

Supplementary information

Table 1: Comparison of functionalities offered by selected published tools for Ribo-seq data quality control and visualization.

	<i>Ribo-seqC</i>	<i>Shoe laces</i> ¹	<i>riboviz</i> ²	<i>riboWaltz</i> ³	<i>Ribo-TISH</i> ⁴	<i>Ribo Profiling</i> ⁵	<i>system PipeR</i> ⁶	<i>RUST</i> ⁷	<i>ribo SeqR</i> ⁸
Automated standalone report	x	-	-	-	x	-	-	-	-
Side-by-side analysis of nuclear & organellar genome	x	-	-	-	-	-	-	-	-
Side-by-side analysis of multiple datasets	x	x	-	-	-	-	x	-	-
Read length distribution	x	x	x	x	x	x	-	x	x**
Read biotype distribution (biotypes covering the whole genome)	x	-	-	x	-	x	x	-	x**
Read length and biotype distribution	x	-	-	-	-	-	-	-	-
Codon usage (transcriptome-wide)	x	-	-	x	-	x	-	-	-
Codon usage (position-specific)	x	-	-	-	-	-	-	-	-
5' profiles for wide read length range (heatmap)	x	-	-	x	-	-	-	-	-
P-site profiles for wide read length range (heatmap)	x	-	-	x	-	-	-	x*	-
Automated selection of P-site read lengths	x	x	?	x	x	x	-	-	-
Automated per read length P-site offset calculation	x	x	?	-	-	-	-	-	-
Frame distribution	x	x	-	x	x	-	-	x	x
Per transcript 5'/P-site profiles	-	x	x	-	-	x	-	-	x

* A- instead of P-site profiles
** Shown in publication, but not documented in package.

References

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