

The background of the slide is white and filled with various yellow abstract shapes, including circles, rectangles, and irregular polygons, some of which are blurred to create a sense of depth and movement.

**B
G** | **ViennaLab**[®]

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

BioVendor Group NGS GENOVESA v. 1.0
| ViennaLab Diagnostics GmbH

Projects

5

ADD PROJECT

Search

ID	Project Name	Workflow	Status	Created	Finished	Description	Actions
289	Run 5	Vienna Lab Hereditary Cancer	PASSED	22. 10. 2021	09. 12. 2021		
281	Run 4	Vienna Lab Hereditary Cancer	PASSED	18. 10. 2021	18. 10. 2021		
279	Run 3	Vienna Lab Somatic Mutations	PASSED	15. 10. 2021	15. 10. 2021		
278	Run 2	Vienna Lab Hereditary Cancer	PASSED	15. 10. 2021	19. 10. 2021		
277	Run 1	Vienna Lab Somatic Mutations	PASSED	12. 10. 2021	12. 10. 2021		

Showing 11 To 15 Of 53 Entries

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

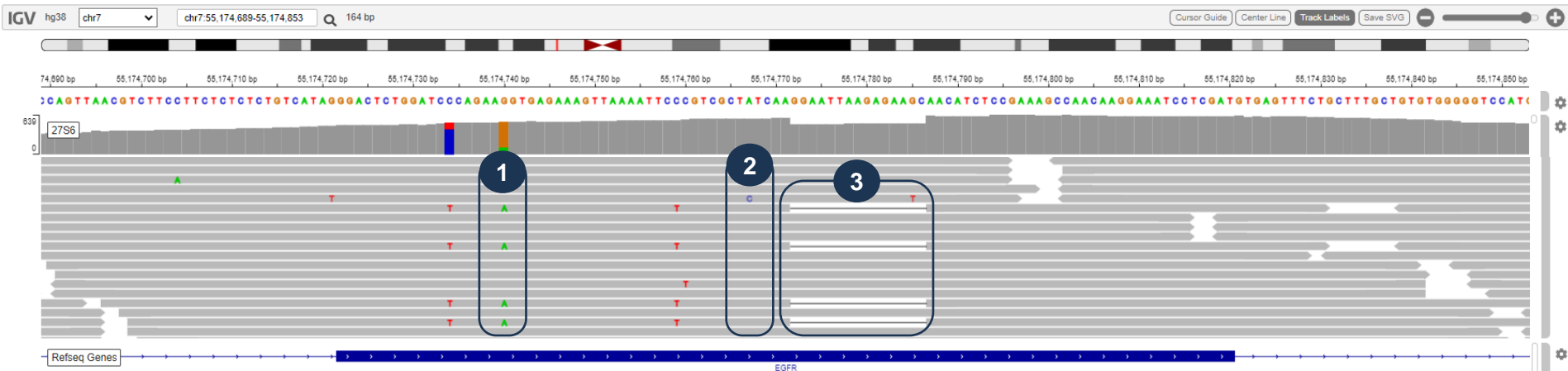
Examples for each workflow:

- 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

ViennaLab Filter														
All Variants Custom Filter Diagnoses Preselected Variants Signed Out Variants														
Transcript system: Ensembl <input checked="" type="checkbox"/> RefSeq														
Filter by: select column for filtering and insert value here ...														
<input type="checkbox"/> IGV <input type="button" value="Refresh"/> <input type="button" value="Menu"/>														
	Sample ID	Int. Cl. A	Int. Cl. B	ClinVar	Freq / Proj	Freq / Ger m	Gene / Transcript	Chr-Position	dbSNP	HGVSc / HGVS p	Type	Consequence	Var Quality	Actions
>	33H1	5	0	5	2 / 8	2 / 3652	BRCA1 NM_007294.4	chr17:43099773	rs80358047	c.547+2T>A	SNV	splice donor variant	good	⋮
>	33H1	5	0	5	2 / 8	2 / 3652	ATM NM_000051.4	chr11:108315856	rs375783941	c.6040G>T p.Glu2014Ter	SNV	stop gained	good	⋮

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**