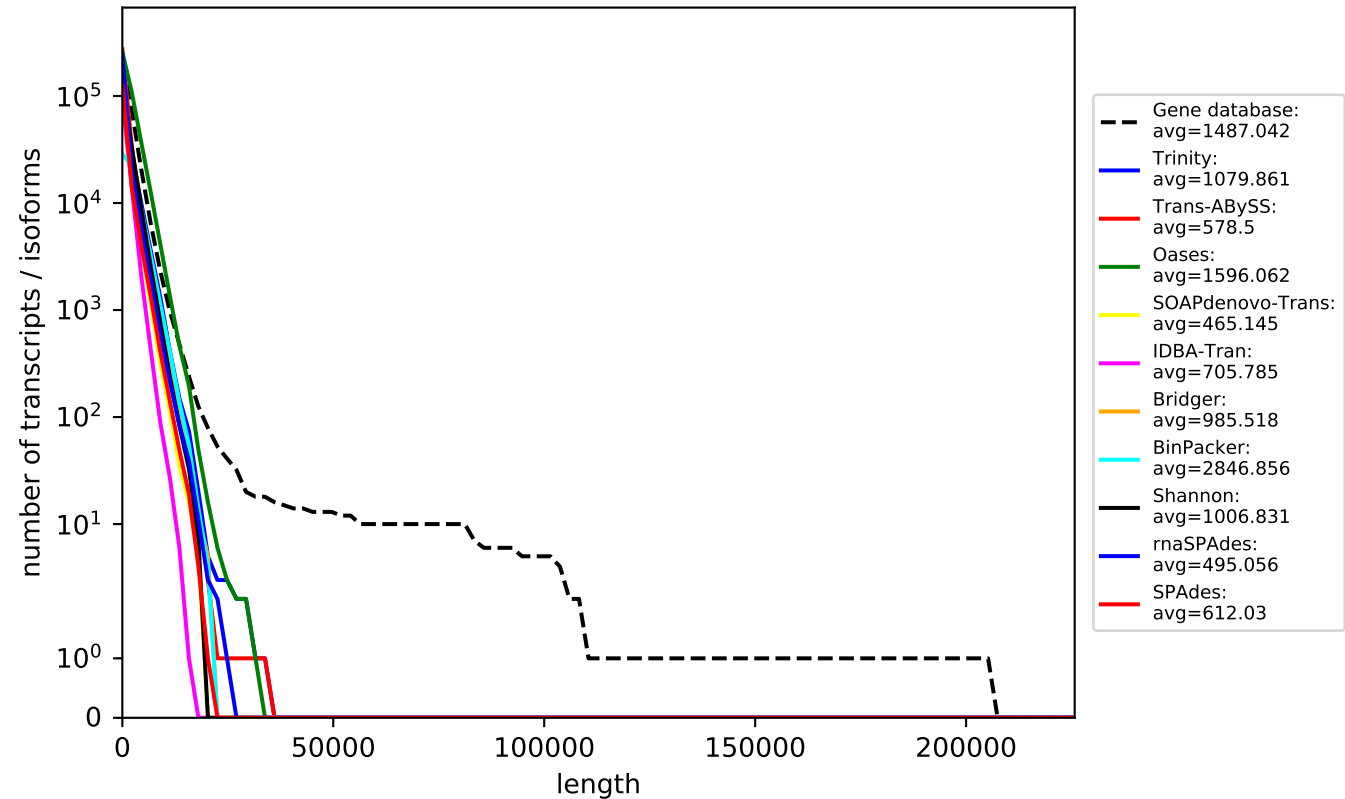


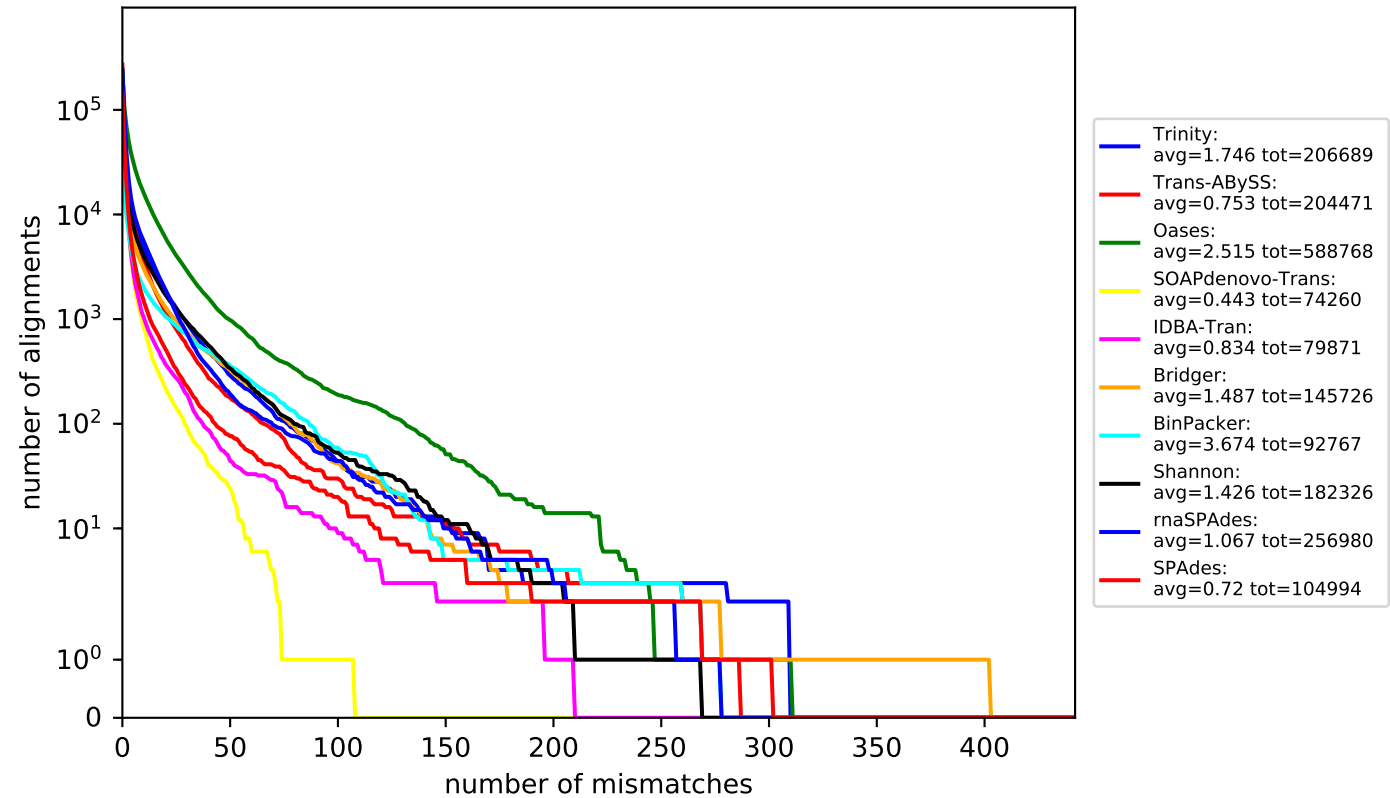
Short report

	Trinity	Trans-ABYSS	Oases	SOAPdenovo-Trans	IDBA-Tran	Bridger	BinPacker	Shannon	rnaSPAdes	SPAdes
Genes	57992	57992	57992	57992	57992	57992	57992	57992	57992	57992
Avg. number of exons per isoform	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971	5.971
Transcripts	121575	275008	259024	165909	95730	103284	28888	133199	243604	125233
Transcripts > 500 bp	50409	69717	163070	29135	37135	40276	26809	56849	39548	31264
Transcripts > 1000 bp	31319	37410	115596	15251	16181	23487	22928	35785	21867	15598
Aligned	121404	274233	257703	165401	95623	103098	28840	133032	241562	124551
Uniquely aligned	116518	263913	229396	162777	94239	96737	25086	125839	236219	110918
Multiply aligned	764	2838	1694	1738	595	529	58	786	1806	7690
Unaligned	171	775	1321	508	107	186	48	167	2042	682
Avg. aligned fraction	0.983	0.982	0.92	0.995	0.992	0.975	0.938	0.981	0.987	0.986
Avg. alignment length	1040.875	534.402	1364.377	455.959	697.748	866.608	2505.426	918.854	470.161	489.2
Avg. mismatches per transcript	1.746	0.753	2.515	0.443	0.834	1.487	3.674	1.426	1.067	0.72
Misassemblies	1294	4769	18893	125	203	2509	2649	2605	1219	2042
Database coverage	0.178	0.21	0.201	0.158	0.15	0.141	0.102	0.167	0.173	0.143
50%-assembled genes	9849	10377	10258	9406	8675	8480	6728	8889	10186	9154
95%-assembled genes	3972	3694	4128	3116	776	2722	2585	2562	3628	2790
50%-covered genes	11338	12053	11355	11234	11103	9903	7054	10747	12078	10454
95%-covered genes	4999	5157	5252	3965	2003	3286	2879	3761	4691	3454
50%-assembled isoforms	14332	17634	17801	11166	10800	10559	8400	12957	12795	10453
95%-assembled isoforms	4696	4004	5115	3225	780	2965	2851	2964	3850	2795
50%-covered isoforms	16823	22458	20319	14018	14855	12587	8796	16167	15837	12569
95%-covered isoforms	5889	5768	6549	4106	2012	3556	3164	4354	4981	3461
Mean isoform coverage	0.514	0.464	0.539	0.385	0.451	0.435	0.678	0.529	0.411	0.422
Mean isoform assembly	0.461	0.4	0.491	0.334	0.38	0.391	0.654	0.456	0.36	0.377
Predicted genes	33592	50018	96132	17801	25350	23585	18234	41533	23967	18444
50%-matched	58201	117092	140767	61852	48574	44187	21827	81027	60734	47018
95%-matched	36579	79703	67696	50736	39613	29804	12271	58664	41312	35929
Unannotated	47498	128019	60426	85681	35089	40608	1173	38169	159251	61658
Mean fraction of transcript matched	0.473	0.42	0.561	0.372	0.508	0.44	0.805	0.609	0.249	0.319

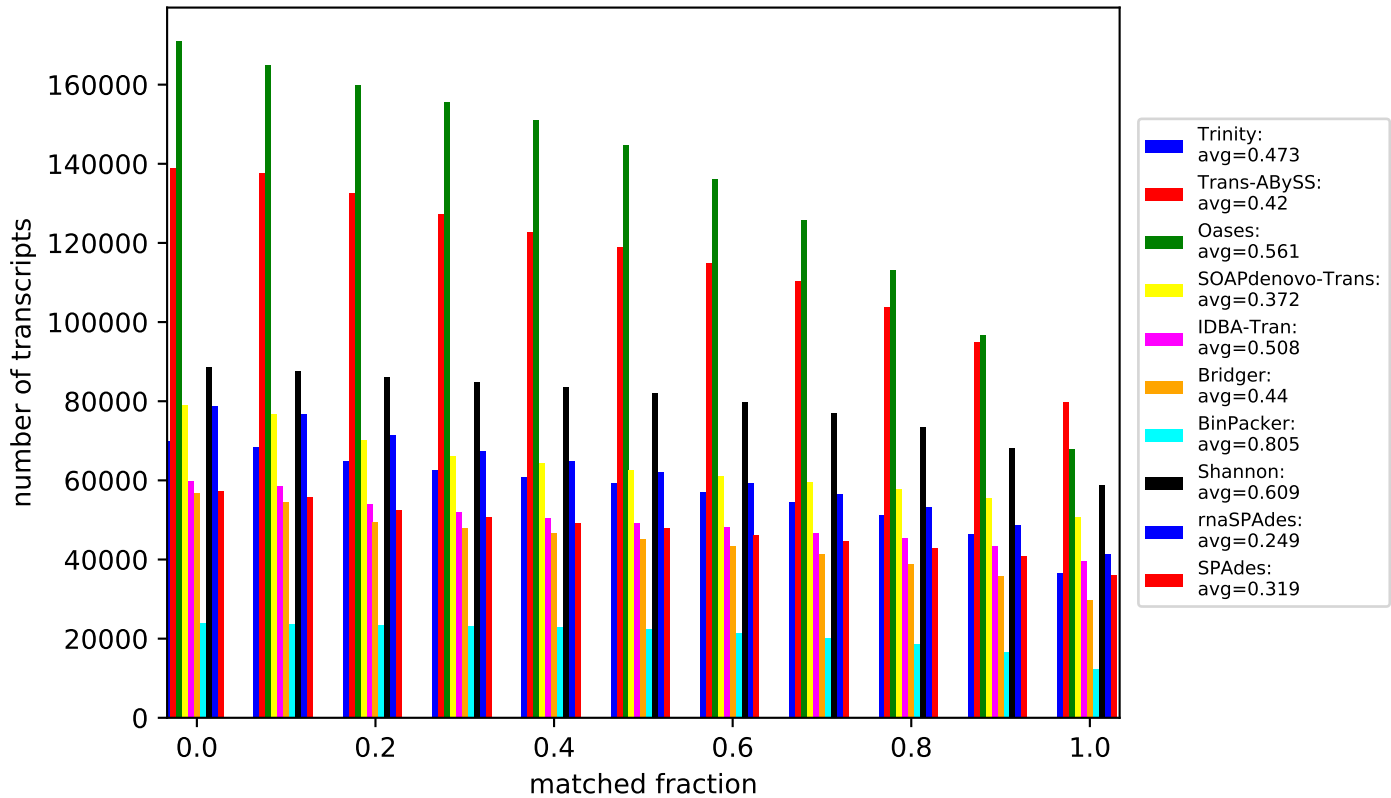
Cumulative transcript / isoform length plot



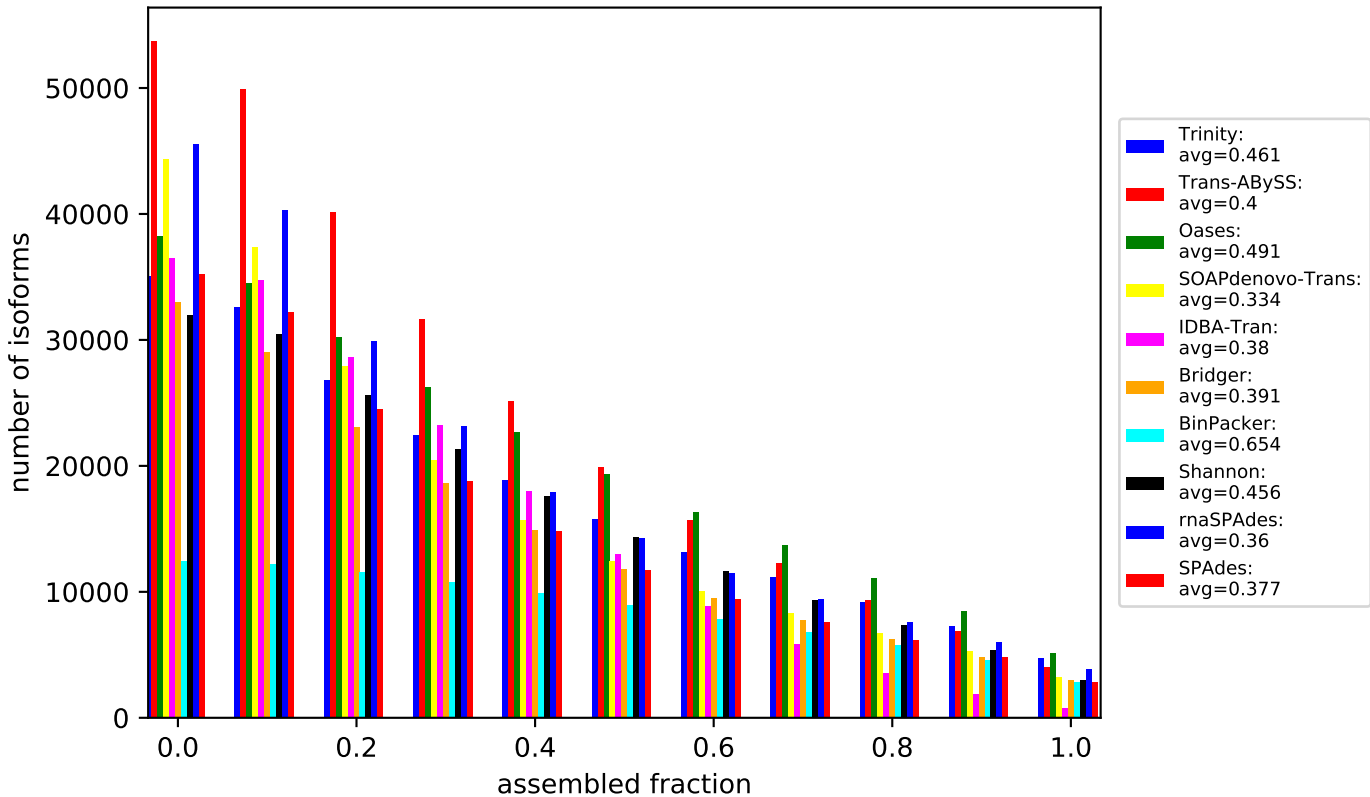
Cumulative substitution errors per alignment plot



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

