Figure S2: Overall microbiome detected across all samples. For each family detected in the microbiome one eOTU with the most drastic change in abundance from biofilm to string-of-pearls community was selected. In case eOTUs within one family behaved non-uniformly, two eOTUs with the most drastic increase and decrease in abundance were selected. HybScores were normalized as z-scores individually for each eOTU across all samples. An idealized tree based on taxonomic assignments was computed and OTUs belonging to the nine major phyla were colored differently from other phyla that are colored in petrol.