

SUPPLEMENTARY FIGURES

Multiple Cold Tolerance Trait Phenotyping Reveals Shared Quantitative Trait Loci in *Oryza sativa*

Authors: Naoki Shimoyama, Melineeh Johnson, André Beaumont, Michael Schläppi*

Department of Biological Sciences, Marquette University, Milwaukee, WI, United States

***Correspondence: michael.schlappi@marquette.edu**

Supplementary Fig. S1 Quantile-Quantile (Q-Q) plots for all cold tolerance trait GWAS mapping. Plots were created using the RDP1 GWAS mapping pipeline (McCouch et al. 2016). Divergence of SNPs from expected (significance cutoff) is apparent at $-\log_{10}(p) > 4$ for all plots.

Supplementary Fig. S2 Approximate genomic locations of 40 Multiple-Trait (*qMT*) QTL. Colored bars show the approximate lengths of Individual Cold Tolerance QTL for 11 traits: Electrolyte Leakage (EL) measured at 4°C, 8°C, 10°C, 12°C, and 16°C (Fig. 4); Low-Temperature Seedling Survivability (LTSS) measured at 4°C, 8°C, 10°C, 12°C, and 16°C (Fig. 5); and Median Lethal Temperature (LT50, Fig. 7). Exact genomic locations are shown in Table 1 and Fig. 9.

Supplementary Fig. S3 Multiple Trait QTL (*qMT*) *Biological Processes* enrichment tree map. GO term enrichment analysis of all genes within *qMT* QTL is shown. GO term similarity was calculated using simRel scores, and a tree map for Biological Processes was constructed using REVIGO.

Supplementary Fig. S4 Multiple Trait QTL (*qMT*) *Cell Component* enrichment tree map. GO term enrichment analysis of all genes within *qMT* QTL is shown. GO term similarity was calculated using simRel scores, and a tree map for Biological Processes was constructed using REVIGO.

Supplementary Fig. S5 Multiple Trait QTL (*qMT*) *Molecular Function* enrichment tree map. GO term enrichment analysis of all genes within *qMT* QTL is shown. GO term similarity was calculated using simRel scores, and a tree map for Biological Processes was constructed using REVIGO.

Supplementary Fig. S6 Filtered Gene List *Biological Processes* enrichment tree map. GO term enrichment analysis for 71 filtered genes within *qMT* QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Biological Processes was constructed by REVIGO.

Supplementary Fig. S7 Filtered Gene List *Cell Component* enrichment tree map. GO term enrichment analysis for 71 filtered genes within *qMT* QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Cell Component was constructed by REVIGO.

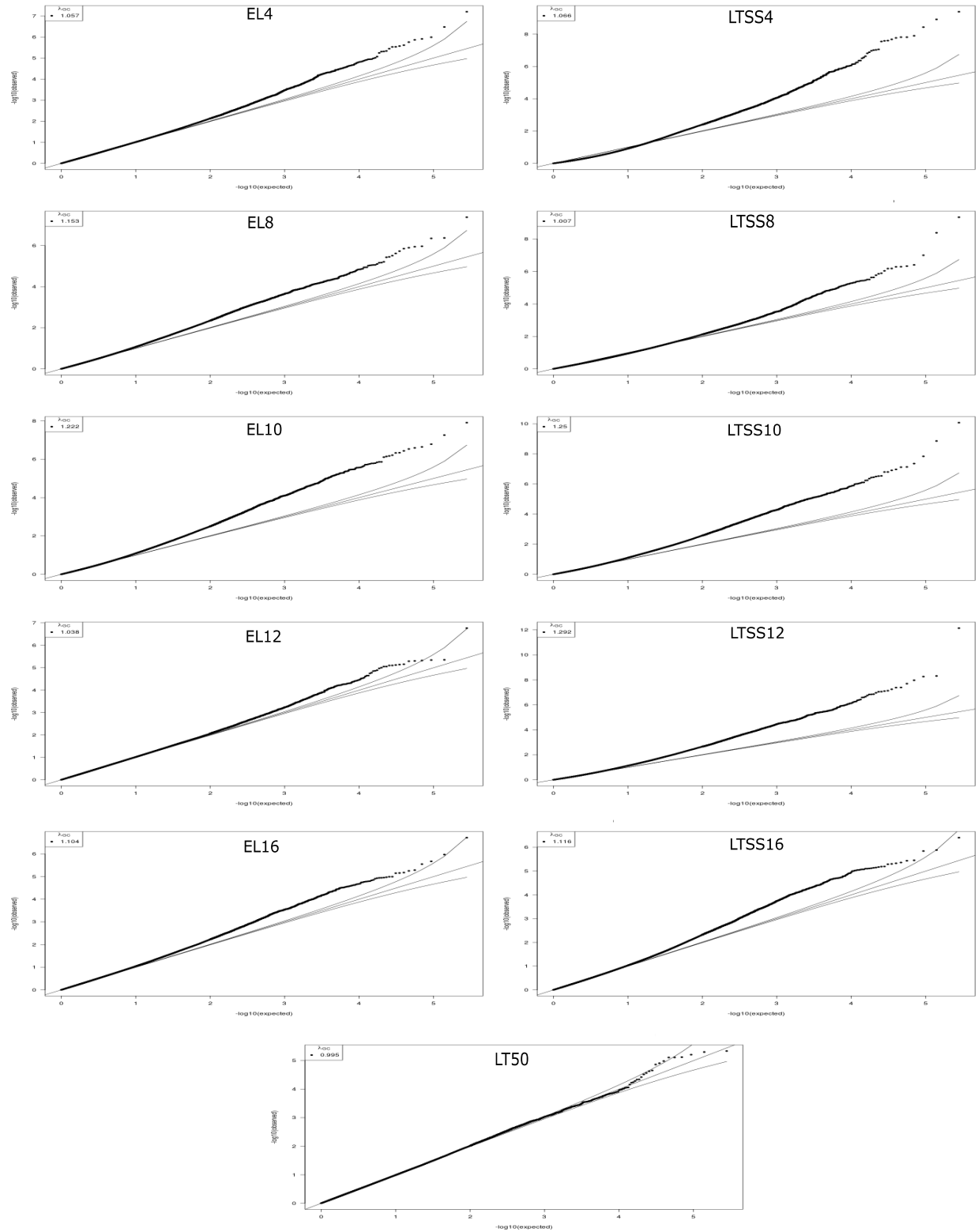
Supplementary Fig. S8 Filtered Gene List *Molecular Function* enrichment tree map. GO term enrichment analysis for 71 filtered genes within *qMT* QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Molecular Function was constructed by REVIGO.

Supplementary Fig. S9 Multiple Trait (*qMT*) QTL + Tolerant & Sensitive Cluster QTL *Biological Process* enrichment map. GO term enrichment analysis of 159 filtered genes within *qMT* + cluster specific QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Molecular Function was constructed by REVIGO.

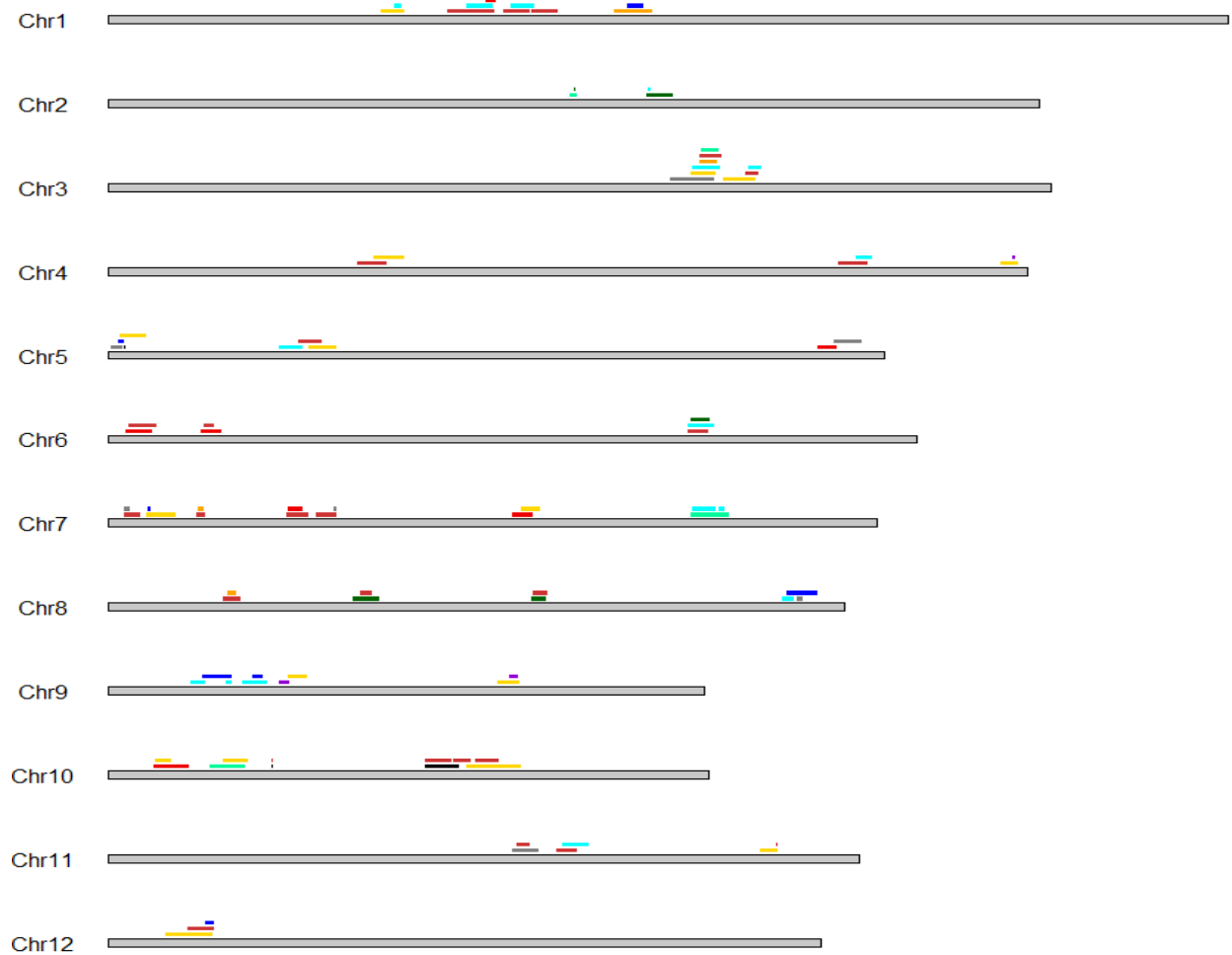
Supplementary Fig. S10 Multiple Trait (*qMT*) QTL + Tolerant & Sensitive Cluster QTL *Cell Component* enrichment map. GO term enrichment analysis of 159 filtered genes within *qMT* + cluster specific QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Molecular Function was constructed by REVIGO.

Supplementary Fig. S11 Multiple Trait (*qMT*) QTL + Tolerant & Sensitive Cluster QTL *Molecular Function* enrichment map. GO term enrichment analysis of 159 filtered genes within *qMT* + cluster specific QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Molecular Function was constructed by REVIGO.

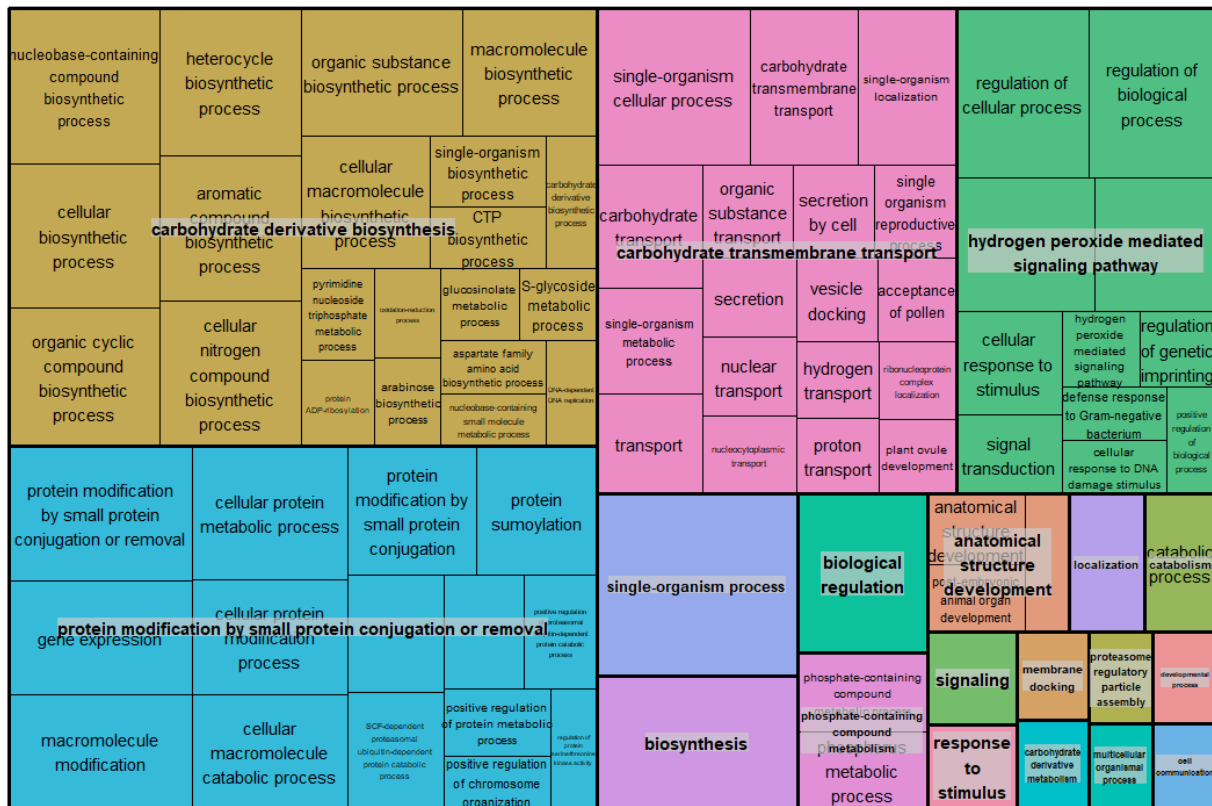
Supplementary Fig. S12 Model for functional associations of candidate term clusters. Shown is one possibility of how candidate genes from different GO term clusters may control cold tolerance through the ABA signaling pathway. Alternative models are possible (not shown).



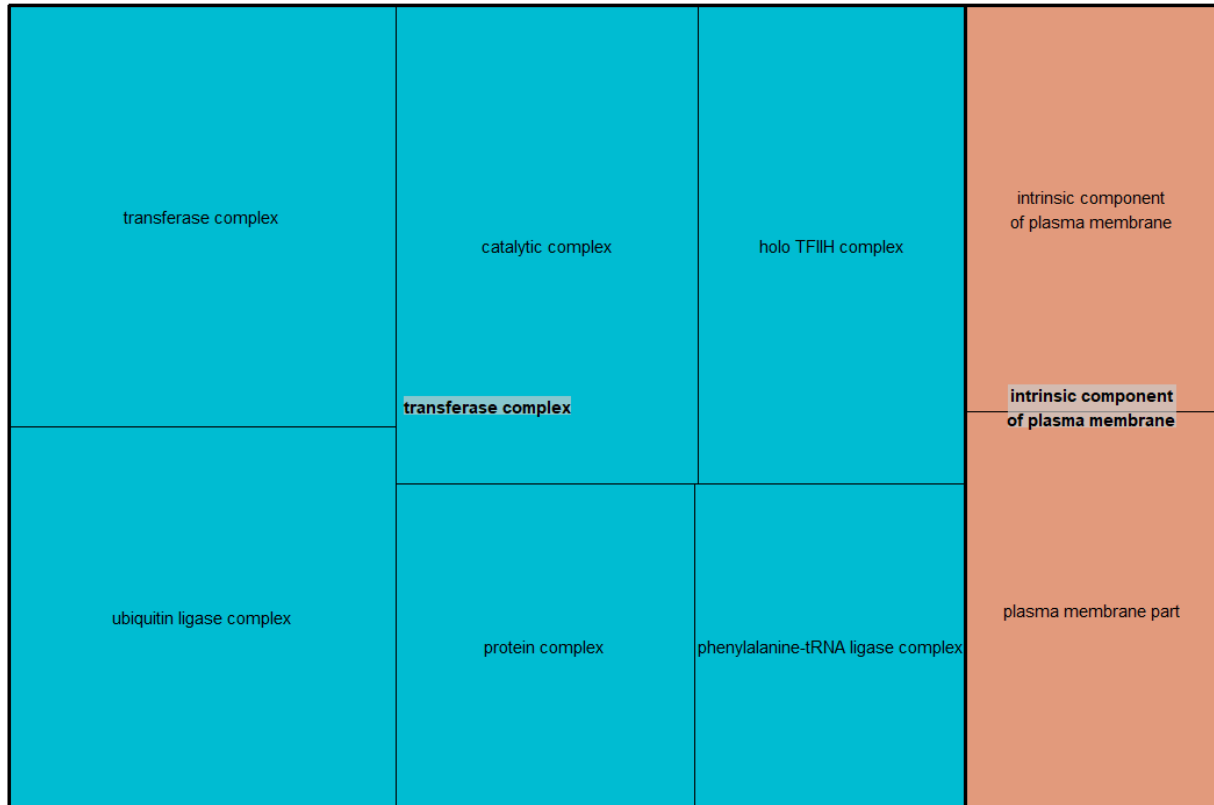
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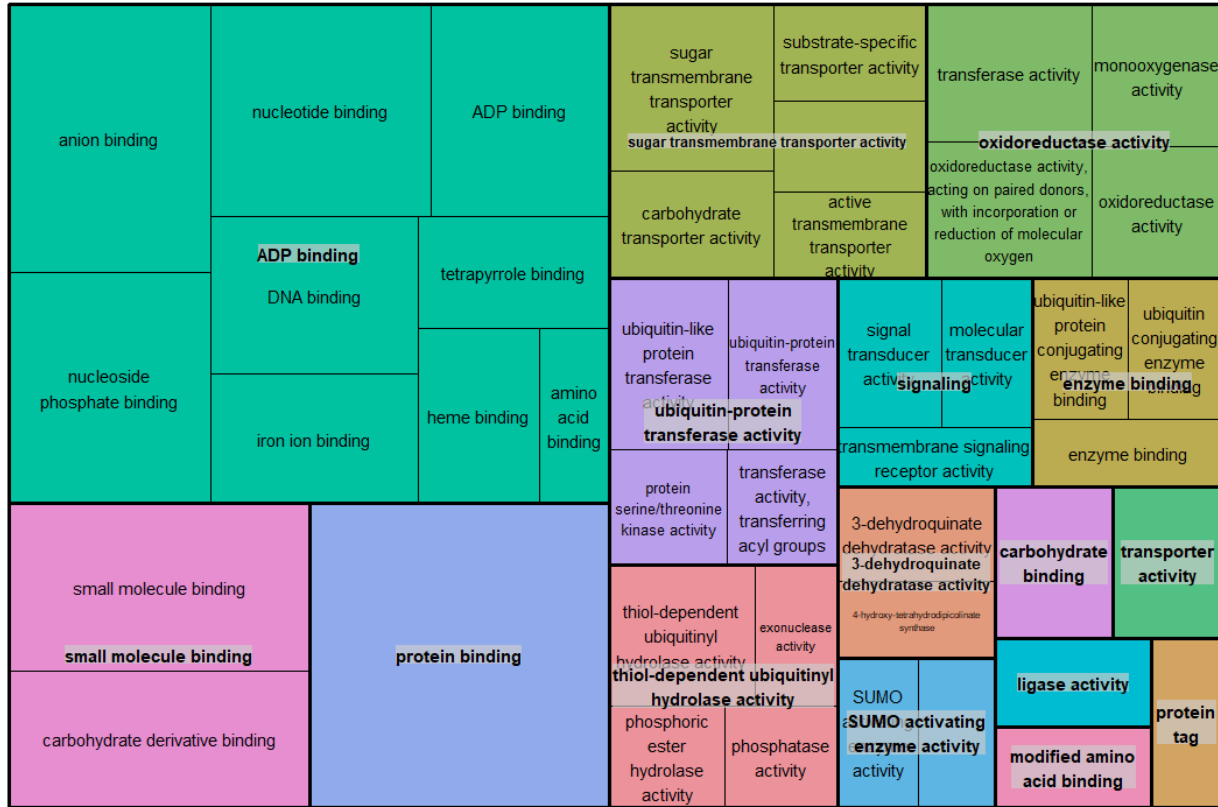
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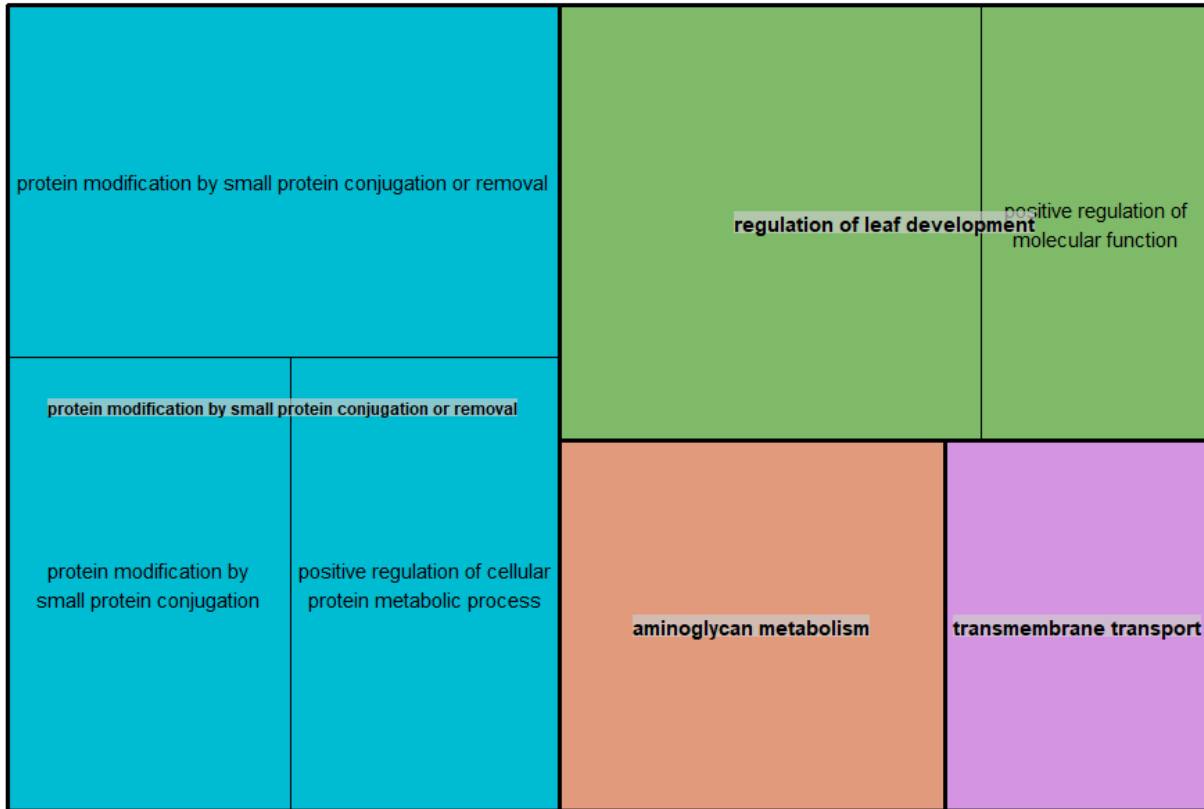
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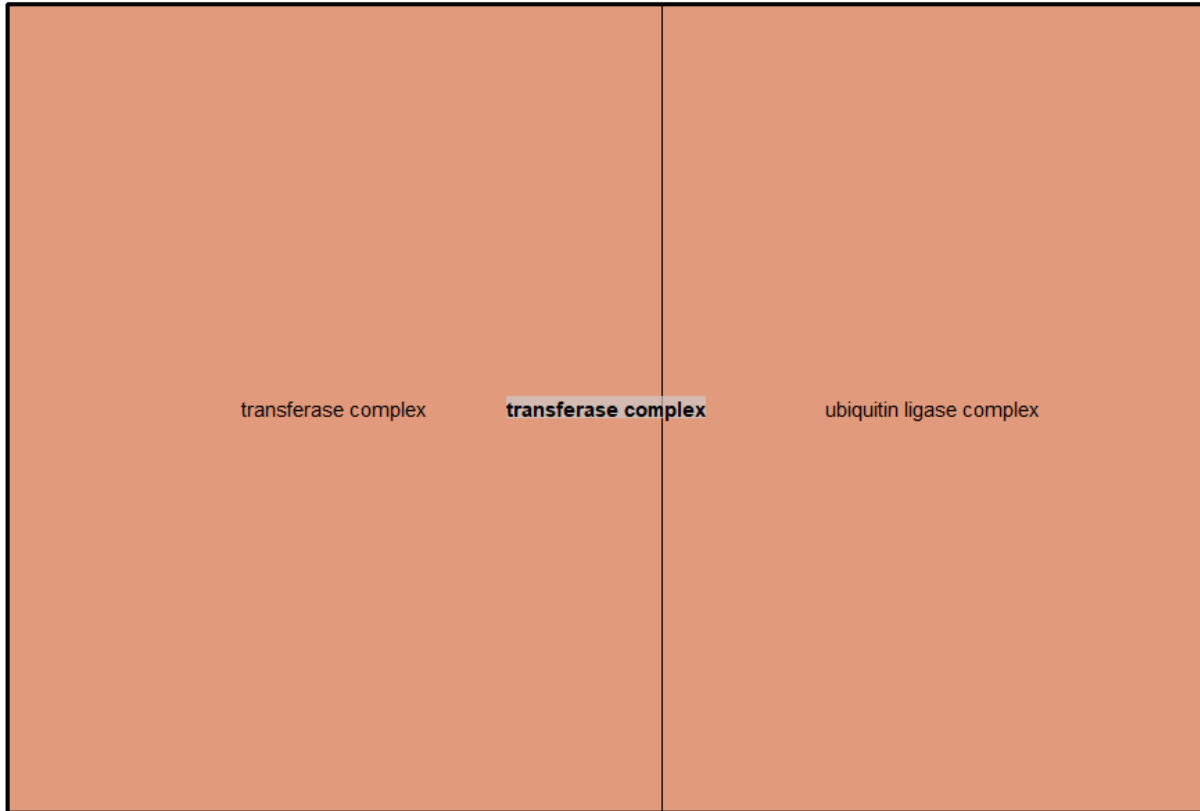
Supplementary Fig. S7 Filtered Gene List *Cell Component* enrichment tree map. GO term enrichment analysis for 71 filtered genes within *qMT* QTL is shown. GO term similarity was calculated by simRel scores and a tree map for Cell Component was constructed by REVIGO.



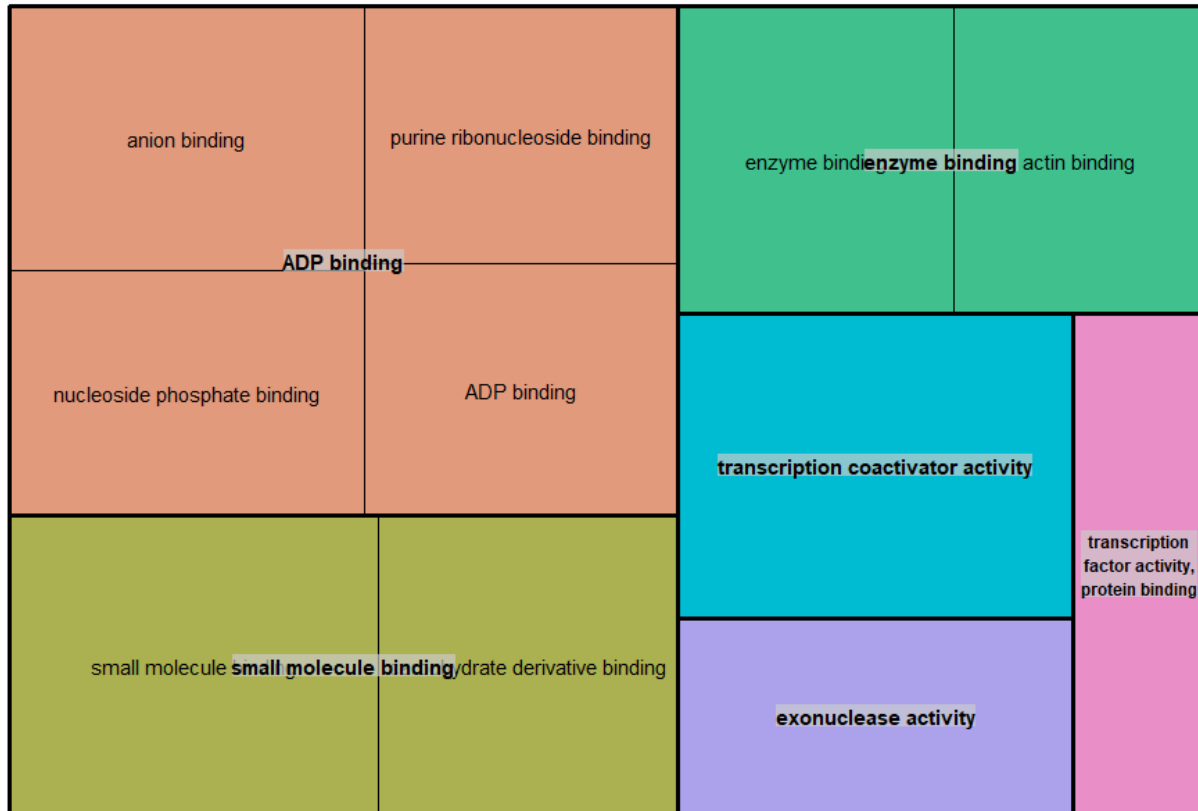
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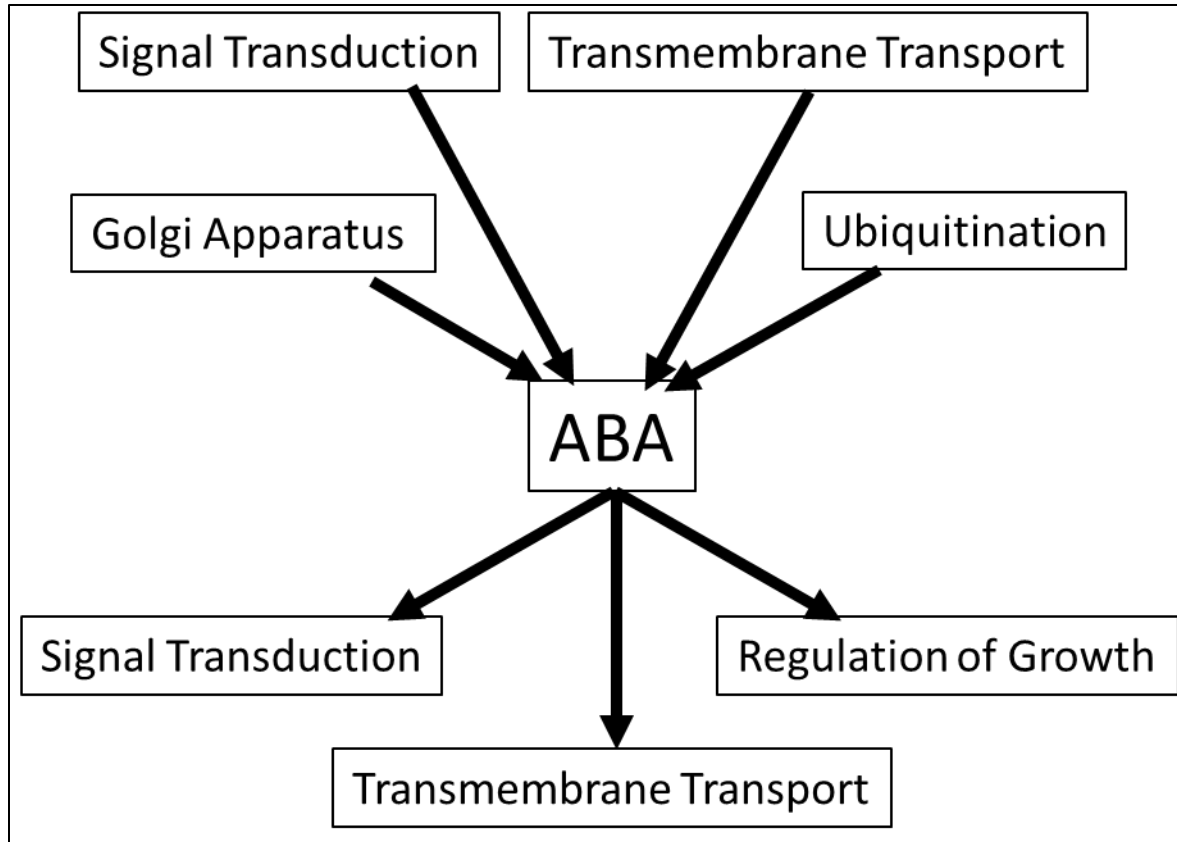
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