**Supp. Table 1. Viral population dynamics of superinfected participants.**

| **Subject** | **Coding Regions** | **Initial Strain** | **Superinfecting Strain** | **Recombination** |
|---|---|---|---|---|
| K6 | RT | Replaced | Persists | No |
| | C2V3 | Replaced | Persists | No |
| K9 | RT | Replaced | Persists | No |
| | C2V3 | Replaced | Persists | No |
| D2 | RT | Persists | Persists | **Yes** |
| | C2V3 | Persists | Transient | No |
| P2 | RT | Persists | Not Detected | No |
| | C2V3 | Persists | Persists | **Yes** |
| P8 | RT | Persists | Transient | No |
| | C2V3 | Persists | Transient | No |
| S1 | RT | Persists | Transient | **Yes** |
| | C2V3 | Replaced | Transient | No |
| U7 | RT | Persists | Persists | No |
| | C2V3 | Persists | Transient | No |

Legend: Viral population dynamics are shown for each superinfected participant over the length of follow-up.

**Supp. Table 2. Population HLA Frequency Comparisons.**

**SI vs. MI**

| **HLA** | **SI (%)** | **MI (%)** | **p** | **q** |
|---|---|---|---|---|
| A29* | 14 | 0 | 0.07 | 0.94 |
| C16* | 14 | 0 | 0.07 | 0.94 |
| DR11 | 0 | 22 | 0.09 | 0.72 |
| B35 | 36 | 14 | 0.11 | 0.60 |
| DR07 | 36 | 17 | 0.25 | 0.93 |

**CI vs. MI**

| **HLA** | **CI (%)** | **MI (%)** | **p** | **q** |
|---|---|---|---|---|
| A29 | 25 | 0 | 0.03 | 0.20 |
| C02 | 25 | 0 | 0.03 | 0.20 |
| C16 | 25 | 0 | 0.03 | 0.20 |

**DI vs. MI**

| **HLA** | **DI (%)** | **MI (%)** | **p** | **q** |
|---|---|---|---|---|
| A29 | 18 | 0 | 0.03 | 0.20 |
| C02 | 18 | 0 | 0.03 | 0.20 |
| DR11 | 0 | 22 | 0.02 | 0.09 |

Legend: Frequency calculated based on two alleles per haplotype. SI: superinfected group, MI: monoinfected group, CI: co-infected group, DI: dual-infected, p: p-value, q: q-value (false discovery). *A29 and C16 were found to be in linkage disequilibrium ($p<0.05$).