTTTTTTGTTTTTTTTTAATATTTGCTCTCACAG
CCAACCCAGCAGATGCAGAGAGAGGGAAGTGGGTTAGAGGTGAGGGGAAC
ACCTTCCCCATCAAAGATCCCCGTTCTCCTCTCCAACGCTGAGACAGCAA
TAACCAAGGCAGCTTTTGAATGTTCCAGCATCACTCTCCCAACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACTATAAATAA
CCACAAGTGTCGTAAGAATAGAAAAACAAAACTAAAACTGTAAATGATGA
CAAATAAGT

397U= ACACCTTCCCCATCAA
397L= TGAGATCATCCCATAAAAAGG

GM83
GNNNAGGTGNNGTGNNACTTTATCTTNTAACANGNNCNCCCAACGTGNCCTCTCATCNCTTT
TGGANNTCGACCGTATCGATAAGCTNGANATCGAATTCCTGCAGCCCANNTNCACCATCTCC
TCTTCAGCCACGAGNGNNTTCCAGTGTAGTGGACCAAGCTCTCACCAAAGCAAAGGCTTAG
AAAGAACACACACACACACACACACACACACACACACACACACACACACACTGATAAAAGAGGGGTA
GTGATAATGGTGGAGGCTTAAGAGCTTCAAATTGCCCAAAATGGAAAGTGTGCTCTCTGCAG
GAGATTGAGAGATAGAGAGGGAACCATGGGTCTGCTATTTTTGGTCTACTAGGGGGATCTA
AATCTGTGGCTGGATGGAAGAAAAGCCTNCTGGGTAATGACCCTAAAAGCCCACATCAAAAA
GAGACACCCACAGTTTTTTTCTGATATTCATGGTGGTGACTGGAACCAGGTGTGATAAAATA
GCTGAAAGCTGAAAACAAAAAGCAACGAATGACAGAGTTCTTATTTTTATCACAGTTTTTAAG
CCAAAAACTGCAAAATCATAANGGGTCAAGTTAANTACCAGATAAANGGCTTTTAATTCATAA
ATNTGGCAANAATAACAAAAANGAAN

83U= CCACAACACCATCTCCTC
83L= CCATTATCACTACCCCTCTTT

GM482

GM39
ANNCCTTTGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCACTCCTCTCAT
TAACCTCTGGTATTTCAGACCAGTTTCCATTTATATTTAATGAGAGTCTCTGCACAAGCGATT
TGTAGTGGTGAGCAGCACCATCACAAATTCTCTTTGACTGTACGGCACACTCCCTCCATGGT
CTTTTACAAGATCCCGCTAAAGGAGCAAATGGGATCCCCACTATCTGAACTATGTGCTATATA
TATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGTAGCAAAGACTGAGCAAGAGAGAGG

Figure 11 XXX

TAATAGGAGAAAGATAAGAGATGCAGAGAGAATGAGAAAAAGCAAAGCAGAAATAGAACCAT
GTCTTGAGGTTGTTTGCTTGGAAAACTTAGCAATCTGCTGCTTGAGTGCCCTTCTCTTTGTCA
CATCCACCTCTGTGGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTC
GAGGGGGGGCCCGGTCCCAGCTTTTGGTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCG
TA

39U= TACAAGATCCCGCTAAAGGAG
39L= GGCACTCAAGCAGCAGATT

GM571

TRANSFERRIN

GM622

GM666
ATATGTTCTGGACACTCAGGTGAAGAGAGGTGCTGAGCTGTCAACTGATTACCAGGTGTTG
GTGAGATGGATCAGCTGGTGGAGAAGAATGCTGGACAGACAGACCTGATAGTAATGGTGCG
CTAGGAATAGCAATAGTATGCTGCTTTTAATTAGAAATCAATATCACATGCCCCCCAGAAAAG
GAAACAATAATTTTTTTCCACATCTTAAAGGCAGGAATAAATTACCCTCAAAAGAATTACACTC
AGTGAAAATGTTGCCTTGCGTGCCAATTGCTCTTCTTCTTTTTTCTTACATTCTTACATGCATG
AATTCTCTCTCTCTCTCTCTCACACACACACACACACACACACACACAAGCTGGAGATGAAAGC
CTCATTCAAGGTGTAACTGTGTTATAAAAAGAAATTANTTGGAGAT

666U= ATGGTGCGCTAGGAATAGCA
666L= TGAATGAGGCTTTCATCTCCA

GM285
GNNNNTNNTNNNTTNNTTGNNNNNNTCCGTTGGGAGCNCCCCGCGGTGGCGGCCGCTCTA
GAACTAGTGGATCCCCCACAATGATAGCAGTGGAATTATCTAACACACAGATACACACGTAA
CAGCCACAGACCCCTAACATGCTTATCTAAGTGGCGATATTACAGTAATACATTATAATCACA
CTCTTTGATCACTCTATCTGGGACACCTGCTGCACTTTGGGGGATGCAGAACTGCTTTGTCT
GCAGATATATACACATAACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACACACACTCTATATGACAACCAAATTTTCCCCTCACAACCGTAATGGAACAAA
CGGCAGAGCTATTAGATTAGCAGGACATGTAACAACACAATAAACTGGGAGCACACCTGAG
GCTGGATGCAGTGTAAGTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACC
TCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCCCTTT
GGGCGTAATCATGGCATAGCTGTTTCCTGTGTGAAAATTGTTATCCGCTCACAATTTCACACA
ACATACGAGCCGGAAGCTTAAAGTGTAAAGCCTNGGGTGNCT

285U= TGCACTTTGGGGGATG
285L= TAATAGCTCTGCCGTTTGTTC

GM648
TTTTTAATACAACACTGACACAAAGTTACATCTCTGACTCGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTGTGTGTTTCGCATTTTGCTAACTTTGTGAGAACATGTTTCAGAGTGAGGTCA
GTTTAATCTTCAGACCTCAGCCTCAGAAACCCACGGTCTGCATGAATACTGCTTTTTTTCTTA

Figure 11 YYY

GCACTTGGAAGTAACTAAGTACATTTACTTAAGTACCTATCAGTTTTAGTAGAATAATTCTCCT
CCACAGTTCAGGTGTAAACTACGTCTTTTACTCCAATTCATTTGACATCTATATCGACATACTT
CAGGTATCA

648U= CACTGACACAAAGTTACATCTCTGA
648L= AGACCGTGGGTTTCTGAGG

GM519
CCCNNCACAGGGTTCACCAAGCCCACCTGAGGCACGCCAGGTCTCACTGGGGTCACACCT
GAAACAGGAAGCAGGAAGTGATACCTGTTGGAGCACCTTTGATTGGTTAGCATTTTTGAATG
AGCCTGCTTTCAAAATAAAGAGCGGTGAGACGTGTGGGCGGAGCAGACTGCCCCAAACTCA
AGATGAGATGTCGTGTGGGTGGAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGT
GTATGTGTGTGGACAGGGCTCAGGTGTTCCTACCTGTGATGACACCTGGAGCCTGGTGGG

519U= CCTGTTGGAGCACCTTTGAT
519L= TAGGAACACCTGAGCCCTGT

GM564
TCGGGAAGGACAAGCTGCTAGACTGGCTCTGGGTGATGGGGGGGAGTGATGGTGGGGTGA
TGGTGTTTGGCTTGTCAGGGCTCAACCCACATNCAAGGAACAGTCTCCACACACACACACA
CACACACACACACACACACACACACACACACACACACACACACACACACACACACACAGATGCTGTCTCA
CACACACCTAACAGAATGTGACAGGTCTGCCTCTGAACAGTGTCCCTGCCACAAAACAGAAT
TTTTCAGTATTTGTCTTTTAGCCACGCTAGCAGCATGACTCCAGGAATAGCAATAGAGAGCT
GAATCGCTACACTATACCAGCTGATTTCTGTTTTTTAAGTCTCAATCACGCCGTAAAAGGCTA
AAACCAGAGTCTGAATGTAAAAGATGGCTGTGGCAACCATAACATCACTCACAGGTTTGAGG
GCTTTTTAAAGCCTTCATGT

564U= GATGGTGTTTGGCTTGTCAG
564L= ATTCCTGGAGTCATGCTGCT

GM202
TNTTTGACTCCTTGGAACTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTG
GATCCCCCACTTGAGTCAATTCCCTGTGAATTAACATAAATGTGGTGATT
CGCCAACATAAGCAGCTGTGTTATGACTGATGTGAATACAGTGGAAGGGT
CTGGAAAAGCAGATGCACAGCTATGAGCTGCTGCATTGCTGCTAGTCAGG
AGCTGTCAGGAAAAGACTAGAAGCAGGTCCCAGATGGGAACGCATGTGAA
CACAAAGTAGAGCTTTGCATGCTCAGCAAACCTTCTTAAGATAAATACAA
TTGTGTGTGTGTGTGTGTGTGTGTGTTTGAGTGCTGGAGGGGTCTTTCAC
AGTTCCTTGGAATAAGCCTGTTCTTGCGTTGTGAGGGTGCAGCTAAACAT
AAATCATGCATTAGGCTTTCTTAGAGGAGAACTTGGTTTCGAACATATCA
GCTTGAATTTCGGACCCGCGTGGGCTGCAGGGAATTCGATATCAAGCTTA
TCGATACCGTCGACCTCGAGGGGGGGCCCCGGGTCCCAGCTTTT

202U= GGTGATTCGCCAACATAAGC
202L= AACTGTGAAAGACCCCTCCAG

Figure 11 ZZZ

LG 19

YDIX2

GM536
CCCCTTGGGGGGACGTTAACCGCTGAGCTGTGTGTGTGTGAGAGAAGTGAAGACAGAAGA
GTCTGATGTTCATTTTTAAATGAAAGAAGATGATGGACAACAGGTATGACAGCAGTAATGGC
AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGCGGAGTGTATTATTGACAAAACACAAATGT
CTTCATCACGTGGACTCCAACATCAGCGCACAGAGTCAGACGCTGTCAGCACGTCTGTCAT
CAGGTGTGTTGCGTCAGTGTGTGTTACACAGCAGACGAGAAAATGTTACCTCCTGCTTTTCT
TAAAAAAGAGCTTTTGAAGCGATGCGTCTCACAGGACCAATCACCTCAGAGCGGTCAAACC
CACCTTGGGTCGGGCTGAAAGGACTCTTGCCTTCCATAAACTTNCATGTTGAAGCTTATTGG
TTACATTTTTGGNACCGTCACACAACTAAACACAAGATGGGGGG

536U= TTAACCGCTGAGCTGTGTGT
536L= GACGCAACACACCTGATGAC

MYOSTATIN

GM581
CCGTGACCTATGTGGGCTGAATGCTAACGGGGGCTAAGGAATGCAGCCGCTGGGGTAAAA
CGCCACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACCCTTCTCTTTTTGGAGGAGCACTTTAAAACGCAGTCAGAGCTGTTGACTTG
TGGCTGCTTTTGGGATAAGAGACAGAGGTGGAGAGATGGGGGTGGATGTGTAGCACTCTG
CCGCCGACCGGCAGGATCAATGAAGGGCACTTATGAAGAGAAAGCTCACTGCTTGGAAGAT
TTACAATGAATGGCTCGG

581U= ACCTATGTGGGCTGAATGCT
581L= CAAAAGCAGCCACAAGTCAA

GM368
TNNTTGTCGNGATCTTTTTGAAAACCCCGCTCCNTNTNGAGGNCGACNGTATCGATAAGCTT
GATATCGAATTCCTGCAGCCCCcccTCCCTCACAGCAAAGGTTTGTTtGAttGGGTCCTGcgGCA
aGGTCACACACACACACACACACACACACACACACACACACACACACACACACACACACACACA
GGGGGAACAATCAATAACGGATGGCTGGATTAAGGTGTCAGGACATCTATGTGTCCAGCCA
GCATACGGCTGAATAACTCTTGAACACACACACACACACACACACACACACACACACACACA
CACACACACCTCCATATCCAGCTTTCCTATTGTCCGCTGTCCATCACCACGGGGGGGATCCA
CTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATT
ACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGGTTACCC
AACTTAATCGNCTTGGAGNACATNCCCCTTTNGCAGGCTNGCGTNATANCGAAAGAGGCCC
GCACCGATCGCCTTCCAACAGTTGCGCAACCTGAATGGCNAATGGAAT

368U= ACAGGGGGAACAATCAATAAC
368L= GACAGCGGACAATAGGAAAG

Figure 11 AAAA

GM63
CNAGGGTNNNTTGCTANTTTCATCTTGTAACTTANTTATNTNCCGTAAAAACNCNNCCCTTTT
GGAGNTCGACCGTATCGATAAGCTTGATATCGAATTCCTGCANNCCCTTNGTGCCGCAGGG
AGAAAACANCATCGGGACAGATCACAAATGTTATTCACTCAATGGAGCTAATGAAACACACA
CACACACACACACACACACACACACCAAATGAATCTTTGCAAATTACTGTATCTGAACCACCT
TTTGACCTGTAATTTATACACATACTTGTTTTTAATCAAAGCATGCAGTTTGTGATTATTCAGT
TTCAGTAACCAAAGGTAAAAAAATAACCATTATTTGAACTGACTCGACTGCATTTGTTTTATCA
GAACAAAAATATGCCCCATCTNAAGGTGTTACAGCTTTGACCTTCACTCTTTTCTAAGTTTTT
CCAACAAAGACACTGTAAATGTTACACAAAATGAAATGNCACGACCTGGCATTTGGGGGATN
CACTAGTTCTAGAGCGGTCGCCACCGCGGTGGAGCCTCCAATTCGCCCTTATAGTGAGTNN
GTATTACCGCGCGCTTNANTGNCCGGTCGTTTTANAANNGTTGTNGACTTGNGGAAAAACCC
NTTNGNGTTTNCNN

63U= GCCGCAGGGAGAAAACA
63L= CAGGTCAAAAGGTGGTTCAGA

GM250
TNTTGACCTANTNAATGCNCTTTTCAACGCGGCCGCGGCTCGCTCTAGAACTAAGTGGATCCC
CCCCGTGTGAAGCTCTCCGCTGCTTGCAGTGCAAACAGGCTTACAGGACTCTAGGCTGTGGCT
GCTCTTCAGTGTGCTCCATGCTTTGTGCAGAAAACTGCAGCTGGTGCATTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGAGGGGGGGTNCAGACCTCGGGTTCTTCATCA
TCCTGCAATGCTGCTGAAGCAGATGGGCTCAGGTGCTGCAGCTGGGCACCTCTCCTCACTCAT
CGGCAGCACCGGCGCTTCAGTCTGACATCAATCATCTAAACACAAACATGCTCCCGTACCTGG
CGATGGCGCTCGGGGTCTCTGTCTGTCTGCGTGTCAANTAAAGCTGCTGTCTTATCTTGCTGTG
CTCTTGGCTAACATTCATCACTGTGCCTGTNTNTGACTAACTGCATGGAGCCCTCTCTGATNAA
TGANAACTAANTTGCTTTGGATGTTCANAAGNTANTTAATCANANGTTTAANCCTNTGTAAGT
CTNNTTTNGGNATGTCAACACTTTGGGGCTNCANGAAATNCATATAAGCTTATCNATACCGNC
AACTNCAAGGGGGGGCCCCGTNNCCCAACNTTNTGTTCCTTNANTGNAGGGTTAAANNCNCC
CCTTGGNNCNNAAACAATGGNCANAANCNTTNNTTCCCGNNNCAAAAANNNTTATCCCNCTN
ACAATTTCCNNACAACNTNNCANNNCNNAANCCNNANAANNNNAANCC

250U= AGTGCAAACAGGCTTACAGGA
250L= AGCATTGCAGGATGATGAAG

GM534
ATCACTTGTTAGCCCTCTACATGCAGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATCTGGAAAGGCTCCATTGG
GGCTGAAAGGTATGAACAGGTTTTAGAGAAACATCTGCTCCATGCAGATGTGTGTTTCAGGA
A

534U= CACTTGTTAGCCCTCTACATGC
534L= TCTGCATGGAGCAGATGTTT

GM278
TGNGTNNNNNTCNGATTCCTTGGGTACCGNGCCCCCCNTCGAGGTCGACGGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCACATGTTAGAGATGGCTGAGGAACAGAGAGGGAGAGG
TAACGGAGGACGGAAACCACACACACACACACACACACACACACACACACACACACACACACA

Figure 11 BBBB

CACACACACACACACACACACACACACAGCGGTATTTGTTTCCAGCAGAATCCGCTGCGA
GAGCCGAGATGAAAATCATCACCACACTCGAGCACAGCAGCATCACCGGTTTTTGGGGGAT
CCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGT
ATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTAC
CCAACTTAATCGCCTTGCAGCACATNCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCC
CGCACCGATCGCCCTTCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTT
AATATTTTGGTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTTATTTTTTAACCAATAGGNCG
AAAN

278U= TTAGAGATGGCTGAGGAACA
278L= ATTCTGCTGGAAACAAATACC

GM255
TANTTTGATNCGNGAANCTTNTTGAAAGCNCCCCTCGAGGTCGACGGTATCGATCAGCTTGA
TATCGAATTCCTGCAGCCCCCATGACCTCACCTGAAACCCTCAGGCTTTGGTTCGGTCGCCA
TGGAGtncaaCACCTcCATCCATACCCGTCTCACCACTGCTAACGAGTGCACTCCATTTCTGCA
GATCTGTGACACCGCTGGTCTGGAACATCTGTCTACAAGAGTGGGTGAGTATTCAGAGAGC
ATATTCCATCCCTGATGGTAGTATGGACAGTTTGAGCCATACTCAGTGCTGTACACTGAGTC
TCTCTCTCTCTCTCTCTCTCACACACACACACACACACACACACACACACACGCAGCATGAGCT
GTAAGATAGGAGCCACGCTCAAGACCTAAATGAGGTCCTGCAgAGGAATCACCACCAGGCT
GAAGGAGACCGNCATCCTTCACCACATCATCACTCTGCACCTGTGGTGACCTGATGATGAG
GTGTGAGCATCCTCCCCTGTAGAAGACAGCAGTCGGGGGGGATCCACTAGTTCTAGAAGCG
GGCGCCACCGNGGTGGAGCTCCAATTCCGCCTATAGTGAGTCGTATTACGCGCGCTCACTG
GCCGTCGTTTTACAACGTNGGNGACTGGGGAAAAACCCTNGCGTTACCCAACTTAATCGGC
TTTGCAGTACAATCCCCTTTTCGCCAGCTTGGCGTTAATAGNCGAANNAGGCCCGNAACCG
AATCGGCCCTTTCCAAACAGTTGCGCAANCCTGAATTGGCNAAATGGAAATTGTAAACCNTT
AANATTT

255U= GCTGGTCTGGAACATCTGTCT
255L= CTTCAGCCTGGTGGTGATT

GM168
TGNNTTTGACAACCTTGGGTACCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGA
TATCGAATTCCTGCAGCCCAAAGCGACAGGTGCACGCTCAGCCTCACGCCCACACACTCCA
TATAAGGACACAGGCGCACCGGGCTGTCACAGCAGGAAATCAGGAGGGTTTGAACTGTCAG
AGGGGAAAGTGGAAAAGCTTAAACAGTGGAGCTGGAATAGGCTCTGCCCCCATCACCCTGA
TTACCTGTTGGACTTTGCTCAGGTGTATTAAAGCAGCTGGACAGATGTTAGAGATTATTTCTG
TTTTGACTGAAAGCTGCTCGTCAGACACACACAGACCGTAACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACAGTGTGTATCAAATTCACTGTTTACAAACCATG
AATGACTCATACCAAAATCATCAATATGATCAATAACACTGATGATTATTATCACTGTGATCAT
TACTGCTACGCGTGTTGTGACGCACCAGCACCAGTGGGGGATCCACTAGTTCTAGAGCGGG
CCGNCACCGGGGGGTGGAGCTCCAATTCGCCCCTATAGGGAGTCGTATTACGCGCGCTNAAT
GGCCGTCGTTTA

168U= TCAGAGGGGAAAGTGGAAAA
168L= CAACACGCGTAGCAGTAATGA

Figure 11 CCCC

GM671
CAATGCCCCTCCAAGGACGGGTGAGCGAGCGAGGAGCGAGCAGAGTAATCACAGTTAAAG
AGAGAGTGTGTGTGTGTGTGTGTGTGTCTGTAGGGAGGTGAATAAACGTACTACAGGGG
ACACAGGAATGGCTTGGTGCTGGAAAAAATGGATGGGGATATGAACCGAGTGGAACATCCT
GTCCCATCTACCATTCTTCACATACTTGCACTCACACACGGAGCGGTTCGGTGTGGTTATGT
TGGTGTTCTTGAGCAGTGGAGTAGACAGATGAGTGAATCCAGGATACGGAATGTGTTCCAG
TACTCCAAACAT

671U= CGAGGAGCGAGCAGAGTAAT
671L= CTCCGTGTGTGAGTGCAAGT

GM56
TTGAANTCGNGAGCNCTNGGAANNCCNGTCCCTTTNGGANGTCGNCGGTNTCGATNAGCTT
GATATNNAATTCCTGTTNCCCTTTAGCCAGAATCGGAGAAAATAAATANGGNGAAGAAAAGC
TTGTGCGCCATCGACACGTCACACACTCCCTCCAGCCTCTTGGCAAGGCTGCAGACAGCAC
TGCAACCAGGACACAATGCCTAAAAATCTGCAACTATCTGGCATATGCTCCTCTGCAAAACT
CTCAAGGCTTCAATACGAGCCTTTCTAGTCAAGCAGACTCTCTGCTCCCAGTGATGCTTAGC
AATAAAAGCTCTACAGAGGTCTATTTATGAATACTAACCACACTCCCACACACACACACACAC
ACACACACATCCAGATAGCTGATGAATTCGAACAGACAGAGAGGGACGGTGAGGCCTGATC
CCTGCCATACCAATATTGCTGTGTGGGTGTCAGTGTGTGTGGNCGTGTATTACTTATTGNTG
TGGGGACACAAATTTGTTACACACTCACATTGTGAGGTCTCGCCTACTTTATGGGGACAAAT
TGCAAGGNAAATCATTCAATTTTAGGGTGAAGGCTTGAC

56U= GACACAATGCCTAAAAATCTG
56L= CCTCACCGTCCCTCTC

LG 20

GM610
ATGAAACAACAGTCAGGAATAAACGGNGAAGAGCCTGAGTGGGTATTAGTGATGTCACTGA
CGCCCATCAnNGTTCTCAGTTACAGCAGATnGGCGTGTCCGCTGTCGGAAAAGATTTGTTCA
AATTAGTGCAAATAAATGAGGATTTTGGAAACAAACACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACATAGATGAAACAAACAAGTGAAGGAAACAAGATG
CCAACTGGTTATCAGAGGAGTTGGCATGGCAACGGGTAAAGTTGCTATGGGAATGGTAGTA
TTAAAAGAGATGAAAGAGGAATTATCAGCACAGTTGGAAAGTA

610U= GATGTCACTGACGCCCATC
610L= CCATAGCAACTTTACCCGTTG

GM333
ACACACCTNTACAGTTCAAATCCACTGGACACATAATGTAAAATCTGNAC
CAGAATCAGTAAAAAACCCACAATAGTAGCGACTGCGCCAACATATTTTT
GGTTGTGTTTGTGATGAAAAAAGCAGACAATCTTACTGAGCGTAGAGAAA
CTTTCATGTGGCTCTATAAACCAATAGAAAATAAGCAAAGTGCCATACAC
GAGCGTATGCTCACACACACACACACACACACACACACACACACACACACAC
ACACACACTGCTTCAAACGCCGTTCGTGTGTTCTCATGTTCTGGAGACAT

Figure 11 DDDD

TACACATCAAATGAGTCCCATAAGCTGAAGTATTTTTAGAATCTGAGGAT
ATTTTGCTAATTCACGCAGCCTCTTTTCACTCACACTGTCAACAGCATCC
CGCTNGTGCACACACNCGTTGNACCGACTGCAAAATGCTGTGAGAAGTCC
AATTCGATGCTTTTTCACCACTGNACAANGGGCTTCANAAGANAACNGAN
CCCAAANTGAAAACCNNATNCCCCTGGTTTTATNATTAAATCTNCCCCAA
GANATTTTGTGGGGGGGGGATTCCCCTTTANTTTTTNAAANATGNGCCNN
CACCCTNGGGNGNAATNTC

333U= AAAATAAGCAAAGTGCCATAC
333L= CTGCGTGAATTAGCAAAATA

GM224
ACTTGTCTGTCTCTGTGAGGACCAATCTGAGTTTGCAGCCTTGAGACTGA
TGTAGTTAGTCTTCACTGTAGGATAAAATCTTCAAAGGCGTGCTTGGAGG
TTCAGACATAGTTTTAAGGTTCAGGTTCGGTTAAGGAGCTCAGTAATGTA
GTATGTCAACAAGAGTCCTCGCAAAGACAGAGGGAAAAATAAGCATGTGT
GTGAGGATGTGATGCTGGCTGTCCGCCTAATAAGAGCAAAGCCTCGCTGA
AGTTGGAGTGTTTGATCTCAACCAGTCACCAGCAGCTATGACAGATGGCT
CTGACTCACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACACACACACACACAGACACACACACGTAGACACACACACG
CAGATGAGCTTTACAGTCTAACCACAGGTGTAATGTGTTGGTTTTGTGTT
CACACAGACCCTACTTCACAGATCAGTGTGTGTGTTACCTTGCAGCAAGT
GAGGTTNCAGGGTGCGATGCTTTCAGGTATGTTT

224U= CAGCTATGACAGATGGCTCT
224L= TGAAGTAGGGTCTGTGTGAAC

GM263
TTTGANANCGTTGGGTACCGGGCCCCCCCTCGAGGTCGACGGTATCGATAAGCTTGATATC
GAATTCCTGCAGCCCCCATGTTGACAAACCAGGATTCATGCTTTTCAAGACTGTCTGTCCAT
CCGTGCCAAGGACCCCCCCATAGAGGCATAGAGCTACAGCCACCATGACCCTGTTCCACAC
ACACGCACGCATACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACACACACACGCCTCTCTCATCTGTCCTTTCACATGTAACCCAGCAGAACAAAAGCA
AAGGACTGGAAACACATTTTCCCGTCCTTATGAGCACTTCACTTCCTGTGTGCATATGTCTGT
TTACATATCACTCCTGCCCTTCATCCAACACGCTTACACAAAAATGCATCACCCATTTGTCCC
CTACTTTTTAGCCCATGCTTGTCTGTAAATATATATGTATGCAGCTTCTTTTTTCATTAGGATC
AGAGTGCAGGAGCCCAGGAACAGGTCCAAGAACTGAAACATAAGGAGATTGGAAAGAAAGC
GTTGTGAAATTTGGAGGGAACCTTCAGCTTTTCACGCTGCTGNGATGGA

263U= GTCCATCCGTGCCAAGG
263L= TTGCTTTTGTTCTGCTGGGTT

GM399
TTTGTGCCAGTGAAGCATGTAGGTGCATGCTTGTGTGTGTCTGTGTGTAT
ATCGATGTCTTAGGAGAGACGTTAATGTCCTGGGAGCAGACCGTCACTTT
GGTGAGAGTAAATATACCTAAAAGCGCCCTGAGAGCAACAGGACTCTTCT
CTCACTGACACAATATTATTCTGCTGTTCTTCACAAGCTCTGGGGAACTC
GTACACACACACACACACACACACACACACACACACACACACACTTTCTCTC

Figure 11 EEEE

TCTCTATCCCACCAGGCTTGTTTATGAGTGTGATTACACAGAGAGAGGTC
CGGTTGTCCAGCTCACCTGAGAGCGCATCAGGTGCAGTGCCCTGGGGCTT
TGTGCCTGTTTGTGTTTGGACAGTGCTGTGTATTTTTGGAACGGCACACT
TTTTGTGCCTGACAGTGAGTTTTTTGGTTTTGTTTCCTGNTTTATTCCTT
CTGTTACTGTGTGAAAAAGAGATATAGTGTTTGTTTAAGGNGTCCCATGT
TGGGTTAGATGCCCCAAACTTCTGGGGTCCTAAAATTCAACC

399U= CGCCCTGAGAGCAACA
399L= AGTGTGCCGTTCCAAAAATAC

GM493

GM57
TNTTNTTGGNAGTAGATCTNTTGGAATCCCCCGTGGTGTTTGGNCGCTCTAGAACTAGTGGAT
CCCCCCCCGGTCCTCGTGCTCTGGTGGACGTTAGCCTGCTAGCTGCCTCCATTCATTAGCTTTAT
TCGCACAACAACAACAAAGCATTGCTGCTCCCCAGATGCAGCCCCCAAAACACACACATACG
AAAGCACACACACACACACACACACACACACACACACACACACACACACACACACACACACAACTGCCTACC
ACAACTACCACCACCCACTGCCACCACCTCATAACCATTTTTTCCATTGTGTGTTCTTCTCCCC
CTCGTTCTCTCCCTCTCCCTCTCTTCATGATAACAACAACAGAGTTGAAGCCTCTTGAAAAACT
CACTTTGAATATCAGATTGGCTTTGTGTGTGTGGGCAGGGGATGTTTGGGAAGNTGTTGACAT
TTTTGGTGAGACAGNTTGGNCNCTACNTTTNGNNCTTACTTTATGGGTTGNGCCCCCTNTGAA
AANGGGTTTNCATGGANATNNCAGTCTNNANNTTTACTTTAAGGNTTTNAGGGGNCCTGTCCC
CTTNCCCCGCCCGCNCNGGTTTAANGAAATTTTGNTNTNA

57U=TAGCTTTATTCGCACAACAAC
57L=GAGGGGGAGAAGAACACA

GM401
TAGACTACGAGCAGATATGATGGGAATAACAATATCTGGAGTCCCGATTC
AACTGTCTGATCCTTATCTCTGCCTGTATGATTCTGACATTTTCAGATGT
TATTACTCACACTCAAGGATTTGTATCCTAAAGCCTCGACAGTGACGACG
GCGCTCAACAGAAATGCTGCATGTGCACAAATCCCACGGCTCTACCCCCT
ATCCGCACACACACACACACACACACACACACACACACACACACACACACAC
ACACAGACAGAAACACCCTTGACAGAGATCTGTGAGCCATTCTTCAGTGT
CACAGTGAGCGACGCCTGGCACATCCTTATACCTGAAGTTGATCAATGCA
GATATGTCCAGGGGGAAATTGAAATCCATAGGAAATTAGGCGGCGCAAGT
GATTTATTGGAACAGTAAATCATGGTGCGTGTGATGTGTGGAGAGTCTGT
GTTCCAGCTTNCGTGCGCCATACT

401U= ACGGCTCTACCCCCTATC
401L= CGCCTAATTTCCTATGGATTT

GM662
TGCAGCTGACCTTCACTCTTATCTCACTTATGGCTGCTAACATGCCTGATGGATGTTTCCTTA
TTGTTTGTACAGACTGACCCGTGTGGAATCTGTTTACAAGACTTGTGTGTATATATGTGTGTG
TGTGTGTGTGTGTGTTAGGGGGGGTCTGGGCTTTCATGCTGTCTGCTCAGTTGTATCCCACA
CTACTGAAAAAAAACCACACACACGATACTGAAATGTTCCTATAACTGGGATTTTAGAGAAAT
TGAAACAGCATATTAGTCT

Figure 11 FFFF

662U= TGCAGCTGACCTTCACTCTT
662L= TGAGCAGACAGCATGAAAGC

GM589
CCCAGATAAAGCATGTCAGCAATATAATATTTACACCTAAGAAAATACATCACGATATAAAGT
AAAAAAAACAAAACATCCAACTCTATGTACTTGCATTCAAGGGATAACCTCCAAACCAGAGA
GCTATTTTAGCACAGATTACATAACGTAAGATAATCACATTTGTGATGTTCTCACACACACAC
ACACACACACACACACCAACAACAACAAAGATTAATTACGAGGG

589U= CCCAGATAAAGCATGTCAGC
589L= CCCTCGTAATTAATCTTTGTTGTTG

GM215
AGGNNGNNNNNAGNTTATCTTNNATNNGGGGNTTNAAGGNANCCTTCCCN
CTANTGGGNAACGACCCTATCGATAAGCTNGANNTCGAATTCCTGCAGCC
CATTNACCATCAAACAGACACTTCATTNGGGGNGCAGTGATAACAAATAC
ATTGTGTAGGATAATGATGGCAGTGGTTCATATTGTTCATTATACGTCTG
GGTGTCATACGGCACTTGCAAATTTATACGTCTGTGGGTGCTTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTGCGCGTGTG
TCTTTGTTTTTGTCATTTTCATGTTTCAGCAAATTAACGTCTGAACCATT
GGGAAGAAAAATATACCATCATTTGCCATTGGNGACAAACAATATATTTT
GGATAATGATTGCATCTATTGGCTTCTGCATTTGNAAATGTGAGGTAATG
AATTTCCTTTGNGAGCAATGAAAGCAAACAGACATATTATGTCACTTTGC
TTGAACAGGGGGGGATCCACTAGTTCTAGAGCGGCCGNCACCCGNGGNGG
ACTCCAATTCCCCTATAGNGANNNCNTANTACGCCGCTCACTGGCCCNCN
N

215U= GGATAATGATGGCAGTGGT
215L= TATTTTTCTTCCCAATGGTTC

GM131
TNNNTNNNNCNANTNATCNCTTGGATACCCNGCCCCCTCTCGAGGTCGACGGTATCGATAA
GCTTGATATCGAATTCCTGCAGCCCACTTTTTATTGCCATTGATTTGTTGACACTGAAAAAAG
AGAGAGATGTCTTAAAACGTTTGAGATCTGACACACACACACACACACACACACACACACAC
ACACACACACAGAGGAGCCACTGTTTGCCGTGCAAGTTTTTACTCGCAGTCTTGGGGTTGTA
TGAAGTTTATTCGAGACTTTCCCTGACATCCCCCGCCTTTACAGTTTCTGTATCTTACTGTGC
TCGGGATTAGTTCTTTCATGCCATTTTGTTGGGCTTTGATCCCTGACCACATTGATCTCAAGG
CATGACTAGATAACGCTCGCCCCAGTTTTTCCTTTCCCTCCTCAAGATACATCTCTGAAGAAT
AGGCTTGCATTACCCTCCAGCCACATCTTAGATTTTTTTTTTAACCAGCCCACTTTTTTTCATG
AGCATATAATCCCTGTTTTTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGG
AGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCN

131U= GCCATTGATTTGTTGACACT
131L= AAAATGGCATGAAAGAACTAA

Figure 11 GGGG

GM615
GAGAGCGTACCTTAGCTGACGCAATGATCTGGCGATGACTGAGTGTTTGCTTCAGCCTTAAG
TAGTGAGCCTGATAACCAGTGAGCCGCAGGTGAGTAATCACAGCTGATTGCCAGCAGCTGC
GTGCACAGAGGAAGGTGGAGAGACAAGAGAAGCCACACTGAGGGTGGGATGCACAACCAT
GCCTACACACAGACTCACACACATGCACTCACACACACACACACACACACCCAGGGAGAAA
AACAACTACAGAGACACAAAAAGGAAAGGAGGGCAAGCAGGAGACAGTAACTATCGAGCTC
CTCTCCTCATAGAAATACACTGGAATGTGTCACTTCTGTTGGTTGNTTAGAATCACAGGTTTA
CTTTAGTAAACTAAATTATTTAGACAGCCAATCTAA

615U= GTGCACAGAGGAAGGTGGAG
615L= CCCTCCTTTCCTTTTTGTGTC

GM155
TCTATNTTTGANAGCGATCTCTTTGGAACTCCCCCNCGGTTNCGGCCGCTCTAGAACTAGTGG
ATCCCCCCCCCACTCATATAAACACAgcAAAAGTGCTACTCACATCAGTGCTAACATCTTAAAG
ATATGCATATTAATATAGATATTCACAGTTCCACTTTTAGTCAGACAGAATTTATTTGTTTCTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGTGTCTCAGTGTTACT
GATGGAGCTGGTGCTGAGAAACACATTTGACTTGAGTGTGGAAATGTCAGTCGCTTTGATTAC
TGCACTTAGGCAGCTGTGACATTTTTCACTACTTTACGTGCACTCAACGCAAAGGTCAAAACA
AAAAGGACCGGGCCTGCTCTATTTCCCAAACCTATCCAGCCAGCGCCTCATGGGATTGGTGGT
GCCCCTGCCCATTGCCTCTCTCCCTANNTGNGGGGNAGCCCCCNCACCCNCTTATCTNATNCT
AACCCTCTNAACCCTCTTTGGCTCNCNNATTCNTNCNTCCCCNTTNTTNAGCNNTCTATCTCNT
AANTGGGTNNNCCNCTNNATCNCTNAAACCTTNATNTNNATATCTCNNCG

155U= CCCACTCATATAAACACAGCA
155L= CGACTGACATTTCCACACTC

LG 21

GM343
GNNNNGNNTTNNNTTNNNCTNNNANNTCTTTGGNANCNCCACCGCGNTGG
CGGCCGCTCTAGAACTAGTGGATCCCCCCCCGCCGTCTTCTCCTNTGACGC
CAGGTCTGTGCAGTGGGATGCCGGGTAAAGCCCCGGGAGAGGCAGCGCTG
TTTCCCTGCTGTTTCCTCCTTCGTGTTAAGACACGATCGCGGTTCAGTTG
AAAAGAATGGAGGAGATGTTAATAAAGGGGAATATCAGTCAGAAGGCACA
CACACACACACACACACACACACACACACACACACACACACACACACACACA
CACACACAGAGTTCAGCTGTCTGAACACGAAAAGCTGATAAGGTGTTTTG
GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGG
GGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCT
TNGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCT
CACAATTCCACACAACATACGAGCCGGNAGCATACAAGTGTAAAGCTTGG
GGTGCTAATGAGTGAGCTTACTCACATTAATTNGNGTTGGGCTTAATGNC
CGNTTTTCANTTGGGAANACNTNTTNNGCCNANTNTTTTNNANAAATTNG
CCCCCCCGGGGGGGGNGGCCT

343U=CCCTGCTGTTTCCTCCT
343L=CCTTATCAGCTTTTCGTGTTC

Figure 11 HHHH

GM613
GGGAATAGCACAGTGTCCTGGGTGACATGTCACAAAGCATAGGGCTTAGAGAGAACACACA
CACACACACACACACACACACATCCTCAAAATCAAACCCATCTCTCTGATAGCACTGCTGCCAC
CCAACACAGCTCCTGCTTAAATTAAGTGTTTTGATTATTCAGTAAGTGTACGTACATTTCATTC
CTATAAGCCAGAGGGAAGGAAGGAAGGCGTGAGTGACACCAGAGGTCAGCAACACTCACT
GCAGCTATACTTACATTTTACAAGGATTACATCTGCTCAGTGATAAGCAGTCTTTGTTTATGT
AATCAATAAAGCAGCACAGTTTGGAACAGTGTGGGACTTCAGCAACCTGATTACCAGCTGTC
TAACTGGCTGACTCGAGCGGCTGTGGGGGAACAGCAGCCCCAATAATNCAGTCGAGGCAG
AGAGAGCTCGGAGGGAGTATTCCGTTTAGCGGTGACCAGCCTC

613U= TAGCACAGTGTCCTGGGTGA
613L= GTGTCACTCACGCCTTCCTT

GM171
TNNTTTGATCCGTNAATCNCTTTGAACCGGCCCCTCCCTTTAGGTCGACGGTCTCGATAAGC
TTGATATCGAATTCCTGCAGCCCACTGCTATcCATTGACAGATATTGAGTTTTCCCTTCAtGTT
GCTGCCATCACCTCTTGCTTATCATGCTCACTCTTTTGCAGCTATAATAGCAGTATGTCACTG
GCTACCATGTATGCACACACACATTATACAGTGACATATACACATTAATCCATAAGATATGCT
AATTGATTATATAAAAGACATAGTCTTTCCTTCGTGTGTGCACACATGCACACACACACACAC
ACACACACACACACACACACACACACACACACTAAAACATGCACACATAACCTCTGCCCTAACT
CACAGTGTTCTTTGTCTCTAATAGCTGCTAACTCATTTAGCACTTCATGTTAGAGAGAGAGTG
GAGTCTGAGTAGGAGGGGGNGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAG
CTCCAATTCGCCCTTATAGTGAGTCGGTATTACGCGCGCTCACTGGGCCGTCTGTTTTACAA
CGTNGTGACTGGGGAAAACCNTGGGCCGTTNCCCCAACTTAAATTGCCTTTGGAANCACATT
CCCCTTTTGCCAGNTTGGGCGNTAATAGCCNNAAAAGGCCN

171U= GCCATCACCTCTTGCTT
171L= GAGTTAGGGCAGAGGTTATGT

GM146
GNGAGNNNGNNGANNTTGTATTNNGTCTANAAANACTTTATTNAAANNCTCCCCCCTTTTGA
GGAAAGACGCCCGTCGGGNAGCTTGATATCGAATTCCTGCAGCCCAAAaTTTCTAAAAAGTC
CTCTGTTACACATCcacttACaccccTgtcaCTTCATGCACACACACACACACACACACACACA
CACACACACACACACACACACACACACATTTATGTATAGAAATACATTTCAGCGTACAACTTAAT
ATATTAAAACAGAAGTTGATCTCTCCAGTTATACAACGGATTAGCTCATTTAGCCTTTTAGGT
ATGCACTGCCTCTTTTCATCATCAAGTCCGGTGTCCCTCTGCAGATCTTCACTCCTTTGTTTG
TTACAGTCAGCTTTATAGAAGTGACCCAATCATAAAACCCCCATGGAGTGTTGCAAACTCTGT
GTTTGTGTGTGTATGTGCNAACACNTNANTGCCTGTGTGTGCCCNTACCCGTGTGTCTATGT
NAGTGCACNTTNAATGACTGTNTNTNCNTACCTGTGTNTATGTNTNAATGCACCTNAATNAAT
NTCCTNTNGNTNTNTNAANTGTAACANTTAAAANCACTGNNTNNNNNTNNTNNTTTTGNNCAC
NTNANTTTCCTNCCCN

146U= CCACTTACACCCCCTGTCACTTC
146L= ACACCGGACTTGATGATGAAAAGAG

Figure 11 IIII

GM62
TTCTCTTGTTNCTACNGATNCTNGGNATTCCCGCCCCTTTCGAGGTCGACCGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCANTTACATTTTTTTGAATGCATTCAGTTTNGNAGNCAAA
TACTTATTTTCAGGTATTCTGCTTTCAAGAGTAAAAGTTTAATTTGTTTCACCTTACCTAGACT
TTTCCTTTCTTCTTTACTGGTCTATTTTTTTCTATAACTGCCCCACACACACACACACACACAC
ACACACACACAGAGTCATGCACCCTCCTCTCCCGTTCAGCCTTTCTTTTTCCTCCCCTGCCC
TCCTTCCTTCTCCTCATCACTGAAGGTGTCAGGACTCTAACGCTGCAGTGCCATCTGGGGG
GGGATCCACTAGTTCTAGAGCGGCCGCCACCGNGGTGGAGCTCCAATTCGCCCTATAGTGA
GTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGC
GTACCCAACTTAATCGCCTTGCAAGCACATTCCCCTTTCGCCAGCTGGCGTTAATAGCCGAA
NAGGCCCCGNACCCGATCGGCCCTTTCCNAANANTTTGCCCANNCCTGAANNGNCCAAAGG

62U= TTCAGTTTTTCAGCCAAATAC
62L= CTGCAGCGTTAGAGTCCT

GM184
TTNTTTGACGACNTGGAGCTCCCCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCCC
GTAGGGATAGAATATCTAATATAGAGGAGCTCTGTGTATTTGGACACTTCCACCTTTACTTTG
ACAGACAGACCTGGACAAGCACACACAAAACCCAGCCACATACCAACTGTGGAAAACATCT
CACACACTCTACTCTTTTTCTTAAAGGTGCATCTCTTACACACACACACACACACACACACAA
GCAGGCACATGCAAAAATGTGGACACACATTGCACAAACATGCAATTTGGACAATAAGCCCT
GTTCTCCGTACAGAATGGCATGTATGTGCGCAAAACTACACAAGAGGTGAGACGGTTCGAT
GAGAAGCTACATGAAAGATGTAAAAGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATAC
CCGTCGACCTCGAGGGGGGGCNCCGGTACCCAGCTTTTTGTTCCCTTTTAGTGAAGGGTTT
AATTGCGCGCTTGGGCGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAAAATTGGTTATCC
GCTCACAATTCCACACAACATACGAGCCGGAAGATAAAAGTGTAAAGCTTGGGGTGCTAAAT
GN

184U= CACTTCCACCTTTACTTTGAC
184L= GGAGAACAGGGCTTATTG

GM510
CCTGGAGAGCGGAAAACTTGGCGGGATATTCGTGTTCTGGGCAATTAGGAATGTTGGAAAC
CTGAACTGAAATCTGCTTTTGGAGGAGCACTCAATCTGTCACTCACAGTCAAAACACAGCAC
GGAAAACTCATCCCTGCACATGGTTCAAACTTGCACACACACACACACACACACACACACAC
ACACACACACACACAGACACACACACACACATGCAGGCACTAGAGTGAAAACCACAACTCA
AATGCATTAATGTACACCTTTAACAAGTGCCTGAAAATACTCGCACCCACAGATAACCAGGG
GCTAGTTAGACCACCCCCGATGG

510U= ACAGCACGGAAAACTCATCC
510L= TAGCCCCTGGTTATCTGTGG

GM153
NNNNNNGGNNNNNNNNNNNNTTANNTTNTNTNTTTGNAGNGGATCTTAANGNGAACNCTCC
NCCCTTTCGAGGTCGACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCTGAAAAT
CTTCCTTGATGAACTGCACTAaGAATAGGGTCCTTTATGAGTCTCATTACCAAACCCAAACTG
TTTCAGGCAGAGCTGTGCGAGACACCCCGACAAGTCCTGGTAATTATCTTTAGTGAGCGGA
GCGCGACACACTGCTGTCGCTTCATGAACACATAGCACAGAGCTAACCGCTCAGAGAGATT

Figure 11 JJJJ

ACAGGCTCATGTGCATCAAAGACGAGCACGCACTCACACACACACACACACACACACAC
ACACACACACACACACACACCGTTTAATACACATGTCCACTTTGCTGATGTAAACCAATTTTT
TTCTTTTTTTTGGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTC
GCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGGTCGTTTTACAACNGTCGTGACT
GGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCAGCTN
GGCGTAATAGCGAA

153U= AAAGACGAGCACGCACTC
153L= GGTTTACATCAGCAAAGTGGA

GM277
TTGAATGCNNTCCCGCGGNNGCGGCCGCTCTAGAACTAGTGGATCCCCCC
TGTGCCCCTAAATTAGCCAATACAACATGGCAAACAACACAAGTAGAATG
TATCATTAACATGCCCGTTTCAGACTGCATTTCATTTTGCCAATATGAGT
ATGTTTAACTGCGCAGGTCTTCATGTGCGTCAGCAGCTGGTTTTTATTTT
AATGAATCTGACTGGAGCCTGAACCAGAGGTCACTTCCACTCTGCAGCAG
AACAAAGCTGGAACATTGGCTCCACACATCAGAAAGATGGAACGAGGCTT
TGTTGTTGTGAGAGACGAGGAGAATGTGTGCACATGCACATATCCTTTTT
ATAGACGTGCAAGGGCTCATATGCACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACAGAGAGGACGTTCAACTGTTTATA
AAAGAAGCATTTTACAAAGGCTTCAACATATAAAGAAAAACGTGTCAGTC
TGCAGAAAGCACTCCCTCAGTGCTTCCTGTTTTAGTAGATTAGGTTTCAG
AAATCACAAACTGTATGCAAGCAGTGGANGTGGGCTGCANGAATTCGATA
TCAAGCTTATTGANACCCGTCGAACTNGAGGGGGGGCCCGGTACCCAGCT
TTNGGTCCCTTTAGTGANGGGTAANTTGCCCCTTGGCGTAATCATGGNCA
TNGCTNTTCCCTGGGTGAAAATGGTATCCCGTNACAATTCCCACAACTTT
CGAGCCGGAGCTTAA

277U= TGTTGTGAGAGACGAGGAGA
277L= GTTGAAGCCTTTGTAAAATGC

GM102
NTTTGATNCGTNANNCNNNTGGAACCGCCTGGCGGTTCGCTCTAGAACTAGTGGATCCCCCCC
ACACAGTGGGACACAACATCGTAGTTCATTTATCCTGACGGCACTCTCGTAGAAGTGCTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGGTGTTTGGGGCTCAAGA
AGAAAAAAAAAGAACCCCCAGCATGTGTGCTTTGGAAAGCTGGGTATTCATCATCCTTCTCCA
CACGGTGTGAGCTCCAAAGAGCGGGAGCGGCGAGATGAGAGGAGAGCAGAGATCGGAAAAT
ATAGGTCTGAGATCAGTGATAACAAGGCAATCTCACACATGGTTTCATGTGAGATGGTGGAG
GAATTTTGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCC
CGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATA
GCTGTTTNCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGACCCGNAAGCAT
AAAAGTGTAAACCCTGGGGTTGCCCTAATGATGAGCTAN

102U=CATTTATCCTGACGGCACTCT
102L=TTTCCGATCTCTGCTCTCCT

Figure 11 KKKK

GM566
ATCTGGAGCAGAGAGCAGAGACCCTGACACACGGCTGTCACCCGAGGCAGACACGCAGAG
ATGTGGACATAGACAAAGTCTGCCCCCGTGTTTCTGCCTCCGCTTCTGTCTATCTGACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACTCTTTCACTCACATGTAAGTGACAGCAGAATGGAGATTGGTGAGTCAAACGGAA
GATGATGGTGAGAAAATTCCTGAGGATTTTACCAGGAGGAAAACTGAATTGCTATCCACCTA
AAAATCCCTCCCCAAATAAAGTGCTTGCTCTTTGATGGGGCAGAAAAGTTGAAAAACAGTAA
GTAGACTTTTTTAATATGAAGACAGGTTGTAAGCAGACTATTGTCATGTATGCTGGTATGATA
AACCATTAAACCACCAACATTATTGATCAGTCTTNCCAATGAAA

566U= CAGACACGCAGAGATGTGGA
566L= TCTTCCGTTTGACTCACCAA

GM55
TTNNAAGCCCTTGGNAGNCCCCCTCGAGGTTGACGGTATCGATNNGCTTGATATCGAATTC
CTGCAGCCCCCTTCCACTGTTGAAGCTGTCACAGGATTTGATAGAAGAGCATATGATTGCTA
CACCTGCACTTGCTTGCTTTTCACTTTTCACCTCTTTAGTTACATTAAAAAGTCTCAGTTTGTT
TGGCTTACACACATGCTTGAAAAGACACACTTATCTCACTCACACACACACACACACACACA
CACACACACACACACACACACACACACACACACACACACACAGACGTcTCACCTgTTTTACTAGGTA
AGGCTCAAAACGGATCATCTAAGCCAAtCACCTTTCAGGAAGCAGGGATCAGCCAAAATCTC
CTCAATTAATAGCTAAAGTAACCTTCAGTGACCTGACTGTGGTCTACCACAAACACACCCAC
ACTTACACACAGACATGCGCGCACTTACACACACACTCTCTCTCTATTGTCGGTCCATTTACC
ATTAGTCTGGGATTTTTTTTNTATTCATTTGAGTATAGCTTAGTATTAGTAAACATGTGAGGAAC
AGGATCAAGNATGTGAGGCACATCTATCTATCTAAACTGTAAGGGTGGACTGACCTTTTCCC
TACCTNTAGGNGCTTAGATGAAAAGATGAATGCCTGTCNGGNGTNAACACCGGATTTTTNTT
TNGGNAACAAAAACTGNTGGACNTTNTNGCTGGCAGCAACCCNTCCTTNGATAGGACTGAA
NAGNCCCCTGTCTNNAACTGGGTTTTTATTTG

55U= CATGCCTGTAAACCTTTTCC
55L= ATCCAGCGTTTACAGAGTGAA

GM594
CCCGGCAATTACAGCGTGGTGTTCACGAAGGACGACTTTCCAAAGAAATGTGCGCAGAGCA
GAGATTCAGATTTTCAGCCTTTGCTCGCTGAGCTGTGATCTGCAGGGTTTCATGATTCTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCCAGGTCAGACGTGTGACCCCAGC
TGTCATAACAGCTCGTGCTGGGCAGCAGGACAGGATCACTGTCAGAGATGTAAGCACACAC
TCCTTCCTGCTCTCACACAGTCGTTCTCTGTACGTTCAAAGTCATGATGATGGTACGTGTCG
ATTGTCTCTCTCTCTCTGTCTGTTTCTGTTAGTCACCAAGCTGCTGTGTGCAGAGCAGTGCA
GCTGGAGGTGTCGGGGG

594U= GCGCAGAGCAGAGATTCAG
594L= AGCAGGAAGGAGTGTGTGCT

GM516
TTCCTCAGCAGCCTGCTCAACTTCAGCAAGGTCACACACACACACACACACACACACACACA
CACTGGTATTATTATACTTGTTCCAGCTGCAGCATAAACCTGAGTTTGAGTCCTCATGTTCAT
GAAGCTTCACACACTCTATTGAAGAAGTGACAGATGGACACACGCTGACCTCACACACTCAG

Figure 11 LLLL

ATGTGTGTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTAGGGGGAAAC
TCCCCTCTCATGGTCTCATCACCTGCTGTCTCTCCGTGTGTCACATACCTGCTAAGCTGTGG
ATCTCTGAGG

516U= CAGCTGCAGCATAAACCTGA
516L= TCAGAGATCCACAGCTTAGCA

GM109
NNTTNNNNCTANTAACNCTCTTTTGGACACCCGGCCCCCTCTCGAGGTCGACGGTATCGAT
AAGCTTGATATCGAATTCCTGCAGCCCCCcTACAGTGCTTACTGACTAATTTAACAaAGTAAC
AACAAACAAACAAAACATTGAAACAAAATATTAACCAACAAATAAACTTGTAAATAAACCCCAA
AATATAAGTAAACTAACAACAAACTTTAACTAATTCAAAAATAATAAAAAAATAAGAACAAATG
GCTCCAACAATTAGTAAATCTTAAAAGCTAAAGCACTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTCCATGTCCATGCTGTCCAGTCTCTTTTCCAGCTGCTAGAACACACCTGTTCAACAT
CTATTCAGTCAATCATGTTTATTTCGCATCTACGGACACATTATAGACGTCTTTTATCAGGCT
GTAGAGCGATAAGCTTTGATCTTTTTTTAGTCTATAAATTTGTCAAATGGCATTTTTCCTGGGA
TGAATTTAAAAGCCTCAAGTGAAAAGGATGCNTTAAATTAAAATTTTGGAAATACCATTAAAAA
TGGCAATGGNAAGAGCNCCAATNTTNGGGATTGCAATGGGAAAAATGCCNNGCTTTTACAC
CTTTAAATTN

109U= ACTTGTAAATAAACCCCAAAA
109L= CCGTAGATGCGAAATAAAC

LG 22

GM674
TTCTGTCTGGTAAAAGGTTATGAGCAGAGGTGCGAGGTGAGACAAAGTGCAGCTGAGGTCG
TGACATACACACACACACACACACACACACACACACACACACACACACACTTAGCAGATTGTAGGT
AAGAGGTTAGACATATTTTGCTTGCAAACTGCATTTTGTGCTTGCATAAGTTACAGATTGTGC
AGGACTGTGCCTGATGGTCCAGACGATAAGCGAGCGTCCGGCAGCGACAGGAAGCACCTG
CCGTGGAGACGAGGCGATGTTCTTTTTTAACTGTGTCACAAGTTGTCAACAGAATATTTGTG
GTTTTGACGTTTGTATTAAATGACTTCTAAAGTCACAGCAGTTGGACTTTCTGTTTCTGACAG
AAACCTGGCTTCAACCCGGTGAGTCTGTAGCTTTTTCGGAACTGGTTCCTCCTAATTTCTCAT
TCTTCAGTCTCCCTC

674U= GGTGCGAGGTGAGACAAAGT
674L= GACGCTCGCTTATCGTCTG

GM175
TTTGATGCCCTTGGCTCCCCGCGGTGGNGGCCGCTCTAGAACTAGTGGATCCCCCACTGAT
GGGCAAACTGACCAAATGACCTCTTCGTGCACACACACACACACACACACACACACACACACA
CACACACACACACACACACACAAACAAAACTCCTCCCAGCTCCCCCACGACACTCTAACTTC
TAATGAACTCACACAAACATATGTATTCACACACATAATACACCCCCTCCACCCAAACACACA
CACATACAGACACTTACAGCCCCCCCACCCCCACCCCTCGAGGGAATAGATCAGCAGGAGA
TGAAAGGTGAGGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG

Figure 11 MMMM

GGGGGCCCGGTACCCAGCTTTTGTTCCCTTTAGTGAGGGTTAATTGCGCGCTTGGGCGTAA
TCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA
GCCGGAAGCATAAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG
CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTTGNTCGGGCAGCTGCATTAATGAA
TC

175U= GCAAACTGACCAAATGACC
175L= GGGGCTGTAAGTGTCTGTATG

GM687
TGGGATTTATAGATCATCTCCCTACAGCTGTCCCTTCTCATCCCCGAACCCCACCCTCCCCT
CCCCTCCCCAAACACACACACACACACACACACACACACACACACACACACACACACACACGC
TAATATTCTGAGGCTCATGATTCCACATCCAAACCCATCTACATCTCCTGTTTTTGTGTGTGA
TCTTTGGAGTCAGTGAACTGGGTCTTGGGAGTCCAGAACAGTAATGCTATCTGGAACCCGG
GTCAGCTAGAAACAA

687U= ACAGCTGTCCCTTCTCATCC
687L= TGTTCTGGACTCCCAAGACC

GM423
TNTNTGGTCCNCGTGNTCTNANGNAATGCTCCNCCNTTTAGGTAAACGGCCTCGATAAGCTN
GATATCGAATTCCTGCAGCCCCCCGGAGTTGGTTGAACTTTGACTTAATTGCAGACNGGGCG
CTGGTGGGTGTCAGGCTCAGCGACAGAGCGGGAGATGGAGGTGGACAGATCGCCAGACTG
CTGTTTGAAATTGTATTCATGCCTCTGGTGTTCTGTCTCCTTCTTCATCGTGTCCTCGCTGCT
CTTTTCTCACTTTCTTTCTTTCTTTTATTCTCTCCTTCCTTTGCTCTCGCTCTCTGCCCCCCTC
CCCTTGTCATATTTATAATGCGTTTGCCTGCAGGGCATTTTTCTATAACCTGACCTTGCAACA
GAGCGACTGTAGGACACGATTATAGTGATGCAACCACTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTNNGGNNGGTATGCCAGCCTCTCAGCCATTCTTAGCATCATGCTGCAGGCGCTGTGT
AACAGCTGCATGGAGAATGTCCTGGACTGCTCTGAGAGGNANAGGCTGCTGCACAGTGGG
GGGGATCCACTAGTTTCTAGAGCGGNCGCACCGCGGGTGGAGCTCCAATTCGCCCTATAGT
GGAGGTCCGAATTACGCGCCGCTCCTGGCCCGTCG

423U= GAGCGACTGTAGGACACGATT
423L= TGATGCTAAGAATGGCTGAGA

GM3
NTNTTNTTCCTAGTGATCTCTTGGANACCCNGCCCCNTTTCGAGGTCGACGGTATCGATAAG
CTTGATATCGAATTCCTGCAGCCCCCCCCAGTCCAAAGCACTCTGTAACAAAGAGACAAAATA
AAAAATGGTGGATGAAAACCAGCAGAGGAGTGTCACATGGGTGAGAGATTTATAATATGAAT
GGTTCAAACTTTCTCATAAATCAGTGCAAAATGCTTTCAGGTAGGTATGCTGACATTTATGCA
TGAGAGATGTCAACAGAACAAGTTCAATGAAGAGATGTGTGGAAGTGCAACTATGTTTATAT
GGTCCCGGTGATAGAAAACACACACACACACACACACACACACACACACACACACACACACAC
ACACAGACGCATACATATTTTTCTCTATAGGGTAAAATCATCCTGAGAATTGTGGTTGTCCCC

Figure 11 NNNN

ACATGTCGGGGAAAAAACATCTCAGTGATTCCTCAAATGTGGGGGATCCACTAGTTCTAGAG
CGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCAC
TGGCCGTCGTTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCACT

3U= GGATGAAAACCAGCAGAGGA
3L= GGGACAACCACAATTCTCAGG

LG 23

GM209
GNGNNNAGNTATTTGTCNCAAANACNAAAAANNNCNCCCCANCTGNGAAA
CNCNCTANCNATAAGCNGGNGATCGAATTCCTGCAGCCCACAAAAGCACC
CAGATGTTCAAACACCGGGGGGACNCAAAAANANTNCACNCACACACACA
CACACACACACACACACACACACACACACTGACACACAAAAGGTTTCATTTG
AATTCAAACCAAATTGACTTCAGGCAAACAAAACGTTGCTGAAATGATAT
TTTGTGTTAGAATCTAAGAATTCAGGAAATATGTTATAATGAATGAATTA
TCAGCAGCTTTGATACTTTCAGACGNNGTATTTGACTCGCTCTGGTAACT
GAAGCTAACCTGTGATGCAGTTTGGTTTGTTCGCGTGTTGTNAGTTGCTT
GTGTNGTTTCTGTTTGCCTTCCTCCTTGNCTTGTGTGGGGGATCCACTAG
TTCTAGAGCGGCCGCCACCGCGGNGGAGCTCCAATTCGCCCTATAGNGAA
NNCNNANTACNCNCGCTCANTGGCCCCNCNNTTTACAANNNNCNNNACNG
GGAAAANCCCNNNNNNNAACCCCAAACTNAAANACCNTGC

209U= AAAGCACCCAGATGTTCA
209L= GCTGCTGATAATTCATTCATT

GM592
AGTAAGTCTGAGCAAAACTCTAAACTGACTCAGAAACAAGAAGATTACACCCTTAGTCCTGA
TACTGAGTCATGCTTGACTTTTTCAAATGCCCAGTCCTGAGGACGTCAGGTTACCTTGTAGC
AGAGGGTTGCCAGGTTTGACGGAGACTCCTCTCTGACGGCTCTGATCTCTGCCGCCGGAAC
CAGAGCGAAAACATCCTGAACCGTGGTGGAGGAGTCGACCCAGAACTGATCCCAGAACAC
GTCGTCTGAGGCTTCGACGGGCTGCAGGAGAGGAAACGCACACAAACATCAGTGTGTGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTTCGACGTGATGAGAAAACCACCACTGCAGCTAT
GACTCTGTGACTTATCTGCTGCTAAACACATCAAATGAAAACAGTATGCAACATTCATTTCAT
TATGACTGTGTTGATGAGAAGG

592U= TCCTCTCTGACGGCTCTGAT
592L= CTGCAGTGGTGGTTTTCTCA

GM104
GGGNNNANNTNTNTGTNCANGNNATCTNAATNTAGACNCGCCCCTTTTGNAGNTCGACCGT
NTCGATAAGCTTGATATCGAATTCCTGCAGCCCCTNGACCACGGGGGCTCTTCTGCTCCTTG
GNGNCTAGAGGAGGGGGGCTCTCCTCGGGGGATGAACCCAGCGATGTCCCCCCCTCCACC
TCCAGAGCCTGGAGCTTCTGCAGGGAACTCTGCAGGCAGAAGCAGAACATGCCAGACACA
CTGGTCCAGAGATTAACCAGGTTCCAGGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGAGTGAGTGAGTGAGAGAGAAGAGGTGGAATGTAGGGCAGTGAGGCACTGTTACAATAAA

Figure 11 OOOO

AGACTCCAGATATTAGCCAGATCTCTGAAACATCACATGTGGAAGCACAGAGCAGGGGTTA
GTGTTCAGGAAATAGTCTGATCCCACAGTTTCAAAGCATAAGTCAATGAGCCTCCCTTCCAG
GAATTAGACCAGCACCATNCANAAAAACACGTNTNCCTNCAGNTTTTTCANATATTNANNATG
NGGGGGGATCCNCTNNNTTAAAANNGGNCNCCNCNNNNGNGN

104U= GAACCCAGCGATGTCCC
104L= ACTAACCCCTGCTCTGTGCTT

GM173
TTATTTNTACCACTATCCCTTTGGAAGCCCCACCGCGTTGGCGGCCGCTCTAGAACTAGTGG
ATCCCCCAAAAGCCATTCTTTGTGAACTTCTAGTCTGCCTCTGCAGAGAGcTTTCACACGCTT
CAAATAGCTATCAGAACAGATGATCGAGCTGGATAATCTCCAGTATCTACAGAGTCTGGTAT
GAGCCTGGCAAAACAGCATTTGTGAATCACTCACTCACACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACACACACACACACACACACACACACACACAC
ACACACACACACACAGCTTGGAATAATACACAAGACAAACTACATTTGGAGACTGTCTTCATA
CCCTGAATCAAAACACCACAGTCAAAACATGAAAAAAATGAATTATTTTGGGCTGCAGGAATT
CGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTTGNT
CCCTTTAGTGAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGA
AATTGTTATTCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGGTGTAAAGCTGG
GGTGCCTATGANTGAGCTAACTCAN

173U= TGAACTTCTAGTCTGCCTCTG
173L= GTGTTTTGATTCAGGGTATGA

GM145
GGNNNNNNNNNANCTTNTNTTNTTCNANAANACTTNANTGAACNCCNCCCCCTTTNGAGGTC
GACGGTATCGATAAGCTTGATATCGAATTCCTGCAGCCCCCcTcAGATCAAGTTTCAAACAGC
CATCCCcgtCTTTCTCCACACTCAAACACACACACACACACCCTTGTATATATATACACACACA
CACACACACACACACACACACCCTTGTATATATATACACACACACACACACACACACACACC
CTTGTATATACACACACACATTTCCCTTCAAGATGCACAATCAAACGGGCTCACAGAAAAT
ATACTCCACTGAACACCCTGTAAAATGTCTTTAGGCTGGAGACATGTGGGGGATCCACTAGT
TCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAATTCGCCCTATAGTGAGTCGTATTACGCG
CGCTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTT
AATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGGCGTAATAGCGAAGAGGCCCGCACC
GATCGCCCTTCCAAACAGTTGCGCAGCCTGAATGGCGAATGGAAAATGGTAAGCGTTNATN

145U= AGCCATCCCCGTCTTTCT
145L= TATTTTCTGTGAGCCCGTTTG

LG 24

GM27
TTTGAANCCCTTTGGAANCCCCGCGGTGNTNGNCGNTCTACCACTAGTGGATCCCCCAAAC
TTTTACACTTCTTGCAAAGACCAGACTATTATAAGAACAGGGTAATTCTCGAAAATCCCTGGC
TCCAGTTAATCCTCTGTTGTTTTGCCATGATGCTGACAGAGAGAGAGAGAGAGAAAGAGAGA
GAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTAAGAGAGAGAGAGAGAGAGCGAGAGTGA

Figure 11 PPPP

ATGACAAAAGGCTTGTGTAGGTTTCAACAGGGTAAATGAATGAGAACATAAGGCTTCGGTTT
TATTACCCAAATTATGTTCTGGAAAGTTAAAGTGTGTCACGTGTCATCACTAACTATGAAGTT
GTATAAGTAATACATGCTTGGTGTTGTATATAATACATTTATACTAAAAGCCTTTTGCCTTGTT
ATTCAAATCTGTTGGCATATTTTATCCATAATCCGTGCTGTGGTTTGTTGTTGCTGAGGTATC
TTCCCTCAGAGAGGAGGTGTCTGAGTTGCAGCGAGCATTGCATGGGCTTTGTGTTACAAATT
GGTTCCTTGNTAATGATACTTCATTTGCCTTTCATCTN

27U= TGGCTCCAGTTAATCCTCT
27L= TCTCATTCATTTACCCTGTTG

GM540
AAATTAGTACTGTTACATGAAGAAAACTcTGGGTTAAGCACACACACACACACACACACACAC
ACACACACACACACACACACACACACACACACTACCAGGGGAGTTGAGAGTCCTGCGCAGCAT
CTTTGCTGTTCCTACGAT

540U= GTACTGTTACATGAAGAAAACTcTGG
540L= TCGTAGGAACAGCAAAGATGC

GM559
ATCAATTGTAGCTGTCTAACTTGGTTTATCAAATAAAATTACAAGTTGAGCACCATTTTTAACC
AGTGCTTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGG
TCTCCAGGACCCTGACAGACCTGCTGAAACAGCAGGGGACTGAGGTGAGCTCGGTGGAAA
ATGCCAC

559U= GCACCATTTTTAACCAGTGCT
559L= ATTTTCCACCGAGCTCACCT

LG 25

GM128
TTGCTTCATTCCTTGCNTCCCCGNGGTGGTCGGCCGCTCTACNACTAGTG
GATCCCCCCCGGGGTGAAAGAGATGAGTGTNTGAGCAAGAGGAATAAAAG
ACAAAGAGAGCAGGGGAAATAGCTAATGATGAGAGAAAGGGAAAGAGGTG
AGCATTTGATGAGACTGTATTTCTATTAAACTGTCAGAGAATTTGCTCTT
TTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGCGCGAGCG
CCCTTCACAGAGGCACAGTAATGTGGCTGACCCAAATGACTAGGAAAATA
TTGGGAGAGTGAAAGACGGAAGCCTCTGTTGAATACTGATGAAGCTCAGC
ACAAAGCTTCCTCCTGGGGGCTGCAGGAATTCNATATCAAGCTTATCGAT
ACCGTCNACCTCGAGGGGGGGCCCGGNACCCAGCTTTTGNTCCCTTTAGT
GAGGGTTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTG
TGAAATTGTTATCCCGCTCACAATTCCACACAACATACGAGCCCGGAAGC
ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGN

128U= ATGATGAGAGAAAGGGAAAGA
128L= CATTACTGTGCCTCTGTGAAG

Figure 11 QQQQ

GM587
CCCATGCCTCCAACACAACCACCGCAACCCACCGTCACTTATGTCACCAGATGGACATCAAA
TGGGTAACAGTCTACGGGACAGCCACCAGCTATGCCAACTGGCTAGGCTCATTATGTTTGA
CTGACTGAGATCCGTGCCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTTTGNTCCAGCTCCTGAGGGAAATATGTGTGTTTTATAACAACCCACATCATTAT
ACAGTACAGCCACAGCGATAACACTTCAGCATGTTGG

587U= GCCAACTGGCTAGGCTCAT
587L= TGCTGAAGTGTTATCGCTGTG

GM526
CCCTCATTTTTTGTTGTCTCCAGACCTCTGCCCATATTTCCACCAGCTTTTTCCTTTTCTTGCT
TCGTTGGTGTGTGTGTGTGAGTCTCTTCCTCAGCCCATCTGTTTGTAACTGTGCACGTCTGT
CTGCCTTACACCAGACTAAACACATACAGACACACAGACACACACACACACACGTACATTCA
GCTTTTCATTAAATATACCAGTGACAGGATATGACAAGCTCTCCCAGCTTTTTAATTTAGCGC
CGGTGTCCGCCCACCTCCTCAGAGAGCTGGTCTAAAACCTGTCACTGCCAACAGTTGAGGG
ATGACAAGGTAATTAATAGTTTCACTACAATGCAGCCAACTCTTTTAGGAGCTGGACAGACA
GGATGAGCAGAAAAACAAGGAAGCATGTGGAGAGAGGAGAGATTAGGAGGCAGGGGATGA
GCAAAAAATATTGACAGACAGAGCAGGAAGATGAACAGAAATAGTCTGGTAAACCAGACGG
GG

526U= TCTTCCTCAGCCCATCTGTT
526L= CAACTGTTGGCAGTGACAGG

Figure 11 RRRR