# COMPASS LE OWC Root Exclusion: Porewater Nutrients

## Apr-May 2024 Samples

### 2025-10-30

## Contents

## 0.1 Run Information

```r
#set the run date & user name
  run_date <- "08/20/2025"
  sample_year <- "2024"
  sample_month <- "Apr-May"
  user <- "Roberta Peixoto"
  QAQC_by <- "Zoe Read"

#identify the files you want to read in
  #read in as a list to accommodate multiple runs in a month
  data_files <- c("Raw Data/Seal_COMPASS_LE_OWC_RootExclusion_NUTR_Apr-May2024.csv")

# Define the file path for QAQC log file - NO Need to change just check year
  file_path <- "Raw Data/SEAL_COMPASS_LE_OWC_RootExclusion_QAQC_Log_2025.csv"
  final_path <- "Processed Data/COMPASS_LE_OWC_RootExclusion_Nutrients_2024_Apr-May2024.csv"

#record any notes about the run or anything other info here:
  run_notes <- "The last CCV check std for Phosphate is very high.
  All other check standards are too low. " #Add notes from QAQC

#Set up file path for metadata
  #downloaded metadata csv - downloaded from Google drive as csv for this year
  Raw_Metadata = "Raw Data/COMPASS_OWC_Root_Exclusion_Nutrient_SampleLog.csv"

  cat(run_notes)
```

```
## The last CCV check std for Phosphate is very high.
##   All other check standards are too low.
```
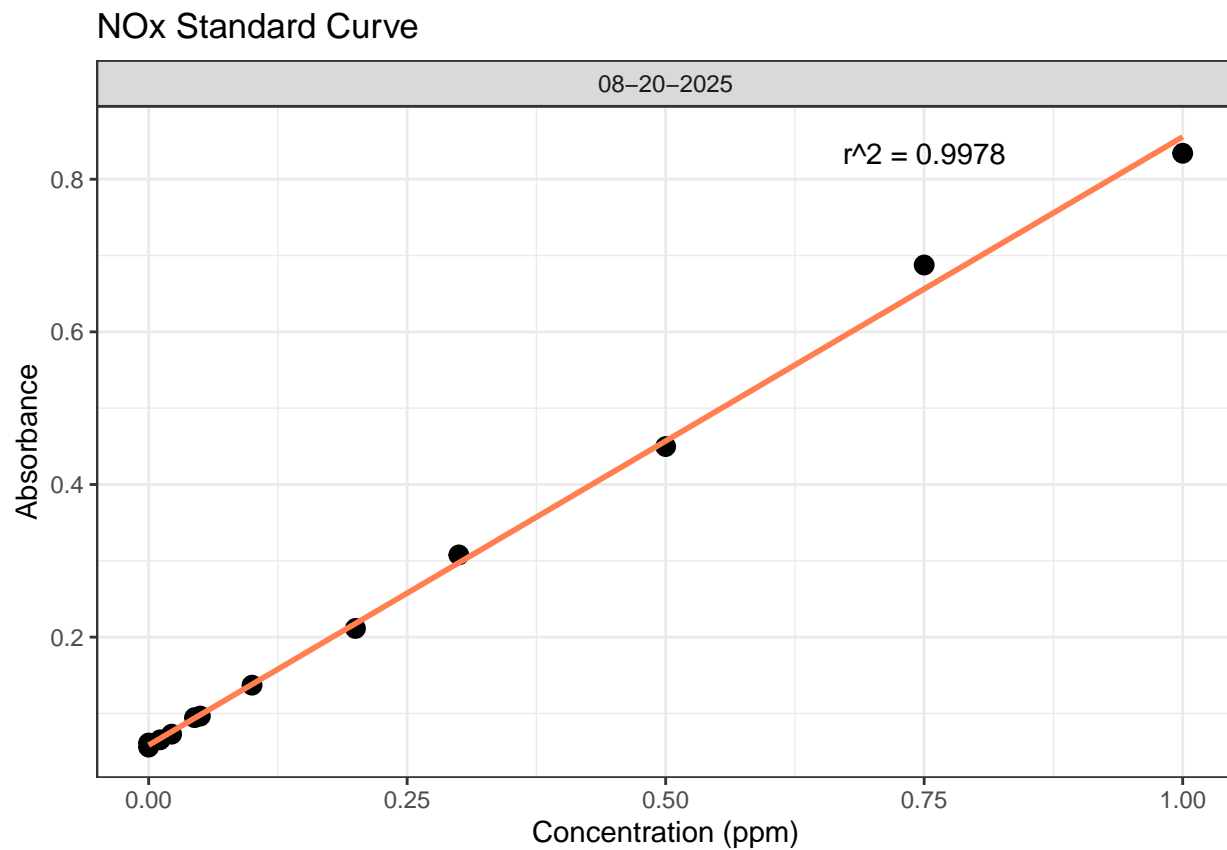
##Setup

##Read in metadata and create similar sample IDs for matching to samples
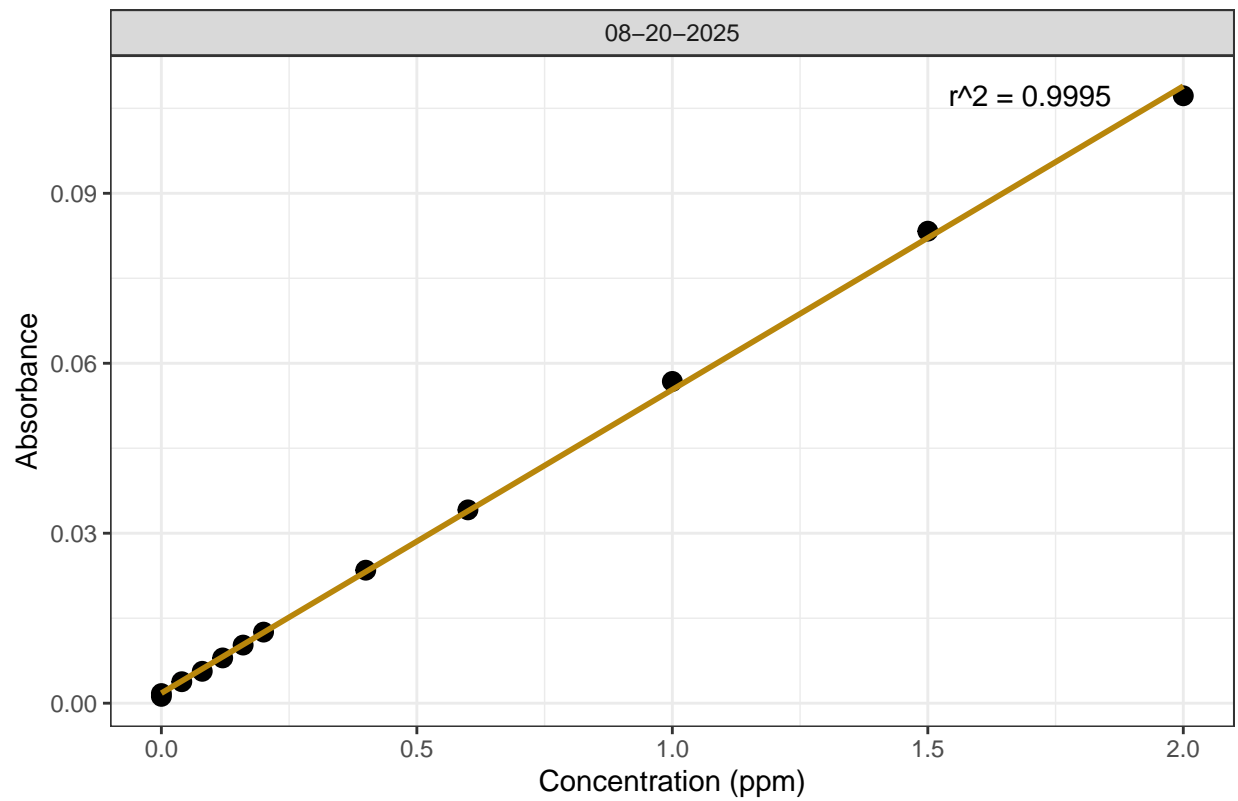
##Import Data & Clean

##Assessing standard Curves

## 0.2 Plot standard curves

## `geom_smooth()` using formula = 'y ~ x'

NOx Standard Curve
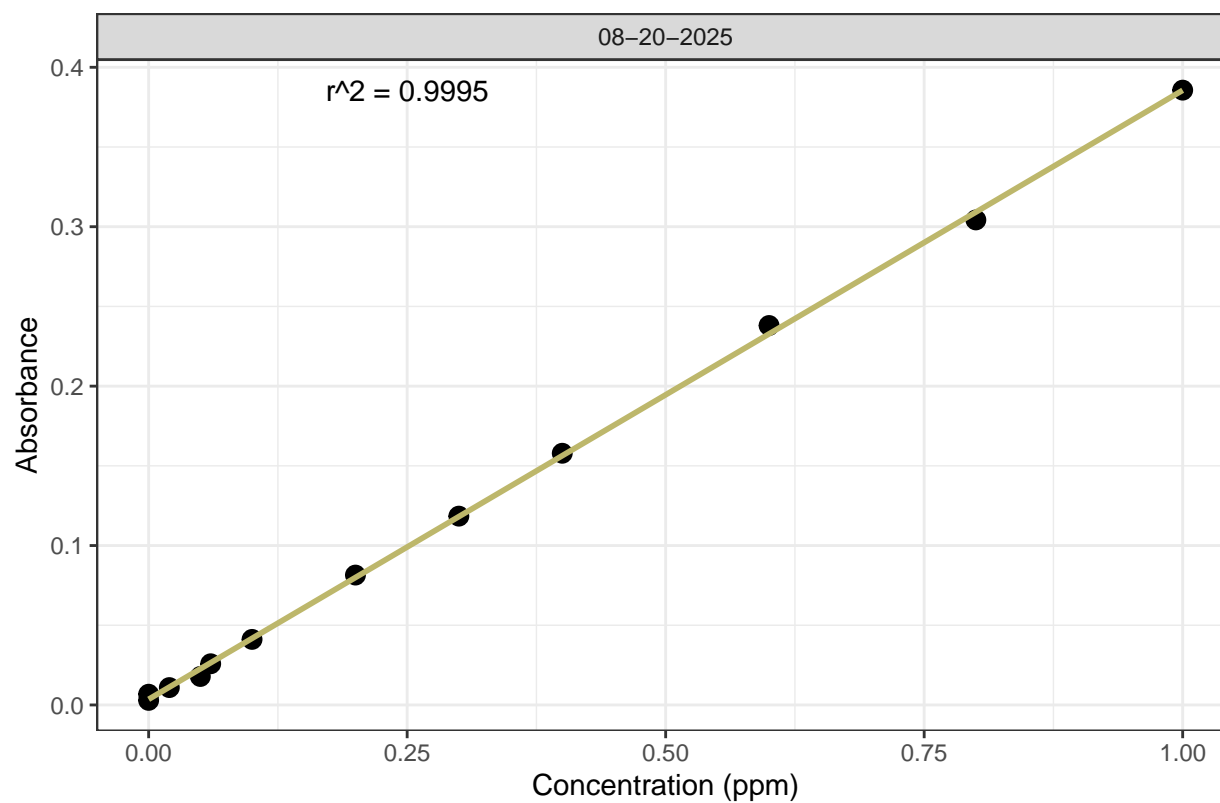


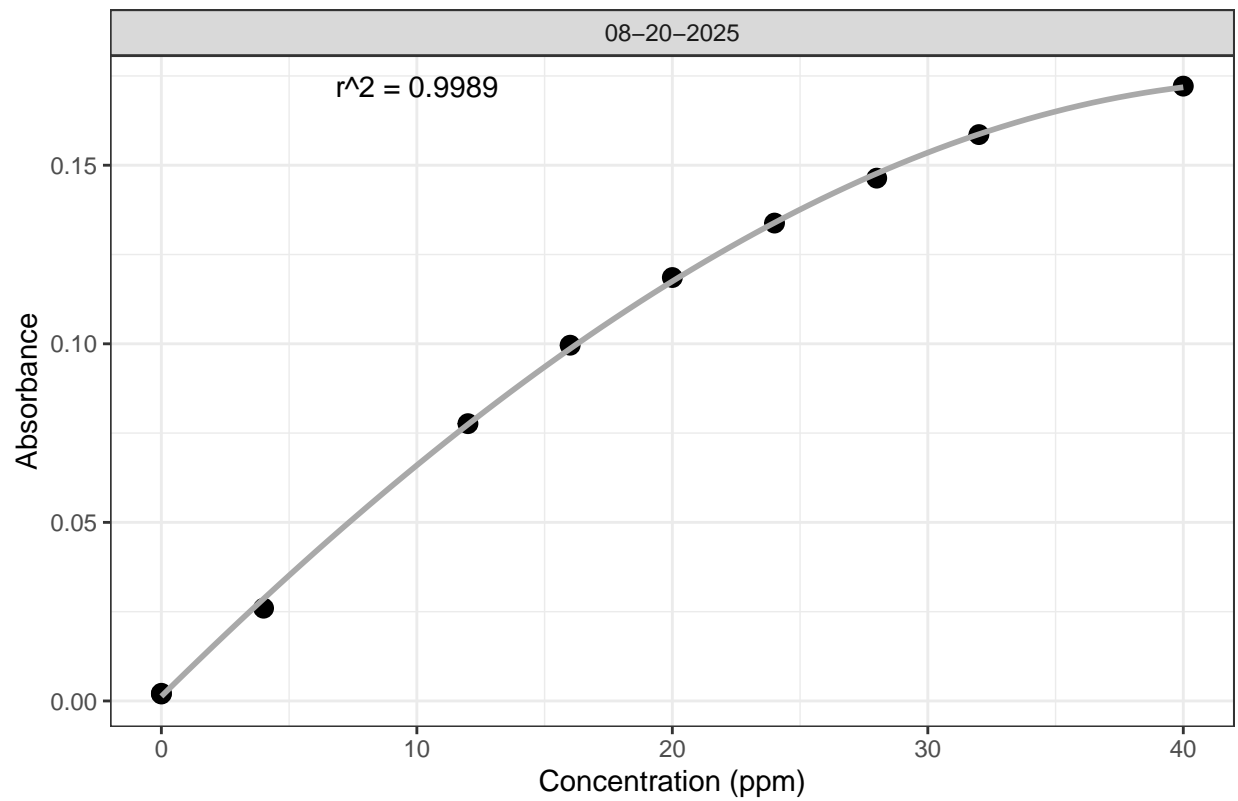## `geom_smooth()` using formula = 'y ~ x'

# NH3 Standard Curve



```
## 'geom_smooth()' using formula = 'y ~ x'
```
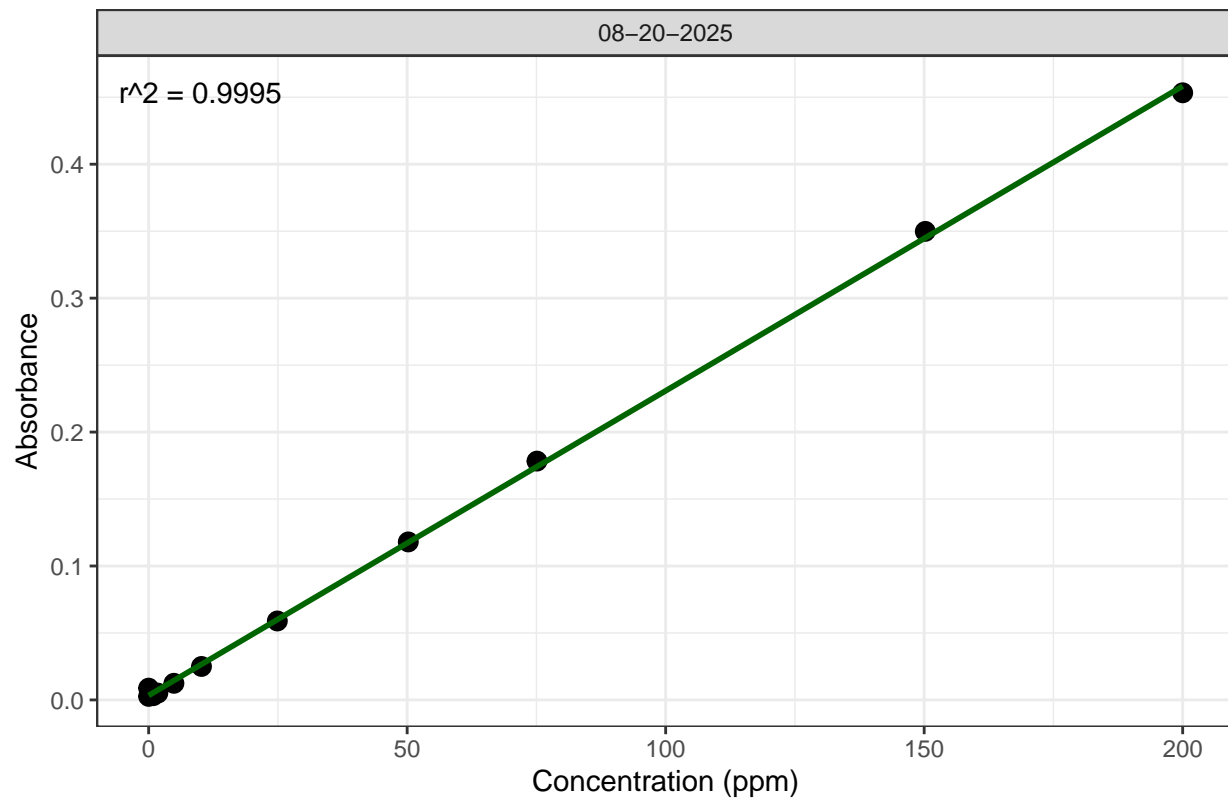
## PO4 Standard Curve

## SO4 Standard Curve



## `geom_smooth()` using formula = 'y ~ x'

## NO2 Standard Curve

| 08−20−2025 |
|---|

r^2 = 0.9995



```
## [1] "NOx Curve r2 GOOD - PROCEED"

## [1] "NH3 Curve r2 GOOD - PROCEED"

## [1] "PO4 Curve r2 GOOD - PROCEED"

## [1] "SO4 Curve r2 GOOD - PROCEED"

## [1] "NO2 Curve r2 GOOD - PROCEED"

## [1] "QAQC log file exists and has been read into the code."

## `geom_line()`: Each group consists of only one observation.
## i Do you need to adjust the group aesthetic?
```
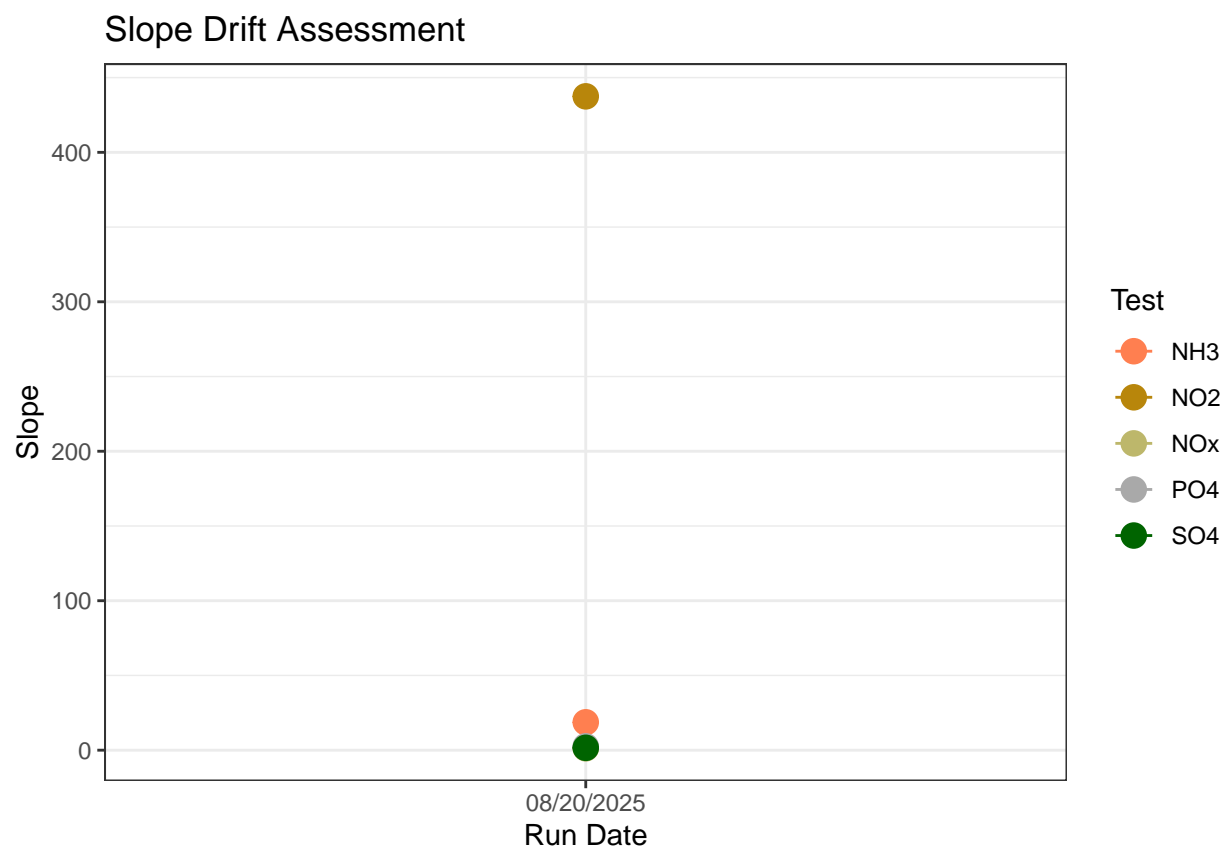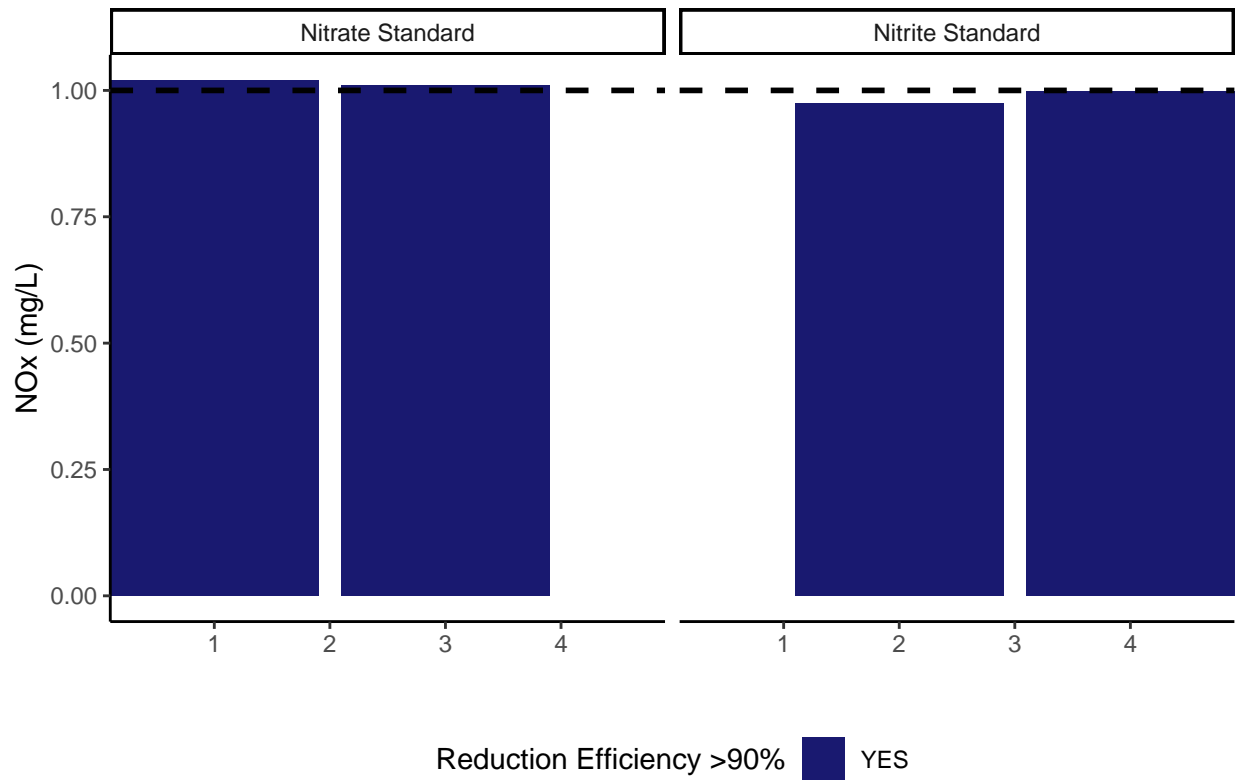
## Slope Drift Assessment



Table 1: Average Slope by Analyte

| Test | avg__slope |
|------|------------|
| NH3  | 18.657     |
| NO2  | 437.467    |
| NOx  | 1.252      |
| PO4  | 2.616      |
| SO4  | 1.570      |

##Dilution Corrections - ensure the latest dilution is kept

```
## No duplicated samples.
```

## 0.3 Check NOx Reduction Efficiency



```
## [1] "Mean NOx Reduction Efficiency >95% - PROCEED"
```

```
## [1] 100.045
```

## 0.4 Analyze the Check Standards

```
## [1] "NOx Check Standard RSD within Range - PROCEED"

## [1] "NH3 Check Standard RSD within Range - PROCEED"

## [1] "PO4 CHECK STANDARD RSD TOO HIGH - REASSESS"

## [1] "SO4 Check Standard RSD within Range - PROCEED"

## [1] "NO2 Check Standard RSD within Range - PROCEED"
```
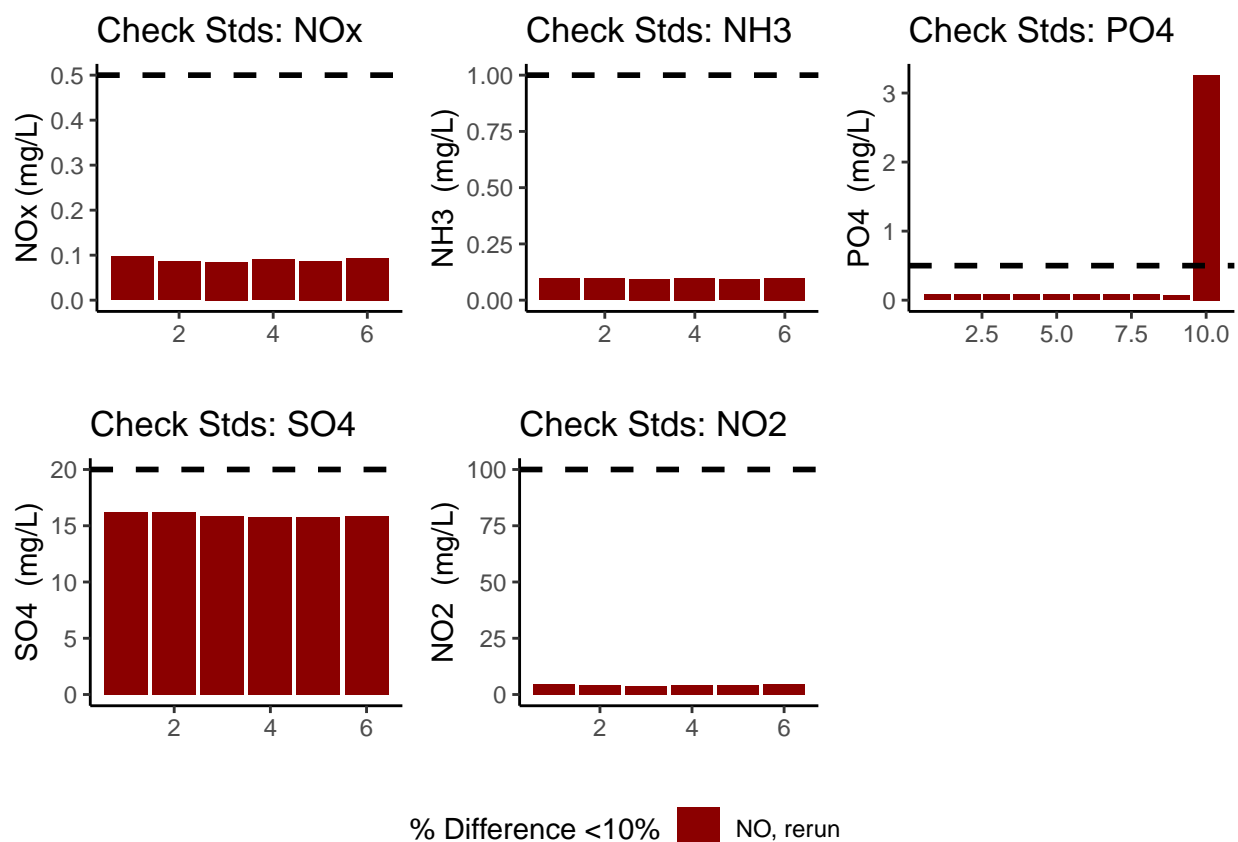


```
## [1] "<60% of NOx Check Standards are within range of expected concentration - REASSESS"

## [1] "<60% of NH3 Check Standards are within range of expected concentration - REASSESS"

## [1] "<60% of PO4 Check Standards are within range of expected concentration - REASSESS"

## [1] "<60% of SO4 Check Standards are within range of expected concentration - REASSESS"

## [1] "<60% of NO2 Check Standards are within range of expected concentration - REASSESS"
```

## 0.5 Analyze Blanks

```
## [1] ">60% of NOx Blanks are below the lower 25% quartile of samples or 1/2 detection limit - PROCEED"
```

```
## [1] ">60% of NH3 Blanks are below the lower 25% quartile of samples - PROCEED"
```

```
## [1] ">60% of PO4 Blanks  are below the lower 25% quartile of samples- PROCEED"
```

```
## [1] ">60% of SO4 Blanks  are below the lower 25% quartile of samples- PROCEED"
```

```
## [1] ">60% of NO2 Blanks  are below the lower 25% quartile of samples- PROCEED"
```
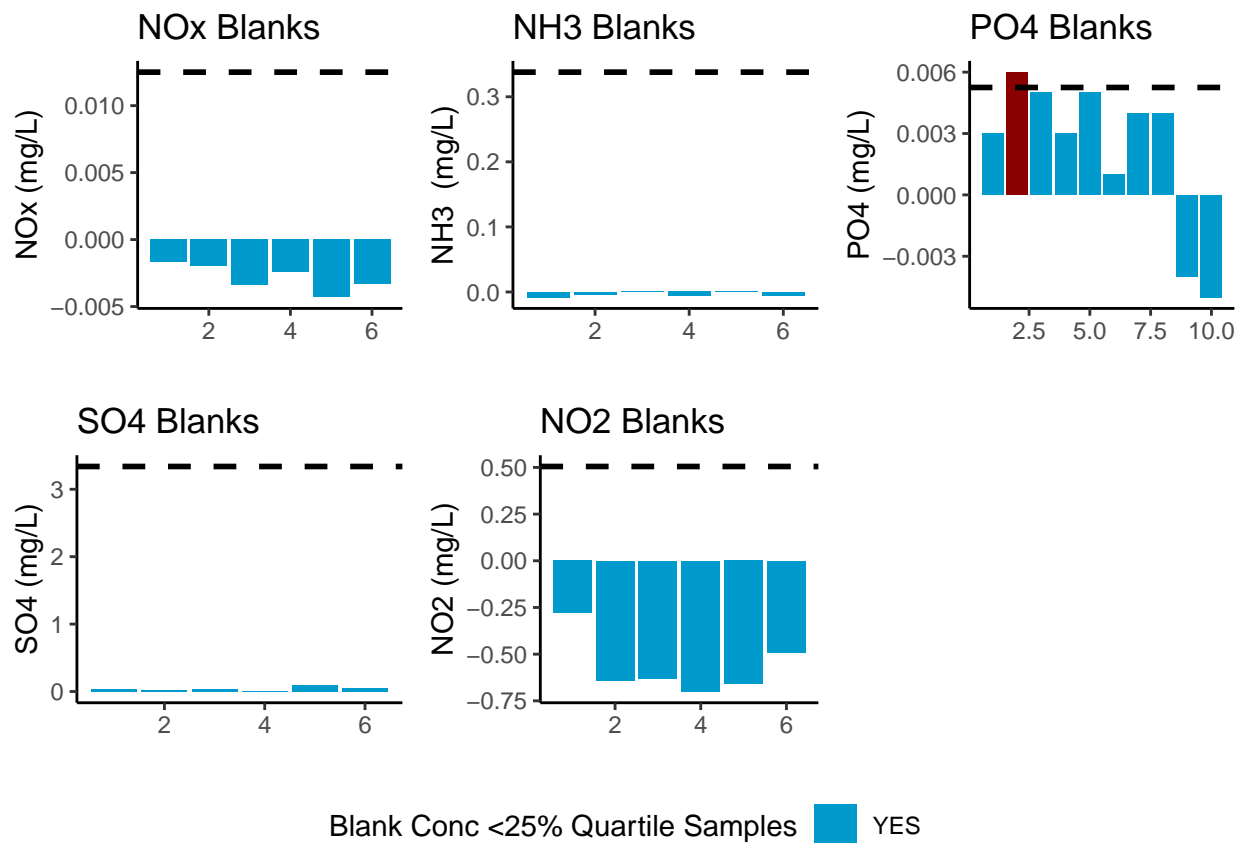


Table 2: Mean Concentration of Blanks

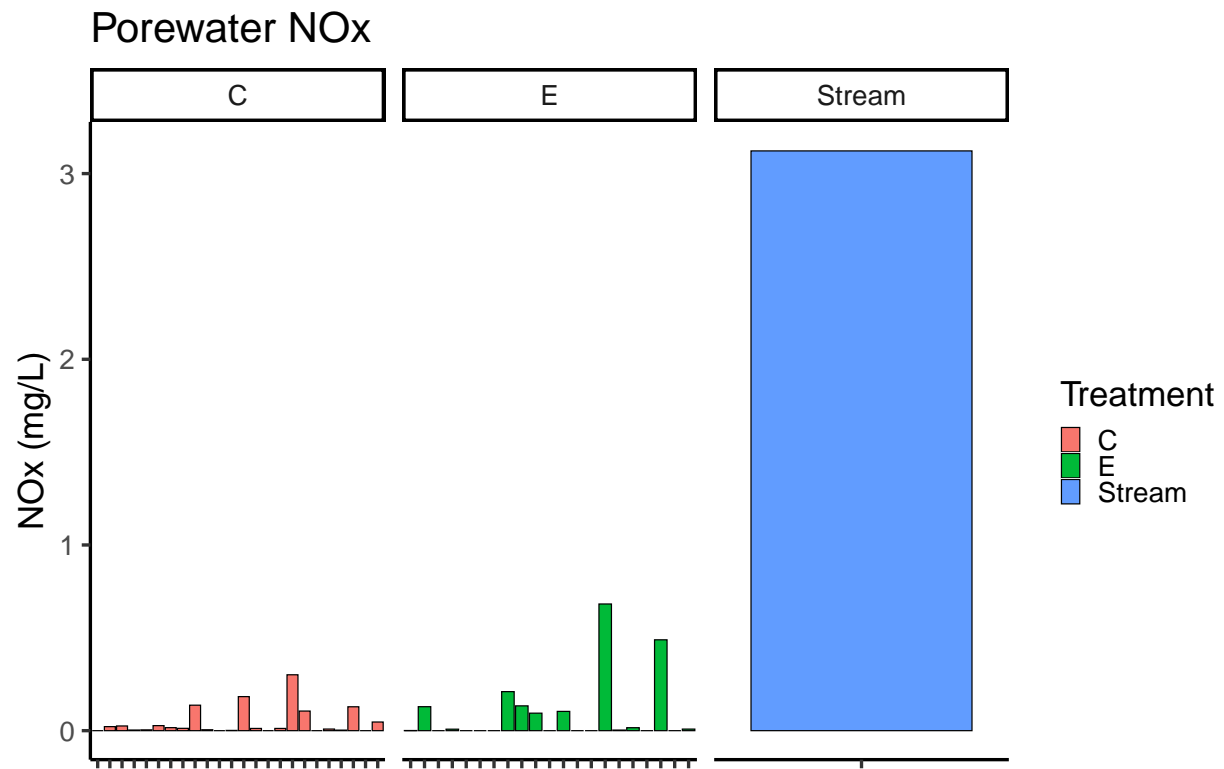| Test | Blank_Mean_Conc |
|------|-----------------|
| NOx  | -0.0029 |
| NH3  | -0.0037 |
| PO4  | 0.0022 |
| SO4  | 0.0433 |
| NO2  | -0.5667 |

##Sample Flagging - Within range of standard curve

##Pull out sample id information

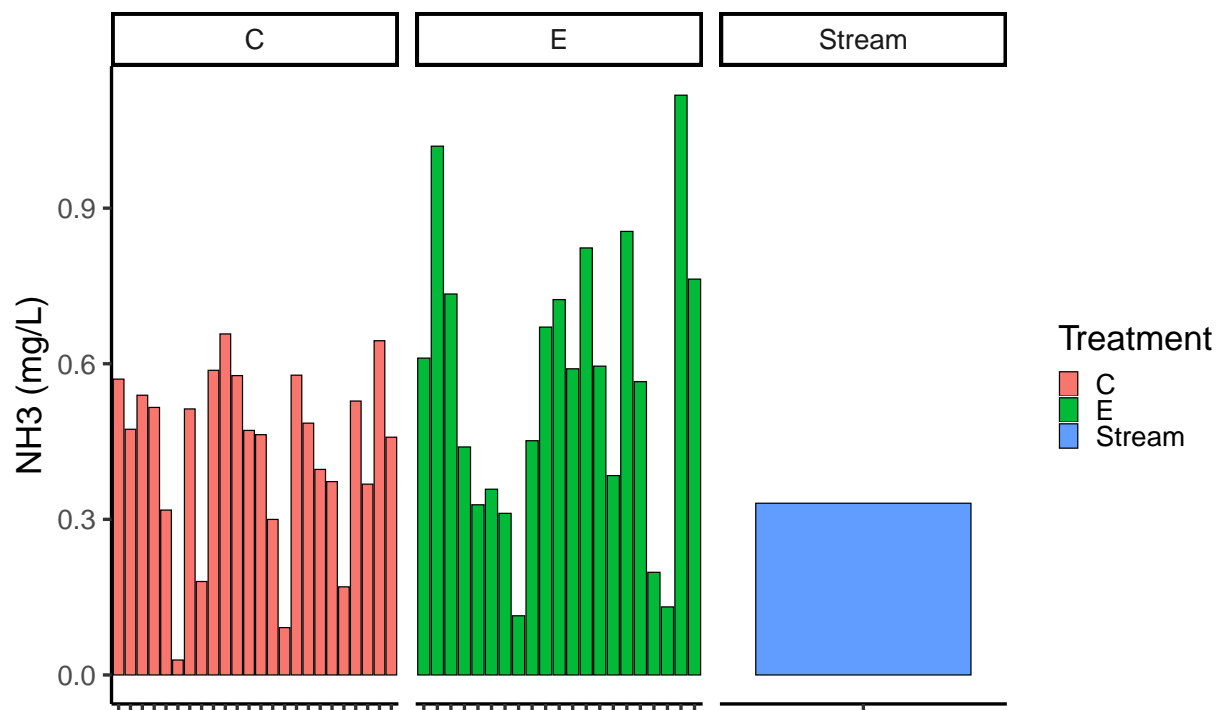## 0.6 Check to see if samples run match metadata & merge info

```
## Check Sample IDs with Metadata
```

```
## All sample IDs are present in metadata.
```
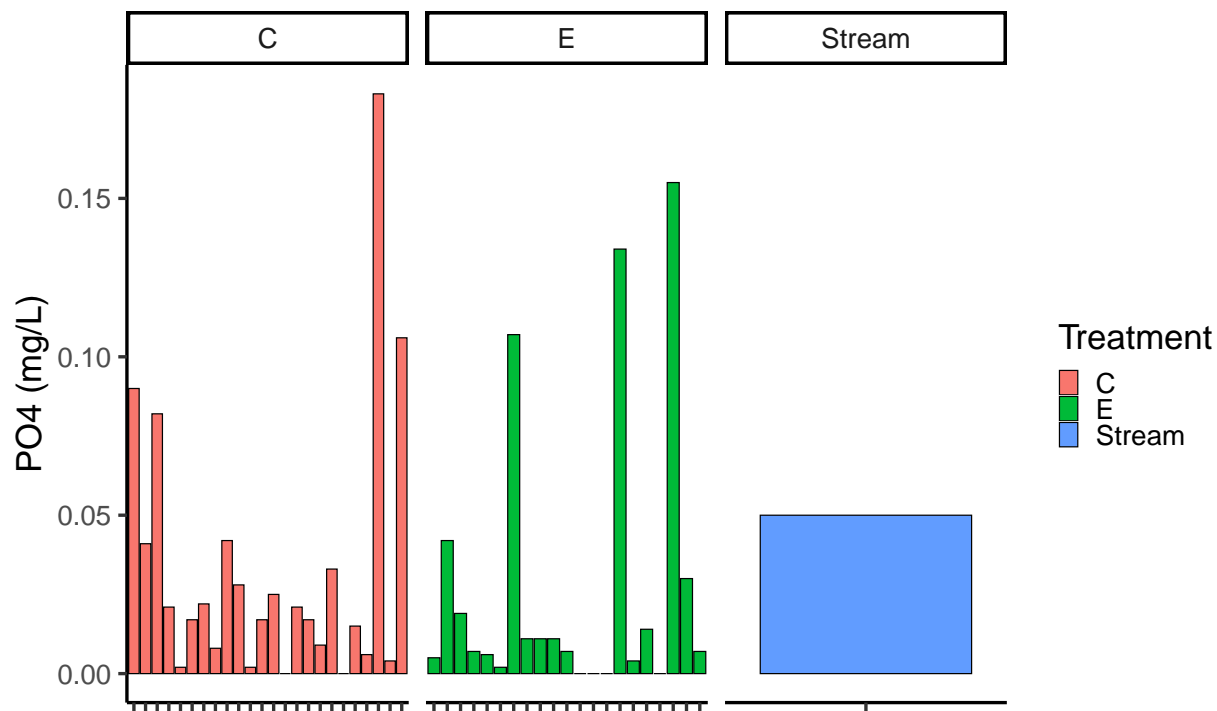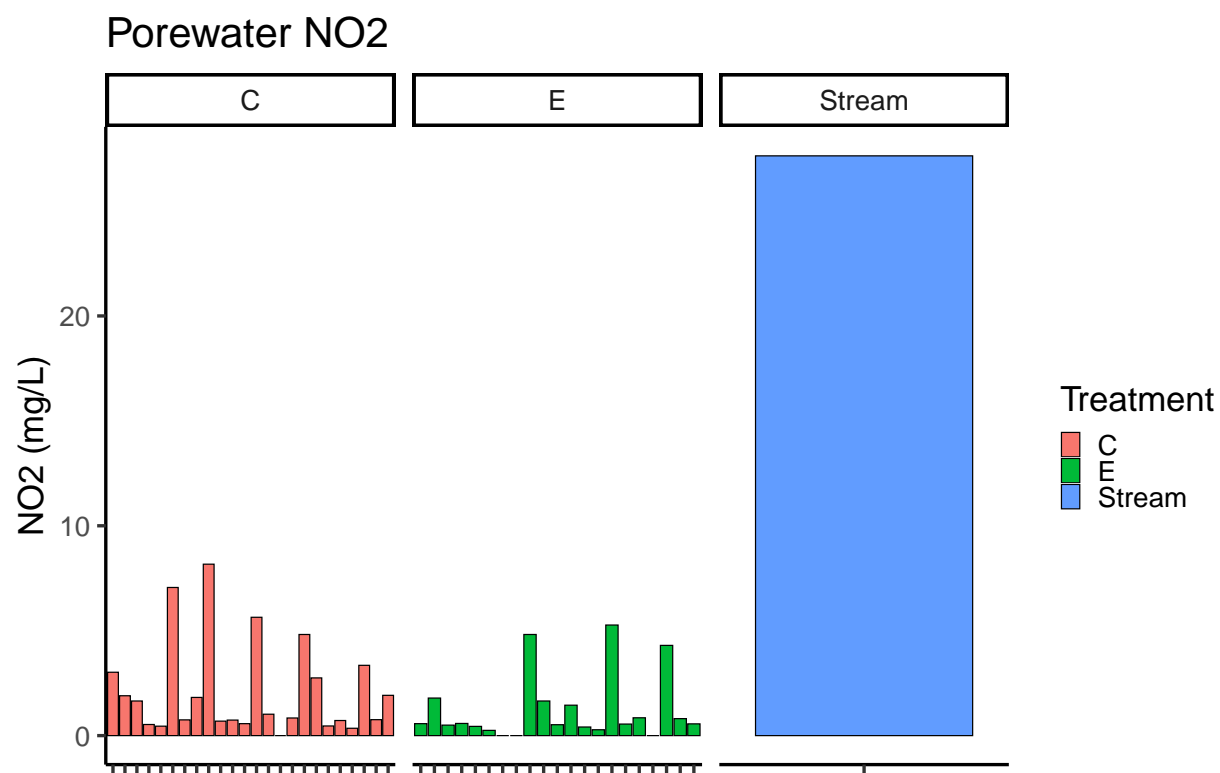
## 0.7 Visualize data
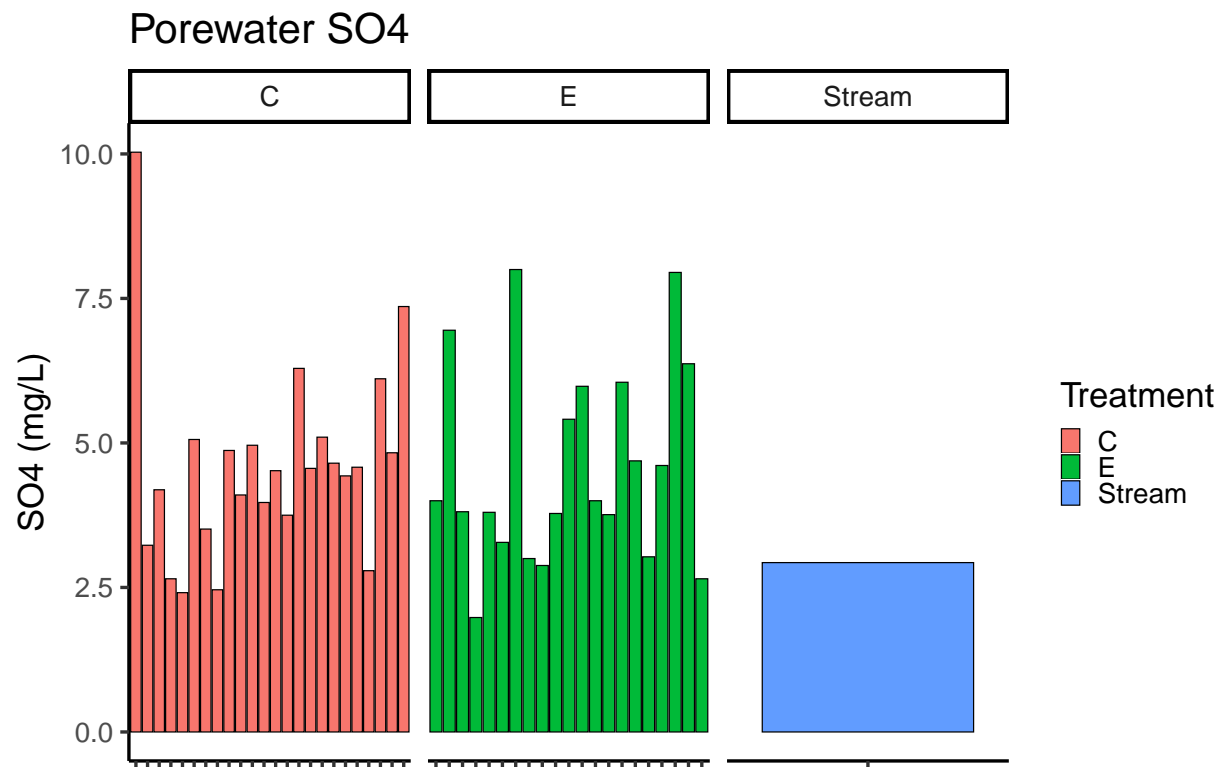
## Visualize Data

# Porewater NOx

Porewater NH3



Porewater PO4

## Porewater SO4



## Porewater NO2



##Export Processed Data

#end