



Supplemental Fig. S27. Retrieving unmapped data against the reference genome. (a) Illustration of OEA (one-end anchored) and orphan reads. The unmapped reads from paired-end sequencing were classified as those that mapped onto the reference assembly with only one end (OEA reads) or orphan reads for which neither end mapped. **(b)** and **(c)**, Retrieving orphan reads from the paired-end short-insert reads (180 and 500 bp) and long-insert reads (2, 5, 6 and 10 kb) of ten assemblies. Summary of high-quality data, unmapping ratio **(b)** and unmapped reads **(c)** against the reference genome. For OEA reads, only one end was counted. Only Rongchang, Large White and Tibetan wild boar had long insert size DNA libraries of 10 kb, and the Tibetan wild boar did not have insert size DNA libraries of 6 kb. The unassembled sequencing reads of Tibetan wild boar were downloaded from the NCBI sequence read archive (SRA) under accession code SRA065461.