### Supplementary Materials

#### Supplementary Table 1. Categorization of the most frequently repeated microsatellite motifs in genomes of *Plasmodium* species

| Plasmodium species | Unit motif length (bp) \(^a\) |
|--------------------|-------------------------------|
|                     | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 |
| *P. falciparum* 3D7 | A(27682) | AT(35293) | AAT(5932) | AAAAT(1715) | AAAAAT(312) | AATATAT(317) | AATATATAT(176) | AATATATATAT(119) |
|                     | C(C) | AC(93) | ATC(389) | ATAT(710) | ATATAT(312) | AATATAT(256) | AAAAAAT(91) | AAAAAAAT(136) | AAAAAAAAT(69) |
|                     | AG(37) | AAG(244) | AAG(112) | AAAAG(178) | AAAAAG(228) | AAAAAAG(104) | ACATATAT(115) | AATATATG(60) | ACATATATAT(54) |
|                     |     | A(183) | AAAC(79) | AAAAC(71) | AATTGAT(64) | AATATAT(55) | AAAAAAG(72) | AAAAAAG(52) | AAAAAATATAT(31) |
| *P. vivax* SAL-1    |     | A(15404) | AG(188) | AAAT(206) | AAAAAT(59) | AAAAAAT(34) | AAAAAAAAT(19) | AAAAAAAAG(26) |
|                     |     | C(140) | AG(116) | AGAT(101) | AAAAAT(55) | AAAAAAT(47) | AACCCGTT(21) | AACCCCT(12) | AAAAAAAAGG(16) |
|                     |     | AG(37) | AT(95) | AAAC(66) | ACAT(31) | ACATAT(29) | AAAAAAG(19) | ACATATAT(19) | AAAAAAAT(12) |
|                     |     |     | ATC(58) | AAAG(45) | AAAGC(24) | AAAAAG(24) | AAAAAAAAT(34) | AAAAAAAAG(11) | AAAAAAAAC(10) |
| *P. malariae* UG01  |     | A(24319) | AT(11597) | AAAAT(1018) | AATATAT(214) | AAAAAAT(10) | ACATATAT(177) | AAAAAAAT(43) | ACATATATAT(89) |
|                     |     | C(1) | AC(222) | AAAAT(842) | AAAAAT(54) | AAAAAAT(238) | AAAAAAAAT(100) | AAAAAAAT(77) | AAAAAAAAG(41) |
|                     |     | AG(38) | ACT(176) | AAAAAT(82) | AAAAC(103) | AAAAAAG(196) | ACATATAT(36) | AAAAAAAAG(64) | AATATATG(17) |
|                     |     |     | ATC(113) | AAAC(76) | AAAT(78) | AATAT(94) | AAAAAATAT(30) | AAAAAAAT(54) | AAAAAAATAT(15) |
| *P. ovale* curtisi GH01 |     | A(20859) | AT(3413) | AAAAT(526) | AAAAAT(91) | AAAAAAT(38) | ACATATAT(35) | AAAAAAAAG(4) | ACATATATAT(11) |
|                     |     | C(126) | AC(214) | AAAAT(256) | AAAAAT(90) | AAAAAAT(33) | AAAAAATAT(28) | AAAAAATAT(13) | AAAAAAAAT(11) |
|                     |     | AG(94) | ATC(55) | AAAAAT(49) | AAAAC(44) | ACATAT(66) | AAAAAAG(16) | AAAAAAAAG(22) | AAAAAAAGG(3) |
|                     |     |     | A(29) | AAAC(27) | AAATAT(41) | AAAAAGG(25) | AAAAAAT(10) | AAAAAAAAAG(14) | AAAAAAATAT(3) |
| *P. knowlesi* STRAIN-H |     | A(23592) | AT(2308) | AAAAT(268) | AAAAT(93) | ACATAT(205) | AAAAACTC(364) | ACATATAT(268) | AAAAAAAAC(63) |
|                     |     | C(215) | AC(307) | AAAAT(159) | AAAAAT(76) | AAAAAAT(79) | AAAAAATAT(59) | AAAAAAATAT(62) | AAAAAAAAGG(25) |
|                     |     | AG(27) | ATC(102) | AAAAG(70) | AAAAG(71) | AAAAAAG(50) | AACCCCT(65) | AAAAAAAG(57) | AAAAAAAG(19) |
|                     |     |     | A(74) | AAAC(48) | AACAC(58) | AAAAAT(48) | AAAAAAT(50) | AAAAAAGG(36) | AAAAAAAAG(43) |

\(^a\) Entire genomes of five *Plasmodium* species causing human malaria were scanned for diversity of microsatellite 1-10 bp unit motif length. List contains four most frequently repeated unique motifs along with their occurrence for each unit motif length.
Supplementary Table 2. Diversity and motif length-wise distribution of chromosomal microsatellite in *P. malariae* UG01

| Chr | Unit motif length (n) |
|-----|-----------------------|
|     | 1                    | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| Chr-1 | 990 | 442 | 85 | 77 | 53 | 69 | 30 | 58 | 47 | 58 |
|       | (51.86%) | (23.15%) | (4.45%) | (2.78%) | (3.61%) | (1.57%) | (3.04%) | (2.46%) | (3.04%) |
| Chr-2 | 758 | 327 | 51 | 62 | 54 | 57 | 25 | 42 | 30 | 50 |
|       | (52.06%) | (22.46%) | (3.5%) | (4.26%) | (3.71%) | (3.91%) | (1.72%) | (2.88%) | (2.06%) | (3.43%) |
| Chr-3 | 978 | 414 | 59 | 113 | 81 | 95 | 16 | 68 | 56 | 51 |
|       | (50.65%) | (21.44%) | (3.06%) | (5.85%) | (4.19%) | (4.92%) | (8.3%) | (3.52%) | (2.9%) | (2.64%) |
| Chr-4 | 914 | 418 | 74 | 71 | 50 | 71 | 28 | 86 | 33 | 72 |
|       | (50.3%) | (23.0%) | (4.07%) | (3.91%) | (2.75%) | (3.91%) | (1.54%) | (4.73%) | (1.82%) | (3.96%) |
| Chr-5 | 1447 | 749 | 105 | 147 | 97 | 101 | 40 | 93 | 80 | 83 |
|       | (49.18%) | (25.46%) | (3.57%) | (5.00%) | (3.3%) | (3.43%) | (1.36%) | (3.16%) | (2.72%) | (2.82%) |
| Chr-6 | 755 | 327 | 70 | 76 | 59 | 64 | 24 | 39 | 38 | 46 |
|       | (50.4%) | (21.83%) | (4.67%) | (5.07%) | (3.94%) | (4.27%) | (1.6%) | (2.6%) | (2.54%) | (3.07%) |
| Chr-7 | 1666 | 766 | 105 | 158 | 103 | 97 | 55 | 112 | 67 | 111 |
|       | (51.42%) | (23.64%) | (3.24%) | (4.88%) | (3.18%) | (2.99%) | (1.7%) | (3.46%) | (2.07%) | (3.43%) |
| Chr-8 | 1892 | 931 | 153 | 173 | 130 | 127 | 41 | 109 | 96 | 104 |
|       | (50.37%) | (24.79%) | (4.07%) | (4.61%) | (3.46%) | (3.38%) | (1.09%) | (2.9%) | (2.56%) | (2.77%) |
| Chr-9 | 2028 | 959 | 171 | 186 | 116 | 180 | 41 | 106 | 122 | 105 |
|       | (50.52%) | (23.89%) | (4.26%) | (4.63%) | (2.89%) | (4.48%) | (1.02%) | (2.64%) | (3.04%) | (2.62%) |
| Chr-10 | 1849 | 849 | 125 | 167 | 99 | 116 | 47 | 122 | 83 | 83 |
|       | (52.23%) | (23.98%) | (3.53%) | (4.72%) | (2.8%) | (3.28%) | (1.33%) | (3.45%) | (2.34%) | (2.34%) |
| Chr-11 | 2075 | 1023 | 190 | 220 | 133 | 159 | 52 | 97 | 94 | 84 |
|       | (50.28%) | (24.79%) | (4.6%) | (5.33%) | (3.22%) | (3.85%) | (1.26%) | (2.35%) | (2.28%) | (2.04%) |
| Chr-12 | 2908 | 1383 | 241 | 271 | 174 | 204 | 64 | 138 | 99 | 122 |
|       | (51.89%) | (24.68%) | (4.3%) | (4.84%) | (3.1%) | (3.64%) | (1.14%) | (2.46%) | (1.77%) | (2.18%) |
| Chr-13 | 2207 | 1066 | 173 | 211 | 122 | 134 | 64 | 112 | 97 | 106 |
|       | (51.42%) | (24.84%) | (4.03%) | (4.92%) | (2.84%) | (3.12%) | (1.49%) | (2.61%) | (2.26%) | (2.47%) |
| Chr-14 | 2890 | 1424 | 229 | 270 | 172 | 154 | 75 | 150 | 104 | 138 |
|       | (51.55%) | (25.4%) | (4.08%) | (4.82%) | (3.07%) | (2.75%) | (1.34%) | (2.68%) | (1.86%) | (2.46%) |

* Entire chromosomal DNA of *Plasmodium malariae* UG01 was scanned for microsatellites and categorized according to unit motif length. Data are expressed as motif-wise number of microsatellites and corresponding percentage within each chromosome.

Supplementary Table 3. Diversity and motif length-wise distribution of chromosomal microsatellite in *P. ovale curtisi*
| Chr-1 | Chr-2 | Chr-3 | Chr-4 | Chr-5 | Chr-6 | Chr-7 | Chr-8 | Chr-9 | Chr-10 | Chr-11 | Chr-12 | Chr-13 | Chr-14 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 651 (74.91%) | 498 (75.23%) | 810 (77.14%) | 663 (76.91%) | 1046 (76.02%) | 852 (75.67%) | 1423 (78.84%) | 1379 (76.95%) | 1766 (77.29%) | 1154 (74.84%) | 1660 (74.77%) | 2541 (73.75%) | 1873 (76.67%) | 2399 (75.02%) |
| 86 (9.9%) | 61 (9.21%) | 81 (7.71%) | 79 (9.16%) | 126 (9.16%) | 99 (8.79%) | 118 (6.54%) | 147 (8.2%) | 186 (8.14%) | 121 (7.85%) | 206 (9.28%) | 311 (9.24%) | 214 (8.76%) | 322 (10.07%) |
| 25 (2.88%) | 14 (2.11%) | 24 (2.29%) | 16 (1.86%) | 26 (1.89%) | 29 (2.58%) | 42 (2.33%) | 50 (1.88%) | 50 (2.19%) | 49 (3.18%) | 50 (2.25%) | 69 (2.05%) | 48 (1.96%) | 79 (2.47%) |
| 16 (2.88%) | 18 (2.72%) | 28 (2.67%) | 20 (2.32%) | 25 (1.82%) | 29 (2.49%) | 34 (1.88%) | 31 (1.83%) | 43 (1.88%) | 27 (1.75%) | 55 (2.48%) | 73 (2.17%) | 40 (1.64%) | 62 (1.94%) |
| 25 (2.99%) | 18 (2.72%) | 27 (2.67%) | 28 (2.57%) | 39 (1.82%) | 32 (2.49%) | 53 (2.94%) | 52 (2.9%) | 73 (2.19%) | 53 (3.44%) | 65 (2.93%) | 96 (2.85%) | 75 (3.07%) | 93 (2.91%) |
| 0 (0.46%) | 2 (0.3%) | 4 (1.14%) | 20 (2.09%) | 16 (1.16%) | 32 (2.84%) | 43 (2.38%) | 45 (2.51%) | 64 (2.8%) | 45 (2.92%) | 77 (3.47%) | 112 (3.33%) | 86 (3.52%) | 86 (2.69%) |
| 0 (0.81%) | 8 (1.21%) | 12 (1.33%) | 18 (0.93%) | 16 (1.16%) | 32 (1.51%) | 13 (0.72%) | 12 (0.72%) | 33 (1.44%) | 22 (1.43%) | 11 (0.57%) | 13 (1.62%) | 37 (1.62%) | 42 (1.04%) |
| 22 (2.53%) | 17 (2.57%) | 14 (1.43%) | 8 (0.93%) | 25 (1.82%) | 5 (0.44%) | 24 (1.33%) | 29 (1.62%) | 29 (1.62%) | 40 (1.36%) | 34 (0.74%) | 20 (1.06%) | 35 (1.87%) | 53 (1.09%) |
| 7 (0.81%) | 12 (1.81%) | 15 (1.05%) | 7 (0.81%) | 16 (1.16%) | 17 (1.16%) | 30 (1.66%) | 29 (1.66%) | 37 (0.88%) | 34 (1.04%) | 41 (2.2%) | 63 (1.82%) | 26 (1.06%) | 35 (1.09%) |

*a* Entire chromosomal DNA of *Plasmodium ovale curtisi* was scanned for microsatellites and categorized according to unit motif length. Data are expressed as motif-wise number of microsatellites and corresponding percentage within each chromosome.