



Figure S4 | Distribution of markers and within contig recombination. Each microsatellite marker is shown as a black bar in its position on one of the 8 largest supercontigs from the *P. marneffei* genome. The MAT idiomorph locus is shown as a white bar. R_M for each contig with multiple markers was determined using dnaSP [1]. For each isolate, alleles were arrayed in their order on the contig, gaps were recoded as characters and flanking sequence variation was not used because only a few isolates were sequenced for most loci, therefore RM reflects only microsatellite repeat variation.

1. Rozas J, Sanchez-DelBarrio JC, Messeguer X, Rozas R (2003) DnaSP, DNA polymorphism analyses by the coalescent and other methods. *Bioinformatics* 19: 2496-2497.