











FIGURE S2.—Genome-wide LD with SNPs in the *AOP* and *MAM* loci. Pairwise linkage disequilibrium between SNPs within coding regions of query genes (*AOP2*, *AOP3*, *MAM1*, and *MAM3*) and all ~240,000 SNPs is shown as a heatmap with significantly strong to weak LD indicated by green to white respectively. The top histogram represents the number of GSL phenotypes showing a significant association with the individual SNP in this region for both the 2007 and 2008 datasets. The right bar-graph shows the minor allele frequency of each SNP within the query genes. The cladogram on the left indicates the hierarchical clustering of SNPs within the query genes.