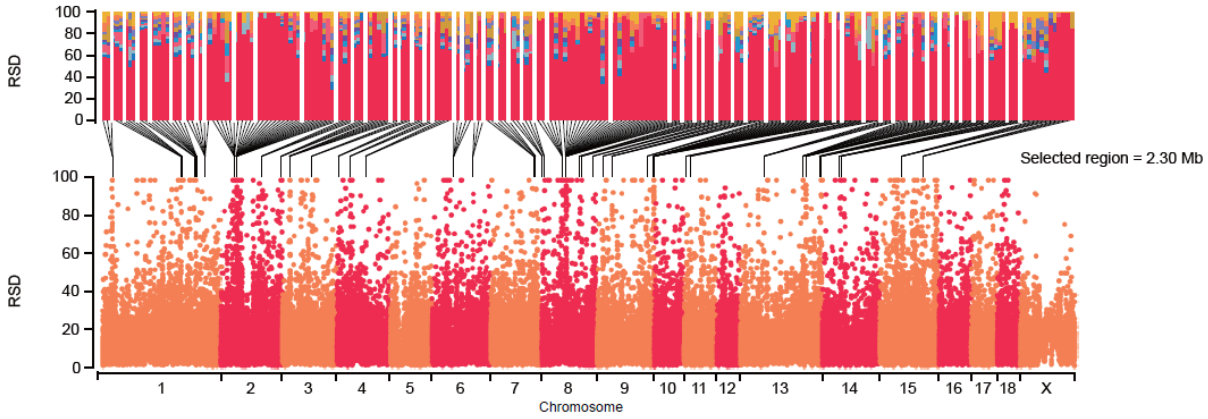
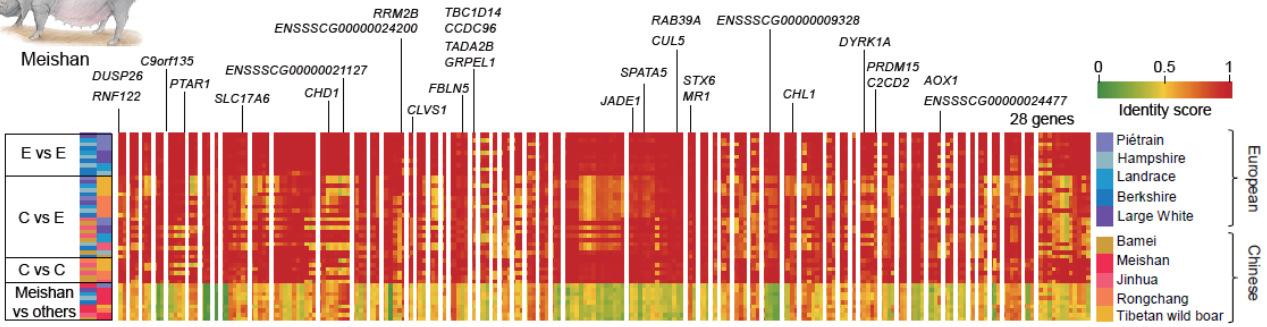
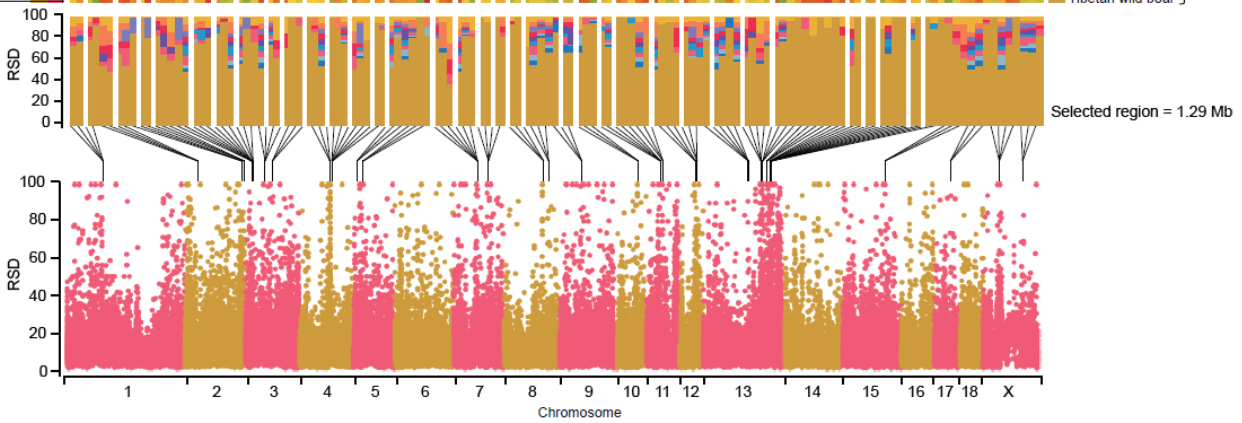
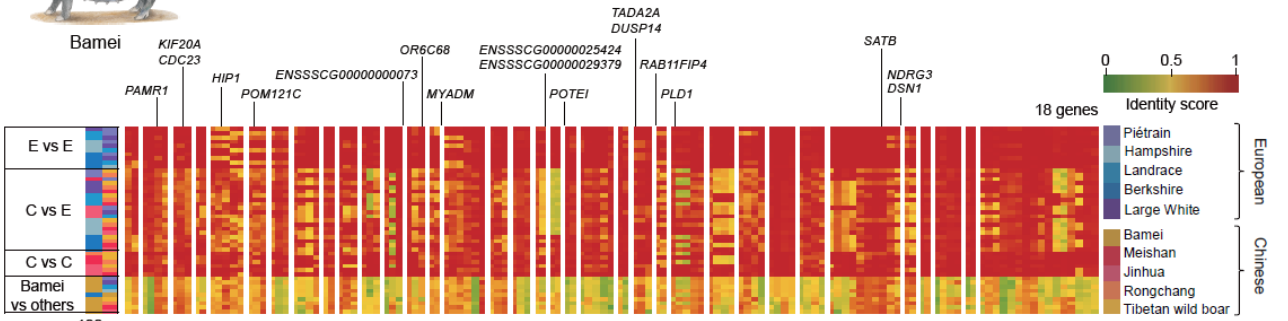


c



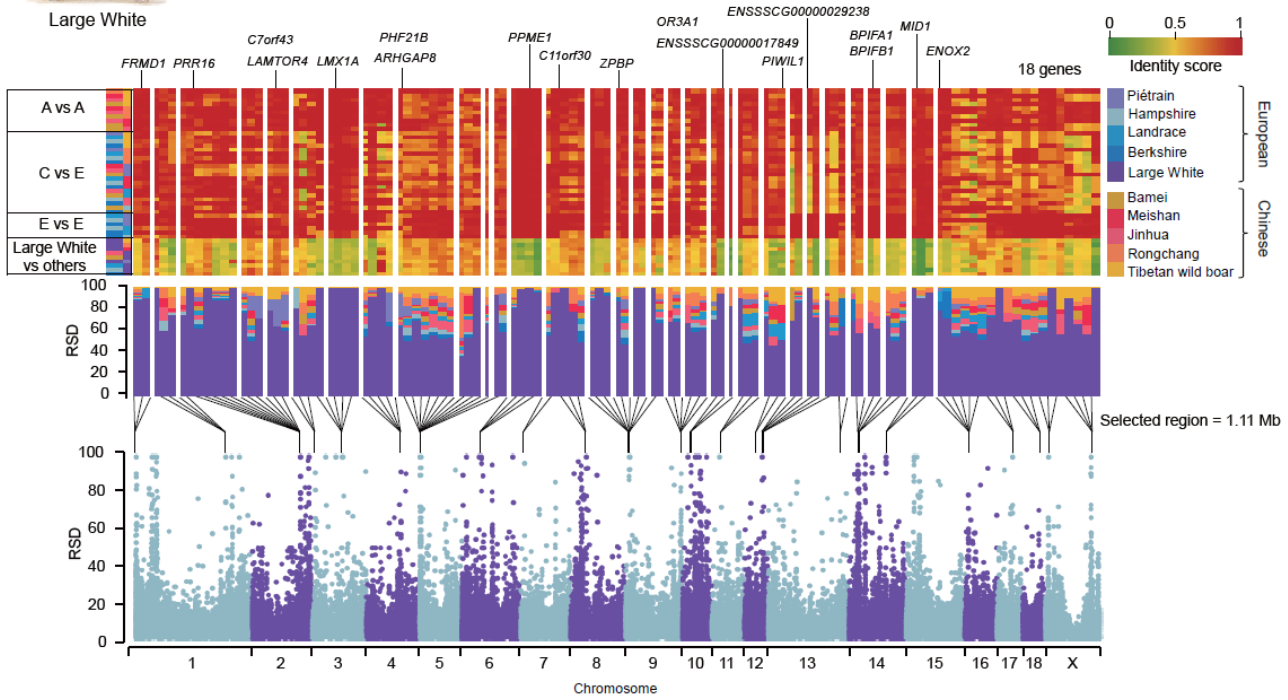
d



e



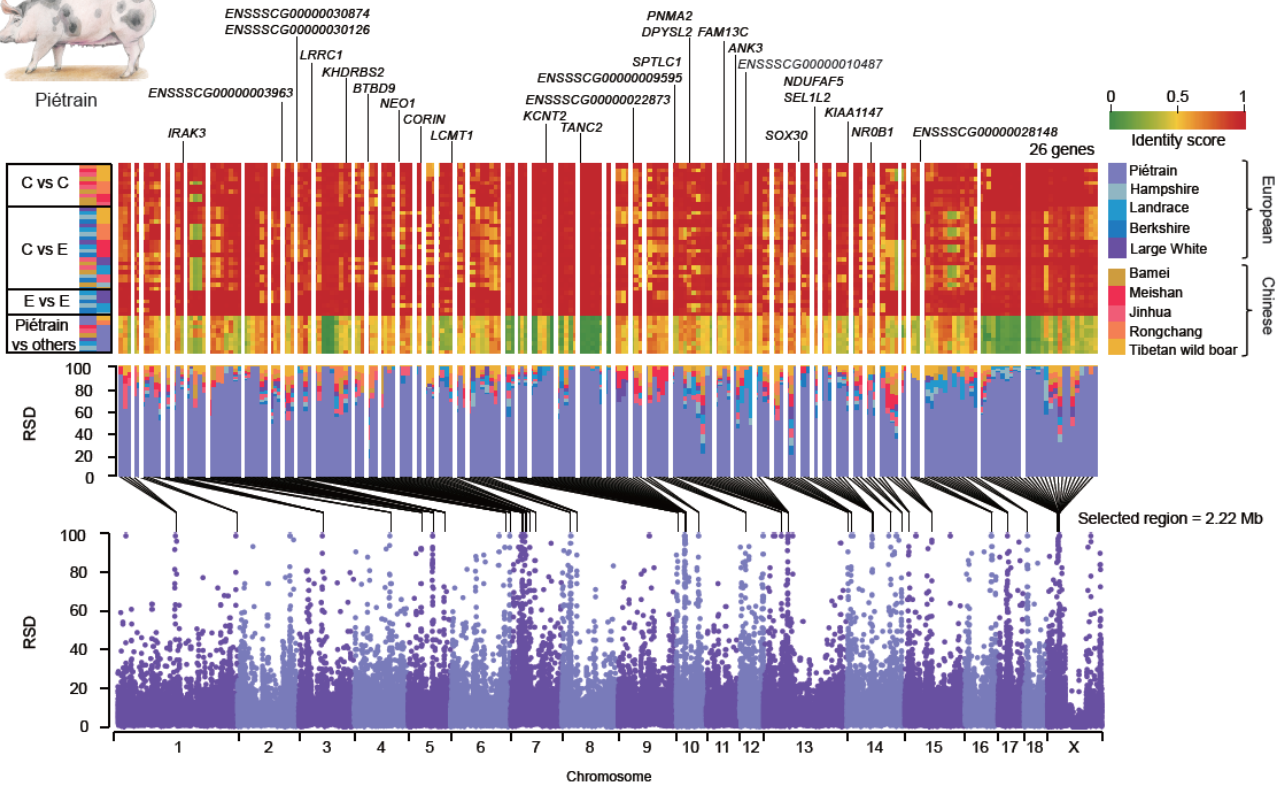
Large White



f



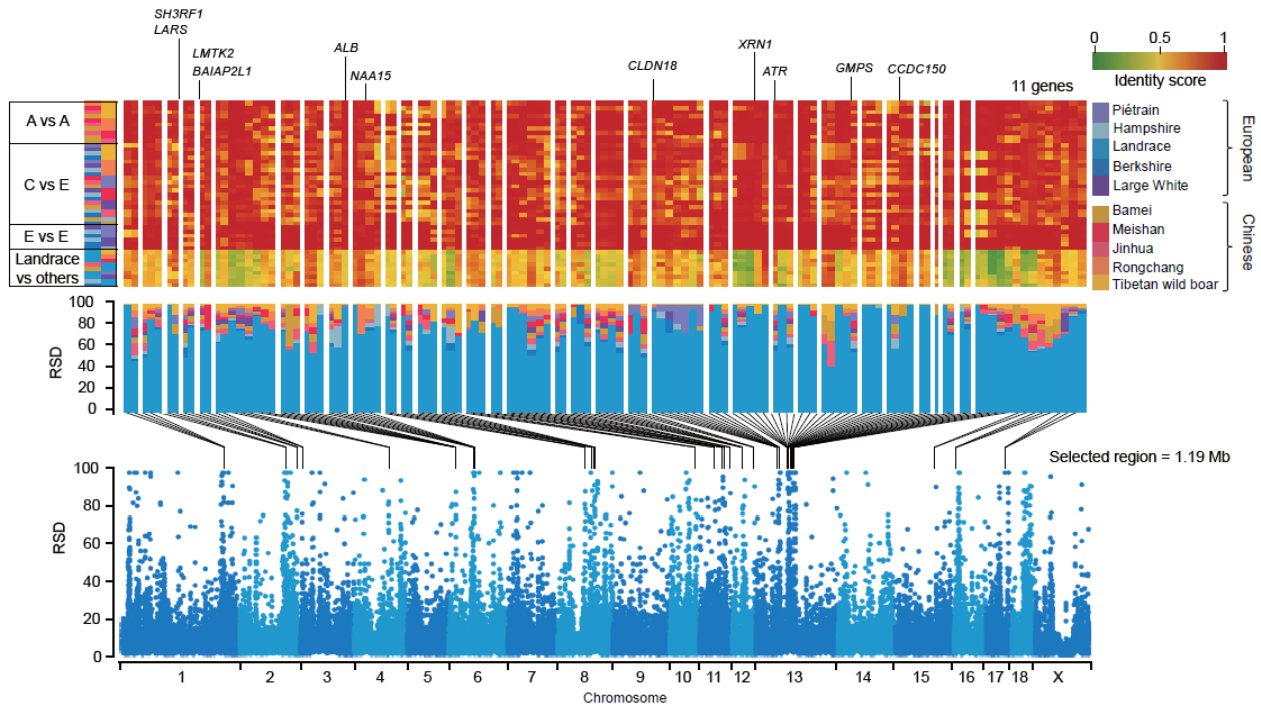
Pietrain



g



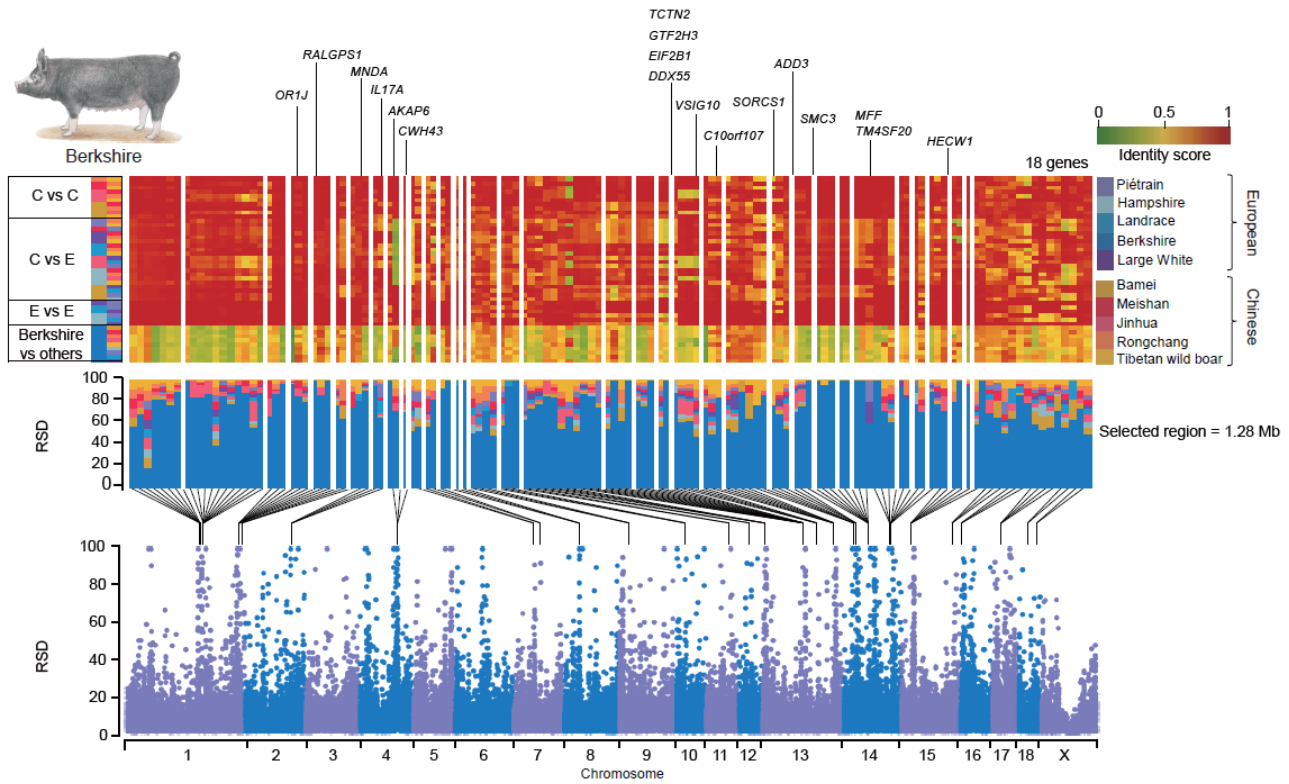
Landrace

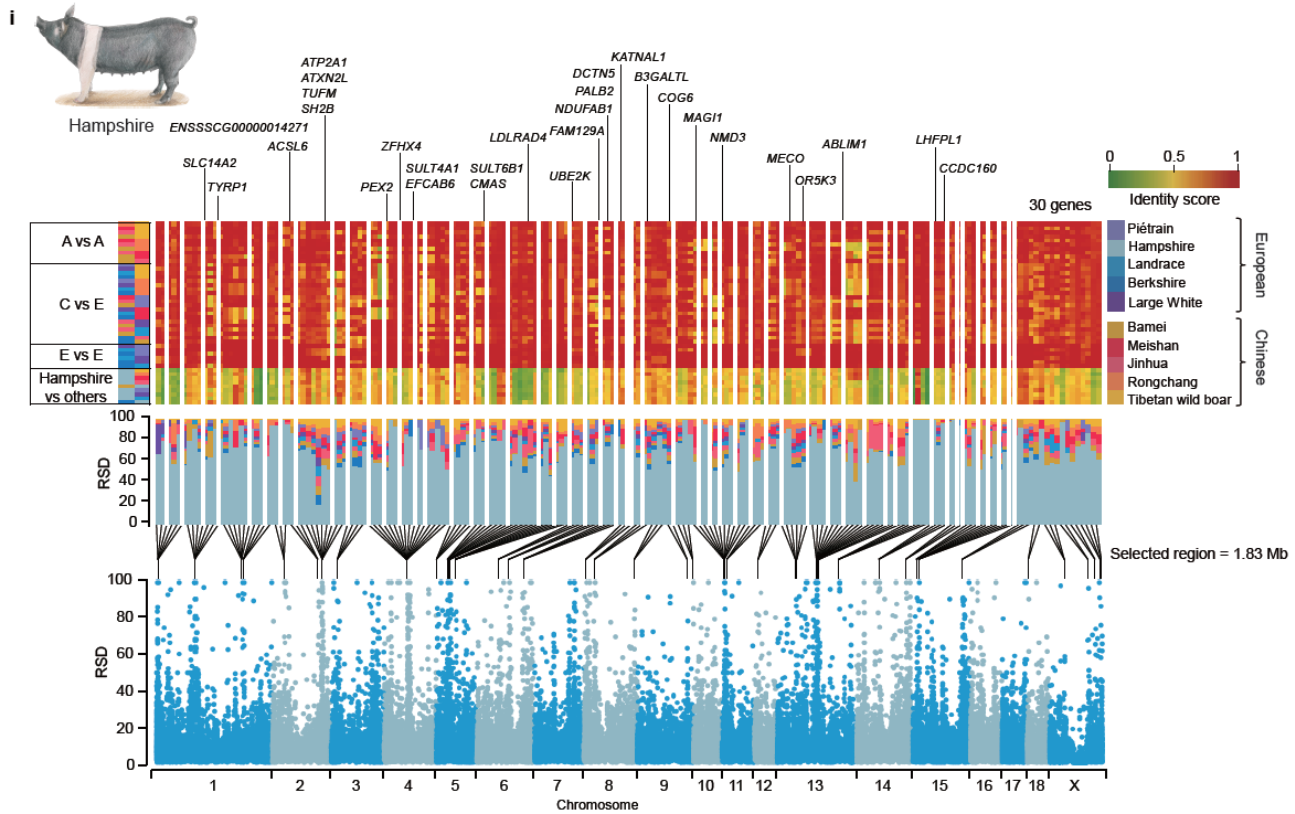


h



Berkshire





**Supplemental Fig. S25. Breed-specific selective sweep regions.** Top panels, top half: Genes residing within or in the vicinity ( $\pm 5$  kb) of selected regions are presented for each chromosome and ordered according to their locations. Top panels, lower half: Degree of haplotype sharing of selected regions in pairwise comparisons among ten breeds. Homozygous SNP frequencies in individual breeds were used to calculate identity scores in 10 kb windows. Boxes (left) indicate pairwise comparison presented on that row (E, European pigs; C, Chinese pigs) according to the colour assigned to each pig breed (right). Heat-map colors indicate identity scores. Second panels: Percentage stacked column showing RSD in the breed-specific selected regions across ten pig breed sequenced. Particular breed showing predominated RSD value than other breeds indicates SNPs against the reference genome in this region. Third panels: RSD in 10 kb windows for particular breed plotted along chromosomes. Black lines indicate selected regions. **(a)** Jinhua; **(b)** Tibetan wild boar; **(c)** Meishan; **(d)** Bamei; **(e)** Large White; **(f)** Piétrain; **(g)** Landrace; **(h)** Berkshire; **(i)** Hampshire. For **(a)**, six selected genes orthologous to the mammalian fat deposition genes, and **(b)**, 16 selected genes related to the high-altitude adaptation, were marked in red.