



phenotype prediction from genotype (version 3.4)

## I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 50	Predicted subtype: B (100%)
Sample type:	Report date: October 7, 2018
Physician:	Reported by:

## II. Substitutions

(relative to the reference strain HXB2)

Protease:	V3I, T4A/T, L10F, I15I/V, K20K/T, E35D, S37N, M46I, I54V, L63P, I64V, A71V, I72L, G73T, V77I/V, I84V, I85V, 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	323.763	16.661	48G <u>84V</u> 11V 74T 88N <u>90M</u> 53F 95C 26T 1P <u>73T</u> 80T 34E <u>72L</u> 47I
IDV	396.539	15.649	82V 88N <u>90M</u> 29D 1P <u>84V</u> 21E 65E <u>46I</u> <u>73T</u> 11V <u>72L</u> 30D 78G 98N
NFV	477.456	13.96	88N 30D <u>90M</u> <u>84V</u> 82V 97L 68G 36M <u>46I</u> 31T 75V 74T 5L 2Q 1P
APV	89.663	13.875	76L 50I <u>84V</u> <u>32V</u> <u>46I</u> <u>10F</u> <u>22A</u> <u>63P</u> 1P 47I 13I 82V <u>90M</u> 97L 45K
LPV	153.621	14.7	82V 50I <u>46I</u> <u>54V</u> <u>84V</u> <u>76L</u> <u>22A</u> <u>10F</u> <u>7Q</u> <u>63P</u> 24L 25D 47I 92Q 2Q
TPV	11.279	5.228	69H <u>46I</u> <u>48G</u> <u>84V</u> <u>33L</u> <u>90M</u> 47I 91T <u>71V</u> <u>15V</u> <u>82V</u> 74T 88N 58Q 19L
DRV	14.212	6.944	47I <u>84V</u> <u>33L</u> <u>76L</u> 74T 43K 36M <u>65E</u> <u>10F</u> <u>48G</u> <u>93I</u> <u>85V</u> <u>15I</u> <u>7Q</u> 8R
ATV	290.614	16.91	48G <u>84V</u> <u>82V</u> <u>90M</u> <u>73T</u> <u>72L</u> 88N <u>7Q</u> 36M 24L <u>76L</u> 45K <u>32V</u> <u>20T</u> <u>46I</u>

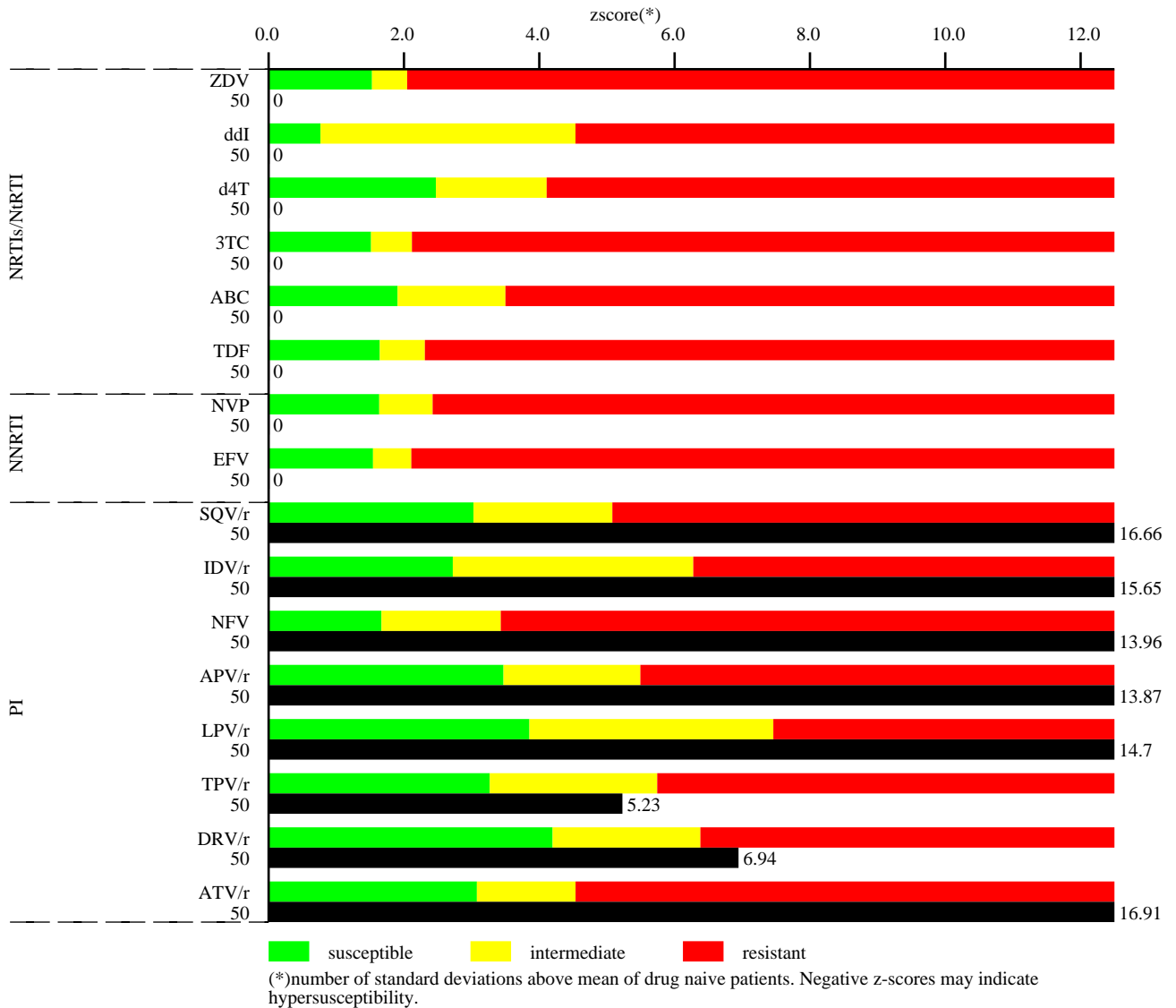
(\*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(\*\*) 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