

Sheep 40K Panel

The GenoBaits® Sheep 40K Panel was developed from resequencing 587 sheep breeds and wild relatives. The SNP discovery project was a collaboration between Molbreeding R&D team and the research teams led by Dr. Jiang Yu from Northwest A&M University and Dr. Liu Yongbin from Inner Mongolia University.

Product Highlight

- Total 40,156 target regions, evenly distributed across the genome; more than 90% SNPs have MAF > 0.1
- Rich informative profiles, of which have high call rates (>99%) and accuracy
- High density multiplexing and high-throughput indexing providing efficiency and cost-effectiveness
- 26 target regions on Y chromosome were designed (NCBI:CM022046.1) for early sex determination

Brucella spp. specific genes designed for infection detection and VirB12, a serological marker of Brucella infection screening.

- ~150 traits related genes that provide better characterization of the flock and breeding value. These include genes significant related to reproduction, growth, immunity, fat deposition, milk production, thoracic vertebrae, tail type, tail fat, horn type, and wool type, etc.

Genes	SNPs	Traits	Reference
BMPR1B	19	Reproduction	Souza et al., 2001
BMP15	5	Reproduction	Dixit et al., 2006
GDF9	7	Reproduction	Hanrahan et al., 2004
LEMD3	3	Ear size	Zhang et al., 2014
MSRB3	4	Ear size	Paris et al., 2020
MSTN	14	Muscle growth	Hickford et al., 2010
RXFP2	13	Horn type	Pan et al., 2018
CSN1S1	10	Milk production	Calvo et al., 2013
DGAT1	3	Milk production	Martin et al., 2017
FBXL3	3	Growth	Godinho et al., 2007
PDGFD	17	Tail type	Dong et al., 2020
TBTX	8	Tail type	Han et al., 2019
IRF2BP2	20	Wool traits	Demars et al., 2017
KRT36	7	Wool traits	Sulayman et al., 2018
BCO2	10	Fat deposition	Våge et al., 2010
NRIP1	1	Fat deposition	Xu et al., 2017
VRTN	5	Vertebra number	Li et al., 2019



Service process



Submit sample for DNA QC



Library construction and sequence capture



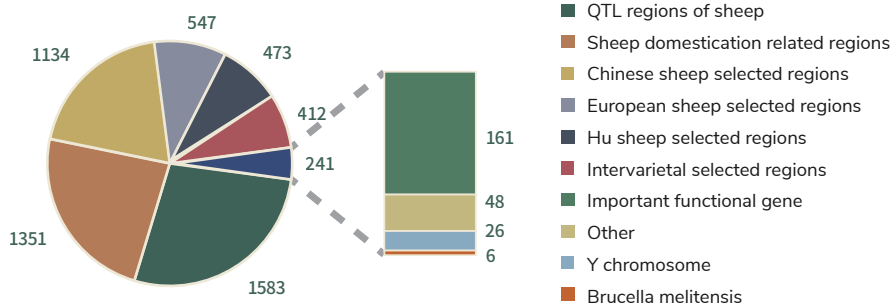
High-throughput sequencing



Data quality control and sequence trimming



Automatic Bioinformatics analysis on cloud



~6K breeding selection regions are also included to differentiate flocks from different regions, Asian and Europe, and Pacific. These regions were very informative in QTL analysis based on their SNP frequency, density and LD etc.

The distribution of markers across the genome

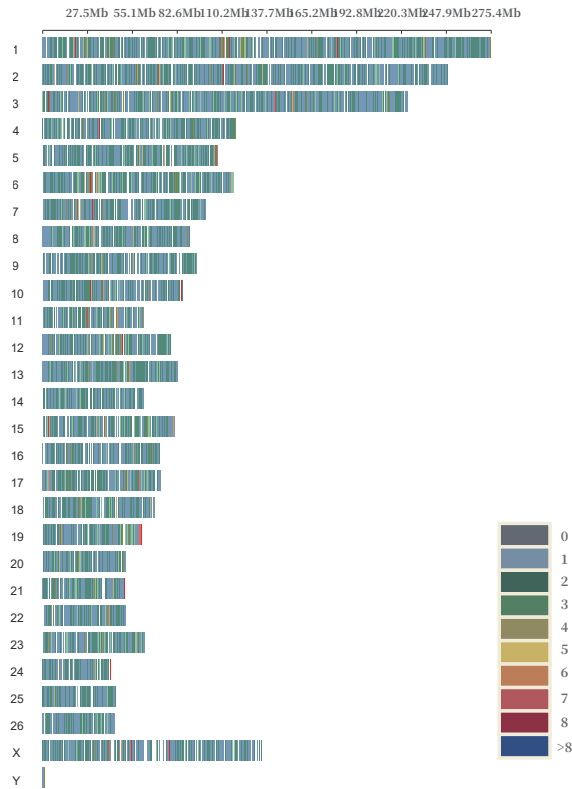


Figure 1. The distribution of 40K SNP markers on chromosomes

In figure 1, there are 40,156 SNPs evenly distributed on 26 autosomes, the different colors represent the number of SNPs that located in a 100 Kb sliding windows.

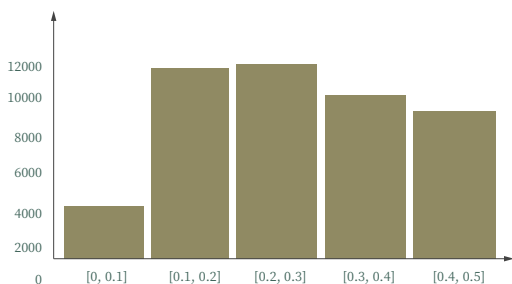


Figure 2. Frequency distribution of 40K SNP MAF

The means of Minor allele frequency (MAF) of this SNP chip in test population is 0.27, which provides great potential for successful genomic studies and genomic selection to majority sheep breeds.

