

Synoptic CB: Porewater SO₄/Cl

November 2025 Samples

2025-11-24

Contents

0.1	Run Information	2
0.2	Assess Standard Curves	3
0.3	Assess Check Standards	4
0.4	Assess Blanks	5
0.5	Assess Duplicates	7
0.6	Calculate mmol/L concentrations & salinity, add dilutions	8
0.7	Assess Analytical Spikes	9
0.8	Check if samples within the range of the standard curve	10
0.9	Check to see if samples run match metadata & merge info	10
0.10	Visualize Data by Plot	11
0.11	Export Processed Data	11

```
##Add Required Packages
```

0.1 Run Information

```
##### Run information - PLEASE CHANGE
Date_Run = "2025-11-20" #Date that instrument was run
Run_by = "Zoe Read" #Instrument user
Script_run_by = "Zoe Read" #Code user
run_notes = "No issues with this run. All sample IDs are present in metadata.
" #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

##Fix samples that were entered incorrectly
samples_to_remove <- NA
Old_ID_1 = NA
New_ID_1 = NA

##### File Names - PLEASE CHANGE
#file path and name for raw summary data file
raw_file_name_cl = "Raw Data/COMPASS_Synoptic_CB_MonMon_202511_Cl.txt"
raw_file_name_so4 = "Raw Data/COMPASS_Synoptic_CB_MonMon_202511_S04.txt"

#file path and name of processed data file
processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_Cl_S04_202511.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_2025.csv"

#qaqc log file path for this year
Log_path = "Raw Data/COMPASS_Synoptic_Cl_S04_QAAClog_2024.csv"
```

```
##Set Up Code - constants and QAQC cutoffs
```

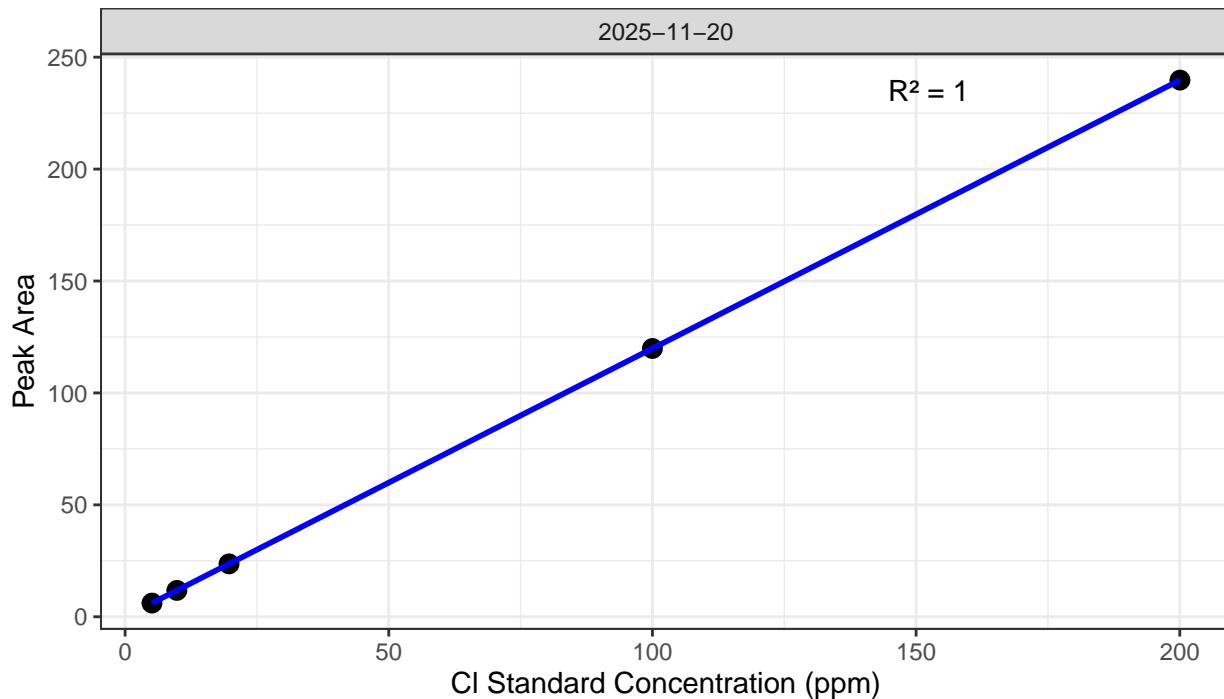
```
##Read in metadata and create similar sample IDs for matching to samples
```

```
##Import Sample Data
```

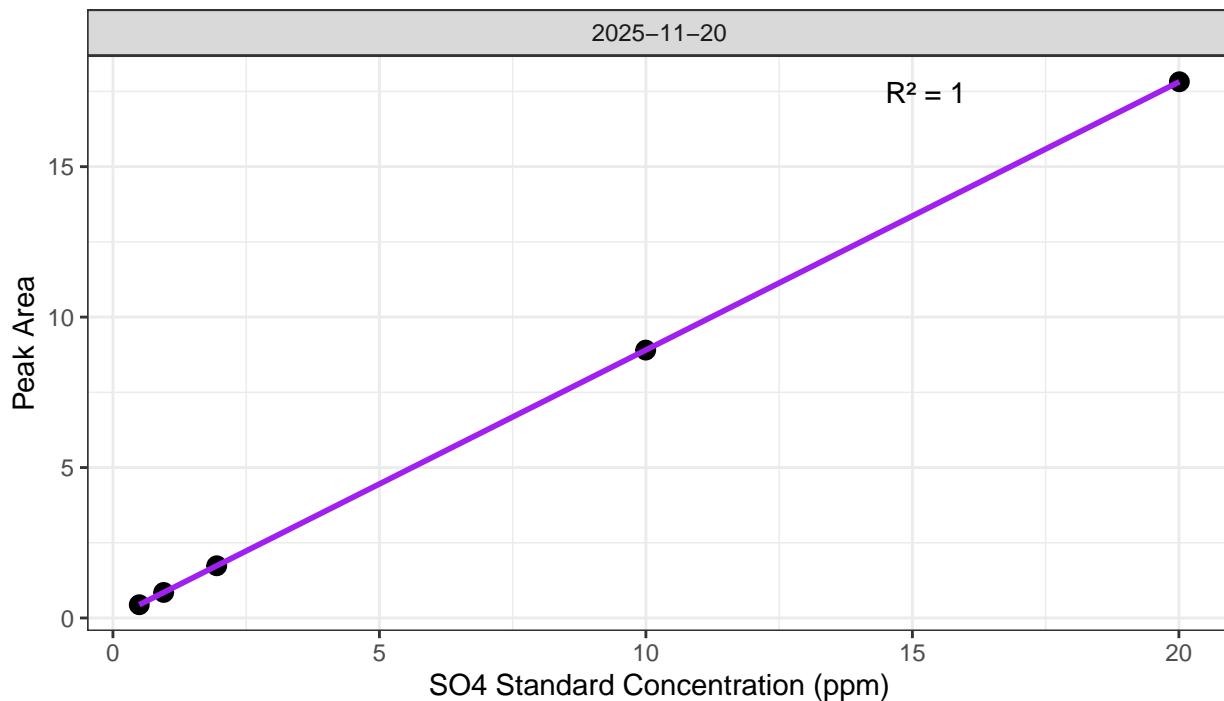
```
##Fix samples entered incorrectly
```

0.2 Assess Standard Curves

Chloride Std Curve

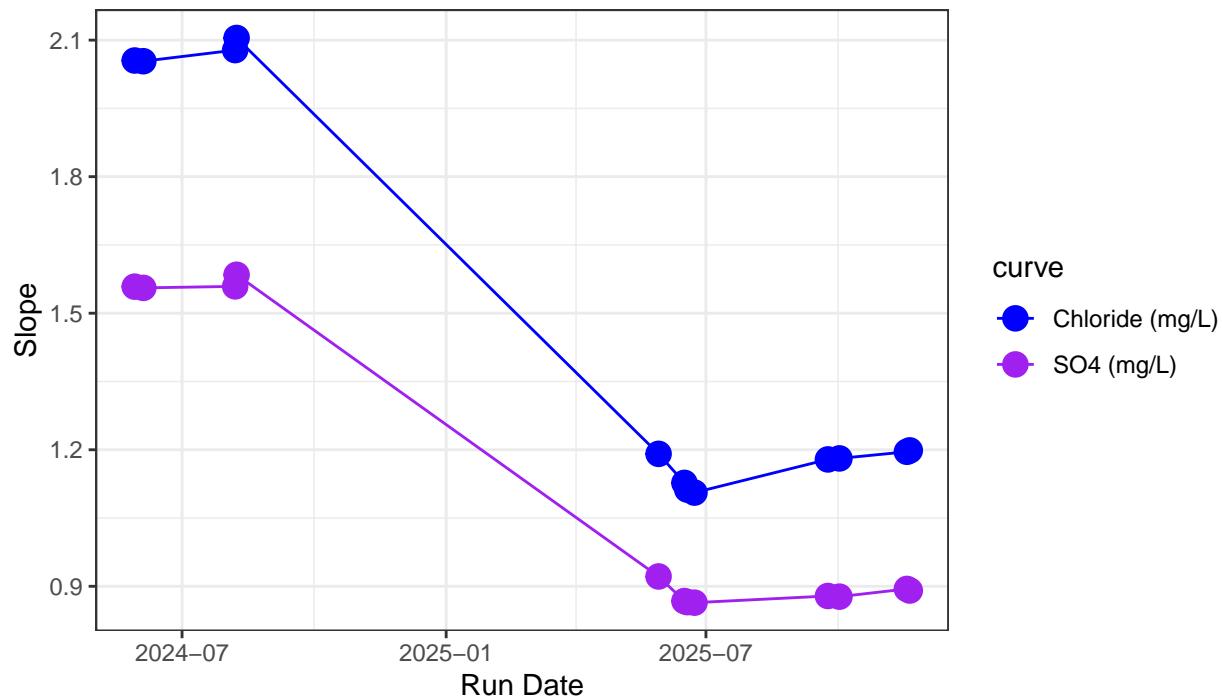


Sulfate Std Curve



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

Slope Drift Assessment



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

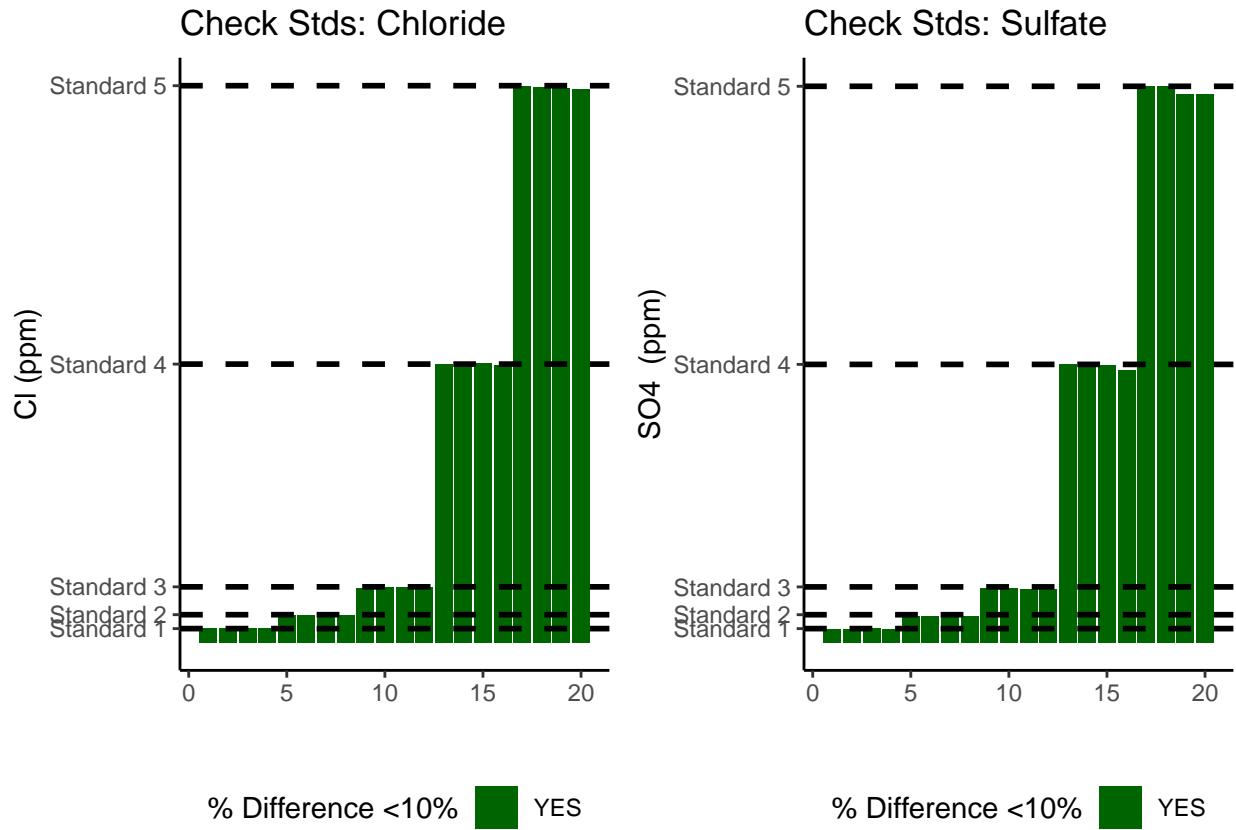
```
## [1] "SO4 Curve r2 GOOD"
```

0.3 Assess Check Standards

```
## # A tibble: 5 x 5
##   sample_ID  mean_Cl    sd_Cl    cv_Cl flag_Cl
##   <chr>       <dbl>    <dbl>    <dbl> <chr>
## 1 Standard 1  5.18  0.0608  0.0117 Chloride Check Standard RSD within Range - ~
## 2 Standard 2  9.96  0.0955  0.00959 Chloride Check Standard RSD within Range - ~
## 3 Standard 3 19.8   0.0874  0.00441 Chloride Check Standard RSD within Range - ~
## 4 Standard 4 100.    0.338   0.00338 Chloride Check Standard RSD within Range - ~
## 5 Standard 5 199.   0.451   0.00226 Chloride Check Standard RSD within Range - ~

## # A tibble: 5 x 5
##   sample_ID  mean_SO4   sd_SO4   cv_SO4 flag_SO4
##   <chr>       <dbl>    <dbl>    <dbl> <chr>
## 1 Standard 1  0.497  0.00686  0.0138 Sulfate Check Standard RSD within Range --~ 
## 2 Standard 2  0.949  0.0105   0.0111 Sulfate Check Standard RSD within Range --~ 
## 3 Standard 3  1.93   0.0175   0.00908 Sulfate Check Standard RSD within Range --~ 
## 4 Standard 4  9.96   0.100    0.0101 Sulfate Check Standard RSD within Range --~ 
## 5 Standard 5 19.9    0.174    0.00878 Sulfate Check Standard RSD within Range --~ 

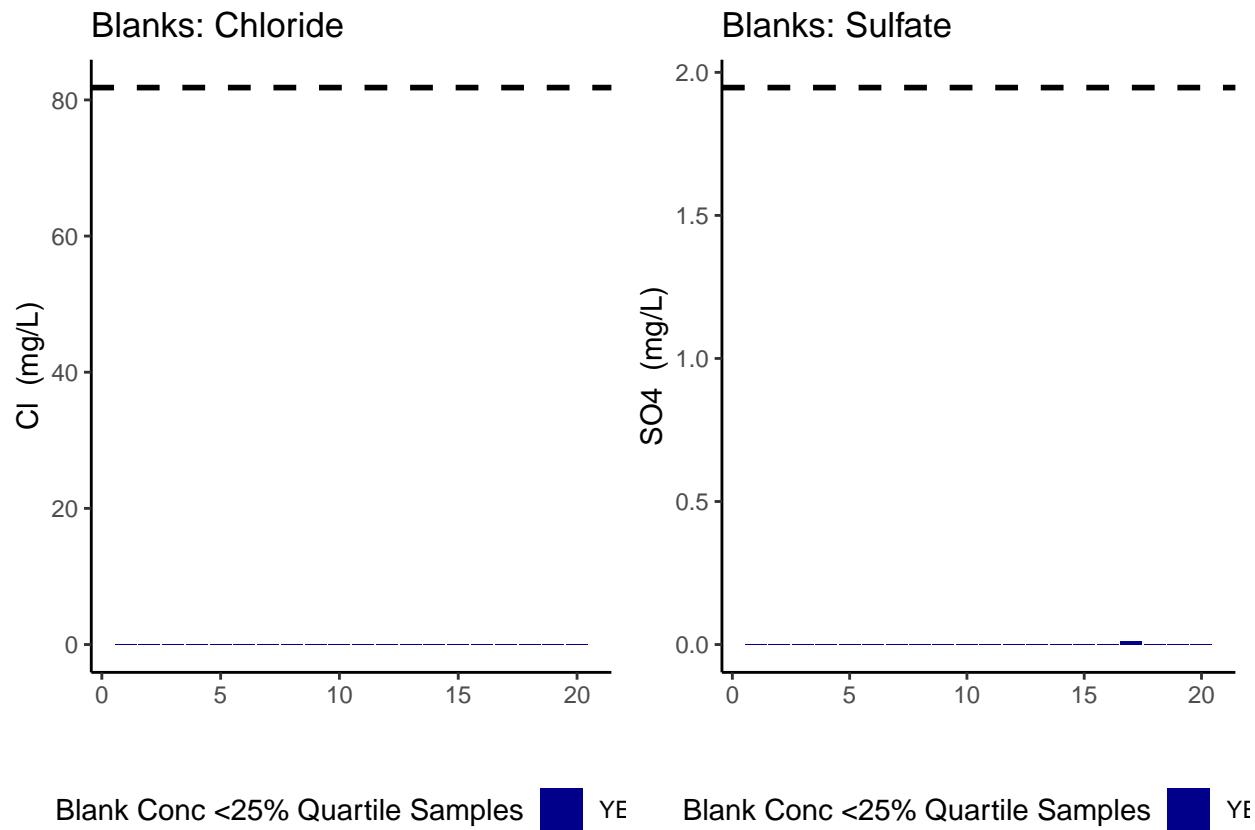
## [1] ">80% of Chloride Check Standards have RSD within range - PROCEED"
## [1] ">80% of Sulfate Check Standards have RSD within range - PROCEED"
```



```
## [1] ">80% of Chloride Check Standards are within range of expected concentration - PROCEED"
## [1] ">80% of Sulfate Check Standards are within range of expected concentration - PROCEED"
```

0.4 Assess Blanks

```
## [1] ">80% of Chloride Blank concentrations are lower 25% quartile of samples"
## [1] ">80% of Sulfate Blank concentrations are lower 25% quartile of samples"
```



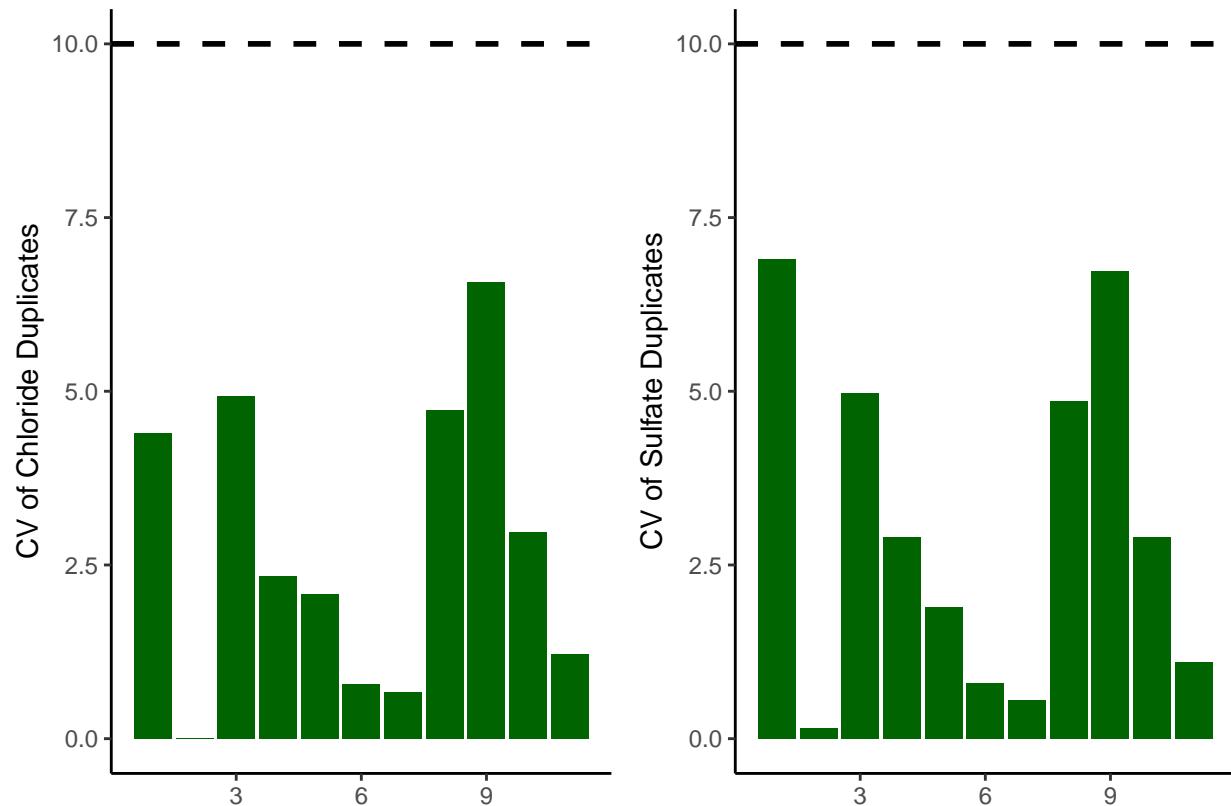
```
## Chloride blanks mean ppm:
```

```
## [1] 0.005505
```

```
## Sulfate blanks mean ppm:
```

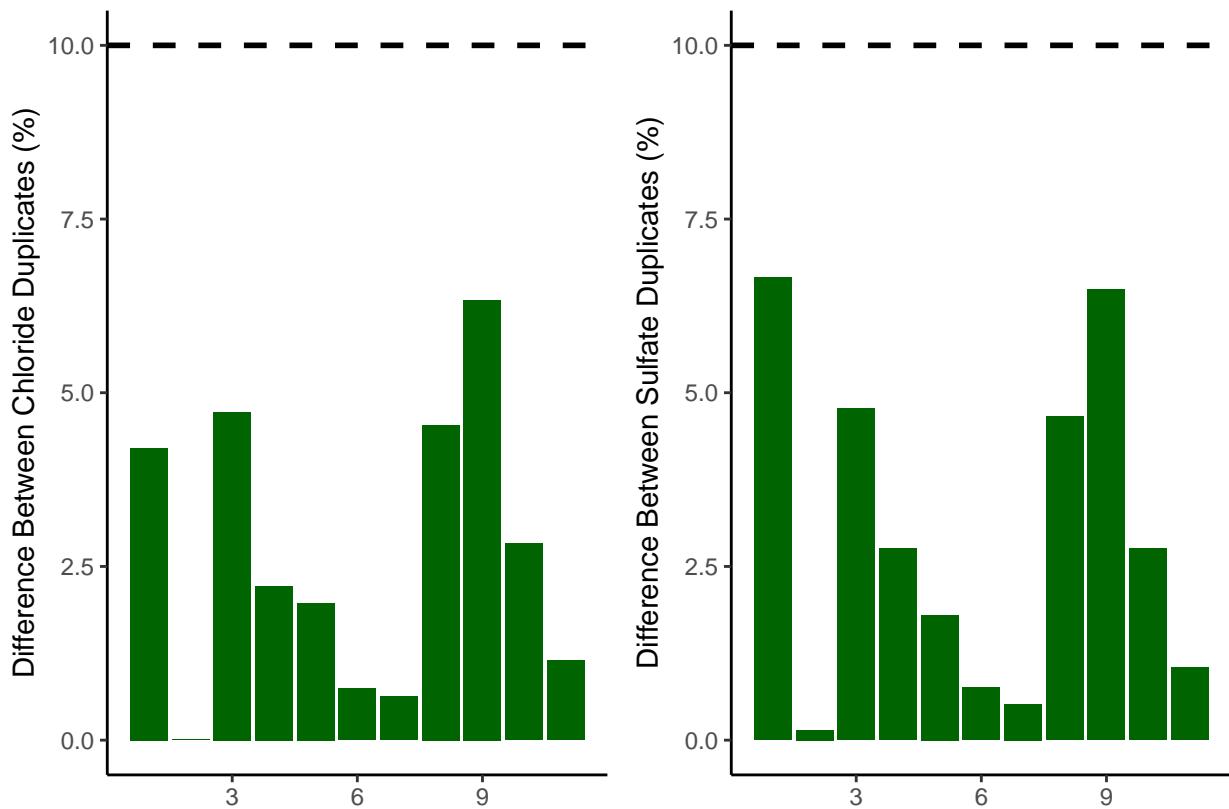
```
## [1] 0.00062
```

0.5 Assess Duplicates



```
## [1] ">80% of Chloride Duplicates have a CV <10% - PROCEED"
```

```
## [1] ">80% of Sulfate Duplicates have a CV <10% - PROCEED"
```



```
## [1] ">80% of Chloride Duplicates have a percent difference <10% - PROCEED"
```

```
## [1] ">80% of Sulfate Duplicates have a percent difference <10% - PROCEED"
```

0.6 Calculate mmol/L concentrations & salinity, add dilutions

```
# Convert ppm to mmol/L
all_dat$SO4_Conc_mM <- (all_dat$SO4_ppm / s_mw)
all_dat$Cl_Conc_mM <- (all_dat$Cl_ppm / cl_mw)

# Calculate Salinity
# calculated using the Knudsen equation
# Salinity = 0.03 + 1.8050 * Chlorinity
# Ref: A Practical Handbook of Seawater Analysis by Strickland & Parsons (P. 11)
# =((1.807*Cl_ppm)+0.026)/1000
all_dat$salinity <- ((1.807 * all_dat$Cl_ppm) + 0.026) / 1000

#Need to determine dilution factors for your samples
#for Steph / COMPASS this depends on the site so...
all_dat$Dilution <- 1
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "MSM") & str_detect(all_dat$sample_ID, "UP"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "MSM") & str_detect(all_dat$sample_ID, "TR"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "MSM") & str_detect(all_dat$sample_ID, "WC"),
```

```

all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "MSM") & str_detect(all_dat$sample_ID, "SW"), 50, all_dat$Dilution)

all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "UP"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "TR"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "WC"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "SW"), 50, all_dat$Dilution)

all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "UP"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "TR"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "WC"), 50, all_dat$Dilution)
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "SW"), 50, all_dat$Dilution)

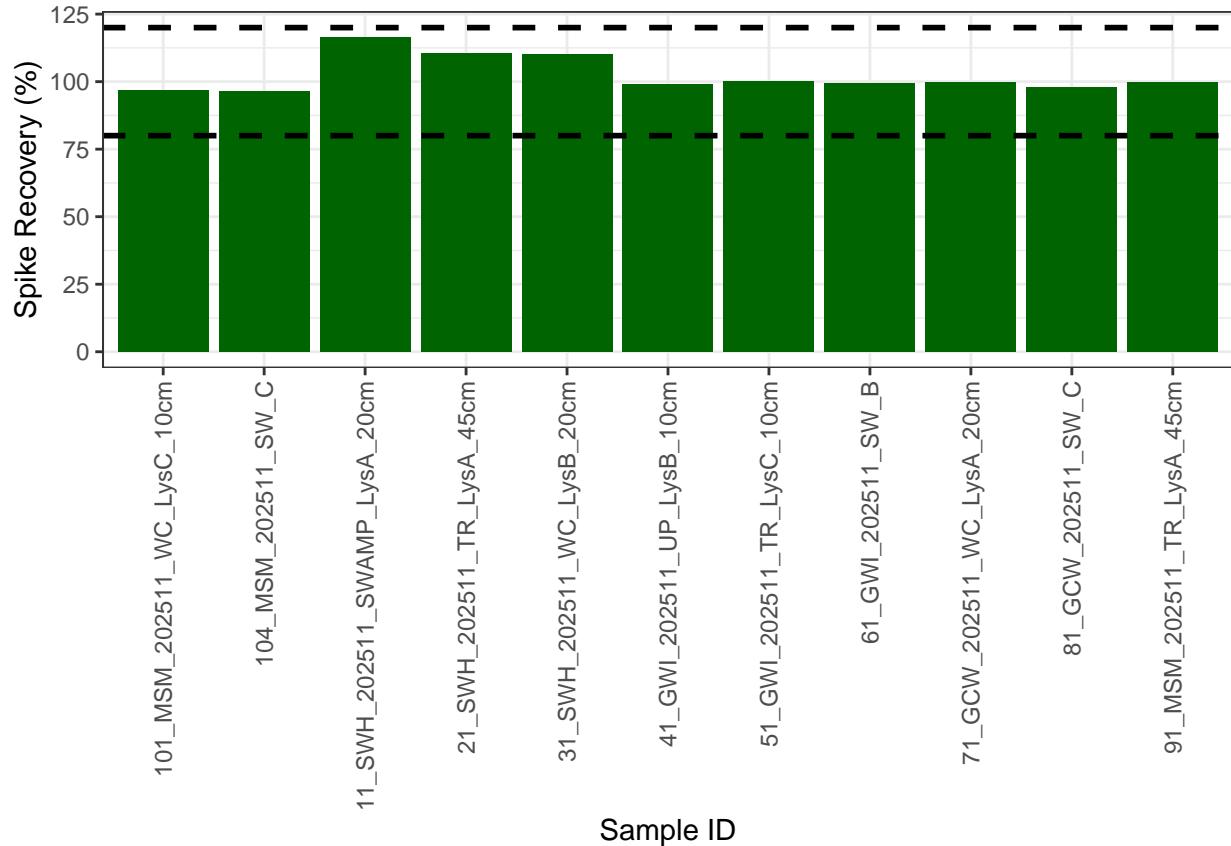
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "SWH"), 50, all_dat$Dilution)

all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "Lucie"), 50, all_dat$Dilution)

# head(all_dat)

```

0.7 Assess Analytical Spikes



```
## [1] ">80% of S04 spikes have a recovery between the high and low cutoff - PROCEED"
```

0.8 Check if samples within the range of the standard curve

```
## Sample Flagging
```

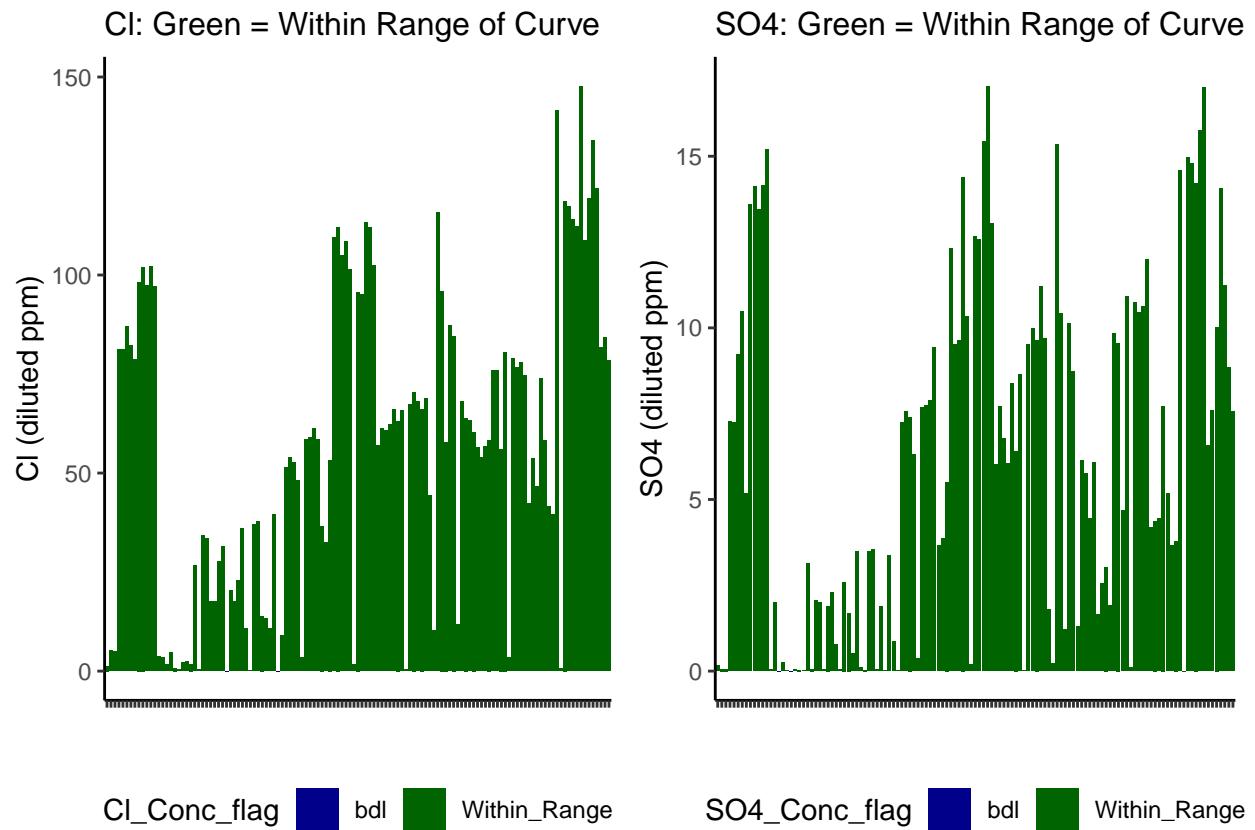


Table 1: SO4 samples

SO4_Conc_flag	Percent_samples
Within_Range	98.425197
bdl	1.574803

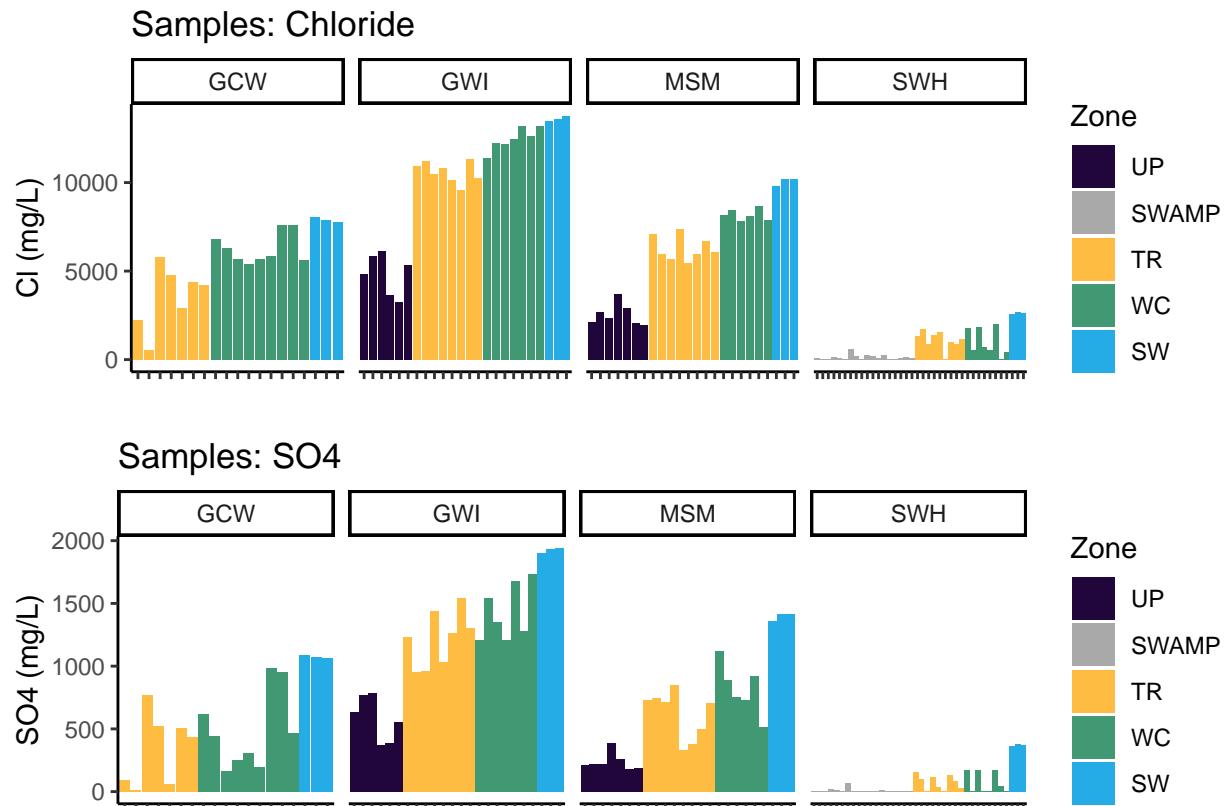
Table 2: Cl samples

Cl_Conc_flag	Percent_samples
Within_Range	98.425197
bdl	1.574803

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

```
## All sample IDs are present in metadata.
```

0.10 Visualize Data by Plot



0.11 Export Processed Data

```
#end
```