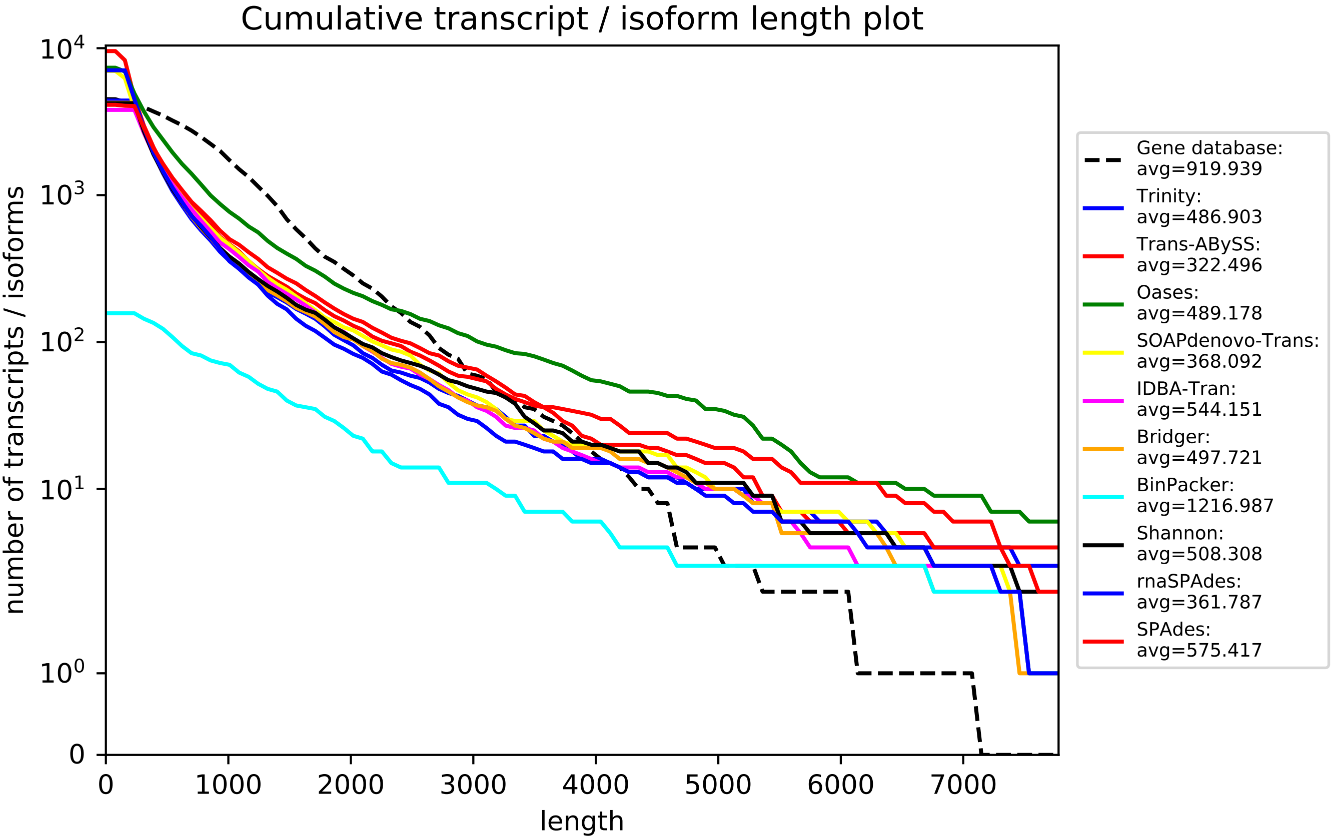
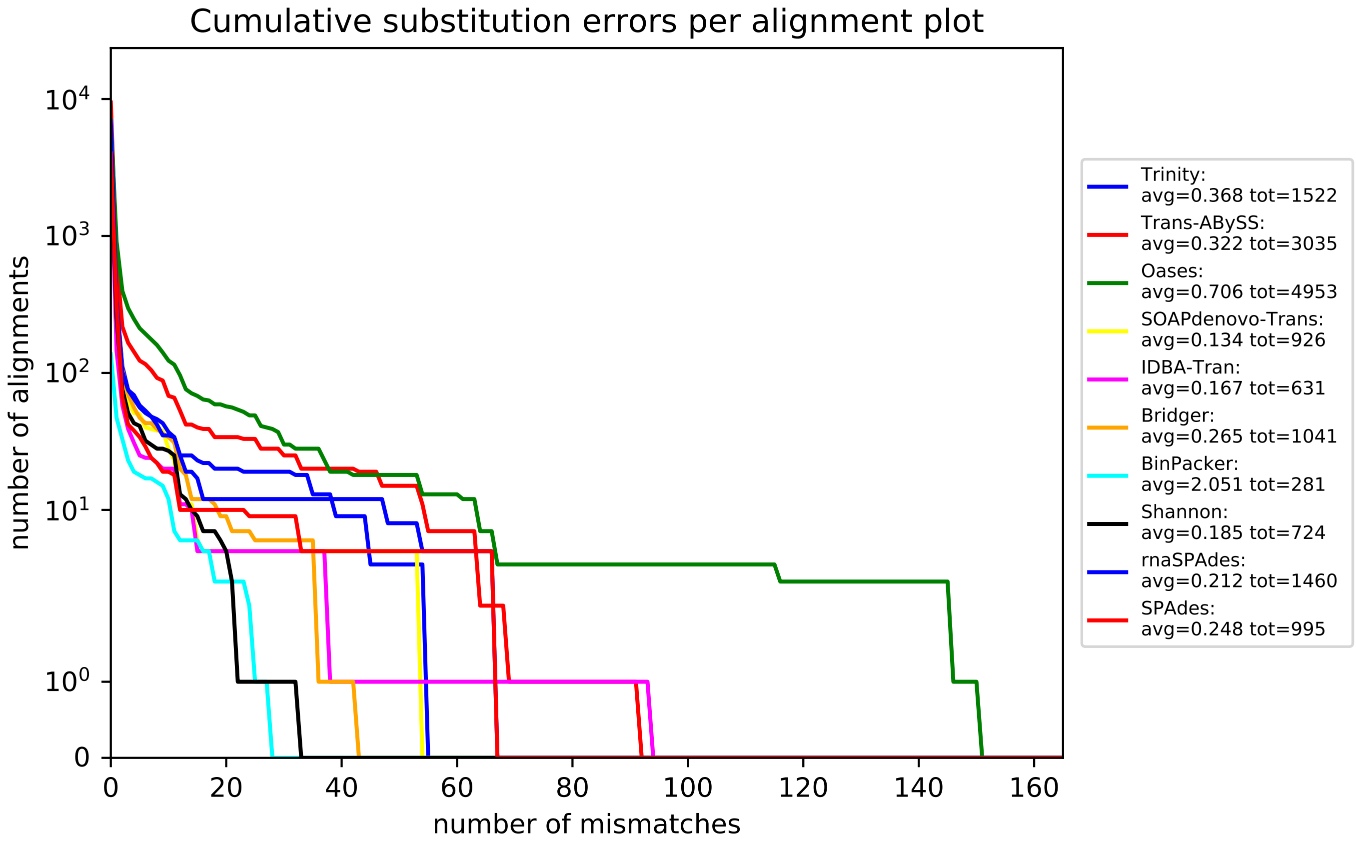
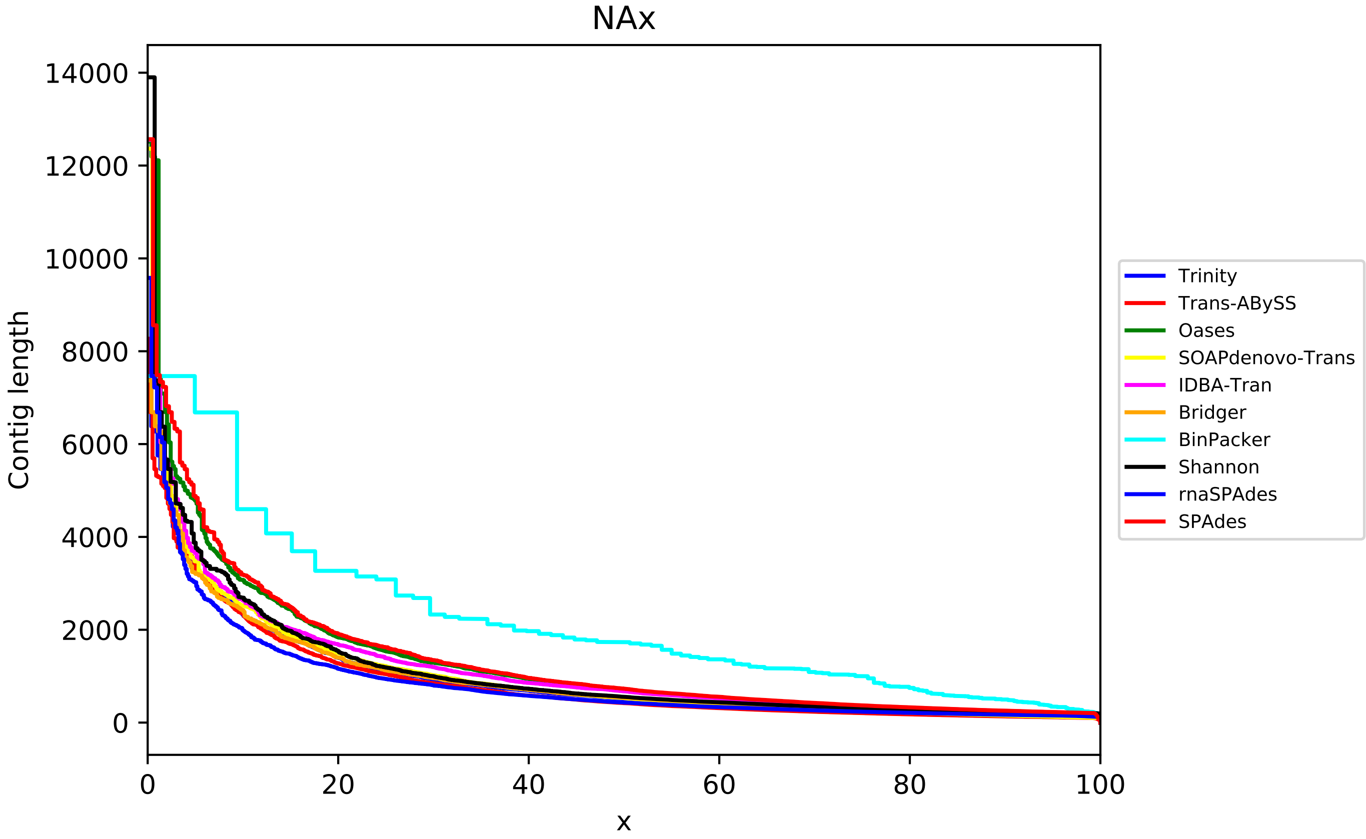
Short report

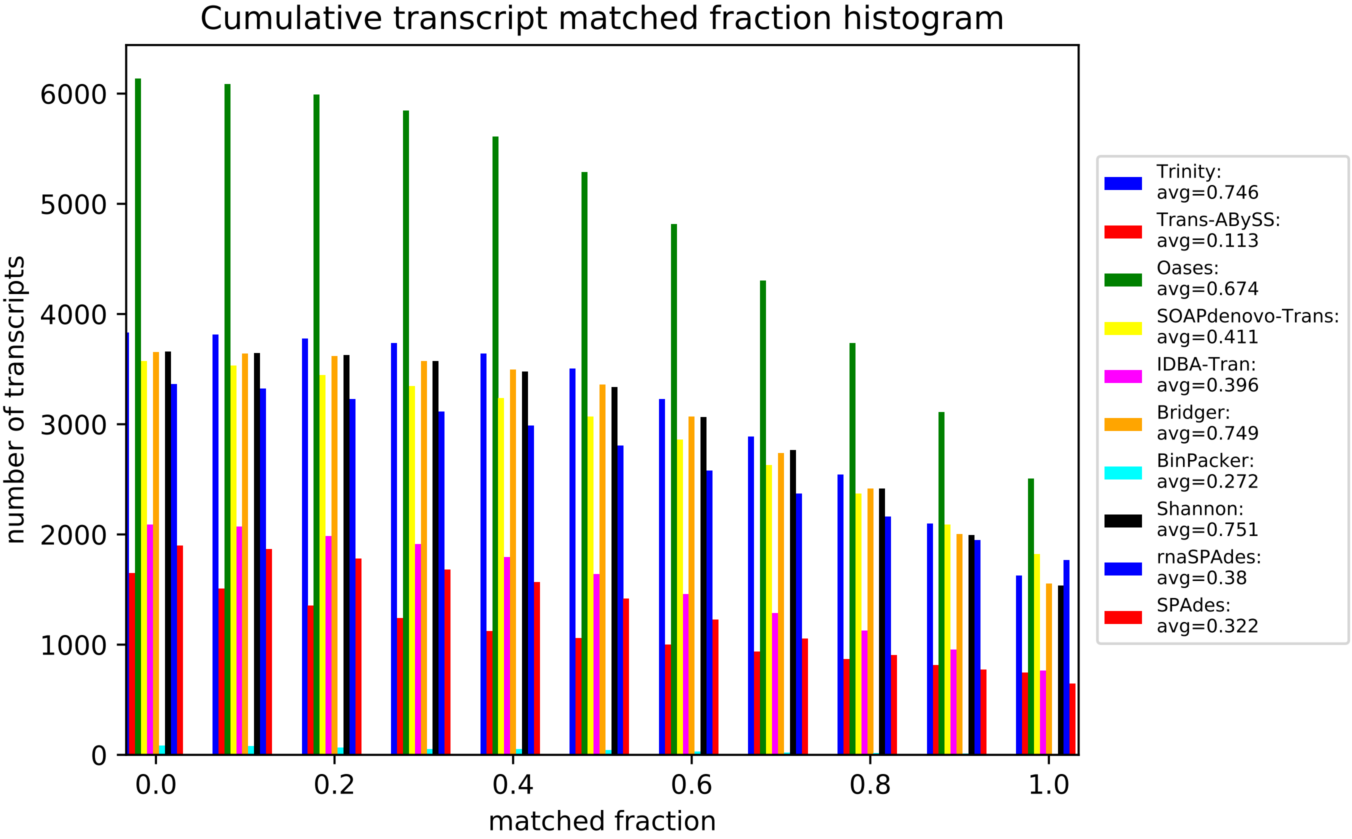
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	4497	4497	4497	4497	4497	4497	4497	4497	4497	4497
Avg. number of exons per isoform	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015	1.015
Transcripts	4403	9555	7364	7007	3803	4254	157	4221	7067	4119
Transcripts > 500 bp	1080	1273	1974	1230	1199	1118	109	1123	1142	1333
Transcripts > 1000 bp	347	446	743	439	414	363	66	372	340	489
Aligned	4173	9163	7139	6848	3757	4048	151	4039	6870	3984
Uniquely aligned	4074	8992	6921	6799	3732	3883	126	3885	6821	3893
Multiply aligned	17	115	26	31	15	16	5	10	21	33
Unaligned	230	392	225	159	46	206	6	182	197	135
Avg. aligned fraction	0.99	0.98	0.988	0.994	0.996	0.991	0.947	0.993	0.992	0.988
Avg. alignment length	467.035	310.442	457.717	364.881	540.828	472.806	1100.774	482.659	359.195	558.904
Avg. mismatches per transcript	0.368	0.322	0.706	0.134	0.167	0.265	2.051	0.185	0.212	0.248
Misassemblies	13	18	103	1	0	52	8	54	10	12
Database coverage	0.334	0.043	0.334	0.225	0.183	0.319	0.009	0.318	0.208	0.16
50%-assembled genes	950	96	916	587	550	920	47	907	469	503
95%-assembled genes	396	32	414	261	250	382	34	393	187	210
50%-covered genes	1435	126	1408	824	699	1376	47	1350	707	591
95%-covered genes	596	38	595	311	294	562	36	565	237	242
50%-assembled isoforms	950	96	916	587	550	920	47	907	469	503
95%-assembled isoforms	396	32	414	261	250	382	34	393	187	210
50%-covered isoforms	1435	126	1408	824	699	1376	47	1350	707	591
95%-covered isoforms	596	38	595	311	294	562	36	565	237	242
Mean isoform coverage	0.647	0.216	0.581	0.447	0.507	0.636	0.728	0.636	0.42	0.478
Mean isoform assembly	0.509	0.191	0.452	0.373	0.45	0.507	0.719	0.509	0.345	0.436
50%-matched	3358	1001	5029	2941	1543	3212	32	3205	2687	1292
95%-matched	1619	724	2492	1814	759	1550	2	1535	1756	638
Unannotated	303	7494	882	3288	1673	273	53	255	3511	2075
Mean fraction of transcript matched	0.746	0.113	0.674	0.411	0.396	0.749	0.272	0.751	0.38	0.322

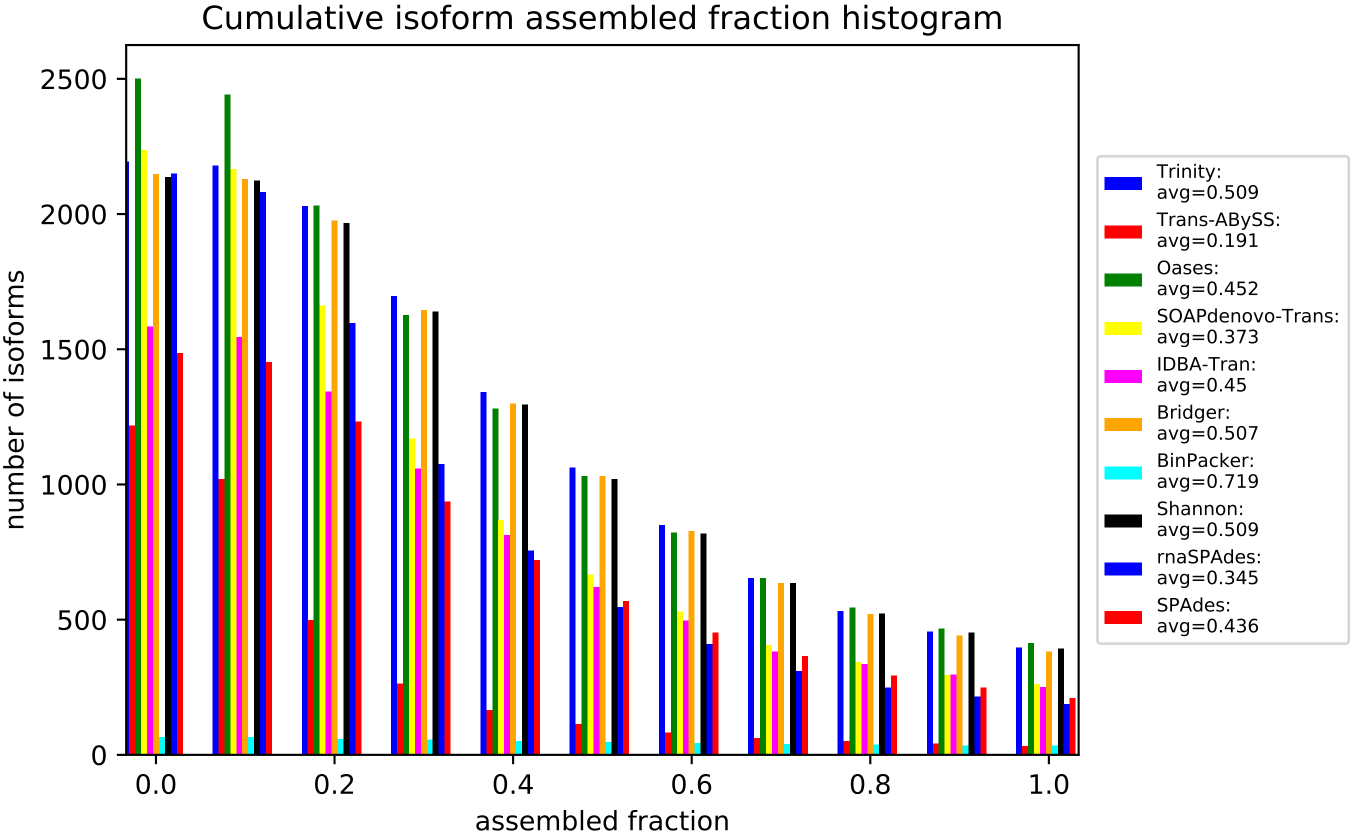
generated by rnaQUAST

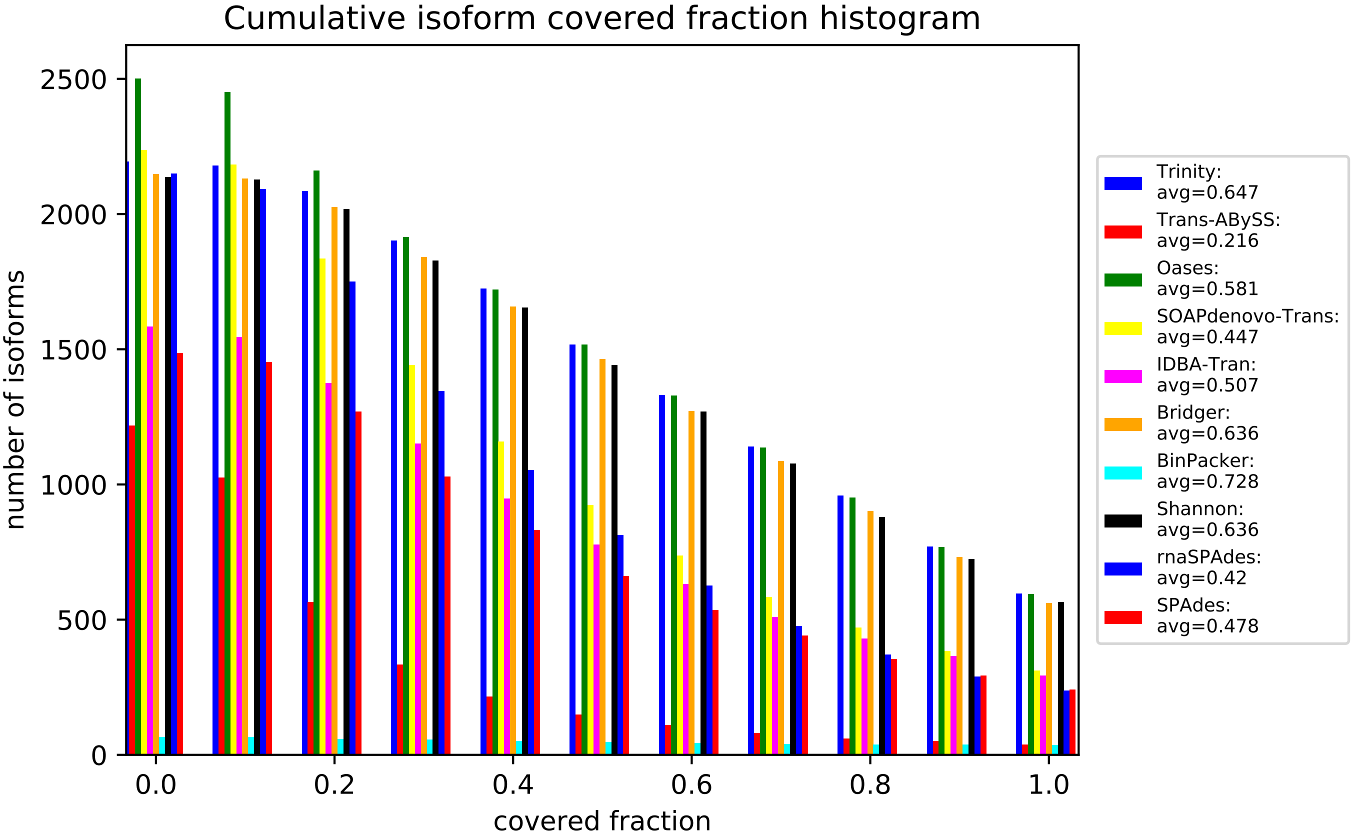

Cumulative transcript / isoform length plot
number of transcripts / isoforms
length
10^4
10^3
10^2
10^1
10^0
0
0
1000
2000
3000
4000
5000
6000
7000
Gene database:
avg=919.939
Trinity:
avg=486.903
Trans-ABySS:
avg=322.496
Oases:
avg=489.178
SOAPdenovo-Trans:
avg=368.092
IDBA-Tran:
avg=544.151
Bridger:
avg=497.721
BinPacker:
avg=1216.987
Shannon:
avg=508.308
rnaSPAdes:
avg=361.787
SPAdes:
avg=575.417


Cumulative substitution errors per alignment plot
number of alignments
number of mismatches
10^4
10^3
10^2
10^1
10^0
0
0
20
40
60
80
100
120
140
160
Trinity:
avg=0.368 tot=1522
Trans-ABySS:
avg=0.322 tot=3035
Oases:
avg=0.706 tot=4953
SOAPdenovo-Trans:
avg=0.134 tot=926
IDBA-Tran:
avg=0.167 tot=631
Bridger:
avg=0.265 tot=1041
BinPacker:
avg=2.051 tot=281
Shannon:
avg=0.185 tot=724
rnaSPAdes:
avg=0.212 tot=1460
SPAdes:
avg=0.248 tot=995


NAx
Contig length
14000
12000
10000
8000
6000
4000
2000
0
x
0
20
40
60
80
100
Trinity
Trans-ABySS
Oases
SOAPdenovo-Trans
IDBA-Tran
Bridger
BinPacker
Shannon
rnaSPAdes
SPAdes


Cumulative transcript matched fraction histogram
number of transcripts
0
1000
2000
3000
4000
5000
6000
0.0
0.2
0.4
0.6
0.8
1.0
matched fraction
Trinity: avg=0.746
Trans-ABySS: avg=0.113
Oases: avg=0.674
SOAPdenovo-Trans: avg=0.411
IDBA-Tran: avg=0.396
Bridger: avg=0.749
BinPacker: avg=0.272
Shannon: avg=0.751
rnaSPAdes: avg=0.38
SPAdes: avg=0.322


Cumulative isoform assembled fraction histogram
number of isoforms
0
500
1000
1500
2000
2500
0.0
0.2
0.4
0.6
0.8
1.0
assembled fraction
Trinity: avg=0.509
Trans-ABySS: avg=0.191
Oases: avg=0.452
SOAPdenovo-Trans: avg=0.373
IDBA-Tran: avg=0.45
Bridger: avg=0.507
BinPacker: avg=0.719
Shannon: avg=0.509
rnaSPAdes: avg=0.345
SPAdes: avg=0.436


Cumulative isoform covered fraction histogram
number of isoforms
covered fraction
0
500
1000
1500
2000
2500
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.647
Trans-ABySS: avg=0.216
Oases: avg=0.581
SOAPdenovo-Trans: avg=0.447
IDBA-Tran: avg=0.507
Bridger: avg=0.636
BinPacker: avg=0.728
Shannon: avg=0.636
rnaSPAdes: avg=0.42
SPAdes: avg=0.478