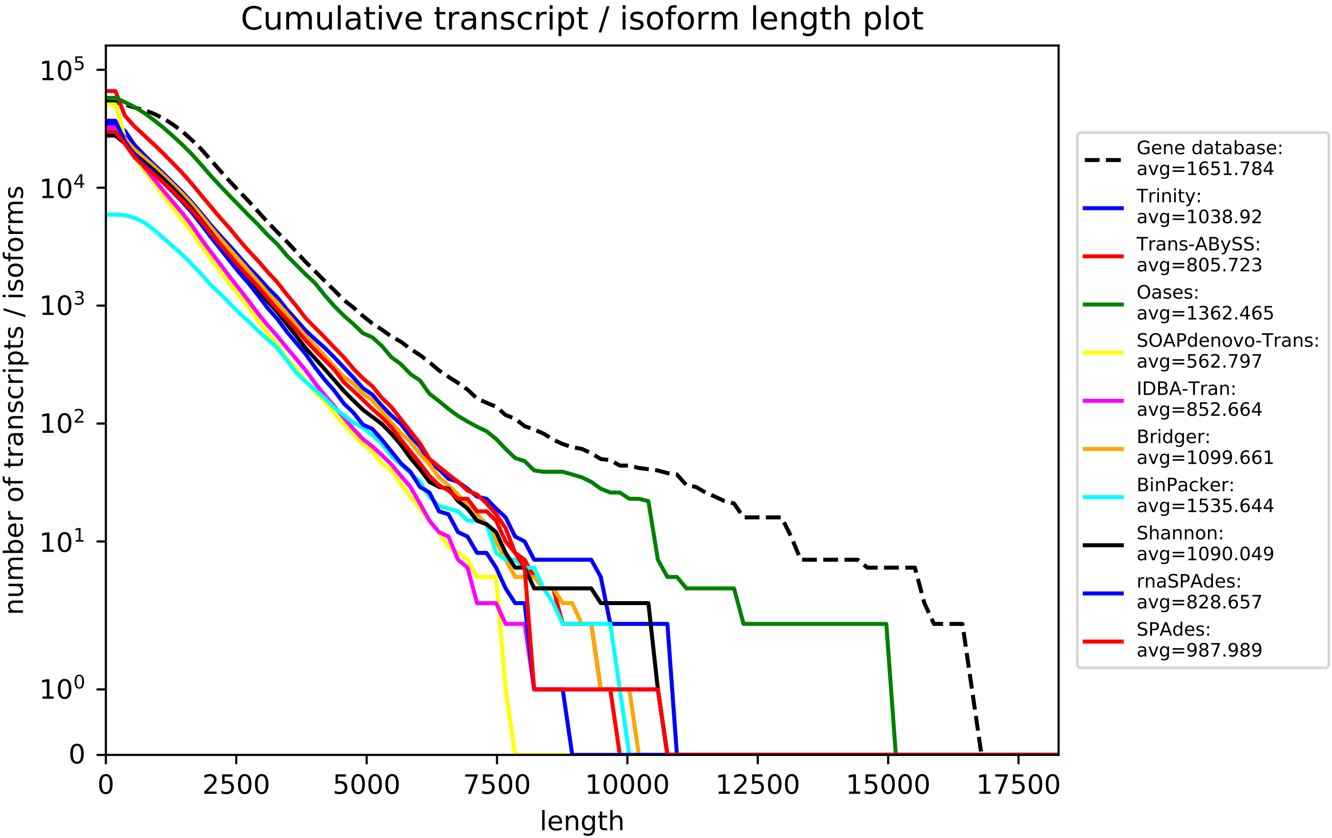
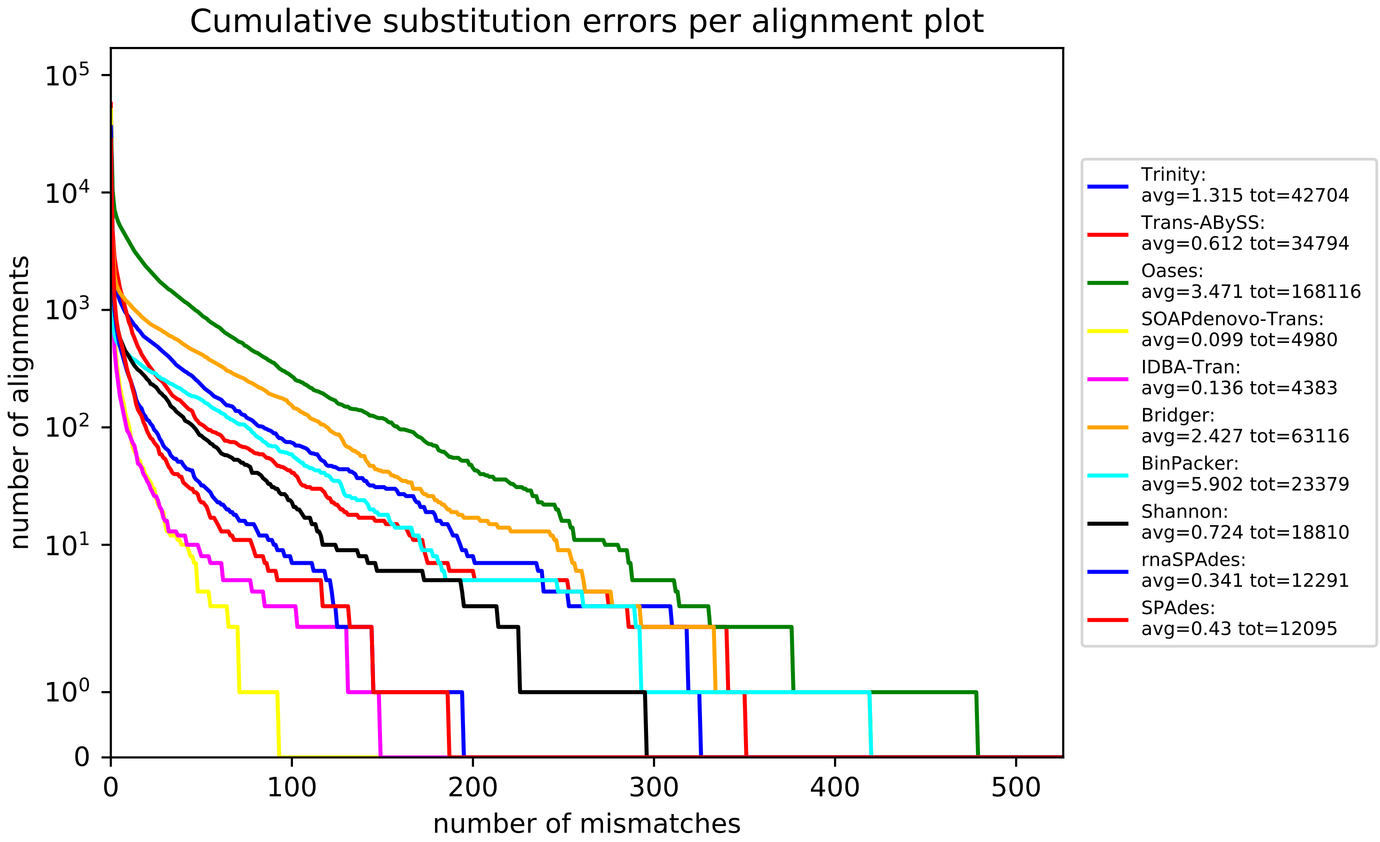
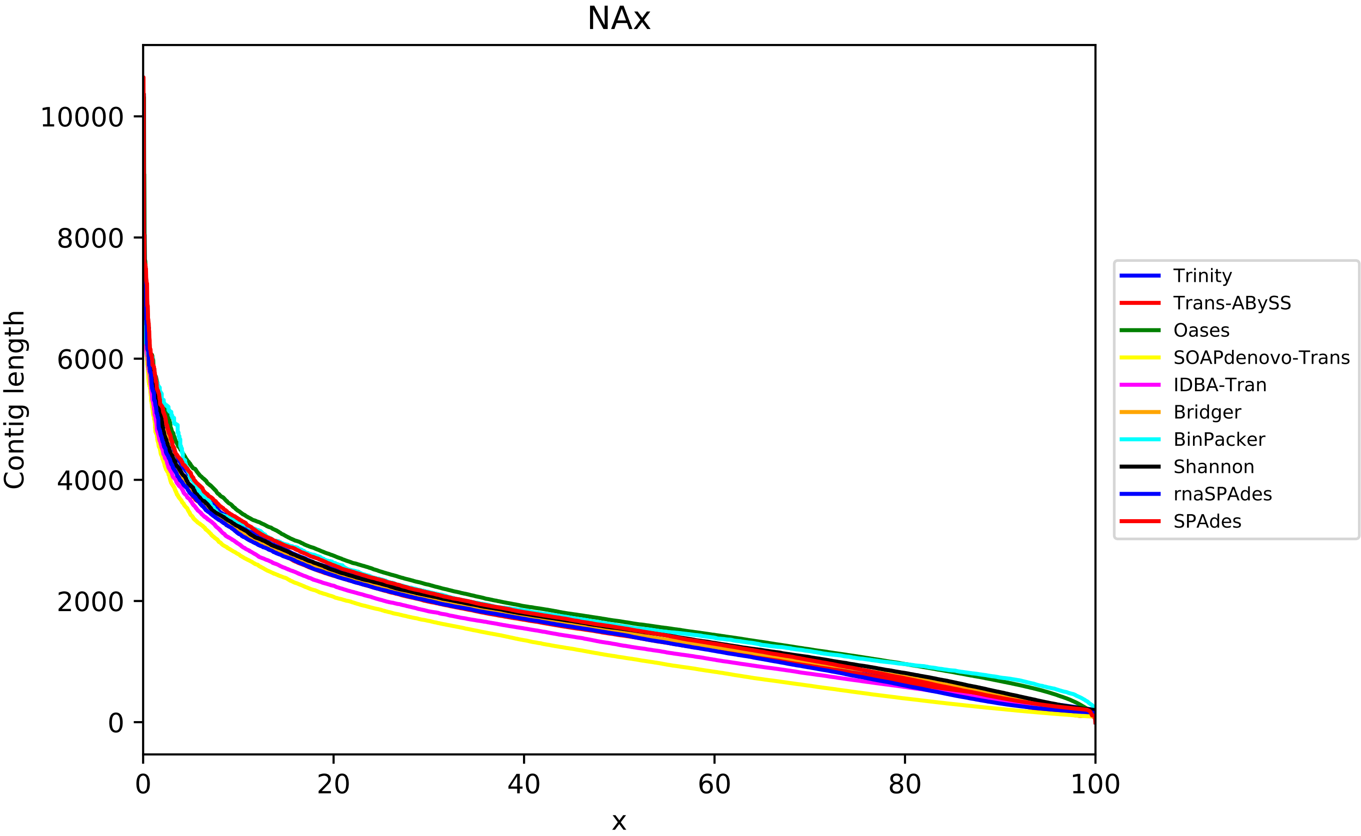
Short report

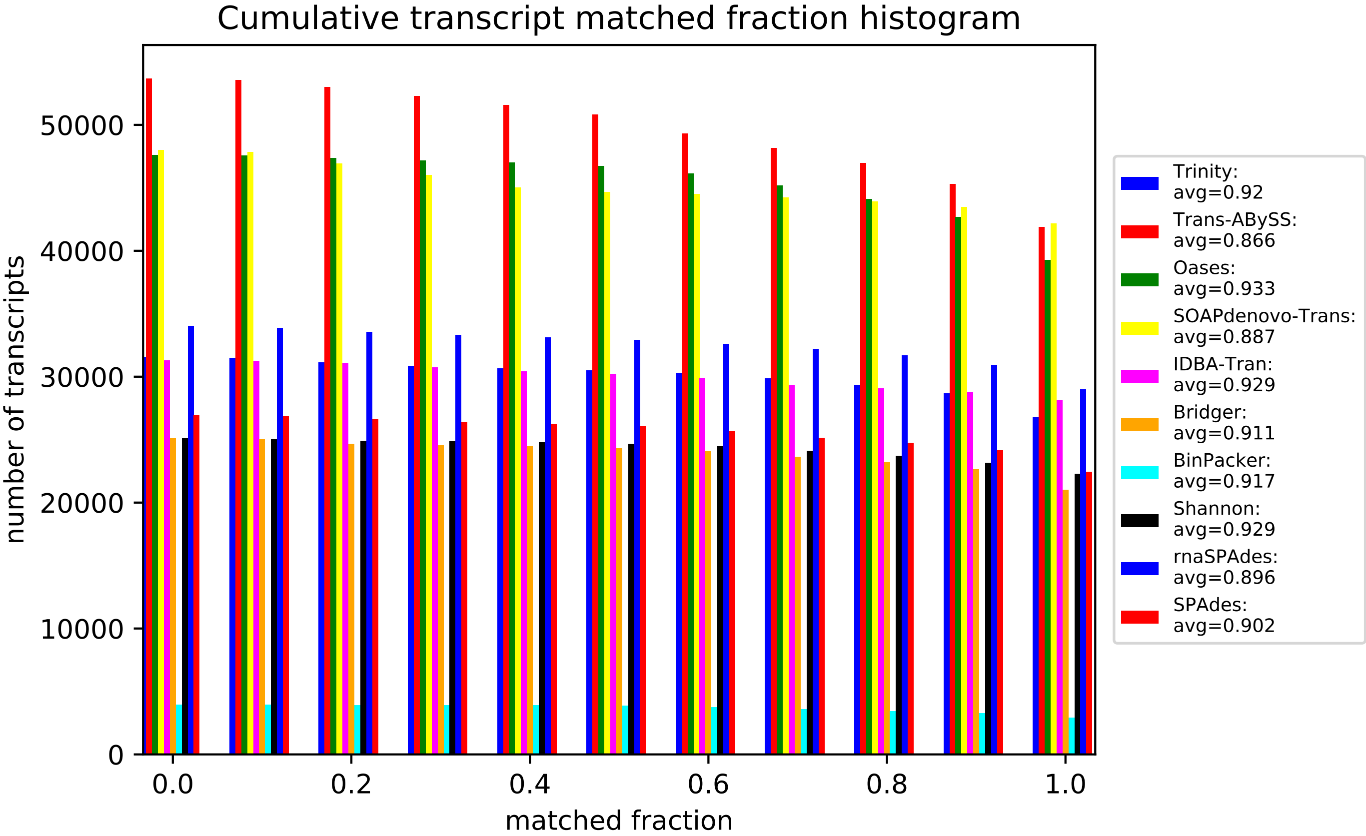
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	32833	32833	32833	32833	32833	32833	32833	32833	32833	32833
Avg. number of exons per isoform	5.813	5.813	5.813	5.813	5.813	5.813	5.813	5.813	5.813	5.813
Transcripts	34617	66004	57809	50876	32447	30017	5914	27685	36953	29929
Transcripts > 500 bp	21969	31763	47279	17326	18147	20235	5458	18623	18068	17390
Transcripts > 1000 bp	13357	19714	32647	8709	9577	12882	3775	12018	11160	11171
Aligned	34432	65463	57441	50525	32366	29822	5891	27478	36628	29691
Uniquely aligned	32388	56460	48302	50289	32020	25907	3945	25912	35821	27985
Multiply aligned	44	176	66	119	54	45	8	37	91	62
Unaligned	185	541	368	351	81	195	23	207	325	238
Avg. aligned fraction	0.993	0.979	0.988	0.997	0.998	0.99	0.976	0.996	0.995	0.993
Avg. alignment length	978.213	745.088	1232.688	561.746	848.356	990.349	1312.171	1044.904	807.422	944.388
Avg. mismatches per transcript	1.315	0.612	3.471	0.099	0.136	2.427	5.902	0.724	0.341	0.43
Misassemblies	1212	7227	6804	51	201	1995	1233	769	505	1189
Database coverage	0.298	0.334	0.321	0.299	0.289	0.256	0.047	0.245	0.3	0.279
50%-assembled genes	12459	13755	13955	11457	12672	11301	2589	11168	12931	12496
95%-assembled genes	2196	1881	2599	1213	1175	1861	477	1962	2233	2318
50%-covered genes	14388	15660	14680	15357	14963	12519	2609	12207	15136	13998
95%-covered genes	2542	2200	2812	1770	1642	2076	488	2103	2607	2570
50%-assembled isoforms	13304	15283	15861	11470	12694	11814	2706	11606	13051	12509
95%-assembled isoforms	2302	1960	2753	1213	1175	1909	489	2004	2237	2318
50%-covered isoforms	15266	17334	16686	15395	15017	13047	2729	12658	15283	14031
95%-covered isoforms	2651	2298	2981	1770	1642	2127	500	2147	2613	2570
Mean isoform coverage	0.684	0.639	0.734	0.591	0.654	0.666	0.751	0.698	0.672	0.681
Mean isoform assembly	0.625	0.582	0.707	0.489	0.579	0.623	0.745	0.657	0.603	0.632
50%-matched	30436	50342	46508	44555	30039	24213	3808	24594	32784	25910
95%-matched	26763	41811	39238	42150	28142	21017	2929	22274	28995	22414
Unannotated	887	3066	788	2479	801	876	23	854	1938	1100
Mean fraction of transcript matched	0.92	0.866	0.933	0.887	0.929	0.911	0.917	0.929	0.896	0.902

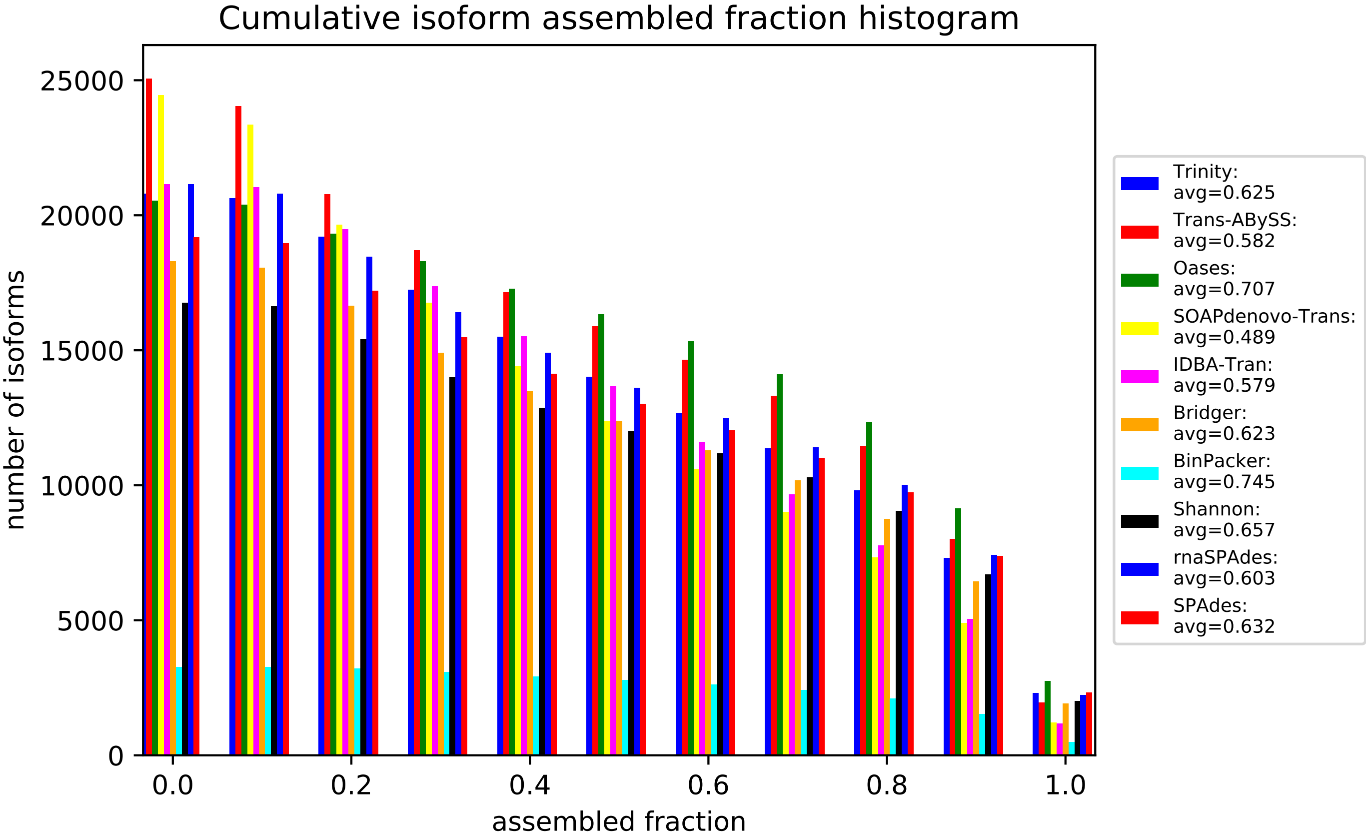
generated by rnaQUAST

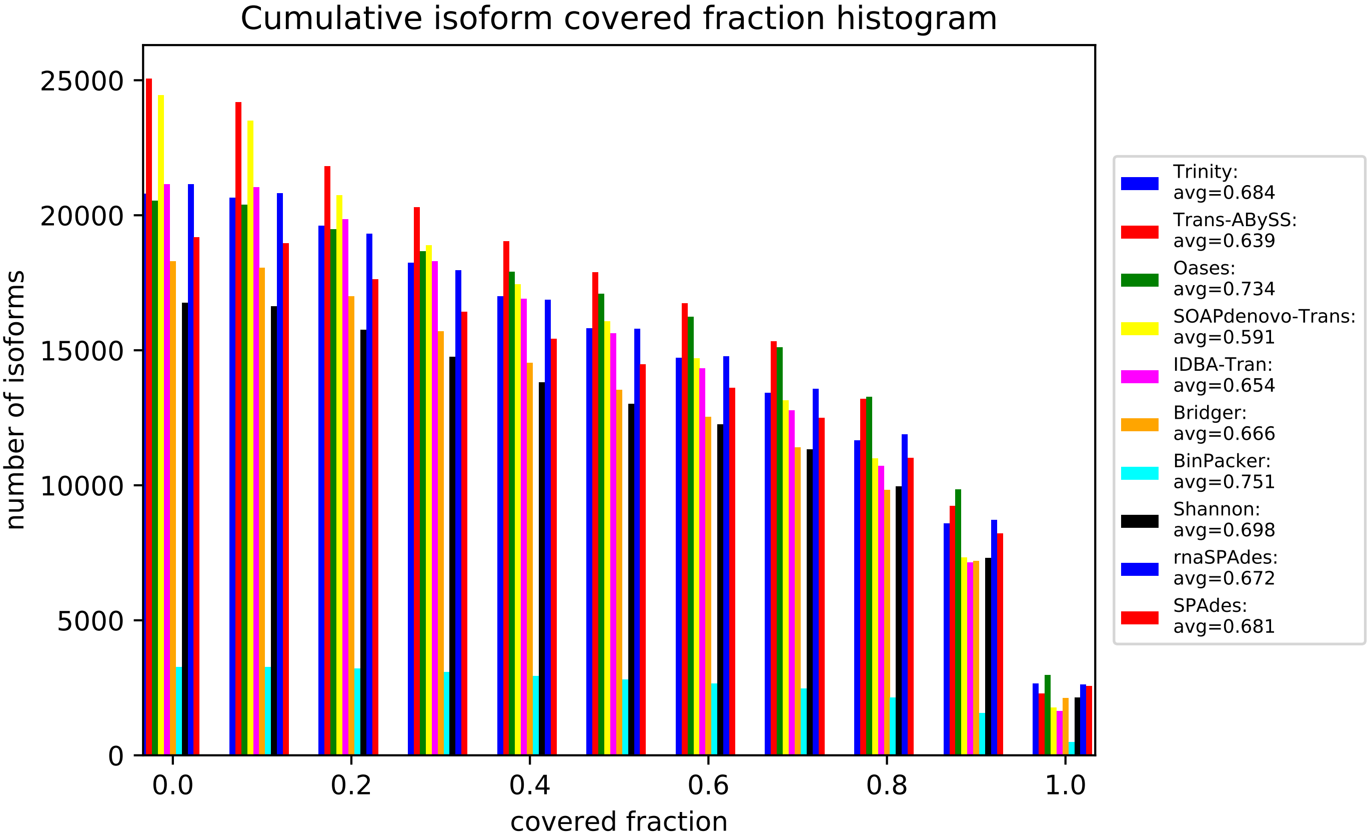

Cumulative transcript / isoform length plot
number of transcripts / isoforms
10^5
10^4
10^3
10^2
10^1
10^0
0
0
2500
5000
7500
10000
12500
15000
17500
length
Gene database:
avg=1651.784
Trinity:
avg=1038.92
Trans-ABySS:
avg=805.723
Oases:
avg=1362.465
SOAPdenovo-Trans:
avg=562.797
IDBA-Tran:
avg=852.664
Bridger:
avg=1099.661
BinPacker:
avg=1535.644
Shannon:
avg=1090.049
rnaSPAdes:
avg=828.657
SPAdes:
avg=987.989


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
100
200
300
400
500
Trinity:
avg=1.315 tot=42704
Trans-ABySS:
avg=0.612 tot=34794
Oases:
avg=3.471 tot=168116
SOAPdenovo-Trans:
avg=0.099 tot=4980
IDBA-Tran:
avg=0.136 tot=4383
Bridger:
avg=2.427 tot=63116
BinPacker:
avg=5.902 tot=23379
Shannon:
avg=0.724 tot=18810
rnaSPAdes:
avg=0.341 tot=12291
SPAdes:
avg=0.43 tot=12095


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
10000
20000
30000
40000
50000
0.0
0.2
0.4
0.6
0.8
1.0
matched fraction
Trinity: avg=0.92
Trans-ABySS: avg=0.866
Oases: avg=0.933
SOAPdenovo-Trans: avg=0.887
IDBA-Tran: avg=0.929
Bridger: avg=0.911
BinPacker: avg=0.917
Shannon: avg=0.929
rnaSPAdes: avg=0.896
SPAdes: avg=0.902


Cumulative isoform assembled fraction histogram
number of isoforms
0
5000
10000
15000
20000
25000
assembled fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.625
Trans-ABySS: avg=0.582
Oases: avg=0.707
SOAPdenovo-Trans: avg=0.489
IDBA-Tran: avg=0.579
Bridger: avg=0.623
BinPacker: avg=0.745
Shannon: avg=0.657
rnaSPAdes: avg=0.603
SPAdes: avg=0.632


Cumulative isoform covered fraction histogram
number of isoforms
0
5000
10000
15000
20000
25000
0.0
0.2
0.4
0.6
0.8
1.0
covered fraction
Trinity:
avg=0.684
Trans-ABySS:
avg=0.639
Oases:
avg=0.734
SOAPdenovo-Trans:
avg=0.591
IDBA-Tran:
avg=0.654
Bridger:
avg=0.666
BinPacker:
avg=0.751
Shannon:
avg=0.698
rnaSPAdes:
avg=0.672
SPAdes:
avg=0.681