source	term name Gene Ontology (Biological process)	term ID	n. of term genes	corrected p-value	ARAB	BELGIAN	FM	FT	ICELANDIC	LUSITANO	MAREMMANO	MORGAN	QH	SB	TB	WP
BP	regulation of protein deacetylation	GO:0090311	28	3.87e-03												4
BP	aminoglycan catabolic process	GO:0006026	23	7.73e-04									5			
BP	signaling	GO:0023052	5192	6.73e-03							44					
BP	response to stimulus	GO:0050896	6747	4.46e-02							50					
BP	detection of stimulus	GO:0051606	1089	5.89e-08			52	39	31		24	36				
BP	detection of chemical stimulus	GO:0009593	1004	2.79e-09			52	24	36		23	36				
BP	system process	GO:0003008	1954	7.29e-03			36				22					
BP	nervous system process	GO:0050877	1525	5.52e-05			35	42	44		22	39				
BP	sensory perception	GO:0007600	1291	2.90e-06			34	45	40		25	38				
BP	sensory perception of chemical stimulus	GO:0007606	1044	1.23e-08			52	24	37		23	36				
BP	sensory perception of smell	GO:0007608	971	7.69e-10			52	24	36		23	36				
BP	detection of stimulus involved in sensory perception	GO:0050906	1019	4.91e-09			52	24	36		23	36				
BP	detection of chemical stimulus involved in sensory perception	GO:0050907	985	1.34e-09			52	24	36		23	36				
BP	detection of chemical stimulus involved in sensory perception ...	GO:0050911	952	3.56e-10			52	24	35		23	36				
BP	cellular process	GO:0009987	14012	1.06e-03			420							377		
BP	cell communication	GO:0007154	5238	8.69e-03							44					
BP	cellular response to stimulus	GO:0051716	5795	7.85e-03							47					
BP	signal transduction	GO:0007165	4877	1.05e-03							44					
BP	G-protein coupled receptor signaling pathway	GO:0007186	1585	7.36e-08			39	17	42		29	23				
BP	regulation of biological process	GO:0050789	9088	2.84e-02							50					
BP	negative regulation of biological process	GO:0048519	3430	1.12e-03									98			
BP	negative regulation of cellular process	GO:0048523	3143	2.64e-03									113			
BP	negative regulation of metabolic process	GO:0009892	1900	6.99e-04									42			
BP	negative regulation of macromolecule metabolic process	GO:0010605	1732	3.57e-03									38			
BP	negative regulation of nitrogen compound metabolic process	GO:0051172	1632	1.68e-02									35			
BP	negative regulation of cellular metabolic process	GO:0031324	1750	1.69e-03									39			
BP	negative regulation of NLRP3 inflammasome complex assembly	GO:1900226	3	3.15e-02		2										
BP	hyaluronan catabolic process	GO:0030214	7	8.19e-03									3			
BP	protein-DNA complex subunit organization	GO:0071824	192	1.75e-07				16			13	20	18			
BP	macromolecular complex assembly	GO:0065003	1227	3.09e-02									53			
BP	cellular macromolecular complex assembly	GO:0034622	799	5.85e-03									41			
BP	protein-DNA complex assembly	GO:0065004	167	1.14e-07				16			13	19	17			
BP	organelle organization	GO:0006996	2788	2.11e-02								72				
BP	chromosome organization	GO:0051276	858	3.47e-07								46	46			43
BP	DNA conformation change	GO:0071103	193	1.40e-06				13				19	18			
BP	DNA packaging	GO:0006323	142	6.00e-08				12				18	17			
BP	chromatin organization	GO:0006325	553	1.47e-10				34			23	41	42			
BP	chromatin assembly or disassembly	GO:0006333	136	2.83e-09				12				19	16			
BP	chromatin assembly	GO:0031497	117	2.07e-09				12			10	18	15			
BP	nucleosome organization	GO:0034728	129	1.07e-09				12				19	16			
BP	nucleosome assembly	GO:0006334	104	2.52e-10				12			10	18	15			
BP	negative regulation of histone deacetylation	GO:0031064	2	2.26e-02												2
BP	negative regulation of megakaryocyte differentiation	GO:0045653	7	2.53e-02								3				
BP	negative regulation of I-kappaB kinase/NF-kappaB signaling	GO:0043124	42	2.52e-02												4
BP	response to UV-B	GO:0010224	15	3.32e-02						5						
BP	cellular response to UV-B	GO:0071493	7	8.19e-03									3			
BP	negative regulation of kinase activity	GO:0033673	193	3.74e-02									9			
BP	negative regulation of MAPK cascade	GO:0043409	105	1.91e-02									9			
BP	calcium activated phosphatidylserine scrambling	GO:0061589	4	3.73e-02				3								
BP	regulation of histone phosphorylation	GO:0033127	8	1.03e-02									4			

source	term name Gene Ontology (Cellular component)	term ID	n. of term genes	corrected p-value	ARAB	BELGIAN	FM	FT	ICELANDIC	LUSITANO	MAREMMANO	MORGAN	QH	SB	TB	WP
CC	nucleoplasm	GO:0005654	2058	1.32e-02									89			
CC	membrane	GO:0016020	7773	4.30e-02							44					
CC	membrane part	GO:0044425	6023	3.81e-03							33					
CC	intrinsic component of membrane	GO:0031224	5275	5.71e-04							32					
CC	integral component of membrane	GO:0016021	5228	4.55e-04							32					
CC	organelle	GO:0043226	9830	1.90e-03									318			294
CC	membrane-bounded organelle	GO:0043227	8940	5.68e-04									297			
CC	organelle part	GO:0044422	5774	5.90e-03												196
CC	cell	GO:0005623	14128	1.82e-03				265				314				418
CC	cell part	GO:0044464	14089	5.83e-03				263				313				
CC	intracellular part	GO:0044424	11151	1.96e-02									347			343
CC	intracellular organelle	GO:0043229	8832	5.99e-04									294			266
CC	intracellular organelle part	GO:0044446	5612	1.83e-03												194
CC	intracellular membrane-bounded organelle	GO:0043231	7514	1.96e-04									259			233
CC	nucleus	GO:0005634	5002	6.48e-04									187			
CC	endoplasmic reticulum-Golgi intermediate compartment	GO:0005793	46	2.34e-02			3									
CC	cell periphery	GO:0071944	3991	2.57e-05							42					
CC	plasma membrane	GO:0005886	3890	1.16e-05							42					
CC	DNA packaging complex	GO:0044815	97	4.68e-17				15	13		14	23	19			
CC	protein-DNA complex	GO:0032993	164	8.29e-14				18	17		15	25	22			
CC	chromosome	GO:0005694	750	5.80e-07								40				
CC	chromosomal part	GO:0044427	695	8.44e-07								38				
CC	nuclear chromosome part	GO:0044454	419	3.34e-02								21				
CC	chromatin	GO:0000785	415	3.73e-09								32	28			
CC	nuclear chromatin	GO:0000790	264	8.90e-03								17				
CC	nucleosome	GO:0000786	90	7.28e-18				15	13		14	23	19			
CC	hemoglobin complex	GO:0005833	5	2.16e-02		2										

source	term name Gene Ontology (Molecular function)	term ID	n. of term genes	corrected p-value	ARAB	BELGIAN	FM	FT	ICELANDIC	LUSITANO	MAREMMANO	MORGAN	QH	SB	TB	WP
MF	histone binding	GO:0042393	149	2.68e-03								16				
MF	chitin binding	GO:0008061	6	1.25e-02									3			
MF	glutathione transferase activity	GO:0004364	27	3.42e-02						4						
MF	protein dimerization activity	GO:0046983	887	5.61e-03								33	47			
MF	protein heterodimerization activity	GO:0046982	349	7.54e-08							18	26	31			
MF	signal transducer activity	GO:0004871	1950	6.16e-06			65	18			25	47				
MF	molecular transducer activity	GO:0060089	1938	5.20e-06			65	17			27					
MF	receptor activity	GO:0004872	1904	3.52e-06			64	17			27					
MF	transmembrane receptor activity	GO:0099600	1684	2.79e-07			38	17	40		25	42				
MF	signaling receptor activity	GO:0038023	1733	5.15e-07			63	17	40		25	43				
MF	transmembrane signaling receptor activity	GO:0004888	1652	1.85e-07			38	17	40		25	42				
MF	olfactory receptor activity	GO:0004984	952	3.56e-10			52	24	35		23	36				
MF	G-protein coupled receptor activity	GO:0004930	1321	7.66e-08			37	25	38		23	23				
MF	hyaluronoglucosaminidase activity	GO:0004415	9	1.95e-02									3			
MF	glycine N-acyltransferase activity	GO:0047961	4	2.04e-02				3								
MF	odorant binding	GO:0005549	224	3.31e-20	25	25	26	20	16	14	22	27				

source	term name Human Phenotype Ontology	term ID	n. of term genes	corrected p-value	ARAB	BELGIAN	FM	FT	ICELANDIC	LUSITANO	MAREMMANO	MORGAN	QH	SB	TB	WP
hp	Gonosomal inheritance	HP:0010985	205	3.78e-27	33						18			32	21	14
hp	X-linked inheritance	HP:0001417	202	2.11e-27	33						18			38	21	14
hp	X-linked dominant inheritance	HP:0001423	73	1.05e-05	7									12		
hp	X-linked recessive inheritance	HP:0001419	134	1.15e-18	19						15			27	16	13
hp	Abnormality of the ileum	HP:0001549	26	4.26e-02											5	
hp	Meckel diverticulum	HP:0002245	25	3.48e-02											5	
hp	Cone-shaped epiphysis	HP:0010579	57	2.58e-02			5									
hp	Lower extremity joint dislocation	HP:0030311	182	1.49e-02											12	
hp	Central nervous system degeneration	HP:0007009	4	3.00e-02												3
hp	Chronic CSF lymphocytosis	HP:0009704	3	4.67e-03									3			
hp	Neurodevelopmental abnormality	HP:0012759	1716	1.83e-02										54		
hp	Intellectual disability	HP:0001249	1226	2.19e-04	15									47		
hp	Enlarged cisterna magna	HP:0002280	4	3.60e-02			2									
hp	Decreased fertility in males	HP:0012041	56	2.94e-02											7	
hp	Alveolar ridge overgrowth	HP:0009085	3	4.56e-02			2									
hp	Flaring of rib cage	HP:0000904	4	3.07e-03					2							
hp	Abnormality of the upper urinary tract	HP:0010935	854	2.18e-03			12									
hp	Abnormality of the kidney	HP:0000077	834	1.66e-03			12									
hp	Abnormal renal morphology	HP:0012210	649	9.02e-05			12									
hp	Abnormality of the renal pelvis	HP:0010944	144	9.92e-03			6									
hp	Dilatation of the renal pelvis	HP:0010946	143	9.52e-03			6									
hp	Hydronephrosis	HP:0000126	143	9.52e-03			6									
hp	Abnormal renal physiology	HP:0012211	433	3.69e-02			8									
hp	Abnormality of the testis	HP:0000035	636	2.59e-02			9									
hp	Abnormal breath sound	HP:0030829	14	4.86e-02							2					
hp	Stridor	HP:0010307	14	4.86e-02							2					
hp	Inspiratory stridor	HP:0005348	6	8.02e-03							2					
hp	Macroorchidism	HP:0000053	13	1.17e-02										4		
hp	Hydroureter	HP:0000072	52	5.09e-03											8	
hp	Neurological speech impairment	HP:0002167	590	1.85e-02												31
hp	Facial wrinkling	HP:0009762	2	3.43e-02										2		
hp	Oligohydramnios	HP:0001562	83	3.42e-02											8	
hp	Progressive forgetfulness	HP:0007017	3	7.60e-03												3
hp	Abnormality of the genital system	HP:0000078	999	3.20e-02			23									
hp	Abnormal reproductive system morphology	HP:0012243	915	6.55e-03			23									
hp	Abnormal sex determination	HP:0012244	26	3.69e-02								4				
hp	Sex reversal	HP:0012245	19	9.94e-03								4				
hp	U-Shaped upper lip vermilion	HP:0010806	5	5.01e-03			2									
hp	Abnormality of the nail	HP:0001597	310	1.29e-02	9											
hp	Increased head circumference	HP:0040194	280	3.94e-02			6									
hp	Macrocephaly	HP:0000256	278	3.78e-02			6									
hp	Abnormal nipple morphology	HP:0004404	128	3.94e-02												7
hp	Aplasia/Hypoplasia of the nipples	HP:0006709	36	1.34e-03												5
hp	Progressive spasticity	HP:0002191	11	4.47e-03										4		
hp	Abnormality of the chin	HP:0000306	182	3.79e-02												12

Supplemental Figure S5. g:Cocoa Gene Ontology and Human Phenotype Ontology enrichment comparisons for the bottom 500 genes by recombination rate across individual breed-specific maps. Each column represents a gene list for a single breed (i.e., Arabian [Arab], Belgian, Franches-Montagnes [FM], French Trotter [FT], Icelandic, Lusitano, Maremmano, Morgan, Quarter Horse [QH], Standardbred [SB], Thoroughbred [TB], and Welsh Pony [WP]), and each row represents association with a functional term (significant terms only). Cell color depicts the strength of association, with darker colored cells representing stronger associations. Cells framed with black lines refer to the strongest association for the term. Enrichment p-values are corrected for multiple testing using g:Profiler's default g:SCS algorithm. Reported p-values correspond to the best (framed) gene list.