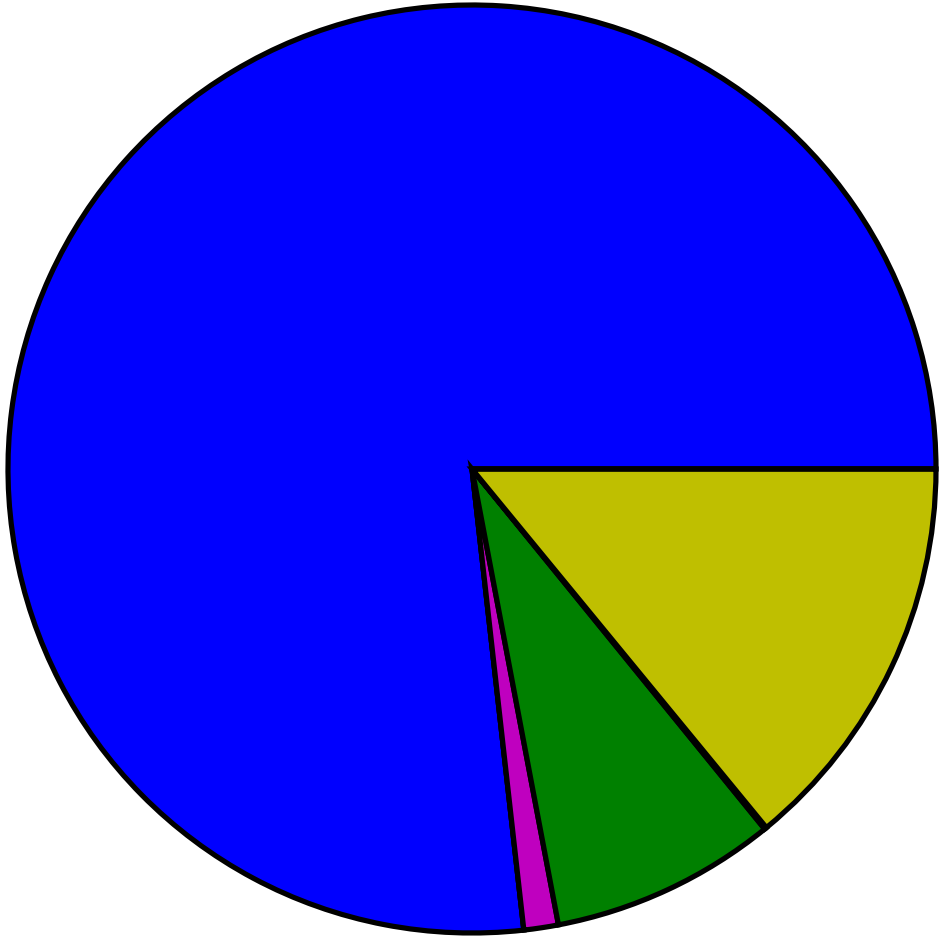
number of read pairs

- aligned (7.1×10^6)
- outside gene (0)
- unaligned (1.1×10^5)
- unpaired (7.3×10^5)
- excess N (7.1×10^3)
- low Q (1.3×10^6)
- filtered (0)