RNA-seq Quality Control Tool Comparison

Features	RNA-SeQC	EVER-seq	CollectRNASeqMetrics
Version	1.1.0	1.0.6	0.1.18
Total and Duplicate Read Counts	Yes	Yes	Yes
Mapping Rate	Yes	Yes	Yes
Read Pairing Stats	Yes	Yes	w/ additional tool[a]
Exon, Intron, Intergenic Rate	Yes	Yes	Yes
Strand Specificity Quantification	Yes	Yes	Yes
Normalization by Downsampling	Yes	No	No
Provides RPKM	Yes	No	No
Coefficient of Variation of Coverage	Yes	No	Yes
3’ / 5’ Coverage Ratios	Yes	No	No
Gaps in Coverage Report	Yes	No	No
Stratification by Expression	Yes	No	No
NCV Plot (nucleotide distribution)	No	Yes	No
Average Transcript Coverage Plot	Yes	Yes	Yes
Coverage Plot – Dist. From 3’ End	Yes	No	No
MA Plot	No	Yes	No
Expression Standard Error	Read counts given	Yes	No
Clipping Profile	No	Yes	No
Alignment Mismatch Rate per Base	Yes	No	w/ additional tool[a]
Report Paired End vs. Single End	No	Yes	No
Fragment size distribution	Yes	Yes	No
rRNA content	Re-alignment or interval method	No	Interval Method
Summarizes metrics for multiple samples	Yes	No	No
Expression Correlation to Arrays	Yes	No	No
Expression Correlation to RNA-seq	Yes	2 Sample Max.	No
GC Content Bias Assessment	Coverage metrics stratified by GC content	Provides histogram of read GC content	None
Peer Reviewed	Yes	No	No

[a] CollectRNASeqMetrics is part of the Picard package of tools, some of which include these additional features.

RNA-SeQC:	http://www.broadinstitute.org/rna-seqc
EVER-seq	http://code.google.com/p/ever-seq
CollectRNASeqMetrics	http://picard.sourceforge.net