Metric (0,1)–norm. scores Homo sapiens + EBOV 7h 0.16 0.22 0.08 0.20 Transcripts 1000 bp Average alignment length 0.29 0.44 0.20 0.12 0.23 Ex90N50 0.56 0.64 0.19 0.35 0.52 0.15 0.32 0.53 0.57 Optimal score 0.35 0.12 0.64 0.33 0.20 0.76 Duplication ratio 0.78 0.80 0.87 0.74 0.72 0.75 0.87 0.87 0.87 0.90 Misassemblies Number of ambiguous bases 0.82 0.74 0.90 0.81 0.85 0.60 0.90 0.70 0.81 Mismatches per transcript 0.36 0.68 0.39 0.35 0.87 0.51 0.20 0.25 0.80 Percentage bases uncovered Nucleotide F1 0.64 0.63 0.86 0.71 0.25 0.42 0.85 0.28 0.69 0.88 Missing BUSCOs Perc95 assembled isoforms 0.74 0.56 0.50 0.50 0.71 0.90 0.48 0.46 Full length transcripts 0.77 0.77 0.67 0.71 0.64 0.76 0.77 0.76 0.71 Complete BUSCOs 0.73 0.83 Overall mapping rate 0.53 0.79 0.72 0.46 0.82 0.87 0.38 0.81 0.85 0.72 0.90 0.52 RSEM EVAL Reference coverage 0.37 0.90 0.27 0.26 0.27 0.28 0.48 0.43 Contig F1 0.27 0.28 0.80 0.23 0.24 0.63 0.28 Mean ORF percentage 0.77 0.75 0.39 0.20 0.51 0.35 0.35 0.61 0.87 0.43 0.58 0.50 0.90 0.36 KC score Bridger Trinity **Oases** Shannon SPAdes.rna Trans.ABySS SOAP denovo. Trans BinPacker SPAdes.sc IDBA.Tran