

**Table S3:** Not considering R=0.125: minimum number of SNP and/or STR loci required per category for a relatedness category assignment with a >95% (>80%) correct classification rate without considering the category R=0.125.

Mating System	Marker	MAF	PO	FS	R=0.25	Unrel <sup>1</sup>
<b>Monogamy</b>	SNP	0.05	3200 (800)	1600 (800)	--	50
		0.25	200 (100)	200 (200)	--	50
		0.5	100 (100)	200 (100)	--	50
	STR	n/a	80 (40)	80 (40)	--	10
	SNP&STR <sup>2</sup>	0.05	800 (100)	400 (100)	--	50
		0.25	100 (50)	200 (50)	--	50
0.5		100 (50)	100 (50)	--	50	
<b>Polygyny</b>	SNP	0.05	1600 (400)	3200 (1600)	--	50
		0.25	200 (100)	400 (400)	--	50
		0.5	100 (100)	400 (200)	--	50
	STR	n/a	80 (40)	- (80)	--	10
	SNP&STR	0.05	400 (100)	1600 (800)	--	50
		0.25	100 (50)	400 (200)	--	50
0.5		50 (50)	400 (200)	--	50	
<b>Promiscuity</b>	SNP	0.05	800 (400)	-	--	50
		0.25	200 (100)	-	--	50
		0.5	100 (100)	-	--	50
	STR	n/a	40 (40)	-	--	10
	SNP&STR	0.05	200 (50)	-	--	50
		0.25	50 (50)	-	--	50
0.5		50 (50)	-	--	50	

Dashes indicate that the category could not be assigned with a >95% (80%) correct classification rate with the simulated number of loci. MAF minor allele frequency, PO parent-offspring, FS full siblings, R=0.25 avuncular, half sibs, grand-parent-grand offspring, unrel unrelated. <sup>1</sup>Note that with the population size and parameters used, more than >95% of individuals are unrelated, so even if all dyads were assigned to the category 'unrelated' the correct classification rate might be >95%. <sup>2</sup>Number of SNP loci required when combined with 20 STR loci.