

Table S2. Relative distribution of genus-level taxonomic bioindicators generated from a DWDS simulator. Values represent abundance (\pm SD) of each taxon as a ratio of all sequences obtained at each operational scheme.

Taxonomy groups (bioindicators)	Lineage	Stable [‡]	Failure
		SS ($n = 24$)	SF ($n = 16$)
Taxa A1	<i>Nitrospira</i>	0.0022 \pm 0.0013	0.0220 \pm 0.0171
Taxa A2	<i>Nitrosomonas</i>	0.0046 \pm 0.0047	0.0495 \pm 0.0383
Taxa A3	<i>Erythromicrobium</i>	0.0012 \pm 0.0010	0.1079 \pm 0.0950
Taxa A4	<i>Sphingomonas</i>	0.0228 \pm 0.0244	0.1391 \pm 0.0446
Taxa A5	<i>Hyphomicrobium</i>	0.0053 \pm 0.0034	0.2217 \pm 0.1733
Taxa B1	<i>Bradyrhizobium</i>	0.0311 \pm 0.0129	0.0038 \pm 0.0040
Taxa B2	<i>Sphingopyxis</i>	0.0365 \pm 0.0431	0.0044 \pm 0.0063
Taxa B3	<i>Mycobacterium</i>	0.4877 \pm 0.2137	0.1071 \pm 0.0612

[‡]Operational schemes: **SS** = stable chloramine residual; **SF** = complete nitrification and minimal chloramine residual