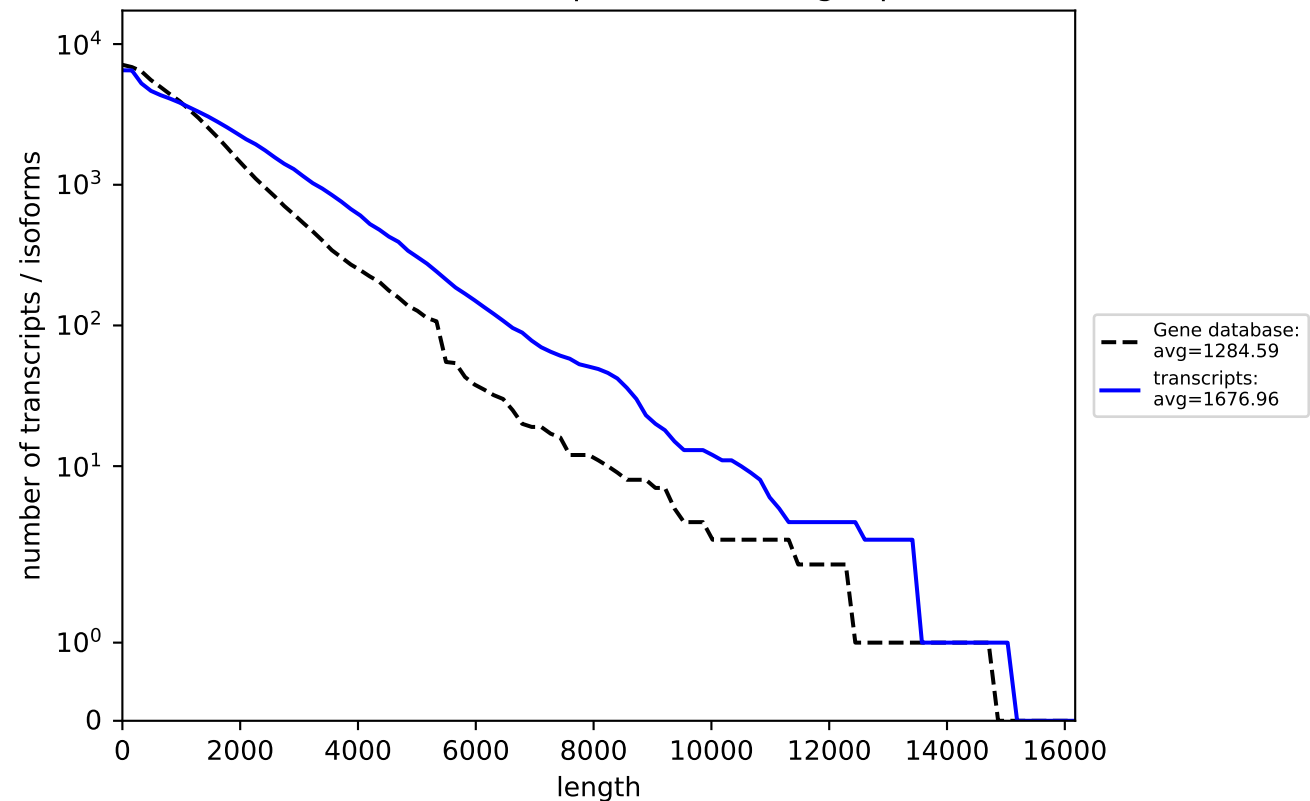


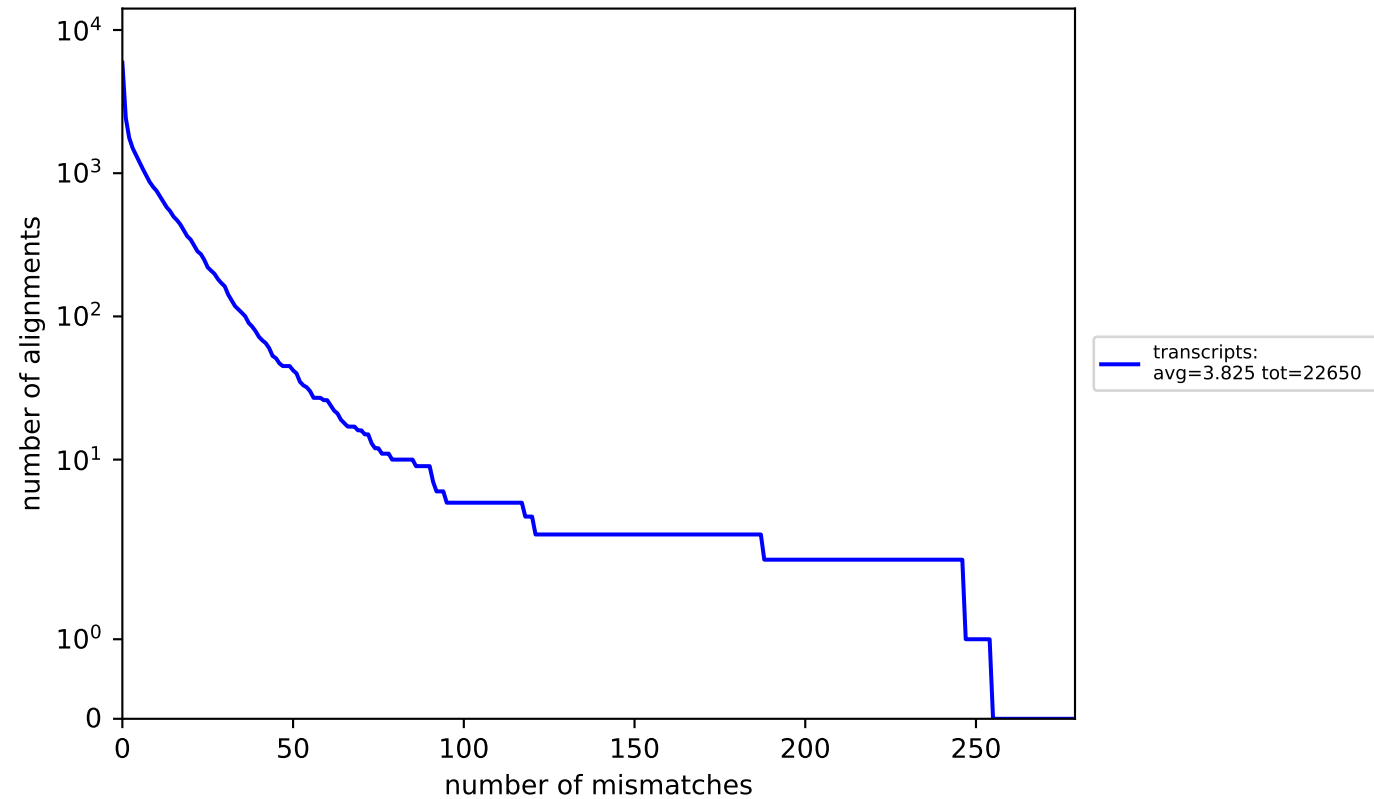
Short report

	transcripts
Genes	7126
Avg. number of exons per isoform	1.06
Transcripts	6512
Transcripts > 500 bp	4448
Transcripts > 1000 bp	3641
Aligned	5933
Uniquely aligned	5798
Multiply aligned	57
Unaligned	579
Avg. aligned fraction	0.987
Avg. alignment length	1775.412
Avg. mismatches per transcript	3.825
Misassemblies	51
Database coverage	0.74
Duplication ratio	1.027
50%-assembled genes	3921
95%-assembled genes	3632
50%-covered genes	4010
95%-covered genes	3753
50%-assembled isoforms	3921
95%-assembled isoforms	3632
50%-covered isoforms	4010
95%-covered isoforms	3753
Mean isoform coverage	0.952
Mean isoform assembly	0.933
50%-matched	3824
95%-matched	604
Unannotated	981
Mean fraction of transcript matched	0.578

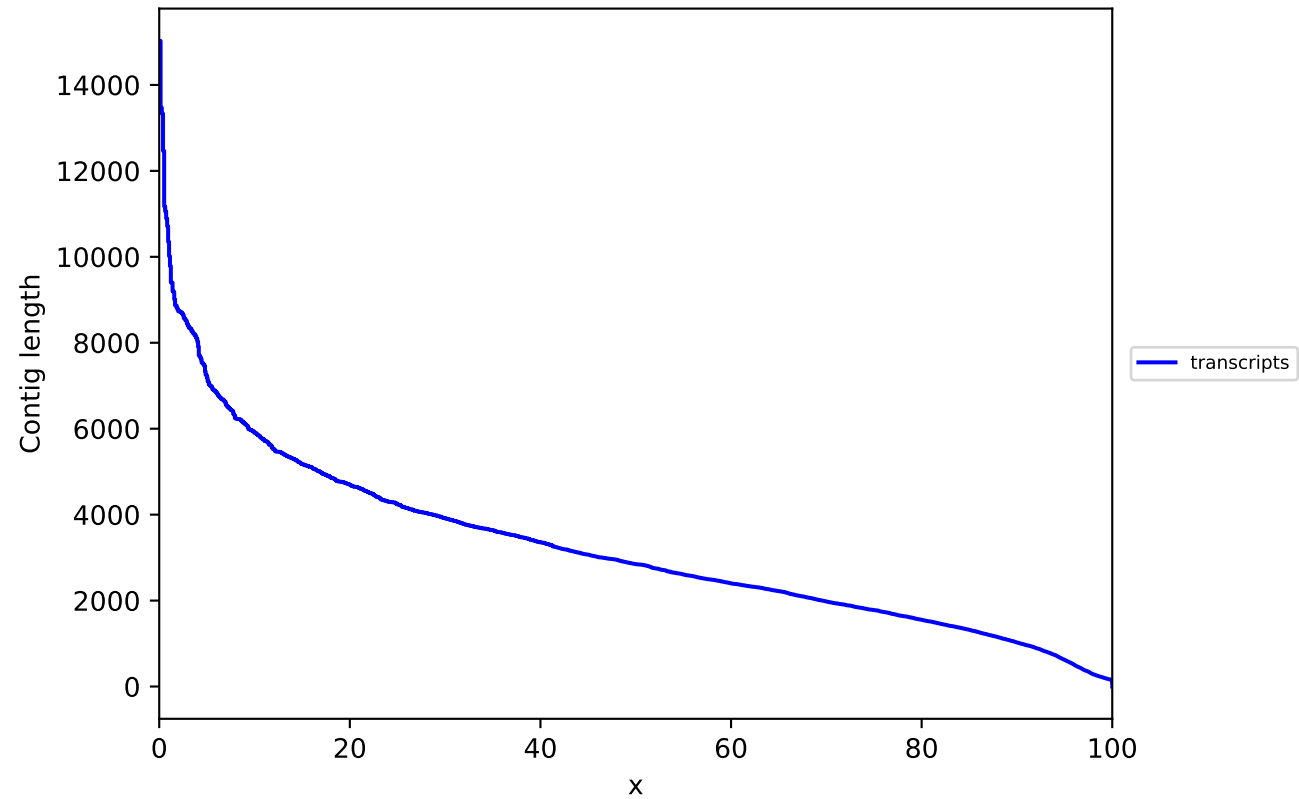
Cumulative transcript / isoform length plot



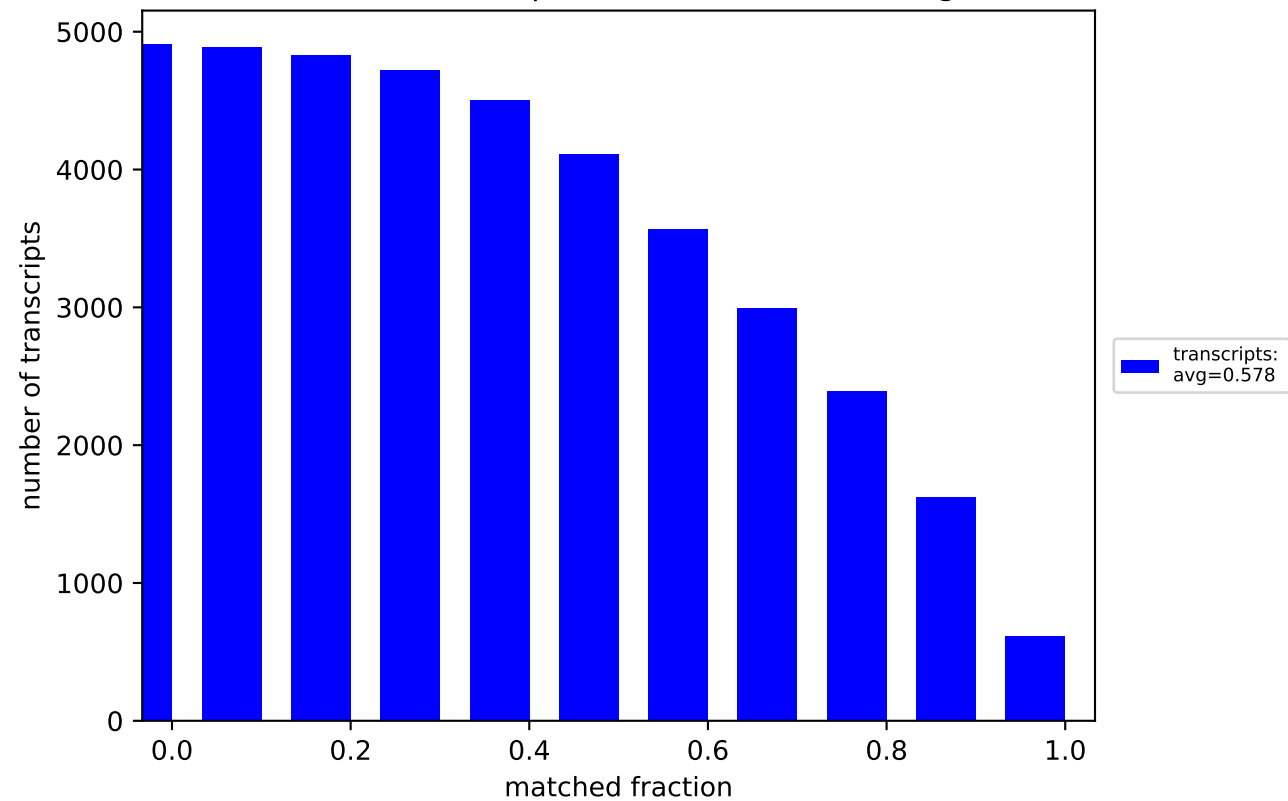
Cumulative substitution errors per alignment plot



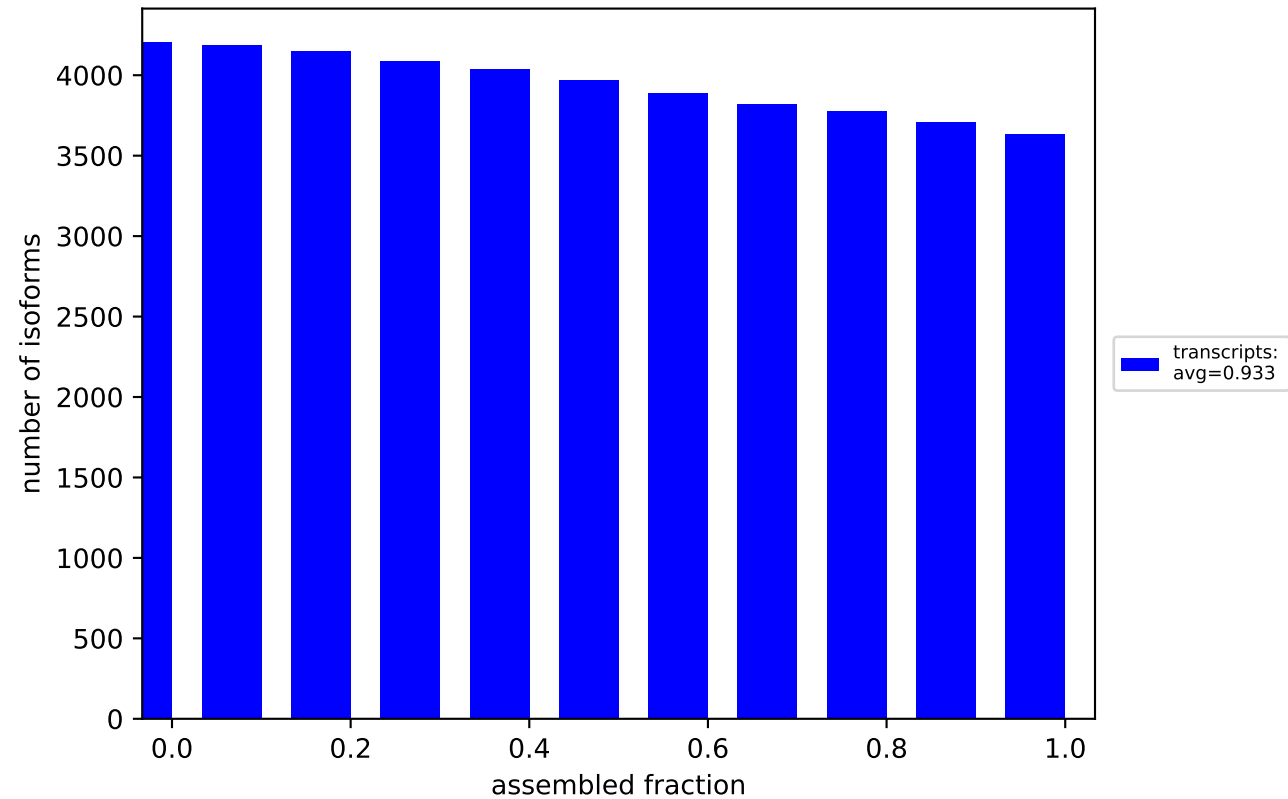
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

