SUPPLEMENTAL MATERIAL FOR KOEPFLI ET AL.

Figure S1. Pedigree of sable antelope SB#2152 reconstructed using the program Lineage 1.0 ([http://jppollak.com/software.html)](http://jppollak.com/software.html). Only known portions of the pedigree are shown with hypothetical animals excluded. Circles are females and squares are males. Colored boxes indicate individuals involved in three rounds of consanguineous matings including one brother-sister pairing (green) and two parent-offspring pairings (red and blue). These are depicted as reticulations in the pedigree. Photograph shows SB#2152 from the Jackson Zoo, Jackson, Mississippi, USA.

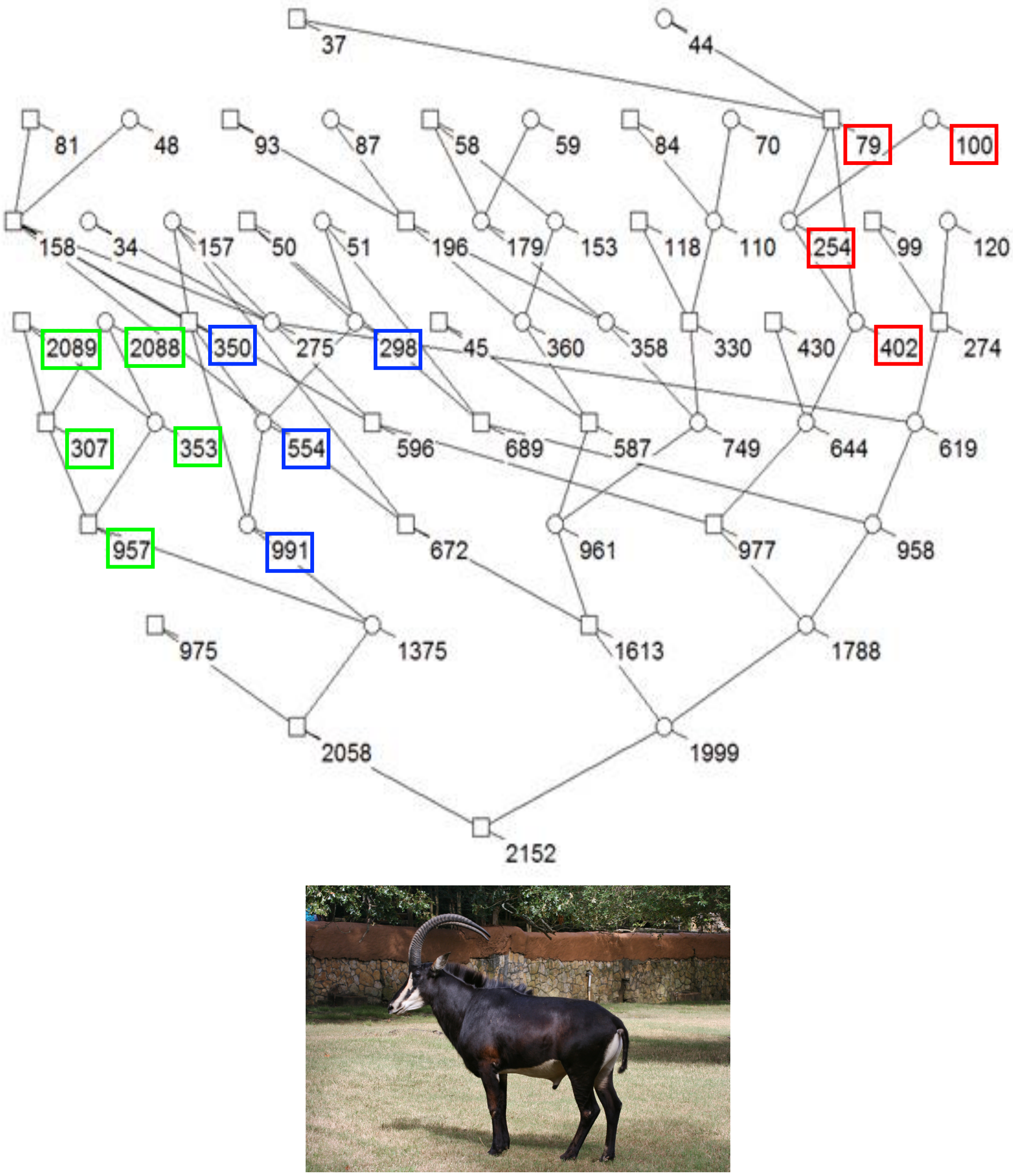

Table S1. Number of sequence reads generated, paired, and mapped from the libraries used for whole genome sequencing or re-sequencing of the eight sable antelope included in this study.

Individual	Library ID	Total reads	Paired in seq.	Mapped	% mapped	Properly paired	% properly paired
SB#2152	HIPNI-shotgun-1	442,370,831	441,109,314	440,315,553	99.54	410,691,642	93.10
SB#2152	HIPNI-shotgun-2	241,356,376	241,029,580	240,567,865	99.67	223,572,370	92.76
SB#2152	HIPNI-shotgun-3	483,404,371	482,615,866	481,838,492	99.68	447,652,944	92.76
SB#2152	5 kbp mate-pair library	211,734,352	211,563,906	209,024,676	98.72	-	-
SB#134	SB134	214,497,304	214,204,982	213,711,283	99.63	196,835,054	91.89
SB#1954	SB1954	204,696,456	204,366,252	202,910,556	99.13	184,495,196	90.28
SB#2027	SB2027	202,152,485	201,869,154	200,800,503	99.33	185,284,522	91.78
SB#2130	SB2130	201,815,490	201,465,082	200,533,758	99.36	187,545,366	93.09
SB#381	SB381	198,289,183	197,976,540	196,929,675	99.31	181,840,384	91.85
HN216	090316_HN216_AD07_CAGATC_L005	39,007,955	38,843,106	38,874,872	99.66	33,679,462	86.71
HN216	090316_HN216_AD07_CAGATC_L006	39,061,759	38,896,542	38,927,842	99.66	33,728,674	86.71
HN216	090316_HN216_AD07_CAGATC_L007	38,945,974	38,780,492	38,812,662	99.66	33,637,592	86.74
HN216	090316_HN216_AD07_CAGATC_L008	39,039,835	38,874,908	38,902,723	99.65	33,721,404	86.74
HN216	190216_HN216_AD07_CAGATC_L007	40,028,195	39,858,324	39,868,324	99.60	34,671,784	86.99
HN216	190216_HN216_AD07_CAGATC_L008	39,759,338	39,590,146	39,602,876	99.61	34,456,884	87.03
HN216	280116_HN216_AD07_CAGATC_L006	39,691,962	39,536,366	39,494,427	99.50	34,438,236	87.11
HN250	090316_HN250_AD13_AGTCAA	186,423,044	185,938,164	185,786,274	99.66	158,006,016	84.98
HN250	190216_HN250_AD13_AGTCAA	95,827,095	95,581,010	95,455,704	99.61	81,650,698	85.43

Table S2. Number of single nucleotide variants filtered and removed from the total set in a multistage approach according to specific criteria.

Filtering Stage	# SNVs Filtered	# SNVs Removed
Exclude insertion-deletion SNVs	15,405,064	1,847,139
Remove SNVs within RepeatMasker repeats	7,168,722	8,236,342
Filter bi-allelic SNVs	7,149,764	18,958
No alternative homozygotes in reference	7,138,537	11,227
Remove SNVs with missing genotypes	6,716,609	421,928
No indels closer than 10 bp	6,587,874	128,735
More than 3 reads supporting each genotype	2,244,440	4,343,434
Variant quality (Q) more than 50	1,987,710	256,730