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 + EBOV 7h* 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	$0.91_{92.58}$	$0.53_{85.78}$	$1.00_{94.22}$	$0.79_{90.52}$	$0.72_{89.14}$	$0.46_{84.63}$	$0.00_{76.39}$	$0.82_{90.99}$	$0.87_{91.94}$	$0.95_{93.4}$
rnaQUAST											
2	Transcripts $\geq 1\,000$ nt	0.16_{31319}	1.00_{115596}	0.22_{37410}	0.00_{15251}	0.08_{23487}	0.08_{22928}	0.01_{16181}	0.20_{35785}	0.00_{15598}	0.07_{21867}
3	Misassemblies	0.94_{1294}	0.00_{18893}	0.75_{4769}	1.00_{125}	0.87_{2509}	0.87_{2649}	1.00_{203}	0.87_{2605}	0.90_{2042}	0.94_{1219}
4	Mismatches per transcript	$0.60_{1.75}$	$0.36_{2.52}$	$0.90_{0.75}$	$1.00_{0.44}$	$0.68_{1.49}$	$0.00_{3.67}$	$0.88_{0.83}$	$0.70_{1.43}$	$0.91_{0.72}$	$0.81_{1.07}$
5	Average alignment length	$0.29_{1040.88}$	$0.44_{1364.38}$	$0.04_{534.4}$	$0.00_{455.96}$	$0.20_{866.61}$	$1.00_{2505.43}$	$0.12_{697.75}$	$0.23_{918.85}$	$0.02_{489.2}$	$0.01_{470.16}$
6	95 %-assembled isoforms	0.90_{4696}	1.00_{5115}	0.74_{4004}	0.56_{3225}	0.50_{2965}	0.48_{2851}	0.00_{780}	0.50_{2964}	0.46_{2795}	0.71_{3850}
7	Duplication ratio	$0.78_{1.757}$	$0.00_{4.347}$	$0.80_{1.663}$	$0.98_{1.06}$	$0.87_{1.451}$	$0.74_{1.884}$	$1.00_{1.007}$	$0.72_{1.954}$	$1.00_{1.013}$	$0.95_{1.161}$
8	Ex90N50	0.56_{2839}	0.64_{3003}	0.19_{2039}	0.35_{2385}	0.52_{2745}	1.00_{3764}	0.15_{1967}	0.32_{2328}	0.53_{2766}	0.00_{1647}
9	# full-length transcripts	0.93_{8458}	1.00_{8861}	0.92_{8405}	0.77_{7569}	0.77_{7540}	0.64_{6844}	0.00_{3197}	0.76_{7524}	0.67_{7004}	0.71_{7226}
TransRate											
10	Reference coverage	$0.37_{0.08}$	$0.90_{0.12}$	$1.00_{0.13}$	$0.27_{0.08}$	$0.26_{0.08}$	$0.00_{0.06}$	$0.27_{0.08}$	$0.92_{0.12}$	$0.28_{0.08}$	$0.48_{0.09}$
11	Mean ORF percentage	$0.77_{52.15}$	$0.00_{43.82}$	$0.75_{51.97}$	$0.51_{49.38}$	$0.35_{47.64}$	$0.35_{47.66}$	$0.61_{50.41}$	$1.00_{54.69}$	$0.39_{48.01}$	$0.20_{45.99}$
12	Optimal score[a]	$0.35_{0.19}$	$0.00_{0.02}$	$0.12_{0.07}$	$0.64_{0.33}$	$0.33_{0.18}$	$0.20_{0.11}$	$0.76_{0.39}$	$0.04_{0.04}$	$1.00_{0.51}$	$0.57_{0.3}$
13	Percentage bases uncovered[a]	$0.39_{0.58}$	$0.00_{0.95}$	$0.35_{0.62}$	$0.87_{0.13}$	$0.51_{0.47}$	$0.20_{0.76}$	$1.00_{0.01}$	$0.25_{0.71}$	$0.98_{0.03}$	$0.80_{0.2}$
14	Number of ambiguous bases	0.82_{131284}	0.00_{413418}	0.74_{159092}	0.97_{77171}	0.90_{101788}	0.96_{82239}	1.00_{67564}	0.81_{134108}	0.97_{76646}	0.85_{120597}
DETONATE											
15	Nucleotide F1	$0.64_{0.46}$	$0.00_{0.2}$	$0.63_{0.46}$	$0.86_{0.55}$	$0.71_{0.49}$	$0.25_{0.3}$	$0.87_{0.56}$	$0.42_{0.37}$	$0.91_{0.57}$	$1.00_{0.61}$
16	Contig F1	$0.27_{0.01}$	$0.28_{0.01}$	$1.00_{0.05}$	$0.80_{0.04}$	$0.23_{0.01}$	0.00_{0}	$0.24_{0.01}$	$0.63_{0.03}$	$0.28_{0.01}$	$0.43_{0.02}$
17	KC score	$0.87_{0.55}$	$0.10_{0.45}$	$1.00_{0.57}$	$0.43_{0.49}$	$0.58_{0.51}$	$0.50_{0.5}$	$0.00_{0.43}$	$0.90_{0.55}$	$0.36_{0.48}$	$0.93_{0.56}$
18	RSEM EVAL	$1.00_{-1.62}$	$0.38_{-2.35}$	$0.98_{-1.64}$	$0.81_{-1.85}$	$0.85_{-1.8}$	$0.72_{-1.95}$	$0.00_{-2.8}$	$0.90_{-1.74}$	$0.52_{-2.19}$	$0.92_{-1.71}$
BUSCO											
19	Complete BUSCOs	1.00_{4119}	0.97_{4055}	1.00_{4121}	0.77_{3667}	0.93_{3979}	0.73_{3590}	0.00_{2134}	0.83_{3777}	0.76_{3644}	0.71_{3542}
20	Missing BUSCOs	1.00_{1759}	0.91_{1817}	0.98_{1771}	0.85_{1855}	0.96_{1785}	0.00_{2392}	0.28_{2217}	0.69_{1955}	0.88_{1835}	0.97_{1780}
Summed up metric (0,1)-score		13.54	8.5	14.11	13.24	11.81	9.17	8.18	12.5	12.7	13.0

[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.