



phenotype prediction from genotype (version 3.4)

I. General information

Patient:	Study Id:
Birth date:	Viral load:
Sample received:	Sample collected:
Sample ID: 42	Predicted subtype: D (100%)
Sample type:	Report date: October 6, 2018
Physician:	Reported by:

II. Substitutions

(relative to the reference strain HXB2)

Protease:	V3I, T12S, I13V, I15V, L19I, K20T, M36I, S37N, R41K/R, M46I/M, K55K/R, R57K/R, D60E, I62V, L63P, I64V, L90M, I93I/L
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	6.967	5.499	48G 73G 84I 54I 11V 74T 88N 90M 53F 95C 26T 1P 71A 80T 34E
IDV	17.895	7.268	54I 82V 88N 90M 29D 1P 73G 21E 65E 84I 46L 11V 71A 85I 30D
NFV	30.193	7.459	88N 54I 30D 90M 82V 97L 73G 68G 71A 46L 31T 75V 74T 84I 5L
APV	8.26	6.329	54I 76L 50I 84I 32V 46L 85I 22A 63P 1P 47I 82V 90M 97L 45K
LPV	6.253	5.432	54I 82V 84I 50I 46L 76L 10L 22A 71A 7Q 63P 24L 25D 47I 92Q
TPV	6.582	4.061	69H 48G 84I 33L 90M 54I 47I 71A 72I 91T 15V 82V 74T 46M 88N
DRV	2.672	2.447	47I 84I 54I 33L 76L 74T 43K 73G 71A 65E 48G 93L 10L 7Q 62V
ATV	10.184	6.542	54I 48G 73G 84I 82V 90M 4T 71A 88N 7Q 24L 76L 45K 32V 20T

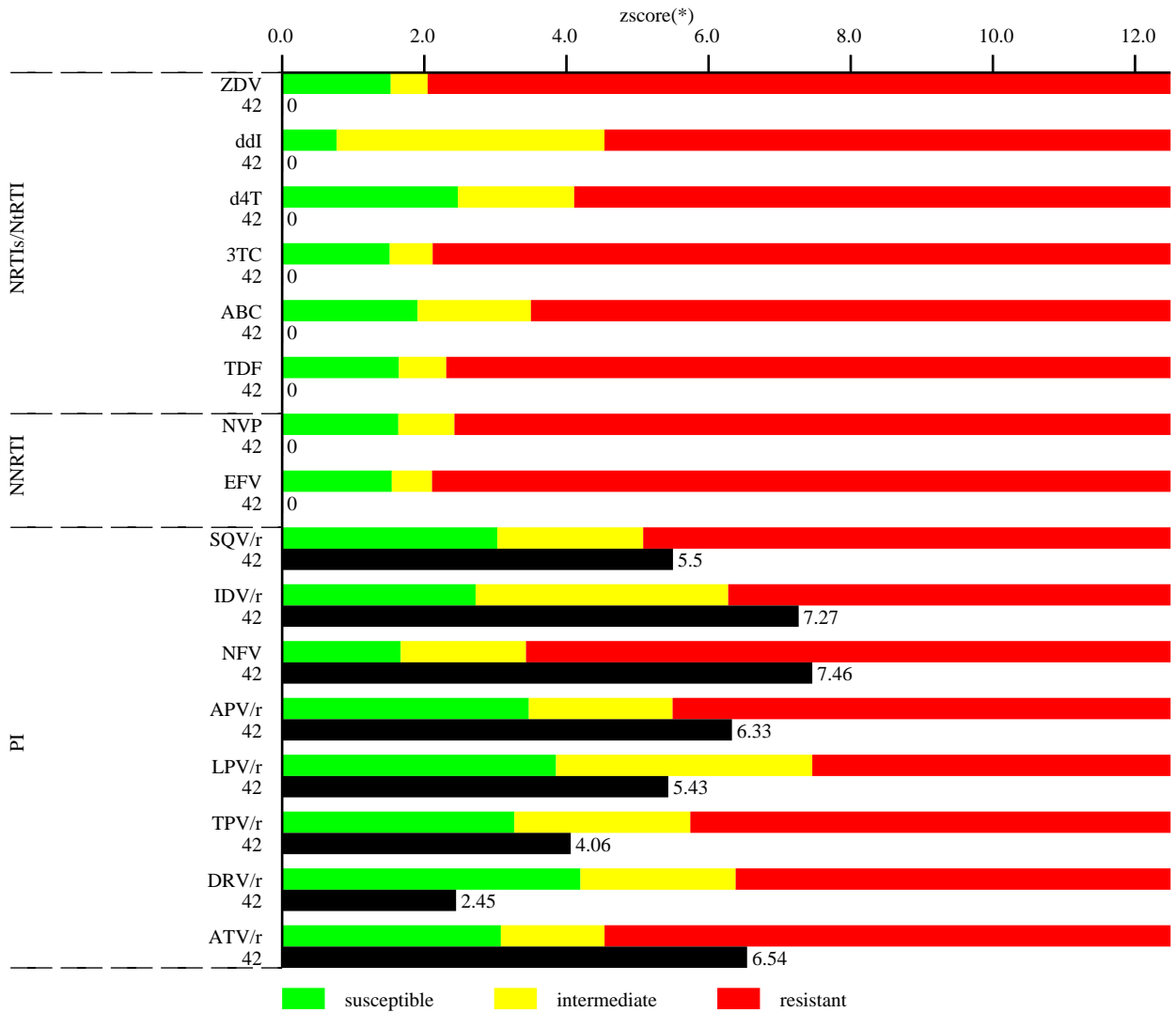
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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