

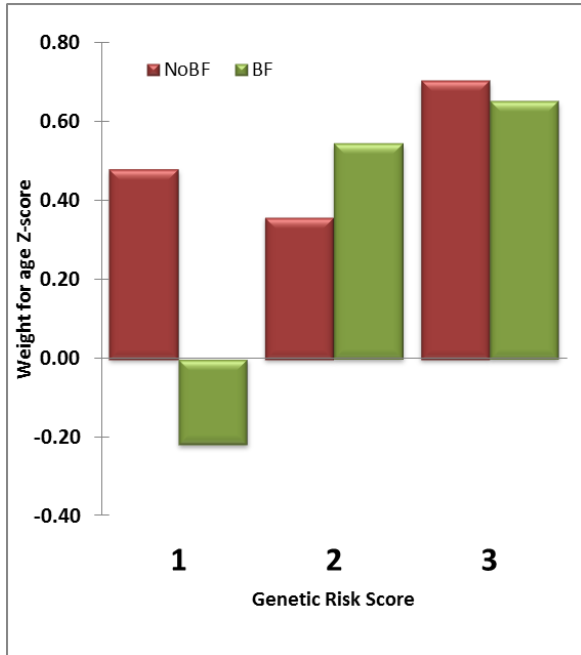
Supplementary material. Percent of variability explained in selected phenotypes by tertiles of genetic risk score (GRS) using bootstrapping modeling and 100, 500 and 1000 replicates.

	MODEL 1	MODEL 2	MODEL 3	MODEL 4	MODEL 5
100replicates					
BMIPCT	1.2	1.3	1.2	2.9	6.0
BMIZ	1.6	1.6	1.6	3.2	6.1
HAZ	3.3	3.6	4.1	7.1	7.8
WAZ	4.5	4.8	4.8	9.4	9.7
WHZ	2.0	2.1	2.0	4.7	7.3
500replicates					
BMIPCT	1.1	1.3	1.1	3.0	6.0
BMIZ	1.4	1.5	1.4	3.1	5.9
HAZ	2.9	3.2	3.7	6.8	7.6
WAZ	4.0	4.4	4.4	9.1	9.5
WHZ	1.8	1.9	1.8	4.7	7.1
1000rep					
BMIPCT	1.2	1.3	1.2	3.0	6.2
BMIZ	1.4	1.5	1.5	3.1	6.0
HAZ	2.8	3.0	3.5	6.6	7.4
WAZ	3.8	4.2	4.2	9.0	9.3
WHZ	1.8	1.9	1.8	4.6	7.2

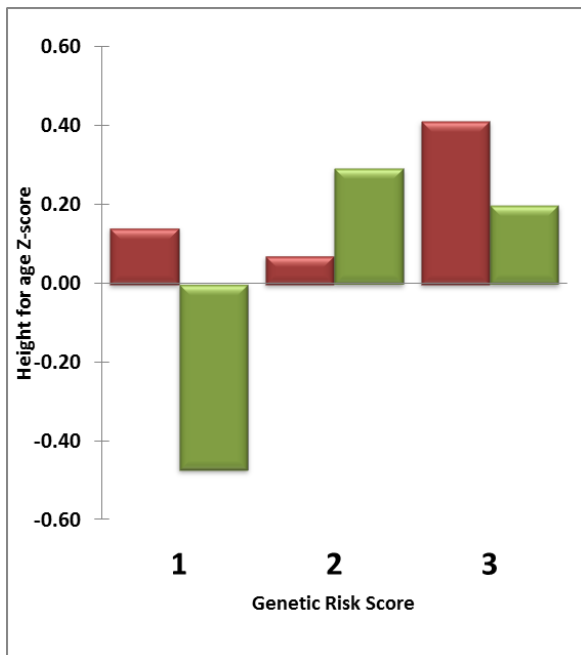
¹ Model 1, genetic association using general linear model; Model 2 includes BF breastfeeding duration as binary covariate (0 = never BF; 1=ever BF); Model 3, includes BF breastfeeding duration in 3 categories (never BF; BF less than 6 months; BF for 6 or more months); Models 4 and 5, same as Models 2 and 3, adding the interaction term.

Data generated using 1000 replicates of Strong Kids cohort genotypes.

The impact of Genetic Risk Scores (GRS) and breastfeeding (BF) on the association on Z-scores for weight (WAZ) and height (HAZ).



GRS*	BF	WAZ MEAN	SE
1	0	0.48	0.008
2	0	0.36	0.006
3	0	0.70	0.009
1	1	-0.22	0.010
2	1	0.54	0.007
3	1	0.65	0.013



GRS*	BF	HAZ MEAN	SE
1	0	0.14	0.009
2	0	0.07	0.007
3	0	0.41	0.010
1	1	-0.47	0.011
2	1	0.29	0.008
3	1	0.20	0.014

* GRS, in tertiles (1, low, 2 median, 3, high); BF duration as binary covariate (0 = never BF; 1=ever BF). Data represents the adjusted means (lsmeans) and standard errors (SE).

Allele frequencies of original data and 1000 replicates of the Strong Kids cohort.

Major allele frequency				
Gene marker	Original set (n=128)	1000 replicates (confidence intervals)		
		2.5%	50%	97.5%
BDNF	0.61	0.53	0.62	0.71
LEPR	0.27	0.19	0.26	0.35
FTO	0.25	0.17	0.25	0.33
PCSK1	0.52	0.41	0.50	0.59
POMC	0.46	0.39	0.48	0.57
TUB	0.47	0.41	0.50	0.59
LEP	0.38	0.29	0.38	0.48
MC4R	0.54	0.48	0.56	0.66