

SUPPLEMENTAL TABLE 1. Detailed MFMAP Results for the Two-Point and Multipoint Linkage Using the African-American Samples

Two-Point Linkage Results												
CHR	Linkage Map	Marker	LOD Assuming Homogeneity (MLOD)		LOD Assuming Admixture (MALOD)							
				Model-Free LOD (MFLOD)	MALOD	α	q	f0	f1	f2	Model	
1	56.7	D1S1622	1.38	1.05	1.38	1.00	0.031	0.050	0.249	0.249	Dominant	
4	78.4	D4S2367	1.35	1.89	1.95	0.30	0.031	0.001	0.999	0.999	Dominant	
6	0.0	D6S942	1.54	0.47	1.65	0.70	0.247	0.038	0.038	0.437	Recessive	
	152.6	D6S2436	1.59	1.00	1.61	0.60	0.031	0.038	0.437	0.437	Dominant	
	164.8	D6S1035	1.23	1.15	1.30	0.60	0.031	0.038	0.437	0.437	Dominant	
	173.3	D6S1277	0.71	0.66	1.03	0.30	0.247	0.025	0.025	0.624	Recessive	
	187.2	D6S1027	1.42	0.08	1.42	1.00	0.247	0.050	0.050	0.249	Recessive	
7	41.7	D7S1808	1.31	1.01	1.34	0.50	0.031	0.038	0.437	0.437	Dominant	
	50.3	D7S817	1.17	1.25	1.30	0.40	0.031	0.025	0.624	0.624	Dominant	
18	115.9	D18S1371	1.46	1.12	1.46	1.00	0.031	0.050	0.249	0.249	Dominant	

Multi-Point Linkage Results												
Linkage Map	Marker Interval	LOD Assuming Homog (MLOD)		LOD Assuming Admixture (MALOD)								
			Model-Free LOD (MFLOD)	MALOD	α	q	f0	f1	f2	Model		
61.0	D1S1622-D1S1255	0.59	0.43	0.89	0.10	0.247	0.001	0.001	0.999	0.999	Recessive	
70.5	D4S2367-D4S3243	0.99	0.84	1.03	0.20	0.031	0.001	0.999	0.999	0.999	Dominant	
156.7	D6S2436-D6S1035	1.40	1.23	1.65	0.60	0.031	0.038	0.437	0.437	0.437	Dominant	
166.0	D6S1035-D6S1277	1.13	1.38	1.46	0.40	0.031	0.025	0.624	0.624	0.624	Dominant	
180.6	D6S1277-D6S1027	1.65	0.00	1.65	1.00	0.247	0.050	0.050	0.249	0.249	Recessive	
46.0	D7S1808-D7S817	1.82	1.65	1.87	0.60	0.031	0.038	0.437	0.437	0.437	Dominant	
54.0	D7S817-D7S2846	0.99	1.10	1.15	0.50	0.247	0.038	0.038	0.437	0.437	Recessive	
120.8	D18S1371-D18S1390	0.22	0.34	0.46	0.20	0.031	0.001	0.999	0.999	0.999	Dominant	

CHR = ? ; LOD = ? ; MALOD = ? ; MFLOD = ? ; MFMAP = ? ; MLOD = ? ;

SUPPLEMENTAL TABLE 2. Detailed MFMAP Results for the Two-Point and Multipoint Linkage in the White Families

Two-Point Linkage Results												
CHR	Linkage Map	Marker	LOD Assuming Homogeneity (MLOD)		Model-Free LOD (MFLOD)		LOD Assuming Admixture (MALOD)					Model
			MLOD	MLOD	MALOD	α	q	f0	f1	f2		
1	136.9	D1S1631	0.87	0.05	1.83	0.30	0.247	0.001	0.001	0.999	Recessive	
6	118.6	D6S474	0.61	0.00	0.74	0.60	0.241	0.0358	0.0358	0.435	Recessive	
	128.9	D6S1040	0.69	1.17	1.17	0.30	0.0295	0.001	0.999	0.999	Dominant	
	137.7	D6S1009	2.86	0.14	2.87	0.90	0.241	0.0242	0.0242	0.623	Recessive	
11	33	ATA34E08	1.12	0.00	1.15	0.90	0.0295	0.0474	0.247	0.247	Dominant	
12	36.1	D12S373	1.15	0.00	1.45	0.40	0.241	0.001	0.001	0.999	Recessive	
	48.7	D12S1042	1.28	0.38	1.29	0.90	0.241	0.0358	0.0358	0.435	Recessive	
	125.3	D12S2070	0.45	1.20	1.20	0.20	0.0295	0.001	0.999	0.999	Dominant	
14	125.9	D14S1426	0.12	0.21	0.73	0.20	0.241	0.001	0.001	0.999	Recessive	
	138.2	D14S1007	0.57	0.45	1.59	0.30	0.241	0.001	0.001	0.999	Recessive	
20	54.1	D20S478	2.46	0.55	2.46	1.00	0.241	0.0358	0.0358	0.435	Recessive	
	62.3	D20S481	1.42	1.12	1.43	0.90	0.241	0.0358	0.0358	0.435	Recessive	
	79.9	D20S480	1.04	1.19	1.50	0.60	0.0295	0.0126	0.811	0.811	Dominant	
	90.1	D20S451	1.07	0.73	1.10	0.80	0.0295	0.0474	0.247	0.247	Dominant	
Multipoint Linkage Results												
Linkage Map	Marker Interval	LOD Assuming Homogeneity (MLOD)		Model-Free LOD (MFLOD)		LOD Assuming Admixture (MALOD)					Model	
		MLOD	MLOD	MALOD	α	q	f0	f1	f2			
138.6	D1S1631-D1S3723	1.08	0.00	1.25	0.4	0.247	0.013	0.013	0.812	Recessive		
146.1	D1S3723-D1S534	1.01	0.00	1.01	1	0.247	0.050	0.050	0.249	Recessive		
121.8	D6S474-D6S1040	0.68	0.28	1.02	0.5	0.241	0.024	0.024	0.623	Recessive		
130.2	D6S1040-D6S1009	2.19	1.09	2.19	1	0.241	0.036	0.036	0.435	Recessive		
139.7	D6S1009-GATA184A08	1.28	0.00	1.41	0.6	0.241	0.024	0.024	0.623	Recessive		
27.2	D11S1981-ATA34E08	1.48	0.35	1.48	1	0.030	0.047	0.247	0.247	Dominant		
42.3	D12S373-D12S1042	2.42	0.23	2.42	1	0.241	0.036	0.036	0.435	Recessive		
52.0	D12S1042-GATA91H06	1.31	0.28	1.31	1	0.241	0.047	0.047	0.247	Recessive		
132.0	D14S1426-D14S1007	0.34	0.44	1.25	0.2	0.241	0.001	0.001	0.999	Recessive		
48.7	D20S477-D20S478	2.01	0.79	2.14	0.7	0.241	0.024	0.024	0.623	Recessive		
56.1	D20S478-D20S481	2.09	1.18	2.09	1	0.241	0.036	0.036	0.435	Recessive		
69.1	D20S481-D20S480	1.34	1.64	1.76	0.6	0.030	0.013	0.811	0.811	Dominant		
CHR = ? ; LOD = ? ; MALOD = ? ; MFLOD = ? ; MFMAP = ? ; MLOD = ? ;												
Results are shown in bold for markers or marker intervals with MALOD scores >2.0.												