

Table S1. HyperGEN EWAS Family Structure					
	Family Size				
	1	2	3	4	5
Members per family	334	82	30	4	2
Parent-child pairs	46				
Full sibling pairs	42				
<i>EWAS: epigenome-wide association study. Members per family describes the number of distinct family clusters. For example, for Family Size = 2, there are 82 families with 2 members (82 x 2 = 164 total participants).</i>					

Table S2. Selected EWAS results from HyperGEN.

Trait	Chr	Gene	CpG	β	SE	FDR
LASD	19	GNA11	cg05370802	-0.0062	0.0009	5.36E-09
			cg18505103	-0.0017	0.0003	2.93E-06
	10	PANK1	cg00257187	-0.0101	0.0017	3.41E-06
	7		cg17512207	-0.0158	0.0027	8.13E-06
	15	SLC24A1	cg07116160	-0.0106	0.0020	1.28E-04
	14		cg05015996	-0.0088	0.0018	2.48E-03
	8	ENTPD4	cg04712321	0.0168	0.0037	0.020
	14	KCNK10	cg12095807	-0.0083	0.0018	0.020
	7		cg22886275	0.0135	0.0030	0.020
	5		cg01195564	-0.0160	0.0036	0.035
	1		cg09132102	-0.0163	0.0037	0.035
	6	TRIM15	cg13252226	-0.0161	0.0037	0.041
	14		cg18991417	0.0147	0.0034	0.041
	10		cg23939236	-0.0087	0.0020	0.044
	13		cg11508437	-0.0085	0.0020	0.071
	17	MPRIIP	cg23842572	0.0119	0.0028	0.071
	LVIDD	16	VAC14	cg00370608	0.0120	0.0025
9		NCRNA00092	cg00462570	0.0169	0.0035	0.056
3		TRAK1	cg23715029	0.0229	0.0049	0.056
6		JARID2	cg26797722	0.0102	0.0022	0.056
MWS	6	MAS1L	cg07511633	0.0024	0.0004	0.012
		B3GAT2	cg10766373	-0.0006	0.0001	0.064
	17		cg05720491	0.0016	0.0003	0.064
	22		cg19115805	-0.0012	0.0003	0.064
RWT	11	DNHD1	cg10703481	-0.129	0.0224	0.076
			cg22908616	-0.1526	0.0270	0.076
			cg16126079	-0.1210	0.0216	0.076
EWAS results with FDR < 0.1. Chr: chromosome. Linear mixed models adjusted for age, sex, BMI, recruitment center, cell counts, ancestry principal components, family relatedness (random), and batch (random). Boldface indicates CpG was part of a significant DMR in main analysis. There were no significant CpG sites associated with EF.						

Table S3. Association of *DNHD1* DMR with RWT in HyperGEN using family and batch-adjusted residuals.

Residuals	β(SE)	P
Family [#]	-0.1194(0.0238)	5.34e-07
Family & batch ^{##}	-0.1236(0.0223)	3.09e-08
[#] Family ID as a random effect. ^{##} Family ID and batch as random effects. Models adjusted for age, sex, BMI, recruitment center, ancestry principal components, cell counts, and batch (family-only residuals).		

