10 20 30 40 50 60 70 80 90 100 110 120 130
TT GGACTTCGTTTTGTCTGTATCACGTAAAGTACAGCTTTCGAGTCAGGTAAGCCGCAACTTCTTACCCATTTAAA GTTT GAGAATAGGTT GAGAGACATTTC GTCCCCAAGGCCTCTAATCATT GTCTTTACC GGAT
140 150 160 170 180 190 200 210 220 230 240 250 260
AAGACT GCAT GTAC GAGCACCAGCTATCCTGGGGGGAAACTTCGGAGGGAACCAGC TACTAG AT GGTTCGATTAGTCTTTCGCCCCTAT ACCCAAGTCTGACGATCGATTTGCACGTCAGAATCGCT
270 280 290 300 310 320 330 340 350 360 370 380
TCGGACCTCCACCAGAGTTTCCTCTGGCTTCGTCCTGCTCAGGCATAGTTCACCAT CTTTCGGGTCCCAACAT GTAAGCTCTGTCTCCACTCCATTGCAAGCAATCGGAAT GGGACTACACTGCGC
390 400 410 420 430 440 450 460 470 480 490 500 510
CGCTCGCCGAAGCTCACGGATCGT GTATCAACAGGCAAGCCTGCTTTACTTTCATTGC GCCCTTAGGTTTTAACACCCAGTGACTCGCTTACAT GTTAGACTCCTTGGTCCGTGTTTCAAG ACGGG
520
TCAAG