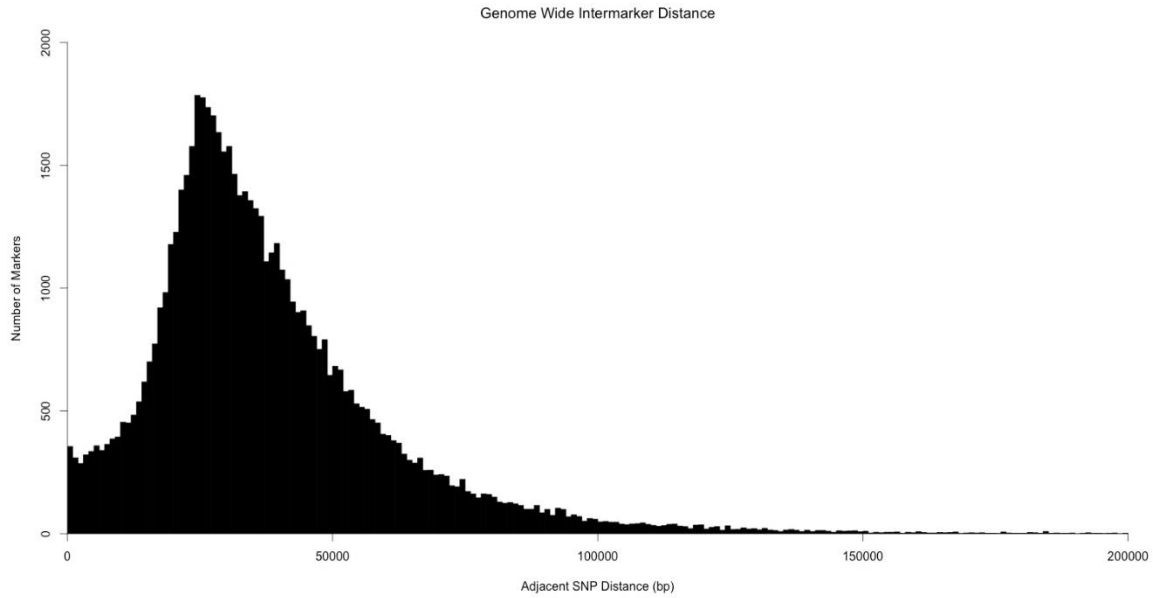


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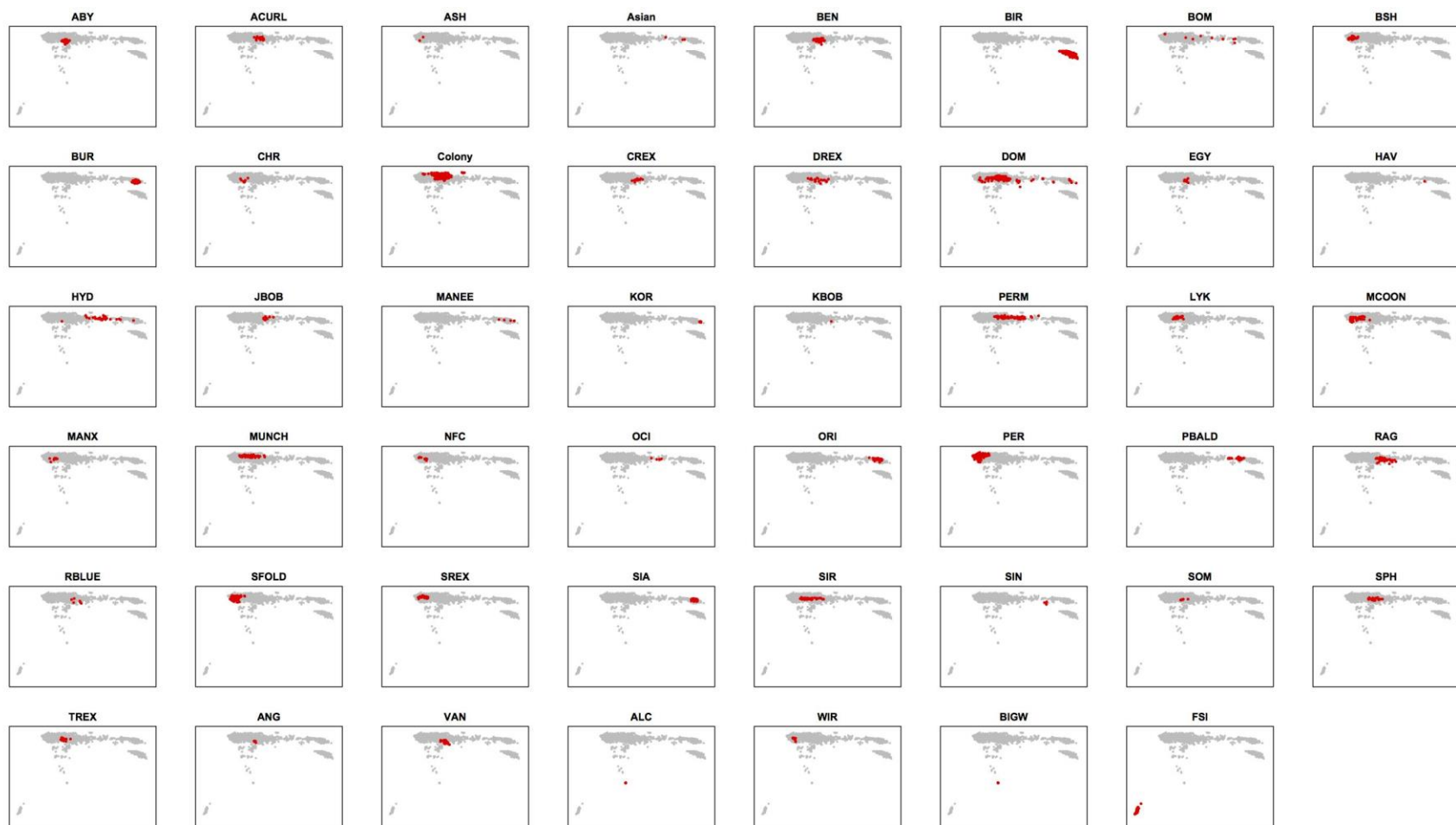
Applications and efficiencies of the first cat 63K DNA array

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Supplementary Figures



Supplementary Figure 1. Genome-wide distribution of intermarker distances. The genome-wide intermarker distribution of array loci is plotted as the marker frequency relative to the distance to the closest adjacent array SNP.



a.

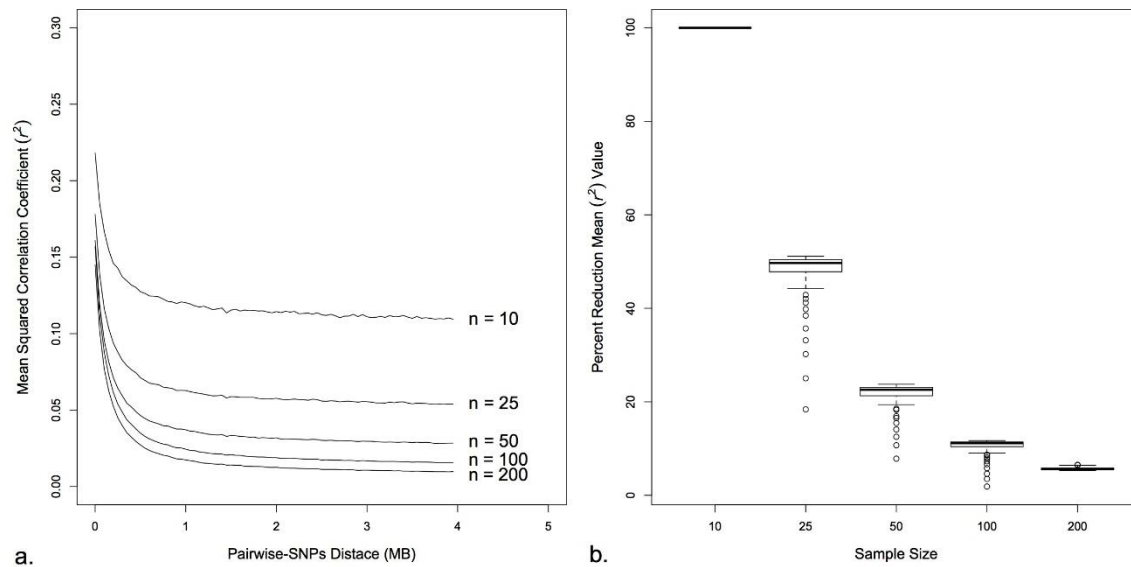


b.

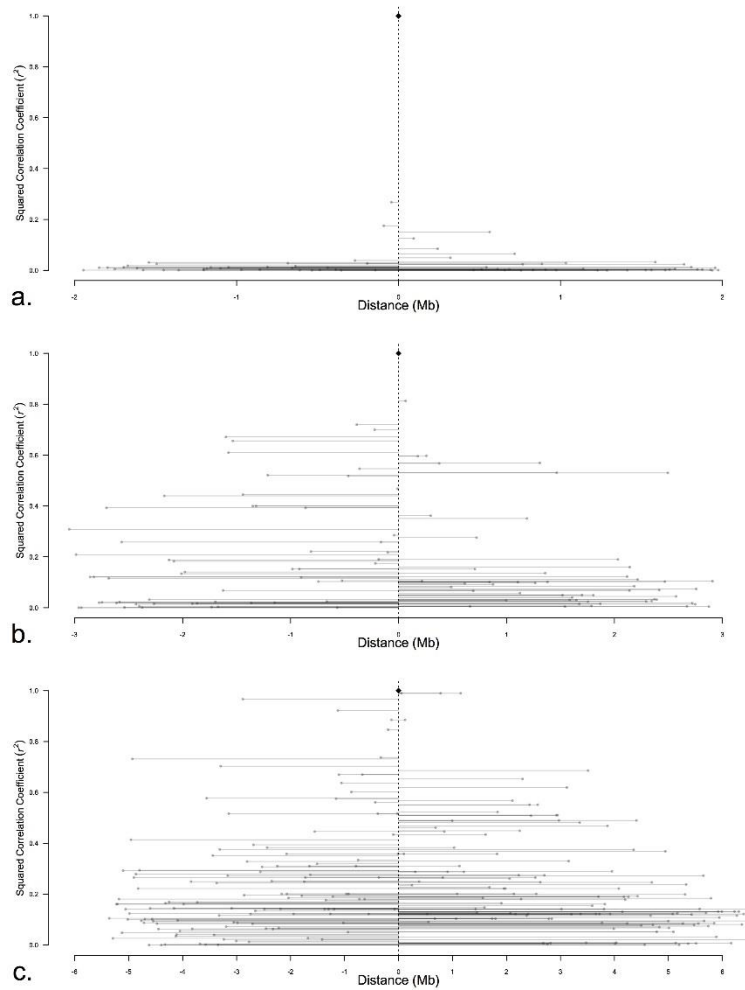


C.

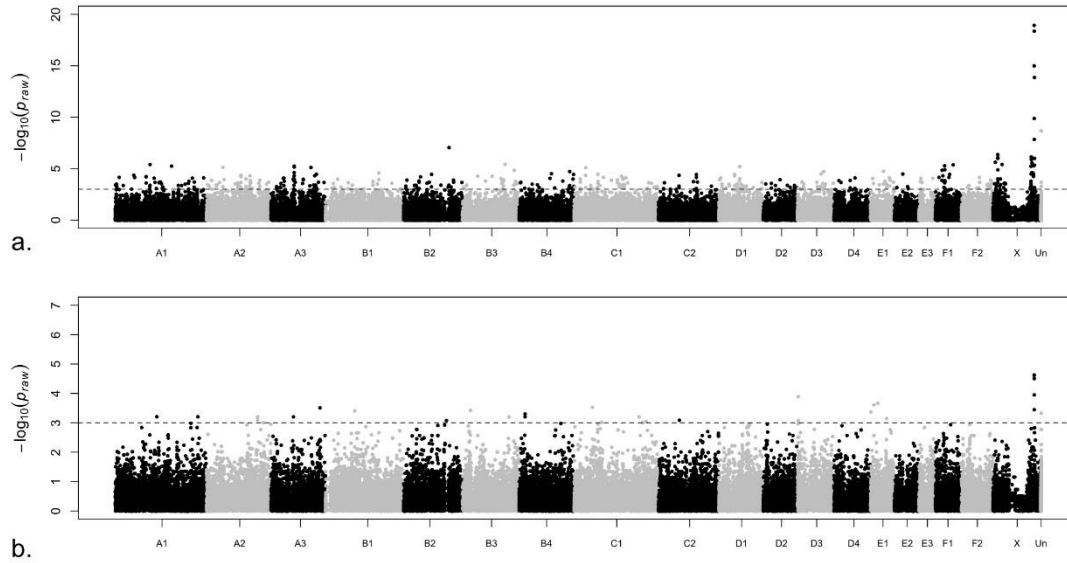
Supplementary Figure 2: Detailed genetic structure of cat populations using Feline array markers. Gray dots represent the individual cats position in the two dimensions plotted while red dots represent the individuals that belong to a specific population. An abbreviated name of population under investigation (red dots) is used as a header for the plot and details can be found in table#. (a-c) are plots of dimension1 vs. dimension2, dimension1 vs. dimension3, dimension2 vs. dimension3, respectively.



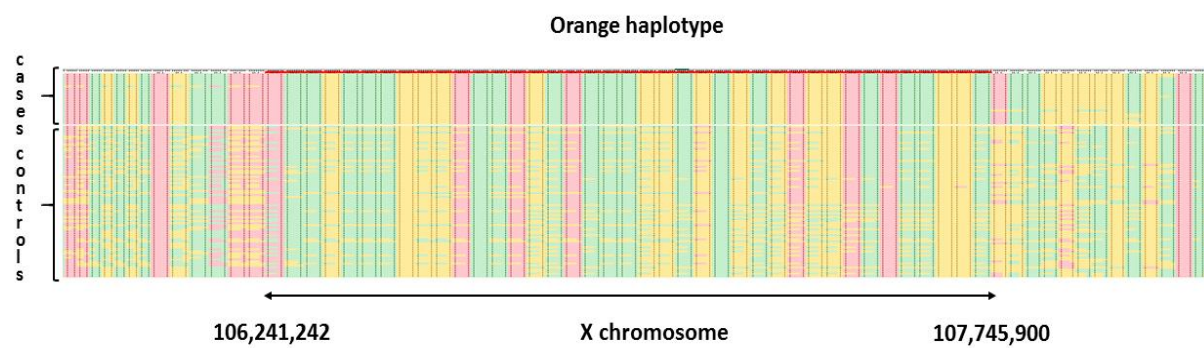
Supplementary Figure 3. Effects of sample size on linkage disequilibrium estimates. (a) Decay of linkage disequilibrium as a function of distance (Mb) for different sample size ($n = 10, 25, 50, 100, 200$) of a random bred population. (b) The reduction in the linkage disequilibrium estimates as the sample size increases. Increasing sample size from 10 to 25 reduces estimates by $\sim 50\%$ (details of the calculations are in Materials and Methods).



Supplementary Figure 4. Linkage disequilibrium between causative mutations and surrounding markers. a-c) vertical dashed line and black dot represent the causative marker of dilute coloration, long hair, and point coloration, respectively. Gray dots represent the SNPs and horizontal lines correspond to the distance to the causative marker. The y-axis is a measure of pair-wise linkage disequilibrium (r^2) between the causative markers and nearby SNPs.



Supplementary Figure 5. Genome-wide association analysis of orange coloration in cats. a) Manhattan plot of the allelic association study across multiple breeds b) CMH association study using the same dataset of the allelic association after pair-wise population concordance (PPC) test.



Supplementary Figure 6. Extent of the orange coloration haplotype. A haplotype block was identified between all cases from position 106,241,242 to position 107,745,900 of the X chromosome.

Supplementary Tables

Supplementary Table 1. Number of markers and average distance for each chromosome.

Chromosome	# of markers	Average distance (bp)
A1	6369	37741
A2	4424	38113
A3	3444	40867
B1	5086	40569
B2	3685	41523
B3	3746	39488
B4	3760	37870
C1	5835	38081
C2	4283	37181
D1	3109	37048
D2	2367	37184
D3	2555	36699
D4	2491	37893
E1	1564	38961
E2	1679	36784
E3	1104	37122
F1	1799	38963
F2	2169	38701
X	2724	46697

Supplementary Table 2. Genotypes mismatches between duplicated samples.
Duplicated samples mismatches number and % including the whole SNPs dataset, and after excluding SNPs with a genotyping rate below 10% and with Mendelian errors.

Sample ID	Category	62897		62272		62051	
		# mismatch	% mismatch	# mismatch	% mismatch	# mismatch	% mismatch
CCL94	control	356	0.57	344	0.55	340	0.55
Cinnamon	control	0	0	0	0	0	0
4406	control	4	0.006	3	0.005	3	0.005
4649	control	4	0.006	3	0.005	3	0.005
Cinnamon vs wga12682	WGA test	1720	2.73	1639	2.63	1628	2.62
16216T	tumor	439	0.7	429	0.69	426	0.69
6223T	tumor	681	1.08	664	1.07	660	1.06
10208	Involuntary	223	0.35	170	0.27	164	0.26
10209	Involuntary	78	0.12	46	0.07	44	0.07
10850	Involuntary	331	0.52	299	0.48	297	0.48
13106	Involuntary	353	0.56	320	0.51	318	0.51
13226	Involuntary	648	1.03	492	0.79	456	0.73
13233	Involuntary	446	0.71	310	0.5	275	0.44
15427	Involuntary	702	1.11	567	0.91	525	0.85
17993	Involuntary	462	0.73	353	0.57	331	0.53
5588	Involuntary	541	0.86	410	0.66	383	0.62
7359	Involuntary	550	0.87	497	0.8	491	0.8
8638	Involuntary	530	0.84	441	0.71	431	0.7
9793	Involuntary	279	0.44	225	0.36	213	0.34
LYM16513	Involuntary	443	0.7	426	0.68	426	0.68
1310	Low calls	28056	44.6	27749	44.56	27652	44.56
13632	Low calls	5810	9.23	5600	9	5551	8.9
15723	Low calls	23959	38.1	23692	38.05	23589	38.01
4439	Low calls	29346	46.7	28968	46.5	28848	46.5
5589	Low calls	27338	43.5	26976	43.3	26861	43.3
6667	Low calls	3952	6.3	3799	6.1	3756	6.05
10988	Low calls	2711	4.3	2548	4.09	2514	4.05

Supplementary Table 3. Number of SNPs in each MAF ranges.

MAF bin	Number SNPs	MAF bin	Number SNPs
0-0.05	7813	0-0.005	2013
0.05-0.1	7537	0.005-0.01	615
0.1-0.15	7469	0.01-0.015	589
0.15-0.2	7187	0.015-0.02	567
0.2-0.25	6477	0.02-0.025	626
0.25-0.3	5977	0.025-0.03	677
0.3-0.35	5327	0.03-0.035	690
0.35-0.4	5027	0.035-0.04	683
0.4-0.45	4797	0.04-0.045	675
0.45-0.5	4661	0.045-0.05	678
		0.05-0.055	691
		0.055-0.06	756
		0.06-0.065	741
		0.065-0.07	724
		0.07-0.075	756
		0.075-0.08	797
		0.08-0.085	736
		0.085-0.09	787
		0.09-0.095	788
		0.095-0.1	761
		0.1-0.105	756
		0.105-0.11	759
		0.11-0.115	776
		0.115-0.12	698
		0.12-0.125	790
		0.125-0.13	762
		0.13-0.135	748
		0.135-0.14	741
		0.14-0.145	732
		0.145-0.15	707
		0.15-0.155	756
		0.155-0.16	723
		0.16-0.165	753
		0.165-0.17	775
		0.17-0.175	733
		0.175-0.18	661

		0.18-0.185	699
		0.185-0.19	670
		0.19-0.195	689
		0.195-0.2	728
		0.2-0.205	676
		0.205-0.21	695
		0.21-0.215	673
		0.215-0.22	635
		0.22-0.225	623
		0.225-0.23	607
		0.23-0.235	639
		0.235-0.24	625
		0.24-0.245	669
		0.245-0.25	635
		0.25-0.255	625
		0.255-0.26	653
		0.26-0.265	654
		0.265-0.27	553
		0.27-0.275	590
		0.275-0.28	603
		0.28-0.285	609
		0.285-0.29	576
		0.29-0.295	543
		0.295-0.3	571
		0.3-0.305	565
		0.305-0.31	519
		0.31-0.315	534
		0.315-0.32	547
		0.32-0.325	553
		0.325-0.33	523
		0.33-0.335	515
		0.335-0.34	529
		0.34-0.345	533
		0.345-0.35	509
		0.35-0.355	536
		0.355-0.36	492
		0.36-0.365	500
		0.365-0.37	491
		0.37-0.375	503

		0.375-0.38	491
		0.38-0.385	496
		0.385-0.39	523
		0.39-0.395	492
		0.395-0.4	503
		0.4-0.405	491
		0.405-0.41	428
		0.41-0.415	492
		0.415-0.42	439
		0.42-0.425	460
		0.425-0.43	483
		0.43-0.435	527
		0.435-0.44	500
		0.44-0.445	508
		0.445-0.45	469
		0.45-0.455	477
		0.455-0.46	509
		0.46-0.465	426
		0.465-0.47	442
		0.47-0.475	465
		0.475-0.48	463
		0.48-0.485	477
		0.485-0.49	477
		0.49-0.495	466
		0.495-0.5	459

Supplementary Table 4. Effect of sample size of random bred cats on average squared correlation coefficient (r^2) estimates of LD at different distance bins.

Distance	DOM10	DOM25	DOM50	DOM100	DOM200
0	0.2181	0.178	0.1609	0.1568	0.1451
50000	0.185	0.1387	0.1189	0.1124	0.1018
100000	0.1669	0.1165	0.0956	0.0879	0.077
150000	0.1547	0.1034	0.0816	0.0726	0.0626
200000	0.146	0.0939	0.0713	0.0616	0.0526
250000	0.1428	0.0879	0.0643	0.0539	0.045
300000	0.1371	0.0825	0.0593	0.0486	0.0398
350000	0.1345	0.0791	0.0545	0.0436	0.0352
400000	0.1318	0.0764	0.052	0.0407	0.0323
450000	0.1302	0.0744	0.049	0.0377	0.0295
500000	0.1274	0.0711	0.0464	0.0349	0.0272
550000	0.1263	0.0694	0.0445	0.0328	0.0251
600000	0.1246	0.0676	0.0429	0.0311	0.0236
650000	0.1245	0.067	0.0419	0.0299	0.0224
700000	0.1241	0.0666	0.041	0.0287	0.0215
750000	0.1226	0.065	0.0398	0.0278	0.0205
800000	0.1211	0.0646	0.0396	0.0273	0.02
850000	0.1207	0.0641	0.0385	0.0261	0.019
900000	0.1197	0.0628	0.0376	0.0253	0.0181
950000	0.1207	0.0629	0.0376	0.0252	0.0179
1000000	0.1202	0.0628	0.0371	0.0244	0.0174
1050000	0.1194	0.062	0.0362	0.0236	0.0169
1100000	0.1181	0.0614	0.036	0.0235	0.0165
1150000	0.1174	0.0609	0.0353	0.0226	0.0158
1200000	0.1179	0.0604	0.0348	0.0223	0.0153
1250000	0.1168	0.0598	0.0342	0.0218	0.0151
1300000	0.1156	0.0593	0.0339	0.0215	0.0148
1350000	0.1162	0.0594	0.0337	0.0213	0.0146
1400000	0.1167	0.0597	0.034	0.0212	0.0147
1450000	0.1135	0.0579	0.0328	0.0205	0.014
1500000	0.1154	0.0588	0.0334	0.0209	0.0141
1550000	0.1159	0.0587	0.0332	0.0204	0.0139
1600000	0.1148	0.0583	0.0328	0.0204	0.0139
1650000	0.1154	0.0583	0.0326	0.0199	0.0133
1700000	0.115	0.0583	0.0323	0.0196	0.0132
1750000	0.1152	0.0583	0.0324	0.0195	0.0131
1800000	0.1148	0.0576	0.0317	0.0193	0.0131
1850000	0.1149	0.0574	0.032	0.0193	0.013
1900000	0.1142	0.0575	0.0318	0.0191	0.0126
1950000	0.1136	0.0574	0.0316	0.0189	0.0125

2000000	0.1144	0.0577	0.0319	0.0189	0.0126
2050000	0.1137	0.0571	0.031	0.0184	0.0122
2100000	0.1146	0.0567	0.0312	0.0184	0.0121
2150000	0.1141	0.0569	0.0311	0.0183	0.012
2200000	0.1145	0.0572	0.031	0.0184	0.012
2250000	0.113	0.0568	0.0309	0.0182	0.0118
2300000	0.1132	0.0568	0.0307	0.018	0.0117
2350000	0.1134	0.0564	0.0306	0.0179	0.0116
2400000	0.1127	0.0571	0.0309	0.0179	0.0116
2450000	0.1137	0.0568	0.0307	0.0179	0.0116
2500000	0.1123	0.0559	0.0302	0.0173	0.0112
2550000	0.1119	0.0557	0.0301	0.0175	0.0112
2600000	0.1126	0.0561	0.0303	0.0173	0.0112
2650000	0.1117	0.0559	0.03	0.0173	0.0112
2700000	0.1104	0.0554	0.0298	0.0172	0.011
2750000	0.1114	0.0557	0.0299	0.017	0.0109
2800000	0.1115	0.0558	0.0299	0.0171	0.011
2850000	0.1126	0.0555	0.0297	0.017	0.0109
2900000	0.1111	0.0552	0.0294	0.0167	0.0105
2950000	0.1125	0.0556	0.0297	0.017	0.0107
3000000	0.111	0.0555	0.0296	0.0168	0.0107
3050000	0.1105	0.0552	0.0296	0.0167	0.0106
3100000	0.1107	0.0547	0.0292	0.0165	0.0105
3150000	0.1113	0.0547	0.0291	0.0164	0.0104
3200000	0.1106	0.0546	0.029	0.0164	0.0104
3250000	0.1118	0.0552	0.0291	0.0164	0.0104
3300000	0.111	0.0548	0.029	0.0164	0.0102
3350000	0.1111	0.0553	0.0289	0.0163	0.0103
3400000	0.1119	0.0554	0.0291	0.0161	0.0101
3450000	0.1108	0.0546	0.029	0.0162	0.0101
3500000	0.11	0.0541	0.0287	0.0159	0.01
3550000	0.1112	0.0545	0.029	0.0161	0.0101
3600000	0.1101	0.0544	0.0287	0.016	0.01
3650000	0.1104	0.0543	0.0289	0.016	0.0099
3700000	0.11	0.054	0.0286	0.0159	0.0098
3750000	0.1095	0.0541	0.0282	0.0157	0.0097
3800000	0.1098	0.054	0.0283	0.0155	0.0097
3850000	0.1096	0.0541	0.0283	0.0156	0.0097
3900000	0.1103	0.0539	0.0284	0.0155	0.0096
3950000	0.1094	0.054	0.0284	0.0156	0.0098
4000000	0.0565	0.031	0.0535	0.019	0.004
5000000	0.109	0.0534	0.0278	0.0151	0.0093
6000000	0.0992	0.0462	0.0226	0.0112	0.0062

Supplementary Table 5. Details of GWAS association results.

Trait	Association	Chro	SNPs	Raw <i>P</i> _{values}	<i>P</i> _{genome} values
Dilution	Allelic	C1	218,100,114 (within <i>MLPH</i>)	1.3e ⁻²⁰	0.00002
		C1	218,055,908	2.1e ⁻⁵	0.8278
		E1	61,374,140	2.2e ⁻⁵	0.8548
Long hair	Allelic	B1	140,077,554 (within <i>FGF5</i>)	8.2e ⁻¹⁰	0.0001
		B1	140,143,322	9.5e ⁻⁸	0.0065
		B1	138,478,128	1.9e ⁻⁶	0.07582
Point coloration	Allelic	D1	46,341,460	2e ⁻⁹	0.00036
		D1	46,396,786 (within <i>TYR</i>)	2.2e ⁻⁹	0.00044
		D1	47,121,808	2.2e ⁻⁹	0.00044
Orange	Allelic	X	107,777,134	1.8e ⁻¹⁹	0.00002
		X	107,994,240	4.3e ⁻¹⁹	0.00002
		X	107,822,242	1e ⁻¹⁵	0.00002
Orange	CMH	X	107,777,134	4.4e ⁻⁵	0.04776
		X	107,822,242	4.4e ⁻⁵	0.04776
		X	107,994,240	3.1e ⁻⁵	0.0751

Supplementary Table 6. List of genes within the Orange haplotype on the X chromosome.

Gene ID	Gene name
<i>ZNF280D</i>	<i>Zinc finger protein 280C isoform 2</i>
<i>TSPAN13</i>	<i>Tetraspanin-13</i>
<i>SLC25A14</i>	<i>Brain mitochondrial carrier protein 1 isoform 1 precursor</i>
<i>GPR119</i>	<i>Glucose-dependent insulinotropic receptor</i>
<i>RBMX2</i>	<i>RNA-binding motif protein X-linked 2</i>
<i>FSIP2</i>	<i>Fibrous sheath-interacting protein 2</i>
<i>ENOX2</i>	<i>Ecto-NOX disulfide-thiol exchanger 2 isoform b</i>
<i>LINC01201</i>	<i>LINC01201</i>
<i>ARHGAP36</i>	<i>Rho GTPase-activating protein 36 isoform 1 precursor</i>
<i>IGSF1</i>	<i>Immunoglobulin superfamily member 1 isoform 4</i>
<i>RPL13P5</i>	<i>RPL13P5</i>
<i>FIRRE</i>	<i>FIRRE</i>

Supplementary Data Files

Supplementary Data File 1. List of wildcat SNPs

Supplementary Data File 2. Map file of the 62,897 SNPs map to *Felis catus* (FelCat 8.0) assembly

Supplementary Data File 3. Remapping information of the 62,897 SNPs to *Felis catus* (FelCat8) assembly, including position of the SNPs, intermarker distances and gap sizes

Supplementary Data File 4. Comparison between the map files generated using *Felis catus* FelCat 6.2 and FelCat 8.0 assemblies

Supplementary Data File 5. Genotype dataset of all cats included in the study (ped file)

Supplementary Data File 6. List of SNPs with >10% missing data across all samples in the dataset

Supplementary Data File 7. List of SNPs with Mendelian errors

Supplementary Data File 8. List of hemizogous SNPs

Supplementary Data File 9. SNPs MAF for each chromosome