

Description of Additional Supplementary Files

Supplementary Data 1. Data sets of 233 new sequencing genomes after different steps of quality control.

Supplementary Data 2. Sample information.

Supplementary Data 3. Sites filter summary.

Supplementary Data 4. Number of SNPs and references used for each analysis.

Supplementary Data 5. Admixture analysis by Haplonet.

Supplementary Data 6. Local ancestry inference by LOTER and F4-ratio.

Supplementary Data 7. New downloaded samples from northernmost Southeast Asia and East Asia during revisions.

Supplementary Data 8. GO enrichment analysis for genes in the top 5% proportion of Banteng introgression based on LOTER.

Supplementary Data 9. List of genes overlapping between top5% Loter and top5% Hmmix.

Supplementary Data 10. List of genes overlapping between top5% Ux and top5% Hmmix.

Supplementary Data 11. List of genes overlapping between top5% Loter and top5% Ux.

Supplementary Data 12. The 29 genes found in the top 5% proportion of introgression based on Loter across five breeds.

Supplementary Data 13. Frequency of high impact non-synonymous mutation in *ASIP* gene between various populations.

Supplementary Data 14. Number of SNP variants not found in other cattle populations (Allele Frequency ≤ 0.05), and fixed in Bantengs (AF ≥ 0.9).