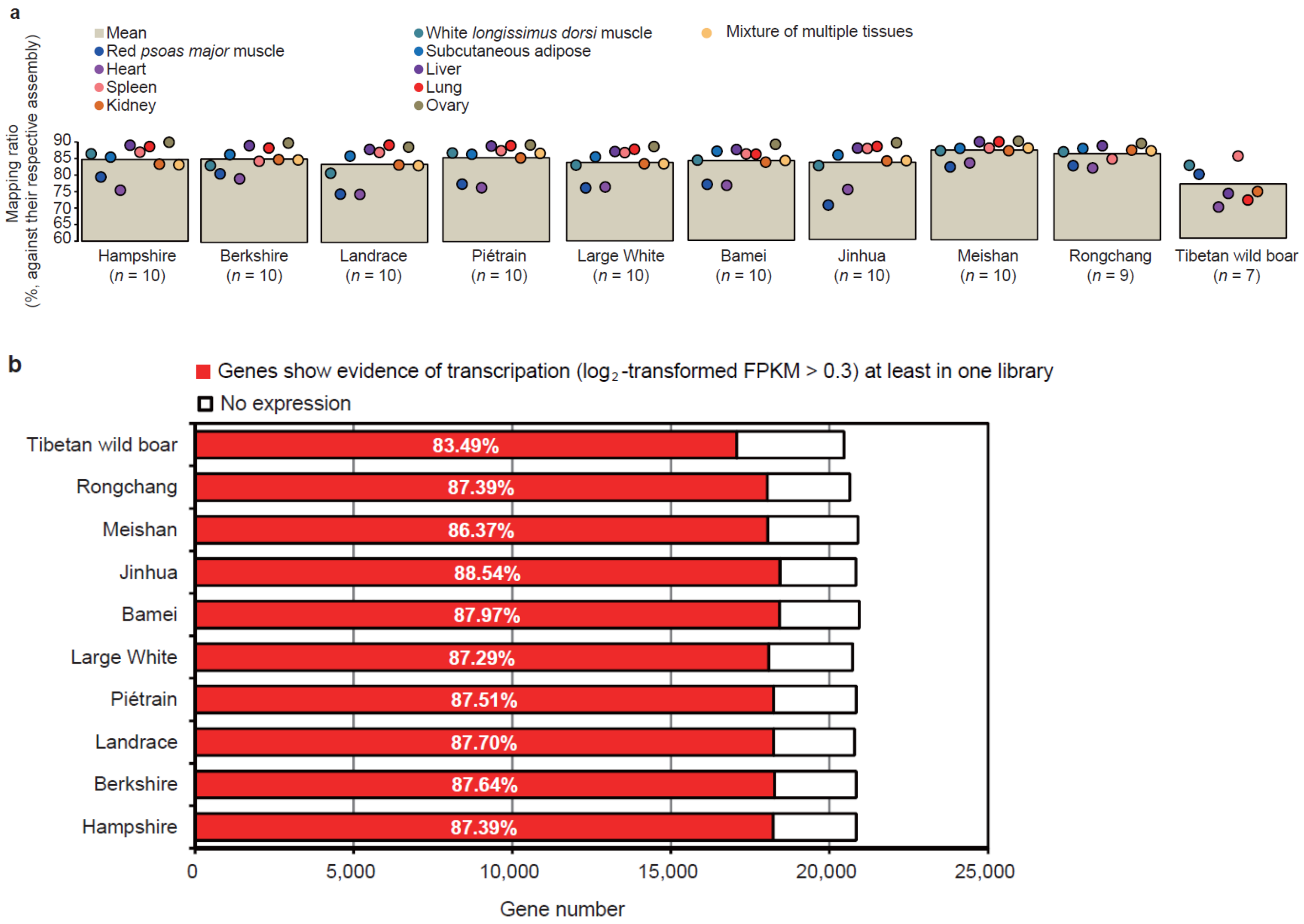

Supplemental Fig. S35. Summary of RNA-seq mapping and genes with evidence of transcription. (a) To enhance genome annotation, 96 mRNA-seq libraries (7 to 10 libraries for each of 10 pig breeds) were constructed using the Illumina mRNA-Seq Prep Kit and ~503.56 Gb (~5,25 Gb per library) of high-quality sequence was generated (125 bp at each end). Of which, RNA-seq data for four tissues of Tibetan wild boar (heart, kidney, liver and lung) were downloaded from the NCBI-Gene Expression Omnibus (GEO) database under accession code GSE43892. **(b)** Evidence of transcription of annotated genes. About 87.13% (18,108 of 20,782) annotated genes in each of ten assemblies had $\log_2$-transformed FPKM expression values greater than 0.3 at least in one library. Expression values were denoted as fragments per kb of transcript per Mb reads, FPKM.