**Table S6. Linkage disequilibrium: comparison with and without MS16 plus msp1f3**

|  |  |  |  |
| --- | --- | --- | --- |
|  | ***I*AS All infections 1  (*n*)** | ***I*AS Low complexity 2 (*n*)** | ***I*AS Unique MLGs 3 (*n*)** |
| **Site** | **8 Markers** | **6 Markers** | **8 Markers** | **6 Markers** | **8 Markers** | **6 Markers** |
| Arbaminch | 0.020\* (35) | 0.021\* (35) | 0.026\* (25) | 0.024\* (27) | 0.020\* (35) | 0.013 NS (34) |
| Halaba | 0.009 NS (44) | 0.004 NS (44) | 0.003 NS (38) | -0.004 NS (38) | 0.006 NS (43) | -0.002 NS (43) |
| Badawacho | 0.322\* (56) | 0.318\* (57) | 0.331\* (53) | 0.339\* (54) | 0.058\* (25) | 0.041\* (25) |
| Hawassa | 0.006\* (46) | 0.015 NS (47) | 0.015 NS (31) | 0.018 NS (34) | 4.0 x 10-4 NS (45) | 0.009 NS (46) |
| All sites | 0.051\* (181) | 0.055\* (183) | 0.074\* (147) | 0.076\* (153) | 7.0 x 10-4 NS (148) | -0.002 NS (148) |

**1**Only samples with no missing data at all loci are included in the analyses.

2 Restricted multi-locus haplotypes from samples with no more than one multi-allelic locus.

3 Unique set of multi-locus genotypes.

NS Not significant (*P* > 0.05).

\* *P* < 0.05.