This set of scripts can be used to re-make all the figures described in the manuscript.

The PlantCV scripts used to generate the phenotype data can be found in the following directory:

~/Feldman\_Ellsworth\_Setaria\_WUE\_2017/script/plantcv\_script

To perform the analysis conducted in manuscript in the scripts in the following order:

1) fetch\_data.R

2) analysis\_fxns.R

3) ril\_biomass\_modeling.R

4) ril\_water\_use.R

5) ril\_water\_use\_supplemental.R

6) ril\_transpiration\_efficiency.R

7) ril\_transpiration\_analysis.R

8) ril\_wue\_major\_axis.R

9) ril\_heritability.R

After this step, output derived from this process is put through the foxy\_qtl\_pipeline:

https://github.com/maxjfeldman/foxy\_qtl\_pipeline

The files that are put into the QTL pipeline are named with the following convention:

ril\_loess\_ **<TRAIT NAME>** \_qtl.csv

The output files are named as described in the documentation associated with the foxy\_qtl\_pipeline github account.

Next fun the scripts in the following order:

10) ril\_qtl\_summary\_table.R

11) ril\_qtl\_trait\_matrix\_plot.R

12) ril\_venn\_qtl\_summary.R

13) ril\_venn\_qtl\_gxe\_summary.R

14) ril\_qtl\_timeseries\_plots.R

15) ril\_qtl\_summary\_table\_fixed\_marker.R

16) ril\_fixed\_fx\_size\_clustering.R

This gives you all final data for plotting and you can run the following R script to generate the figures:

17) manuscript\_figures.R

Please let me know if you have any questions or concerns.