

**Table S1:** Primer details and PCR conditions for amplification of microsatellite loci

Microsatellite marker	Primer sequence	Size range (bp)	Repeat unit	Fluorescent label	T <sub>a</sub> (°C)	Reference
BM415	F: 5'-gct aca gcc ctt ctg gtt tg -3'	131-171	di-nucleotide	FAM	50	Bishop <i>et al.</i> , 1994
BM415	R: 5'-gag cta atc acc aac agc aag -3'					
BM203	F: 5'-ggg tgt gac att ttg ttc cc -3'	201-280	di-nucleotide	FAM	52	Bishop <i>et al.</i> , 1994
BM203	R: 5'-ctg ctc gcc act agt cct tc -3'					
ETH10	F: 5'-ggt cag gac tgg ccc tgc taa ca -3'	200-230	di-nucleotide	VIC	62	Toldo <i>et al.</i> , 1993
ETH10	R: 5'-cct cca gcc cac ttt ctc ttc tc -3'					
OARFCB48	F: 5'-gac tct aga gga tgc caa aga acc -3'	160-180	di-nucleotide	PET	55	Buchanan <i>et al.</i> , 1994
OARFCB48	R: 5'-gag tta gta caa gga tga caa gag gca c -3'					
BM2113	F: 5'-gct gcc ttc tac caa ata ccc -3'	120-145	di-nucleotide	VIC	58	Sunden <i>et al.</i> , 1993
BM2113	R: 5'-ctt cct gag aga agc aac acc -3'					
OARFCB304	F: 5'-ccc tag gag ctt tca ata aag aat cgg -3'	120-160	di-nucleotide	NED	55	Buchanan <i>et al.</i> , 1993
OARFCB304	R: 5'-cgc tgc tgt caa ctg ggt cag gg -3'					
OARCP26	F: 5'-ggc cta aca gaa ttc aga tga tgt tgc -3'	110-170	di-nucleotide	FAM	58	Ede <i>et al.</i> , 1995
OARCP26	R: 5'-gtc acc ata ctg acg gct ggt tcc -3'					
BB03	F: 5'-agc cat gtg cca atc ata tac t -3'	225-290	Tri-nucleotide	FAM	60	Dalton <i>et al.</i> , 2011
BB03	R: 5'-gga cac gga ctg aag cta ctt a -3'					
BB04	F: 5'-ata aag gca tgt acc cca cat c -3'	140-160	Tri-nucleotide	VIC	62	Dalton <i>et al.</i> , 2011
BB04	R: 5'-cag aca gga ctg aag cga att a -3'					
BM1824	F: 5'-gag caa ggt gtt ttt cca atc -3'	190-215	di-nucleotide	FAM	52	Bishop <i>et al.</i> , 1994
BM1824	R: 5'-cat tct cca act gct tcc ttg -3'					
BB05	F: 5'-atg gac aga gga gcc tag tga g -3'	130-145	di-nucleotide	PET	60	Dalton <i>et al.</i> , 2011
BB05	R: 5'-act gtg cct ttc aac act gga -3'					
BB08	F: 5'-acc tcc ctg tgg atg act tct -3'	165-180	di-nucleotide	VIC	60	Dalton <i>et al.</i> , 2011
BB08	R: 5'-gcc atg act gag caa cta aac a -3'					
BB10	F: 5'-aat ggg gac aat gac gta cct a -3'	190-220	di-nucleotide	NED	58	Dalton <i>et al.</i> , 2011
BB10	R: 5'-aac agg aac cag ata gtg agt gg -3'					
BB20	F: 5'-gct ctc cac ctt atg ctc atc t -3'	180-195	di-nucleotide	VIC	58	Dalton <i>et al.</i> , 2011
BB20	R: 5'-aac aca tgg cct gac tct ctt t -3'					
SRCRSP8	F: 5'-tgc ggt ctg gtt ctg att tca c -3'	210-260	di-nucleotide	NED	50	Bhebhe <i>et al.</i> , 1994
SRCRSP8	R: 5'-gtt tct tcc tgc atg aga aag tgc atg ctt ag -3'					
TGLA263	F: 5'-cga att cca aat ctg tta att tgc t -3'	120-170	di-nucleotide	PET	50	Georges & Massey, 1992
TGLA263	R: 5'-aca gac aga aac tca atg aaa gca -3'					
INRA006	F: 5'-agg aat atc tgt atc aac ctc agt c -3'	90-120	di-nucleotide	FAM	50	Vaiman <i>et al.</i> , 1992
INRA006	R: 5'-ctg agc tgg ggt ggg agc tat aaa ta -3'					

Microsatellite marker	Primer sequence	Size range (bp)	Repeat unit	Fluorescent label	T <sub>a</sub> (°C)	Reference
BMC3224	F: 5'- cca tca ctg cta ttc tac ctc c -3'	210-240	di-nucleotide	FAM	55	Bishop et al., 1994
BMC3224	R: 5'- cac agc caa ttt ctg att tca -3'					
SPS113	F: 5'- cct cca caca gg ctt ctc tga ctt -3'	140-170	di-nucleotide	FAM	55	FAO, 2011
SPS113	R: 5'- cct aac ttg ctt gag tta ttg ccc -3'					
INRA128	F: 5'- taa gca ccg cac agc aga tgc -3'	160-210	di-nucleotide	NED	55	Vaiman et al., 1994
INRA128	R: 5'- aga cta gtc agg ctt cct ac -3'					
BMS4008	F: 5'- cgg ccc taa gtg ata tgt tg -3'	140-180	di-nucleotide	VIC	55	Sonstegard et al., 1997
BMS4008	R: 5'- gaa gag tgt gag gga aag act g -3'					

Polymerase Chain Reaction (PCR) amplification was conducted in a 12.5 micro litre (µL) reaction volume consisting of AmpliTaq® DNA polymerase (Roche Molecular Systems, Inc), forward and reverse primers (0.5 micro Molar (µM) each) and 50 nano gram (ng) genomic DNA template. The conditions for PCR amplification were as follows: 5 minutes (min) at 95°C denaturation, 35 cycles for 30 seconds (sec) at 95°C, 30 sec at 50 – 62°C (supplementary Table 1) and 30 sec at 72°C, followed by extension at 72°C for 10 min in a T100™ Thermal Cycler (Bio-Rad Laboratories, Inc. Hercules, CA, USA). PCR products were run against a Genescan™ 500 LIZ™ internal size standard on an ABI 3130 genetic analyser (Applied Biosystems, Inc., Foster City, CA, USA) and were genotyped using GeneMapper® v. 4.0 (Applied Biosystems, Inc., Foster City, CA, USA).

**Table S2:** Null allele estimation for the red hartebeest and blesbok reference populations calculated using four statistical methodologies (Oosterhout, Chakraborty, Brookfield 1 and Brookfield 2) in MICRO-CHECKER. Presence of null alleles is indicated (yes) if the average null allele frequencies are above 0.2 at all four algorithms.

<b>Red hartebeest population</b>					
Locus	Null present	Oosterhout	Chakraborty	Brookfield 1	Brookfield 2
OARFCB48	no	0.0084	0.0069	0.0064	0.0064
OARFCB304	no	0.0268	0.0226	0.0197	0.0197
BM415	no	0.1544	0.2571	0.0845	0.0845
TGLA263	no	0.0594	0.0545	0.0451	0.0451
INRA006	no	-0.0305	-0.0306	-0.028	0
BB03	no	0	0	0	0
BB08	no	0.0565	0.0471	0.0381	0.1965
OARCP26	no	-0.1229	-0.0612	-0.0221	0
BB10	no	0.1205	0.106	0.0697	0.0697
BM2113	no	-0.1229	-0.0612	-0.0221	0
BB20	no	0	0	0	0
BB04	no	-0.1229	-0.0612	-0.0221	0
ETH10	no	-0.0177	0.0038	0.0033	0.0033
BM1824	no	0.0657	0.028	0.0179	0.0179
BM203	no	-0.0267	-0.028	-0.0269	0
BMC3224	no	-0.0385	-0.0256	-0.0222	0
BMS4008	no	0.1274	0.151	0.1194	0.1194
INRA128	no	-0.0534	-0.0269	-0.0246	0
<b>Blesbok population</b>					
Locus	Null Present	Oosterhout	Chakraborty	Brookfield 1	Brookfield 2
OARFCB48	no	-0.1728	-0.0857	-0.0394	0.1687
OARFCB304	no	0.0056	-0.0077	-0.006	0.1392
BM415	no	0.2245	0.392	0.1495	0.2719
TGLA263	no	0.0599	0.072	0.0508	0.1785
INRA006	no	0.1838	0.2024	0.1202	0.2342
BB03	no	-0.2828	-0.127	-0.0812	0.2153
BB08	yes	0.2126	0.286	0.1668	0.3397
OARCP26	yes	0.203	0.3287	0.1511	0.3437
BB10	yes	0.2937	0.5232	0.2387	0.3977
BM2113	yes	0.2352	0.3833	0.1843	0.3612
BB20	no	-0.0121	-0.0272	-0.0205	0.215
BB04	yes	0.2724	0.4693	0.2017	0.3765
ETH10	yes	0.2331	0.3246	0.1728	0.349
BM1824	no	0.1828	0.3112	0.1097	0.2499
BM203	no	0.1921	0.2963	0.1277	0.2542
BMC3224	no	0.0202	0.0478	0.0355	0.1645
BMS4008	no	-0.0261	-0.0256	-0.0175	0.1489
INRA128	yes	0.2138	0.3174	0.1824	0.2789

**Table S3:** Allele frequencies for all loci in red hartebeest and blesbok populations with private allele frequencies indicated in bold.

Locus	Allele	Red hartebeest	Blesbok
<b>OARFCB48</b>			
	149	<b>0,038</b>	0,000
	151	<b>0,192</b>	0,000
	153	<b>0,077</b>	0,000
	161	<b>0,077</b>	0,000
	163	<b>0,192</b>	0,000
	165	0,115	0,825
	167	0,038	0,175
	169	<b>0,192</b>	0,000
	173	<b>0,038</b>	0,000
	179	<b>0,038</b>	0,000
<b>OARFCB304</b>			
	133	0,000	<b>0,300</b>
	135	0,000	<b>0,200</b>
	139	0,000	<b>0,500</b>
	141	<b>0,115</b>	0,000
	143	<b>0,346</b>	0,000
	145	<b>0,154</b>	0,000
	149	<b>0,038</b>	0,000
	151	<b>0,077</b>	0,000
	153	<b>0,038</b>	0,000
	155	<b>0,077</b>	0,000
	157	<b>0,154</b>	0,000
<b>BM415</b>			
	145	0,846	0,225
	147	<b>0,154</b>	0,000
	153	0,000	<b>0,775</b>
<b>TGLA263</b>			
	95	<b>0,115</b>	0,000
	105	<b>0,115</b>	0,000
	107	<b>0,385</b>	0,000
	109	<b>0,115</b>	0,000
	111	<b>0,038</b>	0,000
	115	<b>0,192</b>	0,000
	131	0,000	<b>0,500</b>
	137	0,000	<b>0,375</b>
	139	0,038	0,100
	149	0,000	<b>0,025</b>
<b>INRA006</b>			
	98	0,000	<b>0,625</b>
	100	<b>0,038</b>	0,000
	104	<b>0,038</b>	0,000
	106	0,000	<b>0,175</b>
	108	<b>0,115</b>	0,000
	114	0,000	<b>0,200</b>

Locus	Allele	Red hartebeest	Blesbok
	116	<b>0,115</b>	0,000
	118	<b>0,077</b>	0,000
	120	<b>0,269</b>	0,000
	122	<b>0,308</b>	0,000
	124	<b>0,038</b>	0,000
<b>BB03</b>			
	232	<b>1,000</b>	0,000
	244	0,000	<b>0,026</b>
	264	0,000	<b>0,211</b>
	267	0,000	<b>0,763</b>
<b>BB20</b>			
	185	<b>1,000</b>	0,000
	187	0,000	<b>0,579</b>
	189	0,000	<b>0,289</b>
	191	0,000	<b>0,132</b>
<b>BM1824</b>			
	188	<b>0,077</b>	0,000
	192	<b>0,692</b>	0,000
	194	<b>0,038</b>	0,000
	196	<b>0,038</b>	0,000
	198	0,000	<b>0,825</b>
	200	0,000	<b>0,175</b>
	202	<b>0,154</b>	0,000
<b>BM203</b>			
	224	0,000	<b>0,750</b>
	228	0,000	<b>0,250</b>
	238	<b>0,038</b>	0,000
	244	<b>0,115</b>	0,000
	252	<b>0,231</b>	0,000
	254	<b>0,115</b>	0,000
	256	<b>0,154</b>	0,000
	258	<b>0,038</b>	0,000
	260	<b>0,038</b>	0,000
	262	<b>0,077</b>	0,000
	266	<b>0,077</b>	0,000
	272	<b>0,077</b>	0,000
	276	<b>0,038</b>	0,000
<b>BMC3224</b>			
	213	<b>0,231</b>	0,000
	215	<b>0,038</b>	0,000
	219	<b>0,385</b>	0,000
	221	<b>0,115</b>	0,000
	223	0,231	0,025
	227	0,000	<b>0,525</b>
	231	0,000	<b>0,225</b>
	233	0,000	<b>0,225</b>
<b>BMS4008</b>			
	142	<b>0,038</b>	0,000

<b>Locus</b>	<b>Allele</b>	<b>Red hartebeest</b>	<b>Blesbok</b>
	144	<b>0,077</b>	0,000
	158	0,192	0,650
	162	<b>0,192</b>	0,000
	164	<b>0,038</b>	0,000
	166	0,077	0,250
	168	0,038	0,100
	170	<b>0,038</b>	0,000
	172	<b>0,269</b>	0,000
	180	<b>0,038</b>	0,000