



phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 13	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, K20R, L33F, E34T, E35D, M36I, S37D, K43T, M46I, G48V, I50V, I54S, I62V, L63P, A71I/V, I72V, V77I, V82A, I85V, 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	177.825	14.919	<u>48V</u> 73G 90L 84I 11V 74T 88N 53F 95C 26T 1P 80T 47I 97L 24L
IDV	649.319	16.983	88N 29D 1P <u>48V</u> 73G 21E 65E 84I <u>46I</u> 11V <u>10I</u> 30D <u>54S</u> 90L 78G
NFV	136.899	11.019	88N 30D <u>97L</u> 73G 68G 90L <u>46I</u> 31T 75V 74T 84I 5L 2Q <u>54S</u> 1P
APV	227.363	16.819	<u>33F</u> 76L <u>50V</u> 84I 32V <u>46I</u> <u>37D</u> <u>48V</u> 22A <u>43T</u> <u>63P</u> 1P 47I 13I 97L
LPV	409.877	17.541	84I <u>50V</u> <u>46I</u> <u>33F</u> <u>48V</u> 76L 22A 7Q <u>63P</u> 24L 25D <u>82A</u> <u>37D</u> 47I 92Q
TPV	1.677	1.096	<u>69H</u> <u>82A</u> <u>46I</u> 84I 47I 15I 91T <u>71V</u> 90L 74T 88N 58Q 19L 13I <u>37D</u>
DRV	20.461	7.925	47I <u>33F</u> 84I 76L 74T 73G <u>37D</u> <u>65E</u> <u>43T</u> 93L <u>82A</u> <u>85V</u> 15I 7Q <u>62V</u>
ATV	222.779	16.087	73G 84I <u>82A</u> 4T <u>33F</u> <u>48V</u> 88N 90L 7Q 24L 76L 45K 32V <u>93L</u> <u>46I</u>

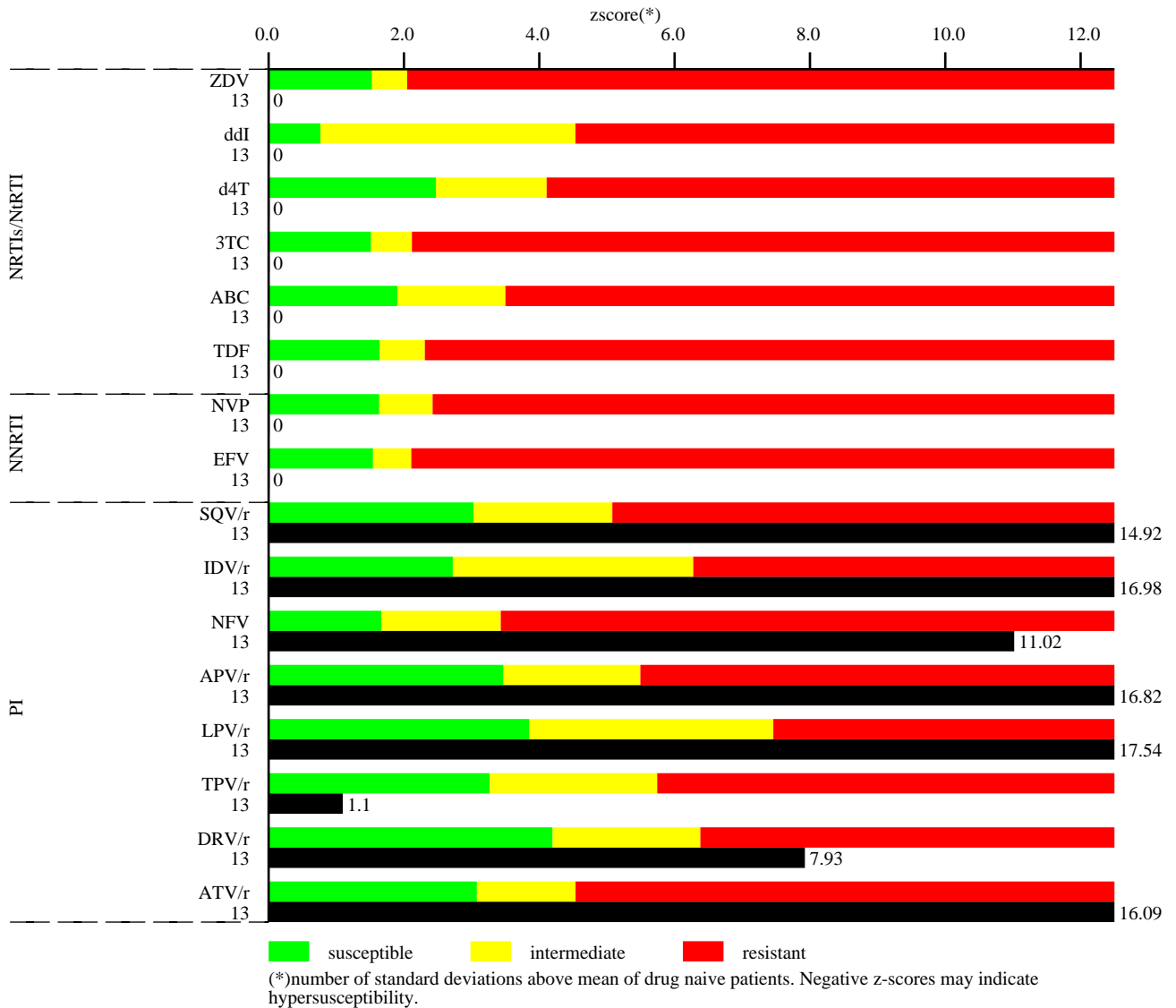
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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