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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).
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.