

Supplementary Information for:

**Chapter 2 | Genome-wide local ancestry and direct evidence for
mitonuclear coadaptation in African hybrid cattle populations (*Bos
taurus/indicus*)**

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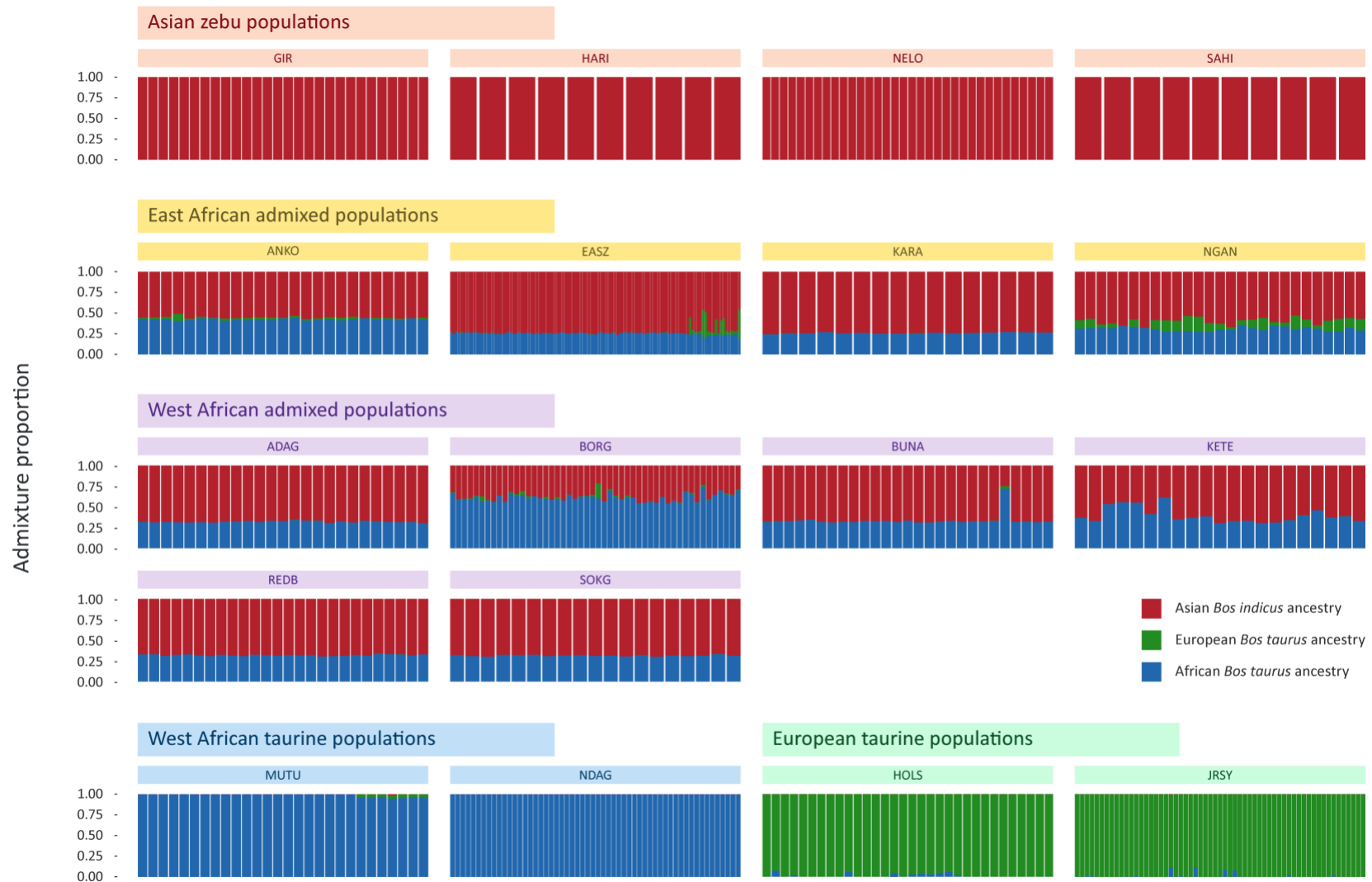
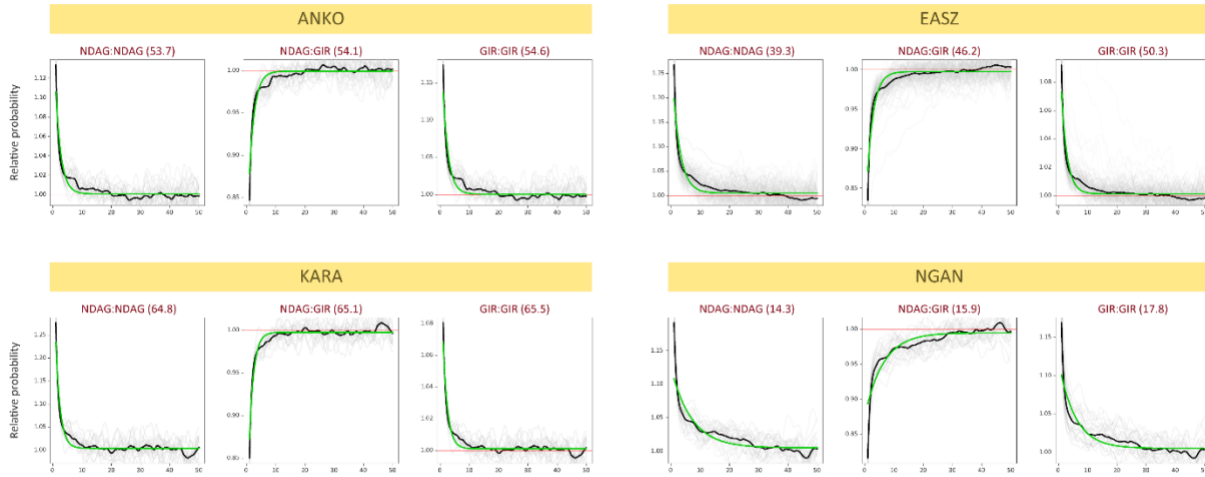


Figure S2.1: Unsupervised genetic structure plot for Asian zebu, East and West African admixed cattle, and West African and European taurine breeds. Results for an inferred number of ancestry clusters of $K = 3$ is shown, which corresponds to Asian *Bos indicus* (red), European *Bos taurus* (green), and African *B. taurus* (blue) ancestral components, respectively.

East African admixed populations



West African admixed populations

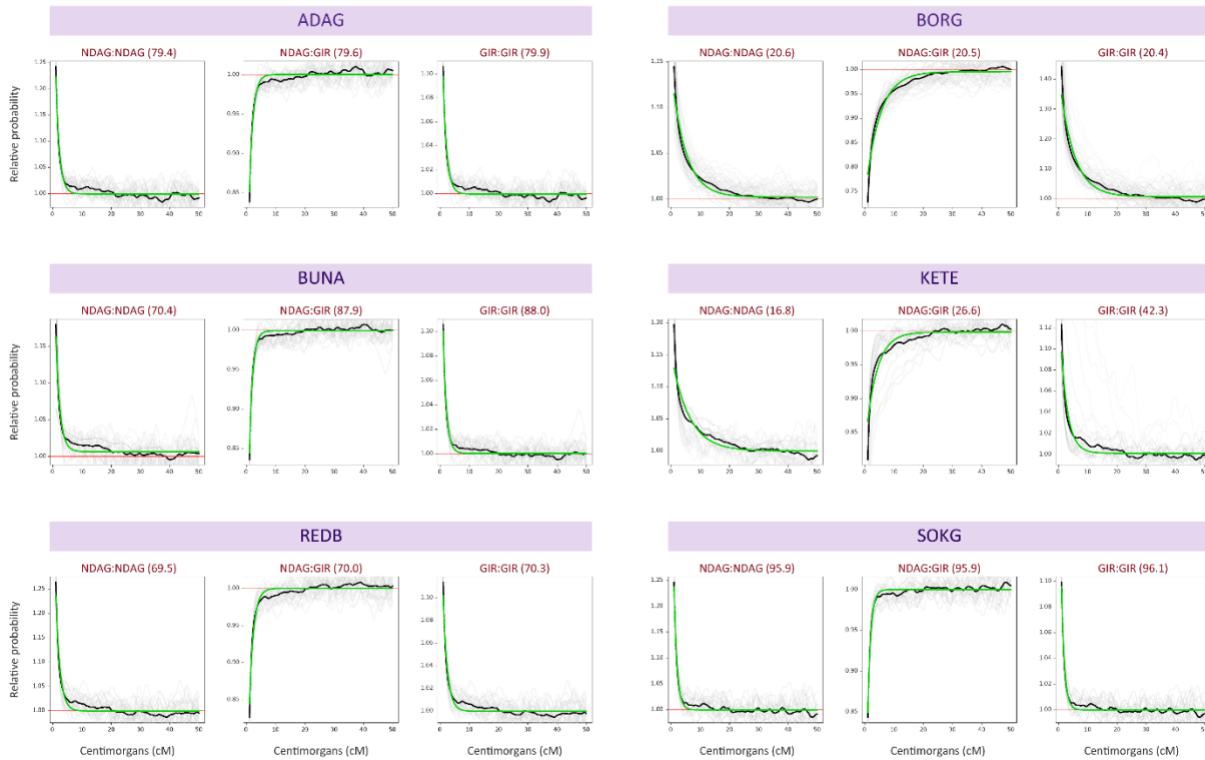


Figure S2.2: Coancestry curve plots generated using MOSAIC for 10 East and West African admixed cattle populations. These curves show the exponential decay of the ratio of probabilities of pairs of local ancestries (y-axis) as a function of genetic distance (x-axis). The pair of ancestries used for each curve is shown on the top of each plot with the estimated number of generations since the start of admixture in brackets. For each plot, the green line represents the fitted curve, the black line shows the across targets ratio, and the grey lines indicate the per target ratio (further information in Salter-Townshend and Myers, 2019).

Table S2.3: Ancestry components estimated using fastSTRUCTURE with estimated times for the start of the admixture process in African admixed cattle populations generated using MOSAIC.

Code	Type/morphology	Country of origin	African taurine ancestry	European taurine ancestry	Asian zebu ancestry	Generations since start of admixture	Start of admixture
MUTU	West African taurine	Nigeria	0.990 ± 0.019	0.010 ± 0.018	0.000 ± 0.003		----
NDAG	West African taurine	Guinea	1.000 ± 0.000	0.000 ± 0.000	0.000 ± 0.000		----
HOLS	European taurine	Netherlands	0.010 ± 0.025	0.990 ± 0.025	0.000 ± 0.000		----
JRSY	European taurine	United Kingdom	0.010 ± 0.022	0.990 ± 0.022	0.000 ± 0.000		----
ANKO	East African admixed	Uganda	0.420 ± 0.010	0.020 ± 0.016	0.550 ± 0.013	54.1	1641 – 1804 CE
EASZ	East African admixed	Kenya	0.250 ± 0.015	0.020 ± 0.065	0.730 ± 0.055	46.2	1697 – 1835 CE
KARA	East African admixed	Uganda	0.260 ± 0.008	0.000 ± 0.001	0.740 ± 0.008	65.1	1564 – 1760 CE
NGAN	East African admixed	Uganda	0.310 ± 0.024	0.100 ± 0.052	0.590 ± 0.039	15.9	1909 – 1956 CE
ADAG	West African admixed	Nigeria	0.320 ± 0.010	0.000 ± 0.001	0.680 ± 0.010	79.6	1463 – 1702 CE
BORG	West African admixed	Benin	0.610 ± 0.047	0.010 ± 0.027	0.370 ± 0.055	20.5	1877 – 1938 CE

BUNA	West African admixed	Nigeria	0.340 ± 0.076	0.000 ± 0.007	0.660 ± 0.083	87.9	1405 – 1668 CE
KETE	West African admixed	Nigeria	0.400 ± 0.093	0.000 ± 0.001	0.600 ± 0.093	26.6	1834 – 1914 CE
REDB	West African admixed	Nigeria	0.320 ± 0.009	0.000 ± 0.001	0.680 ± 0.009	70	1530 – 1740 CE
SOKG	West African admixed	Nigeria	0.320 ± 0.008	0.000 ± 0.000	0.680 ± 0.008	95.9	1349 – 1636 CE
GIR	Asian zebu	India	0.000 ± 0.000	0.000 ± 0.000	1.000 ± 0.000		----
HARI	Asian zebu	India	0.000 ± 0.000	0.000 ± 0.000	1.000 ± 0.000		----
NELO	Asian zebu	Brazil	0.000 ± 0.000	0.000 ± 0.001	1.000 ± 0.001		----
SAHI	Asian zebu	India	0.000 ± 0.000	0.000 ± 0.000	1.000 ± 0.000		----

Note. For each admixed population, the generations since admixture started were obtained from the NDAG:GIR coancestry plots (Fig. S2). A generation interval range of 4–7 years for managed domestic cattle was used. CE = Common Era.

Table S2.4: Fixed nucleotide substitutions determined from alignments of the protein-coding sequences of 13 mitochondrial OXPHOS protein genes for three groups of Bovinae species/subspecies. The taxa examined included African *Bos taurus*, Asian *Bos indicus* and a range of *Bos* species (*Bos gaurus*, *Bos grunniens*, *Bos javanicus*, *Bos mutus*, *Bos frontalis*, and *Bos primigenius*).

Gene name	Gene symbol	Length in bp (aligned)	African <i>B. taurus</i> vs. Asian <i>B. indicus</i>		African <i>B. taurus</i> vs. <i>Bos</i> species		Asian <i>B. indicus</i> vs. <i>Bos</i> species	
			Single	Multiple	Single	Multiple	Single	Multiple
ATP synthase 6	<i>ATP6</i>	692	8	4	30	8	23	14
ATP synthase 8	<i>ATP8</i>	204	5	2	13	4	12	4
Cytochrome b	<i>CYB</i>	1158	14	4	45	15	38	19
Cytochrome c oxidase I	<i>COX1</i>	1570	3	0	29	0	28	0
Cytochrome c oxidase II	<i>COX2</i>	695	2	2	13	2	14	0
Cytochrome c oxidase III	<i>COX3</i>	798	4	4	14	12	13	14
NADH dehydrogenase subunit 1	<i>ND1</i>	972	8	2	24	6	26	6
NADH dehydrogenase subunit 2	<i>ND2</i>	1061	6	2	52	11	51	11
NADH dehydrogenase subunit 3	<i>ND3</i>	353	1	2	6	0	4	2
NADH dehydrogenase subunit 4	<i>ND4</i>	1400	10	6	52	19	53	22
NADH dehydrogenase subunit 4L	<i>ND4L</i>	301	0	2	11	0	10	2
NADH dehydrogenase subunit 5	<i>ND5</i>	1891	7	17	114	46	72	56
NADH dehydrogenase subunit 6	<i>ND6</i>	536	8	2	22	4	22	3

Table S2.5: Results for the branch-site test of positive selection (BSPS) for 13 mitochondrial OXPHOS protein gene sequences in three different *Bos* groups. Significant *P* values (< 0.05) indicating positive selection for individual genes are shown in bold underline.

<i>Bos taurus</i> mitochondrial genome sequences							
Gene symbol	No. param. H_A	No. param. H_0	df	LnL H_A	LnL H_0	LRT($2\Delta\text{LnL}$)	<i>P</i> (χ^2)
<i>ATP6</i>	381	380	1	-2101.88	-2101.79	-0.18280	1.00000
<i>ATP8</i>	381	380	1	-527.49	-526.98	-1.01728	1.00000
<i>CYB</i>	381	380	1	-3334.59	-3334.59	0.00004	<u>0.00479</u>
<i>COX1</i>	381	380	1	-3955.67	-3955.67	-0.00081	1.00000
<i>COX2</i>	381	380	1	-1696.07	-1696.06	-0.01870	1.00000
<i>COX3</i>	381	380	1	-1774.40	-1774.40	0.00000	<u>0.00160</u>
<i>ND1</i>	381	380	1	-2475.83	-2475.83	-0.00070	1.00000
<i>ND2</i>	381	380	1	-3748.60	-3748.60	0.00054	<u>0.01857</u>
<i>ND3</i>	381	380	1	-867.15	-867.15	0.00014	<u>0.00937</u>
<i>ND4</i>	381	380	1	-3826.87	-3826.87	-0.00067	1.00000
<i>ND4L</i>	381	380	1	-781.98	-781.98	0.00000	<u>0.00113</u>
<i>ND5</i>	381	380	1	-5019.63	-5019.63	0.00173	<u>0.03318</u>
<i>ND6</i>	381	380	1	-1931.80	-1931.80	-0.00013	1.00000

<i>Bos indicus</i> mitochondrial genome sequences							
Gene symbol	No. param. H_A	No. param. H_0	df	LnL H_A	LnL H_0	LRT($2\Delta\text{LnL}$)	P (χ^2)
<i>ATP6</i>	381	380	1	-1894.03	-1894.03	0.00019	<u>0.01090</u>
<i>ATP8</i>	381	380	1	-526.98	-526.98	0.00013	<u>0.00900</u>
<i>CYB</i>	381	380	1	-3334.59	-3334.59	0.00193	<u>0.03510</u>
<i>COX1</i>	381	380	1	-3955.67	-3955.67	0.00021	<u>0.01170</u>
<i>COX2</i>	381	380	1	-1696.06	-1696.06	-0.00057	1.00000
<i>COX3</i>	381	380	1	-1774.40	-1774.40	0.00104	<u>0.02570</u>
<i>ND1</i>	381	380	1	-2475.83	-2475.84	0.00159	<u>0.03190</u>
<i>ND2</i>	381	380	1	-3747.84	-3747.84	-0.00085	1.00000
<i>ND3</i>	381	380	1	-866.65	-866.65	-0.00031	1.00000
<i>ND4</i>	381	380	1	-3826.87	-3826.87	-0.00053	1.00000
<i>ND4L</i>	381	380	1	-781.98	-781.98	-0.00041	1.00000
<i>ND5</i>	381	380	1	-5019.63	-5019.63	-0.00374	1.00000
<i>ND6</i>	381	380	1	-1931.80	-1931.80	-0.00007	1.00000

Table S2.6: HMG and LMG functional subset genes detected in multiple studies (≥ 2) of genomic selective sweeps in African cattle populations.

Gene symbol	Gene name	Functional subset	Chromosomal location	Citations
<i>ACO2</i>	Aconitase 2 gene	LMG	BTA5	(Bahbahani et al., 2018a; Taye et al., 2018)
<i>BCL2L13</i>	BCL2 like 13 gene	LMG	BTA5	(Taye et al., 2018; Taye et al., 2017)
<i>CA5A</i>	Carbonic anhydrase 5A gene	LMG	BTA18	(Kim et al., 2017; Taye et al., 2018; Taye et al., 2017)
<i>CMC1</i>	C-X9-C motif containing 1 gene	LMG	BTA22	(Bahbahani et al., 2018a; Kim et al., 2017)
<i>CYP24A1</i>	Cytochrome P450, family 24, subfamily A, polypeptide 1 gene	LMG	BTA13	(Bahbahani et al., 2017; Tijjani et al., 2019)
<i>DARS2</i>	Aspartyl-tRNA synthetase 2, mitochondrial gene	HMG	BTA16	(Bahbahani et al., 2017; Taye et al., 2018)
<i>DNAJC11</i>	DnaJ heat shock protein family (Hsp40) member C11 gene	LMG	BTA16	(Bahbahani et al., 2017; Taye et al., 2018; Taye et al., 2017)
<i>HDHD3</i>	Haloacid dehalogenase like hydrolase domain containing 3 gene	LMG	BTA8	(Kim et al., 2017; Taye et al., 2017)
<i>HIBADH</i>	3-hydroxyisobutyrate dehydrogenase gene	LMG	BTA4	(Kim et al., 2017; Taye et al., 2018; Taye et al., 2017)
<i>HIGD1A</i>	HIG1 hypoxia inducible domain family member 1A gene	LMG	BTA22	(Bahbahani et al., 2018a; Jang et al., 2021; Tijjani et al., 2019)
<i>MRPS33</i>	Mitochondrial ribosomal protein S33 gene	HMG	BTA4	(Kim et al., 2017; Taye et al., 2017)
<i>MSRB3</i>	Methionine sulfoxide reductase B3 gene	LMG	BTA4	(Bahbahani et al., 2017; Kim et al., 2017; Taye et al., 2018; Taye et al., 2017)

<i>NGRN</i>	Neugrin, neurite outgrowth associated gene	LMG	BTA21	(Taye <i>et al.</i> , 2018; Taye <i>et al.</i> , 2017)
<i>PDE12</i>	Phosphodiesterase 12 gene	LMG	BTA22	(Bahbahani <i>et al.</i> , 2017; Taye <i>et al.</i> , 2018)
<i>PUSL1</i>	Pseudouridine synthase like 1 gene	LMG	BTA16	(Taye <i>et al.</i> , 2018; Taye <i>et al.</i> , 2017)
<i>SARDH</i>	Sarcosine dehydrogenase gene	LMG	BTA11	(Bahbahani <i>et al.</i> , 2018a; Tijjani <i>et al.</i> , 2019)
<i>SLC25A11</i>	Solute carrier family 25 member 11 gene	LMG	BTA19	(Bahbahani <i>et al.</i> , 2017; Kim <i>et al.</i> , 2017; Taye <i>et al.</i> , 2018)
<i>SLC25A21</i>	Solute carrier family 25 member 21 gene	LMG	BTA21	(Bahbahani <i>et al.</i> , 2018b; Tijjani <i>et al.</i> , 2019)
<i>SOD1</i>	Superoxide dismutase 1 gene	LMG	BTA1	(Kim <i>et al.</i> , 2017; Taye <i>et al.</i> , 2018; Taye <i>et al.</i> , 2017)
<i>SUCLG2</i>	Succinate-CoA ligase GDP-forming subunit beta gene	LMG	BTA22	(Jang <i>et al.</i> , 2021; Kim <i>et al.</i> , 2020)
<i>TIMM21</i>	Translocase of inner mitochondrial membrane 21 gene	LMG	BTA24	(Bahbahani <i>et al.</i> , 2018a; Tijjani <i>et al.</i> , 2019)
<i>TOMM22</i>	Translocase of outer mitochondrial membrane 22 gene	LMG	BTA5	(Kim <i>et al.</i> , 2017; Taye <i>et al.</i> , 2017)
<i>YME1L1</i>	YME1 like 1 ATPase gene	LMG	BTA13	(Taye <i>et al.</i> , 2018; Taye <i>et al.</i> , 2017)

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