



phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 45	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, I13I/V, K20R, V32I, L33F, E35D, M36I, S37Q, M46I, I47V, I54L, R57K, Q58E, D60E, I62V, L63P, A71V, G73S, V77T, I84V, L89V, 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	64.598	11.975	48G <u>84V</u> 74T 88N <u>90M</u> 47V 53F 95C 26T <u>11I</u> 1P 80T 34E <u>54L</u> 97L
IDV	112.897	12.25	82V <u>54L</u> 88N <u>90M</u> 29D 1P <u>84V</u> 21E 65E <u>32I</u> <u>46I</u> 85I 30D <u>73S</u> 78G
NFV	315.989	12.988	88N 30D <u>90M</u> <u>84V</u> 82V 97L 68G <u>46I</u> 31T 75V 74T <u>54L</u> 5L 2Q 1P
APV	1003.993	21.519	<u>33F</u> 76L 50I <u>84V</u> <u>32I</u> 89V <u>46I</u> <u>54L</u> 85I <u>47V</u> 10F 22A <u>63P</u> 1P 82V
LPV	212.611	15.641	82V 50I <u>46I</u> <u>84V</u> <u>33F</u> 76L <u>54L</u> 89V 22A <u>10F</u> 7Q <u>63P</u> 24L <u>47V</u> 25D
TPV	10.052	4.979	69H <u>46I</u> <u>48G</u> <u>84V</u> <u>90M</u> <u>47V</u> 72I 15I 91T <u>71V</u> <u>54L</u> <u>73S</u> 82V 74T 88N
DRV	127.737	12.854	<u>47V</u> <u>33F</u> <u>84V</u> 76L 74T 43K 65E <u>10F</u> <u>93L</u> <u>48G</u> <u>32I</u> 15I 7Q <u>62V</u> 8R
ATV	311.536	17.125	48G <u>84V</u> 82V <u>90M</u> 4T <u>33F</u> 88N 7Q <u>73S</u> 24L 76L 45K <u>32I</u> <u>54L</u> <u>93L</u>

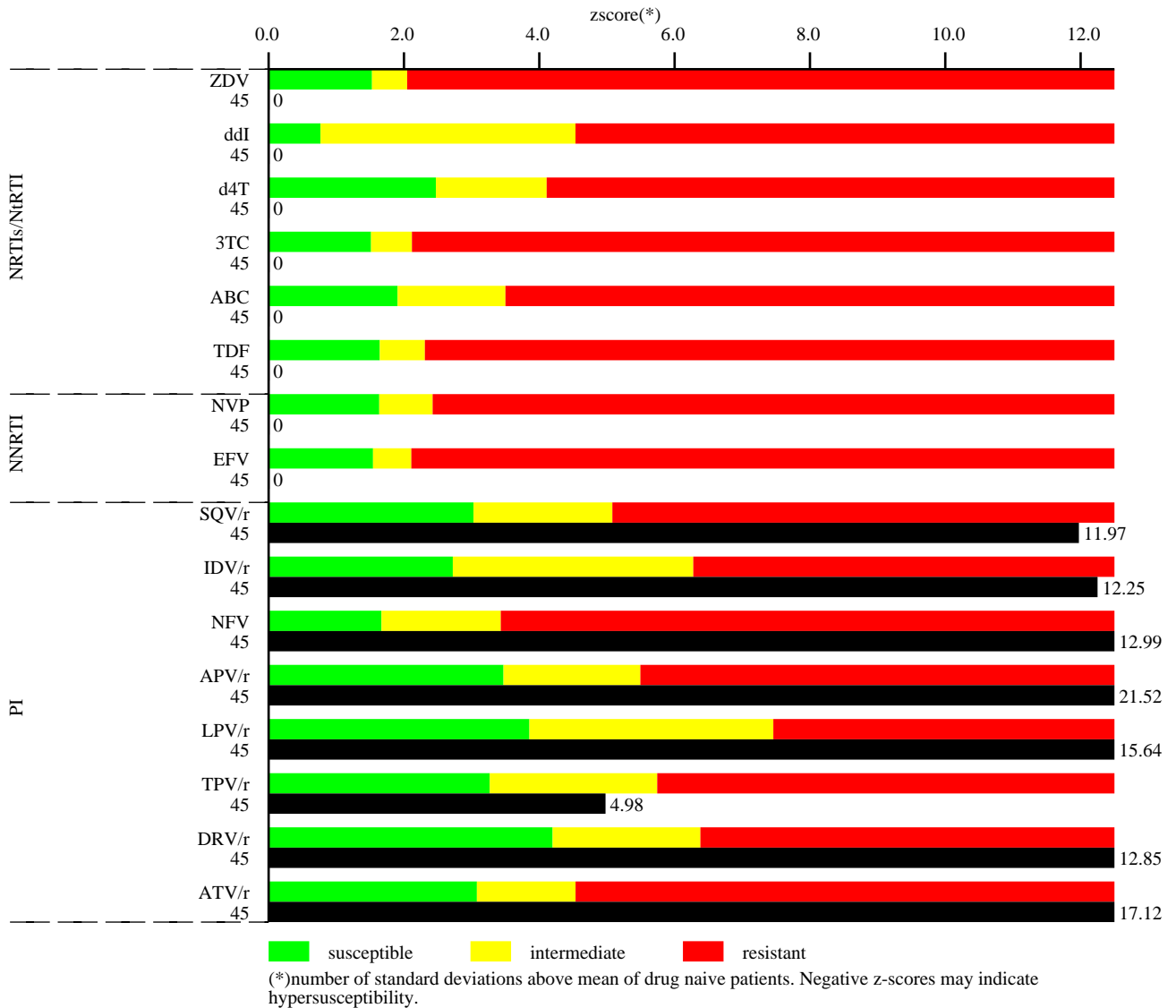
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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:	



NRTIs/NtRTI:

NNRTIs:

PIs:

Previous genotypes:

date

signature