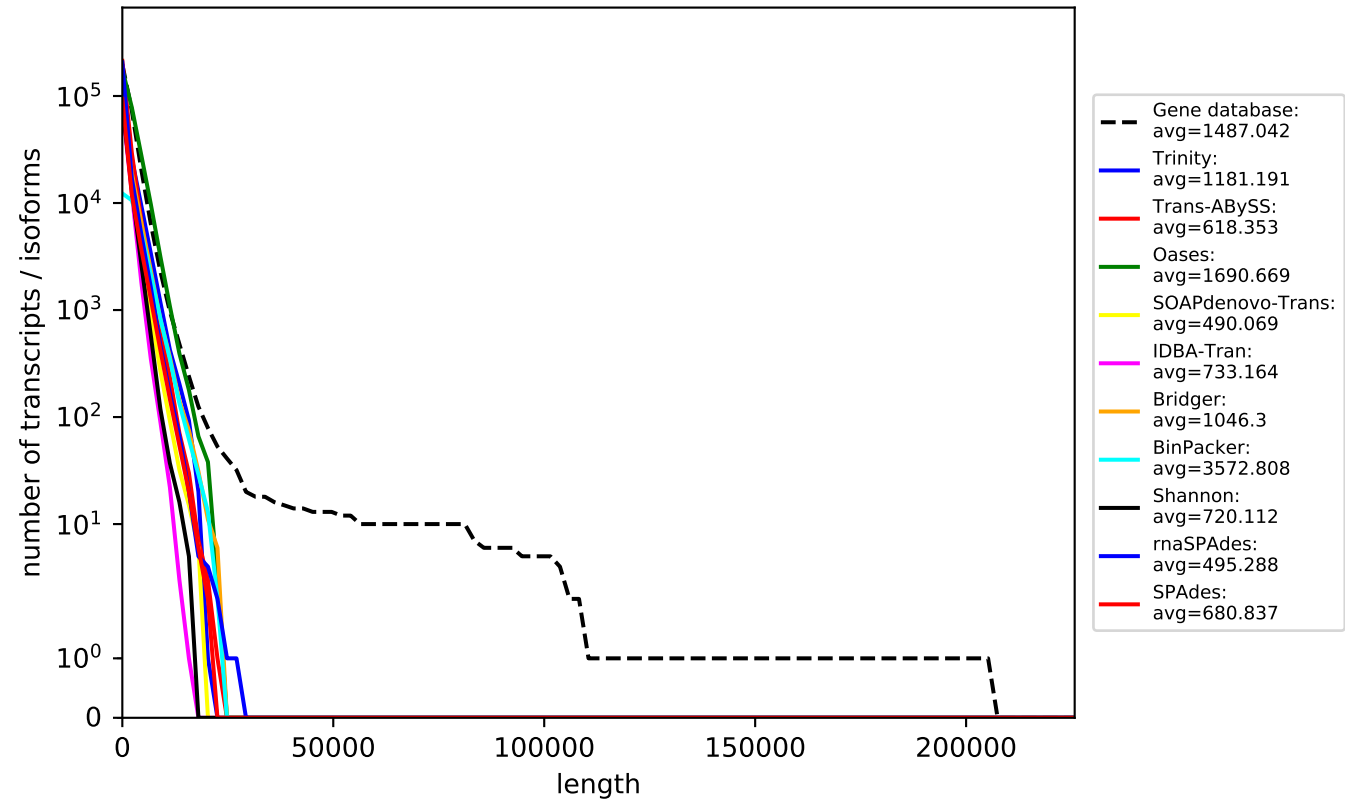


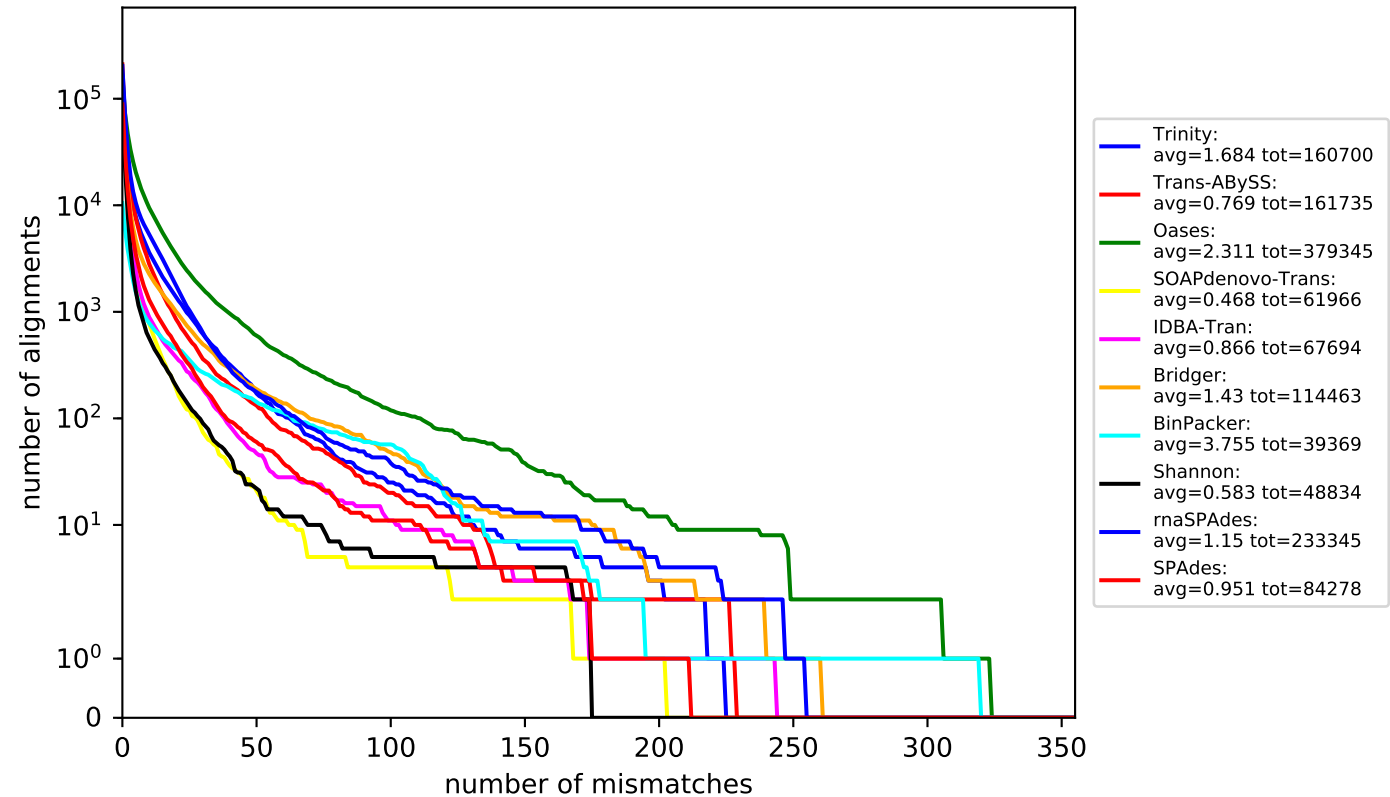
Short report

| | 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 | 97849 | 213005 | 178498 | 131711 | 78116 | 83744 | 12291 | 84456 | 206133 | 93814 |
| Transcripts > 500 bp | 42497 | 58213 | 114976 | 24636 | 31500 | 33578 | 11834 | 27820 | 32697 | 25204 |
| Transcripts > 1000 bp | 27785 | 32866 | 83530 | 13418 | 14196 | 20560 | 10862 | 15007 | 18629 | 13245 |
| Aligned | 97647 | 212044 | 177747 | 130789 | 77999 | 83546 | 12274 | 84373 | 203335 | 87567 |
| Uniquely aligned | 94046 | 204947 | 161313 | 128896 | 77059 | 79021 | 10437 | 82753 | 199122 | 81873 |
| Multiply aligned | 549 | 1999 | 1048 | 1263 | 407 | 404 | 19 | 421 | 1496 | 1707 |
| Unaligned | 202 | 961 | 751 | 922 | 117 | 198 | 17 | 83 | 2798 | 6247 |
| Avg. aligned fraction | 0.984 | 0.984 | 0.937 | 0.995 | 0.993 | 0.977 | 0.929 | 0.994 | 0.987 | 0.984 |
| Avg. alignment length | 1143.492 | 578.881 | 1500.776 | 482.257 | 725.58 | 929.857 | 3072.898 | 703.748 | 476.176 | 649.419 |
| Avg. mismatches per transcript | 1.684 | 0.769 | 2.311 | 0.468 | 0.866 | 1.43 | 3.755 | 0.583 | 1.15 | 0.951 |
| Misassemblies | 1066 | 3253 | 11194 | 94 | 134 | 1844 | 1436 | 381 | 908 | 1206 |
| Database coverage | 0.161 | 0.188 | 0.176 | 0.143 | 0.136 | 0.131 | 0.048 | 0.116 | 0.159 | 0.126 |
| 50%-assembled genes | 8947 | 9467 | 9166 | 8582 | 7964 | 7837 | 3054 | 6519 | 9283 | 8232 |
| 95%-assembled genes | 3486 | 3292 | 3579 | 2667 | 710 | 2492 | 1353 | 1502 | 3363 | 2650 |
| 50%-covered genes | 10329 | 11000 | 10167 | 10251 | 10120 | 9192 | 3115 | 8262 | 11020 | 9329 |
| 95%-covered genes | 4299 | 4434 | 4451 | 3404 | 1744 | 2981 | 1415 | 2188 | 4217 | 3034 |
| 50%-assembled isoforms | 12623 | 15475 | 15176 | 9979 | 9764 | 9616 | 3794 | 8309 | 11326 | 9031 |
| 95%-assembled isoforms | 4065 | 3575 | 4330 | 2749 | 714 | 2736 | 1523 | 1631 | 3535 | 2654 |
| 50%-covered isoforms | 14765 | 19493 | 17208 | 12503 | 13253 | 11421 | 3874 | 10900 | 13922 | 10517 |
| 95%-covered isoforms | 4991 | 4943 | 5457 | 3512 | 1755 | 3246 | 1591 | 2369 | 4440 | 3039 |
| Mean isoform coverage | 0.515 | 0.461 | 0.551 | 0.385 | 0.451 | 0.444 | 0.719 | 0.473 | 0.403 | 0.439 |
| Mean isoform assembly | 0.462 | 0.401 | 0.504 | 0.335 | 0.382 | 0.399 | 0.707 | 0.402 | 0.354 | 0.398 |
| Predicted genes | 30009 | 43585 | 73686 | 16066 | 23174 | 21088 | 8375 | 23879 | 21429 | 15644 |
| 50%-matched | 51949 | 99617 | 109483 | 55068 | 43657 | 40396 | 9462 | 56036 | 56981 | 33929 |
| 95%-matched | 33810 | 70234 | 57036 | 46001 | 36242 | 28362 | 4836 | 48039 | 40135 | 25755 |
| Unannotated | 33696 | 90840 | 35015 | 60913 | 24679 | 29047 | 202 | 23378 | 128667 | 42074 |
| Mean fraction of transcript matched | 0.524 | 0.462 | 0.623 | 0.419 | 0.559 | 0.492 | 0.83 | 0.658 | 0.277 | 0.379 |

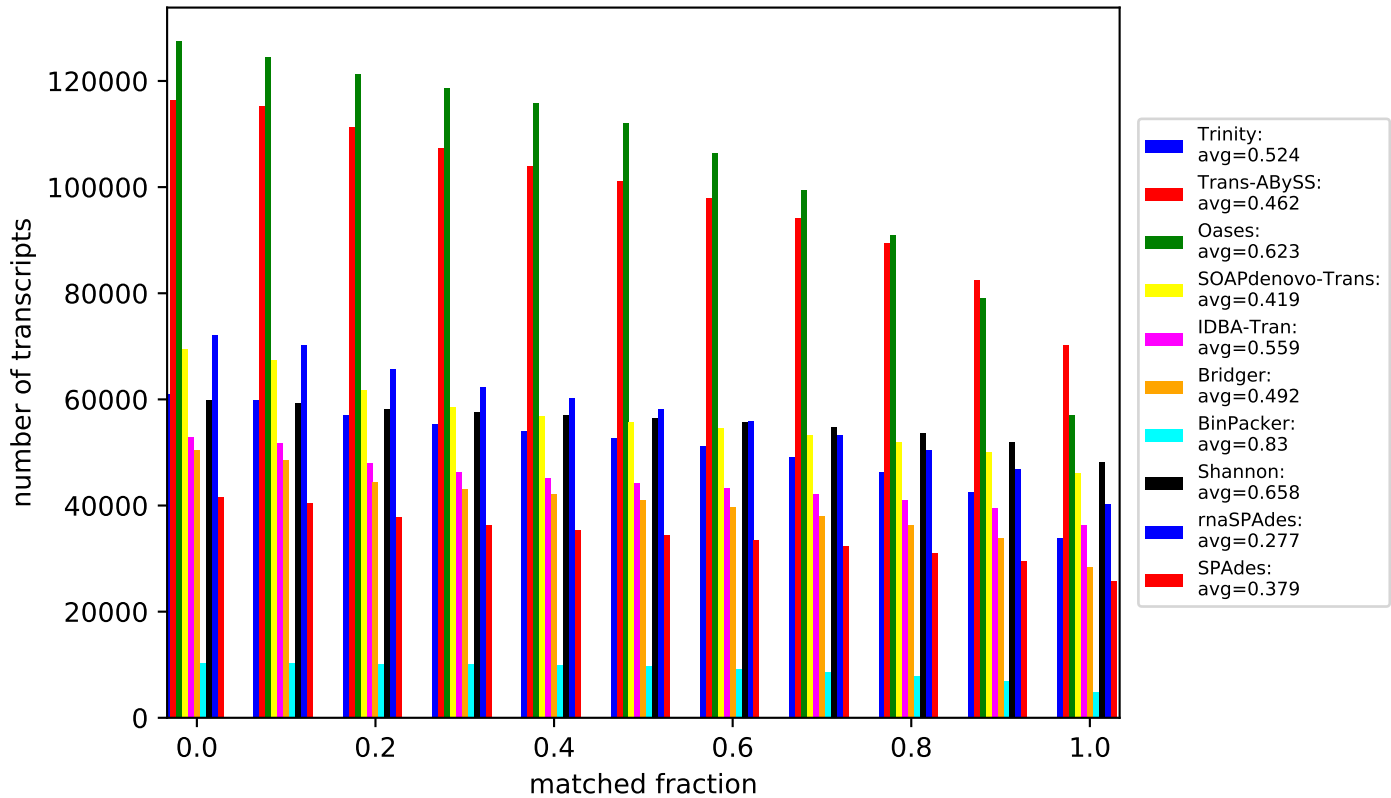
Cumulative transcript / isoform length plot



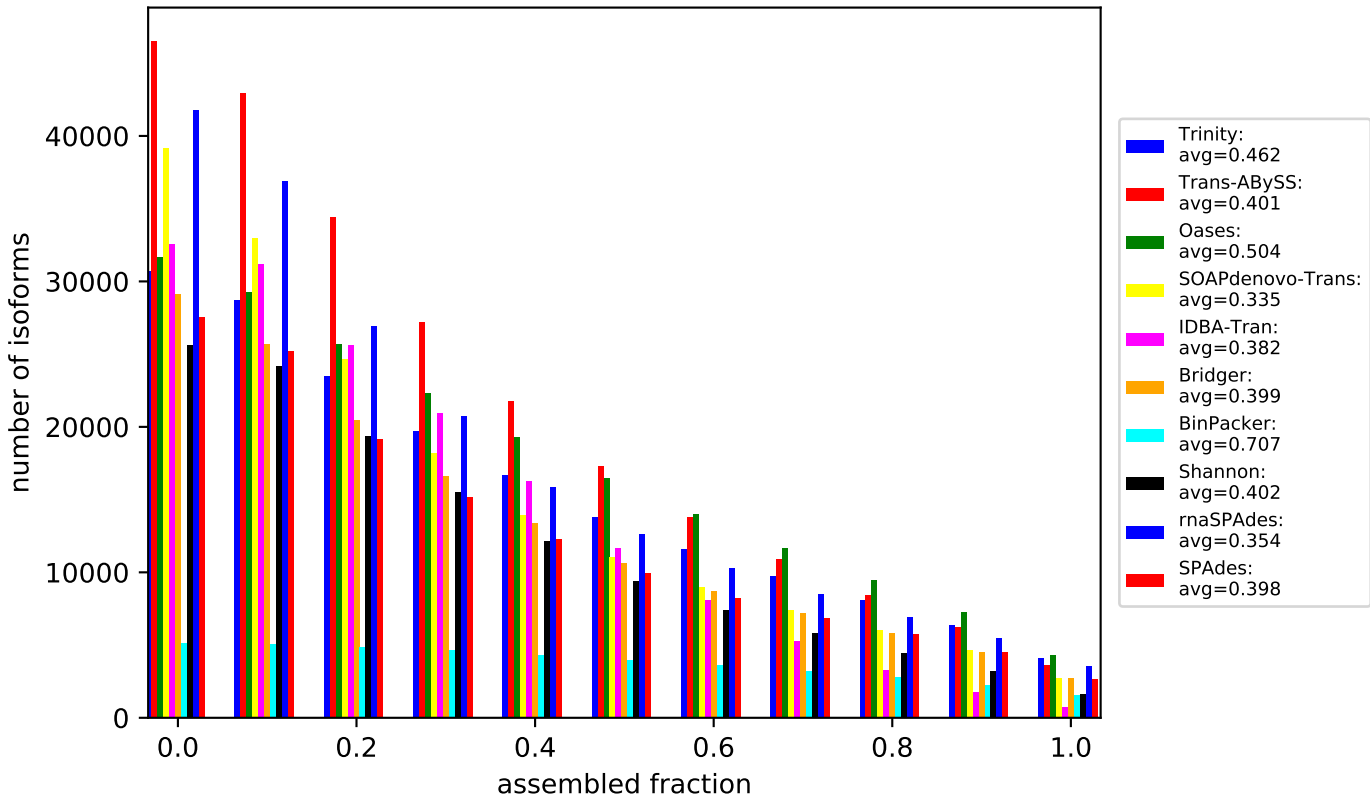
Cumulative substitution errors per alignment plot



Cumulative transcript matched fraction histogram



Cumulative isoform assembled fraction histogram



Cumulative isoform covered fraction histogram

