



Supplementary information, Figure S1 The distribution of 17-kmer frequencies of *C. quinoa*.

The frequency of 17-mers peaks at 67. The genome size is estimated using the formula: Genome size = K-mer number/peak depth. A total of 344,467,594 reads from the two PCR-free libraries were used, which resulted in 99,297,839,479 K-mers.

K-mer Number	Peak Depth	Genome Size (nt)	Used Bases	Used Reads	Depth
99,297,839,479	67	1,482,057,305	86,461,366,094	344,467,594	58.4