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Wilson, R. and Moran, C.N. and Cole, J. and Pitsiladis, Y. and Bailey, M.
(2010) *Evolutionary history of the ADRB2 gene in humans*. American
Journal of Human Genetics, 86 (3). pp. 490-493. ISSN 0002-9297

<http://eprints.gla.ac.uk/25678/>

Deposited on: 23 March 2010

Evolutionary history of the *ADRB2* gene in humans.

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This manuscript was published in *American Journal of Human Genetics* as a Letter to Editor:
Wilson et al., 2010, *Am. J. Hum. Genet.* 86: 490-493

To the editor: Recently, Cagliani *et al.*¹ reported on the evolutionary history of the human β 2-adrenoreceptor gene (*ADRB2*, [MIM 109690]).

The authors presented their analysis of the genealogy of inferred *ADRB2* haplotypes reconstructed through the use of a median-joining network approach. *ADRB2* shows a high level of polymorphism, including three coding variants with altered functional properties (at codons 16, 27 and 164; hereafter referred to as C16, C27 and C164), and several suspected regulatory variants. The network presented by Cagliani *et al.*¹ was prepared using software implementing a model that assumes no recombination, but allows for recurrent mutation. We notice that most SNPs in their network are represented by recurrent mutations in non-reticulated parts of the network, which we find biologically implausible and difficult to interpret in an evolutionary context. We have prepared a network diagram for the evolution of common *ADRB2* haplotypes that can be accounted for by divergence via the accumulation of mutations and rare recombination events between diverged haplotypes (Figure 1). This revised network requires no recurrent mutations (homoplasy) and accounts for the major haplotype groups of Cagliani *et al.*¹, Hawkins *et al.*² and Drysdale *et al.*³, as well as those revealed by the HAPMAP data, with only one recombination event.

To construct this revised network, we generated an alignment of genomic sequences for human, chimpanzee and macaque as an outgroup using GenBank Accession nos. DQ094845, NC_006472 and NC_007863, respectively. The alignment, generated using ClustalX, spanned *ADRB2* from base position -4219 to + 5479 relative to the first base of the initiation codon of the main polypeptide product (Supplementary Figure 1). It was found that the chimpanzee genome sequence used gave poor alignment in the region -600 to -900. We used our own chimpanzee sequence generated by PCR amplification from genomic DNA to replace poorly

aligned regions of NC_006472. In Figure 1 we have shown only the network connecting the major haplogroups. Our network accounts for the generation of the HC1 haplogroup in Cagliani *et al.*¹ (haplogroup 1.1 in Hawkins *et al.*²) by recombination between the 5' end of a haplotype containing the ancestral G alleles at each of the common functional coding SNPs, C16 and C27 (i.e. a 'GG' haplotype), and the 3' end of a doubly-derived C16/C27 AC haplotype. This network, produced by eye, satisfies conditions of parsimony, requiring only one recombination event and no homoplastic mutations. Further mutation and recombination events, especially around the 3' end of the coding region, would account for the full spectrum of rare and region-specific haplotypes observed in Cagliani *et al.*¹ and Hawkins *et al.*² (not shown).

The major difference in network topology we find in relation to the common functional coding SNPs is that the first divergence from the most recent common ancestor (MRCA) of extant haplotypes separates the C16/C27 GG haplogroup from the remaining (GC and AC) haplogroups, with mutation at the C27 site creating a GC haplotype, followed by divergence of the GC and AC haplogroups, indicating that the C16 mutation that created the AC haplotype occurred on a GC haplotype background (Figure 1). The order of mutation events and consequent high degree of linkage disequilibrium between the neighbouring C16 and C27 sites probably explains why AG haplotypes are never found in well-sequenced datasets worldwide.

All the sites represented in the network in Cagliani *et al.*¹ are currently polymorphic, so their node labeled 'chimp' may thus better be represented as the most recent common ancestral human node for this gene. In our revised network we have used comparison with the macaque outgroup to assign all fixed mutations on the branches leading to the chimpanzee and to the ancestral human. Using our sequence for the chimpanzee, we find fewer fixed differences (50 sites) between the chimpanzee and the human common ancestor haplotype than the number

reported in Cagliani *et al.*¹ (77 sites). Of these 50 differences, 32 occur on the chimpanzee branch and 18 occur on the human branch. The ratio of polymorphic to fixed sites within the human lineage will relate to the relative time to most recent common ancestor (TMRCA) of all extant *ADRB2* haplotypes compared with time since the divergence from chimpanzee, although the true value would be affected by differences in generation times, population parameters and per-generation substitution rates within each species and haplotype lineage. Cagliani *et al.*¹ estimate this TMRCA to be in the range 1.05-1.65Myr. The revised network we have generated points to a significantly more ancient MRCA for this gene, since we find that 11, 8, and 13 currently polymorphic sites are found in the GG, AC and GC haplogroups, respectively, compared with the 18 fixed human mutations that have occurred since the human/chimpanzee common ancestor.

The mutation rate analysis in Cagliani *et al.*¹ is constrained by the use of polymorphism data only. Further evidence that *ADRB2* is unusually polymorphic comes from a comparison between the nucleotide substitution frequency in the lineage to the macaque outgroup and those to the fixed and polymorphic sites along the other branches. To illustrate the changes in substitution frequency across *ADRB2* and the differences between lineages, we counted the number of substitutions (of all mutation categories) in each lineage in 500bp windows across the entire region, moving along the gene in 200bp steps, and plotted these values as substitution frequencies per 1000bp on a line graph (Figure 2). To look for statistical differences in substitution frequency between lineages, we used Fisher's exact test to compare the frequency of substitutions in each 500bp window for chimpanzee fixed, human fixed and human polymorphic sites, respectively, with that in the macaque/outgroup. Individual 500bp windows giving $P < 0.05$ in these tests were investigated further by extending the window in each direction and retesting using Fisher's exact test until no further decrease in P value was

observed (i.e. to give the minimum P value). The substitution frequency varied significantly (more than 5-fold) across *ADRB2* in the macaque/outgroup (500bp windows, $P < 10^{-6}$ for heterogeneity, 18 d.f., χ -squared test). For the other branches, 10 out of 144 individual 500bp windows showed differences in substitution frequency (at $P < 0.05$) when compared to the macaque/outgroup branch (Supplementary Table 1). After extension of these 10 windows to find the minimum P values, we found that the two most significant regions were the human polymorphic sites from position -50 to +1300 ($P = 0.00001$) and from position +1300 to +4050 ($P = 0.0013$). The macaque/outgroup substitution frequencies demonstrate a long-term reduction in substitution rate over the coding region, signaling constraint presumably associated with stabilizing selection on the *ADRB2* functional phenotype. In agreement with Cagliani *et al.*¹, we note a relative increase in the density of surviving human polymorphic mutations in the coding region relative to the macaque/outgroup branch. This high diversity in our species may be associated with long-term balancing selection or with relaxed constraint. We also note the low diversity downstream of the transcript, which may be indicative of a selective sweep, although the possibility of incomplete SNP ascertainment in this region cannot be discounted.

We have also characterized the haplotype structure at the 3' end of *ADRB2*, which was not addressed in detail by Cagliani *et al.*¹ or by Hawkins *et al.*², nor addressed completely by another study by the latter group⁴. Table 1 shows the haplotypes obtained by sequencing 83 European individuals from our earlier study of Greek teenagers⁵. This study was approved by both Greek and UK local Research Ethics Committees and all subjects gave parentally-sanctioned informed consent. All sequenced individuals were homozygous for haplotypic combinations at codons 16 and 27 (i.e. GG homozygotes, GC homozygotes or AC homozygotes), apart from one individual heterozygous for a GCt haplotype. Homozygosity facilitated the reading of the sequence electropherogram across the polyC-tract beginning at

position 1266. We found almost complete linkage disequilibrium between the C16/C27 coding polymorphisms and the 3' polymorphisms within the GG and GC haplotypes, but considerable diversity within the AC haplotype. This 3'-end diversity is best explained by a combination of recombination events between haplotypes and variation in C-tract homopolymer length. In addition to the variability in the length of the C-tract, we would emphasise the hitherto unappreciated insertion of a G at position 1275 within the C-tract in certain haplotypes. The functional importance of length variation in the C-tract in relation to mRNA stability has been highlighted by Panebra *et al.*⁴ but no alleles with a C-tract interrupted by the 1275G insertion were tested in their study. The insertion of a G into the homopolymer C-tract would be expected to influence C-tract conformation and interactions involved in mRNA stability at least as much as changes in homopolymer length. Both the C-tract length and the G insertion should be taken into account in future functional studies of variation at the 3' end of the gene.

The degree of linkage disequilibrium between the 3' variants and upstream variants may be a reflection of possible functional interactions between variants in different regions of *ADRB2* in relation to protein function, transcriptional regulation and mRNA stability. There may be additional effects mediated by the polymorphic site at pos. 1239, immediately 5' to the stop codon, affecting translation termination. A complete and accurate picture of variation across the entire gene is required before such interactions can be studied effectively.

References

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Acknowledgements

We are grateful to M. Sironi for unpublished data that enabled us to interpret their Fig. 1.

This research was supported in part by a BBSRC research grant #17/D17566. The authors have no conflicts of interest to declare.

Web Resources

OMIM, <http://www.ncbi.nlm.nih.gov/sites/entrez?db=omim>

dbSNP, <http://www.ncbi.nlm.nih.gov/SNP/index.html>

HAPMAP, <http://www.hapmap.org>

Accession Numbers

The chimpanzee *ADRB2* gene sequence generated by us has been given GenBank Accession number GU373723.

Figure Legends

Figure 1 – Evolutionary network for the common haplotypes of human *ADRB2*

Substituted and polymorphic sites in *ADRB2* are listed along the branches the mutation occurred in. Sites different in macaque but identical in human and chimpanzee are counted but not listed. Nodes connecting lines represent common ancestral haplotypes and are labeled. Sites are coded by position in the aligned human sequence relative to the first base of the initiation codon, derived allele, and whether the change involved insertion or deletion. Insertions and deletions were treated as single mutational events for calculation of the network regardless of the number of bases altered. Within the C-tract at pos. 1275, the co-appearance of adjacent G and C inserted bases were treated as a single mutation (see Table 1). Major haplogroups are indicated in shaded boxes. Within each box, these are coded as Cagliani *et al.* haplogroup (e.g. ‘HC2’), Hawkins *et al.* haplogroup (e.g. ‘2.1’), and C16/C27 functional SNP haplogroup (e.g. ‘GG’). GCt refers to the rare C164 derived haplotype not considered by Cagliani *et al.*¹. Branches rejoining below a node represent formation of a new haplotype via recombination. Regions contributed by each parental haplotype and regions of recombination are indicated with ‘<’ and ‘>’. Rare, population-specific polymorphic sites have not been shown on this network.

Figure 2 – Substitution/polymorphism rates across the *ADRB2* region.

No. of substitutions per kbp are plotted, on a logarithmic scale, vs position along the genomic region analysed for central points in a sliding window of 500 base pairs, with step size of 200bp. Base position 1 is the first base of the initiation codon. The black and white bar represents the *ADRB2* coding region and UTRs, respectively.

Key:

—————	Macaque / outgroup
- - - - -	Chimpanzee / fixed
- - - - -	Human / fixed
—————	Human / polymorphic

Table 1 Allelic composition of 3' polymorphic sites in *ADRB2*

position C16/C27 haplogroup	46	79	491	1053	1239	1263-1282	C-tract ^a	R?	N	% of haplogroup ^b
GG	G	G	C	G	G	AGACCCCCCCC-----CCCAAC	10		2	4
GG	G	G	C	G	G	AGACCCCCCCCC---CCCAAC	11		48	90
GG	G	G	C	G	A	AGACCCCCCCCC---CCCAAC	11	R	2	4
GG	G	G	C	C	A	AGACCCCCCCCC- CG CCCAAC	13 +G	R	1	2
GC	G	C	C	C	A	AGACCCCCCCCC- CG CCCAAC	13 +G		37	97
GC	G	C	C	C	G	AGACCCCCCCCC- CG CCCAAC	13 +G	R	1	3
GCt	G	C	T	C	A	AGACCCCCCCCC- CG CCCAAC	13 +G		3	N/A ^c
AC	A	C	C	G	G	AGACCCCCCCCC---CCCAAC	11		35	56
AC	A	C	C	G	G	AGACCCCCCCCC C ---CCCAAC	12		5	8
AC	A	C	C	C	A	AGACCCCCCCCC- CG CCCAAC	13 +G	R	19	31
AC	A	C	C	G	A	AGACCCCCCCCC- CG CCCAAC	13 +G	R	1	2
AC	A	C	C	C	A	AGACCCCCCCCC CG CCCAAC	14 +G	R	1	2

^aLength of C-tract including polymorphic G insertion if present; '+G' indicates G insertion is present

^bProportion of chromosomes from each of the three major haplogroups (GG, GC and AC); GCt indicates the rare haplotype containing the derived T-allele at the third functional non-synonymous site, codon 164, nucleotide position 491

^cThe GCt chromosomes are not counted as part of the GC haplogroup for this analysis as they were specifically selected.

N = no. of chromosomes observed

R – recombinant after position 79. In some rare cases recombination cannot easily be distinguished from back mutation or gene conversion events.

Derived alleles are shown in bold, including additional C residues appearing within the C-tract.

Figure 1

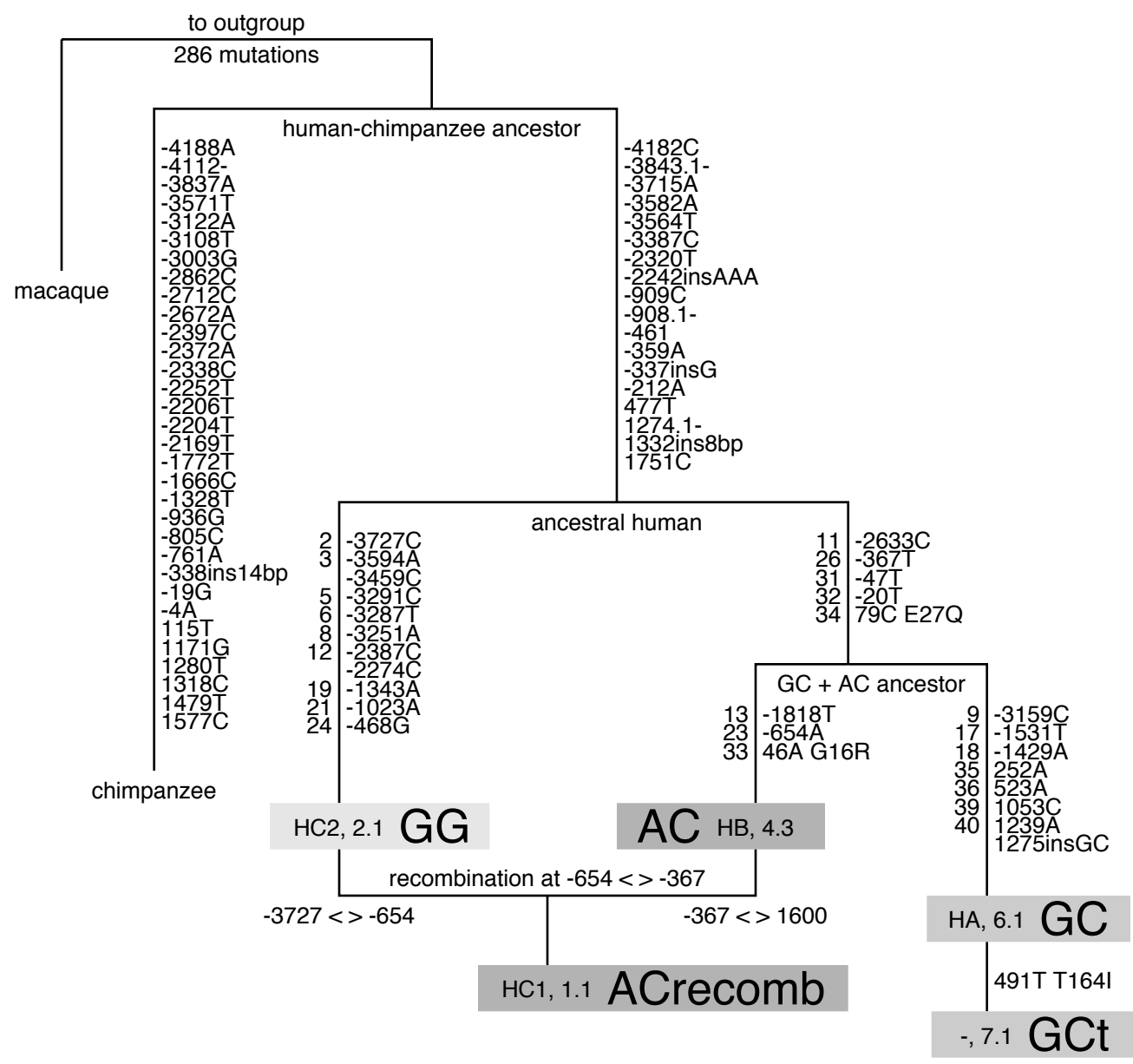
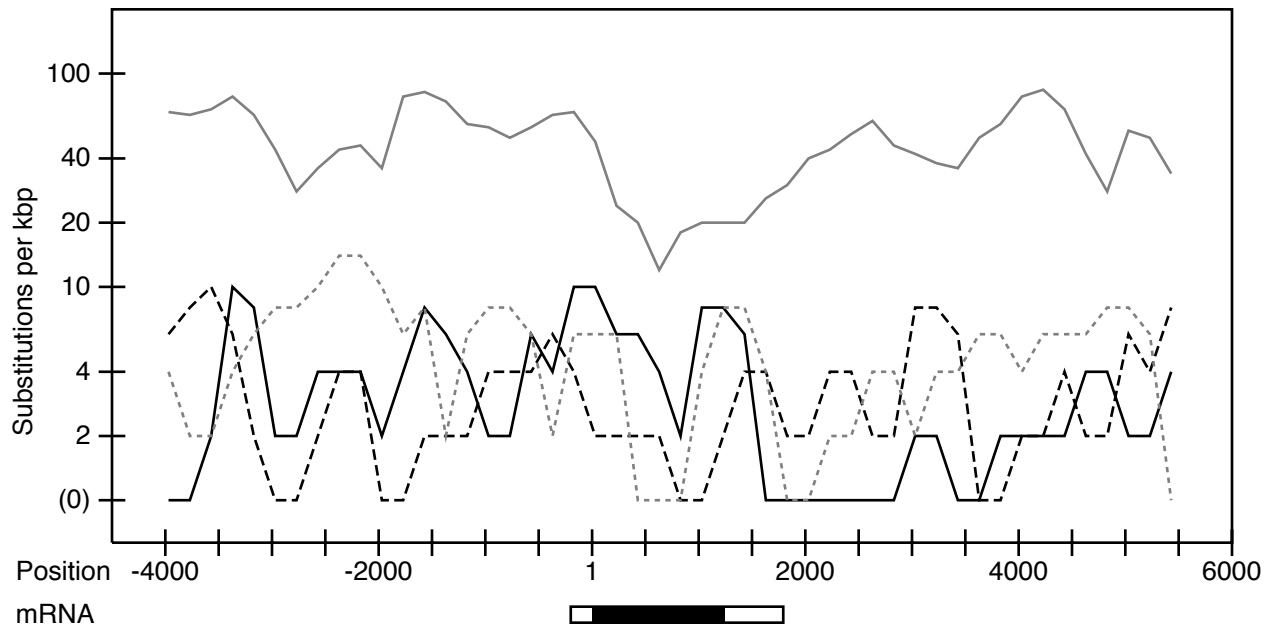


Figure 2



Evolutionary history of the *ADRB2* gene in humans.

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Supplementary Table 1 - Regions around *ADRB2* giving evidence for altered substitution rates.

Species/Site set	Starting pos.	Ending pos.	<i>P</i> (Fisher's Exact)	Rate rel. to outgroup branch	Region of gene
Chimpanzee / fixed	-2900	-1700	0.0017	High	Extended Promoter
Chimpanzee / fixed	1150	1650	0.008	High	3' coding and UTR
Human / fixed	5200	5750	0.04	High	Downstream
Human / polymorphic	-50	1300	0.00001	High	Coding region
Human / polymorphic	1300	4050	0.0013	Low	3' UTR and downstream

Substitution frequencies were calculated at central points of 500bp windows across *ADRB2* with a step size of 200bp (see Fig. 2), and tested for differences against the macaque/outgroup using Fisher's Exact Test. Windows with $P < 0.05$ were extended on either side until overall P value in repeated tests stopped decreasing. Eight windows initially gave P values leading to extensions, and some separate windows became merged into extension regions subsequently. Hence, 5 regions remained, as listed in the Table. Starting and Ending pos. refers to the limits of the extended windows relative to the first base of the initiation codon (+1). The penultimate column states whether the substitution rate is higher or lower than that for the same region in the macaque/outgroup branch. The human polymorphic site set was constrained to contain only sites with minor allele frequency (MAF) > 0.1 .

Supplementary Figure 1 - Alignment used for calculations of substitution rates across *ADRB2*

Sequences are based on the following sequence accession numbers in GenBank: Human – DQ094845; Chimpanzee - NC_006472; Macaque - NC_007863; our own chimpanzee sequence is designated as ‘chimp5pr’. CLUSTAL 2.0.11 was used to align the sequences.

Position in each sequence is indicated at the end of each line.

Overall position in the human gene is indicated below the alignment (position +1 is the first base of the initiation codon).

‘*’ indicates identities across all three species.

‘-‘ indicates a gap or deletion.

We have annotated the alignment, as follows:

‘4’ etc. indicates sites used to prepare the haplotype network in Cagliani *et al.* (Ref. 1).

‘c3’ etc. indicate sites from the full set (1-63) referred to in the Supplementary Material from Cagliani *et al.* (Ref. 1), where these were not used to construct the network in that study. Please note that ‘1’ and ‘c1’ are thus not the same site as they come from different numbering systems.

‘c’ indicates a chimpanzee-specific change.

‘h’ indicates a human-specific change.

Sites that are identical in human and chimpanzee and different in macaque are indicated by lack of a ‘*’ in the consensus trace.

‘?’ indicates that all three sequences are different, so assignment of changes to particular branches in the network is impossible.

‘|’ indicates a mismatch between chimpanzee genome sequence and our own chimpanzee sequence.

‘&’ indicates the site of the G insertion into the polyC tract in the 3’-UTR.

‘>’ indicates the known sites of transcriptional initiation.

‘pA’ indicates the site of addition of the polyA tail in the *ADRB2* cDNA reference sequence.

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                                     c      h
                                     |      |
DQ094845      TGCAAAGACATGAAGTCATCCTTTTTTATGGCTGCACAGTATTCATGGTGTATATGTG 60
Chimp         TGCAAAGACATGAAGTCATCCTTTTTTATGACTGCATAGTATTCCATGGTGTATATGTG 60
Macaque       TGCAAAGAGCCTGAACCTCACCTTTTTTATGGCTGCATAGTATTCCATGGTGTATATGTG 60
              ....5....0....5....0....5....0....5....0....5....0....5....0-4160
              ***** * **** * ** ***** ***** ***** ***** *****

                                               c
                                               |
DQ094845      CCACATTTTCTTTATCAAGTCTATTCTTGATGGGCATTTGGGTTGGTTCCAAGTCTTTGC 120
Chimp         CCACATTTTCTTTATCAAGTCTATTCTTGATGGGCATTTGGGTTGGT-CCAAGTCTTTGC 119
Macaque       CCACATTTTCTTTGTCAAGTCTATTATTAATGGGCATTTGGGTTGGTTCCTAGTCTTTGC 120
              ....5....0....5....0....5....0....5....0....5....0....5....0-4100
              ***** ***** ** ***** ***** ***** ***** *****

c1
|
DQ094845      TATTGTGAACAGTGCTGCAATAAACATACATGTCCATGTGTCTTTATAGTAGAATGATTT 180
Chimp         TATTGTGAACAGTGCTGCAATAAACATACGTGTCCATGTGTCTTTATAGTAGAATGATTT 179
Macaque       TATTGTGAACAGTGCTGCAATAAACATATGTGTCCATGTGTCTTTATAGTAGAATGATTT 180
              ....5....0....5....0....5....0....5....0....5....0....5....0-4040
              ***** ***** ***** ***** ***** ***** ***** *****

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c5
|

DQ094845 TTGATTTGCATTTCACTAATAACCAGTGTCTGATGATCTTTTTCATATGTTTGTTGGCT 779
Chimp TTGATTTGCATTTCACTAATAACCAGTGTCTGATGATCTTTTTTTCATATGTTTGTTGGCT 779
Macaque TTGATTTGCATTTCACTAGTAAGTGTCTGATGATGATCTTTTTTTCATATGTTTGTTGGCT 705
0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3441

h
|

DQ094845 GCATTAATGTCTTCTTTT-GAGAAGTGTCTGTTTCATATCCTTTGCCACTTTTTTCATGGG 838
Chimp GCATTAATGTCTTCTTTT-GAGAAGTGTCTGTTTCATATCCTTTGCCACTTTTTTCATGGG 838
Macaque GCATAAATGTTTTTTTTTTGAGAAGGATCTGTTTCATATCCTTTGCCCAATTTTTTCATGGG 765
0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3382

DQ094845 GCTGTTTGTTTTTTCTTGTAATTTGTTTAAAGTCTTTGTAGATTCTGGATATTAGCCCT 898
Chimp GCTGTTTGTTTTTTCTTGTAATTTGTTTAAAGTCTTTGTAGATTCTGGATATTAGCCCT 898
Macaque GTTGTGTTGTTTTTCTTGTAATTTGTTTACGTTCTTTGTAGATTCTGGATATTAGCCCT 825
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3322
* ****

4 5 6 7
| | | |

DQ094845 TTGTCAGATGGATAGATTGCAAAATTTTCTCCCATTTCTGTAGGTTGCCTGTTCCACCTG 958
Chimp TTGTCAGATGGATAGATTGCAAAATTTTCTCCCATTTCTGTAGGTTGCCTGTTCCACCTG 958
Macaque TTGTCAGATGAGTAGATTGCAAAACATTTTCTCCCATTTCTGTAGGTTGCCTCTTCACTCTG 885
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3262

8
|

DQ094845 ATGATAGTTTCTTTTGCTGTGCAGAAACTCTTTAGTTTAATTAGATCCCATTGTCAATT 1018
Chimp ATGATAGTTTCTTTTGCTGTGCAGAAACTCTTTAGTTTAATTAGATCCCATTGTCAATT 1018
Macaque ACGACAGTTTCTTTTGCTGTGCAGAAAGCTCTTTAGTTTAATTAGATCCCATTGTCAATT 945
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3202
* **

9
|

DQ094845 TTGGCTTTTGTGGCCATTGCTTTTGTATGTTTTAGTCATGAAGTCTTTGCCATGCCTATG 1078
Chimp TTGGCTTTTGTGGCCATTGCTTTTGTATGTTTTAGTCATGAAGTCTTTGCCATGCCTATG 1078
Macaque TTGGCTTTTGTGGCCATTGCTTTTGGTGTTTTAGCCATGAAGTGTGTTGCTCATGCCTATG 1005
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3142

c c
| |

DQ094845 TCCTGGATGTTATTGCCTAGATTTTCTTCTAGGGTTTTTATGGTTTTAGGTCTTACGTTT 1138
Chimp TCCTGGATGTTATTGCCTAAATTTTCTTCTAGGGTTTTTATGGTTTTAGGTCTTACGTTT 1138
Macaque TCCTGAATAGCATTGCCTAGGTTTTTCTTCTAGGGTTTTTATGGTTTTAGGTCTTACGTTT 1065
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3082

DQ094845 AAGTCTTTAATTCATCTTGAGTTAATTTCTTGTATAAGGTGTAAGGAAGGGGTCCAGTTT 1198
Chimp AAGTCTTTAATTCATCTTGAGTTAATTTCTTGTATAAGGTGTAAGGAAGGGGTCCAGTTT 1198
Macaque AAGTATTTAATTCATCTTGAGTTAATTTCTTGTATAAAGTTTAAAGGAAGGGGTGCAGTTT 1125
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-3022

c
|

DQ094845 AGTTTTCTGCATATGGCTAGCCAGTCTTCTTGTATTTAGTATTTGTGGGTTTTAAAAAAG 1258
Chimp AGTTTTCTGCATATGGCTGGCCAGTCTTCTTGTATTTAGTATTTGTGGGTTTTAAAAAAG 1258
Macaque AGTTTTCTTCATATGGCTAGCCAGT--TCTTGTATTTAGCATTGTGGGTTTTAAAAAAG 1182
.0...5...0...5...0...5...0...5...0...5...0...5...0...5...-2962

c12
|
DQ094845 GAGTTTCCCAAAATATTCAGTTAAACTTTTAAGTGACTTACGTGTATATCTAAATACATG 1318
Chimp GAGTTTCCCAAAATATTCAGTTAAACTTTTAAGTGACTTACGTGTATATCTAAATACATG 1318
Macaque GAGTTTCCCAAAATATTCAGTTAAACTTTTAAGTGACTTATGTGTATATTTAAATACATG 1242
.0...5...0...5...0...5...0...5...0...5...0...5...-2902

c
|
DQ094845 ATCAGTTAATATTTGTCTTAAAGGGGTTTTCTTTGTTCTTTTCTTATTATAGGAAGGTTA 1378
Chimp ATCAGTTAATATTTGTCTTAAAGGGGTTTTCTTTGTTCTTTTCTTATTATAGGAAGGTTA 1378
Macaque ATCAGTTAATATTTGTCTTAAAGGGGTTTTCTTTGTTCTTTTCTTATTATAGGAAGGTTA 1302
.0...5...0...5...0...5...0...5...0...5...0...5...-2842

DQ094845 AACAAATATGCTTATTTATGCCATAGCTTCACAAACAGGAAGGAGGTTTTAAATGGTTTAG 1438
Chimp AACAAATATGCTTATTTATGCCATAGCTTCACAAACAGGAAGGAGGTTTTAAATGGTTTAG 1438
Macaque AACAAATATGCTTATTTATGCCATAGCTTCACAAACAGGAAGGAGGTTTTAAATGGTTTAG 1362
.0...5...0...5...0...5...0...5...0...5...0...5...-2782

DQ094845 TTCCACAATTTGAGTAGATGCATATTTAAAGAAACGTTGTTGCATAATAAATACTGCCTC 1498
Chimp TTCCACAATTTGAGTAGATGCATATTTAAAGAAACGTTGTTGCATAATAAATACTGCCTC 1498
Macaque TTCCACAATTTGAGTAGATGTGTATTTAAAGAAACGTTGTTGCATAACAAATACTGCCTC 1422
.0...5...0...5...0...5...0...5...0...5...0...5...-2722

c 10 c
| | |
DQ094845 TTCTTAAATGCATCATGCCACAGCCAATTTTGGAAAACACAAATATGAGGTGAGTGTAT 1558
Chimp TTCTTAAACGCATCATGCCACAGCCAATTTTGGAAAACACAAATATGAAGTGAGTGTAT 1558
Macaque TTCTTAAATGCATCATGCCAGAGCCAATTTTGGAAAACACAAATATGAGGTGAGTGTAT 1482
.0...5...0...5...0...5...0...5...0...5...0...5...-2662

11
|
DQ094845 TTTGAAAACATATGTGAATATAATAGATCCTTAATTCATATTTGTGGATTTTATGGGAAAT 1618
Chimp TTTGAAAACATATGTGAATATAATAGATCCTTAATTCATATTTGTGGATTTTATGGGAAAT 1618
Macaque TTTGAAAACATATGTGAATATAATAGATCCTTAATTAATATTTGTGGATTTTATCGGAAAT 1542
.0...5...0...5...0...5...0...5...0...5...0...5...-2602

DQ094845 ACTTGTTTTCTAAGGCATCTGTCTTGCAAAAAGTCAGTTTCTGCTATGAAGGATGTAAA 1678
Chimp ACTTGTTTTCTAAGGCATCTGTCTTGCAAAAAGTCAGTTTCTGCTATGAAGGATGTAAA 1678
Macaque ACTTGTTTTCTAAGGCATCTGTCTTGCAAAAAGTCAGTTTCTGCTGTGAAGGATGTAAA 1602
.0...5...0...5...0...5...0...5...0...5...0...5...-2542

DQ094845 GGGGATATGTAGGTTAAATTCGTTTCTGAGCTTTGCTTCCAGAGTAAACACCCAACTTA 1738
Chimp GGGGATATGTAGGTTAAATTCGTTTCTGAGCTTTGCTTCCAGAGTAAACACCCAACTTA 1738
Macaque GGGGATATGTAGGTTAAATTCGTTTCTGAGCTTTGCTTCCAGAGTAAACACCCAACTTA 1662
.0...5...0...5...0...5...0...5...0...5...0...5...-2482

DQ094845 CTTTTGCCCTAAAGTATTTTATGTTCTAGTAGAGAAGACTAACAACATATTTCTAAACCA 1798
Chimp CTTTTGCCCTAAAGTATTTTATGTTCTAGTAGAGAAGACTAACAACATATTTCTAAACCA 1798
Macaque CTTTTGCCCTAAAGTATTTTATGTTCTAGTAGAGAAGACTAACAATATATTTCTAAACCG 1722
.0...5...0...5...0...5...0...5...0...5...0...5...-2422

DQ094845 CTAAGTAATTTATGTAAACTTCGCCTTACAAACTATACTTGTGTGACACTTATATGAGCAA 1858
Chimp CTAAGTAATTTATGTAAACTTCGCCTTACAAACTATACTTGTGTGACACTAATATGAGCAA 1858
Macaque CTAAGTAATTTACATAAACTTCACCTTACAAACTGTATTTGTGTGACACTTATATGAGCAA 1782
.0...5...0...5...0...5...0...5...0...5...0...5...-2362
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DQ094845 AAGCATTTTCATATTTCTTACTATATCATTCAATTCTTGCTTACCCCAATGGAAGTGACT 1918
Chimp AAGCATTTTCATATTTCTTACTACATCATTCAATTCTTGCTCACCCCAATGGAAGTGACT 1918
Macaque AAGCATTTTCATATTTCTTACTATATTTCAATTCTTGCTCACCCCAATGGAAGTGACT 1842
.0...5...0...5...0...5...0...5...0...5...0...5...-2302
***** ** *****

DQ094845 TTATGCCCTTTAGAGACAATGAAATCAGGTACTTCGTGATTTCTCTTAAAAAAAAA 1978
Chimp TTATGCCCTTTAGAGACAATGAAATAGGTACTTCGTGATTTCTCTTAAAAAAAAA- 1977
Macaque TTATGCCCTTTAGAGATAATGAAATAGGTACTTT-TGATTTCTCTTAGGAAAAAAAA- 1900
.0...5...0...5...0...5...0...5...0...5...0...5...-2242
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DQ094845 AAATGAAGTAGAAAGCTCCAAGTTGGTGAATCTGGAACCTGGGTATTCCAGTTCAGTT 2038
Chimp --ATGAAGTAGAAAGCTCCAAGTTGGTGAATCTGTATCCTGGGTATTCCAGTTCAGTT 2035
Macaque --ATGAAGTAGAAAGCTCCAAGTTGGTGAATCTGGAACCTGGGTATTCCAATTCCAGTT 1958
.0...5...0...5...0...5...0...5...0...5...0...5...-2182
***** * *****

DQ094845 GTAGCCCTTCCTCCCTATCCATCACTCCTGTCTGCATGTAATTATGCAATACATTGAAAA 2098
Chimp GTAGCCCTTCCTTCCTATCCATCACTCCTGTCTGCATGTAATTATGCAATACATTGAAAA 2095
Macaque GTAGTGCTTCCTCCCTGTCCATCACTCCTGTCTGCATGTAATTATGCAATACATTGAAAA 2018
.0...5...0...5...0...5...0...5...0...5...0...5...-2122
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DQ094845 GATTAAAAGATGGGTCTTGGACTCAGGCAGACCTGGGTCAAATCCAGATTCTGGCACTGC 2158
Chimp GATTAAAAGATGGGTCTTGGACTCAGGCAGACCTGGGTCAAATCCAGATTCTGGCACTGC 2155
Macaque GATTAAAAGATGGGTCTTAGACTCAGGCAGACCTGGGTCAAATCCAGATTCTGGCACAG 2078
.0...5...0...5...0...5...0...5...0...5...0...5...-2062
***** *****

DQ094845 CCAGCCATTGCCCTGGGCAAGCCATTTTCTCTTTGAACCTCATTTGTGAATTAAGCTA 2218
Chimp CCAGCCATTGCCCTGGGCAAGCCATTTTCTCTTTGAACCTCATTTGTGAATTAAGCTA 2215
Macaque CCAGCCATTGCCCTGGGAAGGCCATTTTCTCTTCGAACCTCATTTGTGAATTAAGCTA 2138
.0...5...0...5...0...5...0...5...0...5...0...5...-2002
***** * *****

DQ094845 AAAATAGTCCCCACCCCATGGGACTGTGGGAAGGATTAATAGAAATAATGCATGAAAAG 2278
Chimp AAAATAGTCCCCACCCCATGGGACTGTGGGAAGGATTAATAGAAATAATGCATGAAAAG 2275
Macaque AAAATAGTCCCCACCCCATGGGACTGTGGGAAGGATTAATAGAAATAATGCATGAAAAG 2198
.0...5...0...5...0...5...0...5...0...5...0...5...-1942

DQ094845 CAAATAGCAGAATGGTCCATAAATGTTAACCATTGTTATGTTATTATGTAATCTACAAAG 2338
Chimp CAAATAGCAGAATGGTCCATAAATGTTAACCATTGTTATGTTATTATGTAATCTACAAAG 2335
Macaque CACATAGCAGAATGGTCCATAAATGTTAGCCATTGTTATGTTATTATGTAATCTGCAAAG 2258
.0...5...0...5...0...5...0...5...0...5...0...5...-1882
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DQ094845 TACGTTTAGTTACACTTCATGAAATACTTTTCAGTTTTTCAAAGACACCACTAATACATGG 2398
Chimp TACGTTTAGTTACACTTCATGAAATACTTTTCAGTTTTTCAAAGACACCACTAATACATGG 2395
Macaque TATGTTTAGTTACACTTCATGAAATAGTTTCAGTTTTTCAAAGACACCACTAATACATGG 2318
.0....5....0....5....0....5....0....5....0....5....0....5....-1822
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13 14 c
| | |
DQ094845 GAAATCAAACCCTGAAAATTAATTTCACTTTAGCAGTAAAGTCACATGCCAGATGGAAAG 2458
Chimp GAAATCAAACCCTGAAAATTAATTTCACTTTAGCAGTAAAGTCACATGCTAGATGGAAAG 2455
Macaque GAAATCAAACCCTGAAAATTAATTTCACTTTAGCAGTAAAGTCACATGCCAGATGCAAAG 2378
.0....5....0....5....0....5....0....5....0....5....0....5....-1762

15
|
DQ094845 GATAGTATTTTCATGAACAAAGATCTTACTTTTGAGATTTGGTCTTACTTTTTTCTTTTTC 2518
Chimp GATAGTATTTTCATGAACAAAGATTTTACTTTTGAGATTTGGTCTTACTTTTTTCTTTTTC 2515
Macaque GATAGTATTTTCATGAACAAAGATCTTACTTTTGAGATTTGGTCTTACTTTTTT-TATTTTC 2437
.0....5....0....5....0....5....0....5....0....5....0....5....-1702

DQ094845 TTAAGGGAGAATTAT----- 2533
Chimp TTAAGGGAGAATTAT----- 2530
Macaque ATAAGGAAGAAATATATATATATATATTTATATATTTGGTTTTTATTTATTTGTATATTTAT 2497
.0....5....0....-1687

DQ094845 -----CTTGTGTTT-----TTTGTTT----- 2549
Chimp -----CTTGTGTTT-----TTTGTTT----- 2546
Macaque TTATAATTTGTATTTATATATTTATATATATATATATATATATATATATTTATATTTATTAT 2557
.5....0.. ..5....-1671
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c 16
| |
DQ094845 -----TGTTTTGTTTTGAGATGGAGTCTTGTTCTGTCACCCAGGCTGGAGCGCA 2598
Chimp -----TGTTCTGTTTTGAGATGGAGTCTTGTTCTGTCACCCAGGCTGGAGCGCA 2595
Macaque TTATTTATTTATTTTTTTTTTTGAGATGGAGTCTTGTTCTGTCACCCAGGCTGAAGTGCA 2617
0....5....0....5....0....5....0....5....0....5....-1622
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DQ094845 GTGACGTGATCTCGGCTCACTGCAACCTTCACCTCCCGGGTTCAAGAGATTCTCCTGTCT 2658
Chimp GTGACGTGATCTCGGCTCACTGCAACCTTCACCTCCCGGGTTCAAGAGATTCTCCTGTCT 2655
Macaque GTGGCACGGTCTCGCCTCACTGCAACCTCCACCTCCAGGTTCAAGTATTCTCCTGTCC 2677
.0....5....0....5....0....5....0....5....0....5....0....5....-1562
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17
|
DQ094845 CAGCCTCCCGAGTAGCTGGGACTACAGGTACGTGCCACCACACCTGGCTAATTTTTGTAT 2718
Chimp CAGCCTCCCGAGTAGCTGGGACTACAGGTACGTGCCACCACACCTGGCTAATTTTTGTAT 2715
Macaque CAGCCTCCCGAGTAGCTAAGACTACAAGTGCC-----CGCCTGGCTAATTTTTGTAT 2729
.0....5....0....5....0....5....0....5....0....5....0....5....-1502

c22
|
DQ094845 TTTTAGTAGAGACAAGAGTTACACCATATTGGCCAGGATCTTTTGCTTTCTATAGCTTCA 2778
Chimp TTTTAGTAGAGACAAGAGTTACACCATATTGGCCAGGATCTTTTGCTTTCTATAGCTTCA 2775
Macaque TTTTAGTAGAGACA-GAGTTACACCATATTGGCCAAGATCTTTTGCTTTCTATAGCTCCA 2788
.0....5....0....5....0....5....0....5....0....5....0....5....-1442

18
|
DQ094845 AAATGTTCTTAATGTTAAGACATCTTAATACTCTGAACCATATGAATTTGCCATTTGG 2838
Chimp AAATGTTCTTAATGTTAAGACATCTTAATACTCTGAACCATATGAATTTGCCATTTGG 2835
Macaque AA-TGTTCTTAATGTTAAGACACTCTTAAGACTCTGAACCATATGAATTTGCCATTTGG 2847
.0...5...0...5...0...5...0...5...0...5...0...5...-1382
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19 c
| |
DQ094845 TAAGTCACAGACGCCAGATGGTGGCAATTTACATGGCGCAACCCGAAAGATTAACAAAC 2898
Chimp TAAGTCACAGACGCCAGATGGTGGCAATTTACATGGTGCACCCGAAAGATTTACAAAC 2895
Macaque TAAGTCACAGACACCAGATGGTGGCAATTTACATGGTGCACCCGAAAGATTAACAAAC 2907
.0...5...0...5...0...5...0...5...0...5...0...5...-1322

20
|
DQ094845 TATCCAGCAGATGAAAGGATTTTTTTTAGTTTCATTGGGTTTACTGAAGAAATTGTTGA 2958
Chimp TATCCAGCAGATGAAAGGATTTTTTTTAGTTTCATTGGGTTTACTGAAGAAATTGTTGA 2955
Macaque TATCCAGCAGATGAAAGGATTTTTTT-AGTTGCATTGGGATTACTGAAGAAATTGTTGA 2966
.0...5...0...5...0...5...0...5...0...5...0...5...-1262

DQ094845 ATTCTCATTGCATCTCCAGTTCAACAGATAATGAGTGAGTGATGCCACACTCTCAAGAGT 3018
Chimp ATTCTCATTGCATCTCCAGTTCAACAGATAATGAGTGAGTGATGCCACACTCTCAAGAGT 3015
Chimp5pr -----AAGAGT
Macaque ATTCTCAGTGCATCTCCAGTTCAACAGATAATGAGGGAGTGATGCCACACTCTCAAGAGT 3026
.0...5...0...5...0...5...0...5...0...5...0...5...-1202

DQ094845 TAAAAACAAAACAACAA---AAAAATAAAACAAAAGCACACAACCTTTCTCTCTGTCC 3075
Chimp TAAAAACAAAACAACAA---AAAAATAAAACAAAAGCACACAACCTTTCTCTCTGTCC 3072
Chimp5pr TAAAAACAAAACAACAA---AAAAATAAAACAAAAGCACACAACCTTTCTCTCTGTCC
Macaque TAAAAACAAAACAACAAACAAAAAATAAAACAAAAGTACACAACCTTTCTCTCTCCGTCC 3086
.0...5...0...5...0...5...0...5...0...5...0...5...-1145

DQ094845 CAAAATACATACTTGCATACCCCGCTCCAGATAAAAATCCAAAGGGTAAAACGTCTTCA 3135
Chimp CAAAATACATACTTGCATACCCCGCTCCAGATAAAAATCCAAAGGGTAAAACGTCTTCA 3132
Chimp5pr CAAAATACATACTTGCATACCCCGCTCCAGATAAAAATCCAAAGGGTAAAACGTCTTCA
Macaque CGAAATACATACTTGCATACCTCTGCTCCAGGTGAAATCCAAAGGGTAAAACGTCTTCA 3146
.0...5...0...5...0...5...0...5...0...5...0...5...-1085
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DQ094845 TGCCTGCAAATTCCTAAGGAGGGCACCTAAAGTACTTGACAGCGAGTGTGCTGAGGAAAT 3195
Chimp TGCCTGCAAATTCCTAAGGAGGGCACCTAAAGTACTTGACAGCGAGTGTGCTGAGGAAAT 3192
Chimp5pr TGCCTGCAAATTCCTAAGGAGGGCACCTAAAGTACTTGACAGCGAGTGTGCTGAGGAAAT
Macaque TGCCTGCAAATTCCTAAGGAGGGCACCTAAAGTACTTGACAACGAGTGTGCTGAGGAAAT 3206
.0...5...0...5...0...5...0...5...0...5...0...5...-1025

21
|
DQ094845 CGGCAGCTGTTGAAGTCACCTCCTGTG--CTCTTGCCAAATGTTTGAAGGGAATACACT 3253
Chimp CGGCAGCTGTTGAAGTCACCTCCTGTG--CTCTTGCCAAATGTTTGAAGGGAATACACT 3250
Chimp5pr CGGCAGCTGTTCAAGTCACCTCCTGTG--CTCTTGCCAAATGTTTGAAGGGAATACACT
Macaque CGGCAGCTGTTGAAGTCACCTCCTGTGTGCTCTTGCCAAATGTTTGAAGTGAATATACT 3266
.0...5...0...5...0...5...0...5...0...5...0...5...-967

DQ094845 GGGTTACCGGGTGTATGTTGGGAGGGGAGCATTATCAGTGCTCGGGTGAGGCAAGTTTCG- 3312
Chimp GGGTTACCGGGTGTATGTTGGGAGGGGAGCGTTATCAGTGCTCGGGTGAGGCAAGTTTGT 3310
Chimp5pr GGGTTACCGGGTGTATGTTGGGAGGGGAGCGTTATCAGTGCTCGGGTGAGGCAAGTTTGT
Macaque GGGTTACCGGGTGTATGCTGGGAGGGGGGCATTAGCAGTGCTTGGGTGAGGGAAGTTTGT 3326
.5....0....5....0....5....0....5....0....5....0....5....0... -908
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DQ094845 GAGTACCCAGATGGAGACATCCGTGTCTGTGTGCTCTGGATGCCTCCAAGCCAGCG--T 3370
Chimp GAGTACCCAGATGGAGACATCCGTGTCTGTGTGCTCTGGATGCCTCCAAGCCAGTG--T 3368
Chimp5pr GAGTACCCAGATGGAGACATCCGTGTCTGTGTGCTCTGGATGCCTCCAAGCCAGCG--T
Macaque GAGTACCCAGATGGAGACATCCGTGTCTGTGTGCTCTGGATGCCTCCAAGCCAGCGTGT 3386
.5....0....5....0....5....0....5....0....5....0....5....0 0 -850
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DQ094845 GTGTTTACTTTCTGTGTGTGTCACCATGTCTTTGTGCTTCTGGGTGCTTCTGTGTTTGT 3430
Chimp GTGTTTACTTGTGTGTGTGTCACCATGTCTTTGTGCTTTTGGGTGATTCTGTGTTTGT 3428
Chimp5pr GTGTTTACTTTCTGTGTGTGTCACCATGTCTTTGTGCTTCTGGGCCTTCTGTGTTTGT
Macaque GTGTTTACTTTCTGTGTGTGTCACCATGCCTTTGTGCTTCTGGGTGCTTCTGTGTTTGT 3446
.5....0....5....0....5....0....5....0....5....0....5....0 -790
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DQ094845 TCTGGCCGCGTTTCTGTGTTGGACAGGGGTGACTTTGTGCCGGATGGCTTCTGTGTGAGA 3490
Chimp TTTGGCAGCGCTTTAGTGTGGACAGGGATGAATTTGTGCCGGATGGCTTCTTTTGGAAA 3488
Chimp5pr TCTGGCCGCGTTTCTGTGTTGGACAGGGATGACTTTGTGCCGGATGGCTTCTGTGTGAGA
Macaque TGTGGCCGCGTTTCTGTGTTGGACAGGGGTGACTTTGTGCCGTGACAGCTTCTGTGTGAGC 3506
.5....0....5....0....5....0....5....0....5....0....5....0 -730
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DQ094845 GCGCGCGAGTGTGCATGTCGGTGAGCTGGGAGGGTGTGTCTCAGTGTCTATGGCTGTG 3550
Chimp GGCATCTCGAGTGTGCATGTCT----CTGGACCTTTAGTGAGTTCGTTCCCTGGTTGTG 3543
Chimp5pr GCGCGCGAGTGTGCATGTCGGTGAGCTGGGAGGGTGTGTCTCAGTGTCTATGGCTGTG
Macaque GCGCGCGAGTGTGCATGTCGGTGAGCTGGGAGGGTGTGTCTCAGTGTCTATAGCTGTG 3566
.5....0....5....0....5....0....5....0....5....0....5....0 -670
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DQ094845 GTTCGGTATAAGTCTGAGCATGTCTGCCAGGGTGTATTTGTGCCCTGTATGTGCGTGCCCTC 3610
Chimp GTGCGGTATAAGTTAGAGCA--TTAGGCAG--TTCATTTGTGCCCTGTATGTGCGTGCCCTA 3599
Chimp5pr GTTCGGTATAAGTCTGAGCATGTCTGCCAGGGTGTATTTGTGCCCTGTATGTGCGTGCCCTC
Macaque GTTCCGTATAAGTCTGAGCATGTCTGCCGGGTGTATTTGTGCCCTGTATGTGCGTGCCCTT 3626
.5....0....5....0....5....0....5....0....5....0....5....0 -610
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DQ094845 GGTGGGCACTCTCGTTTCTTCCGAATGTGGGGCAGTGCCGGTGTG--CTGCCCTCTGCC 3668
Chimp GGTGGGCACTCTCGTTTCTTCCGAATGTGGGGCAGTGCCGGTGTG--CTGCCCTCTGCC 3657
Chimp5pr GGTGGGCACTCTCGTTTCTTCCGAATGTGGGGCAGTGCCGGTGTG--CTGCCCTCTGCC
Macaque GGTGGGCACTCTCGTTTCTTCCGAATGTGGGGCAGTGCCGGTGTGCTGCTGCCCTCTGCC 3686
.5....0....5....0....5....0....5....0....5....0....5....0 -552
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DQ094845 TTGAGACCTCAAGCCGCGCAGGCGCCAGGGCAGGCAGGTAGCGGCCACAGAAGAGCCAA 3728
Chimp TTGAGACCTCAAGCCGCGCAGGCGCCAGGGCAGGCAGGTAGCGGCCACAGAAGAGCCAA 3717
Chimp5pr TTGAGACCTCAAGCCGCGCAGGCGCCAGGGCAGGCAGGTAGCGG
Macaque CTGAGACCTCAGGCCGCGCAGGCGCCAGGGCAGGCAGGTAGCGGCCACAGAAGAGCCAA 3746
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... -492

24 h
DQ094845 AAGCTCCCGGGTTGGCTGGTAAGCACACCACCTCCAGCTTTAGCCCTCTGGGGCCAGCCA 3788
Chimp AAGCTCCCGGGTTGGCTGGTAAGCACACCAGCTCCAGCTTTAGCCCTCTGGGGCCAGCCA 3777
Macaque AAGCTGCTGGGTTGGCTGGTAAGCACGCCAGCTCCAGCTTTAGCCCTCTGGGGCCAGCCA 3806
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... -432

25 c32 c33
DQ094845 GGGTAGCCGGGAAGCAGTGGTGGCCCGCCCTCCAGGGAGCAGTTGGGCCCGCCCGGGCC 3848
Chimp GGGTAGCCGGGAAGCAGTGGTGGCCCGCCCTCCAGGGAGCAGTTGGGCCCGCCCGGGCC 3837
Macaque GGGTAGCCGGGAAGGAGTGGTGGCCCGCCCGGGGAGCAGTTGGGCCCGCCCGGGCC 3866
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... -372

26 h C h
DQ094845 AGCCTCAGGAGAAGGAGGGCGAGGGGAGGGGAGG-----GAAAGGGGAGGA 3894
Chimp AGCCCCAGGAGAGGGAGGGCGAGGGGAGGGGAGGAAAGGGGAGGAGGAAAGGGGAGGA 3897
Macaque AGCCCCGAGAAGGAGGGAGGGCGAGAGGAGGGGAGG-----AAAGGGGATGG 3911
.0...5...0...5...0...5...0... ..5...0... -326
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27 28
DQ094845 GTGCCTCGCCCCCTTCGCGGCTGCCGGCGTGCACATTGGCCGAAAGTTCCCGTACGTCACGG 3954
Chimp GTGCCTCGCCCCCTTCGCGGCTGCCGGCGTGCACATTGGCCGAAAGTTCCCGTACGTCACGG 3957
Macaque GTGCCTCGCCCCCTTCGGGCTGCCGGCGTGCACATTGGCCGAAAGTTCCCTTACGTCACGG 3971
5...0...5...0...5...0...5...0...5...0...5...0...5...0... -266

29 30 c39 h > >>
DQ094845 CGAGGGCAGTTCCCTTAAAGTCTGTGCACATAACGGGCAGAACGCACTGCCAAGCGGCT 4014
Chimp CGAGGGCAGTTCCCTTAAAGTCTGTGCACATAACGGGCAGAACGCACTGCCAAGCGGCT 4017
Macaque CGAGGGCAGTTCCCTTAAAGTCTGTGCACATAACGGGCAGAGCGCACTCCGAGGCGGCT 4031
5...0...5...0...5...0...5...0...5...0...5...0...5...0... -206

>>>>
DQ094845 TCTTCAGAGCACGGGCTGGAAC TGGCAGGCACCGCGAGCCCC TAGCACCCGACAAGCTGA 4074
Chimp TCTTCAGAGCACGGGCTGGAAC TGGCAGGCACCGCGAGCCCC TAGCACCCGACAAGCTGA 4077
Macaque TCTCCAGAGCACGGGCTGGAAC TGGCAGGCACCGCGAGCCCC TGGCACCCGACAAGCTAA 4091
5...0...5...0...5...0...5...0...5...0...5...0...5...0... -146
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DQ094845 GTGTGCAGGACGAGTCCCCACCACACCCACACCCAGCCGCTGAATGAGGCTTCCAGGCG 4134
Chimp GTGTGCAGGACGAGTCCCCACCACACCCACACCCAGCCGCTGAATGAGGCTTCCAGGCG 4137
Macaque GTGTACAAGACGTGTCCCCACCACACCCACCCACCGCCGCTGAATGAGGCTTCCAGGAG 4151
5...0...5...0...5...0...5...0...5...0...5...0...5...0... -86

h c50
| |
DQ094845 GATCATTCTGATGGTGTGGATTTGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCA 4734
Chimp GATCATTCTGATGGTGTGGATCGTGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCA 4737
Macaque GATCATTCTGATGGTGTGGATCGTGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCA 4751
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 515

36
|
DQ094845 CTGGTACCGGGCCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGA 4794
Chimp CTGGTACCGGGCCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGA 4797
Macaque CTGGTACCGGGCCACCCACCAGGAAGCCATCAACTGCTATGCCAAGGAGACCTGCTGTGA 4811
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 575

DQ094845 CTTCTTCACGAACCAAGCCTATGCCATTGCCCTTCCATCGTGTCTTCTACGTTCCCCT 4854
Chimp CTTCTTCACGAACCAAGCCTATGCCATTGCCCTTCCATCGTGTCTTCTACGTTCCCCT 4857
Macaque CTTCTTCACGAACCAAGCCTATGCCATTGCCCTTCCATCGTGTCTTCTACGTTCCCCT 4871
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 635

37
|
DQ094845 GGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGGCCAAAAGGCAGCTCCAGAA 4914
Chimp GGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGGCCAAAAGGCAGCTCCAGAA 4917
Macaque GGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGGCCAAAAGGCAGCTCCAGAA 4931
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 695

DQ094845 GATTGACAAATCTGAGGGCCGCTTCCATGTCCAGAACCTTAGCCAGGTGGAGCAGGATGG 4974
Chimp GATTGACAAATCTGAGGGCCGCTTCCATGTCCAGAACCTTAGCCAGGTGGAGCAGGATGG 4977
Macaque GATTGACAAATCTGAGGGCCGCTTCCATGTCCAGAACCTTAGCCAGGTGGAGCAGGATGG 4991
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 755

DQ094845 GCGGACGGGGCATGGACTCCGCAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCT 5034
Chimp GCGGACGGGGCATGGACTCCGCAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCT 5037
Macaque GCGGACGGGGCATGGACTCCGCAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCT 5051
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 815

38
|
DQ094845 CAAGACGTTAGGCATCATCATGGGCACTTTCACCTCTGCTGGCTGCCCTTCTTCATCGT 5094
Chimp CAAGACGTTAGGCATCATCATGGGCACTTTCACCTCTGCTGGCTGCCCTTCTTCATCGT 5097
Macaque CAAGACGTTAGGCATCATCATGGGCACTTTCACCTCTGCTGGCTGCCCTTCTTCATCGT 5111
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 875

DQ094845 TAACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACATCCTCCTAAA 5154
Chimp TAACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACATCCTCCTAAA 5157
Macaque TAACATTGTGCATGTGATCCAGGATAACCTCATCCCTAAGGAAGTTTACATCCTCCTAAA 5171
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 935

DQ094845 TTGGATAGGCTATGTCAATTCGGTTTCAATCCCCTTATCTACTGCCGGAGCCCAGATTT 5214
Chimp TTGGATAGGCTATGTCAATTCGGTTTCAATCCCCTTATCTACTGCCGGAGCCCAGATTT 5217
Macaque TTGGGTGGGCTATGTCAATTCGGTTTCAATCCCCTTATCTACTGCCGGAGCCCAGATTT 5231
...0...5...0...5...0...5...0...5...0...5...0...5...0...5 995
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DQ094845 CAGGATTGCCTTCCAGGAGCTTCTGTGCCTGCGCAGGTCTTCTTTGAAGGCCTATGGGAA 5274
 |
 Chimp CAGGATTGCCTTCCAGGAGCTTCTGTGCCTGCGCAGGTCTTCTTTGAAGGCCTATGGGAA 5277
 Macaque CAGGATTGCCTTCCAGGAGCTTCTGTGTCTGCGCAGGTCTTCTTTGAAGGCCTGTGGGAA 5291
0....5....0....5....0....5....0....5....0....5....0....5.... 1055

DQ094845 TGGCTACTCCAGCAAC-----GGCAACACAGGGGAGCAGAGTGGATATCACGTGGAACA 5328
 |
 Chimp TGGCTACTCCAGCAAC-----GGCAACACAGGGGAGCAGAGTGGATATCACGTGGAACA 5331
 Macaque TGGCTACTCCAGCAACAGCAATGGCAACACAGGGGAGCAGAGTGGATATCACCTGGAACA 5351
0....5....0.5....0....5....0....5....0....5.... 1109

DQ094845 GGAGAAAGAAAATAAACTGCTGTGTGAAGACCTCCAGGCACGGAAGACTTTGTGGGCCA 5388
 |
 Chimp GGAGAAAGAAAATAAACTGCTGTGTGAAGACCTCCAGGCACGGAAGACTTTGTGGGCCA 5391
 Macaque GGAGAAAGAAAATAAACTGCTGTGTGAAGACCTCCAGGCACGGAAGACTTTGTGGGCCA 5411
 0....5....0....5....0....5....0....5....0....5....0....5.... 1169

c55 c c56
 |/
 DQ094845 TCAAGGTACTGTGCCTAGCGATAACATTGATTACAAGGGAGGAATTGTAGTACAAATGA 5448
 |
 Chimp TGAAGGTACTGTGCCTAGCGATAACATTGATTACAAGGGAGGAATTGTAGTACAAATGA 5451
 Macaque TCAAGGTACTGTGCCTAGCGATAACATTGATTACAAGGGAGGAGTTGTAGTACAAATGA 5471
 0....5....0....5....0....5....0....5....0....5....0....5.... 1229
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40 c
 | & |
 DQ094845 CTCACTGCTGTAAAGCAGTTTTTCTACTTTTTAAAGACCCCCCCCCGCCCAACAGAACT 5508
 |
 Chimp CTCACTGCTGTAAAGCAGTTTTTCTACTTTTTAAAGACCCCCCCCC-CCCATCAGAACT 5510
 Macaque CTCACTGCTGTAAAGCAGTTTTTCTACTTTTTAAAGACCCCCCCCCCAACAGAACT 5531
 0....5....0....5....0....5....0....5....0....5....0....5.... 1289

c h
 | |
 DQ094845 AAACAGACTATTTAACTTGAGGGTAATAAACTTAGAATAAAAATTGTAATAATTGTATAGAG 5568
 |
 Chimp AAACAGACTATTTAACTTGAGGGTAATAACCTTAGAATAAAA-----TTGTATAGAG 5562
 Macaque AAACAGACTATTTAACTTGAGGGTAATAAACTTAGAATAAAA-----TTGTATAGAG 5583
 0....5....0....5....0....5....0....5....0....5....0....5.... 1349

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 DQ094845 ATATGCAGAAGGAAGGGCATCCTTCTGCCTTTTTTATTTTTTTAAGCTGTAAAAAGAGAG 5628
 |
 Chimp ATATGCAGAAGGAAGGGCATCCTTCTGCCTTTTTTATTTTTTTAAGCTGTAAAAAGAGAG 5622
 Macaque ATATGCAGAAGGAAGGGCATCCTTCTGCCTTTTTTATTTTTTTAAGCTGTAAAAAGAGAG 5643
 0....5....0....5....0....5....0....5....0....5....0....5.... 1409

DQ094845 AAAACTTATTTGAGTGATTATTTGTTATTTGTACAGTTCAGTTCCTCTTTGCATGGAATT 5688
 |
 Chimp AAAACTTATTTGAGTGATTATTTGTTATTTGTACAGTTCAGTTCCTCTTTGCATGGAATT 5682
 Macaque AAAACTTATTTG-GTGATTATTTGTTATTTGTACAGTTCAGTTCCTCTTTGCATGGAATT 5702
 0....5....0....5....0....5....0....5....0....5....0....5.... 1469

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 DQ094845 TGTAAGTTTATGTCTAAAGAGCTTTAGTCCTAGAGGACCTGAGTCTGCTATATTTTCATG 5748
 |
 Chimp TGTAAGTTTTTGTCTAAAGAGCTTTAGTCCTAGAGGACCTGAGTCTGCTATGTTTTTCATG 5742
 Macaque TGTAAGTTTATGTCTAAAGGGCTTTAGTCCTAGAGGACCTGAGTCTGCTATGTTTTTCATG 5762
 0....5....0....5....0....5....0....5....0....5....0....5.... 1529

DQ094845 ACTTTTCCATGTATCTACCTCACTATTCAAGTATTAGGGGTAATATATTGCTGCTGGTAA 5808
Chimp ACTTTTCCATGTATCTACCTCACTATTCAAGTATTAGGGGTAATATACTGCTGCTGGTAA 5802
Macaque ACTTTTCCATGTATCTACCTCACTATTCAAGTATTAGGGGTAATATATTGCTGCTGGTAA 5822
0...5...0...5...0...5...0...5...0...5...0...5... 1589

DQ094845 TTTGTATCTGAAGGAGATTTTCCTTCCACACCCCTTGGACTTGAGGATTTTGAATATCTC 5868
Chimp TTTGTATCTGAAGGAGATTTTCCTTCCACACCCCTTGGACTTGAGGATTTTGAATATCTC 5862
Macaque TTTGTATCTGAAGGAGATTTTCCTTCCACACCCCTCGGACTTGAGGATTTTGAATATCTC 5882
0...5...0...5...0...5...0...5...0...5...0...5... 1649

DQ094845 GGACCTTTCAGCTGTGAACATGGACTCTTCCCCACTCCTCTTATTTGCTCACACGGGGT 5928
Chimp GGACCTTTCAGCTGTGAACATGGACTCTTCCCCACTCCTCTTATTTGCTCACACGGGGT 5922
Macaque GGACCTTTCAGCTGTGAACATGGACTCTTCCCC-GCTCCTCTTATTTGCTCACACGGGGT 5941
0...5...0...5...0...5...0...5...0...5...0...5... 1709

DQ094845 ATTTTAGGCAGGGATTTGAGGAGCAGCTTCAGTTGTTTTCCCGAGCAAAGTCTAAAGTTT 5988
Chimp ATTTTAGGCAGGGATTTGAGGAGCAGCTTCAGTTGTTTTCCCGAGCAAAGTCTAAAGTTT 5982
Macaque ATTTTAGGCAGGGATTTGAGGAGCAGCTTCAGTTGTTTTCCCGAGCAAAGTCTAAAGTTT 6001
0...5...0...5...0...5...0...5...0...5...0...5... 1769

DQ094845 ACAGTAAATAAATTGTTTGACCATGCCTTCATTGCACCTGTTTCTCCAAAACCCCTTGAC 6048
Chimp ACAGTAAATAAATTGTTTGACCATGCCTTCATTGCACCTGTTTCTCCAAAACCCCTTGAC 6042
Macaque ACAGTAAATAAATTGTTTGACCATGCCTTCATTGCACCTGTTTCTCCAAAACCCCTTGTC 6061
0...5...0...5...0...5...0...5...0...5...0...5... 1829

DQ094845 TGGAGTGCCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTTGTGCCCCAAATCAGTTCTG 6108
Chimp TGGAGTGCCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTTGTGCCCCAAATCAGTTCTG 6102
Macaque TGGAGTGCCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTTGTGAAAAACACAGGTAACACTTGTGTAATAACTGCCCAT 6121
0...5...0...5...0...5...0...5...0...5...0...5... 1889

DQ094845 GACTTAATGTAGAATGATACAAGAATGACATGCACAGATTGCTTAACCCCTTTCATTTGCC 6168
Chimp GACTTAATGTAGAATGATACAAGAATGACATGCACAGATTGCTTAACCCCTTTCATTTGCC 6162
Macaque GACTTAATGTAGAATGATACAAGAATGACATGCACAGATTGCTTAACCCCTTTCATTTGCC 6181
0...5...0...5...0...5...0...5...0...5...0...5... 1949

DQ094845 TTTGAGTCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTTGTGCCCCAAATCAGTTCTG 6228
Chimp TTTGAGTCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTTGTGCCCCAAATCAGTTCTG 6222
Macaque TTTGAATCTGCTGCTGCAAAGCTGCATCTCTCCTGACACTCATGCCCAAATCAGTTCTG 6241
0...5...0...5...0...5...0...5...0...5...0...5... 2009

DQ094845 CCTGCTCTTAGTATAGCTCAACTCTCCCTATGGTTATTGTTCTGTGTTACCTCAGAA 6288
Chimp CCTGCTCTTAGTATAGCTCAACTCTCCCTATGGTTATTGTTCTGTGTTACCTCAGAA 6282
Macaque CCTGCTCTTAGTATAGCTCAACTCTCCCTATGGTTATTGTTCTGTGTTACCTCGGAA 6301
0...5...0...5...0...5...0...5...0...5...0...5... 2069

DQ094845 ACACCTGACTCACAGAAGCGGAGTTAAGGGGATATGTTTTTTT-CTCTCCACGTGCACCCA 6347
Chimp ACACCTGACTCACAGAAGCGGAGTTAAGGGGATATGTTTTTTT-CTCTCCACGTGCACCCA 6341
Macaque ACACCTGACTCACAGAAGCGGAGTTATGGGCATATGTTTTTTTCTCTCCACGCGCCCCA 6361
0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2128
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DQ094845 CCACCCACCTTCCAGTTCTACTTGTTCAAAACGTTTATATTTCTGTCTTGGCCATGTG 6407
Chimp CCACCCACCTTCCAGTTCTACTTGTTCAAAACGTTTATATTTCTGTCTTGGCCATGTG 6401
Macaque CCACCCACCTTCCAGTTCTACTTGTTCATAACTGTTTATATTTATGTCTTGGCCATGTG 6421
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2188

DQ094845 TTACAGTGGAGCTCTTTGTACTGCATCAGGGCTTGGCATTTTAGGGATAAGGAAGATGTT 6467
Chimp TTACAGTGGAGCTCTTTGTACTGCATCAGGGCTTGGCATTTTAGGGATAAGGAAGATGTT 6461
Macaque TTGTGAGGAGCTCTTTGTACTGCATCAGGGCTTGGCATTTTAGGGATAAGGAAGATGTT 6481
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2248
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DQ094845 CTTATGAGGAAGCTACTCAGACATGGCCCCGTAATTCTGAGGGAAAATTCAAAAGGCATT 6527
Chimp CTTATGAGGAAGCTACTCAAACATGGCCCCGTAATTCTGAGGGAAAATTCAGAAGGCATT 6521
Macaque CTTGTGAGGAAGCTACTCGAACATGGCCCCGTAATTCAGGGAAAATTAAGGAAGGCATT 6541
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2308
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DQ094845 GGTCATGGGGAGAAAAGCTGGAGAACACATAACTGATGGATACCTCATGAAC TAGAAACA 6587
Chimp GGTCATGGGGAGAAAAGCTGGAGAACACATAACTGATGGATACCTCATGACCTAGAAACA 6581
Macaque GGTCATGGGGAGAAAAGCTGGAGAACACATAACTGATGGATACCTCATGACCTAGAAATA 6601
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2368
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DQ094845 GAATTTTAACCCCTTTTCCTTCTTCCCTTTGGTCCCTGTTTTCTCTCCACTGACTCTC 6647
Chimp GAATTTTAACCCCTTTTCCTTCTTCCCTTTGGTCCCTGTTTTCTCTCCACTGACTCTC 6641
Macaque GAATTTTAACCCCTTTTCCTTCTTCCCTTTGGTCCCTGTTTTCTCTCCACTGACTCTC 6661
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2428

DQ094845 CTCGATTAGTGTAAACCAAGTTCTGAGTCTTAGCACTGTTAGCATTTTGGACCAGATA 6707
Chimp CTCGATTAGTGTAAACCAAGTTCTGAGTCTTAGCACTGTTAGCATTTTGGACCAGATA 6701
Macaque CTCGGTTAGTGTAAACCAAGTTCTGAGTCTTAGCACTGTTAGCATTTTGGACCAGATA 6721
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2488
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DQ094845 ACTCTTTGTTATGGGGCTGCATCATTGTATGTGTAGCACCTCTGGCCTCTGTTTCATTAG 6767
Chimp ACTCTTTGTTATGGGGCTGCATCATTGTATGTGTAGCACCTCTGGCCTCTGTTTCATTAG 6761
Macaque ACTCTTTGTTATGGGGCTGCATCATTGTATGTGTAGCACCTCTGGCCTCTATTCATTAG 6781
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2548
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DQ094845 ATGCCAATAGCACCCCCTGCTTATAACAAGCAAAAATGTTTCCAGACATTGCAAAAAGAGC 6827
Chimp ATGCCAATAGCACCCCCTGCTTATAACAAGCAAAAATGTTTCCAGACATTGCAAAAAGAGC 6821
Macaque ATGCCAGGAGCATCCCCTGCTTATAACAGGCAAAAATGTTTCCAGATATTGCAAAAAGAGC 6841
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2608
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DQ094845 CCCTGAGGTGCGAATTAGCCCCTGGTTGAGAGTCACTGGTAGAACTGTAAAAATCTCAG 6887
Chimp CCCTGAGGTGCGAATTAGCCCCTGGTTGAGAGTCACTGGTAGAACTGTAAAAATCTCAG 6881
Macaque CCCTGAGGTGTGAATTAGCCCCTGATTGAGAGTCACTGGTAGAACT--AAAAATCTCAG 6899
.0...5...0...5...0...5...0...5...0...5...0...5...0...5... 2668
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DQ094845 CAGATACATACATTCTTTCTAATGCAAGCGCTTGATTGTGCAGAGCCTTAGAGAGGGATT 6947
Chimp CAGATACATACATTCTTTCTAATGCAAGCACTTGATTGCACAGAGCCTTAGAGAGGGATT 6941
Macaque CAGATATATACATTCTTTCT---GCAAGCACTTGATTGTGCCGAGCCTTGGAGAGGGATT 6956
.0...5...0...5...0...5...0...5...0...5...0...5... 2728

DQ094845 TTCACAGTTCACCTAGGCAGTAACAGACCCCTCACCAGCACTCTTTCATTCCATCATGCT 7007
Chimp TTCACAGTTCACCTAGGCAGTAACAGACCCCTCACCAGCACTCTTTCATTCCATCATGCT 7001
Macaque TTCACAGTTCACCTAGGCAGTAACACACCCCTCATCAGCACTCTTTCATTCCATCATGCT 7016
.0...5...0...5...0...5...0...5...0...5...0...5... 2788

DQ094845 GCCTTCTAAACTTGTTTTCTAGCTGCCCAAATAGTGATCATGAAATGTTAAGAAGGCTTT 7067
Chimp GCCTTCTAAACTTGTTTTCTAGCTGCCCAAATAGTGATCATGAAATGTTAAGAAGGCTTT 7061
Macaque GCCTCCTAAACTTGCTTTCTAGCTGCCCAAATAGTGACCCTGAAGTGTTAAGAAGGCTTC 7076
.0...5...0...5...0...5...0...5...0...5...0...5... 2848

DQ094845 AAGTCTGTACATGAATTGTTTGAGAGGGTTTATCAATGGAGGTGAGGCCTGTGGGCCATG 7127
Chimp AAGTCTGTACATGAATTGTTTGAGAGGGTTTATCAATGGAGGTGAGGCCTGTGGGCCATG 7121
Macaque AGGTCTGTACATGAATTGT-----CAATGGAGGTGAGGCCTGTGGGCCATG 7122
.0...5...0...5...0...5...0...5...0...5...0...5... 2908
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DQ094845 ACTCCTGTTTGTGAAGAGATTATAAATACTGTCAAGAGGCACGTTAGGGGAAATCACAAAA 7187
Chimp ACTCCTGTTTGTGAAGAGATTATAAATACTGTCAAGAGGCACGTTAGGGGAAATCACAAAA 7181
Macaque GCTCCTGCTTGTGAAGAGATTAGAATACTGTCAAGAGGCACGTTAGGGGAAATCACAAAA 7182
.0...5...0...5...0...5...0...5...0...5...0...5... 2968

DQ094845 GTAAACACATTTCTTCTCCCAGCCCCTTCTATTTTTGCCTGTGTGTCTGAGCCAGAGCT 7247
Chimp GTAAACACATTTCTTCTCCCAGCCCCTTCTATTTTTGCCTGTGTGTCTGAGCCAGAGCT 7241
Macaque GTAACACATTTCTTCTCCCAGCCCCTTCTATTTTTGCCTGTGTGTCTGAGCCAGAGCT 7242
.0...5...0...5...0...5...0...5...0...5...0...5... 3028

DQ094845 TGGCCAGGTTTGATGAAGTGGATCGTCTCCTTGGCAACGCCAGGCTAGAGCAGATCAG 7307
Chimp TGGCCAGGTTTGATGAAGTGGATCGTCTCCTTGGCAACGCCAGGCTAGAGCAGATCAG 7301
Macaque TGGCCAGGTTTGATGAAGTGGATCGTCTCCTTGGCAACGCCAGGCTAGGGCAGATCGG 7302
.0...5...0...5...0...5...0...5...0...5...0...5... 3088

DQ094845 CCTGCAGGTTTCATTGCCATTTCACTGGCTCATGAAGCTGACTCCACTCCCCTCTTCCTT 7367
Chimp CCTGCAGGTTTCATTGCCATTTCACTGGCTCATGAAGCTGACTCCACTCCCCTCTTCCTT 7361
Macaque CCTACAGGTTTCATTGCCATTTCACTGGCTCATGAAGCTGACTCCACTCCCCTCTTCCTT 7362
.0...5...0...5...0...5...0...5...0...5...0...5... 3148

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DQ094845 TCTGTTGCAGCCAAGGTCCCCAACCAGAAAAGCATTGGCCTTCTCTGCTTCCTGTCAACT 7427
Chimp TCTGTGCGAGCCAAGGTCCCCAACCAGAAAAGCATTGGCCTTCTCTGCTTCCTGTCAACT 7421
Macaque TCTATCCCAGCCAAGGTCCCCAACCAGAAAAGCATTGGCCTTCTCTGCTTCCTGTGAGCT 7422
.0...5...0...5...0...5...0...5...0...5...0...5... 3208
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DQ094845 CAATGATGGGATGTTTGGGTGAGCACCGAGCTATCAGGAGAAGGTTAGGCGCCTGTGATT 7487
Chimp CAATGATGGGACGTTTGGGTGAGCACTGAGCTATCAGGAGAGTGTAGGCGCCTGTGATT 7481
Macaque CAATGATGGGACGTTTGGGTGAGCACTGAGCTATCAGGAGAATGTTAGGCGCCTGTGATT 7482
.0...5...0...5...0...5...0...5...0...5...0...5... 3268

DQ094845 TTGGAACATGCCATGGCAAATTGGAGAATGTGTGCATTCAGTGCTTTTACTTTTTTCCA 7547
Chimp TTGGAACATGCCATGGCAAATTGGAGAATGTGTGCATTCAGTGCTTTTACTTTTTTCCA 7541
Macaque TTGGAACATGCCGTGGCAAATTGGGAATGTGTGCATTCAGTGCTTTTACTTTTTTCCA 7542
.0...5...0...5...0...5...0...5...0...5...0...5... 3328

DQ094845 AGGGTTTTTCATACCTATTGAAAACCTTATTACACATTATCACCTTCTCTTTCTACTGCT 7607
Chimp AGGGTTTTTCATACCTATTGAAAACCTTATTACACATTATCACATTCTCCTTCTACTGCT 7601
Macaque AGGGTTTGCATACCTATT----- 7560
.0...5...0...5...0...5...0...5...0...5...0...5... 3388

DQ094845 ATTATCACATTCTCTTTCTACTGCTCTGGTCTCCACACTCAGAGATTTGGGCAGCTTCTT 7667
Chimp ATTATCACATTCTCTTTCTACTGCTCTGGTCTCCACACTCAGAGATTTGGGCAGCTTCTT 7661
Macaque ---ATCACATTCTCTCTACTGCTCTGGTCCCCACACTCAGAGATTTGGGCAGCTTCTT 7617
.0...5...0...5...0...5...0...5...0...5...0...5... 3448

DQ094845 TG GCTAATATTATGCTCCCTGTAGCCTCATAAGATCTCAGACATGGAAGAGCCCATAGA 7727
Chimp TG GCTAATATTTATGCTCCCTGTAGCCTCATAAGATCTCAGACATGGAAGAGCCCATAGA 7721
Macaque TG GCTAATCTTCACTACTCCCGGTAGCCTCATAAAATCTCAGACATGGAAGAGCCCATAGA 7677
.0...5...0...5...0...5...0...5...0...5...0...5... 3508

DQ094845 AAGTATTTAACATCTGATGAGACTGAAACGCTGTGAGGTGAAGGGCTTGCCCAAGTAAG 7787
Chimp AAGTATTTAACATCTGATGAGACTGAAACGCTGTGAGGTGAAGGGCTTGCCCAAGTAAG 7781
Macaque AAGTATTTAACATCTGAAGAGACTGAAACGCTGTGAGGCGAAGGGCTTGCCCAAGTAAG 7737
.0...5...0...5...0...5...0...5...0...5...0...5... 3568

DQ094845 CAGCCAAGGATGTCAGAGTGGGA-CTCAAGCCAGGGAACCCAACCTGCTATTCCAGGAAC 7846
Chimp CAGCCAAGGATGTCAGAGTGGGA-CTCAAGCCAGGGAACCCAACCTGCTATTCCAGGAAC 7840
Macaque CAGCCAAGGATGTCAGAGTGGGAACCTCAAGCCAGGGAACCCAACCTGCTATTCCAGGAAC 7797
.0...5...0...5...0...5...0...5...0...5...0...5... 3627

DQ094845 GCTGCATTCTCCACCACATTAGCATTGCGTTCTTTCTCACCCTCAACTGGGGCTATA 7906
Chimp GCTGCATTCTCCACCACATTAGCATTGCGTTCTTTCTCACCCTCAACTGGGGCTATA 7900
Macaque GCTGCATTCTCCACCACATTAGCATTGAGTTCTTTCTCACCCTCAACTGGGGCTATA 7857
.0...5...0...5...0...5...0...5...0...5...0...5... 3687

DQ094845 ACATAACACATTCATTTAGCCAATATATTTTTCTTTGTCCTTAACACAAAATTTAGAG 7966
Chimp ACATAACACATTCATTTAGCCAATATATTTTTCTTTGTCCTTAACACAAAATTTAGAG 7960
Macaque ACATAACACATTCATTTAGCCAAGGTATTTTTCTTTGTCCTTAACACAAAATTTAGAG 7917
.0...5...0...5...0...5...0...5...0...5...0...5... 3747

DQ094845 CATAAACAAATAATCTGCAATAGAGACAAAAGAAATAATTGTTTCATTTAACTCAACAAGC 8026
Chimp CATAAACAAATAATCTGCAATAGAGACAAAAGAAATAATTGTTTCATTTAACTCAACAAGC 8020
Macaque CATAAACAAATAATCTGCAATAGGAACAAAAGAAACAATTGCTCATTTAACTCAGCAAGA 7977
.0...5...0...5...0...5...0...5...0...5...0...5... 3807

DQ094845 ATCCACTAGGATATCTTCTGCATTTAGGGAAGCTGGGAGATTCCCTTAGCTCTTTATAACC 8086
Chimp ATCCACTAGGATATCTTCTGCATTTAGGGAAGCTGGGAGATTCCCTTAGCTCTTTATAACC 8080
Macaque GTCCACTAAGATATCTTCTGCATTTAGGGAAGCTGGGAGATTCCCTTAGCCCTTTATAACC 8037
.0...5...0...5...0...5...0...5...0...5...0...5... 3867

DQ094845 AGATGTCGGTGTGTATATATACTCTTTTGCCTAAAGGAATGTCTAATGTAATTTCTGTT 8146
Chimp AGATGTCGGTGTGTATATATACTCTTTTGCCTAAAGGAATGTCTAATGTAATTTCTGTT 8140
Macaque AAATGTCAGTGTGTATATATACTCTTTTGCCTAAAGGAATGTCTAATGTAATTTCTGTT 8097
..0...5...0...5...0...5...0...5...0...5...0...5.. 3927
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DQ094845 AAAA-TTCAGGTATTAATGTTAATTCAGATTCACAGCTAAAAGGAGAGTTTAACCATATT 8205
Chimp AAAA-TTCAGGTATTAATGTTAATTCAGATTCACAGCTAAAAGGAGAGTTTAACCATATT 8199
Macaque AAAAATTCAGGTATTAATGTTAATTCAGATTCACAGCTAAAAGGAGAGTTTAACCATATT 8157
..0. ...5...0...5...0...5...0...5...0...5...0...5. 3986
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DQ094845 CACGTTCCCTTTAGGAATACTGTAGACACAAGAACCTTGATTAGTTTAAAGGGTCCTGATA 8265
Chimp CACGTTCCCTTTAGGAATACTGTAGACACAAGAACCTTGATTAGTTTAAAGGGTCCTGATA 8259
Macaque CACATTCCTTTACGAATATTGTAAGCACAAGAACCTTGATTAGTTTAAAGGGTCCTGATA 8217
...0...5...0...5...0...5...0...5...0...5...0...5. 4046
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DQ094845 AGCAAGAGCATTCTAGGCATATCTTAATCCTTTGCTTTCTACCTCTTTGGTGTGTGCTT 8325
Chimp AGCAAGAGTATGCTAGGCATATCTTAATCCTTTGCTTTCTACCTCTTTGGTGTGTGCTT 8319
Macaque AGCAAGAGTATCTAGCCATATCTTAATCCTTTACTTTCTACCTCTTTGGTGTGTGCTT 8277
...0...5...0...5...0...5...0...5...0...5...0...5. 4106
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DQ094845 TGTTTCTTTTGAGGGGTGGCTTTTGTGTCAGTGTCCCTTCGTCCTCTGTTTGC TGACATG 8385
Chimp TGTTTCTTTTGAGGGGTGGCTTTTGTGTCAGTGTCCCTTCGTCCTCTGTTTGC TGACATG 8379
Macaque TGTTTCTTTTGAGGGGTGGCTTTTGTGTTGGTGTCCCTTTGTCCTCTGTT-GCTGACAAG 8336
...0...5...0...5...0...5...0...5...0...5...0...5. 4166
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DQ094845 CTGGCCACCTAAGGTTTGTGTTGTATTCTCATCGTGAGTTTTTTTTTGCCTGGACAGC 8445
Chimp CTGGCCACCTAAGGTTTGTGTTGTATTCTCATCGTGAGTTTTTTTTT-GCCTGGACAGC 8438
Macaque TTGGCTACCTAAAATTTGTGTTGTATTCTCATCGGAAAGTTTTCTTT-GCCTGGACAGC 8395
...0...5...0...5...0...5...0...5...0...5...0...5. 4226
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DQ094845 AAGTTCTCAGAGTCTGTCAAATAAGAAGAACTTTTTTCTAAGATGCAAGCTGAGAGGTGT 8505
Chimp AAGTTCTCAGAGTCTGTCAAATAAGAAGAACTTTTTTCTAAGATGCAAGCTGAGAGGTGT 8498
Macaque AAGTTCTCAGAGTCTGTCAAATGAGAA--CTTTTTTCTAAGATGCAAGCTGACAGATGT 8452
...0...5...0...5...0...5...0...5...0...5...0...5. 4286
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DQ094845 GAACAGTGGCAGGACAGGGTGAGCCTCCCCACTGCAATAATTAATGGGATAAAGGAATCTG 8565
Chimp GAACAGTGGCAGGACAGGGTGAGCCTCCCCACTGCAATAATTAATGGGATAAAGGAATCTG 8558
Macaque GAACGGTGGCAGGACAGGGTGAGCCTCCCTACTG-AATAATTAATGGGATAAAGGAATCTG 8511
...0...5...0...5...0...5...0...5...0...5...0...5. 4346
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DQ094845 GAGAAAGGGGAGCTTGAGAATAGGAACTGTCTTTACATGATTCTTAGAATGTTTCTTATG 8625
Chimp GAGAAAGGGGAGCTTGAGAATAGGAACTGTCTTTACATGATTCTTAGAATGTTTCTTATG 8618
Macaque GAGAAAAGGGGAGCTTGAGAATAGGAACTATCTTTGCACGATTCTTGAATGTTTCTCATG 8571
...0...5...0...5...0...5...0...5...0...5...0...5. 4406
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DQ094845 GTGAACCTATTGCCAAATGGAGCCTAAACCAGAATCAGTCAGAAAAGTATTTATGGAGCAC 8685
Chimp GTGAACCTATTGCCAAATGAAGCCTAAACCAGAATCAGTCAGAAAAGTATTTATGGAGCAC 8678
Macaque GTGAACCTACTGCCAAATGGAGCCTAAACCAGAATCAATCAGAAAAGTATTTTTGGAGAAC 8631
. . . 0 5 0 5 0 5 0 5 0 5 0 5 0 5 4466
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DQ094845 CTA CTACTGTATGCAGCATGAGAAAAGTATAGGTTTCCATTTCTGCCTTTTGGATCATGATAT 8745
Chimp CTA CTACTGTATGCAGCATGAGAAAAGTATAGGTTTCCATTTCTGCCTTTTGGAGCATGATAT 8738
Macaque CTA CTACTGTGTGTAGCATGAGAAAAGTATAGGTTTCCAGTTTCTGCCTTTTGGAGCATGATAT 8691
. . . 0 5 0 5 0 5 0 5 0 5 0 5 0 5 4526
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DQ094845 TAAGGATACTAAGCAGATACCTTTTATGGAATCTTACTAAAAGTTAGTGACTATGTTAGA 8805
Chimp TAAGGATACTAAGCAGATACCTTTTATGGAATCTTACTAAAAGTTAGTGACTATGTTAGA 8798
Macaque TAATGATACTAAGCAGATAGCTTTTATGGAATCTTACTAAAAGTTAGTGACTATATAGA 8751
. . . 0 5 0 5 0 5 0 5 0 5 0 5 0 5 4586
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DQ094845 CACCTGTTAGGC GTTATGTCCCTC---ACAACGTATGATGTAGGTAGCATAATTGTCCCTC 8862
Chimp CACCTGTTAGGC GTTATGTCCCTC---ACAACGTATGATGTAGGTAGCATACTTGTCCCTC 8855
Macaque CACCTGTTAGGCATTATGTCCCTCTTCAACAACGTATGATGTAGGTAGCATAATTGTCCCTC 8811
. . . 0 5 0 5 0 5 0 5 0 5 0 4643
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DQ094845 ATCTAACAAATGAGGGAGCTGAGGCTCAGAAAGCTTCAGTAAC TTCCAAAGCCATACAA 8922
Chimp ATCTAACAAATGAGGGAGCTGAGGCTCAGAAAGCTTCAGTAAC TTCCAAAGCCATACAA 8915
Macaque ATCTAACAAACGAGGGAGCTGAGGCTCAGAAAGCTTCAGTAAC TTCCAAAGCCATACCA 8871
. 5 0 5 0 5 0 5 0 5 0 5 0 5 0 4703
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DQ094845 CCAACTAGTTGCAGAGTCAGGACGAGAACCCAGGTCTCTGTGATTCCAGGATCCATGGAG 8982
Chimp CCAACTAGTTGCAGAGTCAGGACGAGAACCCAGGTCTCTGTGATTCCAGGATCCATGGAG 8975
Macaque CCAACTAGTTGCAGAGTCAGGACGAGAACCCAGGTCTCTGTGATTCCAGGATCCATGGAG 8931
. 5 0 5 0 5 0 5 0 5 0 5 0 4763
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DQ094845 CCTAGCACCCAGGCAAACCAGGAAGCAGCAGGTTAGCTTAGAATCTGTGCCAGAACAA 9042
Chimp CCTAGCACCCAGGCAAACCAGGAAGCAGCAGGTTAGCTTAGAATCTGTGCCAGAACAA 9035
Macaque CCTAGCACCCAGGCAAACCAGGAAGCAGCAGGTTAGCTTAGAATCTGTGCCAGAACAA 8991
. 5 0 5 0 5 0 5 0 5 0 5 0 4823
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DQ094845 GTGTAAGA AACTGGAAATGCAATACTTTGTTGAGAGAAGACGGAGACTGCTGTGGGTTGAG 9102
Chimp GTGTAAGA AACTGGAAATGCAATACTTTGTTGAGAGAAGAGGGAGACTGCTGTGGGTTGAG 9095
Macaque GTGTAAGA AACTGGAAATGCAATACTTTGTTGAGAGAAGAGGGAGATTGCTGTGGGTTGAG 9051
. 5 0 5 0 5 0 5 0 5 0 5 0 4883
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DQ094845 GCAGGGAGGAATGTTCCCTTCCAAGCATGTGACTGCAGGGTTTCTGGGGACTGACACAAA 9162
Chimp GCAGGGAGGAATGTTCCCTTCCAAGCATGTGACTGCAGGGTTTCTGGGGACTGACACAAA 9155
Macaque GCAGGGAGGAATGTTCCCTTCCAAGCATGTTACTGCAGTGTTCCTGGGGACTGGACAAA 9111
. 5 0 5 0 5 0 5 0 5 0 5 0 4943
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                |                               |
DQ094845      ACCCACCACCCACTCTCTCTCTCTCTGAAGTTGGGTGAGGCGGTTTTCTTCAGCCGACT 9761
Chimp         ACCCACCATCCCACTCTCTCTCTCTCTGAAGTTGGGTGAGGCAGTTTTCTTCAGCCGACT 9754
Macaque      GCCCACC-CCCACTCTCTCTCTCTCTGAAGTTGGGTGAGGCAGTTTTCTTCAGCCGACT 9709
                ..5....0....5....0....5....0....5....0....5....0....5....0... 5542
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DQ094845      TCCGTTTACTCATCTGTAATTTGAGGCCAGTACAGGTGGTATCTAAGCTCTGCTCCCCTC 9821
Chimp         TCCGTTTACTCATCTGTAATTTGAGGCCAGTACAGGTGGTATCTAAGCTCTGCTCCACTC 9814
Macaque      TCCGTTTGTCTCATCTGTAATTTGAGGCCAGTACAGGTGGTATCTAAGCTCTGCTCCACTC 9769
                ..5....0....5....0....5....0....5....0....5....0....5....0... 5602
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                                |             |
DQ094845      TGAAT-----TTATACAGTTGTTAATTTACAGGCTAGAGATAATCATTATATTCTAA 9875
Chimp         TGAAT-----TTATACAGTTGTTAATTTAGAGGCTAGATATAATCATTATATTCTAA 9868
Macaque      TAAATGTAAATTTATACAGTTGTTAATTTAGAGGCTAGAGATAATCATTATATTCTAA 9829
                ..5..           ..0....5....0....5....0....5....0....5....0....5... 5656
                * **          *****

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DQ094845      TTAGAGTTGATGACATTTGCCATATAAACAATGGTTGAATATTCTGAAGTTGTCAGCCT 9935
Chimp         TTAGAGTTGATGACATTTGCCATATAAACAATGGTTGAATATTCTGAAGTTGTCAGCCT 9928
Macaque      TTAGAGTTGATGACATTTGCCATATAAACAATGGTTGAATATTCTGAAGTTGTCAGCCT 9889
                ...0....5....0....5....0....5....0....5....0....5....0....5... 5716
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DQ094845      GCAGAAGAGAATGCTGTGAAGTACTATTTGGTG 9968
Chimp         GCAGAAGAGAATGCTGTGAAGTACTATTTGGTG 9961
Macaque      GCAGAAGAGAATGCTGTGAAGTACTATTTCTGTG 9922
                ...0....5....0....5....0....5.... 5749
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