Supplementary Figure S6 Phylogenetic tree of *Pvs47* gene sequences of *Plasmodium vivax* worldwide isolates.

Maximum Likelihood method based on the HKY+G model. The phylogenetic reconstruction tree was run with 1000 replicates.

A branch of 67% bootstraps separates all isolates of America from other geographic sites, and another branch of 64% bootstraps separated a set of 12 Mexican isolates including three belonging to lineage PvSM-B (**). One Mexican isolate was traced back to lineage PvSM-A (*) that clustered with American isolates. This resembled the clustering of Figure 2.

The analysis involved 100 nucleotide sequences of the complete gene 1302 bp in the final dataset. Data source: https://plasmodb.org/.

