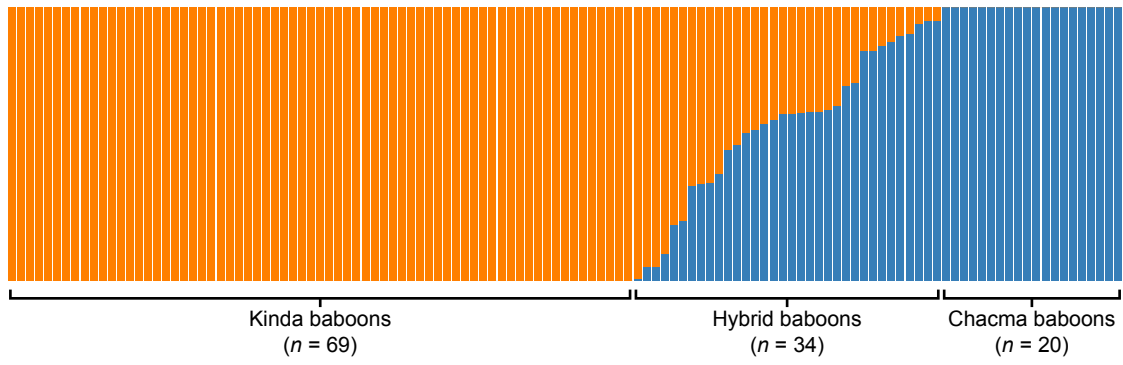
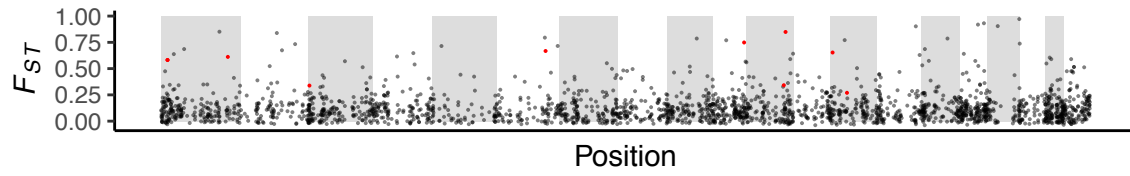


Supplementary Fig. S1: Cross-validated error results from ADMIXTURE runs in which K varied from 1 to 10.



Supplementary Fig. S2: Taxonomic assignment based on ancestry estimates calculated using ADMIXTURE. Of the 129 animals sequenced, 6 were filtered out of the analysis due to excessive missingness and are not shown here.



Supplementary Fig. S3: Distribution of F_{ST} for protein-coding genes. Genes identified as significant by permutation are displayed in red (FDR < 0.05). Background shading indicates the position of the autosomal chromosomes in order (i.e., chromosomes 1 - 20).

Supplementary Table S1: Full list of samples included in this analysis. Samples that were sequenced but failed quality-control filters or exhibited hybrid ancestry are not included in this table.

Sample ID	Tissue type	Locality	Ancestry	SRA Accession
BZ11-001	leukocyte	Chunga	Kinda	SRR7717396
BZ11-002	leukocyte	Chunga	Kinda	SRR7717393
BZ11-003	leukocyte	Chunga	Kinda	SRR7717394
BZ11-004	leukocyte	Chunga	Kinda	SRR7717399
BZ11-005	leukocyte	Chunga	Kinda	SRR7717400
BZ11-006	leukocyte	Chunga	Kinda	SRR7717397
BZ11-007	leukocyte	Chunga	Kinda	SRR7717398
BZ11-008	leukocyte	Chunga	Kinda	SRR7717401
BZ11-009	leukocyte	Chunga	Kinda	SRR7717402
BZ11-010	leukocyte	Chunga	Kinda	SRR7717384
BZ11-011	leukocyte	Chunga	Kinda	SRR7717383
BZ11-012	leukocyte	Chunga	Kinda	SRR7717386
BZ11-013	FTA blood spot	Chunga	Kinda	SRR7717385
BZ11-014	leukocyte	Chunga	Kinda	SRR7717388
BZ11-015	leukocyte	Chunga	Kinda	SRR7717387
BZ11-016	leukocyte	Chunga	Kinda	SRR7717390
BZ11-017	leukocyte	Chunga	Kinda	SRR7717389
BZ11-018	leukocyte	Chunga	Kinda	SRR7717392
BZ11-019	leukocyte	Chunga	Kinda	SRR7717391
BZ11-020	leukocyte	Chunga	Kinda	SRR7717293
BZ11-021	FTA blood spot	Chunga	Kinda	SRR7717294
BZ11-022	FTA blood spot	Chunga	Kinda	SRR7717295
BZ11-023	FTA blood spot	Chunga	Kinda	SRR7717296
BZ11-024	leukocyte	Chunga	Kinda	SRR7717297
BZ11-025	leukocyte	Chunga	Kinda	SRR7717298
BZ11-026	FTA blood spot	Chunga	Kinda	SRR7717299
BZ11-028	leukocyte	Chunga	Kinda	SRR7717300
BZ11-029	leukocyte	Chunga	Kinda	SRR7717301
BZ11-030	leukocyte	Chunga	Kinda	SRR7717302
BZ11-031	leukocyte	Chunga	Kinda	SRR7717281
BZ11-032	leukocyte	Chunga	Kinda	SRR7717280
BZ11-033	leukocyte	Chunga	Kinda	SRR7717279
BZ11-034	leukocyte	Chunga	Kinda	SRR7717278
BZ11-035	leukocyte	Chunga	Kinda	SRR7717277
BZ11-036	leukocyte	Chunga	Kinda	SRR7717276
BZ11-037	leukocyte	Chunga	Kinda	SRR7717275
BZ11-038	leukocyte	Chunga	Kinda	SRR7717274
BZ11-039	leukocyte	Chunga	Kinda	SRR7717283
BZ11-040	leukocyte	Chunga	Kinda	SRR7717282
BZ11-041	leukocyte	Chunga	Kinda	SRR7717321
BZ11-042	leukocyte	Chunga	Kinda	SRR7717322
BZ11-043	FTA blood spot	Chunga	Kinda	SRR7717319
BZ11-045	leukocyte	Chunga	Kinda	SRR7717320
BZ11-046	FTA blood spot	Chunga	Kinda	SRR7717317
BZ11-047	leukocyte	Chunga	Kinda	SRR7717318
BZ11-048	FTA blood spot	Chunga	Kinda	SRR7717315
BZ11-050	leukocyte	Chunga	Kinda	SRR7717316
BZ11-051	FTA blood spot	Chunga	Kinda	SRR7717313
BZ11-052	FTA blood spot	Chunga	Kinda	SRR7717314
BZ11-053	leukocyte	Chunga	Kinda	SRR7717310
BZ11-054	leukocyte	Chunga	Kinda	SRR7717309
BZ11-056	leukocyte	Chunga	Kinda	SRR7717312

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Supplementary Table S1 – continued from previous page

Sample ID	Tissue type	Locality	Ancestry	SRA Accession
BZ11-058	leukocyte	Chunga	Kinda	SRR7717306
BZ11-059	leukocyte	Chunga	Kinda	SRR7717305
BZ11-061	FTA blood spot	Chunga	Kinda	SRR7717308
BZ11-062	FTA blood spot	Chunga	Kinda	SRR7717307
BZ11-063	FTA blood spot	Chunga	Kinda	SRR7717304
BZ11-064	FTA blood spot	Chunga	Kinda	SRR7717303
BZ11-065	FTA blood spot	Chunga	Kinda	SRR7717368
BZ11-066	FTA blood spot	Chunga	Kinda	SRR7717369
BZ11-067	FTA blood spot	Chunga	Kinda	SRR7717370
BZ11-068	FTA blood spot	Chunga	Kinda	SRR7717371
BZ11-070	FTA blood spot	Chunga	Kinda	SRR7717365
BZ11-071	FTA blood spot	Chunga	Kinda	SRR7717366
BZ11-072	FTA blood spot	Chunga	Kinda	SRR7717367
BZ11-073	FTA blood spot	Chunga	Kinda	SRR7717361
BZ11-074	FTA blood spot	Chunga	Kinda	SRR7717362
BZ11-075	FTA blood spot	Chunga	Kinda	SRR7717340
BZ11-076	FTA blood spot	Chunga	Kinda	SRR7717334
BZ07-042	feces	North Nkala Road	chacma	SRR7717329
BZ12-003	plasma	Ngoma Airstrip	chacma	SRR7717341
BZ12-006	plasma	Ngoma Airstrip	chacma	SRR7717338
BZ12-008	plasma	Ngoma Airstrip	chacma	SRR7717360
BZ12-009	plasma	Ngoma Airstrip	chacma	SRR7717344
BZ12-030	plasma	Dendro Park	chacma	SRR7717348
BZ12-031	plasma	Dendro Park	chacma	SRR7717349
BZ12-032	plasma	Dendro Park	chacma	SRR7717346
BZ12-033	plasma	Dendro Park	chacma	SRR7717347
BZ07-029	feces	Nanzhila Plains	chacma	SRR7717328
BZ07-032	feces	Nanzhila Plains	chacma	SRR7717326
BZ07-034	feces	Nanzhila Plains	chacma	SRR7717325
BZ07-004	feces	Choma	chacma	SRR7717356
BZ07-005	feces	Choma	chacma	SRR7717359
BZ07-007	feces	Choma	chacma	SRR7717358
BZ06-218	feces	Lower Zambezi National Park	chacma	SRR7717351
BZ06-220	feces	Lower Zambezi National Park	chacma	SRR7717350
BZ06-221	feces	Lower Zambezi National Park	chacma	SRR7717353
BZ06-225	feces	Lower Zambezi National Park	chacma	SRR7717355
BZ06-227	feces	Lower Zambezi National Park	chacma	SRR7717354

Supplementary Table S2: Full list of genes with significant F_{ST} ($p_{F_{ST}} < 0.05$) prior to correction for multiple testing.

Gene	F_{ST}	$p_{F_{ST}}$
<i>ABCC6</i>	0.29510	0.03379
<i>ADAM19</i>	0.46159	0.04911
<i>AFDN</i>	0.31298	0.01436
<i>AHCTF1</i>	0.41161	0.02608
<i>ALDH7A1</i>	0.32752	0.03378
<i>ALLC</i>	0.31691	0.02241
<i>ALMS1</i>	0.40316	0.00149
<i>ALPK2</i>	0.23213	0.03372
<i>AQP7</i>	0.31983	0.02067
<i>ARCNI</i>	0.26019	0.00734
<i>ATP9B</i>	0.26107	0.02414
<i>ATXN2</i>	0.84882	0.00003
<i>BCAS3</i>	0.57289	0.02749
<i>BCL9L</i>	0.90226	0.00153
<i>BMP7</i>	0.25936	0.00059
<i>C16orf62</i>	0.36272	0.00939
<i>CACNA1D</i>	0.52348	0.03682
<i>CACNA2D4</i>	0.55962	0.02934
<i>CAPN9</i>	0.27515	0.01603
<i>CD226</i>	0.24492	0.00979
<i>CFAP46</i>	0.39592	0.03196
<i>CHST11</i>	0.32745	0.00345
<i>CIB3</i>	0.30536	0.02744
<i>COL27A1</i>	0.57369	0.00249
<i>COPG2</i>	0.51315	0.03892
<i>CTRC</i>	0.58200	< 0.00001
<i>DENND6B</i>	0.56703	0.00256
<i>DIS3L2</i>	0.27283	0.02388
<i>DNA2</i>	0.46812	0.04726
<i>DNER</i>	0.27585	0.04829
<i>DPP6</i>	0.20804	0.04012
<i>ECE2</i>	0.83854	0.00330
<i>EDIL3</i>	0.37468	0.04026
<i>EFHD2</i>	0.58200	< 0.00001
<i>EHD2</i>	0.39810	0.03011
<i>EP300</i>	0.41123	0.02664
<i>EPB41L4B</i>	0.38656	0.03501
<i>ESRRB</i>	0.24742	0.04475
<i>ETV7</i>	0.39259	0.03271
<i>FAF2</i>	0.71554	0.01160
<i>FAM149A</i>	0.24276	0.00791
<i>FAM210A</i>	0.73778	0.01023
<i>FAM3D</i>	0.31282	0.02341
<i>FBRS1</i>	0.64186	0.01737
<i>FBXO10</i>	0.28294	0.02814
<i>FCHSD2</i>	0.46819	0.04708
<i>FDXR</i>	0.93147	0.00050
<i>FGF1</i>	0.66769	0.00004
<i>FLII</i>	0.46240	0.04869
<i>FNTA</i>	0.49563	0.04092
<i>FTO</i>	0.33726	0.02929
<i>GAS6</i>	0.31437	0.00045

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Gene	F_{ST}	$p_{F_{ST}}$
<i>GGNBP2</i>	0.22363	0.03609
<i>GLCC11</i>	0.57015	0.02784
<i>GRAMD1B</i>	0.28781	0.01144
<i>GRM1</i>	0.53937	0.03379
<i>GTF3C1</i>	0.46246	0.04879
<i>H2AFY2</i>	0.22263	0.04506
<i>HSPG2</i>	0.34571	0.00094
<i>HTRA1</i>	0.22455	0.02425
<i>IK</i>	0.79478	0.00539
<i>IP6K1</i>	0.35887	0.04662
<i>IPO9</i>	0.85115	0.00291
<i>IQSEC1</i>	0.38822	0.03422
<i>IQSEC3</i>	0.20883	0.01999
<i>KCNK13</i>	0.49790	0.04120
<i>KDM2A</i>	0.44769	0.01671
<i>KMT2C</i>	0.41598	0.02534
<i>KMT5B</i>	0.44284	0.01807
<i>LAMP3</i>	0.36783	0.00367
<i>LCMT1</i>	0.47434	0.00262
<i>LDLR</i>	0.22747	0.02134
<i>LLGL2</i>	0.47763	0.01119
<i>LPP</i>	0.25330	0.03910
<i>LRP11</i>	0.64726	0.01656
<i>LSM12</i>	0.52516	0.03500
<i>LY96</i>	0.42064	0.00678
<i>MAD1L1</i>	0.26257	0.00400
<i>MED13L</i>	0.29158	0.01028
<i>MED20</i>	0.24371	0.02413
<i>MEGF11</i>	0.19554	0.01331
<i>MOB3B</i>	0.32995	0.00299
<i>MTCL1</i>	0.19511	0.02164
<i>MTO1</i>	0.42405	0.00642
<i>MYL1</i>	0.41734	0.00747
<i>MYO7B</i>	0.39156	0.01150
<i>MYO9B*</i>	0.58992	0.02486
<i>NAA35</i>	0.22633	0.02278
<i>NCOR2</i>	0.59053	0.00209
<i>NDUFS8</i>	0.28450	0.01752
<i>NMUR1</i>	0.26947	0.03795
<i>NOL10</i>	0.32559	0.00224
<i>NTNG2</i>	0.26701	0.00112
<i>NTRK3</i>	0.29037	0.00293
<i>NUDT7</i>	0.28728	0.03905
<i>NUGGC</i>	0.47754	0.01010
<i>NUP93</i>	0.23881	0.04300
<i>ODC1</i>	0.29926	0.00502
<i>ODF2</i>	0.68581	0.01385
<i>PACSI</i>	0.33250	0.00289
<i>PANK2</i>	0.76970	0.00787
<i>PATJ</i>	0.68590	0.01376
<i>PCDH7</i>	0.71470	0.01159
<i>PCID2</i>	0.97146	0.00033
<i>PDGFRL</i>	0.48296	0.04418
<i>PERP</i>	0.24191	0.03173
<i>PHC3</i>	0.67413	0.01424

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Gene	F_{ST}	$p_{F_{ST}}$
<i>PLAUR</i>	0.22857	0.03708
<i>PLEKHA5</i>	0.32369	0.01197
<i>PRDM10</i>	0.62931	0.01903
<i>PRKCE</i>	0.26969	0.00016
<i>PRRC2A</i>	0.33359	0.03057
<i>PTEN</i>	0.78622	0.00603
<i>PUM3</i>	0.78612	0.00612
<i>PYDC1</i>	0.51555	0.03711
<i>RAB11FIP4</i>	0.38858	0.03391
<i>RAD51</i>	0.36802	0.04253
<i>RBFOX1</i>	0.47494	0.01168
<i>RBM33</i>	0.26127	0.04292
<i>RFC5</i>	0.36285	0.04428
<i>RFX4</i>	0.34189	0.00013
<i>RHBDF2</i>	0.36213	0.00897
<i>RPS6KA2</i>	0.21401	0.04906
<i>RUNDC1</i>	0.91873	0.00070
<i>RYR1</i>	0.38968	0.03413
<i>SCO1</i>	0.64062	0.01769
<i>SDR42E2</i>	0.47514	0.04549
<i>SETD3</i>	0.40980	0.02626
<i>SLC24A3</i>	0.45728	0.00364
<i>SLC45A1</i>	0.47461	0.04562
<i>SLC6A13</i>	0.35348	0.04959
<i>SPHKAP</i>	0.26428	0.02997
<i>SRCAP</i>	0.20734	0.04156
<i>SRGN</i>	0.51940	0.03680
<i>ST8SIA1</i>	0.46287	0.04803
<i>SYT9</i>	0.29371	0.00615
<i>TET3</i>	0.50453	0.03953
<i>TF</i>	0.73293	0.01061
<i>TMEFF2</i>	0.31345	0.04249
<i>TMEM178A</i>	0.77110	0.00755
<i>TMPRSS9</i>	0.54854	0.03136
<i>TNKS</i>	0.40762	0.00892
<i>TRBV6-1</i>	0.30260	0.04972
<i>TRIM62</i>	0.63802	0.01795
<i>TRIM72</i>	0.51555	0.03821
<i>TLL5</i>	0.55135	0.03075
<i>UBAC1</i>	0.53118	0.03537
<i>UBAC2</i>	0.43741	0.01960
<i>UBR3</i>	0.37741	0.00705
<i>UMODL1</i>	0.33847	0.00020
<i>UQCRC2</i>	0.59024	0.02441
<i>URB1</i>	0.22569	0.01335
<i>VAC14</i>	0.51243	0.00138
<i>WBSCR17</i>	0.23422	0.03062
<i>WDFY2</i>	0.90447	0.00129
<i>WNT7B</i>	0.23625	0.03621
<i>WRAP53</i>	0.44955	0.01752
<i>XYLT1</i>	0.22870	0.00975
<i>ZBTB3</i>	0.41557	0.02462
<i>ZDHHC14</i>	0.30653	0.00096
<i>ZFPM2</i>	0.26225	0.04439
<i>ZNF3</i>	0.33029	0.00026

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Gene	F_{ST}	$p_{F_{ST}}$
<i>ZNF485</i>	0.27073	0.00497
<i>ZNF536</i>	0.25102	0.03087
<i>ZNF564</i>	0.60466	0.02290
<i>ZSCAN25</i>	0.43668	0.01962
ENSPANG00000004311	0.74849	0.00012
ENSPANG00000010457	0.61534	0.00159
ENSPANG00000017858	0.22827	0.04616
ENSPANG00000023891	0.30260	0.04967
ENSPANG00000027984	0.65318	0.00010
ENSPANG00000028076	0.27890	0.04559
ENSPANG00000028262	0.61153	0.00001
ENSPANG00000028279	0.42387	0.02326
ENSPANG00000028627	0.42785	0.00637

Supplementary Table S3: Genotype frequencies for genes considered to be strong candidates for differentiation (see Table 2). Genome positions and reference alleles are given for the anubis baboon (Panu2.0) genome. The reference allele for the rhesus macaque (Mmul8.0.1) genome was also obtained using a coordinate translation in liftOver (Kent et al., 2002; Rosenbloom et al., 2015). Where the reference alleles differed between genomes, both alleles are listed with the baboon allele listed first. Asterisks (*) indicate that the coordinate could not be converted to Mmul8.0.1, and the reference allele from rheMac2 (an older assembly) is shown instead. Genotype frequencies are shown for each species in the order: homozygous for reference, heterozygous, homozygous for alternate.

Gene	Position		Differentiation		Allelic variants		Genotype frequencies					
	(Panu2.0)		F_{ST}	$p_{F_{ST}}$	Ref.	Alt.	Kinda			chacma		
<i>ATXN2</i>	chr11	110620892	0.84882	0.00003	G	A	54	13	0	0	0	15
	chr11	110620934	0.84882		A	G	0	13	54	15	0	0
	chr1	17875364	0.61707		C	G	64	2	0	4	3	2
	chr1	17875397	0.71940		T	C	66	0	0	4	3	2
<i>EFHD2</i>	chr1	17875411	0.71940	< 0.00001	T	G	66	0	0	4	3	2
	chr1	17875416	-0.00265		G/A	A	9	57	0	3	3	3
	chr1	17875436	0.71940		C/T	T	66	0	0	4	3	2
	chr1	17875441	0.71940		C	T	66	0	0	4	3	2
<i>FGF1</i>	chr6	136137340	0.23022	0.00004	T/T*	C	12	25	26	0	1	15
	chr6	136137374	0.87739		T/T*	C	62	1	0	2	3	11
	chr6	136137439	0.89546		T/T*	G	62	1	0	1	4	11
	chr13	44855469	0.51137		A/G	G	6	25	36	10	0	1
	chr13	44855470	0.51137		C	G	6	25	36	10	0	1
	chr13	44855471	0.51137		A	G	6	25	36	10	0	1
	chr13	44855507	0.51137		G/C	C	6	25	36	10	0	1
	chr13	44898572	0.71643		A	C	66	0	0	5	4	4
	chr13	44898586	-0.01417		C	T	65	2	0	13	0	0
	chr13	44898587	0.52273		G	A	61	6	0	5	4	4
	chr13	44898613	0.51940		G	A	67	0	0	8	3	2
	chr13	44898617	0.51940		G	A	67	0	0	8	3	2
	chr13	44898696	-0.00921		T	A	63	3	1	13	0	0
<i>PRKCE</i>	chr13	45024148	-0.01925	0.00016	A	C	57	7	1	12	1	0
	chr13	45024166	-0.01605		G	A	62	2	1	13	0	0
	chr13	45024206	0.71375		A	C	65	0	0	5	4	4
	chr13	45024265	-0.01925		C/T	T	57	7	1	12	1	0
	chr13	45053068	0.17177		C	T	68	0	0	12	0	1
	chr13	45053077	0.08873		C	T	67	1	0	12	0	1
	chr13	45053155	0.17177		G	A	68	0	0	12	0	1
	chr13	45053159	0.17177		G	C	68	0	0	12	0	1
	chr13	45053165	0.11253		T	G	44	20	4	13	0	0
	chr13	45150212	0.00257		C	T	55	4	0	16	0	0
	chr13	45150236	-0.01482		C	T	58	1	0	16	0	0

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Supplementary Table S3 – continued from previous page

Gene	Position		Differentiation		Allelic variants		Genotype frequencies					
	(Panu2.0)		F_{ST}	$p_{F_{ST}}$	Ref.	Alt.	Kinda			chacma		
<i>RFX4</i>	chr11	105851669	0.72300		C	T	2	13	51	11	3	0
	chr11	105851730	-0.01749		A	G	65	1	0	14	0	0
	chr11	105870425	0.68939		C	T	65	0	0	5	4	3
	chr11	105870454	-0.01573		C	T	63	2	0	12	0	0
	chr11	105870471	0.44224		C	A	66	0	0	9	1	2
	chr11	105870476	0.09165	0.00013	T	C	44	21	1	12	0	0
	chr11	105870506	0.44224		T	G	66	0	0	9	1	2
	chr11	105870520	0.44224		C	T	66	0	0	9	1	2
	chr11	105870526	0.44224		A	G	66	0	0	9	1	2
	chr11	105870586	0.44224		C	T	66	0	0	9	1	2
	chr11	105870588	0.07881		C	G	48	14	4	12	0	0
<i>UMODL1</i>	chr3	4512016	0.40211		A/T	G	68	1	0	10	0	3
	chr3	4512024	0.46734		T/A	G	69	0	0	10	0	3
	chr3	4512027	0.46734		A/T	G	69	0	0	10	0	3
	chr3	4512050	0.46734		G/C	C	69	0	0	10	0	3
	chr3	4512065	0.06414		C/A	T	52	15	2	13	0	0
	chr3	4512066	0.01904	0.00020	G/C	A	68	1	0	13	0	0
	chr3	4512075	0.00457		C/A	T	63	6	0	13	0	0
	chr3	4512076	0.46734		G/C	A	69	0	0	10	0	3
	chr3	4512080	0.46734		C/G	T	69	0	0	10	0	3
	chr3	4512092	0.46734		A/T	G	69	0	0	10	0	3
	chr3	4512098	0.46734		T/A	C	69	0	0	10	0	3
ENSPANG-00000004311	chr10	86441991	0.74849		G	A	50	16	2	0	1	13
	chr10	86441993	0.74849	0.00012	T	A	50	16	2	0	1	13
ENSPANG-00000027984	chr13	5031394	0.75948		C	G	58	7	2	2	1	12
	chr13	5031410	0.44058	0.00010	G	A	67	0	0	10	3	2
	chr13	5031434	0.75948		T	A	58	7	2	2	1	12
ENSPANG-00000028262	chr1	185450553	0.19649		A	G	65	1	0	13	0	2
	chr1	185450577	0.86013		G	A	66	0	0	3	3	9
	chr1	185450607	0.57834	0.00001	C	T	52	12	2	3	2	9
	chr1	185450667	0.81117		T	C	66	0	0	4	3	7

Supplementary Table S4: Gene Ontology (GO) terms (biological process ontology) with significantly enriched differentiation. Terms that are enriched exhibit an overall shift in $p_{F_{ST}}$. Only terms with $p < 0.05$ are shown here.

Accession	Name	GO term	Enrichment (p -value)
GO:0045598	regulation of fat cell differentiation		0.00009
GO:0015850	organic hydroxy compound transport		0.00062
GO:0048639	positive regulation of developmental growth		0.00099
GO:0045839	negative regulation of mitotic nuclear division		0.00130
GO:0061448	connective tissue development		0.00222
GO:0050772	positive regulation of axonogenesis		0.00230
GO:0001936	regulation of endothelial cell proliferation		0.00357
GO:0031667	response to nutrient levels		0.00383
GO:0050680	negative regulation of epithelial cell proliferation		0.00431
GO:0048589	developmental growth		0.00826
GO:0002062	chondrocyte differentiation		0.00864
GO:0006816	calcium ion transport		0.00927
GO:0000122	negative regulation of transcription by RNA polymerase II		0.01012
GO:0034968	histone lysine methylation		0.01084
GO:0051051	negative regulation of transport		0.01102
GO:0097035	regulation of membrane lipid distribution		0.01320
GO:0046677	response to antibiotic		0.01501
GO:0035264	multicellular organism growth		0.01546
GO:0051345	positive regulation of hydrolase activity		0.01546
GO:0051304	chromosome separation		0.01547
GO:0051896	regulation of protein kinase B signaling		0.01583
GO:0051209	release of sequestered calcium ion into cytosol		0.01590
GO:0007600	sensory perception		0.01612
GO:1901565	organonitrogen compound catabolic process		0.01622
GO:0043062	extracellular structure organization		0.01628
GO:0010717	regulation of epithelial to mesenchymal transition		0.01635
GO:0061136	regulation of proteasomal protein catabolic process		0.01748
GO:0090630	activation of GTPase activity		0.01779
GO:0006413	translational initiation		0.01833
GO:0090316	positive regulation of intracellular protein transport		0.01949
GO:0010001	glial cell differentiation		0.02024
GO:0045444	fat cell differentiation		0.02044
GO:0001659	temperature homeostasis		0.02143
GO:0051240	positive regulation of multicellular organismal process		0.02185
GO:0072006	nephron development		0.02412
GO:0051983	regulation of chromosome segregation		0.02472
GO:0007417	central nervous system development		0.02552
GO:0062012	regulation of small molecule metabolic process		0.02644
GO:0009636	response to toxic substance		0.02648
GO:0035148	tube formation		0.02723
GO:0006259	DNA metabolic process		0.02780
GO:0051054	positive regulation of DNA metabolic process		0.02968
GO:1901991	negative regulation of mitotic cell cycle phase transition		0.03032
GO:0000070	mitotic sister chromatid segregation		0.03134
GO:0008361	regulation of cell size		0.03193
GO:0030307	positive regulation of cell growth		0.03522
GO:0048259	regulation of receptor-mediated endocytosis		0.03574
GO:0120161	regulation of cold-induced thermogenesis		0.03639
GO:0048675	axon extension		0.03649
GO:0015914	phospholipid transport		0.03711

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Accession	Name	GO term	Enrichment (<i>p</i> -value)
GO:0048878	chemical homeostasis		0.03773
GO:0010906	regulation of glucose metabolic process		0.03791
GO:0050801	ion homeostasis		0.04018
GO:0051050	positive regulation of transport		0.04124
GO:0031328	positive regulation of cellular biosynthetic process		0.04193
GO:0080090	regulation of primary metabolic process		0.04213
GO:0000724	double-strand break repair via homologous recombination		0.04321
GO:0001568	blood vessel development		0.04374
GO:1901361	organic cyclic compound catabolic process		0.04429
GO:0050921	positive regulation of chemotaxis		0.04542
GO:0007411	axon guidance		0.04563
GO:0050796	regulation of insulin secretion		0.04675
GO:0097306	cellular response to alcohol		0.04691
GO:0006302	double-strand break repair		0.04760
GO:0032956	regulation of actin cytoskeleton organization		0.04812
GO:0006939	smooth muscle contraction		0.04881

Supplementary Table S5: F_{ST} and p values of genes in the CCKR signaling pathway. Genome positions are given for the anubis baboon (Panu2.0) genome.

Gene	Position	F_{ST}	$p_{F_{ST}}$	BH-adjusted $p_{F_{ST}}$
<i>GNBI</i>	chr1 4724905-4839528	0.12757	0.34870	> 0.99999
<i>ODCI</i>	chr1 33711839-33721404	0.29926	0.00502	0.27773
<i>FOXO3</i>	chr4 153548329-153654266	0.02159	0.87560	> 0.99999
<i>PIK3R1</i>	chr6 63980911-64062226	0.05827	0.76380	> 0.99999
<i>LYN</i>	chr8 51971047-52057050	0.12235	0.46480	> 0.99999
<i>PTEN</i>	chr9 80021075-80056543	0.78622	0.00603	0.30886
<i>PRKCE</i>	chr13 44756709-45175428	0.26969	0.00016	0.03934
<i>TPCN2</i>	chr14 5295886-5334864	0.22514	0.06081	0.65791
<i>GUCY2D</i>	chr16 7707896-7725235	0.07230	0.61890	> 0.99999
<i>AKAP1</i>	chr16 38017354-38051906	0.02482	0.70890	> 0.99999
<i>STAT3</i>	chr16 48978970-49012645	0.11931	0.36770	> 0.99999
<i>FOXO1</i>	chr17 19194223-19301111	0.17917	0.22320	0.95342
<i>MAP2K2</i>	chr19 3900243-3938641	0.24289	0.08564	0.76623
<i>RYR1</i>	chr19 32699970-32857343	0.38968	0.03413	0.58253

Supplementary Table S6: Genotype frequencies for all components and genes in the JAK/STAT signaling pathway with identified variants in our dataset. Genome positions and reference alleles are given for the anubis baboon (Panu2.0) genome. The reference allele for the rhesus macaque (Mmul8.0.1) genome was also obtained using a coordinate translation in liftOver (Kent et al., 2002; Rosenbloom et al., 2015). Where the reference alleles differed between genomes, both alleles are listed with the baboon allele listed first. Genotype frequencies are shown for each species in the order: homozygous for reference, heterozygous, homozygous for alternate.

Component	Gene	Position		Differentiation		Allelic variants		Genotype frequencies					
		(Panu2.0)		F_{ST}	$p_{F_{ST}}$	Ref.	Alt.	Kinda			chacma		
JAK	<i>JAK1</i>	chr1	66951070	0.07908	0.14740	A	C	65	0	0	18	0	1
		chr1	66951074	0.07908		C	A	65	0	0	18	0	1
		chr1	66951078	0.07908		C	G	65	0	0	18	0	1
		chr1	66951082	0.59910		T/C	C	0	3	62	6	7	6
PIAS	<i>PIAS1</i>	chr7	42548519	0.39690	0.06619	A	T	54	12	2	4	4	5
	<i>PIAS4</i>	chr19	3844945	0.21996	0.17450	C	T	67	0	0	12	3	0
STAT	<i>STAT3</i>	chr16	48997534	0.11931	0.36770	C	T	59	0	0	14	2	0