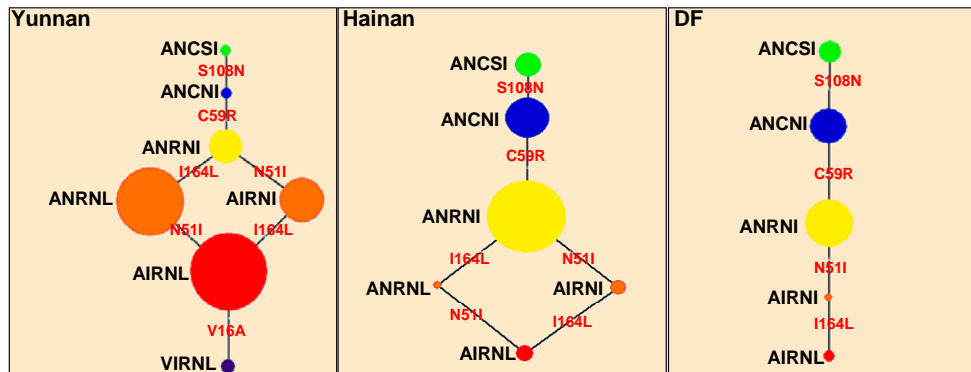


A



B

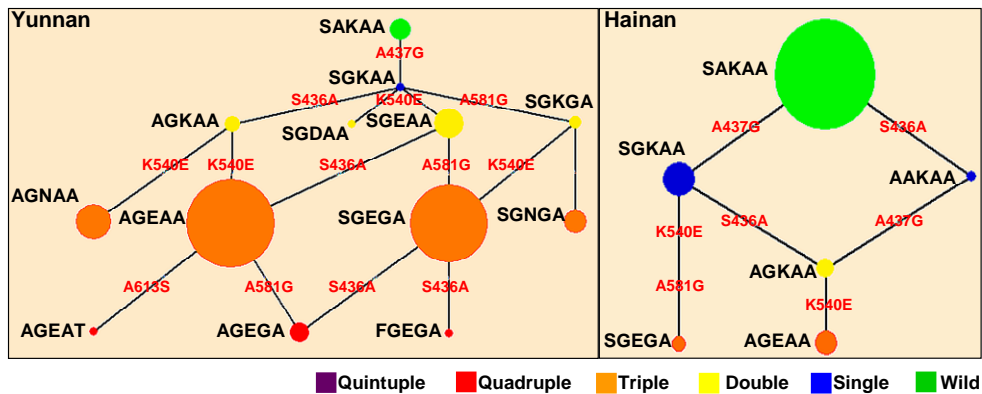


FIG S1 Evolutionary pathway of the drug resistance-conferring mutations in *pfdhfr* and *pfdhps* genes in southern China. The network diagram shows the evolution of the drug resistant *pfdhfr* (A) and *pfdhps* (B) alleles with respect to the site-mutations in the genes. The size of the circle is proportional to the number of isolates with a particular allele. The lines represent evolutionary steps connecting individual SNP haplotypes shown in different colors.

TABLE S1 Geographical distribution of *P. falciparum dhfr* and *dhps* resistant alleles in southern China

Resistance Genes	No. of mutations	DHFR/DHPS Alleles	Yunnan Province				Hainan Province			
			Lazan n=60	Dehong n=78	Tengchong n=92	Total N=230(%)	Ledong n=37	Dongfang n=50	Sanya n=32	Total N=119(%)
DHFR alleles	5	<u>VIRNL</u>			3	1.30				0.00
	4	<u>AIRNL</u>	33	30	44	46.52		2	1	2.52
	3	<u>ANRNL</u>	19	33	19	30.87			1	0.84
		<u>AIRNI</u>	4	10	18	13.91		3		2.52
	2	<u>ANRNI</u>	4	5	7	6.96	35	16	29	67.23
	1	<u>ANCNI</u>				0.00	1	21	1	19.33
	0	<u>ANCSI</u>			1	0.44	1	8		7.56
DHPS alleles	4	<u>AGEGA</u>		1	4	2.17				0.00
		<u>FGEGA</u>			1	0.44				0.00
		<u>AGEAT</u>			1	0.44				0.00
	3	<u>AGNAA</u>	3	3	9	6.52				0.00
		<u>AGEAA</u>	30	36	41	46.52	3	1	1	4.21
		<u>SGEGA</u>	19	29	25	31.74		1	1	1.68
		<u>SGNGA</u>	2	3	1	2.61				0.00
	2	<u>SGEAA</u>	3	2	6	4.78				0.00
		<u>SGDAA</u>			1	0.44				0.00
		<u>AGKAA</u>	1		1	0.87		2	1	2.52
		<u>SGKGA</u>	1		1	0.87				0.00
	1	<u>AAKAA</u>				0.00			1	0.84
		<u>SGKAA</u>	1			0.44	5	5		8.4
0	<u>SAKAA</u>		4	1	2.17	29	41	28	82.35	

Note: only alleles from single infection are presented in this table. Mutant amino acids are in bold and underlined.