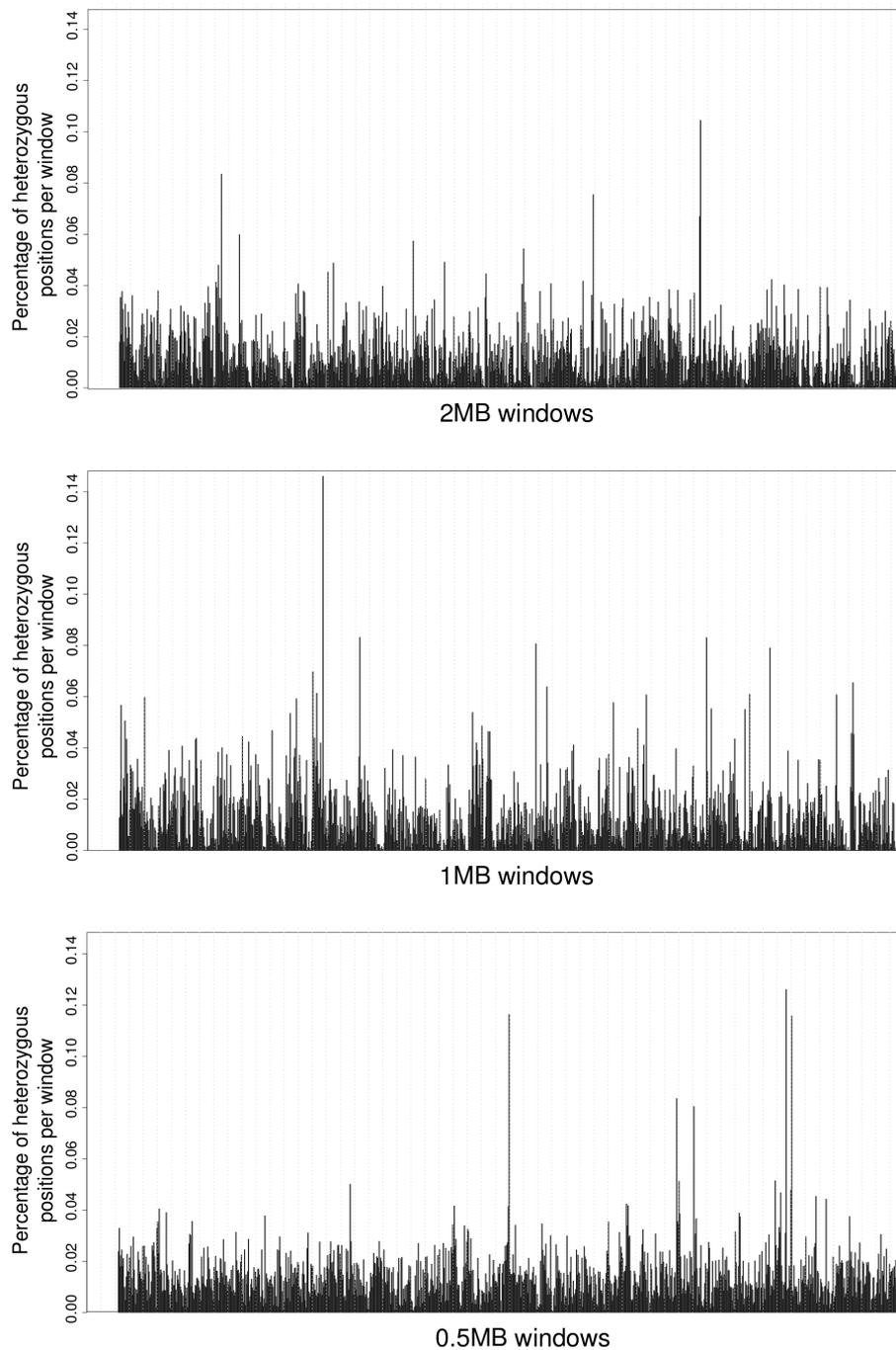
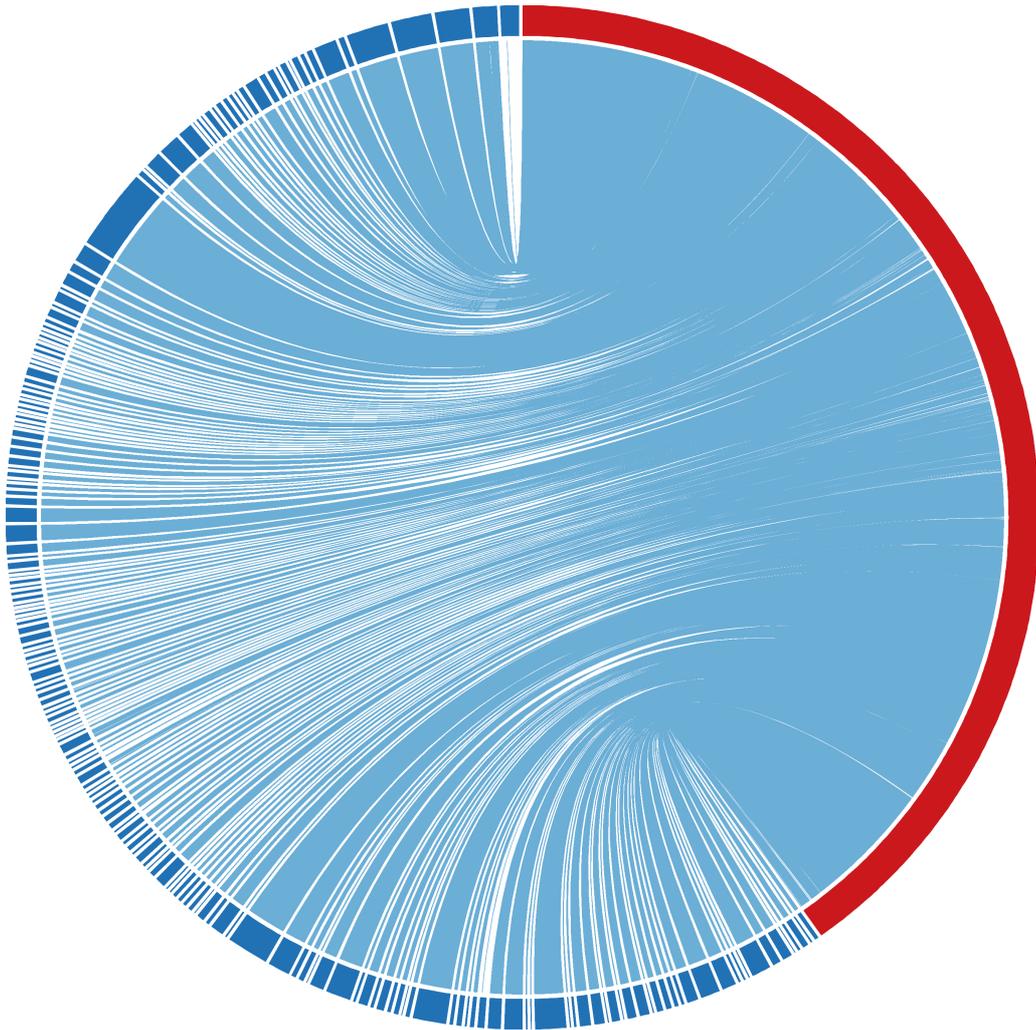


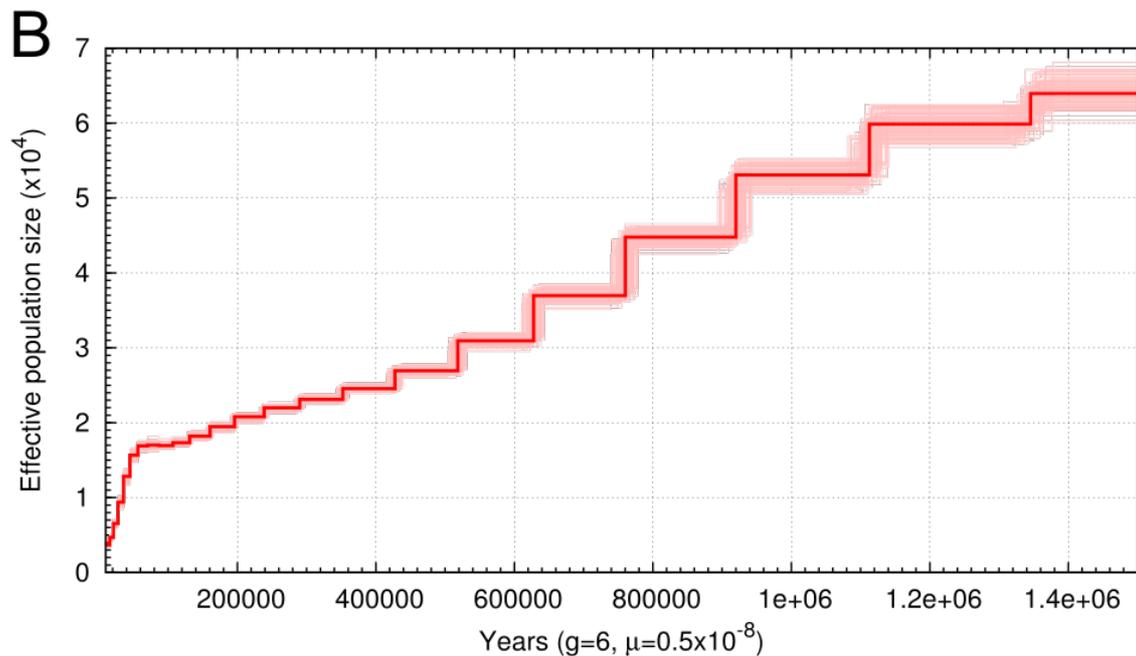
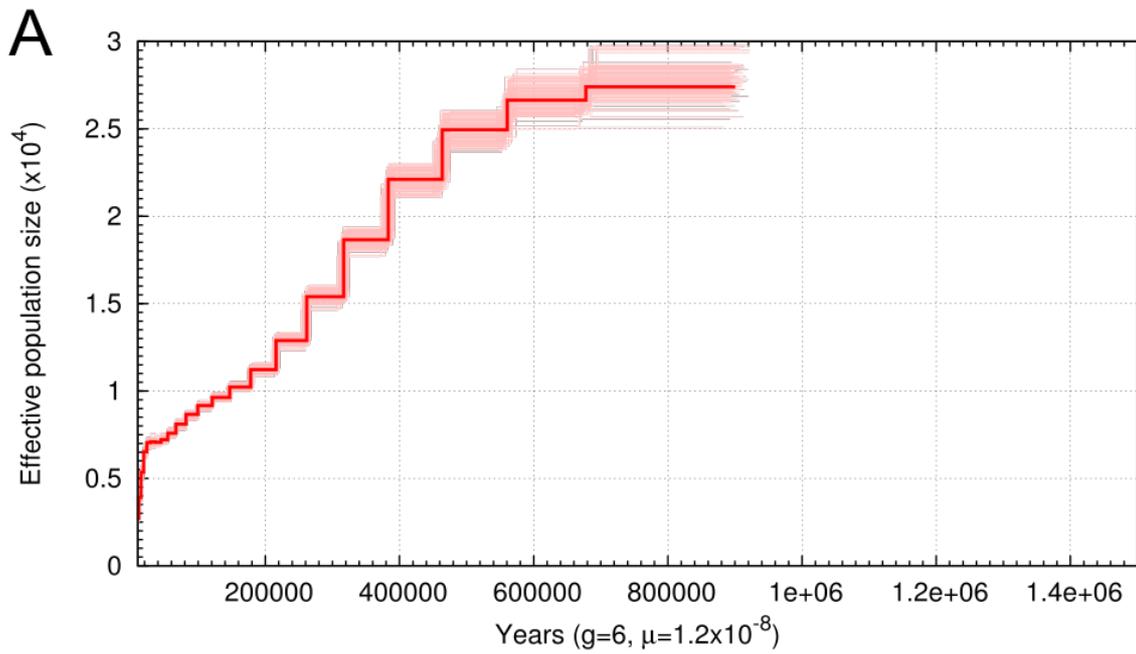
## Supplemental figures



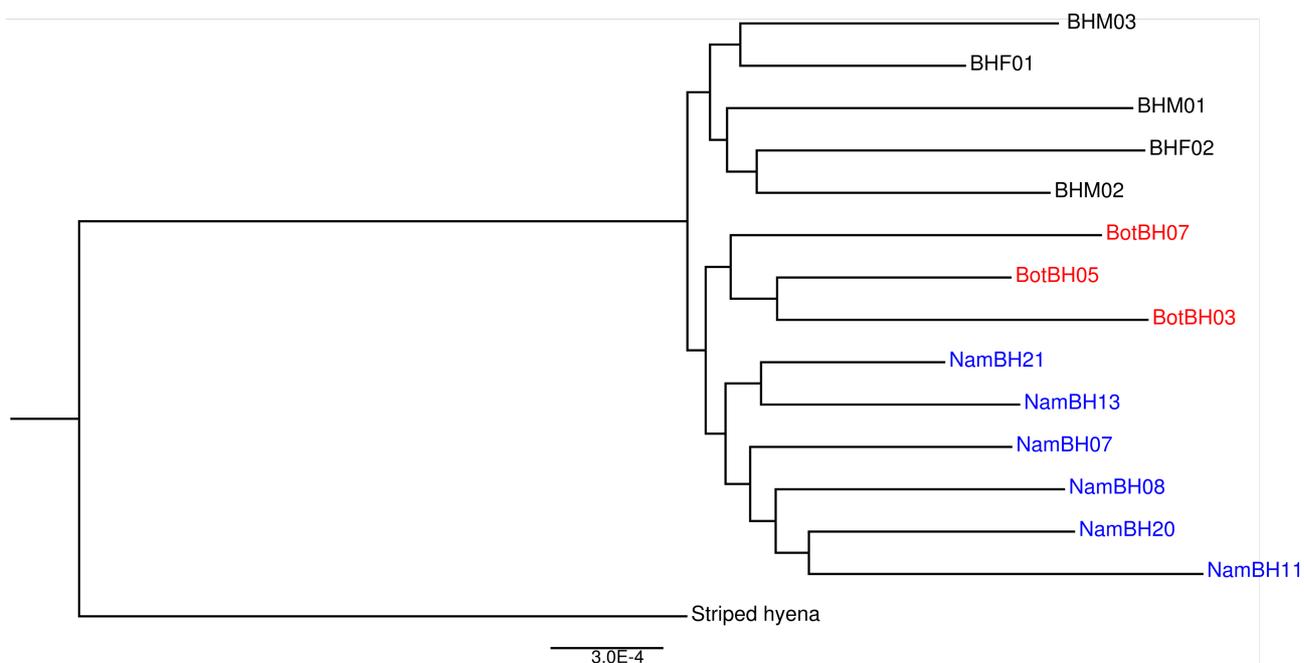
**Supplemental figure S1.** Non-overlapping sliding window analysis of heterozygosity across the captive brown hyena nuclear genome using window sizes of 2Mbp, 1Mbp and 0.5Mbp. Each graph consists of 2000 windows. The Y axis indicates the percentage of the window made up of heterozygous positions. The X axis indicates the window. No considerable stretches of homozygosity can be seen suggesting a lack of inbreeding in this individual.



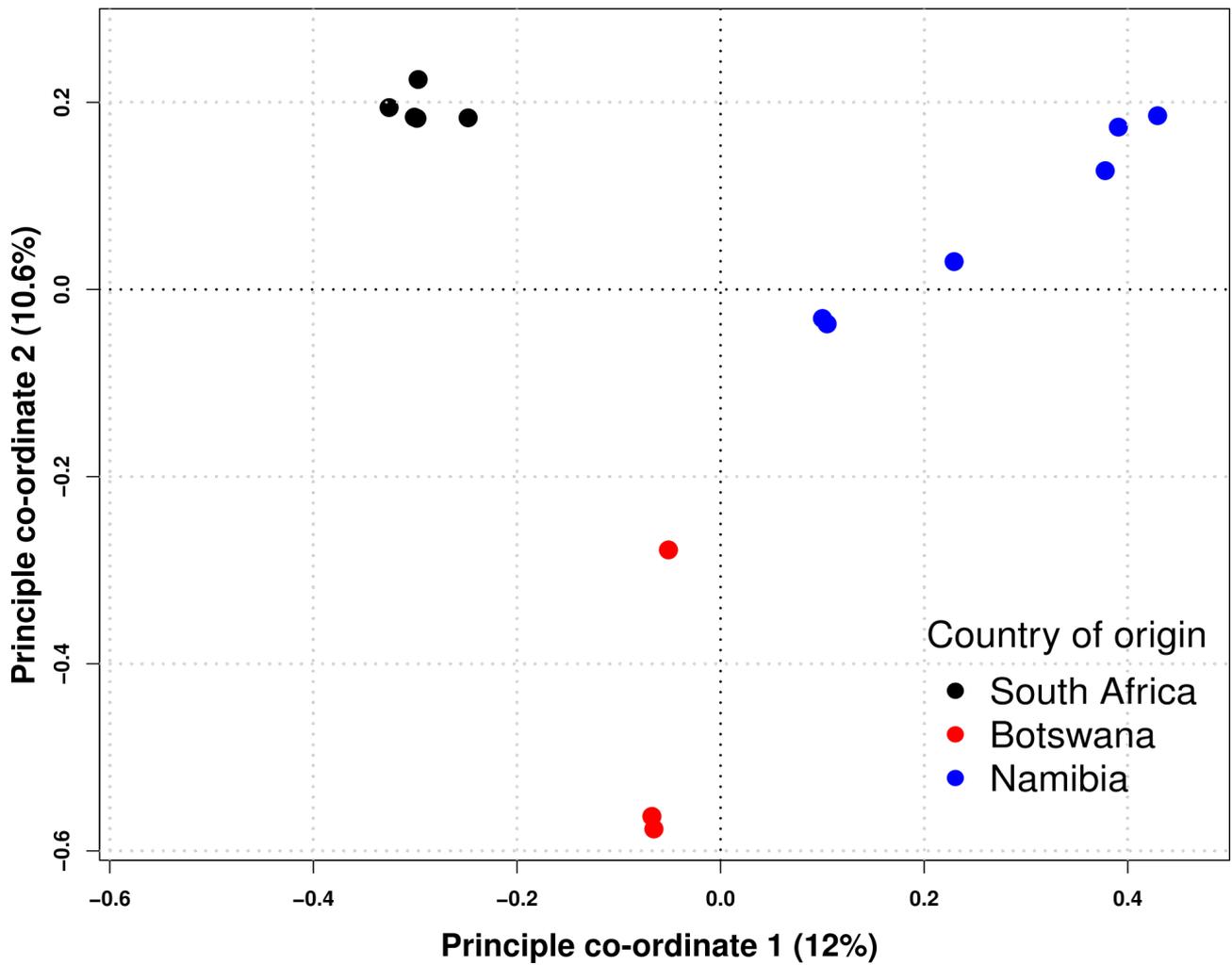
**Supplemental figure S2.** Circos plot of the cat X chromosome (red) and the corresponding scaffolds in the brown hyena (blue). Most of the cat X chromosome is covered by the brown hyena.



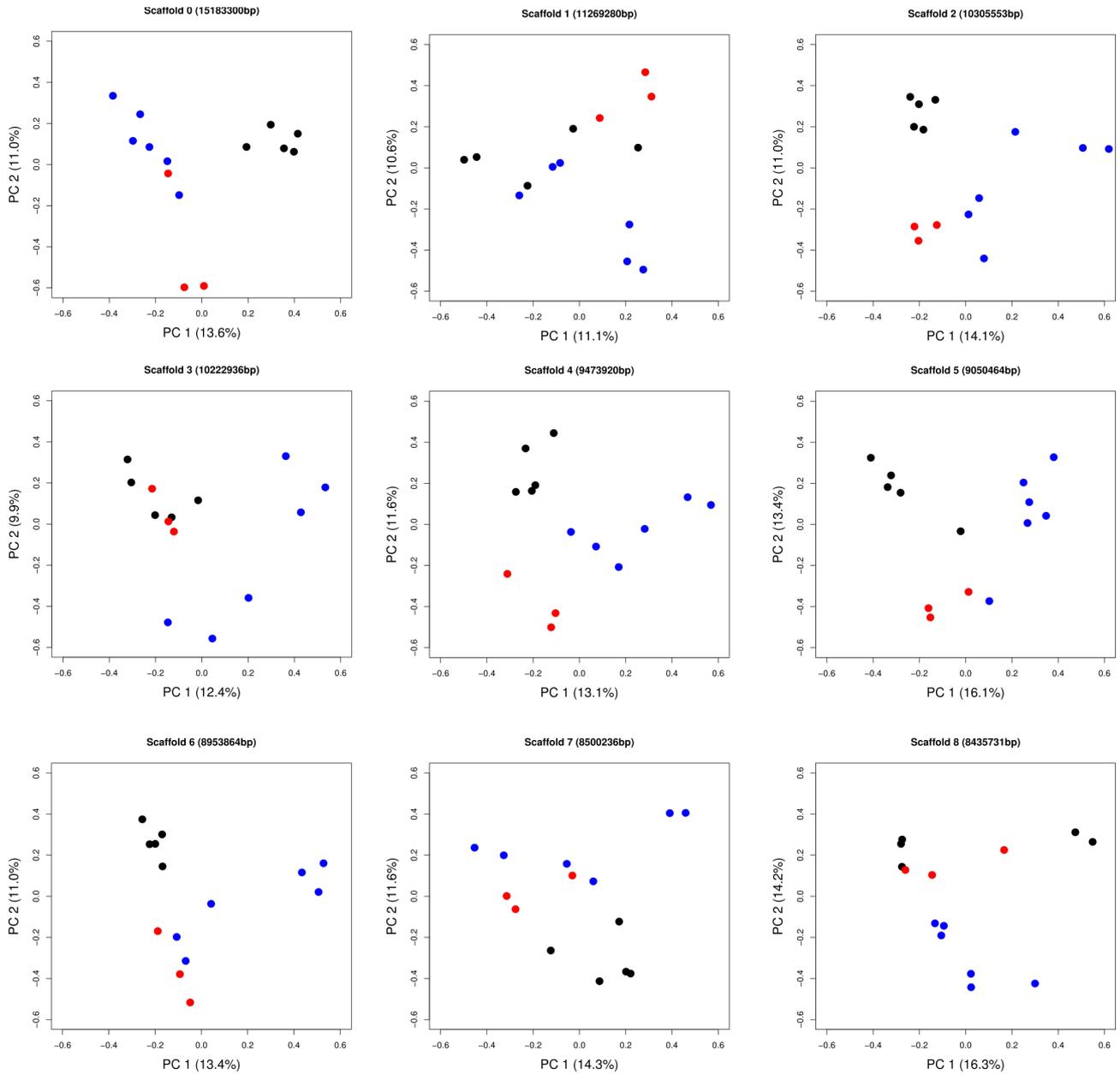
**Supplemental figure S3.** PSMC analyses utilising different per generation mutation rates calculated from the 95% confidence interval of the brown and striped hyena divergence date. A) PSMC plot using a per generation mutation rate calculated assuming a brown and striped hyena divergence date of 2.6mya. B) PSMC plot using a per generation mutation rate calculated assuming a brown and striped hyena divergence date of 6.4mya.  $g$  shows generation time and  $\mu$  shows mutation rate per generation.



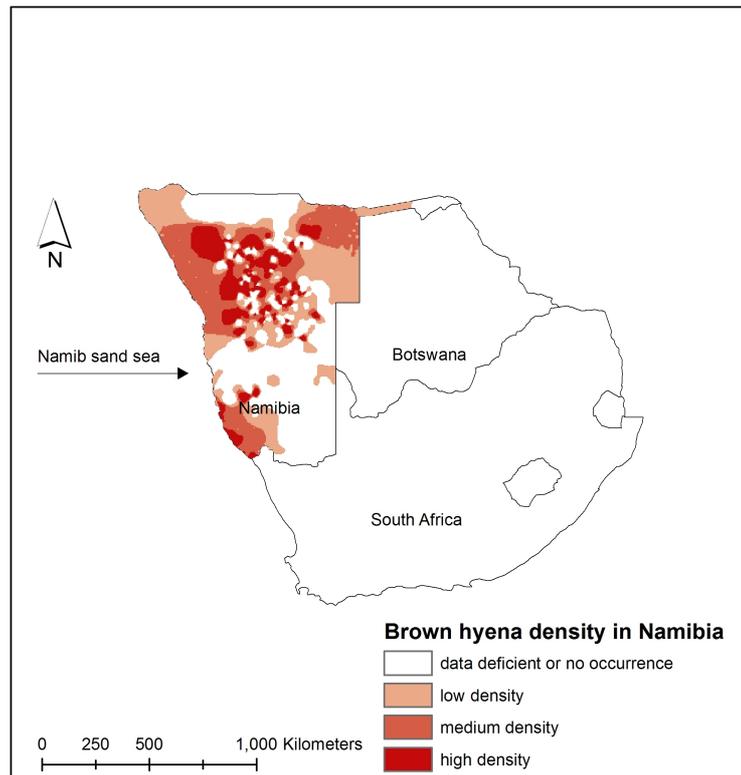
**Supplemental figure S4.** Wild caught brown hyena maximum likelihood tree rooted using the Striped hyena. Different colours represent the country of origin of the samples (blue - Namibia, red - Botswana, black - South Africa). Scale bar indicates substitutions per site.



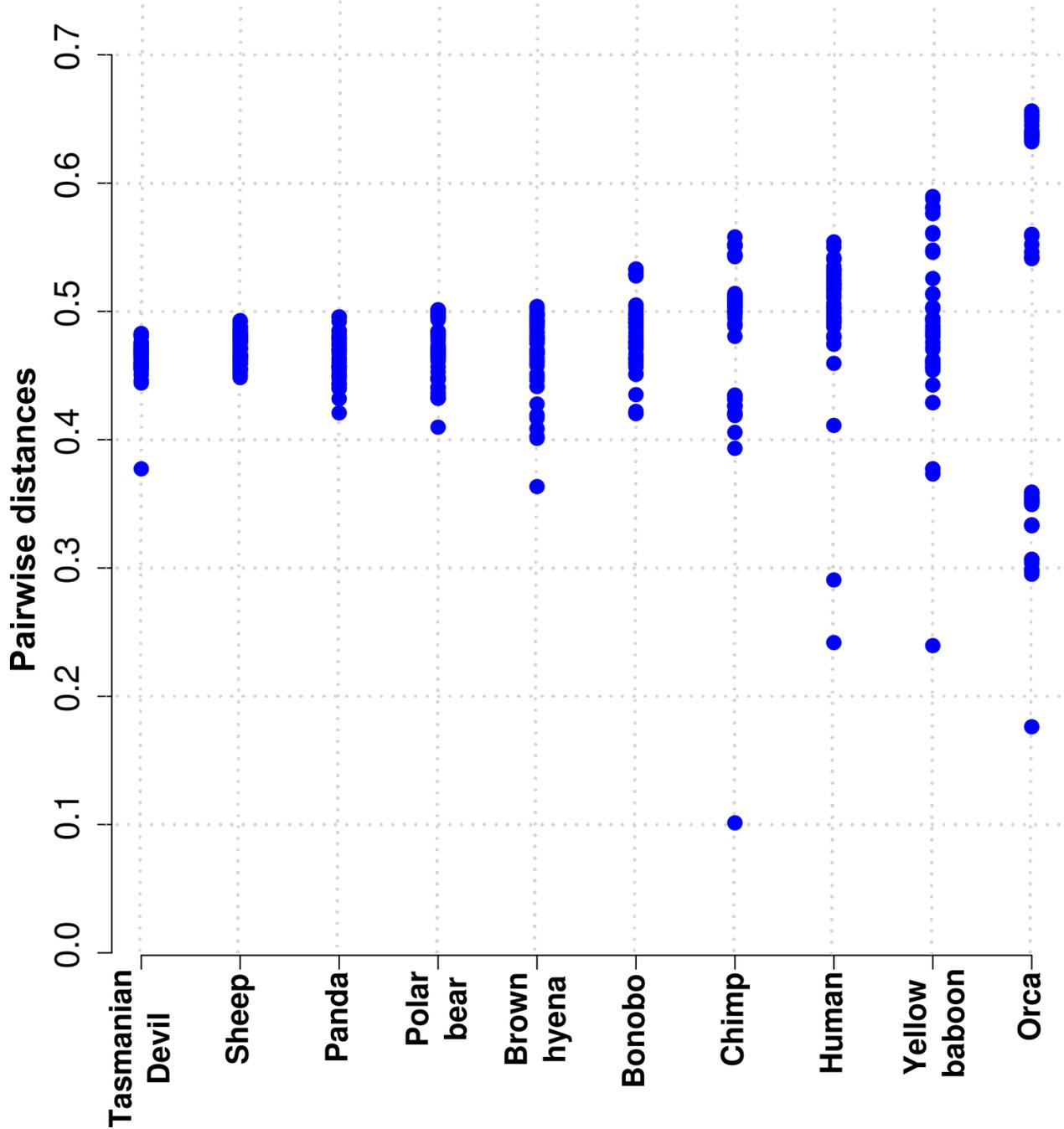
**Supplemental figure S5.** Principal components analysis produced using single site identity by state comparisons of the 14 wild caught brown hyena individuals in this study. Colours represent country of origin (black - South Africa, blue - Namibia, red - Botswana). Percentages on the X and Y axis represent the percentage of variance explained by each respective component. Results found here are consistent with those calculated using genotype likelihoods.



**Supplemental figure S6.** Single scaffold principal components analysis produced using single site identity by state comparisons of the 14 wild caught brown hyena individuals. Colours represent country of origin (black - South Africa, blue - Namibia, red - Botswana). Percentages on the X and Y axis represent the percentage of variance explained by each respective component. Size of scaffolds in base pairs can be seen in each respective main label. These plots do generally support some phylogeographic structure but individuals from different regions partially intermingle in a number of plots suggesting that there is not enough power in these single scaffolds to resolve phylogeographic structure in these cases.



**Supplemental figure S7.** Observed brown hyena density found across Namibia. Differing intensities of red correspond to the brown hyena density in that location. Distribution patterns within Namibia show a lack of overlap between individuals from Southern Namibia and Northern Namibia.



**Supplemental figure S8.** Comparative population structure analyses performed using single base identity by state comparisons while removing singletons. The Y axis indicates pairwise differences while the X axis shows the species. Each point on the plot represents a single pairwise comparison.

## Supplemental tables

**Supplemental table S1.** Striped hyena *de novo* assembly contig/scaffold statistics.

Contig N50	82579
Scaffold N50	2001328
GC %	41.56
Longest scaffold (bp)	15183300
Assembly length (bp)	2374721933
Number of contigs	54939
Number of scaffolds	5760

**Supplemental table S2.** Striped hyena *de novo* assembly BUSCO scores calculated using the Eukaryote and Mammalian BUSCO databases.

	Eukaryote BUSCO scores	Mammalian BUSCO scores
Complete BUSCOs	271	3835
Complete Single-Copy BUSCOs	262	3807
Complete Duplicated BUSCOs	9	28
Fragmented BUSCOs	10	165
Missing BUSCOs	22	104
Total BUSCO groups searched	303	4104

**Supplemental table S3.** Brown hyena sample location and sample type details. \* Indicates these individuals have approximate sample locations.

Codename	Country of Origin	Sample type	latitude	longitude
BHF1*	South Africa	Hair	-33.124584	26.537708
BHF2*	South Africa	Hair	-33.124584	26.537708
BHM1*	South Africa	Hair	-33.124584	26.537708
BHM2*	South Africa	Hair	-33.124584	26.537708
BHM3*	South Africa	Hair	-33.124584	26.537708
NamBH11	Namibia	Blood	-27.608632	15.497852
NamBH13*	Namibia	Blood	-22.79169	14.549477
NamBH20	Namibia	Blood	-26.680351	15.163507
NamBH21*	Namibia	Blood	-20.85327	16.647978
NamBH7	Namibia	Blood	-27.349512	15.912735
NamBH8	Namibia	Blood	-26.99631	15.650119
BotBH3*	Botswana	Tissue	-20.46989	25.12184
BotBH5*	Botswana	Tissue	-20.46989	25.12184
BotBH7*	Botswana	Tissue	-20.46989	25.12184
BH_Love	Tierpark Berlin	Blood		

**Supplemental table S4.** Brown hyena mapping statistics when mapping to the striped hyena nuclear and our reconstructed brown hyena mitochondrial genome.

Codename	Total SE reads after merging and adapter trimming	Unique reads mapped to nuclear genome	bp mapped to nuclear genome	Average coverage	Unique reads mapped to mitochondrial genome	bp mapped to mitochondrial genome	Average coverage
BHF1	64422612	47254713	7363724523	3.100	35110	5776562	335.905
BHF2	38641444	33331195	4975565124	2.095	18976	2850634	165.763
BHM1	49209478	43764811	6384610509	2.688	27345	4048045	235.393
BHM2	52780882	45508271	6744127558	2.839	33391	5084205	295.645
BHM3	53172160	46297247	6833441946	2.877	37079	5684861	330.573
NamBH11	52544400	42170064	6641423313	2.796	23041	3784082	220.043
NamBH13	68581118	56379724	8728844324	3.675	19598	3042953	177.132
NamBH20	55366276	43635935	6874142712	2.894	26319	4230429	245.998
NamBH21	90758418	48688930	7181669430	3.024	20916	3194780	185.948
NamBH7	65777674	50924181	8248476080	3.473	24683	4154046	241.556
NamBH8	63671350	47951458	7818176024	3.292	23623	4002347	232.735
BotBH3	38007734	31490650	4912299215	2.068	38406	6549645	380.860
BotBH5	63924040	52012046	8162041861	3.437	49010	8838756	513.971
BotBH7	54158322	43563771	6920001119	2.914	17771	2878601	167.390
BH_Love	881114120	632326566	97757690887	41.165			

**Supplemental table S5.** List of the numerical IDs of the scaffolds that successfully aligned to the cat X chromosome (CM001396.2) via synteny.

Striped hyena scaffolds aligning to the cat X chromosome
12, 77, 80, 85, 142, 147, 162, 243, 259, 295, 297, 318, 348, 351, 376, 383, 402, 451, 470, 524, 536, 555, 556, 576, 610, 611, 658, 669, 701, 744, 754, 758, 765, 808, 840, 844, 853, 865, 917, 924, 929, 932, 960, 982, 986, 1017, 1019, 1025, 1051, 1070, 1091, 1114, 1115, 1112, 1157, 1130, 1158, 1163, 1165, 1171, 1178, 1181, 1182, 1188, 1217, 1219, 1211, 1230, 1257, 1259, 1254, 1272, 1269, 1292, 1295, 1299, 1318, 1340, 1333, 1349, 1358, 1386, 1388, 1420, 1414, 1421, 1450, 1443, 1461, 1463, 1468, 1471, 1488, 1512, 1508, 1517, 1531, 1547, 1539, 1549, 1567, 1578, 1588, 1615, 1609, 1620, 1635, 1640, 1629, 1630, 1660, 1667, 1677, 1701, 1688, 1705, 1712, 1713, 1765, 1749, 1776, 1789, 1792, 1814, 1825, 1815, 1837, 1849, 1843, 1844, 1845, 1860, 1884, 1881, 1876, 1877, 1879, 1891, 1897, 1898, 1903, 1929, 1955, 1964, 1961, 1974, 2000, 1984, 1995, 1994, 2044, 2022, 2047, 2061, 2054, 2062, 2093, 2098, 2100, 2112, 2111, 2116, 2120, 2125, 2164, 2193, 2183, 2187, 2203, 2221, 2209, 2217, 2226, 2236, 2248, 2261, 2271, 2306, 2335, 2326, 2333, 2350, 2375, 2376, 2388, 2402, 2404, 2418, 2464, 2542, 2557, 2605, 2672, 2719, 3002

**Supplemental table S6.** Accession numbers for the raw reads from the low coverage genomes used in the population structure comparison and the accession number for the reference these were mapped against.

Species	Accession numbers	Reference sequence
Human ( <i>Homo sapien</i> )	ERR010982, ERR010985, ERR010989, ERR010992, ERR011001, ERR011008, ERR019683, ERR019684, ERR019688, ERR033733	PRJNA31257
Sheep ( <i>Ovis aries</i> )	SRR501839, SRR501846, SRR501849, SRR501856, SRR501860, SRR501864, SRR501870, SRR501877, SRR501896, SRR501910	GCA_000005525
Yellow baboon ( <i>Papio cynocephalus</i> )	SRR3151894, SRR3151901, SRR3151905, SRR3151907, SRR3151909, SRR3151922, SRR3151925, SRR3151931, SRR3151932, SRR3151936	AHZZ00000000.2
Polar bear ( <i>Ursus maritimus</i> )	SRR827537, SRR827574, SRR827584, SRR827585, SRR827587, SRR827600, SRR942195, SRR942202, SRR942223, SRR942231	PRJNA210951
Panda ( <i>Ailuropoda melanoleuca</i> )	SRR504865, SRR504868, SRR504877, SRR504884, SRR504885, SRR504888, SRR504893, SRR504895, SRR504900, SRR504904	GCA_000004335
Bonobo ( <i>Pan paniscus</i> )	ERR032963, SRR740773, SRR740792, SRR740800, SRR740807, SRR740821, SRR740823, SRR740833, SRR740941, SRR741276	GCA_000258655.2
Orca ( <i>Orcinus orca</i> )	ERR637310, ERR637314, ERR637317, ERR637322, ERR637329, ERR637332, ERR637336, ERR637344, ERR637347, ERR637352	ANOL000000000
Tasmanian Devil ( <i>Sarcophilus harrisi</i> )	ERR1474982, ERR1474983, ERR1474984, ERR1474985, ERR1474986, ERR789027, ERR789028, ERR789029, ERR789030, ERR789031, ERR789032	GCA_000189315
Chimpanzee ( <i>Pan troglodytes</i> )	ERR032935, ERR032936, ERR032939, ERR032940, ERR032943-ERR032948, ERR032947-ERR032952, ERR032958, ERR032959, ERR032960, ERR032961	GCA_000001515.5

**Supplemental table S7:** Accession numbers for the raw reads used in the nuclear genome heterozygosity estimates and the accession code for the reference these were mapped against.

<b>20x coverage genome species</b>	<b>Accession number</b>	<b>Reference</b>
Bonobo	SRR740794-SRR740801	GCA_000258655.2
Chimpanzee	ERR1709871,ERR1709872	GCA_000001515.5
Cheetah	SRR2737512-SRR2737518	GCA_001443585.1
Iberian lynx	ERR1255587-ERR1255590	FIZN00000000.1
Human (African)	SRR1295432	PRJNA31257
Human (European)	SRR1291026	PRJNA31257
Panda	SRR019734-SRR019754	GCA_000004335
Orca	SRR574970-SRR574972,SRR574975	ANOL00000000
Polar bear	SRR933670-SRR933696	PRJNA210951
Yellow baboon	SRR1513473,SRR1513475-SRR1513478	AHZZ00000000.2
Island fox	SRR5198007,SRR5198009	GCF_000002285.3