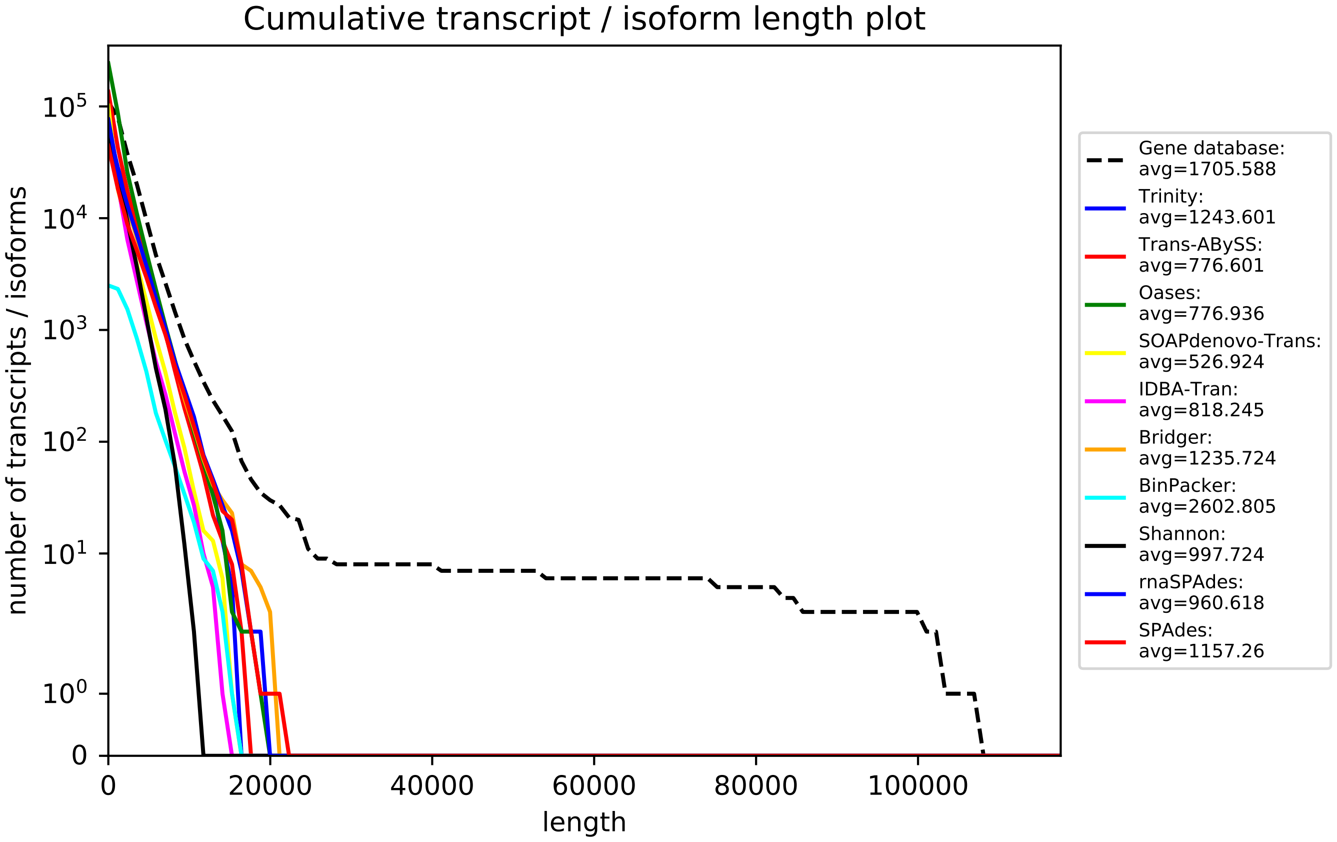
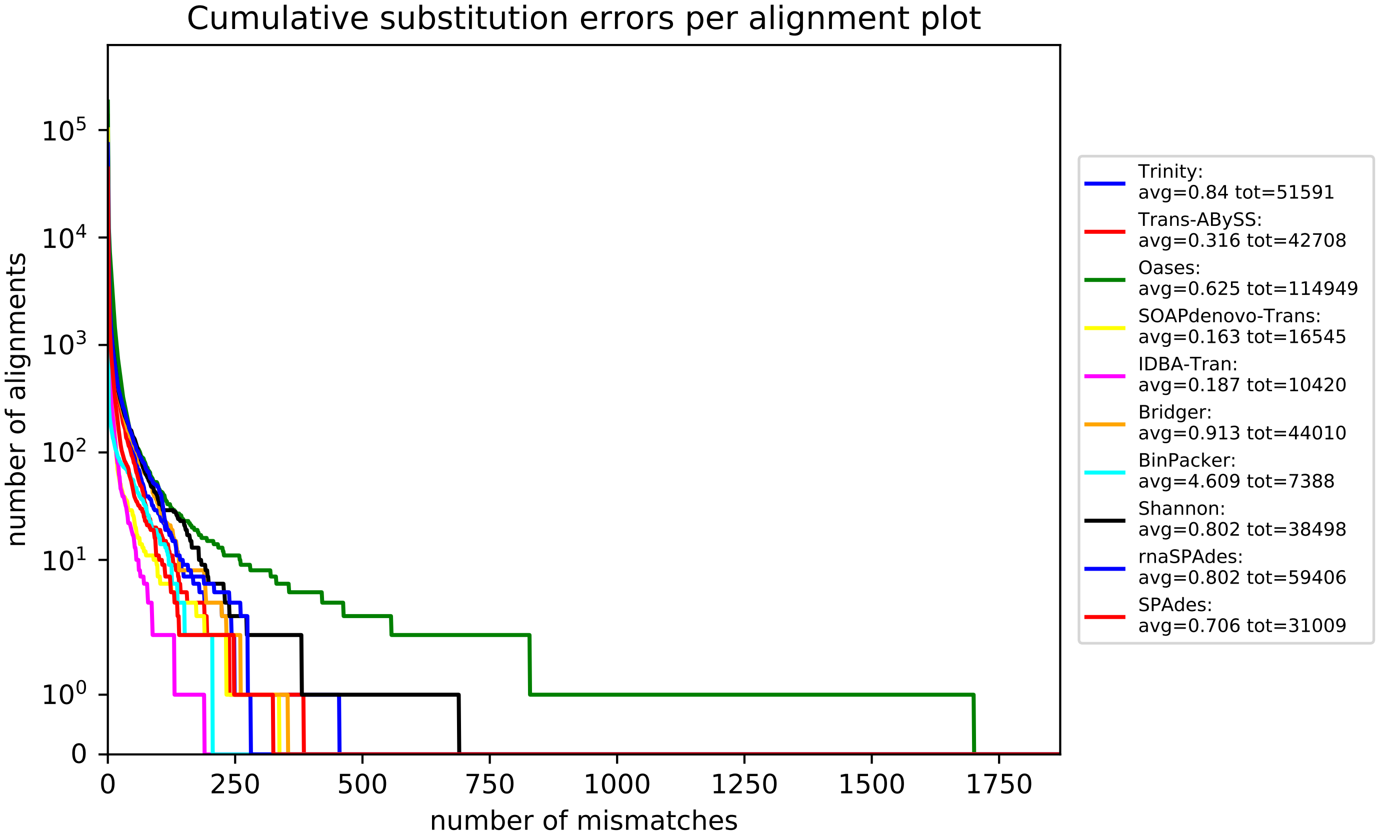
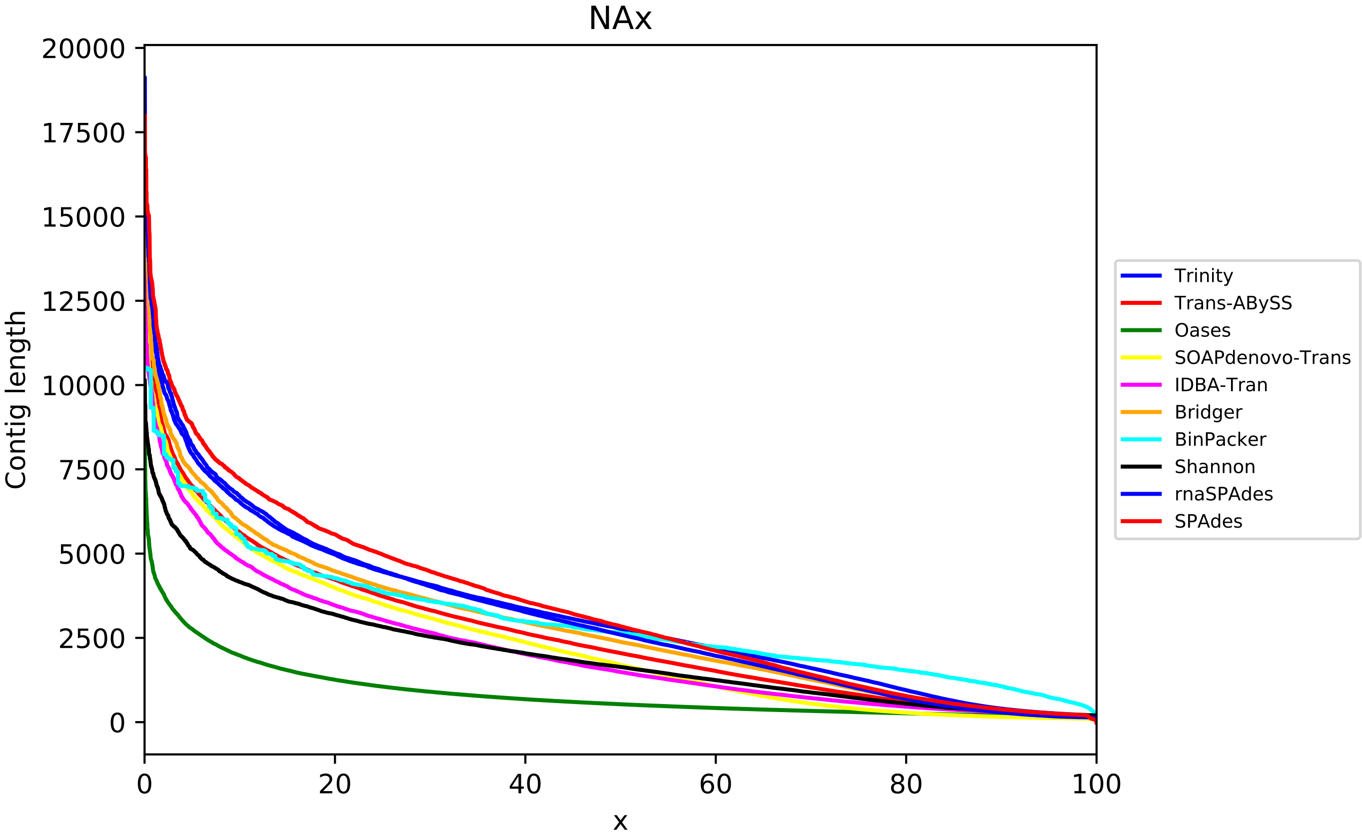
Short report

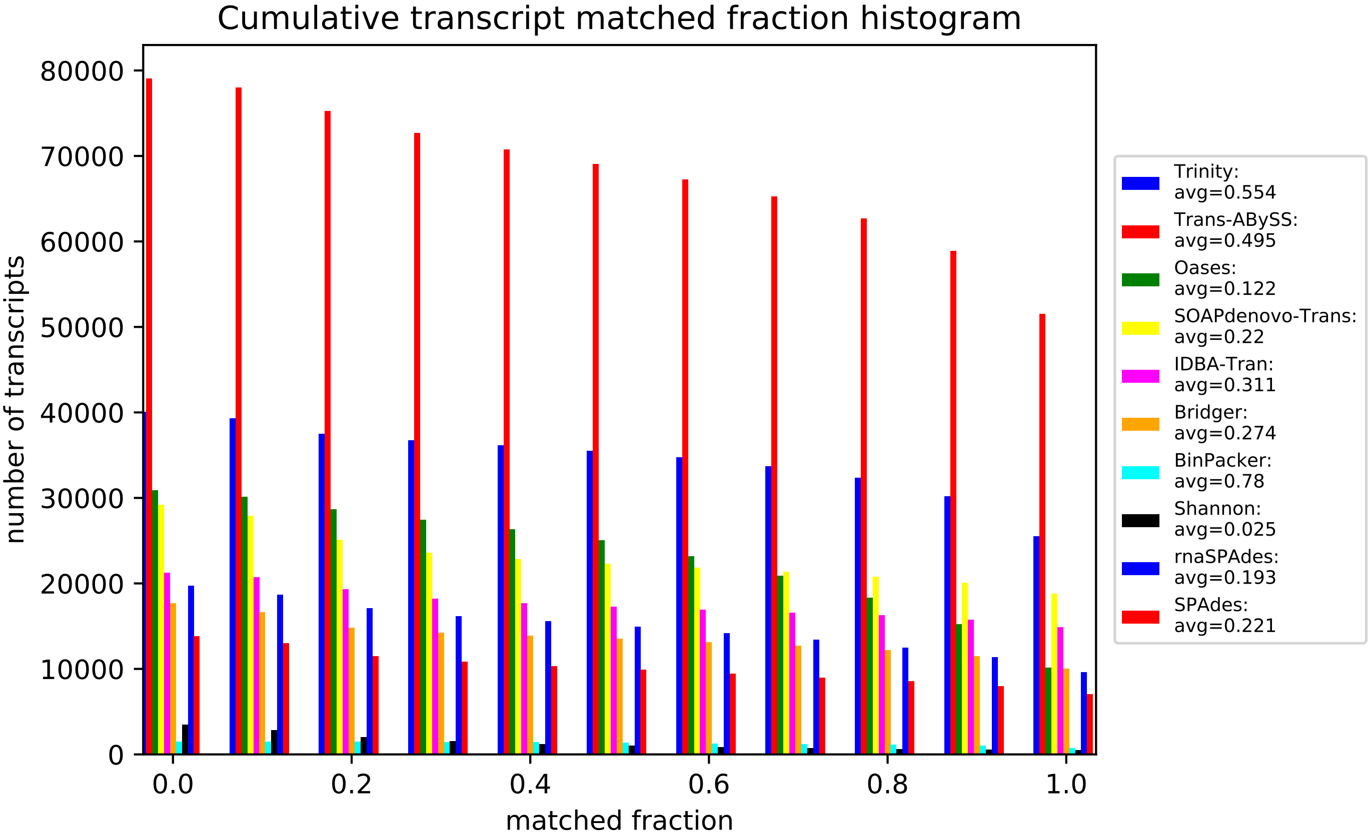
	Trinity	Trans-ABySS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	45792	45792	45792	45792	45792	45792	45792	45792	45792	45792
Avg. number of exons per isoform	6.262	6.262	6.262	6.262	6.262	6.262	6.262	6.262	6.262	6.262
Transcripts	63305	135402	243196	101745	55639	54182	2503	53069	76473	44567
Transcripts > 500 bp	30976	47157	100314	20648	23040	27127	2394	26641	28354	20542
Transcripts > 1000 bp	21804	29719	51832	12603	12294	18266	2037	16915	19367	13099
Aligned	62410	134605	240548	100986	55367	53312	2489	52618	75637	43715
Uniquely aligned	60559	132078	177880	99816	54884	47785	1590	47310	73243	40569
Multiply aligned	310	1098	2382	686	289	161	5	260	306	866
Unaligned	895	797	2648	759	272	870	14	451	836	852
Avg. aligned fraction	0.993	0.995	0.891	0.997	0.998	0.989	0.946	0.991	0.989	0.991
Avg. alignment length	1216.863	752.811	406.084	519.962	811.99	1073.395	1972.809	877.706	910.466	1089.264
Avg. mismatches per transcript	0.84	0.316	0.625	0.163	0.187	0.913	4.609	0.802	0.802	0.706
Misassemblies	564	612	52668	61	41	2643	628	1927	1080	570
Database coverage	0.208	0.244	0.024	0.1	0.096	0.084	0.011	0.004	0.111	0.088
50%-assembled genes	9280	9765	841	4762	4594	4157	811	203	5787	4751
95%-assembled genes	5323	5721	183	2204	967	2100	519	71	3185	2629
50%-covered genes	10171	10804	1206	5293	5313	4421	812	259	6064	4919
95%-covered genes	6275	7145	355	2505	1435	2253	526	85	3447	2781
50%-assembled isoforms	11611	14134	1064	5063	4846	4637	881	206	6289	4955
95%-assembled isoforms	6032	6281	183	2244	967	2236	554	71	3269	2633
50%-covered isoforms	12896	16495	1755	5678	5665	4942	883	264	6622	5155
95%-covered isoforms	7081	8075	360	2548	1436	2397	561	85	3544	2785
Mean isoform coverage	0.649	0.607	0.246	0.376	0.434	0.467	0.808	0.217	0.509	0.504
Mean isoform assembly	0.595	0.539	0.202	0.343	0.391	0.444	0.805	0.195	0.486	0.487
Predicted genes	22949	35418	39050	9941	12246	13562	1924	8919	13269	9048
50%-matched	35166	68154	24164	22053	17105	13327	1321	912	14553	9643
95%-matched	25522	51506	10182	18742	14889	10017	744	469	9593	7028
Unannotated	20832	54198	149381	71364	33923	30247	100	44108	53812	27678
Mean fraction of transcript matched	0.554	0.495	0.122	0.22	0.311	0.274	0.78	0.025	0.193	0.221

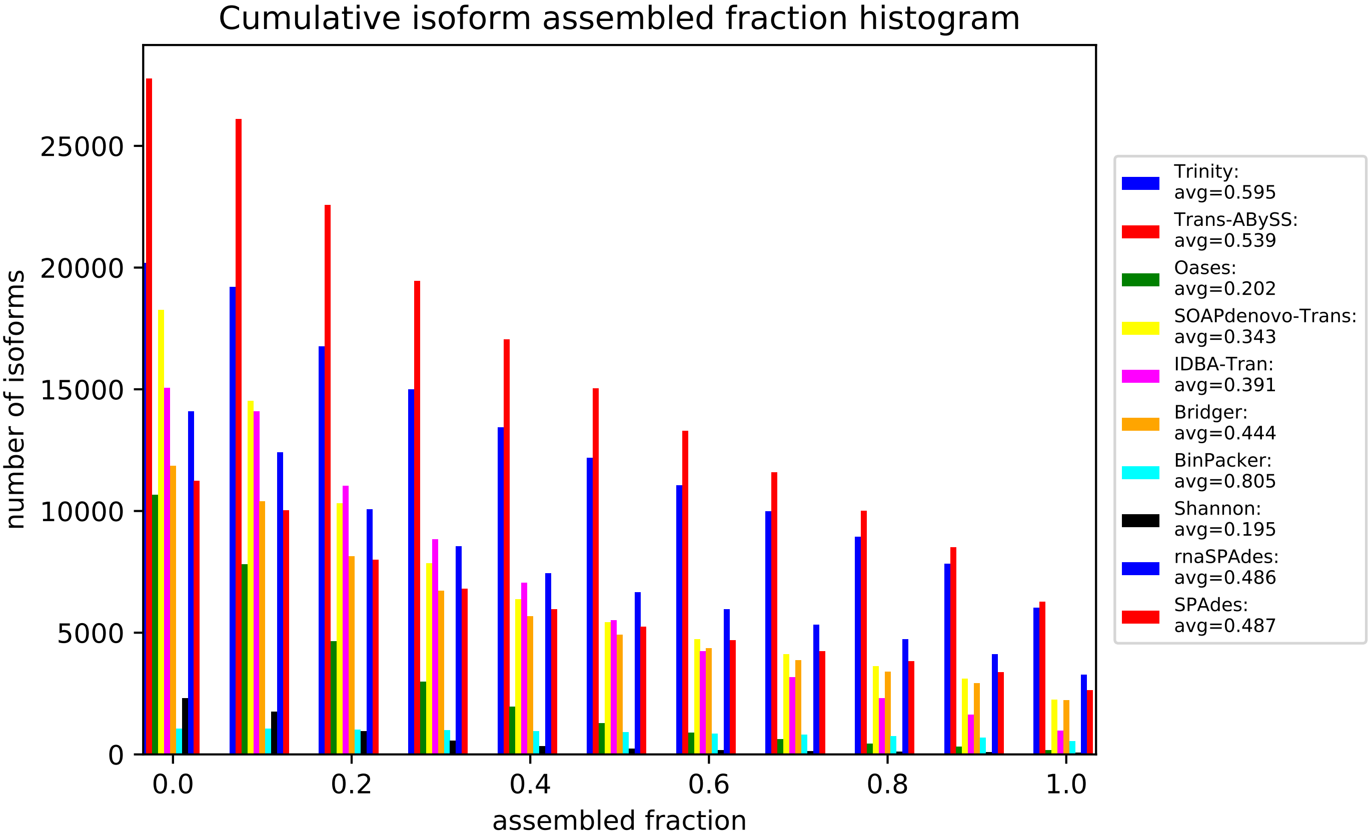
generated by rnaQUAST

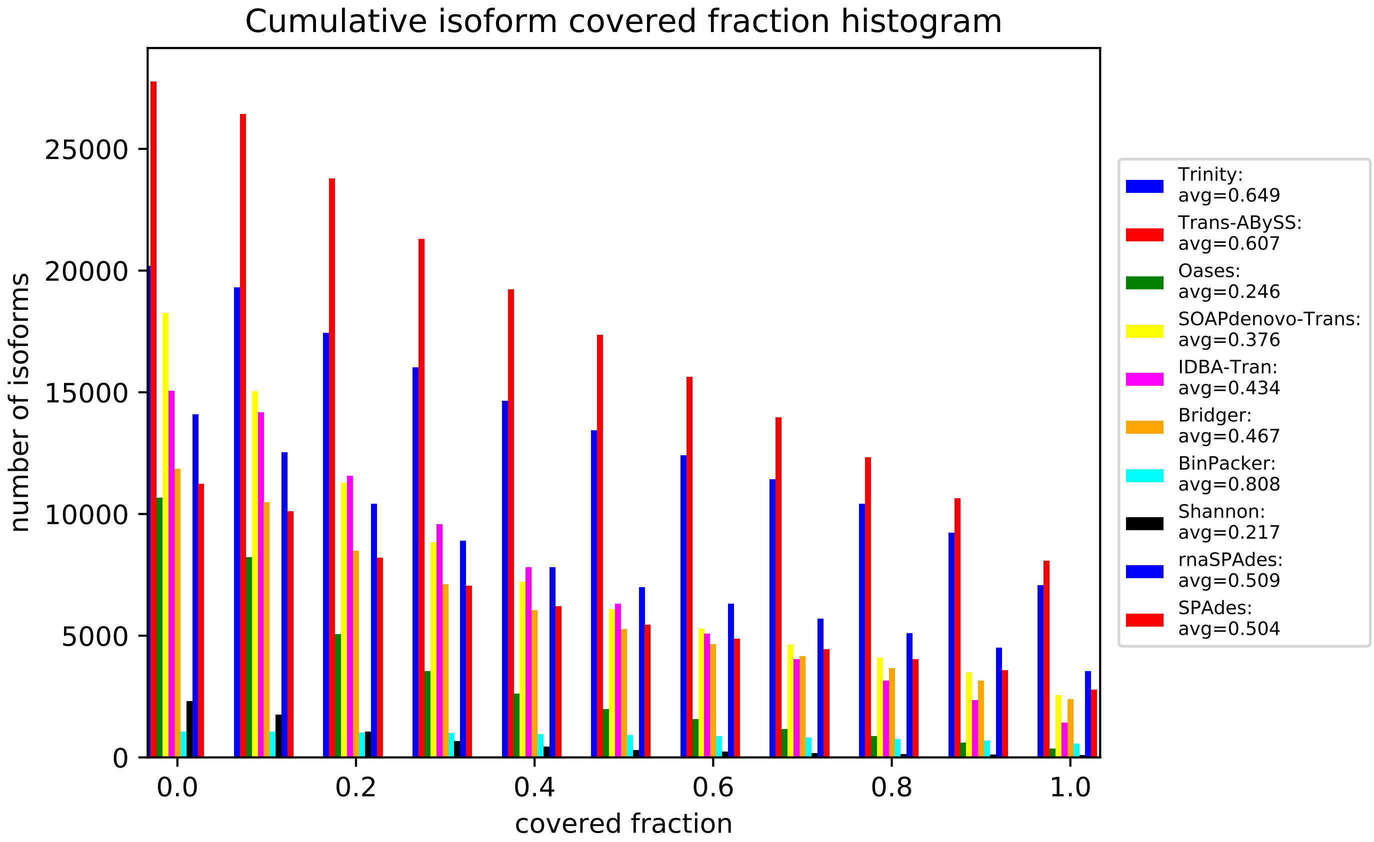

Cumulative transcript / isoform length plot
number of transcripts / isoforms
length
10^5
10^4
10^3
10^2
10^1
10^0
0
0
20000
40000
60000
80000
100000
Gene database:
avg=1705.588
Trinity:
avg=1243.601
Trans-ABySS:
avg=776.601
Oases:
avg=776.936
SOAPdenovo-Trans:
avg=526.924
IDBA-Tran:
avg=818.245
Bridger:
avg=1235.724
BinPacker:
avg=2602.805
Shannon:
avg=997.724
rnaSPAdes:
avg=960.618
SPAdes:
avg=1157.26


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
250
500
750
1000
1250
1500
1750
Trinity:
avg=0.84 tot=51591
Trans-ABySS:
avg=0.316 tot=42708
Oases:
avg=0.625 tot=114949
SOAPdenovo-Trans:
avg=0.163 tot=16545
IDBA-Tran:
avg=0.187 tot=10420
Bridger:
avg=0.913 tot=44010
BinPacker:
avg=4.609 tot=7388
Shannon:
avg=0.802 tot=38498
rnaSPAdes:
avg=0.802 tot=59406
SPAdes:
avg=0.706 tot=31009


NAx
Contig length
20000
17500
15000
12500
10000
7500
5000
2500
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
60000
70000
80000
matched fraction
0.0
0.2
0.4
0.6
0.8
1.0
Trinity:
avg=0.554
Trans-ABySS:
avg=0.495
Oases:
avg=0.122
SOAPdenovo-Trans:
avg=0.22
IDBA-Tran:
avg=0.311
Bridger:
avg=0.274
BinPacker:
avg=0.78
Shannon:
avg=0.025
rnaSPAdes:
avg=0.193
SPAdes:
avg=0.221


Cumulative isoform assembled fraction histogram
number of isoforms
0
5000
10000
15000
20000
25000
0.0
0.2
0.4
0.6
0.8
1.0
assembled fraction
Trinity:
avg=0.595
Trans-ABySS:
avg=0.539
Oases:
avg=0.202
SOAPdenovo-Trans:
avg=0.343
IDBA-Tran:
avg=0.391
Bridger:
avg=0.444
BinPacker:
avg=0.805
Shannon:
avg=0.195
rnaSPAdes:
avg=0.486
SPAdes:
avg=0.487


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=0.649
Trans-ABySS:
avg=0.607
Oases:
avg=0.246
SOAPdenovo-Trans:
avg=0.376
IDBA-Tran:
avg=0.434
Bridger:
avg=0.467
BinPacker:
avg=0.808
Shannon:
avg=0.217
rnaSPAdes:
avg=0.509
SPAdes:
avg=0.504