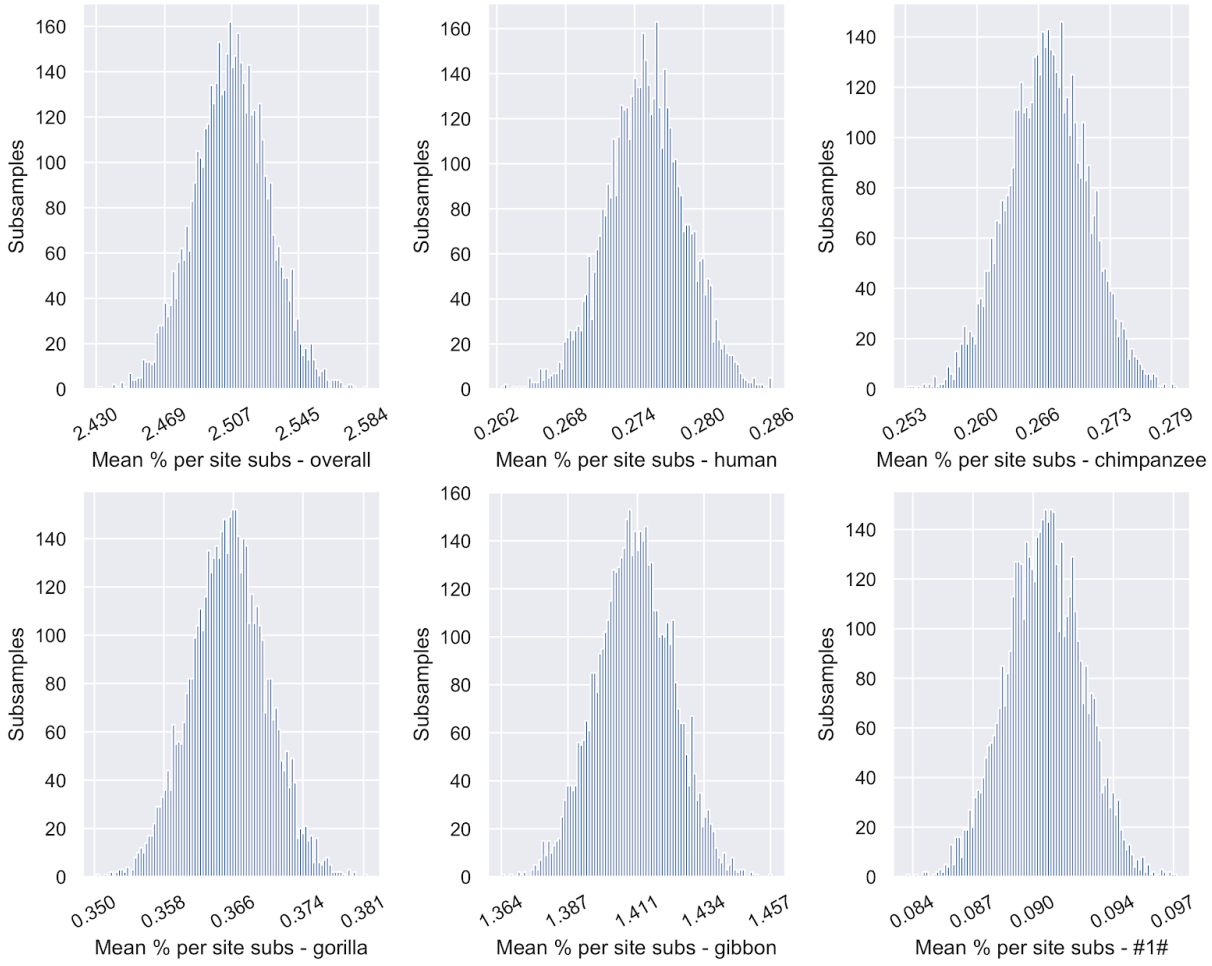
Filtered ortholog families

Three ortholog families (out of 13163) 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.



Supplemental Figure 1: Distribution of the mean % substitutions per site generated from the subsamples for the total and branch-specific substitution frequencies. Each distribution was divided into 100 bins of equal sizes between the maximum and minimum values.

Supplemental Table 1: Overall normalised substitutions and permissive range of the normalised subs in agreement with the molecular clock.

Branch	Normalised subs	Cutoff	
		Minimum subs	Maximum subs
Human	0.11	0.07	0.15
Chimpanzee	0.11	0.07	0.15
Gorilla	0.15	0.12	0.19
Gibbon	0.59	0.55	0.62
#1#	0.04	0.00	0.07

Supplemental Table 2: Evidence for rapidly diverging human genes

Ortholog family / Human transcript	Gene	Tissue-specific expression	Phenotype	Biological Process
ENST00000450565	ADCYAP1	Biased expression in appendix and 12 other tissues	Schizophrenia	Ovarian follicle development, Behavioral fear response, and Inflammatory response
ENST00000369951	OPN1LW	Low expression overall, highest in testis	Blue cone monochromatism, Color blindness	Vision
ENST00000637878	PVALEF	Low expression overall, highest in fat	-	-
ENST00000259845	PSORS1C2	Restricted expression toward skin	Autism spectrum disorder or schizophrenia	-
ENST00000454136	BTNL2	Low expression	Sarcoidosis, Autism spectrum disorder or schizophrenia, Asthma, Blood pressure	Positive regulation of T cell proliferation and interleukin-2 secretion