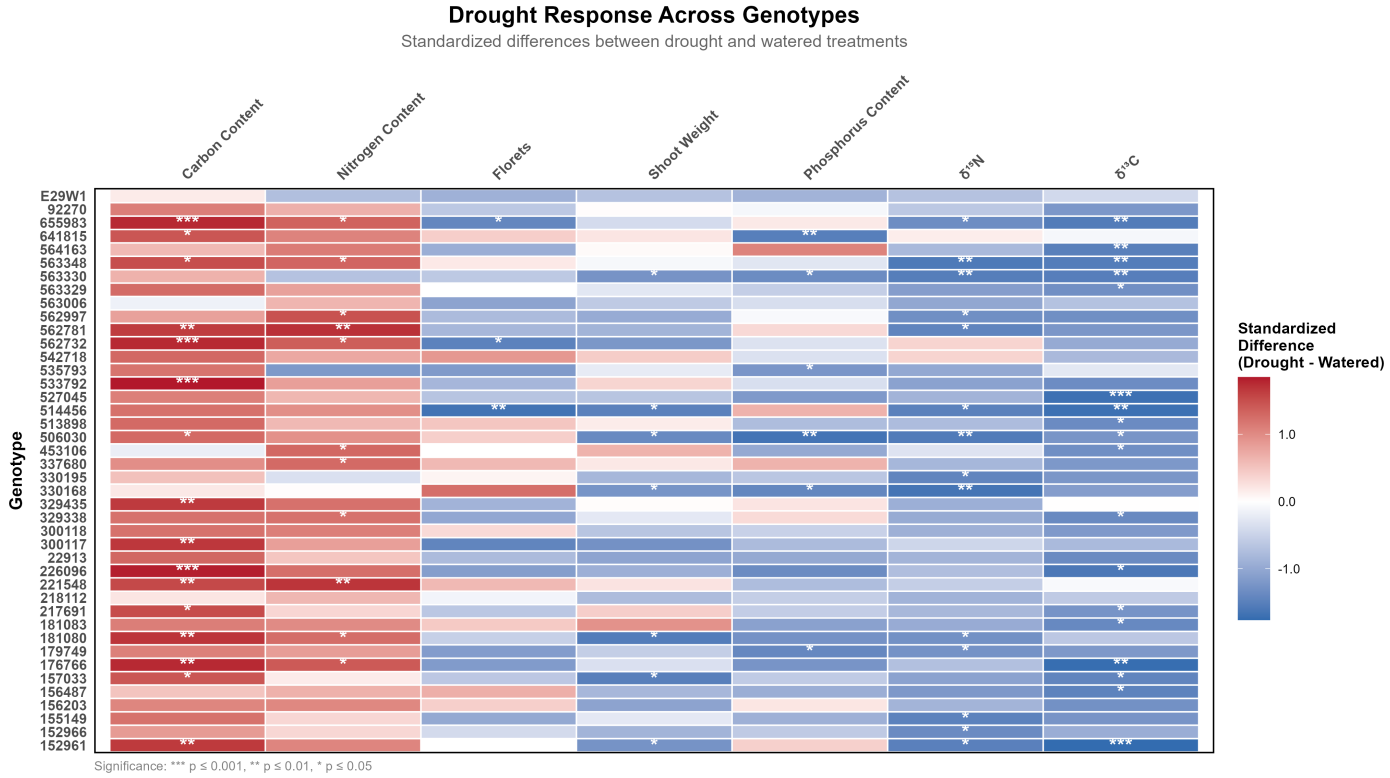
MAC-2022-Drought: Figures and numeric summaries

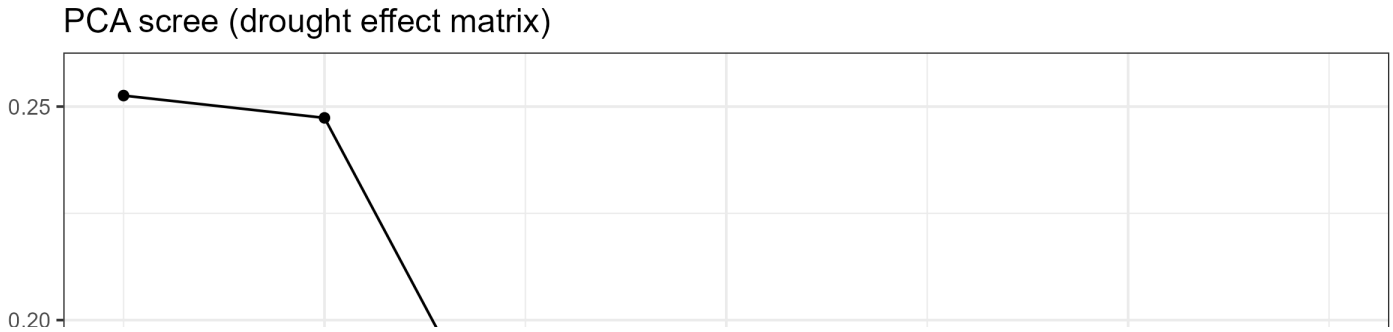
Generated: 2025-08-15

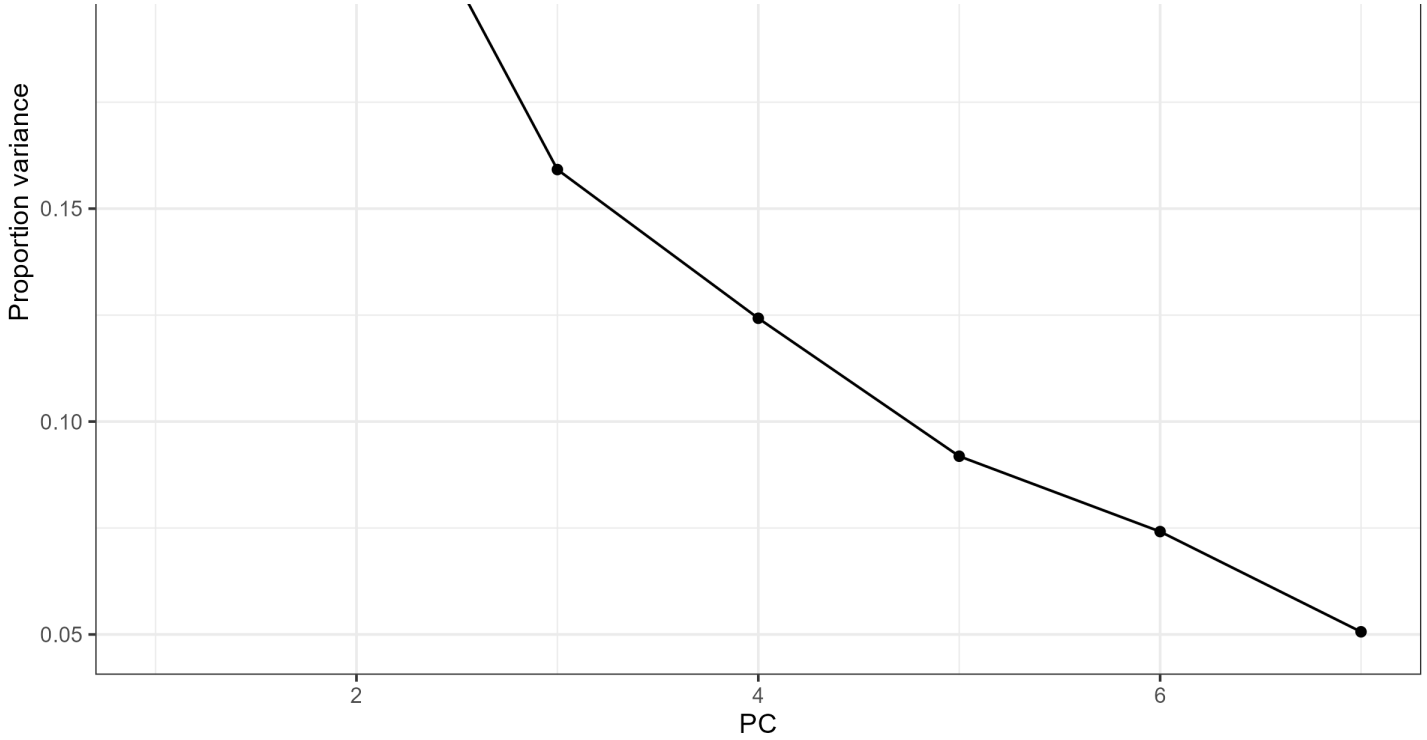
Figures

1) Drought response heatmap

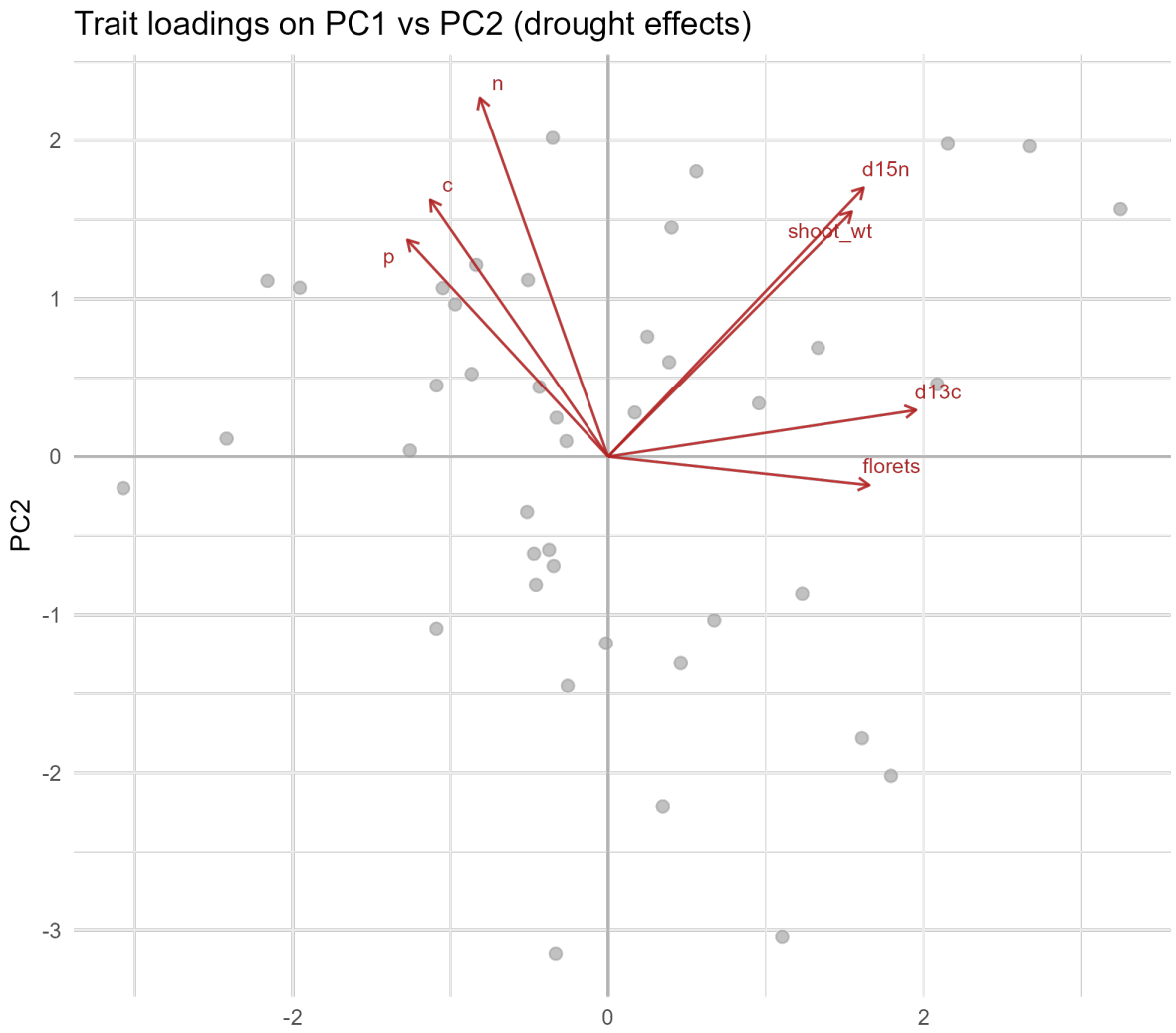


2) PCA scree plot



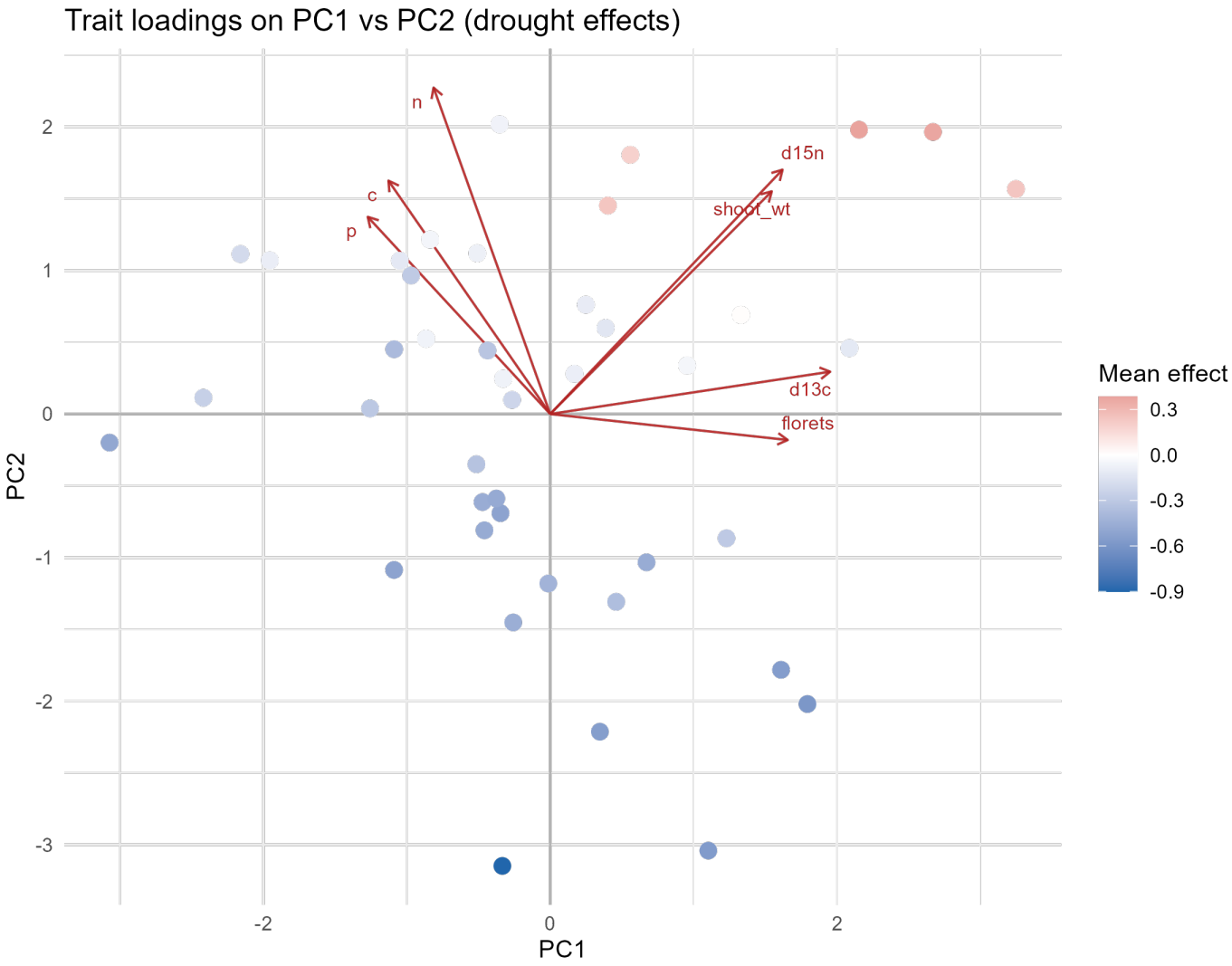


3) PCA trait loadings (biplot)



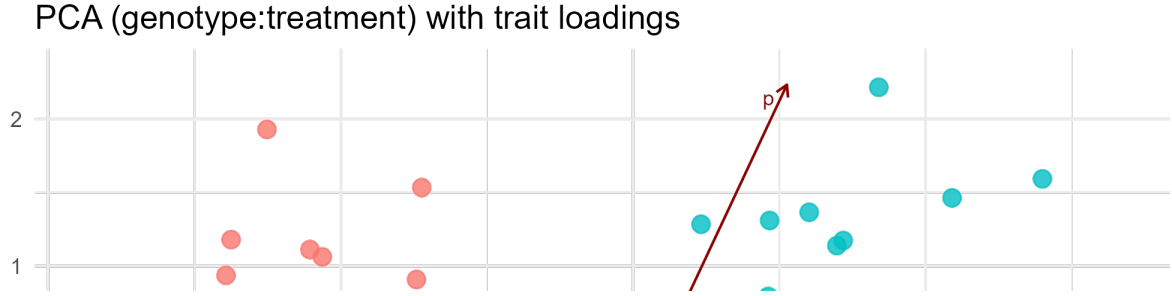
PC1

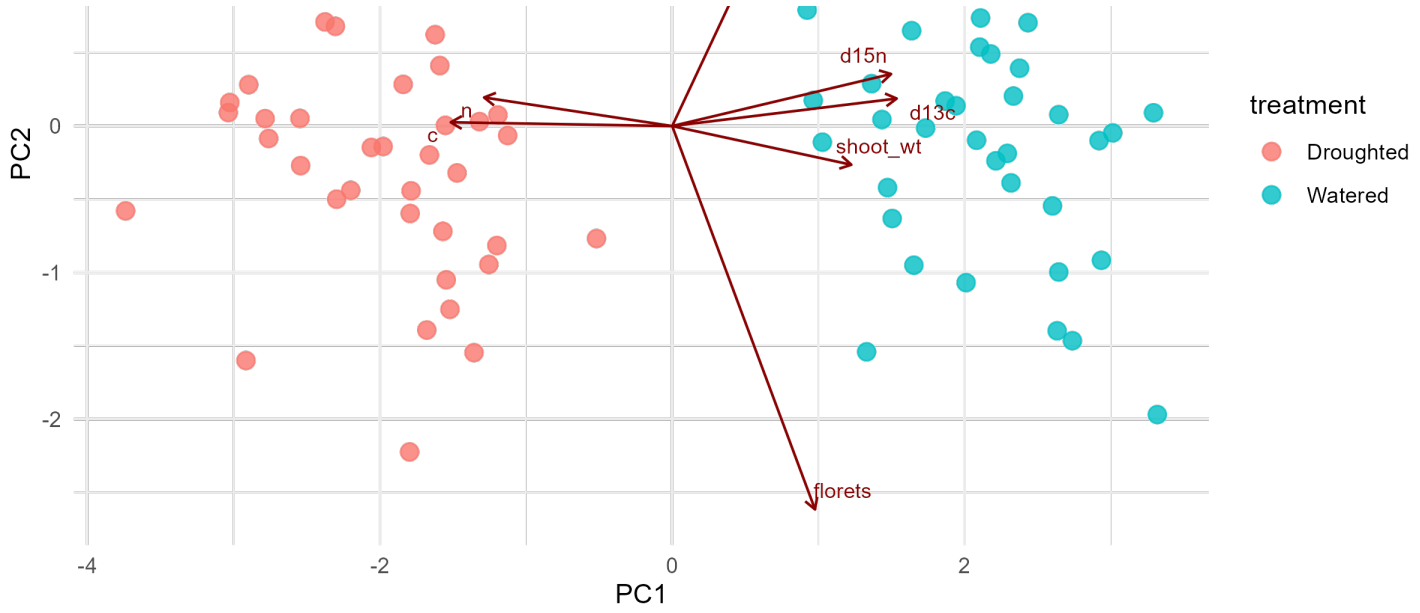
4) PCA trait loadings colored by sensitivity



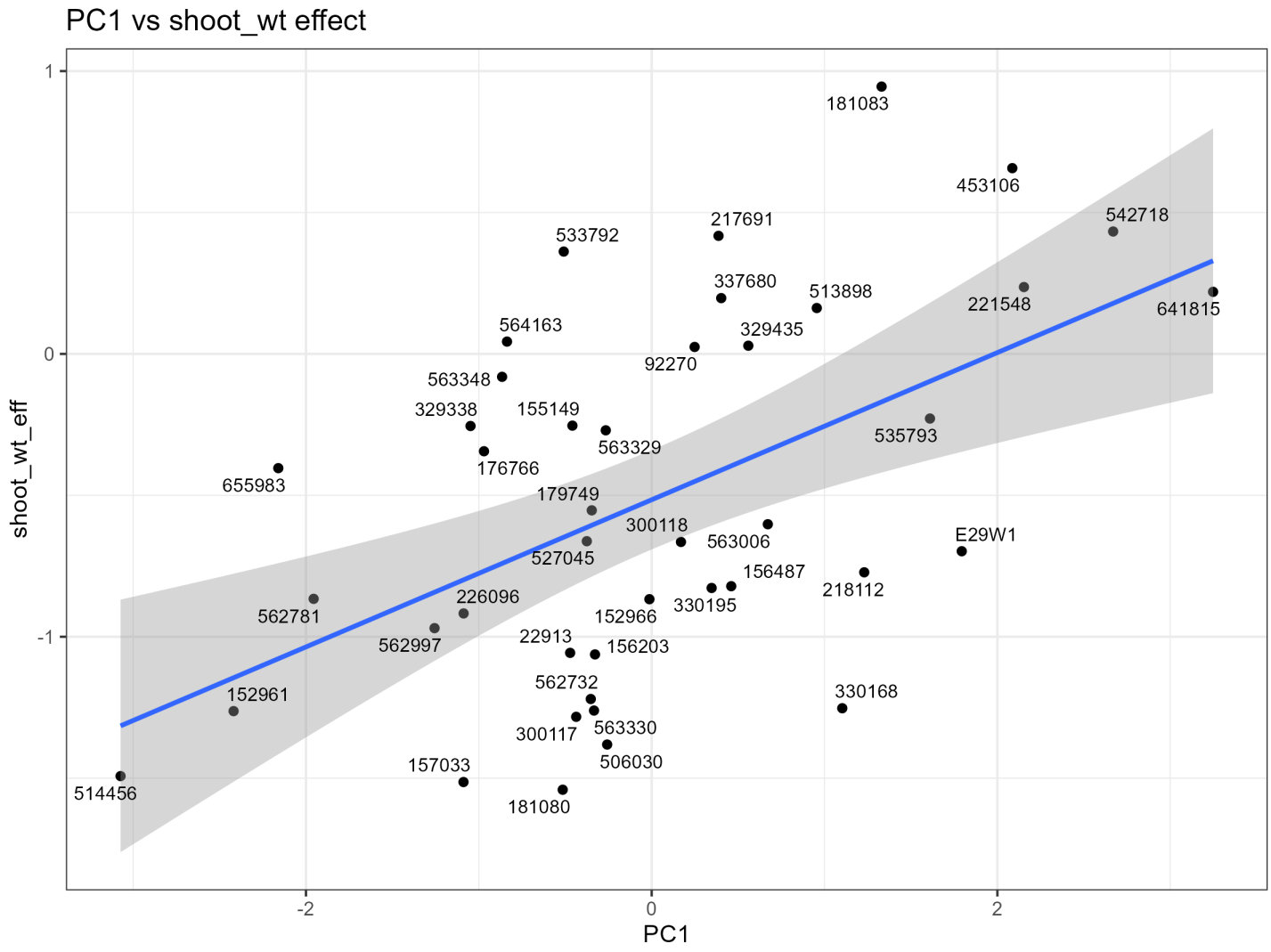
5) PCA genotype:treatment by treatment

6) PCA genotype:treatment biplot

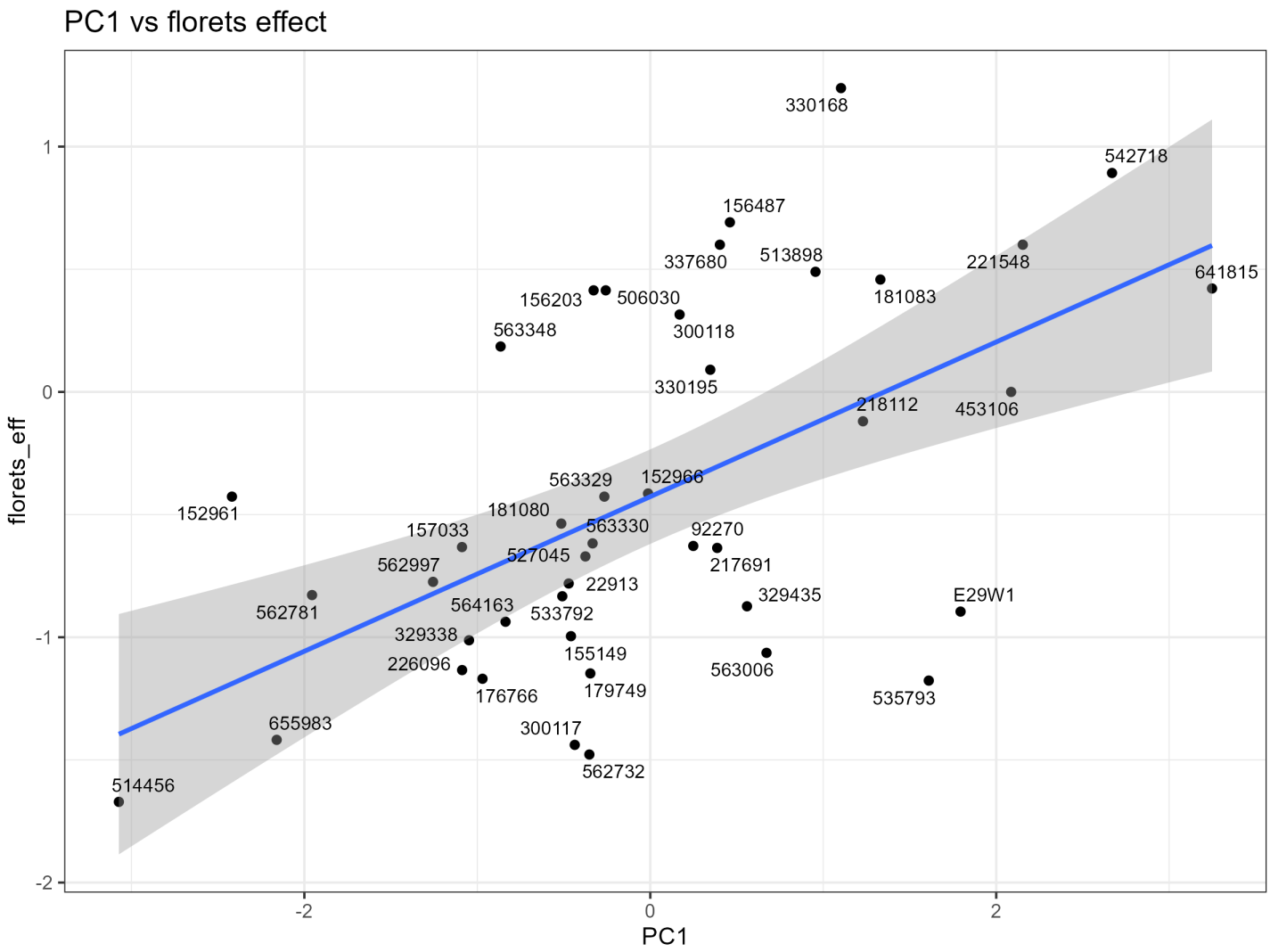




7) PCA vs Shoot weight effect



8) PCA vs Florets effect



Numeric summaries

- 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
```

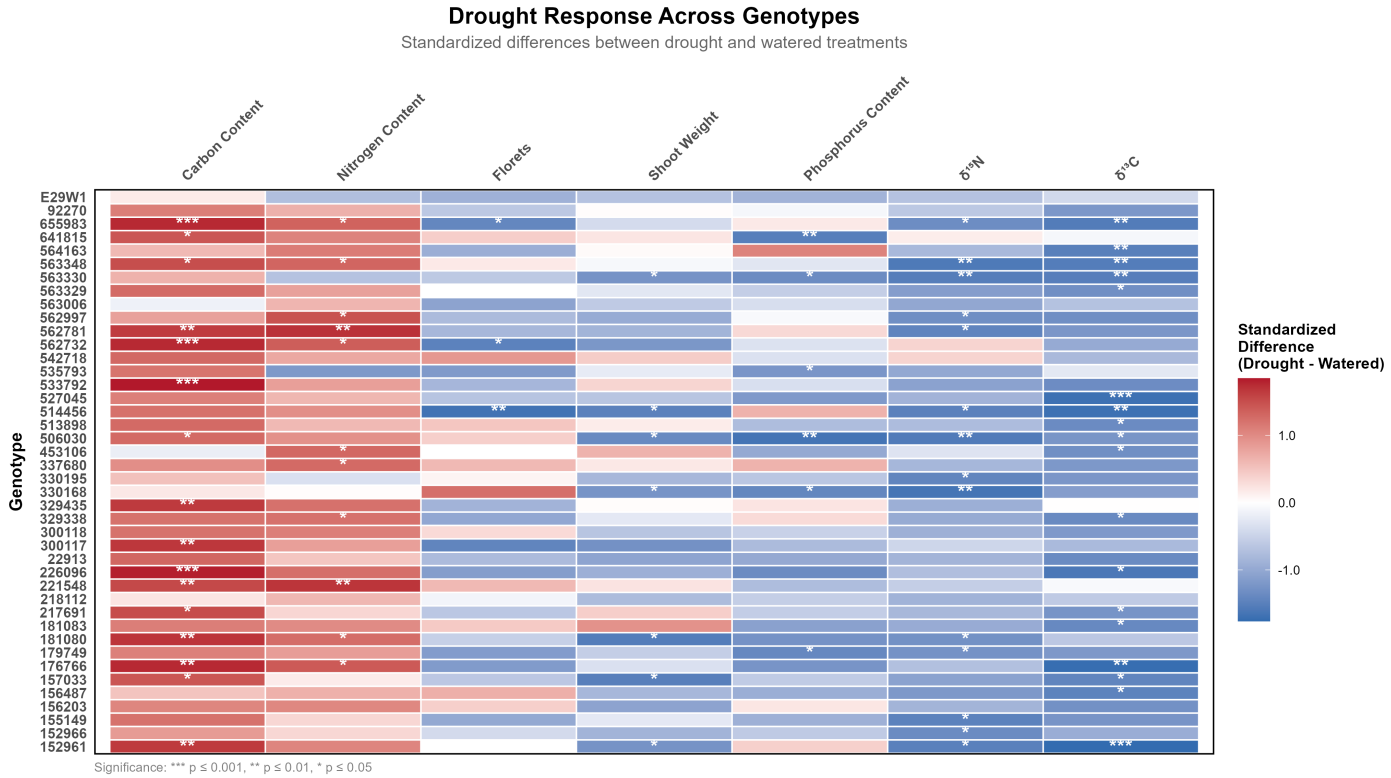
```
Coefficients:

            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
```

Auto-generated: Figures and numeric summaries

Generated: 2025-08-15

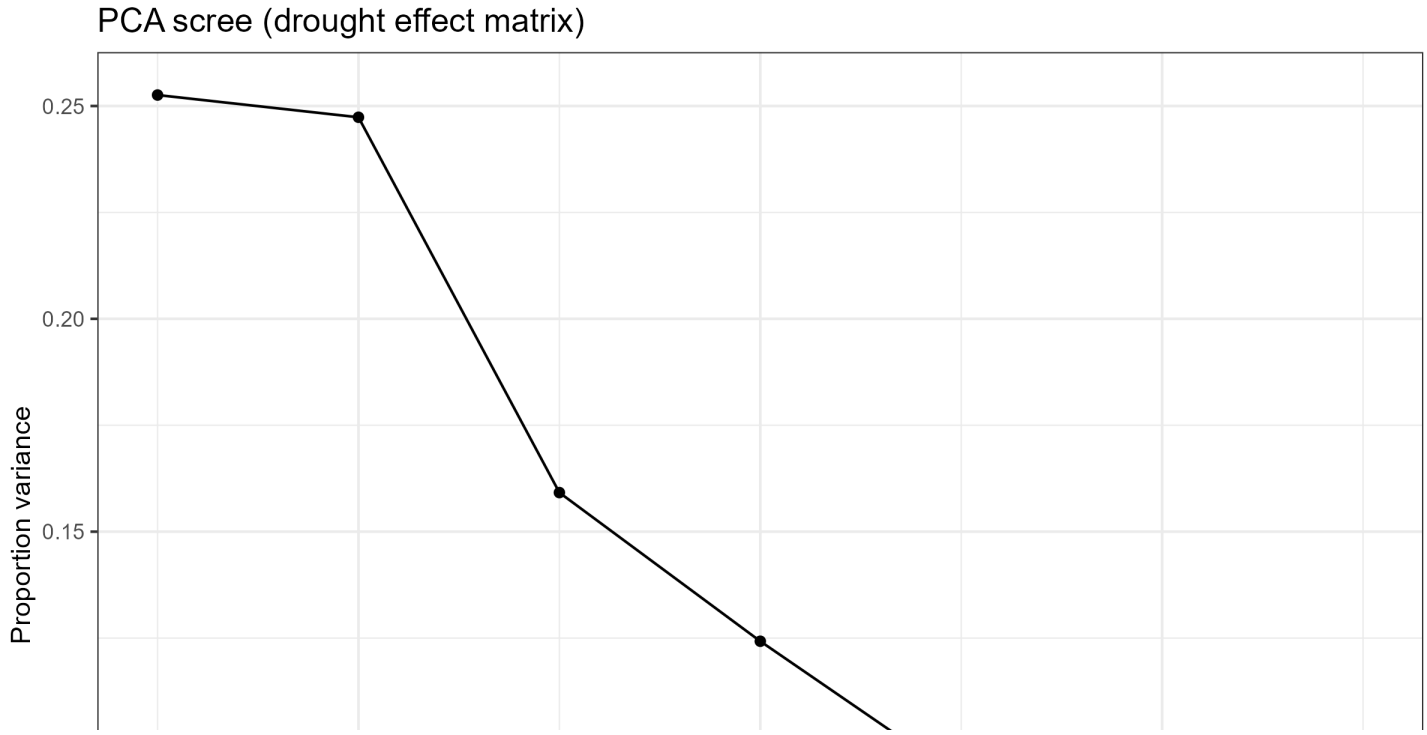
Figures (auto-inserted)

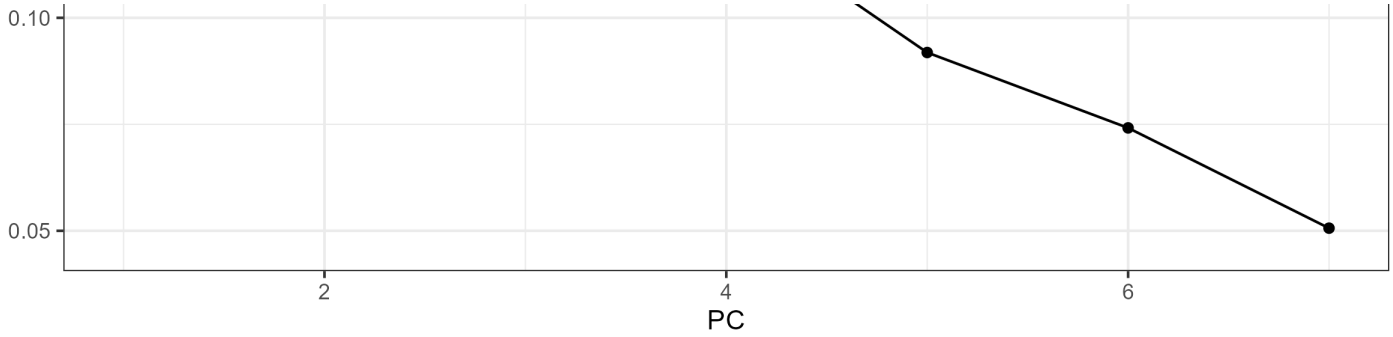
1) Drought response heatmap



Interpretation: This heatmap shows standardized differences (Drought - Watered) per genotype and trait; red = increase, blue = decrease. Stars mark nominal t-test significance.

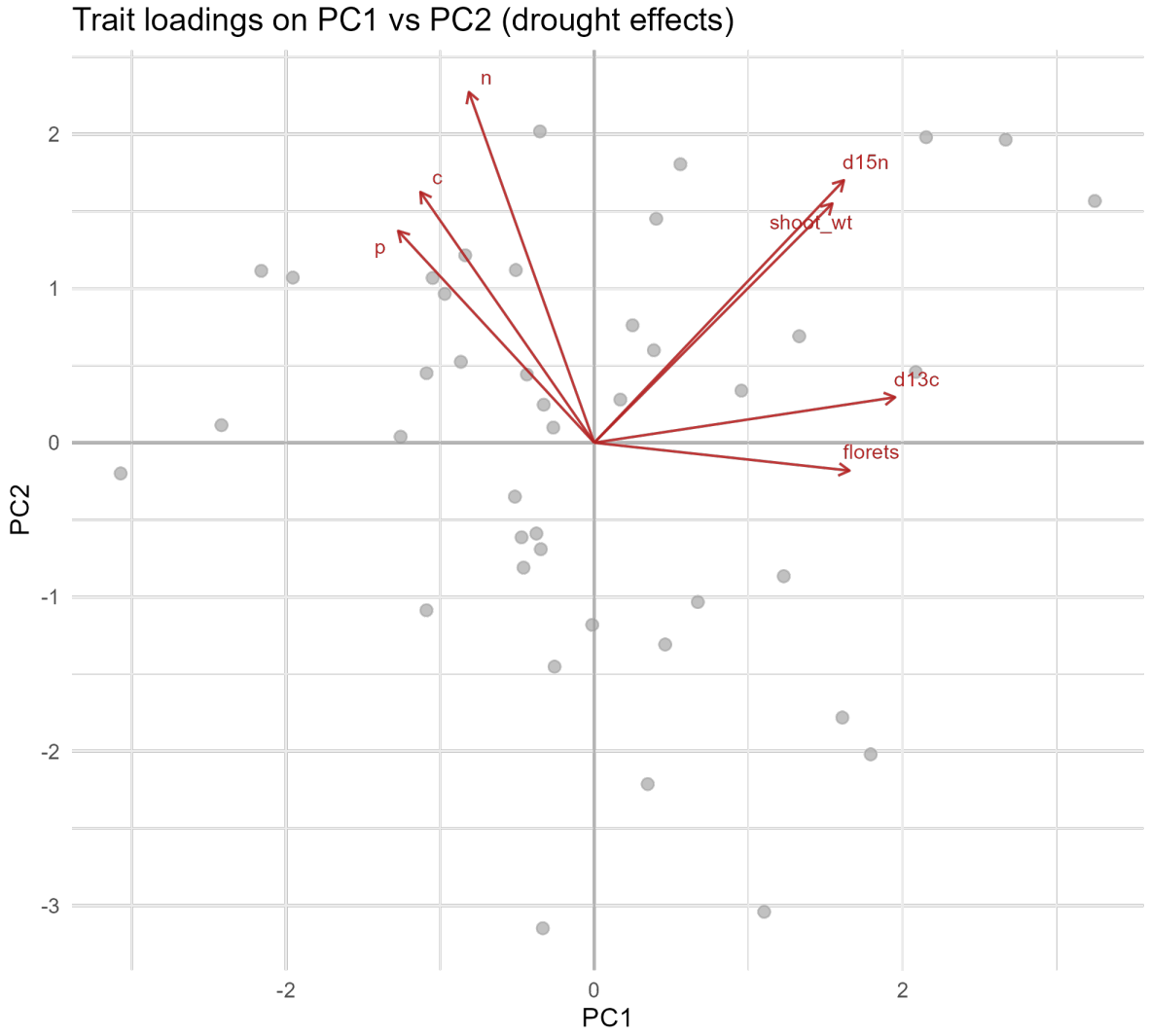
2) PCA scree plot





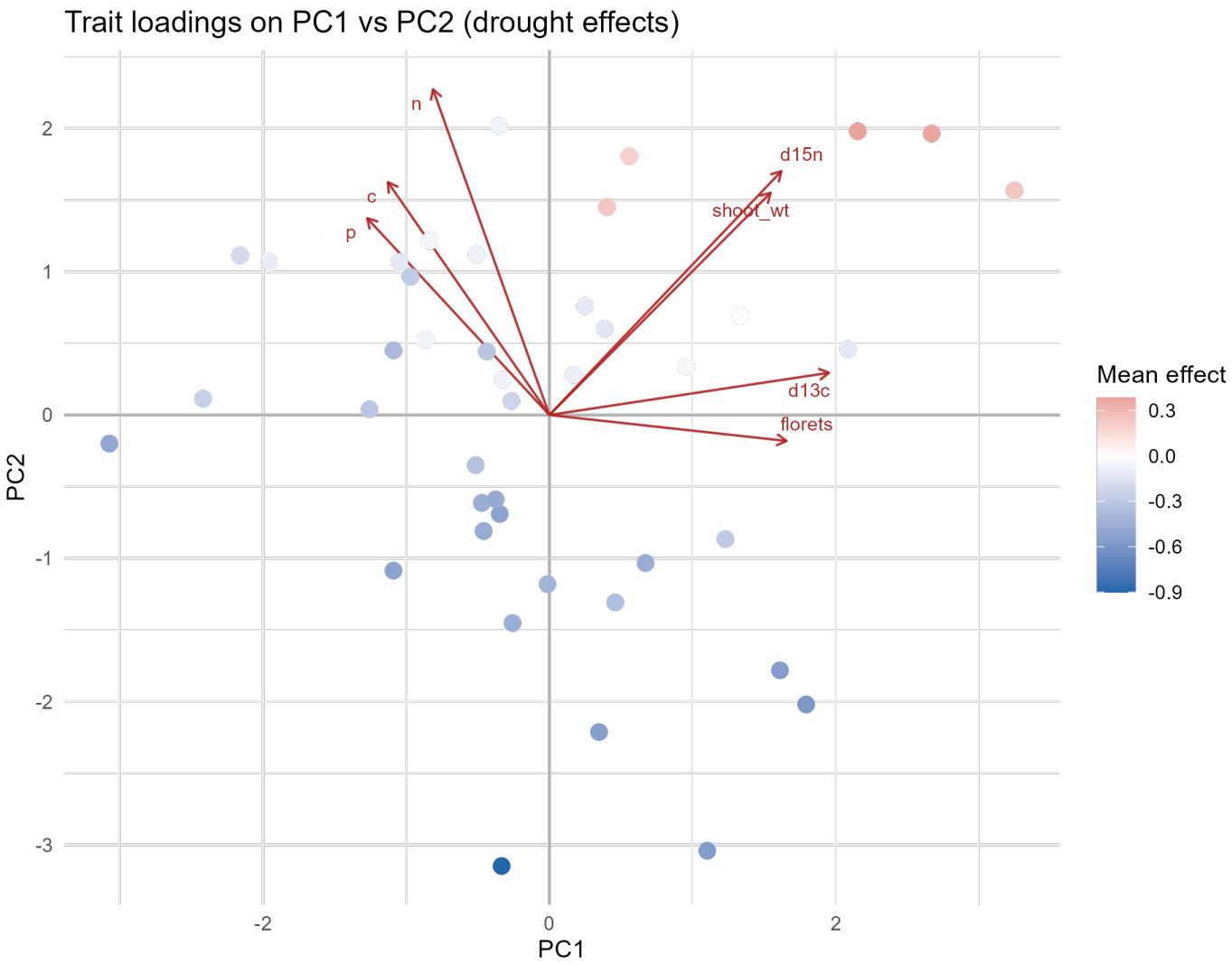
Interpretation: The scree plot shows variance explained by each PC; PC1/PC2 often capture the major response syndromes.

3) PCA trait loadings (biplot)



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

4) PCA trait loadings colored by sensitivity

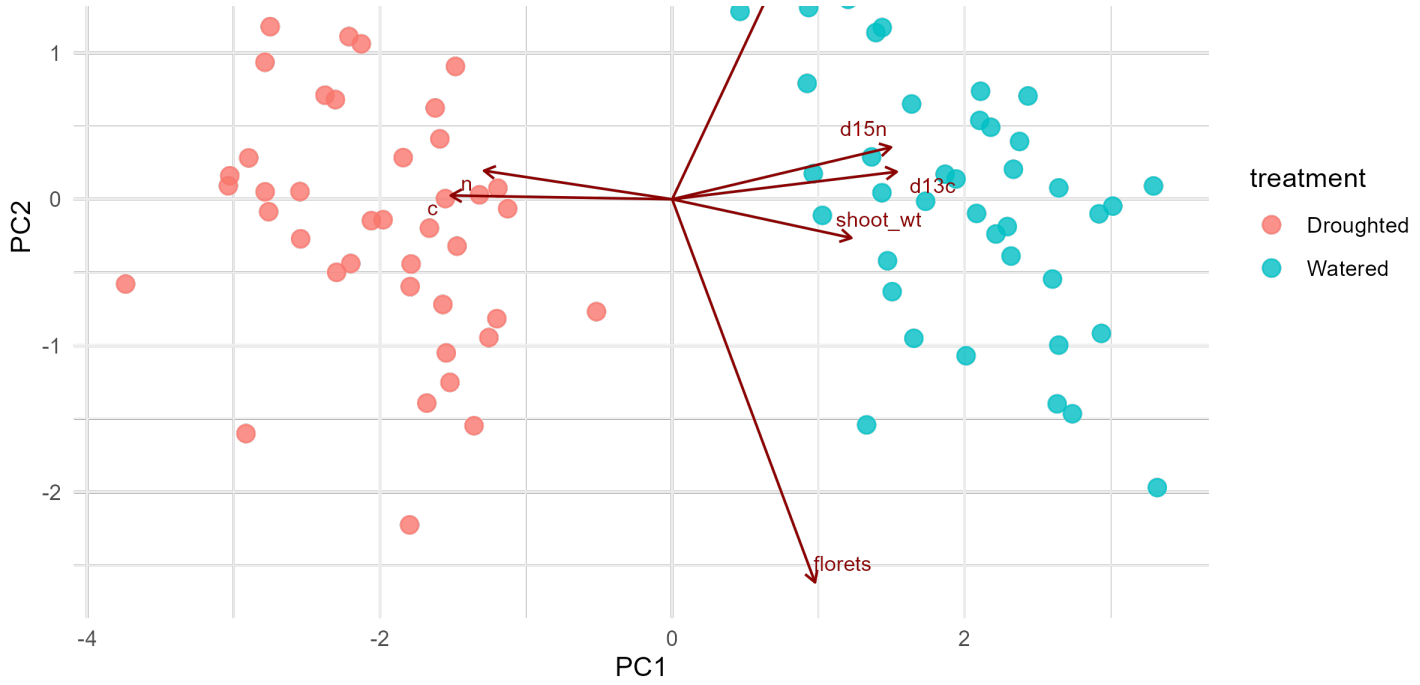


Interpretation: Genotypes colored by mean effect (sensitivity) to highlight clusters.

5) PCA genotype:treatment by treatment

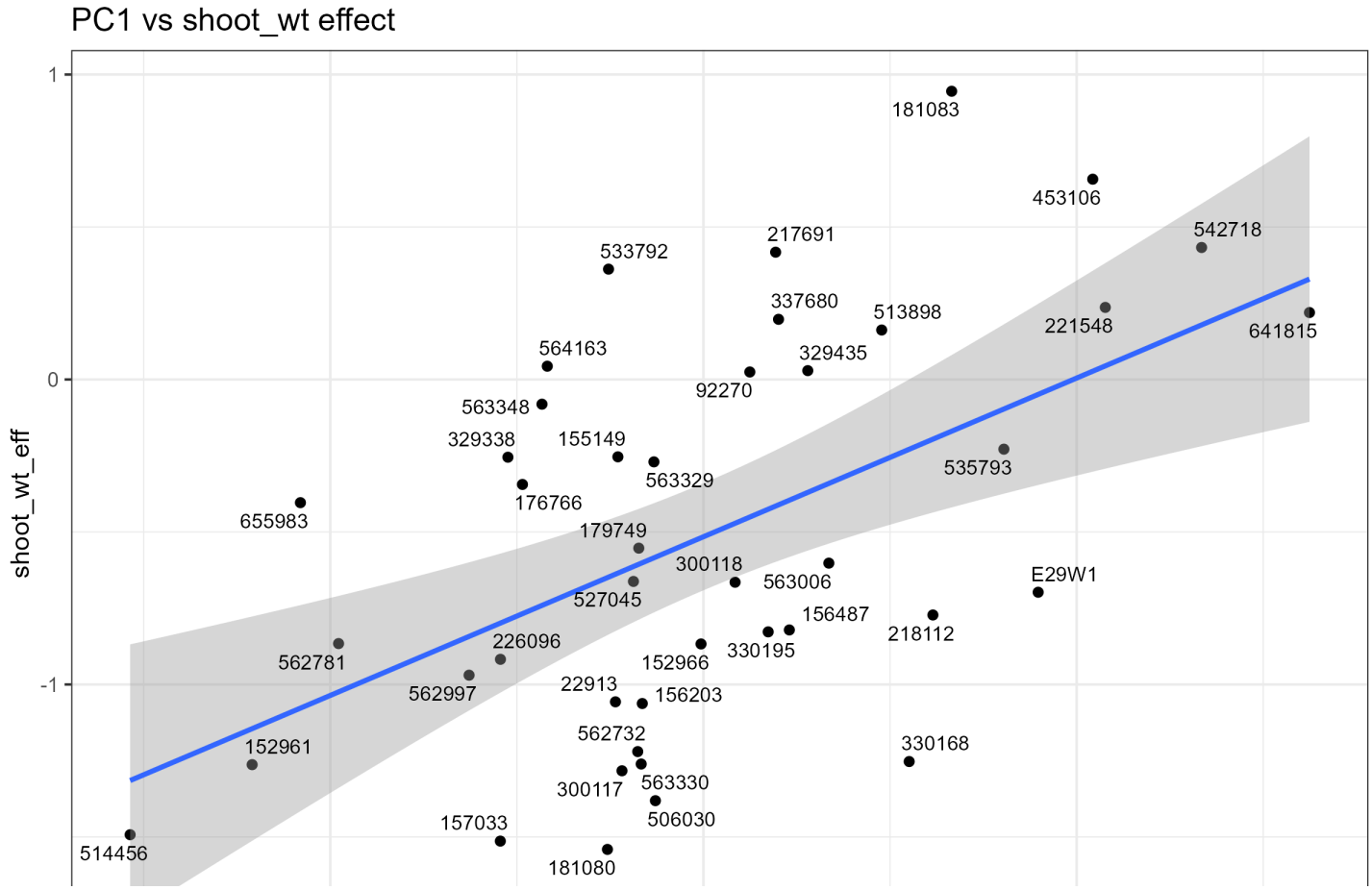
Interpretation: Shows separation (or overlap) between drought and watered states across genotypes.

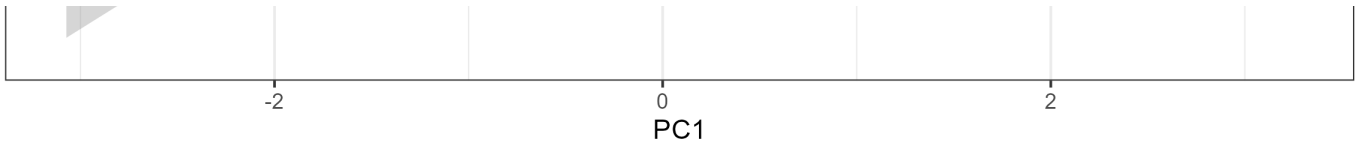
6) PCA genotype:treatment biplot



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

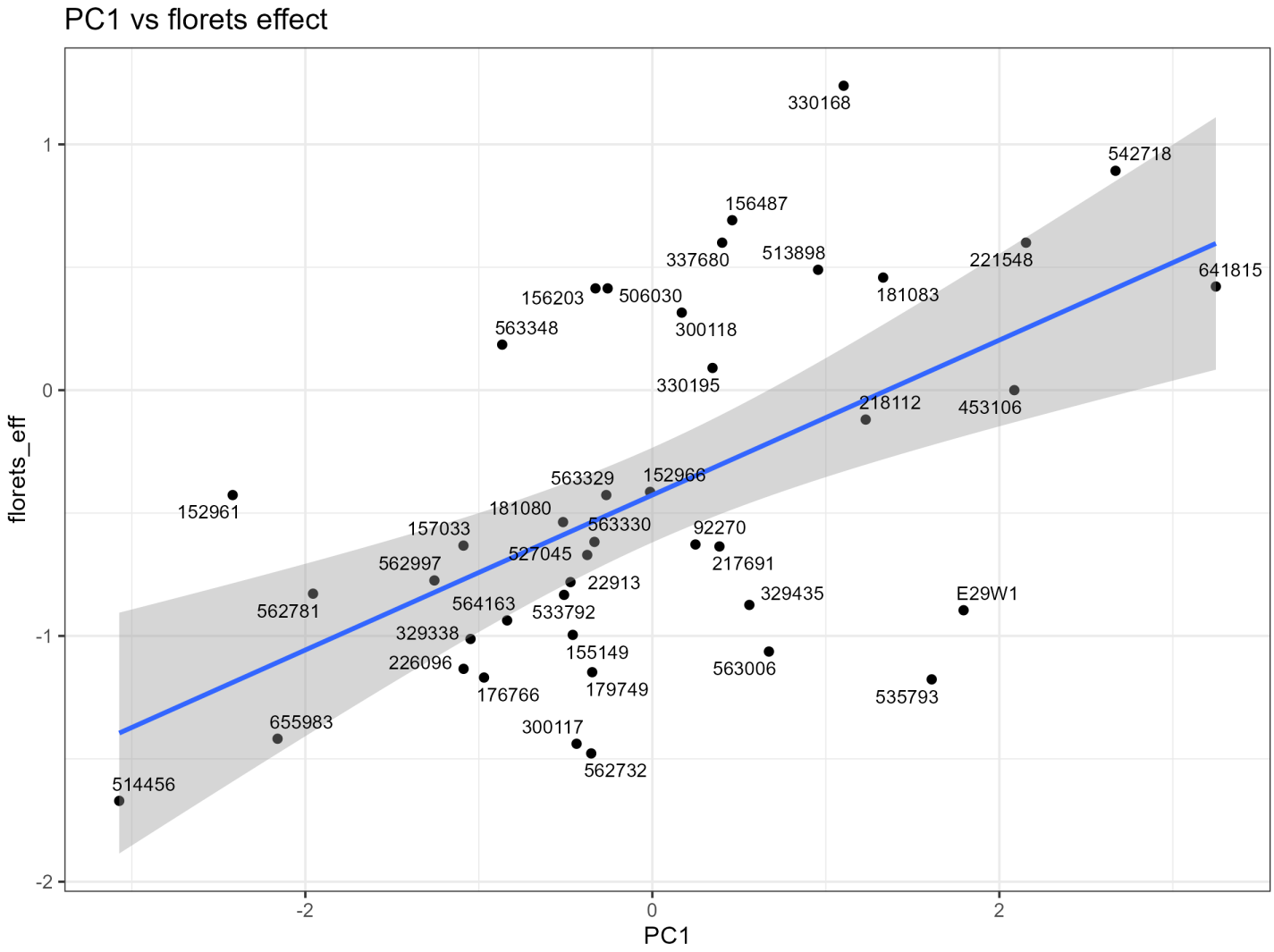
7) PCA vs Shoot weight effect





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

8) PCA vs Florets effect



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

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