

# Variant Report

Variant calling pipelines contains two exclusive sections.

## Mapping

This section provides details of the abundance/mapping statistics. This section also has three sub-sections: This

1. Data Table: This (Fig. 1) shows several alignment statistics such as the number of total processed reads, the number of mapped or multi-mapped reads, and the uniquely mapped reads.
2. Sample Coverage: Allows users to explore the alignment quality through a series of plots. Sample depth of coverage in total read counts. Sample depth of coverage in percentages. On-target mapping quality in a 96-well plate format
3. Read Lengths: Histograms and 96-well plate plots show the read length distributions for mapped and unmapped reads.
4. Genome Browser: Aligned reads against the reference genome can be viewed for each sample. The genome browser is interactive and allows exploratory analysis.

The screenshot displays the Stanome Genotyping Report interface. The main title is "Genotyping Report" and the sub-section is "Sequence Alignment Metrics". The "Data Table" tab is selected, showing a table with 8 columns: Samples, Number of reads, Unmapped reads, Mapped reads, Uniquely mapped reads, Multi mapped reads, On target reads, and Off target reads. The table contains 4 rows of data for samples tomato1, tomato2, tomato3, and tomato4. The interface also includes a search bar, a table toolbar with options like Copy, CSV, Excel, PDF, Print, and Show 10 rows, and a navigation bar with Previous, 1, and Next buttons. A link is provided to switch the Merged BAM file on the Genome Browser.

Samples	Number of reads	Unmapped reads	Mapped reads	Uniquely mapped reads	Multi mapped reads	On target reads	Off target reads
tomato1	9,117,867	72,673	9,045,194	8,639,940	405,254	832,980	8,212,214
tomato2	6,820,857	47,813	6,773,044	6,477,270	295,774	624,091	6,148,953
tomato3	3,825,942	26,180	3,799,762	3,632,419	167,343	350,286	3,449,476
tomato4	11,436,991	95,518	11,341,473	10,833,205	508,268	1,045,004	10,296,469

## Variant Calling

This section provides details of the abundance/mapping statistics. This section also has three sub-sections:

1. Call Rate Summary: Provides a summary of the genotype calls.
2. Target Call Rates: Genotype calling metrics for the top 100 targets are shown in the table format. The complete list can be downloaded from the **Reports** section. The position field is cross-linked to the Variant Browser.

This section also shows:

1. Genotype call distribution
2. Genotype Heatmap
3. Sample Call Rates: Histograms and 96-well plate plots show the call rate distributions from all the samples.
4. Genotypes: Shows table of genotypes obtained for each marker across all the samples
5. Variant Browser: Sequencing reads support for each variant can be viewed for each sample (Fig. 2). The genome browser is interactive and allows exploratory analysis.

The screenshot displays the Stanome Genotyping Report interface. The main header shows the report title "DEMOPROJECT\_VARIANT\_3156181748\_VARIANT SUITE 1412 DEMO\_ANR.HTML" and the "Genotyping Report" title. The left sidebar contains navigation options: Analysis Summary, Sample Quality, Mapping, and Variant Calling (highlighted). The main content area is titled "Variant Calling Metrics" and includes tabs for Variant Summary, Target Call Rates, Sample Call Rates, Genotype Table, and Variant Browser (selected). The Variant Browser view shows a genomic region from 4,684,400 bp to 4,684,435 bp. It displays a sequence of nucleotides (A C A G A G A A T T T G T A G A C C T C A T C C A C A A A C T C C T A G G G A) and a corresponding alignment of sequencing reads. The alignment shows a red vertical bar indicating a variant position at approximately 4,684,420 bp. The interface includes search and zoom controls at the top of the browser view.

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