

Synoptic CB: Porewater DIC

November 2024 Samples

2025-10-21

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

```
#identify section  
cat("Setup Information")
```

```
## Setup Information
```

```
##### Run information - PLEASE CHANGE  
Date_Run = "11/25/2024" #Date that instrument was run  
Run_by = "Stephanie J. Wilsonr" #Instrument user  
Script_run_by = "Stephanie J. Wilson" #Code user  
run_notes = "There was only one duplicate included in this run and it is out of range,  
accepting the run. " #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_" #what did you name your check standards?  
crm_name = "CRM|crm" #what did you name your CRMS?  
  
##### File Names - PLEASE CHANGE  
#file path and name for raw summary data file  
raw_file_name = "Raw Data/TOCTN_COMPASS_Synoptic_DIC_202411.txt"  
  
#file path and name for raw all peaks file  
raw_allpeaks_name = "Raw Data/TOCTN_COMPASS_Synoptic_DIC_202411_allpeaks.txt"  
  
#file path and name of processed data file  
processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_DIC_202411.csv"  
  
##### 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_DIC_QAQClog_2024.csv"
```

```
##Set Up Code
```

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

0.1 Import Data Functions

0.2 Import Sample Data

```
## Import Sample Data
```

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

```
## # A tibble: 6 x 3  
##   sample_name          ic_raw run_datetime
```

```
##   <chr>                                <dbl> <chr>
## 1 202411_SWH_UP_LysA_10cm             3.13 11/26/2024 12:18:08 PM
## 2 202411_SWH_UP_LysA_20cm             5.01 11/26/2024 12:28:48 PM
## 3 202411_SWH_UP_LysA_45cm            15.5 11/26/2024 12:44:57 PM
## 4 202411_SWH_UP_LysB_10cm             3.02 11/26/2024 12:55:18 PM
## 5 202411_SWH_UP_LysB_20cm            11.6 11/26/2024 1:06:21 PM
## 6 202411_SWH_UP_LysC_20cm             5.29 11/26/2024 1:17:01 PM
```

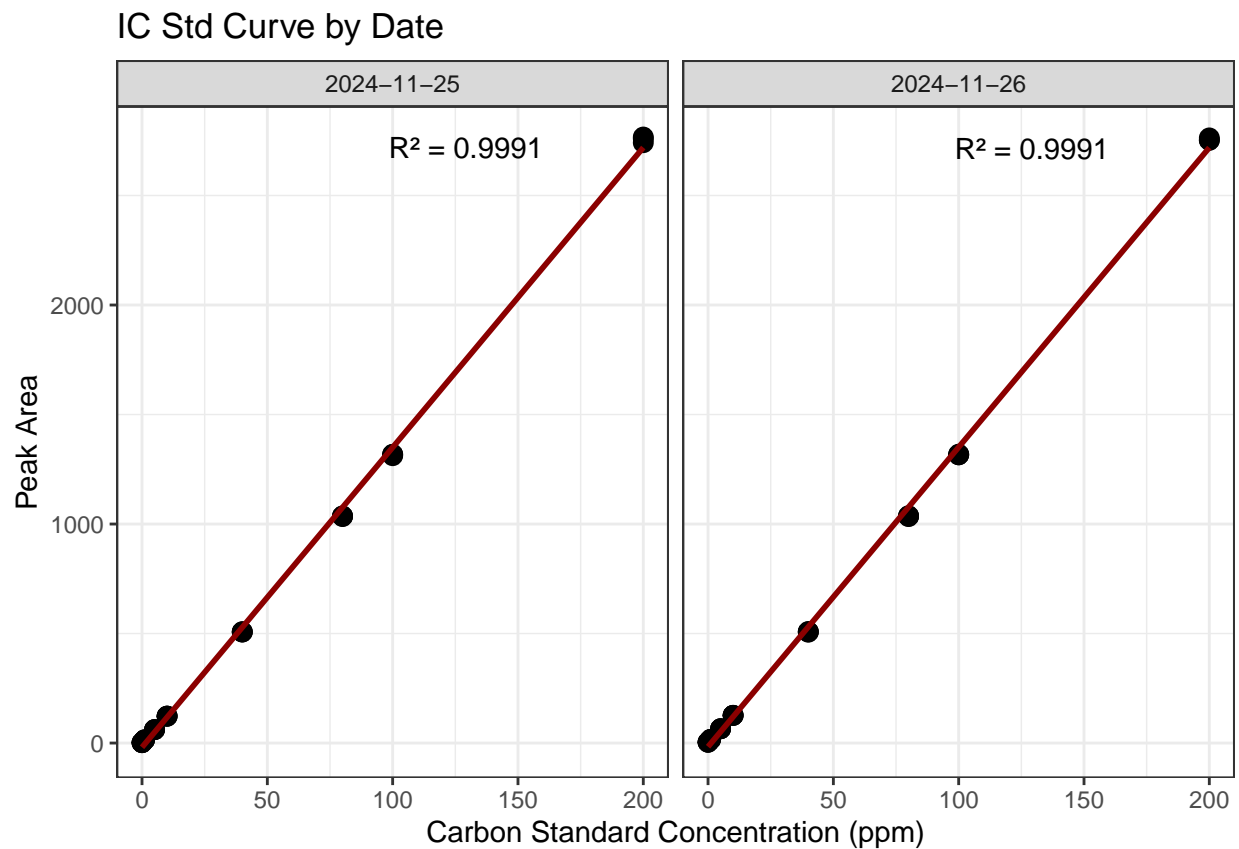
0.3 Assessing Standard Curves

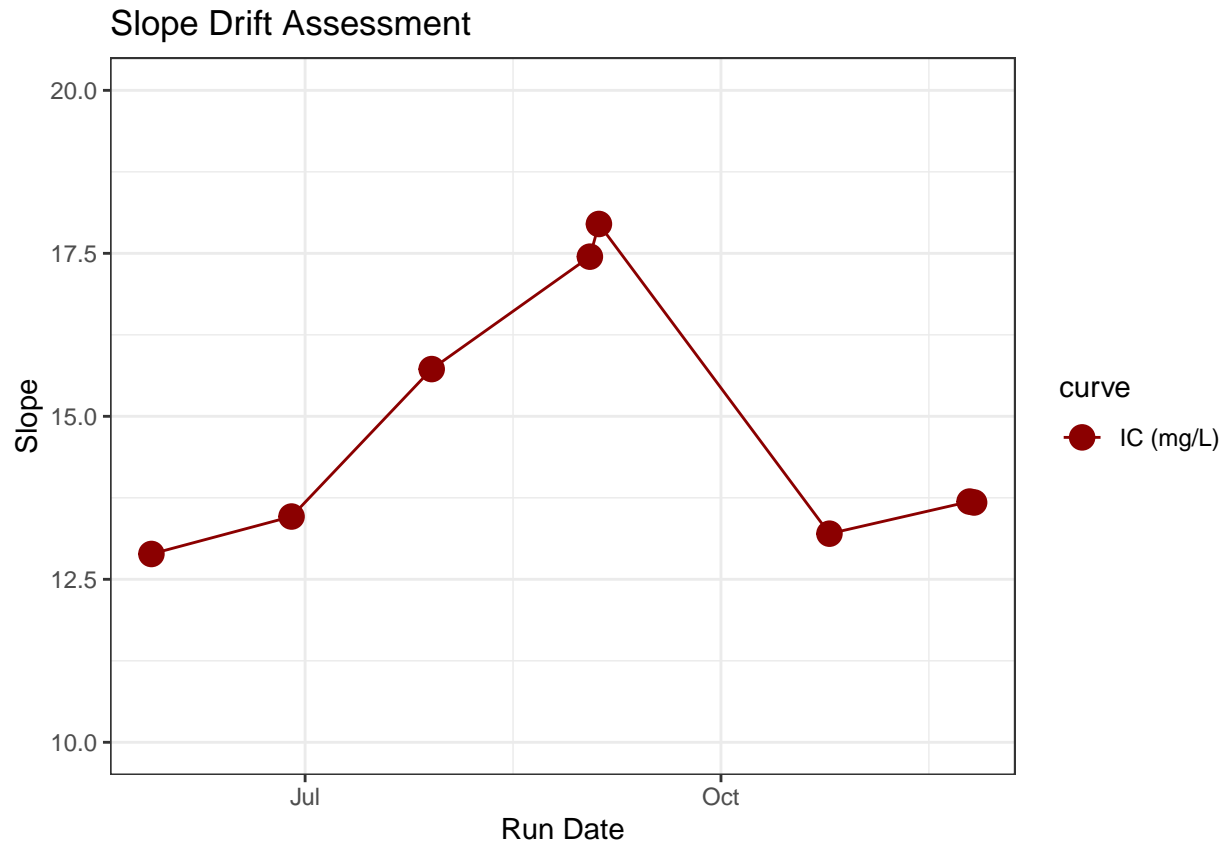
```
## Assess the Standard Curves
```

```
## New names:
## * ' ' -> '...18'
```

```
## Warning: One or more parsing issues, call 'problems()' on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)
```

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





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

0.4 CRM Check - Don't run chunk if no CRMs run

```
## Assess the CRMs
```

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

```
## [1] "IC crm has a % Difference <25% of expected - PROCEED"
```

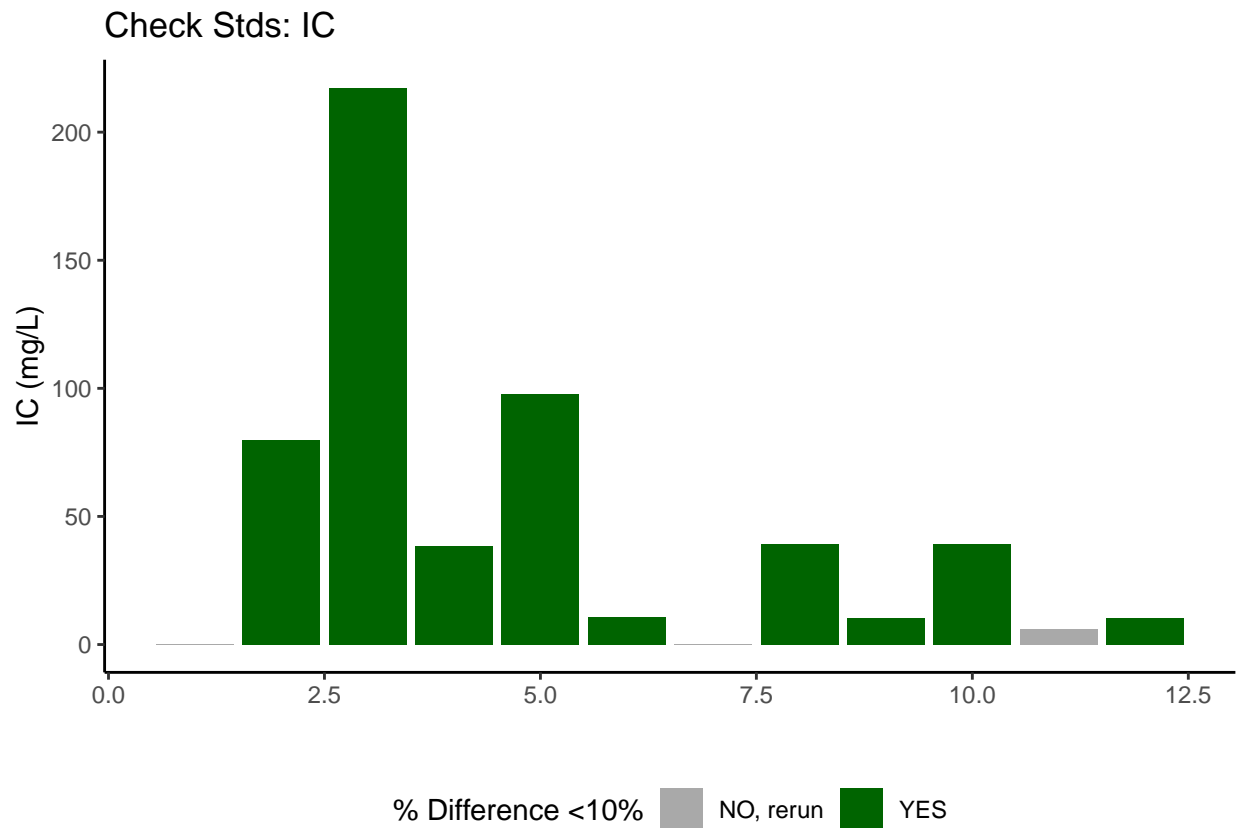
```
## Run mean = 21.95333
```

```
## Expected = 22.19
```

0.5 Assess Check Standards

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

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



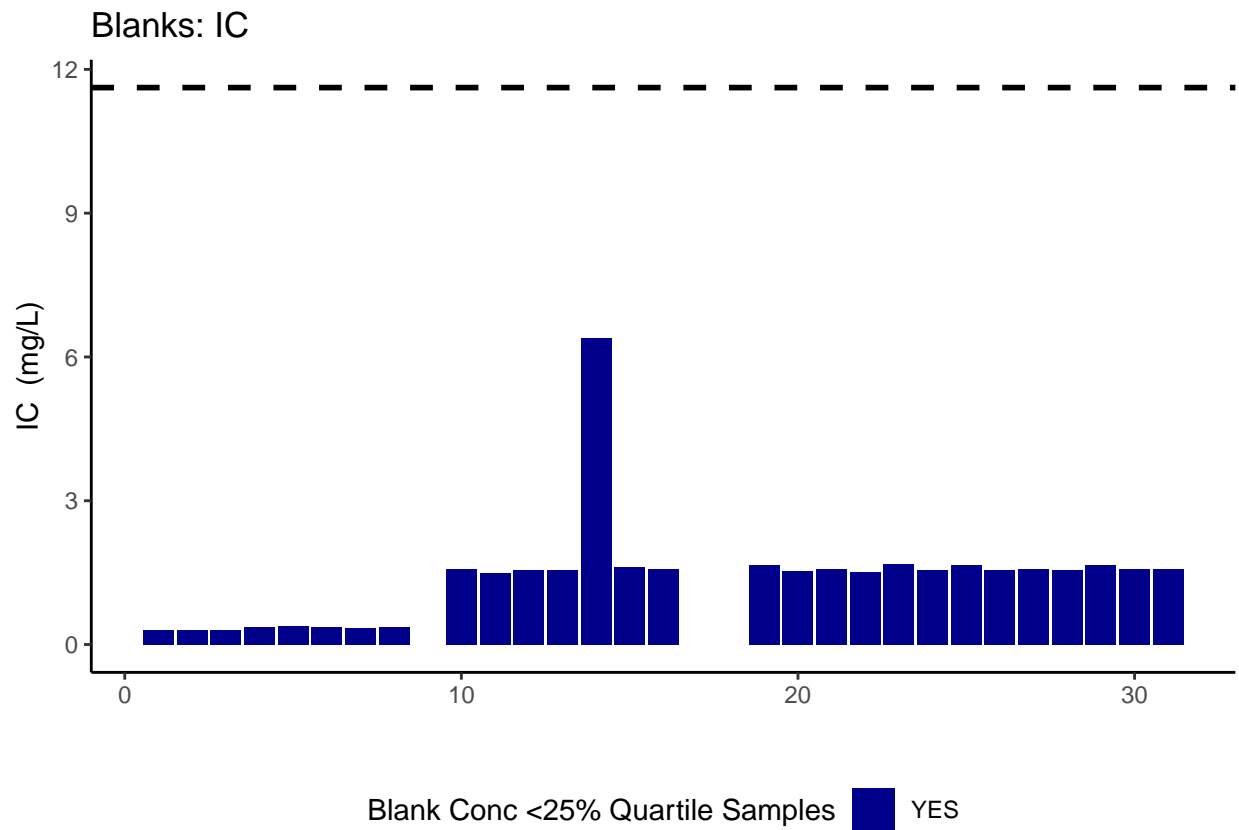
```
## [1] ">60% of IC Check Standards are within range of expected concentration"
```

0.6 Assess Blanks

```
## Assess Blanks
```

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

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

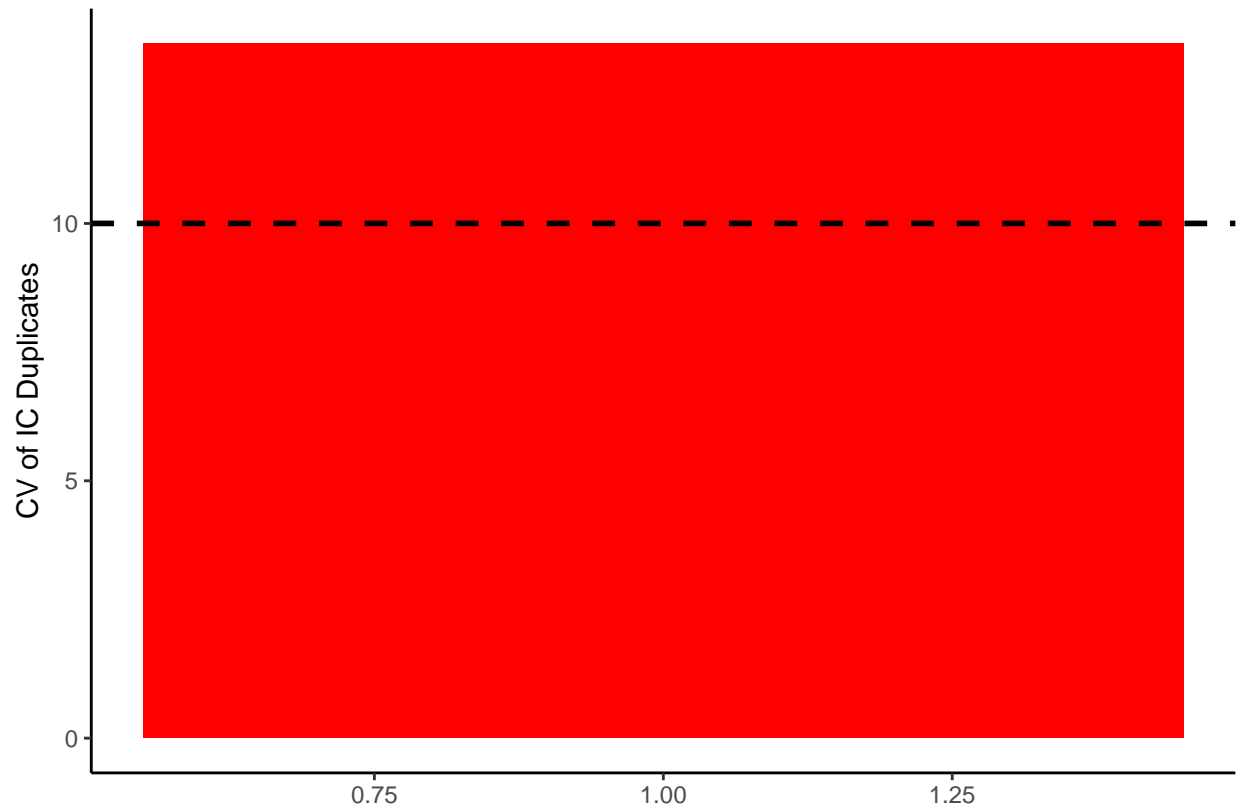


```
## carbon blanks:
```

```
## [1] 1.397504
```

0.7 Assess Duplicates - only one dup and it is out of range...

```
## Assess Duplicates
```

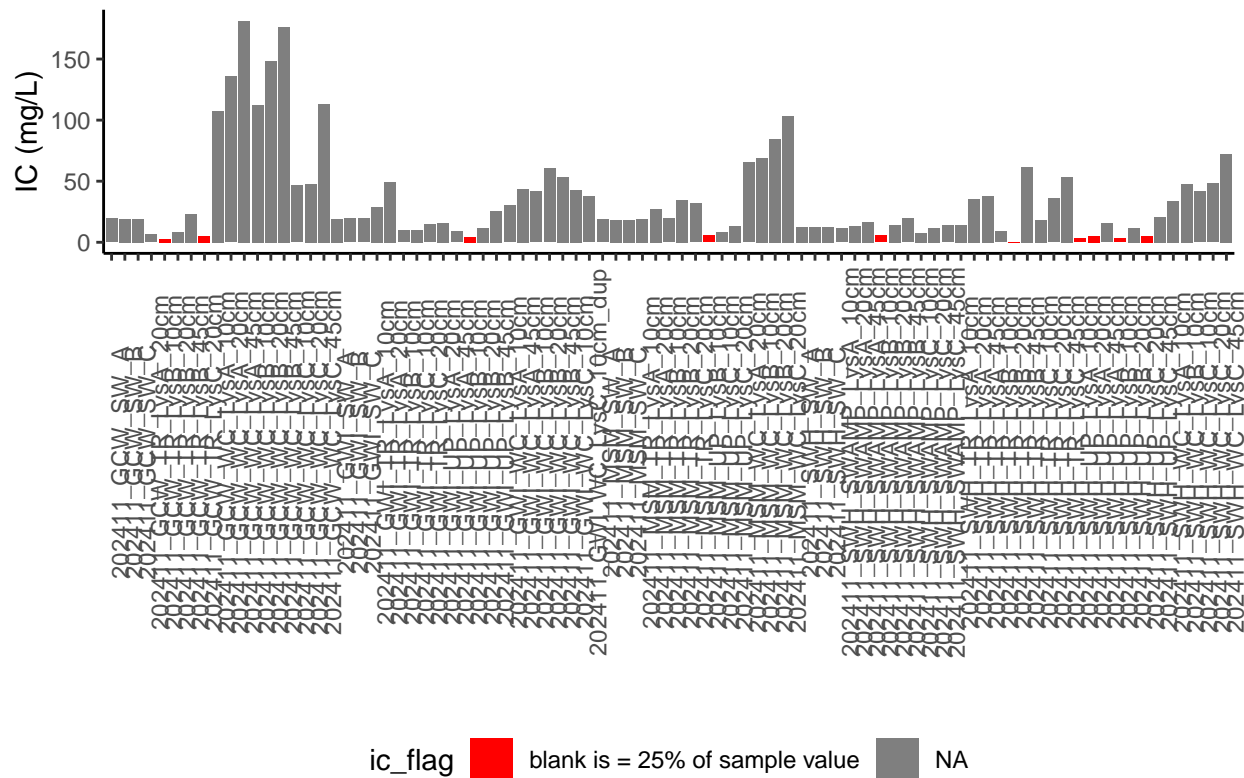


```
## [1] "<60% of Carbon Duplicates have a CV <10% - REASSESS"
```

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

```
## Sample Flagging
```

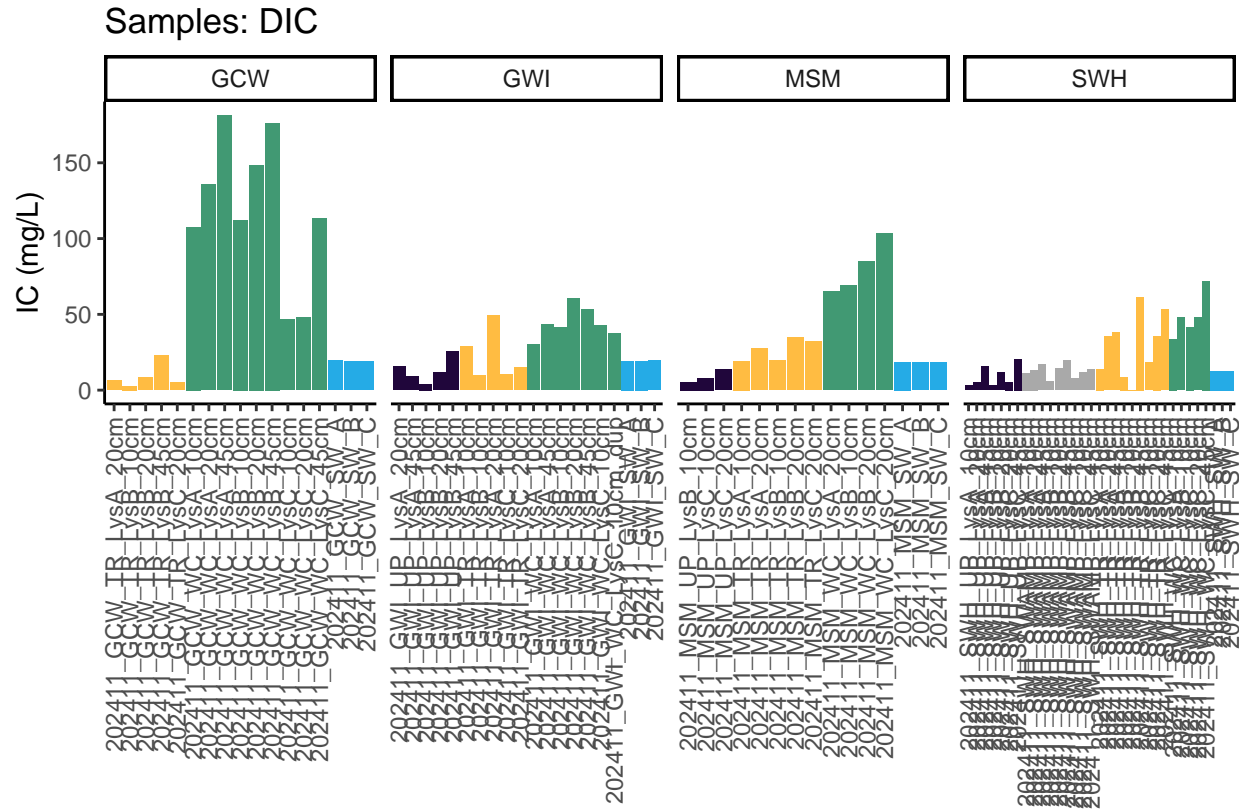
C: Grey = Within Range of Curve



0.9 Visualize Data by Plot

```
## Visualize Data
```

```
## Warning in rbind(c("202411", "SWH", "UP", "LysA", "10cm"), c("202411", "SWH", :
## number of columns of result is not a multiple of vector length (arg 1)
```

0.10 Convert data from mg/L to uMoles/L

0.11 Check to see if samples run match metadata & merge info

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

0.12 Export Processed Data

```
## Export Processed Data

## # A tibble: 6 x 18
##   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 202411_S~ 2024 11 12
## 2 COMPASS: Sy~ CB SWH UP A          20 202411_S~ 2024 11 12
## 3 COMPASS: Sy~ CB SWH UP A          45 202411_S~ 2024 11 12
## 4 COMPASS: Sy~ CB SWH UP B          10 202411_S~ 2024 11 12
## 5 COMPASS: Sy~ CB SWH UP B          20 202411_S~ 2024 11 12
## 6 COMPASS: Sy~ CB SWH UP C          20 202411_S~ 2024 11 12
## # i 8 more variables: Time <chr>, Time_Zone <chr>, ic_mgL <dbl>, ic_uM <dbl>,
## # ic_flag <chr>, Analysis_runtime <chr>, Run_notes <chr>, Field_notes <chr>

#end
```