

# number of read pairs

- aligned ( $2.2 \times 10^7$ )
- outside gene ( $5.8 \times 10^3$ )
- unaligned ( $4.1 \times 10^4$ )
- unpaired ( $8.9 \times 10^6$ )
- excess N ( $2.2 \times 10^4$ )
- low Q ( $5.4 \times 10^5$ )
- filtered ( $4.4 \times 10^5$ )

