



**S3 Fig. Effect Size Heterogeneity Among SNPs With Identical Multivariate Model Assignments.**

Shown are the phenotype effect sizes (points), and  $\pm 2$  standard errors (bars), for four significantly associated SNPs from HaemgenRBC2016. All four SNPs were classified as being “associated” with all six phenotypes (i.e. marginal posterior probability of association  $\geq 95\%$  for each phenotype). However, they clearly show different patterns of effect sizes. Therefore focusing simply on binary calls of “associated” vs “unassociated” can hide different patterns of multivariate association.