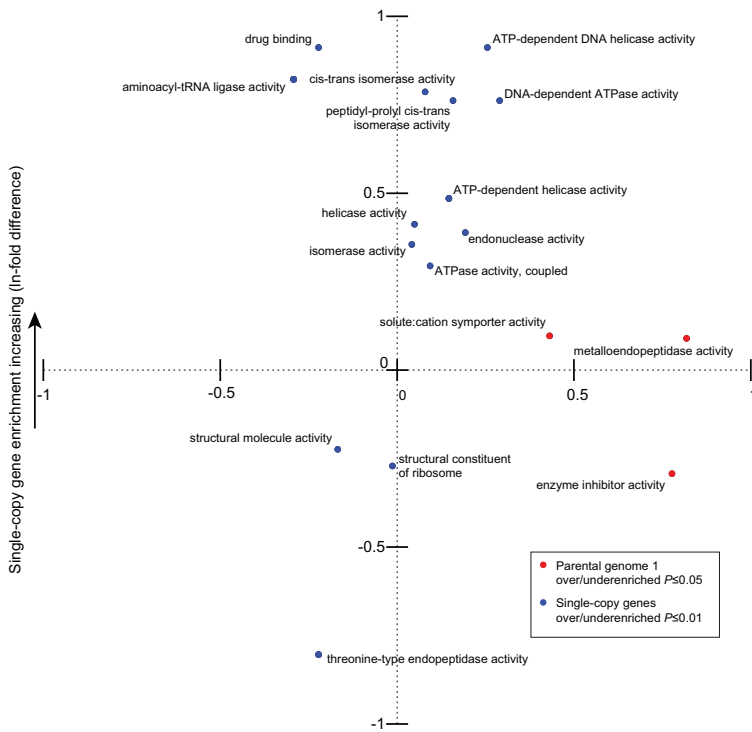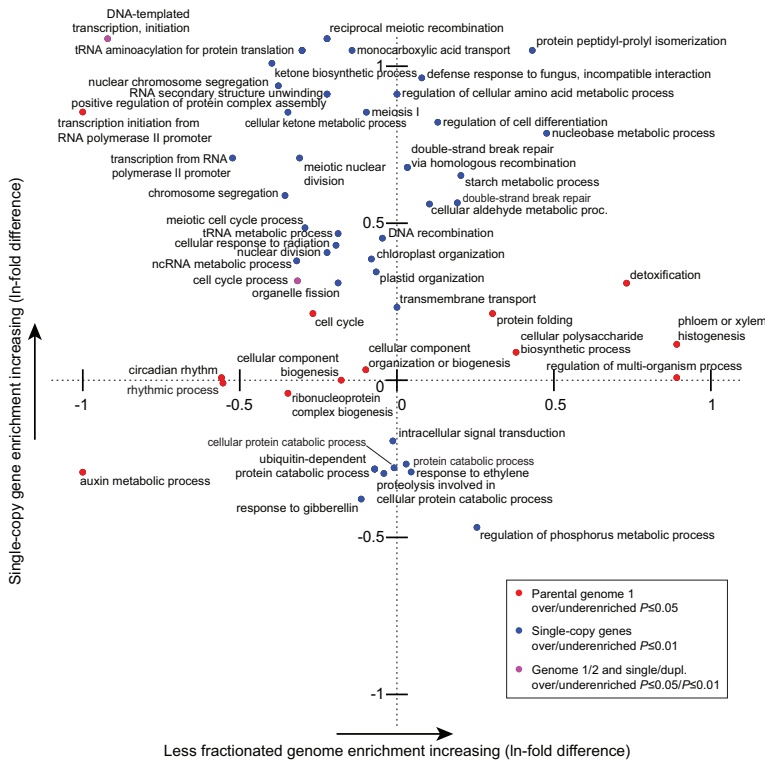**A)** GO Molecular Function

B) GO Biological Process

S3 Fig: Statistically overrepresented GO terms associated with At-α duplication status and parental genome of origin (see *Methods*) **A)** Molecular function hierarchy. **B)** Biological processes hierarchy. On the *y* axis is the ln(fold-enrichment) of the term in

question among the single copy genes relative to the duplicates. Blue dots represent terms that are significantly over/underrepresented in single copy genes relative to duplicates with Bonferroni corrected P-value ≤ 0.01 and are >1.5 fold over/underrepresented. On the *x*-axis is the ln(fold-enrichment) of GO terms of genes from subgenome 1 relative to those from subgenome 2. The GO terms that are over/underrepresented in genes from subgenome 1 (the less fractionated subgenome) with P-value ≤ 0.05 after Bonferroni correction are shown in triangles. GO terms that are significantly different both between the single copy and duplicate genes and between subgenome 1 and subgenome 2 are shown in dark purple.