

Sample ID: CQ012022_PGM

Source ID: CQ012022_PGM

MID: n.a.

Subtype: F2

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC		1	Green	S - Susceptible
ABC	41L (100.0%), 67N (98.4%), 74V (99.2%), 215F (98.4%)	3	Red	R - Resistance
ISL		1	Green	S - Susceptible
TDF_TAF	41L (100.0%), 67N (98.4%), 69D (98.8%), 74V (99.2%), 215F (98.4%)	3	Red	R - Resistance
ZDV	41L (100.0%), 67N (98.4%), 70R (99.1%), 215F (98.4%), 219Q (95.6%)	3	Red	R - Resistance

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	181C (100.0%), 190A (100.0%)	2	Yellow	I - Possible resistance
EFV	181C (100.0%), 190A (100.0%)	3	Red	R - Resistance
ETR	181C (100.0%), 190A (100.0%)	3	Red	R - Resistance
NVP	181C (100.0%), 190A (100.0%)	3	Red	R - Resistance
RPV	181C (100.0%)	3	Red	R - Resistance

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV	10V (100.0%), 16E (99.7%), 33F (100.0%), 90M (100.0%)	3	Red	R - Resistance
DRV_RTV_BID	33F (100.0%)	1	Green	S - Susceptible
DRV_RTV_QD	33F (100.0%)	1	Green	S - Susceptible
LPVr	10V (100.0%), 33F (100.0%), 53L (100.0%), 54V (100.0%), 82F (100.0%), 90M (100.0%)	3	Red	R - Resistance

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC		1	Green	S - Susceptible
CAB		1	Green	S - Susceptible
DTG_BID		1	Green	S - Susceptible
DTG_QD		1	Green	S - Susceptible
EVG		1	Green	S - Susceptible
RAL		1	Green	S - Susceptible

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
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Signature(s)

Sample ID: CQ012022_PGM

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MID: n.a.

Subtype: F2

1	F1	FJ900268	365	296	90.5	28
2	F1	DQ979024	365	296	90.5	28
3	F1	DQ979025	357	296	90.2	29
4	F1	FJ900266	333	296	89.2	32
5	F1	FJ900267	333	296	89.2	32

HIV-1 RT

Consensus length : 1 620

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	F2	AJ249236	1 984	1 617	90.6	150
2	F2	MN153483	1 966	1 616	90.3	156
3	F2	KU749420	1 966	1 616	90.3	156
4	CRF46_BF1	MG365771	1 961	1 621	90.4	154
5	F1	FJ771008	1 943	1 620	90.1	160

HIV-1 IN

Consensus length : 864

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	F2	MN153485	1 302	861	94.1	51
2	D	AF484497	1 302	849	94.3	48
3	A4	AM000054	1 302	861	94.1	51
4	F2	AJ249236	1 287	861	93.8	53
5	F1	FJ900267	1 287	861	93.8	53

Detailed information

IDNS5 version	v3.13.0
Drug resistance algorithm	ANRS (2022.33/sg/b)
Pipeline name	HIV-1 PR+RT_frag+IN
Pipeline version	2.4.6_HIV1_v1.6
Genotyping database version	HIV1_r23u051
Noise filter [%]	0.5
Interpretation cutoff [%]	20.0
Min. read depth [# reads]	50
Number of input reads	752 343
Number of reads mapped	680 565
Mutations HIV-1 PR [(%)]	3I (100.0), 10V (100.0), 12I (98.0), 13V (100.0), 15V (100.0), 16E (99.7), 20V (98.2), 33F (100.0), 35N (96.9), 36I (100.0), 37N (100.0), 39Q (100.0), 41K (97.9), 45V (100.0), 53L (100.0), 54V (100.0), 57K (94.1), 62V (100.0), 63T (100.0), 74A (100.0), 82F (100.0), 89M (85.8), 90M (100.0)

Signature(s)

Sample ID: CQ012022_PGM

Source ID: CQ012022_PGM

MID: n.a.

Subtype: F2

Mutations HIV-1 RT [(%)]

20R (100.0), 35T (100.0), 39M (100.0), 41L (100.0), 67N (98.4), 69D (98.8), 70R (99.1), 74V (99.2), 75T (100.0), 101Q (98.3), 118I (100.0), 171Y (100.0), 173T (98.3), 174K (94.8), 177E (100.0), 178L (100.0), 181C (100.0), 190A (100.0), 203K (100.0), 207E (100.0), 208Y (100.0), 211A (100.0), 215F (98.4), 219Q (95.6), 223Q (100.0), 228H (99.6), 245Q (100.0), 248D (100.0), 250E (100.0), 277K (100.0), 283I (100.0), 286A (100.0), 291D (100.0), 292I (100.0), 293V (100.0), 297Q (99.4), 324E (100.0), 333D (100.0), 334H (100.0), 356K (89.9), 359S (100.0), 365I (100.0), 376C (100.0), 386I (93.4), 390R (100.0), 399G (100.0), 411L (100.0), 431T (100.0), 449Q (99.5), 451R (100.0), 452E (100.0), 460D (99.5), 466A (100.0), 468S (100.0), 483H (98.9), 491S (100.0), 512K (95.4), 527Q (99.5), 534S (100.0)

Mutations HIV-1 IN [(%)]

3E (100.0), 7R (100.0), 10E (100.0), 17N (100.0), 100Y (100.0), 101I (100.0), 112V (100.0), 119P (100.0), 123S (100.0), 125A (100.0), 127K (100.0), 136Q (100.0), 205S (100.0), 218I (99.2), 232D (100.0), 234I (100.0), 255N (100.0), 256E (100.0), 283G (100.0), 288N (94.3)

Created by

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Signature(s)

Sample ID: CQ022022_PGM

Source ID: CQ022022_PGM

MID: n.a.

Subtype: B

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC	65R (31.7%)	3		R - Resistance
ABC	41L (100.0%), 65R (31.7%), 67N (66.6%), 74I (93.4%), 215V (96.8%)	3		R - Resistance
ISL		1		S - Susceptible
TDF_TAF	41L (100.0%), 65R (31.7%), 67N (66.6%), 69D (67.6%), 69N (32.4%), 74I (93.4%), 215V (96.8%)	3		R - Resistance
ZDV	41L (100.0%), 67N (66.6%), 215V (96.8%), 219Q (100.0%)	3		R - Resistance

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	181C (100.0%)	1		S - Susceptible
EFV	181C (100.0%)	3		R - Resistance
ETR	181C (100.0%)	3		R - Resistance
NVP	181C (100.0%)	3		R - Resistance
RPV	181C (100.0%)	3		R - Resistance

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV	10V (99.3%), 33F (99.3%), 46L (100.0%), 60E (100.0%), 71V (100.0%), 84V (100.0%)	3		R - Resistance
DRV_RTV_BID	11I (100.0%), 33F (99.3%), 84V (100.0%)	2		I - Possible resistance
DRV_RTV_QD	11I (100.0%), 33F (99.3%), 84V (100.0%)	3		R - Resistance
LPVr	10V (99.3%), 24I (100.0%), 33F (99.3%), 46L (100.0%), 54V (99.1%), 63P (100.0%), 71V (100.0%), 82A (100.0%), 84V (100.0%)	3		R - Resistance

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC		1		S - Susceptible
CAB		1		S - Susceptible
DTG_BID		1		S - Susceptible
DTG_QD		1		S - Susceptible
EVG		1		S - Susceptible
RAL		1		S - Susceptible

Signature(s)

Sample ID: CQ022022_PGM

Source ID: CQ022022_PGM

MID: n.a.

Subtype: B

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	MG572010	414	297	92.6	22
2	B	AF538303	414	297	92.6	22
3	B	AY835758	414	297	92.6	22
4	BD	MH234642	406	297	92.3	23
5	B	KY112061	406	297	92.3	23

HIV-1 RT

Consensus length : 1 617

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	AY037282	2 385	1 614	93.4	106
2	B	D10112	2 383	1 617	93.4	107
3	B	AY835778	2 369	1 614	93.3	108
4	B	AF004394	2 365	1 614	93.3	108
5	B	M38429	2 361	1 614	93.2	109

HIV-1 IN

Consensus length : 867

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	EF637046	1 513	867	97.0	26
2	B	U34604	1 513	867	97.0	26
3	B	ConsB-IN	1 513	867	97.0	26
4	B	JQ316129	1 505	867	96.9	27

IDNS5 version v3.13.0

Drug resistance algorithm ANRS (2022.33/sg/b)

Pipeline name HIV-1 PR+RT_frag+IN

Pipeline version 2.6.1_HIV1_v1.6

Genotyping database version HIV1_r23u051

Noise filter [%] 0.5

Interpretation cutoff [%] 20.0

Min. read depth [# reads] 50

Number of input reads 337 319

Number of reads mapped 289 704

Mutations HIV-1 PR [(%)

3I (100.0), 10V (99.3), 11I (100.0), 13V (100.0), 16A (100.0), 24I (100.0), 33F (99.3), 37N (100.0), 46L (100.0), 54V (99.1), 60E (100.0), 62V (100.0), 63P (100.0), 71V (100.0), 72T (99.5), 73C (100.0), 82A (100.0), 84V (100.0)

Signature(s)

Sample ID: CQ022022_PGM

Source ID: CQ022022_PGM

MID: n.a.

Subtype: B

5	B	MH234640	1 505	867	96.9	27
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Detailed information

Mutations HIV-1 RT [(%)]

35M (100.0), 39A (100.0), 41L (100.0), 65R (31.7), 67H (33.4), 67N (66.6), 69D (67.6), 69N (32.4), 70M (28.0), 71G (20.6), 74I (93.4), 75T (100.0), 123N (99.1), 135T (100.0), 138D (100.0), 177E (100.0), 178M (100.0), 181C (100.0), 211T (100.0), 214F (97.2), 215V (96.8), 218E (100.0), 219Q (100.0), 293V (100.0), 297A (100.0), 359S (100.0), 360T (100.0), 376A (100.0), 377V (96.0), 386I (83.3), 390R (99.1), 435A (100.0), 437V (100.0), 460D (99.0), 468S (99.4), 470P (100.0), 491P (100.0), 512K (100.0), 517I (100.0), 519S (100.0), 524E (99.5)

Mutations HIV-1 IN [(%)]

10E (100.0), 17N (100.0), 31I (100.0), 45G (97.8), 123S (100.0), 125V (99.3), 127K (100.0), 136N (100.0), 201I (100.0), 232D (100.0)

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Signature(s)

Sample ID: CQ032022_PGM

Source ID: CQ032022_PGM

MID: n.a.

Subtype: B

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC		1		S - Susceptible
ABC	41L (100.0%), 74V (95.6%), 215C (83.2%)	3		R - Resistance
ISL		1		S - Susceptible
TDF_TAF	41L (100.0%), 74V (95.6%), 215C (83.2%)	2		I - Possible resistance
ZDV	41L (100.0%), 215C (83.2%), 219E (91.1%)	3		R - Resistance

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	100I (100.0%), 103N (100.0%)	3		R - Resistance
EFV	100I (100.0%), 103N (100.0%)	3		R - Resistance
ETR	100I (100.0%)	1		S - Susceptible
NVP	98S (100.0%), 100I (100.0%), 103N (100.0%)	3		R - Resistance
RPV	100I (100.0%), 103N (100.0%)	3		R - Resistance

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV	10F (99.1%), 33F (100.0%), 71T (100.0%), 84V (100.0%), 90M (100.0%)	3		R - Resistance
DRV_RTV_BID	32I (100.0%), 33F (100.0%), 54L (98.8%), 84V (100.0%), 89V (100.0%)	3		R - Resistance
DRV_RTV_QD	32I (100.0%), 33F (100.0%), 54L (98.8%), 84V (100.0%), 89V (100.0%)	3		R - Resistance
LPVr	10F (99.1%), 33F (100.0%), 54L (98.8%), 63P (100.0%), 71T (100.0%), 84V (100.0%), 90M (100.0%)	3		R - Resistance

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC	140S (100.0%), 148H (97.8%)	3		R - Resistance
CAB	140S (100.0%), 148H (97.8%)	3		R - Resistance
DTG_BID	140S (100.0%), 148H (97.8%)	2		I - Possible resistance
DTG_QD	140S (100.0%), 148H (97.8%)	3		R - Resistance
EVG	140S (100.0%), 148H (97.8%)	3		R - Resistance
RAL	140S (100.0%), 148H (97.8%)	3		R - Resistance

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Signature(s)

Sample ID: CQ032022_PGM

Source ID: CQ032022_PGM

MID: n.a.

Subtype: B

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	D	MN650444	408	297	91.9	24
2	B	KY658693	408	297	91.9	24
3	B	EF178358	408	297	91.9	24
4	B	GQ372066	402	297	91.6	25
5	D	MN650466	400	297	91.6	25

HIV-1 RT

Consensus length : 1 158

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	JF689873	1 849	1 158	95.1	57
2	B	M38429	1 845	1 156	95.1	57
3	B	AY835769	1 841	1 158	95.0	58
4	B	JQ316130	1 825	1 158	94.8	60
5	B	KJ140264	1 825	1 158	94.8	60

HIV-1 IN

Consensus length : 867

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	ConsB-IN	1 481	867	96.5	30
2	B	KX505396	1 457	867	96.2	33
3	B	MW405324	1 449	867	96.1	34
4	B	OK181205	1 449	867	96.1	34
5	B	KY514083	1 449	867	96.1	34

Detailed information

IDNS5 version	v3.13.0
Drug resistance algorithm	ANRS (2022.33/sg/b)
Pipeline name	HIV-1 PR+RT_frag+IN
Pipeline version	2.4.6_HIV1_v1.6
Genotyping database version	HIV1_r23u051
Noise filter [%]	0.5
Interpretation cutoff [%]	20.0
Min. read depth [# reads]	50
Number of input reads	573 797
Number of reads mapped	490 729
Mutations HIV-1 PR [(%)]	3I (100.0), 10F (99.1), 13V (98.0), 32I (100.0), 33F (100.0), 35D (88.9), 36I (100.0), 37N (100.0), 43Q (20.4), 43T (79.5), 54L (98.8), 63P (100.0), 64V (100.0), 71T (100.0), 72V (100.0), 73T (99.8), 84V (100.0), 89V (100.0), 90M (100.0)

Signature(s)

Sample ID: CQ032022_PGM

Source ID: CQ032022_PGM

MID: n.a.

Subtype: B

Mutations HIV-1 RT [(%)]

6K (100.0), 41L (100.0), 67G (100.0), 68G (100.0), 74V (95.6), 98S (100.0), 100I (100.0), 103N (100.0), 108I (100.0), 135T (100.0), 177N (99.0), 200I (100.0), 214F (98.1), 215C (83.2), 219E (91.1), 228H (100.0), 272A (100.0), 277K (99.5), 286A (100.0), 297K (97.7), 356K (97.2), 376A (100.0), 379G (21.0)

Mutations HIV-1 IN [(%)]

10E (100.0), 20K (100.0), 31I (100.0), 72I (96.6), 101I (96.2), 112M (93.6), 123S (100.0), 124N (100.0), 125V (100.0), 127K (100.0), 140S (100.0), 148H (97.8), 163E (100.0), 207N (99.5), 211T (99.0), 218S (100.0), 232D (100.0), 256E (100.0)

Created by

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Signature(s)

Sample ID: CQ012023_PGM

Source ID: CQ012023_PGM

MID: n.a.

Subtype: B

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC	184V (100.0%)	3		R - Resistance
ABC	74I (97.5%), 184V (100.0%), 215V (99.6%)	3		R - Resistance
ISL	184V (100.0%)	3		R - Resistance
TDF_TAF	74I (97.5%), 215V (99.6%)	1		S - Susceptible
ZDV	215V (99.6%), 219E (98.3%)	3		R - Resistance

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	103N (100.0%)	1		S - Susceptible
EFV	103N (100.0%)	3		R - Resistance
ETR	138G (100.0%)	2		I - Possible resistance
NVP	103N (100.0%)	3		R - Resistance
RPV	103N (100.0%), 138G (100.0%)	3		R - Resistance

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV	10V (96.2%), 33F (100.0%), 60E (100.0%), 71V (100.0%), 84V (100.0%), 90M (100.0%)	3		R - Resistance
DRV_RTV_BID	32I (99.4%), 33F (100.0%), 54L (100.0%), 84V (100.0%), 89V (100.0%)	3		R - Resistance
DRV_RTV_QD	32I (99.4%), 33F (100.0%), 54L (100.0%), 84V (100.0%), 89V (100.0%)	3		R - Resistance
LPVr	10V (96.2%), 33F (100.0%), 54L (100.0%), 63P (100.0%), 71V (100.0%), 84V (100.0%), 90M (100.0%)	3		R - Resistance

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC		1		S - Susceptible
CAB		1		S - Susceptible
DTG_BID	97A (100.0%)	1		S - Susceptible
DTG_QD		1		S - Susceptible
EVG	97A (100.0%), 143R (97.3%), 157Q (100.0%)	3		R - Resistance
RAL	143R (97.3%), 157Q (100.0%)	3		R - Resistance

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
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Signature(s)

Sample ID: CQ012023_PGM

Source ID: CQ012023_PGM

MID: n.a.

Subtype: B

1	B	MF109418	359	297	90.2	29
2	B	AB874132	359	297	90.2	29
3	D	MN694986	351	297	89.9	30
4	B	KY658703	351	297	89.9	30
5	D	AF484480	351	297	89.9	30

HIV-1 RT

IDNS5 version v3.13.0
Drug resistance algorithm ANRS (2022.33/sg/b)
Pipeline name HIV-1 PR+RT_frag+IN
Pipeline version 2.7.0_HIV1_v1.6
Genotyping database version HIV1_r23u051
Noise filter [%] 0.5
Interpretation cutoff [%] 20.0
Min. read depth [# reads] 50
Number of input reads 185 069
Number of reads mapped 125 656
Mutations HIV-1 PR [(%)
3I (100.0), 10V (96.2), 11L (100.0), 13V (100.0), 14R (98.2), 15V (100.0), 20T (100.0), 32I (99.4), 33F (100.0), 35D (99.1), 36I (100.0), 37N (100.0), 41K (99.5), 54L (100.0), 58E (100.0), 60E (100.0), 61E (100.0), 62V (100.0), 63P (100.0), 71V (100.0), 73N (100.0), 84V

Signature(s)

Sample ID: CQ012023_PGM

Source ID: CQ012023_PGM

MID: n.a.

Subtype: B

(100.0), 89V (100.0), 90M (100.0)

Consensus length : 1 158

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	D10112	1 706	1 155	93.6	74
2	B	AF538303	1 704	1 158	93.5	75
3	B	JF689873	1 696	1 158	93.4	76
4	B	AY835778	1 696	1 158	93.4	76
5	B	AF004394	1 696	1 158	93.4	76

HIV-1 IN

Consensus length : 867

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	M17451	1 441	863	96.1	34
2	B	ConsB-IN	1 413	861	95.7	37
3	B	MW924814	1 382	861	95.2	41
4	B	AY173955	1 378	863	95.1	42
5	B	MW059483	1 374	861	95.1	42

Detailed information

Mutations HIV-1 RT [(%)]

35T (100.0), 62V (99.5), 67G (99.4), 68G (100.0), 74I (97.5), 75T (99.6), 103N (100.0), 135V (100.0), 138G (100.0), 162Y (100.0), 173R (88.4), 174K (94.0), 184V (100.0), 194D (87.6), 207A (100.0), 211K (100.0), 214F (100.0), 215V (99.6), 219E (98.3), 232H (100.0), 238T (100.0), 250N (69.1), 277K (100.0), 293V (99.5), 297A (100.0), 333D (98.9), 335C (100.0), 356K (92.6), 357L (99.1), 360T (99.0), 376A (100.0), 379C (21.9), 379G (27.2)

Mutations HIV-1 IN [(%)]

6E (100.0), 31I (100.0), 72I (98.4), 97A (100.0), 101I (100.0), 111T (100.0), 112V (100.0), 119T (100.0), 123S (100.0), 124N (100.0), 127K (100.0), 142A (97.0), 143R (97.3), 157Q (100.0), 160Q (100.0), 167E (100.0), 218S (100.0), 220M (100.0), 227F (99.4), 230N (99.1), 232D (100.0), 283G (100.0)

Created by

CH Versailles

Signature(s)

Sample ID: CQ022023_PGM

Source ID: CQ022023_PGM

MID: n.a.

Subtype: A

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC		1		S - Susceptible
ABC		1		S - Susceptible
ISL		1		S - Susceptible
TDF_TAF		1		S - Susceptible
ZDV		1		S - Susceptible

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	103N (100.0%)	1		S - Susceptible
EFV	103N (100.0%)	3		R - Resistance
ETR		1		S - Susceptible
NVP	103N (100.0%)	3		R - Resistance
RPV	103N (100.0%)	1		S - Susceptible

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV		1		S - Susceptible
DRV_RTV_BID	11I (100.0%)	1		S - Susceptible
DRV_RTV_QD	11I (100.0%)	1		S - Susceptible
LPVr		1		S - Susceptible

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC	74I (100.0%)	1		S - Susceptible
CAB	74I (100.0%)	1		S - Susceptible
DTG_BID	74I (100.0%)	1		S - Susceptible
DTG_QD	74I (100.0%)	1		S - Susceptible
EVG	74I (100.0%)	1		S - Susceptible
RAL	74I (100.0%)	1		S - Susceptible

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Signature(s)

Sample ID: CQ022023_PGM

Source ID: CQ022023_PGM

MID: n.a.

Subtype: A

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	A	MH705157	484	296	95.6	13
2	A1	AB485632	476	296	95.3	14
3	CRF02_AG	AY371146	476	296	95.3	14
4	A7	MH078558	468	296	94.9	15
5	CRF01_AE	JX448296	468	296	94.9	15

HIV-1 RT

Consensus length : 1 530

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	AKU	DQ886038	2 350	1 530	94.1	90
2	A1	M62320	2 092	1 530	92.0	122
3	A3	AY521631	2 068	1 526	91.8	125
4	CRF09_cpx	AY093607	2 068	1 530	91.8	126
5	A1	AB485632	2 064	1 526	91.7	126

HIV-1 IN

Consensus length : 864

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	A3	AY521629	1 411	864	95.6	38
2	AKU	DQ886038	1 411	864	95.6	38
3	CRF45_cpx	FN392874	1 396	864	95.2	41
4	A6	MN703137	1 394	864	95.2	41
5	CRF45_cpx	FN392877	1 392	860	95.3	40

Detailed information

IDNS5 version	v3.13.0
Drug resistance algorithm	ANRS (2022.33/sg/b)
Pipeline name	HIV-1 PR+RT_frag+IN
Pipeline version	2.7.0_HIV1_v1.6
Genotyping database version	HIV1_r23u051
Noise filter [%]	0.5
Interpretation cutoff [%]	20.0
Min. read depth [# reads]	50
Number of input reads	288 596
Number of reads mapped	159 175
Mutations HIV-1 PR [(%)]	3I (100.0), 10M (100.0), 11I (100.0), 13V (100.0), 20I (100.0), 35D (99.6), 36I (100.0), 37N (100.0), 41K (100.0), 69K (91.7), 89M (100.0)

Signature(s)

Sample ID: CQ022023_PGM

Source ID: CQ022023_PGM

MID: n.a.

Subtype: A

Mutations HIV-1 RT [(%)]

6K (98.7), 11T (100.0), 28A (100.0), 35T (100.0), 39E (99.4), 103N (100.0), 123S (98.9), 135T (100.0), 173A (84.3), 174K (96.7), 177E (100.0), 196E (100.0), 203A (100.0), 207E (100.0), 211K (100.0), 245Q (100.0), 248D (100.0), 250E (100.0), 277K (100.0), 286A (100.0), 292I (100.0), 293V (98.3), 297R (97.8), 326V (100.0), 335D (100.0), 356K (100.0), 357K (93.6), 359S (98.7), 369A (100.0), 371V (100.0), 375R (45.6), 375V (43.3), 376V (44.1), 376H (46.6), 377Q (45.2), 377L (42.6), 379C (20.6), 379G (20.2), 395R (99.4), 403V (100.0), 432D (93.8), 435A (99.0), 458I (100.0), 460D (100.0), 461K (99.3), 468S (99.2), 471E (100.0), 480H (98.9)

Mutations HIV-1 IN [(%)]

10E (100.0), 11D (100.0), 24N (99.3), 42R (100.0), 63I (99.4), 72I (87.5), 74I (100.0), 112I (97.1), 113V (100.0), 123S (100.0), 124N (100.0), 125A (100.0), 127K (100.0), 134D (100.0), 167E (100.0), 201I (100.0), 206S (100.0), 232D (100.0), 234I (100.0), 255T (100.0), 283G (100.0)

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Signature(s)

Sample ID: CQ042023_PGM

Source ID: CQ042023_PGM

MID: n.a.

Subtype: B

Drug resistances

Drug resistance algorithm: ANRS (2022.33/sg/b)

Nucleoside Reverse Transcriptase Inhibitors (NRTI)

Drug	Mutations list	Range	Color	Interpretation
3TC_FTC		1	Green	S - Susceptible
ABC	41L (100.0%), 215F (85.2%)	2	Yellow	I - Possible resistance
ISL		1	Green	S - Susceptible
TDF_TAF	41L (100.0%), 215F (85.2%)	1	Green	S - Susceptible
ZDV	41L (100.0%), 70R (100.0%), 215F (85.2%), 219E (93.8%)	3	Red	R - Resistance

Non-Nucleoside Reverse Transcriptase Inhibitors (NNRTI)

Drug	Mutations list	Range	Color	Interpretation
DOR	98G (100.0%), 181C (100.0%)	2	Yellow	I - Possible resistance
EFV	181C (100.0%)	3	Red	R - Resistance
ETR	98G (100.0%), 181C (100.0%)	3	Red	R - Resistance
NVP	181C (100.0%)	3	Red	R - Resistance
RPV	98G (100.0%), 181C (100.0%)	3	Red	R - Resistance

Protease Inhibitors (PI)

Drug	Mutations list	Range	Color	Interpretation
ATV_RTV	10I (99.3%), 71V (100.0%), 90M (100.0%)	3	Red	R - Resistance
DRV_RTV_BID		1	Green	S - Susceptible
DRV_RTV_QD		1	Green	S - Susceptible
LPVr	10I (99.3%), 54V (99.5%), 63P (100.0%), 71V (100.0%), 82A (100.0%), 90M (100.0%)	3	Red	R - Resistance

Integrase Strand Transfer Inhibitors (INSTI)

Drug	Mutations list	Range	Color	Interpretation
BIC		1	Green	S - Susceptible
CAB		1	Green	S - Susceptible
DTG_BID		1	Green	S - Susceptible
DTG_QD		1	Green	S - Susceptible
EVG		1	Green	S - Susceptible
RAL		1	Green	S - Susceptible

Auto-genotyping results

HIV-1 PR

Consensus length : 297

Signature(s)

Sample ID: CQ042023_PGM

Source ID: CQ042023_PGM

MID: n.a.

Subtype: B

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	AB873943	462	293	94.9	15
2	B	FJ469753	462	293	94.9	15
3	B	OK181187	454	293	94.5	16
4	BD	MH234642	454	293	94.5	16
5	B	KY112061	454	293	94.5	16

HIV-1 RT

Consensus length : 1 236

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	FJ469685	1 957	1 239	94.8	62
2	B	AY835778	1 957	1 239	94.8	62
3	B	AF538307	1 957	1 239	94.8	62
4	B	AF538303	1 957	1 239	94.8	62
5	B	K03455	1 957	1 239	94.8	62

HIV-1 IN

Consensus length : 867

Rank	Subtype	AC	Score	Match-length	Similarity [%]	Mismatches
1	B	ConsB-IN	1 497	867	96.8	28
2	B	D10112	1 473	867	96.4	31
3	B	AB564745	1 473	867	96.4	31
4	B	AY173960	1 473	867	96.4	31
5	B	GQ371811	1 467	867	96.3	32

Detailed information

IDNS5 version	v3.13.0
Drug resistance algorithm	ANRS (2022.33/sg/b)
Pipeline name	HIV-1 PR+RT_frag+IN
Pipeline version	2.7.0_HIV1_v1.6
Genotyping database version	HIV1_r23u051
Noise filter [%]	0.5
Interpretation cutoff [%]	20.0
Min. read depth [# reads]	50
Number of input reads	244 915
Number of reads mapped	197 317
Mutations HIV-1 PR [(%)]	3I (100.0), 10I (99.3), 15V (100.0), 35D (99.6), 36I (100.0), 37N (100.0), 41K (99.4), 54V (99.5), 62V (100.0), 63P (100.0), 71V (100.0), 73S (100.0), 82A (100.0), 90M (100.0)

Signature(s)

Sample ID: CQ042023_PGM

Source ID: CQ042023_PGM

MID: n.a.

Subtype: B

Mutations HIV-1 RT [(%)]

4T (100.0), 31M (24.8), 36D (100.0), 41L (100.0), 43E (100.0), 67- (76.1), 69G (99.5), 70R (100.0), 98G (100.0), 108I (100.0), 122K (100.0), 123E (100.0), 135T (100.0), 178M (100.0), 181C (100.0), 211K (100.0), 214F (98.8), 215F (85.2), 219E (93.8), 277K (99.1), 293V (100.0), 334H (100.0), 356K (93.7), 359S (99.1), 360T (100.0), 376A (100.0), 379C (21.3), 399K (32.7), 400A (98.9), 401* (30.7)

Mutations HIV-1 IN [(%)]

10E (100.0), 17N (100.0), 28I (99.7), 30A (100.0), 39C (100.0), 112V (100.0), 119P (100.0), 123S (100.0), 124T (100.0), 127K (100.0), 201I (100.0), 232D (100.0), 234I (100.0), 253E (98.3), 286N (99.3)

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Signature(s)