

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_QAAClog_2024.csv"
```

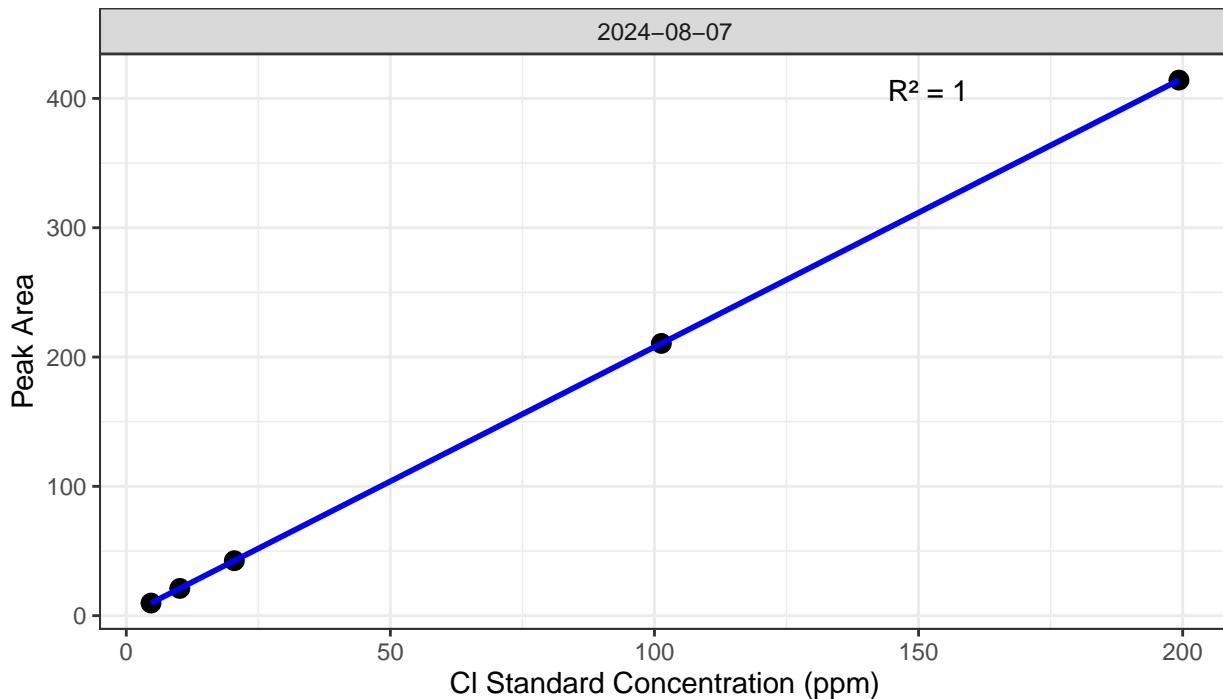
```
##Set Up Code - constants and QAQC cutoffs
```

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

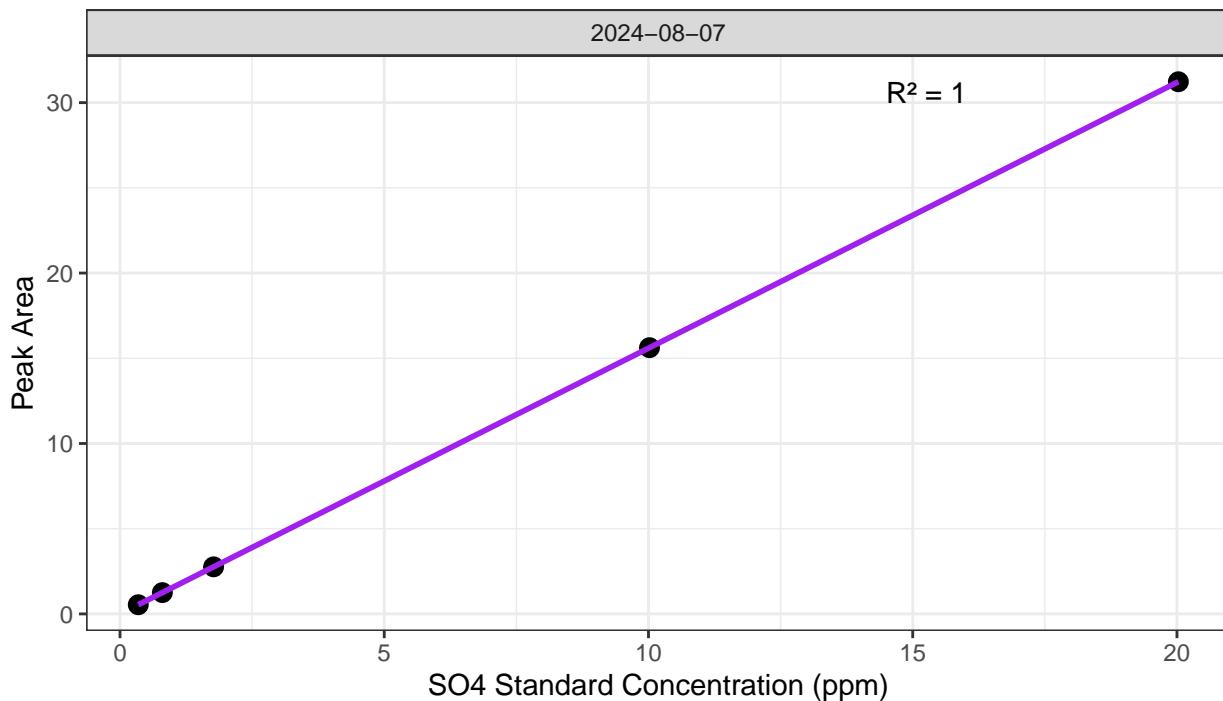
```
##Import Sample Data
```

0.2 Assess Standard Curves

Chloride Std Curve

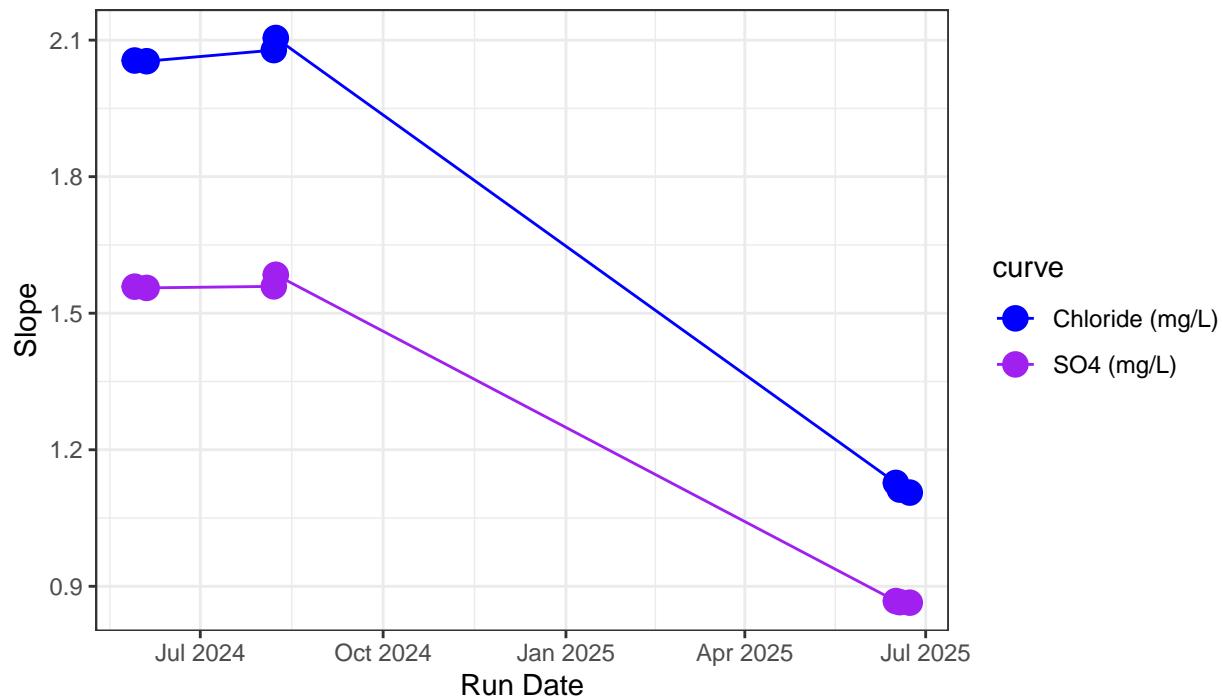


Sulfate Std Curve



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

Slope Drift Assessment



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

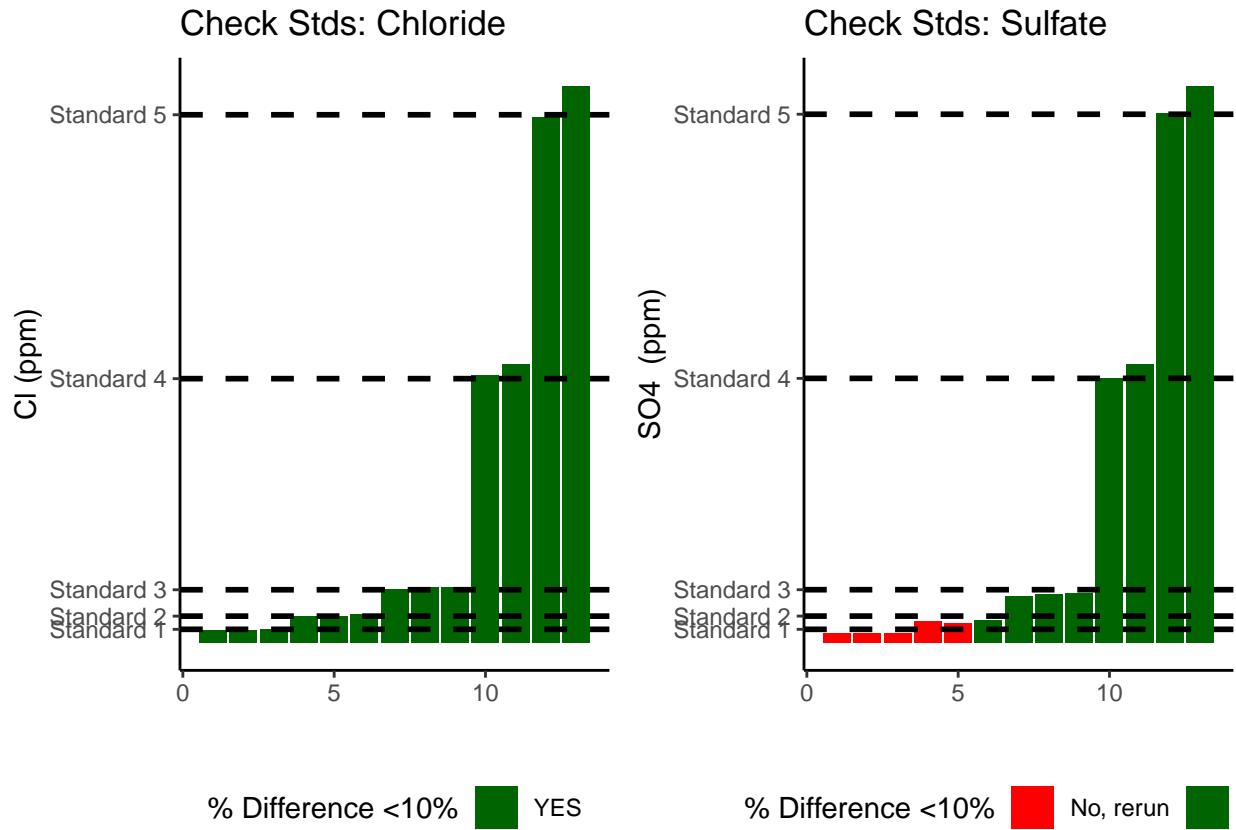
```
## [1] "SO4 Curve r2 GOOD"
```

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  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_SO4  sd_SO4  cv_SO4 flag_SO4
##   <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~

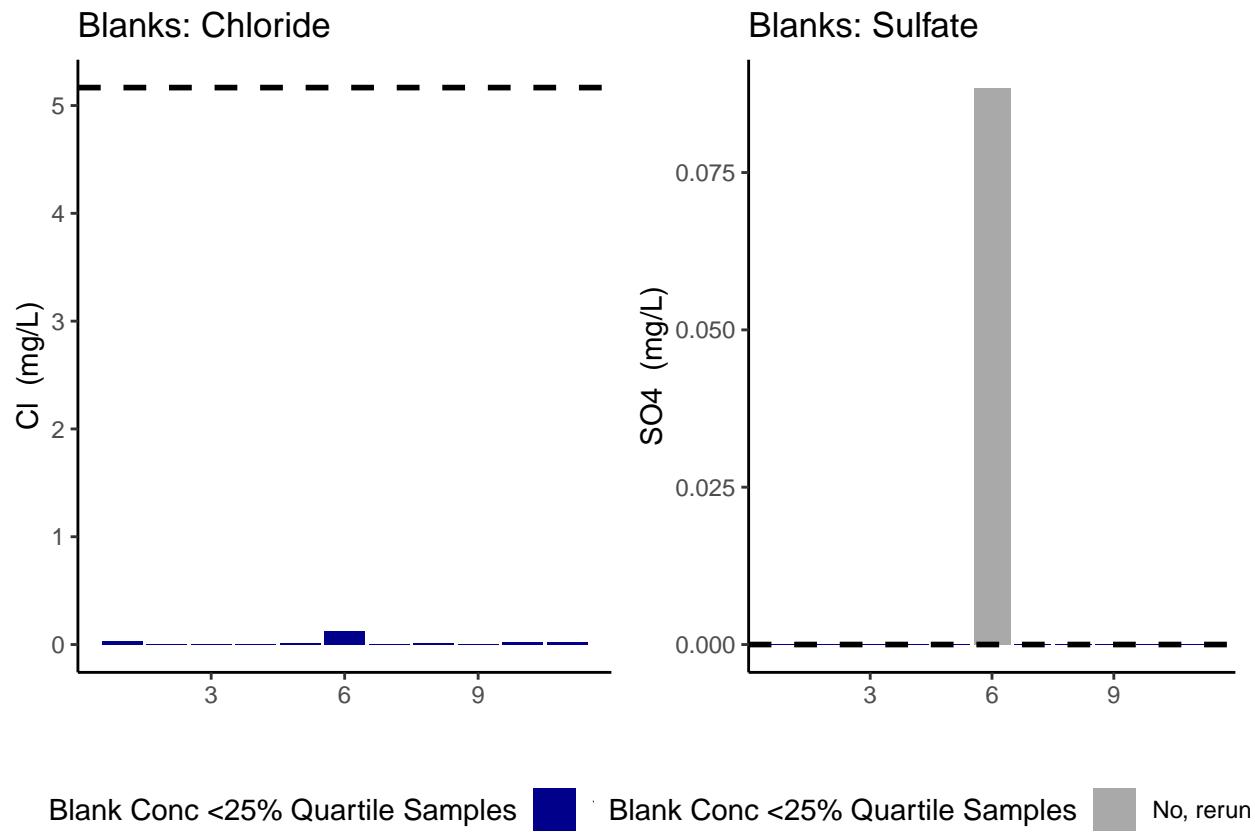
## [1] ">80% of Chloride Check Standards have RSD within range - PROCEED"
## [1] ">80% of Sulfate Check Standards have RSD within range - PROCEED"
```



```
## [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:
```

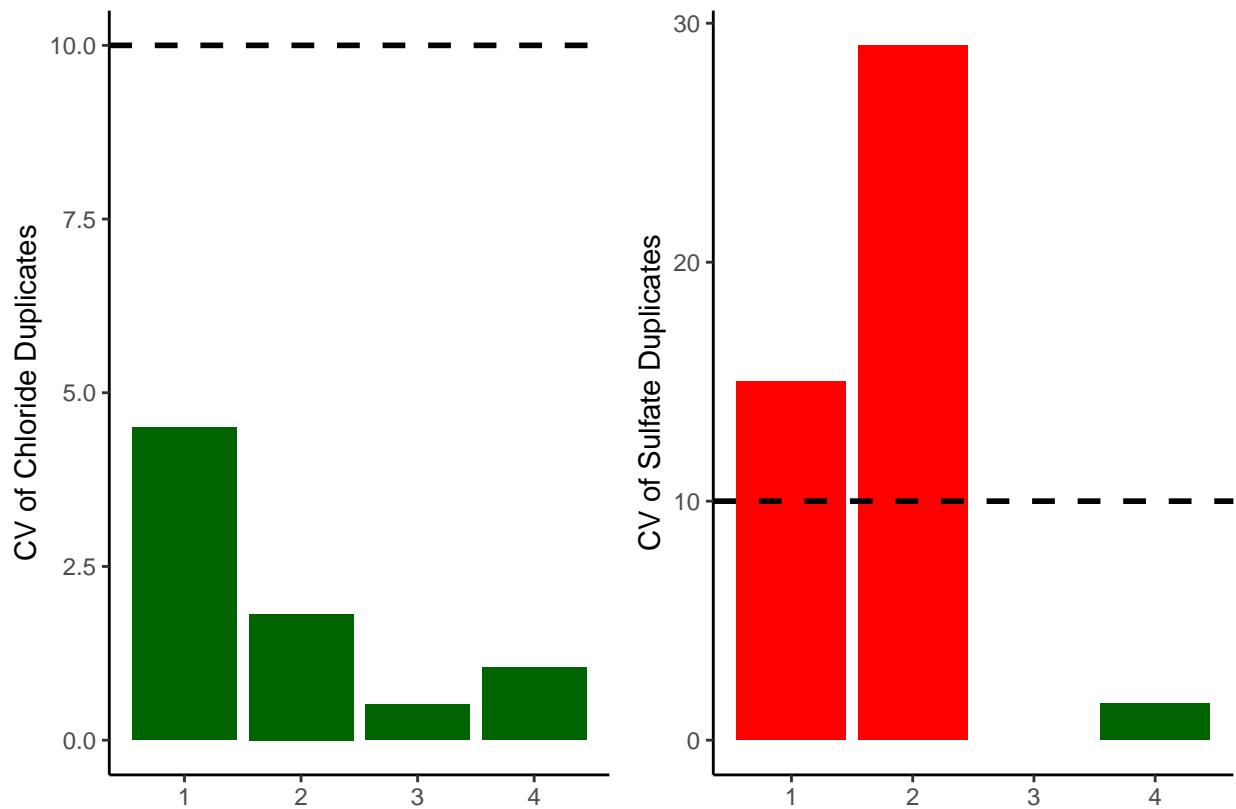
```
## [1] 0.02226364
```

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

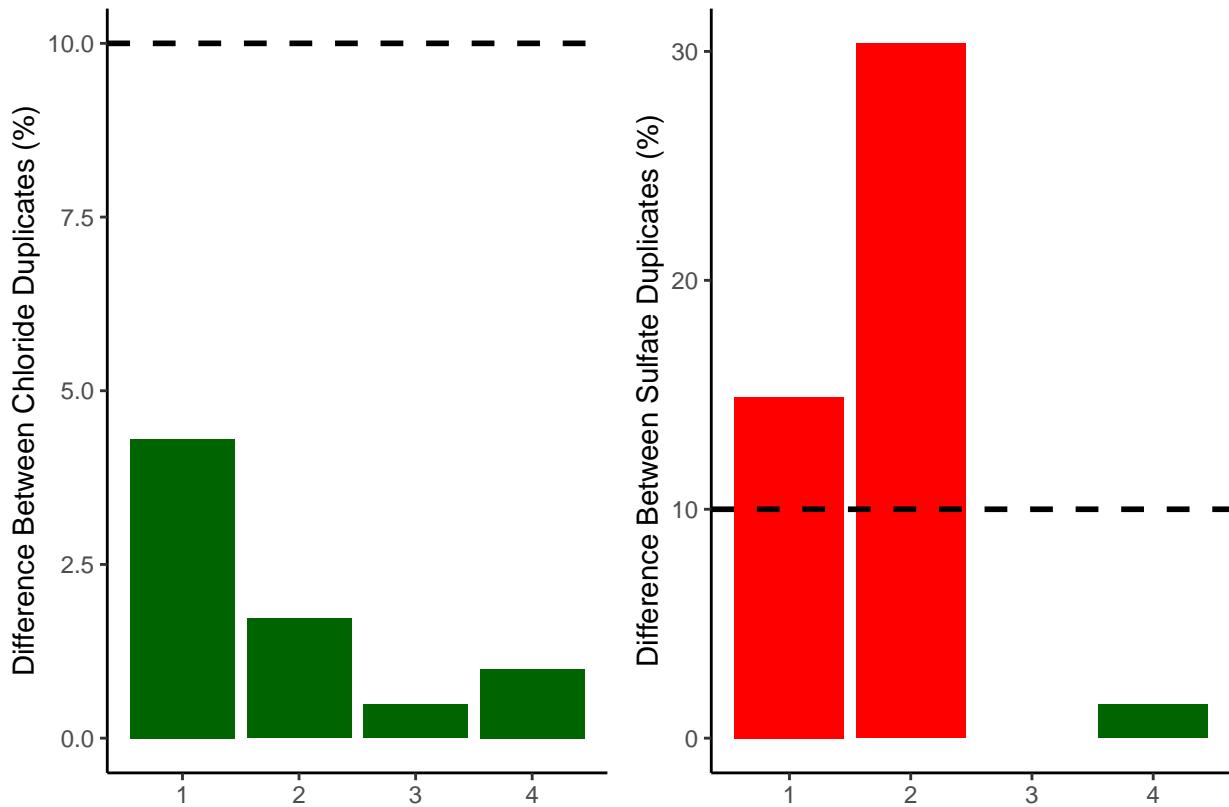
```
## [1] 0.008045455
```

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$SO4_Conc_mM <- (all_dat$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$salinity <- ((1.8070 * all_dat$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"),  

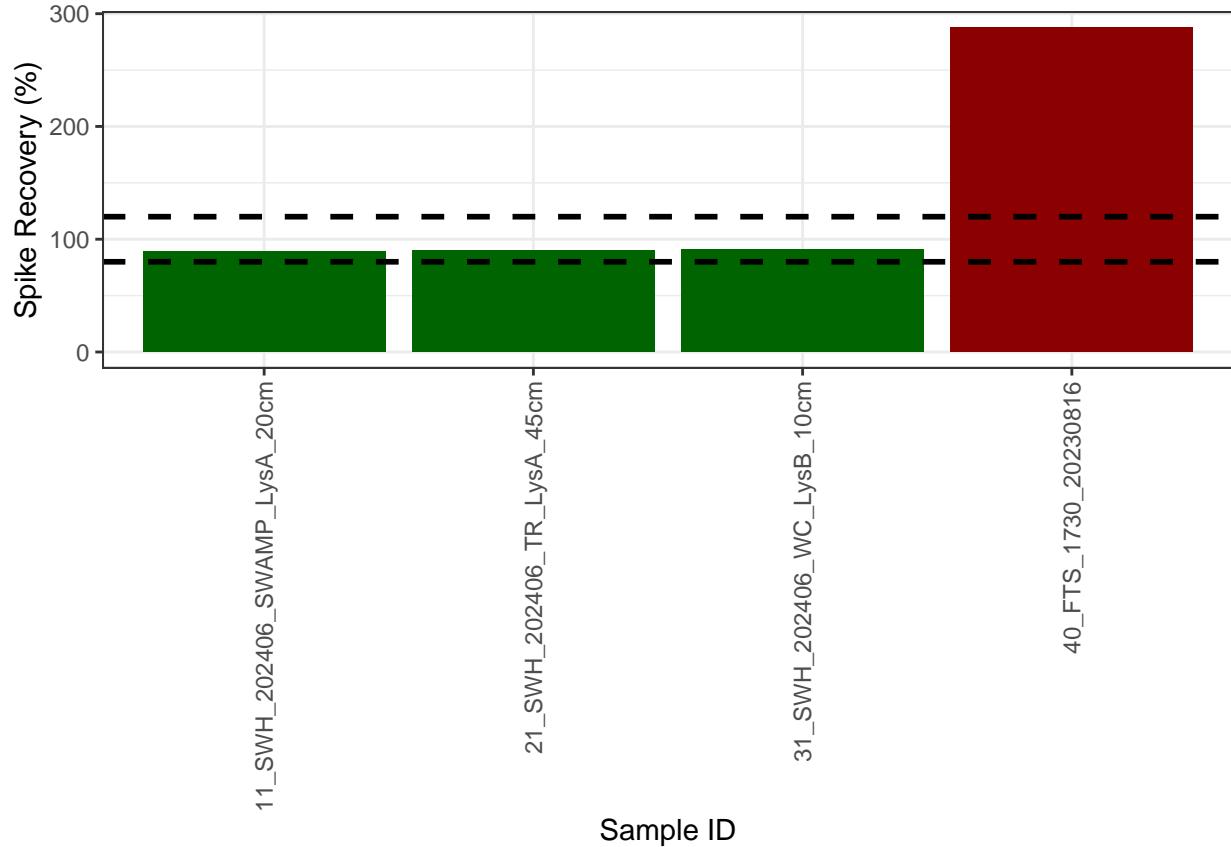
all_dat$Dilution <- ifelse(str_detect(all_dat$sample_ID, "SWH"), 50, all_dat$Dilution)  

# 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
```

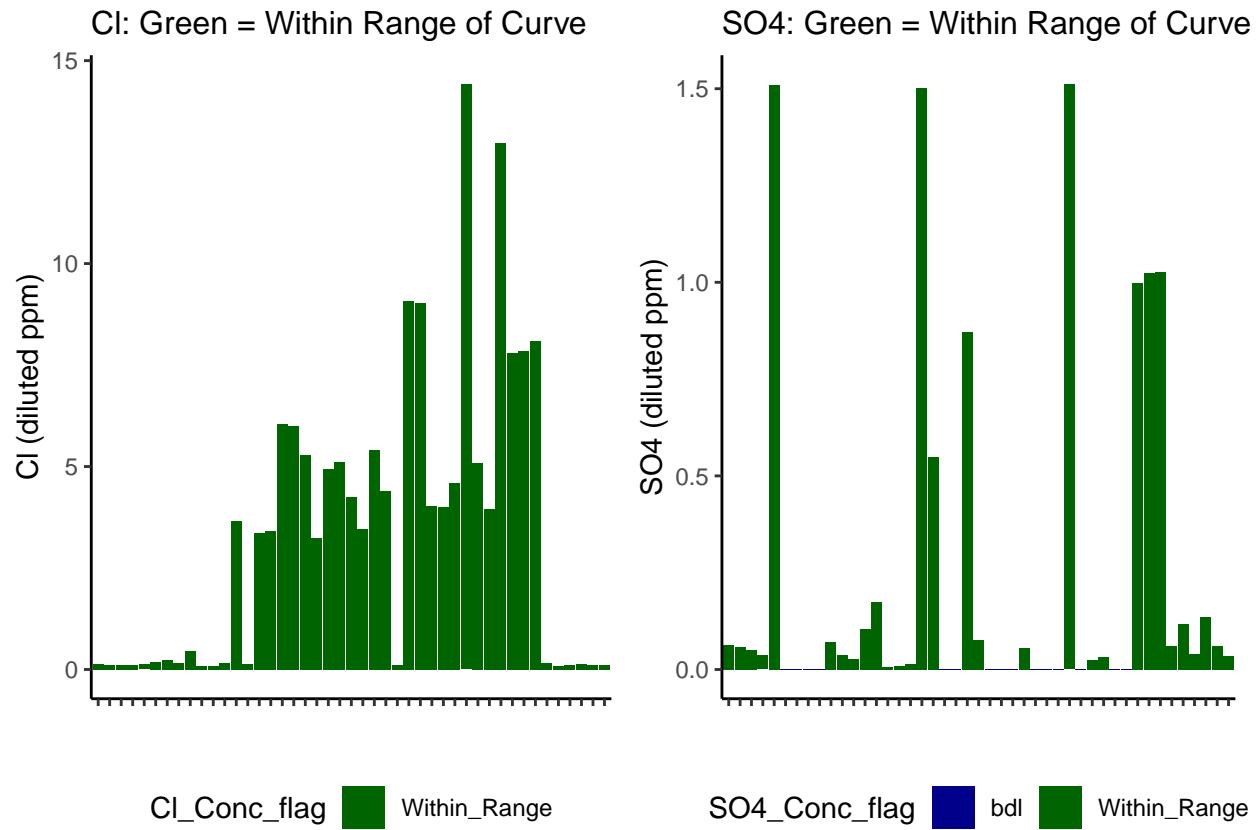


Table 1: SO4 samples

SO4_Conc_flag	Percent_samples
Within_Range	66.66667
bdl	33.33333

Table 2: Cl samples

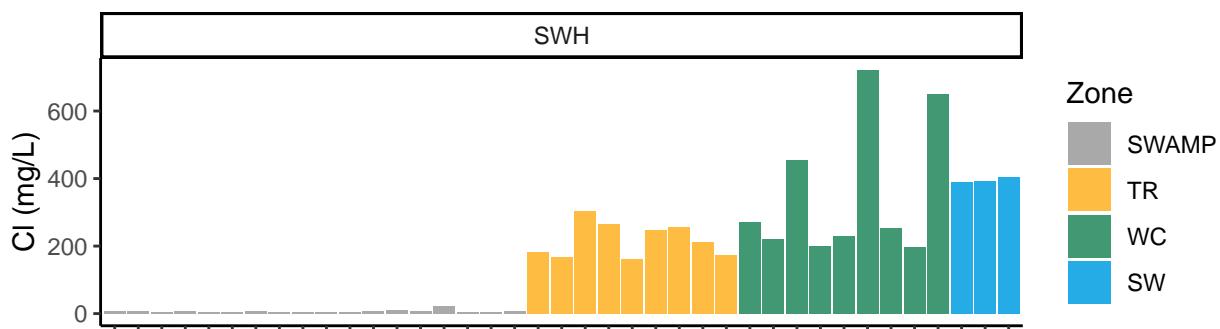
Cl_Conc_flag	Percent_samples
Within_Range	100

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

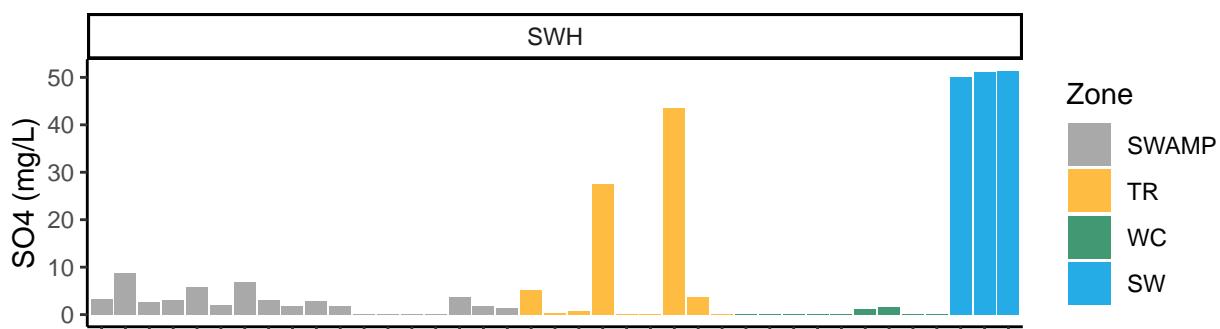
```
## All sample IDs are present in metadata.
```

0.10 Visualize Data by Plot

Samples: Chloride



Samples: SO4



0.11 Export Processed Data

#end