Table 1: Selected metrics based on the output of `rnaQUAST`, `HISAT2`, `DETONATE`, `TransRate` and `BUSCO` for the transcripts assembled by all ten tools on the *Escherichia coli* RNA-Seq data set. Details and much more statistics, complementing this evaluation, can be found in the electronic supplement, content S4–S10. The RSEM-EVAL score is divided by 10^9. Number of ambiguous bases is given in thousand. F1 score – an F1 score of 1 would mean that all nucleotides/contigs in the estimated true assembly were recovered with at least 90 % identity. KC score – k-mer compression score reflecting the similarity of each assembly to `DETONATE`s estimated "true" assembly. The Ex90N50 statistic is computed as usual N50 but limited to the top most highly expressed transcripts that represent 90 % of the total normalized expression data. Normalized scores in the range between 0 and 1 are displayed. Raw values for each metric and assembly tool are given in subscript next to the normalized values. In the last row, the summarized *metric score* (MS) of (0,1)-normalized scores is given for each assembly tool.

		`Trinity`	`Oases`	`Trans-ABySS`	`SOAP-Trans`	`Bridger`	`BinPacker`	`IDBA-Tran`	`Shannon`	`SPAdes-sc`	`SPAdes-rna`
	k-mer size	default	25,35,45,55,65	25,35,45,55,65	default	default	default	25,35,45,55,65	default	default	default
Evaluation metrics 1–20											
`HISAT2`											
1	Overall mapping rate	$0.70_{77.01}$	$0.24_{49.16}$	$1.00_{95.67}$	$0.36_{56.62}$	$0.86_{87.35}$	$0.60_{71.09}$	$0.00_{34.31}$	$0.69_{76.69}$	$0.88_{88.04}$	$0.89_{88.9}$
`rnaQUAST`											
2	Transcripts ≥1 000 nt	0.42_{347}	1.00_{743}	0.56_{446}	0.55_{439}	0.44_{363}	0.00_{66}	0.51_{414}	0.45_{372}	0.62_{489}	0.40_{340}
3	Misassemblies	0.87_{13}	0.00_{103}	0.83_{18}	0.99_{1}	0.50_{52}	0.92_{8}	1.00_{0}	0.48_{54}	0.88_{12}	0.90_{10}
4	Mismatches per transcript	$0.88_{0.37}$	$0.70_{0.71}$	$0.90_{0.32}$	$1.00_{0.13}$	$0.93_{0.27}$	$0.00_{2.05}$	$0.98_{0.17}$	$0.97_{0.19}$	$0.94_{0.25}$	$0.96_{0.21}$
5	Average alignment length	$0.20_{467.04}$	$0.19_{457.72}$	$0.00_{310.44}$	$0.07_{364.88}$	$0.21_{472.81}$	$1.00_{1100.77}$	$0.29_{540.83}$	$0.22_{482.66}$	$0.31_{558.9}$	$0.06_{359.2}$
6	95 %-assembled isoforms	0.95_{396}	1.00_{414}	0.00_{32}	0.60_{261}	0.92_{382}	0.01_{34}	0.57_{250}	0.95_{393}	0.47_{210}	0.41_{187}
7	Duplication ratio	$0.98_{1.012}$	$0.00_{1.443}$	$0.90_{1.044}$	$1.00_{1.002}$	$0.97_{1.014}$	$0.40_{1.267}$	$1.00_{1.001}$	$0.94_{1.027}$	$0.99_{1.006}$	$0.98_{1.009}$
8	Ex90N50	0.46_{369}	0.21_{229}	0.12_{177}	0.11_{173}	0.50_{393}	1.00_{675}	0.34_{304}	0.45_{363}	0.00_{111}	0.24_{245}
9	# full-length transcripts	0.92_{407}	0.94_{418}	0.99_{436}	0.96_{423}	0.90_{402}	0.00_{37}	0.89_{396}	0.90_{399}	1.00_{441}	0.75_{338}
`TransRate`											
10	Reference coverage	$1.00_{0.32}$	$0.97_{0.31}$	$0.07_{0.03}$	$0.61_{0.19}$	$0.98_{0.31}$	$0.00_{0.01}$	$0.50_{0.16}$	$0.96_{0.3}$	$0.44_{0.14}$	$0.55_{0.18}$
11	Mean ORF percentage	$1.00_{75.04}$	$0.69_{65.72}$	$0.92_{72.73}$	$0.90_{71.99}$	$0.99_{74.59}$	$0.00_{45.13}$	$0.90_{71.99}$	$0.94_{73.34}$	$0.81_{69.47}$	$0.96_{73.78}$
12	Optimal score[a]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
13	Percentage bases uncovered[a]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
14	Number of ambiguous bases	0.43_{2143}	0.00_{3602}	0.15_{3081}	0.30_{2579}	0.44_{2117}	1.00_{191}	0.45_{2069}	0.43_{2145}	0.36_{2370}	0.31_{2556}
`DETONATE`											
15	Nucleotide F1	$0.86_{0.64}$	$0.63_{0.49}$	$0.82_{0.61}$	$1.00_{0.74}$	$0.85_{0.64}$	$0.00_{0.06}$	$0.89_{0.66}$	$0.83_{0.62}$	$0.97_{0.71}$	$0.97_{0.72}$
16	Contig F1	$0.46_{0.03}$	$0.38_{0.03}$	$0.47_{0.03}$	$0.89_{0.06}$	$0.43_{0.03}$	0.00_{0}	$0.41_{0.03}$	$0.38_{0.03}$	$0.83_{0.06}$	$1.00_{0.07}$
17	KC score	$0.92_{0.82}$	$0.89_{0.79}$	$0.93_{0.82}$	$0.98_{0.86}$	$0.91_{0.81}$	$0.00_{0.16}$	$0.94_{0.83}$	$0.91_{0.81}$	$1.00_{0.87}$	$0.96_{0.84}$
18	RSEM EVAL	$0.79_{-0.21}$	$0.66_{-0.25}$	$1.00_{-0.15}$	$0.34_{-0.34}$	$0.93_{-0.17}$	$0.62_{-0.26}$	$0.00_{-0.44}$	$0.83_{-0.2}$	$0.86_{-0.19}$	$0.83_{-0.2}$
`BUSCO`											
19	Complete BUSCOs	0.83_{284}	0.88_{299}	0.88_{297}	0.94_{316}	0.83_{285}	0.00_{50}	0.87_{296}	0.82_{280}	1.00_{332}	0.73_{255}
20	Missing BUSCOs	0.96_{190}	1.00_{172}	1.00_{170}	0.99_{178}	0.96_{190}	0.00_{711}	0.95_{196}	0.95_{198}	1.00_{172}	0.96_{189}
Summed up metric (0,1)-score		13.61	10.36	11.53	12.59	13.55	5.55	11.49	13.08	13.37	12.85

[a] Not available for the *E. coli* and *A. thaliana* data set because this metric is only calculated by `TransRate` in the case of paired-end data.