

(13) chr1:10818517-10818704 (NCBI36/hg18)
Target13
TTTCCCTTGGGGAGAAGCAGGAGTCCGGACCCCCAGCCCCACTCGCAGGAGGCAGTGGGCGGCTCCTCTCAGCCAGGCGGGTGAGGGTCTGTGCCGGCGGGGCATGCCACCAGCCAGGCAGGTGTGGAGCCCTCACAATGGTGCACCTGGCGTGGGCGTCAGGCCCTGCCCATTCAGCCCGGAACAATCACTGCTCTGCAGCCGCGCGCCACGCGGCTCCAGGGGCGGGAGGACCGCGGGCGGCAGAGCGGCAGATGGGCCTCGGGTGTCAAGTTTCCAGCTGGA
GGAGGGG

(14) chr1:1385949-1386143 (NCBI36/hg18)
Target14
CCTGAGGGGGCTGAGGAGCACCTGTTCCCTGGGGACAGCTCGGC CGGCAGCCCCAGCGTTTCCCTCCCATCCCGCCC CGCAGATTATGCTGATCCTGGCCAGCTGCCACCCCGAGCAGTTCGACTGGGCCATCAATGCC
TGCATCGACCTGATGGTCCACTTCGACCTGCCAGGGCAGGAGGAGCGGGCGCGCCTGGTGAAGTGTATCTTAAAGAGTATGTTCTTAAGCGGCCACAGAAGGAAAGCGTAAGTGTCCCGCCCCACCAGCCCCGCTCCAGG
GGCCCTCGCTCAGGGTCCACCCCTGCTCCTGTTCTCCGGACACACCAGCAGGCCTGTCTCCAGGATGGG

(15) chr10:53743705-53744974 (NCBI36/hg18)
Target15
GAGGGCAAAAAGTGTCTTTGTCAGAGCCTATCACCCCTCGGCTCTGTAAAGTATTTAGATCGGATAATTAACCCCTTACTGCCAGGCAAGGGCACCCAAAGTCCAGAGTTCCTGCTGCCCGCTGCATTTATTAAGT
CTGCTATAAAGCTCGCTGGTAGCCTTACCCTCGAAGGTGAGCCGGCCAGCCGAGCGACTAAGCAAGGGAGGGGCGGGGTGAAGAGTGTCAAAGGCCCCCTTTCATGTACACAAACACACCCCTCCAGCCCTCCAGCGC
TTTGAATCCCATCCCGGCTTTGTTGTCTCCCTCCCAAGGGGCGGAATGCTCGGGCCCGCGGTATAAAGGCAGCCGCGGTGGCGGTGGCGGCAGAGCTCTGTGCTCCCTGCAGTCAGGACTCTGGGACCGCAGGGGGCT
CCCGACCTGACTTGCAGCCGAACCGGCACGGTTTCTGGGGACCCAGGCTTGCAAGTGAAGGTCATTTCTCTTTCTTCTCCCTCTTGTAGTCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACC
GGGTCTTGTGGATGGTAGCGCGGCTCTCGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTCAATTCCAAAGCTATCAAGAACCTGCCCCACCGCTGGGCGCGCTGCGGGGCACCCAGGCTCTGCAGTCA
GCGCCGCGCCGGAATCCTGTACC CGGGCGGGAATAAGTACCAGCCAT TGACAACCTACCAGGTGAGAGGGGTCGGGCACCTCAGAGGATGCTCTGACCTTGAAGGGTCCCTATCTGGAGA CGAGGAGTAGAACCGTGCTGAAT
GTGTGCGGTTCAAGGAGCATTTGGTAACCTGCATTTGGGAGCAGTGGGCAGTAACAGGTTTGGAGAGGTGGACAGATAAGGACTGTGATCAGCGCCCGGGTCCAAGAGGGCGGGTACCTGGAAGCTCTGGGTGCCTCACCCCT
CTCCCGAACCTTCCACAGCCGTACC CGTGCGCAGAGGACGAGGAGTGGGCCTGATGAGTACTGCGCTAGTCCCACC CGCGGAGGGGACCGCAGGCGTGCAATCTGTCTCGCTGCAGGAAGCGCCGAAAAAGCTGCAT
GCGTCAAGCTATGTGCTGCCCGGGAAATTAAGTGAATAAAGTGGTGAAGTCTCTG

(16) chr11:20588323-20588561 (NCBI36/hg18)
Target16
GGAGAATGACTAGTCTGTGCCCTGTCAAGTGAGACCAGCGGCTTTAAGTGAATAAAGTGGAGCTAGCTGGGTCAAGTAAATAGGAACAACATAAATATCATTTCTATTTCCGGAATGGCTTCATTTTCACTTATAACTTTTAAAT
AAATGATTCCTTTTCTCCCTGGTCTTTTCATGTGCTTTTCATTTAATAAATGCCCCAAGTAAAGAGAATCCATTCACAGCTTCCAATTTAGCAAGATCATTATCGCTGTTCTTTGTTGGGGTTGCTGGGCGCAGAGCTC
TCTGATGAGATGGCCATCATTTCCCTCGCGGGTGGACC CGAAGGCTCGGGCGCTGGGAAGCATGCTCCTGCGCCCGTGGTGGGAGGGATATTCAGGAGGCTTGGGGCTGCGGAGCGAGCGAGCGGGGAGCCTGGGAAC
CCTGCTGCATGCTGCAGGAACGGTGACCTTGTGCTGCTCGGCGGCAGTGCATACAGACATCCAGAGAAGCTCTCTAGTGAGGCTGCCTGCGTGCTTACAATGCAACTTGGGAATCGAGAGATTTGGTGTTCCTCCCTG
TGTTAGTGATCTCTCCGCTCTTGGGTGGAAGTAATGTTTGGCAGGAGGGCTAGAAATAACTTATGTG

(17) chr10:134210902-134211265 (NCBI36/hg18)
Target17
TCCCACCTTGCATGGTGGCTCAGGGTGGTCAAGGAGGGCGTGGCTGTACATGGTTTCTGGACTGTAGCCCTTTGGGCTGAGTGAGGCGTACTGCCATCAGGGGTCCCTGGAGGGGCTCTCTCCATCCTCTTCTGGCGTCA
GGTGTCTCGCGGCCTCTCGGTAAACAGCTGGCCTTTGCTTCTGTGCGGGCGCGTGGCCAGGCTGAGCAGTGCCTCGGCTGCCTAGGTGGTGTGAGGTTCTGTGAGCCCGGGCCAGCTGCCGCTGGTGAATATAACCGG
GAGGGATGCCCGCCTCTGCCACCTGCTGGCATCTGGGGTTCCCGGGAGGCGGGCACCTGCACCTCGCGCTCGCCCTGGGCTGACCTCCATCTCCTCTCTTCTTACCCTAAGCGCCGTGGCTGAACAGGACTTGGTT
TTTACGGCCTTCATGCCCTCAGCTTGGGGCTCTTTTTCAAAGGGTTCTCCGCGGACCGCTCGCCTAGGCAAGCAGGGTTTCTCCTTCAAGGACAGCCCGCGTGCCCCAGCCCTGTGACCGCGCTCTTGGTACTCACC
AAGTGAAGTCCCA

(18) chr5:10702368-10703458 (NCBI36/hg18)
Target18
GCAGTCTGTTAGGAGCTTGGGGCCAGGGGTGGGGGTGGGGGCAGTTTTGCCTTTGCCAGGCTCTGCTGGGAGGGAAGAGTCTTGTGTGCCCGCCACCCTTCTGTTTGTGTTTTGCGTTTTGCAGGGGCGGATGTCCA
CGCGAGGACCCCGCGTGGGATGTCCCGCAGGAGTGGCCACTTACACGGGCGCGTGGATGCCGCTCGTCTCATGCAGAGGCTGCTGGAGCGCCCTGCCCGAGCAGTTCTGGGAGAAGTACCGGCCCGAGCTGCCGCG
CGCCCTGAAGCGCGCGGAAGCCCGCGGGCTCCAAGAAGTGCCTGCAGAGGCTCAGACTGCGTGTGCTCGTGTGCTGACCGCGCGCTCGTGTGGGGCCCGGAGGAAGGGGCGTCTGGACCACATGGTCCGGATGACC
ACGACCTTACAGCCCGCGTGGCCATCGTGTGCCAGACCGTGTGCCCTGAGAGCCCTCCGAGCGTGGGGAAGAGGCGGCTGGCGGTGCAGGAGATCCTGGCGCGCGGGCTGCAGGGGCCCCAGGCGCAGGAGGAGGA
TGAGGTGGGGGCGCGGGCAGCGCGGCGGACCGGACAGGAGGAAGCGGACTCCCGGGAGGGCTCCCGAGAGCCCGCCCTCCCTCCCGCCCTGGGGTCCCGGGGCCCGCAGCGCCCGCCCGCGGAAGGCCAGCCTCTGTC
CCCTGCAGCCCGTGGGAGGAGCGGTCGCGCCCGGTGTGGTGGTGGCCCGGGTCCGAGTCAAGCAAGGCGCCCGCCACCTTCCAGCCCGAGCGCGCGGGAAGGGCAGCACCAGGACAGCGGCCACCTGCAGATC
CCCAAGTGGCGGTACAAGGAGGCCAAGGAGGAGAAGGGAAGGCAGAGGAGGCGAAAAGAGCGCCAGGCGAGGCGCAGAAGGAGAGGCGCACTGCGCCCTGGAAGAAGAGGAGCTGAGGGCCCGTGTGCTGGCGTGGG
GCGGGGCTGGGGCGGGGCGGGGCGCAGGGCTGGGCGCGGAGAAGGAGGCGGCCCGTTGCGCATCGCACCACTTCCGCTCCATGGACCAGGGGCTGCGCGCATTTCCAGGCTGTTGTCCAGGCTGCTTCCAAGAGAGG
GCTGAGGGAGCCACATGGATTGCGTGTGCGCCAGCCCTCTAGCAATCAGTACACCTAGCGGGCACGTTGCTAAAGGCTCCCTTTAGAGAACCT

(19) chr16:85994896-85999172 (NCBI36/hg18)

Target19

ACTTTCAGGAAAATGACTAAGTACTTGAAAGGGTCAGTATGTTCTGTGTTTTTCAGATGAGGAAGTCTGATGACCGCAAAAAGCTCTTCAGACGCGCCGACCTTGGTGGCTTTTGGAGAGATGCATCCGAGCTCGCTGCTGGCA
AACTCTCAAGTCCAAGTGTGCGGCTCCCTCCGGAAAGAGGCTCAAGGATGGGTGGTTCATTTTCTCTCGCTGTGTAGCTCCTACTTACAGCTGACGATTCTCGACTTCGGACGGCCTCCCTGGAGATGTACACGCGCC
CATGCACGTTCAAGAAGACTGGCAGCTCCGAGAGGCCTTCGCTGCTGGGAACACAGCCGTGACAGTGTGGAACTCATCTACCTCAACGCTGAATGGCAGGCTCCAAGTTGAAA

(21) chr5:1010475-1010610 (NCBI36/hg18)

Target21

GGGGCCAAGAGAACCCTCAAAGGCTGAGGTCACCCCGCCAGGGTTCGGTTTAGGTGTGGCGCCTCCTCTGGAAGCCCTGGGATTGCCTGCGCGCCCGGCCCGGAGCTCCTGTTCCAAGCAGGGAGCATCCCTGGACCGTGCCC
TCGTTCCCTTTGAGGTTTTCTGTGGCAGCACCACAGTTTAAATCGACTCACCCAGCCATGCTGGGGCTGGTTTTCTGTTAC

(22) chr2:216945117-216945376 (NCBI36/hg18)

Target22

GGCACTTGGCTCCAGCTTGGTCCTCGCGACTCCCCAAAACCGTATATAAATATATCTCTATAAAAAGCCGAGAGGAAGCAAATCAGATTCCAGGCTGCTGCCAGGTGTTGTCTCGTCTTCCGCGTTGCTCAGCACCCGCGGC
TGCCCCACTGGCTCGATTCCCAAAGGGGTGGTGTGGAAGGGAGGTGGCGGGGCGGCGAGCTGACCGTCCGAGAACTGGAAACAAGGTTCTTGAGCGAGGGAGGCTCTCGGCTATCTCCGCCGCGCGCGCGCGCGCGCG
CTGCTGCATTCAGCACCCCGGGGAGTGGACAGTCCCACCCAGACCCCGCGCGTCAAGCTCGTGGGGGCTGACGCAGACGCGCGGAGGGATGGAGGAGGAAAGGGGATGAGAGGAAAAGAAGCTGGAGGGAGAGGGAGC
AAGAGGAGGAGAGAACTGTGCGAGGGAAGGGGATGGGGAGGGACCAAGGAAAGGGAGGTAACCA