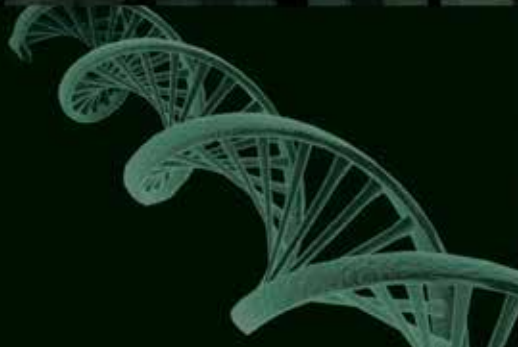


230,000 SNPs



GeneSeek® Genomic Profiler F250

- Utilizes whole genome sequencing data (20x) from more than 1400 cattle
- Approximately 200,000 functional variant assays (non-synonymous, frameshift, premature stop etc.)
- More than 23,000 genes represented with an average of greater than 8 variants per gene
- An additional 35,000 SNPs used to impute GGP chips for genomic selection

GGP



GGP
F250



One Sample, One Simple Comprehensive Solution

Functional variants and whole genome selection:

- Developed in conjunction with the University of Missouri and other collaborators, the GeneSeek Genomic Profiler™ F250 (GGP-F250) genotyping chip makes use of Illumina Infinium chemistry and features nearly 200,000 SNPs for accurate evaluation of functional variants such as non-synonymous, frameshift, and premature stop mutations.
- An additional 35,000 strategically selected SNP assays are included that allows researchers the ability to investigate genetic merit, apply genome wide selection, and the ability to accurately impute to higher density arrays.
- The GGP F250 BeadChip, built on the highly informative Illumina 7k BeadChip, also offers the most informative SNPs from the Illumina Bovine 50k and 770k BeadChips

Imputation accuracy greater than 99% in most well characterized breeds

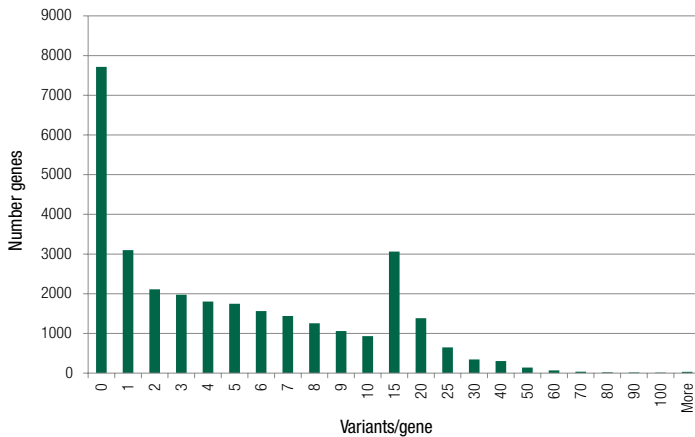
- Call rate success averages above 99%
- Includes a large percentage of SNP overlap with other commercially available arrays including the original Bovine SNP50k

Source of Functional Variants

- 244 *Bos taurus* whole genome sequence data (aligned to UMD3.1)
- 150 *Bos taurus* animals with RNA-seq data
- 16 *Bos indicus* whole genome sequence data
- 1000 Bulls Project variant calls

Figure 1: Number of variants per gene

There are 23,059 genes with at least one variant. There is an average of 8 variants per gene. 7,714 genes do not contain a single variant.



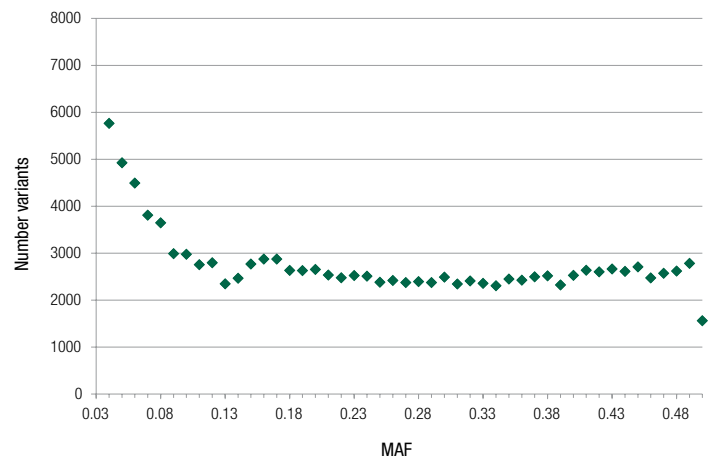
GGP-F250 content and design were performed at the University of Missouri-Columbia by Robert D. Schnabel and Jeremy F Taylor. Denis Larkin at the Royal Veterinary College, London, contributed the annotation for evolutionarily conserved genomic regions. A complete description of the GGP-F250 assay will be available at:

Schnabel RD, Simpson EB, Larkin DM, Hoff JL, Decker JE and Taylor JF. 2016. Design and Application of the Cattle GGP-F250 Assay. Anim. Genet. (in preparation).

No. of Variants	Description
33,730	Selected imputation content from leading bovine arrays
193,503	Functional content variants
227,233	Total number of variants
22,298	Non-synonymous Sift scored deleterious (< 0.05)
48,994	Non-synonymous Sift scored tolerated (0.05 to 1.0)
49,627	Non-synonymous with no Sift prediction
120,919	Total non-synonymous (NS) AA substitutions
1,265	Frameshift indels
585	In-frame indels
20,402	Untranslated region (UTR)
1,573	Ensembl ncRNA (snoRNA, miRNA, snRNA, rRNA, Mt_tRNA, Mt_rRNA)
4,081	Conserved, non-coding elements
6,378	Splice (not mutually exclusive)
23,059	Genes with at least 1 variant
7,714	Genes with no variant

Figure 2: Distribution of Minor Allele Frequency

There are more than 100,000 markers that have a minor allele frequency greater than 0.05.



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