Supplementary Table 1. Transcriptomic datasets and experimental conditions.

Supplementary Table 2. All identified clusters with the average value of |log2(fold change)| in different growth conditions

Supplementary Table 3. The list of coexpressed genes including potential TFs in each cluster, annotated by COG categories, GO terms, KEGG Orthology with predicted operon number

Supplementary Table 4. The list of coexpressed genes from *M.alcaliphilum* 20ZR including potential TFs with their orthologs from *M.buryatense* 5GB1

Supplementary Table 5. Ratio of genes under the control of a each regulator in each cluster to the cluster size

Supplementary Table 6. Reproduction of GCN-based clusters in GRN

Supplementary Table 7. The average operon completeness for each cluster

Supplementary Table 8. Differential gene expression results in three growth conditions

*Legend for each Supplementary Table is represented left of the spreadsheet except Supplementary Table 1-2.*