Supplementary Table S1. Relative rate test results for samples with the reference versus non-reference allele at 31 SNPs located in DNA repair-related genes, identified as highly differentiated in drug-resistant *P. falciparum* populations (Miotto et al., 2013). χ^2 values calculated based on comparison of synonymous sites, with p-values based on 6,000 random permutations of SNP group assignment (reference vs non-reference). NR, non-reference; R, reference; ES, effect size.

			Num. samples		**Synonymous SNPs**						**All SNPs**					
Ch	**Pos.**	**Description**	**R**	**NR**	**m_{NR}-m_R**	**X^2**	**p-val**	**ES**	**95%CI**		**m_{NR}-m_R**	**X^2**	**p-val**	**ES**	**95%CI**	
2	242618	DNA repair endonuclease putative	80	97	-6.433	0.091	0.0273	0.15	-0.14	0.45	-15.815	0.14	0.02567	0.09	-0.21	0.39
5	401707	Hypothetical protein conserved	136	7	2.912	0.018	0.7052	0.06	-0.71	0.82	6.877	0.025	0.735	0.03	-0.73	0.8
5	577697	Deoxyribodipyrimidine photolyase	171	5	6.668	0.102	0.4426	0.19	-0.71	1.08	-2.675	0.004	0.9095	0.02	-0.87	0.91
5	592528	UvrD family helicase	166	11	-10.58	0.269	0.0621	0.27	-0.34	0.89	-27.698	0.47	0.044	0.17	-0.44	0.78
6	238493	RAD50 putative	148	28	-8.312	0.161	0.0308	0.24	-0.17	0.64	-30.127	0.54	0.0015	0.2	-0.21	0.6
7	460125	Hypothetical protein conserved	120	55	-3.706	0.031	0.2303	0.1	-0.22	0.42	-14.073	0.113	0.07117	0.09	-0.23	0.41
7	461139	Hypothetical protein conserved	80	96	3.417	0.026	0.2399	0.08	-0.21	0.38	2.225	0.003	0.752	0.01	-0.28	0.31
7	461364	Hypothetical protein conserved	100	77	-6.23	0.087	0.033	0.16	-0.14	0.46	-14.854	0.126	0.0385	0.09	-0.21	0.39
7	1059929	Exonuclease I putative	158	19	-10.633	0.266	0.0173	0.29	-0.18	0.77	-26.179	0.409	0.0195	0.17	-0.31	0.65
7	1105672	Mismatch repair protein pms1 homolog	161	16	-15.899	0.602	7.0E-04	0.44	-0.07	0.96	-23.261	0.324	0.04883	0.15	-0.37	0.66
9	1346394	DNA excision repair helicase putative	166	11	-9.708	0.219	0.0985	0.3	-0.31	0.91	-19.846	0.232	0.1665	0.15	-0.47	0.76
10	169428	Hypothetical protein	156	21	0.884	0.002	0.8341	0.02	-0.43	0.48	-13.633	0.108	0.20717	0.08	-0.37	0.54
10	256602	Hypothetical protein	168	8	-4.69	0.05	0.4895	0.14	-0.57	0.85	-37.821	0.842	0.02033	0.27	-0.44	0.98

11	255830	RuvB DNA helicase putative	101	74	1.955	0.008	0.5156	0.05	-0.25	0.35	11.977	0.08	0.09867	0.07	-0.23	0.37
11	480718	Hypothetical protein	102	75	8.451	0.156	0.0029	0.2	-0.1	0.5	28.693	0.457	<1.6E-4	0.16	-0.14	0.46
11	676743	DNA mismatch repair MLH1 putative	161	16	-11.914	0.335	0.0124	0.32	-0.19	0.84	-47.859	1.39	<1.6E-4	0.3	-0.21	0.82
12	637652	Hypothetical protein conserved	174	3	7.138	0.121	0.5083	0.19	-0.95	1.34	-0.839	0	1	0.01	-1.14	1.15
12	638469	Hypothetical protein conserved	155	22	-1.572	0.006	0.704	0.04	-0.41	0.48	2.103	0.003	0.8385	0.01	-0.44	0.46
13	187407	Peptidase putative	177	0	-	-	-	-	-	-	-	-	-	-	-	-
13	188355	Peptidase putative	138	38	0.053	0	1	0	-0.36	0.36	3.505	0.007	0.68767	0.02	-0.34	0.38
13	190954	Peptidase putative	161	16	-4.837	0.055	0.3213	0.13	-0.39	0.64	-22.642	0.31	0.05433	0.14	-0.37	0.66
13	192423	Peptidase putative	78	99	-10.139	0.222	2.0E-04	0.25	-0.04	0.55	-30.455	0.51	<1.6E-4	0.17	-0.13	0.47
13	192974	Peptidase putative	123	54	-4.533	0.046	0.1497	0.11	-0.21	0.43	-7.449	0.031	0.33433	0.04	-0.28	0.36
13	197434	Peptidase putative	155	22	-7.853	0.146	0.0617	0.21	-0.24	0.66	-25.718	0.396	0.01067	0.16	-0.28	0.61
13	203538	Peptidase putative	165	12	-5.524	0.07	0.3332	0.17	-0.42	0.76	-17.959	0.191	0.20267	0.13	-0.46	0.72
13	203891	Peptidase putative	171	6	-8.608	0.182	0.2627	0.22	-0.6	1.04	-14.827	0.136	0.44467	0.09	-0.73	0.9
13	204962	Peptidase putative	153	23	-2.53	0.015	0.5351	0.07	-0.37	0.51	-6.509	0.025	0.5325	0.04	-0.4	0.48
13	209856	Peptidase putative	169	7	-18.467	0.763	0.0114	0.58	-0.18	1.34	-40.828	0.961	0.02617	0.32	-0.44	1.07
13	210367	Peptidase putatitve	94	83	-4.309	0.041	0.1437	0.11	-0.19	0.41	-16.315	0.151	0.01733	0.1	-0.2	0.39
13	2732856	DNA repair endonuclease	96	81	-8.004	0.143	0.0043	0.2	-0.1	0.5	-19.845	0.224	0.0035	0.12	-0.18	0.41
14	1179389	ATP-dependent helicase putative	106	71	-2.661	0.016	0.368	0.07	-0.23	0.37	-17.691	0.179	0.01517	0.11	-0.2	0.41
14	2927471	Hypothetical protein	177	0	-	-	-	-	-	-	-	-	-	-	-	-