Supporting Information for

Human-associated fecal qPCR measurements and simulated risk of gastrointestinal illness in recreational waters contaminated with raw sewage

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Human qPCR Marker Concentration Estimates in Raw Sewage

Shanks et al.[1] previously reported concentrations of HF183 and HumM2 qPCR markers in raw sewage collected from 54 wastewater treatment plants throughout the United States. Results were reported as the estimated $\log_{10}$ copies (cp) per ng total nucleic acids. The concentration of total nucleic acids was measured for each DNA extract using a NanoDrop ND-1000 UV spectrophotometer (NanoDrop Technologies, Wilmington, DE) as previously reported [1]. Using this concentration (ng total nucleic acids per µL of DNA extract), the total elution volume (100 µL), and the volume of sewage filtered (25 mL per sample), the concentration of each human qPCR marker in cp/mL sewage was estimated. The distribution of estimated concentrations for the two human-associated qPCR markers is shown in Figure S1.

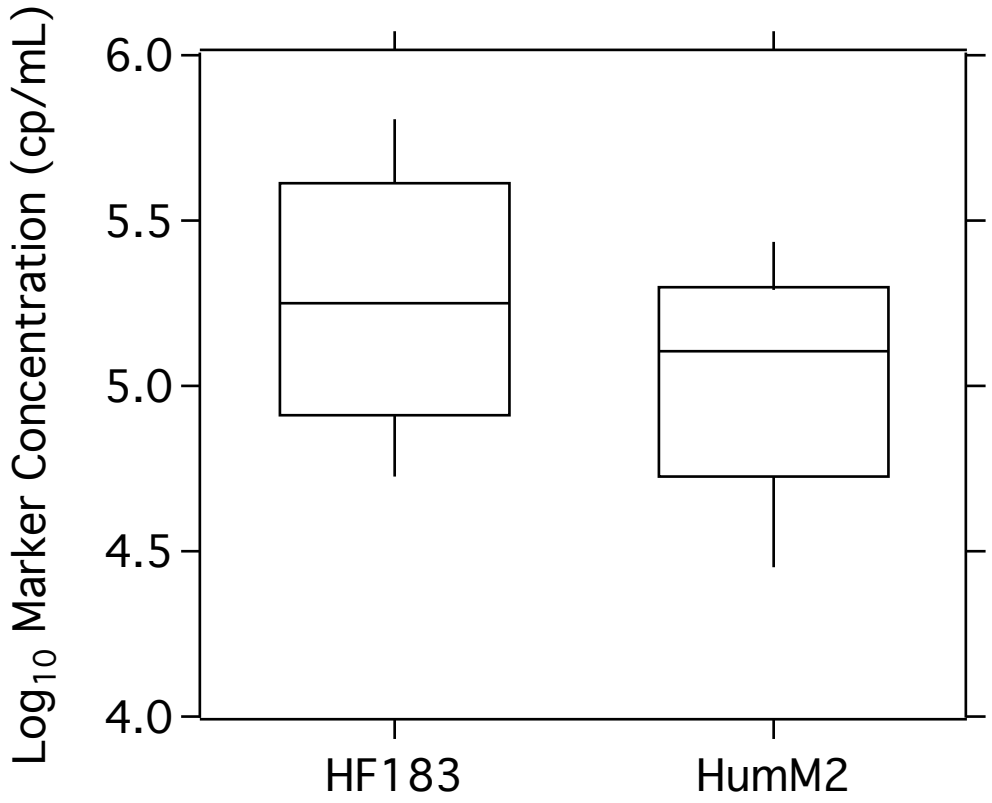

Figure S1. Distribution of human-associated qPCR markers in sewage at 54 geographical locations across the US. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively).

GI Illness Risk From Exposure to Individual Pathogens

The risk of GI illness from exposure to each of the individual pathogens is shown in Figures S2-S7.

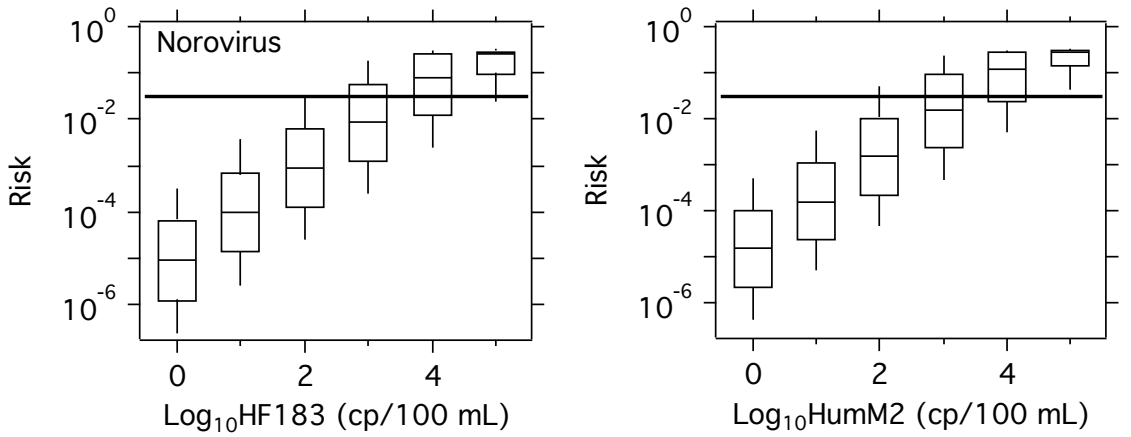

Figure S2. Left panel. GI risk from norovirus as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from norovirus as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

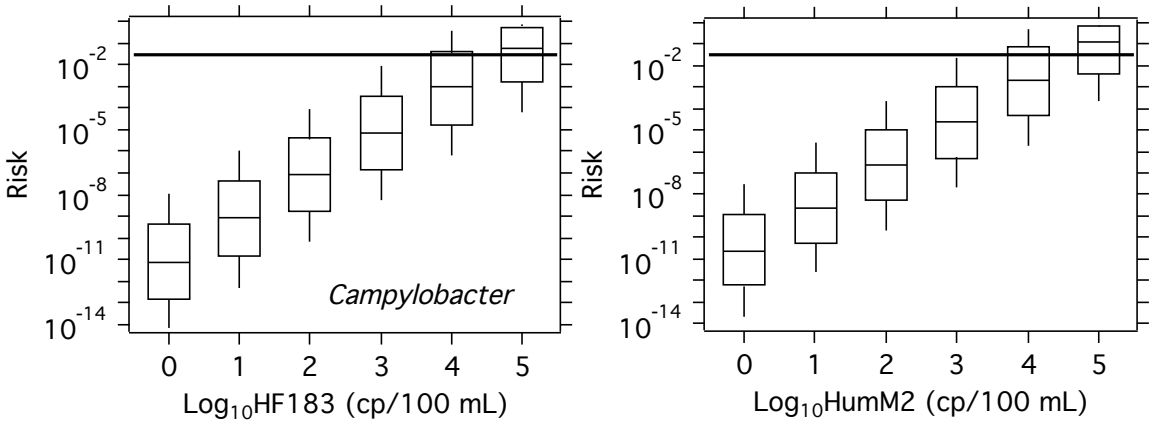

Figure S3. Left panel. GI risk from *Campylobacter* as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from *Campylobacter* as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

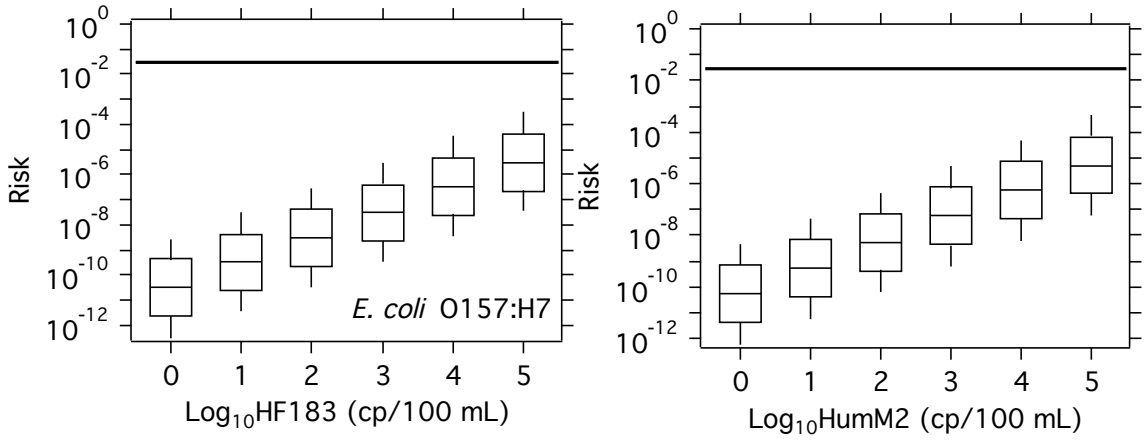

Figure S4. Left panel. GI risk from *E. coli* O157:H7 as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from *E. coli* O157:H7 as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

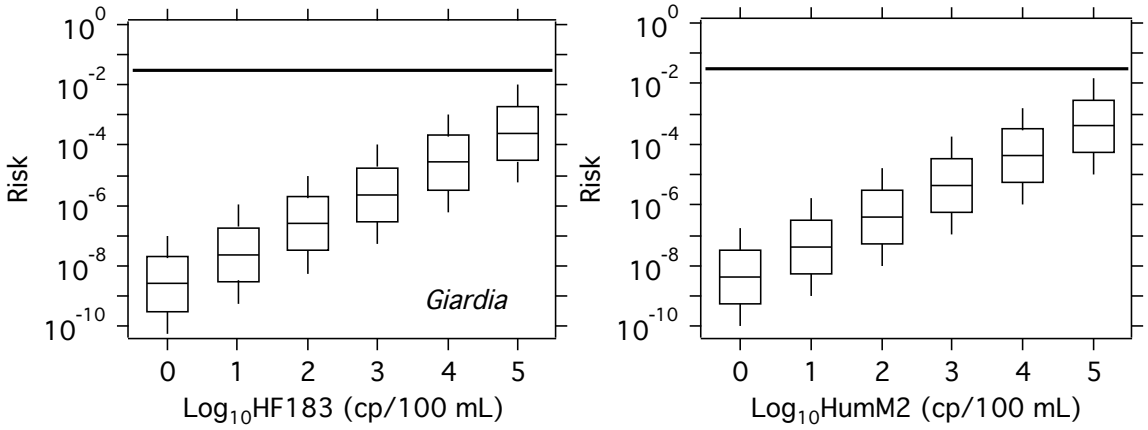

Figure S5. Left panel. GI risk from *Giardia* as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from *Giardia* as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

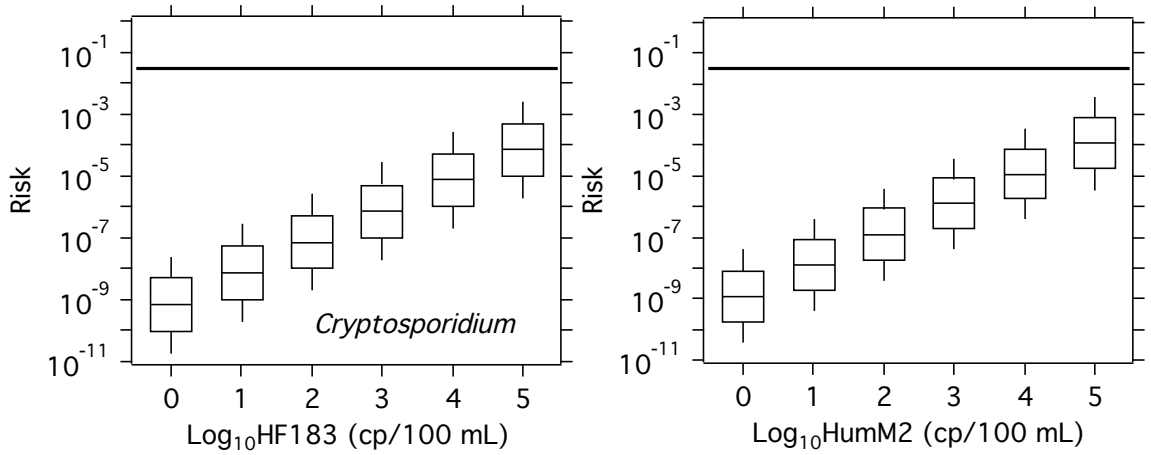

Figure S6. Left panel. GI risk from *Cryptosporidium* as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from *Cryptosporidium* as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

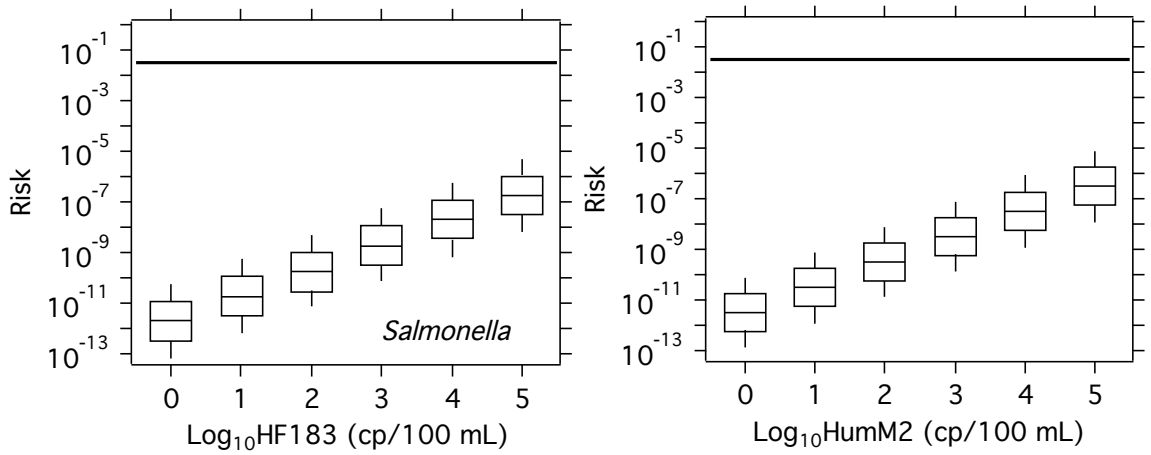

Figure S7. Left panel. GI risk from *Salmonella* as a function of concentration of HF183Taqman marker in ambient water. Right panel. GI risk from *Salmonella* as a function of concentration of HumM2 marker in ambient water. cp is copy. Box and whiskers indicate median (line in middle of box), 25th and 75th percentile (bottom and top of box, respectively), and 10th and 90th percentile (bottom and top of whisker, respectively). The horizontal line indicates a risk of 0.03 which is approximately the USEPA benchmark risk of ~30 GI per 1000 swimmers.

References

(1) Shanks, O. C.; White, K.; Kelty, C. A.; Sivaganesan, M.; Blannon, J.; Meckes, M.; Varma, M.; Haugland, R. A. Performance of PCR-Based Assays Targeting

101 Bacteroidales Genetic Markers of Human Fecal Pollution in Sewage and Fecal
102 Samples. *Environ. Sci. Technol.* **2010**, *44* (16), 6281–6288.
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