

Table S4: Considering R=0.0625: minimum number of SNP loci or SNP loci combined with 20 STR loci required per category for a relatedness category assignment (RCA) with >95% (>80%) correct classification rates. For the simulations shown in this table the category R=0.0625 was assessed. STR only results are not shown because they did not change compared to simulations without R=0.0625 (Table 2).

Mating System	Marker	MAF	PO	FS	R=0.25	R=0.125 ¹	R=0.0625 ¹	unrel ²
Monogamy	SNP	0.05	3200 (800)	1600 (800)	3200 (1600)	- -	--	50
		0.25	200 (200)	200 (200)	1600 (800)	- -	--	50
		0.5	100 (100)	200 (100)	1600 (800)	- -	--	50
	SNP&STR ³	0.05	1600 (100)	800 (200)	3200 (1600)	- -	--	50
		0.25	100 (50)	200 (50)	1600 (800)	- -	--	50
		0.5	100 (50)	200 (50)	1600 (800)	- -	--	50
Polygyny	SNP	0.05	1600 (800)	3200 (1600)	3200 (800)	- -	--	50
		0.25	200 (100)	400 (400)	800 (400)	- (3200)	--	50
		0.5	100 (100)	400 (200)	800 (400)	- (3200)	--	50
	SNP&STR	0.05	800 (100)	1600 (800)	3200 (800)	- -	--	50
		0.25	100 (50)	400 (200)	800 (400)	- (3200)	--	50
		0.5	100 (50)	400 (200)	800 (400)	- (3200)	--	50
Promiscuity	SNP	0.05	800 (400)	- -	3200 (800)	- (3200)	--	50
		0.25	200 (100)	- -	1600 (400)	- (3200)	--	50
		0.5	100 (100)	- -	800 (400)	- (1600)	--	50
	SNP&STR	0.05	200 (50)	- -	3200 (800)	- (3200)	--	50
		0.25	100 (50)	- -	1600 (400)	- (1600)	--	50
		0.5	50 (50)	- -	800 (400)	- (1600)	--	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, R=0.125 full cousins, half avuncular, unrel unrelated. ¹Even though no number of tested loci led to a 95% correct classification rate for the R=0.125 and R=0.0625 categories

under the simulated population conditions these categories are part of this table because it may be important to include them in the RCA. ²Note 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%. ³Number of SNP loci required when combined with 20 STR loci.