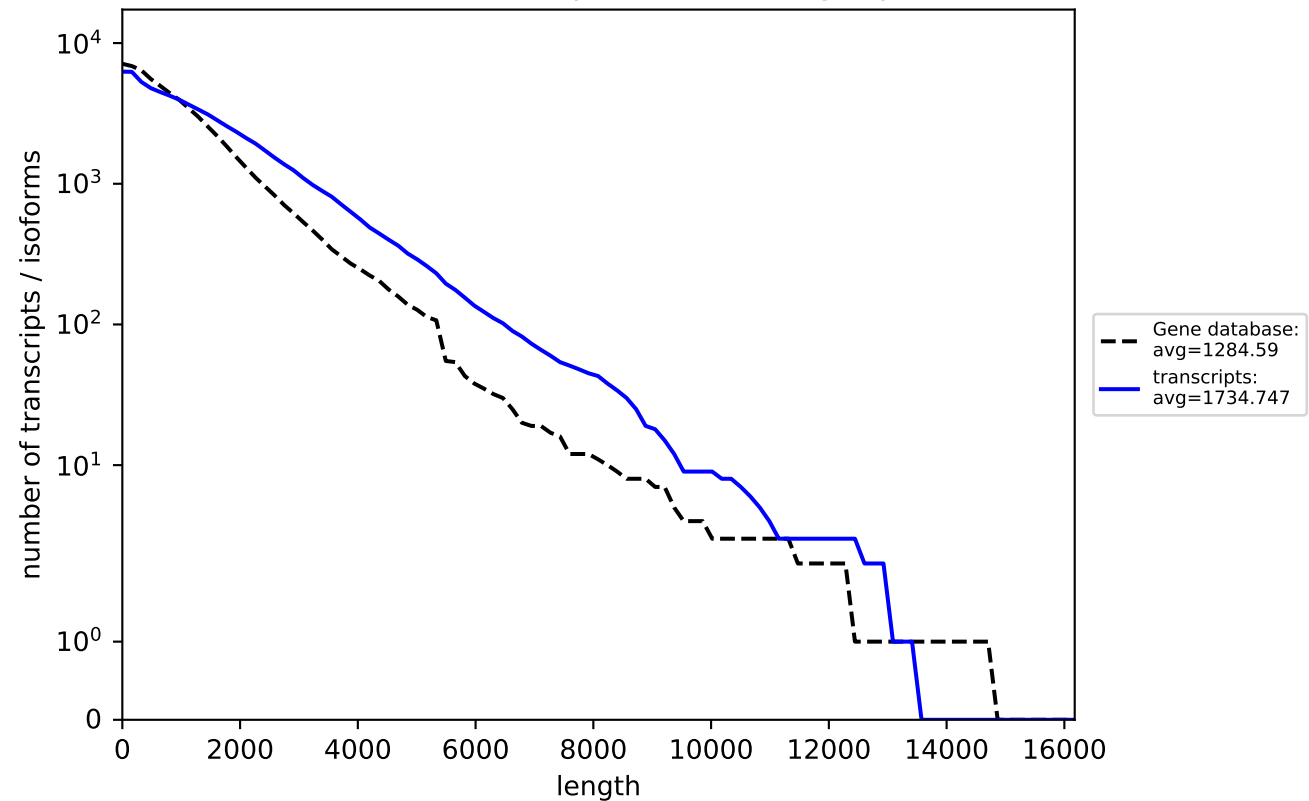


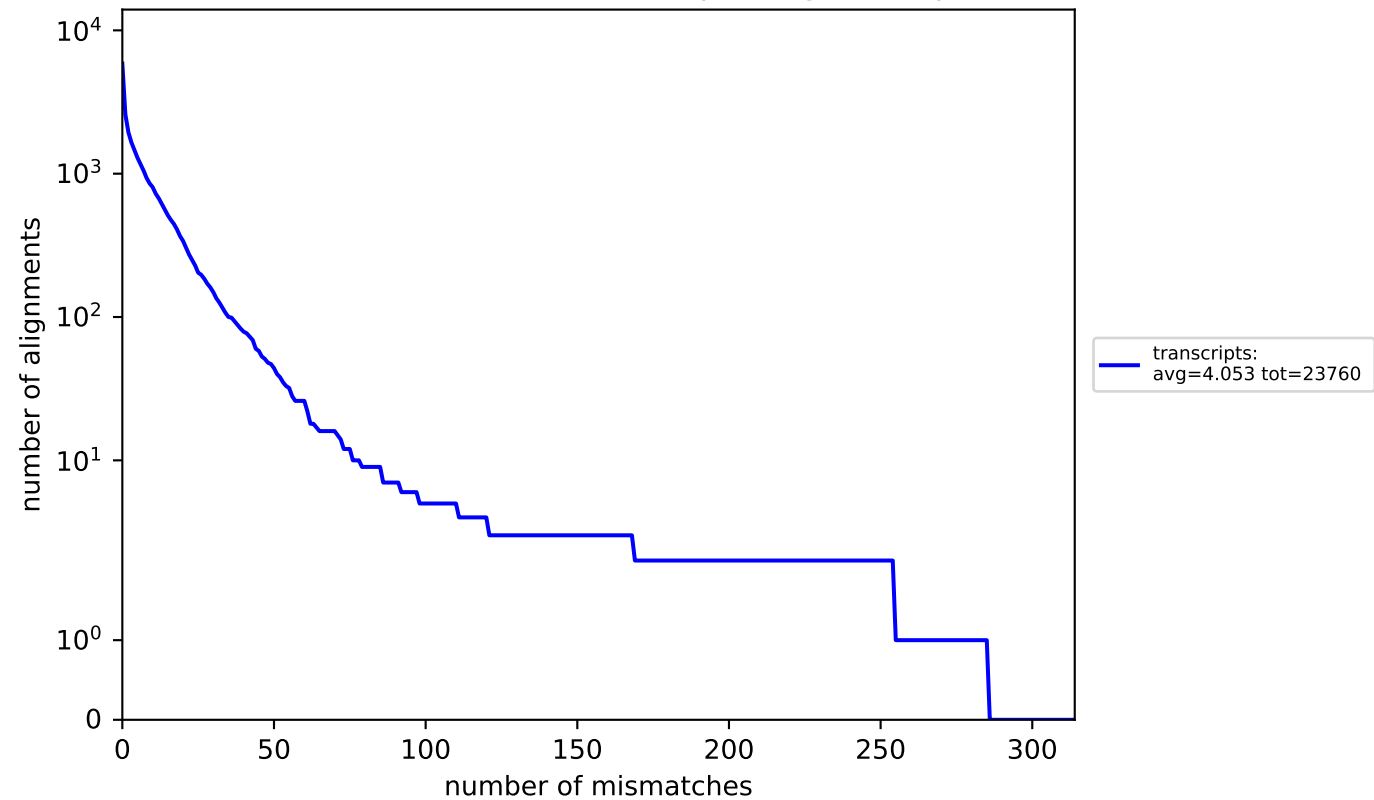
Short report

	transcripts
Genes	7126
Avg. number of exons per isoform	1.06
Transcripts	6264
Transcripts > 500 bp	4601
Transcripts > 1000 bp	3756
Aligned	5947
Uniquely aligned	5774
Multiply aligned	41
Unaligned	317
Avg. aligned fraction	0.983
Avg. alignment length	1771.999
Avg. mismatches per transcript	4.053
Misassemblies	85
Database coverage	0.747
Duplication ratio	1.025
50%-assembled genes	4011
95%-assembled genes	3709
50%-covered genes	4098
95%-covered genes	3817
50%-assembled isoforms	4011
95%-assembled isoforms	3709
50%-covered isoforms	4098
95%-covered isoforms	3817
Mean isoform coverage	0.952
Mean isoform assembly	0.935
Predicted genes	3918
50%-matched	549
95%-matched	911
Unannotated	0.591

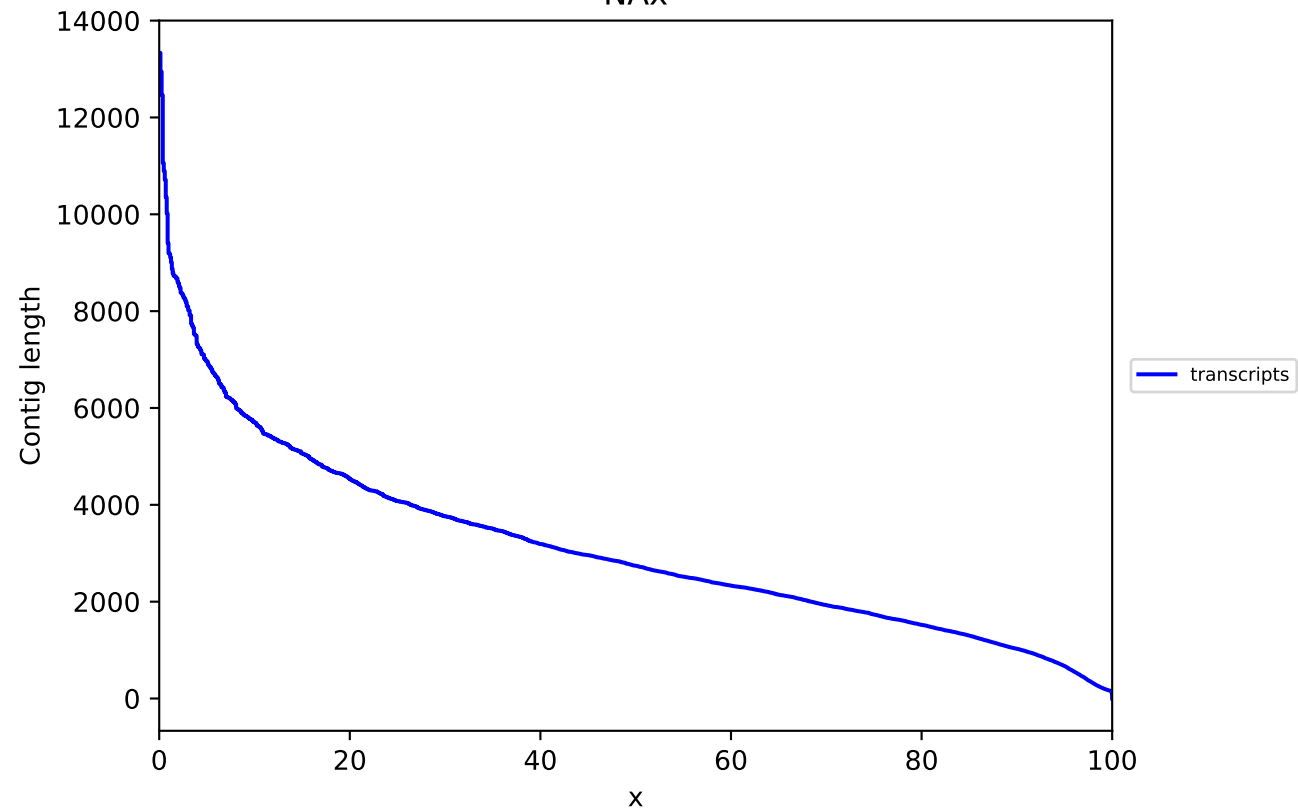
Cumulative transcript / isoform length plot



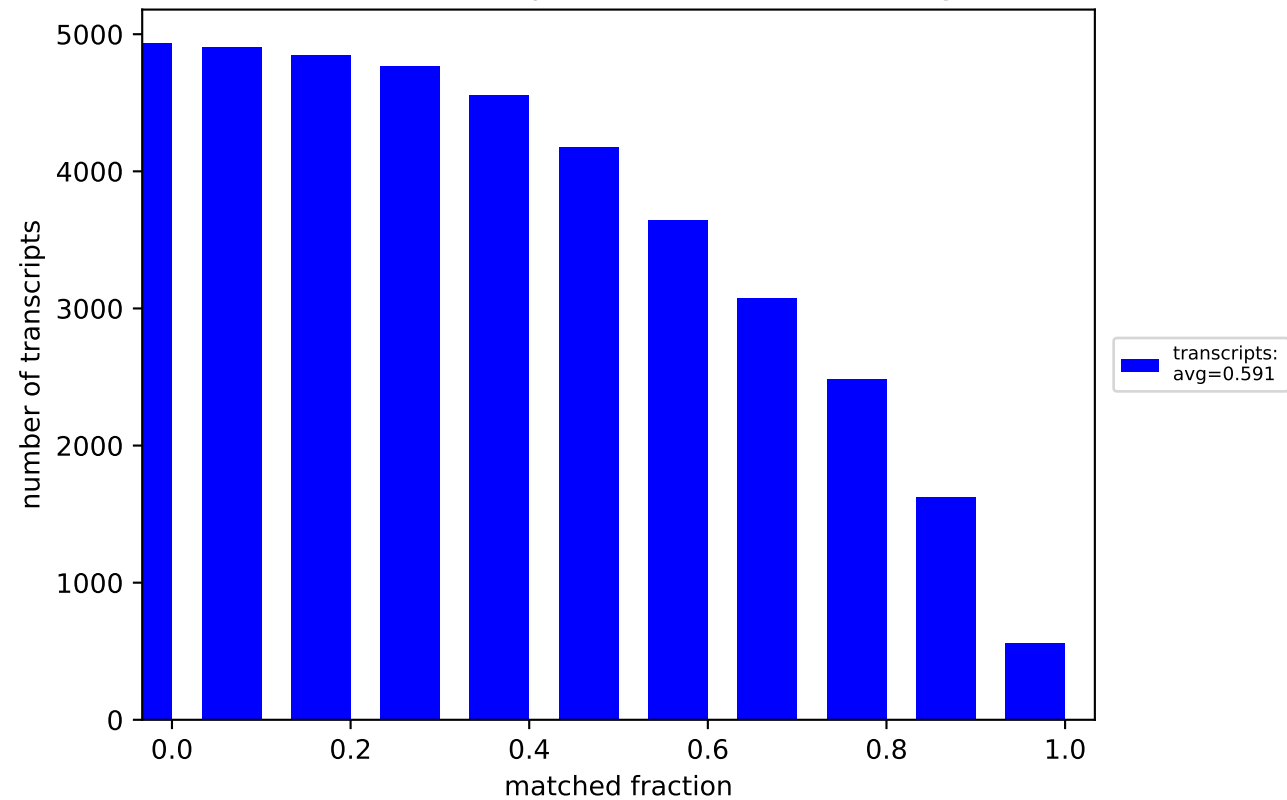
Cumulative substitution errors per alignment plot



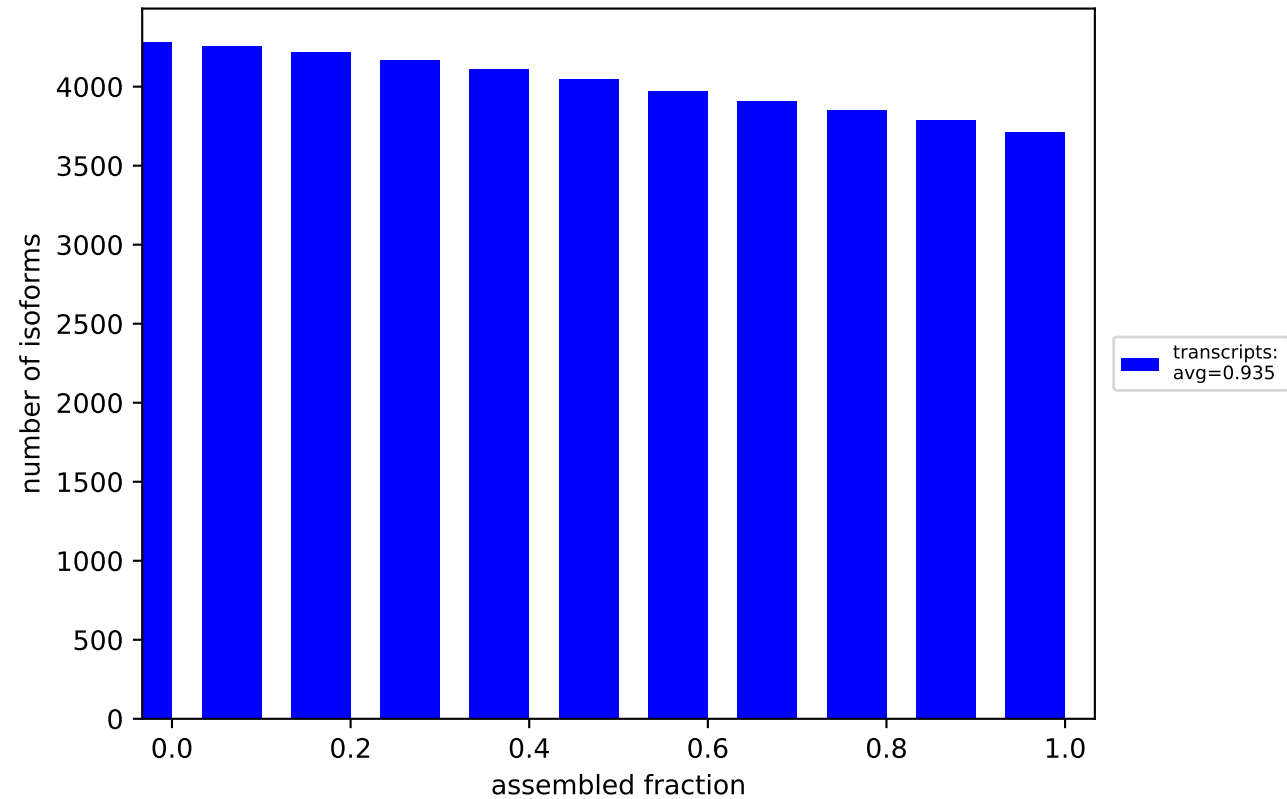
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

