

COMPOSITIONS AND METHODS FOR TREATMENT OF MONOGENIC NEURODEVELOPMENTAL DISORDER

The present application claims priority from AU 2022901557 filed on 7 June 2022,
5 AU 2022902778 filed on 26 September 2022, and AU 2022903040 filed on 17 October
2022, the entire contents of each of which are incorporated herein by reference.

Technical Field

The present disclosure generally is directed to oligonucleotides and related
10 compositions and methods for treating conditions associated with mutations in the
SHANK3 gene.

Background

SHANK3 is a widely expressed scaffolding protein enriched in the post-synaptic
15 density of excitatory synapses in the brain. SHANK3 recruits and stabilizes ionotropic
and metabotropic glutamate receptors (AMPA, NMDA, mGluR) to the post-synaptic
density. *SHANK3* gene mutations/deletions and SHANK3 haploinsufficiency underlie
the rare genetic neurodevelopmental disorder, Phelan-McDermid syndrome, and have
been attributed to 0.5%-1% of autism spectrum disorders (ASD), 2% of intellectual
20 disability diagnoses, and 0.6%-2.16% of atypical schizophrenia diagnoses.

Phelan-McDermid syndrome is characterized by intellectual disability of varying
degrees, neonatal hypotonia, absent to severely delayed speech development, moderate
to profound developmental delay, motor regression and minor dysmorphic features.
Approximately 14-70% of affected individuals develop seizures ranging from mild to
25 severe. Other complications include kidney abnormalities, gastrointestinal issues,
reduced perspiration and risk of overheating, lack of perception of pain, arachnoid cysts,
or other comorbid neuropsychiatric illnesses. Children are typically diagnosed in early
childhood, often due to significant delays in reaching early developmental milestones.
There is currently no effective treatment for conditions caused by SHANK3
30 haploinsufficiency such as Phelan-McDermid syndrome. Thus, there is an ongoing need
to provide effective compositions and methods for treating such conditions.

Summary

The *SHANK3* gene includes 22 exons spanning 58 kb of genomic DNA on the terminal end of chromosome 22 (22q13 region) and its major protein product is a 1,607 amino acid polypeptide. There are at least six known isoforms that are temporally and spatially specific and have distinct functions at the synapse. *SHANK3* contains five protein-protein interaction domains, and each isoform contains distinct combinations of these five domains.

While not wishing to be bound by theory, *SHANK3* haploinsufficiency due to loss of function gene mutation(s), including nonsense, missense and frameshift mutations, as well as partial or whole gene deletions, results in insufficient protein production.

The present disclosure provides antisense oligonucleotides (ASO), antisense RNA (AR) expression vectors, and related compositions and methods to increase *SHANK3* protein levels by modulating the translational efficiency or the stability of *SHANK3* mRNA to increase the level of *SHANK3* mRNAs encoding functional *SHANK3* isoforms. Also disclosed are methods for treating conditions associated with *SHANK3* haploinsufficiency.

Accordingly, in one aspect provided herein is an antisense oligonucleotide that binds within a targeted portion of the:

- (i) 5' untranslated region (UTR) of a *SHANK3* mRNA;
- (ii) 5'-proximal non-coding region (PNCr) of a *SHANK3* pre-mRNA; or
- (iii) 3' UTR of a *SHANK3* mRNA;

whereby binding of the antisense oligonucleotide within the targeted portion of the mRNA or pre-mRNA in a mammalian cell results in an increased level of *SHANK3* protein in the mammalian cell.

In a related aspect provided herein is vector for expression, in a mammalian neuron, of an antisense RNA (AR) that binds within a targeted portion of the:

- (i) 5' UTR of a *SHANK3* mRNA;
- (ii) 5' PNCr of a *SHANK3* pre-mRNA; or
- (iii) 3' UTR of a *SHANK3* mRNA;

whereby binding of the AR within the targeted portion of the RNA in a mammalian cell results in an increased level of SHANK3 protein in the mammalian cell. In some examples the vector includes a neuron-selective promoter for driving expression of the AR in the mammalian neuron. In some examples the neuron-selective promoter is selective for expression in a neuron type selected from the list consisting of: cortical glutamatergic neurons, cortical GABAergic neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons. In some examples the vector includes an inducible promoter. In some examples the vector is a non-viral vector. In some examples a non-viral vector is provided as a composition comprising a transfection agent. In other examples the vector is a viral vector. In some examples, where the vector is a viral vector, the viral vector is a recombinant virus selected from the group consisting of: adeno-associated virus (AAV), adenovirus, lentivirus, and anellovirus.

In some examples the nucleotide sequence of the ASO or AR corresponds to any one of **SEQ ID NOs:293, 299, 301, 302, 304-309, 311, 313, 315, 318, 606, 797, 1193, 1195, 1847, 1934-1937, 2858, 2874, 3510, 12644, 12666, 12669, 12671, 12688, or 12690**. In some examples of any of the ASOs, vectors, or compositions, the binding of the ASO or AR is within a targeted portion of the 5' UTR corresponding to **SEQ ID NO:1**. In other examples of any of the foregoing methods, ASOs, vectors, or compositions, the binding of the ASO or AR is within a targeted portion of the 5' PNCR corresponding to **SEQ ID NO:3**. In other examples of any of the foregoing methods, ASOs, vectors, or compositions, the binding of the ASO or AR is within a targeted portion of the 3' UTR corresponding to **SEQ ID NO:2**.

In some examples the nucleotide sequence of the ASO or AR is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion over the length of the ASO or the AR. In some examples the nucleotide sequence of the ASO or AR corresponds to any one of **SEQ ID NOs:5-622, 4175-4181, or 4184-4186**. In some examples the nucleotide sequence of the ASO or AR corresponds to any one of **SEQ ID NOs:559, 606, or 4178-4181**. In other examples the nucleotide sequence of the antisense oligonucleotide or the AR corresponds to any one of **SEQ ID NOs:1935-4168, 4182, 4183, 12646-12654, or 12664-12671**. In some examples the nucleotide sequence of the ASO or AR corresponds to any one of

SEQ ID NOs:1935-1937, or 2849. In other examples the nucleotide sequence of the ASO or AR corresponds to any one of SEQ ID NOs:623-1934, 4169-4174, 12645, 12655-12663, or 12688. In some examples the nucleotide sequence of the ASO or AR corresponds to any one of SEQ ID NOs:1847, 1852, 1934, 12661-12663, or 12688.

5 In some examples any of the foregoing ASOs include a backbone modification. In some examples the backbone modification includes a phosphorothioate linkage or a phosphorodiamidate linkage. In other examples the ASO includes a phosphorodiamidate morpholino, a locked nucleic acid, a peptide nucleic acid, or a 2'-O- modification such as a 2'-O-methyl, a 2'-Fluoro, or a 2'-O-methoxyethyl moiety. In some examples the
10 ASO includes at least one modified sugar moiety. In other examples each sugar moiety in the ASO is a modified sugar moiety. In some examples the ASO includes a 2'-O-methoxyethyl moiety. In other examples each nucleotide of the ASO includes a 2'-O-methoxyethyl moiety.

In some examples of any of the foregoing ASOs or vectors, the nucleotide
15 sequence of the ASO or AR is 10 to 50 nucleotides, 15 to 40 nucleotides, 17 to 30 nucleotides, 18 to 40 nucleotides, 17 to 25 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 22 to 30 nucleotides, 24 to 30 nucleotides, 25 to 30 nucleotides, or 26 to 30 nucleotides in length. In some examples where the ASO is 17 to 30 nucleotides in length, the ASO includes one or more phosphorodiamidate morpholino moieties.

20 In some examples any of the foregoing ASOs are linked to a functional moiety. In some examples the functional moiety includes a delivery moiety. In some examples the delivery moiety is selected from the group consisting of: lipids, polyethers, peptides, carbohydrates, receptor binding domains (RBDs), and antibodies. In some examples, wherein the ASO includes a delivery moiety, the delivery moiety includes a cell-
25 penetrating peptide (CPP). In some examples the delivery moiety includes a *N*-acetylgalactosamine (GalNAc) or glycan moiety. In some examples the delivery moiety includes a fatty acid or lipid moiety. In some embodiments the fatty acid chain length is about C8 to C20. In other examples the functional moiety includes a stabilising moiety. In some examples the functional moiety is covalently linked to the ASO. In other
30 examples the functional moiety is non-covalently linked to the ASO. In some examples the functional moiety is linked to the 5' end of the ASO. In other examples the functional

moiety is linked to the 3' end of the ASO. In some examples any of the foregoing ASOs also include a delivery nanocarrier, wherein the nanocarrier is complexed with the ASO. In some examples the delivery nanocarrier is selected from the group consisting of: lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures. In
5 some examples the delivery nanocarrier includes a lipid nanoparticle (LNP) encapsulating the ASO.

In a related aspect provided herein is a pharmaceutical composition that includes any of the foregoing ASOs, vectors, or compositions and a pharmaceutically acceptable excipient.

10 In a further related aspect provided herein is a method for preventing or treating a condition associated with SHANK3 haploinsufficiency, the method comprising administering to a subject in need thereof a therapeutically effective amount of the foregoing pharmaceutical composition. In some examples the condition to be treated is Phelan-McDermid syndrome, an autism spectrum disorder, schizophrenia, or an
15 intellectual disability. In some examples the condition to be treated is Phelan-McDermid syndrome. In some examples the subject to be treated is a human subject.

In a further aspect provided herein is the use of any of the foregoing antisense oligonucleotides, vectors, or compositions in the manufacture of a medicament for prevention or treatment of a condition associated with SHANK3 haploinsufficiency.

20 In some examples of the foregoing methods of treatment or uses, the level of SHANK3 protein in at least a plurality of cells in the subject is increased about 1.1 to about 5 fold in cells (*e.g.*, neurons) *in vitro* or *ex vivo*, *e.g.*, 1.2 fold, 1.3 fold, 1.5 fold, 1.7 fold, 2 fold, 2.2 fold, 2.5 fold, 2.7 fold, 3 fold, 3.3 fold, 3.5 fold, 4 fold, 4.3 fold, 4.5 fold, 4.7 fold, or another increase in SHANK3 protein levels from about 1.1 fold to about
25 5 fold in cells in a subject compared to the level in the absence of the pharmaceutical composition.

In yet another aspect provided herein is a genetically modified cell comprising any of the foregoing ASOs or vectors. In some examples the genetically modified cell is a mammalian cell. In some examples the genetically modified mammalian cell is a
30 human cell. In some examples the genetically modified mammalian cell is a neuron or a neural progenitor. In some examples, the genetically modified mammalian cell is a

neuron selected from the group consisting of: cortical glutamatergic neurons, cortical GABAergic neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons. In some examples the genetically modified mammalian cell is from a cell line. In some examples the cell line is a human induced pluripotent stem cell (hiPSC) line or
5 a cell line derived from neurons.

It is also known that *SHANK3* mRNA is subject to alternative splicing, which can have an impact on the overall level of canonical *SHANK3* mRNA and protein levels. The term “alternative splicing” refers to a process whereby exons, or part of an exon of a gene, or introns or part of an intron, may be included within or excluded from the final
10 mRNA transcript. Mature noncanonical mRNA transcripts can be non-productive due to a frame shift that may induce degradation of the transcript via the nonsense mediated decay pathway. In other cases, translation of the noncanonical mRNA can produce a truncated but non-functional protein. Alternative splicing of the *SHANK3* pre-RNA transcripts can downregulate overall *SHANK3* mRNA and protein expression.

15 Introns are removed from maturing transcripts by a large RNA-protein complex termed the spliceosome, which orchestrates complex interactions between primary transcripts, small nuclear RNAs (snRNAs) and a large number of proteins. Spliceosomes assemble on each intron in an ordered manner, starting with recognition of the 5' splice site (5' ss) by U1 snRNA or the 3' splice site (3' ss) by the U2 pathway, which involves
20 binding of the U2 auxiliary factor (U2AF) to the 3' ss region to facilitate U2 binding to the branch point sequence (BPS). U2AF is a stable heterodimer composed of a U2AF2-encoded 65-kD subunit (U2AF65), which binds the polypyrimidine tract (PPT), and a U2AF1-encoded 35-kD subunit (U2AF35), which interacts with highly conserved AG dinucleotides at 3' ss and stabilizes U2AF65 binding. In addition to the BPS/PPT unit
25 and 3' ss/5' ss, accurate splicing requires auxiliary sequences or structures that activate or repress splice site recognition, known as intronic or exonic splicing enhancers or silencers. These elements allow genuine splice sites to be distinguished from cryptic or pseudo-splice sites, which have the same sequence motifs as authentic sites but outnumber them by an order of magnitude in the genomes of higher eukaryotes.

30 Accordingly, in a different aspect provided herein is a method for increasing the amount of functional SHANK3 protein in a mammalian cell expressing a *SHANK3* pre-

mRNA, the method comprising contacting the cell with an antisense oligonucleotide or antisense RNA that binds to a targeted portion of the *SHANK3* pre-mRNA to modulate splicing of a *SHANK3* mRNA derived therefrom, whereby the level of *SHANK3* mRNA encoding full length, functional SHANK3 protein is increased in the mammalian cell.

5 In a further aspect provided herein is antisense oligonucleotide that binds to a targeted portion of a *SHANK3* pre-mRNA to modulate splicing of the *SHANK3* mRNA, whereby the level of *SHANK3* mRNA encoding full length, functional SHANK3 is increased.

10 In a related aspect provided herein is a vector for expression, in a mammalian neuron, of an antisense RNA (AR) that binds within a targeted portion of a *SHANK3* pre-mRNA to modulate splicing of the *SHANK3* mRNA, whereby the level of *SHANK3* mRNA encoding full length, functional SHANK3 is increased. In some examples the nucleotide sequence of the ASO or AR used to modulate splicing corresponds to any one of SEQ ID NOs:4187-12693 or 12695-3953.

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Brief Description of the Accompanying Drawings

Figure 1 – A set of exemplary *SHANK3* PMOs induce variable SHANK3 protein upregulation

Normalized fold-change in expression of SHANK3 protein assessed by western blotting. SHANK3 protein expression is shown relative to the level in transfection control cells (no ASO transfection control). SH-SY5Y cells transfected with PMOs 4-10 (SEQ ID NOs: 4169, 4170, 1934 and 4171-4174 respectively) and 19-37 (SEQ ID NOs:4184-4186, 4175, 559, 4176, 4177, 598, 4178-4183, 606, 1935, 1936, 2849 and 1937 respectively) at 25 μ M and 50 μ M. SHANK3 protein (190 kDa) is normalized to the total amount of protein loaded. Data are presented as mean (n = 3-6 biological replicates, with 1-2 technical replicates per experiment).

Figure 2 – A subset of exemplary *SHANK3* PMOs induce robust upregulation of SHANK3 protein

30 Normalized fold-change in expression of SHANK3 protein assessed by western blotting. SHANK3 protein expression is shown relative to the level in transfection control cells

(no ASO transfection control). SH-SY5Y cells transfected with PMOs 6 (SEQ ID NO: 1934), 33-35 (SEQ ID NOs: 606, 1935 and 1936, respectively), 37 (SEQ ID NOs: 1937), at 25 μ M and 50 μ M demonstrate upregulation of SHANK3 protein, relative to transfection control SH-SY5Y cells (no ASO transfection control). Data are presented as mean $\pm$ SEM (n = 3-6 biological replicates, with 1-2 technical replicates per experiment). Statistical significance calculated as two-way unpaired t-test between treatment and transfection control cells (no ASO transfection control); *:p $\leq$ 0.05, **: p $\leq$ 0.01.

Figure 3 – Screening of PMOs targeting the 5' UTR, 3' UTR, or retained introns of *SHANK3* in human neuroblastoma cell line

SH-SY5Y cells were transfected with PMOs targeting the 5' UTR, 3' UTR, or retained introns of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific), as per the manufacturer's instructions. Total protein was harvested (96 hours) from transfected cells using 15% SDS lysis buffer. SHANK3 protein (190 kDa) expression was analysed by western blotting using rabbit-SHANK3 polyclonal antibody (Bethyl Labs, BLA304178A-T) at 1:10 000 in 5% BSA in TBST. Experimental controls are identified as TFC (transfection control, no ASO), UTC (untreated control), + control (rat cerebellum lysate positive control and NTC (non-targeted negative controls (Smn1 and scrambled PMO). Housekeepers used for normalization include Vinculin (116 kDa; mouse-monoclonal antibody at 1:200 in 5% BSA in TBST, Sigma Aldrich, V9131) and Beclin1 (60 kDa; rabbit-polyclonal antibody at 1:2 000 in 5% BSA in TBST, Cell Signalling Technology, S3495). Blots are representative of n = 2-5 biological replicates. Corresponding SEQ ID NOs through (A) and (B) are indicated above each lane.

Figure 4 – A set of exemplary *SHANK3* PMOs induce variable SHANK3 protein upregulation by targeting the 5' UTR and putative extended 5' UTR of *SHANK3* transcripts

SH-SY5Y cells were transfected with PMOs targeting the 5' UTR and putative extended 5' UTR of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of SHANK3 protein was assessed by western blotting. SHANK3 protein expression is shown relative to the level in

transfection control cells (no PMO, zap). Data are presented as mean $\pm$ SEM (n = 2-5 biological replicates). ASOs (other than positive controls) are identified by their SEQ ID NO and are listed in 5'-3' target site order, as schematically illustrated in Figure 14. Control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control) and UTC (untreated control). SHANK3 protein (190 kDa) is normalized to the total amount of protein loaded.

Figure 5 – A set of exemplary *SHANK3* PMOs induce variable *SHANK3* protein upregulation by targeting the 3' UTR of *SHANK3* transcripts

SH-SY5Y cells were transfected with PMOs targeting the 3' UTR of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of SHANK3 protein was assessed by western blotting. SHANK3 protein expression is shown relative to the level in transfection control cells (no PMO, zap). Data are presented as mean $\pm$ SEM (n = 2-5 biological replicates). ASOs (other than positive controls) are identified by their SEQ ID NO and are listed in 5'-3' target site order, as schematically illustrated in Figure 17. Control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control) and UTC (untreated control). SHANK3 protein (190 kDa) is normalized to the total amount of protein loaded.

Figure 6 – A subset of exemplary *SHANK3* PMOs induce robust upregulation of *SHANK3* protein by targeting the 5' and 3' UTRs of *SHANK3* transcripts

SH-SY5Y cells were transfected with PMOs targeting the 5' and 3' UTR of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of SHANK3 protein was assessed by western blotting. SHANK3 protein expression is shown relative to the level in transfection control cells (no PMO, zap). Data are presented as mean $\pm$ SEM (n = 2-5 biological replicates). ASOs (other than positive controls) are identified by their SEQ ID NO and are listed in 5'-3' target site order, as diagrammed in Figures 14 and 17, and control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control) and UTC (untreated control). SHANK3 protein (190 kDa) is normalized to the total amount of protein loaded.

Figure 7 – A set of exemplary *SHANK3* PMOs induce variable *SHANK3* protein upregulation by modulating splicing of *SHANK3* transcripts

SH-SY5Y cells were transfected with PMOs that modulate alternative splicing of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of *SHANK3* protein was assessed by western blotting. *SHANK3* protein expression is shown relative to the level in transfection control cells (no PMO, zap). Data are presented as mean $\pm$ SEM (n = 2-5 biological replicates). ASOs (other than positive controls) are identified by their SEQ ID NO and are listed in 5'-3' target site order, as diagrammed in Figures 15 and 16. Control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control) and UTC (untreated control). *SHANK3* protein (190 kDa) is normalized to the total amount of protein loaded.

Figure 8 – A subset of exemplary *SHANK3* PMOs induce robust upregulation of *SHANK3* protein by modulating splicing of *SHANK3* transcripts

SH-SY5Y cells were transfected with PMOs that modulate alternative splicing of *SHANK3* at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of *SHANK3* protein was assessed by western blotting. *SHANK3* protein expression is shown relative to the level in transfection control cells (no PMO, zap). Data are presented as mean $\pm$ SEM (n = 2-5 biological replicates). ASOs (other than positive controls) are identified by their SEQ ID NO and are listed in 5'-3' target site order, as illustrated in Figures 15 and 16. Control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control) and UTC (untreated control). *SHANK3* protein (190 kDa) is normalized to the total amount of protein loaded.

Figure 9 – Screening of MOEs targeting the 5' UTR or 3' UTR of *SHANK3* in human neuroblastoma cell line

A panel of MOEs targeting the 5' UTR, 3' UTR, or retained introns of *SHANK3* were screened in SH-SY5Y cells via electroporation (NEON, ThermoFisher Scientific), as per

the manufacturer's instructions. Protein was harvested (96 hours), using 15% SDS protein lysis buffer. SHANK3 (190 kDa) expression was assessed by western blot using rabbit-SHANK3 polyclonal antibody (Bethyl Labs, BLA304-178A-T) at 1:10,000 in 5% BSA in TBST buffer. Beclin1 (60 kDa) and Vinculin (116 kDa) were used as housekeeper proteins and were assessed using rabbit-Beclin1 monoclonal antibody at 1:2,000 in 5% BSA in TBST (Cell Signalling Technology, S3495) and mouse-Vinculin monoclonal antibody at 1:200 in 5% BSA in TBST (Sigma-Aldrich, V9131). Control treatments are identified as NTC (Non-targeted control PMO), TFC (transfection control), UTC (untreated control) and rat cerebellum lysate positive control (+ control). SEQ ID NOs for each MOE are indicated above each lane. Blots are representative of n = 1-3 biological replicates.

Figure 10 – A set of exemplary *SHANK3* MOEs induce variable *SHANK3* protein upregulation by targeting the 5' UTR and putative extended 5' UTR of *SHANK3* transcripts

SH-SY5Y cells were transfected with 2.5 μ M, 5.0 μ M and/or 25 μ M of MOE designed to target the 5' UTR or putative extended 5' UTR of *SHANK3* via electroporation (NEON, ThermoFisher Scientific). SHANK3 protein levels were assessed by western blot and expression was normalized to a housekeeper (HK) protein, Beclin1. Fold-change in SHANK3 expression was measured relative to the transfection control (TFC; no ASO). A subset of MOEs at 5 μ M (SEQ ID NO: 3510, 299, 301, 302, 305, 306, 309 and 318) and 25 μ M (SEQ ID NO: 293, 305, 306, 307, 308, 311, 313 and 315) induced protein upregulation ≥ 1.5 -fold relative to the TFC. Data are presented as mean $\pm$ SEM (n = 1-3 biological replicates, with 1-2 technical replicates per experiment).

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Figure 11 – A subset of exemplary *SHANK3* MOEs induce variable upregulation of *SHANK3* protein by targeting the 3' UTR of *SHANK3* transcripts.

SH-SY5Y cells were transfected with a panel of MOEs targeting the 3' UTR of *SHANK3* via electroporation (NEON, ThermoFisher Scientific). Normalized fold-change in expression of SHANK3 protein (at 96 hours) was assessed by western blotting. SHANK3 protein expression in transfected and un-transfected (UTC) cells is shown relative to the

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transfection control (TFC; no ASO). MOEs were tested at concentrations of 2.5 μ M, 5.0 μ M, or 25 μ M, although not all concentrations were tested for each MOE. Among the sequences tested, one MOE (SEQ ID NO: 1193) induced upregulation of SHANK3 protein at both the lower (5.0 μ M) and higher (25 μ M) concentrations, relative to the TFC. A subset of MOEs (SEQ ID NOs: 797, 1194 and 1195) induced SHANK3 upregulation only when used at 25 μ M. Data are presented as mean $\pm$ SEM (n = 1-3 biological replicates, with 1-2 technical replicates per experiment).

Figure 12 – Screening of an expanded panel of *SHANK3* MOEs targeting the 5' UTR and 3' UTR by lipofectamine™

A panel of MOEs targeting the 5' UTR or 3' UTR were screened in SH-SY5Y cells using Lipofectamine™ 3000 (Life Technologies) to facilitate transfection, as per the manufacturer's instructions. Total protein was harvested (96 hours) from the transfected cells and an untreated control (UTC) using 15% SDS protein lysis buffer, and expression of SHANK3 was assessed by western blot. (A) SHANK3 expression was normalized to housekeeper (HK) proteins and the fold-change in its expression was measured against the transfection control (TFC; no ASO). On average, none of the screened MOEs induced ≥ 1.5 -fold upregulation of SHANK3, relative to the TFC. Data are presented as mean $\pm$ SEM (n = 2-4 biological replicates, 1-2 technical replicates per experiment). Corresponding SEQ ID NOs for each MOE tested are indicated under each graph set. (B) Representative western blot using rabbit anti-SHANK3 polyclonal antibody (Bethyl Labs, A304-178A-T) at 1:10 000 in 5% BSA in TBST to detect SHANK3. HK proteins were measured using rabbit anti-Becn1 monoclonal antibody at 1:2 000 in 5% BSA in TBST (Cell Signalling Technology, S3495) and mouse anti-Vinculin monoclonal antibody at 1:200 in 5% BASA in TBST (Sigma-Aldrich, V9131). Corresponding SEQ ID NOs for each MOE tested are indicated over each lane.

Figure 13 – A subset of exemplary *SHANK3* MOEs induce robust upregulation of SHANK3 protein by targeting the 5' and 3' UTRs of *SHANK3* transcripts

A subset of MOEs targeting the 5' and 3' UTRs of *SHANK3* were tested for their ability to upregulate SHANK3 protein expression in SH-SY5Y cells. Total protein was

harvested (96 hours) from the transfected cells and an untreated control (UTC) using 15% SDS protein lysis buffer. Expression of SHANK3 was assessed by western blot and normalised to total protein levels (Revert™ 700 Total Protein Stain, LI-COR). A transfection control (TFC; no ASO) was used to calculate the fold-change in SHANK3 expression. A subset of MOEs (SEQ ID NOs: 3510, 299, 301, 302, 304, 305, 309, 318 and 1193) caused upregulation at 5.0 µM, relative to the TFC. Select MOEs were also tested at 25 µM and were shown to further increase SHANK3 expression ≥ 1.5 -fold relative to the TFC (SEQ ID NOs: 293, 305-308, 311, 313, 315, 316, 797 and 1195). Data are presented as mean $\pm$ SEM (n = 1-2 biological replicates, with 1-2 technical replicates per experiment).

Figure 14 – PMO 5' UTR diagram

Binding sites of PMOs targeting the putative extended 5' UTR and canonical 5' UTR of *SHANK3* transcripts. Grey rectangles above upper-case sequence (ACGT) represent exons, or exon segments; dashed lines above lower-case sequence (agct) represent introns, or intron segments. Ellipses (...) indicate where part of an exon or intron sequence is omitted from this diagram. =Where necessary, the span of the absent sequence between two shown sequences is written (e.g., in intron 1 -1152 bp-). Black bars indicate the target sites of the PMOs, which are labelled with the corresponding SEQ IDs; grey bars indicate the target site of a single PMO (SEQ ID 598) that bridges exon 3 and exon 4, with asterisks showing where the two target site segments are contiguous in the mature spliced mRNA. *SHANK3* exon/intron boundaries and sequence are derived from ENSEMBL transcript reference sequence ENST00000262795.6.

Figure 15 – PMO retained intron diagram (1 of 2)

Binding sites of PMOs targeting the exons of mature *SHANK3* transcripts. Grey rectangles above upper-case sequence (ACGT) represent exons, or exon segments; dashed lines above lower-case sequence (agct) represent introns, or intron segments. Ellipses (...) indicate where part of an exon or intron sequence is omitted from this diagram. Black bars indicate the target sites of PMOs with sequences corresponding to

the labelled SEQ IDs. *SHANK3* exon/intron boundaries and sequence are derived from ENSEMBL transcript reference sequence ENST00000262795.6

Figure 16 – PMO retained intron diagram (2 of 2)

- 5 Binding sites of PMOs targeting the exons of mature *SHANK3* transcripts. Grey rectangles above upper-case sequence (ACGT) represent exons, or exon segments
dashed lines above lower-case sequence (agct) represent introns, or intron segments. Ellipses (...) indicate where part of an exon or intron sequence is omitted from this
diagram. Black bars indicate the target sites of PMOs with sequences corresponding to
10 the labelled SEQ IDs. *SHANK3* exon/intron boundaries and sequence are derived from
ENSEMBL transcript reference sequence ENST00000262795.6

Figure 17 – PMO 3' UTR diagram

- Binding sites of PMOs targeting the 3' UTR of *SHANK3* transcripts. Grey rectangles
15 above upper-case sequence (ACGT) represent segments of exon 23. Ellipses (...) denote
where part of a sequence has been omitted from the diagram, and the span of the absent
sequence is indicated (i.e., 1128 bp). Black bars represent the target sites of a given
PMOs, which are labelled with the corresponding SEQ IDs. *SHANK3* exon boundaries
and sequence are derived from ENSEMBL transcript reference
20 sequence ENST00000262795.6

Figure 18 – MOE 5' UTR and 3' UTR diagram

- Binding sites of MOEs targeting the 5' UTR (top) and 3' UTR (middle, bottom) of
mature *SHANK3* transcripts. Grey rectangles above upper-case sequence (ACGT)
25 represent exons or exon segments, with vertical black lines indicating exon-exon
junctions. Ellipses (...) denote where part of an exon or intron sequence is omitted from
this diagram. Where necessary, the span of the absent sequence is also indicated. Black
bars represent the target sites of each MOE, , which are labelled with the corresponding
SEQ IDs. *SHANK3* exon/intron boundaries and numbering are derived from GenBank
30 transcript reference sequence NM_001372044.2.

Figure 19 – A subset of exemplary *SHANK3* PMOs induce robust transcript modulation of SHANK3

SH-SY5Y cells were transfected with a subset of PMOs designed to target the 5' UTR or putative extended 5' UTR of *SHANK3* that demonstrated ≥ 1.5 -fold-change upregulation of SHANK3 protein from western blot assessment. SH-SY5Y cells were transfected with PMOs at 25 μ M and 50 μ M via electroporation (NEON, ThermoFisher Scientific), as per the manufacturer's instructions. Cells were harvested (96 hours) and RNA was extracted using MagMAX™-96 Total RNA Isolation Kit (AM1830, ThermoFisher Scientific). Target engagement was determined by the percentage modulation of altered SHANK3 transcript relative to TFC (transfection control) and UTC (untreated control), indicated by RT-PCR gel bands (LabChip GXII, PerkinElmer). Data are presented at mean $\pm$ SEM (n = 3 biological replicates).

15 Detailed Description

General

Throughout this specification, unless specifically stated otherwise or the context requires otherwise, reference to a single step, composition of matter, group of steps or group of compositions of matter shall be taken to encompass one and a plurality (*i.e.*, one or more) of those steps, compositions of matter, groups of steps or groups of compositions of matter. Thus, as used herein, the singular forms "a", "an" and "the" include plural aspects unless the context clearly dictates otherwise. For example, reference to "a" includes a single as well as two or more; reference to "an" includes a single as well as two or more; reference to "the" includes a single as well as two or more and so forth.

Each example of the present disclosure described herein is to be applied *mutatis mutandis* to each and every other example unless specifically stated otherwise.

Those skilled in the art will appreciate that the disclosure herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the disclosure includes all such variations and modifications. The disclosure also includes all of the steps, features, compositions and compounds referred

to or indicated in this specification, individually or collectively, and any and all combinations or any two or more of said steps or features.

The present disclosure is not to be limited in scope by the specific examples described herein, which are intended for the purpose of exemplification only.

- 5 Functionally-equivalent products, compositions and methods are clearly within the scope of the disclosure, as described herein.

The present disclosure is performed without undue experimentation using, unless otherwise indicated, conventional techniques of molecular biology, microbiology, virology, recombinant DNA technology, peptide synthesis in solution, solid phase
10 peptide synthesis, and immunology. Such techniques are described and explained throughout the literature in sources such as Perbal 1984, Sambrook et al., 2001, Brown (editor) 1991, Glover and Hames (editors) 1995 and 1996, Ausubel *et al.* including all updates until present, Coligan *et al.* (editors) (including all updates until present), Maniatis *et al.* 1982, Gait (editor) 1984, Hames and Higgins (editors) 1984, Freshney
15 (editor) 1986.

The term “and/or”, *e.g.*, “X and/or Y” shall be understood to mean either “X and Y” or “X or Y” and shall be taken to provide explicit support for both meanings or for either meaning.

The term “about”, unless stated to the contrary, refers to +/- 20%, more preferably
20 +/- 10%, of the designated value. For the avoidance of doubt, the term “about” followed by a designated value is to be interpreted as also encompassing the exact designated value itself (for example, “about 10” also encompasses 10 exactly).

Throughout this specification the word “comprise”, or variations such as “comprises” or “comprising”, will be understood to imply the inclusion of a stated
25 element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

The term “antisense oligonucleotide” “antisense oligomer” or “ASO,” as used herein, encompasses oligonucleotides and any other oligomeric molecule that comprises nucleobases capable of hybridizing to a complementary sequence on a target RNA
30 transcript, including, but not limited to, those that do not comprise a sugar moiety, such

as in the case of a peptide nucleic acid (PNA). Preferably, the ASO is an ASO that is resistant to nuclease cleavage or degradation.

The phrase “binds to a targeted portion” or “binds within a targeted portion,” in reference to an ASO or AR, as used herein, refers to specific hybridization between the ASO or AR nucleotide sequence and a target nucleotide sequence that is complementary within the ranges set forth herein. In some examples, specific hybridization occurs where, under *ex vivo* conditions, the hybridization occurs under high stringency conditions. By “high stringency conditions” is meant that the ASO or AR, under such *ex vivo* conditions, hybridize to a target sequence in an amount that is detectably stronger than non-specific hybridization. High stringency conditions, then, are conditions that distinguish a polynucleotide with an exact complementary sequence, or one containing only a few scattered mismatches from a random sequence that happened to have a few small regions (*e.g.*, 1-5 bases) that matched the probe. Such small regions of complementarity are more easily melted than a full-length complement of 12-17 or more bases, and moderate stringency hybridization makes them easily distinguishable. In one example, high stringency conditions include, for example, low salt and/or high temperature conditions, such as provided by about 0.02-0.1 M NaCl or the equivalent, at temperatures of about 50--70 °C. The skilled person will appreciate that under *in vivo* conditions, the specificity of hybridization between an ASO or an AR and its target sequence is defined in terms of the level of complementarity between the ASO or an AR and the target sequence to which it hybridizes within a cell.

The term “peptide” is intended to include compounds composed of amino acid residues linked by amide bonds. A peptide may be natural or unnatural, ribosome translated or synthetically derived. Typically, a peptide will consist of between 2 and 200 amino acids. For example, the peptide may have a length in the range of 10 to 20 amino acids or 10 to 30 amino acids or 10 to 40 amino acids or 10 to 50 amino acids or 10 to 60 amino acids or 10 to 70 amino acids or 10 to 80 amino acids or 10 to 90 amino acids or 10 to 100 amino acids, including any length within said range(s). The peptide may comprise or consist of fewer than about 150 amino acids or fewer than about 125 amino acids or fewer than about 100 amino acids or fewer than about 90 amino acids or

fewer than about 80 amino acids or fewer than about 70 amino acids or fewer than about 60 amino acids or fewer than about 50 amino acids.

Peptides, as referred to herein, include "inverso" peptides in which all L-amino acids are substituted with the corresponding D-amino acids, "retro-inverso" peptides in which the sequence of amino acids is reversed and all L-amino acids are replaced with D-amino acids.

Peptides may comprise amino acids in both L- and/or D-form. For example, both L- and D-forms may be used for different amino acids within the same peptide sequence. In some examples the amino acids within the peptide sequence are in L-form, such as natural amino acids. In some examples the amino acids within the peptide sequence are a combination of L- and D-form. Further, peptides may comprise unusual, but naturally occurring, amino acids including, but not limited to, hydroxyproline (Hyp), beta-alanine, citrulline (Cit), ornithine (Orn), norleucine (Nle), 3-nitrotyrosine, nitroarginine, pyroglutamic acid (Pyr). Peptides may also incorporate unnatural amino acids including, but not limited to, homo amino acids, N-methyl amino acids, alpha-methyl amino acids, beta (homo) amino acids, gamma amino acids, and N-substituted glycines. Peptides may be linear peptides or cyclic peptides.

The term "protein" shall be taken to include a single polypeptide chain, *i.e.*, a series of contiguous amino acids linked by peptide bonds or a series of polypeptide chains covalently or non-covalently linked to one another (*i.e.*, a polypeptide complex). For example, the series of polypeptide chains can be covalently linked using a suitable chemical bond or a disulfide bond. Examples of non-covalent bonds include hydrogen bonds, ionic bonds, Van der Waals forces, and hydrophobic interactions.

Percentage amino acid sequence identity with respect to a given amino acid sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical to the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Amino acid sequence identity may be determined using the EMBOSS Pairwise Alignment Algorithms tool available from The European Bioinformatics Institute (EMBL-EBI), which is part of the European Molecular Biology Laboratory. This tool is

accessible at the website located at www.ebi.ac.uk/Tools/emboss/align/. This tool utilizes the Needleman-Wunsch global alignment algorithm (Needleman and Wunsch, 1970). Default settings are utilized, which include Gap Open: 10.0 and Gap Extend 0.5. The default matrix "Blosom62" is utilized for amino acid sequences and the default matrix. Percent (%) or percentage "nucleic acid sequence identity" with respect to the nucleotide sequences disclosed herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are known in the art, for instance, using publicly available computer software such as BLAST or ALIGN. The skilled person can readily determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

The term "cell penetrating peptide" (CPP) refers to a peptide that is capable of crossing a cellular membrane. In one example, a CPP is capable of translocating across a mammalian cell membrane and entering into a cell. In another example, a CPP may direct a conjugate to a desired subcellular compartment. Thus, a CPP may direct or facilitate penetration of a molecule of interest across a phospholipid, mitochondrial, endosomal, lysosomal, vesicular, or nuclear membrane. A CPP may be translocated across the membrane with its amino acid sequence complete and intact, or alternatively partially degraded.

A CPP may direct a molecule of interest, such as an ASO disclosed herein, from outside a cell through the plasma membrane, and into the cytoplasm or a desired subcellular compartment. Alternatively, or in addition, a CPP may direct a molecule of interest across the blood-brain, trans-mucosal, hematoretinal, skin, gastrointestinal and/or pulmonary barriers.

The term "peptide ligand" or "receptor binding domain" refers to a peptide that is capable of binding to a membrane surface receptor to enable translocation of the peptide across a cellular membrane. In one example a peptide ligand may enable translocation across the cellular membrane via the natural endocytosis of the targeted receptor. In

- another example the peptide ligand may utilise a complementary mechanism of translocation across the cellular membrane including utilising a conjugated CPP. In one example, a peptide ligand is capable of translocating across a mammalian cell membrane and to enter a cell. In another example, a peptide ligand may direct a conjugate to a
- 5 desired subcellular compartment. Thus, a peptide ligand may direct or facilitate cellular uptake of a molecule of interest across a phospholipid, mitochondrial, endosomal, lysosomal, vesicular, or nuclear membrane. A peptide ligand may be translocated across the membrane with its amino acid sequence complete and intact, or alternatively partially degraded.
- 10 A peptide ligand via its binding to a target receptor may direct a molecule of interest, such as an ASO disclosed herein, from outside a cell through the plasma membrane, and into the cytoplasm or a desired subcellular compartment. Alternatively, or in addition, a peptide ligand via its binding to a target receptor may direct a molecule of interest across a relevant biological barrier, *e.g.*, the blood-brain, trans-mucosal,
- 15 hematoretinal, skin, gastrointestinal, and/or pulmonary barriers.

Compositions for Increasing SHANK3 Protein Levels

- Secondary structures and upstream open reading frames in the 5' UTR of *SHANK3* mRNA can reduce translational efficiency and transcript stability thereby
- 20 limiting protein production. In addition, the *SHANK3* 5' UTR includes 3 exons, exon 2 contains sequences that can affect translational efficiency, which ultimately affects the level of SHANK3 protein. Exclusion of *SHANK3* exon 2 during splicing of the the 5' PNCR shortens the resulting 5' UTR, removing elements that reduce translational efficiency. Further, microRNAs (miRNAs) typically bind to complimentary RNA
- 25 sequences in the 3' untranslated region (3' UTR) and regulate gene expression by stimulating either mRNA degradation or translational repression. Both classes of mechanisms lead to diminished expression of a gene. Despite such "inefficiencies," in a genetic background of two functional (wild type) alleles, the level of productive RNA transcripts and translation yield a sufficient level of functional protein for a given gene.
- 30 However, in the case of rare, monogenic diseases, the loss of one functional allele, *e.g.*, *SHANK3* allele, can result in haploinsufficiency and the associated disease.

While not wishing to be bound by theory, it is believed that ASOs targeting sequences within the 5' UTR of *SHANK3* mRNA can enhance translation, *e.g.*, by reducing/disrupting the formation of secondary structures that would otherwise reduce translational efficiency. ASOs targeting the 5' PNCr can enhance *SHANK3* transcript translational efficiency. Further, it is believed that an antisense sequence at least partly complementary to the binding sites for miRNAs located within the *SHANK3* mRNA 3' UTR will hybridize to the 3' UTR and sterically hinder ("mask") access of these miRNAs to their binding sites, thereby resulting in an increased level of *SHANK3* mRNA and ultimately allowing increased translation of SHANK3 protein.

Accordingly, disclosed herein is an ASO that binds within a targeted portion of the: (i) 5' UTR of a *SHANK3* mRNA; (ii) 5' PNCr of a *SHANK3* pre-mRNA; or (iii) 3' UTR of a *SHANK3* mRNA;

whereby binding of the antisense oligonucleotide within the targeted portion in a mammalian cell results in an increased level of SHANK3 protein in the mammalian cell.

For reference, the nucleotide sequence of the canonical human *SHANK3* pre-mRNA transcript ("*SHANK3-201*") is provided herein as **SEQ ID NO:4**. The nucleotide sequence of the 5' UTR of the canonical human *SHANK3* mRNA transcript is provided herein as **SEQ ID NO:1**. The nucleotide sequence of the 5' PNCr of the canonical *SHANK3* pre-mRNA is provided herein as **SEQ ID NO:3**. The nucleotide sequence of the 3' UTR of the canonical human *SHANK3* mRNA is provided herein as **SEQ ID NO:2** (Appendix).

Antisense Oligonucleotides (ASOs) and Antisense RNAs (ARs)

In some examples of the compositions and methods described herein, ASOs and ARs have a sequence that is completely or nearly completely complementary across its length to the target sequence. ASOs and ARs are designed so that they bind (hybridize) to a target RNA sequence (*e.g.*, a targeted portion of a mRNA transcript) and remain hybridized under physiological conditions. Selection of suitable sequences for ASOs and ARs generally avoids, where possible, similar nucleic acid sequences in other (*i.e.*, off-target) locations in the genome or in cellular mRNAs or miRNAs, such that the likelihood the ASO or AR will hybridize at such sites is limited. In some examples,

ASOs disclosed herein are useful for attenuating the formation of *SHANK3* mRNA secondary structures, particularly in the 5' UTR region that interfere with translation. In other examples, ASOs disclosed herein bind to a targeted region within the 5' PNCR of a *SHANK3* pre-mRNA, *e.g.*, within an intronic sequence or partly within an intronic sequence and partly within flanking exonic sequence. In other examples, ASOs disclosed herein mask access of miRNAs to their target binding sites in the *SHANK3* 3' UTR thereby reducing the level of miRNA-dependent *SHANK3* mRNA destabilization. Thus, the ASOs disclosed herein result in a net increase in the level of canonical *SHANK3* mRNA and consequently the level of functional SHANK3 protein.

10 In some examples, ASOs or ARs "specifically hybridize" to or are "specific" to a target nucleic acid or a targeted portion of a *SHANK3* mRNA 5' UTR or 3' UTR, or a *SHANK3* pre-mRNA 5' PNCR. At a given ionic strength and pH, the T_m is the temperature at which 50% of a target sequence hybridizes to a complementary oligonucleotide.

15 ASO and AR sequences are "complementary" to their target sequences when hybridization occurs in an antiparallel configuration between two single-stranded polynucleotides. Complementarity is quantifiable in terms of the proportion (*e.g.*, the percentage) of bases in opposing strands that are expected to form hydrogen bonds with each other, according to generally accepted base-pairing rules. The nucleotide sequence of an ASO or AR need not be 100% complementary to that of its target nucleic acid to hybridize. In certain examples, the nucleotide sequences of ASOs or ARs in the compositions disclosed herein can be at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence complementary to the nucleotide sequence of the targeted portion of an RNA transcript over the length of the ASO or AR nucleotide sequence. For example, an ASO or AR in which 18 of 20 nucleotides of ASO or AR sequence are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In such an example, the remaining non-complementary nucleotides of the ASO or AR could be clustered together or interspersed with complementary nucleotides and need not be contiguous. Complementarity of an ASO or AR sequence to a target nucleotide sequence (expressed

as “percent complementarity” to its target sequence; or “percent identity” to its reverse complement sequence) can be determined routinely using algorithms known in the art, as exemplified in the BLAST programs (basic local alignment search tools) and PowerBLAST programs (Altschul, et al., 1990, *J. Mol. Biol.*, 215:403-410; Zhang et al., 5 1997, *Genome Res.*, 7:649-656).

In some examples, an ASO or AR does not hybridize to all nucleotides in a target sequence and the nucleotide positions at which it does hybridize may be contiguous or noncontiguous. ASOs or ARs may hybridize over one or more segments of a *SHANK3* mRNA 5' UTR or 3' UTR; one or more segments of a *SHANK3* mRNA 5' PNCr, such 10 that intervening or adjacent segments are not involved in the hybridization event (*e.g.*, a loop structure or hairpin structure may be formed).

In some examples, the ASOs or ARs disclosed herein are complementary to a targeted portion of the canonical *SHANK3* mRNA 5' UTR sequence corresponding to **SEQ ID NO:1**. In other examples, the ASOs or ARs disclosed herein are complementary 15 to a targeted portion of the canonical *SHANK3* pre-mRNA 5' PNCr sequence corresponding to **SEQ ID NO:3**. In other examples, the ASOs or ARs disclosed herein are complementary to a targeted portion of the canonical *SHANK3* mRNA 3' UTR sequence corresponding to **SEQ ID NO:2**.

In some examples the nucleotide sequence of the ASO or the AR is at least 60%, 20 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion of the *SHANK3* mRNA over the length of the ASO or the AR. In some examples the nucleotide sequence of the ASO or the AR comprises a sequence that: (a) has at least about 40% identity to about 60% identity of the nucleotide sequence of an ASO or AR sequence disclosed herein, *e.g.*, 45% identity, 48% identity, 25 50% identity, 52% identity, 55% identity, 58% identity or another sequence identity from about 40% identity to about 60% identity to the entire length of the sequence of any ASO or AR disclosed herein; and (b) comprises a contiguous sequence of at least 8 bases to 16 bases that is 100% identical to a contiguous sequence of at least 8 to 16 bases in any one of the ASO or AR sequences disclosed herein, *e.g.*, 100% sequence-identical to a 30 contiguous 9 bases, 10 bases, 11 bases, 12 bases, 13 bases, 14 bases, 15 bases, or 16 bases of an ASO or AR sequence disclosed herein. The ASOs or ARs for use in the

compositions described herein may be of any length suitable for specific hybridization to a target sequence. In some examples, the nucleotide sequence of the ASOs or ARs consist of 8 to 50 nucleotides. For example, the ASO or AR sequence can be 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, or 50 nucleotides in length. In some examples, the nucleotide sequence of the ASOs or ARs consist of 8 to 50 nucleotides. For example, the ASO or AR sequence can be 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, or 50 nucleotides in length. In some examples, the ASOs consist of more than 50 nucleotides, but no more than 100 nucleotides in length. In some examples, the ASO or AR nucleotide sequence is from 8 to 50 nucleotides, 8 to 40 nucleotides, 8 to 35 nucleotides, 8 to 30 nucleotides, 8 to 25 nucleotides, 8 to 20 nucleotides, 8 to 15 nucleotides, 9 to 50 nucleotides, 9 to 40 nucleotides, 9 to 35 nucleotides, 9 to 30 nucleotides, 9 to 25 nucleotides, 9 to 20 nucleotides, 9 to 15 nucleotides, 10 to 50 nucleotides, 10 to 40 nucleotides, 10 to 35 nucleotides, 10 to 30 nucleotides, 10 to 25 nucleotides, 10 to 20 nucleotides, 10 to 15 nucleotides, 11 to 50 nucleotides, 11 to 40 nucleotides, 11 to 35 nucleotides, 11 to 30 nucleotides, 11 to 25 nucleotides, 11 to 20 nucleotides, 11 to 15 nucleotides, 12 to 50 nucleotides, 12 to 40 nucleotides, 12 to 35 nucleotides, 12 to 30 nucleotides, 12 to 25 nucleotides, 12 to 20 nucleotides, 12 to 15 nucleotides, 13 to 50 nucleotides, 13 to 40 nucleotides, 13 to 35 nucleotides, 13 to 30 nucleotides, 13 to 25 nucleotides, 13 to 20 nucleotides, 14 to 50 nucleotides, 14 to 40 nucleotides, 14 to 35 nucleotides, 14 to 30 nucleotides, 14 to 25 nucleotides, 14 to 20 nucleotides, 15 to 50 nucleotides, 15 to 40 nucleotides, 15 to 35 nucleotides, 15 to 30 nucleotides, 15 to 25 nucleotides, 15 to 20 nucleotides, 17 to 30 nucleotides, 17 to 25 nucleotides, 17 to 20 nucleotides, 20 to 50 nucleotides, 20 to 40 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 20 to 25 nucleotides, 25 to 50 nucleotides, 25 to 40 nucleotides, 25 to 35 nucleotides, or 25 to 30 nucleotides in length. In some examples, the ASOs or ARs are 17 nucleotides in length. In other examples, the ASOs or ARs are 20 nucleotides in length. In some examples, the nucleotide sequence of the ASO or AR nucleotide is 25 nucleotides in length.

In other examples the ASOs or ARs comprise at least 10 contiguous nucleotides of an ASO or AR sequence described herein. In some examples ASOs or ARs comprise

at least 10 contiguous nucleotides (subsequence) from each of two or more ASO or AR sequences described herein, where the two or more subsequences are not contiguous in a *SHANK3* mRNA sequence.

In some examples for each occurrence of “G” in an ASO or AR sequence disclosed herein, the “G” is guanosine or inosine. In some examples for each occurrence of “T” in an ASO or AR sequence disclosed herein, the “T” is any one of: thymidine, inosine, uracil, or an isomeric or modified form of uracil (e.g., pseudouridine or N1-methyl-pseudouridine). In some examples for each occurrence of “C” in an ASO or AR sequence disclosed herein, the C is cytosine or a modified form of cytosine (e.g., 5'-methyl cytosine).

In some examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:293, 299, 301, 302, 304-309, 311, 313, 315, 318, 606, 797, 1193, 1195, 1847, 1934-1937, 2858, 2874, 3510, 12644, 12666, 12669, 12671, 12688, or 12690. In some examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:5-622, 4175-4181, or 4184-4186. In some examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:5-188, 191-622, 4175-4181, or 4184-4186. In some examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:559, 606, or 4178-4181. In other examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:1935-4168, 4182, 4183, 12646-12654, or 12664-12671. In some examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:1935-1937, 2849, 2858, 2864, 2874, 3510, 12647, 12648, or 12664-12671. In other examples the nucleotide sequence of the ASO or AR comprises the sequence of any one of SEQ ID NOs:623-1934, 4169-4174, 12645, 12655-12663, or 12688. In some examples the nucleotide sequence of the ASO or AR comprises the sequence of SEQ ID NO:1934.

In some examples the nucleotide sequence of the ASO or AR consists of the nucleotide sequence of any one of SEQ ID NOs:5-4186, 12646-12654, or 12664-12671. Sequences for the foregoing SEQ ID NOs are provided in Tables 4 and 5 in the Appendix.

ASO Chemistry and Modifications

The ASOs used in the compositions described herein may comprise naturally-occurring nucleotides, nucleotide analogues, modified nucleotides, or any combination thereof. The term “naturally occurring nucleotides” includes deoxyribonucleotides and ribonucleotides. The term “modified nucleotides” includes nucleotides with modified or substituted sugar groups and/or having a modified backbone. In some examples, all the nucleotides of an ASO are modified nucleotides. Chemical modifications of ASOs or components of ASOs that are compatible with the compositions and methods described herein are known in the art as disclosed in, *e.g.*, in U.S. Patent No. 8,258,109, U.S. Patent No. 5,656,612, U.S. Patent Publication No. 2012/0190728, and Roberts et al., 2020, *Nature Rev. Drug Disc.*, 19:673-694.

One or more nucleotides of an ASO may be any naturally occurring, unmodified nucleobase such as adenine, guanine, cytosine, thymine, uracil and inosine, or any synthetic or modified nucleobase that is sufficiently similar to an unmodified nucleobase such that it is capable of hydrogen bonding with a nucleobase present on a target RNA transcript. Examples of suitable modified nucleobases include, but are not limited to, hypoxanthine, xanthine, 7-methylguanine, 5, 6-dihydrouracil, 5-methylcytosine, and 5-hydroxymethylcytosine.

ASOs include a “backbone” structure, that refers to the connection between nucleotides/monomers of the ASO. In naturally occurring oligonucleotides, the backbone comprises a 3’-5’ phosphodiester linkage connecting sugar moieties of adjacent nucleotides. Suitable types of backbone linkages for the ASOs described herein include, but are not limited to, phosphodiester, phosphorothioate, phosphorodithioate, phosphorodiamidate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate, phosphoramidate, and the like. In some examples, the backbone modification is a phosphorothioate linkage. In other examples, the backbone modification is a phosphorodiamidate linkage. *See, e.g.*, Roberts et al. *supra*; and Agrawal (2021), *Biomedicines*, 9:503. In some examples, the backbone structure of the ASO does not contain phosphorous-based linkages, but rather contains

peptide bonds, for example in a peptide nucleic acid (PNA), or linking groups including carbamate, amides, and linear and cyclic hydrocarbon groups.

In some examples, the stereochemistry at each of the phosphorus internucleotide linkages of the ASO backbone is random. In other examples, the stereochemistry at each of the phosphorus internucleotide linkages of the ASO backbone is controlled and is not random. For example, U.S. Pat. No. 9,605,019 describes methods for independently selecting the handedness of chirality at each phosphorous atom in an oligonucleotide. In some examples, an ASO used in the compositions and methods provided herein, including, but not limited to, the ASOs the sequences of which are disclosed herein as **SEQ ID NOs:5-39535** is an ASO having phosphodiester internucleotide linkages that are not random. In some examples, a composition or composition used in the methods disclosed herein comprises a pure diastereomeric ASO. In other examples, the composition comprises an ASO that has diastereomeric purity of at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, about 100%, about 90% to about 100%, about 91% to about 100%, about 92% to about 100%, about 93% to about 100%, about 94% to about 100%, about 95% to about 100%, about 96% to about 100%, about 97% to about 100%, about 98% to about 100%, or about 99% to about 100%.

In some examples, the ASO has a non-random mixture of Rp and Sp configurations at its phosphorus internucleotide linkages. In some examples, an ASO used in the compositions and methods disclosed herein, comprises about 5-100% Rp, at least about 5% Rp, at least about 10% Rp, at least about 15% Rp, at least about 20% Rp, at least about 25% Rp, at least about 30% Rp, at least about 35% Rp, at least about 40% Rp, at least about 45% Rp, at least about 50% Rp, at least about 55% Rp, at least about 60% Rp, at least about 65% Rp, at least about 70% Rp, at least about 75% Rp, at least about 80% Rp, at least about 85% Rp, at least about 90% Rp, or at least about 95% Rp, with the remainder Sp, or about 100% Rp.

In some examples, the ASOs described herein contain a sugar moiety that comprises ribose or deoxyribose, or a modified sugar moiety or sugar analog, including a morpholine ring. Suitable examples of modified sugar moieties include, but are not

limited to, 2' substitutions such as 2'-O-modifications, 2'-O-methyl (2'-O-Me), 2'-O-methoxyethyl (2'MOE), 2'-O-aminoethyl, 2'F, N3'->P5' phosphoramidate, 2'dimethylaminooxyethoxy, 2'dimethylaminoethoxyethoxy, 2'-guanidinidium, 2'-O-guanidinium ethyl, carbamate modified sugars, and bicyclic modified sugars. In some examples, the sugar moiety modification is selected from among 2'-O-Me, 2'F, and 2'MOE. In other examples, the sugar moiety modification is an extra bridge bond, such as in a locked nucleic acid (LNA). In some examples the sugar analog contains a morpholine ring, such as phosphorodiamidate morpholino (PMO). In some examples, the sugar moiety comprises a ribofuransyl or 2'deoxyribofuransyl modification. In some examples, the sugar moiety comprises 2'4'-constrained 2'-O-methoxyethyl (cMOE) modifications. In some examples, the sugar moiety comprises cEt 2', 4' constrained 2'-O ethyl BNA modifications. In other examples, the sugar moiety comprises tricycloDNA (tcDNA) modifications. In some examples, the sugar moiety comprises ethylene nucleic acid (ENA) modifications. In some examples, the sugar moiety comprises 2'-O-(2-N-methylcarbamoyl ethyl) (MCE). Modifications are known in the art as exemplified in Jarver, et al., 2014, *Nucleic Acid Therapeutics*, 24(1): 37-47.

In some examples, each constituent nucleotide of the ASO is modified in the same way, *e.g.*, every linkage of the backbone of the ASO comprises a phosphorothioate linkage, or each ribose sugar moiety comprises a 2'-O-methyl modification. In other examples, a combination of different modifications is used, *e.g.*, an ASO comprising a combination of phosphorodiamidate linkages and sugar moieties comprising morpholine rings (morpholinos).

In some examples, the ASO comprises one or more backbone modifications. In some examples, the ASO comprises one or more sugar moiety modification. In some examples, the ASO comprises one or more backbone modifications and one or more sugar moiety modifications. In some examples, the ASO comprises a 2'MOE modification and a phosphorothioate backbone. In some examples, the ASO comprises a peptide nucleic acid (PNA).

In some preferred examples, the ASO comprises a phosphorodiamidate morpholino (PMO).

The skilled person in the art will appreciate that ASOs may be modified in order to achieve desired properties or activities of the ASO or reduce undesired properties or activities of the ASO. In some examples, an ASO is modified to alter one or more properties. For example, such modifications can: enhance binding affinity to a target
5 sequence on a pre-mRNA transcript; reduce binding to any non-target sequence; reduce degradation by cellular nucleases (*e.g.*, RNase H); improve uptake of an ASO into a cell and/or particular subcellular compartments; alter the pharmacokinetics or pharmacodynamics of the ASO; and/or modulate the half-life of the ASO *in vivo*.

In some examples, the ASOs comprise one or more 2'-*O*-(2-methoxyethyl)
10 (MOE) phosphorothioate-modified nucleotides, which have been shown to confer significantly enhanced resistance of ASOs to nuclease degradation and increased bioavailability.

Methods for synthesis and chemical modification of ASOs, as well as synthesis of ASO conjugates is well known in the art, and such ASOs are available commercially.

15 In some examples, a composition (*e.g.*, a pharmaceutical composition) provided here includes two or more ASOs with different chemistries but complementary to the same targeted portion of the *SHANK3* mRNA 5' UTR or 3' UTR, or the *SHANK3* pre-mRNA 5' PNCr. In other examples, a composition comprises two or more ASOs that are complementary to different targeted portions of the 5' UTR, 3' UTR, or 5'
20 PNCr.

In some examples, the compositions disclosed herein include ASOs that are linked to a functional moiety. In some examples, the functional moiety is a delivery moiety, a targeting moiety, a detection moiety, a stabilizing moiety, or a therapeutic moiety. In some examples the functional moiety includes a delivery moiety or a targeting moiety.
25 In some examples the functional moiety includes a stabilizing moiety. In some preferred examples the functional moiety is a delivery moiety.

Suitable delivery moieties include, but are not limited to, lipids, polyethers, peptides, carbohydrates, glycans, receptor binding domains (RBDs), and antibodies.

In some examples, the delivery moiety includes a cell-penetrating peptide (CPP).
30 Suitable examples of CPPs are described in, *e.g.*, PCT/AU2020/051397. In some examples the amino acid sequence of the CPP comprises or consists of:

RRSRTARAGRPGRNSSRPSAPR (SEQ ID NO:12694). In other examples, the delivery moiety includes a RBD.

In other examples, the delivery moiety includes a carbohydrate. In some examples, a carbohydrate delivery moiety is selected from among N-acetylgalactosamine (GalNAc), N-Ac-Glucosamine (GluNAc), glycan, and a mannose. In one example, the carbohydrate delivery moiety comprises GalNAc or a glycan moiety.

In other examples, the delivery moiety includes a lipid. Examples of suitable lipids as delivery moieties include, but are not limited to, cholesterol moiety, a cholesteryl moiety, and aliphatic lipids. In some examples the delivery moiety includes a fatty acid or lipid moiety. In some embodiments the fatty acid chain length is about C8 to C20. Examples of suitable fatty acid moieties and their conjugation to oligonucleotides are found in, *e.g.*, International Patent Publication WO 2019232255 and in Prakash et al., (2019).

In further examples, the delivery moiety includes an antibody, as described in, *e.g.*, Dugal-Tessier et al., (2021).

Suitable examples of stabilizing moieties include, but are not limited to, polyethylene glycol (PEG), poly(oligo(ethylene glycol) methyl ether methacrylate) (POEGMA), and Poly(2-oxazoline)s (POx).

In some examples, where an ASO is linked to a functional moiety, the functional moiety is covalently linked to the ASO. In other examples, the functional moiety is non-covalently linked to the ASO.

Functional moieties can be linked to one or more of any nucleotides in an ASO at any of several positions on the sugar, base or phosphate group, as understood in the art and described in the literature, *e.g.*, using a linker. Linkers can include a bivalent or trivalent branched linker. In some examples, the functional moiety is linked to the 5' end of the ASO. In other examples, the functional moiety is linked to the 3' end of the ASO.

In some examples compositions comprising any of the ASOs disclosed herein also include a delivery nanocarrier complexed with ASO. In some examples, a delivery nanocarrier is selected from among lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures. In other examples the delivery nanocarrier

includes a lipid nanoparticle encapsulating the ASO. Various delivery ASO-nanocarrier complex formats are known in the art, as reviewed in, *e.g.*, Roberts et al., *supra*.

Vectors for Expression of SHANK3 Antisense RNA (AR)

5 In some examples provided herein is a vector for expression, in a mammalian neuron or other cell type, of an antisense RNA (AR) that binds within a targeted portion of the: (i) 5' UTR of a *SHANK3* mRNA; (ii) 5' PNCR of a *SHANK3* pre-mRNA; or (iii) 3' UTR of a *SHANK3* mRNA; whereby binding of the AR within the targeted portion in a mammalian cell results in an increased level of SHANK3 protein in the mammalian
10 cell.

In some examples, the promoter used in the expression vector is a neuron type-selective promoter for driving expression of the AR in the mammalian cell. In some examples, the neuronal cell type-selective promoter is selective for expression in neurons selected from the list consisting of: cortical glutamatergic neurons, cortical GABAergic
15 neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons.

In some the promoter is an inducible promoter, *e.g.*, inducible by a ligand-regulated transactivator such as the tet-inducible rtTA, which allows titration of AR transcription in a target mammalian cell. In some examples, the promoter driving AR expression is a U6 or other Pol III promoter, which is particularly suitable for
20 transcription of short RNA sequences such AR sequences disclosed herein. In some examples, an expression vector utilizes hybrid promoter systems, *e.g.*, a Tet-O-regulated U6 promoter system as described in Lin et al. (2004), *FEBS Letters*, 577 (2004) 376–380. In some examples, where both cell type-specificity and inducibility of an AR expression vector are desired, a two-part expression system is used in which expression
25 of a ligand-regulated transactivator is driven by a cell type-selective promoter and expression of an AR disclosed herein is driven by a promoter regulated by the ligand-regulated transactivator.

In some examples, the expression vectors used in the compositions disclosed herein are non-viral expression vectors, *e.g.*, plasmid vectors, minicircle DNA vectors,
30 linear amplicon expression cassettes, and the like.

In some examples, composition containing a non-viral expression virus further comprises a transfection agent. Exemplary transfection agents for transfection include, but are not limited to, jet-PEI® (available from Polyplus-transfection® SA, Strasbourg, France); TurboFect in vivo Transfection Reagent (ThermoFisher), and cationic derivatives of polyisoprenoid alcohols (PTAI) as described in, *e.g.*, Rak et al., (2016).

In other examples, the expression vectors to be used are viral vectors, *i.e.*, non-replicative recombinant viruses suitable for expression of an AR disclosed herein.

Preferably, the recombinant virus for expression of the *SHANK3* AR is a DNA virus. Suitable types of DNA viruses include adeno-associated virus (AAV), adenovirus, lentivirus, herpes simplex virus (HSV), and anelloviruses. Methods for design, production, and use of such types of recombinant DNA viruses are established in the art, as exemplified in Fukazawa et al., (2010), *International J of Mol. Med*, 25(1), 3-10, and in "Gene Therapy Protocols" for adenovirus; "Adeno- Associated Virus: Methods and Protocols" for AAV; Cody et al (2013), *Journal of Genetic Syndromes & Gene Therapy*, 4(1), 126, and "*Herpes Simplex Virus: Methods and Protocols*" for HSV; "*Gene Therapy Protocols Vol. 1: Production and In Vivo Applications of Gene Transfer Vectors*"; and Merten et al. (2016), *Molecular Therapy – Methods & Clinical Development*, 3, 16017, and Emeagi et al. (2013), *Current Molecular Medicine* 13(4), 602-625 for lentivirus. In some preferred examples, the viral vector is a recombinant AAV.

Genetically Modified Cells

Also provided herein are genetically modified cells. In some examples the genetically modified cells are genetically modified bacterial cells (*e.g.*, recombinant *E. coli*, for amplifying an AR expression vector disclosed herein). In other examples the genetically modified cells are genetically modified mammalian cells that have been transfected with any of the ASOs or non-viral AR expression vectors; or transduced with any of the viral AR expression vectors disclosed herein. In some examples, the genetically modified mammalian cells are *ex vivo*, *e.g.*, as a cultured cell population. In other examples, the genetically modified mammalian cells are *in vivo*, *e.g.*, in a mouse. In some examples, the genetically modified mammalian cells are human cells.

In some examples the genetically modified mammalian cells are neurons or neural progenitors. Suitable examples of neurons include, but are not limited to, cortical glutamatergic neurons, cortical GABAergic neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons. In some examples such primary cell types can be obtained by differentiation of a human pluripotent stem cell line, *e.g.*, an hiPSC line or a human embryonic stem cell (hESC) line. Methods for obtaining a variety of different neuronal cell types is known in the art, as reviewed in, *e.g.*, Alia *et al.*, (2019), Fitzgerald *et al.*, (2020) and Kim *et al.* (2014). In other examples, the genetically modified mammalian cells are derived from a cell line. In some examples the cell line is pluripotent stem cell line (*e.g.*, hiPSCs or hESCs) or a neuronal cell line. Suitable neuronal or neuronal stem cell lines include, but are not limited to, SH-SY5Y, NTERA, CTX0E16, ReNcell VM, ReNcell Cx. In some preferred examples, the genetically modified mammalian cells express SHANK3 endogenously.

The genetically modified cells disclosed herein can be genetically modified by any of a number of methods and strategies known in the art, *e.g.*, transient transfection, stable transfection, and viral transduction. In some examples transfection with ASOs or non-viral vectors is carried out by nucleofection. In other examples transfection of cells is by lipofection.

20 *Pharmaceutical Compositions*

Also provided herein are pharmaceutical compositions comprising any of the foregoing ASOs, non-viral expression vectors, and viral expression vectors disclosed herein, and formulated with at least a pharmaceutically acceptable excipient, including a carrier, filler, preservative, adjuvant, solubilizer and/or diluent.

25 Pharmaceutical compositions containing any of the ASOs or expression vector compositions described herein, for use in the methods disclosed herein, can be prepared according to conventional techniques well known in the pharmaceutical industry and described in the published literature. In some examples, a pharmaceutical composition for treating a subject comprises a therapeutically effective amount of any ASO or
30 expression vector disclosed herein.

Pharmaceutically acceptable salts are suitable for use in contact with the tissues of humans and lower animals without undue toxicity, irritation, allergic response, *etc.*, and are commensurate with a reasonable benefit/risk ratio. Examples of pharmaceutically acceptable, nontoxic acid addition salts are salts of an amino group
5 formed with inorganic acids such as hydrochloric acid, hydrobromic acid, phosphoric acid, sulfuric acid and perchloric acid or with organic acids such as acetic acid, oxalic acid, maleic acid, tartaric acid, citric acid, succinic acid or malonic acid. Other pharmaceutically acceptable salts include adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate,
10 citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, formate, fumarate, glucoheptonate, glycerophosphate, gluconate, hemisulfate, heptanoate, hexanoate, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-
15 phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, p-toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like. Further pharmaceutically acceptable salts include, when appropriate, nontoxic ammonium, quaternary ammonium, and amine cations
20 formed using counterions such as halide, hydroxide, carboxylate, sulfate, phosphate, nitrate, lower alkyl sulfonate and aryl sulfonate.

In some examples, pharmaceutical compositions are formulated into any of a number of possible dosage routes or forms including, but not limited to, intravenous administration, intrathecal administration, intramuscular administration, tablets, capsules, gel
25 capsules, liquid syrups, and soft gels. In some examples, the compositions are formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers. In some examples, a pharmaceutical
30 formulation disclosed herein is provided in a form including, but not limited to, a

solution, emulsion, microemulsion, foam or liposome-containing formulation (*e.g.*, cationic or noncationic liposomes).

In some examples, pharmaceutical formulations comprising any of the ASOs or expression vectors described herein may comprise one or more penetration enhancers, carriers, excipients or other active or inactive ingredients as appropriate and known to the skilled person. In some examples, where a pharmaceutical composition includes liposomes, such liposomes can also include sterically stabilized liposomes, *e.g.*, liposomes comprising one or more specialized lipids. These specialized lipids result in liposomes with enhanced circulation lifetimes. In some examples, a sterically stabilized liposome comprises one or more glycolipids or is derivatized with one or more hydrophilic polymers, such as PEG moiety. In some examples, a surfactant is included in the pharmaceutical formulation.

In some examples, a pharmaceutical composition also includes a penetration enhancer to enhance the delivery of ASOs or non-viral expression vectors, *e.g.*, to aid diffusion across cell membranes and /or enhance the permeability of a lipophilic drug. In some examples, the penetration enhancers include a surfactant, a fatty acid, a bile salt, or a chelating agent.

In some examples, where administration is via a systemic route, *e.g.*, intravenous, the method also includes a step to facilitate transfer of any of the ASOs or vectors described herein across the blood brain barrier (BBB) into the CNS, and especially into the brain. In some examples the BBB is transiently disrupted, *e.g.*, by administration of one or more antibodies that disrupt Netrin-1 binding to Unc5B as described in Boyé et al., (2022).

In some examples, a pharmaceutical composition comprises a dose of ASOs or non-viral vectors ranging from about 0.01 mg/kg to 20 mg/kg, *e.g.*, 0.05 mg/kg, 0.1 mg/kg, 0.2 mg/kg, 0.5 mg/kg, 1 mg/kg, 3 mg/kg, 5 mg/kg, 8 mg/kg, 10 mg/kg, 15 mg/kg, or another dose ranging from about 0.01 mg/kg to 20 mg/kg. In some examples, where an ASO disclosed herein is to be administered directly into the CNS or brain, *e.g.*, by intracerebroventricular administration, the total dose ranges from about 50 mg to about 500 mg, *e.g.*, 60 mg, 70 mg, 80 mg, 100 mg, 120 mg, 150 mg, 180 mg, 200 mg, 220 mg, 250 mg, 270 mg, 290 mg, 300 mg, 350 mg, 400 mg, 450 mg, or another dose

from about 50 mg to about 500 mg. This dose range corresponds to approximately 0.050 mg/cm³ of brain volume to about 0.42 mg/cm³ of brain volume assuming an average human brain volume of about 1200 cm³.

5 In some examples, a pharmaceutical composition comprises multiple ASOs or AR expression vectors. In some examples, a pharmaceutical composition comprises, in addition to ASOs or AR expression vectors, another drug or therapeutic agent suitable for treatment of a subject suffering from *SHANK3* haploinsufficiency.

Methods

10 As described herein, a number of conditions (*e.g.*, Phelan-McDermid syndrome) are associated with insufficient levels of functional *SHANK3*. Accordingly, the methods described herein include a method for preventing or treating a condition associated with *SHANK3* haploinsufficiency by administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising any of the ASOs or expression
15 vectors disclosed herein. Likewise, in some examples, any of the ASOs or AR expression vectors disclosed herein are used in the manufacture of a medicament for treating a condition associated with *SHANK3* haploinsufficiency. In some examples the condition associated with *SHANK3* haploinsufficiency to be prevented or treated by the methods or with the compositions disclosed herein is Phelan-McDermid syndrome, an
20 autism spectrum disorder, schizophrenia, or an intellectual disability. In some preferred examples, the condition is Phelan-McDermid syndrome.

Also provided herein is a method for increasing the amount of functional *SHANK3* protein in a mammalian cell expressing *SHANK3* mRNA, the method comprising contacting the cell with any of the ASOs or expression vectors disclosed
25 herein.

In some examples, administration to a subject or contact with cells *in vitro* or *ex vivo* with any of the ASOs, AR expression vectors, or pharmaceutical compositions disclosed herein increases the level of *SHANK3* protein about 1.1 to about 5 fold in cells (*e.g.*, neurons) *in vitro* or *ex vivo*, *e.g.*, 1.2 fold, 1.3 fold, 1.5 fold, 1.7 fold, 2 fold, 2.2
30 fold, 2.5 fold, 2.7 fold, 3 fold, 3.3 fold, 3.5 fold, 4 fold, 4.3 fold, 4.5 fold, 4.7 fold, or

another increase in SHANK3 protein levels from about 1.1 fold to about 5 fold in cells in a subject or *in vitro* or *in vivo*.

Suitable routes of administration for treatment with the compositions, pharmaceutical compositions, or medicaments disclosed herein include, but are not limited to, intravenous, intra-arterial, intraparenchymal, intracerebroventricular, intracisterna magna, intrathecal, intravenous, intra-arterial, subcutaneous, and topical.

As the skilled person will understand, the treatment methods disclosed herein include administration of the compositions and pharmaceutical compositions disclosed herein in a therapeutically effective amount to a subject (*e.g.*, a human subject). The terms "effective amount" or "therapeutically effective amount," as used herein, refer to a sufficient amount of a disclosed ASO, non-viral or viral expression vector being administered to relieve to some extent one or more of the symptoms and/or clinical indicia associated with SHANK3 haploinsufficiency in a particular disease or health condition. In some examples, an "effective amount" for therapeutic uses is the amount of one of the foregoing agents required to provide a clinically significant decrease in disease symptoms to prevent disease symptoms without undue adverse side effects. Examples of suitable symptoms to be reduced by the treatment methods provided herein included, but are not limited to, seizures, anxiety, repetitive behaviors, learning and memory deficits, and impaired sociability. An appropriate "effective amount" in any individual case may be determined using techniques, such as a dose escalation study. The term "therapeutically effective amount" includes, for example, a prophylactically effective amount. It is understood that "an effective amount" or "a therapeutically effective amount" can vary from subject to subject, due to variation in metabolism of the compound of any age, weight, general condition of the subject, the condition being treated, the severity of the condition being treated, and the judgment of the prescribing physician. By way of example only, therapeutically effective amounts may be determined by routine experimentation, including but not limited to a dose escalation clinical trial. Where more than one therapeutic agent is used in combination, a "therapeutically effective amount" of each therapeutic agent can refer to an amount of the therapeutic agent that would be therapeutically effective when used on its own, or

may refer to a reduced amount that is therapeutically effective by virtue of its combination with one or more additional therapeutic agents.

Combination Treatments

- 5 The pharmaceutical compositions comprising any of the ASOs or AR expression vectors, disclosed herein, can also be used in combination with other agents of therapeutic value in the treatment of a condition associated with SHANK3 haploinsufficiency. In general, other agents do not necessarily have to be administered in the same pharmaceutical composition, and may, because of different physical and chemical characteristics,
- 10 preferably be administered by different routes. The determination of the mode of administration and the advisability of administration, where possible, in the same pharmaceutical composition, is well within the knowledge of the skilled clinician. The initial administration can be made according to established protocols known in the art, and then, based upon the observed effects, the dosage, modes of administration and times
- 15 of administration can be modified by the skilled clinician.

Compositions and pharmaceutical compositions comprising ASOs and/or expression vectors, and an additional therapeutic agent may be administered concurrently (*e.g.*, simultaneously, essentially simultaneously or within the same treatment protocol) or sequentially, depending upon the stage and progression of the SHANK3

20 haploinsufficiency-associated condition to be treated, the condition of the patient, and the choice of specific therapeutic agents used. The determination of the order of administration, and the number of repetitions of administration of each therapeutic agent during a treatment protocol, is well within the knowledge of the skilled physician after evaluation of the disease being treated and the condition of the patient.

- 25 It is known to those of skill in the art that therapeutically-effective dosages can vary when the drugs are used in treatment combinations. Methods for experimentally determining therapeutically-effective dosages of drugs and other agents for use in combination treatment regimens are described in the literature. For example, the use of metronomic dosing, *i.e.*, providing more frequent, lower doses in order to minimize toxic
- 30 side effects, has been described extensively in the literature. Combination treatment

further includes periodic treatments that start and stop at various times to assist with the clinical management of the patient.

For combination therapies, dosages of co-administered therapeutic agents will of course vary depending on the type of co-agents employed, ASO or expression vector, and the disease stage of the patient to be treated.

Pharmaceutical compositions comprising ASOs, ARs, or expression vectors, and an additional therapeutic agent that make up a combination therapy disclosed herein may be a combined dosage form or in separate dosage forms intended for substantially simultaneous administration. The pharmaceutical compositions that make up the combination therapy may also be administered sequentially, with either therapeutic agent being administered by a regimen calling for two-step administration. The two-step administration regimen may call for sequential administration of the active agents or spaced-apart administration of the separate active agents. The time period between the multiple administration steps may range from, a few minutes to several hours, depending upon the properties of each pharmaceutical agent, such as potency, solubility, bioavailability, plasma half-life and kinetic profile of the pharmaceutical agent. Circadian variation of various physiological parameters may also be evaluated to determine the optimal dose interval.

Examples of suitable therapeutic agents for co-administration with a composition or a pharmaceutical composition disclosed herein include, but are not limited to, Growth Hormone, Insulin-Like Growth Factor-1, Risperidone, Lumateperone, sodium valproate, lithium, and D-serine.

EXAMPLES

Example 1: Identification of *SHANK3* Target Sequences

Identification of annotated and expressed transcripts that could generate the canonical transcript of the *SHANK3* gene was performed by the sequence alignment of all *SHANK3* protein-coding and NMD transcripts described in Gencode v38. An ASO sequence “micro-walk” of 25-mers and 17mers in 3-base increments was performed across the 5' PNCr of the *SHANK3* canonical pre-RNA transcript and across the 5' UTR and 3' UTR of the *SHANK3* canonical mRNA transcript (ENST00000262795.6). The resulting ASO sequences correspond to **SEQ ID NOs:5-4186, 12646-12671, and 12688**, which are provided in **Table 4** (Appendix).

Example 2: Measurement of SHANK3 Protein Upregulation by PMOs targeting of *SHANK3* mRNA 5' UTR or 3' UTR in a neuronal cell line

A subset of the above-identified ASO sequences were synthesized as phosphorodiamidate morpholino oligonucleotides (PMOs 4-37) targeting the canonical *SHANK3* mRNA 5' UTR, 5' PNCr, and 3' UTR regions. The PMOs, corresponding SEQ ID NOs, and target regions are shown in Table 1 below. The antisense PMOs were electroporated into SH-SY5Y neuronal cell line cultures using the NEON[®] electroporation system (ThermoFisher) at concentrations of 25 μ M and 50 μ M and incubated for 96 hours. At this time, total protein was extracted using 15% SDS complete lysis reagent and the levels of SHANK3 protein assessed by western blot using a mouse anti-SHANK3 monoclonal antibody (Merck, Cat. No. SAB520004) at a dilution of 1:1000 in 5% BSA in TBST buffer followed by goat anti-mouse IgG H&L antibody (Abcam, Cat. number ab216776). Expression levels of the SHANK3 protein were compared to no PMO-transfected cells (untreated), control treated with transfection conditions and scrambled/ non-targeting control sequences. The average signal from SHANK3 following imaging analysis was normalized to the average signal of total protein and ‘housekeeper gene’ proteins (e.g., vinculin, beclin, SRSF4).

Table 1 – Exemplary PMOs Tested for Ability to Increase SHANK3 Protein Levels		
PMO	SEQ ID NO	<i>SHANK3</i> Region (mRNA or pre-mRNA)
PMO4	4169	3'UTR
PMO5	4170	3'UTR
PMO6	1934	3'UTR
PMO7	4171	3'UTR
PMO8	4172	3'UTR
PMO9	4173	3'UTR
PMO10	4174	3'UTR
PMO19	4184	5'UTR
PMO20	4185	5'UTR
PMO21	4186	5'UTR
PMO22	4175	5'UTR
PMO23	559	5'UTR
PMO24	4176	5'UTR
PMO25	4177	5'UTR
PMO26	598	5'UTR
PMO27	4178	5'UTR
PMO28	4179	5'UTR
PMO29	4180	5'UTR
PMO30	4181	5'UTR
PMO31	4182	PNCR
PMO32	4183	PNCR
PMO33	606	5'UTR
PMO34	1935	PNCR
PMO35	1936	PNCR
PMO36	2849	PNCR
PMO37	1937	PNCR
PMO40	1847	3'UTR
PMO41	12662	3'UTR
PMO42	12661	3'UTR
PMO43	12688	3'UTR
PMO44	1852	3'UTR
PMO45	12663	3'UTR
PMO63	12664	PNCR

PMO64	12665	PNCr
PMO65	2858	PNCr
PMO66	12666	PNCr
PMO67	12667	PNCr
PMO68	2864	PNCr
PMO69	12668	PNCr
PMO70	2874	PNCr
PMO71	12669	PNCr
PMO72	12670	PNCr
PMO73	12671	PNCr

As shown in Figs. 1, 4, and 5 some of the tested PMOs induced increased SHANK3 protein levels relative to controls and other PMOs failed to induce any change in SHANK3 protein levels. As shown in Fig. 2 and 6, a subset of the PMOs increased SHANK3 protein levels from about 50% higher than controls to greater than four fold.

Example 3: Measurement of SHANK3 Protein Upregulation by MOE oligonucleotides targeting *SHANK3* mRNA 5' UTR or 3' UTR in a neuronal cell line

A subset of the above-identified ASO sequences were synthesized as 2'-O-(2-methoxyethyl) (MOE)-modified oligonucleotides, which also contained a fully phosphorothioated backbone ("MOEs" 1-6, 13-60) targeting the canonical *SHANK3* mRNA 5' UTR, 5' PNCr, and 3' UTR regions. The numbered MOEs, corresponding SEQ ID NOs, and target regions are shown in Table 2 below. The antisense MOEs were electroporated into SH-SY5Y neuronal cell line cultures using the NEON[®] electroporation system (ThermoFisher) at concentrations of 2.5 μ M and 5.0 μ M and incubated for 96 hours. At this time, total protein was extracted using 15% SDS complete lysis reagent and the levels of SHANK3 protein assessed by western blot using a mouse anti-SHANK3 monoclonal antibody (Merck, Cat. No. SAB520004) at a dilution of 1:1000 in 5% BSA in TBST buffer followed by goat anti-mouse IgG H&L antibody (Abcam, Cat. number ab216776). Expression levels of the SHANK3 protein were compared to no MOE-transfected cells (untreated), control treated with transfection conditions and scrambled/ non-targeting control sequences. The average signal from

SHANK3 following imaging analysis was normalized to the average signal of total protein and ‘housekeeper gene’ proteins (*e.g.*, vinculin, beclin, SRSF4)

Table 2 – Exemplary MOEs Tested for Ability to Increase SHANK3 Protein Levels		
MOE	SEQ ID NO	<i>SHANK3</i> Region (mRNA or pre-mRNA)
MOE1	1191	3'UTR
MOE2	12645	3'UTR
MOE3	12646	PNCr
MOE4	12647	PNCr
MOE5	3510	PNCr
MOE6	12648	PNCr
MOE13	12649	PNCr
MOE14	12650	PNCr
MOE15/34	300	5'UTR
MOE16	12651	PNCr
MOE17/32	298	PNCr
MOE18	12652	PNCr
MOE19	12653	PNCr
MOE20	12654	PNCr
MOE21	12655	3'UTR
MOE22	12656	3'UTR
MOE23	12657	3'UTR
MOE24	12658	3'UTR
MOE25	12659	3'UTR
MOE26	12660	3'UTR
MOE27	293	5'UTR
MOE28	294	5'UTR
MOE29	295	5'UTR
MOE30	296	5'UTR
MOE31	297	5'UTR
MOE33	299	5'UTR
MOE35	301	5'UTR
MOE36	302	5'UTR
MOE37	303	5'UTR

MOE38	304	5'UTR
MOE39	305	5'UTR
MOE40	306	5'UTR
MOE41	307	5'UTR
MOE42	308	5'UTR
MOE43	309	5'UTR
MOE44	310	5'UTR
MOE45	311	5'UTR
MOE46	312	5'UTR
MOE47	313	5'UTR
MOE48	314	5'UTR
MOE49	315	5'UTR
MOE50	316	5'UTR
MOE51	317	5'UTR
MOE52	318	5'UTR
MOE53	1190	3'UTR
MOE54	1192	3'UTR
MOE55	1193	3'UTR
MOE56	1194	3'UTR
MOE57	1195	3'UTR
MOE58	795	3'UTR
MOE59	796	3'UTR
MOE60	797	3'UTR

As shown in Figs. 10, 11, and 12 some of the tested MOEs induced increased SHANK3 protein levels relative to controls and other MOEs failed to induce any change in SHANK3 protein levels. As shown in Fig. 13, a subset of the MOEs increased

5 SHANK3 protein levels from about 50% higher than controls to greater than four fold.

Example 4: Identification of *SHANK3* Target Intron/Exon Sequences

Identification of annotated and expressed transcripts that could generate the canonical transcript of the *SHANK3* gene was performed by the sequence alignment of all *SHANK3* protein-coding and NMD transcripts described in Gencode v38. An ASO sequence “micro-walk” of 25-mers in 5 bp increments of distance was performed over the sequences of intron 7, 17, 21, and exon 21 of the ENST00000262795.6 pre-mRNA transcript and designed to target the intronic splice enhancer motif to mediate exclusion of the retained intron or part thereof and generate productive *SHANK3* mRNA transcript. The resulting ASO sequences correspond to **SEQ ID NOs:4187-12644**.

Example 5: Measurement of SHANK3 Protein Upregulation by PMOs targeting of *SHANK3* pre-mRNA in a neuronal cell line

The above-identified ASO sequences 25 nucleotides in length are synthesized as phosphorodiamidate morpholino oligonucleotides (PMOs). Antisense PMOs targeting intron 7, 18, or 21 (as described in Example 1) are electroporated into the naive SH-SY5Y neuronal cell line cultures using the NEON® electroporation system (ThermoFisher) at concentrations of 25 μ M and 50 μ M and incubated for 96 hours. At this time, total protein is extracted using 15% SDS complete lysis reagent and the levels of SHANK3 protein assessed by western blot using a mouse anti-SHANK3 monoclonal antibody (Merck, Cat. No. SAB520004) at a dilution of 1:1000 in 5% BSA in TBST buffer followed by goat anti-mouse IgG H&L antibody (Abcam, Cat. number ab216776). Expression levels of the SHANK3 protein are compared to no-PMO transfected cells (UT).

Table 3 – Exemplary PMOs Inducing Increased SHANK3 Protein Levels		
PMO	SEQ ID NO	<i>SHANK3</i> Region (mRNA or pre-mRNA)
PMO1	12634	RI21
PMO2	12635	RI21
PMO3	12636	RI21
PMO11	12637	RI7
PMO12	12638	RI7
PMO13	4204	RI7
PMO14	12642	RI17
PMO15	12643	RI17
PMO16	4969	RI17
PMO17	12644	RI17
PMO18	12639	RI21
PMO38	12640	RI21
PMO39	12641	RI21
PMO46	12672	RI17
PMO47	12673	RI17
PMO48	12674	RI17
PMO49	12683	RI17
PMO50	12692	RI17
PMO51	12689	RI17
PMO52	12693	RI17
PMO53	12690	RI17
PMO54	12691	RI17
PMO55	12675	RI17
PMO56	12676	RI17
PMO57	4974	RI17
PMO58	12677	RI17
PMO59	12684	RI17
PMO60	12685	RI17
PMO61	12686	RI17
PMO62	12687	RI17

PMO74	12678	RI21
PMO75	12679	RI21
PMO76	12680	RI21
PMO77	12681	RI21
PMO78	12057	RI21
PMO79	12682	RI21

As shown in Figs. 7 and 8 some of the tested PMOs induced increased SHANK3 protein levels relative to controls and other PMOs failed to induce any change in SHANK3 protein levels.

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It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific examples without departing from the spirit or scope of the invention as broadly described. The present examples are, therefore, to be considered in all respects as illustrative and not restrictive.

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All publications cited herein are hereby incorporated by reference in their entirety. Where reference is made to a URL or other such identifier or address, it is understood that such identifiers can change and particular information on the internet can come and go, but equivalent information can be found by searching the internet. Reference thereto evidences the availability and public dissemination of such information.

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Any discussion of documents, acts, materials, devices, articles or the like that have been included in the present specification is solely for the purpose of providing a context for the present invention. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present invention as it existed before the priority date of each claim of this application.

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References

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Appendix: Sequences and SEQ ID NOs**SEQ ID NO:1**

- 5 *SHANK3* mRNA Canonical Transcript 5' UTR Sequence (*SHANK3*-201
ENST00000262795.7)

CACCACTCAGGCCAGGCCAGTGGCCTTGGGAGGGGCCTGTGATGCTGGGACCACAGTTCCTGG
GCAGGGAGCAACCGTCTAGGCGTGGGGAGAACGCAGGACGTGACCCACACACCGCACTGGAGG
10 CTCCGCTCTGCCGGCTCCGGGACCCCTTCTCCGCCGACCCGCCCCGGTGGTCCGCGGATG
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GCGGCCGACGGGGCTCCGGCGGGGGGGAAGGGGGGGCCGGGGCGCCGCGCGCGGAGTCCCCGG
15 GCGCTCCGTTCGCCGCGCAGCGGCCCGGCCCGGGCCCCGGCGCGGGGATGGACGGCCCCG
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CCCTGGGCCCCGGCGTGGCCCTGCGCTCCCGGCCCGGGATTCCCCACCCCCGCGGGCGCGC
CCGGCGCCCCGGGACCCCGGCCACGGCTACTCACCCCTCCCCGCGCCCTCCGCGGGGACCC
TCCCCATCGCAGGGCGGGGCCCGGGGAAGCCCGGCCCTGGGGCGGGGCTTCGGCCGCGGTT
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25 AACCTGGACACGCCCCCTGCCCTACCTGGAGTTTCGATACAAGCGGCGAGTTTATGCCAGAAC
CTCATCGATGATAAGCAGTTTGCAAAGCTTCACACAAAGGCGAACCTGAAGAAGTTC

SEQ ID NO:2

- 30 *SHANK3* mRNA Canonical Transcript 3' UTR Sequence (*SHANK3*-201
ENST00000262795.7)

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20 **Table 4: Exemplary ASO or AR Sequences Targeting
SHANK3 mRNA 5' UTR or 3' UTR or SHANK3 5' PNCR**

SEQ ID NO	ASO Sequence	ASO Name
5	GCCTGGCCTGAGTGGTG	SHANK3 H1 5UTR(-2178-2162)
6	CTGGCCTGGCCTGAGTG	SHANK3 H1 5UTR(-2175-2159)
7	CCACTGGCCTGGCCTGA	SHANK3 H1 5UTR(-2172-2156)
8	AGGCCACTGGCCTGGCC	SHANK3 H1 5UTR(-2169-2153)
9	CCAAGGCCACTGGCCTG	SHANK3 H1 5UTR(-2166-2150)
10	CTCCCAAGGCCACTGGC	SHANK3 H1 5UTR(-2163-2147)
11	CCCCTCCCAAGGCCACT	SHANK3 H1 5UTR(-2160-2144)
12	AGGCCCCTCCCAAGGCC	SHANK3 H1 5UTR(-2157-2141)
13	CACAGGCCCTCCCAAG	SHANK3 H1 5UTR(-2154-2138)
14	CATCACAGGCCCTCCC	SHANK3 H1 5UTR(-2151-2135)
15	CAGCATCACAGGCCCT	SHANK3 H1 5UTR(-2148-2132)
16	TCCCAGCATCACAGGCC	SHANK3 H1 5UTR(-2145-2129)
17	TGGTCCCAGCATCACAG	SHANK3 H1 5UTR(-2142-2126)
18	CTGTGGTCCCAGCATCA	SHANK3 H1 5UTR(-2139-2123)
19	GAAGTGTGGTCCCAGCA	SHANK3 H1 5UTR(-2136-2120)
20	CAGGAAGTGTGGTCCCA	SHANK3 H1 5UTR(-2133-2117)
21	GCCAGGAAGTGTGGTC	SHANK3 H1 5UTR(-2130-2114)
22	CCTGCCAGGAAGTGTG	SHANK3 H1 5UTR(-2127-2111)

23	CTCCCTGCCCAGGAACT	SHANK3 H1 5UTR(-2124-2108)
24	TTGCTCCCTGCCCAGGA	SHANK3 H1 5UTR(-2121-2105)
25	CGGTTGCTCCCTGCCCA	SHANK3 H1 5UTR(-2118-2102)
26	AGACGGTTGCTCCCTGC	SHANK3 H1 5UTR(-2115-2099)
27	CCTAGACGGTTGCTCCC	SHANK3 H1 5UTR(-2112-2096)
28	ACGCCTAGACGGTTGCT	SHANK3 H1 5UTR(-2109-2093)
29	CCCACGCCTAGACGGTT	SHANK3 H1 5UTR(-2106-2090)
30	CTCCCCACGCCTAGACG	SHANK3 H1 5UTR(-2103-2087)
31	GTTCTCCCCACGCCTAG	SHANK3 H1 5UTR(-2100-2084)
32	TGCGTTCTCCCCACGCC	SHANK3 H1 5UTR(-2097-2081)
33	TCCTGCGTTCTCCCCAC	SHANK3 H1 5UTR(-2094-2078)
34	ACGTCCTGCGTTCTCCC	SHANK3 H1 5UTR(-2091-2075)
35	GTCACGTCCTGCGTTCT	SHANK3 H1 5UTR(-2088-2072)
36	TGGGTCACGTCCTGCGT	SHANK3 H1 5UTR(-2085-2069)
37	GTGTGGGTCACGTCCTG	SHANK3 H1 5UTR(-2082-2066)
38	GGTGTGTGGGTCACGTC	SHANK3 H1 5UTR(-2079-2063)
39	TGCGGTGTGTGGGTCAC	SHANK3 H1 5UTR(-2076-2060)
40	CAGTGCGGTGTGTGGGT	SHANK3 H1 5UTR(-2073-2057)
41	CTCCAGTGCGGTGTGTG	SHANK3 H1 5UTR(-2070-2054)
42	AGCCTCCAGTGCGGTGT	SHANK3 H1 5UTR(-2067-2051)
43	CGGAGCCTCCAGTGCGG	SHANK3 H1 5UTR(-2064-2048)
44	GAGCGGAGCCTCCAGTG	SHANK3 H1 5UTR(-2061-2045)
45	GCAGAGCGGAGCCTCCA	SHANK3 H1 5UTR(-2058-2042)
46	CGGGCAGAGCGGAGCCT	SHANK3 H1 5UTR(-2055-2039)
47	AGGAAGGGGTCCCGGAG	SHANK3 H1 5UTR(-816-800)
48	CGGAGGAAGGGGTCCCG	SHANK3 H1 5UTR(-813-797)
49	CGGCGGAGGAAGGGGTC	SHANK3 H1 5UTR(-810-794)
50	GTGCGGCGGAGGAAGGG	SHANK3 H1 5UTR(-807-791)
51	CGGGTGCGGCGGAGGAA	SHANK3 H1 5UTR(-804-788)
52	GGGCGGGTGCGGCGGAG	SHANK3 H1 5UTR(-801-785)
53	CCGGGGCGGGTGCGGCG	SHANK3 H1 5UTR(-798-782)
54	CCACGGGGCGGGTGCG	SHANK3 H1 5UTR(-795-779)
55	GGACCACGGGGCGGGT	SHANK3 H1 5UTR(-792-776)
56	CGCGGACCACGGGGGCG	SHANK3 H1 5UTR(-789-773)
57	ATCCGCGGACCACGGGG	SHANK3 H1 5UTR(-786-770)
58	GGCATCCGCGGACCACC	SHANK3 H1 5UTR(-783-767)

59	GCGGGCATCCGCGGACC	SHANK3 H1 5UTR(-780-764)
60	AGGGCGGGCATCCGCGG	SHANK3 H1 5UTR(-777-761)
61	GCAAGGGCGGGCATCCG	SHANK3 H1 5UTR(-774-758)
62	GCGGCAAGGGCGGGCAT	SHANK3 H1 5UTR(-771-755)
63	TGAGCGGCAAGGGCGGG	SHANK3 H1 5UTR(-768-752)
64	GGCTGAGCGGCAAGGGC	SHANK3 H1 5UTR(-765-749)
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66	GGGAGTGGCTGAGCGGC	SHANK3 H1 5UTR(-759-743)
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68	TGCGGGGGGAGTGGCTG	SHANK3 H1 5UTR(-753-737)
69	CGGTGCGGGGGGAGTGG	SHANK3 H1 5UTR(-750-734)
70	CCTCGGTGCGGGGGGAG	SHANK3 H1 5UTR(-747-731)
71	AGGCCTCGGTGCGGGGG	SHANK3 H1 5UTR(-744-728)
72	CCTAGGCCTCGGTGCGG	SHANK3 H1 5UTR(-741-725)
73	AGTCCTAGGCCTCGGTG	SHANK3 H1 5UTR(-738-722)
74	GGGAGTCCTAGGCCTCG	SHANK3 H1 5UTR(-735-719)
75	GGCTCAGCTCGGCGCCT	SHANK3 H1 5UTR(-501-485)
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77	GGCCCCGGCTCAGCTCG	SHANK3 H1 5UTR(-495-479)
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79	TGCATCGGCCCCGGCTC	SHANK3 H1 5UTR(-489-473)
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81	CTCAGCTGCATCGGCCC	SHANK3 H1 5UTR(-483-467)
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83	GCGCGGCTCAGTGCAT	SHANK3 H1 5UTR(-477-461)
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86	GCGGCGGCGGCGGCT	SHANK3 H1 5UTR(-468-452)
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101	GCGGGGGACAGCGGCTC	SHANK3 H1 5UTR(-423-407)
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103	GCCGGCGGGGGGACAG	SHANK3 H1 5UTR(-417-401)
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106	GGGGCCGGGGCCGCGC	SHANK3 H1 5UTR(-408-392)
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112	AGGGGGCCGGGGGGGGC	SHANK3 H1 5UTR(-390-374)
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115	CTGCGCGGGAGGGGGCC	SHANK3 H1 5UTR(-381-365)
116	GCGCTGCGCGGGAGGGG	SHANK3 H1 5UTR(-378-362)
117	GCCGCGCTGCGCGGGAG	SHANK3 H1 5UTR(-375-359)
118	TCGGCCGCGCTGCGCGG	SHANK3 H1 5UTR(-372-356)
119	CCGTCGGCCGCGCTGCG	SHANK3 H1 5UTR(-369-353)
120	GCCCCGTCGGCCGCGCT	SHANK3 H1 5UTR(-366-350)
121	GGAGCCCCGTCGGCCGC	SHANK3 H1 5UTR(-363-347)
122	GCCGGAGCCCCGTCGGC	SHANK3 H1 5UTR(-360-344)
123	CCCGCCGAGCCCCGTC	SHANK3 H1 5UTR(-357-341)
124	CCCCCGCCGGAGCCCC	SHANK3 H1 5UTR(-354-338)
125	TTCCCCCGCCGGAGC	SHANK3 H1 5UTR(-351-335)
126	CCCTCCCCCGCCGG	SHANK3 H1 5UTR(-348-332)
127	CCCCCTTCCCCCGC	SHANK3 H1 5UTR(-345-329)
128	GGCCCCCTTCCCCC	SHANK3 H1 5UTR(-342-326)
129	CCCGCCCCCTTCCC	SHANK3 H1 5UTR(-339-323)
130	CGCCCCGCCCCCTT	SHANK3 H1 5UTR(-336-320)

131	CGGCGCCCCGGCCCCC	SHANK3 H1 5UTR(-333-317)
132	GCGCGGCGCCCCGGCCC	SHANK3 H1 5UTR(-330-314)
133	CGCGCGCGGCGCCCCG	SHANK3 H1 5UTR(-327-311)
134	CTCCGCGCGCGGCGCCC	SHANK3 H1 5UTR(-324-308)
135	GGACTCCGCGCGGCG	SHANK3 H1 5UTR(-321-305)
136	CGGGGACTCCGCGCG	SHANK3 H1 5UTR(-318-302)
137	GCCCGGGGACTCCGCGC	SHANK3 H1 5UTR(-315-299)
138	AGCGCCCGGGGACTCCG	SHANK3 H1 5UTR(-312-296)
139	CGGAGCGCCCGGGGACT	SHANK3 H1 5UTR(-309-293)
140	GAACGGAGCGCCGGGG	SHANK3 H1 5UTR(-306-290)
141	GGGGAACGGAGCGCCG	SHANK3 H1 5UTR(-303-287)
142	GCCGGGGAACGGAGCGC	SHANK3 H1 5UTR(-300-284)
143	CGCGCCGGGGAACGGAG	SHANK3 H1 5UTR(-297-281)
144	GCTCGCGCCGGGGAACG	SHANK3 H1 5UTR(-294-278)
145	GCCGCTCGCGCCGGGGA	SHANK3 H1 5UTR(-291-275)
146	GGGGCCGCTCGCGCCGG	SHANK3 H1 5UTR(-288-272)
147	GCCGGGGCCGCTCGCGC	SHANK3 H1 5UTR(-285-269)
148	CGGGCCGGGGCCGCTCG	SHANK3 H1 5UTR(-282-266)
149	GCCCGGGCCGGGGCCGC	SHANK3 H1 5UTR(-279-263)
150	GGGGCCCGGGCCGGGGC	SHANK3 H1 5UTR(-276-260)
151	GCCGGGGCCCGGGCCGG	SHANK3 H1 5UTR(-273-257)
152	CGCGCCGGGGCCCGGGC	SHANK3 H1 5UTR(-270-254)
153	CCCCGCGCCGGGGCCCG	SHANK3 H1 5UTR(-267-251)
154	CATCCCGCGCCGGGGC	SHANK3 H1 5UTR(-264-248)
155	GTCCATCCCCGCGCCGG	SHANK3 H1 5UTR(-261-245)
156	GCCGTCCATCCCCGCGC	SHANK3 H1 5UTR(-258-242)
157	GGGGCCGTCCATCCCCG	SHANK3 H1 5UTR(-255-239)
158	CCCGGGGCCGTCCATCC	SHANK3 H1 5UTR(-252-236)
159	GGCCCCGGGGCCGTCCA	SHANK3 H1 5UTR(-249-233)
160	GCTGGCCCCGGGGCCGT	SHANK3 H1 5UTR(-246-230)
161	GGCGCTGGCCCCGGGGC	SHANK3 H1 5UTR(-243-227)
162	CACGGCGCTGGCCCCGG	SHANK3 H1 5UTR(-240-224)
163	GACCACGGCGCTGGCCC	SHANK3 H1 5UTR(-237-221)
164	CACGACCACGGCGCTGG	SHANK3 H1 5UTR(-234-218)
165	GCGCACGACCACGGCGC	SHANK3 H1 5UTR(-231-215)
166	GACGCGCACGACCACGG	SHANK3 H1 5UTR(-228-212)

167	GCCGACGCGCACGACCA	SHANK3 H1 5UTR(-225-209)
168	GATGCCGACGCGCACGA	SHANK3 H1 5UTR(-222-206)
169	CGGGATGCCGACGCGCA	SHANK3 H1 5UTR(-219-203)
170	GTCCGGGATGCCGACGC	SHANK3 H1 5UTR(-216-200)
171	CAGGTCCGGGATGCCGA	SHANK3 H1 5UTR(-213-197)
172	CTGCAGGTCCGGGATGC	SHANK3 H1 5UTR(-210-194)
173	CTGCTGCAGGTCCGGGA	SHANK3 H1 5UTR(-207-191)
174	CGTCTGCTGCAGGTCCG	SHANK3 H1 5UTR(-204-188)
175	CGAACCGCGGCCGAAGC	SHANK3 H1 5UTR(+1+17)
176	CCGCGAACCGCGGCCGA	SHANK3 H1 5UTR(+4+20)
177	CCTCCGCGAACCGCGGC	SHANK3 H1 5UTR(+7+23)
178	GCGCCTCCGCGAACCGC	SHANK3 H1 5UTR(+10+26)
179	CCCGCGCCTCCGCGAAC	SHANK3 H1 5UTR(+13+29)
180	GACCCCGCGCCTCCGCG	SHANK3 H1 5UTR(+16+32)
181	CGGGACCCCGCGCCTCC	SHANK3 H1 5UTR(+19+35)
182	GCCCGGGACCCCGCGCC	SHANK3 H1 5UTR(+22+38)
183	GGCGCCCGGGACCCCGC	SHANK3 H1 5UTR(+25+41)
184	GCCGGCGCCCGGGACCC	SHANK3 H1 5UTR(+28+44)
185	GGTGCCGGCGCCCGGGA	SHANK3 H1 5UTR(+31+47)
186	TCGGGTGCCGGCGCCCG	SHANK3 H1 5UTR(+34+50)
187	GGCTCGGGTGCCGGCGC	SHANK3 H1 5UTR(+37+53)
188	CGGGGCTCGGGTGCCGG	SHANK3 H1 5UTR(+40+56)
189	GTCCGGGGCTCGGGTGC	SHANK3 H1 5UTR(+43+59)
190	GGAGTCCGGGGCTCGGG	SHANK3 H1 5UTR(+46+62)
191	GAAGGAGTCCGGGGCTC	SHANK3 H1 5UTR(+49+65)
192	GCCGAAGGAGTCCGGGG	SHANK3 H1 5UTR(+52+68)
193	CCCGCCGAAGGAGTCCG	SHANK3 H1 5UTR(+55+71)
194	GCCCCCGCGAAGGAGT	SHANK3 H1 5UTR(+58+74)
195	CGGGCCCCCGCGAAGG	SHANK3 H1 5UTR(+61+77)
196	CCCCGGGCCCCCGCGA	SHANK3 H1 5UTR(+64+80)
197	GAGCCCCGGGCCCCCGC	SHANK3 H1 5UTR(+67+83)
198	GCCGAGCCCCGGGCCCC	SHANK3 H1 5UTR(+70+86)
199	GGTGCCGAGCCCCGGGC	SHANK3 H1 5UTR(+73+89)
200	CGGGGTGCCGAGCCCCG	SHANK3 H1 5UTR(+76+92)
201	ATGCGGGGTGCCGAGCC	SHANK3 H1 5UTR(+79+95)
202	CCCATGCGGGGTGCCGA	SHANK3 H1 5UTR(+82+98)

203	GGCCCCATGCGGGGTGC	SHANK3 H1 5UTR(+85+101)
204	GCCGGCCCCATGCGGGG	SHANK3 H1 5UTR(+88+104)
205	CCCCCGGCCCATGCG	SHANK3 H1 5UTR(+91+107)
206	CGCCCCGCGGCCCCAT	SHANK3 H1 5UTR(+94+110)
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208	CGGACCCGCCCCGCGG	SHANK3 H1 5UTR(+100+116)
209	GCGCGGACCCGCCCCGC	SHANK3 H1 5UTR(+103+119)
210	GGAGCGCGGACCCGCC	SHANK3 H1 5UTR(+106+122)
211	CCGGGAGCGCGGACCCG	SHANK3 H1 5UTR(+109+125)
212	GTCCCGGGAGCGCGAC	SHANK3 H1 5UTR(+112+128)
213	CAGGTCCCGGAGCGCG	SHANK3 H1 5UTR(+115+131)
214	GCTCAGTCCCGGAGC	SHANK3 H1 5UTR(+118+134)
215	TGAGCTCAGTCCCGGG	SHANK3 H1 5UTR(+121+137)
216	TCGTGAGCTCAGTCCC	SHANK3 H1 5UTR(+124+140)
217	GGCTCGTGAGCTCAGGT	SHANK3 H1 5UTR(+127+143)
218	GCGGGCTCGTGAGCTCA	SHANK3 H1 5UTR(+130+146)
219	GGAGCGGGCTCGTGAGC	SHANK3 H1 5UTR(+133+149)
220	AGCGGAGCGGGCTCGTG	SHANK3 H1 5UTR(+136+152)
221	TGCAGCGGAGCGGGCTC	SHANK3 H1 5UTR(+139+155)
222	TTCTGCAGCGGAGCGGG	SHANK3 H1 5UTR(+142+158)
223	CACCTTCTGCAGCGGAGC	SHANK3 H1 5UTR(+145+161)
224	AGGCACTTCTGCAGCGG	SHANK3 H1 5UTR(+148+164)
225	CGCAGGCACTTCTGCAG	SHANK3 H1 5UTR(+151+167)
226	AGGCGCAGGCACTTCTG	SHANK3 H1 5UTR(+154+170)
227	TCCAGGCGCAGGCACTT	SHANK3 H1 5UTR(+157+173)
228	GGGTCCAGGCGCAGGCA	SHANK3 H1 5UTR(+160+176)
229	GCCGGGTCCAGGCGCAG	SHANK3 H1 5UTR(+163+179)
230	GCGGCCGGGTCCAGGCG	SHANK3 H1 5UTR(+166+182)
231	GGCGCGGCCGGTCCAG	SHANK3 H1 5UTR(+169+185)
232	ACGGGCGCGGCCGGGTC	SHANK3 H1 5UTR(+172+188)
233	CACACGGGCGCGCCGG	SHANK3 H1 5UTR(+175+191)
234	GCCCACAGGGCGCGGC	SHANK3 H1 5UTR(+178+194)
235	GCGGCCACACGGGCGC	SHANK3 H1 5UTR(+181+197)
236	TTGGCGGCCACACGGG	SHANK3 H1 5UTR(+184+200)
237	TGCTTGCGGCCACAC	SHANK3 H1 5UTR(+187+203)
238	CGCTGCTTGCGGCCCA	SHANK3 H1 5UTR(+190+206)

239	ACGCGCTGCTTGGCGGC	SHANK3 H1 5UTR(+193+209)
240	AGCACGCGCTGCTTGGC	SHANK3 H1 5UTR(+196+212)
241	CAGAGCACGCGCTGCTT	SHANK3 H1 5UTR(+199+215)
242	GCGCAGAGCACGCGCTG	SHANK3 H1 5UTR(+202+218)
243	AGGGCGCAGAGCACGCG	SHANK3 H1 5UTR(+205+221)
244	TTGAGGGCGCAGAGCAC	SHANK3 H1 5UTR(+208+224)
245	TGGTTGAGGGCGCAGAG	SHANK3 H1 5UTR(+211+227)
246	CTGTGGTTGAGGGCGCA	SHANK3 H1 5UTR(+214+230)
247	AGGCTGTGGTTGAGGGC	SHANK3 H1 5UTR(+217+233)
248	TGGAGGCTGTGGTTGAG	SHANK3 H1 5UTR(+220+236)
249	TCCTGGAGGCTGTGGTT	SHANK3 H1 5UTR(+223+239)
250	GCGTCCTGGAGGCTGTG	SHANK3 H1 5UTR(+226+242)
251	AGCGCGTCTGGAGGCT	SHANK3 H1 5UTR(+229+245)
252	TTGAGCGGTCCTGGAG	SHANK3 H1 5UTR(+232+248)
253	TAGTTGAGCGGTCCTG	SHANK3 H1 5UTR(+235+251)
254	CCATAGTTGAGCGCGTC	SHANK3 H1 5UTR(+238+254)
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256	AAAAGCCCATAGTTGAG	SHANK3 H1 5UTR(+244+260)
257	TGGAAGCCCATAGTT	SHANK3 H1 5UTR(+247+263)
258	GGCTGGAAAGCCCATATA	SHANK3 H1 5UTR(+250+266)
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261	CGGGAGGGCGGCTGGAA	SHANK3 H1 5UTR(+259+275)
262	CCCCGGGAGGGCGGCTG	SHANK3 H1 5UTR(+262+278)
263	CGGCCCGGGAGGGCGG	SHANK3 H1 5UTR(+265+281)
264	GCGCGGCCCCGGGAGGG	SHANK3 H1 5UTR(+268+284)
265	CCGGCGCGGCCCGGGA	SHANK3 H1 5UTR(+271+287)
266	TTGCCGGCGGCCCCG	SHANK3 H1 5UTR(+274+290)
267	AACTTGCCGGCGCGGCC	SHANK3 H1 5UTR(+277+293)
268	AGGAACTTGCCGGCGCG	SHANK3 H1 5UTR(+280+296)
269	TCCAGGAACTTGCCGGC	SHANK3 H1 5UTR(+283+299)
270	TCATCCAGGAACTTGCC	SHANK3 H1 5UTR(+286+302)
271	TCCTCATCCAGGAACTT	SHANK3 H1 5UTR(+289+305)
272	CGCTCCTCATCCAGGAA	SHANK3 H1 5UTR(+292+308)
273	AGCCGCTCCTCATCCAG	SHANK3 H1 5UTR(+295+311)
274	AGGAGCCGCTCCTCATC	SHANK3 H1 5UTR(+298+314)

275	TGCAGGAGCCGCTCCTC	SHANK3 H1 5UTR(+301+317)
276	TCCTGCAGGAGCCGCTC	SHANK3 H1 5UTR(+304+320)
277	TACTCCTGCAGGAGCCG	SHANK3 H1 5UTR(+307+323)
278	GGGTACTCCTGCAGGAG	SHANK3 H1 5UTR(+310+326)
279	GGCGGGTACTCCTGCAG	SHANK3 H1 5UTR(+313+329)
280	TTGGGCGGGTACTCCTG	SHANK3 H1 5UTR(+316+332)
281	AGGTTGGGCGGGTACTC	SHANK3 H1 5UTR(+319+335)
282	TCCAGGTTGGGCGGGTA	SHANK3 H1 5UTR(+322+338)
283	GTGTCCAGGTTGGGCGG	SHANK3 H1 5UTR(+325+341)
284	GGCGTGTCCAGGTTGGG	SHANK3 H1 5UTR(+328+344)
285	AGGGGCGTGTCCAGGTT	SHANK3 H1 5UTR(+331+347)
286	GGCAGGGGCGTGTCCAG	SHANK3 H1 5UTR(+334+350)
287	TAGGGCAGGGGCGTGTC	SHANK3 H1 5UTR(+337+353)
288	AGGTAGGGCAGGGGCGT	SHANK3 H1 5UTR(+340+356)
289	TCCAGGTAGGGCAGGGG	SHANK3 H1 5UTR(+343+359)
290	AACTCCAGGTAGGGCAG	SHANK3 H1:2 5UTR(+346+362)
291	CGAAACTCCAGGTAGGG	SHANK3 H1:2 5UTR(+349+365)
292	TATCGAAACTCCAGGTA	SHANK3 H1:2 5UTR(+352+368)
293	TTGTATCGAAACTCCAG	SHANK3 H1:2 5UTR(+355+371)
294	CGCTTGTATCGAAACTC	SHANK3 H1:2 5UTR(+358+374)
295	CGCCGCTTGTATCGAAA	SHANK3 H2 5UTR(+361+377)
296	ACTCGCCGCTTGTATCG	SHANK3 H2 5UTR(+364+380)
297	TAAACTCGCCGCTTGTA	SHANK3 H2 5UTR(+367+383)
298	GCATAAACTCGCCGCTT	SHANK3 H2 5UTR(+370+386)
299	TGGGCATAAACTCGCCG	SHANK3 H2 5UTR(+373+389)
300	TTCTGGGCATAAACTCG	SHANK3 H2 5UTR(+376+392)
301	AGGTTCTGGGCATAAAC	SHANK3 H2 5UTR(+379+395)
302	ATGAGGTTCTGGGCATA	SHANK3 H2 5UTR(+382+398)
303	TCGATGAGGTTCTGGGC	SHANK3 H2 5UTR(+385+401)
304	TCATCGATGAGGTTCTG	SHANK3 H2 5UTR(+388+404)
305	TTATCATCGATGAGGTT	SHANK3 H2 5UTR(+391+407)
306	TGCTTATCATCGATGAG	SHANK3 H2 5UTR(+394+410)
307	AACTGCTTATCATCGAT	SHANK3 H2 5UTR(+397+413)
308	GCAAACTGCTTATCATC	SHANK3 H2 5UTR(+400+416)
309	TTTGCAAACTGCTTATC	SHANK3 H2 5UTR(+403+419)
310	AGCTTTGCAAACTGCTT	SHANK3 H2 5UTR(+406+422)

311	TGAAGCTTTGCAAAGCTG	SHANK3 H2 5UTR(+409+425)
312	GTGTGAAGCTTTGCAAA	SHANK3 H2 5UTR(+412+428)
313	TTTGTGTGAAGCTTTGC	SHANK3 H2 5UTR(+415+431)
314	GCCTTTGTGTGAAGCTT	SHANK3 H2:3 5UTR(+418+434)
315	TTCGCCTTTGTGTGAAG	SHANK3 H2:3 5UTR(+421+437)
316	AGGTTTCGCCTTTGTGTG	SHANK3 H2:3 5UTR(+424+440)
317	TTCAGGTTTCGCCTTTGT	SHANK3 H2:3 5UTR(+427+443)
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319	AACTTCTTCAGGTTTCGC	SHANK3 H3 5UTR(+433+449)
320	GGCCACTGGCCTGGCCTGAGTGGTG	SHANK3 H1 5UTR(-2178-2154)
321	CAAGGCCACTGGCCTGGCCTGAGTG	SHANK3 H1 5UTR(-2175-2151)
322	TCCCAAGGCCACTGGCCTGGCCTGA	SHANK3 H1 5UTR(-2172-2148)
323	CCCTCCCAAGGCCACTGGCCTGGCC	SHANK3 H1 5UTR(-2169-2145)
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325	ACAGGCCCCCTCCCAAGGCCACTGGC	SHANK3 H1 5UTR(-2163-2139)
326	ATCACAGGCCCCCTCCCAAGGCCACT	SHANK3 H1 5UTR(-2160-2136)
327	AGCATCACAGGCCCCCTCCCAAGGCC	SHANK3 H1 5UTR(-2157-2133)
328	CCCAGCATCACAGGCCCCCTCCCAAG	SHANK3 H1 5UTR(-2154-2130)
329	GGTCCAGCATCACAGGCCCCCTCCC	SHANK3 H1 5UTR(-2151-2127)
330	TGTGGTCCCAGCATCACAGGCCCCCT	SHANK3 H1 5UTR(-2148-2124)
331	AACTGTGGTCCCAGCATCACAGGCC	SHANK3 H1 5UTR(-2145-2121)
332	AGGAACTGTGGTCCCAGCATCACAG	SHANK3 H1 5UTR(-2142-2118)
333	CCCAGGAACTGTGGTCCCAGCATCA	SHANK3 H1 5UTR(-2139-2115)
334	CTGCCCAGGAACTGTGGTCCCAGCA	SHANK3 H1 5UTR(-2136-2112)
335	TCCCTGCCCAGGAACTGTGGTCCCA	SHANK3 H1 5UTR(-2133-2109)
336	TGCTCCCTGCCAGGAACTGTGGTC	SHANK3 H1 5UTR(-2130-2106)
337	GGTTGCTCCCTGCCAGGAACTGTG	SHANK3 H1 5UTR(-2127-2103)
338	GACGGTTGCTCCCTGCCAGGAACT	SHANK3 H1 5UTR(-2124-2100)
339	CTAGACGGTTGCTCCCTGCCAGGA	SHANK3 H1 5UTR(-2121-2097)
340	CGCCTAGACGGTTGCTCCCTGCCCA	SHANK3 H1 5UTR(-2118-2094)
341	CCACGCCTAGACGGTTGCTCCCTGC	SHANK3 H1 5UTR(-2115-2091)
342	TCCCCACGCCTAGACGGTTGCTCCC	SHANK3 H1 5UTR(-2112-2088)
343	TTCTCCCCACGCCTAGACGGTTGCT	SHANK3 H1 5UTR(-2109-2085)
344	GCGTTCTCCCCACGCCTAGACGGTT	SHANK3 H1 5UTR(-2106-2082)
345	CCTGCGTTCTCCCCACGCCTAGACG	SHANK3 H1 5UTR(-2103-2079)
346	CGTCCTGCGTTCTCCCCACGCCTAG	SHANK3 H1 5UTR(-2100-2076)

347	TCACGTCCTGCGTTCTCCCCACGCC	SHANK3 H1 5UTR(-2097-2073)
348	GGGTCACGTCCTGCGTTCTCCCCAC	SHANK3 H1 5UTR(-2094-2070)
349	TGTGGGTCACGTCCTGCGTTCTCCC	SHANK3 H1 5UTR(-2091-2067)
350	GTGTGTGGGTCACGTCCTGCGTTCT	SHANK3 H1 5UTR(-2088-2064)
351	GCGGTGTGTGGGTCACGTCCTGCGT	SHANK3 H1 5UTR(-2085-2061)
352	AGTGCGGTGTGTGGGTCACGTCCTG	SHANK3 H1 5UTR(-2082-2058)
353	TCCAGTGCGGTGTGTGGGTCACGTC	SHANK3 H1 5UTR(-2079-2055)
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355	GGAGCCTCCAGTGCGGTGTGTGGGT	SHANK3 H1 5UTR(-2073-2049)
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357	CAGAGCGGAGCCTCCAGTGCGGTGT	SHANK3 H1 5UTR(-2067-2043)
358	GGGCAGAGCGGAGCCTCCAGTGCGG	SHANK3 H1 5UTR(-2064-2040)
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360	GGGTGCGGCGGAGGAAGGGGTCCCG	SHANK3 H1 5UTR(-813-789)
361	GGCGGGTGCGGCGGAGGAAGGGGTC	SHANK3 H1 5UTR(-810-786)
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364	GACCACCGGGGCGGGTGCGGCGGAG	SHANK3 H1 5UTR(-801-777)
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366	TCCGCGGACCACCGGGGCGGGTGCG	SHANK3 H1 5UTR(-795-771)
367	GCATCCGCGGACCACCGGGGCGGGT	SHANK3 H1 5UTR(-792-768)
368	CGGGCATCCGCGGACCACCGGGGCG	SHANK3 H1 5UTR(-789-765)
369	GGGCGGGCATCCGCGGACCACCGGG	SHANK3 H1 5UTR(-786-762)
370	CAAGGGCGGGCATCCGCGGACCACC	SHANK3 H1 5UTR(-783-759)
371	CGGCAAGGGCGGGCATCCGCGGACC	SHANK3 H1 5UTR(-780-756)
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373	GCTGAGCGGCAAGGGCGGGCATCCG	SHANK3 H1 5UTR(-774-750)
374	GTGGCTGAGCGGCAAGGGCGGGCAT	SHANK3 H1 5UTR(-771-747)
375	GGAGTGGCTGAGCGGCAAGGGCGGG	SHANK3 H1 5UTR(-768-744)
376	GGGGGAGTGGCTGAGCGGCAAGGGC	SHANK3 H1 5UTR(-765-741)
377	GCGGGGGGAGTGGCTGAGCGGCAAG	SHANK3 H1 5UTR(-762-738)
378	GGTGCGGGGGGAGTGGCTGAGCGGC	SHANK3 H1 5UTR(-759-735)
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380	GGCCTCGGTGCGGGGGGAGTGGCTG	SHANK3 H1 5UTR(-753-729)
381	CTAGGCCTCGGTGCGGGGGGAGTGG	SHANK3 H1 5UTR(-750-726)
382	GTCCTAGGCCTCGGTGCGGGGGGAG	SHANK3 H1 5UTR(-747-723)

383	GGAGTCCTAGGCCTCGGTGCGGGGG	SHANK3 H1 5UTR(-744-720)
384	TCGGCCCCGGCTCAGCTCGGCGCCT	SHANK3 H1 5UTR(-501-477)
385	GCATCGGCCCCGGCTCAGCTCGGCG	SHANK3 H1 5UTR(-498-474)
386	GCTGCATCGGCCCCGGCTCAGCTCG	SHANK3 H1 5UTR(-495-471)
387	TCAGCTGCATCGGCCCCGGCTCAGC	SHANK3 H1 5UTR(-492-468)
388	GGCTCAGCTGCATCGGCCCCGGCTC	SHANK3 H1 5UTR(-489-465)
389	CGCGGCTCAGCTGCATCGGCCCCGG	SHANK3 H1 5UTR(-486-462)
390	CGGCGCGGCTCAGCTGCATCGGCC	SHANK3 H1 5UTR(-483-459)
391	CGGCGGCGCGGCTCAGCTGCATCGG	SHANK3 H1 5UTR(-480-456)
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396	CGGCGGCGGCGGCGGCGGCGGCGCG	SHANK3 H1 5UTR(-465-441)
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398	CAGGGGCGGCGGCGGCGGCGGCGGC	SHANK3 H1 5UTR(-459-435)
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404	GCGGCTCCGGGGGCTCCGACAGGGG	SHANK3 H1 5UTR(-441-417)
405	ACAGCGGCTCCGGGGGCTCCGACAGG	SHANK3 H1 5UTR(-438-414)
406	GGGACAGCGGCTCCGGGGGCTCCGC	SHANK3 H1 5UTR(-435-411)
407	CGGGGACAGCGGCTCCGGGGGCTC	SHANK3 H1 5UTR(-432-408)
408	GCGCGGGGACAGCGGCTCCGGGGG	SHANK3 H1 5UTR(-429-405)
409	CCGGCGGGGGACAGCGGCTCCGG	SHANK3 H1 5UTR(-426-402)
410	GGGCCGGCGGGGGACAGCGGCTC	SHANK3 H1 5UTR(-423-399)
411	CCGGGGCCGGCGGGGGACAGCGG	SHANK3 H1 5UTR(-420-396)
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413	CCGGGGCCGGGGCCGGCGGGGGGA	SHANK3 H1 5UTR(-414-390)
414	GGGCCGGGGCCGGGGCCGGCGCGGG	SHANK3 H1 5UTR(-411-387)
415	GGGGGGCCGGGGCCGGGGCCGGCGC	SHANK3 H1 5UTR(-408-384)
416	CGGGGGGGGCCGGGGCCGGGGCCGG	SHANK3 H1 5UTR(-405-381)
417	GGCCGGGGGGGGCCGGGGCCGGGGC	SHANK3 H1 5UTR(-402-378)
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420	GCGGGAGGGGGCCGGGGGGGGCCGG	SHANK3 H1 5UTR(-393-369)
421	TGCGGGGAGGGGGCCGGGGGGGGC	SHANK3 H1 5UTR(-390-366)
422	CGCTGCGCGGGAGGGGGCCGGGGG	SHANK3 H1 5UTR(-387-363)
423	CCGCGCTGCGCGGGAGGGGGCCGGG	SHANK3 H1 5UTR(-384-360)
424	CGGCCGCGCTGCGCGGGAGGGGGCC	SHANK3 H1 5UTR(-381-357)
425	CGTCGGCCGCGCTGCGCGGGAGGGG	SHANK3 H1 5UTR(-378-354)
426	CCCCGTCGGCCGCGCTGCGCGGGAG	SHANK3 H1 5UTR(-375-351)
427	GAGCCCCGTCGGCCGCGCTGCGCGG	SHANK3 H1 5UTR(-372-348)
428	CCGGAGCCCCGTCGGCCGCGCTGCG	SHANK3 H1 5UTR(-369-345)
429	CCGCCGGAGCCCCGTCGGCCGCGCT	SHANK3 H1 5UTR(-366-342)
430	CCCCGCCGGAGCCCCGTCGGCCGC	SHANK3 H1 5UTR(-363-339)
431	TCCCCCGCGCGGAGCCCCGTCGGC	SHANK3 H1 5UTR(-360-336)
432	CCTCCCCCGCGCGGAGCCCCGTC	SHANK3 H1 5UTR(-357-333)
433	CCCCCTCCCCCGCGCGGAGCCCC	SHANK3 H1 5UTR(-354-330)
434	GCCCCCTTCCCCCGCGCGGAGC	SHANK3 H1 5UTR(-351-327)
435	CCGGCCCCCTTCCCCCGCGCGG	SHANK3 H1 5UTR(-348-324)
436	GCCCCGGCCCCCTTCCCCCGCG	SHANK3 H1 5UTR(-345-321)
437	GGCGCCCCGGCCCCCTTCCCCC	SHANK3 H1 5UTR(-342-318)
438	CGCGCGCCCCGGCCCCCTTCCC	SHANK3 H1 5UTR(-339-315)
439	GCGCGCGCGCCCCGGCCCCCTT	SHANK3 H1 5UTR(-336-312)
440	TCCGCGCGCGCGCCCCGGCCCCC	SHANK3 H1 5UTR(-333-309)
441	GACTCCGCGCGCGCGCCCCGGCCC	SHANK3 H1 5UTR(-330-306)
442	GGGGACTCCGCGCGCGCGCCCCGG	SHANK3 H1 5UTR(-327-303)
443	CCCGGGGACTCCGCGCGCGCGCCC	SHANK3 H1 5UTR(-324-300)
444	GCGCCGGGGACTCCGCGCGCGGCG	SHANK3 H1 5UTR(-321-297)
445	GGAGCGCCCGGGGACTCCGCGCGCG	SHANK3 H1 5UTR(-318-294)
446	AACGGAGCGCCGGGGACTCCGCGC	SHANK3 H1 5UTR(-315-291)
447	GGGAACGGAGCGCCGGGGACTCCG	SHANK3 H1 5UTR(-312-288)
448	CCGGGAACGGAGCGCCGGGGACT	SHANK3 H1 5UTR(-309-285)
449	GCGCCGGGAACGGAGCGCCGGGG	SHANK3 H1 5UTR(-306-282)
450	CTCGCGCCGGGAACGGAGCGCCCG	SHANK3 H1 5UTR(-303-279)
451	CCGCTCGCGCGGGGAACGGAGCGC	SHANK3 H1 5UTR(-300-276)
452	GGGCCGCTCGCGCCGGGAACGGAG	SHANK3 H1 5UTR(-297-273)
453	CCGGGGCCGCTCGCGCCGGGAACG	SHANK3 H1 5UTR(-294-270)
454	GGGCCGGGGCCGCTCGCGCCGGGA	SHANK3 H1 5UTR(-291-267)

455	CCCGGGCCGGGGCCGCTCGCGCCGG	SHANK3 H1 5UTR(-288-264)
456	GGGCCCCGGGCGGGGCGCTCGCGC	SHANK3 H1 5UTR(-285-261)
457	CCGGGGCCCCGGGCGGGGCGGCTCG	SHANK3 H1 5UTR(-282-258)
458	GCGCCGGGGCCCGGGCCGGGGCCGC	SHANK3 H1 5UTR(-279-255)
459	CCCGCGCCGGGGCCCGGGCCGGGGC	SHANK3 H1 5UTR(-276-252)
460	ATCCCCGCGCCGGGGCCCGGGCCGG	SHANK3 H1 5UTR(-273-249)
461	TCCATCCCCGCGCCGGGGCCCGGGC	SHANK3 H1 5UTR(-270-246)
462	CCGTCCATCCCCGCGCCGGGGCCCG	SHANK3 H1 5UTR(-267-243)
463	GGGCCGTCCATCCCCGCGCCGGGGC	SHANK3 H1 5UTR(-264-240)
464	CCGGGGCCGTCCATCCCCGCGCCGG	SHANK3 H1 5UTR(-261-237)
465	GCCCCGGGGCCGTCCATCCCCGCGC	SHANK3 H1 5UTR(-258-234)
466	CTGGCCCCGGGGCCGTCCATCCCCG	SHANK3 H1 5UTR(-255-231)
467	GCGCTGGCCCCGGGGCCGTCCATCC	SHANK3 H1 5UTR(-252-228)
468	ACGGCGCTGGCCCCGGGGCCGTCCA	SHANK3 H1 5UTR(-249-225)
469	ACCACGGCGCTGGCCCCGGGGCCGT	SHANK3 H1 5UTR(-246-222)
470	ACGACCACGGCGCTGGCCCCGGGGC	SHANK3 H1 5UTR(-243-219)
471	CGCACGACCACGGCGCTGGCCCCGG	SHANK3 H1 5UTR(-240-216)
472	ACGCGCACGACCACGGCGCTGGCCC	SHANK3 H1 5UTR(-237-213)
473	CCGACGCGCACGACCACGGCGCTGG	SHANK3 H1 5UTR(-234-210)
474	ATGCCGACGCGCACGACCACGGCGC	SHANK3 H1 5UTR(-231-207)
475	GGGATGCCGACGCGCACGACCACGG	SHANK3 H1 5UTR(-228-204)
476	TCCGGGATGCCGACGCGCACGACCA	SHANK3 H1 5UTR(-225-201)
477	AGGTCCGGGATGCCGACGCGCACGA	SHANK3 H1 5UTR(-222-198)
478	TGCAGGTCCGGGATGCCGACGCGCA	SHANK3 H1 5UTR(-219-195)
479	TGCTGCAGGTCCGGGATGCCGACGC	SHANK3 H1 5UTR(-216-192)
480	GTCTGCTGCAGGTCCGGGATGCCGA	SHANK3 H1 5UTR(-213-189)
481	CGCCTCCGCGAACCGCGGCCGAAGC	SHANK3 H1 5UTR(+1+25)
482	CCGCGCCTCCGCGAACCGCGGCCGA	SHANK3 H1 5UTR(+4+28)
483	ACCCCGCGCCTCCGCGAACCGCGGC	SHANK3 H1 5UTR(+7+31)
484	GGGACCCCGCGCCTCCGCGAACCGC	SHANK3 H1 5UTR(+10+34)
485	CCCGGGACCCCGCGCCTCCGCGAAC	SHANK3 H1 5UTR(+13+37)
486	GCGCCGGGACCCCGCGCCTCCGCG	SHANK3 H1 5UTR(+16+40)
487	CCGGCGCCCGGGACCCCGCGCCTCC	SHANK3 H1 5UTR(+19+43)
488	GTGCCGGCGCCCGGGACCCCGCGCC	SHANK3 H1 5UTR(+22+46)
489	CGGGTGCCGGCGCCCGGGACCCCGC	SHANK3 H1 5UTR(+25+49)
490	GCTCGGGTGCCGGCGCCCGGGACCC	SHANK3 H1 5UTR(+28+52)

491	GGGGCTCGGGTGCCGGCGCCCGGGA	SHANK3 H1 5UTR(+31+55)
492	TCCGGGGCTCGGGTGCCGGCGCCCG	SHANK3 H1 5UTR(+34+58)
493	GAGTCCGGGGCTCGGGTGCCGGCGC	SHANK3 H1 5UTR(+37+61)
494	AAGGAGTCCGGGGCTCGGGTGCCGG	SHANK3 H1 5UTR(+40+64)
495	CCGAAGGAGTCCGGGGCTCGGGTGC	SHANK3 H1 5UTR(+43+67)
496	CCGCCGAAGGAGTCCGGGGCTCGGG	SHANK3 H1 5UTR(+46+70)
497	CCCCGCCGAAGGAGTCCGGGGCTC	SHANK3 H1 5UTR(+49+73)
498	GGGCCCCGCCGAAGGAGTCCGGGG	SHANK3 H1 5UTR(+52+76)
499	CCCGGGCCCCGCCGAAGGAGTCCG	SHANK3 H1 5UTR(+55+79)
500	AGCCCCGGGGCCCCGCCGAAGGAGT	SHANK3 H1 5UTR(+58+82)
501	CCGAGCCCCGGGCCCCGCCGAAGG	SHANK3 H1 5UTR(+61+85)
502	GTGCCGAGCCCCGGGCCCCGCCGA	SHANK3 H1 5UTR(+64+88)
503	GGGGTGCCGAGCCCCGGGCCCCGC	SHANK3 H1 5UTR(+67+91)
504	TGCGGGGTGCCGAGCCCCGGGCCCC	SHANK3 H1 5UTR(+70+94)
505	CCATGCGGGGTGCCGAGCCCCGGGC	SHANK3 H1 5UTR(+73+97)
506	GCCCCATGCGGGGTGCCGAGCCCCG	SHANK3 H1 5UTR(+76+100)
507	CCGGCCCCATGCGGGGTGCCGAGCC	SHANK3 H1 5UTR(+79+103)
508	CCGCCGGCCCCATGCGGGGTGCCGA	SHANK3 H1 5UTR(+82+106)
509	GCCCCGCCGGCCCCATGCGGGGTGC	SHANK3 H1 5UTR(+85+109)
510	CCCGCCCCGCCGGCCCCATGCGGGG	SHANK3 H1 5UTR(+88+112)
511	GGACCCGCCCGCCGGCCCCATGCG	SHANK3 H1 5UTR(+91+115)
512	CGCGGACCCGCCCGCCGGCCCCAT	SHANK3 H1 5UTR(+94+118)
513	GAGCGCGGACCCGCCCGCCGGCCC	SHANK3 H1 5UTR(+97+121)
514	CGGGAGCGCGGACCCGCCCGCCGG	SHANK3 H1 5UTR(+100+124)
515	TCCCGGGAGCGCGGACCCGCCCGC	SHANK3 H1 5UTR(+103+127)
516	AGGTCCCGGGAGCGCGGACCCGCC	SHANK3 H1 5UTR(+106+130)
517	CTCAGGTCCCGGGAGCGCGGACCCG	SHANK3 H1 5UTR(+109+133)
518	GAGCTCAGGTCCCGGGAGCGCGGAC	SHANK3 H1 5UTR(+112+136)
519	CGTGAGCTCAGGTCCCGGGAGCGCG	SHANK3 H1 5UTR(+115+139)
520	GCTCGTGAGCTCAGGTCCCGGGAGC	SHANK3 H1 5UTR(+118+142)
521	CGGGCTCGTGAGCTCAGGTCCCGGG	SHANK3 H1 5UTR(+121+145)
522	GAGCGGGCTCGTGAGCTCAGGTCCC	SHANK3 H1 5UTR(+124+148)
523	GCGGAGCGGGCTCGTGAGCTCAGGT	SHANK3 H1 5UTR(+127+151)
524	GCAGCGGAGCGGGCTCGTGAGCTCA	SHANK3 H1 5UTR(+130+154)
525	TCTGCAGCGGAGCGGGCTCGTGAGC	SHANK3 H1 5UTR(+133+157)
526	ACTTCTGCAGCGGAGCGGGCTCGTG	SHANK3 H1 5UTR(+136+160)

527	GGCACTTCTGCAGCGGAGCGGGCTC	SHANK3 H1 5UTR(+139+163)
528	GCAGGCACTTCTGCAGCGGAGCGGG	SHANK3 H1 5UTR(+142+166)
529	GGCGCAGGCACTTCTGCAGCGGAGC	SHANK3 H1 5UTR(+145+169)
530	CCAGGCGCAGGCACTTCTGCAGCGG	SHANK3 H1 5UTR(+148+172)
531	GGTCCAGGCGCAGGCACTTCTGCAG	SHANK3 H1 5UTR(+151+175)
532	CCGGGTCCAGGCGCAGGCACTTCTG	SHANK3 H1 5UTR(+154+178)
533	CGGCCGGGTCCAGGCGCAGGCACTT	SHANK3 H1 5UTR(+157+181)
534	GCGCGGCCGGGTCCAGGCGCAGGCA	SHANK3 H1 5UTR(+160+184)
535	CGGGCGCGGCCGGGTCCAGGCGCAG	SHANK3 H1 5UTR(+163+187)
536	ACACGGGCGCGGCCGGGTCCAGGCG	SHANK3 H1 5UTR(+166+190)
537	CCCACACGGGCGCGGCCGGGTCCAG	SHANK3 H1 5UTR(+169+193)
538	CGGCCACACGGGCGCGGCCGGGTCT	SHANK3 H1 5UTR(+172+196)
539	TGGCGGCCACACGGGCGCGGCCGG	SHANK3 H1 5UTR(+175+199)
540	GCTTGGCGGCCACACGGGCGCGGC	SHANK3 H1 5UTR(+178+202)
541	GCTGCTTGGCGGCCACACGGGCGC	SHANK3 H1 5UTR(+181+205)
542	CGCGCTGCTTGGCGGCCACACGGG	SHANK3 H1 5UTR(+184+208)
543	GCACGCGCTGCTTGGCGGCCACAC	SHANK3 H1 5UTR(+187+211)
544	AGAGCACGCGCTGCTTGGCGGCCCA	SHANK3 H1 5UTR(+190+214)
545	CGCAGAGCACGCGCTGCTTGGCGGC	SHANK3 H1 5UTR(+193+217)
546	GGGCGCAGAGCACGCGCTGCTTGGC	SHANK3 H1 5UTR(+196+220)
547	TGAGGGCGCAGAGCACGCGCTGCTT	SHANK3 H1 5UTR(+199+223)
548	GGTTGAGGGCGCAGAGCACGCGCTG	SHANK3 H1 5UTR(+202+226)
549	TGTGGTTGAGGGCGCAGAGCACGCG	SHANK3 H1 5UTR(+205+229)
550	GGCTGTGGTTGAGGGCGCAGAGCAC	SHANK3 H1 5UTR(+208+232)
551	GGAGGCTGTGGTTGAGGGCGCAGAG	SHANK3 H1 5UTR(+211+235)
552	CCTGGAGGCTGTGGTTGAGGGCGCA	SHANK3 H1 5UTR(+214+238)
553	CGTCCTGGAGGCTGTGGTTGAGGGC	SHANK3 H1 5UTR(+217+241)
554	GCGCGTCCTGGAGGCTGTGGTTGAG	SHANK3 H1 5UTR(+220+244)
555	TGAGCGCGTCCTGGAGGCTGTGGTT	SHANK3 H1 5UTR(+223+247)
556	AGTTGAGCGCGTCCTGGAGGCTGTG	SHANK3 H1 5UTR(+226+250)
557	CATAGTTGAGCGCGTCCTGGAGGCT	SHANK3 H1 5UTR(+229+253)
558	GCCCATAGTTGAGCGCGTCCTGGAG	SHANK3 H1 5UTR(+232+256)
559	AAAGCCCATAGTTGAGCGCGTCCTG	SHANK3 H1 5UTR(+235+259)
560	GGAAAAGCCCATAGTTGAGCGCGTC	SHANK3 H1 5UTR(+238+262)
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562	GCGGCTGGAAAAGCCCATAGTTGAG	SHANK3 H1 5UTR(+244+268)

563	AGGGCGGCTGGAAGGCCATAGTT	SHANK3 H1 5UTR(+247+271)
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565	CCCGGGAGGGCGGCTGGAAGGCC	SHANK3 H1 5UTR(+253+277)
566	GGCCCCGGGAGGGCGGCTGGAAG	SHANK3 H1 5UTR(+256+280)
567	CGCGGCCCGGGAGGGCGGCTGGA	SHANK3 H1 5UTR(+259+283)
568	CGGCGGGCCCCGGGAGGGCGGCTG	SHANK3 H1 5UTR(+262+286)
569	TGCCGGCGGGCCCCGGGAGGGCGG	SHANK3 H1 5UTR(+265+289)
570	ACTTGCCGGCGGGCCCCGGGAGGG	SHANK3 H1 5UTR(+268+292)
571	GGAAGTTGCCGGCGGGCCCCGGGA	SHANK3 H1 5UTR(+271+295)
572	CCAGGAAGTTGCCGGCGGGCCCCG	SHANK3 H1 5UTR(+274+298)
573	CATCCAGGAAGTTGCCGGCGGGCC	SHANK3 H1 5UTR(+277+301)
574	CCTCATCCAGGAAGTTGCCGGCGG	SHANK3 H1 5UTR(+280+304)
575	GCTCCTCATCCAGGAAGTTGCCGG	SHANK3 H1 5UTR(+283+307)
576	GCCGCTCCTCATCCAGGAAGTTGCC	SHANK3 H1 5UTR(+286+310)
577	GGAGCCGCTCCTCATCCAGGAAGTT	SHANK3 H1 5UTR(+289+313)
578	GCAGGAGCCGCTCCTCATCCAGGA	SHANK3 H1 5UTR(+292+316)
579	CCTGCAGGAGCCGCTCCTCATCCAG	SHANK3 H1 5UTR(+295+319)
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582	GCGGGTACTCCTGCAGGAGCCGCTC	SHANK3 H1 5UTR(+304+328)
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585	CCAGGTTGGGCGGGTACTCCTGCAG	SHANK3 H1 5UTR(+313+337)
586	TGTCCAGGTTGGGCGGGTACTCCTG	SHANK3 H1 5UTR(+316+340)
587	GCGTGTCCAGGTTGGGCGGGTACTC	SHANK3 H1 5UTR(+319+343)
588	GGGGCGTGTCCAGGTTGGGCGGGTA	SHANK3 H1 5UTR(+322+346)
589	GCAGGGGCGTGTCCAGGTTGGGCGG	SHANK3 H1 5UTR(+325+349)
590	AGGGCAGGGGCGTGTCCAGGTTGGG	SHANK3 H1 5UTR(+328+352)
591	GGTAGGGCAGGGGCGTGTCCAGGTT	SHANK3 H1 5UTR(+331+355)
592	CCAGGTAGGGCAGGGGCGTGTCCAG	SHANK3 H1 5UTR(+334+358)
593	ACTCCAGGTAGGGCAGGGGCGTGTG	SHANK3 H1:2 5UTR(+337+361)
594	GAACTCCAGGTAGGGCAGGGGCGT	SHANK3 H1:2 5UTR(+340+364)
595	ATCGAACTCCAGGTAGGGCAGGGG	SHANK3 H1:2 5UTR(+343+367)
596	TGTATCGAACTCCAGGTAGGGCAG	SHANK3 H1:2 5UTR(+346+370)
597	GCTTGTATCGAACTCCAGGTAGGG	SHANK3 H1:2 5UTR(+349+373)
598	GCCGCTTGTATCGAACTCCAGGTA	SHANK3 H1:2 5UTR(+352+376)

599	CTCGCCGCTTGTATCGAACTCCAG	SHANK3 H1:2 5UTR(+355+379)
600	AAACTCGCCGCTTGTATCGAACTC	SHANK3 H1:2 5UTR(+358+382)
601	CATAAACTCGCCGCTTGTATCGAAA	SHANK3 H2 5UTR(+361+385)
602	GGGCATAAACTCGCCGCTTGTATCG	SHANK3 H2 5UTR(+364+388)
603	TCTGGGCATAAACTCGCCGCTTGT	SHANK3 H2 5UTR(+367+391)
604	GGTCTGGGCATAAACTCGCCGCTT	SHANK3 H2 5UTR(+370+394)
605	TGAGGTTCTGGGCATAAACTCGCCG	SHANK3 H2 5UTR(+373+397)
606	CGATGAGGTTCTGGGCATAAACTCG	SHANK3 H2 5UTR(+376+400)
607	CATCGATGAGGTTCTGGGCATAAAC	SHANK3 H2 5UTR(+379+403)
608	TATCATCGATGAGGTTCTGGGCATA	SHANK3 H2 5UTR(+382+406)
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610	ACTGCTTATCATCGATGAGGTTCTG	SHANK3 H2 5UTR(+388+412)
611	CAAAGCTTATCATCGATGAGGTT	SHANK3 H2 5UTR(+391+415)
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615	TGTGAAGCTTTCGAAAGCTTATC	SHANK3 H2 5UTR(+403+427)
616	TTGTGTGAAGCTTTCGAAAGCTT	SHANK3 H2 5UTR(+406+430)
617	CCTTGTGTGAAGCTTTCGAAAGCTG	SHANK3 H2:3 5UTR(+409+433)
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619	GGTTCGCCTTGTGTGAAGCTTTCG	SHANK3 H2:3 5UTR(+415+439)
620	TCAGGTTTCGCCTTGTGTGAAGCTT	SHANK3 H2:3 5UTR(+418+442)
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622	ACTTCTTCAGGTTTCGCCTTGTGTG	SHANK3 H2:3 5UTR(+424+448)
623	GGAGTGGGGGTGGGGCG	SHANK3 H22 3UTR(+593+609)
624	GCGGGAGTGGGGGTGGG	SHANK3 H22 3UTR(+596+612)
625	GGGGCGGGAGTGGGGGT	SHANK3 H22 3UTR(+599+615)
626	GCCGGGGCGGGAGTGGG	SHANK3 H22 3UTR(+602+618)
627	ACGGCCGGGGCGGGAGT	SHANK3 H22 3UTR(+605+621)
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631	TGCCGGCAGGGCACGGC	SHANK3 H22 3UTR(+617+633)
632	CCCTGCCGGCAGGGCAC	SHANK3 H22 3UTR(+620+636)
633	GGGCCCTGCCGGCAGGG	SHANK3 H22 3UTR(+623+639)
634	GGGGGGCCCTGCCGGCA	SHANK3 H22 3UTR(+626+642)

635	GGTGGGGGGCCCTGCCG	SHANK3 H22 3UTR(+629+645)
636	GGGGGTGGGGGGCCCTG	SHANK3 H22 3UTR(+632+648)
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659	GGACGATTCATGCAACA	SHANK3 H22 3UTR(+701+717)
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662	CAGCAAACAGGACGATT	SHANK3 H22 3UTR(+710+726)
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667	CGAGTCTCCGAGCAACA	SHANK3 H22 3UTR(+725+741)
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671	CAATGTACAGGGCGAGT	SHANK3 H22 3UTR(+737+753)
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674	GGCACTAAGCAATGTAC	SHANK3 H22 3UTR(+746+762)
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677	GCCGGTGAGGGCACTAA	SHANK3 H22 3UTR(+755+771)
678	GCGGCCGGTGAGGGCAC	SHANK3 H22 3UTR(+758+774)
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683	CGCTGGGTGGGCTGGGC	SHANK3 H22 3UTR(+773+789)
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686	CTGACTGTGCGCTGGGT	SHANK3 H22 3UTR(+782+798)
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692	CCCTGGTCCACGCCCTT	SHANK3 H22 3UTR(+800+816)
693	CCTCCCTGGTCCACGCC	SHANK3 H22 3UTR(+803+819)
694	CAGCCTCCCTGGTCCAC	SHANK3 H22 3UTR(+806+822)
695	CCCCAGCCTCCCTGGTC	SHANK3 H22 3UTR(+809+825)
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697	CTCCGCCCCAGCCTCC	SHANK3 H22 3UTR(+815+831)
698	CACCTCCCGCCCCAGCC	SHANK3 H22 3UTR(+818+834)
699	CGGCACCTCCCGCCCCA	SHANK3 H22 3UTR(+821+837)
700	CCCCGGCACCTCCCGCC	SHANK3 H22 3UTR(+824+840)
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703	GCACCCACCCCGGCA	SHANK3 H22 3UTR(+833+849)
704	AGGGCACCCACCCCG	SHANK3 H22 3UTR(+836+852)
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708	GGTGGTCACGCTAGGGC	SHANK3 H22 3UTR(+848+864)
709	GGAGGTGGTCACGCTAG	SHANK3 H22 3UTR(+851+867)
710	GAAGGAGGTGGTCACGC	SHANK3 H22 3UTR(+854+870)
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714	ACCAGGAGCTGCGAAGG	SHANK3 H22 3UTR(+866+882)
715	GCCACCAGGAGCTGCGA	SHANK3 H22 3UTR(+869+885)
716	ATGGCCACCAGGAGCTG	SHANK3 H22 3UTR(+872+888)
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1027	GGGCGCTGCCTCAAGG	SHANK3 H22 3UTR(+1805+1821)
1028	TGGGGGCGCTGCCTCCA	SHANK3 H22 3UTR(+1808+1824)
1029	AGGTGGGGGCGCTGCCT	SHANK3 H22 3UTR(+1811+1827)
1030	CCAAGGTGGGGGCGCTG	SHANK3 H22 3UTR(+1814+1830)

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1037	CCCTATGATGCCCTCAG	SHANK3 H22 3UTR(+1835+1851)
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1040	TAGGGGTCCCCCTATGA	SHANK3 H22 3UTR(+1844+1860)
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1042	TGACTCTAGGGGTCCCC	SHANK3 H22 3UTR(+1850+1866)
1043	AACTGACTCTAGGGGTC	SHANK3 H22 3UTR(+1853+1869)
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1045	GTGGTGAAGTACTCTA	SHANK3 H22 3UTR(+1859+1875)
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1056	ACCCTCGGGGTCTTTG	SHANK3 H22 3UTR(+1892+1908)
1057	GGCACCTCGGGGTCT	SHANK3 H22 3UTR(+1895+1911)
1058	CTGGGCACCTCGGGGG	SHANK3 H22 3UTR(+1898+1914)
1059	GGGCTGGGCACCTCGG	SHANK3 H22 3UTR(+1901+1917)
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1064	GAGTCACAGTGTGGGGG	SHANK3 H22 3UTR(+1916+1932)
1065	GAGGAGTCACAGTGTGG	SHANK3 H22 3UTR(+1919+1935)
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1069	ATCGCTGAGTGTGAGGA	SHANK3 H22 3UTR(+1931+1947)
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1071	CAGGTCATCGCTGAGTG	SHANK3 H22 3UTR(+1937+1953)
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1073	ACCCACAGGTCATCGC	SHANK3 H22 3UTR(+1943+1959)
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1075	CCCCCACCCACAGGT	SHANK3 H22 3UTR(+1949+1965)
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1098	GAAACTTGTGAGTGACG	SHANK3 H22 3UTR(+2018+2034)
1099	ACAGAACTTGTGAGTG	SHANK3 H22 3UTR(+2021+2037)
1100	TAAACAGAACTTGTGA	SHANK3 H22 3UTR(+2024+2040)
1101	ATATAACAGAACTTG	SHANK3 H22 3UTR(+2027+2043)
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1103	CTAGAAATATAAACAGA	SHANK3 H22 3UTR(+2033+2049)
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1107	TATTAaaaaaaAGCTAGA	SHANK3 H22 3UTR(+2045+2061)
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1114	GTTTCTTTTTTTTTTT	SHANK3 H22 3UTR(+2066+2082)
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1116	ACTTCTGTTTCTTTTT	SHANK3 H22 3UTR(+2072+2088)
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1119	GTTGTGAAAACCTCTGT	SHANK3 H22 3UTR(+2081+2097)
1120	TGGGTTGTGAAAACCTC	SHANK3 H22 3UTR(+2084+2100)
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1135	GGGCCAGGGCGGGGCGG	SHANK3 H22 3UTR(+2129+2145)
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1137	GCCGGTGGGCCAGGGCG	SHANK3 H22 3UTR(+2135+2151)
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1313	GACGATTCATGCAACATTCCTGGCC	SHANK3 H22 3UTR(+692+716)
1314	CAGGACGATTCATGCAACATTCCTG	SHANK3 H22 3UTR(+695+719)
1315	AAACAGGACGATTCATGCAACATTC	SHANK3 H22 3UTR(+698+722)
1316	AGCAAACAGGACGATTCATGCAACA	SHANK3 H22 3UTR(+701+725)
1317	AACAGCAAACAGGACGATTCATGCA	SHANK3 H22 3UTR(+704+728)
1318	AGCAAACAGCAAACAGGACGATTCAT	SHANK3 H22 3UTR(+707+731)

1319	CCGAGCAACAGCAAACAGGACGATT	SHANK3 H22 3UTR(+710+734)
1320	TCTCCGAGCAACAGCAAACAGGACG	SHANK3 H22 3UTR(+713+737)
1321	GAGTCTCCGAGCAACAGCAAACAGG	SHANK3 H22 3UTR(+716+740)
1322	GGCGAGTCTCCGAGCAACAGCAAAC	SHANK3 H22 3UTR(+719+743)
1323	CAGGGCGAGTCTCCGAGCAACAGCA	SHANK3 H22 3UTR(+722+746)
1324	GTACAGGGCGAGTCTCCGAGCAACA	SHANK3 H22 3UTR(+725+749)
1325	AATGTACAGGGCGAGTCTCCGAGCA	SHANK3 H22 3UTR(+728+752)
1326	AGCAATGTACAGGGCGAGTCTCCGA	SHANK3 H22 3UTR(+731+755)
1327	CTAAGCAATGTACAGGGCGAGTCTC	SHANK3 H22 3UTR(+734+758)
1328	GCACTAAGCAATGTACAGGGCGAGT	SHANK3 H22 3UTR(+737+761)
1329	AGGGCACTAAGCAATGTACAGGGCG	SHANK3 H22 3UTR(+740+764)
1330	GTGAGGGCACTAAGCAATGTACAGG	SHANK3 H22 3UTR(+743+767)
1331	CCGGTGAGGGCACTAAGCAATGTAC	SHANK3 H22 3UTR(+746+770)
1332	CGGCCGGTGAGGGCACTAAGCAATG	SHANK3 H22 3UTR(+749+773)
1333	GGGCGGCCGGTGAGGGCACTAAGCA	SHANK3 H22 3UTR(+752+776)
1334	GCTGGGCGGCCGGTGAGGGCACTAA	SHANK3 H22 3UTR(+755+779)
1335	TGGGCTGGGCGGCCGGTGAGGGCAC	SHANK3 H22 3UTR(+758+782)
1336	GGGTGGGCTGGGCGGCCGGTGAGGG	SHANK3 H22 3UTR(+761+785)
1337	GCTGGGTGGGCTGGGCGGCCGGTGGA	SHANK3 H22 3UTR(+764+788)
1338	TGCGCTGGGTGGGCTGGGCGGCCGG	SHANK3 H22 3UTR(+767+791)
1339	CTGTGCGCTGGGTGGGCTGGGCGGC	SHANK3 H22 3UTR(+770+794)
1340	TGACTGTGCGCTGGGTGGGCTGGGC	SHANK3 H22 3UTR(+773+797)
1341	TCCTGACTGTGCGCTGGGTGGGCTG	SHANK3 H22 3UTR(+776+800)
1342	CCTTCCTGACTGTGCGCTGGGTGGG	SHANK3 H22 3UTR(+779+803)
1343	CGCCCTTCCTGACTGTGCGCTGGGT	SHANK3 H22 3UTR(+782+806)
1344	CCACGCCCTTCCTGACTGTGCGCTG	SHANK3 H22 3UTR(+785+809)
1345	GGTCCACGCCCTTCCTGACTGTGCG	SHANK3 H22 3UTR(+788+812)
1346	CCTGGTCCACGCCCTTCCTGACTGT	SHANK3 H22 3UTR(+791+815)
1347	CTCCCTGGTCCACGCCCTTCCTGAC	SHANK3 H22 3UTR(+794+818)
1348	AGCCTCCCTGGTCCACGCCCTTCCT	SHANK3 H22 3UTR(+797+821)
1349	CCCAGCCTCCCTGGTCCACGCCCTT	SHANK3 H22 3UTR(+800+824)
1350	CGCCCCAGCCTCCCTGGTCCACGCC	SHANK3 H22 3UTR(+803+827)
1351	TCCCGCCCCAGCCTCCCTGGTCCAC	SHANK3 H22 3UTR(+806+830)
1352	ACCTCCCGCCCCAGCCTCCCTGGTC	SHANK3 H22 3UTR(+809+833)
1353	GGCACCTCCCGCCCCAGCCTCCCTG	SHANK3 H22 3UTR(+812+836)
1354	CCCGGCACCTCCCGCCCCAGCCTCC	SHANK3 H22 3UTR(+815+839)

1355	ACCCCCGGCACCTCCCGCCCCAGCC	SHANK3 H22 3UTR(+818+842)
1356	CCCACCCCCGGCACCTCCCGCCCCA	SHANK3 H22 3UTR(+821+845)
1357	CACCCACCCCCGGCACCTCCCGCC	SHANK3 H22 3UTR(+824+848)
1358	GGGCACCCACCCCCGGCACCTCCC	SHANK3 H22 3UTR(+827+851)
1359	CTAGGGCACCCACCCCCGGCACCT	SHANK3 H22 3UTR(+830+854)
1360	ACGCTAGGGCACCCACCCCCGGCA	SHANK3 H22 3UTR(+833+857)
1361	GTCACGCTAGGGCACCCACCCCCG	SHANK3 H22 3UTR(+836+860)
1362	GTGGTCACGCTAGGGCACCCACCC	SHANK3 H22 3UTR(+839+863)
1363	GAGGTGGTCACGCTAGGGCACCCCA	SHANK3 H22 3UTR(+842+866)
1364	AAGGAGGTGGTCACGCTAGGGCACCC	SHANK3 H22 3UTR(+845+869)
1365	GCGAAGGAGGTGGTCACGCTAGGGC	SHANK3 H22 3UTR(+848+872)
1366	GCTGCGAAGGAGGTGGTCACGCTAG	SHANK3 H22 3UTR(+851+875)
1367	GGAGCTGCGAAGGAGGTGGTCACGC	SHANK3 H22 3UTR(+854+878)
1368	CCAGGAGCTGCGAAGGAGGTGGTCA	SHANK3 H22 3UTR(+857+881)
1369	CCACCAGGAGCTGCGAAGGAGGTGG	SHANK3 H22 3UTR(+860+884)
1370	TGGCCACCAGGAGCTGCGAAGGAGG	SHANK3 H22 3UTR(+863+887)
1371	GAATGGCCACCAGGAGCTGCGAAGG	SHANK3 H22 3UTR(+866+890)
1372	GGAGAATGGCCACCAGGAGCTGCGA	SHANK3 H22 3UTR(+869+893)
1373	CTGGGAGAATGGCCACCAGGAGCTG	SHANK3 H22 3UTR(+872+896)
1374	CCTCTGGGAGAATGGCCACCAGGAG	SHANK3 H22 3UTR(+875+899)
1375	CCCCCTCTGGGAGAATGGCCACCAG	SHANK3 H22 3UTR(+878+902)
1376	GTTCCCCCTCTGGGAGAATGGCCAC	SHANK3 H22 3UTR(+881+905)
1377	TAGGTTCCCCCTCTGGGAGAATGGC	SHANK3 H22 3UTR(+884+908)
1378	GA TAGGTTCCCCCTCTGGGAGAAT	SHANK3 H22 3UTR(+887+911)
1379	CTGGACTAGGTTCCCCCTCTGGGAG	SHANK3 H22 3UTR(+890+914)
1380	ATGCTGGACTAGGTTCCCCCTCTGG	SHANK3 H22 3UTR(+893+917)
1381	CGCATGCTGGACTAGGTTCCCCCTC	SHANK3 H22 3UTR(+896+920)
1382	CCTCGCATGCTGGACTAGGTTCCCC	SHANK3 H22 3UTR(+899+923)
1383	TGACCTCGCATGCTGGACTAGGTTTC	SHANK3 H22 3UTR(+902+926)
1384	TCCTGACCTCGCATGCTGGACTAGG	SHANK3 H22 3UTR(+905+929)
1385	GGGTCTGACCTCGCATGCTGGACT	SHANK3 H22 3UTR(+908+932)
1386	GGCGGGTCTGACCTCGCATGCTGG	SHANK3 H22 3UTR(+911+935)
1387	CAAGGCGGGTCTGACCTCGCATGC	SHANK3 H22 3UTR(+914+938)
1388	CACCAAGGCGGGTCTGACCTCGCA	SHANK3 H22 3UTR(+917+941)
1389	AGTCACCAAGGCGGGTCTGACCTC	SHANK3 H22 3UTR(+920+944)
1390	CCGAGTCACCAAGGCGGGTCTGAC	SHANK3 H22 3UTR(+923+947)

1391	CCCCCGAGTCACCAAGGCGGGTCCT	SHANK3 H22 3UTR(+926+950)
1392	CTCCCCCGAGTCACCAAGGCGGGT	SHANK3 H22 3UTR(+929+953)
1393	CCCCTCCCCCGAGTCACCAAGGCG	SHANK3 H22 3UTR(+932+956)
1394	TCCCCCTCCCCCGAGTCACCAAG	SHANK3 H22 3UTR(+935+959)
1395	GTCTCCCCCTCCCCCGAGTCACC	SHANK3 H22 3UTR(+938+962)
1396	AATGTCTCCCCCTCCCCCGAGTC	SHANK3 H22 3UTR(+941+965)
1397	CCCAATGTCTCCCCCTCCCCCGA	SHANK3 H22 3UTR(+944+968)
1398	AATCCAATGTCTCCCCCTCCCC	SHANK3 H22 3UTR(+947+971)
1399	GAGAATCCAATGTCTCCCCCTCC	SHANK3 H22 3UTR(+950+974)
1400	ATCGAGAATCCAATGTCTCCCC	SHANK3 H22 3UTR(+953+977)
1401	CCCATCGAGAATCCAATGTCTCC	SHANK3 H22 3UTR(+956+980)
1402	GCCCCATCGAGAATCCAATGTCT	SHANK3 H22 3UTR(+959+983)
1403	TTGGCCCCCATCGAGAATCCAATG	SHANK3 H22 3UTR(+962+986)
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1405	GGCTCCTTGGCCCCCATCGAATC	SHANK3 H22 3UTR(+968+992)
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1407	CAGGGGGGCTCCTTGGCCCCCATCG	SHANK3 H22 3UTR(+974+998)
1408	AAACAGGGGGGCTCCTTGGCCCCCA	SHANK3 H22 3UTR(+977+1001)
1409	GCAAAACAGGGGGGCTCCTTGGCCC	SHANK3 H22 3UTR(+980+1004)
1410	TATGCAAAACAGGGGGGCTCCTTGG	SHANK3 H22 3UTR(+983+1007)
1411	AAATATGCAAAACAGGGGGGCTCCT	SHANK3 H22 3UTR(+986+1010)
1412	TTAAAATATGCAAAACAGGGGGGCT	SHANK3 H22 3UTR(+989+1013)
1413	GGATTAATATGCAAAACAGGGGGG	SHANK3 H22 3UTR(+992+1016)
1414	AGTGGATTAATATGCAAAACAGG	SHANK3 H22 3UTR(+995+1019)
1415	TAGAGTGGATTAATATGCAAAAC	SHANK3 H22 3UTR(+998+1022)
1416	ATATAGAGTGGATTAATATGCAA	SHANK3 H22 3UTR(+1001+1025)
1417	CAAATATAGAGTGGATTAATATG	SHANK3 H22 3UTR(+1004+1028)
1418	TTCAAATATAGAGTGGATTAAT	SHANK3 H22 3UTR(+1007+1031)
1419	TCGTTCAAATATAGAGTGGATTAA	SHANK3 H22 3UTR(+1010+1034)
1420	TTCTCGTTCAAATATAGAGTGGAT	SHANK3 H22 3UTR(+1013+1037)
1421	CTTTTCTCGTTCAAATATAGAGTG	SHANK3 H22 3UTR(+1016+1040)
1422	TTCCTTTTCTCGTTCAAATATAGA	SHANK3 H22 3UTR(+1019+1043)
1423	TTGTTCTTTTCTCGTTCAAATAT	SHANK3 H22 3UTR(+1022+1046)
1424	TATTTGTTCTTTTCTCGTTCCAAA	SHANK3 H22 3UTR(+1025+1049)
1425	AGATATTTGTTCTTTTCTCGTTCC	SHANK3 H22 3UTR(+1028+1052)
1426	CAGAGATATTTGTTCTTTTCTCGT	SHANK3 H22 3UTR(+1031+1055)

1427	GGACAGAGATATTTGTTCTTTTCT	SHANK3 H22 3UTR(+1034+1058)
1428	TACGGACAGAGATATTTGTTCTTT	SHANK3 H22 3UTR(+1037+1061)
1429	TATTACGGACAGAGATATTTGTTCC	SHANK3 H22 3UTR(+1040+1064)
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1431	GGAAACTATTACGGACAGAGATATT	SHANK3 H22 3UTR(+1046+1070)
1432	AGAGGAACTATTACGGACAGAGAT	SHANK3 H22 3UTR(+1049+1073)
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1434	GAGGGGAGAGGAACTATTACGGAC	SHANK3 H22 3UTR(+1055+1079)
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1442	AGTGGGACCAAGTGAAGTAGAAGGG	SHANK3 H22 3UTR(+1079+1103)
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1444	AGCTGCAGTGGGACCAAGTGAAGTA	SHANK3 H22 3UTR(+1085+1109)
1445	GGCAGCTGCAGTGGGACCAAGTGAA	SHANK3 H22 3UTR(+1088+1112)
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1451	GCCGGAGATGGAAGACTGGGCAGCT	SHANK3 H22 3UTR(+1106+1130)
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1453	TGAGGGGCCGGAGATGGAAGACTGG	SHANK3 H22 3UTR(+1112+1136)
1454	CAGTGAGGGGCCGGAGATGGAAGAC	SHANK3 H22 3UTR(+1115+1139)
1455	TGGCAGTGAGGGGCCGGAGATGGAA	SHANK3 H22 3UTR(+1118+1142)
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1460	GTTGTGGGGTGGCAGTGGCAGTGAG	SHANK3 H22 3UTR(+1133+1157)
1461	CCCGTTGTGGGGTGGCAGTGGCAGT	SHANK3 H22 3UTR(+1136+1160)
1462	TGCCCCGTTGTGGGGTGGCAGTGGC	SHANK3 H22 3UTR(+1139+1163)

1463	CCCTGCCCCGTTGTGGGGTGGCAGT	SHANK3 H22 3UTR(+1142+1166)
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1465	AGCGTCCCCTGCCCCGTTGTGGGGT	SHANK3 H22 3UTR(+1148+1172)
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1468	ACCAGCTGGAGCGTCCCCTGCCCCG	SHANK3 H22 3UTR(+1157+1181)
1469	CAGACCAGCTGGAGCGTCCCCTGCC	SHANK3 H22 3UTR(+1160+1184)
1470	CCCCAGACCAGCTGGAGCGTCCCCT	SHANK3 H22 3UTR(+1163+1187)
1471	CAACCCAGACCAGCTGGAGCGTCC	SHANK3 H22 3UTR(+1166+1190)
1472	GGCCAACCCAGACCAGCTGGAGCG	SHANK3 H22 3UTR(+1169+1193)
1473	CCTGGCCAACCCAGACCAGCTGGA	SHANK3 H22 3UTR(+1172+1196)
1474	GGCCCTGGCCAACCCAGACCAGCT	SHANK3 H22 3UTR(+1175+1199)
1475	TAGGGCCCTGGCCAACCCAGACCA	SHANK3 H22 3UTR(+1178+1202)
1476	CACTAGGGCCCTGGCCAACCCAGA	SHANK3 H22 3UTR(+1181+1205)
1477	GGCCACTAGGGCCCTGGCCAACCC	SHANK3 H22 3UTR(+1184+1208)
1478	GCGGGCCACTAGGGCCCTGGCCAAC	SHANK3 H22 3UTR(+1187+1211)
1479	AGGGCGGGCCACTAGGGCCCTGGCC	SHANK3 H22 3UTR(+1190+1214)
1480	CCCAGGGCGGGCCACTAGGGCCCTG	SHANK3 H22 3UTR(+1193+1217)
1481	GGCCCCAGGGCGGGCCACTAGGGCC	SHANK3 H22 3UTR(+1196+1220)
1482	TGGGGCCCCAGGGCGGGCCACTAGG	SHANK3 H22 3UTR(+1199+1223)
1483	AGCTGGGGCCCCAGGGCGGGCCACT	SHANK3 H22 3UTR(+1202+1226)
1484	CCGAGCTGGGGCCCCAGGGCGGGCC	SHANK3 H22 3UTR(+1205+1229)
1485	GGGCCGAGCTGGGGCCCCAGGGCGG	SHANK3 H22 3UTR(+1208+1232)
1486	GAGGGGCCGAGCTGGGGCCCCAGGG	SHANK3 H22 3UTR(+1211+1235)
1487	GGCGAGGGGCCGAGCTGGGGCCCCA	SHANK3 H22 3UTR(+1214+1238)
1488	CGAGGCGAGGGGCCGAGCTGGGGCC	SHANK3 H22 3UTR(+1217+1241)
1489	CAGCGAGGCGAGGGGCCGAGCTGGG	SHANK3 H22 3UTR(+1220+1244)
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1492	ACTAGAGCTCAGCGAGGCGAGGGGC	SHANK3 H22 3UTR(+1229+1253)
1493	CACACTAGAGCTCAGCGAGGCGAGG	SHANK3 H22 3UTR(+1232+1256)
1494	GGGCACACTAGAGCTCAGCGAGGCG	SHANK3 H22 3UTR(+1235+1259)
1495	GTGGGGCACACTAGAGCTCAGCGAG	SHANK3 H22 3UTR(+1238+1262)
1496	TCGGTGGGGCACACTAGAGCTCAGC	SHANK3 H22 3UTR(+1241+1265)
1497	GGGTCGGTGGGGCACACTAGAGCTC	SHANK3 H22 3UTR(+1244+1268)
1498	GAAGGGTCGGTGGGGCACACTAGAG	SHANK3 H22 3UTR(+1247+1271)

1499	CCTGAAGGGTCGGTGGGGCACACTA	SHANK3 H22 3UTR(+1250+1274)
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1501	GCAGCACCTGAAGGGTCGGTGGGGC	SHANK3 H22 3UTR(+1256+1280)
1502	CGAGCAGCACCTGAAGGGTCGGTGG	SHANK3 H22 3UTR(+1259+1283)
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1504	CCACCACGAGCAGCACCTGAAGGGT	SHANK3 H22 3UTR(+1265+1289)
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1510	CGCGGCTGCCGCCCTCCCACCAC	SHANK3 H22 3UTR(+1283+1307)
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1512	AGGACCCGCGGCTGCCGCCCTCC	SHANK3 H22 3UTR(+1289+1313)
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1515	GTGCACAGCAGGACCCGCGGCTGC	SHANK3 H22 3UTR(+1298+1322)
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1517	CCGCGGGTGCACAGCAGGACCCGCG	SHANK3 H22 3UTR(+1304+1328)
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1522	CCAGGCCGGCTGGTCCCGCGGGTGC	SHANK3 H22 3UTR(+1319+1343)
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1524	GGTCTCCAGGCCGGCTGGTCCCGC	SHANK3 H22 3UTR(+1325+1349)
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1526	GCCGATGGTCTCCAGGCCGGCTGG	SHANK3 H22 3UTR(+1331+1355)
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1535	GGCAGGGCCCTGCCCTCATCCCCC	SHANK3 H22 3UTR(+1358+1382)
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1537	TGGAGCGGCAGGGCCCTGCCCTCAT	SHANK3 H22 3UTR(+1364+1388)
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1542	GGAAGATGGCTGCGGTGGAGCGGCA	SHANK3 H22 3UTR(+1379+1403)
1543	TGAGGAAGATGGCTGCGGTGGAGCG	SHANK3 H22 3UTR(+1382+1406)
1544	CTGTGAGGAAGATGGCTGCGGTGGA	SHANK3 H22 3UTR(+1385+1409)
1545	ACCCTGTGAGGAAGATGGCTGCGGT	SHANK3 H22 3UTR(+1388+1412)
1546	GAGACCCTGTGAGGAAGATGGCTGC	SHANK3 H22 3UTR(+1391+1415)
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1550	CCTCCTTGGGGAGAGACCCTGTGAG	SHANK3 H22 3UTR(+1403+1427)
1551	CCCCCTCCTTGGGGAGAGACCCTGT	SHANK3 H22 3UTR(+1406+1430)
1552	TAGCCCCCTCCTTGGGGAGAGACCC	SHANK3 H22 3UTR(+1409+1433)
1553	AGCTAGCCCCCTCCTTGGGGAGAGA	SHANK3 H22 3UTR(+1412+1436)
1554	CCAAGCTAGCCCCCTCCTTGGGGAG	SHANK3 H22 3UTR(+1415+1439)
1555	GGACCAAGCTAGCCCCCTCCTTGGG	SHANK3 H22 3UTR(+1418+1442)
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1558	AGAGCATGGGGACCAAGCTAGCCCC	SHANK3 H22 3UTR(+1427+1451)
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1562	TGTAGTTGCCCAAGAGCATGGGGAC	SHANK3 H22 3UTR(+1439+1463)
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1564	CTCTGCTGTAGTTGCCCAAGAGCAT	SHANK3 H22 3UTR(+1445+1469)
1565	CTTCTCTGCTGTAGTTGCCCAAGAG	SHANK3 H22 3UTR(+1448+1472)
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1567	GGGAGGCTTCTCTGCTGTAGTTGCC	SHANK3 H22 3UTR(+1454+1478)
1568	GCAGGGAGGCTTCTCTGCTGTAGTT	SHANK3 H22 3UTR(+1457+1481)
1569	AAGGCAGGGAGGCTTCTCTGCTGTA	SHANK3 H22 3UTR(+1460+1484)
1570	TCCAAGGCAGGGAGGCTTCTCTGCT	SHANK3 H22 3UTR(+1463+1487)

1571	GGGTCCAAGGCAGGGAGGCTTCTCT	SHANK3 H22 3UTR(+1466+1490)
1572	TTGGGGTCCAAGGCAGGGAGGCTTC	SHANK3 H22 3UTR(+1469+1493)
1573	ACTTTGGGGTCCAAGGCAGGGAGGC	SHANK3 H22 3UTR(+1472+1496)
1574	GAGACTTTGGGGTCCAAGGCAGGGA	SHANK3 H22 3UTR(+1475+1499)
1575	CAGGAGACTTTGGGGTCCAAGGCAG	SHANK3 H22 3UTR(+1478+1502)
1576	GGACAGGAGACTTTGGGGTCCAAGG	SHANK3 H22 3UTR(+1481+1505)
1577	GCAGGACAGGAGACTTTGGGGTCCA	SHANK3 H22 3UTR(+1484+1508)
1578	AGGGCAGGACAGGAGACTTTGGGGT	SHANK3 H22 3UTR(+1487+1511)
1579	TAAAGGGCAGGACAGGAGACTTTGG	SHANK3 H22 3UTR(+1490+1514)
1580	ACATAAAGGGCAGGACAGGAGACTT	SHANK3 H22 3UTR(+1493+1517)
1581	CACACATAAAGGGCAGGACAGGAGA	SHANK3 H22 3UTR(+1496+1520)
1582	CCACACACATAAAGGGCAGGACAGG	SHANK3 H22 3UTR(+1499+1523)
1583	CACCCACACACATAAAGGGCAGGAC	SHANK3 H22 3UTR(+1502+1526)
1584	TTTCACCCACACACATAAAGGGCAG	SHANK3 H22 3UTR(+1505+1529)
1585	CAGTTTCACCCACACACATAAAGGG	SHANK3 H22 3UTR(+1508+1532)
1586	ACCCAGTTTCACCCACACACATAAA	SHANK3 H22 3UTR(+1511+1535)
1587	CGCACCCAGTTTCACCCACACACAT	SHANK3 H22 3UTR(+1514+1538)
1588	AGACGCACCCAGTTTCACCCACACA	SHANK3 H22 3UTR(+1517+1541)
1589	CTCAGACGCACCCAGTTTCACCCAC	SHANK3 H22 3UTR(+1520+1544)
1590	GTGCTCAGACGCACCCAGTTTCACC	SHANK3 H22 3UTR(+1523+1547)
1591	CACGTGCTCAGACGCACCCAGTTTC	SHANK3 H22 3UTR(+1526+1550)
1592	TCCACGTGCTCAGACGCACCCAGT	SHANK3 H22 3UTR(+1529+1553)
1593	GGTCCCACGTGCTCAGACGCACCC	SHANK3 H22 3UTR(+1532+1556)
1594	CACGGCTCCCACGTGCTCAGACGCA	SHANK3 H22 3UTR(+1535+1559)
1595	ACACACGGCTCCCACGTGCTCAGAC	SHANK3 H22 3UTR(+1538+1562)
1596	CACACACACGGCTCCCACGTGCTCA	SHANK3 H22 3UTR(+1541+1565)
1597	AGGCACACACACGGCTCCCACGTGC	SHANK3 H22 3UTR(+1544+1568)
1598	ATCAGGCACACACACGGCTCCCACG	SHANK3 H22 3UTR(+1547+1571)
1599	GTAATCAGGCACACACACGGCTCCC	SHANK3 H22 3UTR(+1550+1574)
1600	TCAGTAATCAGGCACACACACGGCT	SHANK3 H22 3UTR(+1553+1577)
1601	CACTCAGTAATCAGGCACACACACG	SHANK3 H22 3UTR(+1556+1580)
1602	GGCCACTCAGTAATCAGGCACACAC	SHANK3 H22 3UTR(+1559+1583)
1603	GGTGGCCACTCAGTAATCAGGCACA	SHANK3 H22 3UTR(+1562+1586)
1604	CCTGGTGGCCACTCAGTAATCAGGC	SHANK3 H22 3UTR(+1565+1589)
1605	GCCCCTGGTGGCCACTCAGTAATCA	SHANK3 H22 3UTR(+1568+1592)
1606	GCGGCCCTGGTGGCCACTCAGTAA	SHANK3 H22 3UTR(+1571+1595)

1607	AGAGCGGCCCCCTGGTGGCCACTCAG	SHANK3 H22 3UTR(+1574+1598)
1608	TCCAGAGCGGCCCCCTGGTGGCCACT	SHANK3 H22 3UTR(+1577+1601)
1609	TAGTCCAGAGCGGCCCCCTGGTGGCC	SHANK3 H22 3UTR(+1580+1604)
1610	CGCTAGTCCAGAGCGGCCCCCTGGTG	SHANK3 H22 3UTR(+1583+1607)
1611	CCGCGCTAGTCCAGAGCGGCCCCCTG	SHANK3 H22 3UTR(+1586+1610)
1612	GCCCCGCGCTAGTCCAGAGCGGCCC	SHANK3 H22 3UTR(+1589+1613)
1613	ACGGCCCCGCGCTAGTCCAGAGCGG	SHANK3 H22 3UTR(+1592+1616)
1614	TCCACGGCCCCGCGCTAGTCCAGAG	SHANK3 H22 3UTR(+1595+1619)
1615	GCCTCCACGGCCCCGCGCTAGTCCA	SHANK3 H22 3UTR(+1598+1622)
1616	CACGCCTCCACGGCCCCGCGCTAGT	SHANK3 H22 3UTR(+1601+1625)
1617	GTGCACGCCTCCACGGCCCCGCGCT	SHANK3 H22 3UTR(+1604+1628)
1618	ACGGTGACGCCTCCACGGCCCCGC	SHANK3 H22 3UTR(+1607+1631)
1619	CACACGGTGACGCCTCCACGGCCC	SHANK3 H22 3UTR(+1610+1634)
1620	ATGCACACGGTGACGCCTCCACGG	SHANK3 H22 3UTR(+1613+1637)
1621	CGCATGCACACGGTGACGCCTCCA	SHANK3 H22 3UTR(+1616+1640)
1622	CCACGCATGCACACGGTGACGCCT	SHANK3 H22 3UTR(+1619+1643)
1623	ACCCACGCATGCACACGGTGACG	SHANK3 H22 3UTR(+1622+1646)
1624	TACACCCACGCATGCACACGGTGC	SHANK3 H22 3UTR(+1625+1649)
1625	AGGTACACCCACGCATGCACACGG	SHANK3 H22 3UTR(+1628+1652)
1626	CACAGGTACACCCACGCATGCACA	SHANK3 H22 3UTR(+1631+1655)
1627	TCTCACAGGTACACCCACGCATGC	SHANK3 H22 3UTR(+1634+1658)
1628	TGCTCTCACAGGTACACCCACGCA	SHANK3 H22 3UTR(+1637+1661)
1629	GGGTGCTCTCACAGGTACACCCAC	SHANK3 H22 3UTR(+1640+1664)
1630	ACAGGGTGCTCTCACAGGTACACC	SHANK3 H22 3UTR(+1643+1667)
1631	GAGACAGGGTGCTCTCACAGGTACA	SHANK3 H22 3UTR(+1646+1670)
1632	GAGGAGACAGGGTGCTCTCACAGGT	SHANK3 H22 3UTR(+1649+1673)
1633	GAAGAGGAGACAGGGTGCTCACA	SHANK3 H22 3UTR(+1652+1676)
1634	TTGGAAGAGGAGACAGGGTGCTCTC	SHANK3 H22 3UTR(+1655+1679)
1635	TCTTTGGAAGAGGAGACAGGGTGCT	SHANK3 H22 3UTR(+1658+1682)
1636	CTTTCTTTGGAAGAGGAGACAGGGT	SHANK3 H22 3UTR(+1661+1685)
1637	TGACTTTCTTTGGAAGAGGAGACAG	SHANK3 H22 3UTR(+1664+1688)
1638	CTCTGACTTTCTTTGGAAGAGGAGA	SHANK3 H22 3UTR(+1667+1691)
1639	GGCCTCTGACTTTCTTTGGAAGAGG	SHANK3 H22 3UTR(+1670+1694)
1640	GATGGCCTCTGACTTTCTTTGGAAG	SHANK3 H22 3UTR(+1673+1697)
1641	CAGGATGGCCTCTGACTTTCTTTGG	SHANK3 H22 3UTR(+1676+1700)
1642	GTGCAGGATGGCCTCTGACTTTCTT	SHANK3 H22 3UTR(+1679+1703)

1643	AGGGTGCAGGATGGCCTCTGACTTT	SHANK3 H22 3UTR(+1682+1706)
1644	CCCAGGGTGCAGGATGGCCTCTGAC	SHANK3 H22 3UTR(+1685+1709)
1645	GGACCCAGGGTGCAGGATGGCCTCT	SHANK3 H22 3UTR(+1688+1712)
1646	GCTGGACCCAGGGTGCAGGATGGCC	SHANK3 H22 3UTR(+1691+1715)
1647	ACAGCTGGACCCAGGGTGCAGGATG	SHANK3 H22 3UTR(+1694+1718)
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1649	GGGCAAACAGCTGGACCCAGGGTGC	SHANK3 H22 3UTR(+1700+1724)
1650	GCTGGGCAAACAGCTGGACCCAGGG	SHANK3 H22 3UTR(+1703+1727)
1651	CAGGCTGGGCAAACAGCTGGACCCA	SHANK3 H22 3UTR(+1706+1730)
1652	GGACAGGCTGGGCAAACAGCTGGAC	SHANK3 H22 3UTR(+1709+1733)
1653	GAAGGACAGGCTGGGCAAACAGCTG	SHANK3 H22 3UTR(+1712+1736)
1654	CTGGAAGGACAGGCTGGGCAAACAG	SHANK3 H22 3UTR(+1715+1739)
1655	GCTCTGGAAGGACAGGCTGGGCAAA	SHANK3 H22 3UTR(+1718+1742)
1656	GAGGCTCTGGAAGGACAGGCTGGGC	SHANK3 H22 3UTR(+1721+1745)
1657	GGTGAGGCTCTGGAAGGACAGGCTG	SHANK3 H22 3UTR(+1724+1748)
1658	CTGGGTGAGGCTCTGGAAGGACAGG	SHANK3 H22 3UTR(+1727+1751)
1659	AGGCTGGGTGAGGCTCTGGAAGGAC	SHANK3 H22 3UTR(+1730+1754)
1660	CTCAGGCTGGGTGAGGCTCTGGAAG	SHANK3 H22 3UTR(+1733+1757)
1661	CCGCTCAGGCTGGGTGAGGCTCTGG	SHANK3 H22 3UTR(+1736+1760)
1662	ACCCCGCTCAGGCTGGGTGAGGCTC	SHANK3 H22 3UTR(+1739+1763)
1663	GGAACCCGCTCAGGCTGGGTGAGG	SHANK3 H22 3UTR(+1742+1766)
1664	CAGGGAACCCCGCTCAGGCTGGGTG	SHANK3 H22 3UTR(+1745+1769)
1665	CACCAGGGAACCCGCTCAGGCTGG	SHANK3 H22 3UTR(+1748+1772)
1666	ATTCACCAGGGAACCCGCTCAGGC	SHANK3 H22 3UTR(+1751+1775)
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1669	GCAGCAGGGATTACACAGGGAACCC	SHANK3 H22 3UTR(+1760+1784)
1670	CAAGCAGCAGGGATTACACAGGGAA	SHANK3 H22 3UTR(+1763+1787)
1671	CCCCAAGCAGCAGGGATTACACAGG	SHANK3 H22 3UTR(+1766+1790)
1672	CCTCCCAAGCAGCAGGGATTACAC	SHANK3 H22 3UTR(+1769+1793)
1673	GGGCCTCCCAAGCAGCAGGGATTTC	SHANK3 H22 3UTR(+1772+1796)
1674	TTGGGGCCTCCCAAGCAGCAGGGA	SHANK3 H22 3UTR(+1775+1799)
1675	CCCTTGGGGCCTCCCAAGCAGCAG	SHANK3 H22 3UTR(+1778+1802)
1676	GGGCCCTTGGGGCCTCCCAAGCAG	SHANK3 H22 3UTR(+1781+1805)
1677	AAGGGGCCCTTGGGGCCTCCCAAG	SHANK3 H22 3UTR(+1784+1808)
1678	TCCAAGGGGCCCTTGGGGCCTCCCC	SHANK3 H22 3UTR(+1787+1811)

1679	GCCTCCAAGGGGCCCTTGGGGCCTC	SHANK3 H22 3UTR(+1790+1814)
1680	GCTGCCTCCAAGGGGCCCTTGGGGC	SHANK3 H22 3UTR(+1793+1817)
1681	GGCGCTGCCTCCAAGGGGCCCTTGG	SHANK3 H22 3UTR(+1796+1820)
1682	GGGGGCGCTGCCTCCAAGGGGCCCT	SHANK3 H22 3UTR(+1799+1823)
1683	GGTGGGGGCGCTGCCTCCAAGGGGC	SHANK3 H22 3UTR(+1802+1826)
1684	CAAGGTGGGGGCGCTGCCTCCAAGG	SHANK3 H22 3UTR(+1805+1829)
1685	GCCCAAGGTGGGGGCGCTGCCTCCA	SHANK3 H22 3UTR(+1808+1832)
1686	GAAGCCCAAGGTGGGGGCGCTGCCT	SHANK3 H22 3UTR(+1811+1835)
1687	TCAGAAGCCCAAGGTGGGGGCGCTG	SHANK3 H22 3UTR(+1814+1838)
1688	CCCTCAGAAGCCCAAGGTGGGGGCG	SHANK3 H22 3UTR(+1817+1841)
1689	ATGCCCTCAGAAGCCCAAGGTGGGG	SHANK3 H22 3UTR(+1820+1844)
1690	ATGATGCCCTCAGAAGCCCAAGGTG	SHANK3 H22 3UTR(+1823+1847)
1691	CCTATGATGCCCTCAGAAGCCCAAG	SHANK3 H22 3UTR(+1826+1850)
1692	CCCCCTATGATGCCCTCAGAAGCCC	SHANK3 H22 3UTR(+1829+1853)
1693	GGTCCCCCTATGATGCCCTCAGAAG	SHANK3 H22 3UTR(+1832+1856)
1694	AGGGGTCCCCCTATGATGCCCTCAG	SHANK3 H22 3UTR(+1835+1859)
1695	TCTAGGGGTCCCCCTATGATGCCCT	SHANK3 H22 3UTR(+1838+1862)
1696	GACTCTAGGGGTCCCCCTATGATGC	SHANK3 H22 3UTR(+1841+1865)
1697	ACTGACTCTAGGGGTCCCCCTATGA	SHANK3 H22 3UTR(+1844+1868)
1698	TGAACTGACTCTAGGGGTCCCCCTA	SHANK3 H22 3UTR(+1847+1871)
1699	TGGTGAAGTACTCTAGGGGTCCCC	SHANK3 H22 3UTR(+1850+1874)
1700	CTGTGGTGAAGTACTCTAGGGGTCT	SHANK3 H22 3UTR(+1853+1877)
1701	GGCCTGTGGTGAAGTACTCTAGGG	SHANK3 H22 3UTR(+1856+1880)
1702	CAGGGCCTGTGGTGAAGTACTCTA	SHANK3 H22 3UTR(+1859+1883)
1703	CCCCAGGGCCTGTGGTGAAGTACT	SHANK3 H22 3UTR(+1862+1886)
1704	TCTCCCAGGGCCTGTGGTGAAGT	SHANK3 H22 3UTR(+1865+1889)
1705	GACTCTCCCAGGGCCTGTGGTGAA	SHANK3 H22 3UTR(+1868+1892)
1706	TTTGACTCTCCCAGGGCCTGTGGT	SHANK3 H22 3UTR(+1871+1895)
1707	GTCTTTGACTCTCCCAGGGCCTGT	SHANK3 H22 3UTR(+1874+1898)
1708	GGGGTCTTTGACTCTCCCAGGGCC	SHANK3 H22 3UTR(+1877+1901)
1709	TCGGGGGTCTTTGACTCTCCCAGG	SHANK3 H22 3UTR(+1880+1904)
1710	CCCTCGGGGTCTTTGACTCTCCCC	SHANK3 H22 3UTR(+1883+1907)
1711	GCACCCTCGGGGTCTTTGACTCTC	SHANK3 H22 3UTR(+1886+1910)
1712	TGGGCACCCTCGGGGTCTTTGACT	SHANK3 H22 3UTR(+1889+1913)
1713	GGCTGGGCACCCTCGGGGTCTTTG	SHANK3 H22 3UTR(+1892+1916)
1714	GGGGGCTGGGCACCCTCGGGGTCT	SHANK3 H22 3UTR(+1895+1919)

1715	GTGGGGGGCTGGGCACCCTCGGGGG	SHANK3 H22 3UTR(+1898+1922)
1716	AGTGTGGGGGGCTGGGCACCCTCGG	SHANK3 H22 3UTR(+1901+1925)
1717	CACAGTGTGGGGGGCTGGGCACCCT	SHANK3 H22 3UTR(+1904+1928)
1718	AGTCACAGTGTGGGGGGCTGGGCAC	SHANK3 H22 3UTR(+1907+1931)
1719	AGGAGTCACAGTGTGGGGGGCTGGG	SHANK3 H22 3UTR(+1910+1934)
1720	GTGAGGAGTCACAGTGTGGGGGGCT	SHANK3 H22 3UTR(+1913+1937)
1721	AGTGTGAGGAGTCACAGTGTGGGGG	SHANK3 H22 3UTR(+1916+1940)
1722	CTGAGTGTGAGGAGTCACAGTGTGG	SHANK3 H22 3UTR(+1919+1943)
1723	TCGCTGAGTGTGAGGAGTCACAGTG	SHANK3 H22 3UTR(+1922+1946)
1724	TCATCGCTGAGTGTGAGGAGTCACA	SHANK3 H22 3UTR(+1925+1949)
1725	AGGTCATCGCTGAGTGTGAGGAGTC	SHANK3 H22 3UTR(+1928+1952)
1726	CACAGGTCATCGCTGAGTGTGAGGA	SHANK3 H22 3UTR(+1931+1955)
1727	CCCCACAGGTCATCGCTGAGTGTGA	SHANK3 H22 3UTR(+1934+1958)
1728	CCACCCACAGGTCATCGCTGAGTG	SHANK3 H22 3UTR(+1937+1961)
1729	CCCCACCCACAGGTCATCGCTGA	SHANK3 H22 3UTR(+1940+1964)
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1731	CAGGGCCCCCACCCACAGGTCAT	SHANK3 H22 3UTR(+1946+1970)
1732	TCCCAGGGCCCCCACCCACAGGT	SHANK3 H22 3UTR(+1949+1973)
1733	ACGTCCCAGGGCCCCCACCCACA	SHANK3 H22 3UTR(+1952+1976)
1734	AAAACGTCCCAGGGCCCCCACCCC	SHANK3 H22 3UTR(+1955+1979)
1735	TTAAAAACGTCCCAGGGCCCCCAC	SHANK3 H22 3UTR(+1958+1982)
1736	GGTTTAAAAACGTCCCAGGGCCCC	SHANK3 H22 3UTR(+1961+1985)
1737	CTAGGTTTAAAAACGTCCCAGGGCC	SHANK3 H22 3UTR(+1964+1988)
1738	ACCCTAGGTTTAAAAACGTCCCAGG	SHANK3 H22 3UTR(+1967+1991)
1739	CAAACCTAGGTTTAAAAACGTCCC	SHANK3 H22 3UTR(+1970+1994)
1740	CTCCAAACCCTAGGTTTAAAAACGT	SHANK3 H22 3UTR(+1973+1997)
1741	AGACTCCAAACCCTAGGTTTAAAAA	SHANK3 H22 3UTR(+1976+2000)
1742	TCCAGACTCCAAACCCTAGGTTTAA	SHANK3 H22 3UTR(+1979+2003)
1743	TAGTCCAGACTCCAAACCCTAGGTT	SHANK3 H22 3UTR(+1982+2006)
1744	GCTTAGTCCAGACTCCAAACCCTAG	SHANK3 H22 3UTR(+1985+2009)
1745	GGAGCTTAGTCCAGACTCCAAACCC	SHANK3 H22 3UTR(+1988+2012)
1746	GATGGAGCTTAGTCCAGACTCCAAA	SHANK3 H22 3UTR(+1991+2015)
1747	GTGGATGGAGCTTAGTCCAGACTCC	SHANK3 H22 3UTR(+1994+2018)
1748	GACGTGGATGGAGCTTAGTCCAGAC	SHANK3 H22 3UTR(+1997+2021)
1749	AGTGACGTGGATGGAGCTTAGTCCA	SHANK3 H22 3UTR(+2000+2024)
1750	GTGAGTGACGTGGATGGAGCTTAGT	SHANK3 H22 3UTR(+2003+2027)

1751	CTTGTGAGTGACGTGGATGGAGCTT	SHANK3 H22 3UTR(+2006+2030)
1752	AAACTTGTGAGTGACGTGGATGGAG	SHANK3 H22 3UTR(+2009+2033)
1753	CAGAACTTGTGAGTGACGTGGATG	SHANK3 H22 3UTR(+2012+2036)
1754	AAACAGAACTTGTGAGTGACGTGG	SHANK3 H22 3UTR(+2015+2039)
1755	TATAAACAGAACTTGTGAGTGACG	SHANK3 H22 3UTR(+2018+2042)
1756	AAATATAAACAGAACTTGTGAGTG	SHANK3 H22 3UTR(+2021+2045)
1757	TAGAAATATAAACAGAACTTGTGA	SHANK3 H22 3UTR(+2024+2048)
1758	AGCTAGAAATATAAACAGAACTTG	SHANK3 H22 3UTR(+2027+2051)
1759	AAAAGCTAGAAATATAAACAGAAAC	SHANK3 H22 3UTR(+2030+2054)
1760	AAAAAAGCTAGAAATATAAACAGA	SHANK3 H22 3UTR(+2033+2057)
1761	ATTAATAAAGCTAGAAATATAAAC	SHANK3 H22 3UTR(+2036+2060)
1762	TTTATTAATAAAGCTAGAAATATA	SHANK3 H22 3UTR(+2039+2063)
1763	TATTTATTAATAAAGCTAGAAAT	SHANK3 H22 3UTR(+2042+2066)
1764	TTTTATTTATTAATAAAGCTAGA	SHANK3 H22 3UTR(+2045+2069)
1765	TTTTTTATTTATTAATAAAGCT	SHANK3 H22 3UTR(+2048+2072)
1766	TTTTTTTTATTTATTAATAAAAA	SHANK3 H22 3UTR(+2051+2075)
1767	TCTTTTTTTTTATTTATTAATAA	SHANK3 H22 3UTR(+2054+2078)
1768	TTTCTTTTTTTTTATTTATTA	SHANK3 H22 3UTR(+2057+2081)
1769	CTGTTTCTTTTTTTTTATTTTA	SHANK3 H22 3UTR(+2060+2084)
1770	CTTCTGTTTCTTTTTTTTTATT	SHANK3 H22 3UTR(+2063+2087)
1771	AAACTTCTGTTTCTTTTTTTTTT	SHANK3 H22 3UTR(+2066+2090)
1772	TGAAAACCTCTGTTTCTTTTTTTT	SHANK3 H22 3UTR(+2069+2093)
1773	TTGTGAAAACCTCTGTTTCTTTTT	SHANK3 H22 3UTR(+2072+2096)
1774	GGGTTGTGAAAACCTCTGTTTCTT	SHANK3 H22 3UTR(+2075+2099)
1775	CCTGGGTTGTGAAAACCTCTGTTT	SHANK3 H22 3UTR(+2078+2102)
1776	GCCCCTGGGTTGTGAAAACCTCTGT	SHANK3 H22 3UTR(+2081+2105)
1777	CAGGCCCTGGGTTGTGAAAACCTC	SHANK3 H22 3UTR(+2084+2108)
1778	TGCCAGGCCCTGGGTTGTGAAAAC	SHANK3 H22 3UTR(+2087+2111)
1779	GCGTGCCAGGCCCTGGGTTGTGAA	SHANK3 H22 3UTR(+2090+2114)
1780	CCGGCGTGCCAGGCCCTGGGTTGT	SHANK3 H22 3UTR(+2093+2117)
1781	AGACCGGCGTGCCAGGCCCTGGGT	SHANK3 H22 3UTR(+2096+2120)
1782	CACAGACCGGCGTGCCAGGCCCTG	SHANK3 H22 3UTR(+2099+2123)
1783	AGGCACAGACCGGCGTGCCAGGCC	SHANK3 H22 3UTR(+2102+2126)
1784	GGCAGGCACAGACCGGCGTGCCAGG	SHANK3 H22 3UTR(+2105+2129)
1785	GCGGGCAGGCACAGACCGGCGTGCC	SHANK3 H22 3UTR(+2108+2132)
1786	GGGGCGGGCAGGCACAGACCGGCGT	SHANK3 H22 3UTR(+2111+2135)

1787	GGCGGGGCGGGCAGGCACAGACCGG	SHANK3 H22 3UTR(+2114+2138)
1788	CAGGGCGGGGCGGGCAGGCACAGAC	SHANK3 H22 3UTR(+2117+2141)
1789	GGCCAGGGCGGGGCGGGCAGGCACA	SHANK3 H22 3UTR(+2120+2144)
1790	GTGGGCCAGGGCGGGGCGGGCAGGC	SHANK3 H22 3UTR(+2123+2147)
1791	CCGGTGGGCCAGGGCGGGGCGGGCA	SHANK3 H22 3UTR(+2126+2150)
1792	GGGCCGGTGGGCCAGGGCGGGGCGG	SHANK3 H22 3UTR(+2129+2153)
1793	GTGGGGCCGGTGGGCCAGGGCGGGG	SHANK3 H22 3UTR(+2132+2156)
1794	GGAGTGGGGCCGGTGGGCCAGGGCG	SHANK3 H22 3UTR(+2135+2159)
1795	CAGGGAGTGGGGCCGGTGGGCCAGG	SHANK3 H22 3UTR(+2138+2162)
1796	GCCCAGGGAGTGGGGCCGGTGGGCC	SHANK3 H22 3UTR(+2141+2165)
1797	TGTGCCAGGGAGTGGGGCCGGTGG	SHANK3 H22 3UTR(+2144+2168)
1798	CTCTGTGCCAGGGAGTGGGGCCGG	SHANK3 H22 3UTR(+2147+2171)
1799	TGACTCTGTGCCAGGGAGTGGGGC	SHANK3 H22 3UTR(+2150+2174)
1800	GTGTGACTCTGTGCCAGGGAGTGG	SHANK3 H22 3UTR(+2153+2177)
1801	TGGGTGTGACTCTGTGCCAGGGAG	SHANK3 H22 3UTR(+2156+2180)
1802	GAGTGGGTGTGACTCTGTGCCAGG	SHANK3 H22 3UTR(+2159+2183)
1803	GATGAGTGGGTGTGACTCTGTGCC	SHANK3 H22 3UTR(+2162+2186)
1804	AAGGATGAGTGGGTGTGACTCTGTG	SHANK3 H22 3UTR(+2165+2189)
1805	CGGAAGGATGAGTGGGTGTGACTCT	SHANK3 H22 3UTR(+2168+2192)
1806	TGGCGGAAGGATGAGTGGGTGTGAC	SHANK3 H22 3UTR(+2171+2195)
1807	TGTTGGCGGAAGGATGAGTGGGTGT	SHANK3 H22 3UTR(+2174+2198)
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1809	CTGGACTGTTGGCGGAAGGATGAGT	SHANK3 H22 3UTR(+2180+2204)
1810	GACCTGGACTGTTGGCGGAAGGATG	SHANK3 H22 3UTR(+2183+2207)
1811	TGTGACCTGGACTGTTGGCGGAAGG	SHANK3 H22 3UTR(+2186+2210)
1812	CTGTGTGACCTGGACTGTTGGCGGA	SHANK3 H22 3UTR(+2189+2213)
1813	CTGCTGTGTGACCTGGACTGTTGGC	SHANK3 H22 3UTR(+2192+2216)
1814	CTGCTGCTGTGTGACCTGGACTGTT	SHANK3 H22 3UTR(+2195+2219)
1815	TGACTGCTGCTGTGTGACCTGGACT	SHANK3 H22 3UTR(+2198+2222)
1816	CAGTGACTGCTGCTGTGTGACCTGG	SHANK3 H22 3UTR(+2201+2225)
1817	TTACAGTGACTGCTGCTGTGTGACC	SHANK3 H22 3UTR(+2204+2228)
1818	CTGTTACAGTGACTGCTGCTGTGTG	SHANK3 H22 3UTR(+2207+2231)
1819	AGTCTGTTACAGTGACTGCTGCTGT	SHANK3 H22 3UTR(+2210+2234)
1820	GGCAGTCTGTTACAGTGACTGCTGC	SHANK3 H22 3UTR(+2213+2237)
1821	TGTGGCAGTCTGTTACAGTGACTGC	SHANK3 H22 3UTR(+2216+2240)
1822	GTATGTGGCAGTCTGTTACAGTGAC	SHANK3 H22 3UTR(+2219+2243)

1823	TGTGTATGTGGCAGTCTGTTACAGT	SHANK3 H22 3UTR(+2222+2246)
1824	GAGTGTGTATGTGGCAGTCTGTTAC	SHANK3 H22 3UTR(+2225+2249)
1825	ACCGAGTGTGTATGTGGCAGTCTGT	SHANK3 H22 3UTR(+2228+2252)
1826	GAGACCGAGTGTGTATGTGGCAGTC	SHANK3 H22 3UTR(+2231+2255)
1827	TGTGAGACCGAGTGTGTATGTGGCA	SHANK3 H22 3UTR(+2234+2258)
1828	GAGTGTGAGACCGAGTGTGTATGTG	SHANK3 H22 3UTR(+2237+2261)
1829	GGTGAGTGTGAGACCGAGTGTGTAT	SHANK3 H22 3UTR(+2240+2264)
1830	ACAGGTGAGTGTGAGACCGAGTGTG	SHANK3 H22 3UTR(+2243+2267)
1831	CCCACAGGTGAGTGTGAGACCGAGT	SHANK3 H22 3UTR(+2246+2270)
1832	AAACCCACAGGTGAGTGTGAGACCG	SHANK3 H22 3UTR(+2249+2273)
1833	CCAAAACCCACAGGTGAGTGTGAGA	SHANK3 H22 3UTR(+2252+2276)
1834	GAACCAAAACCCACAGGTGAGTGTG	SHANK3 H22 3UTR(+2255+2279)
1835	ACGGAACCAAAACCCACAGGTGAGT	SHANK3 H22 3UTR(+2258+2282)
1836	TGAACGGAACCAAAACCCACAGGTG	SHANK3 H22 3UTR(+2261+2285)
1837	AATTGAACGGAACCAAAACCCACAG	SHANK3 H22 3UTR(+2264+2288)
1838	CCAAATTGAACGGAACCAAAACCCA	SHANK3 H22 3UTR(+2267+2291)
1839	AACCCAAATTGAACGGAACCAAAAC	SHANK3 H22 3UTR(+2270+2294)
1840	AAAAACCCAAATTGAACGGAACCAA	SHANK3 H22 3UTR(+2273+2297)
1841	GTAAAAACCCAAATTGAACGGAAC	SHANK3 H22 3UTR(+2276+2300)
1842	AAAGTTAAAAACCCAAATTGAACGG	SHANK3 H22 3UTR(+2279+2303)
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1844	CCCTGTAAAGTTAAAAACCCAAATT	SHANK3 H22 3UTR(+2285+2309)
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1849	GTGAAGCGGAACTGACCCTGTAAAG	SHANK3 H22 3UTR(+2300+2324)
1850	GAGGTGAAGCGGAACTGACCCTGTA	SHANK3 H22 3UTR(+2303+2327)
1851	AAGGAGGTGAAGCGGAACTGACCCT	SHANK3 H22 3UTR(+2306+2330)
1852	CAAAAGGAGGTGAAGCGGAACTGAC	SHANK3 H22 3UTR(+2309+2333)
1853	ATACAAAAGGAGGTGAAGCGGAACT	SHANK3 H22 3UTR(+2312+2336)
1854	TCCATACAAAAGGAGGTGAAGCGGA	SHANK3 H22 3UTR(+2315+2339)
1855	AACTCCATACAAAAGGAGGTGAAGC	SHANK3 H22 3UTR(+2318+2342)
1856	TGGAACTCCATACAAAAGGAGGTGA	SHANK3 H22 3UTR(+2321+2345)
1857	GGATGGAACTCCATACAAAAGGAGG	SHANK3 H22 3UTR(+2324+2348)
1858	CCCGGATGGAACTCCATACAAAAGG	SHANK3 H22 3UTR(+2327+2351)

1859	CCCCCGGATGGAAGTCCATACAAA	SHANK3 H22 3UTR(+2330+2354)
1860	AAACCCCCCGGATGGAAGTCCATAC	SHANK3 H22 3UTR(+2333+2357)
1861	GTGAAACCCCCCGGATGGAAGTCCA	SHANK3 H22 3UTR(+2336+2360)
1862	GGGGTGAAACCCCCCGGATGGAAGT	SHANK3 H22 3UTR(+2339+2363)
1863	CAGGGGGTGAAACCCCCCGGATGGA	SHANK3 H22 3UTR(+2342+2366)
1864	GAGCAGGGGGTGAAACCCCCCGGAT	SHANK3 H22 3UTR(+2345+2369)
1865	CTGGAGCAGGGGGTGAAACCCCCG	SHANK3 H22 3UTR(+2348+2372)
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1870	CAGGAGGCCTCAGGACTGGAGCAGG	SHANK3 H22 3UTR(+2363+2387)
1871	GGTCAGGAGGCCTCAGGACTGGAGC	SHANK3 H22 3UTR(+2366+2390)
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1873	CGTCAGGGTCAGGAGGCCTCAGGAC	SHANK3 H22 3UTR(+2372+2396)
1874	CAACGTCAGGGTCAGGAGGCCTCAG	SHANK3 H22 3UTR(+2375+2399)
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1881	AGATCTCTGTGGGGCGTATCACAAC	SHANK3 H22 3UTR(+2396+2420)
1882	CATAGATCTCTGTGGGGCGTATCAC	SHANK3 H22 3UTR(+2399+2423)
1883	AAACATAGATCTCTGTGGGGCGTAT	SHANK3 H22 3UTR(+2402+2426)
1884	AAGAAACATAGATCTCTGTGGGGCG	SHANK3 H22 3UTR(+2405+2429)
1885	TATAAGAAACATAGATCTCTGTGGG	SHANK3 H22 3UTR(+2408+2432)
1886	TAATATAAGAAACATAGATCTCTGT	SHANK3 H22 3UTR(+2411+2435)
1887	TAATAATATAAGAAACATAGATCTC	SHANK3 H22 3UTR(+2414+2438)
1888	TAATAATAATATAAGAAACATAGAT	SHANK3 H22 3UTR(+2417+2441)
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1914	CCCTCAAGCAGGCAACTGAGCCATG	SHANK3 H22 3UTR(+2495+2519)
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1917	ACAAATATCCCCTCAAGCAGGCAAC	SHANK3 H22 3UTR(+2504+2528)
1918	GACACAAATATCCCCTCAAGCAGGC	SHANK3 H22 3UTR(+2507+2531)
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1920	GGGACAGACACAAATATCCCCTCAA	SHANK3 H22 3UTR(+2513+2537)
1921	TGAGGGACAGACACAAATATCCCCT	SHANK3 H22 3UTR(+2516+2540)
1922	GTATGAGGGACAGACACAAATATCC	SHANK3 H22 3UTR(+2519+2543)
1923	CCGGTATGAGGGACAGACACAAATA	SHANK3 H22 3UTR(+2522+2546)
1924	TGGCCGGTATGAGGGACAGACACAA	SHANK3 H22 3UTR(+2525+2549)
1925	GTGTGGCCGGTATGAGGGACAGACA	SHANK3 H22 3UTR(+2528+2552)
1926	TTTGTGTGGCCGGTATGAGGGACAG	SHANK3 H22 3UTR(+2531+2555)
1927	AGGTTTGTGTGGCCGGTATGAGGGA	SHANK3 H22 3UTR(+2534+2558)
1928	AGGAGGTTTGTGTGGCCGGTATGAG	SHANK3 H22 3UTR(+2537+2561)
1929	CTGAGGAGGTTTGTGTGGCCGGTAT	SHANK3 H22 3UTR(+2540+2564)
1930	AGGCTGAGGAGGTTTGTGTGGCCGG	SHANK3 H22 3UTR(+2543+2567)

1931	TCCAGGCTGAGGAGGTTTGTGTGGC	SHANK3 H22 3UTR(+2546+2570)
1932	TGGTCCAGGCTGAGGAGGTTTGTGT	SHANK3 H22 3UTR(+2549+2573)
1933	ATGTGGTCCAGGCTGAGGAGGTTTG	SHANK3 H22 3UTR(+2552+2576)
1934	CTGACCCTGTAAAGTTAAACCCA	SHANK3_H3'UTR(+1697+1721)
1935	GGCATAAACTCGCCGCTTGTACTGA	SHANK3 H2A(+3+27)mm
1936	GGCATAAACTCGCCGCTTGTATCGA	SHANK3 H2A(+3+27)
1937	CTCCCCGTGATCCTTTACCTTTGTG	SHANK3 H2D(+7-18)
1938	CCTCCAGGTAGGGCAGGGGCGTGTC	SHANK3 H1D(+24-1)
1939	TTACCTCCAGGTAGGGCAGGGGCGT	SHANK3 H1D(+21-4)
1940	CACTTACCTCCAGGTAGGGCAGGGG	SHANK3 H1D(+18-7)
1941	GGCCACTTACCTCCAGGTAGGGCAG	SHANK3 H1D(+15-10)
1942	GCCGGCCACTTACCTCCAGGTAGGG	SHANK3 H1D(+12-13)
1943	CGCGCCGGCCACTTACCTCCAGGTA	SHANK3 H1D(+9-16)
1944	CCCCGCGCCGGCCACTTACCTCCAG	SHANK3 H1D(+6-19)
1945	CACCCCCGCGCCGGCCACTTACCTC	SHANK3 H1D(+3-22)
1946	GCTCACCCCCGCGCCGGCCACTTAC	SHANK3 H1D(-1-25)
1947	TCAGCTCACCCCCGCGCCGGCCACT	SHANK3 H1D(-4-28)
1948	TCCTCAGCTCACCCCCGCGCCGGCC	SHANK3 H1D(-7-31)
1949	CGCTCCTCAGCTCACCCCCGCGCCG	SHANK3 H1D(-10-34)
1950	GCGCGCTCCTCAGCTCACCCCCGCG	SHANK3 H1D(-13-37)
1951	CCTGCGCGCTCCTCAGCTCACCCCC	SHANK3 H1D(-16-40)
1952	CACCTGCGCGCTCCTCAGCTCACC	SHANK3 H1D(-19-43)
1953	ATCCACCCTGCGCGCTCCTCAGCTC	SHANK3 H1D(-22-46)
1954	GTGATCCACCCTGCGCGCTCCTCAG	SHANK3 H1D(-25-49)
1955	TTGGTGATCCACCCTGCGCGCTCCT	SHANK3 H1D(-28-52)
1956	GGCTTGGTGATCCACCCTGCGCGCT	SHANK3 H1D(-31-55)
1957	CGGGGCTTGGTGATCCACCCTGCGC	SHANK3 H1D(-34-58)
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1960	GTCCCGCCACGGGGCTTGGTGATCC	SHANK3 H1D(-43-67)
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1963	CCTTCACTGGTCCCGCCACGGGGCT	SHANK3 H1D(-52-76)
1964	TGCCCTTCACTGGTCCCGCCACGGG	SHANK3 H1D(-55-79)
1965	CCGTGCCCTTCACTGGTCCCGCCAC	SHANK3 H1D(-58-82)
1966	CTGCCGTGCCCTTCACTGGTCCCGC	SHANK3 H1D(-61-85)

1967	CCACTGCCGTGCCCTTCACTGGTCC	SHANK3 H1D(-64-88)
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1969	GTTTCCCCACTGCCGTGCCCTTAC	SHANK3 H1D(-70-94)
1970	TGTGTTTCCCCACTGCCGTGCCCTT	SHANK3 H1D(-73-97)
1971	ACTTGTGTTTCCCCACTGCCGTGCC	SHANK3 H1D(-76-100)
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1973	CCTCCCACTTGTGTTTCCCCACTGC	SHANK3 H1D(-82-106)
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1975	CTCACCCCTCCCACTTGTGTTTCCC	SHANK3 H1D(-88-112)
1976	CCCCTCACCCCTCCCACTTGTGTTT	SHANK3 H1D(-91-115)
1977	CCACCCCTCACCCCTCCCACTTGTG	SHANK3 H1D(-94-118)
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1979	CAGCCTCCACCCCTCACCCCTCCCA	SHANK3 H1D(-100-124)
1980	ACACAGCCTCCACCCCTCACCCCTC	SHANK3 H1D(-103-127)
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1987	CACACACACACACACACACACACAC	SHANK3 H1D(-124-148)
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1992	GCACACAGCACCACACACACACACA	SHANK3 H1D(-139-163)
1993	TCTGCACACAGCACCACACACACAC	SHANK3 H1D(-142-166)
1994	CACTCTGCACACAGCACCACACACA	SHANK3 H1D(-145-169)
1995	CTGCACTCTGCACACAGCACCACAC	SHANK3 H1D(-148-172)
1996	TCACTGCACTCTGCACACAGCACCA	SHANK3 H1D(-151-175)
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2000	CCCTGTACACGCTCACTGCACTCTG	SHANK3 H1D(-163-187)
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2004	CCGCTCGCTGCACCCTGTACACGCT	SHANK3 H1D(-175-199)
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2006	CTGTGTCCGCTCGCTGCACCCTGTA	SHANK3 H1D(-181-205)
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2012	GCCTACTCATCGCATACACTGTGTC	SHANK3 H1D(-199-223)
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2022	CTCGCCCTGCCCGCTCACTGCACAC	SHANK3 H1D(-229-253)
2023	CTGCTCGCCCTGCCCGCTCACTGCA	SHANK3 H1D(-232-256)
2024	TTACTGCTCGCCCTGCCCGCTCACT	SHANK3 H1D(-235-259)
2025	TCCTTACTGCTCGCCCTGCCCGCTC	SHANK3 H1D(-238-262)
2026	ACATCCTTACTGCTCGCCCTGCCCG	SHANK3 H1D(-241-265)
2027	TGTACATCCTTACTGCTCGCCCTGC	SHANK3 H1D(-244-268)
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2030	TGCCCACACTGTACATCCTTACTGC	SHANK3 H1D(-253-277)
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2032	GCACACTGCCCACACTGTACATCCT	SHANK3 H1D(-259-283)
2033	CTCGCACACTGCCCACACTGTACAT	SHANK3 H1D(-262-286)
2034	ATGCTCGCACACTGCCCACACTGTA	SHANK3 H1D(-265-289)
2035	CACATGCTCGCACACTGCCCACACT	SHANK3 H1D(-268-292)
2036	CTACACATGCTCGCACACTGCCCAC	SHANK3 H1D(-271-295)
2037	TCACTACACATGCTCGCACACTGCC	SHANK3 H1D(-274-298)
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2046	TGCCTGCTAACTGCACACACTGCCT	SHANK3 H1D(-301-325)
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2050	CTGCACACACTGTGCCTGCTAACTG	SHANK3 H1D(-313-337)
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2054	ACTGCCCACTCACTGCACACACTGT	SHANK3 H1D(-325-349)
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2058	CATGCTGTGCACACTGCCCACTCAC	SHANK3 H1D(-337-361)
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2061	CACACTGTACATGCTGTGCACACTG	SHANK3 H1D(-346-370)
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2078	TGCACTGTGCCCCACTCACTACACAT	SHANK3 H1D(-397-421)
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2082	GTGCACACTGACTGCACTGTGCCCA	SHANK3 H1D(-409-433)
2083	TTTGTGCACACTGACTGCACTGTGC	SHANK3 H1D(-412-436)
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2087	CCCACTGCATACTTTGTGCACACTG	SHANK3 H1D(-424-448)
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2100	CTACACACTGCACACCACTCACTGC	SHANK3 H1D(-463-487)
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2102	TGCACACTACACACTGCACACCACT	SHANK3 H1D(-469-493)
2103	CACTGCACACTACACACTGCACACC	SHANK3 H1D(-472-496)
2104	GCTCACTGCACACTACACACTGCAC	SHANK3 H1D(-475-499)
2105	ACTGCTCACTGCACACTACACACTG	SHANK3 H1D(-478-502)
2106	CACACTGCTCACTGCACACTACACA	SHANK3 H1D(-481-505)
2107	GTACACACTGCTCACTGCACACTAC	SHANK3 H1D(-484-508)
2108	GCTGTACACACTGCTCACTGCACAC	SHANK3 H1D(-487-511)
2109	AATGCTGTACACACTGCTCACTGCA	SHANK3 H1D(-490-514)
2110	TGCAATGCTGTACACACTGCTCACT	SHANK3 H1D(-493-517)

2111	CACTGCAATGCTGTACACACTGCTC	SHANK3 H1D(-496-520)
2112	CCACACTGCAATGCTGTACACACTG	SHANK3 H1D(-499-523)
2113	GCCCCACACTGCAATGCTGTACACA	SHANK3 H1D(-502-526)
2114	ACTGCCCCACACTGCAATGCTGTAC	SHANK3 H1D(-505-529)
2115	CTCACTGCCCCACACTGCAATGCTG	SHANK3 H1D(-508-532)
2116	GTA CTCACTGCCCCACACTGCAATG	SHANK3 H1D(-511-535)
2117	ACTGTACTCACTGCCCCACACTGCA	SHANK3 H1D(-514-538)
2118	CACACTGTACTCACTGCCCCACACT	SHANK3 H1D(-517-541)
2119	ACTCACACTGTACTCACTGCCCCAC	SHANK3 H1D(-520-544)
2120	AACACTCACACTGTACTCACTGCCC	SHANK3 H1D(-523-547)
2121	CACAACACTCACACTGTACTCACTG	SHANK3 H1D(-526-550)
2122	AATCACAACACTCACACTGTACTCA	SHANK3 H1D(-529-553)
2123	CACAATCACAACACTCACACTGTAC	SHANK3 H1D(-532-556)
2124	TACCACAATCACAACACTCACACTG	SHANK3 H1D(-535-559)
2125	GCTTACCACAATCACAACACTCACA	SHANK3 H1D(-538-562)
2126	CCTGCTTACCACAATCACAACACTC	SHANK3 H1D(-541-565)
2127	CATCCTGCTTACCACAATCACAACA	SHANK3 H1D(-544-568)
2128	GCGCATCCTGCTTACCACAATCACA	SHANK3 H1D(-547-571)
2129	ACTGCGCATCCTGCTTACCACAATC	SHANK3 H1D(-550-574)
2130	TATACTGCGCATCCTGCTTACCACA	SHANK3 H1D(-553-577)
2131	CTGTATACTGCGCATCCTGCTTACC	SHANK3 H1D(-556-580)
2132	TCACTGTATACTGCGCATCCTGCTT	SHANK3 H1D(-559-583)
2133	TGTTCACTGTATACTGCGCATCCTG	SHANK3 H1D(-562-586)
2134	CACTGTTCACACTGTATACTGCGCATC	SHANK3 H1D(-565-589)
2135	GCACACTGTTCACTGTATACTGCGC	SHANK3 H1D(-568-592)
2136	TGTGCACACTGTTCACTGTATACTG	SHANK3 H1D(-571-595)
2137	CACTGTGCACACTGTTCACTGTATA	SHANK3 H1D(-574-598)
2138	ACACACTGTGCACACTGTTCACTGT	SHANK3 H1D(-577-601)
2139	TGCACACACTGTGCACACTGTTCAC	SHANK3 H1D(-580-604)
2140	CACTGCACACACTGTGCACACTGTT	SHANK3 H1D(-583-607)
2141	CCACACTGCACACACTGTGCACACT	SHANK3 H1D(-586-610)
2142	AGCCACACTGCACACACTGTGCAC	SHANK3 H1D(-589-613)
2143	CACAGCCACACTGCACACACTGTG	SHANK3 H1D(-592-616)
2144	GCACACAGCCACACTGCACACACT	SHANK3 H1D(-595-619)
2145	GTGGCACACAGCCACACTGCACAC	SHANK3 H1D(-598-622)
2146	TCTGTGGCACACAGCCACACTGCA	SHANK3 H1D(-601-625)

2147	GACTCTGTGGCACACAGCCCACACT	SHANK3 H1D(-604-628)
2148	ACTGACTCTGTGGCACACAGCCCAC	SHANK3 H1D(-607-631)
2149	CACACTGACTCTGTGGCACACAGCC	SHANK3 H1D(-610-634)
2150	CACCACACTGACTCTGTGGCACACA	SHANK3 H1D(-613-637)
2151	ACACACCACACTGACTCTGTGGCAC	SHANK3 H1D(-616-640)
2152	TACACACACCACACTGACTCTGTGG	SHANK3 H1D(-619-643)
2153	AACTACACACACCACACTGACTCTG	SHANK3 H1D(-622-646)
2154	TCAAACACTACACACACCACACTGACT	SHANK3 H1D(-625-649)
2155	TGTTCAAACACTACACACACCACACTG	SHANK3 H1D(-628-652)
2156	CACTGTTCAAACACTACACACACCACA	SHANK3 H1D(-631-655)
2157	ACACACTGTTCAAACACTACACACACC	SHANK3 H1D(-634-658)
2158	TGCACACACTGTTCAAACACTACACAC	SHANK3 H1D(-637-661)
2159	CAATGCACACACTGTTCAAACACTACA	SHANK3 H1D(-640-664)
2160	GCTCAATGCACACACTGTTCAAACACT	SHANK3 H1D(-643-667)
2161	GCTGCTCAATGCACACACTGTTCAA	SHANK3 H1D(-646-670)
2162	CATGCTGCTCAATGCACACACTGTT	SHANK3 H1D(-649-673)
2163	ATCCATGCTGCTCAATGCACACACT	SHANK3 H1D(-652-676)
2164	ACCATCCATGCTGCTCAATGCACAC	SHANK3 H1D(-655-679)
2165	CACACCATCCATGCTGCTCAATGCA	SHANK3 H1D(-658-682)
2166	GTCCACACCATCCATGCTGCTCAAT	SHANK3 H1D(-661-685)
2167	AGCGTCCACACCATCCATGCTGCTC	SHANK3 H1D(-664-688)
2168	CTCAGCGTCCACACCATCCATGCTG	SHANK3 H1D(-667-691)
2169	ATGCTCAGCGTCCACACCATCCATG	SHANK3 H1D(-670-694)
2170	ACAATGCTCAGCGTCCACACCATCC	SHANK3 H1D(-673-697)
2171	AGAACAATGCTCAGCGTCCACACCA	SHANK3 H1D(-676-700)
2172	TGGAGAACAATGCTCAGCGTCCACA	SHANK3 H1D(-679-703)
2173	CCCTGGAGAACAATGCTCAGCGTCC	SHANK3 H1D(-682-706)
2174	CCTCCCTGGAGAACAATGCTCAGCG	SHANK3 H2A(-686-662)
2175	ACTCCTCCCTGGAGAACAATGCTCA	SHANK3 H2A(-683-659)
2176	CACACTCCTCCCTGGAGAACAATGC	SHANK3 H2A(-680-656)
2177	GCTCACACTCCTCCCTGGAGAACAA	SHANK3 H2A(-677-653)
2178	CGTGCTCACACTCCTCCCTGGAGAA	SHANK3 H2A(-674-650)
2179	TCTCGTGCTCACACTCCTCCCTGGA	SHANK3 H2A(-671-647)
2180	CTCTCTCGTGCTCACACTCCTCCCT	SHANK3 H2A(-668-644)
2181	GCACTCTCTCGTGCTCACACTCCTC	SHANK3 H2A(-665-641)
2182	CTGGCACTCTCTCGTGCTCACACTC	SHANK3 H2A(-662-638)

2183	CCTCTGGCACTCTCTCGTGCTCACA	SHANK3 H2A(-659-635)
2184	ACCCCTCTGGCACTCTCTCGTGCTC	SHANK3 H2A(-656-632)
2185	CACACCCCTCTGGCACTCTCTCGTG	SHANK3 H2A(-653-629)
2186	CCACACACCCCTCTGGCACTCTCTC	SHANK3 H2A(-650-626)
2187	ACACCACACACCCCTCTGGCACTCT	SHANK3 H2A(-647-623)
2188	CTCACACCACACACCCCTCTGGCAC	SHANK3 H2A(-644-620)
2189	CTGCTCACACCACACACCCCTCTGG	SHANK3 H2A(-641-617)
2190	GCCCTGCTCACACCACACACCCCTC	SHANK3 H2A(-638-614)
2191	ATAGCCCTGCTCACACCACACACCC	SHANK3 H2A(-635-611)
2192	CAGATAGCCCTGCTCACACCACACA	SHANK3 H2A(-632-608)
2193	ACACAGATAGCCCTGCTCACACCAC	SHANK3 H2A(-629-605)
2194	TGCACACAGATAGCCCTGCTCACAC	SHANK3 H2A(-626-602)
2195	ACGTGCACACAGATAGCCCTGCTCA	SHANK3 H2A(-623-599)
2196	CAAACGTGCACACAGATAGCCCTGC	SHANK3 H2A(-620-596)
2197	GAACAAACGTGCACACAGATAGCCC	SHANK3 H2A(-617-593)
2198	AAGGAACAAACGTGCACACAGATAG	SHANK3 H2A(-614-590)
2199	AGAAAGGAACAAACGTGCACACAGA	SHANK3 H2A(-611-587)
2200	TGGAGAAAGGAACAAACGTGCACAC	SHANK3 H2A(-608-584)
2201	AGCTGGAGAAAGGAACAAACGTGCA	SHANK3 H2A(-605-581)
2202	CACAGCTGGAGAAAGGAACAAACGT	SHANK3 H2A(-602-578)
2203	CTTCACAGCTGGAGAAAGGAACAAA	SHANK3 H2A(-599-575)
2204	AGACTTCACAGCTGGAGAAAGGAAC	SHANK3 H2A(-596-572)
2205	ACAAGACTTCACAGCTGGAGAAAGG	SHANK3 H2A(-593-569)
2206	TTCACAAGACTTCACAGCTGGAGAA	SHANK3 H2A(-590-566)
2207	GCCTTCACAAGACTTCACAGCTGGA	SHANK3 H2A(-587-563)
2208	TTGGCCTTCACAAGACTTCACAGCT	SHANK3 H2A(-584-560)
2209	TGGTTGGCCTTCACAAGACTTCACA	SHANK3 H2A(-581-557)
2210	ACTTGGTTGGCCTTCACAAGACTTC	SHANK3 H2A(-578-554)
2211	GGGACTTGGTTGGCCTTCACAAGAC	SHANK3 H2A(-575-551)
2212	GAGGGGACTTGGTTGGCCTTCACAA	SHANK3 H2A(-572-548)
2213	AAGGAGGGGACTTGGTTGGCCTTCA	SHANK3 H2A(-569-545)
2214	GTAAAGGAGGGGACTTGGTTGGCCT	SHANK3 H2A(-566-542)
2215	TGAGTAAAGGAGGGGACTTGGTTGG	SHANK3 H2A(-563-539)
2216	GGGTGAGTAAAGGAGGGGACTTGGT	SHANK3 H2A(-560-536)
2217	CATGGGTGAGTAAAGGAGGGGACTT	SHANK3 H2A(-557-533)
2218	ATGCATGGGTGAGTAAAGGAGGGGA	SHANK3 H2A(-554-530)

2219	ACCATGCATGGGTGAGTAAAGGAGG	SHANK3 H2A(-551-527)
2220	CACACCATGCATGGGTGAGTAAAGG	SHANK3 H2A(-548-524)
2221	CTTCACACCATGCATGGGTGAGTAA	SHANK3 H2A(-545-521)
2222	CATCTTCACACCATGCATGGGTGAG	SHANK3 H2A(-542-518)
2223	ATACATCTTCACACCATGCATGGGT	SHANK3 H2A(-539-515)
2224	TCAATACATCTTCACACCATGCATG	SHANK3 H2A(-536-512)
2225	CACTCAATACATCTTCACACCATGC	SHANK3 H2A(-533-509)
2226	AGGCACTCAATACATCTTCACACCA	SHANK3 H2A(-530-506)
2227	GCAAGGCACTCAATACATCTTCACA	SHANK3 H2A(-527-503)
2228	CTAGCAAGGCACTCAATACATCTTC	SHANK3 H2A(-524-500)
2229	TGCCTAGCAAGGCACTCAATACATC	SHANK3 H2A(-521-497)
2230	CCATGCCTAGCAAGGCACTCAATAC	SHANK3 H2A(-518-494)
2231	TCCCCATGCCTAGCAAGGCACTCAA	SHANK3 H2A(-515-491)
2232	ACGTCCCCATGCCTAGCAAGGCACT	SHANK3 H2A(-512-488)
2233	TCTACGTCCCCATGCCTAGCAAGGC	SHANK3 H2A(-509-485)
2234	CCGTCTACGTCCCCATGCCTAGCAA	SHANK3 H2A(-506-482)
2235	ACCCCGTCTACGTCCCCATGCCTAG	SHANK3 H2A(-503-479)
2236	CTGACCCCGTCTACGTCCCCATGCC	SHANK3 H2A(-500-476)
2237	GGACTGACCCCGTCTACGTCCCCAT	SHANK3 H2A(-497-473)
2238	ACAGGACTGACCCCGTCTACGTCCC	SHANK3 H2A(-494-470)
2239	TCCACAGGACTGACCCCGTCTACGT	SHANK3 H2A(-491-467)
2240	CCTTCCACAGGACTGACCCCGTCTA	SHANK3 H2A(-488-464)
2241	AGACCTTCCACAGGACTGACCCCGT	SHANK3 H2A(-485-461)
2242	CCAAGACCTTCCACAGGACTGACCC	SHANK3 H2A(-482-458)
2243	ACTCCAAGACCTTCCACAGGACTGA	SHANK3 H2A(-479-455)
2244	CAAACCTCAAGACCTTCCACAGGAC	SHANK3 H2A(-476-452)
2245	TGCCAAACTCCAAGACCTTCCACAG	SHANK3 H2A(-473-449)
2246	CCCTGCCAAACTCCAAGACCTTCCA	SHANK3 H2A(-470-446)
2247	CCACCCTGCCAAACTCCAAGACCTT	SHANK3 H2A(-467-443)
2248	CCTCCACCCTGCCAAACTCCAAGAC	SHANK3 H2A(-464-440)
2249	CCCCCTCCACCCTGCCAAACTCCAA	SHANK3 H2A(-461-437)
2250	CACCCCTCCACCCTGCCAAACTC	SHANK3 H2A(-458-434)
2251	GGGCACCCCTCCACCCTGCCAAA	SHANK3 H2A(-455-431)
2252	GTTGGGCACCCCTCCACCCTGCC	SHANK3 H2A(-452-428)
2253	GCAGTTGGGCACCCCTCCACCCT	SHANK3 H2A(-449-425)
2254	ACTGCAGTTGGGCACCCCTCCAC	SHANK3 H2A(-446-422)

2255	CCCACTGCAGTTGGGCACCCCCCTC	SHANK3 H2A(-443-419)
2256	ATGCCCCACTGCAGTTGGGCACCCCC	SHANK3 H2A(-440-416)
2257	TCAATGCCCCACTGCAGTTGGGCACC	SHANK3 H2A(-437-413)
2258	TATTCAATGCCCCACTGCAGTTGGGC	SHANK3 H2A(-434-410)
2259	CTTTATTCAATGCCCCACTGCAGTTG	SHANK3 H2A(-431-407)
2260	AATCTTTATTCAATGCCCCACTGCAG	SHANK3 H2A(-428-404)
2261	CAAAATCTTTATTCAATGCCCCACTG	SHANK3 H2A(-425-401)
2262	TCACAAAATCTTTATTCAATGCCCA	SHANK3 H2A(-422-398)
2263	AGCTCACAAAATCTTTATTCAATGC	SHANK3 H2A(-419-395)
2264	CTCAGCTCACAAAATCTTTATTCAA	SHANK3 H2A(-416-392)
2265	GAGCTCAGCTCACAAAATCTTTATT	SHANK3 H2A(-413-389)
2266	TTTGAGCTCAGCTCACAAAATCTTT	SHANK3 H2A(-410-386)
2267	AACTTTGAGCTCAGCTCACAAAATC	SHANK3 H2A(-407-383)
2268	CCCAACTTTGAGCTCAGCTCACAAA	SHANK3 H2A(-404-380)
2269	CCGCCCAACTTTGAGCTCAGCTCAC	SHANK3 H2A(-401-377)
2270	GGCCCGCCCAACTTTGAGCTCAGCT	SHANK3 H2A(-398-374)
2271	GGAGGCCCGCCCAACTTTGAGCTCA	SHANK3 H2A(-395-371)
2272	CACGGAGGCCCGCCCAACTTTGAGC	SHANK3 H2A(-392-368)
2273	CACCACGGAGGCCCGCCCAACTTTG	SHANK3 H2A(-389-365)
2274	TGCCACCACGGAGGCCCGCCCAACT	SHANK3 H2A(-386-362)
2275	CTGTGCCACCACGGAGGCCCGCCCA	SHANK3 H2A(-383-359)
2276	TTCCTGTGCCACCACGGAGGCCCGC	SHANK3 H2A(-380-356)
2277	ACTTTCCTGTGCCACCACGGAGGCC	SHANK3 H2A(-377-353)
2278	CCCACTTTCCTGTGCCACCACGGAG	SHANK3 H2A(-374-350)
2279	GACCCCACTTTCCTGTGCCACCACG	SHANK3 H2A(-371-347)
2280	ACTGACCCCACTTTCCTGTGCCACC	SHANK3 H2A(-368-344)
2281	AGAACTGACCCCACTTTCCTGTGCC	SHANK3 H2A(-365-341)
2282	GGTAGAACTGACCCCACTTTCCTGT	SHANK3 H2A(-362-338)
2283	CCAGGTAGAACTGACCCCACTTTC	SHANK3 H2A(-359-335)
2284	TCTCCAGGTAGAACTGACCCCACTT	SHANK3 H2A(-356-332)
2285	CACTCTCCAGGTAGAACTGACCCCA	SHANK3 H2A(-353-329)
2286	CTCCACTCTCCAGGTAGAACTGACC	SHANK3 H2A(-350-326)
2287	CCCCTCCACTCTCCAGGTAGAACTG	SHANK3 H2A(-347-323)
2288	ATCCCCCTCCACTCTCCAGGTAGAA	SHANK3 H2A(-344-320)
2289	GACATCCCCCTCCACTCTCCAGGTA	SHANK3 H2A(-341-317)
2290	CTAGACATCCCCCTCCACTCTCCAG	SHANK3 H2A(-338-314)

2291	ATCCTAGACATCCCCCTCCACTCTC	SHANK3 H2A(-335-311)
2292	ACCATCCTAGACATCCCCCTCCACT	SHANK3 H2A(-332-308)
2293	CTTACCATCCTAGACATCCCCCTCC	SHANK3 H2A(-329-305)
2294	AGGCTTACCATCCTAGACATCCCCC	SHANK3 H2A(-326-302)
2295	TCCAGGCTTACCATCCTAGACATCC	SHANK3 H2A(-323-299)
2296	GATTCCAGGCTTACCATCCTAGACA	SHANK3 H2A(-320-296)
2297	CCTGATTCCAGGCTTACCATCCTAG	SHANK3 H2A(-317-293)
2298	AGGCCTGATTCCAGGCTTACCATCC	SHANK3 H2A(-314-290)
2299	TGAAGGCCTGATTCCAGGCTTACCA	SHANK3 H2A(-311-287)
2300	CTCTGAAGGCCTGATTCCAGGCTTA	SHANK3 H2A(-308-284)
2301	CCTCTCTGAAGGCCTGATTCCAGGC	SHANK3 H2A(-305-281)
2302	ACTCCTCTCTGAAGGCCTGATTCCA	SHANK3 H2A(-302-278)
2303	CCCACTCCTCTCTGAAGGCCTGATT	SHANK3 H2A(-299-275)
2304	AATCCCACTCCTCTCTGAAGGCCTG	SHANK3 H2A(-296-272)
2305	CAAAATCCCACTCCTCTCTGAAGGC	SHANK3 H2A(-293-269)
2306	CGGCAAAATCCCACTCCTCTCTGAA	SHANK3 H2A(-290-266)
2307	TCTCGGCAAAATCCCACTCCTCTCT	SHANK3 H2A(-287-263)
2308	GATTCTCGGCAAAATCCCACTCCTC	SHANK3 H2A(-284-260)
2309	CAGGATTCTCGGCAAAATCCCACTC	SHANK3 H2A(-281-257)
2310	CCCCAGGATTCTCGGCAAAATCCCA	SHANK3 H2A(-278-254)
2311	CATCCCCAGGATTCTCGGCAAAATC	SHANK3 H2A(-275-251)
2312	TCCCATCCCCAGGATTCTCGGCAAA	SHANK3 H2A(-272-248)
2313	CCTTCCCATCCCCAGGATTCTCGGC	SHANK3 H2A(-269-245)
2314	TCGCCTTCCCATCCCCAGGATTCTC	SHANK3 H2A(-266-242)
2315	CCGTCGCCTTCCCATCCCCAGGATT	SHANK3 H2A(-263-239)
2316	GTCCCGTCGCCTTCCCATCCCCAGG	SHANK3 H2A(-260-236)
2317	ACTGTCCCGTCGCCTTCCCATCCCC	SHANK3 H2A(-257-233)
2318	TGCACTGTCCCGTCGCCTTCCCATC	SHANK3 H2A(-254-230)
2319	GCCTGCACTGTCCCGTCGCCTTCCC	SHANK3 H2A(-251-227)
2320	GCAGCCTGCACTGTCCCGTCGCCTT	SHANK3 H2A(-248-224)
2321	CCCGCAGCCTGCACTGTCCCGTCGC	SHANK3 H2A(-245-221)
2322	CTGCCCGCAGCCTGCACTGTCCCGT	SHANK3 H2A(-242-218)
2323	TAGCTGCCCGCAGCCTGCACTGTCC	SHANK3 H2A(-239-215)
2324	GCCTAGCTGCCCGCAGCCTGCACTG	SHANK3 H2A(-236-212)
2325	CGTGCCTAGCTGCCCGCAGCCTGCA	SHANK3 H2A(-233-209)
2326	GCACGTGCCTAGCTGCCCGCAGCCT	SHANK3 H2A(-230-206)

2327	AAGGCACGTGCCTAGCTGCCCGCAG	SHANK3 H2A(-227-203)
2328	TGGAAGGCACGTGCCTAGCTGCCCCG	SHANK3 H2A(-224-200)
2329	CGATGGAAGGCACGTGCCTAGCTGC	SHANK3 H2A(-221-197)
2330	GCCCGATGGAAGGCACGTGCCTAGC	SHANK3 H2A(-218-194)
2331	GCAGCCCGATGGAAGGCACGTGCCT	SHANK3 H2A(-215-191)
2332	GATGCAGCCCGATGGAAGGCACGTG	SHANK3 H2A(-212-188)
2333	CATGATGCAGCCCGATGGAAGGCAC	SHANK3 H2A(-209-185)
2334	AGGCATGATGCAGCCCGATGGAAGG	SHANK3 H2A(-206-182)
2335	CTCAGGCATGATGCAGCCCGATGGA	SHANK3 H2A(-203-179)
2336	ACACTCAGGCATGATGCAGCCCGAT	SHANK3 H2A(-200-176)
2337	ACCACACTCAGGCATGATGCAGCCC	SHANK3 H2A(-197-173)
2338	CCCACCACACTCAGGCATGATGCAG	SHANK3 H2A(-194-170)
2339	GCACCCACCACACTCAGGCATGATG	SHANK3 H2A(-191-167)
2340	CATGCACCCACCACACTCAGGCATG	SHANK3 H2A(-188-164)
2341	TGCCATGCACCCACCACACTCAGGC	SHANK3 H2A(-185-161)
2342	AGTGCCATGCACCCACCACACTCA	SHANK3 H2A(-182-158)
2343	AACAGCTGCCATGCACCCACCACAC	SHANK3 H2A(-179-155)
2344	GCTAACAGCTGCCATGCACCCACCA	SHANK3 H2A(-176-152)
2345	AGAGCTAACAGCTGCCATGCACCCA	SHANK3 H2A(-173-149)
2346	GACAGAGCTAACAGCTGCCATGCAC	SHANK3 H2A(-170-146)
2347	GTGGACAGAGCTAACAGCTGCCATG	SHANK3 H2A(-167-143)
2348	ACAGTGGACAGAGCTAACAGCTGCC	SHANK3 H2A(-164-140)
2349	ACCACAGTGGACAGAGCTAACAGCT	SHANK3 H2A(-161-137)
2350	ACTACCACAGTGGACAGAGCTAACA	SHANK3 H2A(-158-134)
2351	CATACTACCACAGTGGACAGAGCTA	SHANK3 H2A(-155-131)
2352	AGTCATACTACCACAGTGGACAGAG	SHANK3 H2A(-152-128)
2353	ATCAGTCATACTACCACAGTGGACA	SHANK3 H2A(-149-125)
2354	ACCATCAGTCATACTACCACAGTGG	SHANK3 H2A(-146-122)
2355	CACACCATCAGTCATACTACCACAG	SHANK3 H2A(-143-119)
2356	GTACACACCATCAGTCATACTACCA	SHANK3 H2A(-140-116)
2357	CCTGTACACACCATCAGTCATACTA	SHANK3 H2A(-137-113)
2358	CCTCCTGTACACACCATCAGTCATA	SHANK3 H2A(-134-110)
2359	TGCCCTCCTGTACACACCATCAGTC	SHANK3 H2A(-131-107)
2360	CACTGCCCTCCTGTACACACCATCA	SHANK3 H2A(-128-104)
2361	CCTCACTGCCCTCCTGTACACACCA	SHANK3 H2A(-125-101)
2362	ACCCCTCACTGCCCTCCTGTACACA	SHANK3 H2A(-122-98)

2363	CGCACCCCTCACTGCCCTCCTGTAC	SHANK3 H2A(-119-95)
2364	CACCGCACCCCTCACTGCCCTCCTG	SHANK3 H2A(-116-92)
2365	CCACACCGCACCCCTCACTGCCCTC	SHANK3 H2A(-113-89)
2366	TGGCCACACCGCACCCCTCACTGCC	SHANK3 H2A(-110-86)
2367	TGCTGGCCACACCGCACCCCTCACT	SHANK3 H2A(-107-83)
2368	TCATGCTGGCCACACCGCACCCCTC	SHANK3 H2A(-104-80)
2369	CGCTCATGCTGGCCACACCGCACCC	SHANK3 H2A(-101-77)
2370	TCCCGCTCATGCTGGCCACACCGCA	SHANK3 H2A(-98-74)
2371	CCGTCCCGCTCATGCTGGCCACACC	SHANK3 H2A(-95-71)
2372	ACCCCGTCCCGCTCATGCTGGCCAC	SHANK3 H2A(-92-68)
2373	CAAACCCCGTCCCGCTCATGCTGGC	SHANK3 H2A(-89-65)
2374	GCACAAACCCCGTCCCGCTCATGCT	SHANK3 H2A(-86-62)
2375	CATGCACAAACCCCGTCCCGCTCAT	SHANK3 H2A(-83-59)
2376	GTCCATGCACAAACCCCGTCCCGCT	SHANK3 H2A(-80-56)
2377	TGAGTCCATGCACAAACCCCGTCCC	SHANK3 H2A(-77-53)
2378	AAGTGAGTCCATGCACAAACCCCGT	SHANK3 H2A(-74-50)
2379	AGCAAGTGAGTCCATGCACAAACCC	SHANK3 H2A(-71-47)
2380	CTGAGCAAGTGAGTCCATGCACAAA	SHANK3 H2A(-68-44)
2381	CGGCTGAGCAAGTGAGTCCATGCAC	SHANK3 H2A(-65-41)
2382	CCCCGGCTGAGCAAGTGAGTCCATG	SHANK3 H2A(-62-38)
2383	CCACCCCGGCTGAGCAAGTGAGTCC	SHANK3 H2A(-59-35)
2384	CCCCACCCCGGCTGAGCAAGTGAG	SHANK3 H2A(-56-32)
2385	ATGCCCCACCCCGGCTGAGCAAGT	SHANK3 H2A(-53-29)
2386	AAAATGCCCCACCCCGGCTGAGCA	SHANK3 H2A(-50-26)
2387	GAGAAAATGCCCCACCCCGGCTGA	SHANK3 H2A(-47-23)
2388	GTAGAGAAAATGCCCCACCCCGGC	SHANK3 H2A(-44-20)
2389	AAGGTAGAGAAAATGCCCCACCCC	SHANK3 H2A(-41-17)
2390	GAAAAGGTAGAGAAAATGCCCCAC	SHANK3 H2A(-38-14)
2391	AAAGAAAAGGTAGAGAAAATGCCCC	SHANK3 H2A(-35-11)
2392	GATAAAGAAAAGGTAGAGAAAATGC	SHANK3 H2A(-32-8)
2393	TCAGATAAAGAAAAGGTAGAGAAAA	SHANK3 H2A(-29-5)
2394	TGCTCAGATAAAGAAAAGGTAGAGA	SHANK3 H2A(-26-2)
2395	ACCTCCAGGTAGGGCAG	SHANK3 H1D(+15-2)
2396	CTTACCTCCAGGTAGGG	SHANK3 H1D(+12-5)
2397	CCACTTACCTCCAGGTA	SHANK3 H1D(+9-8)
2398	CGGCCACTTACCTCCAG	SHANK3 H1D(+6-11)

2399	CGCCGGCCACTTACCTC	SHANK3 H1D(+3-14)
2400	CCGCGCCGGCCACTTAC	SHANK3 H1D(-1-17)
2401	CCCCCGCGCCGGCCACT	SHANK3 H1D(-4-20)
2402	TCACCCCGCGCCGGCC	SHANK3 H1D(-7-23)
2403	AGCTACCCCGCGCCG	SHANK3 H1D(-10-26)
2404	CTCAGCTACCCCGCG	SHANK3 H1D(-13-29)
2405	CTCCTCAGCTACCCCC	SHANK3 H1D(-16-32)
2406	GCGCTCCTCAGCTACC	SHANK3 H1D(-19-35)
2407	TGCGCGCTCCTCAGCTC	SHANK3 H1D(-22-38)
2408	CCCTGCGCGCTCCTCAG	SHANK3 H1D(-25-41)
2409	CCACCCTGCGCGCTCCT	SHANK3 H1D(-28-44)
2410	GATCCACCCTGCGCGCT	SHANK3 H1D(-31-47)
2411	GGTGATCCACCCTGCGC	SHANK3 H1D(-34-50)
2412	CTTGGTGATCCACCCTG	SHANK3 H1D(-37-53)
2413	GGGCTTGGTGATCCACC	SHANK3 H1D(-40-56)
2414	ACGGGGCTTGGTGATCC	SHANK3 H1D(-43-59)
2415	GCCACGGGGCTTGGTGA	SHANK3 H1D(-46-62)
2416	CCCGCCACGGGGCTTGG	SHANK3 H1D(-49-65)
2417	GGTCCCGCCACGGGGCT	SHANK3 H1D(-52-68)
2418	ACTGGTCCCGCCACGGG	SHANK3 H1D(-55-71)
2419	TTCCTGGTCCCGCCAC	SHANK3 H1D(-58-74)
2420	CCCTTCACTGGTCCCGC	SHANK3 H1D(-61-77)
2421	GTGCCCTTCACTGGTCC	SHANK3 H1D(-64-80)
2422	GCCGTGCCCTTCACTGG	SHANK3 H1D(-67-83)
2423	ACTGCCGTGCCCTTAC	SHANK3 H1D(-70-86)
2424	CCCACTGCCGTGCCCTT	SHANK3 H1D(-73-89)
2425	TTCCCCACTGCCGTGCC	SHANK3 H1D(-76-92)
2426	TGTTTCCCCACTGCCGT	SHANK3 H1D(-79-95)
2427	TTGTGTTTCCCCACTGC	SHANK3 H1D(-82-98)
2428	CACTTGTGTTTCCCCAC	SHANK3 H1D(-85-101)
2429	TCCCACTTGTGTTTCCC	SHANK3 H1D(-88-104)
2430	CCCTCCCACTTGTGTTT	SHANK3 H1D(-91-107)
2431	CACCCCTCCCACTTGTG	SHANK3 H1D(-94-110)
2432	CCTCACCCCTCCCACTT	SHANK3 H1D(-97-113)
2433	ACCCCTCACCCCTCCCA	SHANK3 H1D(-100-116)
2434	TCCACCCCTCACCCCTC	SHANK3 H1D(-103-119)

2435	GCCTCCACCCCTCACCC	SHANK3 H1D(-106-122)
2436	ACAGCCTCCACCCCTCA	SHANK3 H1D(-109-125)
2437	CACACAGCCTCCACCCC	SHANK3 H1D(-112-128)
2438	ACACACACAGCCTCCAC	SHANK3 H1D(-115-131)
2439	CACACACACACAGCCTC	SHANK3 H1D(-118-134)
2440	ACACACACACACACAGC	SHANK3 H1D(-121-137)
2441	CACACACACACACACAC	SHANK3 H1D(-124-140)
2442	ACACACACACACACACA	SHANK3 H1D(-127-143)
2443	CACCACACACACACACA	SHANK3 H1D(-139-155)
2444	CAGCACCACACACACAC	SHANK3 H1D(-142-158)
2445	ACACAGCACCACACACA	SHANK3 H1D(-145-161)
2446	TGCACACAGCACCACAC	SHANK3 H1D(-148-164)
2447	CTCTGCACACAGCACCA	SHANK3 H1D(-151-167)
2448	GCACTCTGCACACAGCA	SHANK3 H1D(-154-170)
2449	ACTGCACTCTGCACACA	SHANK3 H1D(-157-173)
2450	CTCACTGCACTCTGCAC	SHANK3 H1D(-160-176)
2451	ACGCTCACTGCACTCTG	SHANK3 H1D(-163-179)
2452	TACACGCTCACTGCACT	SHANK3 H1D(-166-182)
2453	CTGTACACGCTCACTGC	SHANK3 H1D(-169-185)
2454	ACCCTGTACACGCTCAC	SHANK3 H1D(-172-188)
2455	TGCACCCTGTACACGCT	SHANK3 H1D(-175-191)
2456	CGCTGCACCTGTACAC	SHANK3 H1D(-178-194)
2457	GCTCGCTGCACCCTGTA	SHANK3 H1D(-181-197)
2458	TCCGCTCGCTGCACCCT	SHANK3 H1D(-184-200)
2459	GTGTCCGCTCGCTGCAC	SHANK3 H1D(-187-203)
2460	ACTGTGTCCGCTCGCTG	SHANK3 H1D(-190-206)
2461	TACACTGTGTCCGCTCG	SHANK3 H1D(-193-209)
2462	GCATACACTGTGTCCGC	SHANK3 H1D(-196-212)
2463	ATCGCATACACTGTGTC	SHANK3 H1D(-199-215)
2464	CTCATCGCATACACTGT	SHANK3 H1D(-202-218)
2465	CTACTCATCGCATACAC	SHANK3 H1D(-205-221)
2466	CGCCTACTCATCGCATA	SHANK3 H1D(-208-224)
2467	CCGCGCCTACTCATCGC	SHANK3 H1D(-211-227)
2468	ACACCGCGCCTACTCAT	SHANK3 H1D(-214-230)
2469	CACACACCGCGCCTACT	SHANK3 H1D(-217-233)
2470	CTGCACACACCGCGCCT	SHANK3 H1D(-220-236)

2471	TCACTGCACACACCGCG	SHANK3 H1D(-223-239)
2472	CGCTCACTGCACACACC	SHANK3 H1D(-226-242)
2473	GCCCGCTCACTGCACAC	SHANK3 H1D(-229-245)
2474	CCTGCCCCGCTCACTGCA	SHANK3 H1D(-232-248)
2475	CGCCCTGCCCGCTCACT	SHANK3 H1D(-235-251)
2476	GCTCGCCCTGCCCGCTC	SHANK3 H1D(-238-254)
2477	ACTGCTCGCCCTGCCCG	SHANK3 H1D(-241-257)
2478	CTTACTGCTCGCCCTGC	SHANK3 H1D(-244-260)
2479	ATCCTTACTGCTCGCCC	SHANK3 H1D(-247-263)
2480	TACATCCTTACTGCTCG	SHANK3 H1D(-250-266)
2481	CTGTACATCCTTACTGC	SHANK3 H1D(-253-269)
2482	AACTGTACATCCTTAC	SHANK3 H1D(-256-272)
2483	CCCACACTGTACATCCT	SHANK3 H1D(-259-275)
2484	CTGCCCACACTGTACAT	SHANK3 H1D(-262-278)
2485	AACTGCCACACTGTA	SHANK3 H1D(-265-281)
2486	CGCACACTGCCACACT	SHANK3 H1D(-268-284)
2487	GCTCGCACACTGCCAC	SHANK3 H1D(-271-287)
2488	CATGCTCGCACACTGCC	SHANK3 H1D(-274-290)
2489	ACACATGCTCGCACACT	SHANK3 H1D(-277-293)
2490	ACTACACATGCTCGCAC	SHANK3 H1D(-280-296)
2491	CTCACTACACATGCTCG	SHANK3 H1D(-283-299)
2492	CTGCTCACTACACATGC	SHANK3 H1D(-286-302)
2493	TGCCTGCTCACTACACA	SHANK3 H1D(-289-305)
2494	CACTGCCTGCTCACTAC	SHANK3 H1D(-292-308)
2495	ACACACTGCCTGCTCAC	SHANK3 H1D(-295-311)
2496	TGCACACACTGCCTGCT	SHANK3 H1D(-298-314)
2497	AACTGCACACACTGCCT	SHANK3 H1D(-301-317)
2498	GCTAACTGCACACACTG	SHANK3 H1D(-304-320)
2499	CCTGCTAACTGCACACA	SHANK3 H1D(-307-323)
2500	GTGCCTGCTAACTGCAC	SHANK3 H1D(-310-326)
2501	ACTGTGCCTGCTAACTG	SHANK3 H1D(-313-329)
2502	CACACTGTGCCTGCTAA	SHANK3 H1D(-316-332)
2503	GCACACACTGTGCCTGC	SHANK3 H1D(-319-335)
2504	ACTGCACACACTGTGCC	SHANK3 H1D(-322-338)
2505	CTCACTGCACACACTGT	SHANK3 H1D(-325-341)
2506	CCACTCACTGCACACAC	SHANK3 H1D(-328-344)

2507	TGCCCCACTCACTGCACA	SHANK3 H1D(-331-347)
2508	CACTGCCCCACTCACTGC	SHANK3 H1D(-334-350)
2509	GCACACTGCCCCACTCAC	SHANK3 H1D(-337-353)
2510	TGTGCACACTGCCCCACT	SHANK3 H1D(-340-356)
2511	TGCTGTGCACACTGCCC	SHANK3 H1D(-343-359)
2512	ACATGCTGTGCACACTG	SHANK3 H1D(-346-362)
2513	TGTACATGCTGTGCACA	SHANK3 H1D(-349-365)
2514	CACTGTACATGCTGTGC	SHANK3 H1D(-352-368)
2515	TCACACTGTACATGCTG	SHANK3 H1D(-355-371)
2516	CACTCACACTGTACATG	SHANK3 H1D(-358-374)
2517	CACCACTCACACTGTAC	SHANK3 H1D(-361-377)
2518	ACACACCACTCACACTG	SHANK3 H1D(-364-380)
2519	AGCACACACCACTCACA	SHANK3 H1D(-367-383)
2520	CACAGCACACACCACTC	SHANK3 H1D(-370-386)
2521	GCACACAGCACACACCA	SHANK3 H1D(-373-389)
2522	ACGGCACACAGCACACA	SHANK3 H1D(-376-392)
2523	CTCACGGCACACAGCAC	SHANK3 H1D(-379-395)
2524	ATGCTCACGGCACACAG	SHANK3 H1D(-382-398)
2525	CACATGCTCACGGCACA	SHANK3 H1D(-385-401)
2526	CTACACATGCTCACGGC	SHANK3 H1D(-388-404)
2527	TCACTACACATGCTCAC	SHANK3 H1D(-391-407)
2528	CACTCACTACACATGCT	SHANK3 H1D(-394-410)
2529	GCCCCACTCACTACACAT	SHANK3 H1D(-397-413)
2530	TGTGCCCCACTCACTACA	SHANK3 H1D(-400-416)
2531	CACTGTGCCCCACTCACT	SHANK3 H1D(-403-419)
2532	CTGCACTGTGCCCCACTC	SHANK3 H1D(-406-422)
2533	TGACTGCACTGTGCCCA	SHANK3 H1D(-409-425)
2534	CACTGACTGCACTGTGC	SHANK3 H1D(-412-428)
2535	GCACACTGACTGCACTG	SHANK3 H1D(-415-431)
2536	TGTGCACACTGACTGCA	SHANK3 H1D(-418-434)
2537	CTTTGTGCACACTGACT	SHANK3 H1D(-421-437)
2538	ATACTTTGTGCACACTG	SHANK3 H1D(-424-440)
2539	TGCATACTTTGTGCACA	SHANK3 H1D(-427-443)
2540	CACTGCATACTTTGTGC	SHANK3 H1D(-430-446)
2541	GCCCCACTGCATACTTTG	SHANK3 H1D(-433-449)
2542	CGTGCCCCACTGCATACT	SHANK3 H1D(-436-452)

2543	GTACGTGCCCCACTGCAT	SHANK3 H1D(-439-455)
2544	ACGGTACGTGCCCCACTG	SHANK3 H1D(-442-458)
2545	CACACGGTACGTGCCCA	SHANK3 H1D(-445-461)
2546	GCACACACGGTACGTGC	SHANK3 H1D(-448-464)
2547	ACTGCACACACGGTACG	SHANK3 H1D(-451-467)
2548	CTCACTGCACACACGGT	SHANK3 H1D(-454-470)
2549	ACACCACTCACTGCACA	SHANK3 H1D(-460-476)
2550	TGCACACCACTCACTGC	SHANK3 H1D(-463-479)
2551	CACTGCACACCACTCAC	SHANK3 H1D(-466-482)
2552	ACACACTGCACACCACT	SHANK3 H1D(-469-485)
2553	ACTACACACTGCACACC	SHANK3 H1D(-472-488)
2554	CACACTACACACTGCAC	SHANK3 H1D(-475-491)
2555	CTGCACACTACACACTG	SHANK3 H1D(-478-494)
2556	TCACTGCACACTACACA	SHANK3 H1D(-481-497)
2557	TGCTCACTGCACACTAC	SHANK3 H1D(-484-500)
2558	CACTGCTCACTGCACAC	SHANK3 H1D(-487-503)
2559	ACACACTGCTCACTGCA	SHANK3 H1D(-490-506)
2560	TGTACACACTGCTCACT	SHANK3 H1D(-493-509)
2561	TGCTGTACACACTGCTC	SHANK3 H1D(-496-512)
2562	CAATGCTGTACACACTG	SHANK3 H1D(-499-515)
2563	CTGCAATGCTGTACACA	SHANK3 H1D(-502-518)
2564	ACACTGCAATGCTGTAC	SHANK3 H1D(-505-521)
2565	CCCACACTGCAATGCTG	SHANK3 H1D(-508-524)
2566	TGCCCCACACTGCAATG	SHANK3 H1D(-511-527)
2567	CACTGCCCCACACTGCA	SHANK3 H1D(-514-530)
2568	ACTCACTGCCCCACACT	SHANK3 H1D(-517-533)
2569	TGTACTCACTGCCCCAC	SHANK3 H1D(-520-536)
2570	CACTGTACTCACTGCCC	SHANK3 H1D(-523-539)
2571	TCACACTGTACTCACTG	SHANK3 H1D(-526-542)
2572	CACTCACACTGTACTCA	SHANK3 H1D(-529-545)
2573	CAACACTCACACTGTAC	SHANK3 H1D(-532-548)
2574	TCACAACACTCACACTG	SHANK3 H1D(-535-551)
2575	CAATCACAACACTCACA	SHANK3 H1D(-538-554)
2576	CCACAATCACAACACTC	SHANK3 H1D(-541-557)
2577	TTACCACAATCACAACA	SHANK3 H1D(-544-560)
2578	TGCTTACCACAATCACA	SHANK3 H1D(-547-563)

2579	TCCTGCTTACCACAATC	SHANK3 H1D(-550-566)
2580	GCATCCTGCTTACCACA	SHANK3 H1D(-553-569)
2581	TGCGCATCCTGCTTACC	SHANK3 H1D(-556-572)
2582	TACTGCGCATCCTGCTT	SHANK3 H1D(-559-575)
2583	GTATACTGCGCATCCTG	SHANK3 H1D(-562-578)
2584	ACTGTATACTGCGCATC	SHANK3 H1D(-565-581)
2585	TTCACTGTATACTGCGC	SHANK3 H1D(-568-584)
2586	CTGTTCACGTATACTG	SHANK3 H1D(-571-587)
2587	ACACTGTTCACTGTATA	SHANK3 H1D(-574-590)
2588	TGCACACTGTTCACTGT	SHANK3 H1D(-577-593)
2589	CTGTGCACACTGTTCAC	SHANK3 H1D(-580-596)
2590	ACACTGTGCACACTGTT	SHANK3 H1D(-583-599)
2591	CACACACTGTGCACACT	SHANK3 H1D(-586-602)
2592	CTGCACACACTGTGCAC	SHANK3 H1D(-589-605)
2593	ACACTGCACACACTGTG	SHANK3 H1D(-592-608)
2594	CCCACACTGCACACACT	SHANK3 H1D(-595-611)
2595	CAGCCCACACTGCACAC	SHANK3 H1D(-598-614)
2596	ACACAGCCCACACTGCA	SHANK3 H1D(-601-617)
2597	GGCACACAGCCCACACT	SHANK3 H1D(-604-620)
2598	TGTGGCACACAGCCCAC	SHANK3 H1D(-607-623)
2599	CTCTGTGGCACACAGCC	SHANK3 H1D(-610-626)
2600	TGACTCTGTGGCACACA	SHANK3 H1D(-613-629)
2601	CACTGACTCTGTGGCAC	SHANK3 H1D(-616-632)
2602	CCACACTGACTCTGTGG	SHANK3 H1D(-619-635)
2603	ACACCACACTGACTCTG	SHANK3 H1D(-622-638)
2604	CACACACCACACTGACT	SHANK3 H1D(-625-641)
2605	CTACACACACCACACTG	SHANK3 H1D(-628-644)
2606	AAACTACACACCACA	SHANK3 H1D(-631-647)
2607	TTCAAACACTACACACC	SHANK3 H1D(-634-650)
2608	CTGTTCAAACACTACAC	SHANK3 H1D(-637-653)
2609	ACACTGTTCAAACACTACA	SHANK3 H1D(-640-656)
2610	CACACACTGTTCAAAC	SHANK3 H1D(-643-659)
2611	ATGCACACACTGTTCAA	SHANK3 H1D(-646-662)
2612	TCAATGCACACACTGTT	SHANK3 H1D(-649-665)
2613	TGCTCAATGCACACACT	SHANK3 H1D(-652-668)
2614	TGCTGCTCAATGCACAC	SHANK3 H1D(-655-671)

2615	CCATGCTGCTCAATGCA	SHANK3 H1D(-658-674)
2616	CATCCATGCTGCTCAAT	SHANK3 H1D(-661-677)
2617	CACCATCCATGCTGCTC	SHANK3 H1D(-664-680)
2618	CCACACCATCCATGCTG	SHANK3 H1D(-667-683)
2619	CGTCCACACCATCCATG	SHANK3 H1D(-670-686)
2620	CAGCGTCCACACCATCC	SHANK3 H1D(-673-689)
2621	GCTCAGCGTCCACACCA	SHANK3 H1D(-676-692)
2622	AATGCTCAGCGTCCACA	SHANK3 H1D(-679-695)
2623	AACAATGCTCAGCGTCC	SHANK3 H1D(-682-698)
2624	GAGAACAATGCTCAGCG	SHANK3 H2A(-686-670)
2625	CTGGAGAACAATGCTCA	SHANK3 H2A(-683-667)
2626	TCCCTGGAGAACAATGC	SHANK3 H2A(-680-664)
2627	TCCTCCTGGAGAACAA	SHANK3 H2A(-677-661)
2628	CACTCCTCCTGGAGAA	SHANK3 H2A(-674-658)
2629	TCACACTCCTCCTGGA	SHANK3 H2A(-671-655)
2630	TGCTCACACTCCTCCCT	SHANK3 H2A(-668-652)
2631	TCGTGCTCACACTCCTC	SHANK3 H2A(-665-649)
2632	CTCTCGTGCTCACACTC	SHANK3 H2A(-662-646)
2633	ACTCTCTCGTGCTCACA	SHANK3 H2A(-659-643)
2634	GGCACTCTCTCGTGCTC	SHANK3 H2A(-656-640)
2635	TCTGGCACTCTCTCGTG	SHANK3 H2A(-653-637)
2636	CCCTCTGGCACTCTCTC	SHANK3 H2A(-650-634)
2637	CACCCCTCTGGCACTCT	SHANK3 H2A(-647-631)
2638	ACACACCCCTCTGGCAC	SHANK3 H2A(-644-628)
2639	ACCACACACCCCTCTGG	SHANK3 H2A(-641-625)
2640	CACACCACACCCCTCTC	SHANK3 H2A(-638-622)
2641	GCTCACACCACACACCC	SHANK3 H2A(-635-619)
2642	CCTGCTCACACCACACA	SHANK3 H2A(-632-616)
2643	AGCCCTGCTCACACCAC	SHANK3 H2A(-629-613)
2644	GATAGCCCTGCTCACAC	SHANK3 H2A(-626-610)
2645	ACAGATAGCCCTGCTCA	SHANK3 H2A(-623-607)
2646	CACACAGATAGCCCTGC	SHANK3 H2A(-620-604)
2647	GTGCACACAGATAGCCC	SHANK3 H2A(-617-601)
2648	AACGTGCACACAGATAG	SHANK3 H2A(-614-598)
2649	ACAAACGTGCACACAGA	SHANK3 H2A(-611-595)
2650	GGAACAAACGTGCACAC	SHANK3 H2A(-608-592)

2651	AAAGGAACAAACGTGCA	SHANK3 H2A(-605-589)
2652	GAGAAAGGAACAAACGT	SHANK3 H2A(-602-586)
2653	CTGGAGAAAGGAACAAA	SHANK3 H2A(-599-583)
2654	CAGCTGGAGAAAGGAAC	SHANK3 H2A(-596-580)
2655	TCACAGCTGGAGAAAGG	SHANK3 H2A(-593-577)
2656	ACTTCACAGCTGGAGAA	SHANK3 H2A(-590-574)
2657	AAGACTTCACAGCTGGA	SHANK3 H2A(-587-571)
2658	CACAAGACTTCACAGCT	SHANK3 H2A(-584-568)
2659	CTTCACAAGACTTCACA	SHANK3 H2A(-581-565)
2660	GGCCTTCACAAGACTTC	SHANK3 H2A(-578-562)
2661	GTTGGCCTTCACAAGAC	SHANK3 H2A(-575-559)
2662	TTGGTTGGCCTTCACAA	SHANK3 H2A(-572-556)
2663	GACTTGGTTGGCCTTCA	SHANK3 H2A(-569-553)
2664	GGGGACTTGGTTGGCCT	SHANK3 H2A(-566-550)
2665	GGAGGGGACTTGGTTGG	SHANK3 H2A(-563-547)
2666	AAAGGAGGGGACTTGGT	SHANK3 H2A(-560-544)
2667	AGTAAAGGAGGGGACTT	SHANK3 H2A(-557-541)
2668	GTGAGTAAAGGAGGGGA	SHANK3 H2A(-554-538)
2669	TGGGTGAGTAAAGGAGG	SHANK3 H2A(-551-535)
2670	GCATGGGTGAGTAAAGG	SHANK3 H2A(-548-532)
2671	CATGCATGGGTGAGTAA	SHANK3 H2A(-545-529)
2672	CACCATGCATGGGTGAG	SHANK3 H2A(-542-526)
2673	TCACACCATGCATGGGT	SHANK3 H2A(-539-523)
2674	TCTTCACACCATGCATG	SHANK3 H2A(-536-520)
2675	ACATCTTCACACCATGC	SHANK3 H2A(-533-517)
2676	AATACATCTTCACACCA	SHANK3 H2A(-530-514)
2677	CTCAATACATCTTCACA	SHANK3 H2A(-527-511)
2678	GCACTCAATACATCTTC	SHANK3 H2A(-524-508)
2679	AAGGCACTCAATACATC	SHANK3 H2A(-521-505)
2680	AGCAAGGCACTCAATAC	SHANK3 H2A(-518-502)
2681	CCTAGCAAGGCACTCAA	SHANK3 H2A(-515-499)
2682	ATGCCTAGCAAGGCACT	SHANK3 H2A(-512-496)
2683	CCCATGCCTAGCAAGGC	SHANK3 H2A(-509-493)
2684	GTCCCCATGCCTAGCAA	SHANK3 H2A(-506-490)
2685	TACGTCCCCATGCCTAG	SHANK3 H2A(-503-487)
2686	GTCTACGTCCCCATGCC	SHANK3 H2A(-500-484)

2687	CCCGTCTACGTCCCAT	SHANK3 H2A(-497-481)
2688	GACCCCGTCTACGTCCC	SHANK3 H2A(-494-478)
2689	ACTGACCCCGTCTACGT	SHANK3 H2A(-491-475)
2690	AGGACTGACCCCGTCTA	SHANK3 H2A(-488-472)
2691	CACAGGACTGACCCCGT	SHANK3 H2A(-485-469)
2692	TTCCACAGGACTGACCC	SHANK3 H2A(-482-466)
2693	ACCTTCCACAGGACTGA	SHANK3 H2A(-479-463)
2694	AAGACCTTCCACAGGAC	SHANK3 H2A(-476-460)
2695	TCCAAGACCTTCCACAG	SHANK3 H2A(-473-457)
2696	AACTCCAAGACCTTCCA	SHANK3 H2A(-470-454)
2697	CCAAACTCCAAGACCTT	SHANK3 H2A(-467-451)
2698	CTGCCAAACTCCAAGAC	SHANK3 H2A(-464-448)
2699	ACCCTGCCAAACTCCAA	SHANK3 H2A(-461-445)
2700	TCCACCCTGCCAAACTC	SHANK3 H2A(-458-442)
2701	CCCTCCACCCTGCCAAA	SHANK3 H2A(-455-439)
2702	CCCCCTCCACCCTGCC	SHANK3 H2A(-452-436)
2703	GCACCCCCCTCCACCCT	SHANK3 H2A(-449-433)
2704	TGGGCACCCCCCTCCAC	SHANK3 H2A(-446-430)
2705	AGTTGGGCACCCCCCTC	SHANK3 H2A(-443-427)
2706	TGCAGTTGGGCACCCCC	SHANK3 H2A(-440-424)
2707	CACTGCAGTTGGGCACC	SHANK3 H2A(-437-421)
2708	GCCCACTGCAGTTGGGC	SHANK3 H2A(-434-418)
2709	AATGCCCACTGCAGTTG	SHANK3 H2A(-431-415)
2710	TTCAATGCCCACTGCAG	SHANK3 H2A(-428-412)
2711	TTATTCAATGCCCACTG	SHANK3 H2A(-425-409)
2712	TCTTTATTCAATGCCCA	SHANK3 H2A(-422-406)
2713	AAATCTTTATTCAATGC	SHANK3 H2A(-419-403)
2714	ACAAAATCTTTATTCAA	SHANK3 H2A(-416-400)
2715	CTCACAAAATCTTTATT	SHANK3 H2A(-413-397)
2716	CAGCTCACAAAATCTTT	SHANK3 H2A(-410-394)
2717	GCTCAGCTCACAAAATC	SHANK3 H2A(-407-391)
2718	TGAGCTCAGCTCACAAA	SHANK3 H2A(-404-388)
2719	CTTTGAGCTCAGCTCAC	SHANK3 H2A(-401-385)
2720	CAACTTTGAGCTCAGCT	SHANK3 H2A(-398-382)
2721	GCCCAACTTTGAGCTCA	SHANK3 H2A(-395-379)
2722	CCCGCCCAACTTTGAGC	SHANK3 H2A(-392-376)

2723	AGGCCCGCCCAACTTTG	SHANK3 H2A(-389-373)
2724	CGGAGGCCCGCCCAACT	SHANK3 H2A(-386-370)
2725	CCACGGAGGCCCGCCCA	SHANK3 H2A(-383-367)
2726	CCACCACGGAGGCCCGC	SHANK3 H2A(-380-364)
2727	GTGCCACCACGGAGGCC	SHANK3 H2A(-377-361)
2728	CCTGTGCCACCACGGAG	SHANK3 H2A(-374-358)
2729	TTTCCTGTGCCACCACG	SHANK3 H2A(-371-355)
2730	CACTTTCCTGTGCCACC	SHANK3 H2A(-368-352)
2731	CCCCACTTTCCTGTGCC	SHANK3 H2A(-365-349)
2732	TGACCCCACTTTCCTGT	SHANK3 H2A(-362-346)
2733	AACTGACCCCACTTTC	SHANK3 H2A(-359-343)
2734	TAGAACTGACCCCACTT	SHANK3 H2A(-356-340)
2735	AGGTAGAAGTACCCCA	SHANK3 H2A(-353-337)
2736	TCCAGGTAGAAGTACCC	SHANK3 H2A(-350-334)
2737	CTCTCCAGGTAGAAGT	SHANK3 H2A(-347-331)
2738	CCACTCTCCAGGTAGAA	SHANK3 H2A(-344-328)
2739	CCTCCACTCTCCAGGTA	SHANK3 H2A(-341-325)
2740	CCCCCTCCACTCTCCAG	SHANK3 H2A(-338-322)
2741	CATCCCCCTCCACTCTC	SHANK3 H2A(-335-319)
2742	AGACATCCCCCTCCACT	SHANK3 H2A(-332-316)
2743	CCTAGACATCCCCCTCC	SHANK3 H2A(-329-313)
2744	CATCCTAGACATCCCCC	SHANK3 H2A(-326-310)
2745	TACCATCCTAGACATCC	SHANK3 H2A(-323-307)
2746	GCTTACCATCCTAGACA	SHANK3 H2A(-320-304)
2747	CAGGCTTACCATCCTAG	SHANK3 H2A(-317-301)
2748	TTCCAGGCTTACCATCC	SHANK3 H2A(-314-298)
2749	TGATTCCAGGCTTACCA	SHANK3 H2A(-311-295)
2750	GCCTGATTCCAGGCTTA	SHANK3 H2A(-308-292)
2751	AAGGCCTGATTCCAGGC	SHANK3 H2A(-305-289)
2752	CTGAAGGCCTGATTCCA	SHANK3 H2A(-302-286)
2753	TCTCTGAAGGCCTGATT	SHANK3 H2A(-299-283)
2754	TCCTCTCTGAAGGCCTG	SHANK3 H2A(-296-280)
2755	CACTCCTCTCTGAAGGC	SHANK3 H2A(-293-277)
2756	TCCCACTCCTCTCTGAA	SHANK3 H2A(-290-274)
2757	AAATCCCCTCCTCTCT	SHANK3 H2A(-287-271)
2758	GCAAAATCCCCTCCTC	SHANK3 H2A(-284-268)

2759	TCGGCAAAATCCCACTC	SHANK3 H2A(-281-265)
2760	TTCTCGGCAAAATCCCA	SHANK3 H2A(-278-262)
2761	GGATTCTCGGCAAAATC	SHANK3 H2A(-275-259)
2762	CCAGGATTCTCGGCAAA	SHANK3 H2A(-272-256)
2763	TCCCCAGGATTCTCGGC	SHANK3 H2A(-269-253)
2764	CCATCCCCAGGATTCTC	SHANK3 H2A(-266-250)
2765	TTCCCATCCCCAGGATT	SHANK3 H2A(-263-247)
2766	GCCTTCCCATCCCCAGG	SHANK3 H2A(-260-244)
2767	GTCGCCTTCCCATCCCC	SHANK3 H2A(-257-241)
2768	CCCGTCGCCTTCCCATC	SHANK3 H2A(-254-238)
2769	TGTCCCGTCGCCTTCCC	SHANK3 H2A(-251-235)
2770	CACTGTCCCGTCGCCTT	SHANK3 H2A(-248-232)
2771	CTGCACTGTCCCGTCGC	SHANK3 H2A(-245-229)
2772	AGCCTGCACTGTCCCGT	SHANK3 H2A(-242-226)
2773	CGCAGCCTGCACTGTCC	SHANK3 H2A(-239-223)
2774	GCCCGCAGCCTGCACTG	SHANK3 H2A(-236-220)
2775	GCTGCCCGCAGCCTGCA	SHANK3 H2A(-233-217)
2776	CTAGTGCCCGCAGCCT	SHANK3 H2A(-230-214)
2777	TGCCTAGCTGCCCGCAG	SHANK3 H2A(-227-211)
2778	ACGTGCCTAGCTGCCCG	SHANK3 H2A(-224-208)
2779	GGCACGTGCCTAGCTGC	SHANK3 H2A(-221-205)
2780	GAAGGCACGTGCCTAGC	SHANK3 H2A(-218-202)
2781	ATGGAAGGCACGTGCCT	SHANK3 H2A(-215-199)
2782	CCGATGGAAGGCACGTG	SHANK3 H2A(-212-196)
2783	AGCCCGATGGAAGGCAC	SHANK3 H2A(-209-193)
2784	TGCAGCCCGATGGAAGG	SHANK3 H2A(-206-190)
2785	TGATGCAGCCCGATGGA	SHANK3 H2A(-203-187)
2786	GCATGATGCAGCCCGAT	SHANK3 H2A(-200-184)
2787	CAGGCATGATGCAGCCC	SHANK3 H2A(-197-181)
2788	ACTCAGGCATGATGCAG	SHANK3 H2A(-194-178)
2789	CACACTCAGGCATGATG	SHANK3 H2A(-191-175)
2790	CACCACACTCAGGCATG	SHANK3 H2A(-188-172)
2791	ACCCACCACACTCAGGC	SHANK3 H2A(-185-169)
2792	TGCACCCACCACACTCA	SHANK3 H2A(-182-166)
2793	CCATGCACCCACCACAC	SHANK3 H2A(-179-163)
2794	CTGCCATGCACCCACCA	SHANK3 H2A(-176-160)

2795	CAGCTGCCATGCACCCA	SHANK3 H2A(-173-157)
2796	TAACAGCTGCCATGCAC	SHANK3 H2A(-170-154)
2797	AGCTAACAGCTGCCATG	SHANK3 H2A(-167-151)
2798	CAGAGCTAACAGCTGCC	SHANK3 H2A(-164-148)
2799	GGACAGAGCTAACAGCT	SHANK3 H2A(-161-145)
2800	AGTGGACAGAGCTAACA	SHANK3 H2A(-158-142)
2801	CACAGTGGACAGAGCTA	SHANK3 H2A(-155-139)
2802	TACCACAGTGGACAGAG	SHANK3 H2A(-152-136)
2803	TACTACCACAGTGGACA	SHANK3 H2A(-149-133)
2804	TCATACTACCACAGTGG	SHANK3 H2A(-146-130)
2805	CAGTCATACTACCACAG	SHANK3 H2A(-143-127)
2806	CATCAGTCATACTACCA	SHANK3 H2A(-140-124)
2807	CACCATCAGTCATACTA	SHANK3 H2A(-137-121)
2808	ACACACCATCAGTCATA	SHANK3 H2A(-134-118)
2809	TGTACACACCATCAGTC	SHANK3 H2A(-131-115)
2810	TCCTGTACACACCATCA	SHANK3 H2A(-128-112)
2811	CCCTCCTGTACACACCA	SHANK3 H2A(-125-109)
2812	CTGCCCTCCTGTACACA	SHANK3 H2A(-122-106)
2813	TCACTGCCCTCCTGTAC	SHANK3 H2A(-119-103)
2814	CCCTCACTGCCCTCCTG	SHANK3 H2A(-116-100)
2815	CACCCCTCACTGCCCTC	SHANK3 H2A(-113-97)
2816	CCGCACCCCTCACTGCC	SHANK3 H2A(-110-94)
2817	ACACCGCACCCCTCACT	SHANK3 H2A(-107-91)
2818	GCCACACCGCACCCCTC	SHANK3 H2A(-104-88)
2819	CTGGCCACACCGCACCC	SHANK3 H2A(-101-85)
2820	ATGCTGGCCACACCGCA	SHANK3 H2A(-98-82)
2821	CTCATGCTGGCCACACC	SHANK3 H2A(-95-79)
2822	CCGCTCATGCTGGCCAC	SHANK3 H2A(-92-76)
2823	GTCCCGCTCATGCTGGC	SHANK3 H2A(-89-73)
2824	CCCGTCCCGCTCATGCT	SHANK3 H2A(-86-70)
2825	AACCCCGTCCCGCTCAT	SHANK3 H2A(-83-67)
2826	ACAAACCCCGTCCCGCT	SHANK3 H2A(-80-64)
2827	TGCACAAACCCCGTCCC	SHANK3 H2A(-77-61)
2828	CCATGCACAAACCCCGT	SHANK3 H2A(-74-58)
2829	AGTCCATGCACAAACCC	SHANK3 H2A(-71-55)
2830	GTGAGTCCATGCACAAA	SHANK3 H2A(-68-52)

2831	CAAGTGAGTCCATGCAC	SHANK3 H2A(-65-49)
2832	GAGCAAGTGAGTCCATG	SHANK3 H2A(-62-46)
2833	GCTGAGCAAGTGAGTCC	SHANK3 H2A(-59-43)
2834	CCGGCTGAGCAAGTGAG	SHANK3 H2A(-56-40)
2835	ACCCCGGCTGAGCAAGT	SHANK3 H2A(-53-37)
2836	CCCACCCCGGCTGAGCA	SHANK3 H2A(-50-34)
2837	GCCCCACCCCGGCTGA	SHANK3 H2A(-47-31)
2838	AATGCCCCACCCCGGC	SHANK3 H2A(-44-28)
2839	GAAAATGCCCCACCCC	SHANK3 H2A(-41-25)
2840	AGAGAAAATGCCCCAC	SHANK3 H2A(-38-22)
2841	GGTAGAGAAAATGCCCC	SHANK3 H2A(-35-19)
2842	AAAGGTAGAGAAAATGC	SHANK3 H2A(-32-16)
2843	AGAAAAGGTAGAGAAAA	SHANK3 H2A(-29-13)
2844	TAAAGAAAAGGTAGAGA	SHANK3 H2A(-26-10)
2845	AGATAAAGAAAAGGTAG	SHANK3 H2A(-23-7)
2846	CTCAGATAAAGAAAAGG	SHANK3 H2A(-20-4)
2847	CTGCTCAGATAAAGAAA	SHANK3 H2A(-17-1)
2848	AACTGCTCAGATAAAGAAAAGGTAG	SHANK3 H2A(-23+2)
2849	CGAAACTGCTCAGATAAAGAAAAGG	SHANK3 H2A(-20+5)
2850	TATCGAAACTGCTCAGATAAAGAAA	SHANK3 H2A(-17+8)
2851	TTGTATCGAAACTGCTCAGATAAAG	SHANK3 H2A(-14+11)
2852	CGCTTGATCGAAACTGCTCAGATA	SHANK3 H2A(-11+14)
2853	CGCCGCTTGATCGAAACTGCTCAG	SHANK3 H2A(-8+17)
2854	ACTCGCCGCTTGATCGAAACTGCT	SHANK3 H2A(-5+20)
2855	TAAACTCGCCGCTTGATCGAAACT	SHANK3 H2A(-2+23)
2856	GCATAAACTCGCCGCTTGATCGAA	SHANK3 H2A(+2+26)
2857	TGGGCATAAACTCGCCGCTTGATC	SHANK3 H2A(+5+29)
2858	TTCTGGGCATAAACTCGCCGCTTG	SHANK3 H2A(+8+32)
2859	AGGTTCTGGGCATAAACTCGCCGCT	SHANK3 H2A(+11+35)
2860	ATGAGGTTCTGGGCATAAACTCGCC	SHANK3 H2A(+14+38)
2861	TCGATGAGGTTCTGGGCATAAACTC	SHANK3 H2A(+17+41)
2862	TCATCGATGAGGTTCTGGGCATAAA	SHANK3 H2A(+20+44)
2863	TTATCATCGATGAGGTTCTGGGCAT	SHANK3 H2A(+23+47)
2864	TGCTTATCATCGATGAGGTTCTGGG	SHANK3 H2A(+26+50)
2865	AACTGCTTATCATCGATGAGGTTCT	SHANK3 H2A(+29+53)
2866	GCAAACCTGCTTATCATCGATGAGGT	SHANK3 H2A(+32+56)

2867	TTTGCAAAGCTTATCATCGATGA	SHANK3 H2A(+35+59)
2868	AGCTTTGCAAAGCTTATCATCGA	SHANK3 H2A(+38+62)
2869	TGAAGCTTTGCAAAGCTTATCAT	SHANK3 H2A(+41+65)
2870	GTGTGAAGCTTTGCAAAGCTTAT	SHANK3 H2A(+44+68)
2871	TTTGTGTGAAGCTTTGCAAAGCT	SHANK3 H2A(+47+71)
2872	ACCTTTGTGTGAAGCTTTGCAAAG	SHANK3 H2D(+23-2)
2873	TTTACCTTTGTGTGAAGCTTTGCAA	SHANK3 H2D(+20-5)
2874	TCCTTTACCTTTGTGTGAAGCTTTG	SHANK3 H2D(+17-8)
2875	TGATCCTTTACCTTTGTGTGAAGCT	SHANK3 H2D(+14-11)
2876	CCGTGATCCTTTACCTTTGTGTGAA	SHANK3 H2D(+11-14)
2877	TCCCCGTGATCCTTTACCTTTGTGT	SHANK3 H2D(+8-17)
2878	CCCTCCCCGTGATCCTTTACCTTTG	SHANK3 H2D(+5-20)
2879	GCCCCCTCCCCGTGATCCTTTACCT	SHANK3 H2D(+2-23)
2880	GGAGCCCCCTCCCCGTGATCCTTTA	SHANK3 H2D(-2-26)
2881	TCAGGAGCCCCCTCCCCGTGATCCT	SHANK3 H2D(-5-29)
2882	ACCTCAGGAGCCCCCTCCCCGTGAT	SHANK3 H2D(-8-32)
2883	GGAACCTCAGGAGCCCCCTCCCCGT	SHANK3 H2D(-11-35)
2884	GAGGGAACCTCAGGAGCCCCCTCCC	SHANK3 H2D(-14-38)
2885	CAGGAGGGAACCTCAGGAGCCCCCT	SHANK3 H2D(-17-41)
2886	AGGCAGGAGGGAACCTCAGGAGCCC	SHANK3 H2D(-20-44)
2887	GGGAGGCAGGAGGGAACCTCAGGAG	SHANK3 H2D(-23-47)
2888	ACAGGGAGGCAGGAGGGAACCTCAG	SHANK3 H2D(-26-50)
2889	GCCACAGGGAGGCAGGAGGGAACCT	SHANK3 H2D(-29-53)
2890	GCAGCCACAGGGAGGCAGGAGGGAA	SHANK3 H2D(-32-56)
2891	ACAGCAGCCACAGGGAGGCAGGAGG	SHANK3 H2D(-35-59)
2892	GGGACAGCAGCCACAGGGAGGCAGG	SHANK3 H2D(-38-62)
2893	TGGGGGACAGCAGCCACAGGGAGGC	SHANK3 H2D(-41-65)
2894	GGGTGGGGGACAGCAGCCACAGGGA	SHANK3 H2D(-44-68)
2895	CTGGGGTGGGGGACAGCAGCCACAG	SHANK3 H2D(-47-71)
2896	AAGCTGGGGTGGGGGACAGCAGCCA	SHANK3 H2D(-50-74)
2897	CCCAAGCTGGGGTGGGGGACAGCAG	SHANK3 H2D(-53-77)
2898	AGCCCCAAGCTGGGGTGGGGGACAG	SHANK3 H2D(-56-80)
2899	GTCAGCCCCAAGCTGGGGTGGGGGA	SHANK3 H2D(-59-83)
2900	GTGGTCAGCCCCAAGCTGGGGTGGG	SHANK3 H2D(-62-86)
2901	ACTGTGGTCAGCCCCAAGCTGGGGT	SHANK3 H2D(-65-89)
2902	GGGACTGTGGTCAGCCCCAAGCTGG	SHANK3 H2D(-68-92)

2903	TGGGGGACTGTGGTCAGCCCCAAGC	SHANK3 H2D(-71-95)
2904	AGCTGGGGGACTGTGGTCAGCCCCA	SHANK3 H2D(-74-98)
2905	TAAAGCTGGGGGACTGTGGTCAGCC	SHANK3 H2D(-77-101)
2906	AGCTAAAGCTGGGGGACTGTGGTCA	SHANK3 H2D(-80-104)
2907	CTGAGCTAAAGCTGGGGGACTGTGG	SHANK3 H2D(-83-107)
2908	GGAAGCTAAAGCTGGGGGACTG	SHANK3 H2D(-86-110)
2909	AATGGACTGAGCTAAAGCTGGGGGA	SHANK3 H2D(-89-113)
2910	GGAAATGGACTGAGCTAAAGCTGGG	SHANK3 H2D(-92-116)
2911	TGGGGAAATGGACTGAGCTAAAGCT	SHANK3 H2D(-95-119)
2912	TGATGGGGAAATGGACTGAGCTAAA	SHANK3 H2D(-98-122)
2913	TGATGATGGGGAAATGGACTGAGCT	SHANK3 H2D(-101-125)
2914	CCCTGATGATGGGGAAATGGACTGA	SHANK3 H2D(-104-128)
2915	GGCCCCCTGATGATGGGGAAATGGAC	SHANK3 H2D(-107-131)
2916	CTGGGCCCCCTGATGATGGGGAAATG	SHANK3 H2D(-110-134)
2917	GCTCTGGGCCCCCTGATGATGGGGAA	SHANK3 H2D(-113-137)
2918	CAGGCTCTGGGCCCCCTGATGATGGG	SHANK3 H2D(-116-140)
2919	GTACAGGCTCTGGGCCCCCTGATGAT	SHANK3 H2D(-119-143)
2920	CCAGTACAGGCTCTGGGCCCCCTGAT	SHANK3 H2D(-122-146)
2921	CACCCAGTACAGGCTCTGGGCCCCCT	SHANK3 H2D(-125-149)
2922	CCACACCCAGTACAGGCTCTGGGCC	SHANK3 H2D(-128-152)
2923	CAGCCACACCCAGTACAGGCTCTGG	SHANK3 H2D(-131-155)
2924	CTTCAGCCACACCCAGTACAGGCTC	SHANK3 H2D(-134-158)
2925	GCCCTTCAGCCACACCCAGTACAGG	SHANK3 H2D(-137-161)
2926	CCAGCCCTTCAGCCACACCCAGTAC	SHANK3 H2D(-140-164)
2927	TGCCCAGCCCTTCAGCCACACCCAG	SHANK3 H2D(-143-167)
2928	CTGTGCCCAGCCCTTCAGCCACACC	SHANK3 H2D(-146-170)
2929	AATCTGTGCCAGCCCTTCAGCCAC	SHANK3 H2D(-149-173)
2930	AGGAATCTGTGCCAGCCCTTCAGC	SHANK3 H2D(-152-176)
2931	GCCAGGAATCTGTGCCAGCCCTTC	SHANK3 H2D(-155-179)
2932	GGGGCCAGGAATCTGTGCCAGCCC	SHANK3 H2D(-158-182)
2933	CATGGGGCCAGGAATCTGTGCCAG	SHANK3 H2D(-161-185)
2934	AACCATGGGGCCAGGAATCTGTGCC	SHANK3 H2D(-164-188)
2935	CCCAACCATGGGGCCAGGAATCTGT	SHANK3 H2D(-167-191)
2936	GACCCCAACCATGGGGCCAGGAATC	SHANK3 H2D(-170-194)
2937	CCTGACCCCAACCATGGGGCCAGGA	SHANK3 H2D(-173-197)
2938	CCACCTGACCCCAACCATGGGGCCA	SHANK3 H2D(-176-200)

2939	GTACCACCTGACCCCAACCATGGGG	SHANK3 H2D(-179-203)
2940	ACTGTACCACCTGACCCCAACCATG	SHANK3 H2D(-182-206)
2941	ATCACTGTACCACCTGACCCCAACC	SHANK3 H2D(-185-209)
2942	CACATCACTGTACCACCTGACCCCA	SHANK3 H2D(-188-212)
2943	GAACACATCACTGTACCACCTGACC	SHANK3 H2D(-191-215)
2944	CTGGAACACATCACTGTACCACCTG	SHANK3 H2D(-194-218)
2945	TAACTGGAACACATCACTGTACCAC	SHANK3 H2D(-197-221)
2946	ATCTAACTGGAACACATCACTGTAC	SHANK3 H2D(-200-224)
2947	CTGATCTAACTGGAACACATCACTG	SHANK3 H2D(-203-227)
2948	AGTCTGATCTAACTGGAACACATCA	SHANK3 H2D(-206-230)
2949	AAGAGTCTGATCTAACTGGAACACA	SHANK3 H2D(-209-233)
2950	GGCAAGAGTCTGATCTAACTGGAAC	SHANK3 H2D(-212-236)
2951	GTCGGCAAGAGTCTGATCTAACTGG	SHANK3 H2D(-215-239)
2952	GGGGTCTGGCAAGAGTCTGATCTAAC	SHANK3 H2D(-218-242)
2953	AGGGGGGTCTGGCAAGAGTCTGATCT	SHANK3 H2D(-221-245)
2954	GCCAGGGGGGTCTGGCAAGAGTCTGA	SHANK3 H2D(-224-248)
2955	TAAGCCAGGGGGGTCTGGCAAGAGTC	SHANK3 H2D(-227-251)
2956	CCCTAAGCCAGGGGGGTCTGGCAAGA	SHANK3 H2D(-230-254)
2957	AGCCCCTAAGCCAGGGGGGTCTGGCA	SHANK3 H2D(-233-257)
2958	TCCAGCCCCTAAGCCAGGGGGGTCTG	SHANK3 H2D(-236-260)
2959	CACTCCAGCCCCTAAGCCAGGGGGG	SHANK3 H2D(-239-263)
2960	GGACACTCCAGCCCCTAAGCCAGGG	SHANK3 H2D(-242-266)
2961	ACAGGACACTCCAGCCCCTAAGCCA	SHANK3 H2D(-245-269)
2962	CTCACAGGACACTCCAGCCCCTAAG	SHANK3 H2D(-248-272)
2963	CTTCTCACAGGACACTCCAGCCCCT	SHANK3 H2D(-251-275)
2964	CAGCTTCTCACAGGACACTCCAGCC	SHANK3 H2D(-254-278)
2965	ACCCAGCTTCTCACAGGACACTCCA	SHANK3 H2D(-257-281)
2966	TCCACCCAGCTTCTCACAGGACACT	SHANK3 H2D(-260-284)
2967	CTCTCCACCCAGCTTCTCACAGGAC	SHANK3 H2D(-263-287)
2968	TCCCTCTCCACCCAGCTTCTCACAG	SHANK3 H2D(-266-290)
2969	CACTCCCTCTCCACCCAGCTTCTCA	SHANK3 H2D(-269-293)
2970	GTCCACTCCCTCTCCACCCAGCTTC	SHANK3 H2D(-272-296)
2971	CTTGTCCTCCCTCTCCACCCAGC	SHANK3 H2D(-275-299)
2972	ATGCTTGTCCTCCCTCTCCACCC	SHANK3 H2D(-278-302)
2973	CAGATGCTTGTCCTCCCTCTCCA	SHANK3 H2D(-281-305)
2974	CATCAGATGCTTGTCCTCCCTCT	SHANK3 H2D(-284-308)

2975	TCACATCAGATGCTTGCTCACTCCC	SHANK3 H2D(-287-311)
2976	CCATCACATCAGATGCTTGCTCACT	SHANK3 H2D(-290-314)
2977	CAGCCATCAGATGCTTGCTCC	SHANK3 H2D(-293-317)
2978	CGACAGCCATCAGATGCTTG	SHANK3 H2D(-296-320)
2979	TCCCGACAGCCATCAGATGC	SHANK3 H2D(-299-323)
2980	TTGTCCCGACAGCCATCAGACA	SHANK3 H2D(-302-326)
2981	GCCTTGCTCCCGACAGCCATC	SHANK3 H2D(-305-329)
2982	GGTGCCTTGCTCCCGACAGCCATC	SHANK3 H2D(-308-332)
2983	CTGGGTGCCTTGCTCCCGACAGCCAT	SHANK3 H2D(-311-335)
2984	ATGCTGGGTGCCTTGCTCCCGACAGC	SHANK3 H2D(-314-338)
2985	TCGATGCTGGGTGCCTTGCTCCGAC	SHANK3 H2D(-317-341)
2986	CACTCGATGCTGGGTGCCTTGCTCC	SHANK3 H2D(-320-344)
2987	GACCACTCGATGCTGGGTGCCTTG	SHANK3 H2D(-323-347)
2988	GTCGACCACTCGATGCTGGGTGCCT	SHANK3 H2D(-326-350)
2989	CTGGTCGACCACTCGATGCTGGGTG	SHANK3 H2D(-329-353)
2990	GCACTGGTCGACCACTCGATGCTGG	SHANK3 H2D(-332-356)
2991	CTAGCACTGGTCGACCACTCGATGC	SHANK3 H2D(-335-359)
2992	TGCCTAGCACTGGTCGACCACTCGA	SHANK3 H2D(-338-362)
2993	AAATGCCTAGCACTGGTCGACCACT	SHANK3 H2D(-341-365)
2994	CACAAATGCCTAGCACTGGTCGACC	SHANK3 H2D(-344-368)
2995	AATCACAATGCCTAGCACTGGTCG	SHANK3 H2D(-347-371)
2996	TCTAATCACAATGCCTAGCACTGG	SHANK3 H2D(-350-374)
2997	AGGTCTAATCACAATGCCTAGCAC	SHANK3 H2D(-353-377)
2998	GAGAGGTCTAATCACAATGCCTAG	SHANK3 H2D(-356-380)
2999	AATGAGAGGTCTAATCACAATGCC	SHANK3 H2D(-359-383)
3000	ATTAATGAGAGGTCTAATCACAAT	SHANK3 H2D(-362-386)
3001	AGGATTAATGAGAGGTCTAATCACA	SHANK3 H2D(-365-389)
3002	AAGAGGATTAATGAGAGGTCTAATC	SHANK3 H2D(-368-392)
3003	TGGAAGAGGATTAATGAGAGGTCTA	SHANK3 H2D(-371-395)
3004	CTCTGGAAGAGGATTAATGAGAGGT	SHANK3 H2D(-374-398)
3005	TCCCTCTGGAAGAGGATTAATGAGA	SHANK3 H2D(-377-401)
3006	TAGTCCCTCTGGAAGAGGATTAATG	SHANK3 H2D(-380-404)
3007	TAATAGTCCCTCTGGAAGAGGATTA	SHANK3 H2D(-383-407)
3008	TTATAATAGTCCCTCTGGAAGAGGA	SHANK3 H2D(-386-410)
3009	GGGTTATAATAGTCCCTCTGGAAGA	SHANK3 H2D(-389-413)
3010	ACAGGGTTATAATAGTCCCTCTGGA	SHANK3 H2D(-392-416)

3011	GAAACAGGGTTATAATAGTCCCTCT	SHANK3 H2D(-395-419)
3012	TGTGAAACAGGGTTATAATAGTCCC	SHANK3 H2D(-398-422)
3013	ATCTGTGAAACAGGGTTATAATAGT	SHANK3 H2D(-401-425)
3014	CCCATCTGTGAAACAGGGTTATAAT	SHANK3 H2D(-404-428)
3015	GTCCCCATCTGTGAAACAGGGTTAT	SHANK3 H2D(-407-431)
3016	TGTGTCCCCATCTGTGAAACAGGGT	SHANK3 H2D(-410-434)
3017	CTCTGTGTCCCCATCTGTGAAACAG	SHANK3 H2D(-413-437)
3018	GTA CTCTGTGTCCCCATCTGTGAAA	SHANK3 H2D(-416-440)
3019	CGGGTACTCTGTGTCCCCATCTGTG	SHANK3 H2D(-419-443)
3020	AGTCGGGTACTCTGTGTCCCCATCT	SHANK3 H2D(-422-446)
3021	CACAGTCGGGTACTCTGTGTCCCA	SHANK3 H2D(-425-449)
3022	CTACACAGTCGGGTACTCTGTGTCC	SHANK3 H2D(-428-452)
3023	TGTCTACACAGTCGGGTACTCTGTG	SHANK3 H2D(-431-455)
3024	CACTGTCTACACAGTCGGGTACTCT	SHANK3 H2D(-434-458)
3025	CTTCACTGTCTACACAGTCGGGTAC	SHANK3 H2D(-437-461)
3026	CAGCTTCACTGTCTACACAGTCGGG	SHANK3 H2D(-440-464)
3027	CCCCAGCTTCACTGTCTACACAGTC	SHANK3 H2D(-443-467)
3028	CAGCCCCAGCTTCACTGTCTACACA	SHANK3 H2D(-446-470)
3029	GTTCA GCCCCAGCTTCACTGTCTAC	SHANK3 H2D(-449-473)
3030	TGGGTTCA GCCCCAGCTTCACTGTC	SHANK3 H2D(-452-476)
3031	ATCTGGGTTCA GCCCCAGCTTCACT	SHANK3 H2D(-455-479)
3032	CAGATCTGGGTTCA GCCCCAGCTTC	SHANK3 H2D(-458-482)
3033	AGACAGATCTGGGTTCA GCCCCAGC	SHANK3 H2D(-461-485)
3034	ATCAGACAGATCTGGGTTCA GCCCC	SHANK3 H2D(-464-488)
3035	GGAATCAGACAGATCTGGGTTCA GC	SHANK3 H2D(-467-491)
3036	CCTGGAATCAGACAGATCTGGGTTC	SHANK3 H2D(-470-494)
3037	GGGCCTGGAATCAGACAGATCTGGG	SHANK3 H2D(-473-497)
3038	ACAGGGCCTGGAATCAGACAGATCT	SHANK3 H2D(-476-500)
3039	GGCACAGGGCCTGGAATCAGACAGA	SHANK3 H2D(-479-503)
3040	CTGGGCACAGGGCCTGGAATCAGAC	SHANK3 H2D(-482-506)
3041	TGCCTGGGCACAGGGCCTGGAATCA	SHANK3 H2D(-485-509)
3042	GCATGCCTGGGCACAGGGCCTGGAA	SHANK3 H2D(-488-512)
3043	AAGGCATGCCTGGGCACAGGGCCTG	SHANK3 H2D(-491-515)
3044	TCAAAGGCATGCCTGGGCACAGGGC	SHANK3 H2D(-494-518)
3045	ACCTCAAAGGCATGCCTGGGCACAG	SHANK3 H2D(-497-521)
3046	GACACCTCAAAGGCATGCCTGGGCA	SHANK3 H2D(-500-524)

3047	GTAGACACCTCAAAGGCATGCCTGG	SHANK3 H2D(-503-527)
3048	GCAGTAGACACCTCAAAGGCATGCC	SHANK3 H2D(-506-530)
3049	CCAGCAGTAGACACCTCAAAGGCAT	SHANK3 H2D(-509-533)
3050	CACCCAGCAGTAGACACCTCAAAGG	SHANK3 H2D(-512-536)
3051	TGGCACCCAGCAGTAGACACCTCAA	SHANK3 H2D(-515-539)
3052	GGGTGGCACCCAGCAGTAGACACCT	SHANK3 H2D(-518-542)
3053	TGGGGGTGGCACCCAGCAGTAGACA	SHANK3 H2D(-521-545)
3054	AGTTGGGGGTGGCACCCAGCAGTAG	SHANK3 H2D(-524-548)
3055	CCCAGTTGGGGGTGGCACCCAGCAG	SHANK3 H2D(-527-551)
3056	AGGCCAGTTGGGGGTGGCACCCAG	SHANK3 H2D(-530-554)
3057	GTCAGGCCCAGTTGGGGGTGGCACC	SHANK3 H2D(-533-557)
3058	GGGGTCAGGCCCAGTTGGGGGTGGC	SHANK3 H2D(-536-560)
3059	TTTGGGGTCAGGCCCAGTTGGGGGT	SHANK3 H2D(-539-563)
3060	GCATTTGGGGTCAGGCCCAGTTGGG	SHANK3 H2D(-542-566)
3061	AGAGCATTTGGGGTCAGGCCCAGTT	SHANK3 H2D(-545-569)
3062	TCAAGAGCATTTGGGGTCAGGCCCA	SHANK3 H2D(-548-572)
3063	CCCTCAAGAGCATTTGGGGTCAGGC	SHANK3 H2D(-551-575)
3064	CCCCCTCAAGAGCATTTGGGGTCA	SHANK3 H2D(-554-578)
3065	GTGCCCCCTCAAGAGCATTTGGGG	SHANK3 H2D(-557-581)
3066	AAGGTGCCCCCTCAAGAGCATTTG	SHANK3 H2D(-560-584)
3067	AGTAAGGTGCCCCCTCAAGAGCAT	SHANK3 H2D(-563-587)
3068	AATAGTAAGGTGCCCCCTCAAGAG	SHANK3 H2D(-566-590)
3069	GGAAATAGTAAGGTGCCCCCTCAA	SHANK3 H2D(-569-593)
3070	GCGGGAAATAGTAAGGTGCCCCCT	SHANK3 H2D(-572-596)
3071	TCAGCGGGAAATAGTAAGGTGCCCC	SHANK3 H2D(-575-599)
3072	CATTAGCGGGAAATAGTAAGGTGC	SHANK3 H2D(-578-602)
3073	TGACATTAGCGGGAAATAGTAAGG	SHANK3 H2D(-581-605)
3074	CTCTGACATTAGCGGGAAATAGTA	SHANK3 H2D(-584-608)
3075	CCCCTGACATTAGCGGGAAATA	SHANK3 H2D(-587-611)
3076	CTGCCCCTGACATTAGCGGGAA	SHANK3 H2D(-590-614)
3077	ACCCTGCCCCTGACATTAGCGGG	SHANK3 H2D(-593-617)
3078	CCCACCCTGCCCCTGACATTAG	SHANK3 H2D(-596-620)
3079	GCACCCACCCTGCCCCTGACATT	SHANK3 H2D(-599-623)
3080	GTGGCACCCACCCTGCCCCTGAC	SHANK3 H2D(-602-626)
3081	GCTGTGGCACCCACCCTGCCCCTCT	SHANK3 H2D(-605-629)
3082	GGGGCTGTGGCACCCACCCTGCCCC	SHANK3 H2D(-608-632)

3083	GGAGGGGCTGTGGCACCCACCTGC	SHANK3 H2D(-611-635)
3084	TGGGGAGGGGCTGTGGCACCCACCC	SHANK3 H2D(-614-638)
3085	CCCTGGGGAGGGGCTGTGGCACCCA	SHANK3 H2D(-617-641)
3086	AGCCCCTGGGGAGGGGCTGTGGCAC	SHANK3 H2D(-620-644)
3087	GGAAGCCCCTGGGGAGGGGCTGTGG	SHANK3 H2D(-623-647)
3088	GGTGGAAGCCCCTGGGGAGGGGCTG	SHANK3 H2D(-626-650)
3089	GCGGGTGGAAGCCCCTGGGGAGGGG	SHANK3 H2D(-629-653)
3090	GCTGCGGGTGGAAGCCCCTGGGGAG	SHANK3 H2D(-632-656)
3091	TGAGCTGCGGGTGGAAGCCCCTGGG	SHANK3 H2D(-635-659)
3092	CTGTGAGCTGCGGGTGGAAGCCCCT	SHANK3 H2D(-638-662)
3093	GGACTGTGAGCTGCGGGTGGAAGCC	SHANK3 H2D(-641-665)
3094	GCTGGACTGTGAGCTGCGGGTGGA	SHANK3 H2D(-644-668)
3095	CCTGCTGGACTGTGAGCTGCGGGTG	SHANK3 H2D(-647-671)
3096	GTGCCTGCTGGACTGTGAGCTGCGG	SHANK3 H2D(-650-674)
3097	CAAGTGCCTGCTGGACTGTGAGCTG	SHANK3 H2D(-653-677)
3098	AAACAAGTGCCTGCTGGACTGTGAG	SHANK3 H2D(-656-680)
3099	AGCAAACAAGTGCCTGCTGGACTGT	SHANK3 H2D(-659-683)
3100	TCCAGCAAACAAGTGCCTGCTGGAC	SHANK3 H2D(-662-686)
3101	GTATCCAGCAAACAAGTGCCTGCTG	SHANK3 H2D(-665-689)
3102	AAAGTATCCAGCAAACAAGTGCCTG	SHANK3 H2D(-668-692)
3103	CATAAAGTATCCAGCAAACAAGTGC	SHANK3 H2D(-671-695)
3104	GCCCATAAAGTATCCAGCAAACAAG	SHANK3 H2D(-674-698)
3105	ACCGCCCATAAAGTATCCAGCAAAC	SHANK3 H2D(-677-701)
3106	GAGACCGCCCATAAAGTATCCAGCA	SHANK3 H2D(-680-704)
3107	CTCGAGACCGCCCATAAAGTATCCA	SHANK3 H2D(-683-707)
3108	GAGCTCGAGACCGCCCATAAAGTAT	SHANK3 H2D(-686-710)
3109	CCTGAGCTCGAGACCGCCCATAAAG	SHANK3 H2D(-689-713)
3110	TCTCCTGAGCTCGAGACCGCCCAT	SHANK3 H2D(-692-716)
3111	CCCTCTCCTGAGCTCGAGACCGCCC	SHANK3 H2D(-695-719)
3112	GACCCCTCTCCTGAGCTCGAGACCG	SHANK3 H2D(-698-722)
3113	TCTGACCCCTCTCCTGAGCTCGAGA	SHANK3 H2D(-701-725)
3114	CATTCTGACCCCTCTCCTGAGCTCG	SHANK3 H2D(-704-728)
3115	CTCCATTCTGACCCCTCTCCTGAGC	SHANK3 H2D(-707-731)
3116	ACCCTCCATTCTGACCCCTCTCCTG	SHANK3 H2D(-710-734)
3117	GAGACCCCTCCATTCTGACCCCTCTC	SHANK3 H2D(-713-737)
3118	CCAGAGACCCTCCATTCTGACCCCT	SHANK3 H2D(-716-740)

3119	GCTCCAGAGACCCTCCATTCTGACC	SHANK3 H2D(-719-743)
3120	TGGGCTCCAGAGACCCTCCATTCTG	SHANK3 H2D(-722-746)
3121	TCCTGGGCTCCAGAGACCCTCCATT	SHANK3 H2D(-725-749)
3122	CTCTCCTGGGCTCCAGAGACCCTCC	SHANK3 H2D(-728-752)
3123	TTCTCTCTCTGGGCTCCAGAGACCC	SHANK3 H2D(-731-755)
3124	TGATTCTCTCTCTGGGCTCCAGAGA	SHANK3 H2D(-734-758)
3125	TTCTGATTCTCTCTCTGGGCTCCAG	SHANK3 H2D(-737-761)
3126	CAGTTCTGATTCTCTCTCTGGGCTC	SHANK3 H2D(-740-764)
3127	TGACAGTTCTGATTCTCTCTCTGGG	SHANK3 H2D(-743-767)
3128	GGCTGACAGTTCTGATTCTCTCTCT	SHANK3 H2D(-746-770)
3129	CAGGGCTGACAGTTCTGATTCTCTCT	SHANK3 H2D(-749-773)
3130	ACACAGGGCTGACAGTTCTGATTCC	SHANK3 H2D(-752-776)
3131	AGGACACAGGGCTGACAGTTCTGAT	SHANK3 H2D(-755-779)
3132	ATTAGGACACAGGGCTGACAGTTCT	SHANK3 H2D(-758-782)
3133	ACCATTAGGACACAGGGCTGACAGT	SHANK3 H2D(-761-785)
3134	GGGACCATTAGGACACAGGGCTGAC	SHANK3 H2D(-764-788)
3135	GATGGGACCATTAGGACACAGGGCT	SHANK3 H2D(-767-791)
3136	ACTGATGGGACCATTAGGACACAGG	SHANK3 H2D(-770-794)
3137	GTCCTGATGGGACCATTAGGACAC	SHANK3 H2D(-773-797)
3138	AAAGTCACTGATGGGACCATTAGGA	SHANK3 H2D(-776-800)
3139	TCCAAAGTCACTGATGGGACCATTA	SHANK3 H2D(-779-803)
3140	GGCTCCAAAGTCACTGATGGGACCA	SHANK3 H2D(-782-806)
3141	TGAGGCTCCAAAGTCACTGATGGGA	SHANK3 H2D(-785-809)
3142	GCCTGAGGCTCCAAAGTCACTGATG	SHANK3 H2D(-788-812)
3143	GAAGCCTGAGGCTCCAAAGTCACTG	SHANK3 H2D(-791-815)
3144	ACAGAAGCCTGAGGCTCCAAAGTCA	SHANK3 H2D(-794-818)
3145	GGCACAGAAGCCTGAGGCTCCAAAG	SHANK3 H2D(-797-821)
3146	CCTGGCACAGAAGCCTGAGGCTCCA	SHANK3 H2D(-800-824)
3147	AAGCCTGGCACAGAAGCCTGAGGCT	SHANK3 H2D(-803-827)
3148	GAAAAGCCTGGCACAGAAGCCTGAG	SHANK3 H2D(-806-830)
3149	GCAGAAAAGCCTGGCACAGAAGCCT	SHANK3 H2D(-809-833)
3150	GCAGCAGAAAAGCCTGGCACAGAAG	SHANK3 H2D(-812-836)
3151	GGGGCAGCAGAAAAGCCTGGCACAG	SHANK3 H2D(-815-839)
3152	CCTGGGGCAGCAGAAAAGCCTGGCA	SHANK3 H2D(-818-842)
3153	TGCCCTGGGGCAGCAGAAAAGCCTG	SHANK3 H2D(-821-845)
3154	GCCTGCCCTGGGGCAGCAGAAAAGC	SHANK3 H2D(-824-848)

3155	ACCGCCTGCCCTGGGGCAGCAGAAA	SHANK3 H2D(-827-851)
3156	ACCACCGCCTGCCCTGGGGCAGCAG	SHANK3 H2D(-830-854)
3157	TTGACCACCGCCTGCCCTGGGGCAG	SHANK3 H2D(-833-857)
3158	CCGTTGACCACCGCCTGCCCTGGGG	SHANK3 H2D(-836-860)
3159	AGGCCGTTGACCACCGCCTGCCCTG	SHANK3 H2D(-839-863)
3160	CCAAGGCCGTTGACCACCGCCTGCC	SHANK3 H2D(-842-866)
3161	GTGCCAAGGCCGTTGACCACCGCCT	SHANK3 H2D(-845-869)
3162	ATAGTGCCAAGGCCGTTGACCACCG	SHANK3 H2D(-848-872)
3163	GCCATAGTGCCAAGGCCGTTGACCA	SHANK3 H2D(-851-875)
3164	CCAGCCATAGTGCCAAGGCCGTTGA	SHANK3 H2D(-854-878)
3165	TGCCCAGCCATAGTGCCAAGGCCGT	SHANK3 H2D(-857-881)
3166	CTCTGCCCAGCCATAGTGCCAAGGC	SHANK3 H2D(-860-884)
3167	GGACTCTGCCCAGCCATAGTGCCAA	SHANK3 H2D(-863-887)
3168	AGTGGA CTCTGCCCAGCCATAGTGC	SHANK3 H2D(-866-890)
3169	CACAGTGGACTCTGCCCAGCCATAG	SHANK3 H2D(-869-893)
3170	TTCCACAGTGGACTCTGCCCAGCCA	SHANK3 H2D(-872-896)
3171	CCTTCCACAGTGGACTCTGCCCAG	SHANK3 H2D(-875-899)
3172	GGACCTTCCACAGTGGACTCTGCC	SHANK3 H2D(-878-902)
3173	GGGGGACCTTCCACAGTGGACTCT	SHANK3 H2D(-881-905)
3174	AGAGGGGGACCTTCCACAGTGGAC	SHANK3 H2D(-884-908)
3175	AGGAGAGGGGGACCTTCCACAGTG	SHANK3 H2D(-887-911)
3176	GGCAGGAGAGGGGGACCTTCCACA	SHANK3 H2D(-890-914)
3177	AGTGGCAGGAGAGGGGGACCTTCC	SHANK3 H2D(-893-917)
3178	GCCAGTGGCAGGAGAGGGGGACCTT	SHANK3 H2D(-896-920)
3179	AGGGCCAGTGGCAGGAGAGGGGGAC	SHANK3 H2D(-899-923)
3180	GTGAGGGCCAGTGGCAGGAGAGGGG	SHANK3 H2D(-902-926)
3181	CAAGTGAGGGCCAGTGGCAGGAGAG	SHANK3 H2D(-905-929)
3182	GGTCAAGTGAGGGCCAGTGGCAGGA	SHANK3 H2D(-908-932)
3183	CAAGGTCAAGTGAGGGCCAGTGGCA	SHANK3 H2D(-911-935)
3184	TGACAAGGTCAAGTGAGGGCCAGTG	SHANK3 H2D(-914-938)
3185	GGCTGACAAGGTCAAGTGAGGGCCA	SHANK3 H2D(-917-941)
3186	CCAGGCTGACAAGGTCAAGTGAGGG	SHANK3 H2D(-920-944)
3187	AACCCAGGCTGACAAGGTCAAGTGA	SHANK3 H2D(-923-947)
3188	AGGAACCCAGGCTGACAAGGTCAAG	SHANK3 H2D(-926-950)
3189	GGTAGGAACCCAGGCTGACAAGGTC	SHANK3 H2D(-929-953)
3190	TGGGGTAGGAACCCAGGCTGACAAG	SHANK3 H2D(-932-956)

3191	CCATGGGGTAGGAACCCAGGCTGAC	SHANK3 H2D(-935-959)
3192	TGGCCATGGGGTAGGAACCCAGGCT	SHANK3 H2D(-938-962)
3193	AGGTGGCCATGGGGTAGGAACCCAG	SHANK3 H2D(-941-965)
3194	GAGAGGTGGCCATGGGGTAGGAACC	SHANK3 H2D(-944-968)
3195	AGGGAGAGGTGGCCATGGGGTAGGA	SHANK3 H3A(-945-921)
3196	CGGAGGGAGAGGTGGCCATGGGGTA	SHANK3 H3A(-942-918)
3197	ATCCGGAGGGAGAGGTGGCCATGGG	SHANK3 H3A(-939-915)
3198	GAGATCCGGAGGGAGAGGTGGCCAT	SHANK3 H3A(-936-912)
3199	AGAGAGATCCGGAGGGAGAGGTGGC	SHANK3 H3A(-933-909)
3200	TGAAGAGAGATCCGGAGGGAGAGGT	SHANK3 H3A(-930-906)
3201	CACTGAAGAGAGATCCGGAGGGAGA	SHANK3 H3A(-927-903)
3202	GGTCACTGAAGAGAGATCCGGAGGG	SHANK3 H3A(-924-900)
3203	GTTGGTCACTGAAGAGAGATCCGGA	SHANK3 H3A(-921-897)
3204	CTTGTTGGTCACTGAAGAGAGATCC	SHANK3 H3A(-918-894)
3205	TGTCTTGTTGGTCACTGAAGAGAGA	SHANK3 H3A(-915-891)
3206	TCATGTCTTGTTGGTCACTGAAGAG	SHANK3 H3A(-912-888)
3207	CACTCATGTCTTGTTGGTCACTGAA	SHANK3 H3A(-909-885)
3208	AGTCACTCATGTCTTGTTGGTCACT	SHANK3 H3A(-906-882)
3209	GTGAGTCACTCATGTCTTGTTGGTC	SHANK3 H3A(-903-879)
3210	AGAGTGAGTCACTCATGTCTTGTTG	SHANK3 H3A(-900-876)
3211	TTCAGAGTGAGTCACTCATGTCTTG	SHANK3 H3A(-897-873)
3212	TACTTCAGAGTGAGTCACTCATGTC	SHANK3 H3A(-894-870)
3213	ACCTACTTCAGAGTGAGTCACTCAT	SHANK3 H3A(-891-867)
3214	GAGACCTACTTCAGAGTGAGTCACT	SHANK3 H3A(-888-864)
3215	AACGAGACCTACTTCAGAGTGAGTC	SHANK3 H3A(-885-861)
3216	ACAAACGAGACCTACTTCAGAGTGA	SHANK3 H3A(-882-858)
3217	AAAACAAACGAGACCTACTTCAGAG	SHANK3 H3A(-879-855)
3218	CTAAAAACAAACGAGACCTACTTCA	SHANK3 H3A(-876-852)
3219	ATCCTAAAAACAAACGAGACCTACT	SHANK3 H3A(-873-849)
3220	CTCATCCTAAAAACAAACGAGACCT	SHANK3 H3A(-870-846)
3221	AGGCTCATCCTAAAAACAAACGAGA	SHANK3 H3A(-867-843)
3222	TTCAGGCTCATCCTAAAAACAAACG	SHANK3 H3A(-864-840)
3223	AAGTTCAGGCTCATCCTAAAAACAA	SHANK3 H3A(-861-837)
3224	AAGAAGTTCAGGCTCATCCTAAAAA	SHANK3 H3A(-858-834)
3225	TGTAAGAAGTTCAGGCTCATCCTAA	SHANK3 H3A(-855-831)
3226	CTATGTAAGAAGTTCAGGCTCATCC	SHANK3 H3A(-852-828)

3227	GGGCTATGTAAGAAGTTCAGGCTCA	SHANK3 H3A(-849-825)
3228	CACGGGCTATGTAAGAAGTTCAGGC	SHANK3 H3A(-846-822)
3229	AAACACGGGCTATGTAAGAAGTTCA	SHANK3 H3A(-843-819)
3230	CAGAAACACGGGCTATGTAAGAAGT	SHANK3 H3A(-840-816)
3231	AAGCAGAAACACGGGCTATGTAAGA	SHANK3 H3A(-837-813)
3232	GGCAAGCAGAAACACGGGCTATGTA	SHANK3 H3A(-834-810)
3233	CCAGGCAAGCAGAAACACGGGCTAT	SHANK3 H3A(-831-807)
3234	AGCCCAGGCAAGCAGAAACACGGGC	SHANK3 H3A(-828-804)
3235	TGGAGCCCAGGCAAGCAGAAACACG	SHANK3 H3A(-825-801)
3236	AGCTGGAGCCCAGGCAAGCAGAAAC	SHANK3 H3A(-822-798)
3237	GCCAGCTGGAGCCCAGGCAAGCAGA	SHANK3 H3A(-819-795)
3238	AAGGCCAGCTGGAGCCCAGGCAAGC	SHANK3 H3A(-816-792)
3239	GGAAAGGCCAGCTGGAGCCCAGGCA	SHANK3 H3A(-813-789)
3240	GAGGGAAAGGCCAGCTGGAGCCCAG	SHANK3 H3A(-810-786)
3241	GGAGAGGGAAAGGCCAGCTGGAGCC	SHANK3 H3A(-807-783)
3242	AGGGGAGAGGGAAAGGCCAGCTGGA	SHANK3 H3A(-804-780)
3243	ACCAGGGGAGAGGGAAAGGCCAGCT	SHANK3 H3A(-801-777)
3244	ACTACCAGGGGAGAGGGAAAGGCCA	SHANK3 H3A(-798-774)
3245	CTCACTACCAGGGGAGAGGGAAAGG	SHANK3 H3A(-795-771)
3246	GTGCTCACTACCAGGGGAGAGGGAA	SHANK3 H3A(-792-768)
3247	GAAGTGCTCACTACCAGGGGAGAGG	SHANK3 H3A(-789-765)
3248	GAGGAAGTGCTCACTACCAGGGGAG	SHANK3 H3A(-786-762)
3249	GAGGAGGAAGTGCTCACTACCAGGG	SHANK3 H3A(-783-759)
3250	AAAGAGGAGGAAGTGCTCACTACCA	SHANK3 H3A(-780-756)
3251	GTGAAAGAGGAGGAAGTGCTCACTA	SHANK3 H3A(-777-753)
3252	GCAGTGAAAGAGGAGGAAGTGCTCA	SHANK3 H3A(-774-750)
3253	CAGGCAGTGAAAGAGGAGGAAGTGC	SHANK3 H3A(-771-747)
3254	GGCCAGGCAGTGAAAGAGGAGGAAG	SHANK3 H3A(-768-744)
3255	GCGGGCCAGGCAGTGAAAGAGGAGG	SHANK3 H3A(-765-741)
3256	CAGGCGGGCCAGGCAGTGAAAGAGG	SHANK3 H3A(-762-738)
3257	CCTCAGGCGGGCCAGGCAGTGAAAG	SHANK3 H3A(-759-735)
3258	CCTCCTCAGGCGGGCCAGGCAGTGA	SHANK3 H3A(-756-732)
3259	CAACCTCCTCAGGCGGGCCAGGCAG	SHANK3 H3A(-753-729)
3260	AGGCAACCTCCTCAGGCGGGCCAGG	SHANK3 H3A(-750-726)
3261	GGGAGGCAACCTCCTCAGGCGGGCC	SHANK3 H3A(-747-723)
3262	CTTGGGAGGCAACCTCCTCAGGCGG	SHANK3 H3A(-744-720)

3263	TGCCTTGGGAGGCAACCTCCTCAGG	SHANK3 H3A(-741-717)
3264	CCCTGCCTTGGGAGGCAACCTCCTC	SHANK3 H3A(-738-714)
3265	GACCCCTGCCTTGGGAGGCAACCTC	SHANK3 H3A(-735-711)
3266	AGGGACCCCTGCCTTGGGAGGCAAC	SHANK3 H3A(-732-708)
3267	CATAGGGACCCCTGCCTTGGGAGGC	SHANK3 H3A(-729-705)
3268	TGCCATAGGGACCCCTGCCTTGGGA	SHANK3 H3A(-726-702)
3269	GGGTGCCATAGGGACCCCTGCCTTG	SHANK3 H3A(-723-699)
3270	GGAGGGTGCCATAGGGACCCCTGCC	SHANK3 H3A(-720-696)
3271	AGGGGAGGGTGCCATAGGGACCCCT	SHANK3 H3A(-717-693)
3272	AATAGGGGAGGGTGCCATAGGGACC	SHANK3 H3A(-714-690)
3273	AGAAATAGGGGAGGGTGCCATAGGG	SHANK3 H3A(-711-687)
3274	CTCAGAAATAGGGGAGGGTGCCATA	SHANK3 H3A(-708-684)
3275	TACCTCAGAAATAGGGGAGGGTGCC	SHANK3 H3A(-705-681)
3276	GTGTACCTCAGAAATAGGGGAGGGT	SHANK3 H3A(-702-678)
3277	CCAGTGTACCTCAGAAATAGGGGAG	SHANK3 H3A(-699-675)
3278	CACCCAGTGACCTCAGAAATAGGG	SHANK3 H3A(-696-672)
3279	AAACACCCAGTGACCTCAGAAATA	SHANK3 H3A(-693-669)
3280	CATAAACACCCAGTGACCTCAGAA	SHANK3 H3A(-690-666)
3281	TTCCATAAACACCCAGTGACCTCA	SHANK3 H3A(-687-663)
3282	CCCTTCCATAAACACCCAGTGACCT	SHANK3 H3A(-684-660)
3283	GGGCCCTTCCATAAACACCCAGTGT	SHANK3 H3A(-681-657)
3284	CCGGGGCCCTTCCATAAACACCCAG	SHANK3 H3A(-678-654)
3285	AGGCCGGGGCCCTTCCATAAACACC	SHANK3 H3A(-675-651)
3286	CAAAGGCCGGGGCCCTTCCATAAAC	SHANK3 H3A(-672-648)
3287	GGCCAAAGGCCGGGGCCCTTCCATA	SHANK3 H3A(-669-645)
3288	CCTGGCCAAAGGCCGGGGCCCTTCC	SHANK3 H3A(-666-642)
3289	TGCCCTGGCCAAAGGCCGGGGCCCT	SHANK3 H3A(-663-639)
3290	AGGTGCCCTGGCCAAAGGCCGGGGC	SHANK3 H3A(-660-636)
3291	GCAAGGTGCCCTGGCCAAAGGCCGG	SHANK3 H3A(-657-633)
3292	AAGGCAAGGTGCCCTGGCCAAAGGC	SHANK3 H3A(-654-630)
3293	CACAAGGCAAGGTGCCCTGGCCAAA	SHANK3 H3A(-651-627)
3294	ACACACAAGGCAAGGTGCCCTGGCC	SHANK3 H3A(-648-624)
3295	CACACACACAAGGCAAGGTGCCCTG	SHANK3 H3A(-645-621)
3296	CACCACACACACAAGGCAAGGTGCC	SHANK3 H3A(-642-618)
3297	GGACACCACACACAAGGCAAGGT	SHANK3 H3A(-639-615)
3298	TACGGACACCACACACAAGGCAA	SHANK3 H3A(-636-612)

3299	CACTACGGACACCACACACAAGG	SHANK3 H3A(-633-609)
3300	CGGCACTACGGACACCACACACA	SHANK3 H3A(-630-606)
3301	AGCCGGCACTACGGACACCACAC	SHANK3 H3A(-627-603)
3302	CCCAGCCGGCACTACGGACACCACA	SHANK3 H3A(-624-600)
3303	TTCCCCAGCCGGCACTACGGACACC	SHANK3 H3A(-621-597)
3304	CACTTCCCCAGCCGGCACTACGGAC	SHANK3 H3A(-618-594)
3305	CCTCACTTCCCCAGCCGGCACTACG	SHANK3 H3A(-615-591)
3306	AGGCCTCACTTCCCCAGCCGGCACT	SHANK3 H3A(-612-588)
3307	ACAAGGCCTCACTTCCCCAGCCGGC	SHANK3 H3A(-609-585)
3308	CCCACAAGGCCTCACTTCCCCAGCC	SHANK3 H3A(-606-582)
3309	CACCCACAAGGCCTCACTTCCCCA	SHANK3 H3A(-603-579)
3310	ACTCACCCACAAGGCCTCACTTCC	SHANK3 H3A(-600-576)
3311	TTCACTCACCCACAAGGCCTCACT	SHANK3 H3A(-597-573)
3312	TTATTCACCTCACCCACAAGGCCTC	SHANK3 H3A(-594-570)
3313	AGTTTATTCACCTCACCCACAAGGC	SHANK3 H3A(-591-567)
3314	CCCAGTTTATTCACCTCACCCACAA	SHANK3 H3A(-588-564)
3315	TCACCCAGTTTATTCACCTCACCCCA	SHANK3 H3A(-585-561)
3316	CATTACCCAGTTTATTCACCTCACC	SHANK3 H3A(-582-558)
3317	ACTCATTACCCAGTTTATTCACCTC	SHANK3 H3A(-579-555)
3318	TGTA CTATTACCCAGTTTATTCAC	SHANK3 H3A(-576-552)
3319	CCTTGTA CTATTACCCAGTTTAT	SHANK3 H3A(-573-549)
3320	TGGCCTTGTA CTATTACCCAGTT	SHANK3 H3A(-570-546)
3321	TGATGGCCTTGTA CTATTACCCCA	SHANK3 H3A(-567-543)
3322	CTTTGATGGCCTTGTA CTATTAC	SHANK3 H3A(-564-540)
3323	TGACTTTGATGGCCTTGTA CTATT	SHANK3 H3A(-561-537)
3324	ACATGACTTTGATGGCCTTGTA CT	SHANK3 H3A(-558-534)
3325	GTGACATGACTTTGATGGCCTTGTA	SHANK3 H3A(-555-531)
3326	CCTGTGACATGACTTTGATGGCCTT	SHANK3 H3A(-552-528)
3327	CATCCTGTGACATGACTTTGATGGC	SHANK3 H3A(-549-525)
3328	ACCCATCCTGTGACATGACTTTGAT	SHANK3 H3A(-546-522)
3329	GGGACCCATCCTGTGACATGACTTT	SHANK3 H3A(-543-519)
3330	CCAGGGACCCATCCTGTGACATGAC	SHANK3 H3A(-540-516)
3331	ACCCAGGGACCCATCCTGTGACAT	SHANK3 H3A(-537-513)
3332	CCCACCCAGGGACCCATCCTGTGA	SHANK3 H3A(-534-510)
3333	ACCCACCCAGGGACCCATCCTG	SHANK3 H3A(-531-507)
3334	CAGACCCACCCAGGGACCCATC	SHANK3 H3A(-528-504)

3335	CCGCAGACCCCCACCCAGGGACCC	SHANK3 H3A(-525-501)
3336	CCACCGCAGACCCCCACCCAGGGA	SHANK3 H3A(-522-498)
3337	ACCCACCGCAGACCCCCACCCAG	SHANK3 H3A(-519-495)
3338	CTCACCCACCGCAGACCCCCACCC	SHANK3 H3A(-516-492)
3339	CAGCTCACCCACCGCAGACCCCCA	SHANK3 H3A(-513-489)
3340	CTCCAGCTCACCCACCGCAGACCC	SHANK3 H3A(-510-486)
3341	CCTCTCCAGCTCACCCACCGCAGA	SHANK3 H3A(-507-483)
3342	CTTCTCTCCAGCTCACCCACCGC	SHANK3 H3A(-504-480)
3343	CATCTTCTCTCCAGCTCACCCAC	SHANK3 H3A(-501-477)
3344	GCCCATCTTCTCTCCAGCTCACCC	SHANK3 H3A(-498-474)
3345	TCGGCCCATCTTCTCTCCAGCTCA	SHANK3 H3A(-495-471)
3346	TCTTCGGCCCATCTTCTCTCCAGC	SHANK3 H3A(-492-468)
3347	CCTTCTTCGGCCCATCTTCTCTCC	SHANK3 H3A(-489-465)
3348	GCTCCTTCTTCGGCCCATCTTCTC	SHANK3 H3A(-486-462)
3349	CCTGCTCCTTCTTCGGCCCATCTC	SHANK3 H3A(-483-459)
3350	CAACCTGCTCCTTCTTCGGCCATC	SHANK3 H3A(-480-456)
3351	AGACAACCTGCTCCTTCTTCGGCC	SHANK3 H3A(-477-453)
3352	CTGAGACAACCTGCTCCTTCTTCGG	SHANK3 H3A(-474-450)
3353	ACCCTGAGACAACCTGCTCCTTCTT	SHANK3 H3A(-471-447)
3354	AGCACCTGAGACAACCTGCTCCTT	SHANK3 H3A(-468-444)
3355	CTCAGCACCTGAGACAACCTGCTC	SHANK3 H3A(-465-441)
3356	ATCCTCAGCACCTGAGACAACCTG	SHANK3 H3A(-462-438)
3357	TGAATCCTCAGCACCTGAGACAAC	SHANK3 H3A(-459-435)
3358	CCCTGAATCCTCAGCACCTGAGAC	SHANK3 H3A(-456-432)
3359	CAGCCCTGAATCCTCAGCACCTGA	SHANK3 H3A(-453-429)
3360	CAGCAGCCCTGAATCCTCAGCACCC	SHANK3 H3A(-450-426)
3361	CCACAGCAGCCCTGAATCCTCAGCA	SHANK3 H3A(-447-423)
3362	GCCCCACAGCAGCCCTGAATCCTCA	SHANK3 H3A(-444-420)
3363	CCAGCCCCACAGCAGCCCTGAATCC	SHANK3 H3A(-441-417)
3364	GAACCAGCCCCACAGCAGCCCTGAA	SHANK3 H3A(-438-414)
3365	CAGGAACCAGCCCCACAGCAGCCCT	SHANK3 H3A(-435-411)
3366	AGGCAGGAACCAGCCCCACAGCAGC	SHANK3 H3A(-432-408)
3367	CCCAGGCAGGAACCAGCCCCACAGC	SHANK3 H3A(-429-405)
3368	CCACCCAGGCAGGAACCAGCCCCAC	SHANK3 H3A(-426-402)
3369	GGTCCACCCAGGCAGGAACCAGCCC	SHANK3 H3A(-423-399)
3370	CGAGGTCCACCCAGGCAGGAACCAG	SHANK3 H3A(-420-396)

3371	GCCCGAGGTCCACCCAGGCAGGAAC	SHANK3 H3A(-417-393)
3372	AGAGCCCGAGGTCCACCCAGGCAGG	SHANK3 H3A(-414-390)
3373	AGAAGAGCCCGAGGTCCACCCAGGC	SHANK3 H3A(-411-387)
3374	CCTAGAAGAGCCCGAGGTCCACCCA	SHANK3 H3A(-408-384)
3375	TGGCCTAGAAGAGCCCGAGGTCCAC	SHANK3 H3A(-405-381)
3376	GCCTGGCCTAGAAGAGCCCGAGGTC	SHANK3 H3A(-402-378)
3377	CCTGCCTGGCCTAGAAGAGCCCGAG	SHANK3 H3A(-399-375)
3378	CGACCTGCCTGGCCTAGAAGAGCCC	SHANK3 H3A(-396-372)
3379	CCCCGACCTGCCTGGCCTAGAAGAG	SHANK3 H3A(-393-369)
3380	CTGCCCCGACCTGCCTGGCCTAGAA	SHANK3 H3A(-390-366)
3381	CTGCTGCCCCGACCTGCCTGGCCTA	SHANK3 H3A(-387-363)
3382	GCCCTGCTGCCCCGACCTGCCTGGC	SHANK3 H3A(-384-360)
3383	CCGGCCCTGCTGCCCCGACCTGCCT	SHANK3 H3A(-381-357)
3384	TCTCCGGCCCTGCTGCCCCGACCTG	SHANK3 H3A(-378-354)
3385	GTCTCTCCGGCCCTGCTGCCCCGAC	SHANK3 H3A(-375-351)
3386	TCCGTCTCTCCGGCCCTGCTGCCCC	SHANK3 H3A(-372-348)
3387	GGCTCCGTCTCTCCGGCCCTGCTGC	SHANK3 H3A(-369-345)
3388	CCTGGCTCCGTCTCTCCGGCCCTGC	SHANK3 H3A(-366-342)
3389	TGCCCTGGCTCCGTCTCTCCGGCCC	SHANK3 H3A(-363-339)
3390	CACTGCCCTGGCTCCGTCTCTCCGG	SHANK3 H3A(-360-336)
3391	AGTCACTGCCCTGGCTCCGTCTCTC	SHANK3 H3A(-357-333)
3392	CCCAGTCACTGCCCTGGCTCCGTCT	SHANK3 H3A(-354-330)
3393	AGGCCAGTCACTGCCCTGGCTCCG	SHANK3 H3A(-351-327)
3394	TCCAGGCCAGTCACTGCCCTGGCT	SHANK3 H3A(-348-324)
3395	CACTCCAGGCCAGTCACTGCCCTG	SHANK3 H3A(-345-321)
3396	CCCCACTCCAGGCCAGTCACTGCC	SHANK3 H3A(-342-318)
3397	GTCCCCACTCCAGGCCAGTCACT	SHANK3 H3A(-339-315)
3398	CAAGTCCCCACTCCAGGCCAGTC	SHANK3 H3A(-336-312)
3399	AAGCAAGTCCCCACTCCAGGCCCA	SHANK3 H3A(-333-309)
3400	CCCAAGCAAGTCCCCACTCCAGGC	SHANK3 H3A(-330-306)
3401	GGCCCCAAGCAAGTCCCCACTCCA	SHANK3 H3A(-327-303)
3402	TGGGGCCCCAAGCAAGTCCCCACT	SHANK3 H3A(-324-300)
3403	TGGTGGGGCCCCAAGCAAGTCCCC	SHANK3 H3A(-321-297)
3404	CCCTGGTGGGGCCCCAAGCAAGTCC	SHANK3 H3A(-318-294)
3405	TCACCCTGGTGGGGCCCCAAGCAAG	SHANK3 H3A(-315-291)
3406	AGGTCACCCTGGTGGGGCCCCAAGC	SHANK3 H3A(-312-288)

3407	GCCAGGTCACCCTGGTGGGGCCCA	SHANK3 H3A(-309-285)
3408	AAGGCCAGGTCACCCTGGTGGGGCC	SHANK3 H3A(-306-282)
3409	ACCAAGGCCAGGTCACCCTGGTGGG	SHANK3 H3A(-303-279)
3410	CTCACCAAGGCCAGGTCACCCTGGT	SHANK3 H3A(-300-276)
3411	CCCCTCACCAAGGCCAGGTCACCCT	SHANK3 H3A(-297-273)
3412	TAGCCCCTCACCAAGGCCAGGTCAC	SHANK3 H3A(-294-270)
3413	AAGTAGCCCCTCACCAAGGCCAGGT	SHANK3 H3A(-291-267)
3414	CCCAAGTAGCCCCTCACCAAGGCCA	SHANK3 H3A(-288-264)
3415	GTACCCAAGTAGCCCCTCACCAAGG	SHANK3 H3A(-285-261)
3416	CTTGTACCCAAGTAGCCCCTCACCA	SHANK3 H3A(-282-258)
3417	CAGCTTGACCCAAGTAGCCCCTCA	SHANK3 H3A(-279-255)
3418	TGTCAGCTTGACCCAAGTAGCCCC	SHANK3 H3A(-276-252)
3419	GACTGTCAGCTTGACCCAAGTAGC	SHANK3 H3A(-273-249)
3420	CACGACTGTCAGCTTGACCCAAGT	SHANK3 H3A(-270-246)
3421	AGTCACGACTGTCAGCTTGACCCA	SHANK3 H3A(-267-243)
3422	ACCAGTCACGACTGTCAGCTTGAC	SHANK3 H3A(-264-240)
3423	CAAACCAAGTCACGACTGTCAGCTTG	SHANK3 H3A(-261-237)
3424	AGCCAAACCAAGTCACGACTGTCAGC	SHANK3 H3A(-258-234)
3425	GATAGCCAAACCAAGTCACGACTGTC	SHANK3 H3A(-255-231)
3426	CCTGATAGCCAAACCAAGTCACGACT	SHANK3 H3A(-252-228)
3427	CGCCCTGATAGCCAAACCAAGTCACG	SHANK3 H3A(-249-225)
3428	TTGCGCCCTGATAGCCAAACCAAGTC	SHANK3 H3A(-246-222)
3429	TCCTTGCGCCCTGATAGCCAAACCA	SHANK3 H3A(-243-219)
3430	CCTTCCTTGCGCCCTGATAGCCAAA	SHANK3 H3A(-240-216)
3431	AGCCCTTCCTTGCGCCCTGATAGCC	SHANK3 H3A(-237-213)
3432	CAAAGCCCTTCCTTGCGCCCTGATA	SHANK3 H3A(-234-210)
3433	GCTCAAAGCCCTTCCTTGCGCCCTG	SHANK3 H3A(-231-207)
3434	ACGGCTCAAAGCCCTTCCTTGCGCC	SHANK3 H3A(-228-204)
3435	TGCACGGCTCAAAGCCCTTCCTTGC	SHANK3 H3A(-225-201)
3436	CCATGCACGGCTCAAAGCCCTTCCT	SHANK3 H3A(-222-198)
3437	GGCCCATGCACGGCTCAAAGCCCTT	SHANK3 H3A(-219-195)
3438	GTGGGCCCATGCACGGCTCAAAGCC	SHANK3 H3A(-216-192)
3439	CGGGTGGGCCCATGCACGGCTCAAA	SHANK3 H3A(-213-189)
3440	ACTCGGGTGGGCCCATGCACGGCTC	SHANK3 H3A(-210-186)
3441	CCCACTCGGGTGGGCCCATGCACGG	SHANK3 H3A(-207-183)
3442	ATTCCCACTCGGGTGGGCCCATGCA	SHANK3 H3A(-204-180)

3443	CCAATTCCCACTCGGGTGGGCCCAT	SHANK3 H3A(-201-177)
3444	GCCCCAATTCCCACTCGGGTGGGCC	SHANK3 H3A(-198-174)
3445	ACGGCCCCAATTCCCACTCGGGTGG	SHANK3 H3A(-195-171)
3446	ACCACGGCCCCAATTCCCACTCGGG	SHANK3 H3A(-192-168)
3447	CCCACCACGGCCCCAATTCCCACTC	SHANK3 H3A(-189-165)
3448	ACTCCCACCACGGCCCCAATTCCCA	SHANK3 H3A(-186-162)
3449	TGCACTCCCACCACGGCCCCAATTC	SHANK3 H3A(-183-159)
3450	TCCTGCACTCCCACCACGGCCCCAA	SHANK3 H3A(-180-156)
3451	CGGTCCTGCACTCCCACCACGGCCC	SHANK3 H3A(-177-153)
3452	CCACGGTCCTGCACTCCCACCACGG	SHANK3 H3A(-174-150)
3453	CAACCACGGTCCTGCACTCCCACCA	SHANK3 H3A(-171-147)
3454	TGTCAACCACGGTCCTGCACTCCCA	SHANK3 H3A(-168-144)
3455	AATTGTCAACCACGGTCCTGCACTC	SHANK3 H3A(-165-141)
3456	CACAATTGTCAACCACGGTCCTGCA	SHANK3 H3A(-162-138)
3457	CATCACAATTGTCAACCACGGTCCT	SHANK3 H3A(-159-135)
3458	TGACATCACAATTGTCAACCACGGT	SHANK3 H3A(-156-132)
3459	ACCTGACATCACAATTGTCAACCAC	SHANK3 H3A(-153-129)
3460	GTCACCTGACATCACAATTGTCAAC	SHANK3 H3A(-150-126)
3461	CCTGTACCTGACATCACAATTGTC	SHANK3 H3A(-147-123)
3462	TGACCTGTACCTGACATCACAATT	SHANK3 H3A(-144-120)
3463	GTCTGACCTGTACCTGACATCACA	SHANK3 H3A(-141-117)
3464	CCAGTCTGACCTGTACCTGACATC	SHANK3 H3A(-138-114)
3465	CTACCACTGTACCTGTACCTGAC	SHANK3 H3A(-135-111)
3466	TCCCTACCACTGTACCTGTACCT	SHANK3 H3A(-132-108)
3467	ACATCCCTACCACTGTACCTGTCA	SHANK3 H3A(-129-105)
3468	GCCACATCCCTACCACTGTACCTG	SHANK3 H3A(-126-102)
3469	CCCGCCACATCCCTACCACTGTAC	SHANK3 H3A(-123-99)
3470	ACCCCGCCACATCCCTACCACTCT	SHANK3 H3A(-120-96)
3471	GCAACCCCGCCACATCCCTACCAG	SHANK3 H3A(-117-93)
3472	CAGGCAACCCCGCCACATCCCTAC	SHANK3 H3A(-114-90)
3473	CTTCAGGCAACCCCGCCACATCCC	SHANK3 H3A(-111-87)
3474	CACCTTCAGGCAACCCCGCCACAT	SHANK3 H3A(-108-84)
3475	GGCCACCTTCAGGCAACCCCGCCA	SHANK3 H3A(-105-81)
3476	TCAGGCCACCTTCAGGCAACCCCG	SHANK3 H3A(-102-78)
3477	GCCTCAGGCCACCTTCAGGCAACCC	SHANK3 H3A(-99-75)
3478	CAAGCCTCAGGCCACCTTCAGGCAA	SHANK3 H3A(-96-72)

3479	CGGCAAGCCTCAGGCCACCTTCAGG	SHANK3 H3A(-93-69)
3480	CTCCGGCAAGCCTCAGGCCACCTTC	SHANK3 H3A(-90-66)
3481	TTCCTCCGGCAAGCCTCAGGCCACC	SHANK3 H3A(-87-63)
3482	GCCTTCCTCCGGCAAGCCTCAGGCC	SHANK3 H3A(-84-60)
3483	CCCGCCTTCCTCCGGCAAGCCTCAG	SHANK3 H3A(-81-57)
3484	TCACCCGCCTTCCTCCGGCAAGCCT	SHANK3 H3A(-78-54)
3485	ACATCACCCGCCTTCCTCCGGCAAG	SHANK3 H3A(-75-51)
3486	TGAACATCACCCGCCTTCCTCCGGC	SHANK3 H3A(-72-48)
3487	ATCTGAACATCACCCGCCTTCCTCC	SHANK3 H3A(-69-45)
3488	ATCATCTGAACATCACCCGCCTTC	SHANK3 H3A(-66-42)
3489	TCCATCATCTGAACATCACCCGCCT	SHANK3 H3A(-63-39)
3490	GCCTCCATCATCTGAACATCACCCG	SHANK3 H3A(-60-36)
3491	AAGGCCTCCATCATCTGAACATCAC	SHANK3 H3A(-57-33)
3492	ACCAAGGCCTCCATCATCTGAACAT	SHANK3 H3A(-54-30)
3493	GGCACCAAGGCCTCCATCATCTGAA	SHANK3 H3A(-51-27)
3494	CCTGGCACCAAGGCCTCCATCATCT	SHANK3 H3A(-48-24)
3495	CAGCCTGGCACCAAGGCCTCCATCA	SHANK3 H3A(-45-21)
3496	AGTCAGCCTGGCACCAAGGCCTCCA	SHANK3 H3A(-42-18)
3497	GTCACTCAGCCTGGCACCAAGGCCT	SHANK3 H3A(-39-15)
3498	GCCGTCAGTCAGCCTGGCACCAAGG	SHANK3 H3A(-36-12)
3499	CCGGCCGTCAGTCAGCCTGGCACCA	SHANK3 H3A(-33-9)
3500	ACACCGGCCGTCAGTCAGCCTGGCA	SHANK3 H3A(-30-6)
3501	GGAACACCGGCCGTCAGTCAGCCTG	SHANK3 H3A(-27-3)
3502	AAACTGCTCAGATAAAG	SHANK3 H2A(-14+3)
3503	TCGAAACTGCTCAGATA	SHANK3 H2A(-11+6)
3504	GTATCGAAACTGCTCAG	SHANK3 H2A(-8+9)
3505	CTTGTATCGAAACTGCT	SHANK3 H2A(-5+12)
3506	CCGCTTGTATCGAAACT	SHANK3 H2A(-2+15)
3507	TCGCCGCTTGTATCGAA	SHANK3 H2A(+2+18)
3508	AACTCGCCGCTTGTATC	SHANK3 H2A(+5+21)
3509	ATAAACTCGCCGCTTGT	SHANK3 H2A(+8+24)
3510	GGCATAAACTCGCCGCT	SHANK3 H2A(+11+27)
3511	CTGGGCATAAACTCGCC	SHANK3 H2A(+14+30)
3512	GTTCTGGGCATAAACTC	SHANK3 H2A(+17+33)
3513	GAGGTTCTGGGCATAAA	SHANK3 H2A(+20+36)
3514	GATGAGGTTCTGGGCAT	SHANK3 H2A(+23+39)

3515	ATCGATGAGGTTCTGGG	SHANK3 H2A(+26+42)
3516	ATCATCGATGAGGTTCT	SHANK3 H2A(+29+45)
3517	CTTATCATCGATGAGGT	SHANK3 H2A(+32+48)
3518	CTGCTTATCATCGATGA	SHANK3 H2A(+35+51)
3519	AAACTGCTTATCATCGA	SHANK3 H2A(+38+54)
3520	TGCAAACTGCTTATCAT	SHANK3 H2A(+41+57)
3521	CTTTGCAAACTGCTTAT	SHANK3 H2A(+44+60)
3522	AAGCTTTGCAAACTGCT	SHANK3 H2A(+47+63)
3523	GTGAAGCTTTGCAAACT	SHANK3 H2A(+50+66)
3524	TGTGTGAAGCTTTGCAA	SHANK3 H2A(+53+69)
3525	CTTTGTGTGAAGCTTTG	SHANK3 H2A(+56+72)
3526	TACCTTTGTGTGAAGCT	SHANK3 H2D(+14-3)
3527	CTTTACCTTTGTGTGAA	SHANK3 H2D(+11-6)
3528	ATCCTTTACCTTTGTGT	SHANK3 H2D(+8-9)
3529	GTGATCCTTTACCTTTG	SHANK3 H2D(+5-12)
3530	CCCGTGATCCTTTACCT	SHANK3 H2D(+2-15)
3531	CTCCCCGTGATCCTTTA	SHANK3 H2D(-2-18)
3532	CCCCTCCCCGTGATCCT	SHANK3 H2D(-5-21)
3533	AGCCCCCTCCCCGTGAT	SHANK3 H2D(-8-24)
3534	AGGAGCCCCCTCCCCGT	SHANK3 H2D(-11-27)
3535	CTCAGGAGCCCCCTCCC	SHANK3 H2D(-14-30)
3536	AACCTCAGGAGCCCCCT	SHANK3 H2D(-17-33)
3537	GGGAACCTCAGGAGCCC	SHANK3 H2D(-20-36)
3538	GGAGGGAACCTCAGGAG	SHANK3 H2D(-23-39)
3539	GCAGGAGGGAACCTCAG	SHANK3 H2D(-26-42)
3540	GAGGCAGGAGGGAACCT	SHANK3 H2D(-29-45)
3541	AGGGAGGCAGGAGGGAA	SHANK3 H2D(-32-48)
3542	CACAGGGAGGCAGGAGG	SHANK3 H2D(-35-51)
3543	AGCCACAGGGAGGCAGG	SHANK3 H2D(-38-54)
3544	AGCAGCCACAGGGAGGC	SHANK3 H2D(-41-57)
3545	GACAGCAGCCACAGGGA	SHANK3 H2D(-44-60)
3546	GGGGACAGCAGCCACAG	SHANK3 H2D(-47-63)
3547	GTGGGGGACAGCAGCCA	SHANK3 H2D(-50-66)
3548	GGGGTGGGGGACAGCAG	SHANK3 H2D(-53-69)
3549	GCTGGGGTGGGGGACAG	SHANK3 H2D(-56-72)
3550	CAAGCTGGGGTGGGGGA	SHANK3 H2D(-59-75)

3551	CCCCAAGCTGGGGTGGG	SHANK3 H2D(-62-78)
3552	CAGCCCCAAGCTGGGGT	SHANK3 H2D(-65-81)
3553	GGTCAGCCCCAAGCTGG	SHANK3 H2D(-68-84)
3554	TGTGGTCAGCCCCAAGC	SHANK3 H2D(-71-87)
3555	GACTGTGGTCAGCCCCA	SHANK3 H2D(-74-90)
3556	GGGGACTGTGGTCAGCC	SHANK3 H2D(-77-93)
3557	CTGGGGGACTGTGGTCA	SHANK3 H2D(-80-96)
3558	AAGCTGGGGGACTGTGG	SHANK3 H2D(-83-99)
3559	CTAAAGCTGGGGGACTG	SHANK3 H2D(-86-102)
3560	GAGCTAAAGCTGGGGGA	SHANK3 H2D(-89-105)
3561	ACTGAGCTAAAGCTGGG	SHANK3 H2D(-92-108)
3562	TGGACTGAGCTAAAGCT	SHANK3 H2D(-95-111)
3563	AAATGGACTGAGCTAAA	SHANK3 H2D(-98-114)
3564	GGGAAATGGACTGAGCT	SHANK3 H2D(-101-117)
3565	ATGGGGAAATGGACTGA	SHANK3 H2D(-104-120)
3566	ATGATGGGGAAATGGAC	SHANK3 H2D(-107-123)
3567	CTGATGATGGGGAAATG	SHANK3 H2D(-110-126)
3568	CCCCTGATGATGGGGAA	SHANK3 H2D(-113-129)
3569	GGGCCCCTGATGATGGG	SHANK3 H2D(-116-132)
3570	TCTGGGCCCTGATGAT	SHANK3 H2D(-119-135)
3571	GGCTCTGGGCCCTGAT	SHANK3 H2D(-122-138)
3572	ACAGGCTCTGGGCCCT	SHANK3 H2D(-125-141)
3573	AGTACAGGCTCTGGGCC	SHANK3 H2D(-128-144)
3574	CCCAGTACAGGCTCTGG	SHANK3 H2D(-131-147)
3575	ACACCCAGTACAGGCTC	SHANK3 H2D(-134-150)
3576	GCCACACCCAGTACAGG	SHANK3 H2D(-137-153)
3577	TCAGCCACACCCAGTAC	SHANK3 H2D(-140-156)
3578	CCTTCAGCCACACCCAG	SHANK3 H2D(-143-159)
3579	AGCCCTTCAGCCACACC	SHANK3 H2D(-146-162)
3580	CCCAGCCCTTCAGCCAC	SHANK3 H2D(-149-165)
3581	GTGCCCAGCCCTTCAGC	SHANK3 H2D(-152-168)
3582	TCTGTGCCCAGCCCTTC	SHANK3 H2D(-155-171)
3583	GAATCTGTGCCCAGCCC	SHANK3 H2D(-158-174)
3584	CAGGAATCTGTGCCCAG	SHANK3 H2D(-161-177)
3585	GGCCAGGAATCTGTGCC	SHANK3 H2D(-164-180)
3586	TGGGGCCAGGAATCTGT	SHANK3 H2D(-167-183)

3587	CCATGGGGCCAGGAATC	SHANK3 H2D(-170-186)
3588	CAACCATGGGGCCAGGA	SHANK3 H2D(-173-189)
3589	CCCCAACCATGGGGCCA	SHANK3 H2D(-176-192)
3590	TGACCCCAACCATGGGG	SHANK3 H2D(-179-195)
3591	ACCTGACCCCAACCATG	SHANK3 H2D(-182-198)
3592	ACCACCTGACCCCAACC	SHANK3 H2D(-185-201)
3593	TGTACCACCTGACCCCA	SHANK3 H2D(-188-204)
3594	CACTGTACCACCTGACC	SHANK3 H2D(-191-207)
3595	CATCACTGTACCACCTG	SHANK3 H2D(-194-210)
3596	ACACATCACTGTACCAC	SHANK3 H2D(-197-213)
3597	GGAACACATCACTGTAC	SHANK3 H2D(-200-216)
3598	ACTGGAACACATCACTG	SHANK3 H2D(-203-219)
3599	CTAACTGGAACACATCA	SHANK3 H2D(-206-222)
3600	GATCTAACTGGAACACA	SHANK3 H2D(-209-225)
3601	TCTGATCTAACTGGAAC	SHANK3 H2D(-212-228)
3602	GAGTCTGATCTAACTGG	SHANK3 H2D(-215-231)
3603	CAAGAGTCTGATCTAAC	SHANK3 H2D(-218-234)
3604	CGGCAAGAGTCTGATCT	SHANK3 H2D(-221-237)
3605	GGTCGGCAAGAGTCTGA	SHANK3 H2D(-224-240)
3606	GGGGGTCTGGCAAGAGTC	SHANK3 H2D(-227-243)
3607	CAGGGGGGTCTGGCAAGA	SHANK3 H2D(-230-246)
3608	AGCCAGGGGGGTCTGGCA	SHANK3 H2D(-233-249)
3609	CTAAGCCAGGGGGGTCTG	SHANK3 H2D(-236-252)
3610	CCCCTAAGCCAGGGGGG	SHANK3 H2D(-239-255)
3611	CAGCCCCTAAGCCAGGG	SHANK3 H2D(-242-258)
3612	CTCCAGCCCCTAAGCCA	SHANK3 H2D(-245-261)
3613	ACACTCCAGCCCCTAAG	SHANK3 H2D(-248-264)
3614	AGGACACTCCAGCCCCT	SHANK3 H2D(-251-267)
3615	CACAGGACACTCCAGCC	SHANK3 H2D(-254-270)
3616	TCTCACAGGACACTCCA	SHANK3 H2D(-257-273)
3617	GCTTCTCACAGGACACT	SHANK3 H2D(-260-276)
3618	CCAGCTTCTCACAGGAC	SHANK3 H2D(-263-279)
3619	CACCCAGCTTCTCACAG	SHANK3 H2D(-266-282)
3620	CTCCACCCAGCTTCTCA	SHANK3 H2D(-269-285)
3621	CCTCTCCACCCAGCTTC	SHANK3 H2D(-272-288)
3622	CTCCCTCTCCACCCAGC	SHANK3 H2D(-275-291)

3623	CCACTCCCTCTCCACCC	SHANK3 H2D(-278-294)
3624	TGTCCACTCCCTCTCCA	SHANK3 H2D(-281-297)
3625	GCTTGTCCTCCCTCT	SHANK3 H2D(-284-300)
3626	GATGCTTGTCCTCCCTCC	SHANK3 H2D(-287-303)
3627	TCAGATGCTTGTCCTCACT	SHANK3 H2D(-290-306)
3628	ACATCAGATGCTTGTC	SHANK3 H2D(-293-309)
3629	ATCACATCAGATGCTTG	SHANK3 H2D(-296-312)
3630	GCCATCACATCAGATGC	SHANK3 H2D(-299-315)
3631	ACAGCCATCACATCAGA	SHANK3 H2D(-302-318)
3632	CCGACAGCCATCACATC	SHANK3 H2D(-305-321)
3633	GTCCCCGACAGCCATCAC	SHANK3 H2D(-308-324)
3634	CTTGTCCTCCGACAGCCAT	SHANK3 H2D(-311-327)
3635	TGCCTTGTCCTCCGACAGC	SHANK3 H2D(-314-330)
3636	GGGTGCCTTGTCCTCCGAC	SHANK3 H2D(-317-333)
3637	GCTGGGTGCCTTGTCCTCC	SHANK3 H2D(-320-336)
3638	GATGCTGGGTGCCTTG	SHANK3 H2D(-323-339)
3639	CTCGATGCTGGGTGCCT	SHANK3 H2D(-326-342)
3640	CCACTCGATGCTGGGTG	SHANK3 H2D(-329-345)
3641	CGACCACTCGATGCTGG	SHANK3 H2D(-332-348)
3642	GGTCGACCACTCGATGC	SHANK3 H2D(-335-351)
3643	ACTGGTCGACCACTCGA	SHANK3 H2D(-338-354)
3644	AGCACTGGTCGACCACT	SHANK3 H2D(-341-357)
3645	CCTAGCACTGGTCGACC	SHANK3 H2D(-344-360)
3646	ATGCCTAGCACTGGTCG	SHANK3 H2D(-347-363)
3647	CAAATGCCTAGCACTGG	SHANK3 H2D(-350-366)
3648	TCACAAATGCCTAGCAC	SHANK3 H2D(-353-369)
3649	TAATCACAAATGCCTAG	SHANK3 H2D(-356-372)
3650	GTCTAATCACAAATGCC	SHANK3 H2D(-359-375)
3651	GAGGTCTAATCACAAAT	SHANK3 H2D(-362-378)
3652	TGAGAGGTCTAATCACA	SHANK3 H2D(-365-381)
3653	TAATGAGAGGTCTAATC	SHANK3 H2D(-368-384)
3654	GATTAATGAGAGGTCTA	SHANK3 H2D(-371-387)
3655	GAGGATTAATGAGAGGT	SHANK3 H2D(-374-390)
3656	GAAGAGGATTAATGAGA	SHANK3 H2D(-377-393)
3657	CTGGAAGAGGATTAATG	SHANK3 H2D(-380-396)
3658	CCTCTGGAAGAGGATTA	SHANK3 H2D(-383-399)

3659	GTCCCTCTGGAAGAGGA	SHANK3 H2D(-386-402)
3660	ATAGTCCCTCTGGAAGA	SHANK3 H2D(-389-405)
3661	ATAATAGTCCCTCTGGA	SHANK3 H2D(-392-408)
3662	GTTATAATAGTCCCTCT	SHANK3 H2D(-395-411)
3663	AGGGTTATAATAGTCCC	SHANK3 H2D(-398-414)
3664	AACAGGGTTATAATAGT	SHANK3 H2D(-401-417)
3665	TGAAACAGGGTTATAAT	SHANK3 H2D(-404-420)
3666	CTGTGAAACAGGGTTAT	SHANK3 H2D(-407-423)
3667	CATCTGTGAAACAGGGT	SHANK3 H2D(-410-426)
3668	CCCCATCTGTGAAACAG	SHANK3 H2D(-413-429)
3669	TGTCCCCATCTGTGAAA	SHANK3 H2D(-416-432)
3670	CTGTGTCCCCATCTGTG	SHANK3 H2D(-419-435)
3671	ACTCTGTGTCCCCATCT	SHANK3 H2D(-422-438)
3672	GGTACTCTGTGTCCCCA	SHANK3 H2D(-425-441)
3673	TCGGGTACTCTGTGTCC	SHANK3 H2D(-428-444)
3674	CAGTCGGGTACTCTGTG	SHANK3 H2D(-431-447)
3675	ACACAGTCGGGTACTCT	SHANK3 H2D(-434-450)
3676	TCTACACAGTCGGGTAC	SHANK3 H2D(-437-453)
3677	CTGTCTACACAGTCGGG	SHANK3 H2D(-440-456)
3678	TCACTGTCTACACAGTC	SHANK3 H2D(-443-459)
3679	GCTTCACTGTCTACACA	SHANK3 H2D(-446-462)
3680	CCAGCTTCACTGTCTAC	SHANK3 H2D(-449-465)
3681	GCCCCAGCTTCACTGTC	SHANK3 H2D(-452-468)
3682	TCAGCCCCAGCTTCACT	SHANK3 H2D(-455-471)
3683	GGTTCAGCCCCAGCTTC	SHANK3 H2D(-458-474)
3684	CTGGGTTCAGCCCCAGC	SHANK3 H2D(-461-477)
3685	GATCTGGGTTCAGCCCC	SHANK3 H2D(-464-480)
3686	ACAGATCTGGGTTCAGC	SHANK3 H2D(-467-483)
3687	CAGACAGATCTGGGTTC	SHANK3 H2D(-470-486)
3688	AATCAGACAGATCTGGG	SHANK3 H2D(-473-489)
3689	TGGAATCAGACAGATCT	SHANK3 H2D(-476-492)
3690	GCCTGGAATCAGACAGA	SHANK3 H2D(-479-495)
3691	AGGGCCTGGAATCAGAC	SHANK3 H2D(-482-498)
3692	CACAGGGCCTGGAATCA	SHANK3 H2D(-485-501)
3693	GGGCACAGGGCCTGGAA	SHANK3 H2D(-488-504)
3694	CCTGGGCACAGGGCCTG	SHANK3 H2D(-491-507)

3695	ATGCCTGGGCACAGGGC	SHANK3 H2D(-494-510)
3696	GGCATGCCTGGGCACAG	SHANK3 H2D(-497-513)
3697	AAAGGCATGCCTGGGCA	SHANK3 H2D(-500-516)
3698	CTCAAAGGCATGCCTGG	SHANK3 H2D(-503-519)
3699	CACCTCAAAGGCATGCC	SHANK3 H2D(-506-522)
3700	AGACACCTCAAAGGCAT	SHANK3 H2D(-509-525)
3701	AGTAGACACCTCAAAGG	SHANK3 H2D(-512-528)
3702	AGCAGTAGACACCTCAA	SHANK3 H2D(-515-531)
3703	CCCAGCAGTAGACACCT	SHANK3 H2D(-518-534)
3704	GCACCCAGCAGTAGACA	SHANK3 H2D(-521-537)
3705	GTGGCACCCAGCAGTAG	SHANK3 H2D(-524-540)
3706	GGGGTGGCACCCAGCAG	SHANK3 H2D(-527-543)
3707	TTGGGGGTGGCACCCAG	SHANK3 H2D(-530-546)
3708	CAGTTGGGGGTGGCACC	SHANK3 H2D(-533-549)
3709	GCCCAGTTGGGGGTGGC	SHANK3 H2D(-536-552)
3710	CAGGCCCAGTTGGGGGT	SHANK3 H2D(-539-555)
3711	GGTCAGGCCCAGTTGGG	SHANK3 H2D(-542-558)
3712	TGGGGTCAGGCCCAGTT	SHANK3 H2D(-545-561)
3713	ATTTGGGGTCAGGCCCA	SHANK3 H2D(-548-564)
3714	AGCATTTGGGGTCAGGC	SHANK3 H2D(-551-567)
3715	AAGAGCATTTGGGGTCA	SHANK3 H2D(-554-570)
3716	CTCAAGAGCATTTGGGG	SHANK3 H2D(-557-573)
3717	CCCCTCAAGAGCATTTG	SHANK3 H2D(-560-576)
3718	GCCCCCTCAAGAGCAT	SHANK3 H2D(-563-579)
3719	GGTGCCCCCTCAAGAG	SHANK3 H2D(-566-582)
3720	TAAGGTGCCCCCTCAA	SHANK3 H2D(-569-585)
3721	TAGTAAGGTGCCCCCT	SHANK3 H2D(-572-588)
3722	AAATAGTAAGGTGCCCC	SHANK3 H2D(-575-591)
3723	GGGAAATAGTAAGGTGC	SHANK3 H2D(-578-594)
3724	AGCGGGAAATAGTAAGG	SHANK3 H2D(-581-597)
3725	TTCAGCGGAAATAGTA	SHANK3 H2D(-584-600)
3726	ACATTCAGCGGAAATA	SHANK3 H2D(-587-603)
3727	CTGACATTCAGCGGAA	SHANK3 H2D(-590-606)
3728	CCTCTGACATTCAGCGG	SHANK3 H2D(-593-609)
3729	GCCCCTCTGACATTCAG	SHANK3 H2D(-596-612)
3730	CCTGCCCTCTGACATT	SHANK3 H2D(-599-615)

3731	CACCCTGCCCCCTCTGAC	SHANK3 H2D(-602-618)
3732	ACCCACCCTGCCCCCTCT	SHANK3 H2D(-605-621)
3733	GGCACCCACCCTGCCCC	SHANK3 H2D(-608-624)
3734	TGTGGCACCCACCCTGC	SHANK3 H2D(-611-627)
3735	GGCTGTGGCACCCACCC	SHANK3 H2D(-614-630)
3736	AGGGGCTGTGGCACCCA	SHANK3 H2D(-617-633)
3737	GGGAGGGGCTGTGGCAC	SHANK3 H2D(-620-636)
3738	CTGGGGAGGGGCTGTGG	SHANK3 H2D(-623-639)
3739	CCCCTGGGGAGGGGCTG	SHANK3 H2D(-626-642)
3740	AAGCCCTGGGGAGGGG	SHANK3 H2D(-629-645)
3741	TGGAAGCCCTGGGGAG	SHANK3 H2D(-632-648)
3742	GGGTGGAAGCCCTGGG	SHANK3 H2D(-635-651)
3743	TGCGGGTGAAGCCCT	SHANK3 H2D(-638-654)
3744	AGCTGCGGGTGAAGCC	SHANK3 H2D(-641-657)
3745	GTGAGCTGCGGGTGAA	SHANK3 H2D(-644-660)
3746	ACTGTGAGCTGCGGGTG	SHANK3 H2D(-647-663)
3747	TGGACTGTGAGCTGCGG	SHANK3 H2D(-650-666)
3748	TGCTGGACTGTGAGCTG	SHANK3 H2D(-653-669)
3749	GCCTGCTGGACTGTGAG	SHANK3 H2D(-656-672)
3750	AGTGCCTGCTGGACTGT	SHANK3 H2D(-659-675)
3751	ACAAGTGCCTGCTGGAC	SHANK3 H2D(-662-678)
3752	CAAACAAGTGCTGCTG	SHANK3 H2D(-665-681)
3753	CAGCAAACAAGTGCCTG	SHANK3 H2D(-668-684)
3754	ATCCAGCAAACAAGTGC	SHANK3 H2D(-671-687)
3755	AGTATCCAGCAAACAAG	SHANK3 H2D(-674-690)
3756	TAAAGTATCCAGCAAAC	SHANK3 H2D(-677-693)
3757	CCATAAAGTATCCAGCA	SHANK3 H2D(-680-696)
3758	CGCCCATAAAGTATCCA	SHANK3 H2D(-683-699)
3759	GACCGCCCATAAAGTAT	SHANK3 H2D(-686-702)
3760	CGAGACCGCCCATAAAG	SHANK3 H2D(-689-705)
3761	GCTCGAGACCGCCCAT	SHANK3 H2D(-692-708)
3762	TGAGCTCGAGACCGCCC	SHANK3 H2D(-695-711)
3763	TCCTGAGCTCGAGACCG	SHANK3 H2D(-698-714)
3764	CTCTCTGAGCTCGAGA	SHANK3 H2D(-701-717)
3765	CCCCTCTCTGAGCTCG	SHANK3 H2D(-704-720)
3766	TGACCCCTCTCTGAGC	SHANK3 H2D(-707-723)

3767	TTCTGACCCCTCTCCTG	SHANK3 H2D(-710-726)
3768	CCATTCTGACCCCTCTC	SHANK3 H2D(-713-729)
3769	CCTCCATTCTGACCCCT	SHANK3 H2D(-716-732)
3770	GACCCCTCCATTCTGACC	SHANK3 H2D(-719-735)
3771	AGAGACCCCTCCATTCTG	SHANK3 H2D(-722-738)
3772	TCCAGAGACCCCTCCATT	SHANK3 H2D(-725-741)
3773	GGCTCCAGAGACCCCTCC	SHANK3 H2D(-728-744)
3774	CTGGGCTCCAGAGACCC	SHANK3 H2D(-731-747)
3775	CTCCTGGGCTCCAGAGA	SHANK3 H2D(-734-750)
3776	CCTCTCCTGGGCTCCAG	SHANK3 H2D(-737-753)
3777	ATTCTCTCCTGGGCTC	SHANK3 H2D(-740-756)
3778	CTGATTCCTCTCCTGGG	SHANK3 H2D(-743-759)
3779	GTTCTGATTCCTCTCCT	SHANK3 H2D(-746-762)
3780	ACAGTTCTGATTCCTCT	SHANK3 H2D(-749-765)
3781	CTGACAGTTCTGATTCC	SHANK3 H2D(-752-768)
3782	GGGCTGACAGTTCTGAT	SHANK3 H2D(-755-771)
3783	ACAGGGCTGACAGTTCT	SHANK3 H2D(-758-774)
3784	GACACAGGGCTGACAGT	SHANK3 H2D(-761-777)
3785	TAGGACACAGGGCTGAC	SHANK3 H2D(-764-780)
3786	CATTAGGACACAGGGCT	SHANK3 H2D(-767-783)
3787	GACCATTAGGACACAGG	SHANK3 H2D(-770-786)
3788	TGGGACCATTAGGACAC	SHANK3 H2D(-773-789)
3789	TGATGGGACCATTAGGA	SHANK3 H2D(-776-792)
3790	CACTGATGGGACCATTA	SHANK3 H2D(-779-795)
3791	AGTCACTGATGGGACCA	SHANK3 H2D(-782-798)
3792	CAAAGTCACTGATGGGA	SHANK3 H2D(-785-801)
3793	CTCCAAAGTCACTGATG	SHANK3 H2D(-788-804)
3794	AGGCTCCAAAGTCACTG	SHANK3 H2D(-791-807)
3795	CTGAGGCTCCAAAGTCA	SHANK3 H2D(-794-810)
3796	AGCCTGAGGCTCCAAAG	SHANK3 H2D(-797-813)
3797	AGAAGCCTGAGGCTCCA	SHANK3 H2D(-800-816)
3798	CACAGAAGCCTGAGGCT	SHANK3 H2D(-803-819)
3799	TGGCACAGAAGCCTGAG	SHANK3 H2D(-806-822)
3800	GCCTGGCACAGAAGCCT	SHANK3 H2D(-809-825)
3801	AAAGCCTGGCACAGAAG	SHANK3 H2D(-812-828)
3802	AGAAAAGCCTGGCACAG	SHANK3 H2D(-815-831)

3803	AGCAGAAAAGCCTGGCA	SHANK3 H2D(-818-834)
3804	GGCAGCAGAAAAGCCTG	SHANK3 H2D(-821-837)
3805	TGGGGCAGCAGAAAAGC	SHANK3 H2D(-824-840)
3806	CCCTGGGGCAGCAGAAA	SHANK3 H2D(-827-843)
3807	CTGCCCTGGGGCAGCAG	SHANK3 H2D(-830-846)
3808	CGCCTGCCCTGGGGCAG	SHANK3 H2D(-833-849)
3809	CACCGCCTGCCCTGGGG	SHANK3 H2D(-836-852)
3810	GACCACCGCCTGCCCTG	SHANK3 H2D(-839-855)
3811	GTTGACCACCGCCTGCC	SHANK3 H2D(-842-858)
3812	GCCGTTGACCACCGCCT	SHANK3 H2D(-845-861)
3813	AAGGCCGTTGACCACCG	SHANK3 H2D(-848-864)
3814	GCCAAGGCCGTTGACCA	SHANK3 H2D(-851-867)
3815	AGTGCCAAGGCCGTTGA	SHANK3 H2D(-854-870)
3816	CATAGTGCCAAGGCCGT	SHANK3 H2D(-857-873)
3817	AGCCATAGTGCCAAGGC	SHANK3 H2D(-860-876)
3818	CCCAGCCATAGTGCCAA	SHANK3 H2D(-863-879)
3819	CTGCCCAGCCATAGTGC	SHANK3 H2D(-866-882)
3820	ACTCTGCCAGCCATAG	SHANK3 H2D(-869-885)
3821	TGGA CTCTGCCAGCCA	SHANK3 H2D(-872-888)
3822	CAGTGGA CTCTGCCAG	SHANK3 H2D(-875-891)
3823	CCACAGTGGACTCTGCC	SHANK3 H2D(-878-894)
3824	TTTCCACAGTGGACTCT	SHANK3 H2D(-881-897)
3825	ACCTTTCCACAGTGGAC	SHANK3 H2D(-884-900)
3826	GGGACCTTTCCACAGTG	SHANK3 H2D(-887-903)
3827	AGGGGGACCTTTCCACA	SHANK3 H2D(-890-906)
3828	GAGAGGGGGACCTTTCC	SHANK3 H2D(-893-909)
3829	CAGGAGAGGGGGACCTT	SHANK3 H2D(-896-912)
3830	TGGCAGGAGAGGGGGAC	SHANK3 H2D(-899-915)
3831	CAGTGGCAGGAGAGGGG	SHANK3 H2D(-902-918)
3832	GGCCAGTGGCAGGAGAG	SHANK3 H2D(-905-921)
3833	GAGGGCCAGTGGCAGGA	SHANK3 H2D(-908-924)
3834	AGTGAGGGCCAGTGGCA	SHANK3 H2D(-911-927)
3835	TCAAGTGAGGGCCAGTG	SHANK3 H2D(-914-930)
3836	AGGTCAAGTGAGGGCCA	SHANK3 H2D(-917-933)
3837	ACAAGGTCAAGTGAGGG	SHANK3 H2D(-920-936)
3838	CTGACAAGGTCAAGTGA	SHANK3 H2D(-923-939)

3839	AGGCTGACAAGGTCAAG	SHANK3 H2D(-926-942)
3840	CCCAGGCTGACAAGGTC	SHANK3 H2D(-929-945)
3841	GAACCCAGGCTGACAAG	SHANK3 H2D(-932-948)
3842	TAGGAACCCAGGCTGAC	SHANK3 H2D(-935-951)
3843	GGGTAGGAACCCAGGCT	SHANK3 H2D(-938-954)
3844	ATGGGGTAGGAACCCAG	SHANK3 H2D(-941-957)
3845	GCCATGGGGTAGGAACC	SHANK3 H2D(-944-960)
3846	GTGGCCATGGGGTAGGA	SHANK3 H3A(-945-929)
3847	GAGGTGGCCATGGGGTA	SHANK3 H3A(-942-926)
3848	GGAGAGGTGGCCATGGG	SHANK3 H3A(-939-923)
3849	GAGGGAGAGGTGGCCAT	SHANK3 H3A(-936-920)
3850	CCGGAGGGAGAGGTGGC	SHANK3 H3A(-933-917)
3851	GATCCGGAGGGAGAGGT	SHANK3 H3A(-930-914)
3852	AGAGATCCGGAGGGAGA	SHANK3 H3A(-927-911)
3853	AAGAGAGATCCGGAGGG	SHANK3 H3A(-924-908)
3854	CTGAAGAGAGATCCGGA	SHANK3 H3A(-921-905)
3855	TCACTGAAGAGAGATCC	SHANK3 H3A(-918-902)
3856	TGGTCACTGAAGAGAGA	SHANK3 H3A(-915-899)
3857	TGTTGGTCACTGAAGAG	SHANK3 H3A(-912-896)
3858	TCTTGTTGGTCACTGAA	SHANK3 H3A(-909-893)
3859	ATGTCTTGTTGGTCACT	SHANK3 H3A(-906-890)
3860	CTCATGTCTTGTTGGTC	SHANK3 H3A(-903-887)
3861	TCACTCATGTCTTGTTG	SHANK3 H3A(-900-884)
3862	GAGTCACTCATGTCTTG	SHANK3 H3A(-897-881)
3863	AGTGAGTCACTCATGTC	SHANK3 H3A(-894-878)
3864	CAGAGTGAGTCACTCAT	SHANK3 H3A(-891-875)
3865	CTTCAGAGTGAGTCACT	SHANK3 H3A(-888-872)
3866	CTACTTCAGAGTGAGTC	SHANK3 H3A(-885-869)
3867	GACCTACTTCAGAGTGA	SHANK3 H3A(-882-866)
3868	CGAGACCTACTTCAGAG	SHANK3 H3A(-879-863)
3869	AAACGAGACCTACTTCA	SHANK3 H3A(-876-860)
3870	AACAAACGAGACCTACT	SHANK3 H3A(-873-857)
3871	AAAAACAAACGAGACCT	SHANK3 H3A(-870-854)
3872	CCTAAAAACAAACGAGA	SHANK3 H3A(-867-851)
3873	CATCCTAAAAACAAACG	SHANK3 H3A(-864-848)
3874	GCTCATCCTAAAAACAA	SHANK3 H3A(-861-845)

3875	CAGGCTCATCCTAAAAA	SHANK3 H3A(-858-842)
3876	G TTCAGGCTCATCTAA	SHANK3 H3A(-855-839)
3877	GAAGTTCAGGCTCATCC	SHANK3 H3A(-852-836)
3878	TAAGAAGTTCAGGCTCA	SHANK3 H3A(-849-833)
3879	ATGTAAGAAGTTCAGGC	SHANK3 H3A(-846-830)
3880	GCTATGTAAGAAGTTCA	SHANK3 H3A(-843-827)
3881	CGGGCTATGTAAGAAGT	SHANK3 H3A(-840-824)
3882	ACACGGGCTATGTAAGA	SHANK3 H3A(-837-821)
3883	GAAACACGGGCTATGTA	SHANK3 H3A(-834-818)
3884	GCAGAAACACGGGCTAT	SHANK3 H3A(-831-815)
3885	CAAGCAGAAACACGGGC	SHANK3 H3A(-828-812)
3886	AGGCAAGCAGAAACACG	SHANK3 H3A(-825-809)
3887	CCCAGGCAAGCAGAAAC	SHANK3 H3A(-822-806)
3888	GAGCCCAGGCAAGCAGA	SHANK3 H3A(-819-803)
3889	CTGGAGCCCAGGCAAGC	SHANK3 H3A(-816-800)
3890	CAGCTGGAGCCCAGGCA	SHANK3 H3A(-813-797)
3891	GGCCAGCTGGAGCCAG	SHANK3 H3A(-810-794)
3892	AAAGGCCAGCTGGAGCC	SHANK3 H3A(-807-791)
3893	GGGAAAGGCCAGCTGGA	SHANK3 H3A(-804-788)
3894	AGAGGGAAAGGCCAGCT	SHANK3 H3A(-801-785)
3895	GGGAGAGGGAAAGGCCA	SHANK3 H3A(-798-782)
3896	CAGGGGAGAGGGAAAGG	SHANK3 H3A(-795-779)
3897	TACCAGGGGAGAGGGAA	SHANK3 H3A(-792-776)
3898	CACTACCAGGGGAGAGG	SHANK3 H3A(-789-773)
3899	GCTCACTACCAGGGGAG	SHANK3 H3A(-786-770)
3900	AGTGCTCACTACCAGGG	SHANK3 H3A(-783-767)
3901	GGAAGTGCTCACTACCA	SHANK3 H3A(-780-764)
3902	GGAGGAAGTGCTCACTA	SHANK3 H3A(-777-761)
3903	AGAGGAGGAAGTGCTCA	SHANK3 H3A(-774-758)
3904	GAAAGAGGAGGAAGTGC	SHANK3 H3A(-771-755)
3905	AGTGAAAGAGGAGGAAG	SHANK3 H3A(-768-752)
3906	GGCAGTGAAAGAGGAGG	SHANK3 H3A(-765-749)
3907	CCAGGCAGTGAAAGAGG	SHANK3 H3A(-762-746)
3908	GGGCCAGGCAGTGAAAG	SHANK3 H3A(-759-743)
3909	GGCGGGCCAGGCAGTGA	SHANK3 H3A(-756-740)
3910	TCAGGCGGGCCAGGCAG	SHANK3 H3A(-753-737)

3911	TCCTCAGGCGGGCCAGG	SHANK3 H3A(-750-734)
3912	ACCTCCTCAGGCGGGCC	SHANK3 H3A(-747-731)
3913	GCAACCTCCTCAGGCGG	SHANK3 H3A(-744-728)
3914	GAGGCAACCTCCTCAGG	SHANK3 H3A(-741-725)
3915	TGGGAGGCAACCTCCTC	SHANK3 H3A(-738-722)
3916	CCTTGGGAGGCAACCTC	SHANK3 H3A(-735-719)
3917	CTGCCTTGGGAGGCAAC	SHANK3 H3A(-732-716)
3918	CCCCTGCCTTGGGAGGC	SHANK3 H3A(-729-713)
3919	GGACCCCTGCCTTGGGA	SHANK3 H3A(-726-710)
3920	TAGGGACCCCTGCCTTG	SHANK3 H3A(-723-707)
3921	CCATAGGGACCCCTGCC	SHANK3 H3A(-720-704)
3922	GTGCCATAGGGACCCCT	SHANK3 H3A(-717-701)
3923	AGGGTGCCATAGGGACC	SHANK3 H3A(-714-698)
3924	GGGAGGGTGCCATAGGG	SHANK3 H3A(-711-695)
3925	TAGGGGAGGGTGCCATA	SHANK3 H3A(-708-692)
3926	AAATAGGGGAGGGTGCC	SHANK3 H3A(-705-689)
3927	CAGAAATAGGGGAGGGT	SHANK3 H3A(-702-686)
3928	CCTCAGAAATAGGGGAG	SHANK3 H3A(-699-683)
3929	GTACCTCAGAAATAGGG	SHANK3 H3A(-696-680)
3930	AGTGTACCTCAGAAATA	SHANK3 H3A(-693-677)
3931	CCCAGTGTACCTCAGAA	SHANK3 H3A(-690-674)
3932	ACACCCAGTGTACCTCA	SHANK3 H3A(-687-671)
3933	TAAACACCCAGTGTACC	SHANK3 H3A(-684-668)
3934	CCATAAACACCCAGTGT	SHANK3 H3A(-681-665)
3935	CTTCCATAAACACCCAG	SHANK3 H3A(-678-662)
3936	GCCCTTCCATAAACACC	SHANK3 H3A(-675-659)
3937	GGGGCCCTTCCATAAAC	SHANK3 H3A(-672-656)
3938	GCCGGGGCCCTTCCATA	SHANK3 H3A(-669-653)
3939	AAGGCCGGGGCCCTTCC	SHANK3 H3A(-666-650)
3940	CCAAAGGCCGGGGCCCT	SHANK3 H3A(-663-647)
3941	TGGCCAAAGGCCGGGGC	SHANK3 H3A(-660-644)
3942	CCCTGGCCAAAGGCCGG	SHANK3 H3A(-657-641)
3943	GTGCCCTGGCCAAAGGC	SHANK3 H3A(-654-638)
3944	AAGGTGCCCTGGCCAAA	SHANK3 H3A(-651-635)
3945	GGCAAGGTGCCCTGGCC	SHANK3 H3A(-648-632)
3946	CAAGGCAAGGTGCCCTG	SHANK3 H3A(-645-629)

3947	ACACAAGGCAAGGTGCC	SHANK3 H3A(-642-626)
3948	CACACACAAGGCAAGGT	SHANK3 H3A(-639-623)
3949	CCACACACACAAGGCAA	SHANK3 H3A(-636-620)
3950	ACACCACACACACAAGG	SHANK3 H3A(-633-617)
3951	CGGACACCACACACACA	SHANK3 H3A(-630-614)
3952	CTACGGACACCACACAC	SHANK3 H3A(-627-611)
3953	GCACTACGGACACCACA	SHANK3 H3A(-624-608)
3954	CCGGCACTACGGACACC	SHANK3 H3A(-621-605)
3955	CAGCCGGCACTACGGAC	SHANK3 H3A(-618-602)
3956	CCCCAGCCGGCACTACG	SHANK3 H3A(-615-599)
3957	CTTCCCAGCCGGCACT	SHANK3 H3A(-612-596)
3958	TCACTTCCCAGCCGGC	SHANK3 H3A(-609-593)
3959	GCCTCACTTCCCAGCC	SHANK3 H3A(-606-590)
3960	AAGGCCTCACTTCCCCA	SHANK3 H3A(-603-587)
3961	CACAAGGCCTCACTTCC	SHANK3 H3A(-600-584)
3962	CCCCACAAGGCCTCACT	SHANK3 H3A(-597-581)
3963	TCACCCACAAGGCCTC	SHANK3 H3A(-594-578)
3964	CACTACCCACAAGGC	SHANK3 H3A(-591-575)
3965	ATCACTACCCACAA	SHANK3 H3A(-588-572)
3966	TTTATTCACTACCCCA	SHANK3 H3A(-585-569)
3967	CAGTTTATTCACTACC	SHANK3 H3A(-582-566)
3968	ACCCAGTTTATTCACTC	SHANK3 H3A(-579-563)
3969	TTCACCCAGTTTATTCA	SHANK3 H3A(-576-560)
3970	TCATTACCCAGTTTAT	SHANK3 H3A(-573-557)
3971	TACTCATTACCCAGTT	SHANK3 H3A(-570-554)
3972	TTGTACTCATTACCCCA	SHANK3 H3A(-567-551)
3973	GCCTTGTA CTACATTCAC	SHANK3 H3A(-564-548)
3974	ATGGCCTTGTA CTACATTC	SHANK3 H3A(-561-545)
3975	TTGATGGCCTTGTA CT	SHANK3 H3A(-558-542)
3976	ACTTTGATGGCCTTGTA	SHANK3 H3A(-555-539)
3977	ATGACTTTGATGGCCTT	SHANK3 H3A(-552-536)
3978	GACATGACTTTGATGGC	SHANK3 H3A(-549-533)
3979	TGTGACATGACTTTGAT	SHANK3 H3A(-546-530)
3980	TCCTGTGACATGACTTT	SHANK3 H3A(-543-527)
3981	CCATCCTGTGACATGAC	SHANK3 H3A(-540-524)
3982	GACCCATCCTGTGACAT	SHANK3 H3A(-537-521)

3983	AGGGACCCATCCTGTGA	SHANK3 H3A(-534-518)
3984	CCCAGGGACCCATCCTG	SHANK3 H3A(-531-515)
3985	CACCCCAGGGACCCATC	SHANK3 H3A(-528-512)
3986	CCCCACCCAGGGACCC	SHANK3 H3A(-525-509)
3987	GACCCCCACCCAGGGA	SHANK3 H3A(-522-506)
3988	GCAGACCCCCACCCAG	SHANK3 H3A(-519-503)
3989	ACCGCAGACCCCCACCC	SHANK3 H3A(-516-500)
3990	CCCACCGCAGACCCCCA	SHANK3 H3A(-513-497)
3991	CACCCACCGCAGACCC	SHANK3 H3A(-510-494)
3992	GCTCACCCACCGCAGA	SHANK3 H3A(-507-491)
3993	CCAGCTACCCACCGC	SHANK3 H3A(-504-488)
3994	TCTCCAGCTACCCAC	SHANK3 H3A(-501-485)
3995	TCCTCTCCAGCTACCC	SHANK3 H3A(-498-482)
3996	TCTTCCTCTCCAGTCA	SHANK3 H3A(-495-479)
3997	CCATCTTCCTCTCCAGC	SHANK3 H3A(-492-476)
3998	GGCCCATCTTCCTCTCC	SHANK3 H3A(-489-473)
3999	TTCGGCCCATCTTCCTC	SHANK3 H3A(-486-470)
4000	TTCTTCGGCCCATCTTC	SHANK3 H3A(-483-467)
4001	TCCTTCTTCGGCCCATC	SHANK3 H3A(-480-464)
4002	TGCTCCTTCTTCGGCCC	SHANK3 H3A(-477-461)
4003	ACCTGCTCTTCTTCGG	SHANK3 H3A(-474-458)
4004	ACAACCTGCTCCTTCTT	SHANK3 H3A(-471-455)
4005	GAGACAACCTGCTCCTT	SHANK3 H3A(-468-452)
4006	CCTGAGACAACCTGCTC	SHANK3 H3A(-465-449)
4007	CACCCTGAGACAACCTG	SHANK3 H3A(-462-446)
4008	CAGCACCTGAGACAAC	SHANK3 H3A(-459-443)
4009	CCTCAGCACCTGAGAC	SHANK3 H3A(-456-440)
4010	AATCCTCAGCACCTGA	SHANK3 H3A(-453-437)
4011	CTGAATCCTCAGCACCC	SHANK3 H3A(-450-434)
4012	GCCCTGAATCCTCAGCA	SHANK3 H3A(-447-431)
4013	GCAGCCCTGAATCCTCA	SHANK3 H3A(-444-428)
4014	ACAGCAGCCCTGAATCC	SHANK3 H3A(-441-425)
4015	CCCACAGCAGCCCTGAA	SHANK3 H3A(-438-422)
4016	AGCCCCACAGCAGCCCT	SHANK3 H3A(-435-419)
4017	ACCAGCCCCACAGCAGC	SHANK3 H3A(-432-416)
4018	GGAACCAGCCCCACAGC	SHANK3 H3A(-429-413)

4019	GCAGGAACCAGCCCCAC	SHANK3 H3A(-426-410)
4020	CAGGCAGGAACCAGCCC	SHANK3 H3A(-423-407)
4021	ACCCAGGCAGGAACCAG	SHANK3 H3A(-420-404)
4022	TCCACCCAGGCAGGAAC	SHANK3 H3A(-417-401)
4023	AGGTCCACCCAGGCAGG	SHANK3 H3A(-414-398)
4024	CCGAGGTCCACCCAGGC	SHANK3 H3A(-411-395)
4025	AGCCCAGGTCCACCCA	SHANK3 H3A(-408-392)
4026	AAGAGCCCGAGGTCCAC	SHANK3 H3A(-405-389)
4027	TAGAAGAGCCCGAGGTC	SHANK3 H3A(-402-386)
4028	GCCTAGAAGAGCCCGAG	SHANK3 H3A(-399-383)
4029	CTGGCCTAGAAGAGCCC	SHANK3 H3A(-396-380)
4030	TGCCTGGCCTAGAAGAG	SHANK3 H3A(-393-377)
4031	ACCTGCCTGGCCTAGAA	SHANK3 H3A(-390-374)
4032	CCGACCTGCCTGGCCTA	SHANK3 H3A(-387-371)
4033	GCCCCGACCTGCCTGGC	SHANK3 H3A(-384-368)
4034	GCTGCCCCGACCTGCCT	SHANK3 H3A(-381-365)
4035	CCTGCTGCCCCGACCTG	SHANK3 H3A(-378-362)
4036	GGCCCTGCTGCCCCGAC	SHANK3 H3A(-375-359)
4037	TCCGGCCCTGCTGCCCC	SHANK3 H3A(-372-356)
4038	CTCTCCGGCCCTGCTGC	SHANK3 H3A(-369-353)
4039	CGTCTCTCCGGCCCTGC	SHANK3 H3A(-366-350)
4040	CTCCGTCTCTCCGGCCC	SHANK3 H3A(-363-347)
4041	TGGCTCCGTCTCTCCGG	SHANK3 H3A(-360-344)
4042	CCCTGGCTCCGTCTCTC	SHANK3 H3A(-357-341)
4043	CTGCCCTGGCTCCGTCT	SHANK3 H3A(-354-338)
4044	TCACTGCCCTGGCTCCG	SHANK3 H3A(-351-335)
4045	CAGTCACTGCCCTGGCT	SHANK3 H3A(-348-332)
4046	GCCCAGTCACTGCCCTG	SHANK3 H3A(-345-329)
4047	CAGGCCCAGTCACTGCC	SHANK3 H3A(-342-326)
4048	CTCCAGGCCCAGTCACT	SHANK3 H3A(-339-323)
4049	CCACTCCAGGCCAGTCT	SHANK3 H3A(-336-320)
4050	CCCCACTCCAGGCCCA	SHANK3 H3A(-333-317)
4051	AGTCCCCACTCCAGGC	SHANK3 H3A(-330-314)
4052	GCAAGTCCCCACTCCA	SHANK3 H3A(-327-311)
4053	CAAGCAAGTCCCCACT	SHANK3 H3A(-324-308)
4054	CCCAAGCAAGTCCCCC	SHANK3 H3A(-321-305)

4055	GGGCCCCAAGCAAGTCC	SHANK3 H3A(-318-302)
4056	GTGGGGCCCCAAGCAAG	SHANK3 H3A(-315-299)
4057	CTGGTGGGGCCCCAAGC	SHANK3 H3A(-312-296)
4058	ACCCTGGTGGGGCCCCA	SHANK3 H3A(-309-293)
4059	GTCACCTGGTGGGGGCC	SHANK3 H3A(-306-290)
4060	CAGGTCACCTGGTGGG	SHANK3 H3A(-303-287)
4061	GGCCAGGTCACCTGGT	SHANK3 H3A(-300-284)
4062	CAAGGCCAGGTCACCT	SHANK3 H3A(-297-281)
4063	CACCAAGGCCAGGTAC	SHANK3 H3A(-294-278)
4064	CCTCACCAGGCCAGGT	SHANK3 H3A(-291-275)
4065	GCCCCTACCAAGGCCA	SHANK3 H3A(-288-272)
4066	GTAGCCCCTACCAAGG	SHANK3 H3A(-285-269)
4067	CAAGTAGCCCCTACCA	SHANK3 H3A(-282-266)
4068	ACCCAAGTAGCCCCTCA	SHANK3 H3A(-279-263)
4069	TGTACCCAAGTAGCCCC	SHANK3 H3A(-276-260)
4070	GCTTGTACCCAAGTAGC	SHANK3 H3A(-273-257)
4071	TCAGCTTGTACCCAAGT	SHANK3 H3A(-270-254)
4072	CTGTCAGCTTGTACCCA	SHANK3 H3A(-267-251)
4073	CGACTGTGAGCTTGTAC	SHANK3 H3A(-264-248)
4074	TCACGACTGTGAGCTTG	SHANK3 H3A(-261-245)
4075	CAGTCACGACTGTGAGC	SHANK3 H3A(-258-242)
4076	AACCAGTCACGACTGTC	SHANK3 H3A(-255-239)
4077	CCAAACCAGTCACGACT	SHANK3 H3A(-252-236)
4078	TAGCCAAACCAGTCACG	SHANK3 H3A(-249-233)
4079	TGATAGCCAAACCAGTC	SHANK3 H3A(-246-230)
4080	CCCTGATAGCCAAACCA	SHANK3 H3A(-243-227)
4081	GCGCCCTGATAGCCAAA	SHANK3 H3A(-240-224)
4082	CTTGCGCCCTGATAGCC	SHANK3 H3A(-237-221)
4083	TTCCTTGCGCCCTGATA	SHANK3 H3A(-234-218)
4084	CCCTTCCTTGCGCCCTG	SHANK3 H3A(-231-215)
4085	AAGCCCTTCCTTGCGCC	SHANK3 H3A(-228-212)
4086	TCAAAGCCCTTCCTTGC	SHANK3 H3A(-225-209)
4087	GGCTCAAAGCCCTTCCT	SHANK3 H3A(-222-206)
4088	CACGGCTCAAAGCCCTT	SHANK3 H3A(-219-203)
4089	ATGCACGGCTCAAAGCC	SHANK3 H3A(-216-200)
4090	CCCATGCACGGCTCAAA	SHANK3 H3A(-213-197)

4091	GGGCCCATGCACGGCTC	SHANK3 H3A(-210-194)
4092	GGTGGGCCCATGCACGG	SHANK3 H3A(-207-191)
4093	TCGGGTGGGCCCATGCA	SHANK3 H3A(-204-188)
4094	CACTCGGGTGGGCCCAT	SHANK3 H3A(-201-185)
4095	TCCCACTCGGGTGGGCC	SHANK3 H3A(-198-182)
4096	AATTCCCACTCGGGTGG	SHANK3 H3A(-195-179)
4097	CCCAATTCCCACTCGGG	SHANK3 H3A(-192-176)
4098	GGCCCCAATTCCCACTC	SHANK3 H3A(-189-173)
4099	CACGGCCCCAATTCCCA	SHANK3 H3A(-186-170)
4100	CACCACGGCCCCAATTC	SHANK3 H3A(-183-167)
4101	TCCCACCACGGCCCCAA	SHANK3 H3A(-180-164)
4102	CACTCCCACCACGGCCC	SHANK3 H3A(-177-161)
4103	CTGCACTCCCACCACGG	SHANK3 H3A(-174-158)
4104	GTCCTGCACTCCCACCA	SHANK3 H3A(-171-155)
4105	ACGGTCCTGCACTCCCA	SHANK3 H3A(-168-152)
4106	ACCACGGTCCTGCACTC	SHANK3 H3A(-165-149)
4107	TCAACCACGGTCCTGCA	SHANK3 H3A(-162-146)
4108	TTGTCAACCACGGTCCT	SHANK3 H3A(-159-143)
4109	CAATTGTCAACCACGGT	SHANK3 H3A(-156-140)
4110	TCACAATTGTCAACCAC	SHANK3 H3A(-153-137)
4111	ACATCACAATTGTCAAC	SHANK3 H3A(-150-134)
4112	CTGACATCACAATTGTC	SHANK3 H3A(-147-131)
4113	CACCTGACATCACAATT	SHANK3 H3A(-144-128)
4114	TGTCACCTGACATCACA	SHANK3 H3A(-141-125)
4115	ACCTGTACCTGACATC	SHANK3 H3A(-138-122)
4116	CTGACCTGTACCTGAC	SHANK3 H3A(-135-119)
4117	AGTCTGACCTGTACCT	SHANK3 H3A(-132-116)
4118	ACCACTGTGACCTGTCA	SHANK3 H3A(-129-113)
4119	CCTACCACTGTGACCTG	SHANK3 H3A(-126-110)
4120	ATCCCTACCACTGTGAC	SHANK3 H3A(-123-107)
4121	CACATCCCTACCACTCT	SHANK3 H3A(-120-104)
4122	CGCCACATCCCTACCAG	SHANK3 H3A(-117-101)
4123	CCCCGCCACATCCCTAC	SHANK3 H3A(-114-98)
4124	AACCCCCGCCACATCCC	SHANK3 H3A(-111-95)
4125	GGCAACCCCCGCCACAT	SHANK3 H3A(-108-92)
4126	TCAGGCAACCCCCGCCA	SHANK3 H3A(-105-89)

4127	CCTTCAGGCAACCCCG	SHANK3 H3A(-102-86)
4128	CCACCTTCAGGCAACCC	SHANK3 H3A(-99-83)
4129	AGGCCACCTTCAGGCAA	SHANK3 H3A(-96-80)
4130	CTCAGGCCACCTTCAGG	SHANK3 H3A(-93-77)
4131	AGCCTCAGGCCACCTTC	SHANK3 H3A(-90-74)
4132	GCAAGCCTCAGGCCACC	SHANK3 H3A(-87-71)
4133	CCGGCAAGCCTCAGGCC	SHANK3 H3A(-84-68)
4134	CCTCCGGCAAGCCTCAG	SHANK3 H3A(-81-65)
4135	CTTCCTCCGGCAAGCCT	SHANK3 H3A(-78-62)
4136	CGCCTTCCTCCGGCAAG	SHANK3 H3A(-75-59)
4137	ACCCGCCTTCCTCCGGC	SHANK3 H3A(-72-56)
4138	ATCACCCGCCTTCCTCC	SHANK3 H3A(-69-53)
4139	AACATCACCCGCCTTC	SHANK3 H3A(-66-50)
4140	CTGAACATCACCCGCCT	SHANK3 H3A(-63-47)
4141	CATCTGAACATCACCCG	SHANK3 H3A(-60-44)
4142	CATCATCTGAACATCAC	SHANK3 H3A(-57-41)
4143	CTCCATCATCTGAACAT	SHANK3 H3A(-54-38)
4144	GGCCTCCATCATCTGAA	SHANK3 H3A(-51-35)
4145	CAAGGCCTCCATCATCT	SHANK3 H3A(-48-32)
4146	CACCAAGGCCTCCATCA	SHANK3 H3A(-45-29)
4147	TGGCACCAAGGCCTCCA	SHANK3 H3A(-42-26)
4148	GCCTGGCACCAAGGCCT	SHANK3 H3A(-39-23)
4149	TCAGCCTGGCACCAAGG	SHANK3 H3A(-36-20)
4150	CAGTCAGCCTGGCACCA	SHANK3 H3A(-33-17)
4151	CGTCAGTCAGCCTGGCA	SHANK3 H3A(-30-14)
4152	GGCCGTCAGTCAGCCTG	SHANK3 H3A(-27-11)
4153	ACCGGCCGTCAGTCAGC	SHANK3 H3A(-24-8)
4154	AACACCGGCCGTCAGTC	SHANK3 H3A(-21-5)
4155	TGGAACACCGGCCGTC	SHANK3 H3A(-18-2)
4156	CTGGAACACCGGCCGTCAGTCAGCC	SHANK3 H3A(-25-1)
4157	CGCCTGGAACACCGGCCGTCAGTCA	SHANK3 H3A(-22+3)
4158	GTTGCGCTGGAACACCGGCCGTCAG	SHANK3 H3A(-19+6)
4159	CAGGTTGCGCTGGAACACCGGCCGT	SHANK3 H3A(-16+9)
4160	CTTCAGGTTGCGCTGGAACACCGGC	SHANK3 H3A(-13+12)
4161	CTTCTTCAGGTTGCGCTGGAACACC	SHANK3 H3A(-10+15)
4162	GAACTTCTTCAGGTTGCGCTGGAAC	SHANK3 H3A(-7+18)

4163	CCTGGAACACCGGCCGT	SHANK3 H3A(-16+1)
4164	TCGCCTGGAACACCGGC	SHANK3 H3A(-13+4)
4165	GGTTCGCCTGGAACACC	SHANK3 H3A(-10+7)
4166	TCAGGTTTCGCCTGGAAC	SHANK3 H3A(-7+10)
4167	TCTTCAGTTTCGCCTGG	SHANK3 H3A(-4+13)
4168	ACTTCTTCAGTTTCGCC	SHANK3 H3A(-1+16)
4169	ATGGAAGACTGGGCAGCTGCACTGG	SHANK3_H3'UTR(+506+531)
4170	GTGGCAGTTGCACTGAGTGGTCGGA	SHANK3_H3'UTR(+533+557)mm1
4171	GTGAGGTGCCGGAGATGGAAGACTG	SHANK3 H3'UTR(+521+545)mm1
4172	GCAGTGAGGGGCCGGAGATGGAAGA	SHANK3_H3'UTR (+524+548)
4173	GCAGTGAGGGTCCGGAGATGGAAGA	SHANK3_H3'UTR (+524+548)mm1
4174	GCAGTGAGGTGCCGTAGATGGAAGA	SHANK3_H3'UTR (+524+548)mm2
4175	TGGAAAAGCCCATAGTTGAGCGCGT	SHANK3 H1A(+239+263)
4176	GTCCAGGCGCAGGCACTTCTGCAGC	SHANK3 H1A(+150+174)
4177	GCTCCTCATCCAGGAACCTTGCC	SHANK3 H1A(+286+307)
4178	CCCATAGTTGAGCGCGTCCTGGAGG	SHANK3 H1A(+231+255)
4179	CCCATAGTTGAGCGCGTCCTTAATG	SHANK3 H1A(+231+255)mm
4180	CTCATCCAGGAACCTGCCTTAG	SHANK3 H1A(+282+303)mm
4181	CTCATCCAGGAACCTGCCGGCG	SHANK3 H1A(+282+303)
4182	CTTTGTGTGAAGCTTTGCAAACCTGC	SHANK3 H2A(+48+72)
4183	ATCATCGATGAGGTTCTGGGCATAA	SHANK3 H2A(+21+45)
4184	GAGCGGAGCCTCCAGTGCGGTGTGT	SHANK3 5'UTR(-2069-2045)
4185	GGCGAGAAGTGGAAGAAAAACA	SHANK3_5'UTR (-858-837)mm
4186	GGGCACGAAGACCAAGGTAGGG	SHANK3_5'UTR (-879-857)
12646	GGCATAAACTCGCCTGT	SHANK3 H2A(+3+19)mm
12647	GGCATAAACTCGCCGAGG	SHANK3 H2A(+3+21)mm
12648	GGCATAAACTCGCCGCTTG	SHANK3 H2A(+3+21)
12649	GGTTCTGGGCATAAACT	SHANK3 H2A(+22+40)
12650	GGTTCTGGGCATAAACTCG	SHANK3 H2A(+20+40)
12651	TTCTGGGCATAAACTCGCC	SHANK3 H2A(+8+26)
12652	GCATAAACTCGCCGCTTGT	SHANK3 H2A(+12+32)
12653	GCATAAACTCGCCGAAT	SHANK3 H2A(+14+32)mm
12654	GCATAAACTCGCCGCTGAT	SHANK3 H2A(+12+32)mm
12655	AGCGGAAGTACCCTGT	SHANK3_H22P(+1720+1736)
12656	GAAGCGGAAGTACCCTGT	SHANK3_H22P(+1718+1736)
12657	AGCTGAAGTACTCTGT	SHANK3_H22P(+1720+1736)mm
12658	GAAGCTGAAGTACTCTGT	SHANK3_H22P(+1718+1736)mm

12659	AGGGCACTAAGCAATGTA	SHANK3_H22A(+746+763)
12660	TCCTGACTGTGCGCTGGG	SHANK3_H22A(+783+800)
12661	GGAGGTGAAGCGGAACCTGACCTGT	SHANK3_H3'UTR(+1712+1736)
12662	TGAAGCGGAACCTGACCTGTAAAGT	SHANK3_H3'UTR(+1707+1731)
12663	CCTGTAAAGTAAAAACCAAATTG	SHANK3_H3'UTR(+1692+1716)
12664	CTTGATCGAACTGCTCAGATAAA	SHANK3 H2A(-13+12)
12665	AAACTCGCCGCTTGATCGAACTG	SHANK3 H2A(-3+22)
12666	TTCTGGGCATAAACTCGCCGCTGTT	SHANK3 H2A(+8+32)mm
12667	ATCATCGATGAGGTTCTGGGCACGA	SHANK3 H2A(+21+45)mm
12668	CTTTGCAAACCTGCTTATCATCGATG	SHANK3 H2A(+36+60)
12669	CGTGATCCTTTACCTTTGTGTGAAG	SHANK3 H2D(+12-13)
12670	GCCACCTCCTCGTGATCCTTTACCT	SHANK3 H2D(+2-23)mm
12671	CAGGAGCCACCTCCTCGTGATCCTT	SHANK3 H2D(-4-28)mm
12688	GGAGGTGAAGCTGAACTGACTCTGT	SHANK3_H3'UTR(+1712+1736)m
12689	GTGTCAGGCAAAGCCAAGGCTCTGG	SHANK3 H17D(-22-46)mm
12690	AAGCCAAGGCCCTGTGGACACAGGC	SHANK3 H17D(-12-36)mm
12691	AAGGCCCTGTGGACACAGGCAGATG	SHANK3 H17D(-7-31)mm
12692	GGGTCAGGCAAAGCCAAGGCCCTGG	SHANK3 H17D(-22-46)
12693	AGGCAAAGCCAAGGCCCTGTGGACA	SHANK3 H17D(-17-41)mm

**Table 5: Exemplary PMO and MOE Oligonucleotide Sequences Targeting
SHANK3 mRNA 5' UTR or 3' UTR or SHANK3 5' PNCR**

SEQ ID NO	ASO Sequence	ASO Name	PMO/MOE
293	TTGTATCGAACTCCAG	SHANK3 H1:2 5UTR(+355+371)	MOE27
299	TGGGCATAAACTCGCCG	SHANK3 H2 5UTR(+373+389)	MOE33
301	AGGTTCTGGGCATAAAC	SHANK3 H2 5UTR(+379+395)	MOE35
302	ATGAGGTTCTGGGCATA	SHANK3 H2 5UTR(+382+398)	MOE36
304	TCATCGATGAGGTTCTG	SHANK3 H2 5UTR(+388+404)	MOE38
305	TTATCATCGATGAGGTT	SHANK3 H2 5UTR(+391+407)	MOE39
306	TGCTTATCATCGATGAG	SHANK3 H2 5UTR(+394+410)	MOE40
307	AACTGCTTATCATCGAT	SHANK3 H2 5UTR(+397+413)	MOE41
308	GCAAAGCTTATCATC	SHANK3 H2 5UTR(+400+416)	MOE42
309	TTTGCAAAGCTTATC	SHANK3 H2 5UTR(+403+419)	MOE43
311	TGAAGCTTTGCAAAGCTG	SHANK3 H2 5UTR(+409+425)	MOE45
313	TTTGTGTGAAGCTTTGC	SHANK3 H2 5UTR(+415+431)	MOE47
315	TTCGCCTTTGTGTGAAG	SHANK3 H2:3 5UTR(+421+437)	MOE49
318	TTCTTCAGGTTTCGCCTT	SHANK3 H2:3 5UTR(+430+446)	MOE52
606	CGATGAGGTTCTGGGCATAAACTCG	SHANK3 H2 5UTR(+376+400)	PMO33
797	GGCCGGAGATGGAAGAC	SHANK3 H22 3UTR(+1115+1131)	MOE60
1193	GCGGAAGTACCCTGTA	SHANK3 H22 3UTR(+2303+2319)	MOE55
1195	GGTGAAGCGGAAGTAC	SHANK3 H22 3UTR(+2309+2325)	MOE57
1847	CGGAAGTACCCTGTAAAGTTAAAA	SHANK3 H22 3UTR(+2294+2318)	PMO40
1934	CTGACCCTGTAAAGTTAAACCCA	SHANK3_H3'UTR(+1697+1721)	PMO6
1935	GGCATAAACTCGCCGCTTGTACTGA	SHANK3 H2A(+3+27)	PMO34
1936	GGCATAAACTCGCCGCTTGTATCGA	SHANK3 H2A(+3+27)mm	PMO35
1937	CTCCCCGTGATCCTTTACCTTTGTG	SHANK3 H2D(+7-18)	PMO37
2858	TTCTGGGCATAAACTCGCCGCTTGT	SHANK3 H2A(+8+32)	PMO65
2874	TCCTTTACCTTTGTGTGAAGCTTTG	SHANK3 H2D(+17-8)	PMO70
3510	GGCATAAACTCGCCGCT	SHANK3 H2A(+3+19)	MOE5
12644	GCACAGCAAGGAGGCTCCATCTCAG	SHANK3 H20A(-27-3)	PMO17
12666	TTCTGGGCATAAACTCGCCGCTGTT	SHANK3 H2A(+8+32)mm	PMO66
12669	CGTGATCCTTTACCTTTGTGTGAAG	SHANK3 H2D(+12-13)	PMO71
12671	CAGGAGCCACCTCCTCGTGATCCTT	SHANK3 H2D(-4-28)mm	PMO73
12688	GGAGGTGAAGCTGAAGTACTCTGT	SHANK3_H3'UTR(+1712+1736)m	PMO43
12690	AAGCCAAGGCCCTGTGGACACAGGC	SHANK3 H17D(-12-36)mm	PMO53

5

SEQ ID NO:12694

CPP Amino Acid Sequence (Artificial/Synthetic)
RRSRTARAGRPRGRNSSRPSAPR

The sequence listing for this application is provided in five separate accompanying .xml format files, the entire contents of each of which are incorporated herein by reference. The sequence listing .xml file names, (WIPO Sequence program auto-generated) sequence numbering ranges, corresponding Applicant-assigned SEQ ID NO ranges of each of these, and the first sequence in each file is summarised in Table 6 below.

Table 6: Sequence listing file (auto-generated) numbering ranges and corresponding SEQ ID NOs			
File Name (.xml file)	Auto-generated sequence numbering range in corresponding file	Corresponding SEQ ID NO range	First Sequence in file
536829PCT 1 of 5	1-12694	1-12694	SEQ ID NO:1 (auto-numbered as Seq. 1) CACCACTCAGGCCAGGCCAG . . . (first 20 bases only; sequence continues)
536829PCT 2 of 5	1-7307	12695-20001	SEQ ID NO:12695 (auto-numbered as Seq. 1) CAGGGCGGCGGGGCTCA
536829PCT 3 of 5	1-8000	20002-28001	SEQ ID NO:20002 (auto-numbered as Seq. 1) CAGTTTTGTTAATAAGA
536829PCT 4 of 5	1-8000	28002-36001	SEQ ID NO:28002 (auto-numbered as Seq. 1) CGTGAGTCACGCACACACCAGGCTT
536829PCT 5 of 5	1-3536	36002-39537	SEQ ID NO:36002 (auto-numbered as Seq. 1) AGAAGTCTGTTGTCAGTTGGACCAC

If any discrepancies are identified between (i) the accompanying sequence listing files sequences, the numbering corresponding to the SEQ ID NOs, or the corresponding headings/names provided in the accompanying sequence listing files; and (ii) the sequences and SEQ ID NOs disclosed in the present specification and Appendix therein, the sequences and SEQ ID NOs (and SEQ ID NO ranges) provided in the present specification and Appendix are to be accepted as correct.

CLAIMS:

1. An antisense oligonucleotide that binds within a targeted portion of the:
 - (i) 5' untranslated region (UTR) of a *SHANK3* mRNA;
 - (ii) 5'-proximal non-coding region (PNCr) of a *SHANK3* pre-mRNA; or
 - (iii) 3' UTR of a *SHANK3* mRNA;whereby binding of the antisense oligonucleotide within the targeted portion in a mammalian cell results in an increased level of SHANK3 protein in the mammalian cell.
2. A vector for expression, in a mammalian neuron, of an antisense RNA (AR) that binds within a targeted portion of the:
 - (i) 5' untranslated region (UTR) of a *SHANK3* mRNA;
 - (ii) 5'-proximal non-coding region (PNCr) of a *SHANK3* pre-mRNA; or
 - (iii) 3' UTR of a *SHANK3* mRNA;whereby binding of the AR within the targeted portion in a mammalian cell results in an increased level of SHANK3 protein in the mammalian cell.
3. The vector according to claim 2, wherein the mammalian cell is a neuron.
4. The vector according to claim 3, wherein the vector comprises a neuron-selective promoter for driving expression of the antisense RNA in the mammalian neuron.
5. The vector according to claim 4, wherein the neuron-selective promoter is selective for expression in a neuron type selected from the list consisting of: cortical glutamatergic neurons, cortical GABAergic neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons.
6. The vector according to any one of claims 2 to 5, wherein the vector comprises an inducible promoter.

7. The vector according to any one of claims 2 to 6, wherein the vector is a viral vector.
8. The vector according to any one of claim 7, wherein the viral vector is a recombinant virus selected from the group consisting of: adeno-associated virus (AAV), adenovirus, lentivirus, and anellovirus.
9. The vector according to any one of claims 2 to 8, wherein the vector is a non-viral vector.
10. A composition comprising the non-viral vector according to claim 9, wherein the composition further comprises a transfection agent.
11. The antisense oligonucleotide according to claim 1, wherein the antisense oligonucleotide comprises a backbone modification.
12. The method or antisense oligonucleotide according to claim 11 wherein the antisense oligonucleotide comprises a backbone modification comprising a phosphorothioate linkage or a phosphorodiamidate linkage.
13. The antisense oligonucleotide according to claim 11 or claim 12, wherein the antisense oligonucleotide comprises a phosphorodiamidate morpholino, a locked nucleic acid, a peptide nucleic acid, a 2'-*O*-methyl, a 2'-fluoro, or a 2'-*O*-methoxyethyl moiety.
14. The antisense oligonucleotide according to any one of claims 11 to 13, wherein the antisense oligonucleotide comprises at least one modified sugar moiety.
15. The antisense oligonucleotide according to claim 14, wherein each sugar moiety in the antisense oligonucleotide is a modified sugar moiety.

16. The antisense oligonucleotide according to any one of claims 11 to 15, wherein the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.

17. The antisense oligonucleotide according to claim 16, wherein each nucleotide of the antisense oligonucleotide comprises a 2'-*O*-methoxyethyl moiety.

18. The antisense oligonucleotide according to any one of claims 1 or 11 to 17, or the vector according to any one of claims 2 to 9, or the composition according to claim 10, wherein the nucleotide sequence of the antisense oligonucleotide or the AR consists of 10 to 50 nucleotides, 15 to 40 nucleotides, 18 to 40 nucleotides, 17 to 25 nucleotides, 20 to 35 nucleotides, 20 to 30 nucleotides, 22 to 30 nucleotides, 24 to 30 nucleotides, 25 to 30 nucleotides, or 26 to 30 nucleotides.

19. The antisense oligonucleotide according to claim 18, wherein the nucleotide sequence of the antisense oligonucleotide or the AR consists of 17 to 30 nucleotides.

20. The antisense oligonucleotide according to claim 19, wherein the antisense oligonucleotide comprises one or more phosphorodiamidate morpholino moieties.

21. The antisense oligonucleotide according to any one of claims 1 or 11 to 20, wherein the antisense oligonucleotide is linked to a functional moiety.

22. The antisense oligonucleotide according to claim 21, wherein the functional moiety comprises a delivery moiety.

23. The antisense oligonucleotide according to claim 22, wherein the delivery moiety is selected from the group consisting of lipids, polyethers, peptides, carbohydrates, receptor binding domains (RBDs), and antibodies.

24. The antisense oligonucleotide according to claim 22 or claim 23, wherein the delivery moiety comprises a cell-penetrating peptide (CPP).

25. The antisense oligonucleotide according to claim 22 or claim 23, wherein the delivery moiety comprises a *N*-acetylgalactosamine (GalNAc) moiety or a glycan moiety.
26. The antisense oligonucleotide according to claim 22 or claim 23, wherein the delivery moiety comprises a fatty acid or lipid moiety.
27. The antisense oligonucleotide according to claim 26, wherein the fatty acid chain length is about C8 to C20.
28. The antisense oligonucleotide according to claim 21, wherein the functional moiety comprises a stabilising moiety.
29. The antisense oligonucleotide according to any one of claims 21 to 28, wherein the functional moiety is covalently linked to the antisense oligonucleotide.
30. The antisense oligonucleotide according to any one of claims 21 to 28, wherein the functional moiety is non-covalently linked to the antisense oligonucleotide.
31. The antisense oligonucleotide according to any one of claims 21 to 30, wherein the functional moiety is linked to the 5' end of the antisense oligonucleotide.
32. The antisense oligonucleotide according to any one of claims 21 to 30, wherein the functional moiety is linked to the 3' end of the antisense oligonucleotide.
33. The antisense oligonucleotide, vector, or composition according to any one of claims 1 to 32, wherein the nucleotide sequence of the antisense oligonucleotide or the AR is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to the nucleotide sequence of the targeted portion over the length of the antisense oligonucleotide or the AR.

34. The antisense oligonucleotide according to any one of claims 1 or 11 to 33, the vector according to any one of claims 2 to 9, or the composition according to claim 10, wherein the nucleotide sequence of the ASO or AR corresponds to any one of **SEQ ID NOs:293, 299, 301, 302, 304-309, 311, 313, 315, 318, 606, 797, 1193, 1195, 1847, 1934-1937, 2858, 2874, 3510, 12644, 12666, 12669, 12671, 12688, or 12690.**

35. The antisense oligonucleotide according to any one of claims 1 or 11 to 33, the vector according to any one of claims 2 to 9, or the composition according to claim 10, wherein the binding is within a targeted portion of the 5' UTR corresponding to **SEQ ID NO:1.**

36. The antisense oligonucleotide according to any one of claims 1 or 11 to 33, the vector according to any one of claims 2 to 9, or the composition according to claim 10, wherein the binding is within a targeted portion of the 5' PNCr corresponding to **SEQ ID NO:3.**

37. The antisense oligonucleotide according to any one of claims 1 or 11 to 33, the vector according to any one of claims 2 to 9, or the composition according to claim 10, wherein the binding is within a targeted portion of the 3' UTR corresponding to **SEQ ID NO:2.**

38. The antisense oligonucleotide, vector, or composition according to claim 35, wherein the nucleotide sequence of the antisense oligonucleotide or the antisense RNA corresponds to any one of **SEQ ID NOs:5-622, 4175-4181, or 4184-4186.**

39. The antisense oligonucleotide, vector, or composition according to claim 35, wherein the nucleotide sequence of the antisense oligonucleotide or the AR corresponds to any one of **SEQ ID NOs:559, 606, or 4178-4181.**

40. The antisense oligonucleotide, vector, or composition according to claim 36, wherein the nucleotide sequence of the antisense oligonucleotide or the antisense RNA

corresponds to any one of **SEQ ID NOs:1935-4168, 4182, 4183, 12646-12654, or 12664-12671**.

41. The antisense oligonucleotide, vector, or composition according to claim 36, wherein the nucleotide sequence of the antisense oligonucleotide or the AR corresponds to any one of **SEQ ID NOs:1935-1937, 2849, 2858, 2864, 2874, 3510, 12647, 12648, or 12664-12671**.

42. The antisense oligonucleotide, vector, or composition according to claim 37, wherein the nucleotide sequence of the antisense oligonucleotide or the antisense RNA corresponds to any one of **SEQ ID NOs:623-1934, 4169-4174, 12645, 12655-12663, or 12688**.

43. The antisense oligonucleotide, vector, or composition according to claim 37, wherein the nucleotide sequence of the antisense oligonucleotide or the antisense RNA corresponds to any one of **SEQ ID NOs:1847, 1852, 1934, 12661-12663, or 12688**.

44. The antisense oligonucleotide according to any one of claims 1 or 11 to 43, further comprising a delivery nanocarrier, wherein the nanocarrier is complexed with the antisense oligonucleotide.

45. The antisense oligonucleotide according to claim 44, wherein the delivery nanocarrier is selected from the group consisting of: lipoplexes, liposomes, exosomes, inorganic nanoparticles, and DNA nanostructures.

46. The antisense oligonucleotide according to claim 44, wherein the delivery nanocarrier comprises a lipid nanoparticle (LNP) encapsulating the antisense oligonucleotide.

47. A pharmaceutical composition comprising the antisense oligonucleotide, vector, or composition according to any one of claims 1 to 46, and a pharmaceutically acceptable excipient.

48. A method for preventing or treating a condition associated with SHANK3 haploinsufficiency, the method comprising administering to a subject in need thereof a therapeutically effective amount of the pharmaceutical composition according to claim 47.

49. The method according to claim 48, wherein the condition is Phelan-McDermid syndrome, an autism spectrum disorder, schizophrenia, or an intellectual disability.

50. The method according to claim 48 or claim 49, wherein the condition is Phelan-McDermid syndrome.

51. The method according to claim 48 or claim 50, wherein the subject is a human subject.

52. Use of the antisense oligonucleotide, vector, or composition according to any one of claims 1 to 46 in the manufacture of a medicament for prevention or treatment of a condition associated with SHANK3 haploinsufficiency.

53. The method according to any one of claims 48 to 51, or the use according to claim 52, wherein the level of SHANK3 protein in at least a plurality of cells in the subject is increased about 1.1 to about 5 fold in cells, *e.g.*, 1.2 fold, 1.3 fold, 1.5 fold, 1.7 fold, 2 fold, 2.2 fold, 2.5 fold, 2.7 fold, 3 fold, 3.3 fold, 3.5 fold, 4 fold, 4.3 fold, 4.5 fold, 4.7 fold, or another increase in SHANK3 protein levels from about 1.1 fold to about 5 fold compared to the level in the absence of the pharmaceutical composition.

54. A genetically modified cell comprising the antisense oligonucleotide or vector according to any one of claims 1 to 46.

55. The genetically modified cell according to claim 54, wherein the genetically modified cell is a mammalian cell.

56. The genetically modified mammalian cell according to claim 55, wherein the genetically modified mammalian cell is a human cell.

57. The genetically modified mammalian cell according to claim 55 or claim 56, wherein the genetically modified mammalian cell is a neuron or neural progenitor.

58. The genetically modified mammalian neuron according to claim 57, wherein the genetically modified mammalian cell is a neuron selected from the group consisting of: cortical glutamatergic neurons, cortical GABAergic neurons, hippocampal glutamatergic neurons, and striatal inhibitory neurons.

59. The genetically modified mammalian cell according to claim 55 or claim 56, wherein the genetically modified mammalian cell is from a cell line.

60. The genetically modified mammalian cell according to claim 59, wherein the cell line is a hiPSC cell line or a cell line derived from neurons.