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5'          11          21          31          41          51          61          71          81          91
+1 M H E R E R H R I I L S A V Q E K S V V T I Q D I F E L T E A S E
1 ATGCACGAAC GCGAACGCCA TCGCATCATT TTAAGCGCCG TCCAGGAAAA GTCCGTCGTT ACGATCCAGG ACATTTTCGA GCTGACGGAA GCTTCCGAAG
TACGTGCTTG CGCTTGCGGT AGCGTAGTAA AATTCGCGGC AGGTCCTTTT CAGGCAGCAA TGCTAGGTCC TGTA AAAAGCT CGACTGCCTT CGAAGGCTTC
                    ← 5' primer to mutate

5'          11          21          31          41          51          61          71          81          91
+1 A T I R R D I A A L H V Q G K I R R V R G G A E A V H P P Q L G N L
101 CGACAATTCG GCGCGACATT GCGGCTCTGC ACGTGCAGGG AAAAATCCGC CGTGTGCGCG GCGGCGCGGA GCGGTGTCAT CCGCCGAGC TCGGCAATCT
GCTGTAAAGC CGCGCTGTAA CGCCGAGACG TGCACGTCCC TTTT TAGGCG GCACACGCGC CGCCGCGCCT CCGCCACGTA GCGGCGTTCG AGCCGTTAGA

5'          11          21          31          41          51          61          71          81          91
+1 A G R P F R V S E S V N I D K K R A I A R A A V D L C E A G D A I
201 CGCCGCGCCG CCCTTTCGAG TTT CAGAATC GGTC AACATC GATAAGAAAC GCGCAATTGC ACGCGCCGCG GTCGATCTCT GCGAAGCGGG CGACGCCATC
GCGGCGCGCG GGGAAAGCTC AAAGTCTTAG CCAGTTGTAG CTATTCTTTG CCGCTTAAACG TGCGCGCGCG CAGCTAGAGA CGCTTCGCC GCTCGGTTAG

5'          11          21          31          41          51          61          71          81          91
+1 I I N G G T T T F Q M V H Y M A G H R M Q V M T N S F A I A E H L
301 ATCATCAATG GCGGCACGAC CACCTTCCAG ATGGTGCATT ACATGGCCGG CCATCGCATG CAGGTCATGA CCAATCTTTT TGCCATTGCC GAACATCTGG
TAGTAGTTAC CGCCGTGCTG GTGGAAGGTC TACCACGTAA TGTACCGGCC GGTAGCGTAC GTCCAGTACT GGTTAAGAAA ACGGTAACGG CTTGTAGACC

5'          11          21          31          41          51          61          71          81          91
+1 V K H S K N T V T V P G G A I Y R E Q S L I L S P F D N D A I R N F
401 TGAAGCATTC CAAGAACACG GTGACGGTTC CGGGCGGCGC GATCTATCGC GAGCAGAGCC TGATCCTGTC GCCTTTCGAC AATGACGCGA TCCGCAATTT
ACTTCGTAAG GTTCTTGTGC CACTGCCAAG GCCCGCCGCG CTAGATAGCG CTCGTCTCGG ACTAGGACAG CGGAAAGCTG TTACTGCGCT AGGCGTTAAA

5'          11          21          31          41          51          61          71          81          91
+1 Y A R R M F I G A Q G V G P L G I M E A D A L I I Q S E Q K L M H
501 CTATGCGCGG CGCATGTTCA TCGGCGCGCA GGGTGTGCGG CCGCTCGGCA TCATGGAGGC GGATGCTCTC ATCATCCAGA GCGAGCAGAA GCTGATGCAC
GATACGCGCC GCGTACAAGT AGCCGCGCGT CCCACAGCCG GCGGAGCCGT AGTACCTCCG CCTACGAGAG TAGTAGGTCT CGCTCGTCTT CACTACGTT

5'          11          21          31          41          51          61          71          81          91
+1 Q A D E L V V M V D S S K F N R R S S L I L C A L D R V S V V I T
601 CAGGCCGACG AACTCGTCTG CATGGTTCGAT TCAAGCAAAT TCAATCGCCG GTCGAGCCTC ATTCTTTGCG CGCTCGACCG CGTCTCTGTG GTCATCACCG
GTCCGGCTGC TTGAGCAGCA GTACCAGCTA AGTTTCGTTTA AGTTAGCGGC CAGCTCGGAG TAAGAAACGC GCGAGCTGGC GCAGAGACAC CAGTAGTGGC

5'          11          21          31          41          51          61          71          81          91
+1 D D A I S E E A A R M V E N A G I R L V V A S P V T Q A V R E D S S
701 ATGACGCGAT TTCGGAAGAG GCAGCTCGCA TGTCGAGAA TGCCGCGATC CGGCTCGTTG TCGCAAGTCC GGTGACCCAG GCTGTGAGGG AGGATTCCTC
TACTGCGCTA AAGCTTCTC CGTCGAGCGT ACCAGCTCTT ACGGCCGTAG GCCGAGCAAC AGCGTTCAGG CCACTGGGTC CGACTCTCC TCCTAAGGAG

5'          11          21          31          41          51          61          71          81          91
+1 S V A &
801 GTCGGTCGCA TGA
CAGCCAGCGT ACT

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