

GlobalLipids2013:				
New+Prev SNPs				
HDL _ LDL			Mean	Original
TG _ TC	n	Posterior	Prior	
1 _ 2 _ 1 _ 1	100	0.635	0.327	
1 _ 2 _ 2 _ 1	38	0.531	0.138	
1 _ 1 _ 1 _ 2	18	0.751	0.117	
2 _ 1 _ 2 _ 2	17	0.661	0.057	
1 _ 1 _ 1 _ 1	11	0.769	0.078	
 GIANT2014/5:				
New+Prev SNPs				
Height _ BMI			Mean	Original
WHRadjBMI	n	Posterior	Prior	
1 _ 2 _ 0	616	0.443	0.318	
1 _ 1 _ 1	143	0.677	0.161	
1 _ 1 _ 0	89	0.488	0.094	
1 _ 2 _ 1	15	0.387	0.037	
1 _ 2 _ 2	13	0.623	0.257	
 HaemgenRBC2016:				
New+Prev SNPs				
RBC _ MCV _ PCV			Mean	Original
MCH _ Hb _ MCHC	n	Posterior	Prior	
2 _ 1 _ 1 _ 2 _ 2 _ 2	179	0.487	0.17	
2 _ 1 _ 2 _ 2 _ 1 _ 1	162	0.502	0.203	
2 _ 1 _ 0 _ 2 _ 2 _ 1	105	0.498	0.117	
2 _ 1 _ 1 _ 2 _ 2 _ 1	51	0.561	0.155	
2 _ 0 _ 1 _ 2 _ 2 _ 2	33	0.405	0.038	

S7 Table. Top Multivariate Model Examples per SNP.

List of multivariate models that most frequently have the highest posterior probabilities per SNP. Top 5 models are shown from across both the previous univariate associations analyzed and the new multivariate associations discovered in the GlobalLipids2013, GIANT2014/5, and HaemgenRBC2016 datasets. Phenotype ordering is shown in the header, where 0, 1, and 2 refer to the multivariate categories of **U**nassociated, **D**irectly Associated, and **I**ndirectly Associated. n is the number of SNPs that show the specified model as having the largest posterior probability, with Mean Posterior displaying the average posterior probability of the given model across the n SNPs, and Original Prior showing the prior established for the given model from training on all the previous univariate associations from that dataset.