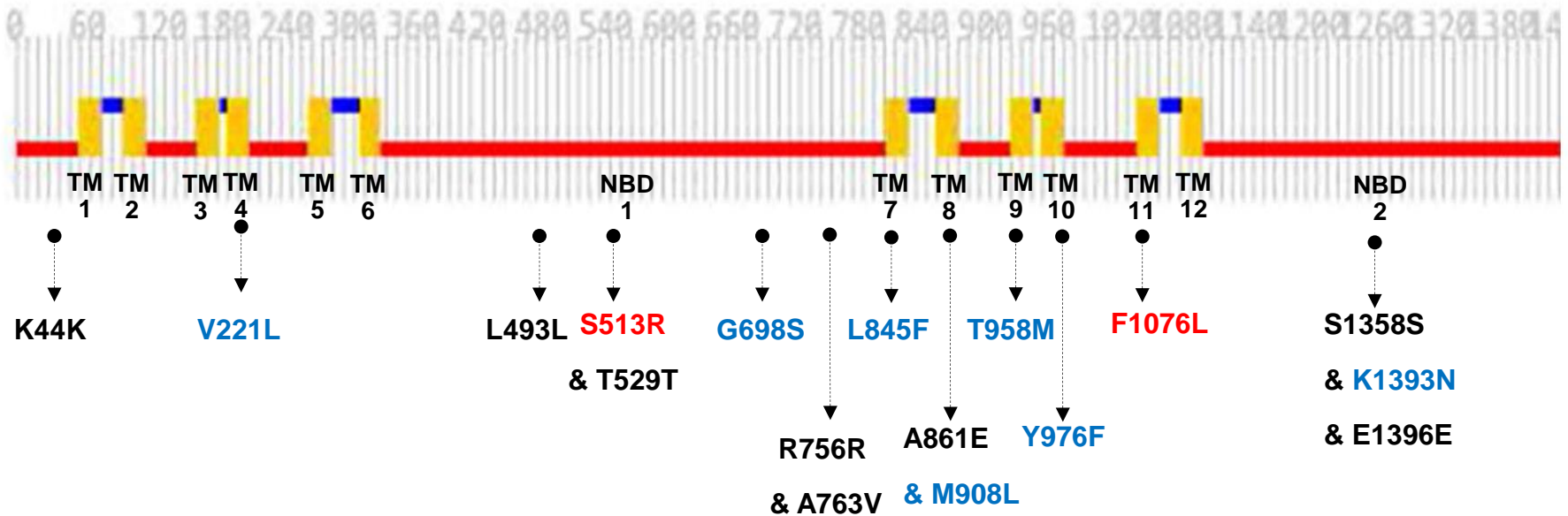
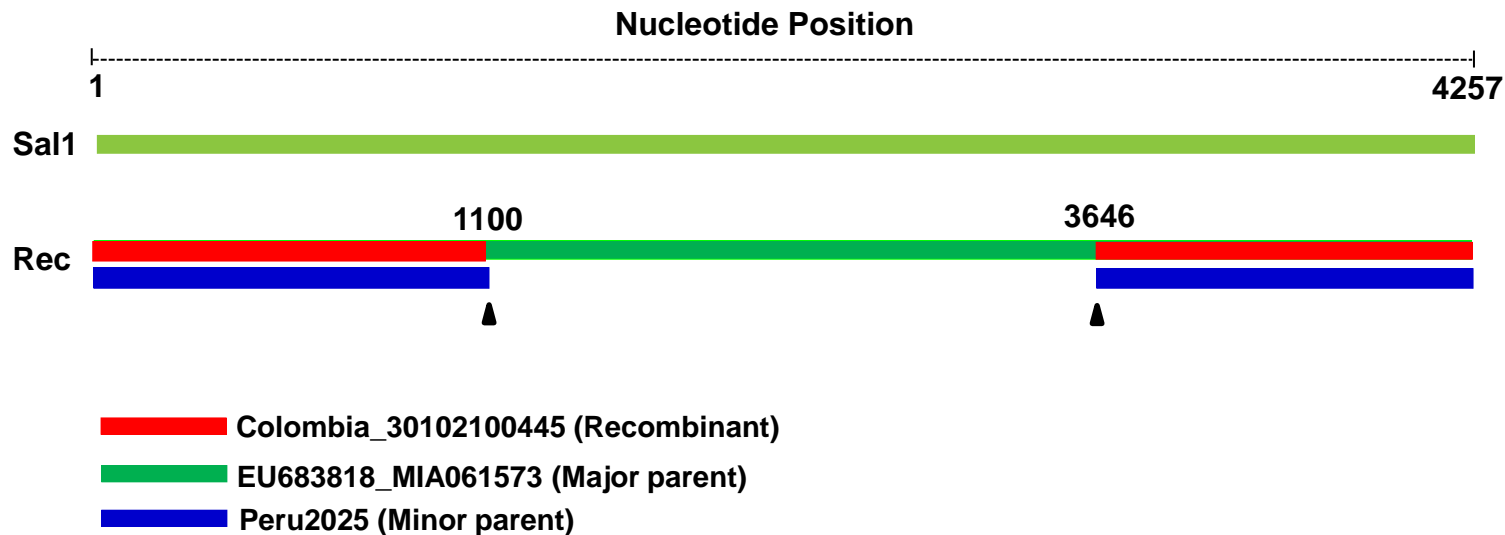


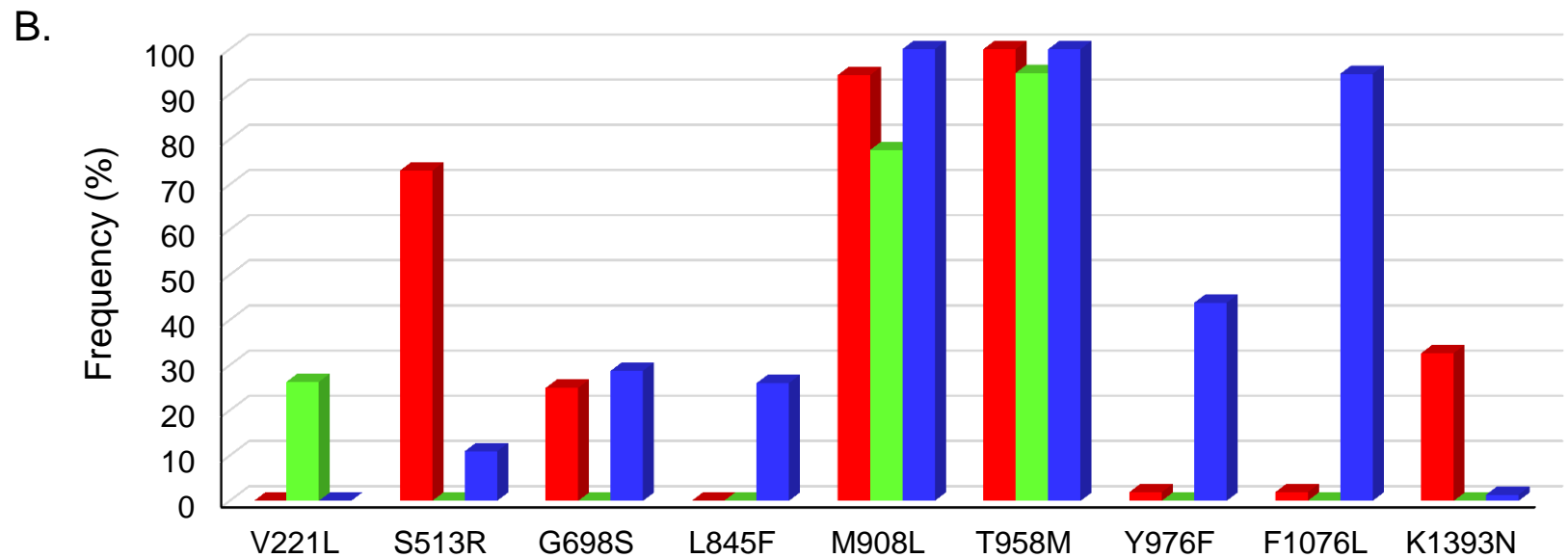
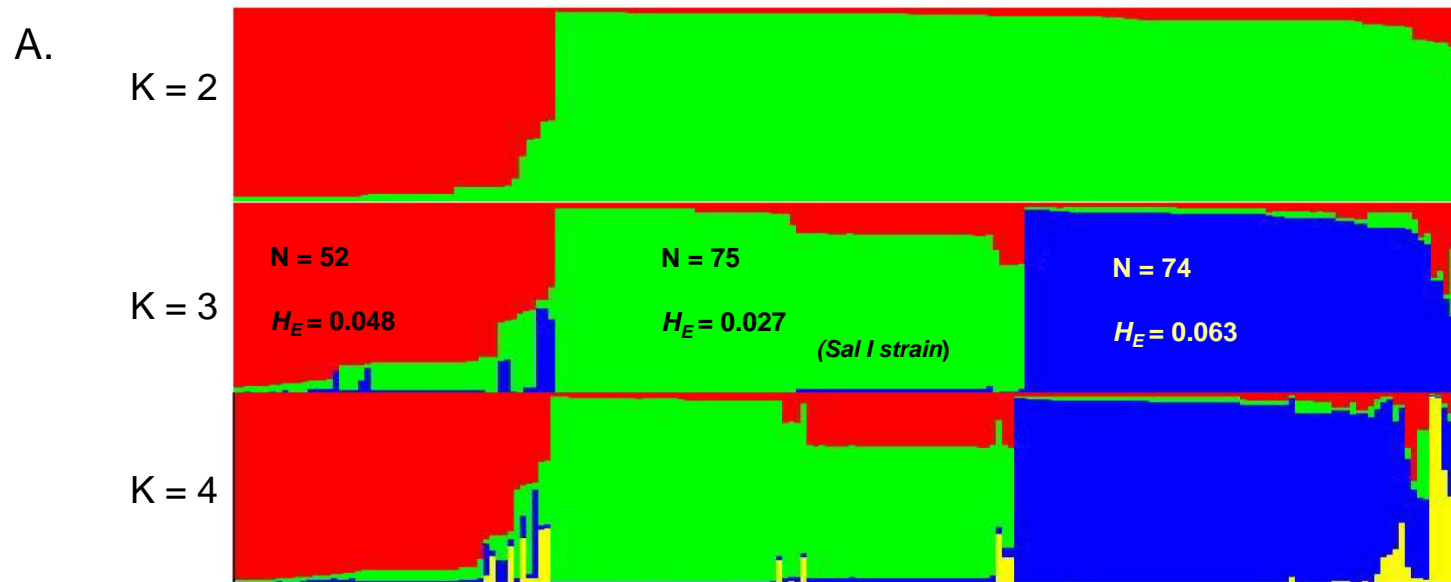
Amino acid position (1-1464)



Supplementary Fig. S1. Predicted domain organization of Pvmdr1 and relative positions of the SNPs. Both synonymous and nonsynonymous SNPs with minor allele frequency of 5% were shown. Black SNPs were only found in Thai's samples but, blue SNPs were found both Thai and global samples. V221L and G698S were not found in Thai' samples. SNPs in red (S513R and F1076L) are the positions under positive selection. Orange bars indicate transmembrane (TM) domains. Red and blue bars indicate loops separating TM domains.



Supplemental Fig. S2. Recombination event. One significant recombination breakpoint ($p < 0.05$) was detected by the MaxChi algorithm in RDP4 package (Rec). Green bar represents the major parent, blue bars the minor parent, and red bars the recombinant. The breakpoint positions (highlighted by the arrow heads) were compared to that of Sal I reference strain.



Supplementary Fig. S3. (A) Genetic structure of global *P. vivax* populations represented by different numbers of clusters. **(B)** The prevalence of each of the nine major SNPs in each cluster.

Supplementary Table S1. Primers used to amplify the near-complete *Pvm_{dr1}* gene.

<i>Primers</i>	<i>Sequence (5'→3')</i>	<i>Position in whole gene</i>	<i>T_m</i>	<i>%GC</i>	<i>Application</i>
MF1	ATGAAAAAGGATCAAAGGCAACCC	1-24	60.26	41.7	PCR & Sequencing
MF2	GACTCACCTCTGCATCACG	593-612	60.46	60.0	Sequencing
MF3	GTTGTATGACCCACCGAGG	1299-1318	60.11	60.0	Sequencing
MF4	GATAAGCAGGAGAAGGGCGG	2044-2063	60.25	60.0	PCR & Sequencing
MF5	AGGATAGTCATGCCCCAGGA	2750-2769	59.73	55.0	Sequencing
MR5	TCCTGGGGCATGACTATCCT	3411-3422	60.04	55.0	PCR
MF6	AGTCCCTCATCGACGTGAGA	3422-3441	60.04	55.0	Sequencing
MF7	AAATGCCACCAGAGAGGACG	3957-3976	60.04	55.0	Sequencing
MR7	CCTGGGCCTGTACAAAGGAG	4327-4308	60.04	60.0	PCR & Sequencing
MF1-MR5			2,770 bp		
MF4-MR7			2,284 bp		

Supplementary Table S2. Distribution of Pvmdr1 haplotypes by countries.

Haplotype	Countries*																Total	% isolate/ Hap
	THA_Tak	THA_Kan	THA_Ubon	THA_DB	MEX	COL	PER	BRA	MAU	MDG	IND	NKR	CHN	PNG	VIE	ESA		
Hap_1	2	2	1			2	25	5									37	18.41
Hap_2	10	8	5														23	11.44
Hap_3						18	2										20	9.95
Hap_4	1	9	5		1		1										17	8.46
Hap_5		3	16														19	9.45
Hap_6					13	1				1							15	7.46
Hap_7	4	1							1	1							7	3.48
Hap_8				3							1		1	4			9	4.48
Hap_9				1						1				3	1		6	2.99
Hap_10		5															5	2.49
Hap_11	1	4															5	2.49
Hap_12				1									3				4	1.99
Hap_13										4							4	1.99
Hap_14				2									1				3	1.49
Hap_15				2									1				3	1.49
Hap_16					1	1										1	3	1.49
Hap_17	1	2															3	1.49
Hap_18	2									1							3	1.49
Hap_19				2													2	1.00
Hap_20	1	1															2	1.00
Hap_21		1	1														2	1.00
Hap_22													1				1	0.50
Hap_23						1											1	0.50
Hap_24										1							1	0.50
Hap_25												1					1	0.50
Hap_26							1										1	0.50
Hap_27				1													1	0.50
Hap_28				1													1	0.50
Hap_29		1															1	0.50
Hap_30			1														1	0.50
No. isolates	22	37	29	13	15	22	30	5	1	8	2	1	7	7	1	1	201	100.00

*Country codes – THA_Tak: Tak province of Thailand, THA_Kan: Kanchanaburi province of Thailand, THA_Ubon: Ubon Ratchathani province of Thailand, THA_DB: Thai isolates from Plasmodb, MEX: Mexico, COL: Colombia, PER: Peru, BRA: Brazil, MAU: Mauritania, MDG: Madagascar, IND: India, NKR: North Korea, CHN: China, PNG: Papua New Guinea, VIE: Vietnam, and ESA: El Salvador.

Supplementary Table S3. Domain-specific polymorphisms and summary statistics of neutrality tests in the near-complete *Pvmdr1* gene in 88Thai isolates.

Domain	Region (Start-end)	Length (bp)	Polymorphic site	Haplotypes		π	Departure of Neutrality		
				No. Hap	Hd \pm VarHd		Tajima's D	Fu & Li's D'	Fu & Li's F'
TM1	1-270	270	0	1	0	0	n.d.	n.d.	n.d.
TM2	273-426	154	0	1	0	0	n.d.	n.d.	n.d.
TM3	459-585	127	3	4	0.049 \pm 0.00045	0.00074	-1.4461	-2.2394 [#]	-2.3437*
TM4	597-729	133	3	4	0.198 \pm 0.00124	0.0015	-0.9738	-2.2394 [#]	-2.1619 [#]
TM5	762-924	163	1	2	0.01 \pm 0.0001	0.0001	-0.9516	-2.202 [#]	-2.1332 [#]
TM6	963-1086	124	1	2	0.01 \pm 0.0001	0.00008	-0.9516	-2.202 [#]	-2.1332 [#]
NBD1	1089-2367	1279	14	13	0.455 \pm 0.00159	0.00055	-1.8732*	-3.5732**	-3.516**
TM7	2370-2562	193	3	4	0.182 \pm 0.0012	0.00171	-0.999	-2.2394 [#]	-2.1716 [#]
TM8	2580-2721	142	0	1	0	0	n.d.	n.d.	n.d.
TM9	2766-2892	127	3	4	0.059 \pm 0.00053	0.00091	-1.4158	-2.2394 [#]	-2.332*
TM10	2907-3081	175	3	3	0.02 \pm 0.00019	0.00022	-1.5076	-3.7453**	-3.5691**
TM11	3120-3255	136	2	3	0.475 \pm 0.00046	0.00307	0.5835	0.6364	0.7309
TM12	3294-3417	124	2	3	0.02 \pm 0.00019	0.00017	-1.2845	-3.0857*	-2.9641*
NBD2	3420-4257	838	9	10	0.263 \pm 0.00164	0.00039	-1.8584*	-3.6864**	-3.6217**
Whole	1-4257	4257	46	53	0.907 \pm 0.00016	0.00069	-2.1456**	-6.4032**	-5.4738**

$p < 0.01$, ** $p < 0.02$ & * $p < 0.05$, and n.d. is not detected.