

## First motif

Name	Strand	Start	p-value	Sites		
Gorilla	+	620	1.87e-24	TCGGGAG ATC	GAGACCAGCCTGACCAACATGGAGAAACA CTGTCTCTACTAAAAATACAA	AATTAGC CAG
Homo	+	624	1.87e-24	TCGGGAG ATC	GAGACCAGCCTGACCAACATGGAGAAACA CTGTCTCTACTAAAAATACAA	AATTAGC CAG
Mandrillus	+	844	4.19e-23	TCAAGAG ATC	GAGACCATCCTGGCCAACAAGGTGAAACC CCGTCTCTACTAAAAACACAA	AAATTAG CTA
Aotus	-	189	2.35e-22	CGGGAGT TGG	GAGACCAGCCTGACCAACATGGAGAAACC CCATCTCTACTAAAAATACAA	AATTAGC TGG
Nomascus	+	605	4.65e-22	TCGGGAG TTC	GAGACCAGCCTGACCAACATGGAGAAACA CCGTCTACTAAAAATACAAA	TTAGCCA GGC
Theropithecus	+	9	5.71e-22	ATGGGTT G	GAGACCAGCCTGGCCAACATGGTGAAACC CTGTCTCTATTAAAAATACAA	GAAATTA GTT
Pongo	+	626	8.43e-22	TCGGGAG TTG	GAGACCAGCCTGACCAACATGGAGAAACA CCGTCTCTACTAAAAATATAA	AATTAGC CAA
Rhinopithecus	-	187	5.09e-21	TCAGGAG TTT	GAGACCAGCCTGACCAACATGGAGAAACC CTGTCTCTACTAAAAATACAA	AATTAGC GCG
M.	-	208	3.54e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGAAGATGAAATA TTACATACGAAAGCTACAATT	CTCACAA AGT
Cercocebus	-	329	3.54e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGAAGATGAAATA TTACATACGAAAGCTACAATT	CTCACAA AGT
Macaca	-	156	3.54e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGAAGATGAAATA TTACATACGAAAGCTACAATT	CTCACAA AGT
Colobus	-	325	4.49e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGGAGATGAAATA TTATATACGAAAGCTACAATT	CTCACAA AGT
Chlorocebus	-	329	4.49e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGAAGATGAAATA TTATATACGAAAGCTACAGTT	CTCACAA AGT
Piliocolobus	-	326	6.54e-20	AGGGACT GAA	CTAGGCCTTTAGGGACAAGGAGATGAAATA TCATATACGAAAGCTACAATT	CTCACAA AGT

## Second motif

Name	Strand	Start	p-value	Sites		
Gorilla	-	92	2.91e-28	GCTACTC AGG	AGGCTGGGACAGGAGAATCGCTTGAACCTGG GAGGTGGAGGTTGCGGTGA	GCCGAG ATCG
Homo	-	96	2.91e-28	GCTACTC AGG	AGGCTGGGACAGGAGAATCGCTTGAACCTGG GAGGTGGAGGTTGCGGTGA	GCCGAG ATCG
Pongo	+	723	7.07e-26	CCTACTA GAG	AGGCTGAGGCAGGAGAATCACTTGAACCTGG GAGGCGGAGGTTGAAGTGA	GCCGAG ATCG
Nomascus	+	700	7.07e-26	ACTACTA GAG	AGGCTGAGGCAGGAGAATCACTTGAACCTGG GAGGCGGAGGTTGAAGTGA	GCCGAG ATCG
Rhinopithecus	-	93	2.99e-25	GCTACCA GGG	AGGCTGAGGCAGGAGAATCGCTTGAACCTGG GAGGCAGAGGTTGCGGTGA	GCCGAG ATCG
Theropithecus	+	573	2.09e-24	TCTACTG GGG	AGGCTGAGGCAGGAGAATCGCTTGAACCCGG GAGGCAGAGGTTGCAGTGA	GCCGAG ATGG
Aotus	-	92	1.53e-22	TCTCCTC GGG	AGGCTGAGGCAGGAGAATTGCTTGAACCTGG GAGGCGGAGATTTTGGTGA	GCTGAG ATTG
Mandrillus	+	52	2.15e-21	GCTACTT GGG	AGGCTGAGACAGGAGAATGCGCATGAACCCAG GAGGTGGAGCTTGCACTGA	GCCGAG ATCG
Chlorocebus	+	83	1.81e-20	AGGAGGG AGG	GTGGTGGGAAGACCGAAGACCTTGGAGCTGC AATGTGGAAAACGGAGGGA	GGCGTG GTGG
Colobus	+	79	3.15e-20	NNNAGGG AGG	GTGGTGGGAAGACCGAAGACCTTCGAGCTGC AATGTGGAAAACGGAGGGA	GGCGTG GTGG
Piliocolobus	+	80	3.15e-20	AGGAGGA TGG	GTGGTGGGAAGACCGAAGACCTTCGAGCTGC AATGTGGAAAACGGAGGGA	GGCGTG GTGG
Cercocebus	+	83	1.10e-19	AGGAGGG AGG	GTGGTGGGAAGACCAAAGACCTTCGAGCTGC AATGTGGAAAACGGAGGGA	GGCGTG GTGG

### Third motif

Name	Strand	Start	p-value	Sites		
Gorilla	+	556	1.05e-24	GCGTGGT GGC	TCATGCCTGTAATCCCAGCACCTTTGGGAG GCCGAGGCAGGTGGATCACCT	GAGGTCG GGA
Homo	+	560	1.05e-24	GCGTGGT GGC	TCATGCCTGTAATCCCAGCACCTTTGGGAG GCCGAGGCAGGTGGATCACCT	GAGGTCG GGA
Pongo	+	562	1.33e-21	GCGTGGT GGC	TTATGCCTGTAATCCCAGCACCTTTGGGAG GCCGAGGCAGGTGGATCACCT	GAGGTCG GGA
Rhinopithecus	-	251	5.25e-21	GGATGGT GGC	TCACACCTGTAATCCCAGCACCTTTGGGAG GCCGAGGTGGGCGGATCACCT	GAGGTCA GGA
M.	+	304	5.97e-21	CTCGCCG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGAGGGCAGAAACCG	CAAGCGC GGC
Colobus	+	421	5.97e-21	CTCGCTG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGAGGGCAGAAACCG	CAAGTGC GGC
Chlorocebus	+	425	5.97e-21	CTCGCCG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGAGGGCAGAAACCG	CAAGCGC CGC
Macaca	+	252	5.97e-21	CTCGCCG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGAGGGCAGAAACCG	CAAGCGC GGC
Piliocolobus	+	422	5.97e-21	CTCGCTG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGAGGGCAGAAACCG	CAAGCGC GGC
Aotus	-	254	2.77e-20	GCGTGGT GGC	TCATGCCTATAAGCCCAGCACCTTTGGGAG GCTGAGGCGGGCGGATCACCT	GAGGTCG GGA
Mandrillus	+	782	8.86e-20	ACGTGGT AGC	TCACGCCTGTAATCCCAGCACCTTTGGGAG GCCGAGGTAGGCGGATCACGA	GGTCAAG AGA
Nomascus	+	541	1.08e-19	GCACGGT GGC	TCATGCCTGTAATCCCAGCACCTTTGGGAG GCCGACATGGGCGGATCACCC	GAGGTCG GGA
Cercocebus	+	425	1.60e-19	CTCGCCG ACT	GATTCAATGCAAGAAAAGAACGATTTCGAG GCGTGGAGACGGCAGAAACCG	CAAGCGC GGC
Theropithecus	+	81	1.64e-14	ACGTGGT AGC	GGGCGCCTGTAATCCCAGCTATTCTGGGAG ACTGAGGCAGGAGAATCCTTT	GAACCCA GGA
Pan	-	198 9	6.01e-12	GTAACAG CTA	GGCCATCAGCAATATCAGGAGGTAGAGAG GCAGAAGGAGATTGTCTATCT	GTGTAGT GTA