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**Abstract Title:** Transcriptomic responses to multi-year drought stress across diverse Switchgrass accessions

**Abstract (250 words or less):** We present gene expression data from a diverse set of 10 Switchgrass (*Panicum Virgatum*) varieties grown from 2012-2014 in the field under rainout shelters with controlled watering conditions. All three years include data from our Temple, TX, location while the final two years include data from our Austin, TX, location. Multiple measurements (across time) were taken within a given year to allow for evaluation of treatment response at key growth cycle time points. Both locations had the same genotypes and same experimental design structure, i.e., at each location each genotype was (vegetatively) replicated 48 times and subjected to 6 water treatment levels. Relative gene expression was measured via next generation sequencing using a 3' tag, poly-A capture protocol which allowed increased efficiency in gene counting and a substantial increase in effective sequencing depth over traditional RNA-Seq protocols. Bioinformatics processing for per gene counts followed best practice procedures, and statistical analysis of the data utilized established data quality and analysis methodology. We present the results of a mixed model analysis framework in which we evaluate the effect of water level on the study genotypes. Based on our analyses, we characterize (drought) treatment responsive genes in terms of their functional roles and promoter classifications, and suggest some possible trends in transcriptomic level responses to drought stress across genotypes.