SUPPLEMENT Table 1: Primers used in qRT-PCR analyses

TargetAccession #Primer_Forward (Fw)Primer_Reverse (Rv)Oct 3/4NM_013633GTTCTCCACCCAGGAACTAGGCTATAAGACCTGCACCCAGGCTCCADNA segment, Chr X, CelltechCTGTGCCACAGACACAACAAGAACCCCCCCTATATTTGGCTCGChinoscience 3'BC027376TCACCTGCCCACTTGAGGTTGCCTTCGGGTGTTCGAAFEbrt: elongation of very longCACTGAGAAGCATGGCCTAAGCATGCCCTGGTCACGGGTGTAGChin fatty acidsNM_019422ACTGAGAGACGCTTACCCATCACCCTGGCCAGGGGTGTAG"EST, similar to CNT1'BC061230GCAGCAGAGCGCTTCAGGTGTCCTGCAGCAACACGGGGGTDKF2P564G2022 protein"NM_173734TGCGTGGCTTCAGGGGTGTCTCTGCAGCAACACGGGGGG"EST, similar toMT12At163083CAGTTCACGAGGCAGGATGTCTGCCTGTTTGCTCTCACTAGCT"Eukaryotic translation initiationAK012338CACTTGCACACGGCGGGGGTGGCAACAGA GCATCGAAGA12000080012 geneBL408065ATCGAGGCCTACGGGAACGGTGGGATTTGGTGTGCCTAT2410146L05 geneBC008295TGACCCTCACCCTGGCGGAGAGGGTGGGACTTGACGGGTGGGG2410146L05 geneBC008295TGACCCTCACCCCGGGAGAGGGTGGACATGGCCCCAGTGGAG2410040019 geneNM_0227532AGGAAACGAGGCACCGAGAGGGCGTCCACATGGCACCTAAGC2410146L05 geneNM_013452ACAGGGCCACGAGGAGAGCACCTCACCCGGAGATG2410146L05 geneNM_02895TGACCTCCACGCTGCCTCATTGGAAATGCATCGCCTCAT2410146L05 geneNM_02895TGACCTCAAGGCACCAGAGGAGCGCTCCACCTGACTAGC2410148L05 geneNM_12352AGGAACGGCCCCCAGGAGAGCGCTCCACGCTCATGTCACGGGG2410148L05 geneNM_118348 <t< th=""><th></th><th></th><th></th><th></th></t<>				
"DNA segment, Chr 19, Wayne CTGTGCCACAGACACAACAAGA ACCCCCCTATATTTGGCTCG State University 57 NM_138595 CTGTGCCACAGACACAACAAGA ACCCCCCTATATTTGGCTCG Chiroscience 3° BC027376 TCACCTGCCACATGGCCTAGACAT GCCTTCGGGTGTTTCGAA FEbrl 1: elongation of very long ACTGAGAAGACATGGCCTAGACAT GCCCTGGTCACGGGTGTAG FEST, similar to cNT1" BC061230 GCAGCAGATGCCTTTACCCA TCACCCGCGGGGGGGGG FEST, similar to NM_173734 TGCGTGGCTTCAGGGGGTGTC CTGCAGCAAACACGGGGG TEST, similar to MT12 AA163083 CAGTTCACGAGGGAGGATGTC TGCCAGCAAAGAGAGGAGGAGGATGTC Tector 2, subunit 2" AK012338 CACTTGTCACACATGCGGGAGGATGTC TGCGCACATGGACAAGGAGGAGGA 1200016D23 gene BI408065 ATCGAGGCCACAGTGGGGGGG GCCACAATGGACATGGCTGGT 241014BL05 gene BC062245 TACCGTCCGCTGTGTCCC CACCCCAGGGCTTCCATGTAG 241014BL05 gene BC08295 TGACCCTGAGCGGAGGAG GGGTGACATGGCTCATGT 2610024N01 gene Bm198522 ACAGGCAATGAGGAGGAG GCGTGACATGGCTCATGT 26100305D13 gene Bm198522 ACGGGAACTGAGGCACAGAGG GGTGGACATGGCCTCATAG <t< td=""><td>Target</td><td>Accession #</td><td>Primer_Forward (Fw)</td><td>Primer_Reverse (Rv)</td></t<>	Target	Accession #	Primer_Forward (Fw)	Primer_Reverse (Rv)
State University 57NM_138595CTGTGCCACAGACACAACAAGAACCCCCCTATATTTGGCTCGChiroscience 3"BC027376TCACCTGCCCACTTGAGGTTGCCTTCGGGTGTTCGAA"Elovi1: elongation of very long-ACTGAGAAGCATGGCCTAGACATGCCCTGGTCACGGGTGTAG"Est, similar to ch11"BC061230GCGTGGCTTCACGGTGTCCTGCAGCAAACACGGGTG"EST, similar to ch12"NM_173734TGCGTGGCTTCAGGTGTCCTGCAGCAAACACGGGTG"EST, similar to ch12"AA163083CAGTTCACGAGGCAGGATGCTGCCTGTTTGCTCACTAGGTG"ELWANVict translation initiationAA163083CAGTTCACGAGGCGGCGGCGGGCTGCCAACAGAGACAAGGAGGAG1200008012 geneBL00065ATCGAGGCCTACGTGGGAGCGCCACAATGGACAAGGACGGT2400008012 geneBC002245TAACCTCCTCGCTGTGTCCCACCCCAGGCTTCAGGTGGCT240000805 geneNM_028030TTCGCTTGACCCAGGGAGAGCGCGGGGATTGCGTAT2410146L05 geneBC008995TGACCCTCAGCCGGAGAGTGCGTACGTTCACTGTGTCCCTAGG2610024N01 geneBC008995TGACCCTCAGGCCGAGAGGAGGTGGACATGGCTCCTAGCT2610024N01 geneBM198522ACAGGGCCAAAGAGAGAGAGGTGGACATGGCTCCTAAGC2610024N01 geneBM008525TGACCCTCAGCCGCGCAAGGAGGAGGTGGACATGGCTCCTAACC2610024N01 geneBM198522TGACCCTCAGGCCCCAATGGTGGACATGGCTCCTAACC2610024N01 geneBM198522TGACCCTCAGCCCCAATGCGTACGTCCCCAT2610024N01 geneBM009309AGGCTCCAAGCCCAAGGCCCAAGGAGGTGGACATGGCTCCTAAGC2610024N01 geneBM0145482TGGAAATGGCATGGCTCCAAGGGTGGACATGGCTCCTAAGC200002M108 geneNM_145482<	Oct 3/4	NM_013633	GTTTCTCCACCCAGGAACTAGGCT	ATAAGACCTGCACCCAGGCTCCA
 "DNA segment, Chr X, Celltech Chiroscience 3" BC027376 TCACCTGCCACTTGAGGTT GCCTTCGGGTGTTTGGAA "EST, similar to cNT1" BC061230 GCAGCAGATGCCTTTACCCA TCACCCTGCTGAGGCTGAGGT TCACCCCCGGTGAGGGTGAG "EST, similar to cNT1" BC061230 GCGTGGCTTCAGGTGTC CTGCAGCAAACACGGGTG "EST, similar to MTF2_HUMAN/now it is Zip110" AA163083 CACTTGTCACGAGGGCAGGATGTC TGCCTGTTTGCTCACTAGGAG "Extaryotic translation initiation Tactor 2, subunit 2" AK012338 CACTTGTCACACATGCCGGT TGGCAACAGA GCACTGAGAA ATCGAGGCCTACGTGGACTCA ATTCGACACGGAGAATGCCTGGT TGGCAACAGA GCACTGAGAA ATGCACGGGAGGAGGAGGAGGA CACTTGTCACACATGCCGGGT TGGCAACAGA GCACGAGAGA ATGCGAGGCCTACGGGAGAGC CCACCTAGGCACAAGCAAGCAGGT 2400008B06 gene NM_02303 TCGCTGCTGTGTCCC CCACCCAAGGGCAATGAGAAGGAGG CACGTCAAGGGAAGGAGG CGGTACGTTCCATGTGAG 2610024N01 gene BC002989 TGACCCTCAGCGGGAGAGG GGTGGACATGGCTCCAAGTGGCTCCAAT TGGAATGCATCGCTCCAAT TGGAATGCATCGCCTCAAT TGGAATGCATCGCCTCAAGGAAGGAACCAAGGAACGGCCCCGAAA CTGGCACGCCTGAACCAACACACGCC CGCCCTTGCACGCAGAA		e		
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 "Elovit: elongation of very long chain fatty acids NM_019422 ACTGAGAAGCATGGCCTAGACAT EST, similar to cNT1* BC061230 GCAGCAGATGCCTTTACCCA TCACCCCTGAGTGCCAGG "EST, similar to cNT1* BC061230 GCAGCAGATGCCTTTACCCA TCACCCCTGAGTGCCAGG "EST, similar to NM_173734 TGCGTGGCTTCAGGTGTC CTGCAGCAAACACGGGGG "EST, similar to NM_173734 TGCGTGCGCAGGGAGTGTC TGCCAGCAAACACGGGGG "EST, similar to NM_173734 TGCGTGCACCAGGCAGGATGTC TGCCCGACTGAAACACGGGGG "Extaryotic translation initiation Tector 2, subunit 2" AK012338 CACTTGTCACACATGCCGGGT TGGCAACAGA GCATCGAGAAA 120008012 gene BL008139 AAGTCCCAGTGCTGCACTCA ATTCGACATGGACAAGCAGGGT 1200016D23 gene BL008030 TTCGCTTGATCCGGAGAC GGTGGAGTTGGTGTGCTCAT 2410146L05 gene BC062245 TAACGTCCTGCCGGGAGAC GGTGGAGTTGGTGTCGCTAT 2410146L05 gene BC062245 TAACGTCCTGCCGGAGAGA CACGCCACAGTGGCTCCATGTAG 2610024N01 gene BC008995 TGACCCTCAGCGCGAGAGA CACGCCTCATGGTCACTGT CCTTTGA 26103024N01 gene BM198522 ACAGGGCAATGAGGAGAGA CACGCTCATATGTGACAAATGATTTATT 200002M19 gene NM_027532 AGGAAACTGAGGCCCACAGAG 9430093H08 gene NM_027532 AGGAAATGCATCGCCTCAT TGGCTGCGACTGCATGAC Brachyury NM_009805 TGGTCCCTCAGCCCAAGAGA GGTGCACAAGCGCCCCTAA Brachyury NM_013422 GGAAATGCATCGCCCAATCT GCACCCTTGCGAATTGTAAG CBC333 BC00206 CAACAAGCAGCACCAATCT CGCCCTTTGCGAATTGTAAA CBCACAAGCAGAAAGGACCAATCT CGCCCTTTCAGAATGGATTGAAAGAGAACAA CDNA E130314M08 gene NM_17554 GAAGCCTTGAACCAGACCACACCC CGCAACAGCAAGAAGGACCGAA CDNA E130314M08 gene NM_178933 TGGTTGCCTTTCCACTCATCAGG CTGGAAAGGAACGAAAGGACCGAA CDNA E130314M08 gene NM_17893 TGGTTGCCTTTCACACAGACCAACACC CDNA E130314M08 gene NM_17893 TGGTTGCCTTTCACCAAGCGCCCCAAGGC CATGTGCCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC				
chain fatty acids NM_019422 ACTGAGAAGCATGGCCTAGACAT GCCTGGTCACGGGTGTAG "EST, similar to cNT1" B0061230 GCAGCAGATGCCTTTACCCA GCCCGTGAGGGCCAGG DKFZP564G2022 protein" NM_173734 TGCGTGGCTTCAGGGTGCT CGGCAGCAGACACGGGGTG "EST, similar to CNT1" CACCCCGGAGGATGCC TGCCGCGCAGGGG TEST, similar to CNT1" AA163083 CAGTTCACGAGGCAGGATGTC TGCCTGTTGCTCTACTAGCT "Extaryotic translation initiation factor 2, subunit 2" AA163083 CACTTGTCACACATGCCGGT TGGCAACAGA GCATCGAGAA 1200008012 gene BL003139 AAGTCCCACGTGCGCACCTCA ATTCGACATGGCACAGGA 1200008008 gene NM_028030 TTCGCTTGACCAGGAGCG GCCCAAATGGAATTGCTGGT 2400008806 gene BL008955 TGACCCTCGGCGGAGAAC GGTGGGATTGGTGGCCTAT 2410146L05 gene BC062245 TAACGGCCAGGGCAGGAGGA GCCCCAAGGCAGCGTCCCATGTAG 2610024N01 gene BC008955 TGACCCTCGCCGGAGAAGC GGTGGACTTGGCCCATGTAG 2610305D13 gene Bm198522 ACAGGGCCATGGGCCCAGGAGG 9330093H08 gene NM_027532 AGGAAACTGAGGCCCAGAGAG GCGTGCACTGTGCCCCTAT ARM1 NM_009665 TTGGTTGCCCCCCAGGGAGAGG GCCCAGAGG GGTGGACTGCGCTCAT ARM1 NM_009668 TTGGTTGTCCCCCAGGGAAGGAG GCGCCCAGGAGG Brachyury NM_009309 AGGCTCCCTGCCCCAGT TGGAAATGCATCGCCTCAT ARM1 NM_013482 GCCAACAGGAGCACCAGCACCCAGT TGCGCCTGCAT ARM1 NM_013482 GCCAACAGCAGCACCAGATCT CGCCCTTGTACG Brachyury NM_013482 GCCAACAGCAGCACCCAGT TGCGCATGTAAGC Brachyury NM_013482 GCCAACAGCAGCACCCAGT TGCGCATGTAAGAGAAGCA CDNA E130314M08 gene NM_175554 GAAGCTGGCCCGAGGA CDNA E130314M08 gene NM_175554 GAAGCCTGAGCACGCCCAGGA CTTGGGCATGGCATGTAAAGGAGAACCA CGCAACAGCAAGCAAGCAAGCAGCACCCAAGTC CGCCAGGATTGTAAAGGAGAACCA CDNA E130314M08 gene NM_175554 GAAGCCTGAAGCACAGCACCCAGTTC TGAAGCATGGAATGGCATGGC			TCACCTGCCCACTTGAGGTT	GCCTTCGGGTGTTTCGAA
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 "EST.similar to MTF2_HUMAN/now it is Zip110" AA163083 CAGTTCACGAGGCAGGATGTC TGCCTGTTTGCTCTCACTAGCT "Eukaryotic translation initiation factor 2, subunit 2" AK012338 CACTTGTCACACATGCCGGT TGGCAACAGA GCATCGAGAA ACGCCCAGTGCTGCACTCA ATTCGACATGGACAAGCAGGAGA 24000080012 gene BI08065 ATCGAGGCCTACGTGGAGC GCCACAATGGAATGGCTGGCT 2400008B06 gene NM_028030 TTCGCTTTGATCCGGAGAAG GGTGGGATTTGGTGTGCCTAT 2410146L05 gene BC008295 TGACCTCAGCCGGAGAGT GCGTACGTCACTGTCACTG TCCTCATGTAG 2610024N01 gene BC008995 TGACCCTCAGCGGAGAGG GGTGGACATGGCCCCAAGGAGAGG 2610305D13 gene Bm198522 ACAGGCCAATGAGGCCAAGGAGAG CACGTCAGTCCACTGCCTGTT 200002M19 gene NM_027532 AGGAAACTGAGGCCCAAGGAGGAG GGTGGACATGGCTCCTAACG YGGAATGCATCGCCTCAT TGGAATGGCTCGCTCATA YAGGTCCCCTGCAATTCCACG TTGGCTCGGACTGCTGCTCT Amd1 NM_009655 TTGGTTGTTCGCTAGTCTCACG TTCGCTCTGGCATTGCACACTGCCCTGCAT TGCGCCCAGCACTGCTGCTCAT AGCAGCCCTTCATACA AGCAGCCCTTCACACG TGCGCCCAAGCAGCACCCATCT CGCCCAATGCAAGAGAGACACGAGAGC CCCCCTTCGCAATTGAAG CCCCCATTGCAAGCAGAACTGGCCCGAGGAA CTTGGAGCATGAAAGGAGAACACA CTGTGAGCATGAAAGGAGGAACA CTGTGGACGCCTTCAACGG CCCCCAAGCCAAGCAAGCAGCACCGTTCCT CGCCCAAGCCATGAAAGAACCAGAAGGACCGGA CTGTGGACGCCAAGCA CTGGCCAAAGAAGAAGAACCGGA CTGTGGCCAAAGCAAGAAGGACCGGA CTGTGGACGCTGGCGC CAAGCCCCAAGCCAAGCCAGACCC CCAACAGCAAGAACGAGAACGGACCCCAAGC		NM 173734	TECETECCTTCACCTETCT	
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Zfp110"AA163083CAGTTCACGAGGCAGGATGTCTGCCTGTTTGCTCTCACTAGCT"Eukaryotic translation initiation"Eukaryotic translation initiationTGCCTGTCACACAGGCGGCTTGGCAACAGA GCATCGAGAA1200008012 geneBC03139AAGTCCCAGTGCTGCACTCAATTCGACATGGACAAGCAGGT1200016D23 geneBI408065ATCGAGGCCTACGTGGAGAACGGTGGGATTTGGTGTCGCGCTAT2400008B06 geneNM_028030TTCGCTTGCTGTGTCCCCCACCCAGGCTTCCATGTAG2410146L05 geneBC062245TACGTCTGCCTGTGTCCCCCACCCAGGCTTCCATGTAG2610024N01 geneBC08295TGACCCTCAGCGGAGAGAGCGTAGGTCACTG TCCTTTGA2610030D13 geneBm198522ACAGGGCAATGAGCAGAGAGACACGTCAATGTGACAATGATTATT3200002M19 geneNM_027532AGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCAT4M1NM_009665TTGGTTGTCGCAGTGTCCCCGCAGGTTCAGTCTGGGGCTCCTGCATARM1NM_019968GAGTTCAAGCGGGACCCAATTCAAGCCCCTTTGGCAGTGTCTARM1NM_019968GCCCACAGCAGCACCAATCTCGCCCCTTCGCAATTGTAAAGCBP300AK042627CTCCAGTGCGCGAGGACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAGAGGCCCGAGGACTTGTGAGGCTTGGCAGACDNA E130314M08 geneNM_17554GAACACAGAAGGACCAGACGCCGCAAGGAGAAGAAGAACAGAACGGAD11Moh45NM_176983TGGTGCCTTTGCACTCTCATCCTTCAAGTTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTGCCTTTGCAGCTGTGGAGGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTGCCTCTCAACCTGCAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTGCCCTTGCCAAGGAAGTGCGAACAGCAAGAAG				
 "Éukaryotic translation initiation factor 2, subunit 2" AK012338 CACTTGTCAACATGCCGGT TGGCAACAGA GCATCGAGAA 1200008012 gene Bl408065 ATCGAGGCCTACGTGGAGC GCCACAATGGACAAGCAGGT 2400008B06 gene NM_028030 TTCGCTTGGTCCGGAGAAC GGTGGGATTTGGTGTGCGCTAT 2410146L05 gene BC062245 TAACGTCCTGCCTGTGTCCC CCACCCAGGCTCACTG TCCTG TCCTG TCCTG 2610024N01 gene BC062245 TAACGTCCAGCGCGAGAGG GCGTACGTTCACTG TCCTTGCACTG TGCTCC CCACCCAGGCTCACTG TCCTTGA 2610305D13 gene Bm198522 ACAGGGCAATGAGGAGAGGAG CACGTCAGTCGCTGTGTCCC CCACCCAGGCTCCAAGC 4630093H08 gene NM_027532 AGGAAACTGAGGCCCAGAGAG GGTGGACATGGCTCCTAGC TGGGTGGCGCGCAGAGAG GGTGGCGGACTGGCGTCT ARM1 NM_009665 TTGGTTGTCGCTAGCTCACG TTGCGTCGGGACTGCTGCAT TGGATGCGGGTACCTCAGT TCGGTCGGACTGCTGCAT ARM1 NM_009309 AGGCTCCCCTGCACATTACA AGCAGCCCCTTCATACACG GCCCCCTTCGAATCG CCCCCTTCGCAATTGTAAG CAGCGCCCTTGAAGCAGGAAC CTTGGTAGCTGGAAC CTTGGTGGCTCCGGGAAC CTTGGTGGCTGGCAGGAA CTTGGAGCATGTAAGGAGAGAACA CTGCAGTGGCCCCCGCAGAA CTGGAGCTTGGACAGGAACA CTGCAGTGGCCCCAGGAA CTTGGAGCATGTAAGGAGAACA CCAAAGCAAGAACAGAACAGACAGACCAGACCAGCA CTGGTGCCTTGCAGTGGCCTGGAC CTGCCAAGGCACAGCAAACA CTGCAGGCAGCAACACCAGACCAGCACCACC CTGCAGGCTGGGACCCGAAAC CTGCAGGCCCCCAGGAACCTTCACCCCTTCAAAGGAAAGGACCGGA CTGGTGCCTTCCAGGCCCCAAGGC CGCAACAGCAAAAGGAACCGGA CTGGTGCCTTTGCAAG		AA163083	CAGTTCACGAGGCAGGATGTC	TGCCTGTTTGCTCTCACTAGCT
factor 2, subunit 2"AK012338CACTTGTCACACATGCCGGTTGGCAACAGA GCATCGAGAA1200008012 geneBC03139AAGTCCCAGTGCTGCACTCAATTCGACATGGACAAGCAGGT1200016D23 geneBI408065ATCGAGGCTACGTGGAGCGCTAGGATTGGTACTGGT240000806 geneNM_028030TTCGCTTGATCCGGAGAACGGTGGATTTGGTGTCGCTAT2410146L05 geneBC062245TAACGTCCTGCCTGTGTCCCCCACCCAGGCTTCATGTAG2610024N01 geneBC082995TGACCTCAGCCGGAGAGGGCTGACATGGACATGACAATGATTTATT320002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGGTGGGCTCCTGCATAmd1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTGGGCTCCTGCATBrachyuryNM_019909AGCTCCCCTGCACATTACAAGCAGCCCCTTCATAAGCBTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATGTGAAGCBP300AK042627CTCCAGTTGCCAGGAGAACTTGTGAGCATGAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCCTGGTAGGCTTGGGACDNA E130314M08 geneNM_175554GAAGCCTTGAACCAGACGACCGACCCCGGAAGACAGAAAGGAACGGAD11Moh45 DNA segmentNM_176983TGGTTGCCTTTTGCAAGTTGTGAAAGACAGAAAGGAACGGADEAD/H box polypeptide 21(RNA helicase II/Gu)NM_176983TGGTTGCCTACTCATCATCAAGT GCACAAGGAAAGGAACGGADNA methyltransferase 3BAF151969CAATGCTGCCCTGCATAGTGGAACCCCCGCGGTTTCCAAGGAATGCAAACADNA methyltransferase 3BAF151969CAATGCTGCC				
1200016D23 geneBI408065ATCGAGGCCTACGTGGAGCGCCACAATGGAATTGCTGGT2400008B06 geneNM_028030TTCGCTTTGATCCGGAGAACGGTGGGATTTGGTGTCCCTAT2410146L05 geneBC062245TAACGTCCTGCCCCCGCGAGAGACGCTACGTTCACTG TCCATGTAG2610024N01 geneBm198522ACAGGGCAATGAGGAAGGAGACACGTCAATGTGACAATGATTTATT3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_019968GAGTTCAAGGGGTACCCCTCAGTTCAGTCTTGGGCTCCTGCATARM1NM_019968GAGTTCCAGGGACACCCCACATCTCGCCCTTTCGCAATTGTAAGBTkNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCCTGCAGGACTTGTGAGCATGGAAAGGAGAACACDNA E130314M08 geneNM_175554GAAACCTGAACCAGAACGCACCCAGGACTGGTAGGCTTGGCTCTGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGACAAGGAAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCCCACAAGCGCGAACAGCAAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCCCAAGGACGGTTGTCGCCCTCCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCCGCAAAGACGGTTGTCGACCTCCTESTAl427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGACACCCCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGACACCACCCCEVAryotic tr	factor 2, subunit 2"	AK012338	CACTTGTCACACATGCCGGT	TGGCAACAGA GCATCGAGAA
2400008B06 geneNM_028030TTCGCTTTGATCCGGAGAACGGTGGGATTTGGTGTCGCTAT2410146L05 geneBC062245TAACGTCCTGCCTGTGTCCCCCACCCAGGCTTCCATGTAG2610024N01 geneBC008995TGACCCTCAGCCGGAGAGTGCGTACGTTCACTG TCCTTTGA2610305D13 geneBm198522ACAGGGCAATGAGGAGGAGACACGTCAATGGACAATGATTATT320002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCTGGACTGCTGTCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCCCTGCATBrachyuryNM_009309AGGCTCCCTGCACATTACAAGCAGCCCTTCATAAGGBTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTGGACATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGAAAAGGAGAACACdca3BC002006CAACAAGCAAGAGCGCCCGCAAGGCTTGGCTGTGGAcoxvib2NM_17554GAAGCCTTGAAGCAACGACGTTCTGTGCCCAAGGAATGCAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATCAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATCAACADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAl427584GACCCCAAGCCAAAATCTACTG <t< td=""><td>1200008O12 gene</td><td>BC03139</td><td>AAGTCCCAGTGCTGCACTCA</td><td>ATTCGACATGGACAAGCAGGT</td></t<>	1200008O12 gene	BC03139	AAGTCCCAGTGCTGCACTCA	ATTCGACATGGACAAGCAGGT
2410146L05 geneBC062245TAACGTCCTGCCTGTGTCCCCCACCCAGGCTTCCATGTAG2610024N01 geneBC008995TGACCCTCAGCCGGAGAGTGCGTACGTTCACTG TCCTTTGA2610305D13 geneBm19852ACAGGCCAATGAGGACGAGACACGTCAATGTGACAAATGATTTATT3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCGGACTGCTGCTARM1NM_019968GAGTTCAAGCGGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGCTCCCCTGCACATTACAAGCAGCCCCTTCATAACAGCBTKNM_013482GCCAACAGCAGCACACCACATCTCGCCCTTTGGACTGTGAACBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGAAAAGGAAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTGGGGACDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAGCACCAGAGCCCGCAAGGCACGGACCGGAChildoh45NM_176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCTCCAACCTGCGAACAGCAAGAACAACADhrs10BC064042CTTGCCCCGCCGCAAAGACGGTTGTCGCCCTCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCGCGGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGACACACCACCEstaryotic translationHi27584GACCCCAAGC	1200016D23 gene	BI408065	ATCGAGGCCTACGTGGAGC	GCCACAATGGAATTGCTGGT
2610024N01 geneBC008995TGACCCTCAGCCGGAGAGTGCGTACGTTCACTG TCCTTTGA2610305D13 geneBm198522ACAGGGCAATGAGGAAGGAGACACGTCAATGTGACAAATGATTTATT3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009655TTGGTTGTCGCAGGCTCCCAGGTTGCGTCGGACTGCTGTCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGBTKNM_013482GCCAACAGCAGGCACCAATCTCGCCCTTTCGCAATTGTAAGCbP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGGCTGGGACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGGCAGGACoxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAAGGAGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTATCCATCCTTCAACGTGCGAACAGCAAGAAGGACCGGADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCAACAACAACADhrs10NM_013514GCTGGCCTGCCAAAGTACGGTTGCGCCTCCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTGGCCCTCCTTEyb4.9NM_013514GCTGGGATTGCAAAGTCAACTCCGCGGTTTCTCAGGAACCACCACCESTAl427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEykaryotic translationHH25252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACC	2400008B06 gene	NM_028030	TTCGCTTTGATCCGGAGAAC	GGTGGGATTTGGTGTCGCTAT
2610305D13 geneBm198522ACAGGGCAATGAGGAAGGAAGGAGACACGTCAATGTGACAAATGATTTATT3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTACCGTTGCGTCGGACTGCTGTCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGGCTCCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcbNA E130314M08 geneNM_175554GAAGCCTTGAAGCAGACCAGCCCCGCAGGGTTGTGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCAAGAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCAACAAAACADNA methyltransferase 3BAF151969TCAATCTGCCCCGCAAAAAACGGTTTGTCAATGAGAATCTESTNM_013514GCTGGGATTGCTAATGTGAACTCCCGCCTTTTCCAGAATCTESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEykaryotic translationHM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACC	2410146L05 gene	BC062245	TAACGTCCTGCCTGTGTCCC	CCACCCAGGCTTCCATGTAG
3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCGGACTGCTGCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGGCTCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM_013482GCCAACAGCAGCAGCACAATCTCGCCCTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAGCACCAGCCCGCAGAGGGTTGTGTGTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCTGCTCCTAACCTGCGAACAGCAACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTGCCTCTTPb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCAGGAATCTEstML_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACACCACEstML_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCACCEukaryotic translationSC3252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCACC	2610024N01 gene	BC008995	TGACCCTCAGCCGGAGAGT	GCGTACGTTCACTG TCCTTTGA
3200002M19 geneNM_027532AGGAAACTGAGGCCCAGAGAGGGTGGACATGGCTCCTAAGC9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCGGACTGCTGCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGGCTCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM_013482GCCAACAGCAGCAGCACAATCTCGCCCTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAGCACCAGCCCGCAGAGGGTTGTGTGTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10BC064042CTTGCCCTGCTCCTAACCTGCGAACAGCAACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTGCCTCTTPb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCAGGAATCTEstML_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACACCACEstML_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCACCEukaryotic translationSC3252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCACC	2610305D13 gene	Bm198522	ACAGGGCAATGAGGAAGGAGA	CACGTCAATGTGACAAATGATTTATT
9430093H08 geneNM_145462TGGAAATGCATCGCCTCATTGGAAATGCATCGCCTCATAmd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCGGACTGCTGTCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGGCTCCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM_013482GCCAACAGCAGGCACCAATCTCGCCCTTTGGAGCATGTAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCGTGGGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAACGCCCGCAAGGCACCAAGTCTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGAACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGAACCGGAD11Moh45NM_019553CATGTGTCCTACTCATCCTTCAAAGTGCGAAAGGAACAGAAAGGACCGGADhrs10BC064042CTTGCCCTGCCCGCAAAGACGGTTGTCGCCTCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCTCTTDNA methyltransferase 3BAF151969TCAATCCTGGCCAAAGCAAACTCACCGGGATTGTAATGAACACESTNM_053252GACCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationStatesStatesStates	3200002M19 gene	NM_027532	AGGAAACTGAGGCCCAGAGAG	GGTGGACATGGCTCCTAAGC
Amd1NM_009665TTGGTTGTTCGCTAGTCTCACGTTGCGTCGGACTGCTGTCTARM1NM_019968GAGTTCAAGCGGGTACCTCAGTTCAGTCTTGGGCTCCTGCATBrachyuryNM_009309AGGCTCCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAACGTTTCTGTGCCCAAGTCCTTCACGATCxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAGGGTTGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTACTCATCCTTCAAAGTGAGGCCAGAAAGGACCGGAD11Moh45NM_019553CATGTGTCCTACTCATCCTTCAAAGTGAGGCACAGAAAGGACCGGADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCTCCTTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEvaryotic translationStaryStaryStaryStartCTACTACT	•	NM_145462	TGGAAATGCATCGCCTCAT	TGGAAATGCATCGCCTCAT
BrachyuryM M 009309AGGCTCCCTGCACATTACAAGCAGCCCCTTCATACATCGBTKNM 013482GCCAACAGCAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM 175554GAAGCCTTGAAGCAACGTTTCTGTGCCCAAGTCCTTCACGATD11Moh45NM 176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGAACCGGAD11Moh45NM 176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGAACCGGAD11Moh45NM 176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGAACGGAD11Moh45NM 176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGAACGGAD11Moh45NM 176983TGGTTGCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADAD/H box polypeptide 21 (RNA helicase II/Gu)NM 019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translation	Amd1	NM_009665	TTGGTTGTTCGCTAGTCTCACG	TTGCGTCGGACTGCTGTCT
BTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAACGTTTCTGTGCCCAAGTCCTTCACGATCoxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAGGGTTGTGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGACCGGAD11Moh45 DNA segmentNM_176983TGGTTGCCTTTTGCAGTTGTGAAAGACAGAAAGGACCGGADAD/H box polypeptide 21CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationSSSS	ARM1	NM_019968	GAGTTCAAGCGGGTACCTCAGT	TCAGTCTTGGGCTCCTGCAT
BTKNM_013482GCCAACAGCAGCACCAATCTCGCCCTTTCGCAATTGTAAGCBP300AK042627CTCCAGTTGCCGCAGGAACTTGTGAGCATGTAAAAGGAGAACACdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAACGTTTCTGTGCCCAAGTCCTTCACGATCoxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAGGGTTGTGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationStationStationStation	Brachyury	NM_009309	AGGCTCCCCTGCACATTACA	AGCAGCCCCTTCATACATCG
Cdca3BC002006CAACAAGCAAGTGGCTCGAGCTGGTAGGCTTGGCTGTGGAcDNA E130314M08 geneNM_175554GAAGCCTTGAAGCAACGTTTCTGTGCCCAAGTCCTTCACGATCoxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAGGGTTGTGTGCTCTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45 DNA segmentNM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADAD/H box polypeptide 21NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCGGCGTTTTCTCAGGAATCTESTAl427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEvkaryotic translationSUM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACC	BTK	NM_013482	GCCAACAGCAGCACCAATCT	CGCCCTTTCGCAATTGTAAG
cDNA E130314M08 gene Coxvib2NM_175554 NM_183406GAAGCCTTGAAGCAACGTTTCT CCCTAACCAGAACCAGACGCGTGCCCAAGTCCTTCACGAT CGCAGGGTTGTGTGCCTTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTG TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGA TGAAAGACAGAAAGGACCGGAD11Moh45 DNA segment DEAD/H box polypeptide 21 (RNA helicase II/Gu)NM_019553CATGTGTCCTACTCATCCTTCAAAGT CCTTGCCCTGCTCCTAACCTGATGCCAAGGAATGCAAACA GCGAACAGCACATTCATCCADhrs10BC064042CTTGCCCCTGCTCCTAACCT CAATCCTGCCCGCAAAGGCGAACAGCACATTCATCCA ACGGTTGTCGCCCTCCTTDNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAG GACCCCAAGCCAAAATCTACTGACGGTTGTCGCCCTCCTT CCGCGTTTTCTCAGGAATCTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTC GACCCCAAGCCAAAATCTACTGCCGCGTTTTCTCAGGAATCT TGATTCTGTAATGAGCACACCACCESTAI427584GACCCCAAGCCAAAATCTACTG GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACC TGATTCTGTAATGAGCACACCACCEukaryotic translationLiningLining	CBP300	AK042627	CTCCAGTTGCCGCAGGAA	CTTGTGAGCATGTAAAAGGAGAACA
Coxvib2NM_183406CCCTAACCAGAACCAGACGCCGCAGGGTTGTGTGTGTCTTTTD11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45 DNA segmentNM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADEAD/H box polypeptide 21NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGCTTTTCCAAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFURAnga Context Contex	Cdca3	BC002006	CAACAAGCAAGTGGCTCGAG	CTGGTAGGCTTGGCTGTGGA
D11Moh45NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGAD11Moh45 DNA segment DEAD/H box polypeptide 21 (RNA helicase II/Gu)NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGCTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFanslationFanslationFanslation	cDNA E130314M08 gene	NM_175554	GAAGCCTTGAAGCAACGTTTCT	GTGCCCAAGTCCTTCACGAT
D11Moh45 DNA segment DEAD/H box polypeptide 21 (RNA helicase II/Gu)NM_176983TGGTTGCCTTTTGCAGTTTGTGAAAGACAGAAAGGACCGGADhrs10NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFanslationFanslationFanslation	Coxvib2	NM_183406	CCCTAACCAGAACCAGACGC	CGCAGGGTTGTGTGCTCTTT
DEAD/H box polypeptide 21 (RNA helicase II/Gu)NM_019553 BC064042CATGTGTCCTACTCATCCTTCAAAGT GCGAACAGCACATTCATCCADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFanslationFanslationFanslation	D11Moh45	NM_176983	TGGTTGCCTTTTGCAGTTTG	TGAAAGACAGAAAGGACCGGA
(RNA helicase II/Gu)NM_019553CATGTGTCCTACTCATCCTTCAAAGTGATGCCAAGGAATGCAAACADhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationCATGTGTAATGAGCACACCACCCATGTCTGTAATGAGCACACCACC	D11Moh45 DNA segment	NM_176983	TGGTTGCCTTTTGCAGTTTG	TGAAAGACAGAAAGGACCGGA
Dhrs10BC064042CTTGCCCCTGCTCCTAACCTGCGAACAGCACATTCATCCADNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFFF				
DNA methyltransferase 3BAF151969TCAATCCTGCCCGCAAAGACGGTTGTCGCCCTCCTTEpb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAl427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationFersonFersonFerson	(RNA helicase II/Gu)	NM_019553	CATGTGTCCTACTCATCCTTCAAAGT	GATGCCAAGGAATGCAAACA
Epb4.9NM_013514GCTGGGATTGCTAATGTGAACTCCCGCGTTTTCTCAGGAATCTESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationEukaryotic translationExternal for the second secon	Dhrs10	BC064042	CTTGCCCCTGCTCCTAACCT	GCGAACAGCACATTCATCCA
ESTAI427584GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCESTNM_053252GACCCCAAGCCAAAATCTACTGTGATTCTGTAATGAGCACACCACCEukaryotic translationEukaryotic translationEukaryotic translation	DNA methyltransferase 3B	AF151969	TCAATCCTGCCCGCAAAG	ACGGTTGTCGCCCTCCTT
EST NM_053252 GACCCCAAGCCAAAATCTACTG TGATTCTGTAATGAGCACACCACC Eukaryotic translation	Epb4.9	NM_013514	GCTGGGATTGCTAATGTGAACTC	CCGCGTTTTCTCAGGAATCT
Eukaryotic translation	EST	AI427584	GACCCCAAGCCAAAATCTACTG	TGATTCTGTAATGAGCACACCACC
	EST	NM_053252	GACCCCAAGCCAAAATCTACTG	TGATTCTGTAATGAGCACACCACC
elongetion factor 1 alpha 1 AVV/210535 ATTCATTTACCOTTCTCACCTTTCTC ACACACTTCCTCTCCCTCTCAT				
	elongation factor 1 alpha 1	AW210535	ATTCATTTAGCCTTCTGAGCTTTCTG	AGACAGTTGCTGTGGGTGTCAT
FOXJ2 NM_021899 ACCAAGTGAACTCTTACGGGCA GCGGTTGTATCCTGCTGAGTC	FOXJ2	NM_021899	ACCAAGTGAACTCTTACGGGCA	GCGGTTGTATCCTGCTGAGTC

FOXM1	NM_008021	CCCAAAGCCCAAGAAGTCCT	ATCGGCTCACCTCCCTTTTC			
Foxp4: forkhead box P4	BC052407	CAGGCCCCCCTTCACCTA	TAGGCGAACATCCTGGTGAAC			
Fshprh1 FSH primary response		CAGGCCCCCTTCACCTA	TAGGEGAACATECTGGTGAAC			
	NM_145924	TGAGCAATGGCTTAGCTCCA	CATGCACTTCAATATCCGTGAGTT			
Human H1F0	BC029046	CCTCGCGCCAGTCCATT	AGGCGCTTGATGGACAACTT			
Human Mybl2	X13293	GCAGAGGGATAGCAAGTGCAA	TCCAGTCCTGCTGTCCAAACT			
IGF1R	NM_010513	ATCCTGAAGGGCAATCTGATT	ACGTAGCCGGTCACCACCT			
IGF2	BC058615	GGGAAGTCGATGTTGGTGCT	TCAACAAgcTccccTccg			
IGF2BP1	AV233540	CGAAGTTCCAGTGAGGAATCCT	ACAACCCAAGCTATGATTGCAA			
IGF2R147	NM_010515	GGGAAGTCGATGTGGTGCT	TCAACAAGCTCCCCTCCG			
Incenp	NM_016692	cTgTTTTgATgTTgggcTggT	CCTCCCAACAGGTCTGGGA			
INSL2	BC023874	GCACCCAAGGAAGGTCTTTG	AGTTCCTTCATGGAGCAGCCT			
Kcnk6 [D7Ertd764e]	AK036882	CGTGTTGCAGACGTCTTTCCGC	CATCCTCATCCTGGCTGAGG			
KU80/X-ray repair	ANU30002	CGIGIIGCAGACIIICCGC	CATCCTCATCCTGGCTGAGG			
complementing defective repair	r NM 009533	CTCCGCAGCCCGTTCA	TTGTCGATTGGAAAAGGCAAA			
LEFTY	MMAJ82	AAAGAGGCTGTCCCCACACA	TGGACACGAGCCTAGAATCGA			
Lin-28	NM_145833	CTGCGGTGGGCTAGACCA	GACACGAGGCCACCATATGG			
Magel-2	NM_013779	ACCTGGCCCCTCTTCTCTAGA	CACCAATGAACATGCGCTCT			
MAZ	MUSPUR	GACATAAGCTGTCGCATTCGG	ATGTGAGCGCACGTGGTAAC			
Mcm3	BC031706	TTGCGTGGTTGGCACTTGT	CGGCTCTCTCAGCACAGTGA			
Mcm5	NM_008566	TCAAGCGGCATTACAACCTG	CGGCTGTTTATGCAAGTGGTC			
MDK1	NM_010784	GGAGACCATCCGCGTGACTA	GGCTCTCTGGCCTCCTGACT			
Mkrn1	BC003329	GTCACGAAACCCAAGCTTTCC	GGGCAGTACGGCCACAGTAG			
mouse EST	AK028828	TGTCCGTCCTGAGGAAGGTG	CAAGATGGATTCCTGCTGAGC			
Mtf2		TTTTCAGGTGATTGAGCTGC	GTATATGGGCCAGGAGGACG			
Mus musculus cAMP responsive	NM_013827	TITICAGGIGATIGAGCIGC	GTATATGGGCCAGGAGGACG			
element binding protein 1 (Creb1)) NM_133828	AGTGCCAACCCCCATTTACC	CCTGTACCCCATCCGTACCA			
Mus musculus cAMP responsive	, 1111_100020					
element binding protein 3-like 3	NM_145365	GGTCCAGTCAACCAGCAAGC	AGTTGAAAGGGCTGATGGAGG			
Mus musculus myeloblastosis	—					
oncogene, mRNA	BC011513	AGGAGGTGGAGTCGCCAACT	AGGAGACGCCTGCGAGAAC			
Mus musculus TATA-binding						
protein associated factor	AY038601	GGCTCCTTCCGGGATGAT	CAACTCAGAGTTTGTGGCCAATAT			
MYBL2	NM_008652	GTGAGGCAGTTTGGACAGCAA	GGATTCAAAACCCTCAGCCA			
myeloblastosis oncogene_like 2						
(Mybl2)	NM_008652	TGCAGTTCCTGGGAACGTGC	TGCAGTTCCTGGGAACGTGC			
Nanog	AK010332	TTTCAGAAATCCCTTCCCTCG	CGTTCCCAGAATTCGATGCT			
Nanog	AK010332	TTCAGATAGGCTGATTTGGTTGG	ATCATAGAAAGAAGAGTTAAATGTCTAATGC			
NEDD8	NM_008683	AccccAAccTgggAAgAAgA	R161ccTTgATTcgcTccAccTTg			
Nvl nuclear VCP-like	BC031847	AGGCGGTTAGCCCTCTTTTC	TCCACCGGGAGTTTTGTCAA			
Oct 3/4	NM_013633	cAATgccgTgAAgTTggAgA	gcTTcAgcAgcTTggcAAAc			
Pea3 (Etv4)	NM_008815	GGCGAACGCTACGTGTACAA	CGGTCAAACTCAGCCTTCAGA			
Reduced expression 3	NM_009052	GAACCCCACCATCTGGAAGA	TTTGGTATGGCCCAGAGAAAGT			
Reduced expression 3	AF097438	ACTCCATTACTCCTGGGCCTATC	AGAGCGGAGCAGGTCTGAGA			
SIRT1	NM_019812	ATGACAGAACGTCACACGCC	AGGATCGGTACCAATCATGA			
SIRT6	NM_181586	TGCCTGCCTCAGCCTCTACT	GGACCTGGACAAGGGACACA			
SIRT7	NM_153056	ACTGCCCTTCACCGACACC	TGCCCTAATGTCCCCCTCTC			
SOP 9	AF071313	TCAACCAACAACCCGTCTGA	GACGACAGGCACTGCTTCAC			
Sox2	NM_011443	AGATGCACAACTCGGAGATCAG	CTTCTCGGTCTCGGACAAAAGT			
Sparc (osteonectin)	NM_009242	GGAACATTGCACCACACGTTT	TTGTTGATGTCCTGCTCCTTGA			
STK38	NM_134115	GTGAGGTGCGGCTTGTTCA	GTCACGCTCCGCACGAAT			
01100			CTOROCOTOCOROCRAT			

Tata- box binding protein	BC016476	TACCGTGAATCTTGGCTGTAAACTT	TTCTCATGATGACTGCAGCAAA
Tcof1	U81030	CCTTAGCTTCTTCTGCCCCG	CCTACCGGTTTTAGGGAGTGC
t-complex testis expressed 1	M25825	GGCCGAGTAGAGATGGAAGACTT	CCGATGGCGCTTTCTATAGC
Tdh L-threonine			
dehydrogenase	NM_021480	GTGGCGTTCTCAGCATCCA	TCTGTGCAGTCCCATTGACC
Tk1	NM_009387	GCATGGAGTGCTTCCGAGAA	GCGGCACACGGAGTGATACT
Tumor-associated calcium			
signal transducer 1	BC005618	CGTCTAAATGCTTGGCGATGA	GTCGTACAGCCCATCGTTGTT
Uhrf1	NM_010931	CACTCTCAGAGCAGCAGGCTAA	GATCTGGTACGGCCCATCCT
ZFP42	NM_009556	CAGCAGCTCCTGCACACAGA	GATCCGCAAACACCTGCTTT