



phenotype prediction from genotype (version 3.4)

## I. General information

|                  |                              |
|------------------|------------------------------|
| Patient:         | Study Id:                    |
| Birth date:      | Viral load:                  |
| Sample received: | Sample collected:            |
| Sample ID: 16    | 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, E35D, M36I, S37N, K43T, I47V, G48M, F53L, I54V, I62V, L63P, I66F, A71V, V82T, I84V, Q92R |
| 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       | 184.139                  | 15.021  | <u>84V</u> 73G 90L 11V 74T 88N 47V 95C <u>53L</u> 26T 1P 80T 34E 97L 24L                            |
| IDV       | 210.29                   | 13.933  | 88N 46M 29D 1P <u>84V</u> 73G 21E 65E <u>92R</u> 11V <u>10I</u> 85I 30D 90L 78G                     |
| NFV       | 153.731                  | 11.292  | 88N <u>48M</u> 30D 46M <u>84V</u> 97L 73G 68G 90L 31T 75V 74T <u>92R</u> 5L 2Q                      |
| APV       | 45.548                   | 11.731  | 76L 50I <u>84V</u> <u>48M</u> 46M 32V 85I <u>82T</u> <u>47V</u> 22A 43T <u>63P</u> 1P 13I 97L       |
| LPV       | 121.938                  | 14.031  | 46M 50I <u>54V</u> <u>84V</u> 76L 22A 7Q <u>63P</u> 24L <u>47V</u> 25D 48M 90L 2Q 74T               |
| TPV       | 9.925                    | 4.951   | <u>69H</u> <u>84V</u> 33L <u>82T</u> <u>47V</u> 72I 15I 91T <u>71V</u> 90L 74T 46M 88N 58Q 19L      |
| DRV       | 39.96                    | 9.727   | <u>47V</u> <u>84V</u> 33L 76L 74T 73G 46M 65E <u>43T</u> <u>93I</u> <u>48M</u> 15I 7Q <u>62V</u> 8R |
| ATV       | 145.211                  | 14.763  | 73G <u>84V</u> <u>48M</u> 4T 88N 90L 7Q 46M 24L 76L 45K 32V <u>71V</u> 41R 2Q                       |

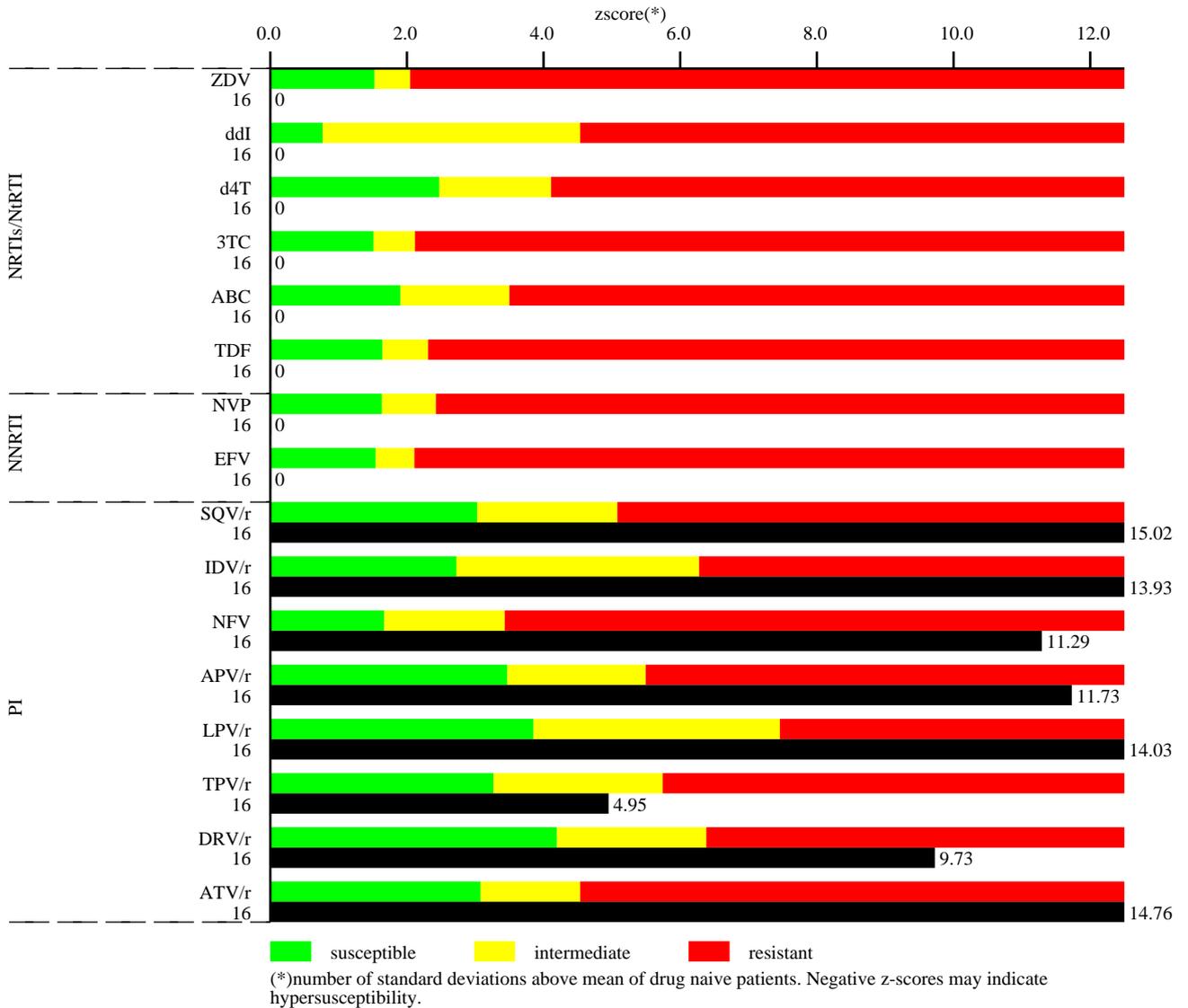
(\*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(\*\*) 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