



phenotype prediction from genotype (version 3.4)

I. General information

| | |
|------------------|------------------------------|
| Patient: | Study Id: |
| Birth date: | Viral load: |
| Sample received: | Sample collected: |
| Sample ID: 11 | Predicted subtype: C (100%) |
| Sample type: | Report date: October 6, 2018 |
| Physician: | Reported by: |

II. Substitutions (relative to the reference strain HXB2)

| | |
|------------------------|--|
| Protease: | L10Y, I15V, K20T, E35G, M36I, S37D, R41K, M46I, F53L, L63V, I64V, H69K, T74A, N88S, L89M, 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 | 7.36 | 5.658 | 48G 73G 90L 84I 54I 11V 95C <u>53L</u> 26T 71A 80T <u>35G</u> 34E <u>10Y</u> 63V |
| IDV | 8.232 | 5.167 | 54I 82V 29D 73G 21E 65E 84I <u>46I</u> 11V 71A 85I <u>30D</u> 90L <u>88S</u> <u>89M</u> |
| NFV | 20.483 | 6.545 | 54I 30D 82V <u>97L</u> 73G <u>68G</u> 90L 71A <u>46I</u> <u>88S</u> <u>31T</u> 75V 84I <u>5L</u> <u>89M</u> |
| APV | 1.528 | 0.988 | 54I 76L 50I 84I 32V <u>88S</u> <u>46I</u> 85I <u>37D</u> <u>22A</u> 47I 13I 82V <u>89M</u> <u>97L</u> |
| LPV | 4.136 | 4.236 | 54I 82V 84I 50I <u>46L</u> 76L <u>22A</u> 71A <u>7Q</u> <u>10Y</u> 24L 25D <u>37D</u> 47I 92Q |
| TPV | 0.447 | -1.77 | <u>46I</u> <u>48G</u> 84I 33L 54I 47I <u>89M</u> 71A 72I <u>91T</u> <u>69K</u> <u>15V</u> 90L 82V 58Q |
| DRV | 0.991 | -0.222 | 47I 84I 54I 33L 76L 43K 73G 71A <u>37D</u> <u>65E</u> <u>93L</u> <u>89M</u> <u>48G</u> <u>7Q</u> |
| ATV | 6.879 | 5.328 | 54I 48G 73G 84I 82V 4T <u>88S</u> 71A 90L <u>35G</u> <u>7Q</u> 24L <u>76L</u> 45K 32V |

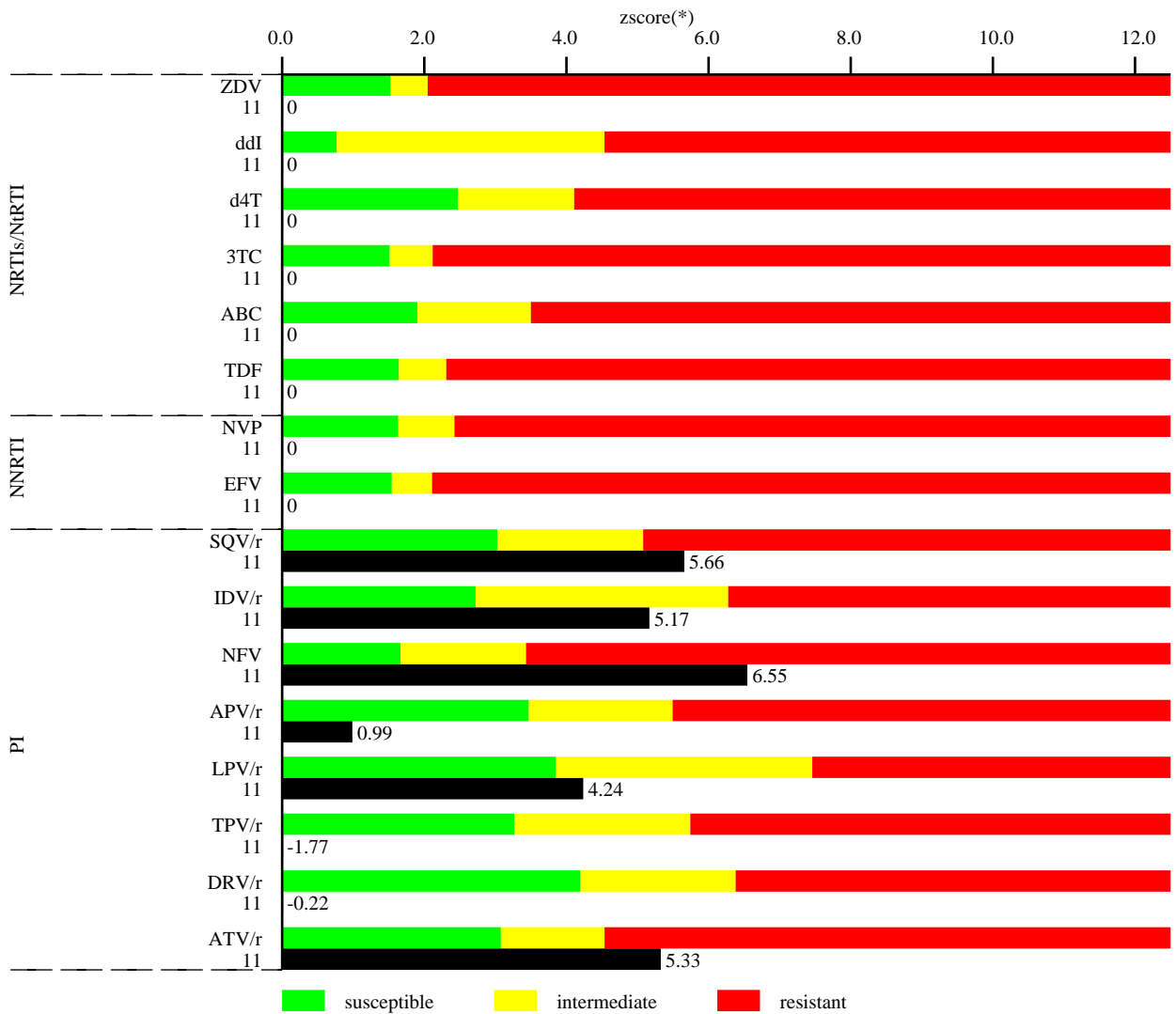
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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

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|------------------|-------------|----------------|
| Patient: | Birth date: | Sampling date: |
| Current therapy: | Viral load: | |



NRTIs/NtRTI:

NNRTIs:

PIs:

Previous genotypes:

date

signature