Supplemental Table S2: List of selected genome profiling tools.

For references, see Supplemental Materials.

Tool	*description*	*url*	*reference*
Kmerfreq	*Estimates genome size from corrected long reads.*	https://github.com/fanagislab/kmerfreq	*[15] [16]*
RESPECT	*Primarily for skimming data; ignores the concept of heterozygosity and is pre-trained on haploid representation of genomes*	https://github.com/shahab-sarmashghi/RESPECT	*[17]*
findGSE	*Modelling* k-*mer coverage with the most complex distribution of all methods - skew normal distributionl,*	https://github.com/schneebergerlab/findGSE	*[16,18]*
tetmer	*focused on polyploids; based on coalescence theory*	https://github.com/hannesbecher/shiny-k-mers	*[19]*
GenomeScope	*using combinatorics and probability;*	https://genomescope.org	*[20]*
GenomeScope 2.0	*using combinatorics and probability; enhanced model accommodates polyploids; fit to transformed* k-*mer spectra*	https://genomescope.org/genomescope2.0/	*[13]*
CovEst		https://github.com/mhozza/covest	*[21]*