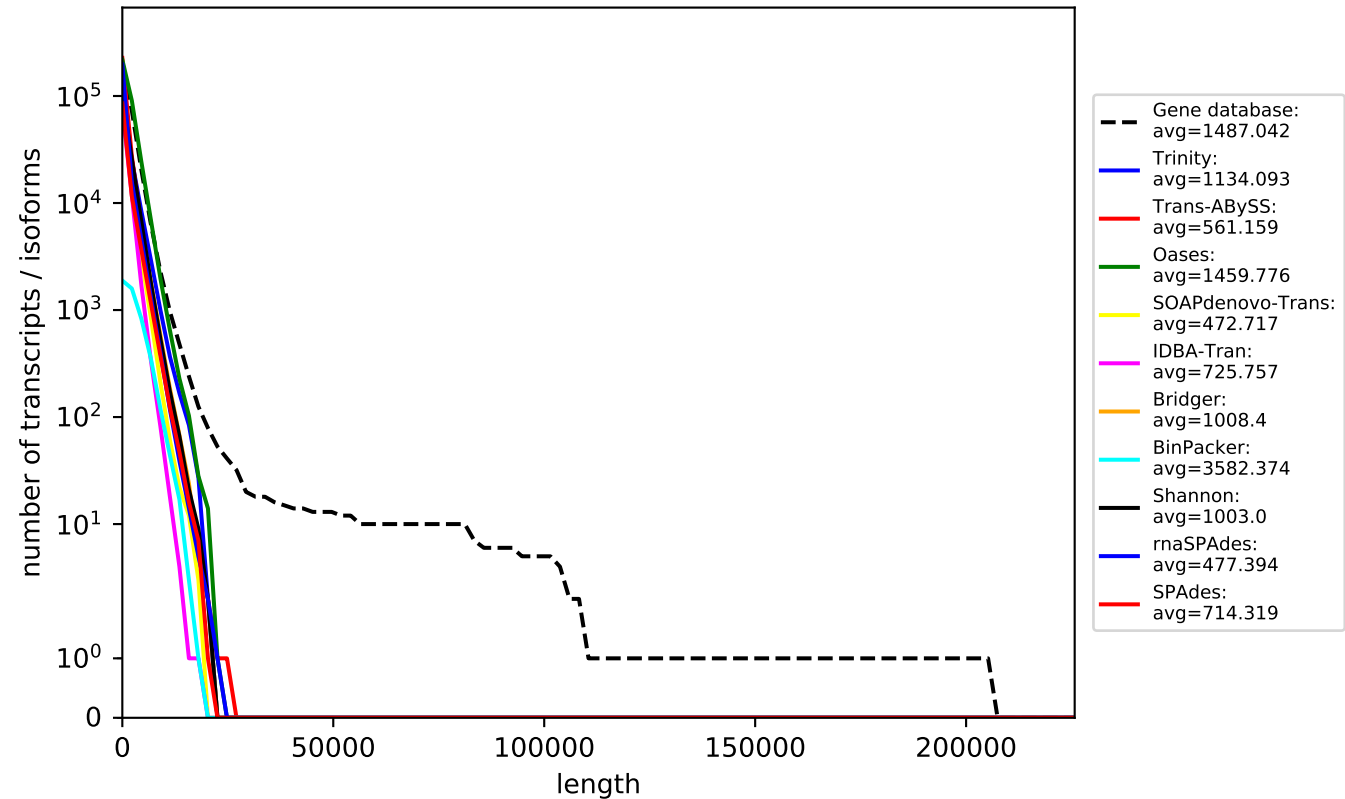


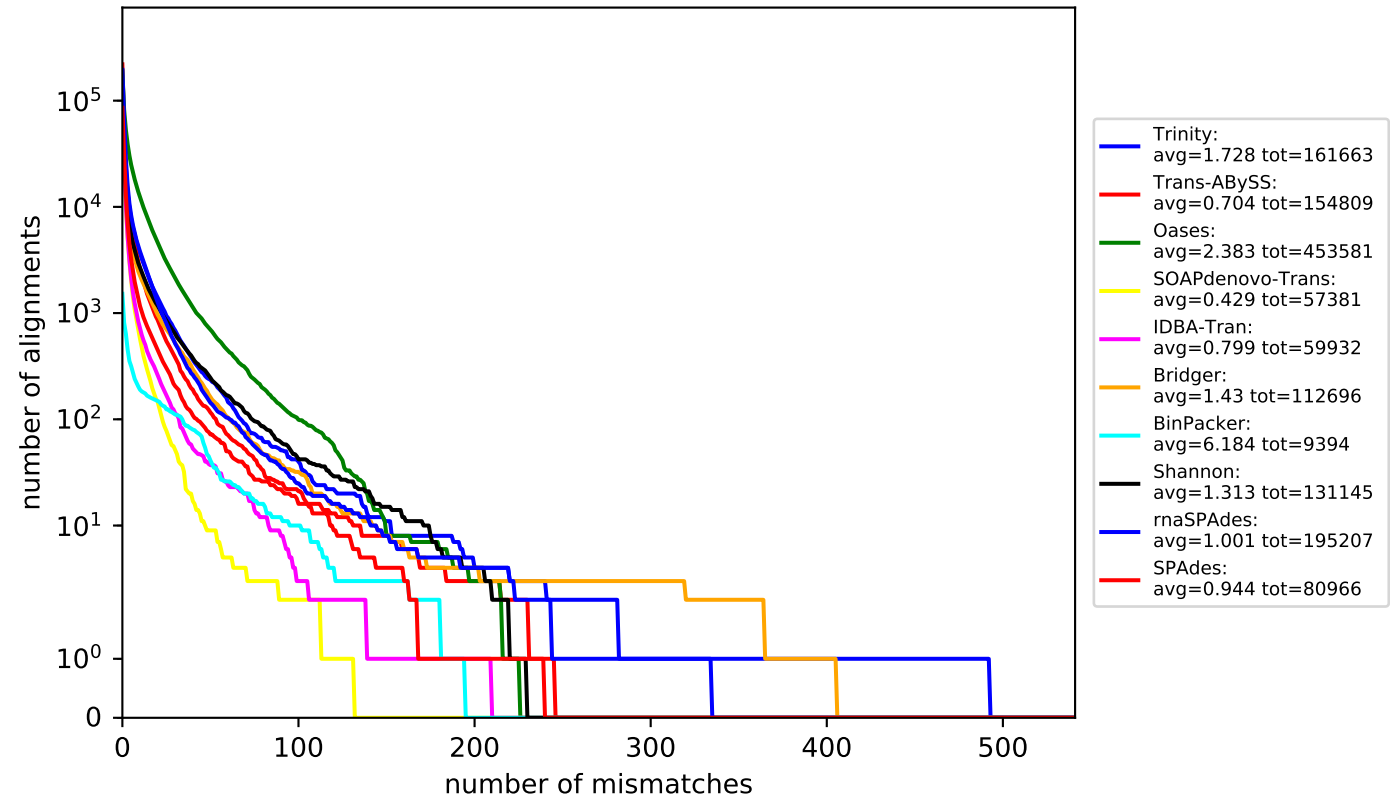
## Short report

|                                     | 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                         | 96550    | 227117      | 218483   | 132751           | 75087     | 82495   | 1885      | 103815  | 197477    | 85257   |
| Transcripts > 500 bp                | 41779    | 56023       | 141416   | 23602            | 29737     | 32853   | 1806      | 45423   | 30090     | 23614   |
| Transcripts > 1000 bp               | 27154    | 30767       | 98196    | 13110            | 13508     | 20434   | 1646      | 28248   | 17195     | 12775   |
| Aligned                             | 96414    | 226264      | 217524   | 132192           | 75016     | 82359   | 1876      | 103729  | 195967    | 85001   |
| Uniquely aligned                    | 92154    | 213998      | 186940   | 130119           | 74003     | 77699   | 1489      | 98368   | 191228    | 79356   |
| Multiply aligned                    | 554      | 2151        | 1224     | 1360             | 402       | 441     | 13        | 565     | 1543      | 1612    |
| Unaligned                           | 136      | 853         | 959      | 559              | 71        | 136     | 9         | 86      | 1510      | 256     |
| Avg. aligned fraction               | 0.982    | 0.974       | 0.925    | 0.993            | 0.992     | 0.978   | 0.908     | 0.982   | 0.986     | 0.983   |
| Avg. alignment length               | 1083.555 | 517.916     | 1308.216 | 464.368          | 718.402   | 925.619 | 2899.392  | 921.046 | 462.087   | 661.322 |
| Avg. mismatches per transcript      | 1.728    | 0.704       | 2.383    | 0.429            | 0.799     | 1.43    | 6.184     | 1.313   | 1.001     | 0.944   |
| Misassemblies                       | 1580     | 7956        | 24845    | 148              | 178       | 1853    | 279       | 2161    | 943       | 1262    |
| Database coverage                   | 0.163    | 0.19        | 0.185    | 0.145            | 0.137     | 0.135   | 0.006     | 0.149   | 0.16      | 0.132   |
| 50%-assembled genes                 | 9238     | 9697        | 9622     | 8709             | 8041      | 8244    | 453       | 8147    | 9604      | 8849    |
| 95%-assembled genes                 | 3275     | 2971        | 3265     | 2481             | 569       | 2540    | 227       | 2047    | 3173      | 2650    |
| 50%-covered genes                   | 10687    | 11339       | 10755    | 10562            | 10360     | 9664    | 458       | 10039   | 11370     | 9988    |
| 95%-covered genes                   | 4162     | 4144        | 4303     | 3195             | 1639      | 3066    | 235       | 3018    | 4129      | 3126    |
| 50%-assembled isoforms              | 12986    | 15150       | 16278    | 9932             | 9681      | 10020   | 550       | 11168   | 11442     | 9529    |
| 95%-assembled isoforms              | 3826     | 3153        | 3948     | 2553             | 569       | 2781    | 255       | 2303    | 3335      | 2653    |
| 50%-covered isoforms                | 15216    | 19670       | 18656    | 12582            | 13221     | 11907   | 556       | 14104   | 14134     | 11049   |
| 95%-covered isoforms                | 4833     | 4480        | 5211     | 3284             | 1642      | 3327    | 264       | 3403    | 4338      | 3132    |
| Mean isoform coverage               | 0.518    | 0.444       | 0.549    | 0.383            | 0.454     | 0.455   | 0.718     | 0.524   | 0.407     | 0.451   |
| Mean isoform assembly               | 0.464    | 0.38        | 0.498    | 0.332            | 0.381     | 0.408   | 0.712     | 0.45    | 0.354     | 0.407   |
| Predicted genes                     | 30445    | 44205       | 95194    | 16217            | 23025     | 22024   | 1376      | 35683   | 20358     | 15761   |
| 50%-matched                         | 53868    | 112373      | 131790   | 58860            | 45371     | 42711   | 1269      | 71978   | 58962     | 35654   |
| 95%-matched                         | 36225    | 75135       | 69556    | 49648            | 38273     | 30697   | 595       | 56189   | 42860     | 27474   |
| Unannotated                         | 31271    | 88770       | 37816    | 61115            | 22079     | 27369   | 86        | 22475   | 120552    | 39000   |
| Mean fraction of transcript matched | 0.555    | 0.49        | 0.645    | 0.441            | 0.602     | 0.529   | 0.769     | 0.698   | 0.298     | 0.41    |

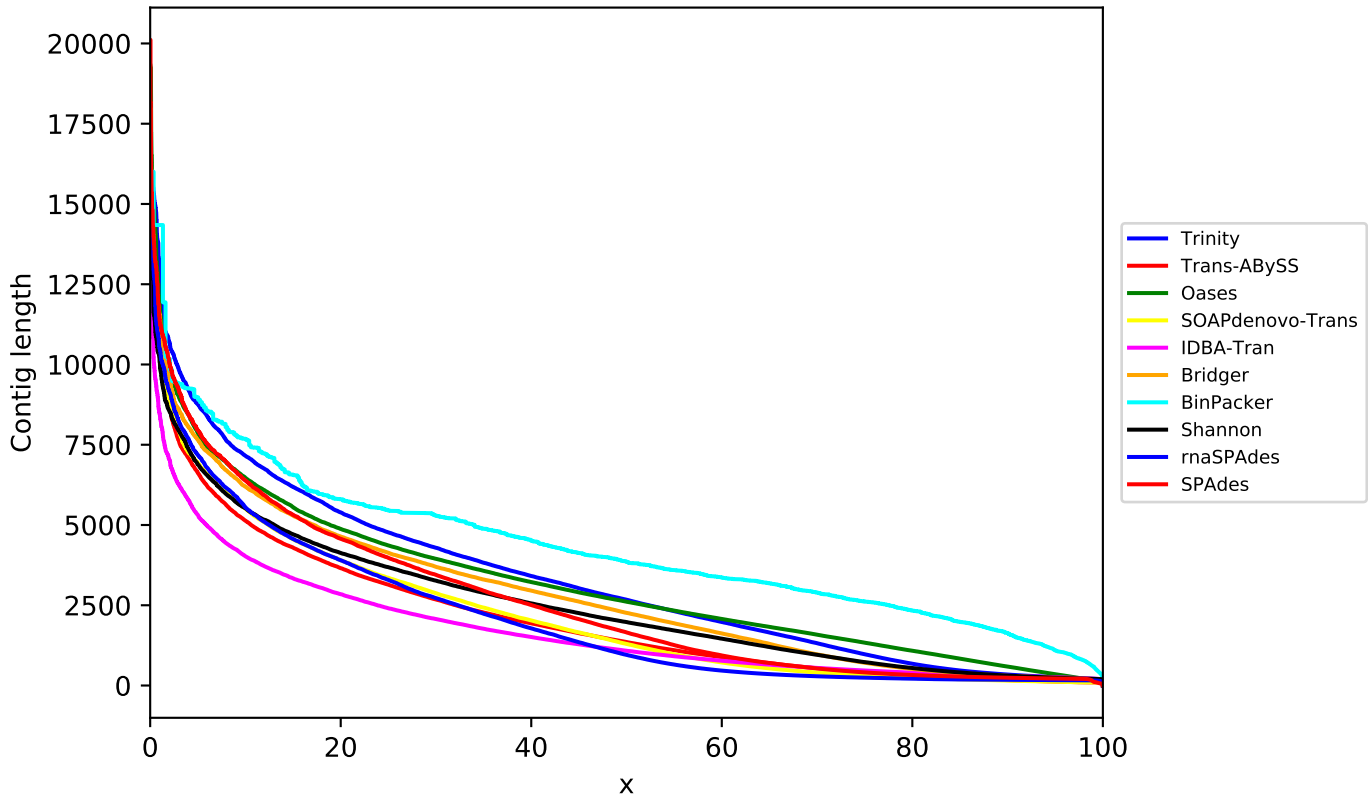
Cumulative transcript / isoform length plot



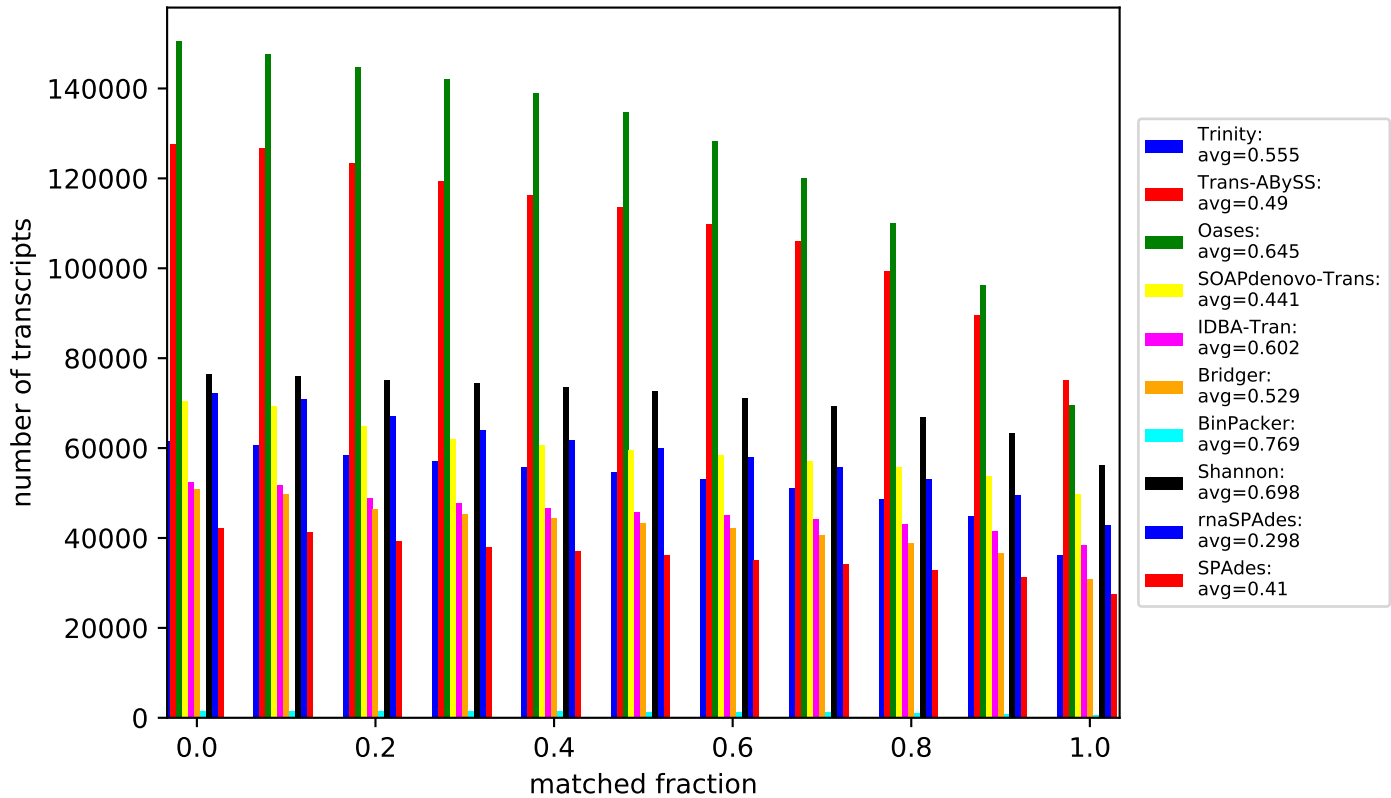
# Cumulative substitution errors per alignment plot



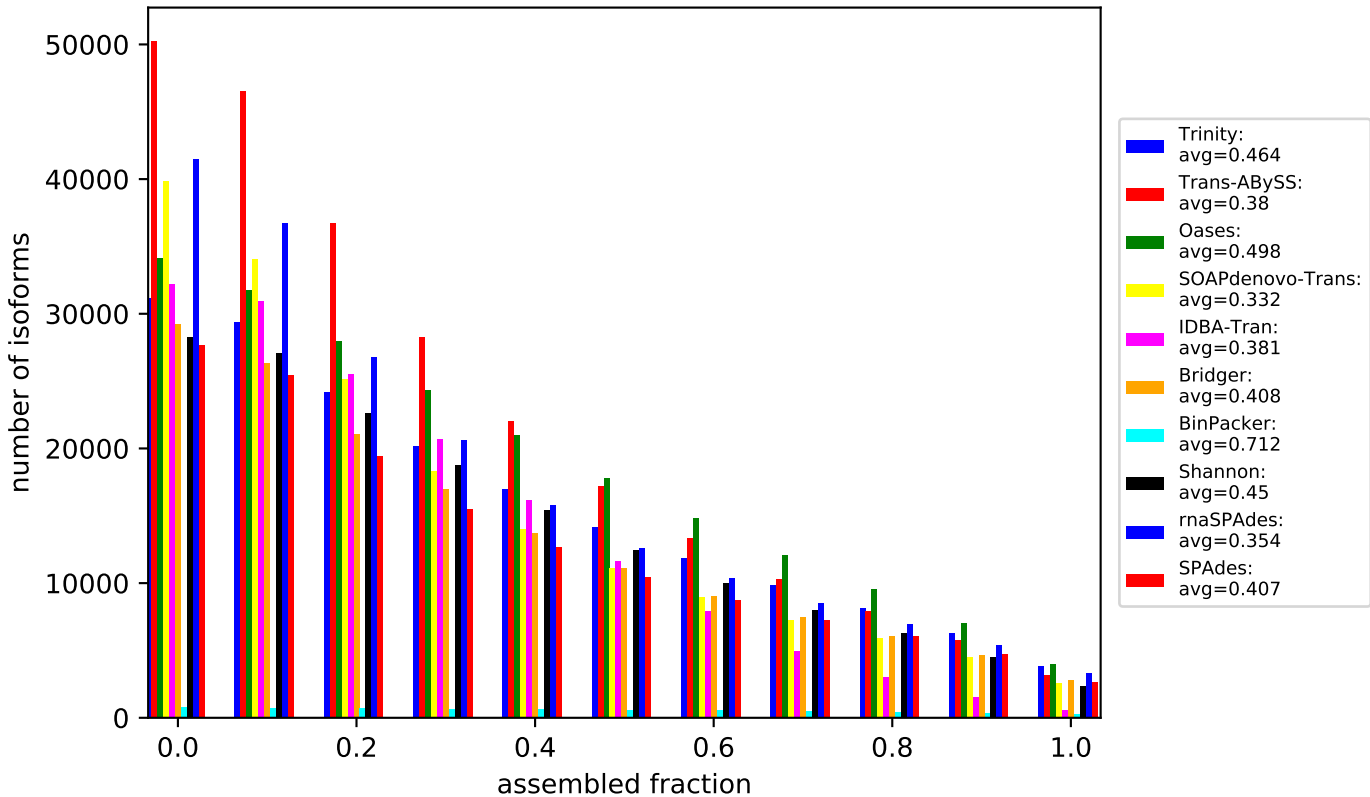
# NAX



# Cumulative transcript matched fraction histogram



# Cumulative isoform assembled fraction histogram



# Cumulative isoform covered fraction histogram

