Table S11. Association results for the B_{12} and folate variants with diseases and traits in deCODE database

Condition	N cases/ controls	Annotation[1]	Allele[2] (effect/ other)	EAF	Effect	OR	P
FUT2 (rs60266) - multiplicative model							
B_{12}	37,283	G258S	A/**G**	0.596	0.16		4.1×10^{-96}
Cancer antigen 19 9	4,493	G258S	A/**G**	0.596	0.48		1.1×10^{-146}
Liver alkaline phosphatase	49,840	G258S	A/**G**	0.596	-0.08		1.1×10^{-73}
Lipase	14,929	G258S	A/**G**	0.596	0.10		2.2×10^{-24}
Psoriasis	1,657/92,792	G258S	A/**G**	0.596		1.14	0.0043
Low BMD[3]		G258S	A/**G**				
Hip, spine or whole body	4,931/69,034	G258S	A/**G**	0.596		1.10	4.6×10^{-4}
Spine	3,015/41,800	G258S	A/**G**	0.596		1.16	1.3×10^{-5}
FUT6 (7788053) - recessive model							
B_{12}	37,283	P124S	A/**G**	0.254	0.046		2.1×10^{-7}
AAA	1,163/61,639	P124S	A/**G**	0.254		0.65	0.037
AAA <65 years	209/41,800	P124S	A/**G**	0.254		0.21	0.010
MTHFR (rs18011339) - recessive model							
Folate	28,913	A222V	**G**/A	0.668	0.096		1.0×10^{-28}
TA	219/31,536	A222V	**G**/A	0.668		0.48	0.0056

Shown are the strongest association results for the folate and B_{12} variants, genome-wide significant or suggestive, with diseases and traits in deCODE's database.

EAF, effect allele frequency; BMD, bone mineral density; AAA, abdominal aortic aneurysm; TA, thoracic aneurysm;

[1]The annotation is based on the RefSeq hg18

[2]The reference alleles based on Build 36 hg18 are shown in bold

[3] The low BMD phenotypes are defined as those BMD values that are below -1 standard deviation (SD) from the mean.