S2 Table. Parasitological parameters and DBLα type sequencing data for the microscopic *P. falciparum* infections during each survey.

Parasitological parameters	Pre-IRS		Post-IRS	
	Survey 1 End of wet season (October 2012)	Survey 2 End of dry season (May/June 2013)	Survey 3 End of wet season (October 2015)	Survey 4 End of dry season (May/June 2016)
Number of participants ^a	1923 (100)	1902 (100)	2022 (100)	2091 (100)
Microscopic <i>P. falciparum</i> prevalence ^b Age groups	808 (42.0)	513 (27.0)	545 (27.0)	272 (13.0)
1-5 years 6-10 years 11-20 years >20 years	173 (48.6) 243 (61.5) 202 (48.9) 190 (25.0)	100 (28.5) 169 (41.8) 159 (39.2) 85 (11.5)	63 (15.6) 167 (40.8) 169 (36.2) 146 (19.7)	28 (7.8) 114 (26.5) 97 (18.9) 33 (4.2)
Microscopic <i>P. falciparum</i> isolates with DBLα type sequencing data ^c Age groups 1-5 years 6-10 years 11-20 years >20 years	685 (84.8) 158 (91.3) 217 (89.3) 167 (82.7) 143 (75.3)	440 (85.8) 94 (94.0) 156 (92.3) 136 (85.5) 54 (63.5)	413 (75.8) 51 (81.0) 146 (87.4) 129 (76.3) 87 (59.6)	238 (87.5) 25 (89.3) 103 (90.4) 85 (87.6) 25 (75.8)

a Number of participants surveyed that were analysed by microscopy.
b Data reflect the number (% (n/N)) of participants sampled that were microscopically positive for *P. falciparum* (including mixed *P. falciparum* infections) relative to the number of participants surveyed in the total population or by the age groups presented.
c Data reflect the number (% (n/N)) of microscopic *P. falciparum* isolates that had DBLα type sequencing data relative the number of participants surveyed

that were microscopically positive for P. falciparum (including mixed P. falciparum infections) in the total population or by the age groups presented. P. falciparum isolates that had low DNA quality and/or sequencing quality (i.e., < 20 DBL α types, S3 Table) were removed when the sequencing dataset was cleaned (please see the Methods for additional details).