


# Supplementary Materials: Co-expression networks for causal gene identification based RNA-seq data of *Corynebacterium pseudotuberculosis*

Edian F. Franco <sup>1,4</sup> , Pratip Rana <sup>2</sup> , Ana Lidia Queiroz Cavalcante <sup>1</sup> , Artur Silva <sup>1</sup> , Adriana R. Carneiro Folador <sup>1</sup> , Vasco Azevedo <sup>3</sup> , Preetam Ghosh <sup>2†</sup>  and Rommel T. J. Ramos <sup>1,3†</sup> \*

1. 1. Supplementary Figures

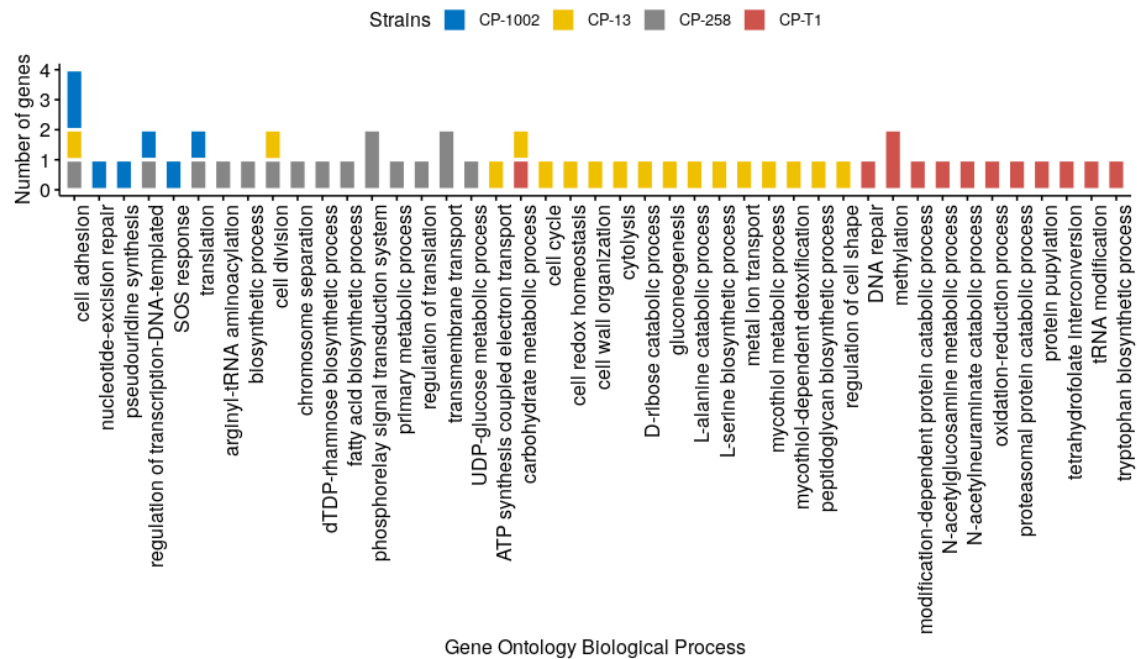
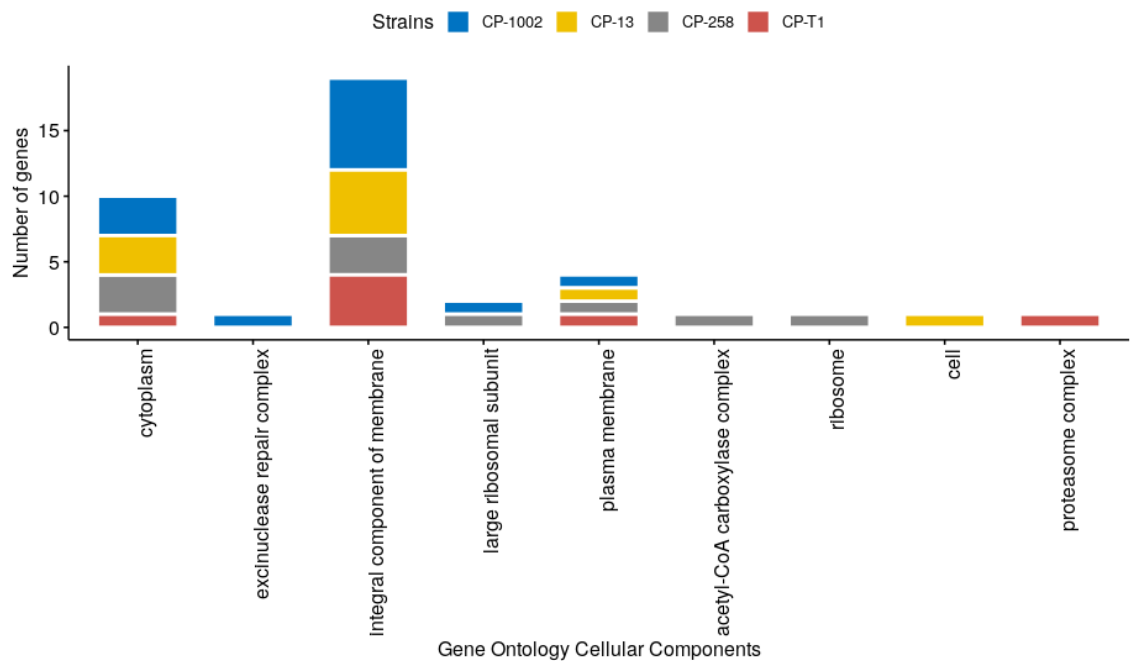
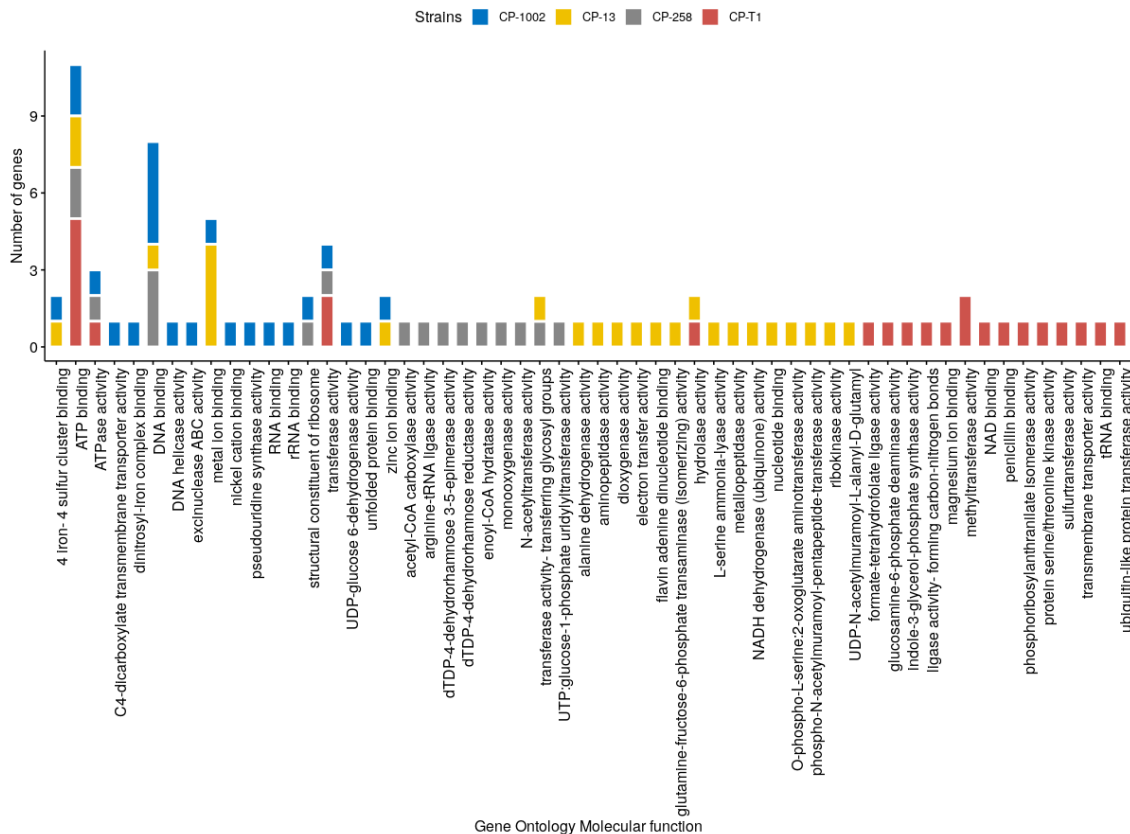


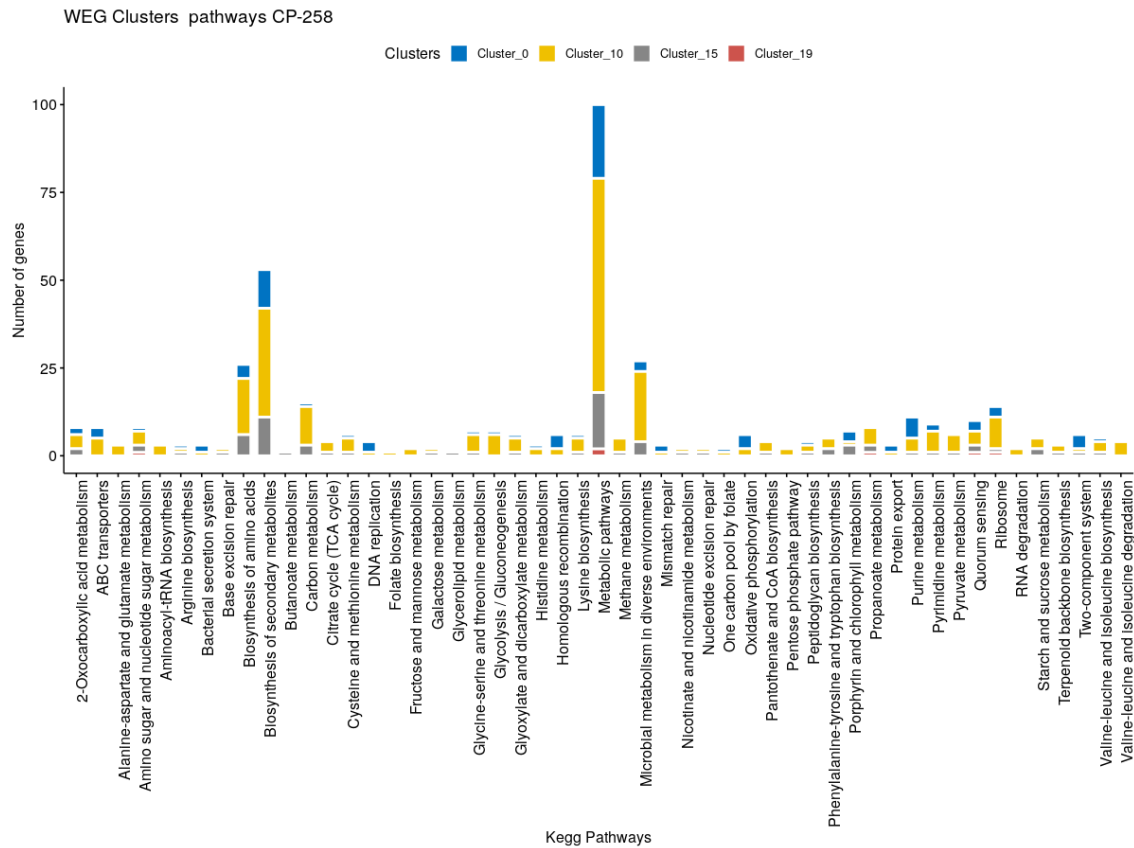
Figure S1. Biological process results of whole expressed genes in CP-1002, CP-258, CP-13, CP-T1



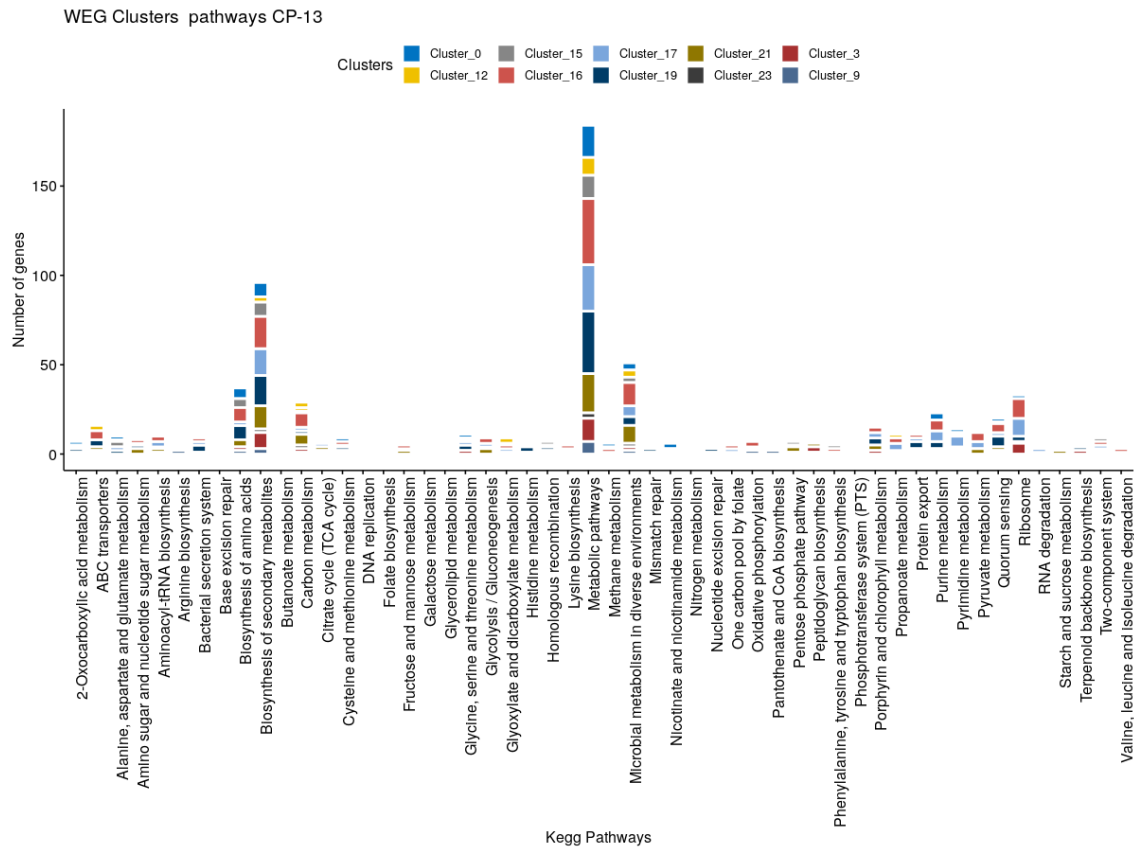
**Figure S2.** Cellular Components results of whole expressed genes in CP-1002, CP-258, CP-13, CP-T1



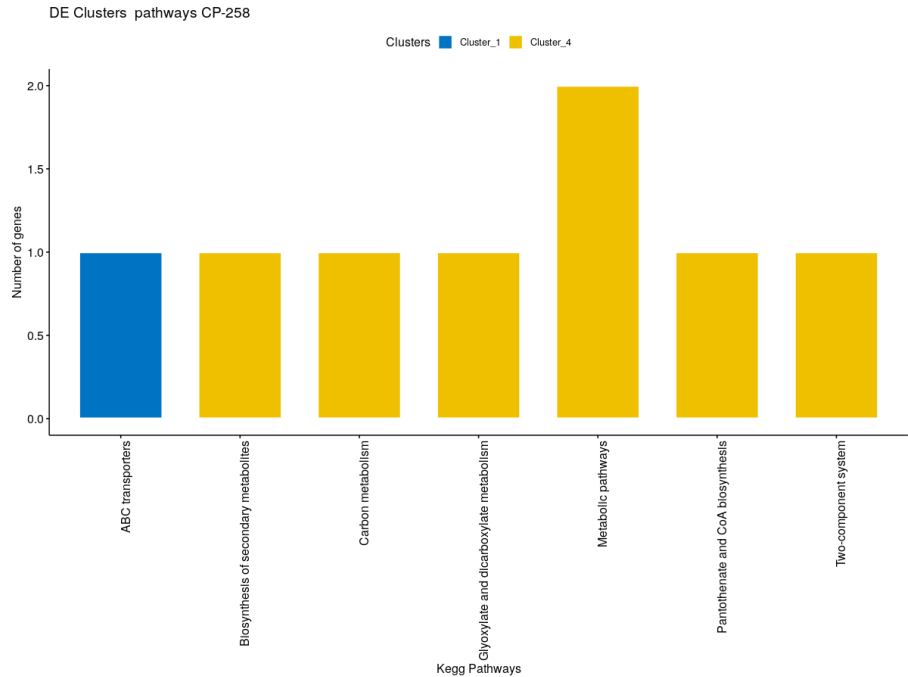
**Figure S3.** Molecular function results of whole expressed genes in CP-1002, CP-258, CP-13, CP-T1



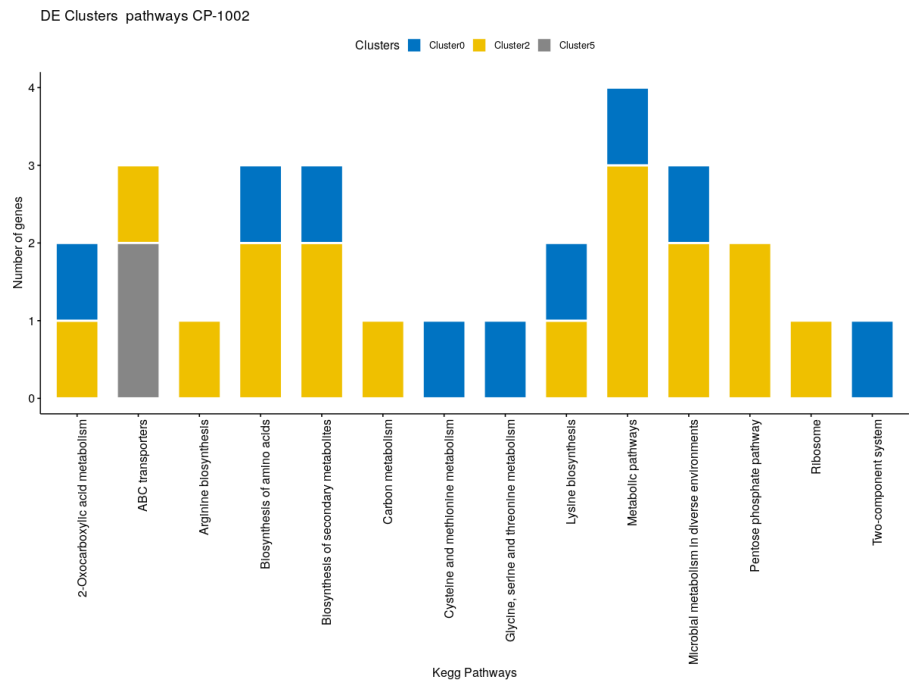
**Figure S4.** Pathways of the clusters where the influential genes are present in the whole expressed genes network in CP-258.



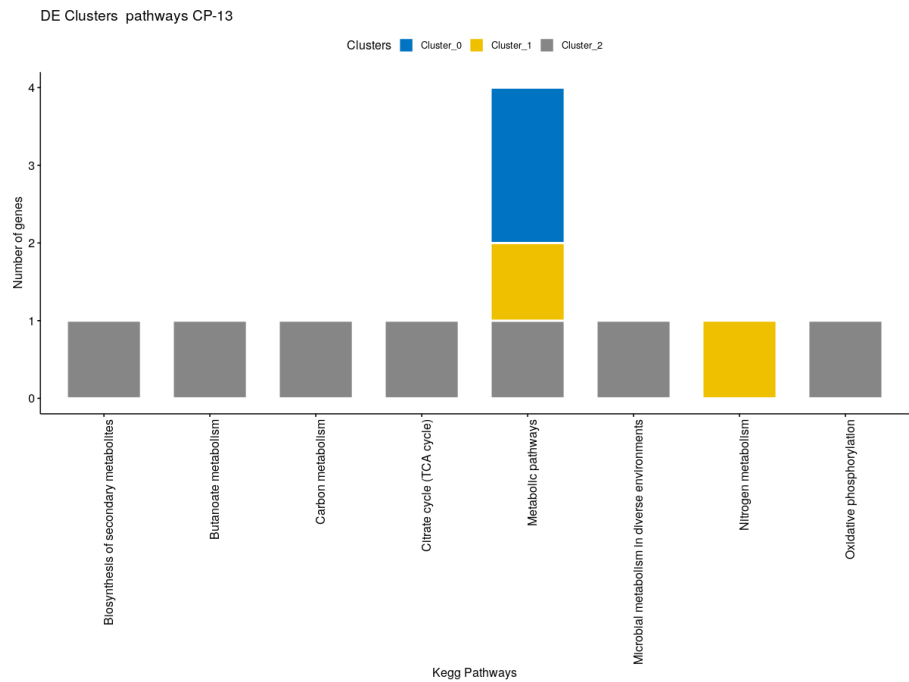
**Figure S5.** Pathways of the clusters where the influential genes are present in the whole expressed genes network in CP-13.



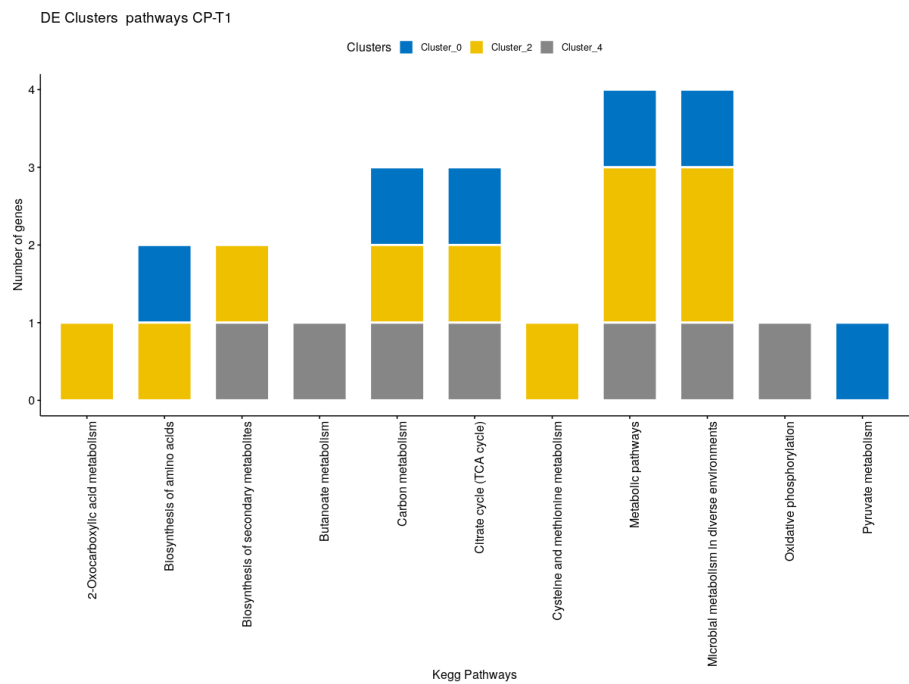
**Figure S6.** Pathways of the clusters where the influential genes are present in the Differentially expressed genes network in CP-258.



**Figure S7.** Pathways of the clusters where the influential genes are present in the Differentially expressed genes network in CP-1002.



**Figure S8.** Pathways of the clusters where the influential genes are present in the Differentially expressed genes network in CP-13.



**Figure S9.** Pathways of the clusters where the influential genes are present in the Differentially expressed genes network in CP-T1.