Supplemental Table S1. Whole-genome sequencing and read trimming statistics. Alignment rates shown are against the sorghum genome.

Genotype	Raw reads (millions)	Raw bases (billions)	High quality reads (millions)	High quality bases (billions)	Alignment rate
KQ228	7,984.80	1,205.70	7,736.15 (96.89 %)	1,133.90 (94.04 %)	37.66 %
SRA5	7,906.10	1,193.82	7,651.47 (96.78 %)	1,121.77 (93.97 %)	38.48 %
Q155	1,595.45	240.91	1,525.27 (95.60 %)	223.38 (92.72 %)	37.31 %
KQB09	1,616.19	244.04	1,541.7 (95.39 %)	225.91 (92.57 %)	37.84 %
SRA1	1,618.08	244.33	1,551.67 (95.90 %)	227.25 (93.01 %)	37.24 %
MQ239	1,523.06	229.98	1,447.08 (95.01 %)	211.52 (91.97 %)	37.10 %
Q186	1,608.74	242.92	1,528.13 (94.99 %)	222.85 (91.74 %)	37.15 %