



Supplemental Fig. S46. Comparison of Shannon entropy values across different tissues within each pig breed between selected and unselected missing genes. Nine RNA-seq libraries from mixture of multiple tissues were excluded. The statistical significance was calculated by Mann-Whitney *U* test. 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.