gi59958357–NM_001003938.2	5'	GGCGCCATGCTCAGCGCCCAGGAGCGCGCCCAAATCGCGCAGGTCTGGGACCTGATTGCGGGCCACGAGGCGCAA
gi59860310–AY698022.2	5'	GGCGCCATGCTCAGCGCCCAGGAGCGCGCCCAAATCGCGCAGGTCTGGGACCTGATTGCGGGCCACGAGGCGCAA
gi23242930–BC035682.1	5'	GGCGCCATGCTCAGCGCCCAGGAGCGCGCCCAAATCGCGCAGGTCTGGGACCTGATTGCGGGCCACGAGGCGCAA
gi61865489–XM_584763.1	5'	AGCGTCATGCTCAGCGCCCAAGAGCGCGCCCACATAACACAGGTCTGGGACCTGATAGCCGGACACGAGGCGCCC

gi59958357–NM_001003938.2	TTCGGGGCGGAGCTGCTGCTCAGGCTCTTCACGGTGTACCCCAGCACCAAGGTCTACTTCCCGCACCTGAGCGCC
gi59860310–AY698022.2	TTCGGGGCGGAGCTGCTGCTCAGGCTCTTCACGGTGTACCCCAGCACCAAGGTCTACTTCCCGCACCTGAGCGCC
gi23242930–BC035682.1	TTCGGGGCGGAGCTGCTGCTCAGGCTCTTCACGGTGTACCCCAGCACCAAGGTCTACTTCCCGCACCTGAGCGCC
gi61865489–XM_584763.1	TTCGGGGCGGAGCTGCTGCGCAGGCTCTTCACTGTGTACCCTAGCACCAAGGTCTACTTCAGACATCTGGGTGAC

gi59958357–NM_001003938.2	TGCCAGGACGCGACGCAGCTGCTGAGCCACGGGCAGCGCATGCTGGCGGCTGTGGGCGCGGCGGGTGCAGCACGTG
gi59860310–AY698022.2	TGCCAGGACGCGACGCAGCTGCTGAGCCACGGGCAGCGCATGCTGGCGGCTGTGGGCGCGGCGGGTGCAGCACGTG
gi23242930–BC035682.1	TGCCAGGACGCGACGCAGCTGCTGAGCCACGGGCAGCGCATGCTGGCGGCTGTGGGCGCGGCGGGTGCAGCACGTG
gi61865489–XM_584763.1	CACCCAGACGGAGGTGCAGCTGCTGAGCCACGGTCAACGCATGCTCCAGGCGGTGGGCGTGGCCGTGCAGTACATG

gi59958357–NM_001003938.2	GACAACCTGCGCGCCGCGCTGAGCCCGCTGGCGGACCTGCACGCGCTCGTGCTGCGCGTGGACCCAGCCAACTTT
gi59860310–AY698022.2	GACAACCTGCGCGCCGCGCTGAGCCCGCTGGCGGACCTGCACGCGCTCGTGCTGCGCGTGGACCCAGCCAACTTT
gi23242930–BC035682.1	GACAACCTGCGCGCCGCGCTGAGCCCGCTGGCGGACCTGCACGCGCTCGTGCTGCGCGTGGACCCAGCCAACTTT
gi61865489–XM_584763.1	GACAACCTGCGCGCAGTCCTGAGCCCGCTTGCCGACCTGCACGCACAAGTGCTGCGCGTGGACCCCACCAACTTC

gi59958357–NM_001003938.2	CCGCTGCTAATCCAGTGTGTTTCCACGTCGTGCTGGCCTCCCACCTGCAGGACGAGTTCACCGTGCAAATGCAAGCG
gi59860310–AY698022.2	CCGCTGCTAATCCAGTGTGTTTCCACGTCGTGCTGGCCTCCCACCTGCAGGACGAGTTCACCGTGCAAATGCAAGCG
gi23242930–BC035682.1	CCGCTGCTAATCCAGTGTGTTTCCACGTCGTGCTGGCCTCCCACCTGCAGGACGAGTTCACCGTGCAAATGCAAGCG
gi61865489–XM_584763.1	CCACTGGTGATCCAGTGTGTTTCCAGGTGGTGCTGGCCTCCCACCTGCAGGGCGAGTTCACGGTGGAGATGCAGGCG

gi59958357–NM_001003938.2	GCGTGGGACAAGTTCCTGACTGGTGTGTGGCCGTGGTGCTGACCGAAAAATACCGCTGAGGCCTGTGCTGCGCAGGC
gi59860310–AY698022.2	GCGTGGGACAAGTTCCTGACTGGTGTGTGGCCGTGGTGCTGACCGAAAAATACCGCTGAGGCCTGTGCTGCGCAGGC
gi23242930–BC035682.1	GCGTGGGACAAGTTCCTGACTGGTGTGTGGCCGTGGTGCTGACCGAAAAATACCGCTGAGCCCTGTGCTGCGCAGGC
gi61865489–XM_584763.1	GCGTGGGATAAGTTCCTGACGGGCGTGGCCGTGGTGCTGACGGAGAAGTACCGCTGAGTTCCGTGCCCCGCGGGT

gi59958357–NM_001003938.2	CTTGGTCTGTGCCTGTCAATAAACAGAGGCCCGAA	3'
gi59860310–AY698022.2	CTTGGTCTGTGCCTGTCAATAAACAGAGGCCCGAA	3'
gi23242930–BC035682.1	CTTGGTCTGTGCCTGTCAATAAACAGAGGCCCGAA	3'
gi61865489–XM_584763.1	CTAGGTCTGCGAAATTCAATAAACAGGCCTCAGTA	3'