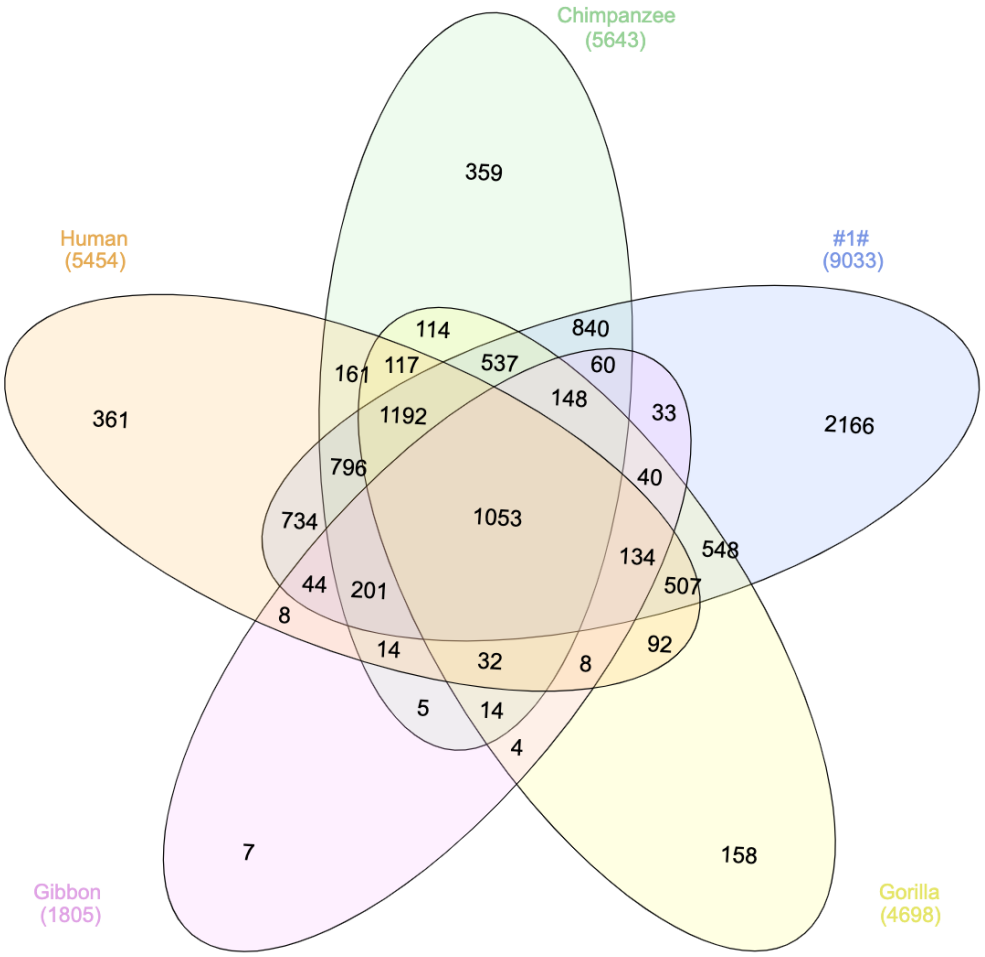
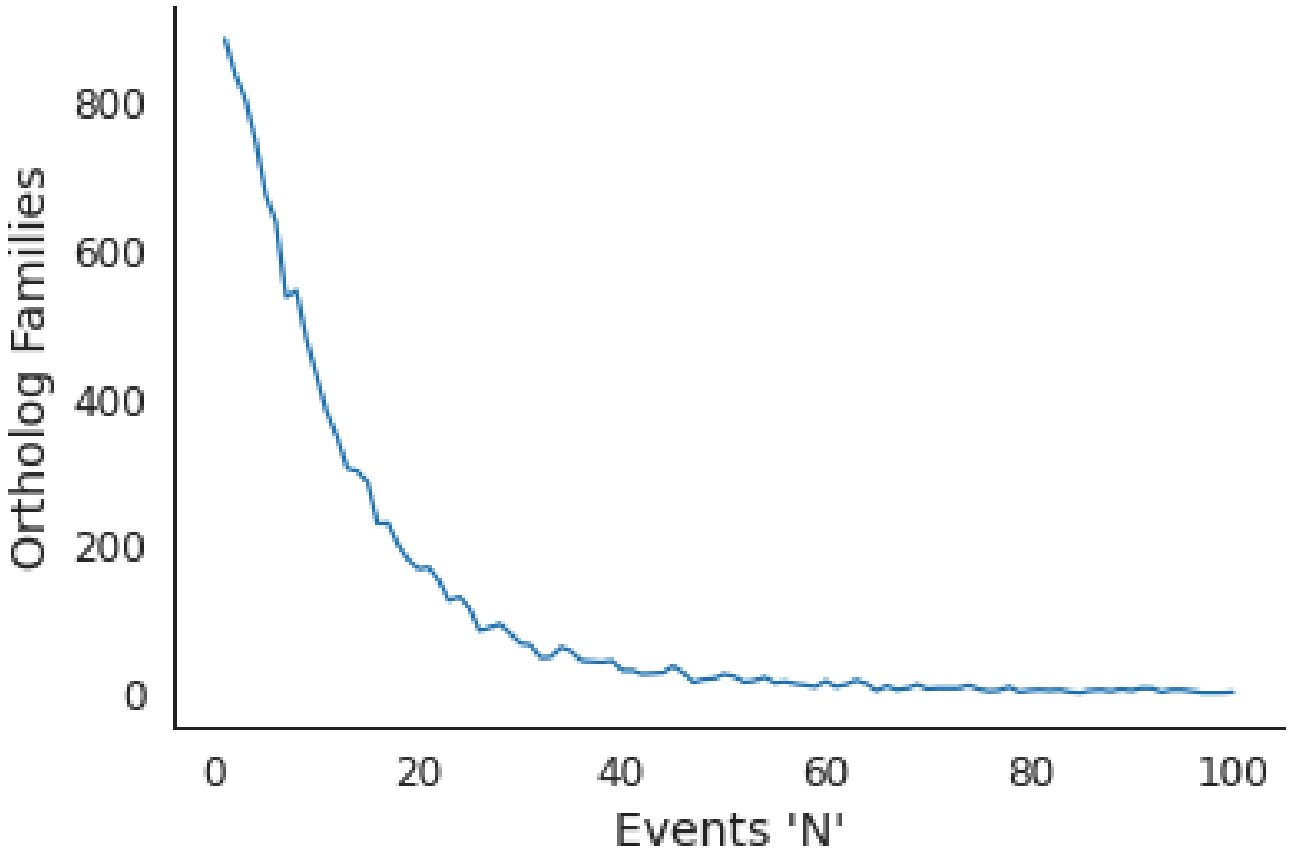
Supporting information

Filtered ortholog families

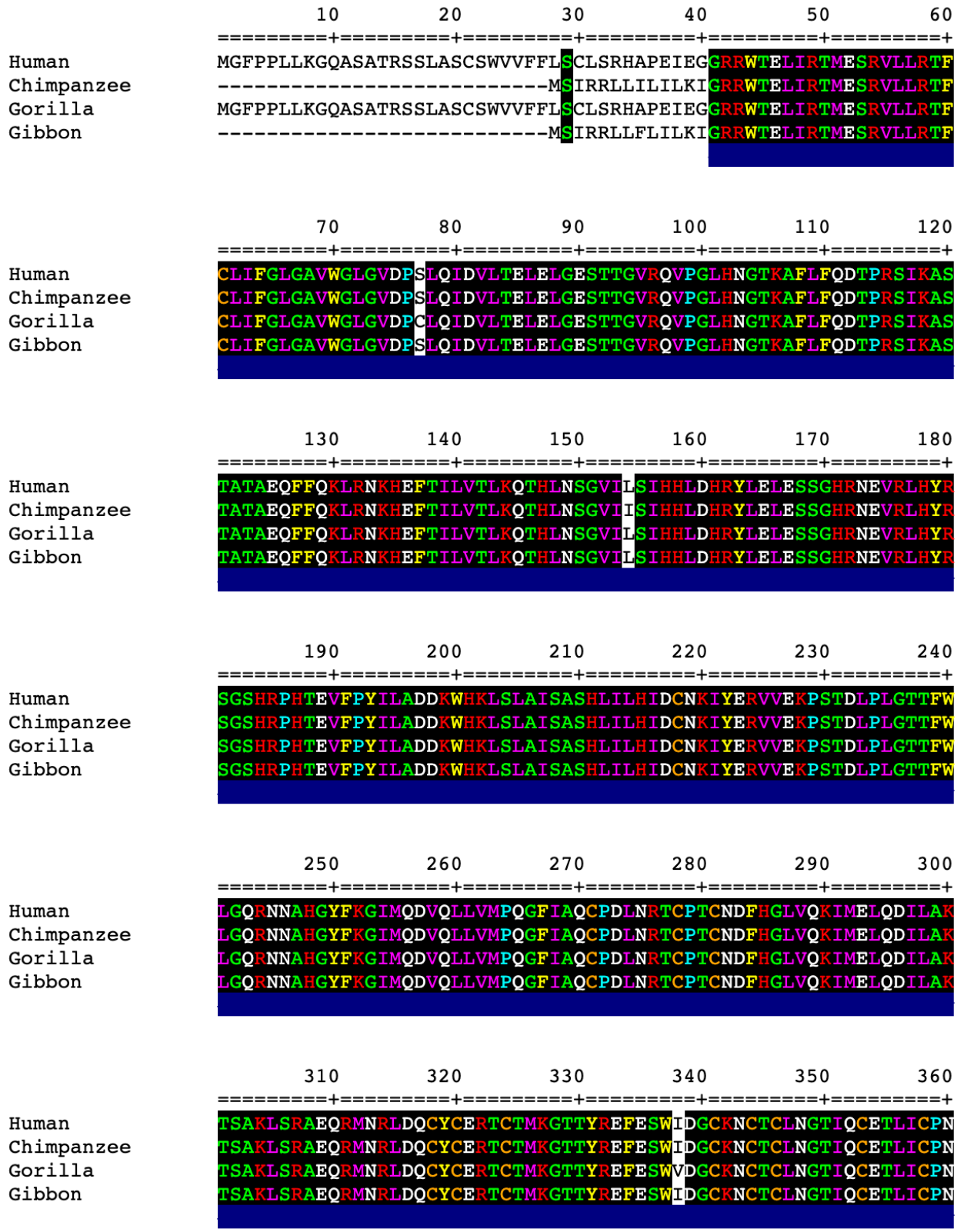
Three ortholog families (out of 12,621) did not contain even a single alignment block. Two of these families (ENST00000262304, ENST00000301788) have truncated genes found next to genome gaps in *Nomascus leucogenys*. *Pan troglodytes* gene from ENST00000397748 family also appears to be truncated due to a genome gap. The truncated version of genes from these families do not share enough sequence overlap with their orthologs, and hence Gblocks does not find any conserved block.



S1 Fig: Families with branch-specific null substitution.



S2 Fig: Distribution of total Branch-specific substitution Events (N) among ortholog families.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Chimpanzee ----------MSIRRLLILILKIGRRWTELIRTMESRVLLRTF
Gorilla MGFPPLLKGQASATRSSLASCSWVVFFLSCLSRHAPEIEGGRRWTELIRTMESRVLLRTF
Gibbon ----------MSIRRLLFLILKIGRRWTELIRTMESRVLLRTF
70 80 90 100 110 120
Human CLIFGLGAVWGLGVDPSLQIDVLTELELGESTTGVRQVPGLHNGTKAFLFQDTPRSIKAS
Chimpanzee CLIFGLGAVWGLGVDPSLQIDVLTELELGESTTGVRQVPGLHNGTKAFLFQDTPRSIKAS
Gorilla CLIFGLGAVWGLGVDPCLQIDVLTELELGESTTGVRQVPGLHNGTKAFLFQDTPRSIKAS
Gibbon CLIFGLGAVWGLGVDPSLQIDVLTELELGESTTGVRQVPGLHNGTKAFLFQDTPRSIKAS
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Chimpanzee TATAEQFFQKLRNKHEFTILVTLKQTHLNSGVIISIHHLDHRYLELESSGHRNEVRLHYR
Gorilla TATAEQFFQKLRNKHEFTILVTLKQTHLNSGVILSIHHLDHRYLELESSGHRNEVRLHYR
Gibbon TATAEQFFQKLRNKHEFTILVTLKQTHLNSGVILSIHHLDHRYLELESSGHRNEVRLHYR
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Gorilla SGSHRPHTEVFPYILADDKWHKLSLAISASHLILHIDCNKIYERVVEKPSTDLPLGTTFW
Gibbon SGSHRPHTEVFPYILADDKWHKLSLAISASHLILHIDCNKIYERVVEKPSTDLPLGTTFW
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Chimpanzee LGQRNNAHGYFKGIMQDVQLLVMPQGFIAQCPDLNRTCPTCNDFHGLVQKIMELQDILAK
Gorilla LGQRNNAHGYFKGIMQDVQLLVMPQGFIAQCPDLNRTCPTCNDFHGLVQKIMELQDILAK
Gibbon LGQRNNAHGYFKGIMQDVQLLVMPQGFIAQCPDLNRTCPTCNDFHGLVQKIMELQDILAK
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Human TSAKLSRAEQRMNRLDQCYCERTCTMKGTTYREFESWIDGCKNCTCLNGTIQCETLICPN
Chimpanzee TSAKLSRAEQRMNRLDQCYCERTCTMKGTTYREFESWIDGCKNCTCLNGTIQCETLICPN
Gorilla TSAKLSRAEQRMNRLDQCYCERTCTMKGTTYREFESWVDGCKNCTCLNGTIQCETLICPN
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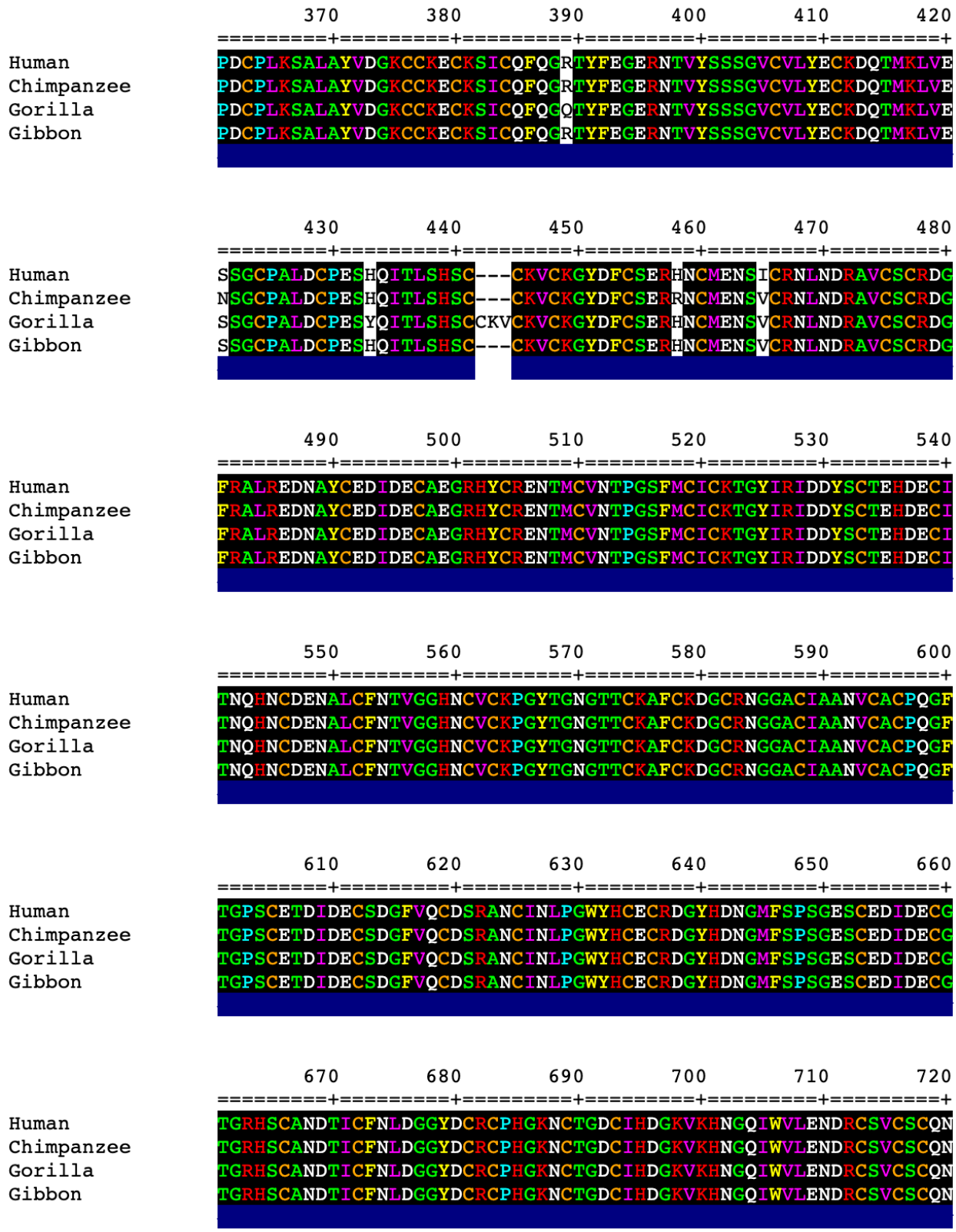
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Chimpanzee PDCPLKSALAYVDGKCCKECKSICQFQGRTYFEGERNTVYSSSGVCVLYECKDQTMKLVE
Gorilla PDCPLKSALAYVDGKCCKECKSICQFQGQTYFEGERNTVYSSSGVCVLYECKDQTMKLVE
Gibbon PDCPLKSALAYVDGKCCKECKSICQFQGRTYFEGERNTVYSSSGVCVLYECKDQTMKLVE
430 440 450 460 470 480
Human SSGCPALDCPESHQITLSHSC---CKVCKGYDFCSERHNCMENSICRNLNDRAVCSCRDG
Chimpanzee NSGCPALDCPESHQITLSHSC---CKVCKGYDFCSERRNCMENSVCRNLNDRAVCSCRDG
Gorilla SSGCPALDCPESYQITLSHSCCKVCKVCKGYDFCSERHNCMENSVCRNLNDRAVCSCRDG
Gibbon SSGCPALDCPESHQITLSHSC---CKVCKGYDFCSERHNCMENSVCRNLNDRAVCSCRDG
490 500 510 520 530 540
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Chimpanzee FRALREDNAYCEDIDECAEGRHYCRENTMCVNTPGSFMCICKTGYIRIDDYSCTEHDECI
Gorilla FRALREDNAYCEDIDECAEGRHYCRENTMCVNTPGSFMCICKTGYIRIDDYSCTEHDECI
Gibbon FRALREDNAYCEDIDECAEGRHYCRENTMCVNTPGSFMCICKTGYIRIDDYSCTEHDECI
550 560 570 580 590 600
Human TNQHNCDENALCFNTVGGHNCVCKPGYTGNGTTCKAFCKDGCRNGGACIAANVCACPQGF
Chimpanzee TNQHNCDENALCFNTVGGHNCVCKPGYTGNGTTCKAFCKDGCRNGGACIAANVCACPQGF
Gorilla TNQHNCDENALCFNTVGGHNCVCKPGYTGNGTTCKAFCKDGCRNGGACIAANVCACPQGF
Gibbon TNQHNCDENALCFNTVGGHNCVCKPGYTGNGTTCKAFCKDGCRNGGACIAANVCACPQGF
610 620 630 640 650 660
Human TGPSCETDIDECSDGFVQCDSRANCINLPGWYHCECRDGYHDNGMFSPSGESCEDIDECG
Chimpanzee TGPSCETDIDECSDGFVQCDSRANCINLPGWYHCECRDGYHDNGMFSPSGESCEDIDECG
Gorilla TGPSCETDIDECSDGFVQCDSRANCINLPGWYHCECRDGYHDNGMFSPSGESCEDIDECG
Gibbon TGPSCETDIDECSDGFVQCDSRANCINLPGWYHCECRDGYHDNGMFSPSGESCEDIDECG
670 680 690 700 710 720
Human TGRHSCANDTICFNLDGGYDCRCPHGKNCTGDCIHDGKVKHNGQIWVLENDRCSVCSCQN
Chimpanzee TGRHSCANDTICFNLDGGYDCRCPHGKNCTGDCIHDGKVKHNGQIWVLENDRCSVCSCQN
Gorilla TGRHSCANDTICFNLDGGYDCRCPHGKNCTGDCIHDGKVKHNGQIWVLENDRCSVCSCQN
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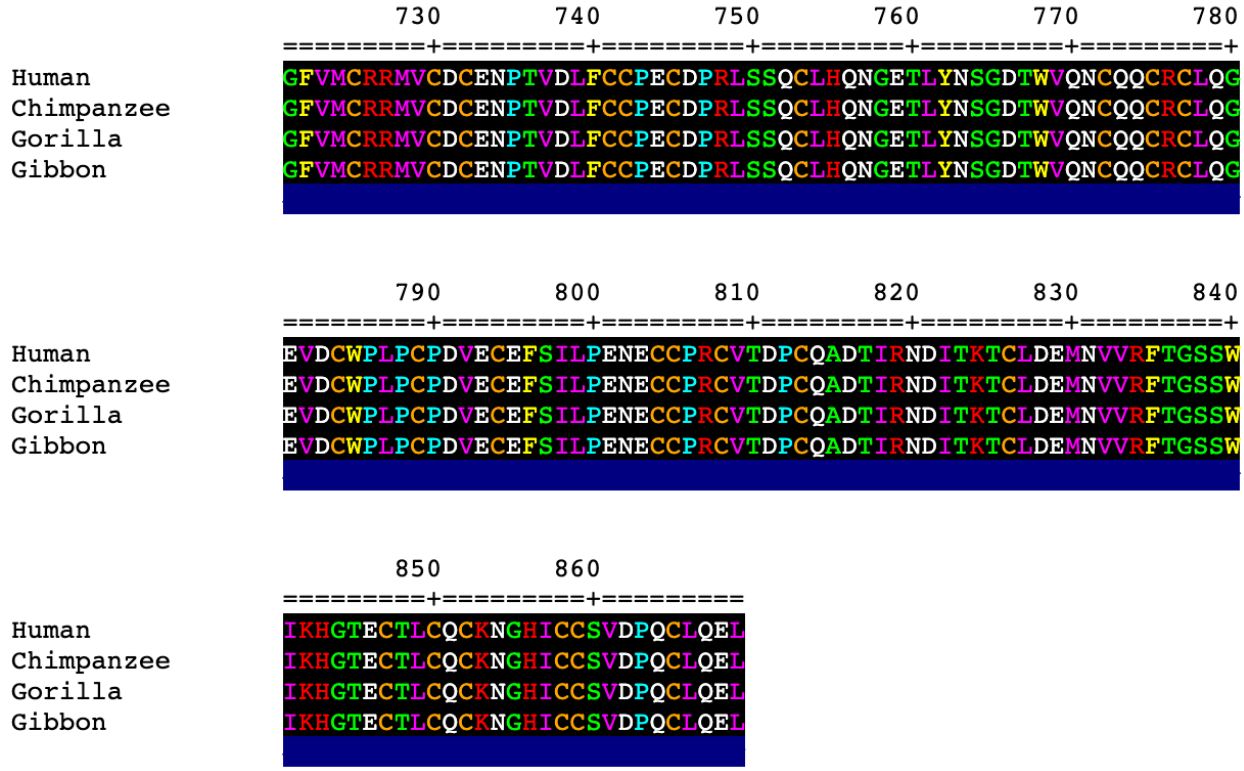
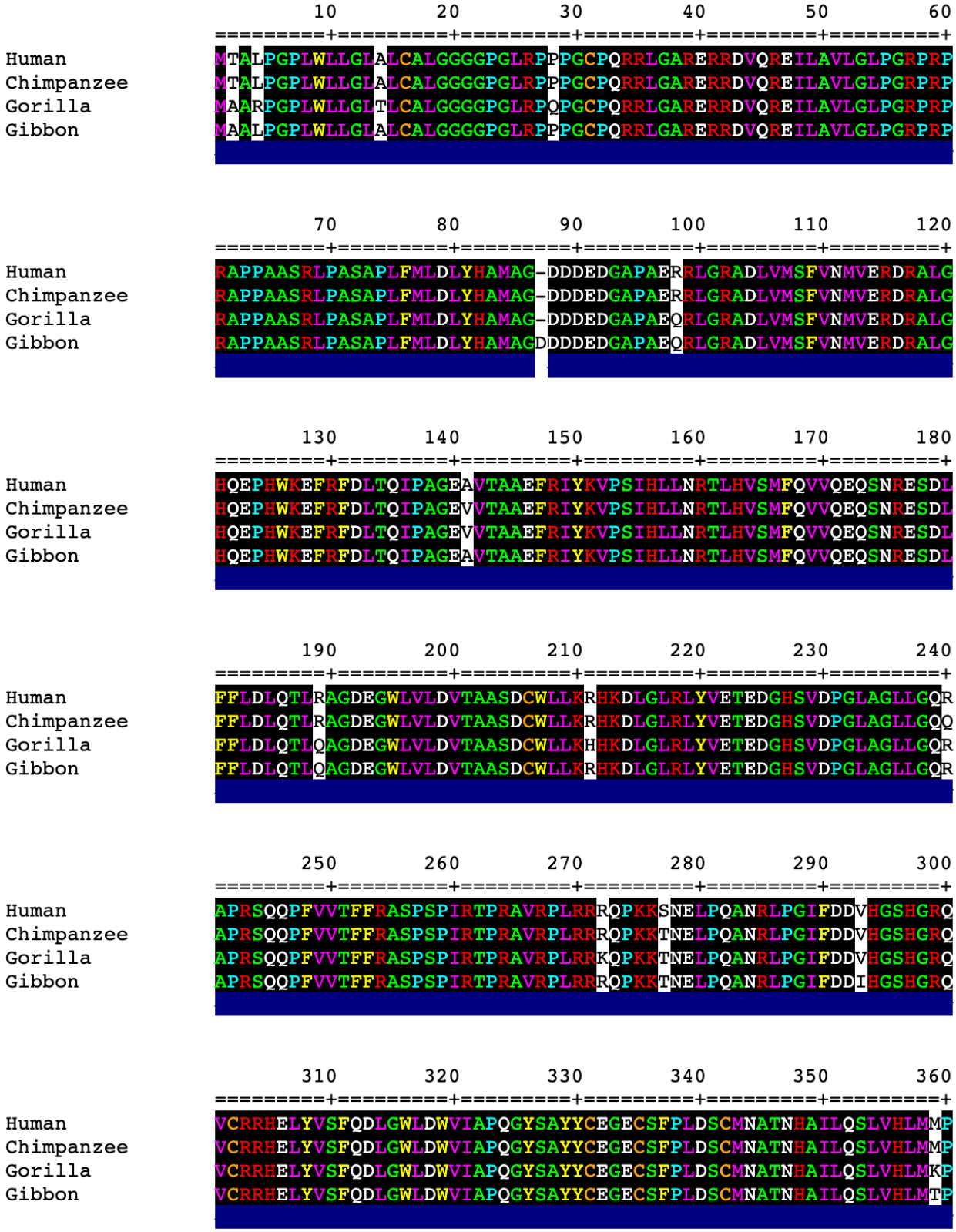


S3 Fig: Protein alignment of the NELL orthologs. Sites retained in the final alignment are underlined by the blue blocks.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Chimpanzee MTALPGPLWLLGLALCALGGGGPGLRPPPGCPQRRLGARERRDVQREILAVLGLPGRPRP
Gorilla MAARPGPLWLLGLTLCALGGGGPGLRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRP
Gibbon MAALPGPLWLLGLALCALGGGGPGLRPPPGCPQRRLGARERRDVQREILAVLGLPGRPRP
70 80 90 100 110 120
Human RAPPAASRLPASAPLFMLDLYHAMAG-DDDEDGAPAERRLGRADLVMSFVNMVERDRALG
Chimpanzee RAPPAASRLPASAPLFMLDLYHAMAG-DDDEDGAPAERRLGRADLVMSFVNMVERDRALG
Gorilla RAPPAASRLPASAPLFMLDLYHAMAG-DDDEDGAPAEQRLGRADLVMSFVNMVERDRALG
Gibbon RAPPAASRLPASAPLFMLDLYHAMAGDDDDEDGAPAEQRLGRADLVMSFVNMVERDRALG
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Human HQEPHWKEFRFDLTQIPAGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDL
Chimpanzee HQEPHWKEFRFDLTQIPAGEVVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDL
Gorilla HQEPHWKEFRFDLTQIPAGEVVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDL
Gibbon HQEPHWKEFRFDLTQIPAGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDL
190 200 210 220 230 240
Human FFLDLQTLRAGDEGWLVLDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQR
Chimpanzee FFLDLQTLRAGDEGWLVLDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQQ
Gorilla FFLDLQTLQAGDEGWLVLDVTAASDCWLLKHHKDLGLRLYVETEDGHSVDPGLAGLLGQR
Gibbon FFLDLQTLQAGDEGWLVLDVTAASDCWLLKRHKDLGLRLYVETEDGHSVDPGLAGLLGQR
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Chimpanzee APRSQQPFVVTFFRASPSPIRTPRAVRPLRRRQPKKTNELPQANRLPGIFDDVHGSHGRQ
Gorilla APRSQQPFVVTFFRASPSPIRTPRAVRPLRRKQPKKTNELPQANRLPGIFDDVHGSHGRQ
Gibbon APRSQQPFVVTFFRASPSPIRTPRAVRPLRRRQPKKTNELPQANRLPGIFDDIHGSHGRQ
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Gorilla VCRRHELYVSFQDLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNATNHAILQSLVHLMKP
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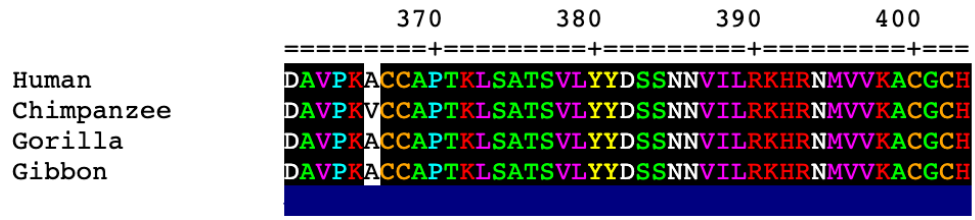
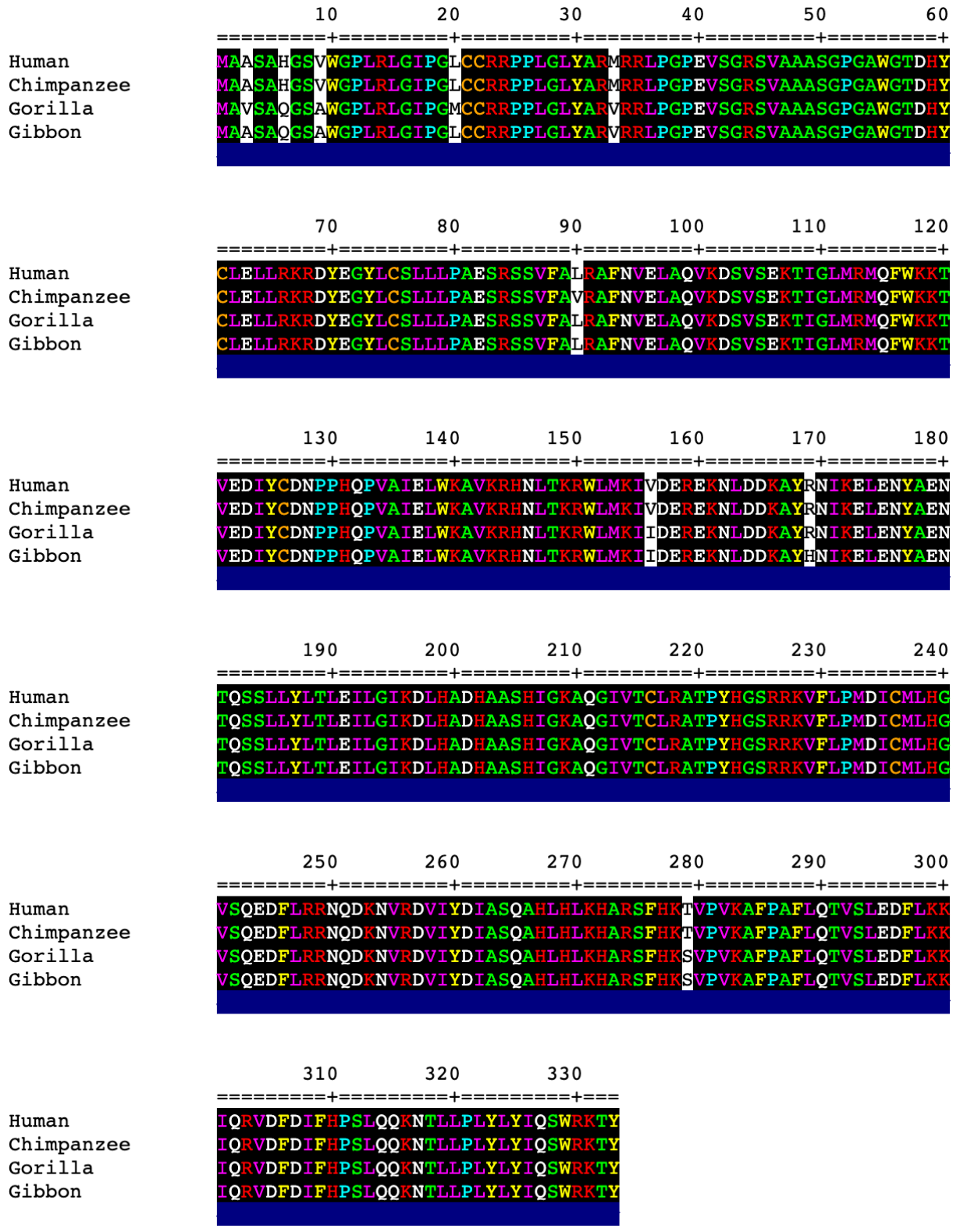
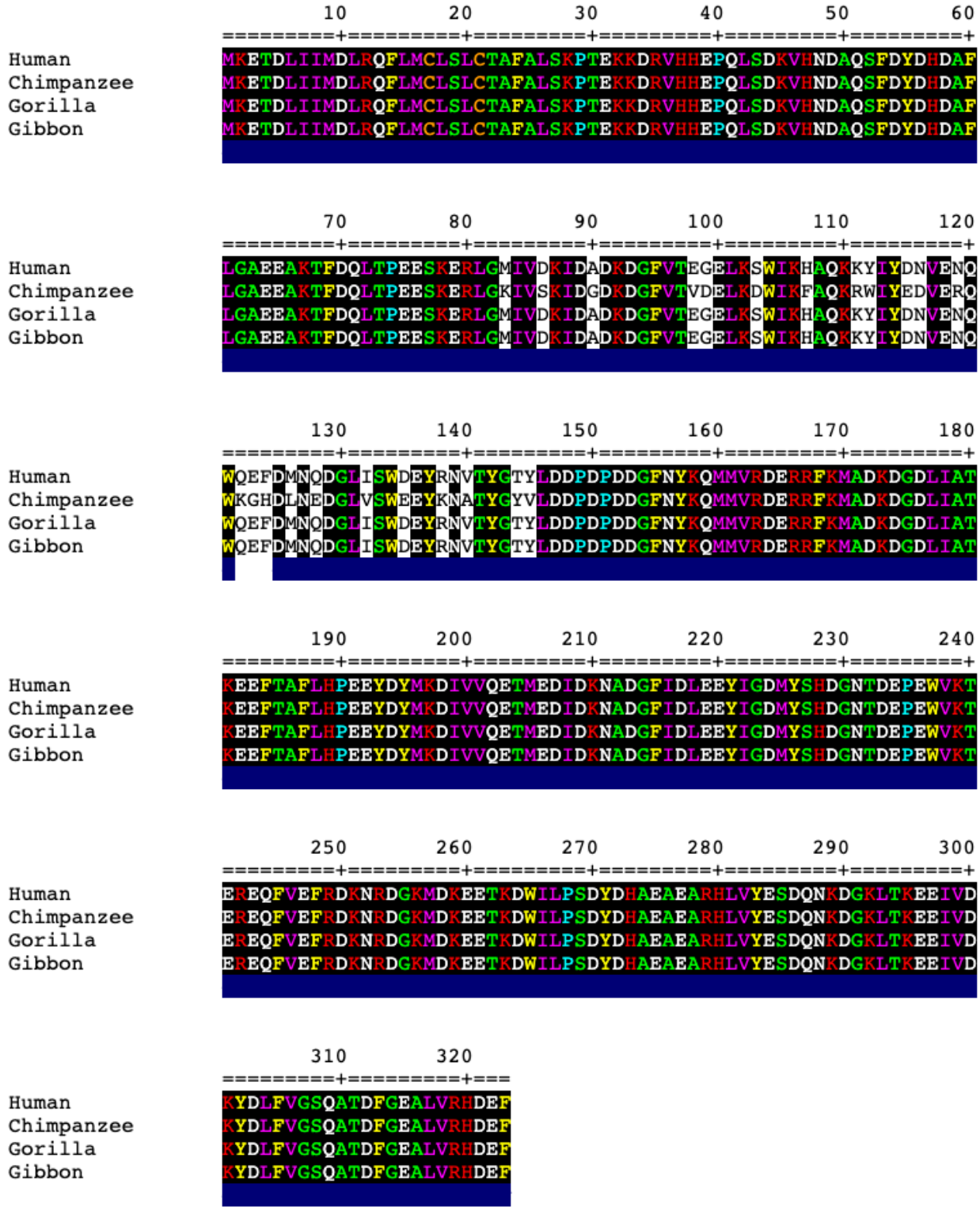


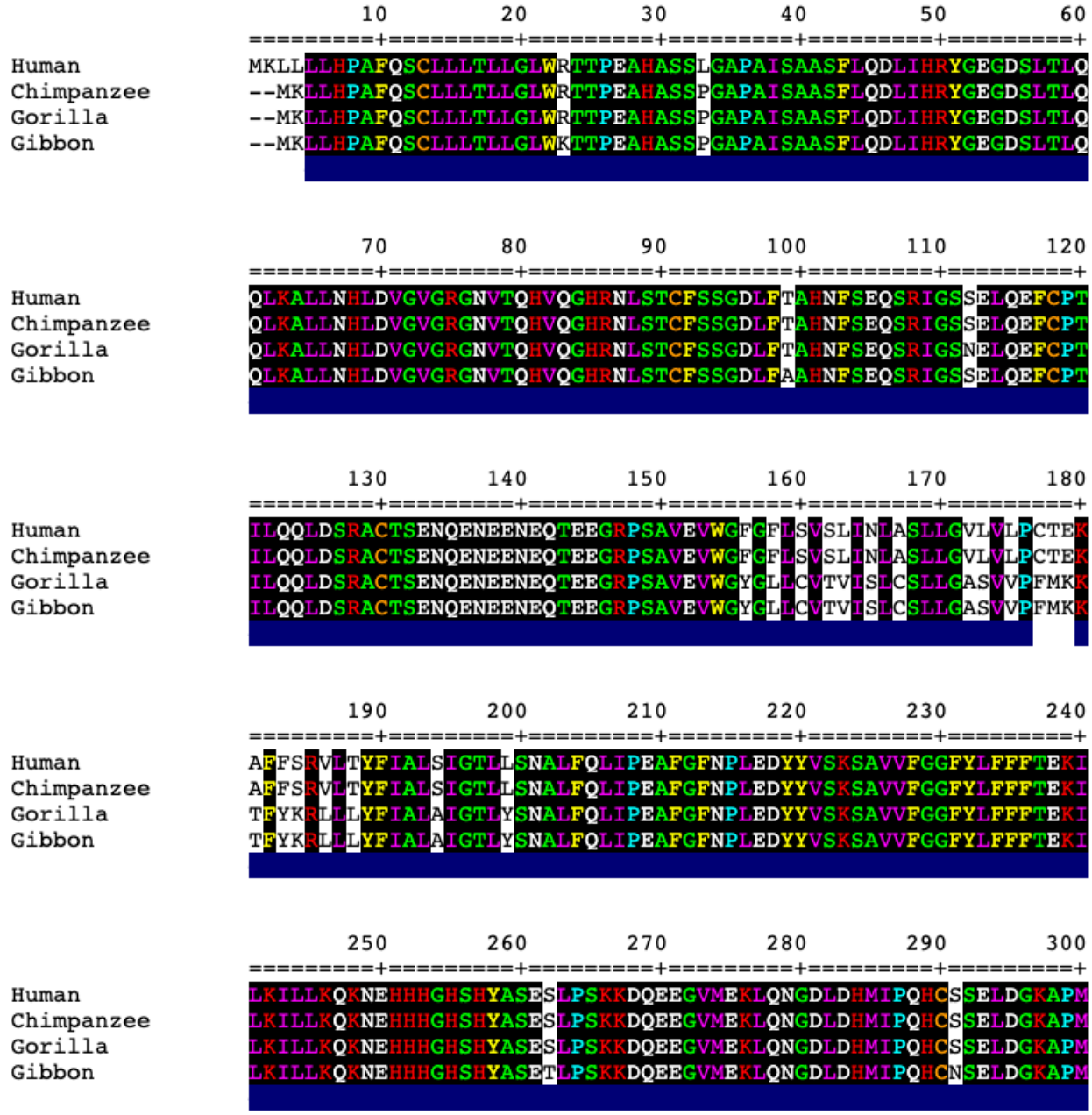
S4 Fig: Protein alignment of the BMP8B orthologs. Sites retained in the final alignment are underlined by the blue blocks.



S5 Fig: Protein alignment of the NDUFAF6 orthologs. Sites retained in the final alignment are underlined by the blue blocks.



S6 Fig: Protein alignment of the CALU orthologs. Sites retained in the final alignment are underlined by the blue blocks.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Gorilla --MKLLHPAFQSCLLLTLLGLWRTTPEAHASSPGAPAISAASFLQDLIHRYGEGDSLTLQ
Gibbon --MKLLHPAFQSCLLLTLLGLWKTTPEAHASSPGAPAISAASFLQDLIHRYGEGDSLTLQ
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Chimpanzee QLKALLNHLDVGVGRGNVTQHVQGHRNLSTCFSSGDLFTAHNFSEQSRIGSSELQEFCPT
Gorilla QLKALLNHLDVGVGRGNVTQHVQGHRNLSTCFSSGDLFTAHNFSEQSRIGSNELQEFCPT
Gibbon QLKALLNHLDVGVGRGNVTQHVQGHRNLSTCFSSGDLFAAHNFSEQSRIGSSELQEFCPT
130 140 150 160 170 180
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Chimpanzee ILQQLDSRACTSENQENEENEQTEEGRPSAVEVWGFGFLSVSLINLASLLGVLVLPCTEK
Gorilla ILQQLDSRACTSENQENEENEQTEEGRPSAVEVWGYGLLCVTVISLCSLLGASVVPFMKK
Gibbon ILQQLDSRACTSENQENEENEQTEEGRPSAVEVWGYGLLCVTVISLCSLLGASVVPFMKK
190 200 210 220 230 240
Human AEFSRVLTYFIALSIGTLLSNALFQLIPEAFGFNPLEDYYVSKSAVVFGGFYLFFFTEKI
Chimpanzee AEFSRVLTYFIALSIGTLLSNALFQLIPEAFGFNPLEDYYVSKSAVVFGGFYLFFFTEKI
Gorilla TEYKRLLLYFIALAIGTLYSNALFQLIPEAFGFNPLEDYYVSKSAVVFGGFYLFFFTEKI
Gibbon TEYKRLLLYFIALAIGTLYSNALFQLIPEAFGFNPLEDYYVSKSAVVFGGFYLFFFTEKI
250 260 270 280 290 300
Human LKILLKQKNEHHHGHSHYASESLPSKKDQEEGVMEKLQNGDLDHMIPQHCSSELDGKAPM
Chimpanzee LKILLKQKNEHHHGHSHYASESLPSKKDQEEGVMEKLQNGDLDHMIPQHCSSELDGKAPM
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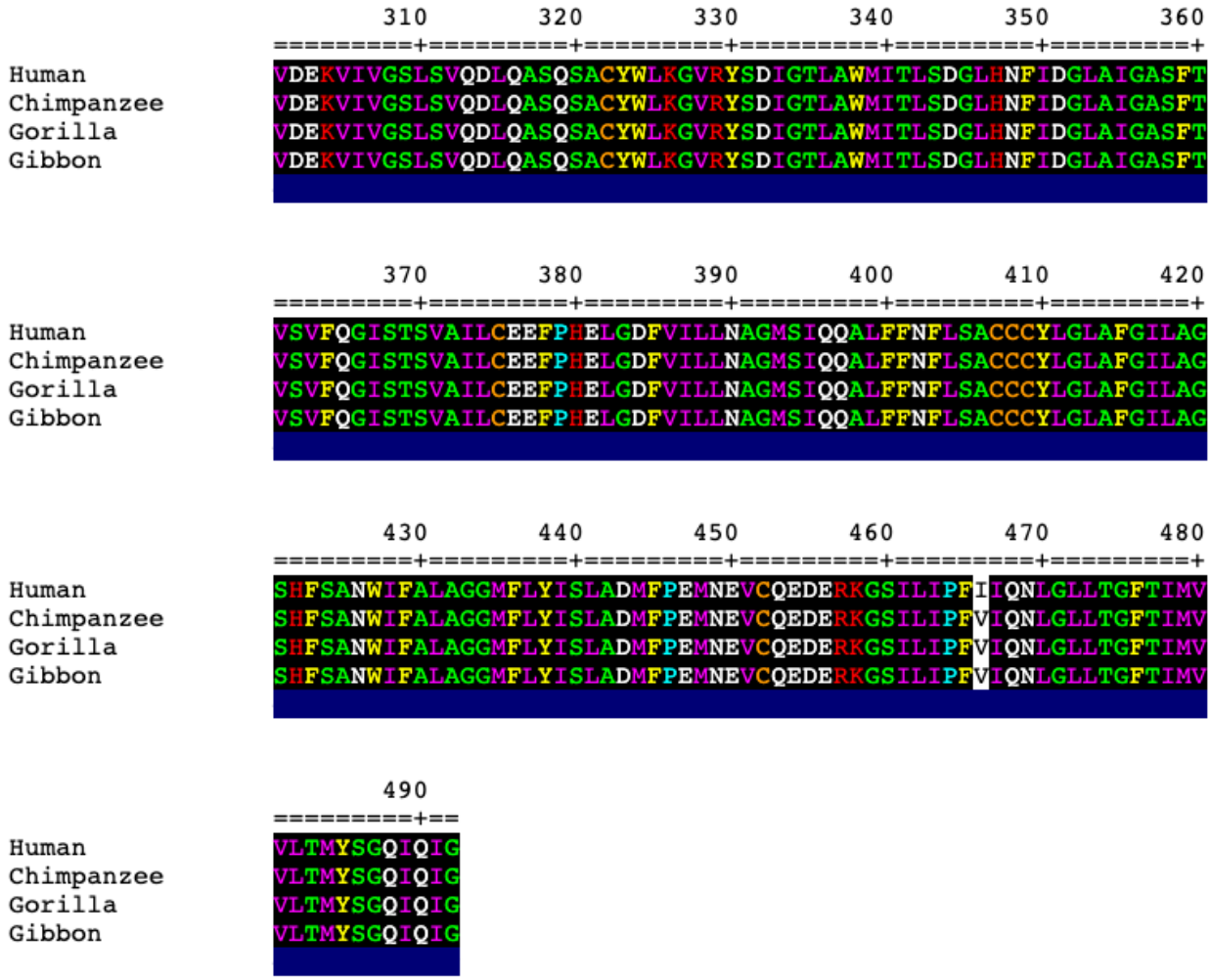
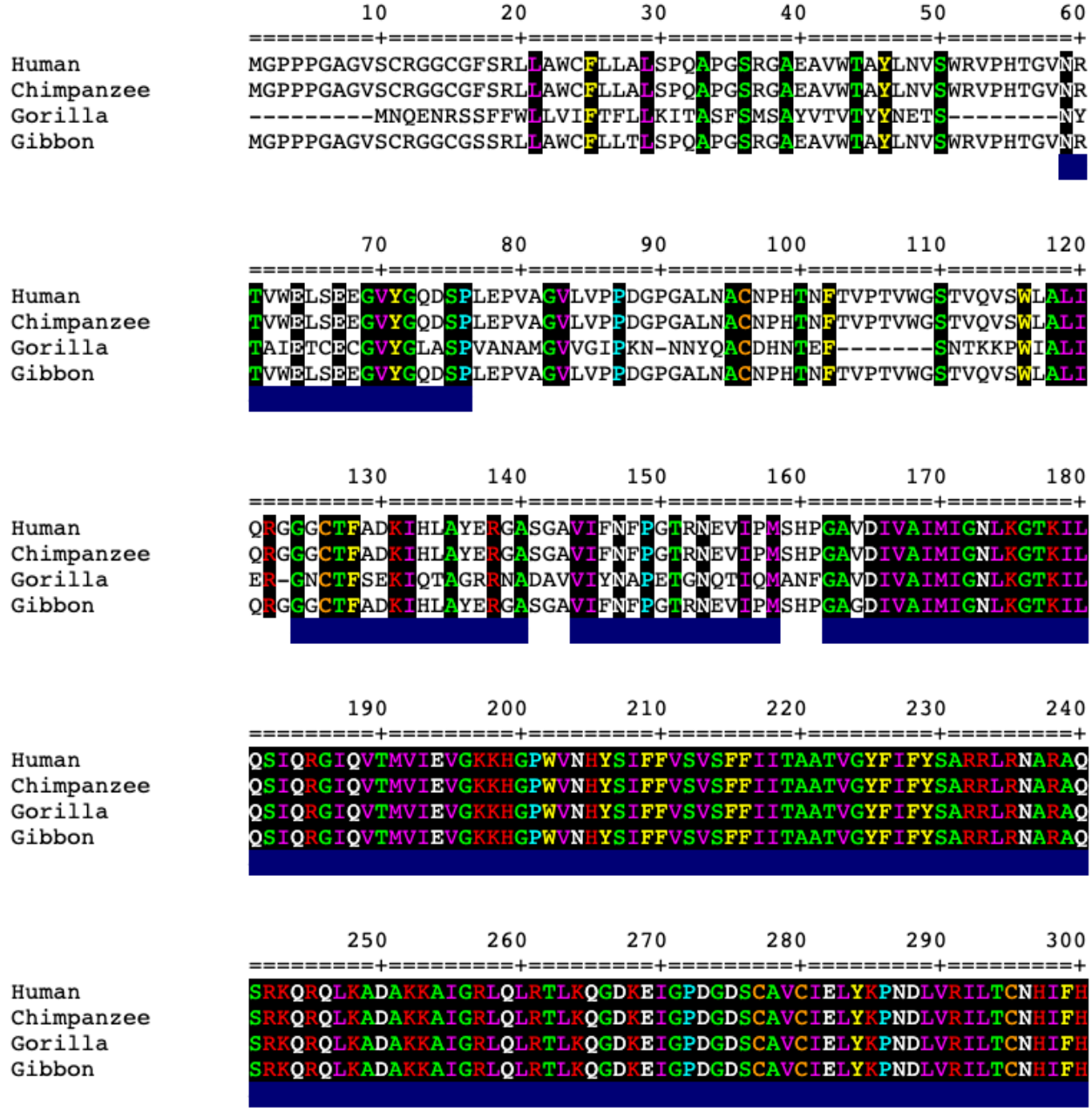


S7 Fig: Protein alignment of the SLC39A14 orthologs. Sites retained in the final alignment are underlined by the blue blocks.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Chimpanzee MGPPPGAGVSCRGGCGFSRLLAWCFLLALSPQAPGSRGAEAVWTAYLNVSWRVPHTGVNR
Gorilla ---------MNQENRSSFFWLLVIFTFLLKITASFSMSAYVTVTYYNETS--------NY
Gibbon MGPPPGAGVSCRGGCGSSRLLAWCFLLTLSPQAPGSRGAEAVWTAYLNVSWRVPHTGVNR
70 80 90 100 110 120
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Chimpanzee TVWELSEEGVYGQDSPLEPVAGVLVPPDGPGALNACNPHTNFTVPTVWGSTVQVSWLALI
Gorilla TAIETCECGVYGLASPVANAMGVVGIPKN-NNYQACDHNTEF-------SNTKKPWIALI
Gibbon TVWELSEEGVYGQDSPLEPVAGVLVPPDGPGALNACNPHTNFTVPTVWGSTVQVSWLALI
130 140 150 160 170 180
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Chimpanzee QRGGGCTFADKIHLAYERGASGAVIFNFPGTRNEVIPMSHPGAVDIVAIMIGNLKGTKIL
Gorilla ER-GNCTFSEKIQTAGRRNADAVVIYNAPETGNQTIQMANFGAVDIVAIMIGNLKGTKIL
Gibbon QRGGGCTFADKIHLAYERGASGAVIFNFPGTRNEVIPMSHPGAGDIVAIMIGNLKGTKIL
190 200 210 220 230 240
Human QSIQRGIQVTMVIEVGKKHGPWVNHYSIFFVSVSFFIITAATVGYFIFYSARRLRNARAQ
Chimpanzee QSIQRGIQVTMVIEVGKKHGPWVNHYSIFFVSVSFFIITAATVGYFIFYSARRLRNARAQ
Gorilla QSIQRGIQVTMVIEVGKKHGPWVNHYSIFFVSVSFFIITAATVGYFIFYSARRLRNARAQ
Gibbon QSIQRGIQVTMVIEVGKKHGPWVNHYSIFFVSVSFFIITAATVGYFIFYSARRLRNARAQ
250 260 270 280 290 300
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Chimpanzee SRKQRQLKADAKKAIGRLQLRTLKQGDKEIGPDGDSCAVCIELYKPNDLVRILTCNHIFH
Gorilla SRKQRQLKADAKKAIGRLQLRTLKQGDKEIGPDGDSCAVCIELYKPNDLVRILTCNHIFH
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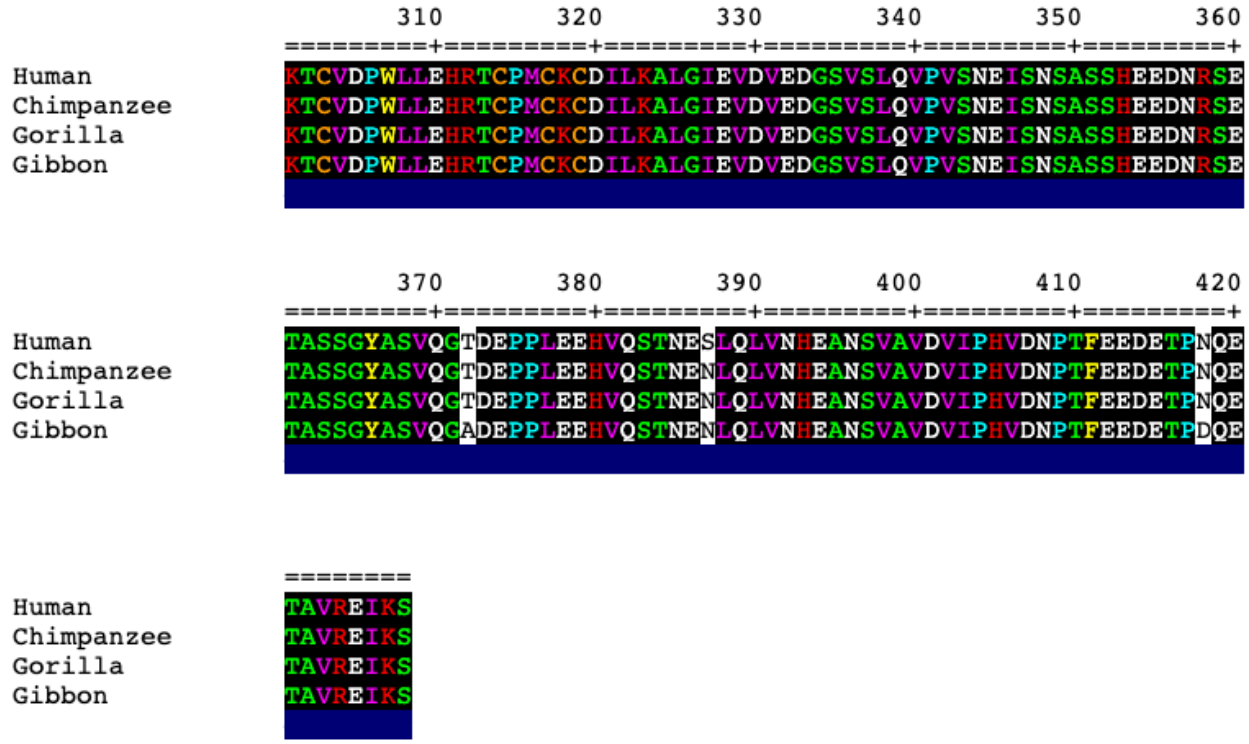
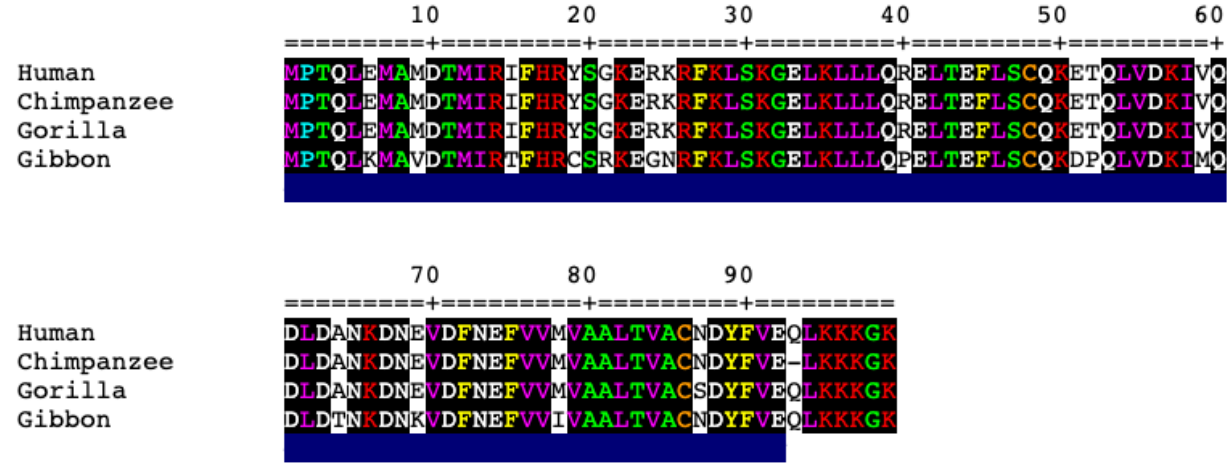


S8 Fig: Protein alignment of the RNF128 orthologs. Sites retained in the final alignment are underlined by the blue blocks.



S9 Fig: Protein alignment of the S100Z orthologs. Sites retained in the final alignment are underlined by the blue blocks.

S1 Table: Lower than expected substitution rate on the gibbon branch

Gene	Gibbon % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Higher in
QDPR	0.00	3	2	1	0	0	243	99.59	
ASIC1	0.00	0	20	0	0	0	307	64.09	Chimpanzee
POLR2A	0.00	12	0	1	0	0	1904	97.14	Human
ZDHHC3	0.00	0	0	12	1	0	274	82.28	Gorilla
HM13	0.00	0	9	0	0	0	363	85.21	Chimpanzee
SRF	0.00	0	1	8	0	0	358	75.69	Gorilla
SNAP25	0.00	0	0	9	0	0	206	100.00	Gorilla
VPS45	0.00	6	0	2	0	0	550	95.16	Human
NELL2	0.00	1	3	4	0	0	826	98.45	
ZNF174	0.00	2	2	3	1	0	407	100.00	
PGM1	0.00	7	0	0	0	0	474	81.72	Human
DACT3	0.00	7	0	0	0	0	180	99.45	Human
XPNPEP2	0.00	3	2	2	0	0	532	81.35	
CALU	0.00	0	20	0	0	0	320	99.07	Chimpanzee
ITPKA	0.00	0	0	7	0	0	312	75.54	Gorilla
GRIA4	0.00	1	5	1	0	0	897	99.45	Chimpanzee
TNKS	0.00	2	2	2	0	0	1248	95.12	
NEURL1	0.00	0	6	0	0	0	446	82.14	Chimpanzee
C2orf68	0.00	2	1	3	0	0	140	100.00	
PPDPF	0.00	0	0	6	0	0	55	50.00	Gorilla
CAAP1	0.00	0	2	4	0	0	342	98.84	Gorilla
SLC25A18	0.00	3	1	2	0	0	314	99.68	
MEIG1	0.00	1	3	1	1	0	88	100.00	
ORC2	0.00	1	3	3	0	0	577	100.00	
GABRD	0.00	0	0	6	0	0	319	70.42	Gorilla
HDAC9	0.00	1	3	2	0	0	1066	100.00	
SPTBN4	0.08	2	4	3	1	2	2389	96.56	
ZC3H7A	0.10	2	2	9	0	1	971	100.00	Gorilla
AASS	0.11	2	1	5	1	1	872	97.76	
ZDHHC8	0.15	0	7	1	0	1	684	89.41	Chimpanzee
ABR	0.16	0	10	0	0	1	628	74.76	Chimpanzee
SLC9A3	0.17	6	1	3	1	1	593	78.54	Human
GMPS	0.20	0	7	1	0	1	506	86.20	Chimpanzee
NUP205	0.20	2	5	5	0	4	1998	99.30	

CIC	0.21	5	2	6	1	5	2353	98.66	
GLDC	0.21	2	2	4	2	2	935	100.00	
COPB2	0.22	1	0	10	0	2	889	99.44	Gorilla
HERC1	0.23	7	6	7	1	11	4854	100.00	
SIPA1L2	0.23	4	3	5	0	4	1722	100.00	
POU2F3	0.23	4	2	2	0	1	427	97.94	
PAICS	0.24	3	2	7	0	1	421	98.14	Gorilla
BMP8B	0.25	1	2	5	3	1	402	100.00	#1#
CACUL1	0.28	1	1	6	0	1	352	95.65	Gorilla
CLIP2	0.30	2	2	9	1	3	1010	96.56	Gorilla
NDUFAF6	0.30	0	1	2	5	1	333	100.00	#1#
NUP107	0.32	5	5	1	1	3	925	100.00	
TMEM245	0.34	4	2	5	0	3	872	99.32	
ADAMTS10	0.36	3	13	0	0	3	828	78.78	Chimpanzee
BIN2	0.38	6	2	3	1	2	532	98.15	Human
SEC23IP	0.40	6	4	2	0	4	992	99.20	Human
ANKLE2	0.44	3	5	3	1	1	225	76.53	
TP53BP2	0.44	5	6	3	1	5	1125	99.21	
SLC25A24	0.46	0	0	10	0	2	436	95.20	Gorilla
SORBS1	0.46	6	3	5	1	6	1293	100.00	
EHMT1	0.47	1	12	0	0	4	857	77.91	Chimpanzee
CDH24	0.50	6	5	2	0	4	793	96.83	
RITA1	0.51	2	1	5	1	1	195	98.48	
TAX1BP1	0.51	3	4	6	1	4	778	99.87	
FAM135A	0.54	4	7	10	2	8	1470	97.03	
STBD1	0.56	3	3	3	1	2	358	100.00	
NID1	0.56	6	5	5	3	7	1247	100.00	
FBXW8	0.57	0	0	11	1	3	527	98.69	Gorilla
NUDT9	0.58	3	3	4	1	2	345	98.85	
CCT6B	0.58	1	3	6	2	3	515	97.17	
ADCYAP1	0.58	13	0	0	0	1	171	97.16	Human
SRI	0.59	0	7	1	0	1	169	85.35	Chimpanzee
CCDC112	0.59	3	0	11	0	3	505	98.44	Gorilla
MYOM1	0.60	13	3	2	1	8	1333	97.16	Human
KIF16B	0.65	4	3	8	4	9	1392	100.00	
RASA3	0.66	0	5	8	0	4	608	82.16	Gorilla
ULK1	0.77	2	12	2	0	5	646	76.00	Chimpanzee

FBXL4	0.81	4	5	4	2	5	621	100.00	
RET	0.82	12	7	3	0	9	1097	98.47	Human
SLC39A14	0.82	2	0	1	17	4	485	98.98	#1#
MKRN1	0.85	1	1	15	1	4	473	98.13	Gorilla
OTUD4	0.88	1	3	16	1	9	1027	97.07	Gorilla
GRIP2	0.88	12	6	7	0	10	1132	99.30	Human
LGR6	0.89	7	6	6	1	8	896	100.00	
CEP128	0.92	6	8	6	1	10	1091	99.73	
PCDH15	0.92	8	11	13	2	17	1847	98.72	
LUZP1	0.93	7	4	6	3	10	1076	100.00	
SMG6	0.94	16	3	3	2	13	1383	98.93	Human
RNF128	0.95	1	0	23	0	3	317	78.86	Gorilla
FER1L6	0.96	8	8	12	1	17	1772	95.99	
VPS37C	0.97	4	1	6	1	3	310	100.00	
WDR81	0.98	5	10	10	2	17	1735	94.65	
TMC3	1.00	7	7	7	1	11	1100	100.00	
RNF180	1.01	3	4	7	1	6	592	100.00	
NOX4	1.08	0	0	12	0	4	371	85.48	Gorilla
UPP2	1.10	5	0	6	1	4	363	100.00	
CELSR1	1.12	12	17	9	3	30	2678	92.60	Chimpanzee
SPG7	1.13	3	10	3	1	7	621	80.34	Chimpanzee
MYLK	1.14	5	7	12	5	18	1574	87.79	
LCT	1.19	11	11	10	9	23	1927	100.00	#1#
TRIM45	1.21	6	4	3	3	7	580	100.00	
COL25A1	1.23	10	4	3	1	8	653	99.85	Human
ALDH16A1	1.24	8	2	4	4	8	647	97.29	Human
FBLN2	1.25	7	5	12	1	14	1119	94.51	
ADGRV1	1.35	33	25	39	7	85	6305	100.00	
TRPM5	1.39	9	2	8	4	13	934	87.37	
SH2D4A	1.45	3	4	6	1	5	346	92.51	
SLC22A31	1.46	4	5	1	0	2	137	40.53	Chimpanzee
IL27RA	1.56	3	7	5	1	7	449	81.05	
EVPL	1.56	9	8	25	0	30	1920	97.96	Gorilla
DNAH11	1.59	24	22	31	6	71	4479	99.58	
ABCB5	1.59	8	9	14	2	19	1198	97.48	
ZNF280C	1.68	3	12	8	4	12	715	99.86	Chimpanzee
HGFAC	1.76	1	7	18	0	11	625	96.60	Gorilla
CEP192	1.93	14	11	28	6	49	2537	100.00	Gorilla

NOM1	1.95	11	6	8	3	16	822	95.80	
KCTD18	1.98	1	2	16	1	7	354	88.06	Gorilla
TYSND1	2.05	4	6	11	0	11	536	99.26	Gorilla
IGFN1	2.40	8	9	19	2	27	1126	90.51	Gorilla
RFPL2	2.97	5	3	10	4	10	337	99.41	
SCART1	3.47	11	52	6	0	23	662	72.51	Chimpanzee
QRICH2	4.59	15	14	40	10	69	1502	88.46	Gorilla
SCML1	4.91	5	17	5	2	16	326	99.09	Chimpanzee

S2 Table: Lower than expected substitution rate on the human branch

Gene	Human % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Higher in
TSGA10	0.00	0	2	1	0	34	494	95.37	Gibbon
CEP295NL	0.00	0	5	9	7	41	589	98.66	
C2orf81	0.00	0	4	9	2	33	537	99.63	
TEX13A	0.00	0	5	8	2	31	383	96.72	
HSF5	0.00	0	3	7	2	32	593	99.50	
PODXL	0.00	0	4	7	1	39	478	85.97	Gibbon
MUC1	0.00	0	3	6	0	29	470	97.31	
LEKR1	0.00	0	1	6	0	31	692	100.00	Gibbon
RIPK1	0.00	0	4	2	2	30	671	100.00	Gibbon
PTCD3	0.00	0	5	6	2	29	686	99.56	
SI	0.06	1	6	6	2	46	1814	99.40	Gibbon
PLB1	0.07	1	3	10	4	47	1369	96.54	
TEX11	0.11	1	10	11	2	36	906	99.34	
C3orf20	0.12	1	3	11	3	39	853	99.53	
CAGE1	0.12	1	6	13	0	42	839	100.00	
PALM3	0.17	1	5	19	4	31	604	92.35	Gorilla
OBSCN	0.46	33	49	92	37	250	7241	89.73	

S3 Table: Lower than expected substitution rate on the chimpanzee branch

Gene	Chimp % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Higher in
SDK2	0.00	3	0	5	1	31	1893	94.65	

TROAP	0.00	3	0	4	2	31	771	97.10	
NSD1	0.00	8	0	5	1	29	2618	99.47	
ANK1	0.00	1	0	11	4	29	1620	91.11	
CYLC1	0.00	1	0	7	5	35	630	97.83	
POLQ	0.14	10	3	18	9	67	2215	90.19	
MUC13	0.21	4	1	9	1	46	474	95.76	Gibbon
NLRP1	0.35	8	5	10	3	93	1428	97.14	Gibbon

S4 Table: Lower than expected substitution rate on the gorilla branch

Gene	Gorilla % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Higher in
LTBP4	0.00	3	6	0	0	19	1483	94.22	
TOP3A	0.00	7	1	0	1	19	1001	100.00	
PSD3	0.00	5	3	0	0	20	911	96.00	
TLR2	0.00	0	3	0	0	26	784	100.00	Gibbon
WDR35	0.00	0	4	0	1	26	1181	100.00	Gibbon
SPN	0.00	1	3	0	1	26	399	100.00	Gibbon
TF	0.00	0	1	0	0	30	672	96.28	Gibbon
CGAS	0.00	3	3	0	1	27	430	96.20	Gibbon
TUBGCP6	0.00	2	18	0	1	18	690	47.85	Chimpanzee
COL16A1	0.08	2	3	1	1	38	1236	83.97	Gibbon
RIPK3	0.20	2	4	1	0	38	501	99.01	Gibbon
TTC3	0.21	13	11	4	4	46	1946	97.79	
ADAM12	0.22	3	5	2	3	57	906	99.67	Gibbon
PTPRC	0.24	2	5	3	3	55	1273	97.62	Gibbon
TDRD15	0.25	11	8	4	1	54	1604	99.75	

S5 Table: Higher than expected substitution rate on the human branch

Gene	Branch-specific % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Lower in
ADCYAP1	7.60	13	0	0	0	1	171	97.16	Gibbon
RNF181	5.08	3	0	0	0	0	59	38.56	
BIRC5	4.40	4	0	1	1	1	91	100.00	
DACT3	3.89	7	0	0	0	0	180	99.45	Gibbon
PVALEF	3.76	5	0	0	0	5	133	99.25	

PGLYRP1	3.57	7	1	5	0	6	196	100.00	
PSORS1C2	2.94	4	1	1	0	1	136	100.00	
BTNL2	2.88	7	2	2	1	5	243	89.67	
DMKN	2.59	9	1	3	0	16	347	74.62	
TMED3	2.48	5	0	0	0	1	202	93.09	
DCXR	2.46	6	0	1	0	5	244	100.00	
DHDH	2.40	8	2	0	0	4	333	99.70	
BLVRB	2.22	4	0	1	0	0	180	87.38	
CD37	2.16	6	3	2	0	4	278	98.93	
TMBIM4	2.12	6	0	0	0	3	283	100.00	
ODF1	2.00	5	0	1	0	2	250	100.00	
NACAD	1.86	19	11	8	0	45	1019	95.06	
TOGARAM2	1.83	18	7	10	1	46	984	97.23	
CBFB	1.76	3	0	1	0	0	170	93.41	
EPCAM	1.71	5	1	0	0	3	292	91.25	
FAM118A	1.68	6	2	0	0	6	357	100.00	
KIF26B	1.58	24	8	6	2	35	1518	98.64	
SOWAHC	1.57	8	2	0	1	10	508	99.61	
EDA2R	1.57	5	1	1	0	2	318	100.00	
MAP7D1	1.56	10	1	1	0	16	640	87.19	
COL25A1	1.53	10	4	3	1	8	653	99.85	Gibbon
VSTM2A	1.53	4	0	2	0	2	262	92.91	
RBM44	1.52	16	6	7	0	25	1050	99.81	
SLC7A2	1.49	10	5	2	0	13	671	96.41	
PGM1	1.48	7	0	0	0	0	474	81.72	Gibbon
ADA	1.42	5	1	0	0	2	352	96.97	
IQCA1L	1.40	10	8	4	0	14	715	99.58	
CARF	1.35	8	0	5	1	9	592	100.00	
PDCL	1.33	4	0	0	0	0	301	100.00	
DCAKD	1.30	3	0	0	0	0	231	100.00	
KLF15	1.24	5	0	0	0	3	403	98.29	
ALDH16A1	1.24	8	2	4	4	8	647	97.29	Gibbon
FAM208B	1.22	29	19	14	0	90	2382	98.96	#1#
SLC15A5	1.22	7	3	3	0	8	575	99.48	
CHPT1	1.20	4	0	0	0	4	332	99.40	
BRCA1	1.19	21	6	12	0	47	1771	97.09	

SMG6	1.16	16	3	3	2	13	1383	98.93	Gibbon
KIAA0825	1.14	14	8	2	0	29	1232	97.70	
BIN2	1.13	6	2	3	1	2	532	98.15	Gibbon
PHACTR2	1.11	7	4	1	0	6	630	99.06	
RET	1.09	12	7	3	0	9	1097	98.47	Gibbon
VPS45	1.09	6	0	2	0	0	550	95.16	Gibbon
GRIP2	1.06	12	6	7	0	10	1132	99.30	Gibbon
DDX18	1.04	7	3	1	1	5	670	100.00	
TG	1.04	28	9	25	1	67	2693	98.11	
COL10A1	1.03	7	3	0	1	5	680	100.00	
SLC9A3	1.01	6	1	3	1	1	593	78.54	Gibbon
PDSS2	1.00	4	0	2	0	2	399	100.00	
WIZ	1.00	7	1	0	1	6	702	80.05	
MYO18B	0.99	22	13	10	4	41	2217	96.94	
MYOM1	0.98	13	3	2	1	8	1333	97.16	Gibbon
NEK6	0.96	3	0	0	0	0	313	90.20	
DCHS2	0.93	25	10	16	4	64	2687	92.21	
ACP5	0.92	3	0	0	0	1	325	100.00	
TRAF5	0.90	5	0	3	0	3	557	100.00	
DHX35	0.89	6	3	0	0	4	675	97.40	
NAP1L4	0.84	3	0	0	0	1	356	92.23	
ESR1	0.84	5	0	0	0	5	594	99.83	
CHPF	0.79	6	1	1	0	3	763	99.22	
EYA2	0.78	4	1	0	0	2	512	100.00	
TIGD4	0.78	4	0	0	0	4	512	100.00	
IGSF22	0.78	10	1	4	0	7	1281	98.69	
NCOA7	0.74	7	1	4	1	7	941	99.89	
PDE4A	0.69	6	0	1	1	4	867	99.77	
FAT1	0.68	30	21	16	2	74	4401	97.56	
CANX	0.68	4	0	1	0	3	592	100.00	
MYEF2	0.67	4	1	1	0	1	600	100.00	
DISP1	0.66	10	2	3	2	18	1514	99.34	
POLR2A	0.63	12	0	1	0	0	1904	97.14	Gibbon
SEC23IP	0.60	6	4	2	0	4	992	99.20	Gibbon
RNF139	0.60	4	0	0	1	2	664	100.00	
UBP1	0.56	3	0	1	0	0	540	100.00	
SIM1	0.52	4	3	0	0	1	765	99.87	

PRDM10	0.52	6	1	0	0	6	1158	100.00	
NR3C2	0.51	5	0	2	0	4	988	100.00	
FNBP1	0.50	3	0	0	0	1	604	99.18	
CACNA1C	0.49	9	2	2	0	7	1845	92.95	
MALT1	0.49	4	0	0	1	2	824	100.00	
LTBP1	0.47	8	5	1	2	9	1689	99.47	
ADAMTS19	0.47	5	0	2	1	2	1059	99.53	
SLC44A1	0.47	3	0	0	0	1	643	97.87	
SYNE1	0.39	34	14	24	7	88	8735	99.44	
SBF2	0.38	7	2	3	0	7	1830	100.00	
PCDH1	0.34	4	0	1	0	3	1187	97.37	
ITPR1	0.30	8	0	1	0	2	2652	98.22	
SLC4A10	0.27	3	0	1	0	0	1097	98.12	
RICTOR	0.23	4	0	0	0	3	1709	100.00	

S6 Table: Higher than expected substitution rate on the chimpanzee branch

Gene	Branch-specific % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Lower in
SCART1	7.85	11	52	6	0	23	662	72.51	Gibbon
ASIC1	6.51	0	20	0	0	0	307	64.09	Gibbon
CALU	6.25	0	20	0	0	0	320	99.07	Gibbon
MASP1	6.18	1	32	0	0	5	518	74.11	
COL23A1	6.09	0	14	1	0	9	230	56.10	
SCML1	5.21	5	17	5	2	16	326	99.09	Gibbon
SRI	4.14	0	7	1	0	1	169	85.35	Gibbon
SLC22A31	3.65	4	5	1	0	2	137	40.53	Gibbon
CXorf67	3.11	1	12	4	3	20	386	97.97	
CARD19	2.99	0	5	0	0	2	167	91.26	
UPRT	2.90	0	4	0	0	0	138	79.77	
NCS1	2.84	0	4	0	0	0	141	81.98	
LYAR	2.65	2	10	4	0	8	378	100.00	
PIMREG	2.61	1	7	1	0	7	268	98.17	
TUBGCP6	2.61	2	18	0	1	18	690	47.85	Gorilla
SPDYE4	2.53	0	6	1	0	10	237	100.00	
PEX11G	2.49	1	6	2	0	3	241	100.00	

RNF168	2.48	2	9	2	0	15	363	77.23	
HM13	2.48	0	9	0	0	0	363	85.21	Gibbon
DFFA	2.44	2	8	2	0	11	328	100.00	
DDX47	2.14	0	9	1	0	4	420	92.31	
FAM53B	2.03	0	6	1	0	2	296	86.55	
MTG1	2.02	1	5	1	0	5	248	82.67	
DERL3	1.93	0	4	3	0	1	207	88.09	
PCBP3	1.92	0	5	0	0	1	260	78.31	
COX10	1.90	0	6	2	0	7	316	79.40	
NIPAL3	1.86	0	6	1	0	2	322	87.50	
ULK1	1.86	2	12	2	0	5	646	76.00	Gibbon
ZNF280C	1.68	3	12	8	4	12	715	99.86	Gibbon
DNAJC9	1.66	0	4	1	0	1	241	97.57	
ARHGAP40	1.63	1	9	2	0	17	553	100.00	
QRFPR	1.62	0	7	3	0	8	431	100.00	
SPG7	1.61	3	10	3	1	7	621	80.34	Gibbon
CYP24A1	1.61	1	7	2	1	7	436	97.32	
ABR	1.59	0	10	0	0	1	628	74.76	Gibbon
ADAMTS10	1.57	3	13	0	0	3	828	78.78	Gibbon
TAF6L	1.52	0	6	0	0	4	395	68.34	
ACER1	1.52	0	4	0	0	3	264	100.00	
NMUR2	1.50	4	6	1	0	6	401	99.50	
CAPS2	1.50	3	7	2	0	6	468	97.91	
CPNE7	1.47	2	6	1	0	5	408	77.57	
PAX6	1.41	0	5	0	0	1	354	81.19	
EHMT1	1.40	1	12	0	0	4	857	77.91	Gibbon
GMPS	1.38	0	7	1	0	1	506	86.20	Gibbon
SCAMP1	1.38	1	4	0	0	1	290	92.65	
GLA	1.35	0	5	1	0	5	370	100.00	
NEURL1	1.35	0	6	0	0	0	446	82.14	Gibbon
ACOX3	1.29	2	8	2	0	7	620	89.86	
CFAP54	1.25	2	7	2	1	9	558	85.71	
DDIAS	1.21	4	12	4	0	25	995	99.70	
TXLNG	1.17	0	6	1	0	7	514	98.09	
ZNF16	1.12	0	7	1	1	11	627	94.86	
SLC16A9	1.09	0	5	0	0	4	459	90.35	
MMRN1	1.06	5	13	2	0	31	1228	100.00	

PROKR2	1.04	1	4	0	0	2	384	100.00	
ZDHHC8	1.02	0	7	1	0	1	684	89.41	Gibbon
TBL1X	1.02	0	5	0	0	2	489	85.64	
RTN4IP1	1.01	0	4	0	0	3	396	100.00	
APBB1	1.01	0	5	0	0	0	495	86.24	
BLM	0.93	6	13	10	1	24	1394	99.64	
LRIG2	0.93	3	8	3	1	7	859	87.03	
PHKB	0.92	0	10	2	0	9	1084	99.18	
SCTR	0.91	0	4	1	0	2	440	100.00	
PAK2	0.90	0	4	1	0	2	442	92.86	
GPN1	0.90	0	3	0	0	0	333	89.04	
KANK1	0.90	7	12	5	0	22	1340	99.63	
SRP68	0.89	0	5	0	0	4	562	93.36	
RUBCN	0.86	1	8	2	0	15	932	96.48	
RAG1	0.85	2	8	5	1	11	942	98.64	
NR2C1	0.84	3	5	1	0	3	592	98.18	
RFC3	0.84	0	3	0	0	0	356	100.00	
INTS9	0.83	0	5	0	0	3	606	95.73	
LARP1	0.77	2	7	0	0	4	907	90.07	
RNF44	0.77	0	3	0	0	1	389	94.42	
CACNA1B	0.76	2	14	2	1	12	1833	87.20	
NFATC1	0.75	1	5	0	0	1	665	77.96	
SPTB	0.74	5	15	7	1	24	2015	88.96	
MAP3K15	0.74	0	7	2	0	6	943	82.43	
PLCD3	0.73	1	5	3	0	2	682	88.57	
CEP83	0.72	0	5	2	0	4	698	99.57	
POLR1A	0.71	5	12	5	1	21	1681	97.90	
GOLGA4	0.71	5	15	9	2	36	2112	98.00	
EIF3A	0.66	1	6	1	0	4	912	77.62	
NBAS	0.64	7	15	3	0	28	2353	99.58	
CELSR1	0.63	12	17	9	3	30	2678	92.60	Gibbon
GALNT3	0.63	1	4	1	0	2	633	100.00	
PHF20L1	0.60	2	6	0	0	3	1005	98.82	
GSPT1	0.60	0	3	0	0	1	504	96.74	
MAP4K1	0.57	0	4	1	0	3	700	88.83	
GRIA4	0.56	1	5	1	0	0	897	99.45	Gibbon
FRMD4A	0.55	0	5	0	0	2	901	93.66	

DOCK8	0.55	5	11	4	1	21	1987	96.60	
PDP1	0.53	0	3	0	0	1	562	100.00	
XPO4	0.46	0	5	0	0	1	1078	94.48	
NCAM1	0.45	1	4	0	0	2	884	100.00	
VPS13C	0.44	15	16	7	1	34	3636	99.32	
CAMSAP2	0.41	2	6	1	2	4	1464	98.32	
PARD3	0.32	0	4	0	1	3	1260	100.00	
PIK3CA	0.31	0	3	0	0	0	960	92.84	
TLN2	0.28	2	6	2	0	3	2125	92.84	
SF3B1	0.27	0	3	0	0	0	1127	88.95	

S7 Table: Higher than expected substitution rate on the gorilla branch

Gene	Branch-specific % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Lower in
PPDPF	10.91	0	0	6	0	0	55	50.00	Gibbon
RNF128	7.26	1	0	23	0	3	317	78.86	Gibbon
KCTD18	4.52	1	2	16	1	7	354	88.06	Gibbon
ZDHHC3	4.38	0	0	12	1	0	274	82.28	Gibbon
SNAP25	4.37	0	0	9	0	0	206	100.00	Gibbon
CARD8	3.67	8	3	13	0	16	354	87.19	
RCC1	3.37	1	0	12	1	6	356	84.16	
WDR38	3.30	4	0	10	0	8	303	98.70	
NOX4	3.23	0	0	12	0	4	371	85.48	Gibbon
MKRN1	3.17	1	1	15	1	4	473	98.13	Gibbon
PALM3	3.15	1	5	19	4	31	604	92.35	Human
APOOL	3.00	0	0	6	0	2	200	86.58	
SAPCD2	2.90	1	1	10	0	6	345	96.64	
HGFAC	2.88	1	7	18	0	11	625	96.60	Gibbon
SPATA32	2.88	3	1	11	3	13	382	100.00	
NSMCE4A	2.83	0	1	7	0	5	247	75.30	
QRICH2	2.66	15	14	40	10	69	1502	88.46	Gibbon
AMACR	2.65	3	3	10	1	9	377	98.69	
THEGL	2.59	1	5	12	1	14	464	100.00	
FGF11	2.54	0	0	5	1	1	197	100.00	
ANO8	2.47	0	0	10	0	4	405	69.71	
IQCD	2.45	1	2	11	2	12	449	100.00	

TBXA2R	2.44	1	0	8	0	2	328	95.63	
DRD4	2.40	0	1	8	0	4	334	86.53	
SLC25A24	2.29	0	0	10	0	2	436	95.20	Gibbon
FAM161B	2.29	4	2	16	3	20	700	99.43	
ITPKA	2.24	0	0	7	0	0	312	75.54	Gibbon
SRF	2.23	0	1	8	0	0	358	75.69	Gibbon
CCDC112	2.18	3	0	11	0	3	505	98.44	Gibbon
IL23A	2.12	0	0	4	1	1	189	100.00	
HMGCLL1	2.09	0	0	5	0	3	239	78.88	
FBXW8	2.09	0	0	11	1	3	527	98.69	Gibbon
GRIN3B	2.07	7	3	15	3	22	726	75.39	
TYSND1	2.05	4	6	11	0	11	536	99.26	Gibbon
MVD	1.97	1	0	7	0	6	356	93.93	
NTF4	1.90	0	0	4	0	2	210	100.00	
SGCB	1.90	1	0	6	0	2	316	99.68	
GABRD	1.88	0	0	6	0	0	319	70.42	Gibbon
DALRD3	1.86	1	0	7	1	4	376	100.00	
RNF39	1.85	2	0	7	0	5	379	100.00	
RGS19	1.84	0	0	4	0	1	217	100.00	
METTL11B	1.84	1	1	5	0	1	272	97.84	
FAM204A	1.72	1	0	4	0	1	233	100.00	
CACUL1	1.70	1	1	6	0	1	352	95.65	Gibbon
IGFN1	1.69	8	9	19	2	27	1126	90.51	Gibbon
SNX32	1.68	0	0	5	0	2	297	90.83	
TMEM62	1.67	1	0	9	0	7	539	92.45	
EFCAB6	1.67	6	9	25	4	45	1501	100.00	
PAICS	1.66	3	2	7	0	1	421	98.14	Gibbon
MEX3A	1.65	0	0	7	0	2	424	94.64	
NACC2	1.57	1	2	6	0	2	382	78.60	
OTUD4	1.56	1	3	16	1	9	1027	97.07	Gibbon
GPN3	1.56	0	1	5	0	3	321	99.69	
ZFAND3	1.55	0	0	3	0	0	193	96.50	
ZCCHC8	1.46	0	2	9	2	5	617	91.54	
GCH1	1.46	0	0	3	0	0	206	91.15	
ITIH6	1.45	5	4	15	0	21	1031	98.10	
CLMN	1.44	2	4	14	2	18	972	100.00	
ECT2L	1.44	3	1	13	2	16	903	100.00	
CAPN15	1.42	0	1	8	0	7	565	80.48	

CWF19L2	1.41	5	4	12	0	12	854	98.96	
PAX5	1.37	0	0	5	0	0	364	93.09	
IQCH	1.37	5	5	14	1	19	1024	99.71	
MAPKBP1	1.34	1	7	20	2	24	1497	98.88	
PGD	1.33	0	0	5	0	3	377	86.87	
RASA3	1.32	0	5	8	0	4	608	82.16	Gibbon
EVPL	1.30	9	8	25	0	30	1920	97.96	Gibbon
CHD1L	1.28	2	3	11	1	11	859	95.76	
BCAM	1.28	0	2	6	0	4	469	80.58	
RANBP1	1.27	0	0	3	0	0	237	100.00	
SLC16A7	1.26	0	0	6	0	3	478	100.00	
LANCL3	1.25	0	0	5	0	0	400	97.09	
ITGA8	1.24	4	4	13	0	13	1045	99.71	
RXFP1	1.24	0	1	9	0	9	726	96.16	
KTN1	1.23	3	5	14	0	14	1136	93.57	
ANO6	1.22	0	1	11	0	7	901	97.83	
HERC2	1.22	0	0	5	0	0	411	78.59	
CFAP61	1.21	2	6	15	1	22	1236	99.92	
ESRRA	1.18	0	0	5	0	1	422	100.00	
NR1I3	1.18	0	0	4	0	2	339	94.96	
FAM171A1	1.18	0	2	10	0	13	851	97.15	
CAAP1	1.17	0	2	4	0	0	342	98.84	Gibbon
UNC93B1	1.17	0	0	4	0	0	343	84.28	
SEPT7	1.16	0	0	4	0	0	346	90.10	
SCARA3	1.15	0	1	5	0	3	433	82.63	
NIM1K	1.15	0	1	5	0	2	436	100.00	
GLIS2	1.15	0	0	6	0	6	524	100.00	
FBXO43	1.14	1	2	8	0	8	700	99.86	
MAPKAPK2	1.14	0	0	3	0	0	264	71.35	
COPB2	1.12	1	0	10	0	2	889	99.44	Gibbon
CEP192	1.10	14	11	28	6	49	2537	100.00	Gibbon
ATP6V0A2	1.05	1	0	9	0	9	856	100.00	
CUBN	1.04	15	17	34	3	66	3280	95.99	
SH3KBP1	1.01	0	1	6	0	4	594	94.44	
ADGRA2	0.97	3	0	10	0	9	1028	91.13	
LDB3	0.97	0	0	7	0	3	724	100.00	
SYT12	0.95	1	0	4	0	1	420	100.00	

ADAMTS12	0.93	4	4	14	3	17	1509	100.00	
ZC3H7A	0.93	2	2	9	0	1	971	100.00	Gibbon
USP14	0.92	0	0	3	0	0	325	70.65	
MEX3B	0.91	1	1	5	0	2	549	96.49	
FOXO3	0.89	0	1	6	0	3	672	100.00	
CLIP2	0.89	2	2	9	1	3	1010	96.56	Gibbon
NUMBL	0.87	0	0	5	1	2	575	95.67	
SFMBT2	0.87	1	2	7	0	6	807	96.65	
DNAH1	0.86	12	15	35	10	67	4060	96.90	
ISL1	0.86	0	0	3	0	0	348	99.71	
COLGALT1	0.86	0	1	5	0	3	582	96.36	
ATP6V0D2	0.86	0	0	3	0	0	350	100.00	
SLC4A2	0.85	1	2	9	0	5	1055	95.39	
EIF2AK3	0.81	3	2	9	0	8	1115	99.91	
DYNC1LI1	0.80	0	0	4	0	2	497	100.00	
EPS15	0.80	1	1	7	0	7	871	97.21	
RCOR3	0.79	0	0	4	0	1	508	92.87	
GFPT2	0.76	0	1	5	1	1	654	98.20	
CYTH3	0.76	0	0	3	0	0	395	99.00	
KDM2A	0.75	0	0	5	0	0	664	91.84	
ZBTB24	0.72	1	1	5	0	2	695	99.86	
CARD10	0.71	0	0	6	0	5	842	93.76	
DYRK2	0.69	0	0	4	0	0	577	96.65	
MPDZ	0.68	2	6	14	3	20	2048	98.27	
MYO9A	0.63	5	6	16	0	27	2547	100.00	
RECQL	0.62	0	0	4	0	2	643	99.08	
LONP1	0.60	0	1	4	0	1	664	91.97	
ARHGAP5	0.60	0	0	9	1	9	1502	100.00	
TNRC6C	0.59	1	2	11	0	18	1865	97.75	
MCM4	0.59	2	0	5	0	2	851	98.84	
SLIT1	0.59	1	1	9	0	11	1534	100.00	
PHLDB1	0.58	2	1	8	0	6	1376	99.93	
GIGYF2	0.58	0	1	7	0	6	1217	94.41	
HNRNPU	0.55	0	0	4	0	2	725	100.00	
GRIA1	0.55	1	1	5	0	1	912	99.56	
ACAP2	0.55	0	0	4	0	0	732	97.21	
GRM5	0.50	0	0	6	0	3	1210	100.00	

ADAM23	0.48	0	0	4	1	1	832	100.00	
LRP5	0.45	0	0	6	1	5	1320	87.42	
TENM1	0.33	2	4	9	0	8	2728	99.89	

S8 Table: Higher than expected substitution rate on the gibbon branch

Gene	Branch-specific % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Lower in
GVQW2	22.92	0	0	0	0	11	48	80.00	
S100Z	15.22	0	0	1	0	14	92	93.88	
DPPA3	14.97	0	1	0	0	22	147	92.45	
TSPAN8	12.66	1	3	3	0	30	237	100.00	
TNNT3	12.57	0	0	0	0	21	167	97.09	
SMIM23	12.14	1	0	0	0	17	140	96.55	
AKAP14	10.15	0	1	0	0	20	197	100.00	
MUC13	9.70	4	1	9	1	46	474	95.76	Chimpanzee
RHEX	9.30	0	1	1	0	16	172	100.00	
DRAM1	9.28	0	0	0	0	22	237	99.58	
NCR3LG1	8.83	1	2	3	2	37	419	96.77	
MISP	8.45	7	4	6	2	56	663	98.51	
PODXL	8.16	0	4	7	1	39	478	85.97	Human
CDKL4	8.14	2	1	3	1	28	344	94.77	
PLA2G4C	8.04	1	1	5	0	37	460	88.63	
MRNIP	7.96	2	0	3	2	27	339	98.83	
MROH9	7.60	4	12	6	4	65	855	99.53	
RIPK3	7.58	2	4	1	0	38	501	99.01	Gorilla
ANKRD7	7.30	0	0	2	0	17	233	91.73	
RNF213	7.15	37	42	36	12	358	5006	95.28	
GP1BA	7.02	2	2	9	0	44	627	96.17	
TSGA10	6.88	0	2	1	0	34	494	95.37	Human
CCDC150	6.74	2	2	2	0	32	475	81.34	
TM4SF19	6.58	1	0	0	1	16	243	81.27	
SPN	6.52	1	3	0	1	26	399	100.00	Gorilla
NLRP1	6.51	8	5	10	3	93	1428	97.14	Chimpanzee
EIF2AK2	6.34	2	1	3	1	31	489	90.06	
ADAM12	6.29	3	5	2	3	57	906	99.67	Gorilla

CGAS	6.28	3	3	0	1	27	430	96.20	Gorilla
TEDC1	6.24	1	2	3	1	28	449	91.82	
PECR	6.11	0	0	1	0	16	262	88.81	
PTPRH	6.00	6	5	5	2	51	850	87.81	
CLDN18	5.98	0	0	0	0	15	251	96.17	
DTX3L	5.68	1	3	5	0	42	740	100.00	
FGR	5.49	0	0	0	0	23	419	88.03	
FBXO39	5.43	0	2	3	0	24	442	100.00	
NDUFB5	5.41	0	0	0	0	10	185	97.88	
AMBN	5.37	1	0	1	1	24	447	100.00	
ITGB2	5.32	0	0	3	0	31	583	76.51	
POLRMT	5.28	3	4	7	3	50	947	93.12	
CD3E	5.26	0	0	0	0	10	190	95.96	
MBL2	4.96	0	1	0	0	12	242	97.98	
C1orf87	4.95	2	0	5	0	27	546	100.00	
CCDC15	4.94	4	2	3	3	44	890	95.19	
MFN1	4.83	3	2	2	0	29	601	91.34	
TBRG4	4.75	2	0	1	2	30	631	100.00	
HS3ST1	4.61	0	0	1	0	14	304	99.02	
BRCA2	4.57	12	12	17	1	156	3411	99.85	
LEKR1	4.48	0	1	6	0	31	692	100.00	Human
RIPK1	4.47	0	4	2	2	30	671	100.00	Human
TF	4.46	0	1	0	0	30	672	96.28	Gorilla
PM20D1	4.40	2	1	1	0	22	500	100.00	
PTPRC	4.32	2	5	3	3	55	1273	97.62	Gorilla
ZNF195	4.27	5	1	1	0	27	633	100.00	
COL9A3	4.25	1	1	1	0	20	471	79.97	
ATP6V0B	4.13	0	0	0	0	10	242	93.80	
MRM3	4.05	0	1	0	0	17	420	100.00	
DHRS13	4.01	0	0	0	0	15	374	99.20	
CD19	3.96	1	0	2	0	22	556	100.00	
TMEM150A	3.93	0	0	0	0	9	229	89.80	
CEP164	3.84	6	3	4	2	54	1405	98.25	
TRPV2	3.82	0	1	2	0	24	629	99.84	
GDF11	3.72	0	0	0	0	12	323	85.68	
MRPS30	3.66	0	1	1	0	16	437	100.00	
ACAD10	3.66	2	1	1	1	25	683	99.56	

SDR16C5	3.60	0	0	0	0	10	278	89.97	
CCDC158	3.60	2	2	5	0	40	1112	100.00	
TAS2R3	3.49	0	0	0	0	11	315	99.68	
IFT81	3.40	0	1	4	0	23	676	100.00	
ZNF703	3.34	0	0	1	0	16	479	91.76	
TLR2	3.32	0	3	0	0	26	784	100.00	Gorilla
TBCD	3.28	6	1	2	0	34	1037	88.48	
OXA1L	3.20	0	0	1	0	13	406	93.33	
ARG2	3.11	0	0	0	0	11	354	100.00	
COL16A1	3.07	2	3	1	1	38	1236	83.97	Gorilla
WISP1	3.06	0	0	0	0	9	294	92.45	
DUSP1	3.04	0	0	0	0	9	296	90.80	
LOXL2	2.99	1	0	0	0	18	602	84.79	
PKN2	2.95	3	0	2	1	29	984	100.00	
B3GNT5	2.91	0	0	0	0	11	378	100.00	
COL11A2	2.90	1	2	4	0	34	1173	87.67	
CEP250	2.88	4	6	10	5	69	2395	98.89	
NAALAD2	2.86	0	1	2	0	18	629	96.62	
NOD1	2.83	0	3	1	0	27	953	100.00	
RBM20	2.69	3	1	3	0	30	1114	93.22	
IKBKE	2.62	0	0	2	0	17	648	95.86	
TDRD7	2.55	2	1	2	2	28	1097	100.00	
SI	2.54	1	6	6	2	46	1814	99.40	Human
DOT1L	2.42	2	1	3	2	33	1363	94.19	
TNK2	2.37	1	0	2	1	23	969	94.17	
RAPGEF3	2.34	1	1	1	0	18	769	90.15	
KIF11	2.30	1	2	0	0	22	957	93.64	
IFT172	2.27	3	1	6	0	37	1629	95.65	
NUP214	2.26	4	3	9	0	47	2080	99.90	
ESPL1	2.22	3	4	3	4	46	2069	97.69	
WDR35	2.20	0	4	0	1	26	1181	100.00	Gorilla
FDPS	2.20	0	0	0	0	9	410	97.85	
SPAG6	2.16	0	0	0	0	10	464	95.87	
DLL1	2.12	0	0	1	0	15	709	98.06	
ARHGEF7	2.11	0	1	1	0	15	710	95.05	
ZNF483	2.11	0	1	1	0	15	712	95.70	
SGIP1	2.08	0	0	1	1	15	721	93.88	

FBXO41	2.06	0	0	0	0	12	582	75.78	
CECR2	2.02	2	3	2	0	28	1383	97.39	
NEK1	1.94	0	2	2	0	22	1133	100.00	
PML	1.85	1	0	1	0	15	809	97.00	
AP3D1	1.83	0	2	1	0	19	1041	90.84	
KLC4	1.69	0	0	0	0	9	534	89.60	
USP33	1.68	1	1	0	0	15	891	98.67	
FERMT1	1.62	0	0	0	0	9	556	94.72	
TRIM28	1.57	0	0	0	0	10	638	91.01	
ZNF326	1.55	0	0	0	0	9	579	100.00	
SMC6	1.51	0	0	2	0	16	1063	99.91	
RPS6KC1	1.50	1	0	0	0	15	1000	96.06	
XAB2	1.40	0	0	0	0	9	641	82.07	
FMNL2	1.33	0	0	0	0	13	975	92.68	
IQSEC2	1.31	0	0	1	0	13	995	75.61	
SRGAP3	1.26	0	0	0	0	13	1034	96.19	
NFKB1	0.93	0	0	0	0	9	969	100.00	
FBN1	0.64	0	0	2	1	18	2821	98.26	
CACNA1E	0.59	0	0	1	0	13	2193	98.34	

S9 Table: Higher than expected substitution rate on the #1# branch

Gene	Branch-specific % subs per site	Human subs	Chimp subs	Gorilla subs	#1# subs	Gibbon subs	Align overlap	Align Sat	Lower in
SLC39A14	3.51	2	0	1	17	4	485	98.98	Gibbon
SUMO3	3.20	0	0	1	4	3	125	89.29	
IL9	2.78	0	0	0	4	6	144	100.00	
HAMP	2.70	1	0	0	2	0	74	88.10	
COX7A2	2.61	0	1	1	3	1	115	100.00	
C16orf78	2.27	1	1	3	6	16	264	100.00	
THAP8	2.16	4	3	5	5	8	231	100.00	
TM2D2	2.10	0	0	0	3	1	143	83.63	
SLC22A18AS	1.99	3	1	5	5	8	251	99.21	
PRG4	1.89	0	0	0	2	0	106	28.65	
CCDC78	1.82	0	2	5	6	11	330	89.19	
TMEM231	1.50	1	0	2	4	3	266	83.91	
NDUFAF6	1.50	0	1	2	5	1	333	100.00	Gibbon
HCFC1R1	1.45	0	0	1	2	0	138	100.00	

RAB6A	1.44	0	0	0	3	1	208	100.00	
BEND2	1.37	7	8	9	10	64	730	96.43	
ZNF778	1.34	5	5	3	8	18	598	98.36	
HEBP1	1.23	0	0	0	2	0	162	85.71	
CCDC121	1.22	0	4	7	5	13	410	100.00	
HUS1	1.15	0	0	0	3	2	260	95.24	
PDZD9	1.14	0	0	2	3	5	264	100.00	
TAF1C	1.04	4	3	6	7	19	673	84.02	
PPP6C	1.02	0	0	3	3	1	294	95.45	
ENKD1	1.00	0	1	1	3	7	299	88.20	
AMZ2	1.00	1	1	1	3	2	301	100.00	
MDFIC	0.96	0	0	1	3	2	313	90.99	
C12orf45	0.95	1	0	0	2	1	211	100.00	
STK31	0.92	5	1	5	7	21	762	90.39	
CCDC91	0.91	3	2	1	4	8	441	100.00	
NEMP1	0.90	1	1	0	4	5	443	99.77	
CLCF1	0.90	0	0	0	2	0	223	99.11	
C11orf80	0.88	3	2	4	5	14	569	99.48	
PLA1A	0.88	1	0	2	4	9	456	100.00	
PITPNA	0.87	0	0	0	2	1	230	85.50	
RECQL4	0.87	8	5	10	9	47	1039	91.38	
ERMAP	0.84	3	1	0	4	7	475	100.00	
ILDR1	0.84	0	0	4	4	14	479	94.85	
NAP1L3	0.80	2	2	2	4	9	502	100.00	
MGAT4B	0.79	0	1	1	4	2	507	92.52	
UNC5CL	0.77	1	0	3	4	9	518	100.00	
SORBS3	0.76	5	2	4	5	11	654	97.47	
BMP8B	0.75	1	2	5	3	1	402	100.00	Gibbon
CNKSR1	0.74	1	3	1	4	12	544	87.60	
SHQ1	0.69	1	0	6	4	10	577	100.00	
NDUFAF7	0.68	1	0	1	3	5	438	99.32	
L3MBTL2	0.68	1	0	0	4	2	586	88.25	
FANCA	0.68	9	9	12	9	50	1319	93.15	
PPHLN1	0.68	0	1	1	3	0	440	100.00	
RTKN2	0.66	2	2	1	4	7	609	100.00	
PKD1L3	0.66	17	11	16	11	69	1679	98.76	
ADAMTS13	0.63	6	7	8	8	41	1260	92.72	
ALPK2	0.63	15	16	14	13	93	2079	99.71	
TCIRG1	0.60	2	0	5	5	15	830	100.00	

DGCR2	0.58	0	0	2	3	3	520	95.94	
ATP13A1	0.54	0	1	3	6	4	1107	96.77	
MAP7D2	0.54	3	0	0	4	10	741	97.24	
ARFIP1	0.54	0	0	1	2	1	373	100.00	
VPS13B	0.53	2	1	1	4	6	748	86.67	
ANKRD31	0.53	13	11	17	10	49	1879	99.95	
FBXW4	0.49	0	0	1	2	0	406	100.00	
CFAP43	0.49	7	11	8	8	26	1632	100.00	
WDR87	0.49	16	19	21	14	92	2879	99.14	
LCT	0.47	11	11	10	9	23	1927	100.00	Gibbon
UNC13B	0.46	20	19	38	19	123	4091	96.99	
CACNA1A	0.45	2	2	1	9	10	1994	83.12	
EXOC5	0.43	0	0	0	2	1	466	89.96	
COL7A1	0.37	13	8	16	11	42	2944	100.00	
PIAS3	0.37	1	0	0	2	1	547	100.00	
DHX57	0.36	3	1	3	5	14	1386	100.00	
NUP160	0.35	1	8	6	5	14	1436	100.00	
LAMA3	0.33	8	13	16	10	55	3005	95.34	
ACTN4	0.33	0	0	0	3	0	911	100.00	
EIF4ENIF1	0.33	1	0	2	3	6	916	95.12	
SVIL	0.33	7	3	7	6	24	1844	94.61	
SCFD1	0.31	0	0	0	2	0	640	99.84	
TRIP11	0.31	6	1	7	6	22	1963	99.95	
TRIM3	0.30	0	0	1	2	0	661	92.71	
KMT2D	0.17	14	9	16	9	43	5194	98.15	
HUWE1	0.07	0	1	3	3	4	4281	97.87	

S10 Table: Evidence for rapidly diverging human genes

Gene	Tissue-specific expression	Phenotype	Biological Process
ADCYAP1	Biased expression in appendix and 12 other tissues	Schizophrenia	Ovarian follicle development, Behavioral fear response, and Inflammatory response
PVALEF	Low expression overall, highest in fat	-	-
PGLYRP1	Restricted expression toward bone marrow	Blood protein levels	Immune response to bacterium
PSORS1C2	Restricted expression toward skin	Autism spectrum disorder or schizophrenia	-
BTNL2	Low expression	Sarcoidosis, Autism spectrum disorder or schizophrenia, Asthma, Blood pressure	Positive regulation of T cell proliferation and interleukin-2 secretion