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(54) Titre : COMPOSITIONS, REACTIFS, ET KITS ET PROCEDE DE DIAGNOSTIC, DE CONTROLE ET DE
TRAITEMENT DE L'OBESITE ET/OU DU DIABETE
(54) Title: COMPOSITIONS, REAGENTS AND KITS FOR AND METHODS OF DIAGNOSING, MONITORING AND
TREATING OBESITY AND/OR DIABETES

(57) **Abrégé/Abstract:**

The present invention concerns thirteen novel variants of alternative splicing of the obesity and/or diabetes related genes.



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DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
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CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

TITLE

COMPOSITIONS, REAGENTS AND KITS FOR AND METHODS OF
DIAGNOSING, MONITORING AND TREATING
OBESITY AND/OR DIABETES

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FIELD OF THE INVENTION

The present invention relates to obesity and diabetes markers, to reagents which can detect, obesity and diabetes marker transcripts and translation products, to kits and methods for detecting obesity and diabetes marker transcripts and translation products, to methods and kits for screening and diagnosing obesity and diabetes in individuals and monitoring response to treatment, disease progression and disease recurrence in patients diagnosed with obesity and diabetes, to compounds which specifically bind to translation products of obesity and/or diabetes marker transcripts, to treating obesity and/or diabetes using one or a composition of several of the obesity and diabetes markers or their translation products as therapeutic agents, to compositions for and methods of treating obesity and/or diabetes.

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BACKGROUND OF THE INVENTION

Obesity is the second most important cause of preventable death in the United States, exceeded only by cigarette smoking. Obesity is estimated to afflict 58,000,000 people and contribute to 300,000 deaths annually in the United States and its prevalence is increasing. Individuals suffering from the disease are at increased risk of illness from hypertension, lipid disorders, coronary heart disease, type II diabetes,

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stroke, gall bladder disease, osteoarthritis, sleep apnea, respiratory problems and certain cancers.

Obesity develops when there is an excess of energy intake over energy usage. The causes of this excess may vary from patient to patient
5 and are believed to stem from various genetic, social and environmental factors. Current research supports the view that under identical environmental conditions, different people gain weight at different rates and the amount they gain seems to be genetically determined. It has been proposed that natural selection caused our distant ancestors to acquire
10 'thrifty genes' which boosted the ability to store fat from each feast in order to sustain the body through the next famine. In today's environment of a surfeit of high fat, high calorie 'western style' food, 'thrifty genes' have become a liability.

More and more scientists and physicians are coming to reject the
15 traditional belief that poor diet and lack of exercise are solely to blame for obesity and are increasingly tending to view it as a medical condition. Health economists, using prospective studies and national health statistics, have calculated the costs of obesity in the US in 1995 at \$99.2 billion. By 2005 it is estimated that more than 120 million people in the world will be obese.
20 The economic impact of obesity in the US is now comparable to that of diabetes and ranks alongside expenditure on heart disease and hypertension. Medical researchers calculate that at least 88% of all cases of type II diabetes, 57% of coronary heart disease cases, 11% of breast cancers, and 10% of colon cancers diagnosed in overweight Americans are
25 attributable to obesity.

The World Health Organization has classified the obesity condition as an epidemic and has set up a special task force to tackle one of the greatest risks to human health and well-being.

There remains a need for obesity and/or diabetes specific markers.
30 There remains a need for reagents and kits which can be used to detect the presence of obesity and/or diabetes markers in samples from patients. There remains a need for reagents and kits which can be used to detect the future

propensity of developing obesity and/or diabetes in samples from patients. There remains a need for methods of screening and diagnosing individuals who have obesity and/or diabetes and methods of monitoring response to treatment, disease progression and disease recurrence in patients
5 diagnosed with obesity and/or diabetes.

There remains a need for reagents, kits and methods for determining the type of obesity and/or diabetes that an individual who is obese has. There remains a need for compositions which can specifically target obesity and/or diabetes related cells. There remains a need for improved methods of
10 treating individuals who are suspected of suffering from obesity and/or diabetes.

GLOSSARY

In the following description and claims use will be made, at times, with
15 a variety of terms, and the meaning of such terms as they should be construed in accordance with the invention is as follows:

“Obesity and/or diabetes nucleic acid sequences” – the sequence shown in any one of SEQ ID NO:1 to SEQ ID NO:4 and of SEQ ID NO:22 to
20 SEQ ID NO:25 sequences having at least *90% identity* (see below, Table 2) to said sequences and *fragments* (see below, Table 2) of the above sequences of least 15 b.p. long. These sequences are sequences coding for naturally occurring, alternative splice variants of the native and known Adiponectin, depicted in Locus Link as locus Hs. 9370 under Accession
25 Number NM_004797 which is the sequence coding for the human 30kDa glycoprotein of 244 amino acids. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of Adiponectin and not merely truncated, mutated or fragmented forms of the gene.

30 – the sequence shown in any one of SEQ ID NO:5 to SEQ ID NO:9 and of SEQ ID NO:26 to SEQ ID NO:30 sequences having at least *90% identity* (see below) to said sequences and *fragments* (see below, Table 2)

of the above sequences of least 15 b.p. long. These sequences are sequences coding for naturally occurring, alternative splice variants of the native and known Adiponectin, depicted in Locus Link as locus Mm. 11450 under Accession Number NM_009605 which is the sequence coding for the mouse 30kDa glycoprotein of 247 amino acids. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of Adiponectin and not merely truncated, mutated or fragmented forms of the gene.

– the sequence shown in any one of SEQ ID NO:10 to SEQ ID NO:11 and of SEQ ID NO:31 to SEQ ID NO:32 sequences having at least 90% *identity* (see below, Table 2) to said sequences and *fragments* (see below, Table 2) of the above sequences of least 15 b.p. long. These sequences are sequences coding for naturally occurring, alternative splice variants of the native and known Ghrelin, depicted in Locus Link as locus Hs. 51738 under Accession Number NM_016362 which is the sequence coding for the human 13kDa glycoprotein of 117 amino acids. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of Ghrelin and not merely truncated, mutated or fragmented forms of the gene.

– the sequence shown in any one of SEQ ID NO:12 to SEQ ID NO:18 and of SEQ ID NO:33 to SEQ ID NO:39 sequences having at least 90% *identity* (see below, Table 2) to said sequences and *fragments* (see below, Table 2) of the above sequences of least 15 b.p. long. These sequences are sequences coding for naturally occurring, alternative splice variants of the native and known 11-beta-HSD, depicted in Locus Link as locus Hs. 3290 under Accession Number NM_005525 which is the sequence coding for the human 32kDa glycoprotein of 292 amino acids. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of 11-beta-HSD and not merely truncated, mutated or fragmented forms of the gene.

– the sequence shown in any one of SEQ ID NO:19 to SEQ ID NO:21 and of SEQ ID NO:40 to SEQ ID NO:42 sequences having at least 90%

identity (see below, Table 2) to said sequences and *fragments* (see below, Table 2) of the above sequences of least 15 b.p. long. These sequences are sequences coding for naturally occurring, alternative splice variants of the native and known 11-beta-HSD, depicted in Locus Link as locus Mm. 15483 under Accession Number NM_008288 which is the sequence coding for the mouse 32kDa glycoprotein of 292 amino acids. It should be emphasized that the novel variants of the present invention are naturally occurring sequences resulting from alternative splicing of 11-beta-HSD and not merely truncated, mutated or fragmented forms of the gene.

The description of the obesity and/or diabetes related gene variants and their difference from the original sequence are summarized in Table 1 as follows:

Table 1

SEQ ID NO:	Obesity and Diabetes related genes	GenBank Human Locus ID	GenBank Mouse Locus ID	Gene Symbol	Variation description
1	Adiponectin -WT (Variant 1)	9370	(11450)	APM	Nucleotide sequence of the human wild type protein (human)
2	Adiponectin Variant 2				Nucleotide sequence of variant 2 (human)
3	Adiponectin Variant 3				Nucleotide sequence of variant 3 (human)
4	Adiponectin Variant 4				Nucleotide sequence of variant 4 (human)
5	Adiponectin -WT (Variant 1)	(9370)	11450	APM	Nucleotide sequence of the mouse wild type protein (mouse)
6	Adiponectin Variant 2				Nucleotide sequence of variant 2 (mouse)
7	Adiponectin Variant 3				Nucleotide sequence of variant 3 (mouse)
8	Adiponectin				Nucleotide

	Variant 4				sequence of variant 4 (mouse)
9	Adiponectin Variant 5				Nucleotide sequence of variant 5 (mouse)
10	Ghrelin- WT (variant 1)	51738	(58991)	GHRL	Nucleotide sequence of the human wild type protein
11	Ghrelin Variant 2				Nucleotide sequence of variant 2 (human)
12	11-beta- HSD – WT (Variant 1)	3290	(15483)	HSD11 B1	Nucleotide sequence of the wild type human protein
13	11-beta- HSD Variant 2				Nucleotide sequence of variant 2 (human)
14	11-beta- HSD Variant 3				Nucleotide sequence of variant 3 (human)
15	11-beta- HSD Variant 4				Nucleotide sequence of variant 4 (human)
16	11-beta- HSD Variant 5				Nucleotide sequence of variant 5 (human)
17	11-beta- HSD Variant 6				Nucleotide sequence of variant 6 (human)
18	11-beta- HSD Variant 7				Nucleotide sequence of variant 7 (human)
19	11-beta- HSD– WT (Variant 1)				Nucleotide sequence of the mouse wild type protein
20	11-beta- HSD Variant 8				Nucleotide sequence of variant 8 (mouse)
21	11-beta- HSD Variant 9				Nucleotide sequence of variant 9 (mouse)
22	Adiponectin- WT (Variant 1)	9370	(11450)	APM	Wild type human protein sequence

23	Adiponectin Variant 2				Alternative initiation (human)
24	Adiponectin Variant 3				
25	Adiponectin Variant 4				
26	Adiponectin-WT (Variant 1)	(9370)	11450	APM	Wild type mouse protein sequence
27	Adiponectin Variant 2				Alternative initiation (mouse)
28	Adiponectin Variant 3				Alternative 45 amino acids from position 111 in the wild type protein creating a variant with 156 amino acids (mouse)
29	Adiponectin Variant 4				Alternative 58 amino acids from position 111 in the wild type protein creating a variant with 169 amino acids (mouse)
30	Adiponectin Variant 5				Short variant 76 amino acids long (mouse)
31	Ghrelin- WT (variant 1)	51738	(58991)	GHRL	Wild type human protein sequence
32	Ghrelin Variant 2				Alternative 70 amino acids from position 35 in the wild type protein creating a variant with 117 amino acids (human)
33	11-beta-HSD – WT (Variant 1)	3290	(15483)	HSD11 B1	Wild type human protein sequence
34	11-beta-HSD Variant 2				Deletion of 18 amino acids from amino acid 64 in the wild type protein and an alternative exon of 16 amino acids replacing the rest

					of the amino acids from amino acid 165 in the wild type protein (human)
35	11-beta-HSD Variant 3				Alternative 9 amino acids from amino acid 286 creating a variant with 295 amino acids (human)
36	11-beta-HSD Variant 4				Deletion of 18 amino acids from amino acid 137 till amino acid 155 in the wild type protein (human)
37	11-beta-HSD Variant 5				Deletion of 20 amino acids from amino acid 64 till amino acid 84 in the wild type protein (human)
38	11-beta-HSD Variant 6				Alternative initiation at amino acid no. 31 in the wild type protein (human)
39	11-beta-HSD Variant 7				Deletion of 48 amino acids from amino acid 173 till amino acid 221 in the wild type protein (human)
40	11-beta-HSD – WT (Variant 1)				Wild type mouse protein sequence
41	11-beta-HSD Variant 8				Deletion of 32 amino acids from amino acid 29 till amino acid 71 in the wild type protein
42	11-beta-HSD Variant 9				Alternative 19 amino acids from amino acid 173 creating a variant with 192 amino

					acids (mouse)
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SEQ ID NOS: 1-21 are nucleotide sequences.

SEQ ID NOS: 22-42 are protein sequences encoded by SEQ ID NOS 1-21.

5

Table 2

SEQ ID NO:1-9 Adiponectin variants:

SEQ ID NO:1: NM_004797_T1 | Length 4517

CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTC
10 TACTGCTATTAGCTCTGCCCCGGGCATGACCAGGAAACCACGACTCAAG
GGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTG
GATGGCGGGCATCCCAGGGCATCCGGGGCCATAATGGGGCCCCCAGGC
CGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGA
TCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACC
15 CGGGGCTGAAGGTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAG
GAGAACCTGGAGAAGGTGCCTATGTATACCGCTCAGCATTCAAGTGTGG
GATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAA
GATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTC
CACTGCAACATTCTGGGGCTGTACTACTTTGCCTACCACATCACAGTCT
20 ATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC
TCTTCACCTATGATCAGTACCAGGAAAATAATGTGGACCAGGCCTCCG
GCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG
GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAATGACAAT
GACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTGATCAC
25 CACTAACTCAGAGCCTCCTCCAGGCCAAACAGCCCCAAAGTCAATTAA
AGGCTTTCAGTACGGTTAGGAAGTTGATTATTATTTAGTTGGAGGCCTT
TAGATATTATTCATTCATTTACTCATTCAATTTATTCATTCATTCATCAAGT
AACTTTAAAAAAATCATATGCTATGTTCCCAGTCCTGGGGAGCTTCACA
AACATGACCAGATAACTGACTAGAAAGAAGTAGTTGACAGTGCTATTTT
30 GTGCCCACTGTCTCTCCTGATGCTCATATCAATCCTATAAGGCACAGG
GAACAAGCATTCTCCTGTTTTTACAGATTGTATCCTGAGGCTGAGAGAG

TTAAGTGAATGTCTAAGGTCACACAGTATTAAGTGACAGTGCTAGAAAT
CAAACCCAGAGCTGTGGACTTTGTTCACTAGACTGTGCCCTTTTATAGA
GGTACATGTTCTCTTTGGAGTGTTGGTAGGTGTCTGTTTCCCACCTCAC
CTGAGAGCCATTGAATTTGCCTTCCTCATGAATTAACCTCCCCCAAG
5 CAGAGCTTCCTCAGAGAAAGTGGTTCTATGATGAAGTCCTGTCTTGGA
AGGACTACTACTCAATGGCCCCTGCACTACTCTACTTCCTCTTACCTAT
GTCCCTTCTCATGCCTTTCCCTCCAACGGGGAAAGCCAACCTCCATCTC
TAAGTGCTGAACTCATCCCTGTTCTCAAGGCCACCTGGCCAGGAGCT
TCTCTGATGTGATATCCACTTTTTTTTTTTTTTTGAGATGGAGTCTCACTC
10 TGTCACCCAGGCTGGAGTACAGTGACACGACCTCGGCTCACTGCAGC
CTCCTTCTCCTGGGTCCAAGCAATTATTGTGCCTCAGCCTCCCGAGTA
GCTGAGACTTCAGGTGCATTCCACCACACATGGCTAATTTTTGTATTTT
TAGTAGAAATGGGGTTTCGTCATGTTGGCCAGGCTGGTCTCGAACTCC
TGGCCTAGGTGATCCACCCGCCTCGACCTCCCAAAGTGCTGGGATTA
15 CAGGCATGAGCCACCATGCCCAGTCGATATCTCACTTTTTATTTTGCCA
TGGATGAGAGTCCTGGGTGTGAGGAACACCTCCCACCAGGCTAGAGG
CAACTGCCCAGGAAGGACTGTGCTTCCGTCACCTCTAAATCCCTTGCA
GATCCTTGATAAATGCCTCATGAAGACCAATCTCTTGAATCCCATATCT
ACCCAGAATTAACCTCCATTCCAGTCTCTGCATGTAATCAGTTTTATCCA
20 CAGAAACATTTTCATTTTAGGAAATCCCTGGTTTAAGTATCAATCCTTGT
TCAGCTGGACAATATGAATCTTTTCCACTGAAGTTAGGGATGACTGTGA
TTTTCAGAACACGTCCAGAATTTTTCATCAAGAAGGTAGCTTGAGCCTG
AAATGCAAAACCCATGGAGGAATTCTGAAGCCATTGTCTCCTTGAGTA
CCAACAGGGTCAGGGAAGACTGGGCCTCCTGAATTTATTATTGTTCTTT
25 AAGAATTACAGGTTGAGGTAGTTGATGGTGGTAAACATTCTCTCAGGA
GACAATAACTCCAGTGATGTTTTTCAAAGATTTTAGCAAAAACAGAGTA
AATAGCATTCTCTATCAATATATAAATTTAAAAAACTATCTTTTTGCTTAC
AGTTTTAAATTCTGAACAATTTCTCTTATATGTGTATTGCTAATCATTAAG
GTATTATTTTTTCCACATATAAAGCTTTGTCTTTTTGTTGTTGTTGTT
30 TTTAAGATGGAGTTTCCCTCTGTTGCCAGGCTAGAGTGCAGTGGCATG
ATCTCGGCTTACTGCAACCTTTGCCTCCCAGGTTTAAGCGATTCTTCTG
CCTCAGCCTCCCGAGTAGCTGGGACCACAGGTGCCTACCACCATGCC

AGGCTAATTTTTGTATTTTGTAGTAAAGACAGGGTTTCACCATATTGGCC
AGGCTGGTCTCGAACTCCTGACCTTGTGATCTGCCCCGCCTCCATTGTG
TTGTTATTTGTGAGAAAGATAGATATGAGGTTTAGAGAGGGATGAAGA
GGTGAGAGTAAGCCTTGTGTTAGTCAGAACTCTGTGTTGTGAATGTCA
5 TTCACAACAGAAAACCCAAAATATTATGCAAACACTACTGTAAGCAAGAAA
AATAAAGGAAAAATGGAAACATTTATTCCTTTGCATAATAGAAATTACCA
GAGTTGTTCTGTCTTTAGATAAGGTTTGAACCAAAGCTCAAAACAATCA
AGACCCTTTTCTGTATGTCCTTCTGTTCTGCCTTCCGCAGTGTAGGCTT
TACCCTCAGGTGCTACACAGTATAGTTCTAGGGTTTCCCTCCCGATATC
10 AAAAAGACTGTGGCCTGCCCAGCTCTCGTATCCCCAAGCCACACCATC
TGGCTAAATGGACATCATGTTTTCTGGTGATGCCCAAAGAGGAGAGAG
GAAGCTCTCTTTCCCAGATGCCCCAGCAAGTGTAACCTTGCATCTCATT
GCTCTGGCTGAGTTGTGTGCCTGTTTCTGACCAATCACTGAGTCAGGA
GGATGAAATATTCATATTGACTTAATTGCAGCTTAAGTTAGGGGTATGT
15 AGAGGTATTTTCCCTAAAGCAAAATTGGGACACTGTTATCAGAAATAGG
AGAGTGGATGATAGATGCAAAATAATACCTGTCCACAACAACTCTTAA
TGCTGTGTTTGAGCTTTCATGAGTTTCCCAGAGAGACATAGCTGGAAA
ATTCCTATTGATTTTCTCTAAAATTTCAACAAGTAGCTAAAGTCTGGCTA
TGCTCACAGTCTCACATCTGGTGGGGGTGGGCTCCTTACAGAACACG
20 CTTTCACAGTTACCCTAAACTCTCTGGGGCAGGGTTATTCCTTTGTGGA
ACCAGAGGCACAGAGACAGTCAACTGAGGCCCAACAGAGGCCTGAGA
GAAACTGAGGTCAAGATTTTCAGGATTAATGGTCCTGTGATGCTTTGAA
GTACAATTGTGGATTTGTCCAATTCTCTTTAGTTCTGTCAGCTTTTGCTT
CATATATTTTAGCGCTCTATTATTAGATATATACATGTTTAGTATTATGTC
25 TTATTGGTGCATTTACTCTCTTATCATTATGTAATGTCCTTCTTTATCTGT
GATAATTTTCTGTGTTCTGAAGTCTACTTTGTCTAAAAATAACATACGCA
CTCAACTTCCTTTTCTTTCTTCCTTCCTTTCTTTCTTCCTTCCTTTCTTTC
TCTCTCTCTCTTTCTTCCTTCCTTCCTTCCTTTTCTCTCTCTCTCTCTCT
CTCTCTCTTTTCTTGACAGACTCTCGTTCTGTGGCCCTGGCTGGAGTTC
30 AGTGGTGTGATCTTGGCTCACTGCTACCTCTACCATGAGCAATTCTCCT
GCCTCAGCCTCCCAAGTAGCTGGAACCTACAGGCTCATGCCACTGCGC
CCAGCTAATTTTTGTATTTTTCGTAGAGACGGGGTTTCACCACATTCGT

12

CAGGTTGGTTTCAAACCTGACTTTGTGATCCACCCGCCTCGGCCTC
CCAAAGTGCTGGGATTACAGGCATGAGCCATCACACCTGGTCAACTTT
CTTTTGATTAGTGTTTTTGTGGTATATCTTTTTCCATCATGTTACTTTAAA
TATATCTATATTATTGTATTTAAAATGTGTTTCTTACAGACTGCATGTAGT
5 TGGGTATAATTTTTATCCAGTCTAAAAATATCTGTCTTTTAATTGGTGTT
TAGACAATTTATATTTAATAAAATGGTGGAATTTAAA

SEQ ID NO:2: NM_004797_T2 | Length 484

ATGACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGGAATCCAAGGC
10 AGGAAAGGAGAACCTGGAGAAGGTGCCTATGTATACCGCTCAGCATT
CAGTGTGGGATTGGAGACTTACGTTACTATCCCCAACATGCCCATTC
GCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCA
CTGGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACC
ACATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAG
15 GACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG
GACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACC
AAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTAT
GCTGATAATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCAT
GACACCAACTGA

20

SEQ ID NO:3: NM_004797_T3 | Length 718

CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTC
TACTGCTATTAGCTCTGCCCCGGGCATGACCAGGAAACCACGACTCAAG
GGCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTG
25 GATGGCGGGCATCCCAGGGCATCCGGGGCCATAATGGGGCCCCAGGC
CGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGA
TCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACC
CGGGGCTGAAGGTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAG
GAGAACCTGGAGAAGGTGCGTTACTATCCCCAACATGCCCATTCGCTT
30 TACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGT
AAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCA
CAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGG

13

CTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTGGACCAGG
CCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTCTGG
CTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATAAT
GACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACT
5 GA

SEQ ID NO:4: NM_004797_T4 | Length 537

CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTT
TACTGCTATTAGCTCTGCCCCGGGCATGACCAGGAAACCACGACTCAAG
10 GGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTG
GATGGCGGGCATCCCAGGGCATCCGGGGCCATAATGGGGCCCCAGGC
CGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGA
TCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACC
CGGGGCTGAAGGTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAG
15 GAGAACCTGGAGAAGGTGCCTATGTATACCGCTCAGCATTCAAGTGTGG
GATTGGAGACTTACGTTACTATCCCCAACATGCCCATTCGCTTTACCAA
GATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTC
CACTGCAACATTCTGGGCTGTACCTTCACAGGCTTTCTTCTCTACCAT
GACACCAACTGA

20

SEQ ID NO:5: U37222_T1 | Length: 1306 WT

ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTG
GATCTGACGACACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTC
CTGTTCTCTTAATCCTGCCCAGTCATGCCGAAGATGACGTTACTACAA
25 CTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCAAGGGAACTTGTG
CAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCACA
CCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAA
AGGAGATGCAGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTG
GAATGACAGGAGCTGAAGGGCCACGGGGCTTCCCCGGAACCCCTGG
30 CAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCGCTCAGCGT
TCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTC
GCTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCAC

TGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTTACCAC
ATCACGGTGTACATGAAAGATGTGAAGGTGAGCCTCTTCAAGAAGGAC
AAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATGTGGAC
CAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGT
5 CTGGCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAG
ATAACGTCAACGACTCTACATTTACTGGCTTTCTTCTCTACCATGATAC
CAACTGACTGCAACTACCCATAGCCCATACACCAGGAGAATCATGGAA
CAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTTTATTGCTTAG
TTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCAATAAA
10 CGACTTTATAAAAAATAATTTGTGTTCCCTAGTCCAGAAAAAAGGCACT
CCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAAATCA
CATTTGGTATGGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAG
ACCATGCTATTTTTCTGCTCACTGTACACAAATATTGTTACATAAACCC
TATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTGASTGT
15 ATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAA
AAAAAAAAAAAAAAAAAAGAAAACTTTAGAGCACACTGGCGGCCGTTAC
TAG

SEQ ID NO:6: U37222_T2 | LENGTH: 1184

20 GCTCATTCACTTTTTAATTCACCCATAAAGGCTTTGAAAACCTAAGGCTG
GAGATGAACTTATAGGAGCCTGCCAGGCCGTGGAGAGTGAGGAAGCA
GAGATGACGGAGATGATGTCTTTCCTTGTCCTGTGAAATGGATTGTGG
GTAGAGGTTCCGGAGATAATGCCTCTTGCTGGAAACAGTCTGGGCAGT
TCTGTTCCCGCCATTCACAGAATTCTTCTCACTTTCTAGGTCTTCTTGG
25 TCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGC
CACGGGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGA
AGCCGCTTATGTGTATCGCTCAGCGTTCAGTGTGGGGCTGGAGACCC
GCGTCACTGTTCCCAATGTACCCATTCGCTTTACTAAGATCTTCTACAA
CCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTGCAACAT
30 TCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGAT
GTGAAGGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTCACCTAC
GACCAGTATCAGGAAAAGAATGTGGACCAGGCCTCTGGCTCTGTGCTC

15

CTCCATCTGGAGGTGGGAGACCAAGTCTGGCTCCAGGTGTATGGGGA
TGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTCTACATT
TACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATA
GCCCATACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCTTA
5 GTTTGAGAGATTGATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCC
ACACGTGTACTCACTTGTTCAATTAACGACTTTATAAAAAATAATTTGTG
TTCCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCACGACTCTTACAT
GGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA
TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTG
10 TACACAAATATTGTTACATAAACCTATAATGTAAATATGAAATACAGT
GATTACTCTTCTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGT
ATTAAAGTGGTAGGGATAAATTGG

SEQ ID NO:7: U37222_T3 | LENGTH: 1209

15 ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTG
GATCTGACGACACCAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTC
CTGTTCTCTTAATCCTGCCAGTCATGCCGAAGATGACGTTACTACAA
CTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCAAGGGAACTTGTG
CAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCACA
20 CCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAA
AGGAGATGCAGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTG
GAATGACAGGAGCTGAAGGGCCACGGGGCTTCCCCGGAACCCCTGG
CAGGAAAGGAGAGCCTGGAGAAGCCGCGTCACTGTTCCCAATGTACC
CATTGCTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGC
25 AGCACTGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTT
ACCACATCACGGTGTACATGAAAGATGTGAAGGTGAGCCTCTTCAAGA
AGGACAAGGCCGTTCTCTTCACCTACGACCAGTATCAGGAAAAGAATG
TGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGAC
CAAGTCTGGCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTA
30 TGCAGATAACGTCAACGACTCTACATTTACTGGCTTTCTTCTCTACCAT
GATACCAACTGACTGCAACTACCCATAGCCCATACACCAGGAGAATCA
TGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATTGATTTTATTG

CTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTCA
TTAAACGACTTTATAAAAAATAATTTGTGTTCTAGTCCAGAAAAAAGG
CACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAA
AATCACATTTGGTATGGGGGCTTCACAATATTCGCATGACTGTCTGGAA
5 GTAGACCATGCTATTTTTCTGCTCACTGTACACAAATATTGTTACATAA
ACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG
AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAAT
TGG

10 SEQ ID NO:8: U37222_T4 | LENGTH: 1028

ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTG
GATCTGACGACACCAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTC
CTGTTCTCTTAATCCTGCCCAGTCATGCCGAAGATGACGTTACTACAA
CTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCAAGGGAACTTGTG
15 CAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCACA
CCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAA
AGGAGATGCAGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTG
GAATGACAGGAGCTGAAGGGCCACGGGGCTTCCCCGGAACCCCTGG
CAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCGCTCAGCGT
20 TCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTC
GCTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCAC
TGGCAAGTTCTACTGCAACATTCCGGGACTCTACATTTACTGGCTTTCT
TCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCATACACCA
GGAGAATCATGGAACAGTCGACACACTTTCAGCTTAGTTTGAGAGATT
25 GATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACT
CACTTGTTCAATTAACGACTTTATAAAAAATAATTTGTGTTCTAGTCCA
GAAAAAAGGCACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATA
ACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAATATTCGCATGA
CTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT
30 TGTTACATAAACCTATAATGTAAATATGAAATACAGTGATTACTCTTC
TCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGT
AGGGATAAATTGG

SEQ ID NO:9: U37222_T5 | LENGTH: 306

ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTG
GATCTGACGACACCAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTC
5 CTGTTCTCTTAATCCTGCCCAGTCATGCCGAAGATGACGTTACTACAA
CTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACCCAAGGGAAC TTGTG
CAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACATAAAAATAT
AATTCGAGGGGGCATCCACCAGGCCGGCTGAATTGTGCCAAAATATGG
CACTTCCTGCAAGATAA

10

SEQ ID NO:10-11 Ghrelin variants:

SEQ ID NO:10: NM_016362_T1 | Length: 665

ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACC
TGACAGCACAGGCACCACTCCGCCAGGACTGCAGGCCACCTGTCTG
15 CAACCCAGCTGAGGCCATGCCCTCCCCAGGGACCGTCTGCAGCCTCC
TGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAGC
TTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAA
GAAGCCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCC
GCCCGGAAGATGGAGGTCAAGCAGAAGGGGGCAGAGGATGAACTGGA
20 AGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGTCAGGGGT
TCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACA
TCCTCTGGGAAGAGGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCC
ACAAGCCTTACTCACCTCTCTCTAAGTTTAGAAGCGCTCATCTGGCTTT
TCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGGAG
25 GCGAATAAATGTTCAAAGTGTATGCTGATGTTCAAATGGGAATTTATT
TCAAAGAGGAAAAGTTAATATTTTACTTTAAAAAAATCAAATAATAC

SEQ ID NO:11: NM_016362_T2 | Length: 579

ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACC
30 TGACAGCACAGGCACCACTCCGCCAGGACTGCAGGCCACCTGTCTG
CAACCCAGCTGAGGCCATGCCCTCCCCAGGGACCGTCTGCAGCCTCC
TGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCTCCAGC

TTCCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCCCACAAA
GCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGAC
CTGGAGCAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCAC
AAAGGACTCTGGGTCTGACCTCACTGTTTCTGGAAGGACATGGGGGCT
5 TAGAGTCCTAAACAGACTGTTTCCCCCTTCCAGCAGAGAAAGGAGTCG
AAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCT
CCGCCCCGGAAGATGGAGGTCAAGCAGAAGGGGGCAGAGGATGAACTG
GAAGTCCGGGTCGGTACCTCTGCAGTTTTATGCTTCTGTGGCAGCGAG
GAGGGTGGGG

10

SEQ ID NO:12-21 HSD11B variants:

SEQ ID NO:12: NM_005525_T1 WT| Length: 1448

GCACTGCCTGAGACTACTCCAGCCTCCCCCGTCCCTGATGTCACAATT
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15 CTCTGTGTGTCCTACAGGAGTCTTCAGGCCAGCTCCCTGTCGGATGGC
TTTTATGAAAAAATATCTCCTCCCCATTCTGGGGCTCTTCATGGCCTAC
TACTACTATTCTGCAAACGAGGAATTCAGACCAGAGATGCTCCAAGGA
AAGAAAGTGATTGTCACAGGGGGCCAGCAAAGGGATCGGAAGAGAGAT
GGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGA
20 GGTCAAAAGAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTG
GAGCAGCCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCT
TCGCAGAGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTA
GACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTCA
TGATGATATTCACCATGTGCGCAAAGCATGGAAGTCAACTTCCTCAGT
25 TACGTGGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAAT
GGAAGCATTGTTGTCGTCTCCTCTCTGGCTGGGAAAGTGGCTTATCCA
ATGGTTGCTGCCTATTCTGCAAGCAAGTTTGCTTTGGATGGGTTCTTCT
CCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATGTATCAATCAC
TCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATGAAGGCAGT
30 TTCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCT
GGAGATCATCAAAGGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGA
CAGCTCACTCTGGACCACTCTTCTGATCAGAAATCCATGCAGGAAGAT

19

CCTGGAATTTCTCTACTCAACGAGCTATAATATGGACAGATTCATAAAC
AAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACT
GTTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCA
GAGTGTCCCCAGAGACATGCAAGTCATGGGTACACCTGACAAATGGA
5 AGGAGTTCCTCTAACATTTGCAAATGGAAATGTAATAATAATGAATGT
CATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGGT
ATAATTACCAGATAGTTATATTAATTTATATCTTATATATAATAATATGT
GATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAAT
TCATAACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAA
10 CCATAAACTGTACAAATGAAATTTTTCAATATTTGTTTCTTAT

SEQ ID NO:13: NM_005525_T2 | LENGTH: 708

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CAGAGGCTGCTGCCTGCTTAGGAGGTTGTAGAAAGCTCTGTAGGTTCT
15 CTCTGTGTGTCCTACAGGAGTCTTCAGGCCAGCTCCCTGTCGGATGGC
TTTTATGAAAAAATATCTCCTCCCCATTCTGGGGCTCTTCATGGCCTAC
TACTACTATTCTGCAAACGAGGAATTCAGACCAGAGATGCTCCAAGGA
AAGAAAGTGATTGTCACAGGGGGCCAGCAAAGGGATCGGAAGAGAGAT
GGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGA
20 GCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCTTCGCAG
AGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTAGACATGC
TCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTTCATGATGAT
ATTCACCATGTGCGCAAAGCATGGAAGTCAACTTCCTCAGTTACGTG
GTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAG
25 CATGTGCGCTCTTCTGCTGGAATGCTATCATGTTGTGCATCTGAGCAG
TNGTTGATGGTCTCTCTCATAGAAGATATCAGGCAGGCATGATATACTT
TGGTCTGCTATACCAGACGCTAGGCGTCTGATGCA

SEQ ID NO:14: NM_005525_T3 | LENGTH: 1394

30 GCACTGCCTGAGACTACTCCAGCCTCCCCCGTCCCTGATGTCACAATT
CAGAGGCTGCTGCCTGCTTAGGAGGTTGTAGAAAGCTCTGTAGGTTCT
CTCTGTGTGTCCTACAGGAGTCTTCAGGCCAGCTCCCTGTCGGATGGC

TTTTATGAAAAAATATCTCCTCCCCATTCTGGGGCTCTTCATGGCCTAC
TACTACTATTCTGCAAACGAGGAATTCAGACCAGAGATGCTCCAAGGA
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GGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGA
5 GGTCAAAGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTG
GAGCAGCCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCT
TCGCAGAGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTA
GACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTCA
TGATGATATTCACCATGTGCGCAAAGCATGGAAGTCAACTTCCTCAGT
10 TACGTGGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAAT
GGAAGCATTGTTGTCGTCTCCTCTCTGGCTGGGAAAGTGGCTTATCCA
ATGGTTGCTGCCTATTCTGCAAGCAAGTTTGCTTTGGATGGGTTCTTCT
CCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATGTATCAATCAC
TCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATGAAGGCAGT
15 TTCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCT
GGAGATCATCAAAGGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGA
CAGCTCACTCTGGACCACTCTTCTGATCAGAAATCCATGCAGGAAGAT
CCTGGAATTTCTCTACTCAACGAGCTATAATATGGAGGGACTGTTCTGT
CTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTC
20 CCCAGAGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTT
CCTCTAACATTTGCAAATGGAAATGTAATAATAATGAATGTCATGCAC
CGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGGTATAATTAC
CAGATAGTTATATTAAATTTATATCTTATATATAATAATATGTGATGATTA
ATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATAACT
25 GGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAA
CTGTACAAATGAAATTTTTCAATATTTGTTTCTTAT

SEQ ID NO:15: NM_005525_T4 | LENGTH: 1394

30 GCACTGCCTGAGACTACTCCAGCCTCCCCCGTCCCTGATGTCACAATT
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TACTACTATTCTGCAAACGAGGAATTCAGACCAGAGATGCTCCAAGGA
AAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAGAGAGAT
GGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGA
GGTCAAAGAACTCTACAGAAGGTGGTATCCCCTGCCTGGAGCTTG
5 GAGCAGCCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCT
TCGCAGAGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTA
GACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTCA
TGATGATATTCACCATGTGCGCCCCATGCTGAAGCAGAGCAATGGAAG
CATTGTTGTCGTCTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTT
10 GCTGCCTATTCTGCAAGCAAGTTTGCTTTGGATGGGTTCTTCTCCTCCA
TCAGAAAGGAATATTCAGTGTCCAGGGTCAATGTATCAATCACTCTCTG
TGTTCTTGGCCTCATAGACACAGAAACAGCCATGAAGGCAGTTTCTGG
GATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGAT
CATCAAAGGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTC
15 ACTCTGGACCACTCTTCTGATCAGAAATCCATGCAGGAAGATCCTGGA
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GAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTGTTCTG
TCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGT
CCCCAGAGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAG
20 TTCCTCTAACATTTGCAAATGGAAATGTAATAATAATGAATGTCATGCA
CCGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGGTATAATTA
CCAGATAGTTATATTAAATTTATATCTTATATATAATAATATGTGATGATT
AATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATAAC
TGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAACCATAAA
25 CTGTACAAATGAAATTTTTCAATATTTGTTTCTTAT

SEQ ID NO:16: NM_005525_T5 | LENGTH: 1394

GCACTGCCTGAGACTACTCCAGCCTCCCCCGTCCCTGATGTCACAATT
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30 CTCTGTGTGTCCTACAGGAGTCTTCAGGCCAGCTCCCTGTCGGATGGC
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TACTACTATTCTGCAAACGAGGAATTCAGACCAGAGATGCTCCAAGGA

AAGAAAGTGATTGTCACAGGGGCCAGCAAAGGGATCGGAAGAGAGAT
GGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGA
GCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCTTCGCAG
AGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTAGACATGC
5 TCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTTCATGATGAT
ATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGTG
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10 TCAGAAAGGAATATTCAGTGTCCAGGGTCAATGTATCAATCACTCTCTG
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GATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGAT
CATCAAAGGGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTC
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15 ATTTCTCTACTCAACGAGCTATAATATGGACAGATTCATAAACAAGTAG
GAACTCCCTGAGGGGCTGGGCATGCTGAGGGATTTTGGGACTGTTCTG
TCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGT
CCCCAGAGACATGCAAGTCATGGGTACACACCTGACAAATGGAAGGAG
TTCCTCTAACATTTGCAAAATGGAAATGTAATAATAATGAATGTCATGCA
20 CCGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGGTATAATTA
CCAGATAGTTATATTAATTTATATCTTATATATAATAATATGTGATGATT
AATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATAAC
TGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAACCATAAA
CTGTACAAATGAAATTTTTCAATATTTGTTTCTTAT

25

SEQ ID NO:17: NM_005525_T6 | LENGTH: 1821

GGTGAAAAGGGAAAACCTGCCCAAATCCAGTTTTTGTTCAGTAACTTC
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GACAGGGGCTCTGTCTGGTATGCCTCTCCCATGTTAAGAGCTAACAAT
30 AGTAATGGATAAGTCTCCAGGGCAACCAGGACCACTTCCAAGCATTCC
TGTCTTGGGCTGCCTCGAGGGCTCCTCTGTCCTTTGGGGAGTACTGAT
TGATGCCTGATGCCCAGAACTGGCCCACTCTGGCTTCTCTTTGGAGCT

GTCTCTGCAGGCGCCTTCTGGCTGCCAGCTCGGTCCTAGCATAAGGG
ACTTCTTCCTTGGCCTGGGTTTCACCTTCTTGTATCAGGTGGCAGACCA
GCTGGTTTCAGTCCCAAATCAGGTCTTCTGACTCCTCCCAGAAACCAA
CCA ACTTCTGAGCAGGAAATCCTGCCCCCTCCCCAAAGAGTGGGAAACC
5 GCAAAGGAAGAGAGAGATGAAACAGAAGGAAAGGCAGAGGAGGAGG
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AGTCAGATTTGTTGAAATCTTGAGAGATGCTCCAAGGAAAGAAAGTG
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10 AA ACTCTACAGAAGGTGGTATCCC ACTGCCTGGAGCTTGGAGCAGCCT
CAGCACACTACATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGC
AATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTAGACATGCTCA
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15 CTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATT
GTTGTCGTCTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCT
GCCTATTCTGCAAGCAAGTTTGCTTTGGATGGGTTCTTCTCCTCCATCA
GAAAGGAATATTCAGTGTCCAGGGTCAATGTATCAATCACTCTCTGTGT
TCTTGGCCTCATAGACACAGAAACAGCCATGAAGGCAGTTTCTGGGAT
20 AGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCAT
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CTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTGTTCTGTCTC
25 ATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCC
AGAGACATGCAAGTCATGGGTCACACCTGACAAATGGAAGGAGTTCCT
CTAACATTTGCAAAATGGAAATGTAATAATAATGAATGTCATGCACCGC
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ATAGTTATATTAAATTTATATCTTATATATAATAATATGTGATGATTAATA
30 CAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATAACTGG
TAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAACCATAAACTG
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SEQ ID NO:18: NM_005525_T7 | LENGTH: 1304

5 GC ACTGCCTGAGACTACTCCAGCCTCCCCCGTCCCTGATGTCACAATT
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10 GGTCAAAGAAACTCTACAGAAGGTGGTATCCCCTGCCTGGAGCTTG
GAGCAGCCTCAGCACACTACATTGCTGGCACCATGGAAGACATGACCT
TCGCAGAGCAATTTGTTGCCCAAGCAGGAAAGCTCATGGGAGGACTA
GACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCTTTTTCA
TGATGATATTCACCATGTGCGCAAAGCATGGAAGTCAACTTCCTCAGT
15 TACGTGGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAAT
GGAAGCATTGTTGTCGTCTCCTCTCTGGCTGAAACAGCCATGAAGGCA
GTTTCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCC
CTGGAGATCATCAAAGGGGGAGCTCTGCGCCAAGAAGAAGTGTATTAT
GACAGCTCACTCTGGACCACTCTTCTGATCAGAAATCCATGCAGGAAG
20 ATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGACAGATTCATAA
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AGAGTGTCCCCAGAGACATGCAAGTCATGGGTCACACCTGACAAATGG
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25 TCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTTAGTAAACATAGG
TATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAATATG
TGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAA
TTCATAACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAA
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SEQ ID NO:19: XM_110304_T1 | Length: 1307 WT

ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGT
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CAGGTCCCTGTTTGATGGCAGTTATGAAAAATTACCTCCTCCCGATCCT
5 GGTGCTCTTCCTGGCCTACTACTACTATTCTACAAATGAAGAGTTCAGA
CCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA
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10 CTATGGAAGACATGACATTTGCGGAGCAATTTATTGTCAAGGCGGGAA
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15 CTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTCTGCAAGCAAGT
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CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACAC
AGAAACAGCTATGAAGGAAATCTCTGGGATAATTAACGCCCAAGCTTC
TCCCAAGGAGGAGTGCGCCCTGGAGATCATCAAAGGCACAGCTCTAC
20 GCAAAGCGAGGTGTACTATGACAAATCGCCTTTGACTCCAATCCTGC
TTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTTCATTACGATATTA
TAATAAGGACATGTTTGTAAGTAACTAGGAACTCCTGAGCCCTGGTGA
GTGGTCTTAGAACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACA
AAAGTATCTTTCCAGAGATACACAAATTTTGGGGTACACCTCATCATGA
25 GAAATTCTTGCAACACTTGACACAGTGAAAATGTAATTGTAATAAATGTC
ACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTAAGTATGGAT
ATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAA
TGATAACTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAA
ATGCA

SEQ ID NO:20: XM_110304_T3 | Length: 1181

ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGT
AGAAAGCTCTGCAGGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGC
CAGGTCCCTGTTTGATGGCAGTTATGAAAAATTACCTCCTCCCGATCCT
5 GGTGCTCTTCCTGGCCTACTACTACTATTCTACAAATGAAGAGTTCAGA
CTCCAGAAGGTAGTGTCTCGCTGCCTTGAACCTCGGAGCAGCCTCTGCT
CACTACATTGCTGGCACTATGGAAGACATGACATTTGCGGAGCAATTT
ATTGTCAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTA
AACCACATCACTCAGACCTCGCTGTCTCTCTTCCATGACGACATCCACT
10 CTGTGCGAAGAGTCATGGAGGTCAACTTCCTCAGCTACGTGGTCATGA
GCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAGCATTGCC
GTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCC
TACTCTGCAAGCAAGTTTGCTCTGGATGGGTCTTTTCCACCATTAGAA
CAGAACTCTACATAACCAAGGTCAACGTGTCCATCACTCTCTGTGTCCT
15 TGGCCTCATAGACACAGAAACAGCTATGAAGGAAATCTCTGGGATAAT
TAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTGGAGATCATCA
AAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTT
TGACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTT
TTTCATTACGATATTATAATAAGGACATGTTTGTAAGTAACTAGGAACTC
20 CTGAGCCCTGGTGAGTGGTCTTAGAACAGTCCTGCCTGATACTTCTGT
AAGCCCTACCCACAAAAGTATCTTTCCAGAGATACACAAATTTTGGGGT
ACACCTCATCATGAGAAATTCTTGCAACACTTGACACAGTGAAAATGTAA
TTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGA
TTGTAACTATGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCAC
25 ACTGAATGAAACAATGATAACTAATGTAAACATTAAATATAATAAAGGTAA
TATCAACTTTGTAAATGCA

SEQ ID NO:21: XM_110304_T4 | Length: 845

ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGT
30 AGAAAGCTCTGCAGGTTTTCTTCGTGTGTCCTACAGGGCGCCCTGAGC
CAGGTCCCTGTTTGATGGCAGTTATGAAAAATTACCTCCTCCCGATCCT
GGTGCTCTTCCTGGCCTACTACTACTATTCTACAAATGAAGAGTTCAGA

27

CCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA
AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCA
TGTGGTATTGACTGCCAGGTCTGGAGGAAGGTCTCCAGAAGGTAGTGT
CTCGCTGCCTTGAACCTCGGAGCAGCCTCTGCTCACTACATTGCTGGCA
5 CTATGGAAGACATGACATTTGCGGAGCAATTTATTGTCAAGGCGGGAA
AGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGA
CCTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCA
TGGAGGTCAACTTCCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGC
CCATGCTGAAGCAGAGCAATGGCAGCATTGCCGTCATCTCCTCCTTGG
10 CTGGGGGAAGAACAGTTCCACAACAGAGAAGTCGCAGTGTTACTCCTG
ACTCCCGCGGCCCGTGATTAATATCACCAGCCACAGAATGGACTGGAA
CCCTGTATCGATCTGGTGGGATTGGATATAACGAACATAGAATTACTCC
TGAGACTACCAGAACTGAATAGTTCAAATCAAATCATGCCAGAATATCA
GACAAATCCAAATGGCAAAACAGTTGCA

15

SEQ ID NO:22-30 Adiponectin variants products:

SEQ ID NO:22: NP_004788_P1 | Length: 244 | Transcript: 1 WT

MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHN
GAPGRDGRDGTTPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQG
20 RKGEPGEGAYVYRSAFSVGLETYVTIPNMPPIRFTKIFYNQNNHYDGSTGK
FHCNIPGLYYFAYHITVYMKDVKVSFLFKKDKAMLFTYDQYQENNVQASG
SVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHDTN

SEQ ID NO:23: NP_004788_P2 | Length: 160 | Transcript: 2

25 MPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPPIRFTKI
FYNQQNNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSFLFKKDKAMLFT
YDQYQENNVQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDST
FTGFLLYHDTN

30 SEQ ID NO:24: NP_004788_P3 | Length: 153 | Transcript: 3

MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHN
GAPGRDGRDGTTPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQG

RKGEPGEGALLSPTCPFALPRSSTISKTTMMAPLVNSTATFLGCTTLPTTS
QSI

SEQ ID NO:25: NP_004788_P4 | Length: 166 | Transcript: 4

5 MLLLGAVLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHN
GAPGRDGRDGTGPGEKGEKGDGPGLIGPKGDIGETGVPGAEGPRGFPGIQG
RKGEPGEGAYVYRSAFSVGLETYVTIPNMPPIRFTKIFYNQQNHYDGSTGK
FHCNIPGLYLHRLSSLP

10 SEQ ID NO:26: NP_033735_P1 | Length: 247 | Transcript: 1 WT

MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPG
HNGTPGRDGRDGTGPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFP
GTPGRKGEPGEAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDG
STGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQ
15 ASGSVLLHLEVGDQWLQVYGDGDHNGLYADNVNDSTFTGFLLYHDTN

SEQ ID NO:27: NP_033735_P2 | Length: 160 | Transcript: 2

MTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSVGLETRVTVPNVPIRFT
KIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLF
20 TYDQYQEKNVDQASGSVLLHLEVGDQWLQVYGDGDHNGLYADNVNDS
TFTGFLLYHDTN

SEQ ID NO:28: NP_033735_P3 | Length: 156 | Transcript: 3

MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPG
25 HNGTPGRDGRDGTGPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFP
GTPGRKGEPGEAASLFPMYPFALLRSSTTNRIIMTAALASSTATFRDSTTS
LTTSRCT

SEQ ID NO:29: NP_033735_P4 | Length: 169 | Transcript: 4

30 MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPG
HNGTPGRDGRDGTGPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFP

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29

GTPGRKGEPGEAAYVYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDG
STGKFYCNIPGLYIYWLSSLP

SEQ ID NO:30: NP_033735_P5 | Length: 76 | Transcript: 5

5 MLLLQALLFLLILPSHAEDDVTTEELAPALVPPPKGTCAGWMAGIPGHPG
HIKIKFEGHPPGRLNCAKIWHFLQD

SEQ ID NO:31-32 Ghrelin variants :

SEQ ID NO:31: NP_057446 | Length: 117 | Transcript: 1 WT

10 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQ
PRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQAL
GKFLQDILWEEAKEAPADK

SEQ ID NO:32: NP_057446 | Length: 117 | Transcript: 2

15 MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQVRPPHKAPHVPA
LPLSNQLCDLEQQRHLWASVFSQSTKDSGSDLTVSGRTWGLRVLNRLFPP
SSRERSRRSHQPSCSPEL

SEQ ID NO:33-42 HSD11B variants:

SEQ ID NO:33: NP_005516 | Length: 292 | Transcript: 1 WT

20 MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
YHLAKMGAAHVVTARSKETLQKVSHCLELGAASAHYIAGTMEDMTFAEQ
FVAQAGKLMGGLDMLILNHITNTSLNLFHDDIHHVRKSMEVNFLSYVLT
AALPMLKQSNGSIVVSSLAGKVAYPMVAAYSASKFALDGGFFSSIRKEYSV
25 SRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEECALEIHKGGALRQEE
VYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK

SEQ ID NO:34: NP_005516 | Length: 163 | Transcript: 2

30 MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
YHLAKMGAAHVVTASSAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILN
HITNTSLNLFHDDIHHVRKSMEVNFLSYVLTVAALPMLKQSNGSMCALLL
ECYHVHLSX

SEQ ID NO:35: NP_005516 | Length: 295 | Transcript: 3

MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
YHLAKMGAHVVTARSKETLQKVSHCLELGAASAHYIAGTMEDMTFAEQ
5 FVAQAGKLMGGLDMLILNHITNTSLNLFHDDIHHVRKSMEVNFLSYVLTVAALPMLKQSNGSIVVSSLAGKVAYPMVAAYSASKFALDGFFSSIRKEYSV
SRVNVSITLCVLGLIDTETAMKAVSGIVHMQAAPKEECALEIIKGGALRQEE
VYYDSSLWTTLLIRNPCRKILEFLYSTSYNMEGLFCLMFI

10 SEQ ID NO:36: NP_005516 | Length: 274 | Transcript: 4

MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
YHLAKMGAHVVTARSKETLQKVSHCLELGAASAHYIAGTMEDMTFAEQ
FVAQAGKLMGGLDMLILNHITNTSLNLFHDDIHHVRPMLKQSNGSIVVSS
LAGKVAYPMVAAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTET
15 AMKAVSGIVHMQAAPKEECALEIIKGGALRQEEVYYDSSLWTTLLIRNPCR
KILEFLYSTSYNMDRFINK

SEQ ID NO:37: NP_005516 | Length: 274 | Transcript: 5

MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
20 YHLAKMGAHVVTASSAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILN
HITNTSLNLFHDDIHHVRKSMEVNFLSYVLTVAALPMLKQSNGSIVVSS
AGKVAYPMVAAYSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETA
MKAVSGIVHMQAAPKEECALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKI
LEFLYSTSYNMDRFINK

25

SEQ ID NO:38: NP_005516 | Length: 262 | Transcript: 6

MLQGKKVIVTGASKGIGREMAYHLAKMGAHVVTARSKETLQKVSHCLE
LGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGLDMLILNHITNTSLNLFHD
DIHHVRKSMEVNFLSYVLTVAALPMLKQSNGSIVVSSLAGKVAYPMVAA
30 YSASKFALDGFFSSIRKEYSVSRVNVSITLCVLGLIDTETAMKAVSGIVHMQ
AAPKEECALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNM
DRFINK

SEQ ID NO:39: NP_005516 | Length: 244 | Transcript: 7

MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMA
YHLAKMGAHVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQ
5 FVAQAGKLMGGLDMLILNHITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTV
AALPMLKQSNGSIVVSSLAETAMKAVSGIVHMQAAPKEECALEIIKGGAL
RQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK

SEQ ID NO:40: XP_110304 | Length: 292 | Transcript: 1 WT

10 MAVMKNYLLPILVLFLAYYYYSTNEEFRRPEMLQGKKVIVTGASKGIGREMA
YHLSKMGAVVLTARSEEGQLQKVVSRCLELGAASAHYIAGTMEDMTFAEQ
FIVKAGKLMGGLDMLILNHITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTA
ALPMLKQSNGSIAVISSLAGKMTQPMIAPYSASKFALDGFFSTIRTELYITKV
NVSITLCVLGLIDTETAMKEISGIINAQASPKEECALEIIKGTALRKSEVYYDK
15 SPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN

SEQ ID NO:41: XP_110304 | Length: 250 | Transcript: 8

MAVMKNYLLPILVLFLAYYYYSTNEEFRLQKVVSRCLELGAASAHYIAGTM
EDMTFAEQFIVKAGKLMGGLDMLILNHITQTSLSLFHDDIHSVRRVMEVNF
20 LSYVVMSTAALPMLKQSNGSIAVISSLAGKMTQPMIAPYSASKFALDGFFS
TIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEECALEIIKGTAL
RKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN

SEQ ID NO:42: XP_110304 | Length: 192 | Transcript: 9

25 MAVMKNYLLPILVLFLAYYYYSTNEEFRRPEMLQGKKVIVTGASKGIGREMA
YHLSKMGAVVLTARSEEGQLQKVVSRCLELGAASAHYIAGTMEDMTFAEQ
FIVKAGKLMGGLDMLILNHITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTA
ALPMLKQSNGSIAVISSLAGGRTVPQQRSRSVTPDSRGP

30 ***“Obesity and/or diabetes Variants products”***, also referred at times as
the ***“obesity and/or diabetes variants proteins”*** or ***“obesity and/or
diabetes variants polypeptides”*** – are amino acid sequences encoded by

the obesity and/or diabetes variants nucleic acid sequences which are naturally occurring mRNA sequences obtained as a result of alternative splicing. The amino acid sequences may be a peptide, a protein, as well as peptides or proteins having *chemically modified* amino acids (see below) such as a glycopeptide or glycoprotein. The obesity and/or diabetes variants products are shown in any one of SEQ ID NO:22 to SEQ ID NO:42. The term also includes *homologs* (see below) of said sequences in which one or more amino acids has been added, deleted, *substituted* (see below) or *chemically modified* (see below) as well as *fragments* (see below) of this sequence having at least 10 amino acids.

“Fragments of obesity and/or diabetes related variants nucleic acid sequences” – a partial sequence of any one of SEQ ID NO:1 to SEQ ID NO:21 which includes the regions which contain the variation in nucleotides between the variant and the original sequences. These regions (in the amino acid level) are as depicted in the above Table 1.

“Fragments of obesity and/or diabetes related variant product” – amino acid sequences coded by the above nucleic acid fragment, containing regions by which the variant differs from the original sequence as indicated in Table 1.

“Nucleic acid sequence” – a sequence composed of DNA nucleotides, RNA nucleotides or a combination of both types and may includes natural nucleotides, chemically modified nucleotides and synthetic nucleotides.

“Amino acid sequence” – a sequence composed of any one of the 20 naturally appearing amino acids, amino acids which have been *chemically modified* (see below), or composed of synthetic amino acids.

“Homologues of variants/products” – amino acid sequences of variants in which one or more amino acids has been added, deleted or replaced.

The altered amino acid shall be in regions where the variant differs from the original sequence, for example, according to the explanation in Table 1.

5 ***“Conservative substitution”***- refers to the substitution of an amino acid in one class by an amino acid of the same class, where a class is defined by common physicochemical amino acid side chain properties and high substitution frequencies in homologous proteins found in nature, as determined, for example, by a standard Dayhoff frequency exchange
10 matrix or BLOSUM matrix. Six general classes of amino acid side chains have been categorized and include: Class I (Cys); Class II (Ser, Thr, Pro, Ala, Gly); Class III (Asn, Asp, Gln, Glu); Class IV (His, Arg, Lys); Class V (Ile, Leu, Val, Met); and Class VI (Phe, Tyr, Trp). For example, substitution of an Asp for another class III residue such as Asn, Gln, or Glu, is a
15 conservative substitution.

“Non-conservative substitution” - refers to the substitution of an amino acid in one class with an amino acid from another class; for example, substitution of an Ala, a class II residue, with a class III residue such as
20 Asp, Asn, Glu, or Gln.

“Chemically modified” - when referring to the product of the invention, means a product (protein) where at least one of its amino acid residues is modified either by natural processes, such as processing or other post-
25 translational modifications, or by chemical modification techniques which are well known in the art. Among the numerous known modifications typical, but not exclusive examples include: acetylation, acylation, octanoylation, amidation, ADP-ribosylation, glycosylation, GPI anchor formation, covalent attachment of a lipid or lipid derivative, methylation,
30 myristylation, pegylation, prenylation, phosphorylation, ubiquitination, or any similar process.

“Biologically active” - refers to the variant product having some sort of biological activity, for example, capability of binding to the obesity and/or diabetes related gene or to other agonists of the original obesity and/or diabetes related gene as known.

5

“Immunologically active” - defines the capability of a natural, recombinant or synthetic variant product, or any fragment thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies. Thus, for example, an immunologically active
10 fragment of variant product denotes a fragment which retains some or all of the immunological properties of the variant product, e.g., can bind specific anti-variant product antibodies or which can elicit an immune response which will generate such antibodies or cause proliferation of specific immune cells which produce variant.

15

“Optimal alignment” - is defined as an alignment giving the highest percent identity score. Such alignment can be performed using a variety of commercially available sequence analysis programs, such as the local alignment program LALIGN using a ktup of 1, default parameters and the
20 default PAM. A preferred alignment is the one performed using the CLUSTAL-W program from MacVectorTM, operated with an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM similarity matrix. If a gap needs to be inserted into a first sequence to optimally align it with a second sequence, the percent identity is calculated using
25 only the residues that are paired with a corresponding amino acid residue (i.e., the calculation does not consider residues in the second sequences that are in the “gap” of the first sequence). In case of alignments of known gene sequences with that of the new variant, the optimal alignment invariably included aligning the identical parts of both sequences together,
30 then keeping apart and unaligned the sections of the sequences that differ one from the other.

“Having at least 90% identity” - with respect to two amino acid or nucleic acid sequence sequences, refers to the percentage of residues that are identical in the two sequences when the sequences are optimally aligned. Thus, 90% amino acid sequence identity means that 90% of the amino acids in two or more optimally aligned polypeptide sequences are identical.

“Isolated nucleic acid molecule having a variant nucleic acid sequence” - is a nucleic acid molecule that includes the obesity and/or diabetes related variant nucleic acid coding sequence. Said isolated nucleic acid molecule may include the obesity and/or diabetes related variant nucleic acid sequence as an independent insert; may include the obesity and/or diabetes related variant nucleic acid sequence fused to an additional coding sequences, encoding together a fusion protein in which the variant coding sequence is the dominant coding sequence (for example, the additional coding sequence may code for a signal peptide); the obesity and/or diabetes related variant nucleic acid sequence may be in combination with non-coding sequences, e.g., introns or control elements, such as promoter and terminator elements or 5' and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host; or may be a vector in which the obesity and/or diabetes related variant protein coding sequence is heterologous.

“Expression vector” - refers to vectors that have the ability to incorporate and express heterologous DNA fragments in a foreign cell. Many prokaryotic and eukaryotic expression vectors are known and/or commercially available. Selection of appropriate expression vectors is within the knowledge of those having skill in the art.

“Deletion” - is a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

“Insertion” or “addition” - is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues, respectively, as compared to the naturally occurring
5 sequence.

“Substitution” - replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively. As regards amino acid sequences, the substitution may be conservative or non-conservative.
10

“Antibody” – refers to IgG, IgM, IgD, IgA, and IgG antibody. The definition includes polyclonal antibodies or monoclonal antibodies. This term refers to whole antibodies or fragments of the antibodies comprising the antigen-binding domain of the anti-variant product antibodies, e.g.
15 antibodies without the Fc portion, single chain antibodies, fragments consisting of essentially only the variable, antigen-binding domain of the antibody, etc.

“Treating a disease” - refers to administering a therapeutic substance
20 effective to ameliorate symptoms associated with a disease, to lessen the severity or cure the disease, or to prevent the disease from occurring.

“Detection” – refers to a method of detection of a disease, disorder, pathological or normal condition. This term may refer to detection of a
25 predisposition to a disease as well as for establishing the prognosis of the patient by determining the severity of the disease.

“Probe” – the obesity and/or diabetes variant nucleic acid sequence, or a sequence complementary therewith, when used to detect presence of
30 other similar sequences in a sample or of sequences having some homology with this sequence. The detection is carried out by identification

of hybridization complexes between the probe and the assayed sequence. The probe may be attached to a solid support or to a detectable label.

“Original obesity and/or diabetes related genes” – the amino acid or
5 nucleic acid sequence from which the obesity and/or diabetes related
variants of the invention have been varied as a result of alternative
splicing. The original nucleic acid sequence is the sequence of the human
obesity and/or diabetes related gene depicted as SEQ ID NO:1 for human
Adiponectin and the original amino acid sequence is the sequence
10 encoded by it; SEQ ID NO:5 for mouse Adiponectin and the original amino
acid sequence is the sequence encoded by it; SEQ ID NO:10 for Ghrelin
and the original amino acid sequence is the sequence encoded by it; SEQ
ID NO:12 for human 11-beta-HSD and the original amino acid sequence is
the sequence encoded by it; SEQ ID NO:19 for mouse 11-beta-HSD and
15 the original amino acid sequence is the sequence encoded by it.

SUMMARY OF THE INVENTION

The present invention relates to isolated nucleic acid molecules
having a sequence selected from the group consisting of: SEQ ID NO:2-4;
20 6-9; 11; 13-18; 20-21 and fragments thereof comprising at least 15
nucleotides. The present invention relates to isolated nucleic acid
molecules comprising SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 and isolated
nucleic acid molecules comprising fragments of SEQ ID NO:2-4; 6-9; 11;
13-18; 20-21 comprising at least 15 nucleotides.

25 The present invention relates to PCR primers which can amplify
products using sequences of SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 as
templates.

The present invention relates to methods of screening, diagnosing
and monitoring individuals for obesity and/or diabetes. The methods
30 comprise detecting the presence, absence, or quantity of a transcription
product that comprises a sequence selected from the group consisting of:
SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 in a sample. The presence or

quantity of said transcription product is indicative of obesity and/or diabetes.

The present invention relates to methods of treating individuals suffering from obesity and/or diabetes comprising the step of administering
5 the translation product of a transcript having a sequence selected from the group consisting of: SEQ ID NO:2-4;6-9;11;13-18;20-21.

The present invention relates to kits for screening, diagnosing and monitoring an individual for obesity and/or diabetes.

The present invention relates to proteins encoded by a nucleic acid
10 sequence selected from the group consisting of: SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 and immunogenic fragments thereof.

The present invention relates to antibodies which specifically bind to an epitope on a protein encoded by a nucleic acid sequence selected from the group consisting of: SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21.

15 The present invention relates to antibodies which specifically bind to an epitope on a protein encoded by a nucleic acid sequence selected from the group consisting of: SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 that are linked to detectable labels or active agents.

The present invention relates to pharmaceutical composition
20 comprising antibodies which specifically bind to an epitope on a protein encoded by a nucleic acid sequence selected from the group consisting of: SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 that are linked to active agents.

The present invention relates to methods of treating an individual suspected of suffering from obesity and/or diabetes. The methods
25 comprise the step of administering to individuals antibodies which specifically bind to an epitope on a protein encoded by a nucleic acid sequence selected from the group consisting of: SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 that are linked to active agents.

The present invention relates to methods of delivering a nucleic
30 acid molecule to obesity and/or diabetic cell of an individual. The methods comprise the step of administering to said individual a pharmaceutical composition comprising antibodies which specifically bind to an epitope on

a protein encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO:2-4; 6-9; 11; 13-18; 20-21 and a nucleic acid molecules.

5

BRIEF DESCRIPTION OF THE DRAWING

Fig. 1 shows multiple alignment of four amino acid sequences of human origin (depicted in SEQ ID NO:22 to SEQ ID NO:25) to each other and to the original sequence;

10 **Fig. 2** shows multiple alignment of five amino acid sequences of mouse origin (depicted in SEQ ID NO:26 to SEQ ID NO:30) to each other and to the original sequence;

Fig. 3 shows alignment of two amino acid sequences of human origin (depicted in SEQ ID NO:31 to SEQ ID NO:32) to the original sequence;

15 **Fig. 4** shows multiple alignment of seven amino acid sequences of human origin (depicted in SEQ ID NO:33 to SEQ ID NO:39) to each other and to the original sequence;

Fig. 5 shows multiple alignment of three amino acid sequences of human origin (depicted in SEQ ID NO:40 to SEQ ID NO:42) to each other
20 and to the original sequence;

Fig. 6 shows multiple alignment of four nucleic acid sequences of human origin (depicted in SEQ ID NO:1 to SEQ ID NO:4) to each other and to the original sequence;

Fig. 7 shows multiple alignment of five nucleic acid sequences of
25 mouse origin (depicted in SEQ ID NO:5 to SEQ ID NO:9) to each other and to the original sequence;

Fig. 8 shows alignment of two nucleic acid sequences of human origin (depicted in SEQ ID NO:10 to SEQ ID NO:11) to the original sequence;

30 **Fig. 9** shows multiple alignment of seven nucleic acid sequences of human origin (depicted in SEQ ID NO:12 to SEQ ID NO:18) to each other and to the original sequence;

Fig. 10 shows multiple alignment of three amino acid sequences of human origin (depicted in SEQ ID NO:19 to SEQ ID NO:21) to each other and to the original sequence.

5 **DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS**

Applicants specifically incorporate the entire content of all cited references in this disclosure. Further, when an amount, concentration, or other value or parameter is given as either a range, preferred range, or a list of upper preferable values and lower preferable values, this is to be understood as specifically disclosing all ranges formed from any pair of any upper range limit or preferred value and any lower range limit or preferred value, regardless of whether ranges are separately disclosed. Where a range of numerical values is recited herein, unless otherwise stated, the range is intended to include the endpoints thereof, and all integers and fractions within the range. It is not intended that the scope of the invention be limited to the specific values recited when defining a range.

Obesity and/or diabetes variants nucleic acid sequence

The nucleic acid sequences of the invention include nucleic acid sequences which encode Obesity and/or diabetes variants products and fragments and analogs thereof. The nucleic acid sequences may alternatively be sequences complementary to the above coding sequences, or to regions of said coding sequence. The length of the complementary sequences is sufficient to avoid the expression of the coding sequence. The nucleic acid sequences may be in the form of RNA or in the form of DNA, and include messenger RNA, synthetic RNA and DNA, cDNA, and genomic DNA. The DNA may be double-stranded or single-stranded, and if single-stranded may be the coding strand or the non-coding (anti-sense, complementary) strand. The nucleic acid sequences may also both include dNTPs, rNTPs as well as non-naturally occurring sequences. The sequence may also be a part of a hybrid between an amino acid sequence and a nucleic acid sequence.

In a general embodiment, the nucleic acid sequence has at least 90% identity with any one of the sequence identified as SEQ ID NO:2 to SEQ ID NO:4 or SEQ ID NO:6 to SEQ ID NO:9 or SEQ ID NO:11 or SEQ ID NO:13 to SEQ ID NO:18 or SEQ ID NO:20 to SEQ ID NO:21.

5 The nucleic acid sequences may include the coding sequence by itself. By another alternative the coding region may be in combination with additional coding sequences, such as those coding for fusion protein or signal peptides, in combination with non-coding sequences, such as introns and control elements, promoter and terminator elements or 5'
10 and/or 3' untranslated regions, effective for expression of the coding sequence in a suitable host, and/or in a vector or host environment in which the variant nucleic acid sequences is introduced as a heterologous sequence.

The nucleic acid sequences of the present invention may also have
15 the obesity and/or diabetes variants products coding sequences fused in-frame to a marker sequence which allows for purification of the variant product. The marker sequence may be, for example, a hexahistidine tag to provide for purification of the mature polypeptide fused to the marker in the case of a bacterial host, or the marker sequence may be a
20 hemagglutinin (HA) tag when a mammalian host, e.g. COS-7 cells, is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson, I., *et al. Cell* **37**:767 (1984)).

Also included in the scope of the invention are fragments as defined above also referred to herein as oligonucleotides, typically having at least
25 17 bases, preferably 17-30 bases corresponding to a region of the coding-sequence nucleic acid sequence. The fragments may be used as probes, primers, and when complementary also as antisense agents, and the like, according to known methods.

As indicated above, the nucleic acid sequence may be substantially
30 as depicted in SEQ ID NO:2 to SEQ ID NO:4 or SEQ ID NO:6 to SEQ ID NO:9 or SEQ ID NO:11 or SEQ ID NO:13 to SEQ ID NO:18 or SEQ ID NO:20 to SEQ ID NO:21 or fragments thereof or sequences having at

least 90% identity to the above sequence as explained above.

Alternatively, due to the degenerative nature of the genetic code, the sequence may be a sequence coding for any one of the amino acid sequences of SEQ ID NO:23 to SEQ ID NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO:39 or SEQ ID NO:41 to SEQ ID NO:42, or fragments or analogs of said amino acid sequence.

A. Preparation of nucleic acid sequences

The nucleic acid sequences may be obtained by screening cDNA libraries using oligonucleotide probes which can hybridize to or PCR-amplify nucleic acid sequences which encode the Obesity and/or diabetes variants products disclosed above. cDNA libraries prepared from a variety of tissues are commercially available and procedures for screening and isolating cDNA clones are well-known to those of skill in the art. Such techniques are described in, for example, Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2nd Edition), Cold Spring Harbor Press, Plainview, N.Y. and Ausubel FM *et al.* (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.

The nucleic acid sequences may be extended to obtain upstream and downstream sequences such as promoters, regulatory elements, and 5' and 3' untranslated regions (UTRs). Extension of the available transcript sequence may be performed by numerous methods known to those of skill in the art, such as PCR or primer extension (Sambrook *et al.*, *supra*), or by the RACE method using, for example, the Marathon RACE^{*} kit (Clontech, Cat. # K1802-1).

Alternatively, the technique of "restriction-site" PCR (Gobinda *et al.* *PCR Methods Appl.* 2:318-22 (1993)), which uses universal primers to retrieve flanking sequence adjacent a known locus, may be employed. First, genomic DNA is amplified in the presence of primer to a linker sequence and a primer specific to the known region. The amplified sequences are subjected to a second round of PCR with the same linker

^{*}-trademark

primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR can be used to amplify or extend sequences using
5 divergent primers based on a known region (Triglia, T. *et al.*, *Nucleic Acids Res.* **16**:8186 (1988)). The primers may be designed using OLIGO® 4.06 Primer Analysis Software (1992; National Biosciences Inc, Plymouth, Minn.), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target
10 sequence at temperatures about 68-72 °C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Capture PCR (Lagerstrom, M. *et al.*, *PCR Methods Appl.* **1**:111-19
15 (1991)) is a method for PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA. Capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered double-stranded sequence into a flanking part of the DNA molecule before PCR.

20 Another method which may be used to retrieve flanking sequences is that of Parker, J.D., *et al.*, *Nucleic Acids Res.* **19**:3055-60 (1991). Additionally, one can use PCR, nested primers and PromoterFinder™ libraries to “walk in” genomic DNA (PromoterFinder™; Clontech, Palo Alto, CA). This process avoids the need to screen libraries and is useful in
25 finding intron/exon junctions. Preferred libraries for screening for full length cDNAs are ones that have been size-selected to include larger cDNAs. Also, random primed libraries are preferred in that they will contain more sequences which contain the 5' and upstream regions of genes.

30 A randomly primed library may be particularly useful if an oligo d(T) library does not yield a full-length cDNA. Genomic libraries are useful for extension into the 5' nontranslated regulatory region.

The nucleic acid sequences and oligonucleotides of the invention can also be prepared by solid-phase methods, according to known synthetic methods. Typically, fragments of up to about 100 bases are individually synthesized, then joined to form continuous sequences up to
5 several hundred bases.

B. Use of Obesity and/or diabetes variants nucleic acid sequences for the production of Obesity and/or diabetes variants products

10 In accordance with the present invention, nucleic acid sequences specified above may be used as recombinant DNA molecules that direct the expression of Obesity and/or diabetes variant products.

As will be understood by those of skill in the art, it may be advantageous to produce Obesity and/or diabetes variants product-
15 encoding nucleotide sequences possessing codons other than those which appear in SEQ ID NO:2 to SEQ ID NO:4 or SEQ ID NO:6 to SEQ ID NO:9 or SEQ ID NO:11 or SEQ ID NO:13 to SEQ ID NO:18 or SEQ ID NO:20 to SEQ ID NO:21 which are those which naturally occur in the human genome. Codons preferred by a particular prokaryotic or
20 eukaryotic host (Murray, E. *et al. Nucleic Acids Res.* **17**:477-508 (1989)) can be selected, for example, to increase the rate of variant product expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than transcripts produced from naturally occurring sequences.

25 The nucleic acid sequences of the present invention can be engineered in order to alter Obesity and/or diabetes variants products coding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the product. For example, alterations may be introduced using techniques
30 which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, etc.

The present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which nucleic acid sequences of the invention have been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the constructs further comprise regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are also described in Sambrook, *et al. (supra)*.

The present invention also relates to host cells which are genetically engineered with vectors of the invention and the production of the product of the invention by recombinant techniques. Host cells are genetically engineered (i.e., transducer, transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the expression of the variant nucleic acid sequence. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art.

The nucleic acid sequences of the present invention may be included in any one of a variety of expression vectors for expressing a product. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host. The appropriate DNA sequence may be inserted into the vector by a variety of

procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Such procedures and related sub-cloning procedures are deemed to be within the scope of those skilled in the art.

5 The DNA sequence in the expression vector is operatively linked to an appropriate transcription control sequence (promoter) to direct mRNA synthesis. Examples of such promoters include: LTR or SV40 promoter, the *E.coli lac* or *trp* promoter, the phage lambda *PL* promoter, and other promoters known to control expression of genes in prokaryotic or
10 eukaryotic cells or their viruses. The expression vectors also contain a ribosome binding site for translation initiation, and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait
15 for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E.coli*.

 The vectors containing the appropriate DNA sequence as described above, as well as an appropriate promoter or control sequence, may be
20 employed to transform an appropriate host to permit the host to express the protein. Examples of appropriate expression hosts include: bacterial cells, such as *E.coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* and *Spodoptera Sf9*; animal cells such as CHO, COS, HEK 293 or Bowes melanoma; adenoviruses;
25 plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein. The invention is not limited by the host cells employed.

 In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the Obesity and/or diabetes
30 variant product. For example, when large quantities of Obesity and/or diabetes variant product are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are

readily purified may be desirable. Such vectors include, but are not limited to, multifunctional *E.coli* cloning and expression vectors such as *Bluescript*® (Stratagene), in which the Obesity and/or diabetes variants polypeptides coding sequence may be ligated into the vector in-frame with
5 sequences for the amino-terminal Met and the subsequent 7 residues of beta-galactosidase so that a hybrid protein is produced; *pIN* vectors (Van Heeke & Schuster *J. Biol. Chem.* **264**:5503-5509 (1989)); *pET* vectors (Novagen, Madison WI); and the like.

In the yeast *Saccharomyces cerevisiae*, a number of vectors
10 containing constitutive or inducible promoters such as alpha factor, alcohol oxidase and PGH may be used. For reviews, see Ausubel *et al.* (*supra*) and Grant *et al.* (*Methods in Enzymology* **153**:516-544 (1987)).

In cases where plant expression vectors are used, the expression of a sequence encoding variant products may be driven by any of a
15 number of promoters. For example, viral promoters such as the 35S and 19S promoters of *CaMV* (Brisson *et al.*, *Nature* **310**:511-514 (1984)) may be used alone or in combination with the omega leader sequence from TMV (Takamatsu *et al.*, *EMBO J.* **6**:307-311 (1987)). Alternatively, plant promoters such as the small subunit of RUBISCO (Coruzzi *et al.*, *EMBO J.*
20 **3**:1671-1680 (1984); Broglie *et al.*, *Science* **224**:838-843 (1984)); or heat shock promoters (Winter J and Sinibaldi R.M., *Results Probl. Cell Differ.* **17**:85-105 (1991)) may be used. These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. For reviews of such techniques, see Hobbs S. or Murry L.E.
25 (1992) in McGraw Hill Yearbook of Science and Technology, McGraw Hill, New York, N.Y., pp 191-196; or Weissbach and Weissbach (1988) *Methods for Plant Molecular Biology*, Academic Press, New York, N.Y., pp 421-463.

Obesity and/or diabetes variants products may also be expressed in
30 an insect system. In one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The Obesity and/or

diabetes variants products coding sequence may be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of Obesity and/or diabetes coding sequences will render the polyhedrin gene inactive
5 and produce recombinant virus lacking coat protein coat. The recombinant viruses are then used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which variant protein is expressed (Smith *et al.*, *J. Virol.* **46**:584 (1983); Engelhard, E.K. *et al.*, *Proc. Nat. Acad. Sci. USA* **91**:3224-7 (1994)).

10 In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, Obesity and/or diabetes variants products coding sequences may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence.
15 Insertion in a nonessential E1 or E3 region of the viral genome will result in a viable virus capable of expressing variant protein in infected host cells (Logan and Shenk, *Proc. Natl. Acad. Sci. USA* **81**:3655-59 (1984). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

20 Specific initiation signals may also be required for efficient translation of variants products coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where Obesity and/or diabetes variants products coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector,
25 no additional translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon must be provided. Furthermore, the initiation codon must be in the correct reading frame to ensure transcription of the entire insert.
30 Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell

system in use (Scharf, D. *et al.*, *Results Probl. Cell Differ.* **20**:125-62 (1994); Bittner *et al.*, *Meth. Enzymol.* **153**:516-544 (1987)).

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher
5 eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, L., Dibner, M., and Battey, I. (1986)
10 *Basic Methods in Molecular Biology*). Cell-free translation systems can also be employed to produce polypeptides using RNAs derived from the DNA constructs of the present invention.

A host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein
15 in the desired fashion. Such modifications of the protein include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation. Post-translational processing which cleaves a "pre-pro" form of the protein may also be important for correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK,
20 293, WI38, etc. have specific cellular machinery and characteristic mechanisms for such post-translational activities and may be chosen to ensure the correct modification and processing of the introduced, foreign protein.

For long-term, high-yield production of recombinant proteins, stable
25 expression is preferred. For example, cell lines which stably express variant products may be transformed using expression vectors which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are
30 switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences.

Resistant clumps of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler M., *et al.*, *Cell* **11**:223-32 (1977)) and adenine phosphoribosyltransferase (Lowy I., *et al.*, *Cell* **22**:817-23 (1980)) genes which can be employed in *tk*- or *aprt*-cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection, for example, *dhfr* which confers resistance to methotrexate (Wigler M., *et al.*, *Proc. Natl. Acad. Sci. USA* **77**:3567-70, (1980)); *npt*, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. *et al.*, *J. Mol. Biol.* **150**:1-14 (1981)); and *als* or *pat*, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, *trpB*, which allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman S.C. and R.C. Mulligan, *Proc. Natl. Acad. Sci.* **85**:8047-51, (1988)). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate, GUS, and luciferase and its substrates, luciferin and ATP, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. *et al.*, *Methods Mol. Biol.* **55**:121-131 (1995)).

Host cells transformed with nucleotide sequences encoding Obesity and/or diabetes variants products may be cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The product produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing nucleic acid sequences encoding Obesity and/or diabetes variants products can be designed with signal sequences which direct

secretion of Obesity and/or diabetes variants products through a prokaryotic or eukaryotic cell membrane.

The Obesity and/or diabetes variants products may also be expressed as recombinant proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of a protease-cleavable polypeptide linker sequence between the purification domain and Obesity and/or diabetes variants products is useful to facilitate purification. One such expression vector provides for expression of a fusion protein comprising a variant polypeptide fused to a polyhistidine region separated by an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography, as described in Porath, *et al.*, *Protein Expr. Purif.* 3:263-281 (1992)) while the enterokinase cleavage site provides a means for isolating variant polypeptide from the fusion protein. *pGEX* vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to ligand-agarose beads (e.g., glutathione-agarose in the case of GST-fusions) followed by elution in the presence of free ligand.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. Microbial cells employed in expression of proteins can be disrupted by any convenient method,

including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, or other methods, which are well known to those skilled in the art.

The Obesity and/or diabetes variants products can be recovered
5 and purified from recombinant cell cultures by any of a number of methods well known in the art, including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite
10 chromatography, and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

15

C. Diagnostic applications utilizing nucleic acid sequences

The nucleic acid sequences of the present invention may be used for a variety of diagnostic purposes. The nucleic acid sequences may be used to detect and quantitate expression of the Obesity and/or diabetes
20 variant in patient's cells, e.g. biopsied tissues, by detecting the presence of mRNA coding for the Obesity and/or diabetes variants products. Alternatively, the assay may be used to detect the soluble variants in the serum or blood. This assay typically involves obtaining total mRNA from the tissue or serum and contacting the mRNA with a nucleic acid probe.
25 The probe is a nucleic acid molecule of at least 20 nucleotides, preferably 20-30 nucleotides, capable of specifically hybridizing with a sequence included within the sequence of a nucleic acid molecule encoding the Obesity and/or diabetes variant product under hybridizing conditions, detecting the presence of mRNA hybridized to the probe, and thereby
30 detecting the expression of variant. This assay can be used to distinguish between absence, presence, and excess expression of Obesity and/or diabetes variants products and to monitor levels of Obesity and/or

diabetes variants expression during therapeutic intervention. In addition, the assay may be used to compare the levels of the Obesity and/or diabetes variant of the invention to the levels of the original Obesity and/or diabetes sequence from which it has been varied or to levels of each
5 other, which comparison may have some physiological meaning.

The invention also contemplates the use of the nucleic acid sequences as a diagnostic for diseases resulting from inherited defective variants sequences, or diseases in which the ratio of the amount of the original Obesity and/or diabetes sequence from which the Obesity and/or
10 diabetes variants were varied to the novel Obesity and/or diabetes variants of the invention is altered. These sequences can be detected by comparing the sequences of the defective (i.e., mutant) Obesity and/or diabetes variants coding region with that of a normal coding region. Association of the sequence coding for mutant Obesity and/or diabetes
15 variants products with abnormal variants products activity may be verified. In addition, sequences encoding mutant Obesity and/or diabetes variants products can be inserted into a suitable vector for expression in a functional assay system (e.g., colorimetric assay, complementation experiments in a variant protein deficient strain of HEK293 cells) as yet
20 another means to verify or identify mutations. Once mutant genes have been identified, one can then screen populations of interest for carriers of the mutant gene.

Individuals carrying mutations in the nucleic acid sequences of the present invention may be detected at the DNA level by a variety of
25 techniques. Nucleic acids used for diagnosis may be obtained from a patient's cells, including but not limited to such as from blood, urine, saliva, placenta, tissue biopsy and autopsy material. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR (Saiki, *et al.*, *Nature* **324**:163-166 (1986)) prior to analysis. RNA or cDNA
30 may also be used for the same purpose. As an example, PCR primers complementary to the nucleic acid of the present invention can be used to identify and analyze mutations in the gene of the present invention.

Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype.

Point mutations can be identified by hybridizing amplified DNA to radiolabeled RNA of the invention or alternatively, radiolabeled antisense
5 DNA sequences of the invention. Sequence changes at specific locations may also be revealed by nuclease protection assays, such RNase and S1 protection or the chemical cleavage method (e.g. Cotton, *et al. Proc. Natl. Acad. Sci. USA* **85**:4397-4401 (1985)), or by differences in melting
10 temperatures. "*Molecular beacons*" (Kostrikis L.G. *et al.*, *Science* **279**:1228-1229 (1998)), hairpin-shaped, single-stranded synthetic oligo-nucleotides containing probe sequences which are complementary to the nucleic acid of the present invention, may also be used to detect point mutations or other sequence changes as well as monitor expression levels of variant product. Such diagnostics would be particularly useful for
15 prenatal testing.

Another method for detecting mutations uses two DNA probes which are designed to hybridize to adjacent regions of a target, with abutting bases, where the region of known or suspected mutation(s) is at or near the abutting bases. The two probes may be joined at the abutting
20 bases, e.g., in the presence of a ligase enzyme, but only if both probes are correctly base paired in the region of probe junction. The presence or absence of mutations is then detectable by the presence or absence of ligated probe.

Also suitable for detecting mutations in the Obesity and/or diabetes
25 variants products coding sequences are oligonucleotide array methods based on sequencing by hybridization (SBH), as described, for example, in U.S. Patent No. 5,547,839. In a typical method, the DNA target analyte is hybridized with an array of oligonucleotides formed on a microchip. The sequence of the target can then be "*read*" from the pattern of target
30 binding to the array.

D. Therapeutic applications of nucleic acid sequences

Nucleic acid sequences of the invention may also be used for therapeutic purposes. Referring to a second aspect of the invention (i.e. inhibition of expression of Obesity and/or diabetes variants), expression of Obesity and/or diabetes variants products may be modulated through antisense technology, which controls gene expression through hybridization of complementary nucleic acid sequences, i.e. antisense DNA or RNA, to the control, 5' or regulatory regions of the gene encoding variant product. For example, the 5' coding portion of the nucleic acid sequence which codes for the product of the present invention is used to design an antisense oligonucleotide of from about 10 to 40 base pairs in length. Oligonucleotides derived from the transcription start site, e.g. between positions -10 and +10 from the start site, are preferred. An antisense DNA oligonucleotide is designed to be complementary to a region of the nucleic acid sequence involved in transcription (Lee *et al.*, *Nucl. Acids Res.* **6**:3073 (1979); Cooney *et al.*, *Science* **241**:456 (1988); and Dervan *et al.*, *Science* **251**:1360 (1991)), thereby preventing transcription and the production of the variant products. An antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the variant products (Okano, *J. Neurochem.* **56**:560 (1991)). The antisense constructs can be delivered to cells by procedures known in the art such that the antisense RNA or DNA may be expressed *in vivo*. The antisense may be antisense mRNA or DNA sequence capable of coding such antisense mRNA. The antisense mRNA or the DNA coding thereof can be complementary to the full sequence of nucleic acid sequences coding for the Obesity and/or diabetes variant protein or to a fragment of such a sequence which is sufficient to inhibit production of a protein product. Antisense technologies can also be used for inhibiting expression of one variant as compared to the other, or inhibiting the expression of the variant/s as compared to the original sequence.

Turning now to the first aspect of the invention, i.e. expression of Obesity and/or diabetes variants, expression of Obesity and/or diabetes variants products may be increased by providing coding sequences for coding for said Obesity and/or diabetes variants products under the control
5 of suitable control elements ending its expression in the desired host.

The nucleic acid sequences of the invention may be employed in combination with a suitable pharmaceutical carrier. Such compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable carrier or excipient. Such a carrier includes
10 but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The formulation should suit the mode of administration.

The products of the invention may also be employed in accordance with the present invention by expression of such polypeptides *in vivo*,
15 which is often referred to as "*gene therapy*." Cells from a patient may be engineered with a nucleic acid sequence (DNA or RNA) encoding a polypeptide *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, cells may be engineered by procedures known in the
20 art by use of a retroviral particle containing RNA encoding a polypeptide of the present invention.

Similarly, cells may be engineered *in vivo* for expression of a polypeptide *in vivo* by procedures known in the art. As known in the art, a producer cell for producing a retroviral particle containing RNA encoding
25 the polypeptides of the present invention may be administered to a patient for engineering cells *in vivo* and expression of the polypeptide *in vivo*. These and other methods for administering products of the present invention by such method should be apparent to those skilled in the art from the teachings of the present invention. For example, the expression
30 vehicle for engineering cells may be other than a retrovirus, for example, an adenovirus which may be used to engineer cells *in vivo* after combination with a suitable delivery vehicle.

Retroviruses from which the retroviral plasmid vectors mentioned above may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape
5 leukemia virus, human immunodeficiency virus, adenovirus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the *PE501*, *PA317*, *psi-2*, *psi-AM*, *PA12*, *T19-14X*, *VT-19-17-H2*, *psi-CRE*, *psi-CRIP*, *GP+E-86*,
10 *GP+envAm12*, and *DAN* cell lines as described in Miller (*Human Gene Therapy*, Vol. 1, pg. 5-14, (1990)). The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO_4
15 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include the nucleic acid sequence(s) encoding the polypeptides.
20 Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express the nucleic acid sequence(s) encoding the polypeptide. Eukaryotic cells which may be transduced include, but are not limited to, embryonic stem cells, embryonic carcinoma cells, as well as
25 hematopoietic stem cells, hepatocytes, fibroblasts, myoblasts, keratinocytes, endothelial cells, and bronchial epithelial cells.

The genes introduced into cells may be placed under the control of inducible promoters, such as the radiation-inducible *Egr-1* promoter, (Maceri, H.J., *et al.*, *Cancer Res.* **56**(19):4311 (1996)), to stimulate variant
30 production or antisense inhibition in response to radiation, e.g., radiation therapy for treating tumors.

Obesity and/or diabetes Variants products

The substantially purified Obesity and/or diabetes variant product of the invention has been defined above as the product coded from the nucleic acid sequence of the invention. Preferably the amino acid
5 sequence is an amino acid sequence having at least 90% identity to a sequence identified as SEQ ID NO:23 to SEQ ID NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO:39 or SEQ ID NO:41 to SEQ ID NO:42. The protein or polypeptide may be in mature and/or modified form, also as defined above, for example, modified
10 by cleavage of the leader sequence. Also contemplated are protein fragments having at least 5 contiguous amino acid residues, preferably at least 5-20 residues, derived from the Obesity and/or diabetes variant products, as well as homologues as explained above.

The sequence variations are preferably those that are considered
15 conserved substitutions, as defined above. Thus, for example, a protein with a sequence having at least 90% sequence identity with the products identified as SEQ ID NO:23 to SEQ ID NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO:39 or SEQ ID NO:41 to SEQ ID NO:42, preferably by utilizing conserved substitutions as
20 defined above is also part of the invention, and provided that it is not identical to the original peptide from which it has been varied (typically the substitutions are in regions where the variant differs from the original sequence as for example in Table 1). In a more specific embodiment, the protein has or contains the sequence identified SEQ ID NO:23 to SEQ ID
25 NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO: 39 or SEQ ID NO:41 to SEQ ID NO:42. The Obesity and/or diabetes variants products may be (i) one in which one or more of the amino acid residues in a sequence listed above are substituted with a conserved or non-conserved amino acid residue (preferably a conserved
30 amino acid residue), or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the Obesity and/or diabetes variants products is fused with another compound, such

as a compound to increase the half-life of the protein (for example, polyethylene glycol (PEG)), or a moiety which serves as targeting means to direct the protein to its target tissue or target cell population (such as an antibody), or (iv) one in which additional amino acids are fused to the

5 Obesity and/or diabetes variant product. Such fragments, variants and derivatives are deemed to be within the scope of those skilled in the art from the teachings herein.

A. Preparation of Obesity and/or diabetes variants products

10 Recombinant methods for producing and isolating the Obesity and/or diabetes variant products, and fragments of the protein are described above.

In addition to recombinant production, fragments and portions of variant products may be produced by direct peptide synthesis using solid-

15 phase techniques (cf. Stewart *et al.*, (1969) Solid-Phase Peptide Synthesis, WH Freeman Co, San Francisco; Merrifield J., *J. Am. Chem. Soc.* **85**:2149-2154 (1963)). *In vitro* peptide synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide

20 Synthesizer (Perkin Elmer, Foster City, Calif.) in accordance with the instructions provided by the manufacturer. Fragments of Obesity and/or diabetes variants products may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

25 B. Therapeutic uses and compositions utilizing the Obesity and/or diabetes variants products

The Obesity and/or diabetes variants products of the invention are generally useful in treating obesity and/or diabetes.

Obesity and/or diabetes variant products or fragments may be

30 administered by any of a number of routes and methods designed to provide a consistent and predictable concentration of compound at the target organ or tissue. The product-containing compositions may be

administered alone or in combination with other agents, such as stabilizing compounds, and/or in combination with other pharmaceutical agents such as drugs or hormones.

Obesity and/or diabetes variants product-containing compositions
5 may be administered by a number of routes including, but not limited to oral, intravenous, intramuscular, transdermal, subcutaneous, topical, sublingual, or rectal means as well as by nasal application. Obesity and/or diabetes variant product-containing compositions may also be administered via liposomes. Such administration routes and appropriate
10 formulations are generally known to those of skill in the art.

The Obesity and/or diabetes variants products can be given via intravenous or intraperitoneal injection. Similarly, the product may be injected to other localized regions of the body. The product may also be administered via nasal insufflation. Enteral administration is also possible.
15 For such administration, the product should be formulated into an appropriate capsule or elixir for oral administration, or into a suppository for rectal administration.

The foregoing exemplary administration modes will likely require that the product be formulated into an appropriate carrier, including, e.g.
20 ointments, gels, or suppositories. Appropriate formulations are well known to persons skilled in the art.

Dosage of the product will vary, depending upon the potency and therapeutic index of the particular polypeptide selected.

A therapeutic composition for use in the treatment method can
25 include the product in a sterile injectable solution, the polypeptide in an oral delivery vehicle, the product in an aerosol suitable for nasal administration, or the product in a nebulized form, all prepared according to well known methods. Such compositions comprise a therapeutically effective amount of the compound, and a pharmaceutically acceptable
30 carrier or excipient. Such a carrier includes but is not limited to saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The product of the invention may also be used to modulate

endothelial differentiation and proliferation as well as to modulate apoptosis either *ex vivo* or *in vitro*, for example, in cell cultures.

Anti-variant antibodies

5 A. Synthesis

In still another aspect of the invention, the purified variants products are used to produce anti-variant antibodies which have diagnostic and therapeutic uses related to the activity, distribution, and expression of the Obesity and/or diabetes variants products.

10 Antibodies to the Obesity and/or diabetes variant may be generated by methods well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, humanized, single chain, Fab fragments and fragments produced by an Fab expression library. Antibodies, i.e., those which inhibit dimer formation, are especially
15 preferred for therapeutic use.

A fragment of the Obesity and/or diabetes variants products for antibody induction is not required to feature biological activity but has to feature immunological activity; however, the protein fragment or oligopeptide must be antigenic. Peptides used to induce specific
20 antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids of the sequences specified in SEQ ID NO:23 to SEQ ID NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO:39 or SEQ ID NO: 41 to SEQ ID NO:42. Preferably they should mimic a portion of the amino acid
25 sequence of the natural protein and may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of Obesity and/or diabetes variants proteins amino acids may be fused with those of another protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule. Procedures well known in the art
30 can be used for the production of antibodies to Obesity and/or diabetes variants products.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, etc may be immunized by injection with Obesity and/or diabetes variants products or any portion, fragment or oligopeptide which retains immunogenic properties. Depending on the host species, various
5 adjuvants may be used to increase immunological response. Such adjuvants include but are not limited to Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. BCG (bacilli Calmette-Guerin) and
10 *Corynebacterium parvum* are potentially useful human adjuvants.

Monoclonal antibodies to Obesity and/or diabetes variants protein may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited, to the hybridoma technique originally described by Koehler
15 and Milstein (*Nature* **256**:495-497 (1975)), the human B-cell hybridoma technique (Kosbor *et al.*, *Immunol. Today* **4**:72 (1983); Cote *et al.*, *Proc. Natl. Acad. Sci. USA* **80**:2026-2030 (1983)) and the EBV-hybridoma technique (Cole, *et al.*, *Mol. Cell Biol.* **62**:109-120 (1984)).

Techniques developed for the production of "*chimeric antibodies*",
20 the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can also be used (Morrison *et al.*, *Proc. Natl. Acad. Sci. USA* **81**:6851-6855 (1984); Neuberger *et al.*, *Nature* **312**:604-608 (1984); Takeda *et al.*, *Nature* **314**:452-454 (1985)). Alternatively, techniques described for the
25 production of single chain antibodies (U.S. Pat. No. 4,946,778) can be adapted to produce single-chain antibodies specific for the variant protein.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in
30 Orlandi *et al.* (*Proc. Natl. Acad. Sci. USA* **86**:3833-3837 (1989)), and Winter G and Milstein C. (*Nature* **349**:293-299 (1991)).

Antibody fragments which contain specific binding sites for the Obesity and/or diabetes variant protein may also be generated. For example, such fragments include, but are not limited to, the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse W.D. *et al.*, *Science* 256:1275-1281 (1989)).

B. Diagnostic applications of antibodies

A variety of protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the formation of complexes between the Obesity and/or diabetes variants products and its specific antibody and the measurement of complex formation. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two noninterfering epitopes on a specific variant product is preferred, but a competitive binding assay may also be employed. These assays are described in Maddox D.E., *et al.* (*J. Exp. Med.* **158**:1211 (1983)).

Antibodies which specifically bind the Obesity and/or diabetes variant product are useful for the diagnosis of conditions or diseases characterized by expression of the novel Obesity and/or diabetes variants of the invention (where normally it is not expressed) by over or under expression of Obesity and/or diabetes variants as well as for detection of diseases in which the proportion between the amount of the Obesity and/or diabetes variants of the invention and the original Obesity and/or diabetes sequence from which it varied is altered. Alternatively, such antibodies may be used in assays to monitor patients being treated with Obesity and/or diabetes variants products. Diagnostic assays for variants proteins include methods utilizing the antibody and a label to detect

variants products in human body fluids or extracts of cells or tissues. The products and antibodies of the present invention may be used with or without modification. Frequently, the proteins and antibodies will be labeled by joining them, either covalently or noncovalently, with a reporter
5 molecule. A wide variety of reporter molecules are known in the art.

A variety of protocols for measuring the Obesity and/or diabetes variants products, using either polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and
10 fluorescent activated cell sorting (FACS). As noted above, a two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on Obesity and/or diabetes variants products is preferred, but a competitive binding assay may be employed. These assays are described, among other places, in Maddox, *et al.*
15 (*supra*). Such protocols provide a basis for diagnosing altered or abnormal levels of Obesity and/or diabetes variants products expression. Normal or standard values for Obesity and/or diabetes variants products expression are established by combining body fluids or cell extracts taken from normal subjects, preferably human, with antibodies to Obesity and/or
20 diabetes variants products under conditions suitable for complex formation which are well known in the art. The amount of standard complex formation may be quantified by various methods, preferably by photometric methods. Then, standard values obtained from normal samples may be compared with values obtained from samples from
25 subjects potentially affected by disease. Deviation between standard and subject values establishes the presence of disease state.

The antibody assays are useful to determine the level of Obesity and/or diabetes variants products present in a body fluid sample, in order to determine whether it is being expressed at all, whether it is being
30 overexpressed or underexpressed in the tissue, or as an indication of how Obesity and/or diabetes variants levels of variable products are responding to drug treatment.

C. Therapeutic uses of antibodies

In addition to their diagnostic use the antibodies may have a therapeutical utility in blocking or decreasing the activity of the obesity and/or diabetes variants products in pathological conditions where
5 beneficial effect can be achieved by such a decrease.

The antibody employed is preferably a humanized monoclonal antibody, or a human Mab produced by known globulin-gene library methods. The antibody is administered typically as a sterile solution by IV
10 injection, although other parenteral routes may be suitable. Typically, the antibody is administered in an amount between about 1-15 mg/kg body weight of the subject. Treatment is continued, e.g., with dosing every 1-7 days, until a therapeutic improvement is seen.

Although the invention has been described with reference to
15 specific methods and embodiments, it is appreciated that various modifications and changes may be made without departing from the invention.

EXAMPLE 1 - Separation

20 Sf-9 cells are infected with Obesity and/or diabetes variants expressing baculovirus (AC-obesity and/or diabetes variant) comprising the amino acid sequence of SEQ ID NO:23 to SEQ ID NO:25 or SEQ ID NO:27 to SEQ ID NO:30 or SEQ ID NO:32 or SEQ ID NO:34 to SEQ ID NO:39 or SEQ ID NO:41 to SEQ ID NO:42 at MOI of 2. The cells are
25 grown in 28 °C at continuous shaking (90 rpm). At 60 hours post-infection (hpi), the medium is collected and cells are separated from the medium by centrifugation at 5000 rpm for 5 minutes. 10 mL medium is separated using cation exchange chromatography with a SP-Sepharose* column. The column is equilibrated with PBS pH 6.5, and, following loading of the
30 sample on the column, the column is washed with PBS to elute the unbound proteins (flow through fraction). Elution is done with increasing concentration of NaCl at a flow rate of 2 mL/min (5% NaCl/min).

*-trademark

The different fractions are subjected to SDS-PAGE electrophoresis and to western blotting using anti-Obesity and/or diabetes variant antibody.

5

EXAMPLE 2- Secretion

Sf-9 cells are infected with Obesity and/or diabetes variants expressing baculovirus (Ac-obesity and/or diabetes variant) at MOI of 2. The cells are grown at 28 °C at continuous shaking (90 rpm), and 1 mL samples are collected at 24, 48, and 60 hours post-infection (hpi).

- 10 Following centrifugation, cell pellets are lysed with lysis buffer (50 mM Tris pH 7.5, 1% triton* X100, and protease inhibitor cocktail) at 4 °C for 30 min and sonicated for 30 seconds. The sample is centrifuged for 10 minutes at 14000 rpm and the supernatant is designated Pellet. 40 µL of the Pellet preparation and of the medium (Designated Medium) are supplemented
- 15 with sample buffer and are electrophoresed on a 15% SDS-PAGE. Following electrophoresis, the gel is subjected to a semi-dry protein transfer onto a nitrocellulose membrane. The membrane is incubated with anti-Obesity and/or diabetes variants antibody for 2 hours and with secondary anti-rabbit antibody for an additional 1 hour.
- 20 Detection of the signal is done using a commercial western blot detection kit.

*trade-mark

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COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

The invention claimed is:

1. An isolated polypeptide coded by nucleotides 112 to 462 of SEQ ID NO:11.
2. The isolated polypeptide of claim 1, wherein said isolated polypeptide has the amino acid sequence of SEQ ID NO:32.
3. An isolated ghrelin variant peptide consisting of amino acids 24-52 of SEQ ID NO:32.
4. The isolated ghrelin variant peptide of claim 3, wherein the amino acid at position number 25 or 26 of SEQ ID NO:32 is acylated.
5. The isolated ghrelin variant peptide of claim 4, wherein the amino acid at position number 25 or 26 of SEQ ID NO:32 is octanoylated.
6. An isolated ghrelin variant peptide consisting of amino acids 24-45 of SEQ ID NO:32.
7. The isolated ghrelin variant peptide of claim 6, wherein the amino acid at position number 25 or 26 of SEQ ID NO:32 is acylated.
8. The isolated ghrelin variant peptide of claim 7, wherein the amino acid at position number 25 or 26 of SEQ ID NO:32 is octanoylated.
9. An isolated ghrelin variant peptide consisting of amino acids 24-47 of SEQ ID NO:32.
10. The isolated ghrelin variant peptide of claim 9, wherein the amino acid at position number 25 or 26 is acylated.
11. The isolated ghrelin variant peptide of claim 10, wherein the amino acid at position number 25 or 26 is octanoylated.
12. An isolated polypeptide comprising the sequence set forth in SEQ ID NO:32, wherein said amino acid sequence has at least one post-translational chemical modification.
13. The isolated polypeptide of claim 12, wherein the amino acid at position number 25 or 26 is acylated.

14. The isolated polypeptide of claim 13, wherein the amino acid at position number 25 or 26 is octanoylated.

15. A pharmaceutical composition comprising a pharmaceutically acceptable carrier and the ghrelin variant peptide of claim 3.

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FIG. 1

SEQID22	MLLLGAVLLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID23	-----	
SEQID24	MLLLGAVLLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID25	MLLLGAVLLLLLALPGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDG	60
SEQID22	TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE	120
SEQID23	-----MPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE	36
SEQID24	TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEA-----	108
SEQID25	TPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLE	120
SEQID22	TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSFLFKKDK	180
SEQID23	TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYMKDVKVSFLFKKDK	96
SEQID24	-----	108
SEQID25	TYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLY-----	158
SEQID22	AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF	237
SEQID23	AMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYAD--NDND-STFTGF	153
SEQID24	-----LLS-PTCPFALPRSSTISKTTMMAP--LVNSTATFLGC	143
SEQID25	-----	158
SEQID22	LLYHDTN-----	244
SEQID23	LLYHDTN-----	160
SEQID24	T----T-LP-TTSQSI-	153
SEQID25	-----LHRLSSLP	166

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FIG. 2

SEQID28	MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG	60
SEQID30	MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGH-----	52
SEQID29	MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG	60
SEQID26	MLLLQALLFLLILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDG	60
SEQID27	-----	
SEQID28	RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-----SL	113
SEQID30	-----	52
SEQID29	RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAA-----	112
SEQID26	RDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAVYRSAFEV	120
SEQID27	-----MTGAEGPRGFPGTPGRKGEPGEAAVYRSAFEV	33
SEQID28	-----	113
SEQID30	-----	52
SEQID29	-----	109
SEQID26	GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLEK	180
SEQID27	GLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLEK	93
SEQID28	-----FPMYP	118
SEQID30	-----IKIK-----FEGHP-----PG-----	63
SEQID29	-----VYRSAFEVGLETRVTVP	129
SEQID26	KDKAVLFTYDQYQEKNVDAQ-----SGSVLLHLEVGDQVWLQ-----	217
SEQID27	KDKAVLFTYDQYQEKNVDAQ-----SGSVLLHLEVGDQVWLQ-----	130
SEQID28	FALLRSSTTNRIIMTAALASSTATFRDSTTSLTTSRCT---	156
SEQID30	--RLNCAKIWHFLQD-----	76
SEQID29	NVPIRFTKIFYNQQN-HYDGSTGKFYCNIPGLYIYWLSSLP	169
SEQID26	--VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----	247
SEQID27	--VYGDGDHNGLYADNVNDSTFTGFLLYHDTN-----	160

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FIG. 3

SEQID31	MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKP-----	44
SEQID32	MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQ-----VRPPHKAPHVV	47
SEQID31	PAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQD	104
SEQID32	PALPLSNQLCDLEQQRHKWASVFSQSTKDSGSDLTVSGRTWGLRV-----	92
SEQID31	ILWEEAKEAPADK-----	117
SEQID32	LNRLFPPSSRERSRRSHQPSCPEL	117

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FIG. 4

SEQID33	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID38	-----MLQGKKVIVTGASKGIGREMAHYHLAKMGAH	30
SEQID36	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID35	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID37	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID39	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID34	MAFMKKYLLPILGLFMAYYYYSANEEFRPEMLQGKKVIVTGASKGIGREMAHYHLAKMGAH	60
SEQID33	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	120
SEQID38	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	90
SEQID36	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	120
SEQID35	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	120
SEQID37	VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	102
SEQID39	VVVTARSKETLQKVVSHCLELGAASAHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	120
SEQID34	VVVTASS-----AHYIAGTMEDMTFAEQFVAQAGKLMGGDLMLILNH	102
SEQID33	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSI VVVSSLAGKVAYPMV	180
SEQID38	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSI VVVSSLAGKVAYPMV	150
SEQID36	ITNTSLNLFHDDIHHVR-----PMLKQSNQSI VVVSSLAGKVAYPMV	162
SEQID35	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSI VVVSSLAGKVAYPMV	180
SEQID37	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSI VVVSSLAGKVAYPMV	162
SEQID39	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSI VVVSSLA-----	172
SEQID34	ITNTSLNLFHDDIHHVRKSMEVNFLSYVVLTVAAALPMLKQSNQSMCAL-----	150
SEQID33	AAYSASKFALDGGFFSSIRKEYSVSRVNV SITLCVLGLIDTETAMKAVSGIVHMQAAPKEE	240
SEQID38	AAYSASKFALDGGFFSSIRKEYSVSRVNV SITLCVLGLIDTETAMKAVSGIVHMQAAPKEE	210
SEQID36	AAYSASKFALDGGFFSSIRKEYSVSRVNV SITLCVLGLIDTETAMKAVSGIVHMQAAPKEE	222
SEQID35	AAYSASKFALDGGFFSSIRKEYSVSRVNV SITLCVLGLIDTETAMKAVSGIVHMQAAPKEE	240
SEQID37	AAYSASKFALDGGFFSSIRKEYSVSRVNV SITLCVLGLIDTETAMKAVSGIVHMQAAPKEE	222
SEQID39	-----ETAMKAVSGIVHMQAAPKEE	192
SEQID34	-----LLECYHVHLSX----	163
SEQID33	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK---	292
SEQID38	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK---	262
SEQID36	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK---	274
SEQID35	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMEGLFCLMFI	295
SEQID37	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK---	274
SEQID39	CALEIIKGGALRQEEVYYDSSLWTTLLIRNPCRKILEFLYSTSYNMDRFINK---	244
SEQID34	-----	

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FIG. 5

SEQID40	MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMG	60
SEQID41	MAVMKNYLLPILVLFLAY-----	18
SEQID42	MAVMKNYLLPILVLFLAYYYYSTNEEFRPEMLQGKKVIVTGASKGIGREMAYHLSKMG	60
SEQID40	VVLTARSEEGLOKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH	120
SEQID41	YYYSTNEEFRLOKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH	78
SEQID42	VVLTARSEEGLOKVVSRCLELGAASAHYIAGTMEDMTFAEQFIVKAGKLMGGDLMLILNH	120
SEQID40	ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGKMTQPMI	180
SEQID41	ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGKMTQPMI	138
SEQID42	ITQTSLSLFHDDIHSVRRVMEVNFLSYVVMSTAALPMLKQSNCSIIVISSLAGGRTVPQQ	180
SEQID40	APYSASKFALDGGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE	240
SEQID41	APYSASKFALDGGFFSTIRTELYITKVNVSITLCVLGLIDTETAMKEISGIINAQASPKEE	198
SEQID42	RSRSVTPDSRGP-----	192
SEQID40	CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN	292
SEQID41	CALEIIKGTALRKSEVYYDKSPLTPILLGNPGRKIMEFFSLRYYNKDMFVSN	250
SEQID42	-----	

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FIG. 6

```

SEQID1      CTGATTCCATACCAGAGGGGCTCAGGATGCTGTTGCTGGGAGCTGTTCTACTGCTATTAG
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CTCTGCCCCGGGCATGACCAGGAAACCACGACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGC
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CCAAGGGGGCCTGCACAGGTTGGATGGCGGGCATCCCAGGGCATCCGGGGCCATAATGGGG
SEQID2      -----
SEQID3      -----
SEQID4      -----

SEQID1      CCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAGAAAGGAGATCCAG
SEQID2      -----ATG-----
SEQID3      -----CTGATTCCAT-----
SEQID4      -----CTGATTCCAT-----
                      **

SEQID1      GTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCG--GGGCTGAAGGTCC
SEQID2      -----ACCCG--GGGCTGAAGGTCC
SEQID3      -----ACCAGAGGGGCTCAGGATGC
SEQID4      -----ACCAGAGGGGCTCAGGATGC
                      *** * ***** * * * *

SEQID1      -----CCGAG-GCT-TTC--CGGG-AAT-----CCAAGGCAGGAA-AGGAGAACCTGG
SEQID2      -----CCGAG-GCT-TTC--CGGG-AAT-----CCAAGGCAGGAA-AGGAGAACCTGG
SEQID3      TGTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
SEQID4      TGTGCTGGGAGCTGTTCTACTGCTATTAGCTCTGCCCGGGCATGACCAGGA-AACCACG
                      * * * * * * * * * * * * * * * * * * * *

SEQID1      A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTTCAGTG-TGGGATTGGA
SEQID2      A--GAAGGTGCCTATGTA----TACCGCT---CA-----GCATTTCAGTG-TGGGATTGGA
SEQID3      ACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
SEQID4      ACTCAAGGGCCCCGGAGTCCTGCTTCCCCTGCCCAAGGGGGCCTGCACAGGTTGGATGGCG
                      * * * * * * * * * * * * * * * *

SEQID1      GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT-----
SEQID2      GACTTACGTTACTATCC---CCAACATG----CCCATTCGCT--TTACCAAGAT-----
SEQID3      GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
SEQID4      GGCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACC
                      * * * * * * * * * * * * * * *

SEQID1      -CTTCT-ACAA---TCAGCAA---AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID2      -CTTCT-ACAA---TCAGCAA---AACCAC-TATGATGGCTCCACTGGTAAATTCCACT
SEQID3      CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGCTTATTGGTCCTAAGGGAGACATCGGT
SEQID4      CCTGGTGAGAAGGGTGAGAAAGGAGATCCAGGCTTATTGGTCCTAAGGGAGACATCGGT
                      ** * * * * * * * * * * * * * * * *

SEQID1      GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID2      GCAAC---ATT--CCTGGGCTGTA---CTACTTTGCCTACCACATCACAGTCTATATGAA
SEQID3      GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG---AATCCA-AGGCA
SEQID4      GAAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGG---AATCCA-AGGCA
                      * * * * * * * * * * * * * * *

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SEQID1 GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID2 GGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGC---TCTTCACCTATGATCA
SEQID3 GGA----AAGGAGAACCT-----GGAGAAGG---TGC-----
SEQID4 GGA----AAGGAGAACCT-----GGAGAAGG---TGCCTATGTATACCGCTCAGCA
*** **** * *** ** * **

SEQID1 GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT
SEQID2 GTACCAGGAAAATAATGTGGACC---AGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGT
SEQID3 -----GTTACTATCC-CCAACATGCCCATTC
SEQID4 TT--CAG-----TGTGGGATTGGAGACTTACGTTACTATCC-CCAACATGCCCATTC
* * * * *

SEQID1 GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID2 GGGCGACCAAG-TCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTG
SEQID3 GCTTTACCAAGATCTT-CTACA-----ATCAGCAAACCACTATGATGG-CTCCA--CTG
SEQID4 GCTTTACCAAGATCTT-CTACA-----ATCAGCAAACCACTATGATGG-CTCCA--CTG
* ***** ** * ** * * * * *

SEQID1 ATAA-TGACAATG---ACTCC-----AC-----
SEQID2 ATAA-TGACAATG---ACTCC-----AC-----
SEQID3 GTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTATA
SEQID4 GTAAATTCCACTGCAACATTCCTGGGCTGTAC-----
*** * ** * * * *

SEQID1 -----
SEQID2 -----
SEQID3 TGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATC
SEQID4 -----

SEQID1 -----
SEQID2 -----
SEQID3 AGTACCAGGAAAATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGG
SEQID4 -----

SEQID1 -----
SEQID2 -----
SEQID3 GCGACCAAGTCTGGCTCCAGGTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATA
SEQID4 -----

SEQID1 -----CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGATCACCAC
SEQID2 -----CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-----
SEQID3 ATGACAATGACTCCACCTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-----
SEQID4 -----CTTCACAGGCTTTCTTCTCTACCATGACACCAACTGA-----

SEQID1 TAACTCAGAGCCTCCTCCAGGCCAAACAGCCCCAAAGTCAATTAAAGGCTTTCAGTACGG
SEQID2 -----
SEQID3 -----
SEQID4 -----

SEQID1 TTAGGAAGTTGATTATTATTTAGTTGGAGGCCTTTAGATATTATTCATTCATTTACTCAT
SEQID2 -----
SEQID3 -----
SEQID4 -----

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FIG. 7

SEQID5	ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC	60
SEQID6	-----GCTCATTTCATCTTTTAATTCA-----	21
SEQID7	ATGAGACCTGGCCACTTTCTCCTCATTTCTGTCTGTACGATTGTCAGTGGATCTGACGAC	60
SEQID8	-----	
SEQID9	-----	
SEQID5	ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCCAG	120
SEQID6	CCCATAAAGGCTTTGAAAATAAGGCTGGAGATGAACTTAT-----AGGAGCCTGCCAGG	76
SEQID7	ACCAAAAGGGCTCAGGATGCTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCCAG	120
SEQID8	-----	
SEQID9	-----	
SEQID5	TCATGCCGAAGATGACGTTACTACAACCTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC	180
SEQID6	CCGTG--GAGAGTGAGGAAGCAGAGATGACGGAGATGATGTCTTTCCTTGTCTGTGA--	132
SEQID7	TCATGCCGAAGATGACGTTACTACAACCTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCACC	180
SEQID8	-----	
SEQID9	-----	
SEQID5	CAAGGGAACCTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC	240
SEQID6	-AATGGATTGTGGGTAGA---GGTTCCGGAGATAATGCCTCTTGCTGGAAACAGT-----	183
SEQID7	CAAGGGAACCTTGTGCAGGTTGGATGGCAGGCATCCCAGGACATCCTGGCCACAATGGCAC	240
SEQID8	-----	
SEQID9	-----	
SEQID5	ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG	300
SEQID6	-CTGGGCAGTTCTGTT---CCCGCCATTC---ACAGAATTCTTCTCACTT---TCTAGG	232
SEQID7	ACCAGGCCGTGATGGCAGAGATGGCACTCCTGGAGAGAAGGGAGAGAAAGGAGATGCAGG	300
SEQID8	-----	
SEQID9	-----	
SEQID5	TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG	360
SEQID6	TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG	292
SEQID7	TCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCCACG	360
SEQID8	-----	
SEQID9	-----	
SEQID5	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG	420
SEQID6	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTATCG	352
SEQID7	GGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGC-----	408
SEQID8	-----	
SEQID9	-----	
SEQID5	CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTTCGCTT	480
SEQID6	CTCAGCGTTCAGTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTTCGCTT	412
SEQID7	-----GTCAGTGTTCCTCAATGTACCCATTTCGCTT	437
SEQID8	-----ATGAGACC--TGGCCACTTTCTCCT	23
SEQID9	-----ATGAGACC--TGGCCACTTTCTCCT	23
	** ** ** * * * * *	

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SEQID5	TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG	540
SEQID6	TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG	472
SEQID7	TACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTACTG	497
SEQID8	CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG	79
SEQID9	CATTTCTGTCTG-TACGATTGTCAG--TGGATCTGACGACACCAAAAG-GGCTCAGGATG * * *** * * * * * * *	79
SEQID5	CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA	600
SEQID6	CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA	532
SEQID7	CAACATTCCGGGACTCTACTACTTCTCTTACCACATCACGGTGTACATGAAAGATGTGAA	557
SEQID8	CTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAGT---CATGCCGAAGATGAC	136
SEQID9	CTACTGTTGCAAGCTCTCCTGTTCTCTTAATCCTGCCAGT---CATGCCGAAGATGAC * * * * * * * * * * *	136
SEQID5	GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTACCTACGACCAGTATCAGGAAAA	660
SEQID6	GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTACCTACGACCAGTATCAGGAAAA	592
SEQID7	GGTGAGCCTCTTCAAGAAGGACAAGGCCGTTCTCTTACCTACGACCAGTATCAGGAAAA	617
SEQID8	GTTACTACAAC---GAAGAGCTAGCTCCTGCTTGGTCCCTCCACCCA---AGGGAAC	189
SEQID9	GTTACTACAAC---GAAGAGCTAGCTCCTGCTTGGTCCCTCCACCCA---AGGGAAC * * * * * * * * * *	189
SEQID5	GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG	720
SEQID6	GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG	652
SEQID7	GAATGTGGACCAGGCCTCTGGCTCTGTGCTCCTCCATCTGGAGGTGGGAGACCAAGTCTG	677
SEQID8	TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACAATG---GCACACC	243
SEQID9	TTGTGCAGGTTGGATGGCAGGCATCCCAGGACATC--CTGGCCACATAA---AAATATA * * * * * * * * * *	243
SEQID5	GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC	780
SEQID6	GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC	712
SEQID7	GCTCCAGGTGTATGGGGATGGGGACCACAATGGACTCTATGCAGATAACGTCAACGACTC	737
SEQID8	AGGCCGTGATGGCAGAGA-TGGCACTCCTGGA---GAGAAGGGAGAGAAAGGA-GATGC	297
SEQID9	ATTC-----GAGG-GGCATCCACCAGG---CCGGCTGAATTGTGCCAA-AATAT * * * * * * * * *	287
SEQID5	TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA	840
SEQID6	TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA	772
SEQID7	TACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGACTGCAACTACCCATAGCCCA	797
SEQID8	AGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGATGTTGGAATGACAGGAGCTGAAGGGCC	357
SEQID9	GGCACTTCCTG-----CAAGATAA----- * * * *	306
SEQID5	TACACCAGGAGAATCATGGAACAGTCGACACACTTTTCAGCTTAGTTTGAGAGATTGATTT	900
SEQID6	TACACCAGGAGAATCATGGAACAGTCGACACACTTTTCAGCTTAGTTTGAGAGATTGATTT	832
SEQID7	TACACCAGGAGAATCATGGAACAGTCGACACACTTTTCAGCTTAGTTTGAGAGATTGATTT	857
SEQID8	ACGGGGCTTCCCCGGAACCCCTGGCAGGAAAGGAGAGCCTGGAGAAGCCGCTTATGTGTA	417
SEQID9	-----	
SEQID5	TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTTATTAAAC	960
SEQID6	TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTTATTAAAC	892
SEQID7	TATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGTACTCACTTGTTTATTAAAC	857
SEQID8	TCGCTCAGCGTTTCACTGTGGGGCTGGAGACCCGCGTCACTGTTCCCAATGTACCCATTCTG	477
SEQID9	-----	
SEQID5	GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA	1020
SEQID6	GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA	952
SEQID7	GACTTTATAAAAAATAATTTGTGTTCCTAGTCCAGAAAAAAGGCACTCCCTGGTCTCCA	977
SEQID8	CTTTACTAAGATCTTCTACAACCAACAGAATCATTATGACGGCAGCACTGGCAAGTTCTA	537
SEQID9	-----	

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SEQID5	CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA	1080
SEQID6	CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA	1012
SEQID7	CGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATTTGGTATGGGGGCTTCACAA	1037
SEQID8	CTGCAACATTCCGGGACTCTACATTTACTGGCTTTCTTCTCTACCATGATACCAACTGAC	597
SEQID9	-----	
SEQID5	TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT	1140
SEQID6	TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT	1072
SEQID7	TATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCTGCTCACTGTACACAAATAT	1097
SEQID8	TGCAACTACCCATAGCCCATACACCAGGAGAATCATGGAACAGTCGACACACTTTCAGCT	657
SEQID9	-----	
SEQID5	TGTTACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG	1200
SEQID6	TGTTACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG	1132
SEQID7	TGTTACATAAACCCTATAATGTAAATATGAAATACAGTGATTACTCTTCTCACAGGCTG	1157
SEQID8	TAGTTTGAGAGATTGATTTTATTGCTTAGTTTGAGAGTCCTGAGTATTATCCACACGTGT	717
SEQID9	-----	
SEQID5	ASTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGGAAAAAAA	1260
SEQID6	AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-----	1184
SEQID7	AGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAGGGATAAATTGG-----	1209
SEQID8	ACTCACTTGTTTCATTAAACGACTTTATAAAAAATAATTTGTGTTCCCTAGTCCAGAAAAA	777
SEQID9	-----	
SEQID5	AAAAAAAAAAGAAAACTTTAGAGCACACTGGCGGCCGTTACTAG-----	1306
SEQID6	-----	
SEQID7	-----	
SEQID8	AGGCACTCCCTGGTCTCCACGACTCTTACATGGTAGCAATAACAGAATGAAAATCACATT	837
SEQID9	-----	
SEQID5	-----	
SEQID6	-----	
SEQID7	-----	
SEQID8	TGGTATGGGGGCTTCACAATATTCGCATGACTGTCTGGAAGTAGACCATGCTATTTTTCT	897
SEQID9	-----	
SEQID5	-----	
SEQID6	-----	
SEQID7	-----	
SEQID8	GCTCACTGTACACAAATATTGTTACATAAACCCTATAATGTAAATATGAAATACAGTGA	957
SEQID9	-----	
SEQID5	-----	
SEQID6	-----	
SEQID7	-----	
SEQID8	TTACTCTTCTCACAGGCTGAGTGTATGAATTCTAAAGACCCATAAGTATTAAAGTGGTAG	1017
SEQID9	-----	
SEQID5	-----	
SEQID6	-----	
SEQID7	-----	
SEQID8	GGATAAATTGG	1028
SEQID9	-----	

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FIG. 8

SEQID10	ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG	60
SEQID11	ACTCTGGATGGGTGCTGTTTAGACAAACGCCGTCTCCTATATAAGACCTGACAGCACAGG	60

SEQID10	CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC	120
SEQID11	CACCACTCCGCCAGGACTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCC	120

SEQID10	CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA	180
SEQID11	CCAGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCA	180

SEQID10	GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAG	240
SEQID11	GGCTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG--GTGAGACCTCCCCACAAAG	238
***** * * * *		
SEQID10	CCACCAGCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGT	300
SEQID11	CCCCACATGTTGTTCAGCCCTGCCACTTAGCAA-CCAGCTCTGT-----GACCT	287
* * * * * * * * * *		
SEQID10	CAAGCAGAAGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGA	360
SEQID11	GGAGCAGCAGCGCCATCTC-TGGGCTTCA-GTCTTCTCCAGAGCACAAAGGACTCTGGG	345
***** * * * * * * * * *		
SEQID10	ATCAAGCTGTCAGGGGTTCAGTACCAGCAGCACAGCC--AGGCCCTGGGGAAGTTTCTTC	418
SEQID11	TCTGACCT--CACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTTC	403
* * * * * * * * * *		
SEQID10	AGGACATCCTCTGGGAAGAG-GCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGC	477
SEQID11	CCCCTTCCAGCAGAGAAAGGAGTCGAAGAAGCC--ACCAGCCAAGCTGCAGCCC-CGAGC	460
* * * * * * * * * *		
SEQID10	CTTACTCACCTCTCTCTAAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGC	537
SEQID11	TCTAGCAGGCTGGCTCC--GCCCGGAAGA-----TGGA-----GGTCAAGCAGA	502
* * * * * * * * * *		
SEQID10	AACTCCCACGACTGTTGTACAAGCTCAGGAGGCGAATAAATGTTCAAACCTGTATGCTGAT	597
SEQID11	AGGGGCAGAGGATGAACTGGAAGTCCGGG---TCGGTACCTCTGCAG-TTTTATGCTTCT	558
* * * * * * * * * *		
SEQID10	GTTCCAAATGGGAATTTATTTCAAAGAGGAAAAGTTAATATTTTACTTTAAAAAAATCAA	657
SEQID11	GTGGCAGCGAGGAGGGTGGGG-----	579
* * * * *		
SEQID10	AATAATAC	665
SEQID11	-----	

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FIG. 9

SEQID15	-----	
SEQID17	GGTGAAAAGGGAAAACCTGCCCAAATCCAGTTTTTGTTCAGTAACTTCCTTTGAGACAA	60
SEQID16	-----	
SEQID12	-----	
SEQID14	-----	
SEQID18	-----	
SEQID13	-----	
SEQID15	-----	
SEQID17	AGTCAGGAATCTGAGAGTAAGCACCTGCTAAGGGTGGGACAGGGGCTCTGTCTGGTATGC	120
SEQID16	-----	
SEQID12	-----	
SEQID14	-----	
SEQID18	-----	
SEQID13	-----	
SEQID15	-----	
SEQID17	CTCTCCCATGTTAAGAGCTAACAATAGTAATGGATAAGTCTCCAGGGCAACCAGGACCAC	180
SEQID16	-----	
SEQID12	-----	
SEQID14	-----	
SEQID18	-----	
SEQID13	-----	
SEQID15	-----	
SEQID17	TTCCAAGCATTCTGTCTTGGGCTGCCTCGAGGGCTCCTCTGTCCTTTGGGGAGTACTGA	240
SEQID16	-----	
SEQID12	-----	
SEQID14	-----	
SEQID18	-----	
SEQID13	-----	
SEQID15	-----	
SEQID17	TTGATGCCTGATGCCCAGAACTGGCCCACTCTGGCTTCTCTTTGGAGCTGTCTCTGCAGG	300
SEQID16	-----	
SEQID12	-----	
SEQID14	-----	
SEQID18	-----	
SEQID13	-----	
SEQID15	-----GCA	3
SEQID17	CGCCTTCTGGCTGCCAGCTCGGTCCTAGCATAAGGGACTTCTTCCTTGGCCTGGGTTTCA	360
SEQID16	-----GCA	3
SEQID12	-----GCA	3
SEQID14	-----GCA	3
SEQID18	-----GCA	3
SEQID13	-----GCA	3

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SEQID15	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
SEQID17	CCTTCTTGTATCAGGTGGCAGACCAGCTGGTTTCAG--TCCCAAATCAG-GTCTTCTGA	416
SEQID16	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
SEQID12	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
SEQID14	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
SEQID18	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
SEQID13	CTGCCTGAGACTACTC--CAGCCTCCCCCGTCCCTGATGTCACAATTCAGAGGCTGCTGC	61
	* ** * * **** * ** * * ** * * * * *	
SEDID15	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
SEQID17	CTCCTCCCAGAAACCAACCACTTCTGAGCAGGAAATC-CTGCCCCTCCCCAAAGAGTGG	475
SEQID16	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
SEQID12	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
SEQID14	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
SEQID18	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
SEQID13	CTGCTTAGGAGGTTGTAGAAAGCTCTG--TAGGTTCTCTCTGTGTGTCTACAGGAGTCT	119
	** * * * * * * * * * * * * * * *	
SEQID15	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
SEQID17	GAAACCGCAAAGGAAGAGAGAGATGAAACAGAAGGAAAGGCAGAGGAGGAGGGAGAGAGA	535
SEQID16	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
SEQID12	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
SEQID14	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
SEQID18	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
SEQID13	TCAG--GCCAGCTCCCTGTCGGATGGCTTTTATGAAAAAATATCTCCTCCCCATTCTGGG	177
	* ** * * * * * * * * *	
SEQID15	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
SEQID17	GAGAAGAGAGAAAAAAGAAAAAGAACATCAATAAAAAGAAAGTCAGATTTGTTTCGAAATC	595
SEQID16	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
SEQID12	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
SEQID14	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
SEQID18	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
SEQID13	GCTCTTCATGGCCTACTACTACTATTCTGCAA-ACGAGGAATTCAGACC-----	225
	* * * * * * * * * * * * * * * *	
SEQID15	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID17	TTGAGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	655
SEQID16	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID12	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID14	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID18	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282
SEQID13	---AGAGATGCTCCAAGGAAAGAAAGTGATTGTACAGGGGCCAGCAAAGGGATCGGAAG	282

SEQID15	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA	342
SEQID17	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA	715
SEQID16	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG-----	336
SEQID12	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA	342
SEQID14	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA	342
SEQID18	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAGGTCAAA	342
SEQID13	AGAGATGGCTTATCATCTGGCGAAGATGGGAGCCCATGTGGTGGTGACAGCGAG-----	336

SEQID15	AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA	402
SEQID17	AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA	775
SEQID16	-----CTCAGCACACTA	348
SEQID12	AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA	402
SEQID14	AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA	402
SEQID18	AGAAACTCTACAGAAGGTGGTATCCCACTGCCTGGAGCTTGGAGCAGCCTCAGCACACTA	402
SEQID13	-----CTCAGCACACTA	348

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SEQID15	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	462
SEQID17	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	835
SEQID16	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	408
SEQID12	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	462
SEQID14	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	462
SEQID18	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA	462
SEQID13	CATTGCTGGCACCATGGAAGACATGACCTTCGCAGAGCAATTTGTTGCCCAAGCAGGAAA *****	408
SEQID15	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	522
SEQID17	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	895
SEQID16	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	468
SEQID12	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	522
SEQID14	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	522
SEQID18	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT	522
SEQID13	GCTCATGGGAGGACTAGACATGCTCATTCTCAACCACATCACCAACACTTCTTTGAATCT *****	468
SEQID15	TTTTTCATGATGATATTCACCATGTGCGC-----	550
SEQID17	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT	955
SEQID16	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT	528
SEQID12	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT	582
SEQID14	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT	582
SEQID18	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT	582
SEQID13	TTTTTCATGATGATATTCACCATGTGCGCAAAAGCATGGAAGTCAACTTCCTCAGTTACGT *****	528
SEQID15	-----CCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	588
SEQID17	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	1015
SEQID16	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	588
SEQID12	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	642
SEQID14	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	642
SEQID18	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCATTGTTGTCGT	642
SEQID13	GGTCCTGACTGTAGCTGCCTTGCCCATGCTGAAGCAGAGCAATGGAAGCAT-----GT ***** **	581
SEQID15	CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT	647
SEQID17	CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT	1074
SEQID16	CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT	647
SEQID12	CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT	701
SEQID14	CTCCTCTCTGGCTGGGAAAGTGGCTTATCCAATGGTTGCTGCC-TATTCTGCAAGCAAGT	701
SEQID18	CTCCTCTCTGGCTG-----	656
SEQID13	GCGCTCTTCTGCTGGAA-----TGCTATCATGTTGTGCATCTGAGC **** *	622
SEQID15	TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG	707
SEQID17	TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG	1134
SEQID16	TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG	707
SEQID12	TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG	761
SEQID14	TTGCTTTGGATGGGTTCTTCTCCTCCATCAGAAAGGAATATTCAGTGTCCAGGGTCAATG	761
SEQID18	-----	
SEQID13	A-GTNGTTGATGG-----TCTCTCTCAT----AGAAGATATCAGG----CAGGCATGATA	668
SEQID15	TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT	766
SEQID17	TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT	1193
SEQID16	TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT	766
SEQID12	TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT	820
SEQID14	TATCAATCACTCTCTGTGTTCTTGGCCTCATAGACACAGAAACAGCCATG-AAGGCAGTT	820
SEQID18	-----AAACAGCCATG-AAGGCAGTT	676
SEQID13	TACT-----TTGGTCTGCTATACCAGACGCTAGGCGTCTGATGCA--- *****	708

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SEQID15	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	826
SEQID17	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	1253
SEQID16	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	826
SEQID12	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	880
SEQID14	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	880
SEQID18	TCTGGGATAGTCCATATGCAAGCAGCTCCAAAGGAGGAATGTGCCCTGGAGATCATCAA	736
SEQID13	-----	
SEQID15	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	886
SEQID17	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	1313
SEQID16	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	886
SEQID12	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	940
SEQID14	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	940
SEQID18	GGGGGAGCTCTGCGCCAAGAAGAAGTGTATTATGACAGCTCACTCTGGACCACTCTTCTG	796
SEQID13	-----	
SEQID15	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC	946
SEQID17	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC	1373
SEQID16	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC	946
SEQID12	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC	1000
SEQID14	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGA-	999
SEQID18	ATCAGAAATCCATGCAGGAAGATCCTGGAATTTCTCTACTCAACGAGCTATAATATGGAC	856
SEQID13	-----	
SEQID15	AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG	1006
SEQID17	AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG	1433
SEQID16	AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG	1006
SEQID12	AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG	1060
SEQID14	-----GGGACTG	1006
SEQID18	AGATTCATAAACAAGTAGGAACTCCCTGAGGGCTGGGCATGCTGAGGGATTTTGGGACTG	916
SEQID13	-----	
SEQID15	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	1066
SEQID17	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	1493
SEQID16	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	1066
SEQID12	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	1120
SEQID14	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	1066
SEQID18	TTCTGTCTCATGTTTATCTGAGCTCTTATCTATGAAGACATCTTCCCAGAGTGTCCCCAG	976
SEQID13	-----	
SEQID15	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1126
SEQID17	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1553
SEQID16	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1126
SEQID12	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1180
SEQID14	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1126
SEQID18	AGACATGCAAGTCATGGGTACACCTGACAAATGGAAGGAGTTCCCTCTAACATTTGCAAA	1036
SEQID13	-----	
SEQID15	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1186
SEQID17	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1613
SEQID16	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1186
SEQID12	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1240
SEQID14	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1186
SEQID18	ATGGAAATGTAATAATAATGAATGTCATGCACCGCTGCAGCCAGCAGTTGTAAAATTGTT	1096
SEQID13	-----	

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SEQID15	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1246
SEQID17	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1673
SEQID16	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1246
SEQID12	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1300
SEQID14	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1246
SEQID18	AGTAAACATAGGTATAATTACCAGATAGTTATATTAAATTTATATCTTATATATAATAAT	1156
SEQID13	-----	

SEQID15	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1306
SEQID17	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1733
SEQID16	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1306
SEQID12	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1360
SEQID14	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1306
SEQID18	ATGTGATGATTAATACAATATTAATTATAATAAAGGTCACATAAACTTTATAAATTCATA	1216
SEQID13	-----	

SEQID15	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1366
SEQID17	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1793
SEQID16	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1366
SEQID12	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1420
SEQID14	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1366
SEQID18	ACTGGTAGCTATAACTTGAGCTTATTCAGGATGGTTTCTTTAAAACCATAAACTGTACAA	1276
SEQID13	-----	

SEQID15	ATGAAATTTTTCATATTTGTTTCTTAT	1394
SEQID17	ATGAAATTTTTCATATTTGTTTCTTAT	1821
SEQID16	ATGAAATTTTTCATATTTGTTTCTTAT	1394
SEQID12	ATGAAATTTTTCATATTTGTTTCTTAT	1448
SEQID14	ATGAAATTTTTCATATTTGTTTCTTAT	1394
SEQID18	ATGAAATTTTTCATATTTGTTTCTTAT	1304
SEQID13	-----	

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FIG. 10

SEQID19	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID20	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60
SEQID21	ACTGTTGGCCTCTGGAWTCAGAGGCTGCTGCCTGCCTGGGAGGTTGTAGAAAGCTCTGCA	60

SEQID19	GGTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT	120
SEQID20	GGTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT	120
SEQID21	GGTTTCTTCGTGTGTCTACAGGGCGCCCTGAGCCAGGTCCCTGTTTGATGGCAGTTAT	120

SEQID19	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA	180
SEQID20	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA	180
SEQID21	GAAAAATTACCTCCTCCCGATCCTGGTGCTCTTCCTGGCCTACTACTACTATTCTACAAA	180

SEQID19	TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA	240
SEQID20	TGAAGAGTTCAGAC-----	194
SEQID21	TGAAGAGTTCAGACCAGAAATGCTCCAGGGAAAGAAAGTGATTGTCACTGGGGCCAGCAA	240

SEQID19	AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC	300
SEQID20	-----	
SEQID21	AGGGATTGGAAGAGAAATGGCATATCATCTGTCAAAAATGGGAGCCCATGTGGTATTGAC	300
SEQID19	TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACCTCGGAGCAGC	360
SEQID20	-----TCCAGAAGGTAGTGTCTCGCTGCCTTGAACCTCGGAGCAGC	234
SEQID21	TGCCAGGTCGGAGGAAGGTCTCCAGAAGGTAGTGTCTCGCTGCCTTGAACCTCGGAGCAGC	360

SEQID19	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	420
SEQID20	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	294
SEQID21	CTCTGCTCACTACATTGCTGGCACTATGGAAGACATGACATTGCGGAGCAATTTATTGT	420

SEQID19	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	480
SEQID20	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	354
SEQID21	CAAGGCGGGAAAGCTCATGGGCGGACTGGACATGCTTATTCTAAACCACATCACTCAGAC	480

SEQID19	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540
SEQID20	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	414
SEQID21	CTCGCTGTCTCTCTTCCATGACGACATCCACTCTGTGCGAAGAGTCATGGAGGTCAACTT	540

SEQID19	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600
SEQID20	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	474
SEQID21	CCTCAGCTACGTGGTCATGAGCACAGCCGCCTTGCCCATGCTGAAGCAGAGCAATGGCAG	600

SEQID19	CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	660
SEQID20	CATTGCCGTCATCTCCTCCTTGGCTGGGAAAATGACCCAGCCTATGATTGCTCCCTACTC	534
SEQID21	CATTGCCGTCATCTCCTCCTTGGCTGGGGGAA-GAACAGTTCACAACAGAGA---AGTC	656

SEQID19	TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC	720
SEQID20	TGCAAGCAAGTTTGCTCTGGATGGGTTCTTTTCCACCATTAGAACAGAACTCTACATAAC	594
SEQID21	-----GCAGTGTTACTCCTGAC-----TCCCGC-----GGCCCGTGATTAATATCAC	754

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SEQID19	CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT	780
SEQID20	CAAGGTCAACGTGTCCATCACTCTCTGTGTCCTTGGCCTCATAGACACAGAAACAGCTAT	654
SEQID21	CAGCCACAGAATGGAC-TGGAACCCTGTATC---GATCTGGTGGGATTGGATATAACGAA ** ** * * * * * * * * *	754
SEQID19	GAAGGAA--ATCTCTGGGATAAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG	838
SEQID20	GAAGGAA--ATCTCTGGGATAAATTAACGCCCAAGCTTCTCCCAAGGAGGAGTGCGCCCTG	712
SEQID21	CATAGAATTACTCCTGAGACTACCAGAACTGAA---TAGTTCAAATCAAATCATGCC--- * *** * *** * * * * *** * ***	808
SEQID19	GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG	898
SEQID20	GAGATCATCAAAGGCACAGCTCTACGCAAAAGCGAGGTGTACTATGACAAATCGCCTTTG	772
SEQID21	-AGAATATC--AGACAAATCCAAATGGCAAAAC-AGTTGCA----- *** *** * * * * * * * * * *	845
SEQID19	ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTTCATTACGATAT	958
SEQID20	ACTCCAATCCTGCTTGGGAACCCAGGAAGGAAGATCATGGAATTTTTTTTCATTACGATAT	832
SEQID21	-----	
SEQID19	TATAATAAGGACATGTTTGTAAGTAAGTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG	1018
SEQID20	TATAATAAGGACATGTTTGTAAGTAAGTAGGAACTCCTGAGCCCTGGTGAGTGGTCTTAG	892
SEQID21	-----	
SEQID19	AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA	1078
SEQID20	AACAGTCCTGCCTGATACTTCTGTAAGCCCTACCCACAAAAGTATCTTTCCAGAGATACA	952
SEQID21	-----	
SEQID19	CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGACAGTGAAAATGT	1138
SEQID20	CAAATTTTGGGGTACACCTCATCATGAGAAATTCTTGCAACACTTGACAGTGAAAATGT	1012
SEQID21	-----	
SEQID19	AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTA ACTA	1198
SEQID20	AATTGTAATAAATGTCACAAACCACTTTGGGGCCTGCAGTTGTGAACTTGATTGTA ACTA	1072
SEQID21	-----	
SEQID19	TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA	1258
SEQID20	TGGATATAAACACATAGTGGTTGTATCGGCTTTACCTCACACTGAATGAAACAATGATAA	1132
SEQID21	-----	
SEQID19	CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA	1307
SEQID20	CTAATGTAACATTAAATATAATAAAGGTAATATCAACTTTGTAAATGCA	1181
SEQID21	-----	