



**SUPPLEMENTARY FIG. S2.** Chromosome-wise fold coverage and percentage coverage of each reference chromosome. Fold coverage was calculated by dividing the total number of mapped bases in a particular chromosome by the length of the chromosome. Fold coverage for the chromosome varied between 30 to 33 times of the reference genome. For the mitochondrial genome the fold coverage was more than 250 times that of the reference mitochondrial genome. Reference genome coverage is calculated by dividing the number of unique mapped bases in a chromosome by the total number of bases in the chromosome. The reference genome coverage is more than 98%, except for the mitochondrial sequence, for which the reference coverage is almost 100%.