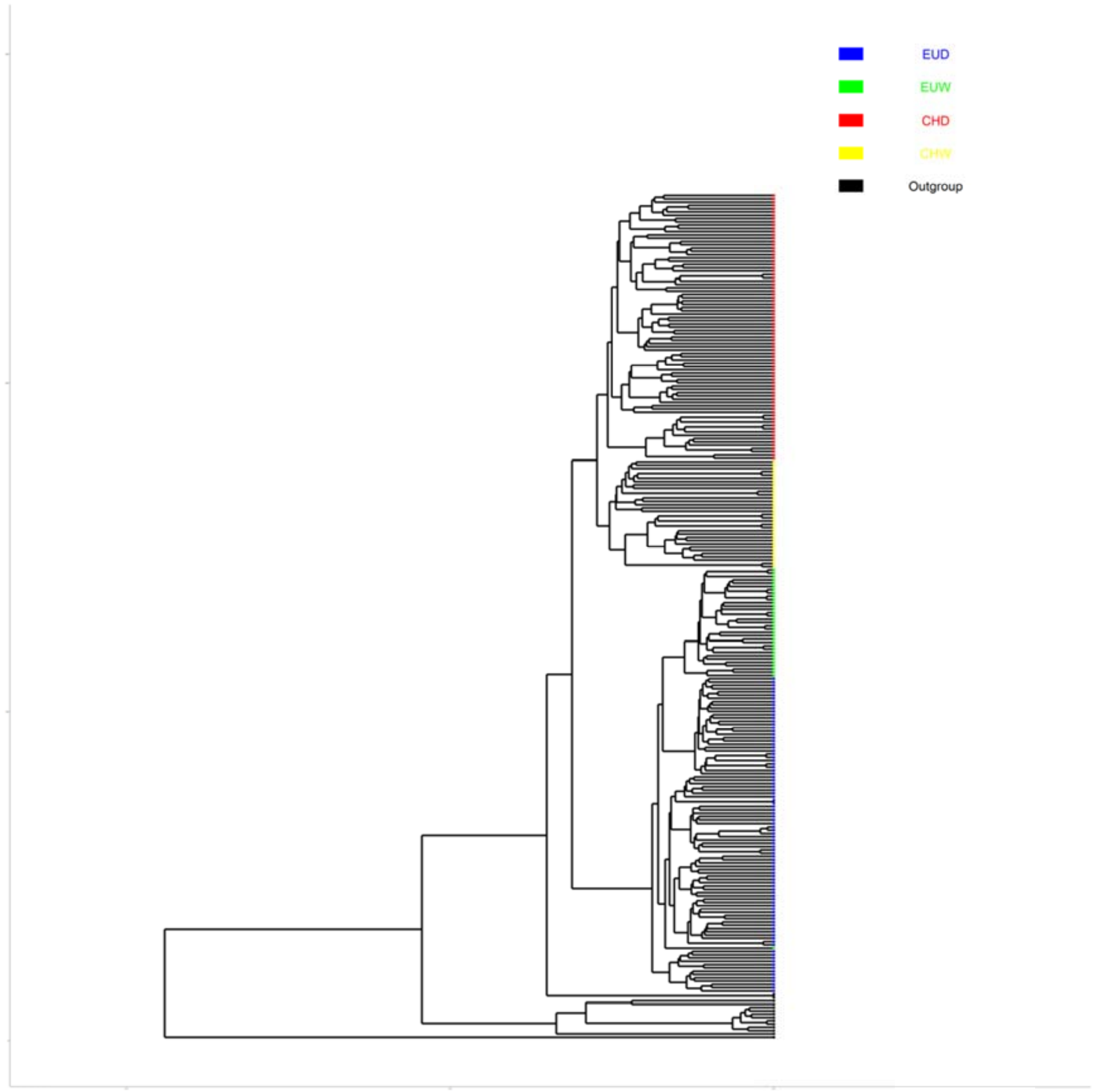
# Convergent and divergent genetic changes in the genome of Chinese and European pigs

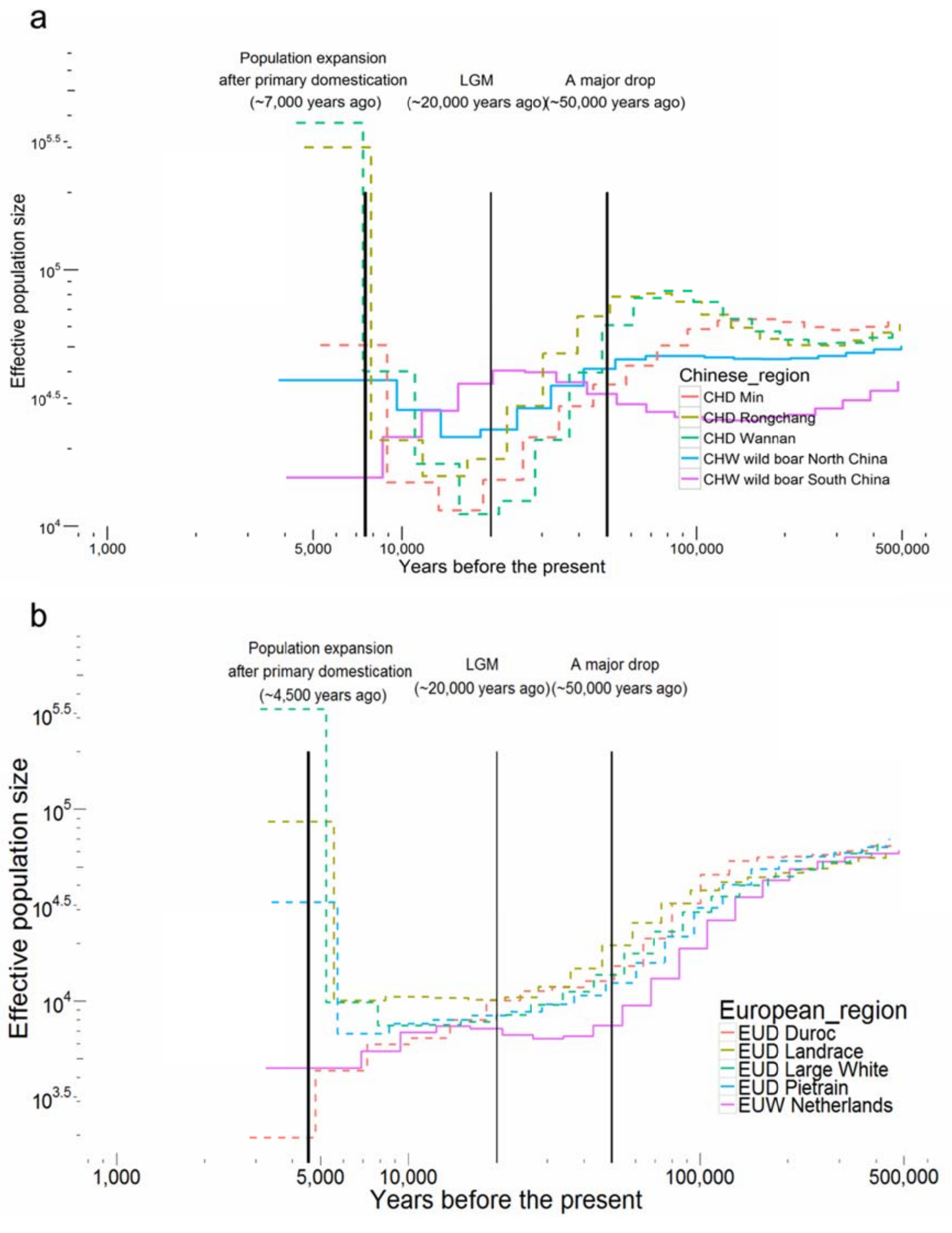
Jing Wang[1,2+], Huiying Zou[2,7+], Lei Chen[3], Xi Long[3], Jing Lan[3], Wenjie Liu[2], Li Ma[2], Chao Wang[4], Xinyu Xu[5], Liming Ren[2], Zhenglong Gu[6], Ning Li[2], Xiaoxiang Hu[2], Yaofeng Zhao[2]* & Yiqiang Zhao[1,2]*.

# Supplemental Information

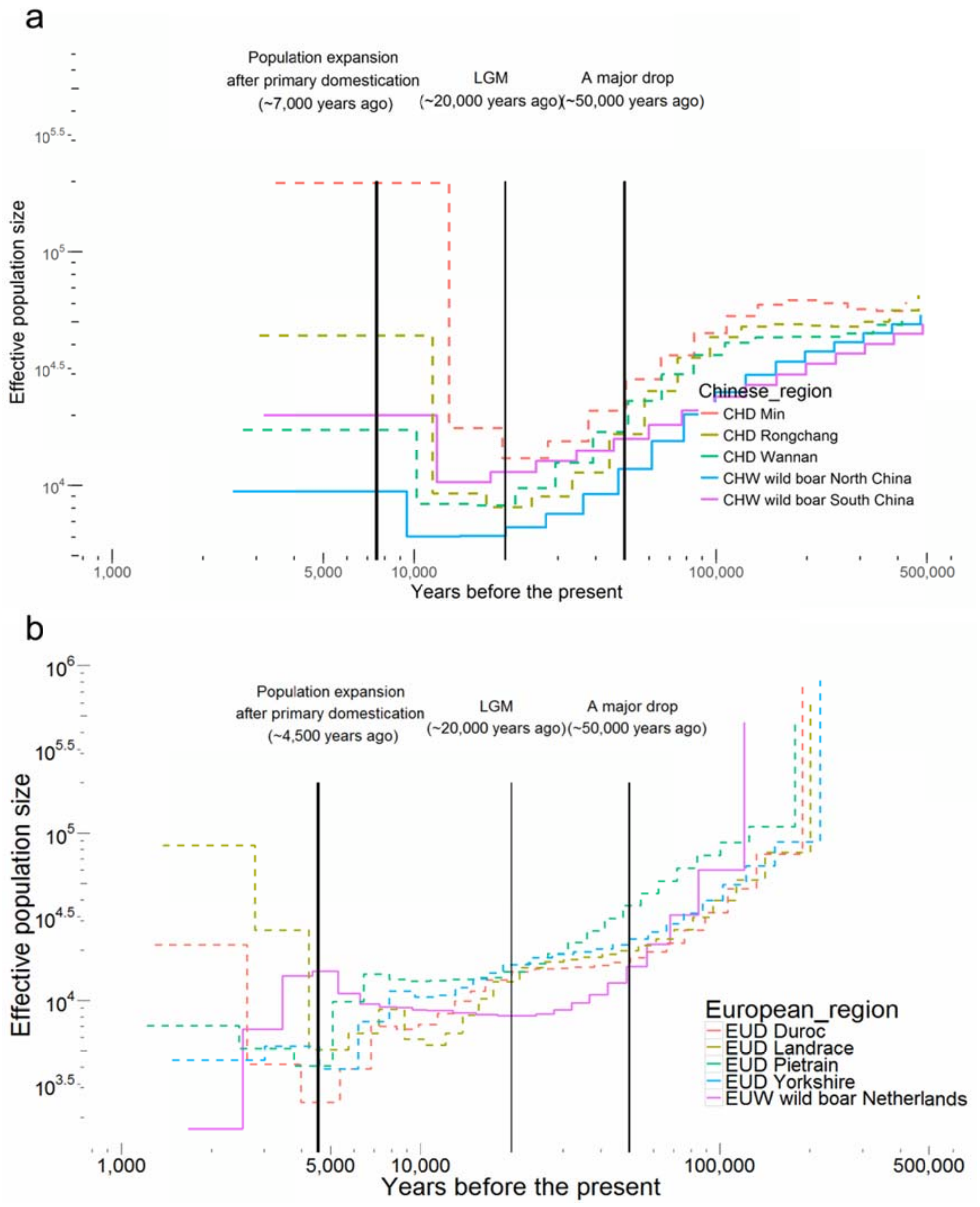
## Supplementary Figures S1-S12



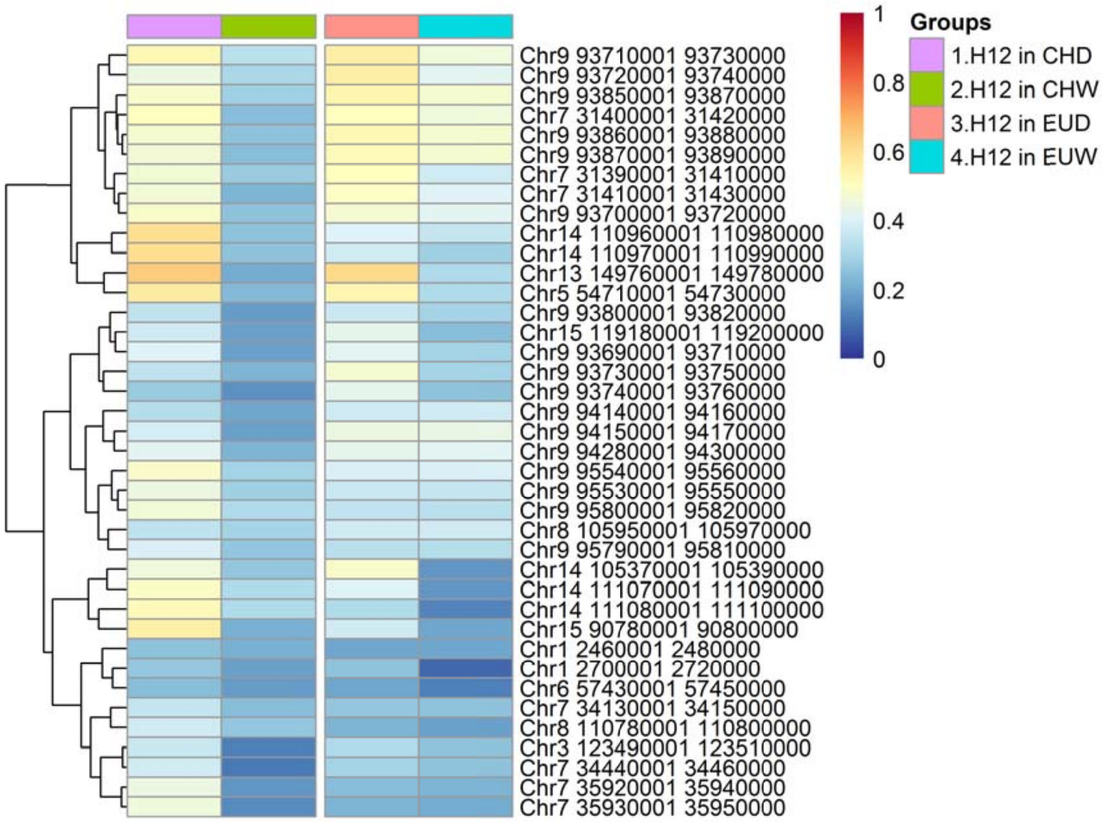
**Supplementary Figure 1. Neighbor-joining tree in whole genome regions.** Neighbor-joining tree is based on an identity-by-state (IBS) distance matrix, using the data in the whole genome regions. The CHD include Mini-pigs.



**Supplementary Figure 2. Demographic history of domestic breeds and wild boars in China and Europe on phased data.** 2 individuals from each breeds were used to infer the demographic history using a hidden Markov model approach as implemented in multiple sequentially Markovian coalescence based on SNP distribution. The Demographic history is inferred based on phased data. **(a),** Demographic history of domestic breeds and wild boars in China. **(b),** Demographic history of domestic breeds and wild boars in Europe.

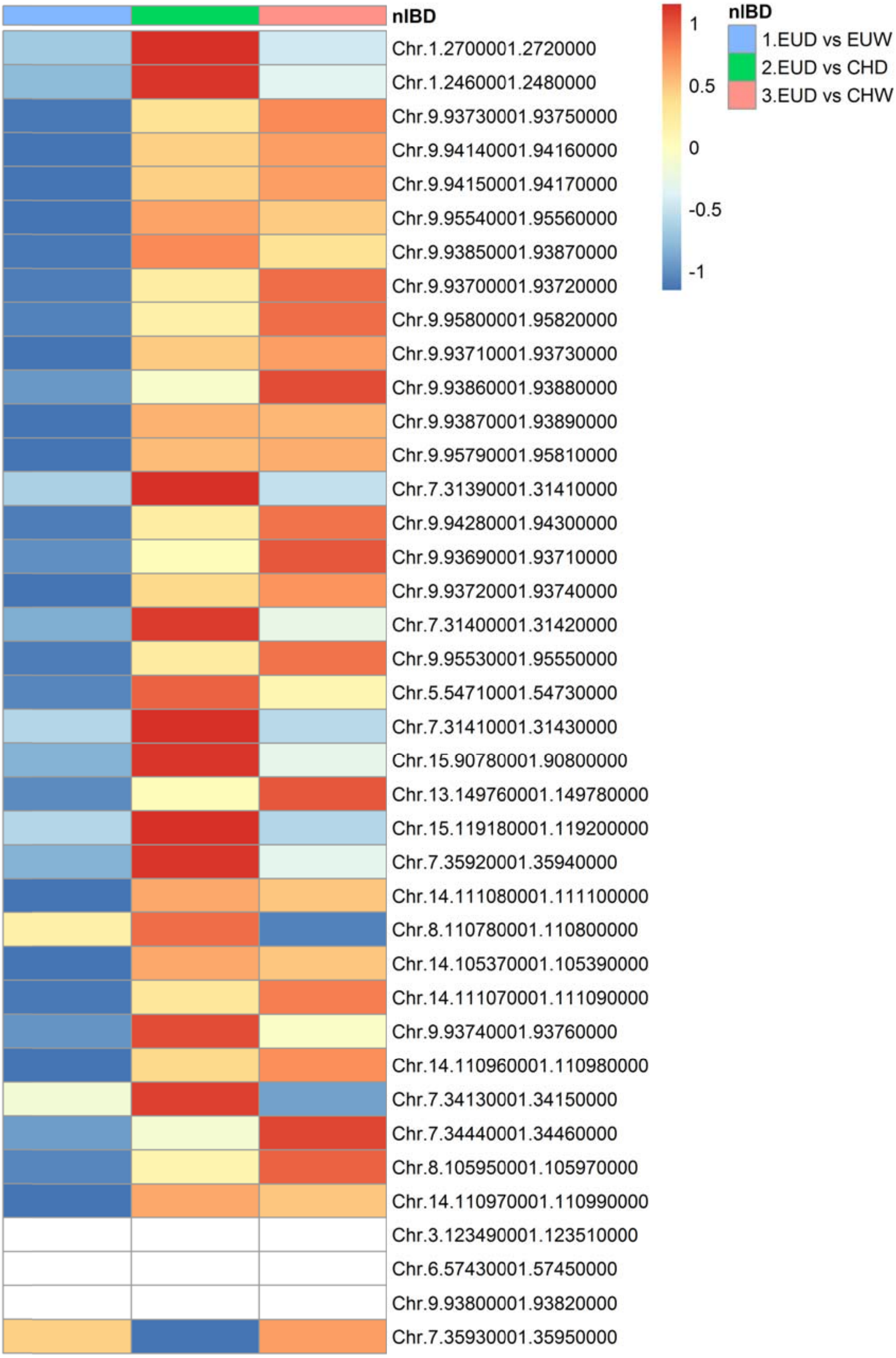


**Supplementary Figure 3. Demographic history of domestic breeds and wild boars in China and Europe on unphased data.** 2 individuals from each breeds were used to infer the demographic history using a hidden Markov model approach as implemented in multiple sequentially Markovian coalescence based on SNP distribution. The Demographic history is inferred based on unphased data. **(a),** Demographic history of domestic breeds and wild boars in China. **(b),** Demographic history of domestic breeds and wild boars in Europe.

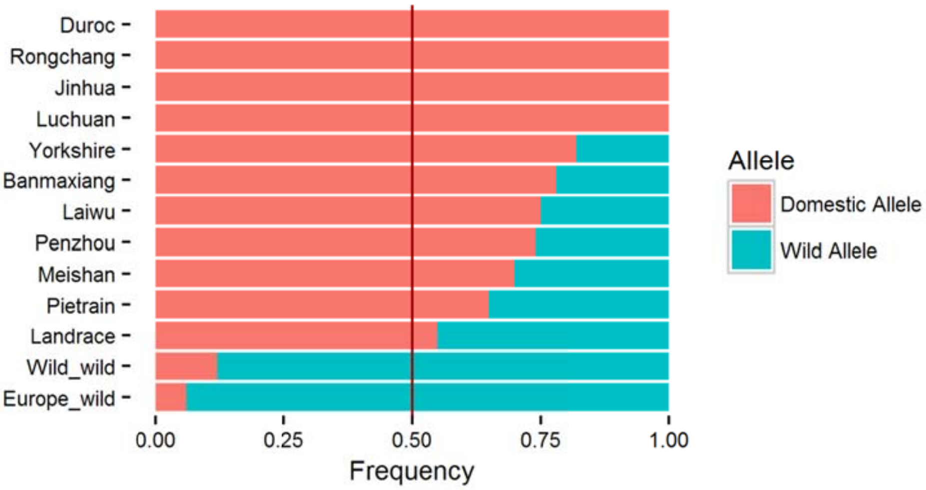


**Supplementary Figure 4. The H12 in unidirectional selection regions for each group.** Heatmap from hierarchical clustering of the H12 value in the 39 unidirectional regions for each group. Heat-map colors (right) indicate the H12 value.

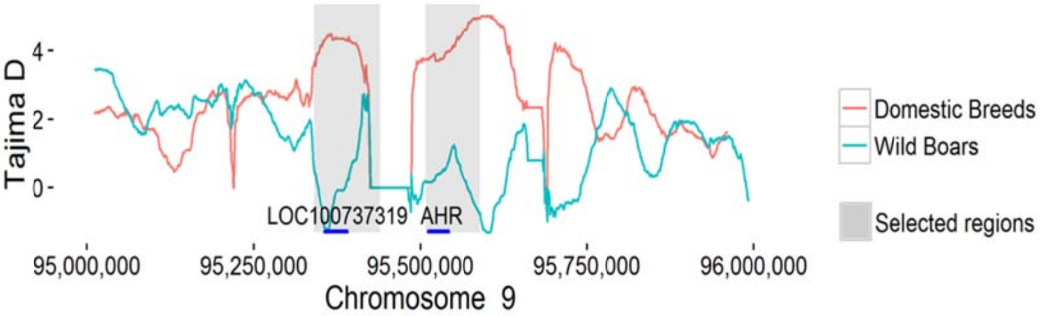
**Supplementary Figure 5. Neighbor-joining tree in unidirectional selection regions.** Neighbor-joining tree is based on an identity-by-state (IBS) distance matrix, using the data in unidirectional selection regions only. The CHD include Mini-pigs.



**Supplementary Figure 6. Pairwise nIBD between EUD and the other three groups in unidirectional selection regions.** Heatmap from pairwise nIBD in the 39 unidirectional regions. The heatmap was plotted scaled by row.

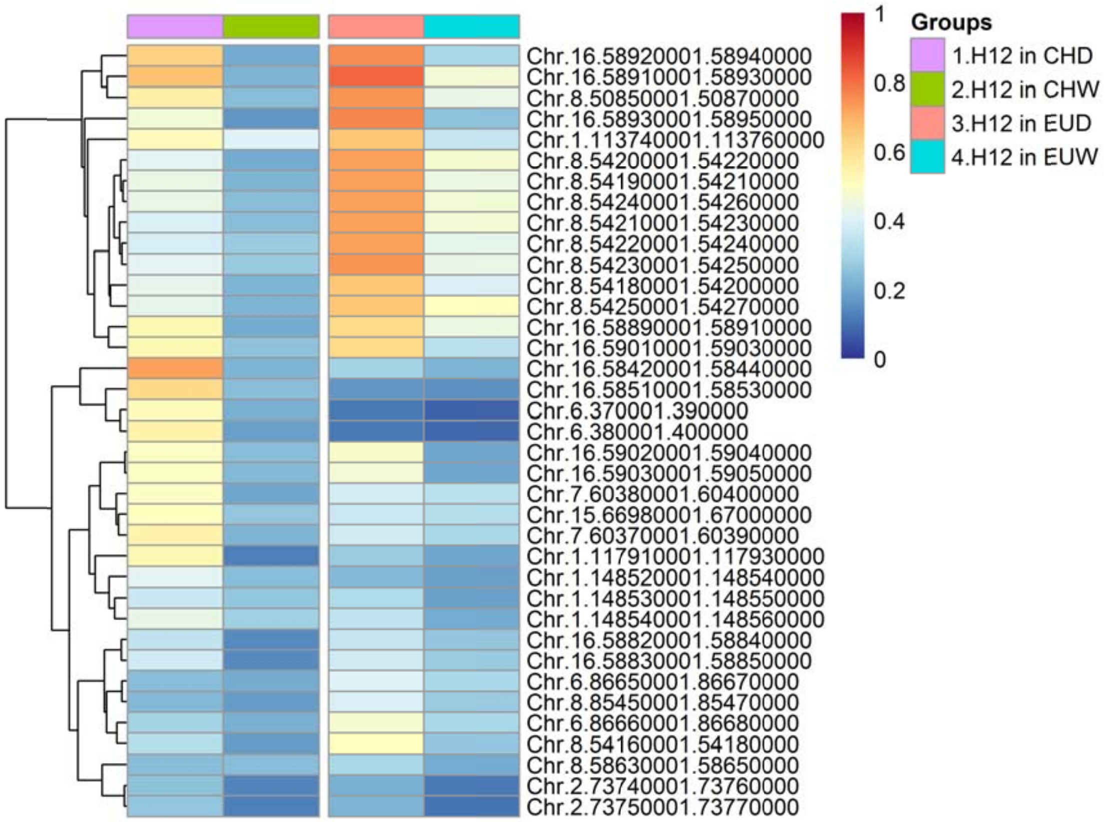


**Supplementary Figure 7. The average frequency of the 5 non-synonymous substitutions in each breed.** The five variants correspond to mutations of amino acids (P419T, K616Q, G717C, F803L, and T839P) in *AHR*.



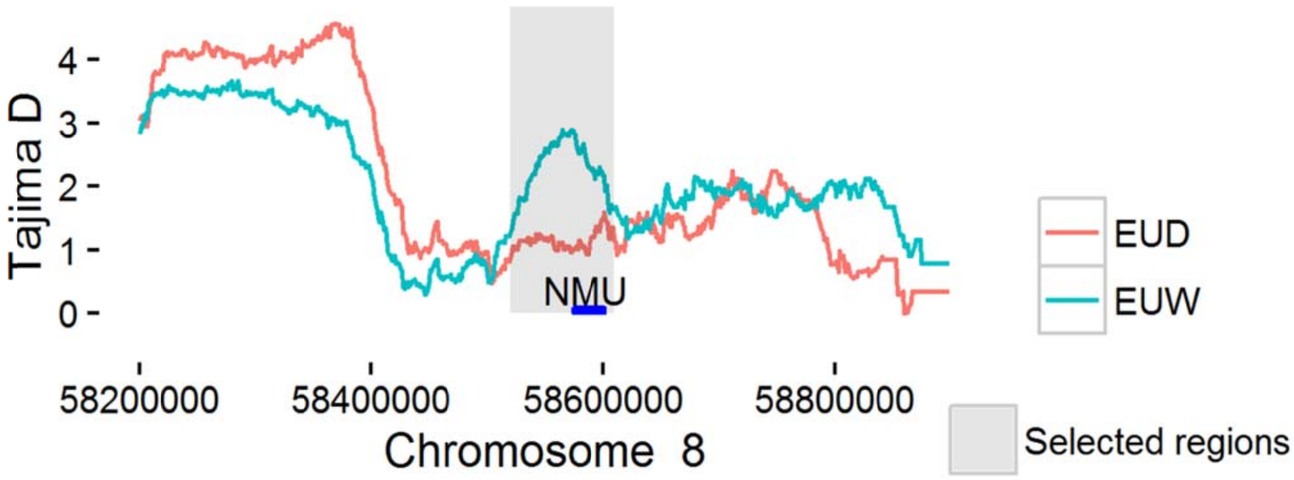
**Supplementary Figure 8. Genomic regions with strong unidirectional selection signals in European domestic breeds and European wild boars.**

Tajima’s D (red and blue lines for domestic breeds and wild boars, respectively) are plotted using a 20 kb sliding window.

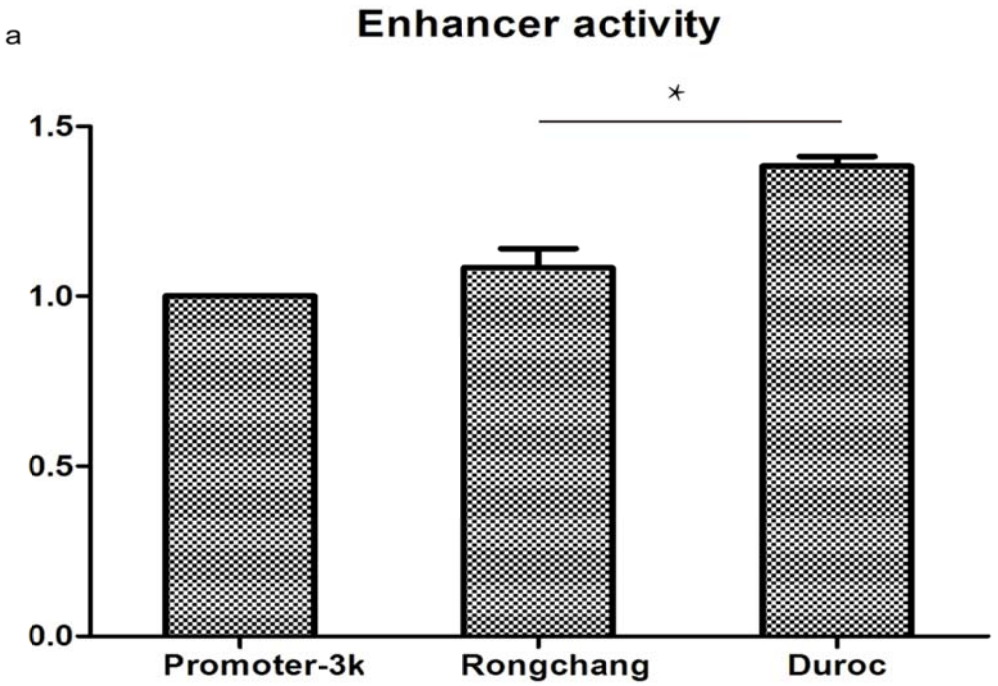


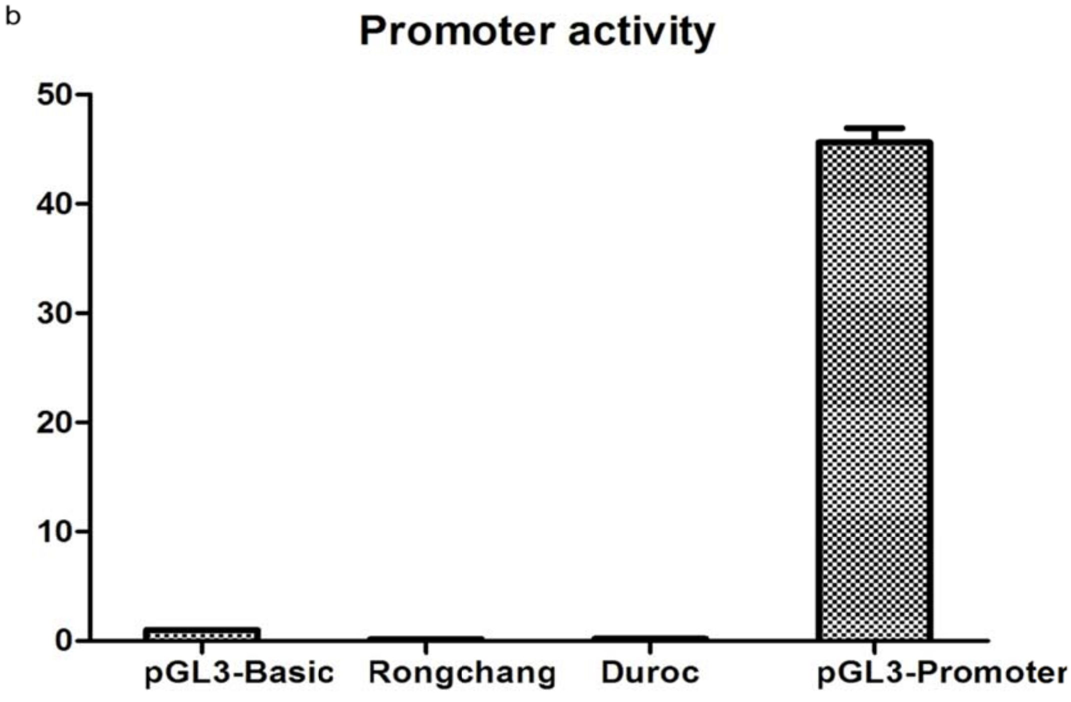
**Supplementary Figure 9. The H12 in unidirectional selection regions for each group.** Heatmap from hierarchical clustering of the H12 value in the 37 bidirectional regions for each group. Heat-map colors (right) indicate the H12 value.

**Supplementary Figure 10. Neighbor-joining tree in bidirectional selection regions.** Neighbor-joining tree is based on an identity-by-state (IBS) distance matrix, using the data in unidirectional selection regions only. The CHD include Mini-pigs.



**Supplementary Figure 11. Genomic regions with strong bidirectional selection signals in European domestic breeds and European wild boars.** Tajima's D (red and blue lines for European domestic breeds and European wild boars, respectively) are plotted using a 20 kb sliding window.





**Supplementary Figure 12. Validation the effect of the mutations in *NMU* using pig fibroblast cells. (a),** Luciferase assay testing the enhancer activity for different allele in the intron of the *NMU* in pig fibroblast cells**. (b),** Luciferase assay testing the promoter activity for different allele in the intron of the *NMU* in pig fibroblast cells.