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* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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**Experiments were performed in three or five replicates. Independent replicate experiments on different days were performed to ensure reproducibility.**

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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**Number of replicates (biological/technical) for each experiment are mentioned in the figure legends. Biological replication refers to the experiments from independent cultures of the same strain whereas technical replicates were those that were done from the same culture of a strain. Data analysis and filtering methods are described in the Methods section “Screening of deletion mutants, classification and functional enrichment analysis**”. **RNA-sequencing data used in this work have been deposited in NCBI GEO with the accession code GSE104343 and reviewer token “mtabqsqebncphaz”.**

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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