

Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:

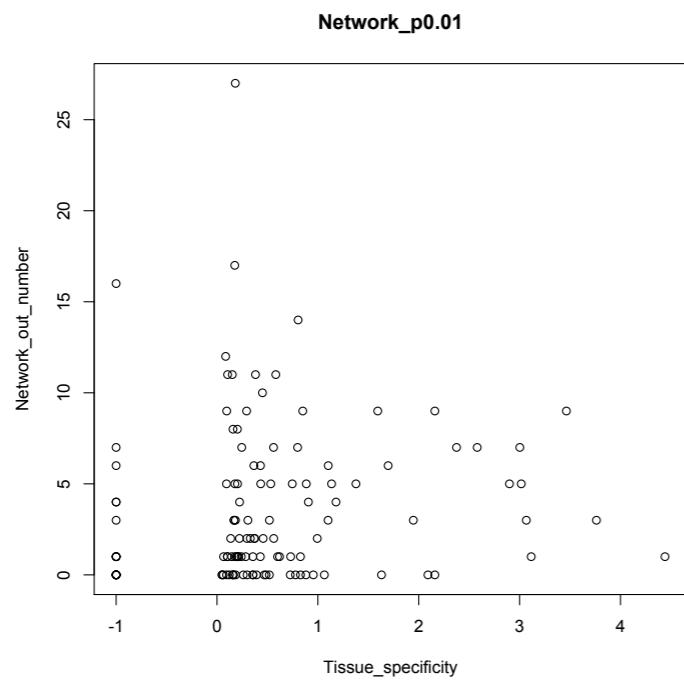
Min	1Q	Median	3Q	Max
-13.825	-3.307	-2.333	2.139	48.578

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.6611	0.7888	2.106	0.0373 *
Tissue_specificity	3.8005	0.6643	5.721	7.91e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.816 on 120 degrees of freedom
Multiple R-squared: 0.2143, Adjusted R-squared: 0.2078
F-statistic: 32.73 on 1 and 120 DF, p-value: 7.914e-08



Call:
lm(formula = Network_out_number ~ Tissue_specificity)

Residuals:

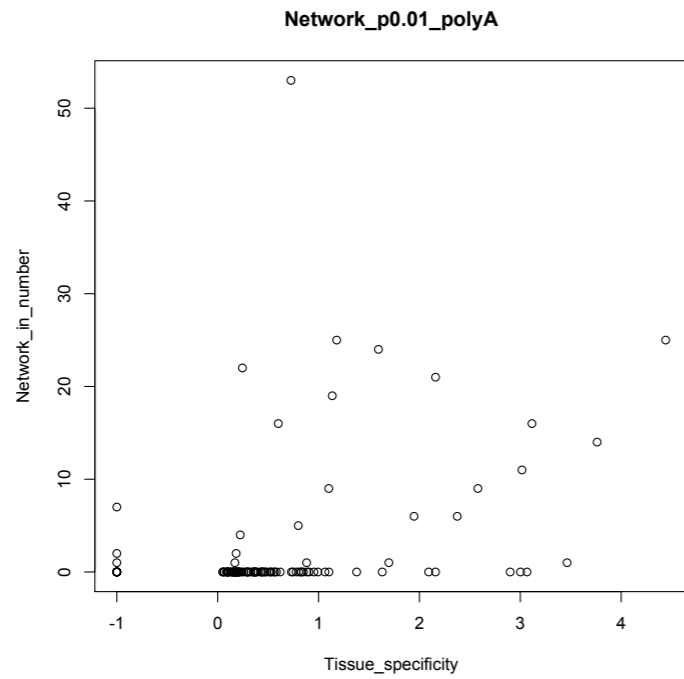
Min	1Q	Median	3Q	Max
-4.207	-2.967	-1.551	1.595	23.569

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.3597	0.4386	7.659	5.31e-12 ***
Tissue_specificity	0.3923	0.3694	1.062	0.290

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.346 on 120 degrees of freedom
Multiple R-squared: 0.009312, Adjusted R-squared: 0.001056
F-statistic: 1.128 on 1 and 120 DF, p-value: 0.2903



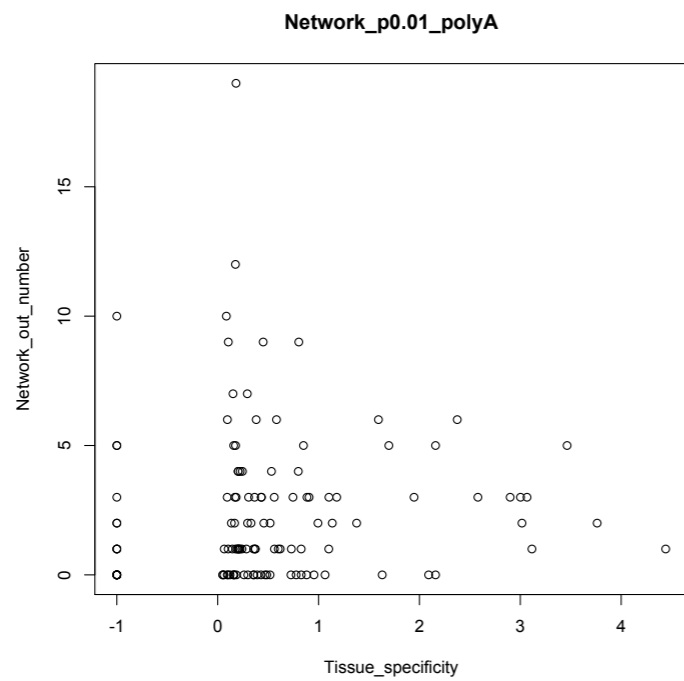
Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:
Min 1Q Median 3Q Max
-8.663 -2.336 -1.634 1.250 50.041

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.1878 0.6846 1.735 0.0853 .
Tissue_specificity 2.4377 0.5765 4.228 4.62e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.783 on 120 degrees of freedom
Multiple R-squared: 0.1297, Adjusted R-squared: 0.1224
F-statistic: 17.88 on 1 and 120 DF, p-value: 4.623e-05



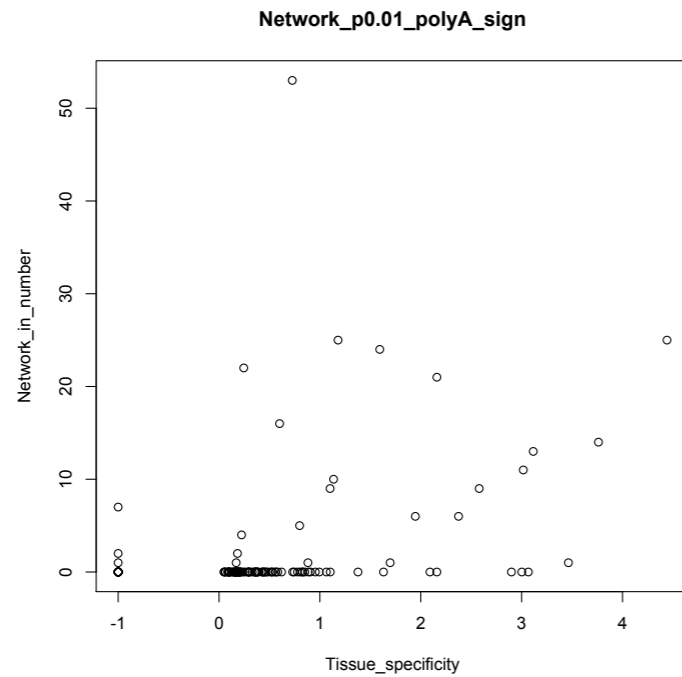
Call:
lm(formula = Network_out_number ~ Tissue_specificity)

Residuals:
Min 1Q Median 3Q Max
-2.6595 -2.1770 -1.1770 0.6438 16.6426

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.3297 0.2997 7.773 2.93e-12 ***
Tissue_specificity 0.1527 0.2524 0.605 0.546

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.97 on 120 degrees of freedom
Multiple R-squared: 0.003041, Adjusted R-squared: -0.005267
F-statistic: 0.3661 on 1 and 120 DF, p-value: 0.5463

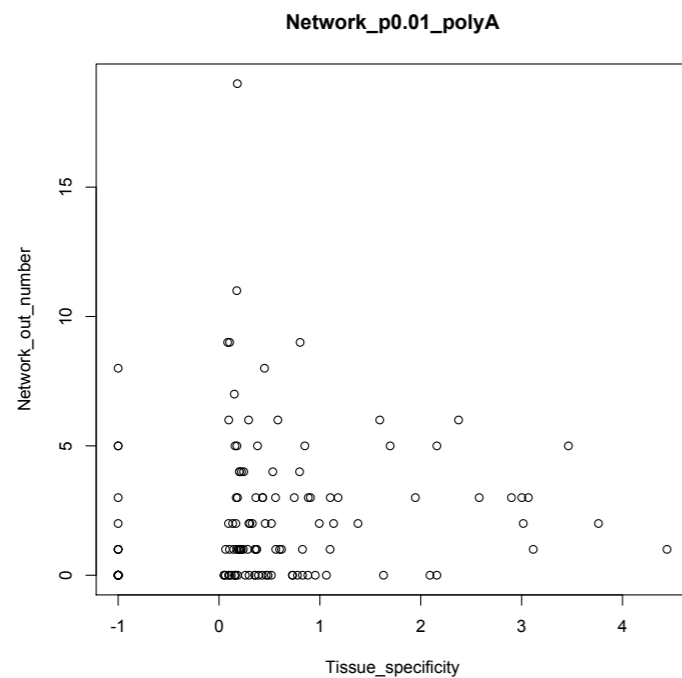


```
Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:
    Min       1Q   Median       3Q      Max
-8.321 -2.231 -1.569  1.202 50.159

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.1398    0.6704   1.700  0.0917 .
Tissue_specificity 2.3418    0.5646   4.148 6.3e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.643 on 120 degrees of freedom
Multiple R-squared:  0.1254, Adjusted R-squared:  0.1181
F-statistic: 17.2 on 1 and 120 DF, p-value: 6.294e-05
```

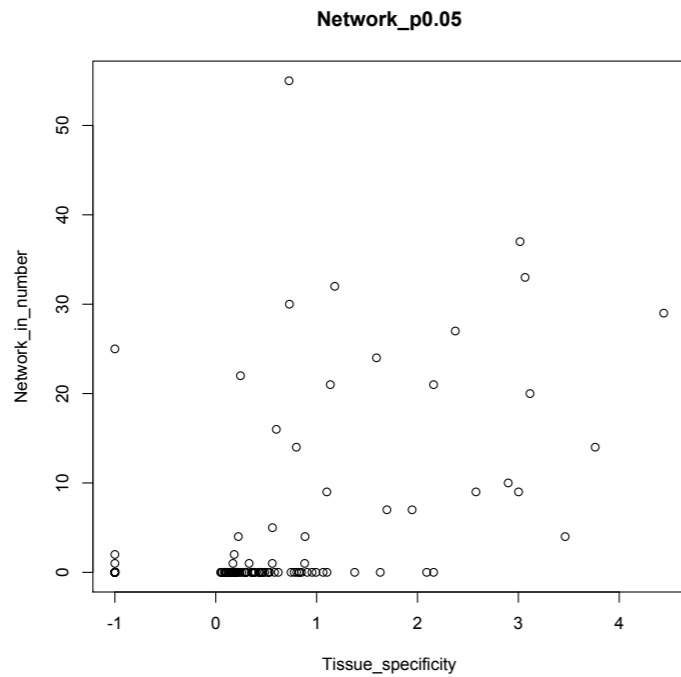


```
Call:
lm(formula = Network_out_number ~ Tissue_specificity)

Residuals:
    Min       1Q   Median       3Q      Max
-2.6530 -1.9929 -0.9929  0.7504 16.7602

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.2018    0.2881   7.641 5.83e-12 ***
Tissue_specificity 0.2089    0.2426   0.861  0.391
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.855 on 120 degrees of freedom
Multiple R-squared:  0.006138, Adjusted R-squared: -0.002144
F-statistic: 0.7411 on 1 and 120 DF, p-value: 0.391
```



Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:

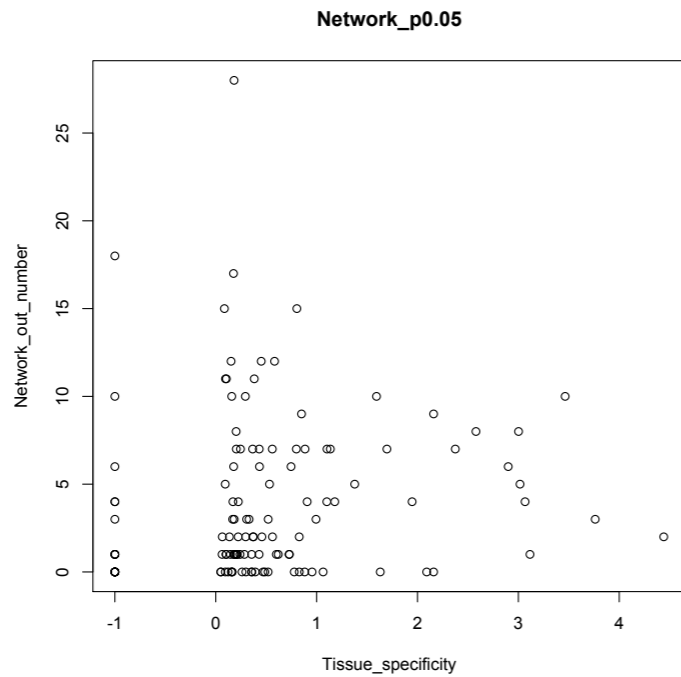
Min	1Q	Median	3Q	Max
-12.879	-3.674	-2.557	2.570	50.048

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.7870	0.8477	2.108	0.0371 *
Tissue_specificity	4.3571	0.7139	6.103	1.31e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.4 on 120 degrees of freedom
Multiple R-squared: 0.2369, Adjusted R-squared: 0.2305
F-statistic: 37.25 on 1 and 120 DF, p-value: 1.314e-08



Call:
lm(formula = Network_out_number ~ Tissue_specificity)

Residuals:

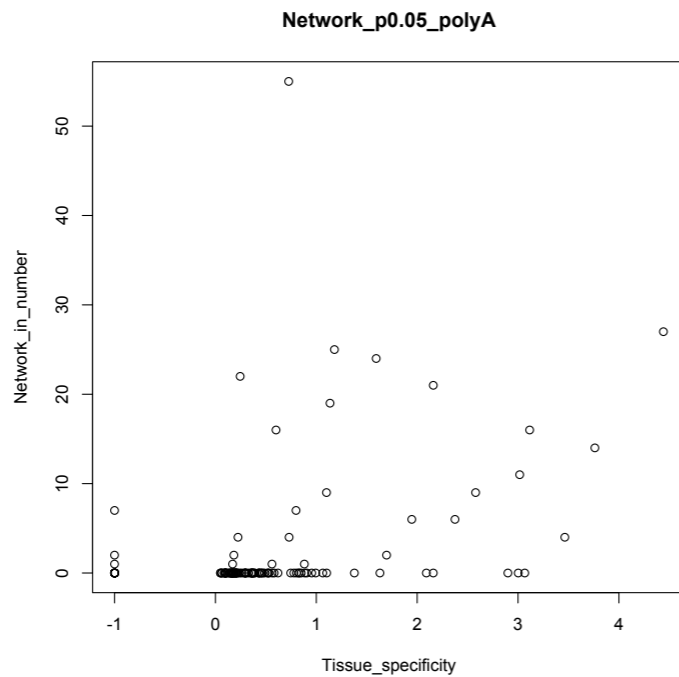
Min	1Q	Median	3Q	Max
-4.725	-3.261	-1.878	2.677	24.192

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.7241	0.4738	7.861	1.84e-12 ***
Tissue_specificity	0.4633	0.3990	1.161	0.248

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.694 on 120 degrees of freedom
Multiple R-squared: 0.01111, Adjusted R-squared: 0.002872
F-statistic: 1.348 on 1 and 120 DF, p-value: 0.2479

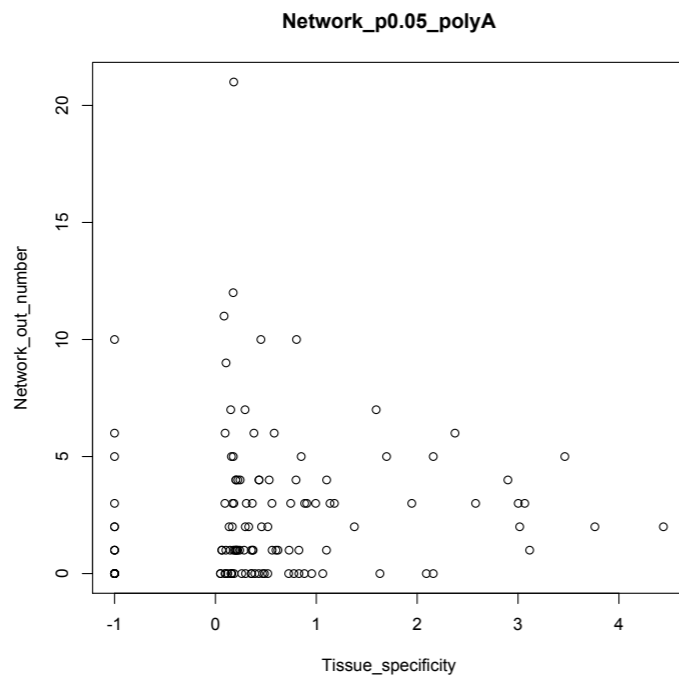


```
Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:
    Min       1Q   Median       3Q      Max
-9.147 -2.412 -1.695  1.343 51.890

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    1.2364    0.6972   1.773  0.0787 .
Tissue_specificity 2.5795    0.5871   4.393 2.42e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.908 on 120 degrees of freedom
Multiple R-squared:  0.1386, Adjusted R-squared:  0.1314
F-statistic: 19.3 on 1 and 120 DF, p-value: 2.421e-05
```

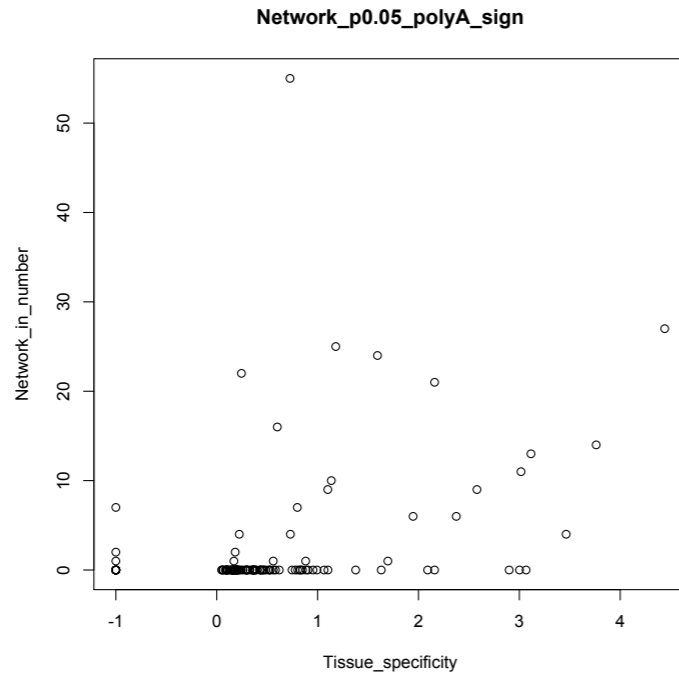


```
Call:
lm(formula = Network_out_number ~ Tissue_specificity)

Residuals:
    Min       1Q   Median       3Q      Max
-2.852 -2.235 -1.235  1.266 18.534

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.4302    0.3174   7.656 5.41e-12 ***
Tissue_specificity 0.1955    0.2673   0.731  0.466
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.145 on 120 degrees of freedom
Multiple R-squared:  0.004438, Adjusted R-squared: -0.003858
F-statistic: 0.5349 on 1 and 120 DF, p-value: 0.466
```



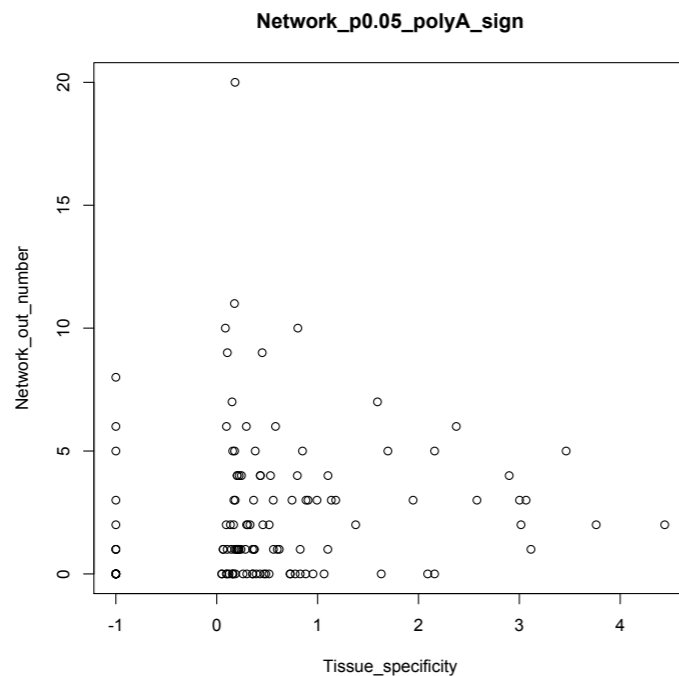
Call:
lm(formula = Network_in_number ~ Tissue_specificity)

Residuals:
Min 1Q Median 3Q Max
-8.775 -2.313 -1.624 1.291 52.017

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.1846 0.6842 1.731 0.086 .
Tissue_specificity 2.4751 0.5761 4.296 3.55e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.779 on 120 degrees of freedom
Multiple R-squared: 0.1333, Adjusted R-squared: 0.1261
F-statistic: 18.46 on 1 and 120 DF, p-value: 3.552e-05



Call:
lm(formula = Network_out_number ~ Tissue_specificity)

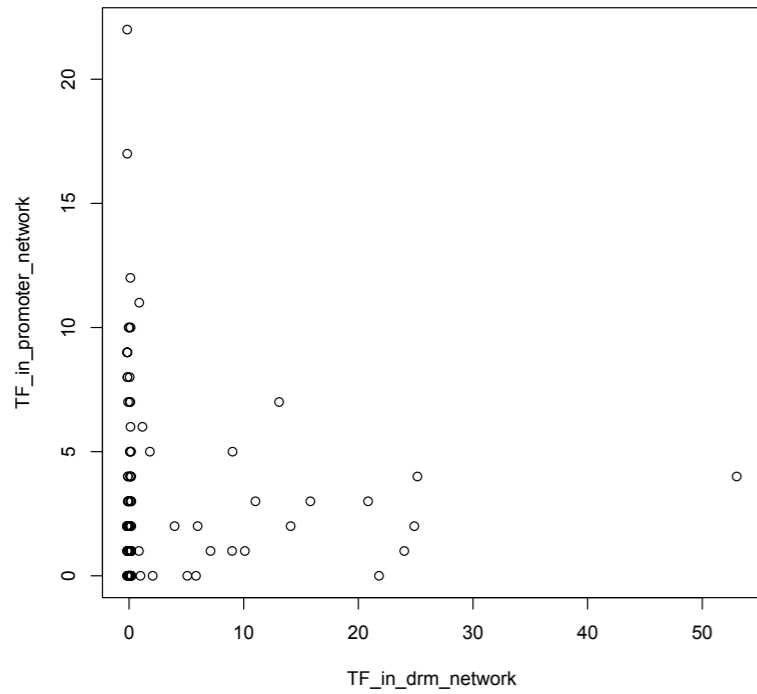
Residuals:
Min 1Q Median 3Q Max
-2.842 -2.039 -1.154 1.313 17.661

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 2.2928 0.3012 7.612 6.8e-12 ***
Tissue_specificity 0.2542 0.2537 1.002 0.318

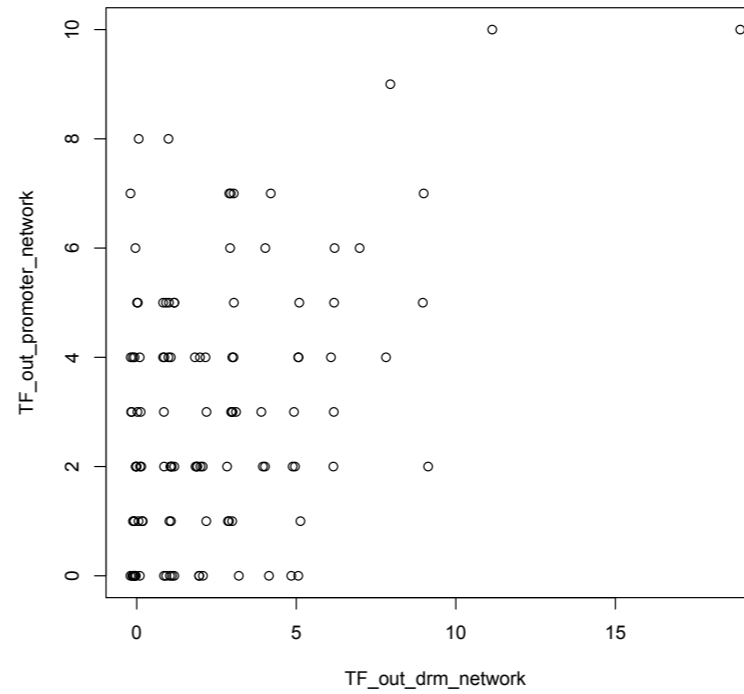
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.985 on 120 degrees of freedom
Multiple R-squared: 0.008298, Adjusted R-squared: 3.423e-05
F-statistic: 1.004 on 1 and 120 DF, p-value: 0.3183

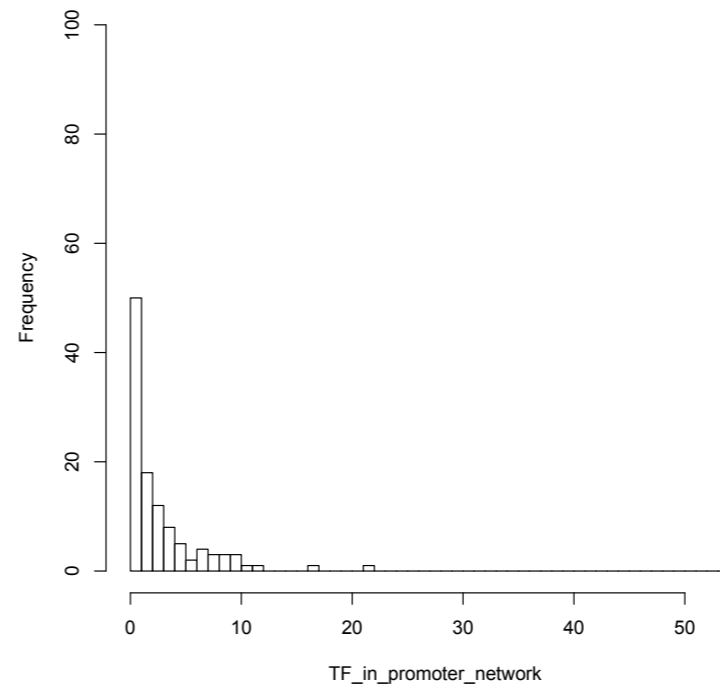
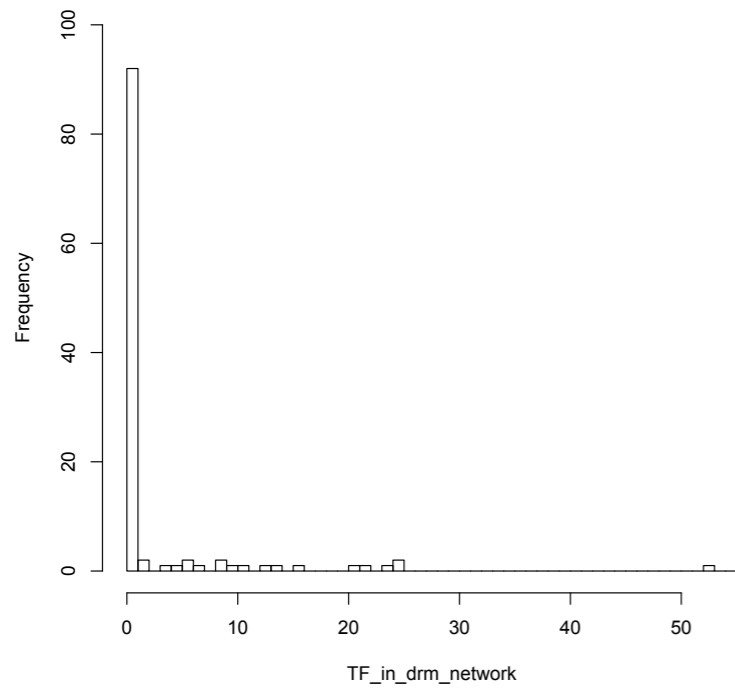
TF_features_DRMnumber_p0.01_polyA_sign



TF_features_DRMnumber_p0.01_polyA_sign



TF_features_DRMnumber_p0.01_polyA_sign



```
> promoter<-hist(TF_features_DRMnumber_p0.01_polyA_sign[TF_features_DRMnumber_p0.01_polyA_sign[,13]>0,35],xlim=c(0,60),breaks=seq(0,60,5))$counts
> drm<-hist(TF_features_DRMnumber_p0.01_polyA_sign[TF_features_DRMnumber_p0.01_polyA_sign[,13]>0,33],xlim=c(0,60),breaks=seq(0,60,5))$counts
> chisq.test(promoter,drm)
```

Pearson's Chi-squared test

data: promoter and drm
X-squared = 44.1429, df = 20, p-value = 0.00144

```
Warning message:
In chisq.test(promoter, drm) : Chi-squared approximation may be incorrect
> sum(promoter/sum(promoter)*log2((promoter+1e-10)/sum(promoter)*12))
[1] 2.748546
> sum(drm/sum(drm)*log2((drm+1e-10)/sum(drm)*12))
[1] 2.706453
```