Supporting materials

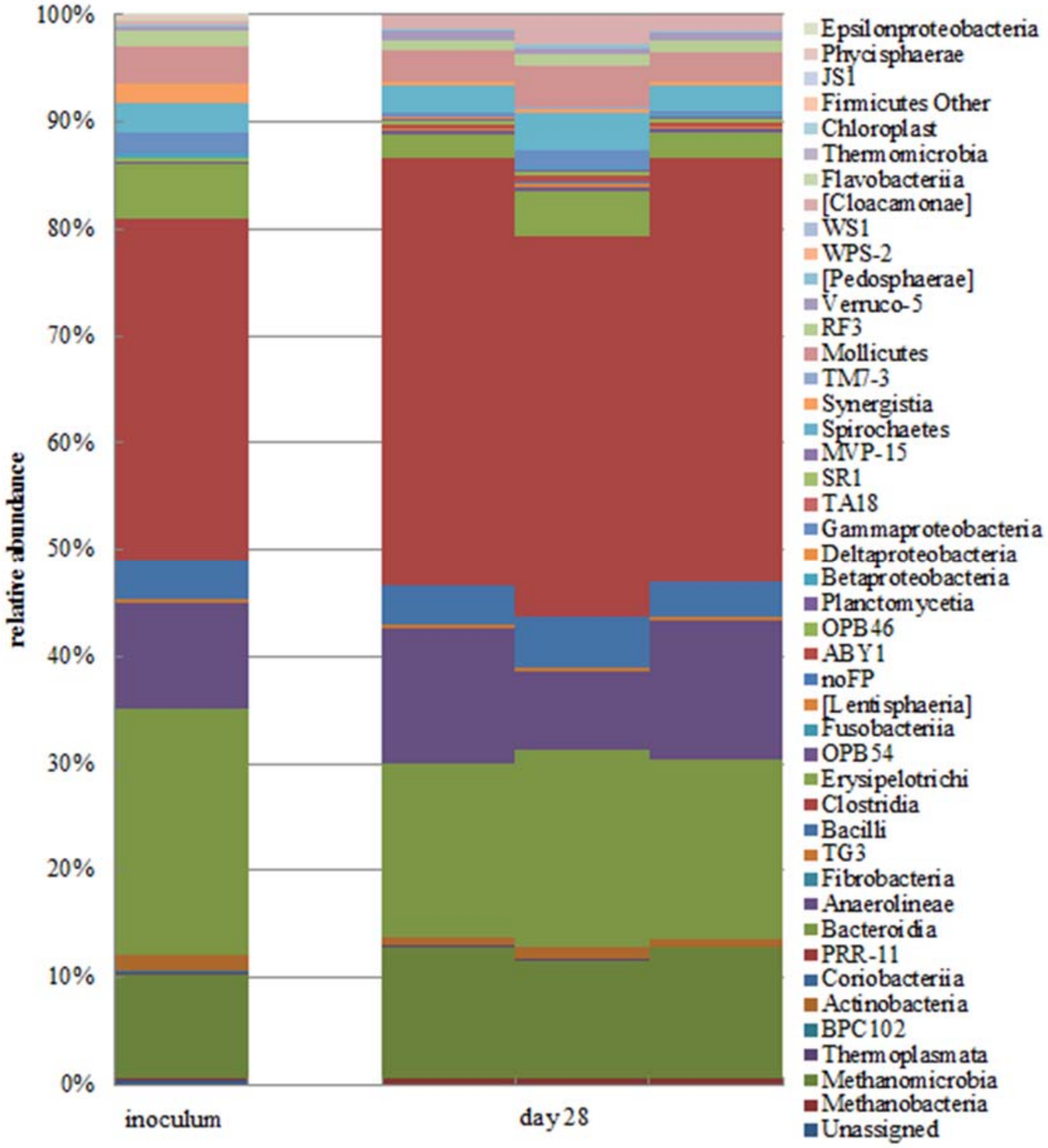

Fig. A1 Comparison of relative abundance of bacterial classes within the inoculum used for digester start-up and digestate sampled from R1, R2 and R3 on day 28

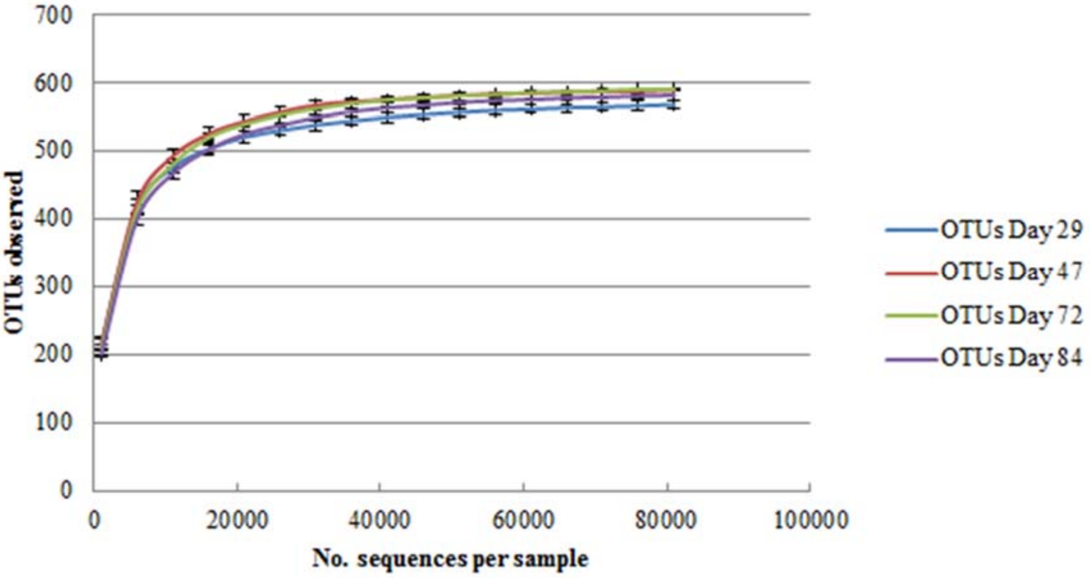

Fig. A2 Rarefaction curves for each sampling day. Error bars denote standard deviation

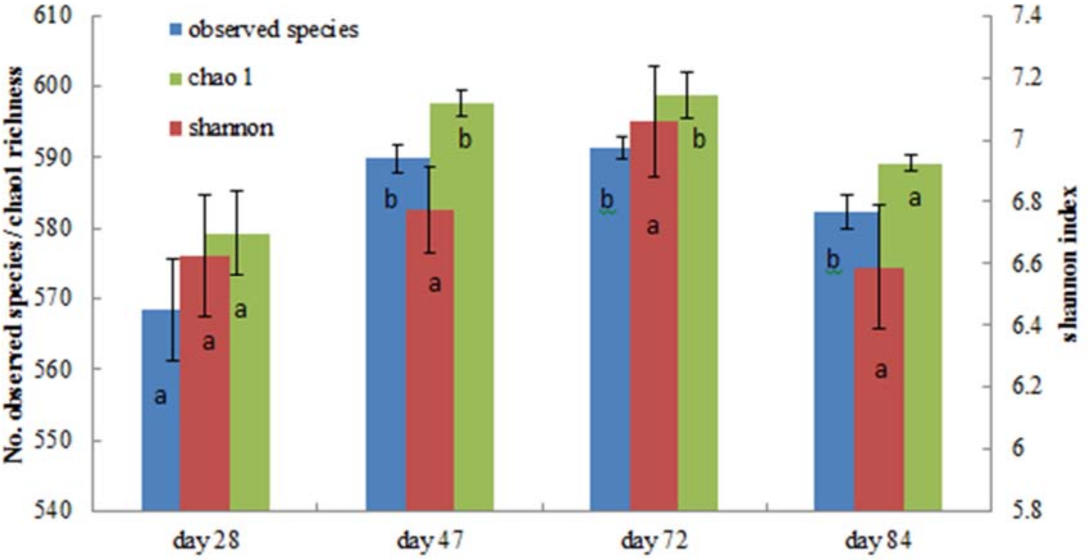

Fig. A3 Shannon index, Chao 1 species richness and number of observed species measured at each sampling point. Values are the mean of three replicates with error bars representing standard deviations. Within each time point, bars sharing a common letter are not significantly different (*P* > 0.05), as measured by the Bonferroni method

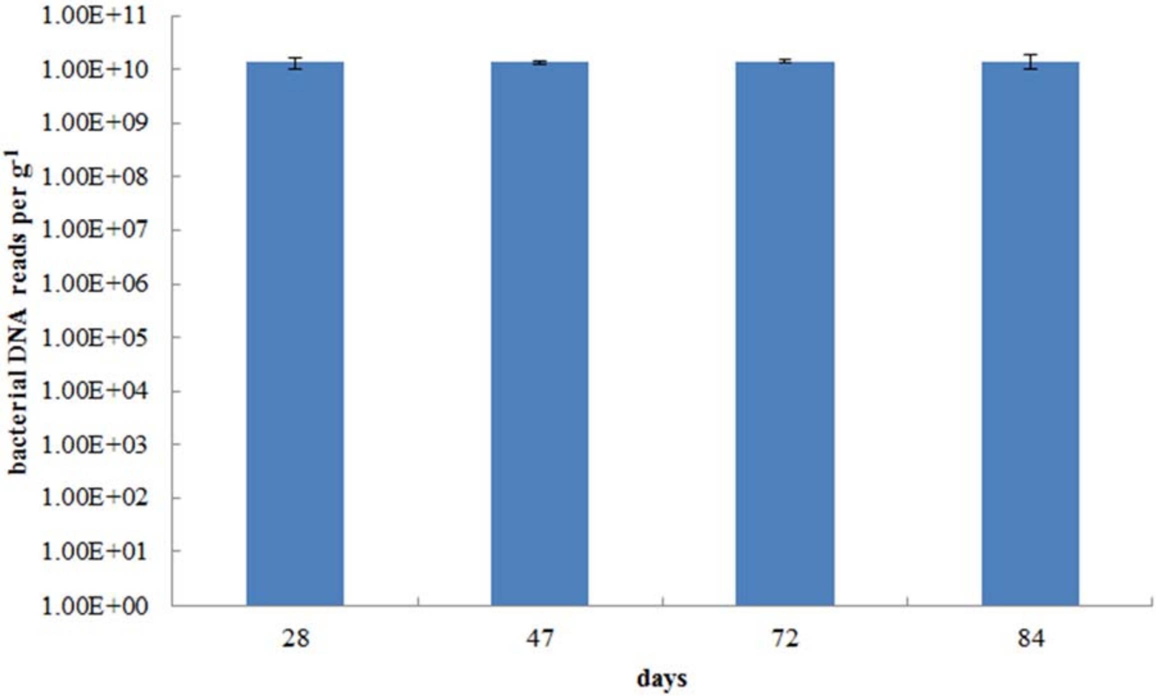

Fig. A4 Bacterial DNA reads per g of digestate as measured by qPCR at each sampling point. Values are the mean of three replicates with error bars representing standard deviations