

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:27:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004026.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6004026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:27:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,075,163
Mapped reads	1,751,310 / 84.39%
Unmapped reads	323,853 / 15.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,604 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	96,051 / 4.63%
Duplication rate	4.38%
Clipped reads	869,626 / 41.91%

2.2. ACGT Content

Number/percentage of A's	31,822,061 / 27.64%
Number/percentage of C's	21,535,660 / 18.71%
Number/percentage of T's	36,171,533 / 31.42%
Number/percentage of G's	25,573,900 / 22.21%
Number/percentage of N's	19,178 / 0.02%
GC Percentage	40.92%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3433
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2.4. Mapping Quality

Mean Mapping Quality	45.53
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2.5. Mismatches and indels

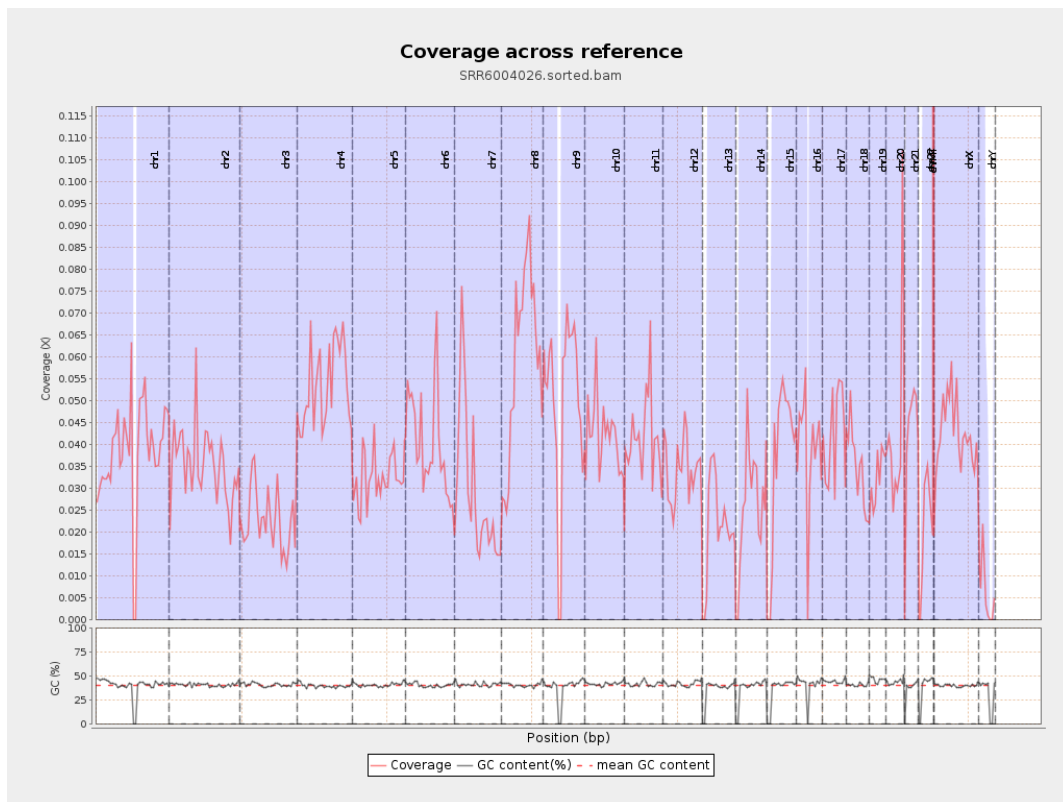
General error rate	0.99%
Mismatches	1,122,228
Insertions	9,088
Mapped reads with at least one insertion	0.51%
Deletions	37,649
Mapped reads with at least one deletion	2.12%
Homopolymer indels	45.03%

2.6. Chromosome stats

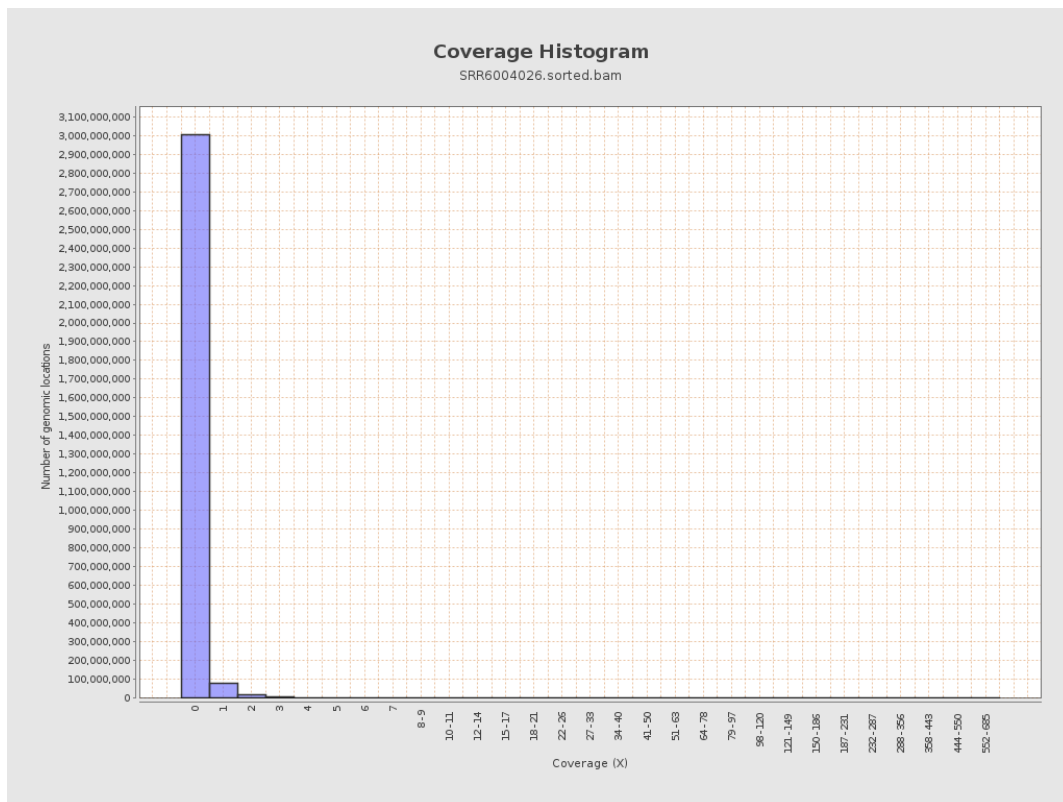
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9489651	0.0381	0.5903
chr2	243199373	8605242	0.0354	0.364
chr3	198022430	4509925	0.0228	0.1805
chr4	191154276	10202408	0.0534	0.3004
chr5	180915260	5862742	0.0324	0.2171
chr6	171115067	6845869	0.04	0.282
chr7	159138663	4741405	0.0298	0.3162

chr8	146364022	8679177	0.0593	0.424
chr9	141213431	7067518	0.05	0.4043
chr10	135534747	5708211	0.0421	0.3456
chr11	135006516	5568802	0.0412	0.3438
chr12	133851895	4558788	0.0341	0.2306
chr13	115169878	2403958	0.0209	0.1749
chr14	107349540	2739349	0.0255	0.2362
chr15	102531392	3812922	0.0372	0.2291
chr16	90354753	3494609	0.0387	0.2644
chr17	81195210	3435504	0.0423	0.2785
chr18	78077248	2752001	0.0352	0.6434
chr19	59128983	1898008	0.0321	0.4557
chr20	63025520	2832039	0.0449	0.2639
chr21	48129895	2036572	0.0423	0.2762
chr22	51304566	1033858	0.0202	0.1667
chrMT	16571	29697	1.7921	1.7657
chrX	155270560	6528748	0.042	0.2737
chrY	59373566	348858	0.0059	0.171

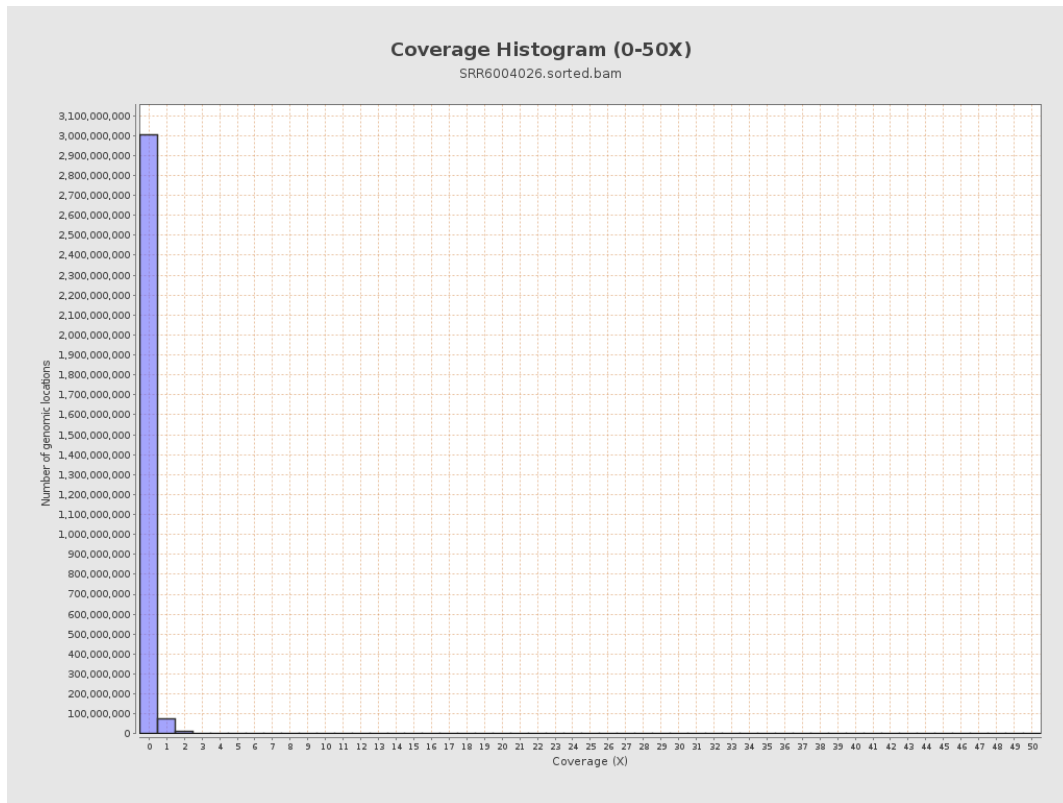
3. Results : Coverage across reference



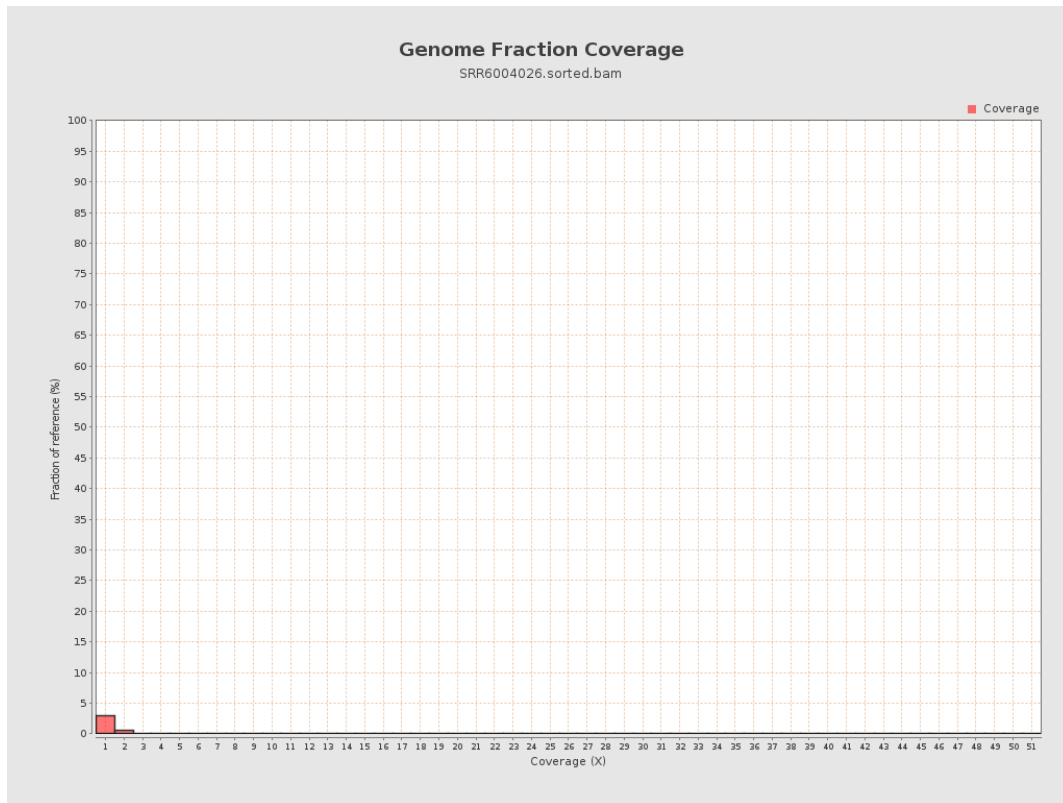
4. Results : Coverage Histogram



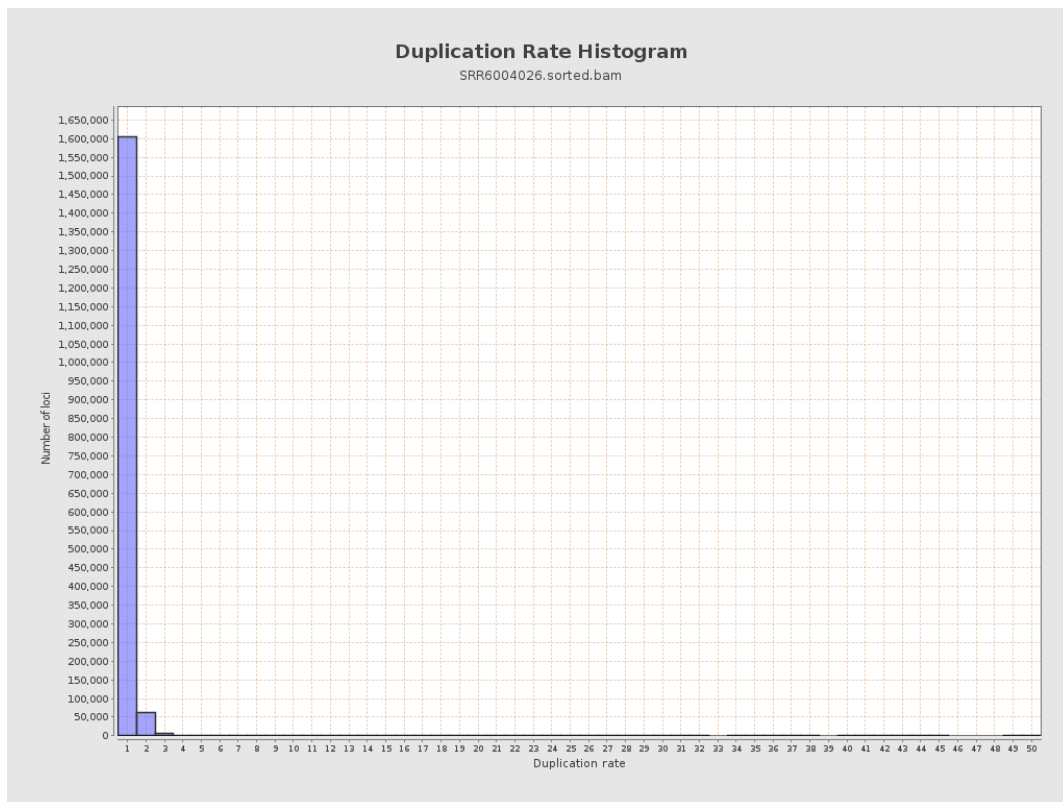
5. Results : Coverage Histogram (0-50X)



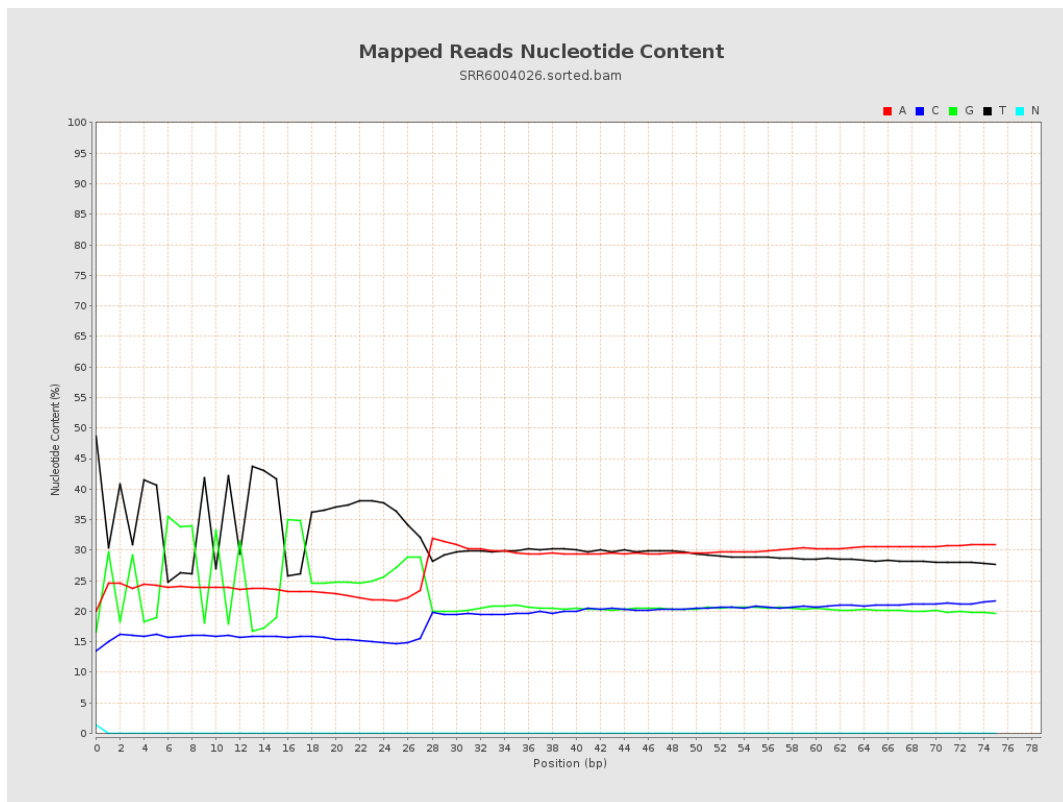
6. Results : Genome Fraction Coverage



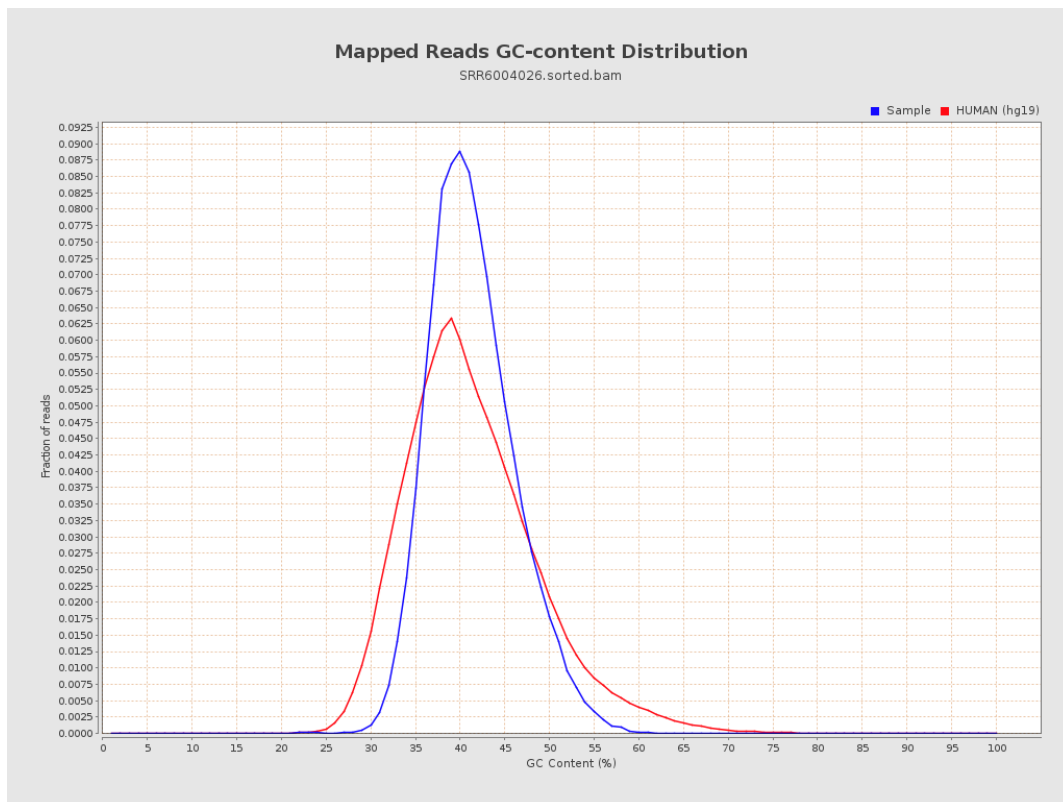
7. Results : Duplication Rate Histogram



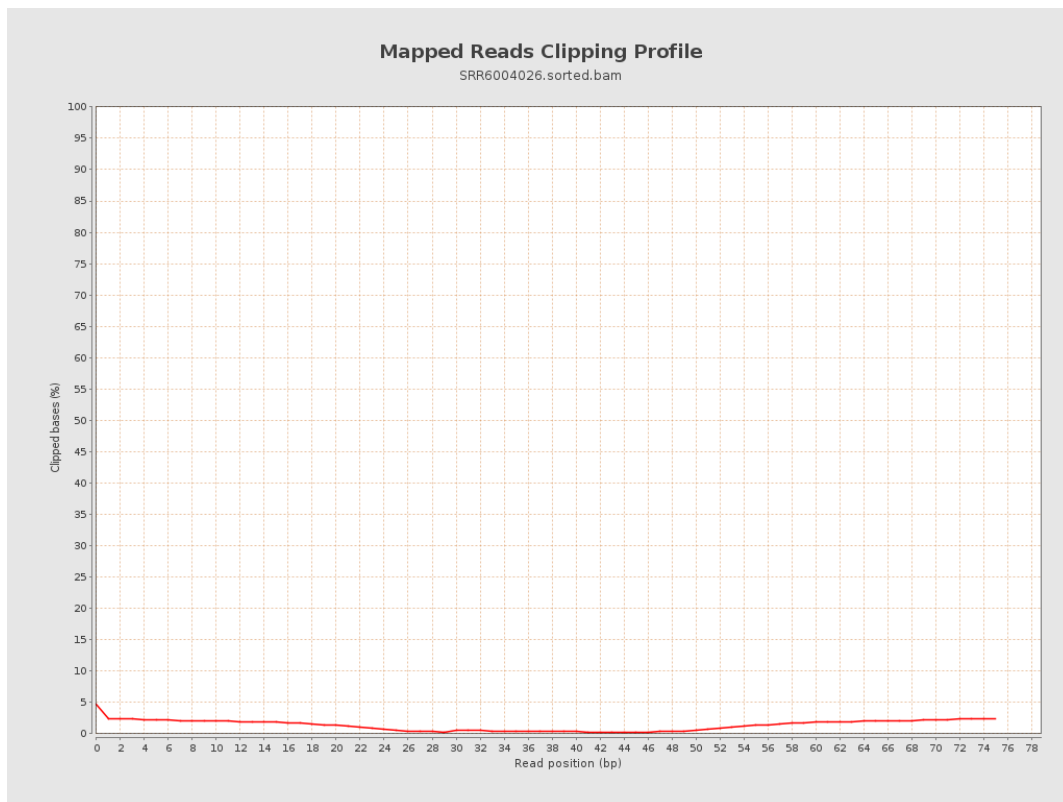
8. Results : Mapped Reads Nucleotide Content



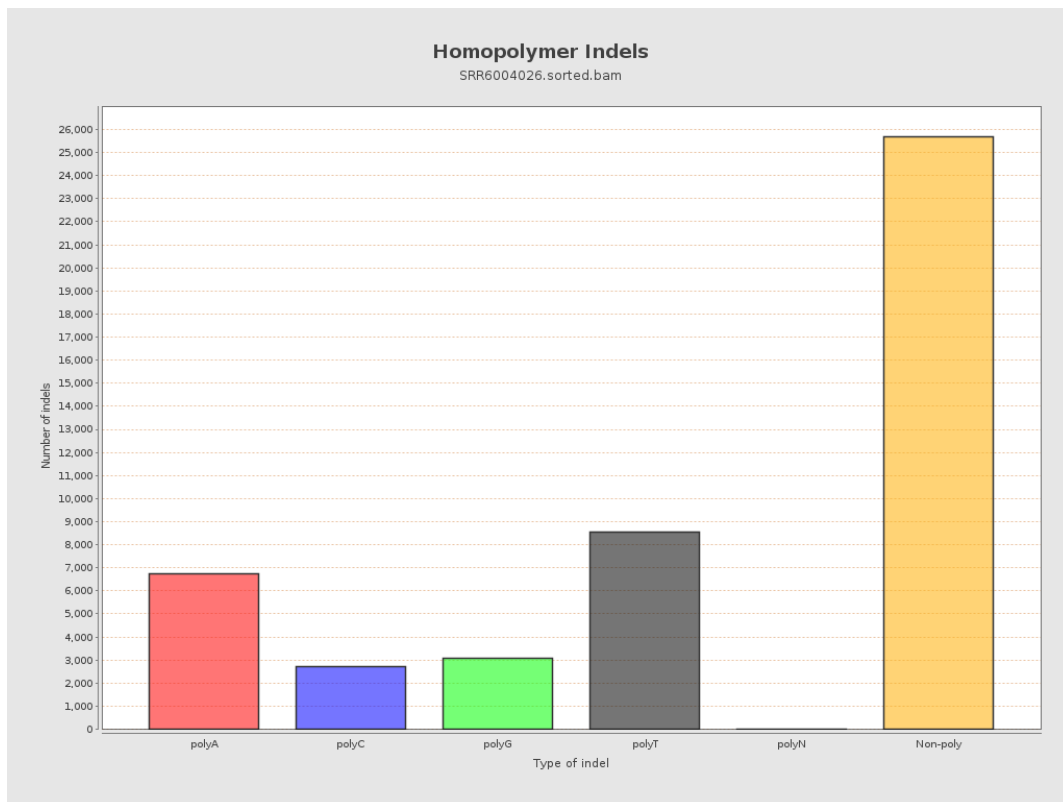
9. Results : Mapped Reads GC-content Distribution



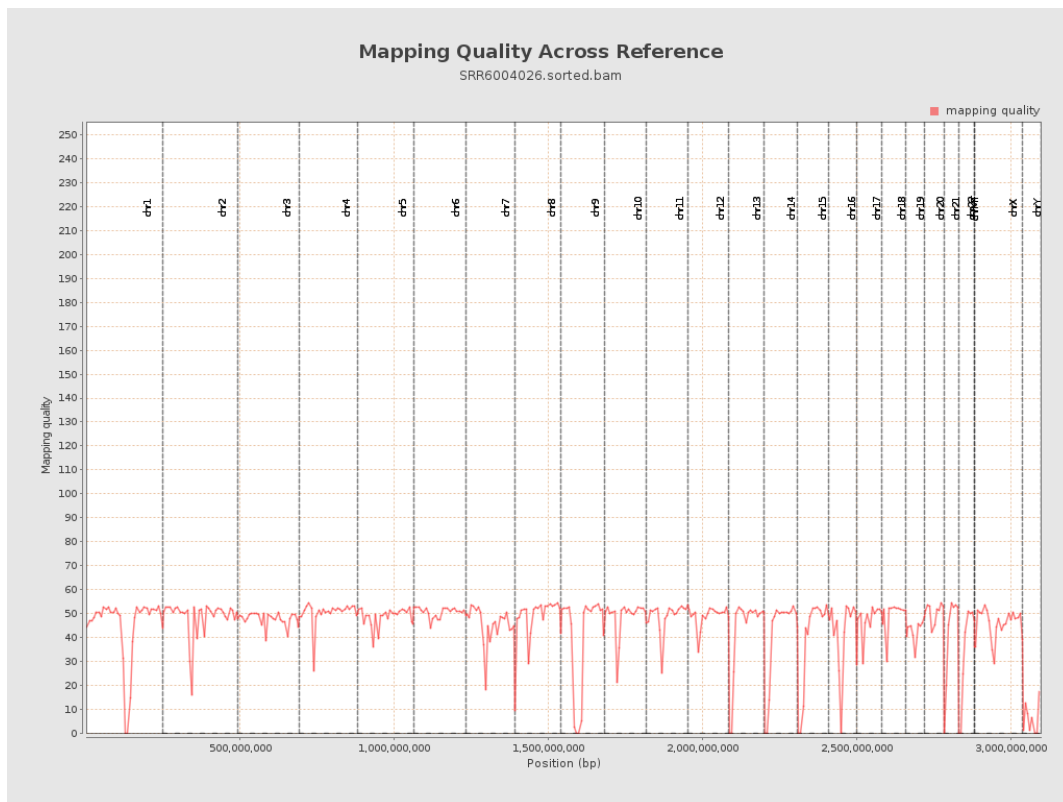
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

