



Supplementary Data

Mitochondrial DNA: hotspot for potential gene modifiers regulating hypertrophic cardiomyopathy

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Supplementary Table S1- mtDNA variants identified by NGS in Family A composed by healthy and HCM individuals bearing the p.E99K-ACTC1 mutation.

Patients displaying more severe phenotypes/ clinical features are labelled in red; healthy or less severe patients are highlighted in green

| Fibroblast sample | Loci | mtDNA Mutation | % Heteroplasmy | Polyphen prediction (score) |
|------------------------|-------------------------|----------------|-----------------------------------|-----------------------------|
| E99K1 | MT-HV2, MT-OHR | m.152T>C | 99.8% | N/A (non-coding) |
| 6;7 | MT-HV2, MT-OHR | m.185G>A | 98.1%; 98.8% | N/A (non-coding) |
| E99K1; 6; 7 | MT-HV2, MT-OHR, MT-CSB2 | m.309_310insCT | 31.7%; 32.3%; 35.8% | N/A (non-coding) |
| E99K1; E99K2; NC; 6; 7 | MT-HV2, MT-OHR, MT-CSB2 | m.310T>C | 53.9%; 13.5%; 17.2%; 57.0%; 58.8% | N/A (non-coding) |
| E99K1; E99K2; NC; 6; 7 | MT-HV2, MT-OHR, MT-CSB2 | m.310_311insC | 33.3%; 65.8%; 62.5%; 32.5%; 31.7% | N/A (non-coding) |
| 6 | MT-OHR, MT-LSP | m.414T>G | 18.7% | N/A (non-coding) |
| 6;7 | MT-ND2 | m.4659G>A | 99.7%; 99.3% | Benign (0.029) |
| E99K1; E99K2; NC; 6; 7 | MT-TA | m.5597A>C | 7.5%; 7.9%; 5.1%; 12.2%; 12.4% | N/A (non-coding) |
| E99K1 | MT-CO1 | m.7109C>T | 91.4% | N/A (redundant) |
| E99K2; NC | MT-ATP6 | m.8952T>C | 99.9%; 99.8% | N/A (redundant) |
| 6; 7 | MT-ATP6 | m.9025G>A | 99.6%; 99.6% | Probably damaging (1.000) |
| E99K1 | MT-ATP6 | m.9116T>C | 99.7% | Benign (0.000) |
| E99K1 | MT-ND4 | m.11176G>A | 99.6% | N/A (redundant) |
| 6; 7 | MT-ND4 | m.11215C>T | 99.7%; 99.6% | N/A (redundant) |
| E99K2; NC | MT-ND5 | m.12715A>G | 99.8%; 99.8% | Probably damaging (0.991) |
| 6; 7 | MT-ND5 | m.12810A>G | 99.9%; 99.9% | Probably damaging (STOP) |
| 6 ;7 | MT-CYB | m.15586T>C | 99.8%; 99.9% | N/A (redundant) |
| E99K1 | MT-HV1, MT-TAS | m.16168C>T | 44.2% | N/A (non-coding) |
| 6; 7 | MT-HV1 | m.16209T>C | 99.9%; 99.9% | N/A (non-coding) |

Supplementary Table S2 - mtDNA variants identified by NGS in Family B composed by healthy and HCM individuals bearing the p.E99K-ACTC1 mutation.

Patients displaying more severe phenotypes/ clinical features are labelled in red; healthy or less severe patients are highlighted in green.

| Fibroblast sample | Loci | mtDNA Mutation | % heteroplasmy | Polyphen score |
|---------------------------------|-------------------------------|------------------|--|---------------------------------|
| 4;5 | MT-HV2, MT-OHR | m.152T>C | 99.8%; 99.8% | N/A (non-coding) |
| 4; 5; 13; 14; 15; 16; 17; 18 | MT-HV2, MT-OHR, MT-CSB2 | m.310T>C | 10.5%; 14.3%; 13.2%; 15.0%; 13.5%; 18.4%; 15.2%; 12.9% | N/A (non-coding) |
| 4; 5; 13;14; 15; 16; 17; 18 | MT-HV2, MT-OHR, MT-CSB2 | m.310_311insC | 67.6%; 67.2%; 67.3%; 65.7%; 68.6%; 57.7%; 65.0%; 67.8% | N/A (non-coding) |
| 13 | MT-HV3 | m.513G>A | 13.0% | N/A (non-coding) |
| 14; 15; 16; 17; 18 | MT-HV3 | m.514_515delCA | 56.3%; 59.4%; 55.6%; 55.0%; 55.4% | N/A (non-coding) |
| 13 | MT-HV3 | m.513_514insCACA | 32.5% | N/A (non-coding) |
| 18 | MT-HV3, MT-TFH | m.540A>C | 11.0% | N/A (non-coding) |
| 14; 15; 16; 17; 18 | MT-HV3, MT-HSP1 | m.567A>G | 99.3%; 99.2%; 99.2%; 99.5%; 99.5% | N/A (non-coding) |
| 15 | MT-HV3 | m.574A>G | 12.3% | N/A (non-coding) |
| 4; 5; 13; 14; 15; 16 | MT-TA | m.5597A>C | 25.7%; 10.5%; 14.0%; 23.8%; 13.8%; 16.8% | N/A (non-coding) |
| 4 | MT-ATP8 | m.8490T>A | 10.0% | Possibly damaging (0.711) |
| 4; 5; 14 | MT-CO3 | m.9716T>C | 100%; 99.9%; 2.4% | N/A (redundant) |
| 4; 5; 14 | MT-ND4 | m.11914G>A | 99.8%; 99.4%; 1.9% | N/A (redundant) |
| 14; 15; 16; 17; 18 | MT-ND4 | m.11950A>G | 97.9%; 99.8%; 99.8%; 99.8%; 99.9% | N/A (redundant) |
| 4 | MT-CYB | m.15639T>C | 18.4% | Probably damaging (0.998) |
| 4; 5; 14 | MT-CYB | m.15670T>C | 99.8%; 99.9%; 2.1% | N/A (redundant) |
| 4 | MT-HV1 | m.16390G>A | 12.7% | N/A (non-coding) |

Supplementary Table S3 - mtDNA variants identified by NGS in Family C composed by healthy and HCM individuals bearing the p.E99K-ACTC1 mutation.

Patients displaying more severe phenotypes/ clinical features are labelled in red; healthy or less severe patients are highlighted in green.

| Fibroblast sample | Loci | mtDNA Position | % heteroplasmy | Polyphen prediction (score) |
|-------------------|-------------------------|------------------|---------------------|-----------------------------|
| 8; 9; 10 | MT-HV2, MT-OHR, MT-CSB2 | m.310T>C | 16.0%; 11.0%; 14.0% | N/A (non-coding) |
| 8; 9; 10 | MT-HV2, MT-OHR, MT-CSB2 | m.310_311insC | 67.1%; 69.6%; 70.1% | N/A (non-coding) |
| 8; 9; 10 | MT-HV3 | m.513G>A | 11.9%; 14.8%; 9.9% | N/A (non-coding) |
| 8; 9; 10 | MT-HV3 | m.513_514insCACA | 31.9%; 33.3%; 34.9% | N/A (non-coding) |
| 8; 10 | MT-TA | m.5597A>C | 11.2%; 10.7% | N/A (non-coding) |

Supplementary Table S4 – Analysis of m.152T>C mtDNA variant frequency in haplogroups (number between brackets) using full length sequence set (left) or control region sequence set (right) deposited in MITOMAP database.

| Using Full Length sequence set | | | |
|--------------------------------|-----------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| L 3913 (63.2%) | L0 1159 (68.3%) | L0 1159 (68.3%) | L0a 405 (58.5%) |
| | | | L0d 582 (70.7%) |
| | | | L0f 40 (80.0%) |
| | | | L0g 9 (90.0%) |
| | | | L0k 121 (100.0%) |
| | L1 792 (90.2%) | L1 792 (90.2%) | L1b 266 (91.1%) |
| | | | L1c 526 (89.8%) |
| | L2 1212 (91.7%) | L2 1207 (91.3%) | L2a 994 (94.6%) |
| | | | L2b 92 (88.5%) |
| | | | L2c 108 (88.5%) |
| | | | L2e 12 (70.6%) |
| | L3 | L3 | L3a 27 (93.1%) |
| | | | L3d 361 (90.5%) |
| | | | L3k 13 (72.2%) |
| | L5 31 (79.5%) | L5 31 (79.5%) | L5a 29 (93.5%) |
| | L6 10 (83.3%) | L6 10 (83.3%) | |
| | M 2251 (21.0%) | D | D1 |
| D4 | | | D4a 154 (99.4%) |
| | | | D4h 81 (69.8%) |

| Using Control Region sequence set | | | | |
|-----------------------------------|-----------------|-------------------------------|-------------------------|-----------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) | |
| L 4405 (52.5%) | L0 | L0 | L0f 50 (71.4%) | |
| | | | L0k 70 (69.3%) | |
| | L1 1057 (88.3%) | L1 1057 (88.3%) | L1b 523 (87.5%) | |
| | | | L1c 534 (89.4%) | |
| | L2 1763 (82.0%) | L2 1755 (81.6%) | L2a 1265 (83.8%) | |
| | | | L2b 225 (89.3%) | |
| | | | L2c 234 (84.2%) | |
| | L3 | L3 | L2e 28 (68.3%) | |
| | | | L3a 21 (56.8%) | |
| | | | L3d 388 (72.7%) | |
| L3k 16 (66.7%) | | | | |
| M 2598 (11.1%) | C | C4 | C4 54 (100.0%) | |
| | | | C4e 12 (66.7%) | |
| | D | D5 | D4 | D4a 306 (57.3%) |
| | | | D5 | D5 16 (76.2%) |
| | | | D5c 24 (85.7%) | |
| | M | M3 | D6 | D6c 44 (100.0%) |
| | | | M4 | M3c 43 (67.2%) |
| | | | M4b 9 (50.0%) | |

| | | | |
|------------------|--------------------|---------------------|-----------------|
| | D5 | D5c 18 (100.0%) | |
| | D6 | D6c 12 (100.0%) | |
| M | M2 | M2b 98 (96.1%) | |
| | M3 | M3c 38 (82.6%) | |
| | M13 48 (71.6%) | M13a 38 (97.4%) | |
| | | M13c 10 (76.9%) | |
| | M20 54 (98.2%) | M20 54 (98.2%) | |
| | M23 224 (96.1%) | M23 224 (96.1%) | |
| | M24 25 (56.8%) | M24a 24 (96.0%) | |
| | M26 10 (100.0%) | M26 10 (100.0%) | |
| | M27 | M27b 63 (100.0%) | |
| | M28 57 (96.6%) | M28a 52 (96.3%) | |
| | M29 13 (100.0%) | | |
| | M36 29 (76.3%) | M36d 27 (96.4%) | |
| | M37 14 (66.7%) | M37 10 (90.9%) | |
| | M45 26 (92.9%) | M45a 19 (100.0%) | |
| | M57 10 (71.4%) | | |
| | M61 18 (69.2%) | M61 9 (52.9%) | |
| | M68 14 (58.3%) | M68a 14 (60.9%) | |
| | M76 | M76 8 (50.0%) | |
| | Z 191 (94.1%) | Z1 88 (100.0%) | Z1a 86 (100.0%) |
| | | Z2 10 (100.0%) | Z2 10 (100.0%) |
| Z3 61 (85.9%) | | Z3 17 (70.8%) | |
| | | Z3a 21 (95.5%) | |

| | | | |
|-------------------|-------------------|---------------------|---------------------|
| | M13 | M13 59 (100.0%) | |
| | | M13c 19 (76.0%) | |
| | M23 23 (74.2%) | M23 23 (74.2%) | |
| | M24 | M24a 13 (86.7%) | |
| | M30 | M30b 14 (100.0%) | |
| | M36 19 (63.3%) | M36a 13 (100.0%) | |
| | M37 18 (56.2%) | M37 17 (89.5%) | |
| | M57 14 (93.3%) | | |
| | M74 | M74 7 (50.0%) | |
| | M75 16 (61.5%) | M75 16 (61.5%) | |
| Z 311 (55.0%) | Z3 58 (93.5%) | Z3 17 (100.0%) | |
| | | Z3a 34 (89.5%) | |
| | Z4 74 (64.9%) | Z4 27 (100.0%) | |
| | | Z4a 47 (54.0%) | |
| N 5863 (14.1%) | A | A2 | A2v 12 (80.0%) |
| | | A5 | A5c 10 (58.8%) |
| | | A6 23 (92.0%) | A6b 16 (88.9%) |
| | | A7 14 (63.6%) | A7 14 (63.6%) |
| | | A11 | A11b 14 (100.0%) |
| | | A14 112 (100.0%) | A14 112 (100.0%) |
| | | A15 152 (93.3%) | A15 141 (98.6%) |
| | | | A15b 11 (55.0%) |
| | | A16 8 (61.5%) | A16 8 (61.5%) |
| | | A24 10 (100.0%) | A24 10 (100.0%) |

| | | | |
|-------------------|----------------|--------------------|---------------------|
| | | | Z3b 8 (80.0%) |
| | | Z4 26 (100.0%) | Z4a 17 (100.0%) |
| N 7119 (21.4%) | A | A | A 57 (86.4%) |
| | | A1 13 (100.0%) | A1a 12 (100.0%) |
| | | A2 | A2v 10 (90.9%) |
| | | A6 16 (100.0%) | |
| | | A8 | A8a 10 (62.5%) |
| | | A11 34 (97.1%) | A11a 22 (95.7%) |
| | | | A11b 10 (100.0%) |
| | | A12 12 (100.0%) | A12a 10 (100.0%) |
| | | A13 19 (100.0%) | A13 19 (100.0%) |
| | | A14 34 (94.4%) | A14 34 (94.4%) |
| | | A15 67 (97.1%) | A15a 10 (100.0%) |
| | | | A15c 53 (98.1%) |
| | | A17 40 (95.2%) | A17 40 (95.2%) |
| | | B | B2 |
| | F | F1 | F1b 93 (66.9%) |
| | | | F1c 46 (97.9%) |
| | | F3 162 (54.9%) | F3b 155 (68.6%) |
| | | F4 | F4a 18 (56.2%) |
| | H | H1 | H1i 17 (89.5%) |
| | | H2 | H2b 28 (96.6%) |
| H3 | | H3g 58 (96.7%) | |
| | | H3k 17 (100.0%) | |
| | | H3q 6 (54.5%) | |
| H8 | H8c 22 (95.7%) | | |

| | | | |
|----|-------------------|--------------------|--------------------|
| | | A25 7 (70.0%) | A25 7 (70.0%) |
| B | B2 | B2b 83 (85.6%) | |
| | | B2u 6 (60.0%) | |
| F | F2 | F2i 14 (58.3%) | |
| H | H9 22 (100.0%) | H9a 22 (100.0%) | |
| | | H32 62 (100.0%) | H32 62 (100.0%) |
| | | H36 12 (70.6%) | H36 12 (70.6%) |
| HV | HV1 | HV1b 23 (50.0%) | |
| | | HV2 58 (65.9%) | HV2a 38 (84.4%) |
| I | I2 27 (71.1%) | I2 24 (80.0%) | |
| | | I3 11 (68.8%) | I3a 11 (68.8%) |
| J | J1 | J1d 84 (52.2%) | |
| | | J2 219 (58.1%) | J2b 126 (84.0%) |
| K | K1 | K1c 145 (91.2%) | |
| | | K2 | K2a 50 (69.4%) |
| N | N1 | N1b 123 (52.1%) | |
| R | R2 63 (61.8%) | R2 52 (61.9%) | |
| | | R2b 10 (76.9%) | |
| | R7 15 (51.7%) | R7 9 (81.8%) | |
| S | S | S 22 (100.0%) | |
| T | T2 | T2d 20 (69.0%) | |
| U | U2 | U2c 45 (68.2%) | |
| | | U2e 170 (63.7%) | |
| | U7 269 (59.1%) | U7a 208 (79.1%) | |
| | U8 | U8c 8 (61.5%) | |
| X | X4 8 (72.7%) | X4 8 (72.7%) | |

| | | | |
|----|-------------------|---------------------|---------------------|
| | | H9 16 (88.9%) | H9a 14 (87.5%) |
| | | H16 | H16a 10 (100.0%) |
| | | | H16d 10 (100.0%) |
| | | H23 58 (65.9%) | H23 58 (65.9%) |
| | | H34 10 (90.9%) | H34 10 (90.9%) |
| | | H36 20 (76.9%) | H36 20 (76.9%) |
| | | H46 15 (78.9%) | H46 8 (72.7%) |
| | | H52 12 (92.3%) | H52 12 (92.3%) |
| HV | HV1 | HV1b 32 (64.0%) | |
| | HV2 40 (88.9%) | HV2a 34 (91.9%) | |
| | HV9 | HV9a 12 (100.0%) | |
| | HV12 | HV12a 7 (58.3%) | |
| I | I2 153 (91.1%) | I2 93 (93.0%) | |
| | | I2a 22 (84.6%) | |
| | | I2c 13 (86.7%) | |
| | | I2d 20 (95.2%) | |
| | I3 64 (98.5%) | I3a 35 (97.2%) | |
| | I3d 12 (100.0%) | | |
| J | J1 | J1d 93 (94.9%) | |
| | J2 575 (86.6%) | J2a 253 (77.1%) | |
| | | J2b 322 (95.8%) | |
| K | K1 | K1c 216 (95.6%) | |
| | K2 188 (62.5%) | K2a 184 (85.6%) | |
| N | N1 201 (67.2%) | N1b 129 (92.1%) | |
| | N7 8 (57.1%) | | |
| | N8 13 (81.2%) | N8 13 (81.2%) | |
| | N11 14 (58.3%) | N11b 14 (93.3%) | |
| P | P1 | P1 15 (78.9%) | |
| | P5 24 (85.7%) | P5 24 (85.7%) | |
| | P9 7 (63.6%) | | |

| | | |
|-----------------|--------------------|-----------------|
| R | R2 65 (95.6%) | R2 27 (100.0%) |
| | | R2b 12 (92.3%) |
| | | R2d 15 (88.2%) |
| | R5 38 (76.0%) | R5a 38 (77.6%) |
| | R21 12 (100.0%) | R21 12 (100.0%) |
| S 26 (53.1%) | S1 13 (59.1%) | S1 13 (92.9%) |
| T | T1 413 (67.4%) | T1a 409 (72.8%) |
| | T2 | T2c 113 (59.2%) |
| | | T2n 10 (100.0%) |
| U | U2 358 (81.7%) | U2b 24 (52.2%) |
| | | U2c 19 (95.0%) |
| | | U2d 24 (100.0%) |
| | | U2e 286 (89.9%) |
| | U7 442 (98.7%) | U7 25 (96.2%) |
| | | U7a 307 (99.7%) |
| U7b 110 (96.5%) | | |
| X | X4 9 (90.0%) | X4 9 (90.0%) |

Supplementary Table S5 - Analysis of m.309_310insCT mtDNA variant frequency in haplogroups (number between brackets) using full length sequence set (left) or control region sequence set (right) deposited in MITOMAP database.

| Using Full Length sequence set | | | |
|--------------------------------|----------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| L 1001 (16.2%) | L6 7 (58.3%) | L6 7 (58.3%) | |
| M 3220 (30.1%) | C | C | C 243 (54.0%) |
| | | C1 161 (51.6%) | C1b 65 (51.6%) |
| | | | C1c 32 (54.2%) |
| | | | C1d 61 (50.8%) |
| | D | D1 | D1j 12 (57.1%) |
| | | D2 50 (58.1%) | D2a 41 (65.1%) |
| | | | D2b 9 (60.0%) |
| | | D4 | D4s 9 (69.2%) |
| | M | M1 | M1b 15 (50.0%) |
| | | M5 | M5b 16 (57.1%) |
| | | M11 19 (50.0%) | M11b 7 (70.0%) |
| | | M13 | M13c 8 (61.5%) |
| | | M21 | M21a 18 (54.5%) |
| | | M33 | M33a 27 (67.5%) |
| | | M34 6 (60.0%) | |
| | | M35 | M35b 41 (71.9%) |
| | M36 30 (78.9%) | M36d 23 (82.1%) | |

| Using Control Region sequence set | | | |
|-----------------------------------|--------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| L 1640 (19.5%) | L4 | L4 | L4 6 (50.0%) |
| M 4047 (17.3%) | C | C4 | C4e 9 (50.0%) |
| | D | D2 129 (64.2%) | D2c 127 (72.2%) |
| | | D4 | D4 22 (59.5%) |
| | | D5 | D5c 16 (57.1%) |
| | | D6 | D6c 25 (56.8%) |
| | M | M5 | M5c 14 (51.9%) |
| | | M10 | M10 8 (72.7%) |
| | | M11 | M11 17 (70.8%) |
| | | M13 | M13 46 (78.0%) |
| | | | M13c 20 (80.0%) |
| | | M38 6 (50.0%) | |
| | | M65 | M65b 7 (58.3%) |
| | M74 | M74 8 (57.1%) | |
| | M91 | M91a 7 (50.0%) | |
| | Q | Q1 | Q1a 37 (50.0%) |
| | Z | Z3 34 (54.8%) | Z3a 23 (60.5%) |
| | | Z4 | Z4 17 (63.0%) |

| | | | |
|-------------------|---|-------------------|--------------------|
| | | M38 13 (56.5%) | |
| | | M52 | M52b 8 (57.1%) |
| | | M57 10 (71.4%) | |
| | | M62 | M62b 10 (55.6%) |
| | | M73 | M73 6 (54.5%) |
| N 9019 (27.1%) | A | A2 | A2a 118 (52.2%) |
| | | | A2b 22 (51.2%) |
| | | | A2p 7 (50.0%) |
| | | | A2w 11 (50.0%) |
| | | | A2y 12 (80.0%) |
| | | A5 63 (60.0%) | A5a 53 (80.3%) |
| | | A13 11 (57.9%) | A13 11 (57.9%) |
| | B | B2 | B2d 7 (58.3%) |
| | | | B2l 7 (50.0%) |
| | H | H1 | H1h 11 (55.0%) |
| | | | H1r 6 (60.0%) |
| | | | H1v 8 (50.0%) |
| | | H7 | H7a 29 (52.7%) |
| | | | H7e 16 (66.7%) |
| | | H10 | H10e 39 (61.9%) |
| | | H31 | H31a 10 (76.9%) |
| | | H35 14 (60.9%) | H35 11 (55.0%) |
| | | H40 7 (53.8%) | |
| | | H49 | H49a 12 (57.1%) |
| H51 6 (54.5%) | | | |
| H52 8 (61.5%) | | H52 8 (61.5%) | |

| | | | |
|-------------------|----|--------------------|--------------------|
| N 6358 (15.3%) | A | A2 | A2g 10 (71.4%) |
| | | | A2m 12 (66.7%) |
| | | A11 | A11b 8 (57.1%) |
| | HV | A24 7 (70.0%) | A24 7 (70.0%) |
| | | HV14 22 (62.9%) | HV14 22 (62.9%) |
| | | S | S 11 (50.0%) |
| | | W | W3 34 (61.8%) |

| | | |
|----|--------------------|---------------------|
| HV | HV0 | HV0d 7 (53.8%) |
| | HV4 56 (58.3%) | HV4a 47 (67.1%) |
| | HV9 | HV9 8 (53.3%) |
| | HV14 46 (80.7%) | HV14a 45 (81.8%) |
| | HV16 10 (66.7%) | HV16 10 (66.7%) |
| I | I1 | I1 11 (52.4%) |
| | | I1b 19 (51.4%) |
| | | I1c 7 (50.0%) |
| | I2 | I2a 13 (50.0%) |
| | I3 38 (58.5%) | I3a 23 (63.9%) |
| | | I3d 6 (50.0%) |
| N | N2 7 (63.6%) | N2a 7 (63.6%) |
| | N7 8 (57.1%) | |
| P | P9 7 (63.6%) | |
| R | R2 | R2d 10 (58.8%) |
| | R8 64 (63.4%) | R8b 42 (87.5%) |
| T | T1 | T1b 25 (62.5%) |
| | T2 | T2n 7 (70.0%) |
| U | U7 | U7b 61 (53.5%) |
| | U8 | U8a 57 (61.3%) |
| | U9 9 (56.2%) | |
| V | V5 7 (70.0%) | V5 7 (70.0%) |
| | V10 15 (62.5%) | V10a 9 (81.8%) |
| | V12 6 (60.0%) | V12 6 (60.0%) |
| | V22 6 (50.0%) | V22 6 (50.0%) |
| W | W1 | W1b 15 (57.7%) |
| | W3 72 (52.2%) | W3a 46 (50.0%) |
| | | W3b 25 (58.1%) |
| | W6 46 (54.1%) | W6a 11 (55.0%) |
| X | X2 | X2p 6 (60.0%) |

Supplementary Table S6 - Analysis of m.309_310insCCT mtDNA variant frequency in haplogroups (number between brackets) using full length sequence set (left) or control region sequence set (right) deposited in MITOMAP database.

| Using Full Length sequence set | | | |
|---------------------------------------|---------------------|--------------------------------------|--------------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| M 689 (6.4%) | M | M50 9 (50.0%) | M50a 8 (61.5%) |
| | | M53 17 (65.4%) | M53b 16 (69.6%) |

| Using Control Region sequence set | | | |
|--|---------------------|--------------------------------------|--------------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| N 2645 (6.4%) | B | B2 | B2y 30 (54.5%) |
| | H | H66 13 (50.0%) | H66a 13 (50.0%) |

Supplementary Table S7 - Analysis of m.310T>C mtDNA variant frequency in haplogroups (number between brackets) using full length sequence set (left) or control region sequence set (right) deposited in MITOMAP database.

| Using Full Length sequence set | | | |
|--------------------------------|---------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| L 2092 (33.8%) | L2 | L2 | L2e 9 (52.9%) |
| | L6 7 (58.3%) | L6 7 (58.3%) | |
| M 4436 (41.4%) | C | C | C 297 (66.0%) |
| | | C1 187 (59.9%) | C1b 74 (58.7%) |
| | | | C1c 44 (74.6%) |
| | | | C1d 66 (55.0%) |
| | | C4 | C4 15 (51.7%) |
| | | | C4c 23 (69.7%) |
| | D | D1 | D1j 13 (61.9%) |
| | | D2 53 (61.6%) | D2a 42 (66.7%) |
| | | | D2b 10 (66.7%) |
| | | D4 | D4 36 (51.4%) |
| | | | D4a 88 (56.8%) |
| | | | D4b 136 (55.3%) |
| | | | D4g 44 (54.3%) |
| | | | D4o 29 (54.7%) |
| | D4s 9 (69.2%) | | |
| | D6 | D6c 7 (58.3%) | |

| Using Control Region sequence set | | | |
|-----------------------------------|--------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| L 1878 (22.4%) | L4 | L4 | L4 7 (58.3%) |
| M 6220 (26.6%) | C | C4 | C4e 10 (55.6%) |
| | | C7 | C7 21 (50.0%) |
| | D | D1 | D1 63 (56.2%) |
| | | | D1a 17 (85.0%) |
| | | | D1e 19 (51.4%) |
| | | | D1f 19 (59.4%) |
| | | D2 178 (88.6%) | D2c 176 (100.0%) |
| | | D4 | D4 26 (70.3%) |
| | | | D4g 91 (54.2%) |
| | | D5 | D5 11 (52.4%) |
| | | | D5c 21 (75.0%) |
| | | D6 | D6c 30 (68.2%) |
| | G | G | G 24 (77.4%) |
| | M | M3 | M3c 33 (51.6%) |
| | | M5 | M5c 15 (55.6%) |
| | | M9 | M9 159 (68.2%) |
| M10 | | M10 9 (81.8%) | |

| | | | | | | |
|---|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| M | M1 116 (53.7%) | M1a 87 (51.5%) | N 12242 (29.5%) | M11 | M11 19 (79.2%) | |
| | | M1b 23 (76.7%) | | M13 | M13 47 (79.7%) | |
| | M3 | M3c 31 (67.4%) | | | M13c 20 (80.0%) | |
| | M5 92 (50.3%) | M5a 66 (50.0%) | | M18 | M18a 14 (51.9%) | |
| | | M5b 19 (67.9%) | | M35 | M35b 25 (56.8%) | |
| | M6 13 (52.0%) | M6a 11 (52.4%) | | M38 6 (50.0%) | | |
| | M7 | M7a 59 (58.4%) | | M42 | M42b 8 (50.0%) | |
| | M8 54 (60.0%) | M8a 53 (59.6%) | | M45 | M45 5 (50.0%) | |
| | M11 24 (63.2%) | M11a 13 (56.5%) | | M62 | M62 10 (55.6%) | |
| | | M11b 7 (70.0%) | | | M62a 38 (70.4%) | |
| | M12 | M12b 30 (69.8%) | | M65 | M65b 8 (66.7%) | |
| | M13 | M13c 9 (69.2%) | | M66 | M66b 8 (50.0%) | |
| | M17 | M17c 20 (50.0%) | | M73 | M73 15 (53.6%) | |
| | M21 45 (55.6%) | M21a 19 (57.6%) | | M74 | M74 11 (78.6%) | |
| | | M21b 26 (54.2%) | | M91 | M91a 8 (57.1%) | |
| | M24 | M24a 13 (52.0%) | | Q | Q1 | Q1a 42 (56.8%) |
| | M33 46 (52.9%) | M33a 28 (70.0%) | | | | Q1c 12 (100.0%) |
| | | | | M33c 12 (57.1%) | Z | Z3 45 (72.6%) |
| | M34 7 (70.0%) | | | | | Z3a 30 (78.9%) |
| | M35 51 (54.3%) | M35b 44 (77.2%) | | Z4 | Z4 19 (70.4%) | |
| | M36 33 (86.8%) | M36d 26 (92.9%) | | A | A2 | A2g 12 (85.7%) |
| | M37 12 (57.1%) | | | | | A2m 12 (66.7%) |
| | M38 15 (65.2%) | | | | | A2v 11 (73.3%) |
| | M39 25 (78.1%) | M39b 18 (94.7%) | | | A6 | A6b 10 (55.6%) |

| | | | |
|--------------------|------------------|-------------------|--------------------|
| | | M42 | M42b 10 (55.6%) |
| | | M44 8 (66.7%) | M44a 7 (63.6%) |
| | | M45 18 (64.3%) | M45a 11 (57.9%) |
| | | M46 10 (83.3%) | |
| | | M50 15 (83.3%) | M50a 12 (92.3%) |
| | | M52 | M52b 11 (78.6%) |
| | | M53 23 (88.5%) | M53b 22 (95.7%) |
| | | M54 6 (54.5%) | M54 6 (54.5%) |
| | | M57 11 (78.6%) | |
| | | M61 14 (53.8%) | |
| | | M62 18 (81.8%) | M62b 15 (83.3%) |
| | | M71 48 (51.6%) | M71a 27 (62.8%) |
| | | M72 10 (52.6%) | M72a 9 (60.0%) |
| | | M73 14 (56.0%) | M73 8 (72.7%) |
| | | M76 15 (60.0%) | M76 13 (81.2%) |
| | | M91 16 (69.6%) | M91a 12 (66.7%) |
| | Z | Z1 50 (56.8%) | Z1a 49 (57.0%) |
| | | Z3 | Z3a 17 (77.3%) |
| | | Z4 | Z4a 9 (52.9%) |
| N 13904 (41.8%) | A 776 (55.6%) | A2 546 (61.0%) | A2 198 (55.9%) |
| | | | A2a 163 (72.1%) |
| | | | A2b 26 (60.5%) |
| | | | A2d 15 (60.0%) |
| | | | A2g 11 (84.6%) |

| | | | | |
|--|--------------------|--------------------|--------------------|----------------|
| | | A11 | A11b 9 (64.3%) | |
| | | A15 109 (66.9%) | A15 99 (69.2%) | |
| | | | A15b 10 (50.0%) | |
| | | A24 8 (80.0%) | A24 8 (80.0%) | |
| | B | B2 384 (61.8%) | B2 11 (68.8%) | |
| | | | B2a 119 (74.8%) | |
| | | | B2b 63 (64.9%) | |
| | | | B2c 64 (69.6%) | |
| | | | B2y 51 (92.7%) | |
| | | B4 | B4e 10 (62.5%) | |
| | | | B4m 42 (66.7%) | |
| | | B6 | B6 8 (53.3%) | |
| | | F | F | F 17 (68.0%) |
| | | | F2 | F2i 12 (50.0%) |
| | H | H1 | H1u 10 (71.4%) | |
| | | H5 | H5b 25 (65.8%) | |
| | | | H5n 5 (50.0%) | |
| | | H7 | H7i 8 (57.1%) | |
| | | H14 | H14b 34 (50.0%) | |
| | | H41 15 (78.9%) | H41a 15 (78.9%) | |
| | | H55 26 (76.5%) | H55b 26 (76.5%) | |
| | H57 88 (59.1%) | H57 88 (59.1%) | | |
| | H66 20 (76.9%) | H66a 20 (76.9%) | | |
| | H101 29 (82.9%) | H101 29 (82.9%) | | |

| | | | |
|--|---|-------------------|--------------------|
| | | | A2h 11 (64.7%) |
| | | | A2j 7 (70.0%) |
| | | | A2p 12 (85.7%) |
| | | | A2q 10 (52.6%) |
| | | | A2v 9 (81.8%) |
| | | | A2w 15 (68.2%) |
| | | | A2y 13 (86.7%) |
| | | A5 69 (65.7%) | A5a 56 (84.8%) |
| | | A11 | A11b 5 (50.0%) |
| | | A13 13 (68.4%) | A13 13 (68.4%) |
| | | A15 | A15a 5 (50.0%) |
| | B | B2 589 (68.5%) | B2 231 (64.9%) |
| | | | B2a 36 (76.6%) |
| | | | B2b 138 (72.3%) |
| | | | B2c 34 (73.9%) |
| | | | B2d 12 (100.0%) |
| | | | B2e 21 (58.3%) |
| | | | B2i 23 (69.7%) |
| | | | B2l 12 (85.7%) |
| | | | B2o 14 (51.9%) |
| | | | B2q 19 (90.5%) |
| | | | B2y 10 (71.4%) |
| | | | B4 |
| | | B4e 8 (57.1%) | |

| | | |
|----|--------------------|--------------------|
| HV | HV0 | HV0f 11 (61.1%) |
| | HV14 33 (94.3%) | HV14 33 (94.3%) |
| I | I1 | I1d 12 (63.2%) |
| | I2 19 (50.0%) | I2 17 (56.7%) |
| J | JT | JT 11 (64.7%) |
| N | N10 | N10b 12 (54.5%) |
| P | P2 6 (60.0%) | P2 6 (60.0%) |
| R | R1 | R1a 8 (66.7%) |
| | R9 | R9 252 (64.0%) |
| | R11 | R11 34 (79.1%) |
| S | S | S 13 (59.1%) |
| T | T2 | T2d 21 (72.4%) |
| U | U1 | U1 7 (63.6%) |
| | U2 | U2 22 (53.7%) |
| | U4 436 (58.4%) | U4a 426 (73.2%) |
| V | V | V 64 (56.6%) |
| W | W3 36 (65.5%) | W3a 34 (64.2%) |
| X | X2 | X2e 31 (53.4%) |
| | X4 7 (63.6%) | X4 7 (63.6%) |
| Y | Y1 | Y1 63 (58.3%) |

| | | | |
|--|---|--------------------|---------------------|
| | | B5 | B5b 78 (50.6%) |
| | F | F1 | F1b 77 (55.4%) |
| | | | F1e 17 (56.7%) |
| | | F3 | F3a 41 (59.4%) |
| | H | H1 | H1h 14 (70.0%) |
| | | | H1j 75 (67.0%) |
| | | | H1n 53 (80.3%) |
| | | | H1r 9 (90.0%) |
| | | | H1v 10 (62.5%) |
| | | | H1z 8 (53.3%) |
| | | H2 457 (55.7%) | H2a 432 (55.5%) |
| | | | H2b 19 (65.5%) |
| | | H3 | H3b 46 (63.0%) |
| | | H5 | H5b 55 (71.4%) |
| | | H6 240 (63.7%) | H6a 214 (66.0%) |
| | | | H6b 19 (70.4%) |
| | | H7 162 (50.8%) | H7a 42 (76.4%) |
| | | | H7c 31 (64.6%) |
| | | | H7e 23 (95.8%) |
| | | H8 29 (53.7%) | H8c 14 (60.9%) |
| | | H10 116 (75.8%) | H10a 21 (72.4%) |
| | | | H10e 53 (84.1%) |
| | | H11 | H11b 8 (61.5%) |
| | | H13 203 (64.4%) | H13a 182 (65.7%) |

| | |
|-------------------|--------------------|
| | H13b 11 (50.0%) |
| | H13c 6 (60.0%) |
| H14 48 (56.5%) | H14a 32 (60.4%) |
| | H14b 15 (55.6%) |
| H15 67 (69.8%) | H15a 46 (73.0%) |
| | H15b 18 (64.3%) |
| H17 | H17a 14 (60.9%) |
| H20 | H20a 12 (50.0%) |
| H26 37 (50.0%) | H26a 29 (58.0%) |
| H30 5 (50.0%) | |
| H31 | H31a 12 (92.3%) |
| H35 18 (78.3%) | H35 15 (75.0%) |
| H39 20 (64.5%) | H39 8 (72.7%) |
| | H39c 7 (63.6%) |
| H40 9 (69.2%) | |
| H41 25 (80.6%) | H41a 25 (80.6%) |
| H44 15 (68.2%) | H44b 12 (85.7%) |
| H49 33 (71.7%) | H49 12 (57.1%) |
| | H49a 17 (81.0%) |
| H51 6 (54.5%) | |
| H52 10 (76.9%) | H52 10 (76.9%) |
| H55 10 (50.0%) | |
| H56 14 (51.9%) | H56 11 (55.0%) |
| H73 6 (60.0%) | |

| | | | |
|--|-------------------|--------------------|---------------------|
| | | H101 7 (50.0%) | H101 7 (50.0%) |
| | HV 442 (57.0%) | HV0 | HV0d 9 (69.2%) |
| | | HV1 81 (60.9%) | HV1a 48 (64.0%) |
| | | | HV1b 30 (60.0%) |
| | | HV2 25 (55.6%) | HV2a 21 (56.8%) |
| | | HV4 76 (79.2%) | HV4 9 (52.9%) |
| | | | HV4a 60 (85.7%) |
| | | HV6 12 (66.7%) | HV6 9 (60.0%) |
| | | HV9 29 (78.4%) | HV9 14 (93.3%) |
| | | | HV9a 8 (66.7%) |
| | | HV12 | HV12a 7 (58.3%) |
| | | HV13 9 (64.3%) | |
| | | HV14 50 (87.7%) | HV14a 49 (89.1%) |
| | | HV16 13 (86.7%) | HV16 13 (86.7%) |
| | | HV18 10 (76.9%) | HV18 10 (76.9%) |
| | I | I | I 14 (51.9%) |
| | | I1 | I1 14 (66.7%) |
| | | | I1b 20 (54.1%) |
| | | | I1c 8 (57.1%) |
| | | | I1f 15 (71.4%) |
| | | I2 93 (55.4%) | I2 56 (56.0%) |
| | | | I2a 18 (69.2%) |
| | | | I2d 16 (76.2%) |
| | | I3 49 (75.4%) | I3a 28 (77.8%) |
| | | | I3d 10 (83.3%) |

| | | | |
|-----|--------------------|-------------------|--------------------|
| | | I4 | I4b 6 (54.5%) |
| K | K1 | | K1b 100 (56.2%) |
| | | | K1d 8 (66.7%) |
| N | | N2 7 (63.6%) | N2a 7 (63.6%) |
| | | N7 9 (64.3%) | |
| | N9 205 (63.1%) | | N9a 180 (63.8%) |
| | | | N9b 25 (58.1%) |
| | N10 | N10a 7 (50.0%) | |
| | N21 | N21a 6 (54.5%) | |
| P | P9 9 (81.8%) | | |
| R | | R0 170 (56.5%) | R0a 151 (58.8%) |
| | | R1 43 (60.6%) | R1a 36 (73.5%) |
| | R2 38 (55.9%) | | R2 14 (51.9%) |
| | | | R2b 12 (92.3%) |
| | | | R2d 10 (58.8%) |
| | R8 70 (69.3%) | | R8a 28 (52.8%) |
| | | | R8b 42 (87.5%) |
| | R9 | R9b 68 (50.4%) | |
| | R11 | R11b 9 (75.0%) | |
| | R21 6 (50.0%) | R21 6 (50.0%) | |
| R30 | R30a 26 (53.1%) | | |
| T | T1 342 (55.8%) | | T1a 310 (55.2%) |
| | | | T1b 29 (72.5%) |
| | T2 | T2 44 (51.8%) | |

| | | |
|-------------------|-------------------|---------------------|
| | | T2d 13 (59.1%) |
| | | T2e 68 (58.1%) |
| | | T2n 8 (80.0%) |
| U | U2 232 (53.0%) | U2e 189 (59.4%) |
| | U4 | U4a 166 (52.5%) |
| | | U4b 83 (53.9%) |
| | U7 238 (53.1%) | U7a 161 (52.3%) |
| | | U7b 65 (57.0%) |
| | U8 80 (56.7%) | U8a 67 (72.0%) |
| | U9 9 (56.2%) | |
| V 453 (63.3%) | V1 83 (71.6%) | V1a 79 (70.5%) |
| | V2 26 (59.1%) | V2b 12 (85.7%) |
| | V3 29 (76.3%) | V3 8 (72.7%) |
| | | V3c 11 (84.6%) |
| | V5 9 (90.0%) | V5 9 (90.0%) |
| | V7 65 (68.4%) | V7 7 (63.6%) |
| | | V7a 55 (68.8%) |
| | V8 12 (75.0%) | V8 12 (75.0%) |
| | V9 16 (80.0%) | V9a 16 (84.2%) |
| | V10 20 (83.3%) | V10a 11 (100.0%) |
| | | V10b 9 (69.2%) |
| | V12 8 (80.0%) | V12 8 (80.0%) |
| | V13 9 (90.0%) | V13 9 (90.0%) |
| V15 9 (60.0%) | V15a 8 (57.1%) | |
| V18 11 (68.8%) | V18a 9 (69.2%) | |

| | | | |
|-------------------|------------------|-------------------|-------------------|
| | | V22 10 (83.3%) | V22 10 (83.3%) |
| W | W1 | | W1a 23 (53.5%) |
| | | | W1b 15 (57.7%) |
| | W3 83 (60.1%) | | W3a 54 (58.7%) |
| | | | W3b 27 (62.8%) |
| | W5 | | W5a 21 (56.8%) |
| | W6 53 (62.4%) | | W6 24 (51.1%) |
| W6a 14 (70.0%) | | | |
| X | X2 | | X2a 20 (55.6%) |
| | | | X2e 29 (67.4%) |
| | | | X2i 12 (70.6%) |
| | | | X2p 7 (70.0%) |
| | X3 6 (50.0%) | | |
| | X4 8 (80.0%) | X4 8 (80.0%) | |
| Y 70 (50.4%) | Y2 29 (53.7%) | Y2a 24 (54.5%) | |

Supplementary Table S8 - Analysis of m.16319G>A mtDNA variant frequency in haplogroups (number between brackets) using full length sequence set (left) or control region sequence set (right) deposited in MITOMAP database.

| Using Full Length sequence set | | | |
|--------------------------------|----------------|-------------------------------|-------------------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) |
| M 939 (8.8%) | D | D3 39 (100.0%) | D3 39 (100.0%) |
| | M | M2 232 (95.1%) | M2a 129 (99.2%) |
| | | | M2b 96 (94.1%) |
| | | M8 88 (97.8%) | M8a 87 (97.8%) |
| | | M32 162 (97.0%) | M32a 10 (100.0%) |
| | | | M32c 152 (99.3%) |
| | | M35 | M35a 14 (50.0%) |
| | | M40 19 (65.5%) | M40a 19 (67.9%) |
| | | M46 7 (58.3%) | |
| | | M55 13 (100.0%) | M55 13 (100.0%) |
| M60 9 (64.3%) | M60a 9 (90.0%) | | |
| N 1810 (5.4%) | A 1356 (97.2%) | A | A 65 (98.5%) |
| | | A1 13 (100.0%) | A1a 12 (100.0%) |
| | | A2 859 (96.0%) | A2 344 (97.2%) |
| | | | A2a 225 (99.6%) |
| | | | A2b 43 (100.0%) |
| | | A2d 21 (84.0%) | |
| | | A2f 18 (94.7%) | |

| Using Control Region sequence set | | | | | |
|-----------------------------------|------------------|-------------------------------|-------------------------|----------------|-----------------|
| Lineage | Top Level HG | Top Level HG Branch (ltr-num) | HG Branch (ltr-num-ltr) | | |
| L 159 (1.9%) | L4 | L4 | L4 7 (58.3%) | | |
| M 1344 (5.7%) | M | M2 124 (53.9%) | M2a 110 (90.9%) | | |
| | | | M2b 14 (66.7%) | | |
| | | M8 435 (75.5%) | M8a 435 (99.1%) | | |
| | | M12 | M12b 82 (59.0%) | | |
| | | M32 50 (98.0%) | M32c 48 (100.0%) | | |
| | | M40 | M40a 8 (50.0%) | | |
| | | M55 22 (100.0%) | M55 22 (100.0%) | | |
| | | M60 13 (54.2%) | M60a 13 (81.2%) | | |
| | | N 4381 (10.6%) | A 3718 (98.6%) | A | A 916 (97.7%) |
| | | | | A1 29 (100.0%) | A1a 29 (100.0%) |
| A2 1570 (98.6%) | A2 797 (98.8%) | | | | |
| | A2a 332 (98.2%) | | | | |
| | A2b 222 (100.0%) | | | | |
| | A2d 98 (100.0%) | | | | |
| A2g 14 (100.0%) | | | | | |
| A2m 18 (100.0%) | | | | | |
| A2q 19 (100.0%) | | | | | |

| | | |
|--|--------------------|---------------------|
| | | A2g 11 (84.6%) |
| | | A2h 15 (88.2%) |
| | | A2i 15 (88.2%) |
| | | A2j 9 (90.0%) |
| | | A2l 13 (100.0%) |
| | | A2m 12 (100.0%) |
| | | A2p 13 (92.9%) |
| | | A2q 18 (94.7%) |
| | | A2u 11 (100.0%) |
| | | A2v 11 (100.0%) |
| | | A2w 22 (100.0%) |
| | | A2y 13 (86.7%) |
| | A5 104 (99.0%) | A5a 66 (100.0%) |
| | | A5b 25 (100.0%) |
| | A6 16 (100.0%) | |
| | A8 23 (100.0%) | A8a 16 (100.0%) |
| | A11 35 (100.0%) | A11a 23 (100.0%) |
| | | A11b 10 (100.0%) |
| | A12 12 (100.0%) | A12a 10 (100.0%) |
| | A13 19 (100.0%) | A13 19 (100.0%) |
| | A14 36 (100.0%) | A14 36 (100.0%) |
| | A15 69 (100.0%) | A15a 10 (100.0%) |
| | | A15c 54 (100.0%) |
| | A17 41 (97.6%) | A17 41 (97.6%) |

| | | |
|--|--------------------|--|
| | | A2u 10 (83.3%) |
| | | A2v 14 (93.3%) |
| | A5 162 (99.4%) | A5a 63 (100.0%) |
| | | A5b 82 (98.8%) |
| | | A5c 17 (100.0%) |
| | A6 24 (96.0%) | A6b 18 (100.0%) |
| | A7 22 (100.0%) | A7 22 (100.0%) |
| | A8 47 (100.0%) | A8a 38 (100.0%) |
| | A11 575 (99.8%) | A11 561 (99.8%) |
| | | A11b 14 (100.0%) |
| | A14 111 (99.1%) | A14 111 (99.1%) |
| | A15 161 (98.8%) | A15 141 (98.6%) |
| | | A15b 20 (100.0%) |
| | A16 11 (84.6%) | A16 11 (84.6%) |
| | A19 54 (100.0%) | A19 54 (100.0%) |
| | A24 10 (100.0%) | A24 10 (100.0%) |
| | A25 10 (100.0%) | A25 10 (100.0%) |
| | N | N2 30 (53.6%) |
| | P | P4 21 (63.6%) P4a 21 (100.0%) |
| | R | R7 29 (100.0%) R7 11 (100.0%) |

| | | |
|---|-------------------|--------------------|
| B | B2 | B2y 8 (57.1%) |
| H | H31 | H31a 12 (92.3%) |
| I | I1 | I1c 12 (85.7%) |
| N | N2 11 (100.0%) | N2a 11 (100.0%) |
| R | R7 28 (100.0%) | R7a 16 (100.0%) |