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

https://www.biorxiv.org/content/early/2018/01/30/234708

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 run the scripts in the following order within RStudio (you will need to enter the correct working directory at the beginning of each script):

1) analysis\_fxns.R

2) fetch\_data.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.

Max Feldman