

Table 4 Simple population genetic summaries. All quantities are means over loci. M is the total fraction of missing genotypes; $\bar{N}_{A,ss}$ is the average number of alleles and $\bar{P}_{poly,ss}$ the fraction of polymorphic loci, after sub-sampling to the smallest sample size per locus; \bar{H}_{exp} and \bar{H}_{obs} are expected and observed heterozygosity, respectively. Population codes are as given in Table 1

Code	M	$\bar{N}_{A,ss}$	$\bar{P}_{poly,ss}$	\bar{H}_{exp}	\bar{H}_{obs}
CRHS	0.008	2.60	0.95	0.398	0.399
SmRF	0.021	2.60	0.95	0.401	0.394
BCkF	0.041	2.59	0.96	0.393	0.382
IGHF	0.028	2.37	0.93	0.356	0.363
TRS	0.036	2.37	0.92	0.353	0.348
TRF	0.031	2.37	0.92	0.352	0.351
ERF	0.022	2.51	0.95	0.364	0.356
RRF	0.037	2.64	0.96	0.398	0.391
SRW	0.338	2.32	0.88	0.338	0.329
BCS	0.046	2.52	0.92	0.379	0.373
MDS	0.082	2.55	0.94	0.394	0.397
FRHS	0.108	2.61	0.95	0.397	0.392
FRHF	0.029	2.63	0.96	0.394	0.398
BCF	0.123	2.60	0.94	0.385	0.370
MDF	0.130	2.59	0.94	0.386	0.383
SJRF	0.012	2.57	0.94	0.384	0.380
CHLF	0.068	2.53	0.94	0.386	0.384