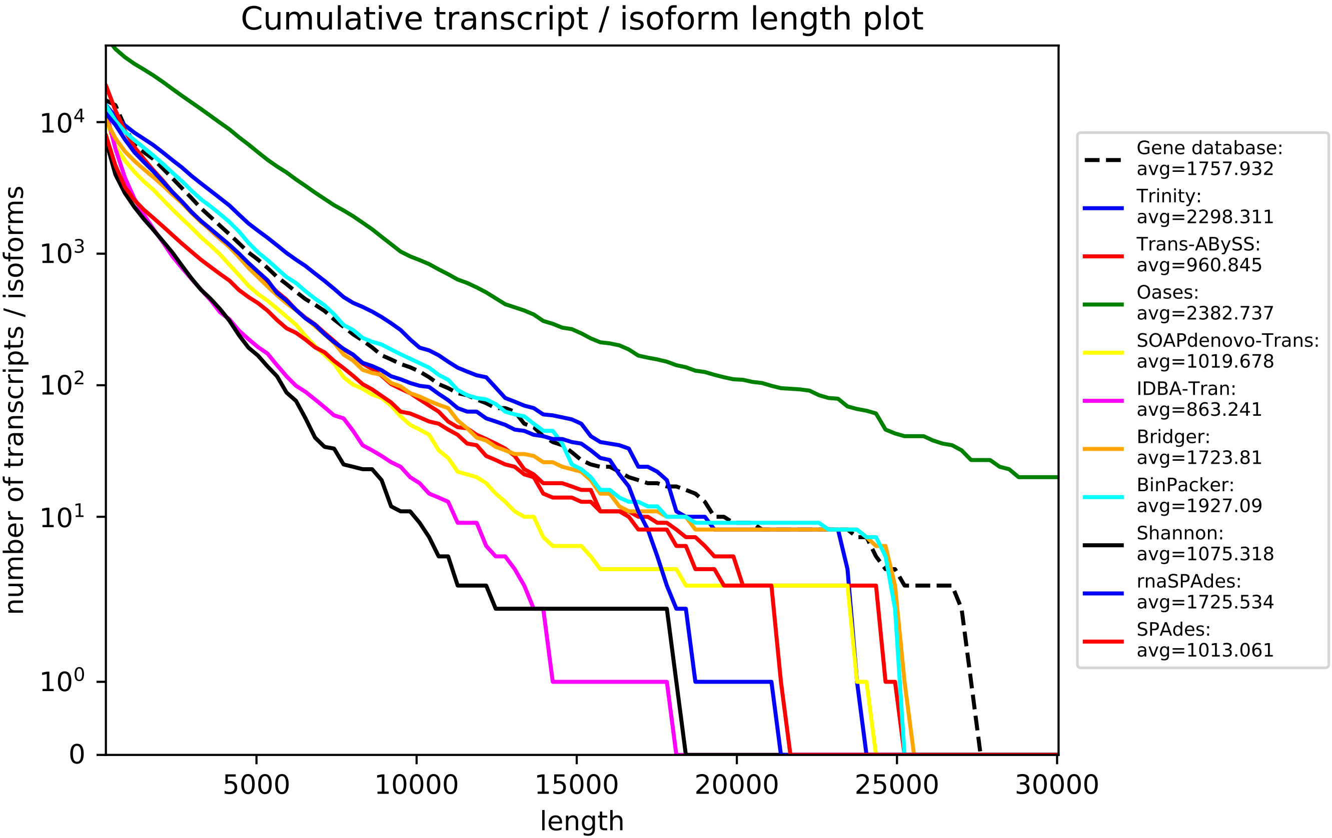
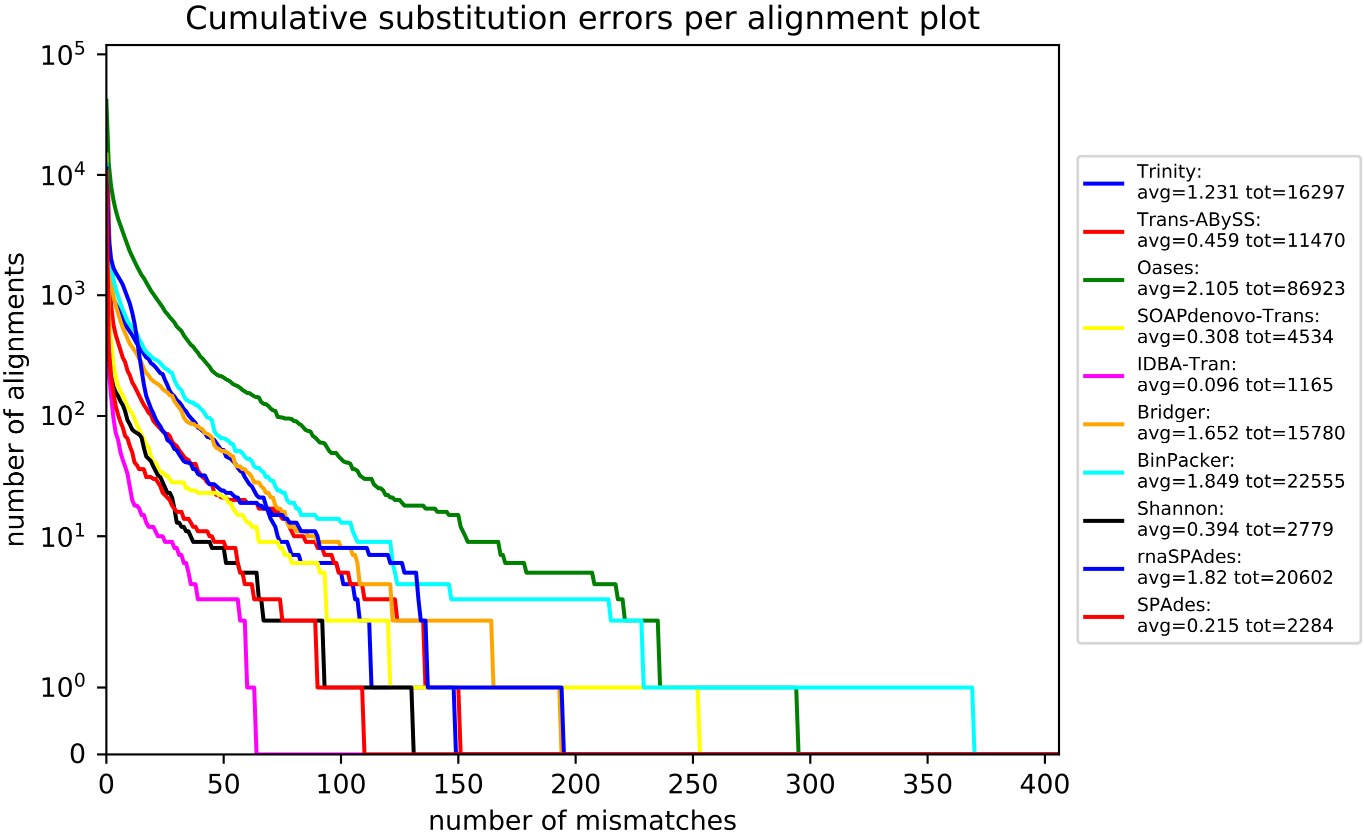
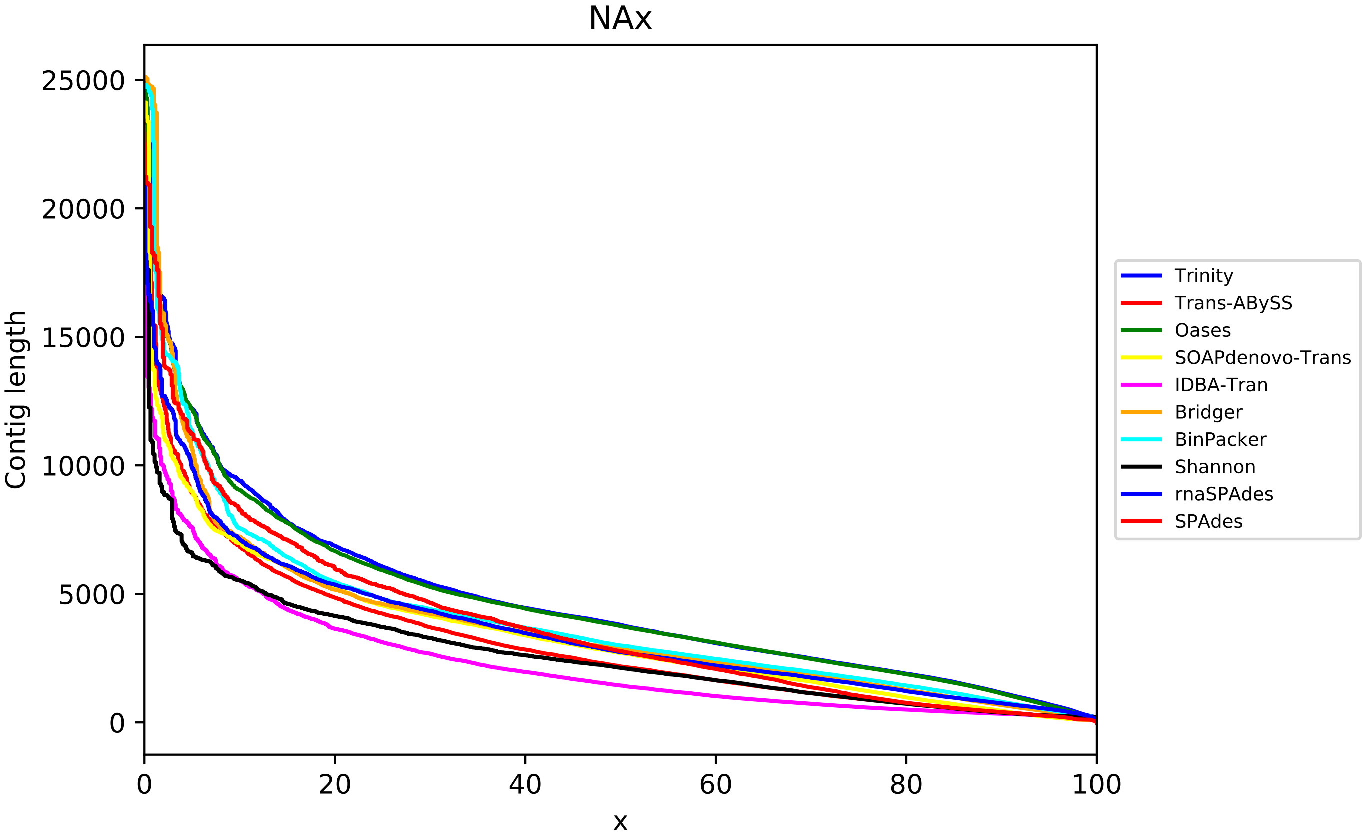
Short report

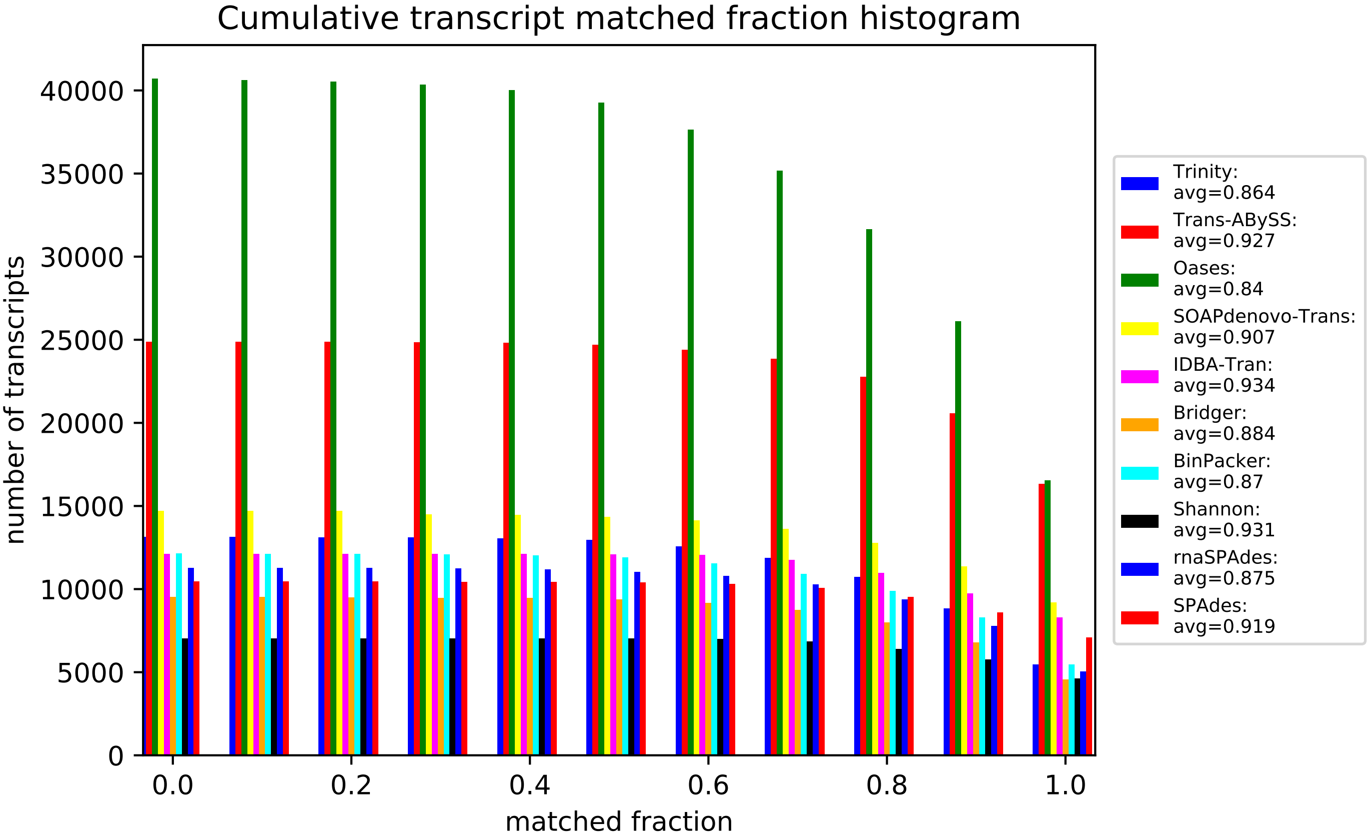
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	3119	3119	3119	3119	3119	3119	3119	3119	3119	3119
Avg. number of exons per isoform	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99
Transcripts	13484	25272	46469	14965	12151	10457	13415	7255	11766	10537
Transcripts > 500 bp	10717	11460	34981	6270	5642	7180	9858	3729	9116	4309
Transcripts > 1000 bp	8451	6703	28143	4263	2740	5167	7424	2341	6053	2623
Aligned	13454	25150	46049	14792	12134	10307	13252	7196	11744	10503
Uniquely aligned	13214	24896	41196	14692	12099	9537	12174	7035	11306	10347
Multiply aligned	12	39	48	18	11	7	10	7	7	87
Unaligned	30	122	420	173	17	150	163	59	22	34
Avg. aligned fraction	0.989	0.994	0.959	0.994	0.998	0.983	0.981	0.996	0.968	0.995
Avg. alignment length	2261.332	939.312	2090.55	1009.08	859.966	1581.299	1755.155	1061.013	1649.147	979.981
Avg. mismatches per transcript	1.231	0.459	2.105	0.308	0.096	1.652	1.849	0.394	1.82	0.215
Misassemblies	139	117	4094	49	8	533	785	66	351	50
Database coverage	0.461	0.535	0.592	0.406	0.382	0.346	0.372	0.189	0.431	0.367
50%-assembled genes	2478	2680	2623	2365	2494	2247	2300	1441	2606	2537
95%-assembled genes	1915	2074	1865	1380	570	1353	1402	854	1760	1566
50%-covered genes	2644	2903	2812	2719	2733	2427	2480	1621	2686	2624
95%-covered genes	2096	2485	2052	1755	1158	1527	1579	954	2025	1772
50%-assembled isoforms	4654	5992	6106	3630	3896	3362	3701	1920	4557	3668
95%-assembled isoforms	2898	2877	2995	1679	577	1570	1660	1056	2220	1625
50%-covered isoforms	5003	6966	6780	4399	4760	3725	4086	2183	4848	4054
95%-covered isoforms	3254	3785	3525	2145	1203	1786	1907	1181	2596	1865
Mean isoform coverage	0.806	0.674	0.737	0.606	0.591	0.655	0.659	0.658	0.717	0.576
Mean isoform assembly	0.759	0.602	0.682	0.531	0.512	0.61	0.614	0.599	0.678	0.538
Predicted genes	6829	8600	21274	3567	4599	4400	6344	2598	6088	2863
50%-matched	12797	24508	38562	14251	12072	9287	11761	7005	10955	10295
95%-matched	5462	16312	16512	9194	8280	4556	5451	4606	5031	7030
Unannotated	96	82	585	24	6	34	62	8	37	44
Mean fraction of transcript matched	0.864	0.927	0.84	0.907	0.934	0.884	0.87	0.931	0.875	0.919

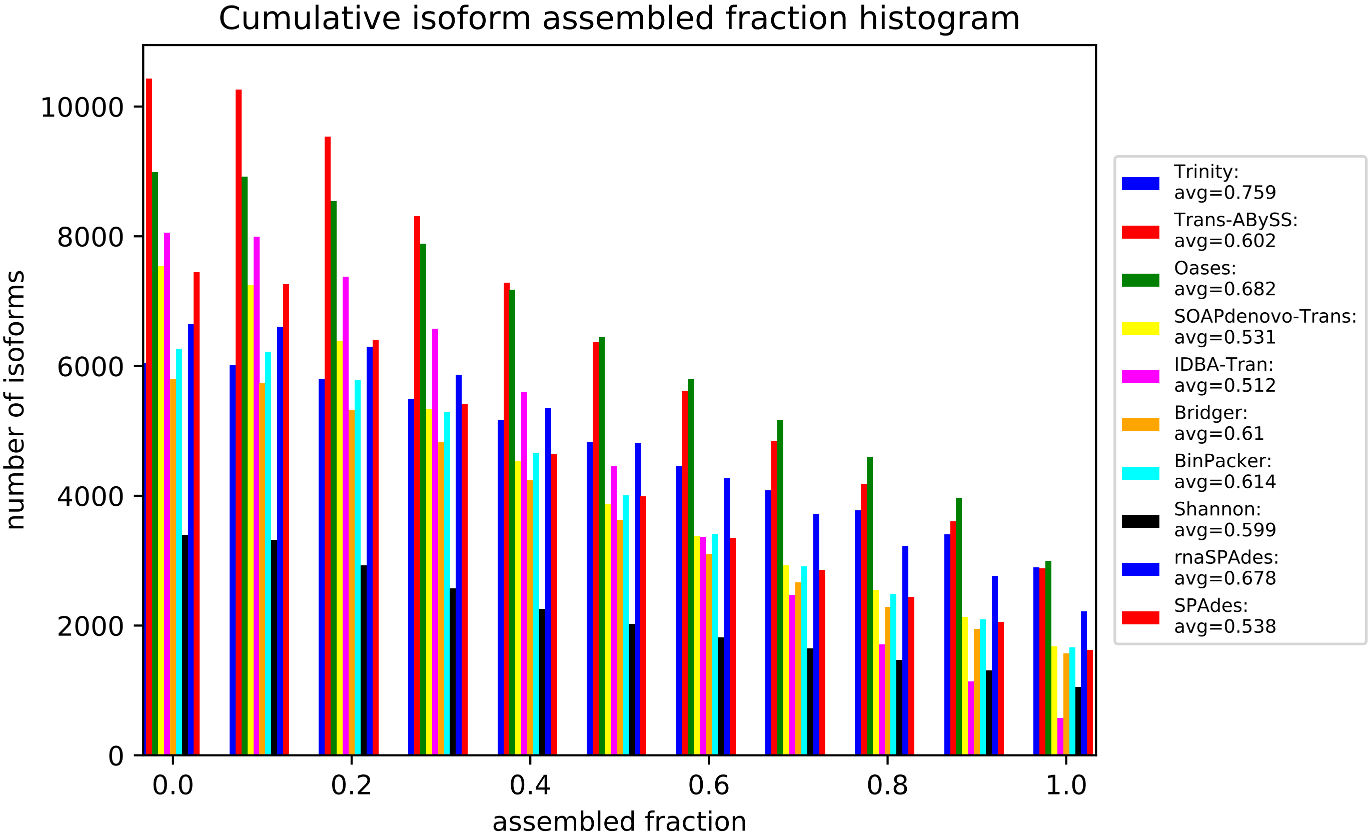
generated by rnaQUAST

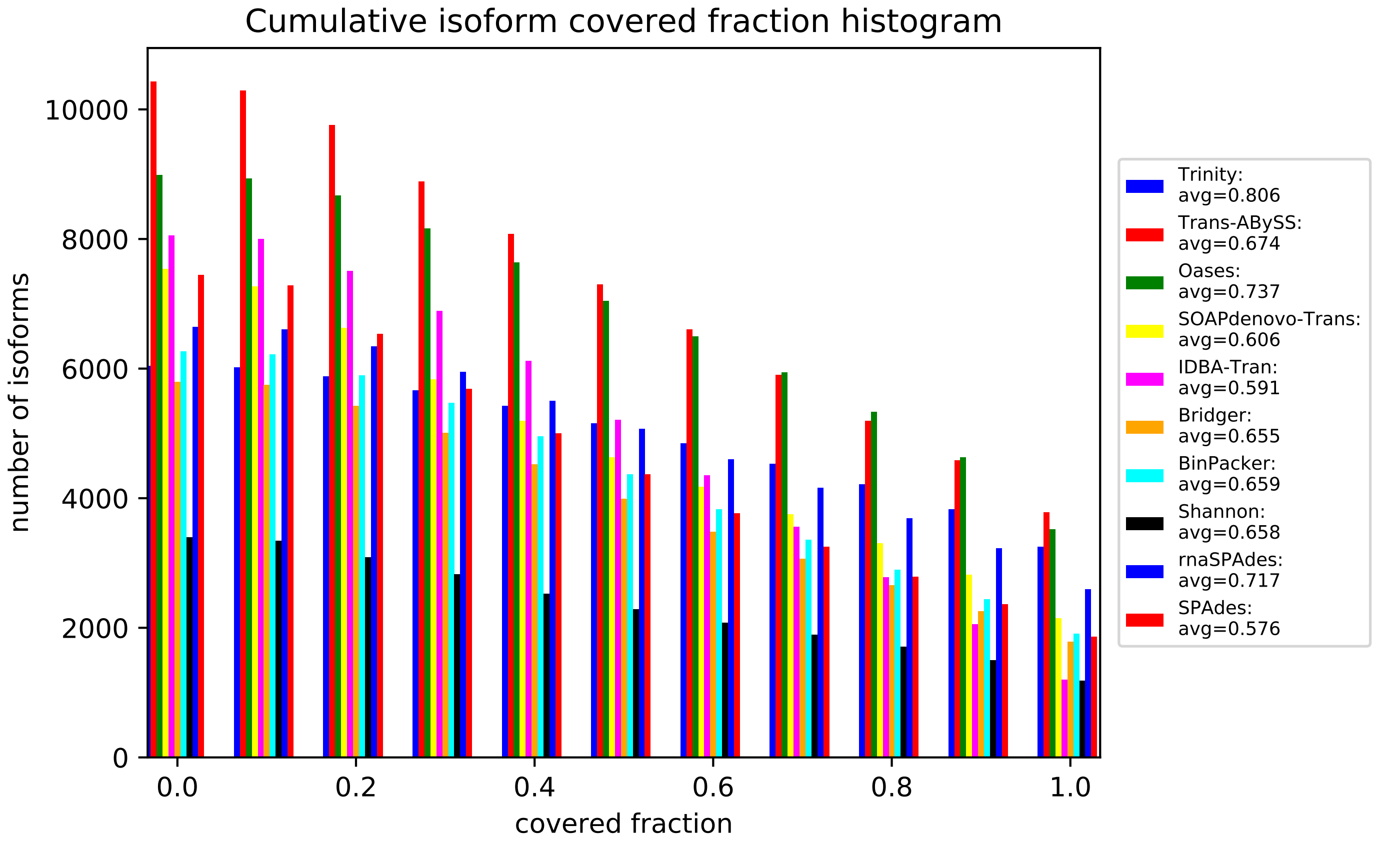

Cumulative transcript / isoform length plot
number of transcripts / isoforms
length
10^4
10^3
10^2
10^1
10^0
0
5000
10000
15000
20000
25000
30000
Gene database:
avg=1757.932
Trinity:
avg=2298.311
Trans-ABySS:
avg=960.845
Oases:
avg=2382.737
SOAPdenovo-Trans:
avg=1019.678
IDBA-Tran:
avg=863.241
Bridger:
avg=1723.81
BinPacker:
avg=1927.09
Shannon:
avg=1075.318
rnaSPAdes:
avg=1725.534
SPAdes:
avg=1013.061


Cumulative substitution errors per alignment plot
number of alignments
10^5
10^4
10^3
10^2
10^1
10^0
0
number of mismatches
0
50
100
150
200
250
300
350
400
Trinity:
avg=1.231 tot=16297
Trans-ABySS:
avg=0.459 tot=11470
Oases:
avg=2.105 tot=86923
SOAPdenovo-Trans:
avg=0.308 tot=4534
IDBA-Tran:
avg=0.096 tot=1165
Bridger:
avg=1.652 tot=15780
BinPacker:
avg=1.849 tot=22555
Shannon:
avg=0.394 tot=2779
rnaSPAdes:
avg=1.82 tot=20602
SPAdes:
avg=0.215 tot=2284


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
5000
10000
15000
20000
25000
30000
35000
40000
matched fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.864
Trans-ABySS: avg=0.927
Oases: avg=0.84
SOAPdenovo-Trans: avg=0.907
IDBA-Tran: avg=0.934
Bridger: avg=0.884
BinPacker: avg=0.87
Shannon: avg=0.931
rnaSPAdes: avg=0.875
SPAdes: avg=0.919


Cumulative isoform assembled fraction histogram
number of isoforms
0
2000
4000
6000
8000
10000
0.0
0.2
0.4
0.6
0.8
1.0
assembled fraction
Trinity:
avg=0.759
Trans-ABySS:
avg=0.602
Oases:
avg=0.682
SOAPdenovo-Trans:
avg=0.531
IDBA-Tran:
avg=0.512
Bridger:
avg=0.61
BinPacker:
avg=0.614
Shannon:
avg=0.599
rnaSPAdes:
avg=0.678
SPAdes:
avg=0.538


Cumulative isoform covered fraction histogram
number of isoforms
0
2000
4000
6000
8000
10000
covered fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity: avg=0.806
Trans-ABySS: avg=0.674
Oases: avg=0.737
SOAPdenovo-Trans: avg=0.606
IDBA-Tran: avg=0.591
Bridger: avg=0.655
BinPacker: avg=0.659
Shannon: avg=0.658
rnaSPAdes: avg=0.717
SPAdes: avg=0.576