



phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 49	Predicted subtype: 08_BC (100%)
Sample type:	Report date: October 7, 2018
Physician:	Reported by:

II. Substitutions (relative to the reference strain HXB2)

Protease:	V3I, T12S, I15V, L19I/M, M36I, S37N, R41K, D60D/E, L63P, H69K, K70R, L89L/M, 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	1.16	0.285	48G 73G 90L 84I 54I 11V 74T 88N 53F 95C 26T 1P 71A 80T 34E
IDV	1.088	-0.308	54I 82V 88N 46M 29D 1P 73G 21E 65E 84I 11V 71A 85I 30D 90L
NFV	1.08	-0.385	88N 54I 30D 46M 82V 97L 20K 73G 68G 90L 71A 31T 75V 74T 84I
APV	1.205	0.238	54I 76L 50I 84I 46M 32V 85I 22A 63P 1P 47I 13I 82V 97L 45K
LPV	0.575	-1.478	54I 82V 46M 84I 50I 76L 10L 22A 71A 7Q 63P 24L 20K 25D 47I
TPV	1.048	0.077	48G 84I 33L 54I 47I 71A 72I 91T 20K 69K 15V 90L 82V 74T 46M
DRV	0.916	-0.434	47I 84I 54I 33L 76L 74T 43K 73G 46M 71A 65E 93L 48G 10L 7Q
ATV	1.146	-0.217	54I 48G 73G 84I 82V 4T 71A 88N 90L 7Q 46M 20K 24L 76L 45K

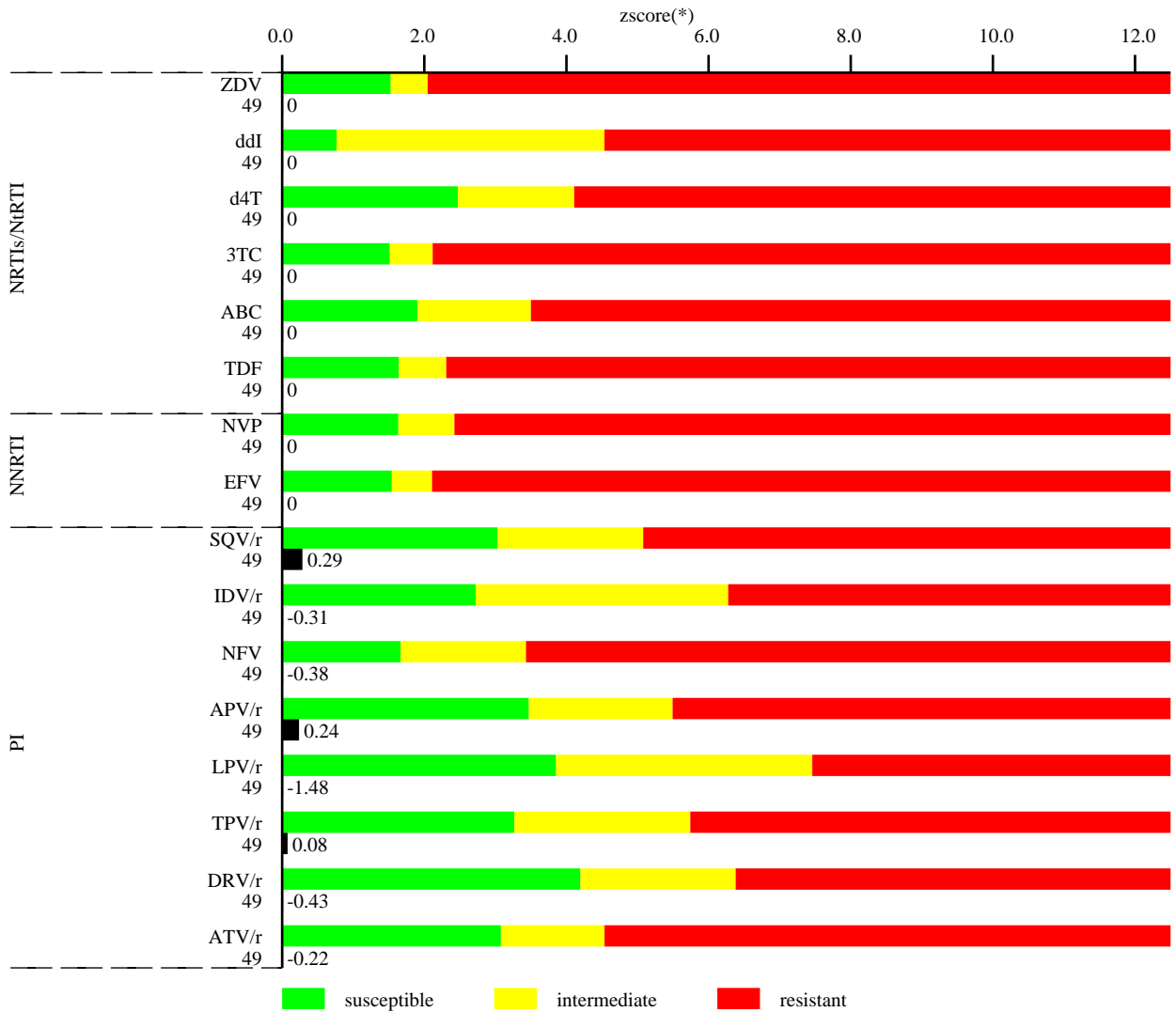
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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