

Supplementary Information

Comparative transcriptome profiling of multi-ovary wheat under heterogeneous cytoplasm suppression

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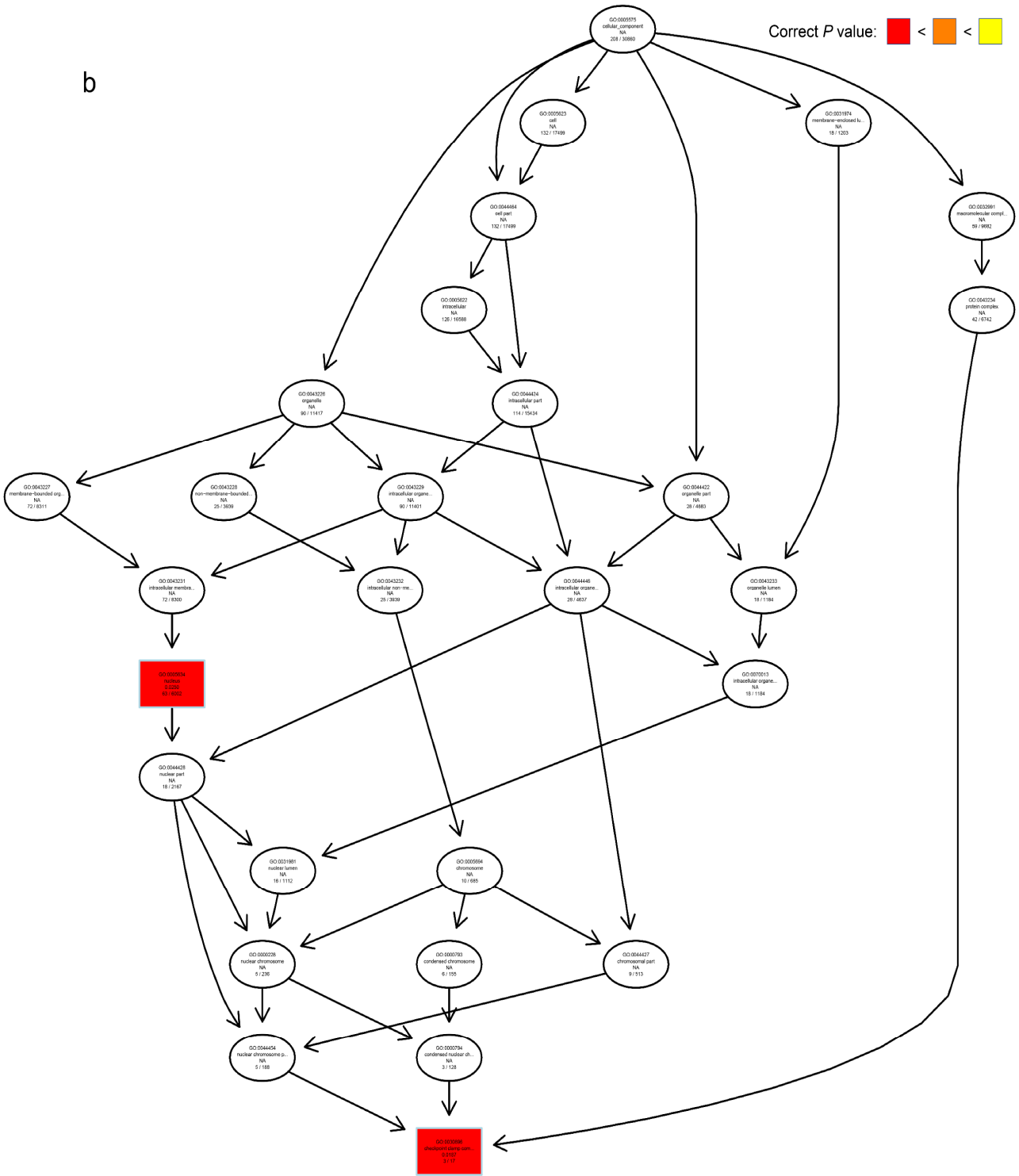
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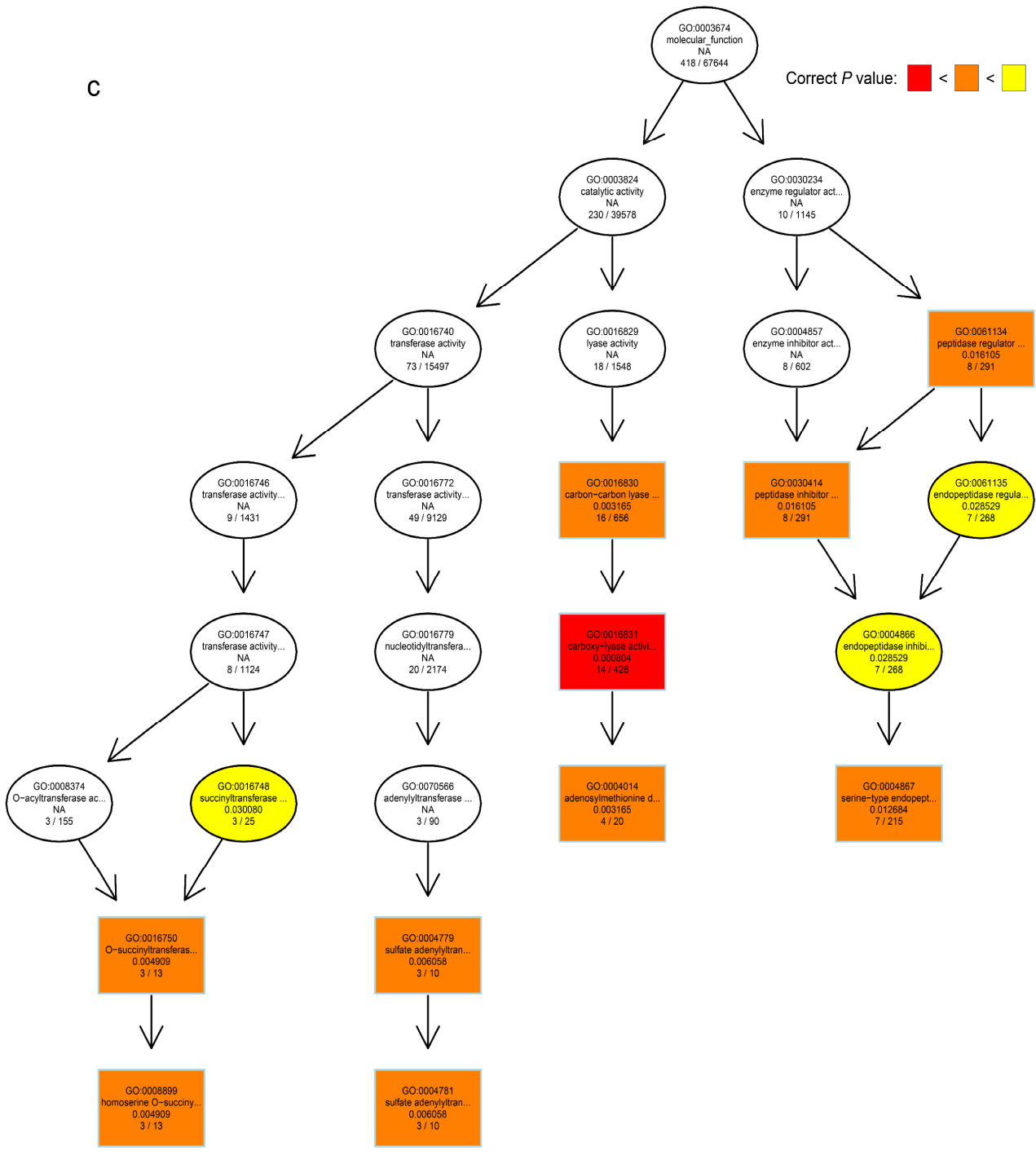
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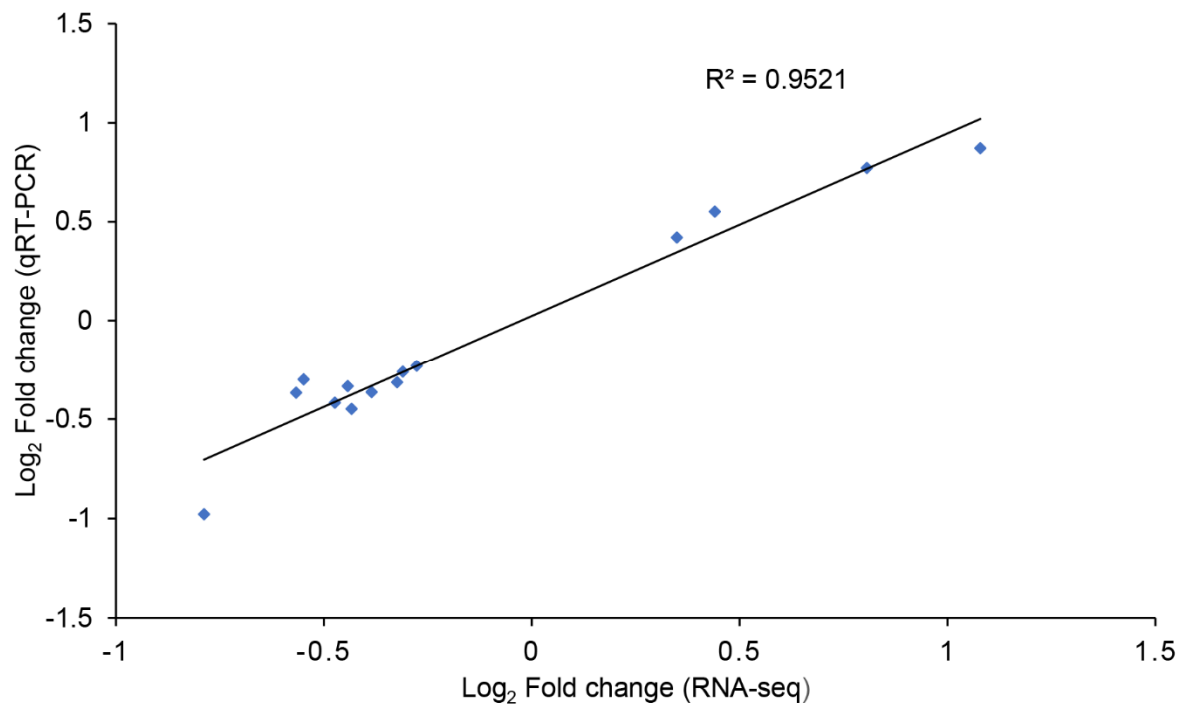
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Supplementary Figure S1. Directed acyclic graphs of enriched GO terms. a, b and c represent directed acyclic graphs of enriched GO terms in biological process, cellular component and molecular function, respectively. The colored terms are significantly enriched GO terms. The darker the color, the smaller the corrected *P* value.

Supplementary Figure S2. Comparison of the \log_2 fold change of 14 selected DEGs using RNA-seq and qRT-PCR.



Supplementary Figure S2. Comparison of the \log_2 fold change of 14 selected DEGs using RNA-seq and qRT-PCR. \log_2 fold change, $\log_2(\text{Mo_HC}/\text{Mu_NC})$, and Mu_NC , F_1 population derived from a cross between DUOII as female parent and TZI as male parent; Mo_HC , F_1 population derived from a cross between TZI as female parent and DUOII as male parent.

Supplementary Table S1. Evaluation Statistics of transcriptome sequencing data

	Mu_NC1	Mu_NC2	Mu_NC3	Mo_HC1	Mo_HC2	Mo_HC3
Raw Reads	89155990	121248314	97911120	116826696	114348164	111194976
Clean Reads	86600650	117629072	94171412	113291774	110660532	107919556
Clean Bases	12.99G	17.64G	14.13G	16.99G	16.60G	16.19G
Q30 (%)	86.61	89.63	89.88	89.91	89.37	89.24
GC (%)	54.86	54.96	55.27	55.06	55.43	54.4
Total Mapped Reads	61145956 (70.61%)	84826134 (72.11%)	66304722 (70.41%)	80667958 (71.20%)	78182672 (70.65%)	78207164 (72.47%)
Multiple Mapped Reads	6867312 (11.23%)	9564989 (11.28%)	7682207 (11.59%)	9301017 (11.53%)	8792795 (11.25%)	8626730 (11.03%)
Uniquely Mapped Reads	54278644 (88.77%)	75261145 (88.72%)	58622515 (88.41%)	71366941 (88.47%)	69389877 (88.75%)	69580434 (88.97%)

Note: Mu_NC, F₁ population derived from a cross between DUOII as female parent and TZI as male parent; Mo_HC, F₁ population derived from a cross between TZI as female parent and DUOII as male parent.

Supplementary Table S2. Primers used for qRT-PCR

Primer name	Sequence (5' to 3')	Annotation
Actin-Forward	CTCCCTCACAACAACCGC	Actin
Actin-Reverse	TACCAGGAACTCCATACCAAC	
Traes_1AS_D0A2B50BE-Forward	AGAGGTTTGTGATGGAGCAC	MCM6-like
Traes_1AS_D0A2B50BE-Reverse	TCTCAACCTTTTCAGCATCGG	
Traes_1BS_ADCD5C43B-Forward	TCCCATAACAATCCATAACAGCG	Ethylene receptor
Traes_1BS_ADCD5C43B-Reverse	CTGCTTGTGTCTGCCTTTATTG	
Traes_1DL_48CC7D8E0-Forward	GGGCTGAACTTTTGTATGTGAG	Trehalose-6-phosphate synthase
Traes_1DL_48CC7D8E0-Reverse	GAAACCCAATATGAGCAAACGG	
Traes_1DL_8809CD0A8-Forward	AAACTTCCCTGATTCCCTG	Ferredoxin--nitrite reductase
Traes_1DL_8809CD0A8-Reverse	CTCCCTGCACTATCTGAAAC	
Traes_2AL_05ECC440C-Forward	GTCTCAAGTTCTGTCTCTGCC	Auxin response factor
Traes_2AL_05ECC440C-Reverse	ACCTTTGTATATGTCCGCACC	
Traes_2AL_A26170C43-Forward	TGTGGCTGGATTAAACTGGG	OsRR6 type-A response regulator
Traes_2AL_A26170C43-Reverse	TGACATTCCACGAGACAAGAC	
Traes_2DL_5B051BFD9-Forward	AGATGGAGAACTGGTAAGCG	DNA polymerase alpha complex subunit
Traes_2DL_5B051BFD9-Reverse	GCAGTATACAAGACGGAGCAC	
Traes_2DL_CB0208DE0-Forward	TGTCACTTACCTTTGCTCTGAG	PCNA
Traes_2DL_CB0208DE0-Reverse	AGCCCATCTCACCAATCTTG	
Traes_4DL_C083C804E-Forward	TCCCTTCTAGCTCTCCAAG	Ethylene-insensitive 3
Traes_4DL_C083C804E-Reverse	CCACTCAAGCAACTCTCCC	
Traes_5DS_76A4D5D4E-Forward	CATTGCAGCTCTCAAACAG	Auxin-responsive Aux/IAA factor
Traes_5DS_76A4D5D4E-Reverse	GTTTGCTTCGCTCCTTTCTG	
Traes_7BL_9ED99FB9E1-Forward	CGTGTCTGGTCTCATCTGTTC	EIN3-binding F-box protein 1-like
Traes_7BL_9ED99FB9E1-Reverse	GAGTGAGGGTGAGGTTTGTG	
Traes_7DS_E5A18AAA4-Forward	AAGTCCGACGTGTTCCAC	Transcription factor HBP-1b(c1)-like
Traes_7DS_E5A18AAA4-Reverse	ATATCAAGGTCGCTCAAGGTG	
TRAES3BF054800030CFD_g-Forward	CCGGCAAGATCTCCTTTACAG	DNA polymerase epsilon complex subunit
TRAES3BF054800030CFD_g-Reverse	AGAGGCAATGGACACAGATG	
TRAES3BF082400010CFD_g-Forward	ATCCATCTTTCCACCCTTCAC	NADP-dependent malic enzyme 1
TRAES3BF082400010CFD_g-Reverse	GCTCTCCGCATATTTCTCCAG	