

Supplementary material

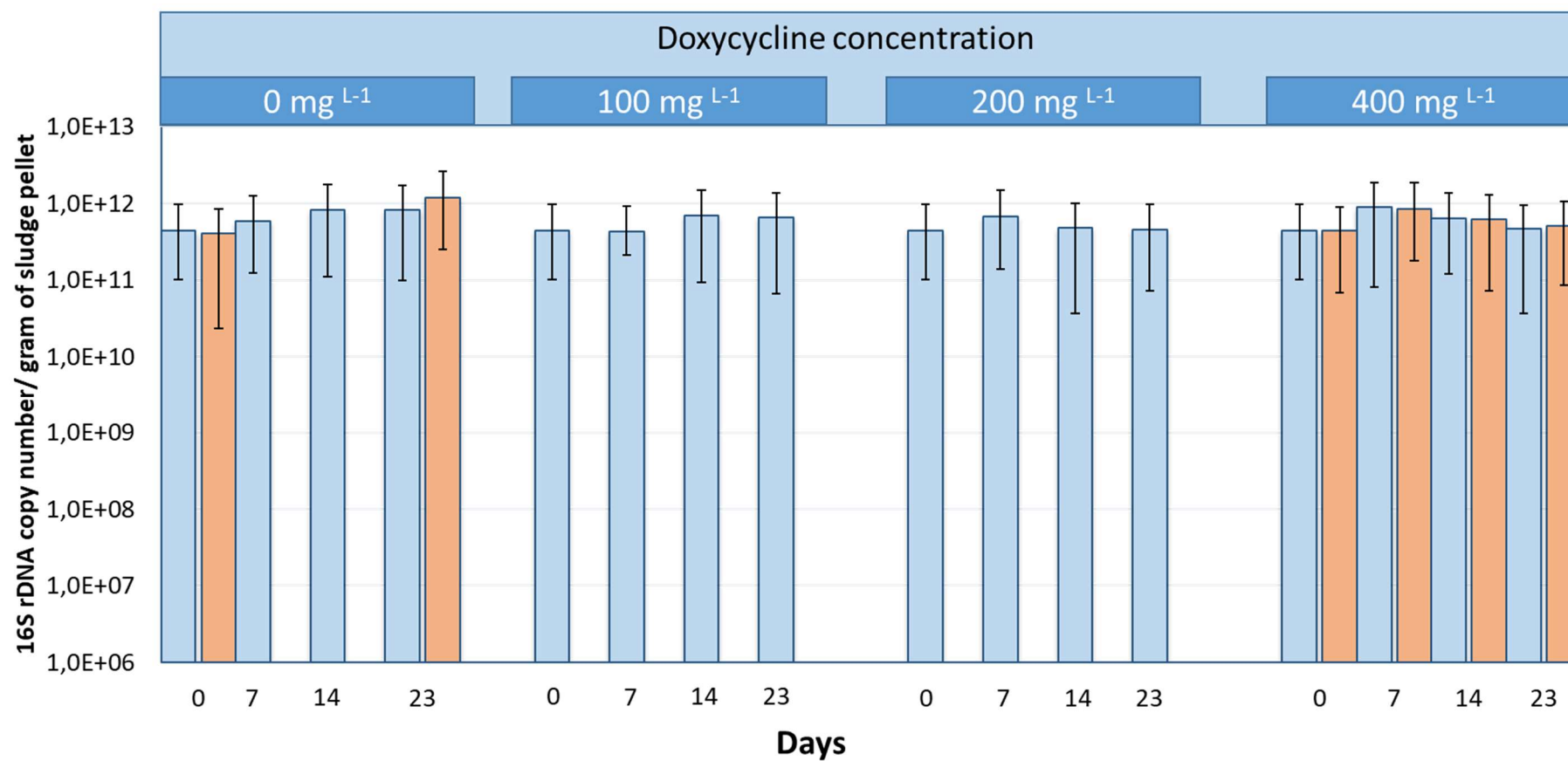


Figure S1: Real time qPCR quantification of the total *Bacteria* according to incubation time and doxycycline concentration. Data are presented as a mean of 6 replicates and minimum and maximum values.

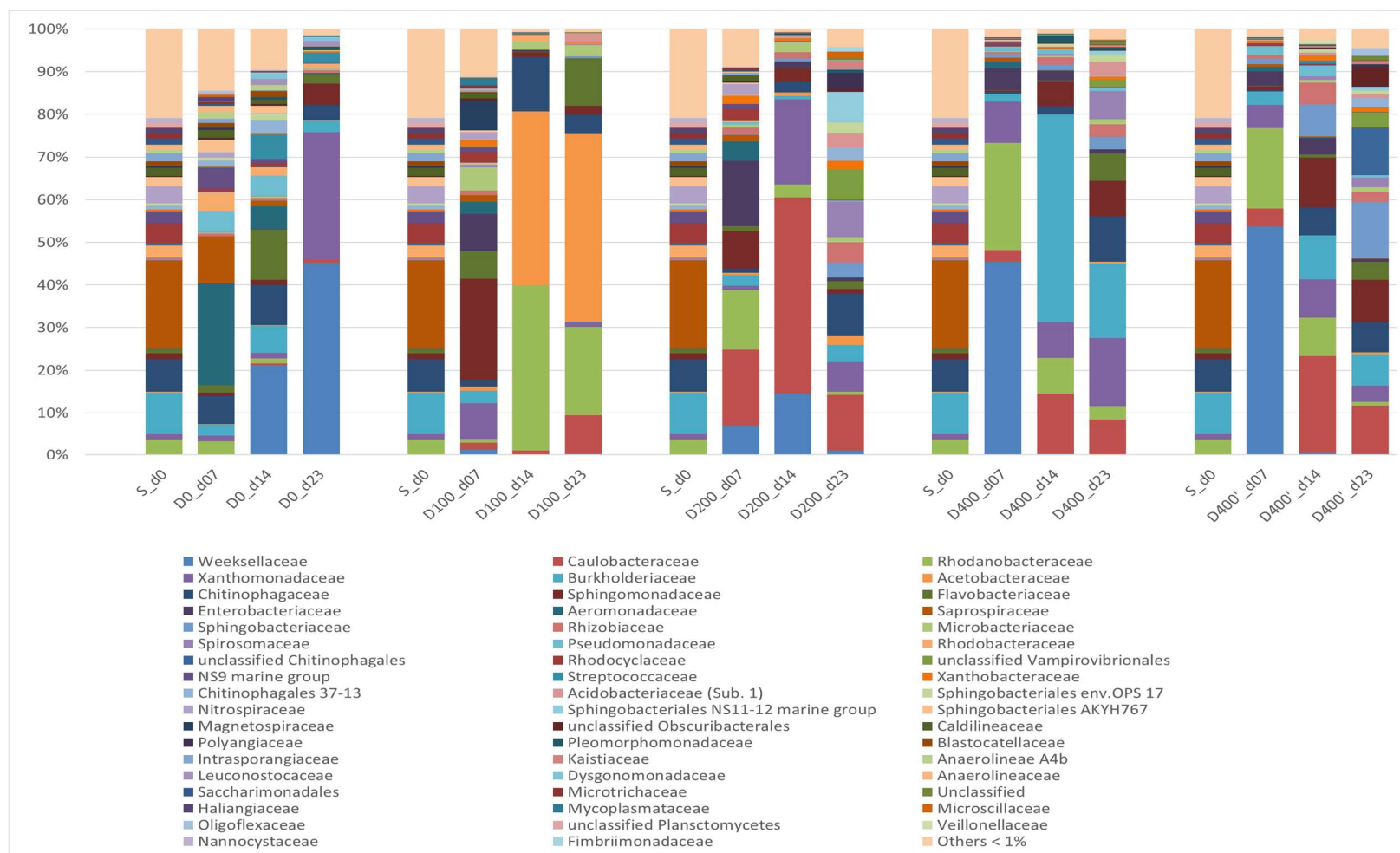


Figure S2: Relative abundance of the different bacterial families according to incubation time and doxycycline concentration. Legend is the same as in Figure 4.

**Table S1. Closest relatives of the microbial populations proposed as representative of sludge variability by PCA of sludge microbial community structures**

	Identification	Acc. Number	% similarity
<b>Day 0</b>			
Cluster_14	Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales; Aeromonadaceae; Tolumonas; Tolumonas auensis	CP001616	100.0
Cluster_26	Bacteria; Bacteroidetes; Bacteroidia; Chitinophagales; Saprospiraceae; unknown genus; unknown species	EU177709	100.0
Cluster_20	Bacteria; Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Nitrospira; Nitrospira defluvii	FP929003	100.0
<b>DC 100</b>			
Cluster_3	Bacteria; Proteobacteria; Alphaproteobacteria; Acetobacterales; Acetobacteraceae; Nguyenibacter; Gluconacetobacter-like organism	AF127400	99.5
Cluster_9	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Dyella; Dyella sp.	FN178370	99.2
Cluster_9	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Frateuria; Frateuria aurantia	AB680411	99.2
Cluster_2	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; SN8; unknown species	EF515229	100.0
<b>DC 400</b>			
Cluster_5	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas; Brevundimonas sp.	DQ341416	99.7
Cluster_6	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Rhodanobacteraceae; Luteibacter; Luteibacter anthropi	FM212561	100.0
Cluster_4	Bacteria; Bacteroidetes; Bacteroidia; Flavobacteriales; Weeksellaceae; Chryseobacterium; Candidatus Chryseobacterium massiliae	FJ812379	100.0
Cluster_10	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Lysobacter; Lysobacter novalis	KM658501	100.0
Cluster_11	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; Burkholderiaceae; Pelomonas; metagenome	FPLS01009417	100.0
Cluster_11	Bacteria; Proteobacteria; Gammaproteobacteria; Betaproteobacteriales; Burkholderiaceae; Roseateles; Mitsuraria sp.	AB560535	100.0
Cluster_13	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium; Novosphingobium sp.	AJ746093	100.0
Cluster_25	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Stenotrophomonas; Stenotrophomonas maltophilia	KP790032	100.0

Cluster_17	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas; Sphingomonas leidyi	JQ723715	100.0
Cluster_16	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Citrobacter; Citrobacter braakii	HQ288930	100.0
Cluster_16	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Enterobacter; unknown species	GQ417323	100.0