Figure S4. Schematic gene order comparison maps between the plastid genomes of *M. hypopitys* MON1-VOLR, *M. hypopitys* MON2-KALR and *Nicotiana tabacum*.

The linear representation of the circular mapping genomes using *rpl32* genes as the starting point does not reflect the actual gene size or spacing between the coding regions. Boxes represent protein-encoding and rRNA genes with the direction of transcription shown by the chamfered top corner. Triangles in *M. hypopitys* maps indicate repeat sequences. The S10 and *rrn* operons are shown by arrows. Locations of IR regions in *N. tabacum* chloroplast genome are shown by gray rectangles.