

phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 24	Predicted subtype: 06_CPX (100%)
Sample type:	Report date: October 6, 2018
Physician:	Reported by:

II. Substitutions (relative to the reference strain HXB2)

Protease:	V3I, L10F, V11I, T12P, I13V, I15V, L19P, K20I, E35G, M36I, S37N, M46I, I54V, L63P, A71V, I72L, G73S, I84V, L90M, I93L
Reverse transcriptase:	

III. Phenotype prediction

Drug	Resistance Factor RF (*)	z-score	Scored Positions (**)
ZDV	0	0	
ddI	0	0	
d4T	0	0	
3TC	0	0	
ABC	0	0	
TDF	0	0	
NVP	0	0	
EFV	0	0	
ETR (***)	Susceptible		
RPV (***)	Susceptible		
SQV	173.461	14.847	48G <u>84V</u> <u>74T</u> 88N <u>90M</u> <u>53F</u> 95C <u>26T</u> <u>11I</u> <u>1P</u> 80T <u>35G</u> <u>34E</u> <u>72L</u> <u>47I</u>
IDV	199.52	13.791	82V 88N <u>90M</u> <u>29D</u> <u>1P</u> <u>84V</u> <u>21E</u> <u>65E</u> <u>46I</u> <u>72L</u> <u>85I</u> 30D <u>73S</u> 78G 98N
NFV	291.072	12.795	88N 30D <u>90M</u> <u>84V</u> <u>82V</u> 97L 68G <u>46I</u> <u>31T</u> 75V 74T <u>5L</u> <u>2Q</u> <u>1P</u> 29D
APV	68.235	13.01	76L 50I <u>84V</u> <u>32V</u> <u>46I</u> <u>85I</u> <u>10F</u> <u>22A</u> <u>63P</u> <u>1P</u> 47I 82V <u>90M</u> <u>97L</u> 45K
LPV	95.561	13.326	82V 50I <u>46I</u> <u>54V</u> <u>84V</u> 76L 22A <u>10F</u> <u>7Q</u> <u>63P</u> 24L 25D 47I 92Q 2Q
TPV	18.552	6.307	69H <u>46I</u> <u>48G</u> <u>84V</u> <u>33L</u> <u>90M</u> <u>47I</u> 91T <u>71V</u> <u>15V</u> 73S 82V 74T 88N 58Q
DRV	9.735	5.926	47I <u>84V</u> <u>33L</u> 76L 74T 43K <u>65E</u> <u>10F</u> <u>93L</u> 48G 7Q <u>8R</u> 16G 2Q 32V
ATV	239.788	16.315	48G <u>84V</u> <u>82V</u> <u>90M</u> <u>4T</u> <u>72L</u> 88N <u>35G</u> <u>7Q</u> <u>73S</u> 24L 76L 45K <u>19P</u> 32V

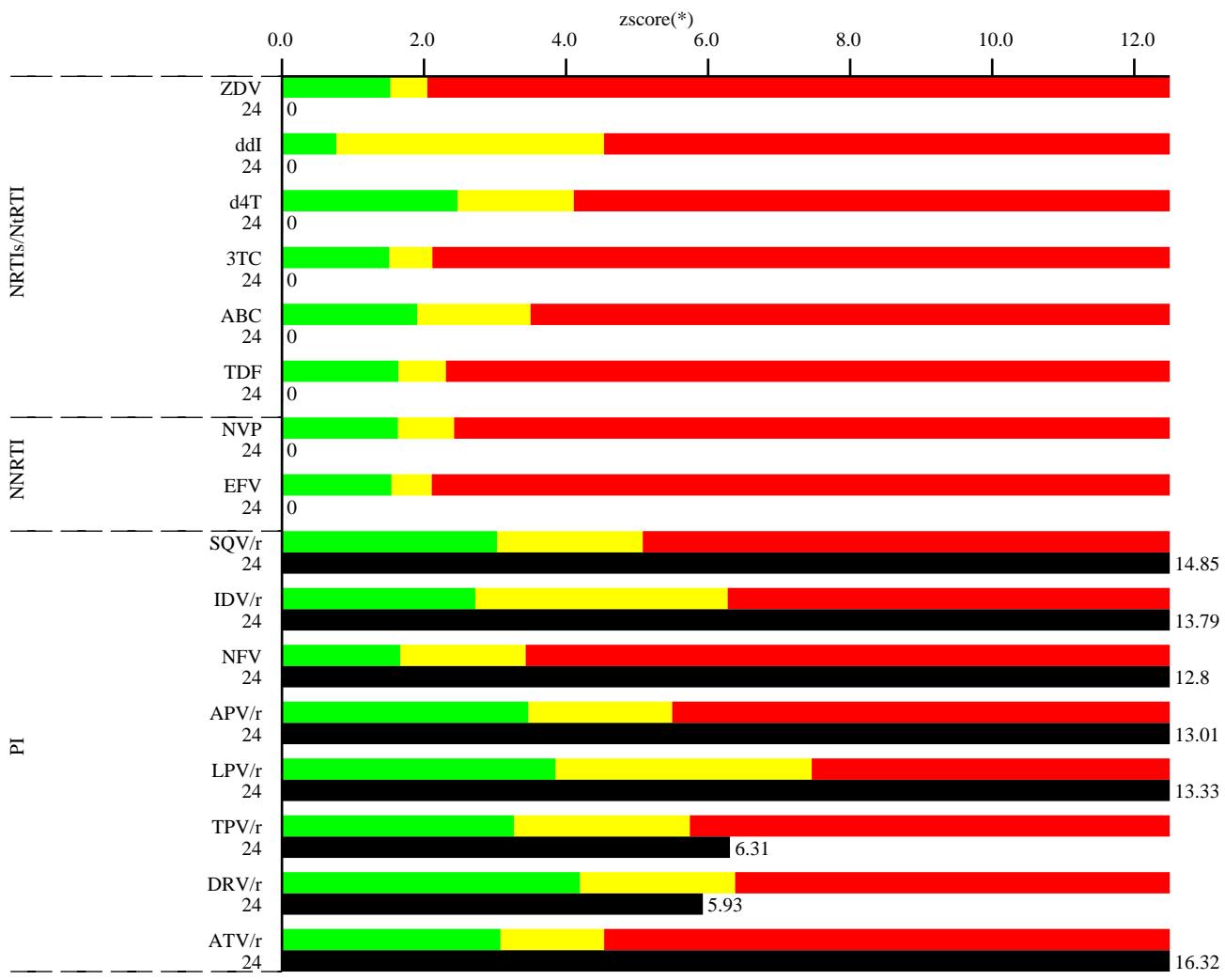
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) Positions are ordered according to their impact on the phenotype prediction. Differences with respect to HXB2 are underlined. Positions shown in red and in green contribute to an increase or decrease in resistance, respectively. At most 15 positions are shown for each drug.

(***) Resistance predictions and scored mutations for ETR and RPV were performed with rules-based drug-resistance interpretation models by HIV-GRADE (<http://www.hiv-grade.de>)

IV. Interpretation

Patient:	Birth date:	Sampling date:
Current therapy:		Viral load:



Legend: █ susceptible █ intermediate █ resistant

(*)number of standard deviations above mean of drug naive patients. Negative z-scores may indicate hypersusceptibility.

NRTIs/NtRTI:

NNRTIs:

PIs:

Previous genotypes:

date

signature