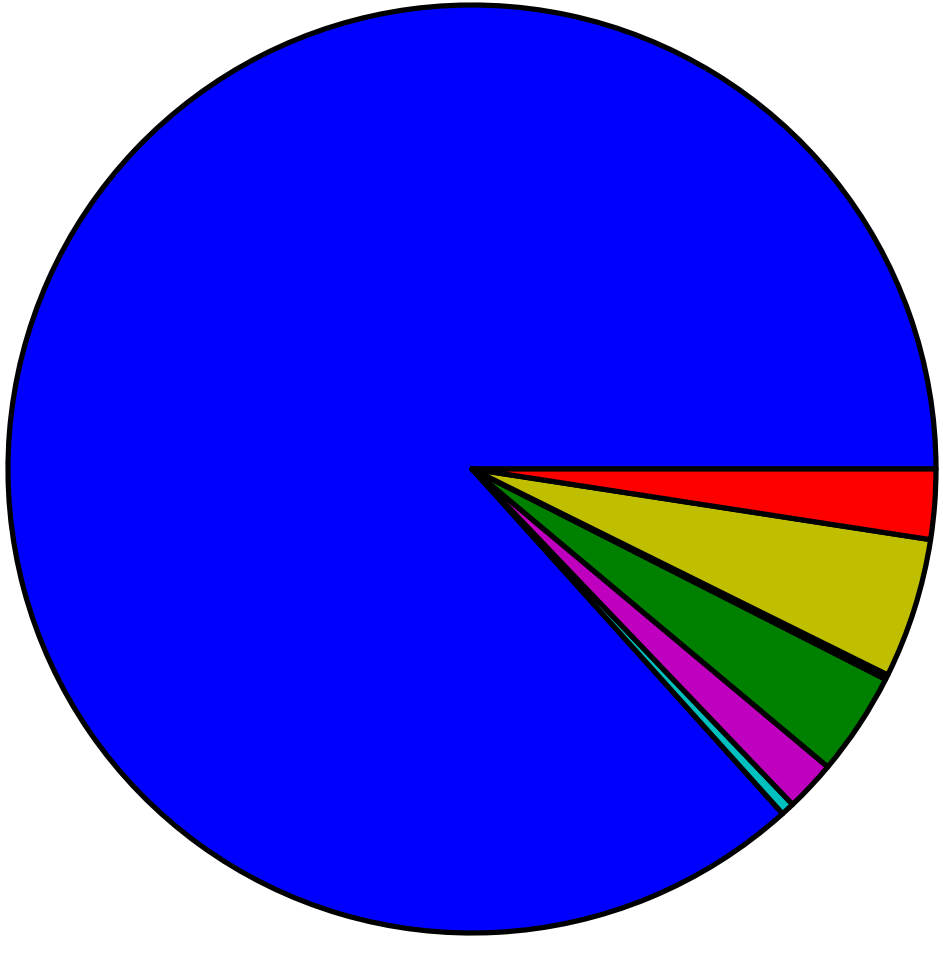
number of read pairs

- aligned (1.9×10^7)
- outside gene (1.0×10^5)
- unaligned (3.9×10^5)
- unpaired (8.0×10^5)
- excess N (3.7×10^4)
- low Q (1.1×10^6)
- filtered (5.4×10^5)