

# COMPASS Synoptic CB Porewater: DOC

September 2024 Samples

2025-10-31

```
##Setup - Change things here & write any notes

#identify section
cat("Setup Information")

## Setup Information

##### Run information - PLEASE CHANGE
Date_Run = "10/10/24" #Date that instrument was run
Run_by = "Stephanie J. Wilson" #Instrument user
Script_run_by = "Stephanie J. Wilson" #Code user
run_notes = "Instrument maintenance before this run, that is why the first standard
curve was off and the blanks decrease concentrations through the run. Some duplicates
out of range." #any notes from the run
samples <- c("GCW", "GWI", "MSM", "SWH") #whatever identifies your samples within the same names
samples_pattern <- paste(samples, collapse = "|")
#samples_pattern <- "GCW" #use this instead of the line above if you have only one site code
chks_name = "Chk_Std_50CN" #what did you name your check standards?

##### File Names - PLEASE CHANGE
#file path and name for raw summary data file
#raw_file_name = "Raw Data/COMPASS_SynopticCB_PW_DOC_202505.txt" #example
raw_file_name = "Raw Data/COMPASS_SynopticCB_PW_DOC_202409.txt"

#file path and name for raw all peaks file
#raw_allpeaks_name = "Raw Data/COMPASS_SynopticCB_PW_DOC_202505_allpeaks.txt" #example
raw_allpeaks_name = "Raw Data/COMPASS_SynopticCB_PW_DOC_202409_allpeaks.txt"

#file path and name of processed data file
#processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_DOC_202505.csv" #example
processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_DOC_202409.csv" #example

##### Log Files - PLEASE CHECK
#downloaded metadata csv - downloaded from Google drive as csv for this year
Raw_Metadata = "Raw Data/COMPASS_SynopticCB_PW_SampleLog_2024.csv"

#qaqc log file path for this year
Log_path = "Raw Data/COMPASS_Synoptic_TOCTN_QAQClog_2024.csv"

##Set Up Code
##Read in metadata and create similar sample IDs for matching to samples
```

## Import Data Functions

### Import Sample Data

```
## Import Sample Data

## New names:
## * `` -> '...14'

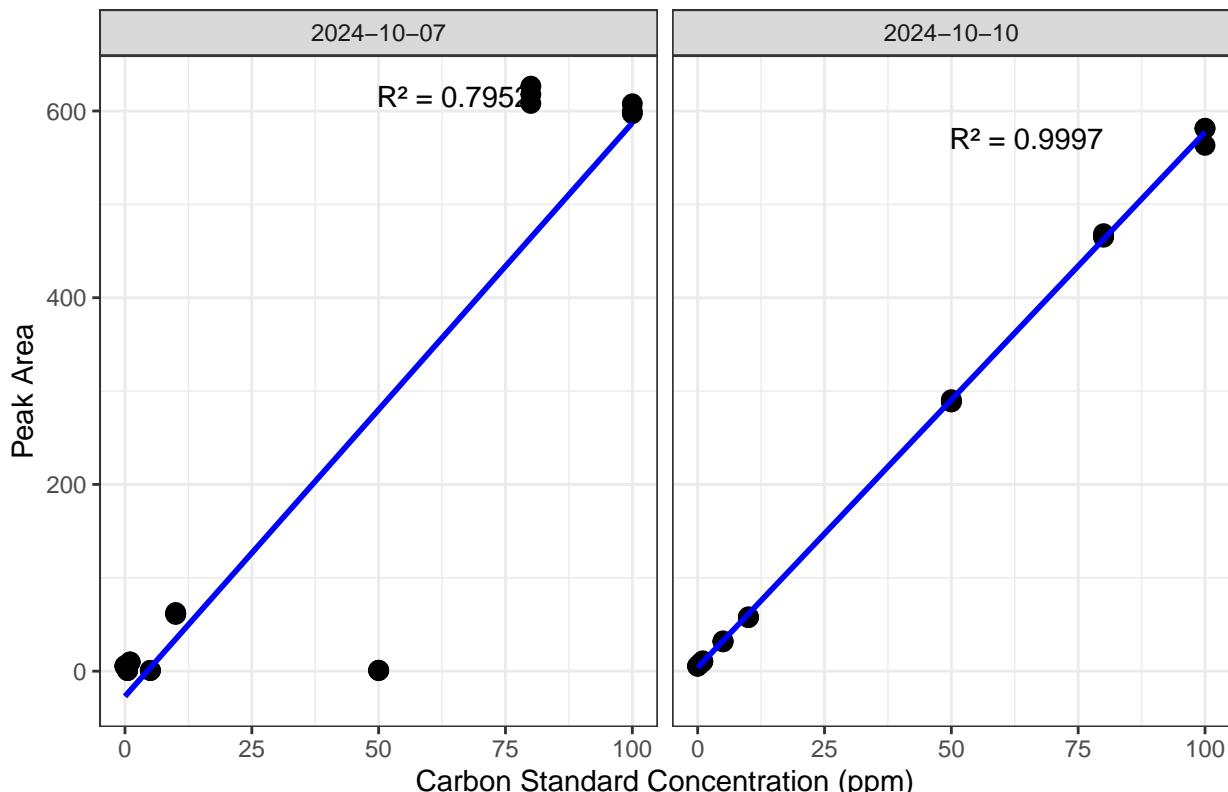
## # A tibble: 6 x 4
##   sample_name      npoc_raw    tdn_raw run_datetime
##   <chr>          <dbl>     <dbl>   <chr>
## 1 202409_GCW_TR_LysA_20cm  2.59    0.109  10/10/2024 5:56:39 PM
## 2 202409_GCW_TR_LysA_45cm  4.95    0.527  10/10/2024 6:25:43 PM
## 3 202409_GCW_TR_LysB_10cm  4.23    0.260  10/10/2024 6:54:21 PM
## 4 202409_GCW_TR_LysB_20cm  2.64    0.812  10/10/2024 7:16:35 PM
## 5 202409_GCW_TR_LysB_45cm  5.41    0.904  10/10/2024 7:47:25 PM
## 6 202409_GCW_TR_LysC_20cm  2.42    0.169  10/10/2024 8:12:45 PM
```

## Assessing Standard Curves

```
## Assess the Standard Curves

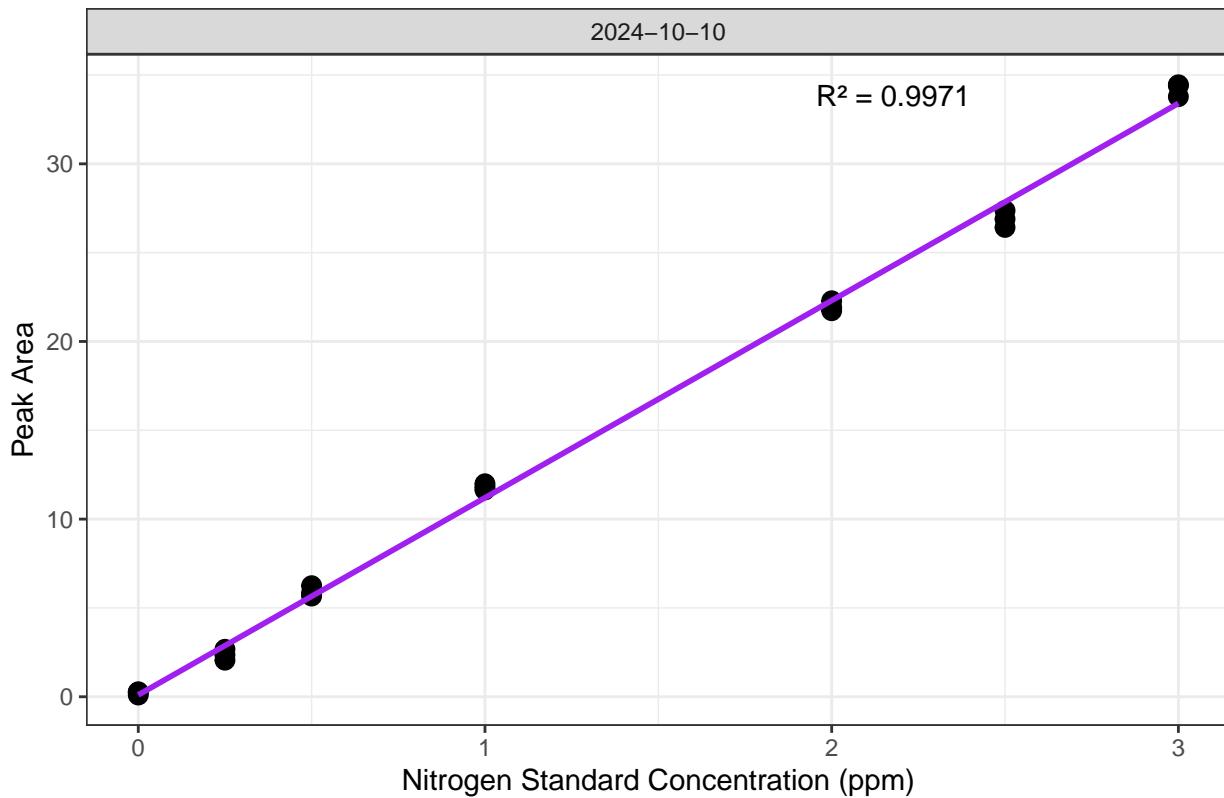
## New names:
## `geom_smooth()` using formula = 'y ~ x'
## * `` -> '...18'
```

NPOC Std Curve by Date

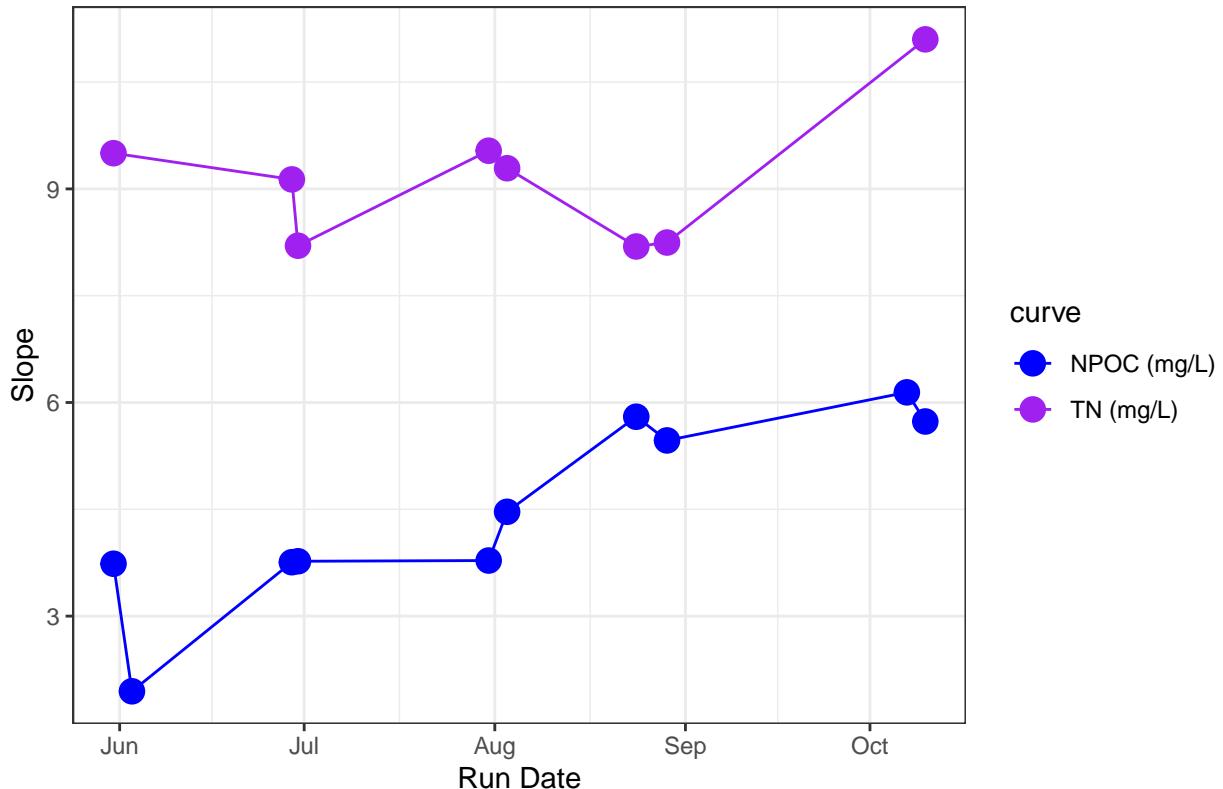


```
## `geom_smooth()` using formula = 'y ~ x'
```

TN Std Curve by Date



## Slope Drift Assessment



```
## [1] "NPOC Curve r2 GOOD"
```

```
## [1] "TN Curve r2 GOOD"
```

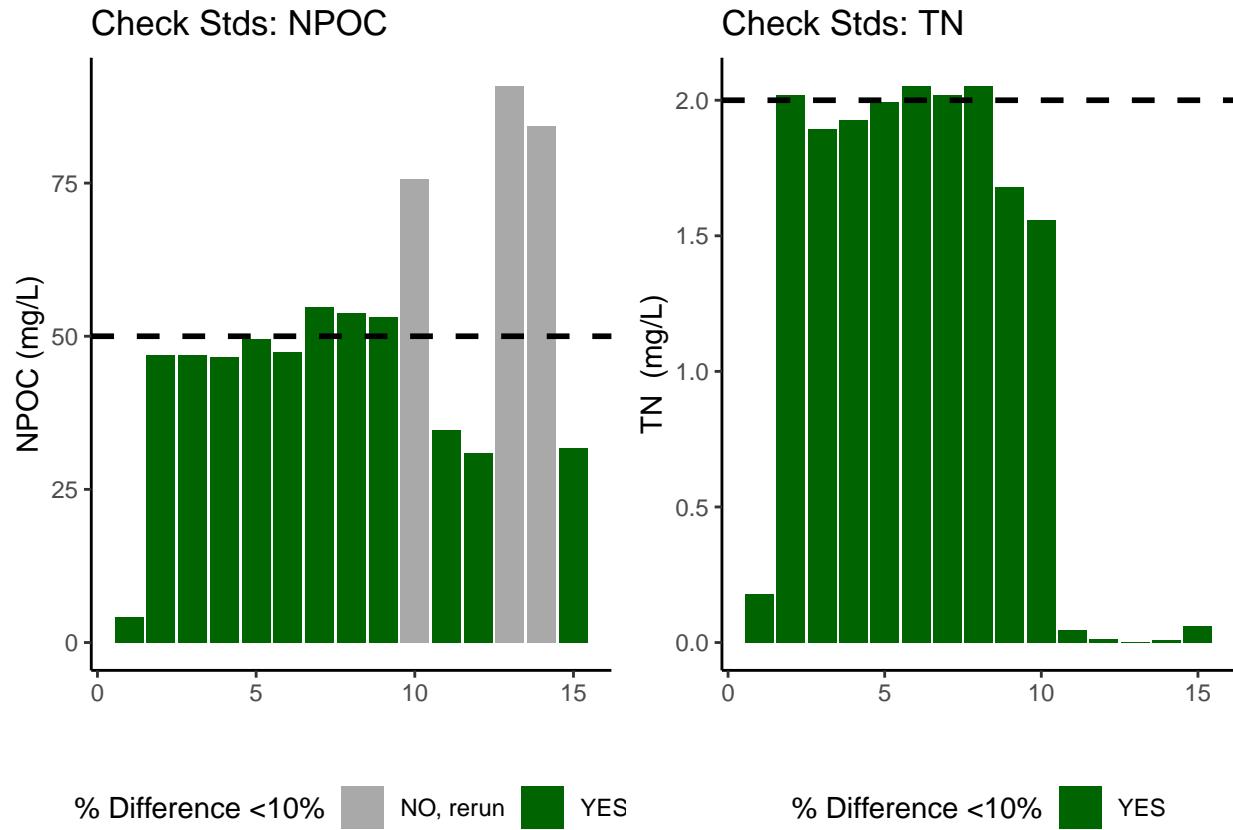
## Assess Check Standards

```
## Assess the Check Standards
```

```
## New names:  
## * ' ' -> '...14'
```

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

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



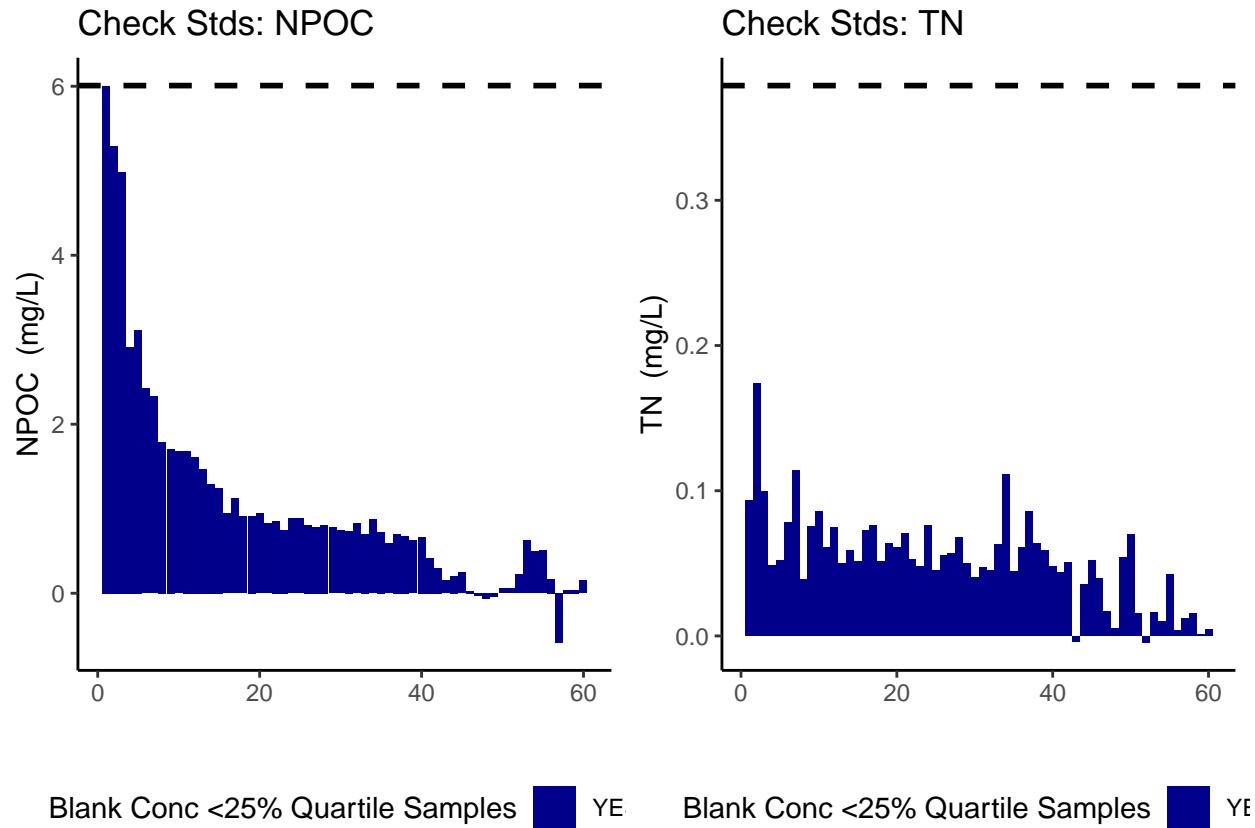
```
## [1] ">60% of Carbon Check Standards are within range of expected concentration"
## [1] ">60% of Nitrogen Check Standards are within range of expected concentration"
```

### Assess Blanks

```
## Assess Blanks

## New names:
## * `` -> '...14'

## [1] ">60% of Carbon Blank concentrations are lower 25% quartile of samples"
## [1] ">60% of Nitrogen Blank concentrations are lower 25% quartile of samples"
```



```
## carbon blanks:
```

```
## [1] 1.04306
```

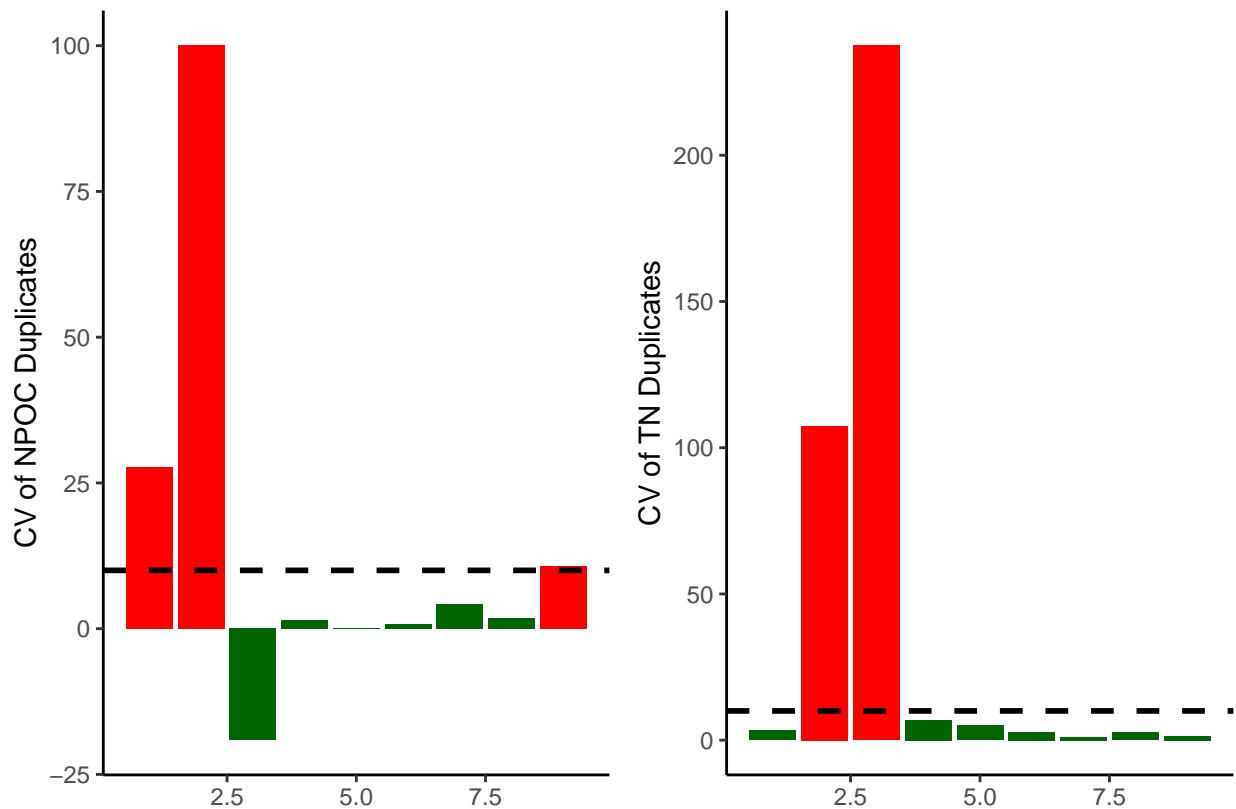
```
## nitrogen blanks:
```

```
## [1] 0.052526
```

## Assess Duplicates

```
## Assess Duplicates
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```



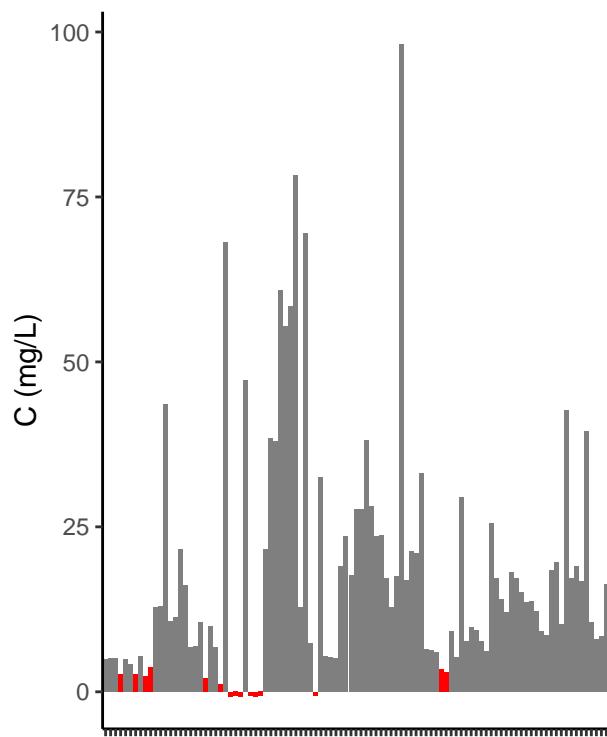
```
## [1] ">60% of Carbon Duplicates have a CV <10%"
```

```
## [1] ">60% of Nitrogen Duplicates have a CV <10%"
```

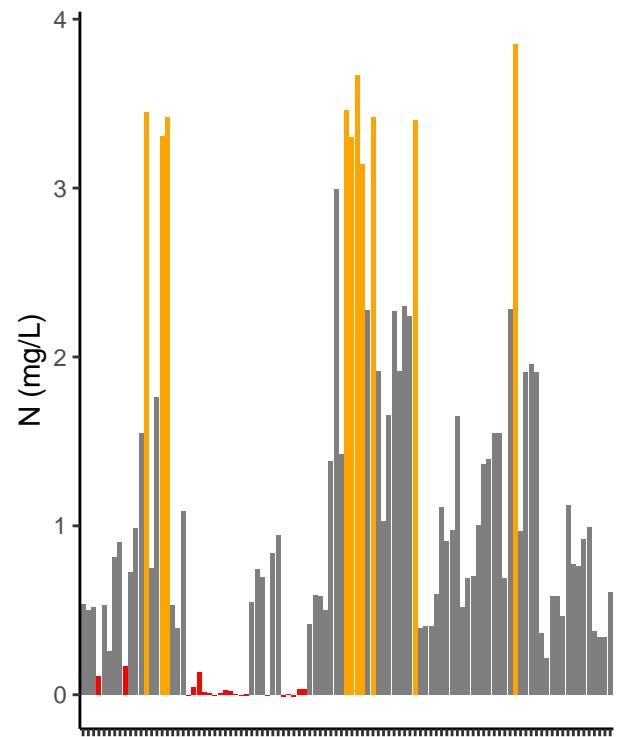
### Sample Flagging - Are samples Within the range of the curve?

```
## Sample Flagging
```

C: Grey = Within Range of Curve



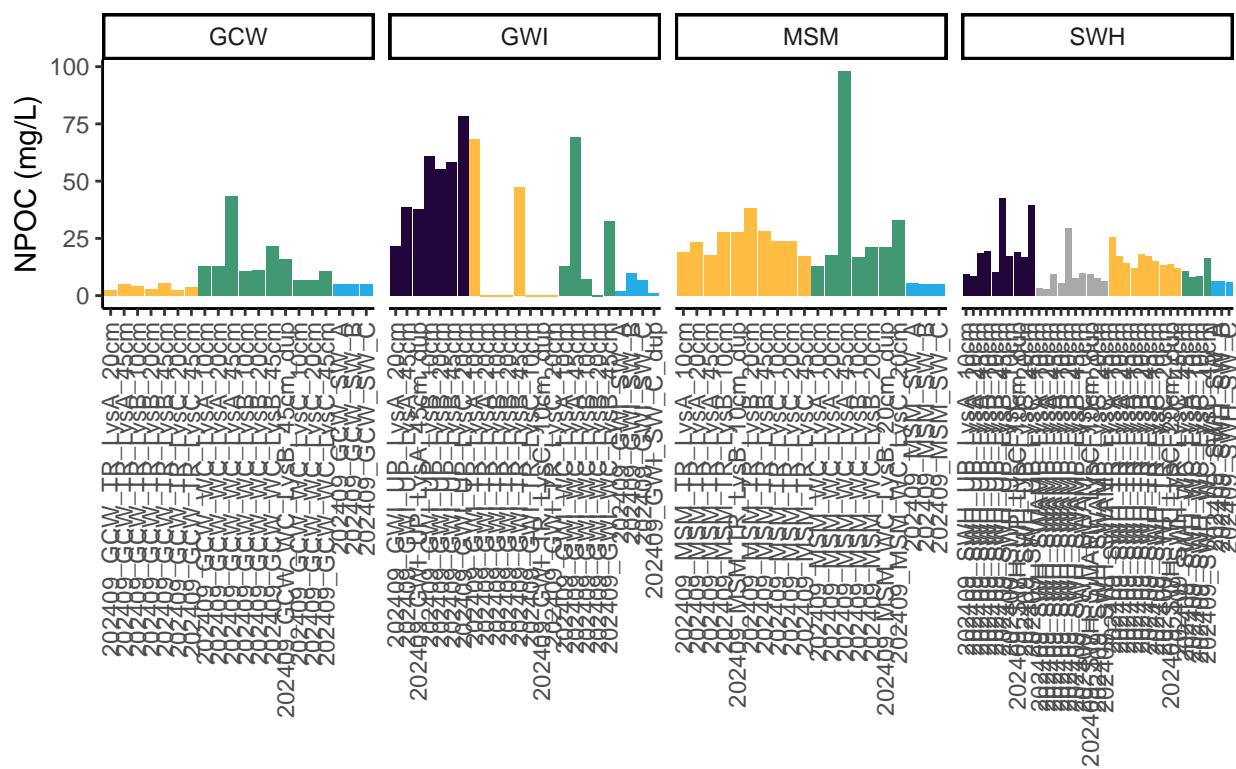
N: Grey = Within Range of Curve

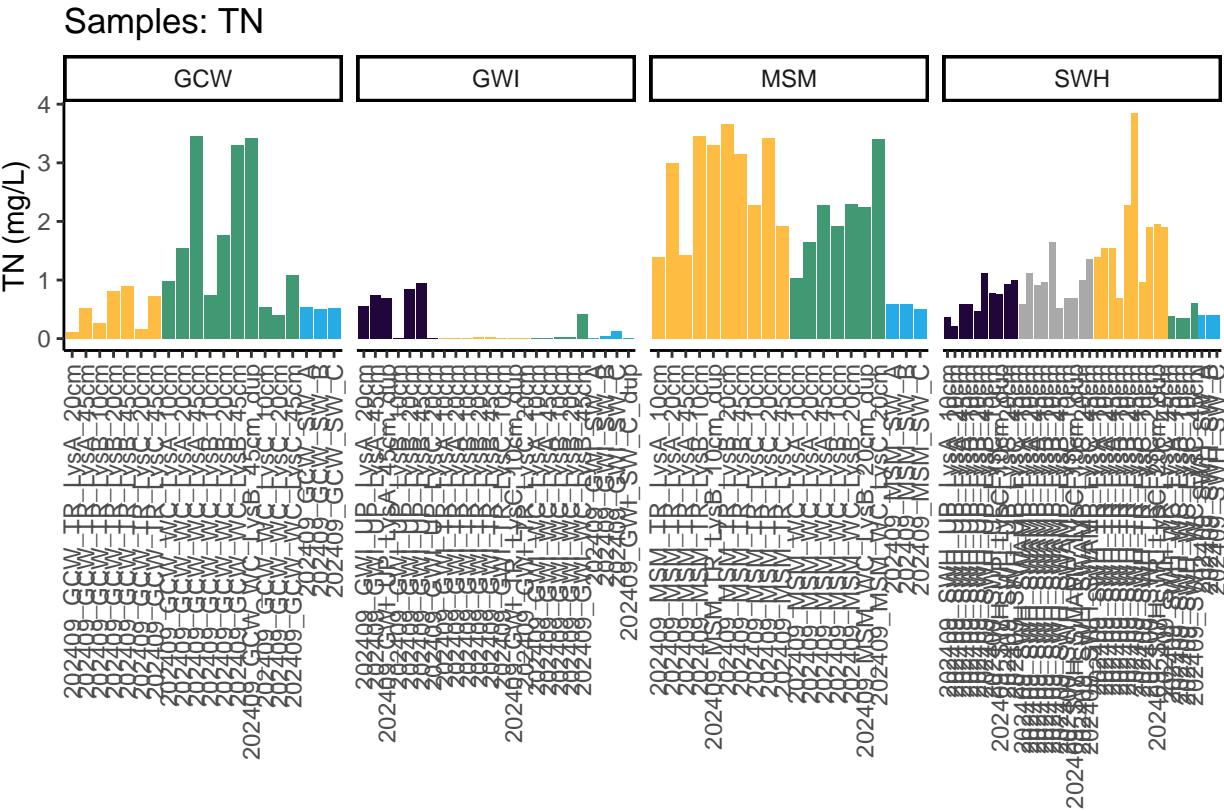


## Visualize Data by Plot

```
## Visualize Data  
  
## Warning in rbind(c("202409", "GCW", "TR", "LysA", "20cm"), c("202409", "GCW", :  
## number of columns of result is not a multiple of vector length (arg 1)
```

### Samples: NPOC





Convert data from mg/L to uMoles/L

Check to see if samples run match metadata & merge info

```
## Check Sample IDs with Metadata
## All sample IDs are present in metadata.
```

## Export Processed Data

```
## Export Processed Data

## # A tibble: 6 x 21
##   Project     Region Site  Zone  Replicate Depth_cm Sample_ID Year Month Day
##   <chr>      <chr>  <chr> <fct> <chr>       <int> <chr>    <int> <int> <int>
## 1 COMPASS: Sy~ CB    SWH   UP    A           10 202409_S~ 2024    9    24
## 2 COMPASS: Sy~ CB    SWH   UP    A           20 202409_S~ 2024    9    24
## 3 COMPASS: Sy~ CB    SWH   UP    A           45 202409_S~ 2024    9    24
## 4 COMPASS: Sy~ CB    SWH   UP    B           10 202409_S~ 2024    9    24
## 5 COMPASS: Sy~ CB    SWH   UP    B           20 202409_S~ 2024    9    24
## 6 COMPASS: Sy~ CB    SWH   UP    B           45 202409_S~ 2024    9    24
## # i 11 more variables: Time <chr>, Time_Zone <chr>, npoc_mgL <dbl>,
## #   npoc_uM <dbl>, npoc_flag <chr>, tdn_mgL <dbl>, tdn_uM <dbl>,
## #   tdn_flag <chr>, Analysis_runtime <chr>, Run_notes <chr>, Field_notes <chr>
```

#end