Additional file 2. Principal component analysis (PCA) of ten clinical isolates based on transcriptome-wide single nucleotide polymorphisms (SNPs). RNAseq data for each clinical isolate was mapped to the *P. vivax* PvPO1 reference genome (5, 838 genes) and SNPs (N = 42,988) were extracted using the Genome Analysis Toolkit, version 3.7. SNPs were filtered using the linkage disequilibrium pruning method and PLINK version 1.9. A sliding window size of 50 was set across the transcriptome, advancing with steps of five SNPs, and SNPs with a threshold value above 0.5 were removed. Isolate identity and Patient Groups are labelled. Geogrpahical origin is denoted by coloured symbols: red circle (Yala), blue square (Ubon Ratchathani).