

Table S4: Performance summary for combining family history and SNPs, including shared environment.

Disease	K	h_L^2	f_{SNPs}	1				S1A				S1B				S1C	
				complete		restricted		complete		restricted		complete		restricted		complete	restricted
				complete	restricted	complete	restricted	complete	restricted	complete	restricted	complete	restricted	complete	restricted	complete	restricted
Coronary artery disease	0.402	0.49	6.9%	0.729	0.713	0.688	0.688	0.688	0.688	0.733	0.732	0.732	0.732	0.725	0.713		
Type 2 diabetes	0.339	0.30	13.0%	0.688	0.670	0.648	0.648	0.688	0.688	0.688	0.688	0.688	0.688	0.683	0.670		
Atrial fibrillation	0.245	0.62	6.1%	0.763	0.747	0.720	0.720	0.768	0.768	0.768	0.768	0.768	0.760	0.747			
Stroke	0.190	0.17	1.9%	0.645	0.617	0.590	0.590	0.590	0.640	0.640	0.640	0.640	0.636	0.617			
Prostate cancer	0.165	0.42	11.9%	0.692	0.674	0.650	0.650	0.650	0.690	0.690	0.690	0.690	0.688	0.674			
Alzheimer disease	0.132	0.79	10.0%	0.814	0.799	0.774	0.774	0.820	0.820	0.820	0.819	0.819	0.811	0.799			
Breast cancer	0.123	0.25	10.5%	0.647	0.628	0.610	0.610	0.642	0.642	0.642	0.642	0.642	0.642	0.628			
Lung cancer	0.069	0.08	2.3%	0.614	0.579	0.558	0.558	0.602	0.602	0.602	0.602	0.602	0.603	0.579			
Bipolar disorder	0.051	0.60	1.1%	0.747	0.708	0.662	0.662	0.747	0.747	0.747	0.747	0.747	0.737	0.708			
Colorectal cancer	0.051	0.13	8.6%	0.635	0.606	0.588	0.588	0.588	0.626	0.626	0.626	0.626	0.625	0.606			
Age-related macular degeneration	0.047	0.71	25.9%	0.836	0.822	0.803	0.803	0.840	0.840	0.840	0.840	0.840	0.832	0.822			
Bladder cancer	0.024	0.08	16.2%	0.621	0.599	0.588	0.588	0.588	0.612	0.612	0.612	0.612	0.613	0.599			
Multiple sclerosis	0.020	0.51	6.1%	0.730	0.700	0.670	0.670	0.731	0.731	0.731	0.731	0.731	0.720	0.700			
Melanoma	0.020	0.21	19.7%	0.682	0.663	0.651	0.651	0.677	0.677	0.677	0.677	0.677	0.675	0.663			
Type 1 diabetes	0.018	0.87	4.5%	0.808	0.781	0.744	0.744	0.816	0.816	0.816	0.816	0.816	0.801	0.781			
Parkinson disease	0.016	0.27	6.0%	0.662	0.634	0.614	0.614	0.657	0.657	0.657	0.657	0.657	0.652	0.634			
Pancreatic cancer	0.015	0.36	1.7%	0.658	0.621	0.594	0.594	0.594	0.652	0.652	0.652	0.652	0.645	0.621			
Ovarian cancer	0.014	0.22	2.0%	0.589	0.571	0.559	0.559	0.581	0.581	0.581	0.581	0.581	0.584	0.571			
Thyroid cancer	0.010	0.53	4.3%	0.712	0.682	0.654	0.654	0.712	0.712	0.712	0.712	0.712	0.701	0.682			
Ulcerative colitis	0.009	0.53	9.2%	0.740	0.718	0.695	0.695	0.742	0.742	0.742	0.742	0.742	0.732	0.718			
Schizophrenia	0.007	0.66	0.4%	0.687	0.647	0.607	0.607	0.689	0.689	0.689	0.689	0.689	0.673	0.647			
Celiac disease	0.007	0.75	12.6%	0.810	0.792	0.769	0.769	0.816	0.816	0.816	0.816	0.816	0.804	0.792			
Crohn disease	0.005	0.56	13.5%	0.767	0.750	0.734	0.734	0.769	0.769	0.769	0.769	0.769	0.761	0.750			

f_{SNPs} provides the proportion of heritability explained by known SNP associations. The last eight columns indicate the AUC achieved when combining these SNP associations with complete and restricted family history models, assuming 10% of the variance in liability is due to shared environment across all individuals in the family, using either the test pedigree in Figure 1 or the additional pedigrees in parts (A), (B), and (C) of Figure S1. Note that the performance of models shown here reflects only currently known genetic factors for European populations and will change as more associations are discovered.