

Tables

Table S2. Meta information of 103 human individuals

Sample	Population	Sex	Depth
HG02095	ACB	Female	10.78
HG02107	ACB	Male	40.28
HG02283	ACB	Male	17.65
HG02332	ACB	Male	17.82
HG02419	ACB	Female	13.21
HG02479	ACB	Female	9.78
HG02484	ACB	Male	12.5
HG02485	ACB	Female	10.64
HG02508	ACB	Female	11.04
HG02537	ACB	Female	17.45
HG02282	ACB	Female	14.74
HG01886	ACB	Female	14.86
HG02009	ACB	Male	15.56
NA19904	ASW	Male	8.91
NA19909	ASW	Female	6.64
NA19914	ASW	Female	17.84
NA19921	ASW	Female	14.94
NA19923	ASW	Female	10.39
NA19984	ASW	Male	11.16
NA19920	ASW	Male	15.26
HG03616	BEB	Female	17.56
HG03796	BEB	Female	14.18
NA12044	CEU	Female	13.96
NA12414	CEU	Female	12.45

NA12812	CEU	Male	10.38
NA12872	CEU	Male	9.64
NA12873	CEU	Female	9.73
NA12874	CEU	Male	11.27
NA10847	CEU	Female	11.97
NA11919	CEU	Male	13.32
NA12342	CEU	Male	16.9
NA18525	CHB	Female	12.35
NA18647	CHB	Male	9.99
NA18747	CHB	Male	9.93
NA18749	CHB	Male	9.81
HG01464	CLM	Male	14.31
HG01486	CLM	Female	16.45
HG00309	FIN	Female	11.05
HG00335	FIN	Male	11.55
HG00337	FIN	Female	11.98
HG00345	FIN	Male	11.51
HG00353	FIN	Female	11.89
HG00097	GBR	Female	10.26
HG00100	GBR	Female	14.24
HG00139	GBR	Male	12.11
HG00140	GBR	Male	11.21
HG00236	GBR	Female	12.92
HG00250	GBR	Female	11.56
HG00256	GBR	Male	11.76
HG00259	GBR	Female	11.68
NA21106	GIH	Female	10.54
NA21119	GIH	Male	10.6
HG02811	GWD	Female	15.45

HG01697	IBS	Female	11.11
HG01770	IBS	Female	13.12
HG01771	IBS	Male	13.99
HG01777	IBS	Male	11.5
HG01756	IBS	Male	14.74
HG01757	IBS	Female	14.7
HG01761	IBS	Male	14.92
HG01762	IBS	Female	14.21
HG01784	IBS	Female	18.35
NA18957	JPT	Female	9.13
NA18960	JPT	Male	13.44
NA18968	JPT	Female	11.07
NA18971	JPT	Male	12.55
NA18974	JPT	Male	12.76
NA18975	JPT	Female	10.69
NA18976	JPT	Female	13.52
NA18998	JPT	Female	10.83
NA19001	JPT	Female	9.89
HG02141	KHV	Male	10.47
NA19031	LWK	Male	10.56
NA19038	LWK	Female	10.62
NA19307	LWK	Male	11.68
NA19308	LWK	Male	11.76
NA19310	LWK	Female	10.18
NA19740	MXL	Female	9.9
HG02089	PEL	Female	11.02
HG02104	PEL	Male	11.09
HG02286	PEL	Female	10.22
HG02301	PEL	Female	11.9

HG00732	PUR	Female	30.95
HG00734	PUR	Female	10.29
HG01049	PUR	Female	7.62
HG01075	PUR	Male	17.01
HG01167	PUR	Male	17.28
HG01176	PUR	Male	17.28
NA20534	TSI	Male	8.46
NA20587	TSI	Female	11.93
NA20588	TSI	Male	11.05
NA18504	YRI	Male	12.19
NA18856	YRI	Male	10.34
NA18868	YRI	Male	11.16
NA19095	YRI	Female	9.33
NA19119	YRI	Male	12.56
NA19131	YRI	Female	11.54
NA19146	YRI	Male	10.67
NA19152	YRI	Female	13.64
NA19171	YRI	Male	10.81
NA19184	YRI	Male	10.02
NA19204	YRI	Female	11.33
NA19102	YRI	Female	14.79

Table S3. Population genetics features for protein coding gene in human.

		Autosome				X Chromosome			
		Median	Mean \pm SD	5%	95%	Median	Mean \pm SD	5%	95%
Nucleotide Diversity ($\pi \times 10^3$)	Synonymous Sites	0.772	1.203 \pm 1.409	0.050	3.794	0.429	0.849 \pm 1.176	0.036	2.915
	Non-synonymous Sites	0.144	0.339 \pm 0.513	0.011	1.268	0.061	0.202 \pm 0.405	0.008	0.767
	CDS	0.331	0.481 \pm 0.533	0.022	1.464	0.151	0.291 \pm 0.411	0.013	1.021
	UTR	0.574	0.747 \pm 0.720	0.053	2.022	0.277	0.434 \pm 0.518	0.028	1.286
	Exon	0.484	0.594 \pm 0.481	0.075	1.464	0.240	0.338 \pm 0.351	0.029	0.969
	Intron	0.758	0.818 \pm 0.452	0.267	1.560	0.418	0.459 \pm 0.331	0.099	0.960
	Intergenic Regions	0.711	0.817 \pm 0.546	0.156	1.836	0.397	0.467 \pm 0.361	0.056	1.198
	Synonymous Sites	1.649	1.895 \pm 1.182	0.530	4.037	1.097	1.388 \pm 1.104	0.362	3.162
	Non-synonymous Sites	0.552	0.693 \pm 0.542	0.144	1.736	0.340	0.457 \pm 0.409	0.098	1.198
	CDS	0.746	0.861 \pm 0.547	0.224	1.882	0.439	0.551 \pm 0.417	0.138	1.299
Population Mutation Rate ($\theta_w \times 10^3$)	UTR	1.081	1.198 \pm 0.670	0.406	2.367	0.670	0.777 \pm 0.500	0.220	1.713
	Exon	0.915	0.990 \pm 0.475	0.366	1.853	0.543	0.607 \pm 0.356	0.178	1.266
	Intron	1.184	1.222 \pm 0.387	0.714	1.860	0.736	0.775 \pm 0.288	0.406	1.261
	Intergenic Regions	1.186	1.229 \pm 0.477	0.508	2.033	0.709	0.772 \pm 0.347	0.354	1.418

Table S4. Population genetics features for protein coding gene in rhesus macaque.

		Autosome				X Chromosome			
		Median	Mean \pm SD	5%	95%	Median	Mean \pm SD	5%	95%
Nucleotide Diversity ($\pi \times 10^3$)	Synonymous Sites	2.738	3.328 \pm 2.670	0.373	8.299	1.297	1.787 \pm 1.785	0.199	4.955
	Non-synonymous Sites	0.419	0.775 \pm 1.037	0.039	2.767	0.263	0.585 \pm 0.837	0.037	2.363
	CDS	0.977	1.263 \pm 1.109	0.142	3.300	0.450	0.681 \pm 0.748	0.066	2.289
	UTR	1.650	2.035 \pm 1.709	0.271	5.011	0.758	1.071 \pm 1.083	0.124	3.217
	Exon	1.277	1.512 \pm 1.087	0.287	3.483	0.537	0.737 \pm 0.703	0.096	2.162
	Intron	2.274	2.334 \pm 1.054	0.979	3.883	1.134	1.247 \pm 0.904	0.395	2.285
	Intergenic Regions	2.107	2.256 \pm 1.135	0.711	4.287	1.012	1.161 \pm 0.717	0.256	2.509
Population Mutation Rate ($\theta_w \times 10^3$)	Synonymous Sites	4.446	4.989 \pm 2.913	1.326	10.462	2.024	2.553 \pm 1.947	0.657	5.669
	Non-synonymous Sites	0.939	1.329 \pm 1.283	0.191	3.903	0.488	0.841 \pm 0.945	0.130	3.030
	CDS	1.709	2.006 \pm 1.343	0.461	4.547	0.706	0.969 \pm 0.850	0.217	2.840
	UTR	2.847	3.179 \pm 1.984	0.880	6.505	1.240	1.583 \pm 1.302	0.420	3.928
	Exon	2.146	2.368 \pm 1.300	0.715	4.760	0.839	1.059 \pm 0.818	0.247	2.801
	Intron	3.327	3.395 \pm 1.165	1.800	5.202	1.515	1.625 \pm 0.928	0.642	2.657
	Intergenic Regions	3.300	3.355 \pm 1.276	1.491	5.643	1.402	1.533 \pm 0.748	0.467	2.922

Table S5. Population genetics features across the rhesus macaque genome.

		300 bps				3M bps			
		Median	Mean \pm SD	5%	95%	Median	Mean \pm SD	5%	95%
Autosome	Nucleotide Diversity ($\pi \times 10^3$)	2.327	2.716 \pm 2.009	0.215	6.515	2.694	2.694 \pm 0.472	1.951	3.445
	Population Mutation Rate ($\theta_w \times 10^3$)	3.549	3.866 \pm 2.109	0.710	7.808	3.829	3.828 \pm 0.584	2.892	4.745
	Tajima's D	-0.746	-0.660 \pm 0.746	-1.700	0.644	-1.067	-1.067 \pm 0.117	-1.222	-0.925
	Fu and Li's D*	-0.470	-0.524 \pm 1.104	-2.433	1.078	-1.171	-1.173 \pm 0.226	-1.491	-0.885
	Fu and Li's F*	-0.608	-0.674 \pm 1.070	-2.595	0.920	-1.352	-1.356 \pm 0.208	-1.656	-1.086
X Chromosome	Nucleotide Diversity ($\pi \times 10^3$)	1.236	1.576 \pm 1.537	0.000	4.577	1.550	1.545 \pm 0.395	1.016	2.138
	Population Mutation Rate ($\theta_w \times 10^3$)	1.558	1.994 \pm 1.537	0.000	4.674	1.956	1.953 \pm 0.432	1.361	2.648
	Tajima's D	-0.411	-0.382 \pm 0.746	-1.484	1.157	-0.817	-0.814 \pm 0.220	-1.052	-0.547
	Fu and Li's D*	-0.045	-0.342 \pm 1.042	-2.439	0.913	-1.006	-1.018 \pm 0.333	-1.434	-0.618
	Fu and Li's F*	-0.024	-0.411 \pm 1.061	-2.505	1.012	-1.123	-1.127 \pm 0.336	-1.462	-0.726

Table S7. New population genetics annotations in RhesusBase PopGateway

Categories	Entries
SNP	46,146,548
Population Mutation Rate (θ_w)	9,020,424
Nucleotide Diversity (π)	9,020,424
Tajima's D	8,937,574
Fu and Li's D*	8,937,574
Fu and Li's F*	8,937,574
Linkage Disequilibrium	8,130,256
McDonald-Kreitman Test	33,776
Total	99,164,150