Description of Additional Supplementary Files

TITLE:

Supplementary Data 1

Description:

Provides the primers list used in this study, the star method table as well as the p-value calculation and numbers of cell counted for the results presented in Figure 2. The non-parametric Wilcoxon test was used to compare means of 2 independent samples. The null hypothesis states that the distributions of both populations are identical. Assuming that the responses are continuous, the alternative is restricted to a shift in location. Data used to produce figures 2, 4a, 4b and 5b are provided in the corresponding spreadsheets. Signal localisation name: DifCyt = Diffuse, GranPeriNu = Granules Perinuclear, PostNuGran = Granules Posterior, AntNuGran = Granules Anterior, STURN = proximal STURN/FP.

TITLE:

Supplementary Data 2

Description:

Results of the proximity proteomes obtained from glucose starvation and during the quorum sensing differentiation process. Statistical enrichment analysis was performed using two-sided moderated t-statistic as described in the Methods section. Data present the p-values and ratio obtained for the given comparison as well as information on the protein localisation (Tryptag, DeepLoc), the presence of low-complexity regions (lcr_005)[1], GO term analysis and their identification in published datasets (Substrate of TbDYRK = Cayla2020[2], Presence in stress granules = Fritz2015[3], Identified as components of the quorum sensing pathway = Sif, Proteins upregulated in Stumpy and Slender =

Dejeung2016upSS/SL[4], Proteins identified as presenting expression regulation in Alba3 knock-out in methyl cellulose-derived stumpy or procyclic = Bevka2023alba3SS/Proc[5], Genes for which mRNA has been identified as cell cycle regulated = CCR[6]). condB = +glucose, condC = -glucose, early = early time point during differentiation, late = late time point during differentiation.

REFERENCES

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