Supplementary Table 2: Genome identity matrix. Genomes are compared using dnadiff tool of MUMmer package.

Genome Accession	**Organism**	**% Coverage of B. japonicum USDA110 genome (M-M Alignments)**	**Average identity**	**% Coverage of query genome (M-M Alignments)**
NC_017325.1	*Sinorhizobium meliloti* SM11	1.06	83.36	2.48
NC_002678	*Mesorhizobium loti*	2.37	83.26	3.07
NC_007406.1	*Nitrobacter winogradskyi*	5.53	84.01	14.82
NC_011386.1	*Oligotropha_carboxidovorans*	6.32	84.01	15.35
NC_007964.1	*Nitrobacter hamburgensis*	8.56	84.34	17.70
NC_008380.1	*Rhizobium leguminosarum*	12.96	83.04	23.34
NC_011004.1	*Rhodopseudomonas palustris* TIE-1	13.12	84.26	20.81
NC_009485	*Bradyrhizobium sp. BTAi*	23.50	84.86	25.90
NC_009445.1	*Bradyrhizobium sp. ORS 278*	24.24	84.98	29.60
NC_017082.1	*Bradyrhizobium sp. S23321*	59.65	89.35	75.01
NC_017249.1	*Bradyrhizobium japonicum* USDA6	74.71	91.04	73.88