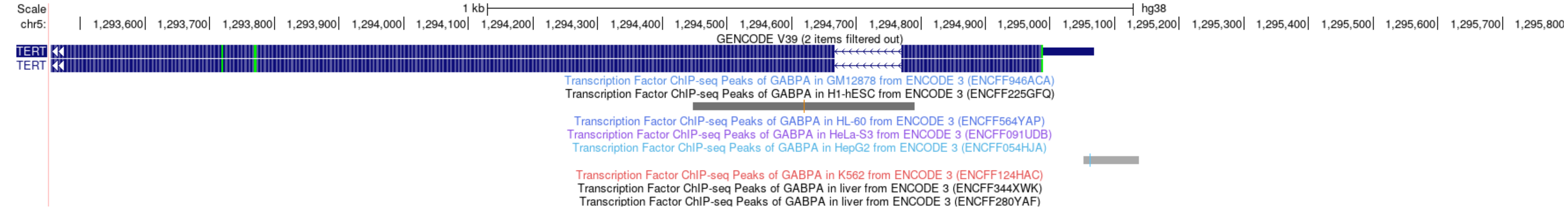
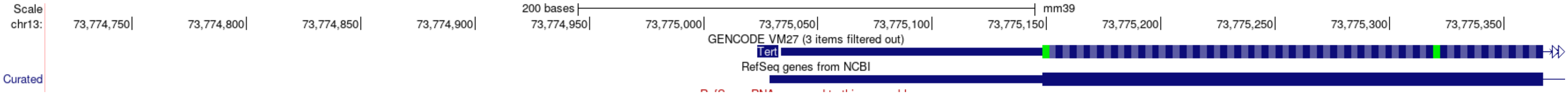
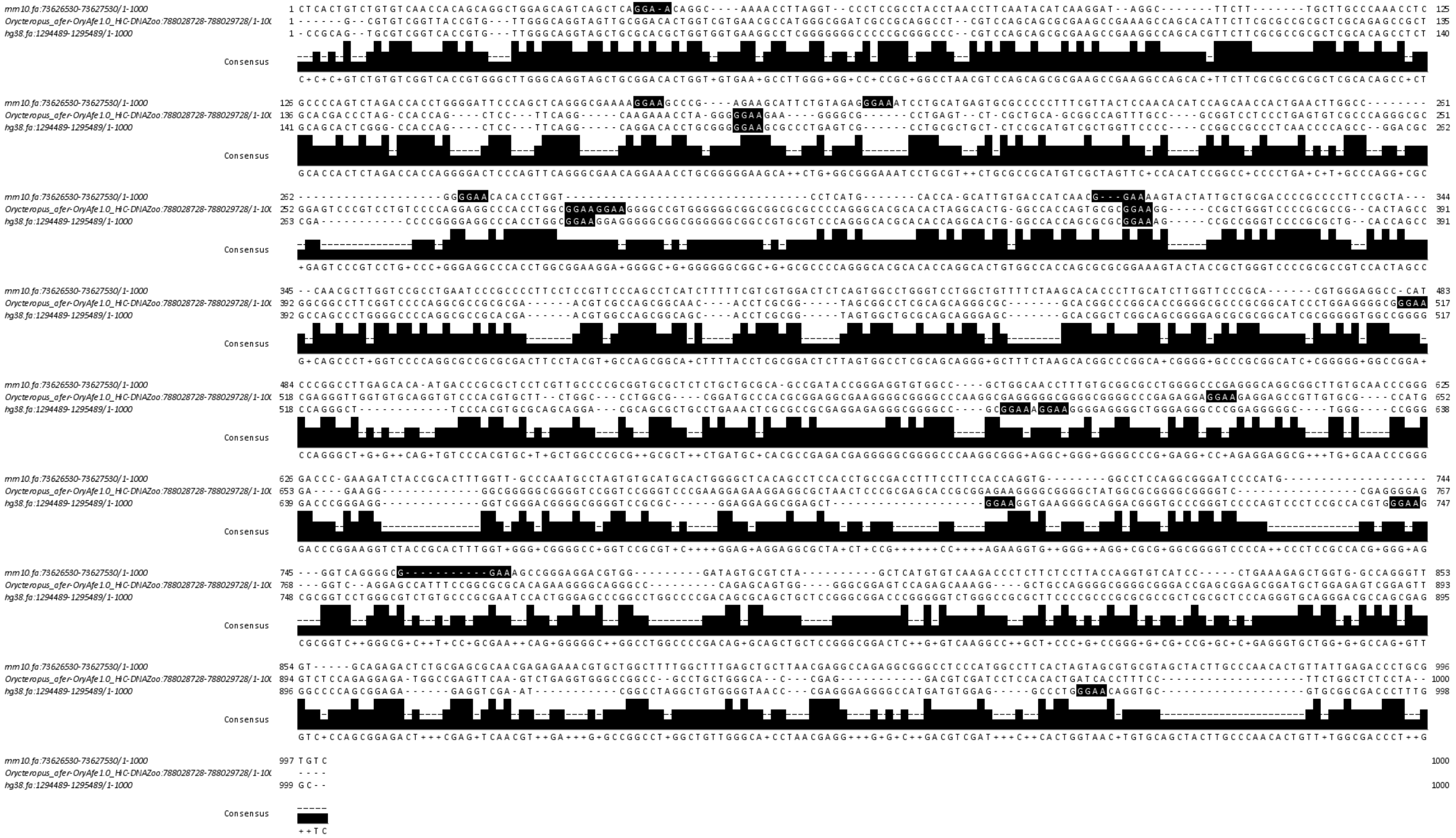
PROCEDURE

- Identified TERT orthologs using tblastn against the available genomes
- Found it in 234 genomes
- Took the 1000bp around the start. Which is not the real TSS, but fortunately the gene has a short 5’UTR in humans and mice, so hopefully it is similar in other mammals
- Did MSA with MUSCLE for each mammalian order including mm10 and hg38

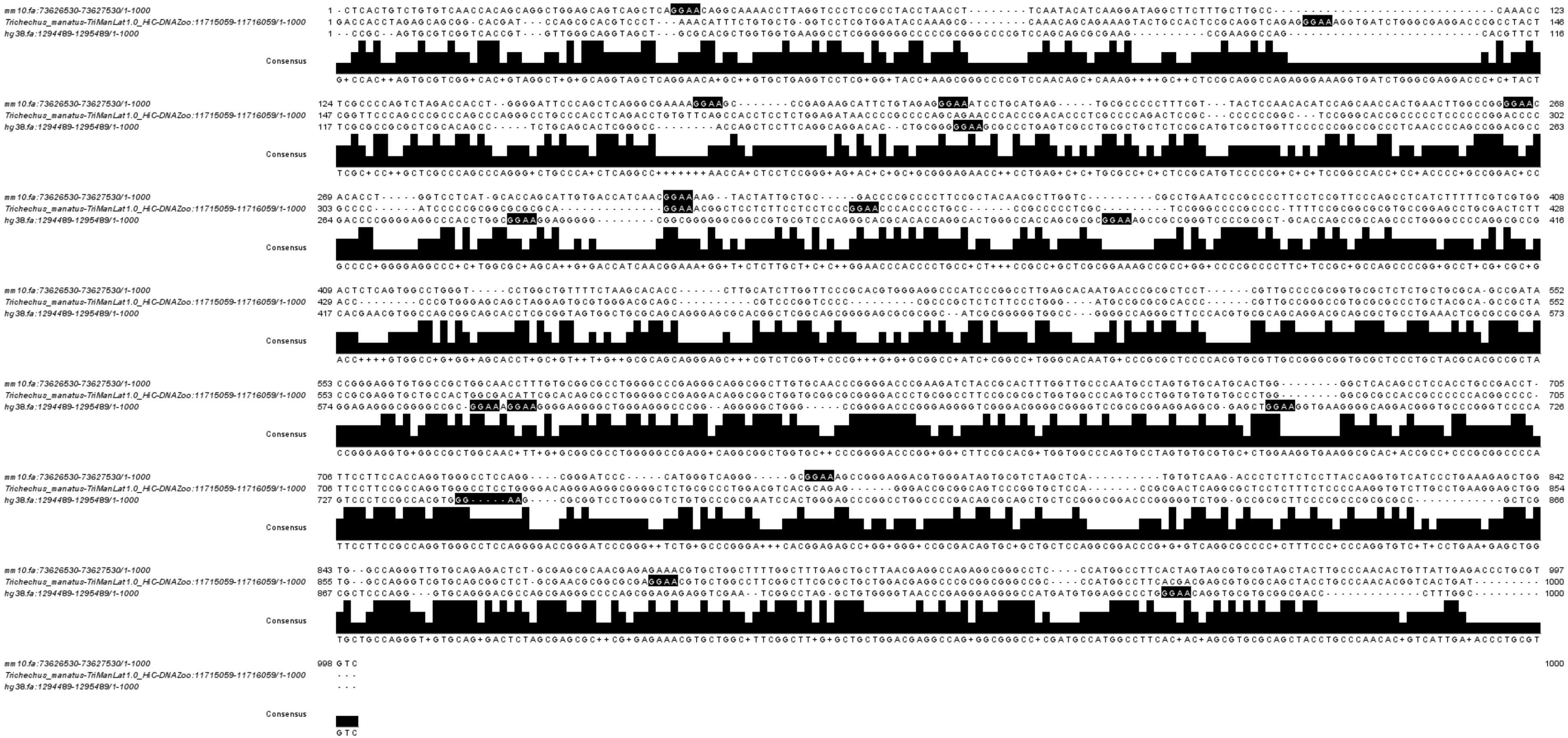




TUBULIDENTATA

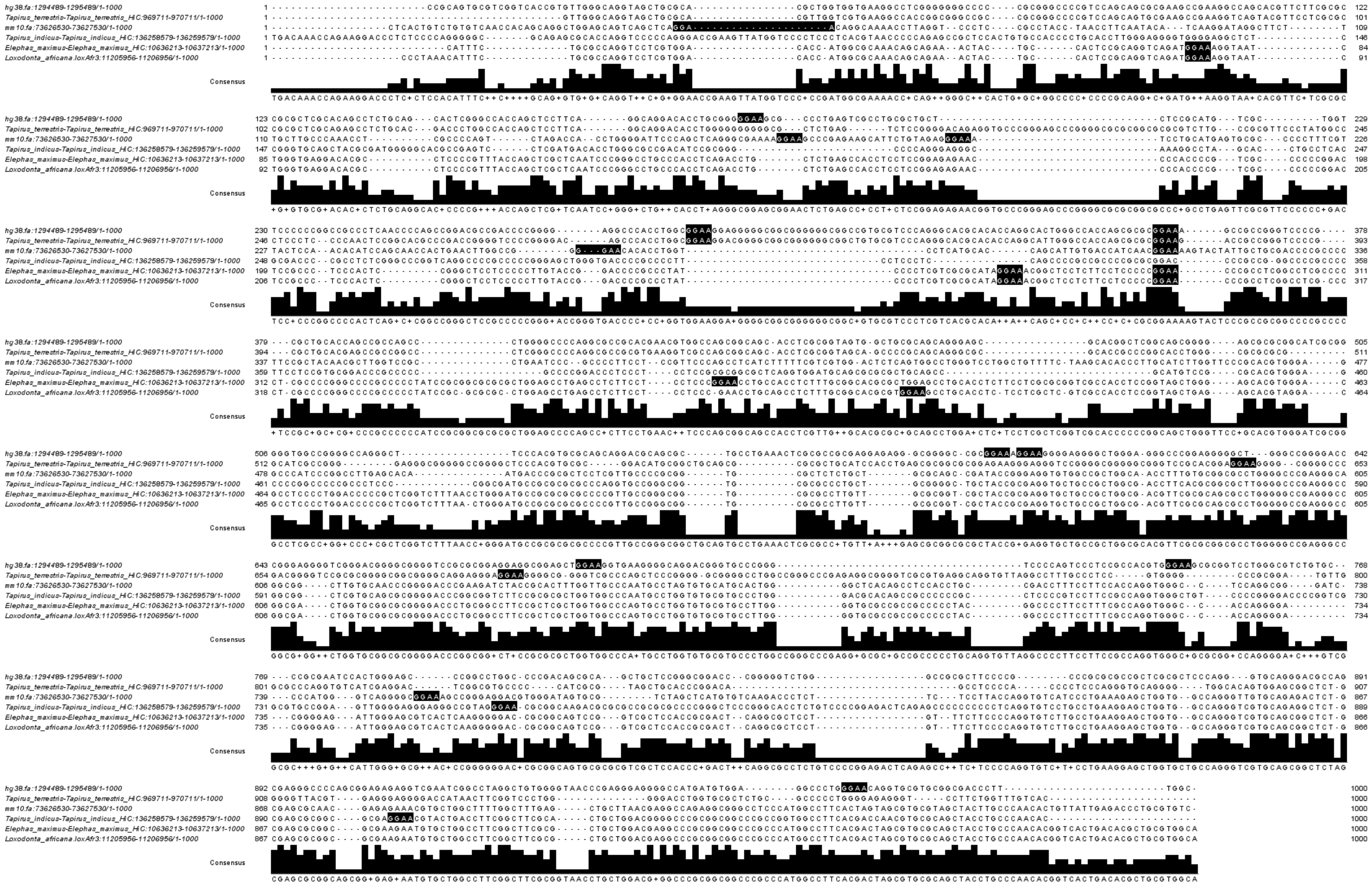


SIRENIA

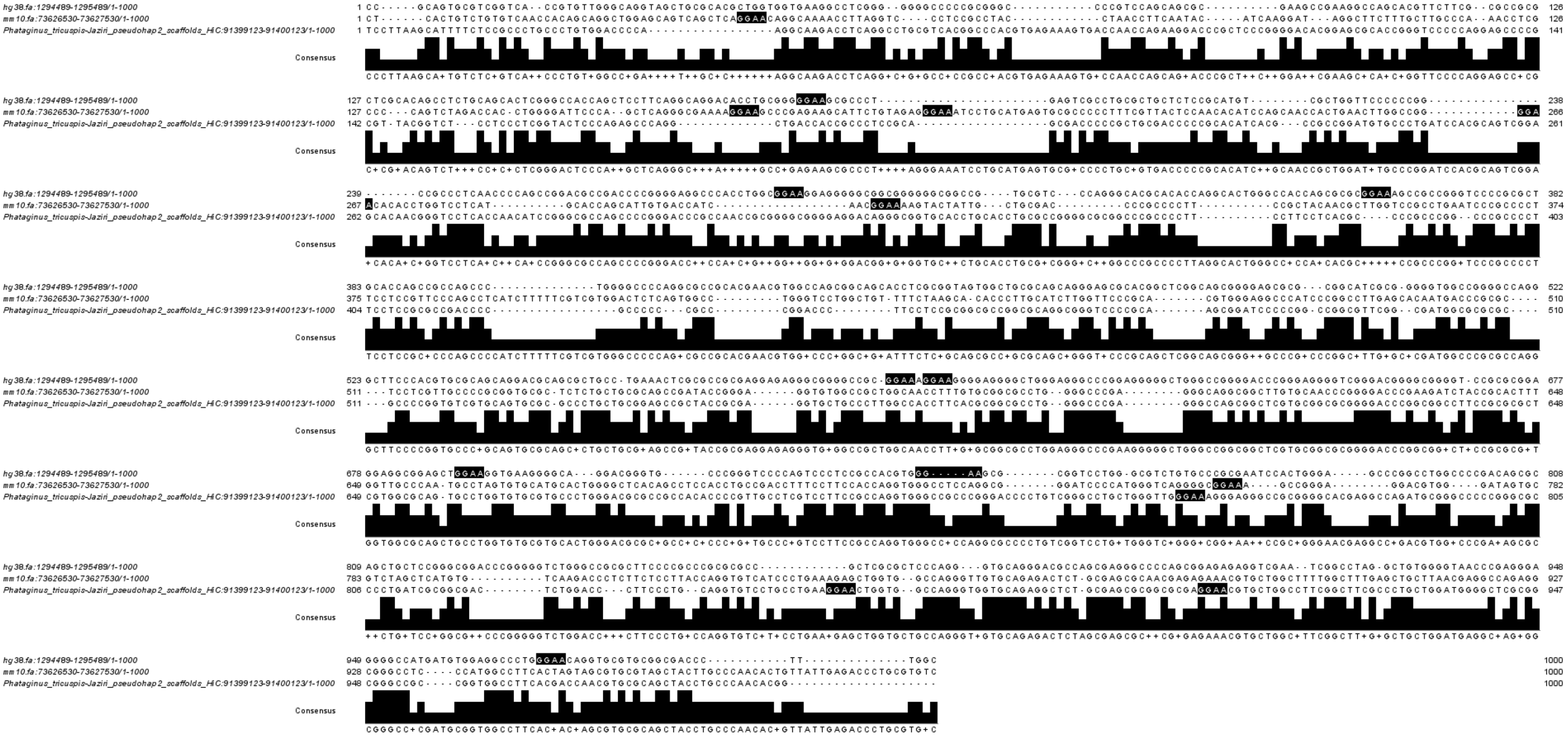


```
mm10.fa:73626530-73627530/1-1000                                     1 -CTCACTGTCTGTGTCAACCACAGCAGGCTGGAGCAGTCAGCTCAGGAACAGGCAAAACCTTAGGTCCCTCCGCCTACCTAACCT--------TCAATACATCAAGGATAGGCTTCTTTGCTTGCC------------------------------CAAACC 123
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000   1 GACCACCTAGAGCAGCGG-CACGAT---CCAGCGCACGTCCCT---AAACATTTCTGTGCTG-GGTCCTCGTGGATACCAAAGCG--------CAAACAGCAGAAAGTACTGCCACTCCGCAGGTCAGAGGGAAAGGTGATCTGGGCGAGGACCCGCCTACT 146
hg38.fa:1294489-1295489/1-1000                                       1 --CCGC--AGTGCGTCGGTCACCGT---GTTGGGCAGGTAGCT---GCGCACGCTGGTGGTGAAGGCCTCGGGGGGGCCCCCGCGGGCCCCGTCCAGCAGCGCGAAG----------CCGAAGGCCAG--------------------------CACGTTCT 116

                                                           Consensus
                                                                       G+CCAC++AGTGCGTCGG+CAC+GTAGGCT+G+GCAGGTAGCTCAGGAACA+GC++GTGCTGAGGTCCTCG+GG+TACC+AAGCGGGCCCCGTCCAACAGC+CAAAG++++GC++CTCCGCAGGCCAGAGGGAAAGGTGATCTGGGCGAGGACCC+C+TACT

mm10.fa:73626530-73627530/1-1000                                   124 TCGCCCCAGTCTAGACCACCT--GGGGATTCCCAGCTCAGGGCGAAAAGGAAGC-------CCGAGAAGCATTCTGTAGAGGGAAATCCTGCATGAG-----TGCGCCCCCTTTCGT---TACTCCAACACATCCAGCAACCACTGAACTTGGCCGGGGAAC 268
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 147 CGGTTCCCAGCCCGCCCAGCCCAGGGCCTGCCCACCTCAGACCTGTGTTCAGCCACCTCCTCTGGAGATAACCCCGCCCCAGCAGAACCCACCCGACACCCTCGCCCCAGACTCCGC---CCCCCCGGC---TCCGGGCACCGCCCCCTCCCCCCGGACCCC 302
hg38.fa:1294489-1295489/1-1000                                     117 TCGCGCCGCGCTCGCACAGCC-----TCTGCAGCACTCGGGCC--------ACCAGCTCCTTCAGGCAGGACAC--CTGCGGGGGAAGCGCCCTGAGTCGCCTGCGCTGCTCTCCGCATGTCGCTGGTTCCCCCCGGCCGCCCTCAACCCCAGCCGGACGCC 263

                                                           Consensus
                                                                       TCGC+CC++GCTCGCCCAGCCCAGGG+CTGCCCA+CTCAGGCC+++++++AACCA+CTCCTCCGGG+AG+AC+C+GC+GCGGGAGAACC++CCTGAG+C+C+TGCGCC+C+CTCCGCATGTCCCCCG+C+C+TCCGGCCACC+CC+ACCCC+GCCGGAC+CC

mm10.fa:73626530-73627530/1-1000                                   269 ACACCT-----GGTCCTCAT-GCACCAGCATTGTGACCATCAACGGAAAAG--TACTATTGCTGC-----GACCCCGCCCCTTCCGCTACAACGCTTGGTC---------CGCCTGAATCCCGCCCCTTCCTCCGTTCCCAGCCTCATCTTTTTCGTCGTGG 408
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 303 GCCCC------ATCCCCCGCGGCGCGCGCA--------------GGAAACGGCTCCTCTTCCTCCTCCCGGAACCCACCCCTGCC------CCGCCCCCTCGC---------TCCGGGCCCCGCCCC-TTTTCCGCGGCGCGTGCCGGAGCCTGCGACTCTT 428
hg38.fa:1294489-1295489/1-1000                                     264 GACCCCGGGGAGGCCCACCTGGCGGAAGGAGGGGG--------CGGCGGGGGGCGGCCGTGCGTCCCAGGGCACGCACACCAGGCACTGGGCCACCAGCGCGCGGAAAGCCGCCGGGTCCCCGCGCT-GCACCAGCCGCCAGCCCTGGGGCCCCAGGCGCCG 416

                                                           Consensus
                                                                       GCCCC+GGGGAGGCCC+C+TGGCGC+AGCA++G+GACCATCAACGGAAA+GG+T+CTCTTGCT+C+C++GGAACCCACCCCTGCC+CT+++CCGCC+GCTCGCGGAAAGCCGCC+GG+CCCCGCCCCTTC+TCCGC+GCCAGCCCCGG+GCCT+CG+CGC+G

mm10.fa:73626530-73627530/1-1000                                   409 ACTCTCAGTGGCCTGGGT-----CCTGGCTGTTTTCTAAGCACACC------CTTGCATCTTGGTTCCCGCACGTGGGAGGCCCATCCCGGCCTTGAGCACAATGACCCGCGCTCCT------CGTTGCCCCGCGGTGCGCTCTCTGCTGCGCA-GCCGATA 552
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 429 ACC--------CCCGTGGGAGCAGCTAGGAGTGCGTGGGACGCAGC----------CGTCCCGGTCCCC---------CGCCCGCTCTCTTCCCTGGG----ATGCCGCGCGCACCC------CGTTGCCGGGCCGTGCGCGCCCTGCTACGCA-GCCGCTA 552
hg38.fa:1294489-1295489/1-1000                                     417 CACGAACGTGGCCAGCGGCAGCACCTCGCGGTAGTGGCTGCGCAGCAGGGAGCGCACGGCTCGGCAGCGGGGAGCGCGCGGC--ATCGCGGGGGTGGCC---GGGGCCAGGGCTTCCCACGTGCGCAGCAGGACGCAGCGCTGCCTGAAACTCGCGCCGCGA 573

                                                           Consensus
                                                                       ACC++++GTGGCC+G+GG+AGCACCT+GC+GT++T+G++GCGCAGCAGGGAGC+++CGTCTCGGT+CCCG+++G+G+GCGGCC+ATC+CGGCC+TGGGCACAATG+CCCGCGCTCCCCACGTGCGTTGCCGGGCGGTGCGCTCCCTGCTACGCACGCCGCTA

mm10.fa:73626530-73627530/1-1000                                   553 CCGGGAGGTGTGGCCGCTGGCAACCTTTGTGCGGCGCCTGGGGCCCGAGGGCAGGCGGCTTGTGCAACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCTAGTGTGCATGCACTGG--------GGCTCACAGCCTCCACCTGCCGACCT- 705
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 553 CCGCGAGGTGCTGCCACTGGCGACATTCGCACAGCGCCTGGGGGCCGAGGACAGGCGGCTGGTGCGGCGCGGGGACCCTGCGGCCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGTGTGCCCTGG--------GGCGCGCCACCGCCCCCCACGGCCCC- 705
hg38.fa:1294489-1295489/1-1000                                     574 GGAGAGGGCGGGGCCGC-GGAAAGGAAGGGGAGGGGCTGGGAGGGCCCGG--AGGGGGCTGGG-----CCGGGGACCCGGGAGGGGTCGGGACGGGGCGGGGTCCGCGCGGAGGAGGCG-GAGCTGGAAGGTGAAGGGGCAGGACGGGTGCCCGGGTCCCCA 726

                                                           Consensus
                                                                       CCGGGAGGTG+GGCCGCTGGCAAC+TT+G+GCGGCGCCTGGGGGCCGAGG+CAGGCGGCTGGTGC++CCCGGGGACCCGG+GG+CTTCCGCACG+TGGTGGCCCAGTGCCTAGTGTGCGTGC+CTGGAAGGTGAAGGCGCAC+ACCGCC+CCCGCGGCCCCA

mm10.fa:73626530-73627530/1-1000                                   706 TTCCTTCCACCAGGTGGGCCTCCAGG----CGGGATCCC-----CATGGGTCAGGG-----GCGGAAAGCCGGGAGGACGTGGGATAGTGCGTCTAGCTCA----------TGTGTCAAG-ACCCTCTTCTCCTTACCAGGTGTCATCCCTGAAAGAGCTGG 842
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 706 TTCCTTCCGCCAGGTGGGCCTCCTGGGGACAGGGAGGGCGGGGCTCTGCGCCCTGGACGTCACGCAGAG------GGGACCGCGGCAGTCCCGGTGCTCCA-------CCGCGACTCAGGCGCTCCTCTTTCTCCCCAAGGTGTCTTGCCTGAAGGAGCTGG 854
hg38.fa:1294489-1295489/1-1000                                     727 GTCCCTCCGCCACGTGGG-----AAG----CGCGGTCCTGGGCGTCTGTGCCCGCGAATCCACTGGGAGCCCGGCCTGGCCCCGACAGCGCAGCTGCTCCGGGCGGACCCGGGGGTCTGG-GCCGCGCTTCCCCGCCCGCGCGCC------------GCTCG 866

                                                           Consensus
                                                                       TTCCTTCCGCCAGGTGGGCCTCCAGGGGACCGGGATCCCGGG++TCTG+GCCCGGGA+++CACGGAGAGCC+GG+GGG+CCGCGACAGTGC+GCTGCTCCAGGCGGACCCG+G+GTCAGGCGCCCC+CTTTCCC+CCCAGGTGTC+T+CCTGAA+GAGCTGG

mm10.fa:73626530-73627530/1-1000                                   843 TG--GCCAGGGTTGTGCAGAGACTCT-GCGAGCGCAACGAGAGAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAGGCCAGAGGCGGGCCTC----CCATGGCCTTCACTAGTAGCGTGCGTAGCTACTTGCCCAACACTGTTATTGAGACCCTGCGT 997
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000 855 TG--GCCAGGGTCGTGCAGCGGCTCT-GCGAACGCGGCGCGAGGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGAGGCCCGCGGCGGGCCGC----CCATGGCCTTCACGACGAGCGTGCGCAGCTACCTGCCCAACACGGTCACTGAT--------- 1000
hg38.fa:1294489-1295489/1-1000                                     867 CGCTCCCAGG---GTGCAGGGACGCCAGCGAGGGCCCCAGCGGAGAGAGGTCGAA--TCGGCCTAG-GCTGTGGGGTAACCCGAGGGAGGGGCCATGATGTGGAGGCCCTGGGAACAGGTGCGTGCGGCGACC-------------CTTTGGC--------- 1000

                                                           Consensus
                                                                       TGCTGCCAGGGT+GTGCAG+GACTCTAGCGAGCGC++CG+GAGAAACGTGCTGGC+TTCGGCTT+G+GCTGCTGGACGAGGCCAG+GGCGGGCC+CGATGCCATGGCCTTCAC+AC+AGCGTGCGCAGCTACCTGCCCAACAC+GTCATTGA+ACCCTGCGT

mm10.fa:73626530-73627530/1-1000                                   998 GTC 1000
Trichechus_manatus-TriManLat1.0_HiC-DNAZoo:11715059-11716059/1-1000     ---
hg38.fa:1294489-1295489/1-1000                                         ---

                                                           Consensus
                                                                       GTC
```

PROBOSCIDEA

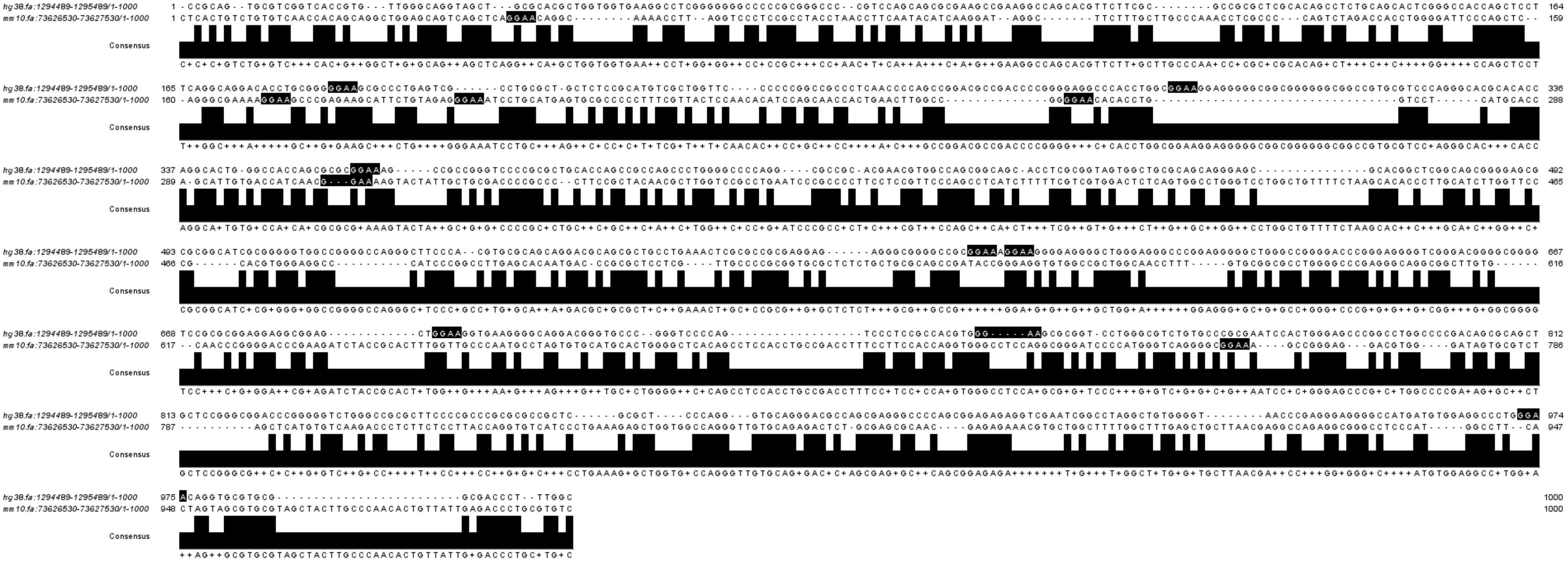


PHOLIDOTA



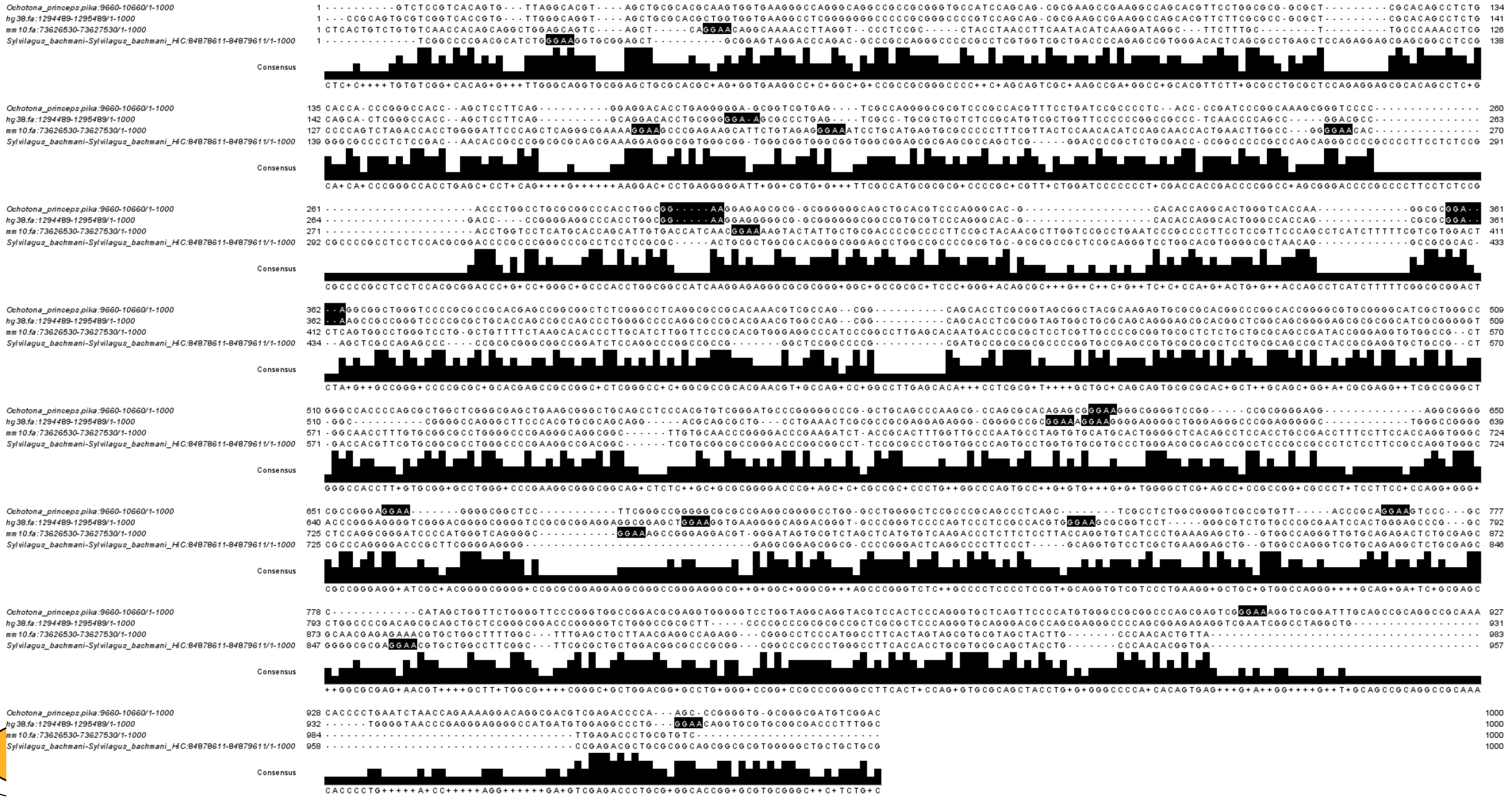
```
hg38.fa:1294489-1295489/1-1000                                              1 CC-----GCAGTGCGTCGGTCA--CCGTGTTGGGCAGGTAGCTGCGCACGCTGGTGGTGAAGGCCTCGGG--GGGGCCCCCGCGGGC-----------CCCGTCCAGCAGCGC----------GAAGCCGAAGGCCAGCACGTTCTTCG--CGCCGCG 126
mm10.fa:73626530-73627530/1-1000                                            1 CT------CACTGTCTGTGTCAACCACAGCAGGCTGGAGCAGTCAGCTCAGGAACAGGCAAAACCTTAGGTC----CCTCCGCCTAC------------CTAACCTTCAATAC-----ATCAAGGAT---AGGCTTCTTTGCTTGCCCA--AACCTCG 126
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 1 TCCTTAAGCATTTTCTCCGCCCTGCCCTGTGGACCCCA-----------------AGGCAAGACCTCAGGCCTGCGTCACGGCCCACGTGAGAAAGTGACCAACCAGAAGGACCCGCTCCCGGGGACACGGAGCGCACCGGGTCCCCAGGAGCCCCG 141
Consensus
CCCTTAAGCA+TGTCTC+GTCA++CCCTGT+GGCC+GA++++T++GC+C+++++AGGCAAGACCTCAGG+C+G+GCC+CCGCC+ACGTGAGAAAGTG+CCAACCAGCAG+ACCCGCT++C++GGA++CGAAGC+CA+C+GGTTCCCCAGGAGCC+CG

hg38.fa:1294489-1295489/1-1000                                              127 CTCGCACAGCCTCTGCAGCACTCGGGCCACCAGCTCCTTCAGGCAGGACACCTGCGGGGGAAGCGCCCT----------------------GAGTCGCCTGCGCTGCTCTCCGCATGT--------CGCTGGTTCCCCCCGG---------------- 238
mm10.fa:73626530-73627530/1-1000                                            127 CCC---CAGTCTAGACCAC-CTGGGGATTCCCA--GCTCAGGGCGAAAAGGAAGCCCGAGAAGCATTCTGTAGAGGGAAATCCTGCATGAGTGCGCCCCCTTTCGTTACTCCAACACATCCAGCAACCACTGAACTTGGCCGG------------GGA 266
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 142 CGT-TACGGTCT---CCTCCCTCGGTACTCCCAGAGCCCAGG-------------CTGACCACCGCCCTCCGCA------------------GCGACCCCCGCTGCGACCCCCGCACATCACG---CCGCCGGATGTGCCCTGATCCACGCAGTCGGA 261
Consensus
C+CG+ACAGTCT+++CC+C+CTCGGGACTCCCA++GCTCAGGGC+++A+++++GCC+GAGAAGCGCCCT++++AGGGAAATCCTGCATGAGTGCG+CCCCTGC+GTGACCCCCGCACATC++GCAACCGCTGGAT+TGCCCGGATCCACGCAGTCGGA

hg38.fa:1294489-1295489/1-1000                                              239 -------CCGCCCTCAACCCCAGCCGGACGCCGACCCCGGGGAGGCCCACCTGGCGGAAGGAGGGGGCGGCGGGGGGCGGCCG----TGCGTC---CCAGGGCACGCACACCAGGCACTGGGCCACCAGCGCGCGGAAAGCCGCCGGGTCCCCGCGCT 382
mm10.fa:73626530-73627530/1-1000                                            267 ACACACCTGGTCCTCAT----------GCACCAGCATTGTGACCATC------------------AACGGAAAAGTACTATTG---CTGCGAC---------CCCGCCCCTT----------CCGCTACAACGCTTGGTCCGCCTGAATCCCGCCCCT 374
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 262 GCACAACGGGTCCTCACCAACATCCGGGCGCCAGCCCCGGGACCCGCCAACCGCGGGGCGGGGAGGACAGGGCGGTGCACCTGCACCTGCGCCGGGGCGCGGCCCGCCCCTT----------CCTTCCTCACGC----CCCGCCCGG--CCCGCCCCT 403
Consensus
+CACA+C+GGTCCTCA+C++CA+CCGGGCGCCAGCCCCGGGACC++CCA+C+G++GG++GG+G+GGACGG+G+GGTGC++CTGCACCTGCG+CGGG+C++GGCCCGCCCCTTAGGCACTGGGCC+CCA+CACGC+++++CCGCCCGG+TCCCGCCCCT

hg38.fa:1294489-1295489/1-1000                                              383 GCACCAGCCGCCAGCCC--------------TGGGGCCCCAGGCGCCGCACGAACGTGGCCAGCGGCAGCACCTCGCGGTAGTGGCTGCGCAGCAGGGAGCGCACGGCTCGGCAGCGGGGAGCGCG---CGGCATCGCG-GGGGTGGCCGGGGCCAGG 522
mm10.fa:73626530-73627530/1-1000                                            375 TCCTCCGTTCCCAGCCTCATCTTTTTCGTCGTGGACTCTCAGTGGCC---------TGGGTCCTGGCTGT-TTTCTAAGCA-CACCCTTGCATCTTGGTTCCCGCA-------CGTGGAGGCCCATCCCGGCCTTGAGCACAATGACCCGCGC---- 510
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 404 TCCTCCGCGCCGACCCC-----------------GCCCCC---CGCC---------CGGACCC--------TTCCTCCGCGGCGCCGGCGCAGGCGGGTCCCCGCA-------AGCGGATCCCCGG-CCGGCGTTCGG--CGATGGCGCGCGC---- 510
Consensus
TCCTCCGC+CCCAGCCCCATCTTTTTCGTCGTGGGCCCCCAG+CGCCGCACGAACGTGG+CCC+GGC+G+ATTTCTC+GCAGCGCC+GCGCAGC+GGGT+CCCGCAGCTCGGCAGCGGG++GCCCG+CCCGGC+TTG+GC+CGATGGCCCGCGCCAGG

hg38.fa:1294489-1295489/1-1000                                              523 GCTTCCCACGTGCGCAGCAGGACGCAGCGCTGCC-TGAAACTCGCGCCGCGAGGAGAGGGCGGGGCCGC-GGAAAGGAAGGGGAGGGGCTGGGAGGGCCCGGAGGGGGCTGGGCCGGGGACCCGGGAGGGGTCGGGACGGGGCGGGGT-CCGCGCGGA 677
mm10.fa:73626530-73627530/1-1000                                            511 ---TCCTCGTTGCCCCGCGGTGCGC-TCTCTGCTGCGCAGCCGATACCGGGA------GGTGTGGCCGCTGGCAACCTTTGTGCGGCGCCTG--GGGCCCGA--------GGGCAGGCGGCTTGTGCAACCCGGGGACCCGAAGATCTACCGCACTTT 648
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 511 ---GCCCCGGTGTCGTGCAGTGCGC-GCCCTGCTGCGGAGCCGCTACCGCGA------GGTGCTGCCCTTGGCCACCTTCACGCGGCGCCTG--GGGCCCGA--------GGGCCAGCGGCTCGTGCGGCGCGGGGACCCGGCGGCCTTCCGCGCGCT 648
Consensus
GCTTCCCCGGTGCCC+GCAGTGCGCAGC+CTGCTGCG+AGCCG+TACCGCGAGGAGAGGGTG+GGCCGCTGGCAACCTT+G+GCGGCGCCTGGAGGGCCCGAAGGGGGCTGGGCCGGCGGCTCGTGCGGCGCGGGGACCCGGCGG+CT+CCGCGCG+T

hg38.fa:1294489-1295489/1-1000                                              678 GGAGGCGGAGCTGGAAGGTGAAGGGGCA---GGACGGGTG------CCCGGGTCCCCAGTCCCTCCGCCACGTGGG-----AAGCG-------CGGTCCTGG-GCGTCTGTGCCCGCGAATCCACTGGGA-----GCCCGGCCTGGCCCCGACAGCGC 808
mm10.fa:73626530-73627530/1-1000                                            649 GGTTGCCCAA-TGCCTAGTGTGCATGCACTGGGGCTCACAGCCTCCACCTGCCGACCTTTCCTTCCACCAGGTGGGCCTCCAGGCG-------GGATCCCCATGGGTCAGGGGCGGAAA----GCCGGGA--------GGACGTGG----GATAGTGC 782
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 649 CGTGGCGCAG-TGCCTGGTGTGCGTGCCCTGGGACGCGCCGCCACACCCCGTTGCCTCGTCCTTCCGCCAGGTGGGCCGCCCGGGACCCCTGTCGGGCCTGCTGGGTTGGGAAAGGGAGGGCCGCGGGGCACGAGGCCAGATGCGGGCCCCCGGGCGC 805
Consensus
GGTGGCGCAGCTGCCTGGTGTGCGTGCACTGGGACGCGC+GCC+C+CCC+G+TGCCC+GTCCTTCCGCCAGGTGGGCC+CCAGGCGCCCCTGTCGGTCCTG+TGGGTC+GGG+CGG+AA++CCGC+GGGAACGAGGCC+GACGTGG+CCCGA+AGCGC

hg38.fa:1294489-1295489/1-1000                                              809 AGCTGCTCCGGGCGGACCCGGGGGTCTGGGCCGCGCTTCCCCGCCCGCGCGCC------------GCTCGCGCTCCCAGG---GTGCAGGGACGCCAGCGAGGGCCCCAGCGGAGAGAGGTCGAA--TCGGCCTAG-GCTGTGGGGTAACCCGAGGGA 948
mm10.fa:73626530-73627530/1-1000                                            783 GTCTAGCTCATGTG----------TCAAGACCCTCTTCTCCTTACCAGGTGTCATCCCTGAAAGAGCTGGTG--GCCAGGGTTGTGCAGAGACTCT-GCGAGCGCAACGAGAGAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAGGCCAGAGG 927
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 806 CCCTGATCGCGGCGAC--------TCTGGACC---CTTCCCTG--CAGGTGTCCTGCCTGAAGGAACTGGTG--GCCAGGGTGGTGCAGAGGCTCT-GCGAGCGCGGCGCGAGGAACGTGCTGGCCTTCGGCTTCGCCCTGCTGGATGGGGCTCGCGG 947
Consensus
++CTG+TCC+GGCG++CCCGGGGGTCTGGACC+++CTTCCCTG+CCAGGTGTC+T+CCTGAA+GAGCTGGTGCTGCCAGGGT+GTGCAGAGACTCTAGCGAGCGC++CG+GAGAAACGTGCTGGC+TTCGGCTT+G+GCTGCTGGATGAGGC+AG+GG

hg38.fa:1294489-1295489/1-1000                                              949 GGGGCCATGATGTGGAGGCCCTGGGAACAGGTGCGTGCGGCGACCC-----------TT--------------TGGC 1000
mm10.fa:73626530-73627530/1-1000                                            928 CGGGCCTC----CCATGGCCTTCACTAGTAGCGTGCGTAGCTACTTGCCCAACACTGTTATTGAGACCCTGCGTGTC 1000
Phataginus_tricuspis-Jaziri_pseudohap2_scaffolds_HiC:91399123-91400123/1-1000 948 CGGGCCGC----CGGTGGCCTTCACGACCAACGTGCGCAGCTACCTGCCCAACACGG-------------------- 1000
Consensus
CGGGCC+CGATGCGGTGGCCTTCAC+AC+AGCGTGCGCAGCTACCTGCCCAACAC+GTTATTGAGACCCTGCGTG+C
```

HYRACOIDEA

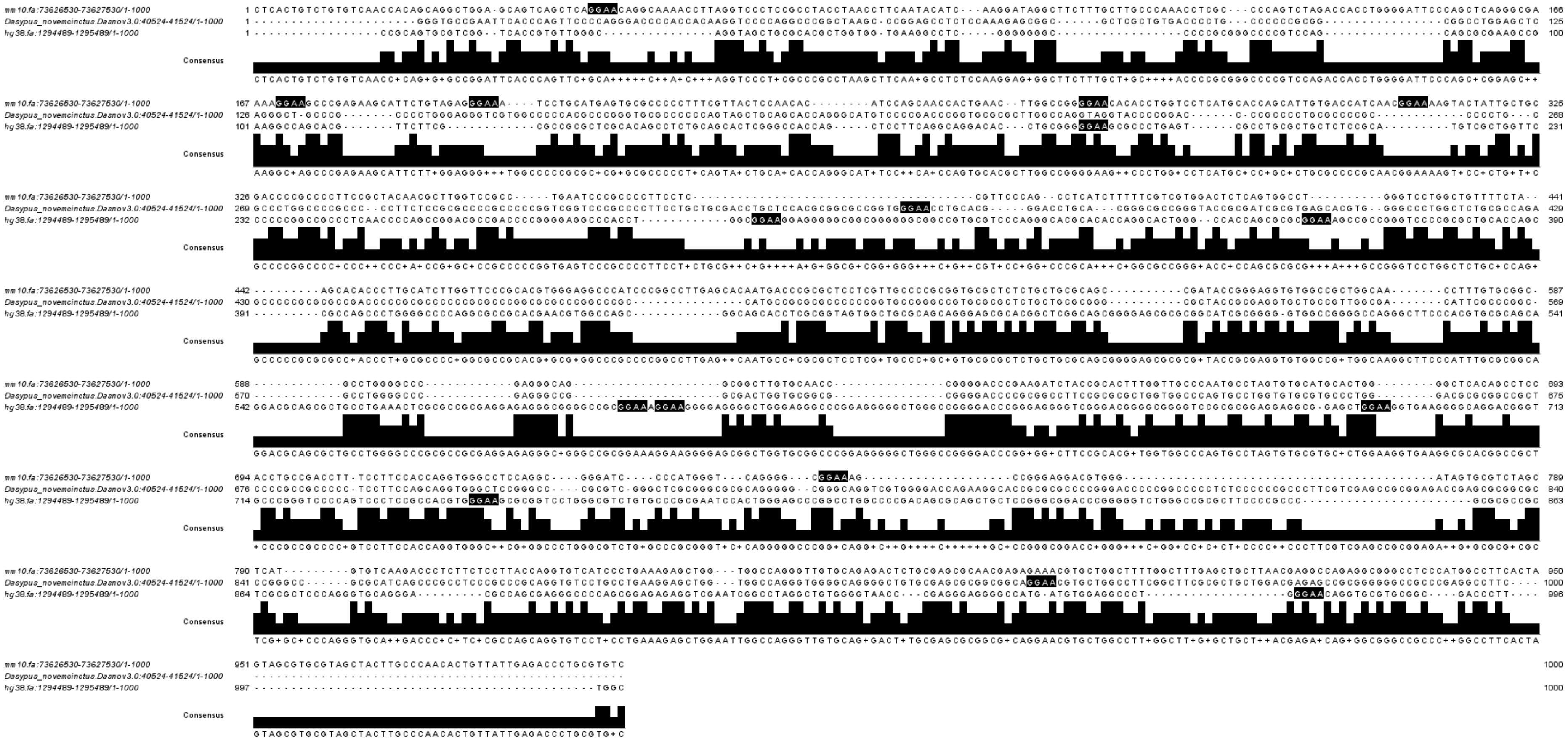


```
hg38.fa:1294489-1295489/1-1000    1 -CCGCAG--TGCGTCGGTCACCGTG---TTGGGCAGGTAGCT---GCGCACGCTGGTGGTGAAGGCCTCGGGGGGCCCCCGCGGGCCC--CGTCCAGCAGCGCGAAGCCGAAGGCCAGCACGTTCTTCGC--------GCCGCGCTCGCACAGCCTCTGCAGCACTCGGGCCACCAGCTCCT 164
mm10.fa:73626530-73627530/1-1000  1 CTCACTGTCTGTGTCAACCACAGCAGGCTGGAGCAGTCAGCTCAGGAACAGGC--------AAAACCTT--AGGTCCCTCCGCCTACCTAACCTTCAATACATCAAGGAT--AGGC-------TTCTTTGCTTGCCCAAACCTCGCCC---CAGTCTAGACCACCTGGGGATTCCCAGCTC-- 159
Consensus                           C+C+C+GTCTG+GTC+++CAC+G++GGCT+G+GCAG++AGCTCAGG++CA+GCTGGTGGTGAA++CCT+GG+GG++CC+CCGC+++CC+AAC+T+CA++A+++C+A+G++GAAGGCCAGCACGTTCTT+GCTTGCCCAA+CC+CGC+CGCACAG+CT+++C++C+++GG++++CCAGCTCCT

hg38.fa:1294489-1295489/1-1000  165 TCAGGCAGGACACCTGCGGGGGAAGCGCCCTGAGTCG------CCTGCGCT-GCTCTCCGCATGTCGCTGGTTC----CCCCCGGCCGCCCTCAACCCCAGCCGGACGCCGACCCCGGGGAGGCCCACCTGGCGGAAGGAGGGGGCGGCGGGGGGCGGCCGTGCGTCCCAGGGCACGCACACC 336
mm10.fa:73626530-73627530/1-1000  160 -AGGGCGAAAAGGAAGCCCGAGAAGCATTCTGTAGAGGGAAATCCTGCATGAGTGCGCCCCCTTTCGTTACTCCAACACATCCAGCAACCACTGAACTTGGCC--------------GGGGAACACACCTG---------------------------------GTCCT------CATGCACC 288
Consensus                           T++GGC+++A+++++GC++G+GAAGC+++CTG++++GGGAAATCCTGC+++AG++C+CC+C+T+TCG+T++T+CAACAC++CC+GC++CC++++A+C+++GCCGGACGCCGACCCCGGGG+++C+CACCTGGCGGAAGGAGGGGGCGGCGGGGGGCGGCCGTGCGTCC+AGGGCAC+++CACC

hg38.fa:1294489-1295489/1-1000  337 AGGCACTG-GGCCACCAGCGCGCGGAAAG-----CCGCCGGGTCCCCGCGCTGCACCAGCCGCCAGCCCTGGGGCCCCAGG----CGCCGC-ACGAACGTGGCCAGCGGCAGC-ACCTCGCGGTAGTGGCTGCGCAGCAGGGAGC---------------GCACGGCTCGGCAGCGGGGAGCG 492
mm10.fa:73626530-73627530/1-1000  289 A-GCATTGTGACCATCAACG---GAAAAGTACTATTGCTGCGACCCCGCCC--CTTCCGCTACAACGCTTGGTCCGCCTGAATCCCGCCCCTTCCTCCGTTCCCAGCCTCATCTTTTTCGTCGTGGACTCTCAGTGGCCTGGGTCCTGGCTGTTTTCTAAGCACACCCTTGCATCTTGGTTCC 465
Consensus                           AGGCA+TGTG+CCA+CA+CGCGCG+AAAGTACTA++GC+G+G+CCCCGC+CTGC++C+GC++C+A++C+TGG++C+CC+G+ATCCCGCC+CT+C++CGT++CCAGC++CA+CT+++TCG++GT+G+++CT++G++GC++GG++CCTGGCTGTTTTCTAAGCAC++C++GCA+C++GG++C+

hg38.fa:1294489-1295489/1-1000  493 CGCGGCATCGCGGGGGTGGCCGGGGCCAGGGCTTCCCA--CGTGCGCAGCAGGACGCAGCGCTGCCTGAAACTCGCGCCGCGAGGAG------AGGGCGGGGCCGCGGAAAGGAAGGGGAGGGGCTGGGAGGGCCCGGAGGGGGCTGGGCCGGGGACCCGGGAGGGGTCGGGACGGGGCGGGG 667
mm10.fa:73626530-73627530/1-1000  466 CG------CACGTGGGAGGCC----------CATCCCGGCCTTGAGCACAATGAC-CCGCGCTCCTCG----TTGCCCCGCGGTGCGCTCTCTGCTGCGCAGCCGATACCGGGAGGTGTGGCCGCTGGCAACCTTT-----GTGCGGCGCCTGGGGCCCGAGGGCAGGCGGCTTGTG------ 616
Consensus                           CGCGGCATC+CG+GGG+GGCCGGGGCCAGGGC+TCCC+GCC+TG+GCA++A+GACGC+GCGCT+C++GAAACT+GC+CCGCG++G+GCTCTCT+++GCG++GCCG+++++GGA+G+G++G++GCTGG+A++++++GGAGGG+GC+G+GCC+GGG+CCCG+G+G++G+CGG+++G+GGCGGGG

hg38.fa:1294489-1295489/1-1000  668 TCCGCGCGGAGGAGGCGGAG------------CTGGAAGGTGAAGGGGCAGGACGGGTGCCC--GGGTCCCAG------------------TCCCTCCGCCACGTGGG-----AAGCGCGGT-CCTGGGCGTCTGTGCCCGCGAATCCACTGGGAGCCCGGCCTGGCCCCGACAGCGCAGCT 812
mm10.fa:73626530-73627530/1-1000  617 --CAACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCTAGTGTGCATGCACTGGGGCTCACAGCCTCCACCTGCCGACCTTTCCTTCCACCAGGTGGGCCTCCAGGCGGGATCCCCATGGTCAGGGGCGGAAA----GCCGGGAG---GACGTGG----GATAGTGCGTCT 786
Consensus                           TCC+++C+G+GGA++CG+AGATCTACCGCACT+TGG++G+++AA+G+++AG+++G++TGC+CTGGGG++C+CAGCCTCCACCTGCCGACCTTTCC+TCC+CCA+GTGGGCCTCCA+GCG+G+TCCC+++G+GTC+G+G+C+G++AATCC+C+GGGAGCCCG+C+TGGCCCCGA+AG+GC++CT

hg38.fa:1294489-1295489/1-1000  813 GCTCCGGGCGGACCCGGGGGTCTGGGCCGCGCTTCCCCGCCCGCGCGCCGCTC------GCGCT----CCCAGG---GTGCAGGGACGCCAGCGAGGGCCCCAGCGGAGAGAGGTCGAATCGGCCTAGGCTGTGGGGT--------AACCCGAGGGAGGGGCCATGATGTGGAGGCCCTGGGA 974
mm10.fa:73626530-73627530/1-1000  787 ----------AGCTCATGTGTCAAGACCCTCTTCTCCTTACCAGGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAGAGACTCT-GCGAGCGCAAC----GAGAGAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAGGCCAGAGGCGGGCCTCCCAT-----GGCCTT--CA 947
Consensus                           GCTCCGGGCG++C+C++G+GTC++G+CC++++T++CC+++CC++G+G+C+++CCTGAAAG+GCTGGTG+CCAGGGTTGTGCAG+GAC+C+AGCGAG+GC++CAGCGGAGAGA+++++++T+G+++T+GGCT+TG+G+TGCTTAACGA++CC++GG+GGG+C++++ATGTGGAGGCC+TGG+A

hg38.fa:1294489-1295489/1-1000  975 ACAGGTGCGTGCG-------------------------GCGACCCT--TTGGC 1000
mm10.fa:73626530-73627530/1-1000  948 CTAGTAGCGTGCGTAGCTACTTGCCCAACACTGTTATTGAGACCCTGCGTGTC 1000
Consensus                           ++AG++GCGTGCGTAGCTACTTGCCCAACACTGTTATTG+GACCCTGC+TG+C
```

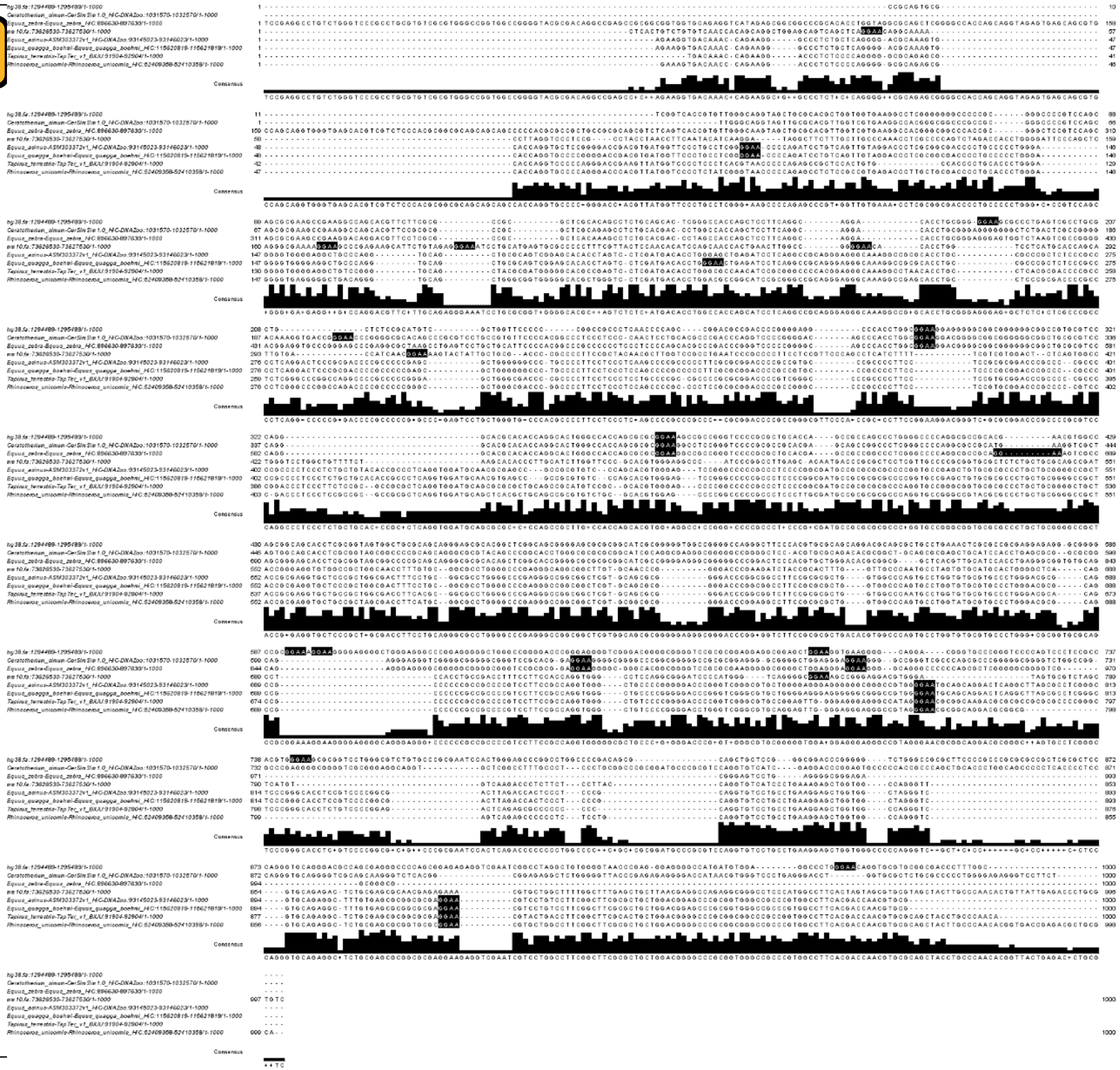
LAGOMORPHA


Ochotona_princeps.pika:9660-10660/1-1000
hg38.fa:1294489-1295489/1-1000
mm10.fa:73626530-73627530/1-1000
Sylvilagus_bachmani-Sylvilagus_bachmani_HiC:84878611-84879611/1-1000
Consensus
GGAA

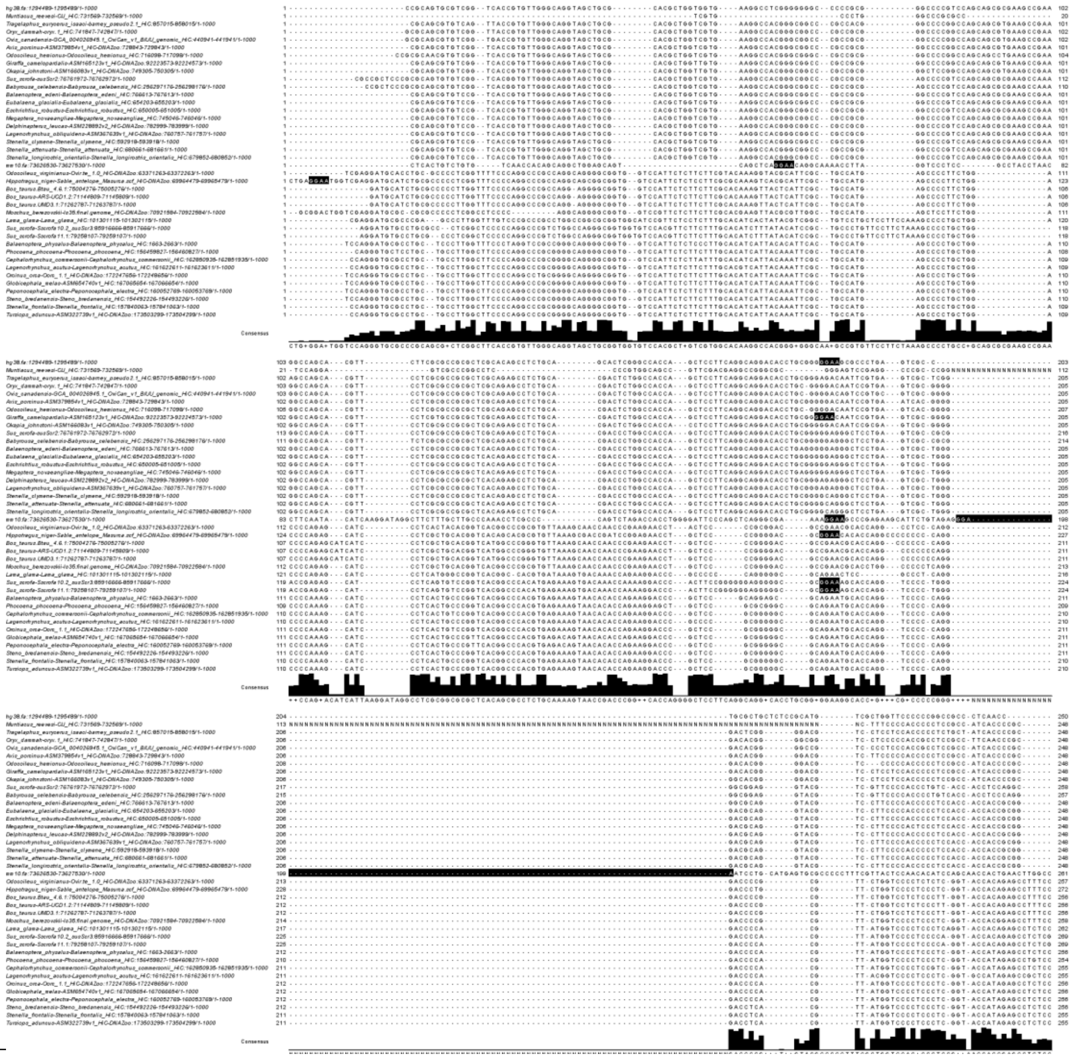
CINGULATA

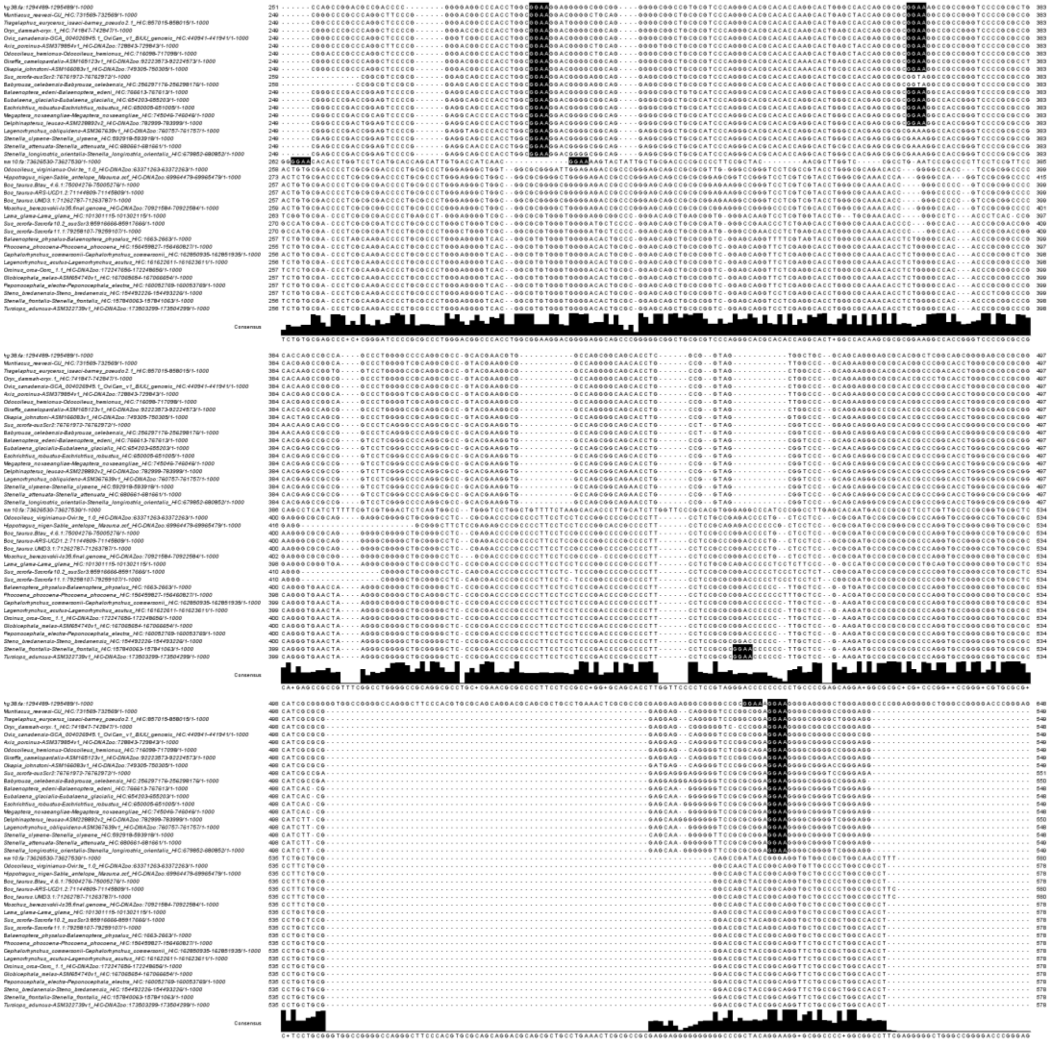

mm10.fa:73626530-73627530/1-1000
Dasypus_novemcinctus.Dasnov3.0:40524-41524/1-1000
hg38.fa:1294489-1295489/1-1000
Consensus
1 166
1 125
1 100
167 325
126 268
101 231
326 441
269 429
232 390
442 587
430 569
391 541
588 693
570 675
542 713
694 789
676 840
714 863
790 950
841 1000
864 996
951 1000
997 1000

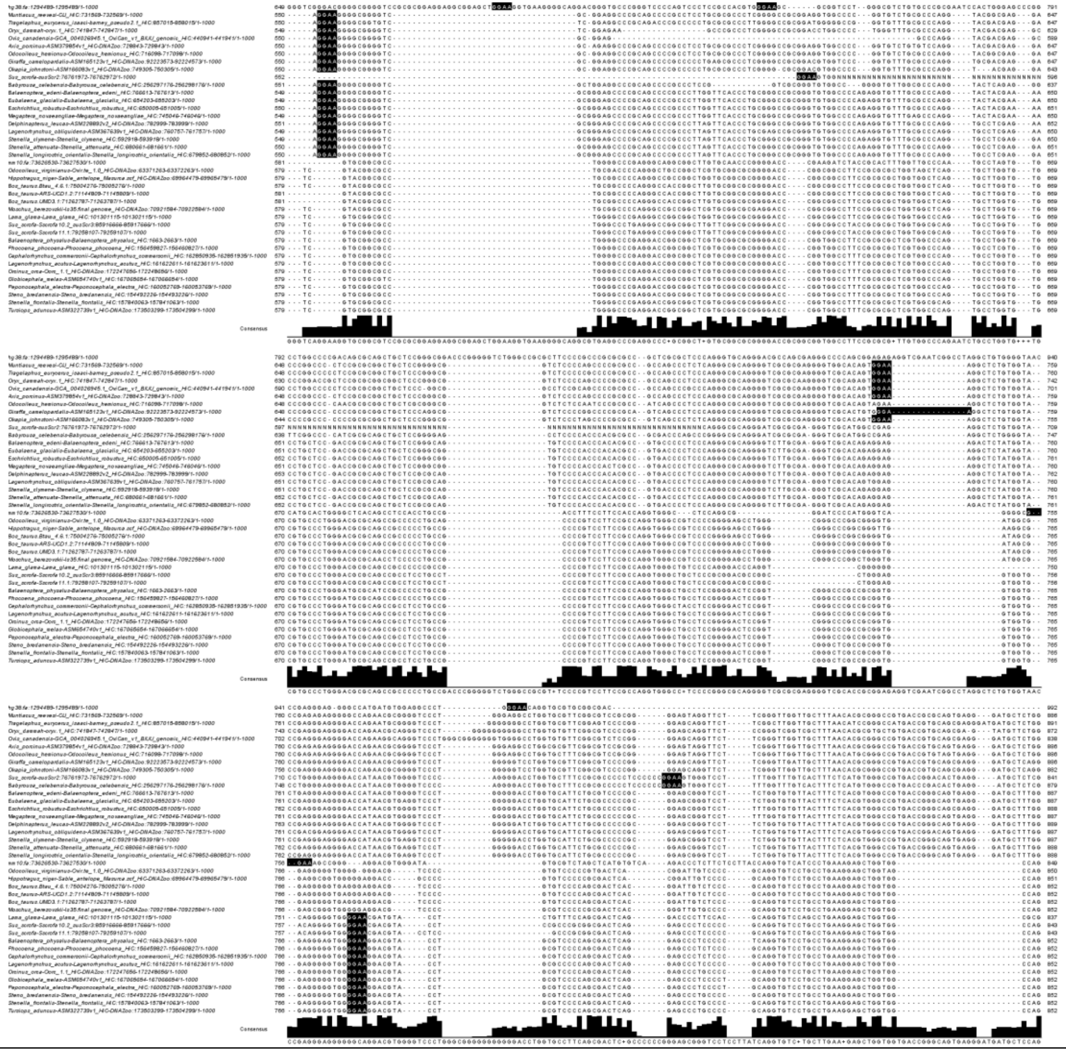
PERISSODACTYLA

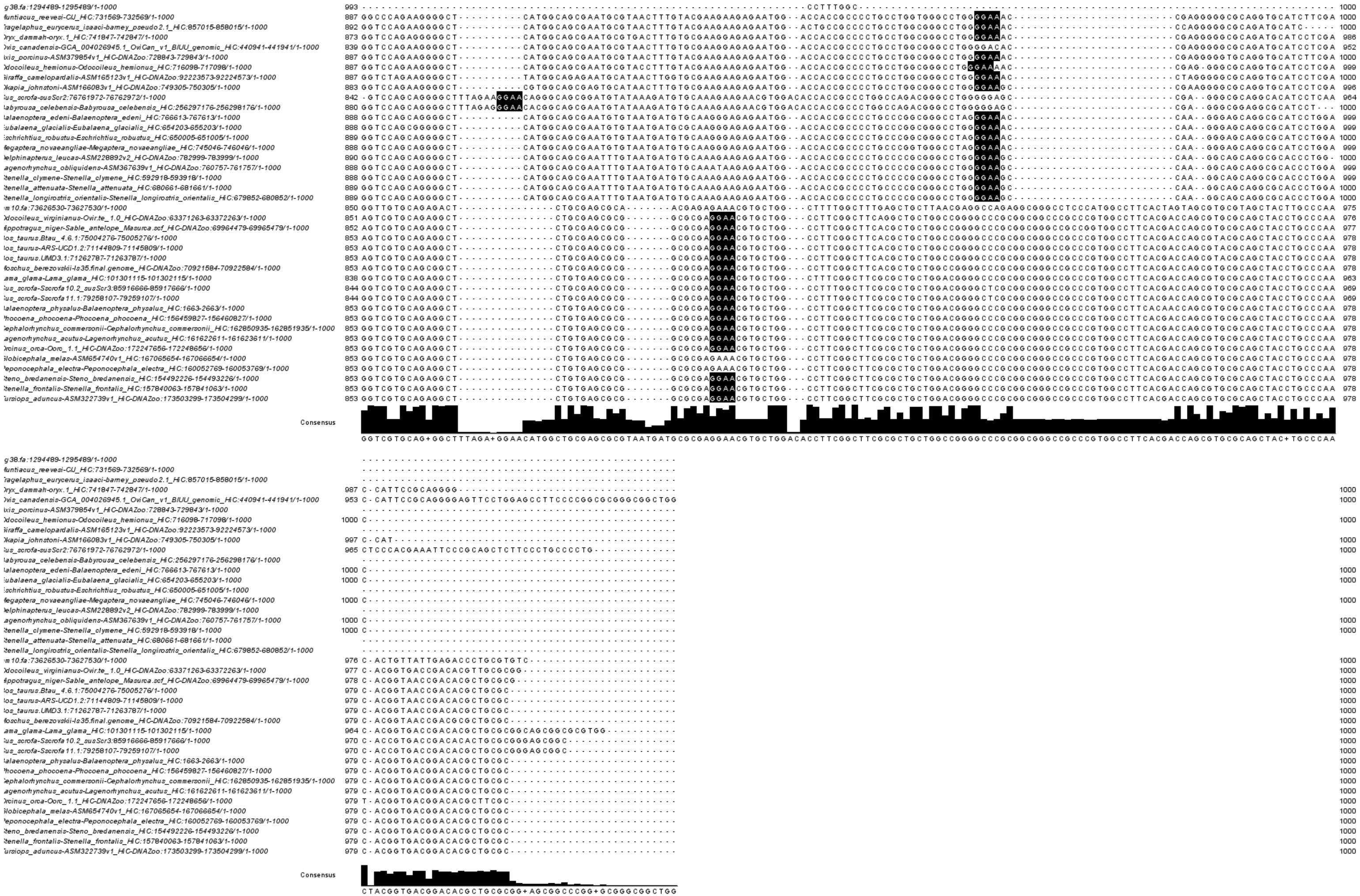


ARTIODACTYLA

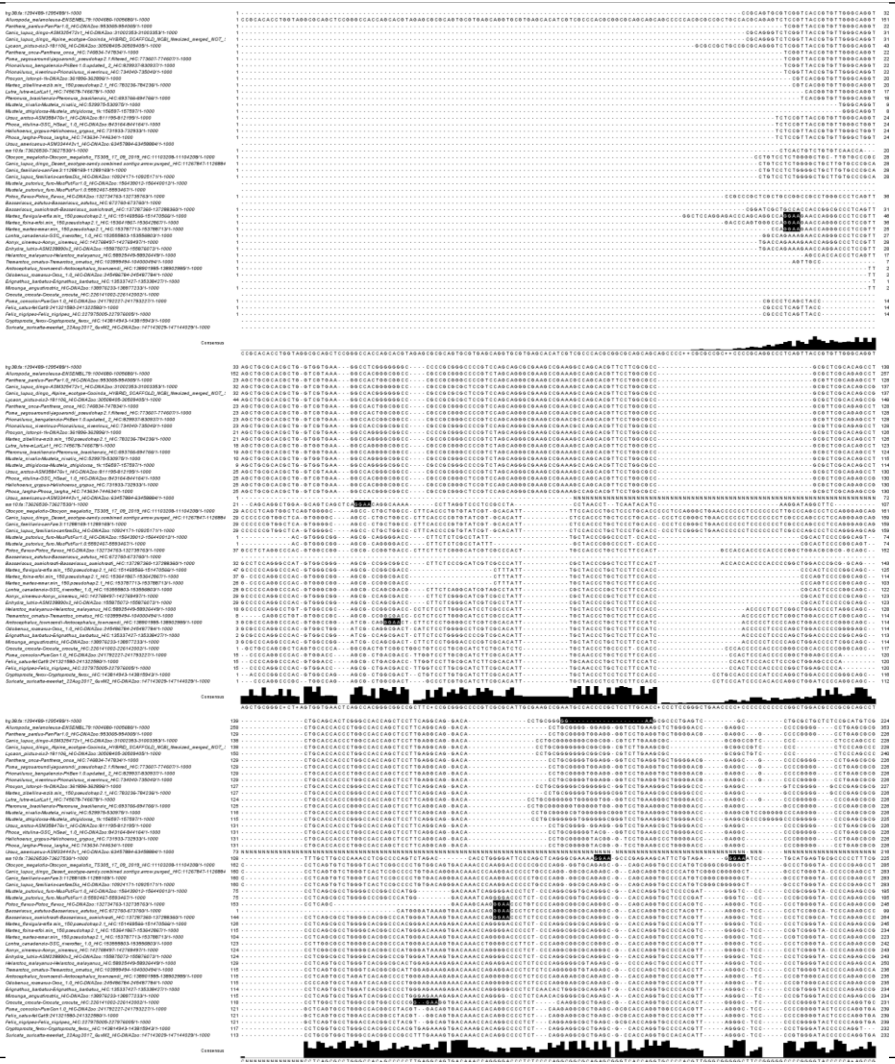


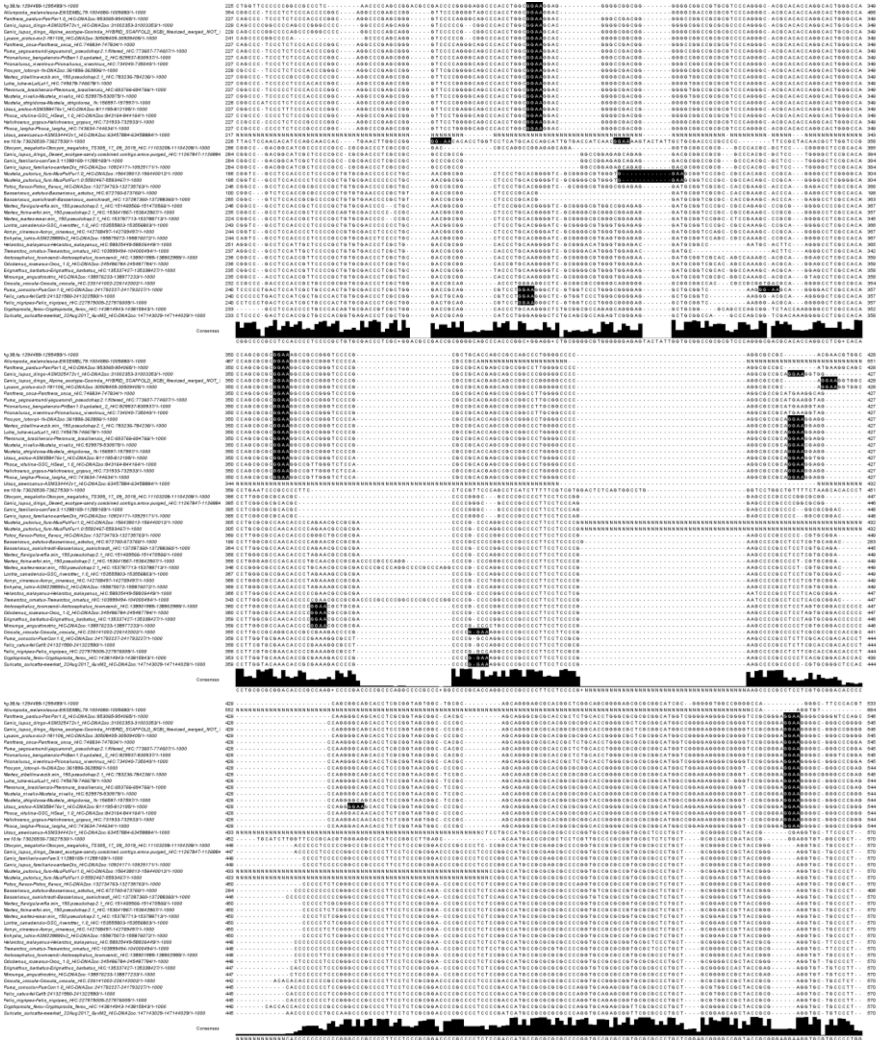


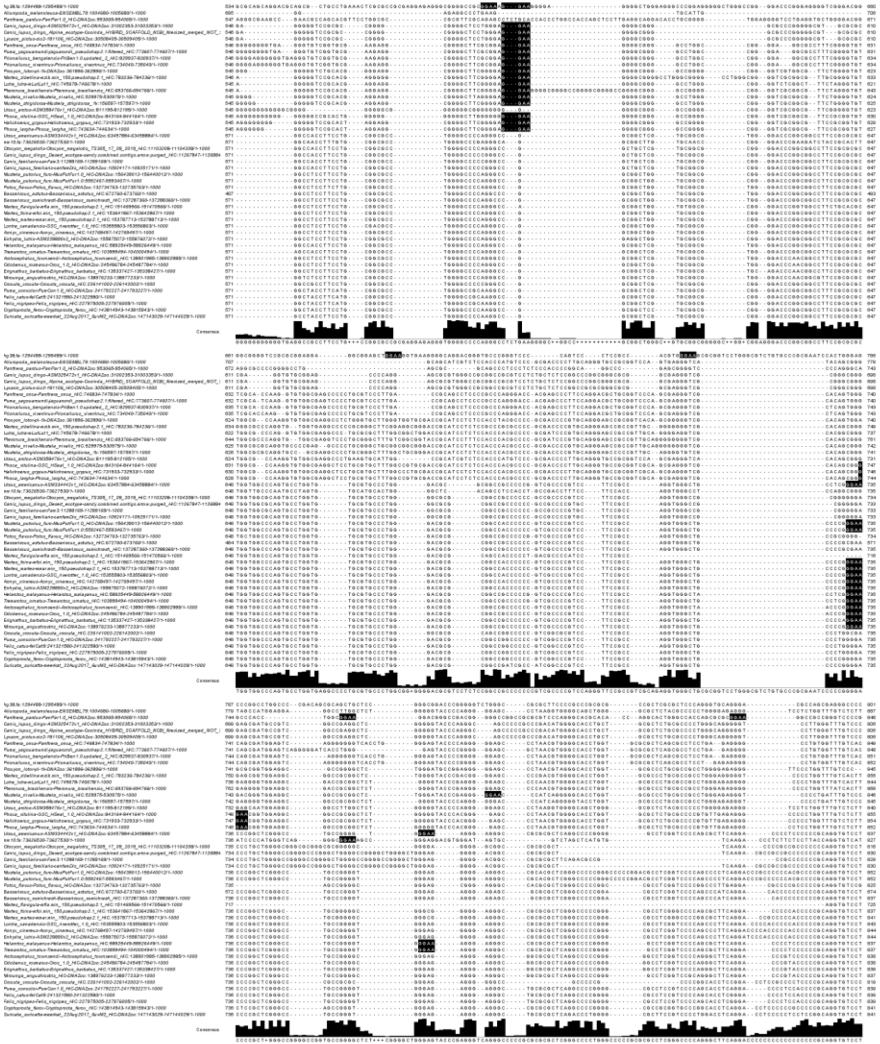




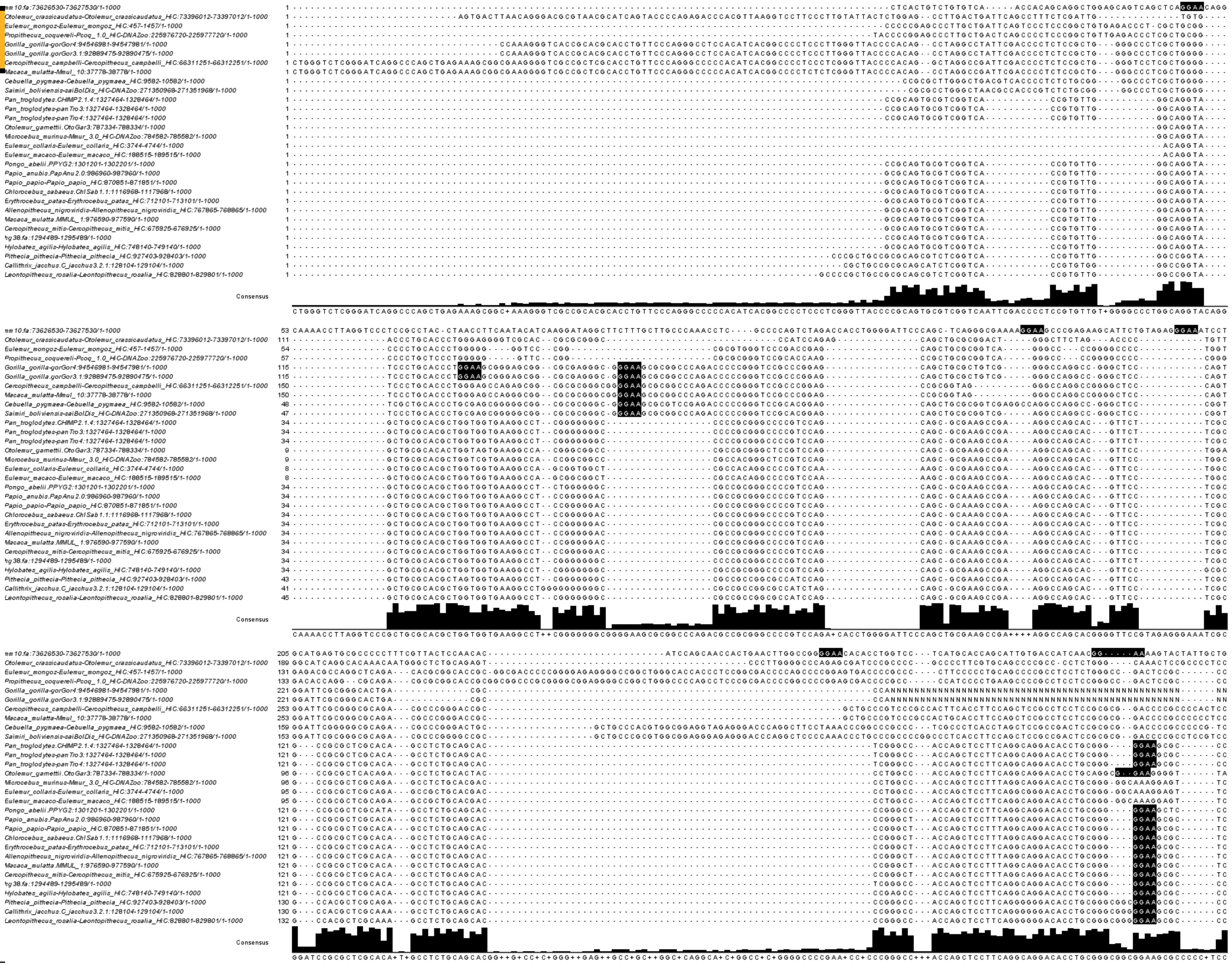
CARNIVORA

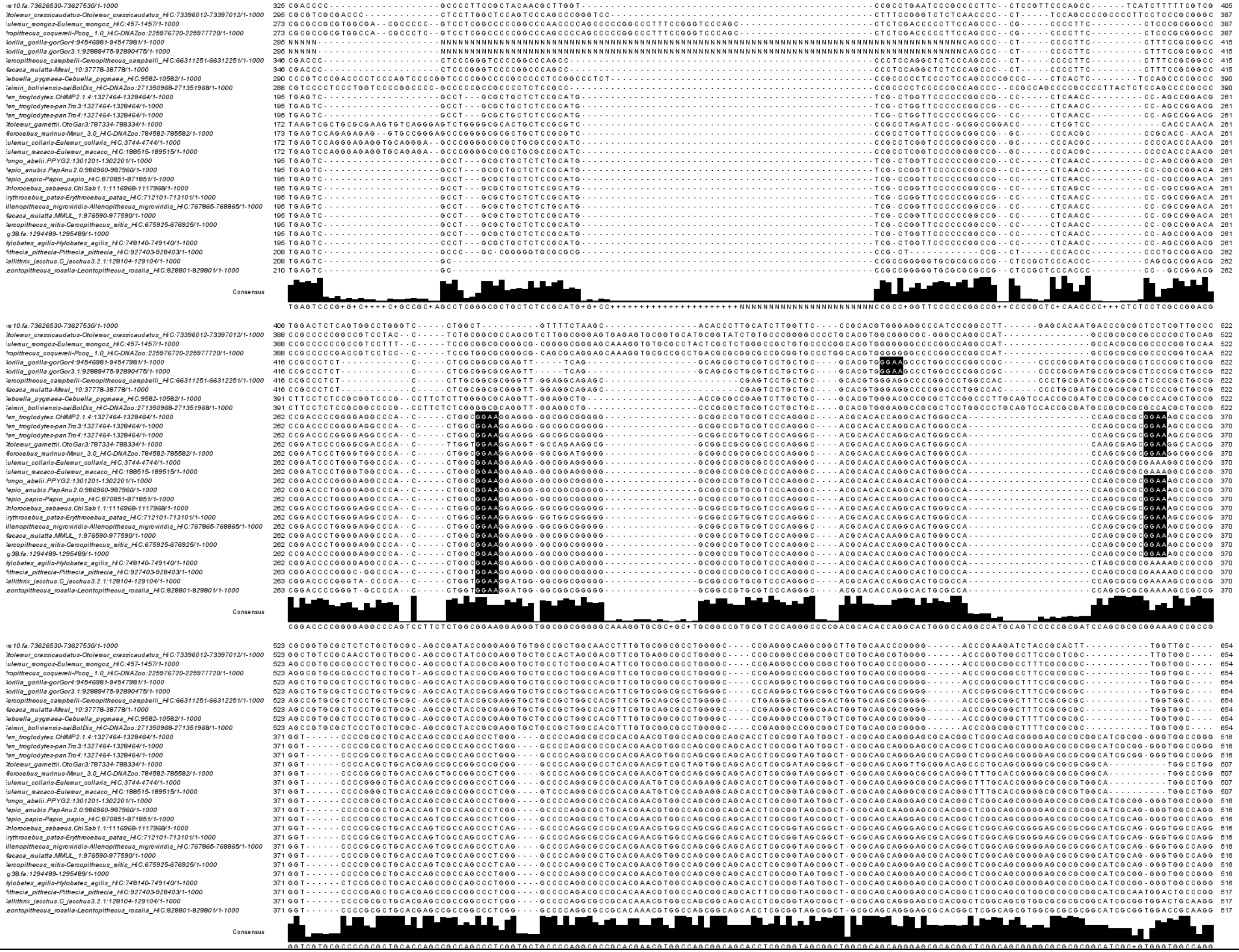


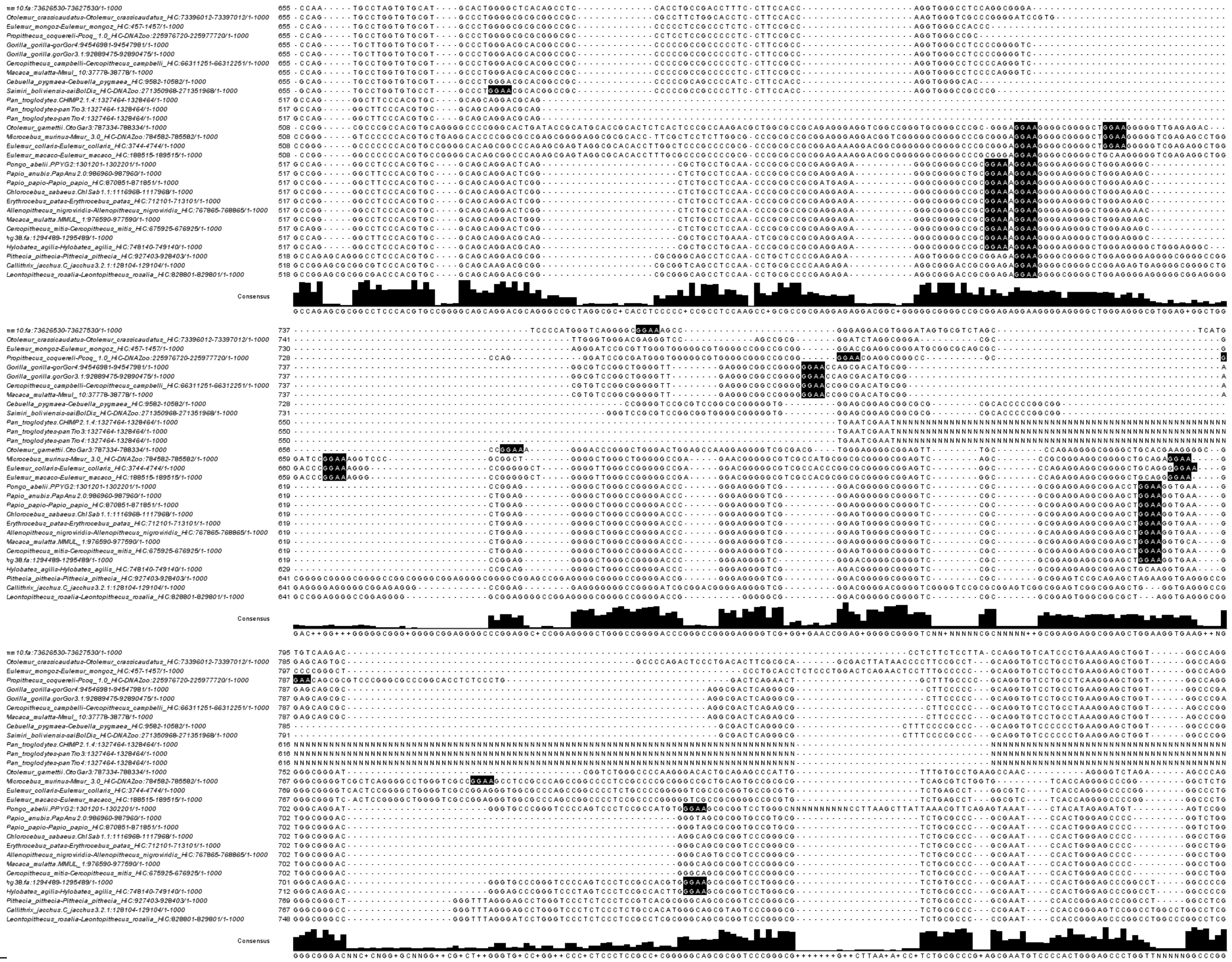


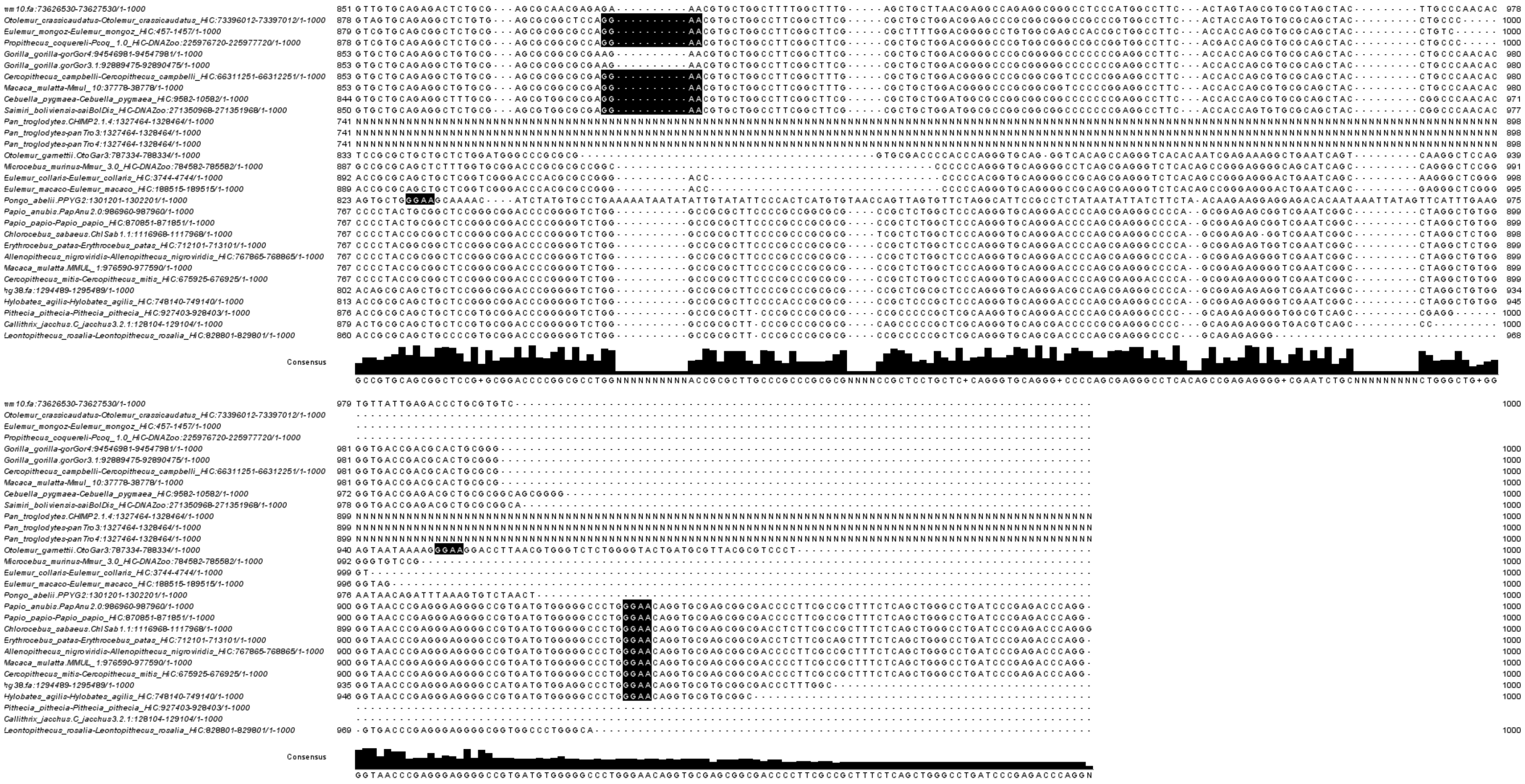


PRIMATES



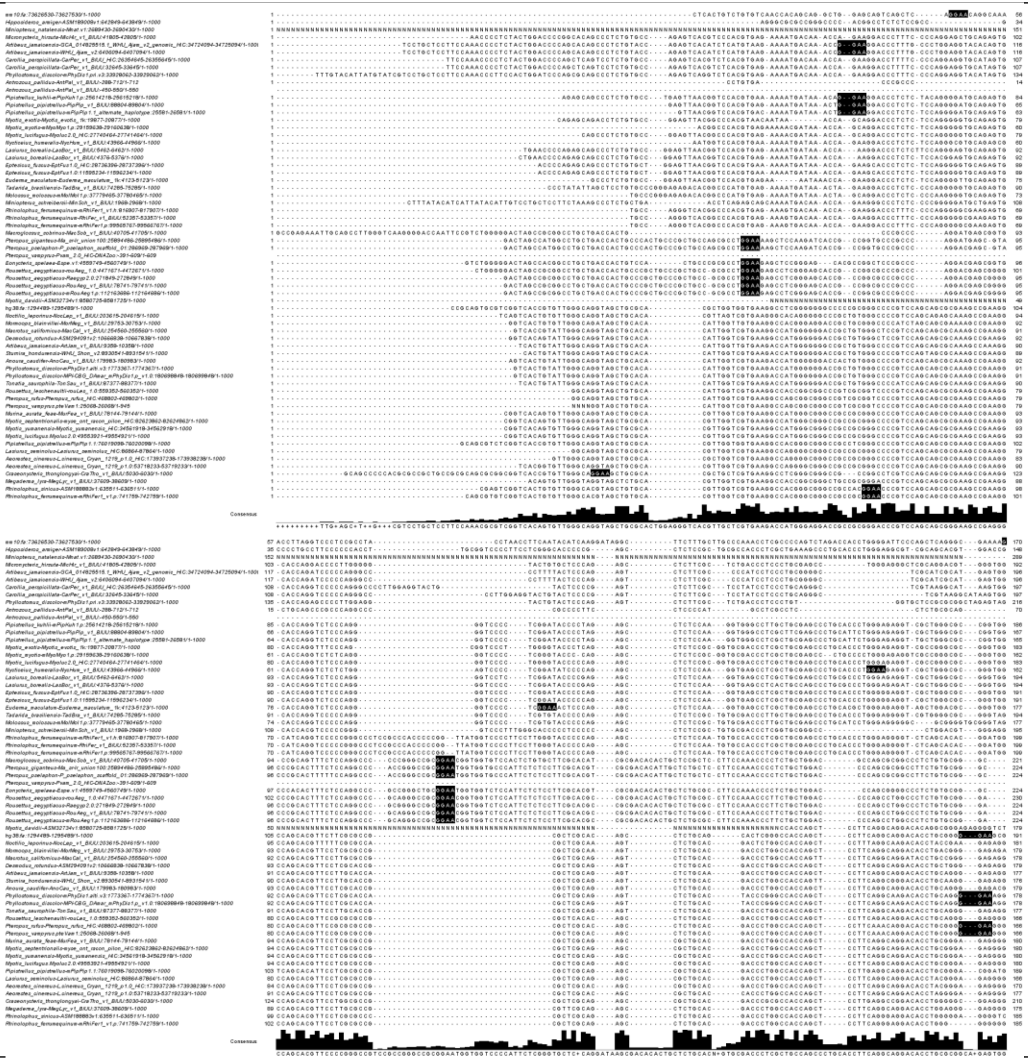


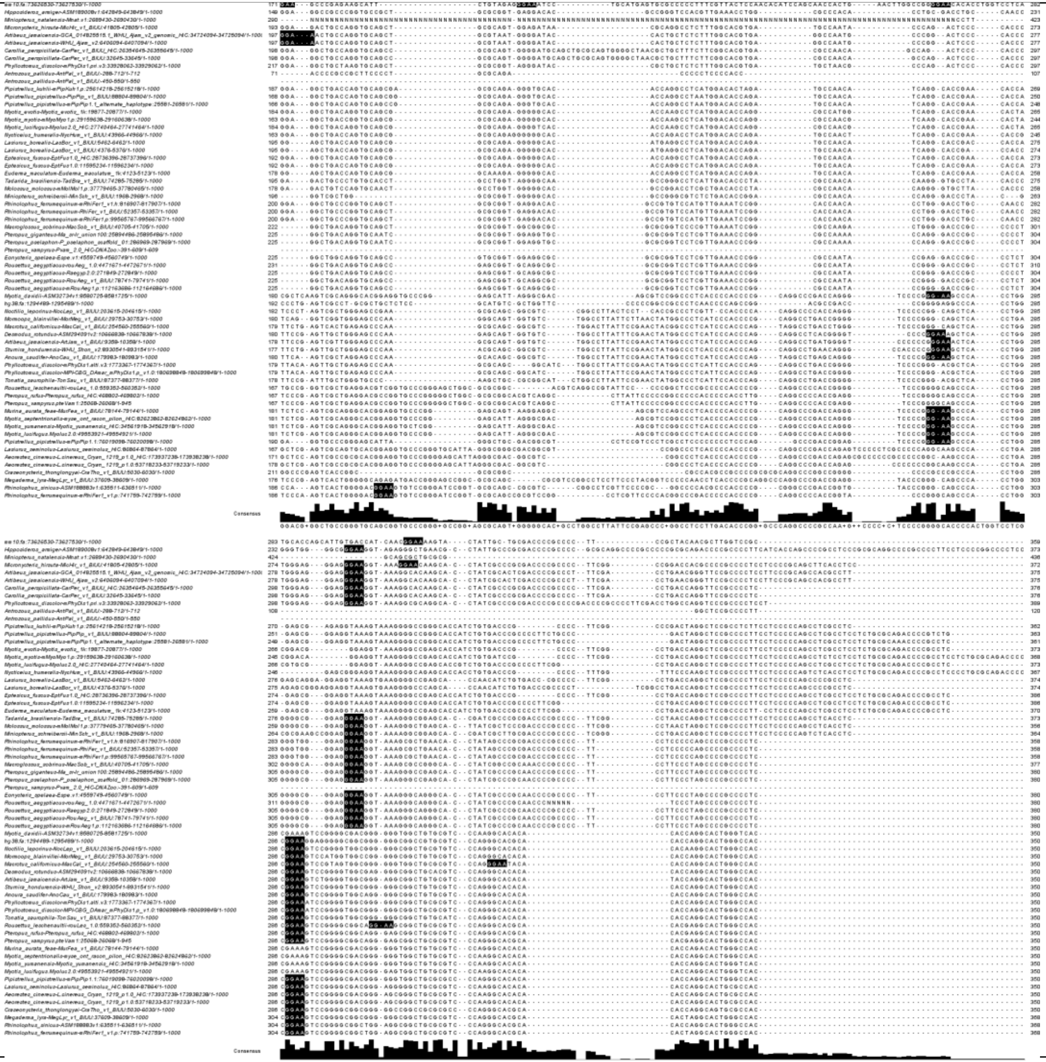

Consensus
Consensus
Consensus

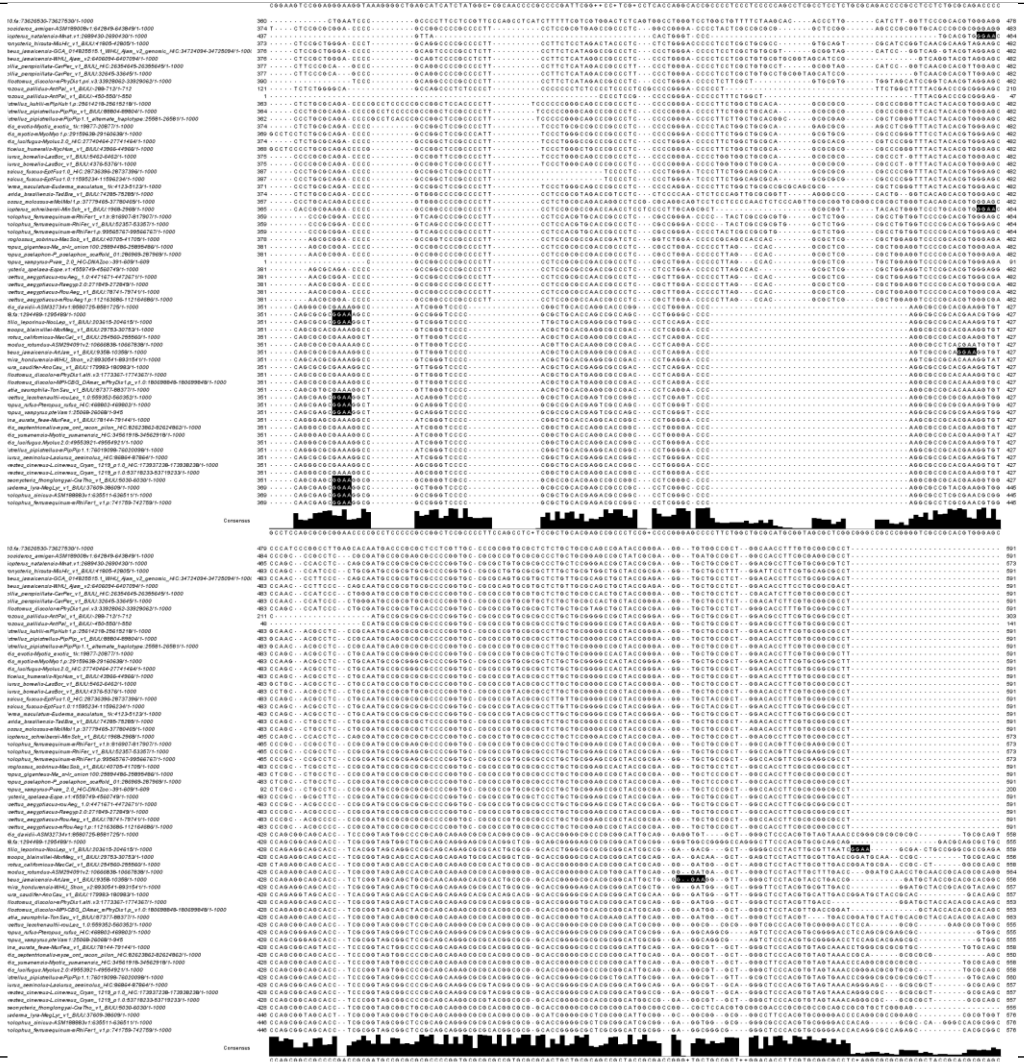


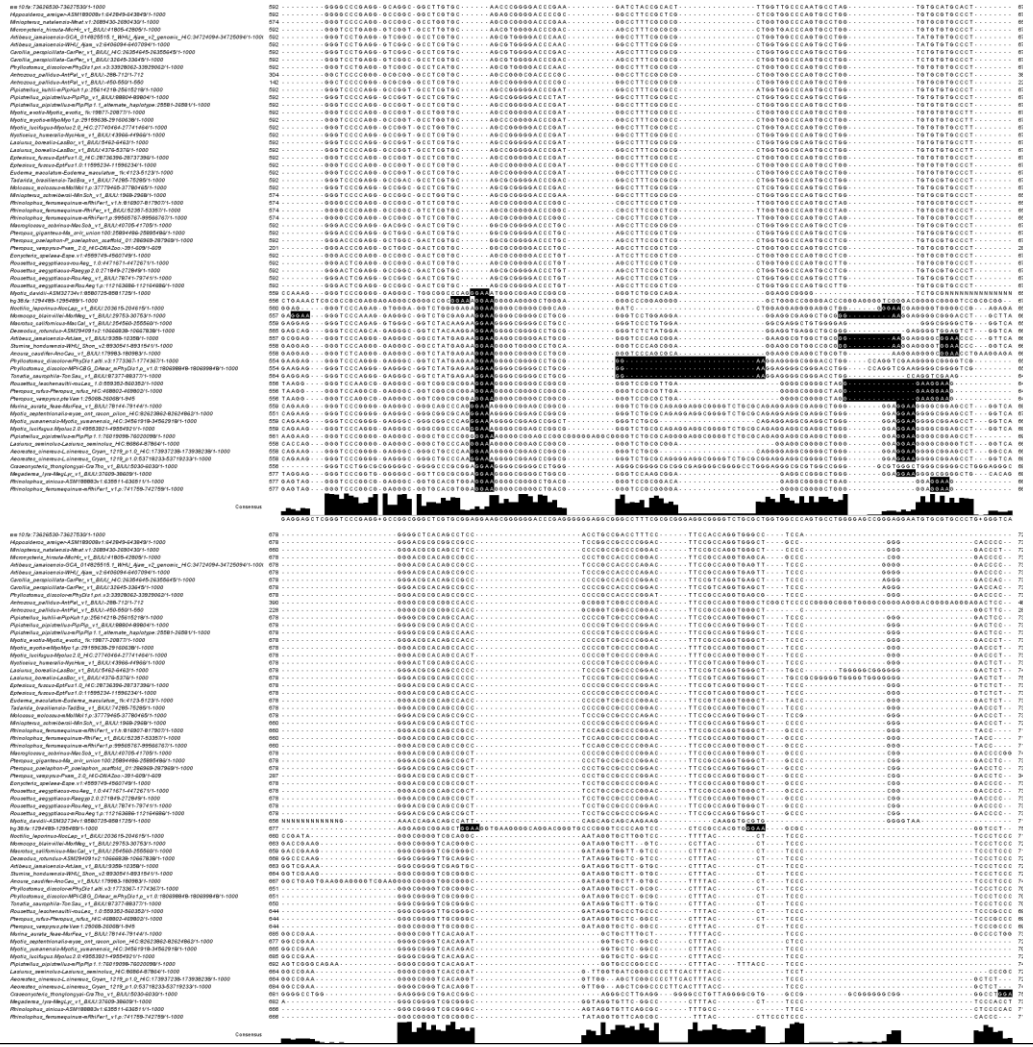
```
mm10.fa:73626530-73627530/1-1000 851 GTTGTGCAGAGACTCTGCG---AGCGCAACGAGAGA----------AACGTGCTGGCTTTTGGCTTTG-----AGCTGCTTAACGAGGCCAGAGGCGGGCCTCCCATGGCCTTC---ACTAGTAGCGTGCGTAGCTAC---------TTGCCCAACAC 978
Otolemur_crassicaudatus-Otolemur_crassicaudatus_HiC:73396012-73397012/1-1000 878 GTAGTGCAGAGGCTCTGTG---AGCGCGGCTCCAGG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGACGGAGCCCGCGGCGGGCCGCCCGTGGCCTTC---ACTACCAGTGTGCGCAGCTAC---------CTGCCC----- 1000
Eulemur_mongoz-Eulemur_mongoz_HiC:457-1457/1-1000 879 GTCGTGCAGCGGCTCTGCG---AGCGCGGCGCCAGG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTTTTGGACGGGGCCTGTGGCGAGCCACCGCTGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CTGTC------ 1000
Propithecus_coquereli-Pcoq_1.0_HiC-DNAZoo:225976720-225977720/1-1000 878 GTCGTGCAGAGGCTCTGCG---AGCGCGGCGCCAGG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGACGGGGCCCGTGGCGGGCCGCCGGTGGCCTTC---ACGACCAGCGTGCGCAGCTAC---------CTGCCC----- 1000
Gorilla_gorilla-gorGor4:94546981-94547981/1-1000 853 GTGCTGCAGAGGCTGTGCG---AGCGCGGCGCGAAG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CTGCCCAACAC 980
Gorilla_gorilla.gorGor3.1:92889475-92890475/1-1000 853 GTGCTGCAGAGGCTGTGCG---AGCGCGGCGCGAAG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CTGCCCAACAC 980
Cercopithecus_campbelli-Cercopithecus_campbelli_HiC:66311251-66312251/1-1000 853 GTGCTGCAGAGGCTGTGCG---AGCGCGGCGCGAGG----------AACGTGCTGGCCTTCGGCTTTG-----CGCTGCTGGACGGGGCCCGCGGCGGTCCCCCGGAGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CTGCCCAACAC 980
Macaca_mulatta-Mmul_10:37778-38778/1-1000 853 GTGCTGCAGAGGCTGTGCG---AGCGCGGCGCGAGG----------AACGTGCTGGCCTTCGGCTTTG-----CGCTGCTGGACGGGGCCCGCGGCGGTCCCCCGGAGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CTGCCCAACAC 980
Cebuella_pygmaea-Cebuella_pygmaea_HiC:9582-10582/1-1000 844 GTGCTGCAGAGGCTTTGCG---AGCGTGGCGCGAGG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGATGGCGCCGGCGGCGGCCCCCCCGAGGCCTTC---ACCACCAGCGTGCGCAGCTAC---------CGGCCCAACAC 971
Saimiri_boliviensis-saiBolDis_HiC-DNAZoo:271350968-271351968/1-1000 850 GTGCTGCAGAGGCTCTGCG---AGCGTGGCGCGAGG----------AACGTGCTGGCCTTCGGCTTCG-----CGCTGCTGGATGGCGCCGGCGGCGGCCCCCCCGAGGCCTTC---ACCACCAGTGTGCGCAGCTAC---------CGGCCCAACAC 977
Pan_troglodytes.CHIMP2.1.4:1327464-1328464/1-1000 741 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 898
Pan_troglodytes-panTro3:1327464-1328464/1-1000 741 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 898
Pan_troglodytes-panTro4:1327464-1328464/1-1000 741 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 898
Otolemur_garnettii.OtoGar3:787334-788334/1-1000 833 TCCGCGCTGCTGCTCTGGATGGGCCCGCGCG-----------------------------------------GTGCGACCCCACCCAGGGTGCAG-GGTCACAGCCAGGGTCACACAATCGAGAAAGGCTGAATCAGT---------CAAGGCTCCAG 939
Microcebus_murinus-Mmur_3.0_HiC-DNAZoo:784582-785582/1-1000 887 GCCGCGCAGCTCTTTGGTGCGGACCCGCGCGCCGGC--------------------------------------------CCCCCCAGGGTGCAGGGGCCTCAGCGAGGGTCTCACAGCCGGGAGGGGCAGCATCAGC---------CAGGGCTCCGG 991
Eulemur_collaris-Eulemur_collaris_HiC:3744-4744/1-1000 892 ACCGCGCAGCTGCTCGGTCGGGACCCACGCGCCGGG----------ACC--------------------------------CCCCCACGGTGCAGGGGCCGCAGCGAGGGTCTCACAGCCGGGAGGGACTGAATCAGC---------AAGGGCTCGGG 998
Eulemur_macaco-Eulemur_macaco_HiC:188515-189515/1-1000 889 ACCGCGCAGCTGCTCGGTCGGGACCCACGCGCCGGG----------ACC--------------------------------CCCCCAGGGTGCAGGGGCCGCAGCGAGGGTCTCACAGCCGGGAGGGACTGAATCAGC---------GAGGGCTCGGG 995
Pongo_abelii.PPYG2:1301201-1302201/1-1000 823 AGTGCTGGGAAGCAAAAC----ATCTATGTGCCTGAAAAATAATATATTGTATATTCCCACTCATGTGTAACCAGTTAGTGTTCTAGGCATTCCGCCTCTATAATATTATCTTCTA-ACAAGAAGGAGGAGACACAATAAATTATAGTTCATTTGAAG 975
Papio_anubis.PapAnu2.0:986960-987960/1-1000 767 CCCCTACTGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCGGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGCGGTCGAATCGGC---------CTAGGCTGTGG 899
Papio_papio-Papio_papio_HiC:870851-871851/1-1000 767 CCCCTACTGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGCGGTCGAATCGGC---------CTAGGCTGTGG 899
Chlorocebus_sabaeus.ChlSab1.1:1116968-1117968/1-1000 767 CCCCTACCGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----TCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAG-GGTCGAATCGGC---------CTAGGCTCTGG 898
Erythrocebus_patas-Erythrocebus_patas_HiC:712101-713101/1-1000 767 CCCCTACGGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGTGGTCGAATCGGC---------CTAGGCTCTGG 899
Allenopithecus_nigroviridis-Allenopithecus_nigroviridis_HiC:767865-768865/1-1000 767 CCCCTACCGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGGGGTCGAATCGGC---------CTAGGCTGTGG 899
Macaca_mulatta.MMUL_1:976590-977590/1-1000 767 CCCCTACCGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGGGGTCGAATCGGC---------CTAGGCTGTGG 899
Cercopithecus_mitis-Cercopithecus_mitis_HiC:675925-676925/1-1000 767 CCCCTACCGCGGCTCCGGGCGGACCCCGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCTGGCTCCCAGGGTGCAGGGACCCCAGCGAGGACCCCA--GCGGAGAGGGGTCGAATCGGC---------CTAGGCTGTGG 899
hg38.fa:1294489-1295489/1-1000 802 ACAGCGCAGCTGCTCCGGGCGGACCCGGGGGTCTGG----------GCCGCGCTTCCCCGCCCGCGCG----CCGCTCGCGCTCCCAGGGTGCAGGGACGCCAGCGAGGGCCCCA--GCGGAGAGAGGTCGAATCGGC---------CTAGGCTGTGG 934
Hylobates_agilis-Hylobates_agilis_HiC:748140-749140/1-1000 813 ACCGCGCAGCTGCTCCGGGCGGACCCGGGGGTCTGG----------GCCGCGCTTCCCCACCCGCGCG----CCGCTCCCGCTCCCAGGGTGCAGGGACCCCAGCGAGGGCCCCA--GCGGAGAGGGGTCGAATCGGC---------CTAGGCTGTGG 945
Pithecia_pithecia-Pithecia_pithecia_HiC:927403-928403/1-1000 876 ACCGCGCAGCTGCTCCGTGCGGACCCGGGGGTCTGG----------GCCGCGCTT-CCCGCCCGCGCG----CCGCCCCCGCTCGCAAGGTGCAGGGACCCCAGCGAGGGCCCC---GCAGAGAGGGGTGGCGTCAGC---------CGAGG------ 1000
Callithrix_jacchus.C_jacchus3.2.1:128104-129104/1-1000 879 ACTGCGCAGCTGCTCCGTGCGGACCCGGGGGTCTGG----------GCCGCGCTT-CCCGCCCGCGCG----CAGCCCCCGCTCGCAGGGTGCAGCGACCCCCGCGAGGGCCCC---GCAGAGAGGGGTGACGTCAGC---------CC--------- 1000
Leontopithecus_rosalia-Leontopithecus_rosalia_HiC:828801-829801/1-1000 860 ACCGCGCAGCTGCCCCGTGCGGACCCGGGGGTCTGG----------GCCGCGCTT-CCCGCCCGCGCG----CCGCCCCCGCTCGCAGGGTGCAGCGACCCCAGCGAGGGCCCC---GCAGAGAGGG------------------------------- 968

Consensus
GCCGTGCAGCGGCTCCG+GCGGACCCCGGCGCCTGGNNNNNNNNNNACCGCGCTTGCCCGCCCGCGCGNNNNCCGCTCCTGCTC+CAGGGTGCAGGG+CCCCAGCGAGGGCCTCACAGCCGAGAGGGG+CGAATCTGCNNNNNNNNNCTGGGCTG+GG

mm10.fa:73626530-73627530/1-1000 979 TGTTATTGAGACCCTGCGTGTC-------------------------------------------------------------------------------- 1000
Otolemur_crassicaudatus-Otolemur_crassicaudatus_HiC:73396012-73397012/1-1000 ------------------------------------------------------------------------------------------------------
Eulemur_mongoz-Eulemur_mongoz_HiC:457-1457/1-1000 ------------------------------------------------------------------------------------------------------
Propithecus_coquereli-Pcoq_1.0_HiC-DNAZoo:225976720-225977720/1-1000 ------------------------------------------------------------------------------------------------------
Gorilla_gorilla-gorGor4:94546981-94547981/1-1000 981 GGTGACCGACGCACTGCGGG---------------------------------------------------------------------------------- 1000
Gorilla_gorilla.gorGor3.1:92889475-92890475/1-1000 981 GGTGACCGACGCACTGCGGG---------------------------------------------------------------------------------- 1000
Cercopithecus_campbelli-Cercopithecus_campbelli_HiC:66311251-66312251/1-1000 981 GGTGACCGACGCACTGCGCG---------------------------------------------------------------------------------- 1000
Macaca_mulatta-Mmul_10:37778-38778/1-1000 981 GGTGACCGACGCACTGCGCG---------------------------------------------------------------------------------- 1000
Cebuella_pygmaea-Cebuella_pygmaea_HiC:9582-10582/1-1000 972 GGTGACCGAGACGCTGCGCGGCAGCGGGG------------------------------------------------------------------------- 1000
Saimiri_boliviensis-saiBolDis_HiC-DNAZoo:271350968-271351968/1-1000 978 GGTGACCGAGACGCTGCGCGGCA------------------------------------------------------------------------------- 1000
Pan_troglodytes.CHIMP2.1.4:1327464-1328464/1-1000 899 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1000
Pan_troglodytes-panTro3:1327464-1328464/1-1000 899 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1000
Pan_troglodytes-panTro4:1327464-1328464/1-1000 899 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1000
Otolemur_garnettii.OtoGar3:787334-788334/1-1000 940 AGTAATAAAAGGGAAGGACCTTAACGTGGGTCTCTGGGGTACTGATGCGTTACGCGTCCCT----------------------------------------- 1000
Microcebus_murinus-Mmur_3.0_HiC-DNAZoo:784582-785582/1-1000 992 GGGTGTCCG--------------------------------------------------------------------------------------------- 1000
Eulemur_collaris-Eulemur_collaris_HiC:3744-4744/1-1000 999 GT---------------------------------------------------------------------------------------------------- 1000
Eulemur_macaco-Eulemur_macaco_HiC:188515-189515/1-1000 996 GGTAG------------------------------------------------------------------------------------------------- 1000
Pongo_abelii.PPYG2:1301201-1302201/1-1000 976 AATAACAGATTTAAAGTGTCTAACT----------------------------------------------------------------------------- 1000
Papio_anubis.PapAnu2.0:986960-987960/1-1000 900 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
Papio_papio-Papio_papio_HiC:870851-871851/1-1000 900 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
Chlorocebus_sabaeus.ChlSab1.1:1116968-1117968/1-1000 899 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCTCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGGG 1000
Erythrocebus_patas-Erythrocebus_patas_HiC:712101-713101/1-1000 900 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCTCTTCGCAGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
Allenopithecus_nigroviridis-Allenopithecus_nigroviridis_HiC:767865-768865/1-1000 900 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
Macaca_mulatta.MMUL_1:976590-977590/1-1000 900 GGTAACCGGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
Cercopithecus_mitis-Cercopithecus_mitis_HiC:675925-676925/1-1000 900 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGG- 1000
hg38.fa:1294489-1295489/1-1000 935 GGTAACCCGAGGGAGGGGCCATGATGTGGAGGCCCTGGGAACAGGTGCGTGCGGCGACCCTTTGGC------------------------------------ 1000
Hylobates_agilis-Hylobates_agilis_HiC:748140-749140/1-1000 946 GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGTGCGGC----------------------------------------------- 1000
Pithecia_pithecia-Pithecia_pithecia_HiC:927403-928403/1-1000 ------------------------------------------------------------------------------------------------------
Callithrix_jacchus.C_jacchus3.2.1:128104-129104/1-1000 ------------------------------------------------------------------------------------------------------
Leontopithecus_rosalia-Leontopithecus_rosalia_HiC:828801-829801/1-1000 969 -GTGACCCGAGGGAGGGGCGGTGGCCCTGGGCA--------------------------------------------------------------------- 1000

Consensus
GGTAACCCGAGGGAGGGGCCGTGATGTGGGGGCCCTGGGAACAGGTGCGAGCGGCGACCCCTTCGCCGCTTTCTCAGCTGGGCCTGATCCCGAGACCCAGGN
```

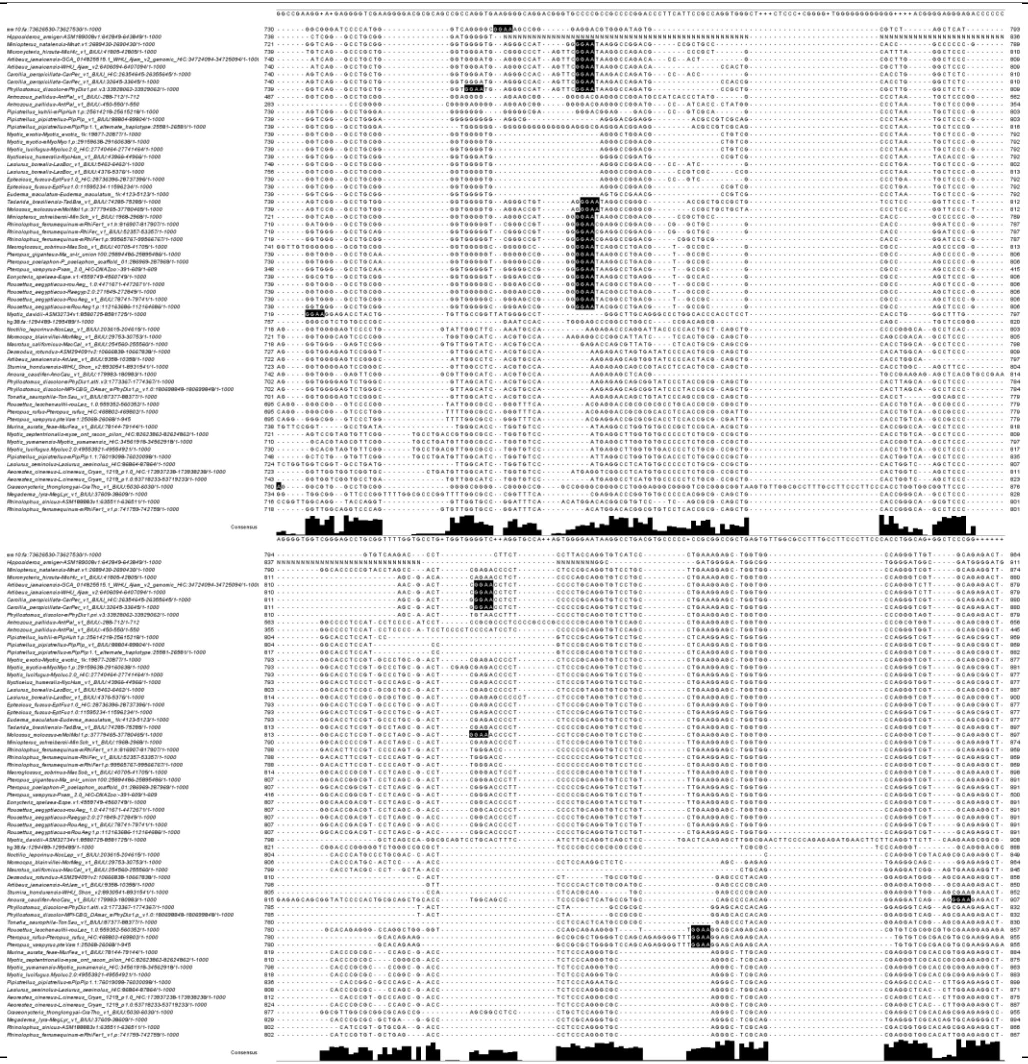
CHIROPTERA

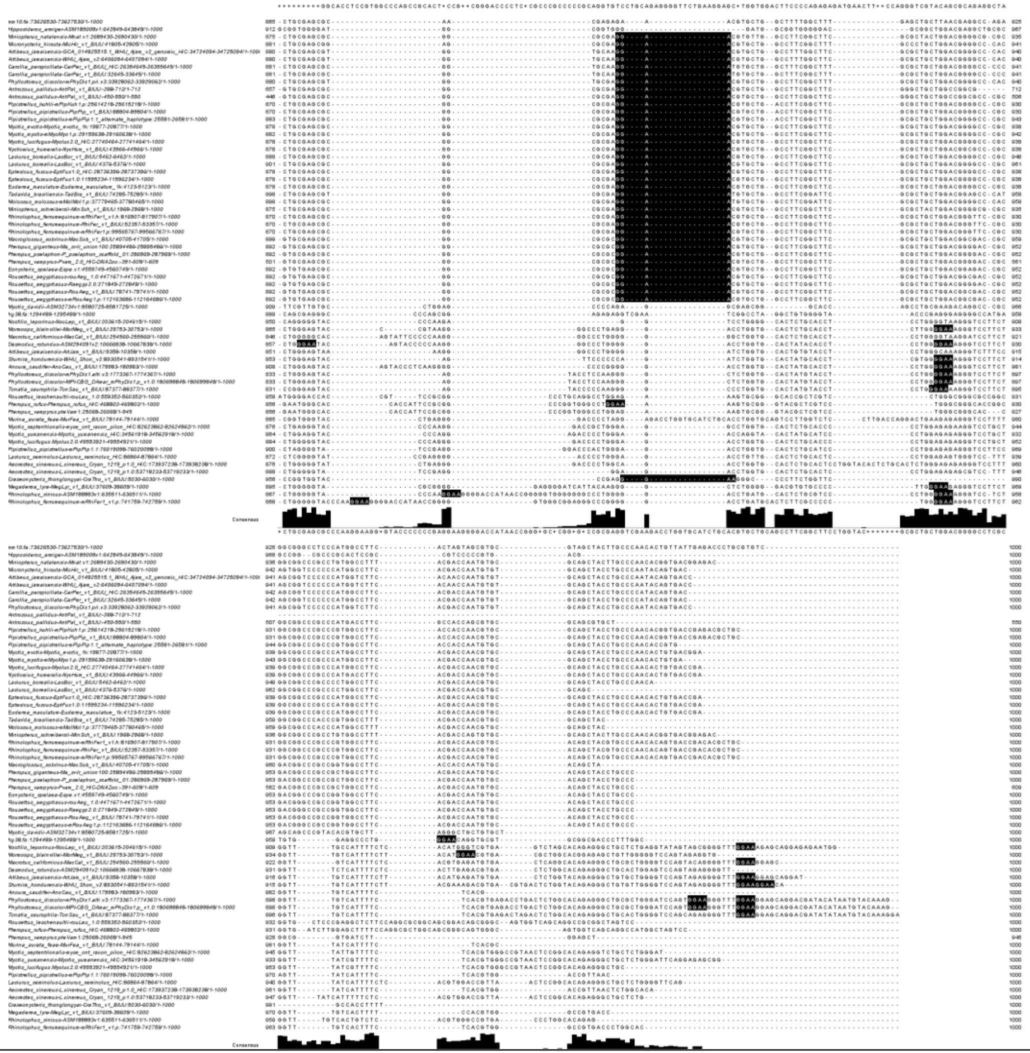




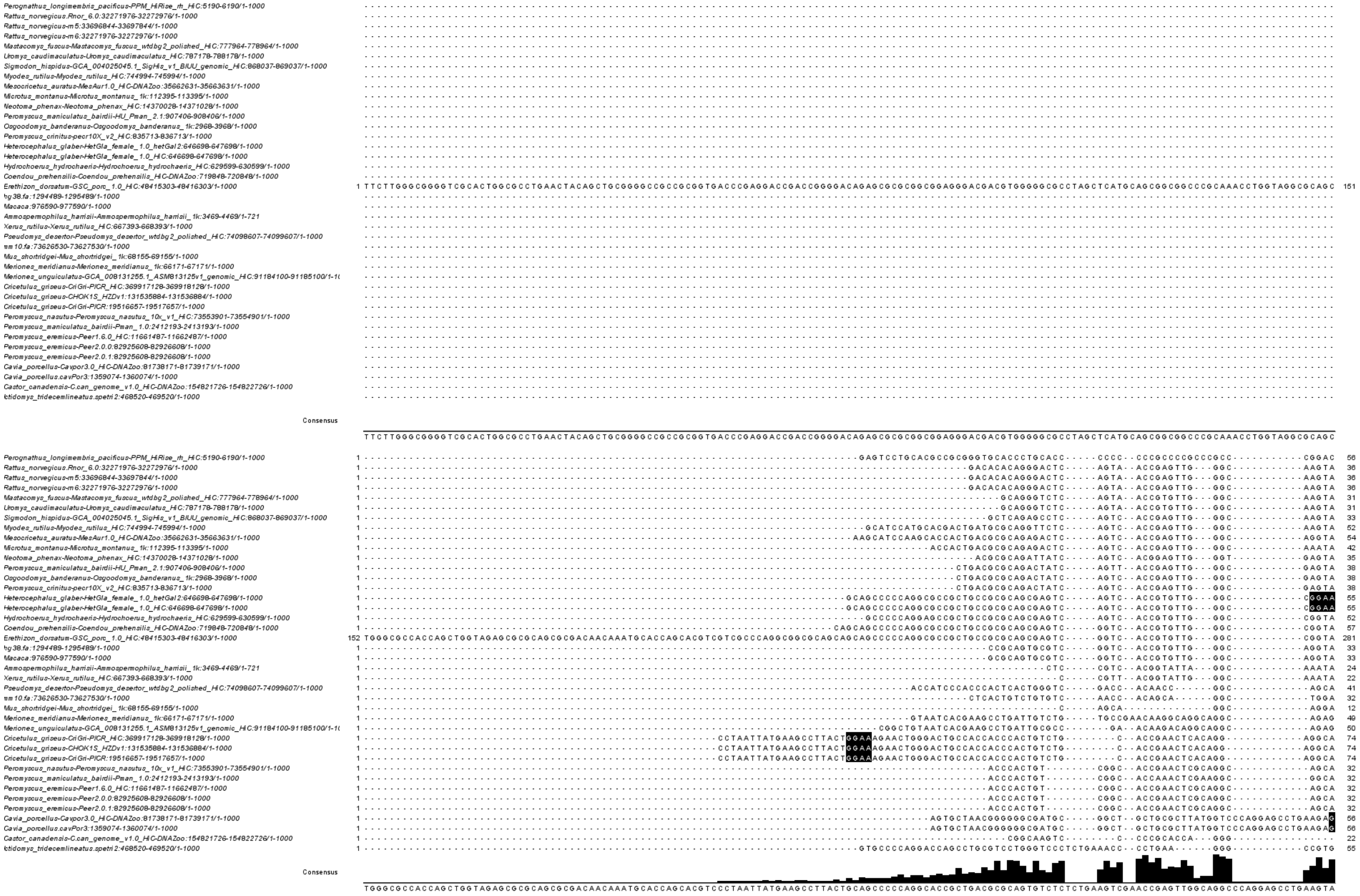


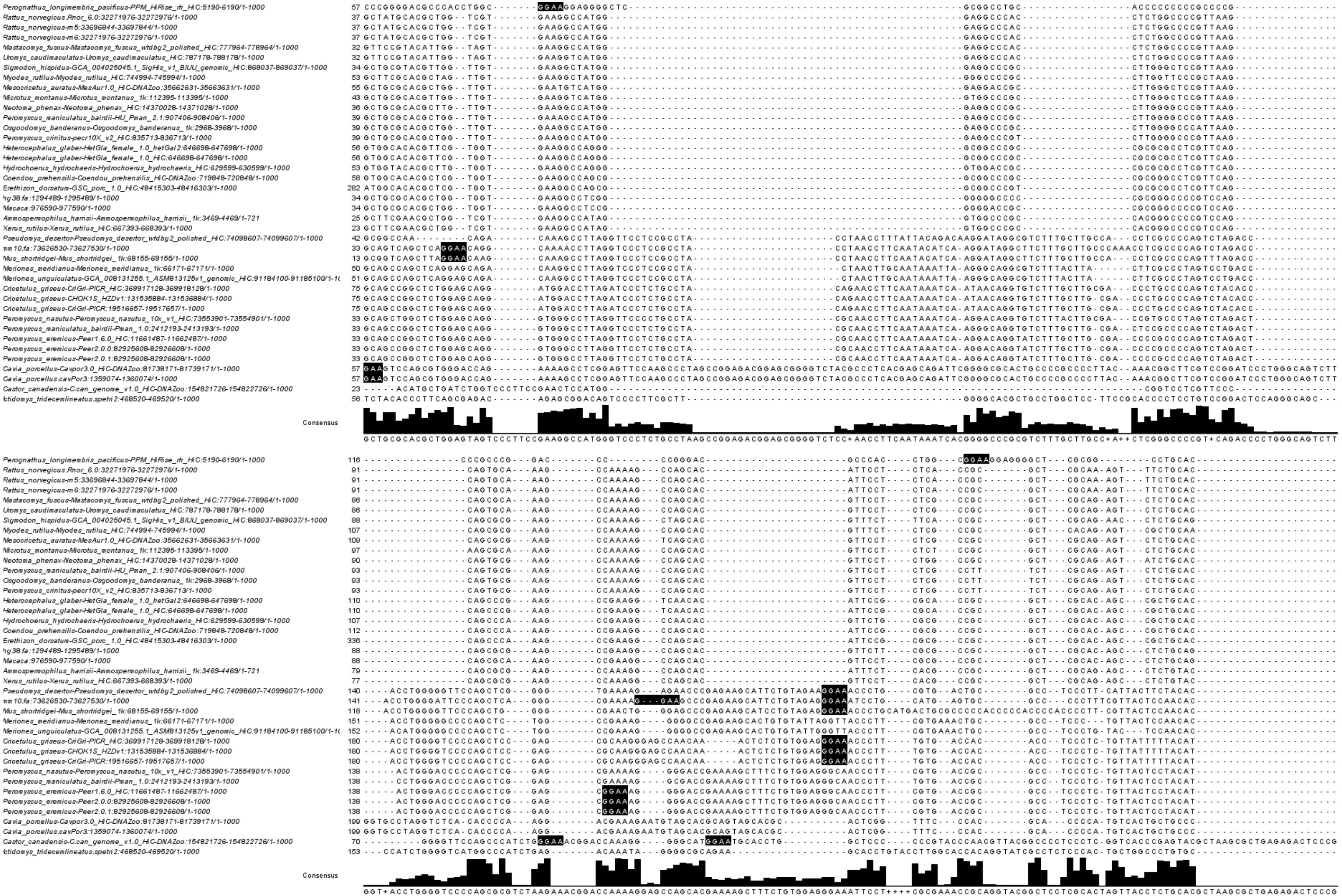


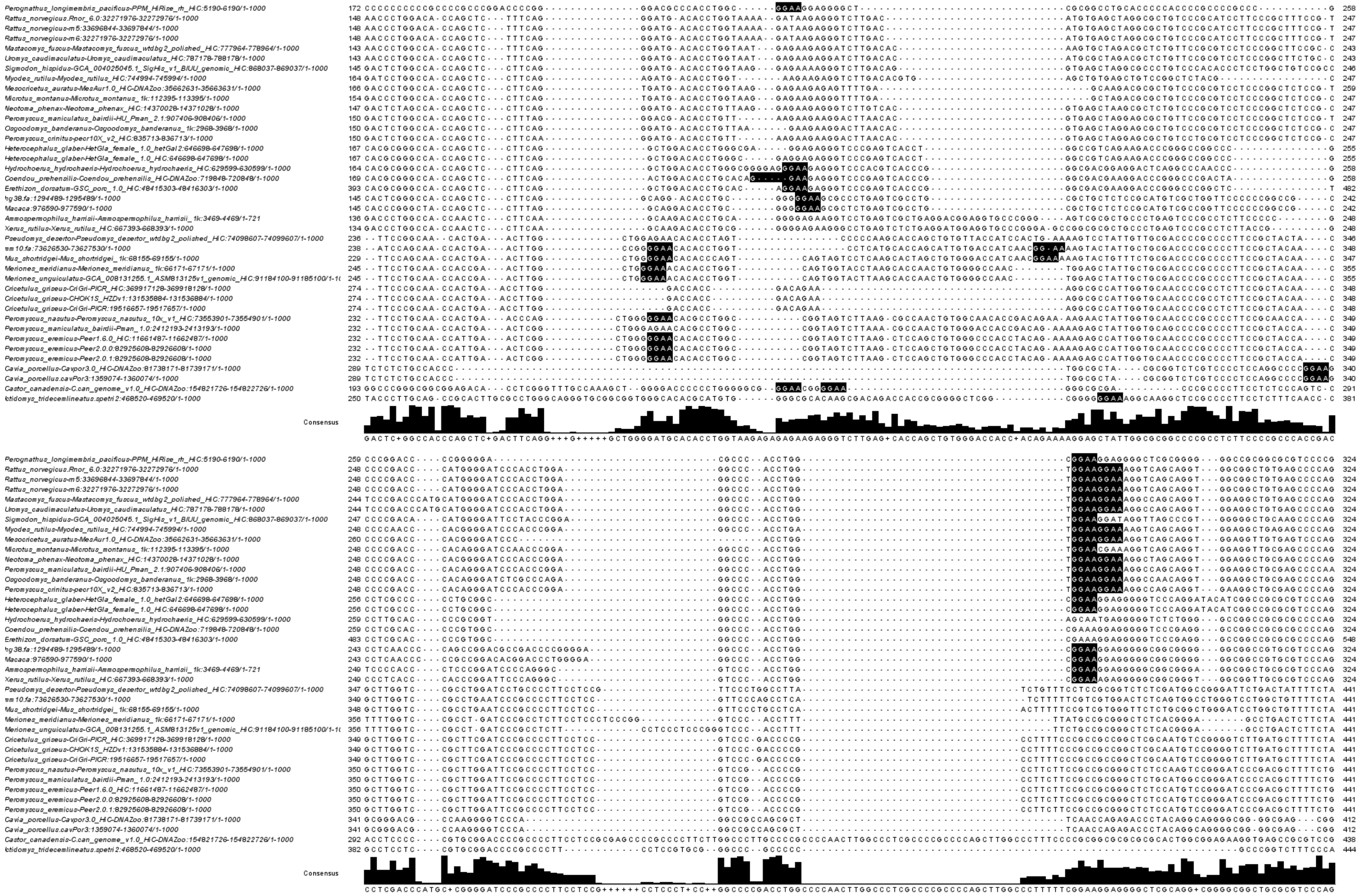


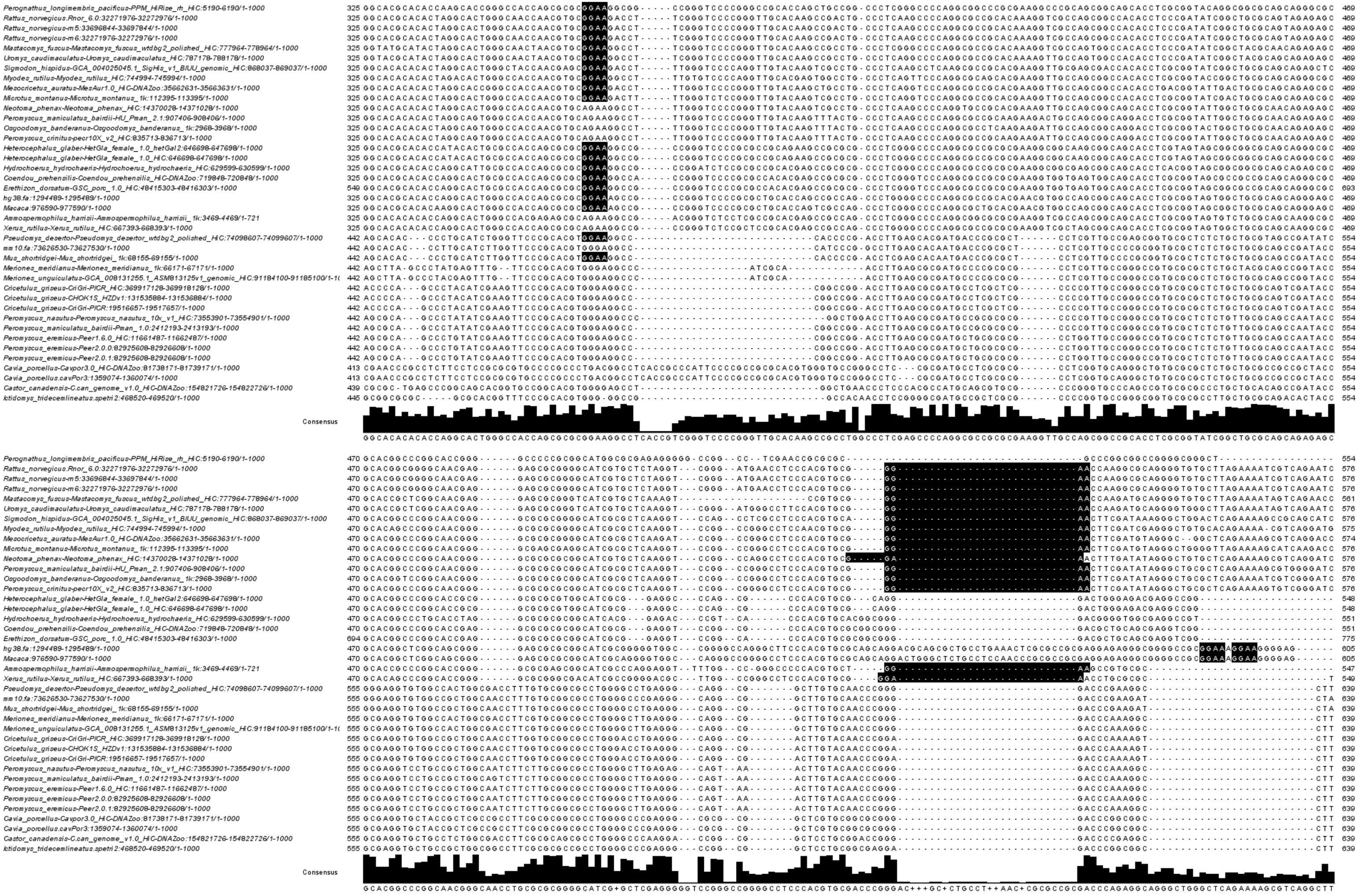

Consensus
Consensus

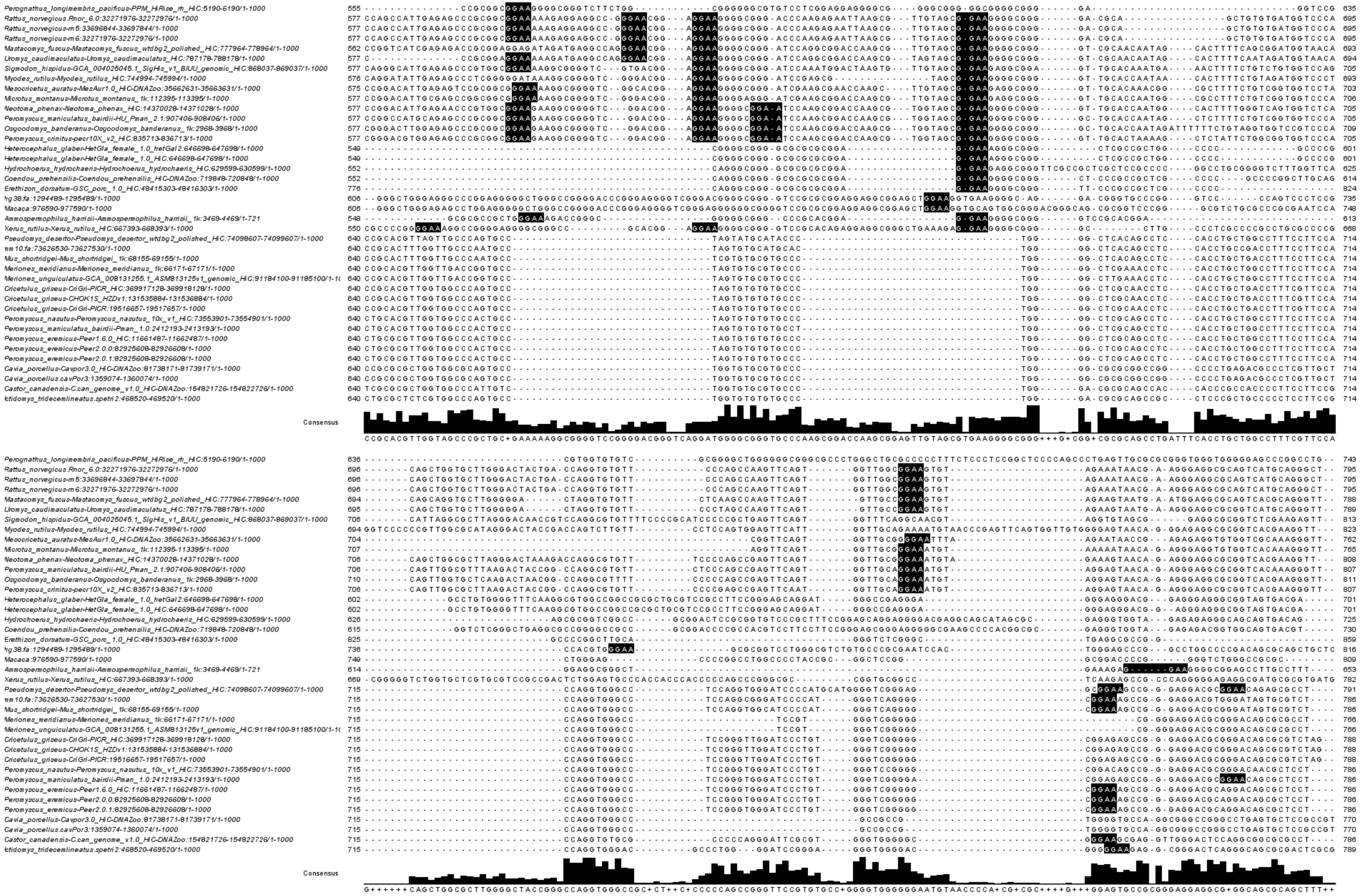
RODENTS

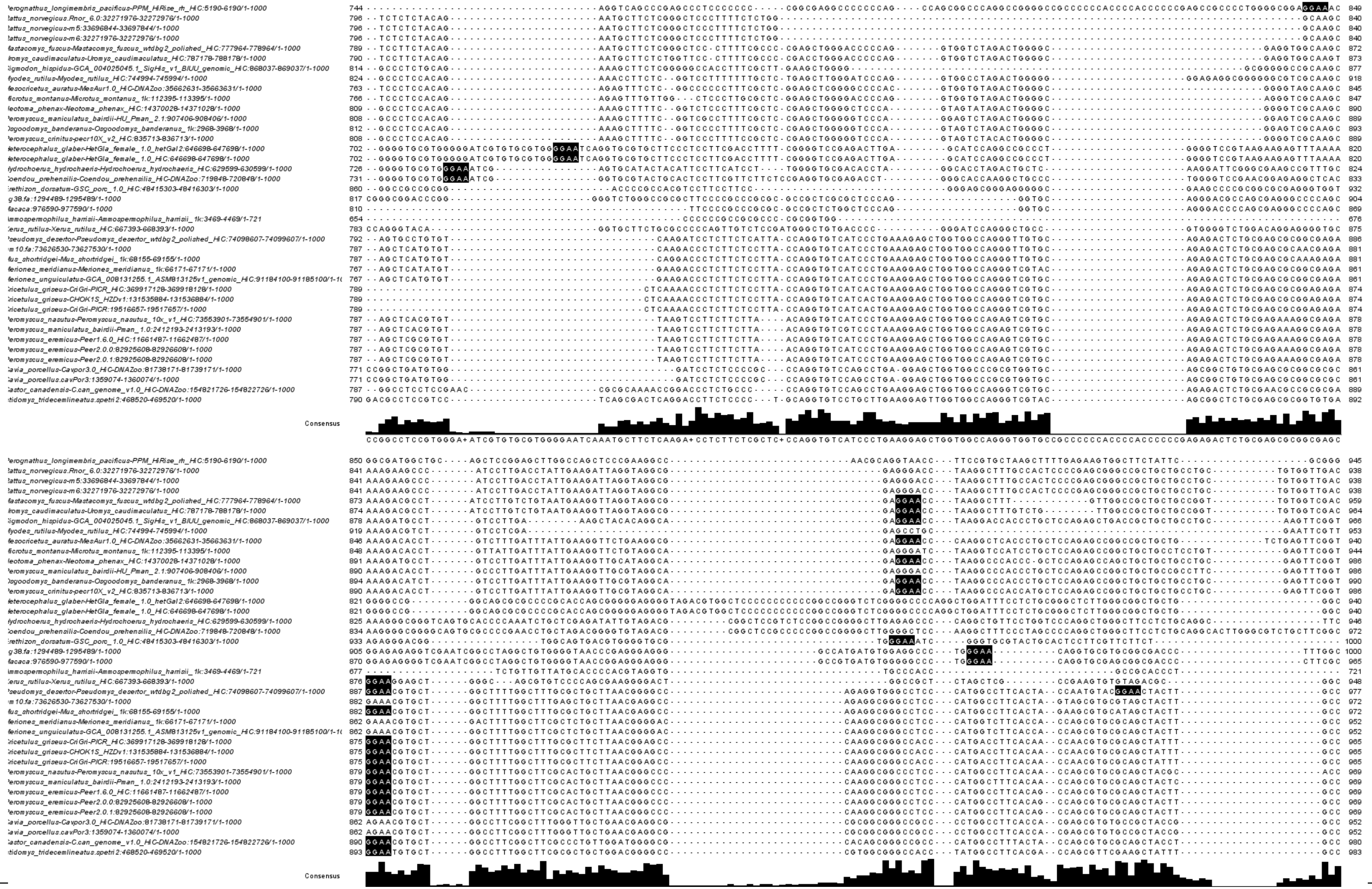



Perognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000
Rattus_norvegicus.Rnor_6.0:32271976-32272976/1-1000
Rattus_norvegicus-rn5:33696844-33697844/1-1000
Rattus_norvegicus-rn6:32271976-32272976/1-1000
Mastacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000
Uromys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000
Sigmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000
Myodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000
Mesocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000
Microtus_montanus-Microtus_montanus_1k:112395-113395/1-1000
Neotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000
Peromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000
Osgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000
Peromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000
Heterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000
Heterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000
Hydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000
Coendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000
Erethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000
hg38.fa:1294489-1295489/1-1000
Macaca:976590-977590/1-1000
Ammospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721
Xerus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000
Pseudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000
mm10.fa:73626530-73627530/1-1000
Mus_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000
Meriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000
Meriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1
Cricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000
Cricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000
Cricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000
Peromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000
Peromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000
Peromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000
Peromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000
Peromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000
Cavia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000
Cavia_porcellus.cavPor3:1359074-1360074/1-1000
Castor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000
ctidomys_tridecemlineatus.spetri2:468520-469520/1-1000
Consensus


Consensus
Consensus


Perognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000
Rattus_norvegicus.Rnor_6.0:32271976-32272976/1-1000
Rattus_norvegicus-rn5:33696844-33697844/1-1000
Rattus_norvegicus-rn6:32271976-32272976/1-1000
Mastacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000
Uromys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000
Sigmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000
Myodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000
Mesocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000
Microtus_montanus-Microtus_montanus_1k:112395-113395/1-1000
Neotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000
Peromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000
Osgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000
Peromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000
Heterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000
Heterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000
Hydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000
Coendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000
Erethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000
hg38.fa:1294489-1295489/1-1000
Macaca:976590-977590/1-1000
Ammospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721
Xerus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000
Pseudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000
mm10.fa:73626530-73627530/1-1000
Mus_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000
Meriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000
Meriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1(
Cricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000
Cricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000
Cricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000
Peromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000
Peromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000
Peromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000
Peromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000
Peromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000
Cavia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000
Cavia_porcellus.cavPor3:1359074-1360074/1-1000
Castor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000
Ictidomys_tridecemlineatus.spetri2:468520-469520/1-1000
Consensus
GGCACACACACCAGGCACTGGGCCACCAGCGCGCGGAAGGCCTCACCGTCGGGTCCCCGGGTTGCACAAGCCGCCTGGCCCTCGAGCCCCAGGCGCCGCGCGAAGGTTGCCAGCGGCCGCACCTCGCGGTATCGGCTGCGCAGCAGAGAGC
Consensus
GCACGGCCCGGCAACGGGCAACCTGCGCGCGGGGCATCG+GCTCGAGGGGGTCCGGGCCGGGGCCTCCCACGTGCGACCCGGGAC+++GC+CTGCCT++AAC+CGCGCCGCGACCCAGAGGCAGGGCTGGGCTCAGAAAAGCGTCAGGCTT


Perognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000
Rattus_norvegicus.Rnor_6.0:32271976-32272976/1-1000
Rattus_norvegicus-m5:33696844-33697844/1-1000
Rattus_norvegicus-m6:32271976-32272976/1-1000
Mastacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000
Uromys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000
Sigmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000
Myodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000
Mesocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000
Microtus_montanus-Microtus_montanus_1k:112395-113395/1-1000
Neotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000
Peromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000
Osgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000
Peromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000
Heterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000
Heterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000
Hydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000
Coendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000
Erethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000
hg38.fa:1294489-1295489/1-1000
Macaca:976590-977590/1-1000
Ammospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721
Xerus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000
Pseudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000
mm10.fa:73626530-73627530/1-1000
Mus_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000
Meriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000
Meriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1
Cricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000
Cricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000
Cricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000
Peromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000
Peromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000
Peromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000
Peromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000
Peromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000
Cavia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000
Cavia_porcellus.cavPor3:1359074-1360074/1-1000
Castor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000
ctidomys_tridecemlineatus.spetri2:468520-469520/1-1000
Consensus
Perognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000
Rattus_norvegicus.Rnor_6.0:32271976-32272976/1-1000
Rattus_norvegicus-m5:33696844-33697844/1-1000
Rattus_norvegicus-m6:32271976-32272976/1-1000
Mastacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000
Uromys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000
Sigmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000
Myodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000
Mesocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000
Microtus_montanus-Microtus_montanus_1k:112395-113395/1-1000
Neotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000
Peromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000
Osgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000
Peromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000
Heterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000
Heterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000
Hydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000
Coendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000
Erethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000
hg38.fa:1294489-1295489/1-1000
Macaca:976590-977590/1-1000
Ammospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721
Xerus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000
Pseudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000
mm10.fa:73626530-73627530/1-1000
Mus_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000
Meriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000
Meriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1
Cricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000
Cricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000
Cricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000
Peromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000
Peromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000
Peromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000
Peromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000
Peromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000
Cavia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000
Cavia_porcellus.cavPor3:1359074-1360074/1-1000
Castor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000
ctidomys_tridecemlineatus.spetri2:468520-469520/1-1000
Consensus



```
erognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000 744 -----------------------------------AGGTCAGCCCGAGCCCTCCCCCCC----CGGCGAGGCCCCCCCAG----CCAGCGGCCCAGGCCGGGGCCGCCCCCCACCCCACCCCCCGAGCCGCCCCTGGGGCGGAGGAAAC 849
attus_norvegicus.Rnor_6.0:32271976-32272976/1-1000 796 --TCTCTCTACAG----------------------AATGCTTCTCGGGCTCCCTTTTCTCTGG--------------------------------------------------------------------------------GCAAGC 840
attus_norvegicus-m5:33696844-33697844/1-1000 796 --TCTCTCTACAG----------------------AATGCTTCTCGGGCTCCCTTTTCTCTGG--------------------------------------------------------------------------------GCAAGC 840
attus_norvegicus-m6:32271976-32272976/1-1000 796 --TCTCTCTACAG----------------------AATGCTTCTCGGGCTCCCTTTTCTCTGG--------------------------------------------------------------------------------GCAAGC 840
astacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000 789 --TCCTTCTACAG----------------------AATGCTTCTCGGGCTCC-CTTTTCGCCC-CGAGCTGGGACCCCCAG-------GTGGTCTAGACTGGGGC--------------------------------GAGGTGGCAAGC 872
romys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000 790 --TCCTTCTACAG----------------------AATGCTTCTCTGGTTCC-CTTTTCGCCC-CGACCTGGGACCCCCAG-------GTGGTCTAGACTGGGGC--------------------------------GAGGTGGCAAGT 873
igmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000 814 --GCCCTCTGCAG----------------------AAAGCTTCTCGGGGGCCACCTTTCGCTT-GAAGCTGGGG------------------------------------------------------------GCGGGGGCCGCAAGC 877
yodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000 824 --GCCCTCCACAG----------------------AAACCTTCTC--GGTCCTTTTTTTGCTC-TGAGCTTGGGATCCCAG-------GTGGCCTAGACTGGGGG---------------------GGAGAGGCGGGGGCGTCGCAAGC 918
esocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000 763 --TCCCTCCACAG----------------------AGAGTTTCTC--GGCCCCCCTTTCGCTC-GGAGCTCGGGGCCCCAC-------GTGGTGTAGACTGGGGC--------------------------------GGGGTAGCAAGC 845
icrotus_montanus-Microtus_montanus_1k:112395-113395/1-1000 766 --TCCCTCCACAG----------------------AGAGTTTGTTGG---CTCCCTTGCGCTC-GGAGCTGGGGACCCCAG-------GTGGTGTAGACTGGGGC--------------------------------AGGGTCGCAAGC 847
eotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000 809 --GCCCTCCACAG----------------------AAAGCTTTTC--GGTCTCCCTTTCGCTC-CGAGCTGGGGCTCCCA--------GTAGTATAGACTGGGGC--------------------------------GGGGTCGCAAGC 890
eromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000 808 --GCCCTCCACAG----------------------AAAGCTTTTC--GGTCGCCTTTTCGCTC-CGAGCTGGGGGTCCCA--------GGAGTCTAGACTGGGGC--------------------------------GGAGTCGCAAGC 889
sgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000 812 --GCCCTCCACAG----------------------AAAGCTTTTC--GGTCCCCTTTTCGCTC-CGAGCTGGGGGTCCCA--------GTAGTCTAGACTGGGGC--------------------------------GGAGTCGCAAGC 893
eromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000 808 --GCCCTCCACAG----------------------AAAGCTTTTC--GGTCCCTTTTCCGCTC-CGAGCTGGGGGTCCCA--------GTAGTCTACACTGGGGC--------------------------------GGGGTCGCAAGC 889
eterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000 702 --GGGGTGCGTGGGGGATCGTGTGCGTGGGGAATCAGGTGCGTGCTTCCCTCCTTCGACCTTTT-CGGGGTCCGAGACTTGA--------GCATCCAGGCCGCCCT-------------------GGGGTCCGTAAGAAGAGTTTAAAA 820
eterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000 702 --GGGGTGCGTGGGGGATCGTGTGCGTGGGGAATCAGGTGCGTGCTTCCCTCCTTCGACCTTTT-CGGGGTCCGAGACTTGA--------GCATCCAGGCCGCCCT-------------------GGGGTCCGTAAGAAGAGTTTAAAA 820
ydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000 726 --GGGGTGCGTGGAAATCG---------------AGTGCATACTACATTCCTTCATCCT----TGGGGTGCGACACCTA--------GGCACCTAGACTGCTC---------------------AAGGATTCGGGCGAAGCCGTTTGC 824
oendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000 731 --GGGGTGCGTGGAAATCG---------------GGTGCGTACTGCACTCCTTCGTTCTTCTCCGAGGTGCGAGACCT---------GGGCACCAAGGCTGCCC--------------------TGGGGTCCGAACGGAGAGGCTCAC 833
rethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000 860 --GGCCGCCGCGG------------------------ACCCCGCCACGTCCTTCCTTCC-----------------------------GGGAGCGGGAGGGGGC---------------------GAAGCCCCGCGGCGCGAGGGTGGT 932
g38.fa:1294489-1295489/1-1000 817 CGGGCGGACCCGG---------------------GGGTCTGGGCCGCGCTTCCCCGCCCGCGC-GCCGCTCGCGCTCCCAG------------------GGTGC---------------------AGGGACGCCAGCGAGGGCCCCAGC 904
acaca:976590-977590/1-1000 810 -------------------------------------------------TTCCCCGCCCGCGC-GCCGCTCTGGCTCCCAG------------------GGTGC---------------------AGGGACCCCAGCGAGGGCCCCAGC 869
mmospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721 654 ------------------------------------------------CCCCCCGCCGCGCCC-CGCGGTGG----------------------------------------------------------------------------- 676
erus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000 783 CCAGGGTACA-------------------------GGTGCTTCTGCGCCCCCAGTTGTCTCCGATGGGCTGTGACCCC----------GGGATCCAGGGCTGCC---------------------GTGGGGTCTGGACAGGAGGGGTGC 875
seudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000 792 --AGTGCCTGTGT-------------------------------CAAGATCCTCTTCTCATTA-CCAGGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGC--------------------AGAGACTCTGCGAGCGCGGCGAGA 886
m10.fa:73626530-73627530/1-1000 787 --AGCTCATGTGT-------------------------------CAAGACCCTCTTCTCCTTA-CCAGGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGC--------------------AGAGACTCTGCGAGCGCAACGAGA 881
us_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000 787 --AGCTCATGTGT-------------------------------CAGGACCCTCTTCTCCTTA-CCAGGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGC--------------------AGAGACTCTGCGAGCGCAAAGAGA 881
eriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000 767 --AGCTCATATGT-------------------------------GAAGACCCTCTTCTCCTTA-CCAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGGGTCGTAC--------------------AGAGACTCTGCGAGCGCGGCGAGA 861
eriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1 767 --AGCTCATGTGT-------------------------------GAAGACCCTCTTCTCCTTA-CCAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGGGTCGTGC--------------------AGAGACTCTGCGAGCGCGGCGAGA 861
ricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000 789 ------------------------------------------CTCAAAACCCTCTTCTCCTTA-CCAGGTGTCATCACTGAAGGAGCTGGTGGCCAGGGTCGTGC--------------------AGAGACTCTGCGAGCGCGGAGAGA 874
ricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000 789 ------------------------------------------CTCAAAACCCTCTTCTCCTTA-CCAGGTGTCATCACTGAAGGAGCTGGTGGCCAGGGTCGTGC--------------------AGAGACTCTGCGAGCGCGGAGAGA 874
ricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000 789 ------------------------------------------CTCAAAACCCTCTTCTCCTTA-CCAGGTGTCATCACTGAAGGAGCTGGTGGCCAGGGTCGTGC--------------------AGAGACTCTGCGAGCGCGGAGAGA 874
eromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000 787 --AGCTCACGTGT-------------------------------TAAGTCCTTCTTCTTA---ACAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGAGTCGTGC---------------------AGAGACTCTGCGAGAAAGGCGAGA 878
eromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000 787 --AGCTCACGTGT-------------------------------TAAGTCCTTCTTCTTA---ACAGGTGTCGTCCCTAAAGGAGCTGGTGGCCAGAGTCGTGC---------------------AGAGACTCTGCGAGAAAGGCGAGA 878
eromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000 787 --AGCTCGCGTGT-------------------------------TAAGTCCTTCTTCTTA---ACAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGAGTCGTGC---------------------AGAGACTCTGCGAGAAAGGCGAGA 878
eromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000 787 --AGCTCGCGTGT-------------------------------TAAGTCCTTCTTCTTA---ACAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGAGTCGTGC---------------------AGAGACTCTGCGAGAAAGGCGAGA 878
eromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000 787 --AGCTCGCGTGT-------------------------------TAAGTCCTTCTTCTTA---ACAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGAGTCGTGC---------------------AGAGACTCTGCGAGAAAGGCGAGA 878
avia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000 771 CCGGCTGATGTGG---------------------------------GATCCTCTCCCCGC---CCAGGTGTCCAGCCTGA-GGAGCTGGTGGCCCGCGTGGTGC---------------------AGCGGCTGTGCGAGCGCGGCGCGC 861
avia_porcellus.cavPor3:1359074-1360074/1-1000 771 CCGGCTGATGTGG---------------------------------GATCCTCTCCCCGC---CCAGGTGTCCAGCCTGA-GGAGCTGGTGGCCCGCGTGGTGC---------------------AGCGGCTGTGCGAGCGCGGCGCGC 861
astor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000 787 --GGCCTCCTCCGAAC-------------------CGCGCAAAACCGGACCCTCTGCCC----CCAGGTGTCCAGCCTGAAGGAGCTGGTGGCCAGGGTCGTGC---------------------AGAGACTCTGCGAACGCCGCGCGA 889
tidomys_tridecemlineatus.spetri2:468520-469520/1-1000 790 GACGCCTCCGTCC----------------------TCAGCGACTCAGGACCTTCTCCCC---T-GCAGGTGTCCTGCTTGAAGGAGTTGGTGGCCAGGGTCGTAC--------------------AGCGGCTCTGCGAGCGCGGTGTGA 892

Consensus
    CCGGCCTCCGTGGGA+ATCGTGTGCGTGGGGAATCAAATGCTTCTCAAGA+CCTCTTCTCGCTC+CCAGGTGTCATCCCTGAAGGAGCTGGTGGCCAGGGTGGTGCCGCCCCCACCCCACCCCCCGAGAGACTCTGCGAGCGCGGCGAGC

erognathus_longimembris_pacificus-PPM_HiRise_rh_HiC:5190-6190/1-1000 850 GGCGATGGCTGC----AGCTCCGGAGCTTGGCCAGCTCCCGAAGGCC--------------------------AACGCAGGTAACC---TTCCGTGCTAAGCTTTTGAGAAGTGGCTTCTATTC--------------------GCGGG 945
attus_norvegicus.Rnor_6.0:32271976-32272976/1-1000 841 AAAGAAGCCC-------ATCCTTGACCTATTGAAGATTAGGTAGGCG-------------------------------GAGGGACC---TAAGGCTTTGCCACTCCCCGAGCGGGCCGCTGCTGCCTGC----------TGTGGTTGAC 938
attus_norvegicus-m5:33696844-33697844/1-1000 841 AAAGAAGCCC-------ATCCTTGACCTATTGAAGATTAGGTAGGCG-------------------------------GAGGGACC---TAAGGCTTTGCCACTCCCCGAGCGGGCCGCTGCTGCCTGC----------TGTGGTTGAC 938
attus_norvegicus-m6:32271976-32272976/1-1000 841 AAAGAAGCCC-------ATCCTTGACCTATTGAAGATTAGGTAGGCG-------------------------------GAGGGACC---TAAGGCTTTGCCACTCCCCGAGCGGGCCGCTGCTGCCTGC----------TGTGGTTGAC 938
astacomys_fuscus-Mastacomys_fuscus_wtdbg2_polished_HiC:777964-778964/1-1000 873 AAAGACGCCT------ATCCTTGTCTGTAATGAAGGTTAGGTAGGCG-------------------------------GAGGAACC---TAAGGCTTT------------GTTGGCCGCTGCTGCCGGT----------TGTGGTCGAC 959
romys_caudimaculatus-Uromys_caudimaculatus_HiC:787178-788178/1-1000 874 AAAGACGCCT------ATCCTTGTCTGTAATGAAGGTTAGGTAGGCG-------------------------------GAGGAACC---TAAGGCTTTGTCTG---------TTGGCCGCTGCTGCCGGT----------TGTGGTCGAC 964
igmodon_hispidus-GCA_004025045.1_SigHis_v1_BIUU_genomic_HiC:868037-869037/1-1000 878 AAAGATGCCT-------GTCCTTGA--------AAGCTACACAGGCA-------------------------------GAGGAACC---TAAGGACCACCCTGCTCCAGAGCTGACCGCTGCTGCCTGC-----------AAGTTCGGT 966
yodes_rutilus-Myodes_rutilus_HiC:744994-745994/1-1000 919 AAAGACGTCT-------GTCCTCGA-----------------------------------------------------GAGCCTGC------------------------------------------------------GAATTCGTT 953
esocricetus_auratus-MesAur1.0_HiC-DNAZoo:35662631-35663631/1-1000 846 AAAGACACCT-------GTCTTTGATTTATTGAAGGTTCTGAAGGCG-------------------------------GAGGAACC---CAAGGCTCACCCTGCTCCAGAGCCGGCCGCTGCTG-------------TCTGAGTTCGGT 940
icrotus_montanus-Microtus_montanus_1k:112395-113395/1-1000 848 AAAGACACCT-------GTTATTGATTTATTGAAGGTTCTGTAGGCA-------------------------------GAGGGATC---TAAGGTCCATCCTGCTCCAGAGCCGGCTGCTGCCTCCTGT-----------GAGTTCGGT 944
eotoma_phenax-Neotoma_phenax_HiC:14370028-14371028/1-1000 891 AAAGATGCCT-------GTCCTTGATTTATTGAAGGTTGCATAGGCA-------------------------------GAGGAACC---TAAGGCCCACCC-GCTCCAGAGCCAGCTGCTGCTGCCTGC-----------GAGTTCGGT 986
eromyscus_maniculatus_bairdii-HU_Pman_2.1:907406-908406/1-1000 890 AAAGACACCT-------GCCCTTGATTTATTGAAGGTTGCGTAGGCA-------------------------------GAGGGACC---TAAGGCCCACCCTGCTCCAGAGCCGGCTGCTGCCGCCTTC-----------GAGTTTGGT 986
sgoodomys_banderanus-Osgoodomys_banderanus_1k:2968-3968/1-1000 894 AAAGACATCT-------GTCCTTGATTTATTGAAGGTTGCGTAGGCA-------------------------------GAGGAACC---TAAGGCCCACCCTGCTCCAGAGCCGGCTGCTGCTGCCTGC-----------GAGTTCGGT 990
eromyscus_crinitus-pecr10X_v2_HiC:835713-836713/1-1000 890 AAAGACACCT-------GTCCTTGATTTATTGAAGGTTGCGTAGGCA-------------------------------GAGGAACC---TAAGGCCCACCATGCTCCAGAGCCGGCTGCTGCTGCCTGC-----------GAGTTCGGT 986
eterocephalus_glaber-HetGla_female_1.0_hetGal2:646698-647698/1-1000 821 GGGGCCG---------GGCAGCGCGCCCCGCACCAGCGGGGGAGGGGTAGACGTGGCTCCCCCCCCCCCGGCCGGGTCTCGGGGCCCCAGGCTGGATTTCCTCTGCGGGCTCTTGGGCGGCTGCTG--------------------GGC 940
eterocephalus_glaber-HetGla_female_1.0_HiC:646698-647698/1-1000 821 GGGGCCG---------GGCAGCGCGCCCCGCACCAGCGGGGGAGGGGTAGACGTGGCTCCCCCCCCCCCGGCCGGGTCTCGGGGCCCCAGGCTGGATTTCCTCTGCGGGCTCTTGGGCGGCTGCTG--------------------GGC 940
ydrochoerus_hydrochaeris-Hydrochoerus_hydrochaeris_HiC:629599-630599/1-1000 825 AAAGGGCGGGTCAGTGCACCCCAAATCTGCTCGAGATATTGTAGACG-------CGGCTCCGTCTCCGGCCGGGGCTTGAGAGCCC---CAGGCTGTTCCTGGTCCCAGGCTGGGCTTCCTCTGCAGGC-----------------TTC 946
oendou_prehensilis-Coendou_prehensilis_HiC-DNAZoo:719848-720848/1-1000 834 AAGGGGCGGGGCAGTGCGCCCCGAACCTGCTAGACGGGGTGTAGACG-------CGGCTCCGCCCCCGGCCGGGGCTTGGGGCTCC---AAGGCTTTCCCTAGCCCCAGGCTGGGCTTCCTCTGCAGGCACTTGGGCGTCTGCTTCGGC 972
rethizon_dorsatum-GSC_porc_1.0_HiC:48415303-48416303/1-1000 933 AGAGGGACGG-----------------TGGCAGTGACGTGGGGTGCG------------------------------TGGGAAATC-----GGGTGCGTACTGCACTCCTTCGTTCTTCT----------------------------- 1000
g38.fa:1294489-1295489/1-1000 905 GGAGAGAGGTCGAATCGGCCTAGGCTGTGGGGTAACCCGAGGGAGGG---------------------GCCATGATGTGGAGGCCC---TGGGAA----------CAGGTGCGTGCGGCGACCC-------------------TTTGGC 1000
acaca:976590-977590/1-1000 870 GGAGAGGGGTCGAATCGGCCTAGGCTGTGGGGTAACCGGAGGGAGGG---------------------GCCGTGATGTGGGGGCCC---TGGGAA----------CAGGTGCGAGCGGCGACCC-------------------CTTCGC 965
mmospermophilus_harrisii-Ammospermophilus_harrisii_1k:3469-4469/1-721 677 --------------------TCTGTTGTTATGCACCCCACGTAGGTG-------------------------------TGCCCACC------------------------GCCGCACCCT----------------------------- 721
erus_rutilus-Xerus_rutilus_HiC:667393-668393/1-1000 876 GGAAGGAGCT------GGGC---AGCGTGTCCCCAGCGAAGGGGACT--------------------------------GGCCGCT---CTAGCTCG--------CCGAAGTGTGTAGACGC------------------------GGC 948
seudomys_desertor-Pseudomys_desertor_wtdbg2_polished_HiC:74098607-74099607/1-1000 887 GGAACGTGCT------GGCTTTTGGCTTTGCGCTGCTTAACGGGGCC-------------------------AGAGGTGGGCCTCC---CATGGCCTTCACTA--CCAATGTACGGAACTACTT----------------------GCC 977
m10.fa:73626530-73627530/1-1000 882 GAAACGTGCT------GGCTTTTGGCTTTGAGCTGCTTAACGAGGCC-------------------------AGAGGCGGGCCTCC---CATGGCCTTCACTA--GTAGCGTGCGTAGCTACTT----------------------GCC 972
us_shortridgei-Mus_shortridgei_1k:68155-69155/1-1000 882 GGAACGTGCT------GGCTTTTGGCTTTGCGCTGCTTAACGAGGCC-------------------------AGAGGCGGGCCTCC---CATGGCCTTCACTA--GAAGCGTGCATAGCTACTT----------------------GCC 972
eriones_meridianus-Meriones_meridianus_1k:66171-67171/1-1000 862 GAAACGTGCT------GACTTTTGGCTTCGCTCTGCTTAACGGGGAC-------------------------CAAGGCGGGCCTCC---CATGGTCTTCACCA--CCAGCGTGCGCAGCTACTT----------------------GCC 952
eriones_unguiculatus-GCA_008131255.1_ASM813125v1_genomic_HiC:91184100-91185100/1-1 862 GAAACGTGCT------GGCTTTTGGCTTCGCTCTGCTTAACGGGGAC-------------------------CAAGGCGGGCCTCC---CATGGTCTTCACCA--CCAGCGTGCGCAGCTACTT----------------------GCC 952
ricetulus_griseus-CriGri-PICR_HiC:369917128-369918128/1-1000 875 GGAACGTGCT------GGCTTTTGGCTTTGCGCTTCTTAACGGAGCC-------------------------CAAGGCGGGCCACC---CATGACCTTCACAA--CCAACGTGCGCAGCTATTT----------------------GCC 965
ricetulus_griseus-CHOK1S_HZDv1:131535884-131536884/1-1000 875 GGAACGTGCT------GGCTTTTGGCTTTGCGCTTCTTAACGGAGCC-------------------------CAAGGCGGGCCACC---CATGACCTTCACAA--CCAACGTGCGCAGCTATTT----------------------GCC 965
ricetulus_griseus-CriGri-PICR:19516657-19517657/1-1000 875 GGAACGTGCT------GGCTTTTGGCTTTGCGCTTCTTAACGGAGCC-------------------------CAAGGCGGGCCACC---CATGACCTTCACAA--CCAACGTGCGCAGCTATTT----------------------GCC 965
eromyscus_nasutus-Peromyscus_nasutus_10x_v1_HiC:73553901-73554901/1-1000 879 GGAACGTGCT------GGCTTTTGGCTTCGCACTGCTTAACGGGCCC-------------------------CAAGGCGGCCCTCC---CATGGCCTTCACAA--CCAGCGTGCGCAGCTACGC----------------------ACC 969
eromyscus_maniculatus_bairdii-Pman_1.0:2412193-2413193/1-1000 879 GGAACGTGCT------GGCTTTTGGCTTCGCACTGCTTAACGGGCCC-------------------------CAAGGCGGGCCTCC---CATGGCTTTCACAA--CCAGCGTGCGCAGCTACTC----------------------GCC 969
eromyscus_eremicus-Peer1.6.0_HiC:11661487-11662487/1-1000 879 GGAACGTGCT------GGCTTTTGGCTTCGCACTGCTTAACGGGCCC-------------------------CAAGGCGGGCCTCC---CATGGCCTTCACAG--CCAGCGTGCGCAGCTACTT----------------------GCC 969
eromyscus_eremicus-Peer2.0.0:82925608-82926608/1-1000 879 GGAACGTGCT------GGCTTTTGGCTTCGCACTGCTTAACGGGCCC-------------------------CAAGGCGGGCCTCC---CATGGCCTTCACAG--CCAGCGTGCGCAGCTACTT----------------------GCC 969
eromyscus_eremicus-Peer2.0.1:82925608-82926608/1-1000 879 GGAACGTGCT------GGCTTTTGGCTTCGCACTGCTTAACGGGCCC-------------------------CAAGGCGGGCCTCC---CATGGCCTTCACAG--CCAGCGTGCGCAGCTACTT----------------------GCC 969
avia_porcellus-Cavpor3.0_HiC-DNAZoo:81738171-81739171/1-1000 862 AGAACGTGCT------GGCCTTCGGCTTTGGGTTGCTGAACGAGGCG-------------------------CGCGGCGGGCCGCC---CCTGGCCTTCACCA--CGAGCGTGTGCCGCTACCG----------------------GCC 952
avia_porcellus.cavPor3:1359074-1360074/1-1000 862 AGAACGTGCT------GGCCTTCGGCTTTGGGTTGCTGAACGAGGCG-------------------------CGCGGCGGGCCGCC---CCTGGCCTTCACCA--CGAGCGTGTGCCGCTACCG----------------------GCC 952
astor_canadensis-C.can_genome_v1.0_HiC-DNAZoo:154821726-154822726/1-1000 890 GGAACGTGCT------GGCCTTCGGCTTCGCCCTGTTGGATGGGGCG-------------------------CACAGCGGGCCGCC---CATGGCCTTTACTA--CCAGCGTGCGCAGCTACCT----------------------GCC 980
tidomys_tridecemlineatus.spetri2:468520-469520/1-1000 893 GGAATGTGCT------GGCCTTTGGCTTCGCGCTGCTGGACGGGGCC-------------------------CGTGGCGGGCCACC---TATGGCCTTCACGA--CCAGCGTTCGAAGCTATTT----------------------GCC 983

Consensus
```