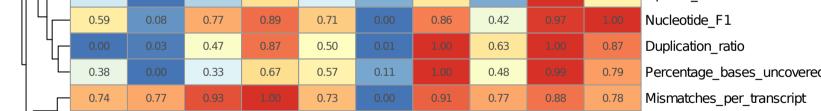
## Metric (0,1)–norm. scores Homo sapiens 0.09 0.08 0.11 0.06 Contig F1 Transcripts 1000\_bp 0.22 0.15 0.20 0.11 Average alignment length 0.27 0.06 0.21 0.13 0.23 0.09 0.09 0.51 0.42 Ex90N50 0.17 0.06 0.19 0.19 0.49 0.22 Full length transcripts 0.83 0.64 0.89 0.26 0.63 0.46 0.69 0.79 0.39 0.13 0.70 0.39 0.58 Complete BUSCOs 0.81 0.69 0.75 0.66 0.24 0.58 0.81 Overall mapping rate RSEM EVAL 0.45 0.72 0.85 0.73 0.42 0.62 KC score 0.87 0.42 0.51 0.40 0.14 0.58 0.47 0.60 Perc95 assembled isoforms 0.31 0.28 0.39 0.23 0.46 0.87 0.33 0.34 0.31 0.27 0.31 0.30 0.42 Reference coverage Mean ORF percentage 0.64 0.72 0.22 0.76 0.30 0.31 0.44 0.57 Optimal score 0.23 0.66 0.13 0.30 0.32 0.14 0.61 0.59 0.77 0.71 0.42 Nucleotide F1 0.08 0.89 0.86



	ŀ	0.00	0.03	0.47	0.87	0.50	0.01	1.00	0.63	1.00	0.87	Duplication_ratio
L		0.38	0.00	0.33	0.67	0.57	0.11	1.00	0.48	0.99	0.79	Percentage_bases_uncovered
		0.74	0.77	0.93	1.00	0.73	0.00	0.91	0.77	0.88	0.78	Mismatches_per_transcript
			0.93	1.00	0.83	0.98		0.63	0.84	0.78	0.92	Missing_BUSCOs
'	]			0.99	1.00		0.98	1.00	0.99	0.99		Misassemblies
	_											

Percentage_bases_uncovered	0.79	0.99	0.48	1.00	0.11	0.57	0.67	0.33	0.00	0.38	
Mismatches_per_transcript	0.78	0.88	0.77	0.91	0.00	0.73	1.00	0.93	0.77	0.74	
Missing_BUSCOs	0.92	0.78	0.84	0.63		0.98	0.83	1.00	0.93	0.99	
Misassemblies	0.98	0.99	0.99	1.00	0.98	0.97	1.00	0.99	0.00	0.99	] _
Number of ambiguous base	0.71	0.86	0.04	0.01	1.00	U 83	0.79	0.53	0.00	0.72	

4 4	0.99	0.93	1.00	0.83	0.98	0.00	0.63	0.84	0.78	0.92	Missing_BUSCOs
	0.99		0.99	1.00	0.97	0.98	1.00	0.99	0.99	0.98	Misassemblies
Ч	0.72	0.00	0.53	0.78	0.83	1.00	0.91	0.94	0.86	0.71	Number_of_ambiguous_bases
	Trinity	Oases	Trans.ABySS	SOAP denovo. Trans	Bridger	BinPacker	IDBA.Tran	Shannon	SPAdes.sc	SPAdes.rna	