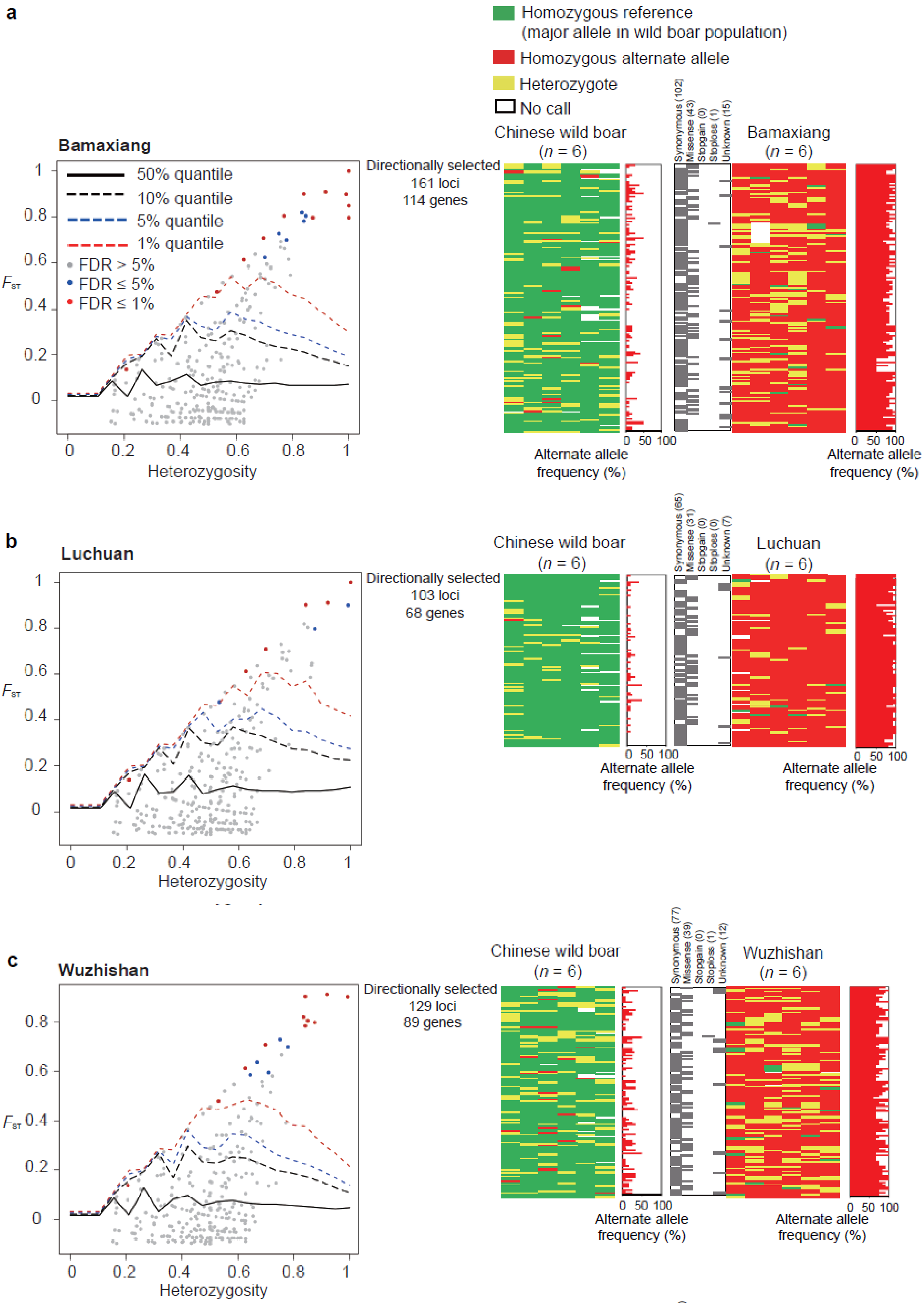
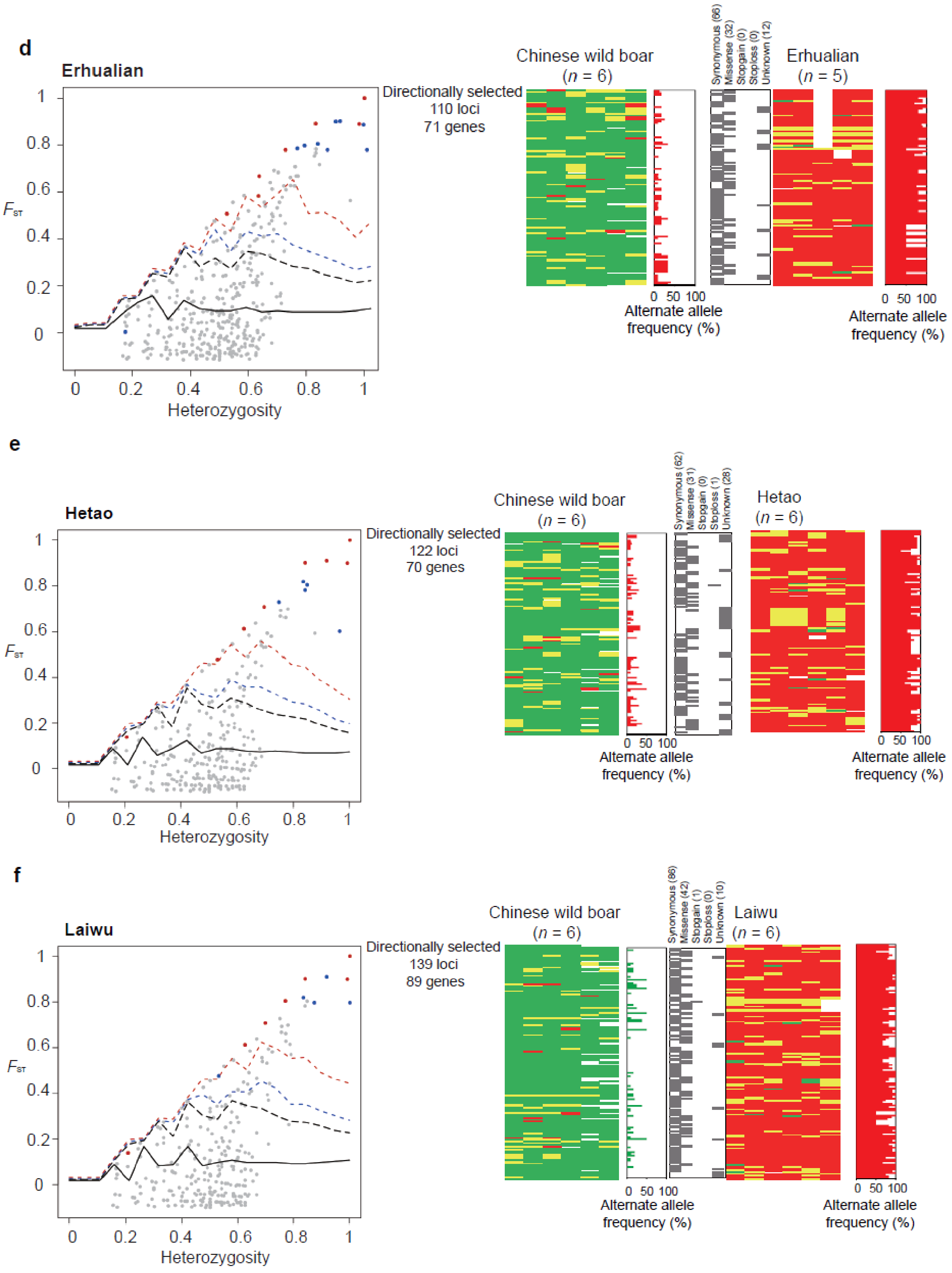
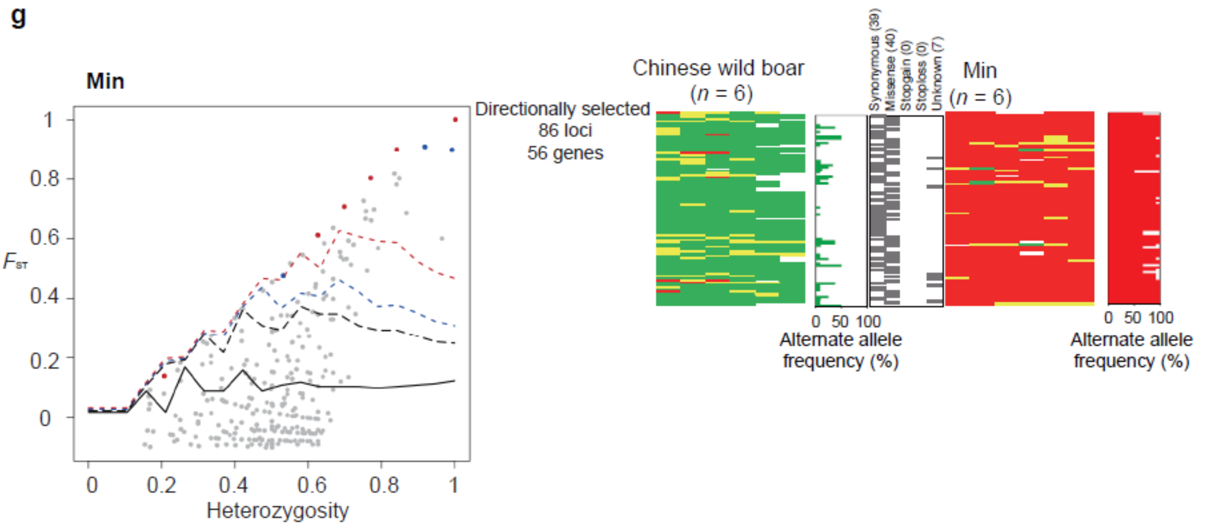

a
🟩 Homozygous reference (major allele in wild boar population)
🟥 Homozygous alternate allele
🟨 Heterozygote
☐ No call
Bamaxiang
1
0.8
0.6
F_{ST}
0.4
0.2
0
50% quantile
10% quantile
5% quantile
1% quantile
● FDR > 5%
● FDR ≤ 5%
● FDR ≤ 1%
0 0.2 0.4 0.6 0.8 1
Heterozygosity
Directionally selected
161 loci
114 genes
Chinese wild boar
(*n* = 6)
Synonymous (102)
Missense (43)
Stopgain (0)
Stoploss (1)
Unknown (15)
Bamaxiang
(*n* = 6)
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)
b
Luchuan
1
0.8
0.6
F_{ST}
0.4
0.2
0
0 0.2 0.4 0.6 0.8 1
Heterozygosity
Directionally selected
103 loci
68 genes
Chinese wild boar
(*n* = 6)
Synonymous (65)
Missense (31)
Stopgain (0)
Stoploss (0)
Unknown (7)
Luchuan
(*n* = 6)
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)
c
Wuzhishan
0.8
0.6
F_{ST} 0.4
0.2
0
0 0.2 0.4 0.6 0.8 1
Heterozygosity
Directionally selected
129 loci
89 genes
Chinese wild boar
(*n* = 6)
Synonymous (77)
Missense (39)
Stopgain (0)
Stoploss (1)
Unknown (12)
Wuzhishan
(*n* = 6)
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)


d
Erhualian
Chinese wild boar
(*n* = 6)
Erhualian
(*n* = 5)
Synonymous (66)
Missense (32)
Stopgain (0)
Stoploss (0)
Unknown (12)
Directionally selected
110 loci
71 genes
F_{ST}
1
0.8
0.6
0.4
0.2
0
0
0.2
0.4
0.6
0.8
1
Heterozygosity
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)
e
Hetao
Chinese wild boar
(*n* = 6)
Hetao
(*n* = 6)
Synonymous (62)
Missense (31)
Stopgain (0)
Stoploss (1)
Unknown (28)
Directionally selected
122 loci
70 genes
F_{ST}
1
0.8
0.6
0.4
0.2
0
0
0.2
0.4
0.6
0.8
1
Heterozygosity
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)
f
Laiwu
Chinese wild boar
(*n* = 6)
Laiwu
(*n* = 6)
Synonymous (86)
Missense (42)
Stopgain (1)
Stoploss (0)
Unknown (10)
Directionally selected
139 loci
89 genes
F_{ST}
1
0.8
0.6
0.4
0.2
0
0
0.2
0.4
0.6
0.8
1
Heterozygosity
0 50 100
Alternate allele frequency (%)
0 50 100
Alternate allele frequency (%)



Supplemental Fig. S43. Detection of coding SNPs under selection between Chinese wild boar and seven domestic populations. **(a)** Bamaxiang, **(b)** Luchuan, **(c)** Wuzhishan, **(d)** Erhualian, **(e)** Hetao, **(f)** Laiwu and **(g)** Min. Left panels: the simulated joint distribution of Heterozygosity-F_{ST} of SNPs from Chinese wild boar and domestic populations under finite island model using Arlequin (v.3.5.2.2)[39]. The upper red and blue dots are outliers subjected to directional selection (FDR < 0.05). Right panels: individual genotype of selected loci. The alternate allele frequency (%) and mutations annotation are also indicated. Allele of the highest frequency in wild boar population was used as the reference allele.