



phenotype prediction from genotype (version 3.4)

I. General information

| | |
|------------------|------------------------------|
| Patient: | Study Id: |
| Birth date: | Viral load: |
| Sample received: | Sample collected: |
| Sample ID: 32 | 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, V11I, T12K, I13V, K20V, V32I, L33F/L, E35G, M36I, S37D/N, M46I, I47V, I54M, R57K, Q58E, L63P, I64V, A71I/V, G73S, I84I/V, L89V, L90M |
| 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 | 141.209 | 14.249 | 48G <u>84V</u> 74T 88N <u>90M</u> 47V 53F 95C 26T <u>11I</u> 1P 80T <u>35G</u> 34E 97L |
| IDV | 315.352 | 15.029 | 82V 88N <u>90M</u> 29D 1P <u>84V</u> 21E 65E <u>20V</u> <u>32I</u> 46L 10I 85I 30D <u>73S</u> |
| NFV | 665.846 | 14.744 | 88N 30D <u>90M</u> <u>84V</u> 82V 97L 68G <u>46I</u> 31T 75V 74T 5L 2Q 1P 29D |
| APV | 1801.621 | 23.369 | <u>33F</u> 76L 50I <u>84V</u> <u>54M</u> <u>32I</u> <u>89V</u> <u>46I</u> <u>85I</u> <u>47V</u> <u>37D</u> 22A 63P 1P 82V |
| LPV | 221.878 | 15.764 | 82V 50I <u>46I</u> <u>84V</u> <u>33F</u> 76L 89V 22A 7Q 63P 24L <u>47V</u> <u>25D</u> <u>54M</u> <u>37D</u> |
| TPV | 27.664 | 7.174 | 69H <u>46I</u> 48G <u>84V</u> <u>90M</u> <u>47V</u> 72I 15I 91T <u>71V</u> <u>73S</u> 82V 74T 88N 19L |
| DRV | 149.725 | 13.281 | <u>47V</u> <u>33F</u> <u>84V</u> 76L 74T 43K <u>54M</u> <u>37D</u> 65E 48G <u>32I</u> 93I 15I 7Q 8R |
| ATV | 468.782 | 18.389 | 48G <u>84V</u> 82V <u>90M</u> 4T <u>33F</u> 88N <u>35G</u> 7Q <u>73S</u> 24L 76L <u>54M</u> 45K <u>32I</u> |

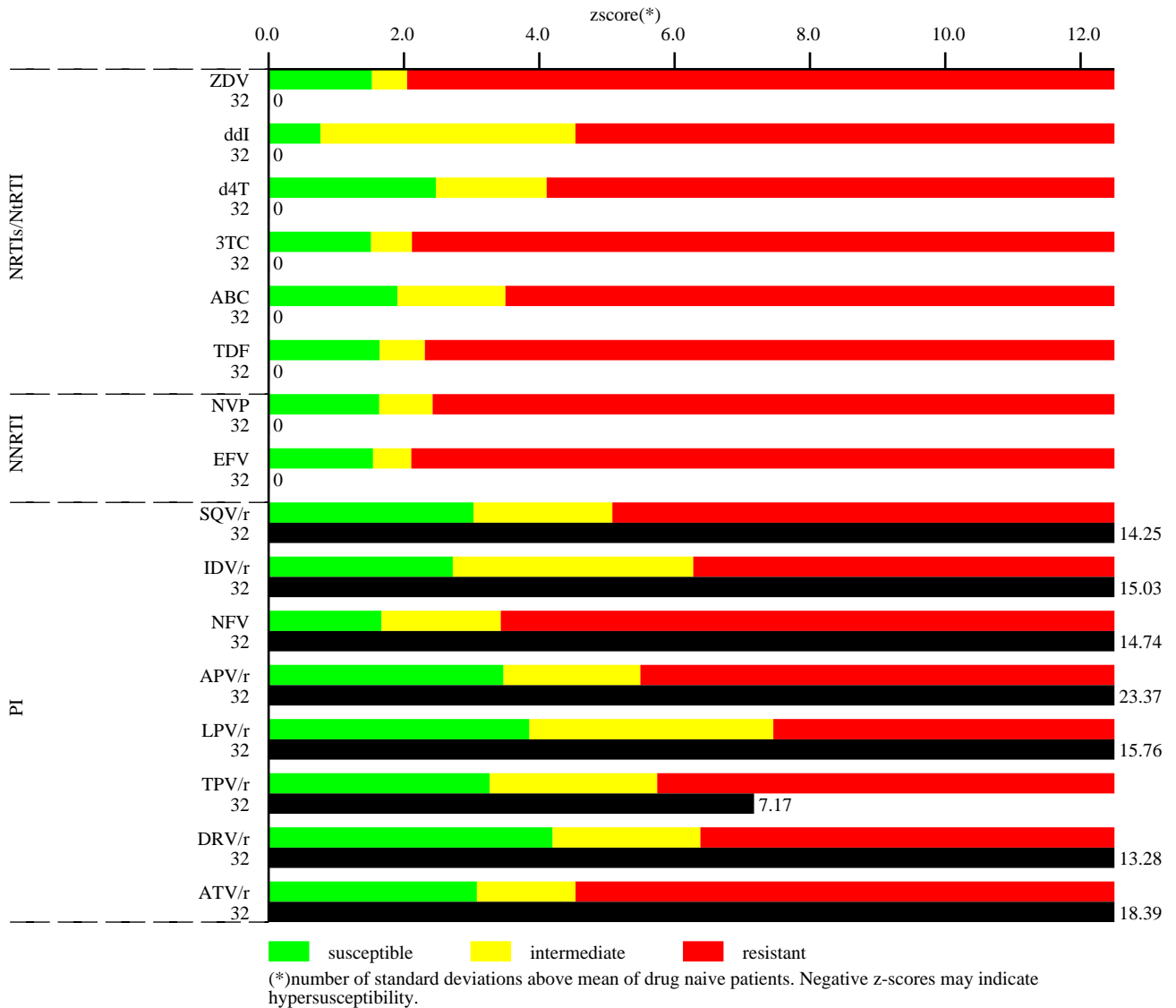
(*) based on LIBSVM, Copyright (c) 2000, Chih-Chung Chang and Chih-Jen Lin

(**) 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