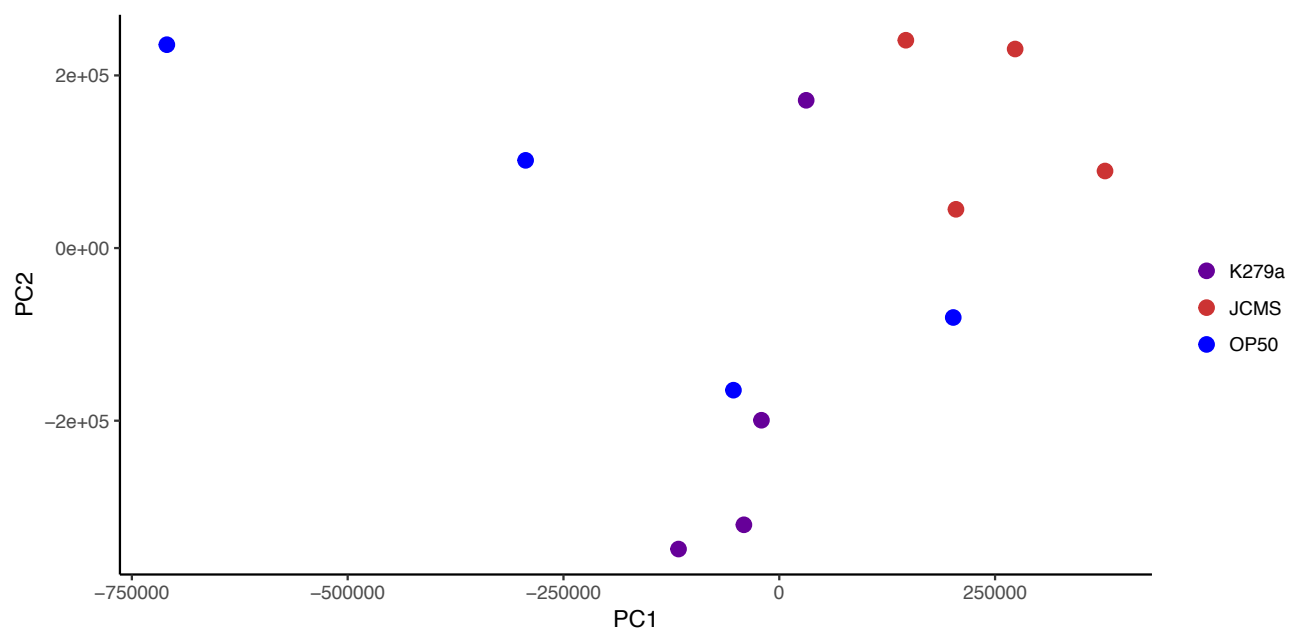


## Supplementary Material

# Transcriptomic, functional and network analyses reveal novel genes involved in the interaction between *Caenorhabditis elegans* and *Stenotrophomonas maltophilia*

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**Figure S1: Principal component analysis of expression profile biological replicates**

Singular value decomposition was used to construct a principle component analysis using the function ggplot in R within the ggplot2 package. PCA was used along with correlation coefficients to evaluate the similarity between four biological replicates for each bacterial treatment. Each point on the PCA represents the normalized expression data on K279a (purple), JCMS (red) and OP50 (blue). Replicates for treatment with JCMS and K279a are more tightly clustered while replicates for OP50 are loosely related. One replicate (556640A12) for OP50 was not included in downstream analysis because this sample had the lowest correlation coefficients (Table S2) and is the most un-clustered (upper left hand corner) sample on this PCA plot. The variance explained for principal component 1 is 32.27% and the variance explained for principal component 2 is 17.83%.