

Table 1 Reference-guided assembly metrics. Illumina reads were mapped to the published H1706 reference genome. *S. gal* = *S. galapagense*; *S. pim* = *S. pimpinellifolium*.

Reference-guided assembly	<i>S. lycopersicum</i>		Wild species	
	H1706	YP-1	<i>S. gal</i>	<i>S. pim</i>
filtered reads in millions	462.7	420.3	363.9	281.5
mapped reads (%mapped)	426.1 (92.1%)	393.1 (93.5%)	324.7 (89.0%)	247.7 (88.0%)
coverage depth	39.3x	45x	32x	25x
coverage of tomato gen	99.2%	99.3%	95.4%	95.0%
no of gaps (total size in mb)	76,276 (5.9)	51,980 (5.4)	227,699 (36.1)	209,919 (38.9)
no of gaps > 500 bp	1,660	1,926	10,751	14,396

¹ after removal of duplicate reads and reads with mapping quality less than 30.

² Gaps in Heinz assembly (“N”s) removed from calculation