

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:47:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004069.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_SRR6004069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:47:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,209,142
Mapped reads	1,092,368 / 90.34%
Unmapped reads	116,774 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,274 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	38,753 / 3.2%
Duplication rate	2.9%
Clipped reads	399,343 / 33.03%

2.2. ACGT Content

Number/percentage of A's	21,683,100 / 28.92%
Number/percentage of C's	13,766,544 / 18.36%
Number/percentage of T's	24,021,462 / 32.04%
Number/percentage of G's	15,490,925 / 20.66%
Number/percentage of N's	13,361 / 0.02%
GC Percentage	39.02%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.247
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2.4. Mapping Quality

Mean Mapping Quality	47.3
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2.5. Mismatches and indels

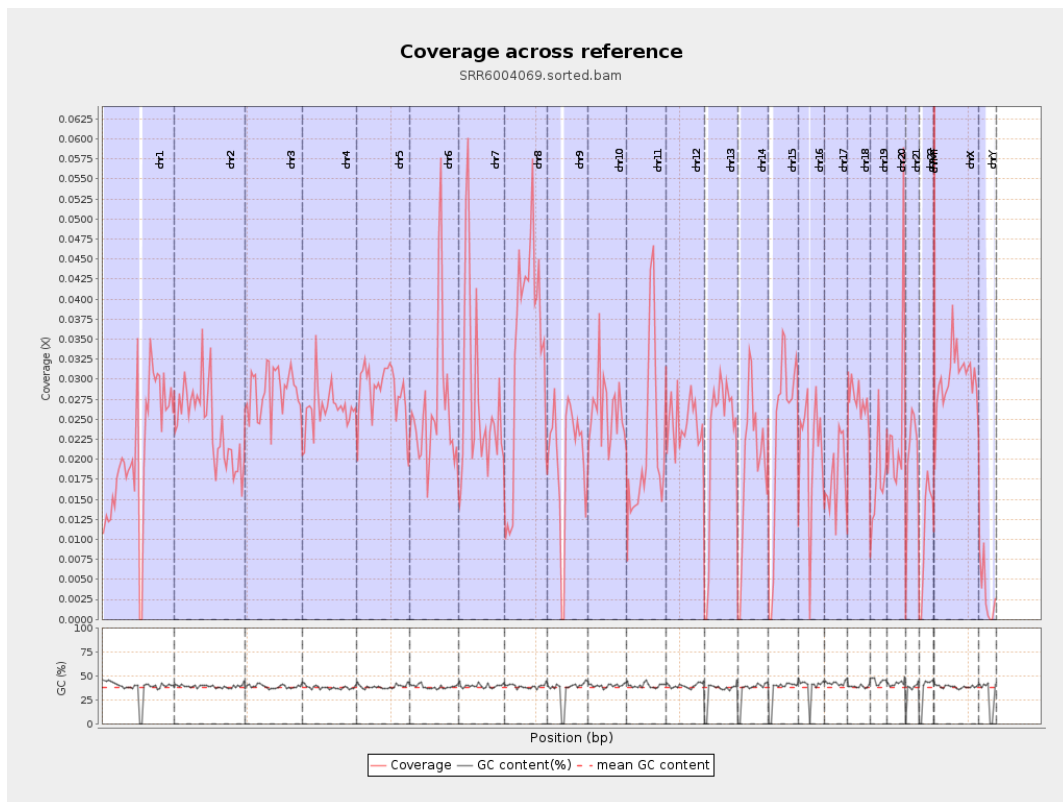
General error rate	0.88%
Mismatches	650,680
Insertions	5,679
Mapped reads with at least one insertion	0.52%
Deletions	18,516
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.5%

2.6. Chromosome stats

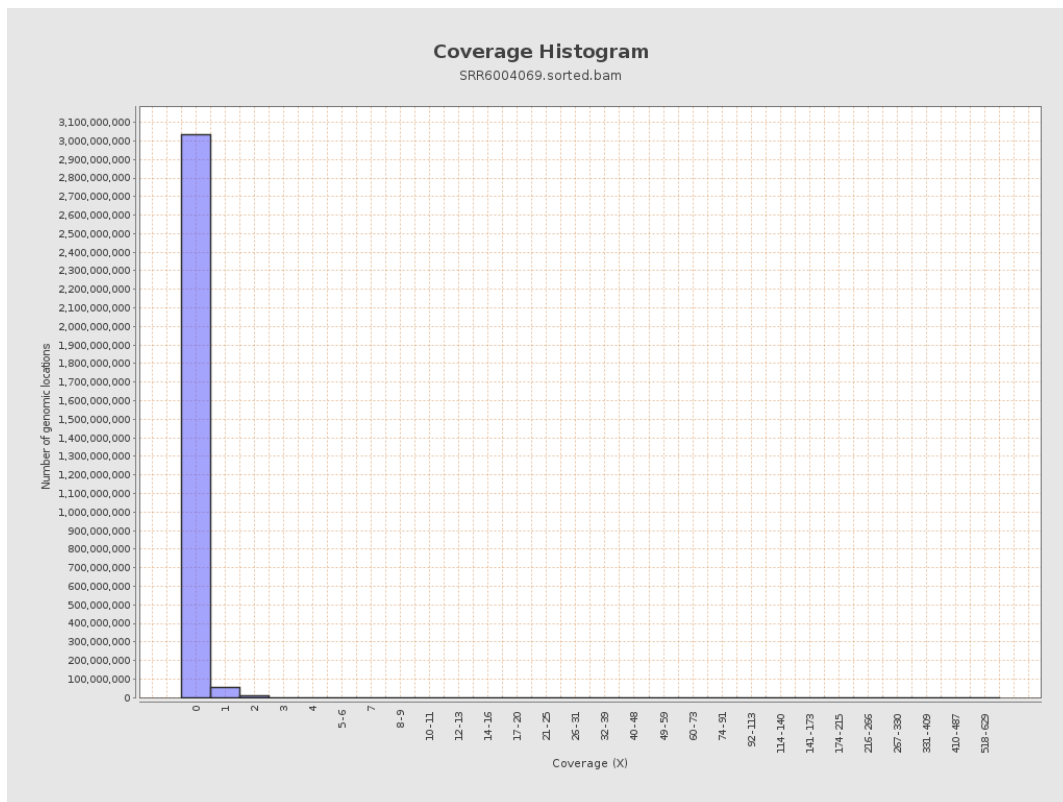
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5237627	0.021	0.4167
chr2	243199373	5903655	0.0243	0.2345
chr3	198022430	5659112	0.0286	0.1902
chr4	191154276	5032486	0.0263	0.1917
chr5	180915260	5206644	0.0288	0.1924
chr6	171115067	4477653	0.0262	0.1934
chr7	159138663	4314315	0.0271	0.3106

chr8	146364022	4988221	0.0341	0.4337
chr9	141213431	2856145	0.0202	0.2142
chr10	135534747	3518082	0.026	0.2332
chr11	135006516	2874790	0.0213	0.1881
chr12	133851895	3273740	0.0245	0.1782
chr13	115169878	2600530	0.0226	0.1709
chr14	107349540	2102204	0.0196	0.1657
chr15	102531392	2438055	0.0238	0.1734
chr16	90354753	1884805	0.0209	0.1724
chr17	81195210	1447277	0.0178	0.1539
chr18	78077248	2136874	0.0274	0.3569
chr19	59128983	1029951	0.0174	0.2566
chr20	63025520	1592682	0.0253	0.1824
chr21	48129895	971822	0.0202	0.1681
chr22	51304566	575049	0.0112	0.1174
chrMT	16571	4294	0.2591	0.5317
chrX	155270560	4694759	0.0302	0.2061
chrY	59373566	186925	0.0031	0.087

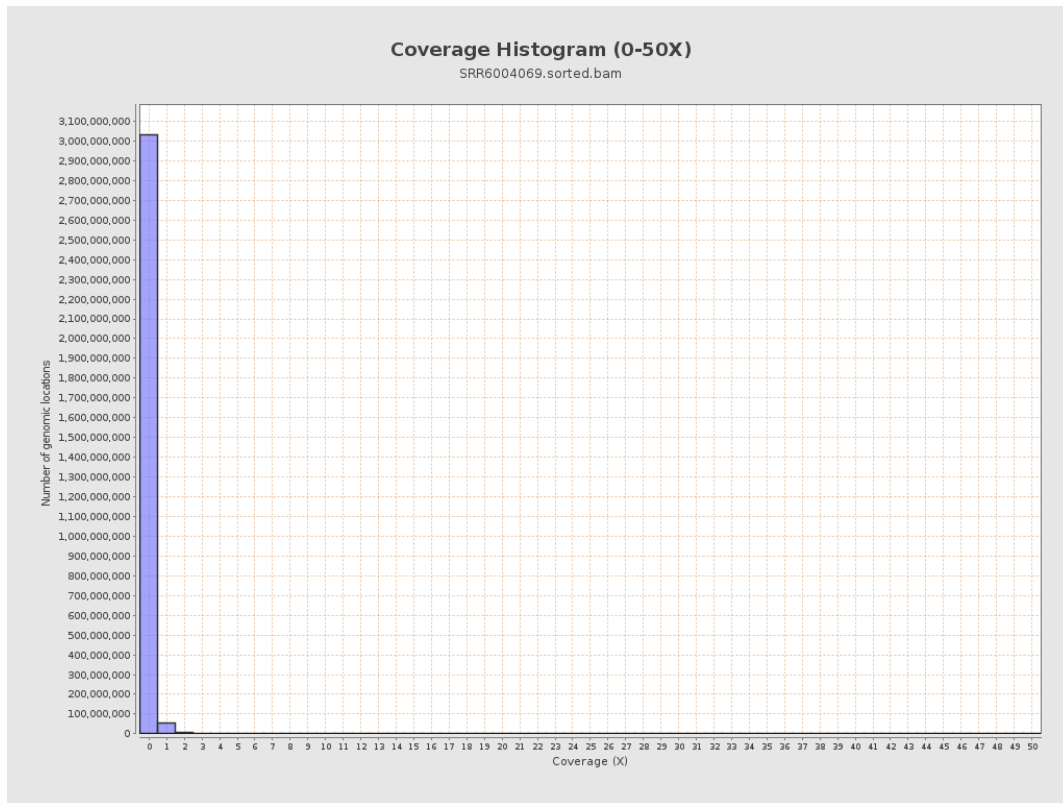
3. Results : Coverage across reference



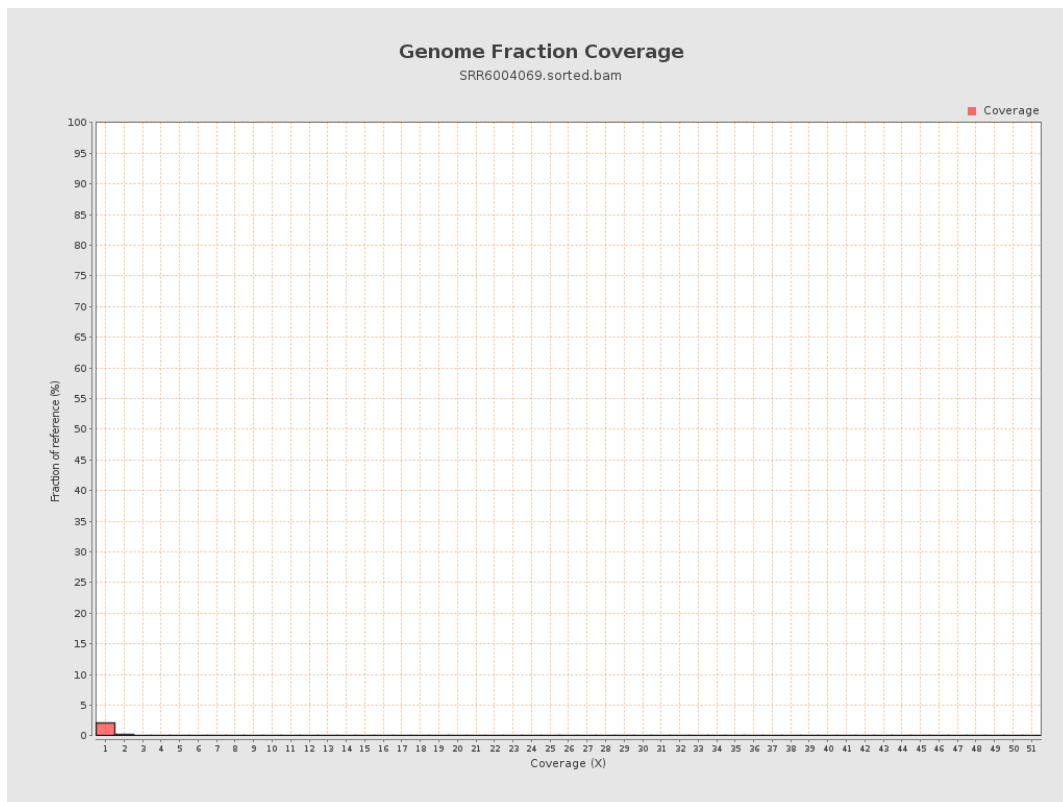
4. Results : Coverage Histogram



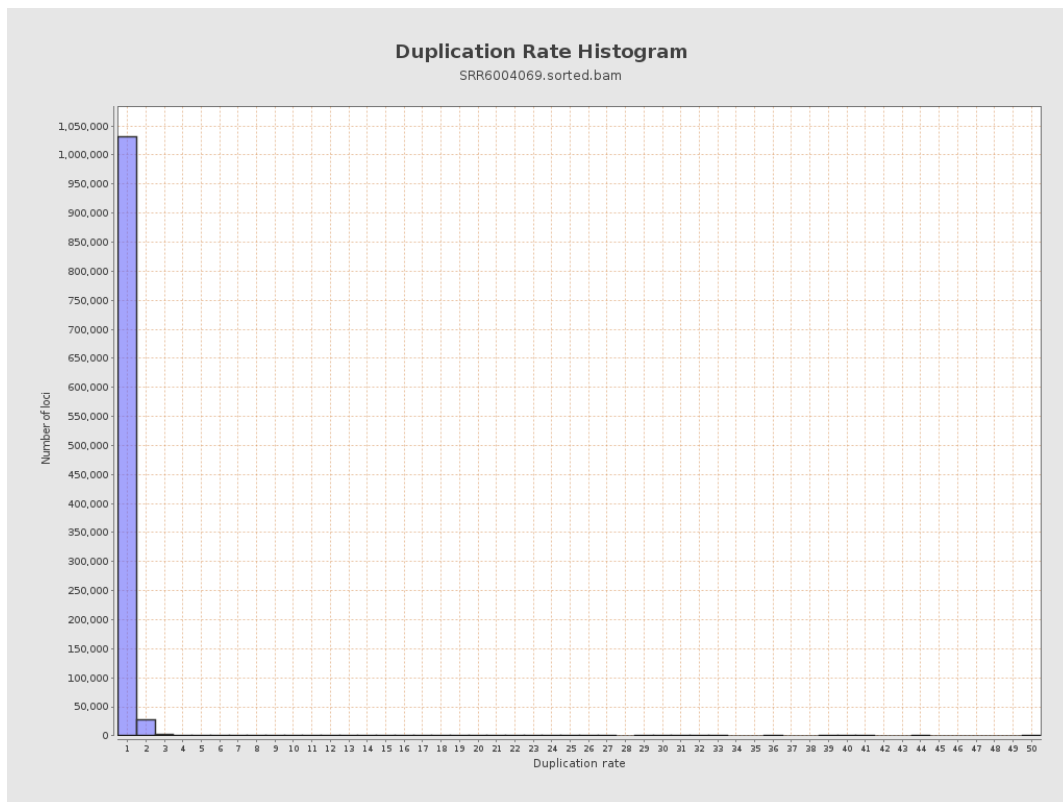
5. Results : Coverage Histogram (0-50X)



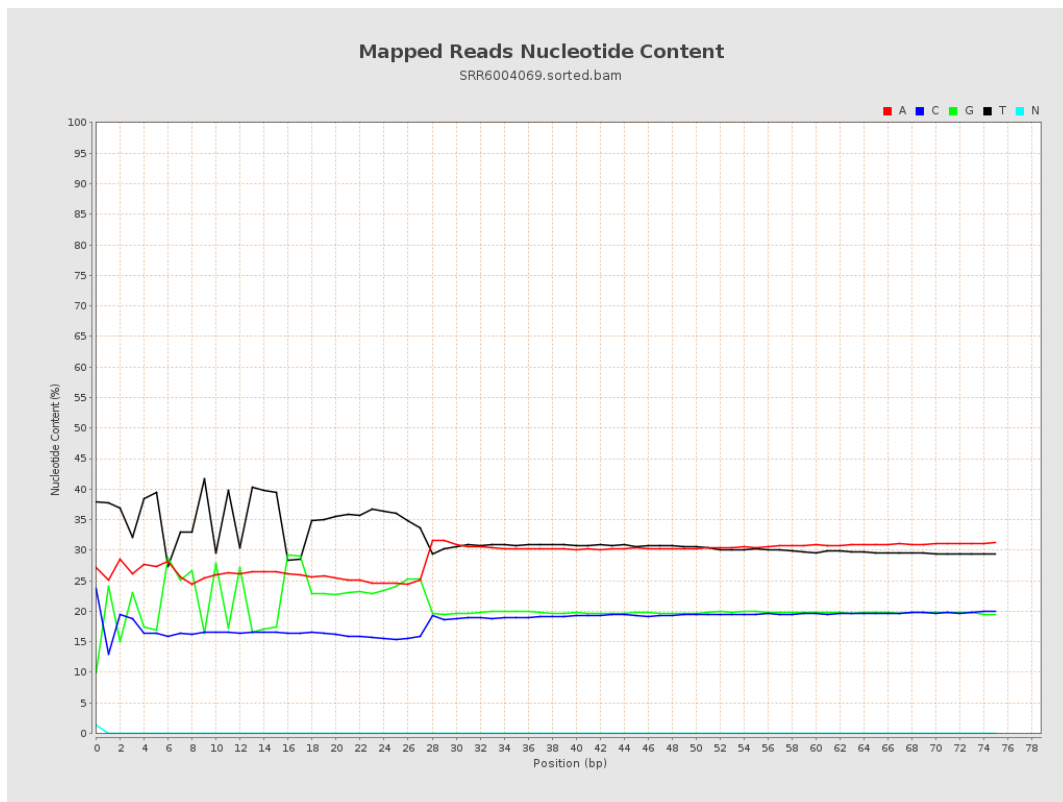
6. Results : Genome Fraction Coverage



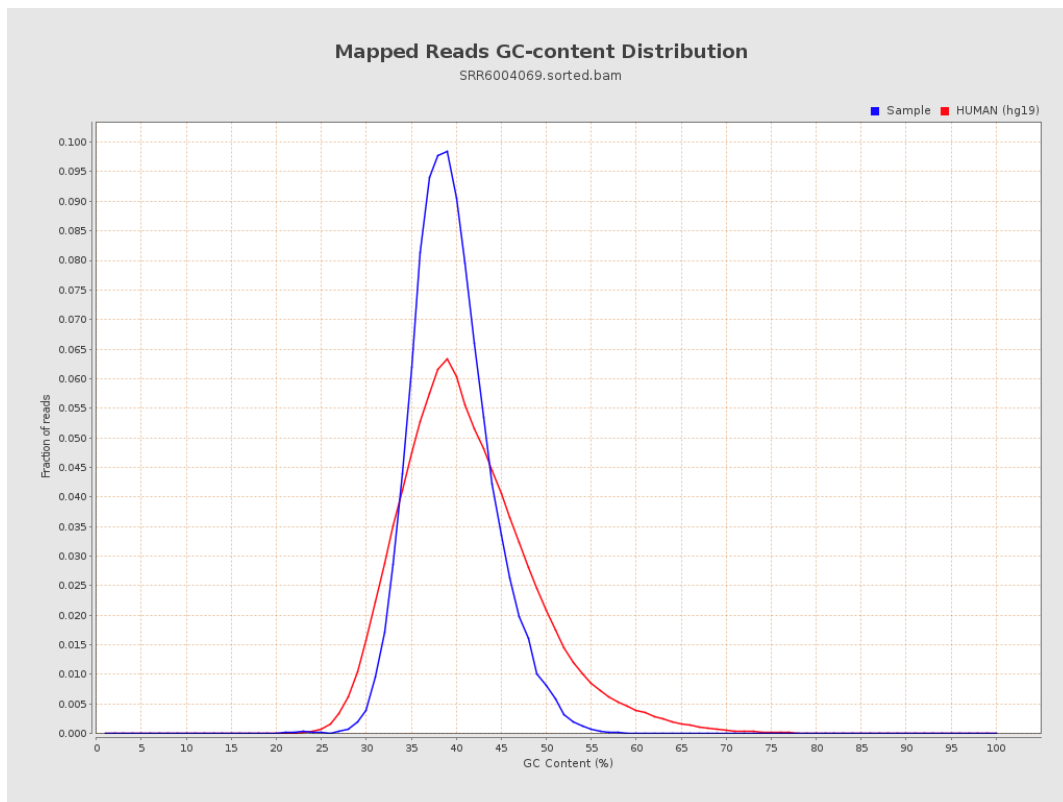
7. Results : Duplication Rate Histogram



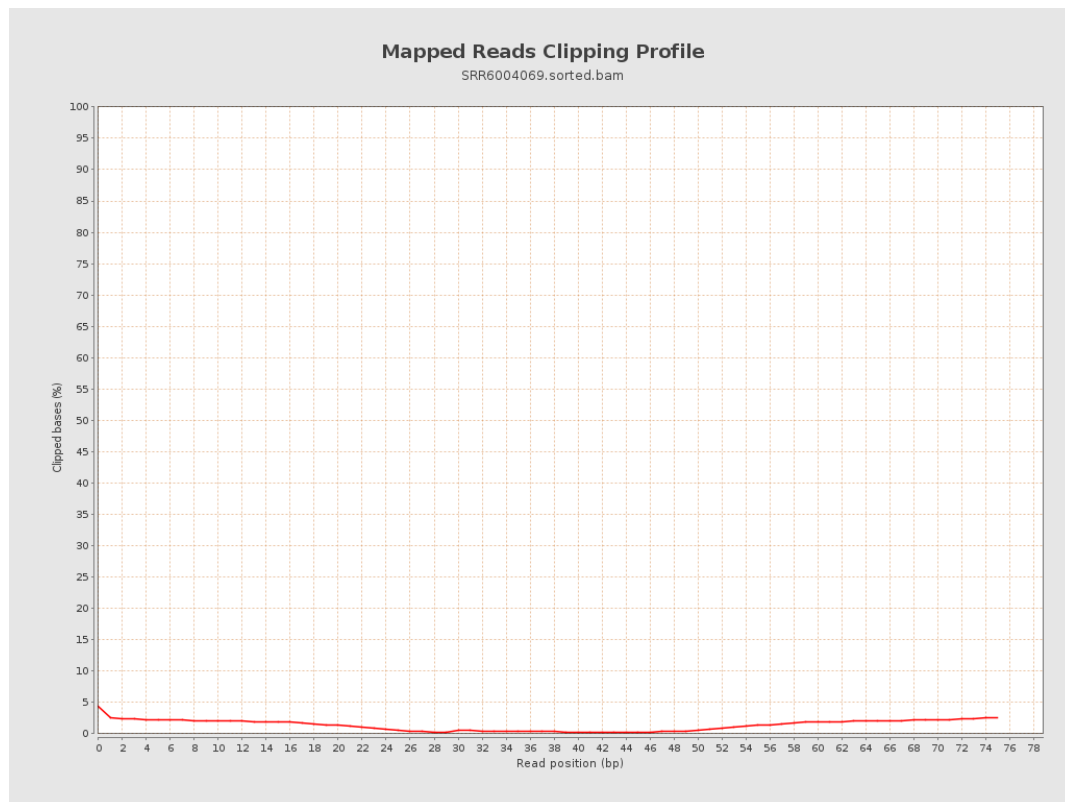
8. Results : Mapped Reads Nucleotide Content



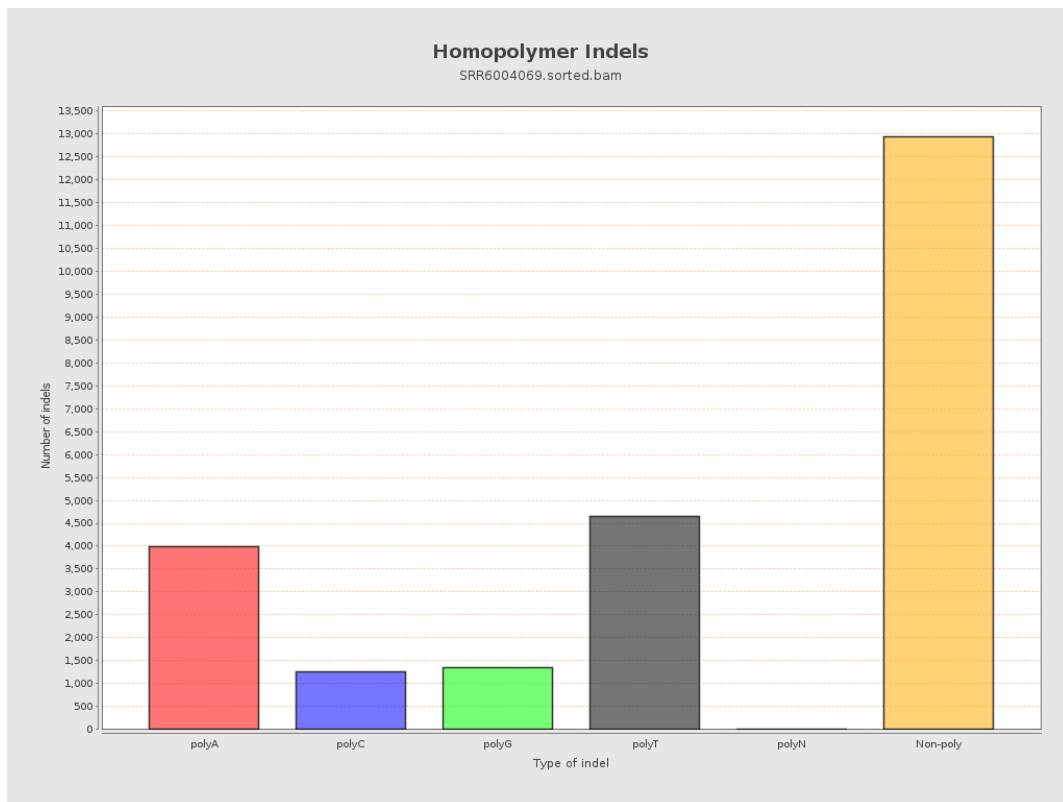
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

