

***Supplementary Data Sheet 3. On the evolution and function of
Plasmodium vivax reticulocyte binding surface antigen (pvrbsa)***

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AMOVA analysis and inter-population F_{ST} values for non-synonymous and synonymous datasets.

$F_{ST}^{Non-syn}$						
Source of variation					% of variation	P- value
Between populations (F_{CT})					2.85	0.061
Amongst subpopulations within populations (F_{SC})					3.93	0.000
Amongst subpopulations (F_{ST})					93.21	0.000
Fst						
	Meta	Chocó	Amazonas	Córdoba	Bolívar	Coastal area
Meta		0.32715	0.00391	0.01367	0.00293	0.03125
Chocó	0.00460		0.00684	0.01074	0.00098	0.01855
Amazonas	0.07397*	0.03688*		0.00000	0.00000	0.00000
Córdoba	0.04013*	0.02756*	0.08040*		0.00000	0.00000
Bolívar	0.05668*	0.05116*	0.08336*	0.06487*		0.14746
Coastal area	0.04170*	0.03657*	0.08821*	0.06487*	0.01369	
F_{ST}^{Syn}						
Source of variation					% of variation	P- value
Between populations (F_{CT})					6.70	0.064
Amongst subpopulations within populations (F_{SC})					2.59	0.019
Amongst subpopulations (F_{ST})					90.71	0.000
Fst						
	Meta	Chocó	Amazonas	Córdoba	Bolívar	Coastal area
Meta		0.09863	0.01953	0.01172	0.02832	0.00781
Chocó	0.04338		0.15332	0.20898	0.00977	0.00488
Amazonas	0.08114*	0.01569		0.09082	0.00098	0.00098
Córdoba	0.10102*	0.01372	0.02589		0.00098	0.00000
Bolívar	0.06661*	0.06218*	0.07859*	0.07804*		0.5595
Coastal area	0.12931*	0.09241*	0.11377*	0.10167*	-0.00907	

F_{ST} was calculated for parasite subpopulations in Colombian and Venezuela taking just the non-synonymous (or synonymous) mutations into account. Values close to 0 indicated low genetic differentiation whilst values close to 1 indicated high genetic differentiation. Values below the diagonal were the F_{ST} value and those above the diagonal represent the respective p values. *: Statistically significant values. $F_{ST}^{Non-syn}$: F_{ST} computed by using just the non-synonymous mutations. F_{ST}^{Syn} : F_{ST} computed by using just the synonymous mutations.