Supplementary material 1

**Imputation of non-genotyped sheep from the genotypes of their mates and resulting progeny**

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**Family imputation**

* If genotype of mate (i.e., the other parent) is known determine phase of heterozygous loci in progeny where genotype of the mate is homozygous
* Impute the genotypes of non-genotyped parent based on allele count in the progeny as follows:
* If SNP to be imputed is on X of male:
	+ If MAF ≥ 0.03 and the number of informative alleles ≥ 2 then call the missing haplotype
* else
	+ If MAF ≥ 0.1 and the number of informative alleles ≥ 2 then call the genotypes as heterozugous
	+ else if MAF < 0.03 and the number of informative alleles ≥ 3+(number of progeny-3)0.8 and frequency of unphased loci < 0.5 then call the genotypes as homozygous
	+ else leave it as missing
* endif

**Population imputation**

* Phase imputed genotypes (for non-genotyped individuals) using parent information (if available) and also population information
* Impute the remaining missing genotypes from population information according to Sargolzaei et al. (2014).

**Reference**

Sargolzaei M, Chesnais JP and Schenkel FS 2014. A new approach for efficient genotype imputation using information from relatives BMC Genomics 15, 478