

<b>GENE</b>	<b>FORWARD</b>	<b>REVERSE</b>	<b>ACCESSION #</b>
<b>ABCC8</b>	ATGCTGCTCTTCGTCCTGGT	CAAACCTTGATGGTCTTGGTGATG	NM_001287174.1
<b>ALS2</b>	TCTGACTGAAGATGGTGAGGTC	ATTCTCTCCCCACATGTACGC	NM_020919.3
<b>APPL1</b>	TTTGTCTTCGACATCAAGCG	GTTTTGCCAGTCCAACAGAATCA	NM_012096.2
<b>ASNS</b>	TGAGATAGAACTGTGAAGAACAACCT	TAGCAGCCAGTAAATCGGGG	NM_133436.3
<b>ATF4</b>	TCTAAAAGAGAGGGCGGATTCC	CTACAGCACTCTATGTACAAGCACA	NM_182810.2
<b>ATF6</b>	GTTATTCAGTCTCGTCTCCTCGG	CAGTCCATTTTCAGTCTTGTTCTTA	NM_007348.3
<b>BLK*</b>	ATGGTGTTGGAAGTTGCTCGT	TGAAGACAACCAGGGGCG	NM_001715.2
	AACACCACTGAAGCATTGCC		
<b>BLOC1S1</b>	CCTCAATGTGGGTGTGGCC	CGAGCCCAGTTCTCCACATC	NM_001487.3
<b>BSCL2</b>	TATATGCCGACAGTCAGCCAC	CCATACATCAGCACCCGATCA	NM_001122955.3
<b>CEL</b>	GACGCCAATCTGCCAGGTAA	CGGATGAGGGCCCTTGTTGTAG	NM_001807.4
<b>COL6A2</b>	AGCCTACGGAGAGTGCTACAA	CTCCAAATTCACCCTTCTCTCCTT	NM_001849.3
<b>DDIT3/CHOP</b>	CCTGGAAATGAAGAGGAAGAATCAA	TCTGACTGGAATCTGGAGAGTGA	NM_001195057.1
<b>DNAJB9</b>	TCGGAGGGTGCAGGATATTAGA	TTGATTTGGCGCTCTGATGC	NM_012328.2
<b>DNAJB11</b>	GGCTCCCCAACTTTGACAAC	AGCTGTTTGATACCTTCTCTCGC	NM_016306.5
<b>DNAJC3</b>	TCAGTGAAGTTCGGGAATGTCTT	TAGCATCTGTGTATCTGCCATCT	NM_006260.4
<b>DUT-M</b>	TTACGTCTCTGCTTCGCTCAG	CGCCTTAGGAAGCTCGCC	NM_001025248.1
<b>DUT-N</b>	GTCTCCTCGCTCGCCTTC	CGTTACTGGGTGAAATGGC	NM_001948.3
<b>EDEM1</b>	ATATGGTGCCCTCCCTGAGA	GGATTCTTGTTGCCTGGTAGA	NM_014674.2
<b>EIF2AK1</b>	CGAGTCTGCCTGTCTTATGTT	TCGGTGCACAATTCCCAGT	NM_014413.3
<b>EIF2AK2</b>	AATTGGCCGCTAAACTTGCA	GATGATTCAGAAGCGAGTGTGC	NM_001135652.2
<b>EIF2AK3</b>	CACACAGGACAAGTAGGGACC	GTTAAGGTCCTGACTCTCTCCATC	NM_004836.6
<b>EIF2AK4</b>	CTCGGCATCAAGTTACAGGTCTT	CCTTCGTTTGATGAAAGCCACAA	NM_001013703.3
<b>EIF2B1</b>	GACTCACGCCTACTCCAGAG	GGCCATTTTCTTACCTGACAAATCA	NM_001414.3
<b>EIF2S1</b>	AGAGACCTGGATATGGTGCCTA	AGCCACTTCAATATCTGCTCGA	NM_004094.4
<b>ERN1/IRE1α</b>	TCCAGTTCTTCCAGGACGTGA	TGATGTTCTCCCGCCAGTC	NM_001433.4
<b>FEN1</b>	CTACCGAGGACATGGACTGC	CCACAACTGTTCTGTTTCAG	NM_004111.5
<b>FOXO3</b>	TAGGGTCCTGAGAACTTCTGAGTTC	CCAGGGTCTGTAAACTGCAAA	NM_001455.3
<b>FOXP3</b>	TTCATCTGTGGCATCATCCGAC	GAGCGTGGCGTAGGTGAAA	NM_001114377.1
<b>GATA4</b>	CTCTACATGAAGCTCCACGGG	TGAAGGAGCTGCTGGTGTCTTA	NM_001308093.1
<b>GATA6</b>	AGCAAGATGAACGGCCTCA	TGGTAGTTGTGGTGTGACAGT	NM_005257.5
<b>GCK</b>	AACAATGTCGTGGGGCTTCT	TGATGGTCTTCGTAGTAGCAGGA	NM_000162.3
<b>GLIS3</b>	TGGACACCAAACCTTATGCTTGT	CTGGACCGCAACTTTTTCTT	NM_001042413.1
<b>HNF1A</b>	CTCATCACCGACACCACCAA	GCTGGAGGACACTGTGGG	NM_000545.6
<b>HNF1B</b>	TGTCAGGAGTGCGCTACAG	GGGAGAGGCTGTGGATATTCG	NM_001304286.1
<b>HNF4A</b>	CTCGTTGAGTGGGCCAAGTA	GTAGTCATTGCCTAGGAGCAGC	NM_001287182.1
<b>HSP90B1</b>	GTGAAAAGCGGCCCGAC	CAAGTCCCCCTTCGATCGCAG	NM_003299.2
<b>HSPA5</b>	TTTTAATGATGCCCAACGCCA	CAGCTGCCGTAGGCTCG	NM_005347.4
<b>IER3IP1</b>	GAGAGAAATCGCTTGGACTTCG	TGGCACTCTCATCACGGTTC	NM_016097.4
<b>IL2RA</b>	GGGGACTGCTCACGTTTCT	GGATCTCTGGCGGGTCTATC	NM_001308243.1
<b>ITCH</b>	ATCATGTGGTTTTGGCAGTTTGTTA	AGAATTTCTGTGGTCCATTGCTCC	NM_001324197.1
<b>KCNJ11</b>	CAGCATCCACTCCTTCTCGTC	GGGCACTCCTCAGTCACCAT	NM_001166290.1
<b>KLF11</b>	CCCATCTTCGCACTCACACA	TGACAGCTCATCCGAACGAG	NM_001177718.1
<b>LRBA</b>	TGCTCATCAAGGTGCTGTACAAG	TTATCCAGAAGCCACAGACG	NM_006726.4
<b>MAFB</b>	AAGAGAGCAACGAGGAAAGGAG	GAGCAGGCAATAAACTGATGAGA	NM_005461.4
<b>MBTPS1</b>	TGGACGCCTTCAACTATGCC	GCTGTTAATTCCACACCTTGTC	NM_003791.3
<b>MBTPS2</b>	TCCCAGTTAGAGCATACAAACGA	TTGCTTCAACTGCTTTCCGG	NM_015884.3
<b>MNX1</b>	GGAGCACCAGTTCAAGCTCA	AATCTTCACCTGGGTCTCGG	NM_005515.3
<b>MSMO1</b>	GCTTTGGTTGTGCAGTCATTGA	GGTCAACCATGCCCAAAGAA	NM_001017369.2
<b>MVK</b>	ACACCAAAGTCCCTCGCAAT	TCTGGGAACTTGAGCAGCC	NM_001301182.1
<b>NEUROD1*</b>	CACTATCCTGCAGCGACACT	CGGAAATGGTGAAACTGGCG	NM_002500.4
	ACTGCTCAGGACCTACTAACAAC	ACACTCGTCTGTCCAGCTTG	
<b>NEUROG3*</b>	CCGGTAGAAAGGATGACGCC	TGCCAACTCGCTCTTAGGC	NM_020999.3
<b>NELFA</b>	AGAACCTGTCCCTCACGAGA	GGCACGGGTTCTCTCGG	NM_005663.4
<b>NFE2L2</b>	CTCCACAGAAGACCCCAACC	AAGTAGCAGGTGAGGGCATG	NM_006164.5

<b>NKX2.2</b>	TACTCCCTGCACGGTCTGG	CCGCTTTCGCTTCTTGCC	NM_002509.3
<b>NR0B2</b>	TTCAACCCCGATGTGCCAG	GATAGGGCGAAAGAAGAGGTCC	NM_021969.2
<b>PAX4</b>	CACGGCTCAGGTCACCAG	CCAGACCCTCACC GTGC	NM_006193.2
<b>PAX6</b>	GTTGGTATCCGGGGACTTCG	TCTCTCAAACCTCTTCTCCAGGG	NM_001310159.1
<b>PCBD1</b>	TTCAAAGACTTCAACAGGGCCT	GGTGGTCCAGTTTCTCAGCC	NM_000281.3
<b>PDIA4</b>	CCTTATGACTACAACGGCCCA	TCAGGTTGTTAGCGGCATCC	NM_004911.4
<b>PDX1</b>	GATGAAGTCTACCAAAGCTCACG	ACATGACAGCCAGCTCCAC	NM_000209.3
<b>PLAGL1</b>	CCCACGACCCCAACAAAATG	CCAGGTGCCTCTTATAGCCC	NM_001317157.1
<b>PPIA</b>	GTGGTATAAAAGGGGGCGGGAG	TGCTGTCTTTGGGACCTTGT	NM_001300981.1
<b>PPP1R15A</b>	GCTCTTATCGGTTCCCATCCC	ATGTGTCTGGGCGGGCTG	NM_014330.3
<b>PSEN1</b>	CCAGAGGAAAGGGGAGTAAACT	GGTTGTGTTCCAGTCTCCACT	NM_000021.3
<b>PTF1A</b>	CGACCCTGATTATGGCCTCC	GATCTTCAGCCGAGTCTGGG	NM_178161.2
<b>RFX6</b>	ATTTTCAGGCAGCACAGACACT	TGACCTTCCATTTTGTGCTGG	NM_173560.3
<b>SIRT1</b>	ACTTCGCAACTATACCCAGAACA	TGTTGCAAAGGAACCATGACAC	NM_001314049.1
<b>SLC2A2</b>	AGGGGAGCACTTGGCACTT	GGTATCTGGGGCTTTCTGGAC	NM_000340.1
<b>SLC19A2</b>	AGCCAGACCGTCTCCTTGTA	ACAGCAACAGCACCCAGTAA	NM_001319667.1
<b>STAT1</b>	GTGATCTCCAACGTCAGCCA	TGGCGTTAGGACCAAGAAGC	NM_139266.2
<b>STAT3</b>	GGAAAGTATTGTGCGCCAGAGA	TTCAGCACCTTCACCATTATTTCCA	NM_213662.1
<b>STAT5B</b>	TGCTTGGAAGTTTGATTCTCAGG	CTTCACGTATCCATCAACAGCTT	NM_012448.3
<b>TMBIM6</b>	TGGTCACTCATTTTCATTCAGGCT	ATCAGCCAAATCATCAATATCAGGG	NM_003217.2
<b>TP53</b>	ATTTTCACCCTTCAGATCCGTGG	TTATGGCGGGAGGTAGACTGA	NM_001126115.1
<b>TRMT10A</b>	AGCACCTTCGCCTTATTATTGA	TGTCAAGTAAACTGCACAGGATG	NM_152292.4
<b>VCP</b>	AGGGGAGCCTATCAAACGAGA	TCTAGGAGGCTTCACACCAATTG	NM_001354927.1
<b>WFS1</b>	TGCGTCTGAAGGTGGTCAAG	GTGGGGATGATGGTGGACAG	NM_006005.3
<b>XBP1s</b>	GTGAGTCCGCAGCAGGTG	GGGTCCTTCTGGGTAGACCT	NM_001079539.1
<b>XBP1u**</b>	CGCACCTGAGCCCCGA	CTAAATCTACCACTTGCTGTTCC	NM_005080.3
<b>ZFP57</b>	GTGAAGAAGAAGCCAGTCACCTT	GATGGACAAACTCTCTCCACTGT	NM_001109809.2

Table S4. Primer sequences

\*PRIMER SET(S) DID NOT AMPLIFY

\*\*THIS PRIMER SET DETECTS BOTH SPLICED AND UNSPLICED MESSAGES