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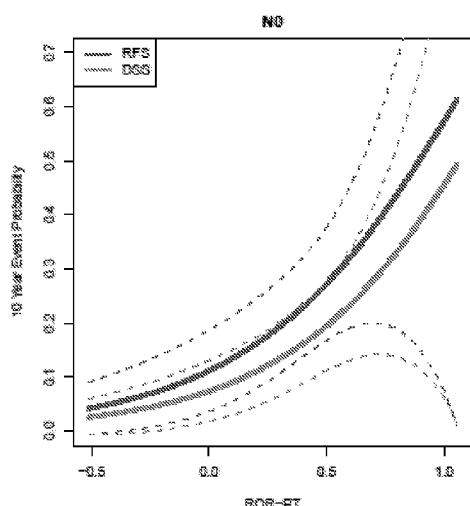
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[Continued on next page]

(54) Title: NANO46 GENES AND METHODS TO PREDICT BREAST CANCER OUTCOME

Figure 4

(57) Abstract: The present invention provides methods for
classifying and for evaluating the prognosis of a subject
having breast cancer are provided. The methods include
prediction of breast cancer subtype using a supervised al-
gorithm trained to stratify subjects on the basis of breast
cancer intrinsic subtype. The prediction model is based on
the gene expression profile of the intrinsic genes listed in
Table 1. Further provided are compositions and methods for
predicting outcome or response to therapy of a subject dia-
gnosed with or suspected of having breast cancer. These
methods are useful for guiding or determining treatment op-
tions for a subject afflicted with breast cancer. Methods of
the invention further include means for evaluating gene ex-
pression profiles, including microarrays and quantitative
polymerase chain reaction assays, as well as kits comprising
reagents for practicing the methods of the invention.



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NANO46 GENES AND METHODS TO PREDICT BREAST CANCER OUTCOME**CROSS-REFERENCE TO RELATED APPLICATIONS**

[01] This application claims the benefit of U.S. Provisional Application No. 61/650,209, filed May 22, 2012 and U.S. Provisional Application No. 61/753,673, filed January 17, 2013. The contents of each of these applications are incorporated herein by reference in their entireties.

FIELD OF THE INVENTION

[02] This disclosure relates generally to the field of cancer biology, and specifically, to the fields of detection and identification of specific cancer cell phenotypes and correlation with appropriate therapies.

BACKGROUND OF THE INVENTION

[03] Current approaches to treating early breast cancer, including adjuvant therapy, have indeed improved survival and reduced recurrence. However, the risk of recurrence may be underestimated in some patients, but overestimated in others.

[04] While the risk of recurrence does diminish somewhat over time, ongoing risk has been observed in many studies, some of them involving tens of thousands of patients with breast cancer. In fact, some of the patients who experienced recurrence after five years in these studies had previously been considered "low risk" - for example, their cancer had not spread to the lymph nodes at the time of their initial diagnosis, or their estrogen receptor status was positive. In one of these studies, a substantial number of recurrences occurred more than five years post-treatment. Thus, there is a need in the art to determine risk of recurrence and determine therapies which reduce that risk and improve overall survival.

SUMMARY OF THE INVENTION

[05] The present invention provides a method of predicting outcome in a subject having breast cancer comprising: providing a tumor sample from the subject; determining the expression of the genes in the NANO46 intrinsic gene list of Table 1 in the tumor sample; measuring the similarity of the tumor sample to an intrinsic subtype based on the expression of the genes in the NANO46 intrinsic gene list, wherein the intrinsic subtype consists of at least Basal-like, Luminal A, Luminal B or HER2-enriched; determining a proliferation score based on the expression of a subset of proliferation genes in the NANO46 intrinsic gene list;

determining the size of the tumor, calculating a risk of recurrence score using a weighted sum of said intrinsic subtype, proliferation score and tumor size; and determining whether the subject has a low or high risk of recurrence based on the recurrence score. In one embodiment a low score indicates a more favorable outcome and high score indicates a less favorable outcome.

[06] The methods of the present invention can include determining the expression of at least one of, a combination of, or each of, the NANO46 intrinsic genes recited in Table 1. In some embodiments, the methods of the present invention can include determining the expression of at least one of, a combination of, or each of, the NANO46 intrinsic genes selected from ANLN, CCNE1, CDC20, CDC6, CDCA1, CENPF, CEP55, EXO1, KIF2C, KNTC2, MELK, MKI67, ORC6L, PTTG1, RRM2, TYMS, UBE2C and/or UBE2T. The expression of the members of the NANO46 intrinsic gene list can be determined using the nanoreporter code system (nCounter® Analysis system).

[07] The methods of the present invention can include determining at least one of, a combination of, or each of, the following: tumor size, tumor grade, nodal status, intrinsic subtype, estrogen receptor expression, progesterone receptor expression, and HER2/ERBB2 expression

[08] The sample can be a sampling of cells or tissues. The sample can be a tumor. The tissue can be obtained from a biopsy. The sample can be a sampling of bodily fluids. The bodily fluid can be blood, lymph, urine, saliva or nipple aspirate.

[09] While the disclosure has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the disclosure, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

[10] The patent and scientific literature referred to herein establishes the knowledge that is available to those with skill in the art. All United States patents and published or unpublished United States patent applications cited herein are incorporated by reference. All published foreign patents and patent applications cited herein are hereby incorporated by reference. Genbank and NCBI submissions indicated by accession number cited herein are hereby incorporated by reference. All other published references, documents, manuscripts and scientific literature cited herein are hereby incorporated by reference.

[11] While this disclosure has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the

scope of the disclosure encompassed by the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

- [12] Figure 1 is a heatmap of the breast cancer intrinsic subtypes and the intrinsic genes of Table 1.
- [13] Figure 2 shows a Kaplan Meier survival curves from a cohort of untreated breast cancer patients.
- [14] Figure 3 shows a Kaplan Meier survival curves from a cohort of node-negative, ER+ Breast Cancer Patients treated with tamoxifen.
- [15] Figure 4 shows a 10 Year event probability as a function of ROR Score in ER+, Node-negative breast cancer patients treated with tamoxifen. The graph shows the sub-population subtyped as Luminal A or B within this population. RFS = Recurrence-free survival; DSS = disease-specific survival
- [16] Figure 5 is a schematic of the breast cancer intrinsic subtyping assay.
- [17] Figure 6 is a schematic of the algorithm process.
- [18] Figure 7 is an illustration showing the hybridization of the CodeSet to mRNA.
- [19] Figure 8 is an illustration showing the removal of excess reporters.
- [20] Figure 9 is an illustration showing the binding of the reporters to the surface of a cartridge.
- [21] Figure 10 is an illustration showing the immobilization and alignment of a reporter.
- [22] Figure 11 is an illustration of data collection.
- [23] Figure 12 is an illustration of the nCounter analysis system breast cancer test assay process.
- [24] Figure 13 is an illustration of the nCounter Prep Station.
- [25] Figure 14 is an illustration of nCounter Digital Analyzer.

DETAILED DESCRIPTION OF THE INVENTION

- [26] The disclosure presents a method of predicting outcome in a subject having breast cancer comprising: providing a tumor sample from the subject; determining the expression of the genes in the NANO46 intrinsic gene list of Table 1 in the tumor sample; determining the intrinsic subtype of the tumor sample based on the expression of the genes in the NANO46 intrinsic gene list, wherein the intrinsic subtype consists of at least Basal-like, Luminal A, Luminal B or HER2-enriched; determining a proliferation score based on the expression of a subset of proliferation genes in the NANO46 intrinsic gene list; determining the size of the

tumor, calculating a risk of recurrence score using a weighted sum of said intrinsic subtype, proliferation score and tumor size; and determining whether the subject has a low or high risk of recurrence based on the recurrence score. In one embodiment a low score indicates a more favorable outcome and high score indicates a less favorable outcome.

[27] Intrinsic genes are statistically selected to have low variation in expression between biological sample replicates from the same individual and high variation in expression across samples from different individuals. Thus, intrinsic genes are used as classifier genes for breast cancer classification. Although clinical information was not used to derive the breast cancer intrinsic subtypes, this classification has proved to have prognostic significance. Intrinsic gene screening can be used to classify breast cancers into five molecular distinct intrinsic subtypes, Luminal A (LumA), Luminal B (LumB), HER2-enriched (Her-2-E), Basal-like, and Normal-like (Perou *et al.* Nature, 406(6797):747-52 (2000); Sorlie *et al.* PNAS, 98(19):10869-74 (2001)).

[28] A NANO46 gene expression assay, as described herein, can identify intrinsic subtype from a biological sample, e.g., a standard formalin fixed paraffin embedded tumor tissue. The methods utilize a supervised algorithm to classify subject samples according to breast cancer intrinsic subtype. This algorithm, referred to herein as the NANO46 classification model, is based on the gene expression profile of a defined subset of intrinsic genes that has been identified herein as superior for classifying breast cancer intrinsic subtypes. The subset of genes, along with primers target-specific sequences utilized for their detection, is provided in Table 1. Table 1A provides the sequences of target specific probe sequences for detecting each gene utilized in Table 1. The sequences provided in Table 1A are merely representative and are not meant to limit the invention. The skilled artisan can utilize any target sequence-specific probe for detecting any of (or each of) the genes in Table 1.

[29] Table 1

GENE	REPRESENTATIVE GENBANK ACCESSION NUMBER	FORWARD PRIMER	SEQ ID NO:	REVERSE PRIMER	SEQ ID NO:
ACTR3B	NM_020445 NM_001040135	AAAGATTCTGGG ACCTGA	1	TGGGGCAGTTCTGTA TTACTTC	47
ANLN	NM_018685	ACAGCCACTTTCA GAAGCAAG	2	CGATGGTTTTGTACA AGATTTCTC	48
BAG1	NM_004323	CTGGAAGAGTTGA ATAAAGAGC	3	GCAAATCCTTGGGC AGA	49
BCL2	NM_000633	TACCTGAACCGGC ACCTG	4	GCCGTACAGTTCCAC AAAGG	50
BLVRA	BX647539	GCTGGCTGAGCAG AAAG	5	TTCTCCATCAAGAG TTCAACA	51
CCNE1	BC035498	GGCCAAAATCGAC AGGAC	6	GGGTCTGCACAGAC TGCAT	52
CDC20	BG256659	CTGTCTGAGTGCC GTGGAT	7	TCCTTGTAATGGGGA GACCA	53
CDC6	NM_001254	GTAAATCACCTTC TGAGCCT	8	ACTTGGGATATGTGA ATAAGACC	54
CDCA1	NM_031423	GGAGGCGGAAGA AACCAG	9	GGGGAAGACAAAG TTTCCA	55
CDH3	BC041846	GACAAGGAGAAT CAAAAGATCAGC	10	ACTGTCTGGGTCCAT GGCTA	56
CENPF	NM_016343	GTGGCAGCAGATC ACAA	11	GGATTTTCGTGGTGGG TTC	57
CEP55	AB091343	CCTCACGAATTGC TGAACCTT	12	CCACAGTCTGTGATA AACGG	58
CXXC5	BC006428	CATGAAATAGTGC ATAGTTTGCC	13	CCATCAACATTCTCT TTATGAACG	59
EGFR	NM_005228	ACACAGAATCTAT ACCCACCAGAGT	14	ATCAACTCCCAAAC GGTCAC	60
ERBB2	NM_001005862	GCTGGCTCTCACA CTGATAG	15	GCCCTTACACATCGG AGAAC	61
ESR1	NM_001122742	GCAGGGAGAGGA GTTTGT	16	GACTTCAGGGTGCTG GAC	62
EXO1	NM_130398	CCCATCCATGTGA GGAAGTATAA	17	TGTGAAGCCAGCAA TATGTATC	63
FGFR4	AB209631	CTTCTTGACCTT GGCG	18	TATTGGGAGGCAGG AGGTTTA	64
FOXA1	NM_004496	GCTACTACGCAGA CACG	19	CTGAGTTCATGTTGC TGACC	65
FOXC1	NM_001453	GATGTTTCGAGTCA CAGAGG	20	GACAGCTACTATTCC CGTT	66
GPR160	AJ249248	TTCGGCTGGAAGG AACC	21	TATGTGAGTAAGCTC GGAGAC	67
HSPC150 (UBE2T)	NM_014176	GGAGATCCGTCAA CTCCAAA	22	AGTGGACATGCGAG TGGAG	68
KIF2C	NM_006845	TGGGTCTGTGTCAG GAAAC	23	CACCGCTGGAAACT GAAC	69

KNTC2	NM_006101	CGCAGTCATCCAG AGATGTG	24	CGTGCACATCCATGA CCTT	70
KRT14	BC042437	ACTCAGTACAAGA AAGAACCG	25	GAGGAGATGACCTT GCC	71
KRT17	AK095281	GTTGGACCAGTCA ACATCTCTG	26	GCCATAGCCACTGCC ACT	72
KRT5	M21389	TGTGGGCTCATTAG GCAAC	27	CTTCGACTGGACTCT GT	73
MAPT	NM_001123066	GACTCCAAGCGCG AAAAC	28	CAGACATGTTGGTAT TGCACATT	74
MDM2	M92424	CCACAAAATATTC ATGGTTCTTG	29	AGGCGATCCTGGGA AATTAT	75
MELK	NM_014791	CCAGTAGCATTGT CCGAG	30	CCCATTGTCTGTCT TCAC	76
MIA	BG765502	GTCTCTGGTAATG CACACT	31	CTGATGGTTGAGGCT GTT	77
MKI67	NM_002417	GTGGAATGCCTGC TGACC	32	CGCACTCCAGCACCT AGAC	78
MLPH	NM_024101	AGGGGTGCCCTCT GAGAT	33	TCACAGGGTCAAAC TTCCAGT	79
MMP11	NM_005940	CGAGATCGCCAAG ATGTT	34	GATGGTAGAGTTCC AGTGATT	80
MYC	NM_002467	AGCCTCGAACAAT TGAAGA	35	ACACAGATGATGGA GATGTC	81
NAT1	BC013732	ATCGACTGTGTAA ACAAC TAGAGAA GA	36	AGTAGCTACATCTCC AGGTTCTCTG	82
ORC6L	NM_014321	TTTAAGAGGGCAA ATGGAAGG	37	CGGATTTTATCAACG ATGCAG	83
PGR	NM_000926	TGCCGCAGAACTC ACTTG	38	CATTTGCCGTCCTTC ATCG	84
PHGDH	AK093306	CCTCAGATGATGC CTATCCA	39	GCAGGTCAAACTC TCAAAG	85
PTTG1	BE904476	CAGCAAGCGATGG CATAGT	40	AGCGGGCTTCTGTAA TCTGA	86
RRM2	AK123010	AATGCCACCGAAG CCTC	41	GCCTCAGATTTCAAC TCGT	87
SFRP1	BC036503	TCGAACTGAAGGC TATTTACGAG	42	CTGCTGAGAATCAA AGTGGGA	88
SLC39A6	NM_012319	GTCGAAGCCGCAA TTAGG	43	GGAACAAACTGCTC TGCCA	89
TMEM45B	AK098106	CAAACGTGTGTTC TGGAGG	44	ACAGCTCTTTAGCAT TTGTGGA	90
TYMS	BQ56428	TGCCCTGTATGAT GTCAGGA	45	GGGACTATCAATGTT GGGTTCTC	91
UBE2C	BC032677	GTGAGGGGTGTCA GCTCAGT	46	CACACAGTTCACTGC TCCACA	92

Table 1a. Probes for detecting NANO46 genes

Gene Name	RefSeq Accession	Target Sequence	SEQ ID NO:
ACTR3B	NM_001040135.1	CCAGAAGAAGTTTGTATAGACGTTGGTTACG AAAGATTCTCTGGGACCTGAAATATTCTTTCAC CCGGAGTTTGCCAACCCAGACTTTATGGAGTC CATC	140
ANLN	NM_018685.2	CGTGCCAGGCGAGAGAATCTTCAGAGAAAAA TGGCTGAGAGGCCACAGCAGCTCCAAGGTC TATGACTCATGCTAAGCGAGCTAGACAGCCA CTTTCAG	141
BAG1	NM_004323.3	CTTCATGTTACCTCCCAGCAGGGCAGCAGTGA ACCAGTTGTCCAAGACCTGGCCCAGGTTGTTG AAGAGGTCATAGGGGTTCCACAGTCTTTTCAG AAAC	142
BCL2	NM_000633.2	CCAAGCACCGCTTCGTGTGGCTCCACCTGGAT GTTCTGTGCCTGTAAACATAGATTGCTTTCC ATGTTGTTGGCCGGATCACCATCTGAAGAGCA GACG	143
BLVRA	NM_000712.3	TTCTGAAAAAAGAAGTGGTGGGGAAAGACC TGCTGAAAGGGTCGCTCCTCTTCACAGCTGGC CCGTTGGAAGAAGAGCGGTTTGGCTTCCCTGC ATTCA	144
CCNE1	NM_001238.1	GAGAACTGTGTCAAGTGGATGGTTCCATTTCG CATGGTTATAAGGGAGACGGGGAGCTCAAAA CTGAAGCACTTCAGGGGCGTCGCTGATGAAG ATGCAC	145
CDC20	NM_001255.1	CCCGAGTGGGCTCCCTAAGCTGGAACAGCTA TATCCTGTCCAGTGGTTCACGTTCTGGCCACA TCCACCACCATGATGTTCTGGGTAGCAGAACA CCATGT	146
CDC6	NM_001254.3	GGGGAAGTTATATGAAGCCTACAGTAAAGTC TGTCGCAAACAGCAGGTGGCGGCTGTGGACC AGTCAGAGTGTTTGTCACTTCAGGGCTCTTG GAAGCC	147
CDCA1	NM_145697.1	GCCTGGCGGTGTTTTTCGTGCTGCTCAGCGGTG GGAGGAGGCGGAAGAAACCAGAGCCTGGGA GATTAACAGGAAACTTCCAAGATGGAAACTT TGTCTTT	148
CDH3	NM_001793.3	CCCTCGACCGTGAGGATGAGCAGTTTGTGAG GAACAACATCTATGAAGTCATGGTCTTGGCCA TGGACAATGGAAGCCCTCCCACCACTGGCAC GGGAAC	149
CENPF	NM_016343.3	AGAAATCTTGCAGAGTCCTCCAAACCAACA GCTGGTGGCAGCAGATCACAAAAGGTCAAAG TTGCTCAGCGGAGCCCAGTAGATTCAGGCAC CATCCTC	150
CEP55	NM_018131.3	GTACTACCGCATTGCTTGAACAGCTGGAAGA GACAACGAGAGAAGGAGAAAGGAGGGAGCA GGTGTGAAAGCCTTATCTGAAGAGAAAGAC GTATTGAA	151
CXXC5	NM_016463.5	AGCTGCCCTCTCCGTGCAATGTCAGTCTCGT GTGGTCTCCAGCAAGGGATTTCGGGCGAAGAC AAACGGATGCACCCGTCCTTAGAACCAAAAA TATTCT	152
EGFR	NM_005228.3	GCAGCCAGGAACGTACTGGTGAAAACACCGC AGCATGTCAAGATCACAGATTTTGGGCTGGCC AAACTGCTGGGTGCGGAAGAGAAAGAATACC	153

		ATGCAG	
ERBB2	NM_004448.2	TGAAGGTGCTTGGATCTGGCGCTTTTGGCACA GTCTACAAGGGCATCTGGATCCCTGATGGGG AGAATGTGAAAATTCCAGTGGCCATCAAAGT GTTGAG	154
ESR1	NM_000125.2	AGGAACCAGGAAAATGTGTAGAGGGCATGG TGGAGATCTTCGACATGCTGCTGGCTACATCA TCTCGGTTCCGCATGATGAATCTGCAGGGAGA GGAGT	155
EXO1	NM_006027.3	TGGCCCACAAAGTAATTAAAGCTGCCCCGGTCT CAGGGGGTAGATTGCCTCGTGGCTCCCTATGA AGCTGATGCGCAGTTGGCCTATCTTAACAAAG CGGG	156
FGFR4	NM_002011.3	CCCACATCCAGTGGCTGAAGCACATCGTCATC AACGGCAGCAGCTTCGGAGCCGACGGTTTCC CCTATGTGCAAGTCCTAAAGACTGCAGACATC AATAG	157
FOXA1	NM_004496.2	TGGATGGTTGTATTGGGCAGGGTGGCTCCAG GATGTTAGGAAGTGTGAAGATGGAAGGGCAT GAAACCAGCGACTGGAACAGCTACTACGCAG ACACGCA	158
FOXC1	NM_001453.1	TTCGAGTCACAGAGGATCGGCTTGAACAAC CTCCAGTGAACGGGAATAGTAGCTGTCAAAT GGCCTTCCCTTCCAGCCAGTCTCTGTACCGCA CGTCCG	159
GPR160	NM_014373.1	GGATTTCAAGTCCTTGCTTATGTTTTGGGAGAC CCAGCCATCTACCAAAGCCTGAAGGCACAGA ATGCTTATTCTCGTCACTGTCTTTCTATGTCA GCAT	160
UBE2T	NM_014176.1	GTGTCAGCTCAGTGCATCCCAGGCAGCTCTTA GTGTGGAGCAGTGAAGTGTGTGTGGTTCCTTC TACTTGGGGATCATGCAGAGAGCTTCACGTCT GAAG	161
KIF2C	NM_006845.2	GTTGTCTACAGGTTACAGCAAGGCCACTGGT ACAGACAATCTTTGAAGGTGGAAAAGCAACT TGTTTTGCATATGGCCAGACAGGAAGTGGCA AGACAC	162
KNTC2	NM_006101.1	AAAAGGTCATAAGCATGAAGCGCAGTTCAGT TTCCAGCGGTGGTGCTGGCCGCCTCTCCATGC AGGAGTTAAGATCCCAGGATGTAAATAAACA AGGCCT	163
KRT14	NM_000526.3	GCAGTCATCCAGAGATGTGACCTCCTCCAGCC GCCAAATCCGCACCAAGGTCATGGATGTGCA CGATGGCAAGGTGGTGTCCACCCACGAGCAG GTCCTT	164
KRT17	NM_000422.1	CTGACTCAGTACAAGAAAGAACCGGTGACCA CCCGTCAGGTGCGTACCATTGTGGAAGAGGT CCAGGATGGCAAGGTCATCTCCTCCCGCGAG CAGGTCC	165
KRT5	NM_000424.2	CTGGTTCTCTTGCTCCACCAGGAACAAGCCAC CATGTCTCGCCAGTCAAGTGTGTCTTCCGGA GCGGGGGCAGTCGTAGCTTCAGCACCGCCTCT GCCA	166
MAPT	NM_016835.3	GCCGGGTCCCTCAACTCAAAGCTCGCATGGTC AGTAAAAGCAAAGACGGGACTGGAAGCGATG ACAAAAAAGCCAAGACATCCACACGTTCCCTC TGCTAA	167

MDM2	NM_006878.2	GGTGAGGAGCAGGCAAATGTGCAATACCAAC ATGTCTGTACCTACTGATGGTGCTGTAACCAC CTCACAGATTCCAGCTTCGGAACAAGAGACC CTGGTT	168
MELK	NM_014791.2	AGAGACAGCCAACAAAATATTCATGGTTCTT GAGTACTGCCCTGGAGGAGAGCTGTTTGACT ATATAATTTCCCAGGATCGCCTGTCAGAAGAG GAGACC	169
MIA	NM_006533.1	CCGGGGCCAAGTGGTGTATGTCTTCTCCAAGC TGAAGGGCCGTGGGCGGCTCTTCTGGGGAGG CAGCGTTCAGGGAGATTACTATGGAGATCTG GCTGCT	170
MKI67	NM_002417.2	GCTTCCAGCAGCAAATCTCAGACAGAGGTTT CTAAGAGAGGAGGAGAAAGAGTGGAACCTG CCTTCAAAAGAGAGTGTCTATCAGCCGAAGT CAACATG	171
MLPH	NM_024101.4	GAGGAAGTCAAACCTCCCGATATTTCTCCCTC GAGTGGCTGGGAACTTGGCAAGAGACCAGA GGACCCAAATGCAGACCCTTCAAGTGAGGCC AAGGCA	172
MMP11	NM_005940.3	AGCAGCCAAGGCCCTGATGTCCGCCTTCTACA CCTTTCGCTACCCACTGAGTCTCAGCCCAGAT GACTGCAGGGGCGTTCAACACCTATATGGCC AGCCC	173
MYC	NM_002467.3	CACCGAGGAGAATGTCAAGAGGCGAACACAC AACGTCCTTGAGCGCCAGAGGAGGAACGAGC TAAACGGAGCTTTTTTGCCCTGCGTGACCAG ATCCCG	174
NAT1	NM_000662.4	AGCACTTCCTCATAGACCTTGGATGTGGGAGG ATTGCATTCACTCTAGTTCTGTTGCCGGCT GAAATAACCTGAATTCAAGCCAGGAAGAAGC AGCAA	175
ORC6L	NM_014321.2	GACTGTGTAAACAACCTAGAGAAGATTGGACA GCAGGTCGACAGAGAACCTGGAGATGTAGCT ACTCCACCACGGAAGAGAAAGAAGATAGTGG TTGAAGC	176
PGR	NM_000926.2	GGGATGAAGCATCAGGCTGTCATTATGGTGTC CTTACCTGTGGGAGCTGTAAGGTCTTCTTTAA GAGGGCAATGGAAGGGCAGCACAACTACTTA TGTGC	177
PHGDH	NM_006623.2	GCGACGGCTTCGATGAAGGACGGCAAATGGG AGCGGAAGAAGTTCATGGGAACAGAGCTGAA TGGAAGACCCTGGGAATTCTTGGCCTGGGC AGGATTG	178
PTTG1	NM_004219.2	CACCAGCCTTACCTAAAGCTACTAGAAAGGC TTTGGGAACTGTCAACAGAGCTACAGAAAAG TCTGTAAAGACCAAGGGACCCCTCAAACAAA AACAGCC	179
RRM2	NM_001034.1	TTCTTTTGGACCGCCGAGGAGGTTGACCTCT CCAAGGACATTCAGCACTGGGAATCCCTGAA ACCCGAGGAGAGATATTTTATATCCCATGTTC TGGCT	180
SFRP1	NM_003012.3	GTGGGTCACACACGCACTGCGCCTGTCAGT AGTGGACATTGTAATCCAGTCGGCTTGTTCTT GCAGCATTCCCCTCCCTTCCCTCCATAGCCA CGCT	181
SLC39A6	NM_012319.2	GATCGAACTGAAGGCTATTTACGAGCAGACT CACAAGAGCCCTCCCACTTTGATTCTCAGCAG CCTGCAGTCTTGGAAGAAGAAGAGGTCATGA TAGCTC	182

TMEM45B	NM_138788.3	CTGGCTGCCCTCAGCATTGTGGCCGTCAACTA TTCTCTTGTCTTACTGCCCTTTTGAATCGGATGAA GAGACACGGAAGGGGAGAAATCATTGGAATT CAGA	183
TYMS	NM_001071.1	TGCTAAAGAGCTGTCTTCCAAGGGAGTGAAA ATCTGGGATGCCAATGGATCCCCGAGACTTTTT GGACAGCCTGGGATTCTCCACCAGAGAAGAA GGGGAC	184
UBE2C	NM_007019.2	GTCTGCCCTGTATGATGTCAGGACCATTCTGC TCTCCATCCAGAGCCTTCTAGGAGAACCCAAC ATTGATAGTCCCTTGAACACACATGCTGCCGA GCTC	185

[30] Table 2 provides select sequences for the NANO46 genes of Table 1.

[31] Table 2

GENBANK ACCESSION NUMBER	SEQUENCE	SEQ ID NO:
NM_020445	CAGCGGCGCTGCGGCGGCTCGCGGGAGACGCTGCGCGCGGGGCTAGCGGGCGGCGGAGCGGACGGCGACG GGGCGCTCTCGGGCTGCCGGCGGGGCCGAGCGCCGCGCGTCCCGAGCATGGCAGGCTCCCTGCCTCCCTG CGTGGTGGACTGTGGCACC GGGTATACCAAGCTTGGCTACGCAGGCAACACTGAGCCCCAGTTTCATTATT CCTTCATGTATTGCCATCAGAGAGTCAGCAAAGGTAGTTGACCAAGCTCAAAGGAGAGTGTGAGGGGAG TTGATGACCTTGACTTTTTTCATAGGAGATGAAGCCATCGATAAACCTACATATGCTACAAAGTGGCCGAT ACGACATGGAATCATTGAAGACTGGGATCTTATGGAAGGTTTCATGGAGCAAGTGGTTTTTAAATATCTT CGAGCTGAACCTGAGGACCATTATTTTTTAATGACAGAACCTCCACTCAATACACCAGAAAACAGAGAGT ATCTTGCAAAATATGTTTGAATCATTTAACGTACCAGGACTCTACATTGCAGTTTCAGGCAGTGTCTGGC CTTGGCGGCATCTTGGACATCTCGACAAGTGGGTGAACGTACGTTAACGGGGATAGTCATTGACAGCGGA GATGGAGTCACCCATGTTATCCAGTGGCAGAAGGTTATGTAATTGGAAGCTGCATCAAACACATCCCGA TTGCAGGTAGAGATATTACGTATTTTCATTCAACAGCTGCTAAGGGAGAGGGAGGTGGGAATCCCTCCTGA GCAGTCACTGGAGACCGCAAAAGCCATTAAGGAGAAATACTGTTACATTGCCCCGATATAGTCAAGGAA TTTGCCAAGTATGATGTGGATCCCCGGAAGTGGATCAAACAGTACACGGGTATCAATGCGATCAACCAGA AGAAGTTTGTATAGACGTTGGTTACGAAAGATTCTTGGGACCTGAAATATTTCTTTCACCCGGAGTTTGC CAACCCAGACTTTATGGAGTCCATCTCAGATGTTGTTGATGAAGTAATACAGAAGTCCCCATCGATGTG CGGCGCCCGCTGTATAAGAATGTCGTACTCTCAGGAGGCTCCACCATGTTTCAGGGATTTTCGACGCCGAC TGCAGAGGGATTTGAAGAGAGTGGTGGATGCTAGGCTGAGGCTCAGCGAGGAGCTCAGCGGCGGGAGGAT CAAGCCGAAGCCTGTGGAGGTCCAGGTGGTCACGCATCAGATGCAGCGCTACGCCGTGTGGTTTCGGAGGC TCCATGCTGGCCTCGACTCCCGAGTTCTTTTCAGGTCTGCCACACCAAGAAGGACTATGAAGAGTACGGGC CCAGCATCTGCCGCCACAACCCCGTCTTTGGAGTCAATGTCCTAGTGTCTGCCTGAACGCGTCTGTTTCGATG GTGTCAGTGTGGGAACAAGTGTCTTTCAGAACCCAGAGAAGGCCGCCGTTCTGTAAATAGCGACGTCGG TGTTGCTGCCAGCAGCGTGCTTGCAATTGCCGGTGATGAGCGCGGCGCGGGCCCTTCAGTAAAGCCA TTTATCCGTGTGCCGACCGCTGTCTGCCAGCTCCTCCTTCTCCCGCCCTCCTACCCCTCGCTCTCCCTC CTCCTCCTCCTCCGAGCTGCTAGCTGACAAAATACAATCTGAAGGAATCCAAATGACTTTGAAAATTTG TTAGAGAAAACAACATTAGAAAATGGCGCAAAATCGTTAGGTCCCAGGAGAGAATGTGGGGGCGCAAAAC CTTTTCCTCCAGCCTATTTTTGTAAATAAAATGTTTAACTTGAAATACAAATCGATGTTTATATTTC TATCATTTTTGTATTTTATGGTATTTGGTACAACTGGCTGATACTAAGCAGCAATAGATATTGATGTTATG GAGTGTGTAATCCAAAGTTTTTAAATGTGAGGCATGTTCTGATATGTTTATAGGCAACAAATAAAACA GCAAACTTTTTTGCACATGTTTGCTAGAAAATGATTATACTTTTATGGAGTGACATGAAGTTTGAACAC TAAACAGTAATGTATGAGAATTACTACAGATACATGTATCTTTTAGTTTTTTTTGTGTTGAACTTTCTGGA GCTGTTTTATAGAAGATGATGGTTTTGTGTGCGGTGAGTGTGGATGAAATACTTCTTGCACCATTTGTA TAAAGCTGTTAGAATATTTGTAAATATC	93
NM_00104013 5	CAGCGGCGCTGCGGCGGCTCGCGGGAGACGCTGCGCGCGGGGCTAGCGGGCGGCGGAGCGGACGGCGACG GGGCGCTCTCGGGCTGCCGGCGGGGCCGAGCGCCGCGCGTCCCGAGCATGGCAGGCTCCCTGCCTCCCTG CGTGGTGGACTGTGGCACC GGGTATACCAAGCTTGGCTACGCAGGCAACACTGAGCCCCAGTTTCATTATT CCTTCATGTATTGCCATCAGAGAGTCAGCAAAGGTAGTTGACCAAGCTCAAAGGAGAGTGTGAGGGGAG TTGATGACCTTGACTTTTTTCATAGGAGATGAAGCCATCGATAAACCTACATATGCTACAAAGTGGCCGAT ACGACATGGAATCATTGAAGACTGGGATCTTATGGAAGGTTTCATGGAGCAAGTGGTTTTTAAATATCTT CGAGCTGAACCTGAGGACCATTATTTTTTAATGACAGAACCTCCACTCAATACACCAGAAAACAGAGAGT ATCTTGCAAAATATGTTTGAATCATTTAACGTACCAGGACTCTACATTGCAGTTTCAGGCAGTGTCTGGC CTTGGCGGCATCTTGGACATCTCGACAAGTGGGTGAACGTACGTTAACGGGGATAGTCATTGACAGCGGA GATGGAGTCACCCATGTTATCCAGTGGCAGAAGGTTATGTAATTGGAAGCTGCATCAAACACATCCCGA TTGCAGGTAGAGATATTACGTATTTTCATTCAACAGCTGCTAAGGGAGAGGGAGGTGGGAATCCCTCCTGA GCAGTCACTGGAGACCGCAAAAGCCATTAAGGAGAAATACTGTTACATTGCCCCGATATAGTCAAGGAA	94

	TTTGCCAAGTATGATGTGGATCCCCGGAAGTGGATCAAAACAGTACACGGGTATCAATGCGATCAACCAGA AGAAGTTTGTATAGACGTTGGTTACGAAAGATTCTTGGGACCTGAAATATCTTTACCCCGGAGTTTGC CAACCCAGACTTTATGGAGTCCATCTCAGATGTTGTTGATGAAGTAATACAGAACCTGCCCATCGATGTG CGGCGCCCGCTGTATAAGCCCGAGTTCTTTCCAGGTCTGCCACACCAAGAAGGACTATGAAGAGTACGGGC CCAGCATCTGCCGCCACAACCCCGTCTTTGGAGTCAATGCTCTAGTGTCTGCTGACGCGTCTGTTTCGATG GTGTACAGTTGGGGAACAAGTGTCTTCAGAACCCAGAGAAGGCCGCCGTTCTGTAATAGCGACGTCGG TGTTGCTGCCAGCAGCGTGTTCGATTGCCGGTGCAITGAGGCGCGGCGGGCCCTTCAGTAAAGGCCA TTTATCCGTGTGCCGACCGCTGTCTGCCAGCCTCCTCCTTCTCCCGCCCTCTCACCCTCGCTCTCCTCT CTCCTCCTCCTCCGAGCTGTAGCTGACAAATACAATTTCTGAAGGAATCCAAATGTGACTTTGAAAATTG TTAGAGAAAACAACATTAGAAAATGGCGCAAAATCGTTAGGTCCCAGGAGAGAATGTGGGGGCGCAAAACC CTTTTCTCCAGCCTATTTTGTAAATAAAATGTTTAACTTGAAATACAAATCGATGTTTATATTTCC TATCATTTTGTATTTTATGGTATTTGGTACAACTGGCTGATACTAAGCAGCAATAGATATTGATGTTATG GAGTGTCTGTAATCCAAAGTTTTTAAATTTGTAGGCATGTTCTGATATGTTTATAGGCAAAACAAATAAACA GCAAACTTTTTTGCCACATGTTTGTAGAAAATGATTATACTTTATGGAGTGACATGAAGTTTGAACAC TAAACAGTAATGTATGAGAATTACTACAGATACATGTATCTTTTAGTTTTTTTGTTTGAACTTTCTGGA GCTGTTTTATAGAAGATGATGGTTTGTGTGCGGTGAGTGTGGATGAAATACTTCCTTGCAACATTGTAA TAAAGCTGTTAGAATATTTGIAAATATC	
NM_018685	CTCGGCGCTGAAATTCAAATTTGAACGGCTGCAGAGGCCGAGTCCGTCAGTGGAGCCGAGAGGAGAGGA CAGCTGGTTTGGGAGAGTTCCCCCGCTCAGACTCCTGGTTTTTTCCAGGAGACACACTGAGCTGAGAC TCATTTTCTCTTCTGAAATTTGAACACCGTTCCTATCGTCTCTAGTCCGACGCTGGGGCGATGGAT CCGTTTACGGAGAAACTGCTGGAGCGAACCCTGCCAGGCGAGAGAATCTTCAGAGAAAAATGGCTGAGA GGCCACAGCAGCTCCAAGGTCTATGACTCATGCTAAGCGAGCTAGACAGCCACTTTTCAAGCAAGTAA CCAGCAGCCCTCTCTGGTGGTGAAGAGAAATCTTGTACAAAACCATCGCCATCAAAAAAACCGTGTCTT GACAACACTGAAGTAGAAGTTTCTAACTTGAAAAATAAACAACCAAGTTGAGTCGACATCTGCAAAATCTT GTTCTCCAAGTCTGTGTCTCCTCAGGTGCAGCCACAAGCAGCAGATACCATCAGTGATTCTGTGTGCTGT CCCGGCATCAGTGTGGGCGATGAGGAGAGGGCTGAATCAAGATTGGAAGCAACTGCAGCCTCCTCAGTT AAAACAGTATGCAAAAACCTTGACAGCAACGGCGCGCTTGGGATAATGATGATGACAGATGACATTC CTGAAAGCTCACTCTTCTCACCAATGCCATCAGAGGAAAAGGCTGCTTCCCTCCGACCTCTGCTTTT AAATGCCTCGGCAACTCCAGTTGGCAGAAGGGGCCGTCTGGCCAATCTTGCTGCAACTATTTGCTCCTGG GAAGATGATGTAATCACTCATTTTCAAAAACAAAACAGTGTACAAGAACAGCTGGTACCGCTTGTTTAT CCAAATTTTCTCTGCAAGTGGAGCATCTGCTAGGATCAATAGCAGCAGTGTAAAGCAGGAAGCTACATT CTGTTTCCCAAGGGATGGCGATGCCTCTTTGAATAAAGCCCTATCCTCAAGTGCTGATGATGCTGTTT GTTAATGCCTCAATTTTCCAGCTCTGTGAAGCTACTTCTCCAGTGAATCTACTACATCTATCACTGATG CTAAAAGTTGTGAGGGACAAAATCCTGAGCTACTTCCAAAACCTCTATTAGTCTCTGAAAACGGGGT ATCGAAACCAATTGTGAAGTCAACTTTATCCAGACAGTTCCATCCAAGGGAGAATTAAAGTAGAGAAATT TGCTGCAATCTCAATCTAAAGACAAATCTACGACACCAGGAGGAACAGGAATTAAAGCCTTTCTTGAAC CGTTTGGAGAGCGTTGTCAAGAACATAGCAAGAAAGTCCAGCTCGTAGCACACCCACAGAACCCCAT TATTACTCCAATAACAAAGGCCATCCAAGAAAGATTATTCAAGCAAGACACATCTTCACTACTACCCAT TTAGCACAACAGCTCAAGCAGGAACGTCAAAAAGAACTAGCATGTCTTCTGTGGCCGATTTGACAAGGGCA ATATATGGAGTGCAGAAAAGGGCGAAACTCAAAAAGCAAACTAGAAACCAAAACAGGAAACTCACTG TCAGAGCACTCCCTCAAAAACACCAAGGTGTTCAAAAACCTCAGTCACTTCCAGTAACAGAAAAGGTG ACCGAAAGACAGATACCAGCCAAAATTTCTAGTACAGAACCTAAAGGTTTCACTGATGATGCGAATGACGA AATCTAGCCCTTTGAAAATAACATTGTTTTTGAAGAGGACAAATCCTTAAAGTAACATCAGACCCAAA GGTTGAGCAGAAAATTGAAGTGATACGTGAAATTGAGATGAGTGTGGATGATGATGATATCAATAGTTCTG AAAGTAATTAATGACCTCTTCAGTGATGTCTAGAGGAAGGTGAAGTAGATGAGAGAGCCAGAGAG AGATGGATCAAGCATTAGCAGAAAGCAGCGAAGAACAGGAAGATGCACTGAATATCTCCTCAATGTCCTT ACTTGCACCATTTGGCACAACAGTTGGTGTGGTAAGTCCAGAGAGTTTGTGTCCACCTAGCTAGCTGAA TTGAAAGACACCAGCAGAAGTGATGAAAGTCCAAAACAGGAAAATTCCAAAGAACTCGTGTCCCTCGAG CTGAATCTGGIGATAGCCTTGGTTCTGAAGATCGTGAICTTTCTTACAGCATTGATGCATATAGATCTCA AAGATTCAAAGAAACAGAACGTCCATCAATAAAGCAGGTGATTGTTCGGAAGGAAGATGTTACTTCAAAA CTGGATGAAAAAATAATGCCTTTTCTTGTCAAGTTAATATCAAAACAGAAAATGCAGGAACCTCAATAACG AAATAAATATGCAACAGACAGTGATCTATCAAGCTAGCCAGGCTCTTAACGTGTGTGTTGATGAAGAACA TGGAAAAGGGTCCCTAGAAGAAGCTGAAGCAGAAAGACTTCTTCTAATTGCAACTGGGAAGAGAACACTT TTGATTGATGAATTGAATAAATTGAAGAACGAAGGACCTCAGAGGAAGAATAAGGCTAGTCCCCAAAGTG AATTTATGCCATCCAAAGGATCAGTTACTTTGTGAGAAATCCGCTTGCCCTCAAAAGCAGATTTTGTCTG CAGTACGGTTCAGAAACAGATGCAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT ATGGTAGCCACACCATTAGCAAGTACTTCAAACCTCTCTTAACGGTGATGCTGTGACATTCACTACTACAT TTACTCTGCAAGATGTATCCAATGACTTTGAAATAAATATTGAAGTTTACAGCTTGGTGCAAAAGAAAGA TCCCTCAGGCCTTGATAAGAAGAAAAAACATCCAAGTCCAAGGCTATTACTCCAAAGCGACTCCTCACA TCTATAACCACAAAAGCAACATTCTTCTCAGTCAATGCCAGTCCAGGAGGTCTTAGTGTGTGCGGAA CCAGCAACTTCGCCCTTGTGGATCTTACACATATCATTTGTCTTTCAGTAGGAAATACTAAGTTTGTCTT GGACAAGGTCCCTTTTTATCTTCTTTGGAAGGTCAATTTTATTTAAAAATAAAATGCAAGTGAATTC AGTGTGGAAGAAAGAGGTTTTCTAACCATATTTGAAGATGTTAGTGGTTTTTGGTGCCTGGCATCGAAGAT GGTGTGTTCTTTCTGAAACTGTATATCTTATTTGGACTTATCCAGATGATGAGAAACGCAAGAATCCCAT AGGAAGGATAAATCTGGCTAATTGTACCAGTCGTGAGATAGAACCAGCCAAACAGAGAATTTTGTGCAAGA CGCAACACTTTTGAATTAATTACTGTCCGACCACAAAGAGAAGATGACCGAGAGACTCTTGTACGCCAAT GCAGGGACACACTCTGTGTACCAAGAAGTGGCTGTCTGCAGATACTAAAGAAAGAGCGGATCTCTGGAT GCAAAAACCTCAATCAAGTTCTTGTGTATATTCGCTCTGGCAACCTGATGCTTGTACAAACCTATTGGA	95

12

	GTTTCATCCTTCAGAATTCAACTCACATGTCTCTTGCATGGAGAACCCTCACCTACTGTGTGAGACCCCTG TCCAGCCCCCAGGTGGGATCCTCTCTCGACTTCCCATACATTTCTTTCACAGCATTTACATAGTCCATGA TAGTTTACTTTGTGGGATTATTTGGTTAATCTTTGCCCTTAACACCAGGGTTCTTGGGTGAAGGAGCTTC TTTATCTTGGTAACAGCATTATTTCAAGCATAACTTGTAAATATAGTTATATTACATATATAACATATATA TATATAACATAACATATATAACATATATAACAAGCATAAATTGTTATATAGTCTTGTATATAGTAAGACC TCAATAAATATTTGGAGAACAAAAA	
NM_000633	TTTCTGTGAAGCAGAAGTCTGGGAATCGATCTGGAAATCCTCCTAATTTTTACTCCCTCTCCCCGCGACT CCTGATTCATTGGGAAGTTTCAAATCAGCTATAACTGGAGAGTGCTGAAGATTGATGGGATCGTTGGCTT ATGCATTTGTTTTGGTTTTACAAAAAGGAACTTGACAGAGGATCATGCTGTACTTAAAAAATACAACAT CACAGAGGAAGTAGACTGATATTAACAATACTTACTAATAATAACGTGCCTCATGAAATAAAGATCCGAA AGGAATTGGAATAAAAAATTTCTCTGCATCTCATGCCAAGGGGGAAACACCAGAAATCAAGTGTTCGCGGTGA TTGAAGACACCCCTCGTCCAAGAAATGCAAAGCACATCCAATAAAATAGCTGGATTATAACTCCTCTTCT TTCTCTGGGGCCCGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTTGGCCCCCGTTGCTTTTCTCTTGGGA AGGATGGCGCACGCTGGGAGAACAGGGTACGATAACCGGGAGATAGTGATGAAGTACATCCATTATAAGC TGTCGCAGAGGGGCTACGAGTGGGATGCGGGAGATGTGGGCGCCGCGCCCCGGGGGGCGCCCCCGCACC GGGCATCTTCTCTCCAGCCCGGGGCACACGCCCCATCCAGCCGCTACCCGGGACCCGGTCCGCCAGGACC TCGCCGCTGCAGACCCCGGCTGCCCGCGCGCGCGCGGGGCTGCGCTCAGCCCGGTGCCACCTGTGG TCCACCTGACCTCCGCCAGGCCGCGACGACTTCTCCGCGCTACCCGCCGACTTCGCCGAGATGTC CAGCCAGCTGCACCTGACGCCCTTACC CGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGG GACGGGGTGAAGTGGGGAGGATTGTGGCCTTCTTTGAGTTCGGTGGGGTTCATGTGTGTGGAGAGCGTCA ACCGGGAGATGTCGCCCCGGTGGGACAACATCGCCCTGTGGATGACTGAGTACCTGAACCGGCACCTGCA CACCTGGATCCAGGATAACCGAGGCTGGGATGCCCTTTGTGGAACGTACGGCCCCAGCATCGGCCCTCTG TTTATTTCTCTGGCTGTCTCTGAAGACTGTCTCAGTTTGGCCCTGGTGGGAGCTTGCATCACCCTGG GTGCCATCTCTGGGCCACAAGTGAAGTCAACATGCCTGCCCAACAAATATGCAAAAGGTTCACTAAAGC AGTAGAAATAATATGCATTGTCTGAGTGTACCATGAAACAAAGCTGCAGGCTGTTTAAAGAAAAATAAC ACACATATAAACATCACACACACAGACAGACACACACACACAACAATTAACAGTCTTCAGGCAAAACG TCGAATCAGCTATTTACTGCCAAAGGAAATATCATTATTTTTACATTATTAAGAAAAAAGATTAT TTATTTAAGACAGTCCCCATCAAACTCCTGTCTTGGAAATCCGACCCTAATTTGCCAAGACCGCTTCG TGTTGCTCCACCTGGATGTTCTGTGCTGTAAACATAGATTGCTTTCCATGTGTGTGGCCGGATCACCA TCTGAAGAGCAGACGGATGGAAGAAAGGACCTGATCATTGGGGAAGCTGGCTTTCTGGCTGCTGGAGGCTG GGGAGAAGGTGTTCACTTGCATTTCTTTGCCCTGGGGGCTGTGATATTAACAGAGGGAGGGTTCTCT TTGGGGGAAGTCCATGCCTCCCTGGCCTGAAGAAGAGACTCTTTGCATATGACTCAGATGATGCATACC TGGTGGGAGGAAAAAGATTGGGAACCTCAGATGGACCTAGTACCCACTGAGATTTCCAGCCGCAAGGACA GCGATGGGAAAAATGCCCTTAAATCATAGGAAAGTATTTTTTAAAGCTACCAATTGTGCCGAGAAAAGCA TTTTAGCAATTTATACAATATCATCCAGTACCTTAAGCCCTGATTGTGTATATTCATATATTTTGATAC GCACCCCCCACTCCCAATCTGGCTCTGTCTGAGTAAGAAACAGAATCCTCTGGAACCTTGAGGAAGTGA ACATTTGCTGACTTCCGCATCAGGAAGGCTAGAGTTACCCAGAGCATCAGGCCCCACAAGTGCCCTGCT TTTTAGGAGACCGAAGTCCGCAGAACCTGCCTGTGTCCAGCTTGGAGGCTGGTCTCTGAGCCGAGCCGG GGCCCTCAGTGGCCTCCTCCAGGGATGATCAACAGGGCAGTGTGGTCTCCGAATGTCTGGAAGCTGATGG AGCTCAGAATTCACCTGTCAAGAAAGAGCAGTAGAGGGGTGTGGCTGGGCCCTGCACCCCTGGGGCCCTCC AGGTAGGCCCGTTTTACGTTGGAGCATGGGAGCCACGACCCCTTCTTAAGACATGTATCACTGTAGAGGGA AGGAACAGAGGCCCTGGGCCCTTCTATCAGAAGGACATGGTGAAGGCTGGGAACCTGAGGAGGCAAT GGCCACGGCCCATTTTGGCTGTAGCAGATGGCACGTTGGCTGTGTGGCCTTGGCCACCTGTGAGTTTAA AGCAAGGCTTTAAATGACTTTGGAGAGGGTCAAAATCTTAAAGAAAGCATTGAAGTGAAGGTGTCTATGGA TTAATTGACCCCTGTCTATGGAATTACATGTAAAACATTATCTTGTCACTGTAGTTTGGTTTTATTGAA AACCTGACAAAAAAAAGTTCAGGTGTGGAATATGGGGGTTATCTGTACATCTGGGGCATTAAAAAAA AAATCAATGGTGGGGAACATAAAGAAGTAACAAAAAGAGTGACATCTTCAGCAAAATAACATAGGAATTT TTTTTTCTTCCAGTTTGAATCAGCCTTGAACATTGATGGAATAACTCTGTGGCATTATTGCATTATA TACCATTTATCTGTATTAACCTTTGGAATGTACTCTGTTCATGTTTAAATGCTGTGGTTGATATTTGAAA GCTGCTTTAAAAAATACATGCATCTCAGCGTTTTTTTGTTTTTTAAATGTATTTAGTTATGGCCTATACA CTATTTGTGAGCAAAGGTGATCGTTTTCTGTTTGTGAGATTTTATCTCTTGATTCTTCAAAAGCATTCTGA GAAGGTGAGATAAGCCCTGAGTCTCAGCTACCTAAGAAAAACCTGGATGTCAGTGGCCCTGAGGAGCTT TGTTTCAACCAAGTCAATGTGCATTTCCACGTCAACAGAAATGTTTTATTGTGACAGTTATATCTGTGTCC CTTTGACCTTGTCTTGAAGGTTTCTCGTCCCTGGGCAATTCGCATTTAATTCATGGTATTTCAGGAT TACATGCATGTTTGGTTAAACCCATGAGATTCATTACAGTTAAAAATCCAGATGGCAATGACCAGCAGAT TCAAATCTATGGTGGTTTACCTTTAGAGAGTTGCTTTACGTGGCCTGTTTCAACACAGACCCACCCAGA GCCCTCCTGCCCTCCTTCCGCGGGGGCTTTCTCATGGCTGTCTTTCAGGGTCTTCTGAAATGCACTGGT GCTTACGCTCCACCAAGAAAGCAGGAAACCTGTGGTATGAAGCCAGACCTCCCCGCGGGCCTCAGGGAA CAGAATGATCAGACCTTTGAATGATTCTAATTTTTAAGCAAAATATATTTTATGAAAGGTTTACATTGT CAAAGTGATGAATATGGAATATCCAATCCTGTGCTGCTATCCTGCCAAATCATTTTAAATGGAGTCAATT TGCAGTATGCTCCACGTGGTAAAGTCTCCAGCTGCTTTAGAAGTAACATGAAGAAGCTGGACGTTTTT TAATATAAAGCTGTTTTGTCTTTTGTGTTGTTCAAACGGGATTACAGAGTATTTGAAAAATGTATAT ATATTAAGAGGTACGGGGGCTAATTGCTGGCTGGCTGCCTTTTGTGTGGGTTTTGTTTACCTGGTTTTT AATAACAGTAAATGTGCCAGCCTCTTGGCCCCAGAAGTGTACAGTATTGTGGCTGCCTTGTCTAAGA GTAGTTGATGTGCATTTTCTTTATTTGTTAAACATGTTAGAAGCAATGAATGTATATAAAGCCTCAA CTAGTCAATTTTTTCTCTCTCTTTTTTTTTCATTATATCTAATTTATTTTGCAGTTGGGCAACAGAGAAC CATCCCTATTTTGTATTTGAAGAGGATTCACATCTGCATCTTAACTGCTCTTTATGAATGAAAAACAGT CCTCTGTATGTACTCCTCTTTACACTGGCCAGGGTACAGATTAAATAGAGTATATGCATTTTCCAAATTG	97

	GGGACAAGGGCTCTAAAAAAGCCCCAAAAGGAGAAGAACATCTGAGAACCTCCTCGGCCCTCCAGTCC CTCGCTGCACAAATACTCCGCAAGAGAGGCCAGAATGACAGCTGACAGGGTCTATGGCCATCGGGTCGTC TCCGAAGATTTGGCAGGGGCAGAAAACCTCTGGCAGGCTTAAGATTTGGAATAAAGTCACAGAATTAAGGA AGCACCTCAATTTAGTTCAAACAAGACGCCAACATTCTCTCCACAGCTCACTTACCTCTCTGTGTTTCA TGIGGCCCTTCCATTTATATGTGATCTTTGTTTTATTAGTAAATGCTTATCATCTAAAGATGTAGCTCTGG CCCAGTGGGAAAAATTAGGAAGTGATTATAAATCGAGAGGAGTTATAATAATCAAGATTAAATGTAAATA ATCAGGGCAATCCCAACACATGTCTAGCTTTACCTCCAGGATCTATTGAGTGAACAGAATTGCAAAATAG TCTCTATTTTGAATTGAACCTTATCCTAAAACAAATAGTTTATAAATGTGAACCTTAAACTCTAATTAATTC CAACTGTACTTTTAAAGGCAGTGGCTGTTTTTAGACTTTCTTATCACTTATAGTTAGTAATGTACACCTAC TCTATCAGAGAAAAACAGGAAAGGCTCGAAATACAAGCCATTCTAAGGAAATTAGGGAGTCAGTTGAAAT TCTATTCTGATCTTATTTCTGTGGTGTCTTTTTCAGCCAGACAAATGTGGTTACACACTTTTTAAGAAAT ACAATCTACATTGTCAAGCTTATGAAGGTTCCAATCAGATCTTTATTGTTATCAATTTGGATCTTTCA GGGATTTTTTTTTTAAATTTATTTAGGGACAAGGACATTTGTTGGAGGGGTGGGAGGGAGGAAGAAATTT TAAATGTAAACATTTCCCAAGTTTGGATCAGGGAGTTGGAAGTTTTTCAGAATAACCAGAACTAAGGGTAT GAAGGACCTGTATTGGGGTCGATGTGATGCCTCTGCGAAGAACCTTGTGTGACAAATGAGAAACATTTTG AAGTTTGTGGTACGACCTTTAGATTCCAGAGACATCAGCATGGCTCAAAGTGCAGCTCCGTTTGGCAGTG CAATGGTATAAATTTCAAGCTGGATATGTCTAATGGGTATTTAAACAATAAATGTGCAGTTTTAACTAAC AGGATATTTAATGACAACCTTCTGGTTGGTAGGGACATCTGTTTTCTAAATGTTTATTATGTACAATACAG AAAAAATTTTATAAATTAAGCAATGTGAACTGAATTGGAGAGTGATAATACAAGTCTTTAGTCTTA CCCAGTGAATCATTTCTGTCCATGTCTTTGGACAACCATGACCTTGGACAATCATGAAATATGCATCTCA CTGGATGCAAGAAAAATCAGATGGAGCATGAATGGTACTGTACCGGTTCTATCTGGACTGCCCCAGAAAA TAACCTCAAGCAAAACCTCTATCAACAACAAGGTTGTTCTGCATACCAAGCTGAGCAGCAAGATGGGAA CACTGGTGGAGGATGGAAGGCTCGCTCAATCAAGAAAAATCTGAGACTATTAATAAATAAGACTGTAGT GTAGATACTGAGTAAATCCATGCACCTAAACCTTTTGGAAAAATCTGCCGTGGGCCCTCCAGATAGCTCAT TTCATTAAGTTTTTCCCTCCAAGGTAGAATTTGCAAGAGTGACAGTGGATTGCATTTCTTTTGGGGAAGC TTTTCTTTGGTGGTTTTGTTTTATTATACCTTCTTAAGTTTTCAACCAAGGTTTGTCTTTTGTGTTT CTGGGTTATTTTTGTTTTTAAATAAAAAATAAGTGACATAAAGTGTTTTTGTATTGAAAGCTTTTGTATT CAAGATTTTTCATACTTTTACCTTCCATGGCTCTTTTTAAGATTGATACTTTTAAAGAGTGGCTGATATTC TGCAACACTGTACACATAAAAAATACGGTAAGGATACTTTACATGGTTAAGGTAAGTAAAGTCTCCAGTT GGCCACCATTAGCTATAATGGCACTTTGTTTTGTGTTGTGGAAAAAGTCACATTGCCATTAAACTTTCCCT TGTCGTCTAGTTAATATTGTGAAGAAAAATAAAGTACAGTGTGAGATACTG	
BX647539	AATGAGGGTATTTATAAACTACTTAAATTATAAAAAGAAATGAGACATCAGACTTACAGTTTTGGATACTA ATTTTTTTCACCTTAACGTTTCAATTTATGTGATAGGAGTTTTCCATCCTATTATACCGCTGTGCGATCTGATC TTGGGCACGTTAACCACCTCTTGTGCTCGATTTTCTCACCTGTAAAAGTGGGGTAAATCATAATGCT TACTTAGTAGGATAGCCCTGAAGAATAAGTGACTTAGCGAACATAAATAGCTTACAATAGGGTTTTTCAGC ATGGGAAGGATTCAGTAAATGTTAGCTGTCTATCATCACCACCTACAAAGGAAGCAATACGTGTCTGAAAG TTTTTCCATTAATGTAAATTTCTATAGTACGATTCCCAAGAAGATATTAAAAATTATGGAATAAAGGT ATTGGTATATTCCTAATTTATTTCCATAAAGATTGTATTGATAAATATGCTCATCTCTTCCCTTAACGGGAT GCATTCAGAAAAACAAGTCAATGTTAGACAAAGTATCAGAAGGGAAATTTCTGTAGCCAGAGAGCTAAA AATTACAATAGGGTCTCTAATTTACTTTCAACTTTTTTAGGAATAATTCTCAGTGTGTTTTCCACATTT CATATGTAATTTTTTTTTTTTTTTTTTTTGTAGACAGAGCCTCGCCCTGTCCACAGGCTGGAGTACAGTG GCGGATCTCGGCTCACTGCACTTCCACCTGCTGGGTTCAAGCAATTCTTCTGACCTCAGGTGATCCAC CCGCCCTCGCCCTCCCAAAGTGCTGGGATTATAACAGGCGTGGCATGAGTCACCGCCCGGCCGATCTTT ACTTTTTTATCTTTGTACCCCTGCTTATCCAGTTAGCATGTGATTAAGTCAAAGATTTGCCACTTTG GGCCACATCTATTAATTTTCACTTTGTTATAATTGATTTAGTTTTGATCTACACTGCTTATTACTCC CAGTCACTTTTTATAGAAGTGAATACTGGTAAAATACCTCAAAATGCACTGACTTCTATGTAGAGGCGA CACCTCATCAGAACCCTGGGCTGACAGGGAATCCCACTGTGACAGGAGCTGCGCGCATTTTCTATTCTGAT TCTCTTTGGCGTATCCAGGACTCTGATGACATGATCATAATTTATCAGTAGTAACAGGTTGGGCCATTT GTTTTTGTGGTAAATCATATATTTAAGATTTTAGAAATAAGTTGATAGCCATGTATTTTGAATTTGAA AAAGACATTGCATTACTCAGCTTCAAATTAAGCTTTAATCAAATAGTGAACTTTCCATTAATGGACAGT GTATACCTTTTTGTGATTTAAAAAAGAACTGAATATAGTGCCTTTGTGACAGGGGAGCTTGGTTCT CTGACAATGTCCTCTTGAGCCTTTTTTTTTTTTTTTGGATGGAGTCTCAGTGTGACCCAGGCTGGAGT GCAGTGGCGCCATCTTGGCTCACTGCAACCTCCGCCCTCGGGTTCAAGTGATTTCTCATTCTCAGCTTC CTAAGTAGCTGGGATTACAGGCACGACCCACCATGACCAGCTAATTTTTTACTTTTTAGTAGAGACAGGG TTTTGCCATGTTGGCTAGGTTGGTCTCGAAGTCTGACCTCAAGTAATCCACCCACCATGGCCTCCCCAA AGTGCTGGGATTACAGGCGTGAGCCATTTACCCCGGCTCTCTTCCGTCTTTGAGCTGTGAGGAAATAGC TACATTACATGAGCTGCTAGATCTGCCTTATGGTCAGAAATGAAGGTTGAACCTCTCAGGAACAGTGACAT ATATACACACTGATATTTCCAAAGTACAATGCCCAAATTTGATCCACAAAGGAATTAAGGTCAATTTGCAA CAAAATCACAGAATAGTAACAAATAAATAGAAATAAATATGGCCAGGGATGCTGCAAACTGATATACTG CCAAGTTTATCAGTTGGGAATCCCAACAGTGAAAAGCATAAAAATGAAAGGAATTTTAAAGGAGACTTTT ATAGAAGAGTGGGAAGGATTGGAGGAGCCAACAAGTGATGGTGAGGCACACAGGGAAGAGCTTCAGTGGG CACCATCCCTCTCTGGTTTGAAGGGGTAGGGAGGGGACCAGAGCTGGGAGAGGGGGCTGGAATCTGCTG TGGAGGAGCCACTCCCTTCCAGACCTGCTGTGGCCATCACAGAATGCAGCCACTGCCAGAGCAGCAGCCC GAGGAACCAAGGAGGGGAGCACAAGTACCCTAGCCTCTCTCTTTCTGTTTCTGCTTCCGATCTCCTC CACTGGCTAAACCCAGCTGGATGCTAAGAGTACAGTCAGCCTGCCTGCTGAGGAGGGACACCAGGGGACC ACCATCAGCAAGGGATCCAATGCTTTCTGCTCTGCAGAATGAAGGTTGGGGCGGGGGGGCGCTCTAC TCTTAGGGATATTGTGGGAATAAAGGAAATAGGCCAAAAATGTTTTTGAAGAAACAAAGCACAATCTGC GCACCCGTGGGCCACTACTGCTTTTGACCCCTGGCTCTGTTTATGAAGTAATGTCGTGTCATTTCTTTT	98

	TTAGGTGCTACAGGATTTCTTTAGGTTTGTCTTCTGTCCACCATATTTCAACTCATGTGTGCTGTTTGT GTGCTAAAAACAAATATTTGCTGATGCTGAGTGAATAGTTGAATATTTATATAAGTCAAATTTATACGT AATGATTTTTCTTTGTAACCTTAGCCGTTTCTCTTTTACAAACTCAGAAAACCTCAGACTTTGAAAAGGCC TGAAGTTCTTCACCTGAAATCTGAGAACTTGGAGCGCCTTAAAAATCTAAAGGAAAAACAAACAGTGAA AGAACATGATATAGTCAGTGTAGAGAATAAATATTTATGTAATTAATATTGAGGATGCAGATAACACA TTGTGAAATCTTGCTTTGTAAAAAATCTCGATCTGCTGAAGAAAGATGTTCTCTCTAGAGATCTTTGAAAG CATAATTATTGAGCTTTTAAATGTTAGAAACAAAGTTAGACCCACACATATCTGGCGTGTGGAAGAT TTGCATTTCTTCCCTGCCCGCCCCGCCACACTTGTGAGTTGTGCTGTACGCAGTTCTCTGTAGC ACTCGGCTGGGCAGAAATCATCTTTAGCAGCTAAGGGAACATAGTTATGATCTGGACCTTCTGGGAGTGG TCAGTGCCCAAGAACAGGTATGGGACTCCAGAAAGTTCTGCTCTCAACCCTATTTGAAATAGAGTTACA CATTGTTCTACAATTATTTGAGTTAATAAGCAGCTCTTTTCAAACGTGATTATGCCCTTCCAAGTTTAA TACACTAGACTTTAGTGAAAGTAATTGACCTCATCTCATTTCTCTCTGTTATATTAAGATCACTTTGAG TAAAGGTAGAAAGCTTTTGAAGTGGTGAGGAGGAGGTAGAGGAGGACATAGAGCAGATAGGGGCTGGAA AGTGGGGTGAGGAAGAGAGTGGCTTCTCTTTGGCAGAGTACCAAGGAAAAGCCCTATCTGTACAGAACCT TTGTGCTTGGGAACCTTGATGGCTGCAACCTGAGCCTCAACCTAGTTTGTCTTGGGAGCCAGAAGAGAAGC TAAAAACCTTCAGTTAACCAAGCCAGACACCAAGAAAGTTAAACCGAAAGAGAACCCCCACCCCCGCA AAAAAAGAGTAAGTGGGTAAAGTGATATCATGTTAGCACAGAAAGAGAACATAAGGGTCACTCTAAG TTCATCTGCCCTCTTCTATTTTCAAGGTGCAGAACTAAGGCACAAGGACCCCGTGTCTGCTCTTGA TCACATAGCTAGTGGGTGCCAAGCCAGGTCTAGAACTCTGTTCTCTGGGTCACAGGCTGGCTCTTCATC CCTCTAGAGAGATAGCTCATCTGTGTGCACCTGAGCCGTTGTGTTTCGGAGTCAAAGCAAATAAAGGCT CAAACCTCAAGACTGTTTTGCAGACCGGCTGCGAGTAGATATGGGGGAGGAGAAACCTGCTTTAAATTGC TTCAAGCAAGTTGTTTTCTGCAAGGTGTTGACTTTTTCTTCAACTTTCTAGCTGAGTCTGAGCTG AGCTGTTATTTGTCTATTATGCAATAATTCAGGAACCTAAGATCTTCTTTTAAATTTATTTGTTTA TTTAGAGACAGAGTCTTGCTCTGTTGCCAGGCTGGAGTGCAGTGGTGTGATCTCGGCTCACTGCAGCCT CTGCTCTCTGGGTTCAGCAATTTCTCATGTCTCAGCCTCCCGAATAGCTGGTATTGCAGGCTCTGTGCCAC CACCCCTGCTAATTTTTGTAAATTTAGTGAGACACCGTTTCGCCATGTTGGCCGGGCTCGTCTTGAGC TCCGCGCTCAGGTGATCCGCCCCGCTCGGCTCCCAAGTGCTGGGATTGAGCCGTGAGCCTCACAC CCGCTCTATTTATTTATTTTAAATTGGCTGCTCTTAGAAAGGCATACCATGTTTCTGGATGGGAAGGCT TATTAATTCACCTAATTTAATGTATAAATTTGATGCAATCATAGTCACAGTCCAGTGGAAATTTTTTAA CTTGATTAAGATGTTCTAAATTAATGAGAGAACTTGAATTACCAGGTATTGAAACACTGTAAAGCCACAA TCAITGTAACAGTATGTTATAACCATGGGAATAGAGGCTGTGATACAGCAGAAAAAAGTGAATAAAGAA ATAACTGTATTCATAAAAAATTTAAATGTGGAGTCACTGGGGGAAAGGATTAAATTCGATAATGTAGAA ACAACTCAACTATTTGGAGAAATGTAAATTTAGAGCCTTATCTCATGCCATATACCAAATACTATTTAG ATTTGATTAAAAAATAAAAAAATAAAAAA	
BC035498	GCGGCGCCAGCGCGGTGTAGGGGGCAGGCGGGATCCCGCCACCGCGCGGCTCGGCGCCGCCGACTCC CGGCGCGCGCCGCCGCTGCGGCTCGCGCGCGCGCTGCGGGGACTGGAGCGCGCGCTCCGCGCGGGAC AAGACCTTGGCTCAGGCGGGAGCAGCCCCATCATGCGGAGGGAGCGCAGGAGCGGATCGGAAGGAGC GGGACACCATGAAGGAGGACGGCGCGCGGAGTTCTCGGCTCGCTCCAGGAAGAGGAAGGCAACGTGAC CGTTTTTTTGCAGGATCCAGATGAAGAAATGGCCAAATCGACAGGACGGCGAGGGACCAGTGTGGGAGC CAGCCTTGGGACAATAATGCAGTCTGTGCAGACCCCTGCTCCCTGATCCCCACACCTGACAAAGAGATG ATGACCGGGTTTACCCAACTCAACGTGCAAGCCTCGGATTATTGCACCATCCAGAGGCTCCCCGCTGCC TGTAAGTGTGGCATAATAGAGAGGAAGTCTGGAAAAATCATGTTAAACAAGGAAAGACATCTAAGG GATCAGCACTTTCTTGAGCAACACCTCTTCTGCAGCCAAAAATGCGAGCAATCTTCTGGATTGTTAA TGGAGGTGTGGAAGTCTATAAACTTCACAGGGAGACCTTTTACTTGGCACAAGATTTCTTTGACCGGTA TATGGCGACACAAGAAATGTTGTAAAAACTCTTTACAGCTTATTGGGATTTCATCTTTATTTATGCA GCCAACTTGAGGAAATCTATCTCCAAAGTTGCACCACTTGGCTATGTGACAGATGGAGGATGTTTTCAG GAGATGAAATCTCACCATGGAATTAATGATTATGAAGGCCCTTAAAGTGGCTTTTAAAGTCCCTGACTAT TGTGTCCTGGCTGAATGTATACATGCAGGTTGCATATCTAAATGACTTACATGAAGTGTACTGCCGAG TATCCCCAGCAATCTTTATACAGATTGCAGAGCTGTGGATCTCTGTGCTCTGGATGTTGACTGCCTTG AATTTCTTTATGGTATACTTGTCTGCTTCGGCCTTGTATCATTTCTCGTCTCATCTGAATTGATGCAAAAGGT TTCAGGGTATCAGTGGTGGACATAGAGAACTGTGTCAAGTGGATGGTTCCATTTGCCATGGTTATAAGG GAGACGGGGAGCTCAAACTGAAGCACTTCAGGGGCGTCTGATGAAGATGCACACAACATACAGACCC ACAGAGACAGCTTGGATTGCTGGACAAAGCCCGAGCAAGAAAGCCATGTTGTCTGAACAAAAATAGGGC TTCCTCTCTCCAGTGGGCTCTTACCCCCGCCACAGAGCGGTAAAGAGCAGAGCAGCGGGCCGGAATG GCGTGACACCCCATCTTCTCCACCAAGACAGTTGCGCGCCTGCTCCACGTTCTCTCTGTCTGTGTC AGCGGAGGCGTGGCTTTTGTCTTTACAGATATCTGAATGGAAGAGTGTCTTCCACAACAGAAGTATTTCT TGTGATGGCATCAAAACAGGGCAAGTGTCTTTTATTGAATGCTTATAGGTTTTTTTTTAAATAAGTGGGT CAAGTACACCAAGCCCTCCAGACACCAAGTGGTGTCTCCGATGCTGCTATGGAAGGTGCTACTTGACCT AAGGACTCCCAACAACAAGCTTGAAGCTGTGGAGGGCCACGGTGGCGTGGCTCTCTCTCGCAGGTG TCTTGGGCTCCGTTGTACCAAGTGGAGCAGGTGGTTGCGGGCAAGCGTTGTGCAGAGCCCATAGCCAGCT GGGCAGGGGGCTGCCCTCTCCACATTATCAGTTGACAGTGTACAATGCCTTTGATGAAGTGTGTTTGTAA TGCTGCTATATCTATCCATTTTTTAAATAAAGATAAATACTGTTTTTGAATAAATAAATAAATAAATAA AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	99
BG256659	GAGGGCACGGGCTCCGTAGGCACCAACTGCAAGGACCCCTCCCCCTGCGGGCGCTCCCATGGCACAGTTT GCGTTCGAGAGTGACCTGCATCTCGTGTCTCAGCTGGATGCACCATCCCCAATGCACCCCTGCGCGCT GGCAGCGCAAGGCAAGGAGCCGAGGCCGCGCCCCCTCACCATGCGGGCGGCCAACCCGATCCACAGT CGCGGCGAGGACTCCGGCGCAACTCTGGCAAACTCCAGTTCCAAAGGTTCCAGGTTCCAGCAACCT GGCGGTGACCGCTATATCCCCATCGCAGTGTGCCAGATGGAGGTGGCCAGCTTCTCTCTGAGCAAGG	100

	AGAACCCAGCCTGAAAACAGCCAGACGCCACCAAGAAGGAACATCAGAAAGCCTGGGCTTTGAACCTGAA CGGTTTTGATGTAGAGGAAGCCAAAGATCCTTCGGCTCAGTGGAAAAACCAAAAAATGCGCCAGAGGGTT ATCAGGAACAGACTGAAAAGTACTCTACAGCCAAAAGGCCACTCCTGGCTCCAGCCGGAAGACCTGCCGTT TACATTCTTCCCTGCCAAGACCGTATCCTGGATGCGCCTGAAATCGAATGACTATTAACCTGAACCTGTG GGACTGGCAGTCCGGGGAATGTCCGGGCCGGGCCACGGCCACGAGGTGTTCCGTGTGGAGTGCAAGCTGG GACACACCGTGGCGCTTGTGCACAGGGCCACGCGGGGAAATAATCCCGGGCGCGCAAGCGGCCTGGC GAGAGCCGCACGGGCCGCTGTGGGGTGGTACAACAGGCCAAAAACAACACAAGGCCAACAAAGACATA CGCGCGCTGACACCACGGTGCAAAGCGCTCAGACGAGTAGTAACCGGCACTGTGGTTGCTGCTCCCCAC CTCTCCCGCTCTCAGCGTAAGATAAAAAGAAAGAGCAAAAAGCAAAAGAAAGAACGAGACGAGACAC ACAGGAACGAACAGTAAAGCAAGCTAAAGCAACCGCAAGACCAGACAACAGAAATAGAAAGAACCAACAG AGAGGAGACAGAACAGGACGCCAGCAACATAGCAACAAACGAACAGAAGAGAGCACTAAACAAAAGCAGC AGCAAGACGAGACAGGAGAGAAGGAGGAAGGAGGGCCGAGCGAGCAGGGAGCGCGAGCGAGGCGGAAG CAGCAGACAAGGGCAGGGCAAGGGCAACGAGAGGAGGCCACCAACAAAAAGGAGAGGGGACAGGAGAAGC AGCGAGAGAAGCGGAGGAGCAACAGAGGAAGAAAAGGAGAGGGAGAGGAGGGAGAGAGCGGAAGGAGGA AGAAACAGCACGAGGCGACGAAGGGGGGAGACGCGGGGGCAGGAAAAGACACAGGAAGGCAGCGCGGAGG AGGAGAAGGGGAAGCAGGAAGGAGACGGAAGGAGAAGAGGGAGAGGACAGCGCAAGAGAGCGCGCGCGGC GACAGCGAGGGACGGAGCGAGAGAGAGGAACGGAAAGCGAGAGGGAAGAGGAGGCAACGACGCAAC CAACCGAAAAACAGCAGAAAGAGAGGAGAAGGACGCGCAAGAGGCAAGCGACGACGACAGGAACGAAG CGAGAGACGAGAAGCCGGTGACGAGCAGGAGAAGGGAGGAGGAGACAGGACAGGCGGAAGAGAGACA CGCGAGACGCAAGAGTGAGCAGAACGAAGCGAAGAGCAACGCACGAGAGAAACGAC	
NM_001254	GAGCGCGGCTGGAGTTTGTCTGCTGCCGCTGTGCAGTTTGTTCAGGGGCTTGTGGTGGTGGTCCGAGAGG CTGCGTGTGAGAGACGTGAGAAGGATCCTGCACTGAGGAGGTGGAAGAAGAGGATTGCTCGAGGAGGCC TGGGCTCTGTGAGGCAGCGGAGCTGGGTGAAGGCTGCGGGTTCCGGCGAGGCTGTAGCTGTCTGTCTGCTC ATGCTCAAACCCGATCCAGGCACAGGCTACAATCAGTTTCCAAAAAGGAAGCTGTCTCGGGCATTGA ACAAAGCTAAAAACTCCAGTGATGCCAAACTAGAACCACAAATGTCCAAACCGTAACCTGTCTCTCTCG TGTAAGCCCTGCTCTCAGCCCCAGGAAACGCTGTGGCGATGACAACCTATGCAACACTCCCCATTTA CCTCTTGTCTCCACCAAAGCAAGGCAAGAAAGAGAATGGTCCCCCTCACTACATACACTTAAGGGAC GAAGATTGGTATTGTACAACTCAGCTGACAATTAAAGTCTCTAGCAAAAAGAGAACTAGCCAAAGTTCCACCA AAACAAAATACTTTCTTCAAGTTAGAAAAAGTCAAGAGATCACAACAAATTTCTGAGCAGAGATGTCCACTG AAGAAAGAATCTGCATGTGTGAGACTATTCAAGCAAGAGGCACCTTGCTACAGCAAGCAAGCTGGTCC TGAACACAGCTGTCCCAGATCGGCTGCCTGCCAGGGAAGGGAGATGGATGTATCAGGAATTTCTTGAG GGAACACATCTGTGGGAAAAAGCTGGAAGCCTTTACCTTTCTGGTGTCTCCGAACTGGAAGAACTGCC TGCTTTAAGCCGATTCTGCAAGACCTCAAGAGGAACCTGAAAGGCTTTAAACTATCATGTCTGAATTTGCA TGTCCTTGAGGACTGCCAGGCTGTATTCCCAGCTATTGCTCAGGAGATTTGTGAGGAAGAGGTATCCAG GCCAGCTGGGAAGGACATGATGAGGAAATTGGAACCAATATGACTGCAGAGAAGGGCCCCATGATTGTG TTGGTATTGGACGAGATGGATCAACTGGACAGCAAAGGCCAGGATGTATTGTACACGCTATTTGAATGGC CATAGGCTAAGCAATTTCTACTTGGTGTGATTGGTATTGCTAATACCCTGGATCTCACAGATAGAATTTCT ACCTAGGCTTCAAGCTAGAGAAAAATGTAAGCCACAGCTGTTGAACCTTCCCACCTTATACCAGAAATCAG ATAGTCACTATTTTGCAAGATCGACTTAATCAGGTATCTAGAGATCAGGTTCTGGACAATGCTGCAGTTC AATCTGTGCCCCGCAAGTCTCTGCTGTTTCAGGAGATGTTTCGCAAGCACTGGATGTTTGCAGGAGAGC TATTGAAATTTAGAGTCAGATGTCAAAAGCCAGACTATTCTCAAACCACTGTCTGAATGTAAATCACCT TCTGAGCCTCTGATTCCCAAGAGGGTTGGTCTTATTCACATATCCCAAGTCACTCAGAAGTTGATGGTA ACAGGATGACCTTGAGCCAAAGAGGAGCACAGATTCTTCCCTCTTCAGCAGAAGATCTTGGTTTGCTC TTTGATGCTCTGATCAGGCAGTTGAAATCAAAGAGGTCACTCTGGGGAAGTTATATGAAGCCTACAGT AAAGTCTGTGCAACAGCAGGTGGCGGCTGTGGACCAGTCAGAGTGTGTTGTCACCTTCAGGGCTCTTGG AAGCCAGGGGCATTTAGGATTAAAGAGAAACAAGGAAACCCGTTTGACAAAGGTGTTTTTCAAGATTGA AGAGAAAGAAATAGAACATGCTCTGAAAGATAAAGCTTTAATTGGAATATCTTAGCTAGTGGATTGCTT TAAATTTCTTCTTACACCCCAACCGAAAGTATTCAGCTGGCATTAGAGAGCTACAGCTTTCATTTTAG TGCTTTACACATTCGGGCTGAAAACAAATATGACCTTTTTTACTTGAAGCCAATGAATTTTAACTATA GATTCTTTAATATTAGCACAGAAATAATATCTTTGGGTCTTACTATTTTACCATAAAAGTGACCAGGTA GACCCTTTTTAATTACATTCACCTTCTTACCCTTGTGTATCTTAGCCAATGTGCTTGCAAGTGTACA GATCTGTGTAGAGGAATGTGTATATTTTACCTCTTCGTTTGCTCAAACATGAGTGGGTATTTTTTGTGTT TGTTTTTTTTGTTGTTGTTGTTTTTGGAGCGCGTCTCACCCCTGTGCCCAGGCTGGAGTGCAATGGCGCG TTCCTGCTCACTACAGCACCCGCTTCCAGGTTGAAGTGATTCTCTTGCCACAGCTCCCGAGTAGCTG GGATTACAGGTGCCACCAACCGCGCCAGCTAATTTTTTAATTTTAGTAGAGACAGGTTTTTACCATGT TGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGAICTGCCACCTTGGCTCCCTAAGTGCTGGGAT TATAGGCGTGAGCCACCATGCTCAGCCATTAAGGTATTTGTTAAGAACTTTAAGTTTAGGGTAAGAAGA ATGAAAATGATCCAGAAAAATGCAAGCAAGTCCACATGGAGATTTGGAGGACACTGGTTAAAGAATTTAT TTCITTTGTATAGTATACTATGTTTATGGTGCAGATACTACAACATTTGTGGCATTTTAGACTCGTTGAGTT TCTTGGGCACTCCCAAGGCGTTGGGGTCATAAGGAGACTATAACTCTACAGATTGTGAATATATTTATT TTCAAGTTGCATTCTTTGCTTTTTTAAGCAATCAGATTTCAAGAGAGCTCAAGCTTTTCAAGTCAATGT GAAAAATTCCTTCCTAGGCTGTCCACAGTCTTTGCTGCCCTTAGATGAAGCCACTGTTTCAAGATGACT ACTTTGGGGTTGGGTTTTTCACTATAACACATTTTTCCAGTCTTATTAGATAAATAGTCCATATGGTTGG TTAATCAAGAGCCTTCTGGGTTTGGTTTGGTGGCATTAAATGG	101
NM_031423	GCGGAATGGGCGGGACTTCCAGTAGGAGGCGGCAAGTTTGAAGAGTGATGACGGTTGACGTTTGCTGAT TTTTGACTTTTGCTTGTAGCTGCTCCCCGAACCTCGCCGCTTCTCTGTCGGCGGCCGCACTGTAGATTAAAC AGGAAACTTCCAAGATGGAACCTTTGTCTTTCCAGATATAATGTAGCTGAGATTGTGATTCTATTCG CAATAAGATCTTAACAGGAGCTGATGGTAAAAACCTCACCAGAATGATCTTTATCCAAATCCAAGCCT	102

	GAAGTCTTGACATGATCTACATGAGAGCCTTACAAATAGTATATGGAATTCGACTGGAACATTTTTTACATGATGCCAGTGAACCTCTGAAGTCATGTATCCACATTTAATGGAAGGCTTCTTACCATTTCAGCAATTTAGTTACTCATCTGGACTCATTTTTTGCCCTATCTGCCGGGTGAATGACTTTGAGACTGCTGATATTTCTATGTCCA AAAGCAAAACGGACAAGTCGGTTTTTAAGTGGCATTATCAACTTTATTCACTTCAGAGAAGCATGCCGTG AAACGTATATGGAATTTCTTTGGCAATATAAATCCTCTGCGGACAAAATGCACAGTTAAACGCCGCACA CCAGGAGGCATTAATGAAACTGGAGAGACTTGATTCTGTTCAGTTGAAGAGCAAGAAGATTCAAGCAG CTTTTCAGATGGAATTCAGGAGCTACAACAATCACTAAATCAGGATTTTCATCAAAAAACGATAGTGCTGC AAGAGGGAATTTCCCAAAAGAAGTCAAATATTTTCAGAGAAAACCAAGCGTTTGAATGAACATAAAATTTGTC GGTGGTTTTCTTTGAAAGAAAATACAAGAGAGTTTGAAGCAAAAATTTGTGGATTCTCCAGAGAAGTTAAAG AATTATAAAGAAAAAATGAAAGATACGGTCCAGAAGCTTAAAAATGCCAGACAAGAAGTGGTGGAGAAAT ATGAAATCTATGGAGACTCAGTTGACTGCCTGCCTTCATGTCTAGTTGGAAGTGCAGTTATATCAAAAGAA AATACAGGACCTTTTCAGATAATAGGGAATAATAGCCAGTATCTTAAAGGAGAGCCCTGAACCTGGAGGAC CAAAATTGAGAGTGATGAGTCAGAACTGAAGAAATTTGAAGACTGAAGAAAATTCGTTTCAAAAGACTGATGA TTGTGAAGAAGGAAAACTTGCCACAGCACAAATCAAAAATAAATAAGAAGCATGAAGATGTTAAGCAATA CAAAACGCACAGTAATTGAGGATTGCAATAAAGTTCAAGAAAAAGAGGTGCTGTCTATGAACGAGTAACC ACAATTAATCAAGAAATCCAAAAATTAACCTTGAATTCACAACTAAAAGATGCTGCTGAAGGGGAGA AAGTGAAGTCCCGAGAAATATTTCTAACTTGAAGAACTGCTTTGGAGAAATACCACGAGCTGATTTGAAAA GGCAGCAGAGGACTCCTATGCTAAGATAGATGAGAAGACAGCTGAACCTGAAGAGGAAGTGTTCAAAATG TCAACCTGATTAAACAAAATTACATGTCTTTTTGTAAATGGCTTGCCATCTTTTAAATTTTCTATTTAGAAA GAAAAGTTGAAGCGAATGGAAGTATCAGAAGTACCAATAATGTTGGCTTCATCAGTTTTTATACACTCT CATAAGTAGTTAATAAGATGAATTTAATGTAGGCTTTTTATTAATTTATAATTAAAAATAACTTGTGCAGCT ATTCATGTCTCTACTCTGCCCTTGTGTAAATAGTTTGAGTAAAACAAACTAGTTACCTTTGAAATAT ATATATTTTTTTCTGTTACTATC	
BC041846	GGCTAGCGCGGAGGTGGAGAAAGAGGCTTGGGCGGCCCCGCTGTAGCCGCGTGTGGGAGGACGCACGGG CCTGCTTCAAAGCTTTGGGATAACAGCGCCTCCGGGGGATAATGAATGCGGAGCCTCCGTTTTTCAGTCTGA CTTCAGATGTGTCTCCACTTTTTTCCGCTGTAGCCGCAAGGCAAGGAAACATTTCTCTTCCCGTACTGAG GAGGCTGAGGAGTGCACCTGGGTGTTCTTTCTCCTTAACCCAGAACTGCGAGACAGAGGCTGAGTCCCT GTAAAGAACAGCTCCAGAAAAGCCAGGAGAGCGCAGGAGGGCATCCGGGAGGCCAGGAGGGTTCCGTGG GGCTCAACCCGACCCACATCGGTCCACCTGCGAGGGGGCGGGACCTCGTGGCGCTGGACCAATCAGCA CCCACCTGCGCTCACCTGGCCTCCCTCCCGCTGGCTCCCGGGGGCTGCGGTGCTCAAAGGGGCAAGAGCTG AGCGGAACACCCGCCCCGCGTCCGCGGACGTGCTTACCCCTCTCTCTGACGCCATGGGGCTCCCTCGTG GACCTCTCGCGTCTCTCTCTCTTCTCCAGGTTTGTCTGGCTGACGTGCGCGGCTCCGAGCCGTCGCGGG GGTCTTCAGGGAGGCTGAAGTGACCTTGGAGCGGGAGCGCGGAGCAGGAGCCCGGCCAGCGCTGGGG AAAGTATTCATGGGCTGCCCTGGGCAAGAGCCAGCTCTGTTTAGCACTGATAATGATGACTTCACTGTGC GGAATGGCGAGACAGTCCAGGAAAGAGGTCACTGAAGGAAAGGAATCCATTGAAGATCTTCCCATCCAA ACGTATCTTACGAAGACACAAGAGAGATTGGGTGGTGTCTCAATATCTGTCCCTGAAAAATGGCAAGGGT CCCTTCCCCAGAGACTGAATCAGCTCAAGTCTAATAAAGATAGAGACCAAGATTTTCTACAGCATCA CGGGGCGGGGCGAGACAGCCCCCTGAGGGTGTCTTCTGCTGTAGAGAAGGAGACAGGCTGGTTGTGT GAATAAGCCACTGGACCGGGAGGAGATTGCCAAGTATGAGCTCTTTGGCCACGCTGTGTGTCAGAGAATGGT GCCTCAGTGGAGGACCCCATGAACATCTCCATCATAGTGACCGACCAAGATGACCACAGCCCAAGTTTA CCCAGGACACCTTCCGAGGGAGTGTCTTAGAGGGAGTCTTACCAGGTACTTCTGTGATGACATGACAGC CAGAGATGAGGATGATGCCATCTACACCTACAATGGGGTGGTTGCTTACTCCATCCATGCAAGAACCA AAGGACCCACAGACCTCATGTTTACAATTCACCGAGCACAGGCACCATCAGCGTCATCTCCAGTGGCC TGGACCGGGGAAAAAGTCCCTGAGTACACACTGACCATCCAGGCCACAGACATGGATGGGGACGGCTCCAC CACCACGGCAGTGGCAGTAGTGGAGATCCTTGATGCCAATGACAATGCTCCCATGTTTGACCCCCAGAAG TACGAGGCCCATGTGCCGTGAGAATGCAGTGGGCCATGAGGTGCAGAGGCTGACGGTCACTGATCTGGACG CCCCCAACTCACAGCGTGGCGTGCCACCTTATCATGCGCGGTGACGACGGGGACCATTTTACCAT CACCACCCACCTGAGAGCAACCAGGGCATCTGACAACCAAGGAGGTTTGGATTTTGGAGCCAAAAAC CAGCACACCCCTGTACGTTGAAGTGACCAACGAGGCCCTTTTGTGCTGAAGCTCCCAACCTCCACAGCCA CCATAGTGGTCCACGTGGAGGATGTGAATGAGGCACCTGTGTTTGTCCACCTCCAAAGTCGTTGAGGT CCAGGAGGGCATCCCCACTGGGGAGCCTGTGTGTGTCTACACTGCAGAAGACCCGTGACAAGGAGAATCAA AAGATCAGCTACCGCATCTCTGAGAGACCCAGCAGGGTGGCTAGCCATGGACCCAGACAGTGGGCAGGTCA CAGCTGTGGGCACCCCTCGACCGTGAGGATGAGCAGTTTGTGAGGAACAACATCTATGAAGTCATGGTCTT GGCCATGGACAATGGAAGCCCTCCACCCACTGGCACGGGAACCCCTTCTGCTAACACTGATTGATGTCAAC GACCATGGCCAGTCCCTGAGCCCCGTGAGTACCATCTGCAACCAAGCCCTGTGCGCCAGGTGCTGA ACATCAGGACAAGGACCTGTCTCCCCACCTCCCCCTTCCAGGCCAGCTCACAGATGACTCAGACAT CTACTGGACGGCAGAGGTCAACGAGGAAGGTGACACAGTGGTCTTGTCCCTGAAGAAGTTCCTGAAGCAG GATACATATGACGTGCACCTTTCTGTGTGTGACCATGGCAACAAAGAGCAGCTGACGGTGATCAGGGCCA CTGTGTGCGACTGCCATGGCCATGTGGAACCTGCCCTGGACCCCTGGAAGGAGGTTTCATCTCTCCCTGT GCTGGGGGCTGTCTGGCTGTGCTGTCTCTCTGCTGGTGTGCTTTTGTGGTGAGAAAGAAGCGGAAG ATCAAGGAGCCCCCTCTACTCCCAAGATGACACCCGTGACAACGCTCTTCTACTATGGCGAAGAGGGGG GTGGCGAAGAGGACGAGACTATGACATCACCCAGCTCCACCGAGTCTGGAGGCCAGGCCGAGGTGGT TCTCCGCAATGACGTGGCACCAACCATCATCCCGACACCCATGTACCGTCTAGGCCAGCCAACCCAGAT GAAATCGGCAACTTTATAATTGAGAACCTGAAGGCGGCTAACACAGACCCACAGCCCCGCCCTACGACA CCCTCTTGGTGTTCGACTATGAGGGCAGCGGCTCCGACGCCGCTCCCTGAGCTCCCTCACTCTCCCG CTCCGACCAAGACCAAGATTACGATTATCTGAACGAGTGGGGCAGCCGCTTCAAGAAGCTGGCAGACATG TACGTGTGGCGGGGAGGACGACTAGGCGGCCCTGCTGACGGGTGAGGACCAACAGCTCAGGACGACGA TCTCCAAGGGGTCTCAGTTCCCCCTTCACTGAGGACTTCGGAGCTGTGACGAAGTGGCCGTAGCAACT	103

	TGGCGGAGACAGGCTATGAGTCTGACGTTAGAGTGGTTGCTTCCTTAGCCTTTCAGGATGGAGGAATGTG GGCAGTTTGACTTCAGCACTGAAAACTCTCCACCTGGGCCAGGGTTGCCCTCAGAGGCCAAGTTTCCAGA AGCCTCTTTACCTGCCGTAAAAATGCTCAACCCCTTGTGCTGGGCCCTGGGCCTGCTGTGACTGACCTACAGT GGACTTTCTCTCTGGAATGGAACCTTCTTAGGCCCTCCTGGTGCAACTTAATTTTTTTTTTAAATGCTATC TTCAAACGTTAGAGAAAGTTCTTCAAAGTGCAGCCCAGAGCTGCTGGGCCCTGCGCGTCTCTGCATT TCTGGTTTCCAGACCCCAATGCCTCCCATTCGGATGGATCTCTGCGTTTTTATACTGAGTGTGCCTAGGT TGCCCTTATTTTTATTTTTCCCTGTGCGTTGCTATAGATGAAGGGTGAGGACAATCGTGATATGTAC TAGAACTTTTTTATTAAAGAACTTTTCCCAAAAAAAAAAAAAAAAAA	
NM_016343	GAGACCAGAAGCGGGCGAATTGGGCACCGGTGGCGGCTGCGGGCAGTTTGAATTAGACTCTGGGCTCCAG CCCCCGAAGCGCGCCAGAAGTGTACTCTCCGAGAGGTCGTTTTCCCGTCCCGAGAGCAAGTTTATTT ACAAATGTTGGAGTAATAAAGAAGGCAGAACAAAATGAGCTGGGCTTTGGAAGAATGGAAGAAGGGCTG CCTACAAGAGCTCTTCAGAAAATTCAGAGCTTGAAGGACAGCTTGACAACTGAAGAAGGAAAAGCAGC AAAGGCAGTTTCAGCTTGACAGTCTCGAGGCTGCGCTGCAGAAGCAAAAACAGAAGTTGAAAAATGAAAA AACCAGGGGTACAAACCTGAAAAGGGAGAATCAAAGATTGATGGAATATGTGAAAGTCTGGAGAAAAC AAGCAGAAGATTTCTCATGAACCTCAAGTCAAGGAGTCACAAGTGAATTTCCAGGAAGGACAACCTGAATT CAGGCAAAAAACAAATAGAAAACTGGAACAGGAACCTTAAAGGTGTAAATCTGAGCTTGAAAGAAGCCA ACAAGCTGCGCAGTCTGCAGATGCTCTCTGAATCCATGCAATACACCACAAAAATTTTTTCAACTCCA CTAACACCAAGTCAATATTATAGTGGTTCCAGTATGAAGATCTAAAAAGAAAAATATAATAAAGAGGTG AAGAACGAAAAAGATTAGAGGCAGAGGTTAAAGCCTTGCAGGCTAAAAAGCAAGCCAGACTCTTCCACA AGCCACCATGAATCACCGCGACATTGCCCGGCATCAGGCTTCATCATCTGTGTCTCATGGCAGCAAGAG AAGACCCCAAGTCATCTTTCATCTAATTTCTCAAAGAAGTCCAAATAGGAGAGATTTCTCTGCATCTTACT TTTTCTGGGGAACAAGAGGTGACTCCAAGTCGATCAACTTTGCAATAGGGAAGAGAGTCTAATAGCAG TTTTCTTTGACAAATTTAGCAGTCTCATCTTTTGGATCAATTAAGAGCGCAGAAATCAAGAGCTAAGAAAC AAGATTAATGAGTTGGAACACGCTGCAAGGACATGAAAAAGAAATGAAAGGCCAAGTGAATAAGTTTC AAGAACTCCAACCTCCAACCTGGAGAAAGCAAAAGTGAATTAATTAAGAAAGAGAAAGTTTGAACAAATG TAGGGATGAAC TAGTGAACAACAGCACAATACGACCAGGCGTCAACCAAGTATACTGCATTGGAACAA AACTGAAAAAATGACGGAAGATTTGAGTTGTGACGACAAAAATGCAGAAAGTGCCAGATGTTCTCTGG AACGAAAAATTAAGGAAAAAGAAAAAGGATTTCAAGAGGAGCTCTCCCGTCAACAGCGTTCTTTCCAAAC ACTGGACAGGAGTGCATCCAGATGAAGGCCAGACTCACCCAGGAGTTACAGCAAGCCAAAGATATGCAC AACGTCTGCGAGGCTGAACTGGATAAACTCACATCAGTAAAGCAACAGCTAGAAAAACAAATTTGGAAGAGT TTAAGCAAAAGTTGTGCGAGCTGAACAGGCGTTCCAGGCGAGTCAGATCAAGGAGAATGAGCTGAGGAG AAGCATGGAGGAATGAAGAAGGAAAAACACCTCCTTAAGAGTCACTCTGAGCAAAAAGGCCAGAGAAGTC TGCCACCTGGAGGCAGAACTCAAGAACATCAACAGTGTTTAAATCAGAGCCAGAAATTTGCAAGAGAAA TGAAAGCGAAGAAATACCTCTCAGGAAACCATGTTAAGAGATCTTCAAGAAAAAATAAATCAGCAAGAAAA CTCCTTGACTTTAGAAAACTGAAGCTTGCTGTGGCTGATCTGGAAAAGCAGCGAGATTGTTCTCAAGAC CTTTTGAAGAAAAGAGAATCATCATTTGAACAACCTTAATGATAAGTTAAGCAAGACAGAGAAAGAGTCCA AAGCATGCTGAGTGTCTTTAGAGTTAAAAAGAAAGAATATGAAGAATTGAAGAAAGAGAAAACTCTGTT TTCTTGTGGAAAAGTGAAGAACGAAAAACTTTTAACTCAGATGGAATCAGAAAAGGAAACTTGCAAGAT AAAATTAATCACTTGGAACCTTGCTGAAGACACAGCAAAATAAAAGTCAATGAATACAACGAGAGAGTAA GAACGCTGGAGATGGACAGAGAAAAACCTAAGTGTGAGATCAGAAACCTTCACAACGTTGTAGACAGTAA GTCAGTGGAGGTAGAGACCCAGAACTAGCTTATATGGAGCTACAGCAGAAAGCTGAGTTCTCAGATCAG AACATCAGAAAGAAATAGAAAAATATGTGTTGAAGACTTCTCAGCTTACTGGGCAAGTTGAAGAACTTAG AACACAAGCTTCAGTTACTGTCAAATGAAATAATGGACAAGACCGGTGTTACCAAGACTTGCATGCCGA ATATGAGAGCCTCAGGGATCTGCTAAAAATCCAAAGATGCTTCTCTGGTGACAAATGAAGATCATCAGAGA AGTCTTTTGGCTTTTGATCAGCAGCTGCCATGCATCATTCCTTTGCAAAATATAATTGGAGAACAAGGAA GCAATGCTTTCAGAGAGGAGTGAATGTCGTTTGAAGCAGACCAAGTCCGAAAAATTTGCTCCATCTTACA AAATGAGGTTGATTCACTTGAATTTTCAATTAGAGTCTCAAAAACAGATGAACCTGCACAAAGCAG TGTAAGAGTTGGTGCAAATCAAAGGAGAAATAGAAGAAAAATCTCATGAAAGCAGAACAGATGCATCAAA GTTTTGTGGCTGAAACAAGTCAGCGCATTAGTAAGTTACAGGAAGACACTTCTGCTCACCAGAATGTTGT TGCTGAAACCTTAAGTGCCTTTGAGAACAAGGAAAAAGAGCTGCAACTTTTAAATGATAAGGTAGAACT GAGCAGGCAGAGATTCAAGAATTAAGAAAGAGCAACCATCTACTTGAAGACTCTCTAAAGGAGCTACAAC TTTTATCCGAAACCTTAAGCTTGGAGAAGAAAGAAATGAGTTCCATCATTCTTCTAAATTAAGGGAAT TGAAGAGCTGACCCAAGAGAATGGGACTCTTAAGGAAATTAATGCATCCTTAAATCAAGAGAAGATGAAC TTAATCCAGAAAAGTGAGAGTTTTGCAACTATATAGATGAAAGGGAGAAAAGCATTTTCAGAGTTATCTG ATCAGTACAAGCAAGAAAAAATTTATTTTACTACAAAGATGTGAAGAAACCGGAAATGCATATGAGGATCT TAGTCAAAAATACAAAGCAGCACAGGAAAAAGAAATCTAAATTAGAATGCTTGCTAAATGAATGCACTAGT CTTTGTGAAAATAGGAAAAATGAGTTGGAACAGCTAAAGGAAGCATTTGCAAGGAACACCAAGAAATTTCT TAACAAAATTAGCATTTTGTGTAAGAAAGAAATCAGAATCTGATGCTAGAGTTGGAGACAGTGCAGCAAGC TCTGAGATCTGAGATGACAGATAACCAAAACAATTTCTAAGAGCGAGGCTGGTGGTTTTAAAGCAAGAAATC ATGACTTTAAAGGAAGAACAAAAACAAATGCAAAAGGAAGTTAATGACTTATACAAAGAGAATGAACAGC TGATGAAGGTAATGAAGACTAAACATGAATGTCAAAAATCTAGAATCAGAACCAATTAGGAACCTCTGTGAA AGAAAGAGAGAGTGAGAGAAATCAATGTAATTTTAAACCTCAGATGGATCTTGAAGTTAAAGAAATTTCT CTAGATAGTTATAATGCGCAGTTGGTGCAATTAGAAGCTATGCTAAGAAATAAGGAATTAAGAACTTCAGG AAAGTGAGAAGGAGAAGGAGTGCCTGCAGCATGAATTACAGACAATTAGAGGAGATCTTGAAACCAGCAA TTTTGCAAGACATGCAGTCAAGAAATTAGTGGCTTAAAGACTGTGAAATAGATGCGGAAGAAAGATAT ATTTGAGGGCTCATGAGTTGTCAACAAGTCAAAACGACAATGCACACCTTCAGTGCTCTCTGCAAAACAA CAATGAACAAGCTGAATGAGCTAGAGAAAAATGTGAATACTGCAGGCTGAAAAGTATGAACCTGTAAC TGAGCTGAATGATTCAAGGTGCAATGTATCAGCAACTAGGAAAAATGGCAGAAGAGGTAGGGAACCTA	104

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AB091343	GGCAGAGGGGCCGACGCGAGCGCCGCGCTTCGCTTCAGCTGCTAGCTGGCCCAAGGGAGGCGACCGCGG AGGGTGGCGAGGGGCCGAGGCCGAGCCCCGGGGCCGGGCGGTCCGGACCGCCAGGAGGGCAGG TCAGTGGGCGAGATCGCGTCCGCGGATTCAAATCTCTGCGCGCTCTGATAACAGTCTCTTTCCCTGGCGCT CACTTCGTGCTGGCACCCGCGCTGGGCGCCTCAAGACCGTTGTCTCTTCGATCGCTTCTTTGGACTTGGC GACCATTTCCAGAGATGTCTCCAGAAGTACCAAAGATTAAATTAAGTAAGTGGGGATCGAAGCCTAGT AACTCCAAATCCGAAACTACATTAGAAAAATTAAGGGAGAAATTCACACTTAAAGACATCAGTGGATG AAATCACAAGTGGGAAAGGAAAGCTGACTGATAAAGAGAGACACAGACTTTGGAGAAAATTCGAGTCTCT TGAGGCTGAGAAGGAGAAGAATGCTTATCAACTCACAGAGAAGGACAAAGAAATACAGCGACTGAGAGAC CAACTGAAGGCCAGATATAGTACTACCGCATTTGCTTGAACAGCTGGAAGAGACAACGAGAGAAGGAGAAA GGAGGGAGCAGGTGTTGAAAGCCTTATCTGAAGAGAAAGACGTATTGAAACACAGTTGTCTGCTGCAAC CTCAGCAATTGCTGAACCTTGAAGCAAAACCAATACACTCCGTTTATCACAGACTGTGGCTCCAACTGC TTCAACTCATCAATAAATAATATTCATGAAATGGAAATACAGCTGAAAGATGCTCTGGAGAAAATCAGC AGTGGCTCGTGTATGATCAGCAGCGGGAAGTCTATGTAAGAGGACTTTTAGCAAAGATCTTTGAGTTGGA AAAGAAAACGGAAACAGCTGCTCATTCACTCCACAGCAGACAAAAAGCCTGAATCAGAAGGTTATCTT CAAGAAGAGAAAGCAGAAATGTTACACAGATCTCTTGGCAAGTGCAAAAAAGATCTTGAGGTTGAACGAC AAACCATAACTCAGCTGAGTTTTTGAAGTGAAGTGAATTTGCAAGAAAATATGAAGAAACCCAAAAAGAAGT TCACAAATTTAAATCAGCTGTTGTATTCACAAAGAAGGGCAGATGTGCAACATCTGGAAGATGATAGGCAT AAAACAGAGAAGATACAAAACCTCAGGGAAGAGAGAATGATATTGCTAGGGGAAAACCTGAAAGAGAAGA AGAGATCCGAAGAGCTCTTATCTCAGGTCCAGTTTCTTTACACATCTCTGCTAAAGCAGCAAGAAGAACA AACAGGGTAGCTCTGTTGGAACAACAGATGCAAGCATGTACTTTAGACTTTGAAAATGAAAACCTCGAC CGTCAACATGTGCAGCATCAATTGCAATGTAATTTCTTAAGGAGCTCCGAAAAGCAAGAAATCAATAACAC AGTTGGAATCCTTGAACAGCTTTCATGAGTTTGCCATCACAGAGCCATTAGTCACTTTCCAAGGAGAGAC TGAAAAACAGAGAAAAGTTGCCGCTCACAAAAAGTCCCACTGCTGCACTCAATGAAAGCCTGTTGGAA TGTCCTCAAGTCAATATACAGTATCCAGCCACTGAGCATCGCGATCTGCTTGTCCATGTGGAATACTGTT CAAAGTAGCAAAATAAGTATTTGTTTTGATATTAAAGATTCAATAGTATTTCTGTAGCTTGTGGG CATTTTGAATTATATATTTTACATTTTGCATAAACTGCCTATCTACCTTTGACACTCCAGCATGCTAGT GAATCAGTATCTTTTAGGCTGCTGTGCAATTTCTCTTGGCAGTGATACCTCCTGACATGACATTGAACTATC AGGTGCAATGACAGAATGTGGTGAGCAGCGTCTACTGAGACTACTAACATTTTGCAGTGTCAAAATACT TGGTGAGGAAAAGATAGCTCAGGTTATTGCTAATGGGTTAATGCACCAGCAAGCAAAATATTTTATGTTT TGGGGGTTTGA AAAATCAAAGATAATTAACCAAGGATCTTAAGTGTTCGCAATTTTTTATCCAAGCACT TAGAAAACCTACAATCCTAATTTTGTATGTCATTTGTTAAGAGGTGGTGATAGATACTATTTTTTTTTTCA TATGTATAGCGGTTATTAGAAAAGTTGGGATTTTCTGTATCTTTATTGCTGTTACGATTGAACCTTA ACCCAGCTGTGTTCCCAACTCTGTTCTGCGCACGAAACAGTATCTGTTTGAAGGCATAATCTTAAGTGGC CACACACAATGTTTTCTCTTATGTTATCTGGCAGTAACTGTAACITGAATTACATTAGCACATTCTGCTT AGCTAAAATTTGTTAAATAAACTTTAATAAACCCATGTAGCCCTCTCATTTGATTGACAGTATTTTAGTT ATTTTTGGCATTTCTTAAGCTGGGCAATGTAATGATCAGATCTTTGTTTGTCTGAACAGGTATTTTTATA CATGCTTTTTGTAAACCAAAAACCTTTAAATTTCTTCAAGTTTTCTAACATGCTTACCCTGGGCTACTG TAAATGAGAAAAGAATAAAATATTTAATGTTTTAAAAA	105
BC006428	GGCGCTGAGCCTGAGCGGGGATGTAGAGGCGGCGGCAGCAGAGGCGGCACTGGCGGCAAGAGCAGACGC CCGAGCCGAGCGAGAAGAGCGGCAGAGCCTTATCCCCTGAAGCCGGGCCCCCGCTCCAGCCCTGCCAG CCCGCGCCAGCCATGCGCGCCCTGCTGAGTCCGGGCGCGCACGCTGAGCCCTCCGCCCGCAGCCG CGCTCAGCTCGGGGGTGATTAGTTGCTTTTTGTTTAAATTTGGGCGCGGGAGGGGAGGAGGG GCAGGTGCTGCAGGCTCCCCCCCCCTCCCGCCTCGGGCCAGCGCGGCGGCGGACTCGGGCTCCGGACC CGGGCACTGCTGGCGGCTGGAGCGGAGCGCACC GCGCGGTGGTGCCAGAGCGGAGCGCAGCTCCCTGC CCCCCCCCCTCCCGCTCGCGGCGACGGCGGCGGTGGCGGCTTGGACGACTCGGAGAGCCGAGTGA AGACATTTCCACCTGGACACCTGACCATGTGCTGCGCTGAGCAGCGAGGCCCCACAGGCATCTCTGTTG TGGGCGCAGGCGCAGGTCCTGCTGTGGACCCCTCGGAGCTTGGCAGGCTCCCTCTGAGTGGGGTCTG GGCTCGGCCCCACCATGTGCGAGCCTCGGCGGTGGCTCCAGGATGCCGCGGCAGTAGCAGCAGCAGCA	106

	CCAATGGCAGCGGTGGCAGTGGCAGCAGTGGCCCAAAGGCAGGAGCAGCAGACAAGAGTGCAGTGGTGGC TGCCGCCGCACCAGCCTCAGTGGCAGATGACACACCACCCCGAGCGTCGGAACAAGAGCGGTATCATC AGTGAGCCCCCTCAACAAGAGCCTGCGCCGCTCCCGCCCGCTCTCCCACTACTCTTTTGGCAGCAGTG GTGGTAGTGGCGGTGGCAGCATGATGGGCGGAGAGTCTGCTGACAAGGCCACTGCGGCTGCAGCCGCTGC CTCCCTGTTGGCCAATGGGCATGACCTGGCGCGCGCCATGGCGGTGGACAAAAGCAACCTTACCTCAAAG CACAAAAGTGGTGCTGTGGCCAGCCTGCTGAGCAAGGCAGAGCGGGCCACGGAGCTGGCAGCCGAGGGAC AGCTGACGCTGCAGCAGTTTGGCGAGTCCACAGAGATGCTGAAGCGCGTGGTGAGGAGCATCTCCCGCT GATGAGCGAGGCGGGTGCTGGCCTGCCTGACATGGAGGCTGTGGCAGGTGCCGAAGCCCTCAATGGCCAG TCCGACTTCCCTTACCTGGGCGCTTTCCCATCAACCCAGGCCTCTTATTATGACCCCGGCAGGTGTGT TCCTGGCCGAGAGCGCGCTGCACATGGCGGGCTGGCTGAGTACCCCATGCAGGGAGAGCTGGCCTCTGC CATCAGCTCCGGCAAGAAGAAGCGGAAACGCTGCGGCATGTGCGCGCCCTGCCGGCGGCATCAACTGC GAGCAGTGCAGCAGTTGTAGGAATCGAAAGACTGGCCATCAGATTTGCAAAATCAGAAAATGTGAGGAAC TCAAAAAGAAGCCTTCCGCTGCTCTGGAGAAGGTGATGCTTCCGACGGGAGCGCCTTCCGGTGGTTTCA GTGACGGCGGGCGGAACCCAAAGCTGCCCTCTCCGTGCAATGTCACTGCTCGTGTGGTCTCCAGCAAGGGA TTCGGGCGAAGACAAACGGATGCACCCGCTTTAGAACCAAAAATATTCTCTACAGATTTTATTCTGT TTTTATATATATATTTTTTGTGTGCTTTTAACTCTCCACGTCCCTAGCATAAAAAGAAAAAGAAAAA ATTTAAACTGCTTTTTTGGGAAGAACAACAACAAAAAGAGGTAAAGACGAATCTATAAAGTACCGAGACT TCCTGGGCAAGAATGGACAATCAGTTTCCCTTCTGTGTCGATGTGATGTTGTCTGTGTCAGGAGATGCA GTTTTGTGTAGAGAATGTAAATTTTCTGTAACTTTTGAATCTAGTTACTAATAAGCACTACTGTAAT TTAGACAGTTTAACTCCACCCTCATTTAACTTCCCTTGATTCTTTCCGACCATGAAATAGTGCATAGT TTGCCTGGAGAATCCACTCAGTTTCATAAAGAGAATGTTGATGGCGCGCTGTAGAAGCCGCTCTGTATCC ATCCAGCGTGCAGAGCTGCCAGCAGGGAGCTCACAGAAGGGGAGGGAGCACCAGGCTGAGTGCATGCA CCCACAGTCCCGAGACTGGGATCCCCACCCCAACAGTGATTTTGGAAAAAAAATGAAAGTTCTGTTCG TTTTATCCATTGCGATCTGGGGAGCCCCATCTCGATATTTCCAATCTGGCTACTTTTCTTAGAGAAAAATA AGTCCTTTTTTCTGGCCTTGCTAATGGCAACAGAAAGAGGGCTCTTTGGCGTGGTCCCTGCTGGTGG GGGTGGGTCCCGAGGGGGCCCCCTGCGGCCTGGGCCCCCTGCCACGGCCAGCTTCTGTGATGAACA TGGCTTTGTATTGTTTTAGGAAACCAAGGCTGTTTTGTGAATAAAACGAATGCATGTTTGTGTACAGAAA AA	
NM_005228	CCCCGGCGCAGCGCGGCCGAGCAGCCTCCGCCCCCGCAGCGTGTGAGCGCCCGACGCGGCCGAGGCGG CCCGAGTCCCCAGCTAGCCCCGGCGGCCGCCGCCGCCAGACCGGACGACAGGCCACCTCGTCGGCGTCC GCCCGAGTCCCCGCTCGCCGCCAACGCCACAACCACCGCGCACGGCCCCCTGACTCCGTCCAGTATTGA TCGGGAGAGCGGAGCGAGCTCTTCGGGGAGCAGCGATGCGACCCCTCCGGGACGGCCGAGCGCTCC TGGCGCTGCTGGCTGCGCTCTGCCCGCGAGTGGGCTCTGGAGAAAAAGAAAGTTTGGCAAGGCACGAG TAACAAGCTCAGCAGTTGGGCACCTTTGAAGATCATTTCTCAGCCTCCAGAGGATGTTCAATAACTGT GAGGTGGTCCCTGGGAATTTGGAATTAACCTATGTGCAGAGGAATTATGATCTTCCCTCTTAAAGACCA TCCAGGAGGTGGCTGGTTATGTCTCATTTGCCCTCAACACAGTGGAGCGAATTCCTTTGGAACCTGCA GATCATCAGAGGAATATGTACTACGAAATTCCTATGCCTTAGCAGTCTTATCTAACTATGATGCAAT AAAACCGACTGAAGGAGCTGCCCATGAGAAATTTACAGGAAATCCTGCATGGCGCGGTGCGGTTACGCA ACAACCTGCCCTGTGCAACGTGGAGAGCATCCAGTGGCGGGACATAGTCAGCAGTGACTTTCTCAGCAA CATGTGATGAGTCTCCAGAACCACTGGGCAGCTGCCAAAAGTGTGATCCAGCTGTCCCAATGGGAGC TGCTGGGGTGCAGGAGAGGAGAACTGCCAGAACTGACCAAAATCATCTGTGCCCAGCTGCTCCGGGC GTGCGCGTGGCAAGTCCCCAGTGACTGTGCCACAACCAAGTGTGCTGCAGGTGTCACAGGCCCGGGGA GAGCGACTGCTGGTCTGCCGCAATTTCCGAGACGAAGCCACGTGCAAGGACACCTGCCCCCCACTCATG CTCTACAACCCCAACACGTACCAGATGGATGTGAACCCGAGGGCAATACAGCTTTGGTGCCACCTGCG TGAAGAAGTGTCCCGTAATTTATGTTGGTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGGGGCCGACAG CTATGAGATGGAGGAAGACGGCGTCCGCAAGTGTGAAGAGTGCAGAGGGCCTTGGCGCAAAGTGTGTAAC GGAATAGGTATTTGGTGAATTTAAAGACTCACTCTCCATAAATGCTACGAATATTAACAACTTCAAAACT GCACCTCCATCAGTGGCGATCTCCACATCCTGCCGTGGCATTTAGGGGTGACTCCTTACACATACTCC TCCCTGGATCCACAGGAACCTGGATATTCTGAAAACCGTAAAGGAAATCACAGGGTTTTTGTGATTTCAG GCTTGGCCTGAAAACAGGACGGACCTCCATGCCTTTGAGAACCTAGAAATCATACGCGCAGGACCAAGC AACATGGTCAGTTTTCTCTTGCACTGCTCAGCCTGAACATAACATCCTTGGGATTACGCTCCCTCAAGGA GATAAGTGATGGAGATGTGATAATTTAGGAAACAAAAATTTGTGCTATGCAATACAAATAAACTGGAAA AAACTGTTTGGGACCTCCGGTCAGAAAACCAAAATTTATAAGCAACAGAGGTGAAAACAGCTGCAAGGCCA CAGGCCAGGCTGCCATGCCTTTGTGCTCCCCGAGGGCTGTGGGGCCCGAGCCAGGGACTGCGTCTC TTGCCGGAATGTGAGCCGAGGACGGGAATGCGTGGACAGTGCAACCTTCTGGAGGGTGAGCCAAGGGAG TTTGTGGAGAACTCTGAGTGACATACAGTGCCACCCAGAGTGCCCTGCCTCAGGCCATGAACATCACCTGCA CAGGACGGGGACAGACAACCTGTATCCAGTGTGCCACTACATTGACGGCCCCCACTGCGTCAAGACCTG CCCCGACAGGATCATGGGAGAAAAACAACCCCTGGTCTGGAAGTACGCAGACGCGCGCCATGTGTGCCAC CTGTGCCATCCAACTGCACCTACGGATGCACTGGGCCAGGTCTTGAAGGCTGTCCAACGAATGGGCCTA AGATCCCGTCCATCGCCACTGGGATGGTGGGGGCCCTCCTCTTGTGCTGTTGGTGGCCCTGGGGATCGG CCTCTTATGCGAAGGCGCCACATCGTTCCGAAGCGCACGCTGCGGAGGCTGCTGCAGGAGAGGGAGCTT GTGAGCCTCTTACACCCAGTGGAGAAGCTCCCAACCAAGCTCTCTTGAGGATCTGAAGGAACTGAAT TCAAAAAGATCAAAGTGTGGGCTCCGGTGGCTTCGGCACGGTGTATAAGGGACTCTGGATCCCAAGG TGAGAAAGTTAAATTTCCGCTCGCTATCAAGGAATTAAGAGAAGCAACATCTCCGAAAGCCAACAAGGAA ATCCTCGATGAAGCCTACGTGATGCCAGCGTGGACAACCCCCACGTGTGCCGCTGCTGGGCATCTGCC TCACCTCCACCGTGCAGCTCATCACGAGCTCATGCCCTTCGGCTGCCCTCTGGACTATGTCCGGGAACA CAAAGACAATATTGGCTCCCGTACCTGCTCAACTGGTGTGTGTCAGATCGCAAGGGCATGAACACTCTTG GAGGACCGTCTGTTGTGACCGCGACCTGGCAGCCAGGAACGTACTGGTGAACACCCGACGATGTCA	107

	AGATCACAGATTTTGGGCTGGCCAACTGCTGGGTGCGGAAGAGAAAAGAAATACCATGCGAGAAGGAGGCCAA AGTGCCATCAAGTGGATGGCATTTGAATCAATTTTACACAGAAATCTATACCCACCAGAGTGATGCTGCG AGCTACGGGGTGACCGTTTGGGAGTTGATGACCTTTTGATCCCAAGCCATATGACGGAATCCCTGCGCAGCG AGATCTCCTCCATCCTGGAGAAAGGAGAACGCCTCCCTCAGCCACCCATATGTACCATCGATGCTACAT GATCATGGTCAAGTGCTGGATGATAGACGCAGATAGTCGCCCAAAGTTCCGTGAGTTGATCATCGAATTC TCCAAAATGGCCCGAGACCCCCAGCGCTACCTTGTCAATTCAGGGGGATGAAAGAATGCATTTTGCCAAAGTC CTACAGACTCCAACCTTCTACCGTGCCCTGATGGATGAAGAAGACATGGACGACGTGGTGGATGCCGACGA GTACCTCATCCACACAGCAGGGCTTCTTCAGCAGCCCCCTCCACGTACGGACTCCCTCCTGAGCTCTCTG AGTGCAACCAGCAACAATTCACCGTGGCTTGCATTGATAGAAATGGGCTGCAAAGCTGTCCCATCAAGG AAGACAGCTTCTTGCAGCGATACAGCTCAGACCCACAGGCGCCTTGACTGAGGACAGCATAGACGACAC CTTCTCCAGTGCCCTGAATACATAAACACAGTCCGTTCCCAAAAGGCCGCTGGCTCTGTGCAGAAATCCT GTCTATCACAATCAGCCTCTGAACCCGCGCCAGCAGAGACCCACACTACCAGGACCCACAGCACTG CAGTGGGCAACCCCGAGTATCTCAACACTGTCCAGCCACCTGTGTCAACAGCATTTCGACAGCCCTGC CCACTGGGCCCCAGAAAGGCAGCCACCAATTAGCCTGGACAACCTGACTACCAGCAGGACTTCTTTCCC AAGGAAGCCAAAGCCAAATGGCATCTTTAAGGGCTCCACAGCTGAAAATGCAGAATACCTAAGGGTCGCGC CACAAAGCAGTGAATTTATGGAGCATGACCACGGAGGATAGTATGAGCCCTAAAAATCCAGACTCTTTC GATACCCAGGACCAAGCCACAGCAGGTCTCCATCCCAACAGCCATGCCCGCATTAGCTCTTAGACCCAC AGACTGGTTTTGCAACGTTTACACCGACTAGCCAGGAAGTACTTCCACCTCGGGCACATTTTGGGAAGTT GCATTCCTTTGTCTTCAAACCTGTGAAGCATTTACAGAAACGCATCCAGCAAGAATATTGTCCCTTTGAGC AGAAATTTATCTTTCAAAGAGGTATATTTGAAAAAAGATATATGTGAGGATTTTATTGATTGG GGATCTTGGAGTTTTTCATTGTCTGCTATTGATTTTACTTCAATGGGCTCTTCCAACAAGGAAGAAGCTT CTGGTAGCACTTGCTACCTTGAGTTTCATCCAGGCCCACTGTGAGCAAGGACACCAAGCCACAGTCTT CCAGAGGATGCTTGATTCCAGTGGTTCTGCTTCAAGGCTTCCACTGCAAAACACTAAAGATCCAAGGAAGG CCTTCATGGCCCCAGCAGGCGGATCGGTACTGTATCAAGTCATGGCAGGTACAGTAGGATAAGCCACTC TGTCCCTTCCCTGGGCAAGAAAGAAACGGAGGGGATGGAATCTTCTTAGACTTACTTTTGTAAAAATGT CCCCACGGTACTTACTCCCCACTGATGGACAGTGGTTTCCAGTCATGAGCGTTAGACTGACTTGTTTGT CTTCCATTCCATTGTTTTGAAACTCAGTATGCTGCCCTGTCTTGTGTCATGAGAAATCAGCAAGAGAGGA TGACACATCAAATAATAACTCGGATTCCAGCCACATTGGATTTCATCAGCATTGGACCAATAGCCACACA GCTGAGAATGIGGAATACCTAAGGATAGCACCGCTTTTGTCTCGCAAAACGTATCTCTAATTTGAGG CTCAGATGAAATGCATCAGGTCTTTGGGGCATAGATCAGAAGACTACAAAATGAAGCTGCTCTGAAAT CTCCTTTAGCCATCACCCCAACCCCCAAAATTAGTTTTGTGTTACTTATGGAAGATAGTTTTCTCCTTTT ACTTCCATTCAAAGCTTTTACTCAAAGAGTATATGTTCCCTCCAGGTACGTCGCCCCAGTCCCTCCT CTTACGCTTTGTACACAAAAAGTGTCTCTGCCTTGAGTCATCTATTCAAGCACTTACAGCTCTGCCCAC AACAGGGCATTTTACAGGTGCGAATGACAGTAGCATTATGAGTAGTGTGGAATTCAGGTAGTAAATATGA AACTAGGGTTTTGAAATTTGATAATGCTTTCACAACATTTGCAGATGTTTTAGAGGAAAAAAGTTCTCTCC TAAATAAATTTCTCTACAATTTGGAAGATTTGGAAGATTTCAGCTAGTTAGGAGCCACCTTTTTCTCTAATC TGTTGTGCCCCGTGAACCTGACTGGTTAACAGCAGTCTTTGTAAACAGTGTTTTAAACTCTTCTGACTCA ATATCCACCCCATCCAATTTATCAAGGAAGAAATGGTTTCAGAAAATATTTTCAGCCTACAGTTATGTTCA GTCACACACATACAAAATGTTCTTTTGTCTTTAAAGTAATTTTGACTCCAGATCAGTCAGAGCCC CTACAGCATTTGTTAAGAAAGTATTTGATTTTTGTCTCAATGAAAATAAACTATATTCAATTTCCACTCTA AAAAA	
NM_00100586 2	GTTCCCGGATTTTGTGGGCGCCTGCCCGCCCTCGTCCCCCTGCTGTGTCCATATATCGAGGCGATAG GGTTAAGGGAAGGCGGACGCCTGATGGGTTAATGAGCAAACTGAAGTGTTTTCCATGATCTTTTTGAGT CGCAATGAAGTACCACCTCCCGAGGGTGATTGCTTCCCATGCGGGGTAGAACCTTTGCTGTCTGTTC ACCCTCTACCTCCAGCAGAAATTTGGCTTATGCCTACTCAATGTGAAGATGATGAGGATGAAAACCTT TGTGATGATCCACTTCCACTTAATGAATGGTGGCAAAGCAAAGCTATATTCAAGACCACATGCAAAGCTA TCTCCTGAGCAAGAGTTCACAGATAAAACGGGGGCACCAAGTAGAATGGCCAGGACAAAGCAGTGACGA CAGAGACTCAGACCTGGCAGCCATGCCTGCGCAGGCAGTGATGAGAGTGACATGTACTGTTGTGGACAT GCACAAAAGTGTGTCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCAGAGACCCACCTGG ACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGCAGGGAACCTGGAACCTCACCTACCTGCCAC CAATGCCAGCCTGTCTTCTGTCAGGATATCCAGGAGGTGCAGGGCTACGTGCTCATCGCTCACAAACCA GTGAGGCAGGTCCCACTGCAGAGGCTGCGGATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCC TGGCCGTGTGACAAATGGAGACCCGCTGAACAATACCAACCCCTGTACAGGGGCTCCCCAGGAGGCCCT GCGGGAGCTGCAGCTTCAAGCCCTACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG CTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTCCACAAGAACCAACAGCTGGCTCTCACACTGA TAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAGGGCTCCCGCTGCTGGGGAGA GAGTTCTGAGGATTGTGACAGCCTGACGCGCACTGTCTGTGCGGTGGCTGTGCCCGTGCAGGGGCCA CTGCCCCTGACTGCTGCCATGAGCAGTGTGCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCCTGG CCTGCCCTCCACTTCAACCACAGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACCTACAACACAGA CACGTTTGAGTCCATGCCAATCCCGAGGGCCGATATACATTCCGCCCCAGCTGTGTGACTGCCTGTCCC TACAACCTACCTTTCTACGGACGTGGGATCTTGCAACCTCGTCTGCCCCCTGCACAACCAAGAGGTGACAG CAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGTTGGGCAT GGAGCACTTGGCAGAGGTGAGGGCAGTTACCAGTGCCAAATATCCAGGAGTTTGTGGCTGCAAGAAGATC TTTGGGAGCCTGGCATTCTGCGGAGAGCTTTGATGGGGACCCAGCCTCCAACACTGCCCGCTCCAGC CAGAGCAGCTCCAAGTGTGAGACTCTGGAAGAGATCAGAGTTACCTATACATCTCAGCATGGCCGGA CAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATCTGTCAACAATGGCGCC TACTCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGCACTGGGCAGTG GACTGGCCCTCATCCACATAACACCCACCTCTGCTTCGTGCACACGGTGCCTGGGACCAGCTCTTTCG	108

	GAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCAGAGGACGAGTGTGTGGGCGAGGGCCTGGCC TGCCACCAGCTGTGCGCCCGAGGGCACTGCTGGGGTCCAGGGCCACCCAGTGTGTCAACTGCAGCCAGT TCCTTCGGGGCCAGGAGTGCCTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGC CAGGCACTGTTTGCCGTGCCACCCTGAGTGTGAGCCCCAGAATGGCTCAGTGACCTGTTTGGACCGGAG GCTGACCAGTGTGTGGCCTGTGCCCACTATAAGGACCCCTCCCTTCTGCGTGGCCCGCTGCCCCAGCGGTG TGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAGGGCGCATGCCAGCCTTGCCC CATCAACTGCACCCACTCCTGTGTGGACCTGGATGACAAGGGCTGCCCGCCGAGCAGAGAGCCAGCCCT CTGACGTCCATCATCTCTGCGGTGGTTGGCATTCTGCTGGTCTGTGGTCTTGGGGTGGTCTTGGGATCC TCATCAAGCGACGGCAGCAGAAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGT GGAGCCGCTGACACCTAGCGGAGCGATGCCAACCCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATCCCTGATGGGG AGAATGTGAAAATTCCAGTGGCCATCAAAGTGTGAGGGAACACATCCCCAAAGCCAACAAAGAAAT CTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCATATGCTCCCGCTTCTGGGCATCTGCGCTG ACATCCACGGTGCAGCTGGTGACACAGCTTATGCCCTATGGCTGCTCTTAGACCATGTCGGGAAAAACC GCGACGCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGA GGATGTGCGGCTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACAGATACCATGTCAGATGGGGCAAGG TGGCCATCAAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTACCCACCAGAGTGATGTGTGGAG TTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCCAAACCTTACGATGGGATCCAGCCCGGAG ATCCCTGACCTGCTGGAAGAGGGGAGCGGCTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGA TCATGGTCAAATGTTGGATGATTGACTCTGAATGTGCGGCAAGATTCCGGGAGTTGGTGTCTGAATTCTC CCGATGGCCAGGGACCCCCAGCGCTTTGTGGTTCATCCAGAATGAGGACTTGGGCTTGGGCTTGGCTT GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCTGAGGAGTATC TGGTACCCAGCAGGGCTTCTTCTGTCCAGACCCCTGCCCGGGCGCTGGGGCATGGTCCACCACAGGCA CCGAGCTCATCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTCTGAAGAGGAGGCC CCCAGGTCTCCACTGGCACCCCTCCGAAGGGGTGGCTCCGATGTATTTGATGGTGACCTGGGAATGGGGG CAGCAAGGGGTGCAAAGCCTCCCCACACATGACCCAGCCCTCTACAGCGCTACAGTGAGGACCCAC AGTACCCCTGCCCTCTGAGACTGATGGCTACGTGCCCCCTGACCTGCAGCCCCAGCCTGAATATGTG AACCAGCCAGATGTTCCGCCCCAGCCCCCTTCCGCCCCGAGAGGGCCCTCTGCCTGCTGCCCGACCTGCTG GTGCCACTCTGAAAGGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGAGCTTTTGGCCTT TGGGGGTGCGGTGGAGAACCCCGAGTACTTGACACCCAGGGAGGAGCTGCCCTCAGCCCCACCCCTCCT CTGCTTTCAGCCAGCCCTTCGACAACCTTATTACTGGGACCAGGACCCAGCCAGCCAGCGGGGCTCCAC CCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCAGAGTACCTGGGTCTGGACGTGCCAGTGTGAAC CAGAAGGCCAAGTCCGCAGAAGCCCTGATGTGTCTCAGGGAGCAGGGAAGGCCTGACTTCTGCTGGCAT CAAGAGGTGGGAGGGCCCTCCGACCACTTCCAGGGGAACCTGCCATGCCAGGAACCTGTCTAAGGAACC TTCTTCTCTGCTTGTAGTTCAGATGGCTGGAAGGGGTCCAGCCTCGTTGGAAGAGGAACAGCACTGGGG AGTCTTTGTGATTCTGAGGCCCTGCCCAATGAGACTCTAGGGTCCAGTGGATGCCACGCCAGCCTTGG CCCTTCTCTCAGATCCTGGGTACTGAAAGCCTTAGGGAAGCTGGCCTGAGAGGGGAAGCGGCCCTAAG GGAGTGTCTAAGAACAAAAGCGACCCATTTCAGAGACTGTCCCTGAAACCTAGTACTGCCCCCATGAGGA AGGAACAGCAATGGTGTGAGTATCCAGGCTTGTACAGAGTGCTTTTCTGTTAGTTTTTACTTTTTTGT TTTTGTTTTTTAAAGATGAAATAAAGACCCAGGGGGAGAATGGGTGTTGTATGGGGAGGCAAGTGTGGG GGGCTTCTCCACACCCACTTTGTCCATTGTCAAATATATTTTGGAAAACAGCTA	
NM_00112274 2	ATGGTCATAACAGCCTCCTGTCTACCGACTCAGAACGGATTTTACCAAAACTGAAAATGCAGGCTCCATG CTCAGAAGCTCTTTAACAGGCTCGAAAGGTCCATGCTCCTTTCTCTGCCCATCTATAGCATAAGAAGA CAGTCTCTGAGTGATAATCTTCTCTTCAAGAAGAAGAAAAGTAGGAAGGAGTAAGCACAAAGATCTCTTC ACATTCTCCGGGACTGCGGTACCAAAATATCAGCACAGCACTTCTTGAAAAGGATGTAGATTTTAAATCTG AACTTTGAACCATCACTGAGGTGGCCGCGGTTTCTGAGCCTTCTGCCCTGCGGGACAGGCTGTCAC CCTGCCCGCGGCCACGGACCATGACCCTCCACACCAAAGCATCTGGATGGCCCTACTGCATCA GATCCAAGGGAACGAGCTGGAGCCCTGAACCGTCCGAGCTCAAGATCCCCCTGGAGCGGCCCTGGGC GAGGTGTACCTGGACAGCAGCAAGCCCGCCGTGTACAACCTACCCCGAGGGCGCCGCTACGAGTTCAACG CCGCGGCCCGCCCAACGCGCAGGCTACGGTCAGACCGGCCTCCCTACGGCCCCGGGTCTGAGGCTGC GGCGTTTCGGCTCCACCGCCTGGGGGGTTTCCCCCACTCAACAGCGTGTCTCCGAGCCGGGCTGATGCTA CTGCACCCCGCCCGCAGCTGTGCGCTTCTCTGCAGCCCCACGGCCAGCAGGTGCCCTACTACCTGGAGA ACGAGCCCAGCGGCTACACGGTGCAGGAGCGGCCCGCCGCGCAATTCTACAGGCCAAATTCAGATAATCG ACGCCAGGGTGGCAGAGAAAGATTGGCCAGTACCAATGACAAGGGAAGTATGGCTATGGAATCTGCCAAG GAGACTCGCTACTGTGCACTGTGCAATGACTATGCTTCAGGCTACCATTAATGGAGTCTGGTCTGTGAGG GCTGCAAGGCCTTCTTCAAGAGAAGTATTCAGGACATAACGACTATATGTGCCAGCCACCAACCATG CACCATTGATAAAAAACAGGAGGAAGAGCTGCCAGGCCTGCCGGCTCCGCAAATGCTACGAAGTGGGAATG ATGAAAGGTGGGATACGAAAAGACCGAAGAGGAGGGAGAATGTTGAAACACAAGCGCCAGAGAGATGATG GGGAGGGCAGGGGTGAAGTGGGGTCTGCTGGAGACATGAGAGCTGCCAACCTTTGGCCAGCCCCGCTCAT GATCAAACGCTCTAAGAAGAAGCAGCTGGCCTTGTCCCTGACGGCCGACAGATGGTCACTGCTTGTG GATGCTGAGCCCCCATACTCTATTCCGAGTATGATCCTACAGACCCCTTCAGTGAAGCTTCAGATGAG GCTTACTGACCAACCTGGCAGACAGGGAGCTGGTTACATGATCAACTGGGCGAAGAGGGTGCCAGGCTT TGTTGATTGACCTCCATGATCAGGTCCACCTTCTAGAATGTGCTGGCTAGAGATCCTGATGATTGGT CTCGTCTGGCGCTCCATGGAGCACCCAGGGAAGCTACTGTTGCTCCTAATTGCTCTTGGACAGGAACC AGGGAAAATGTGTAGAGGGCATGGTGGAGATCTTCGACATGCTGCTGGCTACATCATCTCGGTTCCGCAT GATGAATCTGCAGGGAGAGGAGTTTGTGTGCTCAAATCTATTATTTTGTCTTAATCTGAGGTGTACACA TTTCTGTCCAGCACCCCTGAAGTCTCTGGAAGAGAAGGACCATATCCACCGAGTCTGGACAAGATCACAG	109

	ACACCTTTGATCCACCTGATGGCCAAGGCAGGCCTGACCCTGCAGCAGCAGCACCAGCGGCTGGCCCAGCT CCTCCTCATCCTCTCCACATCAGGCACATGAGTAACAAAGGCATGGAGCACTGTACAGCATGAAGTGC AAGAACGTGGTGCCCTCTATGACCTGCTGCTGGAGATGCTGGACGCCACCAGCTACATGCGCCCACTA GCCGTGGAGGGGCATCCGTGGAGGAGACGGACCAAAGCCACTTGGCCACTGCGGGCTCTACTTCATCGCA TTCCCTTGCAAAAGTATTACATCACGGGGGAGGCAGAGGGTTTCCCTGCCACGGTCTGAGAGCTCCCTGGC TCCCACACGGTTCAGATAATCCCTGCTGCATTTTACCCTCATATGCACCCTTTAGCCAAATTCGTCT CCTGCATACACTCCGGCATGCATCCAACACCAATGGCTTTCTAGATGAGTGGCCATTCAATTTGCTTGCTC AGTTCTTAGTGGCACATCTTCTGTCTTCTGTGGGAACAGCCAAAGGGATTCCAAGGCTAAATCTTTGTA ACAGCTCTCTTTCCCCCTTGCTATGTACTAAGCGTGAGGATTCCCGTAGCTCTTCACAGCTGAAGTACAG TCTATGGGTTGGGGCTCAGATAACTCTGTGCATTTAAGCTACTTGTAGAGACCCAGGCCCTGGAGAGTAGA CATTTTGCCTCTGATAAGCACTTTTTAAATGGCTCTAAGAATAAGCCACAGCAAAGAATTTAAAGTGGCT CCTTTAATTTGGTGACTTGGAGAAAGCTAGGTCAAGGGTTTATTATAGCACCTCTTGTATTCTATGGCA ATGCATCCTTTTATGAAAGTGGTACACCTTAAAGCTTTTATATGACTGTAGCAGAGTATCTGGTGATTGT CAATTCATTCCCCCTATAGGAATACAAGGGGCACACAGGGAAGGCAGATCCCTAGTTGGCAAGACTATT TTAACTTGATACACTGCAGATTAGATGTGCTGAAAGCTCTGCCTCTGGCTTTCCGGTATGGGTTCCAG TTAATTCATGCCTCCCATGGACCTATGGAGAGCAGCAAGTTGATCTTAGTTAAGTCTCCCTATATGAGGG ATAAGTTCTTGATTTTGTGTTTATTTTGTGTTTACAAAAGAAAGCCCTCCCTGAAGTTCAGTAA GGTCAGCTTCAGGACCTGTCCAGTGGGCAGTGTACTTGGATCTTCCCGGCGTGTGTGCTTACACAG GGGTGAAGTGTACTGTGGTGATGCATGATGAGGGTAAATGGTAGTTGAAAGGAGCAGGGGGCCCTGGTG TTGCATTTAGCCCTGGGGCATGGAGCTGAACAGTACTTGTGCAGGATTGTTGTGGCTACTAGAGAACAAAG AGGGAAAGTAGGGCAGAACTGGATACAGTTCTGAGGCACAGCCAGACTTGGCTCAGGGTGGCCCTGCCAC AGGCTGCAGCTACCTAGGAACATTCCTTGCAGACCCCGCATTTGCCCTTTGGGGGTGCCCTGGGATCCCTG GGGTAGTCCAGCTCTTCTTCATTTCCAGCGTGGCCCTGGTTGGAAAGAGCAGCTGTACAGCTGCTGTA GACAGCTGTGTTCTTACAATTTGGCCAGCACCTTGGGGCAGGGGAGAGGGTGGGGACCGTTGCTGTAC TACTCAGGCTGACTGGGGCTGGTGCAGATTACGTATGCCCTTGGTGGTTTATAGATAATCCAAATCAGG GTTTGGTTTGGGGAAGAAATCCTCCCCCTTCTCCCCCGCCCCGTTCCTACCCGCTCCACTCCTGCCA GCTCATTTCCCTCAATTTCCCTTTGACCTATAGGCTAAAAAAGAAAGGCTCATTTCCAGCCACAGGGCAGCC TTCCCTGGGCCTTTGCTTCTCTAGCACAATTTAGGGTTACTTCTTTTCTTAAACAAAAAAGATGTTTG ATTTCTCTGGGTGACCTTATTGCTGTAAATGAAACCTTATTGAGAGGTGATGTCTGTGTTAGCCAATG ACCCAGGTGAGCTGCTCGGGCTTCTCTGGTATGTCTTGTGTTGGAAAAGTGGATTTCATTCATTTCTGAT TGTCAGTTAAGTGATCACCAGGACTGAGAATCTGGGAGGGCAAAAAAAAAAAAAAGTTTTATGTG GCTTAATTTTGGGACAAATTTTATGTATCTGTGTTAAGGATATGTTAAGAACATAATCTTTTGTGTC TGTTTGTGTTAAGAAGCACCTTAGTTTGTGTTAAGAAGCACCTTATATAGTATAATATATATTTTTTGA TTACATTGCTTGTGTTATCAGACAATGAATGTAGTAATCTGTTCTGGATTAAATTTGACTGGGTTAACA TGCAAAAACCAAGGAAAAATATTAGTTTTTTTTTTTTTTTTTGTATACTTTCAAGCTACCTTGTCTATG TATACAGTCATTTATGCCATAAGCCTGGTGATTATTCATTTAAATGAAGATCACATTTATATCAACTTT TGATCCACAGTAGACAAAAATAGCATAATCCAGATGCCATTTGTTGGATACCTGAATGACAGCAACTCTT ATGTAGCAAAGATTATGCCTGAAAAGGAAAAATTTATTCAGGGCAGCTAATTTTGCTTTTACCAAAATATCA GTAGTAATATTTTTGGACAGTAGCTAATGGGTCAGTGGGTTCTTTTAAATGTTTATACTTAGATTTCTT TTAAAAAATTAATAAATAAAAAAATTTCTAGGACTAGACGATGTAATACCAGCTAAAGCCAAAC AATTATACAGTGGAAAGTTTTACATTATTCATCCAATGTGTTTCTATTCAATGTAAAGTACTACTACATT TGAAGTGGGCAGAGAACATCAGATGATTGAATGTTTCCGCCAGGGGTCTCCAGCAACTTTGGAAATCTCT TTGTATTTTTACTTGAAGTGCCACTAATGGACAGCAGATATTTTCTGGCTGATGTGGTATTGGGTGTAG GAACATGATTTAAAAAAAACCTCTTGCTCTGCTTTCCCCCACTCTGAGGCAAGTTAAATGTAAAGAT GTGATTTATCTGGGGGGCTCAGGTATGGTGGGGAAGTGGATTACAGGAATCTGGGGAATGGCAAAATATAT AAGAAGAGTATTGAAAGTATTGGAGGAAAAATGGTTAATCTGGGTGTGCACCAGGGTTAGTAGAGTCC ACTTCTGCCCTGGAGACCACAAATCAACTAGCTCCATTTACAGCCATTCTTAAATGGCATTGCAAGTTT TAGAGAAGAAAGAACACATCAGCAGTAAAGTCCATGGAATAGCTAGTGGTCTGTGTTTCTTTTCGCCAT TGCTAGCTTGCCGTAATGATTCTATAATGCCATCATGCAGCAATTATGAGAGGCTAGGTATCCAAAGA GAAGACCTATCAATGTAGGTGCAAAATCTAACCCCTAAGGAAGTGCAGTCTTTGATTGATTTCCCTA GTAACCTTGCAGATATGTTTAAACCAAGCCATAGCCCATGCCCTTTTGGAGGCTGAACAAATAAGGGACTTA CTGATAAATTTACTTTTGATCACATTAAGGTGTTCTCACCTTGAAATCTTATACACTGAAATGGCCATTGA TTTAGGCCACTGGCTTAGAGTACTCCTTCCCTGCATGACACTGATTACAAATACTTTCTATTTCATACT TTCCAATTATGAGATGGACTGTGGGTACTGGAGTGATCACTAACCCATAGTAATGTCTAATATTACACA GGCAGATCTGCTTGGGGAAGCTAGTTATGTGAAAGGCAATAGAGTCATACAGTAGCTCAAAGGCAACC ATAATCTCTTTGGTGCAGGTCTTGGGAGCGTGATCTAGATTACACTGCACCATTCCCAAGTTAATCCCC TGAAAACTTACTCTCAACTGGAGCAATGAACCTTGGTCCCCAAATATCCATCTTTTCAGTAGCGTTAAT ATGCTCTGTTTCCAACCTGCATTTCTTTCCAATTGAATTAAGTGTGGCCTCGTTTTTGTATTTAAAA TTGTTTTCTAAGTAATTGCTGCCTCTATTATGGCACTTCAATTTTGCAGTGTCTTTTGTAGATTCAAGAAA AATTTCTATTCTTTTTTTTGCATCCAATTGTGCTGAACTTTTAAAAATATGTAATGTGCCATGTTCCA AACCATCGTCAGTGTGTGTTTATAGAGCTGTGCACCCTAGAAACAACATATTGTCCCATGAGCAGGTGC CTGAGACACAGACCCCTTTGCATTCACAGAGAGGTCAATGGTTATAGAGACTTAAATTAATAAGTGACAT TATGCCAGTTTCTGTTCTCTCACAGGTGATAAACAATGCTTTTTTGTGCACTACATACTCTTCAGTGTAGA GCTCTGTTTTATGGGAAAAGGCTCAAATGCCAAATTGTGTTTGTATGGATTAAATATGCCCTTTTGGCGAT GCATACTATTACTGATGTGACTCGGTTTTGTGCGCAGCTTTGCTTTGTTTAAAGAAACACACTTGTAAACC TCTTTTGACATTTGAAAAAGAAATCCAGCGGGATGCTCGAGCACCTGTAAACAAATTTCTCAACCTATTG ATGTTCAAAATAAGAAATTAACATAA	
NM_130398	AAATTGAAAGGTCAGCCTTTTCGCGCGCTGTGTAGGCAAGTTACCCGTGTTCTGCGTTGCCGGCCGTGGGT	110

	GCTCTGGCCACAGTGAAGTTAGGGGCGTCGGAGCGGGTTTCTCCAACCGCAATCGGCTCCGCTCAAGGGGA GGAGGAGAGTCCCTTCTCGGAAGGCCTAAGGAAACGTGTCGTCGGAATGGGCTTGGGGGCCACGCTGC ACATCTCCGCGAGACAGAGGGATAAAGTGAAGATGGTGTGTTATTTGTTACCTCGAGTGCCACATGCGAC CTCTGAGATATGTACACAGTCATTCTTACTATCGCACTCAGCCATTCTTACTACGCTAAAGAGAAATAA TTATTGAGGATATTTGCCCTGGCCAGAAGAACTTATGTAAATTTCTAGTAATTTATATCCGTTTTC TCGGAGTGAGAGAAAACTCTTTTTAGATATCATCTGAGAGAACTAGTGAATCCAGTCACTGAGTGGAGT TGAGAGTCTAAGAACCTCTGAAATTTGAGAACTGCTGGACCAGAGCCTTTAGAGCTCTGATAAGGTGTCA ACAGGGTAGTTAAATTTGGCACCATGGGGATACAGGGATTGCTACAAATTTATCAAAGAAGCTTCAGAACCC ATCCATGTGAGGAAGTATAAAGGGCAGGTAGTAGCTGTGGATACATATTGCTGGCTTTCACAAAGGAGCTA TTGCTTGTGCTGAAAAACTGACAAAGGTGAACCTACTGATAGGTATGTAGATTTTGTATGAAATTTGT AAATATGTTACTATCTCATGGGATCAAGCCTATTCTCGTATTTGATGGATGTACTTTACCTTCTAAAAAG GAAGTAGAGAGATCTAGAAGAGAAAGACGACAAGCCAATCTTCTTAAGGGAAAGCAACTTCTTCGTGAGG GGAAAGTCTCGGAAGCTCGAGAGTGTTTACCCCGGTCTATCAATATCACACATGCCATGGCCCCAAGAT AATTAAGCTGCCCCGTCTCAGGGGGTAGATTGCTCGTGGCTCCCTATGAAGCTGATGCGCAGTTGGCC TATCTTAACAAAGCCGGAAATTTGTGCAAGCCATAATTACAGAGGACTCGGATCTCTGAGCTTTTGGCTGT AAAAGGTAATTTTAAAGATGGACCAGTTTGGAAATGGACTTGAAATTGATCAAGCTCGGCTAGGAATGTG CAGACAGCTTGGGGATGTATTACGGAAGAGAAAGTTTCGTTACATGTGTATTCTTTAGGTTGTGACTAC CTGTCTACTGCGTGGGATTGGATTAGCAAAGGCATGCAAAGTCCTAAGACTAGCCAATAATCCAGATA TAGTAAGGTTATCTCAAGAAATTTGGACATTATCTCAAGATGAATATCACGGTACCAGAGGATTACATCAA CGGGTTTATTCGGGCCAACAAATACCTTCTCTATCAGCTAGTTTTTGTATCCCATCAAAGGAAACTTATT CCTCTGAACGCCTATGAAGATGATGTTGATCCTGAAACACTAAGCTACGCTGGGCAATATGTTGATGATT CCATAGCTCTTCAAATAGCACTTGGAAATAAGATATAAAATCTTTTGAACAGATCGATGACTACAATCC AGACACTGCTATGCTGCCCTCAAGAGTCAATAGTTGGGATGACAAAACATGTCAAAGTCAGCTAAT GTTAGCAGCATTTTGGCATAGGAATTTACTCTCCAGACCAGAGTCGGGTACTGTTTCAGATGCCCAAT TGAAGGAAAAATCCAGTACTGTGGGAGTGGAAAGGATGATTAGTACTAAGGGTTAAATCTCCCAAGGAA ATCATCCATTGTGAAAAGACCAAGAAGTGCAGAGCTGTCAGAAGATGACCTGTTGAGTCAGTATTCTCTT TCATTTACGAAGAAGACCAAGAAAAATAGCTCTGAAGGCAATAAATCATTGAGCTTTTCTGAAGTGTTTG TGCTTGACCTGTTAAATGGACCTACTAACAATAAGAGTGAAGCACTCCACTAGGACAGAGAATAAAT TGCAACATTTTTCAAAGGAAAAATGAAGAAAGTGGTGCAGTTGTGGTTCCAGGACCAAGCAGGCTTT TTTTGCAGTTTCAGATTCTACTGACTGTGTATCAAACAAAGTGAGCATCCAGCTCTGGATGAAATGCTG TCACAGATAAAGAGAACAATCTGCATGAATCAGAGTATGGAGACCAAGAAGGCAAGAGACTGGTTGACAC AGATGTAGCAGTAATTCAGTGATGACATTCCGAATAATCATATTCCAGGTGATCATATCCAGACAAG GCAACAGTGTTTACAGATGAAGAGTCTTACTCTTTGAGAGCAGCAAAATTTACAAGGACCAATTTACCAC CCACTTTGGGAACACTAAGAAGTGTGTTTAGTTGGTCTGGAGGCTTGAGAGATTTTTCAAGAAGCCCGAG CCCCCTCTCCAAGCAGCAGATTGCGAGCAGTTCCGAAGAAAGAGCGATTCCCCCACCCTCTTGCCTGAGAAT AATATGCTGATGTGTGCGAGTTAAAGAGCGAGGAGTCCAGTGACGATGAGTCTCATCCCTTACGAGAAG AGGCATGTTCTTCACAGTCCAGGAAAGTGGAGAATTCTCACTGCAGAGTTCAAATGCATCAAAGCTTTT TCAGTGCTCTAGTAAGGACTCTGATTTCAGAGGAATCTGATTGCAATATTAAGTTACTTGACAGTCAAAG GACCAGACCTCCAAGCTACGTTTATCTCATTTTCTCAAAAAAAGACACACCTCTAAGGCAACAGGTCTCTG GGCTATATAAGTCCAGTTCTGCGAGCTCTCTTTCTACAACCAAGATCAAACCTCTAGGACCTGCCAGAGC CAGTGGGCTGAGCAAGAAGCCGGCAAGCATCCAGAAGAGAAAGCATATAATGCCGAGAACAAGCCGGGG TTACAGATCAAATCAATGAGCTCTGGAAAACTTTGGATTTAAAAAAGATTCTGAAAAGCTTCTCTCTT GTAAGAAACCCCTGTCCCCAGTCAGAGATAAATCAACTAACTCCAGACGGGACGGAAGGAGATATATTAA CAAACCTGAAATGTGCCCGTGTTCAAAGAGCAATATCCAGTAAATGCGAGACTGCTGCAAGGCTTTGCT GCAAGAGAATCTGATCAATTTGAAGTCCCTGTTTGGGAATGAGGCATTTATCAGCATGAAGAATTTTTTC TCATTCTGTGCCATTTTAAAAATAGAATACATTTTGTATATTAATTTATAATGGGTTGTGGTTTTTTT GCTCAGCTTTTTATATTTTATAAAGAGCTAAATAGAAGAATAATTTGATCTCTGACAGGTTTTTGGAGG TTTTAGTGTAAATTTGGGAAATCTCTGGAGTTTATAAAAGTCTACTCTAAATATTTCTGTAATGTTGTC AAGTAGAAGATAGTAAATGGAGAACTCAAAAAAAGGAAAAA	
AB209631	CCATGACCTGCCTTGAGAAGGGGCAGGGGAAGCCAGATGGACTGGAAGTGGAGTGGCAGTGACCAAGGAG GAGGAGGTGTGATAGGCTTCCACAGCAGGGTAGATCCAGAGACACCAGTGCACCCATAGGCCCTTAGGA CTGCAGTGGTACCCGATTCCCTTGTCCCAGCTGAGACTCAGTTCTGAGTGTCTATTTTGGGGAACAGA GGCGTCTCTGTTAGCATTGGAAGAGGATAGCCAGCTGGGGTGTTGTATACACAGCCTGACAGTAACA GCATCCGAACAGAGGTGACTGGCTTAAGGGCAGACCCAGGGCAACAGGTTAACCGTTCTAGGGCCGGCA CAGGGAGGAGAATTTCAACACTCTGTGTGCCAGTGGCGACGACGTTCTCTTTTTATCTCAAAAC AGTCTATGAGGATATAAGCCAGAGAGAGACAGAGACAAGGAATTAACAAGTTGGTGAGAGTCAGGATTTG AACTTGGCTCTGGCAGATGAAAAATTAGGGTCTGTATTTTACAAAACCGTGTTGCCCTCAGATGGAGT TGGTGCAATAACAGCAGGATATCCAGGTCGGGTCCTGTTGCCACGAGGGGCCGCTTGTGCAAT GTGACCAACCCAGCCCTGGAATGTGAGTAATGCTGTAAGGAGTGGGGATCGGATCAGATGCCATCCAGAT GCTGAAGTTTGACCTTGTGTCATTTTCACTTTCTTTTTTGGCTCTTCTGCAATCAATTCATTTATTTAG CAAAAAAGAAATTTATGTGTGCCGAGAGCATGCAGAAGATATGTCTCCGTTCTCTGCTTCCCTCCAAAAA GAATCCCAAAATGCTTTCTGTGAACGTGTGCCAGGGTCCCAGCAGGACTCAGGGAGAGCAGGAAGCCCCA GCCAGACCCCTGTGCAACACTGAGGAGGCTTAGGCTCTGAGTCTGAGTCTGATGAGTCTGTTCCAGTC TGCACTGCCACAGCCTGGCCAGGGACTTGGACACATCTGCTGGCCACTTCTGTCTCAGTTTCTCTATCT GCAAAATAAGGGAAAAGCCCCACAAAGGTGCACGTGTAGCAGGAGCTTTTTTCCCTCCCTATTTTAGGA AGGCATTTGGTGGGAAGTCCAGCTTGGGTCCCTGAGAGCTGTGAGAAGGAGATCGGGCTGCTGCTGGCCC TGTTGGGGGTCCTGCTGAGTGTGCTTGGGCTCCAGTCTTGTCCCTGGAGGCCCTCTGAGGAAGTGGAGCT TGGTATGGCTTCTGAGGTGGGAGGTTGGCAGGGGTGGGAAGAGTGGGACCCAGGAGGGGGCTGCTGGG	111

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	GAAGTTACCTATTCTCCACCTAAATCTCTGAAAAATGGAGAAACCCTCTGACTAGTCCATGTCAAAATTTT ACTAAAAGTCTTTTGGTTAGATTTATTTTCTGCAGCATCTTCTGCAAAATGTACTATATAGTCAGCTT GCTTTGAGGCTAGTAAAAAGATATTTTCTAAACAGATTGGAGTTGGCATATAAAACAAATACGTTTTCTC ACTAATGACAGTCCATGATTTCGGAAATTTTAAAGCCCATGAATCAGCCGCGGCTTACCACGGTGATGCC GTGTGCCGAGAGATGGGACTGTGCGGCCAGATATGCACAGATAAAATATTTGGCTTGTGTATTCCATATAA AATTGCAGTGCATATTATACATCCCTGTGAGCCAGATGCTGAATAGATATTTTCTATTATTTTTCAGTCC TTATAAAAGGAAAAATAAACAGTTTTTAAATGTATGTATATAATTCTCCCCATTTACAATCCTTTCATG TATTACATAGAAGGATTGCTTTTTTAAAAATATACTGCGGGTTGGAAAGGGATATTTAATCTTTTGAGAAA CTATTTTAGAAAAATATGTTTGTAGAACAATTATTTTAAAAAGATTTAAAGCAATAACAAGAAGGAAGG CGAGAGGAGCAGAACATTTTGGTCTAGGGTGGTTTCTTTTTAAACCATTTTTCTTGTTAATTTACAGTT AAACCTAGGGGACAATCCGGATTGGCCCTCCCCCTTTTGTAAATAACCCAGGAAATGTAATAAATTCATT ATCTTAGGGTGATCTGCCCTGCCAATCAGACTTTGGGGAGATGGCGATTGATTACAGACGTTCCGGGGG GTGGGGGGCTTCAGTTTGTTTTGGAGATAATACAGTTTCTGCTATCTGCCGCTCCTATCTAGAGGCAA CACTTAAGCAGTAATTGCTGTGTTGTTGTCAAAATTTGATCATTGTTAAAGGATTGCTGCAATAAAAT ACACTTTAATTTTCAGTCAAAAA	
AJ249248	GTGGCTCGAGGTGGTGGCAGGGCCGCCCCCTGCAGTCCGGAGACGAACGCACGGACCGGGCCTCCGGAG GCAGGTTCCGGCTGGAAGGAACCGCTCTCGCTTCGCTTACACTTGGCGAAAATGTCTCCGAGCTTACTCAC ATAGCATATTGGTATATCAAAATGAAATGCAAGGAACCAAAAATAACATAAATTGAAGGCAGTAAAGTGA AATTAAATAGGAAGATCATCAGTCAAGGAAGACCCACTGGAGAGGACAGAAAAATGAAGCAGTGTTTTATC ATGTGATTTTCAGCAGGTCTTCTTGAATTTAACTAAAAATATGACTGCTCTCTCTTCAGAGAACTGCTC TTTTCAGTACCAGTTACGTCAAAACAAACAGCCCCCTAGACGTTAACTATCTGCTATTCTTGATCATACTT GGGAAAAATATTATTAATATCCTTACACTAGGAATGAGAAGAAAAACACCTGTCAAAATTTTATGGAAT ATTTTTGCATTTCACTAGCATTCGTTGATCTTTTACTTTTGGTAAACATTTCCATTTATTTTTCAG GGATTTTGTACTTTTAAAGCATTAGGTTCACATAAATACCACATCTGCCTATTTACTCAAATATTTCTCTT ACTTATGGCTTTTGCATTATCCAGTTTTCCTGACAGCTTGTATAGATTATGCGCTGAATTTCTCTAAAA CAACCAAGCTTTTCAATTAAGTGTCAAAATTTATTTTATTTCTTTACAGTAATTTTAAATTTGGATTTCAGT CCTTGCCTTATGTTTGGGAGACCCAGCCATCTACCAAGCCTGAAGGCACAGAATGCTTATTTCTCGTCAC TGCTCTTCTATGTGACGATTCAGAGTTACTGGCTGTGCTTTTTCATGGTGATGATTTTATTTGTAGCTT TCATAACCTGTGGGAAGAAGTTACTACTTTGGTACAGGCTATCAGGATAACTTCCTATATGAATGAAAC TATCTTATATTTTCTTTTTCATCCCACTCCAGTTTATCTGTGAGATCTAAAAAAATATCTTATCCAAG CTCATTGCTGTTTTCTCAGTACCTGGTTACCATTGTGTACTACTTCAGGTAATCATTTGTTTTACTTAAAG TTCAGATTCAGCATATATTGAGATGAATATTCCTGGTTATACTTTGTCAATAGTTTCTTCATTGCTAC AGTGATATTGGTTTAAATTTGTCAAGCTTAAATTTAAAGACATTGGATTACCTTTGGATCCATTGTCAAC TGGAAGTGCTGCTTCAATCCACTTACAATTCCTAATCTTGAGCAAATTGAAAAGCCTATATCAATAATGA TTTGTTAATATTATTAATTAAGTTACAGCTGTCAATAGATCATAATTTTATGAACAGAAAGAACTCAG GACATATTAAAAAATAAACTGAACATAAAACAACTTTTGGCCCCCTGACTGATAGCATTTTCAAGATGTGCT TTTGAAAGGCTATACCAGTTATTAATAGTGTTTTATTTTAAAAACAAAATAATTCAGAAGTTTTTAT AGTTATTCAGGACACTATATTACAAATATTACTTTGTTATTAACACAAAAAGTGATAAGAGTTAACATT TGGCTATCTGATGTTTGTGTTACTCAAAAAACTACTGGATGCAAACTGTTATGTAATCTGAGATTTT ACTGACAACCTTAAGATATCAACCTAAACATTTTATTAATAGTTCAAAATGTAAGCAAGAAAAA	114
NM_014176	AGTCAGAGGTCGCGCAGGCGCTGGTACCCCGTTGGTCCGCGCGTTGCTGCGTTGTGAGGGGTGTCAGCTC AGTGCATCCAGGCAGCTCTTAGTGTGGAGCAGTGAACCTGTGTGTGGTTCCCTTCTACTTGGGGATCATGC AGAGAGCTTCACGCTCTGAAGAGAGAGCTGCACATGTTAGCCACAGAGCCACCCCAAGGCATGATGTG GCAAGATAAAGACCAATGGATGACCTGCGAGCTCAAAATATTAGGTGGAGCCAACACACCTTATGAGAAA GGTGTTTTTAAGCTAGAAGTTATCATTCCTGAGAGGTACCCATTTGAACCTCCTCAGATCCGATTCTCA CTCCAATTTATCATCCAAACATTGATTCTGCTGGAAGGATTGTCTGGATGTTCTCAAATTGCCACCAAA AGTGTGCTTGGAGACCATCCCTCAACATCGCACTGTGTTGACCTTATTCAGCTGCTCATGTCAGAACCC AACCTGATGACCCGCTCATGGCTGACATATCCTCAGAATTTAAATATAAATAGCCAGCTTCTCACAAGA ATGCCAGACAGTGGACAGAGAAGCATGCAAGACAGAAACAAAAGGCTGATGAGGAAGAGATGCTTGATAA TCTACCAGAGGCTGGTGAATCCAGAGTACACAACCTCAACACAGAAAAGGAAGGCCAGTCAGCTAGTAGGC ATAGAAAAGAAATTTATCCTGATGTTTAGGGGACTTGTCTGGTTTATCTTAGTTAATGTGTTCTTTGC CAAGGTGATCTAAGTTGCTACCTTGAATTTTTTTTAAATATATTGATGACATAAATTTTGTGTAGTT TATTTATCTTGTACATATGATTTTGAATCTTTTAAACCTGAAAAATAAATAGTCATTTAATGTTGAAA AAAAAAAAAAAAAAAAAAAAAAAAA	115
NM_006845	ACGCTTGCGCGCGGGATTAAACTGCGCGCGTTTACGCGCGGTTAAGACTTCGTAGGGTTAGCGAAATTG AGGTTTTCTTGGTATTGCGCGTTTTCTTCTTCTTGTGACTCTCCGAATGGCCATGGACTCGTCGCTTCAGG CCCGCTGTTCCTCGGTCTCGCTATCAAGATCCAACGCAGTAATGGTTTAAATTCAGAGTGCCAAATGTAAG GACTGTGAACCTGGAGAAATCCTGTGTTTTCAGTGGAAATGGGCAGAAAGGAGGTGCCCAAAAGGGCAAGAG ATTGATTTTGTATGATGTGGCTGCAATAAACCAGAACCTTACAGCTTCTTCTTCTTACATCCGAAGGACA ATCTGCCCTTGCAGGAAAATGTAACAATCCAGAAACAAAACGGAGATCCGTCAACTCCAAAATTCCTGC TCCAAAAGAAAGTCTTCGAAGCCGCTCCACTCGCATGTCCACTGTCTCAGAGCTTCGCATCACGGCTCAG GAGAAATGACATGGAGGTGGAGCTGCTGCACTGCAAACTCCCGCAAGCAGTTTTTCACTTCTCTGCTGCC CCACTAGGCTTCTGCTGCTGAGTGGCTGAAATACCATTTGAGGATGGTCAGCGAGGAGTGAAGAGCA AGTCCATTCCATCCGAGGCAGCTCTTCTGCAAAACCTGTGAACCTCAGTTCCGAGGAAATCATGCTTGTG AAGGAAGTGGAAAAATGAAGAACAAGCGAGAGAGAGAAAGGCCAGAACCTTGAAATGAGAATGAAGA GAGCTCAGGAGTATGACAGTAGTTTTTCAAACCTGGGAATTTGCCGAATGATTAAAGAATTTCCGGCTAC TTTGAATGTCATCCACTTACTATGACTGATCCTATCGAAGAGCACAGAATATGTGCTGTGTTAGGAAA CGCCCACTGAATAAGCAAGAATTGGCCAAGAAAGAAATTTGATGTGATTTCCATTCTTAGCAAGTGTCTCC	116

	TCTTGGTACATGAACCCAAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGA CTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTACAGCAAGGCCACTGGTACAGACA ATCTTTGAAGGTGGAAGCAACTTGTCTTTCATATGGCCAGACAGGAAGTGGCAAGACACATACATATGG GCGGAGACCTCTCTGGGAAAGCCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTCCCGGGACGTCTT CCTCCTGAAGAATCAACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTAC AATGGGAAGCTGTTTGACCTGCTCAACAAGAAGGCCAAGCTGCGCGTGCTGGAGGACGGCAAGCAACAGG TGCAAGTGGTGGGCTGCAGGAGCATCTGGTTAACTCTGCTGATGATGTCAICAGATGATCGACATGGG CAGCGCCTGCAGAACCTCTGGGCAGACATTTGCCAACTCCAATTCTCCCGTCCACGCGTGCTTCCAA ATTATTCTTCGAGCTAAAGGGAGAATGCATGGCAAGTTCTCTTTGGTAGATCTGGCAGGGAATGAGCGAG GCGCGGACACTTCCAGTCTGACCGGCAGACCCGCATGGAGGGCGCAGAAATCAACAAGAGTCTCTTAGC CCTGAAGGAGTGATCAGGGCCCTGGGACAGAACAAGGCTCACACCCCGTTCCGTGAGAGCAAGCTGACA CAGGTGCTGAGGGACTCCTTCATTGGGGAGAACTCTAGGACTTGCATGATTGCCACGATCTCACCAGGCA TAAGCTCCTGTGAATATACCTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAGCTGAGCCCCACAG TGGGCCCAGTGGAGAGCAGTTGATTCAAATGGAAACAGAAGAGATGGAAGCCTGCTCTAACGGGGCGCTG ATTCCAGGCAATTTATCCAAGGAAGAGGAGGAAGTGTCTTCCAGATGTCCAGCTTTAACGAAGCCATGA CTCAGATCAGGGAGCTGGAGGAGAAGGCTATGGAAGAGCTCAAGGAGATCATAACAGCAAGGACCAGACTG GCTTGAGCTCTCTGAGATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAGCGGAATCT GCTCTGGCCCCAGCAAGCCAAGCATTCTCAGCCCTGCGAGATGTATCAAGGCCCTTGGCCCTGGCCATGC AGCTGGAAGAGCAGGCTAGCAGACAAAATAAGCAGCAAGAAACGGCCCCAGTGACGACTGCAAATAAAAAAT CTGTTTGGTTTGACACCCAGCCTCTTCCCTGGCCCTCCCCAGAGAACTTTGGGTACCTGGTGGGTCTAGG CAGGGTCTGAGCTGGGACAGGTTCTGGTAAATGCCAAGTATGGGGGCATCTGGGCCCAGGGCAGCTGGGG AGGGGGTCAGAGTGACATGGGACACTCCTTTCTGTCTCAGTTGTGCGCCCTCAGCAGAGGAGGAGCT CTTAGTTACCCCTTTTGTGTGTCCTTCTTTCCATCAAGGGGAATGTCTCAGCATAGAGCTTTCTCCGCA GCATCTGCTGCGTGGACTGGCTGCTAATGGAGAGCTCCCTGGGGTTGTCTGGCTCTGGGAGAGAGA CGGAGCCTTTAGTACAGCTATCTGCTGGCTCTAAACCTTCTACGCCCTTTGGGCCGAGCAGCTGAATGTCTT GTACTTTAAAAAATGTTTCTGAGACCTCTTTCTACTTTACTGTCTCCCTAGAGATCCTAGAGGATCCCT ACTGTTTCTGTTTATGTGTTTATACATTGTATGTAACAATAAAGAGAAAAAATAAATCAGCTGTTAA GTGTGTGGAAAAAAAAAAAAAAAAAA	
NM_006101	ACTGCGCGCTGCTGCGTAATGACGTGAGCGCCGGCGGAGAATTTCAAATTCGAACGGCTTTGGCGGGCC GAGGAAGGACCTGGTGTTTTGATGACCGCTGTCTCTAGCAGATACTTGACAGGTTTACAGAAATTCG GTCCCTGGGTCGTGTCAGGAACTGGAAAAAGGTCATAAGCATGAAGCGCAGTTTCAGTTTCCAGCGGTG TGCTGGCGCGCTCTCCATGCAGGAGTTAAGATCCAGGATGTAAATAAACAAAGGCCTCTATACCCCTCA AACCAGAGAGAAACCAACCTTTGGAAAGTTGAGTATAAACAAACCGACATCTGAAAGAAAGTCTCGCTA TTTGGCAAAAGAACTAGTGGACATGGATCCCGGAATAGTCAACTTGGTATATTTTCCAGTTCTGAGAAAA TCAAGGACCCGAGACCACTTAATGACAAAGCATTCAATCAGCAGTGTATTCCGACAACCTCTGTGAGTTTCT TACAGAAAATGGTTATGCACATAATGTGTCCATGAATCTCTACAAGCTCCCTCTGTTAAAGACTTCCTG AAGATCTTACATTTCTTTATGGCTTCTGTGCCCCATACAGCAACTTCCTGACACAAGTTTGAAGAAG AGGTTCCAGAATCTTTAAAGACCTTGGGTATCCTTTTGCATATCCAAAAGCTCCATGTACACAGTGGG GGCTCCTCATACTAGGCTCACATTGTGGCAGCCTTAGTTTGGCTAATAGACTGCATCAAGATACATACT GCCATGAAAGAAAGCTCACCTTTATTTGATGATGGGCAGCCTTGGGGAGAAAGAACTGAAGATGGAATTA TGCATAATAAGTTGTTTTTGGACTACACCATAAAATGCTATGAGAGTTTATGAGTGGTGCCGACAGCTT TGATGAGATGAATGCAGAGCTGCAGTCAAACTGAAGGATTTATTTAATGTGGATGCTTTTAAGCTGGAA TCATTAGAAGCAAAAACAGAGCATTGAATGAACAGATTGCAAGATTGGAACAAGAAAGAGAAAAAGAAC CGAATCGTCTAGAGTCGTTGAGAAAACGAAGGCTTCTTACAAGGAGATGTTCAAAGTATCAGGCATA CATGAGCAATTTGGAGTCTCATTACGCCATTCTTGACCAGAAATTAATGGTCTCAATGAGGAAATGTCT AGAGTAGAACTAGAATGTGAAACAATAAAACAGGAGAACTCGACTACAGAAATATCATTGACAACCAGA AGTACTCAGTTGCAGACATTGAGCGAATAAAATCATGAAAGAAATGAATTGCAGCAGACTATTAATAAATT AACCAAGGACCTGGAAGCTGAACAACAGAAGTTGTGGAATGAGGAGTTAAATATGCCAGAGGCAAGAA GCGATTGAAACACAATTAGCAGAGTATCACAAATGGCTAGAAAATTAACCTTATTCCTAAAGGTGCTG AGAAATCCAAAGGTTATGACTTTGAAATTAAGTTTAATCCCGAGGCTGGTGCCAACTGCCTTGTCAAATA CAGGGCTCAAGTTTATGTACCTCTTAAGGAACTCCTGAATGAACTGAAGAAGAAATTAATAAAGCCCTA AATAAAAAAATGGTTTTGGAGGATACTTTAGAACAAATTGAATGCAATGATAACAGAAAGCAAGAGAAGTG TGAGAACTCTGAAAGAAGAAGTTCAAAGCTGGATGATCTTTACCAACAAAAAATTAAGGAAGCAGAGGA AGAGGATGAAAAATGTGCCAGTGAGCTTGAGTCTTGGAGAAACACAAGCACCTGCTAGAAAGTACTGTT AACCAGGGGCTCAGTGAAGCTATGAATGAATTAGATGCTGTTACAGCGGGAATACCAACTAGTTGTGCAAA CCACGACTGAAGAAAGACGAAAAGTGGGAAATAACTTGCAACGCTGTTAGAGATGGTTGCTACACATGT TGGGTCTGTAGAGAAACATCTTGAGGAGCAGATTGCTAAAGTTGATAGAGAATATGAAGAATGCATGTCA GAAGATCTCTCGGAAAATATTAAGAGATTAGAGATAAGTATGAGAAGAAAGCTACTCTAATTAAGTCTT CTGAAGAATGAAGATAAAATGTTGATCATGTATATATCCATAGTGAATAAAATTTGTCTCAGTAAAGTG TAAAAA	117
BC042437	CTCCCTCCTCTGCACCATGACTACCTGCAGCCGCCAGTTACCTCCTCCAGCTCCATGAAGGGCTCCTGC GGCATCGGGGGCGGCATCGGGGGCGGCTCCAGCCGCATCTCCTCGTCTGCGCGGAGGGTCTGCGCGG CCCCAGCACCTACGGGGGCGGCTGTCTGTCTCATCTCCCGCTTCTCCTCTGGGGGAGCCTATGGGTT GGGGGGCGGCTATGGCGGTGGCTTCAGCAGCAGCAGCAGCAGCTTTGGTAGTGGCTTTGGGGGAGGATAT GGTGGTGGCCTTGGTGCTGGCTTGGGTGGTGGCTTTGGTGGTGGCTTTGCTGGTGGTGGTGGCTTCTGG TGGGCAGTGAGAAGGTGACCATGCAGAACCTCAACGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGC TCTGGAGGAGGCCAACGCGACCTGGAAGTGAAGATCCGTGACTGTTACCAGAGGCGCGCTGCTGAG ATCAAGACTACAGTCCCTACTTCAAGACCATTGAGGACCTGAGGAACAAGATTCTCACAGCCACAGTGG	118

	ACAATGCCAATGTCTTCTGCAGATTGACAATGCCCGTCTGGCCGCGGATGACTTCCGCACCAAGTATGA GACAGAGTTGAACCTGCGCATGAGTGTGGAAGCCGACATCAATGGCCTGCGCAGGGTGTCTGGACGAACCTG ACCTTGGCCAGAGCTGACCTGGAGATGCAGATTGAGAGCCTGAAGGAGGAGTGGCCTACCTGAAGAAGA ACCACGAGGAGGAGATGAATGCCCTGAGAGGCCAGGTGGGTGGAGATGTCAATGTGGAGATGGACGCTGC ACCTGGCGTGGACCTGAGCCGCACTTCTGAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAAC CGCAAGGATGCCGAGGAATGGTTCTTACCACAGACAGAGGAGCTGAACCGCGAGGTGGCCACCAACAGCG AGCTGGTGCAGAGCGGCAAGAGCGAGATCTCGGAGCTCCGGCGCACCATGCAGAACCTGGAGATTGAGCT GCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACAGCCTGGAGGAGACCAAGGTGCTACTGTCATG CAGCTGGCCAGATCCAGGAGATGATTGGCAGCGTGGAGGAGCAGCTGGCCAGCTCCGCTGCGAGATGG AGCAGCAGAACCAGGAGTACAAGATCCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGCCACCTA CCGCCGCTGCTGGAGGGCGAGGACGCCACCTCTCCTCCTCCAGTCTCTCTCTGGATCGCAGTCATCC AGAGATGTGACCTCCTCCAGCCGCCAAATCCGCACCAAGGTCTATGATGTGCAGGATGGCAAGGTGGTGT CCACCCACGAGCAGGTCCCTTCGCACCAAGAACTGAGGTGCCAGCCCCGCTCAGGCCTAGGAGGCCCC CGTGTGGACACAGATCCCACTGGAAGATCCCTCTCCTGCCCAAGCACTTCACAGCTGGACCCCTGCTTCA CCCTCAGCCCCCTCCTGGCAATCAATACAGCTTCATTATCTGAGTTGCATAAAAAAAAAAAAAAAAAAAAA AA AA	
AK095281	CTCTTTTGCAGGGGCCGTCTCCTCGGGGCATGACGCTGGCTCCTGCACAGATCCTGCTCCTCTGTGGCCTT CCTGGGCTGCCCTCCCCCTCCTCCGGGACTGCTCTGGACTGACACTGCTCAGGTTCCGATTCCCTCAAAGA CTTTGGGAGACAAGACTTGGTCCCCCTTTTACAAACAAGGGAACCGAGGCTCTAGAAGTACTTCTCTGAA AGGCTTGGATCCAAAGCTCCCTCAGTTTCAGCGGCCACGCTCTATTTCCCTCAGACACAGGGATCCTTGAAC CTGTGGGCTGTATCTCCCCGCGGACTTGGAGAATCCCAAGAGAGTGGGGCTCCCAAGGCTGGAGTGC ATGGTGTGATCTCGGCTCACTGCAACCTCCACCTCCAGGTTCAAGCTATTTCTCTGCTCAGCCTCCTG AGTAGCTGGGATTACAGATCCTGGTGGCTGTGGTTCGTAATTCAGCTTCGTGCTGGCTACAGGTGGATG ATGCCACCTGGCTGCCGATGACCTCTGCACCAAGTGAGGCTGGGTCTCTGAGCTGCCCCAGGGGCTGG ACAAGCTGACCTGGCCGGGGCCAACTGGAGATGCAGATTGAGAACCCTCAAGGAGGACCTGGTCTACCT GAAGAAGAACCACAAGCAGGAAATGAACGTCTCTTGGAGTCAAGTGGATGAGGATGTGCTGAGTGAAGATG GACACTGTGCTGGAGTGAACCTGAGCTGCATCCTGAATGAGATGCGTGACAGGACAGACATTTGGTGG AGAAGAGCTGCAAGGATGCCGAGGGCTGGTTCTTCAGCATGGTGGGTGGCCGTGCGTAAGCAGGTGTGTA CACGTGTGGGCACATGTCTGCATGCTGGTGCAGCTGGAGCACTGGCAGATCCACAGGCTGTCCCAAGTTG GAAGGACTTTTGGAAACAGTTGGACCAGCCCTCATGTTTTAGATGTAAACCGTGAAGGCTCAGAGAGGA CTCAAGCTCACACAGCCCTTCACTGTGGCTGCAAAATAGATCCAGGTCTCTACAAAGCTGGGTGTGGGT TTCCACCACAGCTGTTTTACAGGATGTGCGTATTTGAATACATATGTATACCTTGGCAAGCACAGGCTGA GTATCTCCGGTATCCTAGGGACAGCAACAGGGCGAAAAGAATAACACCCAGTGCCTGTCTTTGAGGTGCT GCAGTTTCAGTAGGAAAAAGAAATGCAAAATGACCGCAGAGCAGGCTGAATTCCTCCAAGTTCCAATGTGGG TGCAGAGGCTCTCTGTGTGCAGAAAGAGGGGCTGAACCTGCGAGGTGGCCACCAACAGAGGGCCCTGCAG AGTGGCTGGATAGAGATATGGAGCTCTACGTCTCTGTGCAGAACCTGAGCCGTCCAGCTCAGCAAGAAA GATGCTGCTGGAGGGCAGCCTGGTGGAGATGGAGGTGTGTACAGGACCTGCCGGCCAGCTGCAGGGGC TTAACAGAAGCATGGAGCAGCAGCTGTGCGAGCTCTGCTGCGACACGGAGCACCAGGACCACAAGCACAG GTCCTTCTGGACGTGAAGACGTGGCTGGAGCAGGAGATCGCCACCTACCGCCGCTTGCTGGAGGTGAGG ACGCCCAGAGGTGATACTGACGATGCAGGCTGGAGTCTGGCTGAGGAGCCTTGAATGCCAAGTTAAAGCG CTCGGACTAGATCAGTAGGCAATGGGGAGCCATGGAGGATTTGGAGCAGGAGATGAATGAACATCA AGAGATTTTAGAACATTCACTCTGGCTGCAGAGGGAGAAATGGATCAGAGGGGTGAGGGCGGGCCAGAG AGATGTGTGAGGGGCTGGAGCAGGGAGTCTGGCCAGAGAAGTCCCGTGGGTGGTGGGTAGTGGGGCAG GGGAAGGAAGGTGGTGCACGCAGAAAGAGAGGTTATAGCTCAAAACAGCGGGACTGGATGCTGGATCTCG GGTAAGCATGGCTCACAGTCAAGGACTCAGTAAGTGTGCGGAGAACACATGAAGGAGCAGGCATTGATGG CCCTGGGTTTTCTGGTTCTGATGACTGTGTGAGTGGTGAAGACAAAGGTGGGTGGGTGGTTGGTCTGAGT TGGGAAGGGTGATCAGGCCTTCAGCTGAGAGTGTCCCGAGTCTCCATGCTTAGTACACGTTGCAGCTT TTTGCTCCCCGAAATGGTGAAGTCCATCTATAGTCTAACACAGTCTCTCCTGCTTTAATTGGGTCTAT TTGTGGGGCCCTCTGGGTATGGAAGAACCACTTGCTCAGCTTCTCCTTGTAATTCCTGGTGGTAGGCC ACAGAGTGGCGCCAGACCTACTGCTGTGCTGTTTTCTTTCTTCTCTGCTGTGCTGAACCCCTGCCCT TTCATTCTTGGGCTGCGCTAATTTCTGTGCATTCCTCACTGTGATTTTTCACCAATTTAGGGGAACCTC CTCTGCCAGGGCCTACTTCTCCCCAGCAGTGTCTGCAGGTGCTGGGCTGGCTGGCATCCCTGGGCTGAT GGGTGCTTCTCTCCCTGCAGGCTGGCCACTCAGTACTCTTGTCCCTGGCCTCGACGCCACCCGGGAAG CCACAGTGACCAGCCACCAGGTGTGCCATCGTGGAGGAAGTCCAGGTGGAGAGGTGGTCTTCTCTGTG AGCAGGTCCACTTCTCCACCCACTGAGACCCCTTCTGTCTGCGACAGCCCCACCTCGAGGGCCACGGCA CAGCCATCAGCTCCAGCTCCAGCATGCTACTGCCACGCCCGAGTGTCCGTCTGGGCCCCGGTGCATGG CCTGTTGTCTTTCTGTATCTACTTTCTGCAGCCCTCACTGAGGAGGCCTCCTGGGTTTTGTCCAGTGCCT ACTATTAAAGCTTTGCTCCAAGTTC	119
M21389	GCATCCCTTTTGGGCTGCTCACAGCCCCAGCCTCTATGGTGAAGACATACTTGTAGCAGCGTCACCAA CTTGCTGCCAAGAGATCAGTGTGCAAGGCAAGGTTATTTCTAACTGAGCAGAGCCTGCCAGGAAGAAAG CGTTTGCACCCACACCACTGTGACGGTGTGACCGGTGAGCTCAGAGCTGCCCCAGGATGCCAGCC CACTTAATCATTACAGCTCGACAGCTCTCTCGCCAGCCAGTCTCTGGAAGGGATAAAAGGGGCGATC ACCGTTCCTGGGTAACAGAGCCACCTTCTGCGTCTGCTGAGCTCTGTTCTCTCCAGCACCTCCCAACCC ACTAGTGCCCTGGTCTCTTGTCTCCACCAGGAACAAGCCACCATGTCTCGCCAGTCAAGTGTGTCTTCCG GAGCGGGGGCAGTCCGTAGCTTCAGCACCGCCTCTGCCATCACCCCGTCTGTCTCCGCAACCAAGCTTACC TCCGTGTCCCGGTCCGGGGTGGCGGTGGTGGTGGCTTCGGCAGGGTCAAGCTTCCGGGTGCTTGTGGAG TGGGTGGCTATGGCAGCCGGAGCCTCTACAACCTGGGGGGCTCCAGAGGATATCCATCAGCACTAGAGG	120

	AGGCAGCTTCAGGAACCGGTTTGGTGTCTGGTGTCTGGAGGCGGCTATGGCTTTGGAGGTGGTGCCGGTAGT GGATTGGTTTCGGCGGTGGAGCTGGTGGTGGCTTTGGGCTCGGTGGCGGAGCTGGCTTTGGAGGTGGCT TCGGTGGCCCTGGCTTTCTGTCTGCCCTCCTGGAGGTATCCAAGAGGTCACTGTCAACCAGAGTCTCCT GACTCCCCCTCAACCTGCAAAATCGACCCAGCATCCAGAGGGTGAGGACCGAGGAGCGGAGCAGATCAAG ACCCCAACAATAAGTTTGCCTCCTTCATCGACAAGGTGCGGTTCTCTGGAGCAGCAGAACAAGGTCTGG ACACCAAGTGGACCTGCTGCAGGAGCAGGGCACCAAGACTGTGAGGCAGAACCTGGAGCCGTTGTTTCGA GCAGTACATCAACAACCTCAGGAGGCAGCTGGACAGCATCGTGGGGGAACGGGGCCGCTGGACTCAGAG CTGAGAAACATGCAGGACCTGGTGAAGACTTCAAGAACAAGTATGAGGATGAAATCAACAAGCGTACCA CTGCTGAGAAATGAGTTTGTGATGCTGAAGAAGGATGTAGATGCTGCCTACATGAACAAGGTGGAGCTGGA GGCCAAGGTTGATGCACTGATGGATGAGATTAACCTTCATGAAGATGTTCTTTGATGCGGAGCTGTCCAG ATGCAGACGCATGTCTCTGACACCTCAGTGGTCTCTCCATGGACAACAACCGCAACCTGGACCTGGATA GCATCATCGCTGAGGTCAAGGCCAGTATGAGGAGATTGCCAACCGCAGCCGACAGAAGCCGAGTCTCTG GTATCAGACCAAGTATGAGGAGCTGCAGCAGACAGCTGGCCGGCATGGCGATGACCTCCGCAACACCAAG CATGAGATCACAGAGATGAACCGGATGATCCAGAGGCTGAGAGCCGAGATTGACAATGTCAAGAAACAGT GCGCCAATCTGCAGAACGCCATTGCGGATGCGAGCAGCGTGGGGAGCTGGCCCTCAAGGATGCCAGGAA CAAGCTGGCCGAGCTGGAGGAGGCCCTGCAGAAGGCCAAGCAGGACATGGCCCGGCTGCTGCGTGAGTAC CAGGAGCTCATGAACACCAAGCTGGCCCTGGAGTGGAGATCGCCACTTACCGCAAGCTGCTGGAGGGCG AGGAATGCAGACTCAGTGGAGAAGGAGTTGGACCAAGTCAACATCTCTGTTGTGACAAGCAGTGTCTCTCT TGGATATGGCAGTGGCAGTGGCTATGGCGGTGGCCTCGGTGGAGGTCTTGGCGGGCGCCTCGGTGGAGGT CTTGGCCGAGGTAGCAGTGGAAAGCTACTACTCCAGCAGCAGTGGGGGTGTGCGGCTAGGTGGTGGCTCA GTGTGGGGGGCTCTGGCTTCAGTGAAGCAGTGGCCGAGGGCTGGGGGTGGGCTTTGGCAGTGGCGGGGG TACTGCTCCAGCGTCAAAATTTGTCTCCACCACCTCCTCTCCCGAAGAGCTTCAAGCAGTGAAGCCGCT GCTGCAAGTCACTGCCTTCCAAGTGCAGCAACCCAGCCCATGGAGATTGCCTCTTCTAGGCAGTTGCTCA AGCCATGTTTTATCCTTTCTGGAGAGTAGTCTAGACCAAGCCAATTCAGAACCCACATTCTTTGGTTCC CAGGAGAGCCCCATTCCAGCCCCCTGGTCTCCCGTGGCGCAGTTCTATATTCTGCTTCAAATCAGCCTTC AGGTTTCCACAGCATGGCCCCCTGCTGACACGAGAACCACAAAGTTTTCCTAAATCTAAATCATCAAAACA GAATCCCCACCCCAATCCCAAAATTTGTTTGGTTCTAACTACCTCCAGAATGTGTTCAATAAAATGCTT TTATAATAT	
NM_00112306 6	GGACGGCCGAGCGGCAGGGCGCTCGCGCGCGCCCACTAGTGGCCGGAGGAGAAGGCTCCCGCGGAGGCCG CGCTGCCCGCCCCCTCCCTGGGGAGGCTCGCGTTCCCGCTGCTCGCGCCTGCGCCGCCCGCCGGCTCA GGAACGCGCCCCCTTCGCGCGCGCGCGCCCTCGCAGTCACCGCCACCCACAGCTCCGGCACCACAGCA GCGCGCTGCCACCGCCACCTTCTGCCCGCGCCACCCAGCCACCTTCTCCTCTCCGCTGCTCCTCTCC CGTCTCGCCTCTGTGACTATCAGGTGAACCTTGAACCAAGGATGGCTGAGCCCCCGCCAGGAGTTCGAAG TGATGGAAGATCACGCTGGGACGTACGGGTGGGGGACAGGAAAGATCAGGGGGGCTACACCATGCACCA AGACCAAGAGGCTGACACGGACGCTGGCCCTGAAAGAATCTCCCTGCGAGACCCCCACTGAGGACGGATCT GAGGAACCGGGCTCTGAAACCTCTGATGCTAAGAGCACTCCAACAGCGGAAGATGTGACAGCACCCCTTAG TGGATGAGGAGCTCCCGCAAGCAGGCTGCGCGCAGCCCCACAGCGAGATCAAGGAGGACACACAGC TGAAGAAGCAGGCATTGGAGACACCCCCAGCCTGGAAGACGAAGCTGCTGGTCACGTGACCCCAAGAGCCT GAAAGTGGTAAGGTGGTCCAGGAAGGCTTCTCCGAGAGCCAGGCCCCCAGGTCTGAGCCACCAGCTCA TGTCGGGCATGCTGGGGCTCCCTCTCTGCTGAGGGCCCCAGAGAGGCCACACGCCAACCTTCGGGGAC AGGACCTGAGGACACAGAGGGCGGCGCCACGCCCCCTGAGCTGCTCAAGCACCAGCTTCTAGGAGACCTG CACCAGGAGGGCGCGCCTGAAGGGGGCAGGGGGCAAGAGAGGGCCGGGAGCAAGGAGGAGTGGATG AAGACCGCGACGTGATGAGTCTCTCCCCCAAGACTCCCTCTCCCAAGGCTCCCAAGCCCAAGATGG GCGGCTCCCAAGACAGCGCCAGAGAAGCCACCAGCATCCAGGCTTCCAGCGGAGGGTGCCATCCCC CTCCTGTGGATTCTCTTCCAAAGTTTCCACAGAGATCCAGCCTCAGAGCCCGACGGGCCAGTGTAG GGCGGGCCAAAGGGCAGGATGCCCCCTGGAGTTACGTTTACGTTGGAATACACACCAACGTGCAGAA GGAGCAGGCGCACTCGGAGGAGCATTTGGGAAGGGCTGCAATTTCCAGGGGCCCTGGAGAGGGCCAGAG GCCCGGGGCCCTCTTTGGGAGAGGACACAAAAGAGGCTGACCTTCCAGAGCCCTCTGAAAAGCAGCCTG CTGCTGCTCCCGGGGGAAGCCCTGAGCCGGGTCCCTCAACTCAAAGCTCGCATGGTCAAGTAAAGCAA AGACGGGACTGGAAGCGATGACAAAAAAGCCAAGACATCCACACGTTCTCTGCTAAAACCTTGAAAAAT AGGCCTTGCCCTAGCCCCAAACACCCCACTCTCTGGTAGCTCAGACCCCTCTGATCCAACCTCCAGCCCTG CTGTGTGCCAGAGCCACCTTCTCTCTCTAAATACGTCTCTTCTGTCACTTCCGAACTGGCAGTTCTGG AGCAAAGGAGATGAAACTCAAGGGGCTGATGGTAAACGAAGATCGCCACACCGCGGGGAGCAGCCCCCT CCAGGCCAGAAGGGCCAGGCCAACGCCACAGGATTCCAGCAAAAAACCCGCGCTCCAAAGACACCAC CCAGCTCTGCGACTAAGCAAGTCCAGAGAAGACCACCCCTGCAGGGCCAGATCTGAGAGAGGTGAACC TCCAAAATCAGGGGATCGCAGCGGTACAGCAGCCCCGGCTCCCAAGGCATCCCGGCAGCCGCTCCCGC ACCCGCTCCCTTCCAACCCACCCACCCGGAGCCCAAGAAGGTGGCAGTGTGCTGATCCACCCAAAGT CGCCGTCTTCCGCCAAGAGCCGCTGCAGACAGCCCCGTGCCATGCCAGACCTGAAGAATGTCAAGTC CAAGATCGGCTCCACTGAGAACCTGAAGCACCAGCCGGGAGGCGGAAGGTGCAGATAATTAATAAGAAG CTGGATCTTAGCAACGTCCAGTCCAAGTGTGGCTCAAAGGATAATATCAAACACGTCCCGGGAGGCGCA GTGTGCAAAATAGTCTACAAACAGTTGACCTGAGCAAGGTGACCTCCAAGTGTGGCTCATTAGGCAACAT CCATCATAAACAGGAGGTGGCCAGGTGGAAGTAAATCTGAGAAGCTTGACTTCAAGGACAGAGTCCAG TCGAAGATTGGGTCCCTGGACAATATCACCCAGTCCCTGGCGGAGGAAATAAAAAGATTGAAACCCACA AGCTGACCTTCCGCGAGAACGCCAAAGCCAAGACAGACCAGGGGCGGAGATCGTGTACAAGTCGCCAGT GGTGTCTGGGGACACGTCTCCACGGCATCTCAGCAATGTCTCTCCACCGGCAGCATCGCATGTTAGAC TCGCCCCAGCTCGCCACGCTAGCTGACGAGGTGTCTGCTCCCTGGCCAAGCAGGGTTTGTGATCAGGCC CCTGGGGCGGTCAATAATTGTGGAGAGAGAGAATGAGAGAGTGTGAAAAAAGAAATAATGACCCGG CCCCCGCCCTCTGCCCCAGCTGCTCTCGCAGTTCGGTTAATTGGTTAATCACTTAACCTGCTTTTGTCT	121

	ACTCGGCTTTGGCTCGGGACTTCAAAATCAGTGATGGGAGTAAGAGCAAATTTTCATCTTTCCAAATTGAT GGGTGGGCTAGTAATAAAATATTTAAAAAAAACATTCAAAAACATGGCCACATCCAACATTTCCCTCAGG CAATTCCCTTTTGATTCTTTTCTTCCCTCCATGTAGAAGAGGGAGAAGGAGGCTCTGAAAGCTGCTG TTCTGGGGGATTTCAAGGGACTGGGGGTGCCAACCCCTCTGGCCCTGTTGTGGGGGTGTACAGAGGCCA GTGGCAGCAACAAAGGATTTGAAACTTGGTGTGTTCGTGGAGCCACAGGCAGACGATGTCAACCTTGTGT GAGTGTGACGGGGGTGGGGTGGGGCGGGAGGCCACGGGGAGGCCGAGGCAGGGGCTGGGCAGAGGGGA GAGGAAGCACAAAGAGTGGGAGTGGGAGAGGAAGCCACGTGCTGGAGAGTAGACATCCCCCTCTTTGCCG CTGGGAGAGCCAAGGCCATGCCCACCTGCAGCGTCTGAGCGGCCGCTGTCTTGGTGGCCGGGGTGGG GGCTGTCTGTGGGTGAGTGTGCCACCTCTGCAGGGCAGCCTGTGGGAGAAGGGACAGCGGGTAAAAAGA GAAGGCAAGCTGGCAGGAGGGTGGCACTTCGTGGATGACCTCCTTAGAAAAGACTGACCTTGATGTCTTG AGAGCGCTGGCCTCTTCTCCCTCCCTGCAGGGTAGGGGGCCTGAGTTGAGGGGCTTCCCTCTGTCTCCAC AGAAACCCTGTTTTATTGAGTTCTGAAGGTGGAACTGCTGCCATGATTTTGGCCACTTTGCAGACCTGG GACTTTAGGGCTAACCACTTCTCTTTGTAAGGACTTGTGCCCTCTTGGGAGAGCTCCACCCGTTTCCAAGC CTGGGCCACTGGCATCTCTGGAGTGTGTGGGGTCTGGGAGGCAGGTCCCGAGCCCCCTGTCTTCCCAC GGCCACTGCAGTCACCCCGTCTGCCCGCTGTGTCTGTCTGCGGTGAGAGCCCAATCACTGCCTATAC CCCTCATCACAGTCACAATGTCCCGAATTTCCAGCCTCACCACCCCTTCTCAGTAATGACCCTGGTTGG TTGACGAGGTACCTACTCTCATCTGAGGGTGAATTAAGGGAAGGCAAGTCCAGGCACAAGAGTGGGA CCCAGCCTCTCACTCTCAGTTCCACTCATCCAAGTGGGACCCCTCACCAGTAATCTCATGTCTGATTCTG GTTCCCTGTCTCTCTCTCCCGTACAGATGTGAGCCAGGGCACTGCTCAGCTGTGACCTAGGTGTTTCT GCCTTGTGACATGGAGAGAGCCCTTTCCCTGAGAAGGCCCTGGCCCTTCTCTGTCTGAGCCACAGCA CAGGCTGGGTGTCTTGGTTGTCTGAGTGGTGGCACCAGGATGGAAGGGCAAGGCACCCAGGGCAGGGCCAC AGTCCCGCTGTCCCCACTTGCACCCCTAGCTGTGAGCTGCCAACCTCCAGACAGCCGACCCGCTGCTC AGCTCCACATGCATAGTATCAGCCCTCCACACCCGACAAAGGGGAACACACCCCTTGGAAATGTTCTT TTCCCCAGTCCCAGCTGGAAGCCATGCTGTCTGTTCTGTCTGGAGCAGCTGAACATATACATAGATGTTG CCCTGCCCTCCCCATCTGCACCCCTGTTGAGTGTAGTTGGATTTGTCTGTTTATGCTTGGATTACCCAGA GTGACTATGATAGTGAAGAAAAAAGGACGCGATGTATCTTGAATGCTTGTAAAGAG GTTTCTAACCCACCCCTCAGCGAGGTGTCTCTACCCCCACACTGGGACTCGTGTGGCCTGTGTGGCCAC CCTGCTGGGGCTCCCAAGTTTTGAAAGGCTTTCCTCAGCACCTGGGACCCAACAGAGACAGCTTCTAG CAGCTAAGGAGGCCGTTAGCTGTGACGAAGCCCTGAAGCACAGGATTAGGACTGAAGCGATGATGTCCC CTTCCCTACTTCCCTTGGGGCTCCCTGTGTGAGGGCAGAGCTAGGTCTTGTGGCTGGTCTGGCTGTGCG GCGCGAGGATGGTTCTCTCTGGTCTATAGCCGAAGTCTCATGGCAGTCCCAAGGAGGCTTACAACCTCT GCATGCACAAGAAAAAGGAAGCCACTGCCAGTGGGGGATCTGCAGCTCCCAGAGCTCCGTGAGCCCTCA GCCACCCCTCAGACTGGGTTCCTCTCCAAGCTCGCCCTCTGGAGGGGCAGCGCAGCCTCCCACCAAGGGC CCTGCGACCACAGCAGGATTGGGATGAATTGCCCTGTCTGGATCTGCTCTAGAGGCCCAAGCTGCCTGC CTGAGGAAGGATGACTTGACAAGTCAGGAGACACTGTTCCCAAGCCCTTGACCAGAGCACTCAGCCCGC TGACCTTGACAAAACCTCCATCTGTCTGCCATGAGAAAAGGGAAGCCGCTTTGCAAAACATTGTCTGCTAA AGAAACTCAGCAGCCTCAGGCCCAATTCTGCCACTTCTGGTTTGGGTACAGTTAAAGGCAACCCCTGAGG ACTTGGCAGTAGAAATCCAGGGCTCCCTGGGGCTGGCAGCTTCGTGTGCAGCTAGAGCTTTACCTGAA AGGAAGTCTCTGGGCCAGAACTCTCCACCAAGAGCCCTCCCTGCCGTTCCGTGAGTCCCAGCAATTCTCC TAAGTTGAAGGATCTGAGAAGGAGAAGGAATGTGGGGTAGATTGGTGGTGGTTAGAGATATGCCCCC CTCATTACTGCCAACAGTTTCGGCTGCATTCTTTCACGCACCTCGGTTCCTCTTCTGAAATCTTGTGTC CCTGCTCTTACGACCACTAGGGCTTCTTATACGGAAGGCTCTGGGATCTCCCTTGTGGGGCAGGCTCT TGGGGCCAGCCTAAGATCATGGTTTAGGGTGATCAGTGTGGCAGATAAATTGAAAAGGCACGCTGGCTT GTGATCTTAAATGAGGACAATCCCCCAGGGCTGGGCACTCCTCCCTCCCTCACTTCTCCACCTGCA GAGCCAGTGTCTTGGTGGGCTAGATAGGATATACTGTATGCCGCTCCTTCAAGCTGCTGACTCACTT TATCAATAGTTCATTAAATGACTTCAGTGGTGAGACTGTATCTGTTTGTCTATTGCTTGTGTGCTA TGGGGGGAGGGGGAGGAATGTGTAAGATAGTTAACATGGGCAAGGGAGATCTTGGGGTGCAGCACTTA AACTGCCTCGTAACCCCTTTTCATGATTTCAACCACATTTGCTAGAGGGAGGGAGCAGCCACGGAGTTAGA GGCCCTTGGGGTTTCTCTTTTCCACTGACAGGCTTTCCAGGCAGCTGGCTAGTTTCACTCCCTCCCAGC CAGGTGCAGGCGTAGGAATATGGACATCTGGTTGCTTTGGCCTGCTGCCCTCTTTCAGGGGTCTTAAGCC CACAATCATGCCTCCCTAAGACCTTGGCATCTTCCCTCTAAGCCGTTGGCACCTCTGTGCCACCTCTCA CACTGGCTCCAGACACACAGCCTGTGCTTTTGGAGCTGAGATCACTCGCTTCAACCTCTCATCTTGT CTCCAAGTAAAGCCACGAGGTGGGGCGAGGGCAGAGGTGATCACCTGCGTGTCCATCTACAGACCTGC AGCTTCATAAACTTCTGATTTCTCTCAGCTTTGAAAAGGGTTACCTTGGGCACTGGCCTAGAGCCTCA CCTCCTAATAGACTTAGCCCCATGAGTTTGCCATGTTGAGCAGGACTATTTCTGGCACTTGCAAGTCCCA TGATTTCTTCGGTAATTTCTGAGGGTGGGGGAGGGACATGAAATCATCTTAGCTTAGCTTTCTGTCTGTG AATGTCTATATAGTGATTTGTGTGTTTTAACAAATGATTACACTGACTGTTGCTGTAAAAGTGAAATTTG GAAATAAGTTATTACTCTGATTAAA	
M92424	GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGGAGCAAGAAGCC GAGCCCCAGGGGCGGCCGACCCCTCTGACCAGATCTGTGCTTTCGAGCCAGGAGCACCGTCCCT CCCCAGATTAGTGGCTACGAGCGCCAGTGCCTGGCCCGGAGAGTGAATGATCCCCAGGGCCCAGGGC GTCGTGCTTCCGAGTAGTCTAGTCCCGGTGAAGGAACTGGGAGTCTTGGGGAGCCCGACTCCCAAGC GCGAAAACCCCGATGGTGAGGAGCAGGCAATGTGCAATACCAACATGTCTGTACCTACTGATGGTGCT GTAACCACCTCACAGATTCCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTTGAAGT TATTAAAGTCTGTTGGTGACAAAAAGACACTTATACATGAAAGAGGTTCTTTTTTATCTTGGCCAGTA TATTATGACTAAACGATTATATGATGAGAAGCAACAATATTGTATATTGTTCAAATGATCTTCTAGGA GATTTGTTGGCGTGCCCAAGCTTCTGTGAAAGAGCACAGGAAAATATATACATGATCTACAGGAACCT TGGTAGTAGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTGA	122

	AGGTGGGAGTGATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAAAACCTTCATCTTCACATTGGTT TCTAGACCATCTACCTCATCTAGAAGGAGAGCAATTAGTGAGACAGAAGAAAATTCAGATGAATTATCTG GTGAACGACAAAAGAAAACGCCACAAATCTGATAGTATTTCCCTTTCCCTTTTGATGAAAGCTGGCTCTGTG TGTAATAAGGGAGATATGTTGTGAAAGAAGCAGTAGCAGTGAATCTACAGGGACGCCATCGAATCCGGAT CTTGATGCTGGTGTAAAGTGAACATTCAGGTGATTGGTTGGATCAGGATTCAGTTTCAGATCAGTTTAGTG TAGAATTTGAAGTTGAATCTCTCGACTCAGAAGATTATAGCCTTAGTGAAGAAGGACAGAAGCTCTCAGA TGAAGATGATGAGGTATATCAAGTTACTGTGTATCAGGCAGGGGAGAGTGATACAGATTCAATTTGAAGAA GATCCTGAAATTTCCCTTAGCTGACTATTGGAAATGCACTTCATGCAATGAAATGAATCCCCCTTCCAT CACATTGCAACAGATGTTGGGCCCTTCGTGAGAATTGGCTTCCCTGAAGATAAAGGGAAAGATAAAGGGGA AATCTCTGAGAAAGCCAACTGGAAAACCTCAACACAAGCTGAAGAGGGCTTTGATGTTCTGATTGTAAA AAAATATAGTGAATGATTCCAGAGAGTCACTGTGTTGAGGAAAATGATGATAAAATTACACAAGCTTCAC AATCACAAGAAAGTGAAGACTATTCTCAGCCATCAACTTCTAGTAGCATTATTTATAGCAGCCAAGAAGA TGTGAAAGAGTTTGAAGGGAAGAAACCCAAAGACAAAGAAGAGAGTGTGGAATCTAGTTTGCCTTAAAT GCCATTGAACCTTGTGTGATTGTGCAAGGTCGACCTAAAAATGGTTGCATTGTCCATGGCAAAACAGGAC ATCTTATGGCTGCTTTACATGTGCAAGAAGCTAAAGAAAAGGAATAAGCCCTGCCAGTATGTAGACA ACCAATTCAAATGATTGTGCTAATTTTCCCTAGTTGACCTGTCTATAAGAGAATTATATATTTCTA ACTATATAACCTAGGAATTTAGACAACCTGAAATTTATTCACATATATCAAAGTGAGAAAATGCCCTCAA TTCACATAGATTTCTTCTCTTTAGTATAATTGACCTACTTTGGTAGTGGAATAGTGAATCTTACTATAA TTTGACTTGAATATGTAGCTCATCTTTACACCAACTCTAATTTTAAATAATTTCTACTCTGTCTTAAA TGAGAAGTACTTGGTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACCTATATTTTTTTTG AGACCGAGTCTTGGCTCTGTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCAAGCTCTGCCC TCCCGGGTTTGCACCATCTCTCTGCTCAGCTCCCAATTAGCTTGGCTTGCCTCATCTGCCACACA CCTGGCTAATTTTTTGTACTTTTAGTAGAGACAGGGTTTACCCTGTTAGCCAGGATGGTCTCGATCTCC TGACCTCGTGATCCGCCACCTCGGCCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG	
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BG765502	GCAGCGGAGGAGCCAGTCCACGATGGCCCGGTCCCTGGTGTGCTTGGTGTGTCATCATCTTGTGCTGCTGC CTTCTCCGACCTGGTGTGAGGGGTGGTCCCTATGCCAAGCTGGCTGACCGGAAGCTGTGTGCGGACCAG GAGTGCAGCCACCCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCCGACTGCCGATTCTCTGA CCATTACCGGGGCCAAGTGGTGTATGTCTTCTCCAAGCTGAAGGGCCGTGGGCGGCTCTTCTGGGGAGG CAGCGTTACAGGAGATTACTATGGAGATCTGGCTGCTCGCCTGGGCTATTTCCCCAGTAGCATTGTCCGA GAGGACCAGACCTGAAACCTGGCAAAGTCGATGTGAAGACAGACAAAATGGGATTTCTACTGCCAGTGAG CTCAGCCTACCGCTGGCCCTGCCGTTTTCCCTCTTGGGTTTATGCAAAATACAAATCAGCCAGTGCAAAA AAAAAAAAAAAAAAAAAACTTCGGAGAAGAGATAGCAACAAAAGGCCGCTTGTGTGAAGGCGCCAAAA	124

	GTTTTGCGCCCAAGAGACCTTCGGCCTCCCCAGGGGCGCGCGCAAAGGCGCCTTGTTTTGACAACCTCTTG GACAACCGGAGGGGCTACCGCCCGGAGACCCCTGTGGTGGACCCCCGGGCAACCCGGTGTGACAGGGTA CTCACCCCCACGGCTTTTGTGCGGGGTCCACCAAAGGCCCCCAAAGAGGCTCTTTCAAGGCACATTTCCCTT GTTGTAGACCTTGTGTGTGCCACAGGCGCCAAAGAAACCTCGGGGGGCTAACAAACGCACGTGCTTGGCA GCTCCGAGAAGGCTCTCTCCACCCGAGGGGTGGACGCAACAGGGGGAATGGGCCATCATATTGTTGCC CCGGTGGGCACCAACTCTTTTCCCCCATAGAGAGCCCTTAGCACACTATGTGGGGCAGCTTATTGCCG CTAGAGAAACCGAGCGCCAGAAAATTCGAAGGGGGGGCGCTTCTCATCATTTTGCGCAAAACCCCTT GTGGGAGTATGCCCCGAACCTCCTCTGGAACACACAAGCGACACTTGC GCGGGGTCTGCAAAAACCTCCT GTTGGGAAGCCGGCTTCACN	
NM_002417	TACCGGGCGGAGGTGAGCGCGCGCGGCTCCTCCTGCGCGGACTTTGGGTGCGACTTGACGAGCGGTG GTTTCGACAAGTGGCCTTTCGGGGCCGGATCGTCCCAGTGGAGAGTTGTAAATTTGCTTCTGGCCTTCCCC TACGGATTATACCTGGCCTTCCCCTACGGATTATCTCAACTTACTGTTTAGAAAAATGTGGCCACAGAGA CGCCTGGTTACTATCAAAAGGAGCGGGGTGACGGTCCCCACTTTCCCTTGAGCCTCAGCACCTGCTTGT TTGGAAGGGGTATTGAATGTGACATCCGTATCCAGCTTCTGTTGTGTCAAACAACATTGCAAAATTGA AATCCATGAGCAGGAGGCAATATTACATAATTTAGTTCCACAAATCCAACACAAGTAAATGGGTCTGTT ATTGATGAGCCTGTACGGCTAAAACATGGAGATGTAATAACTATTATTGATCGTTCCTTCAGGTATGAAA ATGAAAGTCTTCAGAAATGAAGGAAGTCAACTGAATTTCCAAGAAAAATACGTGAACAGGAGCCAGCAG TCGTGTCTCAAGATCTAGCTTCTCTTCTGACCTGATGAGAAAGCTCAAGATTCCAAGGCCATTGCAAAA ATCACTGAAGGAAAAGTTTCAGGAAATCCTCAGGTACATATCAAGAATGTCAAAGAAGACAGTACCGCAG ATGACTCAAAAGACAGTGTGCTCAGGGAACAACTAATGTTTATTCTCAGAACATGCTGGACGTAAATGG CAGAAATGCAGCTGATCCCATTTCTGGGGATTTTAAAGAAATTTCCAGCGTTAAATTAGTGAGCCGTTAT GGAAATTTGAAGTCTGTTCCCACTACACAATGTCTTGACAATAGCAAAAAAATGAATCTCCCTTTTGG AGCTTTATGAGTCAGTGAGAAAGAGTTGGATGTAAAAATCACAAAAAGAAATGTCTCTCAGTATTGTAG AAAACTGATTACAACTGATTACGCAACAGAGAAAGAAAGTGTGATGGTTTACAGGGGGAGACCCAA CTGTTGGTCTCGCGTAAGTCAAGACCAAAATCTGGTGGGAGCGGCCACGCTGTGGCAGAGCCTGCTTCAC CTGAACAAGAGCTTGACCAGAACAAGGGGAAGGGAAGAGACGTGGAGTCTGTTTCACTCCCAGCAAGGC TGTTGGGCGCCAGCTTTCTCTCTATGAGCCGGCTAAAATGAAGACCCCTGTACAATATTACAGCAACAA AATCTCCACAAAAACATAAGAACAAAGACCTGTATATACTACTGGTAGAAGAGAAATCTGTAATCTGGGT AAAGTGAAGGCTTCAAGGCTGGTGATAAACTCTTACTCCCAGGAAGCTTTCACTAGAAATCGAACACC AGCTAAAGTTGAAGATGACGTGACTCTGCCACTAAGCCAGAAAATCTCTCTTCCAAAACAGAGGAAGT ATTCTACAGATGTGGAAGTTCTGCCTACGGAAACTGAAATTCACAATGAGCCATTTTAACTCTGTGGC TCACTCAAGTTGAGAGGAAGATCCAAAAGGATTCCTCAGCAAGCCTGAGAAATTTGGGCATACAGCTGG ACAGTGTGCTCTGGGTTACCTGGTCTTAGTTTCAAGTTGATATCAACAACCTTTGGTGATTCCATTTAG AGTGAGGGAATACCTTTGAAAAGAGGCGTGTGCTCTTTGGTGGGCACCTAAGACCTGAACATTTTATG AAAATCTGCCTCCTAATACGCCTCTCAAAAGGGGAGAGGCCCAACCAAAAGAAAGTCTCTGGTAATGCA CACTCCACCTGTCTGAAGAAAATCATCAAGGAACAGCCTCAACCATCAGGAAAACAAGAGTCAGGTTCA GAAATCCATGTGGAAGTGAAGGCACAAAGCTTGGTTATAAGCCCTCAGCTCCTAGCTTAGGAAACTC CAGTTGCCAGTGATCAACGCGGTAGGTCCTGCAAAACAGCCCTGCTTCCAGCAGCAATCTCAGACAGA GGTTCCTAAGAGAGGAGGAGAAAGAGTGGCAACCTGCCTTCAAGAGAGTGTCTATCAGCCGAAGTCAA CATGATATTTTACAGATGATATGTTCCAAAAGAAAGTGGTGCTTCGGAAGCAAAATCTGATTGTGCAA AATCATGGGCAGATGTAGTAAACTTTGGTGCAAAACAAACACAACTAAAGTCATAAAACATGGTCTCTCA AAGGTCATAGAACAAAAGGCAAGAGACCTGCTACTCCAAGAGCCTGTGGGCGCAAGTTTCACAGTCAA TTTAGTACAGGCCACGCAAACTCTCCTTGTACCATATAATAAGGAAAGCTCATACTGAAAAAGTACATG TGCTGCTCGACCTTACAGAGTGTCTCAACAACCTTCAATTTCCAAACAAAAATGGACTTTAAGGAAGATCT TTCAGTAATAGCTGAAATGTTTCAAGACCCAGTGAAGGAGCAACCGCAGTTGACAAGCACATGTCACATC GCTATTTTCAAAATTCAGAGAATTTGCTTGGAAAACAGTTTCAAGGAACTGATTCAGGAGAAGAACCCTGTC TCCCACCTCAGAGAGTTTGGAGGAAATGTGTTCTTCAAGTGACAGAAATGCAAAAACAGCCATCTGA TAAATGCTCTGCAAGCCCTCCCTTAAAGACGGCAGTGTATTAGAGAAAATGGAACGTAGCAAAAACGCCC AGGAACACCTACAAAATGACTTCTCTGGAGACAAAACCTCAGATACTGAGACAGAGCCTTCAAAAACAG TATCCACTGCAAAACAGGTGAGGAAGGTCTACAGAGTTTCAAGGAATATACAGAAGCTACCTGTGGAAGTAA GAGTGAAGAAACAAATACAGAAATTTGTGAGTGCATCTTAAAAAGAGGTGAGAAGGCAACACTACTACAA CAAAGGAGAGAAGGAGAGATGAAGGAAATAGAAAGACCTTTTGAACATATAAGGAAAAATATTGAATTAA AAGAAAACGATGAAAAGATGAAAGCAATGAAGAGATCAAGAACTTGGGGGCAGAAATGTGCACCAATGTC TGACCTGACAGACCTCAAGAGCTTGCCTGATACAGAACTCATGAAAGACACGGCACGTGGCCAGAAATCTC CTCCAAACCCAGATCATGCCAAGGCACCAAGAGTGAGAAAGGCAAAATCAATAAATGCCCTGCCAGT CATTACAACCAGAACCAATAAACACCCCAACACACAAAACAACAGTTGAAGGCATCCCTGGGGAAAGT AGGTGTGAAAGAGAGCTCCTAGCAGTCGGCAAGTTTACACGGACGTCAGGGGAGACCCAGCACACGCAC AGAGAGCCAGCAGGAGATGGCAAGAGCATCAGAACGTTTAAAGAGTCTCCAAGCAGATCCTGGACCCAG CAGCCCGTGTAACTGGAATGAAGAAGTGGCCAAGAACGCTAAGGAAGAGGGCCAGTCACTAGAAGACCT GGCTGGCTTCAAAGAGCTCTTCCAGACACCAGGTCCCTCTGAGGAATCAATGACTGATGAGAAAACCTACC AAAATAGCCTGCAAAATCTCCACCACCAGAATCAGTGGACACTCCAACAAGCACAAAGCAATGGCCTAAGA AAGTCTCAGGAAAGCAGATGTAGAGGAAGAAATCTTAGCAGTCAAGGAACTAACACACTCAGAGGAA AGCCATGCTTACGCCCCAAACAGCAGGAGGTGATGAGAAAGACATTAAAGCATTTATGGGAACTCCAGTG CAGAAACTGGACCTGGCAGGAACCTTACCTGGCAGCAAAAGACAGCTACAGACTCCTAAGGAAAAGGCC AGGTCTAGAAAGACCTGGCTGGCTTTAAAGAGCTCTTCCAGACTCCTGGTACACCGAGGAATTAGTGGC TGCTGGTAAACCACCTAAAATACCTTGCAGTCTCCACAGTCAGACCCAGTGGACACCCCAACAGCAC AAGCAACGACCAAGAGAGATGATCAGGAAGCAGATGTAGAGGAGAACTCTTAGCTGAGGAATCTAA TGCCATCAGCAGGCAAGCCATGCACACGCTTAAACCATCAGTAGGTGAAGAGAAAGACATCATCATATT	125

TGTGGGAACTCCAGTGCAGAACTGGACCTGACAGAGAAGCTTAACCGGCAGCAAGAGACGGCCACAACT CCTAAGGAAGAGGCCAGGCTCTGGAAGACCTGACTGGCTTTAAAGAGCTCTTCCAGACCCCTGGTCATA CTGAAGAAGCAGTGGCTGCTGGCAAACTACTAAAAATGCCCTGCGAATCTTCTCCACCAAGATCAGCAGA CACCCCAACAAGCACAAGAAGGCAGCCCAAGACACCTTTGGAGAAAAGGGACGTACAGAAGGAGCTCTCA GCCCTGAAGAAGCTCACACAGACATCAGGGGAAACACACACACAGATAAAGTACCAGGAGGTGAGGATA AAAGCATCAACGCGTTTAGGGAACTGCAAAACAGAACTGGACCCAGCAGCAAGTGTAACTGGTAGCAA GAGGACCCCAAACTAAGGAAAAGGCCAACCCCTAGAAGACCTGGCTGGCTTGAAGAGCTCTTCCAG ACACCAGTATGCACTGACAAGCCCAGACTCAGAGAAAACCTACCAAAATAGCCTGCAGATCACAAACAG ACCCAGTGGACACACCAACAGCTCCAAGCCACAGTCCAAGAGAAGTCTCAGGAAAGTGGACGTAGAAGA AGAAATCTTTCGCACTCAGGAAACGAACACCATCAGCAGGCAAGCCATGCACACACCCAAACAGCAGTA AGTGGTGAGAAAAACATCTACGCATTTATGGGAACTCCAGTGCAGAACTGGACCTGACAGAGAAGTTAA CTGGCAGCAAGAGACGGCTACAACTCCTAAGGAAAAGGCCAGGCTCTAGAAGACCTGGCTGGCTTTAA AGAGCTCTTCCAGACACGAGGTACACTGAGGAATCAATGACTAACGATAAACTGCCAAAGTAGCTGC AAATCTTCACAACAGACCCAGACAAAAACCCAGCAAGCTCCAAGCGACGGCTCAAGACATCCCTGGGGA AAGTGGGCGTGAAGAAGAGCTCCTAGCAGTGGCAAGCTCACACAGACATCAGGAGAGACTACACACAC ACACACAGAGCCAACAGGAGATGGTAAGAGCATGAAAGCATTTATGGAGTCTCCAAAGCAGATCTTAGAC TCAGCAGCAAGTCTAAGTGGCAGCAAGAGGCAGCTGAGAAGTCTTAAGGAAAGTCTGAAGTCCCTGAAG ACCTGGCCGGCTTCATCGAGCTCTTCCAGACACCAAGTCACACTAAGGAATCAATGACTAACGAAAAAC TACCAAGTATCTTACAGAGCTTTCAGACCCAGACCTAGTGGACACCCCAACAGCTCCAAGCCACAGCCC AAGAGAAGTCTCAGGAAAGCAGACACTGAAGAAGAAATTTTAGCATTTAGGAAACAAAGGCCATCAGCAG GCAAGCCATGCACACACCCAAACCCAGCAGTAGGTGAAGAGAAAGACATCAACACGTTTTTGGGAACTCC AGTGAGCAAACTGGACCCAGGAAATTTACCTGGCAGCAATAGACGGCTACCAACTCGTAAGGAAAAAG GCCAGGCTCTAGAAGAAGTACTGGCTTCAGAGAGCTTTTCCAGACACCATGCAGTGAATACCCACGA CTGATGAGAAAACTACCAAAAAAATACTCTGCAATCTCCGCAATCAGACCCAGCGGACACCCCAACAAA CACAAAGCAACGGCCCAAGAGAAGCCTCAAGAAAGCAGACGTAGAGGAAGAAATTTTAGCATTCAGGAAA CTAACACCATCAGCAGGCAAGCCATGCACACGCCTAAGCAGCAGTAGGTGAAGAGAAAGACATCAACA GATTTGTGGGACTCCAGTGGAGAACTGGACCTGCTAGGAAATTTACCTGGCAGCAAGAGACGGCCACA AACTCCTAAAGAAAAGGCCAAGGCTCTAGAAGATCTGGCTGGCTTCAAAGAGCTCTTCCAGACACAGGT CACACTGAGGAATCAATGACCGATGACAAAATCAGAGAAGTATCCTGCAAACTCCACAACCCAGACCCAG TCAAAACCCCAACAGCTCCAAGCAACGACTCAAGATATCCTTGGGGAAGTAGGTGTGAAGAAGAGGT CCTACCAGTCCGCAAGCTCACACAGACCTCAGGGAAGACCACACAGACACACAGAGAGACAGCAGGAGAT GGAAAGAGCATCAAAGCGTTTAAGGAATCTGCAAAAGCAGATGCTGGACCCAGCAAACTTGAAGTGGGA TGGAGAGGTGGCCAAGAACACCTAAGGAAGAGGCCCAATCACTAGAAGACCTGGCCGGCTTCAAAGAGCT CTTCCAGACACCAGACCACTGAGGAATCAACAAGTATGACAAAAGTACCAAAATAGCCTGCAAACTCT CCACCACCAGAAATCAATGGACACTCCAACAAGCACAAGGAGGCGGCCCAAAACACCTTTGGGAAAAGGG ATATAGTGAAGAGCTCTCAGCCCTGAAGCAGCTCACACAGACCACACACACAGACAAAGTACCAGGAGA TGAGGATAAAGGCATCAACGTGTTTCAAGGAACTGCAAAACAGAACTGGACCCAGCAGCAAGTGTAACT GGTAGCAAGAGGCAGCCAAAGACTCCTAAGGGAAGGCCCAACCCCTAGAAGACTTGGCTGGCTTGAAG AGCTCTTCCAGACACCAATATGCACTGACAAGCCACGACTCATGAGAAAAGTACCAAAATAGCCTGCAG ATCTCCACAACCCAGACCCAGTGGGTACCCCAACAATCTTCAAGCCACAGTCCAAGAGAAGTCTCAGGAAA CGAGACGTAGAGGAAGAACTCCTTAGCACTCAGGAAACGAACACCATCAGTAGGGAAGCTATGGACACAC CCAAACAGCAGGAGGTGATGAGAAAAGACATGAAAGCATTTATGGGAACTCCAGTGCAGAAATTTGACCT GCCAGGAAATTTACCTGGCAGCAAAAGATGGCCACAACTCCTAAGGAAAAGGCCAGGCTCTAGAAGAC CTGGCTGGCTTCAAAGAGCTCTTCCAGACACCAGGCACTGACAAGCCACGACTGATGAGAAAAGTACCA AAATAGCCTGCAAAATCTCCACAACCCAGACCCAGTGGACACCCAGCAAGCAAAAGACCGGCCAAGAG AAACCTCAGGAAAAGCAGACGTAGAGGAAGAAATTTTAGCACTCAGGAAAACGAACACCATCAGCAGGCAAA GCCATGGACACACCAAAACCCAGCAGTAAGTATGAGAAAATATCAACACATTTGTGGAAGTCCAGTGC AGAACTGGACCTGCTAGGAAATTTACCTGGCAGCAAGAGACAGCCACAGACTCCTAAGGAAAAGGCTGA GGCTCTAGAGGACCTGGTTGGCTTCAAAGAACTCTTCCAGACACCAGGTACACTGAGGAATCAATGACT GATGACAAAATCAGAGAAGTATCCTGTAAATCTCCACAGCCAGAGTCATTCAAACCTCAAGAAGCTCCA AGCAAAGGCTCAAGATACCCCTGGTGAAAGTGGACATGAAAGAAGAGCCCCTAGCAGTCAGCAAGCTCAC ACGGACATCAGGGGAGACTACGCAAAACACACACAGAGCCAACAGGAGATAGTAAGAGCATCAAAGCGTTT AAGGAGTCTCCAAAGCAGATCCTGGACCCAGCAGCAAGTGTAACTGGTAGCAGGAGGCAGCTGAGAACTC GTAAGGAAAAGGCCGTGCTCTAGAAGACCTGGTTGACTTCAAAGAGCTCTTCTCAGCACCAGGTACAC TGAAGAGTCAATGACTATTGACAAAACACAAAAATTCCTGCAAAATCTCCCCACCAGAACTAACAGAC ACTGCCACGAGCAAAAGAGATGCCCAAGACAGTCCCAGGAAAGAAAGTAAAGAGGAGCTCTCAGCAG TTGAGAGGCTCAGCCAAACATCAGGGCAAGCACAACACACACAAAGAACCAAGCGGTGATGAGGG CATCAAAGTATTGAAGCAACGTGCAAAAGAAAGAACCAACCCAGTAGAAGAGGAACCCAGCAGGAGAAGG CCAAGAGCACCTAAGGAAAAGGCCAACCCCTGGAAGACCTGGCCGGCTTACAGAGCTCTCTGAAACAT CAGGTACACTCAGGAATCACTGACTGCTGGCAAAGCCACTAAAATACCTGCGAATCTCCCCACTAGA AGTGGTAGACACCACAGCAAGCACAAGAGGCATCTCAGGACACGTGTGAGAAGGTACAAGTAAAGAA GAGCCTTCAGCAGTCAAGTTTACACAAACATCAGGGGAAACACCGGATGCACAAAGAACCAAGAGGTG AAGATAAAGGCATCAAAGCATTTGAAGGAATCTGCAAAACAGACACCGGCTCCAGCAGCAAGTGTAACTGG CAGCAGGAGACGGCCAAGAGCACCCAGGGAAAGTGCCAAGCCATAGAAGACCTAGCTGGCTTCAAAGAC CCAGCAGCAGGTACACTGAAGAATCAATGACTGATGACAAAACCACTAAAATACCTGCAAAATCATCAC CAGAAGTAGAAGACACCGCAACAAGCTCAAAGAGACGGCCAGGACAGTGGCCAGAAAGTAGAAGTGA GGAGGAGCTGTAGCAGTTGGCAAGCTCACACAAACCTCAGGGGAGACCACGCACACCAAGAGCCG GTAGGTGAGGGCAAAGGCACGAAAGCATTTAAGCAACCTGCAAGCGGAAGCTGGACGCAGAAGATGTAA	
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	TTGGCAGCAGGAGACAGCCAAGAGCACCTAAGGAAAAGGCCCAACCCCTGGAAGATCTGGCCAGCTTCCA AGAGCTCTCTCAAACACCAGGCCACACTGAGGAACCTGGCAAATGGTGTCTGATAGCTTTACAAGCGCT CCAAAGCAAACACCTGACAGTGGAAAACCTCTAAAAATATCCAGAAGAGTTCTTCGGGCCCTTAAAGTAG AACCCTGTTGGGAGACGTGGTAAGCACCAGAGACCCCTGTAAAAATCACAAGCAAAAGCAACACTTCCCTGCC CCCCTGCCCCTCAAGAGGGGAGGTGGCAAAGATGGAAGCGTCACGGGAACCAAGAGGCTGCGCTGCATG CCAGCACCAGAGGAAATTTGTGGAGGAGCTGCCAGCCAGCAAGAAGCAGAGGGTTGCTCCCAGGGCAAGAG GCAAATCATCCGAACCCGTGGTCATCATGAAGAGAAGTTTGAGGACTTCTGCAAAAAGAAATTGAACCTGC GGAAGAGCTGAACAGCAACGACATGAAAACCAACAAAGAGGAACACAAATTACAAGACTCGGTCCCTGAA AATAAGGGAATATCCCTGCGCTCCAGACGCCAAAATAAGACTGAGGCAGAACAGCAAAATAACTGAGGTCT TTGTATTAGCAGAAAGAATAGAAATAAACAGAAATGAAAAGAAGCCCATGAAGACCTCCCCAGAGATGGA CATTGAGAATCCAGATGATGGAGCCCGGAAACCCATACCTAGAGACAAAGTCACTGAGAACAAAAGGTGC TTGAGGTCTGCTAGACAGAATGAGAGCTCCAGCCCTAAGGTGGCAGAGGAGAGCGGAGGGCAGAAAGAGTG CGAAGGTTCTCATGCAAGATCAGAAAGGGAAGGAGAAGCAGGAAATTCAGACTCCATGTGCTGCTGAGATC AAGAAAGACAAAAAGCCAGCCTGCAGCAAGCACTTTGGAGAGCAAACTGTGTCAGAGAGTAACGCGGAGT GTCAGAGGTGTGCAGAAATCCAAAGAAGGTGAGGACAATGTGTGTGTCAGAAAATAGAACCAGAA GTCATAGGGACAGTGAAGATATTTGACAGAAAAATCGAACTGGGAAAAATATAATAAGTTAGTTTTGTG ATAAGTTCTAGTGCAGTTTTTGTCTATAAATTACAAGTGAATTCGTGAAGTAAGGCTGTGAGTCTGCTTAA GGAAGAGAAAACTTTGGATTTGCTGGGTCTGAATCGGCTTCATAAACTCCACTGGGAGCACTGCTGGGCTC CTGGACTGAGAATAGTTGAACACCGGGGGCTTTGTGAAGGAGTCTGGGCCAAGGTTTGCCCTCAGCTTTG CAGAATGAAGCCTTGAGGTCTGTCAACACCCACAGCCACCCCTACAGCAGCCTTAACCTGTGACACTTGCCA CACTGTGTCTGCTGTTTTGTTTGCCTATGTCTCCAGGGCAGGTTGGCAGGAACAATATCCTCGTCTGTCC CAACTGAGCAGGCACTCGGTAAACAGAAATGAATGATGAGCGCAGGATGAATGAGGCTGTACAGATTAAGAT CTGTCTTTCCAAATGGCCGGGGCATTTGGTCCCCAAATTAAGGCTATTGGACATCTGCACAGGACAGTCC TATTTTTGATGTCTTTCTTTCTGTAAAAATAAAGTTTTGTGCTTTTGGAGAATGACTCGTGAGCACATCTT TAGGGACCAAGAGTGACTTTCTGTAAAGGAGTGACTCGTGGCTTGCTTTGGTCTCTTGGGAATACTTTCT AACTAGGGTTGCTCTCACCTGAGACATTTCTCCACCCGCGGAATCTCAGGGTCCCAGGCTGTGGGCCATCA CGACTCAAACCTGGCTCCTAATCTCCAGCTTTCTGTGCTATTGAAAGCTTCGGAAGTTTACTGCTGCTGCT CCCGCTGTTTTCTTTCTGACTCTATCTGGCAGCCCGATGCCACCCAGTACAGGAAGTGACACCAGTACT CTGTAAAGCAICATCATCTTTGGAGAGACTGAGCACTCAGCACCTTCAGCCACGATTTTCAAGATCGCTTC CTTTGTAGCCGCTGCCTCCGAAATCTCTTTGAAGCCAGACATCTTTCTCCAGCTTCAGACTTTGTAGAT ATAACTCGTTTCATCTTCTTTACTTTCCACTTTGCCCTCTGTCTCTGTGTTCCCCAAATCAGAGAA ATGCCCGCATCCCCAGGTCACTGTCTGGATTCTCCCAATTCACCCACCTTGCCAGGTGAGGTGAGG ATGGTGACACCAGACAGGGTAGCTGTCCCCAAATGTGCCCTGTGCGGGCAGTGCCCTGTCTCCACGTTT GTTTCCCCAGTGTCTGGCGGGGAGCCAGGTGACATCATAAATACTTGTGAATGAATGCAGAAATCAGCG GTACTGACTTTGACTATATTGGCTGCCATGATAGGGTTCTCACAGCGTCATCCATGATCGTAAGGGAGAA TGACATCTGCTTTGAGGGAGGGAATAGAAAGGGGCAGGGAGGGGACATCTGAGGGCTTCACAGGGCTGCA AAGGTTACAGGGATTGACCAGGGCAGAACAGGGGAGGGTGTTCAGGAAGAGTGCTCTTAGCAGAGGC ACTTTGGAAGGTGTGAGGCATAAATGCTTCTCTACGTAGGCCAACCTCAAACTTTTCACTAGGAATGT TGCTATGATCAAGTTGTTCTAACACTTTAGACTTAGTAGTAATTATGAACCTCACATAGAAAAATTTTCA CCAGCCATATGCCGTGTGGAGTGGAAATATTCTGTTTAGTAGAAAAATCCTTTAGAGTTCAGCTCTAACAG AAATCTTGCTGAAGTATGTGAGCACCTTTTCTCACCTGGTAAGTACAGTATTTCAAGAGCACGCTAAGG GTGGTTTTTCATTTTACAGGGCTGTGTGATGATGGGTAAATAATGTTCATTTTAAGGGCTACCCCGTGTTA ATAGATGAACACCCTTCTACACAACCCCTCCTTGGTACTGGGGGAGGGAGAGATCTGACAAATACTGCC ATTCCCCTAGGCTGACTGGATTTGAGAACAAATACCCACCCATTTCACCATGGTATGGTAACCTTCTCTG AGCTTCAGTTTTCCAAGTGAATTTCCATGTAATAGGACATTCCTATTAAATACAAGCTGTTTTTACTTTTT CGCTCCCAGGGCCTGTGGGATCTGGTCCCCAGCCTCTCTTGGGCTTTCTTACACTAATCTGTACCTA CCATCTCCTGCCTCCCTTAGGCAGGCACCTCCAACCACACACTCCCTGTGTTTTCCCTGCTGGAA CTTTCCCTCCTGCCCCACCAAGATCATTTTATCCAGTCTCTGAGCTCAGCTTAAGGGAGGCTTCTTGCTG TGGGTTCCCTACCCCCATGCCTGTCTCCAGGCTGGGGCAGGTTCTTAGTTTGCCTGGAATTTGTTCTGT ACCTCTTTGTAGCACGTAGTGTGTGGAACTAAGCCACTAATTGAGTTTCTGGCTCCCTCCTGGGGTT GTAAGTTTTGTTTCACTTATGAGGGCCGACTGCATTTCTGGTTACTCTATCCAGTGACCAGCCACAGGA GATGTCCAATAAAGTATGTGATGAAATGGTCTTAAAAA	
NM_024101	GCGCCGGGACGTGGCCAGTTGCCCGCTGCCCGGAGAGCCAGGCGCTAACAGCCGCTCTGCGCCCCGC GCCCTGCTTGCCCCATTATCCAGCCTTGCCCCGGCGCCTGACCTGACGCCCTGGCCTGACGCCCTGCT TCGTGCGCTCCTTTCTCTCCAGGTGCTGGACCAGGGACTGAGCGTCCCCCGAGAGGGTCCGGTGTGAC CCGACAAGAAGCAGAAATGGGGAAGAACTGGATCTTTCCAAGCTCACTGATGAAGAGGGCCAGCATGT CTTGGAAGTTGTTCAACGAGATTTTGACCTCGAAGGAAAGAAGAGGAACGGCTAGAGCGGTGAAGGGC AAGATTAAGAAGGAAAGCTCCAAGAGGGAGCTGCTTTCCGACACTGCCATCTGAACGAGACCCACTGCG CCCGCTGCCTGCAGCCCTACCAGCTGCTTGTGAATAGCAAAAGGCAGTGCCGGAATGTGGCCTCTTCAC CTGCAAAAGCTGTGGCCCGTCCACCCGAGGAGCAGGGCTGGATCTGTGACCCCTGCCATCTGGCCAGA GTCTGGAAGATCGGCTCACTGGAGTGGTACTATGAGCATGTGAAAGCCCGCTTCAAGAGGTTCGGAAGTG CCAAGGTTCATCCGGTCCCTCCACGGGCGGCTGCAGGGTGGAGCTGGGCTGAACTGATATCTGAAGAGAG AAGTGGAGACAGCGACCAGACAGATGAGGATGGAGAACCTGGCTCAGAGGCCAGGCCAGGCCAGGCC TTTGGCAGCAAAAAAAGCGCTCCTCTCCGTCCACGACTTCGACTTCGAGGGAGACTCAGATGACTCCA CTCAGCCTCAAGGTCACTCCCTGCACCTGTCTCAGTCCCTGAGGCCAGGGACAGCCACAGTCCCTCAC AGATGAGTCTGCTCAGAGAAGGCAGCCCTCACAAGGTGAGGGCCTGGAGGAGGCTGATATGGGGCC TCTGGGTGCCACTCCCTCCGGAAGAGCAGCCGACAGCATCTACCTTCCAGACCGGCCCTGGCTG AGCTCTGCCCGCTGGAGGCTCCACAGGATGGCCCTGGGGACTGCTGCTGCACTCGGGTCAATGTCAAT	126

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	AACATACCTCAATCCTGTCCCAGGCCGGATCCTCCTGAAGCCCTTTTCGCAGCACTGCTATCCTCCAAAG CCATTGTAAATGTGTGTACAGTGTGTATAAACCTTCTTCTCTTTTTTTTTTTTAAACTGAGGATTGTC	
NM_002467	GACCCCGAGCTGTGCTGCTCGCGGCCGCCACCGCCGGGCCCGCGCTCCCTGGCTCCCTCCTGCTC GAGAAGGGCAGGGCTTCTCAGAGGCTTGGCGGAAAAAGAACGGAGGGAGGGATCGCGCTGAGTATAAAA GCCGGTTTTTCGGGGCTTTATCTAATCTCGCTGTAGTAATCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGG CCGGCTAGGGTGGAAAGAGCCGGGCGAGCAGAGCTGCGCTGCGGGCGTCTGGGAAGGGAGATCCGGAGCG AATAGGGGGCTTCGCCCTTGGCCAGCCCTCCCGCTGATCCCCAGCCAGCGGTCCGCAACCCCTTGCCGC ATCCACGAAACTTTGCCCATAGCAGCGGGCGGGCACCTTGCACCTGGAACCTTACAAACCCGAGCAAGGAC GCGACTCTCCCGACGCGGGGAGGCTATTCTGCCCATTTGGGGACACTTCCCGCGCGTCCAGGACCCGC TTCTCTGAAAGCTCTCCTTGCAGCTGCTTAGACGCTGGATTTTTTTCGGGTAGTGGAAAACAGCAGCC TCCCGCGACGATGCCCTCAACGTTAGCTTACCAACAGGAACATATGACCTCGACTACGACTCGGTGCAG CCGTATTTCTACTGCGACGAGGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCTGCAGCCCCCGG CGCCGAGCGAGGATATCTGGAAGAAATTCGAGCTGCTGCCCCACCCGCCCTGTCCCTAGCCCCGCGTC CGGGCTCTGCTCGCCCTCTACGTTGCGGTACACCCCTTCTCCCTTCGGGGAGACAACGACGGCGGTGGC GGGAGCTTCTCCAGGGCGACAGCTGGAGATGGTGACCGAGCTGCTGGGAGGAGACATGGTGAACCAGA GTTTCATCTGCGACCCGGACGACGAGACCTTCATCAAAAACATCATATCCAGGACTGTATGTGGAGCGG CTTCTCGGCCGCCCAAGCTCGTCTCAGAGAAGCTGGCTCCTACCAGGCTGCGCGCAAAGACAGCGGC AGCCGGAACCCCGCCCGCGGCCACAGCGTCTGCTCCACCTCCAGCTTGTACCTGCAGGATCTGAGCGCG CCGCTCAGAGTGCATCGACCCCTCGGTGGTCTTCCCTACCTCTCAACGACAGCAGCTCGCCCAAGTC CTGGCCTCGCAAGACTCCAGCGCTTCTCTCGTCTCCGATTCTCTGCTCTCCTCGACGGAGTCTCC CCGAGGGCAGCCCCGAGCCCTGGTGTCTCATGAGGAGACACCGCCACCAGCAGCGACTCTGAGG AGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTTTCTGTGGAAAAAGAGGAGGCTCTGGCAAAAGGTC AGAGTCTGGATCACCTTCTGCTGGAGGCCACAGCAAACTCCTCACAGCCCTGGTCTCAAGAGGTGC CACGCTCCACACATCAGCACAACCTACGACGCGCTCCCTCCACTCGGAAGGACTATCTGCTGCCAAGA GGGTCAAGTTGGACAGTGTGAGAGTCTGAGACAGATCAGCAACACCGAAATGCACAGCCCCAGGTC CTCGACACCCGAGGAGAAATGTCAAGAGGCGAACACACACGCTTGGAGCGCCAGAGGAGGAACGAGCTA AAACGGAGCTTTTTTGCCCTGCGTGACAGATCCCGGAGTTGGAAAAACAATGAAAGAGCCCCCAAGGTAG TTATCCTTAAAAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAGCAAAAGCTCATTTCTGAAGA GGACTTGTGCGGAAACGACGAGAACAGTTGAAACACAACTTGAACAGCTACGGAACCTTGTGCGTAA GGAAAAGTAAGGAAAACGATTCTTCTAACAGAAATGCTGAGCAATCACCTATGAACCTGTTTTCAAAAT GCATGATCAAAATGCAACCTCACACCTTGGCTGAGTCTTGAAGCTGAAAGATTAGCCATAATGTAACT GCTCAAAATTTGACTTTGGGCATAAAAGAACTTTTTATGCTTACCATCTTTTTTTTTTTTAAACAGAT TTGTATTTAAGAATTGTTTTTAAAAAATTTTAAAGATTTACACAATGTTTCTGTAAATTTGCCATTAA ATGTAAATAACTTTAATAAAACGTTTATAGCAGTTACACAGAATTTCAATCCTAGTATATAGTACCTAGT ATTATAGGTACTATAAAACCTTAATTTTTTTTATTTAAGTACATTTTGCTTTTTAAAGTTGATTTTTTCT ATTGTTTTTAGAAAAAATAAAATAACTGGCAAATATATCATTGAGCCAAATCTTAAAAAATAAAAAA	128
BC013732	GTGGGAGGATTGCATTGCTAGTTCCTGTTGCGGGCTGAAATAACCTGCTCTCCAAATGTCACAA AAGTGACTTAAGTCAGGTTCCCCAAACAGACACCAAGACAAGAAATCCATGTGTGACTGAAGGAA GTGCTGGGAGAGCCCCAGCTGCAGCTTGGATGTGAATGCAACTCCAAAGTGTGTCCAGACTCAAGGCAA GGGCACTAGGCTTTCCAGACCTCCTACTAAGTCATTGATCCAGCACTGCCCTGCCAGGACATAAATCCCT GGCACCTCTTGCTCTCTGCAAAGGAGGGCAAGCAGCTTCAGGAGCCCTTGGGAGTCTCCAAAGAGAGT CTAGGTTACAGGTCCGAAAGTAGAAGAACACAGAAGGCAGGCCAGGGGCACGTGAGATGGTAAAGAGA TCTGAAGGGATCCAGAATTCAAGCCAGGAAGAAGCAGCAATCTGCTTCTGATTAAACTGAAAGTCAA CCTACTTTCAACTTACTAAGAAAGGGGATCATGGACATTGAAGCATATCTTGAAAGAATTGGCTATAAGA AGTCTAGGAACAAATTTGACTTTGGAAACATTAACGTATTTCTTCAACACAGATCCGAGCTGTTCCCTT TGAGAACCTTAAACATCCATTGTGGGGATGCCATGGACTTAGGCTTAGAGGCCATTTTTGATCAAGTTGTG AGAAGAAATCGGGGTGGATGGTGTCTCCAGGTCAATCATCTTCTGTACTGGGCTCTGACCATTATGGTT TTGAGACCAGATGTTGGGAGGGTATGTTTACAGCACTCCAGCCAAAAAATACAGCACTGGCATGATTCA CCTTCTCCTGCAGGTGACCATTGATGGCAGGAACATACATTGTCGATGCTGGGTTTGGACGCTCATACCAG ATGTGGCAGCTCTGGAGTTAATTTCTGGGAAGGATCAGCCTCAGGTGCTTGTGTCTCCGTTTTGACGG AAGAGAATGGATTCTGGTATCTAGACCAATCAGAAGGGAACAGTACATTCCAAATGAAGAATTTCTTCA TCTGATCTCCTAGAAGACAGCAAAATACGAAAAATCTACTCCTTTACTCTTAAGCCTGAACAAATTGAA GATTTTGTGCTATGAATACATACCTGCAGACATCTCCATCATCTGTGTTTTACTAGTAAATCATTTTGT CCTTGCAGACCCAGATGGGGTTCACTGTTTGGTGGGCTTACCCTCACCCATAGGAGATTCAATTATAA GGACAATACAGATCTAATAGAGTTCAAGACTCTGAGTGAGGAAGAAATAGAAAAAGTGTGAAAAATATA TTTAATATTTCTTGCAGAGAAAGCTTGTGCCCAACATGGTGATAGATTTTTTACTATTTAGAATAAGG AGTAAACAACTTGTCTATTGTGATCCAGCTCACCAGTTATCAACTGACGACCTATCATGTATCTTCT GTACCCCTACCTTATTTTGAAGAAATCTAGACATCAAATCATTTACCTATAAAAAATGTCATCATATA TAATTAACAGCTTTTTAAAGAAACATAACCACAAACCTTTCAAATAATAATAATAATAATAATAA ATGTCTTTTAAAGATGGCTGTGGTTATCTTGGAAATGGTGATTATGCTAGAAAGCTTTAATGTGG TTTATTGTTGAATCTAGAAAAGTTTTATGGGTAGATGAGTAAATAAAATATGTAAAAAACTTATTG TCTATAAAGTATATTAACCAATTGTTGGCTAATAATAAAAAAATAAAAAA	129
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[illegible]

	GGTCGACAAGGAGAACACGCCGCCGCCCTGAGCGGGACCCGCGTCTGGCCAGCAAGACCCGCGAGGAGG ATCTTCCAGGAGAAAACCCCGCCGCTTTTGTCATCTTCCCCATCGAGTACCATGATATCTGGCAGATGTA TAAGAAGGCAGAGGCTTCTTTTGGACCGCCGAGGAGGTGGACCTCTCCAAGGACATTCAGCACTGGGAA TCCCTGAAACCCGAGGAGAGATATTTTATATCCCATGTTCTGGCTTTCTTTGACGCAAGCGATGGCATAG TAAATGAAAACCTTGGTGGAGCGATTTAGCCAGAAGTTCAGATTACAGAAGCCCGCTGTTCTATGGCTT CCAAATTGCCATGGAAAACATACATTCTGAAATGTATAGTCTTCTTATTGACACTTACATAAAAGATCCC AAAGAAAGGGAATTTCTCTTCAATGCCATTGAAACGATGCCCTTGTGTCAAGAAGAAGGCAGACTGGGCTT TGCGCTGGATTGGGGACAAAGAGGCTACCTATGGTGAACGTGTTGTAGCCTTTGCTGCGAGTGGAAAGGCAT TTTCTTTTCCGGTTCTTTTGGCTCGATATTCTGGCTCAAGAAACGAGGACTGATGCCCTGGCCTCACATTT TCTAATGAACCTATTAGCAGAGATGAGGGTTTACACTGTGATTTTGTGCTTGCCTGATGTTCAAACACCTGG TACACAAACCATCGGAGGAGAGAGTAAGAGAAATAATTATCAATGCTGTTCCGATAGAACAGGAGTTCCCT CAGTGGGCTTGGCTGTGAAGCTCATTGGGATGAATTGCACCTAATGAAGCAATACATTGAGTTTGTG GCAGACAGACTTATGCTGGAACCTGGGTTTTAGCAAGGTTTTAGAGTAGAGACCCATTGACTTTATAGG AGAATATTTCACTGGAAGGAAAGACTAATTCTTTGAGAAGAGAGTAGGCGAGTATCAGAGGATGGGAGT GATGTCAAGTCCAACAGAGAATTTCTTTTACCTTGGATGCTGACTTCTAAATGAAGTGAAGATGTGCCCTT ACTTGGCTGATTTTTTTTTTTTCCATCTCATAAGAAAAATCAGCTGAAGTGTACCAACTAGCCACACCAT GAATTGTCCGTAATGTTTCATTACAGCATCTTTAAACCTGTGTAGCTACCTCACAACGCTCCTGTCTGT TTATAGTGTCTGTAGTATCACCCTTTGCCAGAAGGCCCTGGCTGGCTGTGACTTACCATAGCAGTGAAT GGCAGTCTTGGCTTTAAAGTGAGGGGTGACCCTTTAGTGAGCTTAGCACAGCGGGATTAAACAGTCTCTT AACCAGCACAGCCAGTTAAAGATGCAGCCTCACTGCTTCAACGAGATTTTAAATGTTTACTTAAATATA AACCTGGCACTTTACAAACAAATAAACATTGTTTGTACTCACAAGGCGATAATAGCTTGATTTATTTGGT TTCTACACCAATACATTCTCTGACCCTAATGGGAGCCATTACAAATCATAAGTGACTAAAGTAA TTTAAACTTGTGTAGACTAAGCATGTAATTTTTAAAGTTTTATTTTAAATGAATTAATAATTTTGTAAACCA ACTTTAAAGTCAGTCTGTGTATACCTAGATATTAGTCAGTTGGTGCCAGATAGAAGACAGGTTGTGTTT TTATCCTGTGGCTTGTGTAGTGTCTGGGATCTCTGCCCCCTCTGAGTAGAGTGTGTGGGATAAAGGA ATCTCTCAGGGCAAGGAGCTTCTTAAAGTTAAATCACTAGAAATTTAGGGGTGATCTGGGCTTTCATATGT GTGAGAAGCCGTTTCAATTTATTTCTCACTGTATTTTCCCTCAACGCTGTGGTGTAGAGAAATTTCTTG AAGAGTTTTTATATGTGGGAGCTAAGGTAGTATTGTAATAATTTCAAGTCATCCTTAAACAAAATGATCCA CCTAAGATCTTGGCCCTGTTAAGTGGTGAAATCAACTAGAGGTGGTTCCTACAAGTTGTTTATTCTAGTT TTGTTGGTGTAAGTAGGTTGTGTGAGTTAATTCATTATATTTACTATGTCTGTAAATCAGAAATTTT TTATTATCTAAGTTCTTCTAGATTTTACCTGTAGTTTCATACTTCAGTCACCCAGTGTCTTATTCTGGCAT TGCTTAATCTGAGCATGTGTCTAGGGGATCTTAAACTTTAGTAGAAACCATGAGCTGTTAATAGCAGTT TCCATTCAAATATTAAATTCAGAATGAAACATAAATTTTTTTTTTTTTTTTGGAGATGGAGTCTCGCTCT GTTGCCAGGCTGGAGTGCAGTGGCGCGATTTTGGCTCACTGTAACTCCAICTCTCTGGGTTCAAGCAAT TCTCTGTCTCAGCCTCCCTAGTAGCTGGGACTGCAGGTATGTGTACCACACCTGGCTAATTTTTGTAT TTTTAGTAGAGATGGAGTTTACCATATTGGTCAGGCTGGTCTTGAACCTCCGACCTCAGGTGATCCACC CACCTCGGCCCTCCCAAAGTGCTGGGATTGCAGGCGTGATAAACAAATATTCTTAATAGGGCTACTTTGAA TTAATCTGCCTTTATGTTTGGGAGAGAAAGCTGAGACATTGCATGAAAGATGATGAGAGATAAATGTTG ATCTTTTGGCCCCATTTGTTAATTGTATTTCAGTATTTGAACGTCGTCTGTTTATTGTTAGTTTTCTTCA TCATTTATTGTATAGACAATTTTTAAATCTCTGTAATATGATACATTTTCCCTATCTTTAAGTTATTGTT ACCTAAAGTTAATCCAGATTATATGGTCTTTATATGTGTACAACATTAATAAGAAAGGCTTTGTCTTGCA TTGTGAGGTACAGGCGGAAGTTGGAATCAGGTTTTAGGATTCGTCTCTCATTAGCTGATAAATGTGAGG ATTAACCTCTGCCAGCTCAGACCATTTCCTAATCAGTTGAAAGGGAAACAAGTATTTCACTCTCAAAAT GAATAATGCACAAGTCTTAAAGTGATTAAATAAAACGTCTTATGTCAGTTT	
BC036503	AGCGGGGGCACTCCAGCCCTGCAGCCTCCGGAGTCAAGTCCGCGCGCGCCCGCGCCCGCGCTTCTGTCT CGCCGCACCTCCGGGAGCCGGGGCGCACCCAGCCCGCAGCGCGCCCTCCCCGCCGCGCCCGCTCCGACC GCAGGCCGAGGGCCGCCACTGGCCGGGGGAGCCGGGCAGCAGCTTGGCGCCGCGGAGCCGGCAACGCTG GGGACTGCGCCTTTTGTCCCCGAGGTTCCCTGGAAGTTTGGCGCAGGACGCGCGCGGGGAGGCGCGGAG GCAGCCCCGACGTCCGGAGAACAGGGCGCAGAGCCGGCATGGGCATCGGGCGCAGCGAGGGGGGCCGCC GCGGGGCAGCCCTGGGCGTGTCTGTGGCGCTGGGCGCGCGCTTCTGGCCGTGGGCTCGGCCAGCGAGTA CGACTACGTGAGCTTCCAGTCCGACATCGGCCCGTACCAGAGCGGGCGCTTCTACACCAAGCCACCTCAG TGCGTGGACATCCCGCGGACCTGCGGCTGTGCCACAACGTTGGGTACAAGAAGATGGTGTCTGCCAACC TGCTGGAGCACGAGACCATGGCGGAGGTGAAGCAGCAGGCCAGCAGCTGGGTGCCCCCTGCTCAACAAGAA CTGCCACGCCGGCACCCAGGTCTTCTCTGTCTGCTCTTTCGCGCCGCTGTGCTTGGACCGGCCATCTAC CCGTGTCTGCTGGCTCTGCGAGGCCGTGCGGACTCGTGCGAGCCGGTCATGCAAGTTCTTGGCTTCTACT GGCCCGAGATGCTTAAGTGTGACAAGTTCCCGGAGGGGACGCTGTCATCGCCATGACGCCGCCCAATGC CACCGAAGCCTCCAAGCCCCAAGGCACAACGGTGTGTCTTCCCTGTGACAACGAGTTGAATCTGAGGCC ATCATTGAACATCTCTGTGCCAGCGAGTTTGCAGTGAAGATGAAAAATAAAGAAAGTGAAGAAAGAAATG GCGACAAGAAGATTGTCCCCAAGAAGAAGAGCCCTGAAGTTGGGGCCCATCAAGAAGAAGGACCTGAA GAAGCTGTGTGTACCTGAAGAATGGGGCTGACTGTCCCTGCCACCAGCTGGACAACCTCAGCCACCAC TTCTCATCATGGGCCGAAGGTGAAGAGCCAGTACTTGTGACGGCCATCCACAAGTGGGACAAGAAAA ACAAGGAGTTTCAAAAACCTCATGAAGAAAATGAAAAACCATGAGTGCCCCACCTTTCAGTCCGTGTTAA GTGATTCTCCCGGGGGCAGGGTGGGGAGGGAGCCTCGGGTGGGGTGGGAGCGGGGGGACAGTGCCCCGG GAACCCGGTGGGTACACACACGCACTGCGCCTGTCTAGTGGACATTTAATCCAGTGGCTTGTCTT GCAGCATTCGCCCTCCCTTCCCTCCATAGCCAGCTCCAAACCCAGGGTAGCCATGGCCGGGTAAAGCA AGGGCCATTTAGATTAGGAAGGTTTTAAGATCCGCAATGTGGAGCAGCAGCCATGCACAGGAGGAGGT GACAAACCATTTCCAACGCAACAGCCACTAAACACAAAAAGGGGGATTGGCGCCAGGTGAGAGCC AGCAGCAAAAACCTACATTTTGAACCTGTTGGTGTGGATCTATTGGCTGATCTATGCCTTTCACTAGAA	135

	AATTCTAATGATTGGCAAGTCACGTTGTTTTTCAGGTCCAGAGTAGTTTCTTTCTGTCTGCTTTAAATGGA AACAGACTCATACCACACTTACAATTAAGGTCAAGCCAGAAAGTGATAAGTGCAGGGAGGAAAAGTGCA AGTCCATTATGTAATAGTGACAGCAAAGGGACCAGGGGAGAGGCATTGCCTTCTCTGCCCCACAGTCTTTTC CGTGTGATTGCTTTGAATCTGAATCAGCCAGTCTCAGATGCCCCAAAGTTTCGGTTCTATGAGCCCGG GGCATGATCTGATCCCCAAGACATGTGGAGGGGCAGCCTGTGCCTGCCTTTGTGTGAGAAAAGGAAACC ACAGTGAGCCTGAGAGAGACGGCGATTTCGGGCTGAGAAGGCAGTAGTTTCAAAACACATAGTTAAAA AAGAAACAAATGAAAAAATTTTGAACAGTCCAGCAAATTGCTAGTCAGGGTGAATTGTGAAATTTGGGT GAAGAGCTTACGATTCTAATCTCATGTTTTTTCCTTTTTCACATTTTAAAAAGAAACATGACAAACCCCA CTTATTTTTCAAGGTTTTTAAACAGTCTACATTGAGCATTGAAAGGTGTGCTAGAACAAGGTCTCTCTGA TCCGTCCGAGGCTGCTTCCAGAGGAGCAGCTCTCCCCAGGCATTGCCAAGGGAGGCGGATTTCCTTGG TAGTGTAGCTGTGTGGCTTTCTTCTCTGAAGAGTCCGTGGTTGCCCCAGAACCTAACACCCCTAGCAAA ACTCACAGAGCTTTCCGTTTTTTCTTCTCTGTAAGAAACATTTTCTTTGAACTTGATTGCCTATGGAT CAAAGAAATTCAGAACAGCCTGCCTGTCCCCCGCACCTTTTACATATATTTGTTTTCATTTCTGCAGATG GAAAGTTGACATGGGTGGGTGTCCCCATCCAGCGAGAGAGTTTAAAAAGCAAAACATCTCTGCAGTTTT TCCCAGTGCCTGAGATACTTCCCAAAGCCCTTATGTTAATCAGCGATGTATATAAGCCAGTTCACTT AGACAACCTTTACCTTCTTGTCCAATGTACAGGAAGTAGTTCTAAAAAATGCAATTAATTTCTTCCC CCAAAGCCGGATTCTTAATCTCTGCAACACTTTGAGGACATTTATGATTGCTCTGGGCCAATGCTT ATACCCAGTGAGGATGCTGCAGTGAGGCTGTAAAGTGGCCCCCTGCGGCCCTAGCCTGACCCGAGGAAA GGATGGTAGATTCTGTAACTCTTGAAGACTCCAGTATGAAAATCAGCATGCCCGCTAGTTACCTACCG GAGAGTTATCTGATAAATTAACCTCTCACAGTTAGTGATCCTGTCTTTTAAACACCTTTTTTGTGGGGT TCTCTCTGACCTTTTATCGTAAAGTGCTGGGGACCTTAAAGTGATTGCTGTAAATTTGGATGATTAAAA AATGTGTATATATATTAGCTAATTAGAAATATCTACTTCTCTGTGTCAAAGTGAATTCAGAGCAAGT TCCTGAGTGCGTGGATCTGGGTCTTAGTTCTGGTTGATTCACTCAAGAGTTTCACTGCTCATACGTATCTG CTCATTTTGACAAAGTGCTCATGCAACCGGGCCCTCTCTCTGCGGCAGAGTCTTAGTGAGGGGTTTA CCTGGAACATTAGTAGTTTACCACAGAATACGGAAGAGCAGGTGACTGTGCTGTGCAGCTCTCTAAATGGG AATTTCTCAGGTAGGAAGCAACAGCTTCAGAAAGAGCTCAAAATAAATTTGAAATGTGAATCGCAGCTGTG GGTTTTTACCACCGTCTGTCTCAGAGTCCCAGGACCTTGAGTGTCATTAGTTTATTTAGAGGTTTTAG ACCCATAGCAGCTTTGTCTCTGTCTCACATCAGCAATTTTCAAGAACAAAAGGGAGGCTCTCTGTAGGCACAG AGCTGCACTATCACGAGCCTTTGTTTTTCTCCACAAAGTATCTAACAAAACCAATGTGCAGACTGATTGG CCTGGTCATTGGTCTCCGAGAGAGGAGGTTTTGCTGTGATTTCCTAATTATCGCTAGGGCCCAAGTGGGA TTTGTAAAGCTTTACAATAATCATTCTGGATAGAGTCTGGGAGGTCTTGGCAGAACTCAGTTAAATCT TTGAAGAATATTTGAGTTATTTAGAAATAGCATGGGAGGTGAGGATTGCGAAAACATTTTATTTTAA AAATATCCTGTGTAACACTTGGCTCTTGGTACCTGTGGGTTAGCATCAAGTTCTCCCCAGGGTAGAATTC AATCAGAGCTCCAGTTTGCATTTGGATGTGTAAATTACAGTAATCCCATTTCCCAAACCTAAAATCTGTT TTTTCTCATCAGACTCTGAGTAACCTGGTTGCTGTGTATAACTTCATAGATGCAAGGAGGCTCAGGTGATCT GTTTGAGCAGAGCACCCTAGGCAGCCTGCAGGGAATAACATACTGGCCGTTTCTGACCTGTTGCCAGCAGA TACAGAGCATGGATGAAATCCCGTTTCCCTCTAGTTTCTTCTCTGAGTACTCTCTTTTAGATCCTAA GTCTCTTACAAAAGCTTTGAATACTGTGAAATGTTTTTACATTCCATTTTCAATTTGTGTTGTTTTTAAAC TGCATTTTACCAGATGTTTTGATGTTATCGCTTATGTTAATAGTAATCCCGTACGTGTTCAATTTATTT TCATGCTTTTTTTCAGCCATGTATCAATATTCATTGACTAAAATCACTCAATTAATCAAAAAAATAAAAAA AA	
NM_012319	AGTCTGGGCGAAGGGGGCGGTGGTTCCCCGCGCGCTGCGCGCGCGGTAATTAGTGATTGTCTTCCAG CTTCGCGAAGGCTAGGGGCGCGGCTGCCGGGTGGCTGCGCGCGCTGCCCGGACCGAGGGGCAGCCAA CCCAATGAAACCACCGCGTGTTCGCGCCTGGTAGAGATTTCTCGAAGACACCAGTGGGCCCGTTCGAGC CCTCTGGACCGCCCGTGTGGAACCAACCTGCGCGCGTGGCCGGGCGTGGGACAAACGAGGCCGCGGAGA CGAAGGCGCAATGGCGAGGAAGTTATCTGTAATCTTGATCCTGACCTTTGCCCTCTCTGTCACAATCC CTTCATGAACATAAAAGCAGCTTTCCTCCAGACCCTGAGAAAATTAGTCCGAATTGGGAATCTGGCA TTAATGTTGACTTGGCAATTTCCACACGGCAATATCATCTACAACAGCTTTTCTACCGCTATGGAGAAAA TAATTTCTTGTGAGTTGAAGGGTTCAGAAAATTACTTCAAAATATAGGCATAGATAAGATTAAAGAATC CATATACACCATGACCACGACCATCACTCAGACCACGAGCATCACTCAGACCATGAGCGTCACTCAGACC ATGAGCATCACTCAGACCACGAGCATCACTCTGACCATGATCATCACTCTCACCATAATCATGTCTGCTTC TGGTAAAAAATAAGCGAAAAGCTCTTTGCCAGACCATGACTCAGATAGTTTCAAGTAAAGATCCTAGAAAAC AGCCAGGGGAAAGGAGCTCACCGACCAGAACATGCCAGTGGTAGAAGGAATGTCAAGGACAGTGTAGTG CTAGTGAAGTGACCTCAACTGTGTACAACACTGTCTCTGAAGGAACCTCACTTTCTAGAGACAATAGAGAC TCCAAGACCTGGAAGAACTCTTCCCAAAGATGTAAGCAGCTCCACTCCACCCAGTGTCAATCAAGAGC CGGGTGAGCCGGCTGGCTGGTAGGAAAACAAATGAATCTGTGAGTGAGCCCCGAAAAGGCTTTATGTATT CCAGAAACACAAATGAAAATCCTCAGGAGTGTTCATGTCATCAAGCTACTGACATCTCATGGCATGGG CATCCAGGTTCCGCTGAATGCAACAGAGTTCAACTATCTCTGTCCAGCCATCATCAACCAAAATTGATGCT AGATCTTGTCTGATTTCATACAAGTAAAAGAGGCTGAAATCCCTCCAAAGACCTATTTCATTACAAATAG CCTGGGTTGGTGGTTTTATAGCCATTTCCATCATCAGTTTCTGTCTGTCTGTTGGGGTTATCTTAGTGCC TCTCATGAATCGGGTGTTTTTCAAAATTTCTCTGAGTTTCTTGTGGCACCTGGCCGTTGGGACTTTGAGT GGTGATGCTTTTTTACACCTTCTTCCACATTTCTCATGCAAGTCAACACCATAGTCAAGCATGAGAAC CAGCAATGGAATGAAAAGAGGACCACTTTTCAGTCACTGTCTTCTCAAAACATAGAAGAAAGTGCCCTA TTTTGATTCCAGTGGAAGGGTCTAACAGCTCTAGGAGGCTGTATTTTCAATGTTTCTTGTGAACATGTC CTCACATTGATCAACAAATTTAAAGATAAGAGAAAAAGAAATCAGAAGAAACCTGAAAATGATGATGATG TGGAGATTAAAGAGCAGTTGTCCAAGTATGAATCTCAACTTTCAACAAATGAGGAGAAAGTAGATACAGA TGATCGAACTGAAGGCTATTTACGAGCAGACTCAACAGAGCCCTCCCACTTTGATTTCTCAGCAGCCTGCA GTCTTGAAGAAGAAGAGGTGATGATGCTCATGCTCATCCACAGGAAGTCTACAATGAATATGTACCCA	136

	GAGGGTGCAAGAATAAATGCCATTACACATTTCCACGATACACTCGGCCAGTCAGACGATCTCATTACCCA CCATCATGACTACCATCATATTTCTCCATCATACCACCACCAAAACCAATCCTCAGAGTCACAGCCAG CGCTACTCTCGGGAGGAGCTGAAAGATGCGGGCGTCCGCACTCTGGCCTGGATGGTGATAAATGGGTGATG GCCTGCACAATTTAGCGATGGCCTAGCAATTTGGTGTCTCTTTTACTGAAGGCTTATCAAGTGGTTTAAAG TACTTCTGTTGCTGTGTTCTGTCTATGAGTTGGCTCATGAATTAGGTGACTTTTGTCTTACTTAAAGGCT GGCATGACCGTTAAGCAGGCTGTCTTTTATAATGCATTGTGAGCCATGCTGGCGTATCTTGGAAATGGCAA CAGGAATTTTTCATTGGTCATTATGCTGAAAATGTTTCTATGTGGATATTTGCACTTACTGCTGGCTTATT CATGTATGTTTGTCTCTGGTTGATATGGTACCTGAAATGCTGCACAATGATGCTAGTGACCATGGATGTAGC CGCTGGGGGTATTTCTTTTACAGAATGCTGGGATGCTTTTGGGTTTTGGAATTATGTTACTTATTTCCA TATTTGAACATAAAATCGTGTTCGTATAAAATTTCTAGTTAAGGTTTAAATGCTAGAGTAGCTTAAAAAG TTGTCATAGTTTCAGTAGGTATAGGGAGATGAGTTTGATGCTGTACTATGCAGCGTTTAAAGTTAGTG GGTTTTGTGATTTTTGTATTGAATATTGCTGTCTGTTACAAAGTCAGTTAAAGGTACGTTTTAATATTTA AGTTATTTCTATCTTGGAGATAAAATCTGTATGTGCAATTCACCGGTATTACCAAGTTTATATGTAAACAA GAGATTTGGCATGACATGTTCTGTATGTTTCAGGGAAAAATGCTTTAATGCTTTTCAAGAACTAACAC AGTTATTCCTATACCTGGATTTTAGGTCTCTGAGAACTGCTGGTGTAGGAAATAAGAAATGTGCATGAAG CCTAAAAATACCAAGAAAGCTTATACTGAATTTAAGCAAGAAATAAAGGAGAAAAAGAGAAGAACTGAGA ATTGGGGAGGCATAGATTTCTTATAAAAAATCACAAAATTTGTTGTAATTTAGAGGGGAGAAATTTAGAAAT AAGTATAAAAAAGGCAGAAATAGTATAGAGTACATTTAATTAACATTTTGTGAGGATTTATTTCCCGTAAA AACGTAGTGAGCACTTTTATATACTAATTTAGTTGTACATTTAATTTGTATAATACAGAAATCTAAAT ATATTTAATGAATTTCAAGCAATATATCACTTGACCAAGAAATTTGAATTTCAAAATGTTGCTGCGGGTAT ATACCAGATGAGTACAGTGAGTAGTTTATGTATCACCAGACTGGGTATTGCCAAGTTATATATCACCA AAAGCTGTATGACTGGATGTTCTGTTTACCTGGTTTACAAAATTTACAGAGTAGTAAACTTTGATATAT ATGAGGATATTTAAACTACACTAAGTATCATTTGATTGATTGAGAAAGTACTTTGATATCTCTCAGTGC TTCAGTGCTATCATTTGTGAGCAATTTGCTTTTATATACGGTACTGTAGCCATACTAGGCTGTCTGTGGC ATTTCTTAGATGTTTCTTTTACACAATAAATTCCTTATATCAGCTTGAAAAAATAAAAAAAAAA	
AK098106	AACGCACTTGGCGCGCGCGCGGGCTGCAGACGGCTGCGAGGCGCTGGGCACAGGTGTCTGTATGGCAAA TTTCAAGGGCCACGCGCTTCCAGGAGTTTCTTCTGATCATTTGGGCTGTGTTGGTCAGTGAAGTACCCG CTGAAGTACTTTAGCCACACGCGGAGAACAGCCCACTACATTACTATCAGGCTCTCGAGTCTGTGAAG CCGCAATTAGGACTTTGTTTTCCGTCAGTGGATCCTGGCAGAGCAGTTTGTTCGGATGGGCCCCACCT GCACCTCTACCATGAGAACCACTGGATAAAGTTAATGAATTGGCAGCACAGACCATGTACCTATCTTT GCAGTCTCAGGAATTGTTGACATGCTCACCTATCTGGTCAGCCACGTTCCCTTGGGGTGGACAGACTGG TTATGGCTGTGGCAGTATTCATGGAAGGTTTCTCTTCTACTACCACGTCACAAACCGCCCTCCGCTGGA CCAGCATCTCACTCACTCTGTATGCTGTGTTCCGAGGGTGTGTTAGTATCTCCCTAGAGTGATC TTCCGGGACCACATTGTGCTGGAATTTTCCGAACCACTCTCATCATTTCTTCCAGGGAACCTGTTTCTGGC AGATTGGGTTTTGTGCTGTTCACCTTTTGGAAACACCCGAATGGGACCAGAAAGGATGATGCCAACCTCAT GTTTCATCACCATGTGCTTCTGCTGGCACTACCTGGCTGCCCTCAGCATTGTGGCCGTCAACTATTTCTCT GTTTACTGCCTTTTGACTCGGATGAAGAGACCGGAAGGGGAGAAATCATTGGAATTTCAAGAACTGAAT CAGATGACACTTACCAGACCGCCCTCTTGGTGGCTCAGATGAGGAATGAGCCGAGATGCGGAGGGCGCA GATGTCCTCAGTGCACAGCTGGAATGAATGGAGTTTATCCCTCCACCTGAATGCCTGTGTGGTCTGATC TTAAGGGTCTATATATTTGCACCTCTCATTTCAACACAGGGCTGGAGGTTCTACAACAGGAAATCAGGCC TACAGCATCTGTGTATCTTGCAGTTGGGATTTTTAAACATACTATAAAGTCTGTGTTGGTATAGTACCC TTCATAAGGAAAAATGAAGTAATGGCTATAAGTAGCAGGCTTTTGTGCTCAGTGTCAGAGAAATCAAG AGATGCTAAAAGCTTTACAATGGAAGTGGCTCATGGATGAATCCGGGGTATGAGCCAGGAGAACGTCG TGCTTTTGGTAACTTATCCCTTTTTCTTTAAGAAAGCAGGTACTTTCTTATTAGAAATATGTTAGAATG TGTAAGCAACGACAGTGCTTTTGAATTAACAATTTCACTTACATATTTTTTGAAAGTAAATATTTCA CAAGCTTTGGTATTTTAAATATTGTTAAACATATCATAACTAATCATACAGGGTACTGCAATACCAC TGTTTATAAGTGACAAAATTAGGCCAAAGGTGATTTTTTTTTTAAATCAGGAAGCTGTTTACTGGCTTAC TGAGAGTTGGAGCCCTGATGTTCTGATTCTTCAAAGTACCCCTAAAAGAAGATCTGACAGGAAAGCTGTA TAATGAGATAGAAAACGTCAGGTATGGAAGGCTTTTCAAGTTTAAATATGGCTGAAAGCAAAGGATAACGA ATTGAGAAATAGTAAATGTAATCTTTGATACCTAATCTTGCTTCTGGATCTGTCTTTTTTAAAAAAA CTTCTTACCGCGCCTATAATCTTAGCACTTTGGGAGGCGGAGGCAGGCAGATCACGGGGTCAGGAGAT CAAGACCATCTGGCTAACATGGTGAAACCCGCTCTCTACTGAAAATACAAAAAATTAGCCGGGTGTGGT GGCGGGCGCCTGTAGTTCCAGCTACTCGGGAGGCTGAGGCAAGAGAATGGCATGAACCCGGTAGGGGAGC TTGCAGTGAGCCAGATCATGCCACTGTACTCCAGCCTAGGTGACAGAGCAAGACTCTGTCTCAAAAACA AGCAAAACAGACTTCTTCAACAAATATTTATTAATATCCACTTTGCAACAGCACTGAAATGGCTGTAAG GACTCTGAGATATGTGTCAGCAAGGAGTTTACAGTCAAAACAGGAGAGACATGCCTGTAGTTACATCCA GTGTGATGGGTGTGAGAGGCAAGTACAAACCCAGATG	137
BQ056428	TCCCGCGCGCCACTTCGCTGCTCCGCTCCCGCGCCGCGCGCCATGCCTGTGGCCGCTCGGAGCTG CCGCGCGCGCCCTTGCCCCCGCGCGACAGGAGCGGGACGCCGAGCCGCTCGCGCGCACGGGGAGCTGC AGTACCTGGGGCAGATCCAACACATCTCTCCGCTGCGGCGTCAGGAAGGACGCCCGCCGGGCACCGGTAC CCTGCCGCTATTCGGCATGACGGCGGCTACAGCCTGAGAGATGAATTTCCCTCTGCTGACAAACCAACGT GTGTTCTGGAACGGTGCTTCGGAGGAGCTGCTGTGGCTTATCAAGGGATCCAAACGCTATAGACCTGT CTTCCCCGGCAGCGAAAAATCTCGGGATGCCACTGGATCCCGACACTCTCTGGACACCTGGGATTCTCCA CCAGAGAAGAACGCGACTTGGGCCAGTTTGTGGCTCTCAGCGGAGGCTCTCTGTGGCAGAAATACATACA TTTTCAATCAGATCACTTCCCGGACACGGACCTGACAGCCTGCCAAAAAGTGGATTTCCTCCCCACCCC AGAACCCANCCCCTGACGCACAGAAACCAACCATTCGTTGTTGCCGCTTGCAGACCCCAACAGAAATC TCTCCCCCTTGGCGGCGCGCTGCGCTGCCAATGCCCTATGGCGGCTCTTGGCGGCTTCCCA TTGGTGCCTGCGCAACCAGCGAGAAAACACTGGCCCGCCGCTCTCCCCCGCTCCGCTACCCCACT	138

	TAATGCGCCTCCGTGGCATGACGCACGCGTTTGGTGTCCGCCGCCGTCTCATGTCCGCCGCGGTGTGGACC CCCITTTCTCTCGCGGCACATCCCCCTATTCCTTTGCCCTTTGGGGGGCACCCCTCTAGACCCGCGCT TCTCTTCTCGTCCGGTGGGGACATTGGTTTGGCTGCCGCGCGGGGGCGNTAAAAATAAAAAACAGCCTG TTAGCCCGGCCAGTACCCCCCGCGCGGGGCGCCTTNCGTTTGCAATTTATACCCCAACCCATAAAG CCGCGCCCCCTTAGCNCCNTAACTTTTGTGGTGTGGCCTCCCCCTTTTCCCGGGGAGCAGCAACGGAC ATCTGTACACTAATGCTGGCCCCGACCTTTCCCAAAAAACCCCCGCCCGTGTCCCGTATAAAATTTGGTGC CAANCTGACNGTTCTCCCCCGCCTCGCCCCGTTGGCCGCCGTTTAAAGCCCCCGGTGGTTGGCG CGCCCAACGAGTCCACCTATAGTTAANTCCACCAACACCCCCACCTTTTCCCTCCCGCCGCATCTTCCCC ACGTACCCCCCTTTGTGCGGAGATGGCCACTCCCCCCCCCTGTTTGTAAAAACAACGAGAATGGTGTCT GCCAACGCTGGTCTTTTCCCCCCCCGACCGCGACCGCCAGGGGGAATACGTACCATAAGCCCCCGCGCC CNCCITTTTCCCCCCTCCCCGCCAATCAAGATCCGCGTCCATTAGACGTATTATTTTCCCGCGATAC ACGAAAAACAGGGCCGCCATTTATACTAAATTCCTGTCGCCGCCGCGCGGATATGTTTCCCAAAATA CCACCCCCCCCCCATTTTCTTTGCCCCCAACTCCTGCGCACCGGTGTTTACCAGCCTCGCGCCGC	
BC032677	GGACGCGTGGGTGACCCACGCGTCCGGACCCACGCGTCCGGTCTGTCTCTCGAGTTCTGTCTCTCTG CCAACGCCCGCGGATGGCTTCCCAAAAACCGGACCCAGCCGCCACTAGCGTCCGCCGCCCGTAAAGG AGCTGAGCCGAGCGGGGGCGCCGCCGGGTCCGGTGGGCAAAAGGCTACAGCAGGAGCTGATGACCCCTC ATGGTGAGTGATTAAGTGGCCAGAACCCAGCCTTCCATCCAATTTTTCAGTAGCCTCCTTTTTCCGTCA GCTTTTTTGTCTAGACATAGGGGTAATGTAATTTGCTCCCTCCTGGGAAAGAAGTTTATACACCCACCTA CACCATTTCTTCCAGCAGTCCCTCCTCCCAATTCATCCCCCACACGAAGTTATCTCGAACACTTCCCT GAAGTCATACAGACCCTCCCTATCCAGTGTGTCCCTACTTCTAGCCCCAACCAAGCTTTACCCACACC CAACTCCCCGCCCTTCTTGGTATTTCTAGCCTATGAATTTGGTTGCTTTATTTTGGATCAGAGTGATGAG ATTAAGGGGAGGCTGGGCGCGGTAGCTCACACCTTATAATCCCAAAGTGCTGGGATTACAGGCGTGAGCC ACCGCGCCCCGCCAGCACTAATATTCTAATTGAACATAAGCACAGGATGCCAATTTACAATCCTTAGAC CAAAGAGTCACTGATGTCTCCACCAGATAAGAGGAAAGCATCAGGCTAGGCATAGTGGCTCACACCTGTA ATCTCAGCACTTTGGGAGGCTGAGGCAGGCAGATCACATGAGCCAGGAGTTTGGAGCTGGCCTGGGCAA CATGGTGAAACCCGTCTCTATAAATAAAAACTAACTAAAAAACTTTTTAAAAAGGCAGTGGGGAGCAT CAGAACCACTCAACAGTTTGTCTACTGTCCGGTCCAGAGAACTCAAGATTCTAGCAAGCCCCCTTGTG TGGGGCTTGGGTTGGGACATGAGGCTGCTGCTGGAGCTTACTCTGCAACTGTTTCTCAAATGCCAGGTA TATGAAGACCTGAGGTATAAGCTCTCGCTAGAGTTCCCCAGTGGCTACCCTTACAATGCGCCACAGTGA AGTTCTCACGCCCTGTCTATCACCCCAACGTGGACACCCAGGGTAACATATGCCTGGACATCCTGAAGGA AAAGTGGTCTGCCCTGTATGATGTCTAGGACCATTCTGTCTCTCATCCAGAGCCTTCTAGGAGAACCCAAAC ATTGATAGTCCCTTGAACACACATGTCTGCCGAGCTCTGAAAAACCCACAGCTTTTAAAGTAGCTGC AAGAAACCTACTCAAAGCAGGTACCCAGCCAGGAGCCCTGACCCAGGCTGCCAGCCTGTCTTTGTGTCG TCTTTTTAATTTTCTTAGATGGTCTGTCTTTTTTGTGATTTCTGTATAGGACTCTTTATCTTGAGCTG TGGTATTTTTGTTTTGTTTTGTCTTTTAAATTAAGCCTCGGTTGAGCCCTTGATATATAAATAAATGCA TTTTGTCTTTTTTAAAAAAAATAA A	139

[32] At least 40, at least 41, at least 42, at least 43, at least 44, at least 46 or all 46 of the genes in Table 1 can be utilized in the methods of the present invention. Preferably, the expression of each of the 46 genes is determined in a biological sample. The prototypical gene expression profiles (*i.e.* centroid) of the four intrinsic subtypes were pre-defined from a training set of FFPE breast tumor samples using hierarchical clustering analysis of gene expression data. A heatmap of the prototypical gene expression profiles (*i.e.* centroids) of these four subtypes is shown in Figure 1, where the level of expression is illustrated by the heatmap. **Table 3** shows the actual values.

[33] **Table 3.**

Tumor Subtype Centroids for Comparison to a Sample				
Target Gene	Basal-like	Her2-enriched	Luminal A	Luminal B
ACTR3B	-0.2052	-0.7965	-0.2790	-0.4380
ANLN	1.0227	0.5006	-0.7289	0.1149
BAG1	-0.4676	-0.3132	0.4716	0.5879
BCL2	-0.7365	-0.7237	0.7234	0.6363
BLVRA	-0.8761	0.2270	0.1628	0.7138

CCNE1	1.3100	0.2201	-0.6231	-0.2729
CDC20	1.0995	0.1445	-1.0518	-0.1173
CDC6	0.5817	0.6601	-0.7032	0.3134
CDCA1	0.9367	0.1623	-0.4509	0.2692
CDH3	0.7639	0.0144	-0.0502	-1.0229
CENPF	1.0222	0.2944	-0.5657	0.2437
CEP55	1.0442	0.4881	-0.6365	0.2921
CXXC5	-0.9732	0.1866	0.5687	0.9463
EGFR	0.3352	-0.1326	-0.0011	-0.9755
ERBB2	-0.7045	1.4182	0.2420	0.1978
ESR1	-1.1847	-0.4926	0.7177	1.0101
EXO1	1.0546	0.4317	-0.7259	0.2559
FGFR4	-0.2073	1.4562	0.1707	-0.2223
FOXA1	-1.3590	0.5726	0.7131	0.7963
FOXC1	1.0666	-0.7362	-0.4078	-0.9877
GPR160	-1.0540	0.5524	0.6032	0.7305
KIF2C	0.9242	0.1104	-1.1001	-0.2771
KNTC2	1.1373	0.2266	-0.7593	0.1656
KRT14	0.4759	-0.5269	0.8187	-0.8879
KRT17	0.6863	-0.3777	0.6149	-1.1415
KRT5	0.7136	-0.4146	0.5832	-0.9462
MAPT	-1.1343	-0.2711	1.0957	0.8372
MDM2	-0.7498	-0.4855	-0.1788	0.2397
MELK	1.0209	0.2678	-0.8016	0.1012
MIA	1.2408	-0.5475	0.3289	-0.6320
MKI67	1.0446	0.4630	-0.6717	0.3161
MLPH	-1.4150	0.4842	0.8829	0.8194
MMP11	-0.1295	0.5220	0.3402	0.5653
MYC	0.5639	-0.9904	-0.3015	-0.2791
NAT1	-0.9711	-0.2708	1.2256	0.9576
ORC6L	1.0086	0.5152	-1.0385	-0.0336
PGR	-0.9216	-0.5755	1.2061	0.9278
PHGDH	0.9192	0.0322	-0.5194	-0.5371
PTTG1	0.9541	0.2079	-1.1207	0.1052
RRM2	0.7895	0.6336	-0.8099	0.3228
SFRP1	0.7694	-0.8271	0.2617	-1.0846
SLC39A6	-0.9992	-0.4573	0.6607	0.9222
TMEM45B	-1.0721	0.7926	0.3190	0.2016
TYMS	0.9823	-0.0960	-0.8593	0.1827
UBE2C	0.8294	0.3358	-1.0141	0.0608
UBE2T	0.6258	0.0617	-0.8652	-0.0487

[34] After performing the Breast Cancer Intrinsic Subtyping test with a test breast cancer tumor sample and the reference sample provided as part of the test kit, a computational algorithm based on a Pearson's correlation compares the normalized and scaled gene expression profile of the NANO46 intrinsic gene set of the test sample to the prototypical expression signatures of the four breast cancer intrinsic subtypes. The intrinsic subtype

analysis is determined by determining the expression of a NANO50 set of genes (which is determining the expression of the NANO46 set of genes and further includes determining the expression of MYBL2, BIRC5, GRB7 and CCNB1) and the risk of recurrence (“ROR”) is determined using the NANO46 set of genes). Specifically, the intrinsic subtype is identified by comparing the expression of the NANO50 set of genes in the biological sample with the expected expression profiles for the four intrinsic subtypes. The subtype with the most similar expression profile is assigned to the biological sample. The ROR score is an integer value on a 0-100 scale that is related to an individual patient’s probability of distant recurrence within 10 years for the defined intended use population. The ROR score is calculated by comparing the expression profiles of the NANO46 genes in the biological sample with the expected profiles for the four intrinsic subtypes, as described above, to calculate four different correlation values. These correlation values are then combined with a proliferation score (and optionally one or more clinicopathological variables, such as tumor size) to calculate the ROR score. Preferably, the ROR score is calculated by comparing only the expression profiles of the NANO46 genes.

[35] **Figure 6** provides a schematic of the specific algorithm transformations. The tumor sample is assigned the subtype with the largest positive correlation to the sample. Kaplan Meier survival curves generated from a training set of untreated breast cancer patients demonstrate that the intrinsic subtypes are a prognostic indicator of recurrence free survival (RFS) in this test population, which includes both estrogen receptor positive/negative and HER2 positive/negative patients, **Figure 2**.

[36] Independent testing on a cohort of node negative, estrogen receptor positive patients treated with tamoxifen shows predominantly Luminal A and B subtype patients with Luminal A patients exhibiting better outcome than Luminal B patients, **Figure 3**. The outcome of Luminal A patients is expected to improve even further using clinical trial specimens that use more modern treatment regimens (*i.e.* aromatase inhibitors) and have better adherence to therapy which will improve outcome

[37] The training set of FFPE breast tumor samples, which had well defined clinical characteristics and clinical outcome data, were used to establish a continuous Risk of Recurrence (ROR) score. The score is calculated using coefficients from a Cox model that includes correlation to each intrinsic subtype, a proliferation score (mean gene expression of a subset of 18 of the 46 genes), and tumor size, **Table 4**.

Table 4. Coefficients to calculate ROR-PT (equation 1)	
Test Variables	Coefficient
Basal-like Pearson's correlation (A)	- 0.0067
Her2-enriched Pearson's correlation (B)	0.4317
Luminal A Pearson's correlation (C)	- 0.3172
Luminal B Pearson's correlation (D)	0.4894
Proliferation Score (E)	0.1981
Tumor Size (F)	0.1133

[38] The test variables in **Table 4** are multiplied by the corresponding coefficients and summed to produce a risk score ("ROR-PT").

[39] **ROR-PT equation** = $-0.0067*A + 0.4317*B + -0.3172*C + 0.4894*D + 0.1981*E + 0.1133*F$

[40] In previous studies, the ROR score provided a continuous estimate of the risk of recurrence for ER-positive, node-negative patients who were treated with tamoxifen for 5 years (Nielsen *et al.* Clin. Cancer Res., 16(21):5222-5232 (2009)). This result was verified on ER-positive, node-negative patients from the same cohort, **Figure 4**. The ROR score also exhibited a statistically significant improvement over a clinical model based in determining RFS within this test population providing further evidence of the improved accuracy of this decision making tool when compared to traditional clinicopathological measures (Nielsen *et al.* Clin. Cancer Res., 16(21):5222-5232 (2009)).

[41] The gene set contains many genes that are known markers for proliferation. The methods of the present invention provide for the determination of subsets of genes that provide a proliferation signature. The methods of the present invention can include determining the expression of at least one of, a combination of, or each of, a 18-gene subset of the NANO46 intrinsic genes selected from ANLN, CCNE1, CDC20, CDC6, CDCA1, CENPF, CEP55, EXO1, KIF2C, KNTC2, MELK, MKI67, ORC6L, PTTG1, RRM2, TYMS, UBE2C and/or UBE2T. Preferably, the expression of each of the 18-gene subset of the NANO46 gene set is determined to provide a proliferation score. The expression of one or more of these genes may be determined and a proliferation signature index can be generated by averaging the normalized expression estimates of one or more of these genes in a sample. The sample can be assigned a high proliferation signature, a moderate/intermediate proliferation signature, a low proliferation signature or an ultra-low proliferation signature. Methods of determining a proliferation signature from a biological sample are as described in Nielsen *et al.* Clin. Cancer Res., 16(21):5222-5232 (2009) and supplemental online material

(these documents are incorporated herein, by reference, in their entireties).

[42] *Description of Intrinsic Subtype Biology*

[43] Luminal subtypes: The most common subtypes of breast cancer are the luminal subtypes, Luminal A and Luminal B. Prior studies suggest that luminal A comprises approximately 30% to 40% and luminal B approximately 20% of all breast cancers, but they represent over 90 % of hormone receptor positive breast cancers (Nielsen *et al.* Clin. Cancer Res., 16(21):5222-5232 (2009)). The gene expression pattern of these subtypes resembles the luminal epithelial component of the breast. These tumors are characterized by high expression of estrogen receptor (ER), progesterone receptor (PR), and genes associated with ER activation, such as LIV1, GATA3, and cyclin D1, as well as expression of luminal cytokeratins 8 and 18 (Lisa Carey & Charles Perou (2009). Gene Arrays, Prognosis, and Therapeutic Interventions. Jay R. Harris et al. (4th ed.), Diseases of the breast (pp. 458-472). Philadelphia, PA: Lippincott Williams & Wilkins).

[44] Luminal A: Luminal A (LumA) breast cancers exhibit low expression of genes associated with cell cycle activation and the ERBB2 cluster resulting in a better prognosis than Luminal B. The Luminal A subgroup has the most favorable prognosis of all subtypes and is enriched for endocrine therapy-responsive tumors.

[45] Luminal B: Luminal B (LumB) breast cancers also express ER and ER-associated genes. Genes associated with cell cycle activation are highly expressed and this tumor type can be HER2(+) (~20%) or HER2(-). The prognosis is unfavorable (despite ER expression) and endocrine therapy responsiveness is generally diminished relative to LumA.

[46] HER2-enriched: The HER2-enriched subtype is generally ER-negative and is HER2-positive in the majority of cases with high expression of the ERBB2 cluster, including ERBB2 and GRB7. Genes associated with cell cycle activation are highly expressed and these tumors have a poor outcome.

[47] Basal-like: The Basal-like subtype is generally ER-negative, is almost always clinically HER2-negative and expresses a suite of “basal” biomarkers including the basal epithelial cytokeratins (CK) and epidermal growth factor receptor (EGFR). Genes associated with cell cycle activation are highly expressed.

[48] *Clinical variables*

[49] The NANO46 classification model described herein may be further combined with information on clinical variables to generate a continuous risk of recurrence (ROR) predictor. As described herein, a number of clinical and prognostic breast cancer factors are known in the art and are used to predict treatment outcome and the likelihood of disease recurrence.

Such factors include, for example, lymph node involvement, tumor size, histologic grade, estrogen and progesterone hormone receptor status, HER-2 levels, and tumor ploidy. In one embodiment, risk of recurrence (ROR) score is provided for a subject diagnosed with or suspected of having breast cancer. This score uses the NANO46 classification model in combination with clinical factors of lymph node status (N) and tumor size (T). Assessment of clinical variables is based on the American Joint Committee on Cancer (AJCC) standardized system for breast cancer staging. In this system, primary tumor size is categorized on a scale of 0-4 (T0: no evidence of primary tumor; T1 : < 2 cm; T2: > 2 cm - < 5 cm; T3 : > 5 cm; T4: tumor of any size with direct spread to chest wall or skin). Lymph node status is classified as N0-N3 (N0: regional lymph nodes are free of metastasis; N1 : metastasis to movable, same-side axillary lymph node(s); N2: metastasis to same-side lymph node(s) fixed to one another or to other structures; N3: metastasis to same-side lymph nodes beneath the breastbone). Methods of identifying breast cancer patients and staging the disease are well known and may include manual examination, biopsy, review of patient's and/or family history, and imaging techniques, such as mammography, magnetic resonance imaging (MRI), and positron emission tomography (PET).

[50] *Sample Source*

[51] In one embodiment of the present disclosure, breast cancer subtype is assessed through the evaluation of expression patterns, or profiles, of the intrinsic genes listed in Table 1 in one or more subject samples. For the purpose of discussion, the term subject, or subject sample, refers to an individual regardless of health and/or disease status. A subject can be a subject, a study participant, a control subject, a screening subject, or any other class of individual from whom a sample is obtained and assessed in the context of the disclosure. Accordingly, a subject can be diagnosed with breast cancer, can present with one or more symptoms of breast cancer, or a predisposing factor, such as a family (genetic) or medical history (medical) factor, for breast cancer, can be undergoing treatment or therapy for breast cancer, or the like. Alternatively, a subject can be healthy with respect to any of the aforementioned factors or criteria. It will be appreciated that the term "healthy" as used herein, is relative to breast cancer status, as the term "healthy" cannot be defined to correspond to any absolute evaluation or status. Thus, an individual defined as healthy with reference to any specified disease or disease criterion, can in fact be diagnosed with any other one or more diseases, or exhibit any other one or more disease criterion, including one or more cancers other than breast cancer. However, the healthy controls are preferably free of any cancer.

[52] In particular embodiments, the methods for predicting breast cancer intrinsic subtypes include collecting a biological sample comprising a cancer cell or tissue, such as a breast tissue sample or a primary breast tumor tissue sample. By "biological sample" is intended any sampling of cells, tissues, or bodily fluids in which expression of an intrinsic gene can be detected. Examples of such biological samples include, but are not limited to, biopsies and smears. Bodily fluids useful in the present disclosure include blood, lymph, urine, saliva, nipple aspirates, gynecological fluids, or any other bodily secretion or derivative thereof. Blood can include whole blood, plasma, serum, or any derivative of blood. In some embodiments, the biological sample includes breast cells, particularly breast tissue from a biopsy, such as a breast tumor tissue sample. Biological samples may be obtained from a subject by a variety of techniques including, for example, by scraping or swabbing an area, by using a needle to aspirate cells or bodily fluids, or by removing a tissue sample (*i.e.*, biopsy). Methods for collecting various biological samples are well known in the art. In some embodiments, a breast tissue sample is obtained by, for example, fine needle aspiration biopsy, core needle biopsy, or excisional biopsy. Fixative and staining solutions may be applied to the cells or tissues for preserving the specimen and for facilitating examination. Biological samples, particularly breast tissue samples, may be transferred to a glass slide for viewing under magnification. In one embodiment, the biological sample is a formalin-fixed, paraffin-embedded breast tissue sample, particularly a primary breast tumor sample. In various embodiments, the tissue sample is obtained from a pathologist-guided tissue core sample.

[53] *Expression Profiling*

[54] In various embodiments, the present disclosure provides methods for classifying, prognosticating, or monitoring breast cancer in subjects. In this embodiment, data obtained from analysis of intrinsic gene expression is evaluated using one or more pattern recognition algorithms. Such analysis methods may be used to form a predictive model, which can be used to classify test data. For example, one convenient and particularly effective method of classification employs multivariate statistical analysis modeling, first to form a model (a "predictive mathematical model") using data ("modeling data") from samples of known subtype (*e.g.*, from subjects known to have a particular breast cancer intrinsic subtype: LumA, LumB, Basal-like, HER2-enriched, or normal-like), and second to classify an unknown sample (*e.g.*, "test sample") according to subtype. Pattern recognition methods have been used widely to characterize many different types of problems ranging, for example, over linguistics, fingerprinting, chemistry and psychology. In the context of the

methods described herein, pattern recognition is the use of multivariate statistics, both parametric and non-parametric, to analyze data, and hence to classify samples and to predict the value of some dependent variable based on a range of observed measurements. There are two main approaches. One set of methods is termed "unsupervised" and these simply reduce data complexity in a rational way and also produce display plots which can be interpreted by the human eye. However, this type of approach may not be suitable for developing a clinical assay that can be used to classify samples derived from subjects independent of the initial sample population used to train the prediction algorithm.

[55] The other approach is termed "supervised" whereby a training set of samples with known class or outcome is used to produce a mathematical model which is then evaluated with independent validation data sets. Here, a "training set" of intrinsic gene expression data is used to construct a statistical model that predicts correctly the "subtype" of each sample. This training set is then tested with independent data (referred to as a test or validation set) to determine the robustness of the computer-based model. These models are sometimes termed "expert systems," but may be based on a range of different mathematical procedures.

Supervised methods can use a data set with reduced dimensionality (for example, the first few principal components), but typically use unreduced data, with all dimensionality. In all cases the methods allow the quantitative description of the multivariate boundaries that characterize and separate each subtype in terms of its intrinsic gene expression profile. It is also possible to obtain confidence limits on any predictions, for example, a level of probability to be placed on the goodness of fit. The robustness of the predictive models can also be checked using cross-validation, by leaving out selected samples from the analysis.

[56] The NANO46 classification model described herein is based on the gene expression profile for a plurality of subject samples using the intrinsic genes listed in Table 1. The plurality of samples includes a sufficient number of samples derived from subjects belonging to each subtype class. By "sufficient samples" or "representative number" in this context is intended a quantity of samples derived from each subtype that is sufficient for building a classification model that can reliably distinguish each subtype from all others in the group. A supervised prediction algorithm is developed based on the profiles of objectively-selected prototype samples for "training" the algorithm. The samples are selected and subtyped using an expanded intrinsic gene set according to the methods disclosed in International Patent Publication WO 2007/061876 and US Patent Publication No. 2009/0299640, which is herein incorporated by reference in its entirety. Alternatively, the samples can be subtyped according to any known assay for classifying breast cancer subtypes. After stratifying the

training samples according to subtype, a centroid-based prediction algorithm is used to construct centroids based on the expression profile of the intrinsic gene set described in Table 1.

[57] In one embodiment, the prediction algorithm is the nearest centroid methodology related to that described in Narashiman and Chu (2002) PNAS 99:6567-6572, which is herein incorporated by reference in its entirety. In the present disclosure, the method computes a standardized centroid for each subtype. This centroid is the average gene expression for each gene in each subtype (or "class") divided by the within-class standard deviation for that gene. Nearest centroid classification takes the gene expression profile of a new sample, and compares it to each of these class centroids. Subtype prediction is done by calculating the Spearman's rank correlation of each test case to the five centroids, and assigning a sample to a subtype based on the nearest centroid.

[58] *Detection of intrinsic gene expression*

[59] Any methods available in the art for detecting expression of the intrinsic genes listed in Table 1 are encompassed herein. By "detecting expression" is intended determining the quantity or presence of an RNA transcript or its expression product of an intrinsic gene. Methods for detecting expression of the intrinsic genes of the disclosure, that is, gene expression profiling, include methods based on hybridization analysis of polynucleotides, methods based on sequencing of polynucleotides, immunohistochemistry methods, and proteomics-based methods. The methods generally detect expression products (*e.g.*, mRNA) of the intrinsic genes listed in Table 1. In preferred embodiments, PCR-based methods, such as reverse transcription PCR (RT-PCR) (Weis *et al.*, TIG 8:263- 64, 1992), and array-based methods such as microarray (Schena *et al.*, Science 270:467- 70, 1995) are used. By "microarray" is intended an ordered arrangement of hybridizable array elements, such as, for example, polynucleotide probes, on a substrate. The term "probe" refers to any molecule that is capable of selectively binding to a specifically intended target biomolecule, for example, a nucleotide transcript or a protein encoded by or corresponding to an intrinsic gene. Probes can be synthesized by one of skill in the art, or derived from appropriate biological preparations. Probes may be specifically designed to be labeled. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

[60] Many expression detection methods use isolated RNA. The starting material is typically total RNA isolated from a biological sample, such as a tumor or tumor cell line, and corresponding normal tissue or cell line, respectively. If the source of RNA is a primary

tumor, RNA (*e.g.*, mRNA) can be extracted, for example, from frozen or archived paraffin-embedded and fixed (*e.g.*, formalin-fixed) tissue samples (*e.g.*, pathologist-guided tissue core samples).

[61] General methods for RNA extraction are well known in the art and are disclosed in standard textbooks of molecular biology, including Ausubel *et al.*, ed., Current Protocols in Molecular Biology, John Wiley & Sons, New York 1987-1999. Methods for RNA extraction from paraffin embedded tissues are disclosed, for example, in Rupp and Locker, Lab Invest. 56:A67, (1987); and De Andres *et al.* Biotechniques 18:42-44, (1995). In particular, RNA isolation can be performed using a purification kit, a buffer set and protease from commercial manufacturers, such as Qiagen (Valencia, CA), according to the manufacturer's instructions. For example, total RNA from cells in culture can be isolated using Qiagen RNeasy mini-columns. Other commercially available RNA isolation kits include MASTERPURE™ Complete DNA and RNA Purification Kit (Epicentre, Madison, Wis.) and Paraffin Block RNA Isolation Kit (Ambion, Austin, TX). Total RNA from tissue samples can be isolated, for example, using RNA Stat-60 (Tel-Test, Friendswood, TX). Total RNA from FFPE can be isolated, for example, using High Pure FFPE RNA Microkit, Cat No. 04823125001 (Roche Applied Science, Indianapolis, IN). RNA prepared from a tumor can be isolated, for example, by cesium chloride density gradient centrifugation. Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (U.S. Pat. No. 4,843,155).

[62] Isolated RNA can be used in hybridization or amplification assays that include, but are not limited to, PCR analyses and probe arrays. One method for the detection of RNA levels involves contacting the isolated RNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 60, 100, 250, or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to an intrinsic gene of the present disclosure, or any derivative DNA or RNA. Hybridization of an mRNA with the probe indicates that the intrinsic gene in question is being expressed.

[63] In one embodiment, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probes are immobilized on a solid surface and the mRNA is contacted with the probes, for

example, in an Agilent gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of expression of the intrinsic genes of the present disclosure.

[64] An alternative method for determining the level of intrinsic gene expression product in a sample involves the process of nucleic acid amplification, for example, by RT-PCR (U.S. Pat. No. 4,683,202), ligase chain reaction (Barany, PNAS USA 88: 189-93, (1991)), self sustained sequence replication (Guatelli *et al.*, Proc. Natl. Acad. Sci USA 87: 1874-78, (1990)), transcriptional amplification system (Kwoh *et al.*, Proc. Natl. Acad. Sci USA 86: 1173-77, (1989)), Q-Beta Replicase (Lizardi *et al.*, Bio/Technology 6:1197, (1988)), rolling circle replication (U.S. Pat. No. 5,854,033), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

[65] In particular aspects of the disclosure, intrinsic gene expression is assessed by quantitative RT-PCR. Numerous different PCR or QPCR protocols are known in the art and exemplified herein below and can be directly applied or adapted for use using the presently-described compositions for the detection and/or quantification of the intrinsic genes listed in Table 1. Generally, in PCR, a target polynucleotide sequence is amplified by reaction with at least one oligonucleotide primer or pair of oligonucleotide primers. The primer(s) hybridize to a complementary region of the target nucleic acid and a DNA polymerase extends the primer(s) to amplify the target sequence. Under conditions sufficient to provide polymerase-based nucleic acid amplification products, a nucleic acid fragment of one size dominates the reaction products (the target polynucleotide sequence which is the amplification product). The amplification cycle is repeated to increase the concentration of the single target polynucleotide sequence. The reaction can be performed in any thermocycler commonly used for PCR. However, preferred are cyclers with real time fluorescence measurement capabilities, for example, SMARTCYCLER® (Cepheid, Sunnyvale, CA), ABI PRISM 7700® (Applied Biosystems, Foster City, Calif.), ROTOR- GENE™ (Corbett Research, Sydney, Australia), LIGHTCYCLER® (Roche Diagnostics Corp, Indianapolis, Ind.), ICYCLER® (Biorad Laboratories, Hercules, Calif.) and MX4000® (Stratagene, La Jolla, Calif.).

[66] In another embodiment of the disclosure, microarrays are used for expression profiling. Microarrays are particularly well suited for this purpose because of the reproducibility between different experiments. DNA microarrays provide one method for the

simultaneous measurement of the expression levels of large numbers of genes. Each array consists of a reproducible pattern of capture probes attached to a solid support. Labeled RNA or DNA is hybridized to complementary probes on the array and then detected by laser scanning. Hybridization intensities for each probe on the array are determined and converted to a quantitative value representing relative gene expression levels. See, for example, U.S. Pat. Nos. 6,040,138, 5,800,992 and 6,020,135, 6,033,860, and 6,344,316. High-density oligonucleotide arrays are particularly useful for determining the gene expression profile for a large number of RNAs in a sample.

[67] In a preferred embodiment, the nCounter® Analysis system is used to detect intrinsic gene expression. The basis of the nCounter® Analysis system is the unique code assigned to each nucleic acid target to be assayed (International Patent Application Publication No. WO 08/124847, US Patent No. 8,415,102 and Geiss *et al.* Nature Biotechnology. 2008. 26(3): 317-325; the contents of which are each incorporated herein by reference in their entireties). The code is composed of an ordered series of colored fluorescent spots which create a unique barcode for each target to be assayed. A pair of probes is designed for each DNA or RNA target, a biotinylated capture probe and a reporter probe carrying the fluorescent barcode. This system is also referred to, herein, as the nanoreporter code system.

[68] Specific reporter and capture probes are synthesized for each target. Briefly, sequence-specific DNA oligonucleotide probes are attached to code-specific reporter molecules. Preferably, each sequence specific reporter probe comprises a target specific sequence capable of hybridizing to no more than one NANO46 gene of Table 1 and optionally comprises at least two, at least three, or at least four label attachment regions, said attachment regions comprising one or more label monomers that emit light. Capture probes are made by ligating a second sequence-specific DNA oligonucleotide for each target to a universal oligonucleotide containing biotin. Reporter and capture probes are all pooled into a single hybridization mixture, the “probe library”. Preferably, the probe library comprises a probe pair (a capture probe and reporter) for each of the NANO46 genes in Table 1.

[69] The relative abundance of each target is measured in a single multiplexed hybridization reaction. The method comprises contacting a biological sample with a probe library, the library comprising a probe pair for the NANO46 genes in Table 1, such that the presence of the target in the sample creates a probe pair – target complex. The complex is then purified. More specifically, the sample is combined with the probe library, and hybridization occurs in solution. After hybridization, the tripartite hybridized complexes (probe pairs and target) are purified in a two-step procedure using magnetic beads linked to

oligonucleotides complementary to universal sequences present on the capture and reporter probes. This dual purification process allows the hybridization reaction to be driven to completion with a large excess of target-specific probes, as they are ultimately removed, and, thus, do not interfere with binding and imaging of the sample. All post hybridization steps are handled robotically on a custom liquid-handling robot (Prep Station, NanoString Technologies).

[70] Purified reactions are deposited by the Prep Station into individual flow cells of a sample cartridge, bound to a streptavidin-coated surface via the capture probe, electrophoresed to elongate the reporter probes, and immobilized. After processing, the sample cartridge is transferred to a fully automated imaging and data collection device (Digital Analyzer, NanoString Technologies). The expression level of a target is measured by imaging each sample and counting the number of times the code for that target is detected. Data is output in simple spreadsheet format listing the number of counts per target, per sample.

[71] This system can be used along with nanoreporters. Additional disclosure regarding nanoreporters can be found in International Publication No. WO 07/076129 and WO 07/076132, and US Patent Publication No. 2010/0015607 and 2010/0261026, the contents of which are incorporated herein in their entireties. Further, the term nucleic acid probes and nanoreporters can include the rationally designed (*e.g.* synthetic sequences) described in International Publication No. WO 2010/019826 and US Patent Publication No. 2010/0047924, incorporated herein by reference in its entirety.

[72] *Data processing*

[73] It is often useful to pre-process gene expression data, for example, by addressing missing data, translation, scaling, normalization, weighting, *etc.* Multivariate projection methods, such as principal component analysis (PCA) and partial least squares analysis (PLS), are so-called scaling sensitive methods. By using prior knowledge and experience about the type of data studied, the quality of the data prior to multivariate modeling can be enhanced by scaling and/or weighting. Adequate scaling and/or weighting can reveal important and interesting variation hidden within the data, and therefore make subsequent multivariate modeling more efficient. Scaling and weighting may be used to place the data in the correct metric, based on knowledge and experience of the studied system, and therefore reveal patterns already inherently present in the data.

[74] If possible, missing data, for example gaps in column values, should be avoided. However, if necessary, such missing data may be replaced or "filled" with, for example, the

mean value of a column ("mean fill"); a random value ("random fill"); or a value based on a principal component analysis ("principal component fill").

[75] "Translation" of the descriptor coordinate axes can be useful. Examples of such translation include normalization and mean centering. "Normalization" may be used to remove sample-to-sample variation. For microarray data, the process of normalization aims to remove systematic errors by balancing the fluorescence intensities of the two labeling dyes. The dye bias can come from various sources including differences in dye labeling efficiencies, heat and light sensitivities, as well as scanner settings for scanning two channels. Some commonly used methods for calculating normalization factor include: (i) global normalization that uses all genes on the array; (ii) housekeeping genes normalization that uses constantly expressed housekeeping/invariant genes; and (iii) internal controls normalization that uses known amount of exogenous control genes added during hybridization (Quackenbush Nat. Genet. 32 (Suppl.), 496-501 (2002)). In one embodiment, the intrinsic genes disclosed herein can be normalized to control housekeeping genes. For example, the housekeeping genes described in U.S. Patent Publication 2008/0032293, which is herein incorporated by reference in its entirety, can be used for normalization. Exemplary housekeeping genes include MRPL19, PSMC4, SF3A1, PUM1, ACTB, GAPD, GUSB, RPLPO, and TFRC. It will be understood by one of skill in the art that the methods disclosed herein are not bound by normalization to any particular housekeeping genes, and that any suitable housekeeping gene(s) known in the art can be used.

[76] Many normalization approaches are possible, and they can often be applied at any of several points in the analysis. In one embodiment, microarray data is normalized using the LOWESS method, which is a global locally weighted scatter plot smoothing normalization function. In another embodiment, qPCR data is normalized to the geometric mean of set of multiple housekeeping genes.

[77] "Mean centering" may also be used to simplify interpretation. Usually, for each descriptor, the average value of that descriptor for all samples is subtracted. In this way, the mean of a descriptor coincides with the origin, and all descriptors are "centered" at zero. In "unit variance scaling," data can be scaled to equal variance. Usually, the value of each descriptor is scaled by $1/\text{StDev}$, where StDev is the standard deviation for that descriptor for all samples. "Pareto scaling" is, in some sense, intermediate between mean centering and unit variance scaling. In pareto scaling, the value of each descriptor is scaled by $1/\sqrt{\text{StDev}}$, where StDev is the standard deviation for that descriptor for all samples. In this way, each descriptor has a variance numerically equal to its initial standard deviation. The pareto

scaling may be performed, for example, on raw data or mean centered data.

[78] "Logarithmic scaling" may be used to assist interpretation when data have a positive skew and/or when data spans a large range, *e.g.*, several orders of magnitude. Usually, for each descriptor, the value is replaced by the logarithm of that value. In "equal range scaling," each descriptor is divided by the range of that descriptor for all samples. In this way, all descriptors have the same range, that is, 1. However, this method is sensitive to presence of outlier points. In "autoscaling," each data vector is mean centered and unit variance scaled. This technique is a very useful because each descriptor is then weighted equally, and large and small values are treated with equal emphasis. This can be important for genes expressed at very low, but still detectable, levels.

[79] In one embodiment, data is collected for one or more test samples and classified using the NANO46 classification model described herein. When comparing data from multiple analyses (*e.g.*, comparing expression profiles for one or more test samples to the centroids constructed from samples collected and analyzed in an independent study), it will be necessary to normalize data across these data sets. In one embodiment, Distance Weighted Discrimination (DWD) is used to combine these data sets together (Benito *et al.* (2004) *Bioinformatics* 20(1): 105-114, incorporated by reference herein in its entirety). DWD is a multivariate analysis tool that is able to identify systematic biases present in separate data sets and then make a global adjustment to compensate for these biases; in essence, each separate data set is a multi-dimensional cloud of data points, and DWD takes two points clouds and shifts one such that it more optimally overlaps the other.

[80] The methods described herein may be implemented and/or the results recorded using any device capable of implementing the methods and/or recording the results. Examples of devices that may be used include but are not limited to electronic computational devices, including computers of all types. When the methods described herein are implemented and/or recorded in a computer, the computer program that may be used to configure the computer to carry out the steps of the methods may be contained in any computer readable medium capable of containing the computer program. Examples of computer readable medium that may be used include but are not limited to diskettes, CD- ROMs, DVDs, ROM, RAM, and other memory and computer storage devices. The computer program that may be used to configure the computer to carry out the steps of the methods and/or record the results may also be provided over an electronic network, for example, over the internet, an intranet, or other network.

[81] *Calculation of risk of recurrence*

[82] Provided herein are methods for predicting breast cancer outcome within the context of the intrinsic subtype and optionally other clinical variables. Outcome may refer to overall or disease-specific survival, event-free survival, or outcome in response to a particular treatment or therapy. In particular, the methods may be used to predict the likelihood of long-term, disease-free survival. "Predicting the likelihood of survival of a breast cancer patient" is intended to assess the risk that a patient will die as a result of the underlying breast cancer. "Long-term, disease-free survival" is intended to mean that the patient does not die from or suffer a recurrence of the underlying breast cancer within a period of at least five years, or at least ten or more years, following initial diagnosis or treatment.

[83] In one embodiment, outcome is predicted based on classification of a subject according to subtype. In addition to providing a subtype assignment, the NANO46 bioinformatics model provides a measurement of the similarity of a test sample to all four subtypes which is translated into a Risk of Recurrence (ROR) score that can be used in any patient population regardless of disease status and treatment options. The intrinsic subtypes and ROR also have value in the prediction of pathological complete response in women treated with, for example, neoadjuvant taxane and anthracycline chemotherapy (Rouzier *et al.*, J Clin Oncol 23:8331-9 (2005), incorporated herein by reference in its entirety). Thus, in various embodiments of the present disclosure, a risk of recurrence (ROR) model is used to predict outcome. Using these risk models, subjects can be stratified into low, medium, and high risk of recurrence groups. Calculation of ROR can provide prognostic information to guide treatment decisions and/or monitor response to therapy.

[84] In some embodiments described herein, the prognostic performance of the NANO46-defined intrinsic subtypes and/or other clinical parameters is assessed utilizing a Cox Proportional Hazards Model Analysis, which is a regression method for survival data that provides an estimate of the hazard ratio and its confidence interval. The Cox model is a well-recognized statistical technique for exploring the relationship between the survival of a patient and particular variables. This statistical method permits estimation of the hazard (*i.e.*, risk) of individuals given their prognostic variables (*e.g.*, intrinsic gene expression profile with or without additional clinical factors, as described herein). The "hazard ratio" is the risk of death at any given time point for patients displaying particular prognostic variables. See generally Spruance *et al.*, Antimicrob. Agents & Chemo. 48:2787-92 (2004).

[85] The NANO46 classification model described herein can be trained for risk of recurrence using subtype distances (or correlations) alone, or using subtype distances with clinical variables as discussed *supra*. In one embodiment, the risk score for a test sample is

calculated using intrinsic subtype distances alone using the following equation:

[86] $ROR = 0.05*Basal + 0.11*Her2 + -0.25*LumA + 0.07*LumB + -0.11*Normal,$

where the variables "Basal," "Her2," "LumA," "LumB," and "Normal" are the distances to the centroid for each respective classifier when the expression profile from a test sample is compared to centroids constructed using the gene expression data deposited with the Gene Expression Omnibus (GEO).

[87] Risk score can also be calculated using a combination of breast cancer subtype and the clinical variables tumor size (T) and lymph nodes status (N) using the following equation:

$ROR (full) = 0.05*Basal + 0.1*Her2 + -0.19*LumA + 0.05*LumB + -0.09*Normal + 0.16*T + 0.08*N,$ again when comparing test expression profiles to centroids constructed using the gene expression data deposited with GEO as accession number GSE2845.

[88] In yet another embodiment, risk score for a test sample is calculated using intrinsic subtype distances alone using the following equation:

[89] $ROR-S = 0.05*Basal + 0.12*Her2 + -0.34*LumA + 0.023*LumB,$ where the variables "Basal," "Her2," "LumA," and "LumB" are as described *supra* and the test expression profiles are compared to centroids constructed using the gene expression data deposited with GEO as accession number GSE2845. In yet another embodiment, risk score can also be calculated using a combination of breast cancer subtype and the clinical variable tumor size (T) using the following equation (where the variables are as described *supra*):

$ROR-C = 0.05*Basal + 0.11*Her2 + -0.23*LumA + 0.09*LumB + 0.17*T.$

[90] In yet another embodiment, risk score for a test sample is calculated using intrinsic subtype distances in combination with the proliferation signature ("Prolif") using the following equation:

[91] $ROR-P = -0.001*Basal + 0.7*Her2 + -0.95*LumA + 0.49*LumB + 0.34*Prolif,$ where the variables "Basal," "Her2," "LumA," "LumB" and "Prolif" are as described *supra* and the test expression profiles are compared to centroids constructed using the gene expression data deposited with GEO as accession number GSE2845.

[92] In yet another embodiment, risk score can also be calculated using a combination of breast cancer subtype, proliferation signature and the clinical variable tumor size (T) using the ROR-PT described in conjunction with Table 3 *supra*.

[93] *Detection of Subtypes*

[94] Immunohistochemistry for estrogen (ER), progesterone (PgR), HER2, and Ki67 was performed concurrently on serial sections with the standard streptavidin–biotin complex method with 3,3'-diaminobenzidine as the chromogen. Staining for ER, PgR, and HER2

interpretation can be performed as described previously (Cheang *et al.*, Clin Cancer Res. 2008;14(5):1368–1376.), however any method known in the art may be used.

[95] For example, a Ki67 antibody (clone SP6; ThermoScientific, Fremont, CA) can be applied at a 1:200 dilution for 32 minutes, by following the Ventana Benchmark automated immunostainer (Ventana, Tucson AZ) standard Cell Conditioner 1 (CC1, a proprietary buffer) protocol at 98°C for 30 minutes. An ER antibody (clone SP1; ThermoFisher Scientific, Fremont CA) can be used at 1:250 dilution with 10-minute incubation, after an 8-minute microwave antigen retrieval in 10 mM sodium citrate (pH 6.0). Ready-to-use PR antibody (clone 1E2; Ventana) can be used by following the CC1 protocol as above. HER2 staining can be done with a SP3 antibody (ThermoFisher Scientific) at a 1:100 dilution after antigen retrieval in 0.05 M Tris buffer (pH 10.0) with heating to 95°C in a steamer for 30 minutes. For HER2 fluorescent *in situ* hybridization (FISH) assay, slides can be hybridized with probes to LSI (locus-specific identifier) HER2/neu and to centromere 17 by use of the PathVysion HER-2 DNA Probe kit (Abbott Molecular, Abbott Park, IL) according to manufacturer's instructions, with modifications to pretreatment and hybridization as previously described (Brown LA, Irving J, Parker R, *et al.* Amplification of EMSY, a novel oncogene on 11q13, in high grade ovarian surface epithelial carcinomas. Gynecol Oncol. 2006;100(2):264–270). Slides can then be counterstained with 4',6-diamidino-2-phenylindole, stained material was visualized on a Zeiss Axioplan epifluorescent microscope, and signals were analyzed with a Metafer image acquisition system (Metasystems, Altlussheim, Germany). Biomarker expression from immunohistochemistry assays can then be scored by two pathologists, who were blinded to the clinicopathological characteristics and outcome and who used previously established and published criteria for biomarker expression levels that had been developed on other breast cancer cohorts.

[96] Tumors were considered positive for ER or PR if immunostaining was observed in more than 1% of tumor nuclei, as described previously. Tumors were considered positive for HER2 if immunostaining was scored as 3+ according to HercepTest criteria, with an amplification ratio for fluorescent *in situ* hybridization of 2.0 or more being the cut point that was used to segregate immunohistochemistry equivocal tumors (scored as 2+) (Yaziji, *et al.*, JAMA, 291(16):1972–1977 (2004)). Ki67 was visually scored for percentage of tumor cell nuclei with positive immunostaining above the background level by two pathologists.

[97] Other methods can also be used to detect subtypes. These techniques include ELISA, Western blots, Northern blots, or FACS analysis.

[98] *Kits*

[99] The present disclosure also describes kits useful for classifying breast cancer intrinsic subtypes and/or providing prognostic information to identify risk of recurrence. These kits comprise a set of capture probes and/or primers specific for the intrinsic genes listed in Table 1. The kit may further comprise a computer readable medium.

[100] In one embodiment of the present disclosure, the capture probes are immobilized on an array. By "array" is intended a solid support or a substrate with peptide or nucleic acid probes attached to the support or substrate. Arrays typically comprise a plurality of different capture probes that are coupled to a surface of a substrate in different, known locations. The arrays of the disclosure comprise a substrate having a plurality of capture probes that can specifically bind an intrinsic gene expression product. The number of capture probes on the substrate varies with the purpose for which the array is intended. The arrays may be low-density arrays or high-density arrays and may contain 4 or more, 8 or more, 12 or more, 16 or more, 32 or more addresses, but will minimally comprise capture probes for the 46 intrinsic genes listed in Table 1.

[101] Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Patent No. 5,384,261, incorporated herein by reference in its entirety for all purposes. The array may be fabricated on a surface of virtually any shape or even a multiplicity of surfaces. Arrays may be probes (*e.g.*, nucleic-acid binding probes) on beads, gels, polymeric surfaces, fibers such as fiber optics, glass or any other appropriate substrate, see U.S. Pat. Nos. 5,770,358, 5,789,162, 5,708,153, 6,040,193 and 5,800,992, each of which is hereby incorporated in its entirety for all purposes. Arrays may be packaged in such a manner as to allow for diagnostics or other manipulation on the device. See, for example, U.S. Pat. Nos. 5,856,174 and 5,922,591 herein incorporated by reference.

[102] In another embodiment, the kit comprises a set of oligonucleotide primers sufficient for the detection and/or quantitation of each of the intrinsic genes listed in Table 1. The oligonucleotide primers may be provided in a lyophilized or reconstituted form, or may be provided as a set of nucleotide sequences. In one embodiment, the primers are provided in a microplate format, where each primer set occupies a well (or multiple wells, as in the case of replicates) in the microplate. The microplate may further comprise primers sufficient for the detection of one or more housekeeping genes as discussed *infra*. The kit may further comprise reagents and instructions sufficient for the amplification of expression products from the genes listed in Table 1.

[103] In order to facilitate ready access, *e.g.*, for comparison, review, recovery, and/or modification, the molecular signatures/expression profiles are typically recorded in a

database. Most typically, the database is a relational database accessible by a computational device, although other formats, *e.g.*, manually accessible indexed files of expression profiles as photographs, analogue or digital imaging readouts, spreadsheets, *etc.* can be used.

Regardless of whether the expression patterns initially recorded are analog or digital in nature, the expression patterns, expression profiles (collective expression patterns), and molecular signatures (correlated expression patterns) are stored digitally and accessed via a database. Typically, the database is compiled and maintained at a central facility, with access being available locally and/or remotely.

[104] *Devices and Tests*

[105] General - The NanoString nCounter Analysis System delivers direct, multiplexed measurements of gene expression through digital readouts of the relative abundance of hundreds of mRNA transcripts. The nCounter Analysis System uses gene-specific probe pairs (**Figure 7**) that are mixed together to form a single reagent called a CodeSet. The probe pairs hybridize directly to the mRNA sample in solution eliminating any enzymatic reactions that might introduce bias in the results.

[106] After hybridization, all of the sample processing steps are automated on the nCounter Prep Station. First, excess capture and reporter probes are removed (**Figure 8**) followed by binding of the probe-target complexes to random locations on the surface of the nCounter cartridge via a streptavidin-biotin linkage (**Figure 9**).

[107] Finally, probe/target complexes are aligned and immobilized (**Figure 10**) in the nCounter Cartridge. The Reporter Probe carries the fluorescent signal; the Capture Probe allows the complex to be immobilized for data collection. Up to 800 pairs of probes, each specific to a particular gene, can be combined with a series of internal controls to form a CodeSet.

[108] After sample processing has completed, cartridges are placed in the nCounter Digital Analyzer for data collection. Each target molecule of interest is identified by the “color code” generated by six ordered fluorescent spots present on the reporter probe. The Reporter Probes on the surface of the cartridge are then counted and tabulated for each target molecule (**Figure 11**).

[109] Reagents and Test Components - The Breast Cancer test will simultaneously measure the expression levels of NANO46 plus eight housekeeping genes in a single hybridization reaction using an nCounter CodeSet designed specifically to those genes. Each assay also includes positive assay controls comprised of a linear titration of *in vitro* transcribed RNA transcripts and corresponding probes, and a set of probes with no sequence homology to

human RNA sequences which are used as negative controls. Each assay run includes a reference sample consisting of *in vitro* transcribed RNA's of the targets and housekeeping genes for normalization purposes. The normalized gene expression profile of a breast tumor sample is correlated to prototypical gene expression profiles of the four breast cancer intrinsic subtypes (Luminal A, Luminal B, HER2-enriched, or Basal-like) that were identified from a training set of breast tumors. The gene expression profile, in combination with selected clinical variables, is used as part of a trained algorithm as a prognostic indicator of risk of distant recurrence of breast cancer.

[110] Figure 12 outlines the assay processes associated with the nCounter Analysis System Breast Cancer Test.

[111] FFPE Tissue Extraction - The Breast Cancer Test will use RNA extracted from Formalin-fixed, Paraffin-embedded (FFPE) tissue that has been diagnosed as invasive carcinoma of the breast. A pathologist first performs an H & E stain of a tumor section mounted onto a slide to identify the region of viable invasive breast carcinoma containing tumor content above a minimum threshold. The pathologist circles the region on the H & E slide. The pathologist then mounts unstained tissue sections onto slides and marks the area of the slides containing invasive tumor. For larger tumors ($>100\text{mm}^2$ of viable invasive carcinoma on the H&E slide), the test requires only a single $10\mu\text{m}$ section. For smaller tumors ($<100\text{mm}^2$), the test requires 3 sections. The identified region of viable invasive breast carcinoma containing sufficient tumor content on the slides is macro-dissected prior to RNA extraction. Procedures for shipping FFPE tissue slides from the collection site to a testing site will be defined as part of the procedure.

[112] Following extraction of total RNA and removal of genomic DNA, the optical density is measured at wavelengths of 260 nm and 280 nm to determine both yield and purity. The assay procedure requires an input range of 125-500ng of total RNA for the subsequent hybridization step. NanoString plans to validate that this input range of RNA is sufficient to reproducibly perform the assay on the nCounter Analysis System. Additionally, the RNA quality will be measured using an OD 260/280 reading, with a target ratio of no less than 1.7 with an upper limit of 2.5. Procedures for storing RNA will be provided to the user so that downstream processing can be performed at a later point in time if desired.

[113] Requirements for Spectrophotometer to measure yield and purity post RNA extraction - RNA isolations from the FFPE sample result in a final sample volume of 30 μL . This volume is too low for the quantitation of nucleic acid abundance using absorbance

measurements in a cuvette-type UV-Vis spectrophotometer; therefore, NanoString's protocol includes a step for quantitating total RNA using a low volume spectrophotometer such as the NanoDrop™ spectrophotometer. NanoString will define performance specifications for the spectrophotometer so that the range of RNA input recommended for the test is above the limit of detection of the low volume spectrophotometer and is reproducibly measurable.

[114] Hybridization - For each set of up to 10 RNA samples, the user will pipette the specified amount of RNA into separate tubes within a 12 reaction strip tube and add the CodeSet and hybridization buffer. A reference sample is pipetted into the remaining two tubes with CodeSet and hybridization buffer. The CodeSet consists of probes for each gene that is targeted, additional probes for endogenous "housekeeping" normalization genes and positive and negative controls. The probes within the CodeSet pertaining to each of these genes within the four groups (target genes, housekeeping genes, and positive and negative controls) are each assigned a unique code and are therefore individually identifiable within each run. The reference sample consists of *in vitro* transcribed RNA for the targeted genes and housekeeping genes. Once the hybridization reagents are added to the respective tubes, the user transfers the strip tube into a heated-lid heatblock for a specified period of time at a set temperature.

[115] Requirement for Heat block with heated lid for hybridization step - The nCounter assay includes an overnight hybridization under isothermal conditions. Because the overnight hybridization is performed in a small volume at elevated temperature, care must be taken to avoid evaporation. Many commercial PCR thermocyclers are equipped with heated lids that will prevent the evaporation of small volumes of liquid. Because the assay does not require any fine control of temperature ramping, any heat block with a programmable heated lid and a block with dimensions that fit the NanoString tubes will work with the NanoString assay. NanoString plans to provide specifications for heat blocks that meet the assay requirements.

[116] Purification and Binding on the Prep Station - Upon completing hybridization, the user will then transfer the strip tube containing the set of 10 assays and 2 reference samples into the nCounter Prep Station along with the required prepackaged reagents and disposables described in **Table 1**. The Prep Plates contain the necessary reagents for purification of excess probes and binding to the cartridge (see section IIIC below for detailed description of purification process). The prep plates are centrifuged in a swinging bucket centrifuge prior to placement on the deck of the Prep Station. An automated purification process then removes excess capture and reporter probe through two successive hybridization-driven magnetic bead

capture steps. The nCounter Prep Station then transfers the purified target/probe complexes into an nCounter cartridge for capture to a glass slide. Following completion of the run, the user removes the cartridge from the Prep Station and seals it with an adhesive film.

[117] Imaging and Analysis on the Digital Analyzer - The sealed cartridge is then inserted into the nCounter Digital Analyzer which counts the number of probes captured on the slide for each gene, which corresponds to the amount of target in solution. Automated software then checks thresholds for the housekeeping genes, reference sample, and positive and negative controls to qualify each assay and ensure that the procedure was performed correctly. The housekeeping genes provide a measure of RNA integrity, and the thresholds indicate when a tested RNA sample is too degraded to be analyzed by the test due to improper handling or storage of tissue or RNA (e.g. improper tumor fixation, FFPE block storage, RNA storage, RNA handling introducing RNase). The positive and negative assay controls indicate a failure of the assay process (e.g. error in assay setup such as sample mixing with CodeSet, or sample processing such as temperature). The signals of each sample are next normalized using the housekeeping genes to control for input sample quality. The signals are then normalized to the reference sample within each run to control for run-to-run variations. The resulting normalized data is entered in the Breast Cancer Intrinsic Subtyping algorithm to determine tumor intrinsic subtype, risk of relapse score, and risk classification.

[118] Instrumentation- The nCounter Analysis System is comprised of two instruments, the nCounter Prep Station used for post-hybridization processing, and the Digital Analyzer used for data collection and analysis.

[119] nCounter Prep Station - The nCounter Prep Station (**Figure 13**) is an automated fluid handling robot that processes samples post-hybridization to prepare them for data collection on the nCounter Digital Analyzer. Prior to processing on the Prep Station, total RNA extracted from FFPE (Formalin-Fixed, Paraffin-Embedded) tissue samples is hybridized with the NanoString Reporter Probes and Capture Probes according to the nCounter protocol described above.

[120] Hybridization to the target RNA is driven by excess NanoString probes. To accurately analyze these hybridized molecules they are first purified from the remaining excess probes in the hybridization reaction. The Prep Station isolates the hybridized mRNA molecules from the excess Reporter and Capture probes using two sequential magnetic bead purification steps. These affinity purifications utilize custom oligonucleotide-modified magnetic beads that retain only the tripartite complexes of mRNA molecules that are bound to both a Capture probe and a Reporter probe.

[121] Next, this solution of tripartite complexes is washed through a flow cell in the NanoString sample cartridge. One surface of this flow cell is coated with a polyethylene glycol (PEG) hydrogel that is densely impregnated with covalently bound streptavidin. As the solution passes through the flow cell, the tripartite complexes are bound to the streptavidin in the hydrogel through biotin molecules that are incorporated into each Capture probe. The PEG hydrogel acts not only to provide a streptavidin-dense surface onto which the tripartite complexes can be specifically bound, but also inhibits the non-specific binding of any remaining excess reporter probes.

[122] After the complexes are bound to the flow cell surface, an electric field is applied along the length of each sample cartridge flow cell to facilitate the optical identification and order of the fluorescent spots that make up each reporter probe. Because the reporter probes are charged nucleic acids, the applied voltage imparts a force on them that uniformly stretches and orients them along the electric field. While the voltage is applied, the Prep Station adds an immobilization reagent that locks the reporters in the elongated configuration after the field is removed. Once the reporters are immobilized the cartridge can be transferred to the nCounter Digital Analyzer for data collection. All consumable components and reagents required for sample processing on the Prep Station are provided in the nCounter Master Kit. These reagents are ready to load on the deck of the nCounter Prep Station which can process up to 10 samples and 2 reference samples per run in approximately 2.5 hours.

[123] nCounter Digital Analyzer - The nCounter Digital Analyzer (**Figure 14**) collects data by taking images of the immobilized fluorescent reporters in the sample cartridge with a CCD camera through a microscope objective lens. Because the fluorescent Reporter Probes are small, single molecule barcodes with features of smaller than the wavelength of visible light, the Digital Analyzer uses high magnification, diffraction limited imaging to resolve the sequence of the spots in the fluorescent barcodes.

[124] The Digital Analyzer captures hundreds of consecutive fields-of-view (FOV) that can each contain hundreds or thousands of discrete Reporter Probes. Each FOV is a combination of four monochrome images captured at different wavelengths. The resulting overlay can be thought of as a four-color image in blue, green, yellow, and red. Each 4-color FOV is processed in real time to provide a “count” for each fluorescent barcode in the sample. Because each barcode specifically identifies a single mRNA molecule, the resultant data from the Digital Analyzer is a precise measure of the relative abundance of each mRNA of interest in a biological sample.

[125] Software - The Prep Station and the Digital Analyzer are stand-alone units that do not require connection to an external PC, but must be networked to one another using a Local Area Network (LAN). The nCounter System software securely manages operations through user accounts and permissions. Both instruments use setup and process wizards on an embedded touch screen user interface to guide the user through the sample processing and data collection steps of the assay. The user is led through the procedure by step-by-step instructions on the Prep Station and Digital Analyzer. The instrument touch screen uses a pressure sensitive method for controlling operations and enables the user to interact with the system by touching a selection on the screen. Because the touchscreen provides a limited human interface for data entry, the system also hosts a web-based application for user accounts management, sample batch definition, and sample status tracking.

[126] When samples are processed, the system software tracks the user account and reagent lots for each sample in a centralized data repository. After expression data for a sample is acquired by the Digital Analyzer, it is first analyzed to ensure that all pre-specified quality control metrics are met. The qualified data are then processed through a locked PAM50 algorithm to generate a report containing intrinsic subtype and risk of recurrence (ROR) score. The sample report is transferred to the central repository where it can be securely accessed for download by a user with the correct permissions.

[127] The Breast Cancer Intrinsic Subtyping Algorithm - The nCounter system will be used to identify the intrinsic subtype of an excised invasive carcinoma of the breast using a 50 gene classifier algorithm originally named the PAM50 (Parker J.S., et al. Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes. *Journal of Clinical Oncology*, 27: 1160-1167 (2009)). The gene expression profile will assign a breast cancer to one of four molecular classes or intrinsic subtypes: Basal-like, Luminal A, Luminal B, and HER2 enriched. A brief description of each subtype is provided below.

[128] Luminal subtypes: The most common subtypes of breast cancer are the luminal subtypes in the hormone-receptor positive population, Luminal A and Luminal B. Prior studies suggest that luminal A comprises approximately 30% to 40% and luminal B approximately 20% of breast cancers² and over 90 % of hormone receptor-positive breast cancers. The gene expression pattern of these subtypes resembles the luminal epithelial component of the breast (Nielsen, TO et al. A comparison of PAM50 intrinsic subtyping with immunohistochemistry and clinical prognostic factors in tamoxifen-treated estrogen receptor positive breast cancer. *Clinical Cancer Research*, 16:5222-5232 (2010)). These tumors are characterized by high expression of estrogen receptor (ER), progesterone receptor (PR), and

genes associated with ER activation² such as LIV1, GATA3, and cyclin D1, as well as expression of luminal cytokeratins 8 and 18.

[129] Luminal A: Luminal A (LumA) breast cancers exhibit low expression of genes associated with cell cycle activation and the ERBB2 cluster resulting in a better prognosis than luminal B. The Luminal A subgroup has the most favorable prognosis of all subtypes and is enriched for endocrine therapy-responsive tumors.

[130] Luminal B: Luminal B (LumB) breast cancers express ER and ER-associated genes, but to a lower extent than LumA. Genes associated with cell cycle activation are highly expressed and this tumor type can be HER2(+) or HER2(-). The prognosis is unfavorable (despite ER expression) and endocrine therapy responsiveness is generally diminished relative to LumA.

[131] Basal-like: The Basal-like subtype is generally ER-negative, is almost always clinically HER2-negative and expresses a suite of “basal” biomarkers including the basal epithelial cytokeratins (CK) and epidermal growth factor receptor (EGFR). Genes associated with cell cycle activation are highly expressed.

[132] HER2-enriched: The HER2-enriched subtype is generally ER-negative and is HER2-positive in the majority of cases with high expression of the ERBB2 cluster, including ERBB2 and GRB7. Genes associated with cell cycle activation are highly expressed and these tumors have a poor outcome.

[133] Cutoffs for the intrinsic subtyping algorithm are pre-defined from training sets that defined the following: 1) intrinsic subtype centroids (i.e. the prototypical gene expression profile of each subtype), 2) coefficients for Risk of Recurrence (ROR) score, and 3) risk classification (Low/Intermediate/High). The intrinsic subtype centroids (Luminal A, Luminal B, Her2-enriched, Basal-like) were trained using a clinically representative set of archived FFPE breast tumor specimens collected from multiple sites. Hierarchical clustering analysis of gene expression data from the FFPE breast tumor samples was combined with breast tumor biology (i.e. gene expression of previously defined intrinsic subtypes) to define the prototypical expression profile (i.e. centroid) of each subtype. A computational algorithm correlates the normalized 50 gene expression profile of an unknown breast cancer tumor sample to each of the prototypical expression signatures of the four breast cancer intrinsic subtypes. The tumor sample is assigned the subtype with the largest positive correlation to the sample.

[134] 304 unique tumor samples with well-defined clinical characteristics and clinical outcome data were used to establish the ROR score. The ROR score is calculated using

coefficients from a Cox model that includes the Pearson correlation (R) to each intrinsic subtype, a proliferation score (P), and tumor size (T), as shown in the equation below.

$$\text{ROR} = aR_{\text{LumA}} + bR_{\text{LumB}} + cR_{\text{Her2e}} + dR_{\text{basal}} + eP + fT$$

[135] To classify tumor samples into specific risk groups (Low Risk/Intermediate Risk/High Risk) based on their calculated ROR score, cutoffs were set based on probability of recurrence free survival in a patient population consisting of hormone receptor positive, post-menopausal patients treated with endocrine therapy alone.

[136] Anticipated Use of NanoString Breast Cancer Test in Clinical Practice - Oncologists currently use a series of tests to develop a treatment protocol for breast cancer patients. Included in these are the IHC / FISH tests such as ER/PR IHC and HER2 IHC / FISH, and the Agendia MammaPrint® assay and the Genomic Health Oncotype Dx® test. These tests offer the oncologist additional information regarding the patient's prognosis and recommended treatment regimens.

[137] These tests, however, have limitations. ER, PgR, and Her2 testing is done locally by pathologists and reference labs, but the challenges with widespread standardization of IHC and FISH testing is well documented (Lester, J et al. Assessment of Tissue Estrogen and Progesterone Receptor Levels: A Survey of Current Practice, Techniques, and Quantitation Methods. The Breast Journal, 6:189-196 (2000); Wolff, A et al. American Society of Clinical Oncology / College of American Pathologists Guideline Recommendations for Human Epidermal Growth Factor Receptor 2 Testing in Breast Cancer. Archives of Pathology and Laboratory Medicine, 131:18-43 (2007)). The MammaPrint test is FDA cleared for use only with frozen or fresh-preserved tissue samples, yet most of the tumor samples collected in the United States are FFPE rather than fresh-frozen. This test is also not distributed and is only available through the Agendia reference labs. The Oncotype Dx test can be used to predict the risk of relapse for stage I/II, node negative, estrogen receptor-positive patients receiving adjuvant Tamoxifen therapy as well as response to cyclophosphamide/methotrexate/5-fluorouracil (CMF) chemotherapy. However this test is only offered as a lab-developed test (LDT) through Genomic Health's CLIA laboratory and is not FDA cleared for prognostic use, or FDA approved for predicting chemotherapy response.

[138] NanoString envisions a model that would have the Breast Cancer test used in conjunction with other sources of clinical data currently available to oncologists for breast cancer prognosis in selected patient segments. The Breast Cancer Test would be an additional source of prognostic information adding significant value to established clinical parameters (i.e tumor size, nodal status) used by oncologists in managing a patient with

breast cancer.

[139] *Methods, Assays and Kits*

[140] The methods, assays and kits of the present invention include a series of quality control metrics that are automatically applied to each sample during analysis. These metrics evaluate the performance of the assay to determine whether the results fall within expected values. Upon successful analysis of these quality control metrics, the Assay gives the following results:

Result	Output Values
The Intrinsic Subtype of the Breast Cancer Specimen	Luminal A Luminal B HER2-Enriched Basal-Like
Individual Estimate of the Probability of Distant Recurrence within 10 years	0-100%
Risk of Recurrence (ROR) Score	Integer value on a 0-100 scale
Risk Category	Low, Intermediate, High

[141] Intrinsic Subtypes

[142] The Intrinsic Subtype of a breast cancer tumor has been shown to be related to prognosis in Early Stage Breast Cancer. On average, patients with a Luminal A tumor have significantly better outcomes than patients with Luminal B, HER2-Enriched, or Basal-like tumors.

[143] The Intrinsic Subtype is identified by comparing the gene expression profile of 50 genes in an unknown sample with the expected expression profiles for the four intrinsic subtypes. The subtype with the most similar profile is assigned to the unknown sample.

[144] The most common subtypes of breast cancer are the luminal subtypes, Luminal A (LumA) and Luminal B (LumB). Prior studies suggest that Luminal A comprises approximately 30% to 40% and Luminal B approximately 20% of breast cancers. However, greater than 90% of hormone-receptor positive patients have luminal tumors. The gene expression pattern of these subtypes resembles the luminal epithelial component of the breast tissue. These tumors are characterized by high expression of estrogen receptor (ER), progesterone receptor (PR), and genes associated with ER activation, such as LIV1, GATA3,

and cyclin D1, as well as expression of luminal cytokeratins 8 and 18. Luminal A breast cancers exhibit lower expression of genes associated with cell cycle activation when compared to Luminal B breast cancers resulting in a better prognosis.

[145] Prior studies suggest that the HER2-Enriched subtype (Her2E) comprises approximately 20% of breast cancers. However, HER2-Enriched tumors are generally ER-negative, so only 5% of the tested ER-positive patient population was found to have HER2-Enriched breast cancer. Regardless of ER-status, HER2-Enriched tumors are HER2-positive in the majority of cases with high expression of the ERBB2 cluster, including ERBB2 and GRB7. Genes associated with cell cycle activation are also highly expressed.

[146] Published data suggest that the Basal-like subtype comprises approximately 20% of breast cancers. However, Basal-like tumors are generally ER-negative, so only 1% of hormone receptor-positive patients have Basal-like breast cancer. The Basal-like subtype is almost always clinically HER2-negative and expresses a suite of “basal” biomarkers including the basal epithelial cytokeratins (CK) and epidermal growth factor receptor (EGFR). Genes associated with cell cycle activation are highly expressed.

[147] ROR Score

[148] The ROR score is an integer value on a 0-100 scale that is related to an individual patient's probability of distant recurrence within 10 years for the defined intended use population. The ROR score is calculated by comparing the expression profiles of 46 genes in an unknown sample with the expected profiles for the four intrinsic subtypes, as described above, to calculate four different correlation values. These correlation values are then combined with a proliferation score and the tumor size to calculate the ROR score.

[149] Probability of 10-Year Distant Recurrence

[150] The ROR scores for a cohort of post-menopausal women with hormone receptor-positive early stage breast cancer were compared to distant recurrence-free survival following surgery and treatment with 5 years of adjuvant endocrine therapy followed by 5 years of observation. This study resulted in a model relating the ROR score to the probability of distant recurrence in this tested patient population including a 95% confidence interval.

[151] Risk Classification

[152] Risk classification is also provided to allow interpretation of the ROR score by using cutoffs related to clinical outcome in tested patient populations.

[153] **Risk classification by ROR range and nodal status**

Nodal Status	ROR Range	Risk Classification
Node-Negative	0-40	Low
	41-60	Intermediate
	61-100	High
Node-Positive (1-3 nodes)	0-15	Low
	16-40	Intermediate
	41-100	High

[154] Quality Control

[155] Each lot of the Assay components is tested using predetermined specifications. All kit-level items are lot tracked, and the critical components contained within each kit are tested together and released as a Master Lot.

[156] The assay kit includes a series of internal controls that are used to assess the quality of each run set as a whole and each sample individually. These controls are listed below.

[157] Batch Control Set: *In vitro* transcribed RNA Reference Sample

[158] A synthetic RNA Reference Sample is included as a control within the Assay kit. The reference sample is comprised of in-vitro transcribed RNA targets from the 50 algorithm and 8 housekeeping genes. The Reference Sample is processed in duplicate in each assay run along with a set of up to 10 unknown breast tumor RNA samples in a 12 reaction strip tube. The signal from the Reference Sample is analyzed against pre-defined thresholds to qualify the run.

[159] The signal from each of the 50 algorithm genes of the breast tumor RNA sample is normalized to the corresponding genes of the Reference Sample.

[160] Positive Control Set: *in vitro* transcribed RNA targets and corresponding Capture and Reporter Probes

[161] Synthetic RNA targets are used as positive controls (PCs) for the assay. The PC target sequences are derived from the External RNA Control Consortium (ERCC) DNA sequence library. The RNA targets are in-vitro transcribed from DNA plasmids. Six RNA targets are included within the assay kit in a 4-fold titration series (128 – 0.125 fM final concentration in hybridization reaction) along with the corresponding Capture and Reporter Probes. The PCs are added to each breast tumor RNA sample and Reference RNA Sample

tested with the Prosigna Assay. A sample will be disqualified from further analysis if the signal intensities from the PCs do not meet pre-defined thresholds.

[162] Negative control set: exogenous probes without targets

[163] Negative control (NC) target sequences are derived from the ERCC DNA sequence library. The probes designed to detect these target sequences are included as part of the assay kit without the corresponding target sequence. The negative controls (NCs) are added to each breast tumor RNA sample and Reference Sample tested with the Prosigna Assay as a quality control measure. The sample will be disqualified from further analysis if the signal intensities from the NCs do not meet pre-defined thresholds.

[164] RNA Integrity Control Set: Housekeeping genes

[165] Capture and Reporter Probes designed to detect 8 housekeeping genes and 50 algorithm genes are included as part of the kit. The expression levels of the 8 housekeeping genes are analyzed to determine the quality of RNA extracted from the FFPE tissue sample and input into the assay. The sample will be disqualified from further analysis if the expression level of the housekeeping genes falls below pre-defined thresholds.

[166] The housekeeping genes are also used to normalize for any differences in the intact RNA amount in a sample prior to Reference Sample normalization.

[167] *Definitions*

[168] For the purposes of the present disclosure, "breast cancer" includes, for example, those conditions classified by biopsy or histology as malignant pathology. The clinical delineation of breast cancer diagnoses is well known in the medical arts. One of skill in the art will appreciate that breast cancer refers to any malignancy of the breast tissue, including, for example, carcinomas and sarcomas. Particular embodiments of breast cancer include ductal carcinoma *in situ* (DCIS), lobular carcinoma *in situ* (LCIS), or mucinous carcinoma. Breast cancer also refers to infiltrating ductal (IDC) or infiltrating lobular carcinoma (ILC). In most embodiments of the disclosure, the subject of interest is a human patient suspected of or actually diagnosed with breast cancer.

[169] The article "a" and "an" are used herein to refer to one or more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, "an element" means one or more element.

[170] Throughout the specification the word "comprising," or variations such as "comprises" or "comprising," will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other

element, integer or step, or group of elements, integers or steps.

EXAMPLES

Example 1. NANO46 Subtyping Test

[171] **Figure 5** outlines the assay processes associated with the Breast Cancer Intrinsic Subtyping test. Following RNA isolation, the test will simultaneously measure the expression levels of 46 target genes plus eight housekeeping genes in a single hybridization reaction using an nCounter CodeSet designed specifically to those genes. For example, the housekeeping genes described in U.S. Patent Publication 2008/0032293, which is herein incorporated by reference in its entirety, can be used for normalization. Exemplary housekeeping genes include MRPL19, PSMC4, SF3A1, PUM1, ACTB, GAPD, GUSB, RPLP0, and TFRC. The housekeeping genes are used to normalize the expression of the tumor sample. Each assay run also includes a reference sample consisting of *in vitro* transcribed RNA's of the 58 targets for normalization purposes.

[172] FFPE Tissue Review/Procurement and RNA Extraction: The Breast Cancer Intrinsic Subtyping Test will use RNA extracted from Formalin-fixed, Paraffin-embedded (FFPE) tissue that has been diagnosed as invasive carcinoma of the breast. A Pathologist reviews an H & E stained slide to identify the tissue area containing sufficient tumor tissue content for the test. Unstained slide mounted tissue sections are processed by macro-dissecting the identified tumor area on each slide to remove any adjacent normal tissue. RNA is then isolated from the tumor tissue, and DNA is removed from the sample.

[173] Assay Setup and Initiation of Hybridization: For each batch of up to 10 RNA samples isolated from a breast tumor, the user will set up a run using the nCounter Analysis x5 system software, which tracks sample processing, reagent lots, and results for each sample. To initiate the assay, the user will pipette the specified amount of RNA into separate tubes within a 12 reaction strip tube and add the CodeSet and hybridization buffer. A reference sample is pipetted into the remaining two tubes with CodeSet and hybridization buffer. The CodeSet consists of probes for each gene that is targeted, additional probes for endogenous "housekeeping" normalization genes and positive and negative controls that are spiked into the assay. The reference sample consists of *in vitro* transcribed RNA for the targeted genes and housekeeping genes. Once the hybridization reagents are added to the respective tubes, the user transfers the strip tube into a heated-lid heatblock for a specified period of time at a set temperature.

[174] Purification and Binding on the Prep Station: Upon completing hybridization, the user will transfer the strip tube containing the set of 10 assays and 2 reference samples onto the

nCounter Prep Station along with the required prepackaged reagents and disposables. An automated purification process then removes excess capture and reporter probe through two successive hybridization-driven magnetic bead capture steps. The nCounter Prep Station then transfers the purified target/probe complexes into an nCounter cartridge for capture to a glass slide. Following completion of the run, the user removes the cartridge from the Prep Station and seals it with an adhesive film.

[175] Imaging and Analysis on the Digital Analyzer: The cartridge is then sealed and inserted into the nCounter Digital Analyzer which counts the number of probes captured on the slide for each gene, which corresponds to the amount of target in solution. Automated software will then check thresholds for the housekeeping genes, reference sample, and positive and negative controls to qualify each assay and ensure that the procedure was performed correctly. The signals of each sample are next normalized using the housekeeping genes to control for input sample quality. The signals are then normalized to the reference sample within each run to control for run-to-run variations. The resulting normalized data is entered in the Breast Cancer Intrinsic Subtyping algorithm to determine tumor intrinsic subtype and risk of recurrence score.

[176] Example 2: Clinical Validation of the NANO46 risk of recurrence (ROR) score for predicting residual risk of distant-recurrence (DR) after endocrine therapy in postmenopausal women with HR+ early breast cancer (EBC): An ABCSG Study.

[177] The aim of the study is to assess the performance of the ROR score in predicting distal recurrence for postmenopausal patients with hormone receptor positive early breast cancer (HR+ EBC) treated with tamoxifen or tamoxifen followed by anastrozole when the NANO46 test is performed in a routine hospital pathology lab. Does the ROR score add prognostic information (Distant RFS) beyond the Clinical Treatment Score in all patients (CTS includes: nodes, grade, tumor size, age, treatment)? Do the ROR-based risk groups add prognostic information (Distant RFS) beyond the Clinical Treatment Score in all patients?

[178] Study Overview: 3,714 patients were enrolled in a ABCSG8. Patients were postmenopausal women with HR+ EBC (node negative and node positive), grade one or two, with no prior treatment. 1,671 patients re-consented for long-term follow-up or are deceased. The median follow-up was 11 years. 1,620 FFPE blocks were collected. 25 had insufficient cancer in the block on path review, 73 had insufficient RNA included, 44 failed QC specs for the NanoString device. 1,478 patients (91.2%) passed the NANO46 analysis.

[179] Methods: Three unstained 10 micron sections and 1 H&E slide for each patient was sent to an independent academic pathology laboratory at BCCA where tissue review, manual

micro-dissection and RNA extraction were performed. NANO46 analysis was then conducted on 250 ng of the extracted RNA using the NanoString nCounter Analysis System; both intrinsic subtype and ROR score were calculated.

[180] Results: The ROR Score adds statistically significant prognostic information (Distant RFS) beyond CTS in all patients (Likelihood ratio test $\Delta LR\chi^2 = 53.5$, $p < 0.0001$). The ROR-based risk groups add statistically significant prognostic information (Distant RFS) beyond CTS in all patients (Likelihood ratio test $\Delta LR\chi^2 = 34.1$, $p < 0.0001$). Differentiation between Luminal A and Luminal B adds statistically significant prognostic information (Distant RFS) beyond CTS in all patients (Luminal B vs. A: HR=2.38, 95% CI; 1.69-3.35, $p < 0.0001$). Results in the node-negative and node-positive subgroups are similar to the results for all patients that are reported in the study.

[181] Conclusions: The results show that both the ROR score and the ROR-based risk groups add statistically significant prognostic information beyond the Clinical Treatment Score. The results demonstrate that a complex, multi-gene-expression test can be performed in a hospital pathology laboratory and meet the same quality metrics as a central reference laboratory. The results of the TransATAC and ABCSG8 studies together provide Level 1 evidence for the clinical validity of the NANO46 test for predicting the risk of distant recurrence in postmenopausal women with HR+ EBC treated with endocrine therapy alone. The results also show that Luminal A subtypes have better outcomes than Luminal B subtypes in postmenopausal women with HR+ EBC treated with endocrine therapy alone.

CLAIMS

What is claimed is:

1. A method of predicting outcome in a subject having breast cancer comprising:
 - providing a tumor sample from the subject;
 - determining the expression of at least the genes in the NANO46 intrinsic gene list of Table 1 in the tumor sample;
 - determining the intrinsic subtype of the tumor sample, wherein the intrinsic subtype is selected from the group consisting of at least Basal-like, Luminal A, Luminal B or HER2-enriched;
 - determining a proliferation score based on the expression of a subset of proliferation genes in the NANO46 intrinsic gene list;
 - calculating a risk of recurrence score using a weighted sum of said intrinsic subtype, proliferation score and optionally one or more clinicopathological variables such as tumor size, nodal status or histological grade; and
 - determining whether the subject has a low or high risk of recurrence based on the risk of recurrence score.
2. The method of claim 1, wherein determining a proliferation signature based on the expression of a subset of proliferation genes in the NANO46 intrinsic gene list comprises determining the expression of each of the NANO46 intrinsic genes selected from ANLN, CCNE1, CDC20, CDC6, CDCA1, CENPF, CEP55, EXO1, KIF2C, KNTC2, MELK, MKI67, ORC6L, PTTG1, RRM2, TYMS, UBE2C and UBE2T.
3. The method of claim 1, further comprising determining at least one of the following: tumor grade, tumor ploidy, nodal status, estrogen receptor expression, progesterone receptor expression, and HER2/ERBB2 expression
4. The method of claim 1, further comprising determining each of the following: tumor grade, tumor ploidy, nodal status, estrogen receptor expression, progesterone receptor expression, and HER2/ERBB2 expression
5. The method of claim 1, wherein the risk of recurrence score is calculated using the following equation:

$$\text{ROR-PT} = -0.0067 * \text{Basal} + 0.4317 * \text{Her2} + -0.3172 * \text{LumA} + 0.4894 * \text{LumB} +$$

$0.1981 * \text{ProliferationScore} + 0.1133 * \text{TumorSize}$.

6. The method of claim 1, wherein the outcome is breast cancer specific survival, event-free survival or response to therapy.

7. The method of claim 1, wherein the expression of the members of the NANO46 intrinsic gene list is determined using the nanoreporter code system (nCounter® Analysis system).

8. A kit comprising a plurality of probes for determining the expression of at least the genes in the NANO46 intrinsic gene list of Table 1 in a tumor sample for use in a method of predicting outcome in a subject having breast cancer.

9. The kit of claim 8, wherein the kit comprises a plurality of probes of Table 1A.

10. The kit of claim 9, wherein the kit comprises each of the probes of Table 1A.

11. The kit of claim 8, comprising probes for determining the expression of each of the NANO46 intrinsic genes selected from ANLN, CCNE1, CDC20, CDC6, CDCA1, CENPF, CEP55, EXO1, KIF2C, KNTC2, MELK, MKI67, ORC6L, PTTG1, RRM2, TYMS, UBE2C and UBE2T.

12. The kit of claim 8, wherein each probe in the plurality of probes comprises a target specific sequence capable of hybridizing to no more than one NANO46 intrinsic gene listed in Table 1, and optionally comprises at least two label attachment regions, said label attachment regions comprising one or more label monomers that emit light.

13. The kit of claim 9, wherein the plurality of probes comprises a probe pair to detect the NANO46 intrinsic genes listed in Table 1, wherein each probe in the probe pair comprises a target specific sequence capable of hybridizing to no more than one NANO46 intrinsic gene listed in Table 1 and wherein the target specific sequences bind to different regions of the same NANO46 intrinsic gene.

14. The kit of claim 13, wherein one probe of the probe pair further comprises at least two

label attachment regions, said label attachment regions comprising one or more label monomers that emit light

15. The kit of claim 8, further comprising one or more reagents for determining one or more clinicopathological variables of the tumor sample such as tumor size, tumor grade, tumor ploidy, nodal status, estrogen receptor expression, progesterone receptor expression, and HER2/ERBB2 expression.

Figure 1

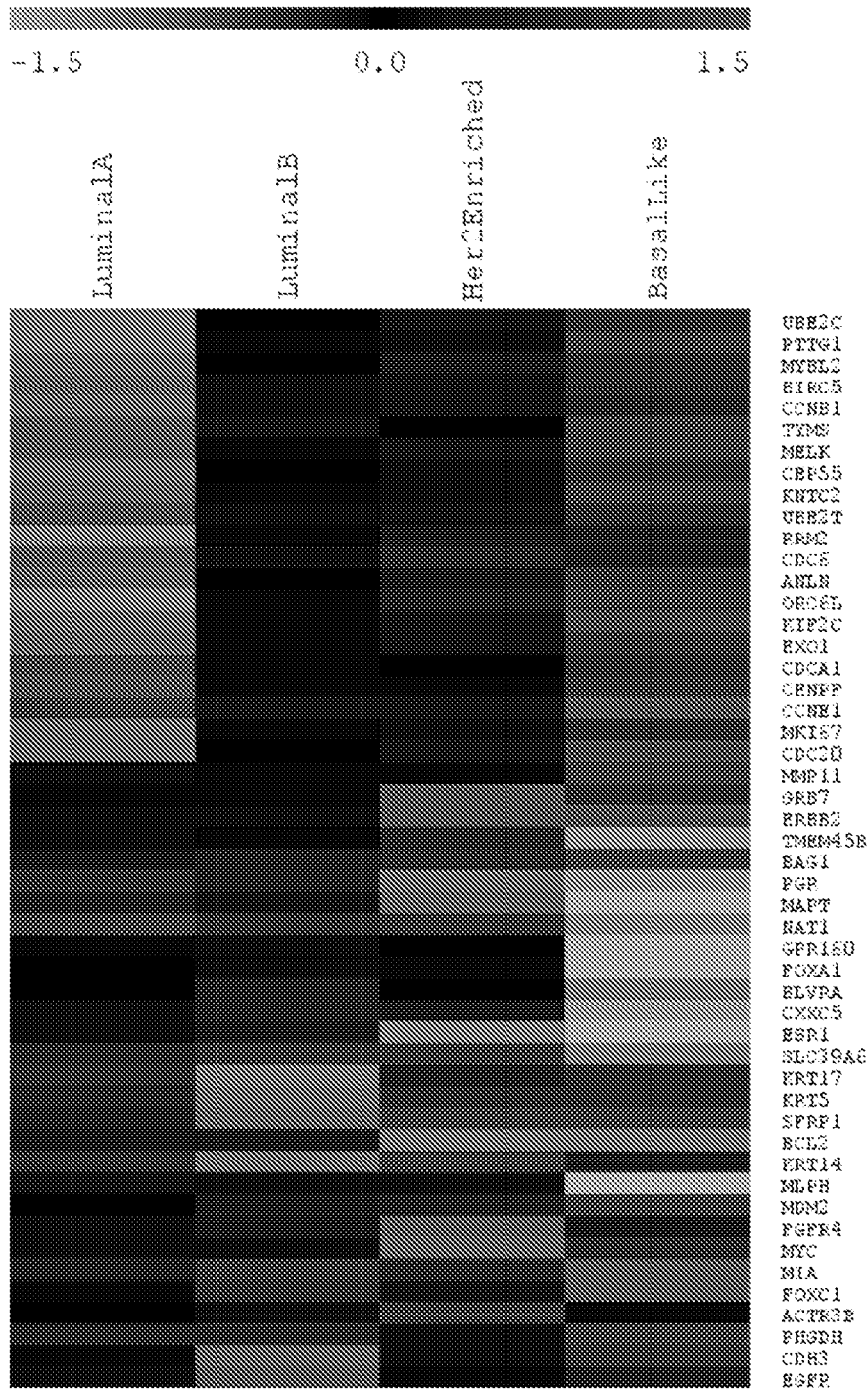


Figure 2

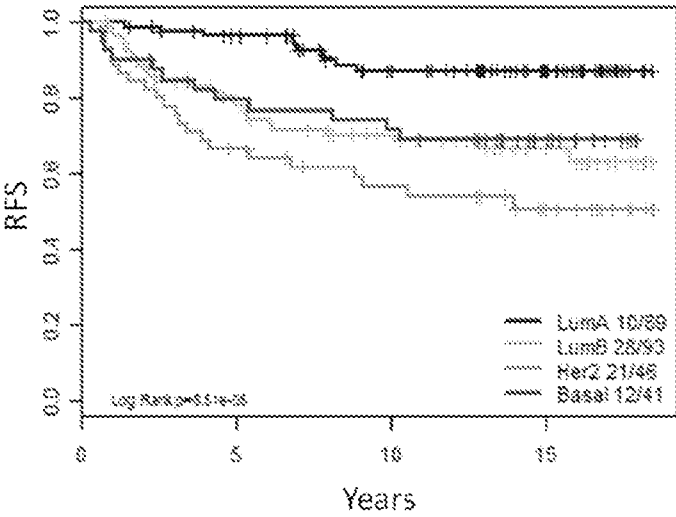


Figure 3

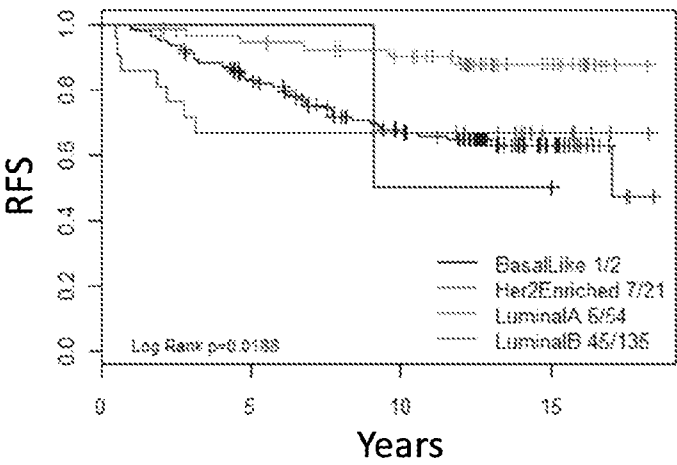


Figure 4

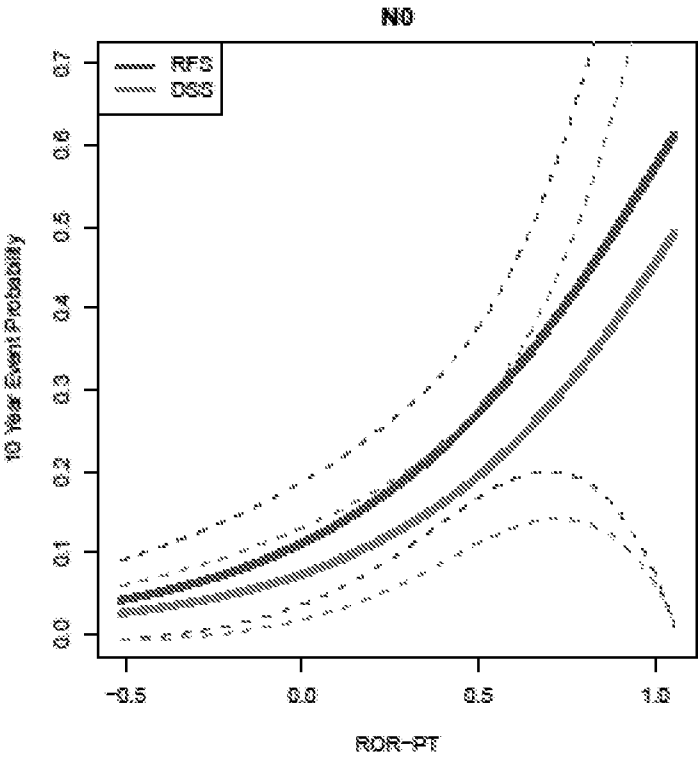


Figure 5

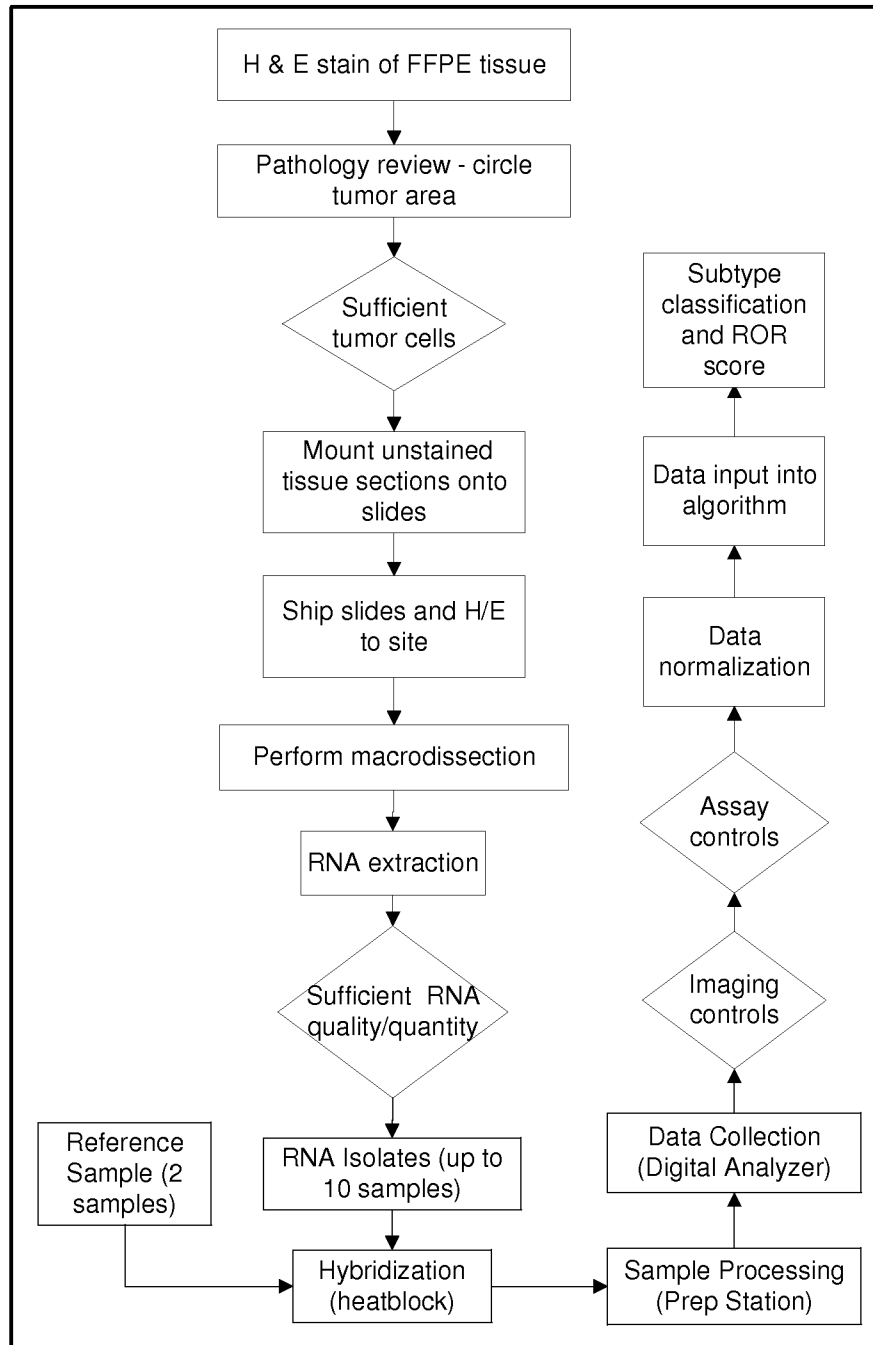


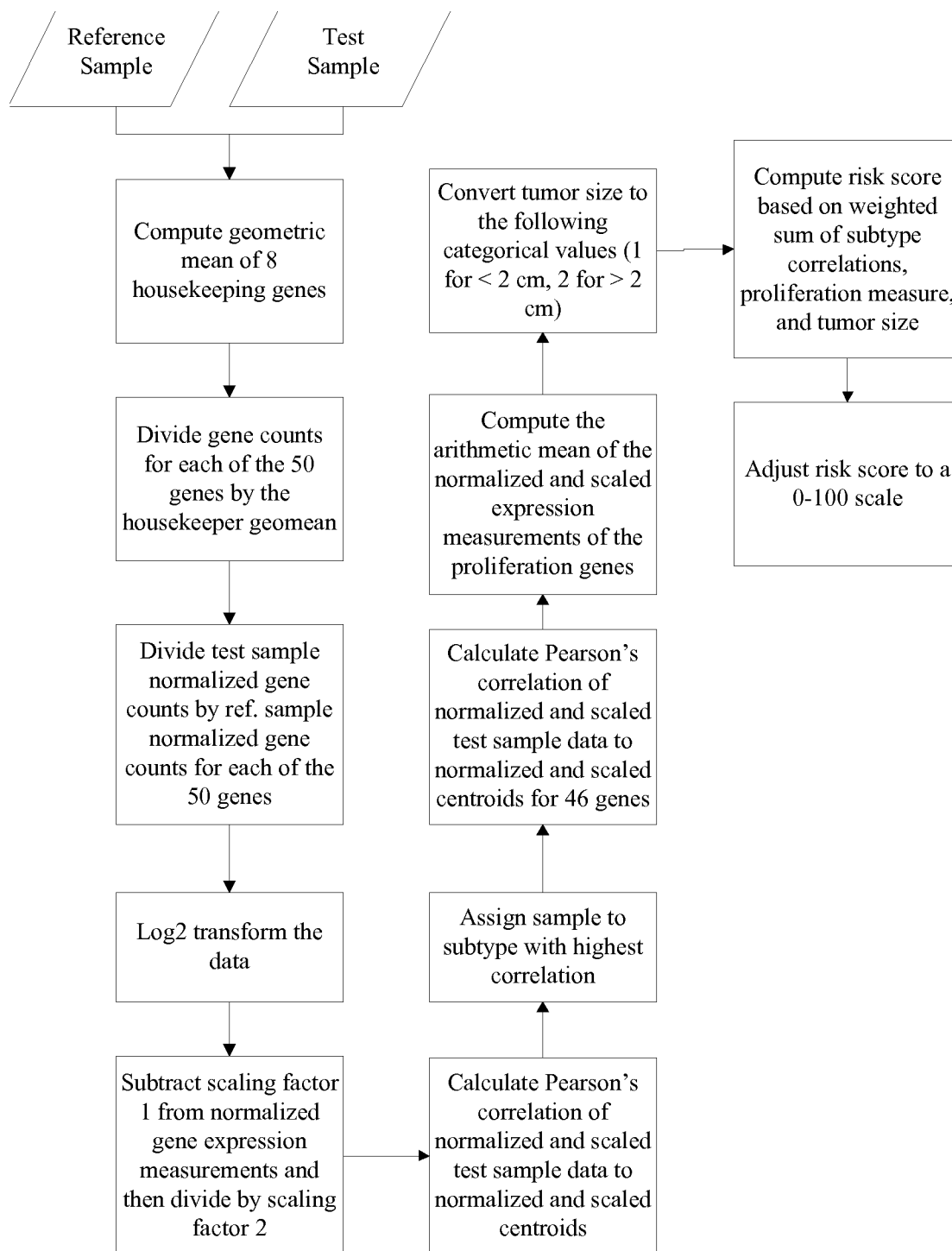
Figure 6

FIGURE 7

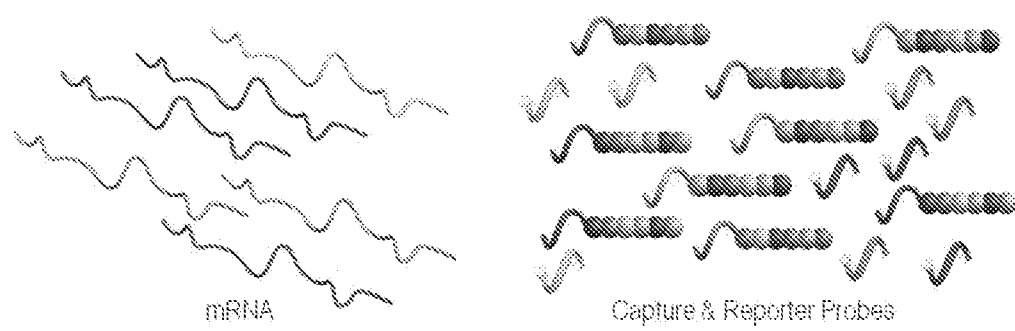


FIGURE 8

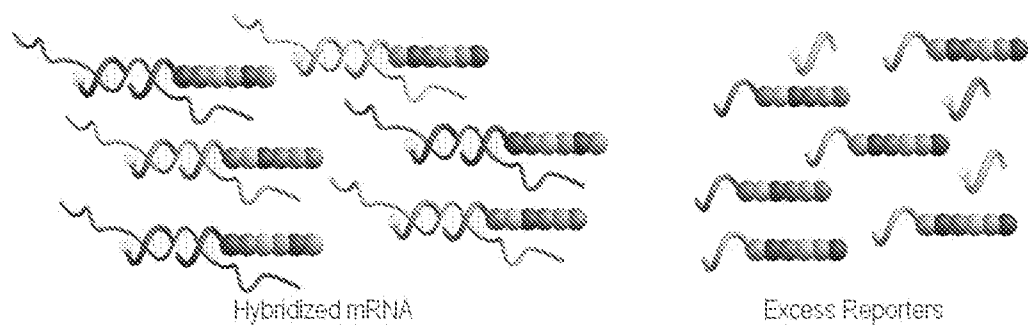


FIGURE 9

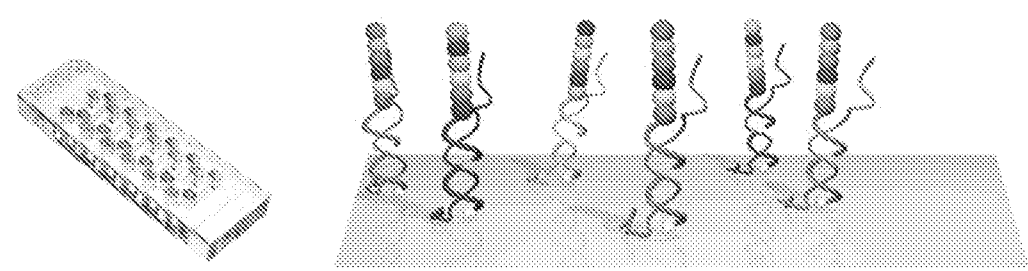


FIGURE 10

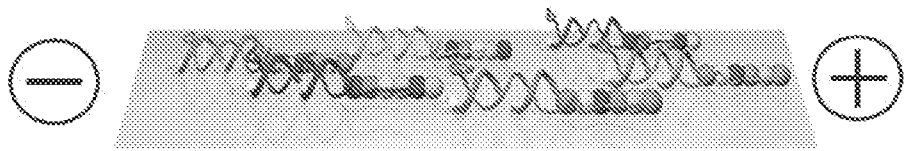


FIGURE 11

Code	Gene	Count
	x	3
	y	1
	z	2

FIGURE 12

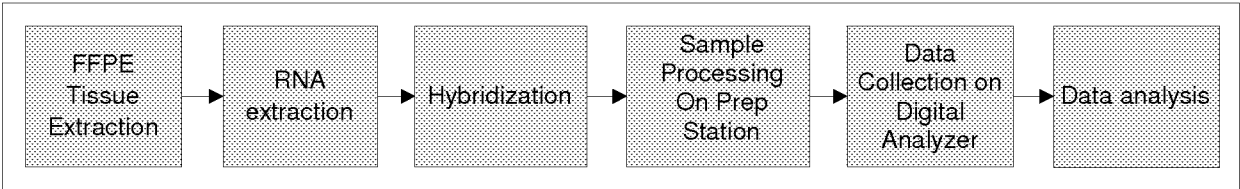


FIGURE 13

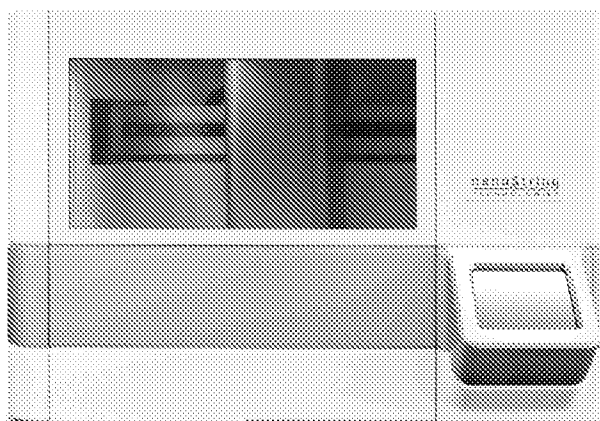


FIGURE 14

