



phenotype prediction from genotype (version 3.4)

## I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 39	Predicted subtype: B (100%)
Sample type:	Report date: October 6, 2018
Physician:	Reported by:

## II. Substitutions (relative to the reference strain HXB2)

Protease:	V3I, L10I, T12P, I15V, K20R, V32I/V, M36I, S37D, M46L, I54L, L63P, A71V, T74S/T, P79S, V82A/V, I84V, I85V, 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	113.167	13.605	48G <u>84V</u> 73G 11V 88N <u>90M</u> 53F 95C 26T 1P 80T 34E <u>54L</u> 47I 97L
IDV	401.033	15.679	<u>54L</u> 88N <u>90M</u> 29D 1P <u>84V</u> 73G 21E 65E <u>32I</u> 11V <u>10I</u> 30D 78G 98N
NFV	202.613	11.942	88N 30D <u>90M</u> <u>84V</u> 97L 73G 68G 31T 75V <u>54L</u> 5L 2Q 1P 29D 48G
APV	198.8	16.394	76L 50I <u>84V</u> <u>32I</u> <u>54L</u> <u>37D</u> 22A <u>63P</u> 1P 47I 13I <u>90M</u> 97L 45K <u>10I</u>
LPV	182.575	15.2	50I <u>84V</u> 76L <u>54L</u> 22A 7Q <u>63P</u> 24L 25D <u>82A</u> 74S <u>37D</u> 47I 92Q 2Q
TPV	13.891	5.68	69H 48G <u>84V</u> 33L <u>90M</u> 47I 72I 91T <u>71V</u> 15V <u>54L</u> <u>82V</u> 74S 88N 58Q
DRV	19.195	7.753	47I <u>84V</u> 33L 76L 43K 73G <u>74S</u> <u>37D</u> 65E <u>93L</u> 48G <u>32I</u> <u>85V</u> 7Q 8R
ATV	371.154	17.667	48G 73G <u>84V</u> <u>90M</u> <u>82A</u> 4T <u>46L</u> 88N 7Q 24L 76L 45K <u>32I</u> <u>54L</u> <u>93L</u>

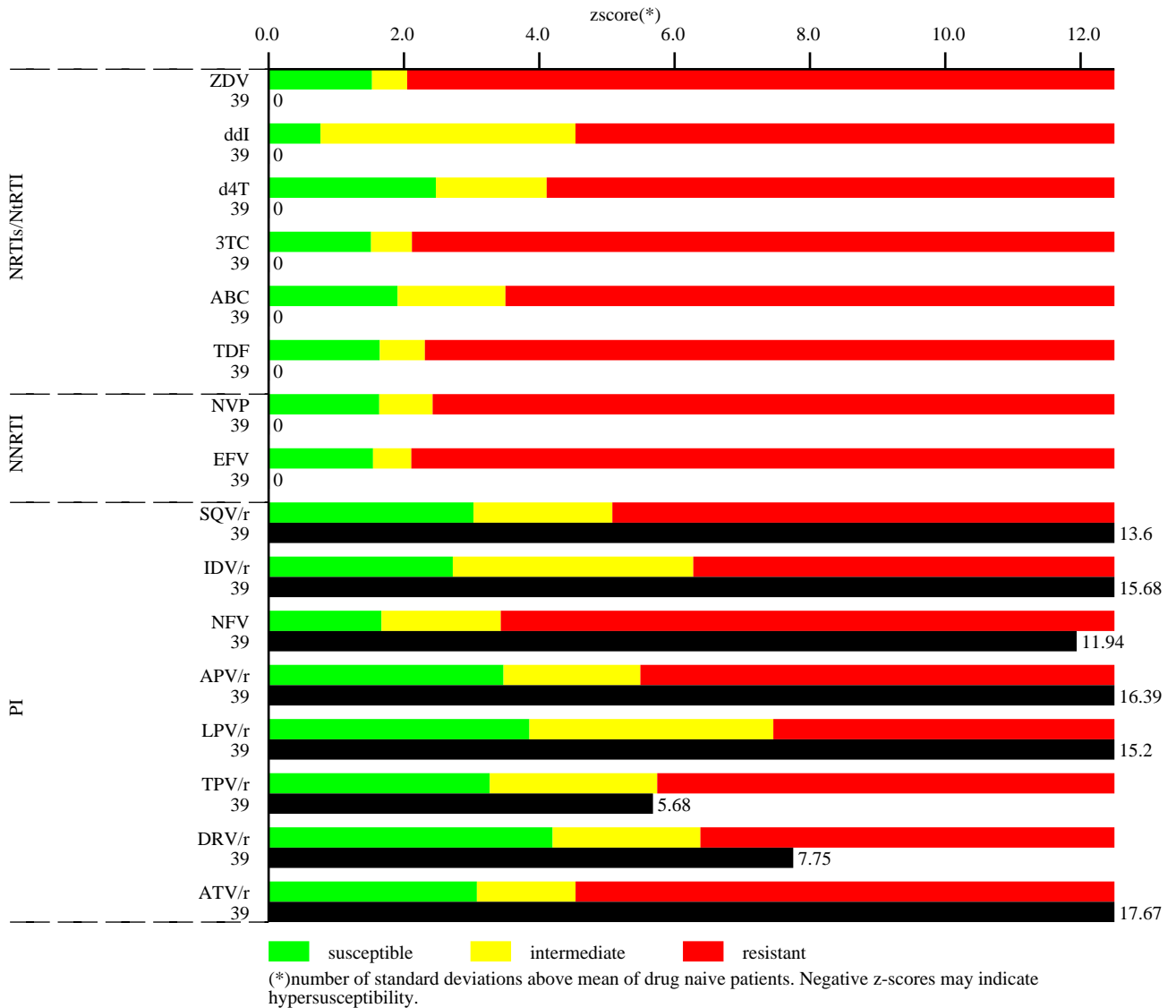
(\*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(\*\*) 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