

Supplementary table 1 Primers' sequence for Sanger-sequencing.

Gene Symbol	M13 PCR primer sequence	PCR primer sequence	start-end	transcript
A2M	ACACAGAGCAGCATAAAGCC	AAGCCTGTGAATCTTCACCG		NM_000014
A2M	AAGGACAGAGCACCTTTTCAC	ACAGCATAGATGAGCAACCGAG		NM_000014
A2M	TCAGACAGTCCAGGCACATTAT	CCTCTCCACGAATCACAGAGTA		NM_000014
A2M	GAGACATGGATCTGGGATTTGG	TTGGGTAATGTGTGCTTCATCG		NM_000014
A2M	ACTCCAGAGATCAAGTCCAAGG	CCTTCTCCTGTCACTTTCATGC		NM_000014
A2M	CTGCAACCAACATCGTGAAGT	TGACCAGAAAAAGTGTTTATTCATC		NM_000014
BEX5	GCATTCATTCCCTCTTCTTGC	GCAGAAGAATGCCAAAAGGT	101409238-101408880	NM_001012978.2
BHLHB9	GGCCATATAACTGGGCTTCA	CATCCAGAACCAGGAATTGA	102003901-102004299	NM_001142524.1
BHLHB9	ATAGGCCCAAGGACTGGTCT	AGATTGCTGTCCCGGTGAGT	102004613- 102005173	NM_001142524.1
BHLHB9	TGTAAAGAAACCATGTCATTTCC	GCCTGCTAGAGTTTGAAGATGG	102005174-102005583	NM_001142524.1
EIF4G1	TCCGAATTCGAGATCCAAAC	CATTTCCCTCCTCTGAGCTG		NM_004953.4
EIF4G1	CAAGGAGGTGACAGCATCAA	TCTTCTTCCCCTCGATCCTT		NM_004953.4
EIF4G1	CCGAAGATATAAACTGAACAAAGC	AATGGTCTTGGGACCCTGAT		NM_004953.4
EIF4G1	AGCCCCGAATGGATCAGTAT	CACCAGACAGCTGCTCAATG		NM_004953.4
EIF4G1	GACATGAAAGAGGCAGTCCAG	CTCCTTCTGCTCGTCACACA		NM_004953.4
EIF4G1	CTCATGACGGCTGTCTGCTA	CACACTACAGGCACCCACTG		NM_004953.4
GRAP	CAGAGGAAGCAGGAAGCTGT	TTAGGAGCCCACGTTCAATC		NM_006613.3
MLL	GTGTTGTCGCCTCTCCCTCT	ATTGGGATGCTCCTCAATCC		NM_001197104
MLL	TCATCGTCCTCAGCCTCTTC	CTTAATGATCCGCGAGGAGA		NM_001197104
MLL	AAAGGGGGCTCAAAAGAAAA	ATGGAGTGGCGAAAACAATC		NM_001197104
MLL	CCTCAGCAAAGTATGCCAAA	CAGCTGTTGTATCCCCAAGAG		NM_001197104
MLL	ATCCTGTGGGTAGGGTTTCC	CTTCTGCAGGTAGGCTTTGG		NM_001197104
MLL	GCCTGAGGACTGTGGTGTTT	GACAGAATTTGCAACGACGA		NM_001197104
MLL	TGCCAGTAGTGGGCATGTAG	GACCATGCTGTTGGCTTTTT		NM_001197104
MLL	CAGGATGATCAGCAGCCTTT	GATCAAATCCCGATGTTCGTT		NM_001197104
MLL	GGGTTGCTGTCTCACATCCT	GGTGGAAGTGTTTTGCCCTA		NM_001197104
MLL	GGCGTCACAGTACCTCTTCC	GTTTCCGTGGTGCCTGTAAT		NM_001197104
MLL	AGTATATGGGCCAACGACCA	CCAAGGAATCTTGTCCCTGT		NM_001197104

MLL	AACAAGGAAAAGCAGCCAGA	GTGGTCTGCATCCATGTGTC		NM_001197104
MLL	CCATCACAGAAAAATCTGTAGCC	GAAGGGGTACTAGAGGGAGCA		NM_001197104
MLL	GGATCCCCAACTTTTGGTTT	CTGCTCCAGTCCCATGCTAT		NM_001197104
MLL	CCAGCAAAACTGGGATTCAT	CACCAGACAGCTGCTCAATG		NM_001197104
MLL	AAGTCCAGGAAGCTCGATCA	ACACTGGGGGAGAAGAGCAG		NM_001197104
MNAT1	GTAGGAACCTGCTTGGTCGC	TGGATGCCCACTGAGAACC	61201491-61201890	NM_001177963
MNAT1	ACTTGGGATACCTATATCTGAAAAGT	TGCTAATCTGTCCACATTTATGAG	61262740-61263186	NM_001177963
MNAT1	AGAACGATGTTTTACACAGTAAGC	TGCATGTACCCATATAGTCTTCC	61264671-61265152	NM_001177963
MNAT1	AGGTAGCTGATTAAGGTCACA	CTGCCTACCTACATACCTATACAGC	61274901-61275310	NM_001177963
MNAT1	GCAAAATCCACTAGTATGGTATAAC	CAAACTAAAGGTGAACCAGATTAC	61278478-61278971	NM_001177963
MNAT1	TTATGTGGGTTTTGGTTATGCTG	CAGGCTCAATCTCAAGAGACCTA	61346265-61346755	NM_001177963
MNAT1	GGCACTCCATGTACAGTTGGTAT	CTTCCATCAGATGAGGCTTATCG	61434762-61435310	NM_001177963
OR3A1	CTGGATGTTTCTTTGCAGGA	TGCCACGTGGATATAGGAGA	3195876-3195240	NM_002550.2
TRIP12	CTAGTGGAAGTTACTGCCGC	TGGCCTGTAATCCAGAAGGT		NM_004238
TRIP12	AGATCAGAACAAGGCCAGGC	TGTCTCCGTGACAACATCTC		NM_004238
TRIP12	GTTGTTCCAGCTTTGATTACG	TACTATTGGCTAACGGGTTAGG		NM_004238
TRIP12	AAAGAAGGCATTTTTGCAGTTG	CTCAATGTTGTTGCTGTTGGAC		NM_004238
TRIP12	CCTCAAGGTCGATTAAGTGATG	CTCATCTGATCCATCGTCATCG		NM_004238
TRIP12	AGGAGGCAGCTTTTCTCTCAAC	CCAATCTAGGTGCAACTCTGCT		NM_004238
TRIP12	AGGCAACTTCAAGATCCTTTAG	TGATTCAAATCCATCTCTGAACG		NM_004238
TRIP12	TCCCAGACCAAAGAGAGTCTAC	CTCATCACAACAACGTTTTAGG		NM_004238
TROVE2	TTTTGTAATTTTATTGTGCCCATC	TTGTAACTGCCAGAGCAAGG	193038109 -193038692	NM_001042369.2
TROVE2	CACAAAGATCTATTAAGATTGTCACAT	AAGGAGCTGATTTGCTTATTGC	193038719- 193039318	NM_001042369.2
TROVE2	TCCTGCATGCTTTTTCAATTC	CCCCAAGTTTATCCTTTTAGCA	193044914- 193045246	NM_001042369.2
TROVE2	CCCTTAATTCCTGGTATTTCTGC	TCACCACATATGAACTAAAGAAAAACA	193045591- 193046321	NM_001042369.2
TROVE2	GCTATGCCAGATGAGCATTTT	TGACAAGCTGAAATGACAGAAA	193050331- 193050729	NM_001042369.2
TROVE2	TTGCTGAAAATTAAGTCCATTG	TTTGGGTGAGGAACCGTATT	193051284-193051872	NM_001042369.2
UBR4	GAAGATGGCGACGAGCGGC	TTCTCCTTCCACCAGAGTCTGTGT		NM_020765
UBR4	ACAGCAATGATGAAATCCGC	CAGTTTGATGGCATGGTTTG		NM_020765
UBR4	TGCTTGGTGCTTGTTAAACAG	AGAAAAAGGAGCCACTCCTAGC		NM_020765

UBR4	CCTCTTCCATGCTGAACTCTCG	TGTCAGTGCAGCATAAAGCTC		NM_020765
UBR4	GGGCAACCACTCCTCTCTATCA	TTGTTCCAGGACTCACACACAG		NM_020765
UBR4	TGACACCTATGCATCGTTCACC	CCCGAACAATGTATGTGGTCAG		NM_020765
UBR4	TTCTTCACCAAACCTCTTCCAGC	TCCATCACTGATGGTAACCTTG		NM_020765
UBR4	TCCTATGCCAAGTATGGATCCT	GCAGGAGAAAATAGAAGGTTGG		NM_020765
UBR4	TGGGCTAAAGGACTGTCATGTG	AAAGTCAATGGGGAAAGTCACC		NM_020765
UBR4	ATGGTTGCTATTAGGCACACGG	GCCCTCTTTGCTAGATGTGTTG		NM_020765
UBR4	TGGCCCAATCATCGAGAAGG	CTGCTGCCTTGTTGGTCCTG		NM_020765
UBR4	CCATGGAGATTTTGAGATGGTG	GTGCAGGCAGTAGTCCACAG		NM_020765
UBR4	ACCTGCTCTCCCAGCTTATTGC	GGCTGAGGAGGAAGAAGCACTG		NM_020765
UBR4	CTGAAAGCCTGTGCAGAGATTG	CTGGCTTGTTTTTCAACTCCAC		NM_020765
UBR4	TCCCTGCCTGGTGTGTAATAAC	AGGACGGATAAAGGCACGGTACT		NM_020765
UBR4	GTTACATCCTGCAGTTGGCTCA	AGTGAAAAGCACTTGTCGCAGC		NM_020765
UBR4	GAGAGACCCCAAGGCATCCTAT	GAGGGCCACTAAGTCACAGTCC		NM_020765
UBR4	CGGTGTTTCATCTTCGAGAGGCT	CATCACCCTGTGATCTTCATCAT		NM_020765
UBR4	ACAGGTGACAAGGATCAACTGG	AGCTGATTCAGGGACATGAGGT		NM_020765
UBR4	CCTGGGCATTTATACCTTCACG	TTAATGCACAAGGAGGGAGAAC		NM_020765
ZDHHC8	ACCCCCAGACTCCACTCTCT	CAGGAACCAAGCCTTCTGAG	20126677- 20127508	NM_001185024.1
ZDHHC8	AGGTTGGGAGGAGGTTTGTC	ACAAGCTACCTCAGGCAAGG	20127543-20127842	NM_001185024.1
ZDHHC8	TCCCGCAAGTATCAGCTTCT	CCCATCCACCTCTTCTAGG	20128032- 20128626	NM_001185024.1
ZDHHC8	GGGCCTAGAAGAGGTGGATG	GGCAGGCTAGGCCTCCTTAC	20128604-20129073	NM_001185024.1
ZDHHC8	GCCTTCTCCCTACAGGTTCC	GATGGTCCTGGACAGGTTGT	20130263- 20130797	NM_001185024.1
ZDHHC8	ACAACCTGTCCAGGACCATC	CGTCCCCAGAGAAAACTCA	20130778-20131401	NM_001185024.1

A2M, MLL, EIF4G1, TRIP12, UBR4, ZDHHC8 primers were designed on cDNA template due to the larger gene region