



Supplementary Figure S2. Unrooted ML tree based on the concatenated sequences of 35 lateral flagellum CDSs (*lafR*, *bll6847*, *flgN*, *flgJ*, *fliR*, *flhA*, *fliQ*, *flgD*, *flbT*, *flaF*, *flgL*, *flgK*, *flgE*, *fliK*, *motB*, *bll6863*, *fliF*, *fliL*, *flgH*, *bll6870*, *flgI*, *flgA*, *flgG*, *fliE*, *flgC*, *flgB*, *flhB*, *fliG*, *fliN*, *bll6880*, *fliM*, *motA*, *flgF1*, *fliI* and *bll6886* as in *B. diazoefficiens* USDA 110^T genome BA000040.2 from position 7,544,342 to 7,577,700) in 66 *Bradyrhizobium* genomes. Bold and ^T indicate type strain.