

**Supplementary Table 2** Parameters of diversity and neutrality tests for *P. vivax dbpII* gene from different geographic origins.

Geographic origin	N	SS	Si	M	H	Hd	$\pi$	$\theta$ -w	Rm	Neutrality tests			S	NS	Test of selection dNS $\neq$ dS	
										Tajima's D	Fu & Li D*	Fu & Li F*			Z test	P value
Nicaragua	63	12	1	12	6	0.704	0.0058	0.0038	1	1.531	0.906	1.326	0	12	3.17	<0.001
Mexico	35	10	0	10	7	0.553	0.004	0.0036	1	0.329	1.404*	1.21*	0	10	3.03	<0.001
Colombia	37	18	2	18	21	0.937	0.0083	0.0064	6	0.985	0.888	1.085	1	17	3.75	<0.001
Peru	11	13	1	13	6	0.855	0.0083	0.0066	4	1.110	1.185	1.319	2	11	1.09	0.28
Ecuador	51	27	9	27	24	0.919	0.0086	0.0089	7	-0.132	-0.846	-0.706	7	20	0.82	0.41
Brazil	122	20	0	20	34	0.934	0.0082	0.0055	6	1.345	1.744***	1.905**	3	17	1.76	0.08
China	124	21	2	21	20	0.907	0.0086	0.0058	7	1.377	0.869	1.275	2	19	2.19	0.03
Sri Lanka	100	27	3	27	39	0.922	0.0097	0.0078	9	0.764	0.814	0.92	4	20	1.54	0.13
Thailand	22	26	8	27	17	0.974	0.0110	0.0106	7	0.000	-0.264	-0.215	4	23	1.92	0.06
India	55	12	1	12	12	0.834	0.0066	0.004	3	1.970*	0.924	1.509*	1	11	2.11	0.04
Iran	19	19	7	19	15	0.977	0.0077	0.0081	5	-0.171	-0.345	-0.341	2	17	1.67	0.1
Pakistan	118	27	0	28	40	0.926	0.00897	0.00752	9	0.44425	1.56246	1.34483	6	19	2.320	0.022
South Korea	13	14	10	14	12	0.987	0.0055	0.0067	1	-0.753	-1.563	-1.540	3	11	1.19	0.24
Myanmar	167	19	2	20	34	0.922	0.0072	0.0050	8	1.052	0.264	0.687	3	17	1.29	0.2
Uganda	31	27	6	27	16	0.929	0.0085	0.0101	3	-0.552	0.241	-0.020	13	14	-1.54	0.13
Sudan	96	19	1	19	16	0.895	0.0071	0.0055	4	0.837	1.252	1.310	4	15	2.1	0.04
Ethiopia	75	18	3	18	21	0.911	0.008	0.0055	8	1.372	0.328	0.839	3	15	2.93	<0.001
PNG	88	61	43	61	42	0.912	0.0094	0.0180	3	-1.562*	-5.573***	-4.740***	15	46	2.13	0.03

A gene sequence of 672 bp was analyzed. N, number of sequences, SS, segregating sites, Si, singletons, M, number of mutations, Hd, number of haplotypes;  $\pi$ , nucleotide diversity;  $\theta$ -w, genetic diversity. S, synonymous and NS, no synonymous mutations. \*0.10>P>0.05, \*\*P<0.05, \*\*\*P<0.02. PNG, Papua New Guinea. All (eight) sequences from Botswana had the same haplotype.