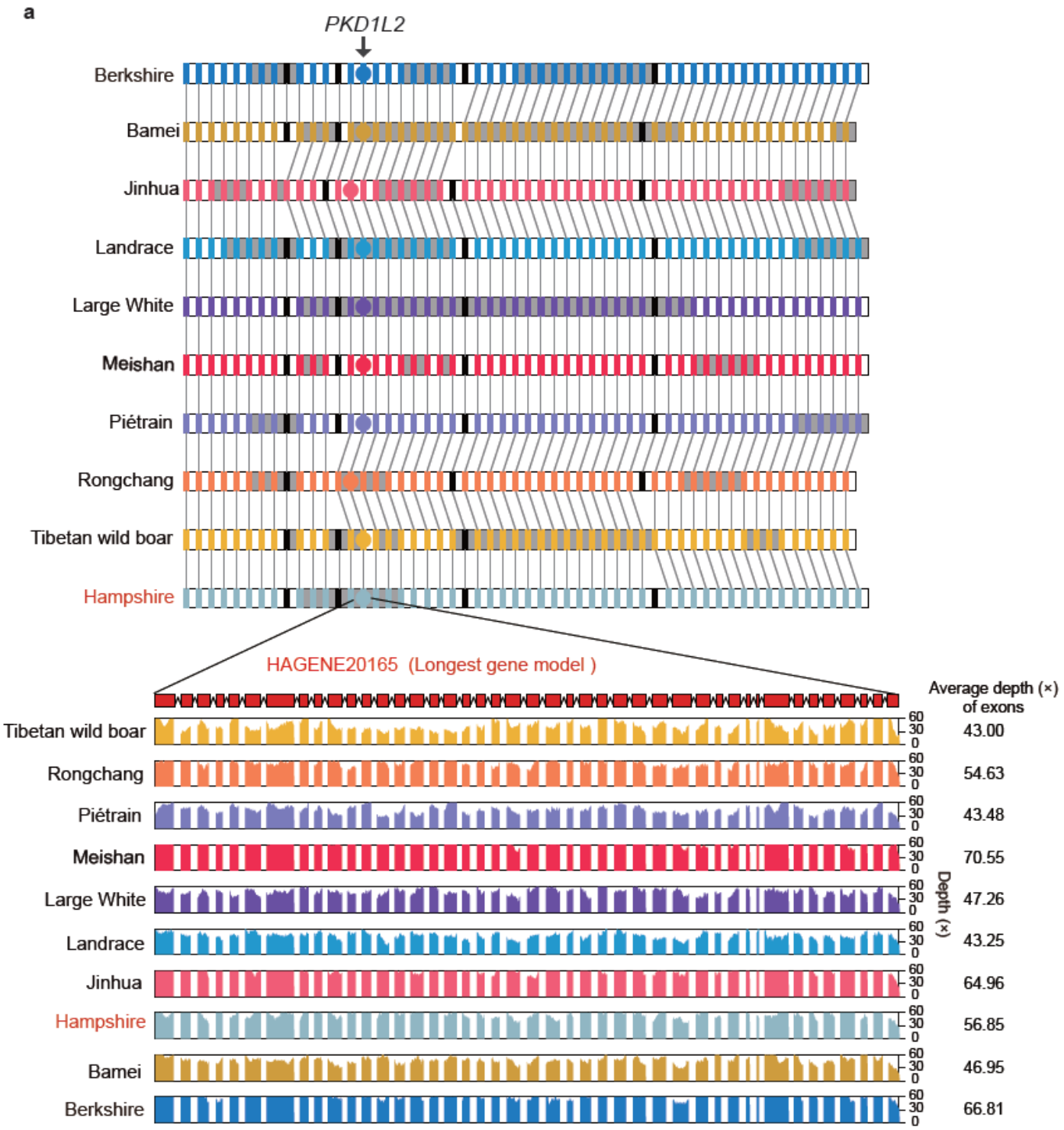
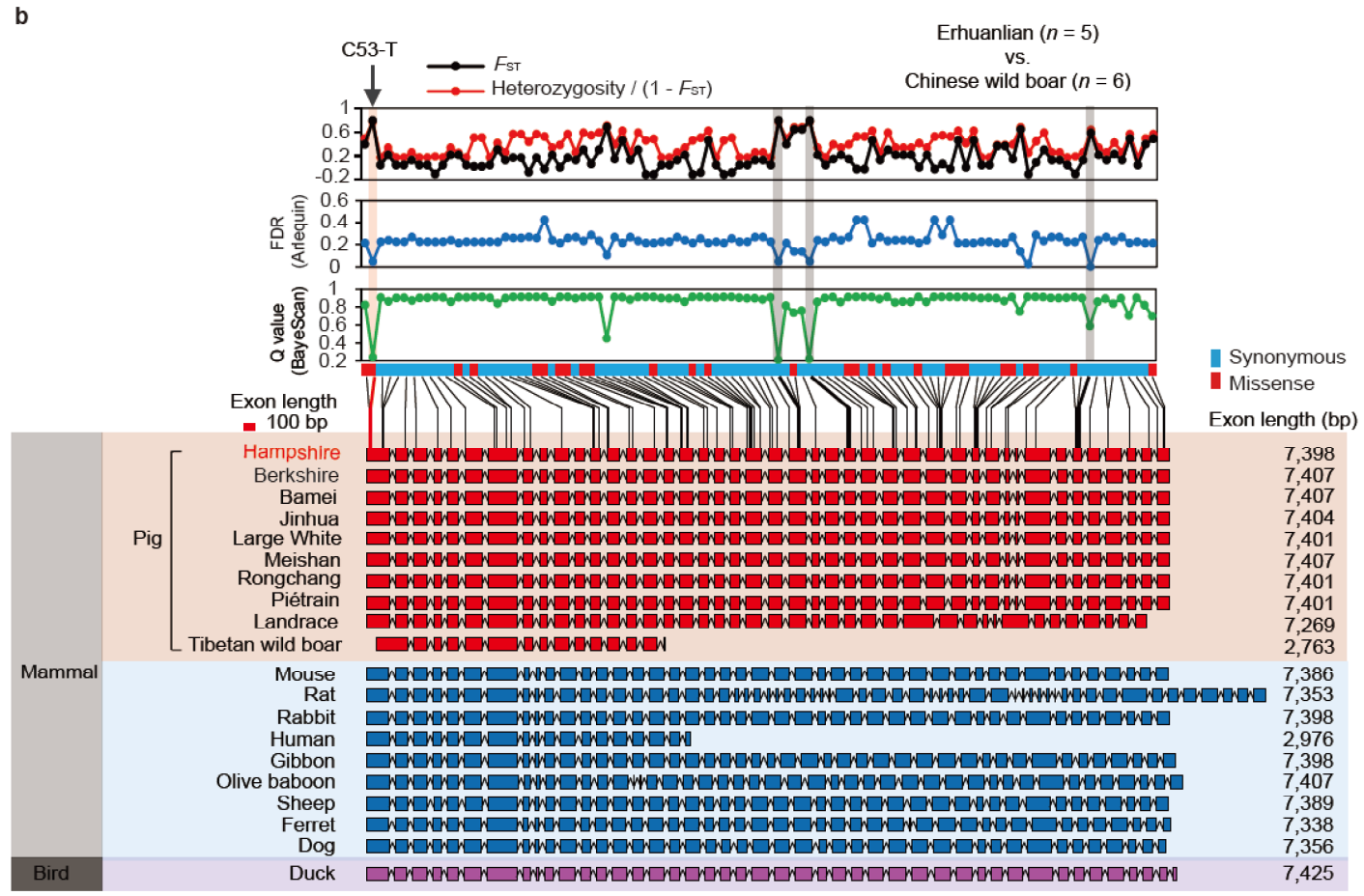
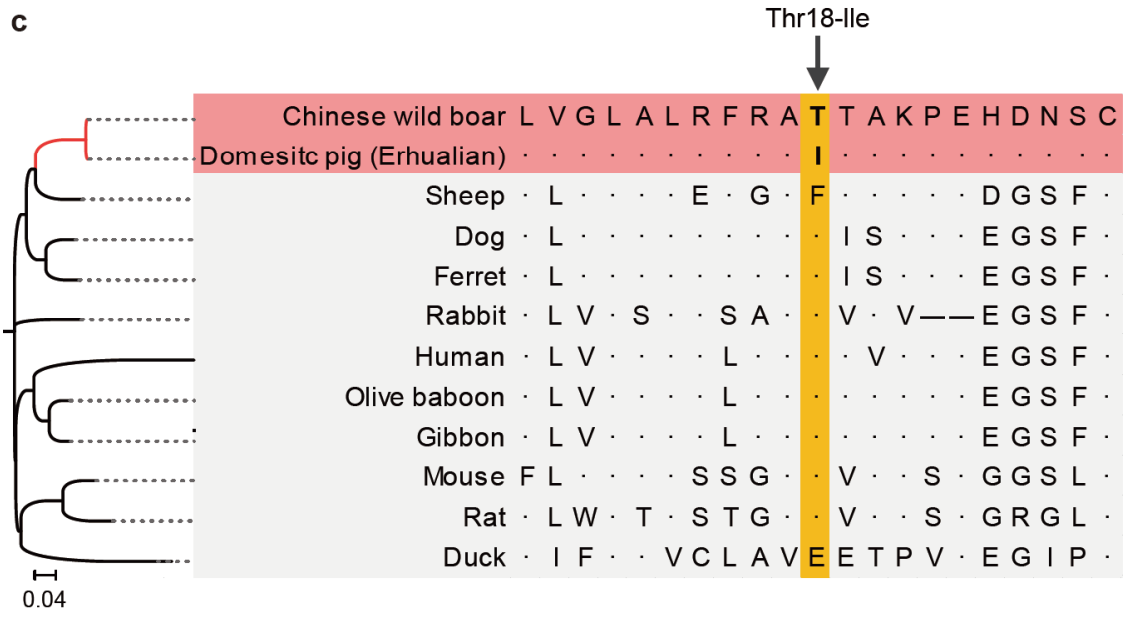
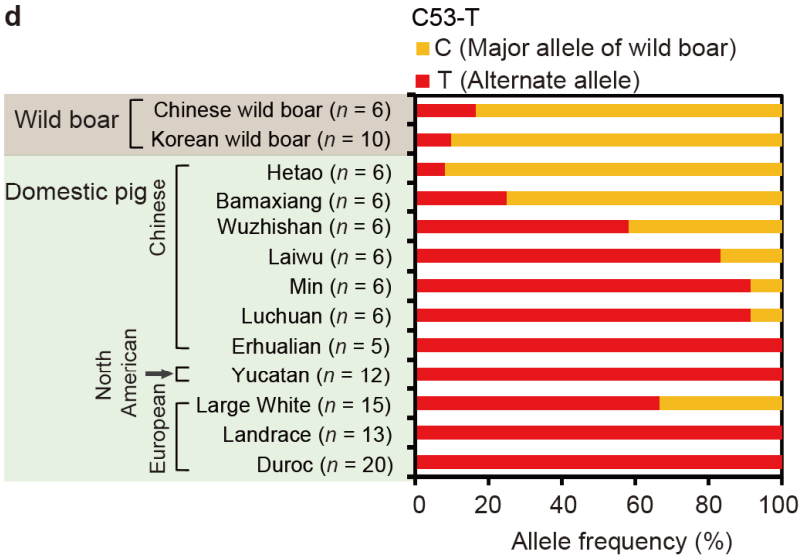

a
PKD1L2
Berkshire
Bamei
Jinhua
Landrace
Large White
Meishan
Piétrain
Rongchang
Tibetan wild boar
Hampshire
HAGENE20165 (Longest gene model)
Average depth (×) of exons
Depth (×)
Tibetan wild boar 43.00
Rongchang 54.63
Piétrain 43.48
Meishan 70.55
Large White 47.26
Landrace 43.25
Jinhua 64.96
Hampshire 56.85
Bamei 46.95
Berkshire 66.81
60
30
0


b
C53-T
F_{ST}
Heterozygosity / (1 - F_{ST})
Erhuanlian (n = 5)
vs.
Chinese wild boar (n = 6)
FDR (Arlequin)
Q value (BayeScan)
Exon length
100 bp
Synonymous
Missense
Exon length (bp)
Pig
Hampshire 7,398
Berkshire 7,407
Bamei 7,407
Jinhua 7,404
Large White 7,401
Meishan 7,407
Rongchang 7,401
Piétrain 7,401
Landrace 7,269
Tibetan wild boar 2,763
Mammal
Mouse 7,386
Rat 7,353
Rabbit 7,398
Human 2,976
Gibbon 7,398
Olive baboon 7,407
Sheep 7,389
Ferret 7,338
Dog 7,356
Bird
Duck 7,425


c
Thr18-Ile
Chinese wild boar L V G L A L R F R A T T A K P E H D N S C
Domesitc pig (Erhualian) I
Sheep L E G F D G S F
Dog L I S E G S F
Ferret L I S E G S F
Rabbit L V S S A V V E G S F
Human L V L V E G S F
Olive baboon L V L E G S F
Gibbon L V L E G S F
Mouse F L S S G V S G G S L
Rat L W T S T G V S G R G L
Duck I F V C L A V E E T P V E G I P
0.04



Supplemental Fig. S49. Details of assembled *PKD1L2* and selected variants. (a) Assembled *PKD1L2*. Top panels: the inter-assembly collinear genes (colorized rectangles) are linked by gray lines, while genes not presented in all of ten assemblies are marked in black. *PKD1L2* is denoted as a circle. Different scaffolds are distinguished by alternant white and gray backgrounds. Second panels: the higher coverage and depth for the longest gene model of the *PKD1L2* by crossly mapping with reads from paired-end DNA libraries (insert sizes of 180 and 500 bp) of ten assemblies. This result suggests the slightly distinct structures of collinear missing genes among ten assemblies (See **b**), which are attributable to the limitations of short reads assembly. Therefore, the longest gene model was considered more reliable and used for subsequent analyses. **(b)** A selected missense mutation (C53-T) in *PKD1L2* between Chinese wild boars (n = 6) and domestic Erhualian pigs (n = 5). Top panels: F_{ST} and Heterozygosity / (1 - F_{ST}), FDR (Arlequin)[39] and q values (BayeScan)[40] are plotted for 102 coding mutations (28 missenses and 74 synonymous mutations). Second panels: structures of *PKD1L2* among ten assemblies and in various species. Boxes and lines indicate exons and introns, respectively. **(c)** An amino acid variant (Thr18-Ile) in *PKD1L2*. Left panels: The phylogenetic tree of the orthologous protein sequences of pig and 10 vertebrates (Ensemble release 83) were derived from multiple alignment as implemented in the Clustal Omega tool[35], which were in accordance with the evolutionary distance with pig lineage. Right panels: Multispecies alignment of proteins for a selected missense mutation. The protein coordinate is based on longest gene model of inter-assembly collinear genes among ten assemblies (HAGENE20165). Dots indicate identities to the Chinese wild boar sequence and dashes indicate missing data. **(d)** Selected missense mutation (C53-T) is highly frequent in domestic pigs.