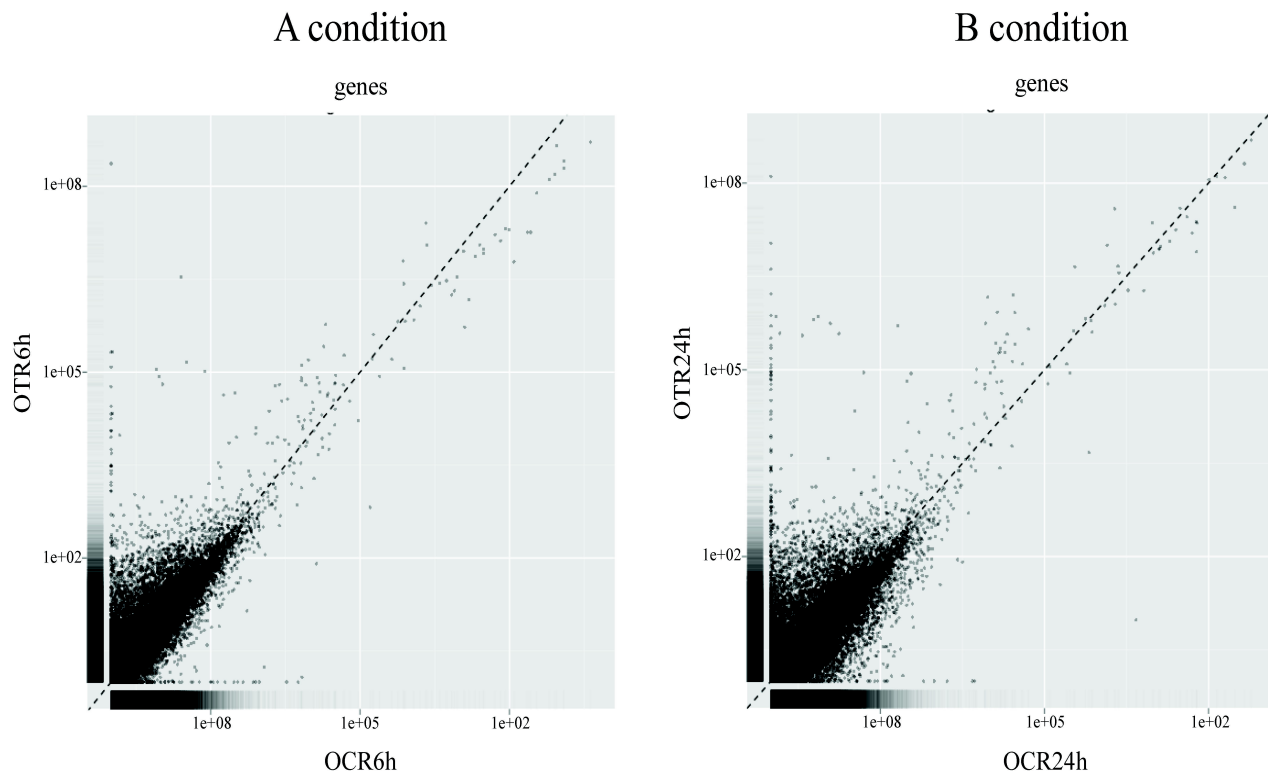
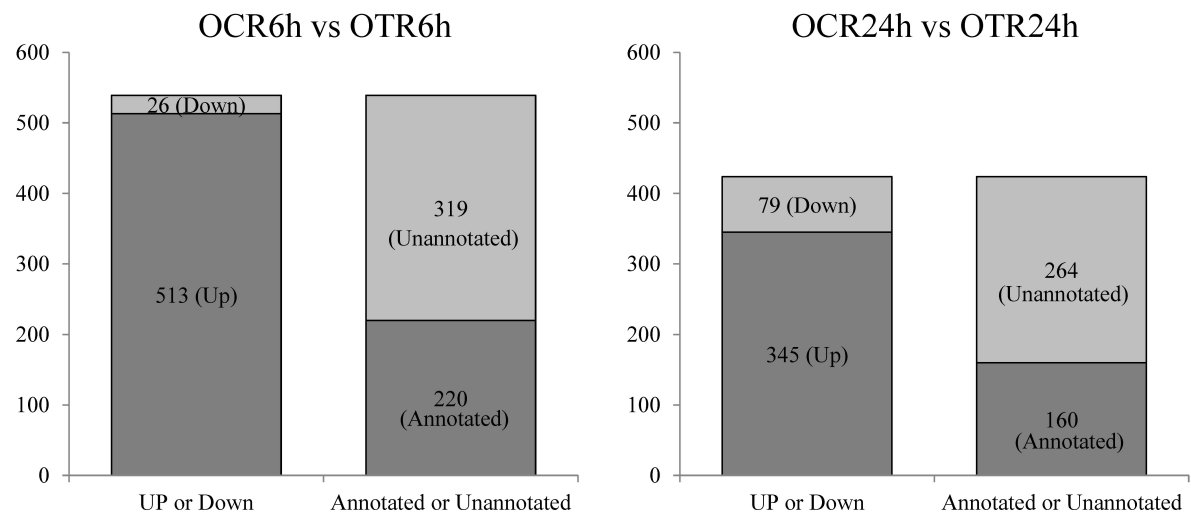


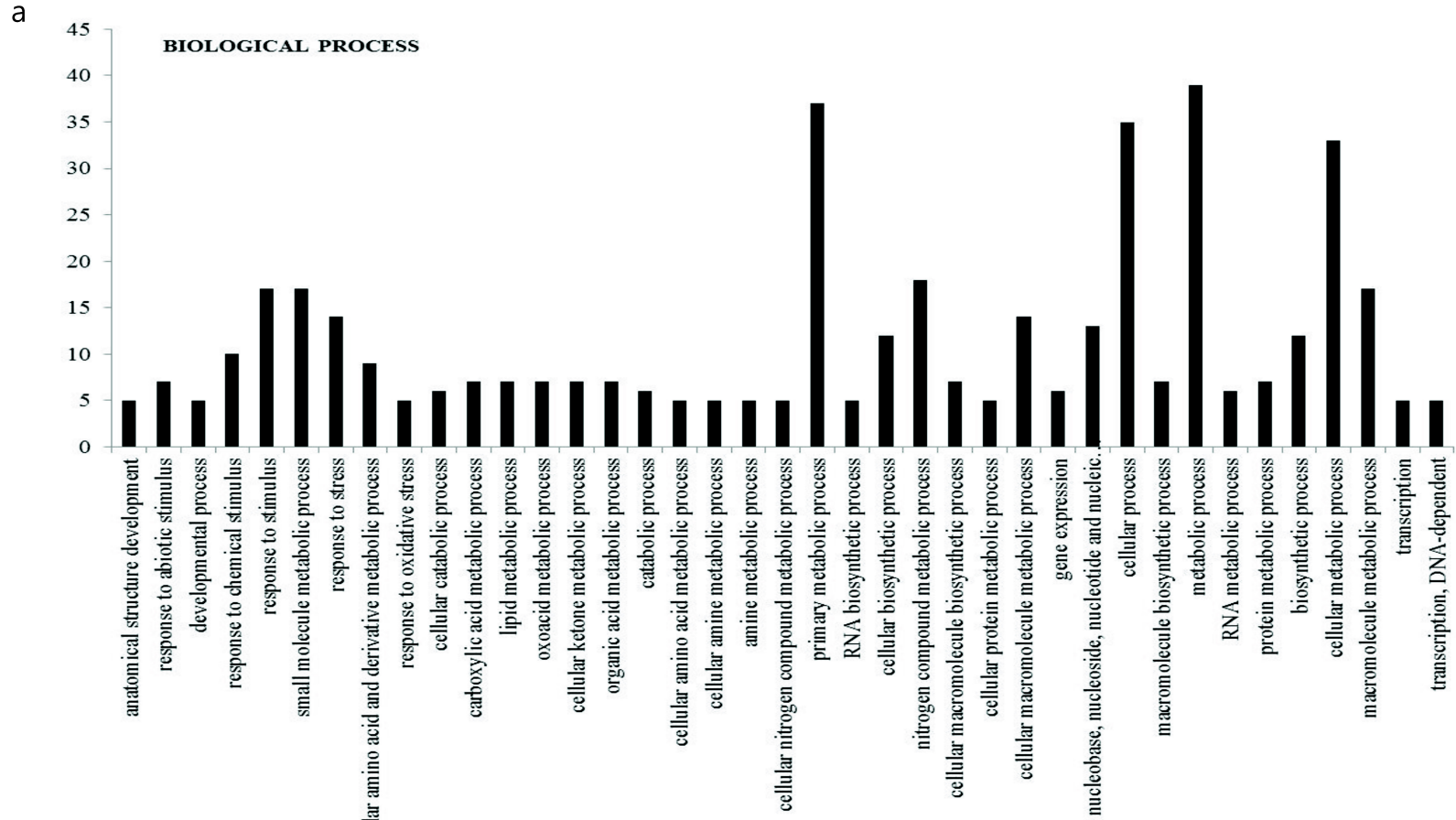
Supplementary Fig. 1. Quantitation and QC for library with a Bioanalyzer 2100. (Redbox indicates that *O. glaberrima* library size ranged from 250 bp to 450 bp with 350 bp of the average)



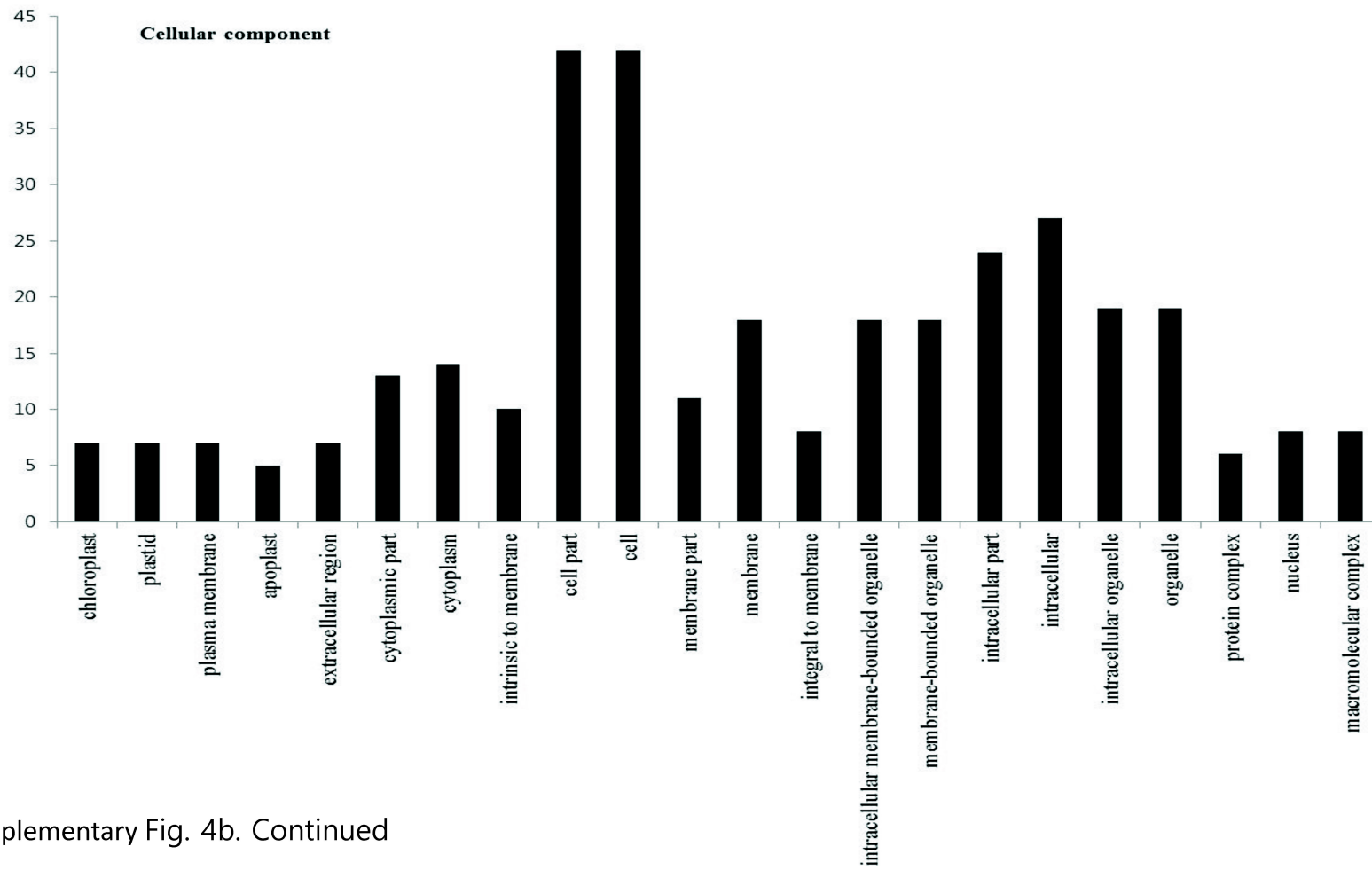
Supplementary Fig. 2. CummeRbund scatter plots highlight general similarities and specific outliers 2 conditions ; A condition: OTR_6h and OCR_6h B condition: OTR_24h and OCR_24h



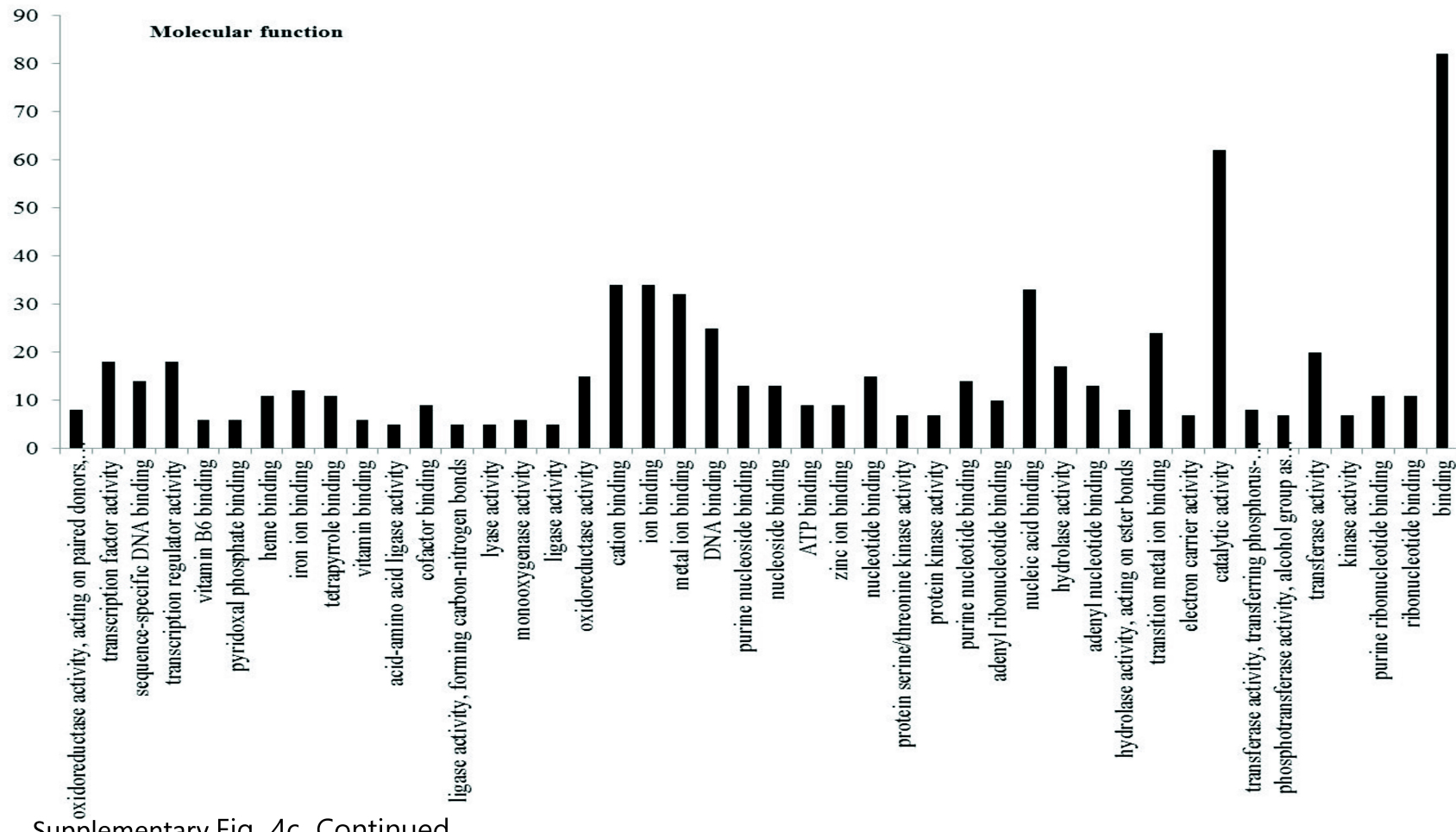
Supplementary Fig. 3. DEGs in each of two time course treatments.



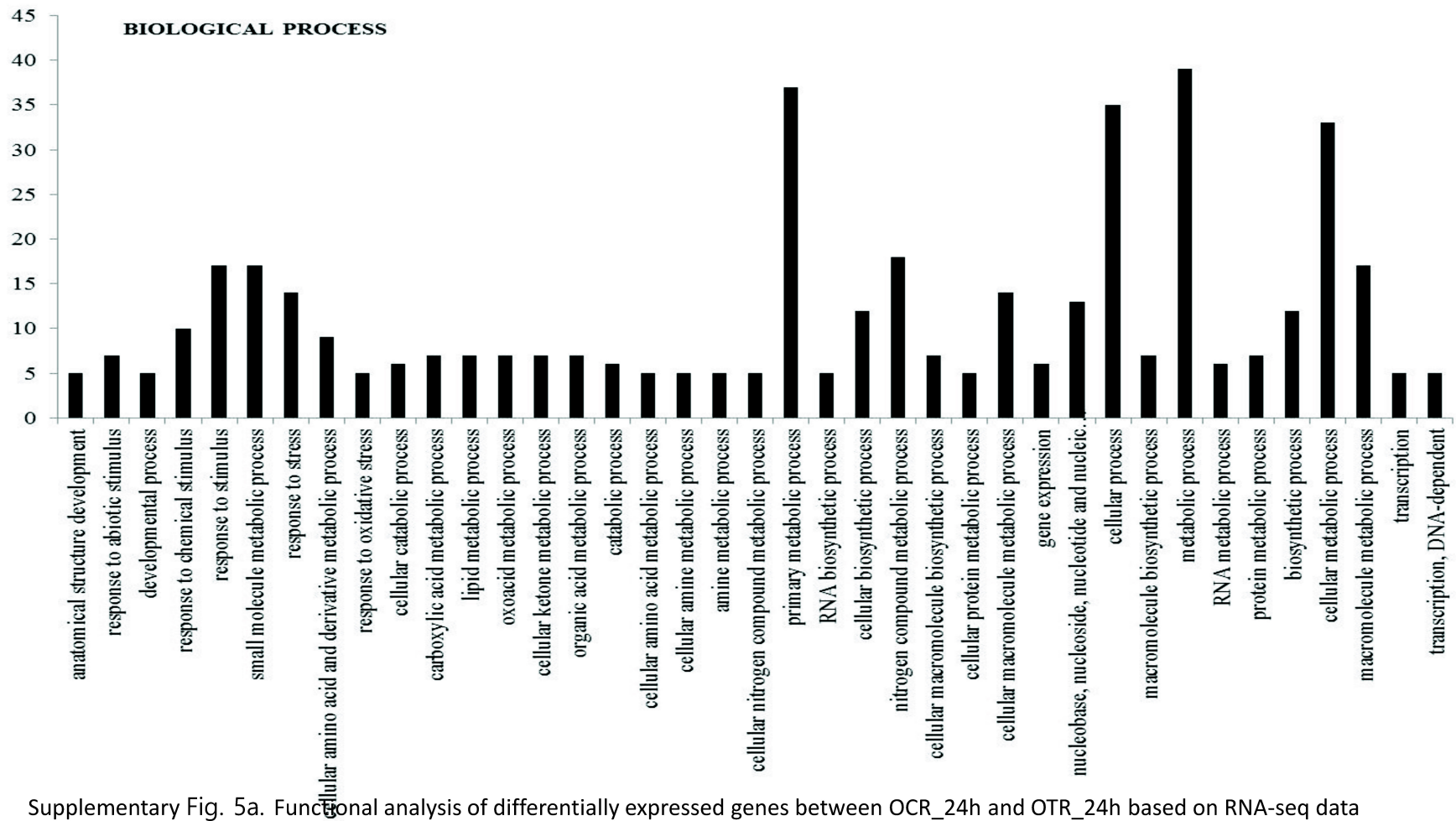
Supplementary Fig. 4a. Functional analysis of differentially expressed genes between OCR_6h and OTR_6h based on RNA-seq data



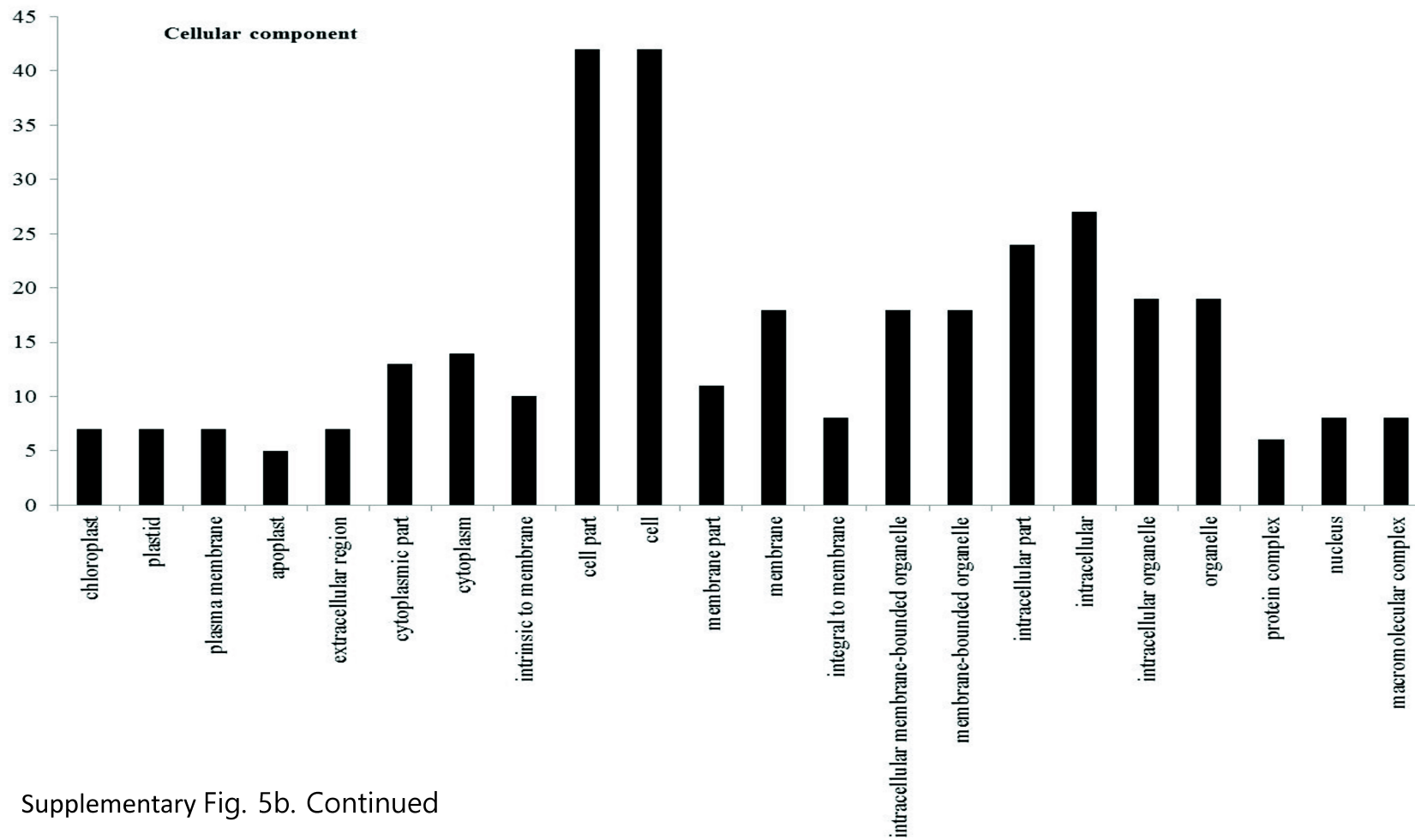
Supplementary Fig. 4b. Continued



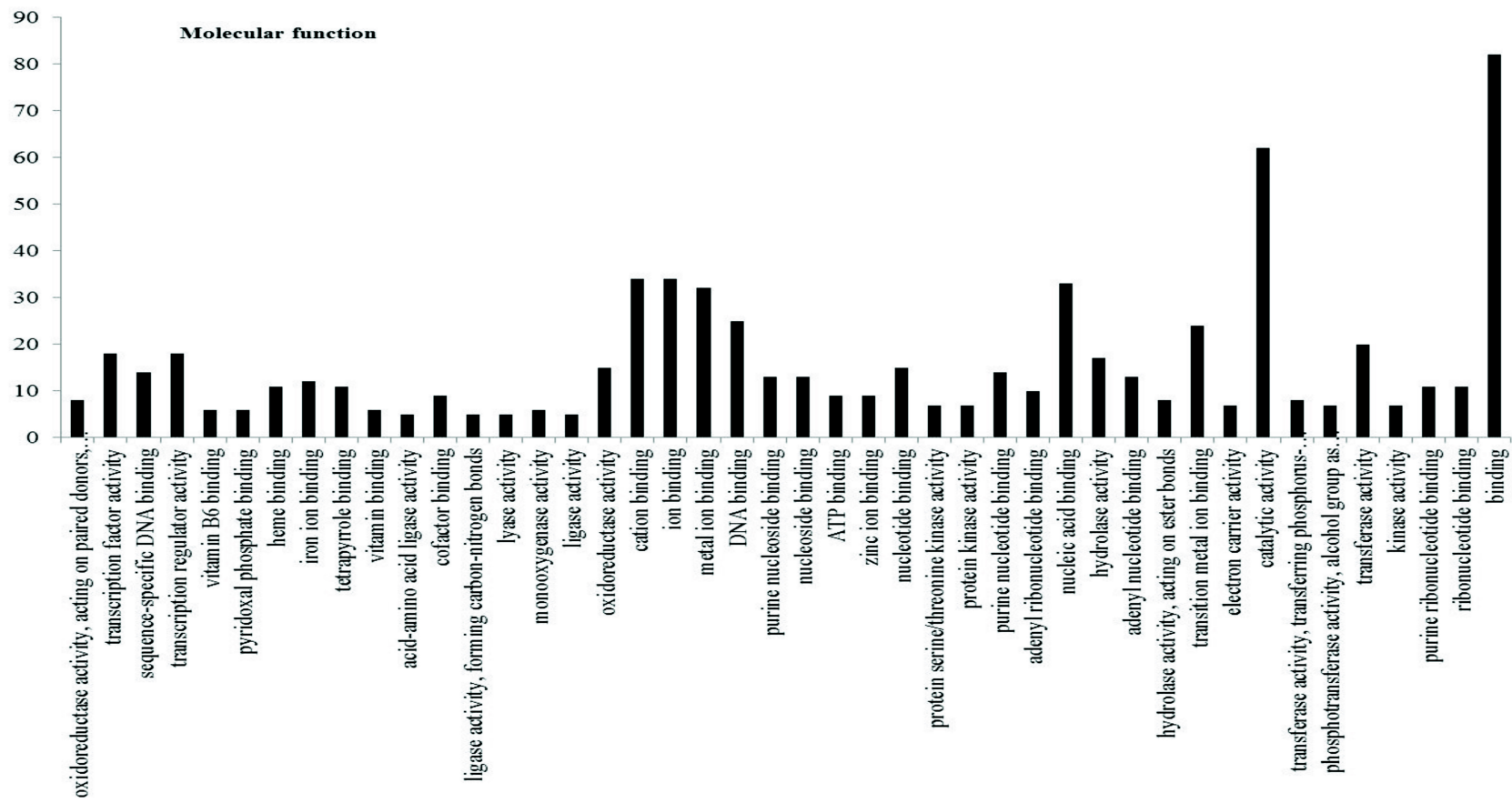
Supplementary Fig. 4c. Continued



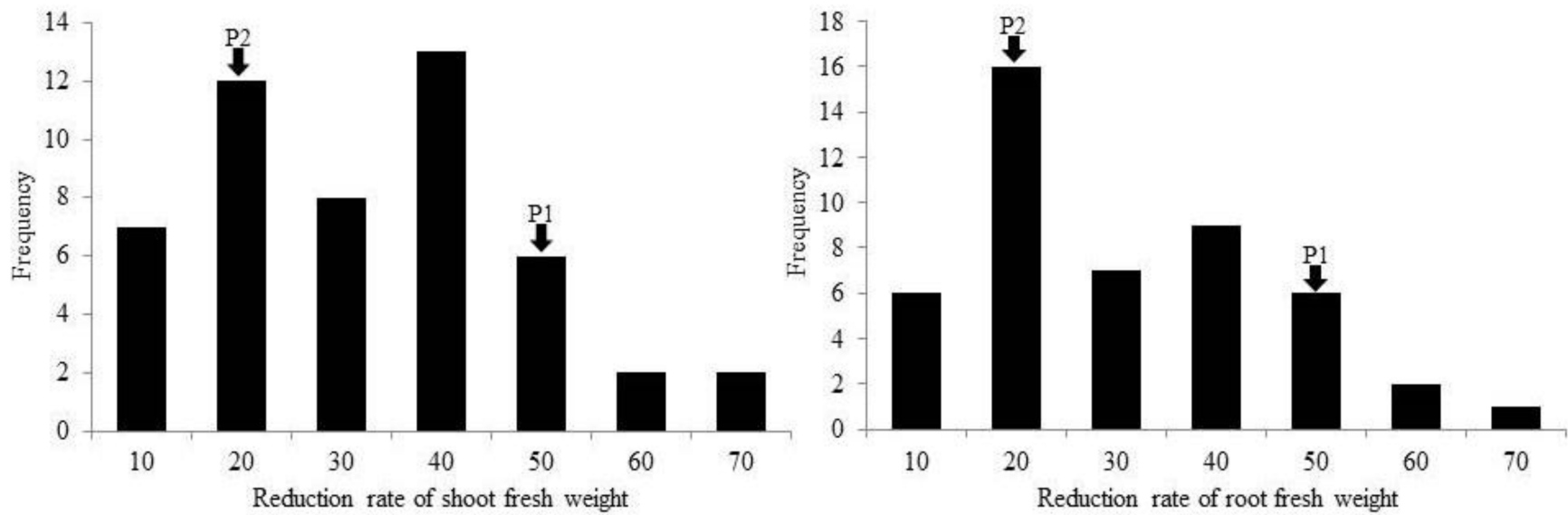
Supplementary Fig. 5a. Functional analysis of differentially expressed genes between OCR_24h and OTR_24h based on RNA-seq data



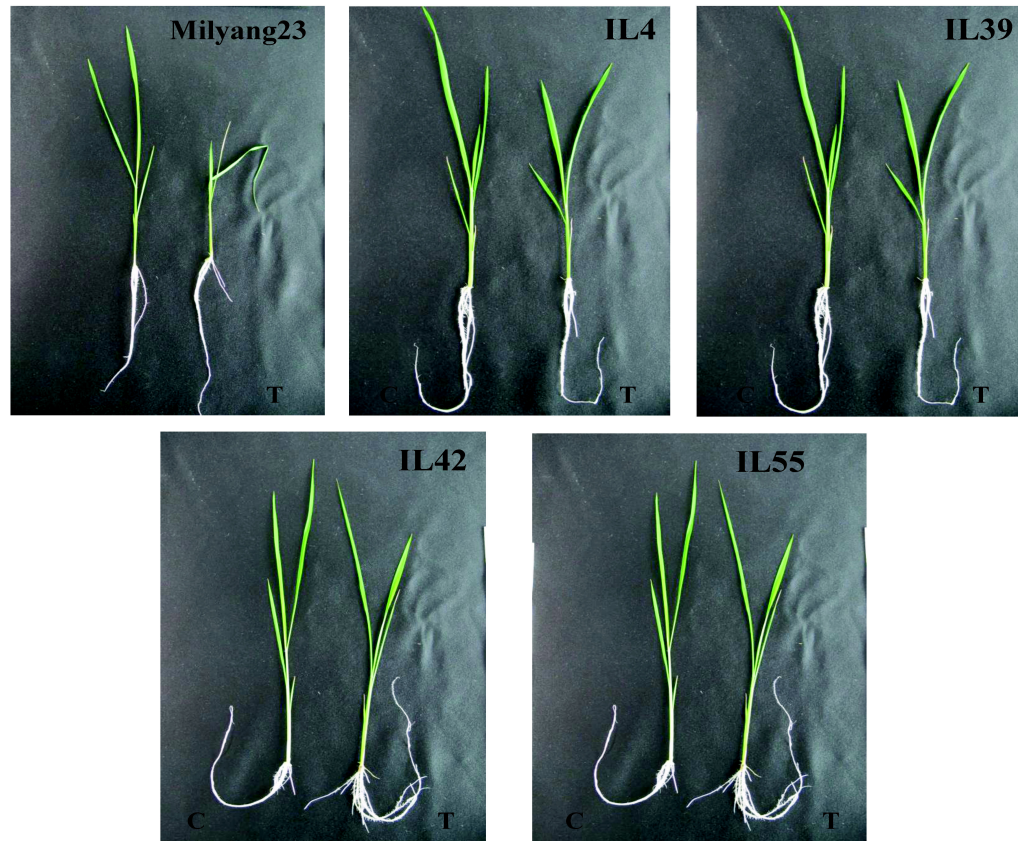
Supplementary Fig. 5b. Continued



Supplementary Fig. 5c. Continued



Supplementary Fig. 6. Frequency distribution of shoot and root reduction rate caused by salt treatment in 55 ILs and parents.
P1 : Milyang23, P2 : *O. glaberrima*



Supplementary Fig. 7. Comparison of Milyang23 and four salt tolerant lines after imposition of 100 mM NaCl stress for five days.