Supplemental Figures

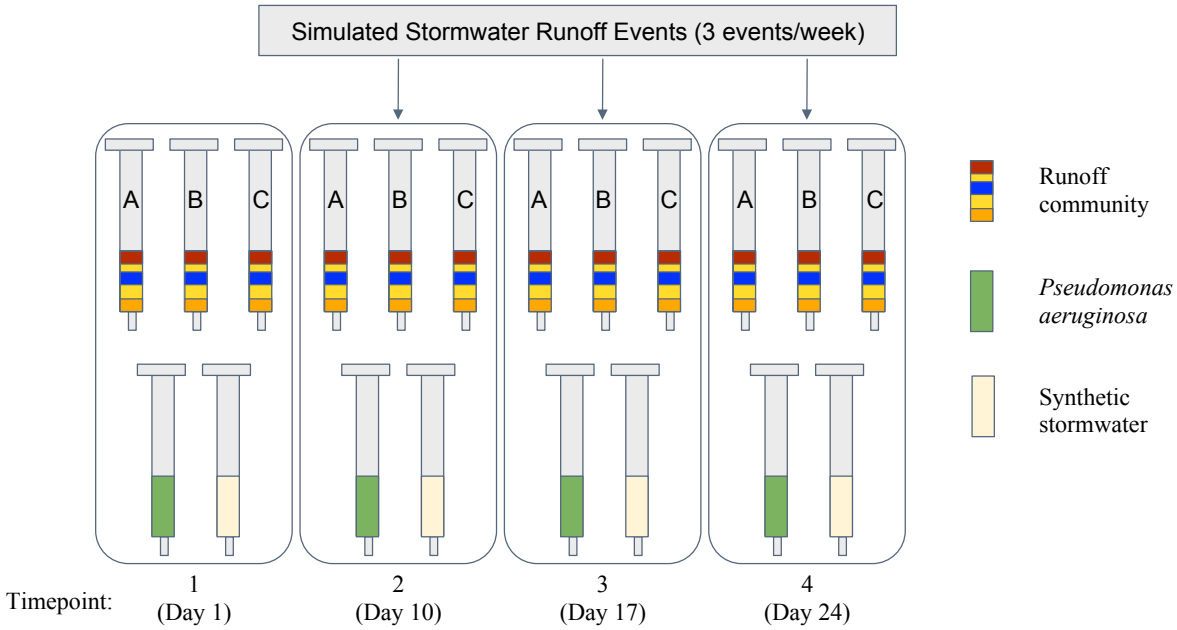

Figure S1. Diagram of experimental plan. A total of 20 columns were analyzed over a 24-day period. On day one, twelve columns were inoculated with stormwater run-off (multi-colored columns), four were inoculated with *Pseudomonas* (green) and four with sterile synthetic stormwater media (cream). After inoculation, day 1 columns were analyzed. Synthetic sterile stormwater was added to the remaining columns 3 times per week to simulate storm events. The columns were analyzed on day 10, 17 and 24 for microbial community analysis and gene quantification.

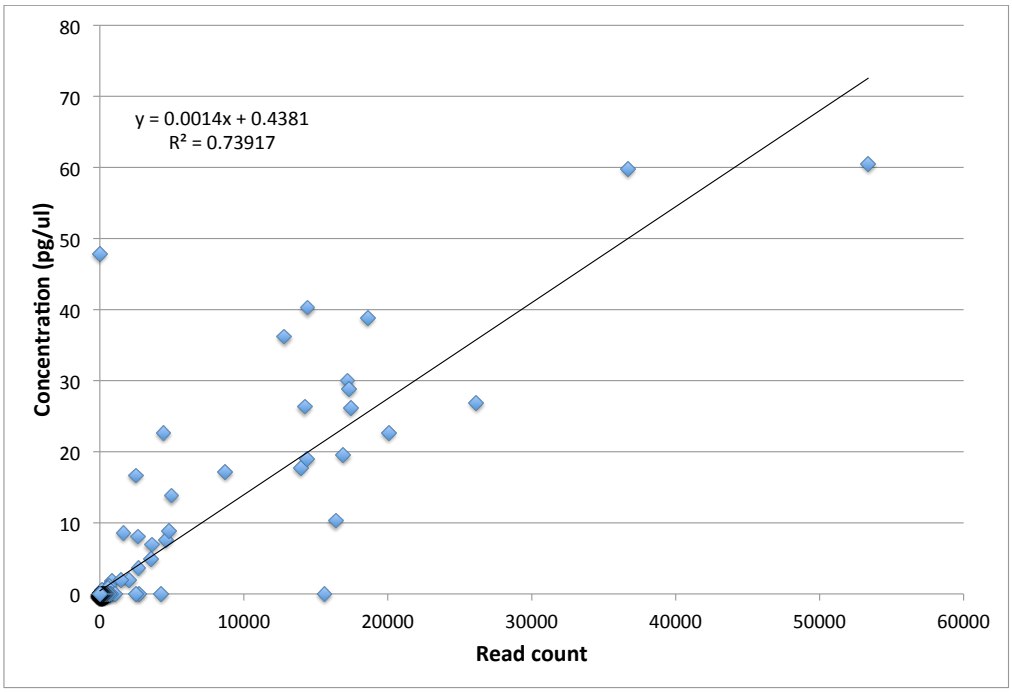

Figure S1. Relationship between input concentration and resulting read count for mock community sequences. Mock community templates were quantified and added together. The resulting total number of reads in the sample correlated to the input concentration for most templates. One template was not observed in the final dataset because it was flagged as a chimera and removed. Another sequence was not a 16S rRNA gene sequence and was removed during subsequent analysis. By analyzing the relationship between the input concentration and resulting read count, we adjusted the analysis parameters to improve correlation (R^2=0.88).

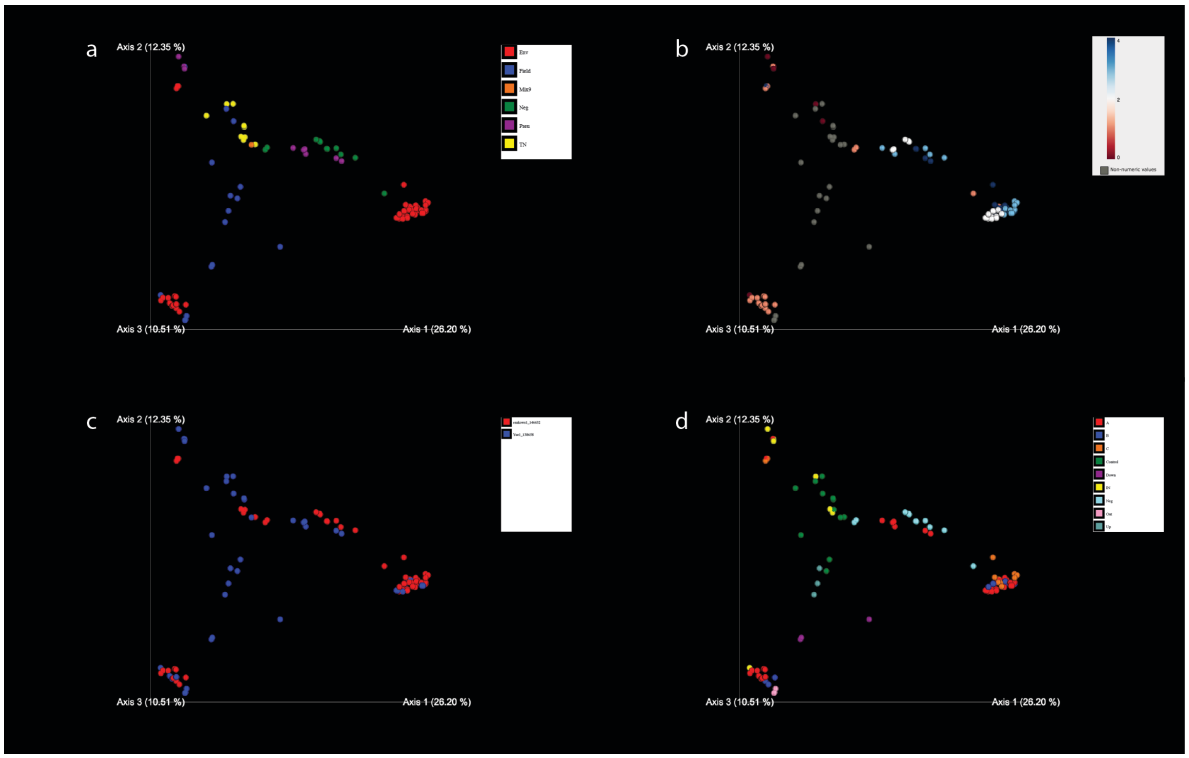

Figure S2. Principle coordinates analysis of all samples colored according to various categories. a.) Colored according to sample type, including column samples (Env, red; Pseu, purple; Neg, Green), environmental samples (Field, blue) and controls (TN, yellow). b.) Colored according to time after inoculation. Input samples in dark red (inoculum), column day 1 samples in pink (week 1), after 10 days (week 2), 17 days (week 3) and 24 days (week 4). Field samples and negative controls not added to the column are in gray. c.) Samples colored according to the two different batches of samples processed and sequenced together. The environmental samples cluster into distinct groups that cannot be explained by batch effects. d.) Samples colored according to replicate description (A, B or C) or field type (Up, Down, Out). Replicate columns were arbitrarily assigned A (red), B (blue) or C (orange), although this designation only describe true biological replicates within week and column type. Control (green) includes positive and negative controls. In (yellow) indicates input inoculum for the environmental, negative and *Pseudomonas* columns. Up (light green) and Down (purple) indicate field samples taken around the outfall and are distinct from the outfall samples (Out, pink) used on the columns.

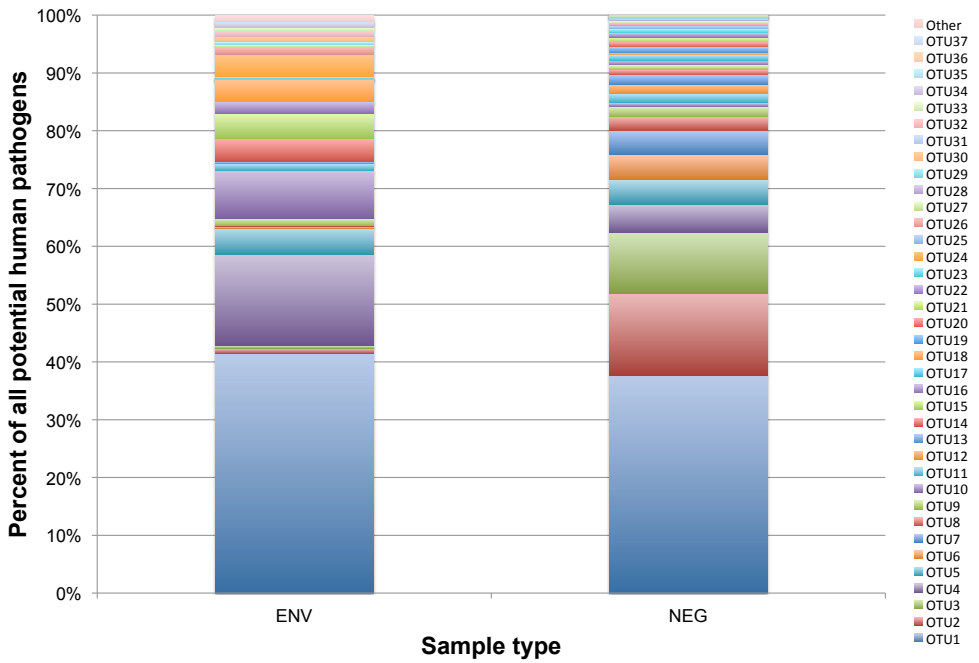

Figure S3. Potentially pathogenic OTUs in stormwater inoculated columns (ENV, left) and non-inoculated columns (Neg) across all time periods. The relative abundance of all OTUs with taxonomic classifications identified as human pathogens by FAPROTAX across all time periods are displayed. OTU composition is slightly different between inoculum types, although the groups share many OTUs. The most abundant OTU (OTU1) is similar to *Stenotrophomonas acidaminiphila*, suggesting that it may have come from the laboratory environment, rather than directly from stormwater. Other OTUs more common in the stormwater columns than the non-inoculated columns (e.g. OTU4, OTU10, OTU14) are classified as *Acinetobacter* and could have originated from the stormwater community.