



EXATYPE™

JOB RESULTS

Job Details

Analysis date: 2024-07-25 - 10:56 am

Job name: **Demo data**

Total samples: **9**

Internal ID: **1725-0977-7410-594**

Job Status: **Completed**

Part 1 - Job overview

Name: Demo data

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Job status: **Completed**

Sequencing platform: CE













Job ID: 1725-0977-7410-594

Samples: 9



Controls: 2

Assay: Thermo Fisher (with Integrase)

1.1 - Samples overview

	Sample name	Exatype sample ID	Pass/fail PRRT	Pass/fail IN
1	A1	1725-0977-7410-596	 Failed	 Failed
2	A2	1725-0977-7410-599	 Passed	 Passed
3	A3	1725-0977-7410-602	 Passed	 Passed
4	A4	1725-0977-7410-605	 Passed	 Failed
5	D1N	1725-0977-7410-608	 Passed	 Passed
6	S1	1725-0977-7410-611	 Passed	N/A
7	S2	1725-0977-7410-613	 Passed	N/A

1.2 - Controls overview

	Control name	Exatype control ID	Region	Control status
1	V1cntrl_POS_IN	1725-0977-7410-615	IN	 Passed
2	V1cntrl_POS_PRRT	1725-0977-7410-617	PRRT	 Passed

Part 2 - Quality control

2.1 - Sequencing controls

Plate name: **Plate 1** +

Sample name: **V1cntrl_POS_IN**

Sample ID: **1725-0977-7410-615**

Plate ID: **1725-0977-7410-595**

Sample type: **Positive**

Region: **IN**

Status: **Passed**

	Locus	Position	Amino acid	Status
	IN	61	*	Present
	IN	74	M	Present
	IN	138	K	Present
	IN	140	S	Present
	IN	148	K	Present
	IN	156	*	Present
	IN	263	K	Present

Plate name: **Plate 1** +

Sample name: **V1cntrl_POS_PRRT**

Sample ID: **1725-0977-7410-617**

Plate ID: **1725-0977-7410-595**

Sample type: **Positive**

Region: **PRRT**

Status: **Passed**

	Locus	Position	Amino acid	Status
	PR	37	S	Present
	PR	41	*	Present
	PR	54	M	Present
	PR	90	M	Present
	RT	41	L	Present
	RT	65	R	Present
	RT	68	*	Present
	RT	103	N	Present
	RT	122	E	Present
	RT	181	C	Present
	RT	183	*	Present
	RT	184	V	Present
	RT	214	L	Present

2.2 - Warnings

2.2.1 - Contamination checks

Samples too similar to positive control

None detected

Samples too similar to selected lab strains

None detected

Samples too similar to other samples from this job

S2 S1

2.2.2 - Unusual mutation checks













Samples with excess APOBEC mutations

D1N

Samples with excess atypical mutations

D1N

Part 3 - Sample results

	Sample name	Exatype sample ID	Pass/fail PRRT	Pass/fail IN
1	A1	1725-0977-7410-596	 Failed	 Failed
2	A2	1725-0977-7410-599	 Passed	 Passed
3	A3	1725-0977-7410-602	 Passed	 Passed
4	A4	1725-0977-7410-605	 Passed	 Failed
5	D1N	1725-0977-7410-608	 Passed	 Passed
6	S1	1725-0977-7410-611	 Passed	N/A
7	S2	1725-0977-7410-613	 Passed	N/A

Name: A1

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Sample status: Failed

Sequencing platform: CE

Exatype version: 24.9.2.5

Assay: Thermo Fisher (with Integrase)

 Sample failed.

Name: **A2 (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **H (5.47%)**
● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	[RT] V106I
	EFV*	S	
	ETR	S	
	NVP*	S	
	RPV	S	
INSTI	BIC	S	
	CAB	S	
	DTG	S	
	EVG	S	
	RAL	S	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-599

Name: **A2 (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **H (5.47%)**

- Susceptible
- Potential low-level resistance
- Low-level resistance
- Intermediate resistance
- High-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	[RT] V106I
	EFV*	S	
	ETR	S	
	NVP*	S	
	RPV	S	
INSTI	BIC	S	
	CAB	S	
	DTG	S	
	EVG	S	
	RAL	S	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-599

Name: **A2 (Supplementary results)**Analysis date: **2024-07-25 10:56**Product: **HIV (Sanger)**Sample status: **Completed**Sequencing platform: **CE**Exatype version: **24.9.2.5**Assay: **Thermo Fisher (with Integrase)**Resistance algorithm: **Stanford HIVDB v9.6**

Mutation summary

PR Region

PI Major: None

PI Accessory: None

PR Other: I13V, G16E, E35D, M36I, R41K, D60E, Q61D, L63T, H69K, L89IM[†]

RT Region

NRTI: None

NNRTI: V106I

RT Other: P4S, K11T, V35T, T39GR[†], T107S, K122E, D123G, A158AS[†], D177E, I178IM[†], L193F, I195L, Q197K, T200A, Q207A, R211K, F227Y, I244V, V245T, E248T

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: E11Q, K14R, S17N, V31I, I72V, I84M, L101I, T112V, I113V, S119P, T124A, T125A, G134D, H171Q, V201I, T218L, N222K, L234I, D256E, A265V, S283G, R284G

[†]Mixed mutation

Phylogenetic summary

Stanford HIVDB v9.6 subtype

H (5.47%): AF190128: Belgium (1993)

H (5.47%): FJ711703: United Kingdom (2000)

H (5.84%): AF005496: Central African Republic (1990)

H (5.84%): KY392778: Congo, the Democratic Republic of the (2001)

H (5.95%): AF190127: Belgium (1993)

H (5.95%): KU168279: Central African Republic (2002)

H (6.00%): KY392777: Congo, the Democratic Republic of the (2001)

H (6.42%): KY392779: Congo, the Democratic Republic of the (2001)

H (6.74%): GQ371946: United States (2003)

H (6.89%): KU168273: Congo, the Democratic Republic of the (2004)

[†]Mixed mutation

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Exatype sample ID: 1725-0977-7410-599

Name: **A3 (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **CRF02_AG (6.00%)**
● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	[PR] V11IT [†]
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	[RT] K103N
	EFV*	R	
	ETR	S	
	NVP*	R	
	RPV	S	
INSTI	BIC	S	
	CAB	S	
	DTG	S	
	EVG	S	
	RAL	S	

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-602

Name: **A3 (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **CRF02_AG (6.00%)**

- Susceptible
- Potential low-level resistance
- Low-level resistance
- Intermediate resistance
- High-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	[PR] V11IT [†]
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	[RT] K103N
	EFV*	R	
	ETR	S	
	NVP*	R	
	RPV	S	
INSTI	BIC	S	
	CAB	S	
	DTG	S	
	EVG	S	
	RAL	S	

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-602

Name: **A3 (Supplementary results)**Analysis date: **2024-07-25 10:56**Product: **HIV (Sanger)**Sample status: **Completed**Sequencing platform: **CE**Exatype version: **24.9.2.5**Assay: **Thermo Fisher (with Integrase)**Resistance algorithm: **Stanford HIVDB v9.6**

Mutation summary

PR Region

PI Major: None

PI Accessory: None

PR Other: L10M, V11I†, T12TI†, I13V, K14KR†, I15IV†, K20I, E35N, M36I, R41K, H69K, L89M, F99FL†

RT Region

NRTI: None

NNRTI: K103N

RT Other: P4T, K11T, V35T, T39N, E40D, K43KR†, K49R, V60I, K102Q, D121H, K122E, K173R, Q174K, D177E, T200A, Q207E, R211K, V245K, D250E

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: E11D, R20K, S24N, L101I, T124A, T125A, G134N, I135V, K136T, D167E, V201I, T206S, L234I, S283G

†Mixed mutation

Phylogenetic summary

Stanford HIVDB v9.6 subtype

CRF02_AG (6.00%): AJ508595: Niger (1997)

G (6.26%): AF316544: Congo, the Democratic Republic of the (1997)

G (6.32%): AY586549: Cuba (1999)

A1 + G (6.47%): AF377957: Cameroon (1997)

CRF02_AG (6.47%): AJ286133: Cameroon (1997)

A1 + G (6.53%): JF683745: Cyprus (2007)

CRF06_cpx (6.58%): FJ183725: Congo, the Democratic Republic of the (1996)

CRF02_AG (6.58%): KT124792: Germany (2009)

CRF02_AG (6.63%): AF107770: Sweden (1994)

CRF02_AG (6.63%): AY444809: United States (1999)

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-602

Name: **A4 (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Discordant**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **B (1.88%)**

● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	
	EFV*	S	
	ETR	S	
	NVP*	S	
	RPV	S	
INSTI	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-605

Name: **A4 (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Discordant**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **B (1.88%)**

- Susceptible
- Potential low-level resistance
- Low-level resistance
- Intermediate resistance
- High-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	S	
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	
NRTI	3TC	S	
	ABC	S	
	AZT	S	
	D4T	S	
	DDI	S	
	FTC	S	
	TDF	S	
NNRTI	DOR*	S	
	EFV*	S	
	ETR	S	
	NVP*	S	
	RPV	S	
INSTI	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-605

Name: A4 (Supplementary results)

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Sample status: **Discordant**

Sequencing platform: CE

Exatype version: 24.9.2.5

Assay: Thermo Fisher (with Integrase)

Resistance algorithm: Stanford HIVDB v9.6

Mutation summary

PR Region

PI Major: None

PI Accessory: None

PR Other: R57RK[†], I62IV[†], L63AP[†], I64IM[†], V77I

RT Region

NRTI: None

NNRTI: None

RT Other: D123E, I178M, Q207E, R211K

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: None

[†]Mixed mutation

Phylogenetic summary

Stanford HIVDB v9.6 subtype

B (1.88%): KJ704787: United States (1983)

B (2.58%): L31963: France (1983)

B (2.84%): AF042100: Australia (1986)

B (2.90%): DQ854716: Spain (1989)

B (2.90%): FJ647145: South Africa (1985)

B (3.11%): D10112: United Kingdom (1983)

B (3.17%): AB873942: Japan (2009)

B (3.17%): EU839600: Haiti (2005)

B (3.22%): AY779554: Canada (1998)

B (3.27%): U34603: Netherlands (1986)

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-605

Name: **D1N (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **B (3.84%)**

● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	I	[PR] D30N, [PR] M46I, [PR] G48S, [PR] G73S
	DRV/r	S	
	FPV/r	I	
	IDV/r	I	
	LPV/r	I	
	NFV	R	
	SQV/r	R	
NRTI	3TC	R	[RT] M41L, [RT] D67N, [RT] L74I, [RT] M184I, [RT] T215C
	ABC	I	
	AZT	I	
	D4T	I	
	DDI	R	
	FTC	R	
	TDF	S	
NNRTI	DOR*	R	[RT] L100V, [RT] K101H, [RT] K103N, [RT] V106I, [RT] V108I, [RT] E138A, [RT] V179F, [RT] Y181C, [RT] M184I, [RT] G190E, [RT] F227FL [†] , [RT] M230I
	EFV*	R	
	ETR	R	
	NVP*	R	
	RPV	R	
INSTI	BIC	I	[IN] G163R, [IN] D232N, [IN] R263K
	CAB	R	
	DTG	I	
	EVG	I	
	RAL	I	

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-608

Name: **D1N (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **B (3.84%)**

- Susceptible
- Intermediate resistance
- Potential low-level resistance
- High-level resistance
- Low-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	I	[PR] D30N, [PR] M46I, [PR] G48S, [PR] G73S
	DRV/r	S	
	FPV/r	L-L	
	IDV/r	I	
	LPV/r	L-L	
	NFV	R	
	SQV/r	R	
	TPV/r	S	
NRTI	3TC	R	[RT] M41L, [RT] D67N, [RT] L74I, [RT] M184I, [RT] T215C
	ABC	I	
	AZT	I	
	D4T	I	
	DDI	R	
	FTC	R	
	TDF	S	
NNRTI	DOR*	R	[RT] L100V, [RT] K101H, [RT] K103N, [RT] V106I, [RT] V108I, [RT] E138A, [RT] V179F, [RT] Y181C, [RT] M184I, [RT] G190E, [RT] F227FL [†] , [RT] M230I
	EFV*	R	
	ETR	R	
	NVP*	R	
	RPV	R	
INSTI	BIC	I	[IN] G163R, [IN] D232N, [IN] R263K
	CAB	R	
	DTG	I	
	EVG	I	
	RAL	I	

[†]Mixed mutation

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Exatype sample ID: 1725-0977-7410-608

Name: D1N (Supplementary results)

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Sample status: Completed

Sequencing platform: CE

Exatype version: 24.9.2.5

Assay: Thermo Fisher (with Integrase)

Resistance algorithm: Stanford HIVDB v9.6

Mutation summary

PR Region

PI Major: D30N, M46I, G48S

PI Accessory: G73S

PR Other: M36MI[†], R41RK[†], L63P, I64V, E65D, K70R, I72V, V77I

RT Region

NRTI: M41L, D67N, L74I, M184I, T215C

NNRTI: L100V, K101H, K103N, V106I, V108I, E138A, V179F, Y181C, G190E, F227FL[†], M230IRT Other: V35M, Q174QR[†], D177E, D186C, Y188S, E203EK[†], Q207E, L210H, R211K, G213H, D218L, K223KE[†], L228LR[†], V245K, D250E

IN Region

INSTI Major: R263K

INSTI Accessory: G163R, D232N

IN Other: L2Y, I5M, E10K, E11K, W19W*[†], I72V, S123G, T124A, K127R, K264R, G277S[†]Mixed mutation

Phylogenetic summary

Stanford HIVDB v9.6 subtype

B (3.84%): KJ704787: United States (1983)

B (3.84%): L31963: France (1983)

B (4.68%): AF042100: Australia (1986)

B (4.79%): FJ647145: South Africa (1985)

B (4.95%): D10112: United Kingdom (1983)

B (5.00%): U34603: Netherlands (1986)

B (5.05%): GQ372188: United States (2003)

B (5.11%): EU839602: Haiti (2005)

B (5.11%): M26727: Gabon (1988)

B (5.16%): AY779554: Canada (1998)

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-608

Name: **S1 (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **A1 (5.22%)**

● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	R	[PR] M46I, [PR] F53L, [PR] I54V, [PR] V82A
	DRV/r	S	
	FPV/r	I	
	IDV/r	R	
	LPV/r	R	
	NFV	R	
	SQV/r	R	
NRTI	TPV/r	I	[RT] M41L, [RT] E44D, [RT] D67N, [RT] T69D, [RT] M184V, [RT] L210W, [RT] T215Y
	3TC	R	
	ABC	R	
	AZT	R	
	D4T	R	
	DDI	R	
	FTC	R	
NNRTI	TDF	R	[RT] A98G, [RT] G190A
	DOR*	I	
	EFV*	I	
	ETR	I	
	NVP*	R	
INSTI	RPV	I	No data
	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-611

Name: **S1 (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **A1 (5.22%)**

- Susceptible
- Potential low-level resistance
- Low-level resistance
- Intermediate resistance
- High-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	R	[PR] M46I, [PR] F53L, [PR] I54V, [PR] V82A
	DRV/r	S	
	FPV/r	I	
	IDV/r	R	
	LPV/r	R	
	NFV	R	
	SQV/r	R	
	TPV/r	L-L	
NRTI	3TC	R	[RT] M41L, [RT] E44D, [RT] D67N, [RT] T69D, [RT] M184V, [RT] L210W, [RT] T215Y
	ABC	R	
	AZT	R	
	D4T	R	
	DDI	R	
	FTC	R	
	TDF	R	
NNRTI	DOR*	L-L	[RT] A98G, [RT] G190A
	EFV*	I	
	ETR	L-L	
	NVP*	R	
	RPV	I	
INSTI	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

†Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-611

Name: S1 (Supplementary results)

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Sample status: Completed

Sequencing platform: CE

Exatype version: 24.9.2.5

Assay: Thermo Fisher (with Integrase)

Resistance algorithm: Stanford HIVDB v9.6

Mutation summary

PR Region

PI Major: M46I, I54V, V82A

PI Accessory: F53L

PR Other: L10I, I13V, G16E, E35D, M36I, N37D, R41K, R57K, L63S, H69K, K70R, L89M

RT Region

NRTI: M41L, E44D, D67N, T69D, M184V, L210W, T215Y

NNRTI: A98G, G190A

RT Other: V35T, V60I, V111I, K122E, D123S, I135T, K173AT[†], Q174K, V179I, T200A, I202V, E203K, Q207D, H208Y, R211N, V245Q, D250E

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: None

[†]Mixed mutation

Phylogenetic summary

Stanford HIVDB v9.6 subtype

A1 (5.22%): AF484493: Uganda (1999)

A1 (5.60%): FJ647148: South Africa (2001)

A1 (5.70%): AF457063: Kenya (1999)

A1 (5.99%): AF107771: Sweden (1995)

A1 (6.18%): AF069670: Somalia (1994)

A1 (6.47%): AF457070: Kenya (2000)

A1 (6.47%): FJ388903: Cyprus (2005)

A1 (6.57%): AF457089: Kenya (2000)

A1 (6.57%): AY322193: Kenya (1997)

A1 (6.57%): DQ676872: Australia (2003)

[†]Mixed mutation

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-611

Name: **S2 (3-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **A1 (5.51%)**

● Susceptible
 ● Intermediate resistance
 ● High-level resistance
 ● No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	I	[PR] M46I, [PR] F53L, [PR] V82A
	DRV/r	S	
	FPV/r	I	
	IDV/r	I	
	LPV/r	I	
	NFV	R	
	SQV/r	I	
	TPV/r	S	
NRTI	3TC	R	[RT] M41L, [RT] E44D, [RT] D67N, [RT] T69D, [RT] M184V, [RT] L210W, [RT] T215Y
	ABC	R	
	AZT	R	
	D4T	R	
	DDI	R	
	FTC	R	
	TDF	R	
NNRTI	DOR*	I	[RT] A98G, [RT] G190A
	EFV*	I	
	ETR	I	
	NVP*	R	
	RPV	I	
INSTI	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-613

Name: **S2 (5-level result)**

 Analysis date: **2024-07-25 10:56**

 Product: **HIV (Sanger)**

 Sample status: **Completed**

 Sequencing platform: **CE**

 Exatype version: **24.9.2.5**

 Assay: **Thermo Fisher (with Integrase)**

 Resistance algorithm: **Stanford HIVDB v9.6**

 HIV subtype: **A1 (5.51%)**

- Susceptible
- Intermediate resistance
- Potential low-level resistance
- High-level resistance
- Low-level resistance
- No data

DRUG CLASS	DRUG	CALL	MUTATIONS
PI	ATV/r	I	[PR] M46I, [PR] F53L, [PR] V82A
	DRV/r	S	
	FPV/r	I	
	IDV/r	I	
	LPV/r	I	
	NFV	R	
	SQV/r	I	
	TPV/r	S	
NRTI	3TC	R	[RT] M41L, [RT] E44D, [RT] D67N, [RT] T69D, [RT] M184V, [RT] L210W, [RT] T215Y
	ABC	R	
	AZT	R	
	D4T	R	
	DDI	R	
	FTC	R	
	TDF	R	
NNRTI	DOR*	L-L	[RT] A98G, [RT] G190A
	EFV*	I	
	ETR	L-L	
	NVP*	R	
	RPV	I	
INSTI	BIC	No data	
	CAB	No data	
	DTG	No data	
	EVG	No data	
	RAL	No data	

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-613

Name: S2 (Supplementary results)

Analysis date: 2024-07-25 10:56

Product: HIV (Sanger)

Sample status: Completed

Sequencing platform: CE

Exatype version: 24.9.2.5

Assay: Thermo Fisher (with Integrase)

Resistance algorithm: Stanford HIVDB v9.6

Mutation summary

PR Region

PI Major: M46I, V82A

PI Accessory: F53L

PR Other: L10I, I13V, G16E, E35D, M36I, N37D, R41K, R57K, L63S, H69K, K70R, L89M

RT Region

NRTI: M41L, E44D, D67N, T69D, M184V, L210W, T215Y

NNRTI: A98G, G190A

RT Other: V35T, V60I, V111I, K122E, D123S, I135T, K173T, Q174K, V179I, T200A, I202V, E203K, R206K, Q207D, H208Y, R211N, V245Q, D250E

IN Region

INSTI Major: None

INSTI Accessory: None

IN Other: None

Phylogenetic summary

Stanford HIVDB v9.6 subtype

A1 (5.51%): AF484493: Uganda (1999)

A1 (5.80%): AF457063: Kenya (1999)

A1 (5.80%): FJ647148: South Africa (2001)

A1 (6.18%): AF107771: Sweden (1995)

A1 (6.38%): AF069670: Somalia (1994)

A1 (6.67%): AF457070: Kenya (2000)

A1 (6.67%): AY322193: Kenya (1997)

A1 (6.67%): FJ388903: Cyprus (2005)

A1 (6.76%): AF457089: Kenya (2000)

A1 (6.86%): DQ676872: Australia (2003)

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*The assay does not cover the entire reverse transcriptase gene region. Therefore, two potential drug-resistance scoring mutations - amino acid position 318 (scoring for DOR, EFV, and NVP) and position 348 (scoring for NVP) - are excluded from the drug-resistance interpretation.

Exatype sample ID: 1725-0977-7410-613