With these data, we evaluated the reaction norms of QTL for elements in the ionome.

Our results allow us to address the following questions:

1. What is the genomic basis for variation in elemental abundances in the switchgrass ionome?
2. What fraction of QTL for distinct elements co-localize, suggesting common genetic architectures underlying their abundances?
3. How frequently do ionomic QTL show GxE?
4. Which QTL colocalize with candidate genes, suggesting avenues for future molecular characterization of the switchgrass ionome?