

## **Supplemental Data**

### **A meta-analysis of genome-wide association studies of asthma in Puerto Ricans**

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**Table S1.** SNPs across the genome with meta-analysis (Hartford-PR, GALA I, GALA II and HCHS/SOL)  $P$ -values  $< 5 \times 10^{-8}$ 

SNP	Chr	Position	Ref	Alt	Gene	Region	Hartford-PR		GALA I		GALA II		HCHS/SOL		Combined
							RAF	$P$ -value	RAF	$P$ -value	RAF	$P$ -value	RAF	$P$ -value	
rs2941522	17	37910368	C	T	<i>GRB7,IKZF3</i>	intergenic	0.44	6.55E-05	0.43	4.77E-01	0.43	5.15E-06	0.44	2.25E-01	2.86E-08
rs12946510	17	37912377	C	T	<i>GRB7,IKZF3</i>	intergenic	0.67	6.23E-06	0.68	3.55E-02	0.67	2.35E-07	0.65	7.78E-02	5.90E-12
rs907092	17	37922259	G	A	<i>IKZF3</i>	exonic	0.69	4.96E-06	0.69	2.33E-02	0.68	3.95E-08	0.66	9.17E-02	1.16E-12
rs10445308	17	37938047	C	T	<i>IKZF3</i>	intronic	0.67	6.15E-06	0.67	4.02E-02	0.66	5.03E-07	0.64	7.08E-02	1.01E-11
rs12942330	17	37939839	C	T	<i>IKZF3</i>	intronic	0.67	6.66E-06	0.67	4.02E-02	0.66	5.81E-07	0.64	7.17E-02	1.23E-11
rs11658993	17	37940808	C	T	<i>IKZF3</i>	intronic	0.67	1.34E-06	0.67	4.60E-02	0.66	5.56E-07	0.65	7.41E-02	5.09E-12
rs4795395	17	37962987	T	A	<i>IKZF3</i>	intronic	0.67	8.49E-06	0.67	4.14E-02	0.66	5.48E-07	0.64	7.86E-02	1.66E-11
rs9909593	17	37970149	A	G	<i>IKZF3</i>	intronic	0.67	9.34E-06	0.67	4.05E-02	0.66	4.66E-07	0.64	7.85E-02	1.51E-11
rs34233420	17	38004929	GATTT	G	<i>IKZF3</i>	intronic	0.67	5.20E-06	0.67	3.04E-02	0.67	1.45E-06	0.64	8.40E-02	2.41E-11
rs4795397	17	38023745	A	G	<i>ZBPB2</i>	upstream	0.67	1.66E-06	0.66	7.50E-03	0.66	8.86E-07	0.64	1.02E-01	3.73E-12
rs11557466	17	38024626	C	T	<i>ZBPB2</i>	exonic	0.69	3.92E-06	0.68	2.86E-03	0.68	1.73E-06	0.65	9.16E-02	5.21E-12
rs11078925	17	38025208	T	C	<i>ZBPB2</i>	intronic	0.69	3.92E-06	0.68	2.86E-03	0.68	1.59E-06	0.65	9.16E-02	4.82E-12
rs200306858	17	38025643	T	TTTCC	<i>ZBPB2</i>	intronic	0.65	5.13E-05	0.65	4.14E-03	0.63	4.02E-05	0.61	3.72E-01	9.16E-09
rs34120102	17	38026035	G	A	<i>ZBPB2</i>	intronic	0.69	4.58E-06	0.68	3.11E-03	0.68	1.73E-06	0.65	7.83E-02	4.52E-12
rs11655198	17	38026169	C	T	<i>ZBPB2</i>	intronic	0.65	5.67E-05	0.63	8.07E-03	0.63	7.65E-05	0.60	3.97E-01	2.83E-08
rs11650661	17	38026286	A	T	<i>ZBPB2</i>	intronic	0.65	5.67E-05	0.63	7.06E-03	0.63	4.85E-05	0.60	3.97E-01	1.77E-08
rs11655292	17	38026361	C	G	<i>ZBPB2</i>	intronic	0.65	5.67E-05	0.63	6.90E-03	0.63	5.86E-05	0.60	3.97E-01	2.05E-08
rs12709365	17	38027400	A	G	<i>ZBPB2</i>	intronic	0.66	4.87E-05	0.65	8.10E-03	0.65	3.11E-05	0.62	2.33E-01	3.80E-09
rs13380815	17	38027583	A	G	<i>ZBPB2</i>	intronic	0.66	4.87E-05	0.65	8.10E-03	0.65	3.11E-05	0.62	2.33E-01	3.80E-09
rs11557467	17	38028634	G	T	<i>ZBPB2</i>	exonic	0.64	2.64E-05	0.61	7.93E-03	0.61	1.15E-04	0.59	3.84E-01	2.29E-08
rs11870965	17	38030205	T	A	<i>ZBPB2</i>	intronic	0.66	4.87E-05	0.65	8.10E-03	0.64	4.54E-05	0.62	2.32E-01	5.26E-09
rs9903250	17	38031030	A	A	<i>ZBPB2</i>	intronic	0.64	2.45E-05	0.63	4.54E-03	0.63	3.38E-05	0.60	3.74E-01	5.26E-09
rs9905959	17	38031138	A	G	<i>ZBPB2</i>	intronic	0.66	4.71E-05	0.66	3.56E-03	0.67	7.64E-05	0.63	2.04E-01	3.87E-09
rs11658278	17	38031164	T	C	<i>ZBPB2</i>	intronic	0.62	3.14E-06	0.62	1.02E-02	0.62	3.19E-04	0.60	2.48E-01	7.62E-09
rs10852935	17	38031674	C	T	<i>ZBPB2</i>	exonic	0.69	4.58E-06	0.68	3.83E-03	0.68	1.69E-06	0.65	9.55E-02	7.43E-12
rs10852936	17	38031714	C	T	<i>ZBPB2</i>	intronic	0.66	1.07E-04	0.65	7.91E-03	0.65	2.80E-05	0.62	2.32E-01	5.66E-09
rs9891174	17	38031802	T	A	<i>ZBPB2</i>	intronic	0.67	4.21E-05	0.65	8.45E-03	0.65	2.92E-05	0.63	3.45E-01	7.87E-09
rs59716545	17	38031857	T	G	<i>ZBPB2</i>	intronic	0.70	7.74E-06	0.70	1.74E-03	0.70	2.65E-06	0.67	9.15E-02	9.11E-12
rs36095411	17	38031865	T	G	<i>ZBPB2</i>	intronic	0.70	6.35E-06	0.69	4.81E-03	0.69	1.00E-06	0.66	6.89E-02	3.87E-12
rs12939457	17	38032188	T	C	<i>ZBPB2</i>	intronic	0.66	4.87E-05	0.66	8.32E-03	0.66	1.05E-04	0.62	2.37E-01	1.19E-08
rs34189114	17	38032460	C	T	<i>ZBPB2</i>	intronic	0.69	4.58E-06	0.68	2.88E-03	0.68	1.69E-06	0.65	9.16E-02	5.65E-12
rs35736272	17	38032680	T	C	<i>ZBPB2</i>	intronic	0.69	3.75E-06	0.68	3.83E-03	0.68	1.54E-06	0.66	8.69E-02	5.04E-12
rs1054609	17	38033277	A	C	<i>ZBPB2</i>	3'UTR	0.66	4.07E-05	0.65	8.10E-03	0.65	3.11E-05	0.62	2.32E-01	3.39E-09
rs9907088	17	38035116	G	A	<i>ZBPB2</i>	downstream	0.66	6.87E-05	0.66	5.27E-03	0.65	1.86E-05	0.63	2.23E-01	2.16E-09
rs36038753	17	38035370	G	T	<i>ZBPB2,GSDMB</i>	intergenic	0.66	6.87E-05	0.65	3.44E-03	0.65	2.50E-05	0.63	2.23E-01	2.14E-09
rs35569035	17	38035624	C	T	<i>ZBPB2,GSDMB</i>	intergenic	0.69	4.58E-06	0.68	2.88E-03	0.68	1.25E-06	0.65	9.16E-02	4.33E-12
rs9910826	17	38035648	A	G	<i>ZBPB2,GSDMB</i>	intergenic	0.67	4.38E-05	0.67	5.41E-03	0.66	1.52E-05	0.63	2.01E-01	1.17E-09
rs34074973	17	38035766	GAGA	G	<i>ZBPB2,GSDMB</i>	intergenic	0.69	4.58E-06	0.68	2.88E-03	0.68	1.69E-06	0.65	9.16E-02	5.64E-12
rs9904624	17	38036586	A	G	<i>ZBPB2,GSDMB</i>	intergenic	0.66	6.87E-05	0.66	6.02E-03	0.65	7.94E-06	0.63	2.23E-01	1.15E-09
rs4795398	17	38038179	C	T	<i>ZBPB2,GSDMB</i>	intergenic	0.69	4.58E-06	0.69	3.02E-03	0.68	1.44E-06	0.65	9.16E-02	5.20E-12
rs62067029	17	38038391	A	T	<i>ZBPB2,GSDMB</i>	intergenic	0.73	2.84E-04	0.73	6.24E-03	0.73	8.26E-05	0.69	7.33E-02	3.54E-09
rs148094956	17	38039561	TAACA	T	<i>ZBPB2,GSDMB</i>	intergenic	0.61	7.07E-06	0.61	1.09E-02	0.61	2.59E-04	0.59	2.97E-01	1.51E-08
rs12232497	17	38040119	T	C	<i>ZBPB2,GSDMB</i>	intergenic	0.69	3.75E-06	0.68	4.00E-03	0.68	1.26E-06	0.66	8.69E-02	4.37E-12
rs12232498	17	38040363	T	C	<i>ZBPB2,GSDMB</i>	intergenic	0.66	6.87E-05	0.66	5.26E-03	0.65	1.88E-05	0.63	2.23E-01	2.17E-09
rs12941333	17	38040534	C	T	<i>ZBPB2,GSDMB</i>	intergenic	0.66	6.87E-05	0.66	5.26E-03	0.65	1.88E-05	0.63	2.23E-01	2.17E-09
rs2872507	17	38040763	G	A	<i>ZBPB2,GSDMB</i>	intergenic	0.66	6.87E-05	0.66	5.26E-03	0.65	1.56E-05	0.63	2.23E-01	1.85E-09
rs9908132	17	38042777	T	A	<i>ZBPB2,GSDMB</i>	intergenic	0.62	8.62E-06	0.61	8.89E-03	0.61	1.68E-04	0.59	3.24E-01	1.19E-08
rs9901146	17	38043343	G	A	<i>ZBPB2,GSDMB</i>	intergenic	0.62	8.62E-06	0.61	8.89E-03	0.61	1.68E-04	0.59	3.23E-01	1.19E-08
rs12936409	17	38043649	C	T	<i>ZBPB2,GSDMB</i>	intergenic	0.69	5.69E-06	0.68	3.56E-03	0.68	1.54E-06	0.65	9.02E-02	6.74E-12

rs12103884	17	38045725	C	T	ZPBP2,GSDMB	intergenic	0.62	8.62E-06	0.61	8.92E-03	0.61	1.84E-04	0.59	3.19E-01	1.26E-08
rs9906951	17	38048244	T	C	ZPBP2,GSDMB	intergenic	0.61	4.26E-06	0.61	1.42E-02	0.61	2.79E-04	0.58	2.73E-01	1.21E-08
rs12950209	17	38049102	T	C	ZPBP2,GSDMB	intergenic	0.62	1.02E-05	0.62	6.04E-03	0.62	1.41E-04	0.59	3.03E-01	7.68E-09
rs12950743	17	38049233	T	C	ZPBP2,GSDMB	intergenic	0.61	6.83E-06	0.61	9.03E-03	0.61	1.99E-04	0.59	3.13E-01	1.15E-08
rs7359623	17	38049589	C	T	ZPBP2,GSDMB	intergenic	0.62	1.07E-05	0.62	6.14E-03	0.62	8.42E-05	0.59	2.89E-01	4.50E-09
rs11651596	17	38056116	T	C	ZPBP2,GSDMB	intergenic	0.66	5.65E-07	0.66	4.63E-03	0.66	1.35E-05	0.64	6.53E-02	6.96E-12
rs12949100	17	38057189	G	A	ZPBP2,GSDMB	intergenic	0.69	7.25E-06	0.68	3.66E-03	0.68	2.30E-06	0.66	7.75E-02	8.70E-12
rs8069176	17	38057197	G	A	ZPBP2,GSDMB	intergenic	0.63	7.37E-06	0.63	7.04E-03	0.64	8.83E-05	0.61	1.52E-01	1.15E-09
rs4795399	17	38061439	T	C	GSDMB	intronic	0.69	5.17E-06	0.69	2.61E-03	0.68	1.10E-05	0.65	7.57E-02	2.26E-11
rs2305480	17	38062196	G	A	GSDMB	exonic	0.70	2.00E-06	0.69	2.97E-03	0.68	6.71E-06	0.66	7.07E-02	7.38E-12
rs2305479	17	38062217	C	T	GSDMB	exonic	0.68	2.24E-06	0.66	4.17E-03	0.66	2.21E-05	0.64	1.55E-01	1.28E-10
rs67786416	17	38062942	A	AC	GSDMB	intronic	0.70	8.70E-06	0.68	4.54E-03	0.69	6.01E-06	0.66	9.18E-02	3.53E-11
rs56750287	17	38062944	A	C	GSDMB	intronic	0.69	1.36E-06	0.68	4.95E-03	0.68	1.32E-05	0.65	7.42E-02	1.66E-11
rs11078926	17	38062976	G	A	GSDMB	intronic	0.70	2.00E-06	0.69	3.32E-03	0.69	7.11E-06	0.66	6.99E-02	8.18E-12
rs883770	17	38063381	C	T	GSDMB	intronic	0.68	2.24E-06	0.66	4.16E-03	0.66	2.36E-05	0.64	1.54E-01	1.35E-10
rs62067034	17	38063738	C	T	GSDMB	intronic	0.68	2.24E-06	0.66	3.83E-03	0.66	2.88E-05	0.64	1.54E-01	1.54E-10
rs36000226	17	38063929	T	C	GSDMB	intronic	0.68	2.24E-06	0.66	4.15E-03	0.66	2.37E-05	0.64	1.54E-01	1.35E-10
rs36084703	17	38063980	CA	C	GSDMB	intronic	0.68	3.50E-06	0.67	9.69E-03	0.67	7.49E-05	0.64	1.95E-01	1.41E-09
rs11078927	17	38064405	C	T	GSDMB	intronic	0.70	1.34E-06	0.69	2.97E-03	0.69	7.91E-06	0.66	7.86E-02	8.13E-12
rs11078928	17	38064469	T	C	GSDMB	splicing	0.70	1.34E-06	0.69	2.97E-03	0.69	6.75E-06	0.66	7.86E-02	7.02E-12
rs12939832	17	38064876	G	A	GSDMB	intronic	0.70	1.09E-06	0.69	2.96E-03	0.69	7.09E-06	0.66	7.83E-02	6.39E-12
rs1008723	17	38066267	G	T	GSDMB	intronic	0.65	4.09E-05	0.64	6.06E-03	0.63	1.94E-04	0.61	2.94E-01	2.30E-08
rs4795400	17	38067020	C	T	GSDMB	intronic	0.69	1.08E-06	0.69	2.22E-03	0.68	1.62E-05	0.66	6.34E-02	7.74E-12
rs4795401	17	38067533	A	G	GSDMB	intronic	0.65	5.59E-05	0.65	7.58E-03	0.65	7.90E-05	0.61	2.32E-01	9.09E-09
rs869402	17	38068043	T	C	GSDMB	intronic	0.33	2.56E-06	0.35	5.01E-03	0.35	7.22E-06	0.38	2.03E-01	9.80E-11
rs1011082	17	38068514	T	C	GSDMB	intronic	0.37	1.14E-05	0.38	3.88E-03	0.38	5.09E-05	0.40	2.04E-01	1.13E-09
rs921650	17	38069076	G	A	GSDMB	intronic	0.34	6.80E-06	0.36	9.59E-03	0.36	8.83E-06	0.38	1.86E-01	2.67E-10
rs921649	17	38069274	C	T	GSDMB	intronic	0.34	6.04E-06	0.36	9.30E-03	0.36	8.48E-06	0.38	1.87E-01	2.37E-10
rs5820308	17	38069364	TCAAAA	T	GSDMB	intronic	0.32	1.84E-06	0.35	3.65E-03	0.34	2.16E-05	0.36	1.15E-01	5.64E-11
rs6503524	17	38069809	C	T	GSDMB	intronic	0.34	6.58E-06	0.36	9.90E-03	0.36	7.79E-06	0.38	1.90E-01	2.51E-10
rs7216389	17	38069949	C	T	GSDMB	intronic	0.34	6.58E-06	0.36	1.31E-02	0.36	1.11E-05	0.38	1.91E-01	4.16E-10
rs7221605	17	38070789	C	T	GSDMB	intronic	0.33	1.33E-05	0.37	6.35E-03	0.37	1.53E-05	0.37	2.77E-01	1.09E-09
rs1031458	17	38072173	G	T	GSDMB	intronic	0.33	1.33E-05	0.35	1.79E-02	0.35	1.82E-05	0.37	2.77E-01	2.66E-09
rs1031460	17	38072247	T	G	GSDMB	intronic	0.33	1.33E-05	0.35	1.86E-02	0.35	3.22E-05	0.37	2.85E-01	4.68E-09
rs8065777	17	38072402	C	T	GSDMB	intronic	0.33	1.33E-05	0.35	2.80E-02	0.35	1.87E-05	0.37	2.77E-01	3.72E-09
rs2872516	17	38072727	C	T	GSDMB	intronic	0.32	4.24E-05	0.36	1.38E-01	0.37	3.19E-05	0.35	1.21E-01	8.66E-09
rs146378727	17	38073837	CCCG	C	GSDMB	intronic	0.36	1.39E-04	0.39	1.99E-02	0.39	3.46E-05	0.41	2.59E-01	1.72E-08
rs9303279	17	38073968	G	C	GSDMB	intronic	0.31	4.52E-06	0.33	3.44E-03	0.33	1.15E-06	0.35	1.22E-01	7.83E-12
rs8076131	17	38080912	G	A	ORMDL3	intronic	0.32	1.52E-05	0.33	2.52E-02	0.34	3.92E-07	0.36	9.22E-02	1.74E-11
rs7221814	17	38089717	A	G	ORMDL3,LRR3C	intergenic	0.33	1.11E-04	0.34	1.15E-01	0.33	5.26E-07	0.36	4.08E-01	6.59E-09

RAF: reference allele frequency

**Table S2.** Chromosome 17q21 LD comparisons across different cohorts using varLD

Cohorts Comparisons	<i>P</i> -values
Hartford-PR PR vs. GALA I PR	0.0835
Hartford-PR PR vs. GALA II PR	0.4591
Hartford-PR PR vs. GALA I MX	0.0002
Hartford-PR PR vs. GALA I MX	0.0007
Hartford-PR PR vs. 1000G EUR	0.0001

**Table S3.** SNPs in *IL33* with meta-analysis (Hartford-PR, GALA I, GALA II and HCHS/SOL) *P*-values < 0.01

SNP	Chr	Position	Ref	Alt	Gene	Hartford-PR			GALA I			GALA II			HCHS/SOL			Combined	
						AAF	OR	<i>P</i> -value	AAF	OR	<i>P</i> -value	AAF	OR	<i>P</i> -value	AAF	OR	<i>P</i> -value	OR	<i>P</i> -value
rs10815393	9	6240324	T	C	<i>IL33</i>	0.20	1.09	0.480	0.23	1.47	0.085	0.20	1.17	0.076	0.20	1.21	0.056	1.18	0.002
rs10975504	9	6235009	A	G	<i>IL33</i>	0.20	1.07	0.588	0.24	1.47	0.087	0.20	1.17	0.073	0.20	1.20	0.059	1.17	0.003
rs10975507	9	6236977	A	T	<i>IL33</i>	0.20	1.06	0.619	0.24	1.47	0.086	0.20	1.18	0.053	0.20	1.18	0.081	1.17	0.003
rs7035413	9	6243119	A	G	<i>IL33</i>	0.19	1.06	0.607	0.23	1.47	0.086	0.19	1.16	0.089	0.19	1.20	0.063	1.16	0.004
rs12339348	9	6233082	A	T	<i>IL33</i>	0.19	1.06	0.636	0.23	1.48	0.083	0.19	1.17	0.086	0.19	1.19	0.075	1.17	0.005
rs72689565	9	6240953	A	C	<i>IL33</i>	0.19	1.08	0.532	0.23	1.48	0.082	0.20	1.15	0.110	0.19	1.19	0.076	1.17	0.005

**Table S4.** Results of the meta-analysis of GWAS of childhood asthma, for SNPs previously associated with asthma in meta-analysis of GWAS of asthma in Europeans (GABRIEL) and ethnically diverse North American populations (EVE)

SNP	Chr	Position	Ref	Alt	Gene	In cited paper	Hartford-PR				GALA I			GALA II			Combined	
						OR	AAF	OR	P-value	AAF	OR	P-value	AAF	OR	P-value	OR	P-value	
Loci reported by the GABRIEL consortium in Moffatt M.F. et al. N Engl J Med 2010; 363:1211-21																		
rs3771166	2	102986222	G	A	IL18R1	0.85*	0.45	0.90	0.500	0.44	0.75	0.114	0.43	0.85	0.018	0.85	0.003	
rs9273349	6	32625869	A	G	HLA-DQ	1.14	0.61	0.98	0.860	NA	NA	NA	NA	NA	NA	0.98	0.860	
rs1342326	9	6190076	A	C	IL33	1.27	0.21	0.90	0.403	0.26	1.12	0.571	0.22	1.05	0.528	1.02	0.804	
rs744910	15	67446785	G	A	SMAD3	0.89	0.43	0.88	0.175	0.42	1.01	0.981	0.45	0.93	0.269	0.91	0.118	
rs2305480	17	38062196	G	A	GSDMB	0.76	0.31	0.62	2.0×10 <sup>-6</sup>	0.31	0.54	0.003	0.32	0.71	6.7×10 <sup>-6</sup>	0.66	1.5×10 <sup>-12</sup>	
rs3894194	17	38121993	G	A	GSDMA	1.26	0.37	1.23	0.034	0.39	0.92	0.648	0.40	1.23	0.002	1.20	0.001	
rs2284033	22	37534034	G	A	IL2RB	0.92	0.41	0.91	0.272	0.39	1.09	0.638	0.40	1.17	0.024	1.06	0.202	
rs2073643	5	131723288	T	C	SLC22A5	0.89	0.50	0.96	0.668	0.48	1.18	0.356	0.50	0.93	0.257	0.96	0.401	
rs1295686	5	131995843	T	C	IL13	0.85	0.59	1.01	0.943	0.62	0.75	0.136	0.62	0.90	0.159	0.90	0.117	
rs11071559	15	61069988	C	T	RORA	0.88	0.26	1.07	0.525	0.25	1.69	0.012	0.24	0.90	0.193	1.01	0.763	
Replicated genes reported by the EVE consortium in Torgerson D.G. et al. Nat. Genet. 2011; 43(9):887-92																		
rs1102000	1	158932907	T	C	PYHIN1	0.76*	0.08	1.09	0.651	0.06	0.50	0.061	NA	NA	NA	0.93	0.562	
rs10173081	2	102957348	C	T	IL1RL1	0.83	0.19	0.84	0.132	0.16	0.85	0.519	0.26	0.78	0.010	0.81	0.003	
rs1837253	5	110401872	C	T	TSLP	0.84	0.25	0.73	0.004	0.23	0.65	0.041	0.27	0.83	0.014	0.78	3.1×10 <sup>-5</sup>	
rs2381416	9	6193455	A	C	IL33	1.18	0.38	0.98	0.847	0.39	1.00	0.980	0.37	1.09	0.249	1.05	0.441	
rs11078927	17	38064405	C	T	GSDMB	0.79	0.30	0.61	1.4×10 <sup>-6</sup>	0.31	0.55	0.003	0.31	0.71	7.9×10 <sup>-6</sup>	0.66	1.4×10 <sup>-12</sup>	

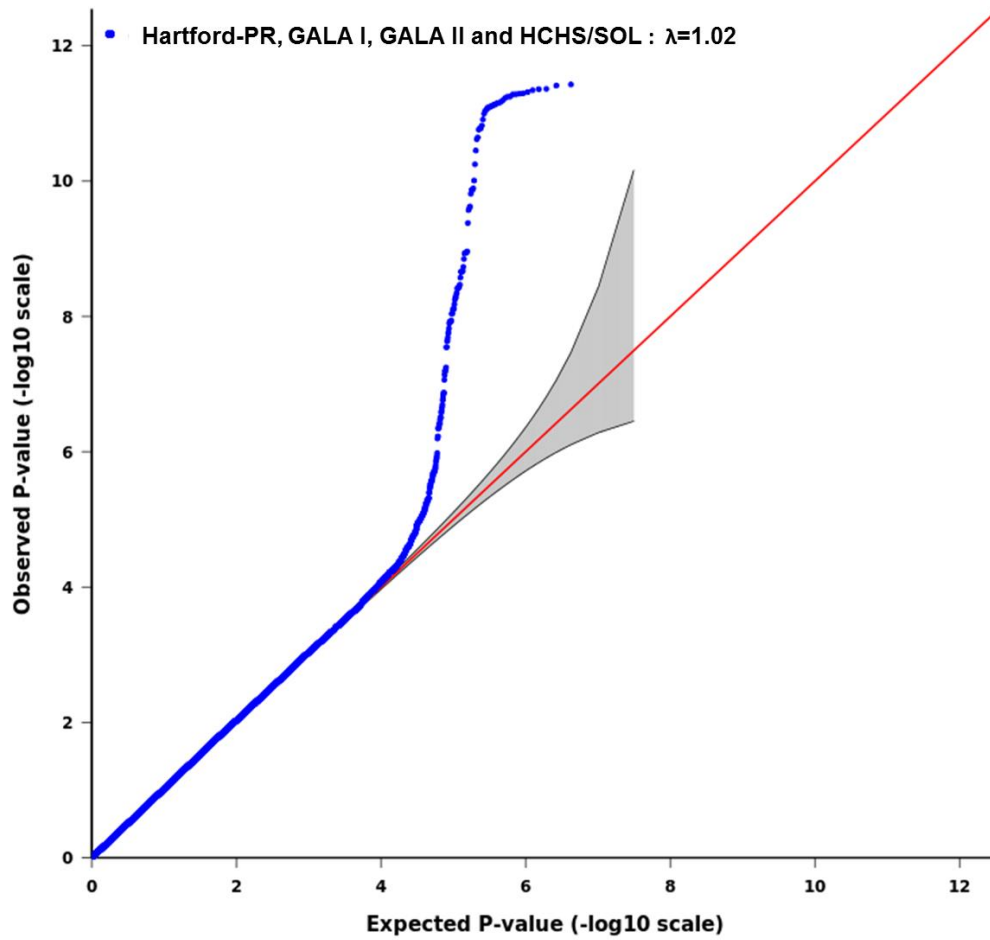
Chr: chromosome; Ref: reference allele; Alt: alternative allele; AAF: alternative allele frequency; OR: odds ratio.

\*: This column is childhood onset odds ratio in Moffatt M.F. et al. N Engl J Med 2010; 363:1211-21.

#: This column is overall odds ratio in Torgerson D.G. et al. Nat. Genet. 2011; 43(9):887-92.

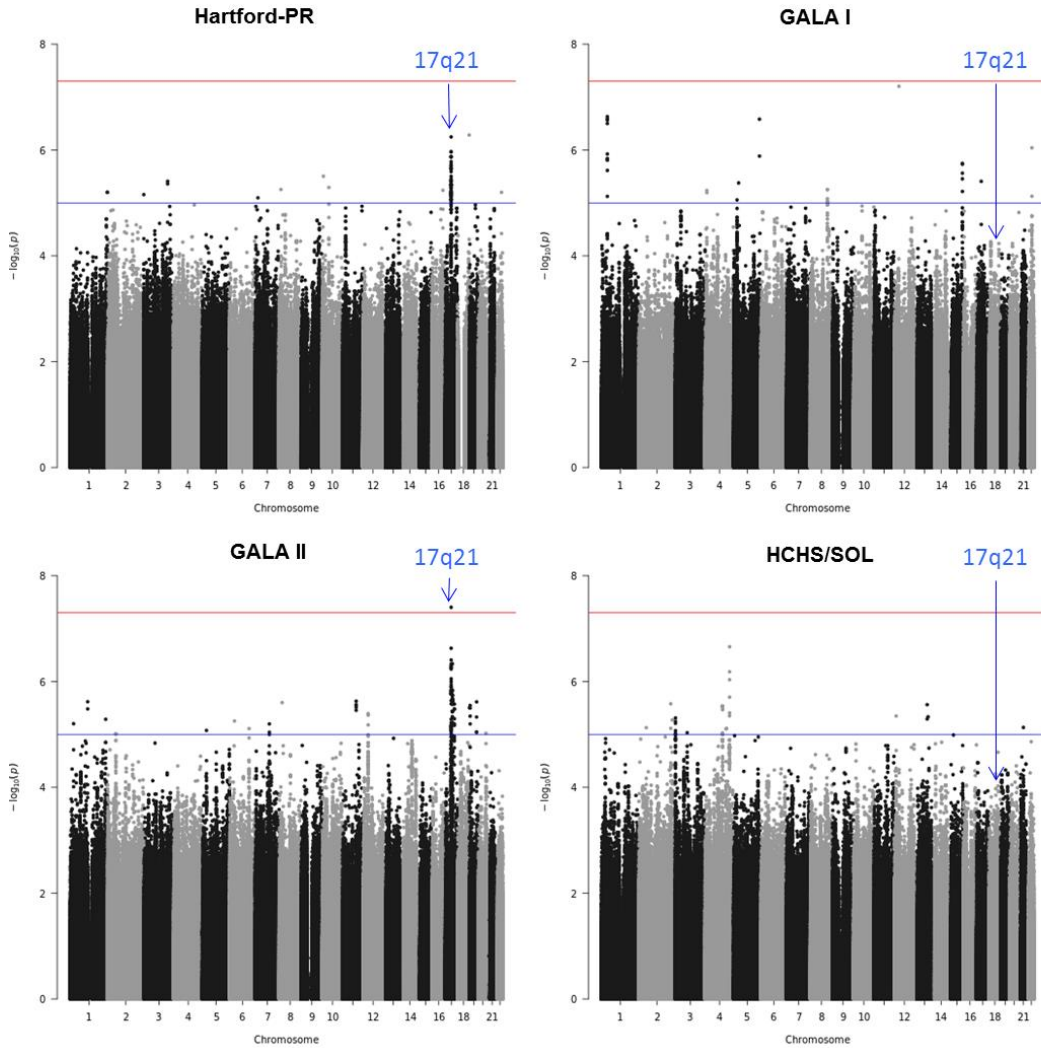
Human Genome version: hg19

**Figure S1. QQ plot for the meta-analysis (Hartford-PR, GALA I, GALA II and HCHS/SOL)**



$\lambda$  is the genomic control value.

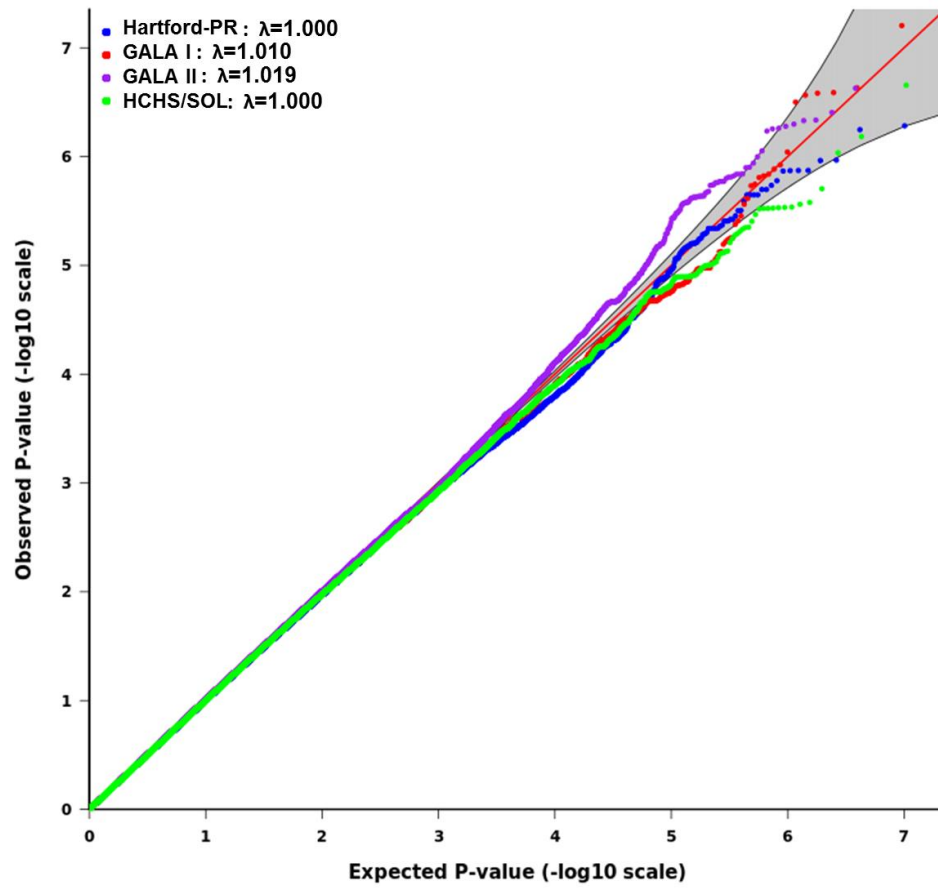
**Figure S2. Manhattan plots showing the GWAS results of Hartford-PR, GALA I, GALA II and HCHS/SOL**



The blue line represents the suggestive significance line ( $P < 1 \times 10^{-5}$ ). The red line represents the conservative significance line ( $P < 5 \times 10^{-8}$ ). The blue arrows mark the 17q21 region on chromosome 17. The detailed information of 17q21 is shown in Figure S6.

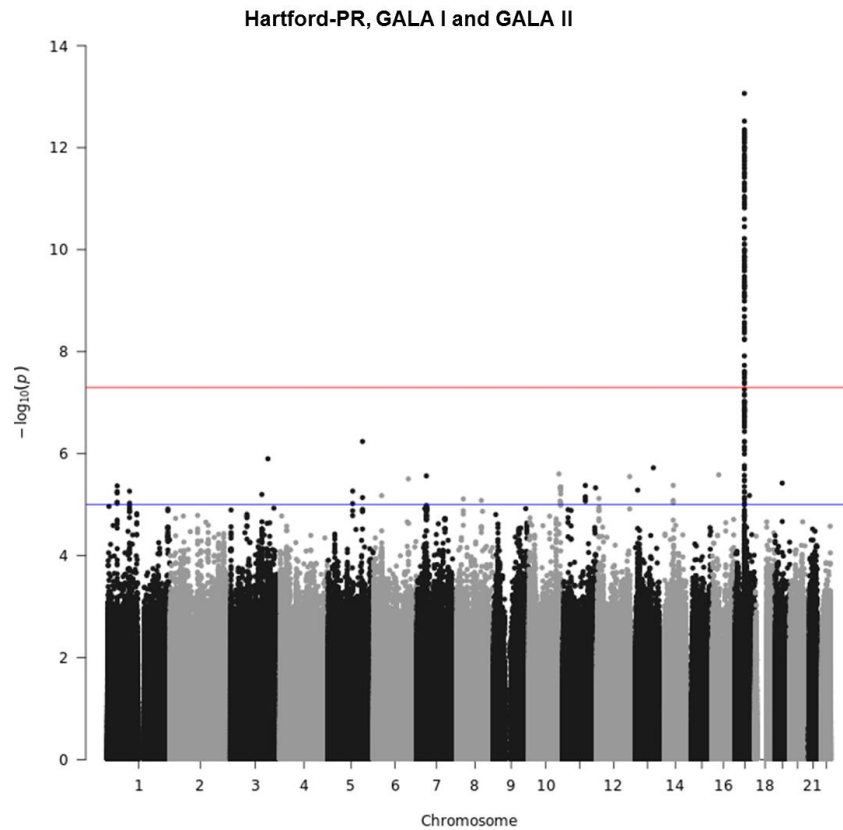


**Figure S3. QQ plot for the GWAS results of Hartford-PR, GALA I, GALA II and HCHS/SOL**



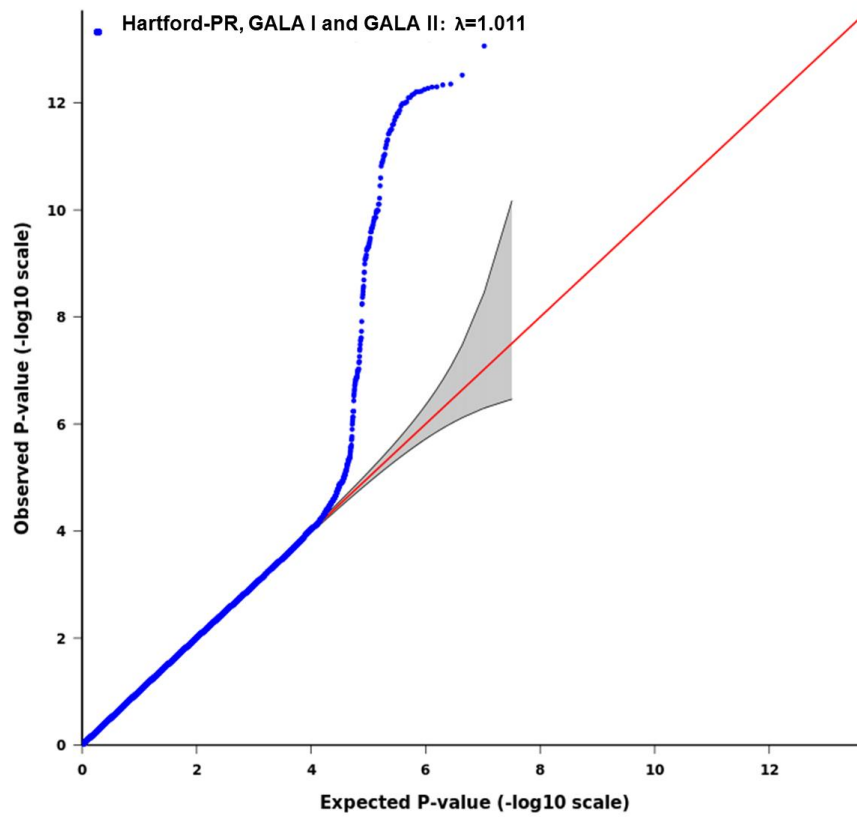
$\lambda$  is the genomic control value.

**Figure S4. Manhattan plot showing the summary meta-analysis results of the Hartford-PR, GALA I, and GALA II**



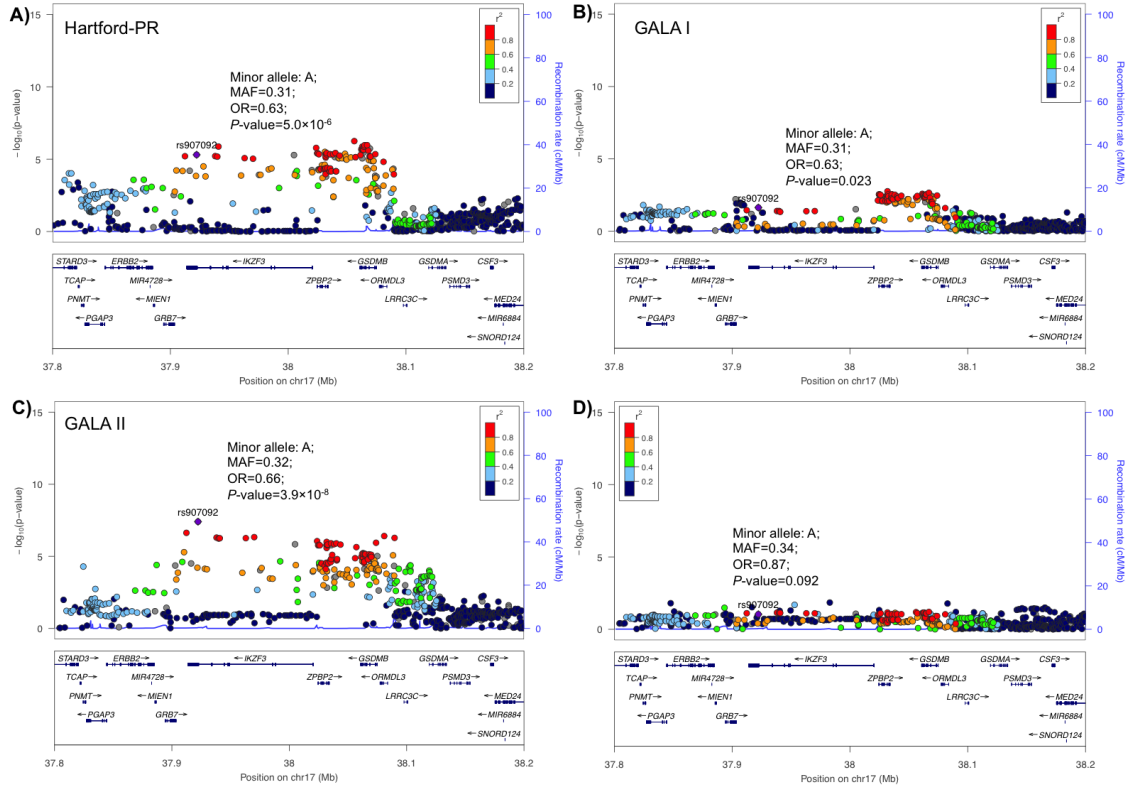
The blue line represents the suggestive significance line ( $P < 1 \times 10^{-5}$ ). The red line represents the significance threshold ( $P < 5 \times 10^{-8}$ ).

**Figure S5. QQ plot for the meta-analysis (Hartford-PR, GALA I and GALA II)**



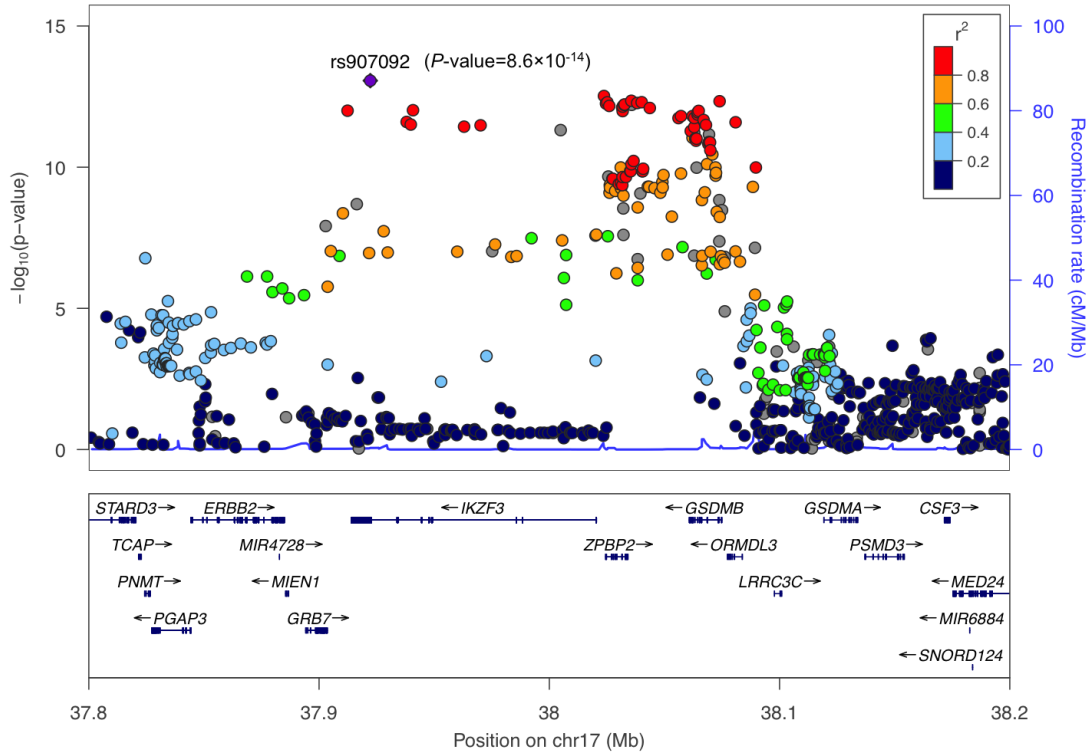
$\lambda$  is the genomic control value.

**Figure S6. GWAS results of Hartford-PR, GALA I, GALA II and HCHS/SOL on the chromosome 17 region**



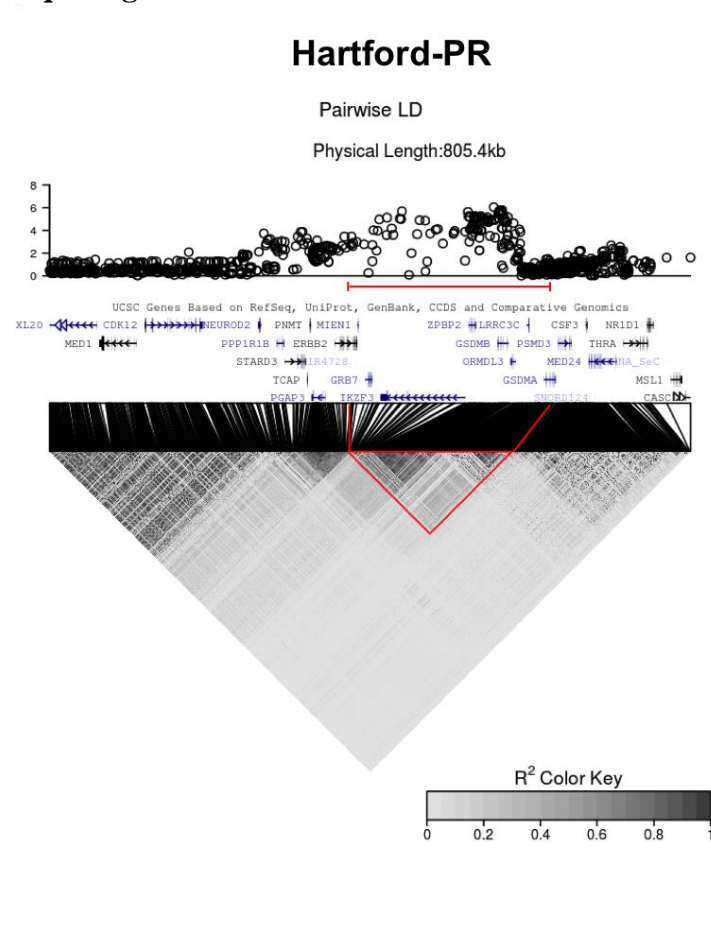
The relative location of genes and the direction of transcription are shown in the lower portion of the figure, and the chromosomal position is shown on the  $x$  axis. The light blue line show the recombination rate across the region (right  $y$  axis), and the left  $y$  axis shows the significance of the associations. The purple diamond shows the  $P$ -value for rs907092 that is the most significant SNP in the meta-analysis (Hartford-PR, GALA I, GALA II and HCHS/SOL). The circles show the  $P$ -values for all other SNPs and are color coded according to the level of LD with rs907092 in the 1000 Genome Project AMR population.

**Figure S7. Results of the meta-analysis (Hartford-PR, GALA I and GALA II) on the chromosome 17 region**



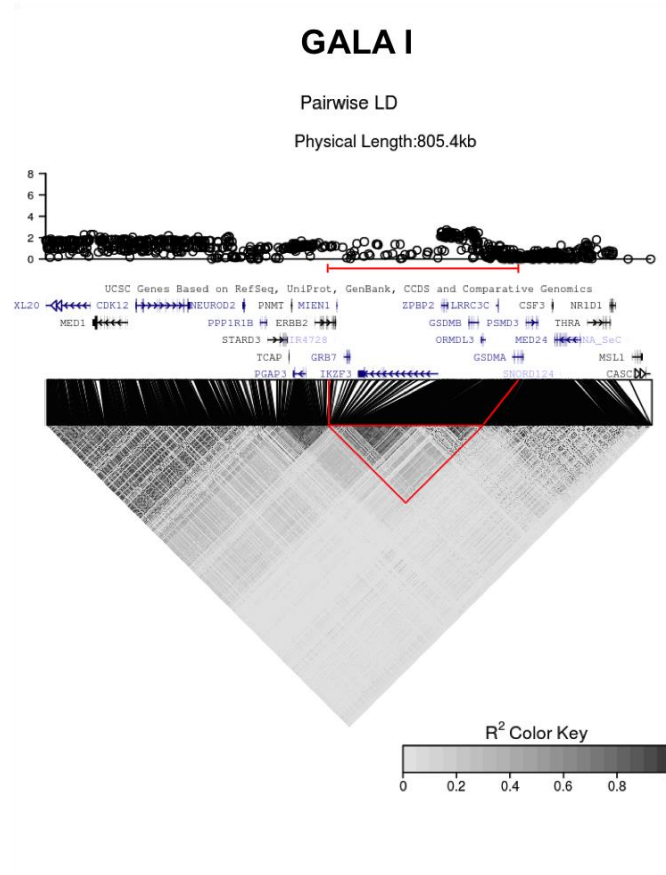
The relative location of genes and the direction of transcription are shown in the lower portion of the figure, and the chromosomal position is shown on the  $x$  axis. The light blue line show the recombination rate across the region (right  $y$  axis), and the left  $y$  axis shows the significance of the associations. The purple diamond shows the  $P$ -value for rs907092 that is the most significant SNP in the meta-analysis (Hartford-PR, GALA I and GALA II). The circles show the  $P$ -values for all other SNPs and are color coded according to the level of LD with rs907092 in the 1000 Genome Project AMR population.

**Figure S8. The 17q21 region of Hartford-PR**



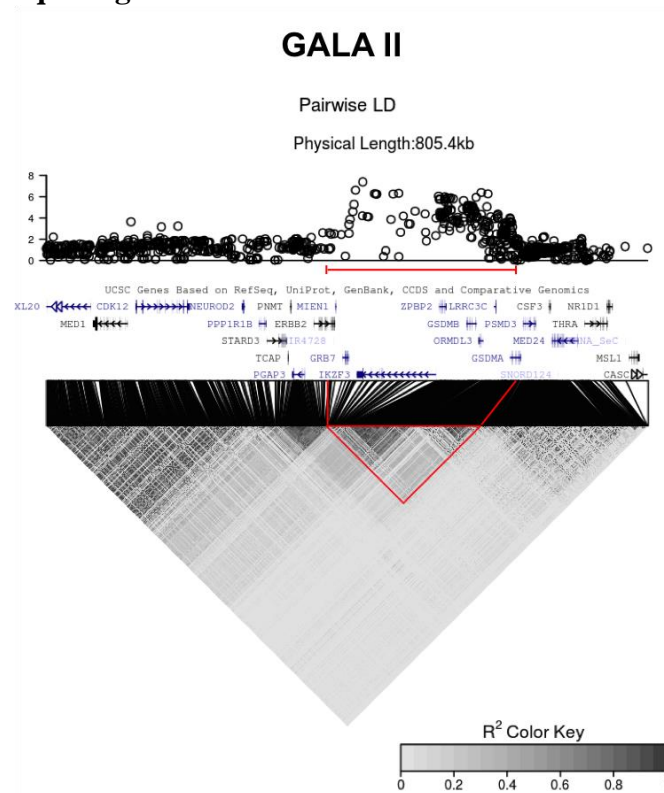
The top portion shows the  $-\log_{10}$  transformed  $P$ -values, the middle portion shows the relative location of genes, and the bottom portion shows the LD structure. The red color marked region shows the second LD block in this region.

**Figure S9. The 17q21 region of GALA I**



The top portion shows the  $-\log_{10}$  transformed  $P$ -values, the middle portion shows the relative location of genes, and the bottom portion shows the LD structure. The red color marked region shows the second LD block in this region.

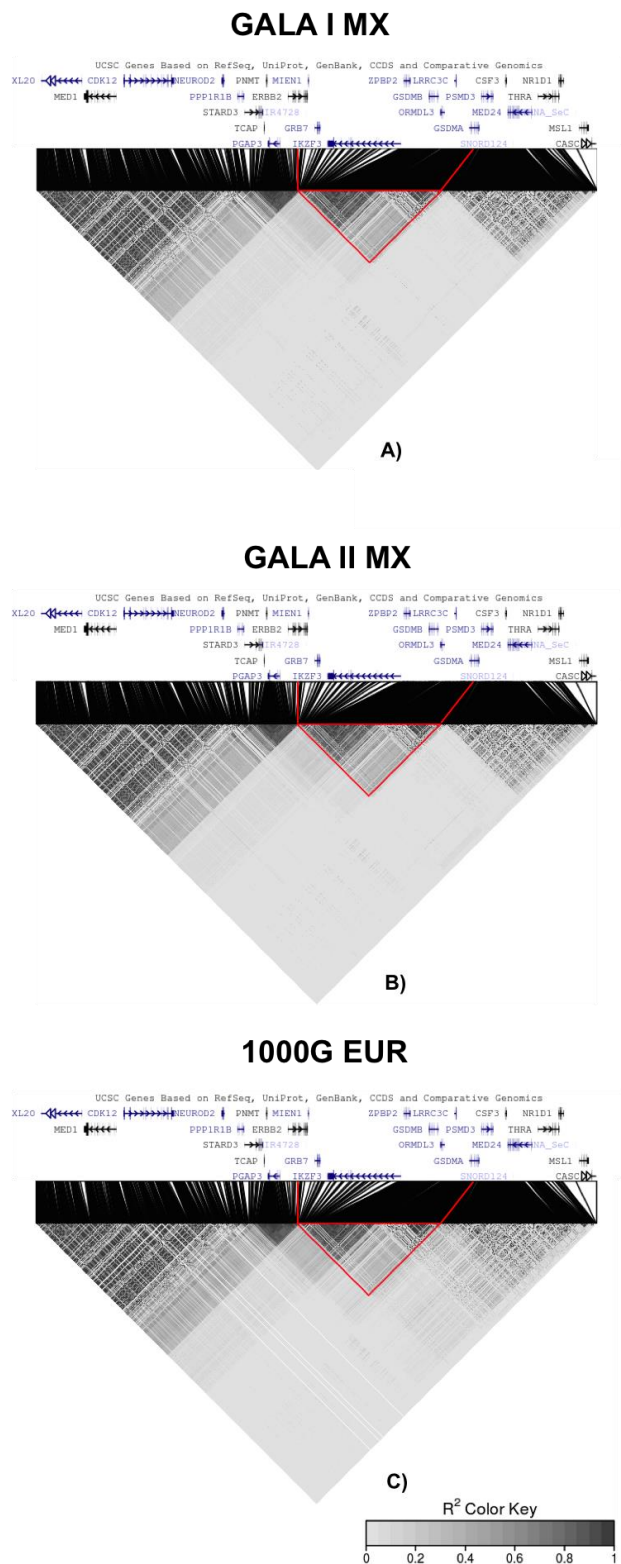
**Figure S10. The 17q21 region of GALA II**



The top portion shows the  $-\log_{10}$  transformed  $P$ -values, the middle portion shows the relative location of genes, and the bottom portion shows the LD structure. The red color marked region shows the second LD block in this region.



**Figure S11. The 17q21 region of Mexican subjects from GALA I and GALA II, and European subjects from 1000 Genome Project.**



**Figure S12. The *IL33* region of Puerto Ricans from Hartford-PR, Mexicans from 1000 Genome Project, and Europeans from 1000 Genome Project.**

