**Figure S1** QTL-specific association scans. Each point is a variant segregating in the DSPR founders. SNP alleles in each RIL are inferred based on the estimated mosaic founder structure of each RIL (see King et al. 2012b), and tested against phenotype using a single marker model. QTL positions are those indicated in Table 1. Variants in blue survive a region-specific 1% FDR threshold, while variants in red survive a region-specific 5% Bonferroni threshold. The clear "stripes" of points across each plot are due to the haplotypic structure of the DSPR RILs; in general, sites are in very tight LD with many other sites.