Twist Genotyping Panel – Bovine 100k and Twist Bovine Blocker Solution

Targeted NGS solutions for improved bovine genomic research

Modern agricultural genomics requires highly scalable, accurate, and flexible tools for large scale genotyping of plant and animal samples. To this end, Twist Bioscience has developed a suite of sequencing solutions for bovine agricultural studies. The Twist Bovine Blocker Solution and Twist Genotyping Panel - Bovine 100k together provide an optimized target enrichment alternative to array-based genotyping for high-throughput bovine genomics.

Target enrichment panels allow for targeted sequencing of regions of interest, which improves efficiency and reduces costs. The Twist Genotyping Panel - Bovine 100k is a targeted sequencing panel designed to target approximately 100k SNP markers, including targets found in the most commonly used SNP arrays such as the Illumina BovineSNP50. The panel covers all 195 International Society for Animal Genetics (ISAG) SNPs for parentage verification and quick discovery,[1] all International Committee for Animal Recording (ICAR) parentage SNPs,[2] as well as all 3552 Council on Dairy Cattle Breeding (CDCB) discovery SNPs.[3,4] Together, these markers have been agreed upon by existing Bovine consortia, including the United States Department of Agriculture-Agricultural Research Service (USDA-ARS) and CDCB, as critical elements for accurate trait selection and understanding parentage. Additionally, by leveraging Twist's Custom Panel solutions, users can add additional SNPs or otherwise improve performance for their specific research and production scaling needs.

Blockers are used to prevent non-specific hybridization between target enrichment probes and sequences that are not of interest. The Twist Bovine Blockers are an accessory reagent used during target enrichment specifically designed to block repetitive regions of the ARS-UCD1.2/bosTau9 genome, thereby reducing off-target binding during enrichment and improving sequencing efficiency. With these Bovine Blockers, users can gain access to more usable sequencing reads, load more samples in a sequencing run, and reduce overall sample processing costs.

Both of these products are optimized for seamless integration with existing Twist library preparation and target enrichment kits, including the high-capacity Twist FlexPrep UHT Library Preparation and Hybridization Kit.

KEY BENEFITS

Expert Selected Content with Built-in Flexibility

- The panel targets markers found in the most commonly used bovine SNP arrays
- All 195 ISAG and all ICAR parentage SNPs, as well as 3552 CDCB SNPs are covered by the panel
- Twist panels are easily customizable, allowing for the addition or removal of any SNPs

Exceptional Performance, Maximized Efficiency

- Blockers reduce off-target reads during capture workflows and increase usable sequencing reads
- Higher plexing capabilities on the sequencer help reduce sequencing cost per sample

End-to-End Workflow Compatibility

- Seamlessly compatible with Twist's library preparation and target enrichment reagents, including the Twist FlexPrep™ UHT Library Preparation and Hybridization Kit

For Research Use Only. Not for use in diagnostic procedures.

Performance metrics are based on internal research data only and may vary depending on sample quality, configuration, and methods used.

Panel performance

Twist target enrichment panels allow for the sequencing of specific regions of interest, which can improve efficiency and lower costs when compared to whole-genome sequencing. When paired with Bovine Blocker Solution, the Twist Genotyping Panel - Bovine 100k delivers high target coverage, uniformity, and concordance with microarray data (**Table 1**). All experiments presented in this product sheet used samples of cow breeds derived from the USMARC Beef Cattle Diversity Panel version 2.9 (MBCDP2.9). This was licensed from the USDA ARS and used to represent the genetic breadth of the US beef industry. This panel comprises 96 sires from breeds that accounted for >99% of US beef germplasm as of year 2000.[5,6] Sires in this panel were selected based on minimal pedigree relationships between ancestors, thereby maximizing the number of unshared haploid genomes sampled. This ensured maximum genetic diversity and minimized lineage redundancy.

% ON TARGET	ESTIMATED LIBRARY SIZE	MEAN TARGET COVERAGE	% ZERO COVERAGE	FOLD 80 BASE PENALTY	AT DROPOUT	GC DROPOUT
88.3% ± 0.72%	9M ± 1.22M	19.14 ± 1.76	1.2% ± 0.12%	1.76 ± 0.2	7.04 ± 1.04	3.09 ± 1.48

Table 1. Ninety-six samples of various masses between 40 - 75 ng of gDNA from 18 different breeds of cows were arrayed out without normalization and loaded into the Twist FlexPrep Library Preparation Workflow. The libraries were then pooled into 96-plex pools and processed through the Twist FlexPrep Target Enrichment Workflow using the Twist Genotyping Panel - Bovine 100k and sequenced on a NextSeq 2000. Analysis was done with bwa-mem and Picard with 100x downsampling.

Blocker performance

Compared to samples put through target enrichment with human or no blocker solution, the use of Bovine Blockers dramatically decreases the off-target observed as a result of blocking repetitive regions in the bovine genome (**Figures 1 and 2**). This targeted performance ensures a higher percentage of usable reads align to the intended SNP markers, directly improving the efficiency and reducing the sequencing cost per sample in large-scale bovine genotyping studies. The robustness of the blocker design is shown by a consistent off-target reduction observed across all 18 breeds tested, despite the ARS-UCD1.2/bosTau9 reference genome used in the blocker design being derived from the Hereford breed.

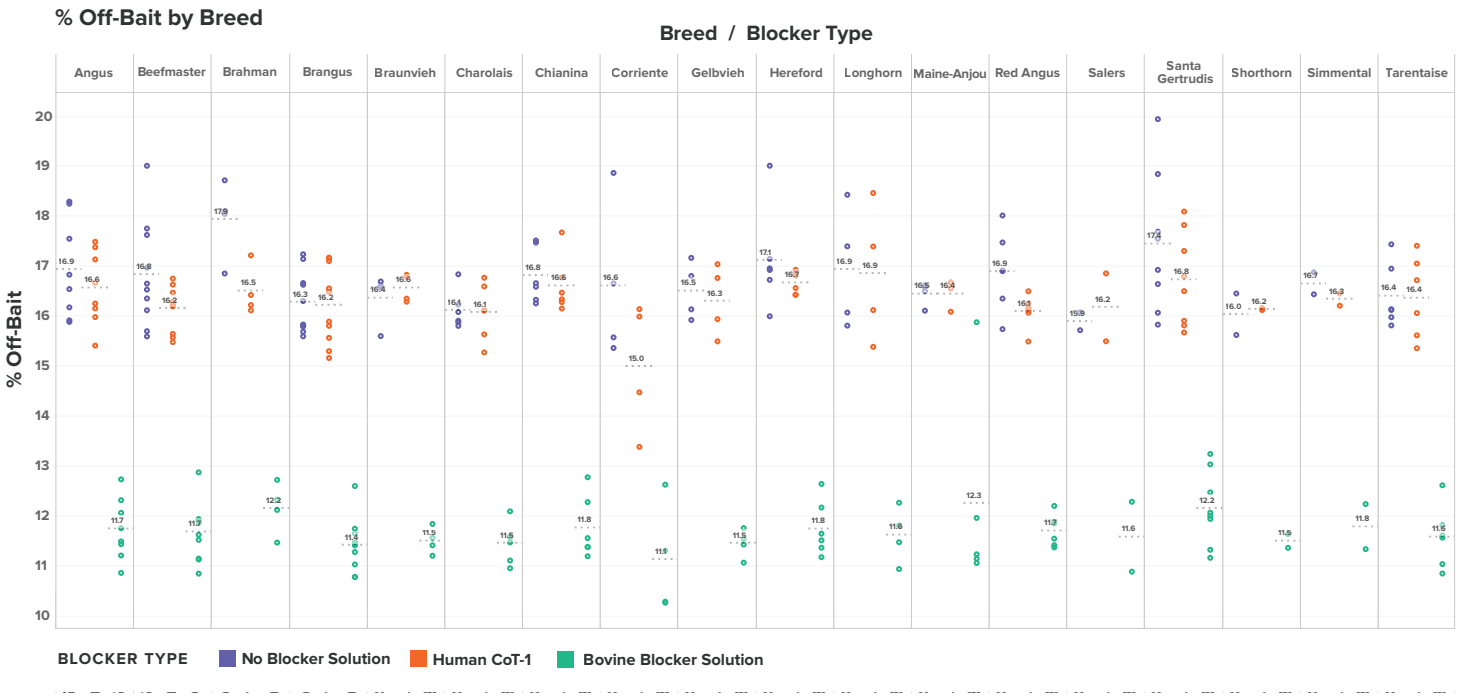

Figure 1. Off-bait performance by specific breed. Ninety-six samples of various masses between 40 - 75 ng of gDNA from 18 different breeds of cows were arrayed out without normalization and loaded into the Twist FlexPrep Library Preparation Workflow. The libraries were then pooled into 96-plex pools and processed through the Twist FlexPrep Target Enrichment Workflow using the Twist Genotyping Panel - Bovine 100k and sequenced on a NextSeq2000. Analysis was done with bwa-mem and Picard with 100x downsampling.

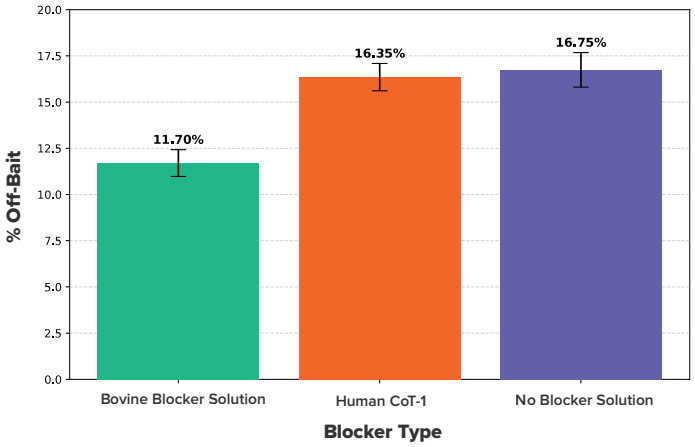

Figure 2. Overall off-bait performance. Ninety-six samples of various masses between 40 - 75 ng of gDNA from 18 different breeds of cows were arrayed out without normalization and loaded into the Twist FlexPrep Library Preparation Workflow. The libraries were then pooled into 96-plex pools and processed in the Twist FlexPrep Target Enrichment Workflow using the Twist Genotyping Panel - Bovine 100k and sequenced on a NextSeq 2000. Analysis was done with bwa-mem and Picard with 100x downsampling.

REFERENCES

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6. Heaton, M.P. et al. Using diverse U.S. beef cattle genomes to identify missense mutations in EPAS1, a gene associated with pulmonary hypertension. F1000Research 5, 2003 (2016). https://doi.org/10.12688/f1000research.9254.2

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ORDERING INFORMATION

Bovine Blocker Solution
126828: Twist Bovine Blockers, 2 Reactions - Illumina Compatible
126829: Twist Bovine Blockers, 12 Reactions - Illumina Compatible
126830: Twist FlexPrep UHT Bovine LP and Enrichment Kit, 192 Samples
126831: Twist FlexPrep UHT Bovine LP and Enrichment Kit, 1152 Samples

Twist Genotyping Panel - Bovine 100k
127890: Twist Genotyping Panel - Bovine 100k, 2 Reactions
127891: Twist Genotyping Panel - Bovine 100k, 12 Reactions
128386: Twist Genotyping Panel - Bovine 100k, 96 Reactions

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