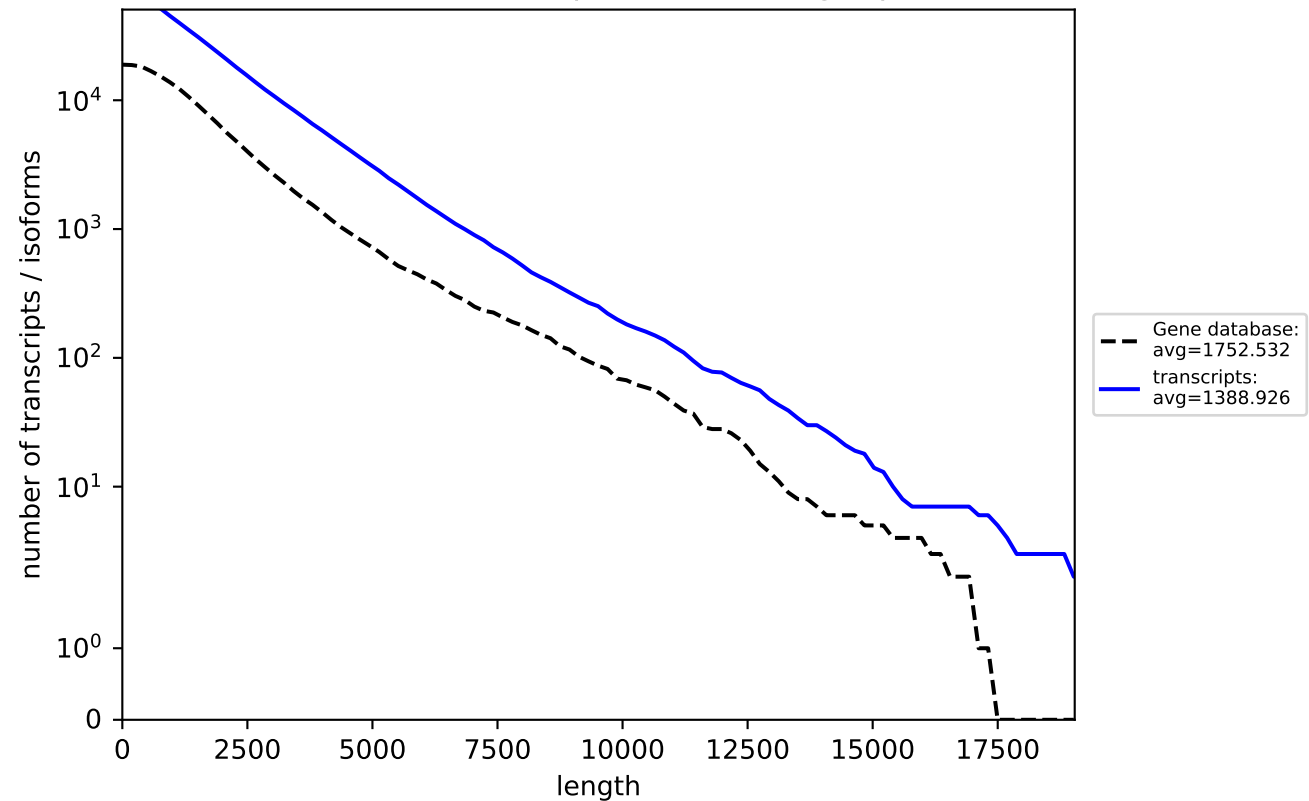


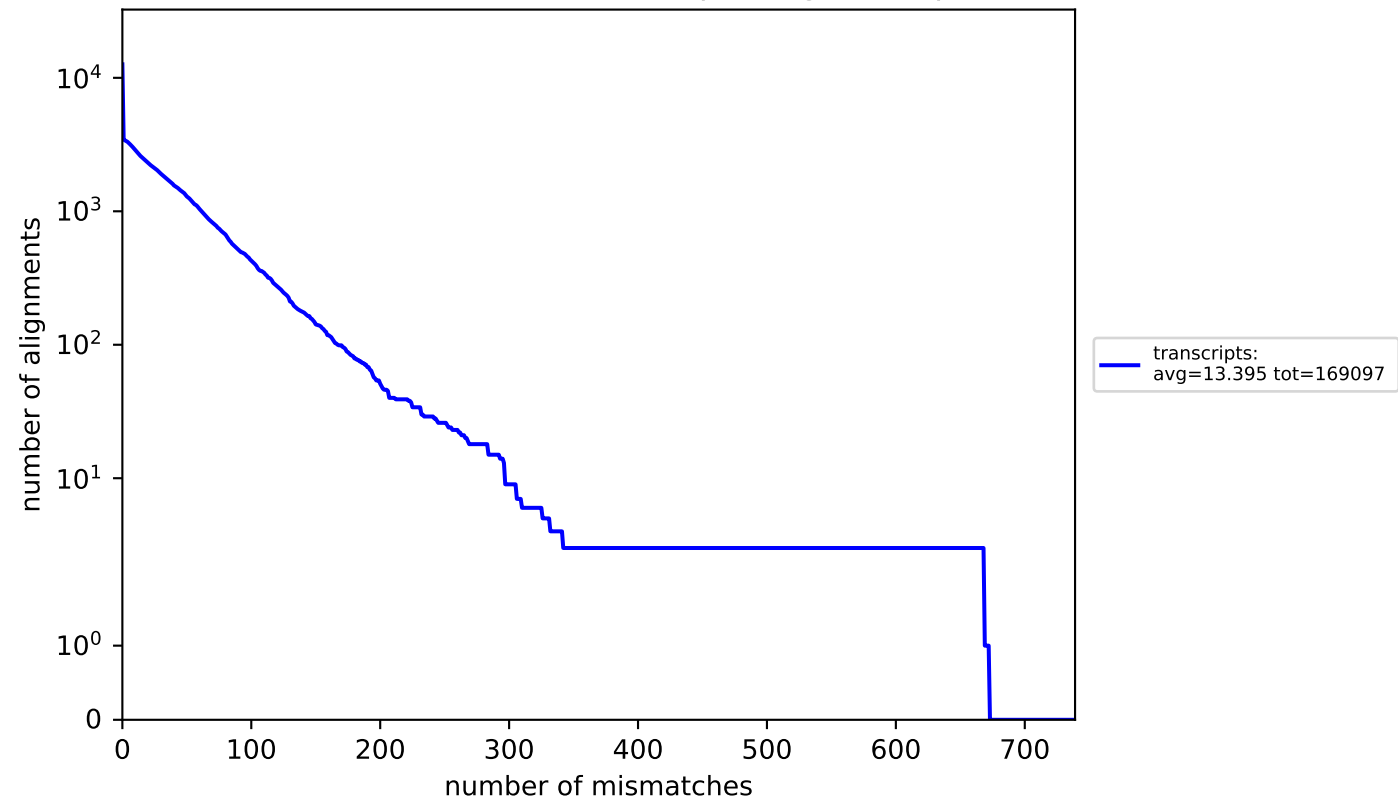
Short report

	transcripts
Genes	16674
Avg. number of exons per isoform	7.715
Transcripts	91092
Transcripts > 500 bp	59829
Transcripts > 1000 bp	41034
Aligned	15285
Uniquely aligned	12426
Multiply aligned	83
Unaligned	75807
Avg. aligned fraction	0.207
Avg. alignment length	366.001
Avg. mismatches per transcript	13.395
Misassemblies	313
Database coverage	0.052
Duplication ratio	1.95
Relative database coverage	0.0
50%-assembled genes	552
95%-assembled genes	12
50%-covered genes	611
95%-covered genes	14
50%-assembled isoforms	554
95%-assembled isoforms	12
50%-covered isoforms	613
95%-covered isoforms	14
Mean isoform coverage	0.254
Mean isoform assembly	0.242
Predicted genes	496
50%-matched	8
95%-matched	5106
Unannotated	0.114

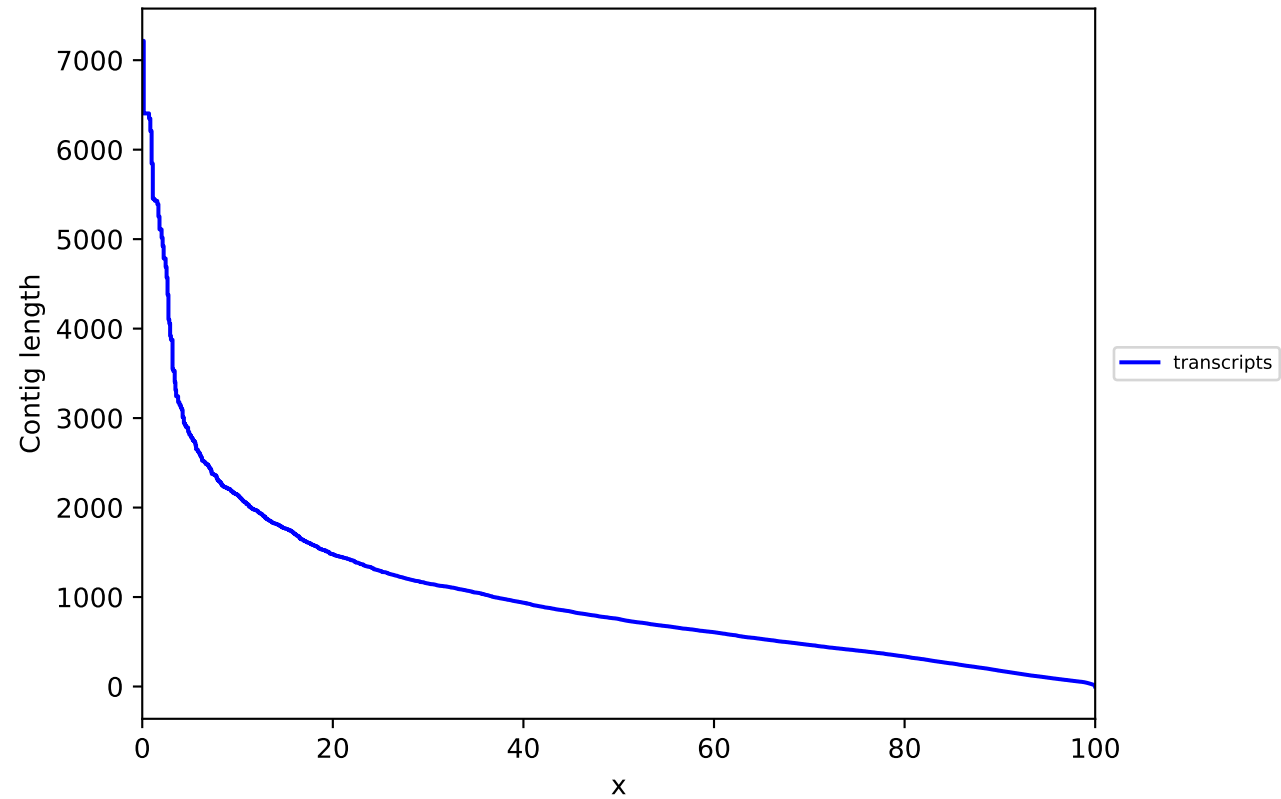
Cumulative transcript / isoform length plot



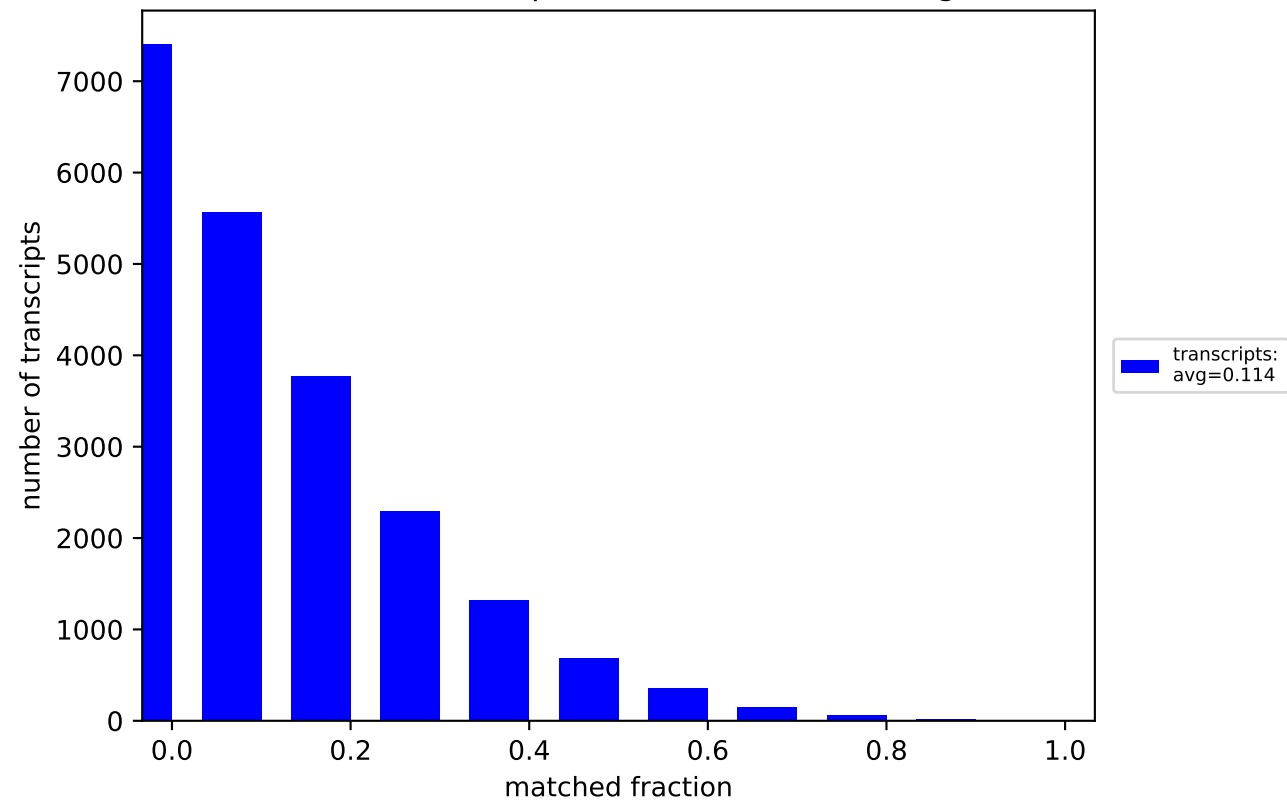
Cumulative substitution errors per alignment plot



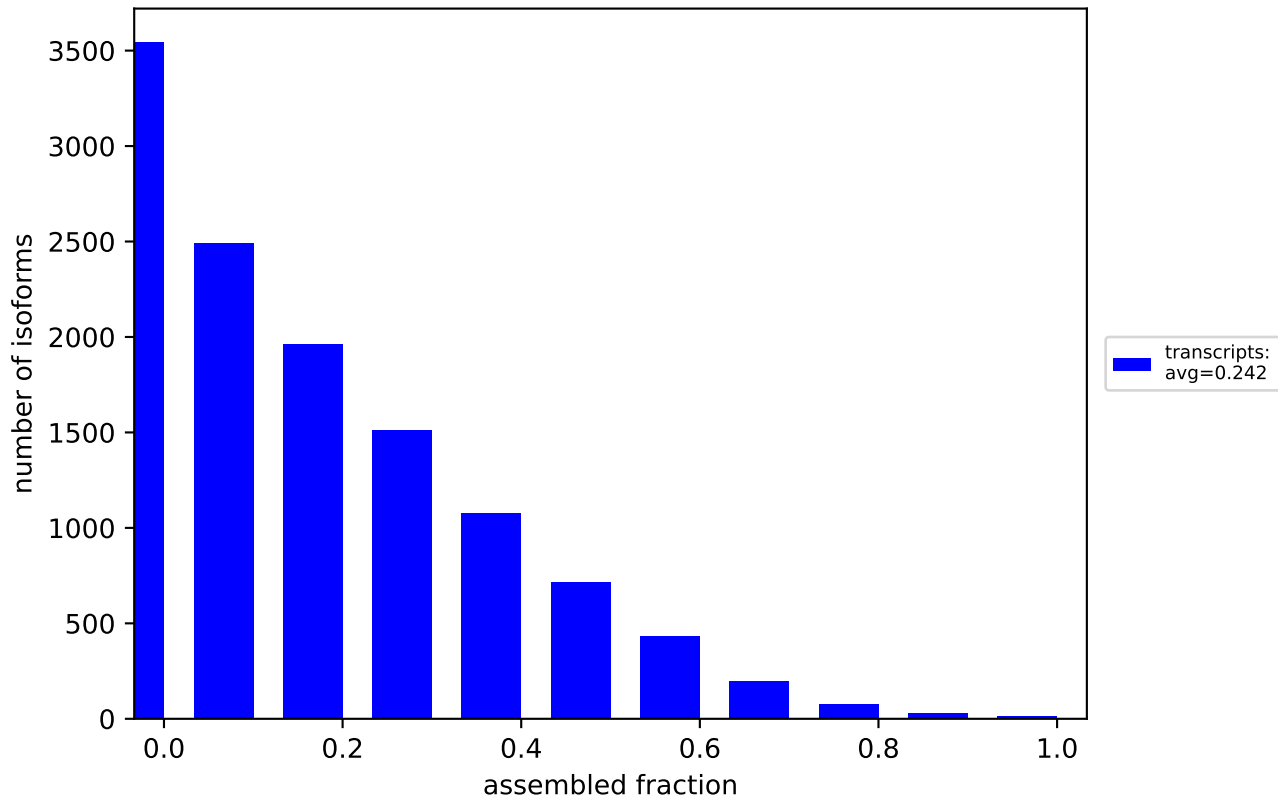
NAX



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

