10   20   30   40   50   60   70   80   90   100   110   120

CA T G TC TATT AT T TG C G GAAC CTAGA GG C C C TT T TTT ATTTT AAA A T TTTT T ACAAAA CGGT TT ACAA GC AT AAAAT CT CT GAT A GAC C GGGG A TTAT CA T CAA CC AGTT ACTC GGGGAGC

130   140   150   160   170   180   190   200   210   220   230   240

AT C C TCAAG GC GAT C GGC CATTC CGA CCAGCAT GTT CACC GT GAT CTT C GC CCT GGCACG TAC C GTGGGCTGGA TCT CGC ACT GG AAAG AAAT GC T CT CCAGC CCGTACAAGAT C GGCC GTCCGC GC

250   260   270   280   290   300   310   320   330   340   350   360

CAGC TGTACACCG GCG AGCAGAAGC GCG A CATC GTTGC CCTG AAAG ACC GCAAGT AAGCT GCAGTAGCCGAAC G CAA G AAGGC T GCCC TCGGG CAGC CTT TTTTTAT TT GTT CCT GT GC CGGC

370   380   390   400   410   420   430   440   450   460   470   480   490   500

T CT TTCGCGGGCCC TT GCC C G CG AAAAA G GCCCGGC ACA G ACC C CA CAAAAAACCT CAA TTTTTTTTTCCC CCCC GCTT C CC GC A CCCCTTTTC A GGGTA TTGGA ACGGGCG C AAC C C C C CACAGAA ATTT

510   520   530   540   550   560   570   580   590   600   610   620

TGTTTGGC CACC A T C G CC CGGAACGGCTT ACCC A CC TG G C TC GGGTGTTGC ACA CTGGGT AG GGTCA CTTTC G GT GCCT GTT C ACCCCTTTGGGGC ACCCAA CT TTCC GAG AAA GTC GT C G ACTTTTT

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  630        640        650        660        670        680        690        700        710        720        730        740        750
TGGCC ACACCGAAAAT AAAAAACC C TT CTTC T T CC  GAGC A GATT A A TTC GGGCTACTCTC T TT T CA GGA T AAC C G ACTC  A A GG CAT GC ACCAT C CGGCGCT CACA CT GA AT GGGTG G GAAAA T G
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       760        770        780        790        800        810        820        830        840        850        860
T G CA A GC A ACGGCGAAAT C T C GGC G G G C G  T C G CGCGCGCCC G TCGTT  A C TAA G  T  CGCCCTCG CG  CT GTTCCA CGT TATT C  AA T TC TTT  T  T CC  GG AT T TG ATG  GA A ATTG CCC  AT  A T
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  870        880        890        900
T T T CT GAAGC GGA  AAT G  A  CCGGGCGGGGT G CG  GA  G   T  T
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