

THE LANCET

Infectious Diseases

Supplementary appendix 2

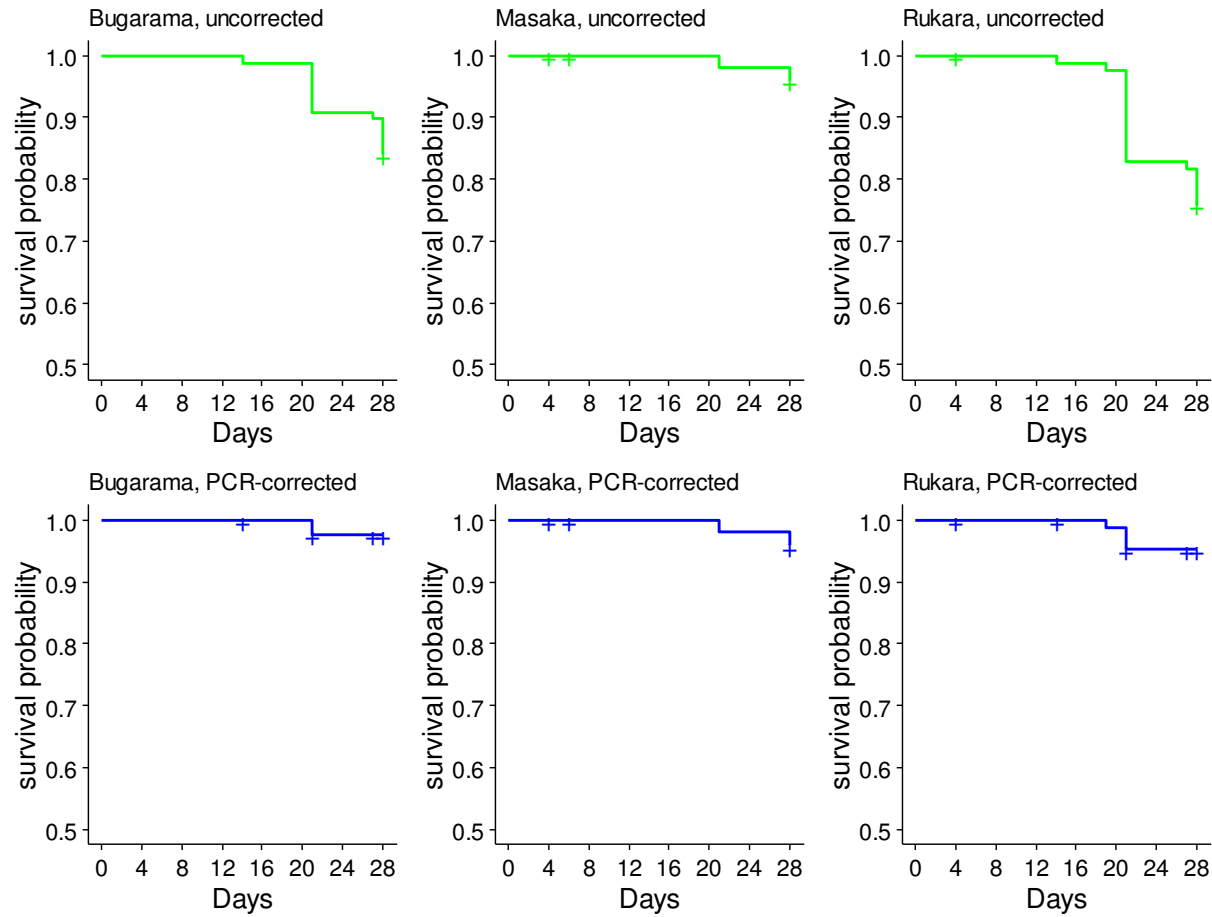
This appendix formed part of the original submission and has been peer reviewed.
We post it as supplied by the authors.

Supplement to: Uwimana A, Umulisa N, Venkatesan M, et al. Association of *Plasmodium falciparum* kelch13 R561H genotypes with delayed parasite clearance in Rwanda: an open-label, single-arm, multicentre, therapeutic efficacy study. *Lancet Infect Dis* 2021; published online April 14. [https://doi.org/10.1016/S1473-3099\(21\)00142-0](https://doi.org/10.1016/S1473-3099(21)00142-0).

Supplementary material

Supplemental Figure 1: Kaplan-Meier curves per site

Uncorrected and PCR-corrected Kaplan-Meier survival curves of time to recurrence among participants enrolled in the 2018 antimalarial therapeutic efficacy study. All participants were treated with artemether-lumefantrine. + signs indicate censoring.



Number at risk (censored) per day by site

Day	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28		
Bugarama - Uncorrected	88	88	88	88	88	88	88	88	88	88	88	88	88	87	87	87	87	87	87	87	80	80	80	80	80	80	80	79	74	
Bugarama - Corrected	88	88	88	88	88	88	88	88	88	88	88	88	88	88 (1)	87	87	87	87	87	87	85 (5)	80	80	80	80	80	80	80 (1)	80 (6)	
Masaka- Uncorrected	52	52	52	52 (1)	51	51 (1)	50	50	50	50	50	50	50	50	50	50	50	50	50	50	49	49	49	49	49	49	49	49	48	
Masaka - Corrected	52	52	52	52 (1)	51	51 (1)	50	50	50	50	50	50	50	50	50	50	50	50	50	50	49	49	49	49	49	49	49	49	48	
Rukara - Uncorrected	88	88	88	88 (1)	87	87	87	87	87	87	87	87	87	86	86	86	86	86	86	85	85	72	72	72	72	72	72	72	71	66 (1)
Rukara - Corrected	88	88	88	89 (1)	87	87	87	87	87	87	87	87	87	87 (1)	86	86	86	86	85	85	82 (10)	72	72	72	72	72	72	72 (1)	71 (6)	

Table S2: Prevalence of *pfmdr1* polymorphisms in pre-treatment and post-treatment samples

	Pre-treatment infections				Post-treatment infections			
	Bugarama, n (%)	Masaka, n (%)	Rukara, n (%)	Total, n (%)	Bugarama, n (%)	Masaka, n (%)	Rukara, n (%)	Total, n (%)
SNPs	N = 85	N = 41	N = 82	208	N = 13	N = 2	N = 20	35
N86	77(91)	41(100)	82(100)	200 (96)	13(100)	2(100)	20(100)	35 (100)
86N/Y	5(6)	0(0)	0(0)	5 (2)	0(0)	0(0)	0(0)	0 (0)
86Y	3(4)	0(0)	0(0)	3 (1)	0(0)	0(0)	0(0)	0 (0)
Y184	55(65)	15(37)	29(35)	99 (48)	8(62)	2(100)	7(35)	17 (49)
184Y/F	10(12)	1(2)	9(11)	20 (10)	0(0)	0(0)	3(15)	3 (9)
184F	20(24)	25(61)	44(54)	89 (43)	5(38)	0(0)	10(50)	15 (43)
D1246	82(96)	38(93)	74(90)	194 (93)	13(100)	2(100)	17(85)	32 (91)
1246D/Y	0(0)	0(0)	4(5)	4 (2)	0(0)	0(0)	1(5)	1 (3)
1246Y	3(4)	3(7)	4(5)	10 (5)	0(0)	0(0)	2(10)	2 (6)
Haplotypes†	N = 101	N = 42	N = 97	240	N = 13	N = 2	N = 25	40
NYD	62(61)	16(38)	36(37)	114 (48)	8(62)	2(100)	10 (40)	20 (50)
YFD	1(1)	0(0)	0(0)	1 (0)	0(0)	0(0)	0(0)	0 (0)
NFD	29(29)	23(55)	51(53)	103 (43)	5(38)	0(0)	11(44)	16 (40)
NFY	1(1)	3(7)	5(5)	9 (4)	0(0)	0(0)	3(12)	3 (8)
NYY	0(0)	0(0)	5(5)	5 (2)	0(0)	0(0)	1(4)	1 (3)
YYD	6(6)	0(0)	0(0)	6 (3)	0(0)	0(0)	0(0)	0 (0)
YFY	0(0)	0(0)	0(0)	0 (0)	0(0)	0(0)	0(0)	0 (0)
YYY	2(2)	0(0)	0(0)	2 (1)	0(0)	0(0)	0(0)	0 (0)

† Each possible haplotype constructed from the mixed infections (wildtype and mutant) was reported.

