

Supplementary Table S2: Genome Sequencing and assembly information of eight *Bradyrhizobium* additional strains.

<i>Bradyrhizobium</i> strain ^a	<i>B. arachidis</i> (LMG 26795 ^T)	GHa	GHvi	RC3b	RC2d	R5	Leo121	Leo170
NCBI BioProject	PRJNA323241	PRJNA323242	PRJNA323243	PRJNA323246	PRJNA323245	PRJNA323244	PRJNA420430	PRJNA420429
Sequencing Platform^b	Illumina HiSeq	Illumina HiSeq	Illumina HiSeq	Illumina HiSeq	Illumina HiSeq	Illumina HiSeq	Ion Torrent™ PGM	Ion Torrent™ PGM
Number of reads	3 890 368	5 263 950	5 424 632	6 776 084	7 952 062	4 030 174	5 781 432	4 239 247
Sequencing depth	59X	94X	100X	119X	121X	63X	104X	76X
N50 (base pairs [bp])	194 418	156 060	801 310	383 119	171 503	142 424	36 967	20 478
Contig count	104	97	44	50	119	128	727	1114
Largest contig (kilo base pairs [kbp])	839.6 kbp	652.8 kbp	1403.5 kbp	751.6 kbp	937.7kbp	476 .1kbp	178.279kbp	104.710kbp
Average contig	99 936	86 876	193 309	170 932	81 865	76 168	17 145	10 914
Genome size (bp)	9 793 799	8 253 313	7 925 674	8 375 670	9 578 216	9 444 915	9 721 730	9 490 515
G +C %	63.6	62.9	63	63.7	62.8	63.6	63.3	63.6

^a LMG = (BCCM/LMG) Belgian Co-ordinated Collections of Microorganisms.

^b Illumina HiSeq sequencing done at JGI for the Genomic Encyclopedia of Type strains Phase III project.

Ion Torrent™ PGM sequencing done at the sequencing facility at the University of Pretoria.