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

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	Tuned for ribo-seq data																							
	Input raw data																							
Imputs	Input alignment files																							
Curation Processing	Input count tables																							
tion	Automated reference genome preparation																							
Cn _{tar.}	Automated CDS reference modification																							
	Pre-processing																							
	Alignment to genome																							
	Alignment to transcriptome																							
rion	Read counts to variable features																							
	Isoform quantification																							
antificati	Quantify reads on motifs																							
Quantification	Translation Efficiency Calculation																							
	Differential Expression Analysis																							
DiscoveN	Novel uORF discovery/functional annotation																							
Disco.	CDS and uORF visualization																							
	General quality control																							
Onality Coutrol	Read size distribution																							
	Pause prediction																							
	Periodicity																							
	Metagene profile (all genes)																							
	rRNA probe summary																							
, net	Other customizable analyses																							
Other	Full automation from pre-processing to analysis																							