



phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 9	Predicted subtype: B (100%)
Sample type:	Report date: October 6, 2018
Physician:	Reported by:

II. Substitutions

(relative to the reference strain HXB2)

Protease:	L10F, I15I/V, K20R, V32I, L33F, E34Q, E35D, M36I, S37N/T, M46I, I47V, F53L, I54L, K55N, Q58E, L63L/P, I64L, T74K, I84V, L89M, Q92K
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	27.51	9.492	48G <u>84V</u> 73G 90L 11V 88N <u>47V</u> 95C <u>53L</u> 26T 71A 80T <u>54L</u> 97L 24L
IDV	11.785	6.138	82V <u>54L</u> 88N 29D <u>84V</u> 73G 21E <u>65E</u> <u>32I</u> <u>46I</u> 11V 71A 85I <u>30D</u> 90L
NFV	22.547	6.771	88N 30D <u>84V</u> 82V 97L 73G <u>68G</u> 90L 71A <u>46I</u> 31T 75V <u>54L</u> <u>5L</u> <u>89M</u>
APV	232.142	16.885	<u>33F</u> 76L 50I <u>84V</u> <u>32I</u> <u>46I</u> <u>54L</u> 85I <u>47V</u> <u>10F</u> 22A <u>63P</u> 13I 82V <u>89M</u>
LPV	98.313	13.408	82V 50I <u>46I</u> <u>84V</u> <u>33F</u> 76L <u>54L</u> 22A 71A <u>10F</u> 7Q <u>63P</u> 24L <u>47V</u> 25D
TPV	5.659	3.733	<u>69H</u> <u>46I</u> <u>48G</u> <u>84V</u> <u>47V</u> <u>89M</u> 71A 72I 91T <u>15V</u> <u>54L</u> 90L 82V 88N 19L
DRV	65.381	11.052	<u>47V</u> <u>33F</u> <u>84V</u> 76L 43K 73G 71A <u>65E</u> <u>10F</u> 89M <u>48G</u> <u>32I</u> <u>93I</u> <u>15L</u>
ATV	42.544	10.965	48G 73G <u>84V</u> 82V 4T <u>33F</u> 71A 88N 90L 7Q 24L 76L 45K <u>32I</u> <u>54L</u>

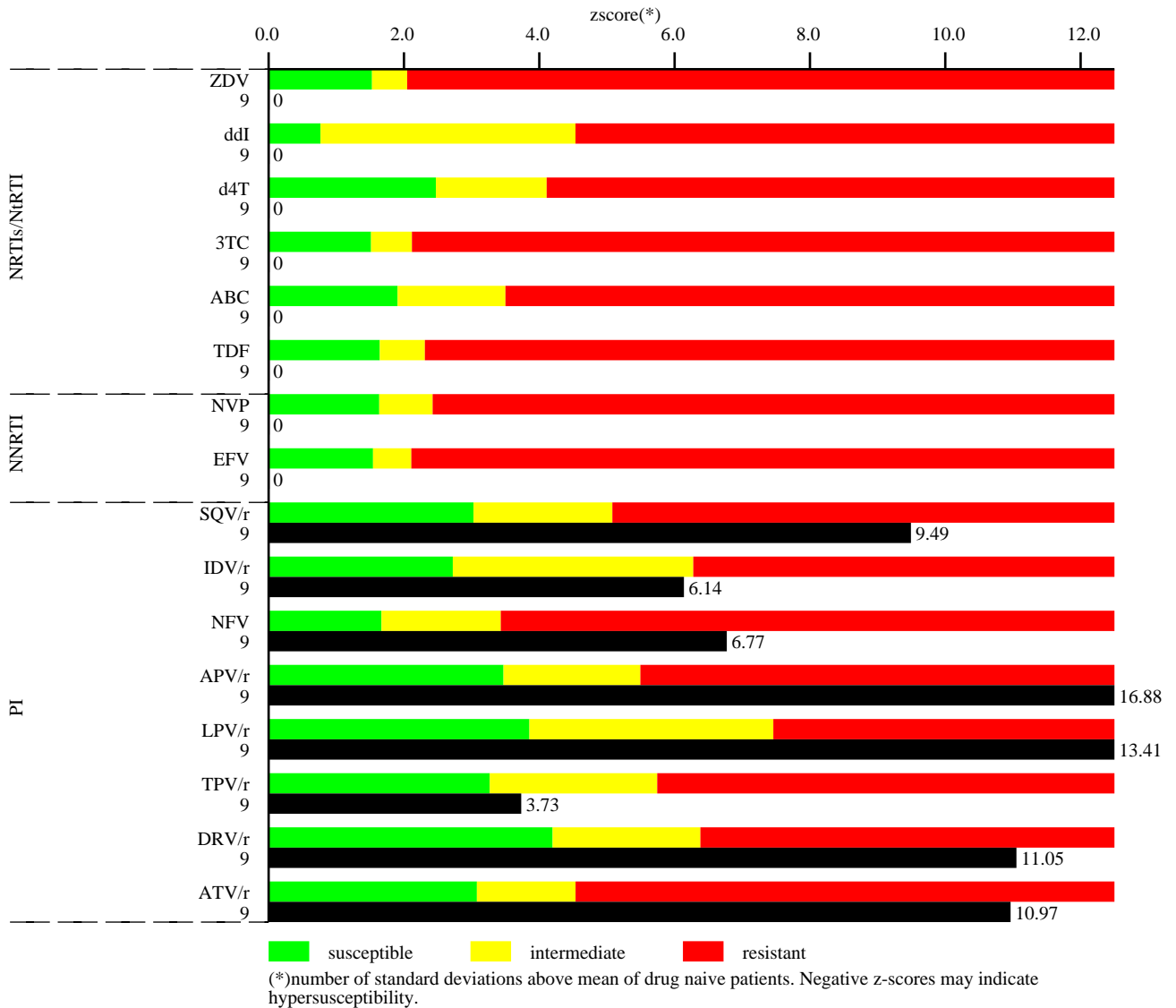
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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