**DATA ACCESS**

Reference files used to generate figures for this paper can be accessed at:

<https://github.com/CEGRcode/2023-Breugel_JournalXXXX>

All data files were de-duplicated

Most of the analyses were performed on **Scriptmanager v.014**, which can be downloaded at:

<https://github.com/CEGRcode/scriptmanager>

**Figures 2C-2H**

* ChIP-exo 5’ tags of TAP-tagged strains were NCIS normalized relative to the no tag [negative control](https://pubmed.ncbi.nlm.nih.gov/33692541/) (PMID: 33692541), and mapped to the TSSs of indicated gene classes.
* **Tag Pileup** function of Scriptmanager v0.14
* Load BED files – tRNA\_TSS\_YEP\_1000bp.bed
* Load BAM files
* Read 1, Strands – combined, tag shift – 6bp, bin size – 1 bp
* Sliding window – 3 bp
* Output file format: CDT
* **Calculate Scaling Factor**
* Load BAM files
* Load Blacklist Filter: YEP\_Blacklist\_181026.bed
* NCIS
* **Apply Scaling Factor**
* Load TAB files – load CDT files generated above
* Scaling factor – input scaling factors obtained above

**Supplemental Figures 2B-2C**

* ChIP-exo 5’ tags of TAP-tagged strains were NCIS normalized relative to the no tag [negative control](https://pubmed.ncbi.nlm.nih.gov/33692541/) (PMID: 33692541), and mapped to the TSSs of indicated gene classes.
* **Tag Pileup** function of Scriptmanager v0.14
* Load BED files – tRNA\_TSS\_YEP\_Fpt1\_250bp\_SORT.bed
* Load BAM files
* Read 1, Strands – combined, tag shift – 6bp, bin size – 1 bp
* Sliding window – 3 bp
* Output file format: CDT
* **Calculate Scaling Factor**
* Load BAM files
* Load Blacklist Filter: YEP\_Blacklist\_181026.bed
* NCIS
* **Apply Scaling Factor**
* Load TAB files – load CDT files generated above
* Scaling factor – input scaling factors obtained above