

Metagenomics-guided Analysis, Isolation and Characterization of Uranium Resistant Microbiota Using a High-throughput Approach

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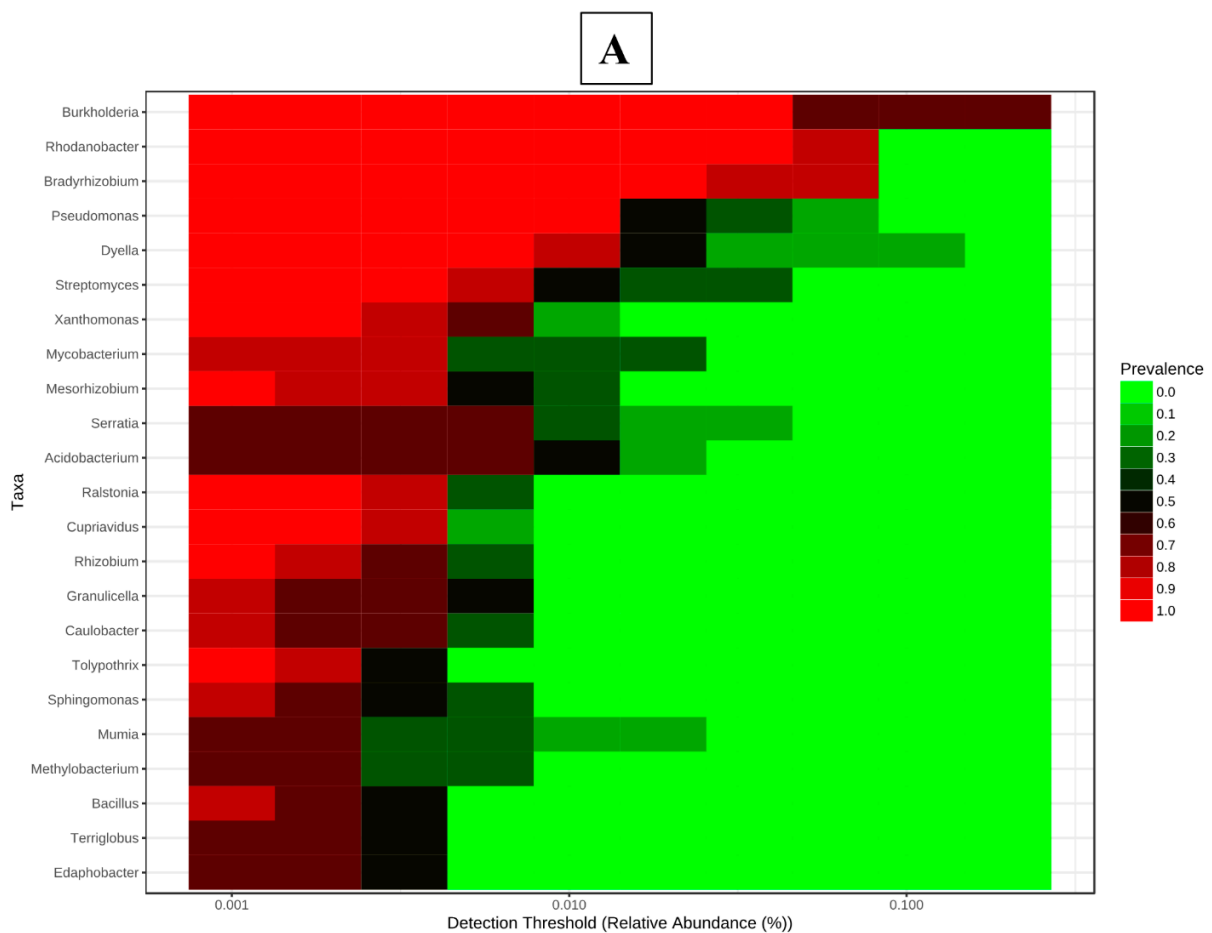
Table S1. Shotgun based sequence reads obtained from the SRS soils and DC/MT culture conditions. total Shown are sequencing depth, number of reads that mapped to taxonomic annotations, number of reads that mapped to a Phylum, and number of reads that mapped to the SEED functional database.

Sample ID	Raw Reads	Total NR (taxonomic) Alignments	Percent	Phylum Sum	Percent	Total Functional Alignments
DC Soil	9827394	2294597	0.23349	2066334	0.210263	1129787
MT Soil	2170172	457303	0.210722	411335	0.18954	225413
DC Gen 1	12630198	3518023	0.278541	3303629	0.261566	1597742
DC Gen 2	12206380	3027513	0.248027	2806697	0.229937	1386391
MT Gen 1	13656466	5622632	0.411719	5336589	0.390774	2782196
MT Gen 2	13852746	4002908	0.288961	3732288	0.269426	1894069

Table S2. Shown are the EDGAR identified set of gene homologues identified in strain MT2 that likely perform a biodegradative or metal resistance function(s)

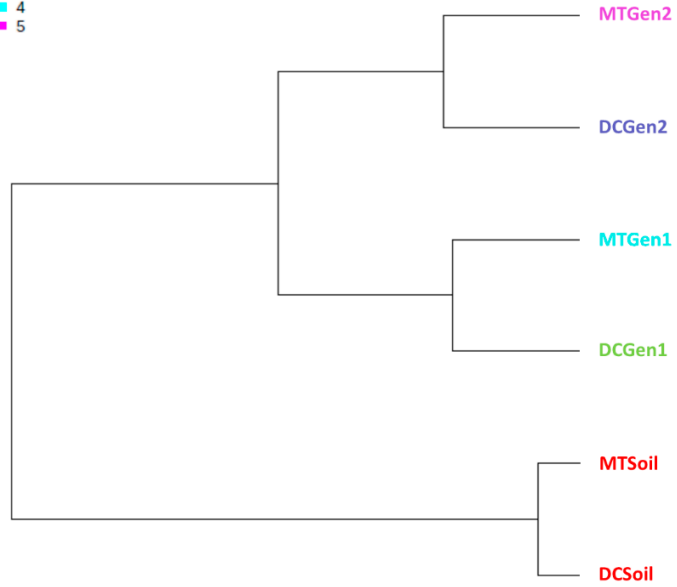
Category	Gene Homologue
Metal Resistance Proteins	Metal tolerance protein 10 ATP-dependent zinc metalloprotease FtsH Copper fist DNA binding domain protein Iron transport multicopper oxidase FET3 Putative Zinc finger CCHC-type protein Iron transport multicopper oxidase FET3 Siderophore iron transporter mirB Iron-sulfur assembly protein 2 Magnesium transporter NIPA2
Transporter Proteins	Tetracycline transporter General substrate transporter CDR ABC transporter ABC transporter substrate-binding protein ABC transporter ATP-binding protein Putative Monocarboxylate transporter
Cytochromes	Cytochrome P450 monooxygenase orf3 NADH-cytochrome b5 reductase 1 Cytochrome C biogenesis protein ResB
Drug Resistance	Multidrug resistance protein fnx1 Multidrug export protein EmrA
Efflux Pumps	Efflux pump FUB11 Efflux pump roqT Efflux pump FUS6 Efflux pump dotC Efflux pump dotC Efflux pump FUB11

Figure S1. A, shown are the bacterial core microbiome at the genus level identified using shotgun metagenomic libraries from the SRS soils. Genera at 50% prevalence cutoff value was used to generate the plot. Also shown are the dendrogram analysis at the bacterial genus level using the Bray-Curtis index and the ward clustering algorithm (B). Groups shown in the plots refer to the metadata in which soils used in DC and MT experiments were binned: group 1 (soils used for DC/MT); group 2 (DC Gen1), group 3 (DC Gen2), group 4 (MT Gen1) and group 5 (MT Gen2), respectively.



B

- 1
- 2
- 3
- 4
- 5



0.6 0.4 0.2 0.0

Figure S2. Shown are the (A), univariate statistical comparisons of *Burkholderia* spp., in soil (class 1) with Gen 1 DC/MT (class 2 and 3) and Gen 2 DC/MT (class 4 and 5) and (B), differential count analysis of *Burkholderia* spp., in soil (class 1) with Gen 1 DC/MT (class 2 and 3) and Gen 2 DC/MT (class 4 and 5).

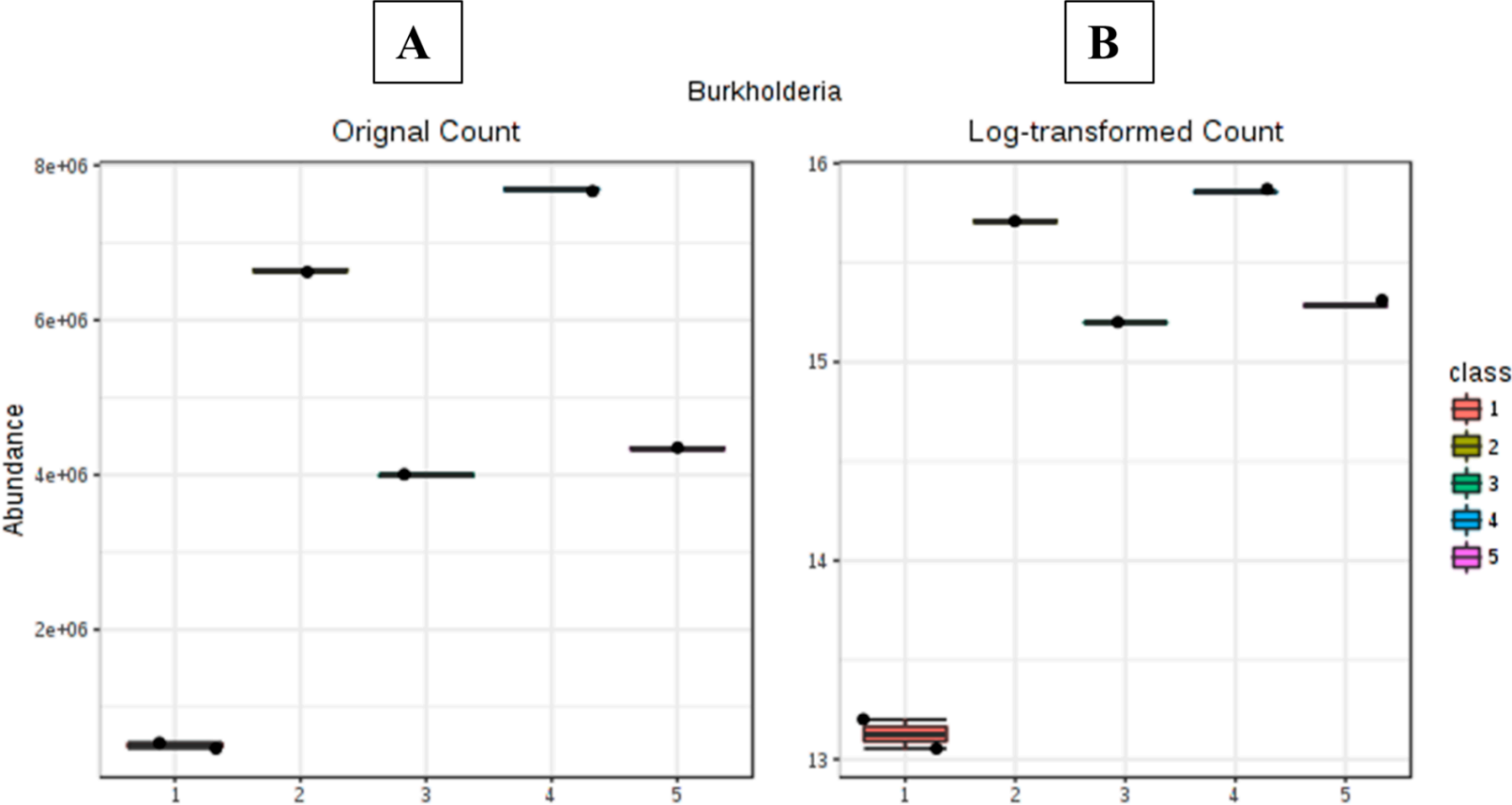
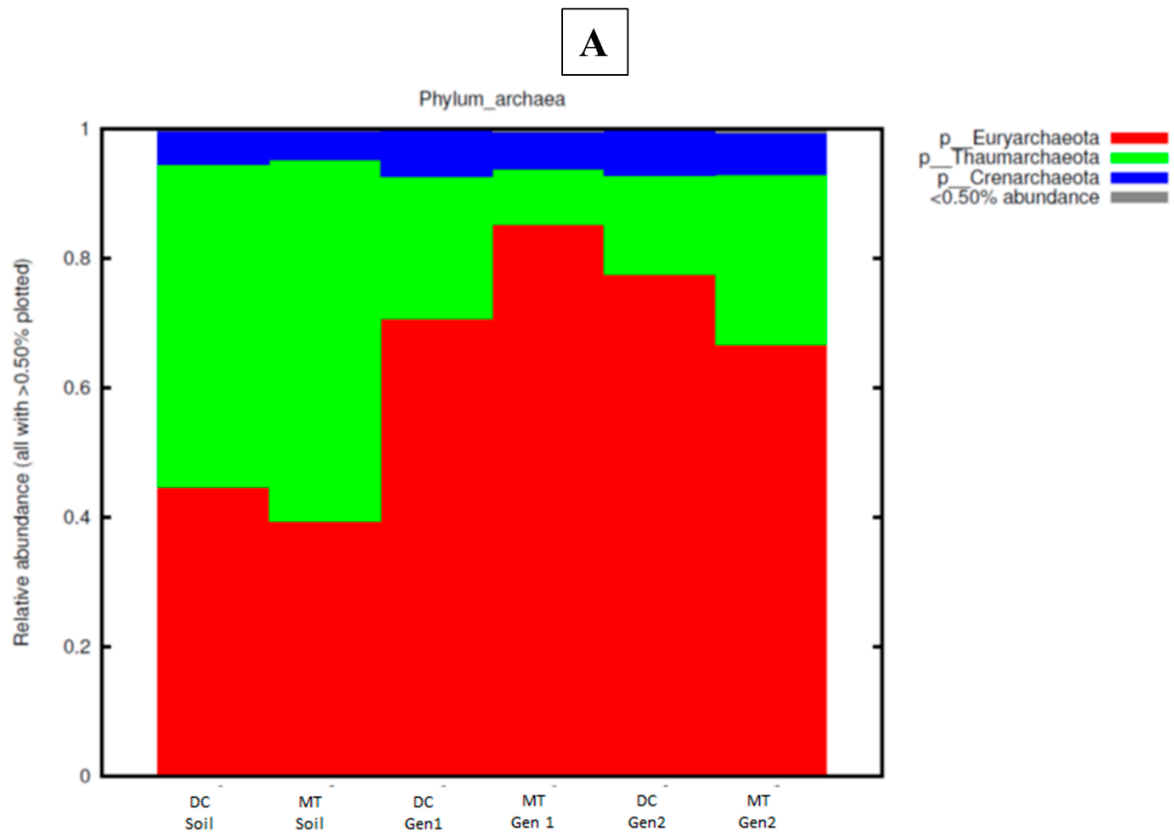


Figure S3. Archaeal relative abundance analysis shown at the phyla (A) and genus (B) levels identified from the soils and DC/MT chambers. Groups shown in the plots refer to the metadata in which soils used in DC and MT experiments were binned: group 1 (soils used for DC/MT); group 2 (DC Gen1), group 3 (DC Gen2), group 4 (MT Gen1) and group 5 (MT Gen2), respectively.



B

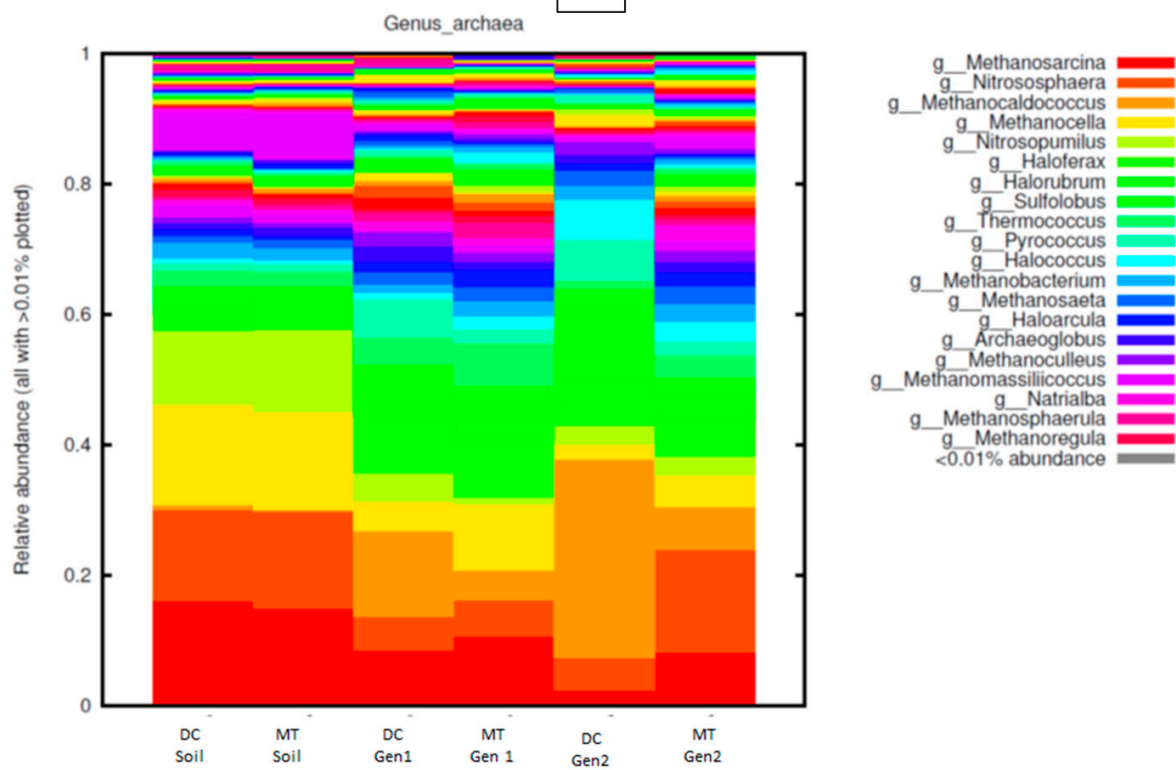
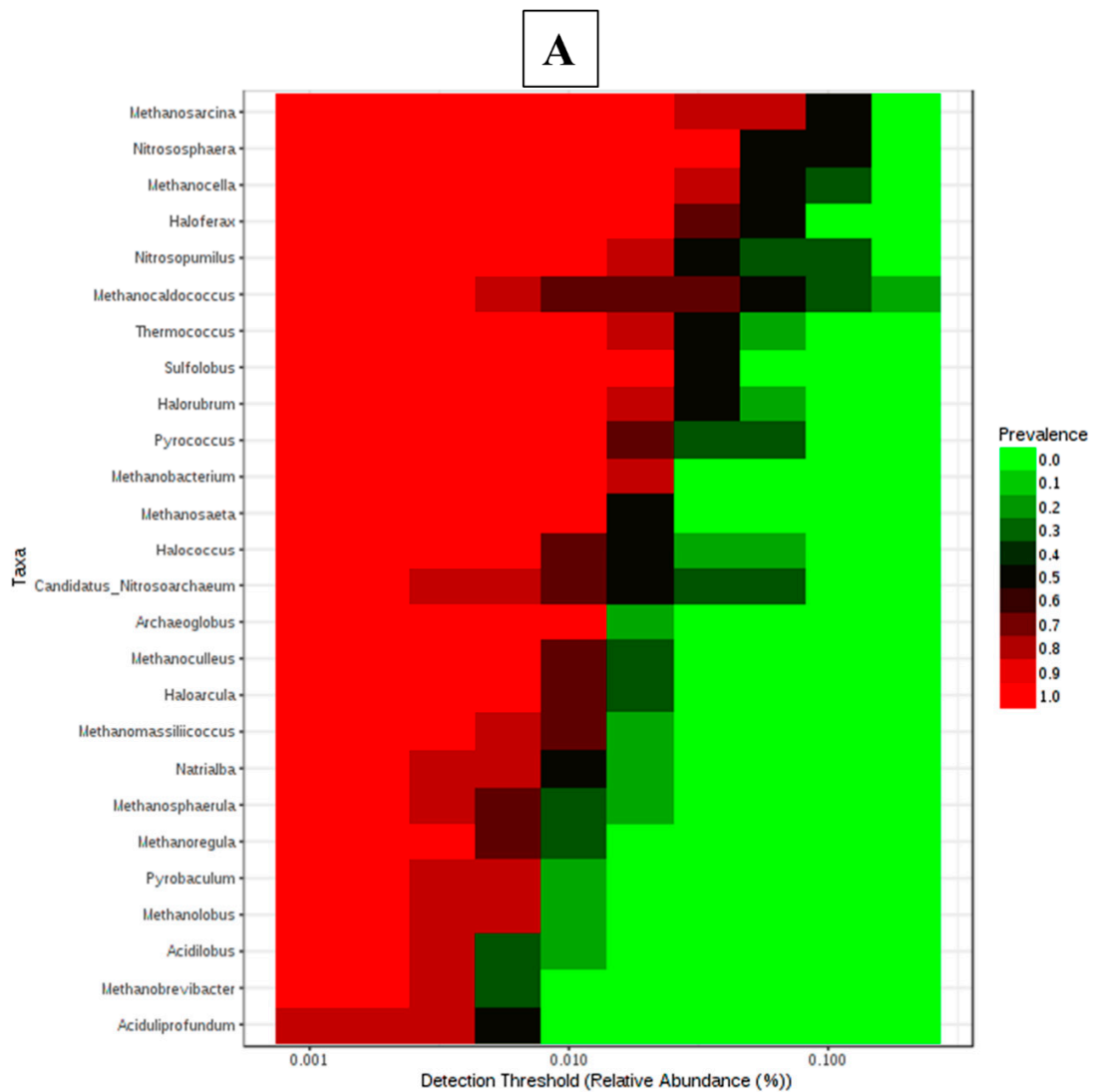


Figure S4. A, shown are the archaeal core microbiome at the genus level identified using shotgun metagenomic libraries from the SRS soils. Genera at 50% prevalence cutoff value was used to generate the plot. Also shown are the dendrogram analysis at the archaeal genus level using the Bray-Curtis index and the ward clustering algorithm (B). Groups shown in the figure refer to the metadata in which soils used in DC and MT experiments were binned: group 1 (soils used for DC/MT); group 2 (DC Gen1), group 3 (DC Gen2), group 4 (MT Gen1) and group 5 (MT Gen2), respectively.



B

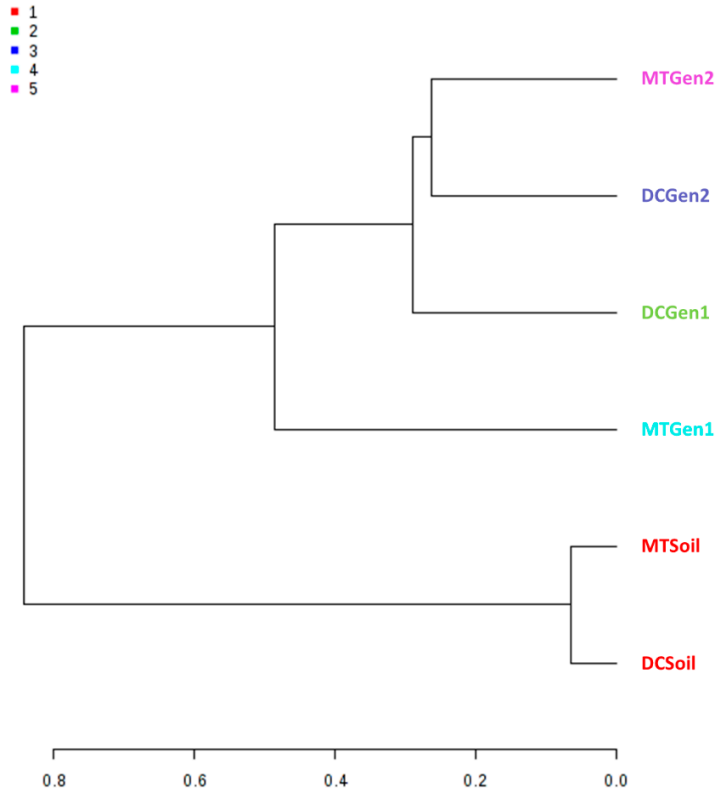
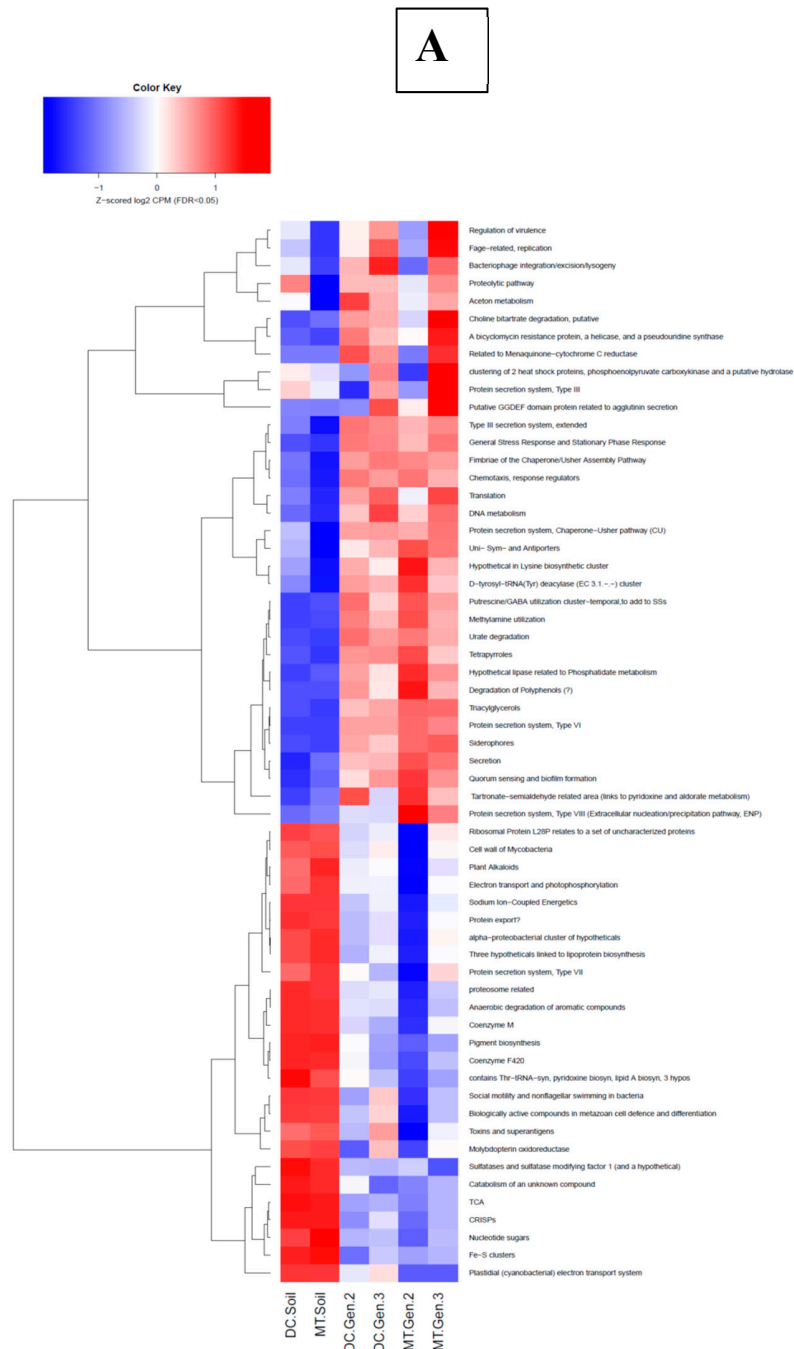
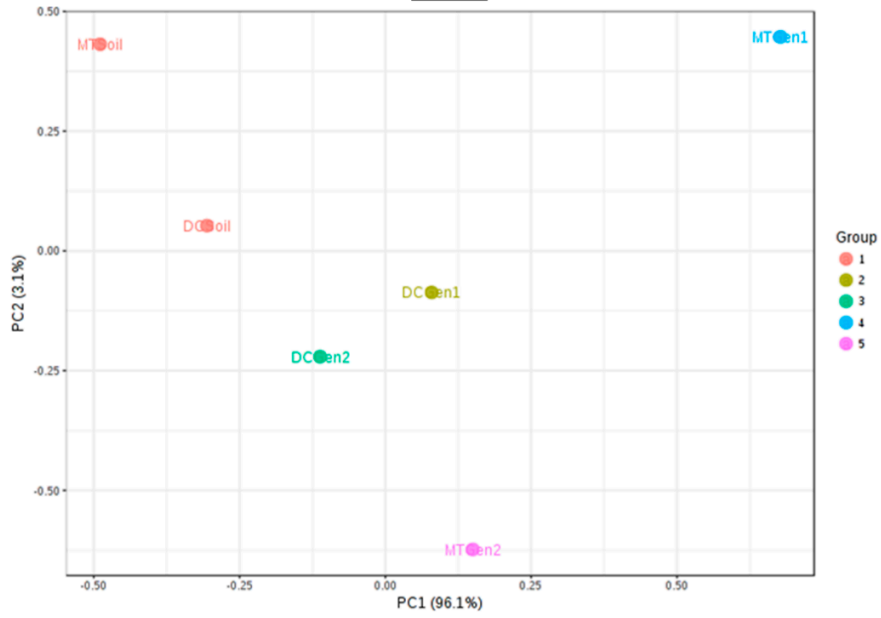


Figure S5. Shown is the heatmap analysis of gene functions identified from the SRS soils across different generations of DC/MT (A); the PCA statistical comparisons of gene functions identified in the SRS soils with different generations of DC/MT (B) and (C), the dendrogram analysis of gene functions using the unweighted UniFrac distance and ward clustering algorithm. Groups shown in the figure refer to the metadata in which soils used in DC and MT experiments were binned: group 1 (soils used for DC/MT); group 2 (DC Gen1), group 3 (DC Gen2), group 4 (MT Gen1) and group 5 (MT Gen2), respectively.



B



C

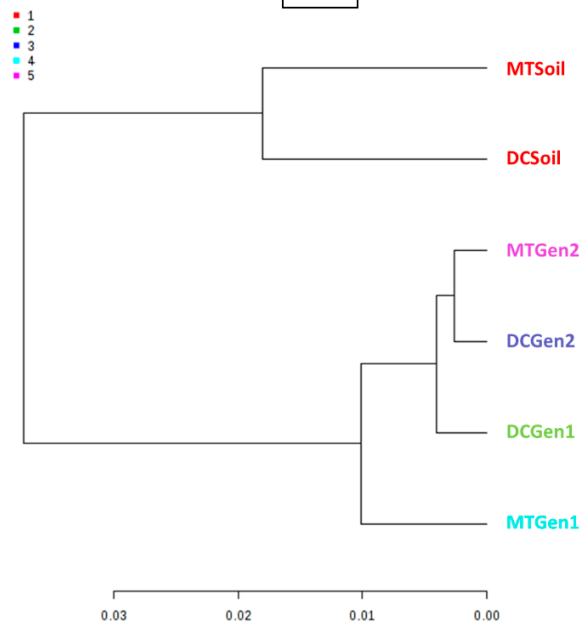
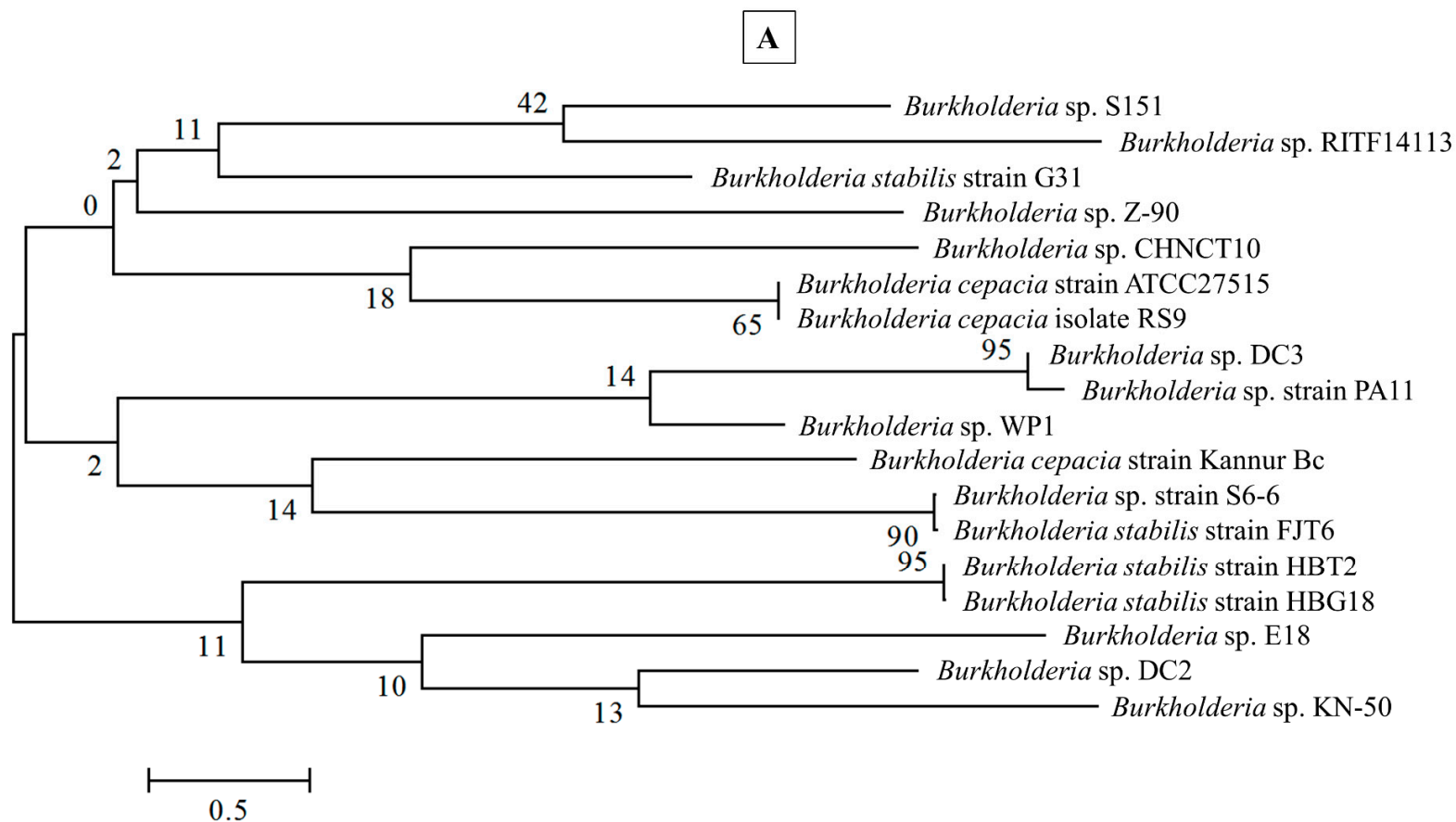


Figure S6. Shown is the 16S gene based phylogenetic tree of the isolated *Burkholderia* strains DC2 and DC3 relative to close taxonomic members (A). Also shown is the 18S gene based phylogenetic tree of isolated *Penicillium* strains DC2, DC3 and MT 2, respectively. The trees were constructed using neighbor joining bootstrap analysis in MEGA.



B

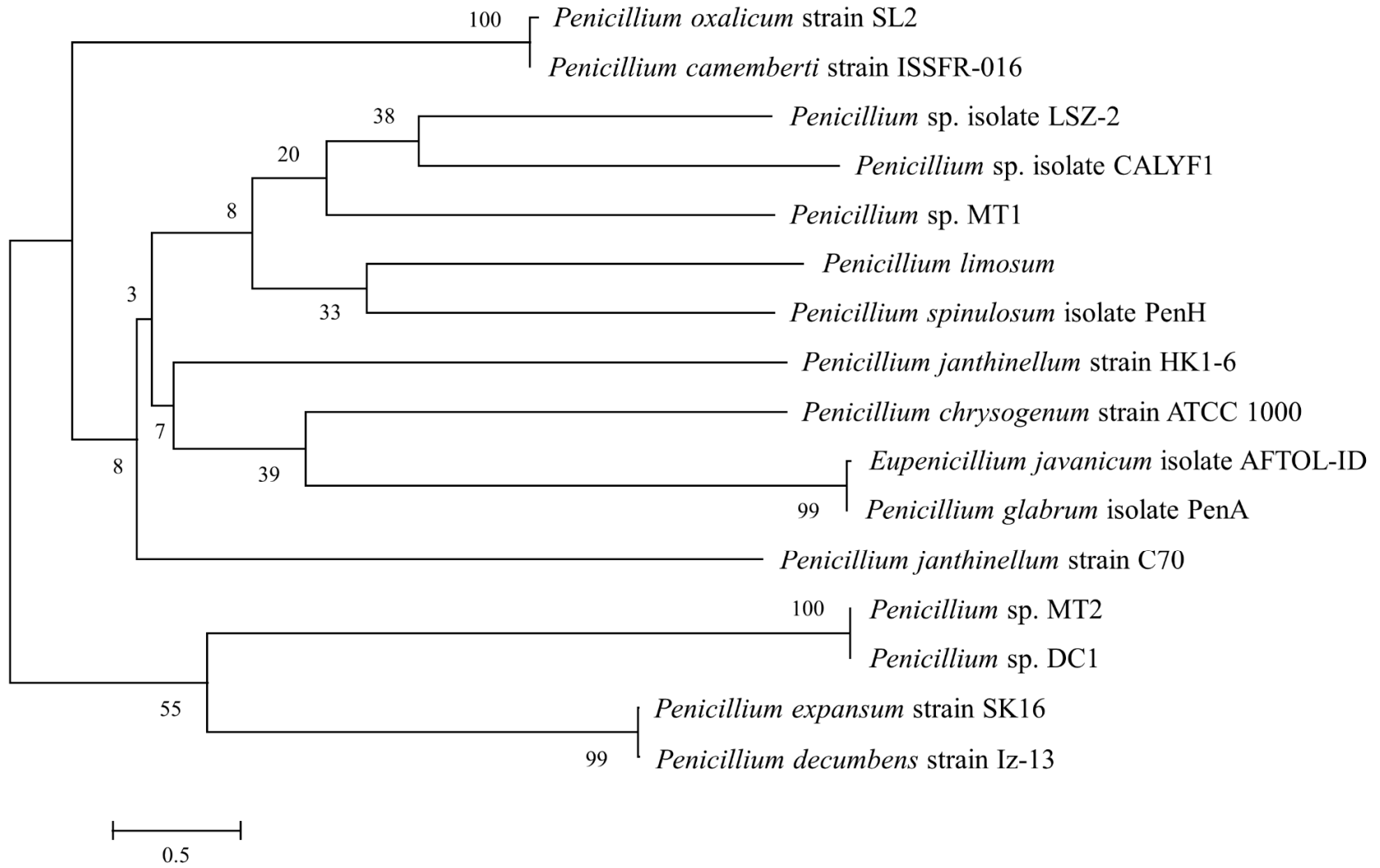


Figure S7. Whole genome sequence based synteny dot plots generated between *Penicillium* sp. strain MT2 and the closest phylogenetic neighbor *P. janthinellum* strain NCIMI366.

