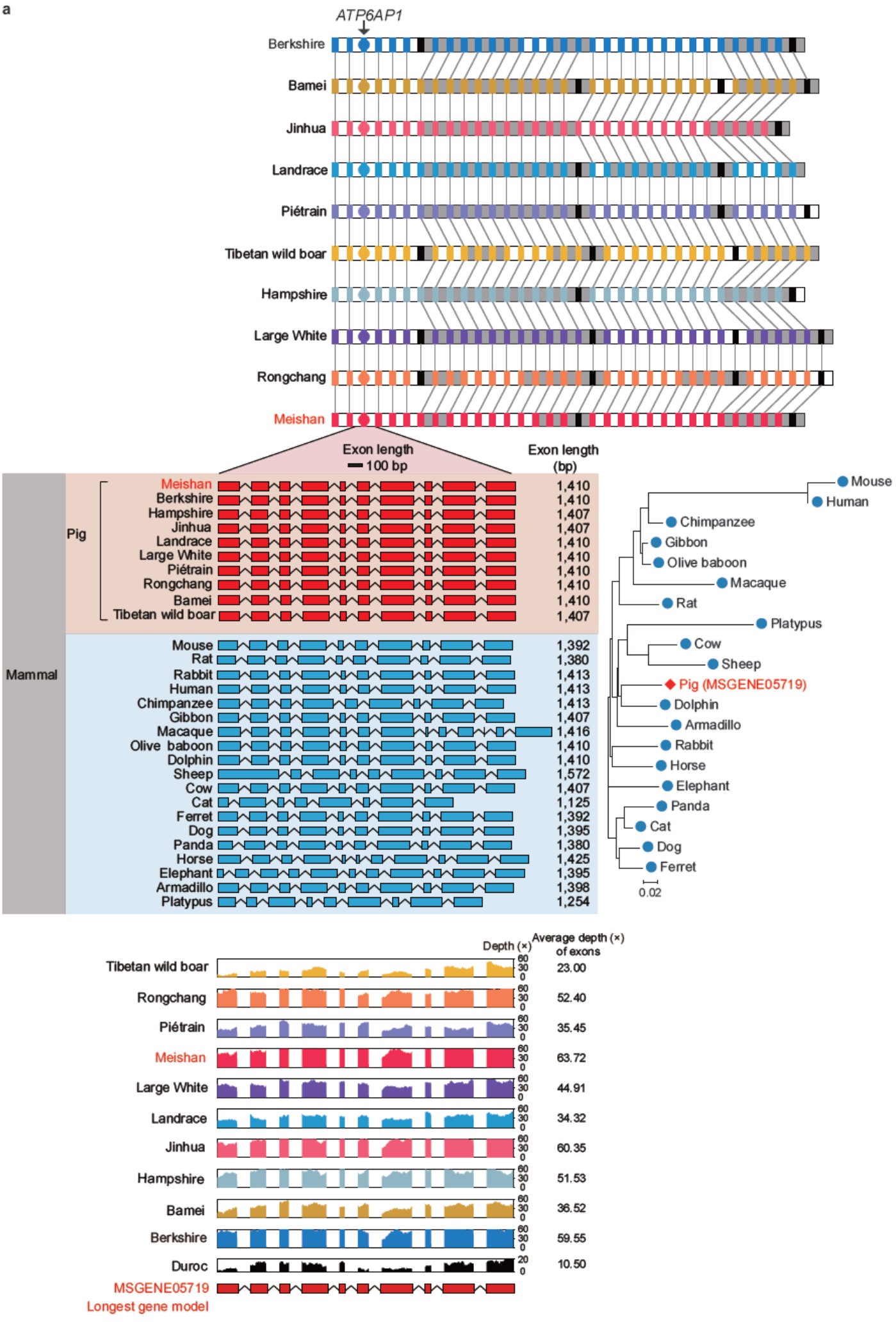
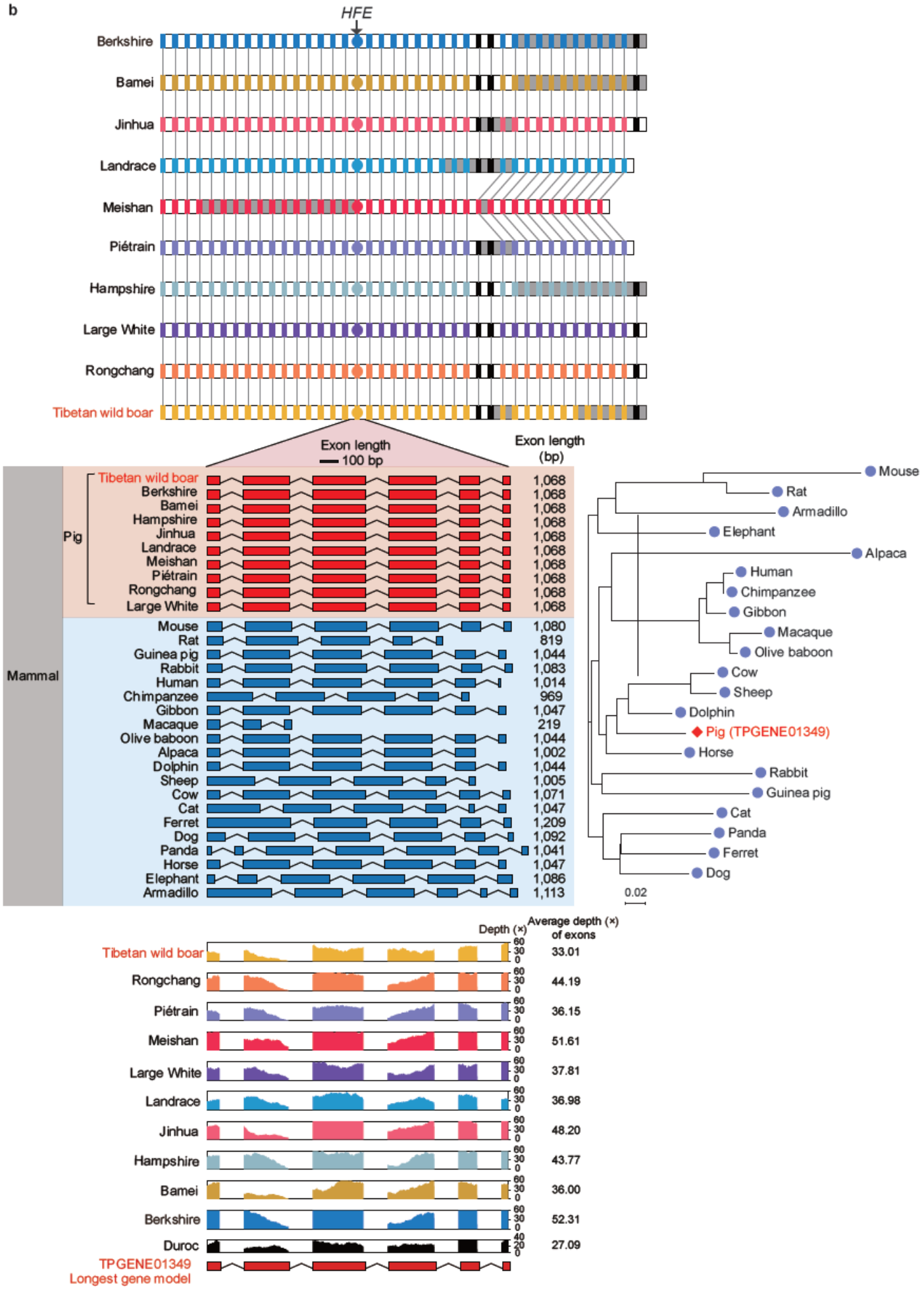
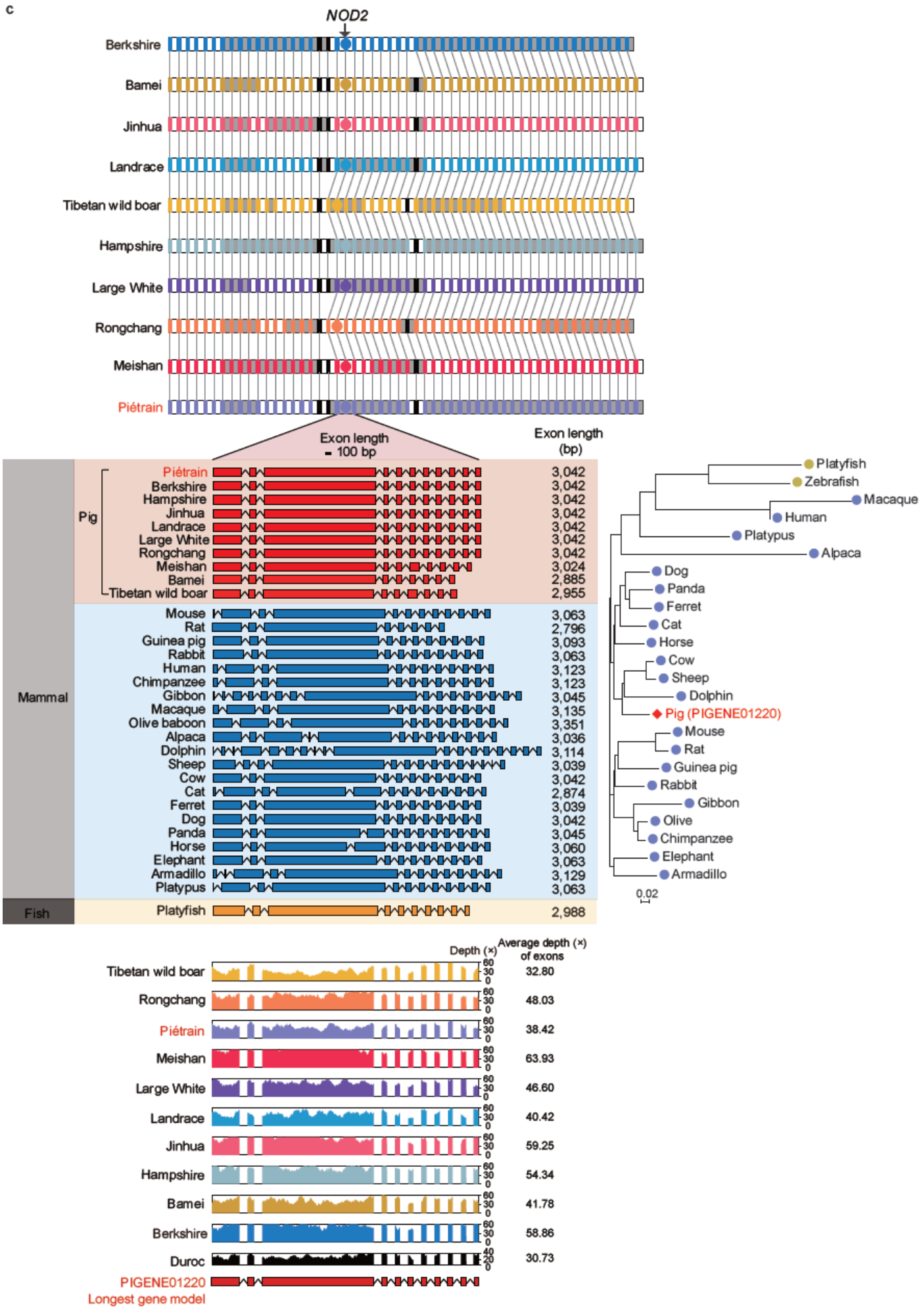
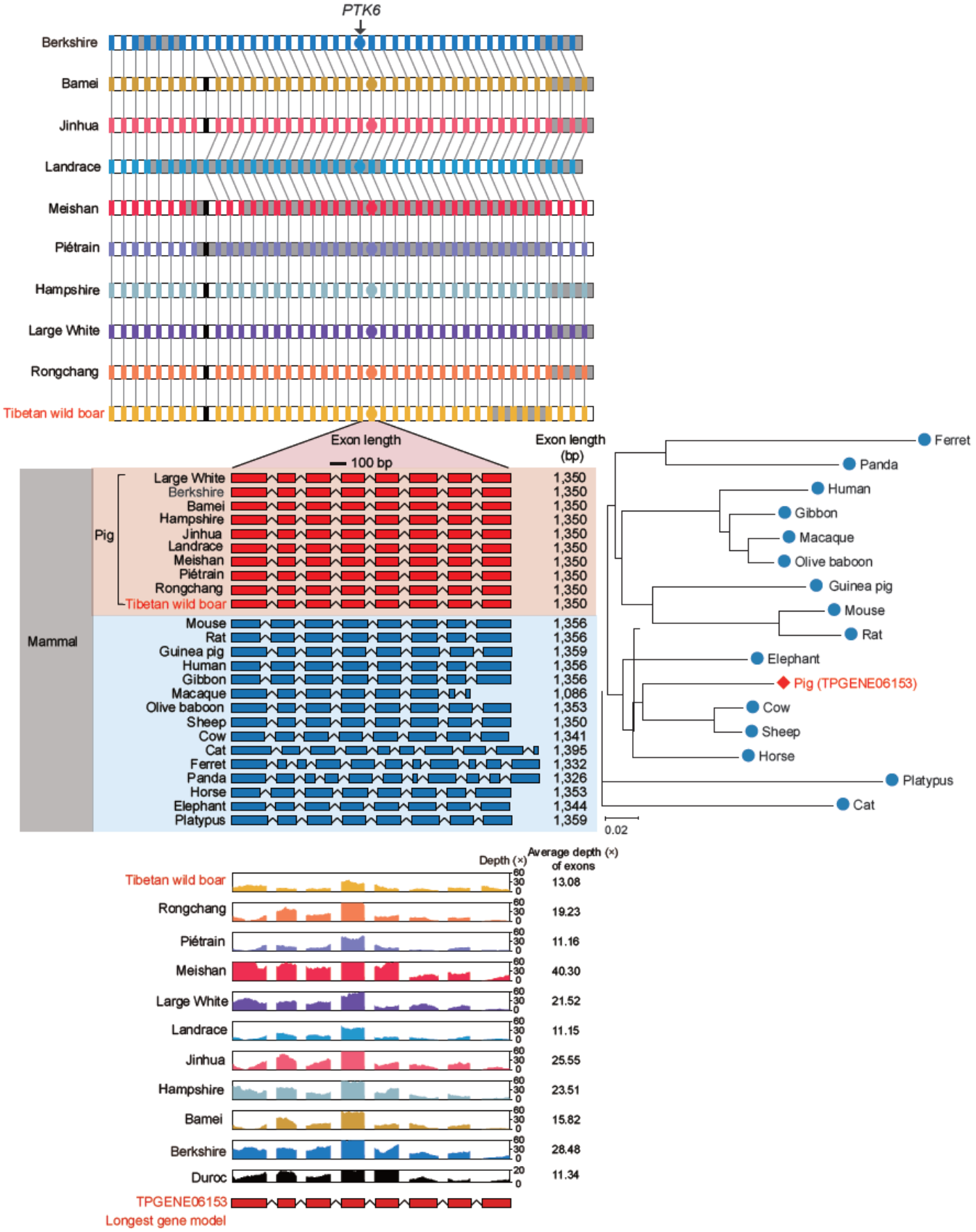
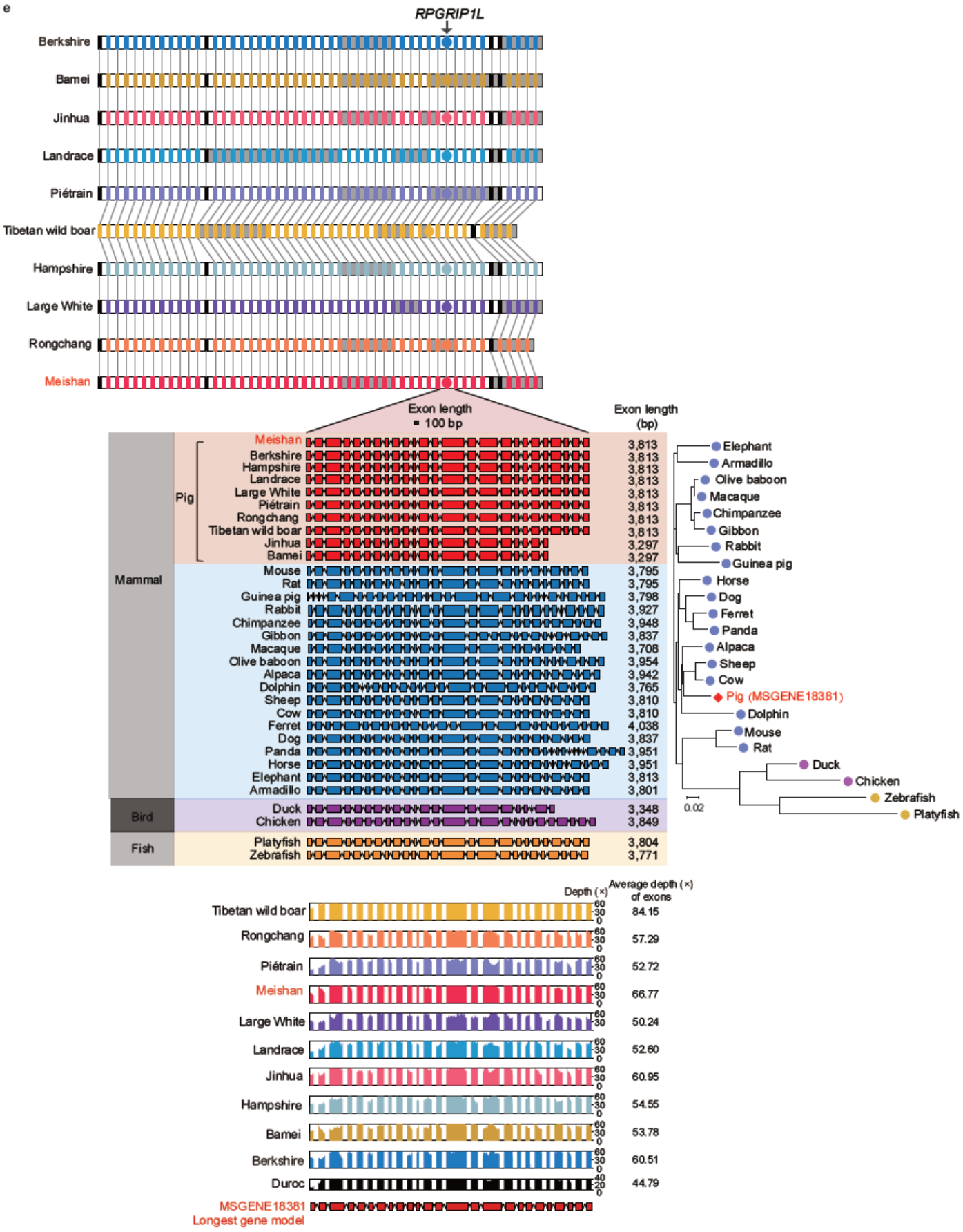

a
ATP6AP1
Berkshire
Bamei
Jinhua
Landrace
Piétrain
Tibetan wild boar
Hampshire
Large White
Rongchang
Meishan
Exon length
100 bp
Exon length
(bp)
Mammal
Pig
Meishan 1,410
Berkshire 1,410
Hampshire 1,407
Jinhua 1,407
Landrace 1,410
Large White 1,410
Piétrain 1,410
Rongchang 1,410
Bamei 1,410
Tibetan wild boar 1,407
Mouse 1,392
Rat 1,380
Rabbit 1,413
Human 1,413
Chimpanzee 1,413
Gibbon 1,407
Macaque 1,416
Olive baboon 1,410
Dolphin 1,410
Sheep 1,572
Cow 1,407
Cat 1,125
Ferret 1,392
Dog 1,395
Panda 1,380
Horse 1,425
Elephant 1,395
Armadillo 1,398
Platypus 1,254
Mouse
Human
Chimpanzee
Gibbon
Olive baboon
Macaque
Rat
Platypus
Cow
Sheep
Pig (MSGENE05719)
Dolphin
Armadillo
Rabbit
Horse
Elephant
Panda
Cat
Dog
Ferret
0.02
Depth (×)
Average depth (×)
of exons
Tibetan wild boar 23.00
Rongchang 52.40
Piétrain 35.45
Meishan 63.72
Large White 44.91
Landrace 34.32
Jinhua 60.35
Hampshire 51.53
Bamei 36.52
Berkshire 59.55
Duroc 10.50
MSGENE05719
Longest gene model


b
HFE
Berkshire
Bamei
Jinhua
Landrace
Meishan
Piétrain
Hampshire
Large White
Rongchang
Tibetan wild boar
Exon length
100 bp
Exon length
(bp)
Mammal
Pig
Tibetan wild boar 1,068
Berkshire 1,068
Bamei 1,068
Hampshire 1,068
Jinhua 1,068
Landrace 1,068
Meishan 1,068
Piétrain 1,068
Rongchang 1,068
Large White 1,068
Mouse 1,080
Rat 819
Guinea pig 1,044
Rabbit 1,083
Human 1,014
Chimpanzee 969
Gibbon 1,047
Macaque 219
Olive baboon 1,044
Alpaca 1,002
Dolphin 1,044
Sheep 1,005
Cow 1,071
Cat 1,047
Ferret 1,209
Dog 1,092
Panda 1,041
Horse 1,047
Elephant 1,086
Armadillo 1,113
Mouse
Rat
Armadillo
Elephant
Alpaca
Human
Chimpanzee
Gibbon
Macaque
Olive baboon
Cow
Sheep
Dolphin
Pig (TPGENE01349)
Horse
Rabbit
Guinea pig
Cat
Panda
Ferret
Dog
0.02
Depth (×)
Average depth (×) of exons
Tibetan wild boar 33.01
Rongchang 44.19
Piétrain 36.15
Meishan 51.61
Large White 37.81
Landrace 36.98
Jinhua 48.20
Hampshire 43.77
Bamei 36.00
Berkshire 52.31
Duroc 27.09
TPGENE01349
Longest gene model

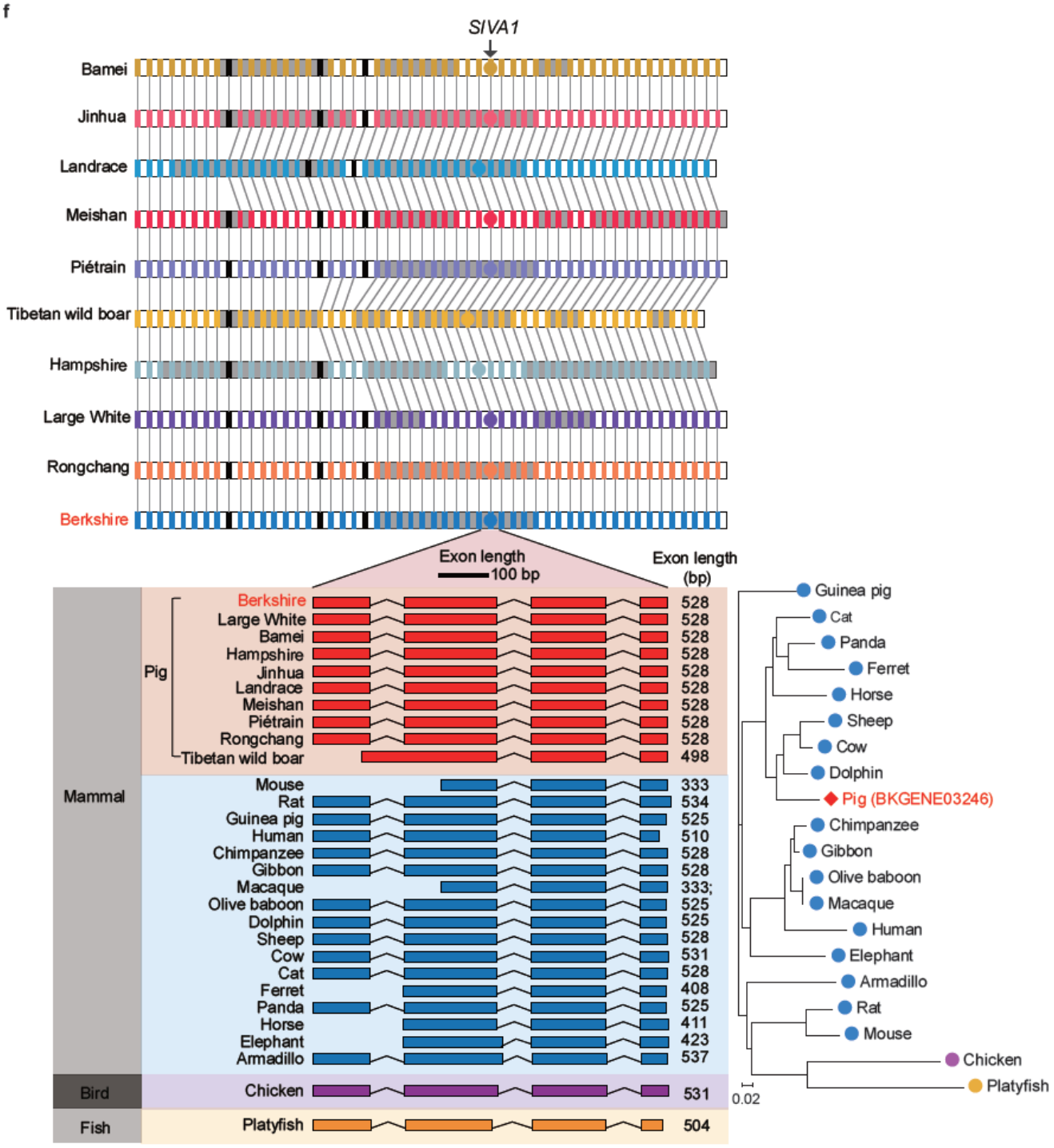

c
NOD2
Berkshire
Bamei
Jinhua
Landrace
Tibetan wild boar
Hampshire
Large White
Rongchang
Meishan
Piétrain
Exon length = 100 bp
Exon length (bp)
Pig
Piétrain 3,042
Berkshire 3,042
Hampshire 3,042
Jinhua 3,042
Landrace 3,042
Large White 3,042
Rongchang 3,042
Meishan 3,024
Bamei 2,885
Tibetan wild boar 2,955
Mammal
Mouse 3,063
Rat 2,796
Guinea pig 3,093
Rabbit 3,063
Human 3,123
Chimpanzee 3,123
Gibbon 3,045
Macaque 3,135
Olive baboon 3,351
Alpaca 3,036
Dolphin 3,114
Sheep 3,039
Cow 3,042
Cat 2,874
Ferret 3,039
Dog 3,042
Panda 3,045
Horse 3,060
Elephant 3,063
Armadillo 3,129
Platypus 3,063
Fish
Platyfish 2,988
Platyfish
Zebrafish
Macaque
Human
Platypus
Alpaca
Dog
Panda
Ferret
Cat
Horse
Cow
Sheep
Dolphin
Pig (PIGENE01220)
Mouse
Rat
Guinea pig
Rabbit
Gibbon
Olive
Chimpanzee
Elephant
Armadillo
0.02
Depth (×)
Average depth (×) of exons
Tibetan wild boar 32.80
Rongchang 48.03
Piétrain 38.42
Meishan 63.93
Large White 46.60
Landrace 40.42
Jinhua 59.25
Hampshire 54.34
Bamei 41.78
Berkshire 58.86
Duroc 30.73
PIGENE01220
Longest gene model

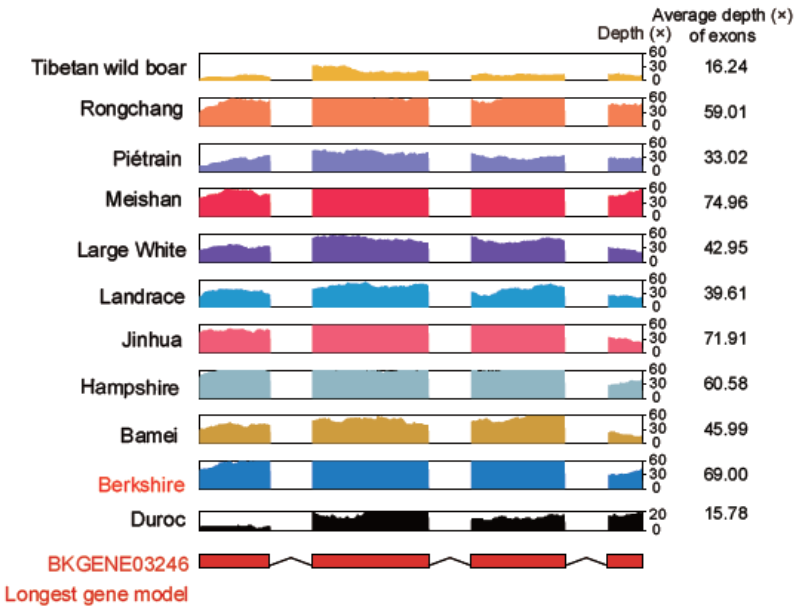
d

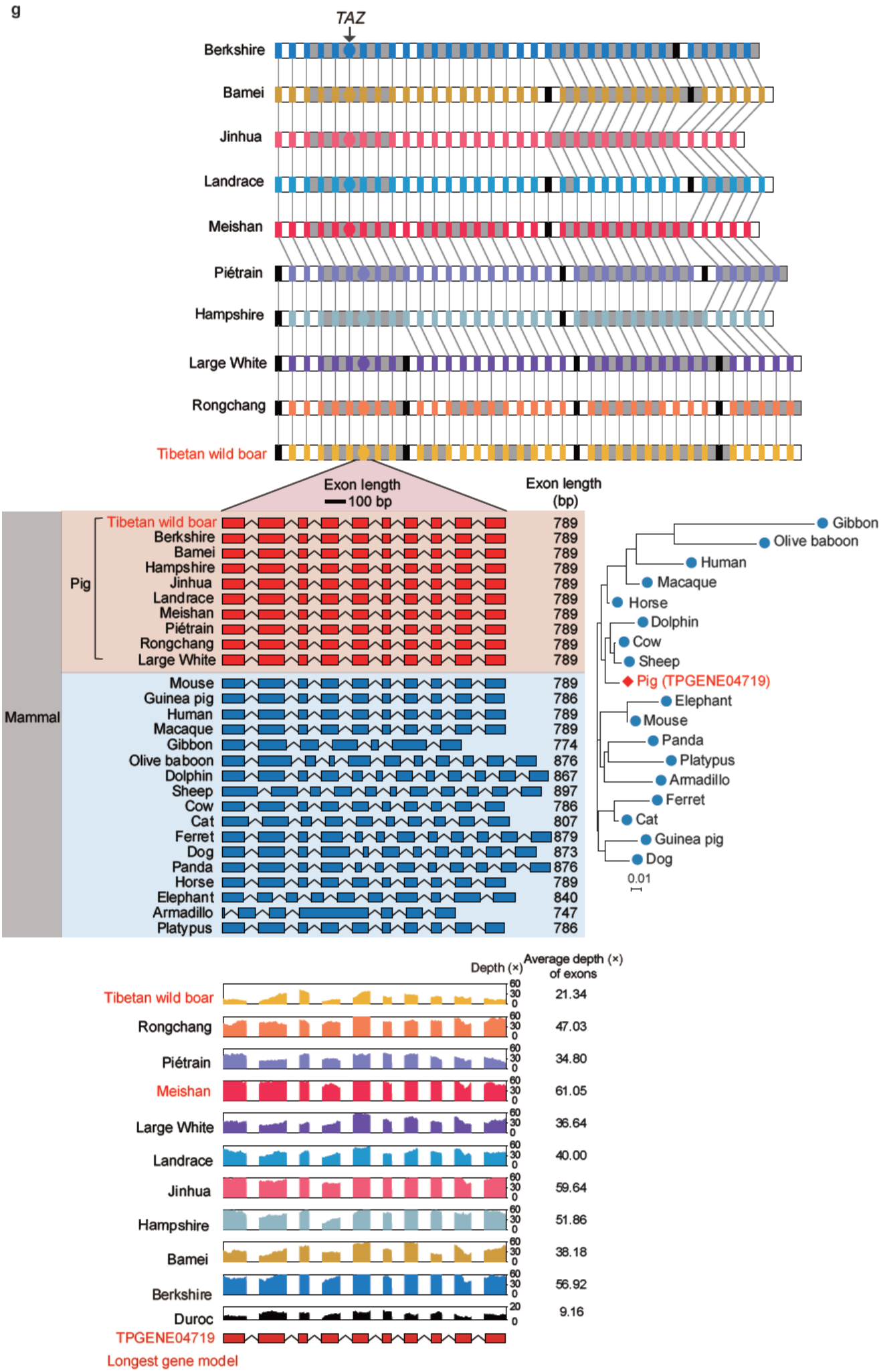

PTK6
Berkshire
Bamei
Jinhua
Landrace
Meishan
Piétrain
Hampshire
Large White
Rongchang
Tibetan wild boar
Exon length
100 bp
Exon length (bp)
Mammal
Pig
Large White 1,350
Berkshire 1,350
Bamei 1,350
Hampshire 1,350
Jinhua 1,350
Landrace 1,350
Meishan 1,350
Piétrain 1,350
Rongchang 1,350
Tibetan wild boar 1,350
Mouse 1,356
Rat 1,356
Guinea pig 1,359
Human 1,356
Gibbon 1,356
Macaque 1,086
Olive baboon 1,353
Sheep 1,350
Cow 1,341
Cat 1,395
Ferret 1,332
Panda 1,326
Horse 1,353
Elephant 1,344
Platypus 1,359
Ferret
Panda
Human
Gibbon
Macaque
Olive baboon
Guinea pig
Mouse
Rat
Elephant
Pig (TPGENE06153)
Cow
Sheep
Horse
Platypus
Cat
0.02
Depth (×)
Average depth (×) of exons
Tibetan wild boar 13.08
Rongchang 19.23
Piétrain 11.16
Meishan 40.30
Large White 21.52
Landrace 11.15
Jinhua 25.55
Hampshire 23.51
Bamei 15.82
Berkshire 28.48
Duroc 11.34
TPGENE06153
Longest gene model

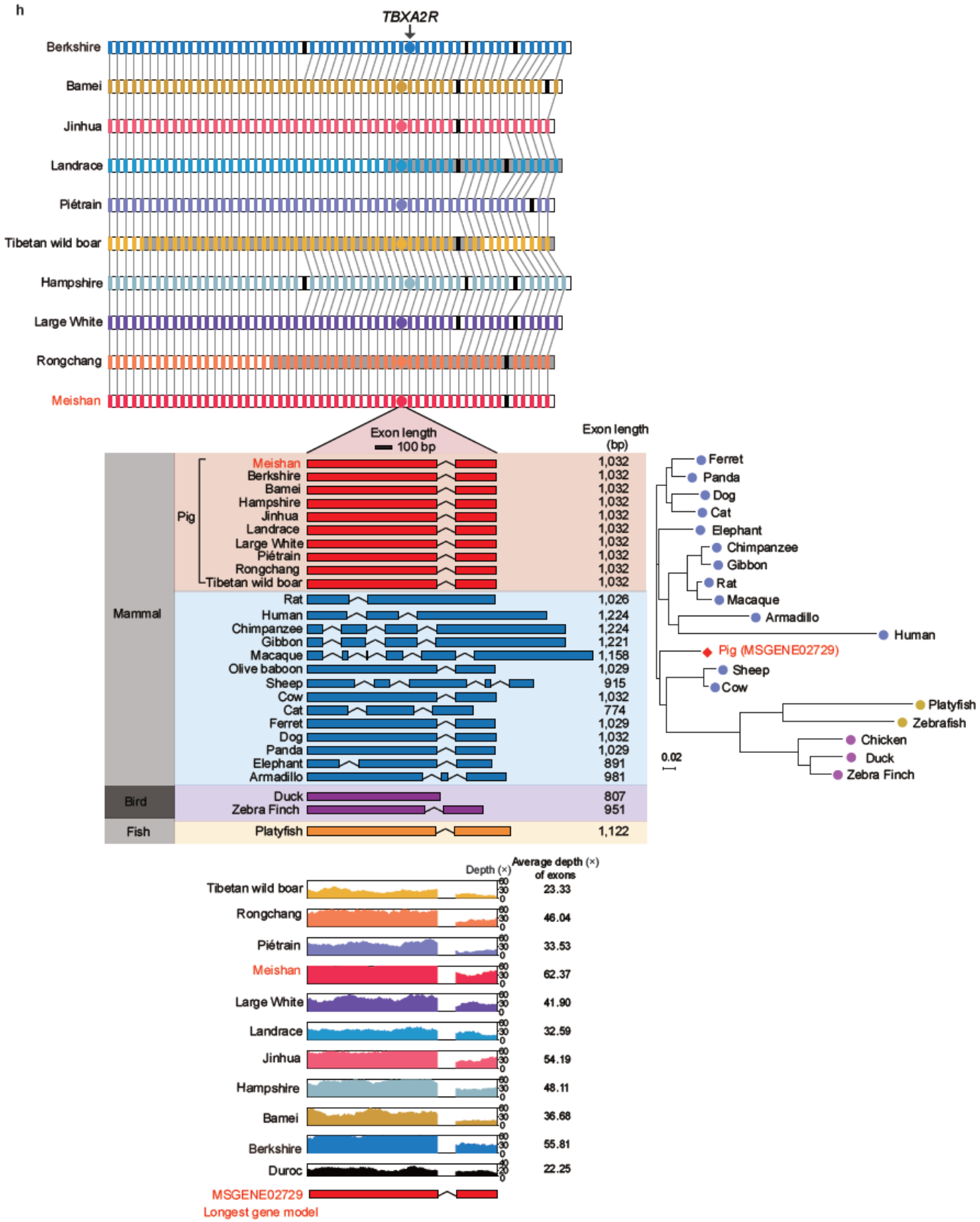

e
RPGRIP1L
Berkshire
Bamei
Jinhua
Landrace
Piétrain
Tibetan wild boar
Hampshire
Large White
Rongchang
Meishan
Exon length
100 bp
Exon length (bp)
Mammal
Pig
Meishan 3,813
Berkshire 3,813
Hampshire 3,813
Landrace 3,813
Large White 3,813
Piétrain 3,813
Rongchang 3,813
Tibetan wild boar 3,813
Jinhua 3,297
Bamei 3,297
Mouse 3,795
Rat 3,795
Guinea pig 3,798
Rabbit 3,927
Chimpanzee 3,948
Gibbon 3,837
Macaque 3,708
Olive baboon 3,954
Alpaca 3,942
Dolphin 3,765
Sheep 3,810
Cow 3,810
Ferret 4,038
Dog 3,837
Panda 3,951
Horse 3,951
Elephant 3,813
Armadillo 3,801
Bird
Duck 3,348
Chicken 3,849
Fish
Platyfish 3,804
Zebrafish 3,771
Elephant
Armadillo
Olive baboon
Macaque
Chimpanzee
Gibbon
Rabbit
Guinea pig
Horse
Dog
Ferret
Panda
Alpaca
Sheep
Cow
Pig (MSGENE18381)
Dolphin
Mouse
Rat
Duck
Chicken
Zebrafish
Platyfish
0.02
Depth (×)
Average depth (×) of exons
Tibetan wild boar 84.15
Rongchang 57.29
Piétrain 52.72
Meishan 66.77
Large White 50.24
Landrace 52.60
Jinhua 60.95
Hampshire 54.55
Bamei 53.78
Berkshire 60.51
Duroc 44.79
MSGENE18381
Longest gene model

f

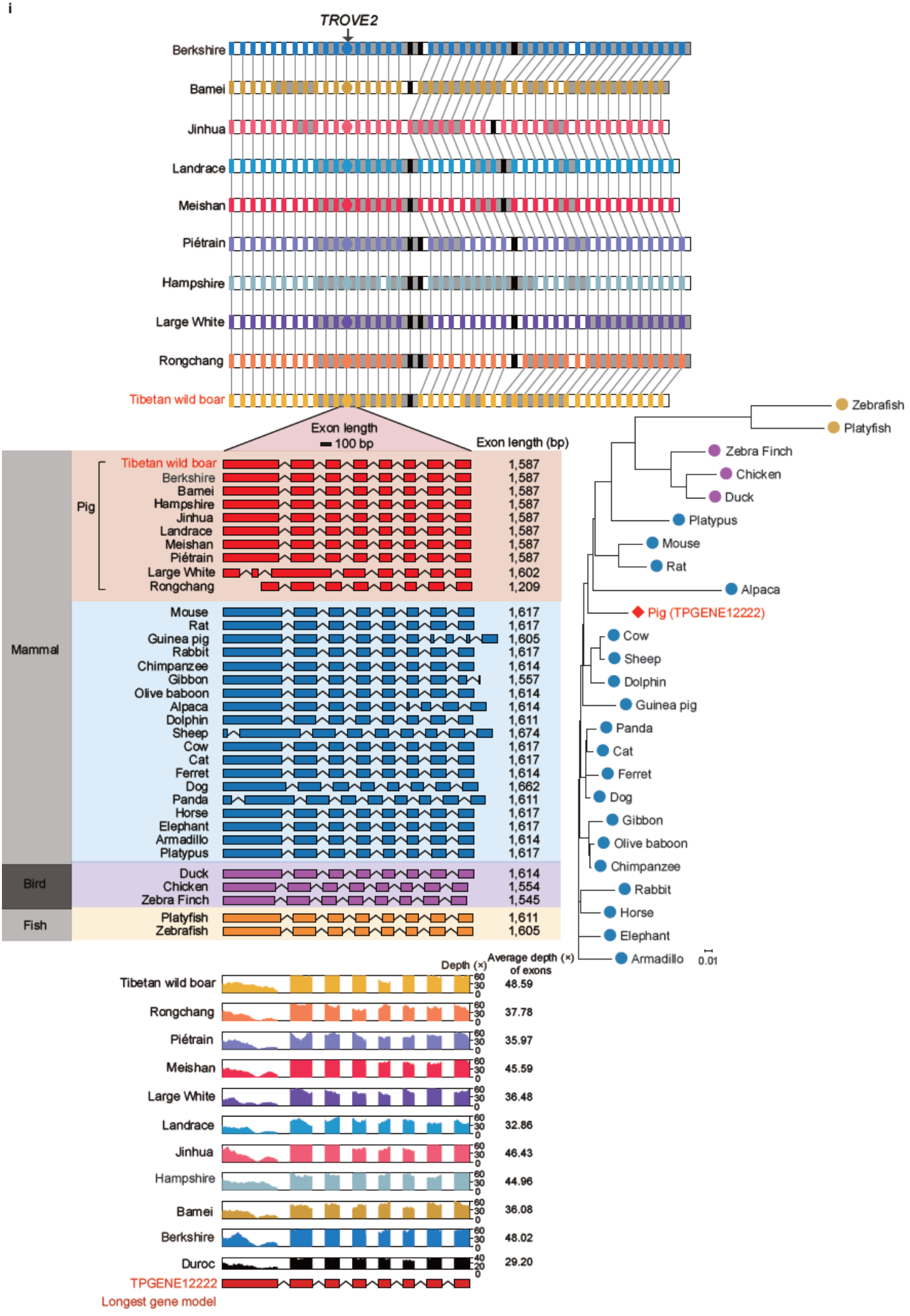

SIVA1
Bamei
Jinhua
Landrace
Meishan
Piétrain
Tibetan wild boar
Hampshire
Large White
Rongchang
Berkshire
Exon length
100 bp
Exon length (bp)
Pig
Berkshire 528
Large White 528
Bamei 528
Hampshire 528
Jinhua 528
Landrace 528
Meishan 528
Piétrain 528
Rongchang 528
Tibetan wild boar 498
Mammal
Mouse 333
Rat 534
Guinea pig 525
Human 510
Chimpanzee 528
Gibbon 528
Macaque 333;
Olive baboon 525
Dolphin 525
Sheep 528
Cow 531
Cat 528
Ferret 408
Panda 525
Horse 411
Elephant 423
Armadillo 537
Bird
Chicken 531
Fish
Platyfish 504
Guinea pig
Cat
Panda
Ferret
Horse
Sheep
Cow
Dolphin
Pig (BKGENE03246)
Chimpanzee
Gibbon
Olive baboon
Macaque
Human
Elephant
Armadillo
Rat
Mouse
Chicken
Platyfish
0.02


Depth (×)
Average depth (×) of exons
Tibetan wild boar 16.24
Rongchang 59.01
Piétrain 33.02
Meishan 74.96
Large White 42.95
Landrace 39.61
Jinhua 71.91
Hampshire 60.58
Bamei 45.99
Berkshire 69.00
Duroc 15.78
BKGENE03246
Longest gene model


g
TAZ
Berkshire
Bamei
Jinhua
Landrace
Meishan
Piétrain
Hampshire
Large White
Rongchang
Tibetan wild boar
Exon length
100 bp
Exon length (bp)
Mammal
Pig
Tibetan wild boar 789
Berkshire 789
Bamei 789
Hampshire 789
Jinhua 789
Landrace 789
Meishan 789
Piétrain 789
Rongchang 789
Large White 789
Mouse 789
Guinea pig 786
Human 789
Macaque 789
Gibbon 774
Olive baboon 876
Dolphin 867
Sheep 897
Cow 786
Cat 807
Ferret 879
Dog 873
Panda 876
Horse 789
Elephant 840
Armadillo 747
Platypus 786
Gibbon
Olive baboon
Human
Macaque
Horse
Dolphin
Cow
Sheep
Pig (TPGENE04719)
Elephant
Mouse
Panda
Platypus
Armadillo
Ferret
Cat
Guinea pig
Dog
0.01
Depth (×)
Average depth (×) of exons
Tibetan wild boar 21.34
Rongchang 47.03
Piétrain 34.80
Meishan 61.05
Large White 36.64
Landrace 40.00
Jinhua 59.64
Hampshire 51.86
Bamei 38.18
Berkshire 56.92
Duroc 9.16
TPGENE04719
Longest gene model


h
TBXA2R
Berkshire
Bamei
Jinhua
Landrace
Piétrain
Tibetan wild boar
Hampshire
Large White
Rongchang
Meishan
Exon length
100 bp
Exon length (bp)
Mammal
Pig
Meishan 1,032
Berkshire 1,032
Bamei 1,032
Hampshire 1,032
Jinhua 1,032
Landrace 1,032
Large White 1,032
Piétrain 1,032
Rongchang 1,032
Tibetan wild boar 1,032
Rat 1,026
Human 1,224
Chimpanzee 1,224
Gibbon 1,221
Macaque 1,158
Olive baboon 1,029
Sheep 915
Cow 1,032
Cat 774
Ferret 1,029
Dog 1,032
Panda 1,029
Elephant 891
Armadillo 981
Bird
Duck 807
Zebra Finch 951
Fish
Platyfish 1,122
Ferret
Panda
Dog
Cat
Elephant
Chimpanzee
Gibbon
Rat
Macaque
Armadillo
Human
Pig (MSGENE02729)
Sheep
Cow
Platyfish
Zebrafish
Chicken
Duck
Zebra Finch
0.02
Depth (×)
Average depth (×) of exons
Tibetan wild boar 23.33
Rongchang 46.04
Piétrain 33.53
Meishan 62.37
Large White 41.90
Landrace 32.59
Jinhua 54.19
Hampshire 48.11
Bamei 36.68
Berkshire 55.81
Duroc 22.25
MSGENE02729
Longest gene model

i


TROVE2
Berkshire
Bamei
Jinhua
Landrace
Meishan
Piétrain
Hampshire
Large White
Rongchang
Tibetan wild boar
Exon length
100 bp
Exon length (bp)
Mammal
Pig
Tibetan wild boar 1,587
Berkshire 1,587
Bamei 1,587
Hampshire 1,587
Jinhua 1,587
Landrace 1,587
Meishan 1,587
Piétrain 1,587
Large White 1,602
Rongchang 1,209
Mouse 1,617
Rat 1,617
Guinea pig 1,605
Rabbit 1,617
Chimpanzee 1,614
Gibbon 1,557
Olive baboon 1,614
Alpaca 1,614
Dolphin 1,611
Sheep 1,674
Cow 1,617
Cat 1,617
Ferret 1,614
Dog 1,662
Panda 1,611
Horse 1,617
Elephant 1,617
Armadillo 1,614
Platypus 1,617
Bird
Duck 1,614
Chicken 1,554
Zebra Finch 1,545
Fish
Platyfish 1,611
Zebrafish 1,605
Zebrafish
Platyfish
Zebra Finch
Chicken
Duck
Platypus
Mouse
Rat
Alpaca
Pig (TPGENE12222)
Cow
Sheep
Dolphin
Guinea pig
Panda
Cat
Ferret
Dog
Gibbon
Olive baboon
Chimpanzee
Rabbit
Horse
Elephant
Armadillo
0.01
Depth (×)
Average depth (×) of exons
Tibetan wild boar 48.59
Rongchang 37.78
Piétrain 35.97
Meishan 45.59
Large White 36.48
Landrace 32.86
Jinhua 46.43
Hampshire 44.96
Bamei 36.08
Berkshire 48.02
Duroc 29.20
TPGENE12222
Longest gene model

j.

Gene symbol	Gene name	Functional description
ATP6AP1	ATPase, H^+ transporting, lysosomal accessory protein 1	An accessory subunit of the vacuolar ATPase complex, which assists in the V-ATPase-mediated acidification of neuroendocrine secretory granules[8] and is associated with several tumors such as adrenal tumor, head and neck carcinoma, leukemia, lung tumor, retinoblastoma and breast cancer[9,10].
HFE	Hemochromatosis	A causal gene of the common iron overload disorder hereditary hemochromatosis[11], which regulates iron uptake and is responsible for the alternation of energy metabolism in adipose tissue in response to an obesity-related alteration of iron homeostasis[12,13].
NOD2	Nucleotide-binding oligomerization domain-containing protein 2	Also known as caspase recruitment domain-containing protein 15 (*CARD15*) or inflammatory bowel disease protein 1 (*IBD1*), an intracellular pattern recognition receptor[14], which could recognize bacterial molecules (peptidoglycans) and stimulate an immune reaction[15]. Mutations in *NOD2* have been associated with Crohn's disease[16], Blau syndrome[17], severe pulmonary sarcoidosis and Graft-versus-host disease[18].
PTK6	Protein-tyrosine kinase 6	Also known as breast tumor kinase (*BRK*), a cytoplasmic non-receptor protein kinase, which functions as an intracellular signal transducer in epithelial tissues[19] and is a mediator of hypoxia-associated breast cancer progression[20].
RPGRIP1L	Retinitis pigmentosa GTPase regulator-interacting protein-1-like	A component of the basal body of the cilium, which modulates leptin sensitivity in the hypothalamic arcuate nucleus[21], thus participates in the control of food intake and energy homeostasis by virtue of the obesity phenotype in the Bardet-Biedl and Alström syndromes[22,23].
SIVA1	Apoptosis-inducing factor 1	A pro-apoptotic gene that is unregulated in various pathological circumstances, which interacts with members of tumor necrosis factor receptor family (TNFR)[24], and has a significant impact on T-cell homeostasis and autoimmune disorders as well as T-cell memory[25].
TAZ	Tafazzin	A mitochondrial transacylase that is expressed at high levels in cardiac and skeletal muscle[26,27], and is unequivocally associated with human Barth syndrome characterized by dilated cardiomyopathy, neutropenia, skeletal myopathy and growth retardation[28].
TBXA2R	Thromboxane A2 receptor	A member of the G-PCR super family, which induces platelet aggregation and regulate hemostasis[29] and is associated with a bleeding disorder[30] and asthma-related phenotypes[31].
TROVE2	TROVE domain family member 2	*TROVE2* encodes a RNA binding protein Ro60, which has a specific RNA recognition domain for Y RNAs but binds additional, possibly misfolded, RNAs through a separate cavity[32]. Autoantibodies to Ro60 are present in individuals with systemic lupus erythematosus, Sjögren's syndrome[33], neonatal lupus with heart block, and other autoimmune disorders[34].

Supplemental Fig. S40. Examples of fat deposition and immunity-related missing genes. (a) *ATP6AP1*; **(b)** *HFE*; **(c)** *NOD2*; **(d)** *PTK6*; **(e)** *RPGRIP1L*; **(f)** *SIVA1*; **(g)** *TAZ*; **(h)** *TBXA2R*; **(i)** *TROVE2*; and **(j)** Summary of gene function. For **(a)** to **(i)**, Top panels: The inter-assembly collinear genes (colorized rectangles) are linked by gray lines, while genes not presented in all of ten assemblies were marked in black. Obesity and immunity-related

missing genes are highlighted and denoted as circles. Different scaffolds are distinguished by alternant white and gray backgrounds. Second panels, left: comparison of structure of emphasized inter-assembly collinear genes and available species in Ensemble (release 83). Boxes and lines indicate exons and introns, respectively. Second panels, right: phylogenetic tree of highlighted missing gene in various species. For pig, the longest gene model of inter-assembly collinear genes was used. The topological relationships were constructed based on protein sequences using a multiple sequence alignment program Clustal Omega tool (v.1.2.1), which uses seeded guide trees and HMM profile-profile techniques to generate alignments[35]. The phylogenetic relationships across species of emphasized missing genes were in accordance with the evolutionary distance with pig lineage. Third panels: Coverage and depth for the longest gene model by crossly mapping with reads from paired-end DNA libraries (insert sizes of 180 and 500 bp) of ten assemblies. The higher coverage depth suggests slightly different structures of missing genes that are mainly attributable to the limitations of short reads assembly, as such the longest gene model is considered more reliable and used for subsequent analyses. We additionally resequenced the whole genomes of a male Duroc pig (same as the breed used as donor for the pig genome project) at 38.69 × depth coverage.