

Supplementary information

Transcriptomic responses to biotic stresses in *Malus x domestica*: a meta-analysis study

Bipin Balan¹, Franco Marra¹, Tiziano Caruso¹, Federico Martinelli¹

¹Dipartimento di Scienze Agrarie e Forestali, Università degli Studi di Palermo, Palermo,
Italy

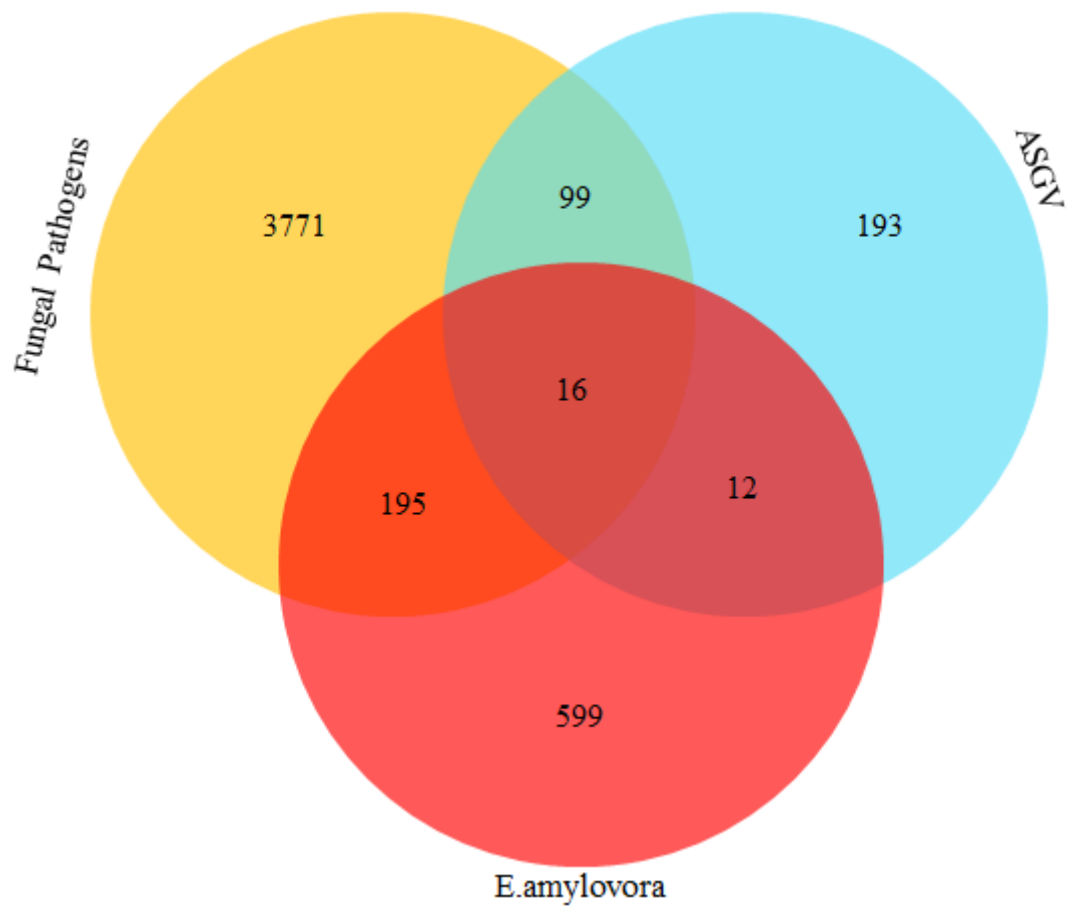


Figure S1. Venn diagram showing the number of specifically and commonly regulated genes for each biotic stresses: Fungal Pathogens, Apple stem grooving virus (ASGV) and Erwinia amylovora (E. amylovora).

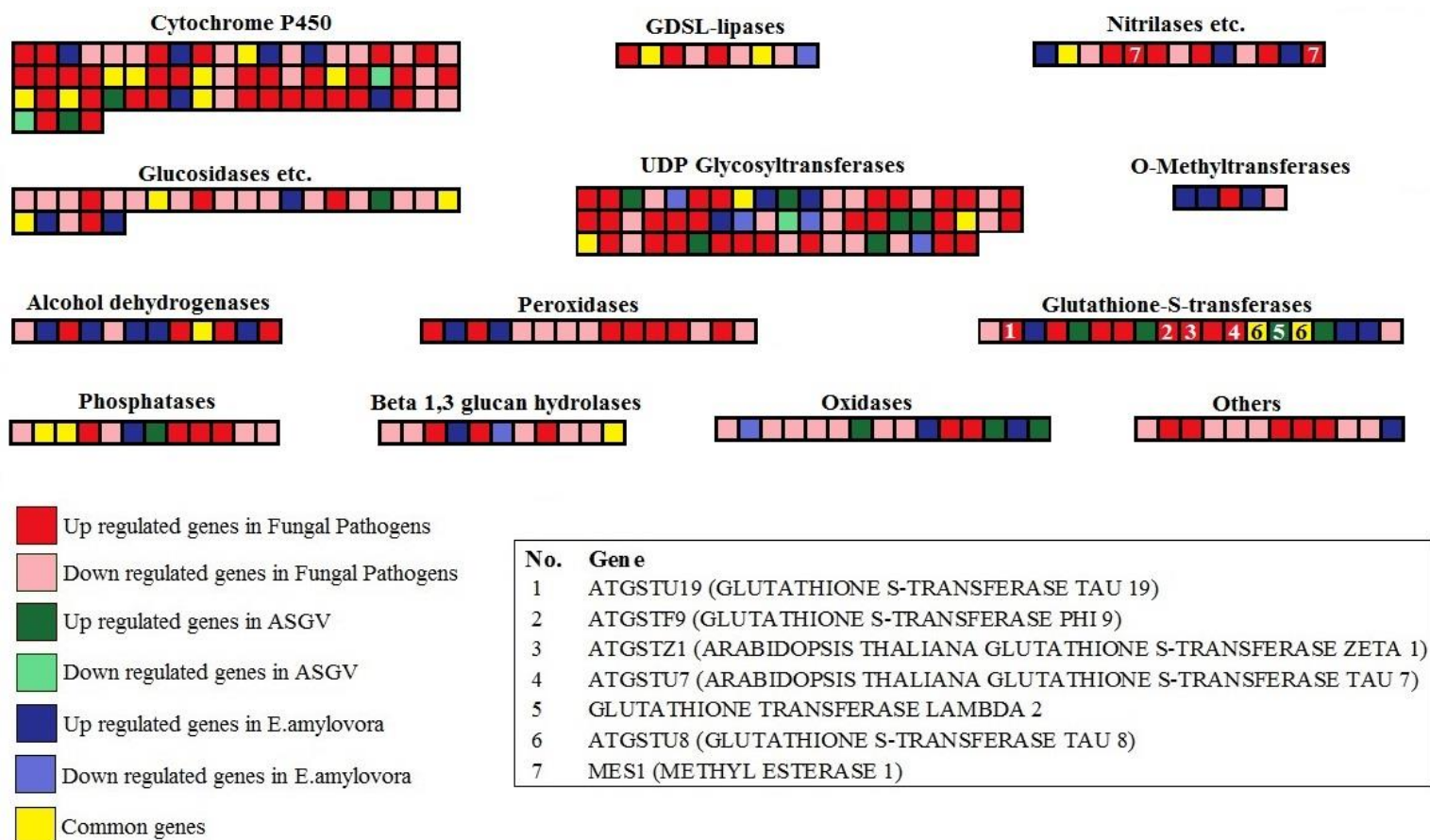
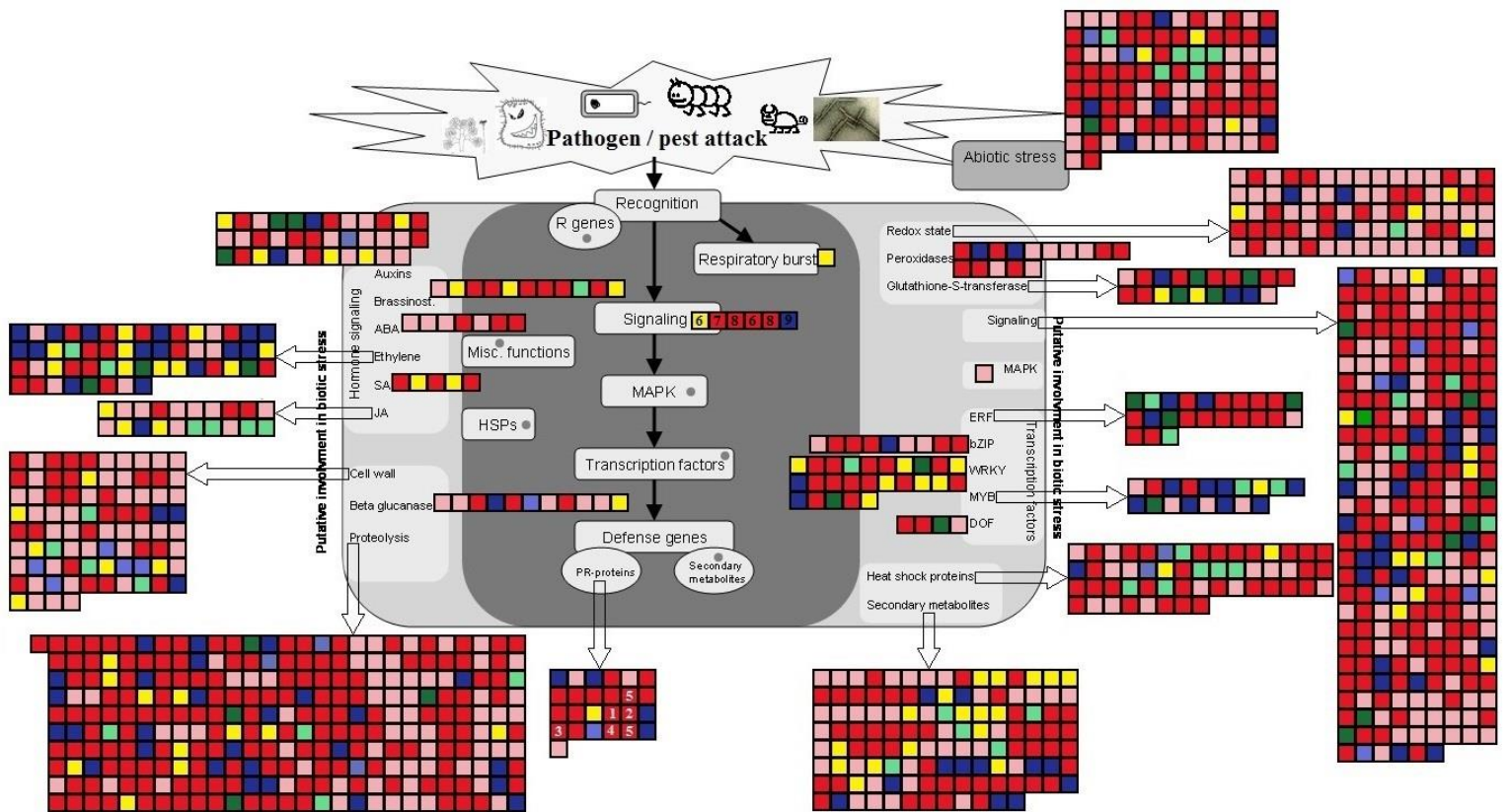


Figure S2. Genes involved in detoxifying pathways and encoding enzymes belonging to different large families. The key genes explained in the manuscript were highlighted in the figure.



- Up regulated genes in Fungal Pathogens
- Down regulated genes in Fungal Pathogens
- Up regulated genes in ASGV
- Down regulated genes in ASGV
- Up regulated genes in E.amylovora
- Down regulated genes in E.amylovora
- Common genes

No.	Gene
1	disease resistance protein (TIR class), putative
2	disease resistance protein (CC-NBS-LRR class), putative
3	ADR1-L1 (ADR1-like 1); ATP binding / protein binding
4	RPP1 (recognition of peronospora parasitica 1); LRR domain binding
5	ATP binding / protein binding / transmembrane receptor
6	MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding
7	MLO3 (MILDEW RESISTANCE LOCUS O 3)
8	MLO1; calmodulin binding
9	MLO12 (MILDEW RESISTANCE LOCUS O 12)

Figure S3. Biotic stress mapman overview showing genes differentially expressed in the 7 transcriptomic articles and divided in three types of stresses and 7 categories depending on their trend of expression. The key genes explained in the manuscript were indicated in the figure.