Supporting Online Material for:

## 3'LIFE: A Functional Assay to Detect miRNA Targets in High-Throughput

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Supplementary Figure 1. Predicted miRNA targets have high false negative rates. We have superimposed all the experimentally validated miRNA targets of five cancer-related miRNAs (x-axis, black dots) to target predictions produced by a panel of widely utilized prediction algorithms, TargetScan (A) (5), DIANA microT-CDS (B) (42), and PicTar (C) (8). The Y-axis represents the normalized targeting score assigned to each prediction, with the black horizontal line representing the normalized mean. We show the same five representative miRNAs in each panel. These miRNAs were selected for this analysis based on 1) their significant presence in the literature, 2) their correlation with oncogenic pathways, and 3) their uncharacteristic high number of validated gene targets when compared to other less studied miRNAs. (D) Among 67 experimentally validated targets for these five miRNAs, 34% were not predicted by TargetScan, 47% were not predicted by DIANA-microT-CDS, and 52% were not predicted by PicTar. Of note, these algorithms produce thousands of predictions that are yet to be tested, representing >98% of predicted targets. This comprehensive list was compiled utilizing miRTarbase (40) and by our own manual literature review of up-to-date



resources.



**Supplementary Figure 2.** 3'LIFE assay plasmid maps (**A**) pLIFE-3'UTR (**B**) pLIFE-miRNA. Positions of restriction sites used to clone various elements are noted. Plasmids are available through DNASU Plasmid Repository (<u>www.DNASU.org</u>, clone IDs:EvNO00601503 and EvNO00601504).

http://dnasu.org/DNASU/GetCloneDetail.do?cloneid=601503 http://dnasu.org/DNASU/GetCloneDetail.do?cloneid=601504

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## **Supplementary Figure 3**



**Supplementary Figure 3.** Expression and splicing of pri-miRNA from pLIFE-miRNA vector (**A**) Top: Total RNA from HEK293T cells transfected with pLIFE-miRNA plasmid was extracted, and cDNA was synthesized using a polydT reverse primer. The second strand PCR reaction was performed using a forward primer that anneals in the open reading frame of RFP, and a reverse primer that anneals downstream of the 3' splice site in the 3'UTR. Middle: Gel electrophoresis depicts PCR of plasmid DNA and cDNA, with a shift of the expected size given proper intron/miRNA splicing. Bottom: Sequencing of the PCR products confirmed that the miRNA is properly spliced out of the RFP mRNA transcript (**B**) Bright field (left) and fluorescent (right) images of HEK293T cells used in the above experiment. RFP expression functions both as a marker for transfection efficiency, and signals transcription of the primary miRNA transcript.

## CMV Max-GFP + CMV-dsRed2-miR-10b



## CMV Max-GFP + PGK-*dsRed2-miR-10b*



B

Α



Supplementary Figure 4: PGK promoter is 80% weaker than CMV Promoter. (A) We have compared the strength of the CMV promoter related to the PGK promoter in cotransfection experiments using fluorescence microscopy. While the expression of GFP driven by a CMV promoter is constant in both experiments (compare panel 1 with 3), the expression of dsRed2 included in the pLIFE is much weaker using the PGK promoter (compare panel 2 with panel 4). (B) Quantification of fluorescence produced by these two promoters shows that CMV promoter is at least five times stronger than the PGK promoter, results comparable to those obtained by Qin, et al. 2010 (52).

## **Supplementary Figure 5**



Supplementary Figure 5. Development of nucleofection transfection buffers. We tested 11 electroporation buffers against 8 different pulse codes. 100k HEK293T cells were transfected with 50 ng pmaxGFP plasmid (Lonza) and compared against the SF cell line solution (Lonza) (data not shown). (A) The highest performing buffers were each retested with various permutations of pH and buffer composition to determine optimal transfection conditions. Based on fluorescence and cell survival PBS 1.5% HEPES pH 7.0 and pulse code FF120 (red box) was chosen for the 3'LIFE assay. (B) HEK293T cells transfected with GFP in PBS 1.5% HEPES pH 7.0 buffer and pulse code FF120 performed in 6 replicates. Cells were cultured for 48 hours following transfection, and fluorescence was analyzed using flow cytometer. Light blue line is negative transfection control without GFP. The percentage of transfected cells is consistent between experiments. (C) Transfection efficiency of previous experiment (b).



Supplementary Figure 6. 3'LIFE cloning pipeline. This cloning pipeline was used to clone the 384 3'UTRs, and the miRNAs used in the 3'LIFE assay. 1. Primers used to amplify 3'UTRs from the human the genome anneal in the terminal exon of each gene and 150 nt downstream of the longest 3'UTR annotation in Refseq HG19 annotation. miRNA were amplified using primers that anneal ~200 nucleotides upstream and downstream from the pre-miRNA annotation from miRbase. All primers contain 5' universal Gateway elements to facilitate cloning in pLIFE Gateway compatible plasmids. 2. 3'UTRs were amplified using touchdown PCR cycling conditions (TD-PCR) in 96-well plates and used in BP cloning reaction. BP reactions were transformed in DH5a cells and plated in 48 well culture plates. Screens for successful clones were performed using colony PCR and size based selection for one colony. If first colony was not positive, up to eight additional colonies were picked and analyzed using colony PCR. 3. Successful 3'UTR clones are re-

arrayed into 96-well plates and tested for targeting by each miRNA in the 3'LIFE assay.

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**Supplementary Figure 7.** miRNA delivered using both weak and strong promoters identify comparable targets. (A) Comparison of 87 genes screened in the 3'LIFE assay using pLIFE (strong promoter) and pLIFE-PGK (weak promoter) for targeting by *let-7c* and *miR10b*. The yellow panel highlights the repression from both miRNA delivery methods. (B) Top hits produced with pLIFE compared with hits produced with pLIFE-PGK. Of the top hits produced using pLIFE-miRNA, 77% of them were also repressed using a weaker promoter, but to a lesser extent. (C) Venn diagram showing the overlap between hits produced using both miRNA delivery vectors. 97% of genes were either repressed or not repressed using both vectors. (D) We studied the seed region in

three statistically significant hits detected using the pLIFE-PGK for *miR-10b* that were not targted by pLIFE (middel panel in C). Two of three have a perfect seed element in their 3'UTRs, suggesting that although at a low frequency (1.7%), some genes may exhibit dosage-dependent targeting.

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CLASH 3'UTR Target	Targeting miRNA	Target Region	Interaction Type	# of chimeric reads	3'LIFE Repression Index	3'LIFE <i>p</i> -value
EZH2	let-7a	CDS, 3'UTR	7-mer	4	0.75	<0.01
EN2	let-7e	3'UTR	noncanonical	1	0.77	<0.025
CCND3	let-7b	3'UTR	none	1	0.83	<0.05
FXR2	let-7b	CDS, 3'UTR	none	1	0.85	
HSF2	let-7a	3'UTR (2x)	noncanonical	2	0.85	
SNX6	let-7a	3'UTR	noncanonical	1	0.91	
NUP153	let-7b	3'UTR	noncanonical	2	0.94	
MYC	let-7b	3'UTR	noncanonical	1	1.00	
HES1	let-7b	3'UTR	none	3	1.00	

B

Α

<i>let-7c:</i> l	JGAGGUA	GUAGGUUGL	JAUGGUU
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- *let-7a:* UGAGGUAGGUUGUAUAGGUUGUAUAGUU
- *let-7b:* UGAGGUAGUUGUGUGUUGUGUU

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let-7e: UGAGGUAGGAGGUUGUAUAGUU
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Supplementary Figure 8: Comparative analysis of 3'LIFE with AGO-HITS-CLIP. (A) In 2011, Kudla, et al. (PNAS), developed a method to isolate RNA:RNA interactions using immunoprecipitation approach, followed by ligation of the two complementary RNAs, resulting in a chimeric sequence composed of the two interacting RNAs. Recently, this technique, termed cross-linking and sequencing of hybrids (CLASH) was applied to the AGO protein and miRNA:mRNA interactions (50), providing a potential solution to the issue of identifying which miRNA is targeting the mRNA footprint obtained from original AGO-HITS-CLIP approach. The CLASH dataset was also conducted in HEK293T cells, which provided a complementary approach to cross validate hits obtained from 3'LIFE. We compared our results with this dataset. Unfortunately, of the 272 chimeric reads obtained for *let-7c* and *miR-10b*, only one gene was present in the 3'LIFE library (EIF3A), and the target footprint mapped to the open reading, thus was not comparable to 3'LIFE. However, CLASH did identify 21 genes which were targeted by a family member of *let-7c* or *miR-10b* which were included in the 3'LIFE library. (B) Alignments of let-7 family members shows that these miRNAs share identical seed regions (red box), and diverge by 1-2 nucleotides in the 3' end of the miRNA (yellow boxes). Of these 21 genes, 12 mapped to coding sequences, while 9 mapped to 3'UTRs. Of the 9 overlapping 3'UTRs in the two datasets, 3 of them were significantly repressed in the 3'LIFE (p<0.05). Of these 3, the gene with the highest repression in 3'LIFE, EZH2, was the only gene with a canonical seed target identified by CLASH and had the highest number of reads sequenced by CLASH. The remaining eight genes had either non-canonical, or unidentifiable target sites. The only gene with canonical seed was the top hit in both 3'LIFE and CLASH, and 7 out of 9 CLASH hits have some degree of repression in 3'LIFE, although only 3 significantly. While there may be subtle differences in miRNA targets by closely related miRNA family members, this comparison suggests that binding (as shown by CLASH) is not an accurate proxy for functional repression (as shown by 3'LIFE).

#### Supplementary Table 1: Primers used for cloning

ARTK     NM_001089395     GGTGAGAGTAAAGAGGCTTGA     CCTCACCEGGGGTGTGCC       ARTI     NM_005163     GCCACGGGCGGCGGCTGA     ACACACCTTACACCCTACAC       AIX3     NM_005163     CCTGACGGGCGGCGCTGA     CCTTTACACCTTACGTTAGGTACAGAC       AIX3     NM_001185     CTGACGTGGACCAGTGA     CCTTTACACCTTACAGTAGAGAG       ARNAA     NM_001231     GCAGAATCCGGAAGCATGA     CTGCTCATGTGGACACGGTGAT       APPL2     NM_01312     GCAGAATCCGCAGTCGT     TTTGGATATGTGGGGGGGTAAG       ARID3A     NM_002224     CACATCTACCTCCTGTGTTTTGAGTGGCGGTGAG     AGTCAAATAAATGAATGGCGGGGGAAG       ARID3A     NM_005452     CCACACGTGGTCCTGGTTTGG     TGGAAGGGGGGGGAAG       ARNDA     NM_005452     CCACAGCTTGGCCCTCTG     TGTGATGGGGGGCAACTGA       ARNT     NM_00512     GGTATTGTGGGGGAATA     TACCCTCCCAAAGAGAGCTCCAAGG       ARTI     NM_00512     GGTATGTGGGGGAATATCCAGAGCTA     CAATCTCCACATGGCTCCCAAG       ARTI     NM_00512     GGTATGTGGGGAATTCCAGACGAGCTA     CAATCTCCACATGGCTCCAAG       ARTI     NM_00512     GGTATGTGGGGAATTCCAGAGCTA     CTATTCCCACTGGCTCAAG       ARTI     NM_00512     GGTAGTATGGGGAAATTCCAGAGCTA     CTATTCCCAAGGGGGG	Alias	RefSeq ID	Forward Primer	Reverse Primer	
ANT1     NM_005133     CCCACCGCACCGCCTGA     ACCACACCTTTCCCTTACTGTTCACACC       ANX37     NM_006942     CTGACTGACCCACGGTA     CCTTTACACCTCTCCTTACTGTCACACC       ANX47     NM_001356     CTGGCTATTGTGGGCCAGTAG     CTTTACACCTTACACTTACAGGTAGAGGA       APPL2     NM_000383     TTCTGGGTCTTACCTTTGTGGCCAGTAA     CTACTCACTTACTGTGTGCGCAGGAGTA       ARD3A     NM_00224     CACATCTACACTCACATAATACTCGTTTGTGTCTACTTGTGTCGCGGGGTGAGG       ARD3A     NM_005244     CACATCTACCTCACATAATACTCGTTGTGTGTCTTTATTGGTCGCGGGTGAGG       ARD3A     NM_005244     CACACTCACTCCCCCTTTA     TGTAGAGGGGTGGCGCACGGC       ARD3A     NM_005244     CACACTGGTCCCCCTTTG     TGTAGAGGGGTGGCCACGG       ARD3A     NM_005244     CACACTGGTCCCCCTTG     TGTAGAGGGGTGGCCACAGG       ARNT     NM_104315     CGACTTACCAACTGGTCACGCCTTA     CAAGGTTGCCACAGGGGCACAGG       ASSL1     NM_003170     TGGTTAGGGGGCACTGGCA     CAAGGTTGCCACAGGGCCACCCC       ASSL1     NM_003170     GAGGACCTGGCTA     CAAGGTTGCCACAGGG       ATTS     NM_003171     GAGGACCCGTAGCTGCTA     CAATTCCCACTGAGGCACAGG       ATTS     NM_00174     ACAGGACCCGTAG     CTATACCACTGCAAGGCGGACTACACAGG	ААТК	NM 001080395	GGTGAGAGTAAAGAGGCTTGA	CCTCCACCGGGGTGTGCC	
AXX3     NM_006432     CTGAACTGGACCACGTGA     CCTTTACACCCTCCTTGTGACGAC       ANXA7     NM_00038     TTCTGGCTATGTGGCCAGTAG     CTGAACCTTAAATTTGCTAAGGTGATGTATA       APPL     NM_00038     TTCTGGGTCTTACCTTGTGACATCTGTTTA     ATTTGGAATTAAAAGGCAAGTTTATTCTAATT       APPL2     NM_00038     TTCTGGGTCTTACCTGTGTGCATA     CTACTCATGTTGACTGGAAGGGTGTTTTTTTGA       ARIDA     NM_00522     CACATCTACCTCAATTACTCGTCATT     AGTTGATGGCTGGCGGGGTGAGAG       ARIDA     NM_00545     CACCAGCTGGTCCCTCTG     TTGAGATGGCCTGGCGGGGTGAGAG       ARNJ     NM_00512     GGCTTACGCACTGGTGGGGGAGATA     CACGGTGGCCCATGG       ASCL1     NM_00512     GGGTTGCCCTGTGGGGGAGAT     TACATAAGGCCCCAAGCA       ASTI     NM_00512     GGGTTGCCCTGTGGGGGAGAT     CAAGGTGCCCCAAGCA       ASTI     NM_00512     GGAGCCCCTACGACTGA     CAAGTTCTCACCTAGGCCCCAAGC       ATF3     NM_00512     GAGGACCCGTACGACTGA     CTTTACAGAGACGCCCAAGCACGAT       ATF3     NM_00522     GCAACAAAGGCACCGTAC     CATCTCCTCTGAGCCAGGGGGGTTTACACCT       ATF3     NM_001268     GAGGACCCTGAAGCAGATCTACAAG     CTCTAGAGCAGGGCCCTTAGACCCTGA       ATTNU     NM_00282     GCACCAACGACAGCTGCTA </td <td>AKT1</td> <td>NM 005163</td> <td>GCCAGCGGCACGGCCTGA</td> <td colspan="2">ACACAGCCTGTCCCCAAAC</td>	AKT1	NM 005163	GCCAGCGGCACGGCCTGA	ACACAGCCTGTCCCCAAAC	
ANXA2     NM_00136     CTGGCTATTGTGGGCCATAG     CTGAACACTTAAAATTGCTAGGTAAGTAATTA       APPL2     NM_000038     TTCTGGGTCTTACCTTGTGACTCGTTTA     ATTGAATTAAAGGCAAGTTTAACTGATTT       ARNDA     NM_018317     GCAGAATCCGAAGCATAA     CTACTCACTGGAACTATATTTGGCCAGTCATG     CTACTCACTGGAACTGGTTTTGACTAGGAAATGCAAGGCAGTGGCGCAGTGG       ARNDA     NM_005242     CACACTCTACTCACTCAATTGCTCGCCTT     TTGGAAAGGCCTGGCCACTGG       ARNDA     NM_005242     CACACACTGGTCCCCTCG     TTGAAGAAGGCCTGGCCACTGG       ASCL1     NM_005130     CGACTTACCAACTGGTTCTG     TGGATGGGACTGGCCAATGC       ASCL2     NM_005130     TGATTGTGCCTTGTGGTGAGATA     TACACCACCAAGGGCTCAA       ATF3     NM_005130     TGATTGTGCCCTTGTGGTGAGATA     TACACTACCAAAGGGCTCCAAGGACTAA       ATF3     NM_005130     TGCAGTAAAAAGGACATTGCAGAGCTTA     CATATCCACTCTGACGCCAAAGAATGACTACAAA       ATF3     NM_015338     TGTATTGCGATGCCCCTAG     GTATTTTCAGTAAGGAAGTTCAACAAA       ATF3     NM_01674     CACCAAACGACTGTGACACCTA     GTATTTTCAGTAAGGAGGACTTCACAAA       ATF3     NM_01785     CACCAAACGCCGTAA     TTTGCATAGGCTTGCCAACTGGCCTCCAAAGAATGACTTTCAGGAAGACTTCAATAAGGACTTGAAGTAAATAGGAGGCTGCCACTA       ATF4     NM_0104282     TAACCCAG	ALX3	NM 006492	CTGAACTGGACCACGTGA	CCTTTACACCCTCCTTAGTGTCAGAC	
APE     NM_00038     TTCTGEGETCTTACCTTGTGACATCTGTTTA     ATTTGAATTAAAAGGCAAGTTAACTTACTTATTAG       ARD1A     NM_018373     GCAGAATCCGAAGCATAA     CTACTCATGTTGACTGGACAGTGATG       ARD1A     NM_00522     CACATCTACCTCAATTAACTCGATGCCATG     TTTTGGATTAGCTGAAATAAATGACAGGGT       ARD3B     NM_00522     CACATCTACCTCAATTACCTCAATTACTGCTTGCCTTA     AGTTCATTGGCTCGCGGGGGGAAG       ARNT     NM_17822     CTACATATGTTTCCCCTCTT     AGTTCATGGCAGCGGGGGTGAGG       ARNT     NM_005170     TGGTTAGGGGGCTACTGA     CGAGTGGCACTGGCCAATGG       ASCL1     NM_005170     TGGTTAGGGGGCTACTGA     CACAGCTAAGCACTGGCTA       ASTI     NM_005170     TGGTTAGGGGGCTACTGA     CACAGATAAAAGAGGAACTTGCAGAGTT       ASTI     NM_005170     TGGTTAGGGGGCTGCTA     CACAGATAAAAGAGGAACATTGCAGAGT     CACAGATCAAAAGAGGGACCTGTA       ATFI     NM_005171     GCAGGCCCTAGCTGA     CTCTACAGCTTTTAGGCAGGGGGTTCACCTT       ATFIS     NM_005273     CACAGATGAGCGCTGTA     CTCTAGCAGGCCTGACAGG       ATFIN     NM_002882     GGAACCTAGTAGCTGAT     CTCTCAGCATTGAGGGGGGTTACCCTT       ATRN     NM_002873     CACAGACAGAAGTGTGAA     CTCTCAGCATTGAGGGGGGTTACCCTT       ATRN	ANXA7	NM 001156	CTGGCTATTGTGGGCCAGTAG	CTGAACACTTAAAATTTGCTAAGGTAGTAG	
APPL2     NM_018371     GCAGATICGGAAGCATAA     CTACTCATGTTGACTGGATGTTTTTTGA       ARIDIA     NM_139333     TGATGTACTGTTTTGATTGGCCATGCATG     TTTTGGATATAGTAAATAAATGACAGGGT       ARID3A     NM_005242     CACATCTACCTCAATATAACTGGTTGCTTA     AGTTCATIGGCCCGCGGC       ARID3     NM_005243     CACATCTACTCAACTGGTTCCCTCTG     TTGAAGAAGGCGTGGCCAATG       ARNT     NM_178427     CTACTACTGTTCCCCCCTTTTCAGAATA     GCACATGCCTCCA       ASCL1     NM_005130     GGATGTGGCCACTGGGCCAATGG     CAAGGTGCCCAATGGCCTCCA       ASL1     NM_005131     GAAGGATCTTTTGCGAGATA     TAACCTCCCAAAGGGGTTCCAAGTAA       ATF3     NM_005131     GAAGGATCCTTTGCGTGAGATA     CTATAAGGTGCCCAAAGGGGTTCCAAGTAA       ATF3     NM_001674     ACAGATAAAGAAGGACATTGCAAGGACTA     GTATTTTCAGAGAGGACTACAGA       ATFS     NM_001674     ACACAAAAAGCTGGAAGACATTGCAAGGACTA     GTATTTTCAGAGAGACAACTAGGGGTTACACAA       ATAU     NM_01288     GAAGGACCCGTAAGCTGATA     GTATTTTCAGAGAGACAACTAGGGGGCAACTAAGG       AGTAGTAGAGAGAGATATTTCAAAGGAGCTGAA     CTTAAAGCTGCCCCCCAAACTAAGGGCCTAAGT     CACCAAACAAAGCGCCTTAAGTCTCGAAGACGCTGA       ATAU     NM_002828     GACGACCCCGTAAGCTGGA     CATTTAAGCTAGAGGACAATTGGCCCCCCCCCCAA <tr< td=""><td>APC</td><td>NM 000038</td><td>TTCTGGGTCTTACCTTGTGACATCTGTTTA</td><td colspan="2">ATTTGAATTAAAAGGCAAGTTTATCTAATT</td></tr<>	APC	NM 000038	TTCTGGGTCTTACCTTGTGACATCTGTTTA	ATTTGAATTAAAAGGCAAGTTTATCTAATT	
ARIDIA     NM_139135     TCATGTACTGTTTTGATTGCCCATCATG     TTTTGAATATATAATAATAATGACAGGGT       ARIDIA     NM_005224     CACATCTACCTCANATAACTCGTGCCTTA     AGTTCATTGGCTCCCCCGGG       ARIDIA     NM_178427     CTAACTAGTCAATTAACTCGTTGCCTTA     AGTTCATTGGCTCCCCCGGG       ARIDIA     NM_109120     CGACTTCACCAACTGGTCCTG     TTGAAGAGCGTGCCCATGG       ASCLI     NM_00130     TGGTTAGGCGGCTACTGA     CAACGTGCCCAAAGAAGAGAGCTCCCAAGCAAAGAAGAGCTCCCAAGTGAA       ASLI     NM_001338     TGTATTGTGCCCTTGTGGTGGGAGAT     TAACCTCCCCAAAAGAAGAGAGCCCCAAGT       ASTI     NM_0013383     TGATGTGCCCAAGTGCCAAAGAGAGCCCCAAAGAAGAGGGCTCCAAGTGCCCAAAGAAGAGCCCCAAAGAAGAGCCCCCAAA     CTATTCCCAAAGGAACTACTACAAA       ATFS     NM_0012058     GAGGACCCGTAGCTAG     CTACTACCACCGAAGTACCTACAACAA       ATFN     NM_002293     CACCAAACACGCGTAG     CTACTACGACCACTAGCTTTGCACTAGACCACAAA       ATNN     NM_002293     CACCAAACACGGTAGCTTTACAATTA     TTGTAGGATACTTAGACCAACAAAGCCGGCTAGTTGAA       BAG3     NM_002293     CACCAAACACGGTAGCTTAAGGCGGA     CATTTAACCATTGAGCGGGGCTAGTTGA       BAG3     NM_002420     CACCAAACACGCGTA     CATTTACAATTGGGCGGCGCTAGTTGA       BAG3     NM_002420     CACCAACACGCGTA     CATT	APPL2	NM 018171	GCAGAATCCGAAGCATAA	CTACTCATGTTGACTGGAAGTATTTTTTGA	
ARID3A     NM_005242     CACATCRACTCACCTCAGTTACTCGTTGCCTTA     AGTTCATTGGCTCGCGGG       ARID3B     NM_005465     CACCAGCTGGTCCCTTG     TTGAAGAGGCGTGGGTGAGG       ARID3A     NM_005455     CACCAGCTGGTCCTGG     TTGAAGAGGCGTGGGTGAAGG       ASCL1     NM_005130     TGGTTAGGGGCTCTGG     GCAGGTGCCCATAGC       ASCL2     NM_005131     GGATGTCACCAACTGGTGGGAGATA     TAACCTCCCAAAGGCTGCCAAGGC       ATF1     NM_005131     GAAGGATCTTTATTCCAATAAAGTGTTTG     TCATAAAGTGCTGCCCAAGGCCAAGGA       ATF3     NM_015338     TGTATTGGGGCTACTGA     CAACGTACCTCAAGGCTGCCCAAGGCAAGCAA       ATF3     NM_01567     ACAGGATCAAGGAATTACATTGCAGAGCTA     ACTTACCCTCAAGGCCCCAAG       ATF3     NM_01568     GAGGACCCGTAGCTGCTA     GTATTTCCAATGGCAACCAGACTTGCTTGATGTGGGGTTTCACCTT       ATOH7     NM_145178     TTCCAACTGGCAACTAG     TTCTCATCAGCACCAGAACTAATGCTGAAGCACACGAACCAGAACTAAGGG       BAG2     NM_002281     TAACCCAGCACCAGCAGTTCATAT     TTTGTATCAATAGGACCAGACTACTTTCAACTGAG       BAG2     NM_002281     TAACCCCAGCAGCAGTTCTTAAGCTCAATA     TTTGAACTCAGCCCCTA       BAG2     NM_002281     TAACCCCAGCAGCAGTTCTTAAGCTCCATTTTCAATGAGGCCTATATATA	ARID1A	NM 139135	TGATGTACTGTTTTTGATTGGCCAGTCATG	TTTTGGAATATAGTAAATAAATGACAGGGT	
ARID3B     NM_D06465     CACCAGCTGGTCCCTCTG     TTGAAGAAGGCGTGGGGTGAAG       ARNT     NM_178427     CTAACTATGTTTCCCCCCTTTTCAGAATAG     AGCCAAGATCGTCGCCATGG       ASCL1     NM_D0510     TGGATTGGACKTGGCCCATTGG     TGGATGGACKTGGCCCATGGC       ASKL1     NM_D05170     TGGTTAGGCGGCTACTGG     CAAGGTCCCCAAAGGACGCCCCAAAGCAAGGCCCCCAAAGCAAGGAGCTCCCAAGTGAAAGAAGGACCTCCAAGTGAAAGAGAGCCCCAAAGCAAGGAGCCCCAAAGCAAGGAGCTCCCAAGTGAAAGAGAGCCCCAAAGCAAGGAGCCCCAAAGCAAGGCCCCAAAGCAAGGCAGCTCCCAAGTGCAAAGGAGCACCCCAAAGGAGCCCCAAAGCAAGC	ARID3A	NM 005224	CACATCTACCTCAAATAACTCGTTGCCTTA	AGTTCATTGGCTCCGCGG	
ARNT     NM_179427     CTAACTATGETTCCCCCCTTTTCAGAATAG     ACCAAGATCGGGCCATGG       ASCL1     NM_004316     CGACTTCACCAACTGGTTCTG     TGGATGGGGCATGGC       ASCL2     NM_005130     TGGTTAGGGGCTACTGA     CAAGGTGTCCCAATGGCTCC       ASSL1     NM_005131     GTGATGGGGCATACTGA     CAAGGTGTCCCAATGGCCCCAGGCTAC       ATF1     NM_005171     GAAGGATCTTTATTCCAATAAACAGGACATTGCAGCACT     CCAAGGTGCTGCCCAAGGCAACGAA       ATF3     NM_005174     ACAGGATTAAAACAAGGACATTGCAGGGCTA     CAATTCCCACTGCAGGCACCTAG     TCTCATCAGGACCACGAGATTCACTT       ATNP     NM_102058     GAGGACCCGTAGCTGCTA     GTATTTTCAGTAGAGACTGACCCAAGA     ATTACCCACAGCACGCACTTGA       ATNP     NM_102393     CACCAACAGCAGTTGTAA     TTCTCATCAGGACCACGGGGCTATT     ATTACCCAGGACCCGGCACCGTA       BAG2     NM_004281     TAACCCAGCAGCAGCTTAA     CATTTCTCTTGAGGACACGATTATCATAGA     GCACAAATTCATTCGGAAATGA       BAG2     NM_004281     TAACCCAGGCAGCCTTAAGTTCTGAAGCGGA     CACTTATCTTTCAGAAGGACCCTTTAGTTCCCCCCA       BCCIP     NM_004281     TAACCCAGGCAGCCTGA     CACTTATCTTATAGGGCTCTCCCCA       BCCIP     NM_0131450     AGGGGACGCAGCTTCAAGTTCTGAAGCCCAGGACCACCCCGA     CCCCCCTTACGTTCAGGATAGACCACAGACCCCCCCCA	ARID3B	NM 006465	CACCAGCTGGTCCCTCTG	TTGAAGAAGGCGTGGGTGAAG	
ASCL1     NM_00316     CGACTTCACCAACTGGTTCTG     TGGTTAGGACGCATAGC       ASCL2     NM_003170     TGGTTAGGGTGCTGCTGA     CAAGGGTCCCAATGGCTCC       ASSL1     NM_015338     TGATTGGCTTGGCTGGGAGAT     TAACCTCCCCAAAGAGAGCAACTGCCAAGAGA       ATF3     NM_01573     ACAGATAAAGAGAAGAACATGCAGGAGTA     GTATTGTGGCTGCCAAGTGAAGAGAACTGCCAAGTGCAAGAGAACTACCATCTGGAGGCCCCAAGTGAAGAGAACTACCTAGGATGCCCCAAGTCAACAGA       ATF5     NM_012068     GAGGACCCGTAGCTGCAA     GTATTTTCAGGAAGACTACTACAA       ATN0     NM_012088     GAGACCCGTAGCTAA     GTATTTTCAGGAAGTACTTCAACAGACTACTTGAGCAGGCTTACAA       ATN0     NM_002821     CACCAACAGCACGTTAA     TCTCAGAGACTCATGCAGCCGGCTATTTAGAGCAGACTCATTGAAGCCCGGGCTATTT       BAG2     NM_002821     CACCAACAGCAGCAGTA     CAATTCATCTCATGCGGGCTATTTGCACCCGGGCTATTTGGAGCGGGCGATAATTTGAAGCCTCATTCCACCCCCCAAGCCGGTA       BC111     NM_018010     TCGCAGAGCCCTTAGGTTCTGA     CTCTCTTAAGCTCTAGCGGGAATAATTCACCCCCCCTA       BC111     NM_0180191     TCCCCAAGCGGCGCTGA     ACCTGAGCGGAAAGGCAAGTACTTAGCCCGGGCAAATTCAGA       BC111     NM_001918     CAGCTCCCCCCAAAGCCGCGTA     CACCCGTAGGCAAAGCGC       BC111     NM_001918     CAGCTCCTCAGCCGTA     ACCTGAGCGCGAAAGGCACGTA       BC121     NM_001918 </td <td>ARNT</td> <td>NM 178427</td> <td>CTAACTATGTTTCCCCCCTTTTCAGAATAG</td> <td>AGCCAAGATCGTGCCACTG</td>	ARNT	NM 178427	CTAACTATGTTTCCCCCCTTTTCAGAATAG	AGCCAAGATCGTGCCACTG	
ASCL2     NM_005170     TGGTTAGGGGGCTACTGA     CAAGGTGTCCCAAATGGCTCC       ASXL1     NM_005171     GAAGGATCTTTATTGCCATGGGGAGATA     TAACCTCCCCAAAAGGAGCCCCAAAGGACATTA       ATF1     NM_005171     GAAGGATCTTTATTCCAATAAAAGTGTTTG     TCATATAAGGAGTGAGCCCCAAAGA       ATF3     NM_001674     ACAGATAAAAGAAGGAACATTGCAGAGCTA     ACTATCCCACATGGATGCCCCAAA       ATF5     NM_012068     GAGGACCTTTATTTATTCCAATAAAAGTGTTTG     GTATTAAGGACTAGGACCCCTAA       ATW1     NM_02293     CACCAACAGCAGCACCTAA     TTCTAAGAGATACTTGAACGAGATACTTACAA       BAG2     NM_002821     TAACCCAGCAGCACCGTA     CAATTCTCTCTTGAGCGGGGCTATT       BAG2     NM_002821     TAACCCAGGAGCACCGTA     CAATTCTCTCTTGAGCGGGGCTAATTGA       BAG2     NM_002821     TAACCCAGGAGCACCGTA     CATTAAACTCAACCCAGCGGGCTATTGA       BAG2     NM_002821     TAACCCAGGAGCACCTAA     CATTAATACTAATGGGCCACCTCACCCAA       BCCIP     NM_03810     TCGCTCTCTGAGCAGATTCAA     CATTAAACTCAACCAGGGGGATAATTCAG       BCL11     NM_03112     TCACTCTTAGGGGAATGCA     CACCAGATCAAGGGGGGATAAATTCAG       BCL211     NM_001312     CACCCATAGCGGAAAGCATTA     TAAGCAGGGGGATAAATTCAG       BLC12     NM_001312	ASCL1	NM 004316	CGACTTCACCAACTGGTTCTG	TGGATGGGACTGGCCATAGC	
ASXL1     NM_015338     TGTATTGTGCCTTGTGGTGAGATA     TAACCTCCCCAAAGAAGAGAGCCCCAAGGTATA       ATF1     NM_001512     GAAGGATCTTTATTCCAATAAAGTGTTTG     TCTATAAGGTGCTGCCAAGGTAAGAGAGAACTACTACAAAA       ATF3     NM_001574     ACGATACAAGAGAGAGACTTTGCGAGGCTT     ACTATCCCCATCTAGTGATGCCCCAAGT       ATF3     NM_001574     ACGATACAAGAGAGAGACTTCTAGCAGGCT     GTATTTTCAGTAGAGCCCCAAGTACCACATA       ATF0     NM_002893     CACCAACAGCAGTGTAA     TCTCAGAGGCAGCTGTAAGTCTCTTGAGCCGGGCTATT       ATNN     NM_002892     GCAACAAAATGCTGCAAGAGCAGATTCAATTA     TTTGTATACAATAGGCCTTAAGCCCCCTA       BAG3     NM_002893     GTCTGTTCCCCCAGTATTAGAAGCAGATTCAATTA     CAACTTATCAGACGCCTTATCCCCCAGGATATTTCAAGTGTGGCCCTTATCTCCACCCA       BCCIP     NM_018014     TGGAGGACAGATACTTCAA     CACCCAATGCTGTGA     CACCAATCTATATTAGACCACGAG       BCL11A     NM_0018014     TCGAGGGCAGCTG     CACCAATCTATATATAGCCCACGAG     BCL11A       BCL11A     NM_0018014     TGGAGGCAGCTGTA     TCACTTACTGAGGCTAAAGTCACACGAG       BCL11A     NM_0018014     TCGAGGCGCCTTA     TCACCGTACAGCTGGGTAAAGTCACACGAG       BCL11A     NM_0018014     TCGAGAGCCCTTA     TCACCGTACAGCTGGGTAAAATTCAG       BCL11A     NM_0018014	ASCL2	NM 005170	TGGTTAGGGGGCTACTGA	CAAGGTGTCCCAATGGCTCC	
ATF1     NN_005171     GAAGGATCTTTATTCCAATAAAAGTGTTTG     TCATAAAGTGCTGCCAAGTCAACAGA       ATF3     NN_012068     GAGGACCCTACGTGCTGCTA     GTATTTCCATAGTGATGCGCCACCTA       ATF3     NN_012068     GAGGACCCTACGTGCTGCTA     GTATTTTCCATAGGAGAGGGGCTTCACCTT       ATN1     NN_002373     CACCAACAGCAGGTGTAA     TCTCATCAGCTTTTGAGCCAGGACTACTACAA       ATXN2     NM_002381     TAACCCAGCAGCCCGTA     CAACAAATGCTGAAAGCGAGATTCAATTA       BAG2     NM_002381     TAACCCAGCAGCCCGTA     CAATTTCTCCTTCAGCCGGGCTTTT       BA228     NM_013420     AAGTGGCACAGAATGCTTAAAGTAGCGGA     ACTTAAACTCACCCCTTATTTCCAACCA       BCL11     NM_010141     TCGAGAGCCCTCTAAGTTCTGA     TCTCTTACTGAGTGGGCACCTG     AGAGTCCCACAGGCGCG       BCL211     NM_00134250     GGAAGTTAAAGAGAATGA     TCACTCTCAGCGGAGACCTG     AGAGTCCCACAGGCACACACAG       BCL31     NM_001342530     GGAAGTTAAAGGAATGTATTGAACATGTA     TAAGTGTAAAGAGGAAATTCAAATACTGAGGG       BHLHB9     NM_001342     CAAGCCTCCCCAGCCCTAA     TAAGTCCTAGAGGAAAGGCACTTCAA       BHLHB9     NM_001342530     GGAAGTGAAAGGCATTATTGAAACATGTA     TAAACAAGTAAAATTAGGGCAACTCTCAA       BHL1     NM_00134250     GGAAGTGTAAGAGAGCTTA     T	ASXL1	NM 015338	TGTATTGTGCCTTGTGGTGAGATA	TAACCTCCCAAAAGAAGAGCTCCAAGTATA	
ATF3     NN_001574     ACAGATAAAAGAAGGAACATTGCAGAGCTA     ACTATCCCATCTAGTGATGCCCCCAAA       ATF5     NN_012068     GAGGACCCGTAGCTGCTA     GTATTTTCAGTAGAGATGGGACTCATTA       ATH5     NN_002873     CACCAACAGCGCTAG     TCTCAGCTTTTTAGAGATGGGACTCATTA       ATN0     NN_002828     GCAACAACAGCGCACCTAG     TCTCAGAGTACCTGAAGGACTAGTTACATTG       BAG3     NN_002821     TAACCCAGCAGCACCACTA     CAATTATCCTCTTCTGGGGGCATT       BAG3     NN_002821     TAACCCAGCAGCACCATA     CAATTAAGGACTAGTTACATTGA       BAG3     NN_002831     TAACCCCAGCAGCATA     CAATTAATGCCTTTAGTGTCTCTCTTGGA       BAG2     NM_002831     TAACCCCAGCAGCATA     CACCAATCTATATAGGACTTACTTCACAGCGGGGGCT       BAG2     NM_00380     AGTTGGACAGATTATGAATA     CACCCAATCTATATAGGACTTACTTCACACG       BCL11     NM_0018014     TCGAGAGGCAGCTG     AGAAGTCCCAAACACAG       BCL3     NM_00178     AGCTCCTCAGAGGCAGCTG     AGAGTCCAAAGGGAAAGCTCAACAG       BCL4     NM_00174     CAAGCCTCTCAACCCTA     TAAGTGTTAAGGGACAACTCTAGTTAAATTCAG       BHHE92     NM_001214     CAAGCCTCTCACCCCTA     ATGTCCAGAGGAGACTCTAATTT       BMP1     NM_001214     CAAGCCTCCTCACCCCTA	ATF1	NM 005171	GAAGGATCTTTATTCCAATAAAAGTGTTTG	TCATAAAGTGCTGCCAAGTCAACAGA	
ATFSNN_012068GAGGACCCGTAGCTGCTAGTATTTTCAGTAGAGATGGGGTTTCACCTTATW1NN_020273CACCAACAGCCACCTAGTCTCATCACTTTTTTGAGGAACTACTACAAGGBAG2NM_002821CACCAACAATGCTGAAAGCAGATTCAATTATTTGCATCACCACACACAAAGGGBAG3NM_002821TAACCCAGCAGCACCTACAATTCCTCTTGTAGGCCGGGCTATTBAG3NM_002821TAACCCAGCAGCACCTACAATTCCTCTCTTGAGCCGGGCTATTBAC8NM_002821TAACCCAGCAGCACCTACAATTCCTCTCTTGCAGCCGGGCTATTBAC9NM_002821TAACCCAGCAGCACCTACACTAAACTCACCCCTCTCCCCCCABC111NM_018014TCGAGAGCCCTTAAGTTCGACTCTTTAACGATGGGCCTCTGGBC1211NM_001919TCACTCTTCAGTGGGAATGATCACCGTACAGGTGGAAAAATTCAGBC1211NM_001919TCACTCTCCAGCAGAAGCACTATAAGCGCTAACGCGCBHHB9NM_001142530GGAAGTTAAAGAGATTATTGAAACAATGTATAAGCGTAAAGAGGCAAGCCTCAABC101NM_001142530GGAAGTTAAAGAGATTATTGAAACAATGTATAAACAGGTAAAATTAGGGCAAAGCCTCAABH1H89NM_001142530GGGATGTGGGTGCCCCTATAAACATTAAAAATTAGGCTTATTAAATTATTTBM14NM_00112CAAGCCTCCTCACCCCTATAAACATTAAAATTAGGCTATTAAATTATTTBM14NM_001200GGGTTGGGTGGCCCCTATAAAACTTACAAACTTAACTTGCCCAAACATTAAATTATTTAT	ATF3	NM 001674	ACAGATAAAAGAAGGAACATTGCAGAGCTA	ACTATCCCATCTAGTGATGCCCCAAA	
AT0H7NM_145178TTCCAGATGGCCACCTAGTCTCATCAGCTTTTTGAGGAACTACTACAAATXN2NM_002973CACCAACAGCAGTTGTAATCTCAGAGATACCTTGAACCAGAACTAACGGGBAG2NM_004281TAACCCAGCAGCAGCGTATCTTGAGACTACCTTGAACCAGAACTTTTGABAG3NM_004281TAACCCAGCAGCACCGTACAATTCTCTCTTGAGCCGGGCCTATTBAG2NM_013450AAGTGGACAGATACTTTCAAAGTGGAGCTGAACTTTAACTTCACCCTCTTCCACCCABCCIPNM_018014TCGAGGACCCTTAAGTTCTGACCACCATCTCTATATTAGCCTTATTCCACCABCL11ANM_018014TCGACGAGGCGCGGAAATGATCCTCTTCTGAGGGGGATAAATTCAGBCL3NM_001919TCACTCTCCCAGGAGGCGCGAGAGTCCCAGGGGGATAAATTCAGBCL3NM_001196CTCCCCCAAGGCTGCTGAACCTAGCCTACCGGGGAAAAGGCCACABCL3NM_001142530GGAAGTTAAAGAGGATTATTGAACAATGTATAAGCAGGAAAAGGCCAAGTCTCAAABMHHE9NM_001214CAAGCCCCCTCCACCCCTATAAACAAGGAAAACTCTATACAGTTAAAAATABM11NM_005180ATCAGCAACTTCTTGGTGGTGTCGGCTATCAACAAAGGAAAACTCTTAACAATTTTBMP6NM_00129GATGGGTGCGGCGCGCGCATCTCTGCATCAAAAAACTATCCCCCAAAAAATAACTTGCCTCCAACAACTCTACACCBMP6NM_00129GATGGGTGCGGCGCGCAATCTCTGCGCTAAAAAAACAATAACTTGCCTCCAAAAAAAA	ATF5	NM 012068	GAGGACCCGTAGCTGCTA	GTATTTTCAGTAGAGATGGGGTTTCACCTT	
ATXN2   NM_002973   CACCAACAGCAGTTGTAA   TCTAGAGATACCTTGAAAGCAGATACTTAAGGG     BAG2   NM_004282   GCAACAAATGCTGAAAGCAGATTCAATTA   TTTGTATATCAATAGGACTAGTTACTTTGA     BAG3   NM_004282   GCAACAAAATGCTGAAAGCAGATTCAATTA   CATTCATCTCTGTAGCCGGGGAGTATT     BAG3   NM_004280   AAGTGGACAGATACTTTCAAAGTGAGCTGA   ACTTAAACTCACCCCTCTATTCCACCCA     BC111   NM_013014   TCGACGCCCTTAAGTTGTGA   CACCAATCTATATATAGCCTTATTCCACAA     BC111   NM_0101191   TCACCTCTCAGTCGGAAATGA   TCACCGTACAGGGGAGTAAATTCAG     BC1211   NM_00114   TCGACGCAGCTG   AGAAGTCCACAGAGGCCGC     BC1211   NM_001142530   GGAAGTTAAAGAGATTATTGAAACAATGTA   TAAGTGTTAAAGAGGAAAAGGCAAGCTCAA     BHLHB9   NM_001142530   GGAAGTTAAAGAGAACTTATGAAACAATGTA   TAAGTGTTAAAGAGGAAAAGGCAAGTCTCAA     BHLHB9   NM_001714   CAAGCCTCACCCCTA   TTAAACAAGTTAATGGGCTACTTCTAATT     BHLB   NM_001714   CAAGCCTCACCCCTA   TGACTTACCAAACAACATTATT     BMP4   NM_001200   GGATGTGGGTCGCGCTA   TACTTCCCTAAACAACTTAACCACAC     BMP4   NM_0012120   GATGGGTGGACGCCCTA   ACTTCAACACCTTTATATATACCCACAC     BMP4   NM_001229   GATGGGTGGACGCCCCAT   ACTTTCCCTAACCACCACCCCCCCCCC	ATOH7	NM 145178	TTCCAGATGGCCACCTAG	TCTCATCAGCTTTTTGAGGAACTACTACAA	
BAG2NM_004282GCAACAAAATGCTGAAAGCAGATTCAATTATTTGTATATCAATAGGACTAGTTACTTTGABAG3NM_004281TAACCCASCACCGTACAATTCTCTTTGACGCGGCGCTATBA228NM_013450AAGTGGACAGATACTTTCAAAGTGAGCTGACATTCATCTTTGACCCGGGCTATTBC111NM_013801TCGAGGCCCTTAAGTTCTGACACCAATCTATATATAGCCTTATTCCACABCL11NM_00111TCACTCTTCACTCGGAAAATGATCACCGTACGGGGCAGCAGCGBCL21NM_001178AGCTCCAGGAGGCAGCTGAGCAGGCCAGAGGGCAGCACACAGGBCL3NM_001176CTCCCCCAAGCCTGCTGCAACCTAGCTCACTCTCTCTCTCAAAAGCGCCBHLB9NM_0011203GGAAGTAAAGCAATTATGAACAATGTATAACGTAAAGGGCAAAAGCCAAGCCBHLB9NM_0011203GGAAGTAAAGGCAATATGGAACAATGTATAAACAAGTAAAATGAGGCTACTTCTAATTBIC01NM_001214CAAGCCCCCTCACCCCTAATGTCCAGTGAAAAGCCAAATATATTTBM11NM_001200GGGTGTGGGGTGTCGCTATCACCTATCAAATAACTTGCCCTGCCCGCAAATTTTGCATCAACAACTCTTACACCCBMP6NM_00129GATGGTGAATCCCAAGATGGCAAAATCTGGATGTGATATAATCACACTTTACCCCBMP81NM_001299GATGGTGAATCCCAAGATGGTAAAATCTGGATGTGATATAAACAAAGGTAATTAACCACCTTTACCCCBMP81NM_003972CCTGGAAAATTTATGCATCTCCAAGAAATTACAAGGAAACACAAAAGGTAATTAACCACCTTTCAAAAAAAA	ATXN2	NM 002973	CACCAACAGCAGTTGTAA	TCTAGAGATACCTTGAACCAGAACTAAGGG	
BAG3NM_004281TAACCCAGCAGCACCGTACAATTCTCTCTTGAGCCGGGCTATTBA228NM_013450AAGTGGACAGATACTTTCAAAGTGAGCTGAACTTAAAACTCACCCCTCTCCACCCABCCIPNM_0138450GTCTGTTTCCCCCAGTATTAGAATACACCAATCTATATATAGCCTTATCCCACABCL11ANM_018014TCGAGAGCCCTTAAGTTCTGATCTCTTACTGATGGGCCTCTGGBCL21NM_001191TCACCTTTCCGCTGGATGGATCACCGTGCACAGGTGGACACAGBCL3NM_005178AGCTCCAGGAGGCGGGACCTAGCCCGACAGGGACACACGBCL4NM_001142530GGAAGTTAAAGAGCTTATTGAAACAATGTATAAAGCAGAAAATTAGGGCTACTTCAATBHLH82NM_001142530GGAAGTTAAAGAGAATATTTGAACACATGTATAAAGCAAGAAAATTAGGGCTACTTCAAATBHLH822NM_001142530GGAAGTTGAGGGAGCCCTTATAAAGCAAGAAAATTAGGGCTACTTCAAATBM1NM_001142CAAGCCACCTCCTCACCCCTAATGTCCAGTGAAGACCTTCTTTAAAAATABM1NM_001200GGGTTGTGGGTGCCGCTATGACTTAACAACATAACTTAGCCACATTTTBMP2NM_001218AAGAGCTTGTGGATGCCCACTAACTTTGCATCAACACTTAACCACBMP81NM_001218AAGGCTTGTGGTGCCCACTAACTTGCATCAACACTTTAGCCTCCAAAAAAAABMP81ANM_00299GGATGTTGGGTGCCCCATAACTTGACACAGAGCTCCACTTTAGCCBMP81ANM_000393GGACACAATTACAACTAAAAATATATCTAACAAAGCAAGACTCCACTCTCCAAAAAAAAABTAC1NM_000393GGACACAATTACAACTAAAAATATATCTAACAAAGCAAGACTCCACACTCTCCAAAAAAAAABTAC1NM_000393GGACACAATTACAACAAAAGGGAGGGAGGAAAATTACTGGGGAGCAGAATTACACCACGGAAGGCTCACCTTGABTAC1NM_0012393AATGGGCAGCACACTCAAAAAAAATATCCAAGAAAAAAAA	BAG2	NM 004282	GCAACAAAATGCTGAAAGCAGATTCAATTA	TTTGTATATCAATAGGACTAGTTACTTTGA	
BA22BNM_013450AAGTGGACAGATACTTTCAAAGTGAGCTGAACTTAAACTCACCCTTTCCACCCABC21PNM_078469GTCTGTTCCCCCAGTATTAGAATACACCAATCTATATATAGCCTTATTCCACAABC111ANM_018014TCGACGCCCTAAGTATGAATACACCATCTATATATAGCCTTATTCCAGBC121NM_001191TCACTCTTCAGTGGGAAATGATCACCGTACAGGTGGATAATTCAGBC121NM_00112530GGAAGTTAAAGAGATTATTGAAACAATGTATAACGGCTACTCCAAAAGACGCCBHLHB9NM_00112530GGAAGTTAAAGAGATTATTGAAACAATGTATAAGTGTTAAGAGGAAAAGGCAAGTCTCAABHLHE2NM_001214CAAGCCTCCTCACCCCTAATGTCCAAGGAAAAGGCAAGTCTCAAATTABIN1NM_001200GGGTTGTGGGTGTCGCTATGACATGACAGAAAAGCCTTGACCCCGCAAAATTTTBMP2NM_001200GGGTTGTGGGTGTCGCGTATGACTTATCAAAATTAACTGCCTGCAAAATTTTBMP4NM_130850GGATGTGGGTGCCGCTGATACTTCCTGTCCCTACAACTTAACCACBMP6NM_001218AAGAGCTTGTGGAGTGCCACTAACTTTGGATCCAAACTTAATCAACCACCBMP6NM_00299AATTGGGCAGATGTGAACAGGAAATCAAAAGGTATTTAAGCTGCCTBRCA1NM_00299AATTGGGCAGATGTGGACAGGAAATCCAAACGAATTTATTATTTTTATGTTBRCA2NM_00059GGACACATTACAACAAAGGTGAACATCACAAAGCAAGCTCCACCACAAAAAAAAAAAAAAAAAAAA	BAG3	NM 004281	TAACCCAGCAGCACCGTA	CAATTCTCTCTTGAGCCGGGCTATT	
BCCIPNM_078469GTCTGTTCCCCCAGATTAGAATACACCAATCTATATATAGCCTTATTCCACAABCL11NM_018014TCGAGAGCCCTTTAGTTCTGATTCTTACTGATGTGGCCCTCTGGBCL211NM_001917TCACTCTTCATGTGGAATGATCACCGTACAGGTGGACAATATTCAGBCL211NM_001706CTCCCCAAGGCAGCTGAGAAGTCCCAGAGGGAAAAAGCACACAGBCL3NM_001705CTCCCCAAAGCCTGCTGAACCTAGCCTCATCTCAAAAGAGCAGBHHB9NM_001142530GGAAGTTAAAGAGATTATTGGAACAATGTATAAGGTGTAAGAGGAAAAGGCAAGTCTCAABHHB22NM_001142CAAGCCTCCTCACCCCTATAAACAGTGATAAATAGGCATCTTAATTBICD1NM_001714CAAGCCTCCTCACCCCTAATGCTCAGTGAAAAGAGCATCTTATTTBMP1NM_001210GGGTTGTGGGTGCGCGCTGTTAAAGTTTTTAGCCTTTAAAAAATATTTTBMP2NM_001200GGGTTGTGGGTGCGCCGCTGATACTTCCTGCTCCACACACTTTAACCACBMP4NM_003850GGATGTGGGTGCCGCTGATACTTCCTGCTCCACACACTTAACCACBMP41NM_003299GATGGTGGATGCGCACTAACTTGCATCCAAACACTCTTAACCACBMP81ANM_007299AATTGGCAGATGTGGACAGGAAATACAAAAGGTATTTAAGCTGCTBRCA1NM_000399GGACACATTACAACTAAAAATATTCTCACAGGAAATACAAAAGGTAATTAAGCTGCATBRCA1NM_000399GCTGGAAAATTGCATCGCAAGGTGACGAAAATTACCTGGAAAATTAACAAATTATCAACTCAAATATACAACTTCGAAGAGGTGAGGAAAATTABRCA1NM_003972CCTGGAAGCTGAGGAAGGTGACGTTAAGCTCCAAGACTCAATATACTGGATGGGBZvu1NM_014670ATTGAACCAAGAAGGTGAAGAAATTACCTGGAATCAAACAGAGAGGGGGGGGAGAAAATTACCTGAATACGAAGCTGAAGAAGGTGAACTAAATTTGACACACAGGCAAAATCGAAAGGTGAGGAAAGCCCTACCTGGGATCAAACCGAAGGTGAGAAAAGCACCAACN	BAZ2B	NM 013450	AAGTGGACAGATACTTTCAAAGTGAGCTGA	ΑCTTAAACTCACCCTCTTCCACCCA	
BCL11ANM_018014TCGAGAGCCCTTAAGTTCTGATCTCTTACTGATGTGGCCTCTGGBCL21NM_001191TCACTCTTCAGTCGGAAATGATCACCCTACGGTGGATAAATTCAGBCL3NM_005178AGCTCCAGGAGGCAGCTGAGAAGTCCCAGAGTGACACACAGBCL4NM_001142530GGAAGTTAAAGAGATTATTGAAACAATGTATAAGTGTTAAGAGGAAAAGGCAGTCTCAABHLH82NM_01142530GGAAGTTAAAGAGCCTTATAAACAAGTAAATTAGGGCTACTTCAAATTABHLH822NM_001214CAAGCCCCCCCCCCAATGTCCAGTGAAGAAATTAGGGCTACTTCAATTABM1NM_001214CAAGCCTCCTCACCCCTAATGTCCAGTGAAGAACTTAGTGAAAAATABM11NM_001210GGGTTGTGGGTGCCGCTATTAAAGTTTTTAGCCTTTTAAAAATATTTTBMP2NM_001200GGATGTGGGGTGCCGCTGATACTTCCTGCTCCAACCTTAACCCACBMP6NM_001218AAGAGCTTGTGGATGCCACTAACTTTCCATCCAAACTTAACCACBMP8NM_001229GATGTGTGAATCCCAAGATGTGAAAAATCTGGATGGTATAATACACATTTATAGCTCCCACABRA1NM_00229AATGGGCAGATGTGAGACAGGAAATACAAAAGGCAAGCTCCATCCCCAAAAAAABTA1NM_003972CCTGGAAAATTACACAAAAAAAAAAAAAAAAAAAAAAAA	BCCIP	 NM_078469	GTCTGTTCCCCCAGTATTAGAATA	CACCAATCTATATATAGCCTTATTCCACAA	
BCL2L1   NM_001191   TCACTCTTCAGTCGGAAATGA   TCACCGTACAGGGGGATAAATTCAG     BCL3   NM_005178   AGCTCCAGGAGGCAGCTG   AGAGTCCCAGAGTGACACAG     BCL6   NM_001706   CTCCCCAAAGCCTGGA   ACCTAGCTCAACGCAGCAGCG     BHLHB9   NM_001123530   GGAAGTTAAAGAGATTATTGAAACAATGTA   TAAGTGTTAAAGAGGAAAAGGCAAGTCTCAAT     BHLHE2   NM_00174   CAAGGTCCCCCCTA   TAAGCGTAAATTAGGGCAACTCTCAATT     BID1   NM_005180   ATCAGCAACTTCTTCTGGTG   TTAAAGTTTTAGCCTTTAAAAAATATTTT     BMP2   NM_00174   CAAGCTTCTGCGTGCCCTA   TGACTTATCAAAATAATTGCCCGCATTTTAAAAATATTTT     BMP2   NM_001718   AAGAGCTTGTGGGTGCCCCTA   TGACTTATCAAATTACACACCAACTTTTACCACC     BMP4   NM_001718   AAGAGCTTGTGGATGCCACTA   ACTTTGCATCCAACACTCTTCACCC     BMP81   NM_001718   AAGAGCTTGTGGATGCACATG   CATGTGATATACACACTTTTACCCCC     BMP81   NM_001718   AAGAGCTGTGTGAT   CATGTGATATACCACATTTTTTAGCATCTCACC     BMP811   NM_000329   GGACACAATTACAACTAAAAATCTG   GATGGATTAATGCACACACCCCT     BRCa2   NM_000329   GGACACAATTACAACTAAAAAATATAACAAATATACAACAAAAAA	BCL11A	NM 018014	TCGAGAGCCCTTAAGTTCTGA	TCTCTTACTGATGTGGCCTCTGG	
BCL3 NM_005178 AGCTCCAGGAGGCAGCTG AGAAGTCCCAGAGTGACACACAG   BCL6 NM_001706 CTCCCCAAAGCCTGCTGA ACCTAGCCTCATCTCAAAAGCACGC   BHHB9 NM_001142530 GGAAGTTAAAGAGATTATTGAAACATGTA TAAGGTGTAAAGGAAAAGGCTTCA   BHHHE2 NM_01142530 GGAAGTTAAAGAGAATTATGAACATGTA TAAACAAGTAAAATTAGGGCTACTTCTAATT   BICD1 NM_001714 CAAGTCCCCCCCCCACCCCTA ATGTCCAGTGAAGAAACTCTAGGTTAAAAATA   BM11 NM_005180 ATCAGCAACTTCTTCTGGTTG TTAAACAATAACTTGCCCTACAACTAAATTTTT   BMP2 NM_001200 GGGTTGTGGGTGCCGCTA TGACTTATCAAATAACTTGCCCAACATTTTT   BMP4 NM_01380 GAATGTGGGTGCCGCTGA TACTTCCTGCCTACACCTCAACTTAACCAC   BMP5 NM_001718 AAGAGCTTGTGGATGCCACTA ACTTTGCATCAACACACACTTTATTTACCAC   BMP6 NM_001739 AATGGCAAGTGTGTGAA CAGGAAATACACAACACACCAC   BMP71A NM_004329 GAGTGTGGCAAGTGTGTGAA CAGGAAATACACAAAAAAAAAAAAAAAAAAAAAAAAAAA	BCL2L1	NM 001191	TCACTCTTCAGTCGGAAATGA	TCACCGTACAGGTGGATAAATTCAG	
BCL6NM_001706CTCCCCAAAGCCTGCTGAACCTAGCCTCATCTCAAAAGAGCGCBHLHB9NM_001142530GGAAGTTAAAGAGATTATTGAAACAATGTATAAGTGTTAAGAGGAAAAGGCAAGTCTCAABHLHE22NM_01142530GGAAGTCCCCCCACCCCTATAAACAAGTAAAGAGGCTACTTCTAATTBHLHE22NM_001714CAAGCCCTCCTCACCCCTAATGTCCAGTGAAAACTCTAGTTAAAAATABMI1NM_001714CAAGCCTCCTCCACCCCTAATGTCCAGTGAAACTCTAGTTAAAAATABMI1NM_001200GGGTTGTGGGTGCGCTATGACTTATCAAATAACTTGCCTGCAAATTTTBMP2NM_001200GGGTTGTGGGTGCCCCTATGACTTATCAAATAACTTGCCTGCAACCCCBMP4NM_01218AAGAGCTGGTGGATGCCACTAACTTTCCATCCAACACTCTTAACCABMP6NM_001718AAGGCTGGATGCCACTAACTTTGCATCCAACACTCTTAACCABMP71ANM_00329GATGGTTGAATCCCAAGATGTAAAAATCTGGATGTGATATAATCACATTTATTTTATGTTBRCa1NM_0007299AATTGGCAAGATGTGTGACAGGAAATACAAAAGGATTCTAACCAAAAAAAABTAF1NM_0003972CCTGGAAATTTTAGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAAAAAAABTAF1NM_014670ATCTGAAGCTGAAGAGGGAGACTGTTTAGCTACACGCCAGGAAACGCACCND3NM_01136017GATGCAAGCCAATCGGAAGGGGAGGAAAATTACTGGGGTTGACCAGGAAACGCAACCND3NM_00136017GATGTCAAGCCATACACCTGAGGAACTGACTATATTGGATCAACCACAGGGAACCND2NM_001789TACAGTGGTCGGAGGAAACCTAAATCTTGCAAATCTGAAGAAGGCACATGCCNL0NM_0010299ACAGTGGTCGCGGGGAACTGTGTGTGTGTAACAGCATGACCTTGATCDK12NM_001360AGAACCACCAGGAAACCTAAATCTTGACCAGGCAGGAAACCTTAACCTCGGATCGCAGAGAGCCCTACTGTGGTGTCTGCACAGGCTGGGGCGGGTGA	BCL3	NM 005178	AGCTCCAGGAGGCAGCTG	AGAAGTCCCAGAGTGACACACAG	
BHLHB9NM_001142530GGAAGTTAAAGAGATTATTGAAACAATGTATAAGTGTTAAGAGGAAAAGGCAAGTCTCAABHLHE22NM_152414ACAGTGCACCGGAGAGCCTTATAAACAAGTAAATTAGGGCTACTTCTAATTBICD1NM_001714CAAGCCTCCTCCCCCCTATTAAAGAGAGAAAATTAGGGCTACTTATTAAAAATABMI1NM_001718ATCAGCAACTTCTTCTGGTTGTTAAAGTTTTTAGCCTTTTAAAAATAATTTTBMP2NM_001718AAGAGCTGGGGTGCCGCTGATACTTCCTGTCCCACAACTTAACCACBMP4NM_001718AAGAGCTTGTGGATGCCACTAACTTTCCTGTCCAACACTTTAACCACBMP6NM_001718AAGAGCTTGTGAGTGCCACTAACTTTGCATCCAAACTTTATTTTATGTTBRCA1NM_00329GATGGTTGAATCCCAAGATGTGAACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_000392GGACCAATTACAACAACTATACAAAATTATCTAACAAAGCAAGACTCCACAAAAAAAAABTAF1NM_0003972CCTGGAAAATTTAGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAAAAAAAABZW2NM_0114670ATTCGAAGCGGAAGGGGAGAAATTACTGGGATTACAAGAGGGGAGGGGBZW2NM_01136017GATGTCACAGCCATACACCTGAAGACTCTGACCACGCCAGGGAACCND3NM_00136017GATGTCACAGCCATACACCTGAGACTCTGACACCCCGGAGAACACCTGCCND3NM_001789TACAGTCGTCGAAGAGGTAATCCGGAGGATTCCTTGCCCATATACTGGATCAGACCACCTGCDKN12NM_00075CTACATAGGAGAAGCTCTGACTGTGCATATACAGGACACCCTGACCCTGCDKN14NM_00075CCACATAAGGAGAAGCCTCTACTGTGCATATACTGGATCAACCACAGTTTTCDKN2NM_001789TACAGTCGTCGAGAGAGCTCCAGATTCTCTGACAACCACCCTGGACCCCGCTGCDKN14NM_000075CTACATAAGGAGAAGCCCTACTGTGCTTATATTGGACAACCACCAGGATTCCAGGCDKN2NM_001289 <td>BCL6</td> <td>NM_001706</td> <td>CTCCCCAAAGCCTGCTGA</td> <td>ACCTAGCCTCATCTCAAAAGACGC</td>	BCL6	NM_001706	CTCCCCAAAGCCTGCTGA	ACCTAGCCTCATCTCAAAAGACGC	
BHLHE22NM_152414ACAGTGCACGGAGAAGCCTTATAAACAAGTAAATTAGGGCTACTTCTAATTBICD1NM_001714CAAGCCTCCTCACCCCTAATGTCCCAGTGAAGAACTCTAGTTAAAAATABMI1NM_001700GGGTTGTGGGTGCCGTGTTAAAGTTTTTAGCATCTAATTTTBMP2NM_001200GGGTTGTGGGTGCCGCTATGACTTATCAAATAACTTGCCTGCAAATTTTBMP4NM_130850GGATGTGGGTGCCGCTGATACTTCCTGTCCCTACAACTTAACCACBMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTTCATCCCBMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTTTATTTTATGTTBRCA1NM_004329GATGGTGAATCCCAAGATGTAAAAATTGGATGTGAATTAAACGTACCCAACGTGCCTBRCA2NM_00059GGACACAATTACAACTAAAAAATATTCTAACAAAGCAAAAGGTACTTCCCAAAAAAAABTAF1NM_003972CCTGGAAAATTTACAACTAAAAAATATTCTAACAAAGCAACACAAAAATATTCAACTGAAAAAAABZW2NM_014670ATCTGAAGCGGAAGGGGAGGGACTGGGATTACAGGTGGAGGAAAATTACTGGAATAGCAATCGGAATGGGAAGGGGAACTCTGACCAGGCAGGGAAACCND3NM_001136017GATGTCACAGCCATACACCTGTAGGAACTGACTATATTTGGGTCAGAGACCATGCCN2NM_001380CTTCTCCAAGAAGGTAACCTAAATTTTTGCACACACCTCAAACACCACAGGAAACCTAACDKN1NM_00075CTACATAAGGATGAAGGTAATCCGGAGGTGATCCTGGTGTGGCTAGAGACCCTTCDKN1NM_00189TACAGTCTCCGAGGAGAACCCTACTGTGCTGTTGTTTTTGCAGCACACCTGGCGGGGCDKN1NM_00189CTTCTCCAAGAGGAGTCCTGATCTTGCAAGAGGCTGCCGTGGACDKN1NM_00180ATGGGGCCGCGGGGACCCAGGCCCAGGCCAGGCCAGCCCAGCDKN1NM_00180ATGGGGCAGGCTGCGGGGACCCAGGCCCAGCCCAG <td< td=""><td>BHLHB9</td><td>NM_001142530</td><td>GGAAGTTAAAGAGATTATTGAAACAATGTA</td><td>TAAGTGTTAAGAGGAAAAGGCAAGTCTCAA</td></td<>	BHLHB9	NM_001142530	GGAAGTTAAAGAGATTATTGAAACAATGTA	TAAGTGTTAAGAGGAAAAGGCAAGTCTCAA	
BICD1NM_001714CAAGCCTCCTCACCCCTAATGTCCAGTGAAGAACTCTAGTTAAAAATABMI1NM_005180ATCAGCAACTTCTTCTGGTTGTTAAAGTTTTTAGCCTTTTAAAAATATTTTBMP2NM_001200GGGTTGTGGGTGTCGCTATGACTTATCAAATAACTTGCCTGCAATTTTBMP4NM_0130850GGATGTGGGTGCCGCTGATACTTCCTGTCCTACAACTTAACCACBMP4NM_001209GATGTTGGATGGATGCCACTAACTTTGCCTACAACACTTAACCACBMP6NM_001718AAGA6CTTGTGGATGCCACTAACTTTGCATCCAACACTTTATTTATGTTBRP61NM_004329GATGGTTGAATCCCAAGATGTAAAAATCTGGATGTGATATAATCACATTTATTTTATGTTBRCA1NM_00059GGACACAATTACCACAGATGTAAAAATATATCTAACAAGCAAAGGCTCCATCTCCAAAAAAAAABTAF1NM_000392CCTGGAAATTTATGCATCTCAAGATATAAAAAAATATTCCAACACCAGAATTACCGAAABZW1NM_014038AGAATCCGAAAGGTGAGGAAAGTGATTTAGCTACACGAGATTACAGGTGAGGCAGAATAGCAS21NM_01136017GATGTCACAGCCATGGAAGAGGTGAGGAAAATTACTGGGATTACAGGTGAGGCAGAAAGCCND3NM_00138017GATGTCCAAGCCATGAGGAAACACTAAATTTTGCAACACCACGGAAACACCTGCDK4NM_00075CTACATAAGGATGAAGGTCATGATCTTGCAAATCAATCTGGATCACCTCDKN1CNM_001289GTCTCCCAAGAAGGCTCTGATCTGGGCCAGGCCAGCCAGCDNN_001800ATGGTGGCCCCGCGTGATGGGCCAGGCCACACCAGCDNN_001800ATGGTGGCCCCCGCTGTGACCCCAGCTCACACACCTGCDKN12NM_001804GAAAGAGGAGCTCTGAGGAGGCTGTCTCCAAGGCCDNF1NM_001804GAAAGAGGAGTTCTGCCATAGTGGGCAGCCACCATTTTTACGTACDN2NM_001265CCCAACAAACCATCGTAAGGAGAGCCCTACTGGGAGGCTGTCCCACCTCDN2 <t< td=""><td>BHLHE22</td><td>NM_152414</td><td>ACAGTGCACGGAGAAGCCTTA</td><td colspan="2">TAAACAAGTAAATTAGGGCTACTTCTAATT</td></t<>	BHLHE22	NM_152414	ACAGTGCACGGAGAAGCCTTA	TAAACAAGTAAATTAGGGCTACTTCTAATT	
BMI1NM_005180ATCAGCAACTTCTTCTGGTTGTTAAAGTTTTTAGCCTTTTAAAAATATTTTBMP2NM_001200GGGTTGTGGGTGCCGCTATGACTTATCAAAATAACTTGCCGCAATTTTBMP4NM_130850GGATGTGGGTGCCGCTGATACTTCCTGTCCCTACAACTAACCACBMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTCTTAACCACBMP81NM_004329GATGGTTGAATCCCAAGACTGTAAAAATCTGGATGGTATAATCACACTTTATTTTATGTTBRCA1NM_007299AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_00059GGACACAATTACAACTAAAAAATATATCTAACAAAGCAAGACTCCACTCCAAAAAAAAAABTAF1NM_003972CCTGGAAAATTTACAACTACTACTCTCCAAGTATAAAAAAAATATTCAACTCAAATATACTGAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGAGCTGTTTAGCTACACCAGAATTCCTGTGTAGGGGGBZW2NM_014670ATCCGAACTGGAAAGAGTGAGAGTGTTTAGCTACACCAGGAGAAATAGCAS21NM_017766CTCCAGTTCCAGGAGAAGGAACTCTGACCAGGCCAAGGAGAGGCCND3NM_00136017GATGTCACAGCCATACACCTGAGGAACTGACTATATTTGGACCAGGAAACACTACDC25ANM_00075CTACATAAGGATGAAAGCCTAATCTTGCAAAACAACCACCAGGAAACACTAACDK41NM_000389CTTCTCCAAAGAGGTAACCCTGATCGTGTGTTTTTGCAGACAGCCAGGCCAGCDKN12NM_001800ATGGGGCCCGCTGGAGGAAGCCCTACTGTGGTTTTCCAGGACGAGCCDKN20NM_001289GCCACAAAACTCTCAATAATCATCAAGAGAGAGAGCTCAGCTCDKN12NM_001804GAAAGAGGCCTGGGTGATGGAGGCCGACCAGCCCAGCCAGCDKN20NM_001804GAAAGAGGCCCCGAGTGGTGGAGGCCGCCCCCCGCGTGACDKN20NM_001804GAAAGAGGCCTGGAGCTGATGGAGGCCGCCCCC	BICD1	NM_001714	CAAGCCTCCTCACCCCTA	ATGTCCAGTGAAGAACTCTAGTTAAAAATA	
BMP2NM_001200GGGTTGTGGGTGTCGCTATGACTTATCAAATAACTTGCCTGCAATTTTBMP4NM_130850GGATGTGGGTGCCGCTGATACTTCCTGTCCCTACAACTTAACCACBMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTCTTCACCBMP81ANM_004329GATGGTTGAATCCCAAGATGTAAAAATCTGGATGTGATATAATCACAATTATTTTATGTTBRCA1NM_000329AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_000059GGACACAATTACAAATATATCTAACAAAGCAAGACTCCCATCTCCCAAAAAAAAABTAF1NM_003972CCTGGAAAATTTATGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAATATACTGAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGACTGTTTAGCTACACCAGGAATTCGTGTAGGTGGBZW2NM_01136017GATGTCACAGCAGAGAGGGACTCTGGCCAGGGAACCND3NM_001136017GATGTCACAGCCATACACCTGAGGGAACTGACTTATCAGGTGAGCAGGAACCND3NM_001136017GATGTCACAGCCATACACCTGAGGAACTGACTATATTGGGTCAGAGACCATGCDC25ANM_001789TACAGTCGTCTGAAGAAGCTCTGATCTTGCCAATCAACTCAAACTCACACTCDK11ANM_000389CTTCTCCCAAGAGGAAGCCCTACTGTTGTTTTTTCGACACACCACAAGTTTTTCGTTTCDKN12NM_001800ATGGTGGCCCGGCGGATGGGCCAGGCCAGCCAGCDNFNM_00129954CCCAAAACAGAGCTCTGACCGAGGCCGACCACCTCDNFNM_001289CCCCACCCGCTGTGAGAAATGTTTTTCCCAAGCACTCDNF1NM_207327CCCGGTTCTCGGACGTGATGGGCCAGGCTGTCTCCAACCTCDNFNM_001804GAAAGAGGCTCTGAGCTTACAAAATGGACTCACCTCDNF1NM_207327CCCGGTCACCCAGTGAGACTGGAGCCACACATTTTTACGTACDNF1NM_207327 </td <td>BMI1</td> <td>NM_005180</td> <td>ATCAGCAACTTCTTCTGGTTG</td> <td colspan="2">TTAAAGTTTTTAGCCTTTTAAAAATATTTT</td>	BMI1	NM_005180	ATCAGCAACTTCTTCTGGTTG	TTAAAGTTTTTAGCCTTTTAAAAATATTTT	
BMP4NM_130850GGATGTGGGTGCCGCTGATACTTCCTGTCCCTACAACTTAACCACBMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTCTTCACCBMP6NM_004329GATGGTGAATCCCAAGATGTAAAAATCTGGATGGTGATATAATCACATTTATTTTATGTTBRCA1NM_007299AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_000059GGACACAATTACAACTAAAAAATATATCTAACAAAGCAAGACTCCATCTCCAAAAAAAAAABTAF1NM_013972CCTGGAAAATTTAGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAATAATACTGAABZW1NM_014670ATCTGAAGCTGAAGAGGTGAGGGAGAGATGGTTTAGCTACACCAGAATTCTGTGTAGGTGGBZW2NM_014670ATCTGAAGCTGAAGAGGTGAGGAAAATTACTGGGATTACAGGTGTGAGCAGAATAGCAS21NM_011766CTCCAGTTCCAGGAGAGGTGAACTCTGACCAGGCCAGGGAACCND3NM_001136017GATGTCACACCCAGGCATACACCTGTAGGAACTGACTATATTTGGGTCAGAGAACCATTCDC25ANM_001789TACAGTCGTCTGAAGAAGGTAATCCGGAGTGATCCTCGTGCCATATACTGGATCACCTCDKN1ANM_000389CTTCCCAAGGAGAGGCCTACTGTGTTTTTTGCAGCAGCACACCCDKN2CNM_001800ATGGTGGCCCCGCTGTGATGGGCCAGGCCAGCCAGCDKN2DNM_001800ATGGTGGCCCCGCTGTGACCCAGGCTCACCCAGCCAGCDNF1NM_00129954CCCAAAACAGAGCTCTGATGGGGCCAGCAGATTCTCAAGGATTCCCAGTACDNF1NM_0012804GAAAGAGGAGTTCTGCATAGATCTTCCAAGAGATTCCACGTCDX1NM_001265CCCACCGTCCCCGTGAAGAGCCACGCATTCCAAGGCCDX1NM_001265CCCACCGTCCCAGTGAGAGCCACGCATTCCAAGGCCDNF1NM_0122075CTCAATAACAACCATCGTAAGAATGACTGACCCAGCTAGATTTTTAGTAGAGG	BMP2	NM_001200	GGGTTGTGGGTGTCGCTA	TGACTTATCAAATAACTTGCCTGCAATTTT	
BMP6NM_001718AAGAGCTTGTGGATGCCACTAACTTTGCATCCAACACTCTTCACCBMPR1ANM_004329GATGGTGAATGCCAAGATGTAAAAATCTGGATGGTGATATAATCACATTTATTTTATGTTBRCA1NM_007299AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_00059GGACACAATTACAACTAAAAAATATATCTAACAAAGCAAGACTCCATCTCCAAAAAAAAABTAF1NM_014670ATCTGAAGCTGAAGATGTGACTGTTTAGCTACACCAGAATTCGAATATACGAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGACTGTTTAGCTACACCAGGACAGAATAGCCAS21NM_014670ATCTGACGAGAGGTGAGGAAAATTACTGGGATTACAGGTGGAGCAGAATAGCCND3NM_001136017GATGTCACAGCCATACACCTGTAGGAACTGACTATATTTGGGTCAGAGACCATGCCNE2NM_057749GAAAAACACACCAGGAAAACCTAAATTCTTGCACACACCTCTAATAACAACACAGAGTCACCTCDK4NM_00075CTACATAAGGATGAAGGTAATCCGGAGTGATCCTCGTGTCCATATACTGGATCACCTCDKN1ANM_001262GGGAGCCCACAAATCTCAATATTCTTTTTTTGCAGCAGGCAGCACTCGTTTTTCDKN2CNM_001800ATGGTGGCCCCGGTGATGGGCCCAGGCCAGCCAGCDNF1NM_001804GAAAGGGGCTCTGAAGAACTTTTTTCCAGAGAGAGTATGTCTAGTTTTCCAGGCDNF1NM_00129954CCCAAAACAGAGCTCTGATGGAGCCTCCACCTGCDNF1NM_001205CTCAATAACAAGGAGTCATGAGCTACAAAAGGAGCTCTCAAGGAGCDX1NM_001205CTCAATAACAAGGACTCGCATAGCTTACAAAATGGACTCACACTTTTACGTACDK12NM_001804GAAAGAGGAGTTTCTCCGAAGCCAGGCTGCCCCCGCCDK12NM_001804GAAGAGGAGCTCGGAGCCAGGCTGCCCCCGCDNFNM_00120954CCCCACCGCGCGGAGAGCCAGCCTCACCCAGCCTCCCCGC <td>BMP4</td> <td>NM_130850</td> <td>GGATGTGGGTGCCGCTGA</td> <td colspan="2">TACTTCCTGTCCCTACAACTTAACCAC</td>	BMP4	NM_130850	GGATGTGGGTGCCGCTGA	TACTTCCTGTCCCTACAACTTAACCAC	
BMPR1ANM_004329GATGGTTGAATCCCAAGATGTAAAAATCTGGATGTGATATAATCACATTTATTTTATGTTBRCA1NM_007299AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_00059GGACACAATTACAACTAAAAAATATATCTAACAAAGCAAGACTCCATCTCCAAAAAAAAABTAF1NM_003972CCTGGAAAATTTTATGCATTCTCTCAAGTATAAAAAAATATTCAACTAAAAAAAAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGACTGTTTAGCTACACCAGAATTCTGTGTAGGTGGBZW2NM_014038AGAATCCGAATCGGAAGGTGAGGAAAATTACTGGGATTACAGGTGGGACAGAAAGCAS21NM_01766CTCCAGTTCCAGGAGAGTGAACTCTGACCAGGCCAGGGAACCND3NM_001136017GATGTCACAGCCATACACCTGTAGGAACTGACTATATTTGGGTCAGAGACCATGCCN22NM_001789TACAGTCGTCTGAAGAAGCTCTGATCTTGCAAATCAATCTGAACCACACACTTTCD25ANM_001789TACAGTCGTCTGAAGAAGGTCATGATTCCTCTGTCCATATACTGGATCACCTCDKN1ANM_000075CTACATAAGGATGAAGGTAATCCGGAGTGATTGCGCCAGGCCAGGCAGGACTTTCTGTTTCDKN2CNM_001262GGGAGCCACAAATCTTCAATAATGATGCAGGGCCCAGGCCAGGCDKN2DNM_001289CTCTCCGAGAGGCTGCGGTGATGGGCCAGGCCAGCCAGCDKN2DNM_001800ATGGTGGCCCCGCTGGACCCAGGCTCACCCTGGCDNFNM_001262GGAAGCCCCCGCTGGAGAAATGTTTTTCAGTATTCCCCAGCTGACDPF1NM_207327CCCGGTTCTCGACGTGAGCTACAAATGGACTCACATTTTACGTACDX1NM_001265CCCACACGCATCCCAGTGAGAGCCACGCATTCCAAGGCCERS2NM_001265CCCACCGCTCCGCGTGAGAGCCACGCATTCCAAGGCCERS2NM_001265CCCACCGCATCCAGTGAGAGCCACGCATTCTAAGGCCE	BMP6	NM_001718	AAGAGCTTGTGGATGCCACTA	ACTTTGCATCCAACACTCTTCACC	
BRCA1NM_007299AATTGGGCAGATGTGTGACAGGAAATACAAAAGGTATTTAAGCTGCCTBRCA2NM_000059GGACACAATTACAACTAAAAAATATATCTAACAAAGCAAGACTCCATCTCCCAAAAAAAAABTAF1NM_003972CCTGGAAAATTTATGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAACTCAAAAAAAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGACTGTTTAGCTACACCAGAATTCTGTGTAGGTGGBZW2NM_014038AGAATCCGAATCGGAAGGTGAGGAAAATTACTGGGATTACAGGTGGAGCAGAATAGCAS21NM_01766CTCCAGTTCCAGGAGAGGGAAGGTGAGACTCTGACCAGGCCAGGGAACCND3NM_001136017GATGTCACAGCCATACACCTGTAGGAACTGACCAGGCCAGGGAACCN22NM_001789GAAAAACACACCAGGAAAACCACTAAATTTTGACACACCCTCTAATAACACACACTATCD25ANM_001789TACAGTCGTCTGAAGAAGGTAATCCGGAGGATCCTCCTGTCCATATACTGGACACACTCDK4NM_000075CTACATAAGGATGAAGGTAATCCGGAGGATTCCTCTGTCCATATACTGGATCACCTCDKN1ANM_000389CTTCTCCCAAGAGGAAGCCCTACTGTTGTTTTTGCAGCAGTCTTAGTTTTCCAGCDKN2CNM_001262GGGAGCCACAAATCTTCAATAATCATCAAGAGAGATATGTCTAGTTTTCCAGCDKN2DNM_001280ATGGTGGCCCGGCTGGATGGGCCAGGCCCAGCCAGCDNFNM_00129954CCCAAACAGAGCTCTGAGCAAGAGGCTGTCCCACCTCDX1NM_001265CCCACCGTCACCAGTGAGGAGCCACGCATTCCAAGGCCERS2NM_01265CCCACCGTCACCCAGTGAGAGCCACGCATTCCAAGGCCERS2NM_01265CCCACCGTCACCAGGAAGAGCCACGCATTCCAAGGCCCRR52NM_01265CCCACCGTCACCATGTAACACTGAATGACTGAACTCTGGTGAGACAAGCTCTGCChMP48NM_176812GAACTGGGCTGGATCCATGTAACTCTGGTGAGACAAGCTCTG	BMPR1A	NM_004329	GATGGTTGAATCCCAAGATGTAAAAATCTG	GATGTGATATAATCACATTTATTTTATGTT	
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BTAF1NM_003972CCTGGAAAATTTTATGCATTCTCTCAAGTATAAAAAAATATTCAACTCAAATATACTGAABZW1NM_014670ATCTGAAGCTGAAGAAGGTGACTGTTTAGCTACACCCAGAATTCTGTGTAGGTGGBZW2NM_014038AGAATCCGAATCGGAAGGGGAGAGGACTGGGATTACAGGTGTGAGCAGAAATAGCAS21NM_011766CTCCAGTTCCAGGACAGTGAACTCTGACCAGGCCAGGGAACCND3NM_001136017GATGTCACAGCCATACACCTGTAGGAACTGACTATATTTGGGTCAGAGACCATGCDK2NM_057749GAAAAACCACCAGGAAAACACTAAATTTTTGACACACCTCTAATAACACTCACTTCDC25ANM_001789TACAGTCGTCTGAAGAAGCTCTGATCTTGCAAATCAATCTGAACCACAAGTTTTCDK4NM_000075CTACATAAGGATGAAGGTAATCCGGAGTGATTCCTCTGTCCATATACTGGATCACCTCDKN1ANM_000389CTTCTCCAAGAGGAGGCCCTACTGTTGTTTTTGCAGCAGCAGTCTTGTTTCDKN1CNM_001262GGGAGCCACAAATCTTCAATAATCATCAAGAGAGTATGCTAGTTTTCCAGCDKN2CNM_001800ATGGTGGCCCGGGTGATGGGCCCAGGCCAGGCCAGGCDNFNM_001800ATGGTGGCCCGCTGTGACCCAGCTCACCCTGCDNFNM_001804GAAACAGAGAGCTCTGAGAAATGTTTTTCCAGATTCCCCAGCTGTACDPF1NM_001804GAAAGAGGAGTTCTGCCATAGCTTACAAAATGGACTCACACTTTTTACGTACDX1NM_001804GAAAGAGGAGTTCTGCCATAGCTTACAAAATGGACTCCACGCCERS2NM_022075CTCAATAACAACCATCGTAAGAATGACTGACCAGCTAGAGTATTTTAGGAGAGAGGGCHMP48NM_176812GAACTGGCCGCGTGGATCCATGTAACTTCTGGTGAGACAAGCTCTGC	BRCA2	NM_000059	GGACACAATTACAACTAAAAAATATATCTA	ACAAAGCAAGACTCCATCTCCAAAAAAAAA	
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CDKN1C   NM_000076   CGCAAGAGGCTGCGGTGA   TGGGCCAGGCCAGCCAGC     CDKN2C   NM_001262   GGGAGCCACAAATCTTCAATA   ATCATCAAGAGAGATATGTCTAGTTTTCCAG     CDKN2D   NM_001800   ATGGTGGCCCCGCTGTGA   CCCAGCTCACTCACCCGG     CDNF   NM_001029954   CCCAAAACAGAGGCTCTGA   GAAATGTTTTTTCAGTATTCCCCAGCTGTA     CDPF1   NM_207327   CCCGGTTCTCGGACGTGA   TGGAGGCTGTCTCCACCT     CDX1   NM_001804   GAAAGAGGAGTTTCTGCCATA   GCTTACAAAATGGACTCACATTTTTACGTA     CDX2   NM_001265   CCCACCGTCACCCAGTGA   GAGCCACGCATTCCAAGGC     CERS2   NM_022075   CTCAATAACAACCATCGTAAGAATGACTGA   CCAGCTAGATGTATTTTTAGTAGAGAATGGG     CHMP4B   NM_176812   GAACTGGGCTGGATCCATGTA   ACTTCTGGTGAGACAAGCTCTGC	CDKN1A	NM_000389			
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CDNR2D   NM_001800   ATGGTGGCCCCGCTGTGA   CCCAGCTCACTCACCCGCTGTG     CDNF   NM_001029954   CCCAAAACAGAGCTCTGA   GAAATGTTTTTTCAGTATTCCCCAGCTGTA     CDPF1   NM_207327   CCCGGTTCTCGGACGTGA   TGGAGGCTGTCTCCACCT     CDX1   NM_001804   GAAAGAGAGGAGTTTCTGCCATA   GCTTACAAAATGGACTCACATTTTTACGTA     CDX2   NM_001265   CCCACCGTCACCCAGTGA   GAGCCACGCATTCCAAGGC     CERS2   NM_022075   CTCAATAACAACCATCGTAAGAATGACTGA   CCAGCTAGATGTATTTTTAGTAGAGAATGGG     CHMP4B   NM_176812   GAACTGGGCTGGATCCATGTA   ACTTCTGGTGAGACAAGCTCTGC	CDKN2C	NM_001262			
CDNF   NM_001029954   CCCAAAACAGAGCTCTGA   GAAATGTTTTTCAGTATTCCCCAGCTGTA     CDPF1   NM_207327   CCCGGTTCTCGGACGTGA   TGGAGGCTGTCTCCACCT     CDX1   NM_001804   GAAAGGGAGTTTCTGCCATA   GCTTACAAAATGGACTCACATTTTTACGTA     CDX2   NM_001265   CCCACCGTCACCCAGTGA   GAGCCACGCATTCCAAGGC     CERS2   NM_022075   CTCAATAACAACCATCGTAAGAATGACTGA   CCAGCTAGATGTATTTTTAGTAGAGAATGGG     CHMP4B   NM_176812   GAACTGGGCTGGATCCATGTA   ACTTCTGGTGAGACAAGCTCTGC	CDKNZD	NM_001800			
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CDX1 NM_001204 GAAAGAGGAGTTTCTGCCATA GCTTACAAAATGGACTCACATTTTTACGTA   CDX2 NM_001265 CCCACCGTCACCCAGTGA GAGCCACGCATTCCAAGGC   CERS2 NM_022075 CTCAATAACAACCATCGTAAGAATGACTGA CCAGCTAGATGTATTTTTAGTAGAGATGGG   CHMP4B NM_176812 GAACTGGGCTGGATCCATGTA ACTTCTGGTGAGACAAGCTCTGC		NINI_207327			
CERS2 NM_022075 CTCAATAACAACCATCGTAAGAATGACTGA CCAGCTAGATGTATTTTTAGTAGAGATGGG CHMP4B NM_176812 GAACTGGGCTGGATCCATGTA ACCATCGTAGAGATGACAAGCTCTGC		NM 001265			
CHMP4B NM_176812 GAACTGGGCTGGATCCATGTA ACAGCATGA ACCTGGGGGAGACAAGCTCTGC	CERS2	NM 022075			
		NIM 176912			
	CNNM2	NM 017649		ΑΓΑΑΑΑΓΓΩΤΟΤΟΤΟΓΟΤΤΤΟΟΤΑΓΓΑΤ	
	CODSE	NM 006933			
	COPSE	NM 006710		CTCCTGATCCTCTGACTTCTTGAATTC	
	CPI X1	NM 006651	CAGGACATGCTCAAGAAGTAG		
	CREB3L3	NM 032607	GGCGGGAGACGAGCTGTG	TGCCCGGCGCCTCTCCCT	
	CREB3L3	NM_032607	GGCGGGAGACGAGCTGTG	TGCCCGGCGCCTCTCCCT	

CREB3L4	NM_001255981	GCATGCAGATGAGATGTG	GGTTTCCTTCCCTTCTGTAACTTGGA	
CREG1	NM_003851	TAATTCTTCTCTGTTCCCCTTTCTAGGTGA	GCTTTTTGCCAATTAGAAAGAGTGGTATTA	
CREM	NM_182721	CAAAGATCTTTATTGCCATAAAGTAGAGTA	TCTCCCACCACACACTGATCAGAT	
CRK	NM_016823	CCCGATGAGGACTTCAGCTGA	AGGAATCCTTAGGACTTGAGTAGCG	
CTCF	NM 006565	CAGCATGATGGACCGGTG	CCCGCCAAGATCATATCGTCC	
CTF1	NM 001142544	GCCCGGGGGCTCGGCCTG	GGGCTGGCAGAGGGCACC	
CTNNB1	NM 001904	CTGGTTTGATACTGACCTGTA	AAGTAGGGCCCTCTCTATCGCTA	
DEC1	NM 017418	GCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		
	NM 022105	CCACTTCCACCTTCTCTCTAA		
	NM 005618			
	NM 019074			
	NM 001028402			
	NM 005220			
	NIM_003220			
	NIVI_001934			
DIVIRTI	NIM_021951			
DNIVITI	NIVI_001379			
DINIVIT3B	NM_175848	GAAGGACTACTTIGCATGTGAATA		
DOCK11	NM_144658			
DONSON	NM_017613	AGAGACIACATITATAATIGGAGATCCIGA		
DPF1	NM_004647	GCTTACATCACCCTCACCTAG	CAAAGCCGGGGAGAGGGCA	
DPF2	NM_006268	CIACCAGAACCAGAACTCCTCTTG	CATAITGGGGTTCCACAAAAAATTTTAAT	
E2F1	NM_005225	ACCCCCTGGATTTCTGA	AGCCCACTGTATTTGTTACATGTTTACTAA	
E2F4	NM_001950	TGATGTGCCTGTTCTCAACCTCTG	CCCGCCCCACACCAAGGT	
E2F5	NM_001083589	TCTGTTTGATGTCCAGATACTAAATTATTA	TATTGTTGTCTGTGTTTTTAAATATAATAC	
E2F6	NM_198256	AGTGAAGAATTGCTTGAAGTAAGCAACTGA	GGATCGCTCAAGGTTTCTGAAGGAA	
EBF4	NM_001110514	GGGCCTGGCATACTCCTA	CCAACAGTCCCCAAGAACAGAC	
EBP	NM_006579	AAAAGCCAAGAGCAAGAAGAACTG	TCTGGCGGGGGGGTCAGTG	
EGR1	NM_001964	CTTTTCTCCCAGGACAATTGAAATTTGCTA	ATACTCAGTCCTCATAAATAACGAACTCCA	
EGR2	NM_000399	CGGACCCGGACACCTTGA	CAGGCTAGCAAAGAAGATCTGGAGA	
EGR4	NM_001965	TCCTTCGCTTCTCTCTGA	CGCAGTTCCTGGCAGGTGT	
EHMT1	NM_024757	TGCCGCCGACCCCCTATG	CTGCCTGGAACGTCCCCT	
EHMT2	NM_025256	CCCCCTGTCAACACATGA	CATAGTGGCCCCCCACCT	
EIF3A	NM_003750	GGATGGACCACAGTACGACGTTAA	TCCTAGCCACATATGCTTTCTTTGTTATAT	
EIF3J	NM_003758	ATATGTACAAGACTATGAAGACTTCATGTG	TTCCTATTTAAAATAGATTGATTTTAGATG	
EIF4A2	NM 001967	CATGAATGTGGCTGACCTTATTTA	GCAGATGGTGCTGATGAACATTTG	
ELF1	NM 172373	CTGCTGGAACCCAACTCTTTTAG	TCTCAAAAACAAAACAAAACAAAAGTGTGT	
ELF2	NM 201999	ACAGAAGGACTAGTGACATGTGAGAAATAA	CAAAAGGTCTGATTGTGAAACAAATGGTTT	
ELF3	NM 004433	GGTTCTCCAGAGTCGGAACTG	TGTAAGTAAAAGCCTTTTTCCAAATGGCTC	
ELF5	NM 001422	CAGGAAGACAAGCTATGA	CTTGGGCAACAAGCAAGAACC	
ELK1	NM 005229	GGGCCCCAGAAGCCATGA	GATATGCAGTCCCTACTATTGTTTCTCACA	
ELK3	NM 005230	ACTGCTTTCTTCAAACTCTCAGAAATCCTG	CCTGGAATAGCATGAACTTGATGTAGCTTT	
FMX1	NM 004097	CATCGATGTCACCTCCAATGACTA	GGTCTGGATGTCGTAAGGGAAAGACTTA	
EMX2	NM 004098	GGAGGAAATAGACGTGACCTCAGATGATTA	ATCTTTCTTTAAAATGCCTGAGAATCCATC	
FN1	NM 001426	GACAAAGACGAGAGCGAGTAG	TCTGGGTCGCGCTTCCCC	
FN2	NM 001427			
FPHA8	NM 020526	GCCCCGCCGCACCTCTG	GCACTAATCCTACCTCCCCAGACA	
FRBR2	NM 004448			
FRBB3	NM 001982			
EDE	NM 006494		CCTCCATTCCCCCATTCTCATTA	
ECD3	NNA 001214002			
	NIM_001214902			
	NNL 001202240			
	NIVI_004460			
FHLI	NM_001449			
FIZ1	NIVI_032836			
FOS	NM_005252			
FOSL1	NM_005438	ACCCICCICGCITTGTGA	GCGGATGTAGCCCCACTTGT	
FOXA1	NM_004496	CCCGTCCTAAACACTTCCTAG	ATGCAAAATAGCGGCTACCCTAAAATGT	
FOXA2	NM_021784	CCCATTATGAACTCCTCTTAA	TTGAAGTGGATTTAGAGAAATAAGATGGAT	
FOXC1	NM_001453	CGTCTACGACTGTAGCAAGTTTTG	CCAGCGAGATTTAAACGGGGC	

FOXD2	NM_004474	TAGTGGCTGCCACTTCTG	CTTGCATCCTCTAAGCTCAAACCC		
FOXE3	NM_012186	GCTGGAGCGCTACCTGTG	CCTGCTGGAGAATCACTTCCTAATC		
FOXI1	NM_144769	GGAGGGCACCGAGGTCTA	AGAGGTGAAAAGAGTCTTGATATGCATTCT		
FOXL1	NM 005250	CACGGTACTCCACTTCCAGTA	TCTCCACTCCTTCCCCTCCAT		
FOXL2	NM 023067	TCGCGCCTCGATCTCTGA	ACAAAGCAGCAGCGACAG		
FOXM1	NM 021953	CAGTTTATTCCTGAGCTACAGTAG	TGTGTGCCTGTGCAAGTGCT		
FOXN1	NM 003593	GCCCGTGGCCCTGGCATG	TTTCTGGAGGAGGAGGAGTGAGATTGTG		
FOXO4	NM 005938	GTTTCTTCTTCCCACAGATCCCTG			
FOX01	NM_033260				
ECT	NM 006250				
ELITO	NIM 004490				
	NIM 004960				
FARZ	NINI_004860				
GATAZ	NINI_052058				
GATAS	NIM_002051	GGTCACCGCCATGGGTTA			
GATA6	NM_005257		CACTGGCTATGGACACTGTCCC		
GCFC1	NM_016631	GAATTTAAGTCTTIGATCGAAGGAAAATAG			
GCM2	NM_004752		ACAACIGIIICCCAGGICAIAAIAIGAACA		
GGNBP2	NM_024835	GACAACGGCTGGAGCAAATTA	CAATTCTCATCAAAGGAAGATTTTTGTCTT		
GNAI1	NM_002069	AAATAATCTAAAAGATTGTGGTCTCTTTTA	CCAAATGTGGCATCACATCTCATAGCT		
GNAI2	NM_002070	GGACTGCGGCCTCTTCTG	TGAAGCTCAGAGCGTGGG		
GNAQ	NM_002072	TTGAACCTGAAGGAGTACAATCTGGTCTAA	AACAATGTCATCTTAAGGACAAAGAAAAGA		
GTF2H1	NM_005316	GCGTCTGATGAAGAAAACGTG	GCATGTGCTACCATGCCTG		
GTF2I	NM_001518	ACCAGACCCCACGTGGTA	TCTGAGAAACACCGCAAGTGG		
HDAC1	NM_004964	GGAGGTCAAGTTGGCCTG	AAACCTCAAGGGAGGAGTTAAGGC		
HDAC3	NM_003883	AATGACAAGGAAAGCGATGTGGAGATTTAA	AATAATAAATGTAGAATACATACACAGGGC		
HDAC5	NM_005474	CAGGAGCCTGCCCTGTGA	TACAGGACAGATCTTGCGCC		
HDAC6	NM 006044	TATGCCCCACCCACACTA	TTCAGTTAGTTTTTTGGGGGCAATGGA		
HES1	NM 005524	GAGGCCGTGGCGGAACTG	TAGTTCATGGAGGATTGGTGAAAAGTTTGA		
HES5	NM 001010926	CTCTGGCGGCCCTGGTGA	GACCCCACCCTTCTTCCG		
HES7	NM 001165967	TGGAGACCTTGGCCCTGA	AAGTAAGGAATGGGGGCAAATCTTAAGAGTG		
ΗΗΔΤ	NM 018194	GACCTACGCCACGGACTA	GCACCACCATTCAGAGTAACTACAAGATTT		
HIF1A	NM 181054		TACATTAAGGTGATGGCACTAAGATAAATG		
	NM 002114		TTTCACATGGTAGAAAGGCGAGTAAAGTCT		
	NM 006724				
	NM 005516	CTCTCACTCTCACACCTTCTA			
	NIM 002071				
	NIM 021059				
	NINI_021956				
HIVIBUXI	NIVI_024567	GGCCCTGGATGATGACTG			
HNFIA	NIM_000545				
HOXA1	NM_005522				
HOXA10	NM_018951	GAGCICACAGCCAACIIIAAIIIIICCIGA			
HOXA3	NM_030661	AAGCICACCIGIGA	AATTIGATICCTTICTCGAGGAATCCTTAA		
HOXA9	NM_152739	GACCGAGCAAAAGACGAGTGA	GCGGACTGGTTGTGGCAG		
HOXC11	NM_014212	TTTCTCGGGAAATCCTCTGCTGTA	CGGCTAGCACCGGCCTAT		
HOXC4	NM_014620	AGAGGACATTACCAGGTTATA	CCTTGCTTGTTCTTCTAAGGACATTGGAAG		
HOXC5	NM_018953	TTCCAAAATGAAAAGCAAAGAGGCTCTTTA	AATTTCACCTCCCTCTACTCACTG		
HOXC6	NM_004503	AGAAGAGGAGAAGCAGAAAGAGTG	GAAGGCCGGGGCCGGGCG		
HOXD1	NM_024501	GTCCCAAGAGCCTTCGTG	AACAGAGCAAGACTCCGTGTCAAAAAAAAA		
HOXD10	NM_002148	CGCCAACCTCACGTTTTCTTA	CCTCCAGCTTTTCTCCCCCAT		
HOXD11	NM_021192	GCAGTATTTCACTGGAAACCCCTTATTTTG	TCGATTTTCAGTTGCATGGGTTCTG		
HOXD3	NM 006898	CAAACTGACGCATCTGTA	CCCGAGAACCAATTTATGCACTAGACT		
HOXD8	NM 019558	AGCCGAAGGCCTGACAAATTA	TTTTTTTTTTTAAACAGCGCGGAATGTGT		
HOXD9	NM_014213	GAAATGCCCCAAAGGAGACTG	GAGACACATCAGAGAGATCTGTCAGGT		
HRAS	NM 005343	AAGTGTGTGCTCTCCTGA	GAGCACCACAGCCCAGAC		
HSF1	NM 005526	GGACCCCACTGTCTCCTA	CTGGGGAGTCGGGCAGGC		
HSF2	NM 001135564	GGATAGTGATATGCCACTTTTAGATAGCTA	TCCAGTGATAATATTCTTACACTATTTGGG		
ID1	NM 181353	GAGATCCAGATCCGACCACTA	TTAAAGACACCGGAAACACTCATTCAG		
ID2	NM 002166		CALCENCIE CONVICTOR CONTINUES		
102	NM 002167				
105	NIM 002107				
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IKF5	NIVI_001242452		TGAGATACTATCTCACCTGTCAGGTTG		

ITFG2	NM_018463	CCTCCAGGATCCCACCTA	AGTATAATTGAGAGGAATTTGAAAGCAATG	
JAK2	NM_004972	GGATCAAATAAGGGATAACATGGCTGGATG	GATTTCTGCATCCAGAACTATTAAAATGCT	
JARID2	NM_004973	CAAAAGTGCTTCGAGCTCATCATG	ATGGAAACCATTAGGTTAGGCTGAAG	
JUN	NM 002228	ACGCAGCAGTTGCAAACATTTTGA	TTCTAGTTTGACTCTTCCTAAATTCTTTGC	
KL	NM 004795	CTCGAAGAAAGGCAGAAGAAGTTACAAATA	TGGGTCGCCCTCCCACCC	
KLF4	NM 004235	CTCGCCTTACACATGAAGAGGCATTTTTAA	GTTTTTTTTAATAAAAAAGGTATTTTAA	
KLF5	NM 001730	TATGAAGAGGCACCAGAACTG	CAGAGCGAGACTCCGTCTCAAAAAATAAAT	
KRT1	NM 006121	TCTACCACTTATTCCGGAGTAACCAGATAA	GGTGAAATGTTGCCTGGTTGG	
KRT12	NM 000223	CAAGTTCAGGAAATTGAAGAACTAATGTAA	CTTAATCCTCAAACCCTGACATCTTCATCC	
LMX1A	NM 177398	TCCATGCAGAATTCTTACTTCACATCTTGA	TTGAAGACCCTTTTCTCCTTATGTTTTGCT	
LRFN1	NM 020862	CTGGAGAGTACCGTGTGA	ATCTTCCCATCTTCCTTCAGTCTCACTTAG	
LRFN2	NM 020737	ATGGAGAGCACGGTCTAG	TCTTGTCAATTGGCAACAATTACCCACTAC	
LRRN1	NM 020873	CGACACATCCAGAAGCTATTACATGTGGTA	CACTGCCCATTAGGTGCTAGTCAGT	
	NM 005583	AGCCCAGAGGTGCGGTGA	CTTCTGTCCAAGCGCCGG	
MAB2111	NM 005584	ACCAACCCGAAAAGTTTGGAAAAACTTTAG	ΑΤGCACTGTATTTTATTTTAAAATAACTTA	
MAF	NM 005360		GTCAGATACATTGTAAAAAAATTATTACATG	
MAF1	NM 032272	GGTCCCAGTGATCTGTATTTG	CTCTGCCTCCATTTCAGCAACT	
ΜΔΕΔ	NM 201589	CCCGACTTCTTCCTGTAG	CTECTCACTTTCTCCCTECT	
MAER	NM 005461			
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MAG	NIM_001101373			
MAY	NM 1/5112			
	NNA_005596			
	NM_005586			
IVIED 28	NM_025205			
INICB	NM_005931			
MILL3	NM_170606		AACTTATTIGAAAATCTAAGAAAACCAAGT	
MILL4	NM_014727			
MLL5	NM_182931			
MLPH	NM_024101	GGTGGCCCACCAGTCCTA	GAGAAACCACTGACTTCTGTCAATCTTTAG	
MLX	NM_170607		GAGGCAGAAGTACTGTAAGGAGTGGA	
MMP11	NM_005940	TGCCAACACTTTCCTCTG	GCAGAAGGAGCCCTGAGCA	
MSH3	NM_002439	GGAAGAAACACAGACTTCTCTTCTTCATTA	GTTAATGAACAGAAAGGTCCCAAATGAACA	
MSX2	NM_002449	TGGCATGTACCACCTGTCCTA	CCCCACCACCACCAATCAC	
MTOR	NM_004958	CTTAGGTGCCCTTTCTGGTAA	TGGGAACAGTCTGAGGAAAGGGA	
МҮВ	NM_005375	CCGGACGCTGGTCATGTG	TGTTCTTTCTTTTCCATTGTAATGATTCCT	
MYBBP1A	NM_014520	AAGGCAGGGAAGCCCTGA	CAGGTGGAATACTCACCCACCAA	
MYBL2	NM_002466	TCGGACCCTCATCTTGTCCTG	AAACAGGGTCAAGGGCTCAG	
MYC	NM_002467	GCTACGGAACTCTTGTGCGTA	GAACTTAAAGACCTTAAGGCCCCCA	
MYCBP	NM_012333	GAGGAGAAGCGTGCTGAATAG	TTTAGGCCCAGCAGTTTGGGTATT	
MYCL1	NM_001033082	AAAAGAATTGCATACCTCACTGGCTACTAA	ATGTCTGAAATGGCATTTCAGGAACC	
MYCN	NM_005378	AATTGAACACGCTCGGACTTGCTA	GGGACAATGACTCATGCCCC	
MYF5	NM_005593	TAGTTCCAGGCTTATCTATCATGTGCTATG	CCTAAACTGGGTACATGAGAATGGTAAATA	
MYF6	NM_002469	GGAGGAAGTGGTGGAGAAGTA	AGGAAAGCCAAATTTCCTTTCAATTGG	
MYOD1	NM_002478	CCCGATATACCAGGTGCTCTG	TTTGCACCCCTCCTTCCTTC	
MYOG	NM_002479	GATGAAACCATGCCCAACTGA	AAGAGCAGGGGTCCCCAG	
MZF1	NM_001267033	AACGCAGCAACCTGCTGA	ATGCTAGGAGCCACCTCTCTCA	
NAB2	NM_005967	TGAGGCCAGCCGGCAGTG	CCAGGGTGAGAGTCTGGGTC	
NANOG	NM_024865	CATGCAACCTGAAGACGTGTG	AGGTTCAAGCGATTCTCCTGC	
NCOA6	NM_014071	TCCAAGCGAAGAAAATCCAAGTAA	AAGCCAAGAATGAGGTGAGGGA	
NCOR2	NM_006312	CTCTCCGACAGCGAGTGA	TTACCAAGGGTATAAATATTCAACTTGCAA	
NFE2L2	NM_001145413	AGTAAGAAGCCAGATGTTAAGAAAAACTAG	TATTTCTCTGTAACCCTGGTACTAGAAATG	
NFKB1	NM_003998	AGGACCTCTAGAAGGCAAAATTTA	AAACACTTTCCTTTTGATAATTATTTGTTC	
NFXL1	NM_152995	TACATCACCCATGATGTCAATTAA	AACATATCTACTTTTAGATACTTTTAGGT	
NFYC	NM_014223	CCAGGTGACCGGCGACTG	AGGTACACAGCATTAAGTTCCCTTAGCT	
NHLH1	NM_005598	CCACGTGCTGGACGTCTG	TGTGGCCCCTTTTCTCTGTCTT	
NHLH2	NM 005599	CACGTCCTGGACGTGTAG	ΑΤCAAATATTTCACTACATAAATATGTTTA	
NKX2-1	NM 003317	TACGGTCGGACCTGGTGA	CCTGGCCTCCTTACCTCCTTAA	
NKX2-5	NM 004387	GGTATCCGAGCCTGGTAG	AACCAGTATGGTTCCAGCAAGG	
NRF1	NM 005011	GGTGGTGACATTGGAACAGTG	CTTTACGGAGGTCCCCAGC	
NRL	NM 006177	TCCCACCTCTTCCTCTGA	GCCTGCCCTCCACCCCA	
NRM	NM 001270710	CCTGGCTCACGGGCTTGA	GGGGGCGGGTCTGCGGGG	

NRN1L	NM_198443	CCTGAGGCCTCTGGCCTA	TGGGAAATGAGTGTTTGTAAGGAGGAAGAT	
NUAK2	NM_030952	TGCTCAAAGCTCACCTGA	GAGCTACTGAGCTCACGTTTGTTTTGATTC	
NUP153	NM_005124	ATAAAGACTGCTGTTAGACGCAGGAAATAA	CAGATACTTTCAGATACTTTCCCTTTCTCT	
OGN	NM_014057	AAAAGATTACCGATAGGGTCATACTTTTAA	AATTTGAGAGTTATTTGATGGTGTTTTGCT	
OLFM1	NM 014279	CCGCTCCGACGAGTTGTA	TGGAGATCCAACAGGGACCTGT	
OLFM3	NM 058170	CATATCATCAAGACAGAGGATGACACATAG	GAATCTCTTAAATTTTCCAACTCCCAGTAG	
OLFM4	NM 006418	TGTCTTGCAGAAGCCCCAGTA	TTATAAAAGTTATTGATGTGATCTGTTGTT	
ORC5	NM 002553	ATAATAAAATACTTGTATGATTTCTTGTGA	TGGGTAGCTAATTTTAAGAAAGTGACCAGA	
OTX2	NM 021728	TGGAAATTCCAGGTTTTGTGA	TCTATTTTATGCATAGATTAGCAAAAAAAA	
PAX3	NM 001127366	TTTCATTATCTCAAGCCAGATATCGCGTAA	ATACAACTGTGGGTTGTGTGTAACCTTATTTG	
PBX3	NM 006195	TGTGCACTCGGATACCTCTAACTA	GCAGCTGTTCCTTCCCTCC	
PRXIP1	NM 020524		GAGCAAAATGGAGCCAGGGT	
DITY1	NM 002653		GAATGGTGGTGGGGAAGCG	
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PTHLH	NIVI_002820			
PTIVIS	NM_002824			
QSOX1	NM_002826			
RARA	NM_000964	GGCCACCCACTCCCCGTG	GGCAGCTTGGAAGGGTGC	
RARB	NM_000965	TCAGTCACCACTCGTGCAATA	ATAGACTGCCGTGCATTAGCACA	
RARG	NM_001042728	CTGAAGTCCCCAGCCTGA	TGTCCCCACCACAATCCAG	
RB1	NM_000321	CATGGATACCTCAAACAAGGAAGAGAAATG	GAAGAAATAAATTTGGAAATCTCTAGCATA	
RB1CC1	NM_014781	AAAGCCGTATCATGGAATAAGAAAGTATAA	GAAGGGTACCAATTAAGTCAAAATGGCCTA	
REV1	NM_016316	ACTTATGGAAGCACATTAAAAGTTACATAA	TTCCTGATATTTGGGCTTAGTGCTTCTAAA	
RFX1	NM_002918	GCGCTGCCCTCCAGCTAA	CCAGGCCGGCAACCTGGC	
RFX2	NM_134433	TCCCTGCAGGGCATCTAG	GGGGGACAGGGCCTAGAG	
RFX3	NM_002919	GACTGTGGAGTTATTGCAAGAGTTCCTTAA	GAAGTGGAAAAGATGAATATTTCAACTGAC	
RFX5	NM_000449	AAAGCAACACCCCCATGA	ΤΑΑΑΑΑΑCAAGCAAAATTAAACACATTTT	
RFX6	NM_173560	AGCAGCTGGAGGCACTTA	GGATATGATATGCAAATGTTTTTAAATTAT	
RHEB	NM 005614	TCTTCATGCTCGGTGATGTGA	ACAGAGTGAGACCCTGTCTTTAAAAATGTA	
RHO	NM 000539	CCAGGTGGCCCCGGCCTA	GCCTCCCAAAGTGCTGGGATTA	
RHOA	NM 001664	AAATCTGGGTGCCTTGTCTTGTGA	CCAGATTAGCTGCTGGGTGG	
RHOB	NM 004040	CAACTGCTGCAAGGTGCTATG	ATGCTCTCAAAGGGACTTCATCCTCATTTA	
RHOC	NM 175744	GGCTGTCCCATTCTCTGA	GAGCCAGGCATGACCTCATC	
RHOF	NM 019034	CTCTGCCTGCTGCTCTGA	GGCACCTGCGTTTGCCCT	
RHOG	NM 001665	TCCTGCATCCTCTTGTGA	GGGAGCCTAGAGCTTTGTTAGGGA	
RHOH	NM 004310	CTTCTCCATCAATGAGTGCAAGATCTTCTA	AAAGTGACACTCTCTTGCTTCTGTTC	
RHOT1	NM 001033566	TATGTACAAAGCATTATTGAAACAGCGATG	CCAAAGTGCTGGGATTACACGATTGA	
RHOV	NM 133639	AAGAAGTTCTTCTGCTTCGTTTGA		
RINS	NM 024832	GGAGCCCAACTTCCTGTG		
	NM 012421	GACAGATGAGCTTTGTGTGGGAAGTTCATA		
DNE1E2	NIM 172557	ΑΓΤΟΤΟΛΟΕΤΤΤΟΤΟΤΛΟΟΛΛΟΤΤΕΛΤΑ		
DNE42	NIM 017762			
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ROCKZ	NIVI_004850			
RURB	NM_006914		GGAAACIIIACAAAGCAGGGGIIIGIAIGI	
RURC	NIM_005060			
RICA	NM_003729	AGGAATIGGGATGACAAATCCAAATCTATA		
RXRB	NM_001270401			
RYK	NM_002958		GGAGICIGAGCCAGCIIAACIGI	
SDC1	NM_002997	AAACAGGAGGAATTCTATGCCTGA		
SDC4	NM_002999	AAIGAGTTCTACGCGTGA	CICIGCCCCCACCCTCTG	
SETDB1	NM_012432	TGAATGCAGAGGACGTCTTCTTTA	CGAGAACTCCATCTAAAAAAATTCACATGC	
SIM2	NM_005069	CATCACCAACGGGAGGTG	AAAGGAATTCCTTTCCCTGGGAG	
SIX1	NM_005982	GTGGACTTGGGGTCCTAA	GAACAGAAATAGGAAAGAGTAAGAAAGAAA	
SIX2	NM_016932	GTGGACCTGGGCTCCTAG	ACCTAGCGACTGACACAAGTCG	
SIX6	NM_007374	CAGCGAGTGCGACATCTG	GTTTAAAACATATACCAGGAAGCACCAAAG	
SMAD6	NM_005585	CCTCCTCAACAACCCCAGATA	AGAGTAAATGTGACTTTCCTCCCTTTTCAA	
SMARCE1	NM_003079	CCCATACCAGAAGATGAGAAAAAAGAATAA	AGTTGGGTGAGACAAGGGC	
SNAI1	NM_005985	CTCAGGATGTCCCCGCTG	GTGACACCCAGGACTCCAAAG	

SNAI2	NM_003068	TGCTGTGTAGCACACTGA	TTTTTGTTAAAGTGGTATGCTAACAAACCA	
SNAPC1	NM_003082	ATCCAAGAAGAGGAGAAAACACTG	AGTGGGGCCAATAATGGATCTACA	
SNF8	NM 007241	AGAGAAGCCCTCCCCTGA	TTTTCTTTCCTCCAATTTAGCCACGATTGG	
SNX4	NM 003794	AATGCTAAGGAATGCTTTAGCAAGATGTAA	TGTGTACTCAATGTTTAGCTCTCACTGATA	
SNX6	NM 021249	GCAGTGTTAAATGGAGACACATAA	AGGGGCCAAGGGATGCAC	
SOHLH1	NM 001012415	GCTGGTCCCCCGCGTAA	CTACCCCAGGGCACCAGG	
SOLH	NM 005632	TEGECCCCEACCECTETE	CTTGTGAGTCACCCCAC	
SON	NM 138927		GTGTGTGTGTGTGTGTGTGTGTGTG	
SOX13	NM 005686		GCATTCCCTTCCATTAACCCAATTCC	
50/15	NM 002106			
5072	NINI_005100			
2012	NINI_005054			
50X8	NIVI_014587			
5089	NIVI_000346			
SPZ	NM_003110			
SP7	NM_152860	AGCAACTIGCIGGAGATCIGA		
SP8	NM_182700		AGCITIGCCAAATAGATCTTTCCATCTAAC	
SPDEF	NM_012391	TTCGTGCACCCCATCTGA	CAATCAATTATCCCTTGCCCTTTAGGCT	
SPEN	NM_015001	GATTGTCATTGCCTCCGTGTG	GGACTGACTGACTAGGAGGCAGAA	
SPI1	NM_003120	CGCCACCCGCCCCACTGA	TGTGTCATTGGTCCTCATGTTCC	
SREBF1	NM_001005291	ACTGTCACTTCCAGCTAG	GTAAACGTGTGTATTATATCTGGCCTCGTT	
SREBF2	NM_004599	TGCCATTGCCGCCTCCTG	TGGGGTAGGGGGGGGGGGGG	
SSRP1	NM_003146	GCGTCAGGATCCGATGAGTAG	AATGCTCGTCCAGCCGGG	
SSX1	NM_005635	CCCTGAGGAAGATGACGAGTA	GCGCTCAGCACGAGGACA	
STAT1	NM_007315	TTTGTCTTTTTACAGATGAACACAGTATAG	TAGGGCAGGTAAGGACAACATTTAGGAAAA	
STAT2	NM 005419	TTGATGCCTTCTGACTTCTAG	AAGGGAAGAAGAAATATGACAAGAGGAATG	
STAT5A	NM 003152	CAGAGGCTCCCTCTCATG	AAACCACAGCAAAGCGGG	
STAT6	NM 003153	GCCAACCCCAGTTGGTGA	CCCCAAGTCCTTTGCAATTTCTTC	
STRA13	NM 001271007	CAGCTCCTGGACTTCTAG	CCTGGGGGTGGGGCCGAG	
SUV420H2	NM 032701	CGGCGGTGAAGAGCTGTG	CCTAGTCCATCACGCTCCCAAAT	
SWI5	NM 001040011		TTATGCTAATTCCTCACAGGATGATTTTAA	
TAF4	NM 003185			
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	NN4 000102			
TBX5	NM_000192			
IBX6	NIVI_004608			
TCERG1	NM_006706			
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TCF19	NM_007109	GGCTGGCATTCAGACCTA	GCCTGGGACACAGTAGATAGACAC	
TCF7L2	NM_030756	GCTCGTCACCAAGTCTTTAGAATA	GAGTCCAAGACCACGTTCTGGTATCTAA	
TEK	NM_000459	TGCTGAAGAAGCGGCCTA	AGGAGACCTTTTCAATCTGATGAGCTTC	
TERT	NM_198253	TTCAAGACCATCCTGGACTGA	TGACCACAACCCCATTCACTCATAG	
TFAP2A	NM_003220	AAAGAGGAGAAGCACAGAAAGTGA	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
TFDP1	NM_007111	CGAGAATGACGAGGACGACTG	ACAACATGTGGTGGTGGGGTTT	
TFE3	NM_006521	AGCATGGAAGAGGAGTCCTGA	TTTGCATATTGTCTTCCTCCATGCC	
TFEB	NM_001167827	GAGGGCGATGTGCTGTGA	TGAGGCGTGTGACAAGCGT	
TFG	NM_001195479	ACCTGGACCTGGTTATCGATA	ACCAAATGGCACTGTTTTCTCTGAAT	
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TOPORS	NM 005802	TGTCTTGGTAGAGACTGTGATATGTCTTAA	AGGCAAAGGCAAACTGAAGGC	
TP53	NM 000546	GGGCCTGACTCAGACTGA		
TP53RP2	NM 005426		GCAAATGGGTTTGGAAACAATTCACAAA	
TRIM29	NM 021253	CCCAACAGATTGGGAGTG	CTCTGTCTCATAAATAAAATGTAGATGTCC	
TDIM71	NM 001020111			
	NIM 007344			
1111	NN4_002504			
	INIVI_003594			
	NIVI_000474			
UBIE	NIVI_014233			
USF1	NM_207005	GILAILAAGAAIGACAGCAACTAA		
USF2	NM_003367	CGAGGGCACCCGGCAGTG	CCATCCAACCAACCACTGGGTAAT	
USP6	NM_004505	TGATTACGAAAAGTACTCTATGTTACAGTA	GTACTGGTCTGTAGCCCAGGAGT	

VAMP2	NM_014232	CCTCTCTCCACAGTTTACTTCAGCACTTAA	CTCTTGCAAAGTCCAGTCCATTACCAAT
VEGFA	NM_001171627	TGTTTTCCATTTCCCTCAGATGTG	ACAACAAGGTGGGTCACCC
VIM	NM_003380	AACTTCTCAGCATCACGATGACCTTGAATA	GTGAGGTCTATCAAAAATGACAAAATTAAG
VIMP	NM_203472	TCTGGCGGATGAGGCTAA	TCCCCTCCATTATCTCCTAATCATTCTC
WT1	NM_024424	CTCCAGCTGGCGCTTTGA	TGAAGTTTGACAGAGAGAAATAAATTGTGG
XBP1	NM_005080	AGCTGGAAGCCATTAATGAACTAA	AAAGCAGGCAGTAATTAAGGTGGAAAA
XRCC3	NM_005432	GGGACCCAGTCCCACTGA	AGCTACTTAACGGTTCTGGGCC
XRCC4	NM_022550	AGAAGACCTCTTTGATGAGATTTA	ΑΤΑΑΑΤCTTTTATCAATAATCCCTGAAAAA
XRCC5	NM_021141	TTGTTCTTGTTCACAGTTGGACATGATATA	TCCTAGAAGCCCAAAGTAAAGCACT
YBX2	NM_015982	ACCACCATCCTGGAGTGA	AACCCATGATAGGGGCACTCTTC
YY1	NM_003403	TAAGGCCAAAAACAACCAGTG	TCAATAATCACTGTAATTGAGTGCAAAATA
ZCCHC3	NM_033089	CGGCGTGGCCGGGCACTA	CAACGTAGTAGGTGCTAAGTGTTGC
ZFP36L1	NM_004926	TTCAGCAGACTTTCCATCTCAGATGACTAA	GCTATAGGCTTAGCTTATAGGGATGAGAGA
ZFYVE1	NM_178441	AATAAAAAGCCCGGTGACCTTTAA	GTAAAAGACTGCAGTATTTGCAGGTAAAAT
ZKSCAN5	NM_014569	TACCTTAAGTGTAGAGGGGTCTCTGTTGTA	ATTAACAGTGATGCGGGTCTTCACT
ZMYND11	NM_006624	CTGCCGCCGGAAAAGATG	GTTTAAGTGAACAAATGATGTTTAACACAC
ZNF282	NM_003575	GCCTCCTGAGCGAGACTA	CACTACCCCCCTCCCCCA
ZNF331	NM_001079906	ACATCAGAGGATCCACAACAGTTG	CTCTGGGCCCTGACCCCG
ZNF362	NM_152493	GCGAATCTCTCTCATCTG	CTCAGTTCAGCACCTGGAGTGA
ZSWIM4	NM_023072	GCGGGAGCGTTTTGGTTG	CTGGGCAACAGAGAAAGACCAAAAAAAAAA

Primer	Sequence
SV40 let-7c target mutagenesis F	CTTGTTTATTGCAGCTTATAATGACATGTAACCATACAACCTACTACCAGTTACAAATAAAGCAATAGCATCAC
SV40 let-7c target mutagenesis R	GTGATGCTATTGCTTTATTTGTAACTGAGGTAGTAGGTTGTATGGTTACATGTCATTATAAGCTGCAATAAACAAG
SV40 miR-10b target mutagenesis F	CTTGTTTATTGCAGCTTATAATGACATGTACAAATTCGGTTCTACAGGGTAGTTACAAATAAAGCAATAGCATCAC
SV40 miR-10b target mutagenesis R	GTGATGCTATTGCTTTATTTGTAACTACCCTGTAGAACCGAATTTGTACATGTCATTATAAGCTGCAATAAACAAG
SV40 gateway F	GGGGACAGCTTTCTTGTACAAAGTGGAACTTGTTTATTGCAGCTTATAATGGT
SV40 gateway R	GGGGACAACTTTGTATAATAAAGTTGGACGGTATACAGACATGATAAGATACA
pmiRint pro mut F	GTATCATATGCCAAGTACGCCCCCCTCGAGATGGCCTCCTCCGAGAACGTC
pmiRint pro mut R	GACGTTCTCGGAGGAGGCCATCTCGAGGGGGGGCGTACTTGGCATATGATAC
CMV (Spel)	ATGACTAGTAGTTCCGCGTTACATAACTTACGGT
CMV (Sacl)	GAGCTCTGCTTATATAGACCTCCCACCGTA
L2R3 (AsiSI) F	ACGTGCGATCGCACCCAGCTTTCTTGTACAAAGTTGG
L2R3 (Mlul) R	ACGTACGCGTGTAAAACGACGGCCAGTGAATTATC
miR10b 400 asisi F	ACGTGCGATCGCAAGAATATTCTGGTTGTTCGCC
mir10b 400 noti R	ACGTGCGGCCGCTCTTTCTTTCTTTCAGCACCC
let7c 400 asisi F	ACGTGCGATCGCGACATTTTACGTGACCTATGCTG
let7c 400 noti R	ACTGGCGGCCGCCCATTAGAAATACCATTTTGACA
PGK BamHI F	CATGGATCCTGGTACCTACCGGGT
PGK Pstl R	CATCTGCAGTGTCTAGAGTCGAAAGG
TIC mut Pstl F	GGACGTGGTTTTCCTTTGAAAAACACCTGCAGTAATCCATGGAAGACGCC
TIC mut Pstl R	GGCGTCTTCCATGGATTACTGCAGGTGTTTTTCAAAGGAAAACCACGTCC
SV40 pA For (Nsil)	ACGTATGCATAACTTGTTTATTGCAGCTTATAATGGT
SV40 pA Rev (XmaJI)	ACGTCCTAGGGACGGTATACAGACATGATAAGATACA
TIC P2RP3 mut F	GTCCAAATTGTAACTAGAGATCTCCGCGCGCGCTAGCGGGACGCGCCCTGTAGCGG
TIC P2RP3 mut R	CCGCTACAGGGCGCGTCCCGCTAGCGCGCGGGGGGAGATCTCTAGTTACAATTTGGAC
P2R-P3 BgIII F	CATAGATCTGTAAAACGACGGCCAGTCTTAAGC
P2R-P3 Nhel R	CATGCTAGCCAGGAAACAGCTATGACCATG
MS2 BgIII F	ACGTACAGATCTACATGAGGATCACCCATGTCT
MS2 Apal R	ACGTACGGGCCCACATGGGTGATCCTCATGTTT
pLIFE ampli F	GGCGGAAAGTCCAAATTGTAACTAGAGATC
pLIFE ampli R	CAGGAAACAGCTATGACCATGTAATACGACTCACTATAG

Supplementary Table 2a - 3'LIFE hits - let-7c

Rank	Score	Refseq	Position	Alignment (top 3'UTR, bottom miRNA)
1	0.52	E2F5	1-37	5' GAUUCCAUGGAAACUUGGGACUGUUAUC <mark>UACCUC</mark> UAA 3'     :
2	0.58	CREM	779-804	5' AGUAAACCACAAAAAAUACCUCAGG 3'                 3' UUGGUAUGUUGGAUGAUGGAGU 5'
3	0.58	RHOB	922-951	5' CUGACCACACUUGUACGCUGUAACCUCAUC 3' :             ::        3' UUGGUAUGUUGGAUGAUGGAGU 5'
4	0.60	HOXD1	510-535	5' UUUAAAAAAGCGGUUUC <mark>UACCUC</mark> UCU 3'       : :         3' UUGGUAUGUUGGAUGAUGGAGU 5'
5	0.60	XBP1	798-836	5' GGAACACCUGCUGAGGGGGGCUCUUUCCCUCAUG 3'        :  :: : :        3' UUG-GUAUGUUGGAUGAUGGAGU 5'
6	0.65	SETDB1	330-351	5' GGAGCCUGUGUAUCUAC <mark>UAUCUC</mark> CAG 3'  :    :     :    3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
7	0.65	SREBF1	805-837	5' GGCCUCCAUGGGGUCAGUUGUCCCUUCUCACCUCCCA 3'     :   :              3' UUGGUAUGUUGGAUG <mark>A-UGGAG</mark> U 5'
8	0.66	РВХЗ	892-923	5' UGUAGCUUAGAGUGCUCACUUAC <mark>UACCUC</mark> UGA 3'            :          3' UUGGUAUGUUGGAUGAUGGAGU 5'
9	0.68	ID1	173-199	5' CGUCCCUUCCAACCCGCC <mark>GGUCUC</mark> AUU 3'           :   ::     3' UUGGUAUGUUGGAU-G <mark>AUGGAG</mark> U 5'

10	0.69	MAF1	246-274	5' ACUGCCCUGCCCAAAUGAACUGCCACAGC 3' :            :      3' UUGGUA-UGUUGGAUGAUGGAGU 5'
11	0.70	BHLHB9	1802-1825	5' CUUUGCAUGUCAAUAAAUAUGCCUCUAC 3'    :    :  :  :     3' UUGGUAU-GUUGGAUG-AUGGAGU 5'
12	0.70	NRM	-2-25	5' UGAUCAGCAAGACCUCCGCUACCUCCGG 3'     :   :     :       3' UUGGUAUGUUGGAUGAUGGAGU 5'
13	0.70	BCCIP	215-247	5' UUUUCCUUUUCUAACCUAUUAAAAUACCUCACU 3'             :        3' UUGGUA-UG-UUGGAUGAUGGAGU 5'
14	0.71	RFX6	450-474	5' AAAGUCAAAUGUGUAUGUUC <mark>UACCUC</mark> CAA 3'  ::    ::  :          3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
15	0.71	МІСВ	732-757	5' GGUUCAAGCACUUCUCG <mark>UACCUC</mark> AGA 3'     :          3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
16	0.72	HSF1	287-319	5' AGAAUUGUAUUUUGGAUUUUUACACAAC <mark>UGUCCC</mark> GUU 3'   :::    : ::    : 3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
17	0.72	DLX4	165-196	5' CUAACCCUAACAGCUAAAUCAAGGACCUCAGC 3'           :            3' UUGGUA-UGUUGGAUGAUGGAGU 5'
18	0.73	RHOV	807-828	5' AAGGUCACACAGCCUAG <mark>AAGCUA</mark> GAG 3' :::      :          : 3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'

19	0.73	CNNM2	1207-1232	5' GAGGGCUCUGUGCCUCC <mark>UGCCUC</mark> AGA 3' ::   :     :     3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
20	0.73	USF2	296-323	5' GAGGCCCUGCCACGUCCCGC <mark>UGCCUC</mark> CUG 3' ::       :   :  !   3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
21	0.73	RARB	1026-1060	5' ACUCCCAAAGAAACAGGCAUAGAAUC <mark>UGCCUC</mark> CUU 3'                       3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
22	0.73	OLFM4	714-736	5' AAAGUCAGUAGAAUCUUCUACCUCAUA 3'  ::        :           3' UUGGU-AUGUUGGAUGAUGGAGU 5'
23	0.73	CRK	1950-1971	5' GCUAAUUUAAUGUAUUUUACCUCACA 3'   :    ::   :       3' UUGGUAUGUUGGAUGAUGGAGU 5'
24	0.74	DNMT1	293-317	5' GUAGUUUUUAUAUGUUGUAA <mark>UAUUUC</mark> UU 3'  :: :   :: :     ::   3' UUGGUAUGUUGGAUGAUGGAGU 5'
25	0.74	SMAD6	99-127	5' AAAACCCCCCAGAUAUCAUC <mark>UACCUA</mark> GAU 3'          :        : 3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
26	0.75	ETNK2	387-413	5' GGAGGCGGGGGGGGGCUCCUUUC <mark>UACCUC</mark> CAG 3'  :  : :  :  :         3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
27	0.75	ARID3A	382-414	5' ACAGCAGUGUGGGCCGAUCCUGUUUACCUCAUA 3'  :  : ::      : :        3' UUGGUAUGUUGGAU-GAUGGAGU 5'

28	0.76	EZH2	15-38	5' GAAAUCCCUUGACAUCUGCUACCUCCUC 3'        :  :  :      3' UUGGUAUGUUGGAUGAUGGAGU 5'
29	0.76	STAT2	1192-1214	5' GGGUUCAAGUGACUCUCC <mark>UGCCUC</mark> AGC 3' : :   :::       :     3' UUGGUAUGUUG-GAUG <mark>AUGGAG</mark> U 5'
30	0.76	ННАТ	695-725	5' AGAGAAGUAUAACAUGGUAGUUCCUCUACCUUACA 3'  : :  :            :  3' UUGGUAUGUUGGAUGAUGGAGU 5'
31	0.76	MYCL1	548-569	5' UGAUCAACAUUGACCAUUACCUCACU 3'        : :    :      3' UUGGUAUGUUGGAUGAUGGAGU 5'
32	0.77	TRIM71	174-204	5' AGAAAAGUACAACAUUGCUUAAGUCCUACCUCAUC 3'    :      :          3' UUGGUAUGUUGGAUGAUGGAGU 5'
33	0.77	SPDEF	36-63	5' GCCUCUCCUGCCUGCCC <mark>UGCCUC</mark> AGC 3'  :     :   :       3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
34	0.77	EN2	1371-1396	5' ACAGUUCUGAAACAUGUGGCUACCUUGUC 3'  ::: :      :     :: 3' UUGGUAUGUUGGAUG <mark>AUGGAG</mark> U 5'
35	0.78	TTF1	96-118	5' GUGGUAGUGCACACCUGUAAUUUCAAC 3' ::: : :       ::  ::    3' UUGGUAUGU-UGGAUGAUGGAGU 5'
36	0.79	HES5	50-76	5' ACGACCAGAGGGCGAGCCUGC <mark>UCCUCUC</mark> GCC 3' :     :  :   :      : 3' UUGGUAUGUUGGAUG <mark>AUG-GAG</mark> U 5'

37	0.80	RNF7	226-254	5' UAAUUUAUUAAAGGUGGUCCUUCCUACCUCUGU 3'   ::       :         3' UUGGUAUGUUGGAUGAUGGAGU 5'

Supplementary Table 2b: 3'LIFE hits - miR-10b

Rank	Score	Refseq	Position	Alignment (top 3'UTR, bottom miRNA)
1	0.44	ZMYND11	524-551	5' GGUAUAUGAUUGAAUUUAGGGAA <mark>CAGGGU</mark> UGA 3' : :  :  :   :         3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
2	0.47	SDC1	734-759	5' GUCGCUCAUGUG-UGCAA <mark>CAGGGU</mark> AUG 3'  :     :            3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
3	0.57	RARG	439-473	5' GUGCCUAAUGCUGUGUGAUGCACCUG <mark>CAGGGU</mark> GUG 3' 
4	0.58	LYL1	151-178	5' GGGGCAAGGUCUCGGGGGUCCGGAAGGGUGAU 3' :   :         :      : 3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
5	0.64	OLFM3	30-67	5' AGGCAAAUGUGACAUGUUUUCAUUGAUUUAAACAGUGUGAU 3' :      :     :      : 3' GUGUUUAAGCCAAGAUGUCCCAU 5'
6	0.67	NCOR2	668-695	5' GAUGUAAAUGAUGUGUUGGUUUA <mark>CAGGGU</mark> AUA 3' :::         :        3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
7	0.68	TCF15	249-273	5' AAAACAAAGACUGUUGGUGA <mark>CAGGGU</mark> GUG 3'             :       : 3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
8	0.69	MYF5	278-306	5' AUUUCUGAUAGGGGGCCAUUGAUUGAGGGUAGC 3' :   :         :       3' GUGUUUAAGCCAAGAUGUCCCAU 5'
9	0.70	CRK	78-104	5' AGUCUUAAUUACCAUAUUCAGGGUACG 3' : :                 3' GUGUUUAAGCCAAGAUGUCCCAU 5'

10	0.71	USP6	1960-1988	5' AUCAAAAGUAUUGGUAAUUGUAUAUGGGGUGUA 3'      :   :        ::    : 3' GUGUUUA-AGCCAAGAUGUCCCAU 5'
11	0.71	DPF2	283-311	5' GGCCCAGCCCCUGGUGAUCACAGGGUUCA 3'     :     :        3' GUGUUUAAGCCAAGAUGUCCCAU 5'
12	0.72	TCF19	1350-1382	5' AGUAUAAAGCCAUUUAAGAAUUCCAGAGUAGGGUGGG 3' : :         : 3' GUGUUUAAGCCAAGAUGUCCCAU 5'
13	0.72	SREBF1	717-760	5' CUUAGUGGCUUUUUUCCUCCUGUGUACAGGGAAGA 3' :  ::  :             3' GUGUUUAAGCCAAGAUGUCCCAU 5'
14	0.73	DLX1	791-817	5' UGAGGCUGUUUGCCAAUUCAGGGUUCU 3' : :  :           3' GUGUUUAAGCCAAGAUGUCCCAU 5'
15	0.73	ANXA7	94-133	5' ACCGAAAGAGCUUUCUGUCAAGGACCGUAU <mark>CAGGGU</mark> AA 3'           : 3' GUGUUUAAGCCAAGAUGUCCCAU 5'
16	0.75	FXR2	174-205	5' UCCAGGAGCUAGUGGAGGGGUGUGUAACAGGGUCAU 3'    : :                  :        3' GUGUUUAAGCCAAGAUGUCCCAU 5'
17	0.76	HOXD11	382-409	5' CCUUCCUCUUCGGUGAAUG <mark>CAGGUU</mark> AUU 3' :          :        3' GUGUUUAAGCCAAG-AU <mark>GUCCCA</mark> U 5'
18	0.77	NCOA6	267-302	5' UUCACAUUUCCUAAGCAGCCUAGAGUACAGGGUGAG 3'                   : 3' GUGUUUAAGCCAAGAUGUCCCAU 5'
19	0.77	HOXD10	257-285	5' AUUAUUUUUUCAUCGUAAUGCAGGGUAAC 3' : :         :       3' GUGUUUAAGCCAAGAUGUCCCAU 5'

20	0.77	ННАТ	252-278	5' GUGUCUUACCCAGCUACA <mark>CAGGGU</mark> GAC 3'                  3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
21	0.77	NUAK2	701-737	5' CCGGCUAAUUUUGUAUUUUUAGUAGAGACAGGGUUUC 3' :      :    :
22	0.78	HOXD1	442-468	5' UUUUGAGAUGACCAAAGCUAGU <mark>UAGGGU</mark> CUC 3' :  :         :      3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'
23	0.78	STAT6	920-955	5' UCCACACCUCCAAUGCUGCCUGGGAGCCAGGGUGAG 3'            :       : 3' GUGUUUAAGCCAAGAUGUCCCAU 5'
24	0.78	ASCL2	1112-1138	5' GACACGAGCAGUCCCUGAGGGGCGGGGUCCC 3'    : :        : :     3' GUGUUUAAGCCAAGAUGUCCCAU 5'
25	0.79	HIVEP2	1267-1289	5' AGCCGGUUUACAUGGGAACAGGGUUAA 3'   :            3' GUGUUUAAGCCAAGAUGUCCCAU 5'
26	0.79	GATA3	240-262	5' CUCAUAUCCCCUAUUUAA <mark>CAGGGU</mark> CUC 3'   :      :        3' GUGUUUAAGCCAAGAU <mark>GUCCCA</mark> U 5'

#### Supplementary table 3 - Literature review

The following references were used to define genes detected by 3'LIFE as either having a positive or a negative role in tumorigenesis.

#### *let-7c Targets:*

Gene	References:
E2F5	(Umemura, Shirane et al. 2009; Zhao, Wu et al. 2013)
CREM	(Passon, Puppin et al. 2012; Healey, Crow et al. 2013)
RHOB	(Marlow, D'Innocenzi et al. 2010; Zhou, Zhu et al. 2011; Kazerounian, Gerald et al. 2013; Medale-Giamarchi, Lajoie-Mazenc et al. 2013)
HOXD1	(Faryna, Konermann et al. 2012; Pussila, Sarantaus et al. 2013)
XBP1	(Doane, Danso et al. 2006; Sengupta, Sharma et al. 2010)
SETDB1	(Rodriguez-Paredes, Martinez de Paz et al. 2013; Noh, Kim et al. 2014)
SREBF1	(Furuta, Pai et al. 2008; Pandey, Xing et al. 2013)
PBX3	(Ramberg, Alshbib et al. 2011; Han, Gu et al. 2012)
ID1	(Kalas, Yu et al. 2005; Swarbrick, Roy et al. 2008; Pillai, Rizwani et al. 2011)
MAF1	
BHLHB9	
NRM	(Chen, Chen et al. 2012)
BCCIP	(Liu, Yuan et al. 2001; Meng, Liu et al. 2003; Lu, Yue et al. 2007)
RFX6	(Takata, Akamatsu et al. 2010; Huang, Whitington et al. 2014)
MICB	(Groh, Wu et al. 2002; Holdenrieder, Stieber et al. 2006; Kohga, Takehara et al. 2008)
HSF1	(Stanhill, Levin et al. 2006; Dai, Whitesell et al. 2007; Dai, Santagata et al. 2012; Xi, Hu et al. 2012)
DLX4	(Tomida, Yanagisawa et al. 2007; Zhang, Yang et al. 2012; Trinh, Ko et al. 2013)
RHOV	(Cavalli, Man et al. 2008; Peng, Zhou et al. 2011; Shepelev and Korobko 2013)
CNNM2	
USF2	(Ismail, Lu et al. 1999; Pawar, Szentirmay et al. 2004)
RARB	(Farias, Arapshian et al. 2002; Liu, Nugoli et al. 2011)
OLFM4	(Koshida, Kobayashi et al. 2007; Huang, Wang et al. 2012; Li, Rodriguez-Canales et al. 2013)
CRK	(Tsuda and Tanaka 2012; Kumar, Fajardo et al. 2014)
DNMT1	(Gazin, Wajapeyee et al. 2007; Huang, Stewart et al. 2013; Wajapeyee, Malonia et al. 2013)
SMAD6	(Kleeff, Maruyama et al. 1999; Jeon, Dracheva et al. 2008)
ETNK2	
ARID3A	(Peeper, Shvarts et al. 2002; Ma, Araki et al. 2003)
EZH2	(Chase and Cross 2011; Deb, Thakur et al. 2013)
STAT2	(Yu and Jove 2004)
HHAT	(Konitsiotis, Chang et al. 2014; Petrova, Matevossian et al. 2014)
MYCL1	(Kim, Girard et al. 2006; Xiong, Wu et al. 2011; Rudin, Durinck et al. 2012)
TRIM71	(Chen, Yuan et al. 2013)
SPDEF	(Steffan, Koul et al. 2012; Buchwalter, Hickey et al. 2013; Fletcher, Castro et al. 2013; Mukhopadhyay, Khoury et al. 2013; Noah, Lo et al. 2013)
EN2	(Martin, Saba-El-Leil et al. 2005; Bose, Bullard et al. 2008)
TTF1	(Lessard, Morin et al. 2010)

HES5	(Osipo, Patel et al. 2008; Mittal, Subramanyam et al. 2009; Aste-Amezaga, Zhang et al. 2010)
	also RAS implication
RNF7	(Tan, Li et al. 2011; Lazar, Suo et al. 2013; Yang, Huh et al. 2013)

## miR-10b Targets:

ZMYND11	(Wen, Li et al. 2014)
SDC1	(Yang, MacLeod et al. 2007; Ishikawa and Kramer 2010; Nguyen, Grizzle et al. 2013)
RARG	(Chen, Goyette et al. 2004; Goranov, Campbell Hewson et al. 2006; Zhao, Graves et al. 2009; Yan, Wu et al. 2010; Huang, Luo et al. 2013)
LYL1	(Nagel, Venturini et al. 2010; McCormack, Shields et al. 2013)
OLFM3	
NCOR2	(Cheng and Kao 2009; van Agthoven, Sieuwerts et al. 2009; Varlakhanova, Hahm et al. 2011)
TCF15	
MYF5	
CRK	(Tsuda and Tanaka 2012; Kumar, Fajardo et al. 2014)
USP6	(Pringle, Young et al. 2012; Rueckert and Haucke 2012)
DPF2	
TCF19	
SREBF1	(Furuta, Pai et al. 2008; Pandey, Xing et al. 2013)
DLX1	
ANXA7	(Srivastava, Torosyan et al. 2007; Torosyan, Dobi et al. 2010; Jin, Wang et al. 2013)
FXR2	
HOXD11	(Shiraishi, Sekiguchi et al. 2002; Miyamoto, Fukutomi et al. 2005)
NCOA6	(Lee, Lee et al. 2006)
HOXD10	(Ma, Teruya-Feldstein et al. 2007; Ma, Reinhardt et al. 2010; Sekar, Bharti et al. 2014)
HHAT	(Konitsiotis, Chang et al. 2014; Petrova, Matevossian et al. 2014)
NUAK2	(Suzuki, Kusakai et al. 2003; Tsuchihara, Ogura et al. 2008)
HOXD1	(Faryna, Konermann et al. 2012; Pussila, Sarantaus et al. 2013)
STAT6	(Gooch, Christy et al. 2002; Wei, He et al. 2014)
ASCL2	(de Sousa, Colak et al. 2011; Reed, Tunster et al. 2012; Zhu, Yang et al. 2012)
HIVEP2	(Fujii, Gabrielson et al. 2005; Yin, Wang et al. 2010)
GATA3	(Chou, Lin et al. 2013; Chu, Lai et al. 2013; Li, Ishiguro et al. 2014)

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#### 3'LIFE/High-throughput Nucleofection and Dual Luciferase Protocols V1 Developed by Justin Wolter, Mangone Lab, 5-21-2013

This portion of the protocol describes a method to transfect plasmid-DNA in 96-well format using the Lonza Nucleofector 96-well shuttle plates. This protocol is optimized for HEK293T cells. Each cell line will have optimal transfection efficiency/survival with individualized buffer conditions, pulse code, and number of cells. These conditions must be optimized for each cell line used.

#### **General Comments:**

- For consistent transfections, cells should be plated at a sufficient density that they are rapidly dividing, and not be more than 90% confluent at time of transfection. This is typically achieved by calculating the doubling time of the cell line, and seeding cells 24-48 hours prior to transfection at a density that will result in 70-90% confluency at the time of transfection. Cells should not be allowed to become 100% (and thus growth inhibited) at any time prior to transfection, as this will reduce transfection efficiency, growth rate, and thus expression of the miRNA and luciferase reporter.
- The Lonza Nucleofector and HEK293T cells are extremely sensitive to the buffer conditions used to transfect cells. Extreme accuracy when preparing buffers will ensure consistent performance of the equipment. Additionally, extra care must be taken when performing the assay to minimize evaporation of buffers. We have observed that this is the most significant source of errors when using the Nucleofector and in-house buffers. Specifically, special care must be taken to minimize evaporation following loading the buffer/DNA/cell mixture into the 96-well shuttle device. In our hands, loading the shuttle device immediately before transfection reduces errors in transfection.
- Owing to the sensitivity of the nucleofection buffer conditions, the total volume of transfected materials (including cells and plasmids) should not exceed 10% of the total liquid pipetted into each well of the 96-well shuttle device. To achieve this the pLIFE-miRNA plasmid should be at a concentration of least 500ng/uL.
- Transfection buffer is composed of PBS supplemented with 1.5% HEPES, pH to 7.00. This should typically be prepared fresh, although can be stored for up to 1 month at 4°.
- In formulating buffer and plasmid DNA volumes, we have found that assuming 120 reactions for each 96-well plate sufficiently accounts for errors in pipetting and volume lost using liquid reservoirs and multichannel pipettes.

The following protocol assumes transfecting 3 96-well plates in one experiment. Each plate will correspond to the same 96-well mini-prepped sample of pLIFE-3'UTR plasmids, and be treated with either pLIFE-miRNA-blank, pLIFE-miRNA-#1, pLIFE-miRNA-#2.

1. (24-48 hrs prior to transfection): Seed sufficient quantity of HEK293T cells based on the number of 96-well plates being transfected. Each well in a 96-well plate will require

75,000 cells, and each plate requires  $9 \times 10^6$  cells (equivalent of 120 wells to account for use of reservoir and multichannel pipette). In our lab, the doubling time of HEK293T cells is ~20 hrs, which can be used to calculate the seeding density based on the number of hours prior to transfection the seeding is occurring. We use 145mm circular culture plates, which, when grown to ~90% confluency, is sufficient for 3 96-well transfections, with ~10% of cells to spare to reseed a new plate.

#### 2. Items to be prepared prior to transfection

- a. Transfection Buffer: 18 uL per well, 120 wells/96-well plate = 2.16 mL per plate. Set this aside into an epindorf tube and set aside (being careful not to leave buffer exposed to prevent evaporation).
- b. Plasmids:
  - pLIFE-3'UTR: In 96-well format, resuspended to ~100 ng/uL per well. We typically observe insufficient luciferase signal if plasmid concentration falls below 40 ng/uL. 4 wells must be reserved for the following controls: 1) no pLIFE-3'UTR (to measure background of luciferase assay), 2) pLIFE-SV40 3'UTR (negative target control), 3) positive control for miRNA #1, 4) positive control for miRNA #2. We typically reserve wells A1-A4 for these controls.
  - ii. pLIFE-miRNA: At a concentration of 500 ng/uL for each miRNA and Blank control plasmids.
- c. 96-well cell culture plates: Each well should possess 200 uL of DMEM supplemented with 10% FBS, 1% Pen/Strep, and placed in a 37° incubator for use following transfection.
- d. Warm media, trypsin (0.25%) to 37°.
- e. Turn on all Nucleofector hardware followed by Nucleofector Shuttle software. Pulse code used for HEK293T cells and PBS/HEPES buffer should be set to FF120.

#### 3. Preparation of Plasmid DNA and cells:

- Prepare 3 stocks of pLIFE-miRNA + transfection buffer for each miRNA. This stock should account for 50% (10uL) of total volume of each well, multiplied by 120 wells. Thus, each stock should contain 1.08 mL buffer + 120 uL plasmid DNA (pLIFE-miRNA).
- b. Remove cells from plate by eluting media, washing *gently* with PBS, and treating with ~5mLs 0.25% trypsin for 5 minutes. Neutralize trypsin with an equal volume of media, and pellet cells at 300g for 5 minutes.
- c. Remove trypsin/media, and resuspend pellet in ~5-10 mLs media (depending on cell density).
- d. Count cells. Mangone lab uses the Countess from Invitrogen. Cells should be >95% viable and within accurate range of machine. Inaccurate count can result from having extremely high cell concentrations (>6.0x10<sup>6</sup>/mL). Transfecting too many cells can drastically reduce efficiency of miRNA targeting by reducing plasmid:cell ratio and/or decreasing transfection efficiency.
- e. Aliquot three tubes of cells, each containing 9x10<sup>6</sup> cells, corresponding to the cells required for transfection of one 96-well plate. Spin cells at 300g for 3 minutes.

- f. Remove media. Be sure to remove as much as possible with minimal disturbance of the pellet. Excess media can impact transfection efficiency.
- g. Resuspend cells in 1.2 mLs buffer/plasmid mixture, and set aside.
- h. The following steps detail resuspension of pLIFE-3'UTR plasmid in transfection buffer. As this occurs in 96 well plates, care should be taken to avoid evaporation of buffer by covering plates at all times.
  - i. Using a multichannel pipette, move 32.4 uL transfection buffer into each well of a 96 well PCR plate (9 uL [per transfection] \* 3 [plates] \* 1.2 [to account for pipette error]).
  - ii. Add 3.6 uL of mini-prepped pLIFE-3'UTR plasmid.
  - iii. Mix thoroughly.
  - iv. Pipette 10 uL of this mixture into each well of the 96-well shuttle device. Cover 96-well shuttle device.

#### 4. Transfection:

- a. Move 1.2 mLs of first cell/buffer/pLIFE-miRNA plasmid mixture into reservoir. Mix well. Add 10 uL of this mixture into the first 96-well shuttle already containing 10 uL buffer/pLIFE-3'UTR. <u>Mix well by pipetting up and down several times.</u> Equal suspension of cells in the buffer will entail even and thorough passage of the electrical current through the cuvette and maximize transfection efficiency. Place 96-well shuttle on the Nucleofector device and initiate transfection.
- b. Once transfection is complete, add 100 uL of prewarmed media from 96-well culture plate to each well of the 96-well shuttle and mix well. Move 100 uL from each well into the 96-well culture plate. Mix well, with pipette positioned vertically, as cells will tend to move to the sides of the well unless mixed properly.
- c. Repeat 3a-3b for the remaining two plates.
- d. Culture cells for 48-72 hours at 37°, followed by the dual luciferase assay (see below).
- 5. Cleaning 96-well shuttle plates: These plates can be reused following transfection and proper washing to ensure no carry over between nucleic acids between experiments. We perform two 70% EtOH washes using a spray bottle to completely fill each well, followed by wiping down excess EtOH on the electrode strips (bottom side) and allowing cuvettes to completely dry in the culture hood. We have tested for carry-over contamination by transfecting 12 wells with 2 ug pmaxGFP plasmid each into HEK293T cells, followed by a single wash with 70% EtOH, and a second transfection with no plasmid DNA. With this extremely high plasmid concentration, extremely bright reporter, and only one wash we observed no fluorescence in the second transfection for all 12 wells. We have reused each cuvette >30 times each with no detectable decrease in transfection efficiency.

**Buffer preparation for dual-luciferase assay:** The following buffer components can be prepared ahead of time and stored at room temperature (unless otherwise noted).

#### Firefly Luciferase Assay Buffer Components:

Stock solutions prepared separately and stored at 10x concentration: Reagent: Final Concentration (1x)

Glycylglycine	25mM	
K <sub>x</sub> PO <sub>4</sub> (pH 7.8)	15 mM	
MgSO <sub>4</sub>	15 mM	
DTT (store at 4°)	1 mM	
EGTA	4 mM	
Note: EGTA will not go into solution a completely.	at neutral pH.	Slowly add NaOH to EGTA until it dissolves

Reagents added just before luciferase	assay:
ATP	2 mM
Beetle luciferin	200 uM

#### Renilla luciferase assay buffer:

*Renilla* luciferase buffer can be prepared ahead of time to 1x concentration and stored at room temperature:

Reagent:	Final Concentration (1x)
NaCl	1.1 M
Na <sub>2</sub> EDTA	2.2 mM
KH <sub>2</sub> PO <sub>4</sub>	.22 M
NaN <sub>3</sub>	1.3 mM
pH to 5.0	

Reagents added just before luciferase	assay:
BSA	.44 mg/mL
Coelenterazine	2.5 uM

#### Beetle Luciferin (firefly luciferase substrate) Reconstitution:

- 50 mg luciferin in 7.134 mLs  $H_20$  (25 mM). Aliquot into 105 uL tubes.
- Store @ -80°. Per Promega technical support, this should be stable for >6 months, but may be light sensitive.

#### Coelenterazine (Renilla luciferase substrate) Reconstitution:

- Acidify methanol by adding HCI to final concentration of 5 mM (<3 pH).
- Reconstitute 250 ug coelenterazine with 2.36 mL acidified methanol (250 uM)
- Aliquot 100 uL into 1.5 mL tubes for use on 1 96-well plate.
- Store @ -80°C (stable for at least 6 months at -80°, but may be light sensitive).

# Protocol for buffer preparation and 96-well dual-luciferase assay using Promega Glomax 96-well dual injection luminometer

1. Lysis buffer: 4 parts water, 1 part 5x passive lysis buffer (Promega) in a reservoir. You need 26 uL/well, so calculate accordingly with ~20 wells extra to account for loss in the reservoir. Buffer is stored at -20° and can be extremely viscous, thus prior to allowing the

5x buffer to approach room temperature will improve accuracy. Mix 1x lysis buffer well prior to use.

- 2. Analyze each well for transfection efficiency using fluorescence microscopy. Note any inconsistent wells that did not transfect efficiently, or are expressing low levels of RFP. These can cause inconsistencies in data and should be removed from the analysis.
- 3. <u>Completely</u> remove the media from the cells, being careful not to elute too quickly and lose cells. Remaining media will dilute the lysate and cause fluctuations in values across experiments. Add 26 uL of lysis buffer to each well, and place on a plate shaker/rocker at low/moderate speed.
- 4. **Start the timer.** For consistency I allow 30 minutes from addition of lysis buffer to the start of measurement. This time is used to prepare buffers, wash and prime the luminometer(s), and transfer lysate to opaque measurement plates. Any of these steps can be completed beforehand (with the exception of the final steps of buffer preparation and lysate transfer) to ensure that you do not go exceed 30 minutes of lysis.

# Wrap tubes (typically Falcon 15/50mL tubes) containing of the firefly and *Renilla* buffers with tinfoil as substrates may be light sensitive.

The following instructions are for 1 96-well plate. If multiple plates are being measured simultaneously (with multiple luminometers) then multiply all volumes by then number of luminometers/plates. If multiple plates are being measured sequentially on one luminometer, create buffer master mixes with everything except ATP and substrates, and add these reagents followed by pHing immediately before the beginning of the luciferase assay. ATP and substrates may degrade over time; consistency in the amount of time these reagents are in the buffer will improve consistency across multiple plates.

- **5. Firefly luciferase buffer:** Have the five reagents for the firefly buffer prepared to 10x concentration. Prepare a master mix with the following:
- For each 96-well plate, add 1mL of each reagent to 5mLs water, adding EGTA last.
- Add .025 g ATP (powder) per plate just before you add the firefly substrate. Keep ATP on ice at all times. ATP will degrade over time, so if you are measuring more than one plate consecutively buffer must be made fresh beginning at this step for each additional plate.
- Add 100 uL beetle luciferin (substrate) (previously aliquoted and stored at 100x conc.) Buffer should change to yellowish color based on pH.

#### 6. To Renilla buffer:

- Per 96-well plate, aliquot 10 mLs of "Renilla buffer".
- Add 100 uL of BSA (44 mg/mL stock) per plate
- If screening more than one plate, separate master mix into 10mL aliquots.
- Add 100 uL coelenterazine to buffer (previously aliquoted and stored at 100x conc.)
- **7. pH Buffers:** pH the firefly to 8.0, followed by the Renilla to 5.0 using NaOH and HCI. The activity of each buffer, and the ability of the *Renilla* buffer to quench the Firefly luciferase activity is highly dependent on pH. For consistent results be extremely accurate in this step. Bring volume of each buffer (corresponding to 1 96-well plate) to 10.5 mLs to accommodate for luminometer priming.

- 8. Transfer lysate to opaque white plates: At this point the cells should be close to done lysing (~20 min has passed?), and are ready to be transferred to white opaque plates. Take 25 uL from each well using a multichannel pipette, be sure to pipet up and down vigorously to break up the clumps of cells and homogenizing the lysate. Once transferred to white plates, lysate may appear pinkish. This may be due to poor removal of culture media, but is also commonly observed with high-quality transfections (RFP).
- **9.** Setting up the luminometer: Turn on the luminometer and select the program. The program is a promega protocol, is listed in the 'DLR' folder, and is called DLR with two injections, <u>not</u> column format. Select the wells you wish to test (all is the default), and make sure to extend the "Delay before measurement" setting to 5 seconds, with a 10 second measurement time (see Dyer, et al. 2000, *Analytical Biochem*, for explanation).
- **10. Capillary wash steps**: water 3x, EtOH 3x, water 3x, dry 3x. Prime buffers once into the waste, and then prime a second time back into the buffer tubes to ensure mixing. Firefly buffer is injected first and should be primed in the left capillary, followed by *Renilla* in the right capillary.
- **11.Luciferase assay**: Each plate takes ~48 minutes to read. After you are done save the file first, and then repeat the wash steps and shut off the luminometer.
- **12. Reading multiple plates:** Multiple plates can be read and data stored on the same excel file, however we have encountered issues with multiple plate reads where the luminometer program will crash. Be sure to save all data between measurements and take screenshots if program crashes before save is possible! Replace old buffers with new, being sure to prime at least twice with new buffers before starting the new plate
- **13.Considerations**: White opaque plates can be reused following a wash with DI water, 70% EtOH, DI water, and spun upside down in a centrifuge to remove any liquid before it can evaporate.