Table S1. Effect sizes of the genome-wide significant SNPs in 23andMe GWAS and CONVERGE GWAS (discovery stage)

					23andMe GWAS	
SNP	**CHR**	**POS**	**A1**	**A2**	**OR**	**SE**
rs10514299	5	87663610	T	C	1.051	0.007
rs1518395	2	58208074	G	A	1.034	0.0062
rs2179744	22	41621714	A	G	1.038	0.0067
rs11209948	1	72811904	T	G	1.036	0.0063
rs454214	5	88003403	C	T	1.035	0.0061
rs301806	1	8482078	C	T	1.029	0.0061
rs1475120	6	105389953	A	G	1.03	0.0061
rs10786831	10	106614571	A	G	1.031	0.0062
rs12552	13	53625781	A	G	1.045	0.0061
rs6476606	9	37005561	A	G	1.028	0.0063
rs8025231	15	37648402	C	A	1.036	0.0061
rs12065553	1	80793118	G	A	1.034	0.0067
rs1656369	3	158280085	T	A	1.036	0.0065
rs4543289	5	164484948	G	T	1.031	0.0061
rs2125716	12	84941429	A	G	1.038	0.0071
rs2422321	1	73293393	G	A	1.029	0.0061
rs7044150	9	2982931	C	T	1.033	0.0062
					CONVERGE GWAS	
SNP	**CHR**	**POS**	**A1**	**A2**	**OR**	**SE**
rs12415800	10	69624180	A	G	1.164	0.028
rs35936514	10	126244970	C	T	1.192	0.032

Abbreviation

SNP, single nucleotide polymorphism; CHR, chromosome; POS, position; OR, odds ratio; SE, standard error; A1, allele 1; A2, allele 2. OR was calculated according to allele 1.