# geno2pheno®

phenotype prediction from genotype (version 3.4)

## I. General information

| | |
|---|---|
| Patient: | Study Id: |
| Birth date: | Viral load: |
| Sample received: | Sample collected: |
| Sample ID:      2 | Predicted subtype:      07_BC (100%) |
| Sample type: | Report date:      October 6, 2018 |
| Physician: | Reported by: |

## II. Substitutions
(relative to the reference strain HXB2)

| | |
|---|---|
| Protease: | L10I, I13V, G16A, K20K/M, S37N, M46I, I54V, L63P, I66F, C67Y, H69K, A71V, I72F, G73T, I84V, L90M, I93L |
| Reverse transcriptase: | |

## III. Phenotype prediction

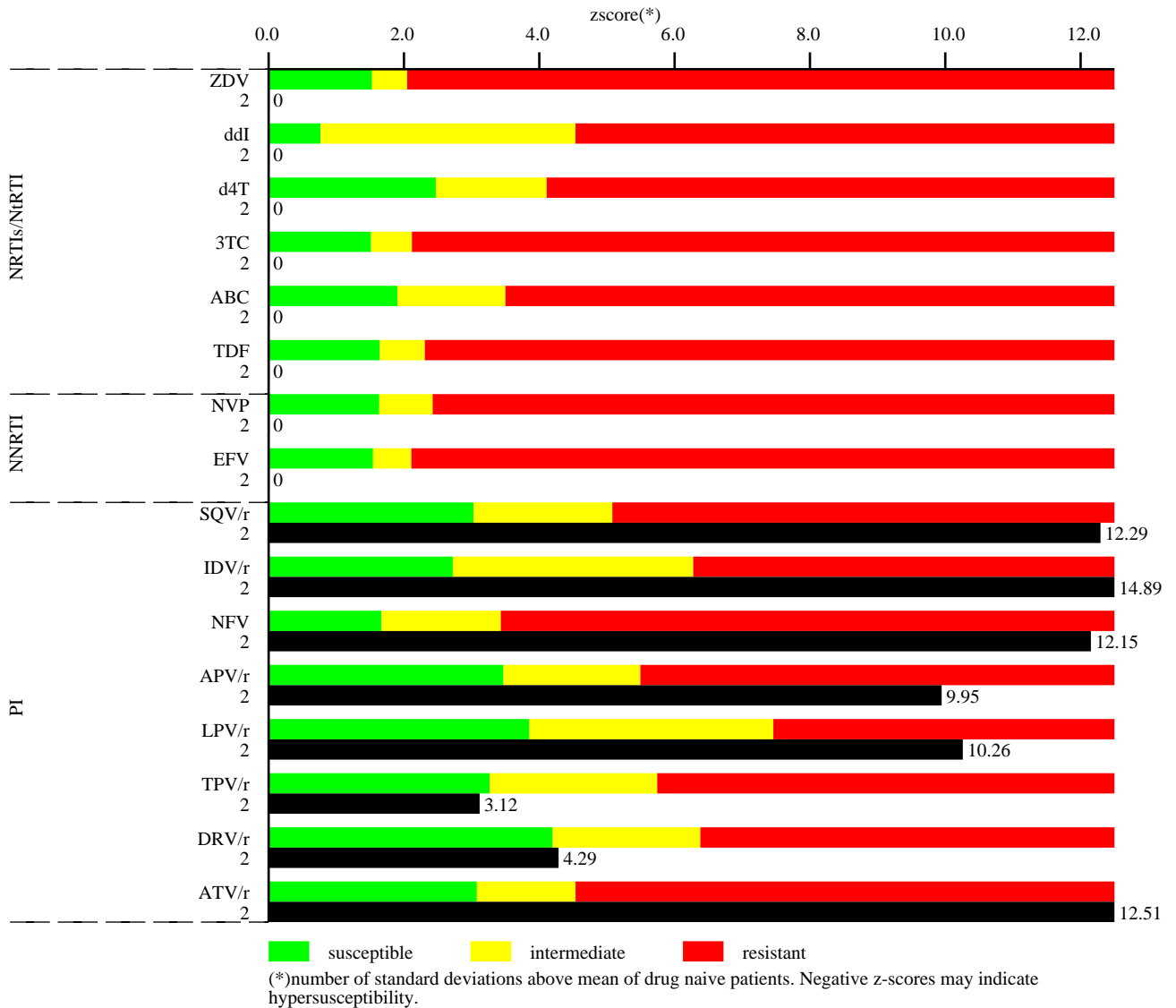| Drug | Resistance Factor RF (*) | z-score | Scored Positions (**) |
|---|---|---|---|
| ZDV | 0 | 0 | |
| ddI | 0 | 0 | |
| d4T | 0 | 0 | |
| 3TC | 0 | 0 | |
| ABC | 0 | 0 | |
| TDF | 0 | 0 | |
| NVP | 0 | 0 | |
| EFV | 0 | 0 | |
| ETR (***) | Susceptible | | |
| RPV (***) | Susceptible | | |
| SQV | 72.095 | 12.294 | 48G 84V 11V 74T 88N 90M 53F 95C 26T 73T 80T 34E 47I 97L 24L |
| IDV | 299.658 | 14.891 | 82V 88N 90M 29D 84V 21E 65E 46I 67Y 73T 11V 10I 85I 30D 78G |
| NFV | 221.514 | 12.152 | 88N 30D 90M 84V 82V 97L 68G 36M 46I 31T 75V 74T 5L 29D 48G |
| APV | 25.91 | 9.946 | 76L 50I 84V 32V 46I 85I 22A 63P 47I 82V 90M 97L 45K 10I 21E |
| LPV | 33.129 | 10.259 | 82V 50I 46I 54V 84V 76L 22A 7Q 63P 24L 25D 47I 92Q 48G 74T |
| TPV | 4.262 | 3.118 | 46I 48G 84V 33L 90M 47I 15I 91T 71V 69K 82V 74T 88N 58Q 19L |
| DRV | 5.29 | 4.285 | 47I 84V 33L 76L 74T 43K 36M 65E 93L 48G 15I 7Q 8R 32V |
| ATV | 69.993 | 12.505 | 48G 84V 82V 90M 73T 4T 88N 7Q 36M 24L 76L 45K 32V 93L 46I |

(*) 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, repectively. 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)

# geno2pheno®

phenotype prediction from genotype (version 3.4)

IV. Interpretation

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

zscore(*)

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 0.0 | 2.0 | 4.0 | 6.0 | 8.0 | 10.0 | 12.0 |

**NRTIs/NtRTI**

- ZDV / 2 / 0
- ddI / 2 / 0
- d4T / 2 / 0
- 3TC / 2 / 0
- ABC / 2 / 0
- TDF / 2 / 0

**NNRTI**

- NVP / 2 / 0
- EFV / 2 / 0

**PI**

- SQV/r / 2 / 12.29
- IDV/r / 2 / 14.89
- NFV / 2 / 12.15
- APV/r / 2 / 9.95
- LPV/r / 2 / 10.26
- TPV/r / 2 / 3.12
- DRV/r / 2 / 4.29
- ATV/r / 2 / 12.51

susceptible    intermediate    resistant

(*)number of standard deviations above mean of drug naive patients. Negative z-scores may indicate hypersusceptibility.

NRTIs/NtRTI:

NNRTIs:

PIs:

Previous genotypes:

_____      _____

date           signature