

Supplemental File 1. Predicted Upstream TICs Identified in Cancer Genes.

Below are the 5'UTRs of mRNAs from genes overexpressed in cancer. Codons colored in red have KSSs ≥ 0.8 . Upstream ATGs that may be used for translation are bolded. Potential alternative TISs are followed by their KSS score. NCBI Nucleotide accession numbers for each sequence are in parentheses.

EPHA4 (NM_001304536.2)

ACGCGTGCTCATCTTGTGTAAAAGTAAAAGTTGCTCATGTCATTAGCTCGGCTCTGAGTTTGCATGAGA
sAACCAGCGCAGCTCTCGAGCCACGGGAGAAAACACGATCTGCTGCGGAGCCCAGTGACCTGAAACT
GTAGCAGTGACTCGAGACCTGTCCTCTCCTCGACGTGCCCCATAACCCTCCCGCTTTATTTAGGATCC
GCTTTTCCGAGAGCAGCCACTCAGGCAACCCCCGGAAGAAGCGGCAGGAGCAGCG**TTG(0.82)**GCACC
GGCGAACC

YY1 (NM_003403.5)

CTCCCTCTGCCTTCCTTCCCCACGGCCGGCCGCTCCTCGCCCGCCCGCCCGCAGCCGAGGAGCCGAG
GCCGCCGCGGCC**GTG(0.91)**GCGGCGGAGCCCTCAGCC

ERBB2 (NM_004448.4)

CCCCTCCATTGGGACCGGAGAAACC**AGG(0.87)**GGAGCCCCCGGGCAGCCGCGCGCCCCCTTCCCACG
GGGCCCTTTACTGCGCCGCGCGCCCGGCCCCACCCCTCGCAGCACCCCGCGCCCCGCGCCCTCCCA
GCCGGGTCCAGCCGGAGCC**ATG(0.86)**GGGCCGGAGCCGCAGTGAGCACC

FOX2 (NM_001031695.4)

CTTCAGCCATCTGCCTGAGATATGGGAGGGAGCTGGAGAAAG**AAG(0.81)**GAGGGGGAGAGACTGCC
AGAGAGGAAGAGAAAAGAAAGGAAGAAACATTAGAAAGAAAAAGGAAGGAAAACGGTATAAAGAG
AGATCAATTACCCACCCTTAAATAGCTAGATTGGGGGGGGAGGGGGGTGGAAAAGAAAGCTGTGGA
GGTGTGCCCCAGC**ACG(0.88)**GCTGCTTTGAAAGGTTTATCATCTATCCGTTTGTTT

KIT (OM304357.1)

TCTGGGGGCTCGGCTTTGCCGCGCTCGCTGCACTTGGGCGAGAGCTGGAAC**GTG(0.82)**GACCAGAGC
TCGGATCCCATCGCAGCTACCGCG

AXL (NM_021913.5)

GAGAAGGCGGCTGCTGGGCAGAGCCGGTGGCAAGGGCCTCCCCTGCCGCTGTGCCAGGCAGGCAGT
GCCAAATCCGGGGAGC**CTG(0.87)**GAGCTGGGGGGAGGGCCGGGGACAGCCCGGCCCTGCCCCCTCC
CCCGCTGGGAGCCCAACAACCTTCTGAGGAAAGTTTGGCACCC

MYC (NM_002467.6)

AACTCGCTGTAGTAATTCCAGCGAGAGGCAGAGGGAGCGAGCGGGCGGCCGGCTAGG**GTG(0.80)**GA
AGAGCCGGGCGAGCAGAGCTGCGCTGCGGGCGTCCTGGGAAGGGAGATCCGGAGCGAATAGGGGG
CTTCGCCTCTGGCCCAGCCCTCCCGCTGATCCCCAGCCAGCGGTCCGCAACCCTTGCCGCATCCACG
AACTTTGCCCATAGCAGCGGGCGGGCACTTTGCACTGGAACCTACAACACCCGAGC**AAG(0.84)**GAC
GCGACTCTCCCGACGCGGGGAGGCTATTCTGCCCATTTGGGGACACTTCCCGCCGCTGCCAGGACCC
GCTTCTCTGAAAGGCTCTCCTTGCACTGCTTAGACG

MET (NM_001127500.3)

AGACACGTGCTGGGGCGGGCAGGCGAGCGCCTCAGTCTGGTCGCCTGGCGGTGCCTCCGGCCCCAA
CGCGCCCCGGGCCGCCGCGGGCCGCGCGCGCCGATGCCCGGTGAGTCACTGGC**AGG(0.82)**GCAGCG
CGCGTGTGGGAAGGGGCGGAGGGAGTGCGGCCGCGGGCGGGCGGGGCGCTGGGCTCAGCCCGGC
CGCAGGTGACCCGAGGCCCTCGCCGCCCGCGGCGCCCCGAGCGCTTTGTGAGCAGATGCGGAGCC
GAGTGGAGGGCGCGAGCCAGATGCGGGGCGACAGCTGACTTGCTGAGAGGAGGCGGGGAGGCGCG
GAGCGCGCGTGTGGTCCTTGCGCCGCTGACTTCTCCACTGGTTCCTGGGCACCGAAAGATAAACCTCT
CATA

HP (AF026219.1)

CCCAGCCAGGAC**ATG(0.81)**GCCGCACCTCTCCTCATCAGGAGCGCCGGCTCACGGACTTCTCGCCCA
ACTCCCTGAGCGCTCCCTCGTTTCGATCTTTAGAAAACCCTGCTTTCTTTCTGGGGCCGTGACG**AGG(0.82)**
GGCAGGGAGCGGCGAGCAAG(0.90)GATGCGTTGAGGACCGCGAGGGCGCGCGTCTCGGGTGCCG
CCGTG(0.86)GGTCCCGACGCGGAAGCCGAGCCGCCTCCGCCTGCCTCGACTTCCCCACAGCGTTCC
GCCGCCGCCTGCCGTGCTTGATGTGCAGAAAGAAGCCGGACACC

EPHA1 (NM_005232.5)

GCAAC**CTG(0.80)**GCGCTGCCATCCGGGCCACTGTCCCAGGTCCCGGCCCGGAGCT

MYCN (NM_001293228.2)

AGGCTGTGACAGTCATCTGTCTGGACGCGCTGGGTGGATGCGGGGGGCTCCTGGGAACCTGTGTTGGA
GCCGAGCAAGCGCTAGCCAGGCGCAAGCGCGCACAGACTGTAGCCATCCGAGGACACCCCCGCCCC
CCCGGGCCACCCGGAGACACCCGCGCAGAATCGCCTCCGGATCCCCTGCAGTCGGCGGGAGGTAAG
GAGCAGG(0.83)GCTTGCAAACCGCCCGGCGCCAGGGAAGCGACGAGCGCCGGGGCAAGGCAAGC
CTG(0.80)GACGGGATT(0.82)GCGACGTGCGCACCGGGCGCCCTAATATGCCCCGGGGGACTGTTTCT
GCTTCCGAAACAAAACCATCTCTGGGTTTTCCAGAAAAGCCAGTTCAGCCCCGAAGGCATCTG(0.
87)GCTAGAGGAGACCCGCCCTAATCCTTTTGAGCCCTTACCGGGGGGAGTAATGGCTTCTGCGAAA
AGAAATTCCCTCGGCTCTAGAAGATCTGTCTGTGTTTGAGCTGTGCGAGAGCCGTGTTGGAGGTCGGC
GCCGGCCCCCGCCTTCCGCGCCCCCCCACGGGAAGGAAGCACCCCCGGTATTAACGAACGGGGCG
GAAAGAAGCCCTCAGTCGCCGGCCGGGAGGCGAGCCG

FOXM1 (NM_202002.3)

AACGCTCCGCCGGCGCCAATTTCAAACAGCGGAACAACTGAAAGCTCCGGTGCCAGACCCACCCC
CGGCCCCGGCCCGGACCCCTCCCTCCCGGGATCCCCGGGGTTCACCCCGCCCGCACCGCCG
GGGACCCGGCCGGTCCGGCGCGAGCCCCCGTCCGGGGCCCTG(0.84)GCTCGGCCCCCAGGTTG(0.85)
GAGGAGCCCGGAGCCCGCCTTCGGAGCTACGGCCTAACGGCGGCGGCGACTGCAGTCTGGAGGGTC
CACACTTGTGATTCTCAATGGAGAGTGAAAACGCAGATTCATA

KPNA2 (NM_001320611.2)

GTTGACTAGGCCTCGGGGGCGACGTTTATTGACCAGGCGGCTGAGTTTCGCGGGGTCTGCGGGTTTA
GGGCGCCGACGCTCTGCAAACGGCAGCGGAGGCCTTAACGCGTCGCGGCCGGGAGAATCGGAGCGA
GCCAGGCTTGAGGGCGAATGTCCCGGGAGGACTTGTGGCGGCCCTG(0.81)GTTTCGCCTCCTCCTTC
TCGTTGCATCTTCCCCGGCCTG(0.83)GGGGCAGGGGCTGGGGGTGGCAGTTGGGAGCACCGTCTCTG
ACACCTAGGCCCCGGGGGTGGCTCTGCCACCAG(0.84)TCGTAGGCGAGCGTAATGAAAGCAAAGAT
AGCAAATTGTAAGGAGGGCTTTGACTTTTGTATCTTCTGAATGACGCACAGCTGATGTCATCCTAATT
AAGCGCATTCACTCCTAGTCTCTGGAAATGCAATCAAATATGCGAGATGCGGCACTGCATTTTAAATG
TTGACCATAATGTAATGATGAAGCAAATTTTATTTAATTTTCGAGTCTGCACCTATTTTGGCCAAGTAA
AGACAGTAAAATAGGGAGAGCCTCCTGAGGATCTGAATTTATTGCCCTGGCACATAATTTTAGCTCTT
TCTCCCTTTGTCTCATAACC

STAMBP (NM_006463.6)

GTTTCCGGAACCTCCGGGTGTCATCCGCGGGGAAAGGTGGGGAAGGGTCCCGGGAACCTG(0.88)GTG
GGGCAGG(0.80)GCCTCCGAGCGTGGTTGACTTTGAAGGGGATCGGCCGCCATGCTGCATCCCCTTTT

TGGAATTGCTCAACCAGGTGGTAACCGGCGCCGCTTCCTGGCCTTGGGAGGTGGTTCCTTTCTTAACCC
ACAAGAACCTCTCCCAAGAGAACTTGGTCCTG

MAP3K8 (NM_005204.4)

ACTCGTCCGCTCCGCTCTGGACTGCGCGCCACGCTCTGGGGTCCGGCGCCCTG(0.82)GTTTCCTGCTTCT
GCCGCTGCCGCCGCCGGATCCCACTGGCCCCGGCGTGCTCGGCTCCACAGGCCTGCAGCCAGCATC(9
0)GCACCGAACCTTCGGGGGGCGCGGCTGGAGCGCTCGGCCGGCCTG(0.83)GGAGCGCCAAAG(0.85)
GCCGCAGATGCAATCTTCTTACCGCGAAGAAGCCAGGGGAATAGGTAGCCACATCTTGTTCAGATA
AGAAAGGAAGCTAACGCAGTATCTGCAAAGCCAGGAGTCTGACTCAGTACTTTTCTCACTCATGCATA
CAAAGCAGCTAAAAATGACACAGCTTATTTACCATGCCCTGACACTGCACTGAGCACTTTATGAGCTT
GAACTCTGTTAATCCTCACGACCACCTCATGAGACTCTCCAGAAAGAGCAACAGTA

CDKN3 (NM_005192.4)

ACCGGTGAGTCGCCGGCGCTGCAGAGGGAGGCGGCACTGGTCTCGACCTG(0.80)GGGCGGCCAGCG

ADAR (NM_001111.5)

GAACCGGAGCCATCTTG(0.88)GGCCCCGGCGCGCAGACCCGCGGAGTTTCCCGTGCCGACGCCCCGGG
GCCACTTCCAGTGCGGAGTAGCGGAGGCTG(0.81)GGGGCCTCGAGGGGCTGGCGCGGCCAGCGG
TCGGGGCCAGG(0.80)GTCGTGCCGCCGGCGGGTCGGGCCGGGCAATGCCTCGCGGGCGCA

RCC1 (NM_001048194.4)

AGAGGCCTGCAGAGCGCATGCTCTGGGGCAGTTCGCGGCCCGGCGGGGAGCGCCGGAGTTCCTTGT
GGCCGACGTGCACCAG(0.85)GACAGGAAG

COL11A1 (NM_001854.4)

ACTGACGGCATGAAGCCTTTAGGGGCACACAGTACTCTCAGCTTGTTGGTGGAAGCCCCTCATCTGCC
TTCATTCTGAAGGCAAG(0.81)GCCCCGGCAGAGGAAGGATCAGAGGGTCGCGGCCGGAGGGTCCCCG
CCGGTGGGGCCAACTCAGAGGGAGAGGAAAGGGCTAGAGACACGAAGAACGCAAACCATCAAATTT
AGAAGAAAAAGCCCTTTGACTTTTTCCCCCTCTCCCTCCCCAATGGCTGTGTAGCAAACATCCCTGGCG
ATACCTTG(0.85)GAAAGGACGAAGTTGGTCTGCAGTCGAATTCGTGGGTTGAGTTCACAGTTGTGA
GTGCGGGGCTCGGAG

BUD31 (NM_003910.4)

GTCGAGAAGCAGCTACCCAAGCTCCAGGAGCTTCCGGTATGTGTTTTCCCTCTGTTCTCGATTACCTTG(0.86)GCAACGGCTGAGGCGGGAGACCGGTGGTCTGCACCGTCCTG(0.80)GAGGGAGATATGAGTGGCTGGACTCTCAGCCAGCCACTGGGATGTGTTCTGGGCTTTGGACCTTGAGGCCGGAGAGAGCTCCCGAGAGGAGGCGGCGCCACGTTCTGTTCTTCTGAGGGGACGGTAGATTTGGGGGTTTTCTCTAGGATTCTCGCGCCGTTTCTCTGAAGAAACAGGACCAGAGAGGGAAGGTGACCTGAAAGTCACAGAATAATTTTTTA
GAGCTGAACAAGAATCCAAGCCTGCAACTGCAGAGACGAGAGATCTTTCTGCTGTCTATACTCTTGGA
AAGCACATCCTAAGATCTTTCAGATTATCCTGTGGAAGGAAA

KCNH2 (NM_000238.4)

AACCCTTCCGCGGCCCGGGCCGAGCCGCAGGCGCTGCCCCAGCCGCGGGCGCTGGAGCGGCTGTCCGCGCGGTG(0.82)GCAGGCGGGAGCCAGGAGTCCGGGGCTCGGGCGGGCGGAGCGCAGCGCGGGGACGCGGCGGAGCGGGGCCCCGCGGCTCGGCGGGGGCCGGCAGACAGGTGTGCCGGCGGCGGGCGGCTCGCGTCAAGCGGCTCCAGGCCGGGCCCCGGGGTCCGGAGCGGGGAGCCGGGAGCCGAGCGAGGACC
CGGCGCCCCGAGTCCAGTCTTG(0.82)GCCGCGCCCCGTGCTCGGCTTG(0.86)GCCGCGGGGTGCGGGG
ACCACG(0.91)GCCCCGCCGGGCCACCCGAAGCCTAGTGCTGGGCCGGGCCGGGCCGGGGTGGGTGG
GGGCCCGCCCCGCCCCGCCCATGGGCTCAGG

BCAP31 (NM_001139457.2)

GATGGGCCTCCGGGACGGTGTGCCAGGCCGGGGCCAAGTCGGAGGCCCTCGCTCTGGGTGGGCGCTGGGGCCCGCGAGG(0.80)GCTACTGTAAGGACCCCTGGCTTCTGAGGATACTGCGTCTAGAACTTTCTCCGTATGGGGCCTTGAGGTGCTTGGTCGAGACCTGCCTTTGCGCTTGGTCCCGAATCCTGCCCTCTAGGAGTCGCTCTTGCGGGCCTCCAGCCCACCGGAGGCGAAGCGGCCCGGGCGGAAGGCCGCTGGATCCTCGAGGGAGGTGCCGTTTCTCTCCGCGGGCGCCGTG(0.89)GGGACGTG(0.82)GGAGGCGGGGCGTCGGCAGCGCTTGACTAGGTGCGGCCCTTG(0.82)GGCCTGCCTGGTAGCGGGGATTTGGGCCCGCAGAGCGCCCGCCTCTGCGGCTGAGTTCTGCCTGGCGGGGAAGGGAGCGCCCG

NME1 ([NM_198175.1](#))

GCAGAAGCGTTCCGTGCGTGCAAGTGCTGCGAACCACGTGGGTCCCGGGCGCGTTTCGGGTGCTGGCGGCTGCAGCCGAGTTCAAACCTAAGCAGCTGGAAGGGCCCTGTGGCTAGGTACCATA(0.84)GAGTCTCTACACAGGACTAAGTCAGCCTG(0.86)GTGTGCAGGGGAGGCAGACACACAAACAGAAAATTGGACTACAGTGCTAAGATGCTGTAAGAAGAGGTTAACTAAAGGACAGGAAGATGGGGCCAAGAG

RPA3 (NM_002947.5)

AAGCTACTCAGATAAGAGGCTCCAAGAGGACATTTTTGGATGTGAAAAACAATGAGAAGGAGGACAA
CACACATTTACAATCGTCTTAATTTTGTACTCAGAAAAAGGATGTGAAGACAATGCACAGGGAATACA

ATAGTTTCAGATCTGTGTACAGTTTCCTTTTGCTTCATCTCCTGCAACAATGTAATGAAGACACCATGAT
ATCATTAACATTTACACAAAAGGAAAATGAGGCTGAAATGGTGTGGGC **AAG(0.80)**GCCCAGGAATCT
GGAGCATCCCTAACCAAGCAGGAGAGCACCTGGGATAGAGAAAGTGCTCAAGAATGTTCACTTACTG
ATTACTACAATCAAAAAAAGATACGACACTAATTTACCACATTCTTCTTACTTATTTTATGAGATACTATT
CTTCCAAG **GTG(0.81)**GAGAAAGTGGAGAAAGTAGAGTGACGCAGCTAAGGGAGTAAATCGACCCCTCA
GCCAACAAGTGGCAAAAGCCTGAAGAAAGTGATCAAGATCACTGATGACCCCGCTGCCCATCTCCAA
GGGGGCGGGTATCACAACCCCGACGCCACACCACGTATCATTCCGCAAACTCCCGCGCCTCCACG
CAGAACTGGCAAG **AGG(0.82)**GAAGGCGAGACAGCAGTGAACAGCTGGTACGCAGCACCCACAGCAC
CGCGGCAGCAGCTAGTGCCGACTCCCGCCTAGCTCTTTTGA CTCTGTTCGCGGGAAGAATGGGGAAAC
AGTAAGGTTGCGGCGCCTCCCGCGAGACGAGGTACCTGAGG **CTG(0.80)**GCCCCGCAGTCCCCCGCCG
CACCAGCACCGGAGCTTCACACCCCACTTCCGGGGTCAAGTCACCGCCGGGAATCCTGTGATCGCAG
AAAGGTAGTCTCAGGTTCCGCCCCTATCCAAGTCCCGCCTCCACTGCCTCTCGCCCTGTATCTGTCAAC
TTCCGGGACGCCGCGCTACTAAGCAGCCAATCTCCACTTCCGGACTCATCCAGCCCCTTCTCCACC
CCTTTCAGAGACAGCGCG **ATT(0.81)**GCGATTTAGGTTTCCGCGCATTTAATTGGCGAAG **CTG(0.81)**GA
GCGCTAGTCTTCGCTGATTGGTGCCGAGAAATCTGCCCCATAGACACCCGCGGGGCGCACAGTTTCAG
TCGTCCGTGGGTTTCCCGCCAGCCGCAGTCTTGACCATAATC

ELOC (NM_005648.4)

CTTTCGACTGCCCCGGAACCCACCGGAGCAGGCAGCTGGGGGTGGGGGGGCGGCC **CTG(0.81)**GGAT
AGGGGCTGTGGCAGTACGCGGGGACCCGGCTGCG **GTG(0.81)**GCTGCGGGACTGACGAGAACTACT
AAAGTTCCTGGGGAAGCAAAGTAGAATTCATAAGAACAAA

DRAP1 (NM_006442.4)

GGGCGGCGAGCAGGCCCGGGAGCCGGGAGGCTGCGGGCGGCGGCG **CTG(0.81)**GACCCGACGCGGC
GAGAGAGGCCCCGAG

UBE2S (NM_014501.3)

GGCTCAGTGCTGCCGGGCACCGGGGCGGCGGGTTGGTCTACGCTGTGCGCGGCGGACGTCCGAGGC
AGCGGGGAGCGGAGCGGGGCCCGGGGCTCTCCAGGGCCGCAGCGGCAGCAGTTGGGCCCCC
GCCCCGCGCGGCGGACCGAAGAACGCAGG **AAG(0.83)**GGGGCCGGGGGACCCGCCCCCGGCCGCG
CGCAGCC

PSMB8 (NM_004159.5)

AAACTCCGCAGTGCTCAGCCAAGC **AGG(0.81)**GAGCAACGCTAGGAAGGGCGGGCAGAA **AAG(0.80)**GG
CACGCTCTTGTGGGTGACTACAGGTTAGGAGACCGTTGAAC **CTG(0.85)**GAGGGGCCCTAGG **ATG(0.8**

CTCGCGGGGTGCGCCTCTGGGATAGGCGACCACG(0.85)GTGTCTTCAAAAGCCCCGTCAGGGTTGGC
TTCCTGGGGCCGGACCGACTGTGGGTCAGTTTGACCAGCGCTCTGGAATCGAGTTACGCGCGAAAG

GGCAGAGTTTCTGGAGGAAACCGCAGCCTCTCAACCGCTGACCGGGTCTCAGAAGGCCCCCGGCAGG
(0.86)GCCGCTTGGCGGGAAGTACCACGCGCCAGTCAGGCTCTCCAGGGACCTGCGCAGGCGCGTGT
GGGCGGAGTCGTGCGCAGGGGGCGGGGCTTCGGGAAGGAGCCACAGAGAGG(0.80)GCGGGGCGTA
GGACCTGCGCTTCGGGGGTGGAGTCGGAGCGGCGCGGCGGCGGTC

NUTF2 (NM_005796.3)

GCAGACCGCGCTGGGTTGCCGCTGCCGCTGCCGCCATC(0.86)GTGCCAGCCCCTCGGGTCTCCGTGA
GGCCGGGTGACGCTCCAGA

TRIM28 (NM_005762.3)

AGTGACGCAGAGGCTGGAGACGACTCTACGGCGGCGAAGAGACGCGGGTTGAGGAAGAGGGACGG
ATTGCCCATGCGCTTGGGCGCACAGCGGCCCGCTTCTGTGTGGTCTGGAGGTGGAGCTGAGAGGGGA
ATCACACTCTATAAAGTTTCGCATACCCCACTGGCGGATTCAATTGCGGCAGTGACGTCACAGAGGCC
CCGCCCCGCCCCACAAGAGCCCCACCGACGTG(0.83)GGGTTG(0.82)GCGGTGGTGAAGGACTAG
GAGTTGGCGCGTGCGTACTGGCGGCCTCTCCCGACCGACCGGCCTG(0.80)GGCCCCGCCCCGGGC
GTGAGGCGCCCAATGCGCGTGCGCGGCGGCGTCGGCGCCAGTTATTTCTGTCCCGCCCCCGGCCTC
GGCTCTTTCTGCGAGCGGGCGCGCGGGCGAGCGGTTGTGCTTGTGCTTGTGGCGCGTGGTGCGGGTTT
CGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCAGGCAGCAGTTGGCCGT
GCCGTAGCAGCGTCCCGCGCGCGGGCGGGCAGCGGCCAGGAGGCGCGTGGCGGCGCTCGGCCTCGC
GGCGGCGGCGGCGGCAGCGGCCAGCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGCGGCGGGCCC
CGCGCCCCTCCTCCCCCCTGGGCGCCCCCGGCGGCGTGTGA

PTDSS1 (NM_014754.3)

CCCTCTGCTCCAGCCTTTGCTGGGCGCCAGACCCGGCTTTGCCGTCCGGCTATTAGCCTACTGTGGCT
AGTACCCCCGGGTCCCGGCCTTCTCGGGCTGGGGCCCGGCCACCGCGGCAGGACG(0.83)GGGA
GGCGGGCC

TCEA1 (NM_006756.4)

AGCCGGAAGCCACGCCTGCCCCTAGCCCGACGCCCGCCTGGCGGGAACATG(0.85)GGCTCGCCCC
TCACCAGCGATCTGCAGTCAGTTGGTAGCGCCTGCACGTCGCGCGCGGTGTTTCGATTGTCGCTGCCTG
GGGAGGAGGAGCCGGAGCCCGCCGCCGCCGCCGCCGCCGGGCTTCGTTTCGTAAGGAAG(0.82)
GGGGCCTAGGCCCGGGCCTGCGGTGGTGGGGTTGCTGCGCGCCGGGGTTCGCTCCTGCTGTGTCTT
CCGCTCCAGCTTCGCCCACTTCCCCTTGCCAGCGGGGTGGGCGCGGAGAAGACCTGCCGGAGCC

PCNA (NM_002592.2)

GGATGGCCGGAGCTGGCGCCCTG(0.85)GTTCTGGAGGTAACCGGTTACTGAGGGCGAGAAGCGCCAC
CCGGAGGCTCTAGCCTGACAAATGCTTGCTGACCTGGGCCAGAGCTCTTCCCTTACGCAAGTCTCAGC
CGGTCGTCGCGACGTTGCCCCGCTCGCTCTGAGGCTCCTGAAGCCGAAACCAGCTAGACTTTCCTCCT
TCCCGCCTGCCTGTAGCGGCGTTGTTGCCACTCCGCCACC

FDPS (NM_002004.4)

GGGAACTACTCGACCCACAGAGCCGATCGCGGAGCGGATTCTGCTTTTAGGAGTACCCGCCAACAG(0.80)CGGGACCGAGCAGGAATCCGTATCTGGGAACAGG

PSMD2 (NM_002808.5)

GCAGCGGGCCGGCAGTG(0.81)GCGGCGGAG

HMGA1 (NM_145899.3)

CTTTTAAAGTCCCCTGAGCCGGTGCTGCGCTCCTCTAATTGGGACTCCGAGCCGGGGCTATTTCTGGC
GCTGGCGCGGCTCCAAGAG(0.83)GCATCCGCATTTGCTACCAGCGGCGGCCGCGGCGGAGCCAGG
CCGGTCCTCAGCGCCCAGCACCGCCGCTCCCGGCAACCCGGAGCGCGCACCGCAGGCCGGCGGCCG
AGCTCGCGCATCCCAGCCATCACTCTTCCACCTGCTCCTTAGAGAAGGGAAG

KPNB1 (NM_002265.6)

CCCTCCCTGCGCGCCGCTCTCACTCACAGCCTCCCTTCCTTCTTTCTCCCTCCGCCTCCCGAGCACCA
GCGCGCTCTGAGCTGCCCCAGGGTCCCTCCCCCGCCGCCAGCAGCCCATTGGAGGGAGGAAGTAA
GGGAAGAGGAGAGGAG(0.80)GGGAGCCGGACCGACTACCCAGACAGAGCCGGTGAATGGGTTTGT
GGTGACCCCCGCCCCCACCACCCCTCCCTTCCCACCCGACCCCCAACCCCCATCCCCAGTTCGAGC
CGCCGCCCCGAAAGGCCGGGCGCGTCTTAGGAGGAGTCGCCGCCGCCGCCACCTCCGCC

DYNLL1 (NM_001037494.2)

CTTCGGGCGCTGACAGG(0.84)GAGAGCCTG(0.85)GGGCCGGGCCGTGTGGATGCCATCCCCGAGCGC
GGTTCGCGCTCGGCTGAGGCGCTGGACAAGTGGCTTGGGCTCCCGCGCCTCAGTTTCTCTCTGTGGCG
CCGCCTACCTCACAGACTTGTGAGCACTCACTGACGTGGGTAGCGCCAGGGCCTGCGGGGCGCAGG

AGAGCTG(0.80)GAGTCAGGCGGAGACCGCAGGCTGACCCCGCAGCGGCCGGGCTGTCGCGGCCCCC
ACCTCAGGTAACC

RUNX (NM_001024630.4)

ATTGCGCTCACAAACAACACAGAACCAAGTGCGGTGCAAACCTTCTCCAGGAGGACAGCAAG(0.8
1)AAGTCTCTGGTTTTTAAATGGTTAATCTCCGCAGGTCCTACCAGCCACCGAGACCAACAGAGTCAT
TTAAGGCTGCAAGCAGTATTTACAACAGAGGGTACAAGTTCTATCTGAAAAAAAAAAGGAGGGACT

MRPL3 (NM_007208.4)

CAGAGAGCATC(0.82)GGCCGGCGACCGTTCCGGCGGCCATT(0.84)GCGAAACTTCCCCACGGCTAC
TGCGTCCACGTGGCGGTGGCGTGGGGACTCCCTGAAAGCAGAGCGGCAGG(0.83)GCGCCCGGAAGT
CGTGAGTCGAGTCTTCCCGGGCTAATCC

SPP1 (NM_001040058.2)

AGCAGCAGGAGGAGGCAGAGCACAGCATC(0.84)GTCGGGACCAGACTCGTCTCAGGCCAGTTGCAG
CCTTCTCAGCCAAACGCCGACCAG(0.83)GAAAACTCACTACC

SNRPD2 (NM_004597.6)

GCGTCCCAGAGGGAAGAGGGGCGGTGCCTGTCTCCGAAGCGAGGAGCGGATTGGCTTCACGGAGGC
CGCGCCCCCGAAGTCACG(0.83)GCCGGCGGGCATTGGAAATAGCTTGTCATTTCCCTCCTTCAACCT
GTACCATTCTTCAAGAAACGGCGCCAACGGAAGTGGGTCGCAGGAAGAGGAAGTCCCGCCTCTCTCT
CCTCAGGCAGCAGCAACGCGGAGGAAACGGGAGTGAACGGAGAGCGTAGTGACCATC

UCHL3 (NM_001270952.2)

GCTCGGCAAGGCTCGGCTCGGAAGAGTCCAAGCGTGAGGGGAGAGGGCTGTGGATTCAGATACTGTT
TTTCTCCCGAAATAGGAAATTGGCTTATTTTTTCTCCTCGGCAGCATCTTAATTTAAAATATGACACTTG
ACCTACGGCCCTGCACGGAGCGGTTAAGAGG(0.80)GTCACCAACCAGTTTCTTAAACAATTAGGTCTA
CATCCTAACTGGCAATTCGTTGATGTATATGGA