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ViennaLab®

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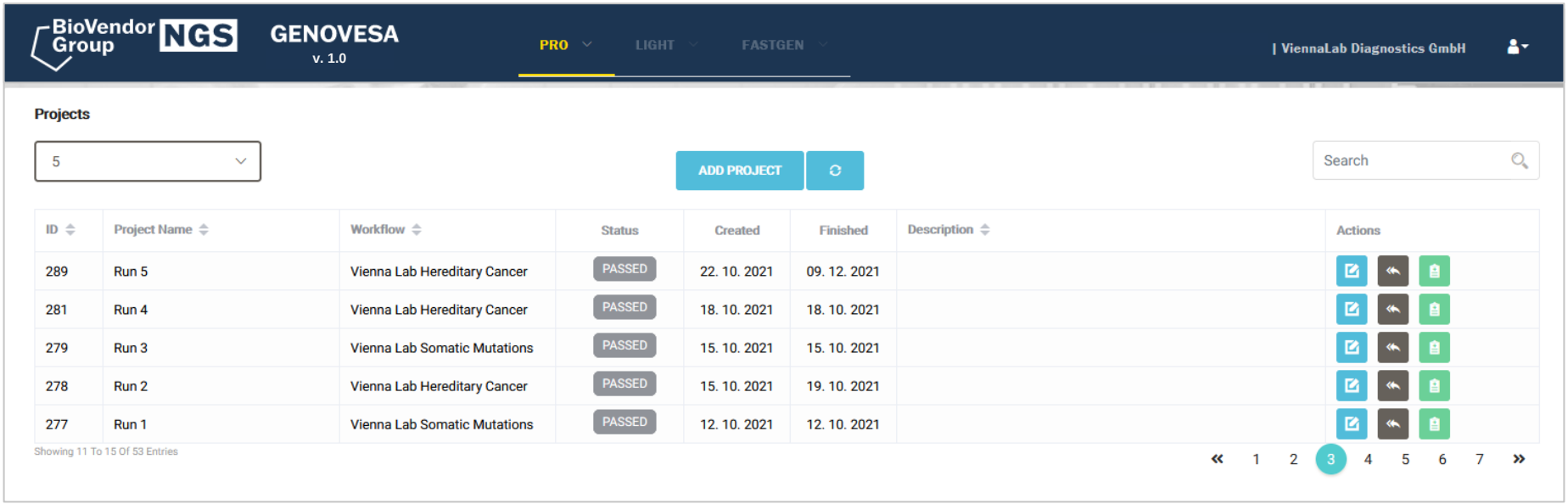
GENOVESA – a web-based platform for automated bioinformatic analysis of NGS data

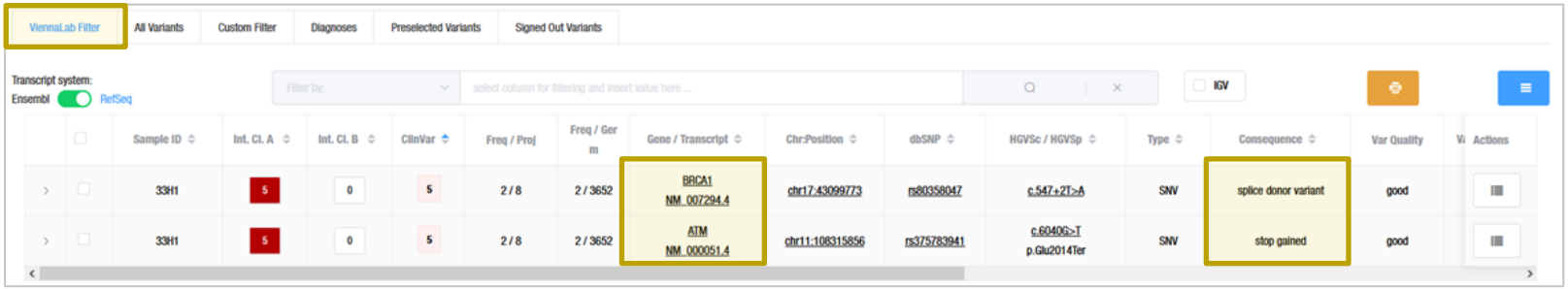


ViennaLab filter – preset filters optimized for simplified and time-saving identification of clinically relevant variants

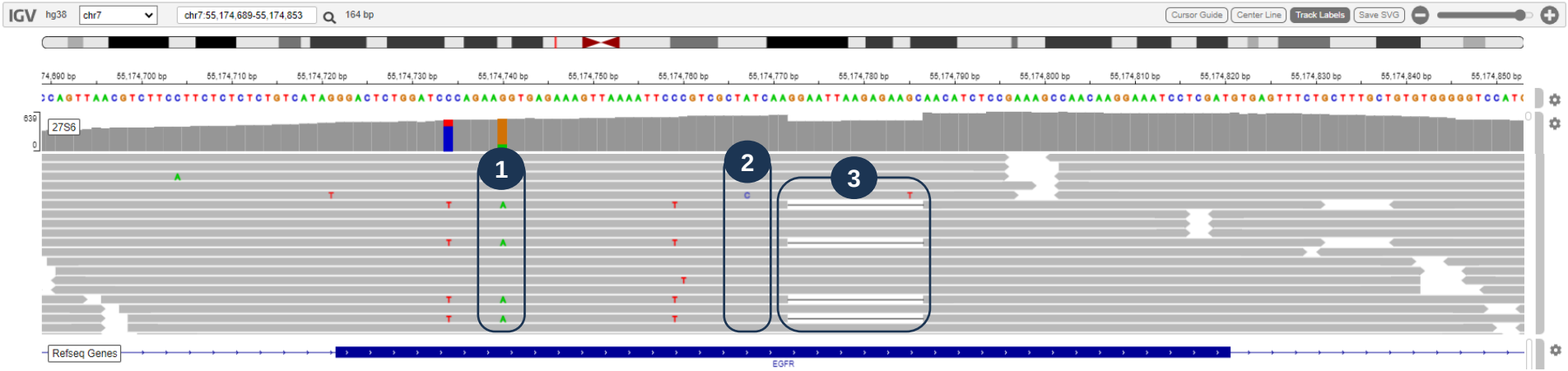
Examples for each workflow:

- ViennaLab Hereditary Cancer: from **170** variants down to **2** relevant variants
- ViennaLab Somatic Mutations: from **107** variants down to **8** relevant variants
- ViennaLab CES: from **12854** variants down to **307** relevant variants

SampleID	Status	Total reads	Total Variants
33H1	PASSED	1 485 196	170



IGV visualization of SNV and InDel variants



1. Single Nucleotide Variant (SNV) shown as colored letter
2. SNV variant observed only once/few times, likely sequencing artifact
3. InDel variant (short deletion: sequence missing shown as line)

→ **NGS allows qualitative and quantitative information of each sequenced DNA molecule**

Key features of the new ViennaLab NGS assays

- ✓ Suitable for FFPE and intact DNA
- ✓ Compatible with Illumina sequencing platforms
- ✓ Full package: library preparation, bioinformatic analysis, genetic variant report generation
  - ✓ Web-based data analysis pipeline: **GENOVESA**
  - ✓ **Automatic QC** and data processing
  - ✓ **Preset filters** optimized to identify clinically relevant variants
  - ✓ **Custom filters** allow comprehensive investigation of data
  - ✓ **Visual display** of variants for both SNVs, InDels – one-click integrated IGV
  - ✓ **CNV and SVs analysis** available upon request
  - ✓ Meaningful **report**