

S4 Table. The main *pfgch1* amplifications with the most frequent *pfdhfr*/*pfdhps* genotypes in Africa and Asia (%).

| Duplication | N | Genotypes * | Number of genotypes | West Africa | Central Africa | East Africa | Southern Africa | Horn of Africa | Southeast Asia |
|-------------|-----|---------------------|---------------------|-------------|----------------|-------------|-----------------|----------------|----------------|
| A | 3 | NCSIS-ISAKAA | 3 | - | - | - | - | - | 100 |
| B | 2 | IRNIS-ISGEAA | 2 | - | - | - | - | 100 | - |
| C | 5 | IRNIS-ISGKAA | 2 | - | - | - | - | - | 40 |
| | | IRNLS-IFGKAA | 3 | - | - | 60 | - | - | - |
| D | 2 | IRNIS-ISGKGA | 2 | - | - | - | 100 | - | - |
| E | 289 | IRNIS-ISGEAA | 20 | - | - | - | - | - | 6.9 |
| | | IRNIS-IAGEAA | 36 | - | - | - | - | - | 12.5 |
| | | IRNLS-ISGNGA | 16 | - | - | - | - | - | 5.5 |
| | | IRNLS-ISGEAA | 124 | - | - | - | - | - | 42.9 |
| | | IRNLS-IAGEAA | 45 | - | - | - | - | - | 15.6 |
| F * | 101 | NRNIS-IAGEAA | 7 | - | - | - | - | - | 6.9 |
| | | IRNIS-ISGEAA | 10 | - | - | - | - | - | 9.9 |
| | | IRNLS-ISGEAA | 49 | - | - | - | - | - | 48.5 |
| | | IRNLS-IAGEAA | 11 | - | - | - | - | - | 10.9 |
| G ** | 68 | IRNIS-ISGKAA | 5 | 4.4 | - | - | - | - | 2.9 |
| | | IRNLS-ISGNGA | 16 | - | - | - | - | - | 23.5 |
| | | IRNLS-ISGEAA | 13 | - | - | - | - | - | 19.1 |
| | | IRNLS-IFGEAS | 17 | - | - | - | - | - | 25.0 |
| H *** | 20 | IRNIS-ISGKAA | 10 | 15.0 | 35.0 | - | - | - | - |
| | | IRNIS-VAGKAA | 2 | - | 10.0 | - | - | - | - |
| | | IRNIS-VAGKGS | 3 | 10.0 | 5.0 | - | - | - | - |
| I + | 347 | IRNIS-ISGKAA | 43 | 7.8 | 4.6 | - | - | - | - |
| | | IRNIS-ISGEAA | 214 | - | - | 23.1 | 38.6 | - | - |
| | | IRNIS-ISGEAA | 30 | - | 0.3 | 8.1 | 0.3 | - | - |
| I ++ | 207 | IRNIS-ISGKAA | 46 | 8.2 | 14.0 | - | - | - | - |
| | | IRNIS-ISGEAA | 88 | 0.5 | - | 12.6 | 29.5 | - | - |
| | | IRNIS-ISGEAA | 18 | - | 0.5 | 8.2 | - | - | - |
| | | IRNIS-IAGKAA | 18 | 7.2 | 1.4 | - | - | - | - |
| I +++ | 125 | NCSIS-ISGKAA | 8 | 6.4 | - | - | - | - | - |
| | | IRNIS-ISGKAA | 39 | 30.4 | 0.8 | - | - | - | - |
| | | IRNIS-IAAKAA | 7 | 5.6 | - | - | - | - | - |
| | | IRNIS-IAGKAA | 32 | 24.8 | 0.8 | - | - | - | - |
| | | IRNIS-IAGKAS | 9 | 7.2 | - | - | - | - | - |

* GB4, T996; ** KH02; *** NF54; + KE01; ++ KE01/ML01; +++ ML01; gDupA - H are gene amplifications; pDupI (3 types) and pDupJ are promoter amplifications; * based on *pfdhfr* (N51I, C59R, S108N, I164L and I306F) and *pfdhps* (I431V, S436A, A437G, K540E/K540N, A581G and A613S); frequencies of at least 10% are bolded