



Supplemental Fig. S24. Analysis of relatedness of ten pig breeds using homozygous SNPs in breed-specific selected regions. (a) A neighbor-joining phylogenetic tree. The scale bar represents p distance. **(b)** Two-way PCA plot. Homozygous SNPs that had greater than 10% missing ratio were discarded. Homozygous SNPs from these regions formed two distinct clusters or groups (i.e. pigs with specific selected regions and other pigs).