Variant Analysis

Variations in nucleotide sequence, in the form of single nucleotide variants (SNVs) and insertion and deletion events (INDELs), can either be neutral in nature or can have functional effects. Partek® Flow® provides all the tools necessary to interrogate and prioritize variants for further analysis. Variants stored in Variant Call Format (vcf) files can be analyzed to filter, annotate, summarize, visualize, and validate your panel of identified variants. Multiple vcf processing tools are available under the *Variant analysis* section of the context sensitive menu

- Fusion Gene Detection
- Annotate Variants
- Annotate Variants (SnpEff)
- Annotate Variants (VEP)
- Filter Variants
- Summarize Cohort Mutations
- Combine Variants

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

Your Rating: Results: 39 rates