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 *Arabidopsis thaliana* 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	$0.96_{95.71}$	$0.88_{91.93}$	$1.00_{97.55}$	$0.73_{85.31}$	$0.85_{90.64}$	$0.34_{67.15}$	$0.82_{89.04}$	$0.00_{51.53}$	$0.93_{94.29}$	$0.92_{93.67}$
`rnaQUAST`											
2	Transcripts ≥1 000 nt	0.33_{13357}	1.00_{32647}	0.55_{19714}	0.17_{8709}	0.32_{12882}	0.00_{3775}	0.20_{9577}	0.29_{12018}	0.26_{11171}	0.26_{11160}
3	Misassemblies	0.84_{1212}	0.06_{6804}	0.00_{7227}	1.00_{51}	0.73_{1995}	0.84_{1233}	0.98_{201}	0.90_{769}	0.84_{1189}	0.94_{505}
4	Mismatches per transcript	$0.79_{1.32}$	$0.42_{3.47}$	$0.91_{0.61}$	$1.00_{0.1}$	$0.60_{2.43}$	$0.00_{5.9}$	$0.99_{0.14}$	$0.89_{0.72}$	$0.94_{0.43}$	$0.96_{0.34}$
5	Average alignment length	$0.55_{978.21}$	$0.89_{1232.69}$	$0.24_{745.09}$	$0.00_{561.75}$	$0.57_{990.35}$	$1.00_{1312.17}$	$0.38_{848.36}$	$0.64_{1044.9}$	$0.51_{944.39}$	$0.33_{807.42}$
6	95 %-assembled isoforms	0.80_{2302}	1.00_{2753}	0.65_{1960}	0.32_{1213}	0.63_{1909}	0.00_{489}	0.30_{1175}	0.67_{2004}	0.81_{2318}	0.77_{2237}
7	Duplication ratio	$0.88_{1.128}$	$0.00_{1.976}$	$0.66_{1.341}$	$1.00_{1.008}$	$0.94_{1.067}$	$0.85_{1.149}$	$1.00_{1.01}$	$0.82_{1.185}$	$1.00_{1.007}$	$0.98_{1.027}$
8	Ex90N50	0.83_{1451}	0.71_{1305}	0.41_{940}	0.00_{449}	0.99_{1636}	0.83_{1452}	0.30_{805}	1.00_{1654}	0.48_{1030}	0.66_{1239}
9	# full-length transcripts	0.81_{7219}	1.00_{8361}	0.96_{8133}	0.52_{5411}	0.80_{7163}	0.00_{2227}	0.63_{6087}	0.70_{6541}	0.91_{7800}	0.86_{7501}
`TransRate`											
10	Reference coverage	$0.69_{0.16}$	$0.90_{0.19}$	$1.00_{0.21}$	$0.65_{0.15}$	$0.57_{0.13}$	$0.00_{0.03}$	$0.64_{0.15}$	$0.65_{0.15}$	$0.67_{0.15}$	$0.69_{0.15}$
11	Mean ORF percentage	$0.57_{74.79}$	$0.38_{72.07}$	$0.41_{72.5}$	$1.00_{80.78}$	$0.56_{74.66}$	$0.00_{66.84}$	$0.99_{80.71}$	$0.66_{76.08}$	$0.55_{74.47}$	$0.63_{75.67}$
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	0.61_{35964}	0.00_{78762}	0.37_{53180}	0.72_{28632}	0.66_{33008}	1.00_{9081}	0.73_{27666}	0.70_{30178}	0.71_{29569}	0.69_{30621}
`DETONATE`											
15	Nucleotide F1	$0.85_{0.71}$	$0.31_{0.42}$	$0.62_{0.59}$	$0.95_{0.77}$	$0.86_{0.72}$	$0.00_{0.26}$	$0.95_{0.76}$	$0.70_{0.63}$	$1.00_{0.79}$	$0.99_{0.79}$
16	Contig F1	$0.73_{0.05}$	$0.43_{0.03}$	$0.59_{0.04}$	$0.59_{0.04}$	$0.58_{0.04}$	0.00_{0}	$0.44_{0.03}$	$0.57_{0.04}$	$0.87_{0.06}$	$1.00_{0.07}$
17	KC score	$0.90_{0.71}$	$0.77_{0.66}$	$1.00_{0.74}$	$0.66_{0.62}$	$0.79_{0.66}$	$0.29_{0.48}$	$0.77_{0.66}$	$0.00_{0.37}$	$0.92_{0.71}$	$0.94_{0.72}$
18	RSEM EVAL	$0.99_{-0.46}$	$0.83_{-0.6}$	$1.00_{-0.45}$	$0.69_{-0.73}$	$0.90_{-0.54}$	$0.43_{-0.96}$	$0.75_{-0.67}$	$0.00_{-1.34}$	$0.84_{-0.59}$	$0.87_{-0.57}$
`BUSCO`											
19	Complete BUSCOs	1.00_{1117}	0.99_{1108}	1.00_{1119}	0.93_{1058}	0.98_{1103}	0.00_{262}	0.78_{930}	0.92_{1049}	0.95_{1074}	0.88_{1012}
20	Missing BUSCOs	1.00_{219}	0.97_{248}	0.99_{224}	0.97_{248}	0.99_{229}	0.00_{1162}	0.95_{269}	0.92_{296}	0.99_{225}	0.95_{264}
Summed up metric (0,1)-score		14.15	11.53	12.36	11.9	13.31	5.57	12.6	11.03	14.18	14.3

[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.