

Genomic Patterns of Homozygosity in Chinese Local Cattle

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Supplementary files

Supplementary File1:

Table S1. The identified individual ROH across 179 individuals and ROH summary statistics per individual.

Supplementary File2:

Table S2. The nonredundant ROH regions in Chinese native cattle. ROH regions were determined by merging ROH identified across all samples within/across breed.

Supplementary File3:

Table S3. The DAVID annotations for the top annotated genes for each of eight breeds.

Supplementary File4:

Table S4. The full names, associated abbreviation for each breeds and additional information on the locations of the sampling areas.