Title:

Integrative comparative analyses of metabolite and transcript profiles uncovers complex regulatory network in tomato (*Solanum lycopersicum L.*) fruit undergoing chilling injury

Authors:

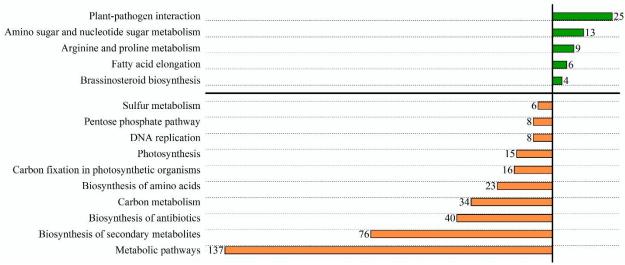
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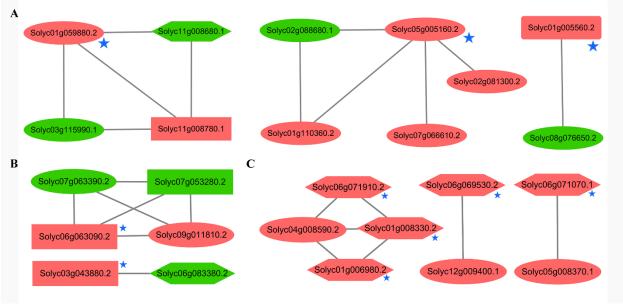
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Supplementary Fig. S1:



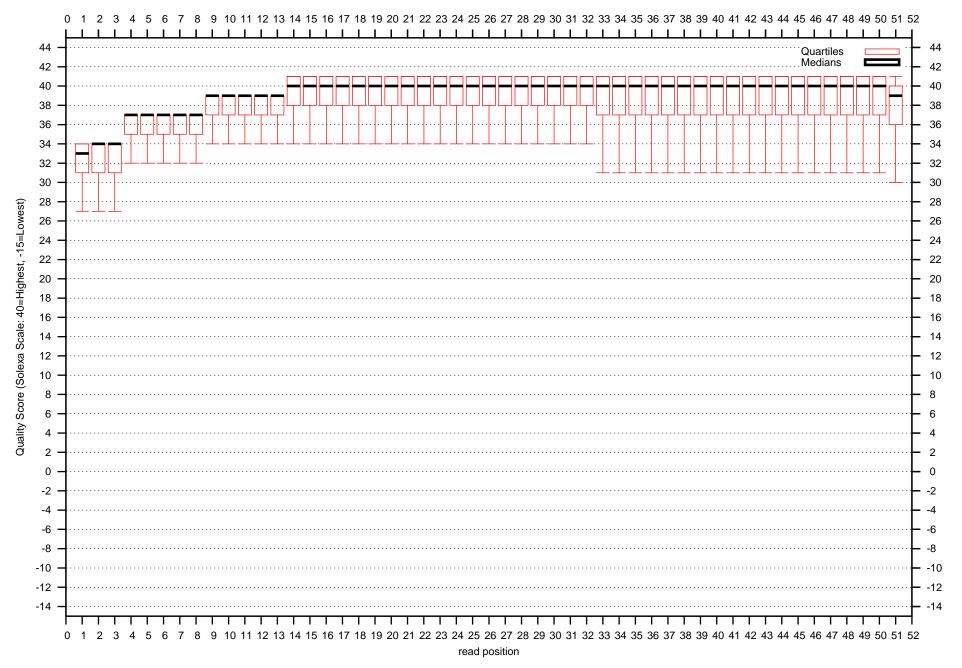
Supplementary Fig. S1: KEGG analysis of up-regulated genes (colored in orange) and down-regulated genes (colored in green).

Supplementary Fig. S2:

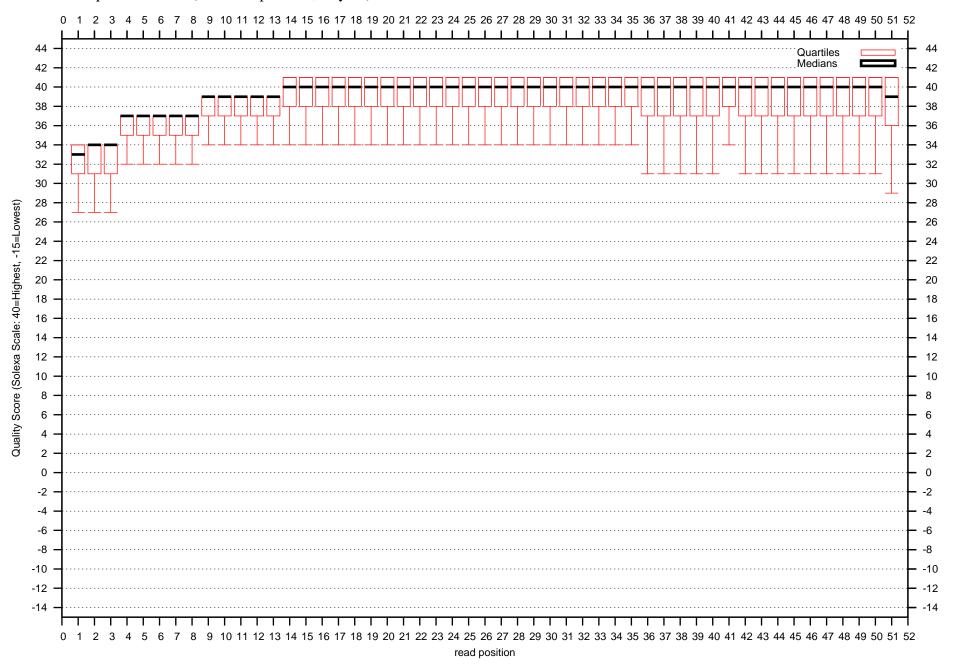


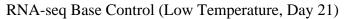
Supplementary Fig. S2: Co-expression analysis of genes involved in sugar and organic acid (A), amino acid (B) as well as fatty acid (C) schematic pathway. Up-regulated genes were colored in red while down-regulated genes were colored in green.

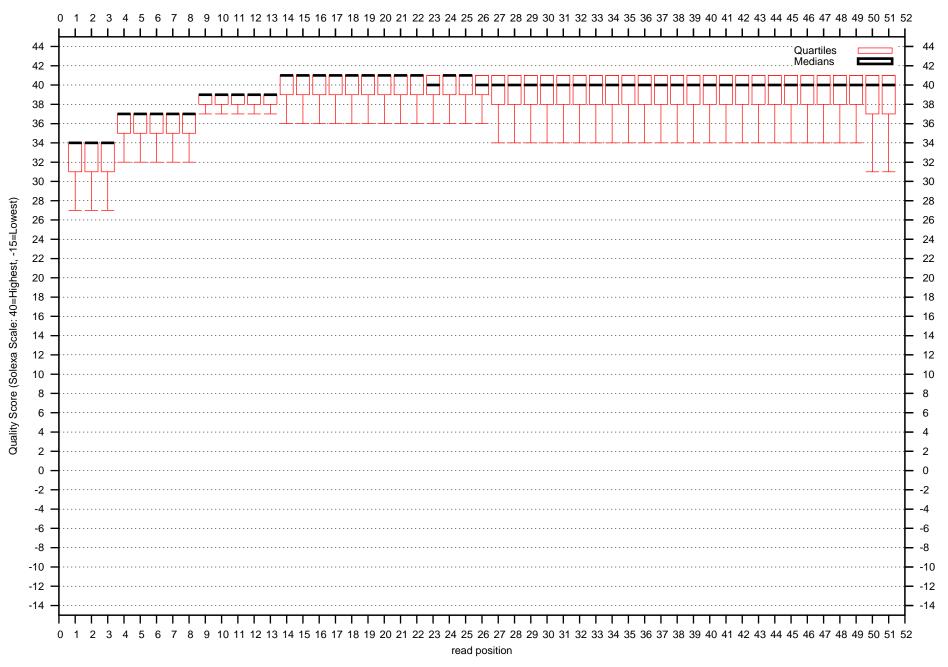
RNA-seq Base Control (Low Temperature, Day 7)



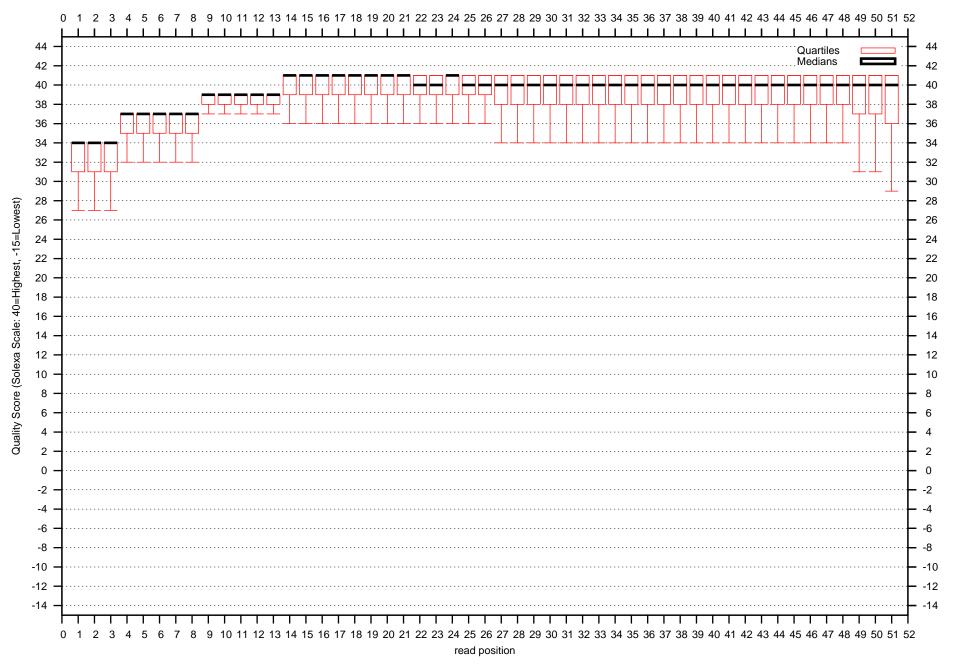






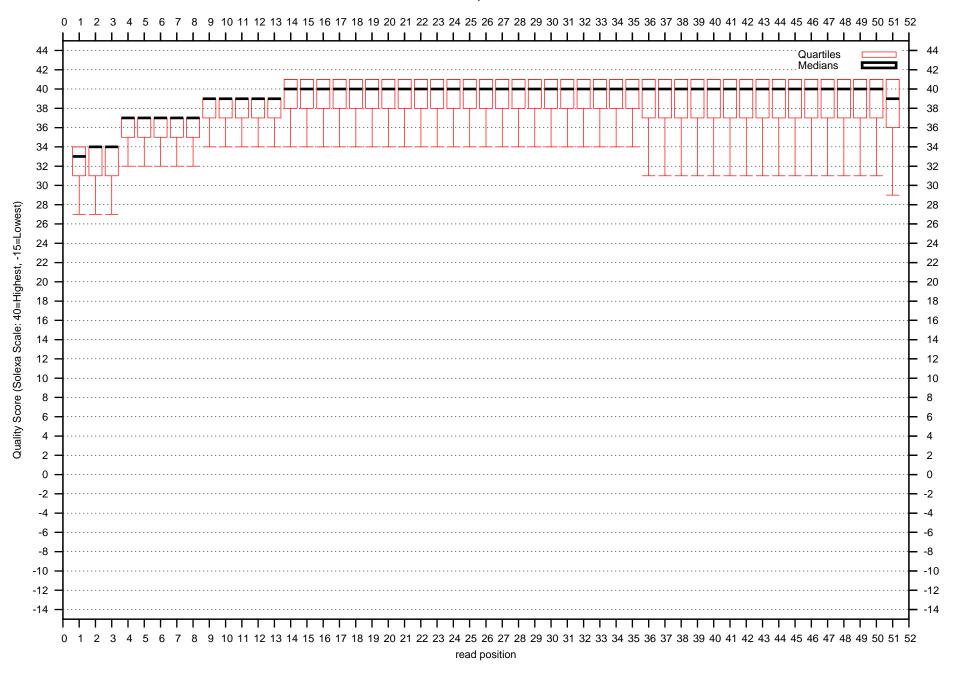






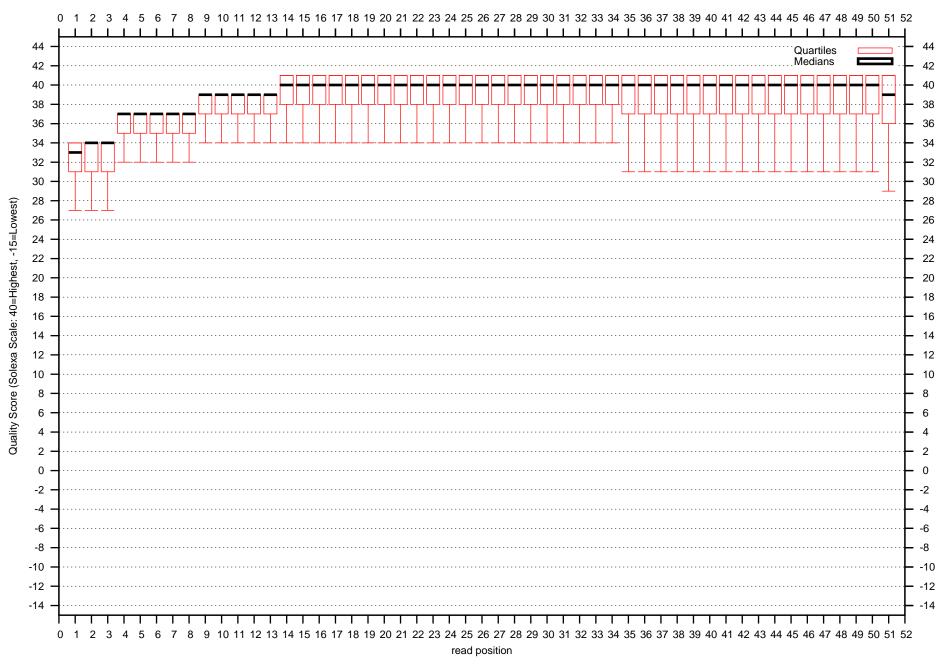


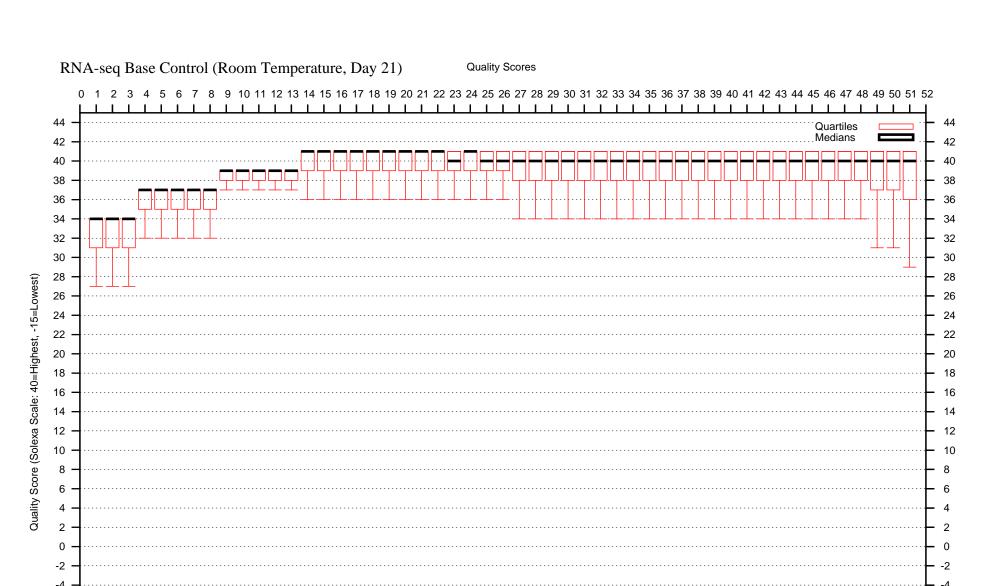










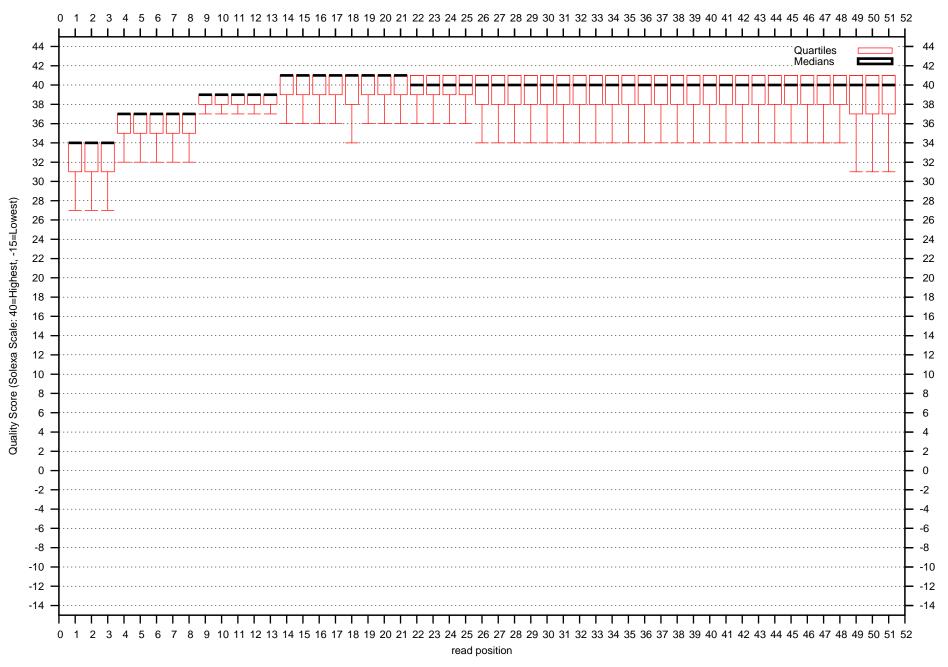


read position

-12







RNA-seq reads quality of room temperature (RT) and low temperature (LT) on day 7, 14, 21 and 28. Raw data has been filtered to get clean data and Q20 correspond to 1 in 100 error probability.

Sample Name	Raw Reads Number	Raw Base number (bp)	≥ Q20(%)	Clean Reads Number	Clean Base Number (bp)	≥ Q20(%)
RT-7d	18181514	927257214	98.25	16705619	830158190	98.7
RT-14d	18681722	952767822	98.27	17142445	851827204	98.69
RT-21d	19558618	997489518	98.66	17920013	890635024	99.02
RT-28d	16323527	832499877	98.67	14992449	745662775	99.02
LT-7d	29983796	1529173596	98.19	27561428	1370110456	98.64
LT-14d	20394797	1040134647	98.3	18770644	933444094	98.7
LT-21d	18864564	962092764	98.66	17338724	862492901	99.05
LT-28d	15787151	805144701	98.63	14499691	720972504	99.03