Primer design report for chr: 1 position: 55039774

ID	%GC	TM	Primer sequence	Best primer	Mapping(s)
LEFT_0	55.00	60.04	ATCTGACGCTGTTTGGGGAG		unique mapping
LEFT_1	55.00	60.11	CTAGAAGGTTTCCGCAGCGA		unique mapping
LEFT_2	60.00	60.32	GTCAAGCACCCACACCCTAG		unique mapping
LEFT_3	55.00	59.90	TCTTCCCTCTGCGCGTAATC		unique mapping
LEFT_4	60.00	60.46	GCCGAAACCTGATCCTCCAG		unique mapping
RIGHT_0	60.00	60.04	GACCTGCACTCCACTTCCTC		unique mapping
RIGHT_1	50.00	60.04	AAGATCGTGCCAAGCGAAGA		unique mapping
RIGHT_2	60.00	60.74	CTGCAGTCCCCAAGATCGTG		unique mapping
RIGHT_3	57.90	59.85	TGGAAGGTGGCTGTGGTTC		unique mapping
RIGHT_4	57.90	60.00	GTCCCCAAGATCGTGCCAA		unique mapping

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55039274   CAGAACTTGGAGTCTGGCATCCCACGCAGGGTGAGAGGCGGGAGAGGAGGAGCCCCTAGGGCGCCGGCCTGCCTTCCAGC

55039354   CCAGTTAGGATTTGGGAGTTTTTTCTTCCCTCTGCGCGTAATCTGACGCTGTTTGGGGAGGGCGAGGCCGAAACCTGATC
                              >>>>>> LEFT_3 >>>>>>                        >>>>>> LEFT_4
                                                  >>>>>> LEFT_0 >>>>>>

55039434   CTCCAGTCCGGGGGTTCCGTTAATGTTTAATCAGATAGGATCGTCCGATGGGGCTCTGGTGGCGTGATCTGCGCGCCCCA
           >>>>>>

55039514   GGCGTCAAGCACCCACACCCTAGAAGGTTTCCGCAGCGACGTCGAGGCGCTCATGGTTGCAGGCGGGCGCCGCCGTTCAG
              >>>>>> LEFT_2 >>>>>>
                              >>>>>> LEFT_1 >>>>>>

55039594   TTCAGGGTCTGAGCCTGGAGGAGTGAGCCAGGCAGTGAGACTGGCTCGGGCGGGCCGGGACGCGTCGTTGCAGCAGCGGC

55039674   TCCCAGCTCCCAGCCAGGATTCCGCGCGCCCCTTCACGCGCCCTGCTCCTGAACTTCAGCTCCTGCACAGTCCTCCCCAC
                                                                  ------------------------------

55039754   CGCAAGGCTCAAGGCGCCGCCGGCGTGGACCGCGCACGGCCTCTAGGTCTCCTCGCCAGGACAGCAACCTCTCCCCTGGC
           ---------------------*------------------------------------------------------------

55039834   CCTCATGGGCACCGTCAGCTCCAGGCGGTCCTGGTGGCCGCTGCCACTGCTGCTGCTGCTGCTGCTGCTCCTGGGTCCCG

55039914   CGGGCGCCCGTGCGCAGGAGGACGAGGACGGCGACTACGAGGAGCTGGTGCTAGCCTTGCGTTCCGAGGAGGACGGCCTG

55039994   GCCGAAGCACCCGAGCACGGAACCACAGCCACCTTCCACCGCTGCGCCAAGGTGCGGGTGTAGGGATGGGAGGCCGGGGC
                              <<<<< RIGHT_3 <<<<<

55040074   GAACCCGCAGCCGGGACGGTGCGGTGCTGTTTCCTCTCGGGCCTCAGTTTCCCCCCATGTAAGAGAGGAAGTGGAGTGCA
                                                                              <<<<< RIGHT_0 <<

55040154   GGTCGCCGAGGGCTCTTCGCTTGGCACGATCTTGGGGACTGCAGGCAAGGCGGCGGGGGAGGACGGGTAGTGGGGAGCAC
           <<<<          <<<<< RIGHT_1 <<<<<<
                               <<<<< RIGHT_4 <<<<<
                                   <<<<< RIGHT_2 <<<<<<

55040234   GGTGGAGAGCGGGGACGGCCGGCTCTTTGGGGACTTGCTGG
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primer-designer version: 1.0-rc2 using dbSNP 150 for SNP checking, and human reference GRCh38.
Common SNP annotation: A common SNP is one that has at least one 1000Genomes population with a minor allele of frequency >= 1% and for which 2 or more founders contribute to that minor allele frequency.