Table S2 Threshold values for the –log(p-value) for all the models and traits for the dent and flint groups and for the joint connected study.

	DMC	DMY	DtSILK	DtTAS	PH	**Mean**
Dent						
Connected	3.71	3.91	3.88	4.11	3.83	**3.89**
LDLA - 5cM	4.18	4.38	4.62	4.87	4.42	**4.49**
LDLA - 2cM	4.26	4.46	4.61	4.94	4.50	**4.55**
LDLA – 1-marker [a]	5.64	5.64	5.64	5.64	5.64	**5.64**
Flint						
Connected	3.43	3.65	4.15	4.37	3.83	**3.89**
LDLA - 5cM	4.07	4.20	4.84	5.13	4.53	**4.55**
LDLA - 2cM	4.30	4.36	5.04	5.23	4.60	**4.71**
LDLA – 1-marker [a]	5.61	5.61	5.61	5.61	5.61	**5.61**
Joint						
Connected	3.49	3.94	4.02	4.85	3.74	**4.00**

[a] The threshold value for the LDLA – 1-marker corresponded to a Bonferroni threshold for a genome-wide risk of 10 %. The other thresholds were calculated using 5,000 intra-family permutations of the phenotypes for a type I risk of 10 % across all families and the total genome.