

Table S1: Summary of allele size standardization

Set		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	Overall ^a
B	#alleles	7	4			9	7		6	11	19	10	15		14	11	9		122
	<i>r</i>	0.998	0.998 ^c			0.956	0.962		0.986	0.979	0.876	0.946	0.974		0.939	0.877	0.909		0.970
	<i>F_{ST}</i>	0.002	0.003			0.012	0.011		0.005	0.003	0.004	0.006	0.003		0.003	0.003	0.005		0.005
	<i>P</i> value	0.606	0.418			0.038	0.046		0.204	0.571	0.330	0.188	0.711		0.538	0.549	0.363		0.116
C	#alleles	6	13				6			13	16	11	13		13	9	9		109
	<i>r</i>	0.974	0.969				0.994			0.733 ^b	0.626 ^e	0.962	0.874		0.912	0.825	0.944		0.932
	<i>F_{ST}</i>	0.005	0.007				0.003			0.007	0.011	0.002	0.005		0.004	0.003	0.003		0.005
	<i>P</i> value	0.197	0.119				0.401			0.048	<u>0.003</u>	0.760	0.291		0.428	0.522	0.566		0.063
D	#alleles		4	3	3	9	8	4	8	12	19			14		11		13	108
	<i>r</i>		0.9996	0.9995	0.9994	0.983	0.995	0.969	0.958	0.927	0.966			0.918		0.974		0.903	0.983 ^d
	<i>F_{ST}</i>		0.001	0.000	0.001	0.002	0.005	0.004	0.008	0.008	0.005			0.003		0.003		0.003	0.004
	<i>P</i> value		0.755	0.731	0.686	0.604	0.198	0.305	0.060	0.043	0.205			0.559		0.448		0.347	0.214
E	#alleles			5										14				12	31
	<i>r</i>			0.883										0.394 ^e				0.781	0.763
	<i>F_{ST}</i>			0.058										0.031				0.007	0.029
	<i>P</i> value			<u>0.0005</u>										<u>0.003</u>				0.620	<u>0.0001</u>
F	#alleles	7										11							18
	<i>r</i>	0.988										0.887							0.958
	<i>F_{ST}</i>	0.004										0.011							0.008
	<i>P</i> value	<u>0.023</u>										<u>0.0001</u>							<u>0.0001</u>

1: *BM3517*, 2: *BM4028*, 3: *ETH010*, 4: *ETH225*, 5: *INRA006*, 6: *INRA128*, 7: *TGLA227*, 8: *TGLA263*, 9: *CSSM019*, 10: *DIK020*, 11: *TGLA057*, 12: *BM0719*, 13: *BM1824*, 14: *BM3205*, 15: *ILSTS026*, 16: *TGLA159*, 17: *SPS115*. Underlined: significance ($\alpha = 0.05$) of individual locus (after Bonferroni) or μsat set. a: Overall Pearson *r* obtained by correlating frequencies of all alleles across loci, b: low correlation due to high frequency of allele 138 in set C (0.157 vs. 0.047 in set B). Pearson *r* = 0.886 without this allele. c: low correlation due to low frequency of allele 188 in set C (0.072 vs. 0.218 in set B). Pearson *r* = 0.861 without this allele. d: when #alleles ≤ 4 : frequencies of the most common allele (> 0.54) differ by a factor < 1.03 . e: Pearson *r* = 0.781 with the pooled sample of Mana Pools NP, Nyakasanga, Gorongosa NP and Marromeu GR, which are located 730 km further south. *F_{ST}* values and G-statistics derived *P* values (9999 randomizations) were estimated with the Genalex add-in for Excel (version 6.503).

Allele size changes relative to microsatellite set A (set A minus other set)

B: μ sat 1: -8; μ sat 2, 6: -2, μ sat 5: -11; μ sat 8: -1; μ sat 9: if ≤ 143 : -5, if ≥ 146 : -4, 144-145: not observed in any population; μ sat 10: if ≤ 181 : -3, if ≥ 182 : -2; μ sat 11: if ≤ 97 : -6, if ≥ 98 : -5; μ sat 12: if ≤ 147 : -1, if ≥ 150 : -2, 148-149: not observed in any population; μ sat 14: if ≤ 210 : -4, if ≥ 213 : -5, 211-212: not observed in any population; μ sat 15: if ≤ 149 : +2, if ≥ 152 : +1, 150-151: not observed in any population; μ sat 16: -5.

C: μ sat 1, 2, 6: -2; μ sat 9: if ≤ 135 : -3, if ≥ 139 : -5, 137: not observed in any population; μ sat 10: if ≤ 195 : -3, if ≥ 197 : -5. Allele sizes 195 and 197 resulted both in an adjusted allele size of 192. For the allele size range 195-199 it was unclear whether the shift should be -3 or -5, because allele size 197 was only observed in Laikipia NP at low frequency (frequency = 0.029). This inconsistency did not affect our analyses as allele sizes 193-201 (190-196 after adjustment) were rare in KNP (i.e., not considered as an MDTA or wild-type associated allele); μ sat 11: if ≤ 87 : 0, if ≥ 91 : -2; μ sat 12: if ≤ 145 : -1, if ≥ 147 : -3 Allele sizes 145 and 147 resulted both in an allele size of 144. Allele size 145 was only observed in Nairobi NP at low frequency (frequency = 0.026). It was unclear whether allele size 145 should be decreased by -1 or -3. This inconsistency did not affect our results as both allele size 142 and allele size 144 were rare in KNP (i.e., not considered as an MDTA or wild-type associated allele); μ sat 14: no change; μ sat 15: if ≤ 150 : -1, if ≥ 152 : -3, Allele sizes 150 and 152 were both adjusted to an allele size of 149, which constitutes a male-deleterious-trait-associated allele. These size shifts represent a conservative choice as they resulted in a more positive Pearson r when correlating allele frequencies against latitude (i.e., less significant allele-frequency cline); μ sat 16: -3.

D: μ sats 2-4, 6-8, 10, 13, 15: no change; μ sat 5: -4; μ sat 9: if ≤ 148 : no change, if ≥ 152 : -2, 150: not observed in any population; μ sat 17: if ≤ 233 : -4, if ≥ 237 : -6, 235: not observed in any population.

E: μ sat 3: no change; μ sat 13: if 167: +2, if ≥ 175 : no change, 169-173: not observed in Serengeti NP; μ sat 17: if ≤ 234 : -1, if ≥ 236 : +1

F: μ sat 1: -5, : μ sat 11: -2