

phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 25	Predicted subtype: B (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, K20T, V32I, L33F, E35G, M36I, S37N, I54I/V, I62V, L63P, K70T, A71I, G73S, P79A, I84V, L89V, L90M
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	117.905	13.724	48G <u>84V</u> 74T 88N <u>90M</u> 53F 95C <u>26T</u> <u>11I</u> <u>1P</u> 80T <u>35G</u> <u>34E</u> 47I 97L
IDV	68.937	10.916	82V 88N 46M <u>90M</u> 29D <u>1P</u> <u>84V</u> <u>21E</u> 65E <u>32I</u> 85I 30D <u>73S</u> 78G 98N
NFV	202.891	11.945	88N 30D <u>90M</u> 46M <u>84V</u> 82V 97L 68G 31T 75V 74T <u>5L</u> 2Q <u>1P</u> 29D
APV	271.857	17.385	<u>33F</u> 76L 50I <u>84V</u> 46M <u>32I</u> 89V 85I <u>10F</u> 22A <u>63P</u> <u>1P</u> 47I 82V <u>90M</u>
LPV	93.157	13.252	82V 46M 50I <u>54V</u> <u>84V</u> <u>33F</u> 76L <u>89V</u> 22A <u>10F</u> <u>7Q</u> <u>63P</u> 24L 25D 47I
TPV	18.574	6.31	69H 48G <u>84V</u> <u>90M</u> 47I 72I <u>91T</u> <u>15V</u> <u>73S</u> 82V 74T 46M 88N 58Q 39P
DRV	31.223	9.063	47I <u>33F</u> <u>84V</u> 76L 74T 43K 46M 65E <u>10F</u> 48G <u>32I</u> 93I 7Q <u>62V</u> 8R
ATV	171.332	15.275	48G <u>84V</u> 82V <u>90M</u> <u>4T</u> <u>33F</u> 88N <u>35G</u> <u>7Q</u> <u>73S</u> 46M 24L <u>76L</u> 45K <u>19P</u>

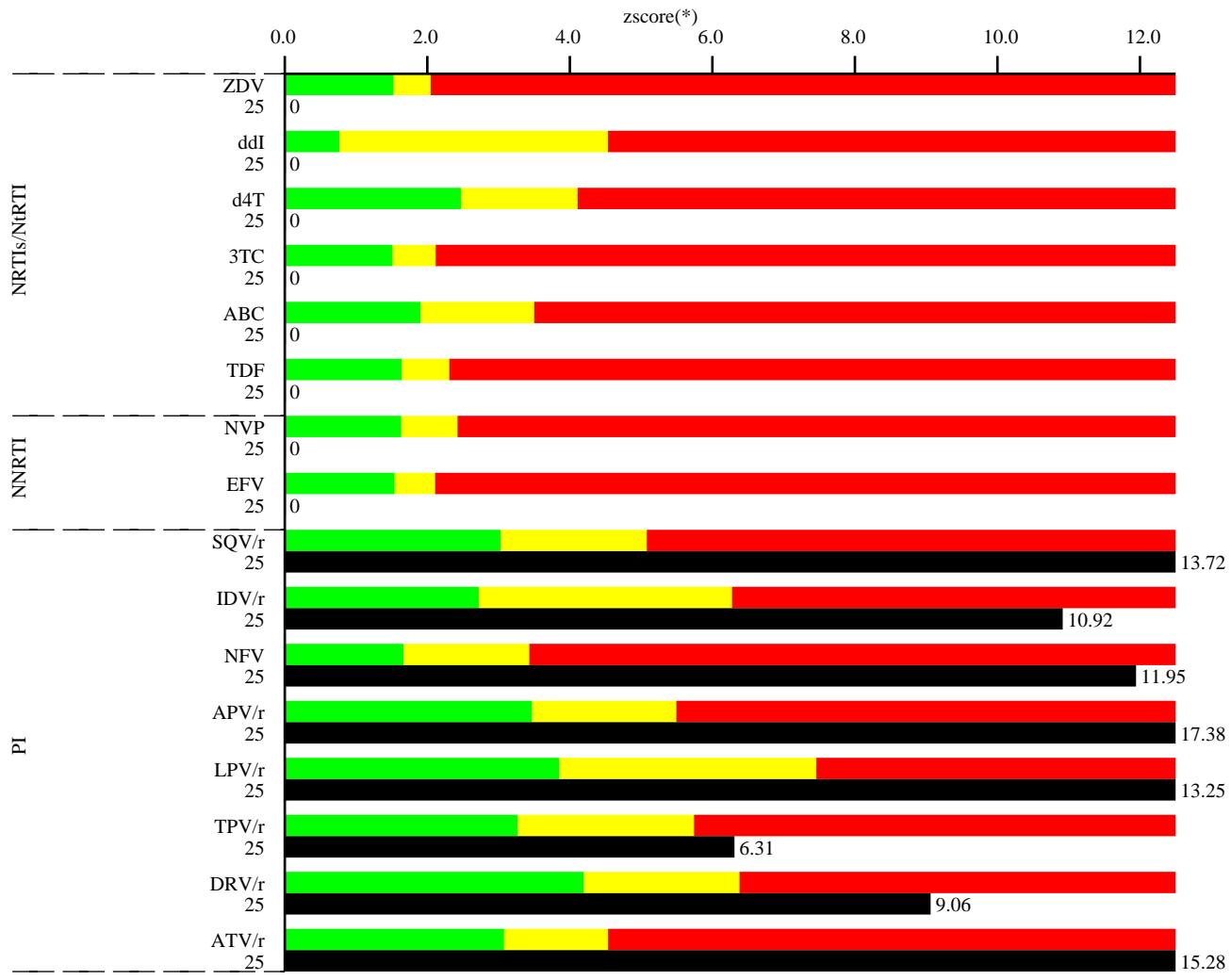
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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