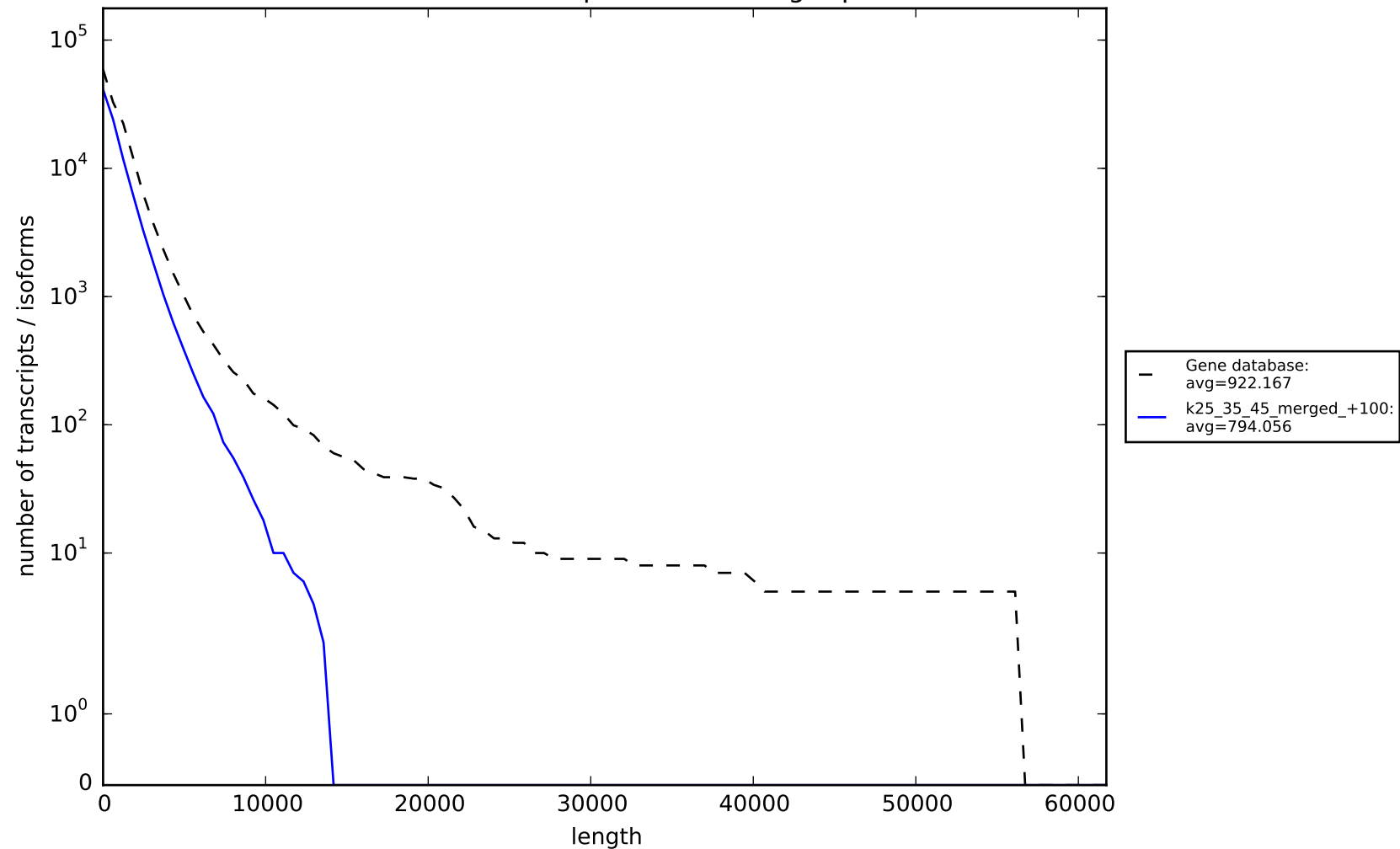


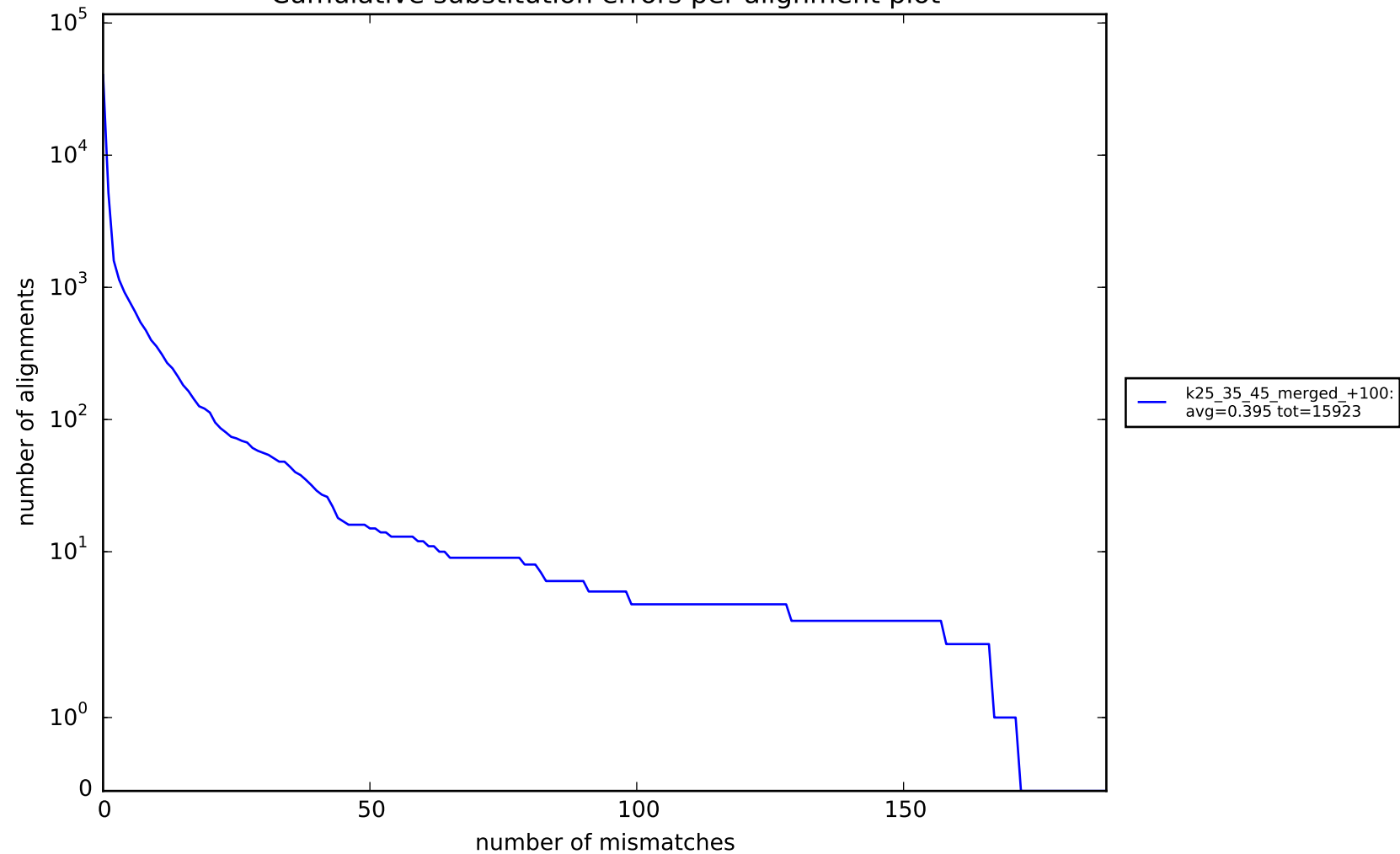
Short report

	k25_35_45_merged_+100
Genes	46739
Avg. number of exons per isoform	4.266
Transcripts	41126
Transcripts > 500 bp	18549
Transcripts > 1000 bp	10913
Aligned	41101
Uniquely aligned	39923
Multiply aligned	161
Unaligned	25
Avg. aligned fraction	0.991
Avg. alignment length	782.832
Avg. mismatches per transcript	0.395
Misassemblies	0
Database coverage	0.357
50%-assembled genes	9665
95%-assembled genes	5824
50%-covered genes	10844
95%-covered genes	6354
50%-assembled isoforms	10835
95%-assembled isoforms	6194
50%-covered isoforms	12193
95%-covered isoforms	6767
Mean isoform coverage	0.761
Mean isoform assembly	0.699
50%-matched	38563
95%-matched	32904
Unannotated	1092
Mean fraction of transcript matched	0.934

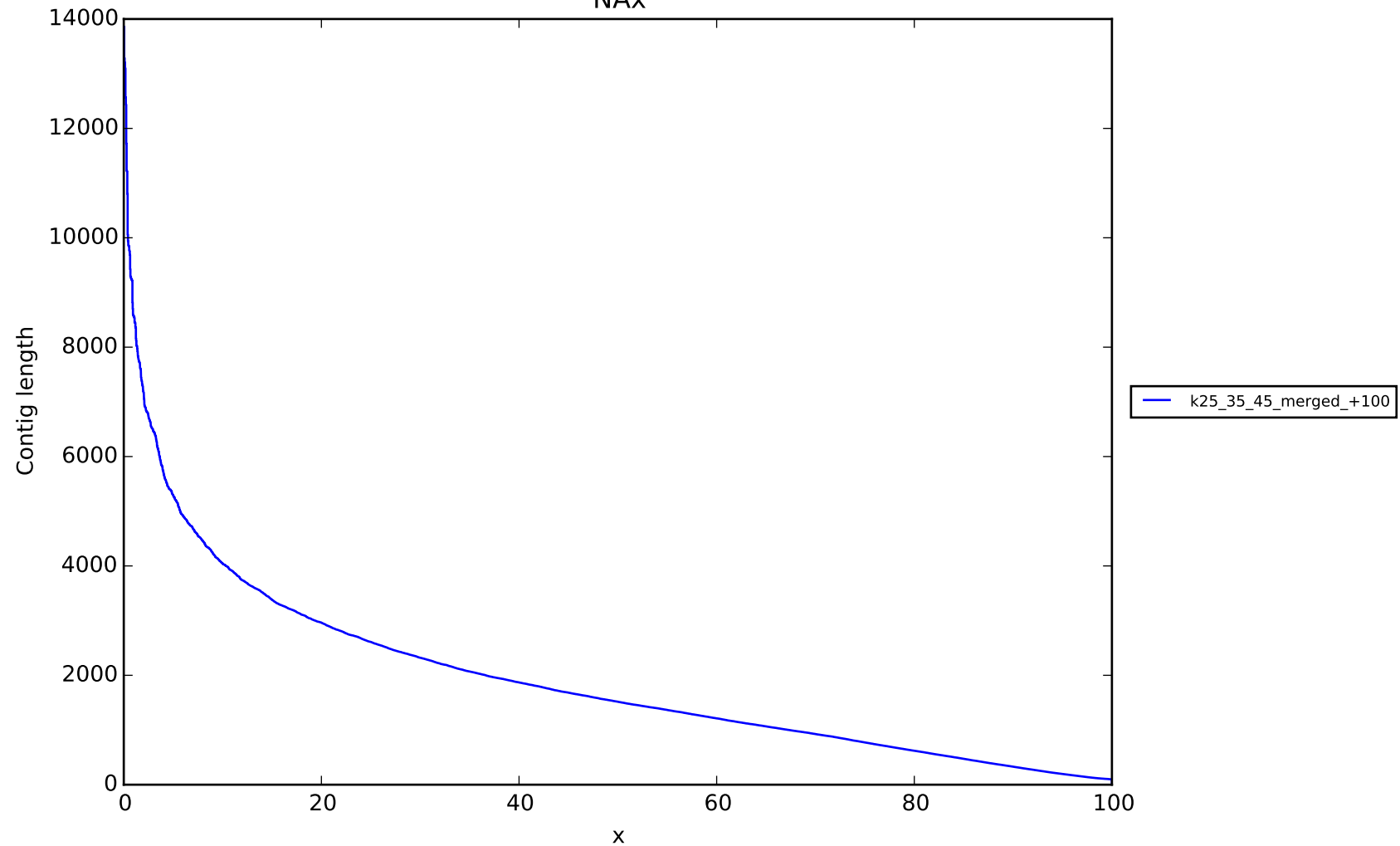
Cumulative transcript / isoform length plot



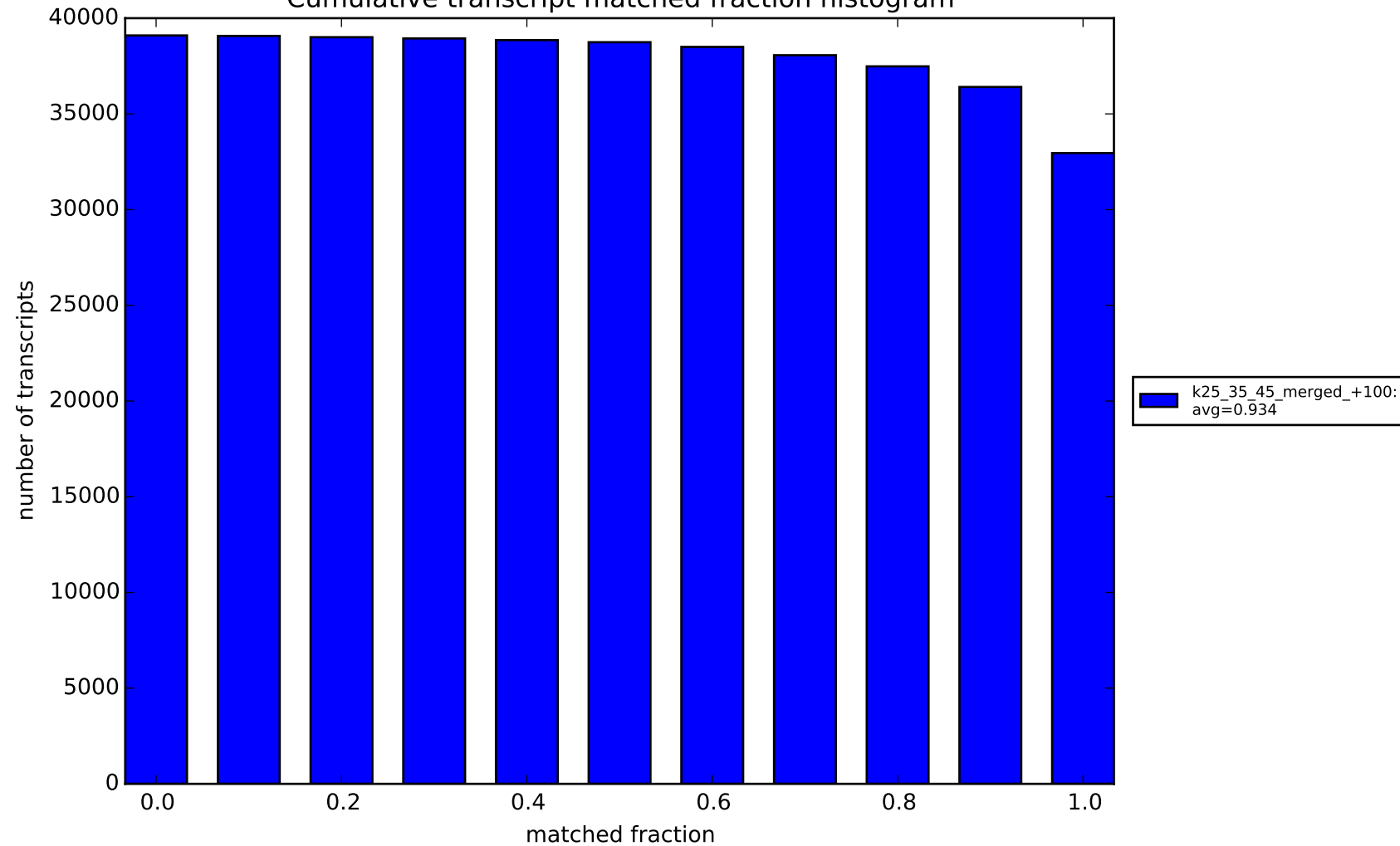
Cumulative substitution errors per alignment plot



NAX

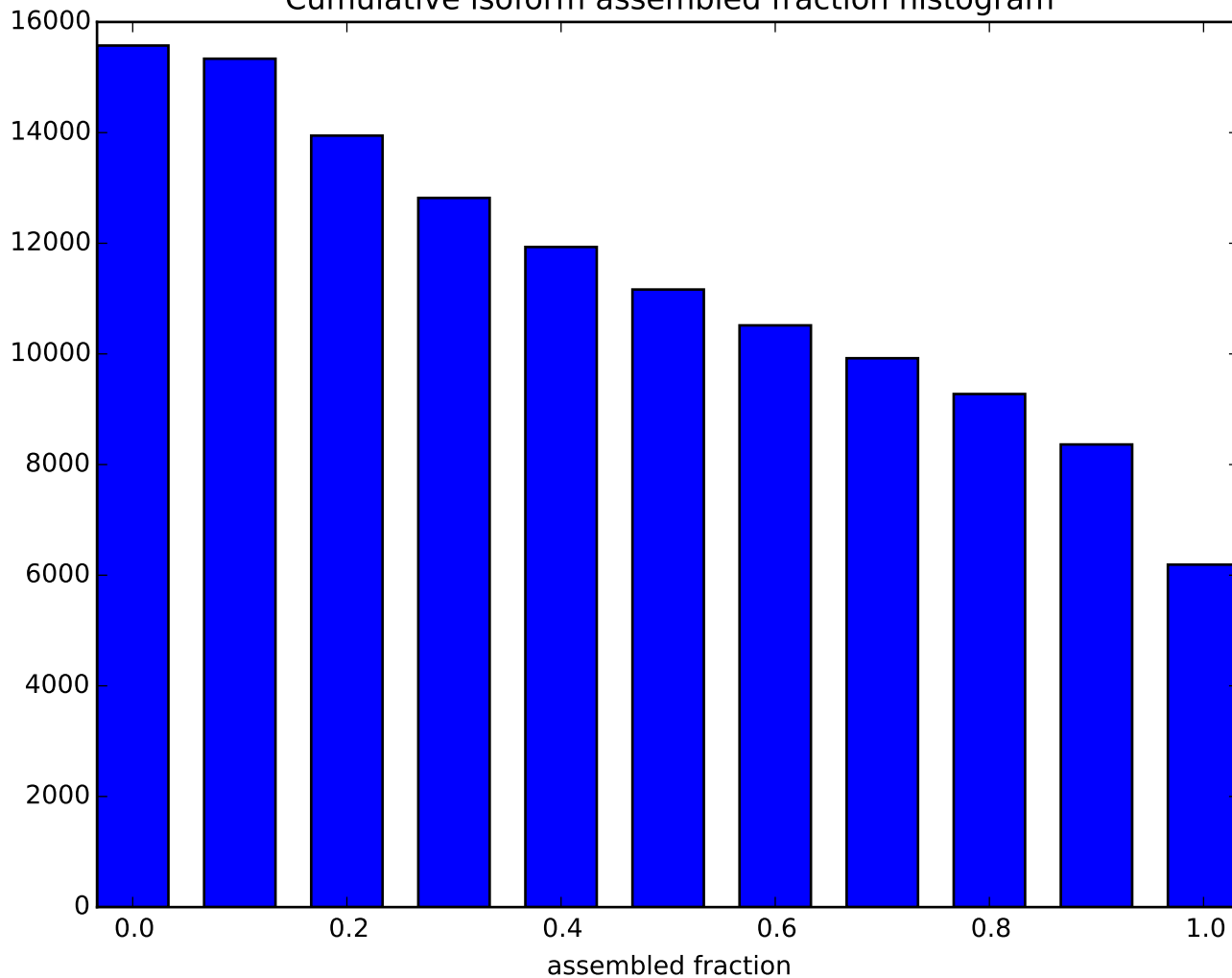


Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram

number of isoforms



k25_35_45_merged_+100:
avg=0.699

Cumulative isoform covered fraction histogram

