

Note: Data shown here are  
preliminary, and not to be cited.

# Microbial Source Tracking in the Love Creek Watershed of Delaware's Inland Bays

Christopher R. Main, Sergio Huerta, Robin M. Tyler  
Department of Natural Resources and Environmental Control  
Division of Water, Environmental Laboratory Section

Naomi S. Bates, A. Scott Andres  
The Delaware Geological Society



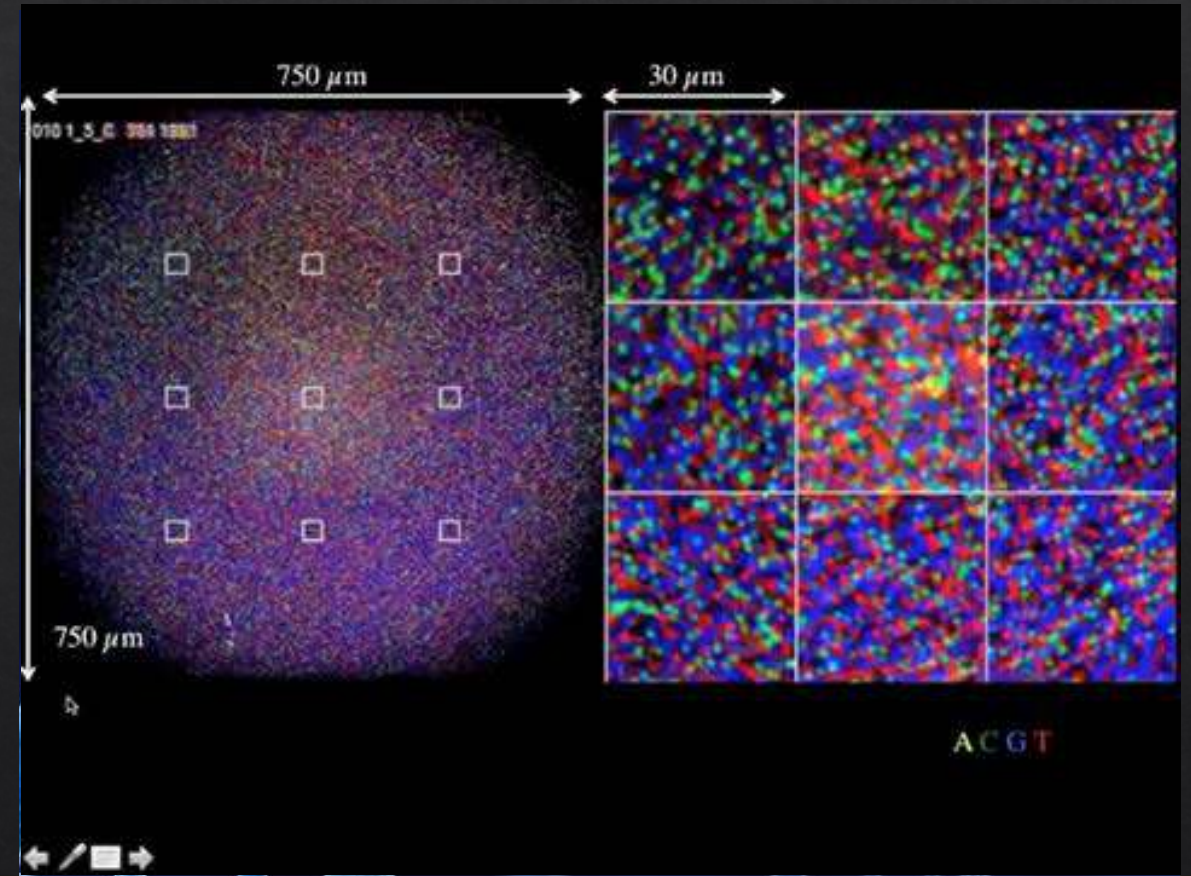
# Objectives

- ◆ Develop a preliminary study to examine the microbial community within the Love Creek Watershed
  - ◆ Can we determine the source of high bacteria loads within the watershed?



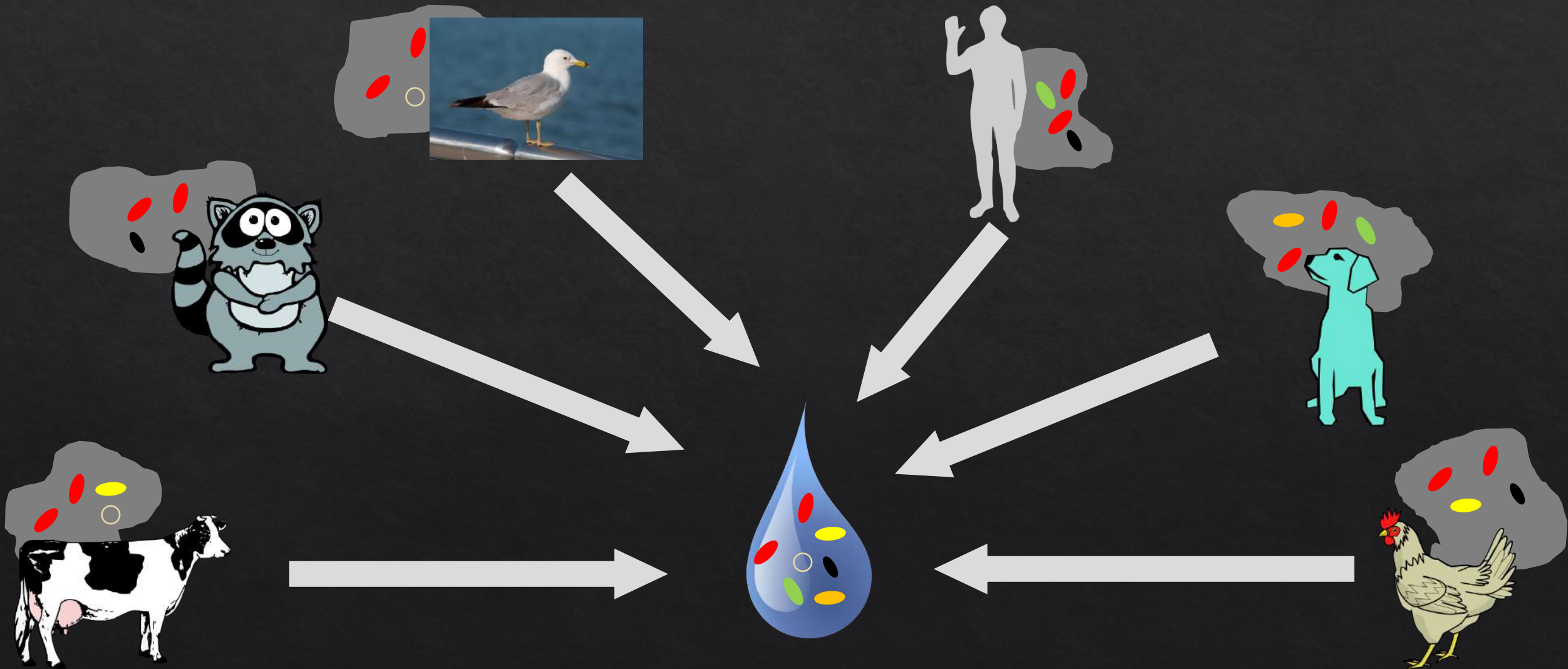
# DNA Sequencing

- ◇ Sanger Sequencing (1<sup>st</sup> Generation)
  - ◇ The Gold Standard for sequencing
  - ◇ Larger sequences (>700 bp)
  - ◇ Increased cost, sequencing and analysis times
- ◇ Next Generation Sequencing (NGS)
  - ◇ Shorter sequences (50 – 300 bp)
  - ◇ Less cost and DNA required
  - ◇ Increased computational power



From: <http://www.intachopen.com/books/next-generation-sequencing-advances-applications-and-challenges/next-generation-sequencing-in-aquatic-models>  
From: [https://www.abmgood.com/marketing/knowledge\\_base/next\\_generation\\_sequencing\\_introduction.php](https://www.abmgood.com/marketing/knowledge_base/next_generation_sequencing_introduction.php)

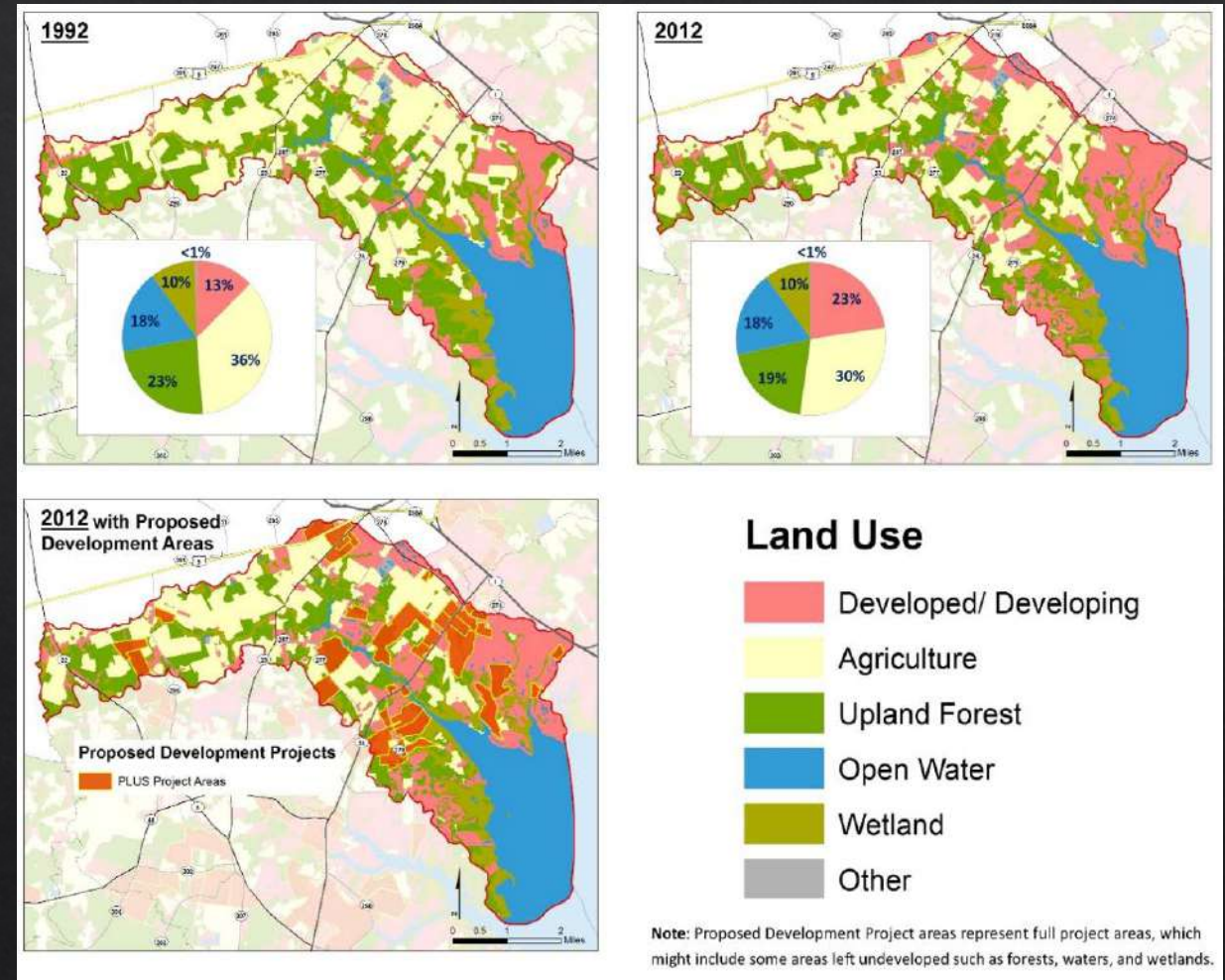
# Microbial Source Tracking





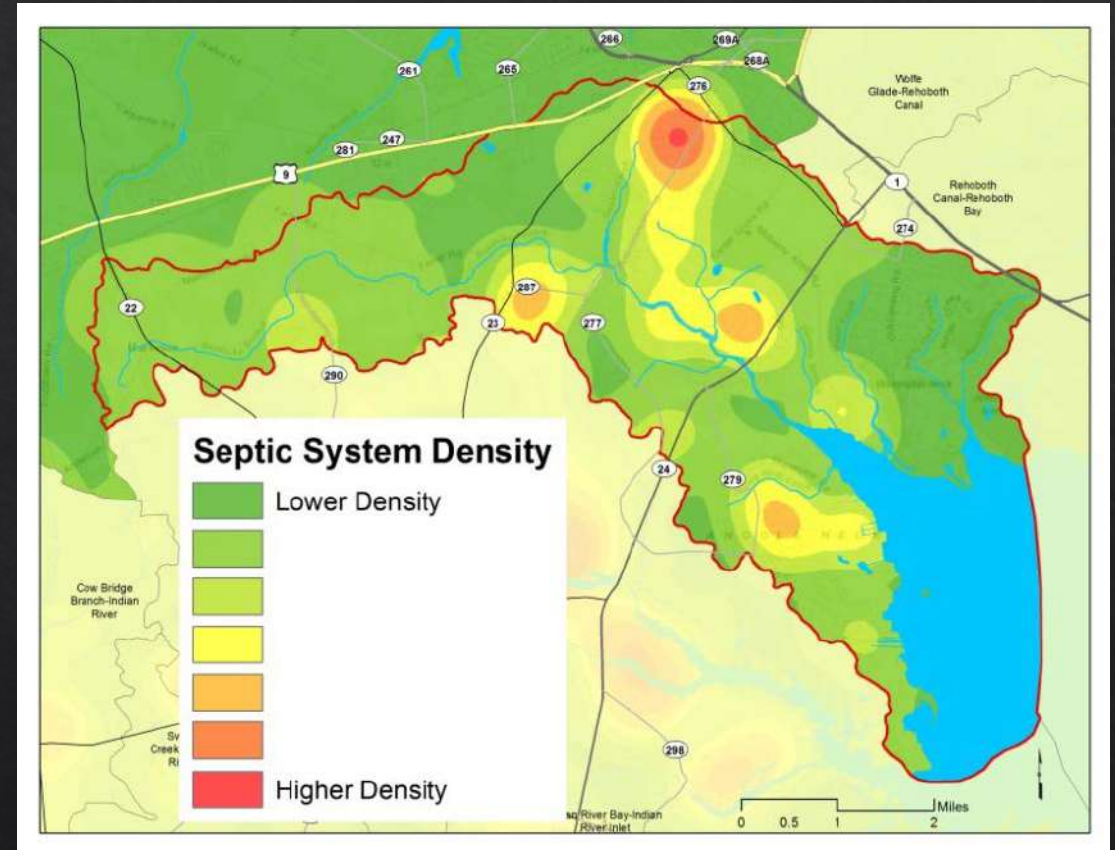
# Love Creek Watershed

- ◆ Major tributary of Rehoboth Bay
- ◆ Watershed approximately 24 square miles
- ◆ Last several decades increased urbanization with decreased agriculture and forested areas



# Love Creek Watershed

- ◆ Nutrient input sources
  - ◆ Agricultural and residential fertilizers
  - ◆ Stormwater runoff
  - ◆ Wastewater disposal including septic systems
- ◆ Currently listed as impaired under the CWA for both bacteria and nutrients



From: <https://www.inlandbays.org/wp-content/uploads/State-of-Love-Creek-Report-FINAL-.pdf>



# Study Area

- ◇ Tidally driven till Goslee Pond at Robinsonville Road (308291)
- ◇ Monthly Samples March to October
  - ◇ 7 Sites along within the watershed
  - ◇ 3 Non-tidal
  - ◇ 4 Tidal
  - ◇ 2 replicates at RB34
- ◇ One sampling event after major rainfall





# Sampling

## ◆ Nutrients

- ◆ DOC/TOC,  $\text{NO}_x$ , Orthophosphate,  $\text{NH}_3$ , Total N and P, TSS, TDS, Turbidity

## ◆ Bacterial

- ◆ Enterococci via Enterolert
- ◆ Microbial community via Illumina MiSeq

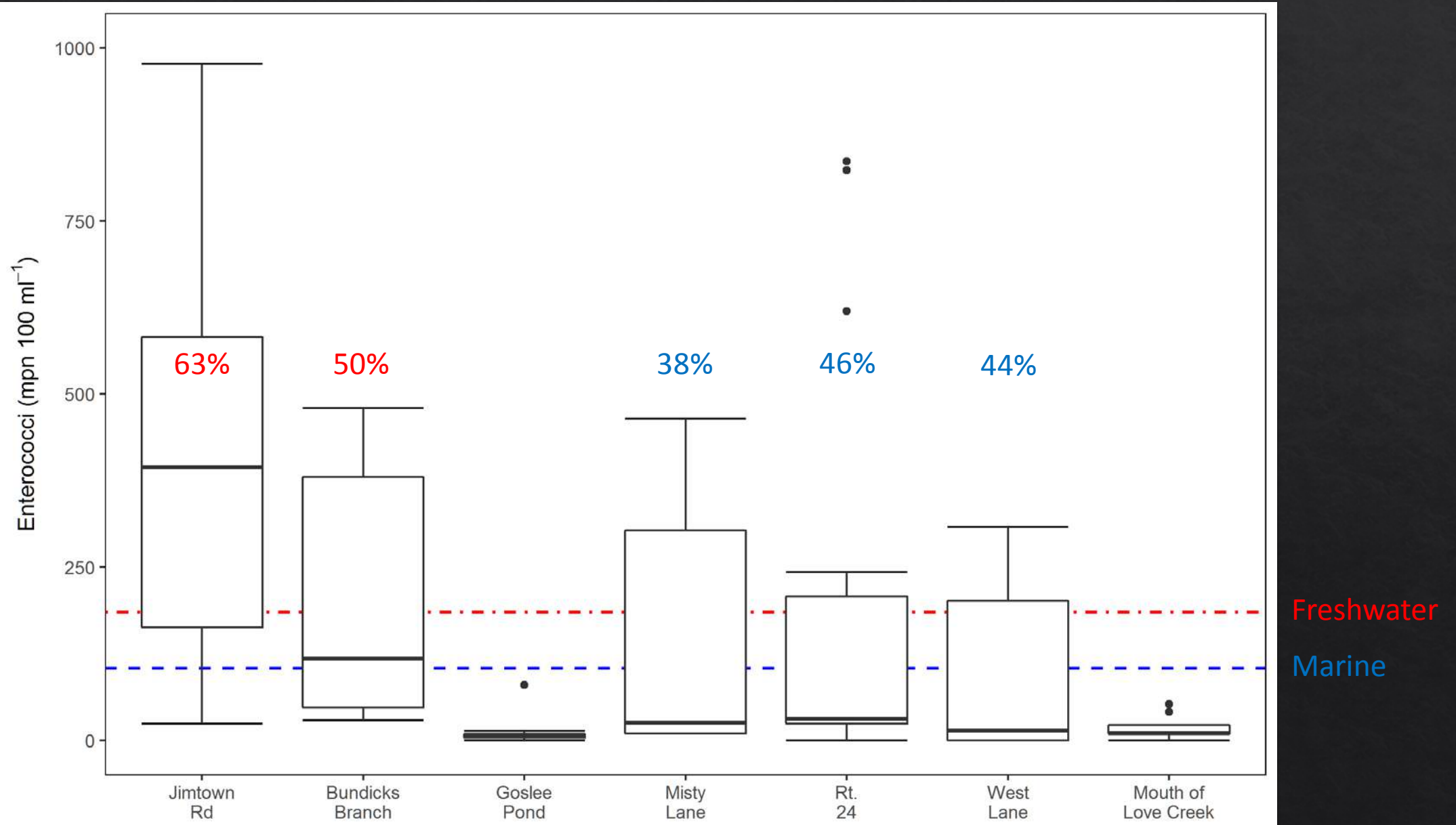
## ◆ Fecal Samples

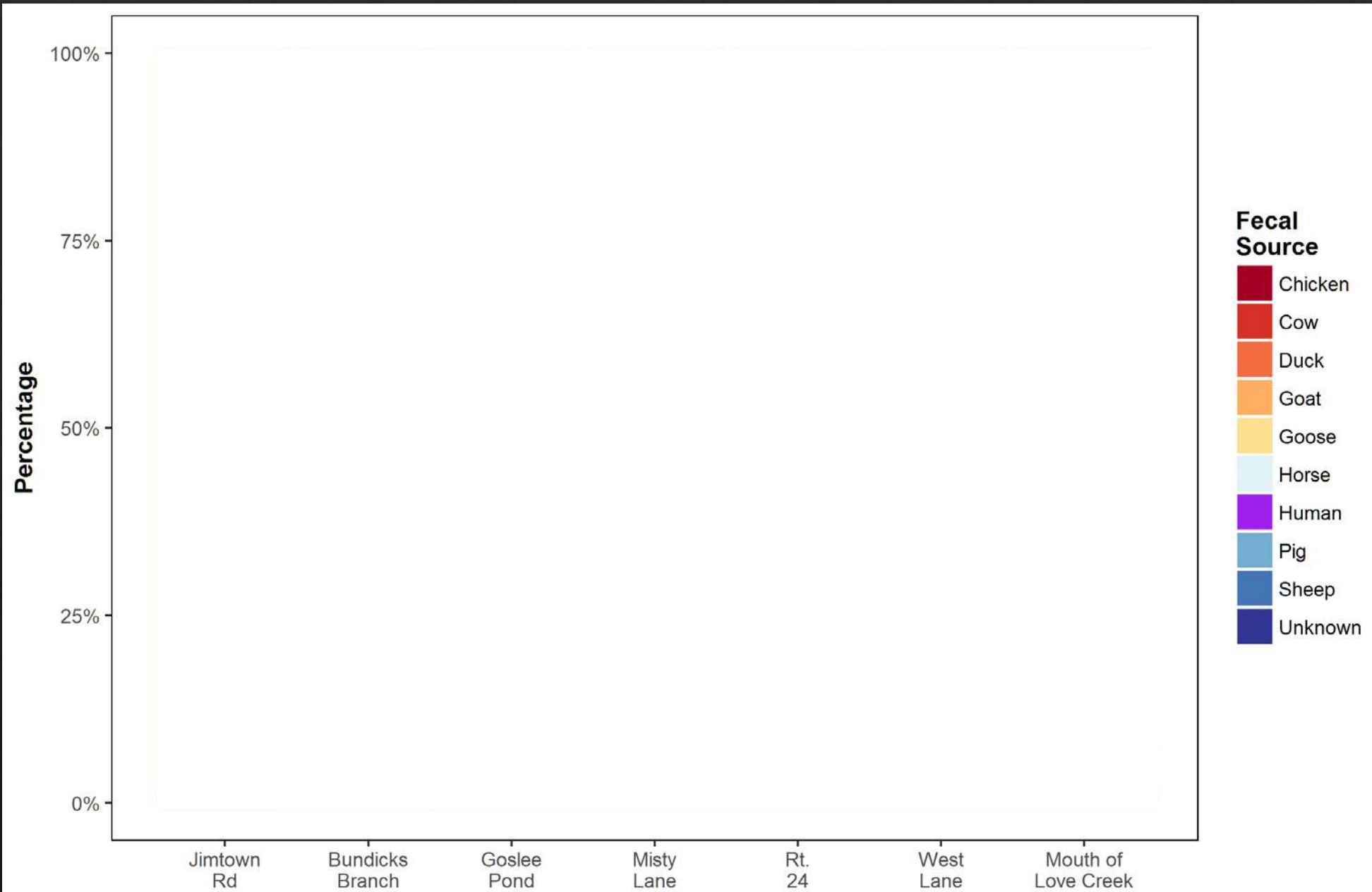
- ◆ Chicken, Cow, Duck, Goat, Goose, Horse, Human, Pig, Sheep





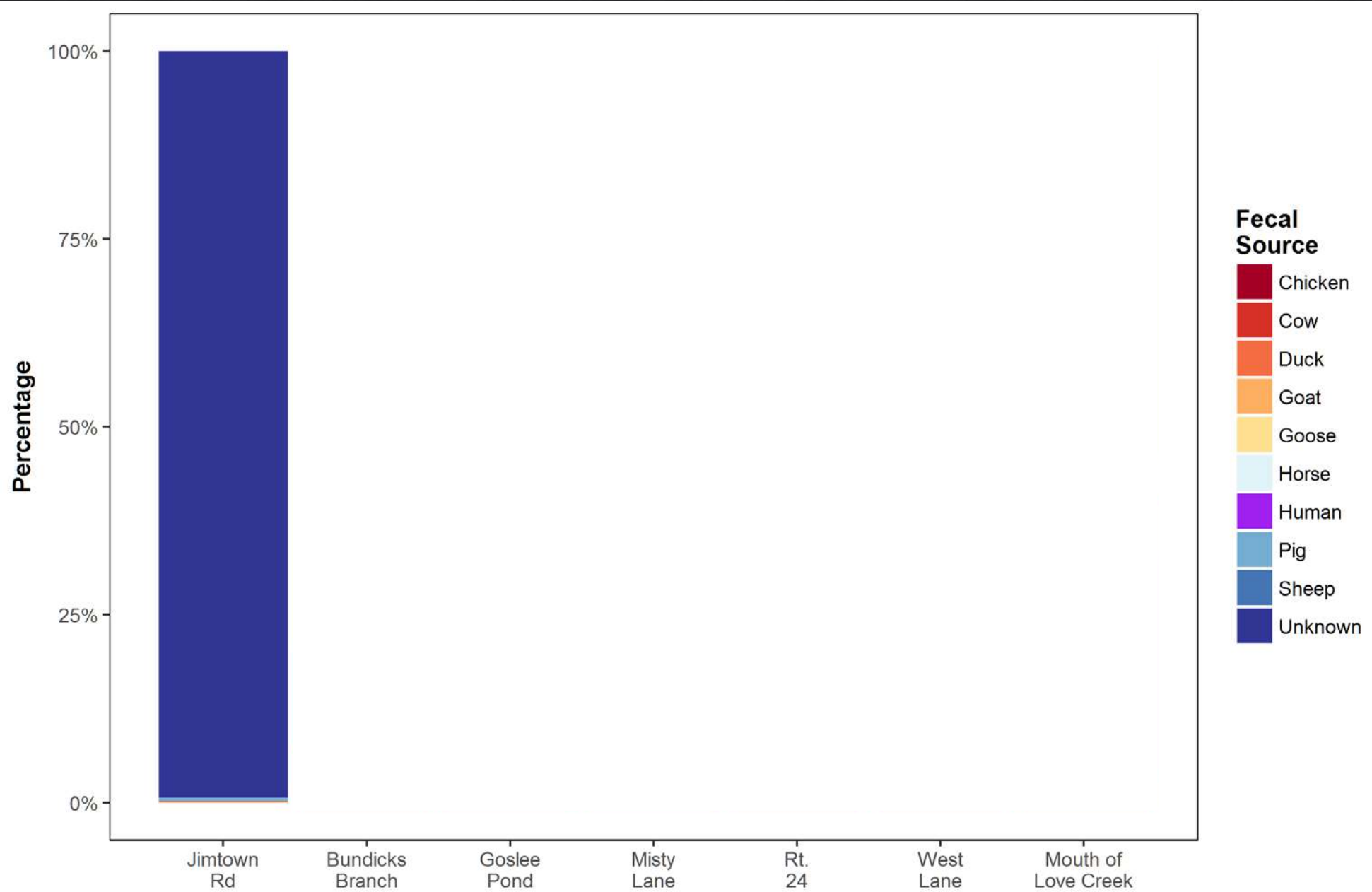
# Enterolert

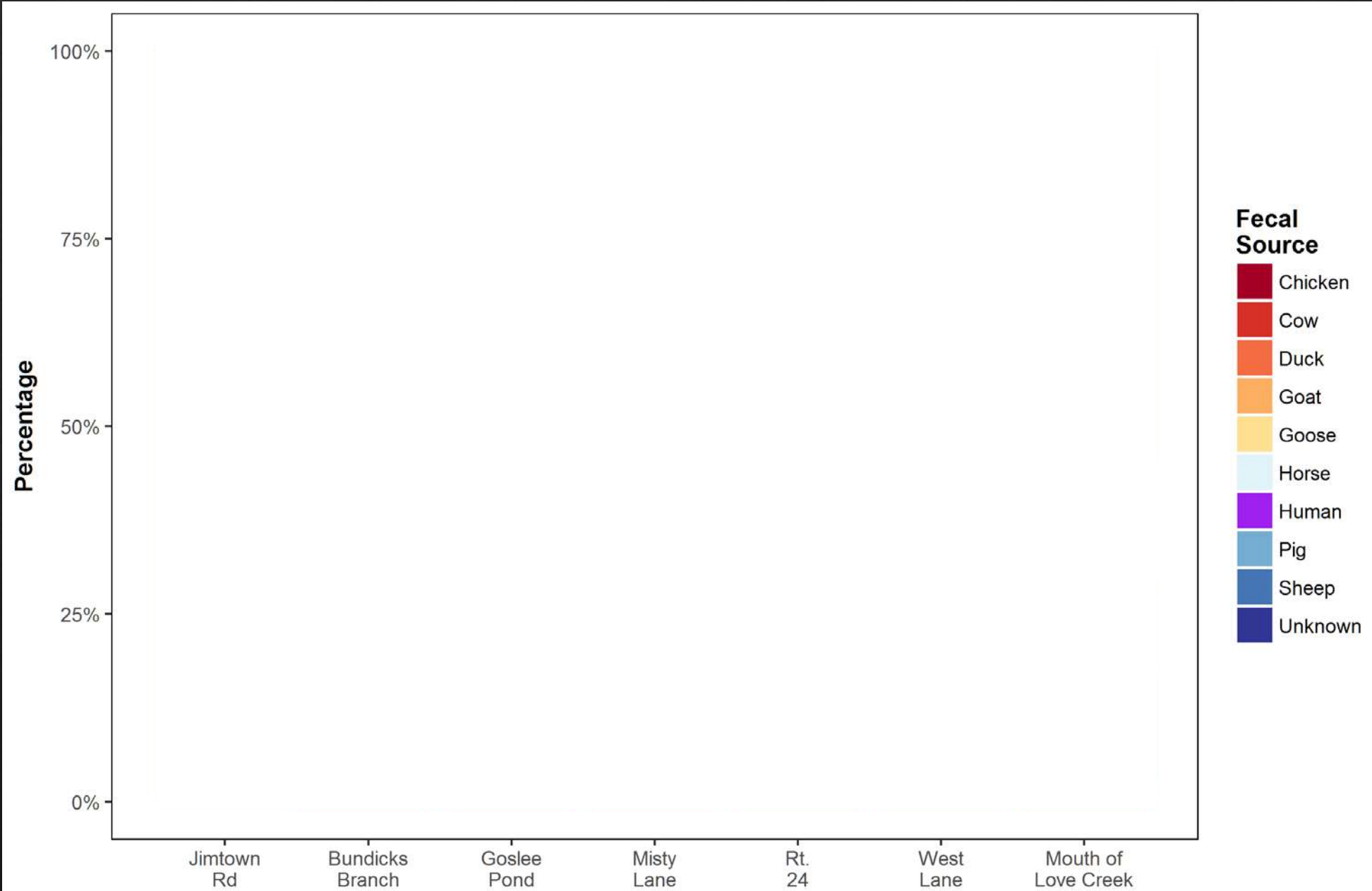




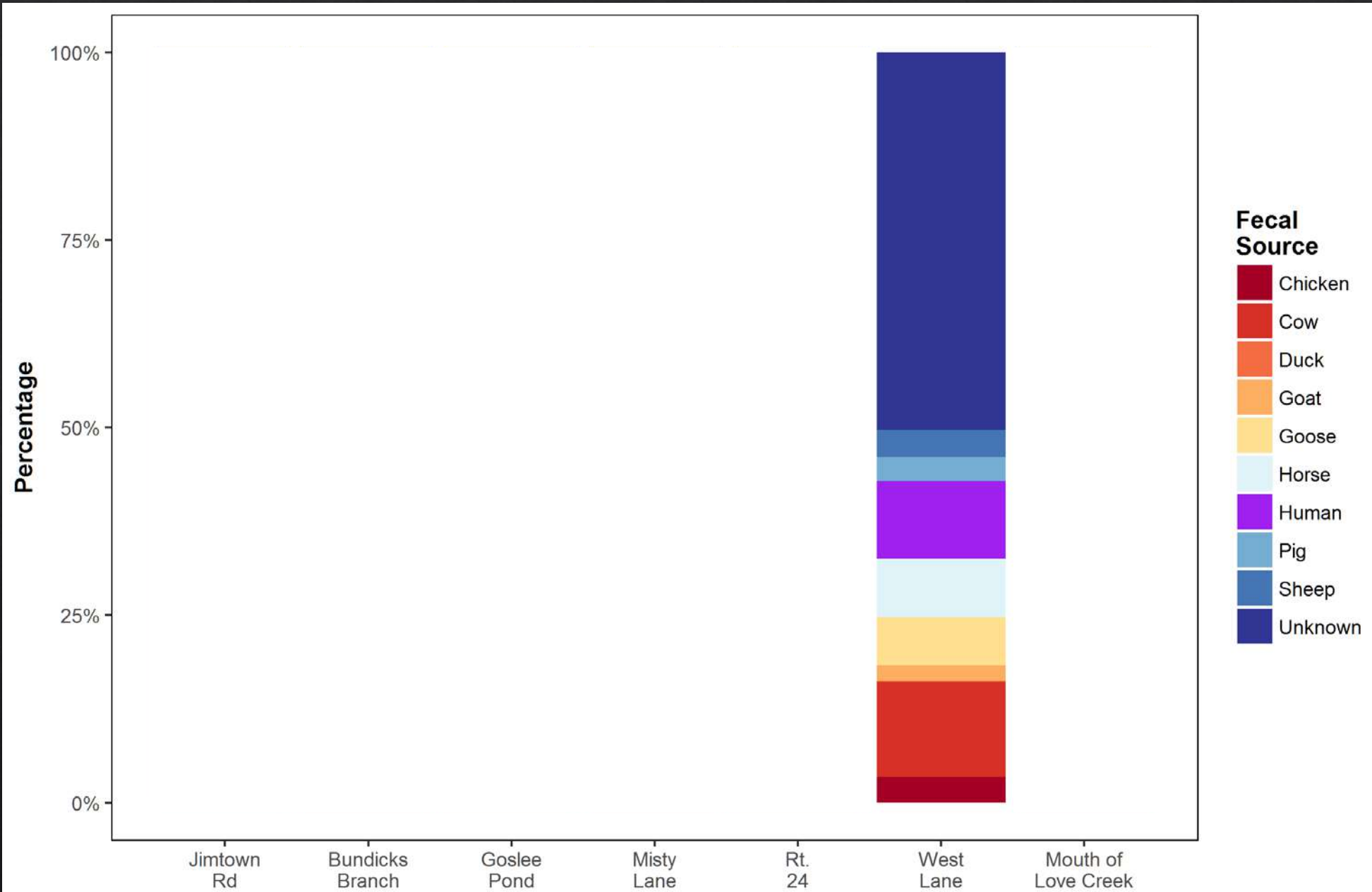


# April

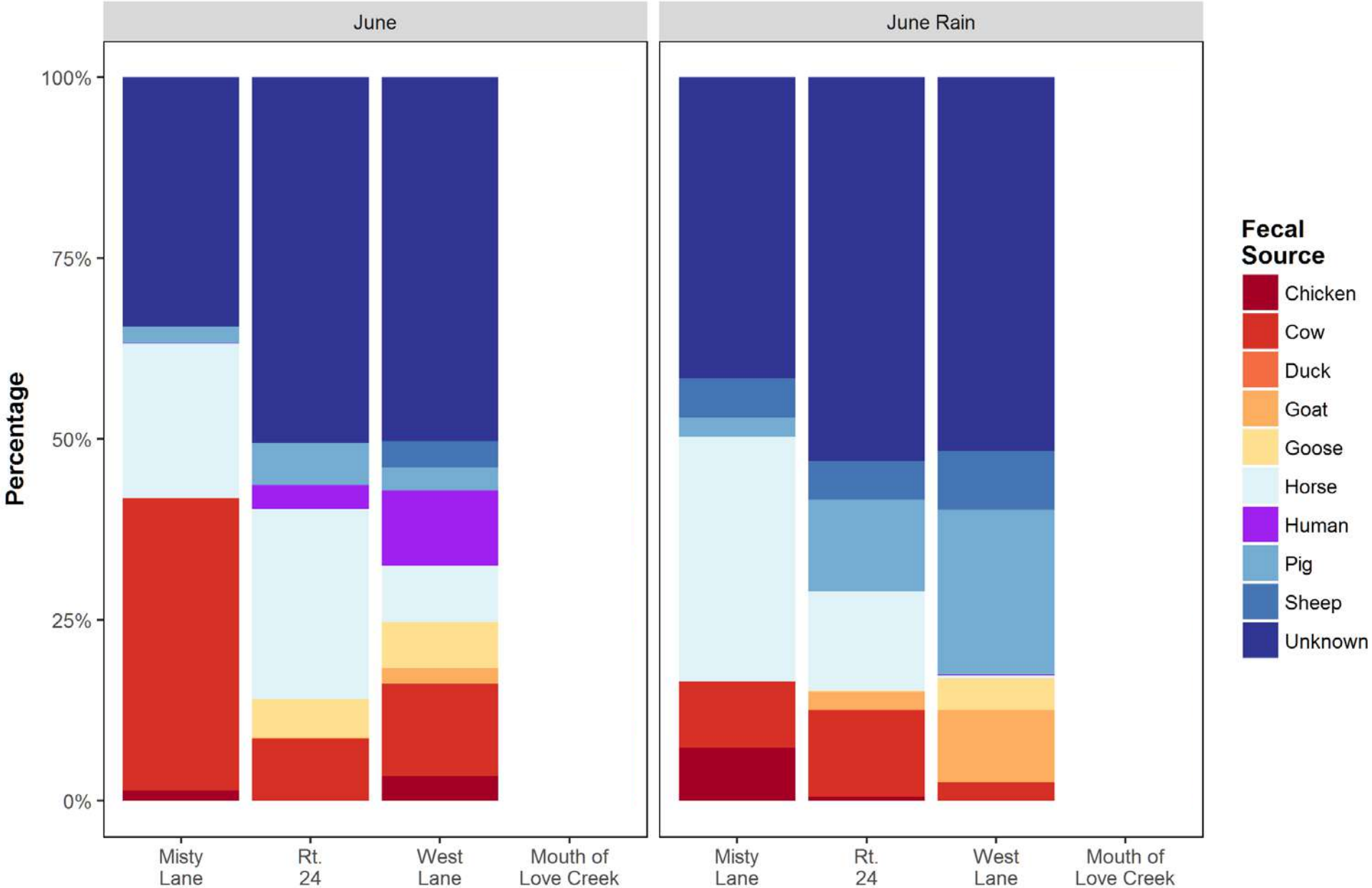






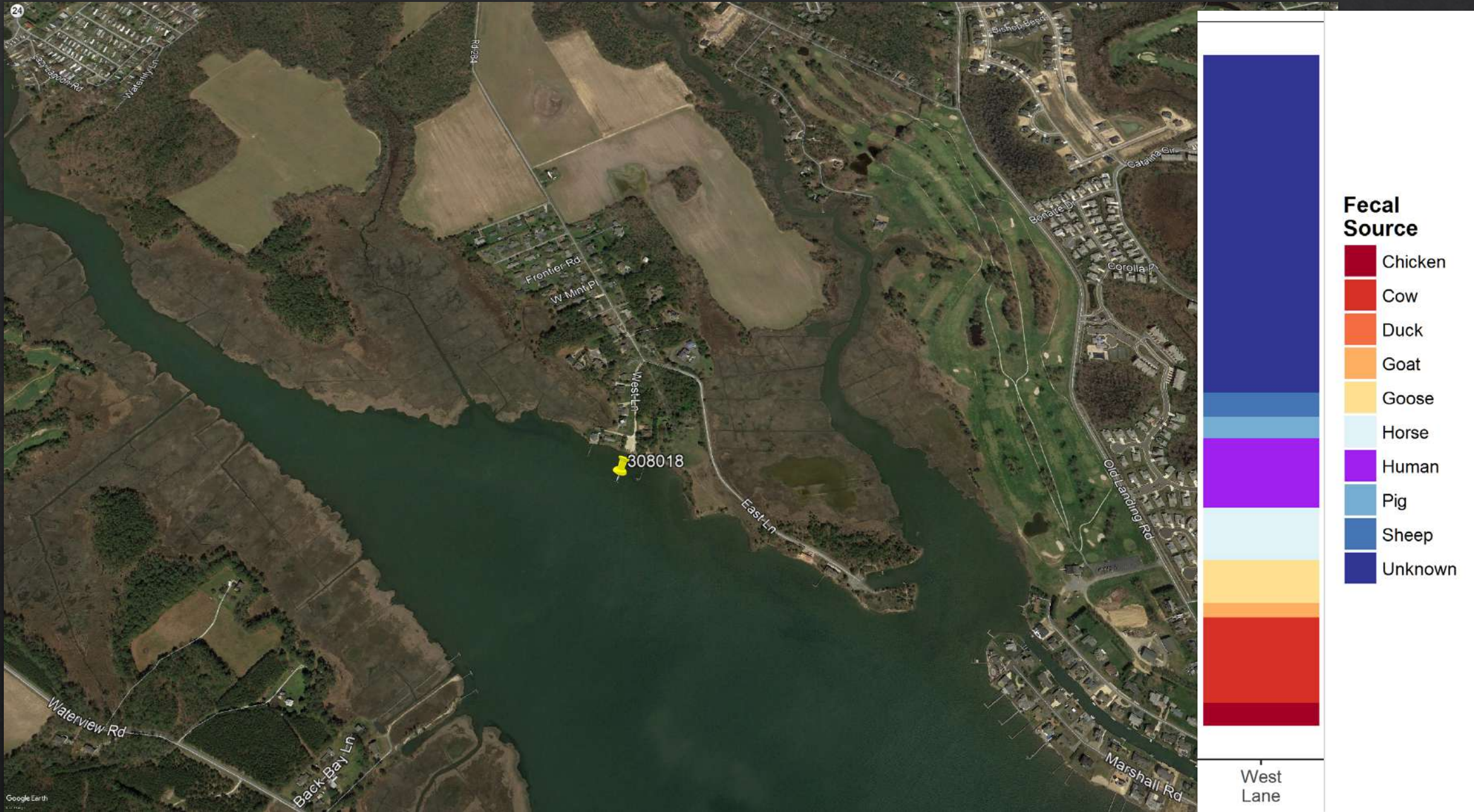


# June Rain Event





# West Lane





# Conclusions

- ◆ Next Generation Sequencing techniques are able to determine potential sources of bacterial contamination
  - ◆ Ground truthing must occur to find potential sources
  - ◆ Greater fidelity can occur from fecal samples collected within the watershed
- ◆ NGS microbial source tracking is another tool to add to the monitoring toolbox



# Future Analysis

- ◆ Functional analysis of the microbial community
- ◆ Emerging pathogens
- ◆ Viral source tracking
- ◆ Linkages between nutrients and the microbial community?



# Acknowledgements

- ◆ DNREC Environmental Lab Section
- ◆ EPA Multipurpose Grant XXXX

