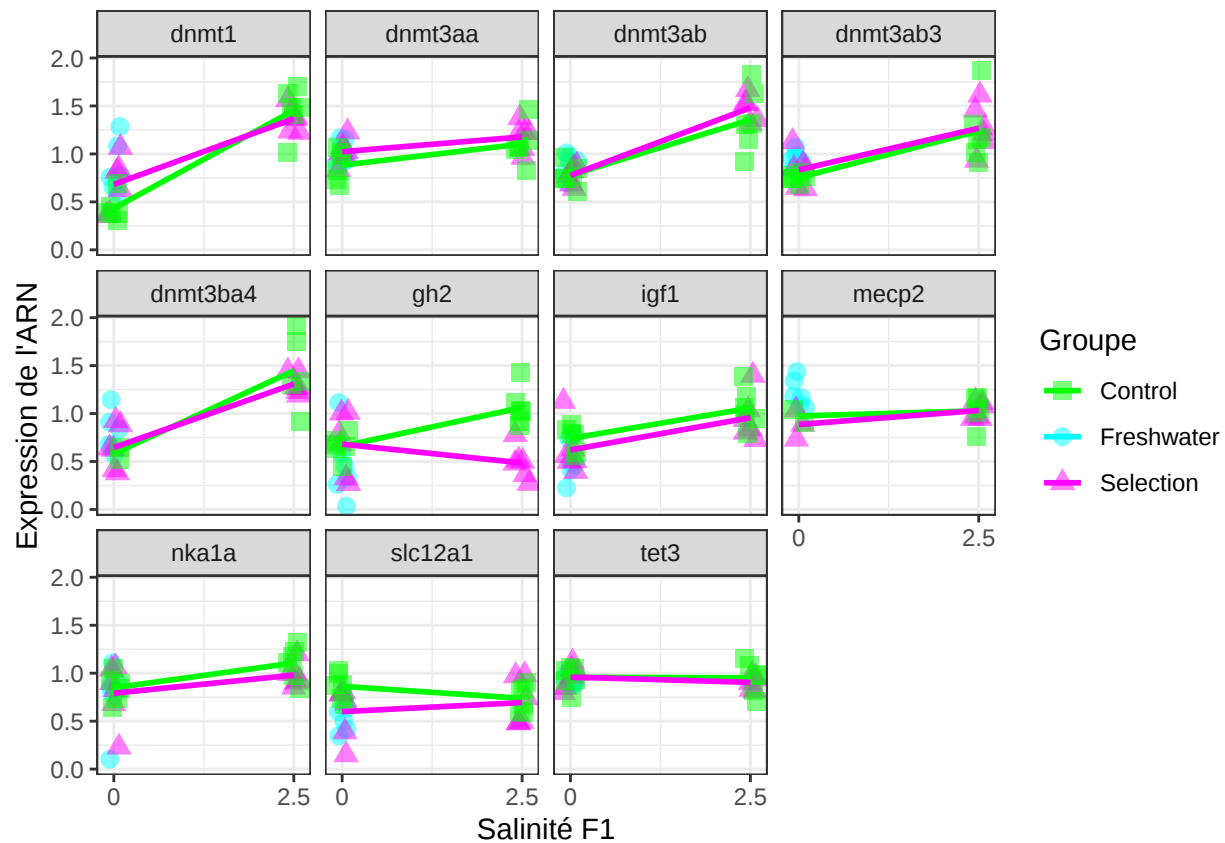


Pangasionodon hypophthalmus Test 6dph

Simon De Pooter

décembre 15, 2021,08:23

Contents



```
##
## Call:
## lm(formula = Gene$dnmt1 ~ as.numeric(Gene$Salinity_F1) * Gene$Group,
##     data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.43748 -0.11912 -0.02123  0.15752  0.42834
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.43294    0.09006   4.807 6.14e-05
```

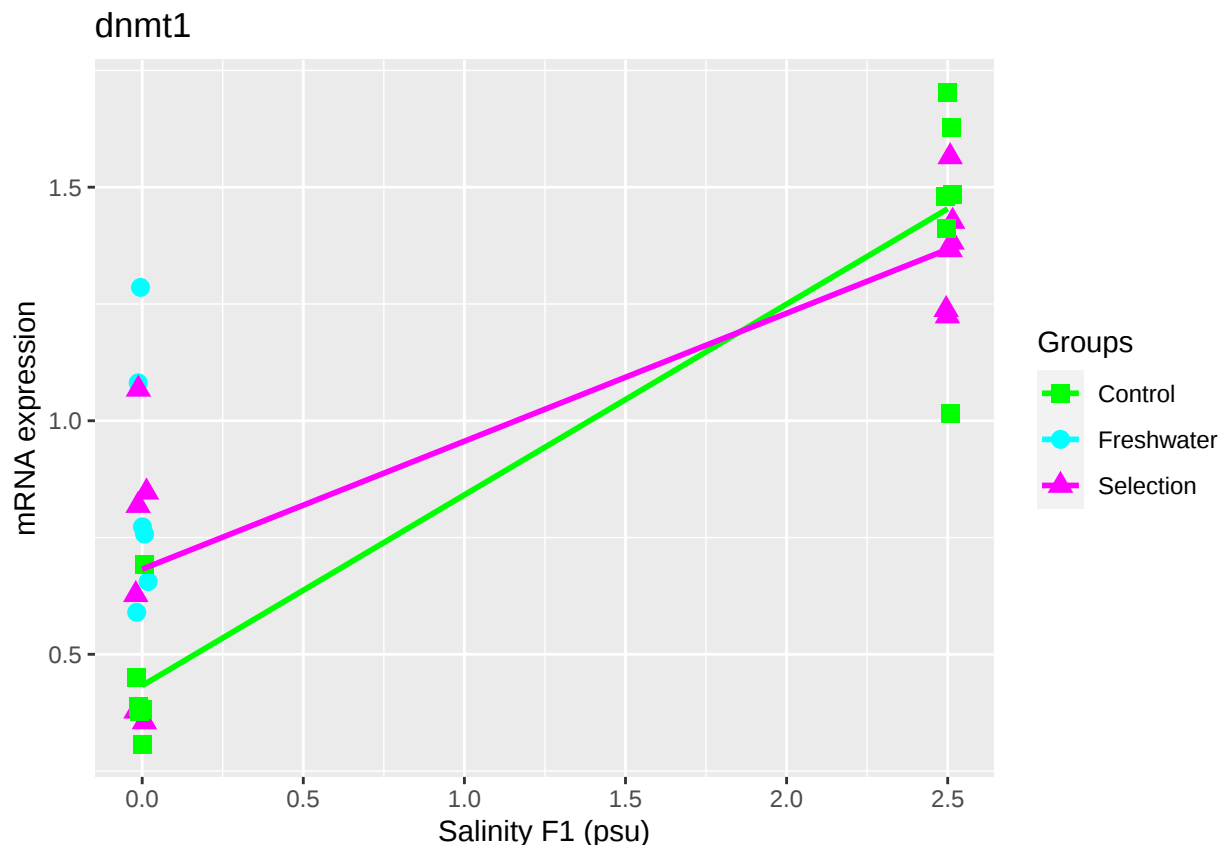
```

## as.numeric(Gene$Salinity_F1)          0.40831    0.05094    8.015 2.27e-08
## Gene$GroupFw                          0.42414    0.12736    3.330 0.0027
## Gene$GroupS                           0.24938    0.12736    1.958 0.0615
## as.numeric(Gene$Salinity_F1):Gene$GroupFw      NA          NA          NA          NA
## as.numeric(Gene$Salinity_F1):Gene$GroupS -0.13444    0.07205   -1.866 0.0738
##
## (Intercept)                          ***
## as.numeric(Gene$Salinity_F1)          ***
## Gene$GroupFw                          **
## Gene$GroupS                           .
## as.numeric(Gene$Salinity_F1):Gene$GroupFw
## as.numeric(Gene$Salinity_F1):Gene$GroupS .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2206 on 25 degrees of freedom
## Multiple R-squared:  0.7926, Adjusted R-squared:  0.7594
## F-statistic: 23.89 on 4 and 25 DF,  p-value: 3.146e-08

##                                2.5 %    97.5 %
## (Intercept)                   0.24746320 0.61841527
## as.numeric(Gene$Salinity_F1)   0.30338563 0.51322781
## Gene$GroupFw                   0.16184149 0.68644693
## Gene$GroupS                    -0.01292694 0.51167850
## as.numeric(Gene$Salinity_F1):Gene$GroupFw      NA          NA
## as.numeric(Gene$Salinity_F1):Gene$GroupS -0.28282046 0.01394119

## Gene$dnmt1 groups
## S 1.0246489 a
## C 0.9433226 a
## Fw 0.8570834 a

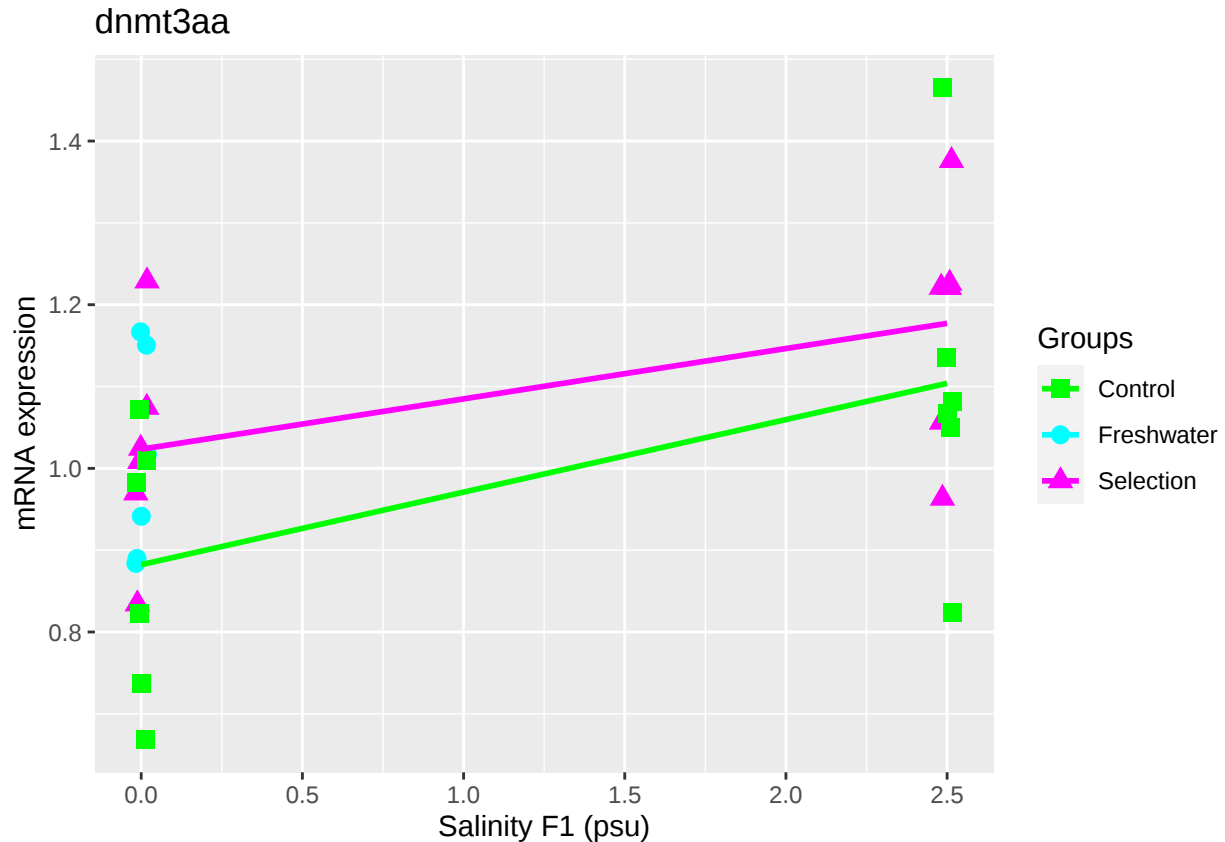
```



```
##
## Call:
## lm(formula = Gene$dnmt3aa ~ Gene$Salinity_F1 * Gene$Group, data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.27952 -0.10549 -0.00702  0.08830  0.36147
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.88229    0.06409   13.766 3.59e-13 ***
## Gene$Salinity_F1    0.08865    0.03626    2.445  0.0219 *
## Gene$GroupFw       0.12597    0.09064    1.390  0.1769
## Gene$GroupS        0.14110    0.09064    1.557  0.1321
## Gene$Salinity_F1:Gene$GroupFw      NA         NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.02712    0.05127   -0.529  0.6015
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.157 on 25 degrees of freedom
## Multiple R-squared:  0.3233, Adjusted R-squared:  0.215
## F-statistic: 2.986 on 4 and 25 DF,  p-value: 0.03824
##
##              2.5 %      97.5 %
## (Intercept)      0.75028601 1.01428651
## Gene$Salinity_F1    0.01397757 0.16331880
## Gene$GroupFw      -0.06070903 0.31264405
```

```
## Gene$GroupS          -0.04557776 0.32777532
## Gene$Salinity_F1:Gene$GroupFw      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.13271943 0.07848097

## Gene$dnmt3aa groups
## S      1.1002962      a
## Fw     1.0082538      a
## C      0.9930965      a
```

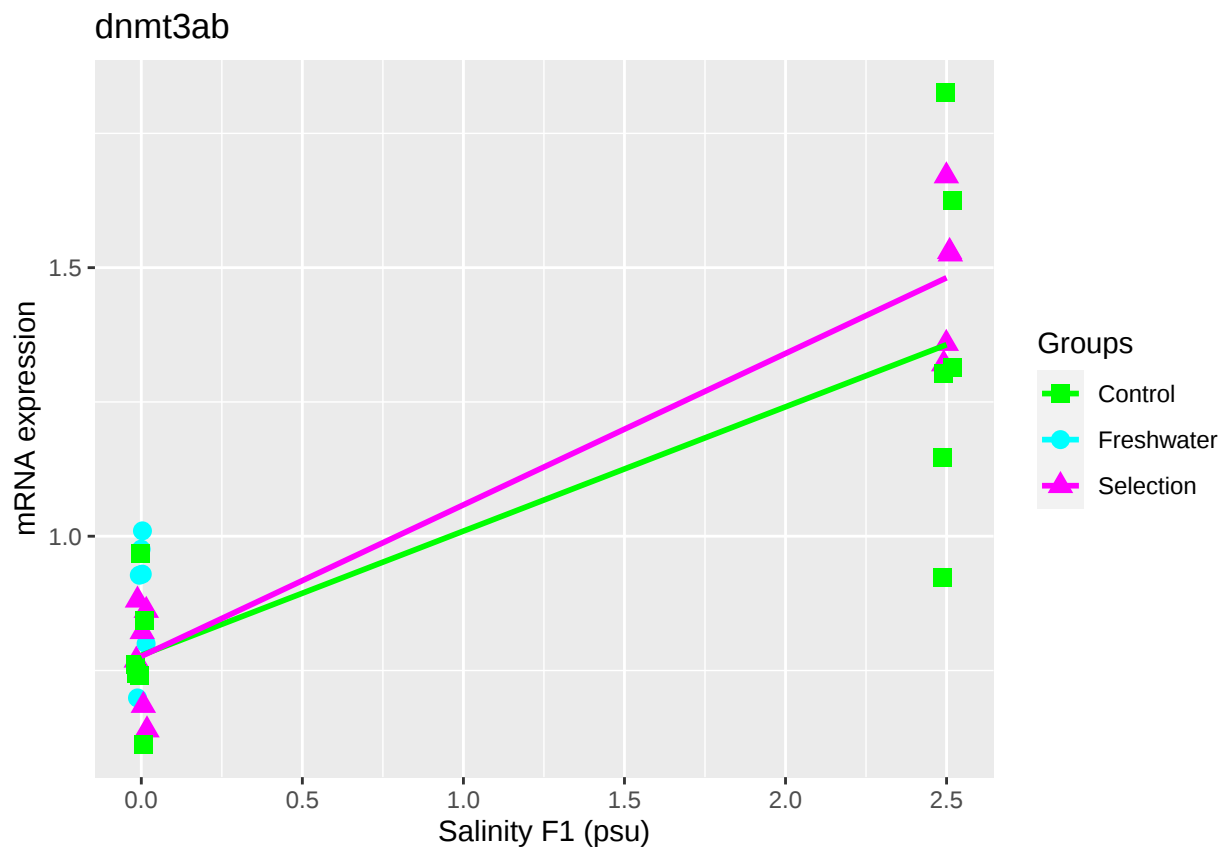


```
##
## Call:
## lm(formula = Gene3ab$dnmt3ab ~ Gene3ab$Salinity_F1 * Gene3ab$Group,
##     data = Gene3ab)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.43344 -0.09108 -0.00679  0.08495  0.46985
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.77828    0.07436  10.466 2.00e-10 ***
## Gene3ab$Salinity_F1  0.23131    0.04206   5.499 1.18e-05 ***
## Gene3ab$GroupFw     0.11208    0.10516   1.066  0.297
## Gene3ab$GroupS     -0.00180    0.10516  -0.017  0.986
## Gene3ab$Salinity_F1:Gene3ab$GroupFw      NA      NA      NA      NA
## Gene3ab$Salinity_F1:Gene3ab$GroupS  0.05056    0.06096   0.829  0.415
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1821 on 24 degrees of freedom
## Multiple R-squared:  0.7611, Adjusted R-squared:  0.7212
## F-statistic: 19.11 on 4 and 24 DF,  p-value: 3.508e-07

##               2.5 %    97.5 %
## (Intercept)      0.6248034 0.9317479
## Gene3ab$Salinity_F1 0.1444941 0.3181281
## Gene3ab$GroupFw    -0.1049655 0.3291197
## Gene3ab$GroupS     -0.2188427 0.2152424
## Gene3ab$Salinity_F1:Gene3ab$GroupFw      NA      NA
## Gene3ab$Salinity_F1:Gene3ab$GroupS    -0.0752468 0.1763728

## Gene3ab$dnmt3ab groups
## S      1.0967870      a
## C      1.0674145      a
## Fw      0.8903527      a
```

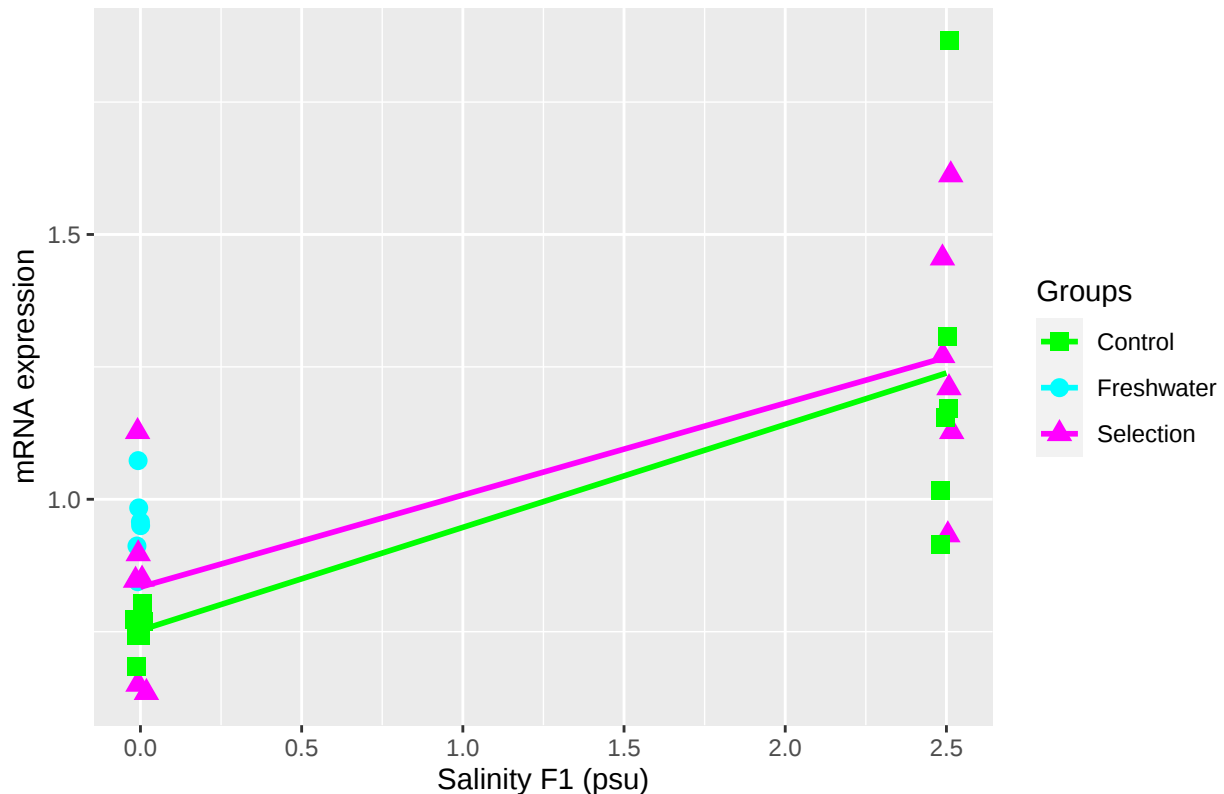


```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.75276    0.08387   8.975 2.71e-09 ***
## Gene$Salinity_F1  0.19422    0.04744   4.094 0.000389 ***
## Gene$GroupFw      0.20066    0.11861   1.692 0.103115
## Gene$GroupS       0.08159    0.11861   0.688 0.497854
## Gene$Salinity_F1:Gene$GroupFw      NA         NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.02065    0.06710  -0.308 0.760842
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2054 on 25 degrees of freedom
## Multiple R-squared:  0.5547, Adjusted R-squared:  0.4835
## F-statistic: 7.786 on 4 and 25 DF,  p-value: 0.0003217

##               2.5 %    97.5 %
## (Intercept)      0.58003164 0.9254943
## Gene$Salinity_F1  0.09650932 0.2919325
## Gene$GroupFw     -0.04361762 0.4449403
## Gene$GroupS      -0.16268910 0.3258689
## Gene$Salinity_F1:Gene$GroupFw      NA         NA
## Gene$Salinity_F1:Gene$GroupS -0.15883184 0.1175383

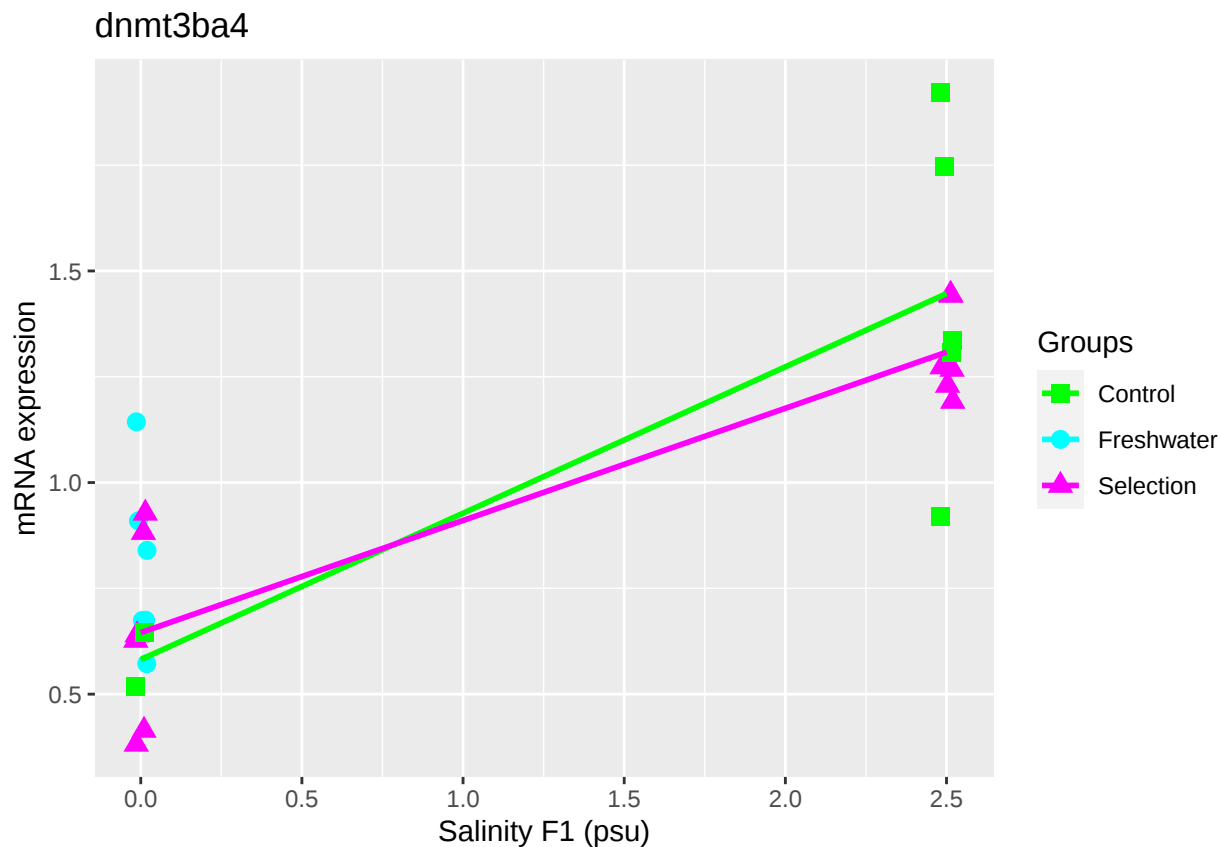
## Gene$dnmt3ab3 groups
## S      1.0513205      a
## C      0.9955391      a
## Fw      0.9534243      a
```

dnmt3ab3



##

```
## Call:
## lm(formula = Gene3ba4$dnmt3ba4 ~ Gene3ba4$Salinity_F1 * Gene3ba4$Group,
##     data = Gene3ba4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.52550 -0.12776 -0.03483  0.13416  0.47555
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.58164    0.17070   3.407 0.002793 **
## Gene3ba4$Salinity_F1  0.34592    0.08079   4.282 0.000364 ***
## Gene3ba4$GroupFw      0.22063    0.19711   1.119 0.276257
## Gene3ba4$GroupS       0.06370    0.19711   0.323 0.749929
## Gene3ba4$Salinity_F1:Gene3ba4$GroupFw      NA         NA      NA      NA
## Gene3ba4$Salinity_F1:Gene3ba4$GroupS -0.08082    0.09816  -0.823 0.420028
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2414 on 20 degrees of freedom
## Multiple R-squared:  0.7137, Adjusted R-squared:  0.6564
## F-statistic: 12.46 on 4 and 20 DF,  p-value: 3.012e-05
##
##              2.5 %    97.5 %
## (Intercept)      0.2255724 0.9377143
## Gene3ba4$Salinity_F1  0.1774002 0.5144473
## Gene3ba4$GroupFw     -0.1905264 0.6317842
## Gene3ba4$GroupS     -0.3474589 0.4748518
## Gene3ba4$Salinity_F1:Gene3ba4$GroupFw      NA      NA
## Gene3ba4$Salinity_F1:Gene3ba4$GroupS -0.2855704 0.1239370
##
## Gene3ba4$dnmt3ba4 groups
## C      1.1993644      a
## S      0.9767237      ab
## Fw     0.8022723      b
```

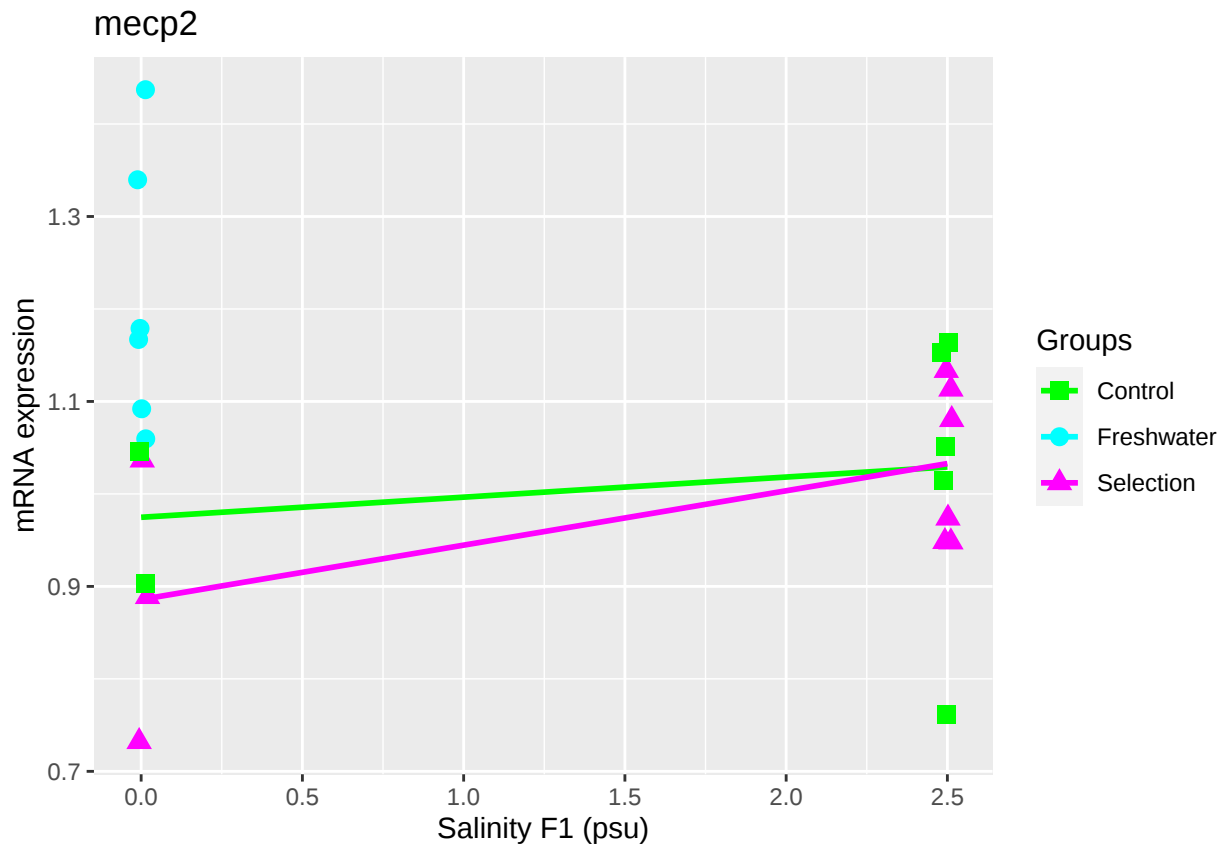


```
##
## Call:
## lm(formula = Genemecp2$mecp2 ~ Genemecp2$Salinity_F1 * Genemecp2$Group,
##     data = Genemecp2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.267349 -0.081217 -0.005586  0.095565  0.224673
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.97472    0.09498  10.262 1.06e-08
## Genemecp2$Salinity_F1      0.02176    0.04495   0.484  0.6345
## Genemecp2$GroupFw      0.23757    0.10968   2.166  0.0448
## Genemecp2$GroupS     -0.08894    0.12262  -0.725  0.4781
## Genemecp2$Salinity_F1:Genemecp2$GroupFw      NA         NA      NA      NA
## Genemecp2$Salinity_F1:Genemecp2$GroupS      0.03704    0.05886   0.629  0.5375
##
## (Intercept)                ***
## Genemecp2$Salinity_F1
## Genemecp2$GroupFw          *
## Genemecp2$GroupS
## Genemecp2$Salinity_F1:Genemecp2$GroupFw
## Genemecp2$Salinity_F1:Genemecp2$GroupS
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.1343 on 17 degrees of freedom
## Multiple R-squared:  0.4525, Adjusted R-squared:  0.3237
## F-statistic: 3.513 on 4 and 17 DF,  p-value: 0.02895

##                                2.5 %   97.5 %
## (Intercept)                   0.774324999 1.1751198
## Genemecp2$Salinity_F1         -0.073081894 0.1166088
## Genemecp2$GroupFw             0.006172089 0.4689700
## Genemecp2$GroupS              -0.347649792 0.1697740
## Genemecp2$Salinity_F1:Genemecp2$GroupFw      NA      NA
## Genemecp2$Salinity_F1:Genemecp2$GroupS      -0.087138392 0.1612251

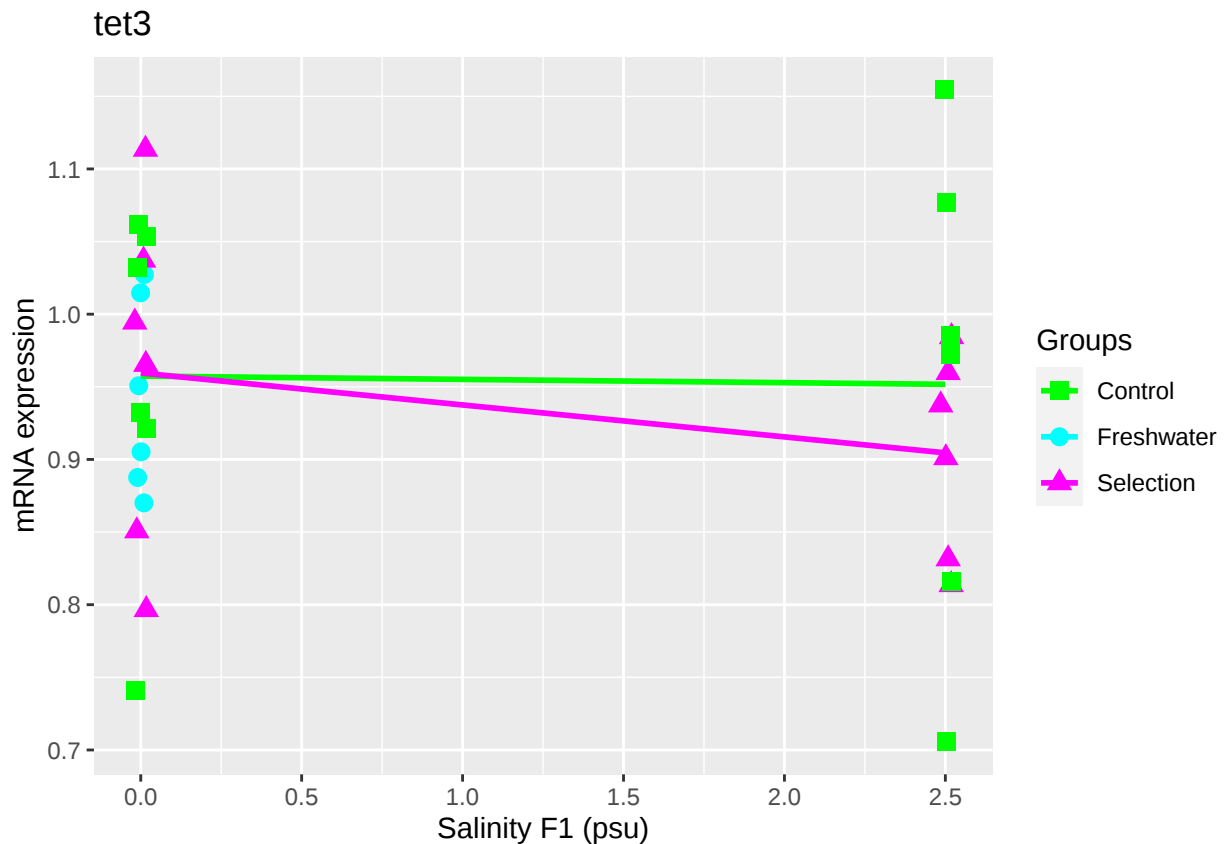
## Genemecp2$mecp2 groups
## Fw      1.2122935      a
## C       1.0135857      b
## S       0.9837958      b
```



```
## (Intercept)                0.957409    0.046753   20.478   <2e-16 ***
## Gene$Salinity_F1           -0.002277    0.026448   -0.086    0.932
## Gene$GroupFw               -0.015090    0.066119   -0.228    0.821
## Gene$GroupS                0.002108    0.066119    0.032    0.975
## Gene$Salinity_F1:Gene$GroupFw      NA          NA          NA          NA
## Gene$Salinity_F1:Gene$GroupS -0.019716    0.037402   -0.527    0.603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1145 on 25 degrees of freedom
## Multiple R-squared:  0.03593,    Adjusted R-squared:  -0.1183
## F-statistic: 0.2329 on 4 and 25 DF,  p-value: 0.9172

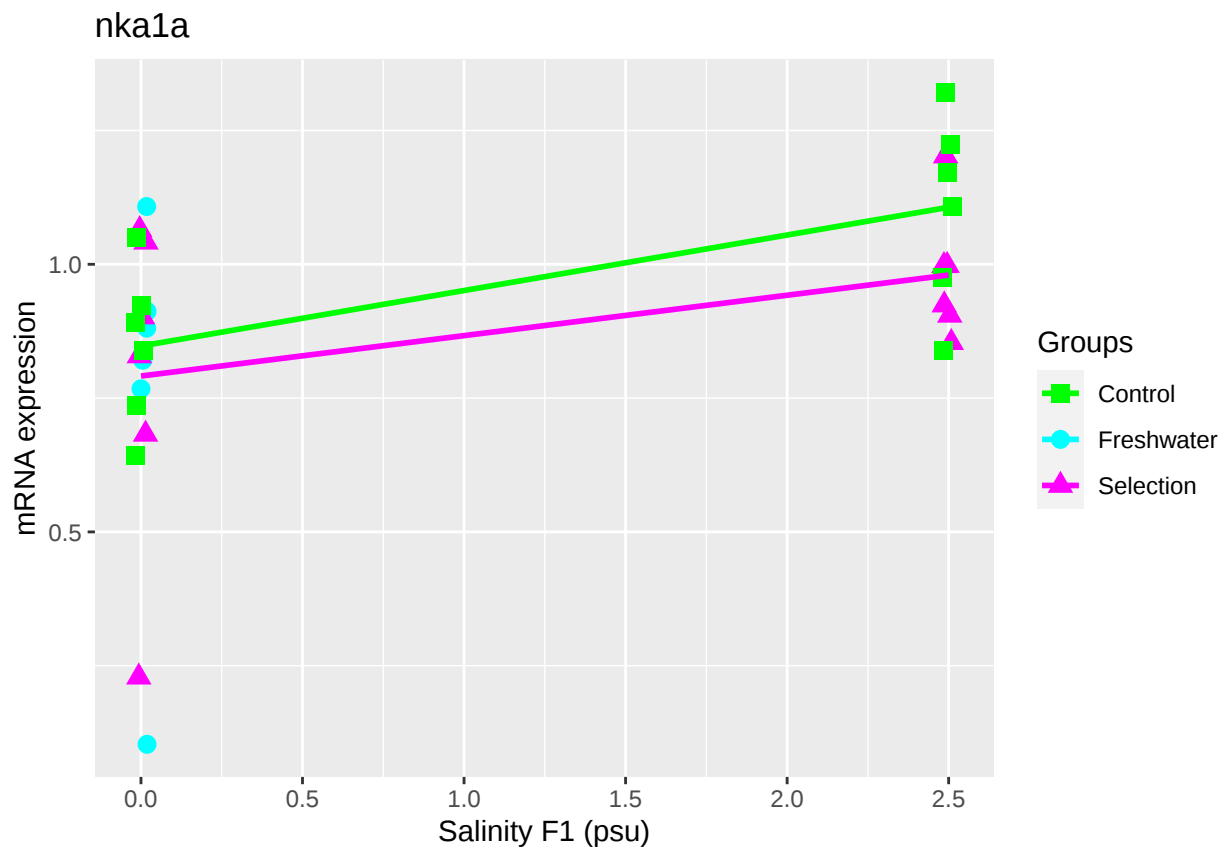
##                2.5 %    97.5 %
## (Intercept)      0.86111951 1.05369914
## Gene$Salinity_F1 -0.05674691 0.05219258
## Gene$GroupFw     -0.15126390 0.12108483
## Gene$GroupS      -0.13406620 0.13828253
## Gene$Salinity_F1:Gene$GroupFw      NA          NA
## Gene$Salinity_F1:Gene$GroupS -0.09674822 0.05731549

## Gene$tet3 groups
## C 0.9545629    a
## Fw 0.9423198   a
## S 0.9320256    a
```



```
##
## Call:
```

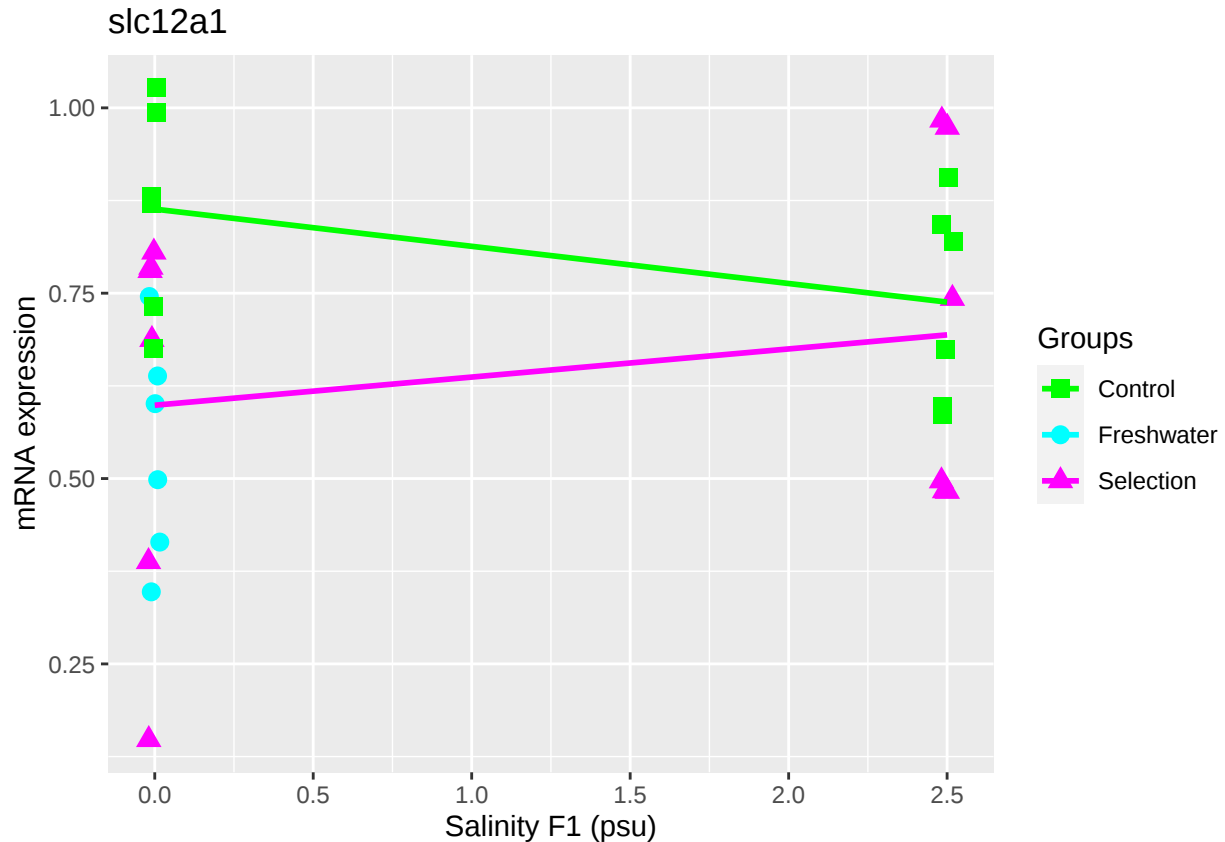
```
## lm(formula = Gene$nkala ~ Gene$Salinity_F1 * Gene$Group, data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.66212 -0.10041  0.02764  0.11638  0.34254
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.84731    0.09675   8.757 4.34e-09 ***
## Gene$Salinity_F1    0.10368    0.05473   1.894  0.0698 .
## Gene$GroupFw     -0.08200    0.13683  -0.599  0.5544
## Gene$GroupS      -0.05608    0.13683  -0.410  0.6854
## Gene$Salinity_F1:Gene$GroupFw      NA         NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.02820    0.07740  -0.364  0.7186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.237 on 25 degrees of freedom
## Multiple R-squared:  0.2589, Adjusted R-squared:  0.1403
## F-statistic: 2.184 on 4 and 25 DF,  p-value: 0.1001
##
##              2.5 %    97.5 %
## (Intercept)      0.648043528 1.0465774
## Gene$Salinity_F1 -0.009039259 0.2164056
## Gene$GroupFw     -0.363803316 0.1998087
## Gene$GroupS      -0.337882145 0.2257299
## Gene$Salinity_F1:Gene$GroupFw      NA         NA
## Gene$Salinity_F1:Gene$GroupS -0.187617956 0.1312092
##
## Gene$nkala groups
## C  0.9769144    a
## S  0.8855828    a
## Fw 0.7653132    a
```



```
##
## Call:
## lm(formula = Gene$slc12a1 ~ Gene$Salinity_F1 * Gene$Group, data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.45057 -0.14894  0.03334  0.15582  0.28903
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.86343    0.07990  10.807 6.55e-11 ***
## Gene$Salinity_F1 -0.05017    0.04520  -1.110  0.27752
## Gene$GroupFw    -0.32238    0.11299  -2.853  0.00857 **
## Gene$GroupS     -0.26454    0.11299  -2.341  0.02749 *
## Gene$Salinity_F1:Gene$GroupFw      NA         NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS  0.08814    0.06392   1.379  0.18012
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1957 on 25 degrees of freedom
## Multiple R-squared:  0.2825, Adjusted R-squared:  0.1677
## F-statistic: 2.461 on 4 and 25 DF,  p-value: 0.07143
##
##              2.5 %      97.5 %
## (Intercept)    0.69888352  1.02798547
## Gene$Salinity_F1 -0.14325635  0.04291182
## Gene$GroupFw    -0.55509496 -0.08967452
```

```
## Gene$GroupS          -0.49725071 -0.03183027
## Gene$Salinity_F1:Gene$GroupFw      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.04350116  0.21978039

## Gene$slc12a1 groups
## C      0.8007192      a
## S      0.6463532     ab
## Fw     0.5410498     b
```

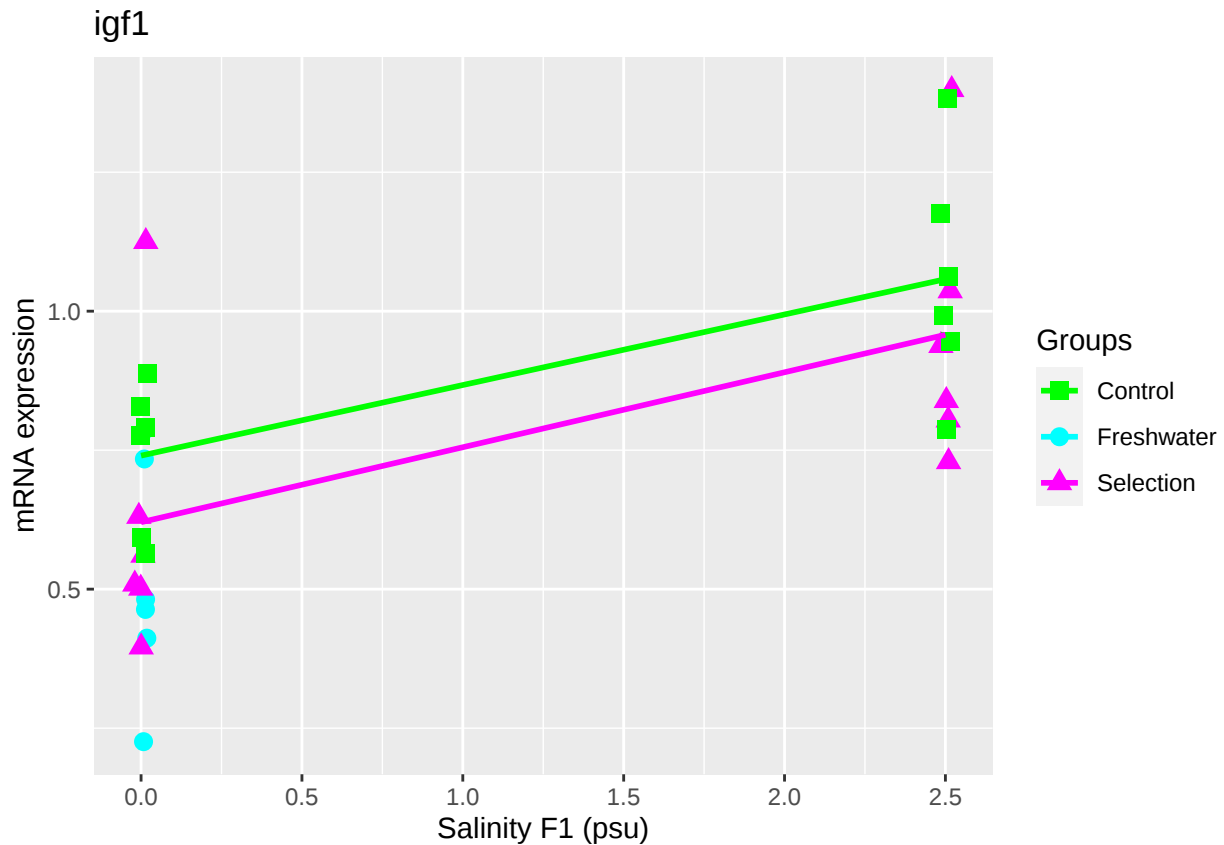


```
##
## Call:
## lm(formula = Gene$slc12a1 ~ Gene$Salinity_F1 * Gene$Group, data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.29168 -0.11866 -0.04438  0.08613  0.50558
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.740203   0.087276   8.481 7.97e-09 ***
## Gene$Salinity_F1  0.126939   0.049371   2.571  0.0165 *
## Gene$GroupFw    -0.223201   0.123427  -1.808  0.0826 .
## Gene$GroupS     -0.119806   0.123427  -0.971  0.3410
## Gene$Salinity_F1:Gene$GroupFw      NA      NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS  0.007921  0.069821   0.113  0.9106
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.2138 on 25 degrees of freedom
## Multiple R-squared:  0.5181, Adjusted R-squared:  0.441
## F-statistic: 6.721 on 4 and 25 DF,  p-value: 0.0008131

##                2.5 %    97.5 %
## (Intercept)      0.56045422 0.91995251
## Gene$Salinity_F1  0.02525782 0.22862076
## Gene$GroupFw     -0.47740448 0.03100288
## Gene$GroupS      -0.37400976 0.13439760
## Gene$Salinity_F1:Gene$GroupFw      NA      NA
## Gene$Salinity_F1:Gene$GroupS     -0.13587807 0.15172056

## Gene$igf1 groups
## C 0.8988775    a
## S 0.7889729    a
## Fw 0.5170026    b
```



```
##
## Call:
## lm(formula = Gene$gh2 ~ Gene$Salinity_F1 * Gene$Group, data = Gene)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.43108 -0.14363 -0.00287  0.09734  0.64824
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)                0.65866    0.10393    6.338 1.24e-06 ***
## Gene$Salinity_F1           0.16177    0.05879    2.752 0.01087 *
## Gene$GroupFw              -0.19291    0.14698   -1.313 0.20127
## Gene$GroupS                0.02232    0.14698    0.152 0.88052
## Gene$Salinity_F1:Gene$GroupFw      NA          NA      NA      NA
## Gene$Salinity_F1:Gene$GroupS -0.24015    0.08314   -2.888 0.00788 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2546 on 25 degrees of freedom
## Multiple R-squared:  0.4607, Adjusted R-squared:  0.3744
## F-statistic:  5.34 on 4 and 25 DF,  p-value: 0.003003

##                2.5 %      97.5 %
## (Intercept)      0.44461893 0.87270523
## Gene$Salinity_F1  0.04068959 0.28285178
## Gene$GroupFw     -0.49561083 0.10979463
## Gene$GroupS      -0.28038275 0.32502271
## Gene$Salinity_F1:Gene$GroupFw      NA          NA
## Gene$Salinity_F1:Gene$GroupS -0.41138192 -0.06891287

##      Gene$gh2 groups
## C 0.8608754      a
## S 0.5830112      b
## Fw 0.4657540     b
```

