**Supplementary Material S4 – Required characteristics of genotypes when computing individual specific imputation accuracy**

The required characteristics of true and imputed genotypes when computing individual specific imputation accuracy can be derived theoretically similarly as for the locus specific imputation accuracy as shown in Appendix C. Considering the individual specific imputation accuracy for an imputed individual *i*, the distribution can be represented as:

 $\left[\begin{matrix}\begin{matrix}X\_{RP}\\X\_{i}\end{matrix}\\\hat{X\_{i}}\\ε\_{i}\end{matrix}\right]=MVN\left[0,\left(\begin{matrix}A\_{RP}σ\_{g}^{2}&A\_{RP,i}σ\_{g}^{2}&A\_{RP}^{-1}A\_{RP,i}σ\_{g}^{2}&0\\A\_{i,RP}σ\_{g}^{2}&A\_{i,i}σ\_{g}^{2}+σ\_{ε}^{2}&A\_{RP}^{-1}A\_{RP,i}σ\_{g}^{2}&σ\_{ε}^{2}\\A\_{i,TRP}A\_{RP}^{-1}σ\_{g}^{2}&A\_{i,RPN}A\_{TRP}^{-1}σ\_{g}^{2}&A\_{i,i}A\_{i,RP}A\_{RP}^{-1}σ\_{g}^{2}&0\\0&σ\_{ε}^{2}&0&σ\_{ε}^{2}\end{matrix}\right)\right] $

where subscript *i* denotes imputed animal *i* and $σ\_{g}^{2}$ denotes variance of the genotypes at locus *j*.

In order to not violate the assumptions of the Pearson correlation coefficient used to compute individual imputation accuracy, all true and imputed genotypes should follow the same distribution. In the above equation, therefore, $X\_{i}$and $\hat{X\_{i}}$should have the same mean and variance across loci. Getting the same mean at each locus is simply achieved by centring both$X\_{i}$and $\hat{X\_{i}}, $i.e. by subtracting the mean gene dosage from each SNP in both $X\_{i}$and $\hat{X\_{i}}$, while the same variance is obtained by scaling across loci, such that $σ\_{g}^{2}=1$ for all loci.