# 1) Drought response heatmap

**Drought Response Across Genotypes**

Standardized differences between drought and watered treatments



Significance: *** p ≤ 0.001, ** p ≤ 0.01, * p ≤ 0.05
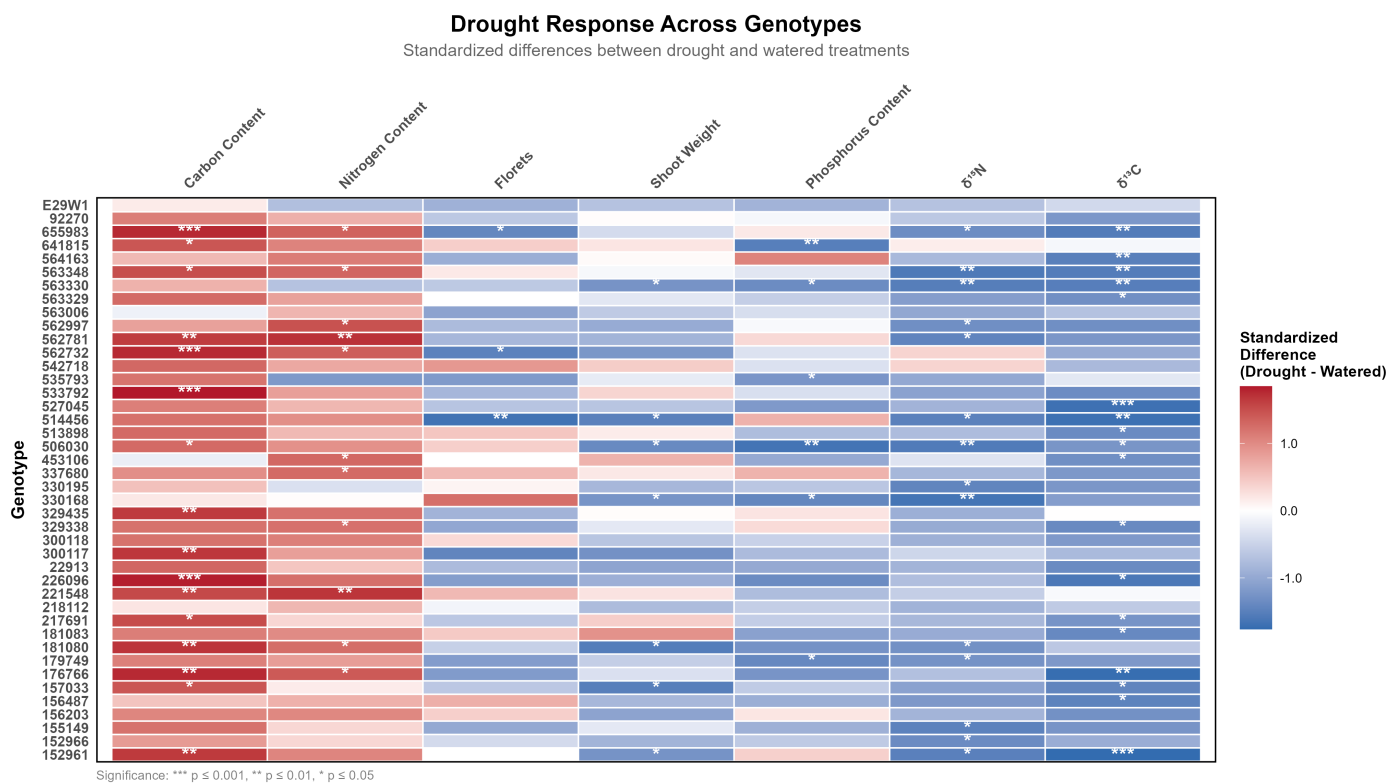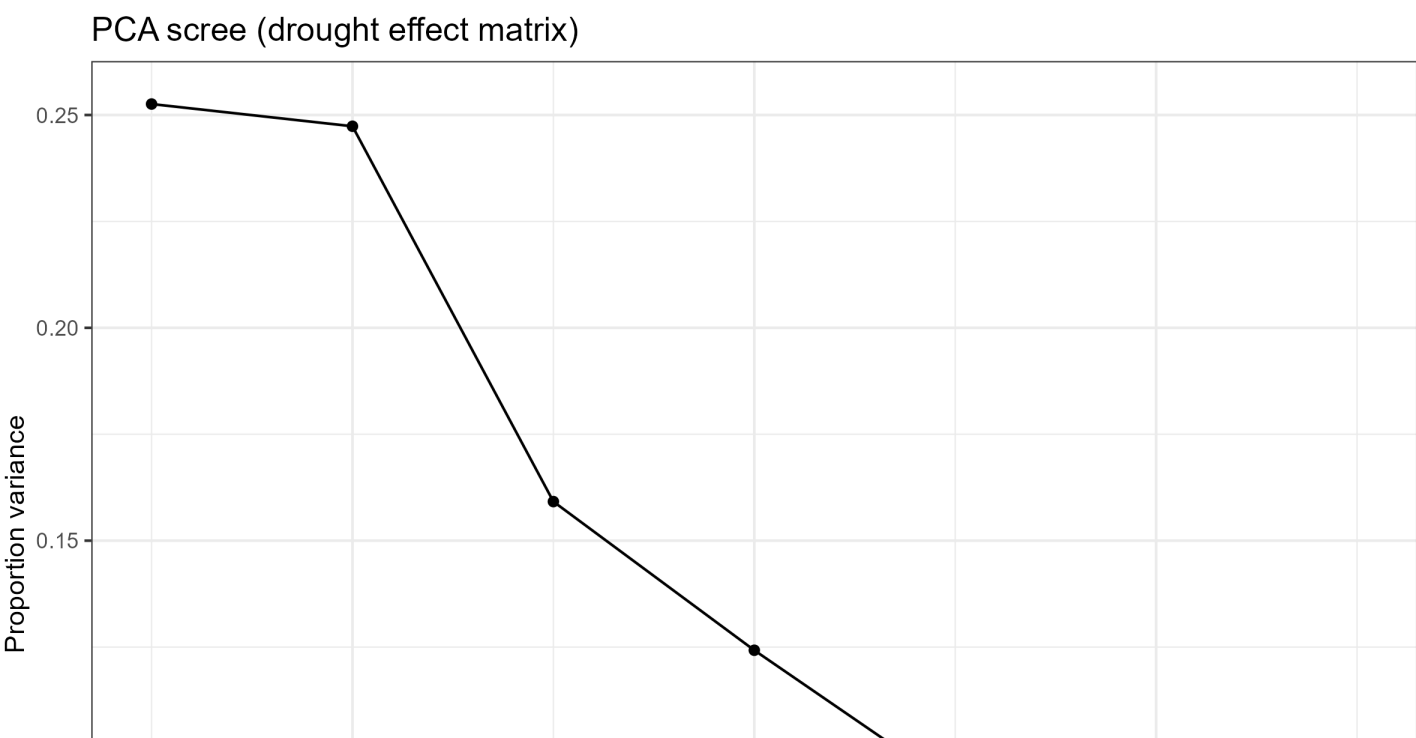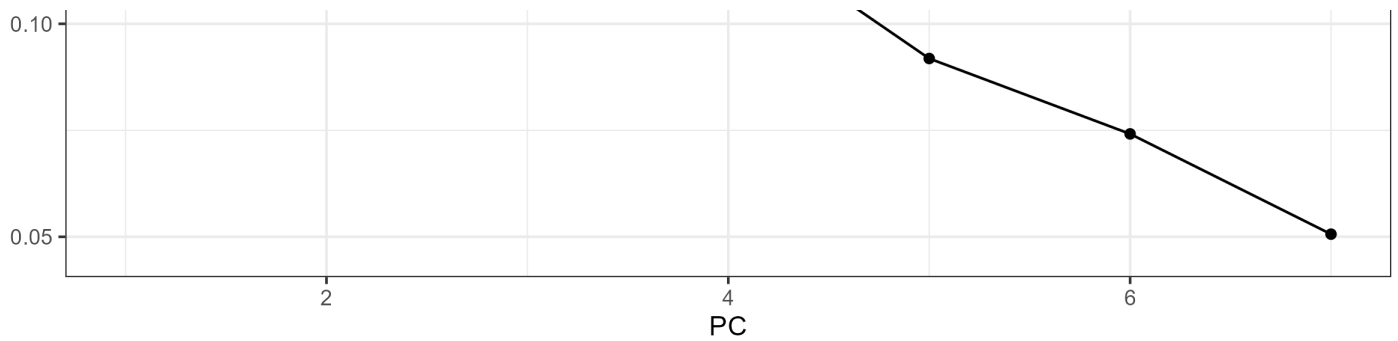
Interpretation: This heatmap shows standardized differences (Drought - Watered) per genotype and trait; red = increase, blue = decrease. Stars mark nominal t-test significance.
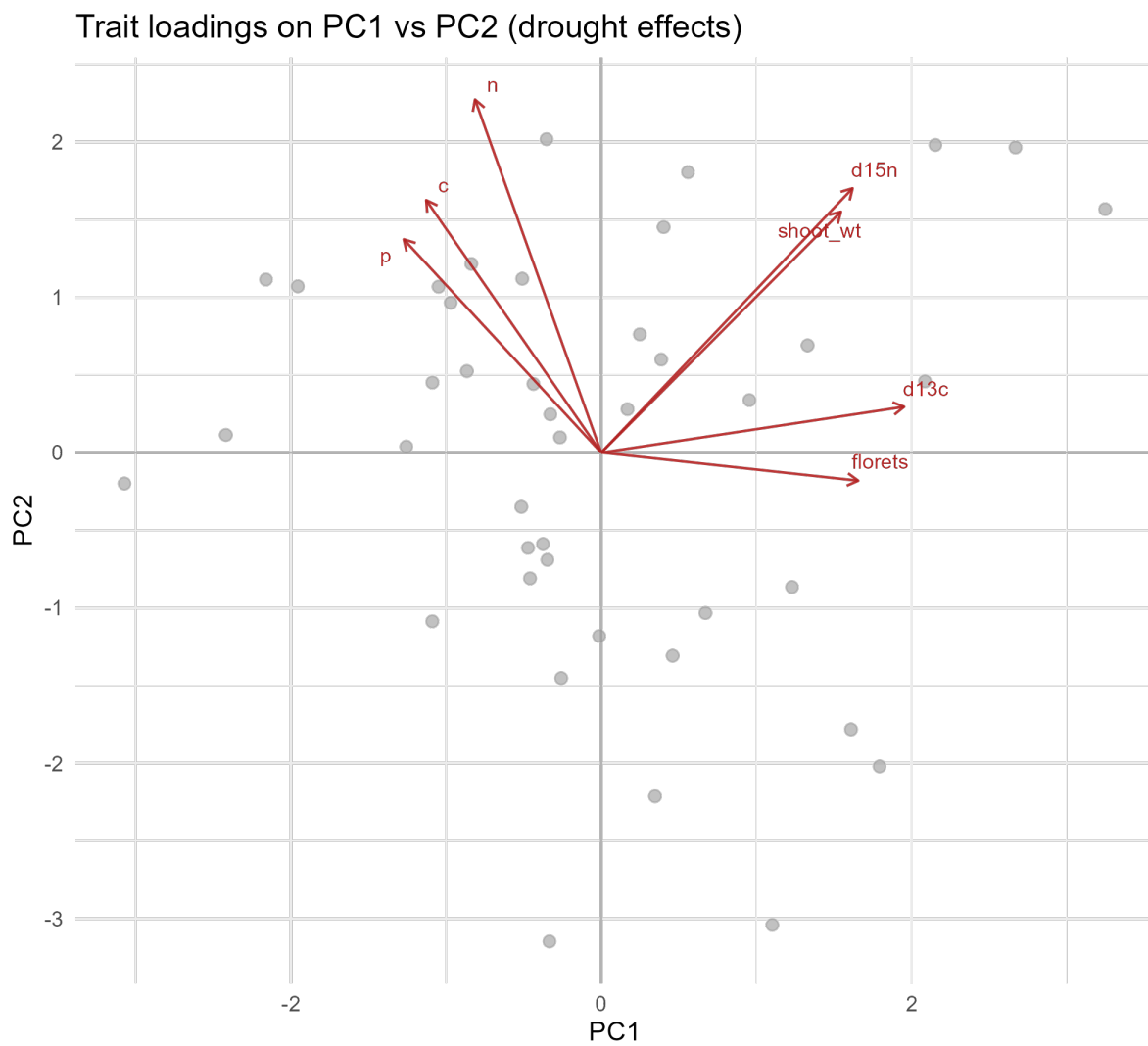
# 2) PCA scree plot

Interpretation: The scree plot shows variance explained by each PC; PC1/PC2 often capture the major response syndromes.

# 3) PCA trait loadings (biplot)



Trait loadings on PC1 vs PC2 (drought effects)

Interpretation: Arrows indicate trait contributions to PC axes; similar directions = correlated drought responses.

# 4) PCA trait loadings colored by sensitivity
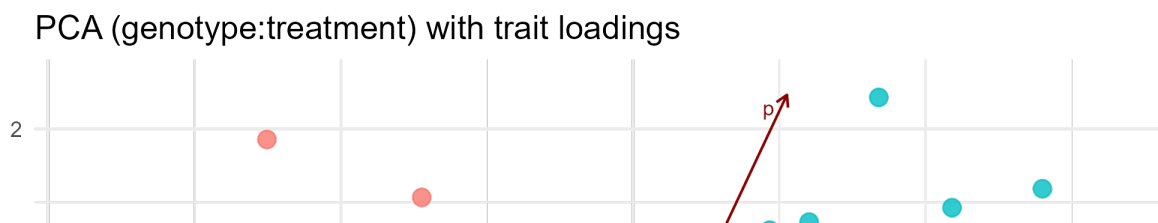


Trait loadings on PC1 vs PC2 (drought effects)
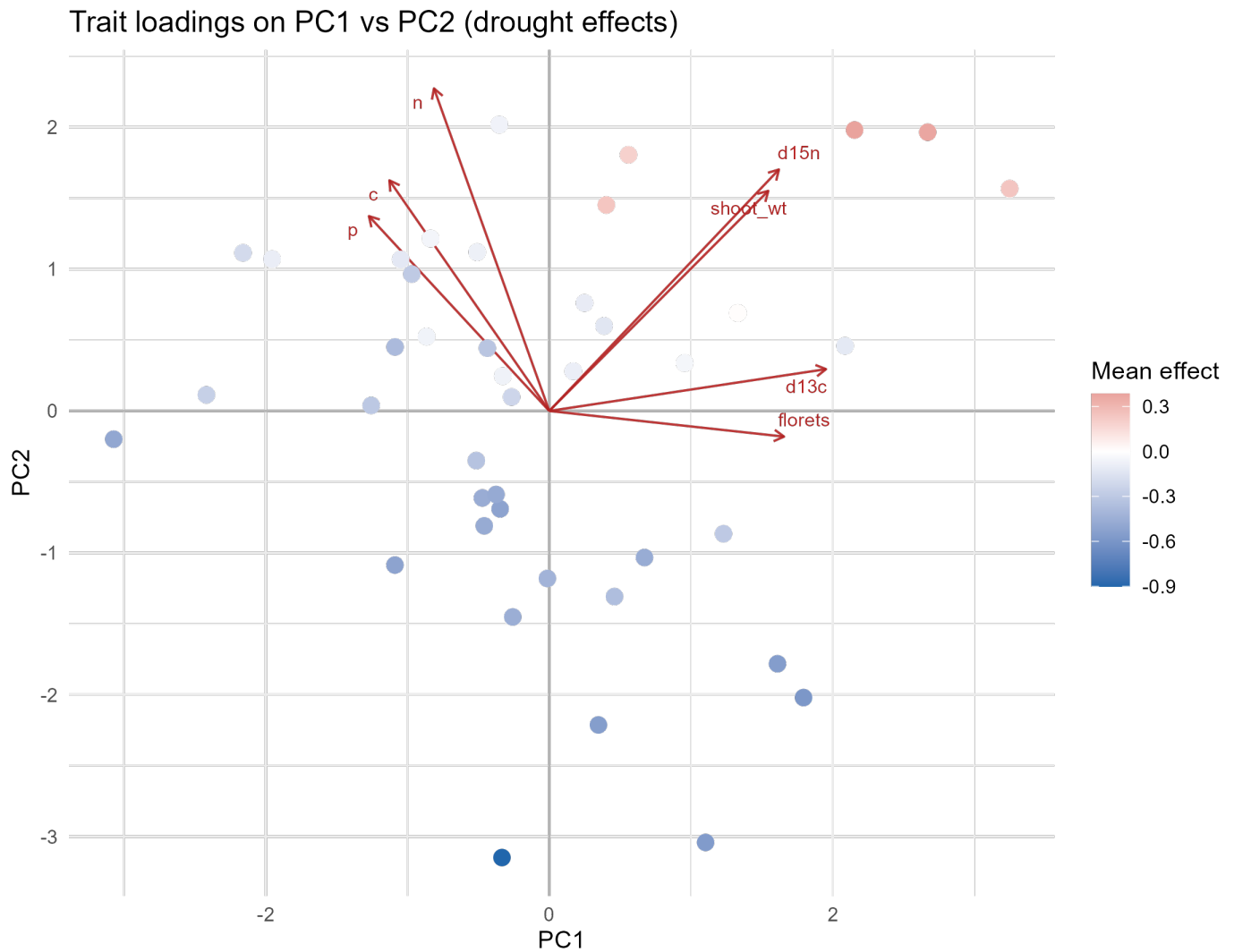
Interpretation: Genotypes colored by mean effect (sensitivity) to highlight clusters.

# 5) PCA genotype:treatment by treatment

Interpretation: Shows separation (or overlap) between drought and watered states across genotypes.

# 6) PCA genotype:treatment biplot



PCA (genotype:treatment) with trait loadings

Interpretation: Overlays trait loadings on genotype:treatment points to identify drivers of separation.

# 7) PCA vs Shoot weight effect

PC1 vs shoot_wt effect

-2                    0                    2
                      PC1

Interpretation: Relationship between PC1 and genotype-level shoot weight effect; regression summary included below.

# 8) PCA vs Florets effect

PC1 vs florets effect
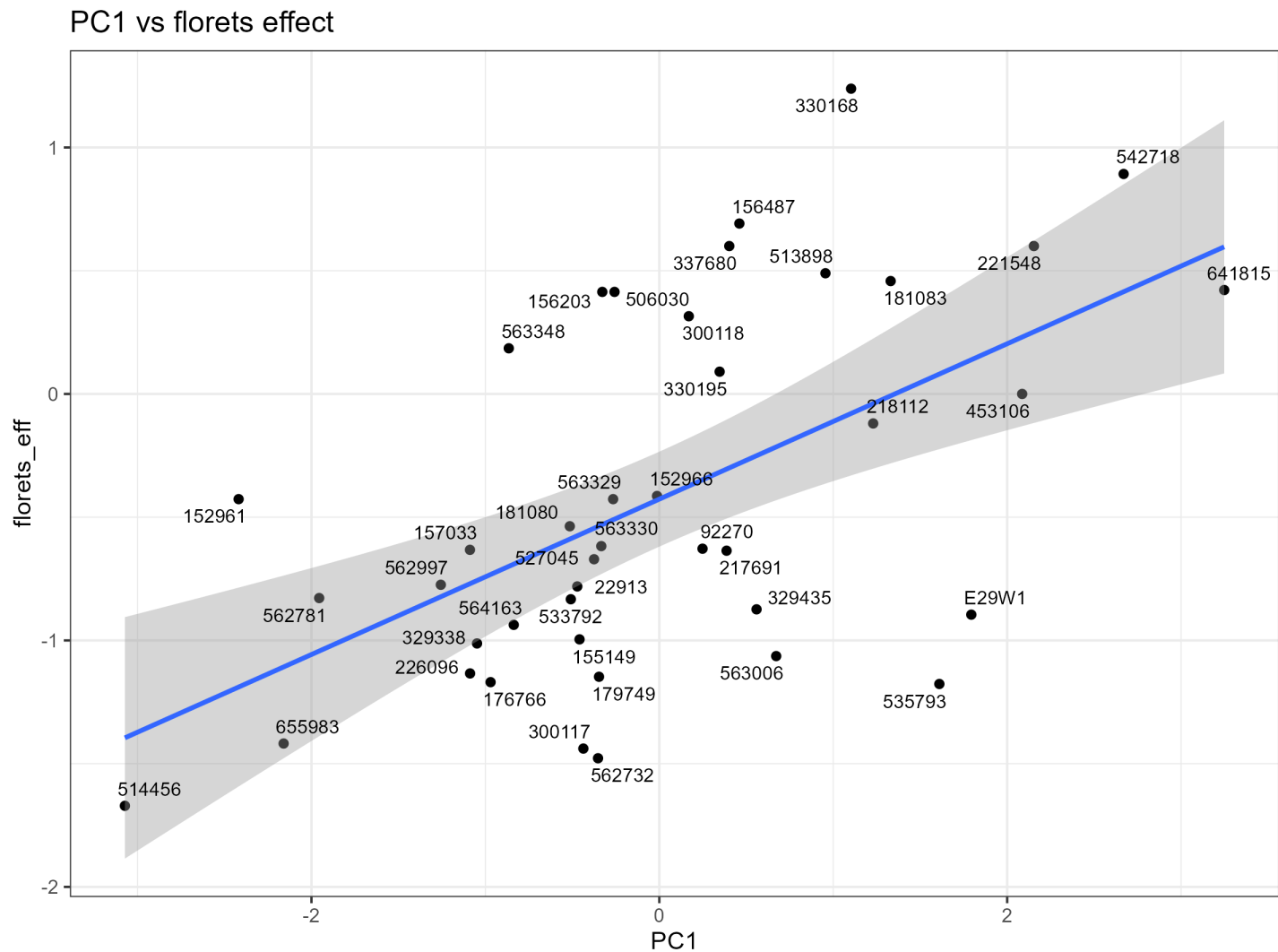


Interpretation: Relationship between PC1 and floret effect; regression summary included below.

# Numeric summaries (auto-inserted)

- Number of significant genotype x trait t-tests (p < 0.05): **75**

# Top 10 absolute effects (genotype, variable, effect)

```
# A tibble: 10 × 3
   genotype variable effect
   <chr>    <chr>     <dbl>
 1 533792   c          1.85
 2 226096   c          1.82
 3 655983   c          1.77
 4 176766   c          1.76
 5 562732   c          1.76
 6 152961   d13c      -1.76
 7 176766   d13c      -1.74
 8 562781   n          1.72
 9 514456   d13c      -1.70
10 527045   d13c      -1.70
```

## PCA variance explained (first 6 PCs)

```
  PC VarPct CumPct
1  1   25.3   25.3
2  2   24.7   50.0
3  3   15.9   65.9
4  4   12.4   78.3
5  5    9.2   87.5
6  6    7.4   94.9
```

## Shoot weight model: shoot_wt_eff ~ PC1 + PC2

```
Call:
lm(formula = shoot_wt_eff ~ PC1 + PC2, data = scores_perf)


Residuals:
    Min      1Q  Median      3Q     Max
-1.1399 -0.2591 -0.0560  0.2860  0.9344


Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.51567    0.06912  -7.460 5.04e-09 ***
PC1          0.26016    0.05261   4.945 1.49e-05 ***
PC2          0.26120    0.05317   4.913 1.65e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Residual standard error: 0.448 on 39 degrees of freedom
Multiple R-squared:  0.5547,        Adjusted R-squared:  0.5319
F-statistic: 24.29 on 2 and 39 DF,  p-value: 1.406e-07
```

# Florets model: florets_eff ~ PC1 + PC2

```
Call:
lm(formula = florets_eff ~ PC1 + PC2, data = scores_perf)


Residuals:
    Min      1Q  Median      3Q     Max
-1.3187 -0.3035 -0.1335  0.4711  1.2130


Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.42678    0.09622  -4.436 7.29e-05 ***
PC1          0.31519    0.07324   4.304 0.000109 ***
PC2         -0.03443    0.07401  -0.465 0.644363
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Residual standard error: 0.6236 on 39 degrees of freedom
Multiple R-squared:  0.3245,         Adjusted R-squared:  0.2899
F-statistic: 9.369 on 2 and 39 DF,  p-value: 0.0004757
```