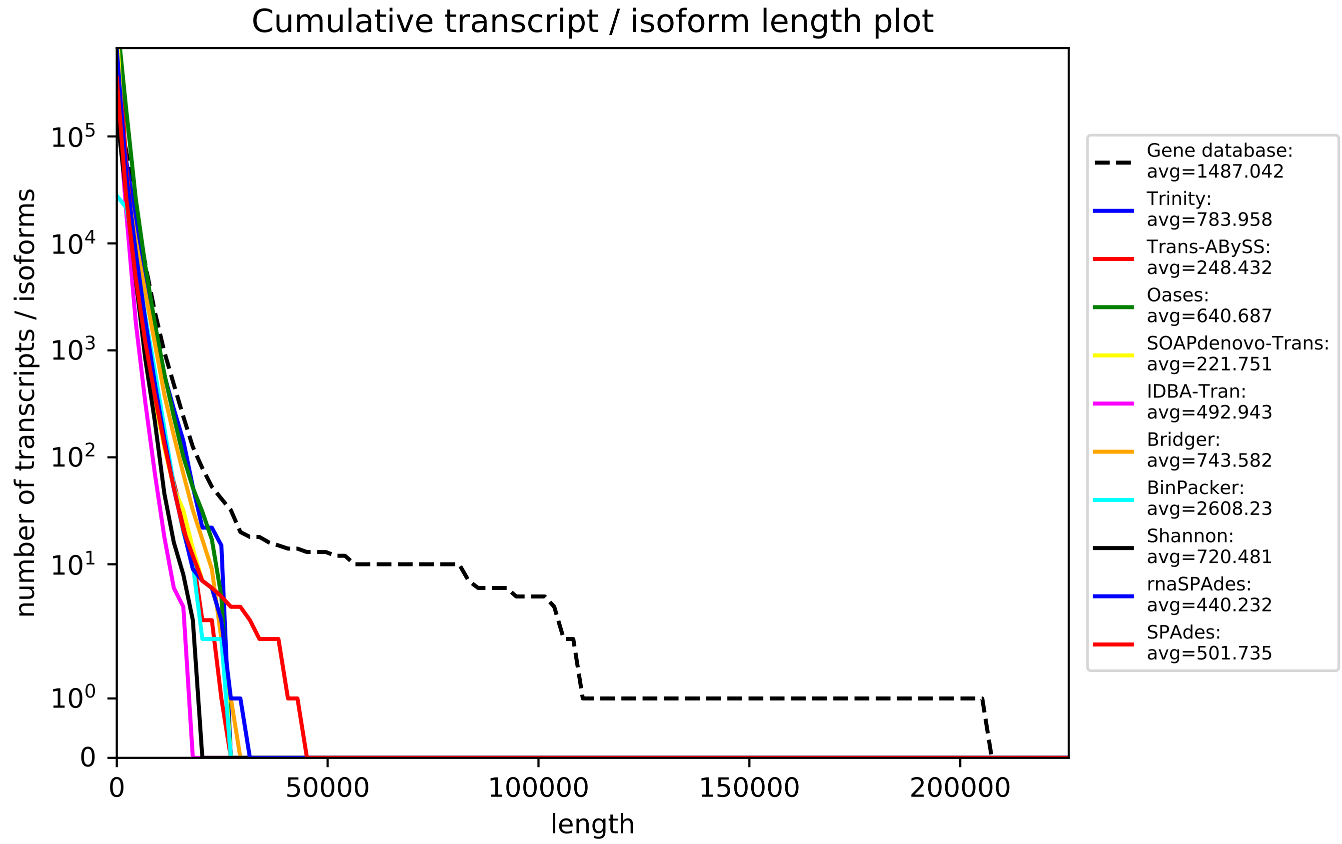
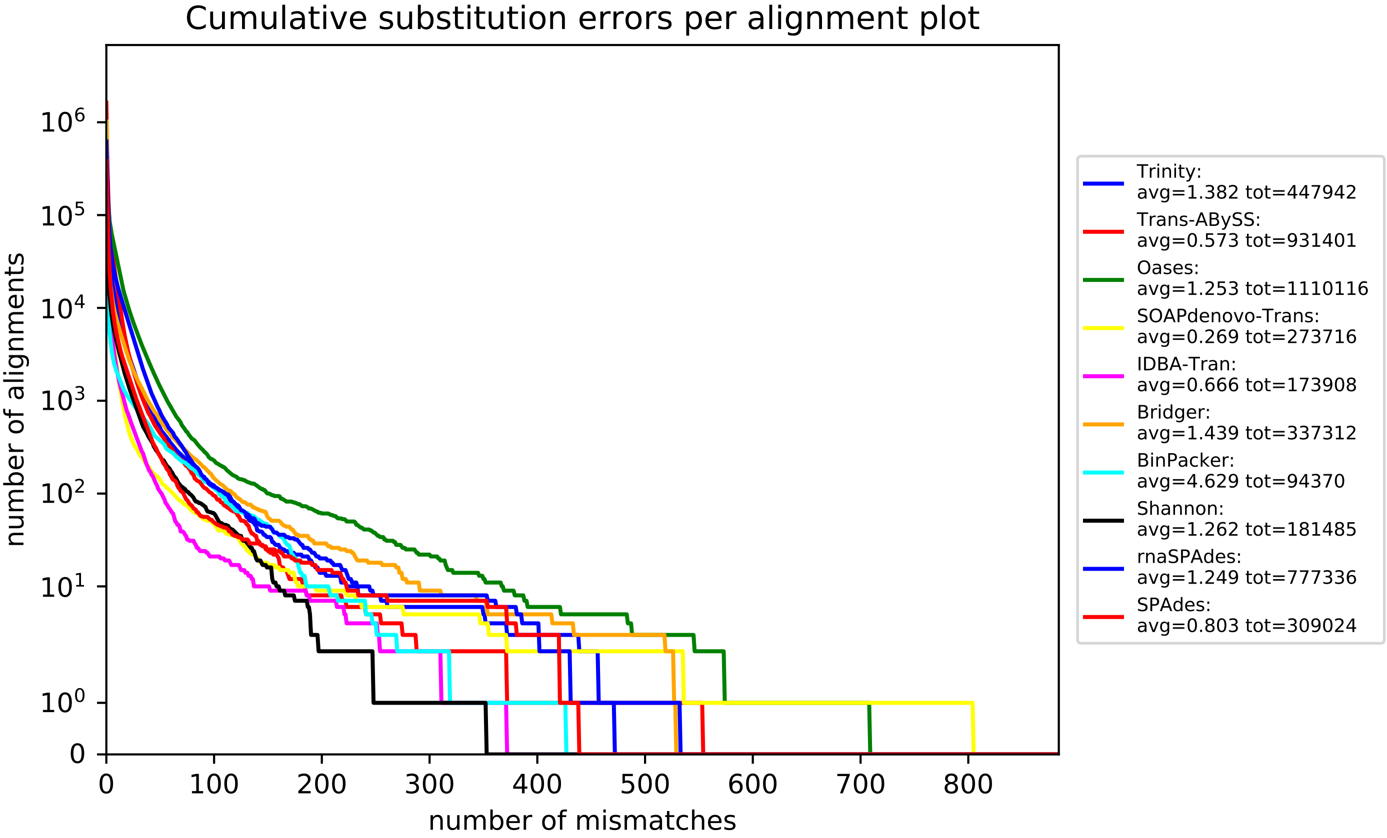
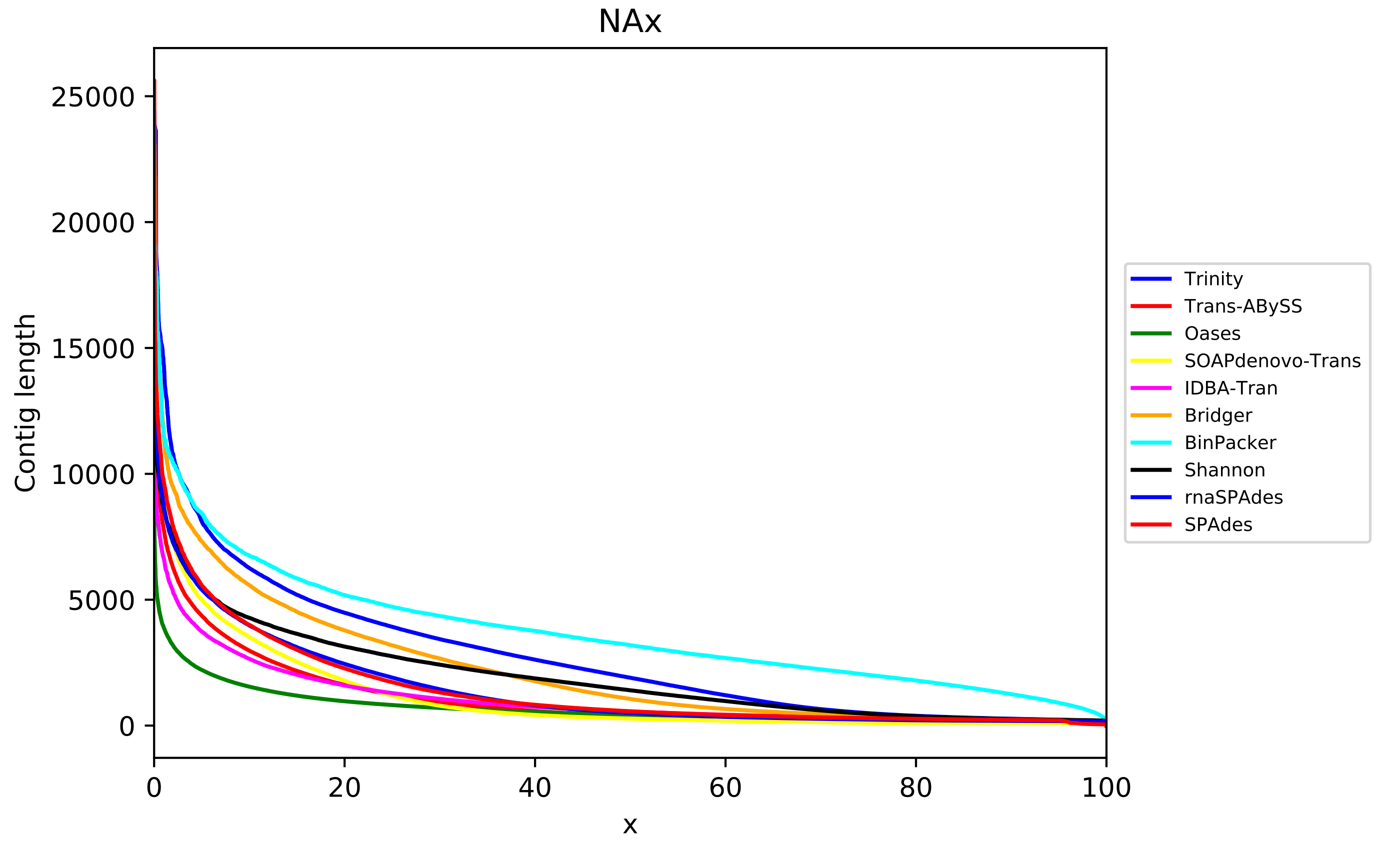
Short report

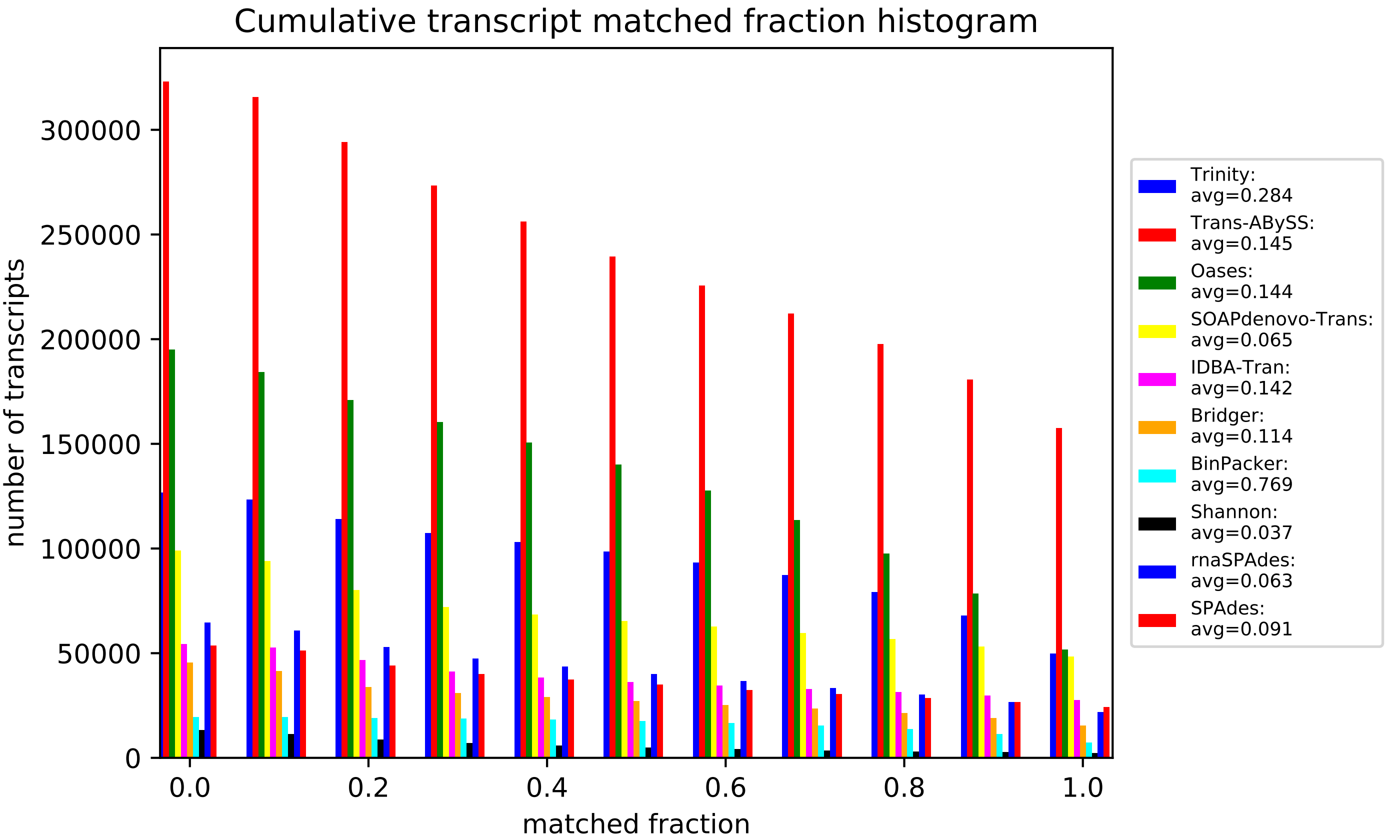
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	57992	57992	57992	57992	57992	57992	57992	57992	57992	57992
Avg. number of exons per isoform	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971
Transcripts	365427	1762439	1316143	1087869	281371	277892	27957	162486	668019	353728
Transcripts > 500 bp	113994	151362	479414	65513	71446	92081	26426	54363	112806	82573
Transcripts > 1000 bp	64061	59779	207474	27529	23516	43201	22611	31328	49860	31039
Aligned	330366	1606696	1209240	1008316	259491	255022	27709	150324	632083	332617
Uniquely aligned	317880	1576053	858267	994920	255855	230696	20274	140216	611585	303526
Multiply aligned	2514	18809	10571	8998	2087	1530	43	1451	4264	18281
Unaligned	35061	155743	106903	79553	21880	22870	248	12162	35936	21111
Avg. aligned fraction	0.992	0.992	0.884	0.996	0.997	0.99	0.969	0.992	0.99	0.994
Avg. alignment length	795.225	246.846	343.479	218.0	487.106	654.413	2335.729	711.831	412.238	410.224
Avg. mismatches per transcript	1.382	0.573	1.253	0.269	0.666	1.439	4.629	1.262	1.249	0.803
Misassemblies	3378	2743	216127	279	302	7329	5603	2837	5126	2022
Database coverage	0.216	0.282	0.083	0.103	0.09	0.074	0.055	0.008	0.118	0.086
50%-assembled genes	11313	12672	4206	6435	6471	5308	4121	934	8695	6626
95%-assembled genes	5228	5896	791	2110	709	1856	2358	242	3046	1747
50%-covered genes	12931	15579	5541	7760	7884	5818	4159	1195	9781	7556
95%-covered genes	6497	8459	1470	2494	1086	2028	2442	306	3540	2115
50%-assembled isoforms	20780	27440	7605	8091	7734	6725	6170	964	11077	7725
95%-assembled isoforms	6788	6824	868	2264	709	2105	2824	242	3253	1755
50%-covered isoforms	24709	40372	12584	9907	9846	7390	6254	1252	12681	9207
95%-covered isoforms	8548	10910	1718	2684	1087	2310	2952	307	3780	2124
Mean isoform coverage	0.505	0.479	0.332	0.265	0.35	0.331	0.698	0.284	0.369	0.337
Mean isoform assembly	0.45	0.382	0.268	0.231	0.311	0.312	0.689	0.252	0.339	0.306
Predicted genes	64574	83312	184371	33207	37937	40025	18636	21295	47886	33968
50%-matched	95985	232064	133920	63948	35324	26146	17124	4476	38308	33552
95%-matched	49795	157467	51746	48307	27491	15406	7291	2263	21942	24135
Unannotated	193800	1272363	674247	905050	203569	186773	860	128462	551412	268461
Mean fraction of transcript matched	0.284	0.145	0.144	0.065	0.142	0.114	0.769	0.037	0.063	0.091

generated by rnaQUAST

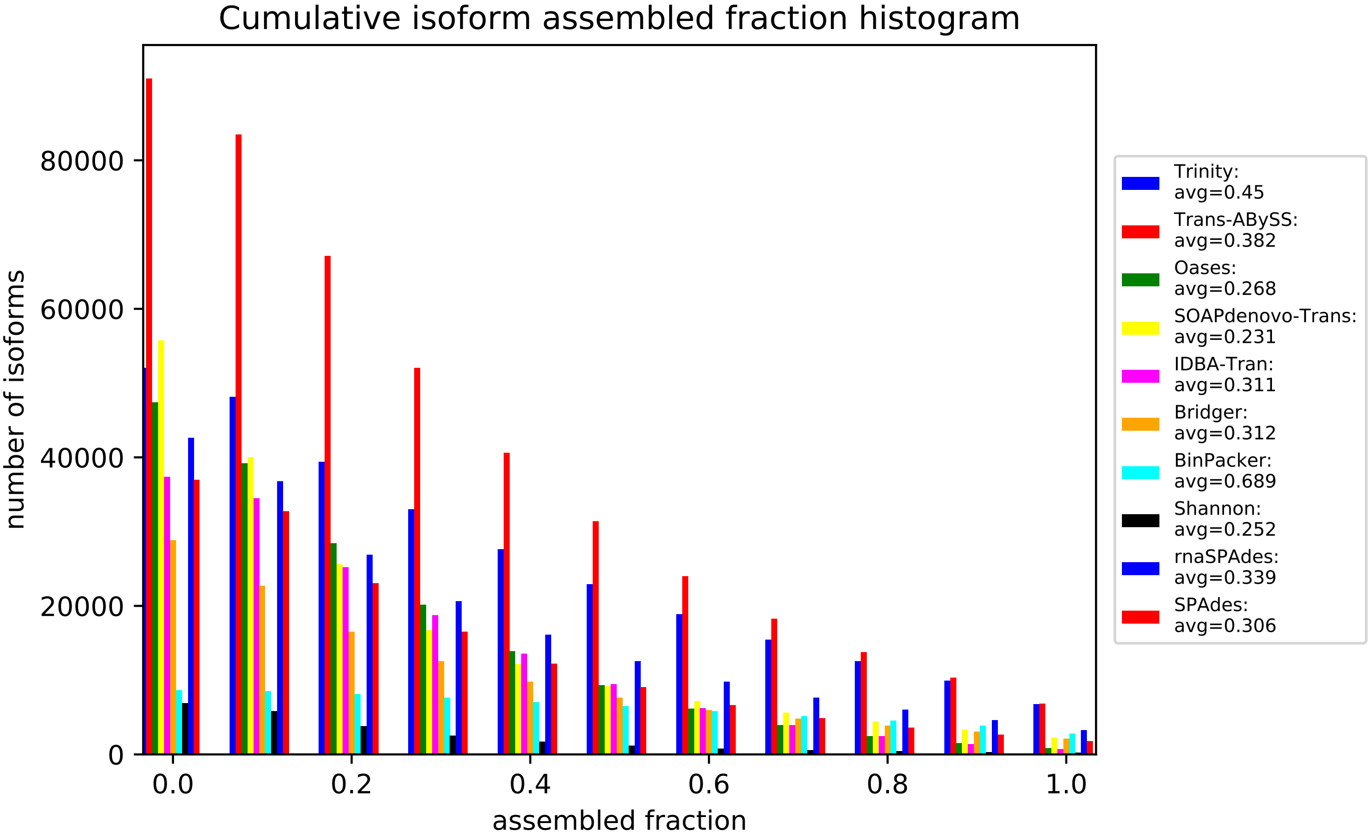

Cumulative transcript / isoform length plot
number of transcripts / isoforms
length
10^5
10^4
10^3
10^2
10^1
10^0
0
0
50000
100000
150000
200000
Gene database:
avg=1487.042
Trinity:
avg=783.958
Trans-ABySS:
avg=248.432
Oases:
avg=640.687
SOAPdenovo-Trans:
avg=221.751
IDBA-Tran:
avg=492.943
Bridger:
avg=743.582
BinPacker:
avg=2608.23
Shannon:
avg=720.481
rnaSPAdes:
avg=440.232
SPAdes:
avg=501.735

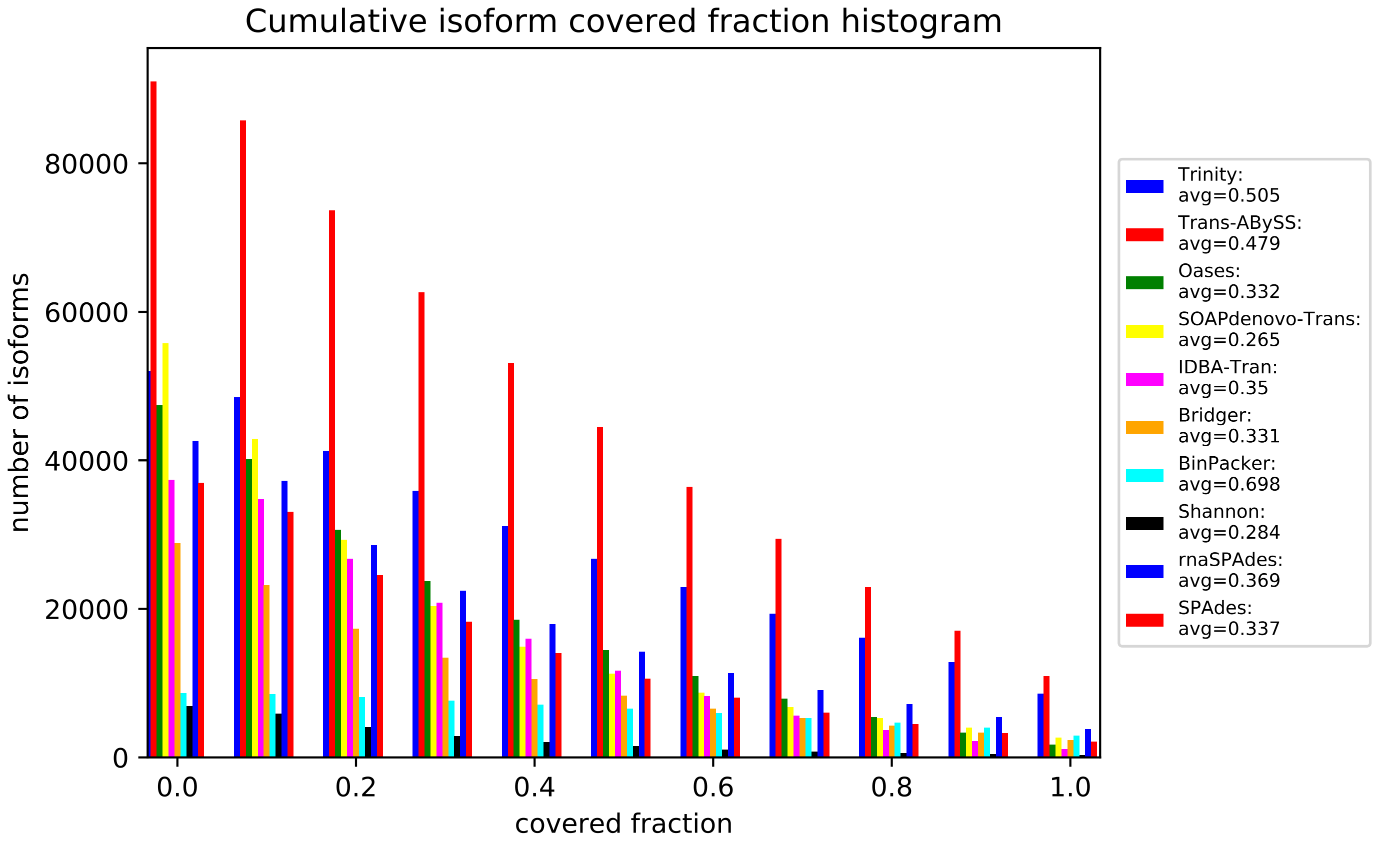

Cumulative substitution errors per alignment plot
number of alignments
number of mismatches
10^6
10^5
10^4
10^3
10^2
10^1
10^0
0
0
100
200
300
400
500
600
700
800
Trinity:
avg=1.382 tot=447942
Trans-ABySS:
avg=0.573 tot=931401
Oases:
avg=1.253 tot=1110116
SOAPdenovo-Trans:
avg=0.269 tot=273716
IDBA-Tran:
avg=0.666 tot=173908
Bridger:
avg=1.439 tot=337312
BinPacker:
avg=4.629 tot=94370
Shannon:
avg=1.262 tot=181485
rnaSPAdes:
avg=1.249 tot=777336
SPAdes:
avg=0.803 tot=309024


NAx
Contig length
25000
20000
15000
10000
5000
0
0
20
40
60
80
100
x
Trinity
Trans-ABySS
Oases
SOAPdenovo-Trans
IDBA-Tran
Bridger
BinPacker
Shannon
rnaSPAdes
SPAdes



Cumulative transcript matched fraction histogram
number of transcripts
0
50000
100000
150000
200000
250000
300000
matched fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity:
avg=0.284
Trans-ABySS:
avg=0.145
Oases:
avg=0.144
SOAPdenovo-Trans:
avg=0.065
IDBA-Tran:
avg=0.142
Bridger:
avg=0.114
BinPacker:
avg=0.769
Shannon:
avg=0.037
rnaSPAdes:
avg=0.063
SPAdes:
avg=0.091


Cumulative isoform assembled fraction histogram
number of isoforms
0
20000
40000
60000
80000
assembled fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.45
Trans-ABySS: avg=0.382
Oases: avg=0.268
SOAPdenovo-Trans: avg=0.231
IDBA-Tran: avg=0.311
Bridger: avg=0.312
BinPacker: avg=0.689
Shannon: avg=0.252
rnaSPAdes: avg=0.339
SPAdes: avg=0.306


Cumulative isoform covered fraction histogram
number of isoforms
0
20000
40000
60000
80000
covered fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.505
Trans-ABySS: avg=0.479
Oases: avg=0.332
SOAPdenovo-Trans: avg=0.265
IDBA-Tran: avg=0.35
Bridger: avg=0.331
BinPacker: avg=0.698
Shannon: avg=0.284
rnaSPAdes: avg=0.369
SPAdes: avg=0.337