SUPPLEMENTARY DATA

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Supplementary Table 1. Genotype distributions of the 12 genotyped *PROX1* SNPs in the HELENA study.

SNP	**Position in *PROX1***	**Genotype**	**n (frequency)**	**MAF**	***P* HWE**
rs340877	promoter	AA	304 (0.27)	0.47	0.20
		AG	579 (0.52)		
		GG	237 (0.21)		
rs340874	promoter	CC	291 (0.26)	0.48	0.55
		CT	568 (0.51)		
		TT	258 (0.23)		
rs340837	intron 1	TT	268 (0.24)	0.49	0.02
		TG	602 (0.54)		
		GG	254 (0.22)		
rs340835	intron 1	GG	321 (0.29)	0.45	0.05
		GA	593 (0.52)		
		AA	216 (0.19)		
rs4655313	intron 1	AA	768 (0.68)	0.18	0.19
		AG	316 (0.28)		
		GG	42 (0.04)		
rs11802122	intron 2	GG	789 (0.70)	0.16	0.95
		GT	310 (0.27)		
		TT	30 (0.03)		
rs2289002	intron 2	TT	597 (0.54)	0.27	0.99
		TC	437 (0.39)		
		CC	80 (0.07)		
rs3754138	intron 3	GG	650 (0.57)	0.24	0.60
		GT	420 (0.37)		
		TT	62 (0.06)		
rs12748973	intron 3	CC	1057 (0.95)	0.02	0.39
		CT	56 (0.05)		
		TT	0 (0.00)		
rs4655482	intron 4	GG	1063 (0.94)	0.03	0.03
		GA	59 (0.05)		
		AA	3 (0.01)		
rs12092859	intron 4	CC	1078 (0.95)	0.02	4.11x10-6
		CG	43 (0.04)		
		GG	4 (0.01)		
rs10494972	intron 4	TT	1034 (0.91)	0.05	4.73x10-4
		TA	93 (0.08)		
		AA	8 (0.01)		

MAF, minor allele frequency. HWE, Hardy-Weinberg equilibrium. Positions are based on the sequence NM_002763 (chr1: 212,223,454…212,281,411).

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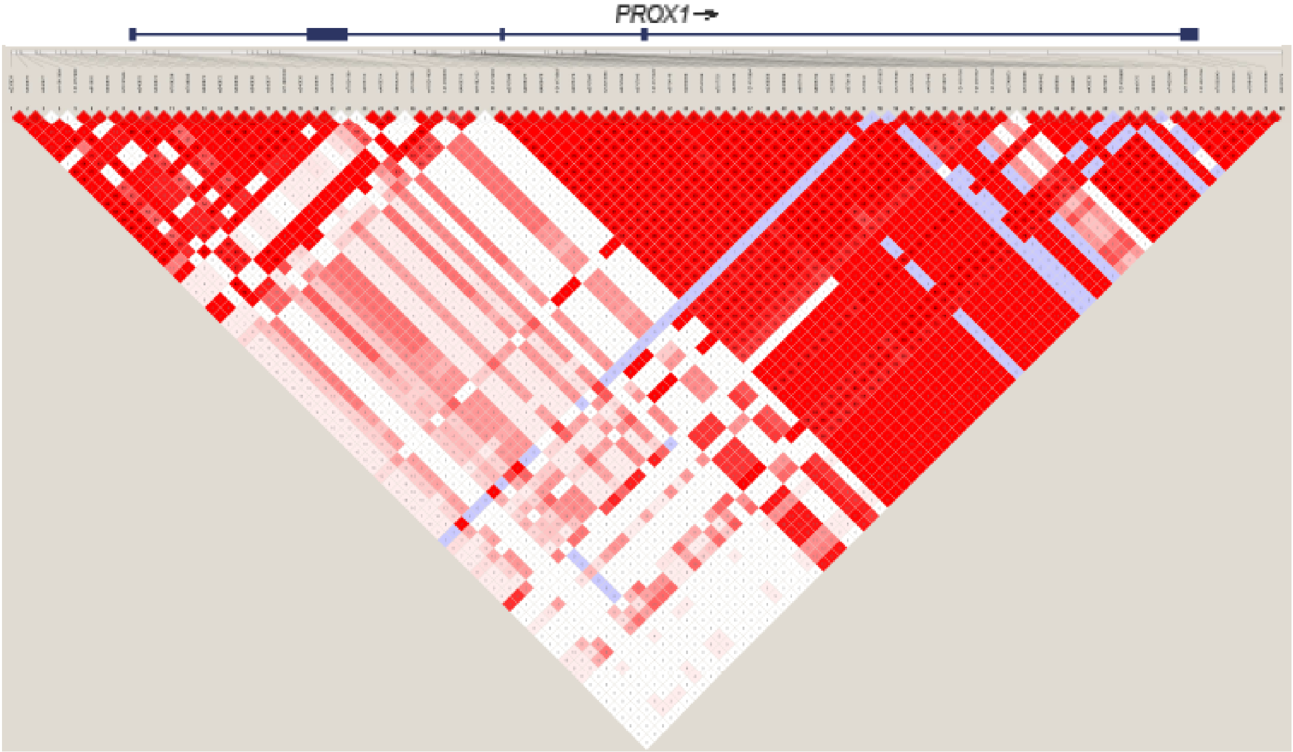
Supplementary Figure 1. Linkage disequilibrium pattern across *PROX1*.



Schematic representation of the linkage disequilibrium by measurements of D' values (red color scale) and r² coefficients (values in the squares) for 80 *PROX1* SNPs based on the 1000 Genomes EUR reference panel.