

Table S1. Summary statistics of RNA-seq data of the 9 libraries mapped to the tomato reference genome (*Solanum lycopersicum* ITAG4.0).

Samples	WT			SIHB8-ox			SIHB8-cr		
Library	WT-1	WT-2	WT-3	HB8-ox-1	HB8-ox-2	HB8-ox-3	SIHB8-cr-1	SIHB8-cr-2	SIHB8-cr-3
Clean reads	50428308	49843612	53550906	49366488	45490476	39049388	43901952	63555660	49914082
High quality clean reads (%)	50336792 (99.82%)	49761328 (99.83%)	53457896 (99.83%)	49276912 (99.82%)	45419064 (99.84%)	38982904 (99.83%)	43826050 (99.83%)	63450750 (99.83%)	49845336 (99.86%)
Removed rRNA reads (%)	50188458 (99.71%)	49628866 (99.73%)	53313056 (99.73%)	49143478 (99.73%)	45302194 (99.74%)	38879150 (99.73%)	43712426 (99.74%)	63292294 (99.75%)	49710888 (99.73%)
Mapped reads (%)	48861307 (97.36%)	48326637 (97.38%)	51861046 (97.28%)	47706778 (97.08%)	44064712 (97.27%)	37727049 (97.04%)	42601874 (97.46%)	61843685 (97.71%)	48411175 (97.39%)
Unique mapped reads (%)	47717462 (95.08%)	47197528 (95.10%)	50647131 (95.00%)	46514713 (94.65%)	42962616 (94.84%)	36785345 (94.61%)	41597363 (95.16%)	60333093 (95.32%)	47246911 (95.04%)
Multiple mapped reads	1143845 (2.28%)	1129109 (2.28%)	1213915 (2.28%)	1192065 (2.43%)	1102096 (2.43%)	941704 (2.42%)	1004511 (2.30%)	1510592 (2.39%)	1164264 (2.34%)
All genes	22546 (64.97%)	22534 (64.94%)	22644 (65.25%)	22568 (65.03%)	22414 (64.59%)	22265 (64.16%)	22447 (64.69%)	22885 (65.95%)	22593 (65.11%)
Known genes (%)	21968 (64.47%)	21961 (64.45%)	22063 (64.75%)	21985 (64.52%)	21831 (64.07%)	21681 (63.63%)	21870 (64.18%)	22307 (65.46%)	22016 (64.61%)
Novel transcripts	578	573	581	583	583	584	577	578	577