

Synoptic CB: Porewater SO₄/Cl

June 2024 Samples

2025-09-19

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##Add Required Packages

0.1 Run Information

```
##### Run information - PLEASE CHANGE
Date_Run = "2024-08-07" #Date that instrument was run
Run_by = "Zoe Read" #Instrument user
Script_run_by = "Zoe Read" #Code user
run_notes = "2/4 of Sulfate Duplicates have a CV <10%,
although one of the dups had a CV of 15 which was not too much higher than the cutoff of 10;
3/4 of SO4 spikes have a recovery between the high and low cutoff;
This run did not have a lot of samples so we are lowering the cutoff for percentage dups/spks
that need to pass and accepting this run.
Check standards 1 and 2 were lower than expected.
Removed FTS samples from the final dataset.
" #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

##### File Names - PLEASE CHANGE
#file path and name for raw summary data file
raw_file_name_cl = "Raw Data/COMPASS_Synoptic_CB_MonMon_202406_Cl.txt"
raw_file_name_so4 = "Raw Data/COMPASS_Synoptic_CB_MonMon_202406_SO4.txt"

#file path and name of processed data file
processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_Cl_SO4_202406.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_Cl_SO4_QAQClog_2024.csv"
```

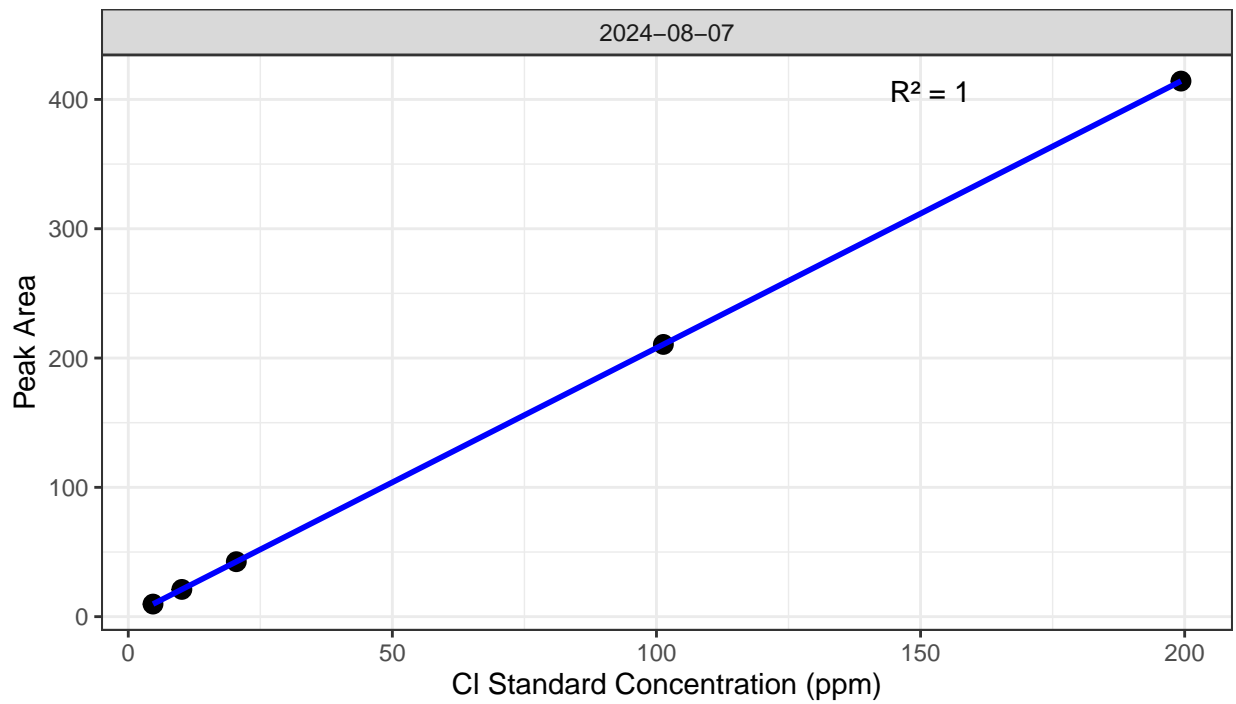
##Set Up Code - constants and QAQC cutoffs

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

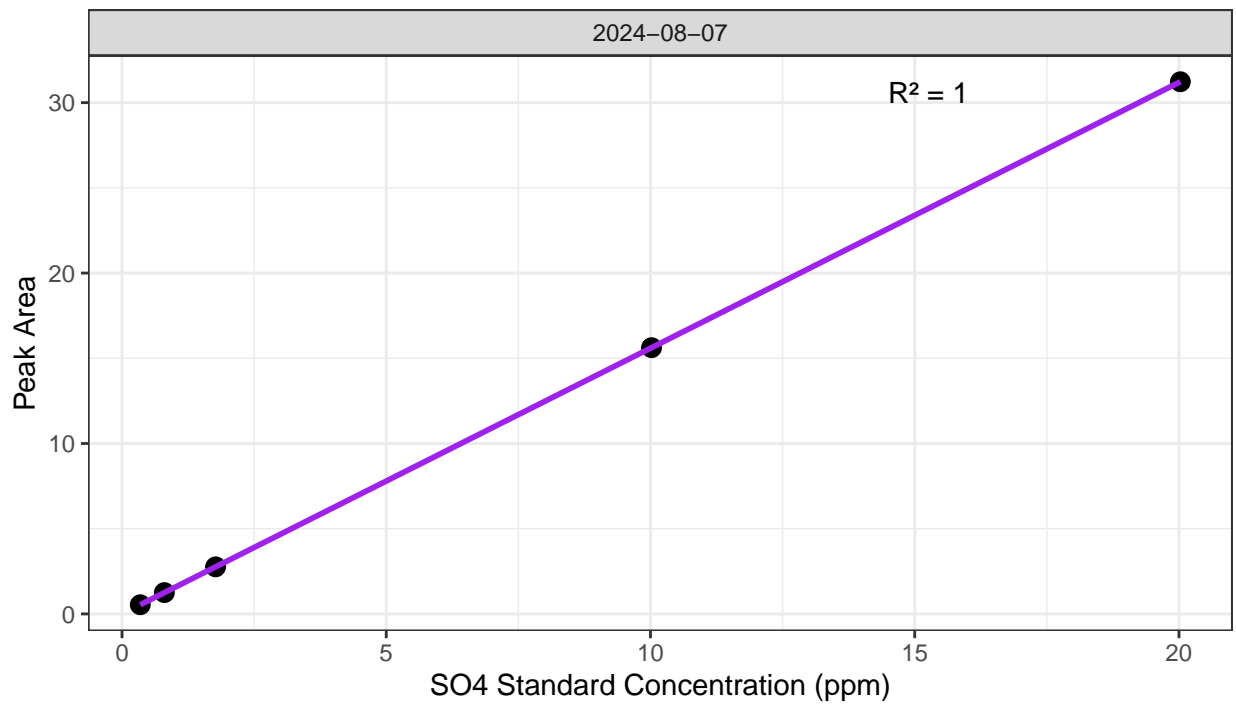
##Import Sample Data

0.2 Assess Standard Curves

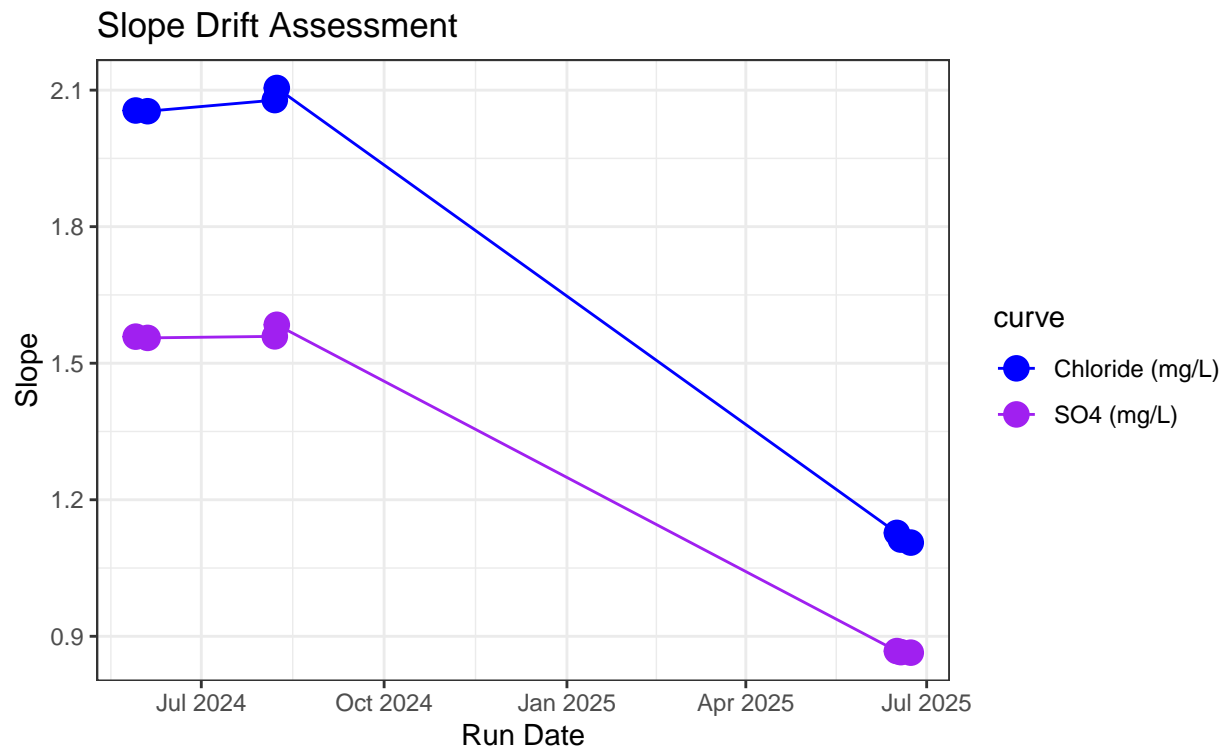
Chloride Std Curve



Sulfate Std Curve



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



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

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

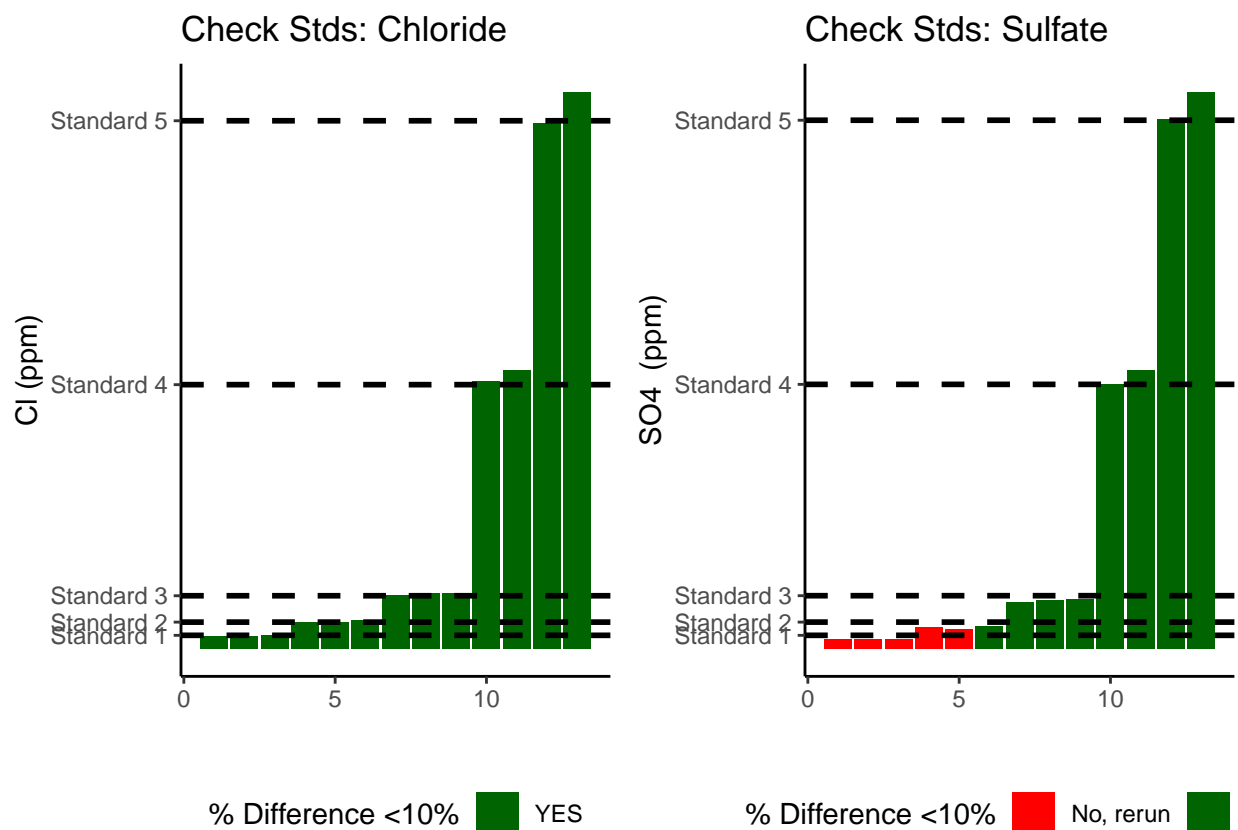
0.3 Assess Check Standards

```
## # A tibble: 5 x 5
##   sample_ID mean_Cl sd_Cl cv_Cl flag_Cl
##   <chr>      <dbl> <dbl> <dbl> <chr>
## 1 Standard 1 4.84 0.164 0.0338 Chloride Check Standard RSD within Range - PR~
## 2 Standard 2 10.2 0.373 0.0364 Chloride Check Standard RSD within Range - PR~
## 3 Standard 3 20.8 0.315 0.0151 Chloride Check Standard RSD within Range - PR~
## 4 Standard 4 103. 2.98 0.0289 Chloride Check Standard RSD within Range - PR~
## 5 Standard 5 205. 8.32 0.0405 Chloride Check Standard RSD within Range - PR~
```

```
## # A tibble: 5 x 5
##   sample_ID mean_S04 sd_S04 cv_S04 flag_S04
##   <chr>      <dbl> <dbl> <dbl> <chr>
## 1 Standard 1 0.359 0.0128 0.0356 Sulfate Check Standard RSD within Range - P~
## 2 Standard 2 0.802 0.0599 0.0746 Sulfate Check Standard RSD within Range - P~
## 3 Standard 3 1.83 0.0496 0.0271 Sulfate Check Standard RSD within Range - P~
## 4 Standard 4 10.3 0.369 0.0359 Sulfate Check Standard RSD within Range - P~
## 5 Standard 5 20.6 0.748 0.0364 Sulfate Check Standard RSD within Range - P~
```

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

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



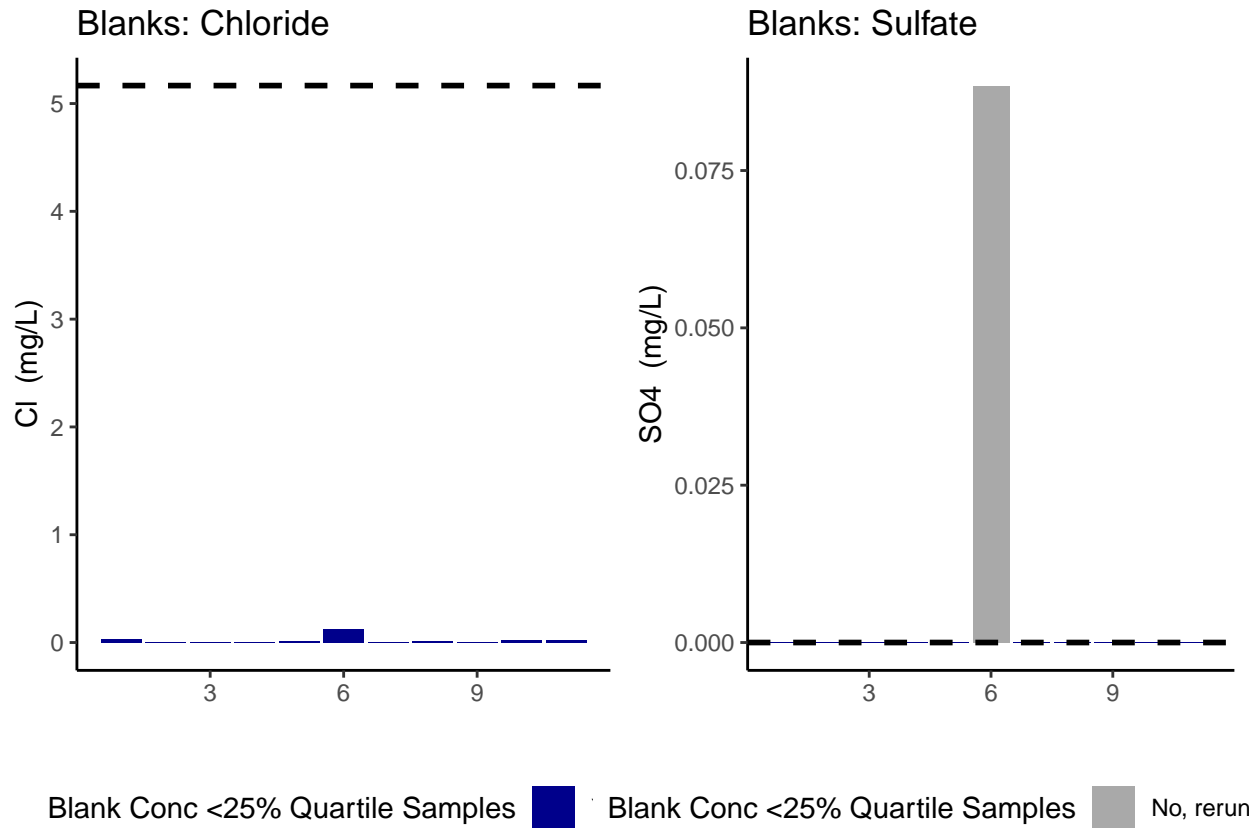
```
## [1] ">80% of Chloride Check Standards are within range of expected concentration - PROCEED"
```

```
## [1] "<80% of Sulfate Check Standards are within range of expected concentration - REASSESS"
```

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:
```

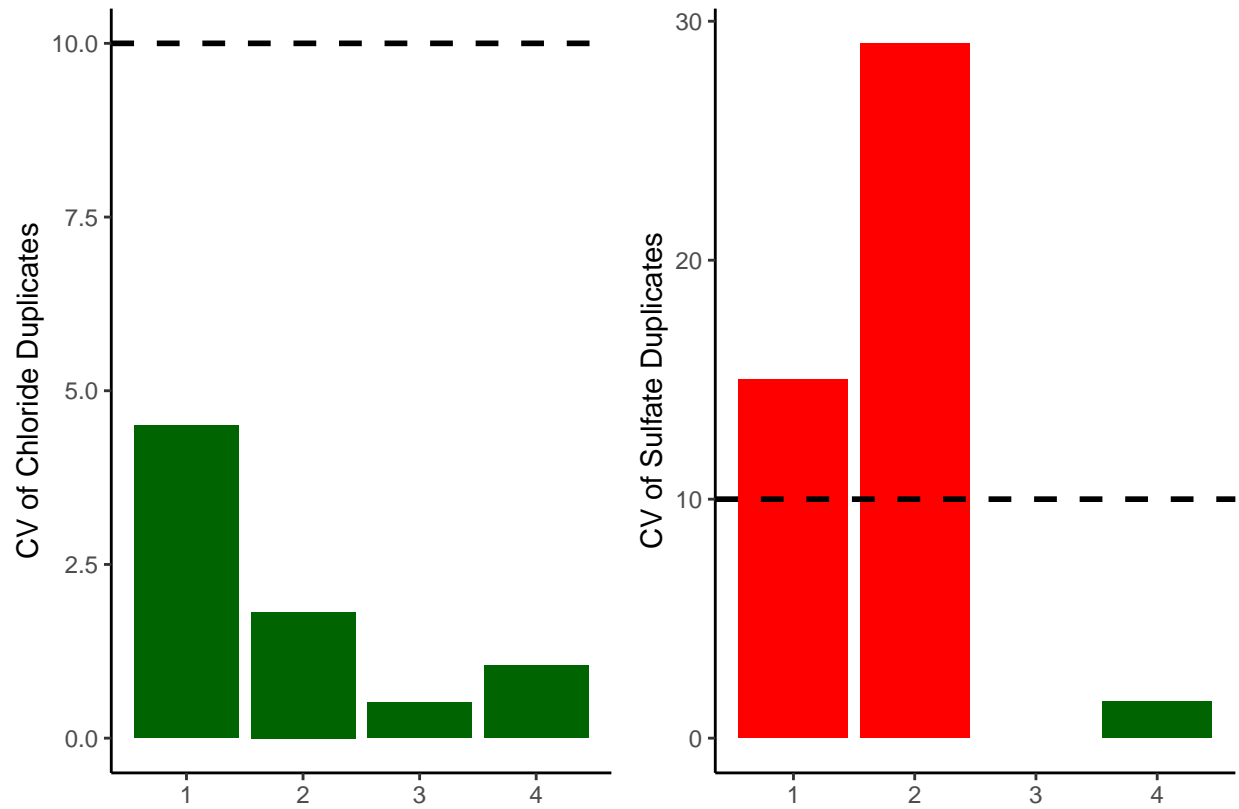
```
## [1] 0.02226364
```

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

```
## [1] 0.008045455
```

0.5 Assess Duplicates

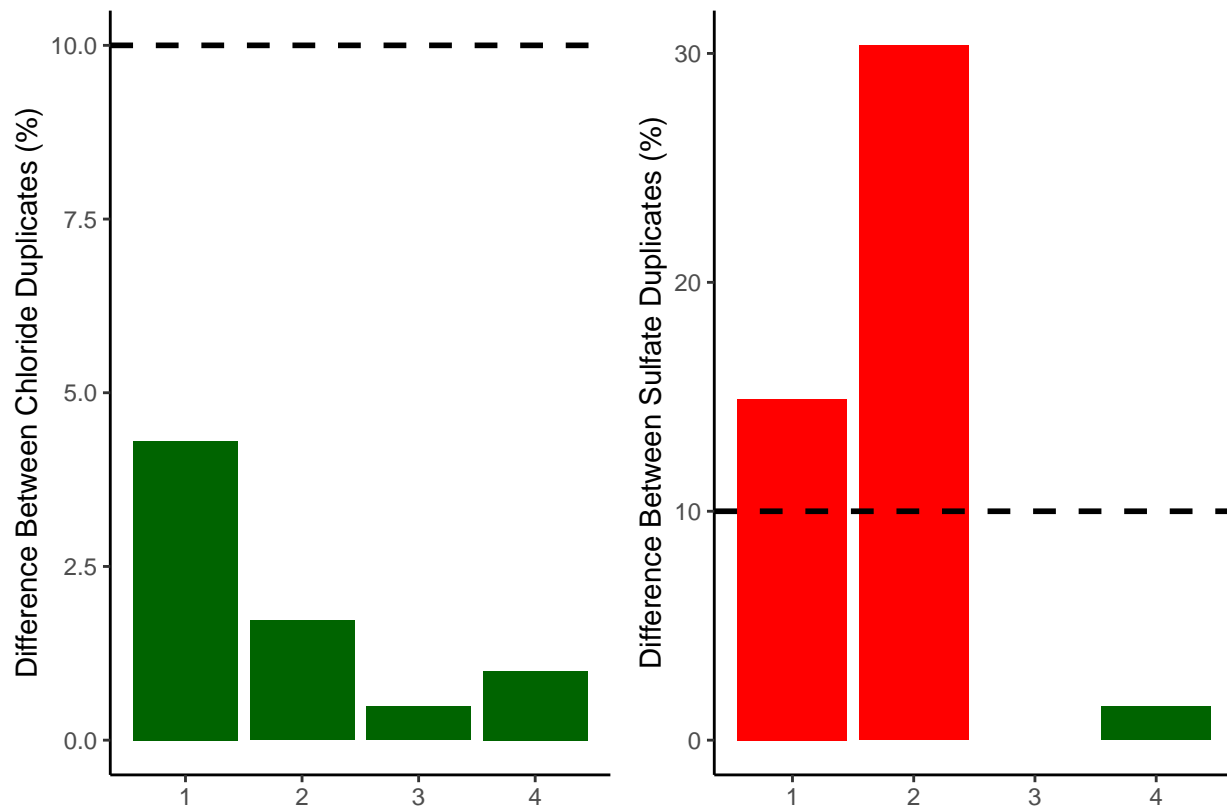
```
## Warning: Removed 1 row containing missing values or values outside the scale range
## ('geom_bar()').
```



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

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

```
## Warning: Removed 1 row containing missing values or values outside the scale range
## ('geom_bar()').
```



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

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

0.6 Calculate mmol/L concentrations & salinity, add dilutions

```
# Convert ppm to mmol/L
all_dat$S04_Conc_mM <- (all_dat$S04_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$salinity <- ((1.8070 * all_dat$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$sample_ID, "SW"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "UP"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "TR"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "WC"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GCW") & str_detect(all_dat$sample_ID, "SW"),

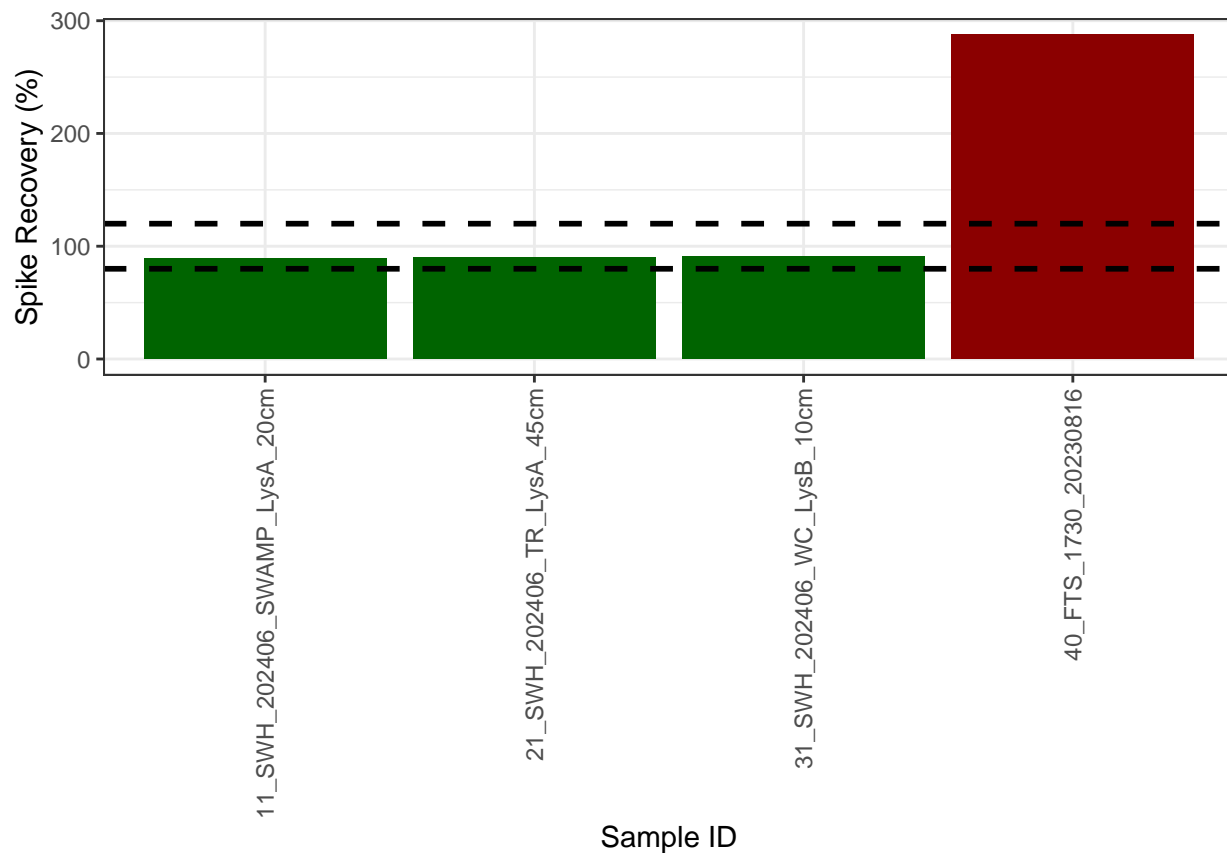
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "UP"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID, "TR"),
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "GWI") & str_detect(all_dat$sample_ID,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

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

0.8 Check if samples within the range of the standard curve

```
## Sample Flagging
```

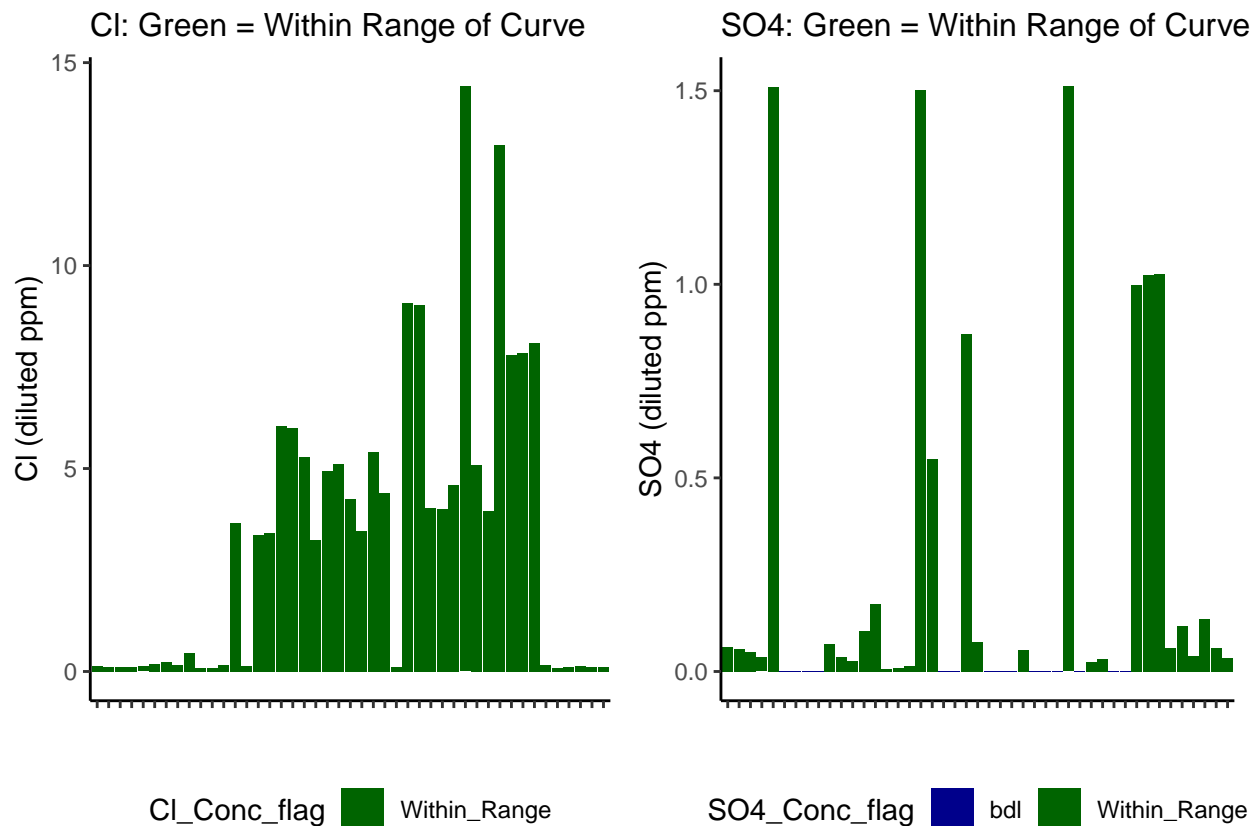


Table 1: SO4 samples

SO4_Conc_flag	Percent_samples
Within_Range	66.66667
bdl	33.33333

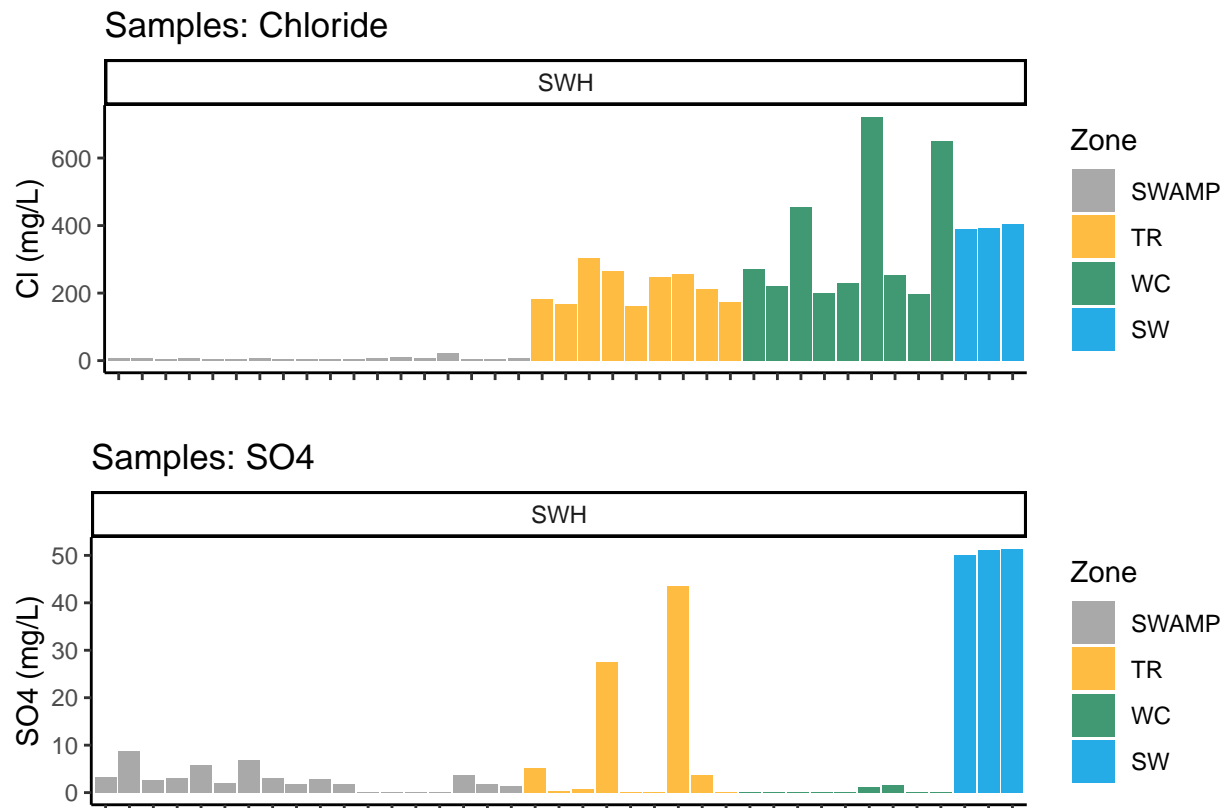
Table 2: Cl samples

Cl_Conc_flag	Percent_samples
Within_Range	100

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