



**SWEEP: a tool for filtering high quality SNPs in polyploid crops.**

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DOI: [10.1534/g3.115.019703](https://doi.org/10.1534/g3.115.019703)

**Table S1** Assembly statistics of *de novo* Trinity assembly

	<b>New Mexico Valencia A Assembly</b>
Transcripts	124,357
N50 (bp)	1,927
Average (bp)	1,118
Total Assembled (bp)	139,090,891

**Table S2 Sequence statistics for all genotypes sequenced in this study.** Percentage of mapped reads are to the New Mexico Valencia *A de novo* assembly

<b>Genotype</b>	<b>Total Reads</b>	<b>Mapped Reads</b>
		<b>%</b>
Florida 07	13,881,744	60.30
NC3033	15,736,991	55.98
SPT06-06	16,252,634	56.48
Tifrunner	35,457,450	61.97
C76-16	9,949,147	63.36

**Table S3 Sys time for –ultimate filtering using one 8-core node (Intel Xeon processors) and 32 Gb of RAM.**

<b>Genotypes</b>	<b>sys (sec)</b>	<b>sys (min)</b>	<b>Total SNPs visited</b>	<b>Rate (SNP/sec)</b>
5	18,121	302.02	49,876	2.75
4	15,020	250.33	47,227	3.14
3	10,207	170.12	26,052	2.55
2	7,542	125.70	16,880	2.24