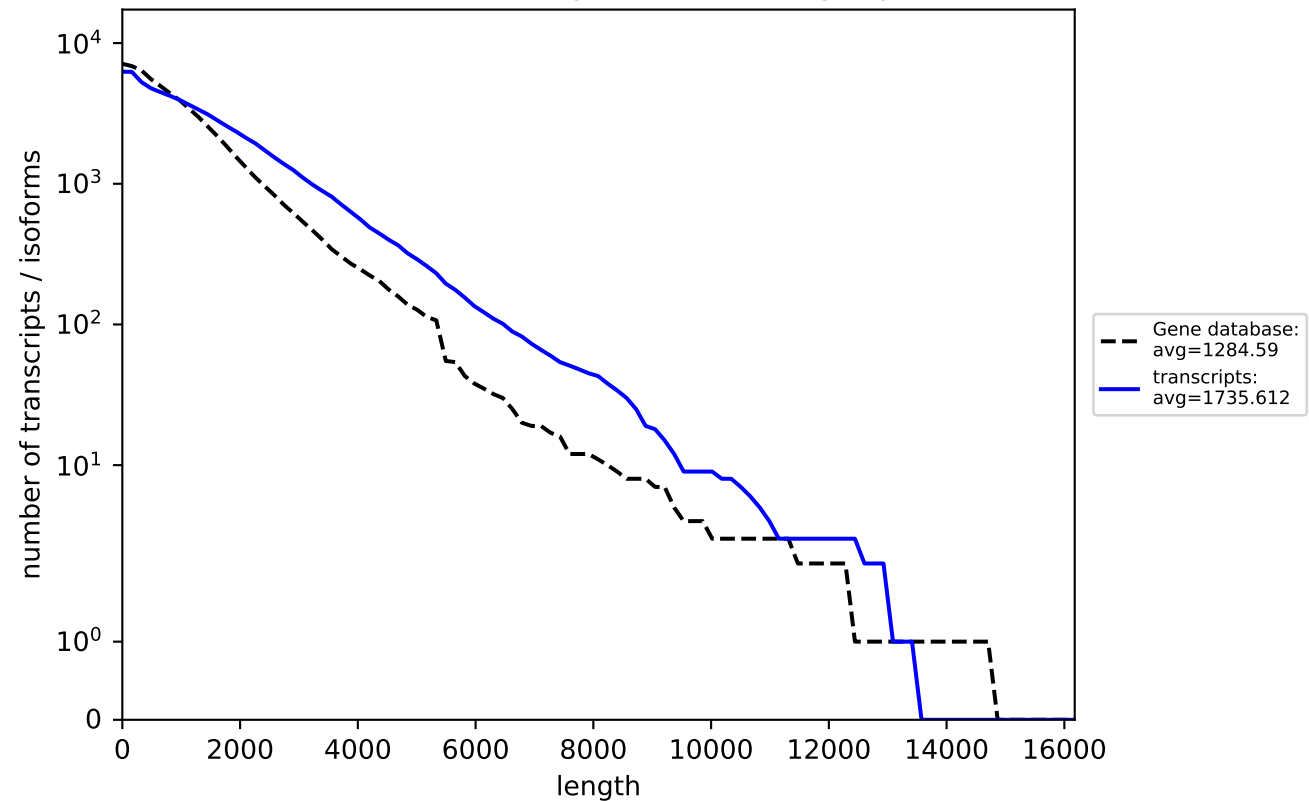


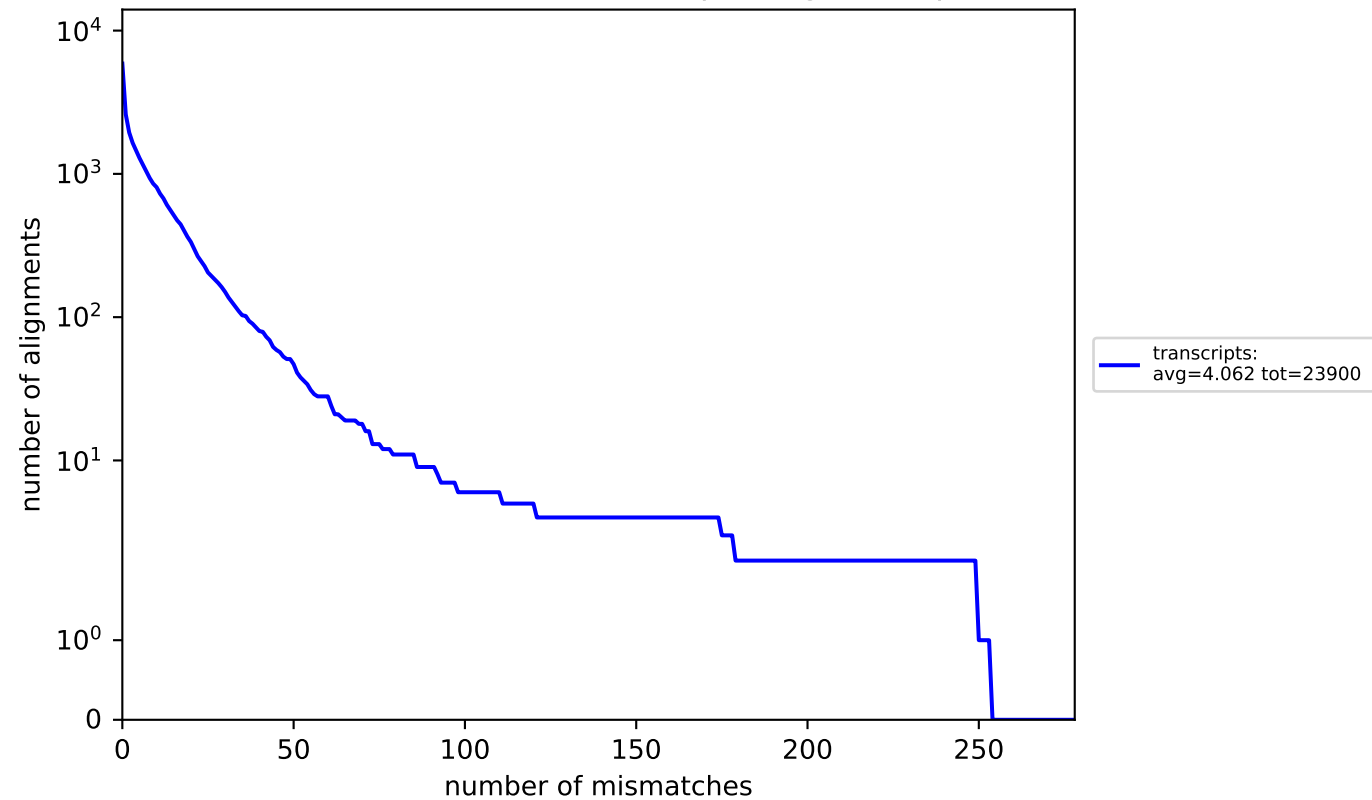
# Short report

	transcripts
Genes	7126
Avg. number of exons per isoform	1.06
Transcripts	6261
Transcripts > 500 bp	4599
Transcripts > 1000 bp	3754
Aligned	5937
Uniquely aligned	5790
Multiply aligned	45
Unaligned	324
Avg. aligned fraction	0.982
Avg. alignment length	1777.73
Avg. mismatches per transcript	4.062
Misassemblies	58
Database coverage	0.75
Duplication ratio	1.026
50%-assembled genes	4030
95%-assembled genes	3726
50%-covered genes	4114
95%-covered genes	3834
50%-assembled isoforms	4030
95%-assembled isoforms	3726
50%-covered isoforms	4114
95%-covered isoforms	3834
Mean isoform coverage	0.953
Mean isoform assembly	0.936
50%-matched	3927
95%-matched	548
Unannotated	910
Mean fraction of transcript matched	0.59

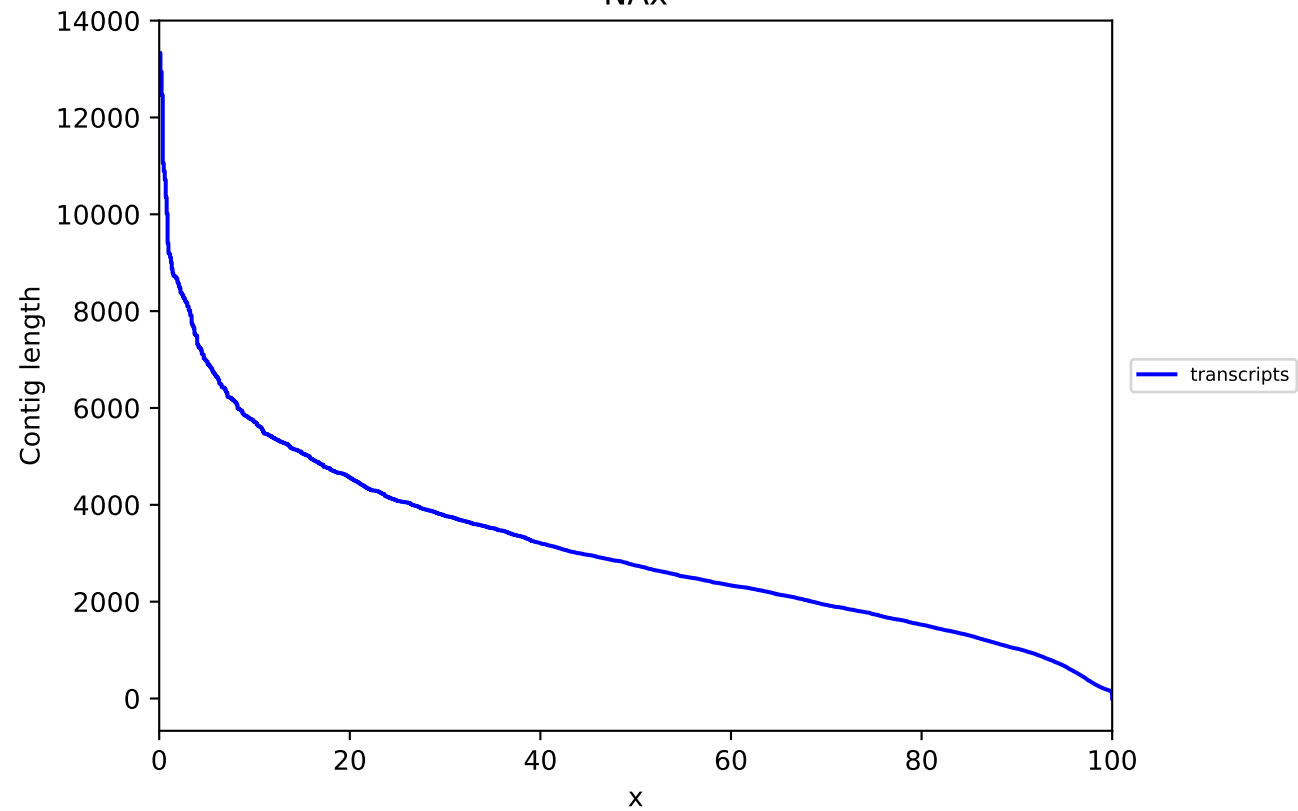
Cumulative transcript / isoform length plot



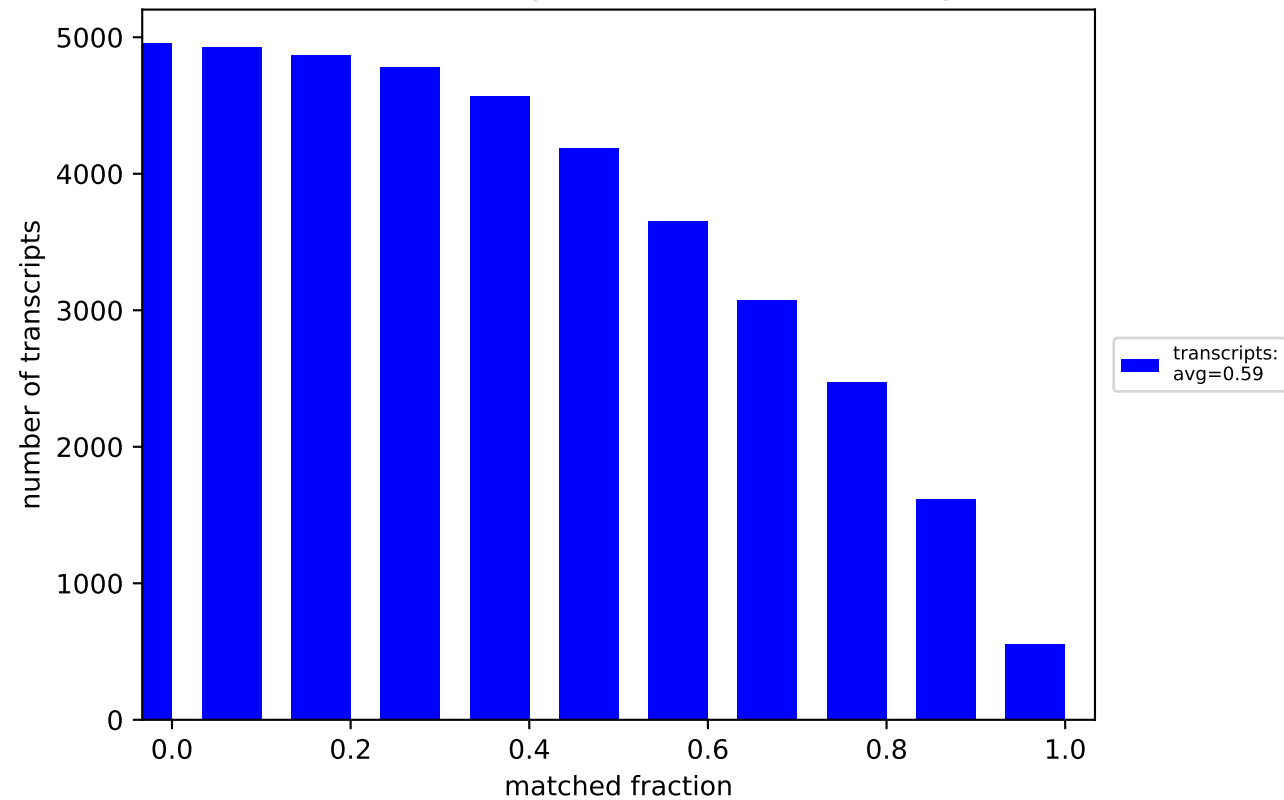
Cumulative substitution errors per alignment plot



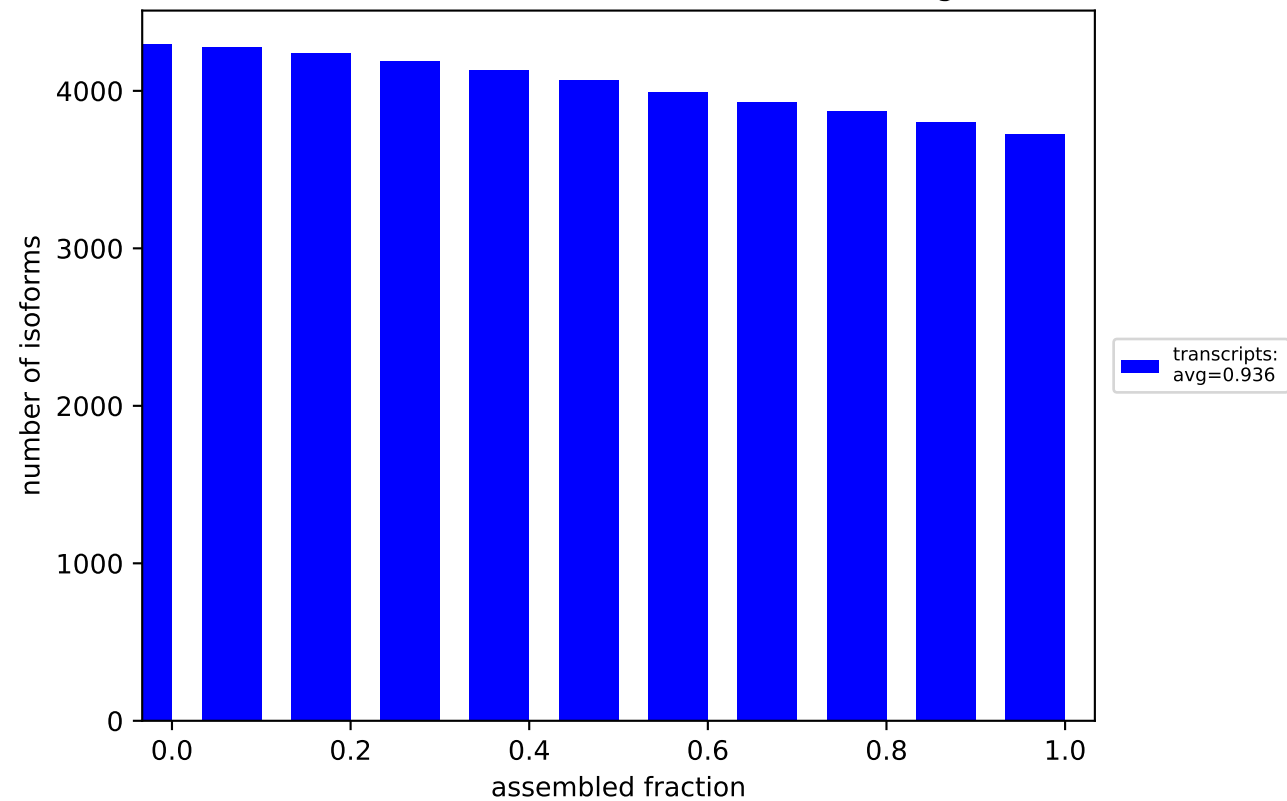
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

