Graphical depiction of data and analyses used to assess genotypes imputed from low-pass sequence to predict genetic merit. Available pedigree, performance and SNP array genotypes from animals in the Germplasm Evaluation (GPE) project were used to in (G)BLUP procedures to predict (G)EBV for all (genotyped) GPE animals. The steers used to test imputation from low-pass sequence were a subset of GPE that had been extracted for an RNA-Seq experiment to determine differences in gene expression associated with extremely high or low feed intake and gain in postweaning tests. Whole genome sequence obtained from that project was downsampled to mimic low-pass sequence. Imputed genotypes were compared to available SNP array genotypes and genotypes called from transcriptome sequence that had been mapped to the ARS-UCD 1.2 assembly. Genotypes and phenotypes of the test steers was removed from GBLUP analyses to predict SNP effects using the remaining GPE data. Predicted SNP effects were applied to genotypes imputed from downsampled sequence to obtain molecular breeding values for the test steers. Those MBV were compared to (G)EBV predicted from the complete GPE data.