Additional file 3: Table S3. (A) Plasmodium falciparum and (B) P. vivax data: Two-sided bootstrap test for differences in heterozygosity per marker. The test statistic (difference in heterozygosity), and p-value of bootstrap test based on B=10,000 bootstrap repeats using bias correction and acceleration are shown. The lower and upper bounds of the 95% bias-corrected and accelerated (BCa) bootstrap condensed interval of the test statistic based on B= 10,000 bootstrap repeats, as well as the p-value for a permutation test to compare the underlying frequency distributions using the differences in heterozygosity as test statistic, are also shown. The permutation test was approximated using 10,000 permutations. Note, that the permutation test will have relatively low power because of the employed test statistic. Namely, different frequency distributions can have similar heterozygosity values. Only some markers show a difference in MOI.

(A)		test stat	p-val	low	up	p-val perm
` '	$\overline{\text{Poly}\alpha}$	-0.2284	0.0000	-0.3376	-0.0818	0.0000
	TAA81	-0.4057	0.0250	-0.4828	-0.2388	0.0000
	TAA42	0.5332	0.0000	0.4783	0.6011	0.0000
	TAA109	0.3625	0.0000	0.2662	0.5663	0.0000
	ARA2	-0.3928	0.0995	-0.4450	-0.2185	0.0000
	Pfg377	-0.1709	0.0192	-0.2644	-0.0412	0.0000
	PfPK2	0.1257	0.0001	0.0606	0.2163	0.0012
	TAA60	0.0115	0.8476	-0.0844	0.1440	0.7814

(B)		test stat	p-val	low	up	p-val perm
` ,	$\overline{\mathrm{MS2}}$	-0.0412	0.1437	-0.1190	0.0134	0.0000
	MS5	-0.2637	0.0000	-0.3580	-0.1769	0.0000
	MS6	0.0270	0.3944	-0.0407	0.0876	0.0361
	MS15	0.0002	0.9830	-0.0773	0.0589	0.9916
	14.185	-0.1097	0.0600	-0.2231	0.0034	0.0128
	2.21	0.0543	0.0973	-0.0090	0.1440	0.0030
	MS8	-0.0595	0.0317	-0.1118	-0.0043	0.0000
	MS1	-0.1251	0.0008	-0.1977	-0.0557	0.0000
	MS10	0.0511	0.2437	-0.0315	0.1724	0.0878