-Supplementary Information for:

Chapter 4 | Population and Functional Genomics of West African Cattle

This PDF file includes:

Supplementary Table 4.2: f_3 statistics calculated using EAT;NDG and AAI as reference populations.

pop1	pop2	pop3	est	se	Z	P-value
BAO	EAT	AAI	0.01120	0.00042	26.88	3.87E-159
BAO	NDG	AAI	-0.00550	0.00031	-17.60	2.62E-69
BIC	EAT	AAI	0.01334	0.00054	24.48	2.17E-132
BIC	NDG	AAI	-0.00303	0.00044	-6.81	1.00E-11
BRG	EAT	AAI	-0.01167	0.00056	-20.71	2.68E-95
BRG	NDG	AAI	-0.02345	0.00051	-46.11	0
DJK	EAT	AAI	-0.01781	0.00038	-46.31	0
DJK	NDG	AAI	-0.02752	0.00037	-75.33	0
KAP	EAT	AAI	-0.00980	0.00057	-17.05	3.25E-65
KAP	NDG	AAI	-0.02114	0.00050	-42.00	0
KUR	EAT	AAI	-0.01683	0.00038	-43.86	0
KUR	NDG	AAI	-0.02714	0.00033	-82.45	0
LAG	EAT	AAI	0.02618	0.00047	55.26	0
LAG	NDG	AAI	0.00849	0.00037	22.80	4.42E-115
MBO	EAT	AAI	-0.00715	0.00067	-10.67	1.42E-26
MBO	NDG	AAI	-0.01408	0.00068	-20.64	1.14E-94
NAM	EAT	AAI	-0.00112	0.00065	-1.73	0.0842
NAM	NDG	AAI	-0.01605	0.00057	-28.39	3.07E-177
NDA	EAT	AAI	0.01059	0.00049	21.77	4.69E-105
NDA	NDG	AAI	-0.00829	0.00037	-22.37	7.30E-111
SHK	EAT	AAI	-0.01495	0.00038	-39.18	0
SHK	NDG	AAI	-0.02107	0.00038	-56.06	0
SKG	EAT	AAI	-0.01084	0.00066	-16.31	8.28E-60
SKG	NDG	AAI	-0.01714	0.00067	-25.43	1.06E-142
SOM	EAT	AAI	0.01630	0.00046	35.57	3.97E-277
SOM	NDG	AAI	-0.00041	0.00038	-1.06	0.2896
WHF	EAT	AAI	-0.01659	0.00052	-32.15	9.55E-227
WHF	NDG	AAI	-0.02313	0.00052	-44.09	0
ZBP	EAT	AAI	-0.01117	0.00057	-19.53	6.53E-85
ZBP	NDG	AAI	-0.01811	0.00058	-31.09	2.90E-212

Supplementary Table 4.3: *D*-statistics calculated using EAT,NDG, AAI and OUT as reference populations.

pop1	pop2	pop3	pop4	est	se	Z	P-value
EAT	KUR	AAI	OUT	-0.0059	0.0003	-18.19	6.48E-74
EAT	KAP	AAI	OUT	-0.0049	0.0003	-16.13	1.59E-58
EAT	NAM	AAI	OUT	-0.0019	0.0002	-8.59	8.36E-18
EAT	LAG	AAI	OUT	0.0007	0.0001	5.84	5.17E-09
EAT	SOM	AAI	OUT	0.0005	0.0001	3.91	9.07E-05
EAT	BRG	AAI	OUT	-0.0050	0.0003	-16.23	2.94E-59
EAT	ZBP	AAI	OUT	-0.0103	0.0005	-20.76	1.00E-95
EAT	MBO	AAI	OUT	-0.0103	0.0005	-19.90	3.72E-88
EAT	SKG	AAI	OUT	-0.0100	0.0005	-20.37	2.90E-92
EAT	WHF	AAI	OUT	-0.0101	0.0005	-20.91	4.27E-97
EAT	BIC	AAI	OUT	6.68E-05	0.0001	0.51	0.61347
EAT	DJK	AAI	OUT	-0.0082	0.0004	-20.34	5.82E-92
EAT	SHK	AAI	OUT	-0.0089	0.0004	-21.42	8.62E-102
EAT	NDA	AAI	OUT	-0.0007	0.0001	-5.00	5.73E-07
EAT	BAO	AAI	OUT	-0.0005	0.0001	-3.77	0.00016
EAT	NDG	AAI	OUT	0.0009	0.0001	8.51	1.69E-17
NDG	KUR	AAI	OUT	-0.0068	0.0003	-22.00	2.90E-107
NDG	KAP	AAI	OUT	-0.0058	0.0003	-20.15	2.63E-90
NDG	NAM	AAI	OUT	-0.0028	0.0002	-13.89	7.13E-44
NDG	LAG	AAI	OUT	-0.0002	9.27E-05	-1.74	0.08239
NDG	SOM	AAI	OUT	-0.0004	9.37E-05	-4.15	3.33E-05
NDG	BRG	AAI	OUT	-0.0059	0.0003	-20.07	1.38E-89
NDG	ZBP	AAI	OUT	-0.0112	0.0005	-23.31	3.22E-120
NDG	MBO	AAI	OUT	-0.0112	0.0005	-22.20	3.74E-109
NDG	SKG	AAI	OUT	-0.0109	0.0005	-22.74	1.62E-114
NDG	WHF	AAI	OUT	-0.0110	0.0005	-23.44	1.69E-121
NDG	BIC	AAI	OUT	-0.0008	0.0001	-7.58	3.47E-14
NDG	DJK	AAI	OUT	-0.0090	0.0004	-23.53	1.95E-122
NDG	SHK	AAI	OUT	-0.0097	0.0004	-24.48	2.16E-132
NDG	NDA	AAI	OUT	-0.0016	0.0001	-13.82	1.93E-43
NDG	BAO	AAI	OUT	-0.0014	9.62E-05	-14.16	1.53E-45
NDG	NDG	AAI	OUT	4.51E-19	3.32E-16	0.00	0.99892

Supplementary Table 4.4: Regions identified by Population Branch Statistics (PBS) analysis of African taurine populations.

| Chromosome	Genomic Range	NumVariants	Mean PBS
1	1:6382001-6456000	497	0.5399952386
1	1:72001-128000	51	0.4887224484
1	1:67926001-67978000	249	0.472475885
2	2:70356001-70422000	358	0.5190776566
3	3:54150001-54256000	476	0.62730989
5	5:28290001-28346000	314	0.4886572406
5	5:74520001-74572000	619	0.4756725571
5	5:70070001-70120000	152	0.4633686179
6	6:4362001-4430000	317	0.5269084562
6	6:87480001-87598000	442	0.4965430087
9	9:3408001-3510000	459	0.545304252
9	9:43486001-43562000	591	0.4907822924
10	10:27846001-27928000	1111	0.5142565813
11	11:32110001-32208000	673	0.5953079984
15	15:55694001-55748000	230	0.4803306572
17	17:22126001-22200000	326	0.5332284725
17	17:59070001-59120000	175	0.4861010476
17	17:68156001-68216000	302	0.4710301407
22	22:10822001-10878000	25	0.5007855537
25	25:40038001-40120000	409	0.5255056706
26	26:38346001-38428000	229	0.4928684679
29	29:42460001-42636000	144	0.5170256347

Supplementary Table 4.5: Genes identified in the regions found using PBS analysis and some traits for which some genes are associated with a traits mentioned in the manuscript.

ENSEMBL_ID	SYMBOL	CHROM
ENSBTAG00000023607	HACD2	BTA1
ENSBTAG00000034854	GRIK1	BTA1
ENSBTAG00000051986		BTA10
ENSBTAG00000053279		BTA10
ENSBTAG00000047107	TNIP3	BTA17
ENSBTAG00000054284		BTA17
ENSBTAG00000016563	GOLGA4	BTA22
ENSBTAG00000004035	SDK1	BTA25
ENSBTAG00000008644	KCNK4	BTA29
ENSBTAG00000008645	ESRRA	BTA29
ENSBTAG00000008646	TRMT112	BTA29
ENSBTAG00000008648	PRDX5	BTA29
ENSBTAG00000012511	BAD	BTA29
ENSBTAG00000012512	GPR137	BTA29
ENSBTAG00000013606	FKBP2	BTA29
ENSBTAG00000015663	STIP1	BTA29
ENSBTAG00000016555	TRPT1	BTA29
ENSBTAG00000016559	NUDT22	BTA29
ENSBTAG00000016560	DNAJC4	BTA29
ENSBTAG00000017181	MACROD1	BTA29
ENSBTAG00000040190	CCDC88B	BTA29
ENSBTAG00000045862	FERMT3	BTA29
ENSBTAG00000047265		BTA29
ENSBTAG00000047567	VEGFB	BTA29
ENSBTAG00000053576		BTA29
ENSBTAG00000001143		BTA3
ENSBTAG00000037634		BTA3
ENSBTAG00000000147	RIC8B	BTA5
ENSBTAG00000017950	SLC4A8	BTA5
ENSBTAG00000038652		BTA5
ENSBTAG00000039524		BTA5
ENSBTAG00000006507	ADAMTS3	BTA6

ENSBTAG00000010634	NDNF	BTA6
ENSBTAG00000017527	CRYBG1	BTA9

Supplementary Table 4.9: Trypanosoma species identified using HAYSTAC and the samples they were identified in.

Taxon	Mean Posterior Abundance	95 CI lower	95 CI upper	Minimum Read Num	Maximum Read Num	Dirichlet Read Num	Evenness of Coverage Ratio	Fraction of Genome Covered	Coverage	Aligned Read Num	Sample	Breed
Trypanosoma vivax	9,18E-07	7,99E-07	1,05E-06	184	241	211	6.84	0.0025	0.0174	226	WG03	Kuri
Trypanosoma vivax	6,20E-05	6,10E-05	6,31E-05	13788	14252	14018	1.21	0.1560	0,1896	14486	WG04	Kuri
Trypanosoma congolense	1,98E-05	1,92E-05	2,04E-05	4314	4576	4443	1.43	0.0312	0,0445	7403	WG15	N'Dama Gambian
Trypanosoma vivax	9,89E-06	9,47E-06	1,03E-05	1998	2177	2086	1.67	0.0253	0,0423	2189	WG44	White Fulani
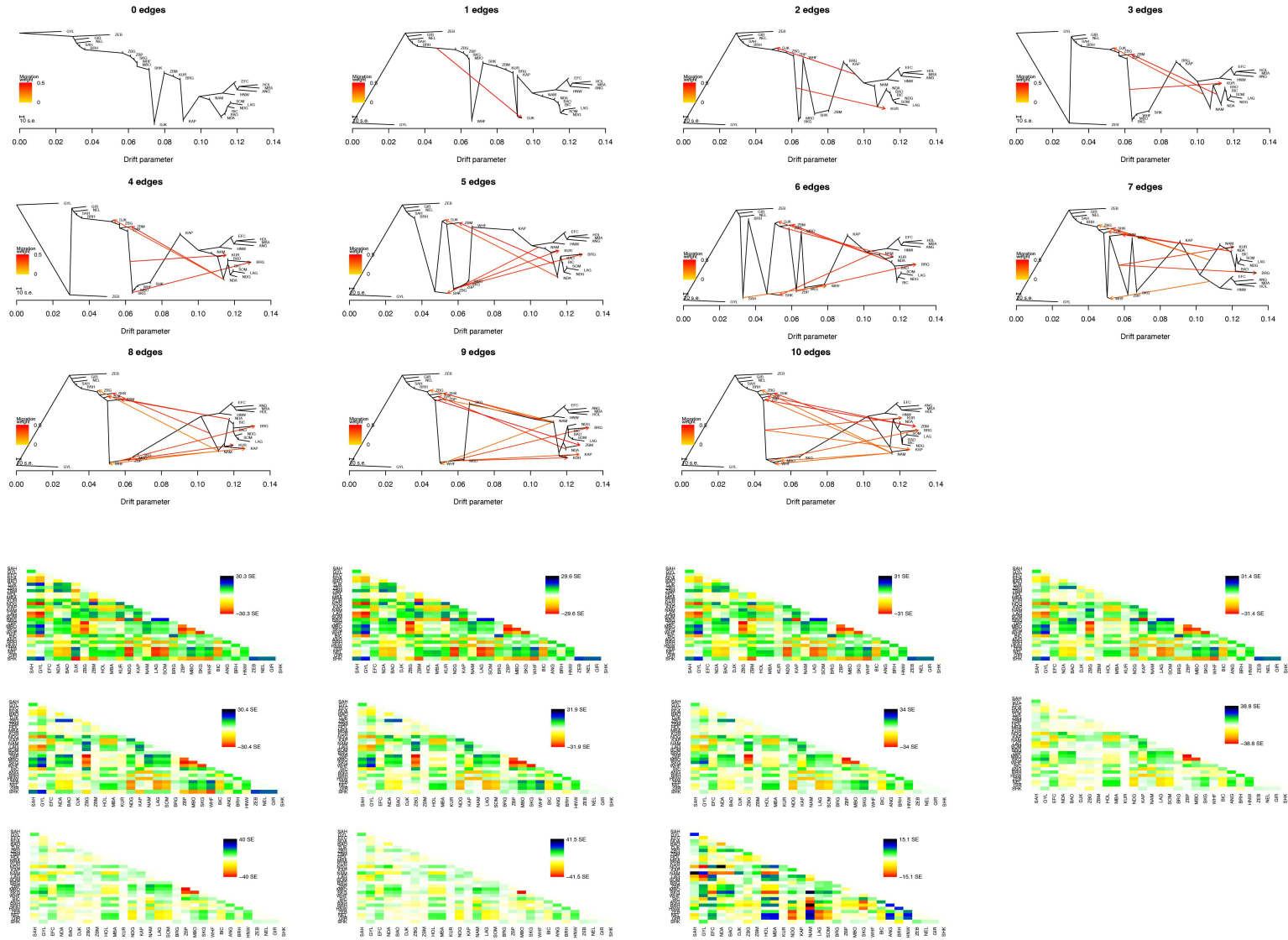
Supplementary Figure 4.1: Results from Treemix analysis for sequentially adding migration edges from 0 to 10. Each tree has its respective residual matrix below.