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 *Homo sapiens* 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	$0.81_{91.9}$	$0.69_{88.04}$	$1.00_{98.34}$	$0.75_{89.93}$	$0.66_{86.83}$	$0.24_{72.6}$	$0.00_{64.61}$	$0.58_{84.27}$	$0.81_{92.04}$	$0.93_{95.95}$
`rnaQUAST`											
2	Transcripts ≥1 000 nt	0.22_{64061}	1.00_{207474}	0.20_{59779}	0.03_{27529}	0.11_{43201}	0.00_{22611}	0.00_{23516}	0.05_{31328}	0.05_{31039}	0.15_{49860}
3	Misassemblies	0.99_{3378}	0.00_{216127}	0.99_{2743}	1.00_{279}	0.97_{7329}	0.98_{5603}	1.00_{302}	0.99_{2837}	0.99_{2022}	0.98_{5126}
4	Mismatches per transcript	$0.74_{1.38}$	$0.77_{1.25}$	$0.93_{0.57}$	$1.00_{0.27}$	$0.73_{1.44}$	$0.00_{4.63}$	$0.91_{0.67}$	$0.77_{1.26}$	$0.88_{0.8}$	$0.78_{1.25}$
5	Average alignment length	$0.27_{795.23}$	$0.06_{343.48}$	$0.01_{246.85}$	0.00_{218}	$0.21_{654.41}$	$1.00_{2335.73}$	$0.13_{487.11}$	$0.23_{711.83}$	$0.09_{410.22}$	$0.09_{412.24}$
6	95 %-assembled isoforms	0.99_{6788}	0.10_{868}	1.00_{6824}	0.31_{2264}	0.28_{2105}	0.39_{2824}	0.07_{709}	0.00_{242}	0.23_{1755}	0.46_{3253}
7	Duplication ratio	$0.00_{2.396}$	$0.03_{2.355}$	$0.47_{1.743}$	$0.87_{1.187}$	$0.50_{1.708}$	$0.01_{2.389}$	$1.00_{1.012}$	$0.63_{1.53}$	$1.00_{1.015}$	$0.87_{1.192}$
8	Ex90N50	0.00_{326}	0.17_{666}	0.06_{441}	0.19_{711}	0.51_{1370}	1.00_{2381}	0.19_{708}	0.49_{1324}	0.42_{1186}	0.22_{782}
9	# full-length transcripts	0.97_{8930}	0.83_{8024}	1.00_{9110}	0.64_{6806}	0.89_{8440}	0.26_{4456}	0.00_{2783}	0.63_{6758}	0.46_{5676}	0.69_{7155}
`TransRate`											
10	Reference coverage	$0.87_{0.23}$	$0.33_{0.09}$	$1.00_{0.26}$	$0.34_{0.09}$	$0.31_{0.09}$	$0.27_{0.07}$	$0.31_{0.08}$	0.00_{0}	$0.30_{0.08}$	$0.42_{0.11}$
11	Mean ORF percentage	$0.64_{50.82}$	$0.00_{42.09}$	$0.72_{51.92}$	$0.44_{48.02}$	$0.22_{45.1}$	$0.04_{42.57}$	$0.76_{52.46}$	$1.00_{55.7}$	$0.30_{46.13}$	$0.31_{46.25}$
12	Optimal score[a]	$0.30_{0.13}$	$0.00_{0.02}$	$0.23_{0.11}$	$0.66_{0.27}$	$0.32_{0.14}$	$0.14_{0.07}$	$0.61_{0.25}$	$0.13_{0.07}$	$1.00_{0.4}$	$0.57_{0.23}$
13	Percentage bases uncovered[a]	$0.38_{0.59}$	$0.00_{0.94}$	$0.33_{0.63}$	$0.67_{0.33}$	$0.57_{0.42}$	$0.11_{0.84}$	$1.00_{0.02}$	$0.48_{0.5}$	$0.99_{0.03}$	$0.79_{0.21}$
14	Number of ambiguous bases	0.72_{286479}	0.00_{843235}	0.53_{437845}	0.78_{241236}	0.83_{206635}	1.00_{72918}	0.91_{138699}	0.94_{117068}	0.86_{177477}	0.71_{294083}
`DETONATE`											
15	Nucleotide F1	$0.59_{0.43}$	$0.08_{0.18}$	$0.77_{0.51}$	$0.89_{0.57}$	$0.71_{0.48}$	$0.00_{0.15}$	$0.86_{0.55}$	$0.42_{0.35}$	$0.97_{0.61}$	$1.00_{0.62}$
16	Contig F1	$0.08_{0.02}$	$0.09_{0.02}$	$0.99_{0.2}$	$1.00_{0.21}$	$0.05_{0.01}$	0.00_{0}	$0.08_{0.02}$	$0.11_{0.02}$	$0.07_{0.01}$	$0.06_{0.01}$
17	KC score	$0.87_{0.51}$	$0.00_{0.24}$	$1.00_{0.55}$	$0.42_{0.37}$	$0.51_{0.4}$	$0.40_{0.37}$	$0.14_{0.29}$	$0.58_{0.42}$	$0.47_{0.39}$	$0.60_{0.43}$
18	RSEM EVAL	$0.98_{-6.51}$	$0.45_{-11.82}$	$1.00_{-6.26}$	$0.72_{-9.03}$	$0.85_{-7.72}$	$0.62_{-10.03}$	$0.00_{-16.3}$	$0.73_{-8.96}$	$0.42_{-12.12}$	$0.91_{-7.16}$
`BUSCO`											
19	Complete BUSCOs	0.96_{4004}	0.79_{3588}	1.00_{4106}	0.39_{2625}	0.92_{3909}	0.13_{2009}	0.00_{1682}	0.70_{3385}	0.39_{2625}	0.58_{3089}
20	Missing BUSCOs	0.99_{1804}	0.93_{1922}	1.00_{1770}	0.83_{2164}	0.98_{1812}	0.00_{4078}	0.63_{2615}	0.84_{2133}	0.78_{2268}	0.92_{1949}
Summed up metric (0,1)-score		12.38	6.31	14.24	11.92	11.13	6.59	8.61	10.3	11.47	12.03

[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.