
# Extending the Curio Genomics Platform for the Wheat Research Community

## DNA Sequences to Analysis Results

*Presented April 30th, 2020 to the IWGSC Community*

*Author: Shawn Quinn (CTO, Curio Genomics)*

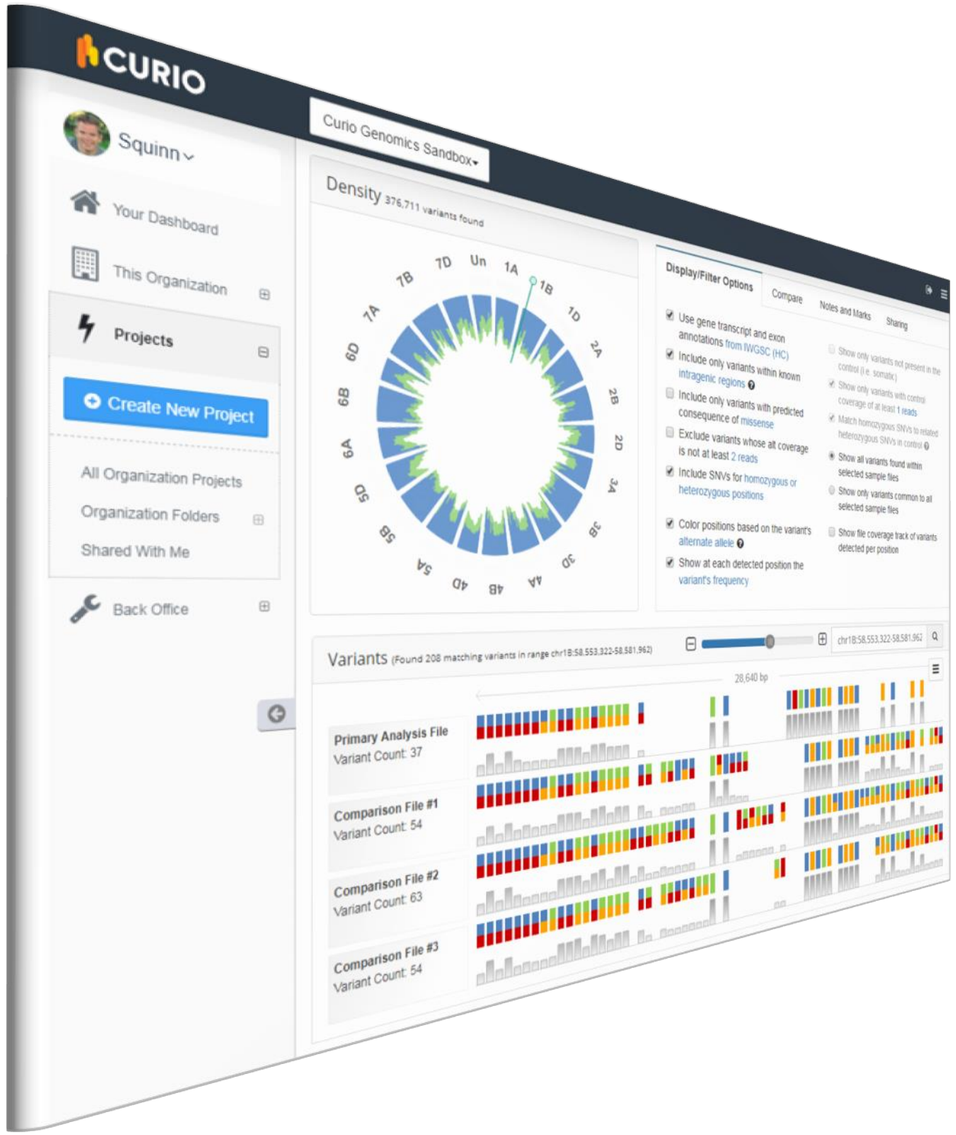
# Extending the Curio Genomics Platform for the Wheat Research Community: *DNA Sequences to Analysis Results*

# Presentation Overview

- What is Curio
- Demonstration of Several Crop/Wheat Research Examples
  - DNA-Seq and RNA-Seq
  - Read Mapping Analysis
  - Variant Analysis
  - Coverage Analysis
  - Expression Analysis
- Looking Ahead
- Acknowledgements

# What is Curio?

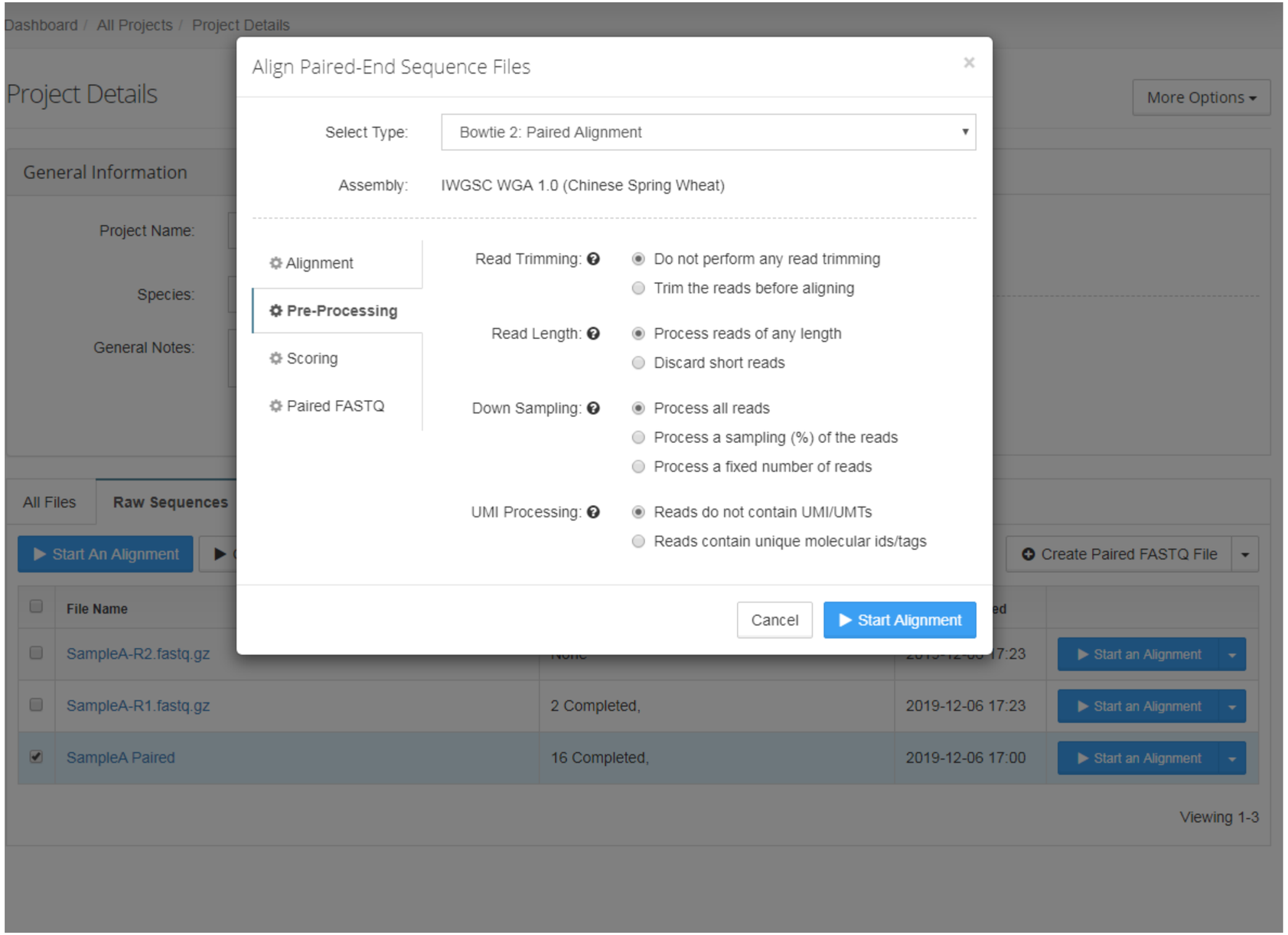
- Modern big data management and genomic analysis platform, fully web-based, collaboration ready
- Supports both bioinformatic processing and scientific interpretive analysis
- Provides scalable data processing and interactive data visualizations using real-time databases and clustering technologies
- Designed for extensibility to continuously support new analysis methods, data types, etc.
- Includes complex crop research solutions, including tetraploid and hexaploid wheat DNA-Seq and RNA-Seq analysis



# DNA-Seq Hexaploid Wheat: Read Mapping and Visualization

# Hexaploid Wheat: Read Mapping

- Incorporates Chinese Spring Wheat (*Triticum aestivum*) reference assembly from the IWGSC (i.e. the International Wheat Genome Sequencing Consortium)



# Hexaploid Wheat: Read Mapping

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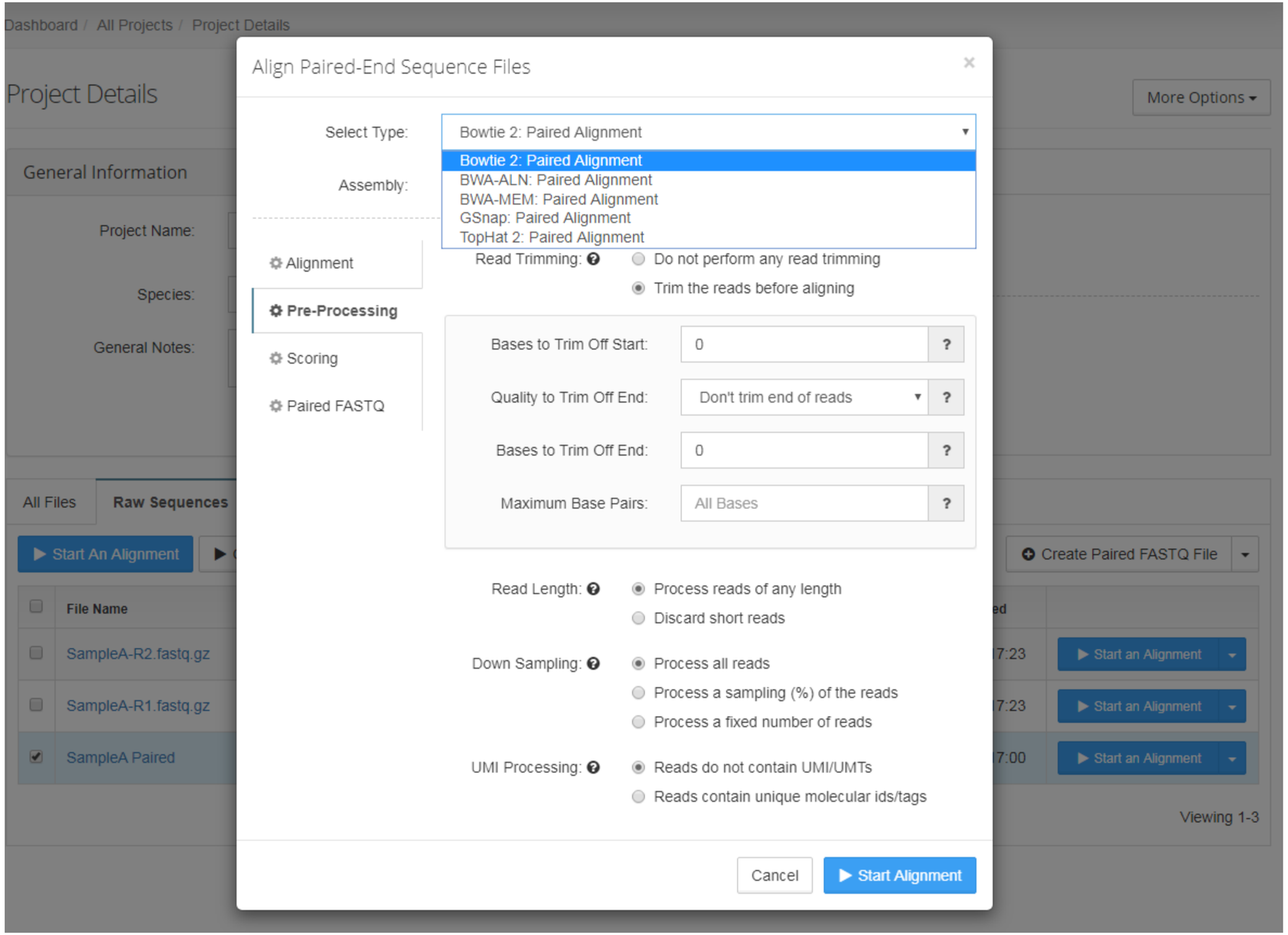
- Multiple read mapping algorithms with pre-built indexes that are deployed and ready on a computational cluster
- Experiment with various alignment and read processing options without requiring any pipeline configuration



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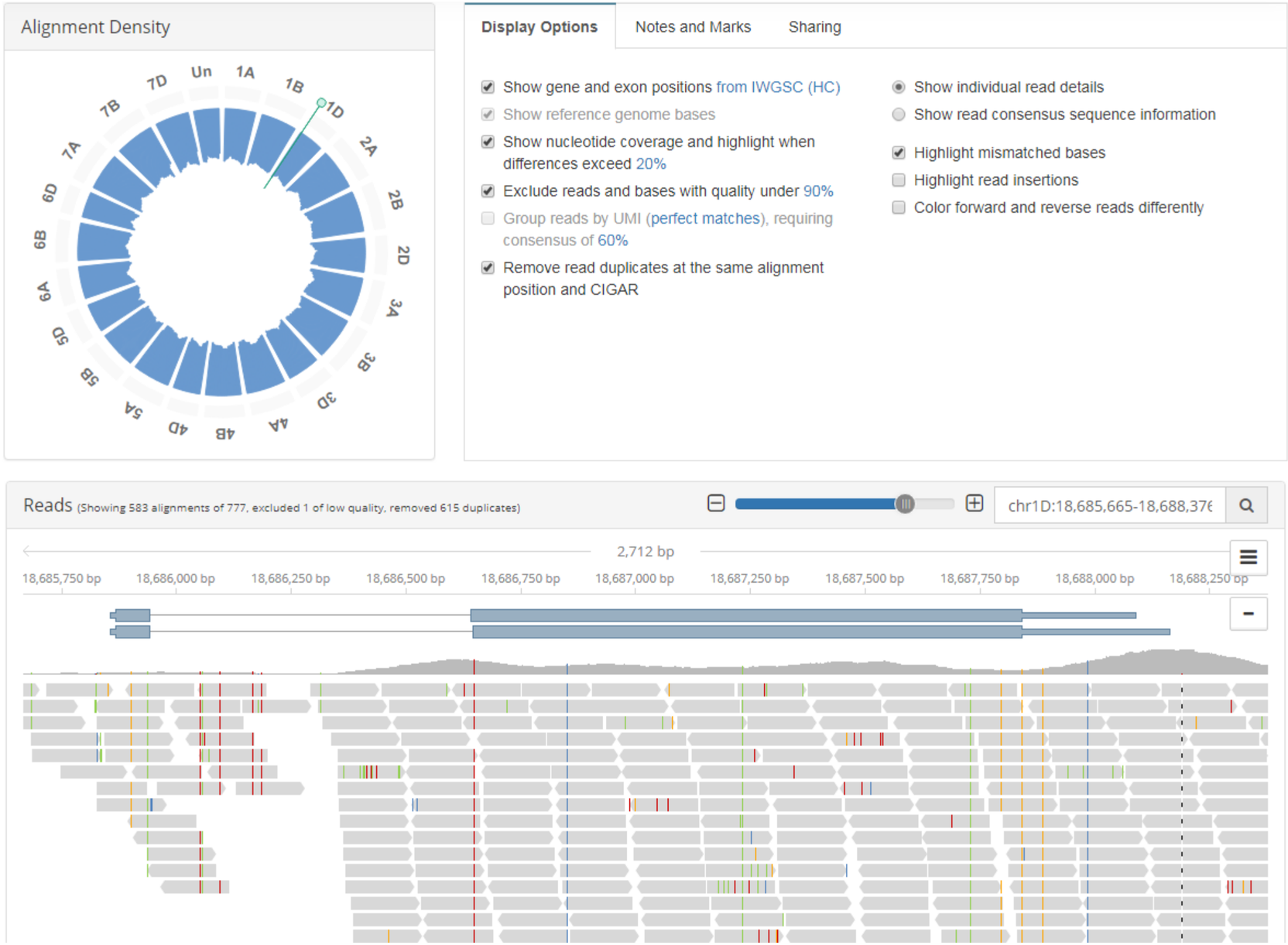
- Quickly browse and visualize reads from samples of any size, anywhere in the genome



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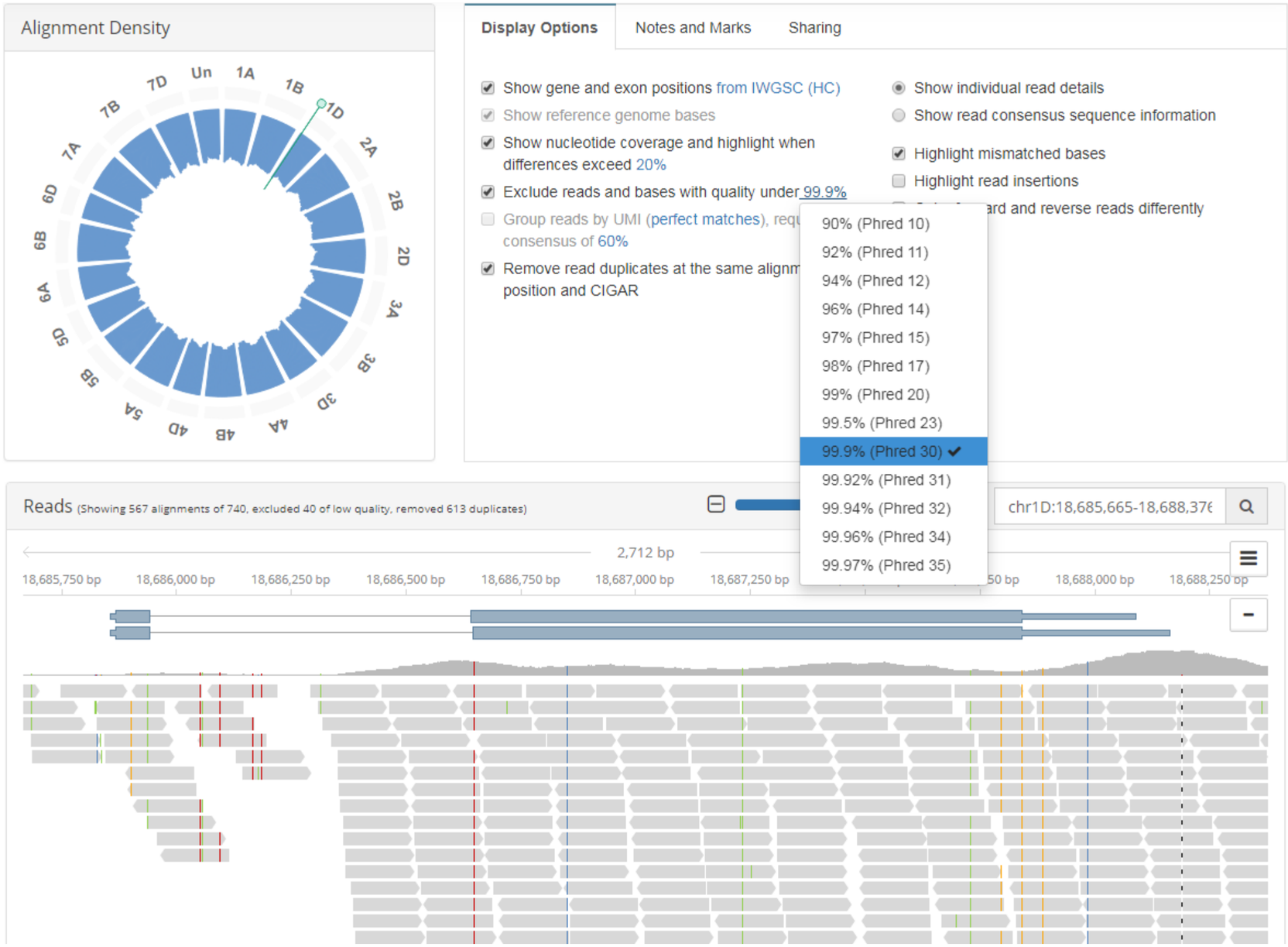

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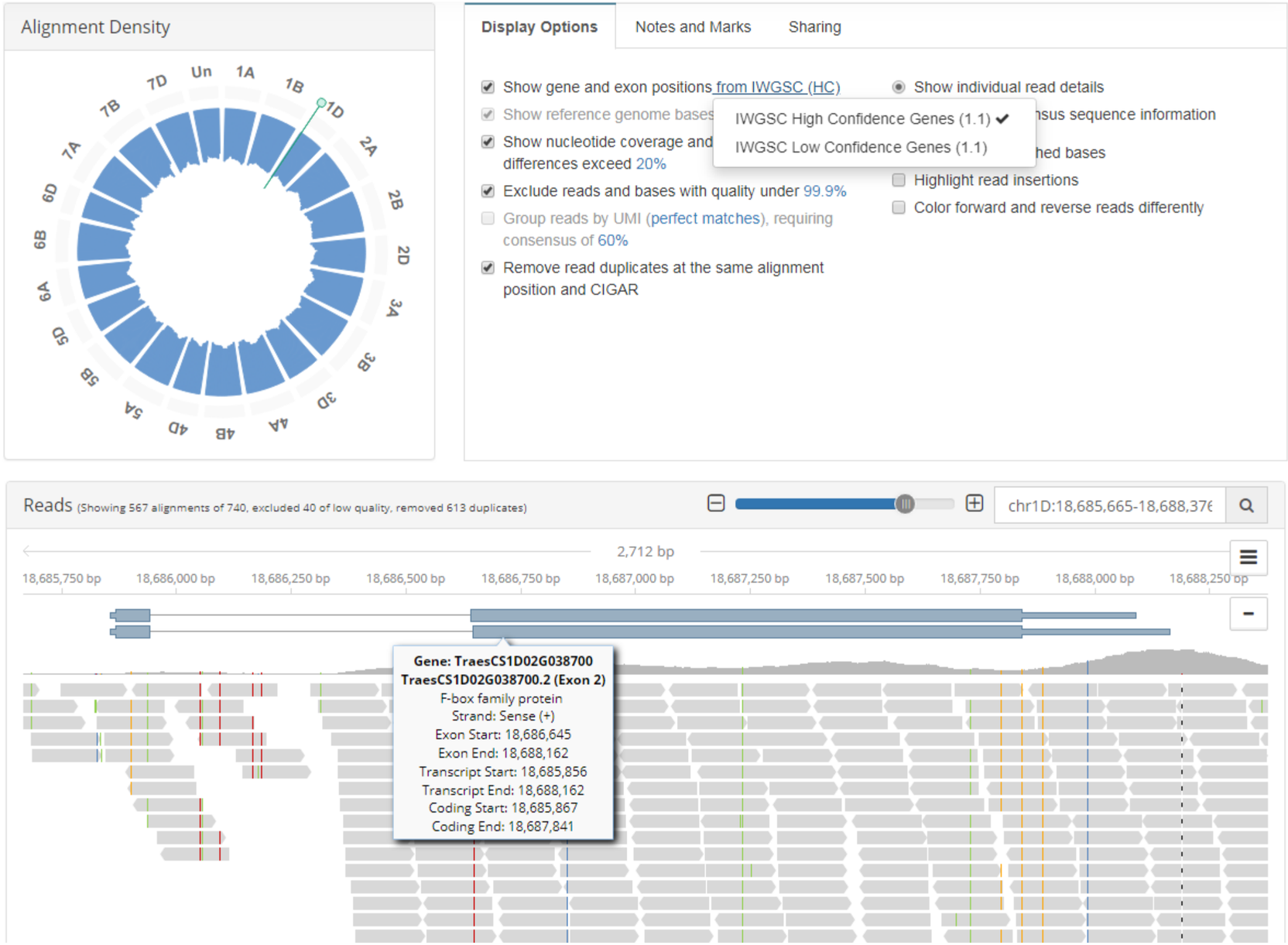

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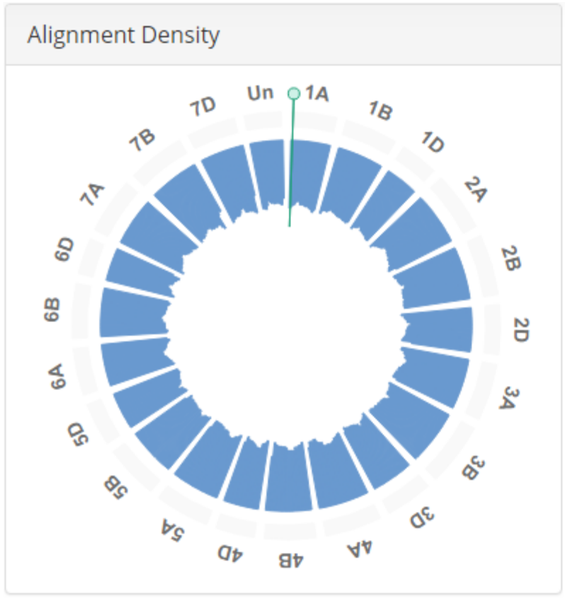


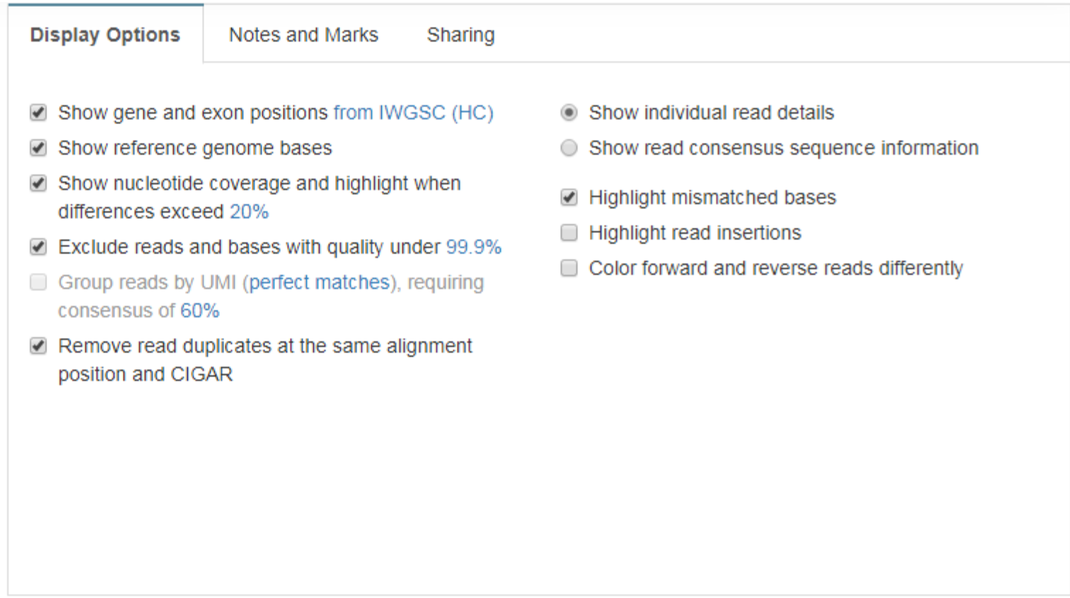


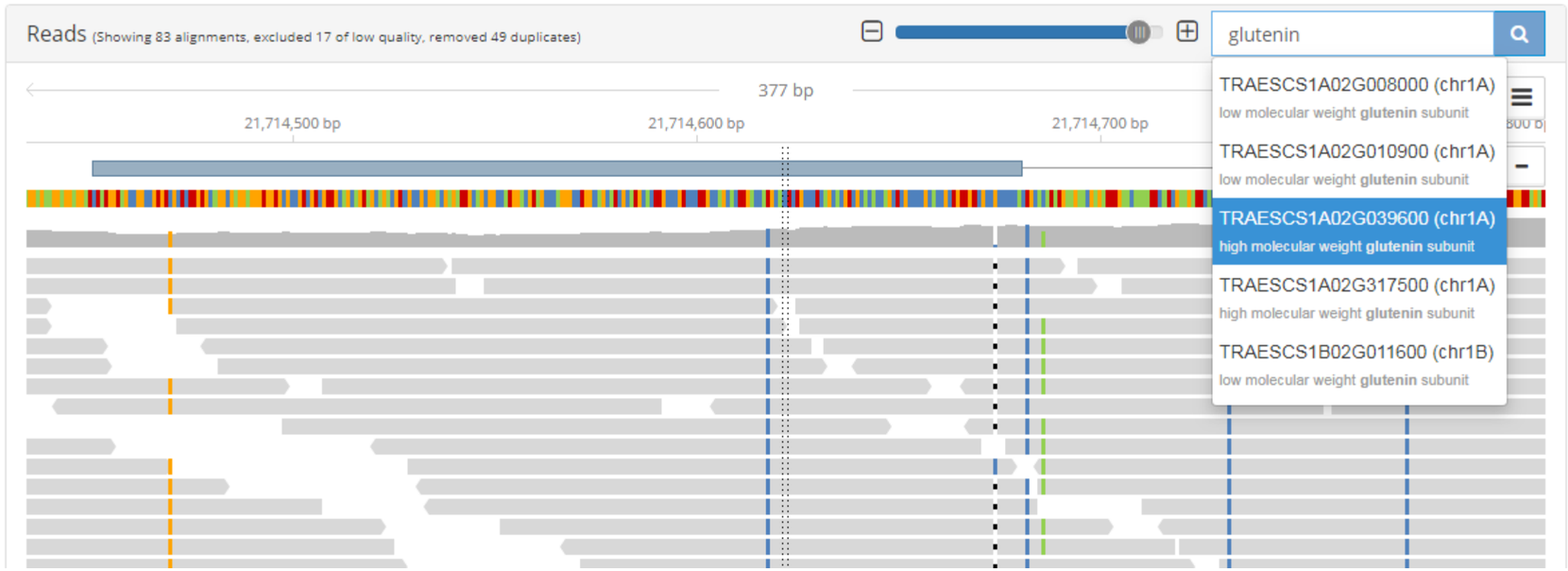

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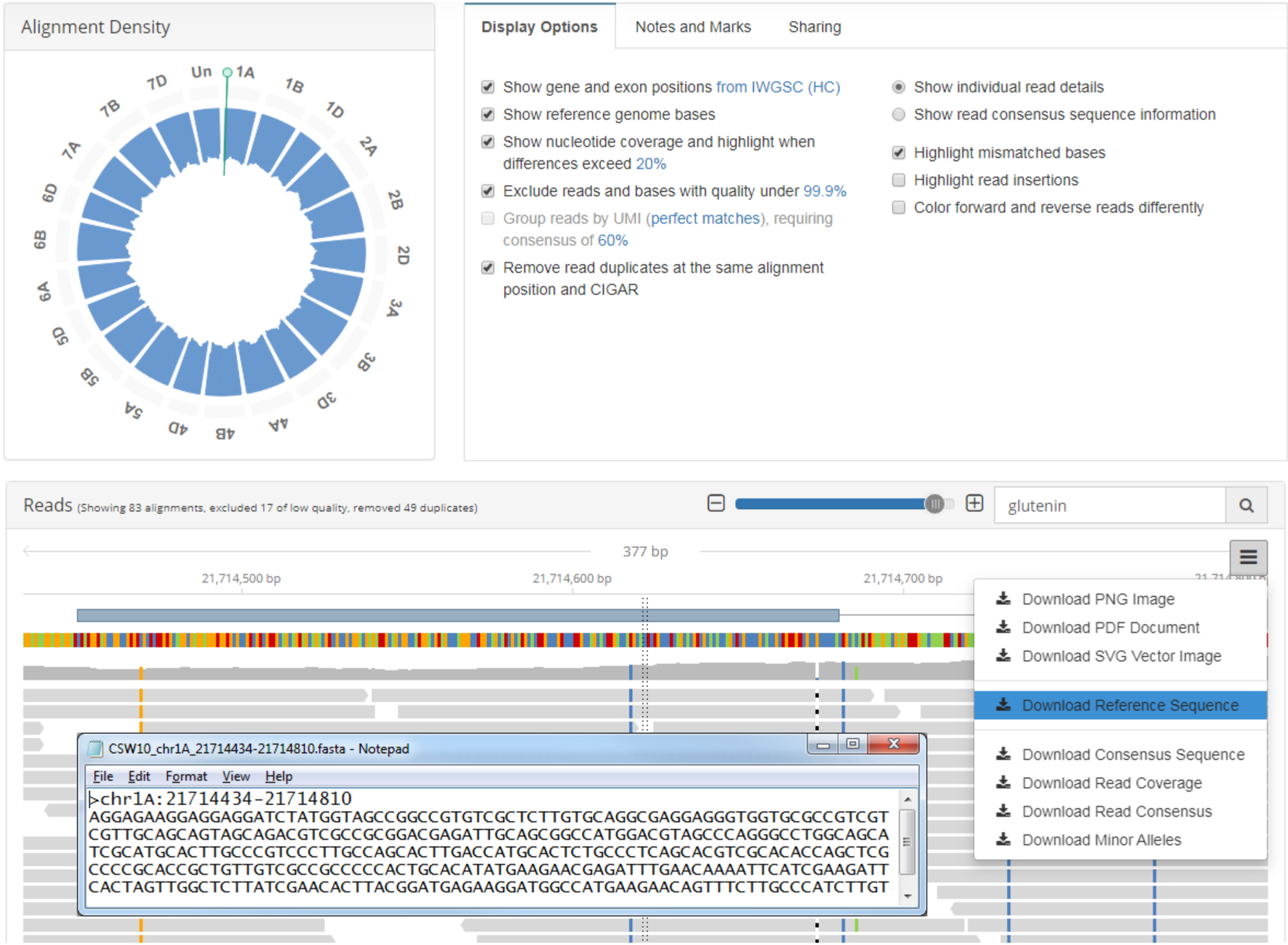

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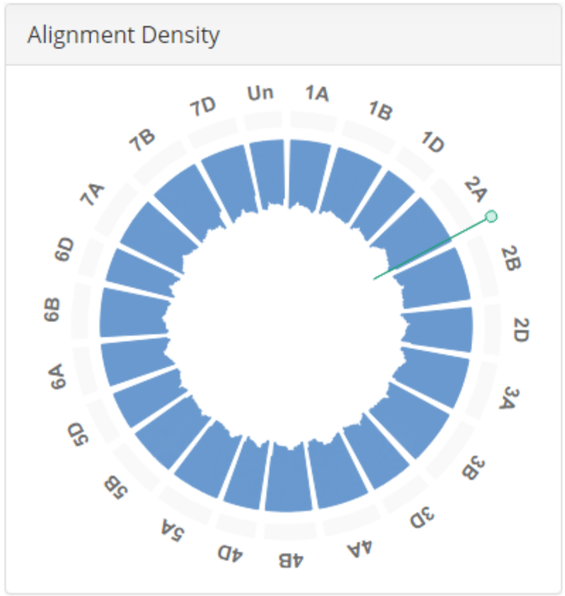
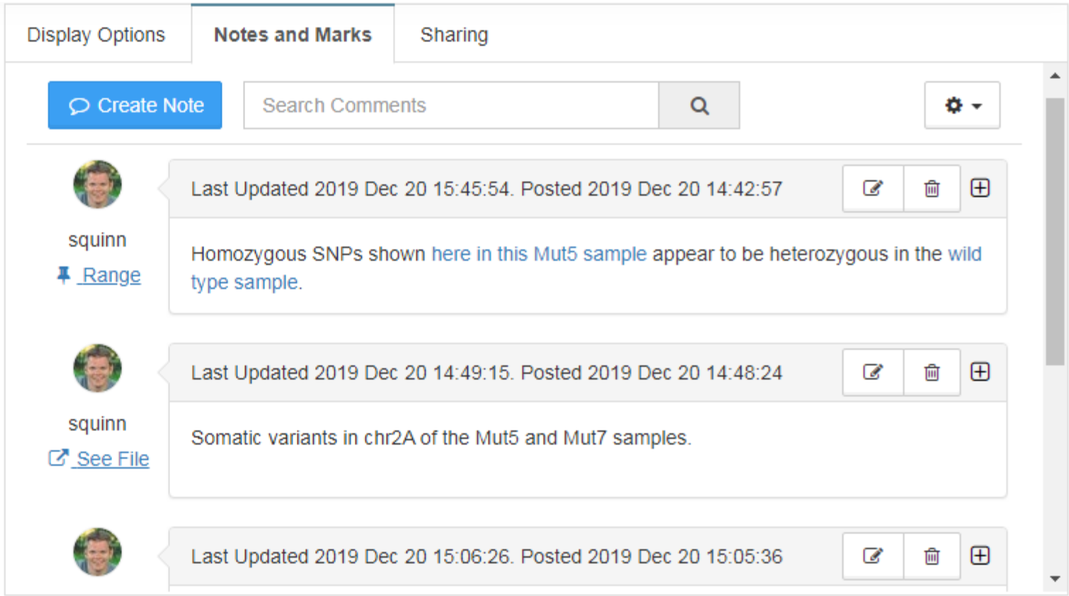
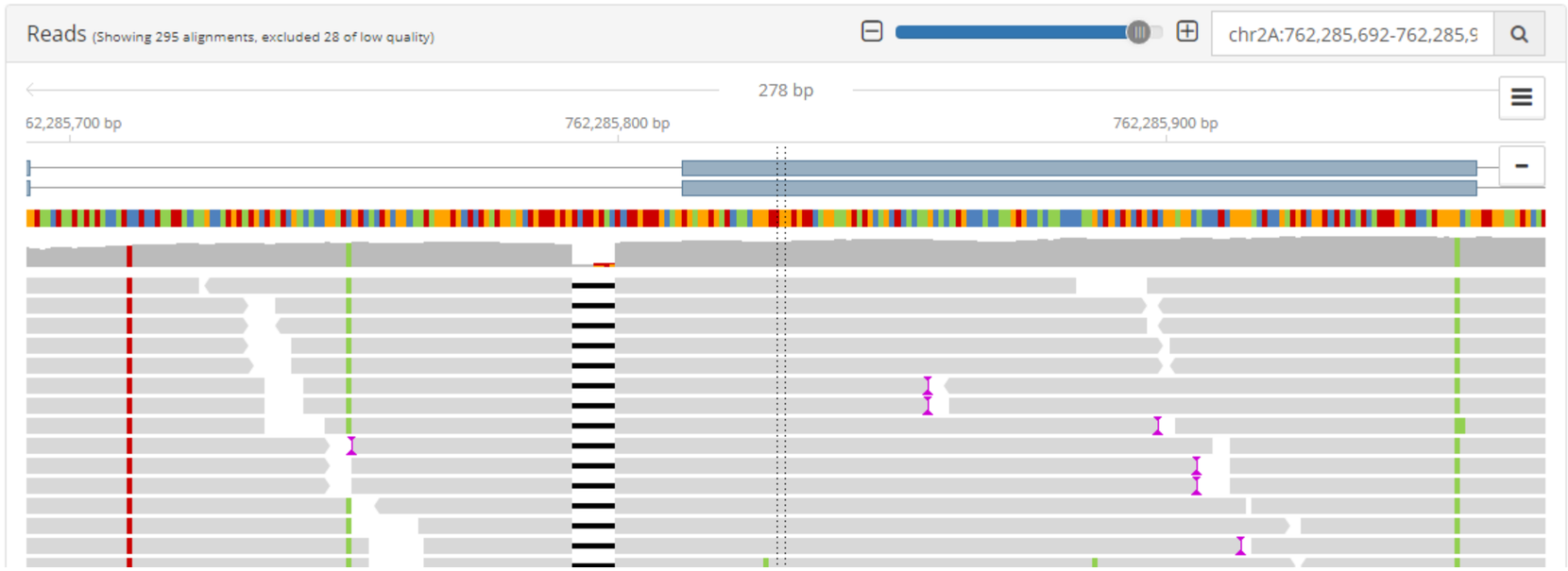
- Navigate and collaborate through annotated comments



# DNA-Seq Hexaploid Wheat: Variant Analysis

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- Call variants leveraging the Chinese Spring Wheat reference assembly and related annotations from the IWGSC
- Operate on one or multiple samples of any read depth simultaneously
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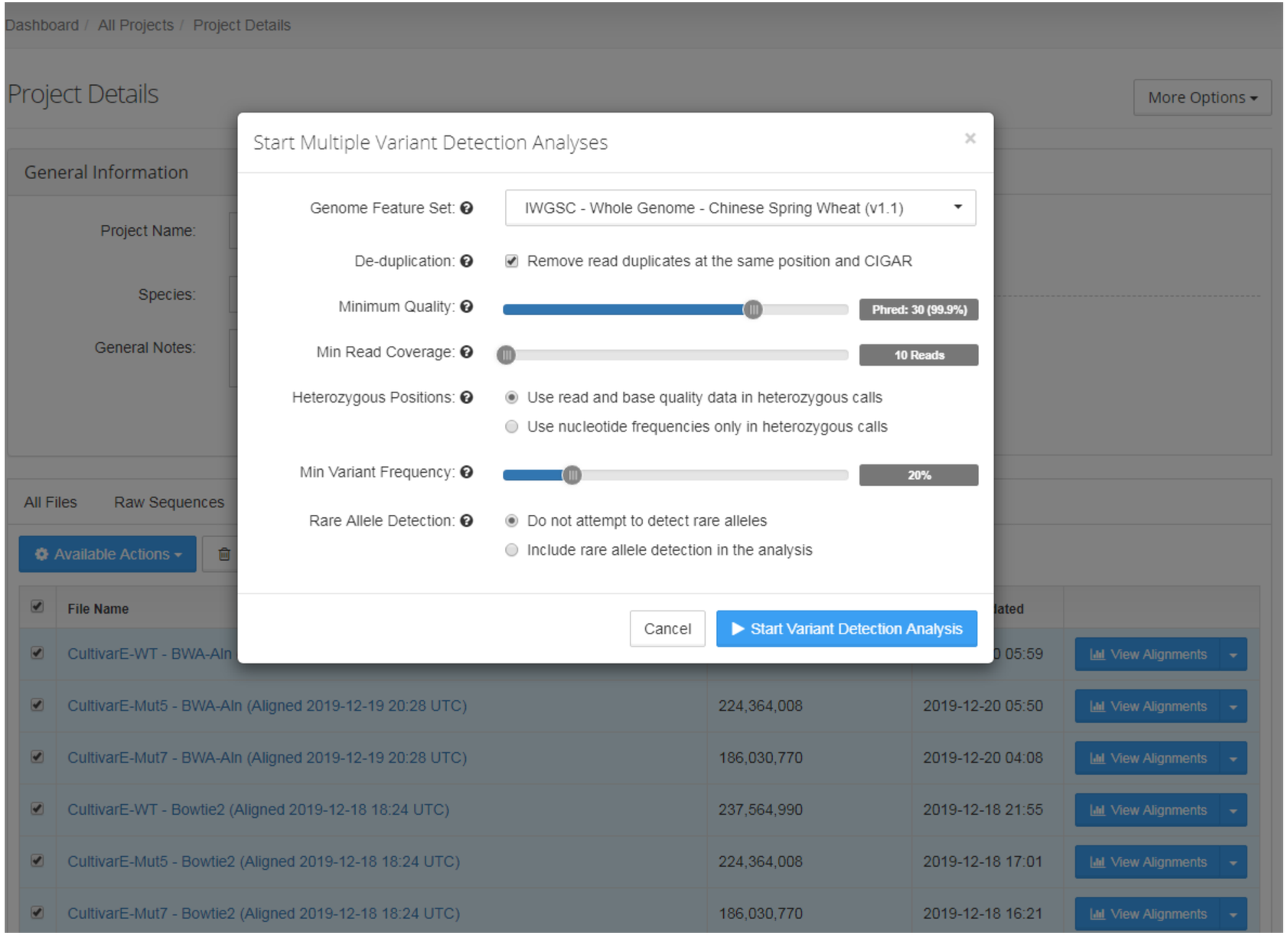

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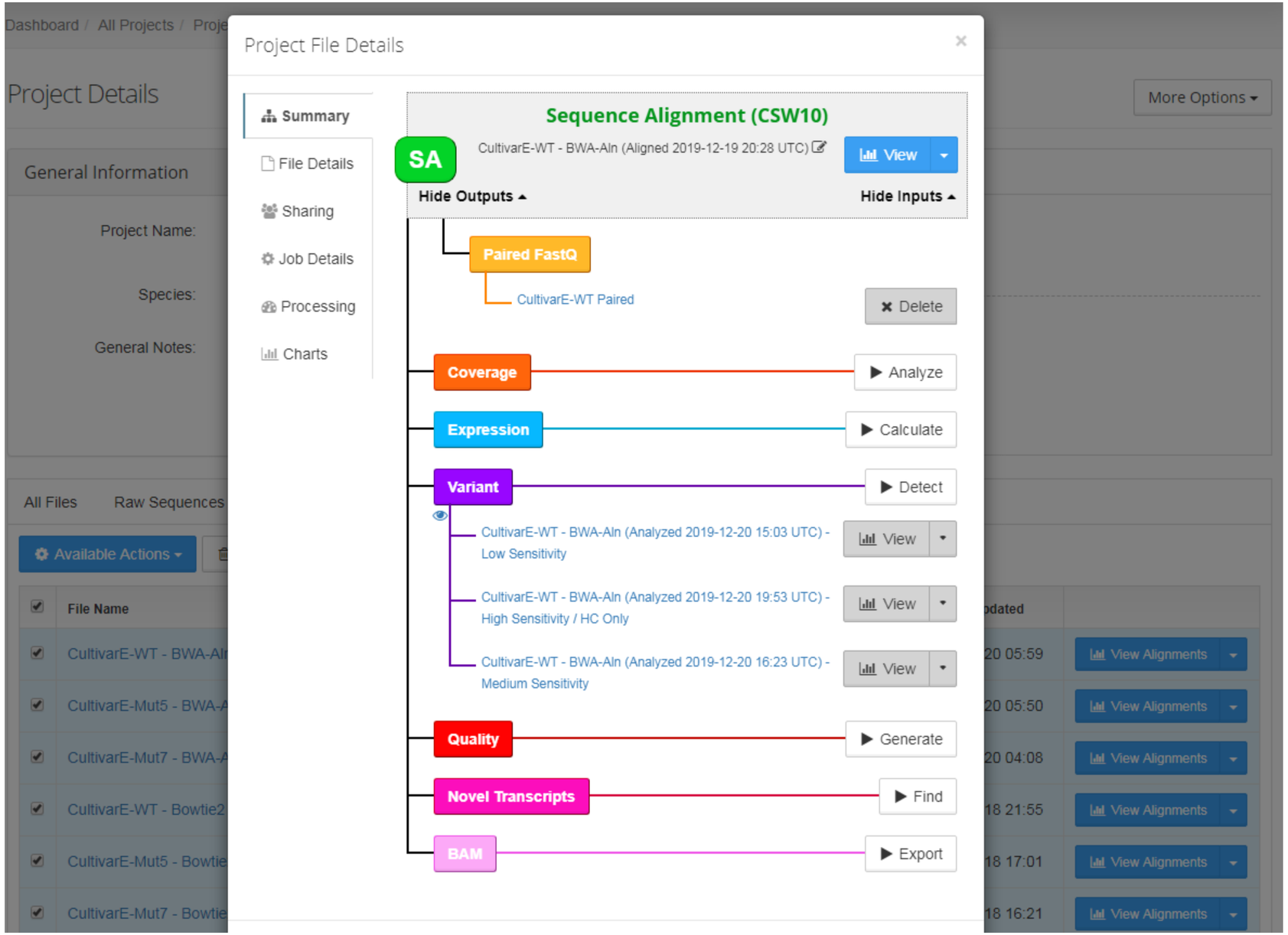

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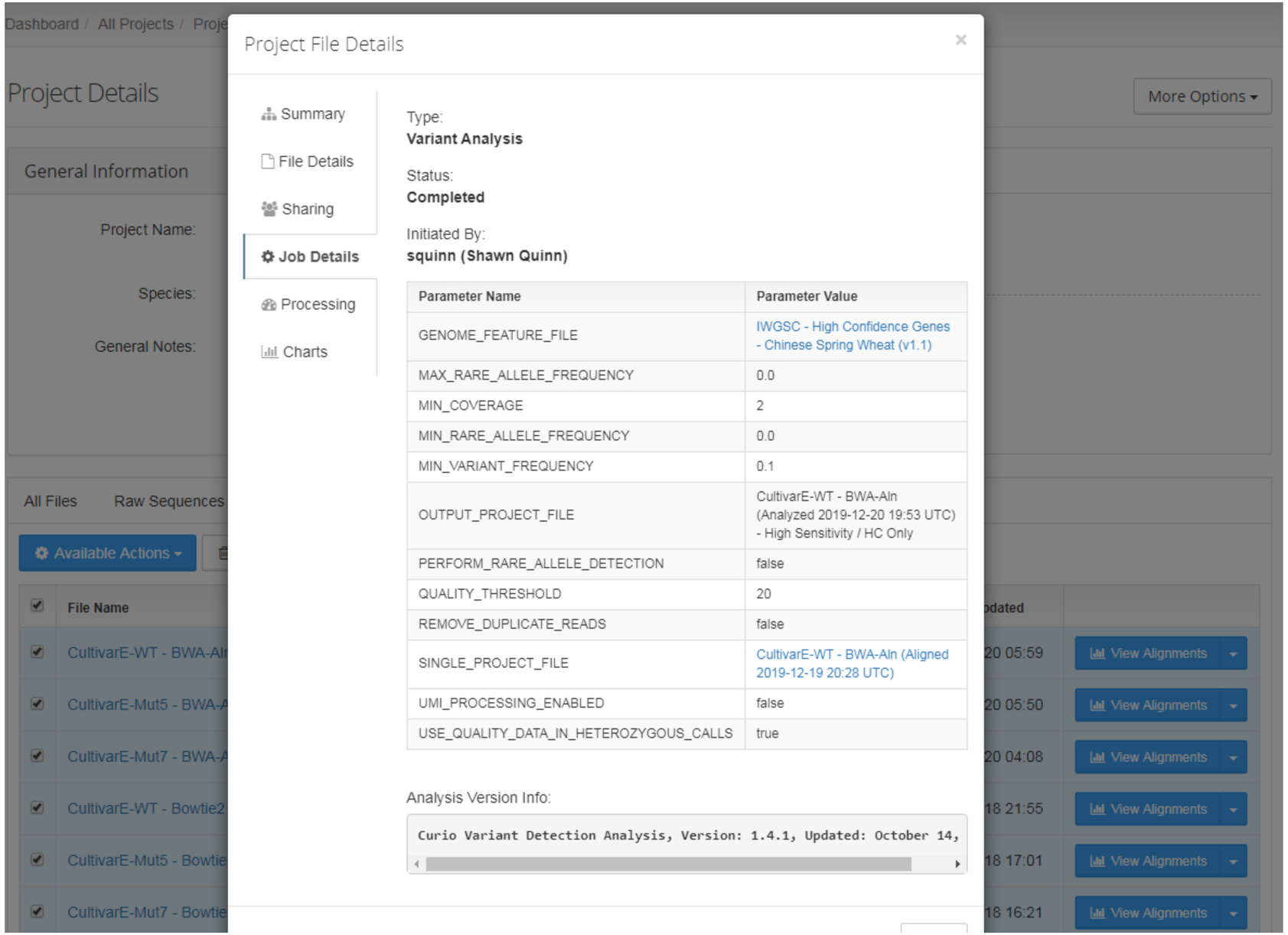

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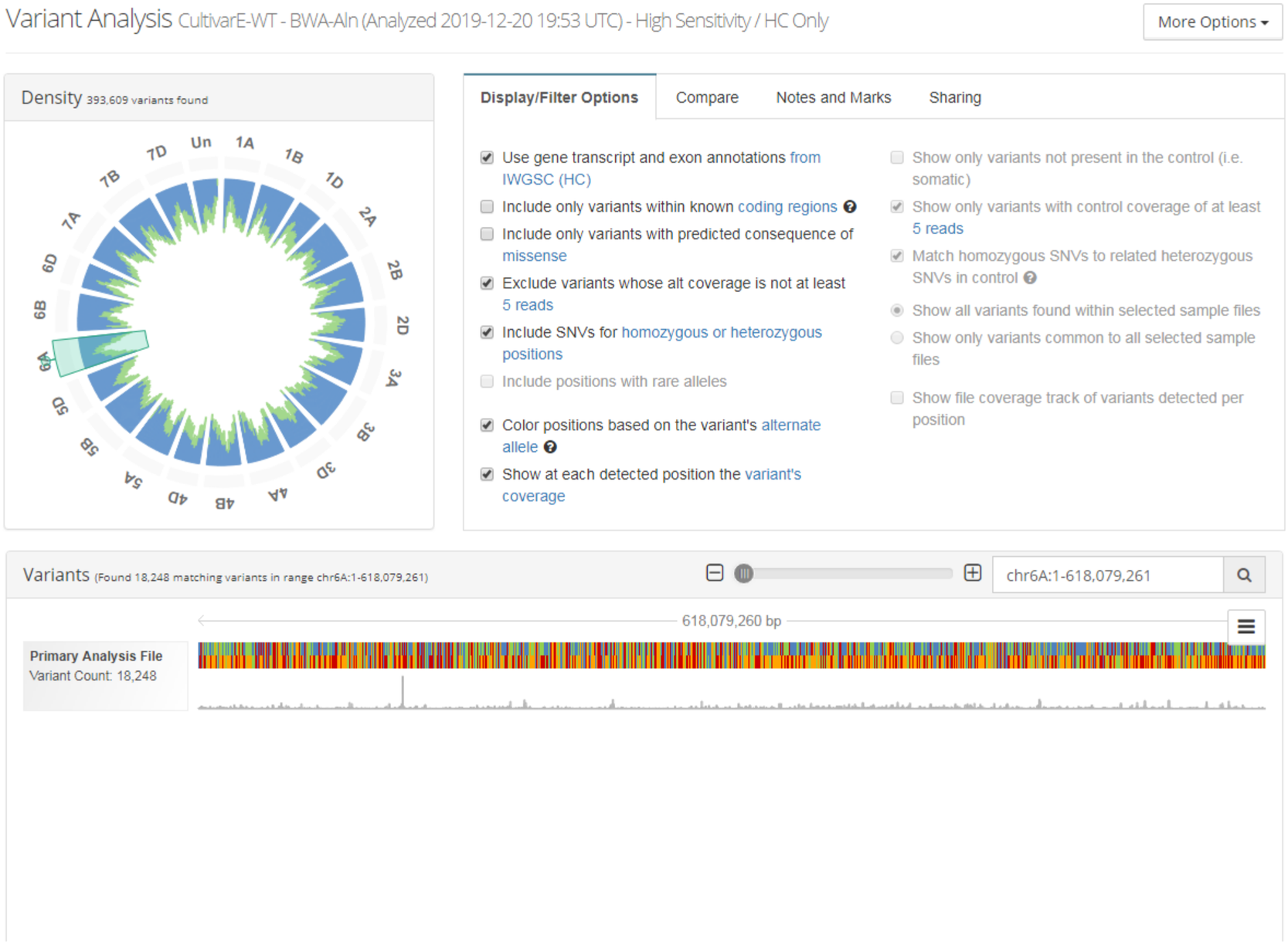

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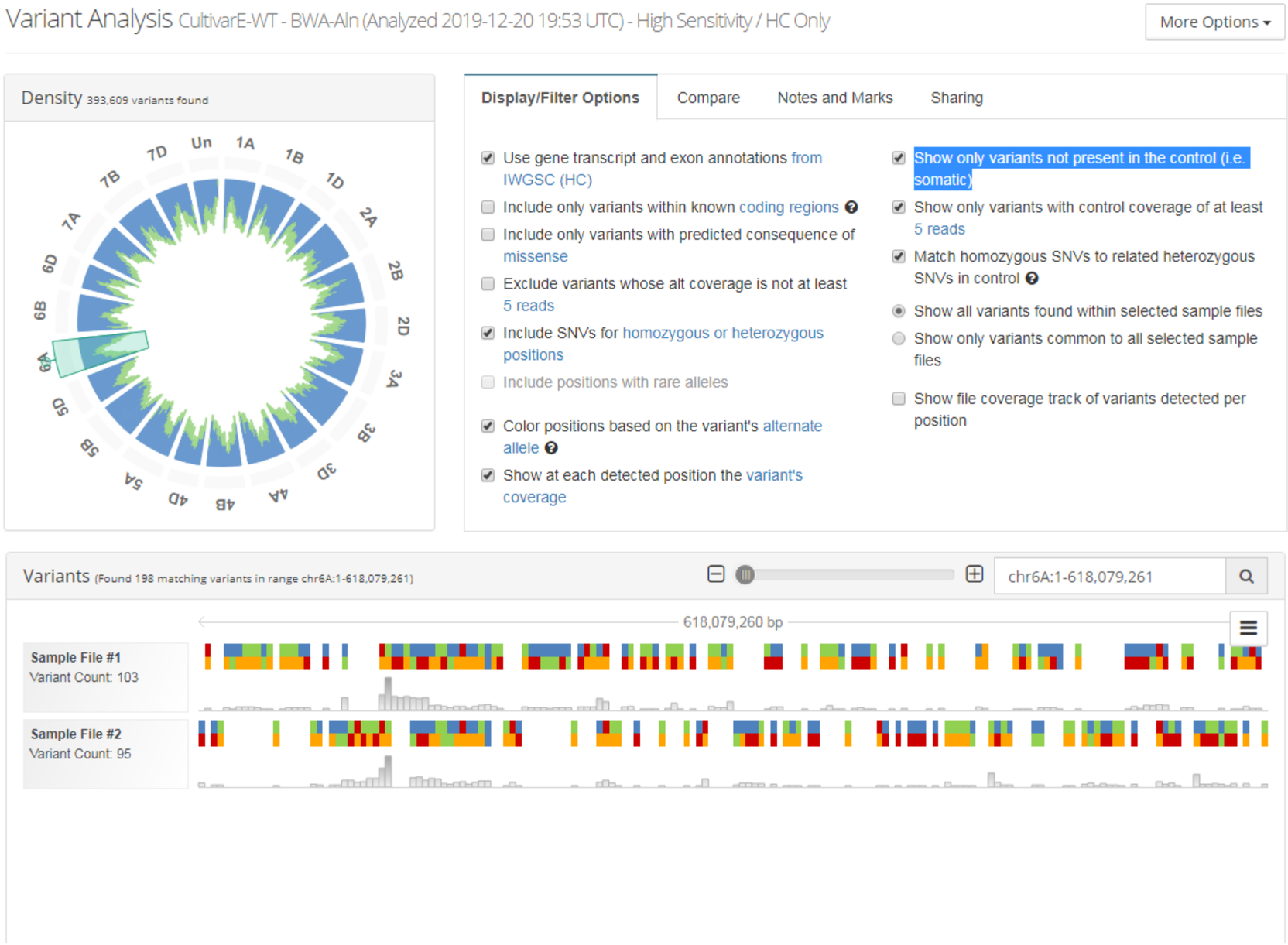

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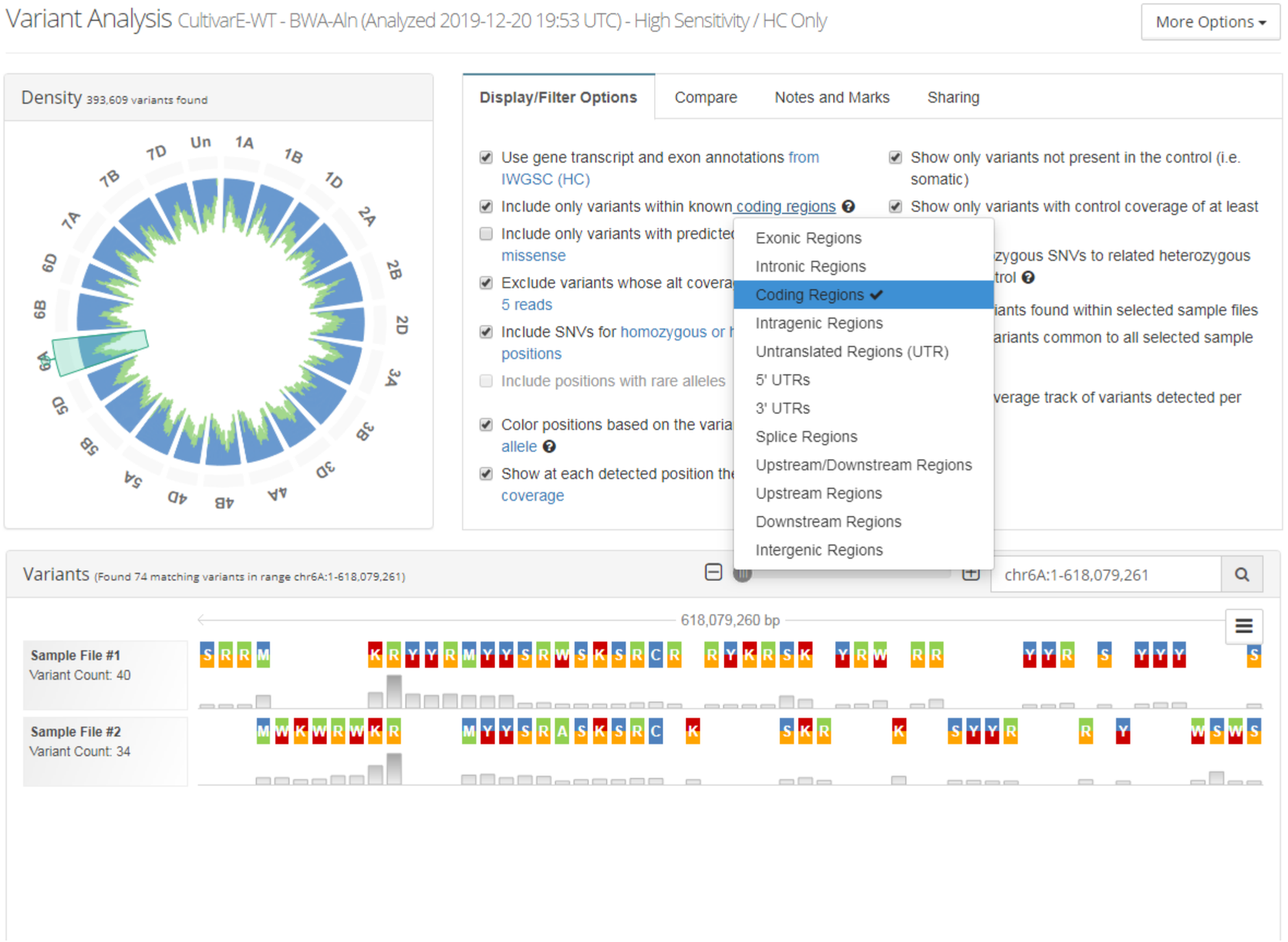

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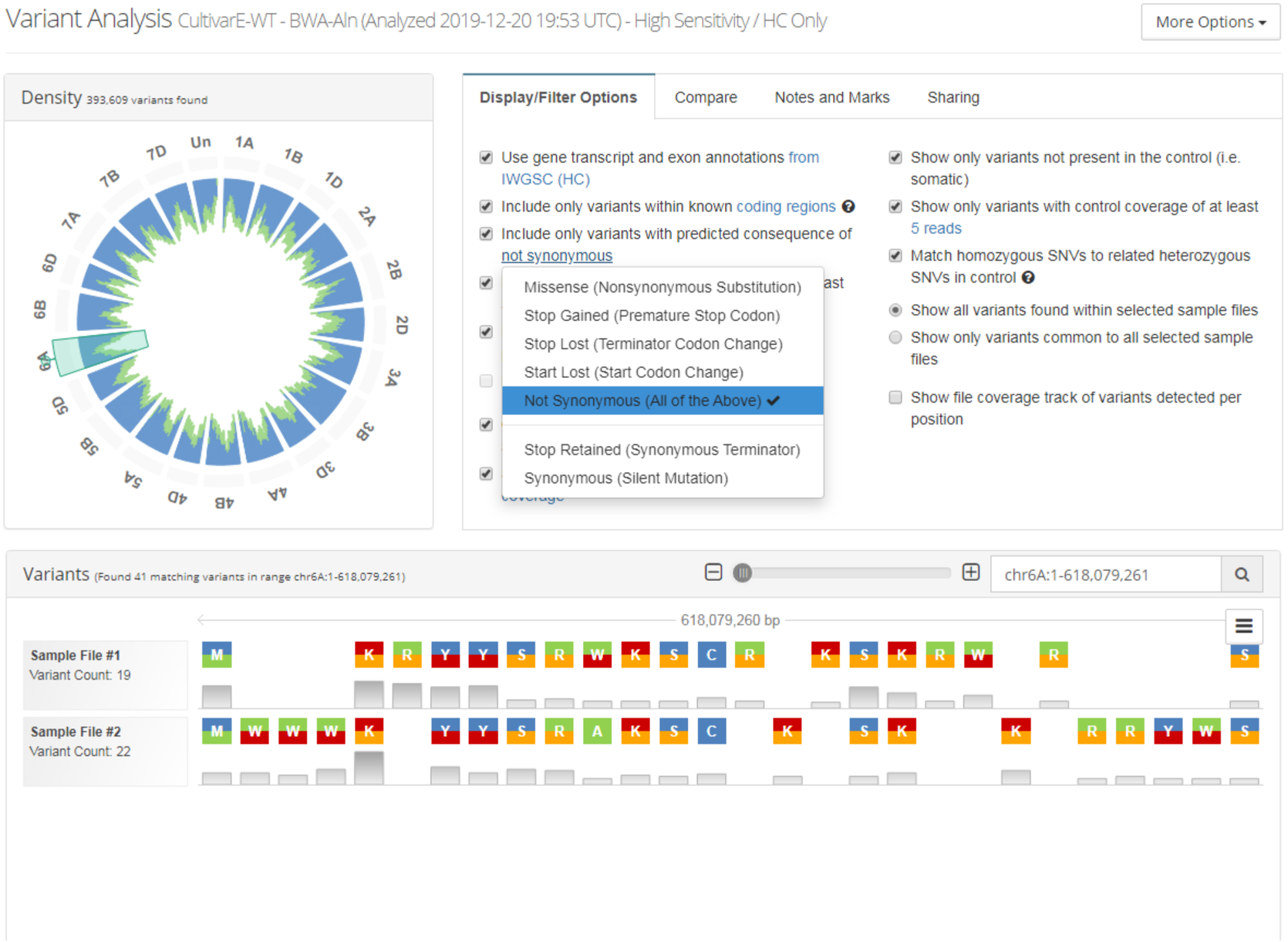

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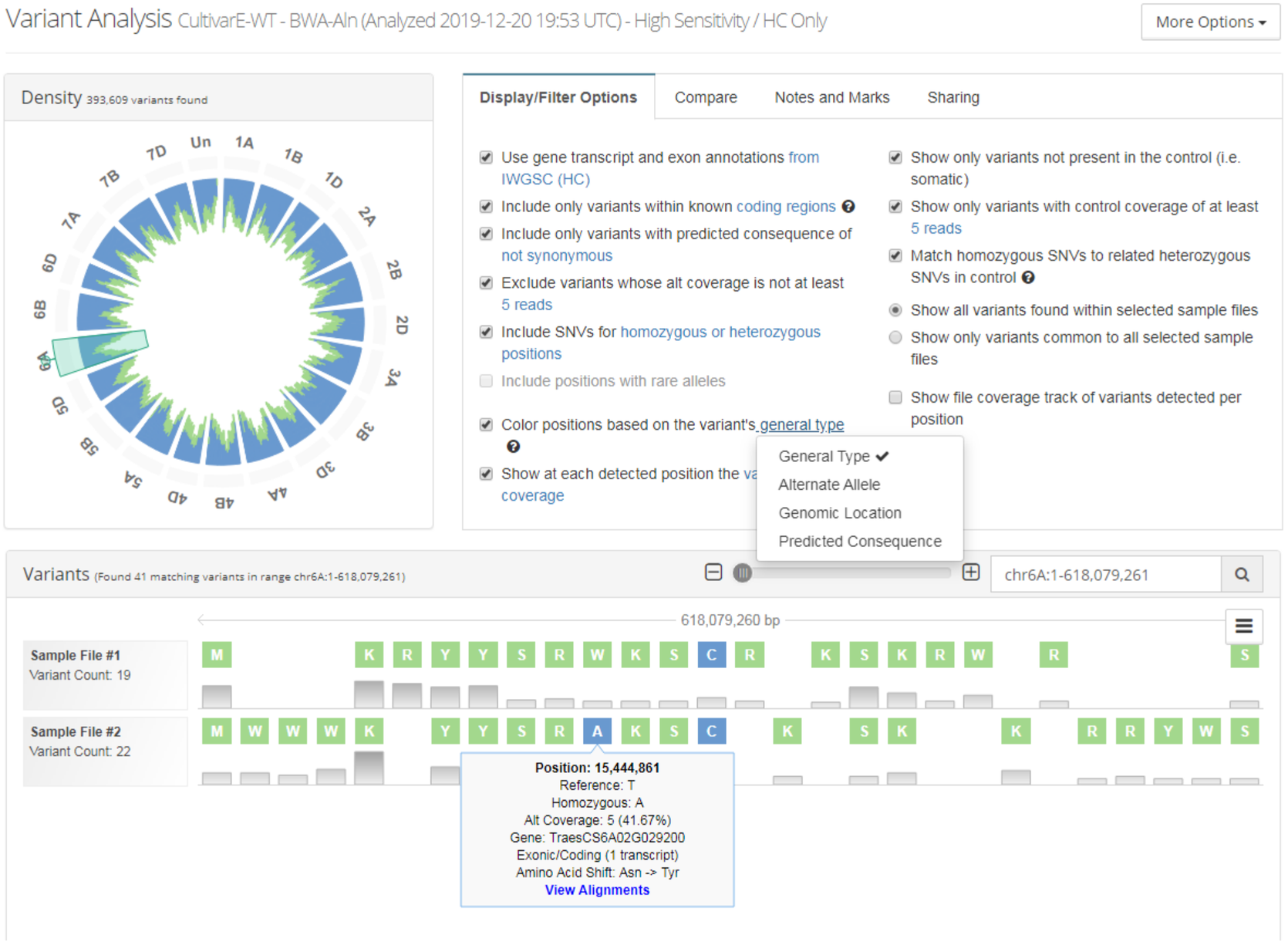
- Interactive visualizations provide deeper access to the information behind each call



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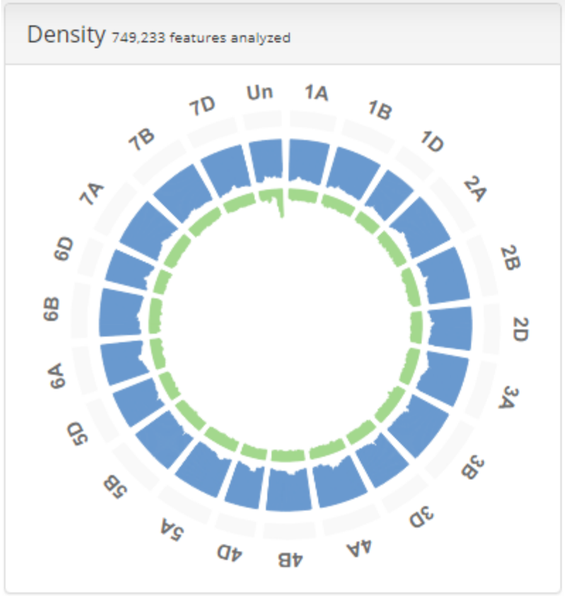





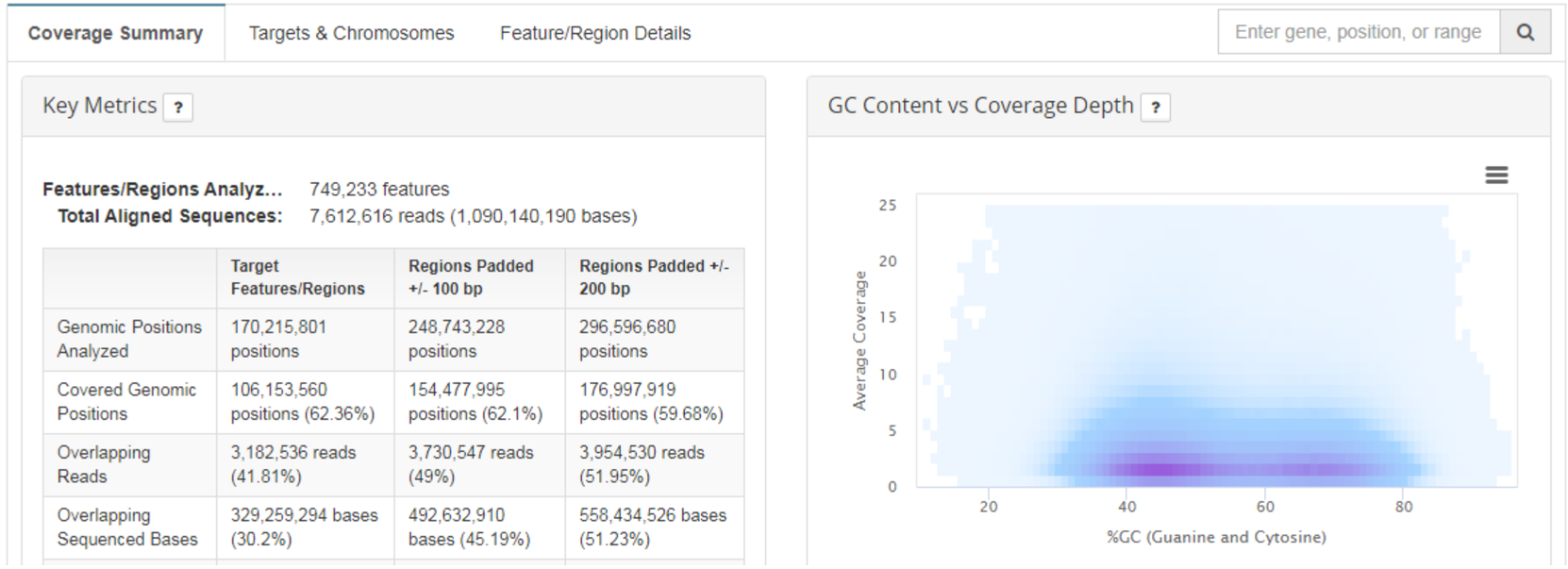


| | Target Features/Regions | Regions Padded +/- 100 bp | Regions Padded +/- 200 bp |
|---|---|---|---|
| Genomic Positions Analyzed | 170,215,801 positions | 248,743,228 positions | 296,596,680 positions |
| Covered Genomic Positions | 106,153,560 positions (62.36%) | 154,477,995 positions (62.1%) | 176,997,919 positions (59.68%) |
| Overlapping Reads | 3,182,536 reads (41.81%) | 3,730,547 reads (49%) | 3,954,530 reads (51.95%) |
| Overlapping Sequenced Bases | 329,259,294 bases (30.2%) | 492,632,910 bases (45.19%) | 558,434,526 bases (51.23%) |

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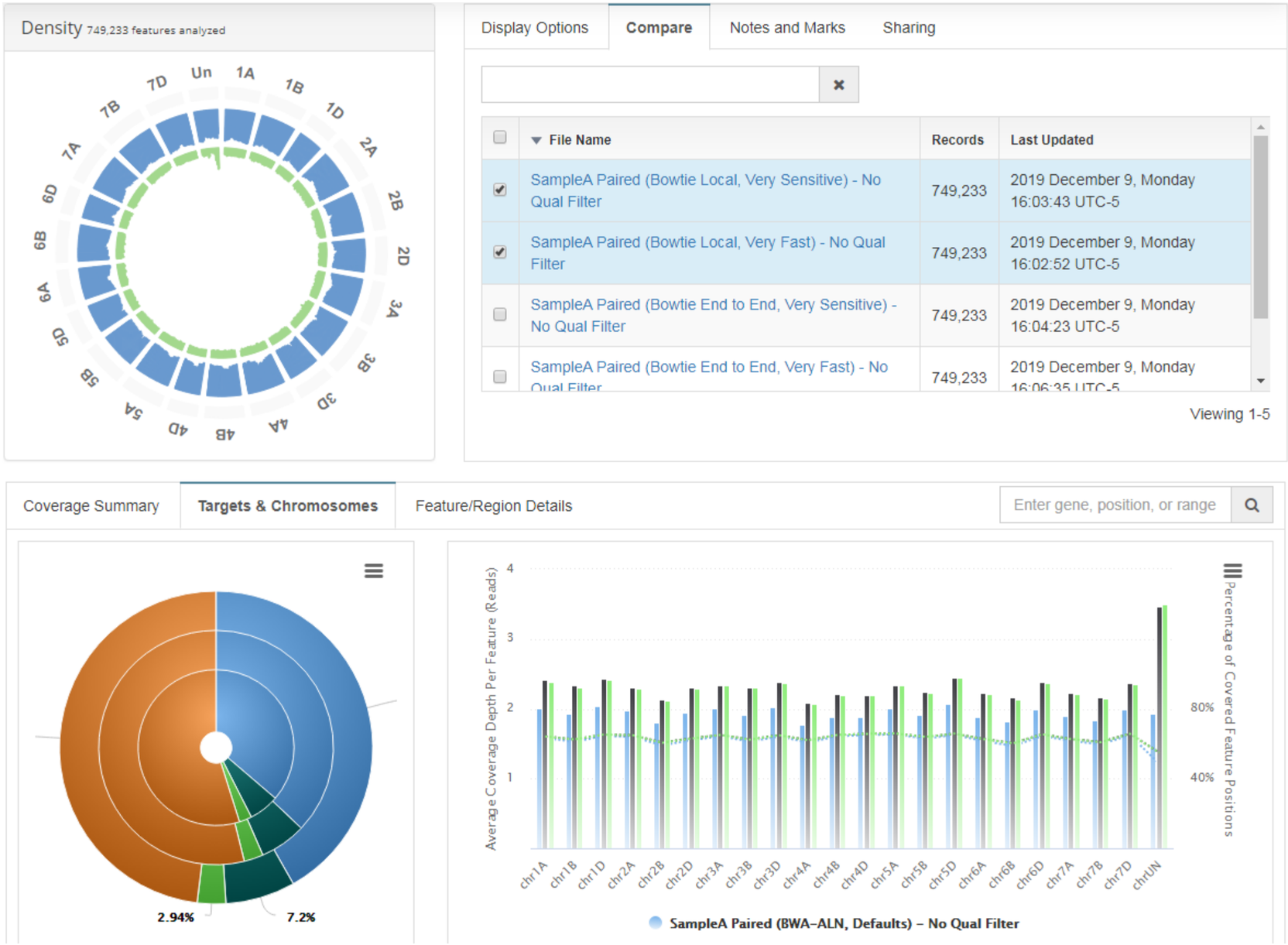

# Hexaploid Wheat: Coverage Analysis

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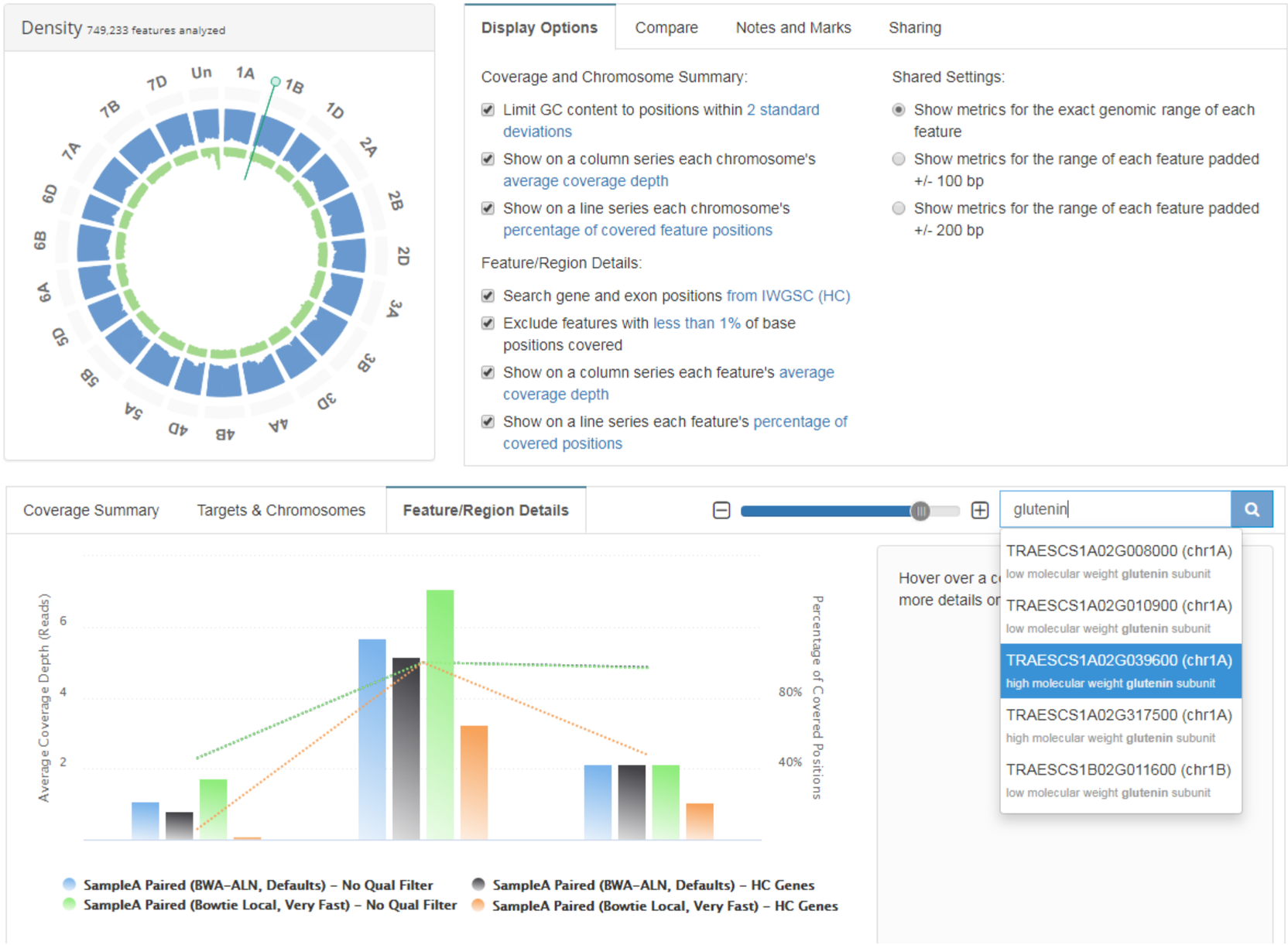
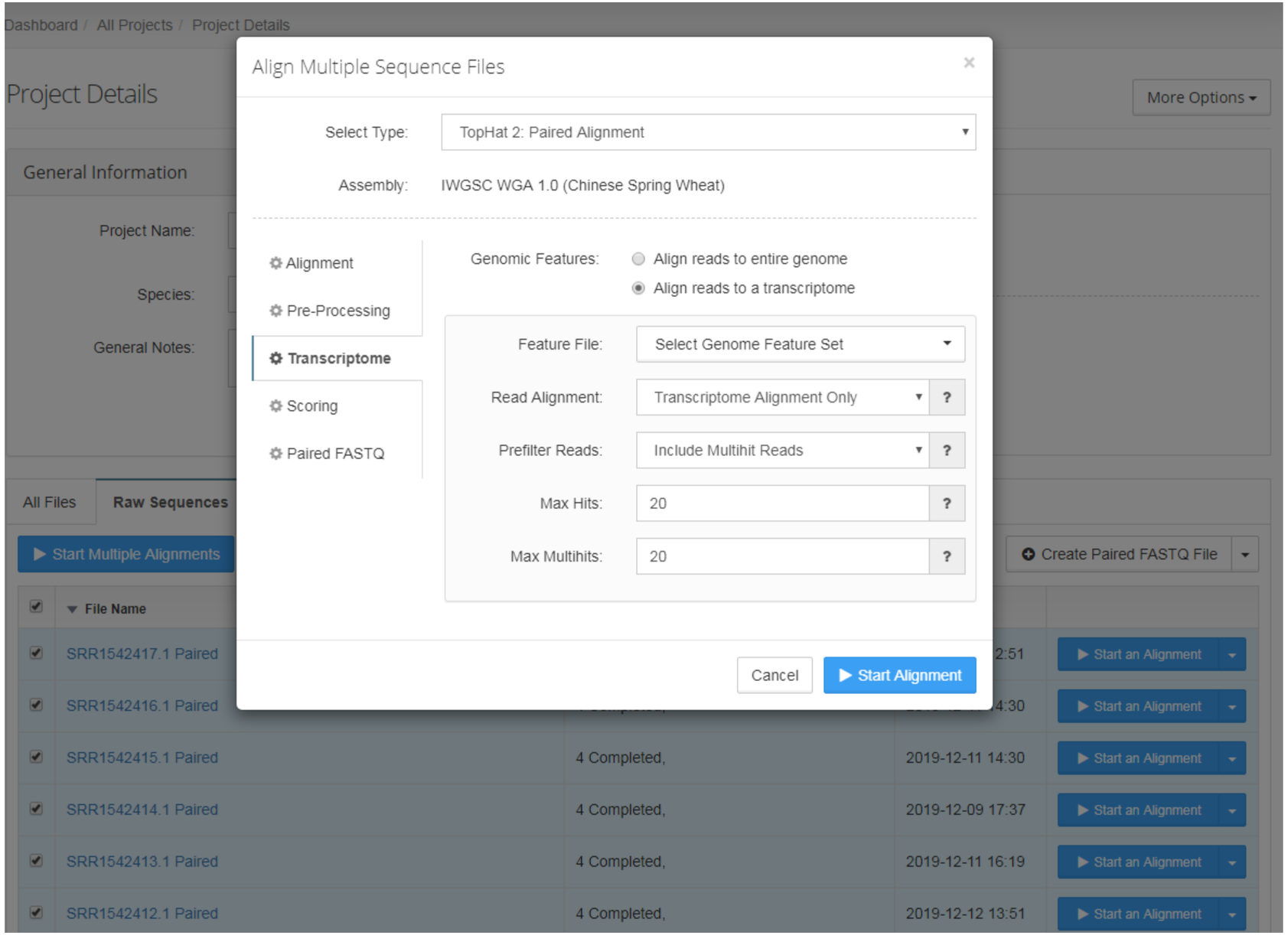
- Access individual gene or transcript coverage metrics leveraging IWGSC annotation sets



# RNA-Seq Hexaploid Wheat : Read Mapping and Visualization

# Bread Wheat: RNA-Seq Read Mapping

- Conveniently select to align to either the full Chinese Spring Wheat genome or a transcriptome



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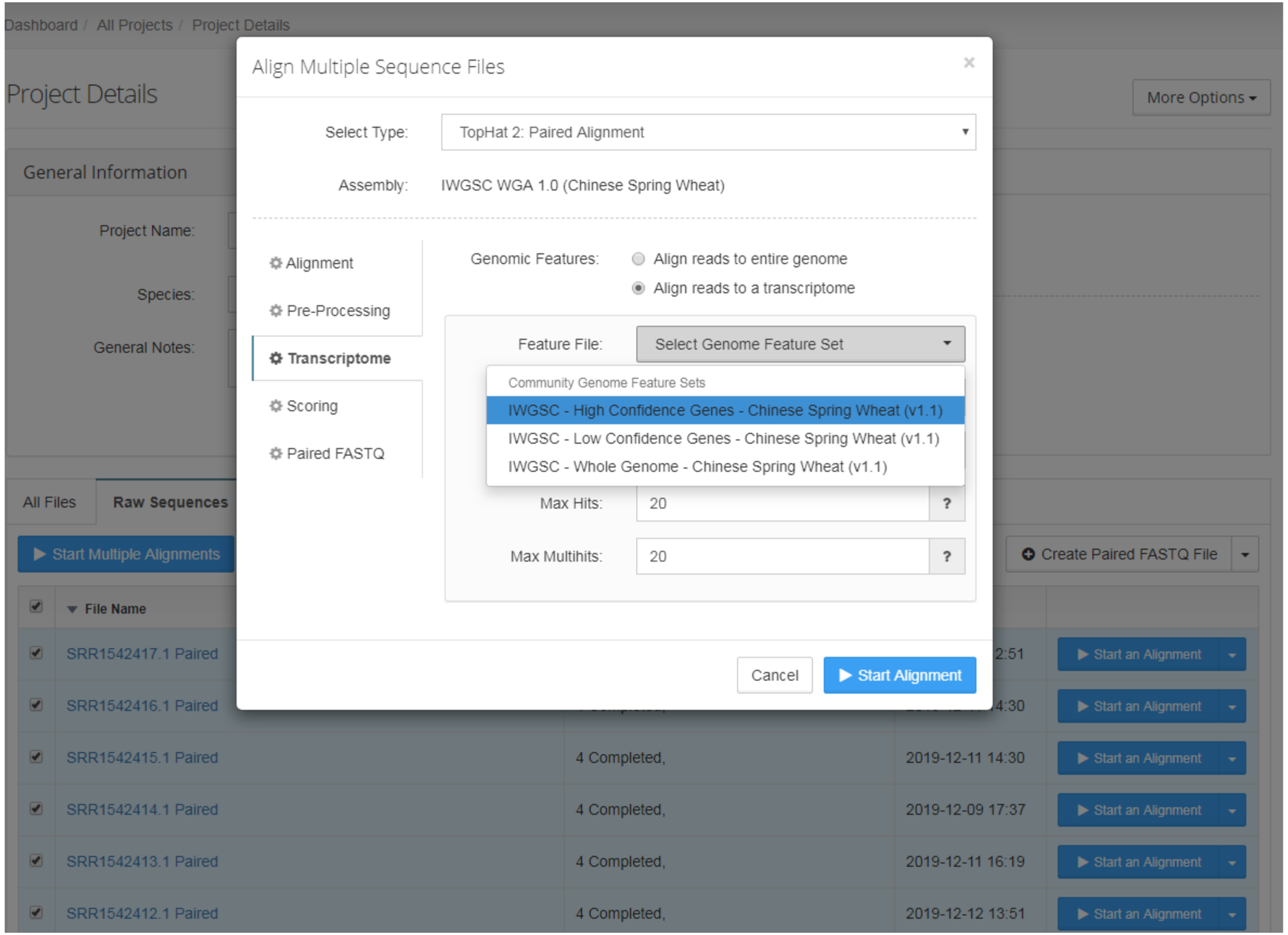

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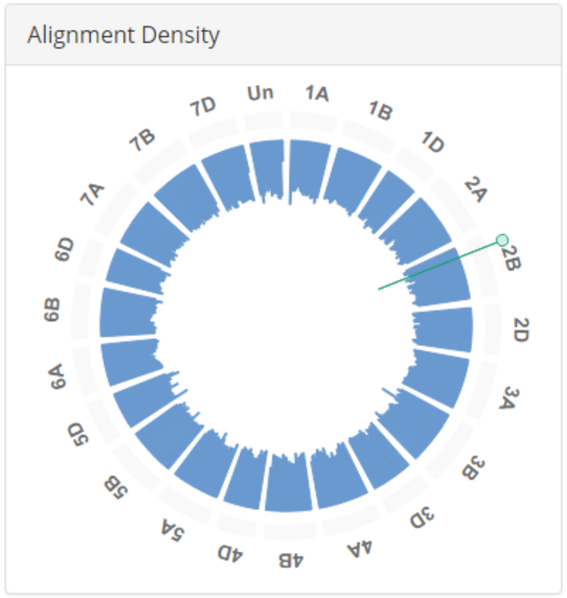
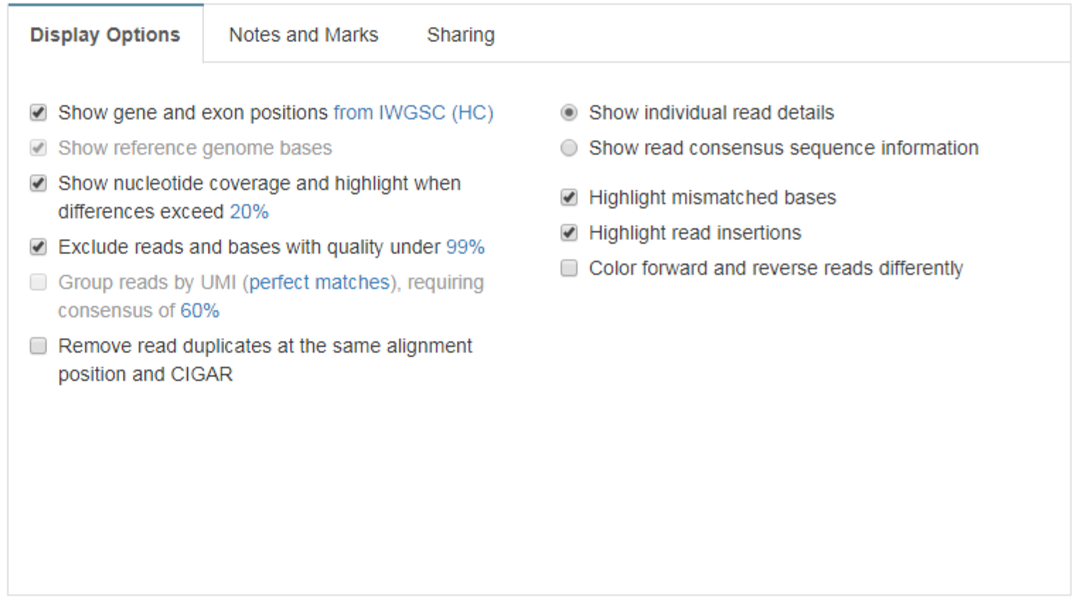
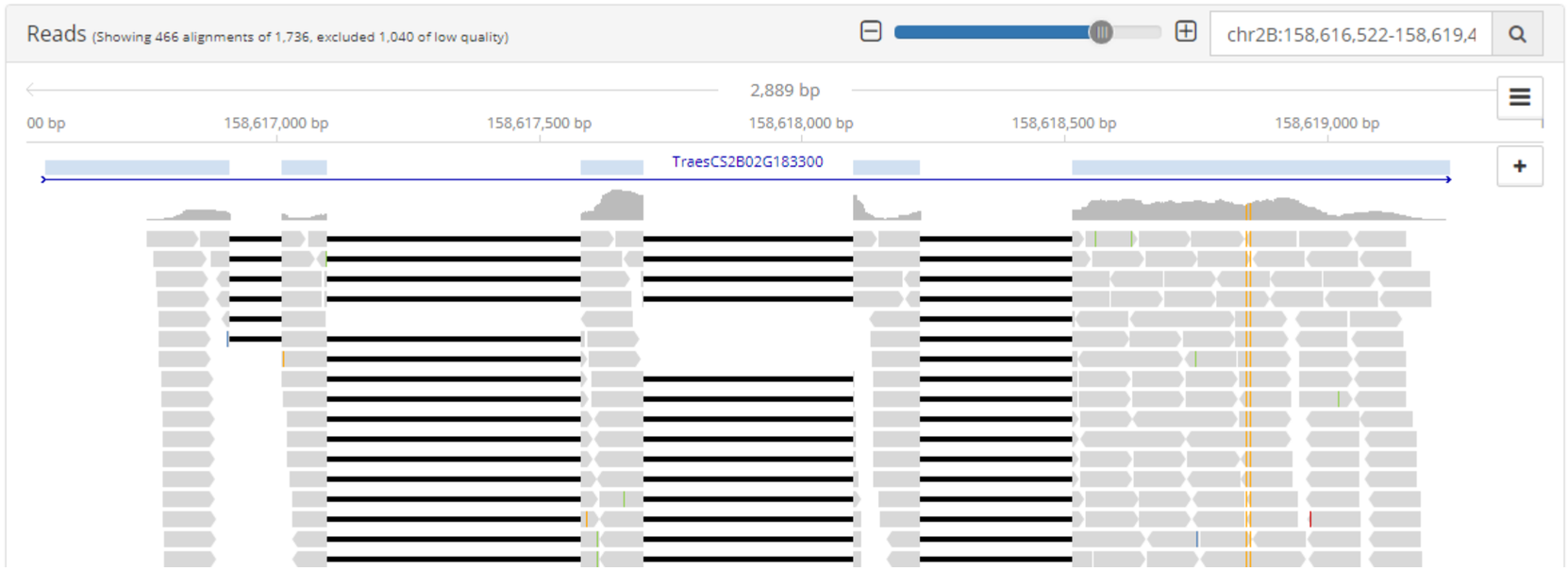
- Quickly visualize and navigate RNA-Seq data from samples of any size



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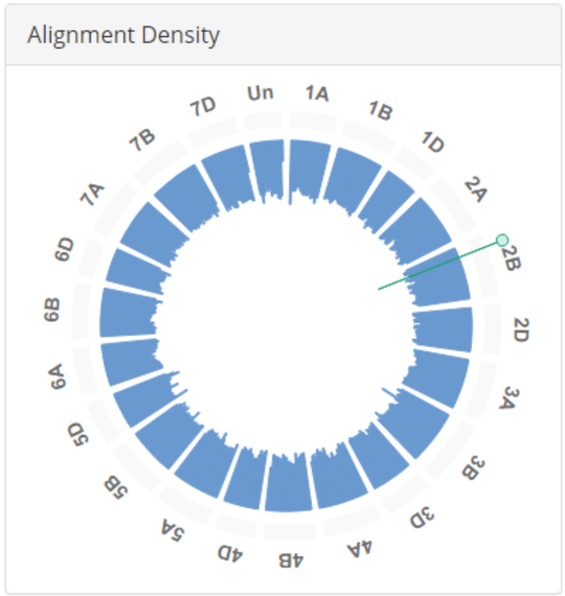
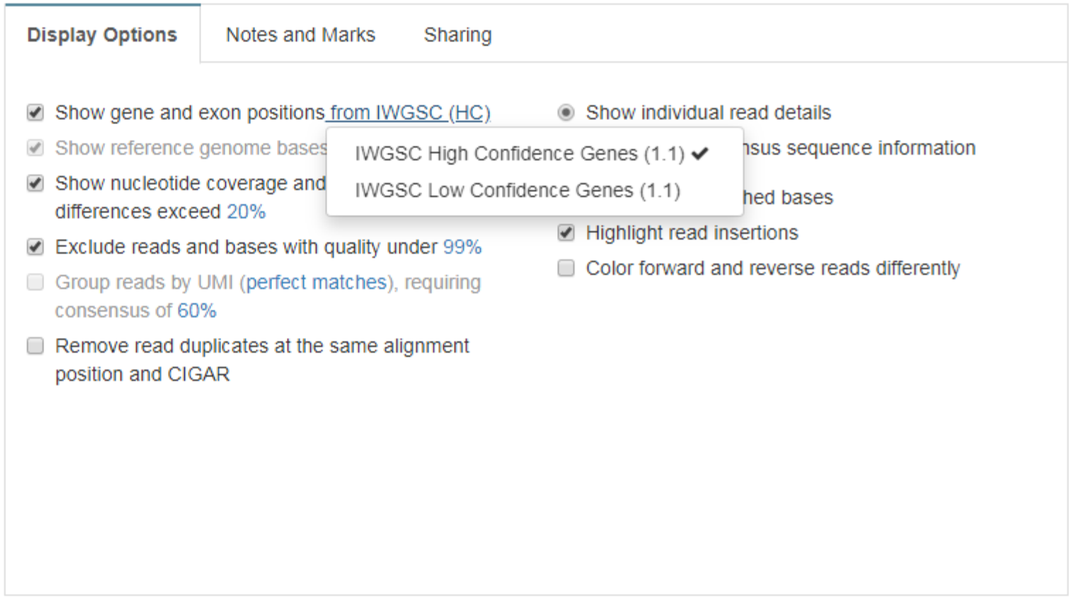
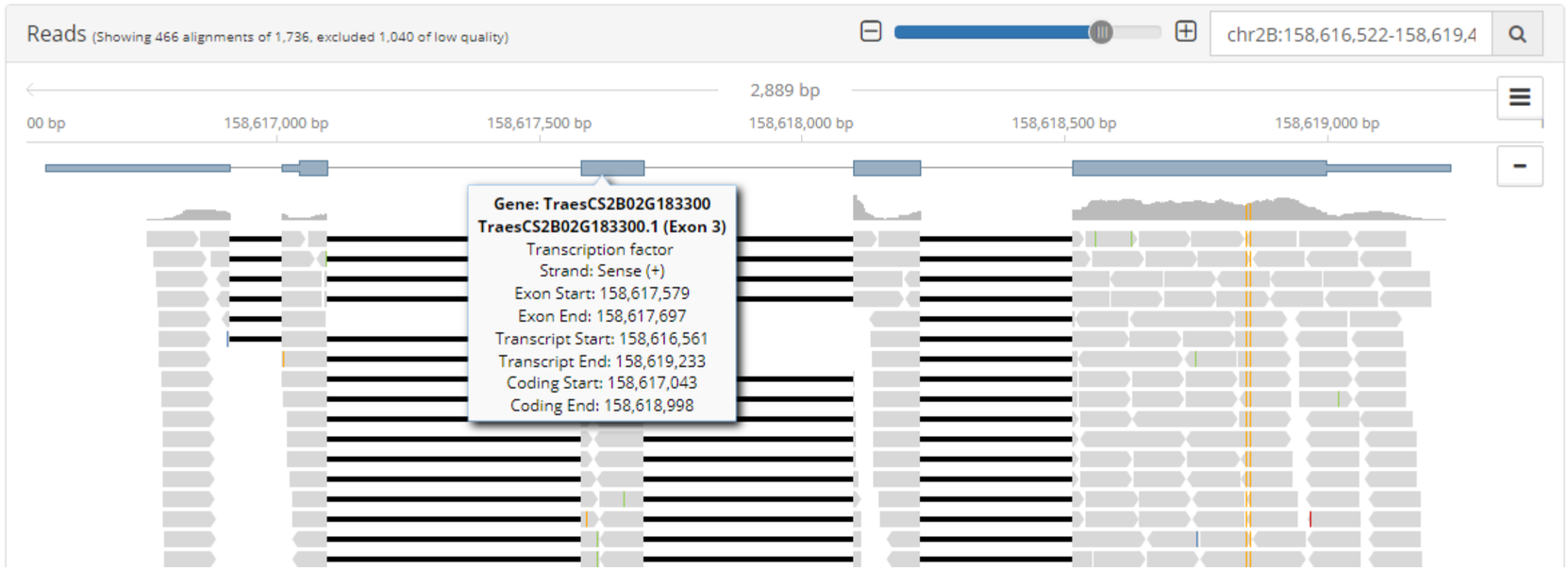
- Reference IWGSC transcript and functional annotations on the fly



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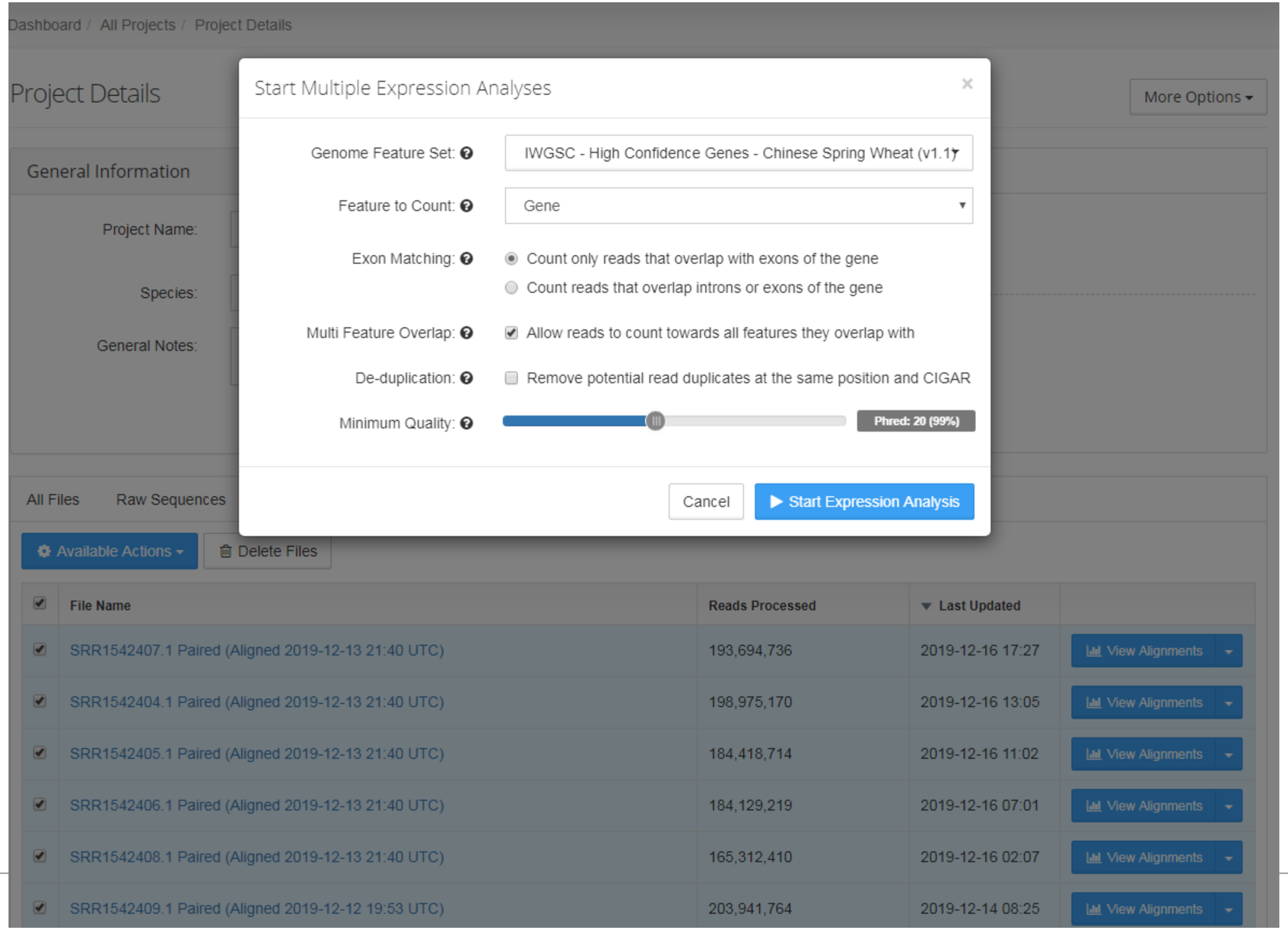
- Analyze feature expression utilizing the Chinese Spring Wheat reference assembly



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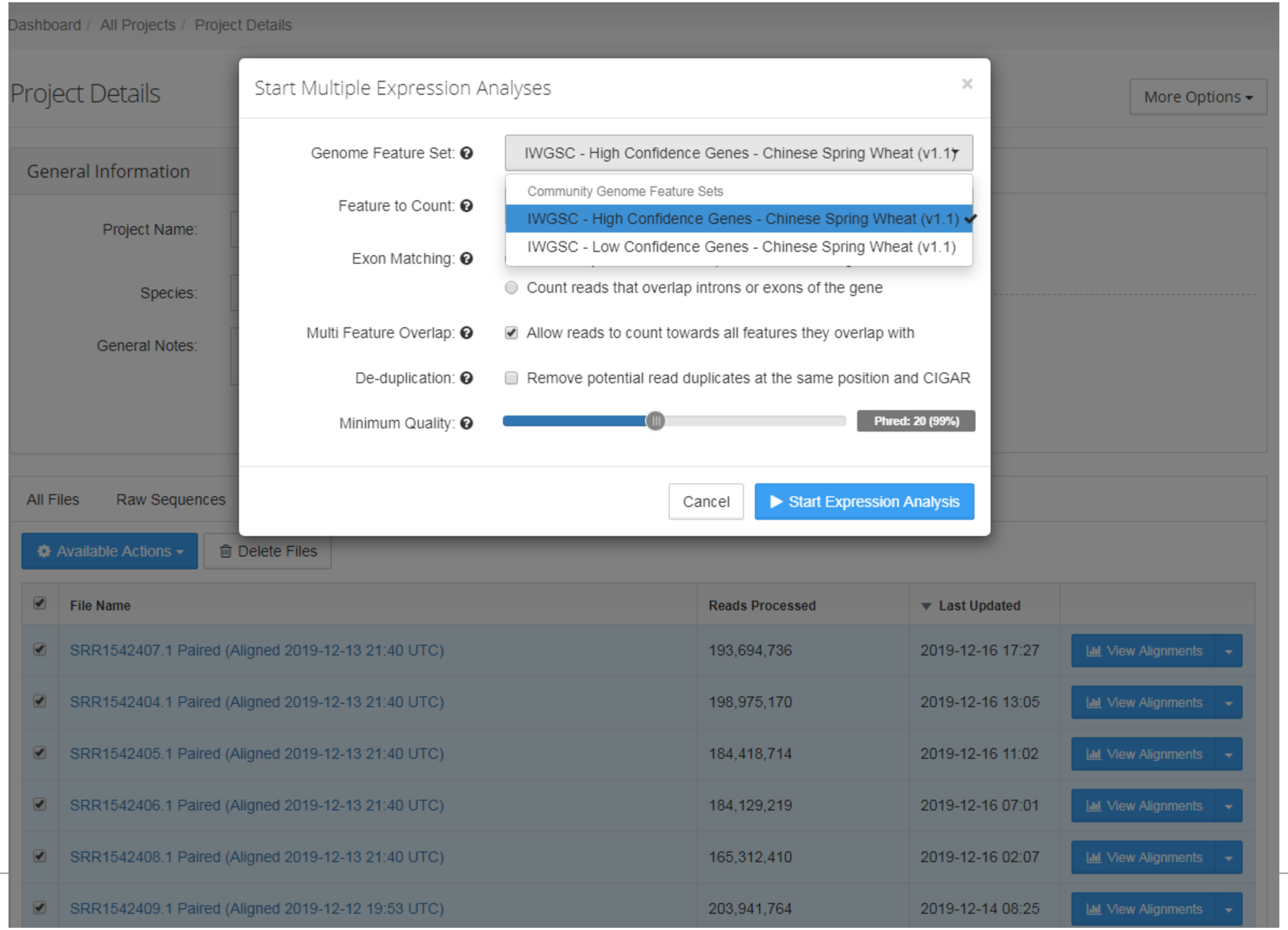
- Leverage either the IWGSC “High Confidence” or “Low Confidence” annotation sets



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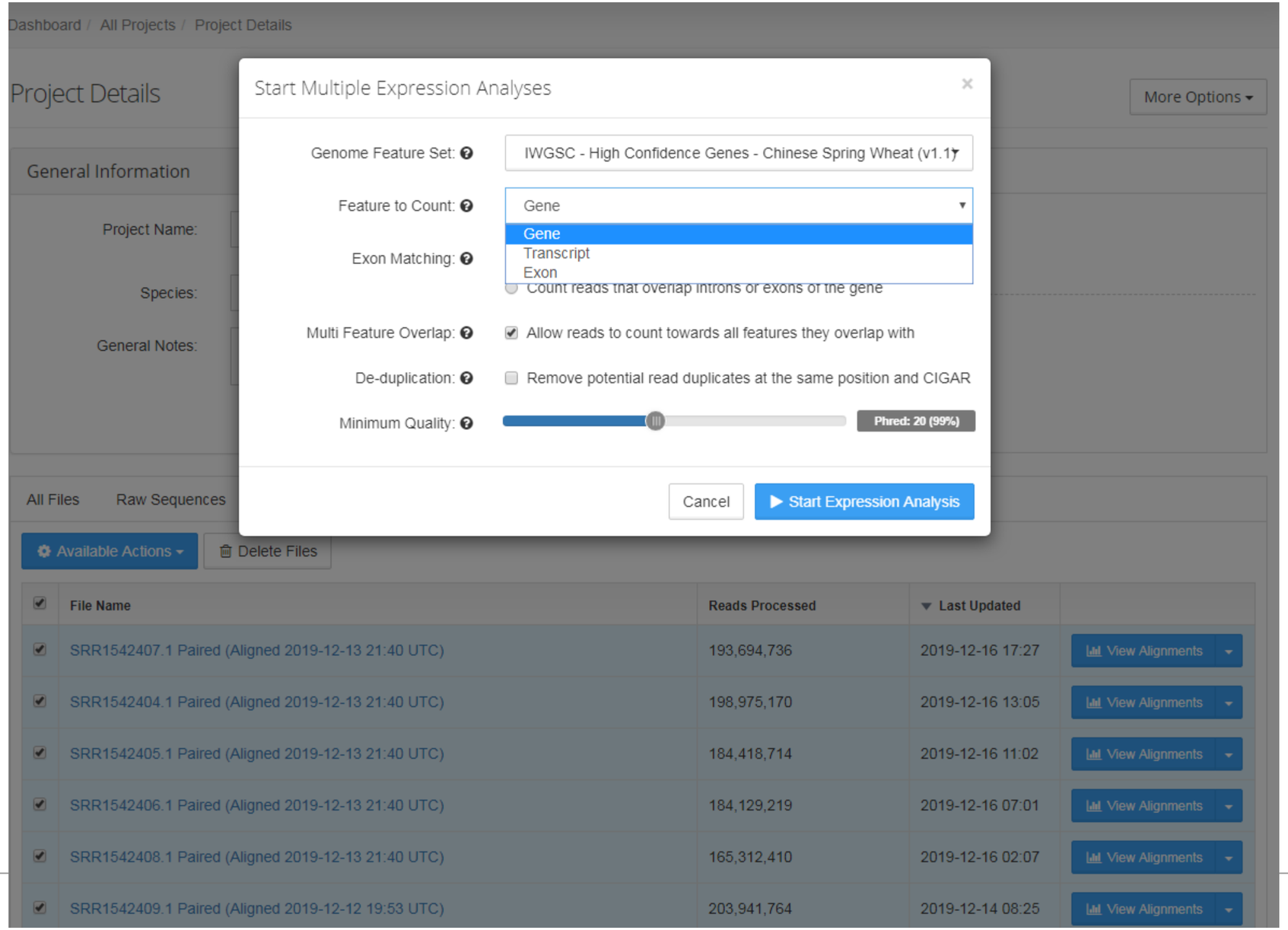

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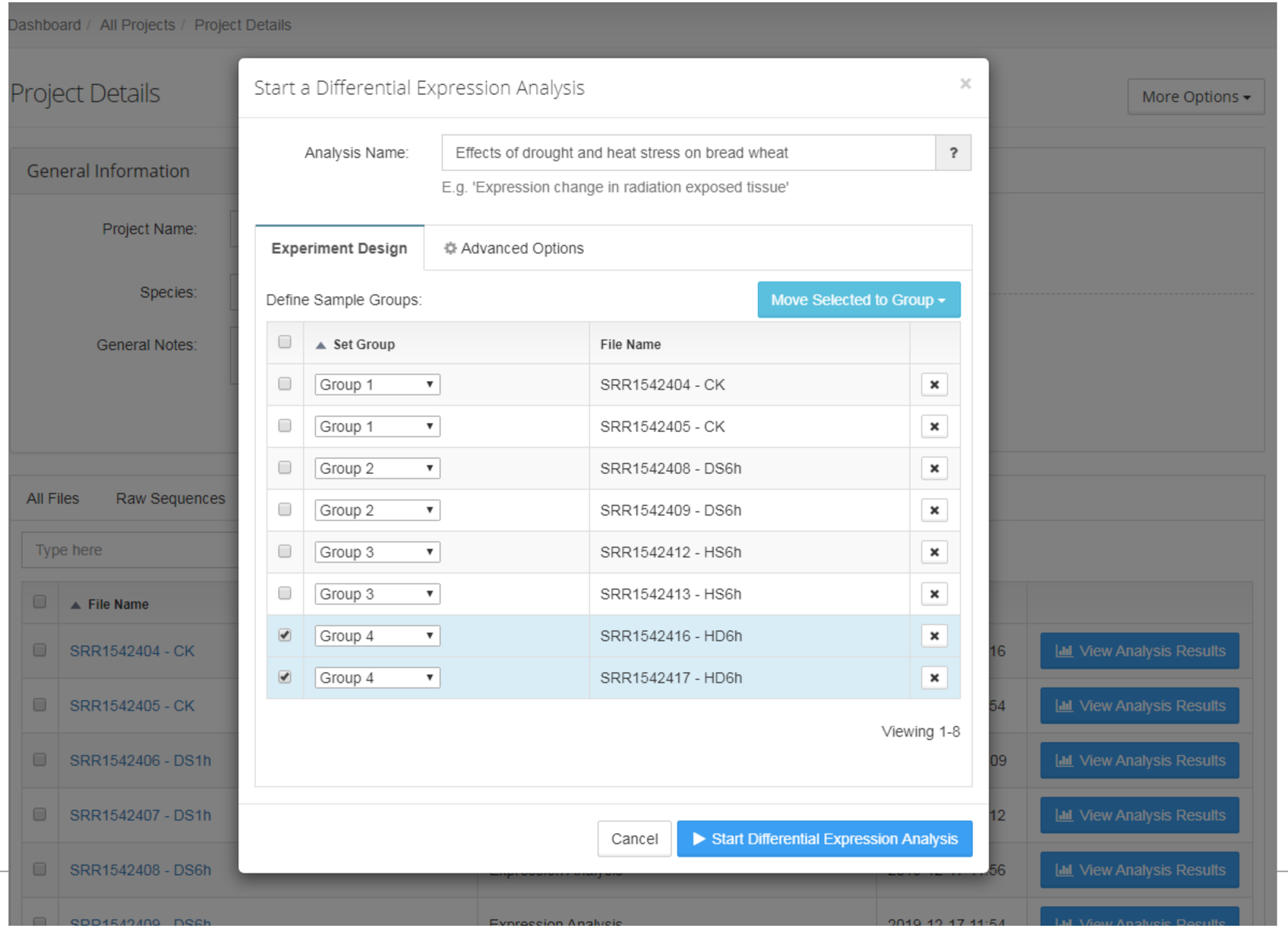

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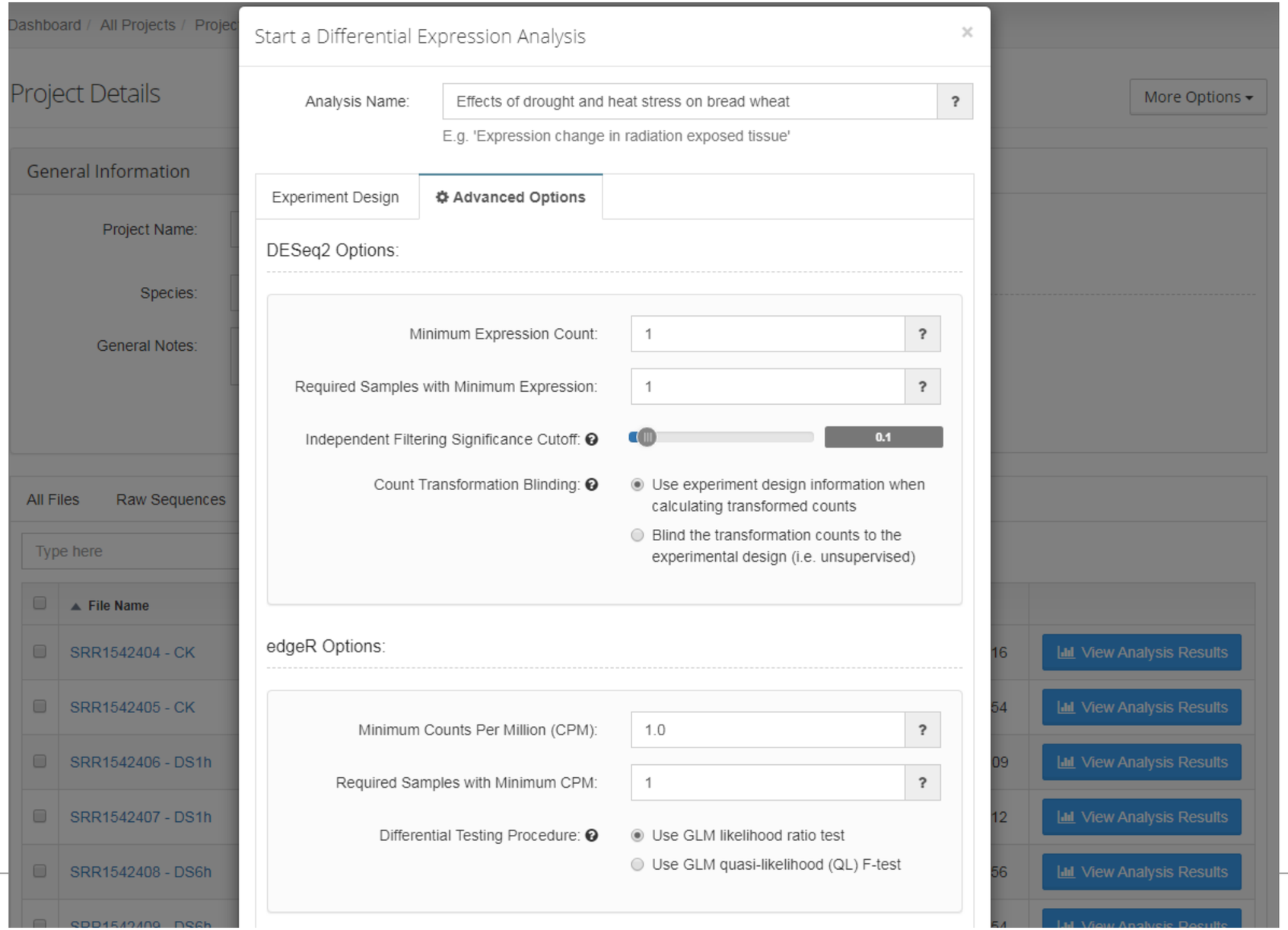
- Group samples for a differential expression analysis…
- …and conveniently tune industry standard ‘R’ based algorithms



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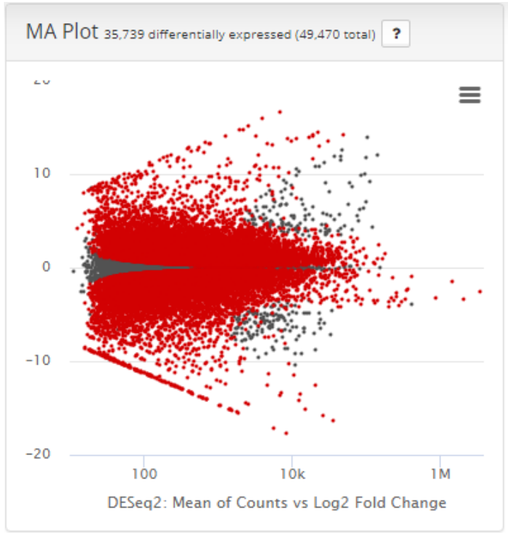
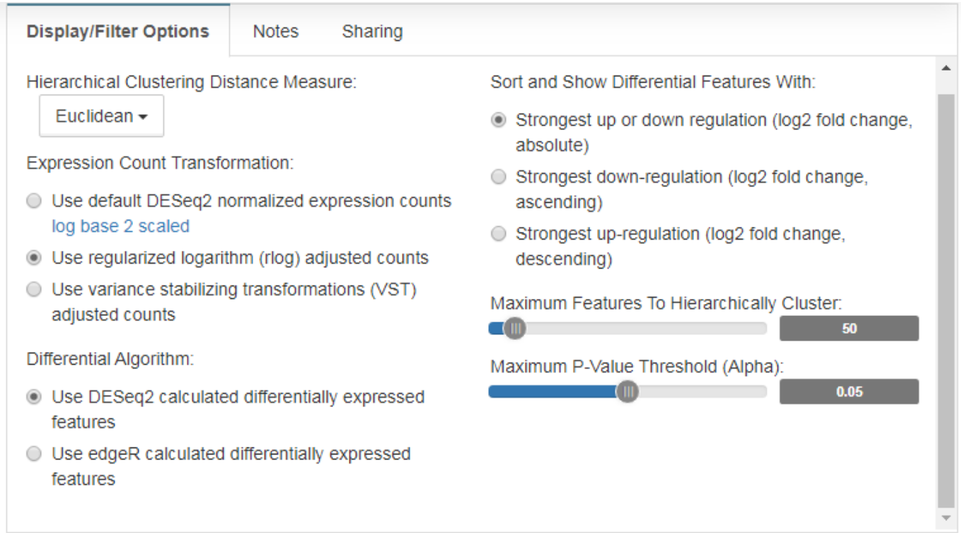
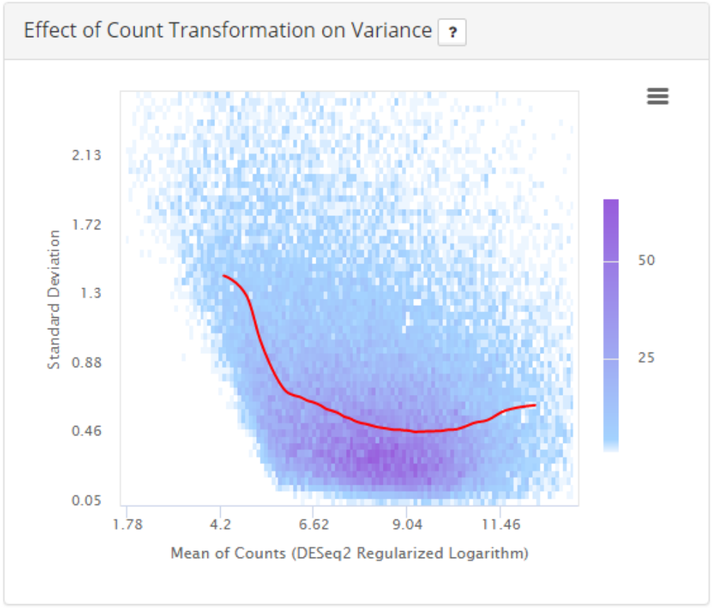
- Visualize expression levels utilizing transcriptome-based alignments leveraging IWGSC annotation sets







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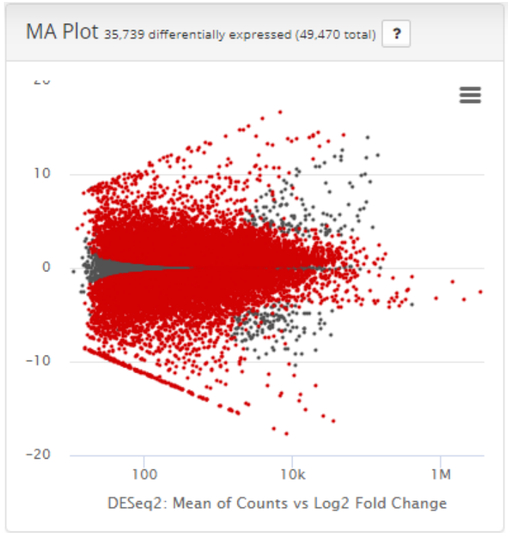
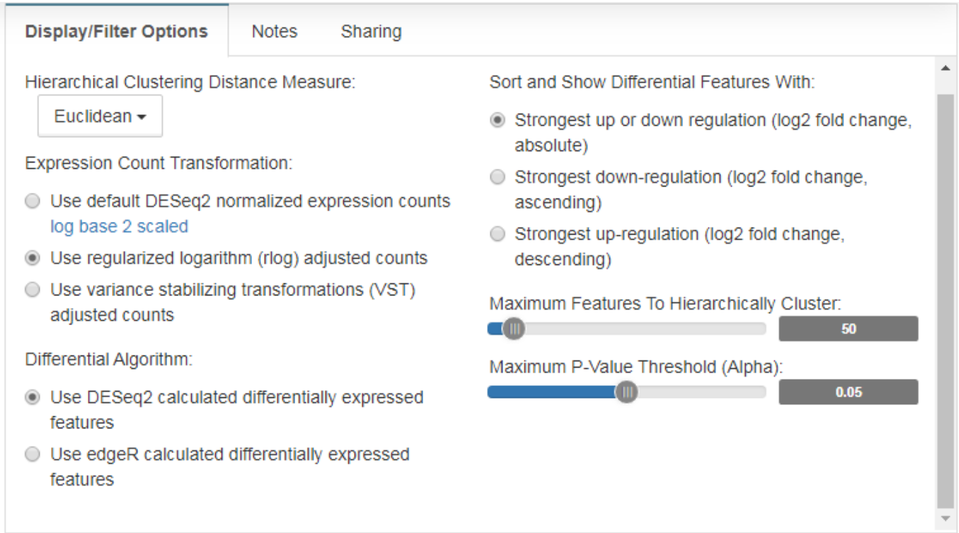
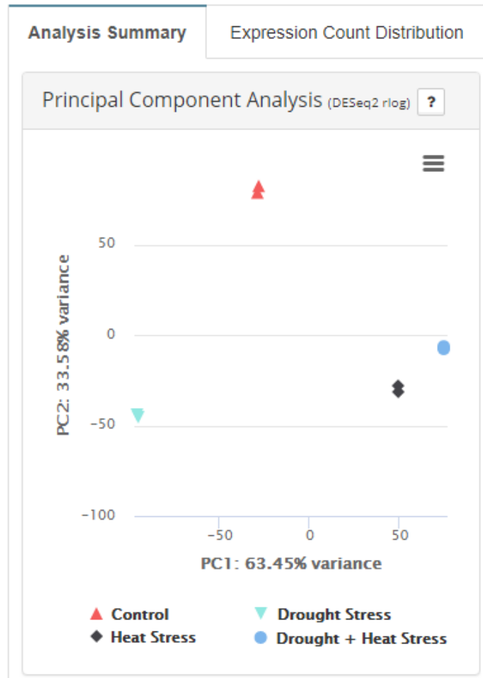
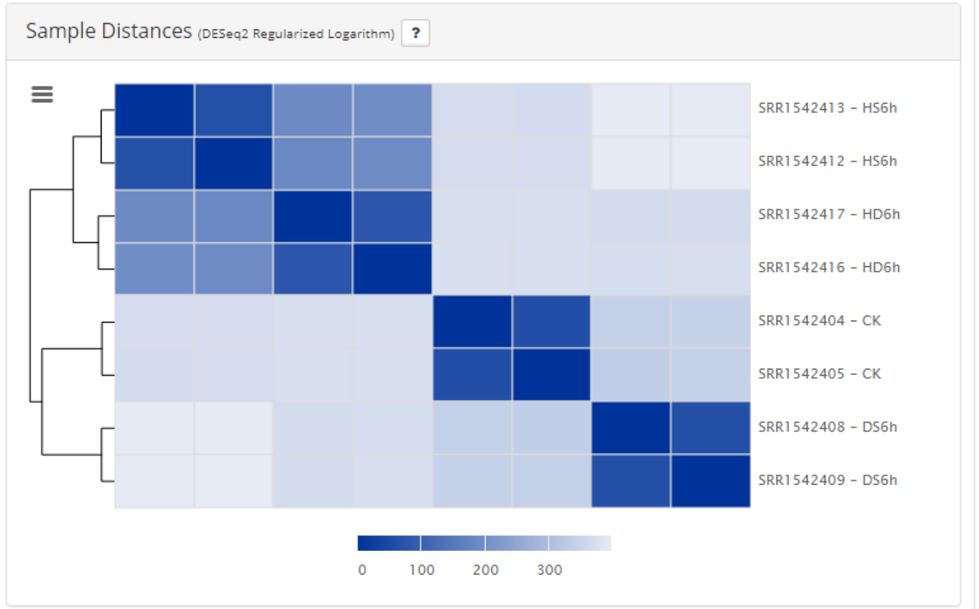
- Visualize expression levels utilizing transcriptome-based alignments leveraging IWGSC annotation sets
- Validate sample distances through principal component analysis



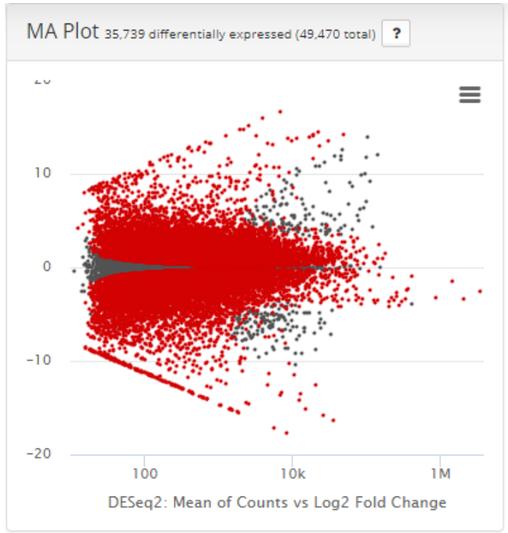



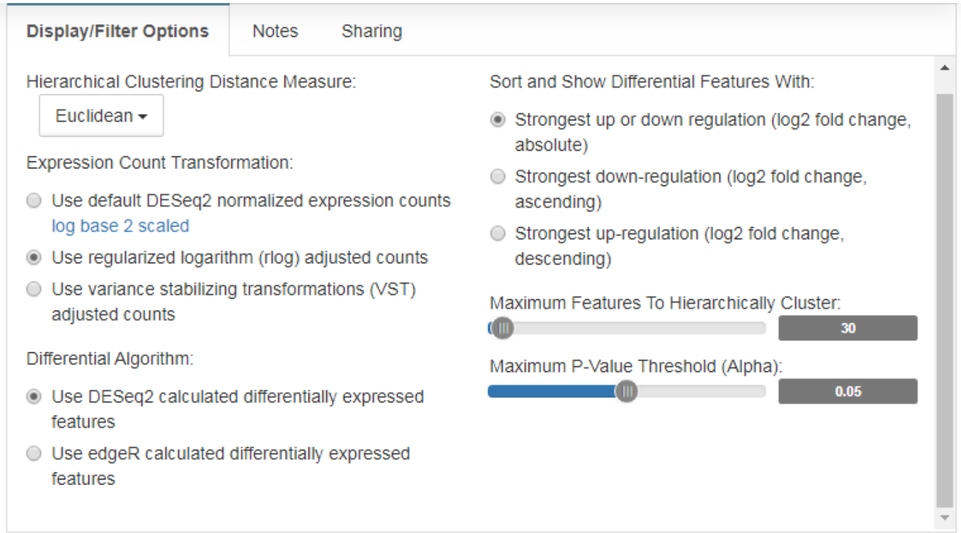



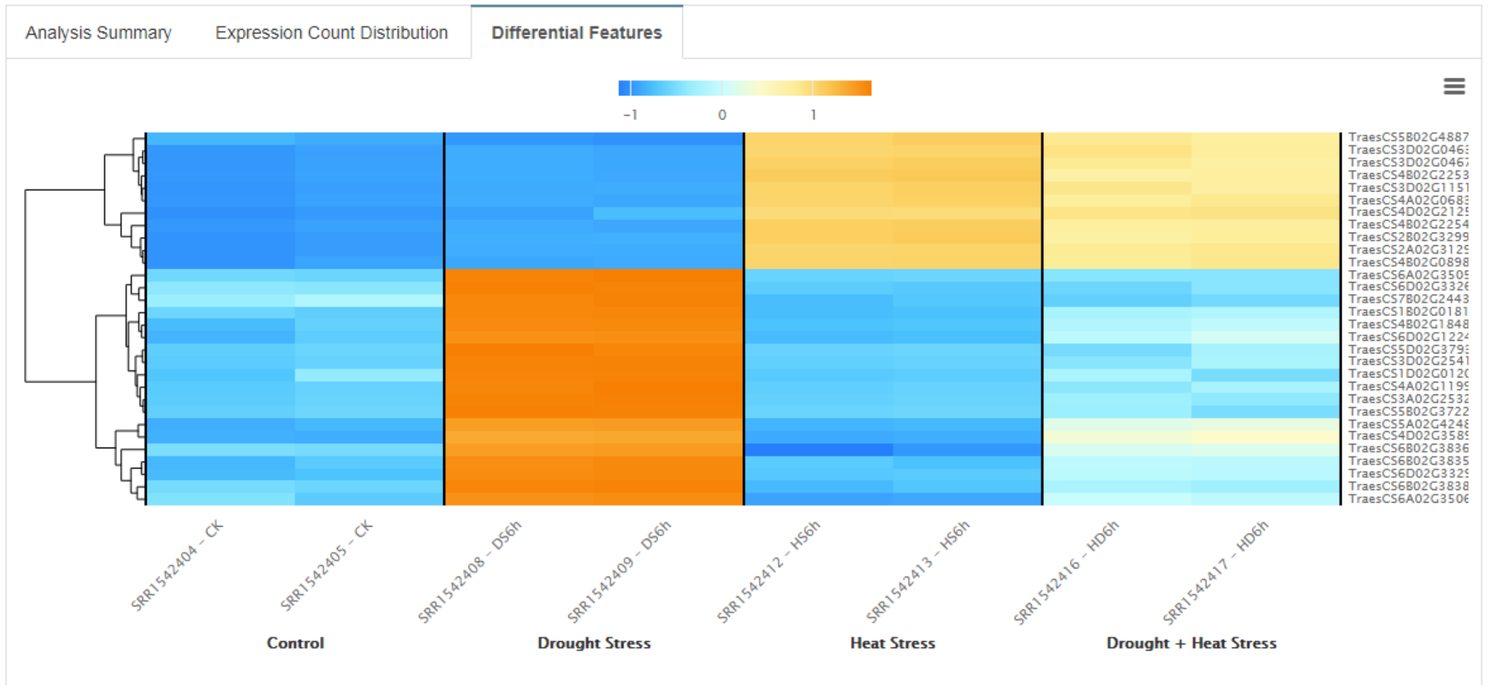



# Bread Wheat: Differential Expression

- Visualize expression levels utilizing transcriptome-based alignments leveraging IWGSC annotation sets
- Validate sample distances through principal component analysis
- Highlight up or down regulated genes through interactive heat maps

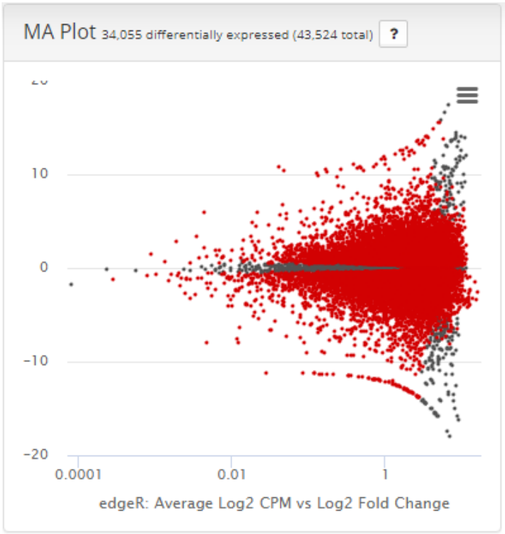


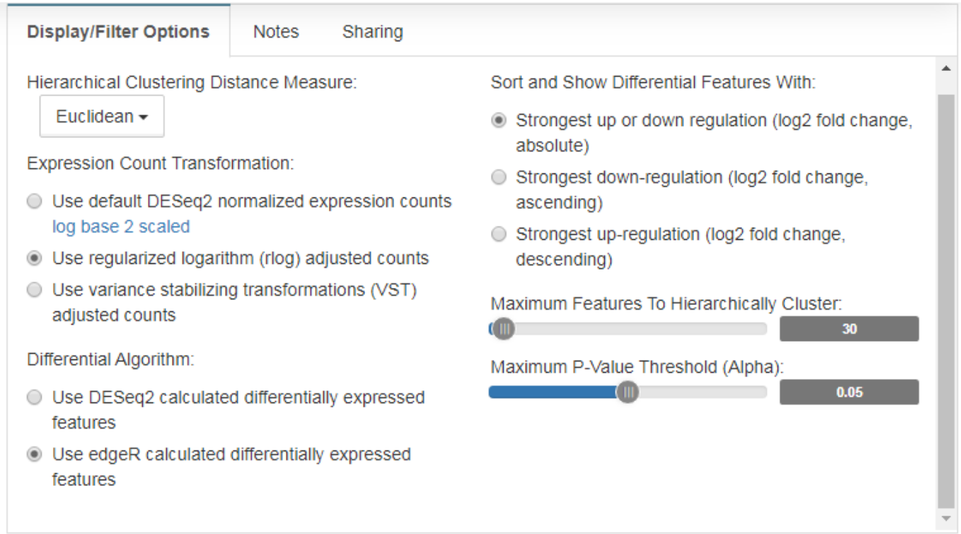



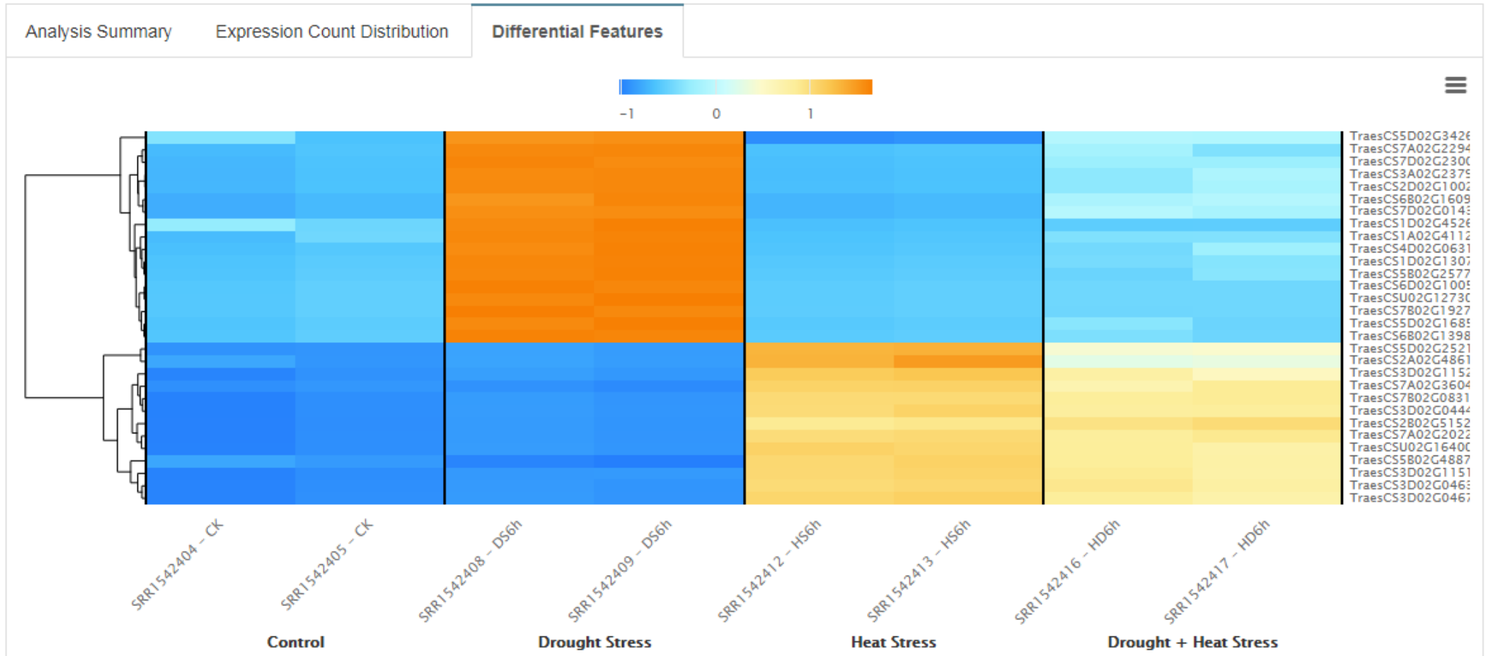



# Bread Wheat: Differential Expression

- Visualize expression levels utilizing transcriptome-based alignments leveraging IWGSC annotation sets
- Validate sample distances through principal component analysis
- Highlight up or down regulated genes through interactive heat maps
- Compare and contrast different industry standard algorithms in real-time



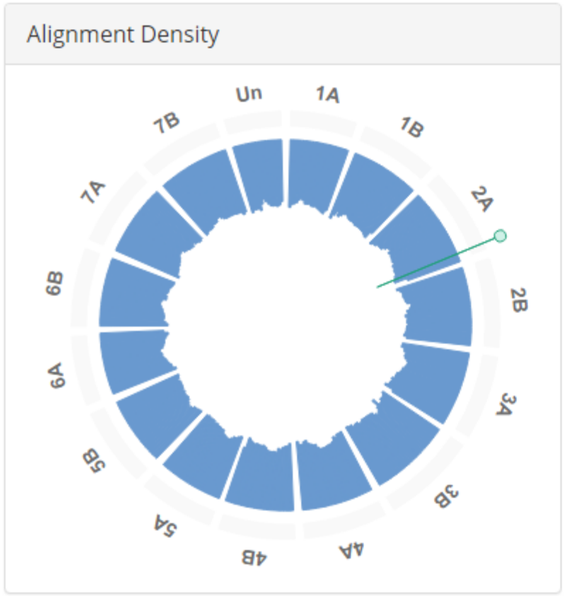



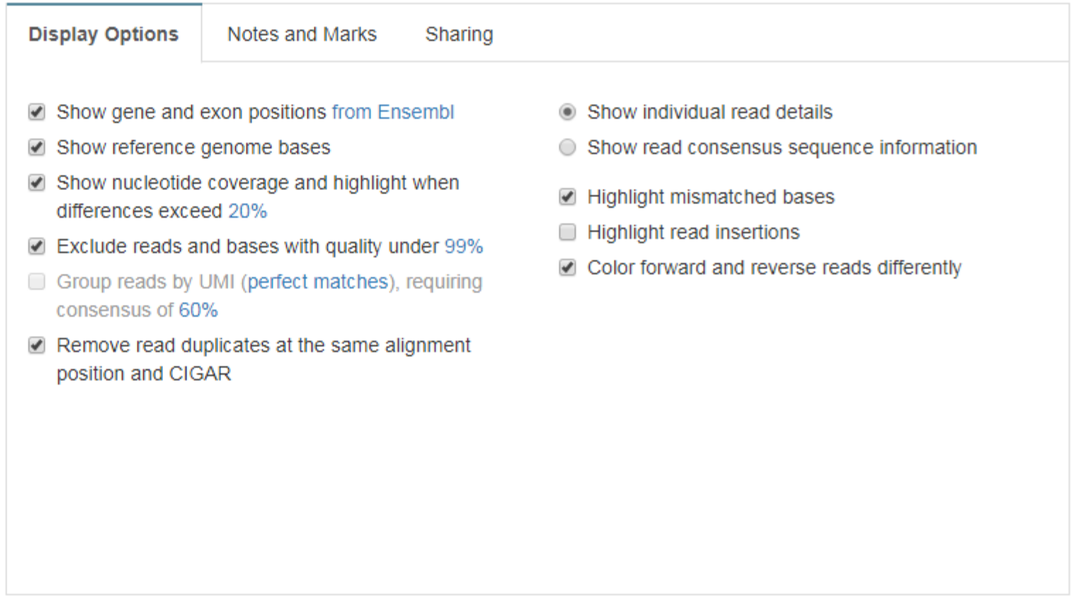



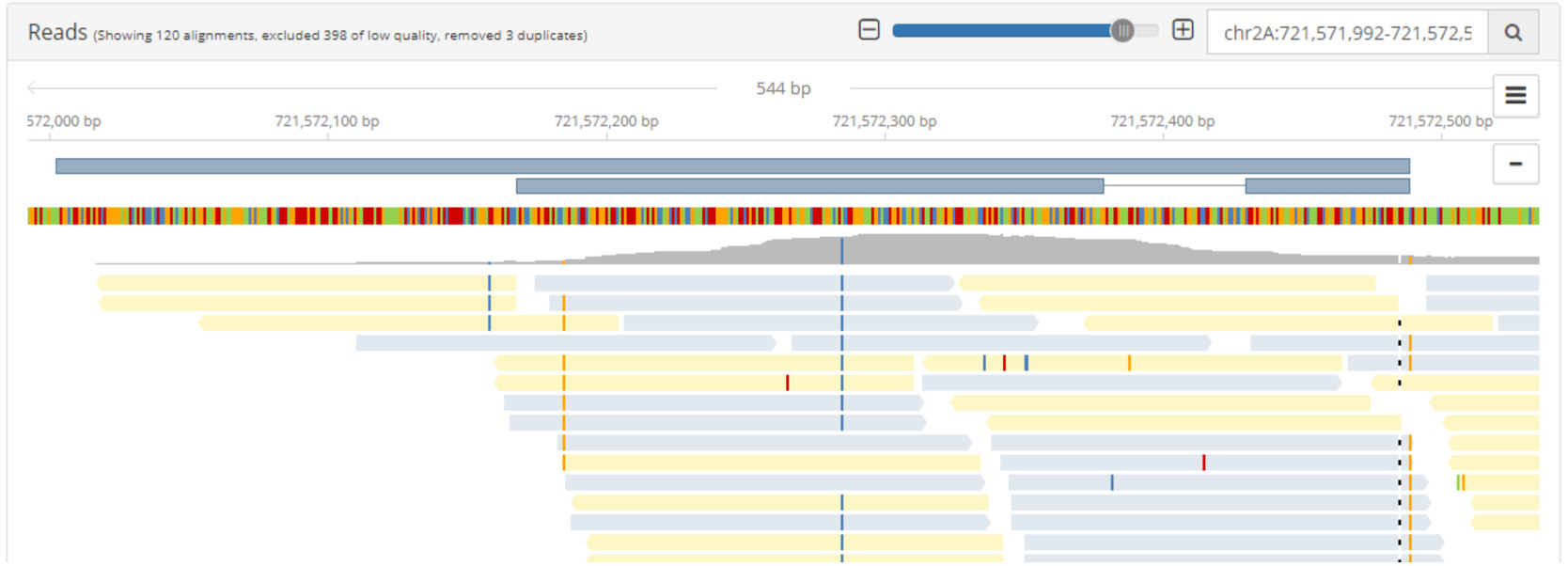
# DNA-Seq: Tetraploid Wheat

# Tetraploid Wheat: Read Mapping

- Also incorporates the Svevo (*Triticum turgidum*) reference assembly from the IDWGSC (i.e. the International Durum Wheat Genome Sequencing Consortium)
- Instantly browse any portion of the IDWGSC reference sequence and visualize read alignments of samples of any size
- Dynamically leverage gene/transcript/exon annotations for Svevo from Ensembl

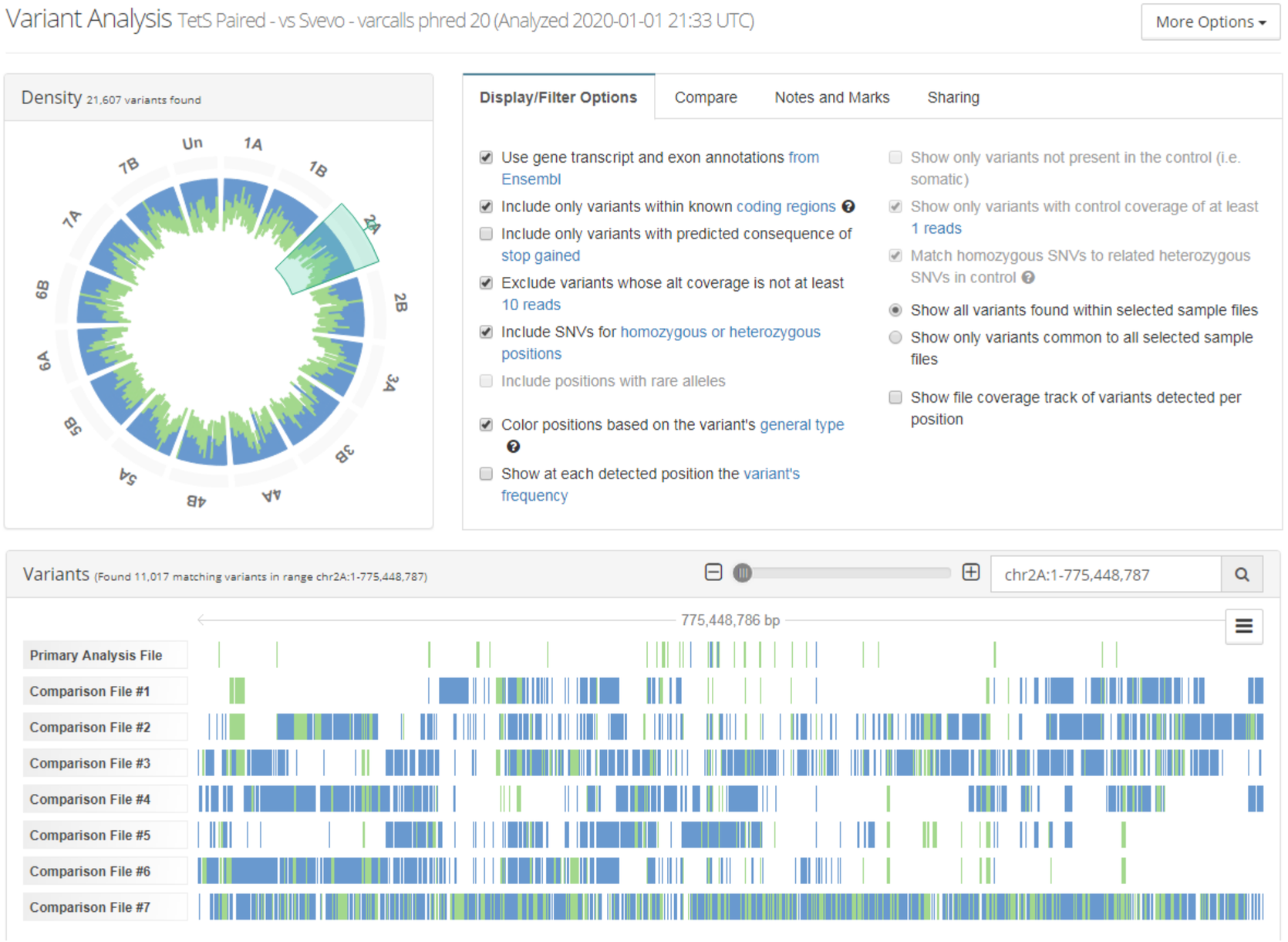


# Tetraploid Wheat: Variant Analysis

- Call and analyze variants leveraging the Svevo 1.0 reference assembly
- Simultaneously compare and visualize variant density across multiple samples
- Dynamically filter to different genomic region types based on annotations published by the IDWGSC via Ensembl



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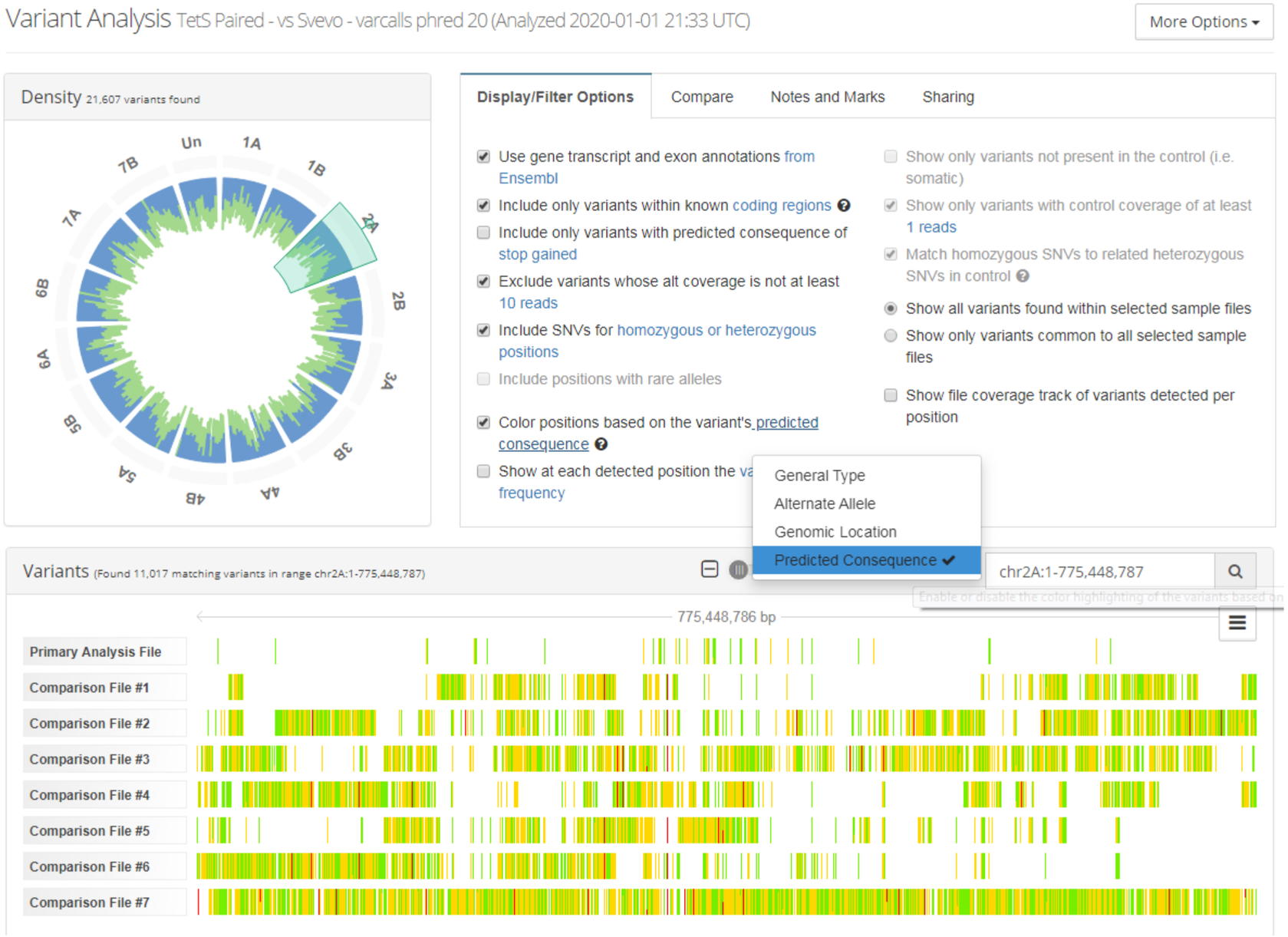
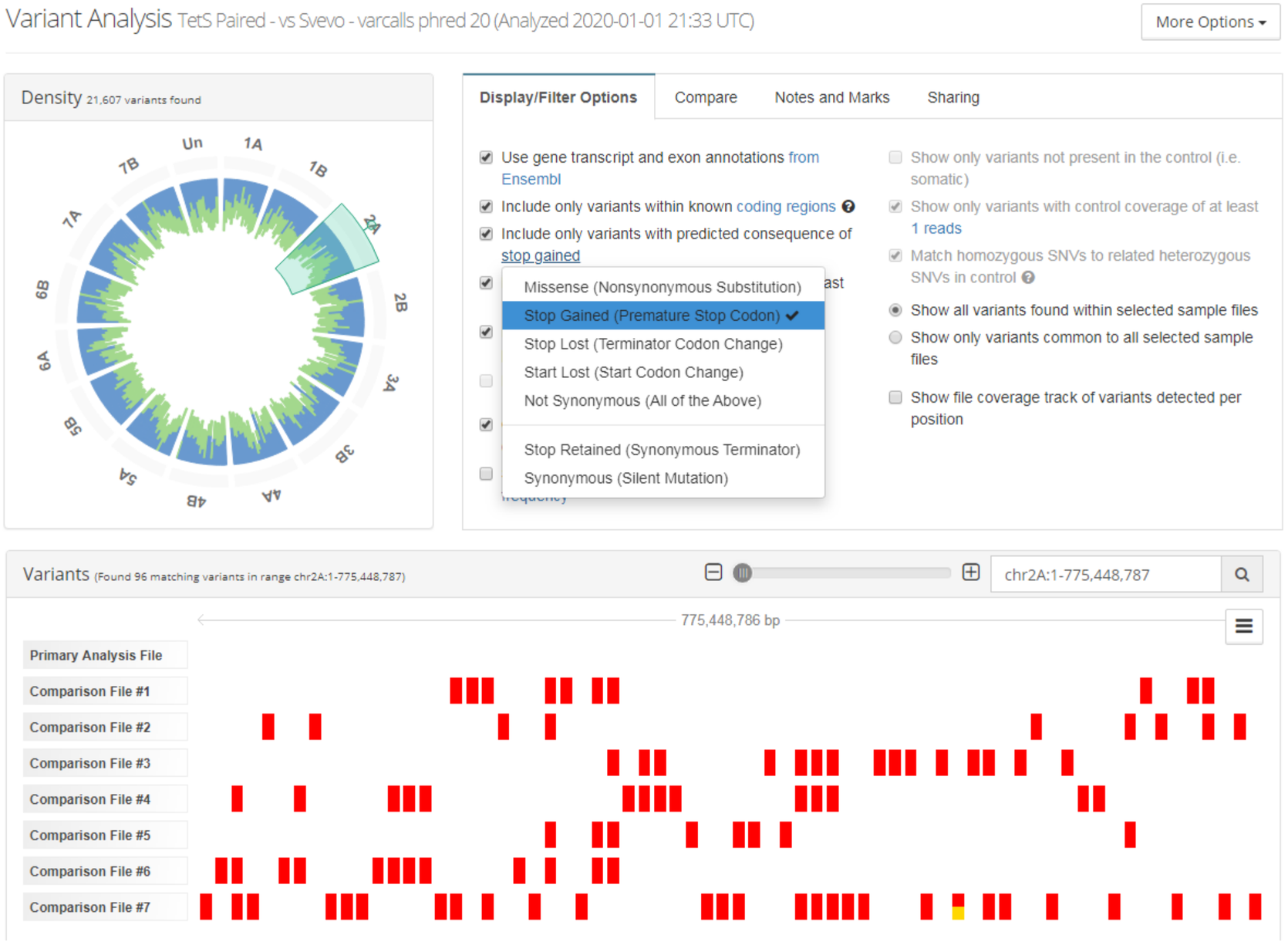
- Call and analyze variants leveraging the Svevo 1.0 reference assembly
- Simultaneously compare and visualize variant density across multiple samples
- Dynamically filter to different genomic region types based on annotations published by the IDWGSC via Ensembl
- Access predicted biological consequences based on calculated amino acid shifts



# Tetraploid Wheat: Variant Analysis

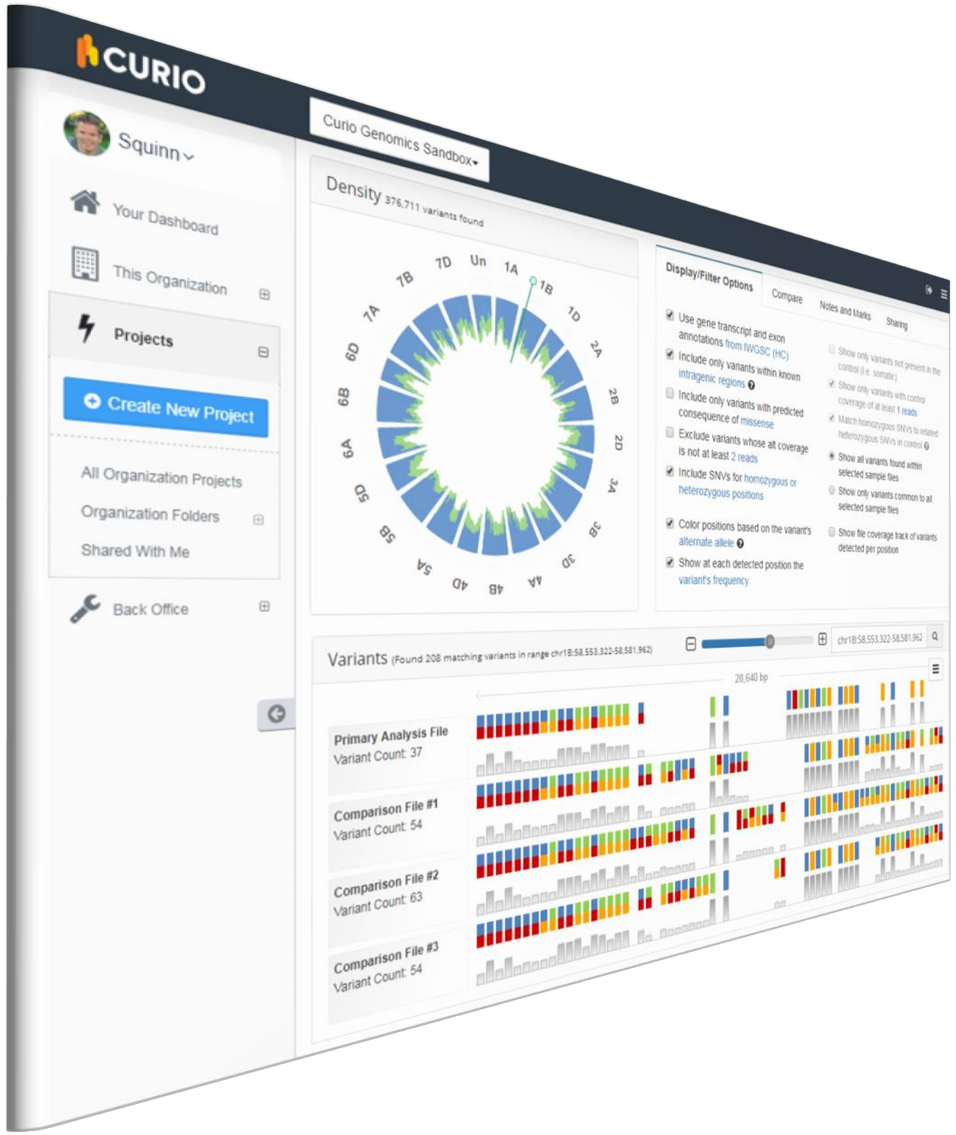
- Call and analyze variants leveraging the Svevo 1.0 reference assembly
- Simultaneously compare and visualize variant density across multiple samples
- Dynamically filter to different genomic region types based on annotations published by the IDWGSC via Ensembl
- Access predicted biological consequences based on calculated amino acid shifts
- Filter down to consequences of interest



# In Conclusion

# Looking Ahead

- Incorporation of the recently released IWGSC 2.0 reference assembly
- Addition of the soon-to-be released IWGSC 2.0 transcript and functional annotations
- Consideration of other wheat and related species, along with related annotation sets
- Support for custom reference assemblies
- Additional crop-research-specific analysis types and interpretive visualizations



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- John Innes Centre (JIC)
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- University of Adelaide, Plant Genomics Centre

**And the collective efforts of the:**

- International Wheat Genome Sequencing Consortium (IWGSC)
- International Durum Wheat Genome Sequencing Consortium (IDWGSC)

**Differential expression analysis utilized FASTQ files published as part of the following study:**

- Liu Z, et al. Temporal transcriptome profiling reveals expression partitioning of homeologous genes contributing to heat and drought acclimation in wheat (*Triticum aestivum* L.)
  BMC Plant Biol. 2015;15:152. doi: 10.1186/s12870-015-0511-8.

# Q&A