

Supplementary Table S2. Linkage disequilibrium values (D') between pairs of the studied SNPs across populations from the 1000 Genomes Project

Gene / SNP ID	MAF	Population	<i>GSS</i>		<i>GGT7</i>	
			rs6088660	rs13041792	rs6119534	rs11546155
<i>GSS</i>	rs1801310	Russian	0.9802	0.8986	0.8333	0.8165
		AFR	0.4512	0.9382	0.9471	1.0000
		AMR	0.9831	0.9660	0.9896	0.9549
		EAS	0.9839	0.9747	0.9873	0.4751
		EUR	1.0000	0.9770	0.9816	0.8487
		SAS	0.9873	0.9678	0.9877	0.8487
	rs6088660	Russian	*	0.9828	0.3813	0.6067
		AFR	*	1.0000	0.3411	0.3608
		AMR	*	1.0000	0.5012	0.6217
		EAS	*	1.0000	0.9018	0.5499
		EUR	*	1.0000	0.3201	0.6629
		SAS	*	1.0000	0.8170	0.7098
	rs13041792	Russian		*	0.7978	0.9014
		AFR		*	0.5859	1.0000
		AMR		*	0.8409	0.4258
		EAS		*	0.9502	0.8000
		EUR		*	0.9050	0.7247
		SAS		*	0.9236	0.9712
<i>GGT7</i>	rs6119534	Russian			*	0.8228
		AFR			*	0.9741
		AMR			*	0.8828
		EAS			*	0.9333
		EUR			*	0.9755
		SAS			*	0.9889
	rs11546155	Russian				*
		AFR				*
		AMR				*
		EAS				*
		EUR				*
		SAS				*

D' -values estimated by LDpair Tool (<https://ldlink.nci.nih.gov/?tab=ldpair>). Only statistically significant D' -values are shown.

* Populations: Russian (the studied population); AFR, African; AMR, Ad Mixed American; EAS, East Asian; EUR, European; SAS, South Asian. MAF, minor allele frequency.