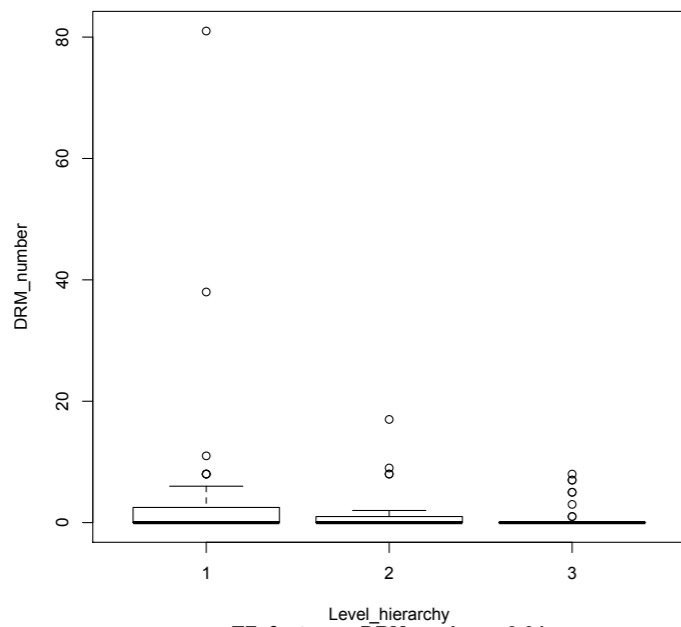
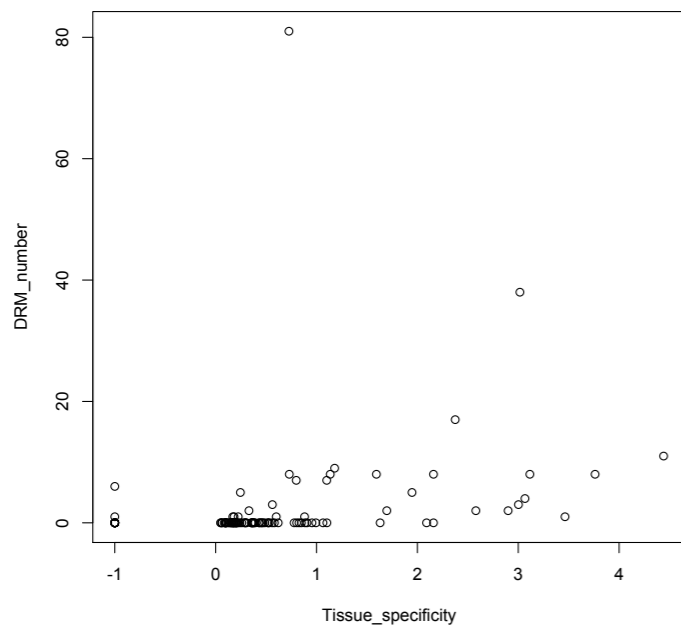


I

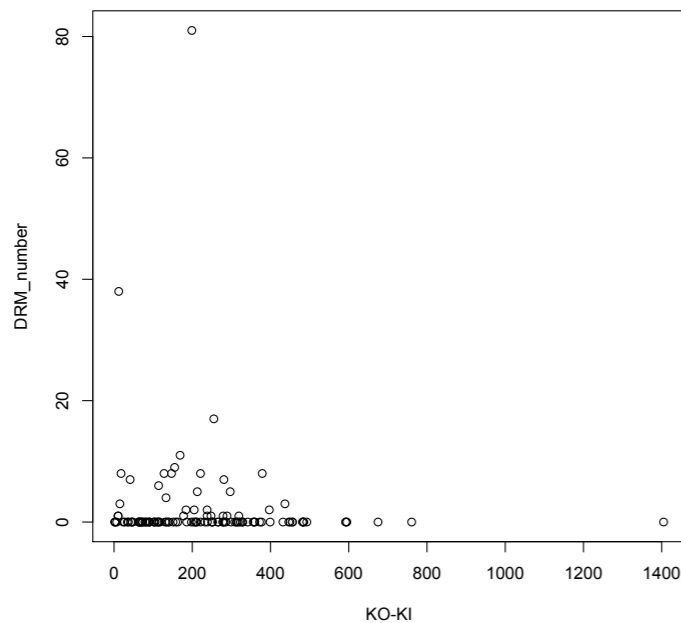
TF_features_DRMnumber_p0.01



TF_features_DRMnumber_p0.01



TF_kin_kout_DRMnumber_p0.01



Pairwise comparisons using Wilcoxon rank sum test

data: DRM_number and Level_hierarchy

```

1 2
2 0.43 -
3 0.33 0.43
    
```

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

data: DRM_number and Level_hierarchy

```

1 2
2 0.28 -
3 0.28 0.45
    
```

P value adjustment method: BH

Call:

lm(formula = Tissue_spec ~ DRM_number)

Residuals:

Min	1Q	Median	3Q	Max
-2.4982	-0.3661	-0.1832	0.3481	3.5845

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.48456	0.10225	4.739	6.47e-06 ***
DRM_number	0.03383	0.01133	2.986	0.00349 **

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

Residual standard error: 1.046 on 110 degrees of freedom

Multiple R-squared: 0.07496, Adjusted R-squared: 0.06655

F-statistic: 8.913 on 1 and 110 DF, p-value: 0.003490

Call:

lm(formula = O_I ~ DRM_number)

Residuals:

Min	1Q	Median	3Q	Max
-236.27	-148.02	-27.27	84.22	1166.73

Coefficients:

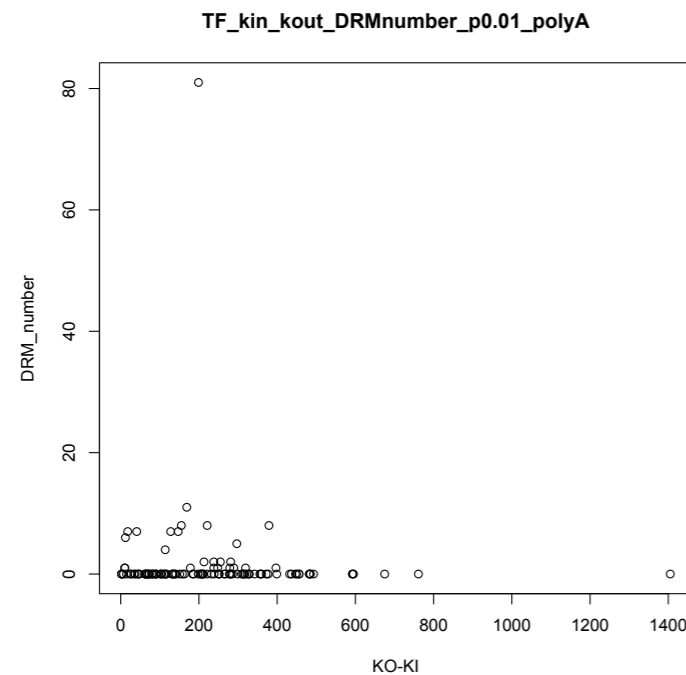
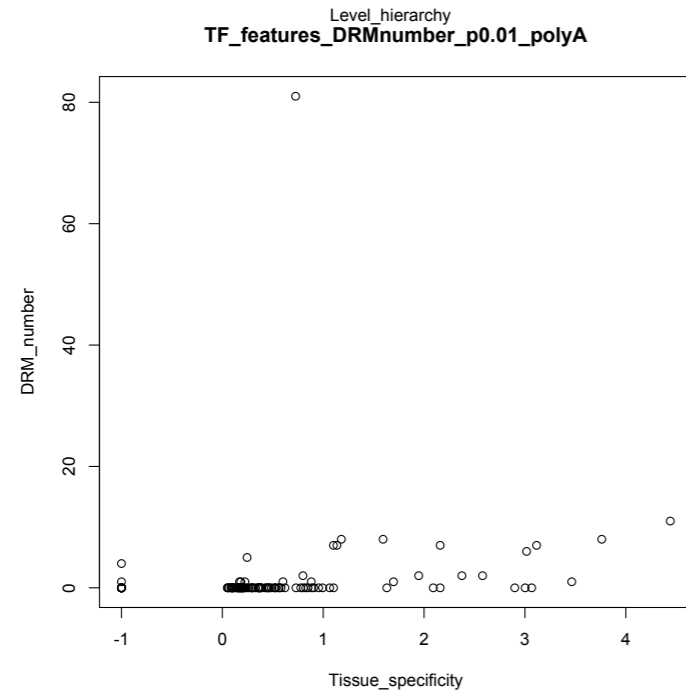
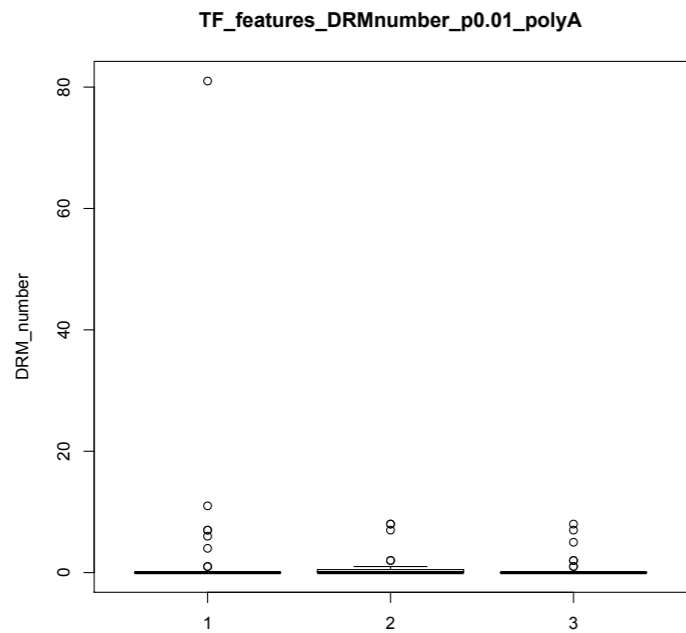
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	238.267	18.483	12.891	<2e-16 ***
DRM_number	-1.958	2.110	-0.928	0.355

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

Residual standard error: 194.7 on 116 degrees of freedom

Multiple R-squared: 0.007374, Adjusted R-squared: -0.001183

F-statistic: 0.8618 on 1 and 116 DF, p-value: 0.3552



Pairwise comparisons using Wilcoxon rank sum test

data: DRM_number and Level_hierarchy

```

1 2
2 0.98 -
3 0.69 0.69

```

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

data: DRM_number and Level_hierarchy

```

1 2
2 0.44 -
3 0.44 0.62

```

P value adjustment method: BH

Call:

```
lm(formula = Tissue_spec ~ DRM_number)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-1.6162 -0.3961 -0.2101  0.3048  3.6718

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.52858    0.10344   5.110 1.37e-06 ***
DRM_number   0.02190    0.01293   1.694  0.0932 .
---

```

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

Residual standard error: 1.074 on 110 degrees of freedom
Multiple R-squared: 0.02542, Adjusted R-squared: 0.01656
F-statistic: 2.869 on 1 and 110 DF, p-value: 0.09315

Call:

```
lm(formula = O_I ~ DRM_number)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-234.00 -145.75 -25.00   83.71 1169.00

```

Coefficients:

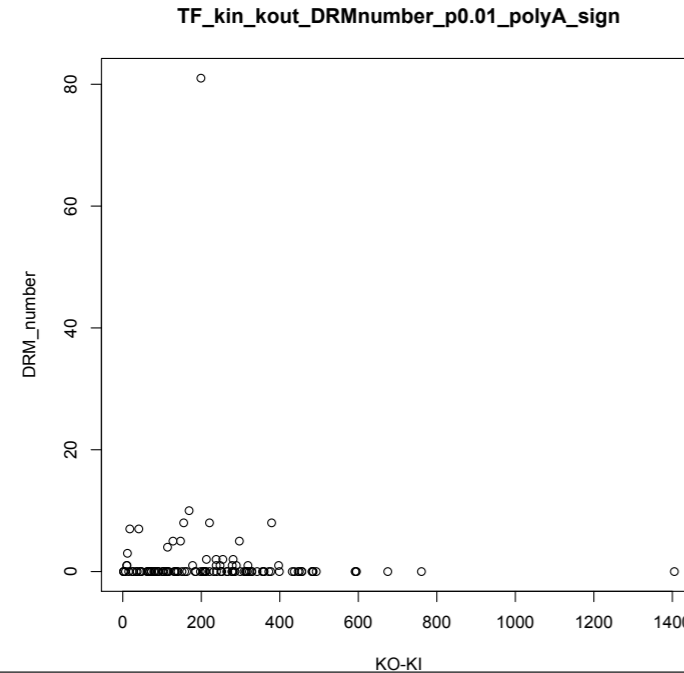
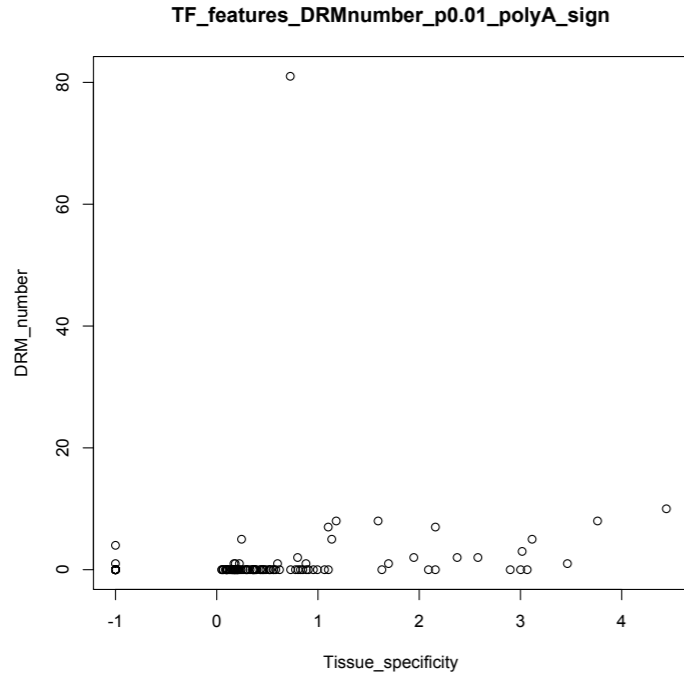
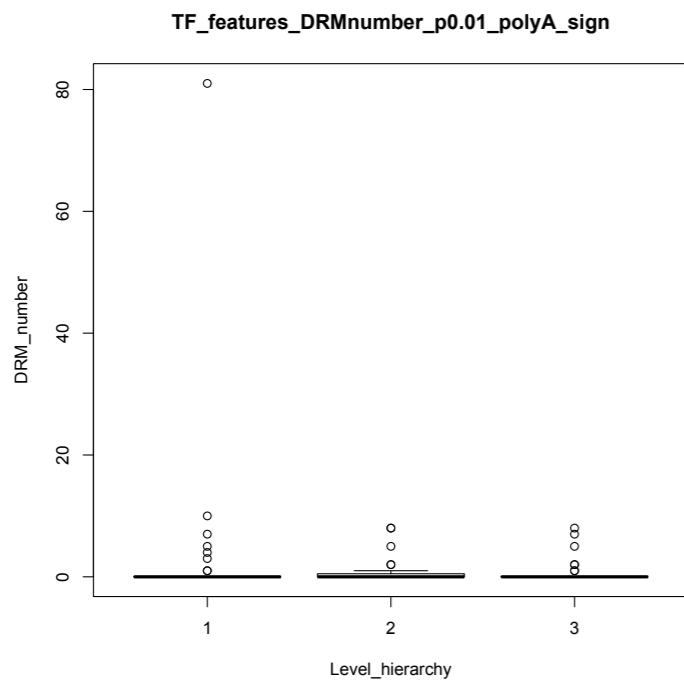
```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  236.003    18.307  12.891 <2e-16 ***
DRM_number   -1.286     2.348  -0.548  0.585
---

```

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

Residual standard error: 195.2 on 116 degrees of freedom
Multiple R-squared: 0.00258, Adjusted R-squared: -0.006019
F-statistic: 0.3 on 1 and 116 DF, p-value: 0.5849



Pairwise comparisons using Wilcoxon rank sum test

```
data: DRM_number and Level_hierarchy
```

1	2
2	0.98 -
3	0.72 0.72

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

```
data: DRM_number and Level_hierarchy
```

1	2
2	0.47 -
3	0.47 0.70

P value adjustment method: BH

Call:
lm(formula = Tissue_spec ~ DRM_number)

Residuals:

Min	1Q	Median	3Q	Max
-1.6119	-0.4011	-0.2152	0.2997	3.7120

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.53362	0.10357	5.152	1.14e-06 ***
DRM_number	0.01956	0.01303	1.501	0.136

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

Residual standard error: 1.077 on 110 degrees of freedom
Multiple R-squared: 0.02008, Adjusted R-squared: 0.01117
F-statistic: 2.254 on 1 and 110 DF, p-value: 0.1362

Call:
lm(formula = O_I ~ DRM_number)

Residuals:

Min	1Q	Median	3Q	Max
-233.70	-145.45	-24.70	83.90	1169.30

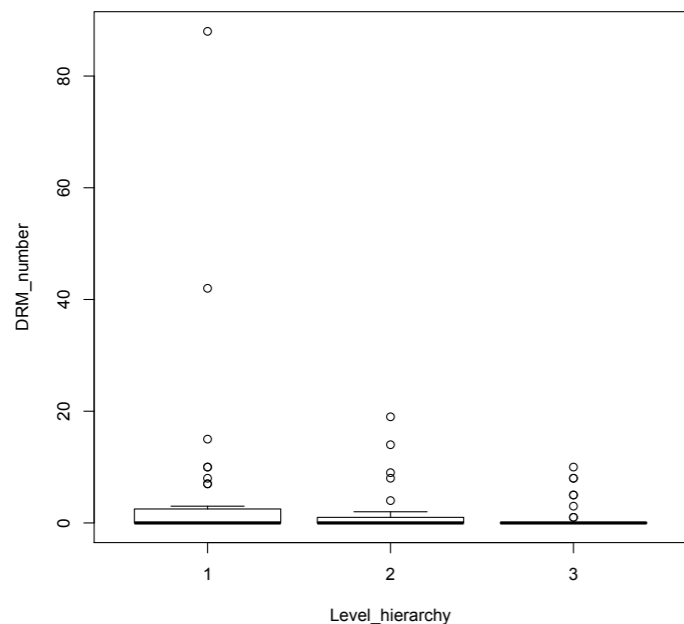
Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	235.703	18.286	12.890	<2e-16 ***
DRM_number	-1.136	2.361	-0.481	0.631

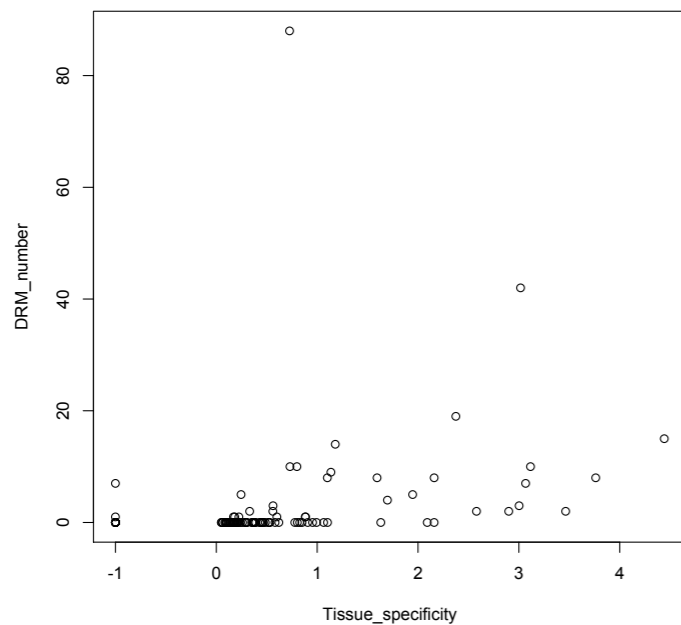
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 195.3 on 116 degrees of freedom
Multiple R-squared: 0.001992, Adjusted R-squared: -0.006611
F-statistic: 0.2316 on 1 and 116 DF, p-value: 0.6313

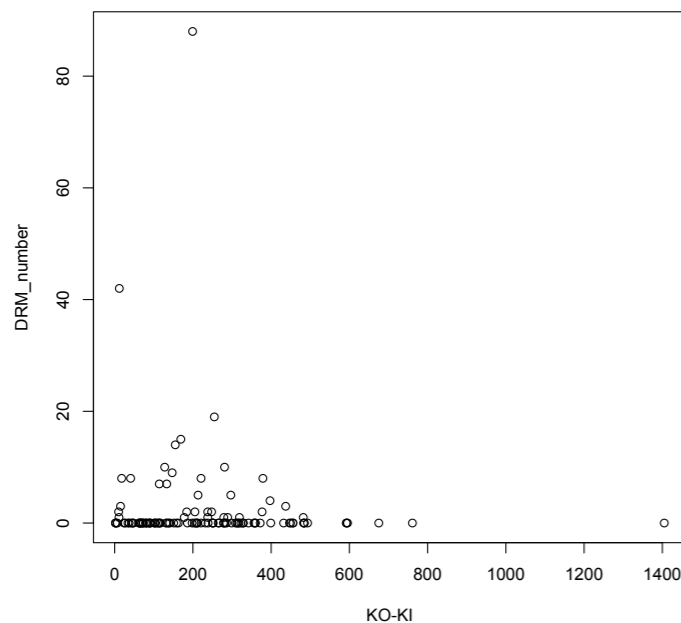
TF_features_DRMnumber_p0.05



TF_features_DRMnumber_p0.05



TF_kin_kout_DRMnumber_p0.05



Pairwise comparisons using Wilcoxon rank sum test

data: DRM_number and Level_hierarchy

```

1 2
2 0.65 -
3 0.31 0.31
    
```

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

data: DRM_number and Level_hierarchy

```

1 2
2 0.28 -
3 0.28 0.34
    
```

P value adjustment method: BH

Call:

```
lm(formula = Tissue_spec ~ DRM_number)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-2.6453 -0.3562 -0.1733  0.3353  3.4728
    
```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.47460    0.10199   4.653 9.16e-06 ***
DRM_number   0.03292    0.01023   3.219 0.00169 **
---

```

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

```

Residual standard error: 1.04 on 110 degrees of freedom
Multiple R-squared:  0.08608,    Adjusted R-squared:  0.07777
F-statistic: 10.36 on 1 and 110 DF,  p-value: 0.001692
    
```

Call:

```
lm(formula = O_I ~ DRM_number)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-236.54 -148.29  -27.54   83.91 1166.46
    
```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  238.536    18.541  12.865 <2e-16 ***
DRM_number   -1.799     1.917  -0.938  0.35
---

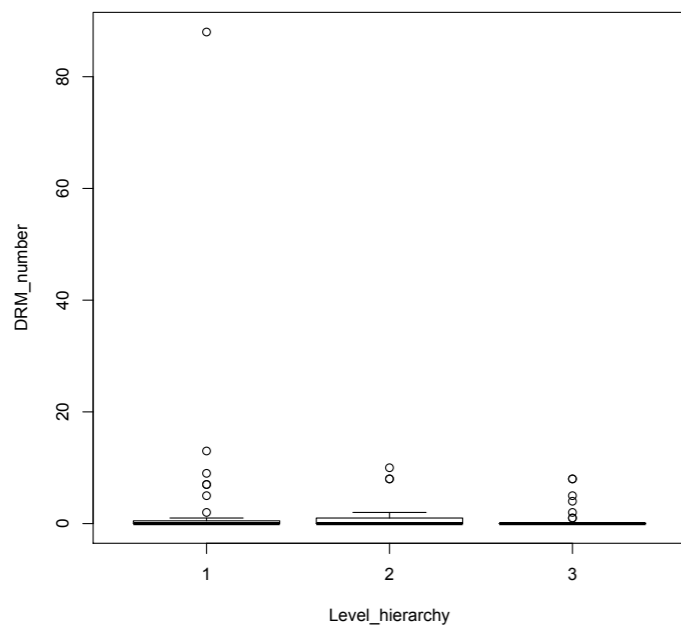
```

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

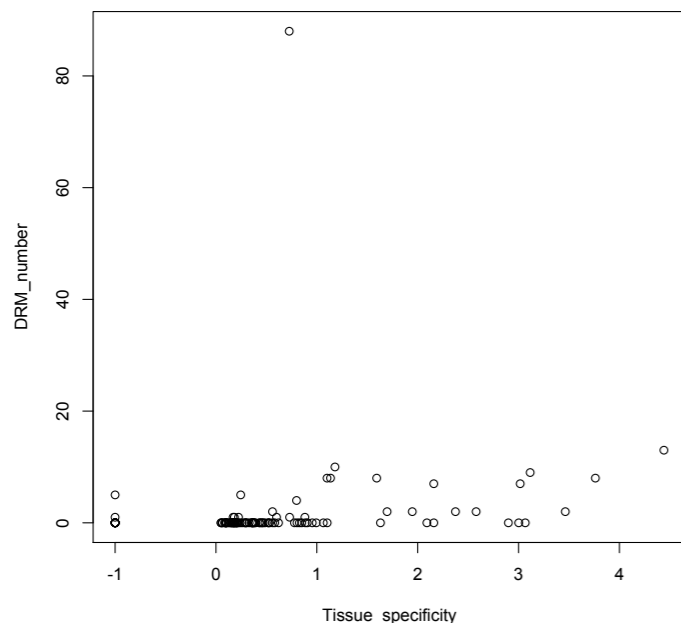
```

Residual standard error: 194.7 on 116 degrees of freedom
Multiple R-squared:  0.007534,    Adjusted R-squared: -0.001022
F-statistic: 0.8806 on 1 and 116 DF,  p-value: 0.35
    
```

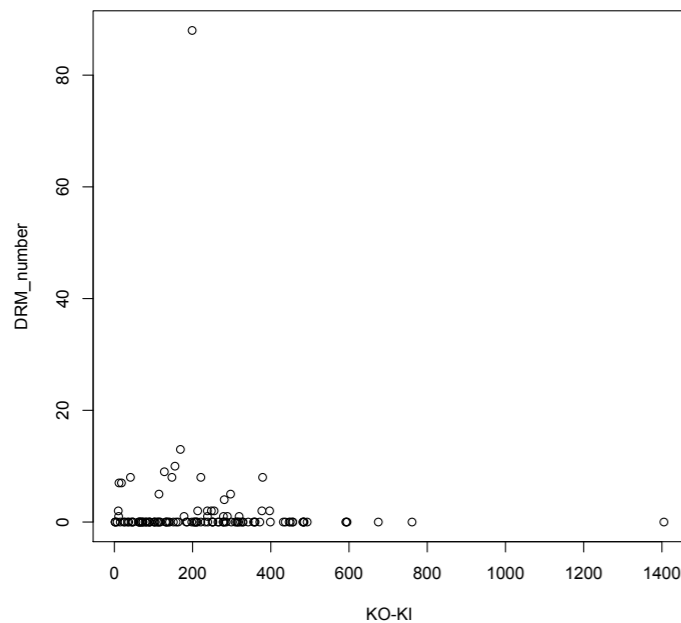
TF_features_DRMnumber_p0.05_polyA



TF_features_DRMnumber_p0.05_polyA



TF_kin_kout_DRMnumber_p0.05_polyA



Pairwise comparisons using Wilcoxon rank sum test

data: DRM_number and Level_hierarchy

```

1 2
2 1.00 -
3 0.46 0.46
    
```

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

data: DRM_number and Level_hierarchy

```

1 2
2 0.43 -
3 0.43 0.53
    
```

P value adjustment method: BH

Call:

```
lm(formula = Tissue_spec ~ DRM_number)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.6567	-0.3928	-0.2068	0.3081	3.6415

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.52528	0.10348	5.076	1.58e-06 ***
DRM_number	0.02111	0.01185	1.782	0.0775 .

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

Residual standard error: 1.072 on 110 degrees of freedom

Multiple R-squared: 0.02806, Adjusted R-squared: 0.01923

F-statistic: 3.176 on 1 and 110 DF, p-value: 0.07749

Call:

```
lm(formula = O_I ~ DRM_number)
```

Residuals:

Min	1Q	Median	3Q	Max
-234.13	-145.88	-25.13	83.52	1168.87

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	236.134	18.335	12.879	<2e-16 ***
DRM_number	-1.209	2.154	-0.561	0.576

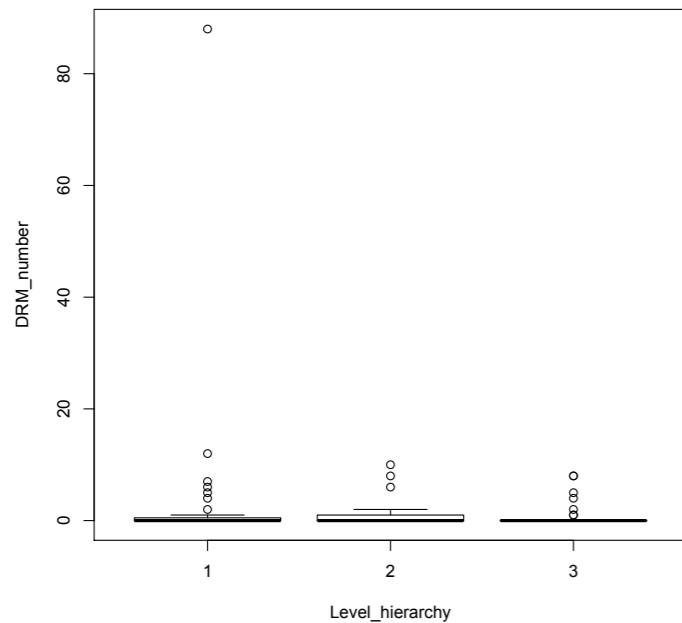
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 195.2 on 116 degrees of freedom

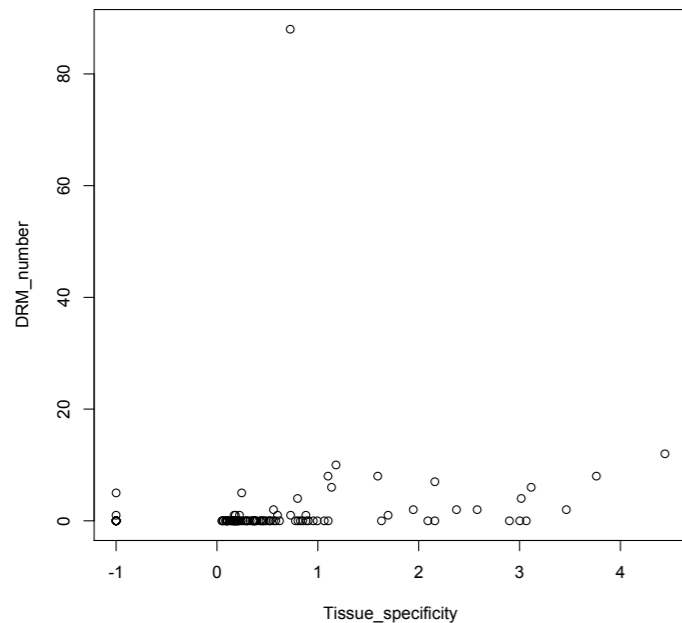
Multiple R-squared: 0.002707, Adjusted R-squared: -0.00589

F-statistic: 0.3149 on 1 and 116 DF, p-value: 0.5758

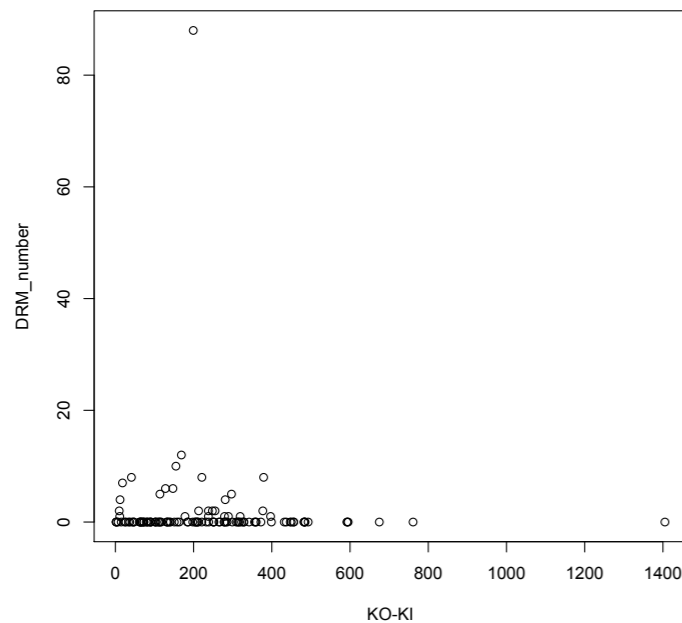
TF_features_DRMnumber_p0.05_polyA_sign



TF_features_DRMnumber_p0.05_polyA_sign



TF_kin_kout_DRMnumber_p0.05_polyA_sign



Pairwise comparisons using Wilcoxon rank sum test

data: DRM_number and Level_hierarchy

```
1 2
2 1.0 -
3 0.5 0.5
```

P value adjustment method: BH

Pairwise comparisons using t tests with non-pooled SD

data: DRM_number and Level_hierarchy

```
1 2
2 0.46 -
3 0.46 0.63
```

P value adjustment method: BH

Call:

```
lm(formula = Tissue_spec ~ DRM_number)
```

Residuals:

```
Min      1Q  Median      3Q      Max
-1.6249 -0.3986 -0.2127  0.3022  3.6850
```

Coefficients:

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.53114    0.10362   5.126 1.28e-06 ***
DRM_number   0.01875    0.01196   1.568  0.120
```

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

Residual standard error: 1.076 on 110 degrees of freedom

Multiple R-squared: 0.02188, Adjusted R-squared: 0.01298

F-statistic: 2.46 on 1 and 110 DF, p-value: 0.1196

Call:

```
lm(formula = O_I ~ DRM_number)
```

Residuals:

```
Min      1Q  Median      3Q      Max
-233.84 -145.59 -24.84   83.73 1169.16
```

Coefficients:

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  235.845    18.308  12.882 <2e-16 ***
DRM_number   -1.093     2.168  -0.504  0.615
```

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

Residual standard error: 195.2 on 116 degrees of freedom

Multiple R-squared: 0.002186, Adjusted R-squared: -0.006416

F-statistic: 0.2541 on 1 and 116 DF, p-value: 0.6151