

Additional file 5 Amino acid haplotypes in the critical binding motif **(A)** and Duffy-binding protein ligand domain of PvDBP **(B)** among Thai isolates

A

Haplotype	Amino acid position		No. Sequences (Total n = 246)	Percent
	2223333333	333333334		
	6682233444	55777890		
	1382609015	39249025		
Salvador 1	FRLIKNDEKR STNILNWP			
I			6	2.36
II	R		2	0.79
III	I.R.		1	0.39
IV	K.I.R.		19	7.48
V	G..H		19	7.48
VI	E.G... ..KMI.R.		1	0.39
VII	E.G..H ..K.I.R.		14	5.51
VIII	E.G.Q. ..K.I.R.		1	0.39
IX	...T..G..HI...		15	5.91
X	..F..... ..I.R.		32	12.60
XI	..F...G..HI.R.		1	0.39
XII	..F...G.QH ..K.I.R.		1	0.39
XIII	..F...GKN. ..K.I.R.		1	0.39
XIV	..F..DGKNH ..K.I.R.		6	2.36
XV	..F.E.GKN. ..K.I.R.		34	13.39
XVI	.S....GKNH TR..I...		6	2.36
XVII	.SF..DGKNHR.		1	0.39
XVIII	.SF..DGKNH ..K.I.R.		68	26.77
XIX	LS....GKNH TR..I...		25	9.84
XX	LS....GKNH TR..IS..		1	0.39

B

Haplotype	Amino acid position			No. Sequences Total n = 246)	Percent
	2222233333	3333333334	4444455		
	1166822334	4455777890	1334551		
	0513826090	1539249025	7031487		
Salvador 1	QKFRLIKNDE KRSTNILNWP GPQQSIQ				
I				6	2.36
II	R			2	0.79
III	I.R.K.			1	0.39
IV	G. .H.....			5	1.97
V	G. .H.....K.			8	3.15
VI	G. .H.....E...			6	2.36
VII	E.G.KMI.R.			1	0.39
VIII	E.G. .H..K.I.R.K.			14	5.51
IX	E.G. Q...K.I.R.KH			1	0.39
X	T..G. .H....I... ..K.			15	5.91
XI	F..... ..I.R.			1	0.39
XII	F..... ..I.R.K.			1	0.39
XIII	F..... ..I.R. .A...K.			30	11.81
XIV	F...G. .H....I.R.K.			1	0.39
XV	F...G. QH..K.I.R.K.			1	0.39
XVI	F...GK N...K.I.R.K.			1	0.39
XVII	F..DGK NH..K.I.R.K.			6	2.36
XVIII	F.E.GK N...K.I.R.			29	11.42
XIX	F.E.GK N...K.I.R. ..R....			1	0.39
XX	F.E.GK N...K.I.R.K.			2	0.79
XXI	F.E.GK N...K.I.R. R...L..			2	0.79
XXII	...S....GK NHTR..I... ..			1	0.39
XXIII	...S....GK NHTR..I... ..E...			5	1.97
XXIV	...SF..DGK NH.....R.K.			1	0.39
XXV	...SF..DGK NH..K.I.R.			1	0.39
XXVI	...SF..DGK NH..K.I.R.K.			64	25.20
XXVII	...SF..DGK NH..K.I.R.KH			2	0.79
XXVIII	..LS....GK NHTR..I... ..			24	9.45
XXIX	..LS....GK NHTR..I...K.			1	0.39
XXX	..LS....GK NHTR..IS... ..H			1	0.39
XXXI	.E..... ..K.I.R.K.			19	7.48
XXXII	H..SF..DGK NH..K.I.R.K.			1	0.39