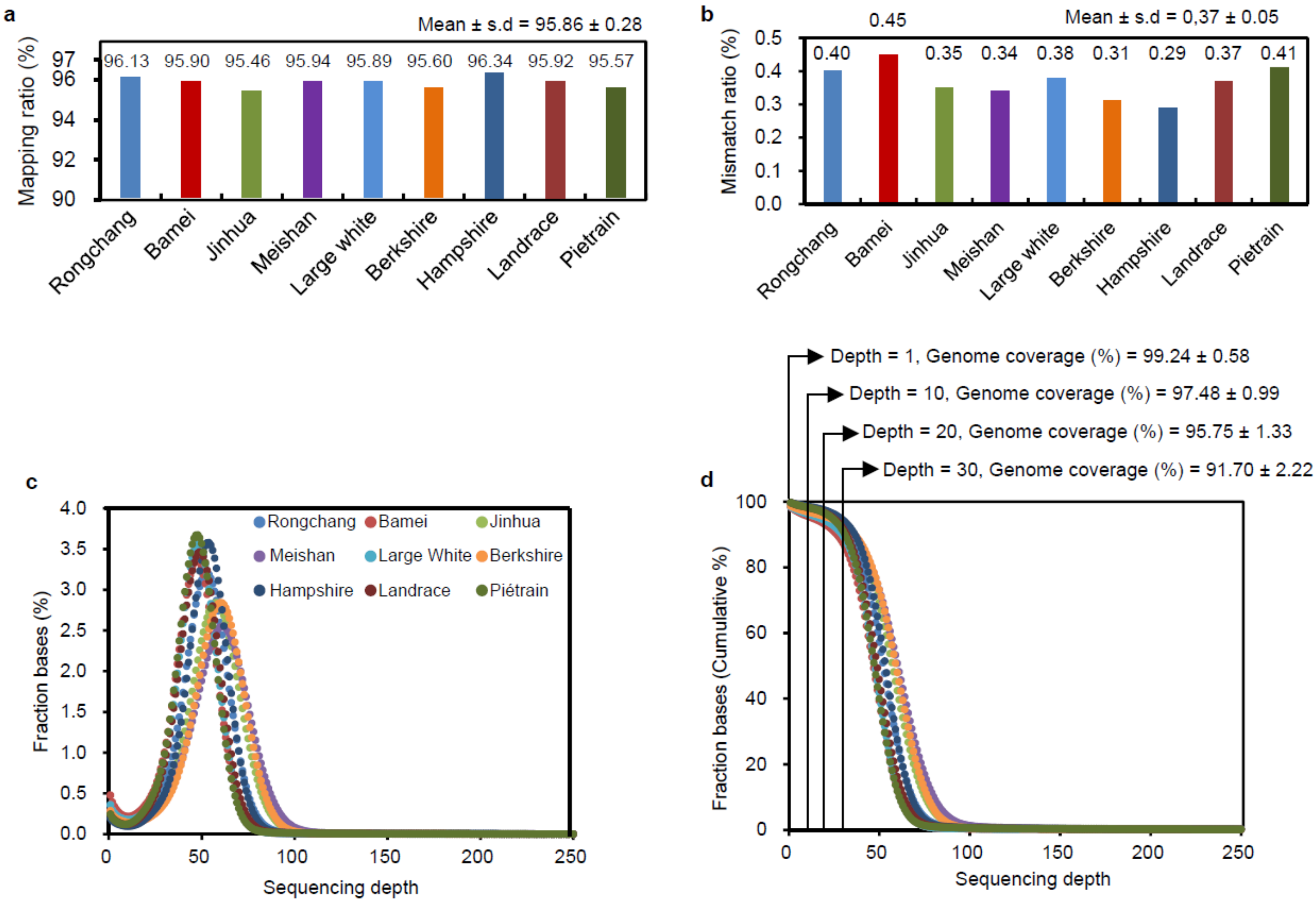

Supplemental Fig. S7. Summary of mapping and coverage depth. The high-quality short-insert reads (180 and 500 bp) were realigned onto the assembly scaffolds. **(a)** mapping ratio; **(b)** mismatch ratio; **(c)** depth distribution of fraction bases; **(d)** depth distribution of cumulative fraction bases. For **(c)** and **(d)**, the x-axis represents sequencing depth, and the y-axis fraction of bases.