

**Table S4 Substitution rates and estimates of most recent common ancestor (MRCA) of the clonal lineages**

**A. Protein coding genes**

| Gene         | Groups   | Total     | Sequenced Region          |                            |          | Synonymous polymorphisms | Age in years since TMRCA |                        | No of Strains | Haplo-group |
|--------------|----------|-----------|---------------------------|----------------------------|----------|--------------------------|--------------------------|------------------------|---------------|-------------|
|              |          |           | Two fold degenerate sites | Four fold degenerate sites | Total bp |                          | M1                       | M2                     |               |             |
|              |          |           |                           |                            |          |                          |                          |                        |               |             |
| <i>ROP18</i> | Type I   | Total adj | 1374                      | 1710                       | 10026    | 0                        | NA                       | NA                     | 6             | 1           |
|              |          | Total obs | 1374                      | 1710                       | 10026    | 2.99 <sup>†</sup>        | 6.56 X 10 <sup>5</sup>   | 3.28 X 10 <sup>5</sup> | 6             | 1           |
|              | Type II  | Total adj | 1143                      | 1427                       | 8355     | 0                        | NA                       | NA                     | 5             | 2           |
|              |          | Total obs | 1143                      | 1427                       | 8355     | 2.99 <sup>†</sup>        | 7.87 X 10 <sup>5</sup>   | 3.93 X 10 <sup>5</sup> | 5             | 2           |
|              | Type III | Total adj | 1362                      | 1740                       | 10026    | 0                        | NA                       | NA                     | 6             | 3           |
|              |          | Total obs | 1362                      | 1740                       | 10026    | 2.99 <sup>†</sup>        | 6.51 X 10 <sup>5</sup>   | 3.24 X 10 <sup>5</sup> | 6             | 3           |
| <i>SAG1</i>  | Type I   | Total adj | 726                       | 1134                       | 6066     | 3                        | 1.07 X 10 <sup>6</sup>   | 5.27 X 10 <sup>5</sup> | 6             | 1           |
|              |          | Total obs | 726                       | 1134                       | 6066     | 7.75 <sup>††††</sup>     | 2.77 X 10 <sup>6</sup>   | 1.36 X 10 <sup>6</sup> | 6             | 1           |
|              | Type II  | Total adj | 610                       | 945                        | 5055     | 0                        | NA                       | NA                     | 5             | 2           |
|              |          | Total obs | 610                       | 945                        | 5055     | 2.99 <sup>†</sup>        | 1.28 X 10 <sup>6</sup>   | 6.29 X 10 <sup>5</sup> | 5             | 2           |
|              | Type III | Total adj | 732                       | 1134                       | 6066     | 0                        | NA                       | NA                     | 6             | 3           |
|              |          | Total obs | 732                       | 1134                       | 6066     | 2.99 <sup>†</sup>        | 1.06 X 10 <sup>6</sup>   | 5.25 X 10 <sup>5</sup> | 6             | 3           |
|              | Type I   | Total adj | 384                       | 702                        | 3384     | 0                        | NA                       | NA                     | 6             | 1           |
|              |          | Total obs | 384                       | 702                        | 3384     | 2.99 <sup>†</sup>        | 1.80 X 10 <sup>6</sup>   | 8.80 X 10 <sup>5</sup> | 6             | 1           |

|             |          |           |     |     |      |                   |                        |                        |   |   |
|-------------|----------|-----------|-----|-----|------|-------------------|------------------------|------------------------|---|---|
| <i>SAG2</i> | Type II  | Total adj | 325 | 585 | 2820 | 0                 | NA                     | NA                     | 5 | 2 |
|             |          | Total obs | 325 | 585 | 2820 | 2.99 <sup>¶</sup> | 2.16 X 10 <sup>6</sup> | 1.05 X 10 <sup>6</sup> | 5 | 2 |
|             | Type III | Total adj | 384 | 702 | 3384 | 0                 | NA                     | NA                     | 6 | 3 |
|             |          | Total obs | 384 | 702 | 3384 | 2.99 <sup>¶</sup> | 1.81 X 10 <sup>6</sup> | 8.80 X 10 <sup>5</sup> | 6 | 3 |

## B. Introns

| Introns                             | Groups   | Total bp <sup>a</sup> | Polymorphisms      |                    | M1*                    | M2*                    | No of Strains | Haplogroups |
|-------------------------------------|----------|-----------------------|--------------------|--------------------|------------------------|------------------------|---------------|-------------|
|                                     |          |                       | SNPs               | Indels             | 1.7 X 10 <sup>-9</sup> | 3.8 X 10 <sup>-9</sup> |               |             |
|                                     |          |                       |                    |                    | SNPs                   | SNPs                   |               |             |
| <i>UPRT, BTUB, MIC2, HP and EF1</i> | Type I   | 15140                 | 1                  | 1                  | 3.8 X 10 <sup>4</sup>  | 1.7 X 10 <sup>4</sup>  | 4             | 1           |
|                                     |          |                       | 4.74 <sup>¶¶</sup> | 4.74 <sup>¶¶</sup> | 1.8 X 10 <sup>5</sup>  | 8.2 X 10 <sup>4</sup>  | 4             | 1           |
|                                     | Type II  | 11355                 | 0                  | 0                  | NA                     | NA                     | 3             | 2           |
|                                     |          |                       | 2.99 <sup>¶</sup>  | 2.99 <sup>¶</sup>  | 1.5 X 10 <sup>5</sup>  | 6.9 X 10 <sup>4</sup>  | 3             | 2           |
|                                     | Type III | 11355                 | 1                  | 0                  | 5.2 X 10 <sup>4</sup>  | 2.3 X 10 <sup>4</sup>  | 3             | 3           |
|                                     |          |                       | 4.74 <sup>¶¶</sup> | 2.99 <sup>¶</sup>  | 2.4 X 10 <sup>5</sup>  | 1.1 X 10 <sup>5</sup>  | 3             | 3           |

NA, Not applicable, M1 (Hughes AL, Verra F (2001) A very large long-term effective population size in the virulent human malaria parasite *Plasmodium falciparum*. Proc Roy Soc Lond 268: 1855-1860.), and M2 (Rich SM, Licht MC, Hudson RR, Ayala FJ (1998) Malaria's Eve: evidence for a recent population bottleneck throughout the world populations of *Plasmodium falciparum*. Proc Natl Acad Sci (USA) 95: 4425-4430.), are different age estimates for the neutral mutation rate

<sup>¶</sup>Total adjusted (Total adj) was calculated by using Poisson upper 95% confidence limit for zero observation: 2.99 “total observed” (Total obs) mutations

¶¶ Total adjusted (Total Adj) was calculated by using Poisson upper 95% confidence limit for 2 observations: 6.29 “total observed” (total obs) mutations

¶¶¶ Total adjusted (Total Adj) was calculated by using Poisson upper 95% confidence limit for 3 observations: 7.75 “total observed” (total obs) mutations

<sup>a</sup> All sites calculated as four fold degenerate since they are noncoding.

M1\*, Mutation rate at four fold degenerate sites., M2\*, Mutation rate at four fold degenerates sites.

MRCA Calculation:  $\text{Total synonymous number of SNPs} / (\text{Two fold codon sites} \times \text{Number of strains} \times \text{Two fold mutation rate}) + (\text{Four fold codon sites} \times \text{Number of strains} \times \text{Four fold mutation rate})$

Strains used:

Type I: RH, GT1, ENT, VEL, OH3, MOR

Type II: ME49, DEG, PIH, ARI, B41

Type III: CTG, VEG, STRL, T61, EDZ, M7741