

**Forward**

Primer Sequence	Position
CGCGCTCTGATCCGAGGAGA	1785-1805
CCCTGATCCTTCTGATGCAT	2287-2307
ACAGGAATTGGACAAAGCCAT	3237-3258
GCCTGAGATGTCTGAAGGAC	4188-4208
CTCACCATGGAGAATCATGA	4829-4849
AGGCACGTAGCACTGAACA	5309-5328
CACCTCTGCCTTCTCACGGT	6049-6069
CGGTCTTGTAAGGGTAACTG	6650-6670
GCACACTGTTTCTCATGATG	7132-7152
TG TTCAGCCGCAGAGACTTG	7730-7750
GTGGTCTGTCTAATGAAGTT	8274-8294
TGATGGTGATGGTGTCATCATA	8769-8791
GGATCTCATCCAAGAGTTAC	9513-9533
TGGACACTCCCAGATGTGCA	10034-10054
GTGAACTTTGTTGGAAACACATTG	10530-10554
TCTGCTGGTAAGGGCTGCCA	11179-11199
CCAAGGATGCTGTGTAGATAAG	11708-11730
CTGGTGAGTCGAATCACGGA	12251-12271
GATCCCAGTGCTGCTGAAACAC	12577-12599
AGGTTAAGAGCGTGTGAACCT	13079-13100
TGTTACTACTATCAACTGTC	13459-13479
ACTCACCAGGACGTGTCCTTCT	13944-13967

**Reverse**

Primer Sequence	Position
AGGGTTCTCAGTCCACAAGC	2001-2021
GCTTTCTAGAACAAGGCACGA	2943-2964

AGCAGAGACCTCACTCATAGCCA	3752-3775
GCCACTGAACGACCATCCTA	4530-4550
CTAATACACGAACTTCCTAG	5085-5105
TGTAATGCACTTGAATCATGCTG	5719-5742
AAACGTAGCAAGCACAGAGC	6328-6348
GAATTCACATTCCCAAGACA	6952-6972
AGAGGTGAAGCAAAGTGCAT	7397-7417
CGGTCCCTAAGTAATGACCT	8037-8057
GAATTGGTGAAGCATCTGCT	8492-8512
TGTCCTTGGTCAGCCTTGATGT	Not_Found
TACTAATAGCACAGTACCTG	9815-9835
ACCATGCTCAGTGCTAAGCA	10290-10310
CCTATACCTATATCAAGGCATG	10745-10767
CTCACTCAATGGTGAAGGCA	11407-11427
TCAGGAAAGCCAGCCCATGTC	12004-12025
AGCGGGTGCTCCACCGAGTA	12445-12465
ACGGCTCATTATAGACAAC TTC	12840-12862
GAATTCAAGCCCAGCGTCCAT	13266-13287
ACCTGTAAACATACAGCATGC	13730-13750
GAACGATCTCTGAACTCCACT	14433-14454