Includes feature
Partial functionality
Uses old or insufficient methods
Unique to XPRESSyourself

The short of the s

	Tuned for ribo-seq data											
Inputs	Input raw data											
	Input alignment files											
	Input count tables											
Curation	Automated reference genome preparation											
	Automated CDS reference modification											
processing	Pre-processing											
	Alignment to genome											
	Alignment to transcriptome											
Quantification	Read counts to variable features											
	Isoform quantification											
	Quantify reads on motifs											
	Translation efficiency calculation and analysis											
	Differential expression analysis											
Discovery	Novel uORF discovery/functional annotation											
	CDS and uORF visualization											
Onality Countrol	General quality control											
	Read size distribution											
	Pause prediction											
	Periodicity											
	Metagene profile (all genes)											
	rRNA probe summary and design											
Other	Other customizable analyses											
	Flexible organism choice											
	End-to-end automation											