

Supplementary Material

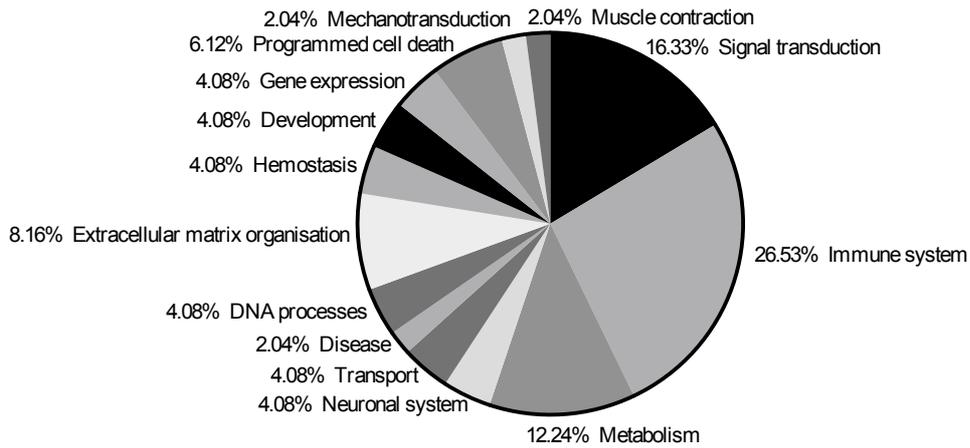


Figure S1. Representation of the main functions of the genes differentially expressed in the monocyte U937 cell line treated with 15 $\mu\text{g}/\text{ml}$ lysozyme for 1 h and analysed immediately at the end of the treatment (1h). Every single gene can possess more than one function.

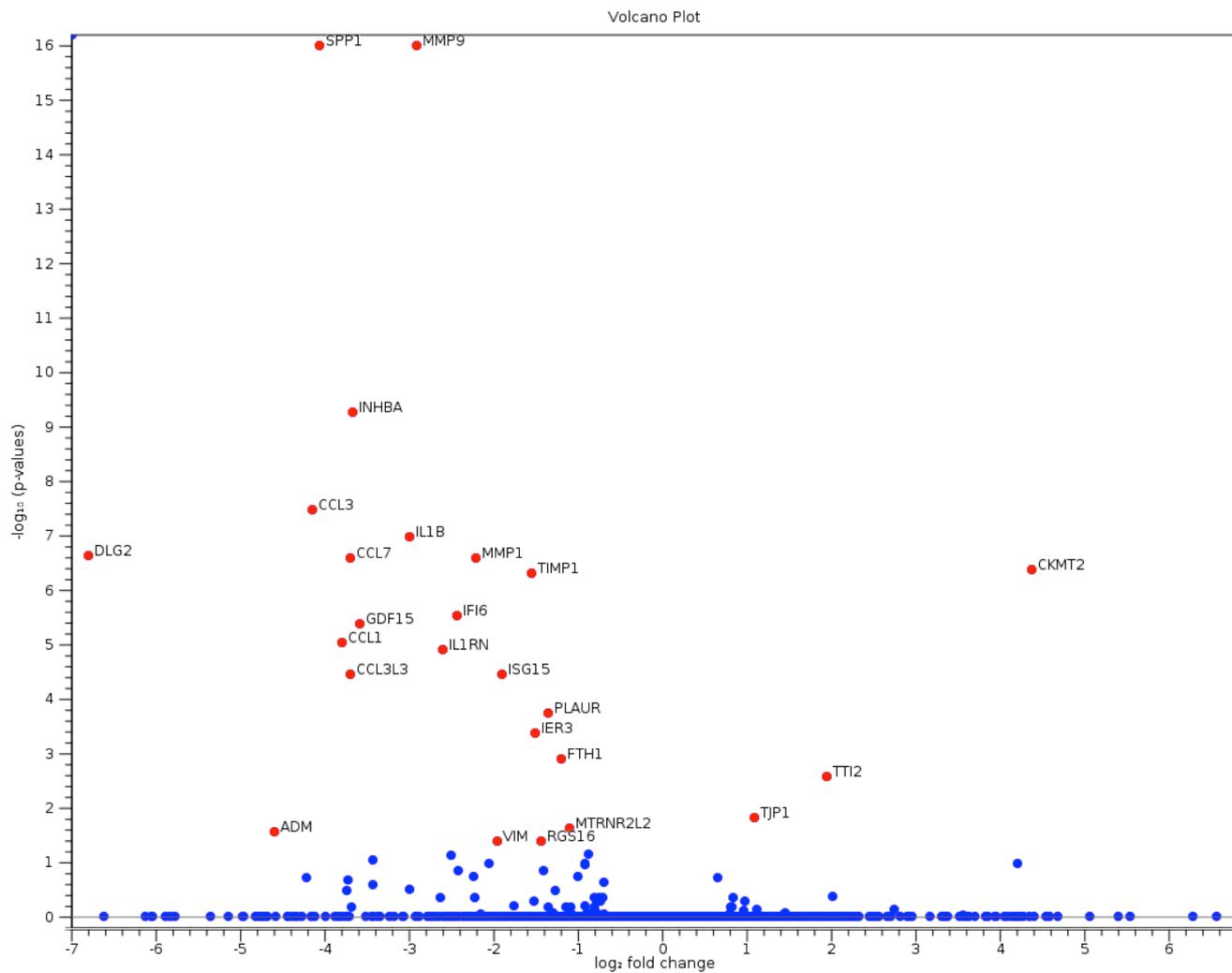


Figure S2: Volcano plot of differential expression between LZ and C at 1h. DEGs are plotted as red dots and labeled with names

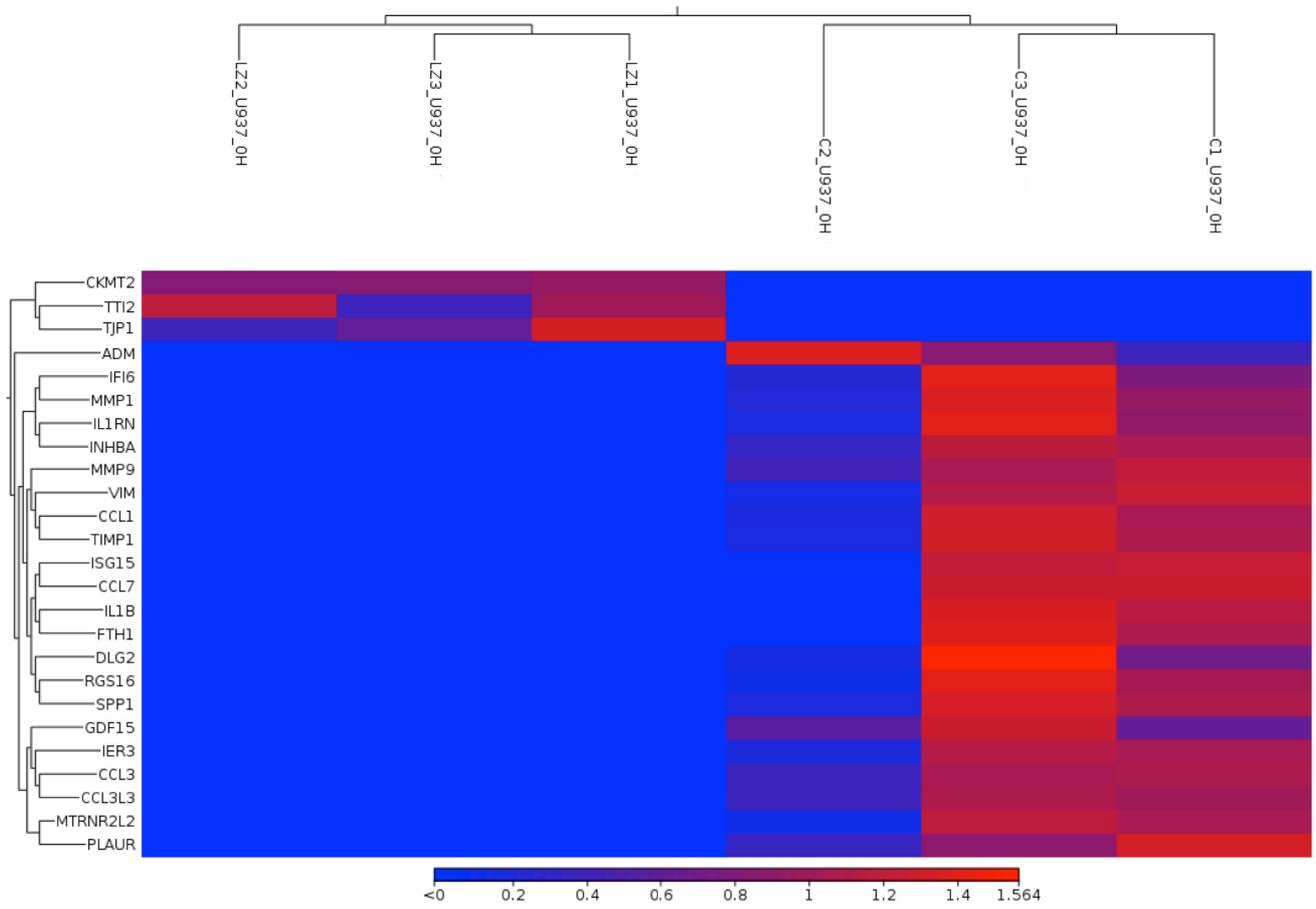


Figure S3: Heatmap of DEGs between LZ and C at 1h. Clusters from both rows and columns are merged by the maximum euclidean distance of their members.

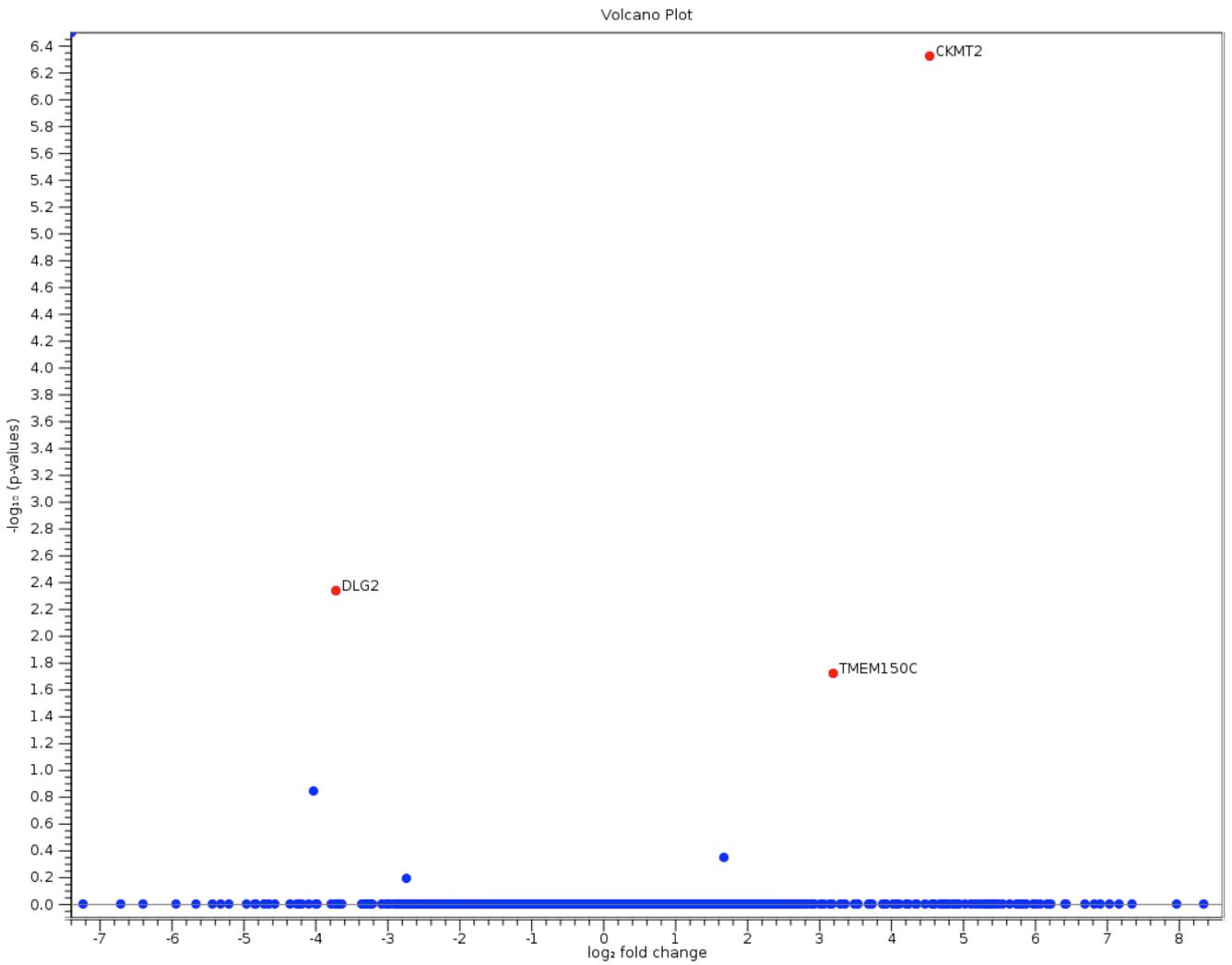


Figure S4: Volcano plot of differential expression between LZ and C at 1h+2. DEGs are plotted as red dots and labeled with names

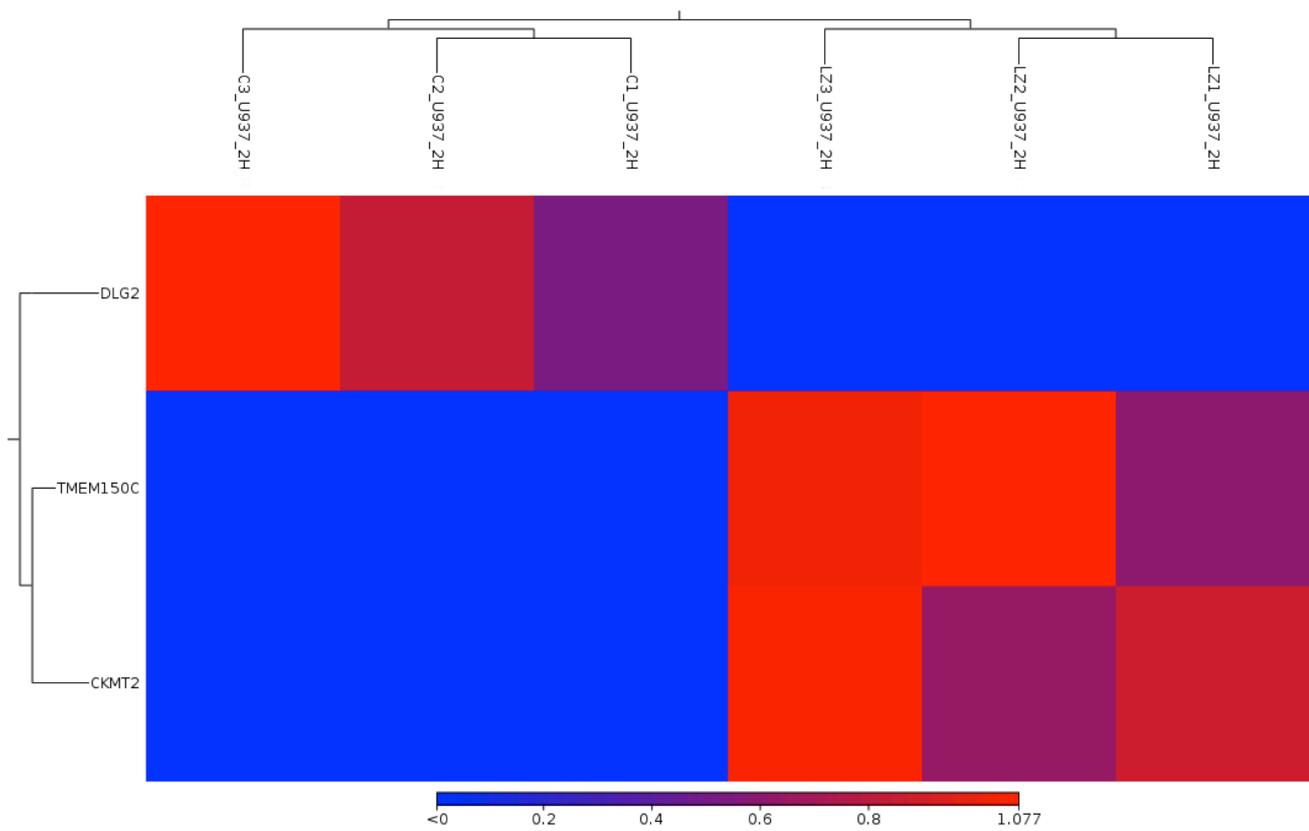


Figure S5: Heatmap of DEGs between LZ and C at 1h+2. Clusters from both rows and columns are merged by the maximum euclidean distance of their members.

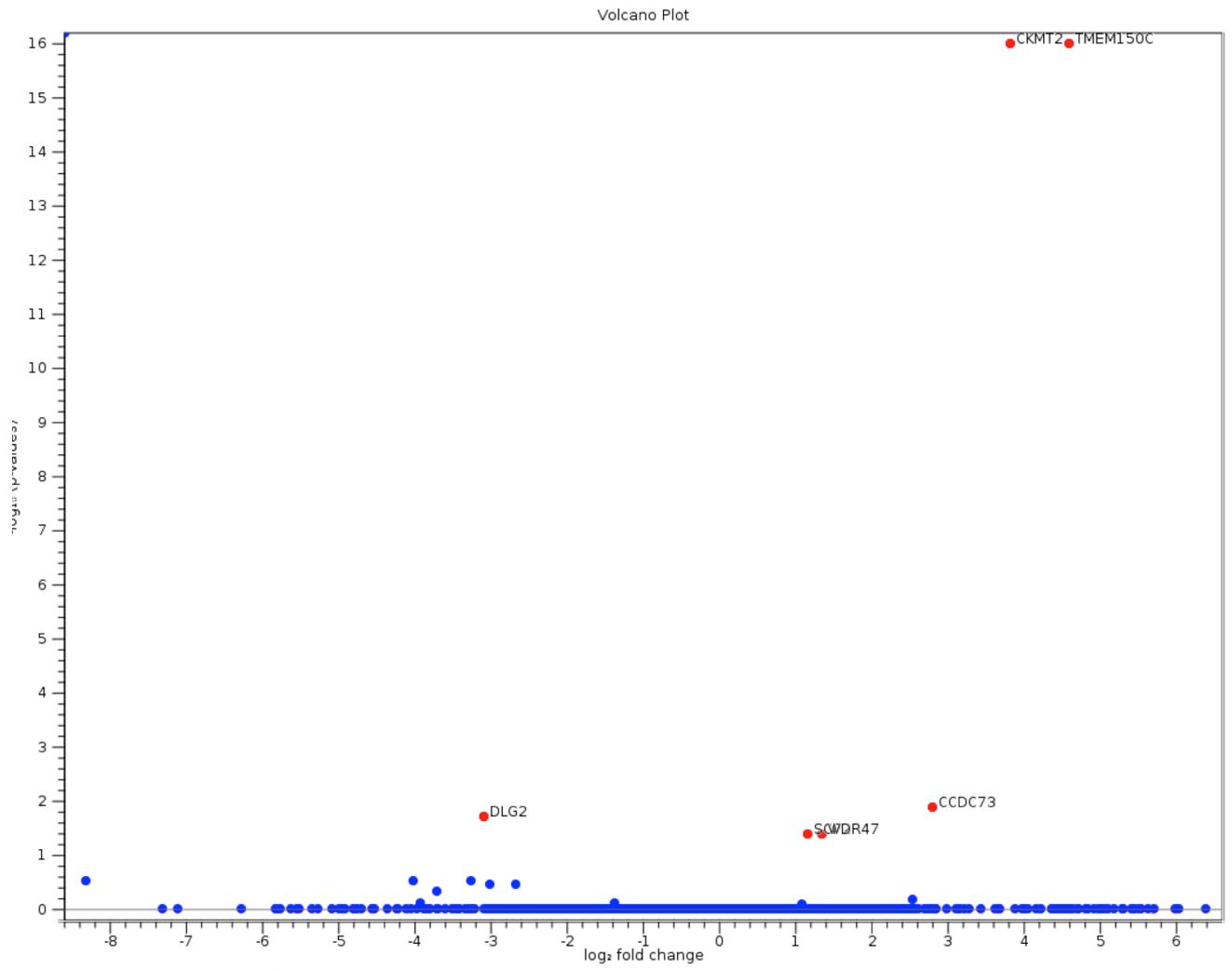


Figure S6: Volcano plot of differential expression between LZ and C at 24h. DEGs are plotted as red dots and labeled with names

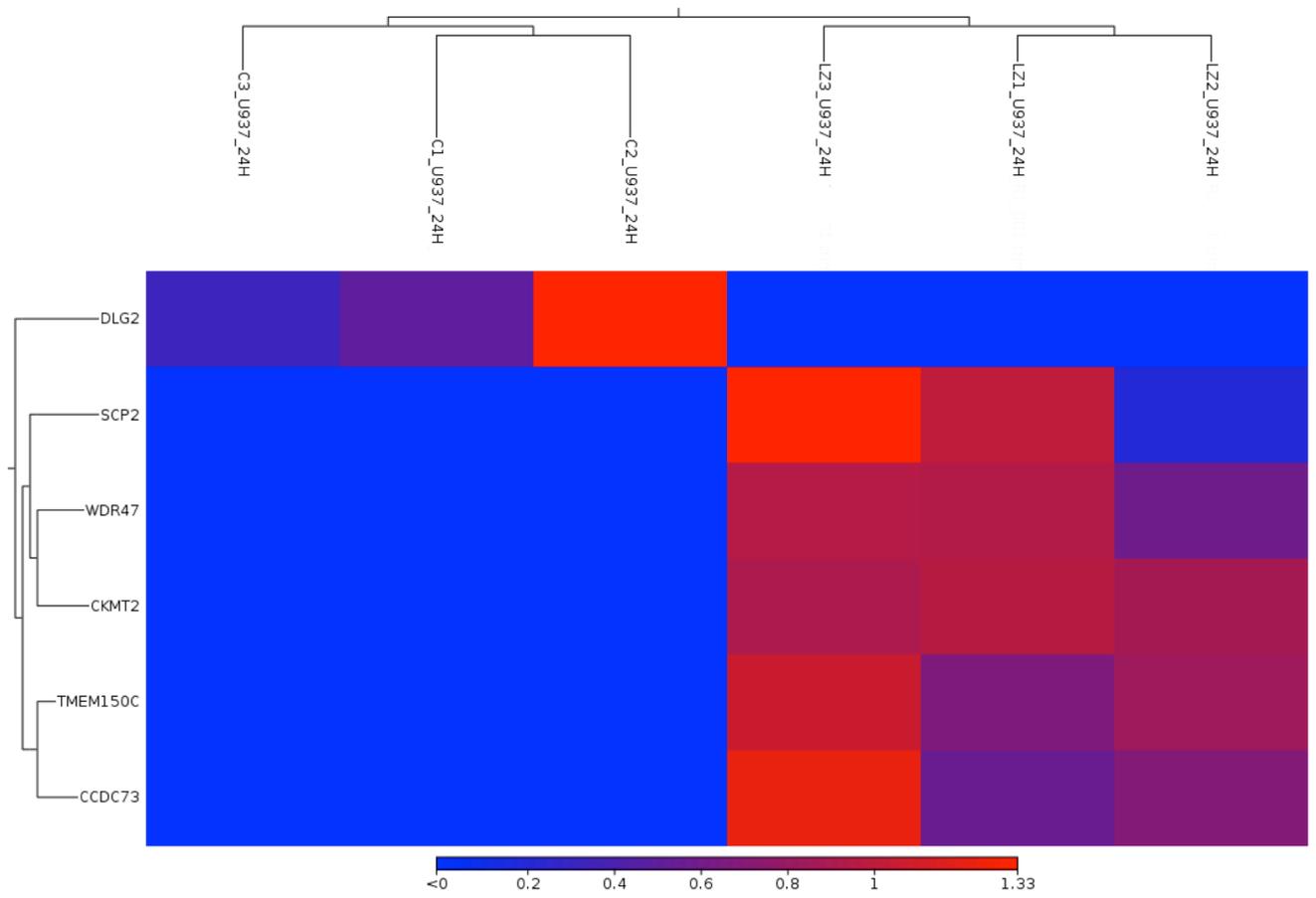


Figure S7: Heatmap of DEGs between LZ and C at 24h. Clusters from both rows and columns are merged by the maximum euclidean distance of their members.

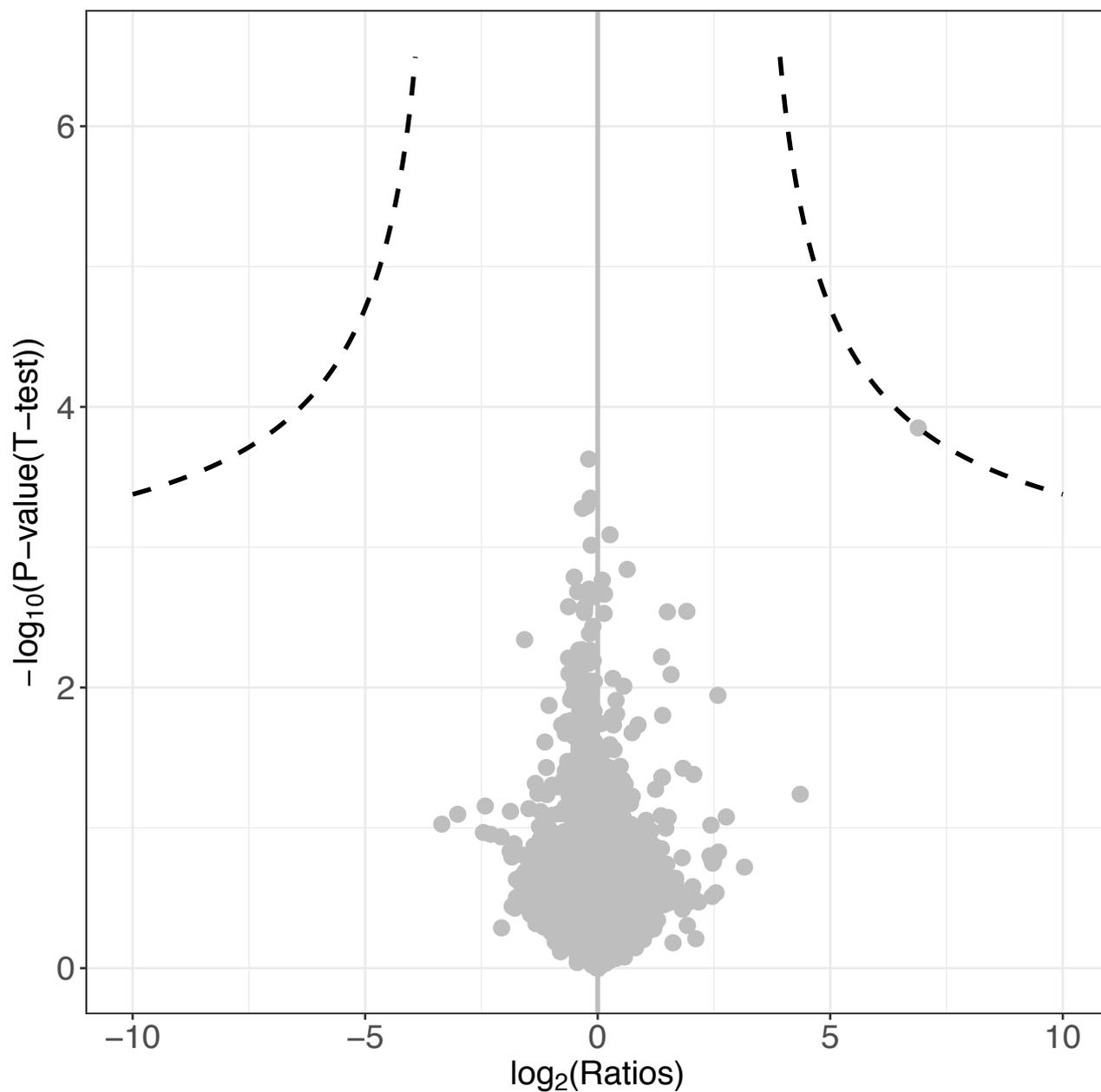


Figure S8. LC-MS/MS analysis, volcano plot shows the differences of protein abundance comparing Lysozyme-treated cells at 1h+24 vs Control cells at 1h+24. The dashed line marks the threshold of statistical significance with FDR < 0.05.

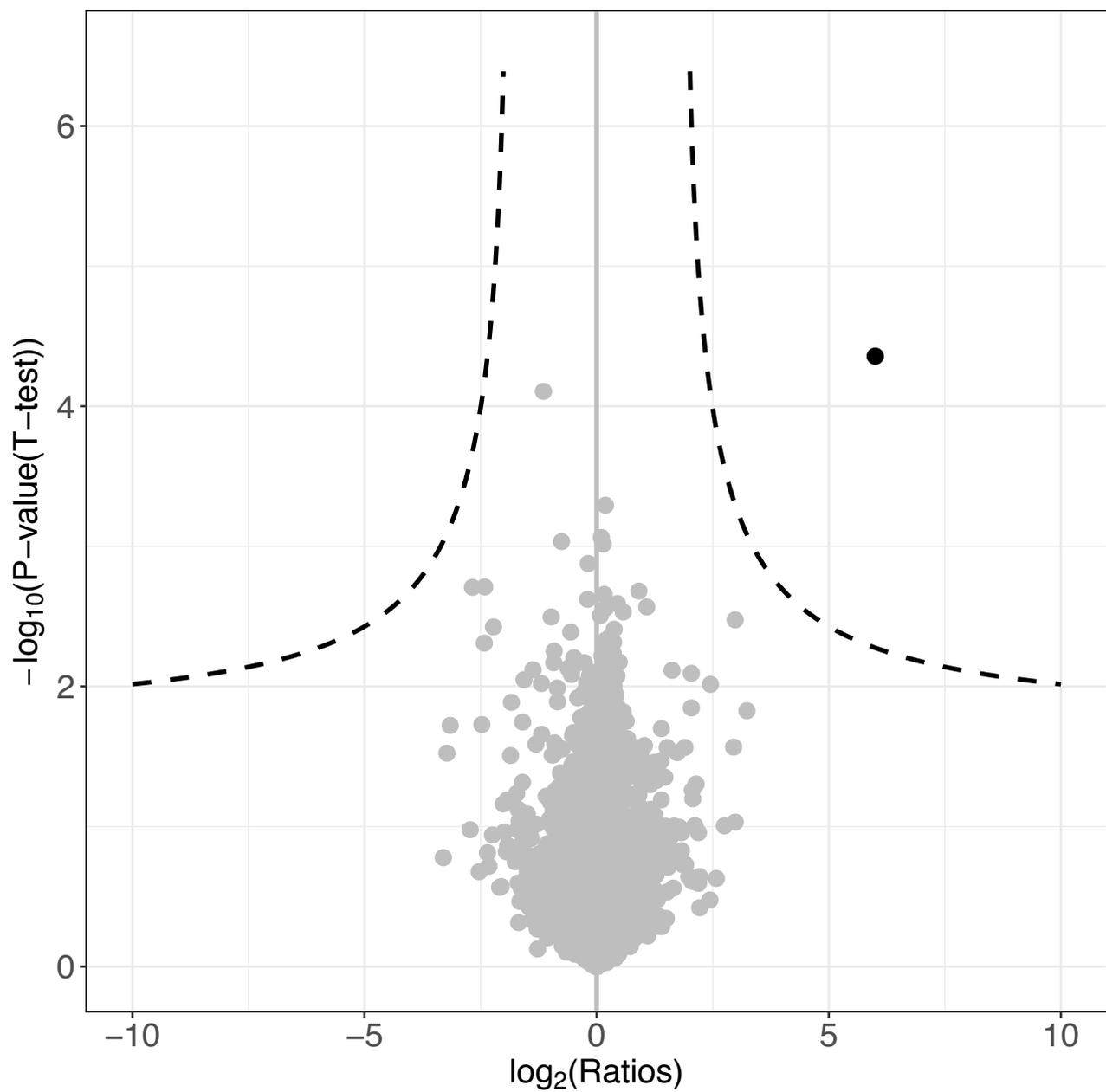


Figure S9. LC-MS/MS analysis, volcano plot shows the differences of protein abundance comparing Lysozyme-treated cells at 24h+24 vs Control cells at 24h+24. The dashed line marks the threshold of statistical significance with FDR < 0.05.