

Supplementary Materials

Multiple Lines of Evidences Reveal Mechanisms Underpinning Mercury Resistance and Volatilization by *Stenotrophomonas* sp. MA5 Isolated from the Savannah River Site (SRS), USA

Table S1: List of primers and probes used for qRT-PCR analysis

Target gene	Forward primer	Reverse primer	Probe
16s	CTCGGAATTACTGGGCGT AAAG	CGCTACCCTCTACCACATT CTA	AACGGACTTAAACGACCAC CTACGC
<i>merA</i>	CCAAGTACGAAGGCATC CTG	TCGTTCAAACGGACGGTAA G	ACAACGGTGATGGCCGGAT TACC
<i>merD</i>	GGTGAGCGTGCATATCGT	TCATCGAACAAGCCGTAGC	TACCTGCTGCGCGGATTGCT
<i>merT</i>	CAAACCGGGTGAGGTCTG	TGGCATGACGTAGGGAAAT C	CCCAAGTGCGAGCTACTTAC AAGCT
<i>merE</i>	CGTCCGAGACGCACAAA	CACGACAGCGAGGATGG	ACTGGCTGTGCTGACTTGCC
<i>merR</i>	CGTGCTGTCTGAGTTGGT	CTAAGGCATAGCCGAACCT G	AAGCTTGCTCCACCCTGTAG TGAC
<i>merP</i>	AGTTGACGTGACTTTCGA GAC	CTTGACGCTGGACGGATAG	ACCTTCGACGATGCCAAGA CCAG

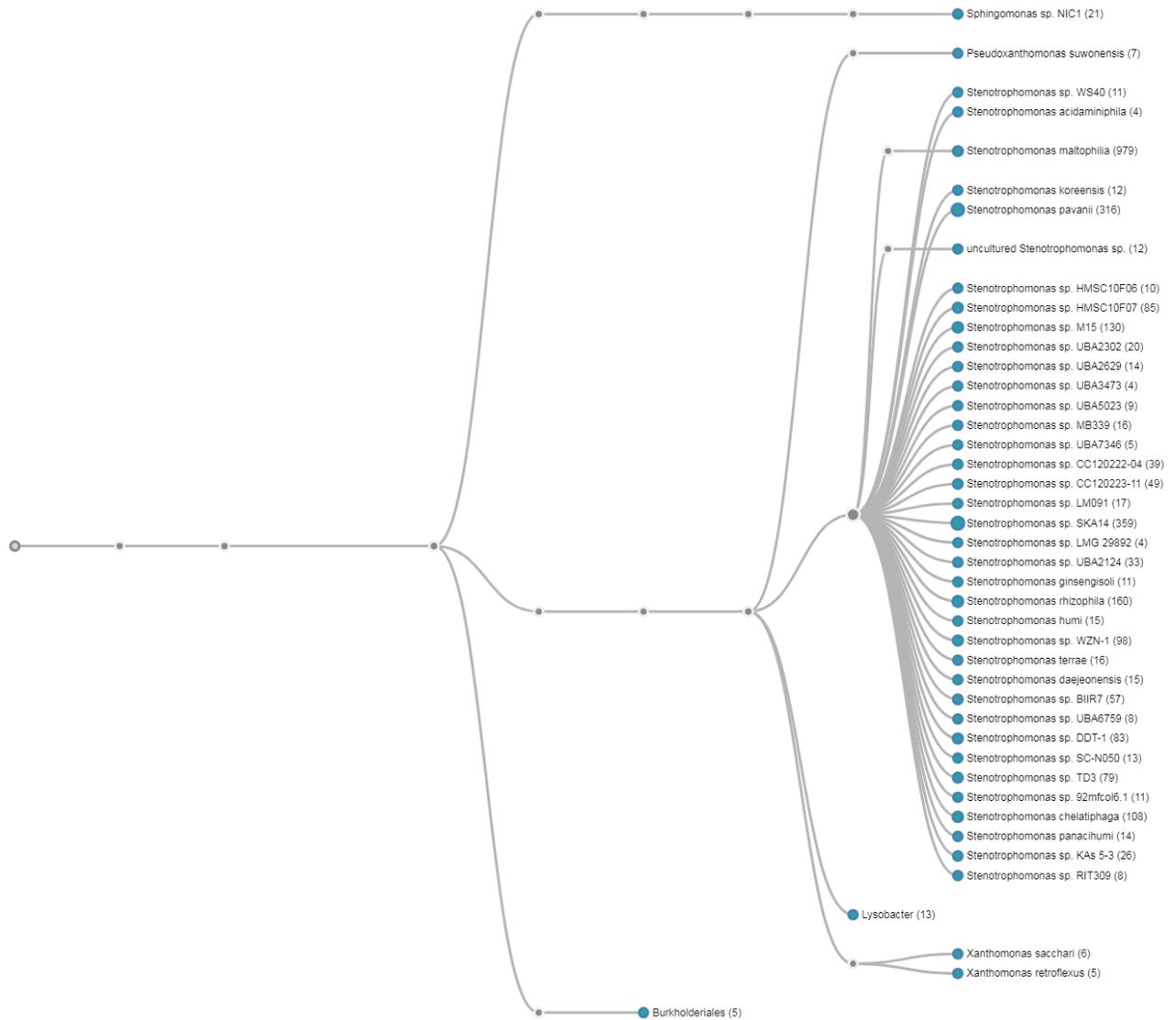


Figure S1: Whole genome sequence-based phylogenetic tree of isolated strain *Stenotrophomonas* sp. strain MA5. The highest taxonomic affiliation of strain was found with *Stenotrophomonas maltophilia* based on highest number of whole genome sequence reads (979; shown in parenthesis). Displayed nodes are those with at least 4 reads (<1% classified reads). This tree was generated by using one codex database.