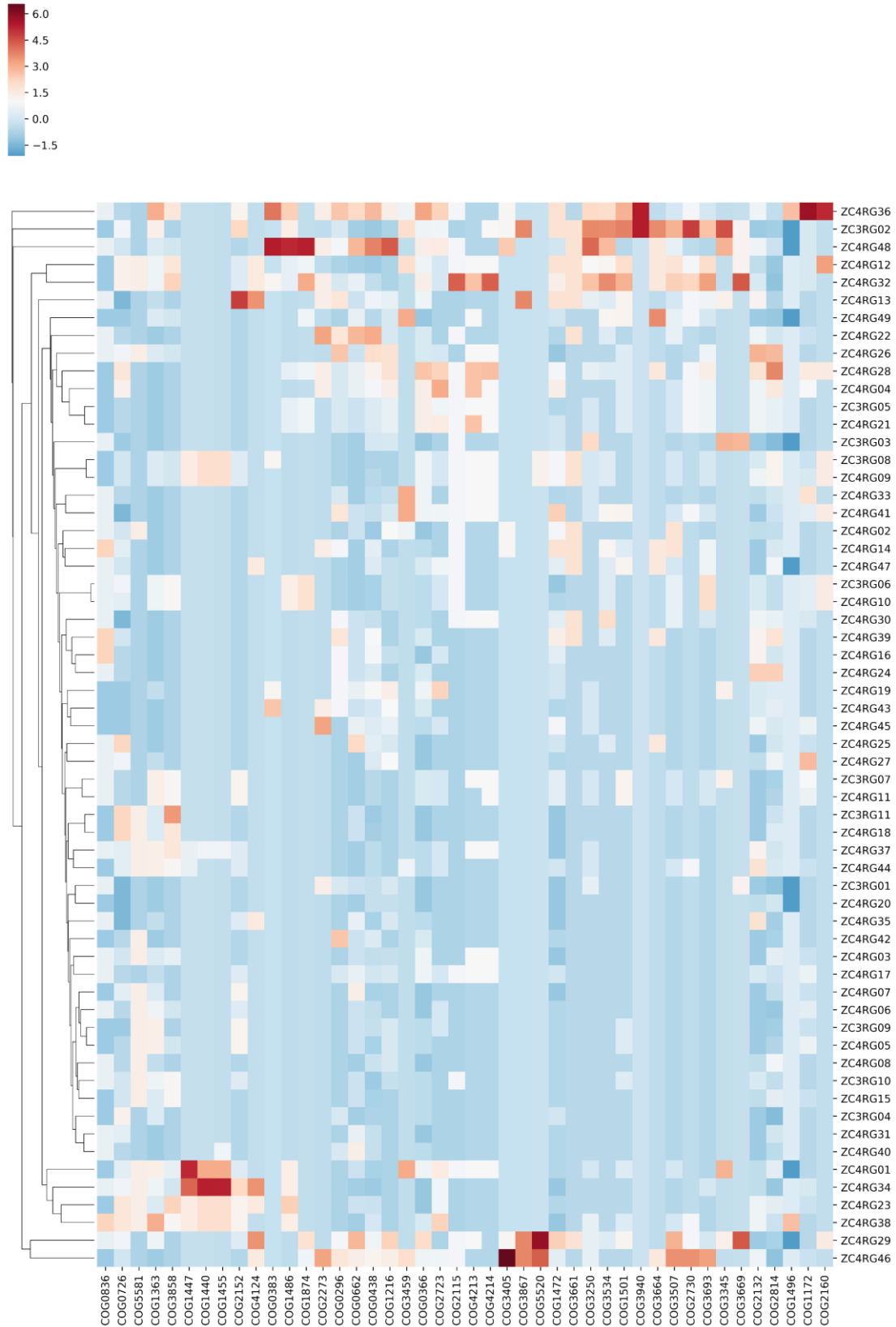
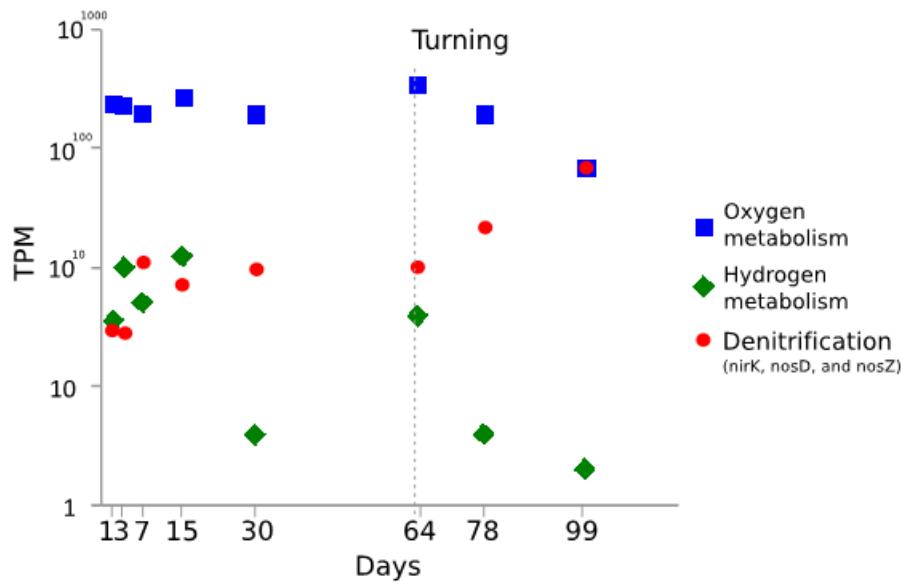


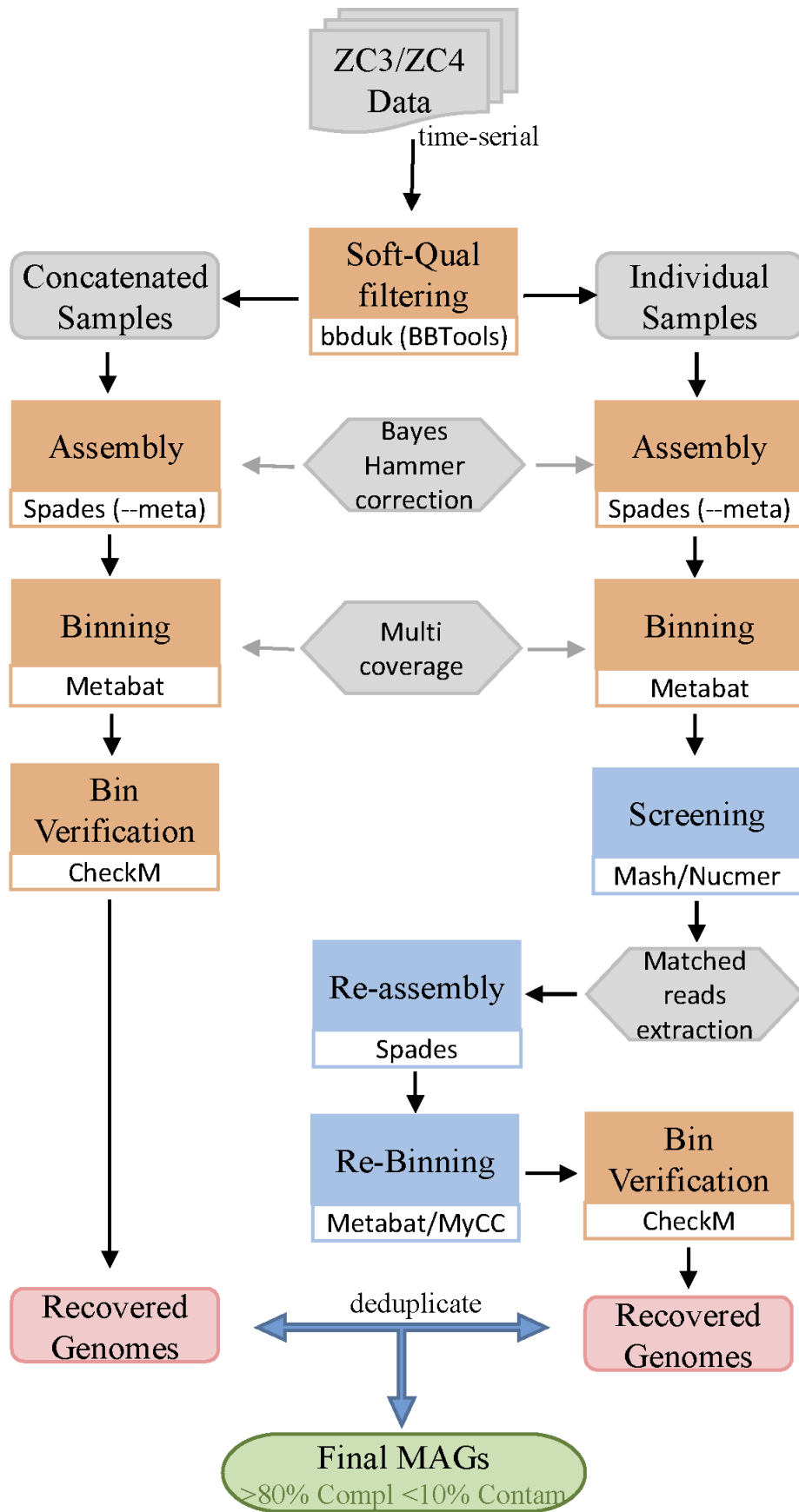
## Supplementary Figures



Supplementary Figure 1 - Hierarchical clustering of ZC3 and ZC4 MAGs. The heatmap is based on the number of COGs associated to lignocellulose breakdown. Abundant COGs are shown in red.



Supplementary Figure 2 – Variation in transcript abundance (TPM) of genes in MAGs that were associated to the indicated metabolic functions. Y-axis is in log scale.



Supplementary Figure 3 – Workflow employed for recovering the ZC3 and ZC4 MAGs.