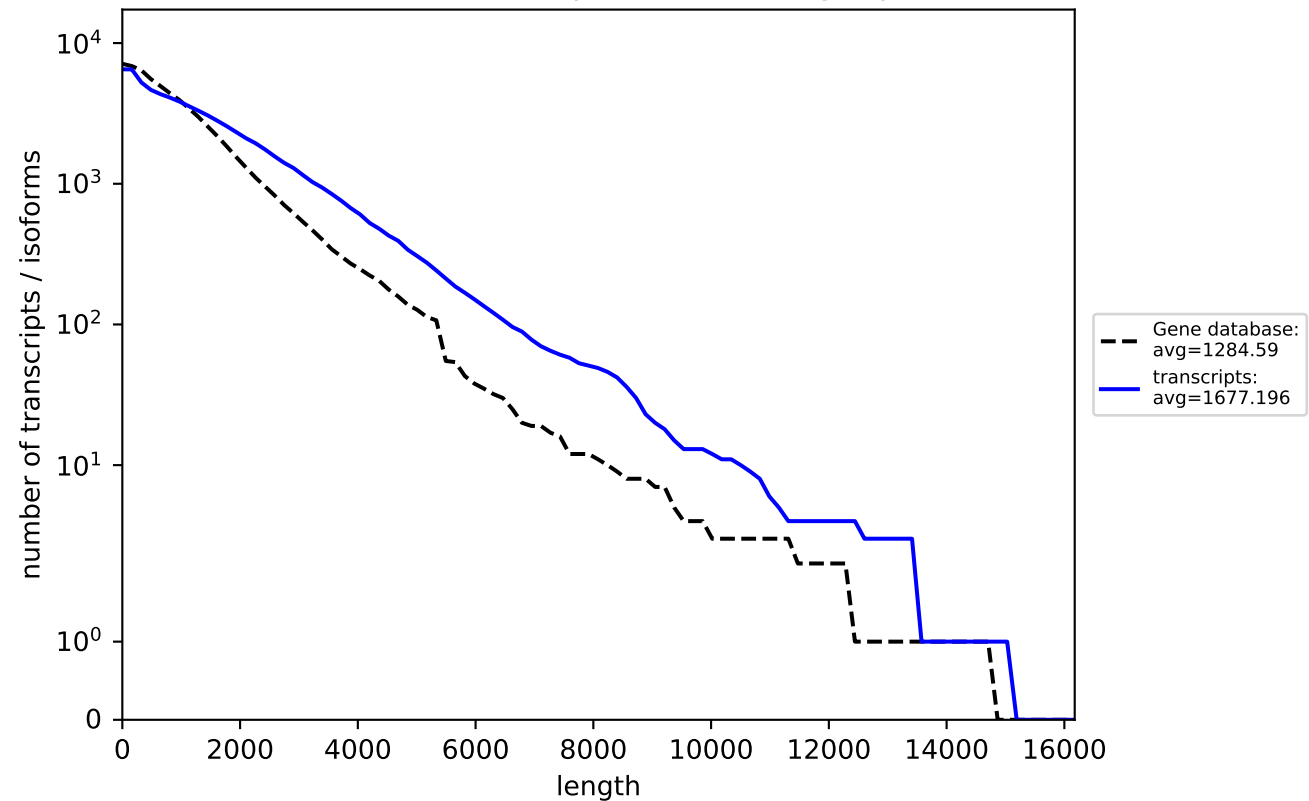


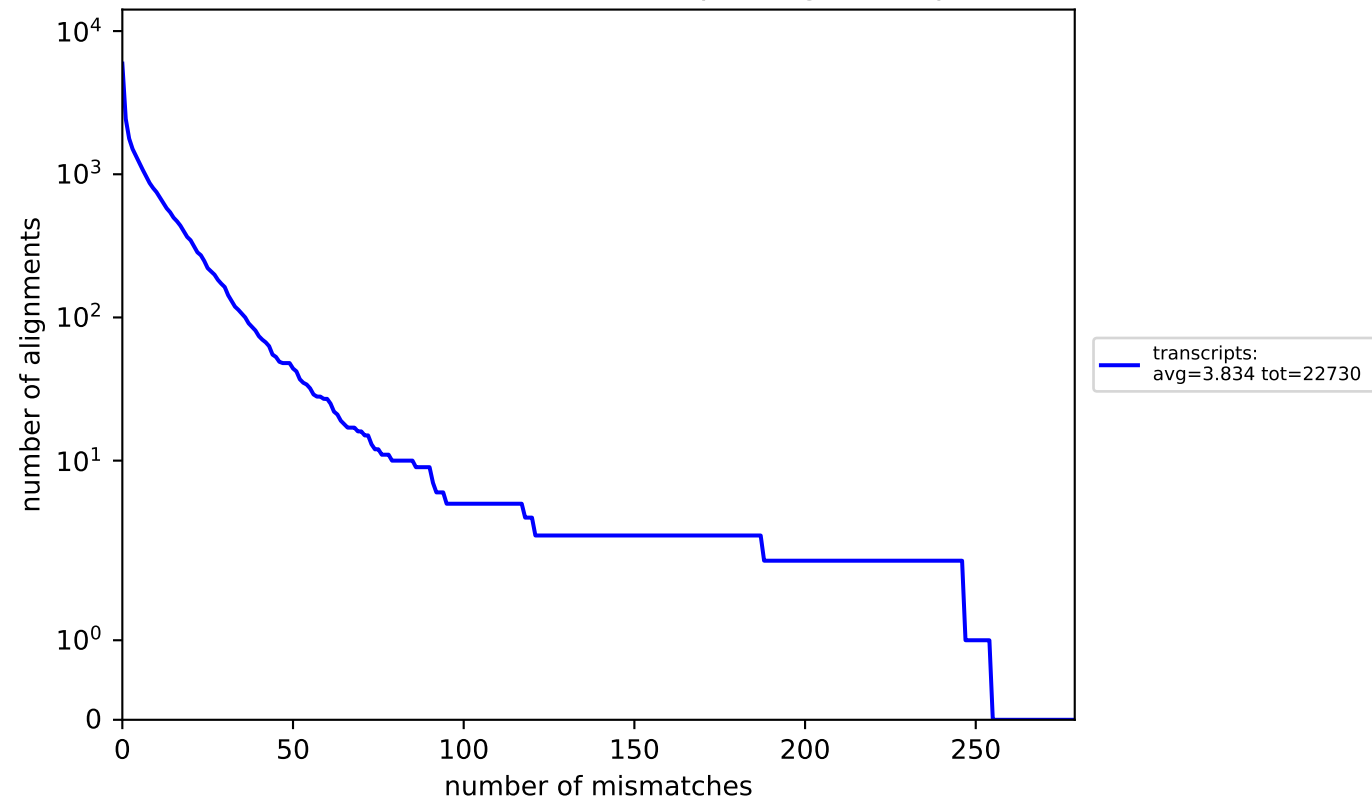
Short report

	transcripts
Genes	7126
Avg. number of exons per isoform	1.06
Transcripts	6511
Transcripts > 500 bp	4448
Transcripts > 1000 bp	3641
Aligned	5933
Uniquely aligned	5800
Multiply aligned	59
Unaligned	578
Avg. aligned fraction	0.987
Avg. alignment length	1774.548
Avg. mismatches per transcript	3.834
Misassemblies	48
Database coverage	0.74
Duplication ratio	1.028
50%-assembled genes	3923
95%-assembled genes	3634
50%-covered genes	4012
95%-covered genes	3756
50%-assembled isoforms	3923
95%-assembled isoforms	3634
50%-covered isoforms	4012
95%-covered isoforms	3756
Mean isoform coverage	0.951
Mean isoform assembly	0.933
Predicted genes	3825
50%-matched	604
95%-matched	979
Unannotated	0.578

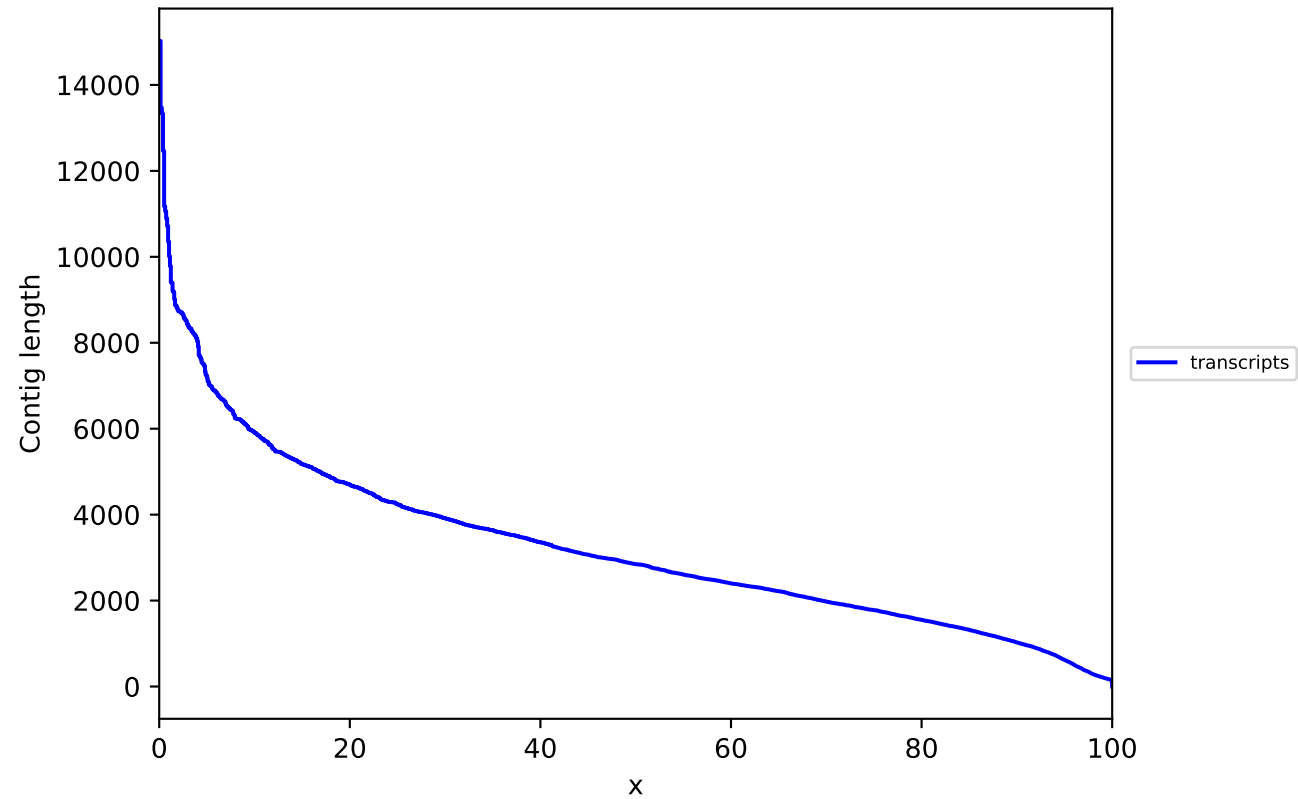
Cumulative transcript / isoform length plot



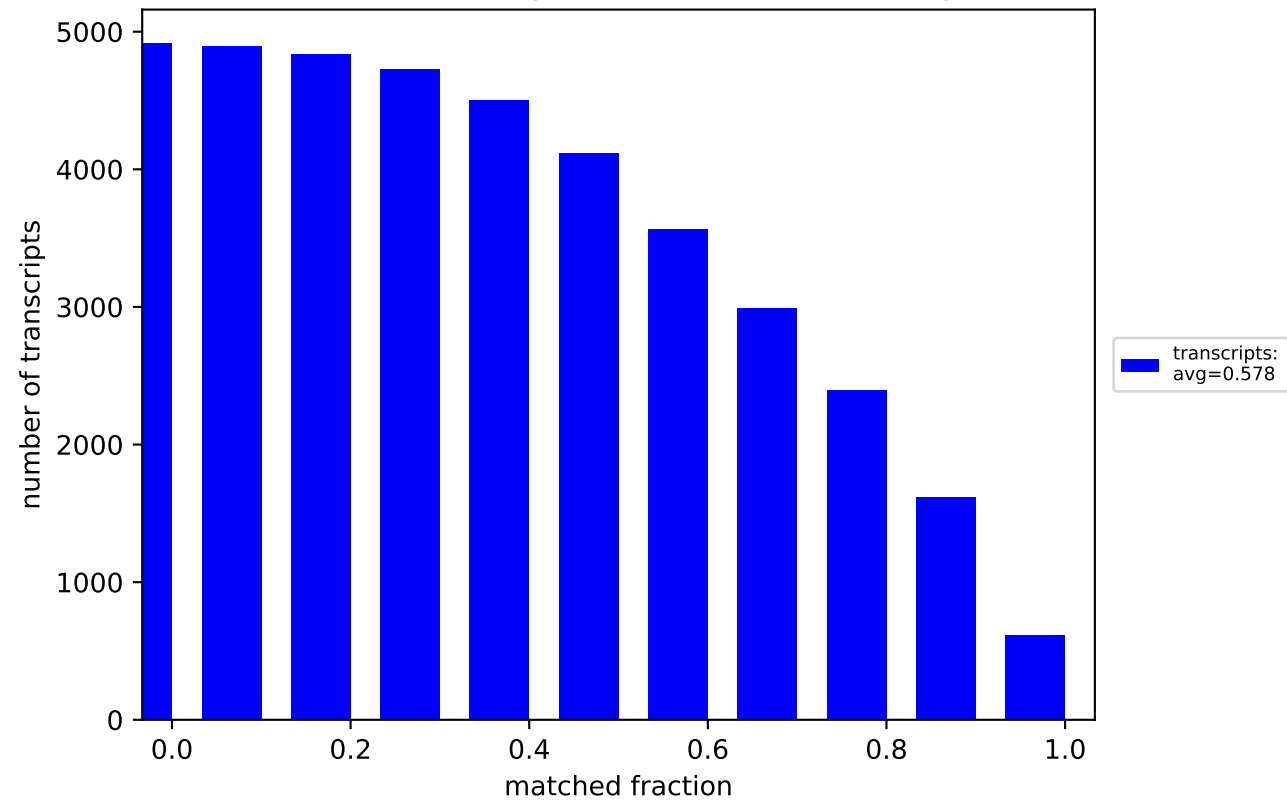
Cumulative substitution errors per alignment plot



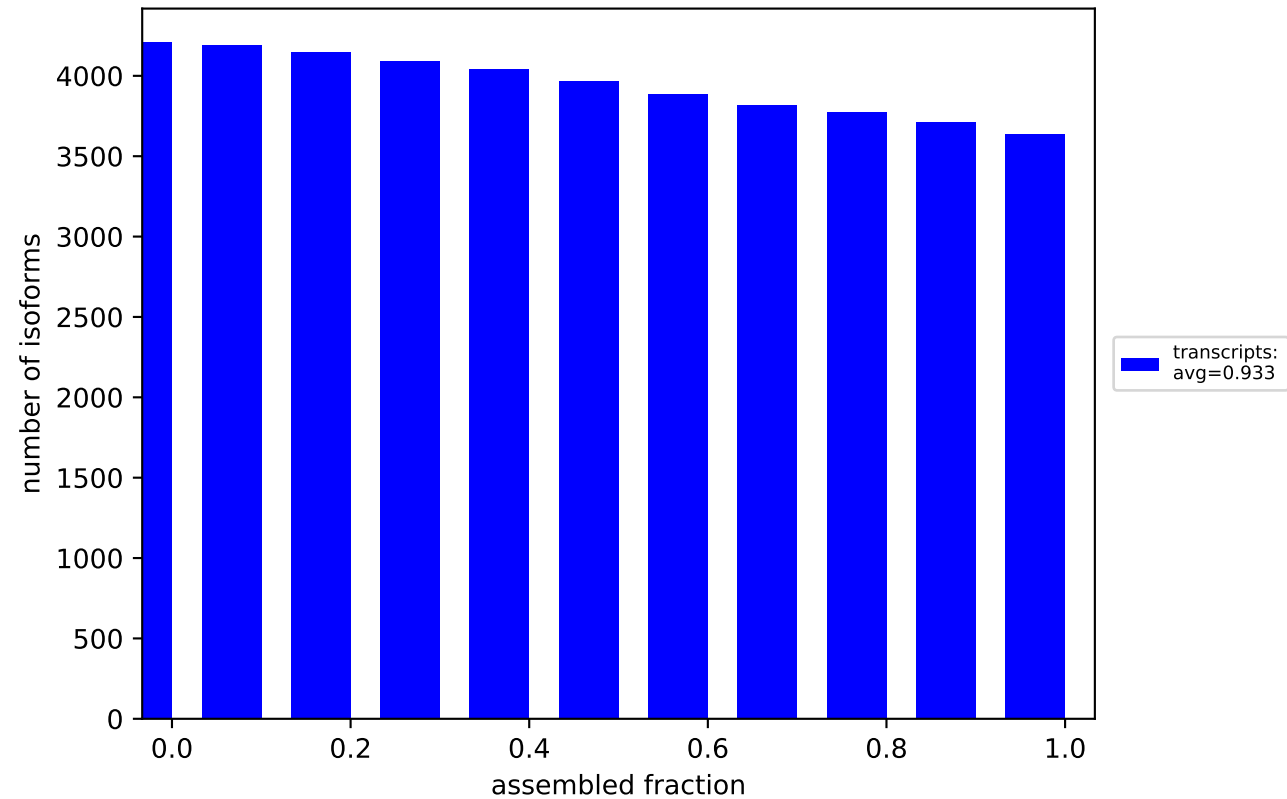
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

