

**Supplemental Digital Content 1. Aligned HIV-1 polymerase sequences from plasma, cervical secretions, and vaginal secretions collected from five women with incident antiretroviral resistance detected in genital tract secretions.**

Nucleotide sequences spanning codons 98-190 of HIV-1 polymerase are included; all isolates that could be sequenced are included. Sequences are identified by participant identification number (e.g., D717), time of collection (e.g., 0M = Baseline, 3M = Month 3 from ART initiation), and compartment (P = plasma, C = cervical, V = vaginal). The reference sequence for each woman is that of the baseline plasma isolate. This reference sequence is followed by cervical and vaginal sequences (if available) from the same time-point, then sequences from subsequent time-points are presented in the same order. Sites that differ from the reference sequence are indicated, and those conferring resistance mutations are highlighted in yellow. Standard IUPAC nucleotide codes are used (see key below).

|            |  |  |                                      |
|------------|--|--|--------------------------------------|
| C648.0M.P  | GGATTAAGAAAGA<br>103                             | AAAATCAGTAACAGTACTAGATGTAGGGGACGCATATTTCCGTCCTTAGATGAAGACTTCAGAAAATATACTGCATTCAACCACCTAGTATAAACAAATGAGACACCAGGAATTAGGTATCAGTACAATGTGCTTCCACAGGGATGAAAGGATCACCGCAATATTCAA<br>WGTAGTATGACAAAAAATCTTAGARCCCTTAGAAAACAAAAYCCAGAGATAGTTATCTATCAACATGGATGACTTATGTC | 184                                  |
| C648.0M.C  | -  | -T-----R-R-----  | G-----T-----K-----                   |
| C648.12M.P | T  | -G-----  | T-----A-G-----T-----G-----           |
| C648.12M.C | T  | -G-----  | T-----A-G-----T-----G-----           |
| D717.0M.P  | GGCCTRAAAAAR<br>103                              | PARAAWYMRKWACAGTATTAGATGTGGGGACGCATATTTCACTGAAAGCTTCTACATGAAAGCTTCTACAGATACCTAGTATAAACAAATGAGACACCAGGAATCAGATATCAGTACAATGTGCTTCCACAGGGATGAAAGGATCACCGCAATATTCCAGAGTAGCATGACAAAAAATCTTAGAGCCCTT<br>TAGAAAATCCAGAAATAATTATCTATCAACATGGATGACTTATGTC             | 190                                  |
| D717.0M.C  | -A-----GARA-TCAGTA-----                          | -Y-----  | R-----Y-----                         |
| D717.0M.V  | -GA-A-TCAGTA-----                                | -R-----T-----  | R-----R-----                         |
| D717.3M.P  | -A-----GARA-TCAGTA-----                          | -T-----  | W-----R-----Y-----A-----             |
| D717.3M.C  | -A-----GA-A-TCAGTA-----                          | -T-----  | A-----                               |
| D717.3M.V  | -A-----GARA-TCAGTA-----                          | -T-----  | A-C-T-----Y-----A-----               |
| D717.6M.P  | -A-----GA-W-TCAGTA-----                          | -R-----Y-----T-----G-----  | K-----W-----R-----Y-----A-----       |
| D717.6M.C  | -A-----GA-C-TCAGTA-----                          | -R-----T-----  | R-----R-----M-----                   |
| D717.6M.V  | -A-----GA-H-TCAGTA-----                          | -R-----T-----  | R-----A-----S-----                   |
| F383.0M.P  | GGCCTAAAGA<br>103 106                            | AAAATCAGTAACAGTAYTAGATGTGGGGATGCATATTTCACTGAAAGCTTCTACATGAAAGCTTCTACAGTACAATGAGACACCAGGAATCAGGTATCAGTACAATGTGCTTCCACAGGGATGAAAGGATGCCAGCAATATTCCAGAGYAGCATGACAAAAAATCTTAGAGCC<br>CTT TAGAGCAGAAAATCCAGRAMTAATTATCTATCAACATGGATGACTTATGTC                     | 190                                  |
| F383.0M.C  | -G-----Y-----T-----A-----Y-----                  | -T-----A-----Y-----  | A-A-----Y-----                       |
| F383.0M.V  | -C-----T-----C-----                              | -T-----C-----  | T-----G-A-----                       |
| F383.3M.P  | M-----Y-----R-----T-----A-----R-----Y-----R----- | -T-----A-----R-----  | A-A-----                             |
| F383.3M.C  | M-----R-----T-----C-----C-----R-----             | -T-----C-----R-----  | A-A-----S-----                       |
| F383.3M.V  | C-----T-----T-----A-----C-----A-----             | -T-----C-----A-----  | T-----A-----                         |
| F383.6M.P  | M-----T-----                                     | -T-----  | M-----T-----A-----                   |
| F383.6M.C  | M-----R-----T-----C-----                         | -T-----C-----  | T-----A-----                         |
| F383.6M.V  | M-----R-----T-----C-----                         | -T-----C-----  | T-----A-----                         |
| F383.12M.P | C-----T-----                                     | -Y-----R-----  | R-----T-----A-A-----                 |
| F383.12M.C | C-----T-----                                     | -Y-----R-----  | T-----A-----A-A-----                 |
| F383.12M.V | C-----T-----                                     | -R-----Y-----R-----  | R-----T-----A-----A-A-----           |
| F987.0M.P  | GGCCTAAAGA<br>181 184                            | AAAATCAGTAACAGTACTAGATGTGGGRAGGCATATTTCACTGTTCTTACATGAAAGACTTCTACAGTACAATGAGACACCAGGAATCAGRTATCAGTAYATGTGCTTCCACAGGGATGAAAGGTACCGCAATATTCCARAGTAGCATGACAAAAAATCTTAGAGCC<br>CTT TAGATCAAATCCAGAGATARTTATYATGCAATTACATGGATGACTTATGTC                           | 184 184                              |
| F987.0M.C  | -G-----T-----G-----C-----A-----A-----G-----      | -T-----G-----C-----A-----A-----G-----  | A-----A-----                         |
| F987.0M.V  | -G-----T-----G-----C-----A-----A-----G-----      | -T-----G-----C-----A-----A-----G-----  | A-----T-----A-----                   |
| F987.3M.P  | -A-----T-----A-----T-----                        | -A-----T-----A-----T-----  | G-----C-----G-----                   |
| F987.6M.P  | -A-----T-----A-----T-----                        | -A-----T-----A-----T-----  | G-----C-----G-----R-----R-----G----- |
| F987.6M.C  | -A-----A-----T-----                              | -A-----T-----A-----T-----  | G-----C-----G-----G-----             |
| F987.6M.V  | -A-----A-----T-----                              | -A-----T-----A-----T-----  | G-----C-----G-----A-----G-----       |
| F987.12M.P | -A-----K-----                                    | -Y-----G-----T-----  | G-----Y-----R-----R-----G-----       |
| H368.0M.P  | GGCYTAAAGA<br>184 190                            | AAAATCAGTAACAGTWCTRGATGTGGGGATGCATATTTCACTGAAAGCTTCTTACATGAAAGCTTCTACAGTACAATGAGACACCAGRATTAGGTATCAGTACAATGTGCTTCCACAGGGATGAAAGGTACCGCAATATTCCAGAGTAGCATGACAAAAAATCTTAGAGC<br>AGAAAATCCAGAAATRATTATCTATCAACATGGATGACTTATGTC                                  | 184 190                              |
| H368.0M.C  | -C-----A-G-----A-----                            | -A-----  | A-----                               |
| H368.6M.P  | -C-----T-A-----                                  | -A-----  | G-----G-----C-----C-----             |
| H368.12M.P | -C-----T-A-----                                  | -A-----  | A-----G-----C-----C-----             |
| H368.12M.V | -C-----T-A-----                                  | -A-----  | G-----G-----G-----C-----             |

IUPAC Code: A = Adenine, C = Cytosine, G = Guanine, T = Thymine, R = A or G (purine), Y = C or T (pyrimidine), S = G or C, W = A or T, K = G or T, M = A or C