Feature comparison matrix — columns (tools), left to right:

XPRESSyourself, Galaxy, RiboGalaxy, PausePred, Rfeet, anota2seq, RiboProfiling, Riborex, mQC, Shoelaces, SuperTranscripts, systemPipeR, ORFik, coMET, riboSeqR, Deeptools, Picard, ROSE, RUST, Xtail, RiboDiff, RiboTaper, Ribomap, Plastid, Riboviz, riboStreamR

Rows (features), top to bottom:

- Tuned for ribo-seq data
- Input raw data
- Input alignment files
- Input count tables
- Automated reference genome preparation
- Automated recursive CDS reference modification
- Pre-processing
- Alignment to genome
- Alignment to transcriptome
- Read counts to variable features
- Isoform quantification
- Quantify reads on motifs
- Differential Expression Analysis
- Read size distribution
- Pause prediction
- Periodicity
- Novel uORF discovery/functional annotation
- General quality control
- CDS and uORF visualization
- Metagene profile (all genes)
- rRNA probe summary
- Other customizable analyses
- Full automation from pre-processing to analysis

Legend:
- Includes feature (black)
- Partial functionality (light blue)
- Uses old or insufficient methods (gray)
- Unique to XPRESSyourself (green)