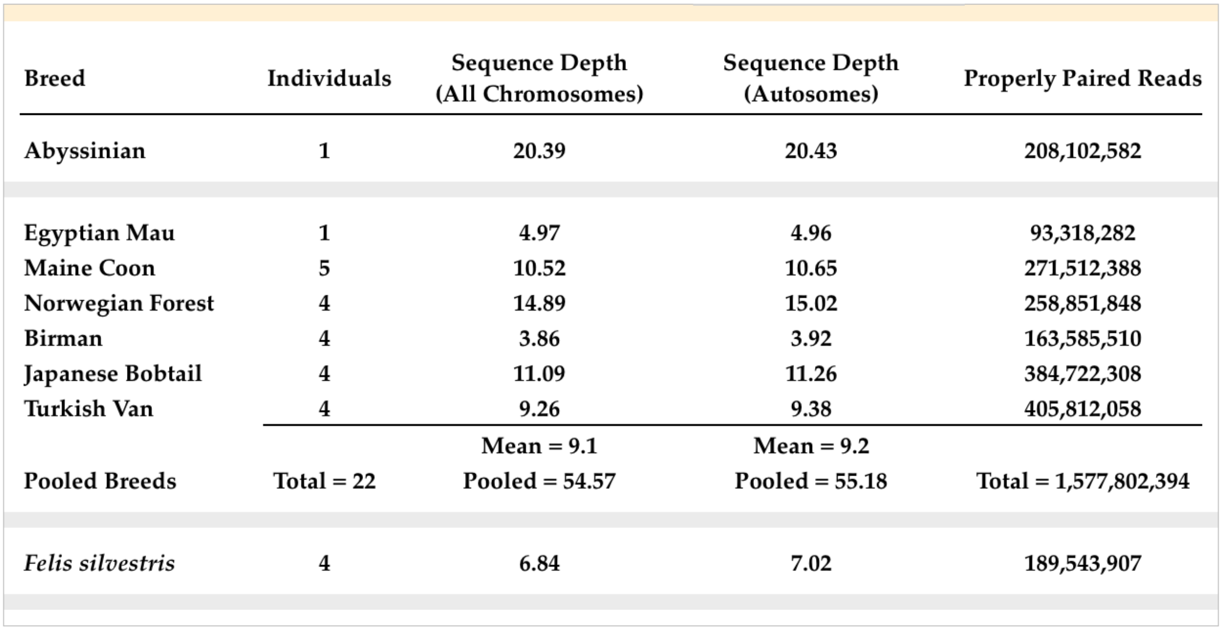
Dataset S2.1. Coverage statistics per pool.



Breed	Individuals	Sequence Depth (All Chromosomes)	Sequence Depth (Autosomes)	Properly Paired Reads
Abyssinian	1	20.39	20.43	208,102,582
Egyptian Mau	1	4.97	4.96	93,318,282
Maine Coon	5	10.52	10.65	271,512,388
Norwegian Forest	4	14.89	15.02	258,851,848
Birman	4	3.86	3.92	163,585,510
Japanese Bobtail	4	11.09	11.26	384,722,308
Turkish Van	4	9.26	9.38	405,812,058
Pooled Breeds	Total = 22	Mean = 9.1 Pooled = 54.57	Mean = 9.2 Pooled = 55.18	Total = 1,577,802,394
Felis silvestris	4	6.84	7.02	189,543,907

Dataset S2.2(a). Genes underlying regions of low H_p in the pooled domestic cat variant dataset following annotation of 100kb windows that fell below four standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With F_{ST} List
A1	8396110	8766675	ENSFCAG00000014322	MTUS2	microtubule associated tumor suppressor candidate 2	
A1	8776308	8797912	ENSFCAG00000014326	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	
A1	40039128	40039239	ENSFCAG00000023540	5S_rRNA	5S ribosomal RNA	
A1	52410273	52410385	ENSFCAG00000028097	5S_rRNA	5S ribosomal RNA	
A1	52479995	52528867	ENSFCAG00000000561	RBM26	RNA binding motif protein 26	
A1	52625952	52688765	ENSFCAG00000025797	NDFIP2	Nedd4 family interacting protein 2	
A1	84103052	84104082	ENSFCAG00000015576			
A1	84167672	84168631	ENSFCAG00000022722			
A1	84208569	84209522	ENSFCAG00000031931			
A1	88361081	88362067	ENSFCAG00000026872	OR2G3	olfactory receptor, family 2, subfamily G, member 3	
A1	88391241	88392229	ENSFCAG00000008196			
A1	88521633	88522592	ENSFCAG00000002236	OR2C3	olfactory receptor, family 2, subfamily C, member 3	
A1	88551982	88552917	ENSFCAG00000024148			
A1	88616973	88617956	ENSFCAG00000021910			
A1	88647235	88648721	ENSFCAG00000008976			
A1	88667669	88668640	ENSFCAG00000010456	OR2B11	olfactory receptor, family 2, subfamily B, member 11	
A1	88708791	88709744	ENSFCAG00000031962			
A1	88723599	88774919	ENSFCAG00000009344	NLRP3	NLR family, pyrin domain containing 3	
A1	89064612	89073091	ENSFCAG00000023784			
A1	89091044	89092033	ENSFCAG00000006397	RNF187	ring finger protein 187	
A1	89124037	89124141	ENSFCAG00000024726	5S_rRNA	5S ribosomal RNA	
A1	89136000	89136365	ENSFCAG00000024427			
A1	89140926	89141306	ENSFCAG00000032040	HIST3H2BB	histone cluster 3, H2bb	
A1	89141619	89142011	ENSFCAG00000024530	HIST3H2A	histone cluster 3, H2a	
A1	89163922	89164322	ENSFCAG00000006396			
A1	89176315	89184314	ENSFCAG00000029709	TRIM17	tripartite motif containing 17	
A1	89187378	89192375	ENSFCAG00000028702	TRIM11	tripartite motif containing 11	
A1	89211477	89214157	ENSFCAG00000025004			
A1	89215471	89216301	ENSFCAG00000023698			
A1	89216810	89218801	ENSFCAG00000022817			
A1	89227536	89243984	ENSFCAG00000030432			
A1	89246495	89247270	ENSFCAG00000025517			
A1	95458053	95465888	ENSFCAG00000031517			
A1	95498785	95504740	ENSFCAG00000030457			
A1	95525507	95744069	ENSFCAG00000025195	COMMD10	COMM domain containing 10	
A1	117462646	117535510	ENSFCAG00000022810	PCDHA1	protocadherin alpha 1	X
A1	117574779	117620293	ENSFCAG00000003685	PCDHAC2	protocadherin alpha subfamily C, 2	
A1	117653631	117656087	ENSFCAG00000003687	PCDHB1	protocadherin beta 1	
A1	117675941	117678295	ENSFCAG00000001367	PCDHB2	protocadherin beta 2	
A1	117694636	117729173	ENSFCAG00000013156	PCDHB4	protocadherin beta 4	X
A1	124586618	124647903	ENSFCAG00000025994	SLC38A9	solute carrier family 38, member 9	
A1	124685687	124778148	ENSFCAG00000012560	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	
A1	124828501	124867387	ENSFCAG00000010857	IL31RA	interleukin 31 receptor A	
A1	124892755	124943980	ENSFCAG00000010859	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	
A1	125019663	125086857	ENSFCAG00000010860	ANKRD55	ankyrin repeat domain 55	
A1	182239426	182624612	ENSFCAG00000008547	EBF1	early B-cell factor 1	
A1	182675442	182769870	ENSFCAG00000012160			
A1	182768748	182791531	ENSFCAG00000026371	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	
A1	182815541	182825071	ENSFCAG00000015571	IL12B	Interleukin-12 subunit beta	
A1	192916759	193132695	ENSFCAG00000014984	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	
A1	193168465	193168577	ENSFCAG00000026163	5S_rRNA	5S ribosomal RNA	X
A1	193262073	193280914	ENSFCAG00000028091	MFAP3	microfibrillar-associated protein 3	X
A1	193286712	193315803	ENSFCAG00000023708	FAM114A2	family with sequence similarity 114, member A2	X
A1	193479446	193624866	ENSFCAG00000005223	GRIA1	glutamate receptor, ionotropic, AMPA 1	X
A1	219080923	219081031	ENSFCAG00000027389	5S_rRNA	5S ribosomal RNA	
A2	110372750	110413021	ENSFCAG00000005018	AHR	aryl hydrocarbon receptor	
A2	110810088	110898682	ENSFCAG00000024117	SNX13	sorting nexin 13	
A3	24313334	24397487	ENSFCAG00000002305	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	
A3	24398183	24399185	ENSFCAG00000022040	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	
A3	24418275	24429758	ENSFCAG00000002304	DYNLRB1	dynein, light chain, roadblock-type 1	
A3	24443756	24584348	ENSFCAG00000008780	ITCH	itchy E3 ubiquitin protein ligase	
A3	24642489	24656544	ENSFCAG00000007301			
A3	24671683	24676154	ENSFCAG00000011037	ASIP	Agouti-signaling protein	
A3	50153794	50156025	ENSFCAG00000030154			
A3	50157809	50158123	ENSFCAG00000027566			
A3	50222873	50229392	ENSFCAG00000022966			
A3	76497901	76527797	ENSFCAG00000003522	CCDC104	coiled-coil domain containing 104	
A3	76529028	76595389	ENSFCAG00000026457	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	
A3	76618801	76664057	ENSFCAG00000013236	PNPT1	polyribonucleotide nucleotidyltransferase 1	
A3	96863689	96865875	ENSFCAG00000024660			

Dataset S2.2(b). Genes underlying regions of low H_p in the pooled domestic cat variant dataset following annotation of 100kb windows that fell below four standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With F_{ST} List
A3	96889747	96889859	ENSFCAG00000028765	5S_rRNA	5S ribosomal RNA	
A3	96900604	96902810	ENSFCAG00000027440			
A3	126610231	126619976	ENSFCAG00000028084			
A3	126698895	126761424	ENSFCAG00000027520	PUM2	pumilio homolog 2 (Drosophila)	
A3	126775239	126796393	ENSFCAG00000005354	SDC1	syndecan 1	
A3	141321118	141464325	ENSFCAG00000013984	MYT1L	myelin transcription factor 1-like	
B1	44313905	44415983	ENSFCAG00000031578			
B1	44440898	44568664	ENSFCAG00000000589			
B1	44593908	44639323	ENSFCAG00000030919			
B1	44605069	44605181	ENSFCAG00000031785	5S_rRNA	5S ribosomal RNA	
B1	44691591	44732046	ENSFCAG00000028945			
B1	44746128	44770572	ENSFCAG00000028120			
B1	44774622	44784782	ENSFCAG00000023569			
B1	44792973	44919764	ENSFCAG00000002595	ADAM9	ADAM metallopeptidase domain 9	
B1	44794749	44795624	ENSFCAG00000002701			
B1	44920372	44925151	ENSFCAG00000002593	TM2D2	TM2 domain containing 2	
B1	44928099	44938386	ENSFCAG00000002591	HTRA4	HtrA serine peptidase 4	
B1	44938751	44984295	ENSFCAG00000030276	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	
B1	45043315	45101607	ENSFCAG00000024992	TACC1	transforming, acidic coiled-coil containing protein 1	
B1	104880577	104998796	ENSFCAG00000010364	PDE5A	cGMP-specific 3',5'-cyclic phosphodiesterase	
B1	105033096	105036707	ENSFCAG00000026257	FABP2	fatty acid binding protein 2, intestinal	
B1	105069890	105121855	ENSFCAG00000014472	USP53	ubiquitin specific peptidase 53	
B1	105153960	105193563	ENSFCAG00000003007	MYOZ2	myozenin 2	
B1	105252135	105424698	ENSFCAG00000028738	SYNPO2	synaptopodin 2	
B1	143593440	143685242	ENSFCAG00000010427	CCDC158	coiled-coil domain containing 158	
B1	172072490	172152353	ENSFCAG00000003209			
B1	172191715	172262048	ENSFCAG00000025531	UBE2K	ubiquitin-conjugating enzyme E2K	
B1	191450950	191588878	ENSFCAG00000029474	LCORL	ligand dependent nuclear receptor corepressor-like	
B1	191619013	191665923	ENSFCAG00000030778	NCAPG	non-SMC condensin I complex, subunit G	
B2	82062518	82106450	ENSFCAG00000030695			
B2	82129137	82129462	ENSFCAG00000022894			
B2	82190939	82198755	ENSFCAG00000029256	SRSF12	serine/arginine-rich splicing factor 12	
B2	82233859	82249448	ENSFCAG00000014224	PM20D2	peptidase M20 domain containing 2	
B2	82263854	82290954	ENSFCAG00000022082	GABRR1	gamma-aminobutyric acid (GABA) A receptor, rho 1	
B3	18642298	18719149	ENSFCAG00000007543	CERS3	ceramide synthase 3	
B3	33511989	33516370	ENSFCAG00000000344	CYP1A2	Cytochrome P450 1A2	X
B3	33532067	33538470	ENSFCAG00000002016	CYP1A1	Cytochrome P450 1A1	X
B3	33564717	33611587	ENSFCAG00000002014	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	X
B3	33611037	33628940	ENSFCAG00000031747	CLK3	CDC-like kinase 3	X
B3	33648267	33702607	ENSFCAG00000002012	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	X
B3	33785369	33799296	ENSFCAG00000027852	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	
B3	33820675	33830309	ENSFCAG00000008142	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	
B3	93427038	93427596	ENSFCAG00000023471			
B3	111258215	111397325	ENSFCAG00000014176	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	
B3	111427724	111428887	ENSFCAG00000025276	WDR89	WD repeat domain 89	
B3	111434101	111434478	ENSFCAG00000029391			
B3	111477502	111477894	ENSFCAG00000013027			
B3	111505184	111540616	ENSFCAG00000031669	SGPP1	sphingosine-1-phosphate phosphatase 1	
B3	114616480	114684401	ENSFCAG00000011076	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	
B3	114689401	114711272	ENSFCAG00000011078	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	
B3	114715814	114732784	ENSFCAG00000031891	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	
B3	114733231	114742902	ENSFCAG00000011080	PLEK2	pleckstrin 2	
B3	114809050	114809553	ENSFCAG00000031183	TMEM229B	transmembrane protein 229B	
B3	114877701	114926189	ENSFCAG00000014084	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	X
B4	39020791	39064360	ENSFCAG00000029824	AKAP3	A kinase (PRKA) anchor protein 3	
B4	39067047	39103662	ENSFCAG00000005951			
B4	39141172	39189805	ENSFCAG00000005953	GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	
B4	39221313	39222899	ENSFCAG00000002340	KCNA6	potassium voltage-gated channel, shaker-related subfamily, member 6	
B4	51667745	51689061	ENSFCAG00000024292	STRAP	serine/threonine kinase receptor associated protein	
B4	51747458	51817466	ENSFCAG00000012551	DERA	deoxyribose-phosphate aldolase (putative)	
B4	83180790	83186313	ENSFCAG00000010156			
B4	83201595	83207215	ENSFCAG00000031316			
B4	83212103	83250831	ENSFCAG00000010157	NCKAP1L	NCK-associated protein 1-like	
B4	83256882	83284307	ENSFCAG00000010158	PDE1B	phosphodiesterase 1B, calmodulin-dependent	
B4	83285929	83289181	ENSFCAG00000010159	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	
B4	85201642	85213246	ENSFCAG00000012017	ANKRD52	ankyrin repeat domain 52	
B4	85212877	85212953	ENSFCAG00000021736			
B4	85219509	85222879	ENSFCAG00000012018	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)	
B4	85223591	85251393	ENSFCAG00000012019	CS	Citrate synthase	
B4	85256805	85258874	ENSFCAG00000012020			
B4	85261031	85272858	ENSFCAG00000012021	PAN2	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	

Dataset S2.2(c). Genes underlying regions of low H_p in the pooled domestic cat variant dataset following annotation of 100kb windows that fell below four standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With F_{ST} List
B4	85277282	85279111	ENSFCAG00000012022	IL23A	interleukin 23, alpha subunit p19	
B4	85281059	85298979	ENSFCAG00000012023	STAT2	signal transducer and activator of transcription 2, 113kDa	
B4	85300402	85302055	ENSFCAG00000028837	APOF	apolipoprotein F	
B4	85313463	85330693	ENSFCAG00000012024	TIMELESS	timeless circadian clock	
B4	85345392	85348942	ENSFCAG00000012025	MIP	major intrinsic protein of lens fiber	
B4	85359827	85362487	ENSFCAG00000023005	SPRYD4	SPRY domain containing 4	
B4	85360205	85376232	ENSFCAG00000012027	GLS2	glutaminase 2 (liver, mitochondrial)	
B4	85400194	85463992	ENSFCAG00000012028	RBMS2	RNA binding motif, single stranded interacting protein 2	
C1	10640571	10657545	ENSFCAG00000011590	FBLIM1	filamin binding LIM protein 1	
C1	10732129	10795582	ENSFCAG00000010165	SPEN	spen homolog, transcriptional regulator (Drosophila)	
C1	10796361	10827960	ENSFCAG00000023421	ZBTB17	zinc finger and BTB domain containing 17	
C1	10837025	10839250	ENSFCAG00000010166	C1orf64	chromosome 1 open reading frame 64	
C1	10848258	10852249	ENSFCAG00000026415	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	
C1	58101938	58102050	ENSFCAG00000031207	5S_rRNA	5S ribosomal RNA	
C1	78698661	78717765	ENSFCAG00000031703	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	
C1	78722799	78738417	ENSFCAG00000026377	GCLM	glutamate-cysteine ligase, modifier subunit	
C1	78772870	78906672	ENSFCAG00000015512	ABCA4	ATP-binding cassette, sub-family A (ABC1), member 4	
C1	84943030	84960266	ENSFCAG00000011031	VCAM1	vascular cell adhesion molecule 1	
C1	85015454	85015558	ENSFCAG00000025299	5S_rRNA	5S ribosomal RNA	
C1	85064668	85071066	ENSFCAG00000023298	EXTL2	exostoses (multiple)-like 2	
C1	85087065	85167096	ENSFCAG00000011033	SLC30A7	solute carrier family 30 (zinc transporter), member 7	
C1	85133519	85134071	ENSFCAG00000028505			
C1	85186588	85225405	ENSFCAG00000022542	DPH5	DPH5 homolog (S. cerevisiae)	
C1	153704054	153753962	ENSFCAG00000004699	GRB14	growth factor receptor-bound protein 14	
C1	154302722	154384425	ENSFCAG00000024761	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	
C1	181824781	181826420	ENSFCAG00000010136			
C1	181987901	182031850	ENSFCAG00000029020	SLC39A10	solute carrier family 39 (zinc transporter), member 10	
C2	77632001	77703504	ENSFCAG00000000693	ATP13A5	ATPase type 13A5	
C2	77706977	77717650	ENSFCAG00000000692			
C2	78412932	78673284	ENSFCAG00000025224	FGF12	fibroblast growth factor 12	
C2	108304270	108463279	ENSFCAG00000012834	PLCH1	phospholipase C, eta 1	
C2	108510488	108510600	ENSFCAG00000031412	5S_rRNA	5S ribosomal RNA	
C2	128014862	128022609	ENSFCAG00000009596	RAB6B	RAB6B, member RAS oncogene family	
C2	128027632	128059443	ENSFCAG00000026858	SRPRB	signal recognition particle receptor, B subunit	
C2	128061749	128090487	ENSFCAG00000009592	TF	transferrin	
C2	128112530	128155615	ENSFCAG00000027859			
C2	128189988	128251128	ENSFCAG00000005146	TOPBP1	topoisomerase (DNA) II binding protein 1	
D1	1607316	1636408	ENSFCAG00000029835	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	
D1	1651507	1992762	ENSFCAG00000028573	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	
D1	30227928	30233580	ENSFCAG00000011024	SPATA19	spermatogenesis associated 19	
D1	30287365	30324514	ENSFCAG00000007138	IGSF9B	immunoglobulin superfamily, member 9B	
D1	53604863	53604975	ENSFCAG00000030335	5S_rRNA	5S ribosomal RNA	
D1	107809557	107915426	ENSFCAG00000008866	UBXN1	UBX domain protein 1 [Source:HGNC Symbol;Acc:18402]	
D1	107850747	107857696	ENSFCAG00000008861	MTA2	metastasis associated 1 family, member 2	
D1	107858491	107867300	ENSFCAG00000008862	EML3	echinoderm microtubule associated protein like 3	
D1	107868913	107870543	ENSFCAG00000008863	ROM1	retinal outer segment membrane protein 1	
D1	107870916	107875681	ENSFCAG00000008864	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	
D1	107876904	107892987	ENSFCAG00000008865	GANAB	glucosidase, alpha; neutral AB	
D1	107889470	107890314	ENSFCAG00000030933			
D1	107893127	107897937	ENSFCAG00000022488	INTS5	integrator complex subunit 5	
D1	107901491	107905417	ENSFCAG00000025454			
D1	107906121	107907032	ENSFCAG00000019062	METTL12	methyltransferase like 12	
D1	107910273	107910654	ENSFCAG00000026508	C11orf83	chromosome 11 open reading frame 83	
D1	107918401	107919123	ENSFCAG00000008867	LRRN4CL	LRRN4 C-terminal like	
D1	107920655	107930057	ENSFCAG00000018428	BSCL2	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	
D1	107931091	107931596	ENSFCAG00000006326			
D1	107937649	107947789	ENSFCAG00000014766			
D1	107948981	107954599	ENSFCAG00000014768	TTC9C	tetratricopeptide repeat domain 9C	
D1	107961224	107964011	ENSFCAG00000027690	ZBTB3	zinc finger and BTB domain containing 3	
D1	107973264	107976548	ENSFCAG00000026072	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	
D1	107984157	107992940	ENSFCAG00000022346	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	
D1	107993688	107994689	ENSFCAG00000014773	TMEM179B	transmembrane protein 179B	
D1	107995077	107996089	ENSFCAG00000025098	TMEM223	transmembrane protein 223	
D1	107996609	108006783	ENSFCAG00000014774	NXF1	nuclear RNA export factor 1	
D1	108008793	108027809	ENSFCAG00000014778	STX5	syntaxin 5	
D1	108029559	108035227	ENSFCAG00000014780	WDR74	WD repeat domain 74	
D1	108066532	108073223	ENSFCAG00000014781	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	
D1	108091101	108092483	ENSFCAG00000000336	CHRM1	cholinergic receptor, muscarinic 1	
D1	111390904	111406979	ENSFCAG00000007404	SYT12	synaptotagmin XII	
D1	111418646	111423350	ENSFCAG00000007405	RHOD	ras homolog family member D	
D1	111493966	111569206	ENSFCAG00000003383	KDM2A	lysine (K)-specific demethylase 2A	

Dataset S2.2(d). Genes underlying regions of low H_p in the pooled domestic cat variant dataset following annotation of 100kb windows that fell below four standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With F_{ST} List
D1	111590001	111597609	ENSFCAG00000003386	ADRBK1	adrenergic, beta, receptor kinase 1	
D1	111598900	111611310	ENSFCAG00000003388	ANKRD13D	ankyrin repeat domain 13 family, member D	
D1	111612360	111620131	ENSFCAG00000003389	SSH3	slingshot homolog 3 (Drosophila)	
D1	111642857	111644862	ENSFCAG00000026317	POLD4	polymerase (DNA-directed), delta 4, accessory subunit	
D2	129076	129188	ENSFCAG00000029175	5S_rRNA	5S ribosomal RNA	
D2	57260928	57261537	ENSFCAG00000031023			
D2	57304321	57346173	ENSFCAG00000014012	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	
D2	57377604	57453891	ENSFCAG00000024547			
D3	16753418	16765475	ENSFCAG00000023496	UNC119B	unc-119 homolog B (C. elegans)	
D3	16767557	16779781	ENSFCAG00000002402	ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	
D3	16818395	16846475	ENSFCAG00000030187	SPPL3	signal peptide peptidase like 3	
D3	27486649	27511914	ENSFCAG00000004294	UFD1L	ubiquitin fusion degradation 1 like (yeast)	
D3	27514585	27517737	ENSFCAG00000025374	C22orf39	chromosome 22 open reading frame 39	
D3	27522219	27526181	ENSFCAG00000002752	MRPL40	mitochondrial ribosomal protein L40	
D3	27545550	27619849	ENSFCAG00000002750	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	
D3	27661078	27763200	ENSFCAG00000002747	CLTCL1	clathrin, heavy chain-like 1	
D3	28412397	28523536	ENSFCAG00000006001	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha	
D3	28460397	28469039	ENSFCAG00000006002	SERPIND1	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	
D3	28532228	28532992	ENSFCAG00000003742			
D3	28549103	28552706	ENSFCAG00000023903	HIC2	hypermethylated in cancer 2	
D3	28587145	28591887	ENSFCAG00000008005			
D3	28601226	28653670	ENSFCAG00000008008	UBE2L3	ubiquitin-conjugating enzyme E2L 3	
D3	28659840	28661374	ENSFCAG00000008011	YDJC	YdjC homolog (bacterial)	
D3	28663783	28666362	ENSFCAG00000027678	CCDC116	coiled-coil domain containing 116	
D3	28672570	28674479	ENSFCAG00000008014	SDF2L1	stromal cell-derived factor 2-like 1	
D3	28677737	28677830	ENSFCAG00000024408			
D3	28678081	28678140	ENSFCAG00000029099			
D3	28680749	28690369	ENSFCAG00000031033			
D3	28692128	28720327	ENSFCAG00000002622	PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	
D3	28724636	28743087	ENSFCAG00000028941	YPEL1	yippee-like 1 (Drosophila)	
D3	28767507	28877605	ENSFCAG00000023435	MAPK1	mitogen-activated protein kinase 1	
D3	28905826	28929444	ENSFCAG00000002630	PPM1F	protein phosphatase, Mg2+/Mn2+ dependent, 1F	
D3	28941162	28961110	ENSFCAG00000002631	TOP3B	topoisomerase (DNA) III beta	
D3	29050629	29085036	ENSFCAG00000011848			
D3	29119195	29120502	ENSFCAG00000004058	VPREB3	pre-B lymphocyte 3	
D3	29124112	29125589	ENSFCAG00000004065	C22orf15	chromosome 22 open reading frame 15	
D3	29126680	29128333	ENSFCAG00000004059	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10	
D3	29130819	29140423	ENSFCAG00000015309	MMP11	matrix metallopeptidase 11 (stromelysin 3)	
D3	29141586	29176322	ENSFCAG00000004068	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	
D3	29178943	29181128	ENSFCAG00000004069	DERL3	derlin 3	
D3	29194518	29214625	ENSFCAG00000004070			
D3	29230481	29231130	ENSFCAG00000004071	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	
D3	32440361	32440473	ENSFCAG00000028017	5S_rRNA	5S ribosomal RNA	
D3	73217674	73955407	ENSFCAG00000012953	DCC	deleted in colorectal carcinoma	X
E1	29838089	29850820	ENSFCAG00000018819	PRR11	proline rich 11	
E1	29867217	29867300	ENSFCAG00000022665			
E1	29878598	29878667	ENSFCAG00000023049			
E1	29884263	29908906	ENSFCAG00000022802			
E1	29914732	30045189	ENSFCAG00000013333	TRIM37	tripartite motif containing 37	
E2	45291420	45336043	ENSFCAG00000003492	CTCF	CCCTC-binding factor (zinc finger protein)	
E2	45340148	45352135	ENSFCAG00000009279	RLTPR	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	
E2	45344436	45344645	ENSFCAG00000023723			
E2	45352266	45355166	ENSFCAG00000009280	ACD	adrenocortical dysplasia homolog (mouse)	
E2	45355872	45357527	ENSFCAG00000009281	PARD6A	par-6 partitioning defective 6 homolog alpha (C. elegans)	
E2	45358052	45361200	ENSFCAG00000009282	ENKD1	enkurin domain containing 1	
E2	45361603	45363331	ENSFCAG00000026033	C16orf86	chromosome 16 open reading frame 86	
E2	45369230	45375475	ENSFCAG00000003493	GFOD2	glucose-fructose oxidoreductase domain containing 2	
E2	45408032	45469729	ENSFCAG00000003494	RANBP10	ran-binding protein 10	
E2	45440127	45440219	ENSFCAG00000029801			
E2	45468767	45482371	ENSFCAG00000012848	TSNAXIP1	translin-associated factor X interacting protein 1	
E2	45482659	45488605	ENSFCAG00000012849	CENPT	centromere protein T	
E2	45492005	45492928	ENSFCAG00000012850	THAP11	THAP domain containing 11	
F2	78455289	78455684	ENSFCAG00000023697			
F2	78470381	78470478	ENSFCAG00000031046			

Dataset S2.3(a). Genes underlying regions of high F_{ST} in the pooled domestic cat variant dataset relative to the pooled wildcat variant dataset

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With Low Domestic H_p
A1	11398212	11455078	ENSFCAG00000025587	BRCA2	breast cancer type 2 susceptibility protein homolog	
A1	11458331	11465570	ENSFCAG00000024257	N4BP2L1	NEDD4 binding protein 2-like 1	
A1	11495916	11500421	ENSFCAG00000022569	N4BP2L2	NEDD4 binding protein 2-like 2	
A1	11500635	11566192	ENSFCAG00000027199			
A1	117311206	117312333	ENSFCAG00000001278	CD14	CD14 molecule	
A1	117316550	117322265	ENSFCAG00000001280	TMCO6	transmembrane and coiled-coil domains 6	
A1	117322928	117325000	ENSFCAG00000001282	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	
A1	117325316	117335480	ENSFCAG00000001279	IK	IK cytokine, down-regulator of HLA II	
A1	117339751	117346166	ENSFCAG00000031277	WDR55	WD repeat domain 55	
A1	117344253	117346522	ENSFCAG00000001285	DND1	dead end homolog 1 (zebrafish)	
A1	117347249	117360519	ENSFCAG00000001286	HARS	histidyl-tRNA synthetase	
A1	117360312	117367965	ENSFCAG00000001288	HARS2	histidyl-tRNA synthetase 2, mitochondrial	
A1	117368560	117373405	ENSFCAG00000001289	ZMAT2	zinc finger, matrin-type 2	
A1	117462646	117535510	ENSFCAG00000022810	PCDHA1	protocadherin alpha 1	X
A1	117694636	117729173	ENSFCAG00000013156	PCDHB4	protocadherin beta 4	X
A1	117745827	117769414	ENSFCAG00000003467	PCDHB14	protocadherin beta 14	
A1	117799797	117801198	ENSFCAG00000029398	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2	
A1	117809591	117810640	ENSFCAG00000025624	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	
A1	117822381	117986226	ENSFCAG00000027095	PCDHGC4	protocadherin gamma subfamily C, 4	
A1	193168465	193168577	ENSFCAG00000026163	5S_rRNA	5S ribosomal RNA	X
A1	193262073	193280914	ENSFCAG00000028091	MFAP3	microfibrillar-associated protein 3	X
A1	193286712	193315803	ENSFCAG00000023708	FAM114A2	family with sequence similarity 114, member A2	X
A1	193353906	193354042	ENSFCAG00000030338			
A1	193479446	193624866	ENSFCAG00000005223	GRIA1	glutamate receptor, ionotropic, AMPA 1	X
A2	18272574	18306642	ENSFCAG00000031387	BSN	bassoon presynaptic cytomatrix protein	
A2	18315503	18324298	ENSFCAG00000028315	APEH	N-acylaminoacyl-peptide hydrolase	
A2	18324835	18329543	ENSFCAG00000025772	MST1	macrophage stimulating 1 (hepatocyte growth factor-like)	
A2	18331960	18361039	ENSFCAG00000022451	RNF123	ring finger protein 123	
A2	18358000	18359547	ENSFCAG00000010675	AMIGO3	adhesion molecule with Ig-like domain 3	
A2	18361478	18363484	ENSFCAG00000010676	GMPPB	GDP-mannose pyrophosphorylase B	
A2	18367013	18386714	ENSFCAG00000010677	IP6K1	inositol hexakisphosphate kinase 1	
A2	18422363	18430166	ENSFCAG00000029853	CDHR4	cadherin-related family member 4	
A2	18433891	18435481	ENSFCAG00000010679	FAM212A	family with sequence similarity 212, member A	
A2	18435671	18444581	ENSFCAG00000010680	UBA7	ubiquitin-like modifier activating enzyme 7	
A2	18450943	18472637	ENSFCAG00000010682	TRAIP	TRAF interacting protein	
A2	18475364	18478459	ENSFCAG00000010683	CAMKV	CaM kinase-like vesicle-associated	
A2	18489446	18493192	ENSFCAG00000024955			
A2	20299485	20562418	ENSFCAG00000015704	POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	
A2	20524053	20596054	ENSFCAG00000015710	DNAH1	dynein, axonemal, heavy chain 1	
A2	20596545	20605161	ENSFCAG00000015711	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	
A2	20605964	20617985	ENSFCAG00000015712	PHF7	PHD finger protein 7	
A2	20628755	20638133	ENSFCAG00000015713	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	
A2	20643522	20646338	ENSFCAG00000015714	TNNC1	troponin C type 1 (slow)	
A2	20648138	20682140	ENSFCAG00000015715	NISCH	nischarin	
A2	20684301	20710994	ENSFCAG00000015716	STAB1	stabilin 1	
A2	56358682	56359374	ENSFCAG00000001739	DNAJB8	DnaJ (Hsp40) homolog, subfamily B, member 8	
A2	56408518	56572045	ENSFCAG00000006153	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	
B1	104314018	104319723	ENSFCAG00000023700			
B3	562402	612682	ENSFCAG00000010511	TBC1D2B	TBC1 domain family, member 2B	
B3	614460	645400	ENSFCAG00000019139	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7	
B3	692868	709793	ENSFCAG00000012197			
B3	724131	733861	ENSFCAG00000012198	CTSH	cathepsin H	
B3	752155	849199	ENSFCAG00000012199	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	
B3	23976933	24067525	ENSFCAG00000027111	UBE3A	ubiquitin protein ligase E3A	
B3	26496373	26600819	ENSFCAG00000023805	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3	

Dataset S2.3(b). Genes underlying regions of high F_{ST} in the pooled domestic cat variant dataset relative to the pooled wildcat variant dataset

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With Low Domestic H_p
B3	31880462	31899698	ENSFCAG00000022033	RCN2	reticulocalbin 2, EF-hand calcium binding domain	
B3	31953456	31981469	ENSFCAG00000010953	PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	
B3	31986675	32018232	ENSFCAG00000025746	TSPAN3	tetraspanin 3	
B3	32061239	32135509	ENSFCAG00000026195			
B3	32120379	32121889	ENSFCAG00000031049			
B3	32401108	32428309	ENSFCAG00000022539	HMG20A	high mobility group 20A	
B3	32540693	32558379	ENSFCAG00000013212	LINGO1	leucine rich repeat and Ig domain containing 1	
B3	33511989	33516370	ENSFCAG00000000344	CYP1A2	Cytochrome P450 1A2	X
B3	33532067	33538470	ENSFCAG00000002016	CYP1A1	Cytochrome P450 1A1	X
B3	33564717	33611587	ENSFCAG00000002014	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	X
B3	33611037	33628940	ENSFCAG00000031747	CLK3	CDC-like kinase 3	X
B3	33648267	33702607	ENSFCAG00000002012	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	X
B3	113916112	114542162	ENSFCAG00000013487	GPHN	gephyrin	
B3	114877701	114926189	ENSFCAG00000014084	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	X
B3	114924265	114931845	ENSFCAG00000014087	PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	
B3	114944868	114977046	ENSFCAG00000014088	ARG2	arginase, type II	
B3	114976632	115008847	ENSFCAG00000014090			
B3	114997195	114997263	ENSFCAG00000021393			
B3	115012454	115028806	ENSFCAG00000014091	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	
B3	115040768	115049236	ENSFCAG00000014092	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	
B3	115064179	115135168	ENSFCAG00000007653	ZFYVE26	zinc finger, FYVE domain containing 26	
B3	115157242	115190375	ENSFCAG00000007657	RAD51B	RAD51 homolog B (S. cerevisiae)	
B3	126320314	126713029	ENSFCAG00000007824	CEP128	centrosomal protein 128kDa	
B3	126725185	126884461	ENSFCAG00000011083	TSHR	thyrotropin receptor precursor	
B4	143787880	143800787	ENSFCAG00000011914	PLXNB2	plexin B2	
B4	143815714	143824099	ENSFCAG00000011915	DENND6B	DENN/MADD domain containing 6B	
B4	143870997	143920737	ENSFCAG00000004431	PPP6R2	protein phosphatase 6, regulatory subunit 2	
B4	143923211	143944516	ENSFCAG00000004434	SBF1	SET binding factor 1	
B4	143955788	143956879	ENSFCAG00000022957	ADM2	adrenomedullin 2	
B4	143960792	143962760	ENSFCAG00000013030	MIOX	myo-inositol oxygenase	
B4	143974923	143979512	ENSFCAG00000013032	LMF2	lipase maturation factor 2	
B4	143979545	143979666	ENSFCAG00000028233			
B4	143979850	143995006	ENSFCAG00000013034	NCAPH2	non-SMC condensin II complex, subunit H2	
B4	143992569	143993369	ENSFCAG00000013035	SCO2	SCO2 cytochrome c oxidase assembly protein	
B4	143998592	144000511	ENSFCAG00000021933	ODF3B	outer dense fiber of sperm tails 3B	
C1	81116342	81201784	ENSFCAG00000027655	PTBP2	polypyrimidine tract binding protein 2	
C1	87218356	87218468	ENSFCAG00000028148	5S_rRNA	5S ribosomal RNA	
C1	87333358	87358352	ENSFCAG00000024312	RNPC3	RNA-binding region (RNP1, RRM) containing 3	
C1	102252296	102252706	ENSFCAG00000029741	HIST2H3D	histone cluster 2, H3d	
C1	102253768	102254160	ENSFCAG00000026932			
C1	102254475	102254892	ENSFCAG00000027797			
C1	102288465	102288845	ENSFCAG00000023970	HIST2H2BE	histone cluster 2, H2be	
C1	102289173	102289562	ENSFCAG00000024806	HIST2H2AC	histone cluster 2, H2ac	
C1	102289719	102290111	ENSFCAG00000028667	HIST2H2AB	histone cluster 2, H2ab	
C1	102300828	102301241	ENSFCAG00000010103	BOLA1	bolA homolog 1 (E. coli)	
C1	102306044	102313944	ENSFCAG00000010104	SV2A	synaptic vesicle glycoprotein 2A	
C1	102328326	102332748	ENSFCAG00000010106	SF3B4	splicing factor 3b, subunit 4, 49kDa	
C1	102334404	102341438	ENSFCAG00000010108	MTMR11	myotubularin related protein 11	
C1	102347722	102369563	ENSFCAG00000010110	OTUD7B	OTU domain containing 7B	
C1	103510046	103513819	ENSFCAG00000005568	RFX5	regulatory factor X, 5 (influences HLA class II expression)	
C1	103523531	103532221	ENSFCAG00000001859	SELENBP1	selenium binding protein 1	
C1	103572933	103576251	ENSFCAG00000001861	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	
C1	103579750	103629870	ENSFCAG00000001864	POGZ	pogo transposable element with ZNF domain	
C1	103669485	103693186	ENSFCAG00000004072	CGN	cingulin	
C1	103694358	103735432	ENSFCAG00000004073	TUFT1	tuftelin 1	
C1	104304676	104409375	ENSFCAG00000022223	FLG2	filaggrin family member 2	

Dataset S2.3(c). Genes underlying regions of high F_{ST} in the pooled domestic cat variant dataset relative to the pooled wildcat variant dataset

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With Low Domestic H_p
C1	104308093	104310222	ENSFCAG00000025915	HRNR	hornerin	
C1	104341706	104342582	ENSFCAG00000028908	FLG	filaggrin	
C1	104478129	104480640	ENSFCAG00000030196	CRNN	cornulin	
C1	142020467	142037136	ENSFCAG00000027956	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	
C1	142068033	142135438	ENSFCAG00000029742	RIF1	RAP1 interacting factor homolog (yeast)	
C1	142149853	142362875	ENSFCAG00000006778	NEB	nebulin	
D1	87552960	87615211	ENSFCAG00000015003	DCDC1	doublecortin domain containing 1	
D3	73217674	73955407	ENSFCAG00000012953	DCC	deleted in colorectal carcinoma	X
E1	2012450	2018802	ENSFCAG00000001360	ASGR1	asialoglycoprotein receptor 1	
E1	2062948	2084818	ENSFCAG00000002824	DLG4	discs, large homolog 4 (Drosophila)	
E1	2071965	2654649	ENSFCAG00000009629	CHD3	chromodomain helicase DNA binding protein 3	
E1	2085784	2091265	ENSFCAG00000002826	ACADVL	acyl-CoA dehydrogenase, very long chain	
E1	2089360	2089473	ENSFCAG00000020094			
E1	2092041	2099011	ENSFCAG00000024333	DVL2	dishevelled, dsh homolog 2 (Drosophila)	
E1	2099343	2103630	ENSFCAG00000025727	PHF23	PHD finger protein 23	
E1	2105175	2106741	ENSFCAG00000030191	GABARAP	GABA(A) receptor-associated protein	
E1	2108629	2114091	ENSFCAG00000018399	CTDNEP1	CTD nuclear envelope phosphatase 1	
E1	2115255	2120631	ENSFCAG00000002827	ELP5	elongator acetyltransferase complex subunit 5	
E1	2121374	2122689	ENSFCAG00000031173			
E1	2133863	2138934	ENSFCAG00000003061	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	
E1	2140924	2144812	ENSFCAG00000018097	YBX2	Y box binding protein 2	
E1	2160740	2165161	ENSFCAG00000010886			
E1	2166294	2168525	ENSFCAG00000030260			
E1	2169030	2180923	ENSFCAG00000010887			
E1	2182103	2185125	ENSFCAG00000030827			
E1	2186123	2197946	ENSFCAG00000010890	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	
E1	2202287	2203655	ENSFCAG00000010892	TMEM95	transmembrane protein 95	
E1	2213358	2218182	ENSFCAG00000010893	TNK1	tyrosine kinase, non-receptor, 1	
E1	2219417	2222502	ENSFCAG00000010894	PLSCR3	phospholipid scramblase 3	
E1	2239238	2240164	ENSFCAG00000029899			
E1	2245191	2253571	ENSFCAG00000031923	NLGN2	neuroligin 2	
E3	19523974	19531163	ENSFCAG00000006398	TRIM72	tripartite motif containing 72	
E3	19542074	19543165	ENSFCAG00000002608	PYCARD	PYD and CARD domain containing	
E3	19551867	19563123	ENSFCAG00000027928	FUS	fused in sarcoma	
E3	19590723	19599388	ENSFCAG00000002607	PRSS36	protease, serine, 36	
E3	19602108	19605310	ENSFCAG00000002606	PRSS8	protease, serine, 8	
E3	19606046	19617514	ENSFCAG00000002605	KAT8	K(lysine) acetyltransferase 8	
E3	19619822	19623515	ENSFCAG00000002604	BCKDK	branched chain ketoacid dehydrogenase kinase	
E3	19631084	19634172	ENSFCAG00000029684			
E3	19635291	19640292	ENSFCAG00000002602	PRSS53	protease, serine, 53	
E3	19638036	19647917	ENSFCAG00000021918	ZNF646	zinc finger protein 646	
E3	19656066	19658480	ENSFCAG00000008954	ZNF668	zinc finger protein 668	
E3	19670742	19679273	ENSFCAG00000030459	STX4	syntaxin 4	
E3	19700268	19707021	ENSFCAG00000002598	STX1B	syntaxin 1B	
E3	19710473	19714090	ENSFCAG00000002594	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	
E3	19715271	19736956	ENSFCAG00000002588	SETD1A	SET domain containing 1A	
E3	19740874	19745210	ENSFCAG00000023192	ORAI3	ORAI calcium release-activated calcium modulator 3	
E3	19747142	19766168	ENSFCAG00000002585	FBXL19	F-box and leucine-rich repeat protein 19	

Dataset S2.4. Summary of genes underlying regions of elevated F_{ST} and low H_p in the pooled domestic cats.

Genes Underlying Putative Regions of Selection in the Domestic Cat

Region	Chr:Pos	Gene ID	Gene Name	Description	Domestic Z(H_p)	Z(F_{ST})	Wildcat Z(H_p)
1	A1:117462646-117535510	ENSFCAG00000022810	**PCDHA1**	**protocadherin alpha 1**	**-4.6 to -4.2**	**4.0 to 4.5**	**-2.6 to -1.5**
	A1:117694636-117729173	ENSFCAG00000013156	**PCDHB4**	**protocadherin beta 4**			
2	A1:193168465-193168577	ENSFCAG00000026163		5S ribosomal RNA	**-4.4 to -4.1**	**4.5 to 5.2**	**0 to 0.6**
	A1:193262073-193280914	ENSFCAG00000028091	**MFAP3**	**microfibrillar-associated protein 3**			
	A1:193286712-193315803	ENSFCAG00000023708	**FAM114A2**	**family with sequence similarity 114, member A2**			
	A1:193479446-193624866	ENSFCAG00000005223	**GRIA1**	**glutamate receptor, ionotropic, AMPA 1**			
3	B3: 33511989-33516370	ENSFCAG00000000344	**CYP1A2**	**cytochrome P450 1A2**	**-8.9 to -5.6**	**4.7 to 5.2**	**0.7 to 0.8**
	B3:33532067-33538470	ENSFCAG00000002016	**CYP1A1**	**cytochrome P450 1A1**			
	B3:33564717-33611587	ENSFCAG00000002014	**EDC3**	**enhancer of mRNA decapping 3 homolog**			
	B3:33611037-33628940	ENSFCAG00000031747	**CLK3**	**CDC-like kinase 3**			
	B3:33648267-33702607	ENSFCAG00000002012	**ARID3B**	**AT rich interactive domain 3B (BRIGHT-like)**			
4	B3: 114877701-114926189	ENSFCAG00000014084	**PLEKHH1**	**pleckstrin homology domain containing, family H (with MyTH4 domain) member 1**	**-4.6**	**4.1**	**0.3**
5	D3: 73217674-73955407	ENSFCAG00000012953	**DCC**	**deleted in colorectal carcinoma**	**-4.3**	**4.2**	**-0.8**

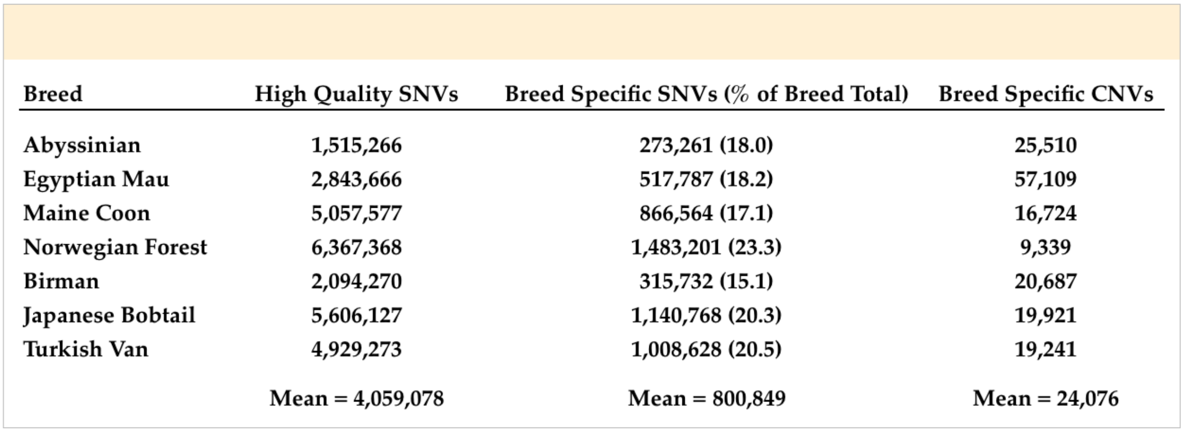
Dataset S2.5. Pathway enrichment results using all genes underlying regions of elevated F_{ST} in the pooled domestic cats relative to the pooled wildcats

KEGG Pathway	Pathway ID	C	O	E	R	rawP	adjP	Genes
Retinol metabolism	830	64	4	0.20	20.12	4.90E-05	0.0009	**RDH12, CYP1A1, CYP1A2, RDH11**
Systemic lupus erythematosus	5322	136	4	0.42	9.47	0.0009	0.0081	**HIST2H3D, HIST2H2BE, HIST2H2AC, HIST2H2AB**
Metabolic pathways	1100	1130	10	3.51	2.85	0.0029	0.0153	**ARG2, CYP1A1, NDUFA2, CYP1A2, PIGH, GMPPB, RDH12, ACADVL, HSD3B7, RDH11**
Homologous recombination	3440	28	2	0.09	22.99	0.0034	0.0153	**BRCA2, RAD51B**
Tryptophan metabolism	380	42	2	0.13	15.33	0.0076	0.0198	**CYP1A1, CYP1A2**
SNARE interactions in vesicular transport	4130	36	2	0.11	17.88	0.0056	0.0198	**STX4, STX1B**
Axon guidance	4360	129	3	0.40	7.48	0.0077	0.0198	**SEMA3G, DCC, PLXNB2**
NOD-like receptor signaling pathway	4621	58	2	0.18	11.10	0.0141	0.0317	**PSTPIP1, PYCARD**
Aminoacyl-tRNA biosynthesis	970	63	2	0.20	10.22	0.0165	0.0330	**HARS2, HARS**
Metabolism of xenobiotics by cytochrome P450	980	71	2	0.22	9.07	0.0207	0.0339	**CYP1A1, CYP1A2**
Huntington's disease	5016	183	3	0.57	5.28	0.0196	0.0339	**DLG4, NDUFA2, DNAH1**
Wikipathway								
AhR pathway	WP2100	39	3	0.12	24.76	0.0002	0.0034	**CYP1A1, FLG, CYP1A2**
Tryptophan metabolism	WP465	69	3	0.21	13.99	0.0013	0.0055	**CYP1A1, UBE3A, CYP1A2**
Fatty Acid Omega Oxidation	WP206	15	2	0.05	42.91	0.0010	0.0055	**CYP1A1, CYP1A2**
mRNA processing	WP411	132	4	0.41	9.75	0.0008	0.0055	**FUS, SF3B4, PTBP2, CLK3**
Striated Muscle Contraction	WP383	38	2	0.12	16.94	0.0063	0.016	**TNNC1, NEB**
Tamoxifen metabolism	WP691	38	2	0.12	16.94	0.0063	0.016	**CYP1A1, CYP1A2**
NOD pathway	WP1433	39	2	0.12	16.50	0.0066	0.016	**PYCARD, ACAP1**
Estrogen metabolism	WP697	44	2	0.14	14.63	0.0083	0.0176	**CYP1A1, CYP1A2**
Selenium Metabolism and Selenoproteins	WP28	49	2	0.15	13.14	0.0102	0.0193	**SELENBP1, EEFSEC**
cytochrome P450	WP43	65	2	0.20	9.90	0.0175	0.027	**CYP1A1, CYP1A2**
Proteasome Degradation	WP183	65	2	0.20	9.90	0.0175	0.027	**PSMB4, UBA7**
Integrated Pancreatic Cancer Pathway	WP2256	181	3	0.56	5.33	0.0191	0.0271	**BRCA2, DCC, MST1**

USER DATA & PARAMETERS - N= 137 genes submitted, Genes mapped to unique Entrez Gene IDs: 134, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2, Enrichment Analyses: KEGG and Wikipathways

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).

Dataset S2.6. Variant calls per individual breed pools



Breed	High Quality SNVs	Breed Specific SNVs (% of Breed Total)	Breed Specific CNVs
Abyssinian	1,515,266	273,261 (18.0)	25,510
Egyptian Mau	2,843,666	517,787 (18.2)	57,109
Maine Coon	5,057,577	866,564 (17.1)	16,724
Norwegian Forest	6,367,368	1,483,201 (23.3)	9,339
Birman	2,094,270	315,732 (15.1)	20,687
Japanese Bobtail	5,606,127	1,140,768 (20.3)	19,921
Turkish Van	4,929,273	1,008,628 (20.5)	19,241
	Mean = 4,059,078	Mean = 800,849	Mean = 24,076

Dataset S2.7. SNPs analyses of *KIT* in the domestic cat

			Exon(E) or intron(I) nucleotide site																					
ID	**Breed**[1]	**Type**[2]	10	281	396	522	531	-67	1035	1036	-5	1473	1479	-18	1617	+34	2054	2325	-30	-3	+37	2805	2856	2862
			E1	E2	E3	E3	E3	I3	E6	E6	I8	E9	E9	I9	E10	I10	E14	E16	I17	I17	I18	E20	E21	E21
	Wild-type sequence		**G**	**A**	**G**	**T**	**C**	**A**	**G**	**C**	**T**	**G**	**G**	**G**	**T**	**G**	**G**	**C**	**T**	**C**	**T**	**T**	**A**	**C**
4910	PE	Black	G	M	G	Y	C	A	G	C	T	G	G	R	C	G	G	Y	T	C	W	T	R	C
4406	RB	Orange	G	M	R	C	Y	M	G	C	Y	G	G	G	W	R	G	Y	Y	Y	A	Y	G	C
9299	RG	Seal pt	G	A	G	K	C	M	S	M	T	G	G	G	C	R	G	C	Y	Y	A	T	R	Y
5337	PE	White	R	A	R	Y	Y	M	G	C	Y	G	G	G	Y	R	G	C	Y	Y	W	T	A	C
10630	AC	Bicolor	G	M	G	Y	C	A	G	C	T	G	G	R	C	G	G	Y	T	C	W	T	R	C
H1001[3]	RB	Bicolor	G	A	R	Y	Y	A	G	C	T	G	G	G	Y	G	G	C	T	C	T	T	R	Y
5779	RG	Bicolor	G	A	G	T	C	A	G	C	T	G	G	G	C	G	G	C	T	C	W	T	A	C
11555	RG	Bicolor	G	A	G	T	C	A	G	C	T	G	G	R	C	G	R	C	T	C	W	T	A	C
11556	RG	Bicolor	G	A	G	T	C	A	G	C	T	G	G	R	C	G	G	C	T	C	W	T	A	C
10660	BI	Gloves	G	C	G	C	C	A	C	A	T	G	G	A	T	G	G	C	T	C	A	T	R	T
11558	RG	Mitted	G	A	R	K	Y	A	G	C	Y	G	G	G	Y	G	R	C	T	C	T	T	R	C
H1174[3]	RB	Van	G	A	G	T	C	A	G	C	T	G	G	G	C	G	G	C	T	C	T	T	A	C
8592	RB	Van	G	M	G	Y	C	M	S	M	Y	G	G	G	Y	G	G	C	Y	Y	W	T	R	Y
11608	TV	Van	G	A	G	T	C	A	G	C	T	G	G	G	C	G	G	C	T	C	T	T	A	C
11618	TV	Van	G	A	R	Y	C	M	G	C	T	R	R	G	W	G	G	C	Y	Y	W	T	R	C
NM_001009 837.3	/	/	G	A	A	C	T	/	G	C	/	G	G	/	T	/	G	C	/	/	/	T	G	C
ENSFCAT0 0000003113	AB	Cinnamon	/	A	G	T	C	A	G	C	T	G	G	G	T	G	G	C	T	C	T	T	A	C
Amino Acid change			**A4T**	**N94T**					**E345D**	**H346N**		**A491T**					**R685K**							

[1] Breed designations: RB = random bred, PE = Persian, RG = Ragdoll, AC = American Curl, BI = Birman, TV = Turkish Van, AB = Abyssinian. [2] Type indicates coloration of the cat, including the white spotting patterns. Some colors have epistasis, for example, dominant white. A cat may be a seal point (pt) or a bicolor, but dominant white will override these colors as melanocytes are absent, preventing the expression of the melanin. Alleles for bicolor and van may be different between breeds and may be additive. Birmans all have “gloves’ and are pointed according to breed standards. Mitted Ragdolls may or may not be pointed.

[3] Cats from the WALTHAM pedigree used for the linkage analysis of the *Spotting* locus.

Dataset S2.8. Frequency of the glove haplotype in cat breed

Observed Genotypes/Phenotypes														
Breed	No.	Gloves/mitted			Solid			Ambiguous			Unknown			Frequency c. 1035_1036delinsCA haplotype
		GG	GN	NN	GG	GN	NN	GG	GN	NN	GG	GN	NN	
Birman	182	177	3	2	0	0	0	0	0	0	0	0	0	0.98
Birman outcrosses	5	0	0	0	0	5	0	0	0	0	0	0	0	0.50
Ragdoll	171	1	7	19	0	11	30	0	7	55	0	15	26	0.12
Random Bred	315	0	0	3	2	15	48	2	10	56	4	22	153	0.10
American Shorthair	11	0	0	0	0	0	5	0	0	1	0	0	5	0.00
American Wirehair	3	0	0	0	0	0	0	0	0	1	0	0	2	0.00
Egyptian Mau	6	0	0	0	0	1	5	0	0	0	0	0	0	0.08
Exotic	10	0	0	0	0	0	0	0	0	0	0	1	9	0.05
Japanese Bobtail	12	0	0	0	0	0	4	0	0	7	0	0	1	0.00
Korat	11	0	0	0	0	0	11	0	0	0	0	0	0	0.00
Maine Coon	10	0	0	0	0	2	1	0	0	1	0	0	6	0.10
Manx	13	0	0	0	0	1	1	0	4	7	0	0	0	0.19
Norwegian Forest Cat	11	0	0	0	0	0	3	0	0	3	0	0	5	0.00
Persian	8	0	0	0	0	0	5	0	0	1	0	0	2	0.00
Russian Blue	11	0	0	0	0	0	11	0	0	0	0	0	0	0.00
Seychellois	2	0	2	0	0	0	0	0	0	0	0	0	0	0.50
Siamese	52	0	0	0	0	3	49	0	0	0	0	0	0	0.03
Siberian	20	0	0	0	1	3	2	1	0	12	0	0	1	0.17
Singapura	8	0	0	0	0	0	8	0	0	0	0	0	0	0.00
Snowshoe	2	0	0	2	0	0	0	0	0	0	0	0	0	0.00
Sphynx	14	0	0	0	0	0	0	1	0	2	3	6	2	0.50
Turkish Angora	14	0	0	0	0	0	0	0	0	12	0	0	2	0.00
Turkish Van	20	0	0	0	0	0	1	0	1	17	0	0	1	0.02
TOTAL	911	178	12	26	3	41	183	4	22	176	7	44	215	/

G (gloves) implies the c.1035_1036delinsCA haplotype, the gloves haplotype. N implies the wildtype allele. 1. Gloves/mitted are cats with white feet. 2. Solid implies a cat with no white spotting pattern. 3. Ambiguous implies a cat with a white spotting pattern that is epistatic and may mask the glove pattern, such as bicolor or dominant white. 4. Cats with no phenotypic description available are listed as unknown. 5.Two random bred cats were included from the WALTHAM pedigree.

Dataset S2.9. Primer sequences and PCR condition for the analysis of feline KIT

			Genomic Primers		
Exon	Exon Size (bp)	Product Size (bp)	Forward Primer 5’-3’	Reverse Primer 5’-3’	Tm/$[Mg^{2+}]$ μM
1	154	173	TCTGGGGGCTCGGCTTTGC	GTCCGCGGCGCTCTCCCAC	60/1.75
2	270	366	ATGCTTTATTTCGCCAAGGA	TCCAAAGCATAGCATGAAAGAA	58/2.25
3	282	395	GCAAAGAGAAACGTCGGAGT	CCCAGAAGAACGCGAGAA	58/1.75
4	140	237	AGGCCACCGAATAAGTTGTG	CGGGCTGTTTTCCTTGATCCA	58/2.25
5	169	361	GACAGACTTGTCATGATGCTTTATT	CATTTATAGAGATACGCTTG	58/2.25
6	190	248	TTCATTAACATCTTCCCTATGATGAA	AGGCCCTGGTAAGCCAAG	60/2.00
7	116	245	CAGGCCCTTCACAAGTGATT	CCAACACGAGCCACAACTTA	58/2.25
8	115	212	GGTGAGGTTTTCCAGCAGTC	GTCCTTCCCTTACGCATGTC	58/2.25
9	194	295	CTTTCTGGAGTAAATCGGGTTG	TGACTGATATGGCAGGCAGA	60/1.75
10-11	107-127	394	CTGCCAATAGATTGTGATTCC	AAAGCCCCGGCTTCATAC	58/2.25
12-13	105-111	380	ACACCACCACGTGCTCTCT	TTTGAAAGATAATAAAAGGTAATTTGG	58/2.25
14	151	496	TTGCCAGCAGTGTCAATAGG	TTCTGATTTTGTGCCTCGAA	58/1.75
15	92	259	CTCCCCTTTTTCCCATTTTG	GCACTGTTATTGGGGGCTAC	58/2.25
16	128	245	CCTTGCTTTGAGGTTTAATTGCT	CTCCAAAGTGGGGCTTGG	58/1.75
17	123	263	CGAAACACACATCATTCAGAG	GGGTACTTACGTTTCCTTTG	60/1.75
18-19	112-100	456	CCTCAGCAGGAGCAATGTCT	AGGGGAAGCACTATCTGAAGG	58/1.75
20	106	288	GCCCTGGAATTTGAGATTGT	AAAGGTCTTCACCCCCAGAG	60/2.00
21	132	159	GGTGTAGGGACTGGCATGTAA	GAACCAAAAGAAGAGGGATCG	60/1.75
5’UTR	/	185	GeneRacer 5’ Primer (Invitrogen)	GAGCAGGAGGAGCAGGACG	62/1.50
Primer name			Allele Specific PCR primers		
KITgloA-VIC		168	GGCATATCCCAAGCCTGACA	AGGCCCTGGTAAGCCAAG	60/1.50
KITgloB-FAM		168	GGCATATCCCAAGCCTGAGC	AGGCCCTGGTAAGCCAAG	60/1.50
Primer name			Microsatellites primers		
UCDC259b		117	AGACCTTCAGAGTTGCCAGTG	TGTCCTCATTACCGTCCTACC	58/2.00
UCDC489		212	GCTCTGCTCCAACATTGC	GGACCATGCTAATCTAATCGAC	58/2.00
UCDC487		158	CCTCCTCCTCAACAACCTG	CTTGAAGCATTGTAGCTGGAAC	58/2.00
UCDC443		148	GCAACTAGCCAGCTCCAG	ACTCCACTTGTTGACGATCC	58/2.00

Dataset S2.10. Pathway enrichment results using all genes underlying regions of low H_p in the pooled domestic cats

KEGG Pathway	Pathway ID	C	O	E	R	rawP	adjP	Genes
Purine metabolism	230	162	6	0.73	8.23	9.80E-05	0.0023	**PDE5A, ENTPD1, POLR2G, PDE1B, POLD4, PNPT1**
Metabolic pathways	1100	1130	16	5.08	3.15	5.84E-05	0.0023	**ACADS, GCLM, ATP6V1D, CYP1A1, POLR2G, GLS2, CYP1A2, GALNT8, B3GAT3, CS, PI4KA, PIGU, GALNT10, POLD4, GANAB, EXTL2**
Ubiquitin mediated proteolysis	4120	135	5	0.61	8.23	0.0004	0.0061	**TRIM37, UBE2K, ITCH, UBE2L3, PPIL2**
Pyrimidine metabolism	240	99	4	0.45	8.98	0.0011	0.0126	**ENTPD1, POLR2G, POLD4, PNPT1**
Axon guidance	4360	129	4	0.58	6.89	0.0028	0.0222	**SEMA7A, MAPK1, DCC, RHOD**
Regulation of actin cytoskeleton	4810	213	5	0.96	5.22	0.0029	0.0222	**SSH3, MAPK1, NCKAP1L, CHRM1, FGF12**
RNA degradation	3018	71	3	0.32	9.39	0.0041	0.0236	**PNPT1, PAN2, EDC3**
Long-term potentiation	4720	70	3	0.31	9.53	0.0039	0.0236	**GRIA1, MAPK1, PPP1R1A**
Homologous recombination	3440	28	2	0.13	15.88	0.0070	0.0268	**TOP3B, POLD4**
Jak-STAT signaling pathway	4630	155	4	0.70	5.74	0.0054	0.0268	**IL23A, IL6ST, IL12B, STAT2**
Protein processing in endoplasmic reticulum	4141	165	4	0.74	5.39	0.0067	0.0268	**EIF2S1, UFD1L, DERL3, GANAB**
Glycosaminoglycan biosynthesis - heparan sulfate	534	26	2	0.12	17.10	0.0061	0.0268	**EXTL2, B3GAT3**
Mucin type O-Glycan biosynthesis	512	30	2	0.13	14.82	0.0081	0.0287	**GALNT10, GALNT8**
African trypanosomiasis	5143	35	2	0.16	12.70	0.0109	0.0358	**VCAM1, IL12B**
Endocytosis	4144	201	4	0.90	4.42	0.0132	0.0405	**PARD6A, ADRBK1, CLTCL1, ITCH**
Tryptophan metabolism	380	42	2	0.19	10.59	0.0154	0.0443	**CYP1A1, CYP1A2**
Wikipathway								
Adipogenesis	WP236	130	7	0.58	11.97	2.21E-06	7.29E-05	**EBF1, MIF, ASIP, BSCL2, AHR, IL6ST, STAT2**
AhR pathway	WP2100	39	3	0.18	17.10	0.0007	0.0115	**CYP1A1, CYP1A2, AHR**
Fatty Acid Omega Oxidation	WP206	15	2	0.07	29.64	0.002	0.022	**CYP1A1, CYP1A2**
Integrated Breast Cancer Pathway	WP1984	68	3	0.31	9.81	0.0036	0.0297	**MAPK1, AHR, SMEK2**
Regulation of Actin Cytoskeleton	WP51	157	4	0.71	5.66	0.0057	0.0336	**SSH3, MAPK1, FGF12, CHRM1**
Physiological and Pathological Hypertrophy of the Heart	WP1528	26	2	0.12	17.10	0.0061	0.0336	**MAPK1, IL6ST**

USER DATA & PARAMETERS - N= 208 genes submitted, Genes mapped to unique Entrez Gene IDs: 194, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2, Enrichment Analyses: KEGG and Wikipathways

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).

Dataset S2.11. Pathway enrichment results using genes underlying regions of elevated F_{ST} in the pooled domestic cats relative to the pooled wildcats and genes underlying regions of low H_p in the pooled domestic cats

KEGG Pathway	Pathway ID	C	O	E	R	rawP	adjP	Genes
Metabolic pathways	1100	1130	24	8.33	2.88	4.40E-06	0.0003	**ACADS, ARG2, GCLM, POLR2G, B3GAT3, PIGH, PI4KA, PIGU, HSD3B7, RDH11, ATP6V1D, CYP1A1, NDUFA2, CYP1A2, GLS2, GALNT8, CS, GMPPB, RDH12, GALNT10, ACADVL, POLD4, GANAB, EXTL2**
Homologous recombination	3440	28	4	0.21	19.37	5.16E-05	0.0015	**TOP3B, BRCA2, POLD4, RAD51B**
Ubiquitin mediated proteolysis	4120	135	7	1	7.03	6.86E-05	0.0015	**UBE3A, TRIM37, UBE2K, UBA7, ITCH, UBE2L3, PPIL2**
Axon guidance	4360	129	6	0.95	6.31	0.0004	0.0066	**SEMA7A, SEMA3G, MAPK1, DCC, RHOD, PLXNB2**
Systemic lupus erythematosus	5322	136	6	1	5.98	0.0005	0.0066	**HIST2H3D, HIST2H2BE, HIST3H2BB, HIST2H2AC, HIST2H2AB, HIST3H2A**
NOD-like receptor signaling pathway	4621	58	4	0.43	9.35	0.0009	0.0099	**MAPK1, NLRP3, PYCARD, PSTPIP1**
Purine metabolism	230	162	6	1.19	5.02	0.0013	0.0107	**PDE5A, ENTPD1, POLR2G, PDE1B, POLD4, PNPT1**
Retinol metabolism	830	64	4	0.47	8.48	0.0013	0.0107	**RDH12, CYP1A1, CYP1A2, RDH11**
SNARE interactions in vesicular transport	4130	36	3	0.27	11.30	0.0024	0.0176	**STX4, STX1B, STX5**
Regulation of actin cytoskeleton	4810	213	6	1.57	3.82	0.0052	0.0343	**SSH3, CD14, MAPK1, NCKAP1L, CHRM1, FGF12**
Pyrimidine metabolism	240	99	4	0.73	5.48	0.0063	0.0378	**ENTPD1, POLR2G, POLD4, PNPT1**
Wikipathway								
Adipogenesis	WP236	130	8	0.96	8.35	5.96E-06	0.0003	**EBF1, MIF, BSCL2, SLC2A4, IL6ST, ASIP, AHR, STAT2**
AhR pathway	WP2100	39	4	0.29	13.91	0.0002	0.0051	**CYP1A1, FLG, CYP1A2, AHR**
Integrated Breast Cancer Pathway	WP1984	68	4	0.50	7.98	0.0016	0.0255	**BRCA2, MAPK1, AHR, SMEK2**
Hypothetical Network for Drug Addiction	WP666	35	3	0.26	11.62	0.0022	0.0255	**GRIA1, MAPK1, NISCH**
mRNA processing	WP411	132	5	0.97	5.14	0.003	0.0255	**NXF1, FUS, SF3B4, PTBP2, CLK3**
NOD pathway	WP1433	39	3	0.29	10.43	0.003	0.0255	**NLRP3, PYCARD, ACAP1**
Regulation of Actin Cytoskeleton	WP51	157	5	1.16	4.32	0.0063	0.0357	**SSH3, CD14, MAPK1, CHRM1, FGF12**
Fatty Acid Omega Oxidation	WP206	15	2	0.11	18.08	0.0053	0.0357	**CYP1A1, CYP1A2**
Mitochondrial LC-Fatty Acid Beta-Oxidation	WP368	16	2	0.12	16.95	0.0061	0.0357	**ACADS, ACADVL**

USER DATA & PARAMETERS - N= 345 genes submitted, Genes mapped to unique Entrez Gene IDs: 378, Organism: hsapiens, Id Type: gene_symbol, Ref Set: entrezgene, Significance Level: .05, Statistics Test: Hypergeometric, MTC: BH, Minimum: 2, Enrichment Analyses: KEGG and Wikipathways

COLUMN HEADINGS - number of reference genes in the category (C), number of genes in the gene set and also in the category (O), expected number in the category (E), Ratio of enrichment (R), p value from hypergeometric test (rawP), and p value adjusted by the multiple test adjustment (adjP).

Dataset S2.12(a). Genes underlying regions of high F_{ST} in the pooled domestic cat X-chromosome variant dataset relative to the pooled wildcat variant dataset

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With Low Domestic H_p
X	41887246	41908184	ENSFCAG00000002568	HDAC6	histone deacetylase 6	
X	41911909	41912610	ENSFCAG00000011221	ERAS	ES cell expressed Ras	
X	41913754	41919251	ENSFCAG00000011223	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	
X	41934479	41938238	ENSFCAG00000002569	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	
X	41938194	41942483	ENSFCAG00000002570	PQBP1	polyglutamine binding protein 1	
X	41942562	41951493	ENSFCAG00000002571	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	
X	41952709	41957926	ENSFCAG00000022467	PIM2	pim-2 oncogene	
X	41961788	41988147	ENSFCAG00000002572	OTUD5	OTU domain containing 5	
X	41991981	41998591	ENSFCAG00000002579	KCND1	potassium voltage-gated channel, Shal-related subfamily, member 1	
X	42002178	42025194	ENSFCAG00000002573	GRIPAP1	GRIP1 associated protein 1	
X	42059037	42068974	ENSFCAG00000002574	TFE3	transcription factor binding to IGHM enhancer 3	
X	42086076	42092788	ENSFCAG00000028936	CCDC120	coiled-coil domain containing 120	
X	42093264	42096118	ENSFCAG00000002576	PRAF2	PRA1 domain family, member 2	
X	42096851	42101817	ENSFCAG00000002577			
X	42129150	42136833	ENSFCAG00000003818	GPKOW	G patch domain and KOW motifs	
X	42149508	42149825	ENSFCAG00000028597			
X	42872212	42934297	ENSFCAG00000015279	CCNB3	cyclin B3	X
X	42969241	43078360	ENSFCAG00000015283			X
X	46413121	46442443	ENSFCAG00000008699	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	
X	46490447	46490559	ENSFCAG00000022607	5S_rRNA	5S ribosomal RNA	
X	49084155	49256064	ENSFCAG00000008079	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	X
X	49256901	49256994	ENSFCAG00000020519			
X	49353869	49353981	ENSFCAG00000030238	5S_rRNA	5S ribosomal RNA	
X	53226451	53260915	ENSFCAG00000030156	ZC4H2	zinc finger, C4H2 domain containing	X
X	53707791	53708303	ENSFCAG00000022560			X
X	53752218	53752715	ENSFCAG00000026187			X
X	53897284	53962444	ENSFCAG00000013821	MSN	moesin	
X	53999183	53999682	ENSFCAG00000031039			
X	54021127	54021234	ENSFCAG00000030106	5S_rRNA	5S ribosomal RNA	
X	57120311	57122215	ENSFCAG00000013727	PJA1	praja ring finger 1, E3 ubiquitin protein ligase	
X	57461705	57487956	ENSFCAG00000000752	FAM155B	family with sequence similarity 155, member B	X
X	62121214	62344089	ENSFCAG00000014128	ZDHHC15	zinc finger, DHHC-type containing 15	
X	62258432	62259126	ENSFCAG00000030281			
X	62407545	62409116	ENSFCAG00000027322	MAGEE2	melanoma antigen family E, 2	
X	62859874	62859986	ENSFCAG00000027539	5S_rRNA	5S ribosomal RNA	
X	62950563	62950675	ENSFCAG00000027233	5S_rRNA	5S ribosomal RNA	
X	62990509	62991208	ENSFCAG00000025177			
X	64307801	64308823	ENSFCAG00000024786	CYSLTR1	cysteinyl leukotriene receptor 1	
X	64322586	64322696	ENSFCAG00000024593	5S_rRNA	5S ribosomal RNA	
X	64453218	64453330	ENSFCAG00000022019	5S_rRNA	5S ribosomal RNA	
X	64983078	64984100	ENSFCAG00000012066	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	
X	64997854	64997966	ENSFCAG00000027429	5S_rRNA	5S ribosomal RNA	
X	65054928	65056011	ENSFCAG00000022899			
X	65077240	65077352	ENSFCAG00000023385	5S_rRNA	5S ribosomal RNA	
X	65091920	65092786	ENSFCAG00000023690			
X	65852774	65860885	ENSFCAG00000002301	TBX22	T-box 22	
X	69515199	69515308	ENSFCAG00000023760	5S_rRNA	5S ribosomal RNA	
X	69533113	69538158	ENSFCAG00000012662	CYLC1	cylicin, basic protein of sperm head cytoskeleton 1	
X	69578192	69578304	ENSFCAG00000022168	5S_rRNA	5S ribosomal RNA	
X	69687439	69829396	ENSFCAG00000009130	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6	
X	70028313	70186830	ENSFCAG00000005781	HDX	highly divergent homeobox	
X	70466196	70466308	ENSFCAG00000028603	5S_rRNA	5S ribosomal RNA	
X	72446722	72446834	ENSFCAG00000024434	5S_rRNA	5S ribosomal RNA	
X	74987292	74987597	ENSFCAG00000024785			
X	76506764	76565232	ENSFCAG00000025687			
X	76745486	76757291	ENSFCAG00000031194			
X	76768969	76774841	ENSFCAG00000027080			
X	76776829	76779222	ENSFCAG00000029591			
X	76853016	76853919	ENSFCAG00000028074			
X	77857129	77857212	ENSFCAG00000028826			
X	77885307	77888089	ENSFCAG00000031149			
X	78058091	78058203	ENSFCAG00000024847	5S_rRNA	5S ribosomal RNA	
X	80450058	80592747	ENSFCAG00000013438	PCDH19	protocadherin 19	X
X	80616295	80616399	ENSFCAG00000023489	5S_rRNA	5S ribosomal RNA	X
X	80649550	80650477	ENSFCAG00000026700	ANXA2	annexin A2	X
X	80741994	80757092	ENSFCAG00000024939	TNMD	tenomodulin	

Dataset S2.12(b). Genes underlying regions of high F_{ST} in the pooled domestic cat X-chromosome variant dataset relative to the pooled wildcat variant dataset

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With Low Domestic H_P
X	82163945	82164473	ENSFCAG00000023241			X
X	82185302	82186069	ENSFCAG00000022838			X
X	82201194	82201535	ENSFCAG00000013057	BEX5	brain expressed, X-linked 5	X
X	82233303	82256641	ENSFCAG00000013704			X
X	83182109	83182975	ENSFCAG00000013517	MORF4L2	mortality factor 4 like 2	
X	83212584	83234142	ENSFCAG00000013518	GLRA4	glycine receptor, alpha 4	
X	83215743	83219091	ENSFCAG00000028808	TMEM31	transmembrane protein 31	
X	83280484	83296694	ENSFCAG00000029818	PLP1	proteolipid protein 1	
X	83331532	83332137	ENSFCAG00000000424	RAB9B	RAB9B, member RAS oncogene family	
X	83491286	83491820	ENSFCAG00000026463			
X	83499961	83528634	ENSFCAG00000006496	FAM199X	family with sequence similarity 199, X-linked	
X	83591368	83596306	ENSFCAG00000007095	ESX1	ESX homeobox 1	
X	83679272	83679384	ENSFCAG00000025445	5S_rRNA	5S ribosomal RNA	
X	84656031	84656372	ENSFCAG00000024474			
X	85860177	85861301	ENSFCAG00000026273			
X	85885076	85885160	ENSFCAG00000024140	5S_rRNA	5S ribosomal RNA	
X	103563484	103563596	ENSFCAG00000029982	5S_rRNA	5S ribosomal RNA	
X	103728395	103728504	ENSFCAG00000031724	5S_rRNA	5S ribosomal RNA	
X	105790212	105795802	ENSFCAG00000022024	APLN	apelin	
X	105873179	105898315	ENSFCAG00000008070	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	
X	105876930	105877062	ENSFCAG00000020596			
X	105908858	105920969	ENSFCAG00000005733	SASH3	SAM and SH3 domain containing 3	
X	105928883	105963235	ENSFCAG00000025956	ZDHHC9	zinc finger, DHHC-type containing 9	
X	121763118	121818915	ENSFCAG00000004331	MAMLD1	mastermind-like domain containing 1	
X	121893254	121967078	ENSFCAG00000004332	MTM1	myotubularin 1	
X	125095537	125102445	ENSFCAG00000011399	FAM50A	family with sequence similarity 50, member A	
X	125116074	125128684	ENSFCAG00000011400	PLXNA3	plexin A3	
X	125134531	125136460	ENSFCAG00000029129	LAGE3	L antigen family, member 3	
X	125140852	125143560	ENSFCAG00000025607	UBL4A	ubiquitin-like 4A	
X	125144336	125145769	ENSFCAG00000022989	SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	
X	125152456	125159000	ENSFCAG00000011403	FAM3A	family with sequence similarity 3, member A	
X	125167043	125177827	ENSFCAG00000011404	G6PD	glucose-6-phosphate dehydrogenase	
X	125182326	125199683	ENSFCAG00000029840	IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	
X	125244852	125245838	ENSFCAG00000028188			

Dataset S2.13(a). Genes underlying regions of low H_p in the pooled domestic cat X-chromosome variant dataset following annotation of 100kb windows that fell below 1.5 standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With High F_{ST} (>1.5)
X	21630	63492	ENSFCAG00000025306			
X	69519	101606	ENSFCAG00000015077	PPP2R3B	protein phosphatase 2, regulatory subunit B'', beta	
X	193651	210731	ENSFCAG00000010308			
X	216285	223908	ENSFCAG00000013263			
X	258750	260256	ENSFCAG00000022728			
X	297649	299085	ENSFCAG00000029324			
X	788985	801017	ENSFCAG00000030897	IL3RA	interleukin 3 receptor, alpha (low affinity)	
X	802775	805108	ENSFCAG00000001211	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
X	810005	827797	ENSFCAG00000014304	ASMTL	acetylserotonin O-methyltransferase-like	
X	832290	833503	ENSFCAG00000029147			
X	832943	833542	ENSFCAG00000025999			
X	836793	839803	ENSFCAG00000031505	ASMT	acetylserotonin O-methyltransferase	
X	982130	1057940	ENSFCAG00000025503			
X	1076513	1078597	ENSFCAG00000012522	ZBED1	zinc finger, BED-type containing 1	
X	2583245	2591210	ENSFCAG00000022434			
X	3110376	3385224	ENSFCAG00000000375			
X	4013126	4013238	ENSFCAG00000024922	5S_rRNA	5S ribosomal RNA	
X	4042639	4093472	ENSFCAG00000023323	HDHD1	haloacid dehalogenase-like hydrolase domain containing 1	
X	4206218	4291197	ENSFCAG00000024019	STS	steroid sulfatase (microsomal), isozyme S	
X	4770564	4800388	ENSFCAG00000004082	PNPLA4	patatin-like phospholipase domain containing 4	
X	5336558	5408176	ENSFCAG00000004854	KAL1	Kallmann syndrome 1 sequence	
X	6295756	6440915	ENSFCAG00000011563	TBL1Y	transducin (beta)-like 1, Y-linked	
X	6470618	6495329	ENSFCAG00000021932	GPR143	G protein-coupled receptor 143	
X	6513656	6514431	ENSFCAG00000025783			
X	6596578	6677533	ENSFCAG00000011183	SHROOM2	shroom family member 2	
X	6690557	6691192	ENSFCAG00000028772			
X	6710553	6711562	ENSFCAG00000022520			
X	6789548	6865297	ENSFCAG00000011192	WWC3	WWC family member 3	
X	6780137	6953135	ENSFCAG00000007631	CLCN4	chloride channel, voltage-sensitive 4	
X	7112953	7216047	ENSFCAG00000002582	MID1	midline 1 (Opitz/BBB syndrome)	
X	7699738	7710351	ENSFCAG00000022393	HCCS	holocytochrome c synthase	
X	7720243	7791414	ENSFCAG00000002122	ARHGAP6	Rho GTPase activating protein 6	
X	7830735	7835138	ENSFCAG00000023640	AMELX	Amelogenin	
X	8074048	8074539	ENSFCAG00000030523			
X	8099270	8099635	ENSFCAG00000024727			
X	8259014	8271418	ENSFCAG00000002794	MSL3	male-specific lethal 3 homolog (Drosophila)	
X	8513291	8513384	ENSFCAG00000017961			
X	9076358	9162154	ENSFCAG00000006682	FRMPD4	FERM and PDZ domain containing 4	
X	9305798	9308923	ENSFCAG00000027513	TLR8	Toll-like receptor 8	
X	9354701	9356802	ENSFCAG00000022748			
X	9885613	9886440	ENSFCAG00000027185			
X	9931463	9964979	ENSFCAG00000012437	EGFL6	EGF-like-domain, multiple 6	
X	9981863	9982885	ENSFCAG00000024286			
X	10023119	10023736	ENSFCAG00000023992	RAB9A	RAB9A, member RAS oncogene family	
X	10027827	10039663	ENSFCAG00000023912			
X	10039520	10081402	ENSFCAG00000014870	OFD1	oral-facial-digital syndrome 1	
X	10103285	10143181	ENSFCAG00000014877	GPM6B	glycoprotein M6B	
X	10305715	10316101	ENSFCAG00000014428	GEMIN8	gem (nuclear organelle) associated protein 8	
X	10529330	10529398	ENSFCAG00000025105			
X	10538216	10538293	ENSFCAG00000027438			
X	10784014	10784129	ENSFCAG00000022459	5S_rRNA	5S ribosomal RNA	
X	10741200	10911440	ENSFCAG00000011448	GLRA2	glycine receptor, alpha 2	
X	11018197	11033965	ENSFCAG00000029176	FANCB	Fanconi anemia, complementation group B	
X	11041578	11095832	ENSFCAG00000022388	MOSPD2	motile sperm domain containing 2	
X	11187292	11187374	ENSFCAG00000029611			
X	11286501	11288251	ENSFCAG00000031484	CBX4	chromobox homolog 4	
X	11413677	11441669	ENSFCAG00000010484	ASB9	ankyrin repeat and SOCS box containing 9	

Dataset S2.13(b). Genes underlying regions of low H_p in the pooled domestic cat X-chromosome variant dataset following annotation of 100kb windows that fell below 1.5 standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With High F_{ST} (>1.5)
X	11450862	11475292	ENSFCAG00000022236	ASB11	ankyrin repeat and SOCS box containing 11	
X	11478140	11488483	ENSFCAG00000010727	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A	
X	11497779	11531651	ENSFCAG00000010485	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	
X	11532692	11621888	ENSFCAG00000010486	PIR	pirin (iron-binding nuclear protein)	
X	11631474	11678324	ENSFCAG00000010487	BMX	BMX non-receptor tyrosine kinase	
X	11681716	11720452	ENSFCAG00000009320	ACE2	Angiotensin-converting enzyme 2 Processed angiotensin-converting enzyme 2	
X	11746176	11777544	ENSFCAG00000009328	TMEM27	transmembrane protein 27	
X	11828552	11828664	ENSFCAG00000029736	5S_rRNA	5S ribosomal RNA	
X	11788172	11901542	ENSFCAG00000031216	CA5B	carbonic anhydrase VB, mitochondrial	
X	11906051	11933524	ENSFCAG00000009333			
X	11936136	11962265	ENSFCAG00000024224	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	
X	12787190	12837643	ENSFCAG00000006523	TXLNG	taxilin gamma	
X	12837168	12864998	ENSFCAG00000028919	RBBP7	retinoblastoma binding protein 7	
X	12996604	13134277	ENSFCAG00000006527	REPS2	RALBP1 associated Eps domain containing 2	
X	13935586	13935741	ENSFCAG00000018915			
X	14086539	14119271	ENSFCAG00000006437	BEND2	BEN domain containing 2	
X	14172289	14250913	ENSFCAG00000006438	SCML2	sex comb on midleg-like 2 (Drosophila)	
X	17399416	17399526	ENSFCAG00000017180	5S_rRNA	5S ribosomal RNA	
X	17175933	17401205	ENSFCAG00000026807	CNKSR2	connector enhancer of kinase suppressor of Ras 2	
X	17833482	17848892	ENSFCAG00000023168			
X	17988539	18006475	ENSFCAG00000023221			
X	18029515	18031154	ENSFCAG00000010060	ZNF645	zinc finger protein 645	
X	18790237	18791979	ENSFCAG00000013616	DDX53	DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	
X	19109565	19159869	ENSFCAG00000031503	PTCHD1	patched domain containing 1	
X	19250902	19251014	ENSFCAG00000027204	5S_rRNA	5S ribosomal RNA	
X	19308144	19308597	ENSFCAG00000031952			
X	19393444	19413380	ENSFCAG00000004028	PRDX4	peroxiredoxin 4	
X	19420080	19443002	ENSFCAG00000004030	ACOT9	acyl-CoA thioesterase 9	
X	19476530	19479076	ENSFCAG00000004032	SAT1	spermidine/spermine N1-acetyltransferase 1	
X	19912217	19915290	ENSFCAG00000022717			
X	19931048	19934125	ENSFCAG00000026176			
X	20018240	20085226	ENSFCAG00000002134	PDK3	pyruvate dehydrogenase kinase, isozyme 3	
X	20104464	20200081	ENSFCAG00000002136	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	
X	20249684	20553632	ENSFCAG00000002138	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	
X	20868777	20869679	ENSFCAG00000031841	FELCATV1R3	vomeronasal 1 receptor felCatV1R3	
X	26713585	26713773	ENSFCAG00000028835			
X	26746658	26767210	ENSFCAG00000022029			
X	26860944	26917110	ENSFCAG00000028265			
X	26971105	26971226	ENSFCAG00000029796			
X	30543947	30544592	ENSFCAG00000030015			
X	30661122	30662084	ENSFCAG00000030986	MAGEB16	melanoma antigen family B, 16	
X	30790586	30849071	ENSFCAG00000018231	CXorf22	chromosome X open reading frame 22	
X	38356463	38359279	ENSFCAG00000007766			
X	38214551	38413159	ENSFCAG00000007765	EFHC2	EF-hand domain (C-terminal) containing 2	
X	38876657	39013854	ENSFCAG00000009445	KDM6A	lysine (K)-specific demethylase 6A	
X	39054031	39099121	ENSFCAG00000009449	CXorf36	chromosome X open reading frame 36	
X	40057175	40084354	ENSFCAG00000027707			
X	40134846	40135831	ENSFCAG00000025461	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	
X	40163495	40226463	ENSFCAG00000003541	SLC9A7	solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7	
X	41093658	41108251	ENSFCAG00000008192	ELK1	ELK1, member of ETS oncogene family	
X	41109294	41118283	ENSFCAG00000028638	UXT	ubiquitously-expressed, prefoldin-like chaperone	
X	41127225	41128098	ENSFCAG00000023763			
X	41165141	41169982	ENSFCAG00000027976			
X	41220128	41306403	ENSFCAG00000022818	ZNF81	zinc finger protein 81	
X	41320923	41321464	ENSFCAG00000026947			
X	41394530	41395849	ENSFCAG00000030362			
X	41428902	41431781	ENSFCAG00000008528			

Dataset S2.13(c). Genes underlying regions of low H_p in the pooled domestic cat X-chromosome variant dataset following annotation of 100kb windows that fell below 1.5 standard deviations from the mean H_p

Chromosome Name	Gene Start (bp)	Gene End (bp)	Ensembl Gene ID	Associated Gene Name	Description	Overlap With High F_{ST} (>1.5)
X	41488558	41490795	ENSFCAG00000027919			
X	42702287	42741226	ENSFCAG00000008619	CLCN5	chloride channel, voltage-sensitive 5	
X	42750538	42750651	ENSFCAG00000017254	5S_rRNA	5S ribosomal RNA	
X	42836383	42851018	ENSFCAG00000031319	AKAP4	A kinase (PRKA) anchor protein 4	
X	42872212	42934297	ENSFCAG00000015279	CCNB3	cyclin B3	X
X	42969241	43078360	ENSFCAG00000015283			X
X	43193426	43193530	ENSFCAG00000026630	5S_rRNA	5S ribosomal RNA	
X	48251045	48253353	ENSFCAG00000005774			
X	48582110	48582823	ENSFCAG00000003939	SPIN4	spindlin family, member 4	
X	48716489	48717304	ENSFCAG00000024136			
X	48773862	48773974	ENSFCAG00000031522	5S_rRNA	5S ribosomal RNA	
X	49049755	49049858	ENSFCAG00000027820	5S_rRNA	5S ribosomal RNA	
X	49084155	49256064	ENSFCAG00000008079	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	X
X	53226451	53260915	ENSFCAG00000030156	ZC4H2	zinc finger, C4H2 domain containing	X
X	53639070	53640170	ENSFCAG00000031009			
X	53707791	53708303	ENSFCAG00000022560			X
X	53752218	53752715	ENSFCAG00000026187			X
X	57343796	57343908	ENSFCAG00000030304	5S_rRNA	5S ribosomal RNA	
X	57461705	57487956	ENSFCAG00000000752	FAM155B	family with sequence similarity 155, member B	X
X	57631690	57632265	ENSFCAG00000028821			
X	58391478	58449666	ENSFCAG00000008636	DLG3	discs, large homolog 3 (Drosophila)	
X	58465920	58707117	ENSFCAG00000029781	TEX11	testis expressed 11	
X	59100432	59101007	ENSFCAG00000021936			
X	59107833	59192395	ENSFCAG00000014809			
X	59250509	59286633	ENSFCAG00000002182	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	
X	59802421	59806881	ENSFCAG00000023693	CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	
X	59828592	60051076	ENSFCAG00000005065	HDAC8	histone deacetylase 8	
X	60058404	60229276	ENSFCAG00000007121	PHKA1	phosphorylase kinase, alpha 1 (muscle)	
X	69165483	69166568	ENSFCAG00000011964	POU3F4	POU class 3 homeobox 4	
X	73345566	73346382	ENSFCAG00000023461			
X	73348095	73348790	ENSFCAG00000030624			
X	73490123	73490814	ENSFCAG00000026491			
X	75676071	75676176	ENSFCAG00000022654	5S_rRNA	5S ribosomal RNA	
X	75747036	75747148	ENSFCAG00000026298	5S_rRNA	5S ribosomal RNA	
X	80450058	80592747	ENSFCAG00000013438	PCDH19	protocadherin 19	X
X	80616295	80616399	ENSFCAG00000023489	5S_rRNA	5S ribosomal RNA	X
X	80649550	80650477	ENSFCAG00000026700	ANXA2	annexin A2	X
X	82163945	82164473	ENSFCAG00000023241			X
X	82185302	82186069	ENSFCAG00000022838			X
X	82201194	82201535	ENSFCAG00000013057	BEX5	brain expressed, X-linked 5	X
X	82233303	82256641	ENSFCAG00000013704			X
X	82327996	82335121	ENSFCAG00000010017			

Dataset S2.14. Summary of genes underlying regions of elevated F_{ST} and low H_p along the X-chromosome in domestic cats

Genes Underlying Putative Regions of Selection in the Domestic Cat Along the X-Chromosome

Region	Chr:Pos	Gene ID	Gene Name	Description	Domestic $Z(H_p)$	$Z(F_{ST})$	Wildcat $Z(H_p)$
1	X:42872212-42934297	ENSFCAG00000015279	**CCNB3**	**cyclin B3**	-2.4 to -1.7	1.6 to 1.7	-0.8 to 0.6
	X:42969241-43078360	ENSFCAG00000015283		unknown			
2	X:49084155-49256064	ENSFCAG00000008079	**ARHGEF9**	**Cdc42 guanine nucleotide exchange factor (GEF) 9**	-2.3	1.5	0.30
3	X:53226451-53260915	ENSFCAG00000030156	**ZC4H2**	**zinc finger, C4H2 domain containing**	-2.3 to -1.6	1.5 to 1.8	0.2 to 0.5
	X:53707791-53708303	ENSFCAG00000022560		unknown			
	X:53752218-53752715	ENSFCAG00000026187		unknown			
4	X:57461705-57487956	ENSFCAG00000000752	**FAM155B**	**family with sequence similarity 155, member B**	-3.1 to -1.5	1.5	-0.8 to 0.5
5	X:80450058-80592747	ENSFCAG00000013438	**PCDH19**	**protocadherin 19**	-2.1 to -1.7	1.60	0.3 to 0.6
	X:80616295-80616399	ENSFCAG00000023489	**5S_rRNA**	5S ribosomal RNA			
	X:80649550-80650477	ENSFCAG00000026700	**ANXA2**	**annexin A2**			
6	X:82163945-82164473	ENSFCAG00000023241		unknown	-2.1	1.7	0.6
	X:82185302-82186069	ENSFCAG00000022838		unknown			
	X:82201194-82201535	ENSFCAG00000013057	**BEX5**	**brain expressed, X-linked 5**			
	X:82233303-82256641	ENSFCAG00000013704		unknown			