SNP Preparation for Association

All available individuals were genotyped on the Latino Axiom SNP chip, as described in the main text. After applying the custom Affymetrix processing script and removing incompatible duplicates, 666,853 SNPs were available for analysis, of which 654,194 could be placed on the Rutgers v3 map. A total of 32,166 monomorphic SNPs were removed; 35,848 SNPs were removed for excess missingness (> 5%); 2 SNPs were removed for excess Mendel errors and all remaining Mendel errors were zeroed out (set to missing); 26,290 SNPs with MAF<0.01 were removed, as were 27 SNPs showing violations of Hardy-Weinberg equilibrium with p-value < 0.0001 and 6 with a U-shaped likelihood (a cleaning step unique to the PPLD; see [1]). This left 559,855 for final analysis.

Statistical Analysis

Trait-marker LD was evaluated using the posterior probability of linkage disequilibrium (PPLD) as described in detail in [1]. The PPLD is on the probability scale, and assumes a prior probability of LD of 0.0004.

Results

Figure S3 1 below shows genome-wide PPLD results together with the PPL (see main text). There were no notable PPLDs under the linkage peaks on chromosomes 1 or 14. However, on chromosomes 15 and X there was some evidence for LD under the linkage peaks (Figure S3 2 and Table S3 1).

1. Huang, Y. and V.J. Vieland, *Association statistics under the PPL framework.* Genet Epidemiol, 2010. **34**(8): p. 835-45.

Figure S3 1 Genome-wide PPLD and PPL results

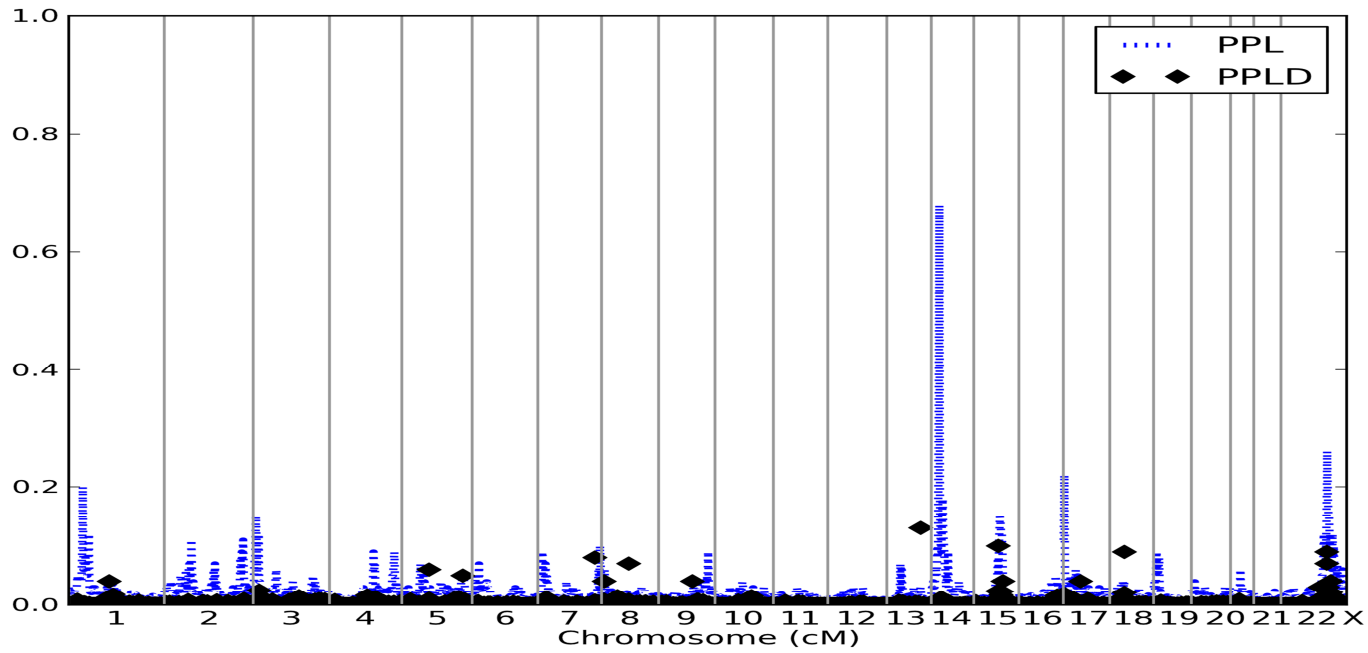

Figure S3 2 PPLD and PPL results on selected chromosomes.

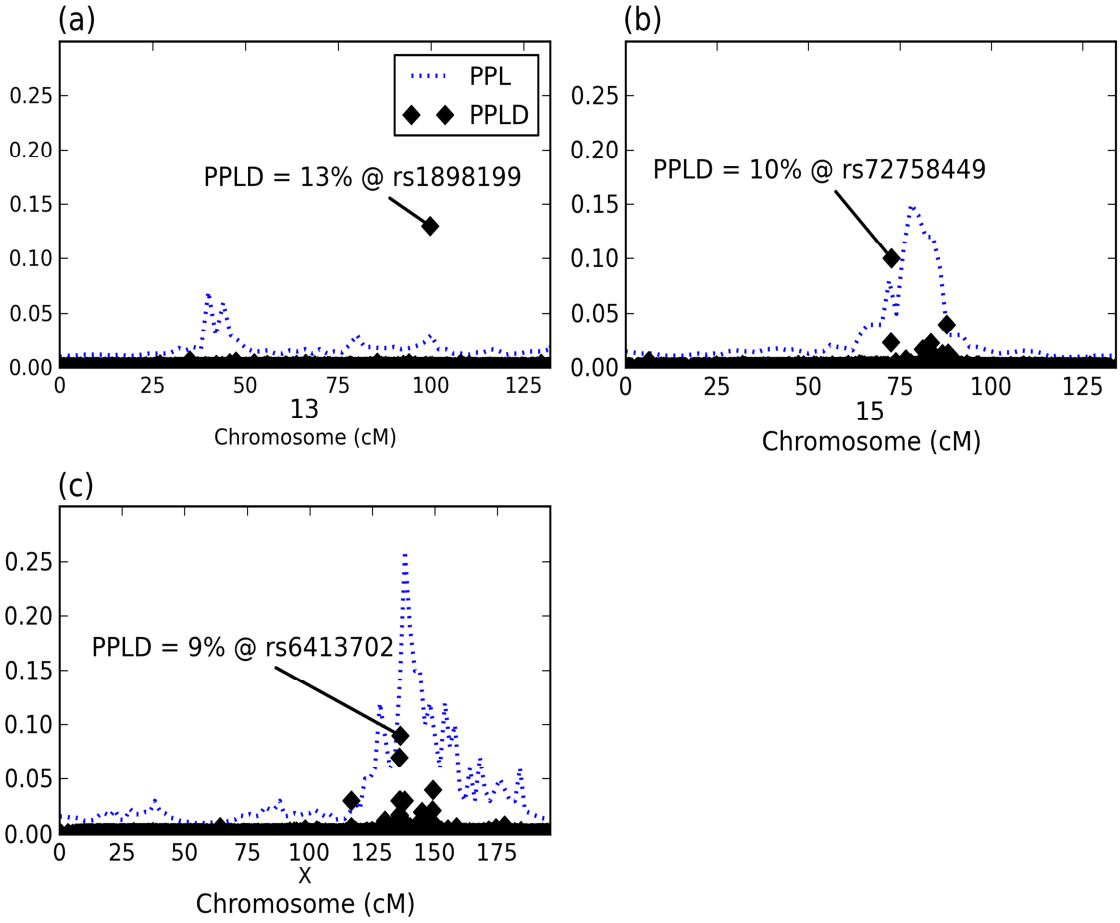

Table S3 1 All SNPs with PPLD ≥ 5%

Chrom	Band	Marker	Position (basepair)	Position (cM)	Frequency in CAPS (SE, n=187)[1]	Frequency in dbSNP (SE, n varies)[2]	PPL[3]	PPLD	Genes	Tier[4] (basepair)
5	q13.1	rs6865369	67696944	80.9	0.41 (0.04)	0.36 (0.01)	0.03	0.06	PIK3R1	250,000
5	q35.1	rs296004	168518373	181.2	0.39 (0.04)	0.45 (0.01)	0.04	0.05	SLIT3	25,000
7	q36.1	rs13234992	152388978	168.8	0.39 (0.04)	0.39 (0.01)	0.02	0.08	XRCC2	25,000
8	q13.2	rs56282096	69654722	81.9	0.25 (0.03)	0.33 (0.01)	0.01	0.07	C8orf34	25,000
13	q33.1	rs1898199	102304894	99.7	0.30 (0.04)	0.29 (0.01)	0.03	0.13	ITGBL1	25,000
15	q23	rs72758449	69810310	72.7	0.06 (0.02)	0.02 (0.01)	0.07	0.10	GLCE,PAQR5,KIF23, RPLP1,LOC145837	250,000
18	p11.21	rs2542170	12800820	43.3	0.46 (0.04)	0.42 (0.01)	0.03	0.09	PTPN2	25,000
23	q24	rs5957600	120393548	135.9	0.41 (0.04)	0.52 (0.01)[5]	0.14	0.07	GLUD2	250,000
23	q24	rs6413702	120603707	136.3	0.33 (0.04)	0.36 (0.01)	0.16	0.09	CT47A10[6],GLUD2	500,000

[1] Family-based frequency estimates and asymptotic standard errors were computed using Mendel.

[2] Global minor allele frequencies from dbSNP (http://www.ncbi.nlm.nih.gov/snp) are based on 1000Genome phase 1 worldwide genotypes.

[3] PPL is the multipoint PPL, see main text.

[4] Tier indicates the half-width of the smallest window, centered on the marker position, in which the genes listed to the left were detected. The search begins at tier = 25,000 basepairs (bp); if no genes are found within a given tier, tier is increased to 250k, 500k and then 1M bp, until either a gene is found or the maximum tier of 1M bp is reached.

[5] The dbSNP listed the opposite allele as minor for this marker.

[6] Additional genes at this location are: CT47A9, CT47A1, CT47A8, CT47A5, CT47A4, CT47A3, CT47A6, CT47A2, CT47A1.