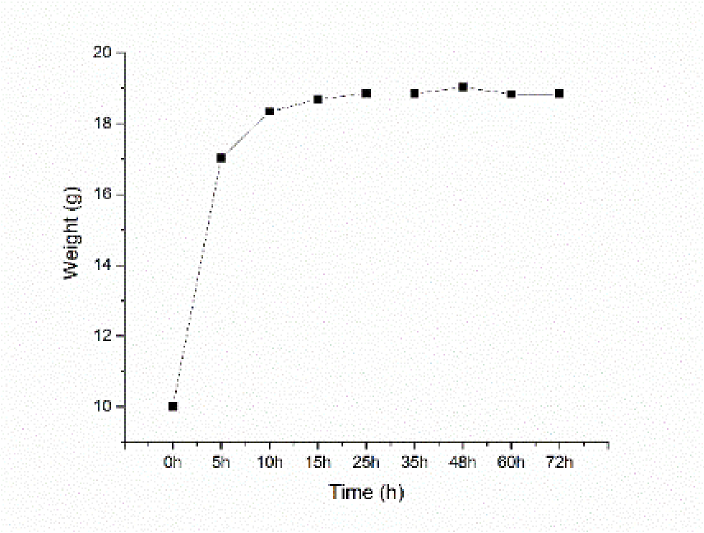
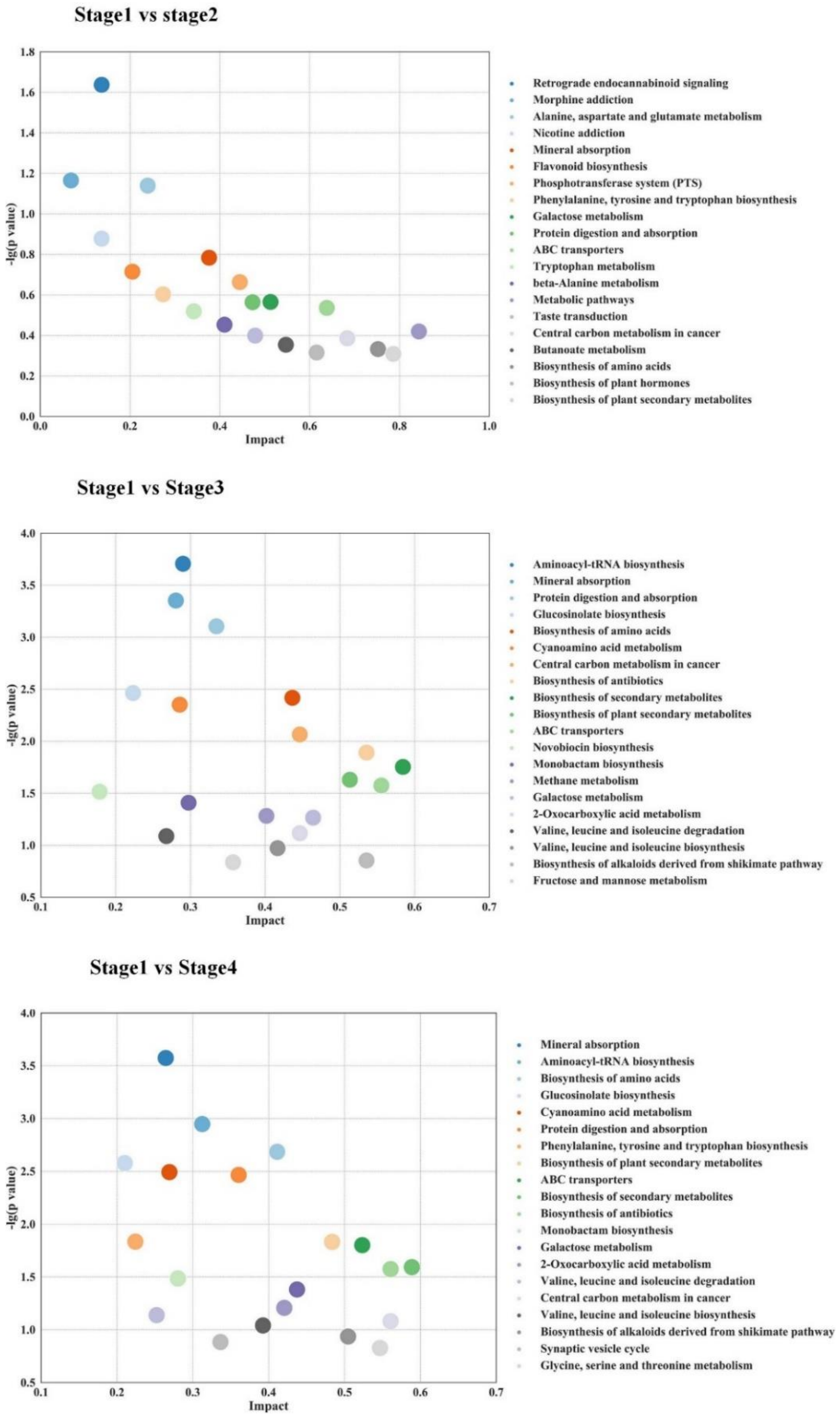
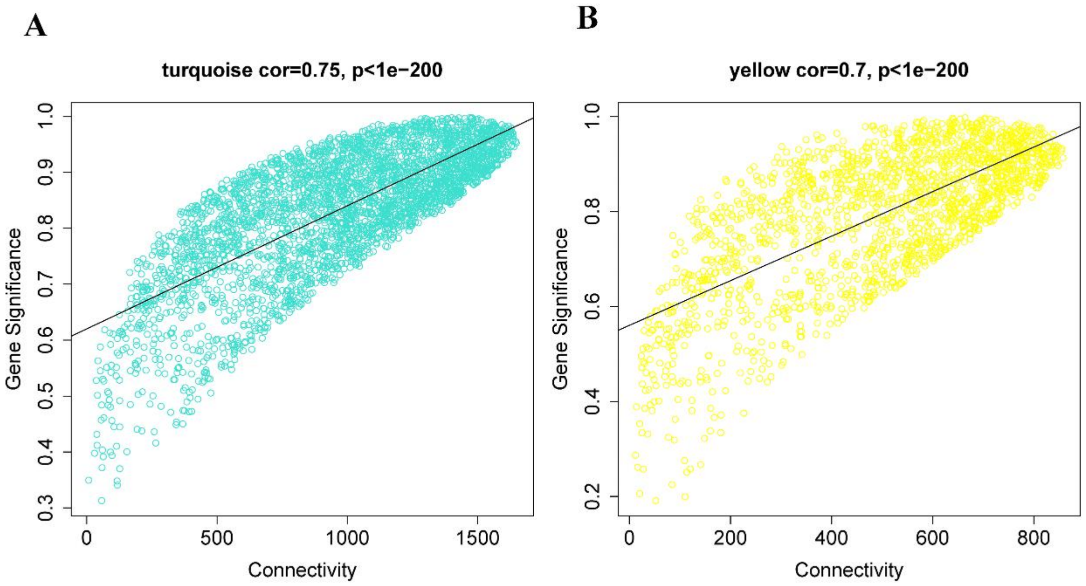


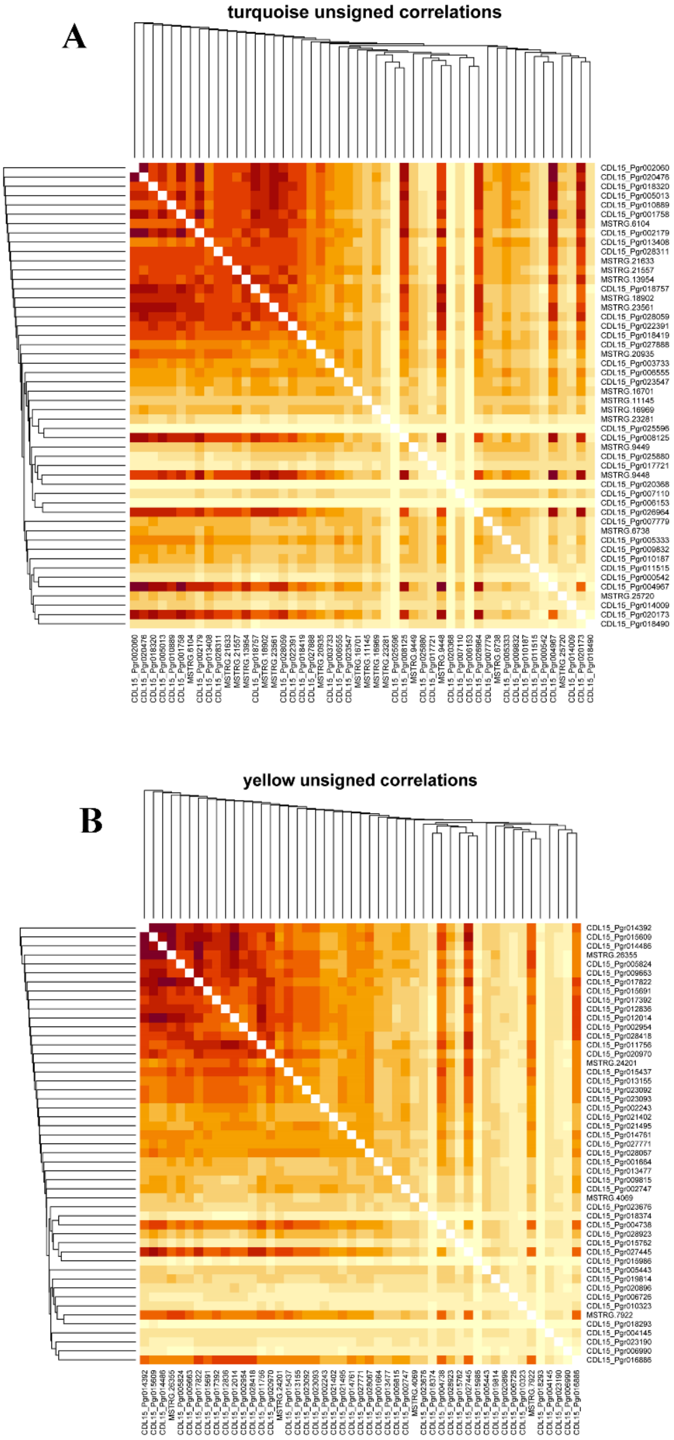
Appendix A Development of water absorption of pomegranate seed during the germination.



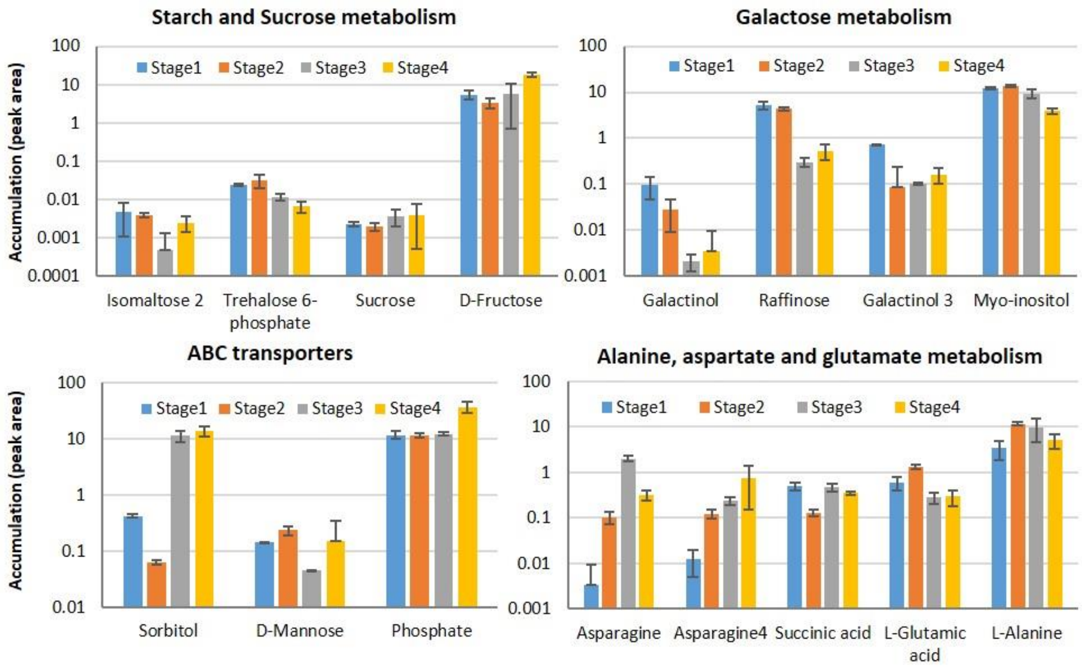
Appendix B Top 20 enriched KEGG pathways of differentially accumulating metabolites during *Punica granatum* seed germination.



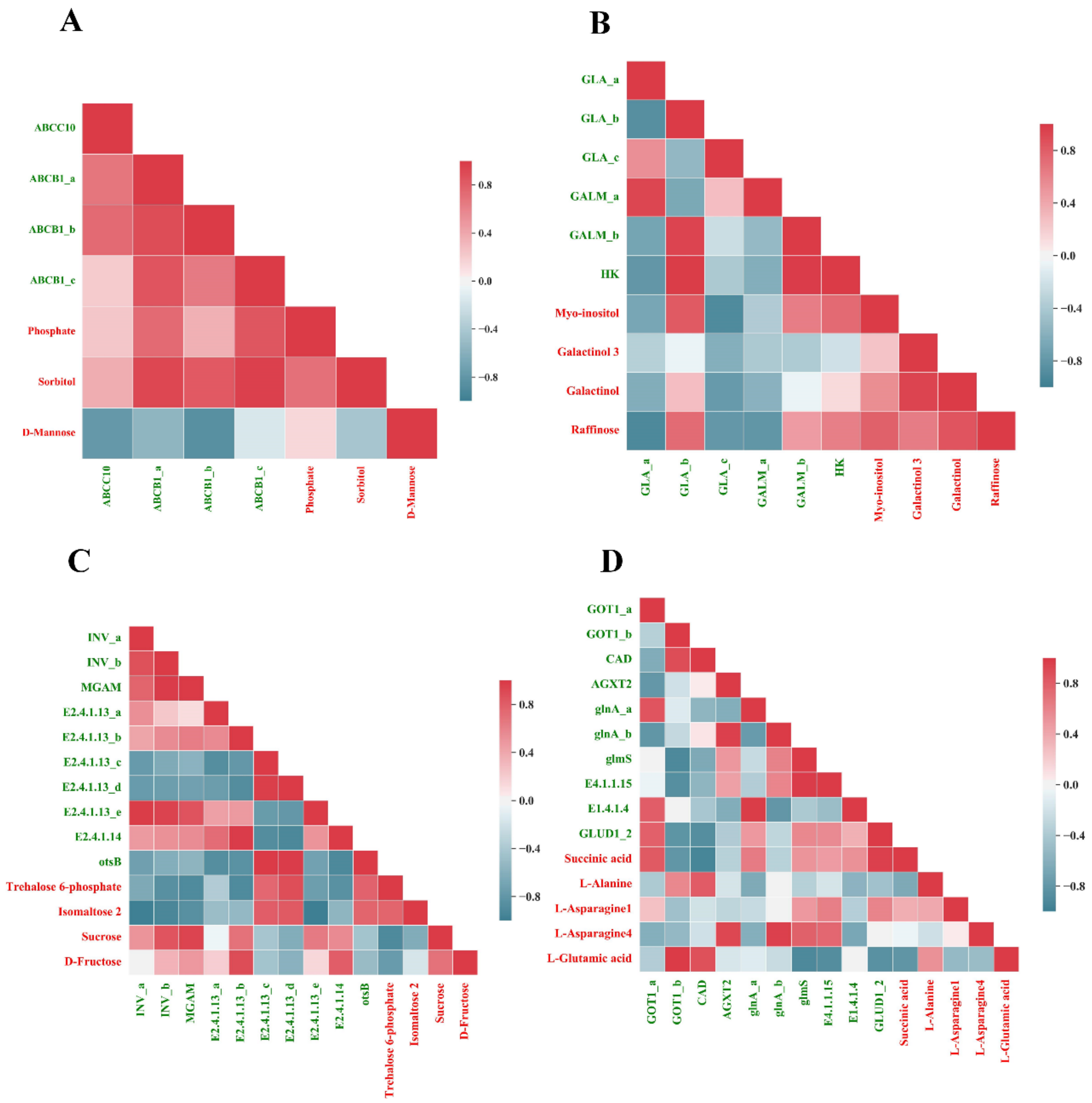
Appendix C Gene associated within modules related with the early and late stage of the germination: **(A)** Turquoise module and **(B)** Yellow module.



Appendix D Top 50 hub genes with the highest internal connectivity in the module: **(A)** Turquoise module and **(B)** Yellow module. The darker the color is the higher the topological overlap and the higher the connectivity of genes.



Appendix E Accumulation of metabolites associated with four important primary metabolic pathways.



Appendix F Pearson's correlation plot based on the correlations of metabolites with the genes in the four primary metabolic pathways: **(A)** ABC transporters, **(B)** Galactose metabolism, **(C)** Starch and sucrose metabolism, and **(D)** Alanine, aspartate and glutamate metabolism. The red and green colors represent positive and negative correlations, respectively. The darker the color is, the stronger the correlation coefficient. The green names represent metabolites, and the red names represent genes.

Appendix G Expression profiles of differentially expressed genes (DEGs) and differentially accumulated metabolites (DAMs) (|log2(FC)| > 1, FDR < 0.001) involved in the flavonoid biosynthesis pathway.

DEG/DAM	**ID**	**Stage1**	**Stage2**	**Stage3**	**Stage4**
DEGs					
CYP73A	MSTRG.2101	0.36	0.84	1.27	0.36
CHS_a	CDL15_Pgr014039	0.27	152.01	598.01	768.17
CHS_b	CDL15_Pgr026373	0.18	1.70	7.04	9.26
E5.5.1.6_a	CDL15_Pgr022663	0.01	1.19	3.56	19.90
E5.5.1.6_b	CDL15_Pgr025966	4.98	14.63	34.38	38.44
E5.5.1.6_c	CDL15_Pgr022664	18.10	3.42	2.77	2.03
E5.5.1.6_d	CDL15_Pgr013918	0.90	0.39	0.14	0.81
F3H	CDL15_Pgr020918	0.42	0.16	0.76	3.59
DFR	MSTRG.15098	0.00	0.53	4.03	11.92
FLSI	CDL15_Pgr003851	5.22	80.11	67.92	66.60
ANS	CDL15_Pgr017842	9.68	14.97	30.95	30.95
DAMs					
Prunin		1.13	0.55	0.17	0.03