

Gencove's low-pass sequencing technology

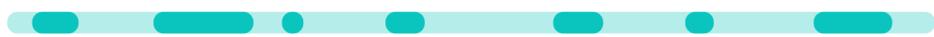
Whole genome information at the cost of genotyping arrays

What is low-pass sequencing?

The genome is shotgun sequenced at a very low depth (between 0.4x and 1x) and the raw sequence data is then uploaded to Gencove's imputation platform. This results in over 99% accurate variant calls across the whole genome.

In one single assay, low-pass sequencing returns millions of variant calls, including all the content from the commonly used arrays. This makes Gencove's low-pass sequencing platform the go-to technology for high-throughput genomic in agriculture.

low-pass sequencing



genotyping array



Solutions

Ready-to-run

We set up and validated our low-pass sequencing solution for a variety of agricultural and companion animal species and model organisms including cattle, pig, chicken, dog, cat, rat, mice, corn, soybean, peas and rice.



Sample results of concordance studies in different species performed with different industry partners

SPECIES	SEQUENCING COVERAGE	SITES CALLED AFTER IMPUTATION	CONCORDANCE WITH WGS	REFERENCE PANEL SIZE (INDIVIDUALS)
Cattle	0.4x	70 million	99.30%	946
Chicken	0.5X	26 million	99.00%	124
Dogs	1X	46 million	99.20%	435
Cats	0.4X	56 million	98.40%	78
Corn	1X	81 million	99.30%	277

Benefits:

- A single assay replacing all common arrays
- > **99%** accurate whole genome variant calls
- High-throughput and cost-efficient (Up to ~1500 samples per run using NovaSeq)
- Flexible setup of new species or custom populations
- Low DNA input required

Applications:

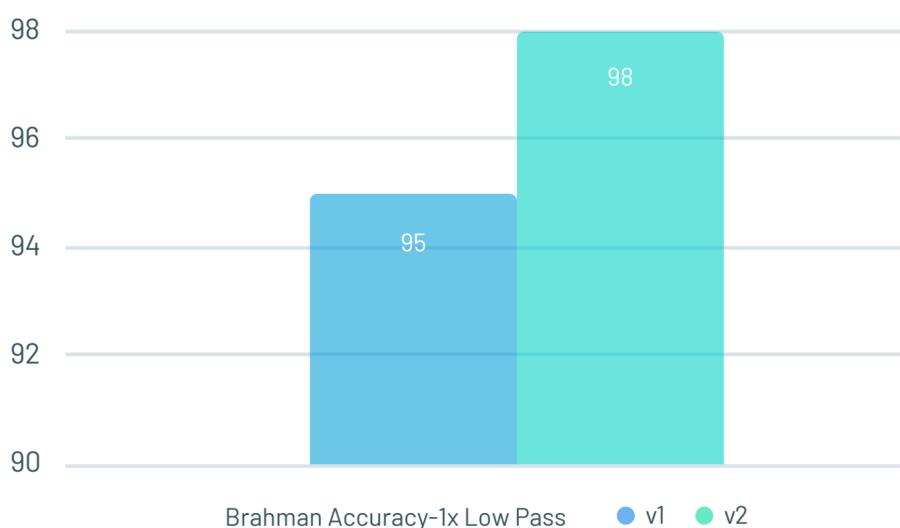
- Genomic selection
- Parentage analysis
- Marker-assisted breeding
- Breed/variety analysis
- QTL mapping
- Embryo genotyping

Advanced solutions

Customized set up for specific species or populations

We can easily set up a custom reference panel for a specific population. The process only requires the selection of key individuals for deeper sequencing (>4x) to add to the imputation reference panel.

Improvement in accuracy through reference panel augmentation



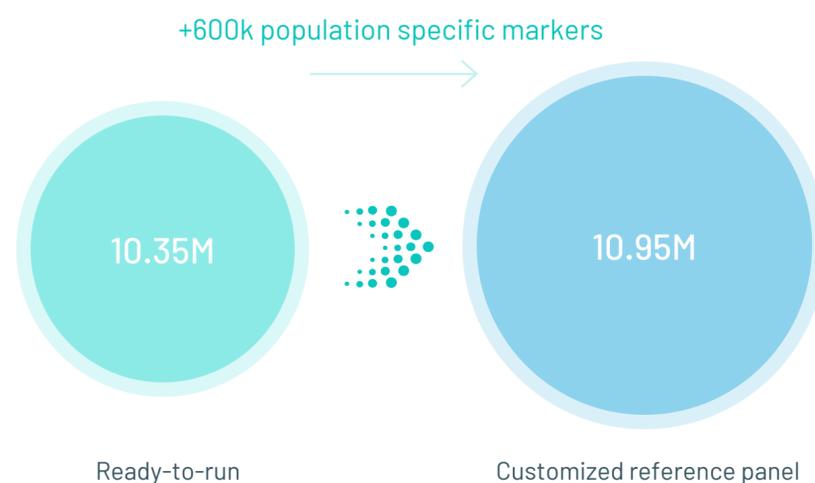
Through the addition of 49 more Indicine cattle to our v2 reference panel, imputation accuracy for Indicine influenced animals increased from 95 % to over 98%

Flexible and efficient optimization of prediction marker set

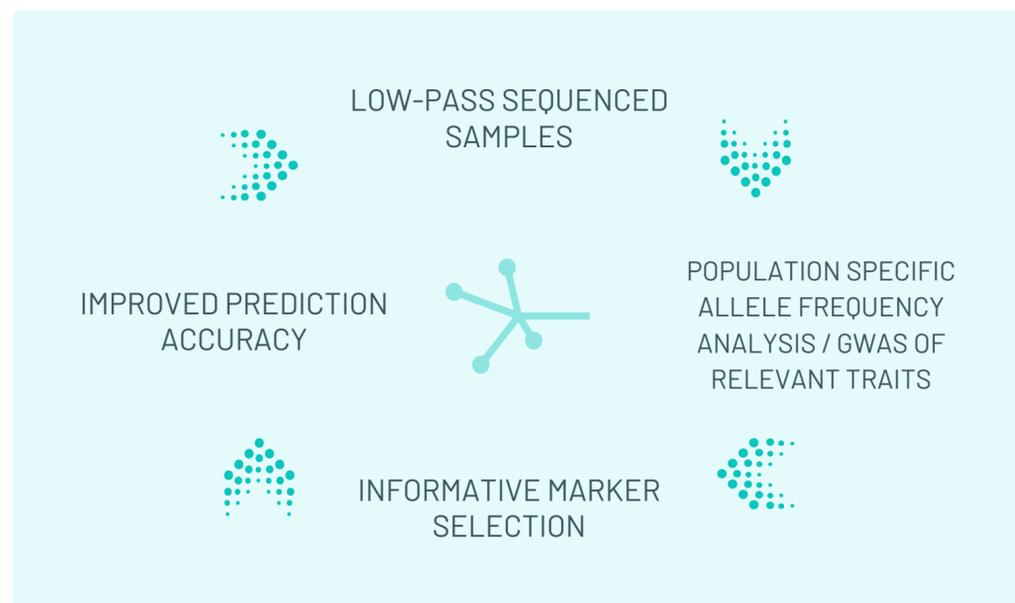
Gencove's platform allows frequent software-based updates to improve a genomic prediction market set through two different processes:

1. With the low-pass sequencing data, identifying the high frequency genetic markers for a specific population
2. With low-pass data and relevant trait phenotypes, through frequent QTL mapping

Reference panel augmentation for specific chicken lines



An increase in the number of polymorphic variants (MAF > 5%) in a custom reference panel designed for a specific line relative to Gencove's ready-to-run chicken reference panel



TRUSTED BY:



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