

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);

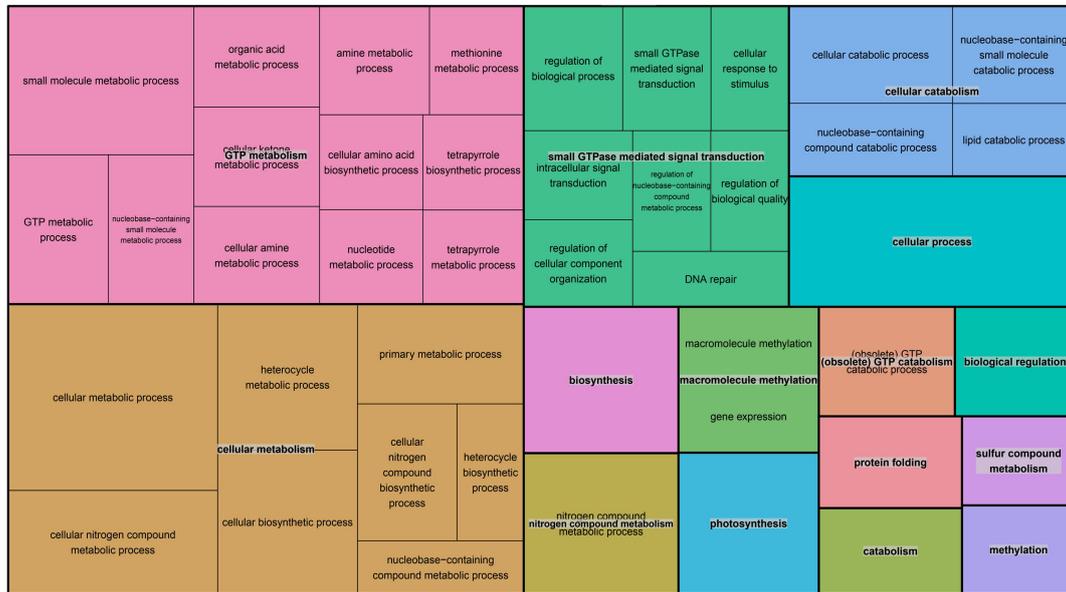


Figure S2 Treemap of the enriched gene ontology (GO) terms (P value <0.01) in co-expression module M26

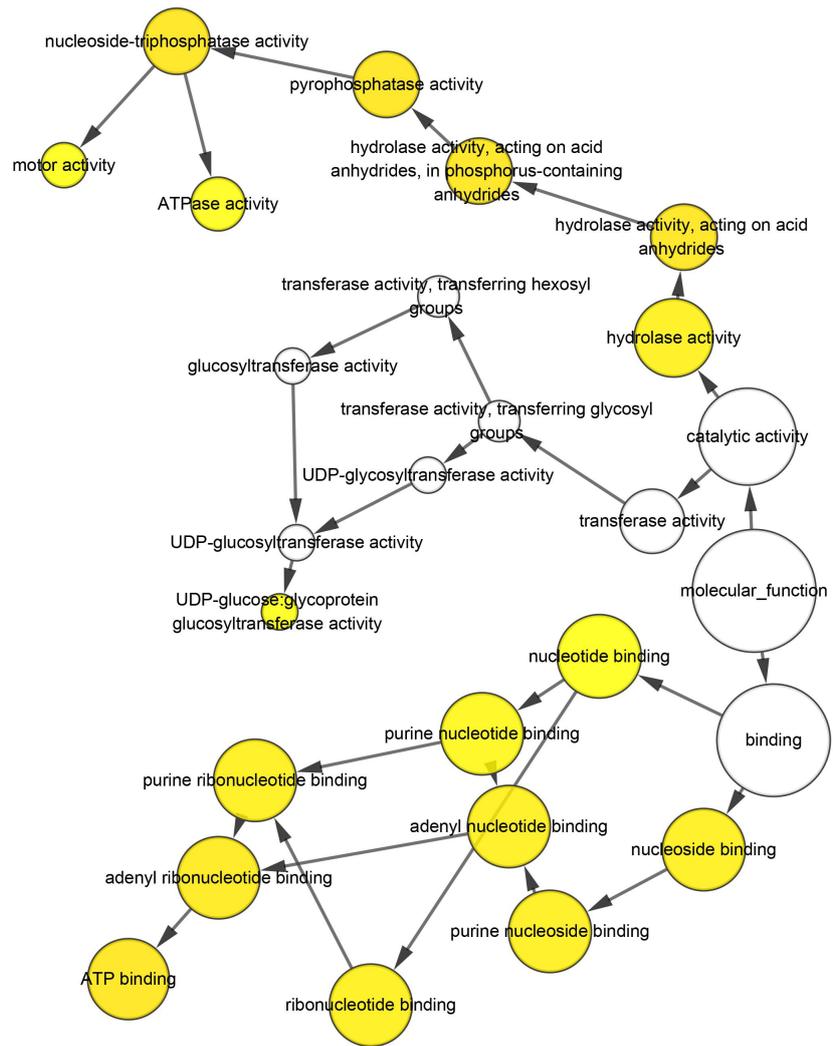


Figure S3 Enriched GO terms (P < 0.05) in the top 100 hub genes of M19

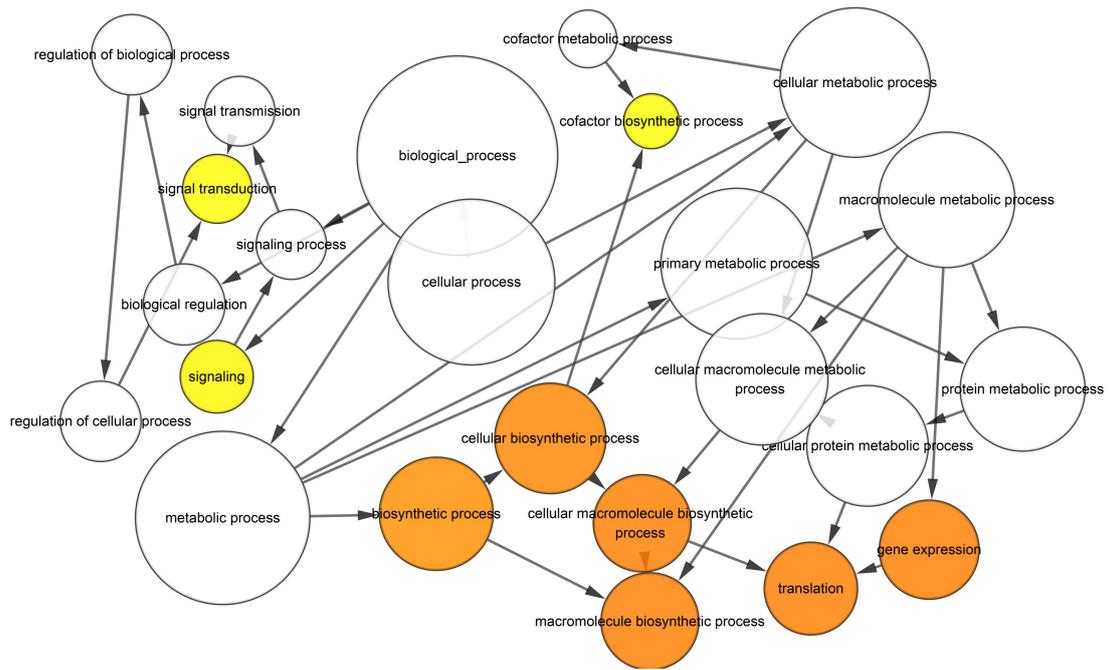
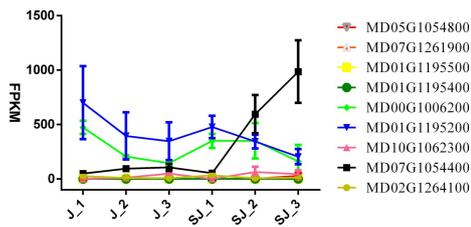
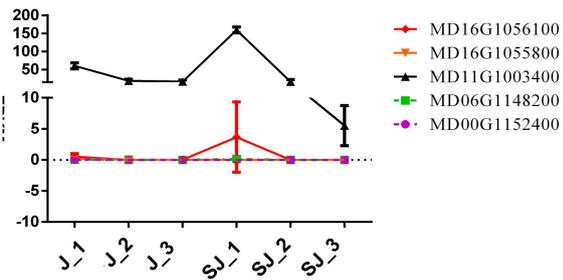


Figure S4 Significantly enriched GO terms (P value <0.05) in the co-expression M8

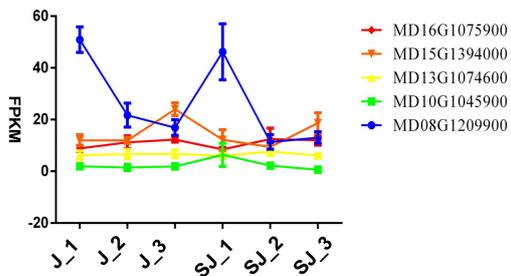
The expression of SDH genes in apple fruit development



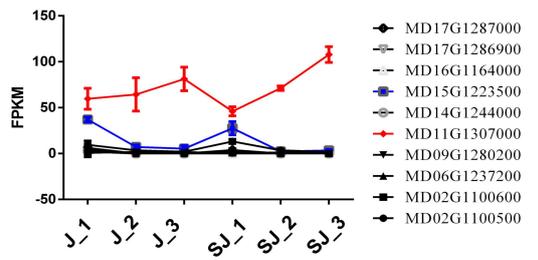
Expression of SOT genes across fruit development



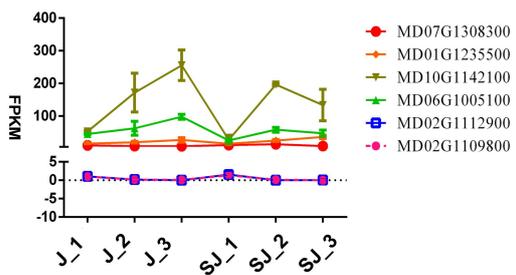
Expression of SUC genes across fruit development



Expression of SUSY genes across fruit development



Expression of TMTs and vGT genes across fruit development



Expression of INV genes across fruit developmental stages

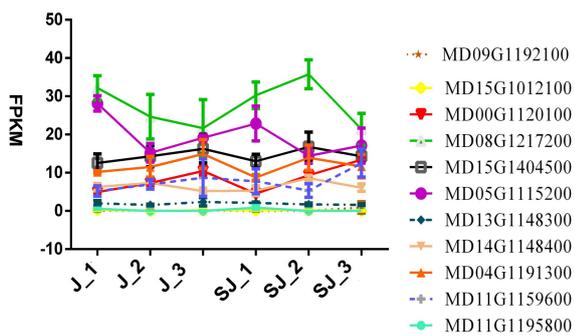
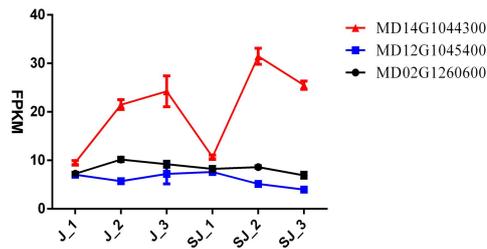


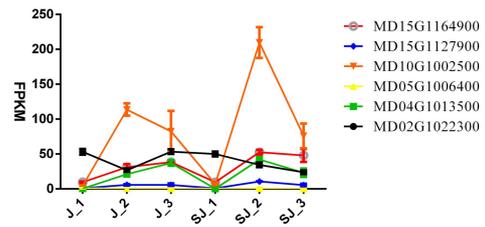
Figure S5 Expression profile of important genes in the sugar accumulation during apple fruit development process

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);

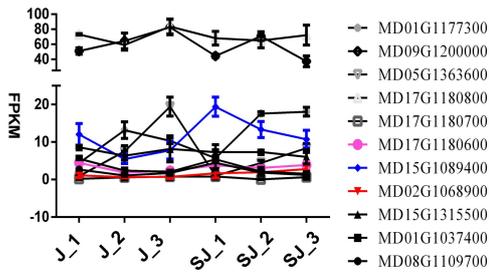
The expression of SPP genes in the apple fruit development



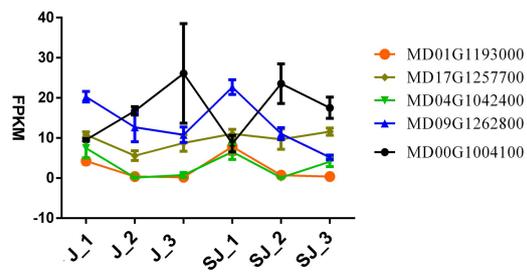
The expression of SPSA genes in the apple fruit development



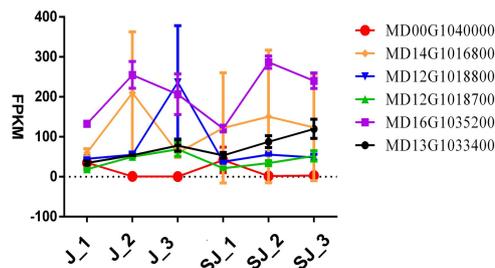
Expression of genes encoding 6-phosphofruktokinase across fruit development stages



Expression of fructokinase genes across fruit developmental stages



Expression of fructose-bisphosphate aldolase genes across fruit developmental stages



Expression of hexokinase genes across fruit developmental stages

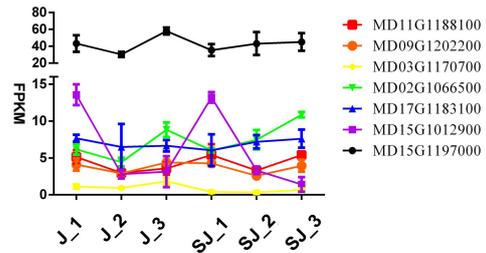


Figure S6 Expression profile of important genes in the sugar accumulation during apple fruit development process

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);

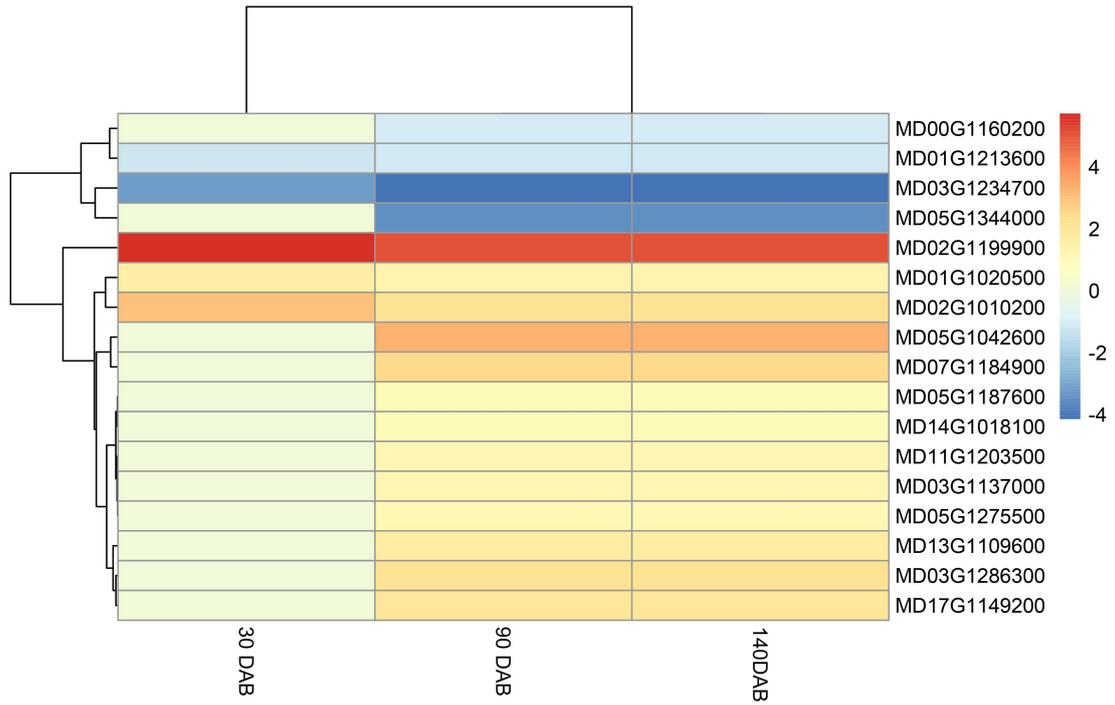
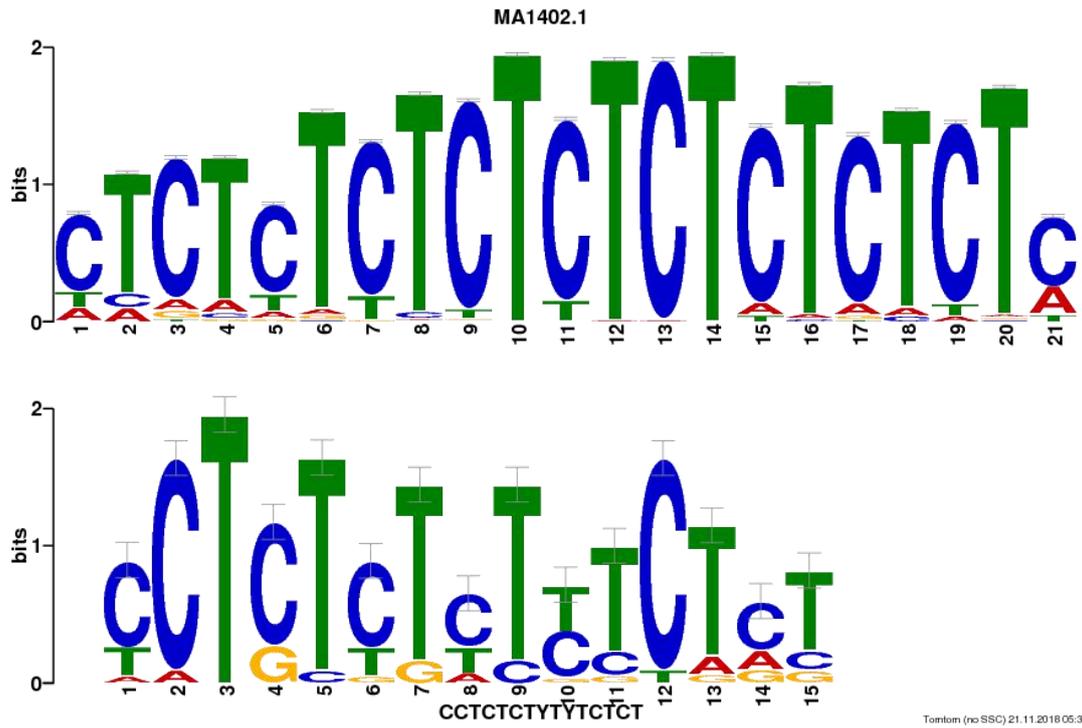


Figure S8

Heatmap shows the log₂ change fold ('Sweet Jonathan' vs 'Jonathan') of the differentially expressed ATP-binding cassette (ABC) transporter genes.



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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

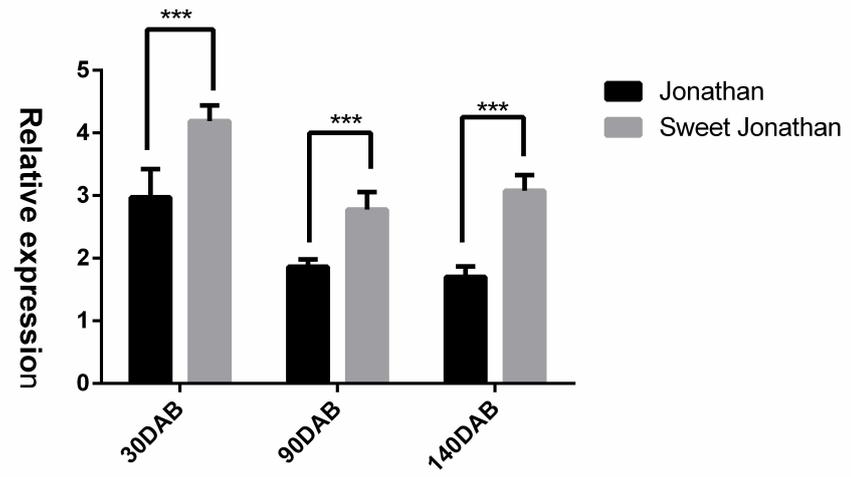


Figure S9b RT-qPCR relative expression of *Md*BPC6

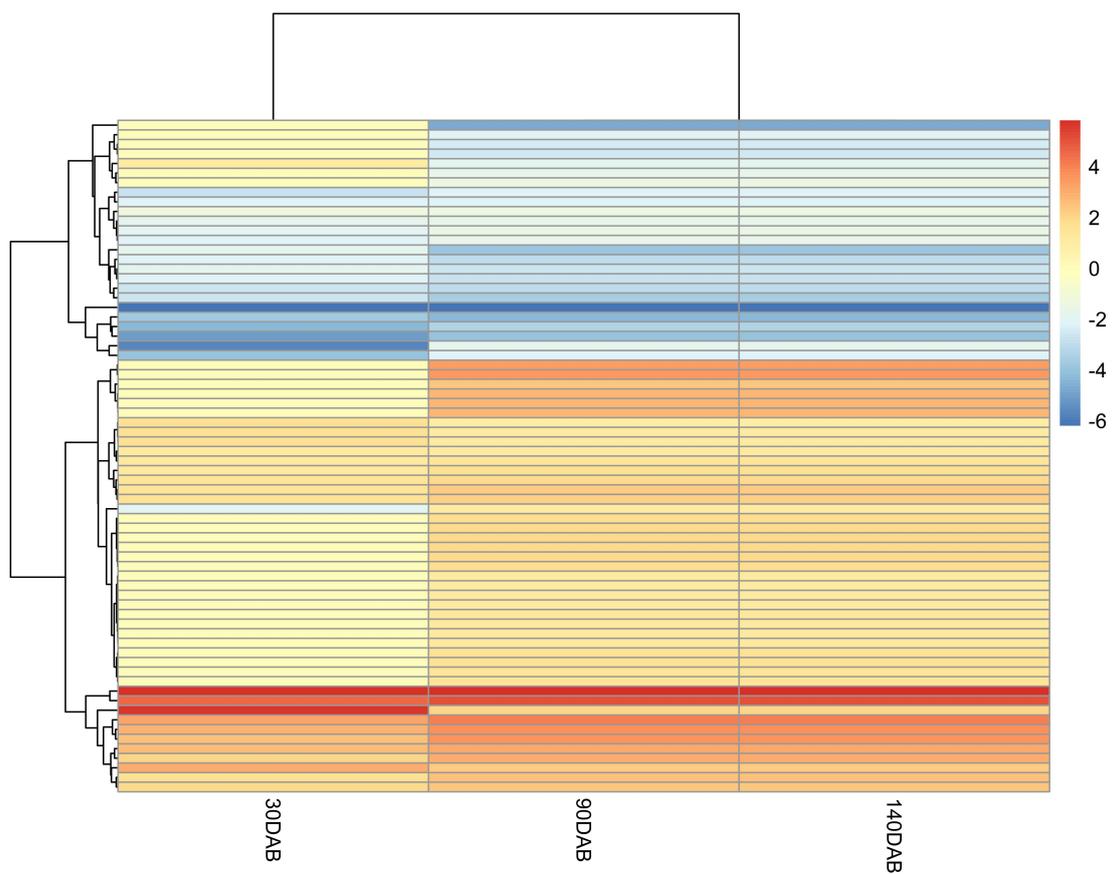


Figure S10 Heatmap shows the log₂change fold ('Sweet Jonathan' vs 'Jonathan') of the differentially expressed disease resistant genes