

## Description of Additional Supplementary Files

Supplementary Data 1: Overview of the sampling information and sequencing statistics.

Supplementary Data 2: Common candidate genomic regions identified in South Asian indicine cattle based on the CLR,  $iHS$ ,  $F_{ST}$ , and  $\vartheta\pi$  analyses.

Supplementary Data 3: Common candidate genomic regions shared by South Asian indicine (SAI) and African indicine (AFI) cattle based on the  $iHS$  (proportion of SNPs with  $|iHS| \geq 2$ ) and CLR analyses.

Supplementary Data 4:  $D$  statistic among indicine, taurine cattle, banteng, and gaur to select pure indicine, taurine, banteng, and gaur samples.

Supplementary Data 5: Results of the  $D$  statistics (swamp buffalo as outgroup) tests performed to detect admixtures among 4 banteng, 2 gaur, 15 South Asian indicine, and 15 taurine cattle.

Supplementary Data 6: Statistics on introgressed intervals from banteng into 97 East Asian and Southwest Chinese indicine cattle.

Supplementary Data 7: Statistics on introgressed intervals from gaur into 97 East Asian and Southwest Chinese indicine cattle.

Supplementary Data 8: Sampling information of taurindicine cattle breeds from North-Central China.