

Samuel H. Pepkowitz, MD, Medical Director
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Patient Name	DOB	Patient ID/Medical Record #	Gender	Monogram Accession #
Date Collected	Date Received	Date Reported	Mode	Report Status
Referring Physician			Reference Lab ID/Order #	
Comments			HIV-1 Subtype: B	

Drug		GenoSure [®] MG		Assessment*	Comments
Generic Name	Brand Name	Drug Resistance Associated Mutations Detected		Drug	
NRTI	Abacavir	Ziagen	None	ABC	Sensitive
	Didanosine	Videx	None	ddI	Sensitive
	Emtricitabine	Emtriva	None	FTC	Sensitive
	Lamivudine	Epivir	None	3TC	Sensitive
	Stavudine	Zerit	None	d4T	Sensitive
	Tenofovir	Viread	None	TFV	Sensitive
	Zidovudine	Retrovir	None	ZDV	Sensitive
	NNRTI	Efavirenz	Sustiva	K103N	EFV
Etravirine		Intelence	None	ETR	Sensitive
Nevirapine		Viramune	K103N	NVP	Resistant
Rilpivirine		Eduvant	K103N	RPV	Sensitive
PI	Atazanavir	Reyataz	A71V	ATV	Sensitive
		Reyataz / r†	A71V	ATV/r	Sensitive
	Darunavir	Prezista / r†	V11I	DRV/r	Sensitive
	Fosamprenavir	Lexiva / r†	V11I	AMP/r	Sensitive
	Indinavir	Crixivan / r†	A71V	IDV/r	Sensitive
	Lopinavir	Kaletra†	A71V	LPV/r	Sensitive
	Nelfinavir	Viracept	A71V	NFV	Sensitive
	Ritonavir	Norvir	A71V	RTV	Sensitive
	Saquinavir	Invirase / r†	A71V	SQV/r	Sensitive
	Tipranavir	Aptivus / r†	A71V	TPV/r	Sensitive

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- * Assessment of drug susceptibility is based upon detected mutations and interpreted using an advanced proprietary algorithm (version 16).
 † Interpretation algorithms for ritonavir-boosted protease inhibitors appropriate for the following dosages: AMP/r 600mg/100mg BID; ATV/r 300mg/100mg QD; IDV/r 800mg/200mg BID; LPV/r 400mg/100mg BID; SQV/r 1000mg/100mg BID; TPV/r 500mg/200mg BID; and DRV/r 600mg/100mg BID.
 * **Mixtures** are indicated by amino acids separated by a slash. Deletions in the amino acid sequence are indicated by a ^ symbol.

Summary of Mutations Observed

RT K13R, Q102K, K103N, I142T, C162S, Q197E, R211K, A272S, V276I, R277K, V292I, E297V, I326V, A327V, Y339F, P345Q, M357I, K358R, T377V, V381I, T386I, A400T
PR V11I, I64V, K70R, A71V, I72E, V77I, I93L

Assay Performance Characteristics

- Assay is highly reproducible and sufficiently sensitive to allow testing of patient samples with viral loads as low as **500 copies/mL**.
- Detects **mixtures** of wild-type and drug-resistant viruses when present at levels as low as **10% of the total population**.
- Uses Monogram's HIV genotyping algorithm, which is based on a large database of **over 100,000 matched HIV genotype-phenotype results** and is reviewed and updated on a regular basis.
- **Includes HIV-1 subtype** which provides information that can be important for long-term drug treatment strategy and genotype interpretation.

For more information on interpreting this report, please visit www.MonogramBio.com or call Customer Service at 800-777-0177 between the hours of 6:30am to 5:00pm PT Monday through Friday.

This assay is performed using a next-generation sequencing platform that analyzes the protease (amino acids 1-99) and reverse transcriptase (amino acids 1-400) coding regions in HIV-1. Variants are reported at a sensitivity that has been demonstrated to be equivalent to that of Sanger/population sequencing. This assay meets the standards for performance characteristics and all other quality control and assurance requirements established by the Clinical Laboratory Improvement Amendments. This test is validated for testing specimens with HIV-1 viral loads equal to or above 500 copies/mL and should be interpreted only on such specimens. The results should not be used as the sole criteria for patient management. The results have been disclosed to you from confidential records protected by law and are not to be disclosed to unauthorized persons. Further disclosure of these results is prohibited without specific consent of the persons to whom it pertains, or as permitted by law.