Metric (0,1)–norm. scores Homo sapiens simulated 0.72 0.50 0.84 0.85 0.51 0.77 0.79 KC score RSEM EVAL 0.75 0.68 0.86 0.86 0.44 0.74 0.83 Overall mapping rate 0.62 0.89 0.79 Missing BUSCOs 0.74 0.65 0.90 Ex90N50 0.78 0.75 0.79 0.51 0.60 0.46 0.41 0.45 0.20 0.43 0.68 Perc95 assembled isoforms Full length transcripts 0.71 0.45 0.62 0.65 0.18 0.46 0.57 Complete BUSCOs 0.77 0.78 0.47 0.61 0.80 0.16 Mean ORF percentage 0.63 0.81 0.52 0.64 0.29 0.36 Misassemblies 0.81 0.70 0.85 0.76 0.89 0.86 Duplication ratio 0.77 0.84 0.90 0.82 0.88 Number of ambiguous bases Percentage bases uncovered 0.40 0.63 0.81 0.74 0.80 0.71 0.49 0.90 0.86 0.83 0.61 0.81 0.67 0.41

Nucleotide F1 Average alignment length 0.06 0.11 0.51 0.64 0.14 0.09 0.56 0.24 0.17 0.11 0.20 0.14 Transcripts 1000 bp

Reference coverage 0.34 0.74 0.16 0.17 0.22 0.14 0.09 0.35 Contig F1 0.06 0.13 0.31 0.54 0.43 Mismatches per_transcript 0.44 0.82 0.85 0.14 0.23 0.13 0.22 0.47 0.43 0.29 0.26 0.74 0.40 Optimal score 0ases Bridger Trinity SPAdes.sc SPAdes.rna Trans.ABySS SOAP denovo. Trans BinPacker Shannon IDBA.Tran