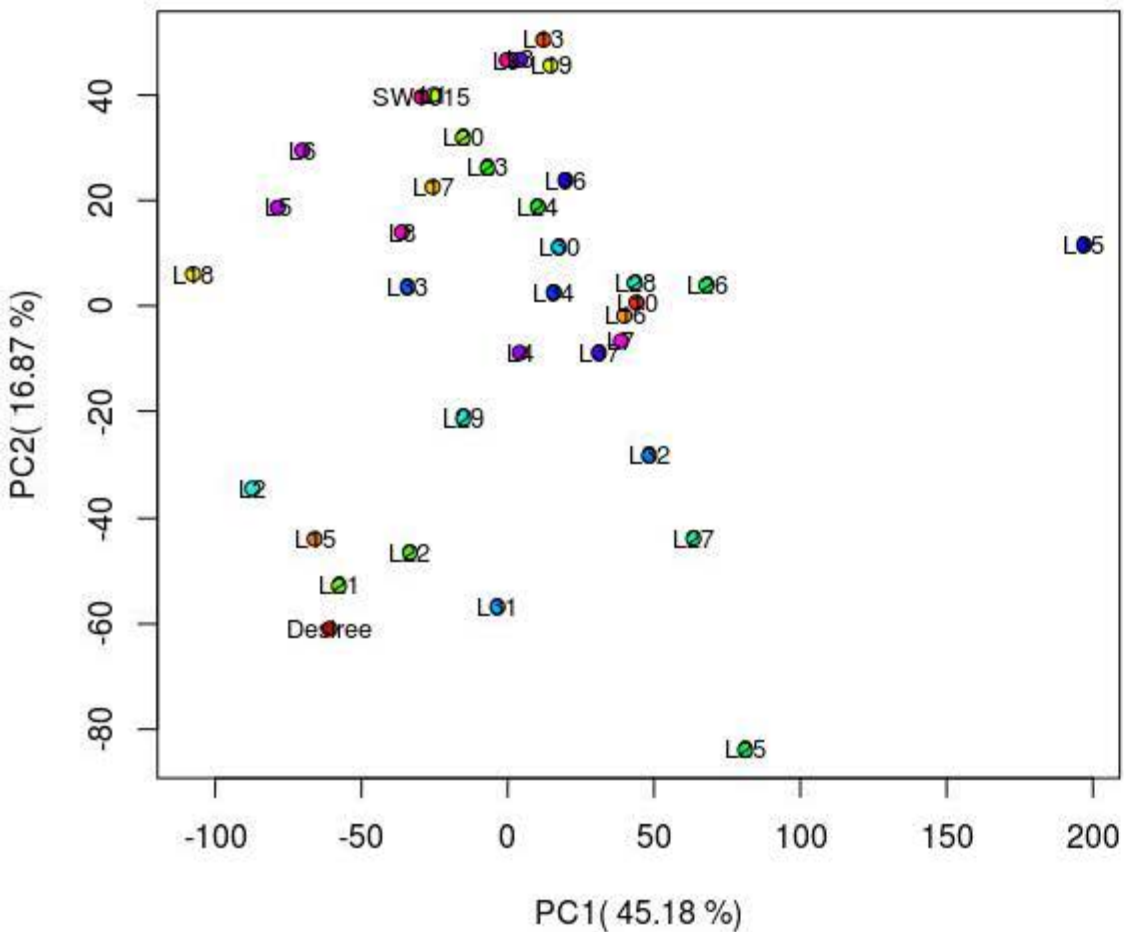
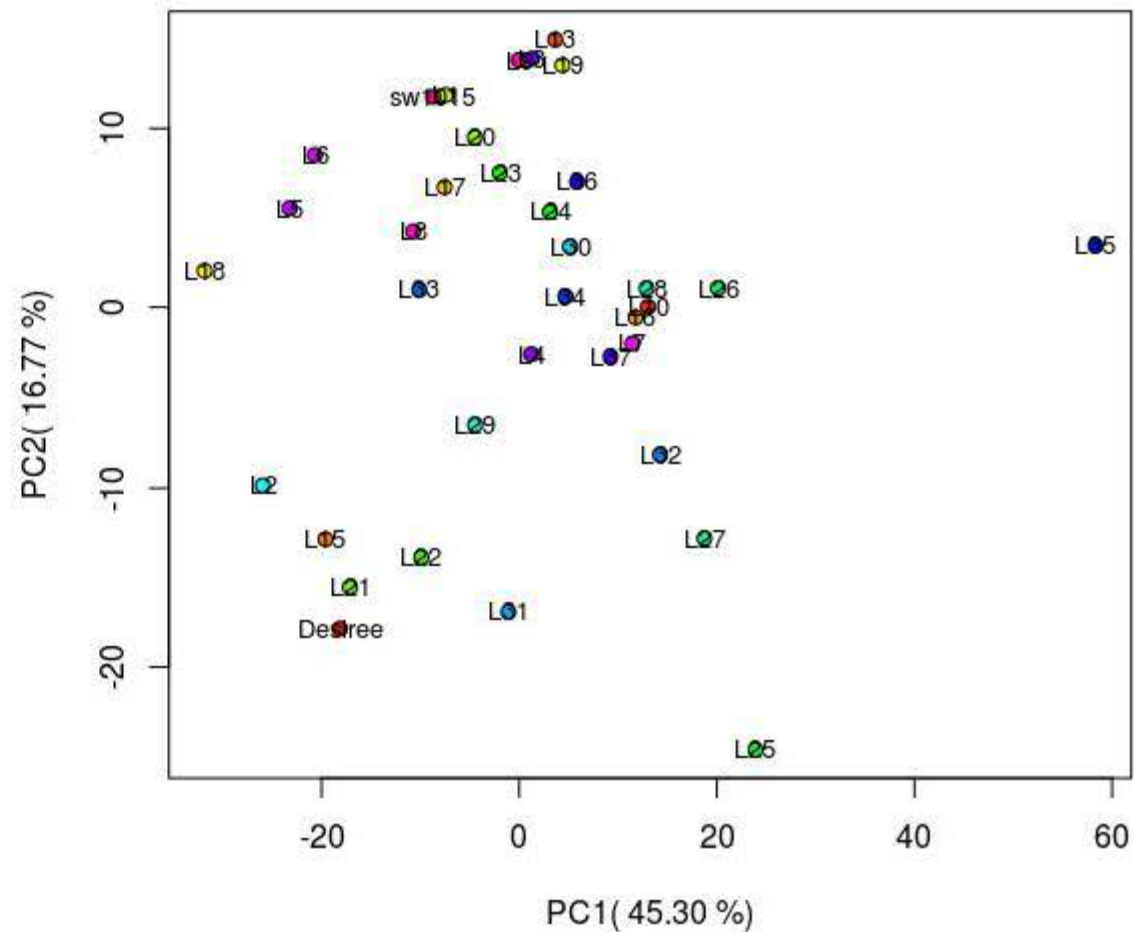
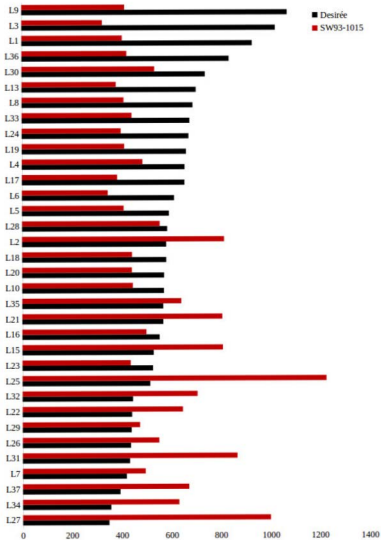


Normalized unfiltered transcriptome



Normalized filtered transcriptome





Method S1: Gene expression of progeny lines with respect to their parental lines

A comparative study was performed to identify differentially expressed genes between progeny lines and the parents. Differential gene expression analysis was performed by edgeR [1] through Trinity version trinityrnaseq_r20140717 to find differentially expressed genes between the individual progeny lines and the two parents separately.

Since no biological replicates existed to determine differentially expressed genes between the individual lines and the parents, we had to define a dispersion value for biological variation. This is possible in edgeR, and for biological variation in genetically identical organisms a dispersion value of 0.1 is suggested. We therefore tried dispersion values from 0.1 to 0.39 and we only had minor variation depending on the dispersion value in the number of differentially expressed genes with respect to the parents. So, we chose to go for the dispersion recommended for genetically identical organisms, 0.1.

1. Robinson MD, McCarthy DJ, Smyth GK: **edgeR: a Bioconductor package for differential expression analysis of digital gene expression data.** *Bioinformatics* 2010, **26**(1):139-140.