

AmpliconName	GenomicSequenceTemplate	LeftPrimer	RightPrimer	Direction	TargetSequence	TaregtLength	TargetCpG	CpGANalyzedInT
COL1A1__05	TTCTCTGTTTTGGAGAGGTCCTCAG CATGCCTCTTTATGCCCTCCCTTAG CTCTTGCCAGGATATCAGAGGGTGA CTGGGGCACAGCCAGGAGGACCCC CTCCCCAACACCCCCAACCTTCCAC CTTTGGAAGTCTCCCCACCCAGCTCC CCAGTTCGCCAGTCCACTTCTTCTA GATTGGAGGTCCAGGAAGAGAGC AGAGGGGCACCCCTACCCACTGGTT AGCCACGCCATTCTGAGGACCCAG CTGCACCCTACCACAGCACCTCTG	TTTTAAATTT TTGGGAGTGT AAGGA	AAACAATCTTT CCTTATAAATC ATCCC	F	TCCCAAACCTTTGGGAG TGCAAGGATACTCTATA TCGCGCCTTGCGCTTGG TCCCGGGGCGCGGCT TAAAACGAGACGTGGA TGATCCGGAGACTCGG GAATGGAAGGGAGATG ATGAGGGCTCTTCTCG GCGCCCTGAGACAGGA GGGAGCTCACCTGGG GCGAGTTGGGTTGA	392	30	23
CRIP1__07	TGCAGAGAGAGGGCTCCCCTGCTCA GTGACAGGAGAGGGGGCTGACAGT GACCTGGGCTCCCTTCTGAGGCTG GCCAGTCAGCTAGAGGGCTGACCCC AAAGCCCGAGGCCAGCGCAGCCCC CTTGCCCTCTGAATCTGGGGGGC GGGTGAGGCGGGACAGACTCCGCCT GGCACCGGACCATCTCCGCCTCA ACTTTGACAGCTACTTGACCGCTCT GGCCGCCCTGGGCGCTACCCGAGA GATAAGGGCCCTCCCTGCGCCCG	GGATTAGAT GATTTTTTT GGGTTT	CACCTCCTAT TACACTAAA ACACTT	F	GGACCAGATGATCTTTC TTGGCCCTGGGCCTAG ATTGAGGTCCCCAGGG TCCAAGTCTGGGTCA GAGGCGGGGCGCGAG GGGCGGGTCTCCAAG GGGCGGGTCCCGGG TCCCTGAAAGCGCGG ACCAGGCCGATCCAC CCAGTCTCGCCTGCA GCCCGTCCGCCCCAGC	246	19	17
CRIP2__30	AGAGTGGGGTGTGGGGTGCGGT GACTGGCATGACCCCTCAATCTCCC GCCTGACCCCTCAGGTCAGGCCCT GGGCCCCAGGCACGCAGCTGTGTC TGGGCGGTGCGGGAGAAGGACTG GAGTGTGACCCAGCCCGGGGAC AGAGGGCAGCCCACTCTCCCTC CCTTCCCTTCTAACTCTCACCGCT CCCCGCCGCCCTGGGTGGAAGT GCTTGGGGTGGACGCTTAAGCGCG GATCCCTCGGCCTGTGTCGCCCG	TTTGTTAGG GTTGTTTTGA TTTTG	AAACCTAAAC CCTTCTCTA AACC	R	CCTGTCCAGGCTGTTT TGACCTTGGAGGCA GGGATCCTGGACACCTG GGTGCTTGACACAA GGTCCCTCTCACGTTG CGGGAATCGCGTGTCA CACCCGCCCCACCCTA CCCCCGTGTGAAACTCC TGGGGAACTGGCGCC AAGGGAATGCGTCGGG ACAAGCAGGAGGCAGA	341	18	18
S100A4intron__01	ACTTCCAAGAATCTTTATTGAACTTG CTCAGCATCAAGCACGTGTCTGAAG GAGCCAGGGTGGAAAAAAAAAAGT GCCCACTGGCGACAGGGAGGGCCC CAGCTGGCAGACCCCAACCACAT CAGAGGAGTTTTTCATTTCTCTGGG CTGCTTATCTGGGAAGCCTTCAAAG AATTCGTTACACATCATGGCGATGC AGGACAGGAAGACACAGTACTCTTG GAAGTCCACCTCGTTGTCCTGTGTC TGTCCAAGTTGCTCATCAGCTTCTGG	TTTTAAGGTT AAGTTAGGG TGAGAA	TTCCAAAATA ATCAATATAC ACAA	F	CCTCAAGGCTAAGCTAG GGTGGAGAAGGTGCTC CTTGATAAGGAAGTCT GAGTACTGGTGAATG GAAAAATGACGGGACC ACTACATTTTACCCAA GGTTGTTCTAATAATCC CATGAGGTAGTAATAGT CATGAAAACAATATAT AAACTGTGTTATGTTG ATACAAATATACATTGT	348	4	4
S100A4intron__05	ACTTCCAAGAATCTTTATTGAACTTG CTCAGCATCAAGCACGTGTCTGAAG GAGCCAGGGTGGAAAAAAAAAAGT GCCCACTGGCGACAGGGAGGGCCC CAGCTGGCAGACCCCAACCACAT CAGAGGAGTTTTTCATTTCTCTGGG CTGCTTATCTGGGAAGCCTTCAAAG AATTCGTTACACATCATGGCGATGC AGGACAGGAAGACACAGTACTCTTG GAAGTCCACCTCGTTGTCCTGTGTC TGTCCAAGTTGCTCATCAGCTTCTGG	GTATGGGGTT AGGTAGTGA GTGGT	CCTACTCCAA ATCCTAACTAC TATCAT	F	GCATGGGGCCAGGCAG TGAGTGGTGGTGTCAA TGTGTTCCACCCAGG CAGCCACCCCACTGATA GATGCCCTCTGTAGCTA ATGCTCTAGAGCAAGA CTGCTGCCCTCTCTGTG GGAAATGCCCCACGTG GGGACTCACTCAGGCA CTACCCACTACCCCA AGAAGCTGGGAGCTC	329	4	4