

**Table S1 Primer sequence and fragment length of genes for RT-PCR**

Genes	Primer sequence (5'- 3')	Fragment length (bp)
c24076	F: AACCCCTCGTTGCTGAGACTG R: AGCCATTCCCTTGTTGACTG	270
c31255	F: AAATGCGAATCAATGCACAG R: TCCACCTCCACTGCCTTTAC	304
c15787	F: ACCAATGCCAACGACAAAT R: ACAAGCCGAGTGGGTGTAAT	300
c22126	F: AATGCTTGTGGCTCTGTCGT R: GTGGCTGGGTGGAATGAAT	284
c23128	F: CATCCTGCTGCTCTTTCACA R: ACTGTTTTCTGGTCCCTCTCC	311
c29314	F: GATTGGGTGTGGATTGTTCC R: CGCATTGGTTCGTGTTCTTA	298
c30388	F: TACGACAATGCTGCCGATAA R: GCGACTGACGATGATAAAAAGG	323
c10499	F: TTCACCAGGCAACAACAGAC R: ACCAAAGACAAGCGGAAAAG	304
c11110	F: CTCCTCAAATCCCCTCCAG R: AGCCAGTTCCTCCAATGCT	297
c28873	F: ATCTCAGCGAAGCAACCATT R: TTCATACCATCCCCAAAGGA	328
c11649	F: TATTCACACCAACGGTCCAA R: TATCACCACCCATCCATTCA	257
c11748	F: GGGAACGGACAAGAATACCA R: CCCTCACGAACCAACAAAAT	336
c12361	F: AGCTGCGGAGATGGTTCA R: TTGGTTATTGACAGCGTGGA	246
c14093	F: CTGCGAAACGGTAATGAACC R: GGGTGGACAGGAACTCACTC	265
c15398	F: TTTGTATGGATGTGGTGACAGA R: GTCCCGAGCGATTCTTGA	227
c15420	F: TCCGCTTGTGATTGTTGAAG R: AGTCGCGCACGTAAAACATT	303
c15931	F: TGGAGCAAGCGTAAAACCTCA R: TGAACCGTCTAACCAAACCTCC	298
c16124	F: CCAGGCAACTTTATCGCAGT R: TGTCCAACAAGGTCATTTCG	290
c16652	F: AGGTGGACGAGGGTGTAGAG R: TTTGTTGGTGTGACTGTAGGC	299
c17315	F: GCATCATCTCGGACTGTGAA R: CGCATCTTGTGTTTCTGGTC	357

c18264	F: CGGTTTTCCGTCTATCTCTCC R: ATTATCTGTGAAGCAGCAATGG	333
c19009	F: CTATGATTGTGCCGATGGTG R: TGGAAGAAGCCAGCAGTTTAT	308
c19179	F: CGCTGGCTGTTGTTAGGAG R: CGCACTTGGAACGATACTG	296
c19361	F: TCCAGCCCTTCGTTACTACAA R: CCACCGAGCAATCTCTTAGC	285
c19381	F: TCTGGTGTCGTTACAAAGG R: ATGGCAGTCCAAGACGCTAC	296
c20839	F: ATGGAACACTGGGAAAATCG R: TCGGACATAGCAAAAGAATGC	316
c20905	F: ATGGTCAACGACACAGCACT R: GGAAAAATGGAACCGTCAAA	330
c21426	F: GGAAAATCCGTTGTGTTTCGT R: TAACTCCGTCAGCCCAAAT	287
c21548	F: CCAAGCGTATTCTCATCCACT R: GGGCACAGTTCAGTTTCTCTC	349
c22526	F: TGTCGGAAATAGATGATGTTTCG R: TCCCAGATTTCGTTTTGAAGC	292
c22953	F: ACTCAAACCGCACTTGGCTA R: ATTGCTTACCGTTCCATTCG	323
c24446	F: TGCGTTTCTGGTGTCTGATT R: TCATTCGTCTGCTTTCCTGA	308
c24628	F: GACTGGAAGCAATCCTCGTC R: TGTGCGATACTGAGCGTTTC	313
c24808	F: AGGACTGTATCCGCCGTAAT R: GAATGGTTGCCGCTTATTTT	318
c26169	F: CAGCCGATAAAAATCCCGTA R: ACAAGGGCAAGTCAATGTCC	305
c26376	F: TGGCGTTGATGCTAACTGAA R: AAAGCGGGTAGTGTGACTGG	283
c26581	F: CAGGAAACGAGACGGATTGT R: ATGCCCCGAGTAAGGCTATC	317
c27111	F: CGTCAGCATCACAAATCCAT R: GCAGTGGCAAAAGAGGAAAA	313
c27263	F: GATTTGATGTTCCGCCGTTG R: CATTTGGTGGTGTGGATTTC	295
c27821	F: ATACCAATGCGGAAGAGACG R: CCAGTCAACGGCAAAGAAAT	272
c30916	F: TTCAGCCACAGCGACTACAC R: TCTCCGACCACTCACAAACA	290
c31983	F: GACCAAATGTCTCCATCCGTA R: GGACCCTCAAGCAAACACA	267

c4936	F: GTCTTGTTGCGGGTCAATCT R: GTCACACCACACTTGGAACG	218
c8174	F: TTGTTCCGCACCTTCCAC R: GTTTTCAATGGGCTTCGGTA	305
c9832	F: TTCTCTGCTTTTCCCTCAGC R: AAGTGGACCGTTTCTGTGC	246

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