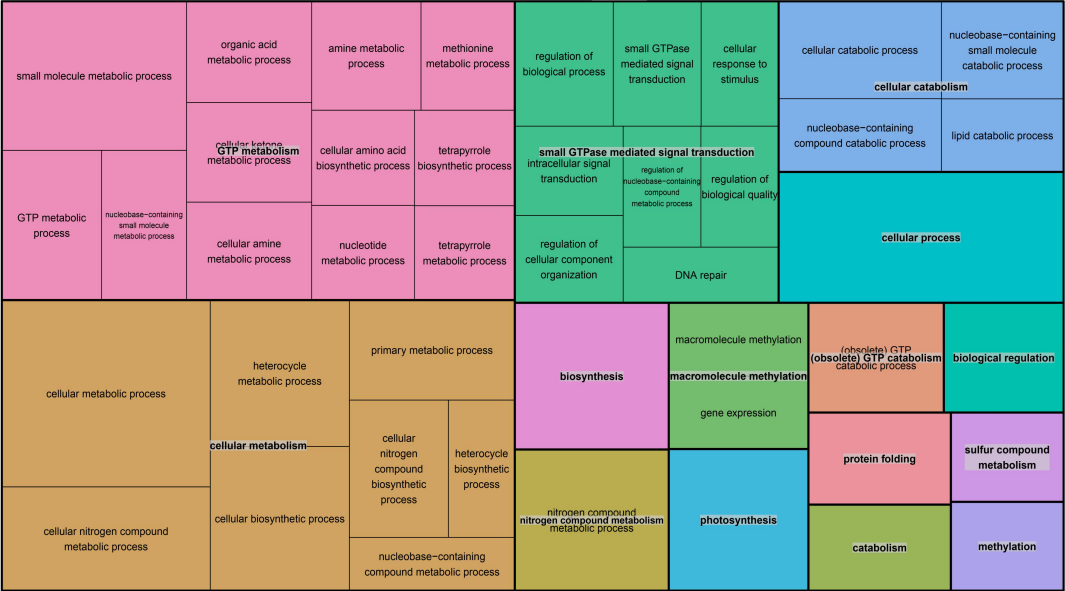
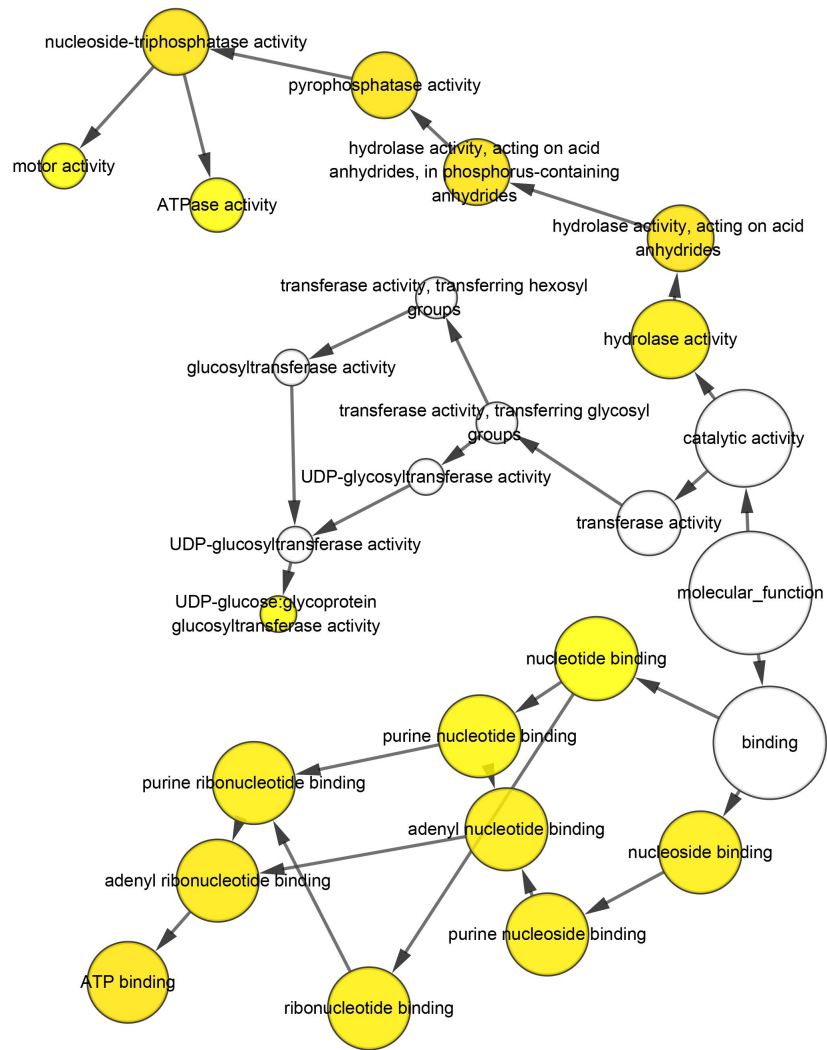


**Figure S1 Correlation analysis between RNA-sequencing and RT-qPCR of three representative genes**

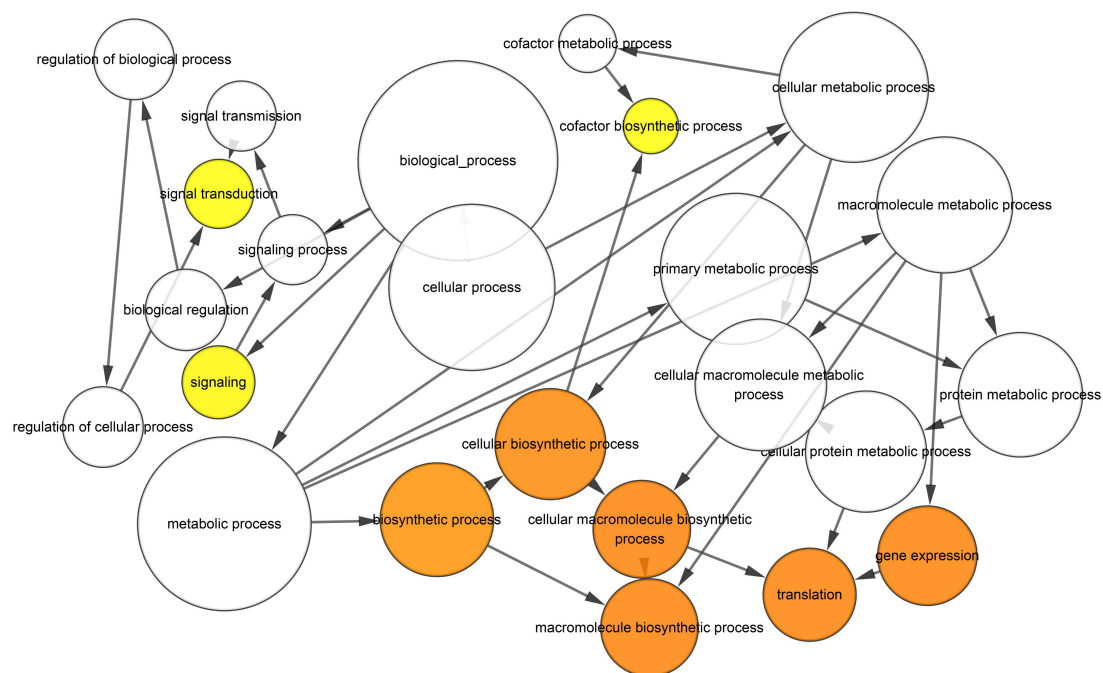
J\_1 ( or SJ\_1): samples from ‘Jonathan’ (or ‘Sweet Jonathan’) and sampled at 30 days after bloom (30 DAB); J\_2 (SJ\_2) : samples from ‘Jonathan’ ( or ‘Sweet Jonathan’) and sampled at 90 days after bloom (90 DAB); J\_3 (SJ\_3): samples from ‘Jonathan’ (or ‘Sweet Jonathan’) and sampled at 140 days after bloom (140 DAB);



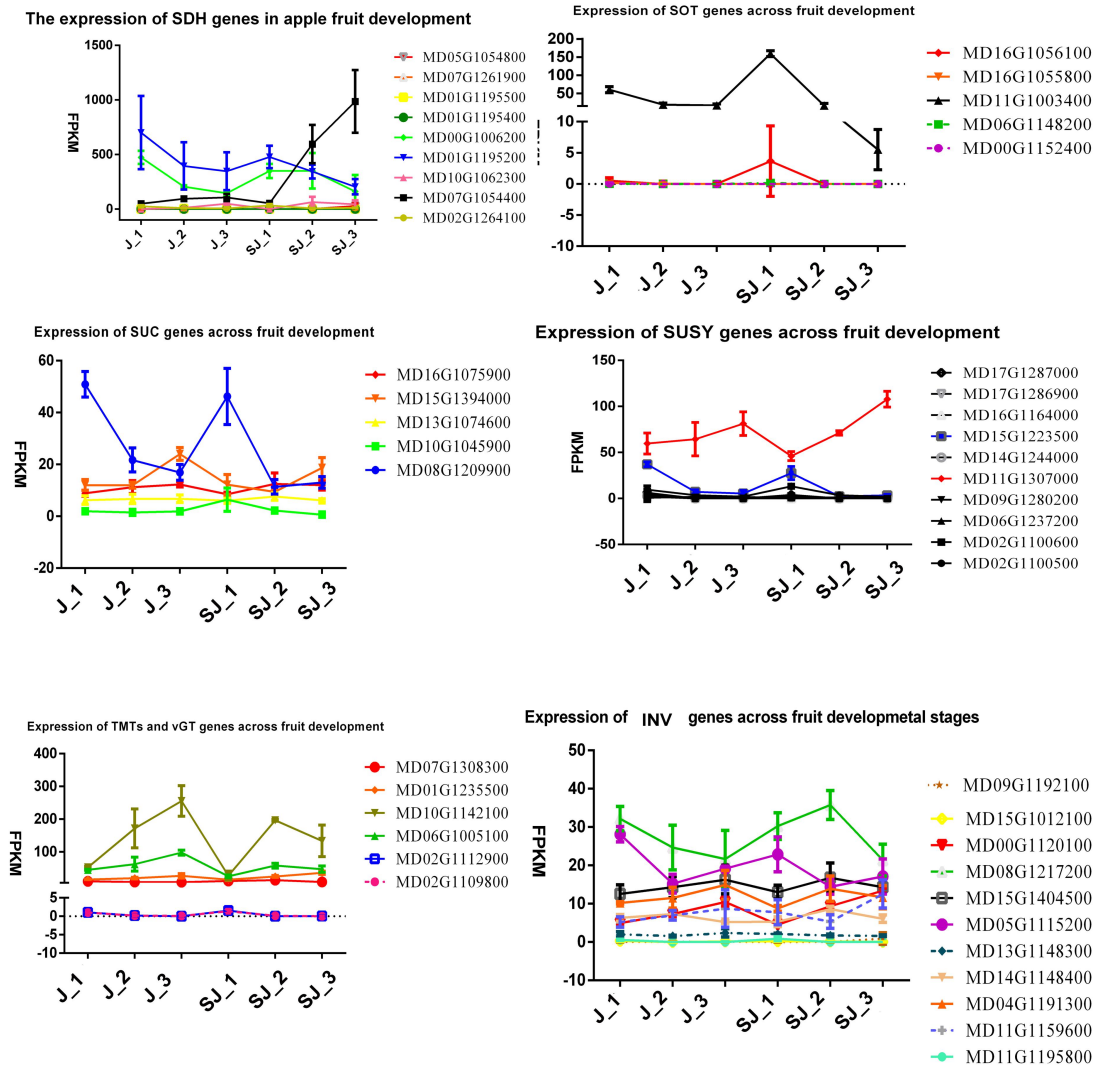
**Figure S2** Treemap of the enriched gene ontology (GO) terms ( $P$  value  $<0.01$ ) in co-expression module M26



**Figure S3 Enriched GO terms ( $P < 0.05$ ) in the top 100 hub genes of M19**



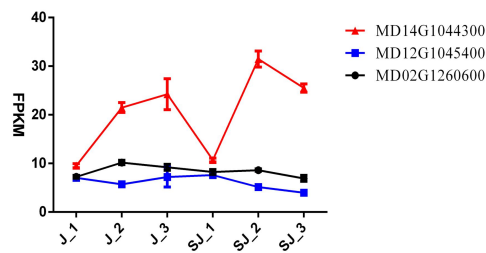
**Figure S4 Significantly enriched GO terms (P value < 0.05) in the co-expression M8**



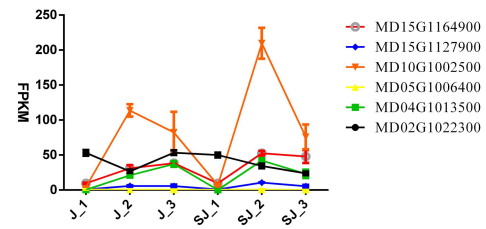
**Figure S5 Expression profile of important genes in the sugar accumulation during apple fruit development process**

J\_1 (or SJ\_1): samples from 'Jonathan' (or 'Sweet Jonathan') and sampled at 30 days after bloom (30 DAB); J\_2 (SJ\_2) : samples from 'Jonathan' (or 'Sweet Jonathan') and sampled at 90 days after bloom (90 DAB); J\_3 (SJ\_3): samples from 'Jonathan' (or 'Sweet Jonathan') and sampled at 140 days after bloom (140 DAB);

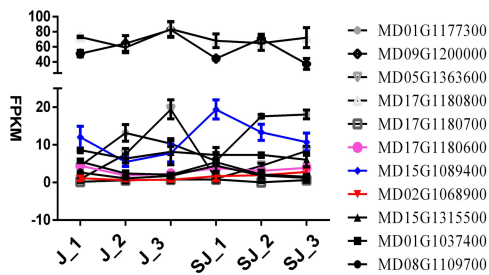
The expression of SPP genes in the apple fruit development



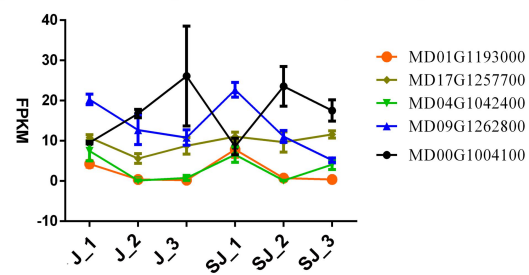
he expression of SPSA genes in the apple fruit development



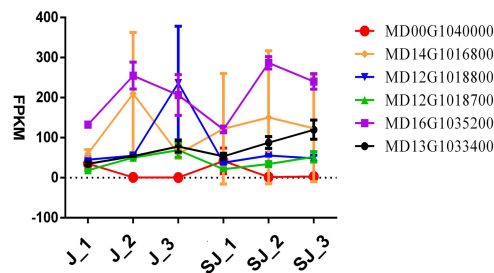
Expression of genes encoding 6-phosphofructokinase across fruit development stages



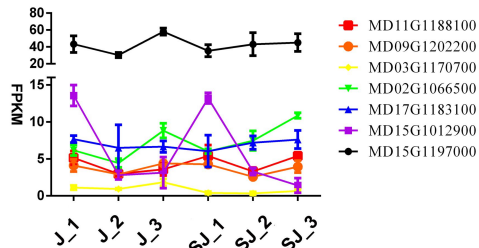
Expression of fructokinase genes across fruit development stages



Expression of fructose-bisphosphate aldolase genes across fruit developmental stages



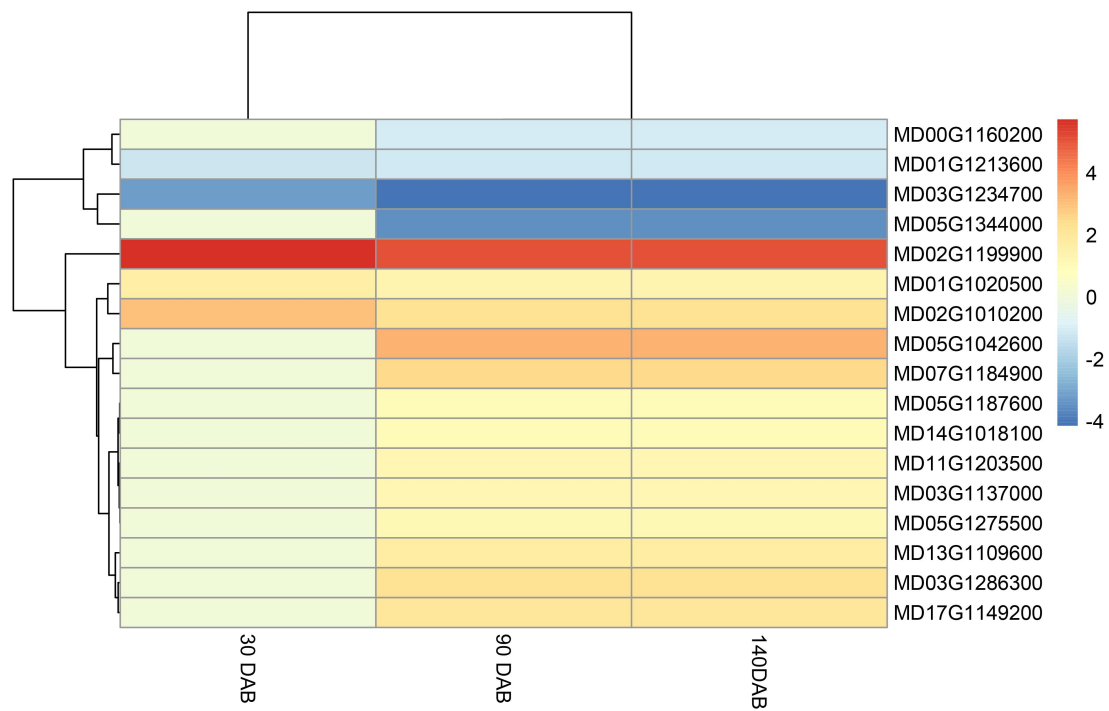
Expression of hexokinase genes across fruit development stages



**Figure S6 Expression profile of important genes in the sugar accumulation during apple fruit development process**

J\_1 ( or SJ\_1): samples from ‘Jonathan’ (or ‘Sweet Jonathan’) and sampled at 30 days after bloom (30 DAB); J\_2 (SJ\_2) : samples from ‘Jonathan’ ( or ‘Sweet Jonathan’) and sampled at 90 days after bloom (90 DAB); J\_3 (SJ\_3): samples from ‘Jonathan’ (or ‘Sweet Jonathan’) and sampled at 140 days after bloom (140 DAB);

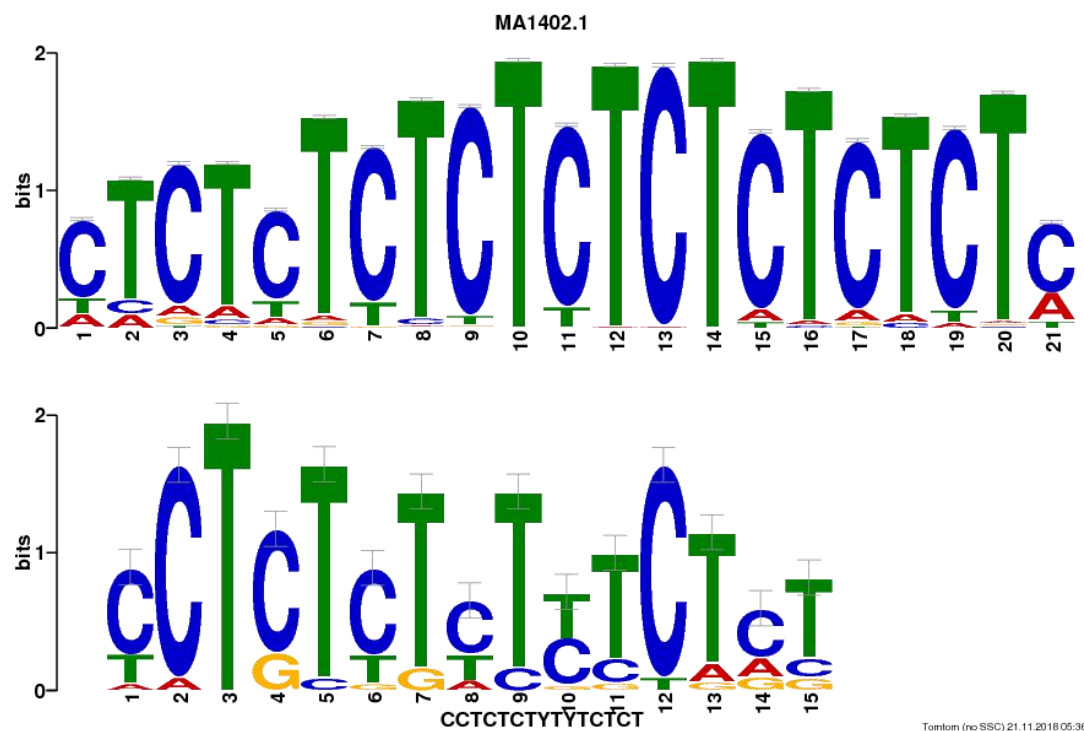




**Figure S8**

Heatmap shows the log<sub>2</sub>change fold ('Sweet Jonathan' vs 'Jonathan') of the differentially expressed ATP-binding cassette (ABC) transporter genes.





Tomtom (no SSC) 21.11.2018 05:36

**Figure S9a** TOMTOM motif alignment result of motif MA1402.1 and the consensus motif, detected in the 17 differentially expressed genes.

RT-qPCR relative expression of *Md*BPC6

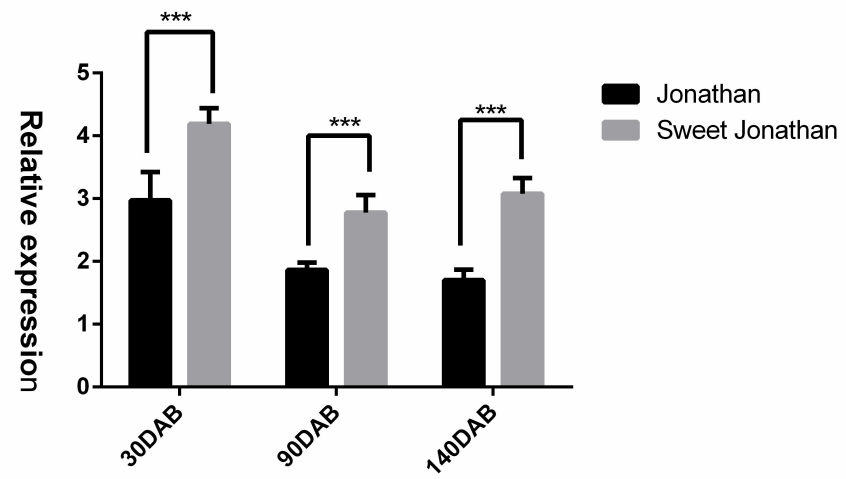
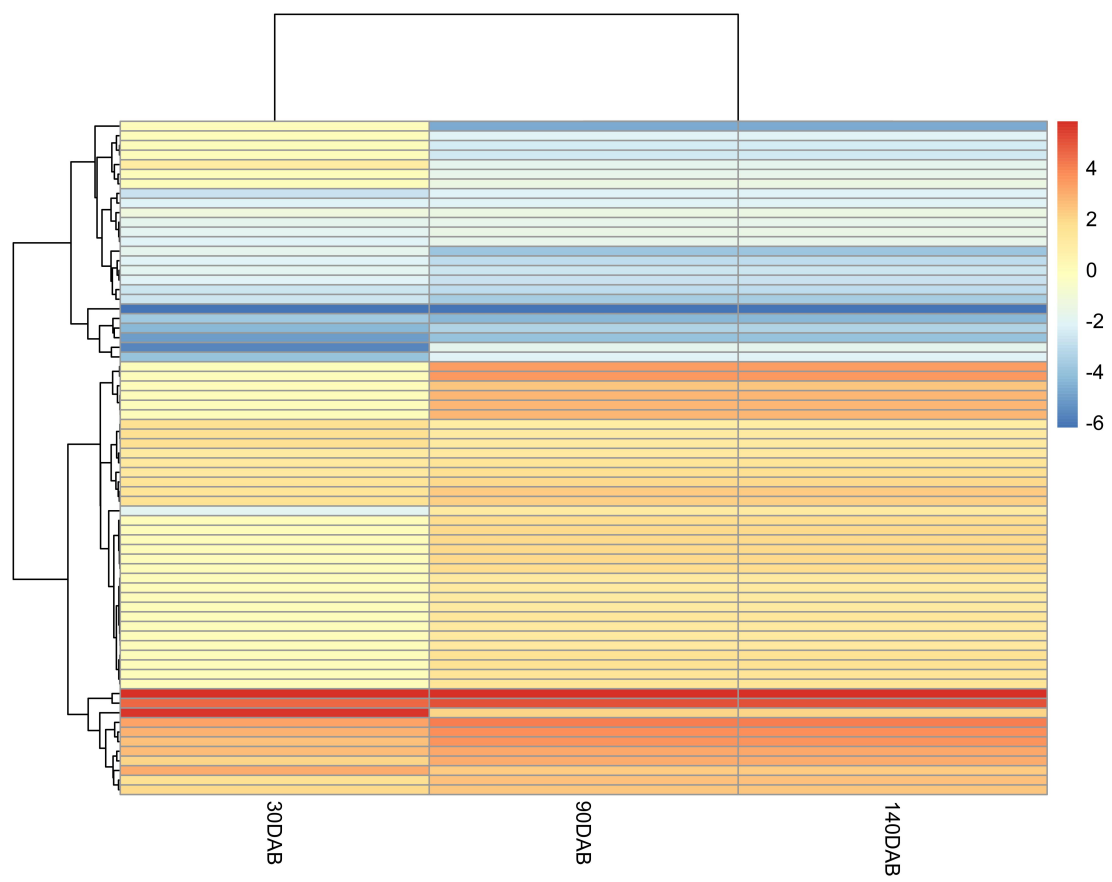


Figure S9b RT-qPCR relative expression of *Md*BPC6



**Figure S10 Heatmap shows the log2change fold ('Sweet Jonathan' vs 'Jonathan') of the differentially expressed disease resistant genes**