

Summary results DE analysis Miscanthus 2014 AU-IBERS

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Description of the data

- Counts table for the 2014 experiment at AU-IBERS (produced by IGATS)
- RNAseq data from Miscanthus mapped to Sorghum Bicolor
- Originally 33032 genes in the table → after data cleaning ¹ 16343 genes in table
- 96 samples were taken from this green house experiment in two harvests (May 31, 2014 and June 15, 2014). The experiment ran from May 5, 2014 to June 18, 2014 (application of drought treatment as of May 12, 2014).
- Two treatments: control and drought (check %); five genotypes (WAT03 -sacchariflorus; WAT04 -sacchariflorus; WAT09 -giganteus; WAT10 -sinensis; WAT11 -sinensis).
- The greenhouse design was not officially randomized, but it seems fairly "random". We have information on the row/column position and a block number.
- Replications: each genotype was harvest replicated 9-10 times per harvest which leads to a replication of about 4-5 samples per harvest/genotype/treatment combination.

Plot of the experimental design?

¹Genes with no expression in any of the samples were removed. Additionally all genes with a mean expression for the non-zero counts of 10 or less were removed.

DE analysis using DESeq2

Before starting the statistical analysis using DESeq2 we ran some check on whether the greenhouse design or sampling scheme (through 2 harvests) might have an effect on the expression (analysis). To this end we used `glm.nb` including the design terms and checked for the significance of these factors. Based on the results we decided to include **Harvest** into the model in order to control for it.