SkimSEEK

Low-pass skim sequencing & imputation from NEOGEN® Genomics

The next advancement in genomic technology

Leverage low-pass sequence data with SkimSEEK™ and explore deeper into the genome

ADVANTAGES OF SKIMSEEK

- Reduce dependence on linkage disequilibrium between 50K fixed chips and Quantitative Trait Loci (QTL) that are impacting the desired phenotypes
- Much lower cost than population-specific genotyping panels
- Complete genotyping of entire breeding populations, which reduces bias in genetic evaluations due to selective genotyping
- Data report contains millions of other SNP variants to improve genomic selection or help discover novel, population-specific causative variants
- >99% accuracy

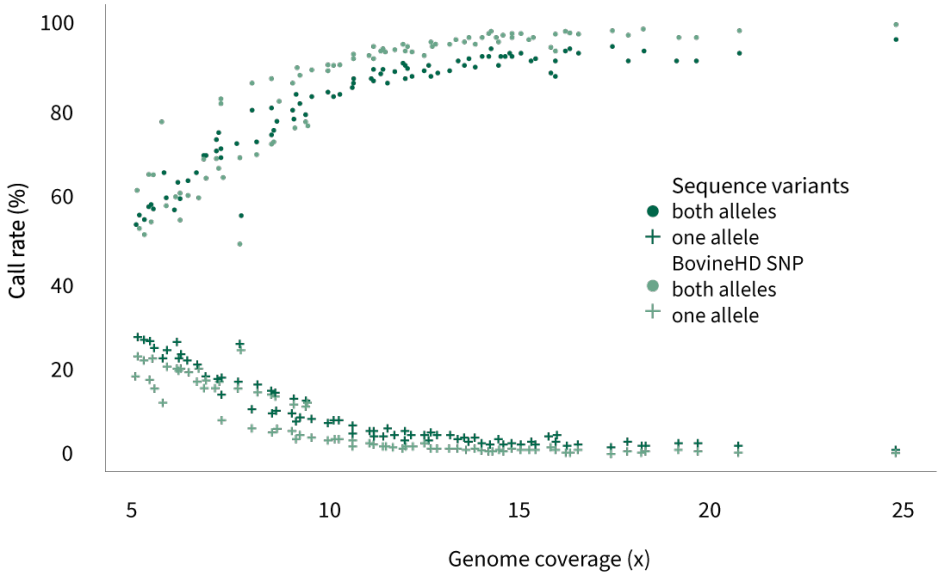
VARIANT (SNP) DISCOVERY

- Same cost and effort to genomically sequence many individuals at low coverage when compared to sequencing a few individuals at high coverage

USING SEQUENCE DATA TO GENOTYPE

- Imputation – match low-coverage reads to well-characterized reference haplotypes
- Utilize pre-determined fixed panels of SNP reports to augment the genomic selection
- Utilize a data report of millions of other SNP variants to improve genomic selection or help discover novel, population-specific causative variants

Ready to learn more? Contact GeneSeekInfo@Neogen.com for more information on SkimSEEK

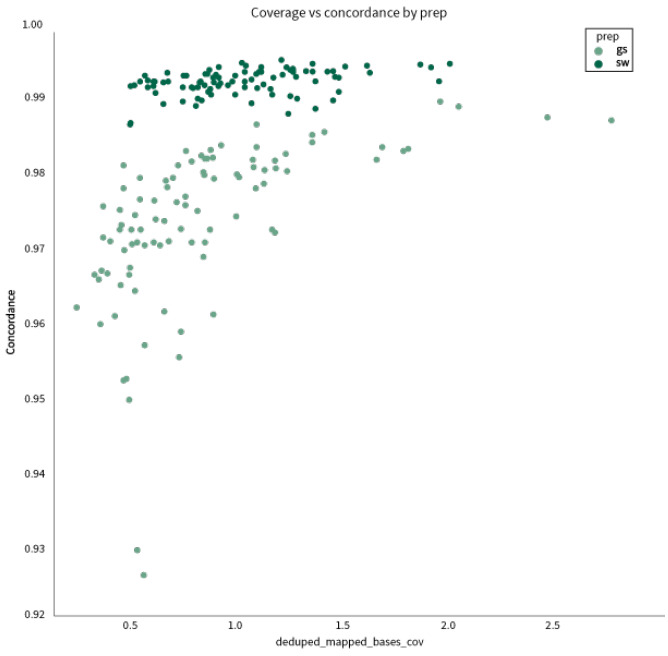


Imputation is a critical step in the data analysis.

The correct algorithms need to be coupled with highly informative reference genomes specific to the population for greatest accuracy and appropriate resolution of genotyping

54 cattle samples sequenced with analysis at various levels of coverage. Data were compared to known genotype calls for the same animals genotyped on an Illumina Bovine HD chip (77K SNPs)

Snelling et. Al. BIF 2019



Genotype Concordance to the GGP Bovine 50K Chip Versus Coverage

- Two replicates of 96 samples from the USDA-MARC Beef Diversity Panel
- Genomic coverage from 0.5 to 3.0 X
- Concordance averages 99.3% in normalized DNA samples (blue)
- Concordance averages 97.3% for the same samples but unnormalized DNA samples