

S3 Table. DBL α type sequencing results for all isolates that were positive for a *P. falciparum* infection by microscopy.

Survey	<i>P. falciparum</i> positive isolates sequenced	<i>P. falciparum</i> isolates with DBL α type sequencing data (i.e., ≥ 20 DBL α types) ^a	<i>P. falciparum</i> isolates with no DBL α type sequencing data (i.e., 0 DBL α types) ^b	<i>P. falciparum</i> isolates with limited DBL α type sequencing data (i.e., 1 to < 20 DBL α types) ^c
1	808	685 (84.8)	66 (8.2)	57 (7.0)
2	513	440 (85.8)	45 (8.8)	28 (5.4)
3	545	413 (75.8)	35 (6.4)	97 (17.8)
4	272	238 (87.5)	13 (4.8)	21 (7.7)
TOTAL	2,138	1,776 (83.1)	159 (7.4)	203 (9.5)

^a Data reflect the number (% (n/N)) of *P. falciparum* isolates that had DBL α type sequencing data relative to the number of participants sampled that had microscopically positive for *P. falciparum* (including mixed *P. falciparum* infections).

^b Data reflect the number (% (n/N)) of microscopic *P. falciparum* isolates that had no DBL α type sequencing data relative to the number of participants sampled that were microscopically positive for *P. falciparum* (including mixed *P. falciparum* infections).

^c Data reflect the number (% (n/N)) of microscopic *P. falciparum* isolates that had between DBL α type sequencing data (i.e., 1 to < 20 DBL α types) relative the number of participants sampled that were microscopically positive for *P. falciparum* (including mixed *P. falciparum* infections).