

Here we provide browsable metagene analysis for 5'P mRNA degradation profiles regarding samples analyzed in the manuscript:

*A functional connection between translation elongation and protein folding at the ribosome exit tunnel in Saccharomyces cerevisiae. Rodríguez-Galán, Juan J. García-Gómez, Iván V. Rosado, Wu Wei, Alfonso Méndez-Godoy, Benjamin Pillet, Alisa Alekseenko, Lars M. Steinmetz, Vicent Pelechano, Dieter Kressler and Jesús de la Cruz.*

Raw and processed sequencing data are deposited at Gene Expression Omnibus (GEO) with accession numbers GSE114899. Data was analyzed using *fivepseq* pipeline <http://pelechanolab.com/software/fivepseq/>

To explore interactive html files please go to the folder *fivepseq\_plot* and click on the html files. Please see additional information at the *fivepseq* manual.

Two different batch of experiments were performed. Same names as in GEO deposit where used for legend.

Batch 1, using 5Pseq:	Batch 2, using HT-5Pseq:
<ul style="list-style-type: none"><li>• rpl</li><li>• rpl_ssz</li><li>• rpl_zuo</li><li>• ssz</li><li>• wt</li><li>• zuo</li></ul>	<ul style="list-style-type: none"><li>• S14A_S14B_R136A</li><li>• W303</li><li>• Itv1</li><li>• ubi3_ub</li><li>• ubi3_ub_zuo1</li><li>• zuo1</li></ul>

## References:

Computational pipeline: Lilit Nersisyan, Maria Ropat, Vicent Pelechano. Improved computational analysis of ribosome dynamics from 5'P degradome data using *fivepseq*. bioRxiv 2020.01.22.915421; doi: <https://doi.org/10.1101/2020.01.22.915421>

5PSeq protocol: Pelechano V, Wei W, Steinmetz LM. Genome-wide quantification of 5'-phosphorylated mRNA degradation intermediates for analysis of ribosome dynamics. Nat Protoc. 2016 Feb;11(2):359-76. doi: 10.1038/nprot.2016.026. Epub 2016 Jan 28. PMID: 26820793; PMCID: PMC4732566.

HT-5PSeq protocol: Yujie Zhang, Vicent Pelechano. High-throughput 5'P sequencing reveals environmental regulated ribosome stalls at termination level. bioRxiv 2020.06.22.165134; doi: <https://doi.org/10.1101/2020.06.22.165134>