

**Table S5:** Effect of typing error: minimum number of SNP and/or STR loci with 2% typing error required per category for a relatedness category assignment with >95% correct classification rates.

Mating System	Marker	MAF	PO	FS	R=0.25	R=0.125 <sup>1</sup>	Unrelated <sup>2</sup>	
Monogamy	SNP	0.05	-	3200	3200	-	50	
		0.25	400	400	3200	-	50	
		0.5	400	400	3200	-	50	
	STR	n/a	80	80	-	-	10	
	SNP&STR <sup>3</sup>	0.05	1600	1600	3200	-	10	
		0.25	200	200	3200	-	50	
		0.5	200	200	1600	-	50	
	Polygyny	SNP	0.05	1600	-	1600	-	50
			0.25	400	800	1600	-	50
0.5			400	800	1600	-	50	
STR		n/a	40	-	-	-	10	
SNP&STR		0.05	400	-	1600	-	50	
		0.25	200	400	1600	-	50	
		0.5	200	800	1600	-	50	
Promiscuity		SNP	0.05	800	-	1600	-	50
			0.25	400	-	1600	-	50
	0.5		200	-	1600	-	50	
	STR	n/a	40	-	-	-	10	
	SNP&STR	0.05	400	-	1600	-	50	
		0.25	100	-	1600	-	50	
		0.5	100	-	1600	-	50	

Dashes indicate that the category could not be assigned with a >95% 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, R=0.125 full cousins, half avuncular. <sup>1</sup>Even though no number of tested loci led to a 95% correct classification rate for the R=0.125 category under the simulated population conditions; R=0.125 is part of this table because it is important to include it in the relatedness category assignment for the correct classification rate of R=0.25. <sup>2</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>3</sup>Number of SNP loci required when combined with 20 STR loci.