

# PROJECT: Porewater Nutrients

Month YEAR Samples

2026-02-25

## Contents

0.1	Run Information . . . . .	2
0.2	Assessing standard Curves . . . . .	3
0.3	Update Standard Log . . . . .	5
0.4	Dilution Corrections - ensure the latest dilution is kept . . . . .	7
0.5	Performance Check . . . . .	7
0.6	Check NOx Reduction Efficiency . . . . .	8
0.7	Analyze the Check Standards . . . . .	9
0.8	Analyze Blanks . . . . .	10
0.9	Analyze Duplicates . . . . .	11
0.10	Spikes . . . . .	12
0.11	Matrix Effects . . . . .	13
0.12	Check to see if samples run match metadata & merge info . . . . .	13
0.13	Visualize Data by Plot . . . . .	14

## 0.1 Run Information

```
cat("Run Information: NAME ") #lets you know what section you're in
```

```
## Run Information: NAME
```

```
#set the run date & user name
sample_year <- "2024"
user <- "NAME"

#identify the files you want to read in
#read in as a list to accomodate ultiple runs in a month
NOx_files <- c("Raw Data/20260120_Tempest2024_NH3_P04_Run1.csv")
NH3_P04_files <- c("Raw Data/20260209_Tempest2024_VNOx_Run1.csv")

# Define the file path for QAQC log file - NO Need to change just check year
file_path <- "Raw Data/SEAL_TEMPEST_QAQC_Log_2024.csv"
final_path <- "Processed Data/COMPASS_Synoptic_Nutrients_202407.csv"

#record any notes about the run or anything other info here:
run_notes <- ""

#Set up file path for metadata
#downloaded metadata csv - downloaded from Google drive as csv for this year
Raw_Metadata = "Raw Data/COMPASS_SynopticCB_PW_SampleLog_2024.csv"

cat(run_notes)
```

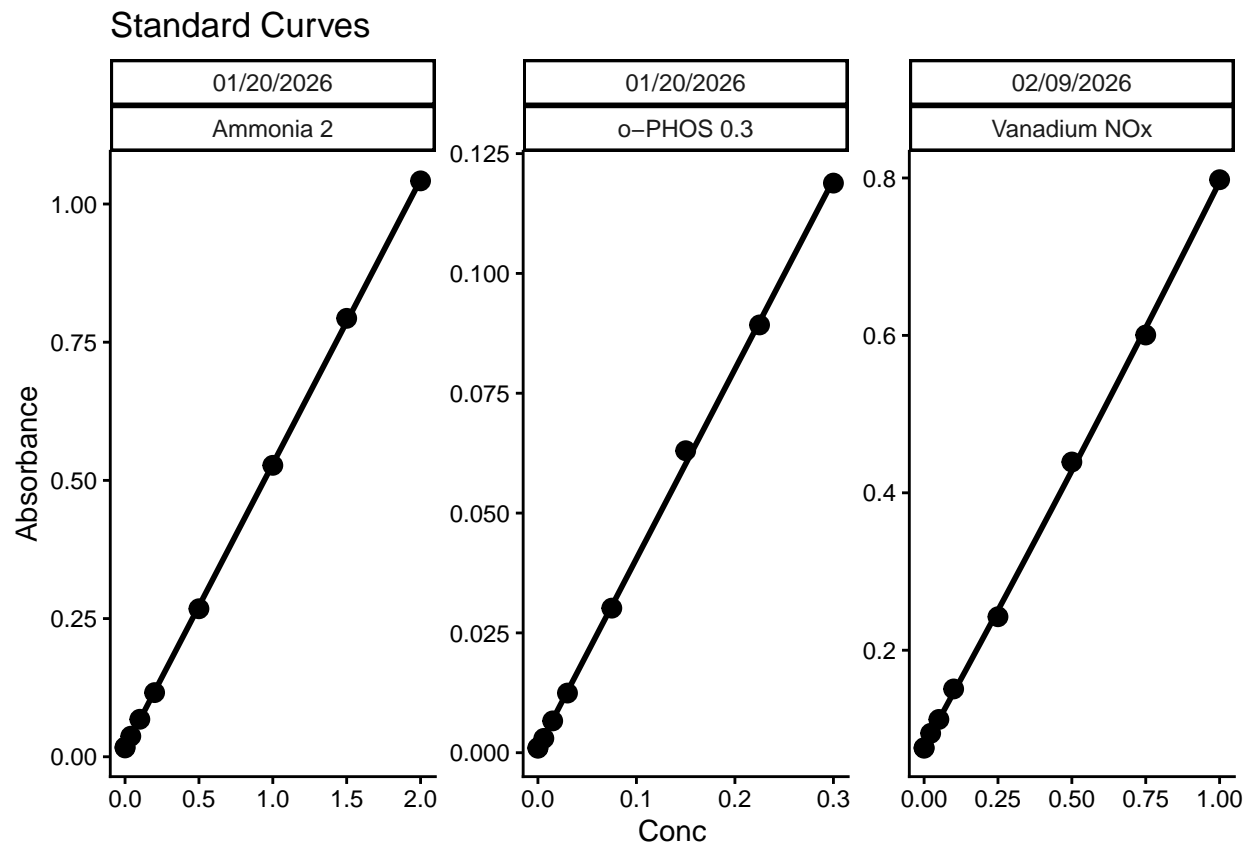
```
##Setup
```

```
##Pull in active porewater tracking inventory sheet from Google Drive:
```

```
##Create similar sample IDs to match with run samples
```

```
##Import Data & Clean
```

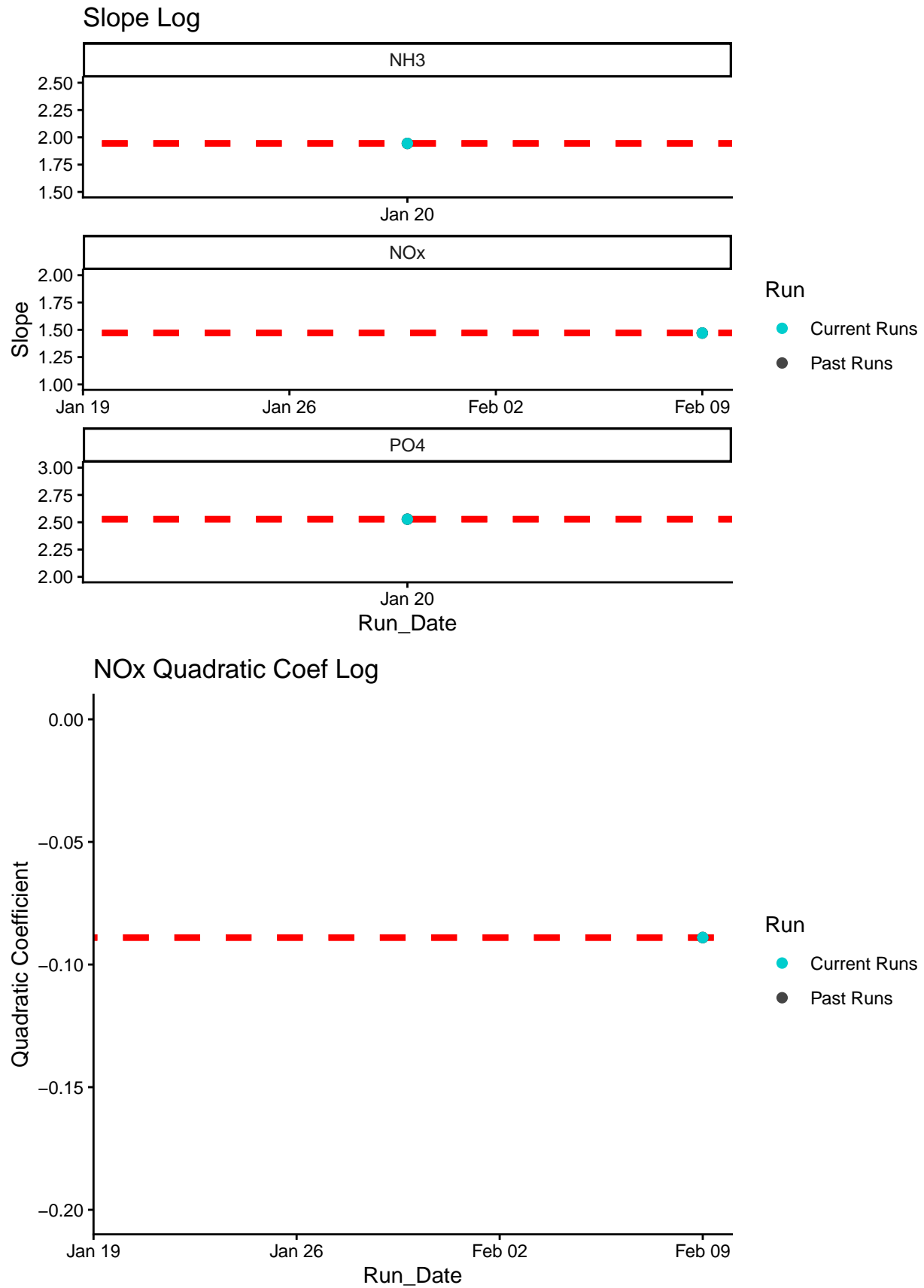
## 0.2 Assessing standard Curves

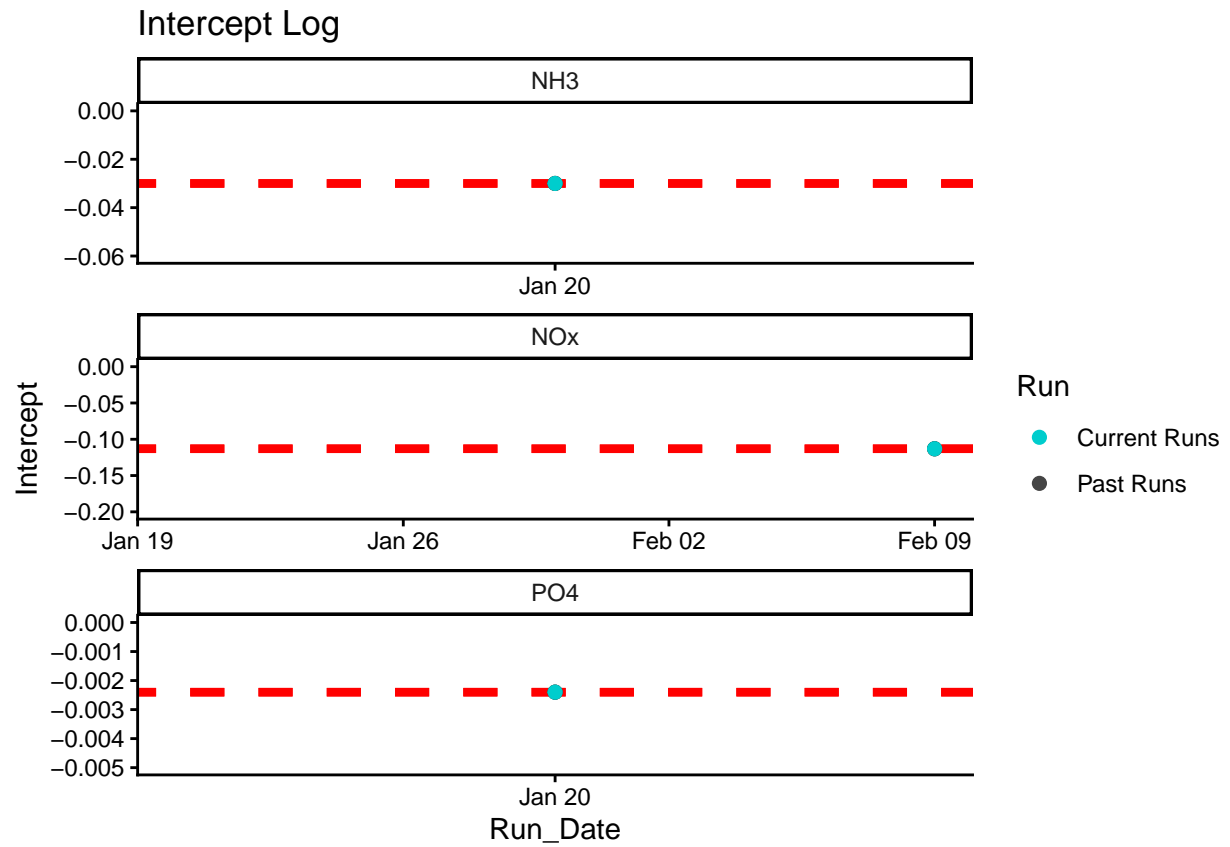


Test	Run_Date	R2_Flag	R2
Ammonia 2	01/20/2026	R2_Pass	0.9999133
o-PHOS 0.3	01/20/2026	R2_Pass	0.9993311
Vanadium NOx	02/09/2026	R2_Pass	0.9992713



### 0.3 Update Standard Log





#### 0.4 Dilution Corrections - ensure the latest dilution is kept

```
## [1] "No Reruns"
```

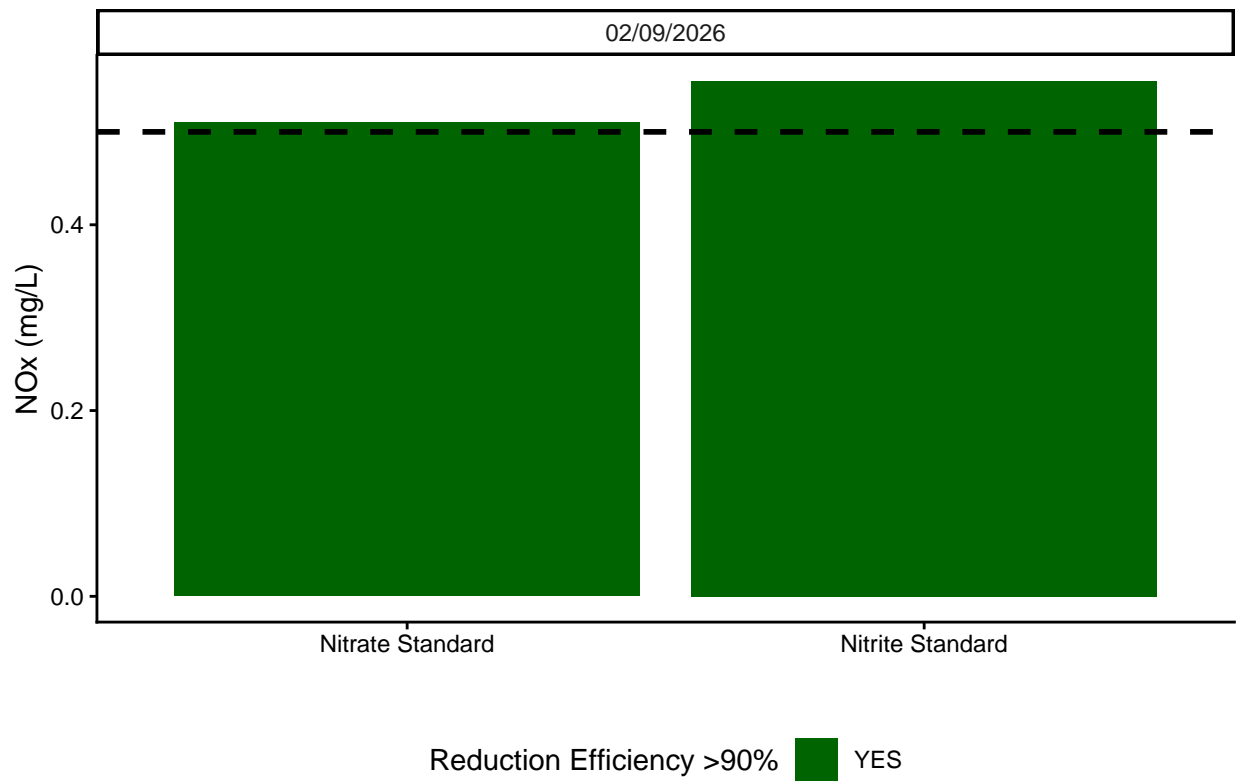
```
## [1] "No Dilutions"
```

```
## [1] "No Naming Issues Detected"
```

#### 0.5 Performance Check

Test	Run_Date	PE_Flag	PE_Conc	PE_Target_Conc
o-PHOS 0.3	01/20/2026	Performance Check Within 25% - PROCEED	0.8646825	0.824
Vanadium NOx	02/09/2026	Performance Check Within 25% - PROCEED	1.7939875	1.510
Ammonia 2	01/20/2026	Performance Check Within 25% - PROCEED	1.1758200	1.034

## 0.6 Check NOx Reduction Efficiency

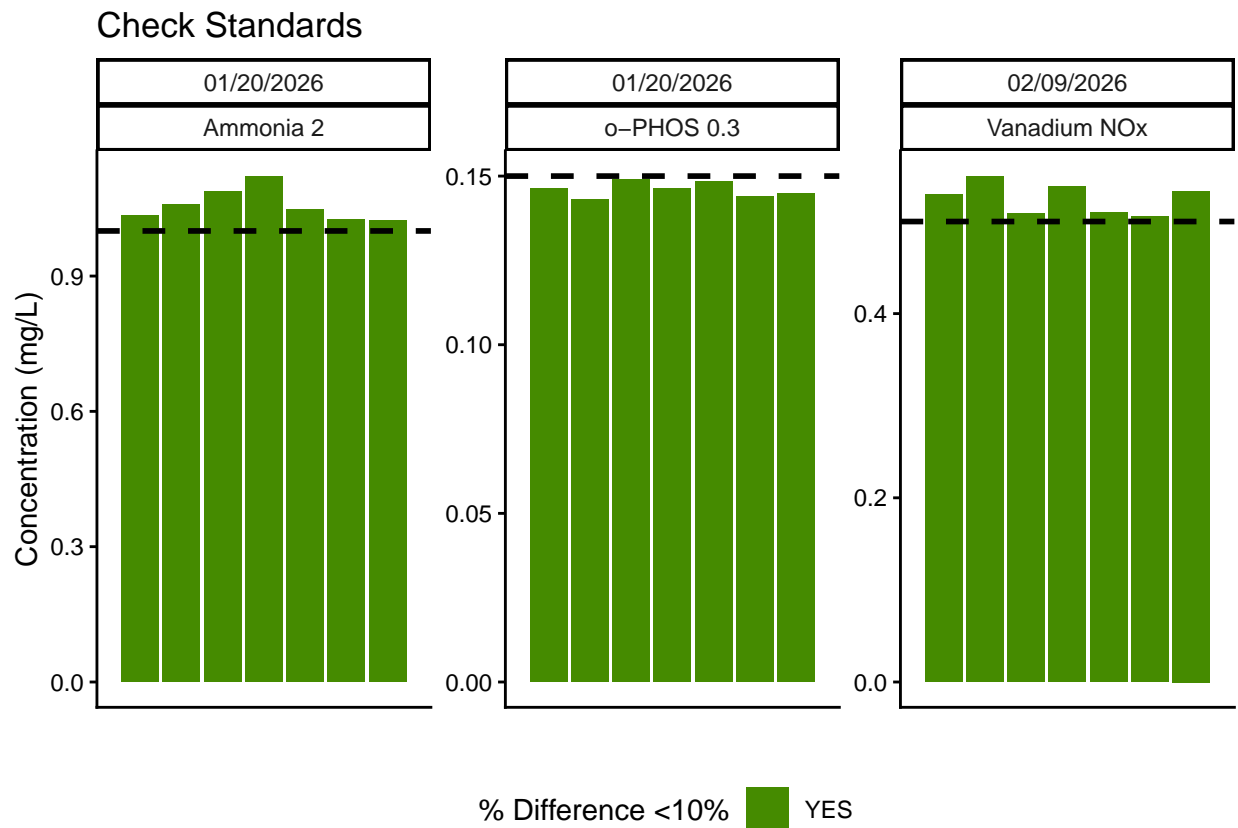


Test	Run_Date	Red_Eff_Flag
Vanadium NOx	02/09/2026	Mean NOx Reduction Efficiency >90% - PROCEED
Vanadium NOx	02/09/2026	Mean NOx Reduction Efficiency >90% - PROCEED



## 0.7 Analyze the Check Standards

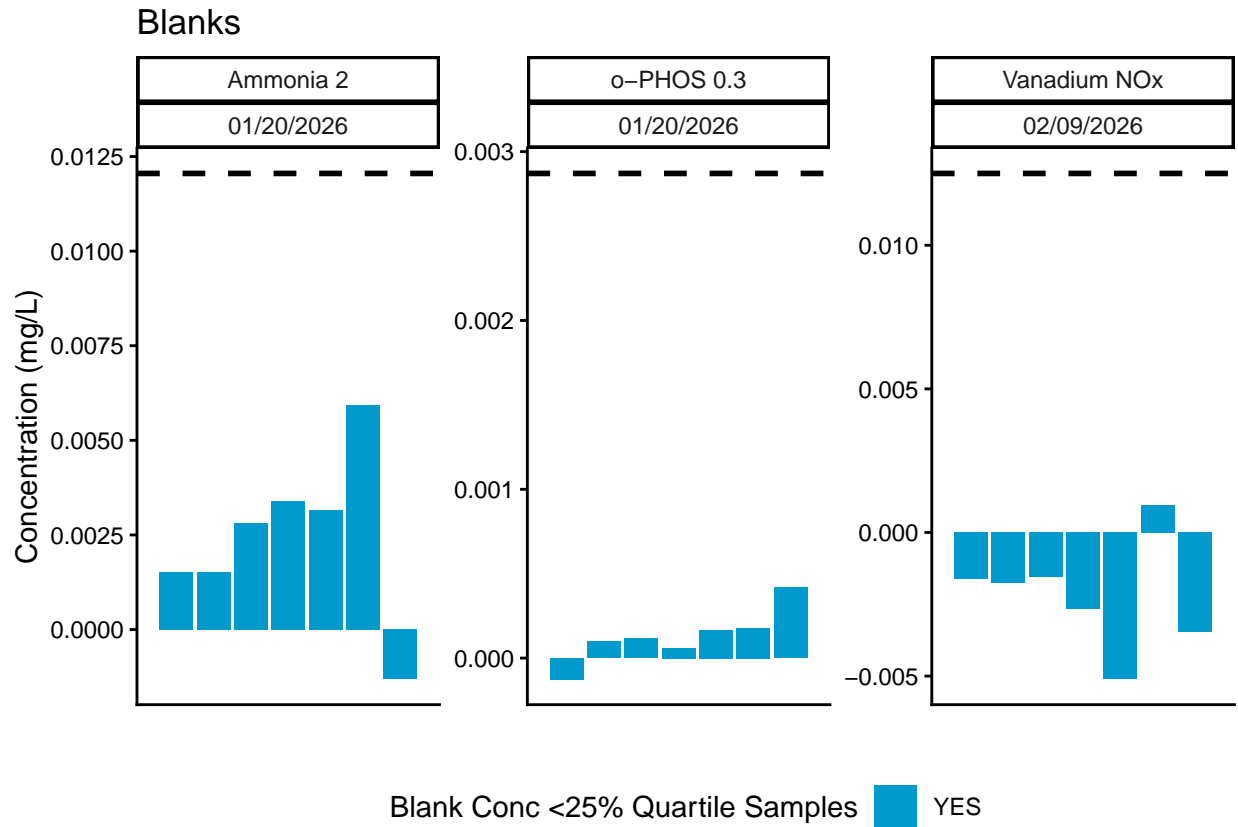
Test	Run_Date	RSV_Flag	RSV	RSV_Cutoff
Ammonia 2	01/20/2026	RSV WITHIN RANGE - PROCEED	0.0341261	0.25
o-PHOS 0.3	01/20/2026	RSV WITHIN RANGE - PROCEED	0.0150141	0.25
Vanadium NOx	02/09/2026	RSV WITHIN RANGE - PROCEED	0.0320678	0.25



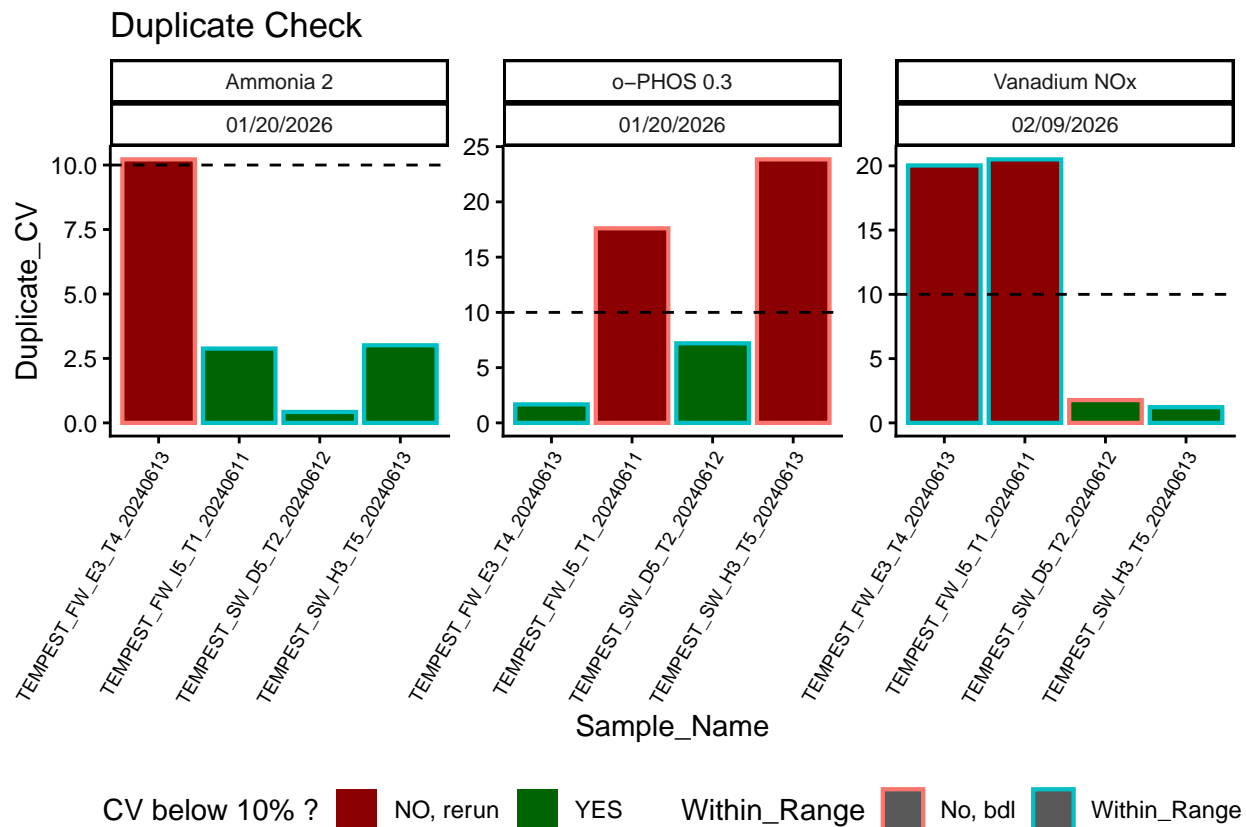
Test	Run_Date	CHK_Flag
Ammonia 2	01/20/2026	>60% of Checks Pass - PROCEED
o-PHOS 0.3	01/20/2026	>60% of Checks Pass - PROCEED
Vanadium NOx	02/09/2026	>60% of Checks Pass - PROCEED

## 0.8 Analyze Blanks

Test	Run_Date	BLK_Pct_Flag	Mean_Blkc_Conc	Quantile_25
Ammonia 2	01/20/2026	>60% of Blanks Pass - PROCEED	0.0024320	0.012053
o-PHOS 0.3	01/20/2026	>60% of Blanks Pass - PROCEED	0.0001294	0.002871
Vanadium NOx	02/09/2026	>60% of Blanks Pass - PROCEED	-0.0021684	0.012500

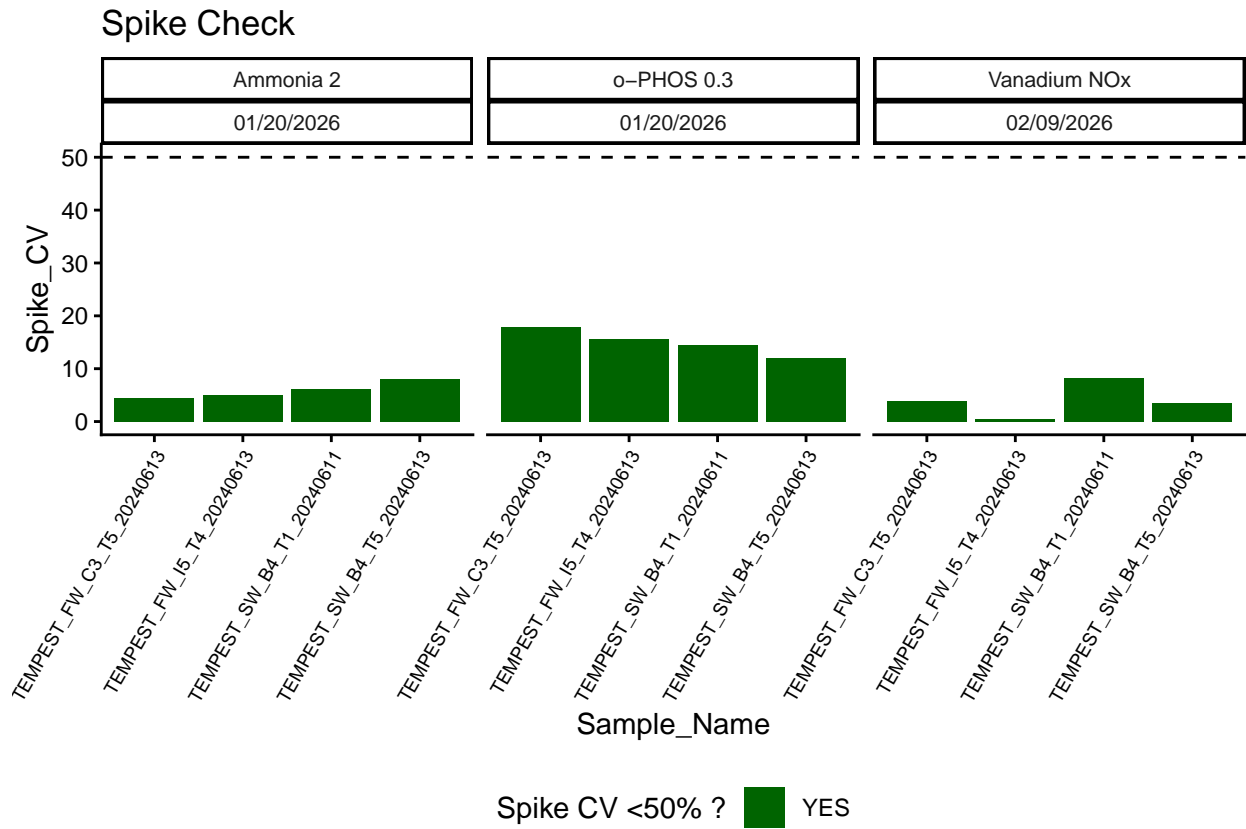


## 0.9 Analyze Duplicates

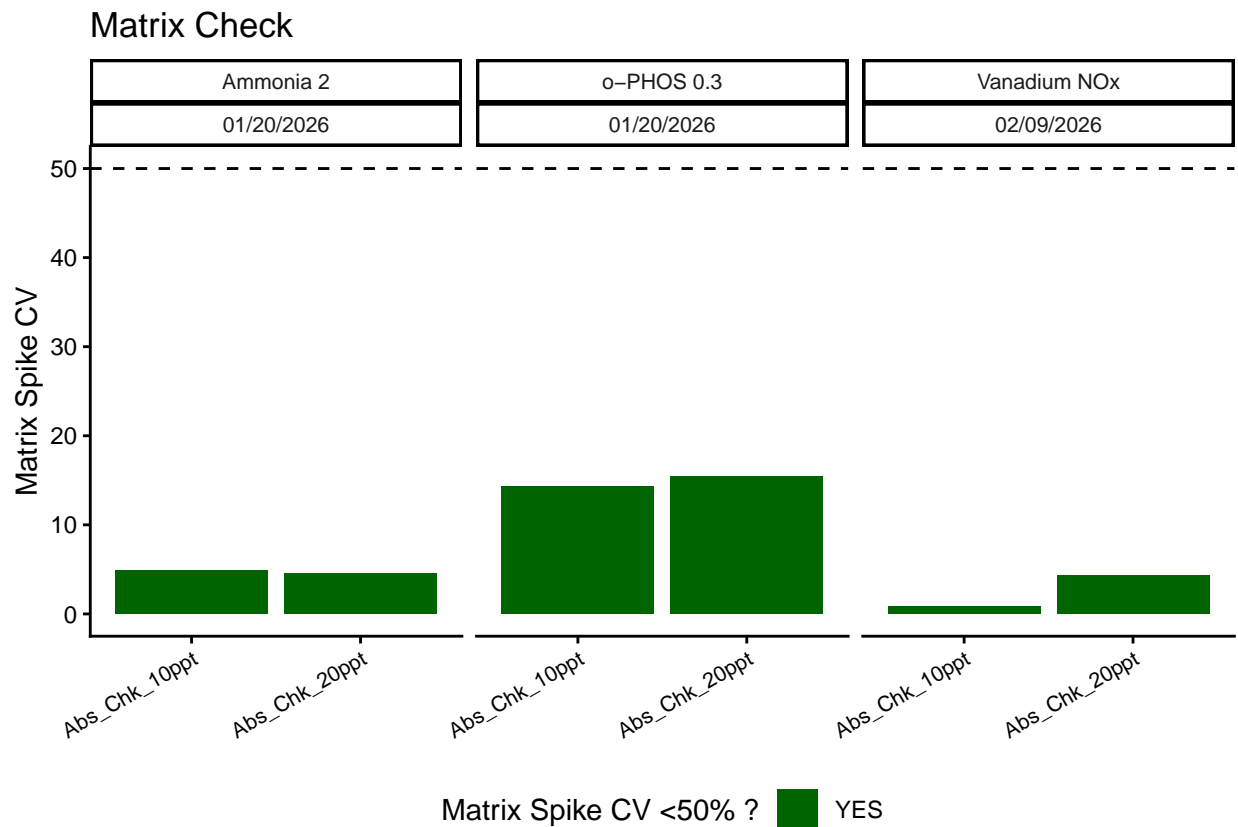


Test	Run_Date	Dup_Flags
Ammonia 2	01/20/2026	>60% of Dups Pass - PROCEED
o-PHOS 0.3	01/20/2026	<60% of Dups Pass - REASSESS
Vanadium NOx	02/09/2026	<60% of Dups Pass - REASSESS

## 0.10 Spikes



## 0.11 Matrix Effects



Test	Run_Date	Matrix_Flags
Ammonia 2	01/20/2026	Matrix Has CV <50% - PROCEED
o-PHOS 0.3	01/20/2026	Matrix Has CV <50% - PROCEED
Vanadium NOx	02/09/2026	Matrix Has CV <50% - PROCEED

##Sample Flagging - Within range of standard curve

##Add QAQC Flags

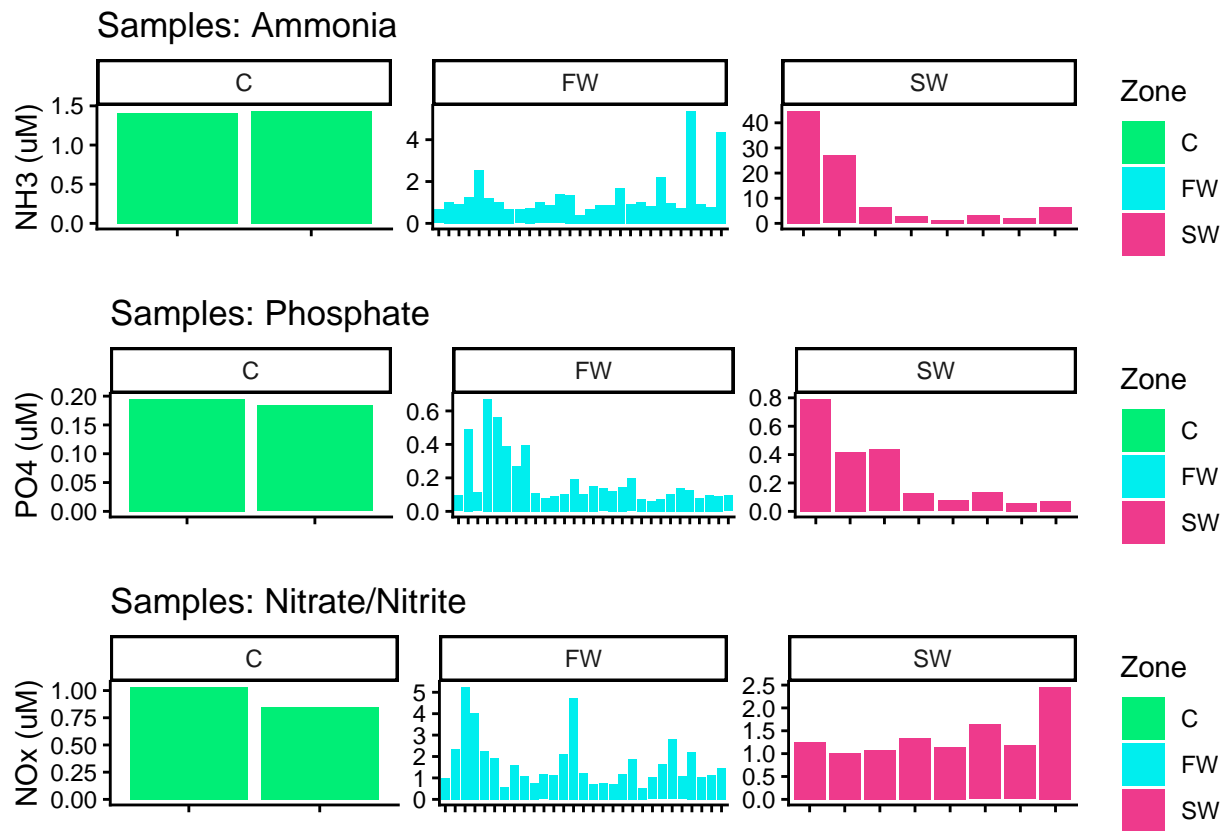
## 0.12 Check to see if samples run match metadata & merge info

## All sample IDs are present in metadata.

```
## [1] "Sample_Name" "Run_Number" "Conc" "Absorbance" "Dilution"
## [6] "Unit" "Test" "Run_Time" "Run_Date" "Keep"
## [11] "Pair_ID" "Conc_uM" "Conc_flag"
```

##Format Data

### 0.13 Visualize Data by Plot



##Write Out Data

#end