

Supplementary Information for:

Chapter 3 | Genomic Insights into the Population History and Adaptive Traits of South American Criollo Cattle

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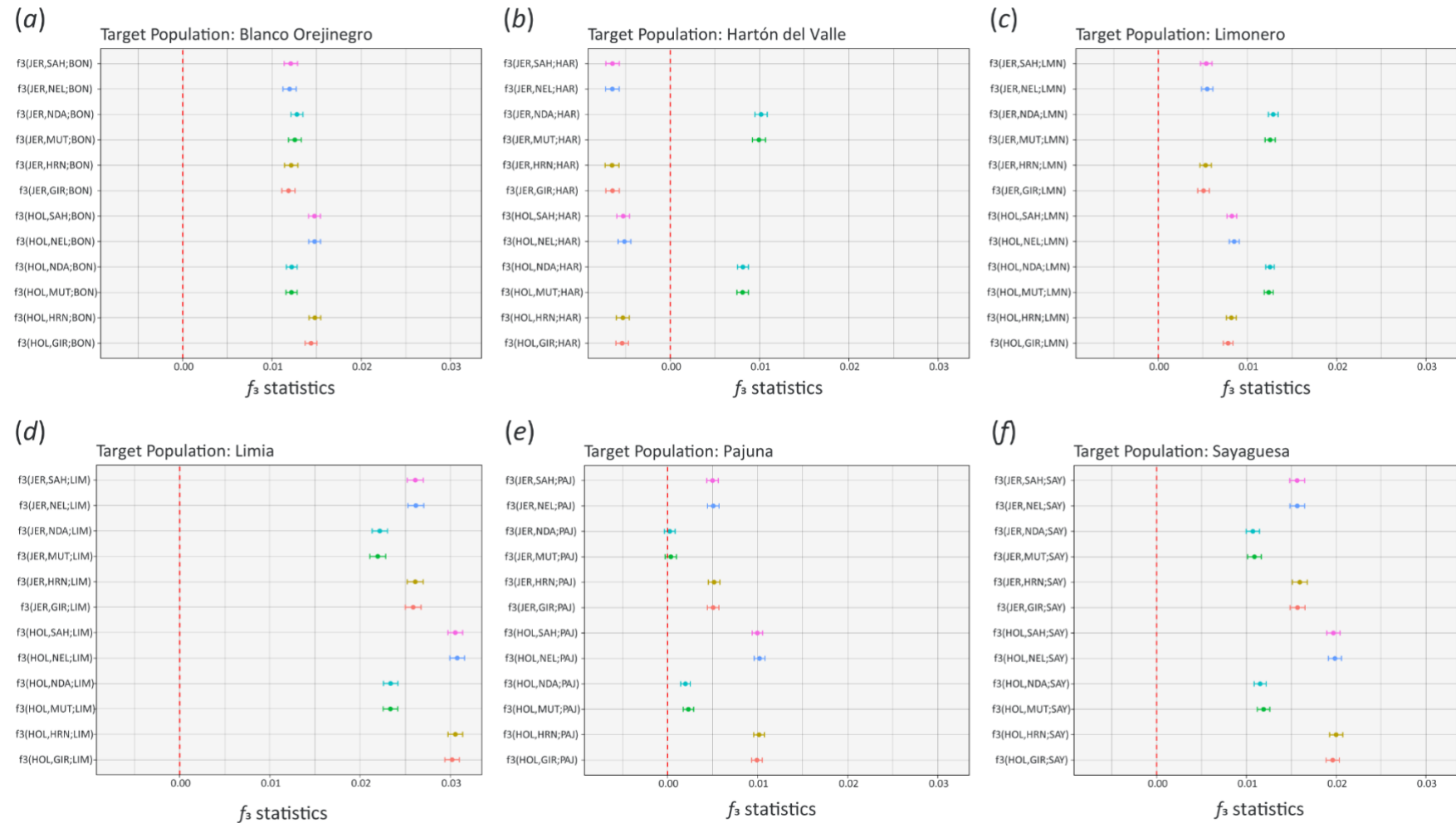
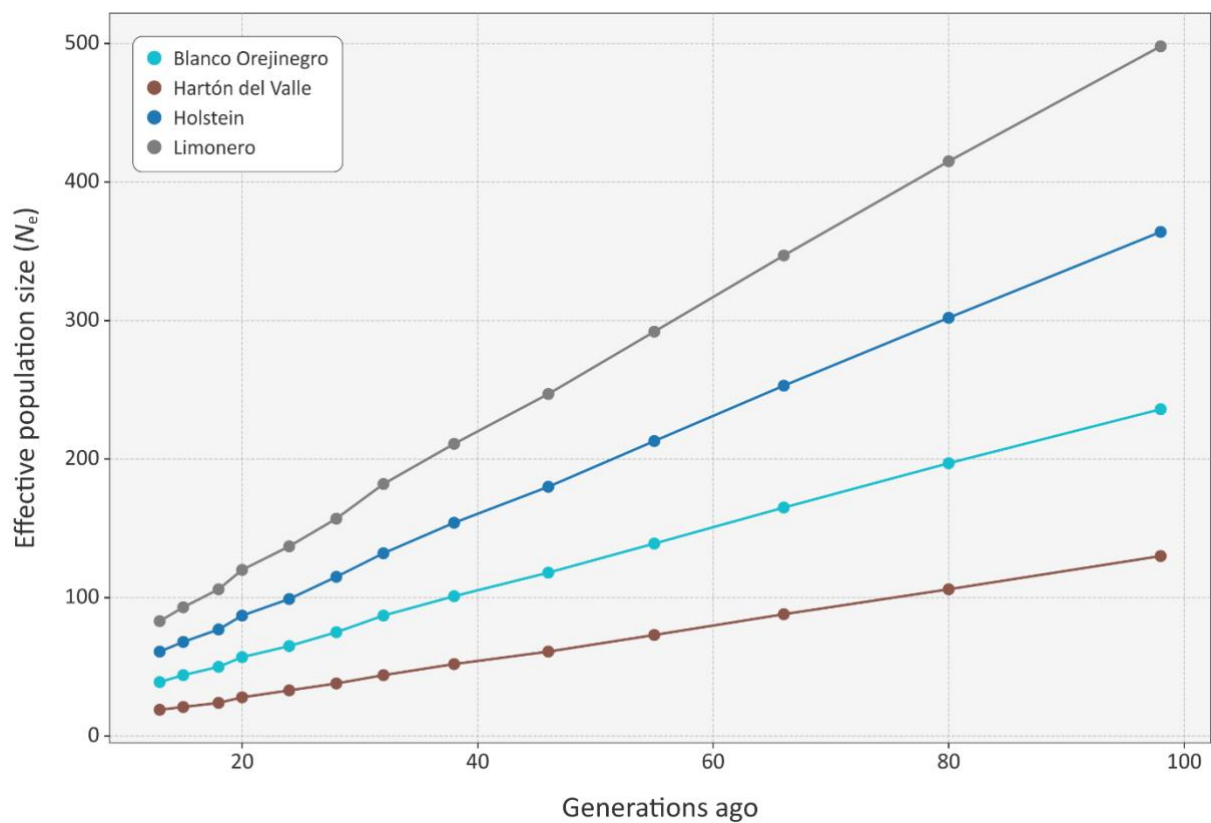


Figure S3.1. Three-population tests using the combined whole-genome sequence (WGS) and remapped BovineHD 777K BeadChip data for the Blanco Orejinegro – BON (a), Hartón del Valle – HAR (b), and Limonero – LMN (c) Limia – LIM (d), Pajuna – PAJ (e), and Sayaguesa – SAY (f) as target populations. The reference populations used were two European taurine populations (Jersey – JER; and Holstein – HOL), four indicine breeds (Gir – GIR; Hariara – HRN; Nelore – NEL; and Sahiwal – SAH), and two African taurine populations (N'Dama – N'DA; and Muturu – MUT). Each coloured data point shows the f_3 statistics value and the horizontal line represents plus or minus the standard error (\pm SE). Further details on the breeds/populations are also provided in Table S2.



Supplementary Figure S3.2. Modelled effective population size (N_e) values across time for the Blanco Orejinegro, Hartón del Valle, Limonero, and Holstein cattle breeds.

Supplementary Tables

Supplementary Table S3.1: Cattle samples with whole-genome sequence (WGS) data.

Sample sequence code	Breed/ pop. code	Lab code	Breed	Lineage	Phenotype	Source
SRR3693229	AFT	NDA01	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693373	AFT	NDA06	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693375	AFT	NDA07	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693376	AFT	NDA04	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693378	AFT	NDA05	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693379	AFT	NDA02	N'Dama	African Taurine	N/A	PRJNA312138
SRR3693419	AFT	NDA03	N'Dama	African Taurine	N/A	PRJNA312138
SRR3694478	AFT	NDA08	N'Dama	African Taurine	N/A	PRJNA312138
SRR3694578	AFT	NDA09	N'Dama	African Taurine	N/A	PRJNA312138
SA01	BON	BON01	Blanco Orejinegro	American Criollo	N/A	This study
SA02	BON	BON02	Blanco Orejinegro	American Criollo	N/A	This study
SA03	BON	BON03	Blanco Orejinegro	American Criollo	N/A	This study
SA04	BON	BON04	Blanco Orejinegro	American Criollo	N/A	This study
SA05	BON	BON05	Blanco Orejinegro	American Criollo	N/A	This study
SA06	BON	BON06	Blanco Orejinegro	American Criollo	N/A	This study
SA07	BON	BON07	Blanco Orejinegro	American Criollo	N/A	This study
SA08	BON	BON08	Blanco Orejinegro	American Criollo	N/A	This study
SA09	BON	BON09	Blanco Orejinegro	American Criollo	N/A	This study
SA10	BON	BON10	Blanco Orejinegro	American Criollo	N/A	This study
SRR7170787	CCC	CCC01	Costeño con Cuernos	American Criollo	N/A	PRJNA471656
SRR7170788	CCC	CCC02	Costeño con Cuernos	American Criollo	N/A	PRJNA471656
G13	HAR	HAR01	Hartón del Valle	American Criollo	N/A	This study
G16	HAR	HAR02	Hartón del Valle	American Criollo	N/A	This study
G17	HAR	HAR03	Hartón del Valle	American Criollo	N/A	This study
G20	HAR	HAR04	Hartón del Valle	American Criollo	N/A	This study

Sample sequence code	Breed/ pop. code	Lab code	Breed	Lineage	Phenotype	Source
G9	HAR	HAR05	Hartón del Valle	American Criollo	N/A	This study
G18	HAR	HAC01	Hartón del Valle/Carora	American Criollo	N/A	This study
G1	LMN	LMN01	Limonero	American Criollo	N/A	This study
G10	LMN	LMN02	Limonero	American Criollo	N/A	This study
G11	LMN	LMN03	Limonero	American Criollo	N/A	This study
G12	LMN	LMN04	Limonero	American Criollo	N/A	This study
G14	LMN	LMN05	Limonero	American Criollo	N/A	This study
G19	LMN	LMN06	Limonero	American Criollo	N/A	This study
G2	LMN	LMN07	Limonero	American Criollo	N/A	This study
G21	LMN	LMN08	Limonero	American Criollo	N/A	This study
G22	LMN	LMN09	Limonero	American Criollo	N/A	This study
G3	LMN	LMN10	Limonero	American Criollo	N/A	This study
G5	LMN	LMN11	Limonero	American Criollo	N/A	This study
G6	LMN	LMN12	Limonero	American Criollo	N/A	This study
G7	LMN	LMN13	Limonero	American Criollo	N/A	This study
G8	LMN	LMN14	Limonero	American Criollo	N/A	This study
SRR6371016	LMN	LMN15	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371017	LMN	LMN16	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371018	LMN	LMN17	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371019	LMN	LMN18	Limonero	American Criollo	Long coat	PRJNA422135
SRR6371020	LMN	LMN19	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371021	LMN	LMN20	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371022	LMN	LMN21	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371023	LMN	LMN22	Limonero	American Criollo	Slick coat	PRJNA422135
SRR6371024	LMN	LMN23	Limonero	American Criollo	Normal coat	PRJNA422135
G23	LAR	LAR01	Limonero/Romosinuano	American Criollo	N/A	This study
G24	LAS	LAS01	Limonero/Senepol	American Criollo	N/A	This study
G4	LAS	LAS02	Limonero/Senepol	American Criollo	N/A	This study

Sample sequence code	Breed/ pop. code	Lab code	Breed	Lineage	Phenotype	Source
SRR7170789	SAM	SAM01	San Martinero	American Criollo	N/A	PRJNA471656
SRR7170790	SAM	SAM02	San Martinero	American Criollo	N/A	PRJNA471656
G25	UKN	UKN01	Unknown Criollo breed	American Criollo	N/A	This study
SAMN05788494	AMI	BRA01	Brahman	American Indicine	N/A	PRJNA343262
SAMN05788495	AMI	BRA02	Brahman	American Indicine	N/A	PRJNA343262
SAMN05788496	AMI	BRA03	Brahman	American Indicine	N/A	PRJNA343262
SAMN05788512	AMI	GIR01	Gir	American Indicine	N/A	PRJNA343262
SAMN05788513	AMI	GIR02	Gir	American Indicine	N/A	PRJNA343262
SAMN05788514	AMI	GIR03	Gir	American Indicine	N/A	PRJNA343262
SAMN05788515	AMI	GIR04	Gir	American Indicine	N/A	PRJNA343262
SAMN05788520	AMI	NEL01	Nelore	American Indicine	N/A	PRJNA343262
SAMN05788521	AMI	NEL02	Nelore	American Indicine	N/A	PRJNA343262
SAMN05788522	AMI	NEL03	Nelore	American Indicine	N/A	PRJNA343262
SAMN05788523	AMI	NEL04	Nelore	American Indicine	N/A	PRJNA343262
SAMN05788524	AMI	NEL05	Nelore	American Indicine	N/A	PRJNA343262
SAMN05788525	AMI	NEL06	Nelore	American Indicine	N/A	PRJNA343262
SRR4477870	EUT	ANG01	Angus	European Taurine	N/A	PRJNA343262
SAMN05788492	EUT	HOL01	Holstein	European Taurine	N/A	PRJNA343262
SAMN05788508	EUT	HOL02	Holstein	European Taurine	N/A	PRJNA343262
SRR4279977	EUT	HOL03	Holstein	European Taurine	N/A	PRJNA343262
SRR4279978	EUT	HOL04	Holstein	European Taurine	N/A	PRJNA343262
SRR4279979	EUT	HOL05	Holstein	European Taurine	N/A	PRJNA343262
SRR4280060	EUT	HOL06	Holstein	European Taurine	N/A	PRJNA343262
SRR8587906	EUT	HOL07	Holstein	European Taurine	N/A	PRJNA343262
SRR8587907	EUT	HOL08	Holstein	European Taurine	N/A	PRJNA343262
SRR8587979	EUT	HOL09	Holstein	European Taurine	N/A	PRJNA343262
SRR8587980	EUT	HOL10	Holstein	European Taurine	N/A	PRJNA343262
SRR8587981	EUT	HOL11	Holstein	European Taurine	N/A	PRJNA343262

Sample sequence code	Breed/ pop. code	Lab code	Breed	Lineage	Phenotype	Source
SRR934405	EUT	HOL12	Holstein	European Taurine	N/A	PRJNA210521
SRR934406	EUT	HOL13	Holstein	European Taurine	N/A	PRJNA210521
SRR934407	EUT	HOL14	Holstein	European Taurine	N/A	PRJNA210521
SRR934408	EUT	HOL15	Holstein	European Taurine	N/A	PRJNA210521
SRR934409	EUT	HOL16	Holstein	European Taurine	N/A	PRJNA210521
SAMN05788516	EUT	JER01	Jersey	European Taurine	N/A	PRJNA343262
SAMN05788518	EUT	JER02	Jersey	European Taurine	N/A	PRJNA343262
SRR3497161	EUT	JER03	Jersey	European Taurine	N/A	PRJNA318089
SRR3497162	EUT	JER04	Jersey	European Taurine	N/A	PRJNA318089
SRR3497451	EUT	JER05	Jersey	European Taurine	N/A	PRJNA318089
SRR3497462	EUT	JER06	Jersey	European Taurine	N/A	PRJNA318089
SRR3497464	EUT	JER07	Jersey	European Taurine	N/A	PRJNA318089
SRR8426539	IBT	LIM01	Limia	European Taurine	N/A	PRJNA514237
SRR8426540	IBT	MAR01	Maronesa	European Taurine	N/A	PRJNA514237
SAMN10721584	EUT	PAJ01	Pajuna	European Taurine	N/A	PRJNA514237
SAMN10721579	EUT	SAY01	Sayaguesa	European Taurine	N/A	PRJNA514237
SRR10752679	EUT	SRH01	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752680	EUT	SRH02	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752681	EUT	SRH03	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752682	EUT	SRH04	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752683	EUT	SRH05	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752684	EUT	SRH06	Shorthorn	European Taurine	N/A	PRJNA343262
SRR10752677	EUT	SIM01	Simmental	European Taurine	N/A	PRJNA343262
SRR10752700	EUT	SIM02	Simmental	European Taurine	N/A	PRJNA343262
SRR10752701	EUT	SIM03	Simmental	European Taurine	N/A	PRJNA343262

Supplementary Table S3.4: Composite selection signatures (CSS) cluster gene ontology (GO) term overrepresentation analysis for the Blanco Orejinegro breed.

GO source	Term name	GO ID	FDR- P_{adj}	Term size	Query size	Intersect. size	Effect. domain size
GO:MF	immunoglobulin receptor binding	GO:0034987	3.06E+07	26	296	10	18,136
GO:MF	antigen binding	GO:0003823	0.00001	57	296	10	18,136
GO:MF	RAGE receptor binding	GO:0050786	0.00021	6	296	4	18,136
GO:BP	phagocytosis, recognition	GO:0006910	6.33E+08	37	304	10	19,448
GO:BP	B cell receptor signaling pathway	GO:0050853	0.00000	63	304	11	19,448
GO:BP	complement activation, classical pathway	GO:0006958	0.00000	48	304	10	19,448
GO:BP	humoral immune response mediated by circulating immunoglobulin	GO:0002455	0.00002	60	304	10	19,448
GO:BP	phagocytosis, engulfment	GO:0006911	0.00002	59	304	10	19,448
GO:BP	plasma membrane invagination	GO:0099024	0.00005	67	304	10	19,448
GO:BP	positive regulation of B cell activation	GO:0050871	0.00006	87	304	11	19,448
GO:BP	membrane invagination	GO:0010324	0.00008	73	304	10	19,448
GO:BP	complement activation	GO:0006956	0.00008	73	304	10	19,448
GO:BP	humoral immune response	GO:0006959	0.00009	187	304	15	19,448
GO:BP	cell recognition	GO:0008037	0.00011	118	304	12	19,448
GO:BP	regulation of B cell activation	GO:0050864	0.00015	123	304	12	19,448
GO:BP	positive regulation of cellular process	GO:0048522	0.00068	4,242	304	101	19,448
GO:BP	phagocytosis	GO:0006909	0.00099	175	304	13	19,448
GO:BP	positive regulation of biological process	GO:0048518	0.00117	4,871	304	111	19,448
GO:BP	immune response-activating cell surface receptor signaling pathway	GO:0002429	0.00117	208	304	14	19,448
GO:BP	immune response-regulating cell surface receptor signaling pathway	GO:0002768	0.00243	223	304	14	19,448
GO:BP	immunoglobulin mediated immune response	GO:0016064	0.00269	117	304	10	19,448

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:BP	B cell mediated immunity	GO:0019724	0.00269	117	304	10	19,448
GO:BP	defense response to bacterium	GO:0042742	0.00269	258	304	15	19,448
GO:BP	antigen receptor-mediated signaling pathway	GO:0050851	0.00320	146	304	11	19,448
GO:BP	response to bacterium	GO:0009617	0.00470	487	304	21	19,448
GO:BP	B cell activation	GO:0042113	0.01092	230	304	13	19,448
GO:BP	positive regulation of lymphocyte activation	GO:0051251	0.01142	232	304	13	19,448
GO:BP	vesicle-mediated transport	GO:0016192	0.01240	1,175	304	36	19,448
GO:BP	endocytosis	GO:0006897	0.01811	502	304	20	19,448
GO:BP	immune response-activating signaling pathway	GO:0002757	0.02362	287	304	14	19,448
GO:BP	neutrophil aggregation	GO:0070488	0.02515	2	304	2	19,448
GO:BP	learned vocalization behavior	GO:0098583	0.02515	2	304	2	19,448
GO:BP	mastication	GO:0071626	0.02515	2	304	2	19,448
GO:BP	regulation of lymphocyte activation	GO:0051249	0.02515	363	304	16	19,448
GO:BP	thorax and anterior abdomen determination	GO:0007356	0.02515	2	304	2	19,448
GO:BP	negative regulation of saliva secretion	GO:1905747	0.02515	2	304	2	19,448
GO:BP	hard palate morphogenesis	GO:1905748	0.02515	2	304	2	19,448
GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO:0002460	0.02522	227	304	12	19,448
GO:BP	positive regulation of leukocyte activation	GO:0002696	0.02637	263	304	13	19,448
GO:BP	immune response-regulating signaling pathway	GO:0002764	0.03001	303	304	14	19,448
GO:BP	positive regulation of cell activation	GO:0050867	0.03450	272	304	13	19,448
GO:BP	membrane organization	GO:0061024	0.04225	554	304	20	19,448
GO:BP	positive regulation of nitrogen compound metabolic process	GO:0051173	0.04225	2,405	304	58	19,448

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:CC	immunoglobulin complex, circulating	GO:0042571	2.87E+05	22	322	10	19,665
GO:CC	immunoglobulin complex	GO:0019814	1.11E+07	26	322	10	19,665
GO:CC	organelle	GO:0043226	0.00345	13,089	322	248	19,665
GO:CC	intracellular organelle	GO:0043229	0.01247	12,824	322	241	19,665
GO:CC	side of membrane	GO:0098552	0.02013	435	322	18	19,665
GO:CC	external side of plasma membrane	GO:0009897	0.02013	322	322	15	19,665
GO:CC	intracellular anatomical structure	GO:0005622	0.02013	14,419	322	263	19,665

Supplementary Table S3.5: Composite selection signatures (CSS) cluster gene ontology (GO) term overrepresentation analysis for the Hartón del Valle breed.

GO source	Term name	GO ID	FDR- P_{adj}	Term size	Query size	Intersect. size	Effect. domain size
GO:MF	structural constituent of skin epidermis	GO:0030280	6.41E-08	21	276	16	18,136
GO:BP	keratinization	GO:0031424	2.18E-01	34	289	16	19,448
GO:BP	intermediate filament cytoskeleton organization	GO:0045104	3.39E-02	72	289	20	19,448
GO:BP	intermediate filament-based process	GO:0045103	3.39E-02	73	289	20	19,448
GO:BP	intermediate filament organization	GO:0045109	9.82E+00	50	289	16	19,448
GO:BP	keratinocyte differentiation	GO:0030216	2.10E+06	106	289	17	19,448
GO:BP	epidermal cell differentiation	GO:0009913	1.89E+08	161	289	18	19,448
GO:BP	epidermis development	GO:0008544	0.00000	256	289	19	19,448
GO:BP	cytoskeleton organization	GO:0007010	0.00001	1,205	289	44	19,448
GO:BP	skin development	GO:0043588	0.00002	223	289	17	19,448
GO:BP	epithelial cell differentiation	GO:0030855	0.00004	498	289	25	19,448
GO:BP	epithelium development	GO:0060429	0.00006	899	289	35	19,448
GO:BP	supramolecular fiber organization	GO:0097435	0.00023	628	289	27	19,448
GO:BP	tissue development	GO:0009888	0.00107	1,444	289	44	19,448
GO:BP	ureteric bud formation	GO:0060676	0.02615	7	289	3	19,448
GO:BP	embryonic epithelial tube formation	GO:0001838	0.03174	102	289	8	19,448
GO:BP	sno(s)RNA catabolic process	GO:0016077	0.03429	2	289	2	19,448
GO:BP	epithelial tube formation	GO:0072175	0.03429	109	289	8	19,448
GO:BP	organelle organization	GO:0006996	0.03429	2,783	289	64	19,448
GO:BP	ureteric bud elongation	GO:0060677	0.03429	8	289	3	19,448
GO:BP	olfactory placode development	GO:0071698	0.03429	2	289	2	19,448

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:BP	olfactory placode morphogenesis	GO:0071699	0.03429	2	289	2	19,448
GO:BP	olfactory placode formation	GO:0030910	0.03429	2	289	2	19,448
GO:BP	anatomical structure development	GO:0048856	0.03539	4,196	289	88	19,448
GO:CC	keratin filament	GO:0045095	3.64E-15	90	304	31	19,665
GO:CC	intermediate filament	GO:0005882	1.28E-08	142	304	31	19,665
GO:CC	intermediate filament cytoskeleton	GO:0045111	1.56E-08	172	304	33	19,665
GO:CC	polymeric cytoskeletal fiber	GO:0099513	6.63E+04	524	304	36	19,665
GO:CC	supramolecular fiber	GO:0099512	4.53E+05	675	304	38	19,665
GO:CC	supramolecular complex	GO:0099080	4.53E+05	956	304	46	19,665
GO:CC	supramolecular polymer	GO:0099081	4.78E+05	683	304	38	19,665
GO:CC	cytoskeleton	GO:0005856	0.00010	1,766	304	53	19,665
GO:CC	non-membrane-bounded organelle	GO:0043228	0.00031	4,965	304	111	19,665
GO:CC	intracellular non-membrane-bounded organelle	GO:0043232	0.00031	4,964	304	111	19,665
GO:CC	cornified envelope	GO:0001533	0.00275	29	304	5	19,665
GO:CC	immunoglobulin complex, circulating	GO:0042571	0.01107	22	304	4	19,665
GO:CC	intracellular organelle	GO:0043229	0.01776	12,824	304	225	19,665
GO:CC	immunoglobulin complex	GO:0019814	0.01847	26	304	4	19,665
GO:CC	organelle	GO:0043226	0.02203	13,089	304	228	19,665
GO:CC	intracellular anatomical structure	GO:0005622	0.04658	14,419	304	245	19,665

Supplementary Table S3.6: Composite selection signatures (CSS) cluster gene ontology (GO) term overrepresentation analysis for the Limonero breed.

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:MF	immunoglobulin receptor binding	GO:0034987	5.54E+06	26	311	10	18,136
GO:MF	antigen binding	GO:0003823	0.00001	57	311	10	18,136
GO:MF	RAGE receptor binding	GO:0050786	0.00029	6	311	4	18,136
GO:MF	L-glutamine aminotransferase activity	GO:0070548	0.00276	4	311	3	18,136
GO:MF	oxidoreductase activity, acting on the aldehyde or oxo group of donors, oxygen as acceptor	GO:0016623	0.00276	4	311	3	18,136
GO:MF	calcium-dependent protein binding	GO:0048306	0.01677	47	311	6	18,136
GO:MF	signaling receptor binding	GO:0005102	0.02561	1,134	311	36	18,136
GO:MF	cysteine-S-conjugate beta-lyase activity	GO:0047804	0.02561	2	311	2	18,136
GO:BP	plasma membrane invagination	GO:0099024	8.58E+05	67	325	15	19,448
GO:BP	phagocytosis, engulfment	GO:0006911	8.58E+05	59	325	14	19,448
GO:BP	complement activation, classical pathway	GO:0006958	8.58E+05	48	325	13	19,448
GO:BP	membrane invagination	GO:0010324	8.80E+05	73	325	15	19,448
GO:BP	humoral immune response mediated by circulating immunoglobulin	GO:0002455	1.15E+08	60	325	13	19,448
GO:BP	complement activation	GO:0006956	1.32E+09	73	325	13	19,448
GO:BP	phagocytosis, recognition	GO:0006910	1.70E+09	37	325	10	19,448
GO:BP	humoral immune response	GO:0006959	1.70E+09	187	325	19	19,448
GO:BP	phagocytosis	GO:0006909	0.00000	175	325	17	19,448
GO:BP	B cell receptor signaling pathway	GO:0050853	0.00000	63	325	11	19,448
GO:BP	positive regulation of B cell activation	GO:0050871	0.00001	87	325	12	19,448
GO:BP	immunoglobulin mediated immune response	GO:0016064	0.00002	117	325	13	19,448
GO:BP	B cell mediated immunity	GO:0019724	0.00002	117	325	13	19,448

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:BP	regulation of B cell activation	GO:0050864	0.00004	123	325	13	19,448
GO:BP	lipoprotein metabolic process	GO:0042157	0.00006	129	325	13	19,448
GO:BP	immune response-activating cell surface receptor signaling pathway	GO:0002429	0.00010	208	325	16	19,448
GO:BP	immune response-regulating cell surface receptor signaling pathway	GO:0002768	0.00025	223	325	16	19,448
GO:BP	lipid transport	GO:0006869	0.00031	314	325	19	19,448
GO:BP	lipid localization	GO:0010876	0.00045	354	325	20	19,448
GO:BP	cell recognition	GO:0008037	0.00085	118	325	11	19,448
GO:BP	lymphocyte mediated immunity	GO:0002449	0.00101	224	325	15	19,448
GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO:0002460	0.00113	227	325	15	19,448
GO:BP	activation of immune response	GO:0002253	0.00144	355	325	19	19,448
GO:BP	establishment of meiotic spindle localization	GO:0051295	0.00266	4	325	3	19,448
GO:BP	positive regulation of biological process	GO:0048518	0.00266	4,871	325	115	19,448
GO:BP	leukocyte mediated immunity	GO:0002443	0.00270	278	325	16	19,448
GO:BP	immune response-activating signaling pathway	GO:0002757	0.00384	287	325	16	19,448
GO:BP	defense response to bacterium	GO:0042742	0.00405	258	325	15	19,448
GO:BP	B cell activation	GO:0042113	0.00426	230	325	14	19,448
GO:BP	antigen receptor-mediated signaling pathway	GO:0050851	0.00426	146	325	11	19,448
GO:BP	establishment of localization	GO:0051234	0.00603	3,760	325	92	19,448
GO:BP	immune response-regulating signaling pathway	GO:0002764	0.00620	303	325	16	19,448
GO:BP	membrane organization	GO:0061024	0.00691	554	325	23	19,448
GO:BP	positive regulation of DNA replication	GO:0045740	0.00802	27	325	5	19,448
GO:BP	synapse pruning	GO:0098883	0.00920	6	325	3	19,448

GO source	Term name	GO ID	FDR- P_{adj}	Term size	Query size	Intersect. size	Effect. domain size
GO:BP	positive regulation of cellular process	GO:0048522	0.00953	4,242	325	100	19,448
GO:BP	localization	GO:0051179	0.00989	4,302	325	101	19,448
GO:BP	transport	GO:0006810	0.00996	3,622	325	88	19,448
GO:BP	positive regulation of response to stimulus	GO:0048584	0.01449	1,627	325	47	19,448
GO:BP	adaptive immune response	GO:0002250	0.01780	304	325	15	19,448
GO:BP	positive regulation of cell activation	GO:0050867	0.01832	272	325	14	19,448
GO:BP	response to bacterium	GO:0009617	0.01880	487	325	20	19,448
GO:BP	neutrophil aggregation	GO:0070488	0.02097	2	325	2	19,448
GO:BP	learned vocalization behavior	GO:0098583	0.02097	2	325	2	19,448
GO:BP	mastication	GO:0071626	0.02097	2	325	2	19,448
GO:BP	hard palate morphogenesis	GO:1905748	0.02097	2	325	2	19,448
GO:BP	thorax and anterior abdomen determination	GO:0007356	0.02097	2	325	2	19,448
GO:BP	negative regulation of saliva secretion	GO:1905747	0.02097	2	325	2	19,448
GO:BP	endocytosis	GO:0006897	0.02387	502	325	20	19,448
GO:BP	vesicle-mediated transport	GO:0016192	0.02402	1,175	325	36	19,448
GO:BP	cell migration	GO:0016477	0.02741	1,141	325	35	19,448
GO:BP	defense response	GO:0006952	0.02741	1,185	325	36	19,448
GO:BP	organonitrogen compound metabolic process	GO:1901564	0.03104	5,570	325	121	19,448
GO:BP	positive regulation of leukocyte activation	GO:0002696	0.03418	263	325	13	19,448
GO:BP	positive regulation of lymphocyte activation	GO:0051251	0.03666	232	325	12	19,448
GO:BP	defense response to other organism	GO:0098542	0.04058	818	325	27	19,448
GO:BP	positive regulation of immune response	GO:0050778	0.04740	497	325	19	19,448
GO:BP	protein metabolic process	GO:0019538	0.04898	4,814	325	106	19,448

GO source	Term name	GO ID	FDR- $P_{adj.}$	Term size	Query size	Intersect. size	Effect. domain size
GO:BP	vestibulocochlear nerve formation	GO:0021650	0.04978	3	325	2	19,448
GO:BP	zygotic determination of anterior/posterior axis, embryo	GO:0007354	0.04978	3	325	2	19,448
GO:CC	immunoglobulin complex, circulating	GO:0042571	3.85E+05	22	332	10	19,665
GO:CC	immunoglobulin complex	GO:0019814	1.49E+07	26	332	10	19,665
GO:CC	extracellular region	GO:0005576	0.01611	1,632	332	48	19,665
GO:CC	complement component C1q complex	GO:0062167	0.03083	2	332	2	19,665

Supplementary Table S3.8: Composite selection signatures (CSS) genes and functional inference.

Breed	Associated trait	Gene	Functional inference	References
Blanco Orejinegro	Coat colour	<i>PAX3</i>	Mutations in <i>PAX3</i> cause a spectrum of white spotting to entirely white.	[1]
Blanco Orejinegro	Coat colour	<i>SLC45A2</i>	Mutations in <i>SLC45A2</i> cause oculocutaneous albinism.	[2]
Blanco Orejinegro	Coat colour	<i>KITLG</i>	<i>KITLG</i> is linked to the roan coat type.	[3]
Limonero, Hartón del Valle	Coat colour	<i>MC1R</i>	<i>MC1R</i> regulates tyrosinase levels affecting coat colour.	[4]
Blanco Orejinegro, Hartón del Valle	Heat tolerance	<i>PRLR</i>	Mutations in <i>PRLR</i> cause the "slick" phenotype, causing increased thermotolerance and milk yields under tropical conditions.	[5-12]
All breeds	Heat tolerance	<i>MVD</i>	Identified to be under selection in North African cattle; may confer thermotolerance.	[13]
Limonero	Heat tolerance	<i>CCM2</i>	Involved in blood vessel development and morphogenesis; might aid heat stress adaptation.	[13]
Blanco Orejinegro, Hartón del Valle	Heat tolerance	<i>SENS2</i>	Downregulated in heat-stress response, helps combat protein denaturation from heat-induced stress.	[14, 15]
Limonero	Heat tolerance	<i>FBXO4</i>	Involved in regulation of body temperature through interactions with Hsp20.	[16, 17]
Blanco Orejinegro	Heat tolerance	<i>DNAJA2</i>	Part of the Hsp40 family, upregulated in response to heat stress.	[18]
All breeds	Heat tolerance	<i>HIGD1A</i> , <i>CBFA2T3</i>	Associated with cellular responses to hypoxia, could indicate a response to oxidative stress in heat-stressed cows.	[19, 20]
Blanco Orejinegro	Fertility and reproduction	<i>CATSPER3</i>	Exclusively expressed in the testis and encodes a sperm-specific ion channel, linked to sperm function and male fertility.	[21]
Blanco Orejinegro	Fertility and reproduction	<i>SPEF2</i>	Involved in the formation and functionality of sperm flagella.	[22]
Blanco Orejinegro, Hartón del Valle	Fertility and reproduction	<i>CREM</i> , <i>MISP3</i>	Implicated in spermatogenesis.	[23, 24]
Hartón del Valle	Fertility and reproduction	<i>HKDC1</i>	Shows high expression in the testes.	[25]
Limonero	Fertility and reproduction	<i>FSIP1</i>	Crucial for normal spermiogenesis and flagella development.	[26]
Limonero	Fertility and reproduction	<i>PTGES</i>	Encodes an enzyme involved in the synthesis of prostaglandin E2 (PGE2), a signalling molecule playing a crucial role in reproductive processes.	[27]
All breeds	Immune response	<i>CBFA2T3</i>	Plays a role in the cattle immune response to mammary gland inflammation.	[28]
Blanco Orejinegro, Limonero	Immune response	<i>CXCL14</i>	Its regulation by mRNAs and miRNAs plays a role in the immune response to bovine mastitis.	[29]
Limonero	Immune response	<i>LRRC8A</i>	Essential for both the development and function of T lymphocytes.	[30]

Breed	Associated trait	Gene	Functional inference	References
Blanco Orejinegro, Hartón del Valle	Resistance to anaemia	<i>EPB41</i>	Associated with resistance to anaemia, encodes proteins that form the skeletal structure of red blood cells and is linked to haematological disorders in humans.	[31]
Blanco Orejinegro, Limonero	Resistance to anaemia	<i>RPS20,</i> <i>RPS27</i>	Mutations in both genes have been shown to be responsible for Diamond-Blackfan anaemia.	[32, 33]
Blanco Orejinegro	Resistance to anaemia	<i>ZFPM1</i>	Plays a significant role in both cardiac and hematopoietic development, implicated in the regulation of haematopoiesis in <i>Trypanosoma congolense</i> -infected mice.	[34]

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