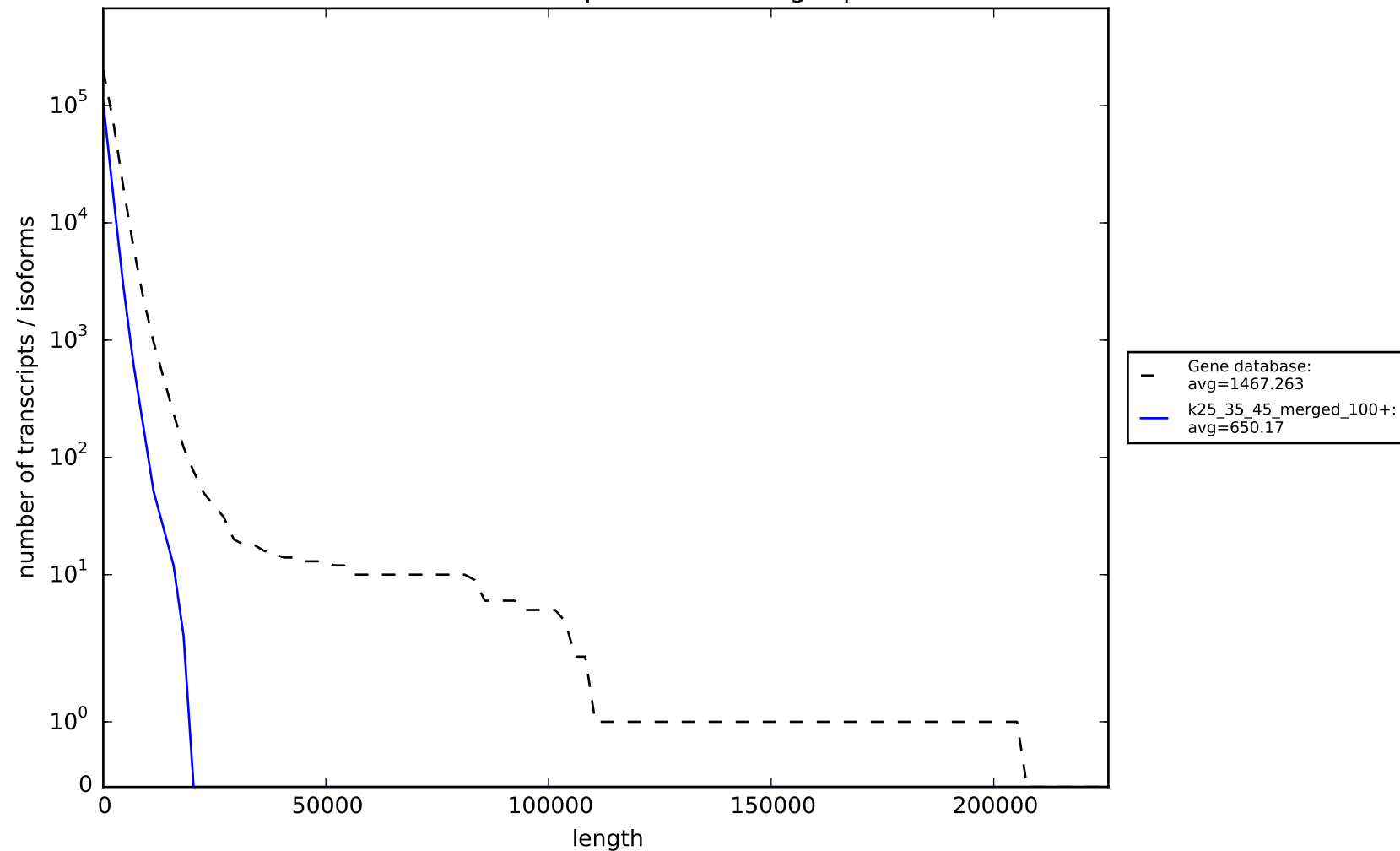


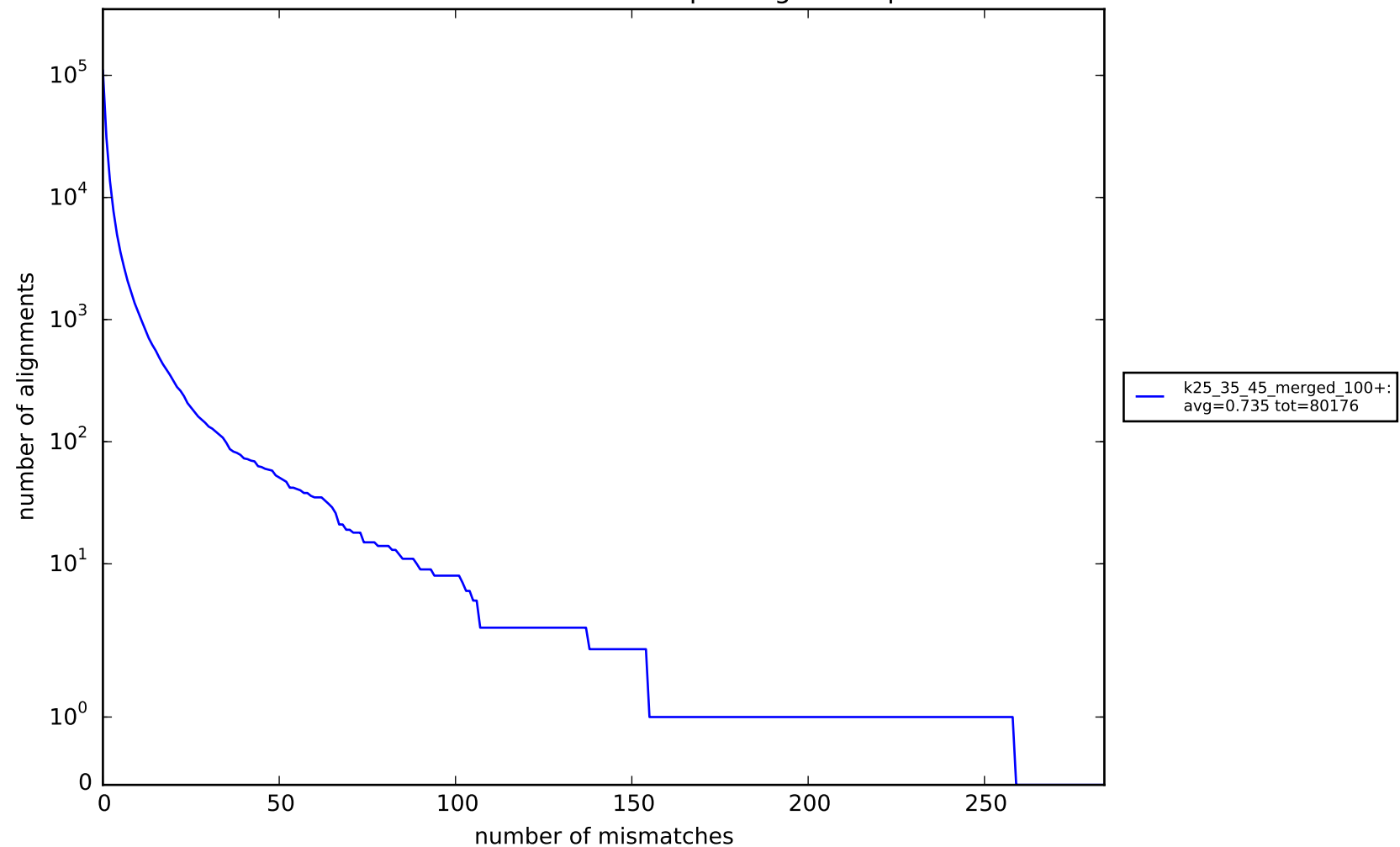
Short report

	k25_35_45_merged_100+
Genes	60675
Avg. number of exons per isoform	5.908
Transcripts	105469
Transcripts > 500 bp	33360
Transcripts > 1000 bp	19089
Aligned	105198
Uniquely aligned	101492
Multiply aligned	2668
Unaligned	271
Avg. aligned fraction	0.996
Avg. alignment length	622.966
Avg. mismatches per transcript	0.735
Misassemblies	531
Database coverage	0.143
50%-assembled genes	7938
95%-assembled genes	2106
50%-covered genes	9739
95%-covered genes	2899
50%-assembled isoforms	11856
95%-assembled isoforms	2308
50%-covered isoforms	15143
95%-covered isoforms	3257
Mean isoform coverage	0.489
Mean isoform assembly	0.418
50%-matched	71617
95%-matched	60867
Unannotated	28594
Mean fraction of transcript matched	0.645

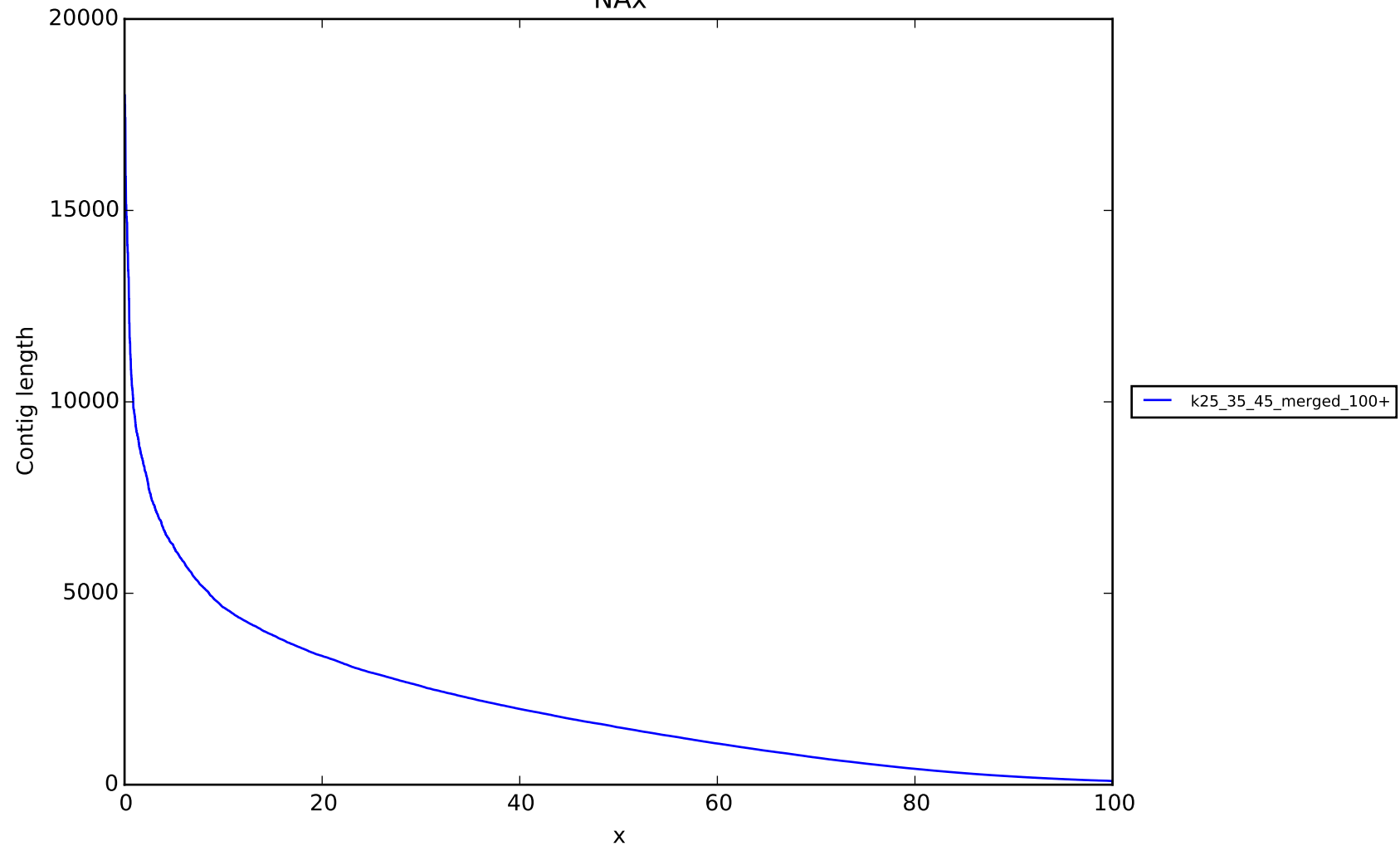
Cumulative transcript / isoform length plot



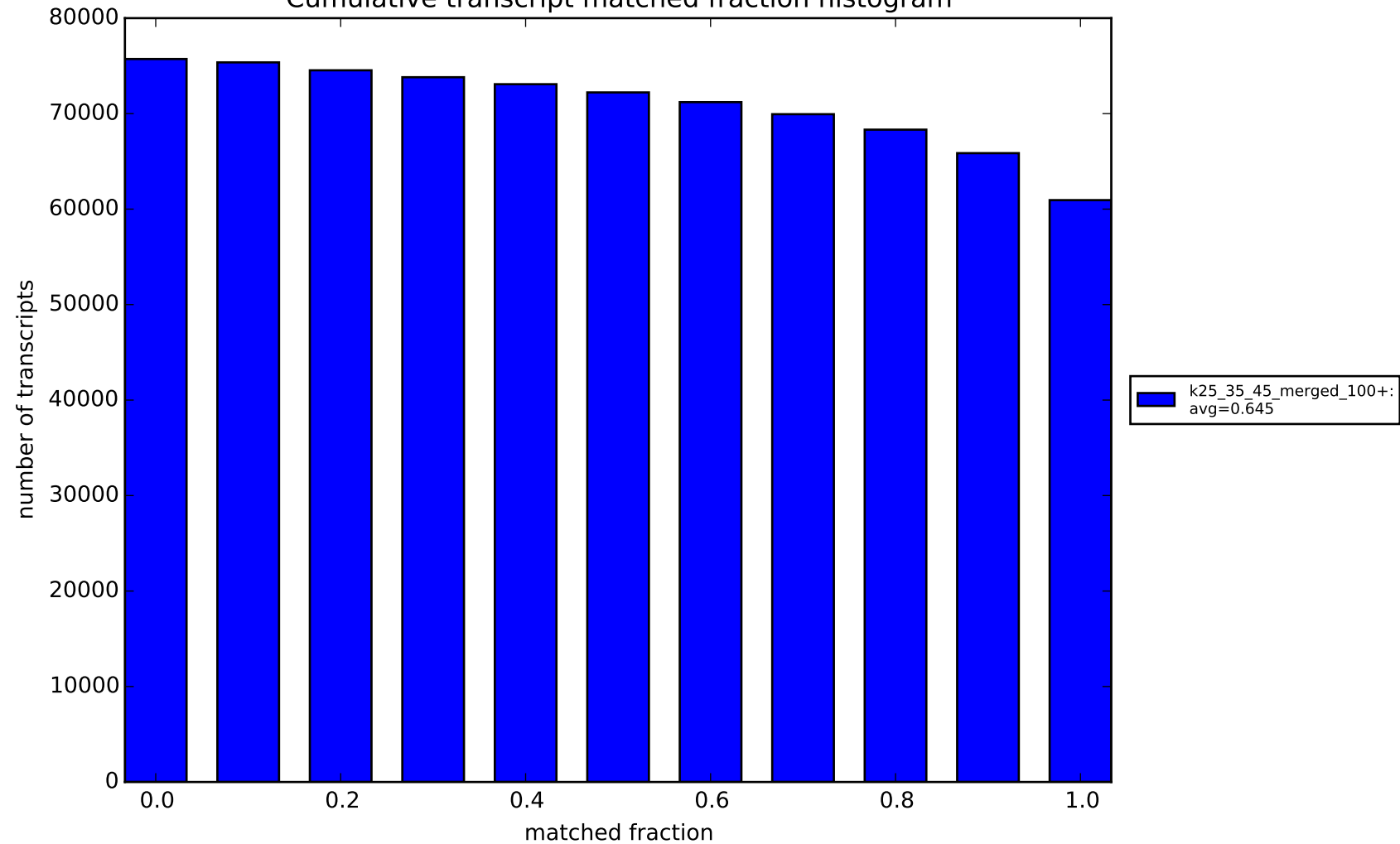
Cumulative substitution errors per alignment plot



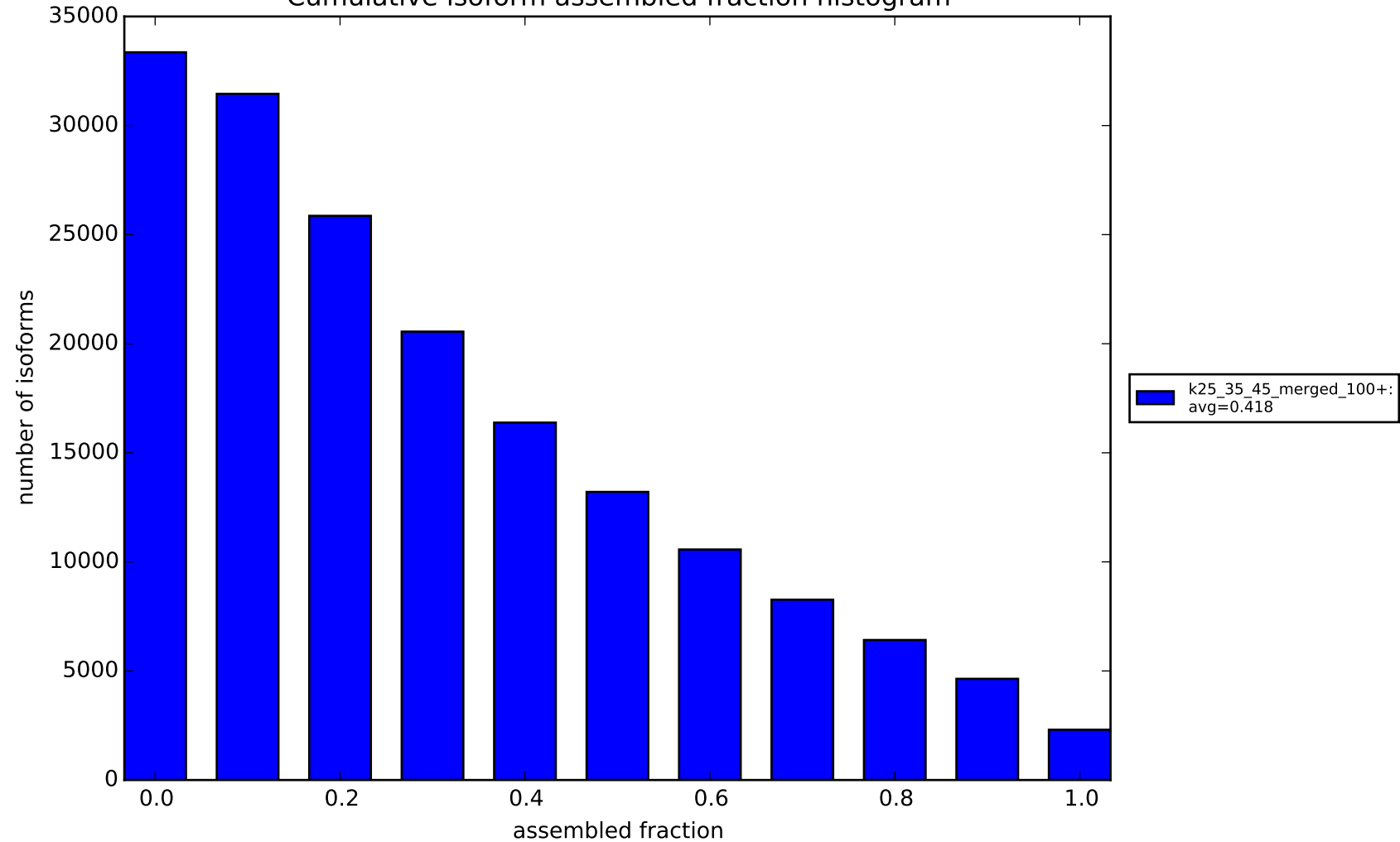
NAx



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

