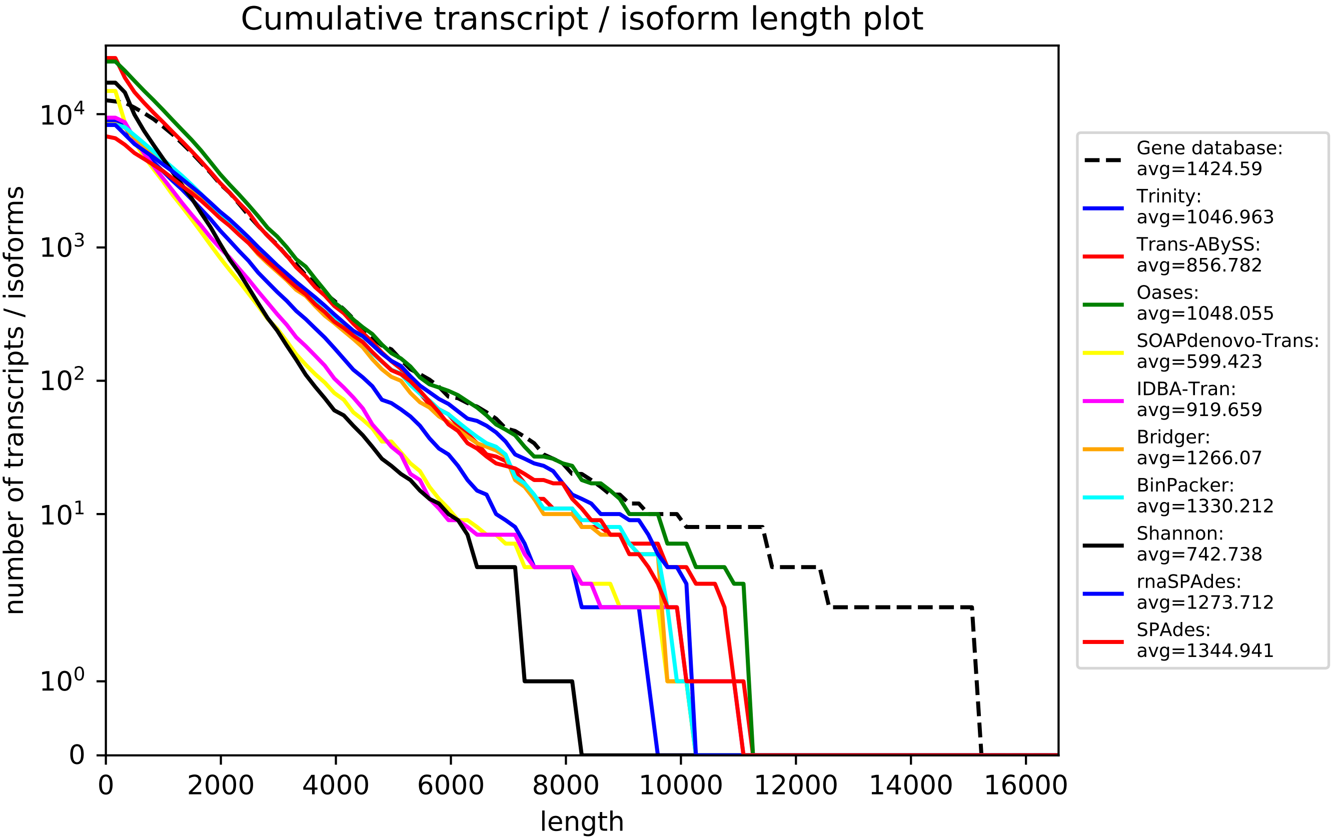
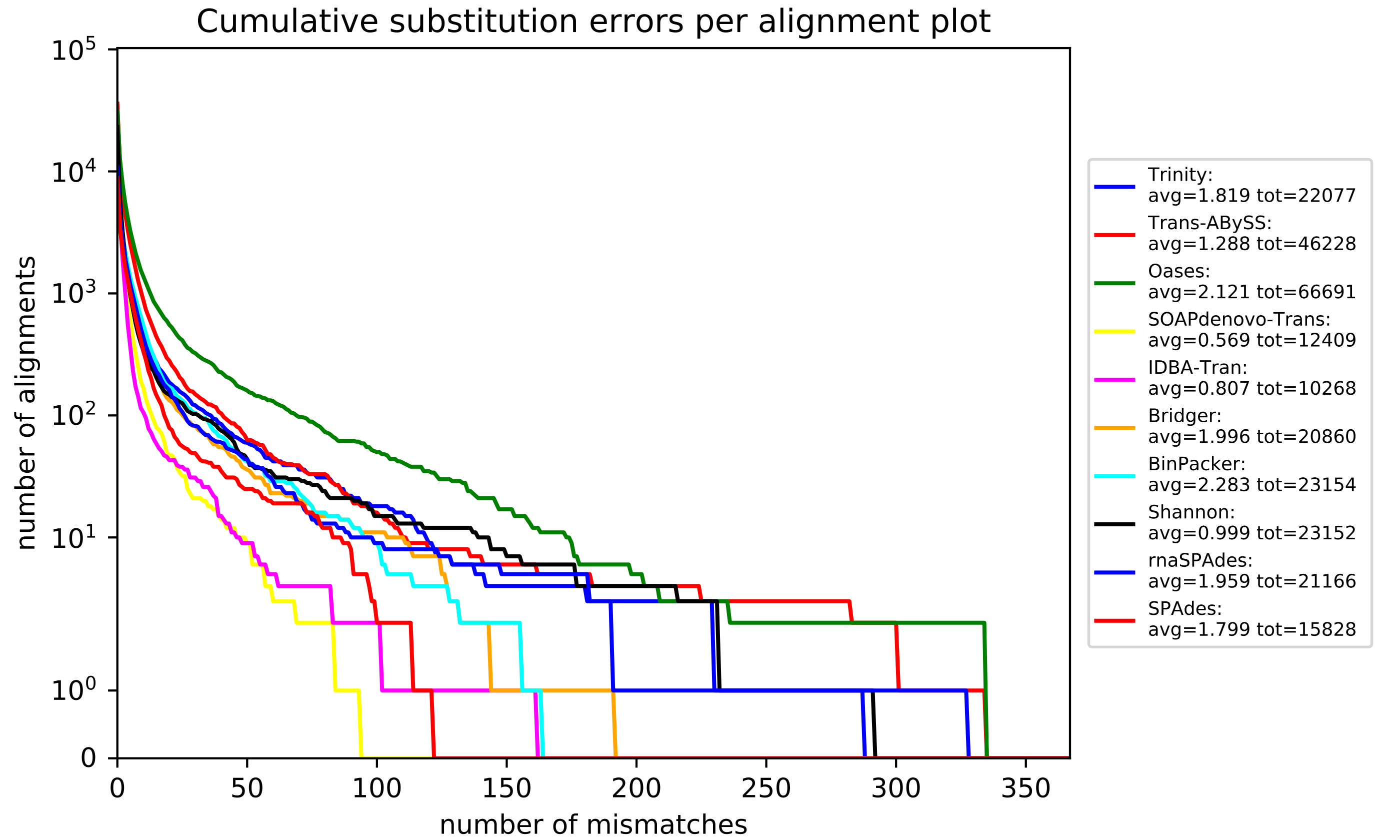
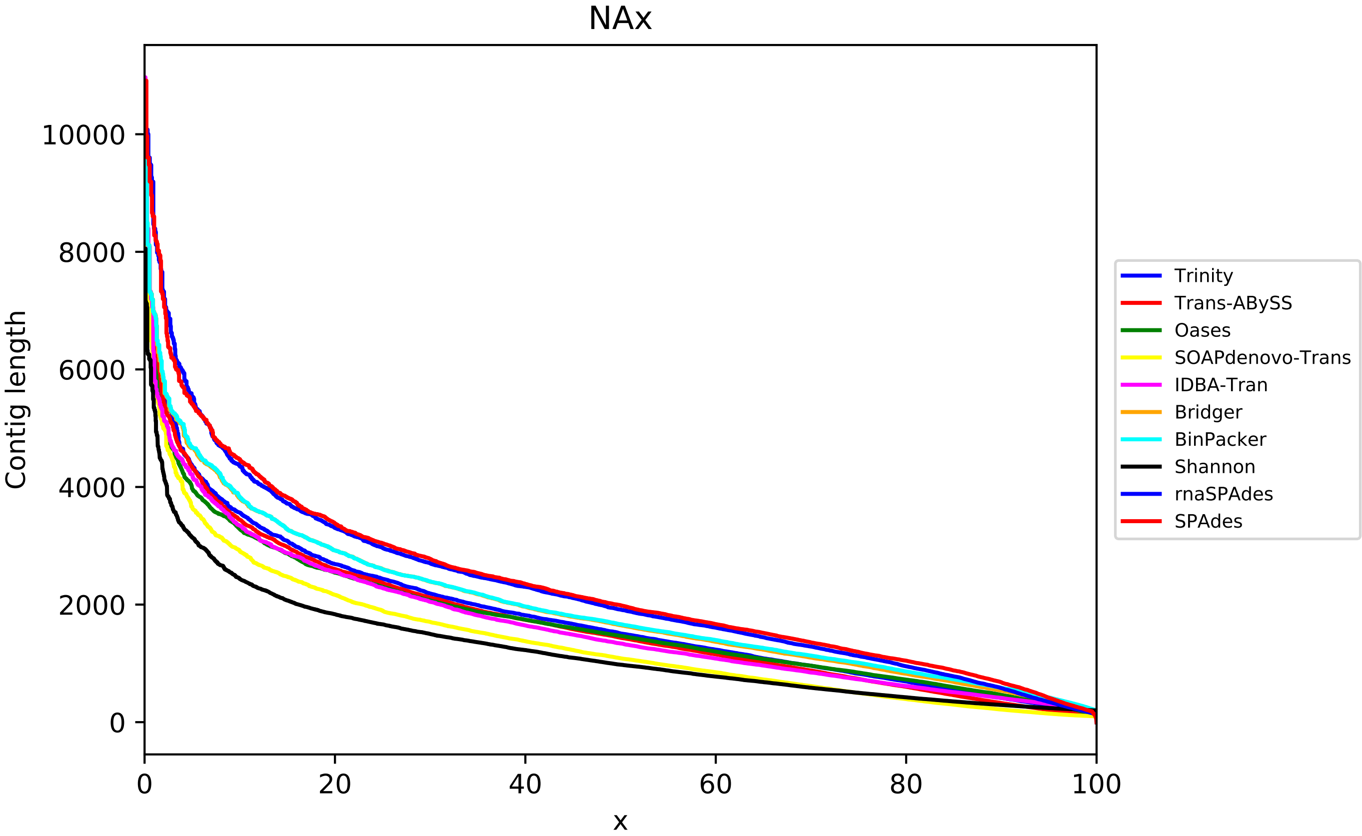
Short report

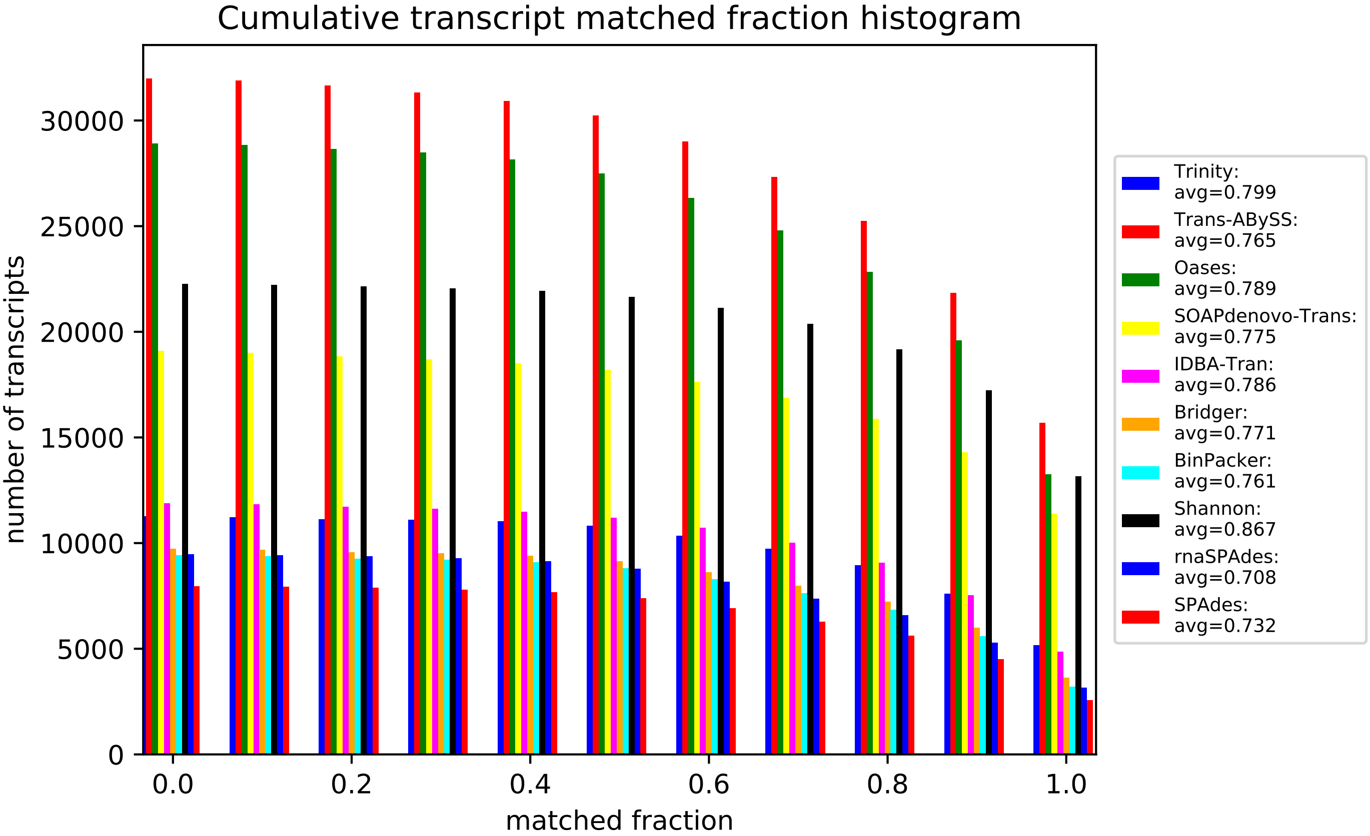
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	12867	12867	12867	12867	12867	12867	12867	12867	12867	12867
Avg. number of exons per isoform	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075	1.075
Transcripts	8970	26356	24818	14927	9408	8413	8324	17225	8297	6821
Transcripts > 500 bp	5578	13304	16371	5424	5711	6159	6485	8567	5614	4858
Transcripts > 1000 bp	3417	7979	9813	2769	2949	4038	4267	4077	3939	3504
Aligned	8786	25928	24192	14724	9238	8226	8138	17071	8092	6502
Uniquely aligned	5000	14459	14556	7606	5725	4853	4905	8573	4847	3983
Multiply aligned	3565	10667	8399	7073	3484	2796	2610	7282	2961	2393
Unaligned	184	428	626	203	170	187	186	154	205	319
Avg. aligned fraction	0.994	0.988	0.986	0.997	0.996	0.987	0.985	0.993	0.988	0.99
Avg. alignment length	969.327	773.584	941.6	567.169	922.096	1131.326	1189.552	678.947	1171.714	1279.411
Avg. mismatches per transcript	1.819	1.288	2.121	0.569	0.807	1.996	2.283	0.999	1.959	1.799
Misassemblies	72	449	613	9	8	236	259	362	82	60
Database coverage	0.511	0.653	0.604	0.564	0.527	0.476	0.47	0.541	0.508	0.485
50%-assembled genes	5302	6734	6425	5362	5380	5136	5162	5475	5413	5266
95%-assembled genes	4146	5214	4808	3290	3238	4005	4033	3736	4533	4437
50%-covered genes	6011	7833	7237	6742	6229	5581	5556	6884	5819	5529
95%-covered genes	4585	5884	5450	4522	4003	4322	4343	4562	4783	4542
50%-assembled isoforms	5302	6734	6425	5362	5380	5136	5162	5475	5413	5266
95%-assembled isoforms	4146	5214	4808	3290	3238	4005	4033	3736	4533	4437
50%-covered isoforms	6011	7833	7237	6742	6229	5581	5556	6884	5819	5529
95%-covered isoforms	4585	5884	5450	4522	4003	4322	4343	4562	4783	4542
Mean isoform coverage	0.817	0.832	0.819	0.756	0.771	0.809	0.82	0.771	0.849	0.852
Mean isoform assembly	0.746	0.748	0.749	0.629	0.687	0.76	0.776	0.66	0.806	0.822
50%-matched	7488	20937	19840	12185	7998	6537	6370	14640	6225	5246
95%-matched	3529	10745	9568	7596	3595	2587	2313	8873	2206	1793
Unannotated	591	2559	1653	1706	574	502	495	604	884	568
Mean fraction of transcript matched	0.799	0.765	0.789	0.775	0.786	0.771	0.761	0.867	0.708	0.732

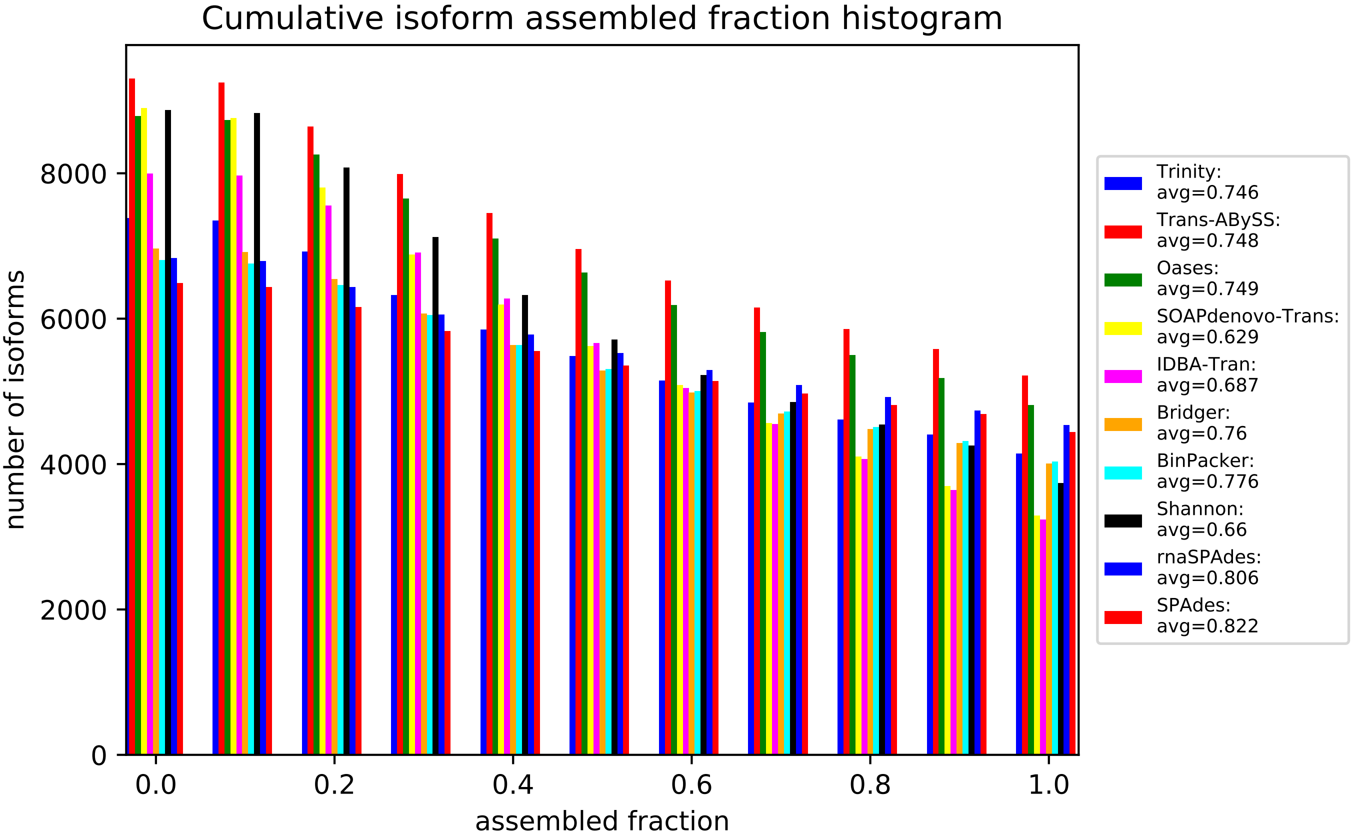
generated by rnaQUAST

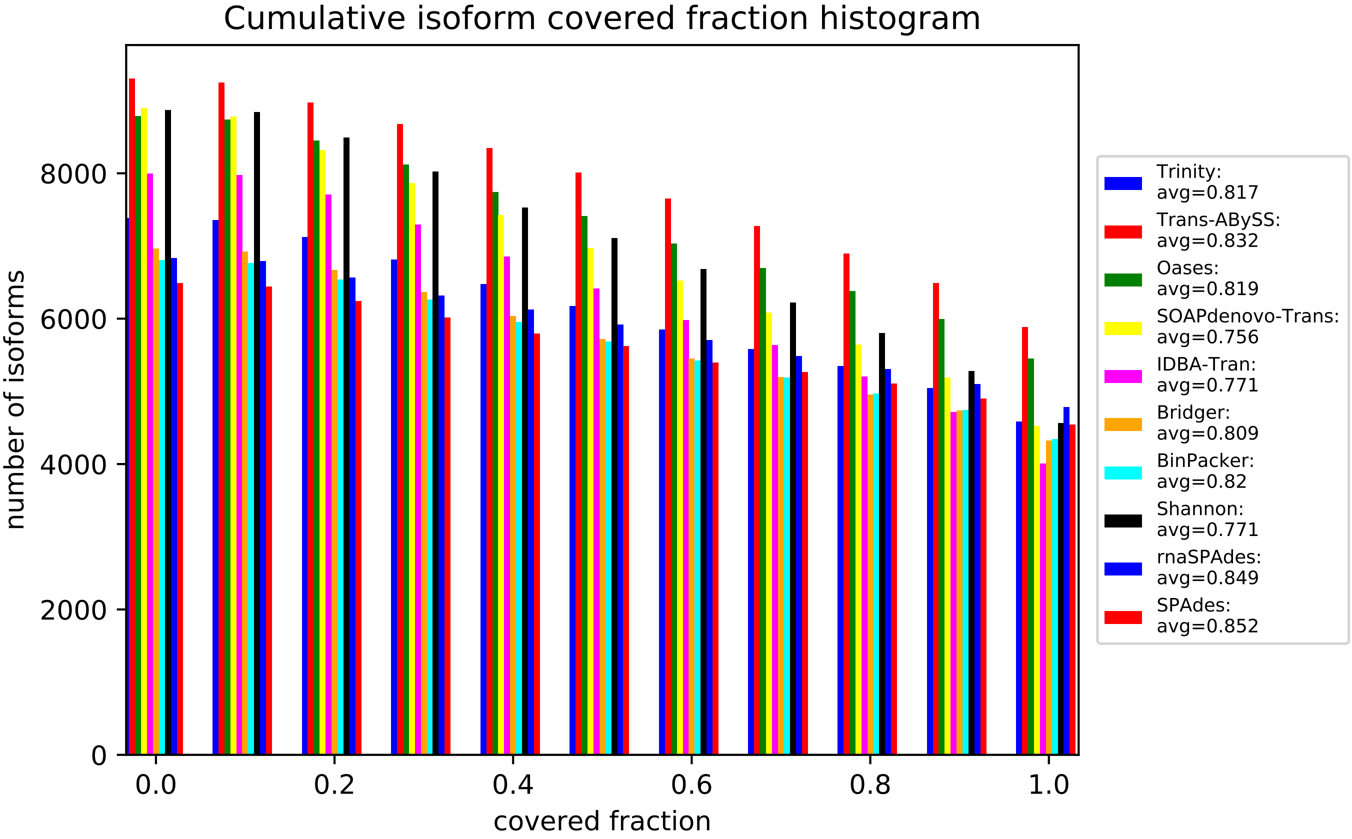

Cumulative transcript / isoform length plot
number of transcripts / isoforms
10^4
10^3
10^2
10^1
10^0
0
0
2000
4000
6000
8000
10000
12000
14000
16000
length
Gene database: avg=1424.59
Trinity: avg=1046.963
Trans-ABySS: avg=856.782
Oases: avg=1048.055
SOAPdenovo-Trans: avg=599.423
IDBA-Tran: avg=919.659
Bridger: avg=1266.07
BinPacker: avg=1330.212
Shannon: avg=742.738
rnaSPAdes: avg=1273.712
SPAdes: avg=1344.941


Cumulative substitution errors per alignment plot
number of alignments
number of mismatches
10^5
10^4
10^3
10^2
10^1
10^0
0
0
50
100
150
200
250
300
350
Trinity:
avg=1.819 tot=22077
Trans-ABySS:
avg=1.288 tot=46228
Oases:
avg=2.121 tot=66691
SOAPdenovo-Trans:
avg=0.569 tot=12409
IDBA-Tran:
avg=0.807 tot=10268
Bridger:
avg=1.996 tot=20860
BinPacker:
avg=2.283 tot=23154
Shannon:
avg=0.999 tot=23152
rnaSPAdes:
avg=1.959 tot=21166
SPAdes:
avg=1.799 tot=15828


NAx
Contig length
10000
8000
6000
4000
2000
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
5000
10000
15000
20000
25000
30000
0.0
0.2
0.4
0.6
0.8
1.0
matched fraction
Trinity: avg=0.799
Trans-ABySS: avg=0.765
Oases: avg=0.789
SOAPdenovo-Trans: avg=0.775
IDBA-Tran: avg=0.786
Bridger: avg=0.771
BinPacker: avg=0.761
Shannon: avg=0.867
rnaSPAdes: avg=0.708
SPAdes: avg=0.732


Cumulative isoform assembled fraction histogram
number of isoforms
0
2000
4000
6000
8000
0.0
0.2
0.4
0.6
0.8
1.0
assembled fraction
Trinity: avg=0.746
Trans-ABySS: avg=0.748
Oases: avg=0.749
SOAPdenovo-Trans: avg=0.629
IDBA-Tran: avg=0.687
Bridger: avg=0.76
BinPacker: avg=0.776
Shannon: avg=0.66
rnaSPAdes: avg=0.806
SPAdes: avg=0.822


Cumulative isoform covered fraction histogram
number of isoforms
0
2000
4000
6000
8000
0.0
0.2
0.4
0.6
0.8
1.0
covered fraction
Trinity: avg=0.817
Trans-ABySS: avg=0.832
Oases: avg=0.819
SOAPdenovo-Trans: avg=0.756
IDBA-Tran: avg=0.771
Bridger: avg=0.809
BinPacker: avg=0.82
Shannon: avg=0.771
rnaSPAdes: avg=0.849
SPAdes: avg=0.852