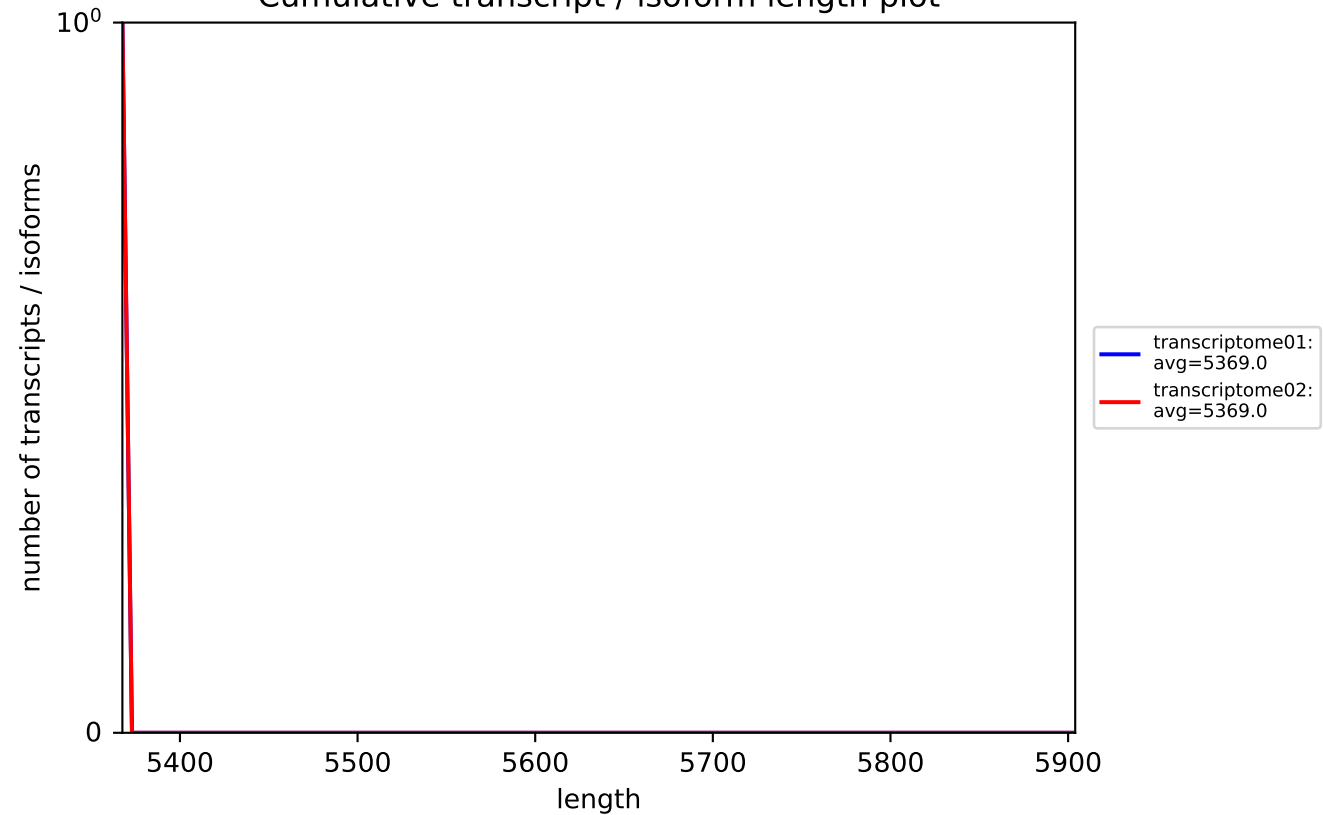


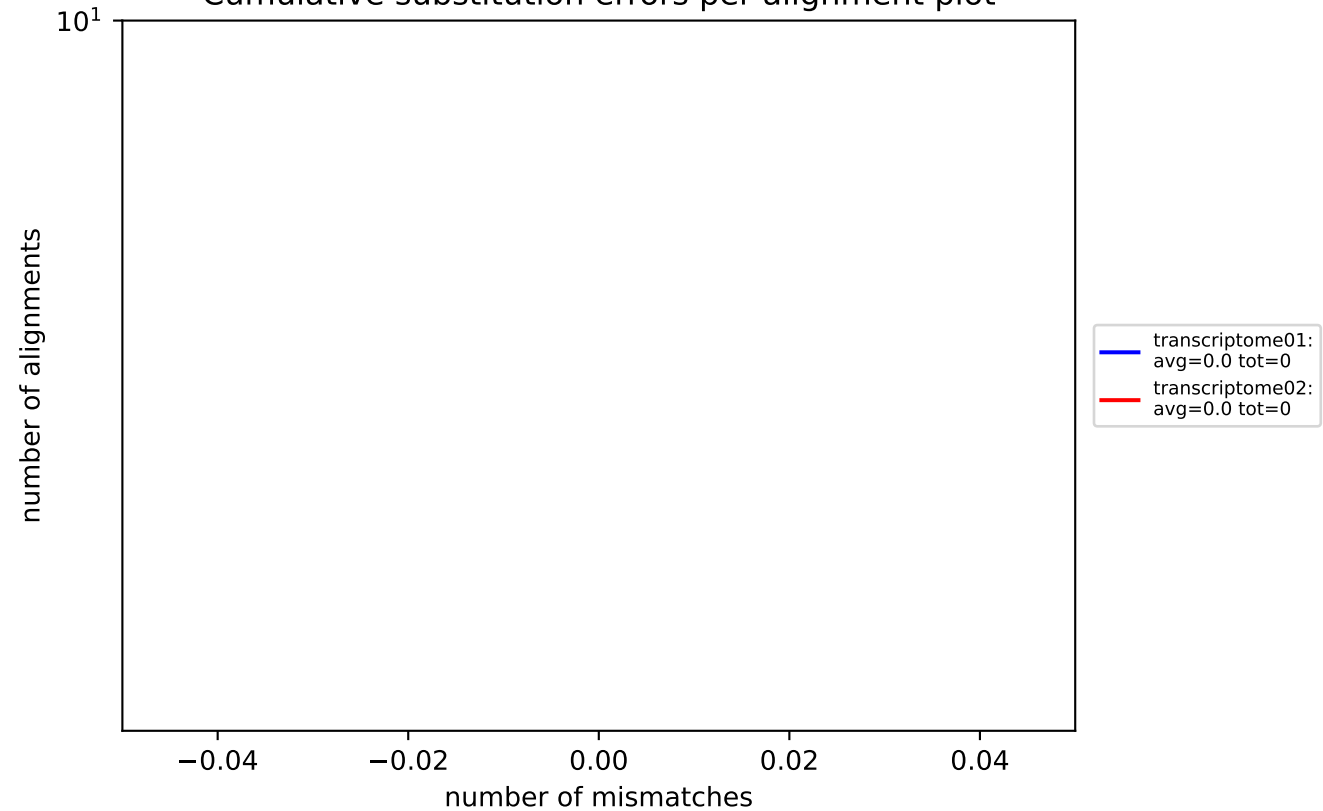
# Short report

	transcriptome01	transcriptome02
Genes	1	1
Avg. number of exons per isoform	1.0	1.0
Transcripts	1	1
Transcripts > 500 bp	1	1
Transcripts > 1000 bp	1	1
Aligned	1	1
Uniquely aligned	0	0
Multiply aligned	1	1
Unaligned	0	0
Avg. aligned fraction	1.0	1.0
Avg. alignment length	5369.0	5369.0
Avg. mismatches per transcript	0.0	0.0
Misassemblies	0	0
Database coverage	1.0	1.0
Duplication ratio	4.0	8.0
Relative database coverage	0.0	0.0
5000%-assembled genes	0	0
9500%-assembled genes	0	0
5000%-covered genes	0	0
9500%-covered genes	0	0
5000%-assembled isoforms	0	0
9500%-assembled isoforms	0	0
5000%-covered isoforms	0	0
9500%-covered isoforms	0	0
Mean isoform coverage	1.0	1.0
Mean isoform assembly	1.0	1.0
5000%-matched	0	0
9500%-matched	0	0
Unannotated	0	0
Mean fraction of transcript matched	1.0	1.0

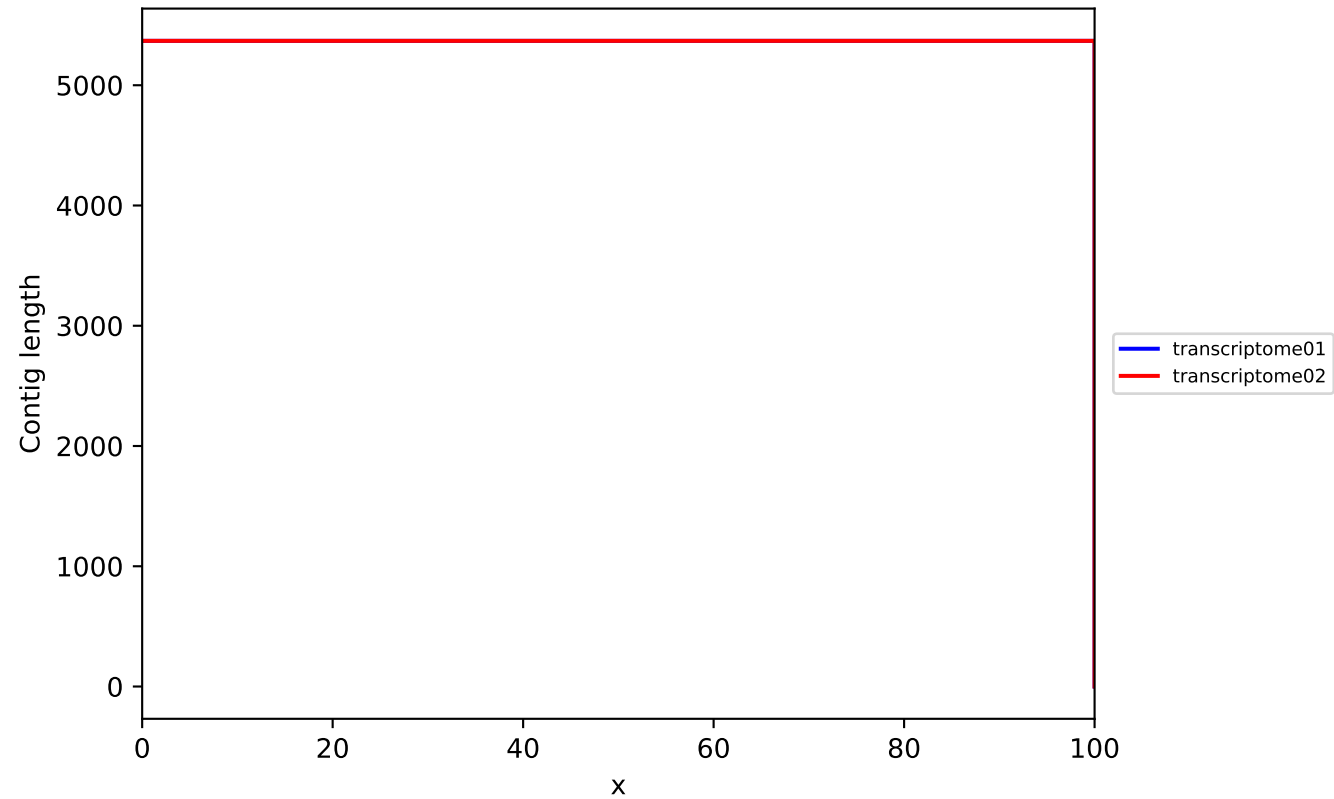
Cumulative transcript / isoform length plot



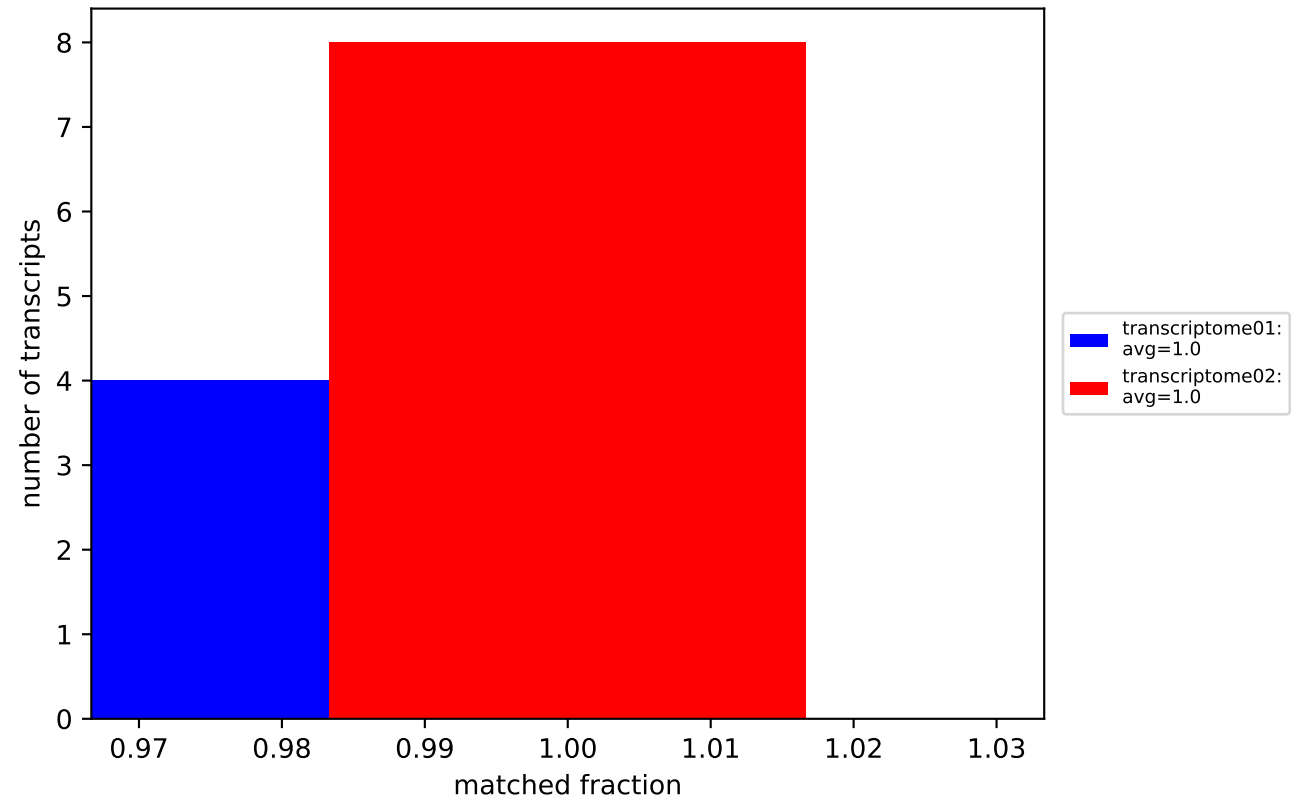
Cumulative substitution errors per alignment plot



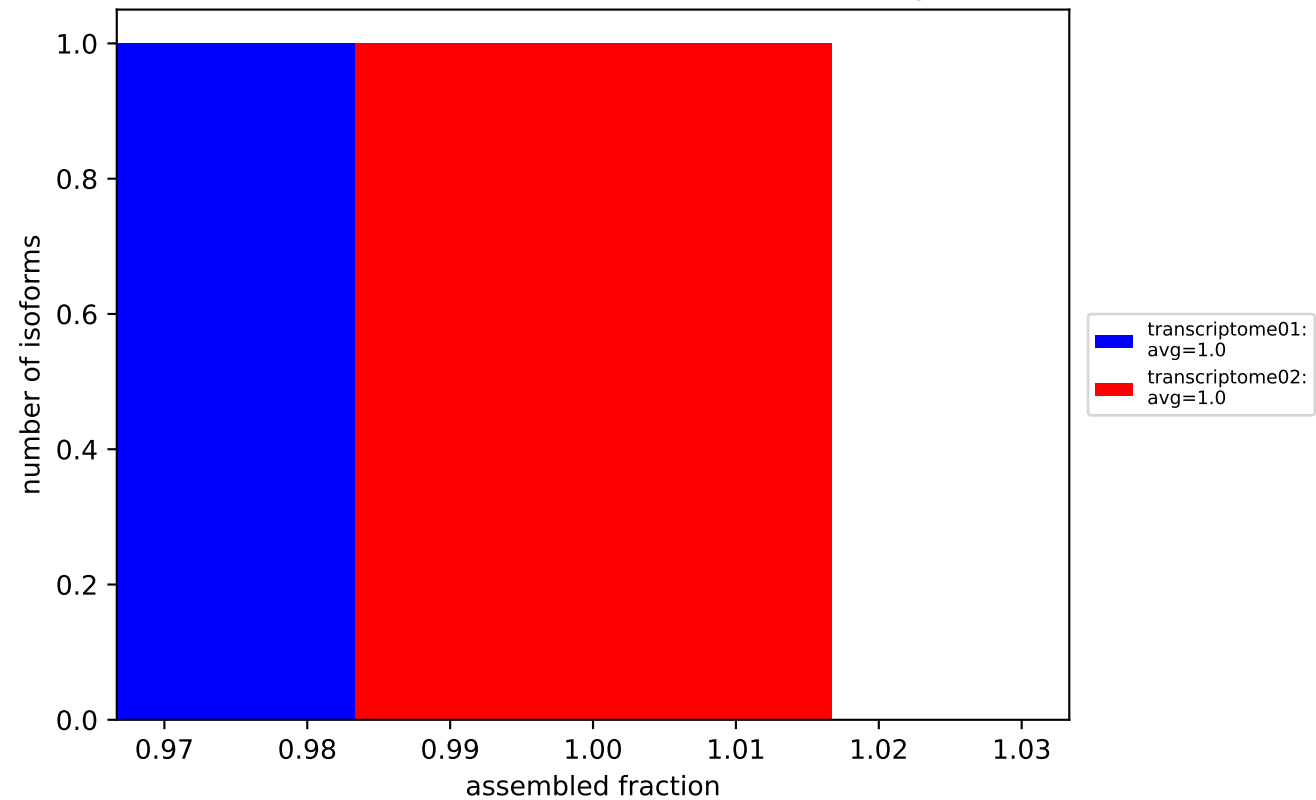
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

