Applying genotypic principal component scores as latent phenotypes in genome- wide and epistatic analyses of soybean agronomic traits.

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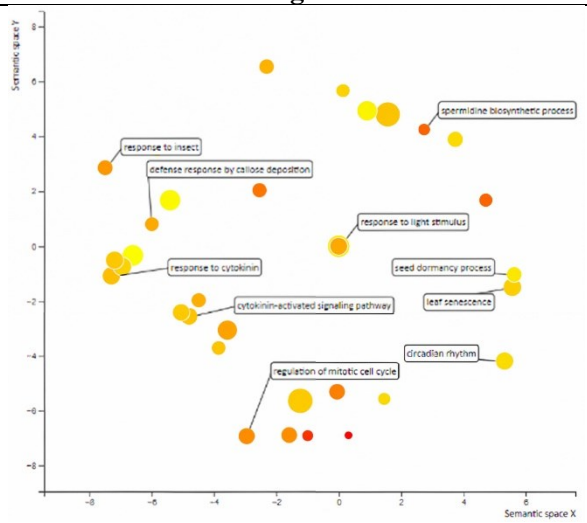
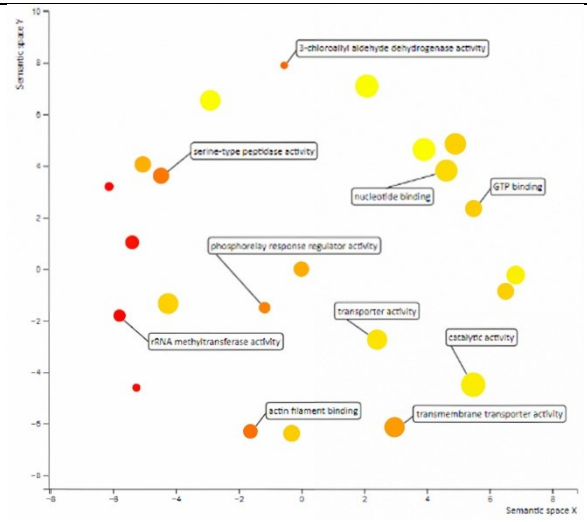
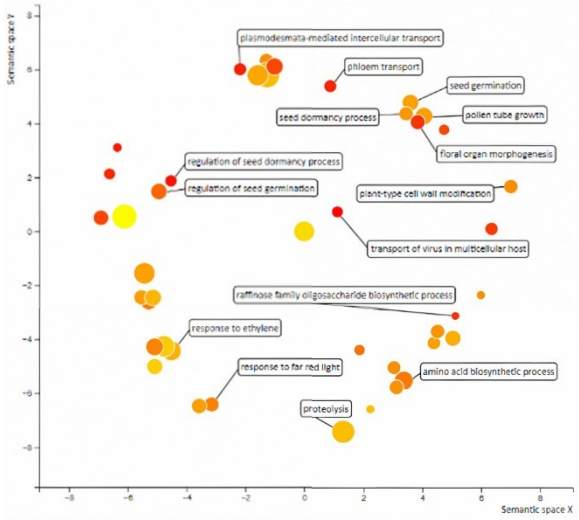
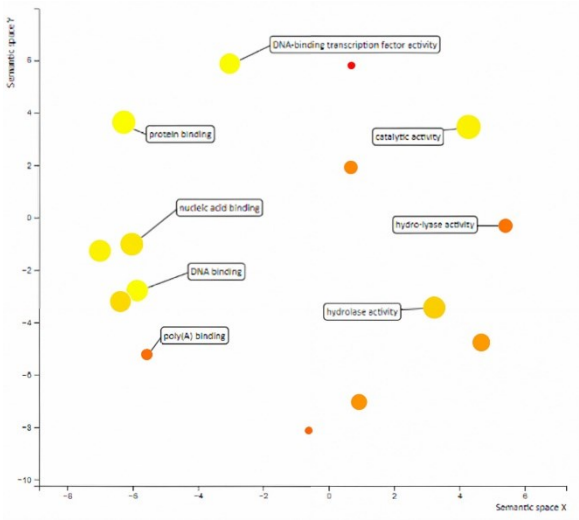
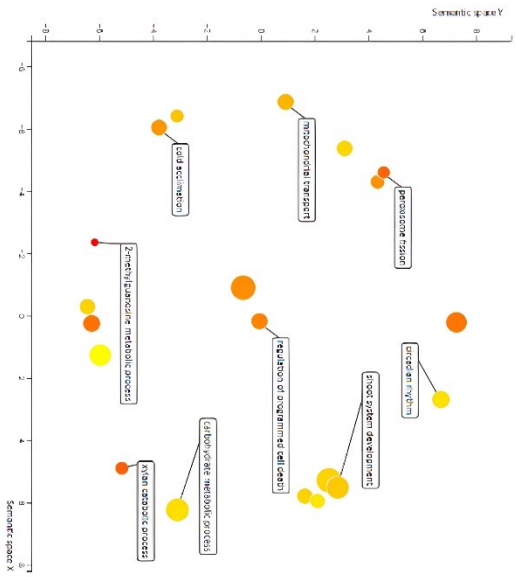
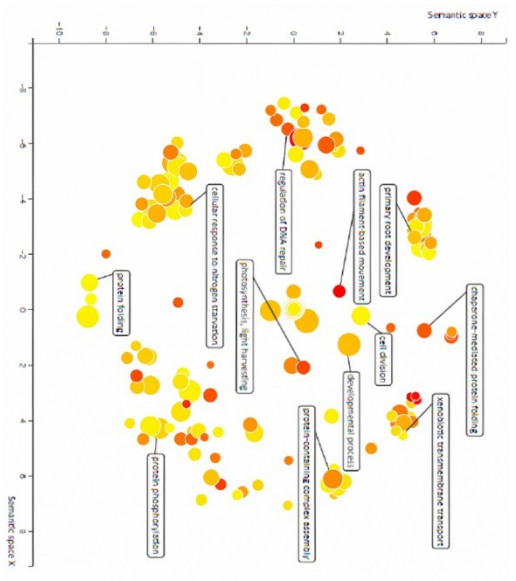
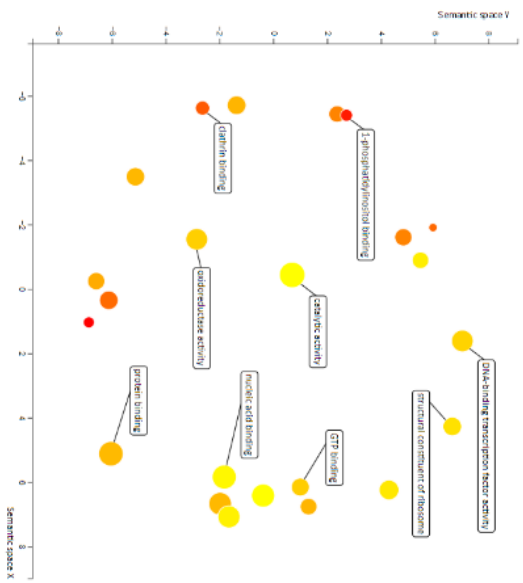
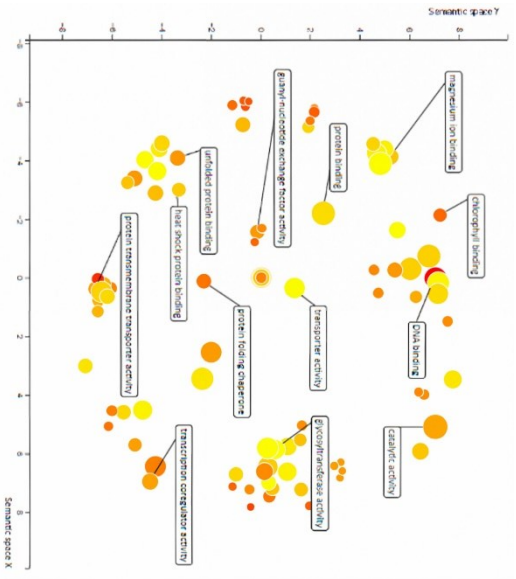
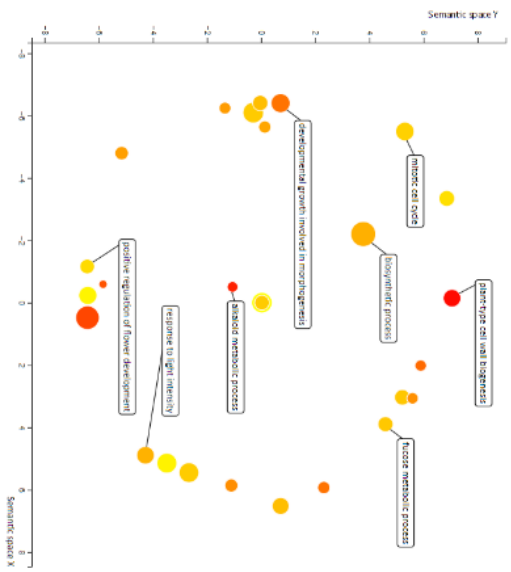
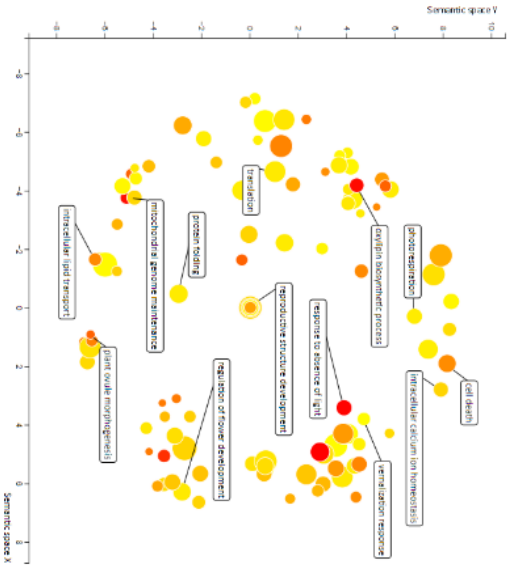
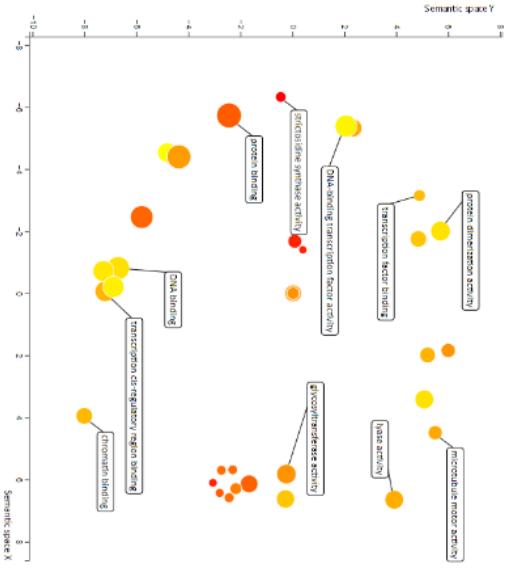
QTL	Biological Process	Molecular Function
Mat-5-PC1-1/Yld-5-PC1-1		
Sdwt-20-PC1-1		

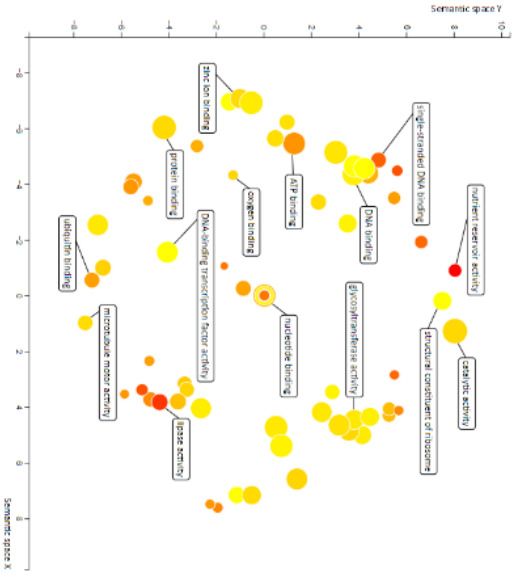
Oil-5-PC1-3	Oil-14-PC1-4/Prot-14-PC1-2/Prot-14-PC1-3
	
	

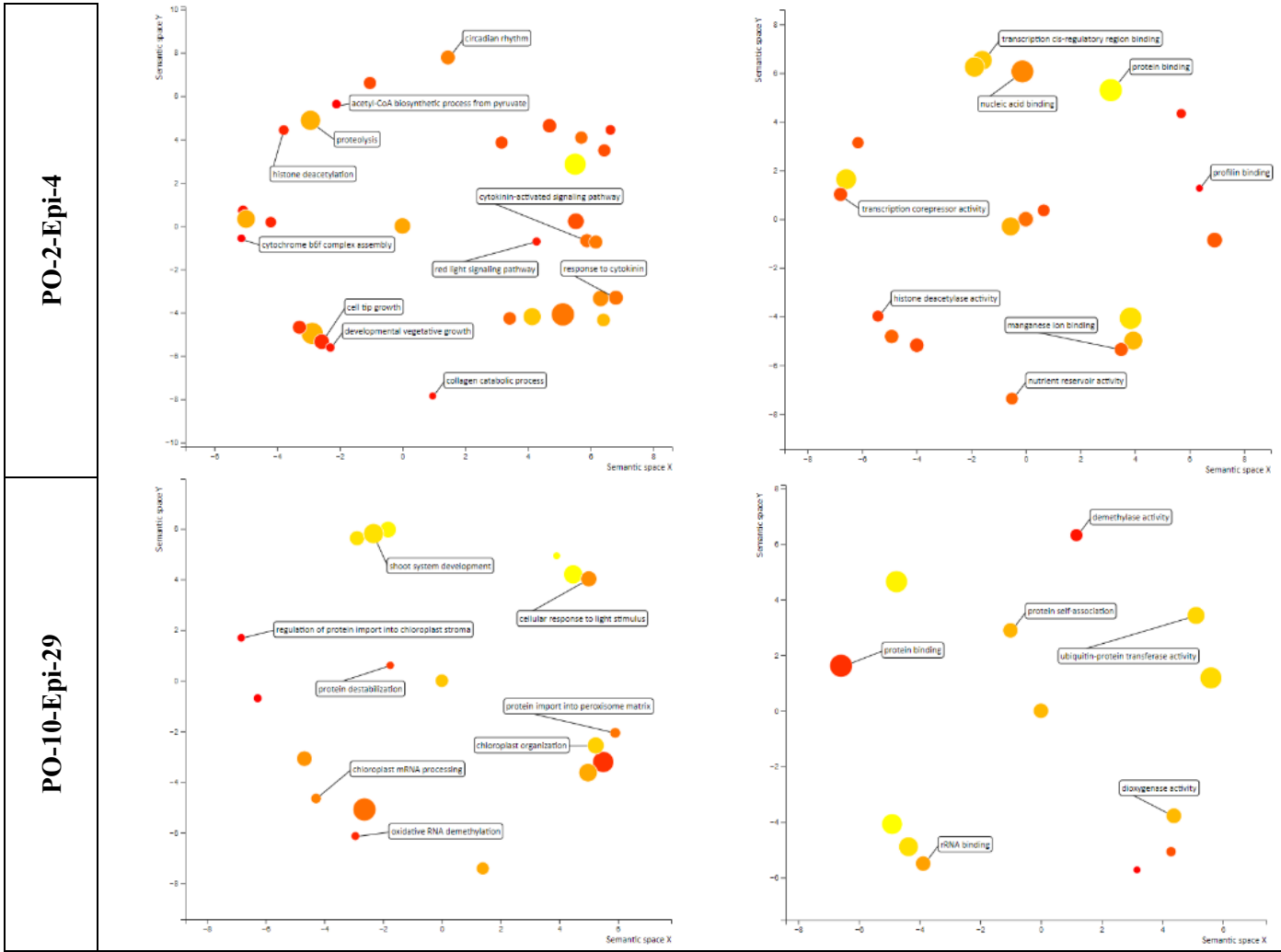
Prot-6-PC1-1 / Plht-6-PC1-1	Mat-14-PC2-3











Supplementary Fig. S5 REVIGO (Reduce and Visualize Gene Ontology) semantic plots for biological processes and molecular functions of each significant QTL. Terms are plotted in semantic space where proximity between terms represents the similarity between the gene ontology descriptions. The size of the circle represents the term's frequency in the underlying database and the color of the circle represents the p-value provided with the input data