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 *Candida albicans* 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$_{97.32}$	0.60$_{93.61}$	1.00$_{98.45}$	0.73$_{95.12}$	0.86$_{96.72}$	0.85$_{96.66}$	0.00$_{86.34}$	0.84$_{96.51}$	0.92$_{97.51}$	0.92$_{97.43}$
`rnaQUAST`											
2	Transcripts $\geq$1 000 nt	0.09$_{3417}$	1.00$_{9813}$	0.74$_{7979}$	0.00$_{2769}$	0.18$_{4038}$	0.21$_{4267}$	0.03$_{2949}$	0.19$_{4077}$	0.10$_{3504}$	0.17$_{3939}$
3	Misassemblies	0.89$_{72}$	0.00$_{613}$	0.27$_{449}$	1.00$_{9}$	0.62$_{236}$	0.59$_{259}$	1.00$_{8}$	0.41$_{362}$	0.91$_{60}$	0.88$_{82}$
4	Mismatches per transcript	0.27$_{1.82}$	0.09$_{2.12}$	0.58$_{1.29}$	1.00$_{0.57}$	0.17$_{2}$	0.00$_{2.28}$	0.86$_{0.81}$	0.75$_{1}$	0.28$_{1.8}$	0.19$_{1.96}$
5	Average alignment length	0.56$_{969.33}$	0.53$_{941.6}$	0.29$_{773.58}$	0.00$_{567.17}$	0.79$_{1131.33}$	0.87$_{1189.55}$	0.50$_{922.1}$	0.16$_{678.95}$	1.00$_{1279.41}$	0.85$_{1171.71}$
6	95 %-assembled isoforms	0.46$_{4146}$	0.79$_{4808}$	1.00$_{5214}$	0.03$_{3290}$	0.39$_{4005}$	0.40$_{4033}$	0.00$_{3238}$	0.25$_{3736}$	0.61$_{4437}$	0.66$_{4533}$
7	Duplication ratio	0.97$_{1.039}$	0.00$_{2.25}$	0.27$_{1.916}$	1.00$_{1.007}$	0.92$_{1.105}$	0.89$_{1.136}$	1.00$_{1.003}$	0.67$_{1.412}$	1.00$_{1.001}$	0.95$_{1.059}$
8	Ex90N50	0.73$_{1862}$	0.40$_{1588}$	0.49$_{1664}$	0.14$_{1374}$	0.80$_{1923}$	0.74$_{1876}$	0.00$_{1257}$	0.08$_{1321}$	1.00$_{2090}$	0.93$_{2034}$
9	# full-length transcripts	0.76$_{1732}$	0.91$_{1836}$	1.00$_{1895}$	0.08$_{1274}$	0.71$_{1698}$	0.71$_{1701}$	0.00$_{1223}$	0.38$_{1480}$	0.93$_{1847}$	0.91$_{1837}$
`TransRate`											
10	Reference coverage	0.06$_{0.18}$	0.31$_{0.24}$	1.00$_{0.38}$	0.13$_{0.2}$	0.00$_{0.17}$	0.00$_{0.17}$	0.12$_{0.2}$	0.62$_{0.3}$	0.02$_{0.17}$	0.13$_{0.2}$
11	Mean ORF percentage	0.51$_{81.69}$	0.33$_{79.54}$	0.49$_{81.47}$	0.71$_{84.15}$	0.32$_{79.4}$	0.26$_{78.65}$	0.65$_{83.37}$	1.00$_{87.69}$	0.13$_{77.02}$	0.00$_{75.46}$
12	Optimal score[a]	0.83$_{0.46}$	0.05$_{0.06}$	0.00$_{0.03}$	0.88$_{0.48}$	0.65$_{0.36}$	0.66$_{0.37}$	0.75$_{0.41}$	0.04$_{0.05}$	1.00$_{0.54}$	0.73$_{0.41}$
13	Percentage bases uncovered[a]	0.85$_{0.13}$	0.00$_{0.87}$	0.05$_{0.82}$	0.98$_{0.02}$	0.64$_{0.31}$	0.59$_{0.36}$	1.00$_{0}$	0.44$_{0.48}$	1.00$_{0}$	0.82$_{0.16}$
14	Number of ambiguous bases	0.96$_{9391}$	0.00$_{26010}$	0.20$_{22581}$	0.98$_{8947}$	0.88$_{10651}$	0.86$_{11072}$	1.00$_{8652}$	0.76$_{12793}$	0.97$_{9173}$	0.89$_{10567}$
`DETONATE`											
15	Nucleotide F1	0.92$_{0.73}$	0.00$_{0.51}$	0.37$_{0.59}$	0.94$_{0.73}$	0.99$_{0.74}$	0.92$_{0.73}$	0.93$_{0.73}$	0.54$_{0.64}$	1.00$_{0.74}$	0.97$_{0.74}$
16	Contig F1	0.81$_{0.08}$	0.78$_{0.08}$	1.00$_{0.08}$	0.44$_{0.06}$	0.49$_{0.06}$	0.50$_{0.07}$	0.00$_{0.05}$	0.60$_{0.07}$	0.42$_{0.06}$	0.25$_{0.06}$
17	KC score	0.70$_{0.68}$	0.36$_{0.62}$	1.00$_{0.73}$	0.28$_{0.6}$	0.71$_{0.68}$	0.71$_{0.68}$	0.00$_{0.55}$	0.92$_{0.72}$	0.85$_{0.71}$	0.77$_{0.69}$
18	RSEM EVAL	1.00$_{-0.33}$	0.68$_{-0.42}$	0.96$_{-0.34}$	0.57$_{-0.45}$	0.93$_{-0.35}$	0.89$_{-0.36}$	0.00$_{-0.61}$	0.89$_{-0.36}$	0.86$_{-0.37}$	0.93$_{-0.35}$
`BUSCO`											
19	Complete BUSCOs	0.65$_{1355}$	0.71$_{1382}$	0.87$_{1461}$	0.00$_{1042}$	0.78$_{1416}$	0.78$_{1416}$	0.06$_{1070}$	0.10$_{1088}$	1.00$_{1523}$	0.95$_{1499}$
20	Missing BUSCOs	0.70$_{164}$	0.79$_{140}$	0.90$_{109}$	0.40$_{248}$	0.81$_{133}$	0.81$_{135}$	0.43$_{240}$	0.00$_{359}$	1.00$_{81}$	0.97$_{88}$
Summed up metric (0,1)-score		13.63	8.33	12.49	10.28	12.64	12.24	8.31	9.63	15.0	13.86

[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.