

## S1 Fig:

### A

CACAACTTATCATTTCACACTCACCTAGATCTATGGAGACGTGCTCCTGTGGAAGGGAGT -587  
AGTTGTGATCATGGAGAATGGAAGAGCTGGAAGAGCCGAGAACATCCCGCGATACTGAGG -527  
GACTGAGCAGAGAGCTCAGTAAATCCTCTACCTCCCAGTCGCTCAGTTCTTGCACGGAGT -467  
TCTATCAAATTCAAAGGCCTTGATTTATTTCCGTACCTTGGGTCTCGCGGACATCCCTAG -407  
CTTCCCCACTGGGAACACCCACCCACCCACCTCGGAAGGTGACAGCTCTAAGTCCAGCG -347  
GAGCCTTCACGTCCGGCTCAGTCGCAGCCCACAAATCTCCGCTTTCCTCTAGCAGGAAGC -287  
CCAGCAGGTCTGATCACCGGATCCAAAGCTAGCAGATCCTGACCACCAGGATCCATTT -227  
GGGATATCTATGGATAGAAATCCCTCCGCGCAGATCCAACCTCCGAACCTCAGGCACGAC -167  
CCCTCAGTCTGTCCAGTCGGCTCGACTTAACCTCCGTCACTCCGGGACAAGGGCCTAGCT -107  
GTCACTCTAAACCGCACCCGTCTCTCAGCTTCTGTATTCTCAGCTTCCAACACAACGGA -47  
AGTGGTGCACATAGCCCCGTGGAATCCTGGGACTTGGAGTTCTCTCCAACTCGGAAGTGG +13  
**CTCTGGGCTGCGCCACGTCCCGGGGGCTATGCAAATTATGGGGACGTCCTTTCAAGCTT** +73  
**CCCACGCCCCAGGGCGGGGATTCTGAGGATCCTTGTCCGCCTTCGCCTCGAGCTATTAAA** +133  
**AAAAAAAAACTTAAGCGTTTTAAAAGGGAAC**TCCAGCTTAGTTTCGGGCGTTCTCTCCAGAGC +193  
TCTGCACGCTCGCTTCTGCTGGGGAGGGGCGGCCAGGCTTCGCGGGCGCCCGAGCATCG +253  
AGAACTACGGCCAGAGCAGCTTCTGAGTCTCCGCTACCATAGAGCGCGGGCCAGGGC +313  
GCCGCCGGCGGGTGGGGACGTTTCCAGGACGGAAGTGCCGAGAGTGTGTCTGAAGGGAG +373  
GGCGAGGCCGGAGCCCCAAAAGCGACCCGGGAGAAGGAGCGGGTAGCGGGCCAGGGCGGG +433  
CGCAGAGCCGGGCAGCGCAGGTAGGCCGGACGGGCTGGGCGGAGCTTCTAGGTGGGGCT +493

### B

CCGAGCCATGGCGGGTATGAAGACAGCCTCCGGGGACTATATCGACTCTTCCTGGGAGC +572  
TGAGGGTGTTTGTGGGCGAGGAGGACCCTGAGGCCAGTCTGTACACTCCGAGTCACGG +632  
GGGAGTCGCACATTGGTGGGTACTTCTGAAGATCGTGGAGGAAATCAGTGAGTCCCCGT +692  
GACCCTATGTATCCAGTCATGACAGCTCTCCCTGGCTTTTCTAGGCCATTCTCGCCTCTA +752  
CTCATAACCTTGTACAGTGACTCAGGCAACAGTCTTTAATTATTTGGTTCCAAAGAAGG +812  
TATTTCTTCAACTTCCCCTCTCCATACTTCTCCAGCTCCTACTGGTTCTGTCTAGTCTC +872  
CAAGAGACAGACAACATGGTCCCCTGTGTGCTTGCCTGTGCCGAGGCTTATTATGTTCC +932  
TGAGGGATGGCTAGGAGGTTCTTGGGGACCTGGCACCTACTCTCCTAAATTTCTCCCCA +992  
GCAAACCACTTGGCAGGCTGCTGACAGTGGGTGAGAGGCCCTGCCCCACAGGAAGTTAC +1052  
GGCAGAGTAGGCTAGGGCGATATCAGTCACCCAGAAGGCCCATGAGGCTTCTCATCAAC +1112  
TTTACCAGCAGAGAATGAGAGTTATCACTTCTTGGGAGGATGGCAGGAAAGCCCCGATAG +1172  
TCAGAGCCGGAAGACATCCCACCATGAGCTCCCGATAGTCAGAGCCGGAAGACATCCCAC +1232  
CATGAGCTCCCATAGCCAGAGACAGAAGGCATCTCACCATGAGTGTGGGTCTTAGGCCT +1292  
CTGGAATTGGGACAGGGATAGAAGGCAGGTTTTCTAGACCCACCCAACCCTCTATGTGTA +1352  
TGCAGTCCAAGACGGACCAGAGTGACTGAGCAGGACAAGCCCCAACACAGCCAAATAACA +1412  
GGGTGAGACAGAAGGGAAGTCCCGGAAGCAGGGCCAAAGAGGCTGTGAAAGCAGAAGT +1462  
GGGAAGAGGGTTAGTCCCTCAGAAACTGGA +1492