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 *Mus musculus* 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	$0.89_{92.14}$	$0.82_{89.29}$	$0.93_{93.96}$	$0.86_{90.98}$	$0.88_{91.66}$	$0.00_{54.31}$	$0.38_{70.64}$	$0.76_{86.6}$	$0.93_{93.83}$	$1.00_{96.86}$
`rnaQUAST`											
2	Transcripts $\geq$1 000 nt	0.40_{21804}	1.00_{51832}	0.56_{29719}	0.21_{12603}	0.33_{18266}	0.00_{2037}	0.21_{12294}	0.30_{16915}	0.22_{13099}	0.35_{19367}
3	Misassemblies	0.99_{564}	0.00_{52668}	0.99_{612}	1.00_{61}	0.95_{2643}	0.99_{628}	1.00_{41}	0.96_{1927}	0.99_{570}	0.98_{1080}
4	Mismatches per transcript	$0.85_{0.84}$	$0.90_{0.63}$	$0.97_{0.32}$	$1.00_{0.16}$	$0.83_{0.91}$	$0.00_{4.61}$	$0.99_{0.19}$	$0.86_{0.8}$	$0.88_{0.71}$	$0.86_{0.8}$
5	Average alignment length	$0.52_{1216.86}$	$0.00_{406.08}$	$0.22_{752.81}$	$0.07_{519.96}$	$0.43_{1073.4}$	$1.00_{1972.81}$	$0.26_{811.99}$	$0.30_{877.71}$	$0.44_{1089.26}$	$0.32_{910.47}$
6	95 %-assembled isoforms	0.96_{6032}	0.02_{183}	1.00_{6281}	0.35_{2244}	0.35_{2236}	0.08_{554}	0.14_{967}	0.00_{71}	0.41_{2633}	0.51_{3269}
7	Duplication ratio	$0.39_{1.547}$	$0.00_{1.9}$	$0.17_{1.75}$	$0.97_{1.031}$	$0.62_{1.348}$	$0.62_{1.346}$	$1.00_{1.005}$	$0.75_{1.23}$	$1.00_{1.003}$	$0.85_{1.135}$
8	Ex90N50	0.00_{420}	0.48_{2044}	0.03_{530}	0.70_{2796}	0.79_{3100}	0.68_{2715}	0.37_{1672}	0.49_{2067}	1.00_{3814}	0.88_{3418}
9	# full-length transcripts	0.97_{8210}	0.71_{6293}	1.00_{8401}	0.86_{7375}	0.90_{7639}	0.00_{1014}	0.43_{4208}	0.57_{5248}	0.91_{7736}	0.93_{7859}
`TransRate`											
10	Reference coverage	$0.88_{0.22}$	$0.09_{0.02}$	$1.00_{0.25}$	$0.38_{0.1}$	$0.40_{0.1}$	$0.06_{0.02}$	$0.37_{0.09}$	0.00_{0}	$0.34_{0.08}$	$0.43_{0.11}$
11	Mean ORF percentage	$0.82_{52.21}$	$0.40_{45.36}$	$0.92_{53.79}$	$0.78_{51.45}$	$0.66_{49.56}$	$0.00_{38.86}$	$0.95_{54.28}$	$1.00_{55.04}$	$0.37_{44.85}$	$0.29_{43.58}$
12	Optimal score[a]	$0.53_{0.22}$	$0.00_{0.02}$	$0.25_{0.12}$	$1.00_{0.4}$	$0.42_{0.18}$	$0.29_{0.13}$	$0.72_{0.29}$	$0.43_{0.18}$	$0.94_{0.38}$	$0.41_{0.18}$
13	Percentage bases uncovered[a]	$0.43_{0.52}$	$0.00_{0.91}$	$0.31_{0.63}$	$0.88_{0.12}$	$0.55_{0.41}$	$0.34_{0.6}$	$1.00_{0.02}$	$0.54_{0.43}$	$1.00_{0.01}$	$0.64_{0.33}$
14	Number of ambiguous bases	0.60_{78726}	0.00_{188947}	0.46_{105153}	0.74_{53611}	0.67_{66954}	1.00_{6514}	0.79_{45526}	0.75_{52948}	0.75_{51575}	0.63_{73461}
`DETONATE`											
15	Nucleotide F1	$0.78_{0.42}$	$0.26_{0.19}$	$0.73_{0.4}$	$0.97_{0.51}$	$0.84_{0.45}$	$0.00_{0.07}$	$0.94_{0.5}$	$0.69_{0.38}$	$1.00_{0.52}$	$0.95_{0.5}$
16	Contig F1	$0.37_{0.01}$	0.07_{0}	$1.00_{0.02}$	$0.95_{0.02}$	$0.27_{0.01}$	0.00_{0}	$0.44_{0.01}$	$0.30_{0.01}$	$0.21_{0.01}$	$0.58_{0.01}$
17	KC score	$0.88_{0.66}$	$0.42_{0.47}$	$0.90_{0.67}$	$0.62_{0.55}$	$0.74_{0.6}$	$0.00_{0.28}$	$0.57_{0.53}$	$0.64_{0.56}$	$0.94_{0.69}$	$1.00_{0.71}$
18	RSEM EVAL	$0.97_{-2.23}$	$0.59_{-3.34}$	$1.00_{-2.15}$	$0.83_{-2.64}$	$0.92_{-2.38}$	$0.05_{-4.89}$	$0.00_{-5.03}$	$0.73_{-2.94}$	$0.70_{-3.01}$	$0.90_{-2.45}$
`BUSCO`											
19	Complete BUSCOs	0.97_{3895}	0.75_{3066}	1.00_{3992}	0.90_{3616}	0.98_{3914}	0.00_{310}	0.64_{2679}	0.68_{2829}	0.95_{3823}	0.94_{3773}
20	Missing BUSCOs	0.98_{1959}	0.85_{2476}	0.99_{1926}	0.97_{1987}	0.99_{1926}	0.00_{5871}	0.92_{2188}	0.84_{2534}	1.00_{1877}	1.00_{1880}
Summed up metric (0,1)-score		14.21	7.36	14.43	15.05	13.5	5.1	12.13	11.58	14.98	14.46

[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.