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Pervasive introgression facilitated domestication and adaptation in the *Bos* species complex

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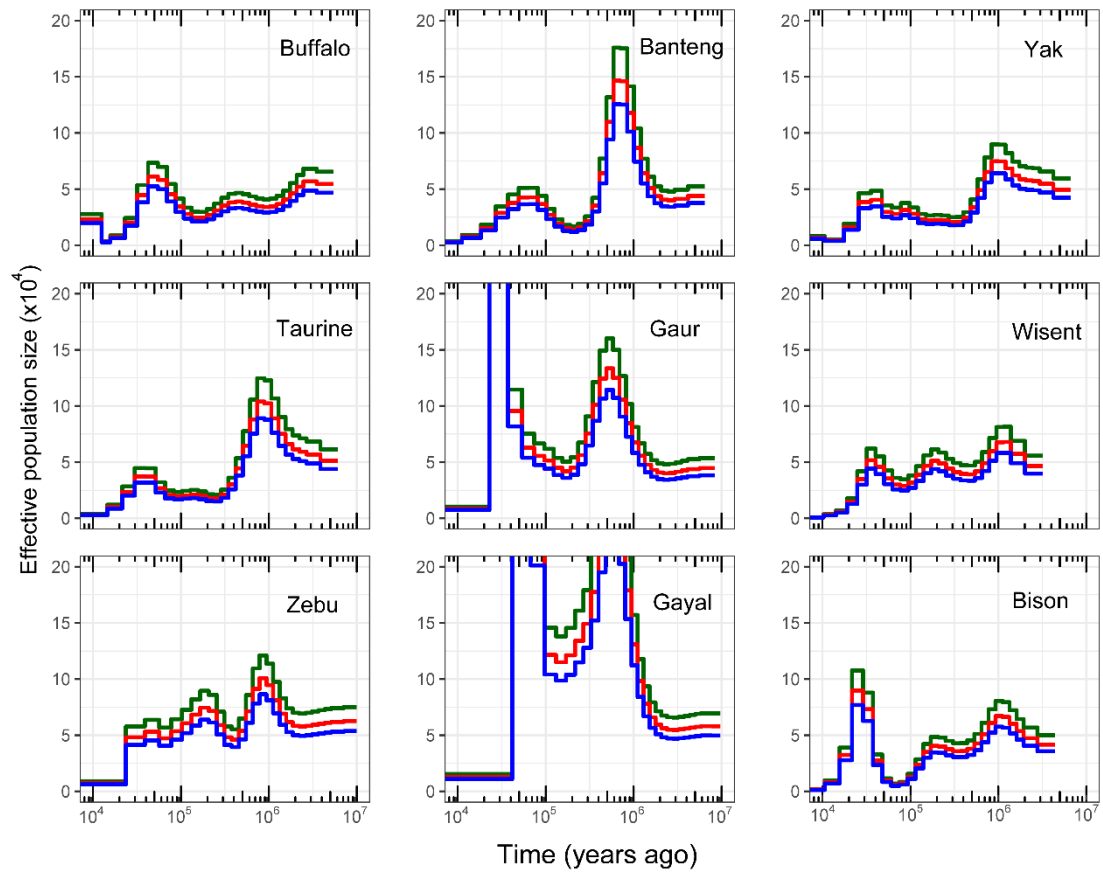
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Supplementary Information:

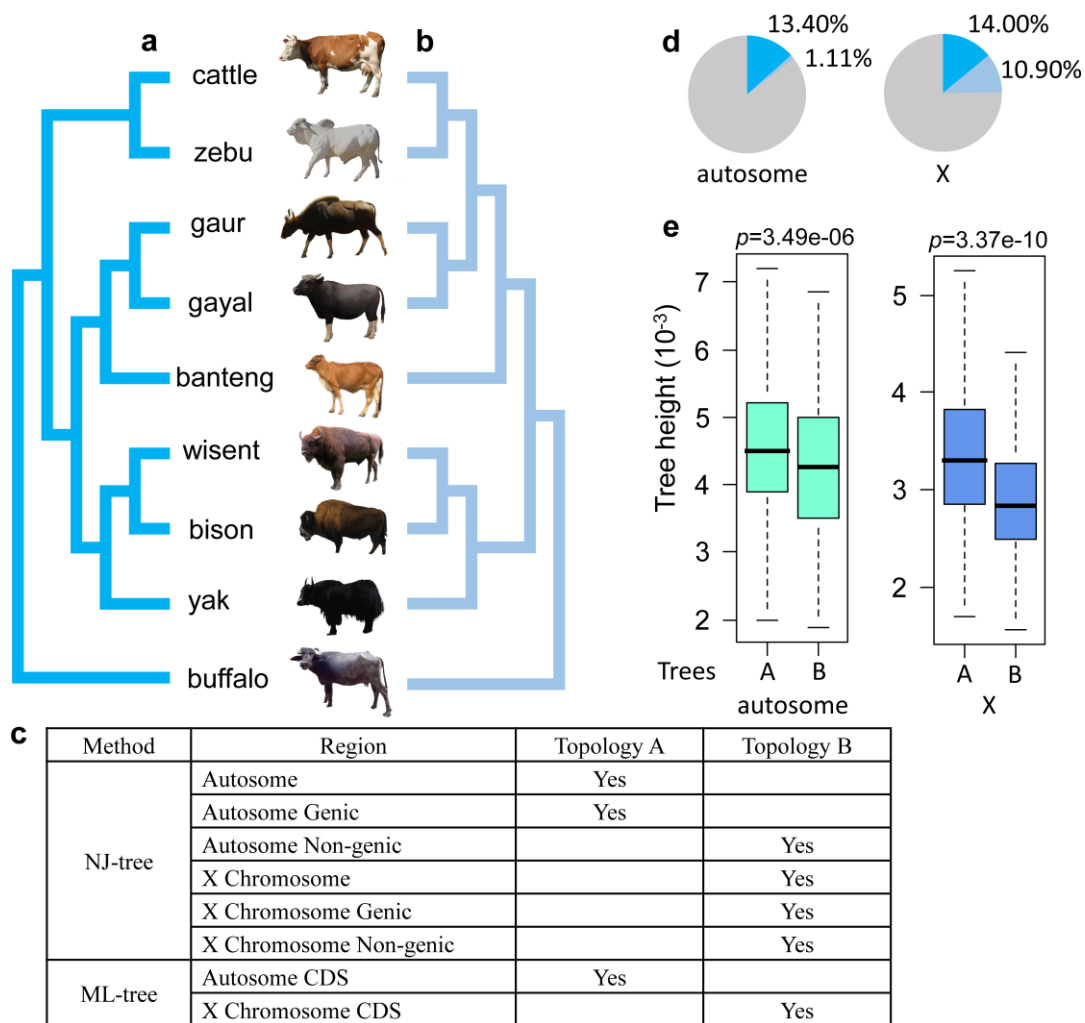
Pervasive introgression facilitated domestication and adaptation in the *Bos* species complex.

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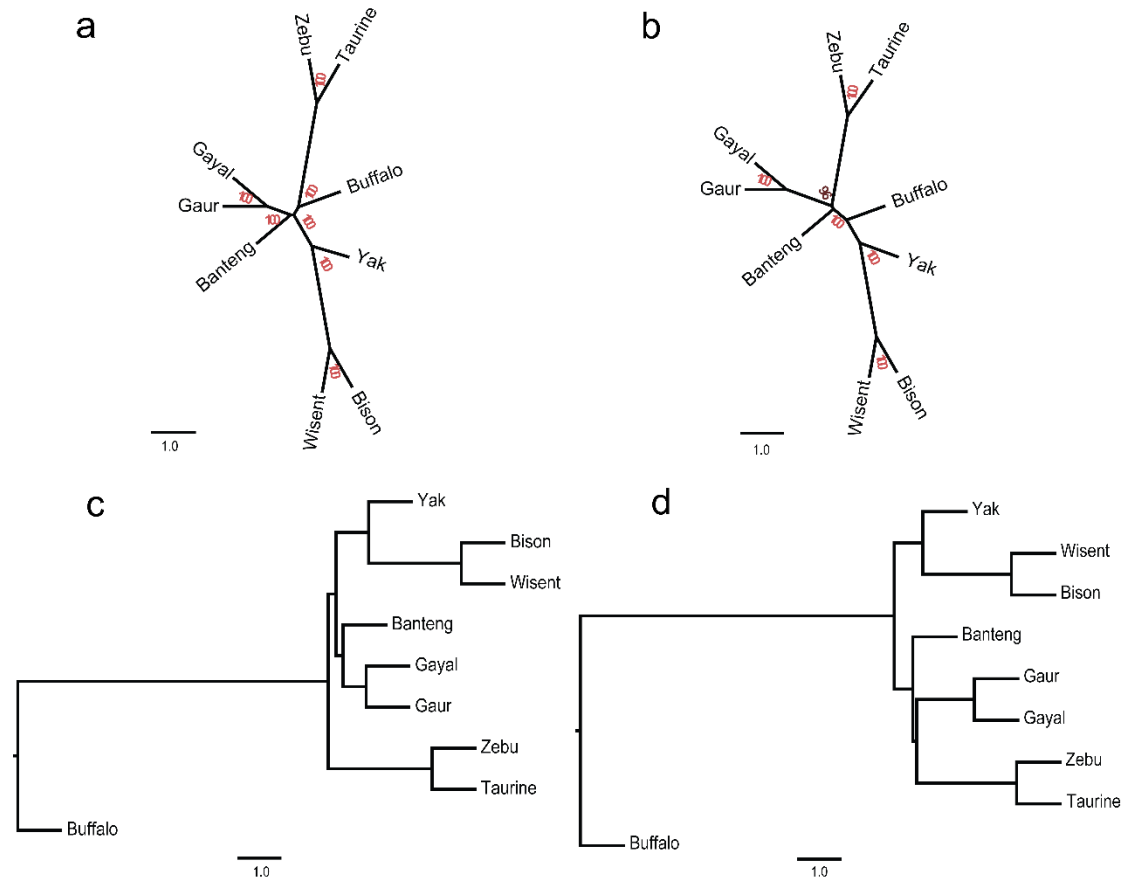
1. State Key Laboratory of Genetic Resources and Evolution, Yunnan Laboratory of Molecular Biology of Domestic Animals, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming 650223, China
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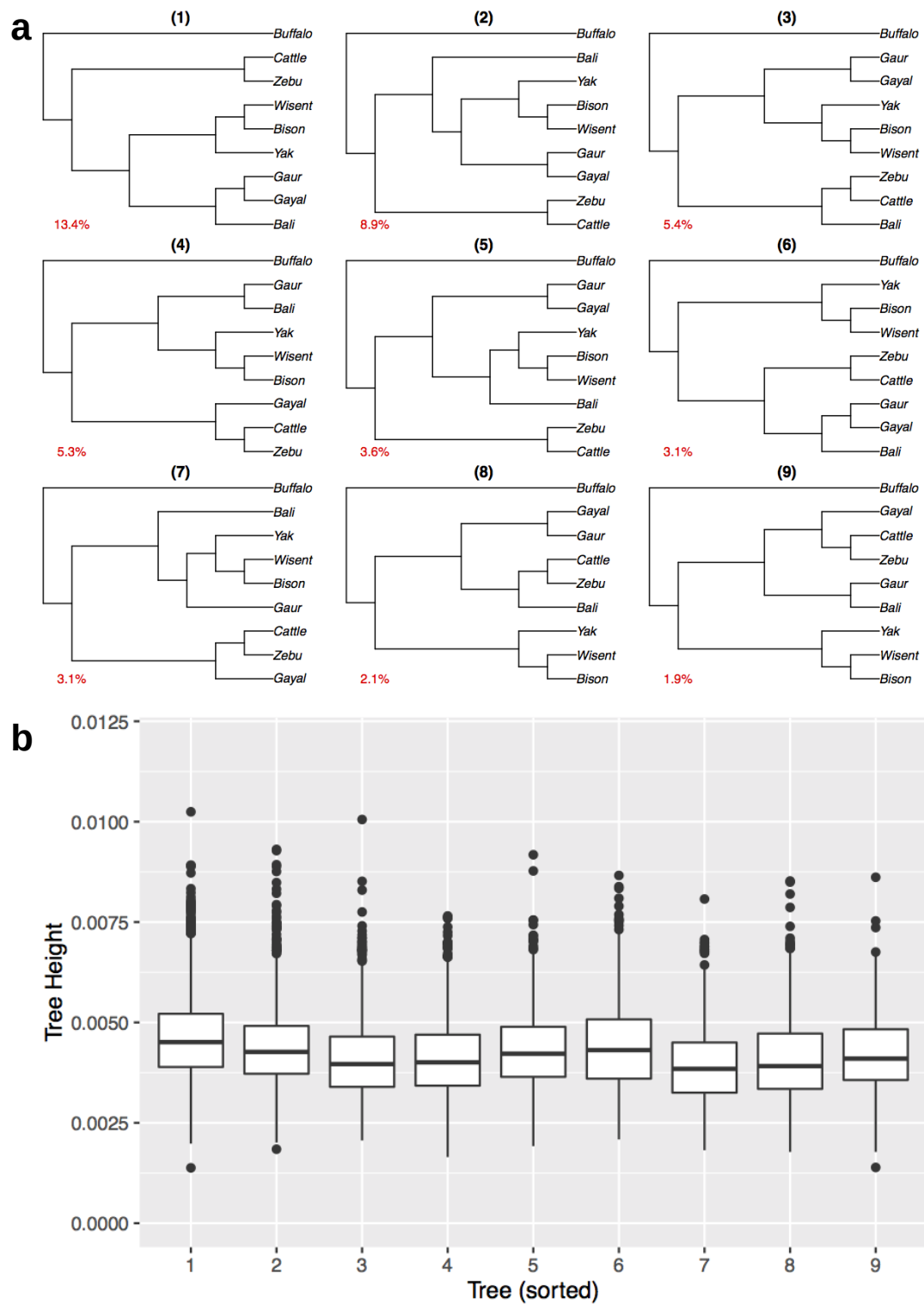
Supplementary Fig. 1: Dynamic changes of effective population size inferred by the PSMC program for nine high-coverage genomes. Colors of the lines indicate different generation times: 5 years (green), 6 years (red) and 7 years (blue). A mutation rate of $2.2\text{e-}9$ per site per year was applied.



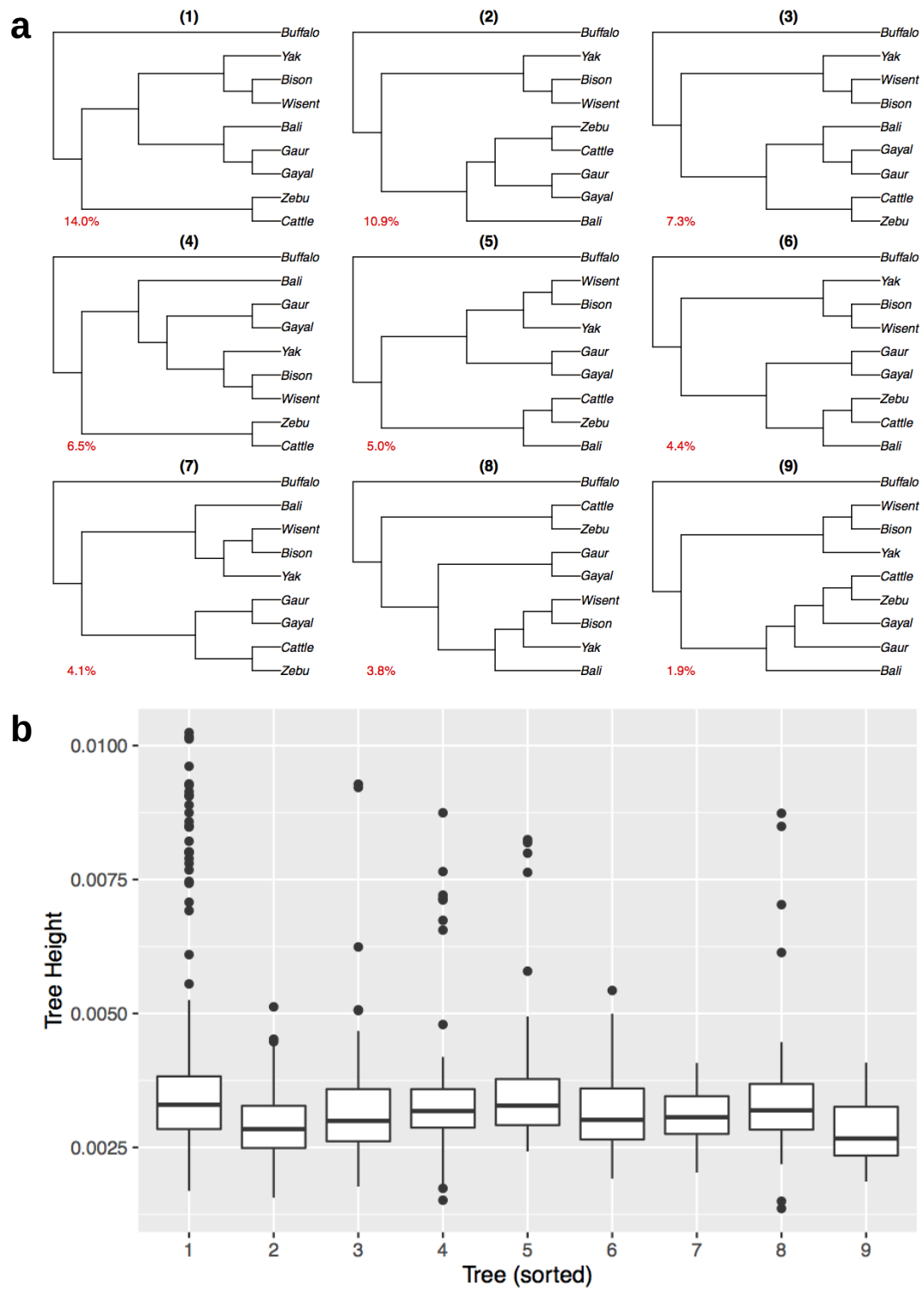
Supplementary Fig. 2: Phylogenetic analysis of species among *Bos* genus by RAxML program. (a) Phylogenetic topology A constructed based on whole autosome sequences by RAxML program. (b) Phylogenetic topology B constructed based on whole X-chromosome sequences by RAxML program. (c) Summarization of phylogenetic trees using different methods and regions. (d) Proportion of different phylogenetic topologies constructed by 25127 and 1489 non overlapping 100-kb windows from autosome and X chromosome. The most common tree topology is A, with 13.40% autosome windows, and 14.00% X windows. The proportions of B topology is 1.11% among autosome windows, and 10.90% among X windows, respectively. (e) Tree heights of topology A and B constructed by autosome sequences and X-chromosome sequence. The heights of A trees are significantly higher than the heights of B trees, with $p=3.49e-6$ using autosome windows, and $p=3.37e-10$ using X windows.



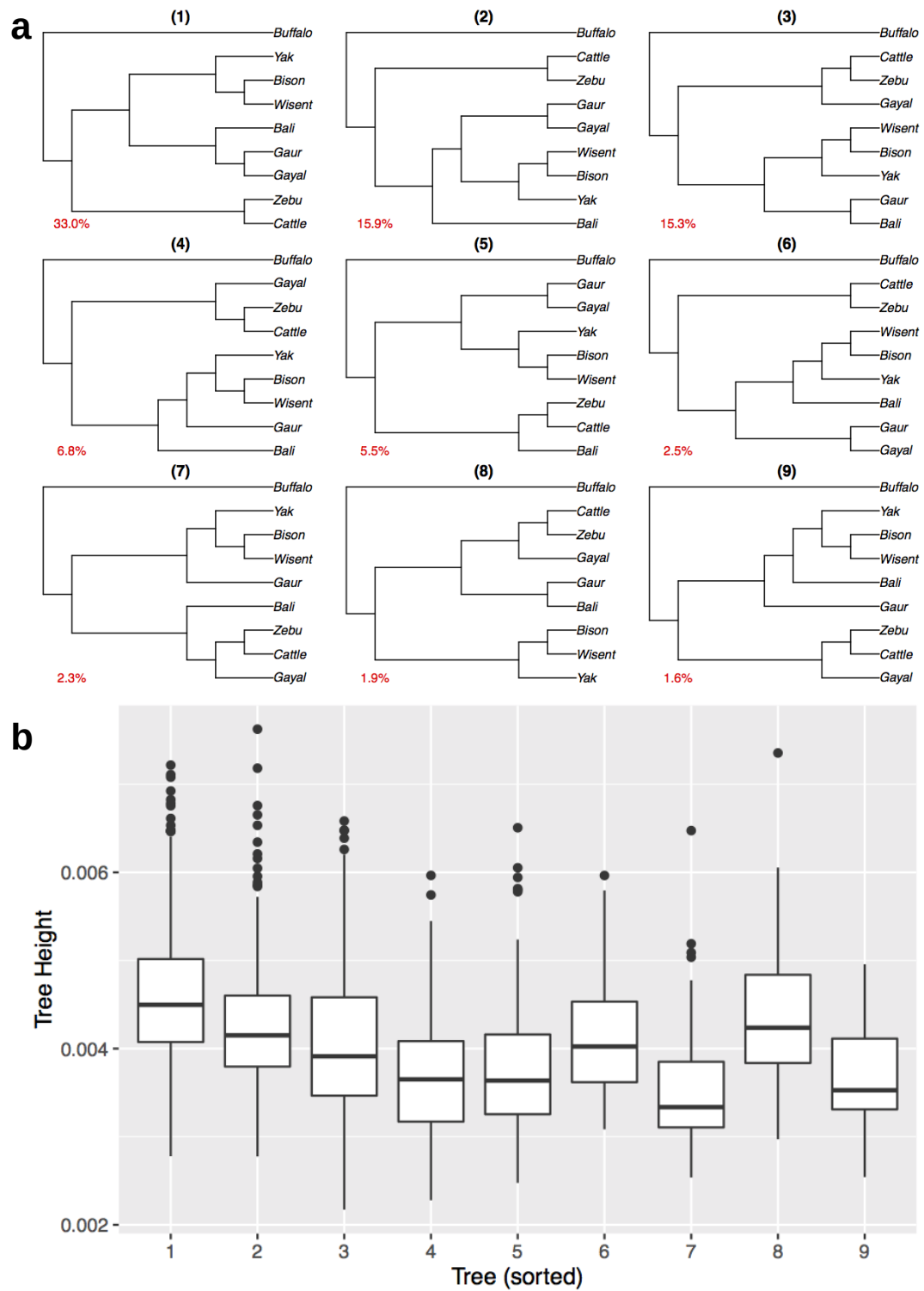
Supplementary Fig. 3: Construction of species tree using ASTRAL (a: all autosomes, b: X chromosome) and MP-EST (c: all autosomes, d: X chromosome) based on gene trees built from completed gene regions.



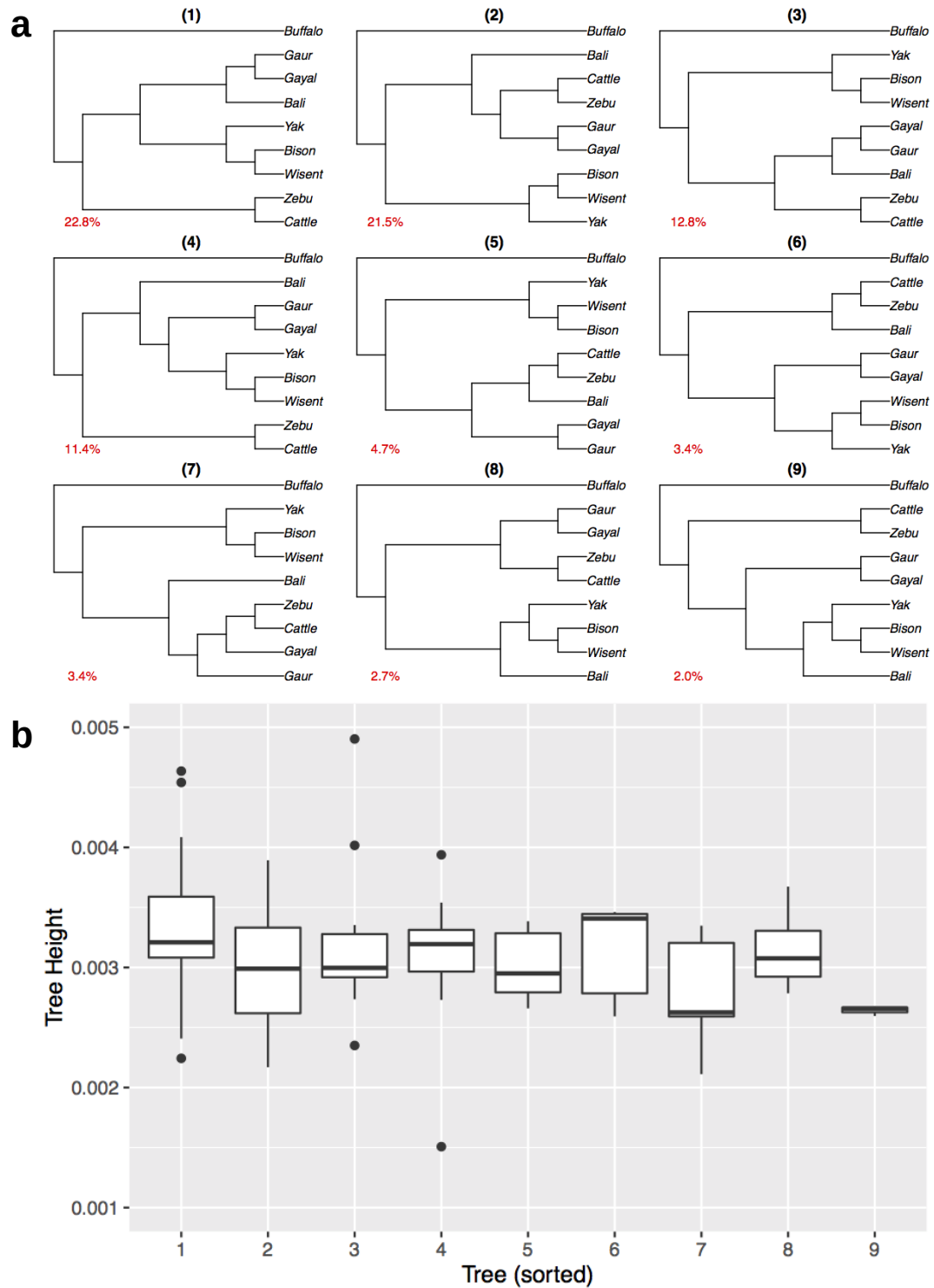
Supplementary Fig. 4: Construction of phylogenetic trees using 100-kb non-overlapping sliding windows at autosome. (a) The proportion of top 9 different topologies. (b) The box plots of tree height of top 9 window-bases trees.



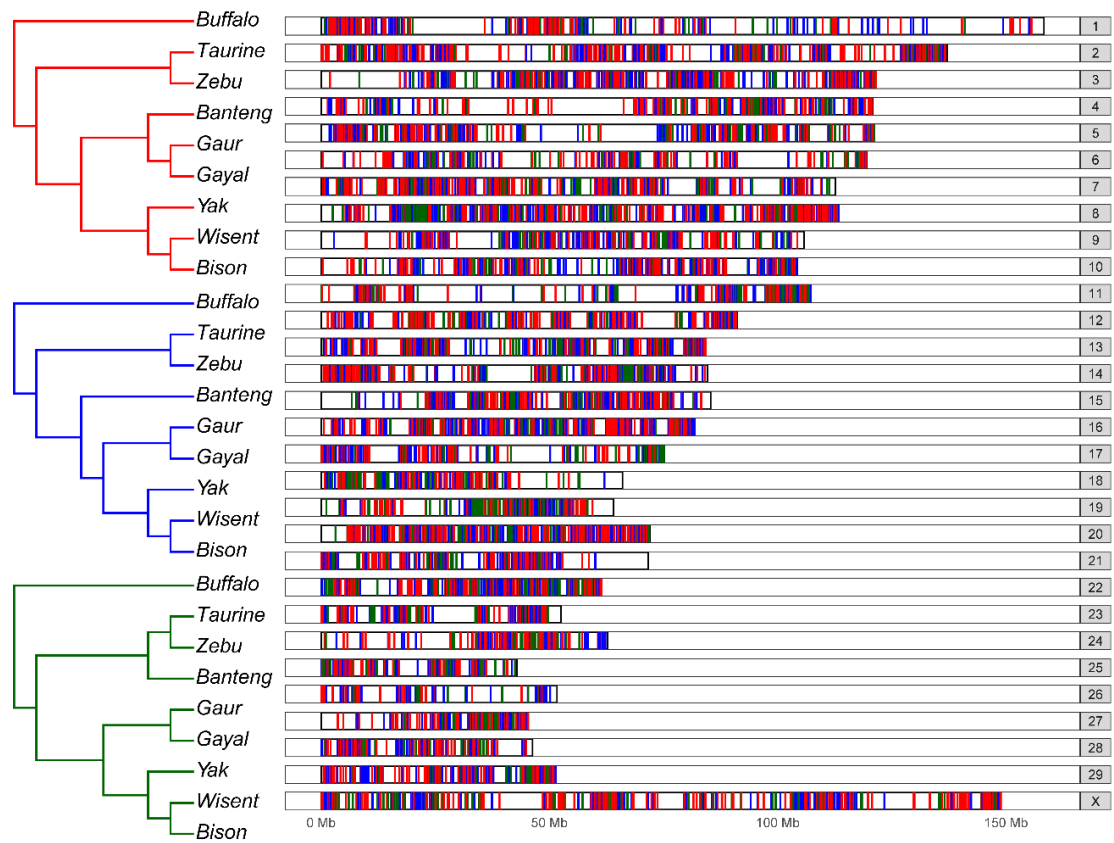
Supplementary Fig. 5: Construction of phylogenetic trees using 100-kb non-overlapping sliding windows at X chromosome. (a) The proportion of top 9 different topologies. (b) The box plots of tree height of top 9 window-bases trees.



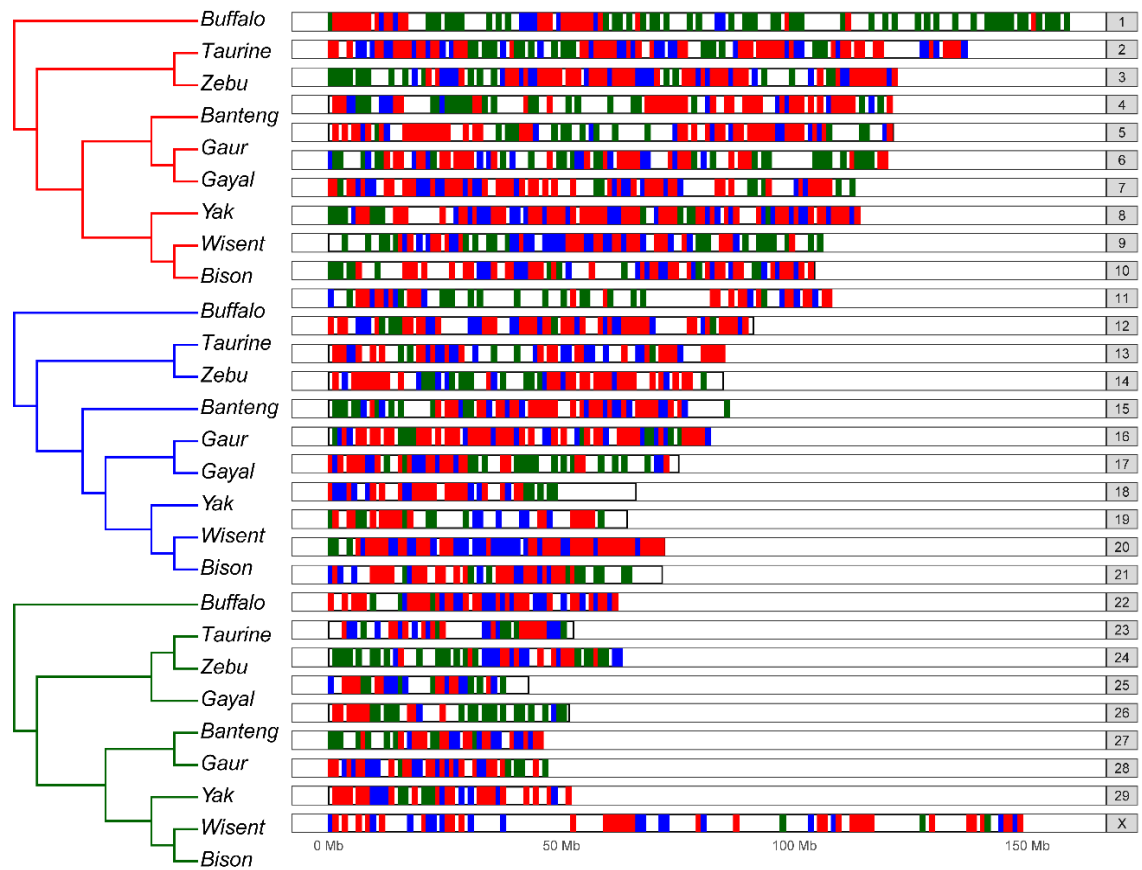
Supplementary Fig. 6: Construction of phylogenetic trees using 1-Mb non-overlapping sliding windows at autosome. (a) The proportion of top 9 different topologies. (b) The box plots of tree height of top 9 window-bases trees.



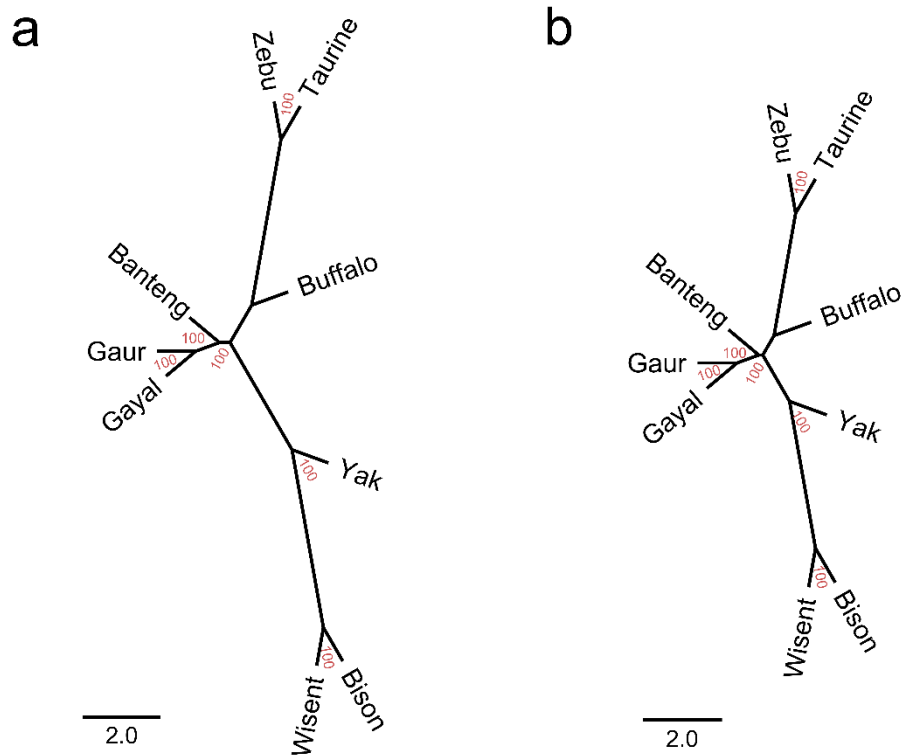
Supplementary Fig. 7: Construction of phylogenetic trees using 1-Mb non-overlapping sliding windows at X chromosome. (a) The proportion of top 9 different topologies. (b) The box plots of tree height of top 9 window-bases trees.



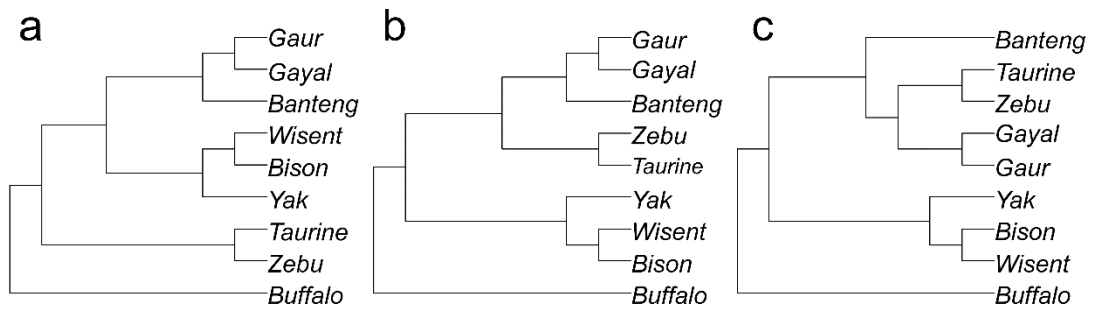
Supplementary Fig. 8: Chromosome painter of top 3 topologies across all 100-Kb non-overlapping sliding windowed trees. The colors of the chromosome segments are corresponding to the left three trees.



Supplementary Fig. 9: Chromosome painter of top 3 topologies across all 1-Mb non-overlapping sliding windowed trees. The colors of the chromosome segments are corresponding to the left three trees.

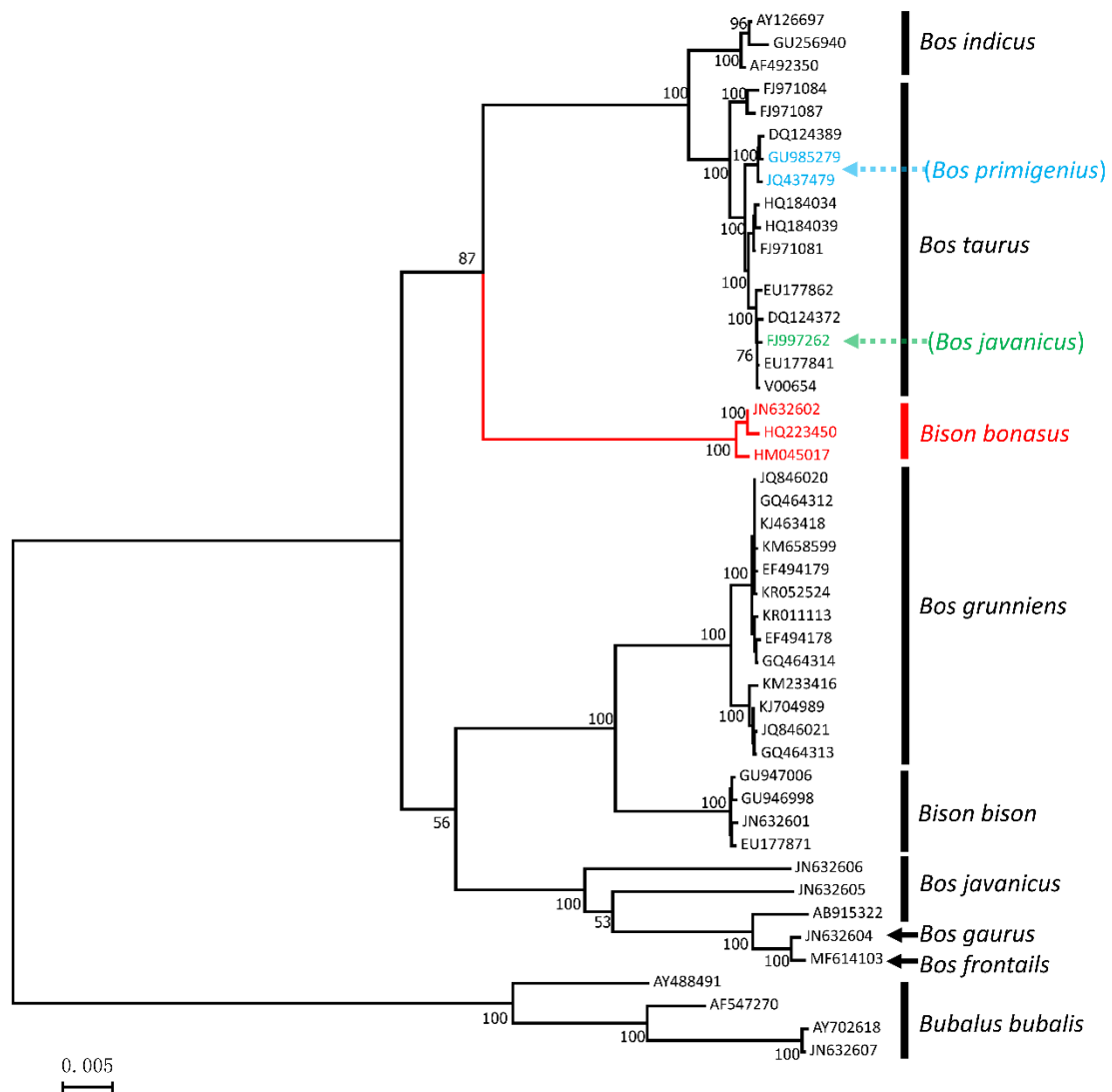


Supplementary Fig. 10: Construction of species tree using ASTRAL based on all 1-Mb (a) and 100-Kb (b) non-overlapping sliding windowed trees. We repeated 1000 resampling genes to get the node support value (red number in picture). Internal branch lengths are in coalescent unit. All terminal branch lengths were assigned the value 1 for plot.

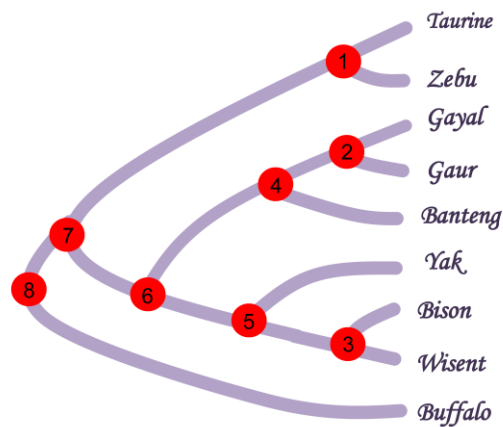


Length of CDS regions	Autosome		X chromosome	
	Number of CDS regions	MP-EST Tree	Number of CDS regions	MP-EST Tree
$\geq 100\text{bp}$	18807	b	797	c
$\geq 500\text{bp}$	16651	b	690	c
$\geq 1\text{kbp}$	11165	b	478	c
$\geq 5\text{kbp}$	644	b	19	c
$\geq 10\text{kbp}$	91	a	2	-

Supplementary Fig. 11: Construction of species tree using MP-EST based on gene trees built from CDS (protein coding sequences) regions.

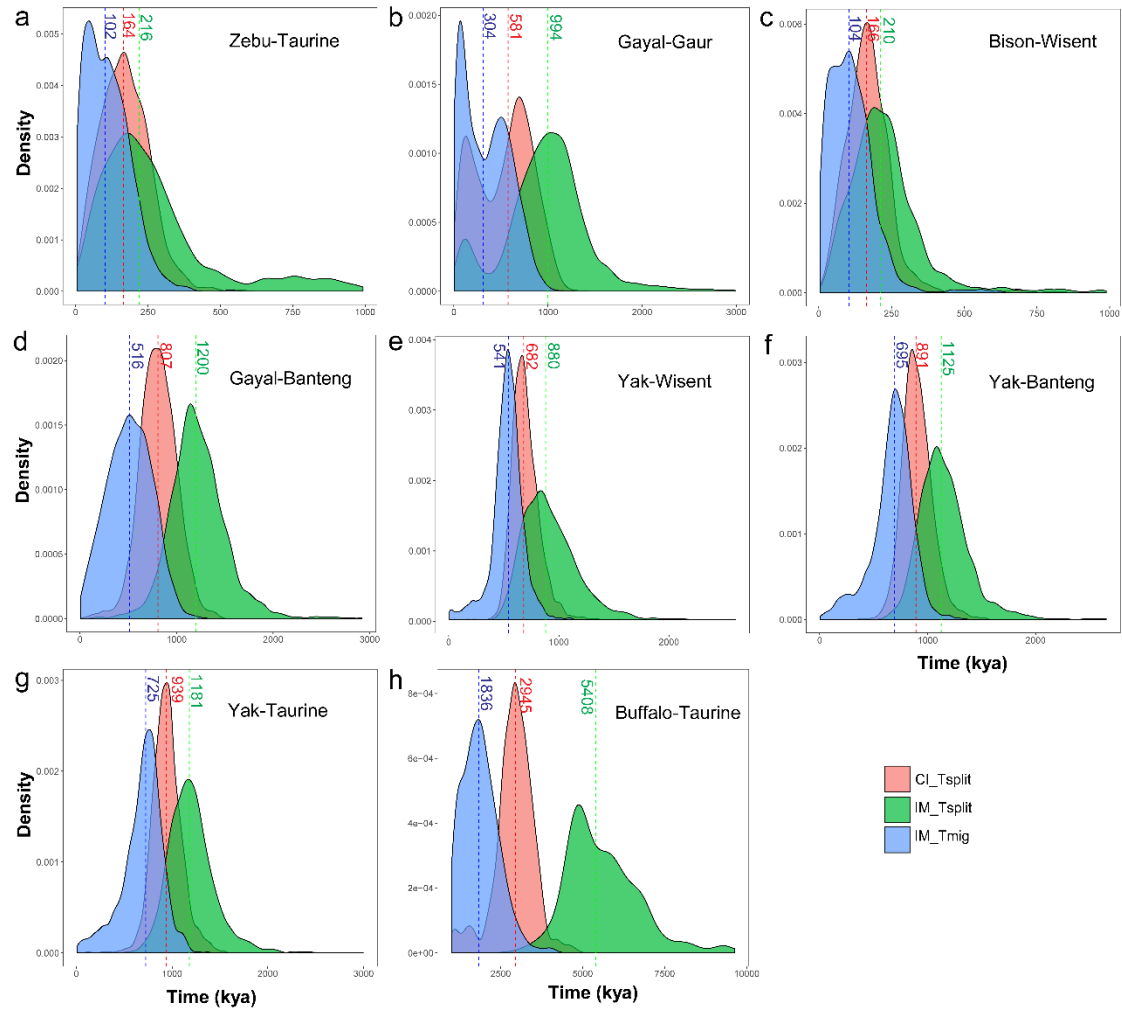


Supplementary Fig. 12: Construction of maximum likelihood tree using complete mitochondrial DNA. The IDs of leaf nodes in the tree are GenBank accession numbers.

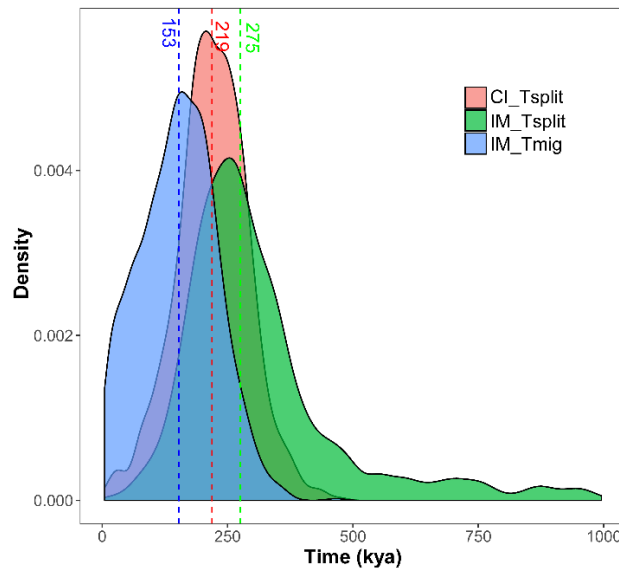


Methods	1	2	3	4	5	6	7	8
CoalHMM (CI model)	163.5 [30.8, 338.4]	580.7 [48.2, 1028.8]	165.6 [467.0, 341.6]	806.7 [446.1, 1179]	681.9 [505.8, 991.0]	890.8 [662.3, 1208]	939.2 [669.8, 1288]	2945 [1263, 3953]
CoalHMM (IM model)	102.2 [7.4, 271.9]	304.0 [12.3, 820.0]	104.4 [9.5, 283.3]	515.5 [81.5, 946.0]	540.7 [168.8, 799.1]	695.3 [184.7, 986.8]	724.6 [169.6, 1061]	1836 [1056, 3083]
	215.7 [42.0, 844.1]	993.5 [83.9, 1958.6]	210.3 [54.1, 610.7]	1200 [714.5, 1871]	880.1 [558.2, 1543]	1125 [793.6, 1718]	1181 [806.8, 1794]	5408 [3870, 8387]

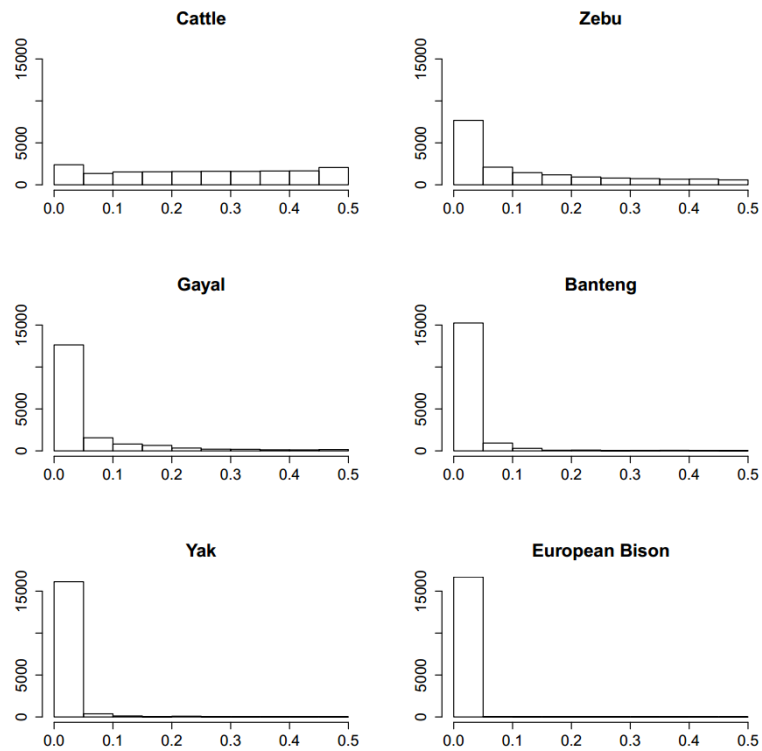
Supplementary Fig. 13: Divergence time (Thousand Years Ago, 95% confidence interval included) induced by CoalHMM. CI model: Complete isolation model; IM model: Isolation with migration model (time interval showed in table).



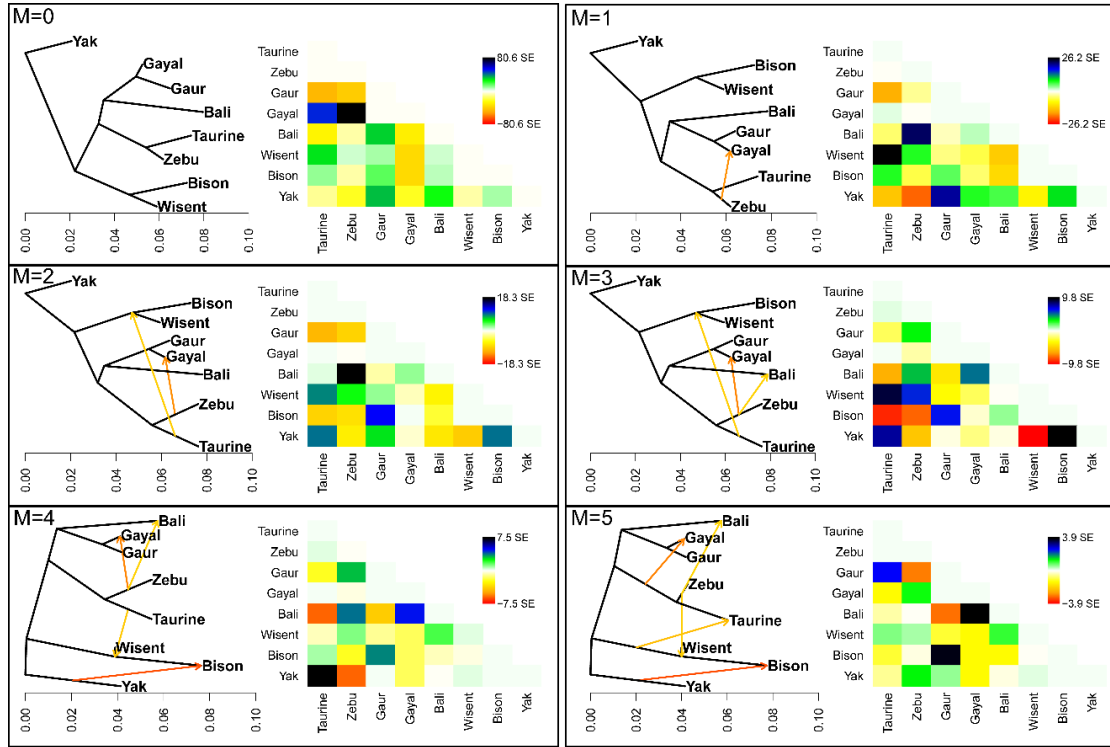
Supplementary Fig. 14: The density plot of divergence time from 8 pairs of species estimated by CoalHMM. The red color distribution shows the split time estimated by complete-isolation model while green color shows the time of initial divergence and blue color shows the end of gene flow estimated by the isolation-with-migration model. The vertical dotted lines represent the median values of distribution with same color. The windows with split time below 5 thousand years or above 3 million years are removed in estimated divergence time. Particularly, the filter criterion for zebu and taurine is below 5 thousand or above 1 million years, buffalo and taurine below 1 million or above 100 million years.



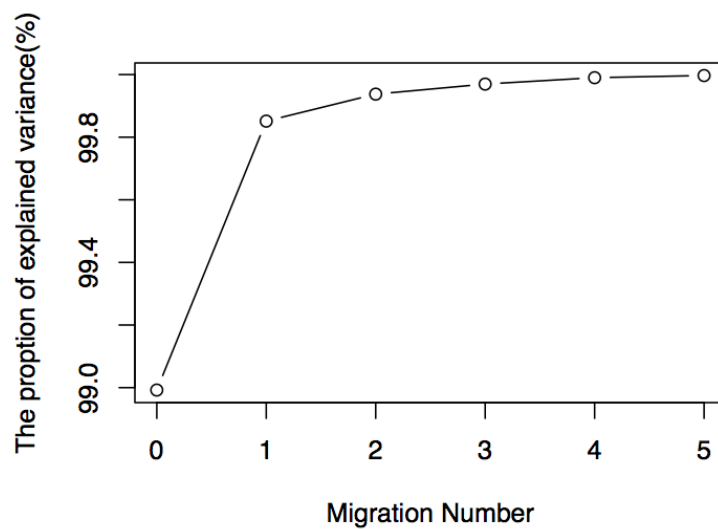
Supplementary Fig. 15: The density plot of divergence time between *bos taurus* and *bos indicus* estimated by CoalHMM. The red color distribution shows the split time estimated by complete-isolation model while green color shows the time of initial divergence and blue color shows the end of gene flow estimated by the isolation-with-migration model. The vertical dotted lines represent the median of distribution with same color. The individual of *bos indicus* downloaded from NCBI SRA database (BioSample ID: SRS1705836, Breed: Gir, Depth: 12x, Coverage: 0.98).



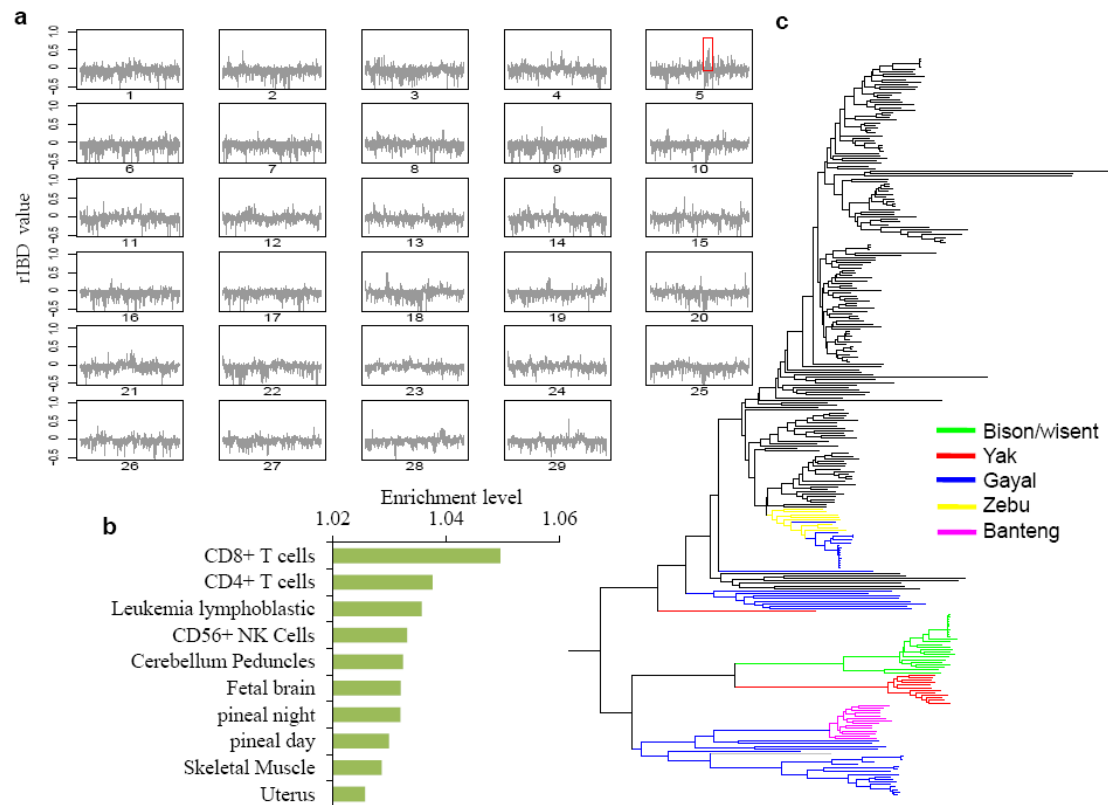
Supplementary Fig. 16: The histogram of minor allele frequency of SNPs used in Illumina UMD3.1 50k chips (version 2) within populations of six species. By comparison with previously generated SNP genotyping array for cattle (Illumina UMD3.1 50k), we document a strong ascertainment bias and reduced ability to detect variants in other species, in the SNP chip data. This illustrates that the cattle SNP genotyping array is not suitable for comparative studies of diversity in other species than cattle.



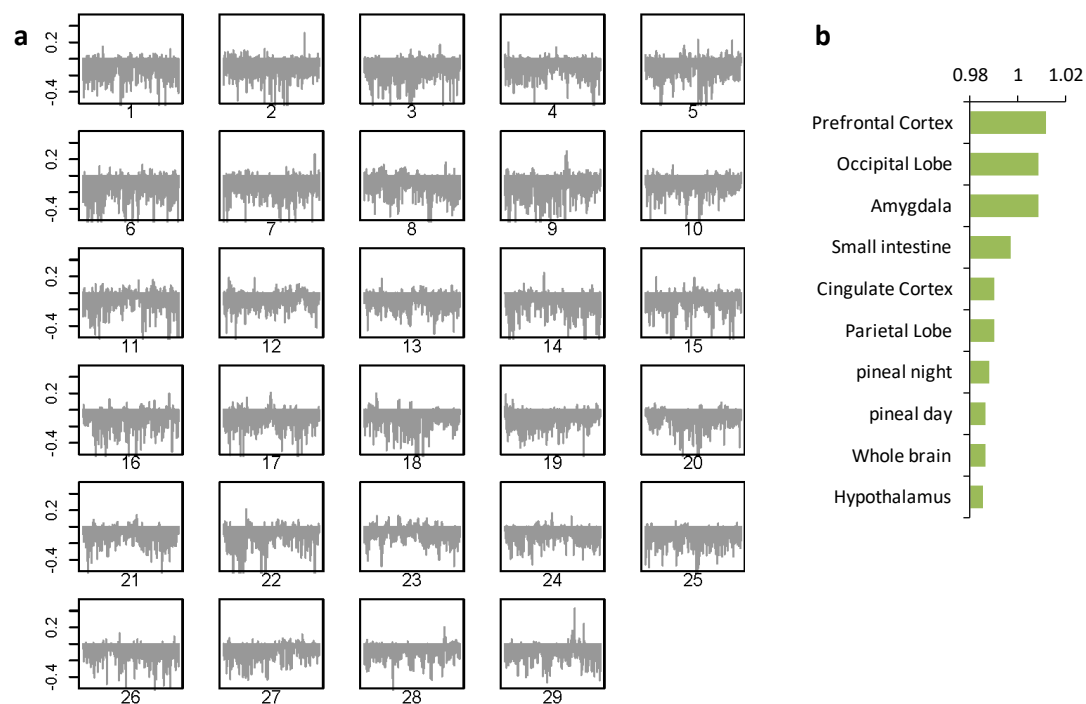
Supplementary Fig. 17: Genetic migration inferred by TreeMix (migration number from 1 ~ 5, 0 means no migration).



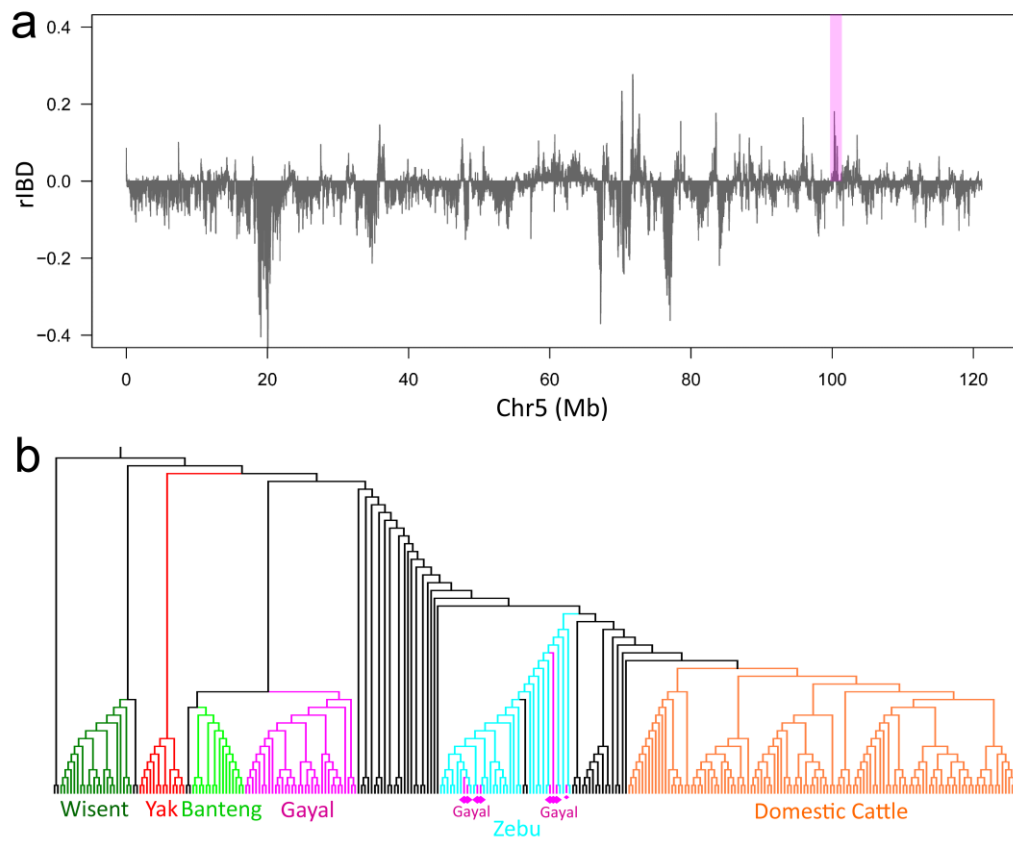
Supplementary Fig. 18: The proportion of explained variance under six model (Migration number from 1 ~ 5, 0 means no migration) described in supplementary figure 17.



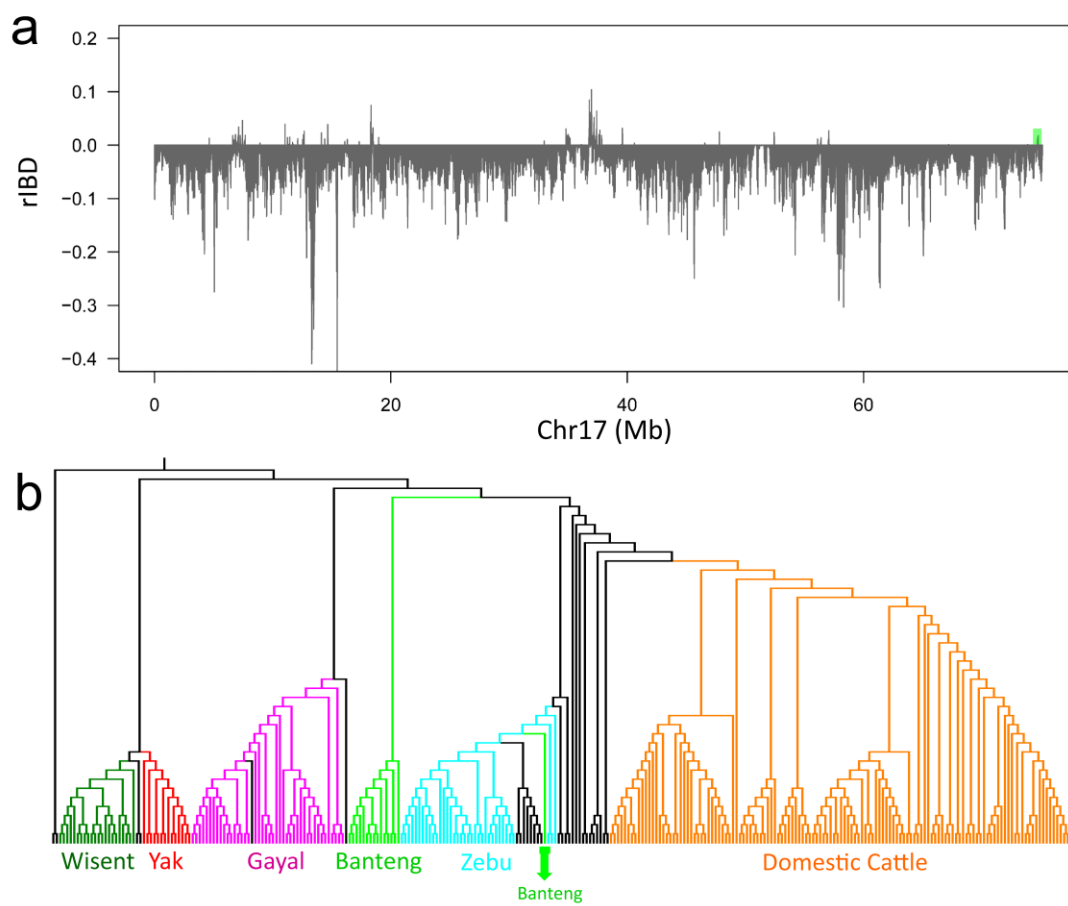
Supplementary Fig. 19: Distribution of regions in the genome where introgression occurred between zebu and gayal. (a) Landscape of rIBD values across genomes. Positive rIBD values indicated potential introgression between zebu and gayal. The most significant window across gene *SYN3* is marked by a red square. (b) Top ten tissues/cells with high expression level. The value in each tissue/cell was calculated as the averaged log 2 transformed expression values of genes showing introgression between zebu and gayal in the tissue/cell divided by the averaged log 2 transformed genome-wide expression in the tissue/cell. The expression value for each gene (HGNC gene symbol) was from human gene expression data (Human U133A Gene Atlas) in 84 tissues or cells, which were downloaded from BioGPS (<http://biogps.org>) with GEO code GSE1133. (c) Phylogenetic tree of *SYN3* gene haplotype sequences indicated its introgression from zebu to gayal.



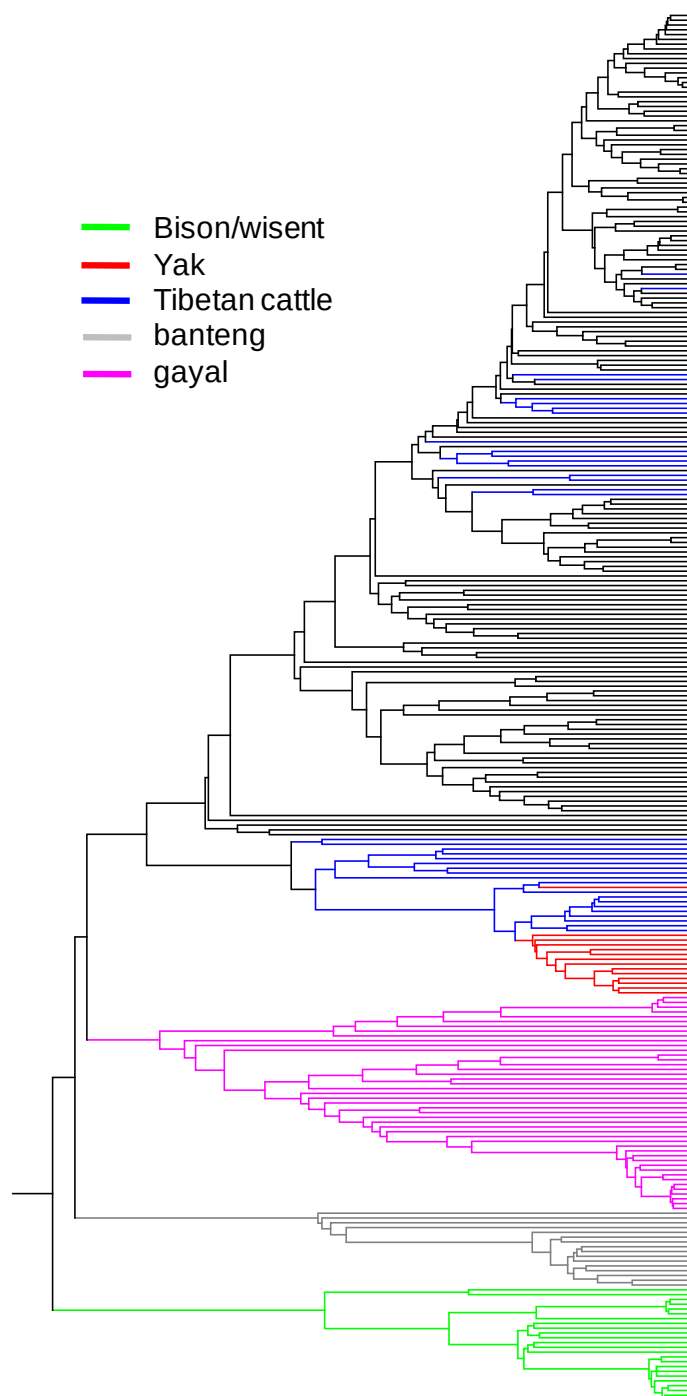
Supplementary Fig. 20: Distribution of regions in the genome where introgression occurred between zebu and bali cattle. (a) Genomic landscape of rIBD values detecting introgression between zebu and bali cattle across all 29 autosome. (b) Top ten tissues/cells with high expression level of genes showing introgression between zebu and bali cattle. The value in each tissue/cell was calculated as the averaged log 2 transformed expression values of genes showing introgression between zebu and bali cattle in the tissue/cell divided by the averaged log 2 transformed genome-wide expression in the tissue/cell. The expression value for each gene (HGNC gene symbol) was from human gene expression data (Human U133A Gene Atlas) in 84 tissues or cells, which were downloaded from BioGPS (<http://biogps.org>) with GEO code GSE1133.



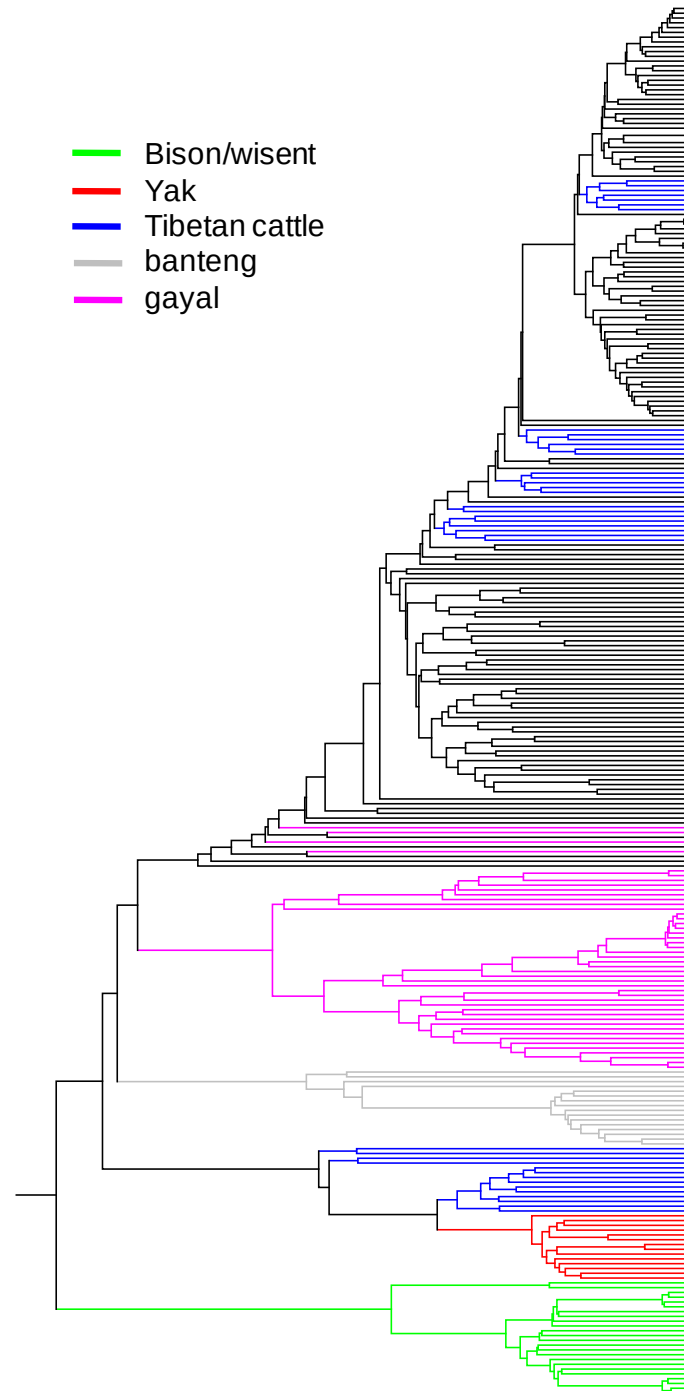
Supplementary Fig. 21: Genetic introgression of region chr5:100300001-100770001 from zebu to gayal.



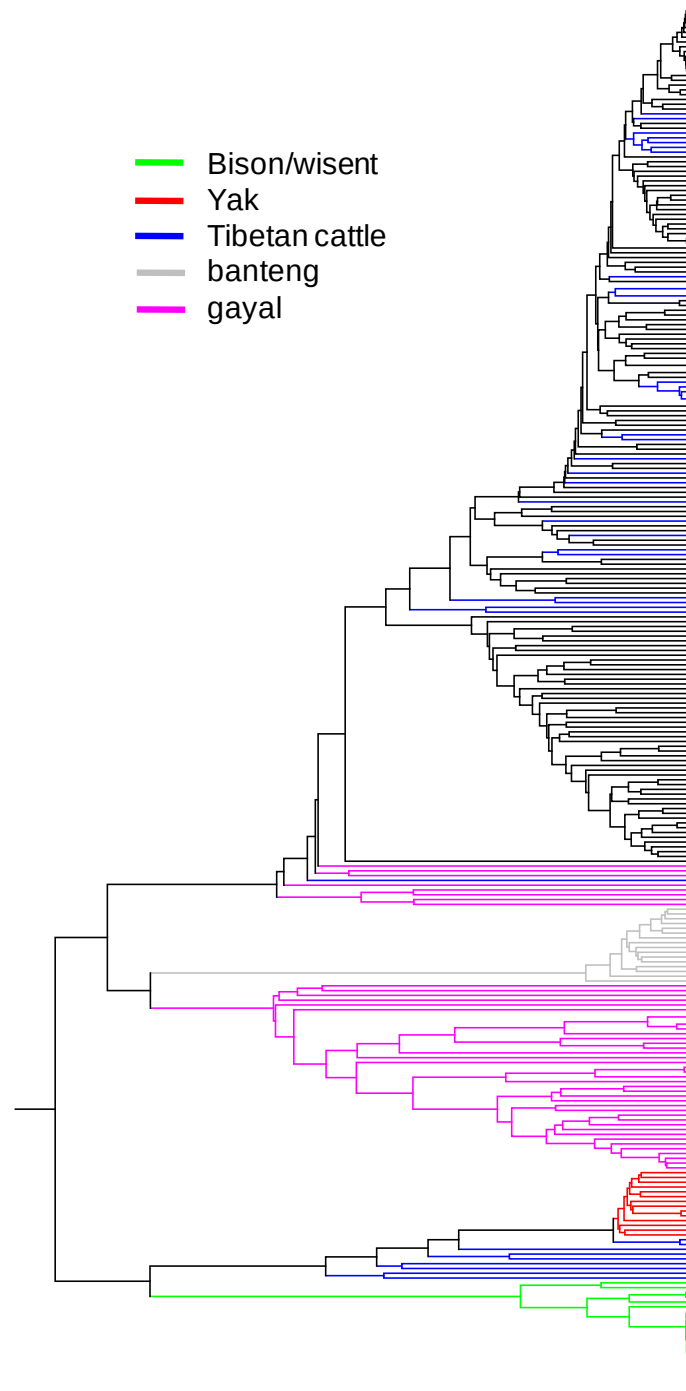
Supplementary Fig. 22: Genetic introgression of region chr17:74800001-74820001 from zebu to bali cattle.



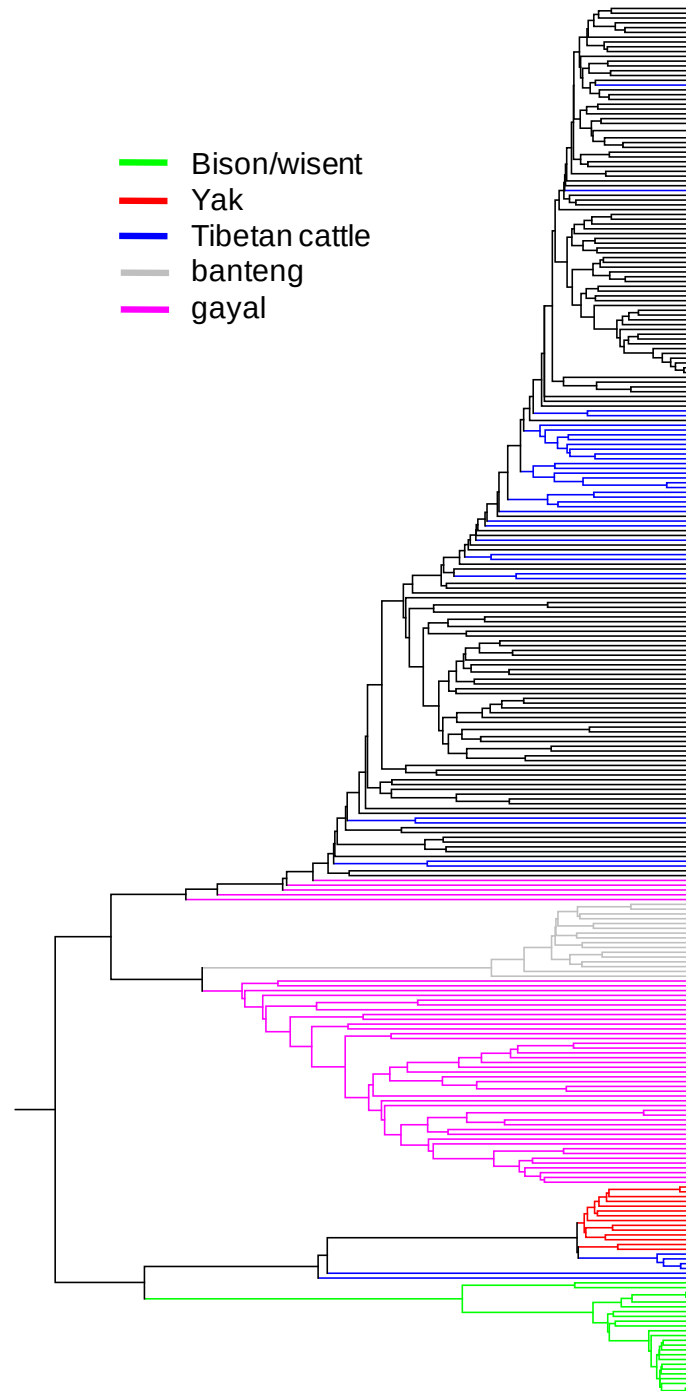
Supplementary Fig. 23: Phylogenetic tree constructed by haplotype sequences of region chr 28: 1300001-1940000. The tree was constructed using UPGMA method in MEGA 6.0. The black lines are others.



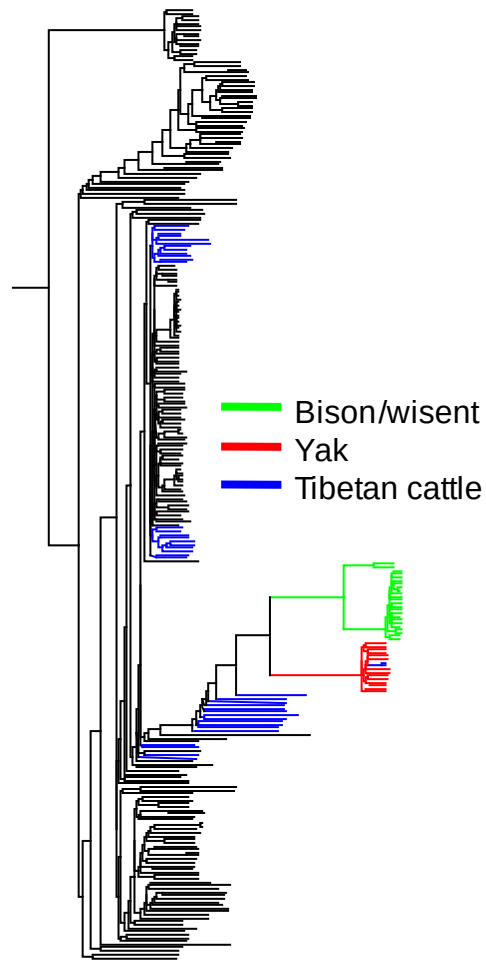
Supplementary Fig. 24: Phylogenetic tree constructed by haplotype sequences of region chr 28: 3000001-4590000. The tree was constructed using UPGMA method in MEGA 6.0. The black lines are others.



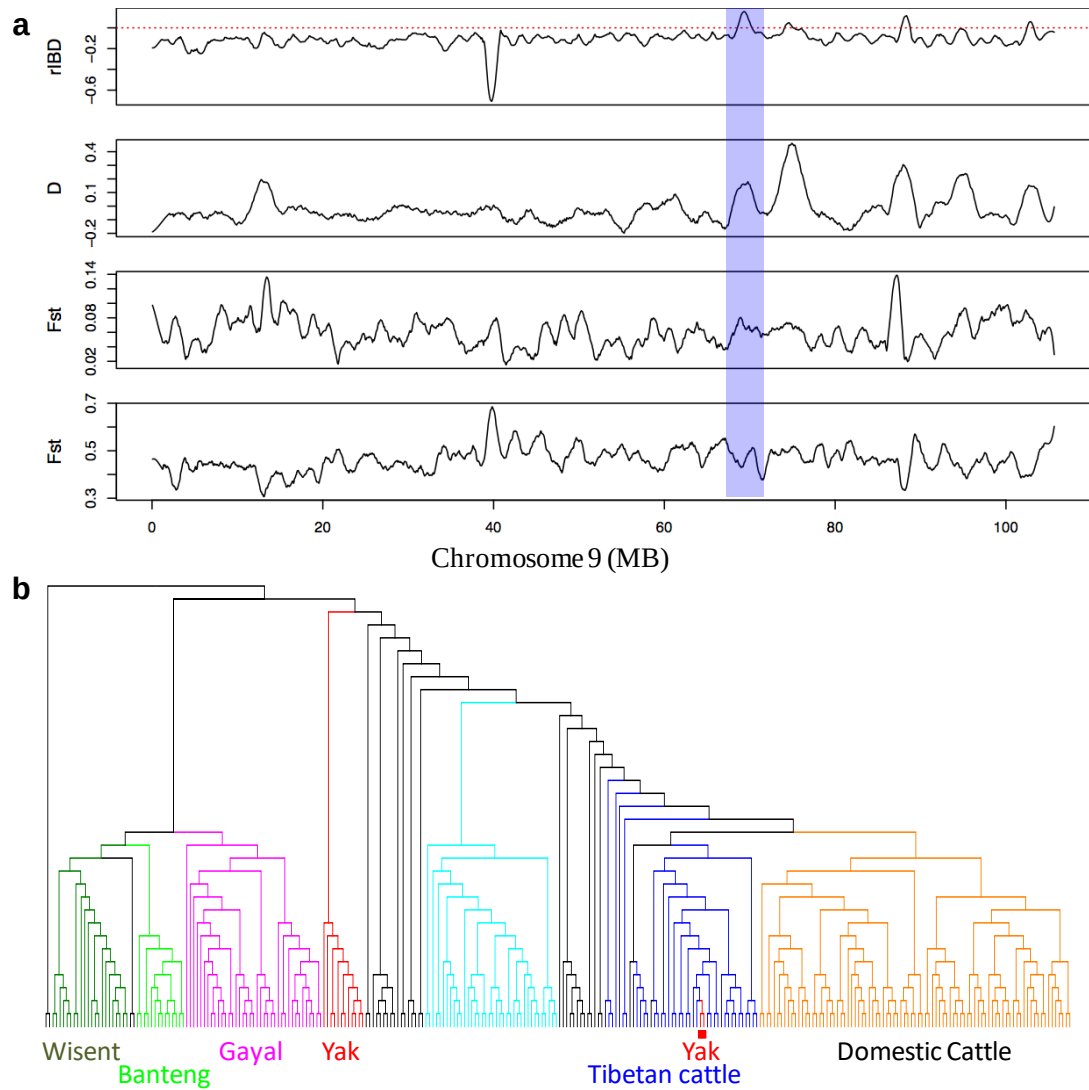
Supplementary Fig. 25: Phylogenetic tree constructed by haplotype sequences of region chr 28: 34530001-35110000. The tree was constructed using UPGMA method in MEGA 6.0. The black lines are others.



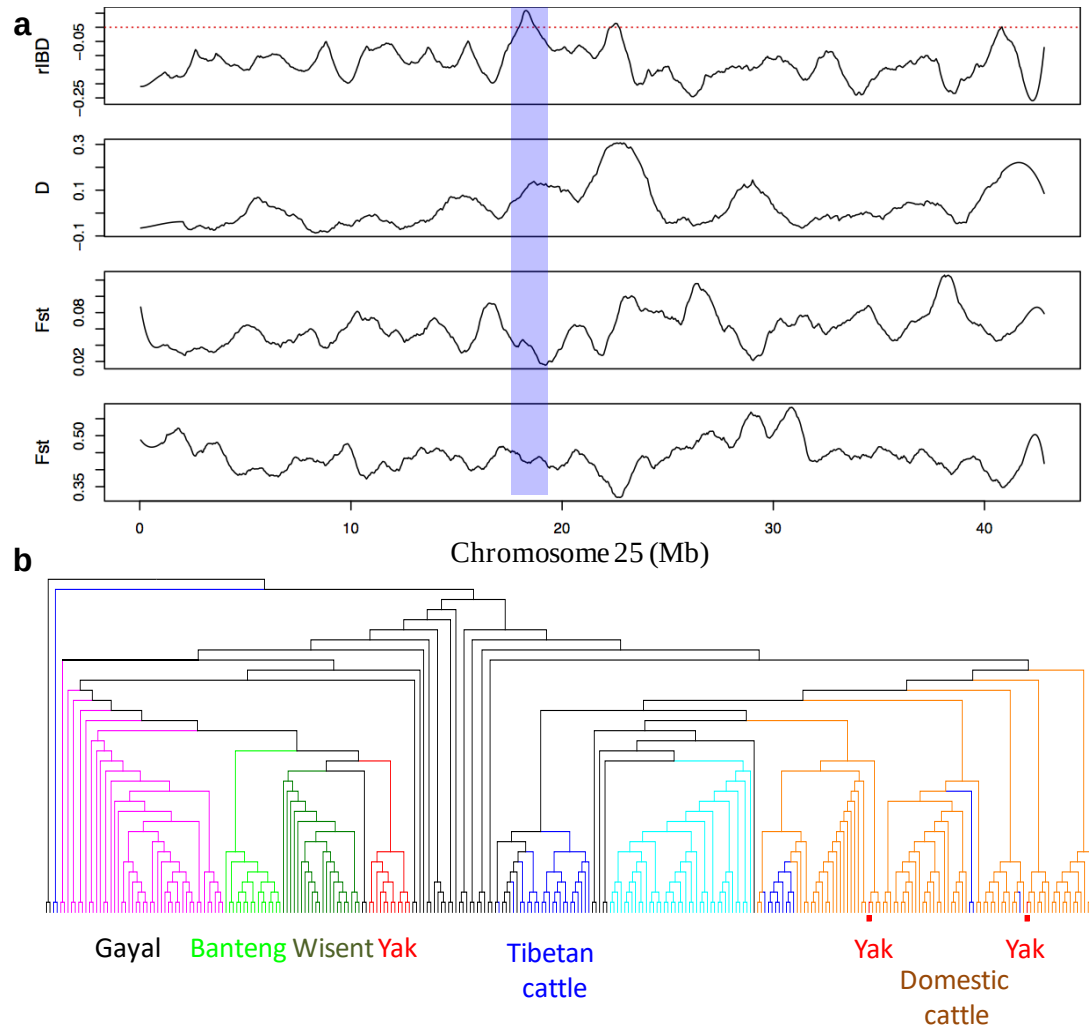
Supplementary Fig. 26: Phylogenetic tree constructed by haplotype sequences of region chr 28: 37040001-43000000. The tree was constructed using UPGMA method in MEGA 6.0. The black lines are others.



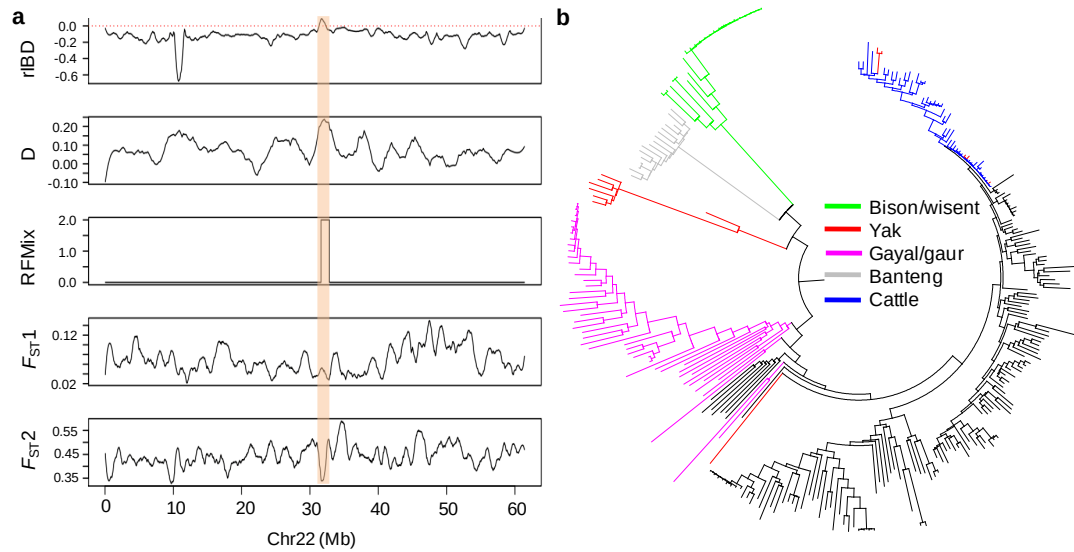
Supplementary Fig. 27: Phylogenetic tree constructed by haplotype sequences of region chr18: 46080001-56110000 indicated its introgression from yak to Tibetan cattle. The black lines are others.



Supplementary Fig. 28: Signal of introgression of chromosome 9 between yak and domestic cattle. (a) Values of rIBD, $D(\text{Zebu, Tibetan cattle, Yak; Buffalo})$, $F_{st}(\text{Tibetan cattle, zebu})$, $F_{st}(\text{Tibetan cattle, yak})$ across chromosome 9. (b) Phylogenetic tree of the introgressive region marked in (a) indicated introgression from domestic cattle to yak.



Supplementary Fig. 29: Signal of introgression of chromosome 25 between yak and domestic cattle. (a) Values of rIBD, $D(\text{Zebu, Tibetan cattle, Yak; Buffalo})$, $F_{st}(\text{Tibetan cattle, zebu})$, $F_{st}(\text{Tibetan cattle, yak})$ across chromosome 25. (b) Phylogenetic tree of the introgressive region marked in (a) indicated introgression from domestic cattle to yak.



Supplementary Fig. 30: genetic introgression of gene *MITF* from domestic cattle to yak. (a) Values of rIBD, D(ABBA-BABA), RFMix, $F_{ST} 1$ (between Tibetan cattle and zebu), $F_{ST} 2$ (between Tibetan cattle and yak) across chromosome 22. The window across *MITF* gene exhibiting singal of introgression with positive rIBD value was marked. (b) phylogenetic tree indicated several yak sequences of *MITF* are close to domestic cattle from China.

Supplementary Table 1: The information of nine high coverage species.

Abbreviation	Species Name	Latin Name	Depth	Sex	Coverage (≥1X)	Source
WB	Water Buffalo	<i>Bubalus bubalus</i>	18.91	F	0.957	PRJNA33659*
YK	Yak	<i>Bos grunniens</i>	65.74	F	0.982	PRJNA221623*
AB	American Bison/Bison	<i>Bison bison</i>	23.29	F	0.969	this study
EB	European Bison/Wisent	<i>Bison bonasus</i>	25.92	F	0.971	this study
GR	Gaur	<i>Bos gaurus</i>	16.75	F	0.971	this study
BT	Banteng/Bali	<i>Bos javanicus</i>	19.74	M	0.975	this study
GY	Gayal	<i>Bos frontalis</i>	33.70	F	0.979	this study
BV	Cattle	<i>Bos taurus</i>	49.27	F	0.981	PRJNA238491*
AZ	African Zebu	<i>Bos indicus</i>	68.17	F	0.982	PRJEB6174*

*: download from Sequence Read Archive (SRA) database on NCBI.

Supplementary Table 2: D statistic (buffalo as outgroup) using single high depth genomes.

P1	P2	P3	D	Z-score	No. BABA	No. ABBA
Bali	Gayal	Zebu	0.3411	25.398	44297	90135
Gaur	Gayal	Zebu	0.487	40.367	26179	75843
Bali	Gayal	Cattle	0.3238	24.655	44345	86782
Gaur	Gayal	Cattle	0.4637	38.269	26572	72472
Cattle	Zebu	Gayal	0.0832	9.783	22689	26806
Cattle	Zebu	Bali	0.0194	4.023	18118	18834
Cattle	Zebu	Gaur	0.0098	2.282	17865	18218
Zebu	Cattle	Wisent	-0.0077	-1.672	17208	16944
Bali	Cattle	Wisent	-0.1104	-33.091	62816	50322
Gayal	Cattle	Wisent	-0.2076	-50.596	59824	39256
Gaur	Cattle	Wisent	-0.2334	-64.021	74646	46396
Zebu	Cattle	Bison	-0.0033	-0.705	17147	17033
Bali	Cattle	Bison	-0.1058	-23.151	62821	50799
Gayal	Cattle	Bison	-0.2005	-35.377	59728	39780
Gaur	Cattle	Bison	-0.2281	-46.368	74605	46888
Zebu	Cattle	Yak	0.0122	2.24	16987	17406
Bali	Cattle	Yak	-0.0998	-17.141	62786	51387
Gayal	Cattle	Yak	-0.185	-27.835	59052	40610
Gaur	Cattle	Yak	-0.2111	-33.159	73520	47887
Yak	Wisent	Cattle	-0.0232	-3.174	42376	40460
Yak	Wisent	Gayal	0.0024	0.614	44858	45070
Yak	Wisent	Gaur	0.0076	2.164	45930	46631
Yak	Wisent	Bali	-0.0095	-2.424	43680	42858
Yak	Wisent	Zebu	-0.015	-2.341	41920	40686
Bison	Wisent	Cattle	-0.021	-1.707	15503	14866
Bison	Wisent	Gayal	-0.0005	-0.089	16130	16116
Bison	Wisent	Gaur	-0.0031	-0.575	16574	16470
Bison	Wisent	Bali	-0.0052	-0.955	15807	15642
Bison	Wisent	Zebu	-0.0161	-1.386	15486	14999

Supplementary Table 3: Samples and alignment information.

Species Name	Country, Province/City	Sample Name	Sex	Genome Coverage (UMD3.1, >= 1X)	Mean Depth	Mapped Reads (%)
Water Buffalo	India	SRS009460	F	0.957	18.91	65.30
Yak	China, Tibet	yak_QH1	F	0.982	65.74	82.79
	China, Tibet	SRR1047220	F	0.959	5.38	98.40
	China, Tibet	SRR1047221	M	0.957	5.25	99.59
	China, Tibet	SRR962824	M	0.942	4.43	98.73
	China, Tibet	SRR962825	M	0.949	4.94	99.06
	China, Tibet	SRR962826	M	0.942	4.53	98.99
	China, Tibet	SRR962827	F	0.947	4.50	99.04
American Bison	America	american_bison	F	0.969	23.29	99.68
European Bison/Wisent	Europe	11,european_bison	F	0.971	25.92	99.69
	Europe	10,MRI865	F	0.944	4.96	99.67
	Europe	12,MRI1200	F	0.941	4.72	99.66
	Europe	13,MRI1197	F	0.942	4.57	99.70
	Europe	1,MRI1161	F	0.927	4.02	95.49
	Europe	2,MRI1163	F	0.928	4.00	99.63
	Europe	3,MRI1169	M	0.941	4.65	99.67
	Europe	4,MRI1177	M	0.932	4.27	99.35
	Europe	5,MRI1K	F	0.929	4.29	99.65
	Europe	8,MRI1211	M	0.943	4.89	99.67
	Europe	9,MRI1167	M	0.935	4.28	99.63
Gaur	China	YPR1115	F	0.971	16.75	99.32
Banteng/Bali	Indonesia	bali,ypt2230	M	0.975	19.74	99.72
	Indonesia	ypt2224	F	0.922	4.03	99.57
	Indonesia	ypt2225	F	0.838	3.74	99.58
	Indonesia	ypt2226	F	0.943	4.69	99.35
	Indonesia	ypt2227	F	0.946	5.64	99.61
	Indonesia	ypt2228	F	0.925	4.19	99.71
	Indonesia	ypt2231	F	0.916	3.89	99.52
	Indonesia	ypt2234	F	0.940	4.46	99.57
Gayal/Mithun	China	gayal	F	0.979	33.70	98.27
	China	kcb200013	F	0.956	4.89	99.65
	China	kcb91002	M	0.872	2.59	99.57
	China	1107	F	0.955	5.65	99.61
	China	201045	F	0.940	4.72	99.69
	China	201048	F	0.936	4.41	99.70
	China	223	M	0.956	5.81	99.30

	China	90005	F	0.943	4.75	99.67
	China	90016	M	0.934	4.55	99.67
	China	YPR397	F	0.939	4.65	99.74
	India	ypr151	M	0.971	7.96	99.40
	India	ypr153	M	0.974	11.06	99.47
	India	ypr155	F	0.965	6.11	99.51
	India	ypr158	F	0.876	2.67	99.39
	Bangladesh	G13	M	0.932	4.19	99.49
	Bangladesh	G16	M	0.953	5.55	99.08
	Bangladesh	G21	M	0.933	4.15	99.61
	Bangladesh	G23	M	0.966	6.90	99.70
	Bangladesh	G24	M	0.956	5.63	99.67
	Bangladesh	G3	M	0.925	3.87	99.56
	Bangladesh	G6	M	0.936	4.42	99.48
	Bangladesh	G7	M	0.953	5.38	99.47
	Bangladesh	G9	M	0.934	4.27	99.57
Bovine	Europe	SRR1262779	F	0.981	49.27	100.00
	Europe	SRR1262620	M	0.977	10.16	100.00
	Europe	SRR1262650	M	0.978	11.06	100.00
	Europe	SRR1262707	M	0.976	16.56	100.00
	Europe	SRR1262760	M	0.981	16.43	100.00
	Europe	SRR1262763	M	0.980	14.53	100.00
	Europe	SRR1262791	M	0.970	8.38	100.00
	Europe	SRR1262793	M	0.978	12.13	100.00
	Europe	SRR1262797	M	0.972	9.61	100.00
	Europe	SRR1262799	M	0.968	10.64	100.00
	Europe	SRR1262802	M	0.972	10.51	100.00
	Europe	SRR1262803	M	0.980	11.37	100.00
	Europe	SRR1262808	M	0.975	8.21	100.00
	Europe	SRR1262819	M	0.975	8.66	100.00
	Europe	SRR1262846	M	0.973	8.09	100.00
	Japan	DRS001212	F	0.978	15.71	86.15
	Japan	DRS001213	F	0.977	13.40	82.47
	Japan	DRS001214	F	0.978	13.21	85.87
	Japan	DRS001215	F	0.971	9.38	93.86
	Japan	DRS001216	F	0.976	11.13	94.44
	Japan	DRS001217	F	0.974	13.08	94.55
	Japan	DRS001218	F	0.974	11.93	94.29
	Japan	DRS001219	M	0.976	11.06	94.34
	Korea	SRR934415	M	0.983	13.33	99.31
	Korea	SRR934416	M	0.984	13.95	99.32
	Korea	SRR934417	M	0.983	13.25	99.26

Korea	SRR934418	M	0.983	13.84	99.21
Korea	SRR934419	M	0.983	12.78	99.30
Korea	SRR934433	M	0.983	12.48	98.60
Korea	SRR934434	M	0.983	12.64	99.32
Korea	SRR934435	M	0.982	11.40	99.36
Korea	SRR934436	M	0.982	11.41	99.26
Korea	SRR934437	M	0.983	11.66	99.35
China, Tibet	100	F	0.932	3.74	99.76
China, Tibet	105	F	0.648	4.61	99.69
China, Tibet	110	M	0.715	3.85	99.67
China, Tibet	113	F	0.903	3.12	99.72
China, Tibet	114	F	0.932	3.59	99.78
China, Tibet	115	F	0.970	5.31	99.49
China, Tibet	116	F	0.970	5.55	99.71
China, Tibet	117	F	0.944	3.84	99.60
China, Tibet	118	F	0.663	3.91	99.68
China, Tibet	119	F	0.948	5.18	99.58
China, Tibet	121	F	0.960	4.68	99.74
China, Tibet	89	F	0.975	6.26	99.58
China, Tibet	92	F	0.900	5.11	99.66
China, Tibet	93	F	0.872	4.66	99.73
China, Tibet	95	F	0.722	4.29	99.71
China, Tibet	96	F	0.695	5.63	99.61
China, Tibet	98	F	0.972	5.70	99.73
China, Tibet	99	F	0.735	5.43	99.66
China, Tibet	xizang_1	M	0.979	8.96	99.68
China, Tibet	xizang_2	M	0.981	11.17	99.69
China, Inner Mongolia	menggu_1	M	0.981	11.20	99.73
China, Inner Mongolia	menggu_2	M	0.982	11.27	99.76
China, Xinjiang	hasake_1	M	0.982	10.17	99.76
China, Xinjiang	hasake_2	M	0.982	10.99	99.75
China, Liaoning	yanbian_1	M	0.982	10.55	99.77
China, Liaoning	yanbian_2	M	0.982	10.49	99.76
China, Shandong	luxi_1	M	0.980	10.99	99.64
China, Shandong	luxi_2	M	0.980	10.44	99.68
China, Hebei	nanyang_1	M	0.983	10.51	99.74
China, Hebei	nanyang_2	M	0.983	11.49	99.73
China, Shaanxi	qinchuan_1	M	0.981	10.53	99.70
China, Shaanxi	qinchuan_2	M	0.981	10.30	99.73
China, Jiangxi	dabieshan_1	M	0.979	10.71	99.40

	China, Jiangxi	dabieshan_2	M	0.979	10.70	99.01
	China, Sichuan	dengchuan_1	M	0.980	10.81	99.66
	China, Sichuan	dengchuan_2	M	0.980	11.06	99.67
	China, Guizhou	guanling_1	M	0.980	10.78	99.73
	China, Guizhou	guanling_2	M	0.980	10.65	99.72
	China, Guizhou	liping_1	M	0.978	10.71	99.72
	China, Guizhou	liping_2	M	0.978	10.41	99.66
	China, Zhejiang	wenling_1	M	0.978	9.96	99.67
	China, Zhejiang	wenling_2	M	0.978	9.97	99.69
	China, Fujian	fujian_1	M	0.979	10.73	99.67
	China, Fujian	fujian_2	M	0.977	10.12	99.70
	China, Yunnan	dehong_1	M	0.978	10.56	99.66
	China, Yunnan	dehong_2	M	0.979	10.58	99.67
	China, Yunnan	ms17	F	0.971	6.49	99.70
	China, Yunnan	ms18	F	0.873	2.45	99.64
	China, Yunnan	ms1	F	0.967	5.36	99.63
	China, Yunnan	ms24	F	0.968	5.53	99.66
	China, Yunnan	ms25	F	0.973	6.86	99.73
	China, Yunnan	ms29	F	0.966	5.73	99.69
	China, Yunnan	ms2	M	0.700	2.86	99.46
	China, Yunnan	ms30	F	0.966	5.29	99.62
	China, Yunnan	ms3	M	0.958	4.70	99.54
	India	ypr114	M	0.861	2.81	99.47
	India	ypr115	M	0.948	7.74	99.49
	India	ypr117	M	0.889	4.60	99.58
	India	ypr119	M	0.968	5.47	99.66
Zebu	Kenya, Western	ERS445101	F	0.982	68.17	82.19

Supplementary Table 4: D statistic (buffalo as outgroup) and numbers of ABBA, BABA sites on all 4,739,555 SNPs.

P1	P2	P3	D	Z-score	No. ABBA	No. BABA
European Cattle	Zebu	Gayal	0.0911	28.53	34546	28779
Japanese Cattle	Zebu	Gayal	0.0996	30.818	35224	28841
Northern Cattle*	Zebu	Gayal	0.0841	26.973	34180	28877
Tibetan Cattle	Zebu	Gayal	0.0726	26.376	33442	28916
European Cattle	Zebu	Bali	0.0582	16.606	28653	25499
Japanese Cattle	Zebu	Bali	0.0685	18.476	29332	25573
Northern Cattle	Zebu	Bali	0.0515	14.719	28334	25561
Tibetan Cattle	Zebu	Bali	0.0471	15.321	27866	25361
Zebu	European Cattle	Wisent	-0.0205	-6.042	23922	24923
Zebu	Japanese Cattle	Wisent	-0.0339	-9.449	23951	25630
Zebu	Northern Cattle	Wisent	-0.015	-4.575	23898	24627
Zebu	Tibetan Cattle	Wisent	-0.0024	-0.783	23991	24107
Bali	European Cattle	Wisent	-0.1116	-35.19	50719	63468
Bali	Japanese Cattle	Wisent	-0.117	-36.304	50670	64097
Bali	Northern Cattle	Wisent	-0.1095	-34.608	50716	63193
Bali	Tibetan Cattle	Wisent	-0.1041	-33.377	51024	62888
Gayal	European Cattle	Wisent	-0.2186	-65.157	43114	67241
Gayal	Japanese Cattle	Wisent	-0.2235	-65.661	43095	67900
Gayal	Northern Cattle	Wisent	-0.2168	-64.996	43080	66934
Gayal	Tibetan Cattle	Wisent	-0.2116	-63.135	43289	66531
Zebu	European Cattle	Yak	-0.0087	-2.497	24327	24755
Zebu	Japanese Cattle	Yak	-0.0214	-5.855	24386	25454
Zebu	Northern Cattle	Yak	-0.0039	-1.133	24276	24466
Zebu	Tibetan Cattle	Yak	0.0418	6.915	25787	23717
European Cattle	Tibetan Cattle	Yak	0.0905	9.633	15056	12560
Northern Cattle	Tibetan Cattle	Yak	0.0827	8.707	14800	12541
Japanese Cattle	Tibetan Cattle	Yak	0.1117	11.826	15621	12484

*: The group of Northern Cattle included Chinese Yanbian, Menggu, Hasake and Korean cattle.

Supplementary Table 5: Genetic introgression between gayal and zebu.

To detect the direction of introgression between zebu and gayal, windows with significant rIBD values were merged within 1Mb. Genes within windows with significant rIBD values are showed. Weir and Cockerham's pairwise F_{ST} between two populations was calculated by Vcftools with window size of 20 kb and a step size of 10 kb. Each segment might contain many windows, and the max window F_{ST} value is used to show the differentiation value of this segment.

Supplementary Table 6: Genetic introgression between bali cattle and zebu.

To detect the direction of introgression between zebu and bali cattle, windows with significant rIBD values were merged within 1Mb. Genes within windows with significant rIBD values are showed. Weir and Cockerham's pairwise F_{ST} between two populations was calculated by Vcftools with window size of 20 kb and a step size of 10 kb. Each segment might contain many windows, and the max window F_{ST} value is used to show the differentiation value of this segment.

Supplementary Table 7: Gene enrichment analysis genes within regions showing genetic introgression between zebu and gayal.**Supplementary Table 8: Gene enrichment analysis genes within regions showing genetic introgression between zebu and bali cattle.****Supplementary Table 9: Genetic introgression between yak and Tibetan cattle.**

To detect the direction of introgression between yak and Tibetan cattle, windows with significant rIBD values were merged within 1Mb. Genes within windows with significant rIBD values are showed. Weir and Cockerham's pairwise F_{ST} between two populations was calculated by Vcftools with window size of 20 kb and a step size of 10 kb. Each segment might contain many windows, and the max window F_{ST} value is used to show the differentiation value of this segment.

Supplementary Table 10: Gene enrichment analysis genes within regions showing genetic introgression between yak and Tibetan cattle.