



Figure S5: Gene ontology (GO) analysis for categories unique to a specific cross show enrichment for specific developmental processes. Significantly enriched GO terms are listed for zygotically transcribed genes that change in *trans* regulation between each pair of species compared. Again, zygotically transcribed genes are limited to those that are mostly zygotic (see Methods), in comparison to the maternal stage of development. Terms are listed for the biological processes category. Gene categories identified uniquely in a single cross primarily represent specific types of developmental processes, and may indicate evolved differences in parental genomes in these processes.