

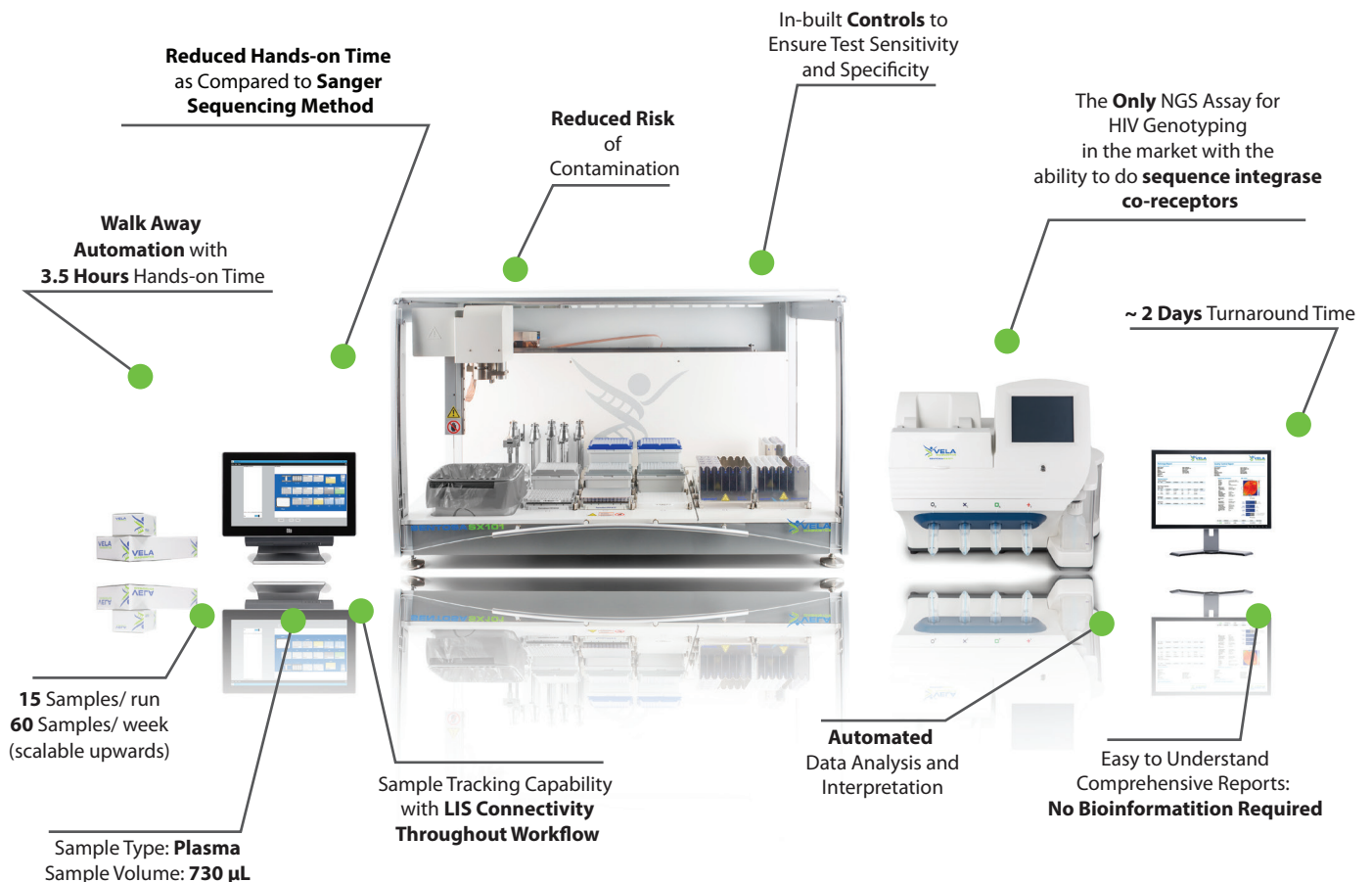
Precise Detection of HIV Drug Resistant Mutations

Automated End-to-End NGS Solution

The **Sentosa[®] SQ HIV Genotyping Assay** detects resistant mutations in HIV positive samples from plasma, to rapidly detect variants in the relevant regions of Protease, Reverse Transcriptase and Integrase genes.

- Overall detection correctness: 99.06%¹
- Assay reproducibility: 100%²
- Interpretation report generated by *Sentosa[®] SQ Reporter* is based on **Stanford HIV drug resistance database**
- Targeted mutation variant frequency of 20% can be detected by assay at **1000 copies/mL**;
Targeted mutation variant frequency of 5% can be detected by assay at **4000 copies/mL**³
- Codon coverage:
 - Protease: 1 - 99
 - Reverse Transcriptase: 1 - 376
 - Integrase: 1 - 288

The *Sentosa[®]* NGS Workflow- Automated from Sample-to-Mutation Detection



Resistance of HIV to antiretroviral drugs is the most common cause for therapeutic failure in people infected with Human Immunodeficiency Virus (HIV).⁴ Detection and reporting of DRMs is critical for optimal selection of Highly Active Antiretroviral Therapy (HAART) regimen and can prevent or minimize the development of resistance to antiviral drugs.

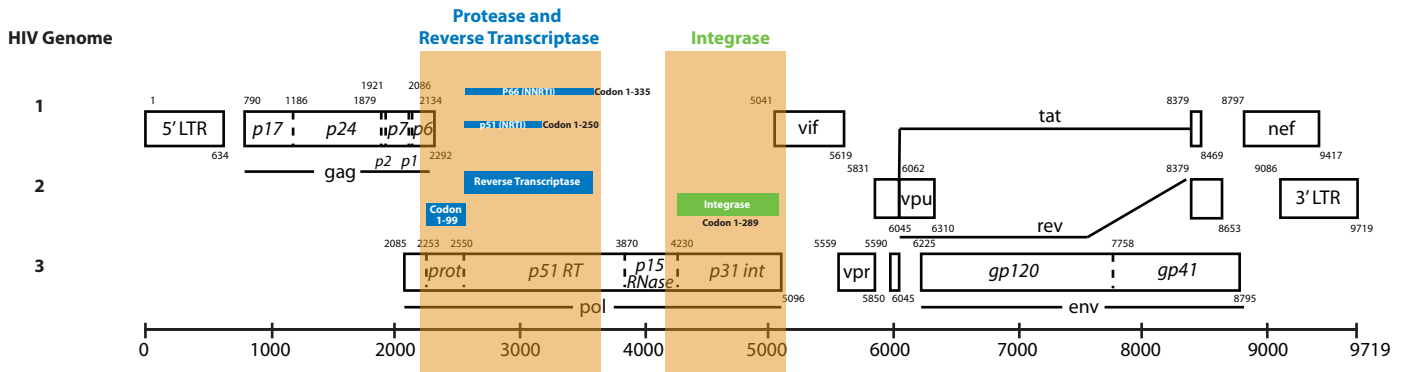


Figure 1: Regions targeted by the Sentosa® SQ HIV Genotyping Assay- The Sentosa® SQ HIV Genotyping Assay provides simultaneous detection of major drug resistant mutations for Reverse Transcriptase, Protease and Integrase, targeting first line HIV treatment. It is currently also the only NGS system validated to detect drug resistant mutations from less than 1,000 copies of viral load for first line treatment simultaneously in one sample.

Quality Control Report

Pathology Report

Target Variants

No.	Gene	CDS Mutation	A/A Mutation	Cov	Ref Cov	Var Cov (%)	COSSMIC
1	EGFR	c.236T>G-A	p.D767Q	4915	2401	2504(50%)	COSSM145180
2	EGFR	c.2544G>A	p.P848P	5059	4342	717(14%)	0
3	FGFR3	c.1952G>A	p.T651T	4953	14	488(99%)	-

Non-Target Variants

Intragenomic

No.	Gene	CDS Mutation	A/A Mutation	Cov	Ref Cov	Var Cov (%)	COSSMIC
1	EGFR	c.236T>G-A	p.D767Q	4915	2401	2504(50%)	COSSM145180
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Intergenic

No.	Gene	CDS Mutation	A/A Mutation	Cov	Ref Cov	Var Cov (%)	COSSMIC
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Figure 2: Automated sequence analysis and reporting- The Sentosa® SQ Reporter automatically generates a Pathology and Quality Control Report. The Pathology report provides information of the HIV Genotyping Assay, genotypes detected and the contigs and target variants. The QC report generates the run QC data, sequencing information, genotypes and coverage and all technical measurements of sequencing quality.

Visit www.veladx.com/NGS-Virology for more information about the workflow and to download a sample report.

References
^{1,2,3} Data on file
⁴ Vella S., Palmisano L. Clin Infect Dis. 2005 41(4): 5239-5246

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