

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008691.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_SRR6008691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:12:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,406,900
Mapped reads	1,054,179 / 74.93%
Unmapped reads	352,721 / 25.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,704 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	27,710 / 1.97%
Duplication rate	1.94%
Clipped reads	515,669 / 36.65%

2.2. ACGT Content

Number/percentage of A's	20,702,346 / 29.91%
Number/percentage of C's	12,306,193 / 17.78%
Number/percentage of T's	21,177,408 / 30.6%
Number/percentage of G's	15,014,243 / 21.69%
Number/percentage of N's	12,725 / 0.02%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2294
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.11
----------------------	-------

2.5. Mismatches and indels

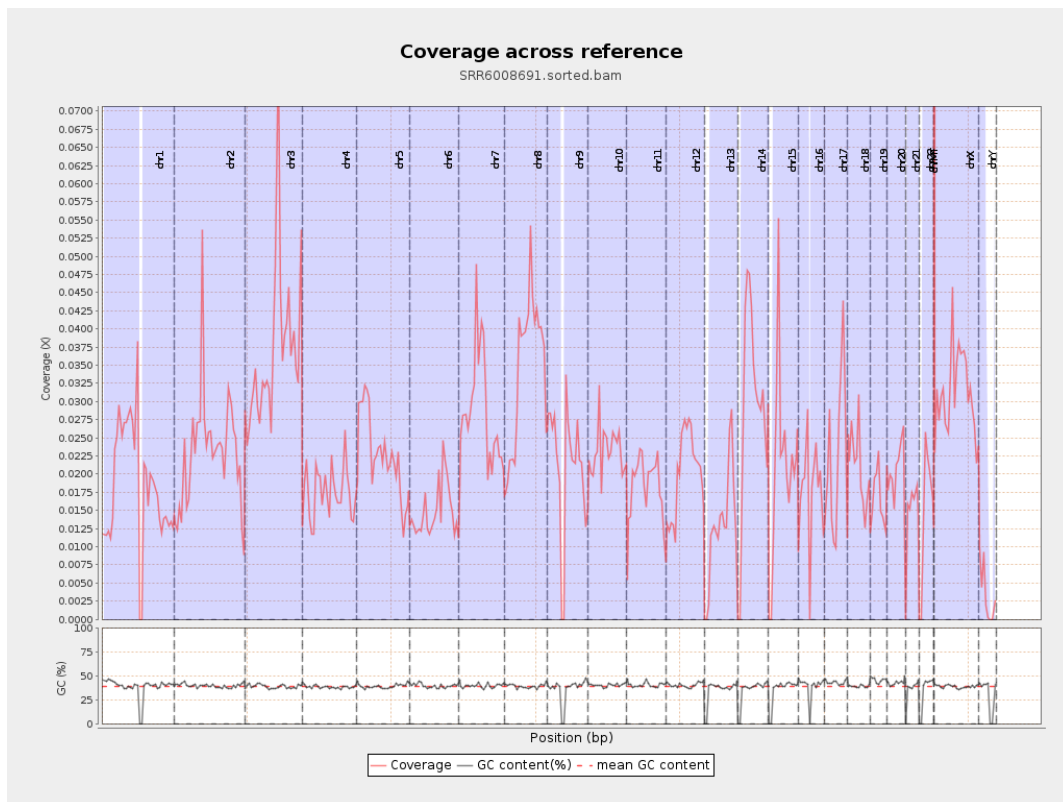
General error rate	0.93%
Mismatches	634,081
Insertions	6,088
Mapped reads with at least one insertion	0.57%
Deletions	20,252
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.16%

2.6. Chromosome stats

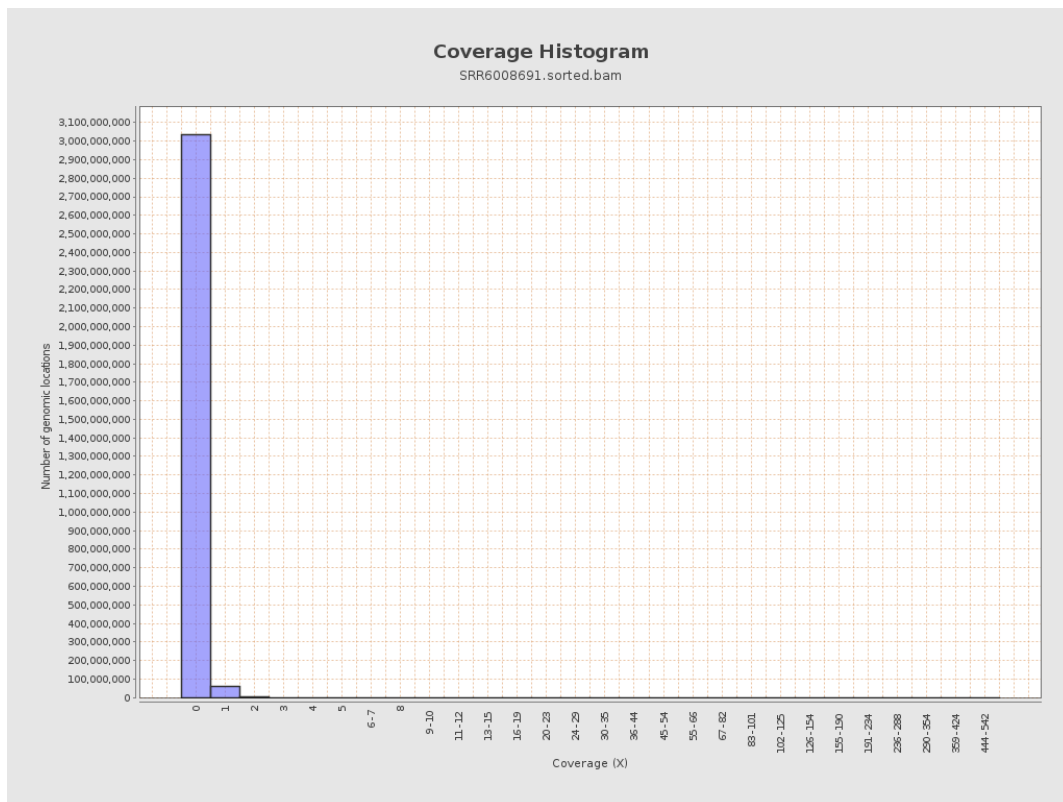
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4583008	0.0184	0.308
chr2	243199373	5613507	0.0231	0.2616
chr3	198022430	7284724	0.0368	0.2044
chr4	191154276	3352292	0.0175	0.1451
chr5	180915260	4144493	0.0229	0.1609
chr6	171115067	2563058	0.015	0.1352
chr7	159138663	4506871	0.0283	0.3309

chr8	146364022	5072549	0.0347	0.3881
chr9	141213431	2999930	0.0212	0.2303
chr10	135534747	3142310	0.0232	0.2001
chr11	135006516	2501018	0.0185	0.2098
chr12	133851895	2692217	0.0201	0.1538
chr13	115169878	1479707	0.0128	0.1209
chr14	107349540	3156134	0.0294	0.1952
chr15	102531392	2167502	0.0211	0.1552
chr16	90354753	1585408	0.0175	0.1608
chr17	81195210	1852038	0.0228	0.1902
chr18	78077248	1635958	0.021	0.4159
chr19	59128983	996510	0.0169	0.2364
chr20	63025520	1293300	0.0205	0.1544
chr21	48129895	719565	0.015	0.1372
chr22	51304566	785990	0.0153	0.1309
chrMT	16571	50209	3.0299	2.5466
chrX	155270560	4872096	0.0314	0.2074
chrY	59373566	195157	0.0033	0.0768

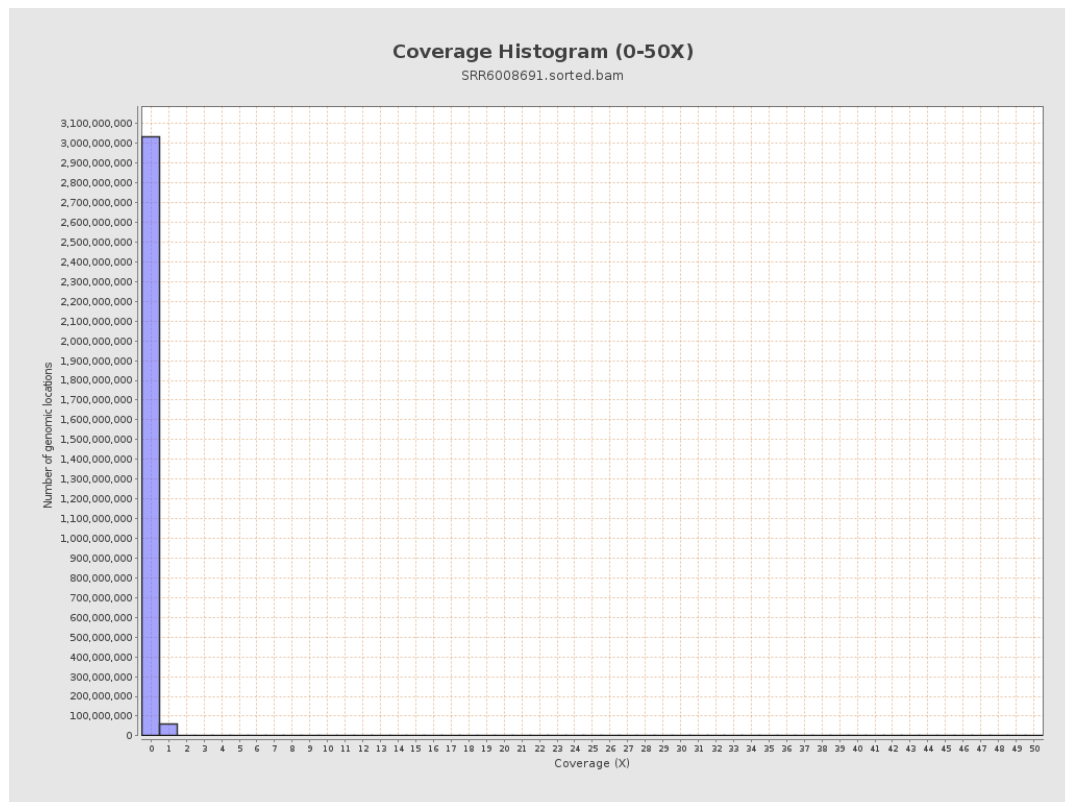
3. Results : Coverage across reference



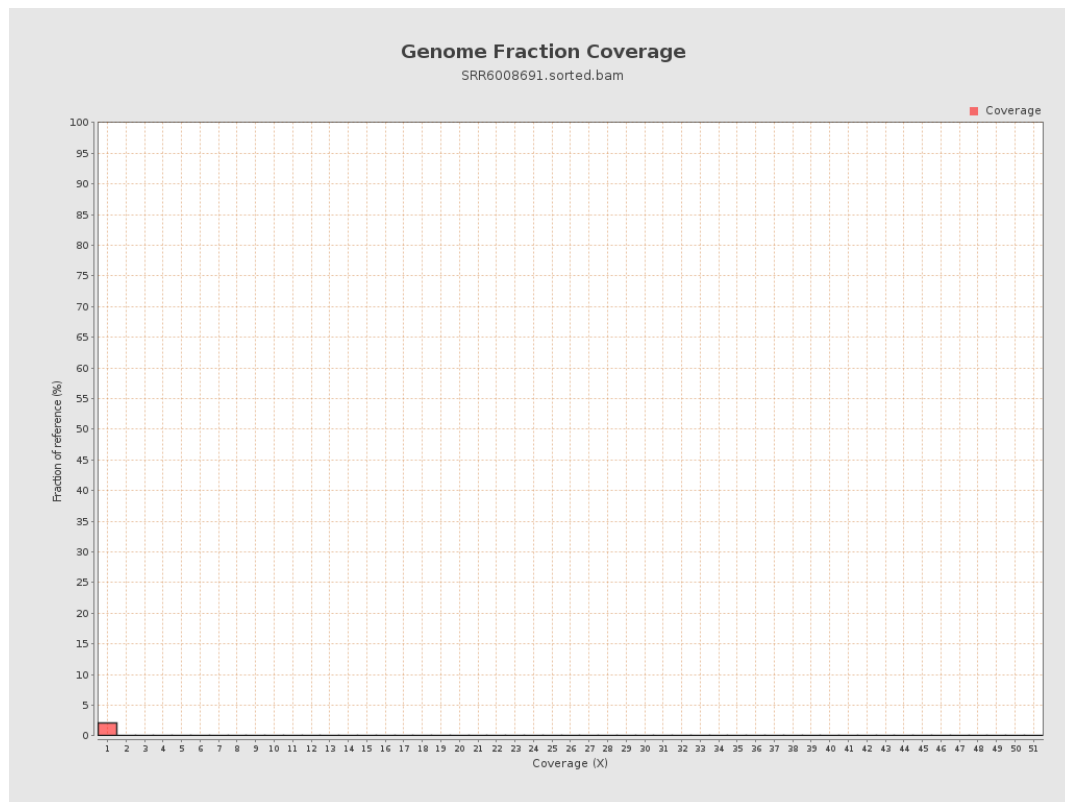
4. Results : Coverage Histogram



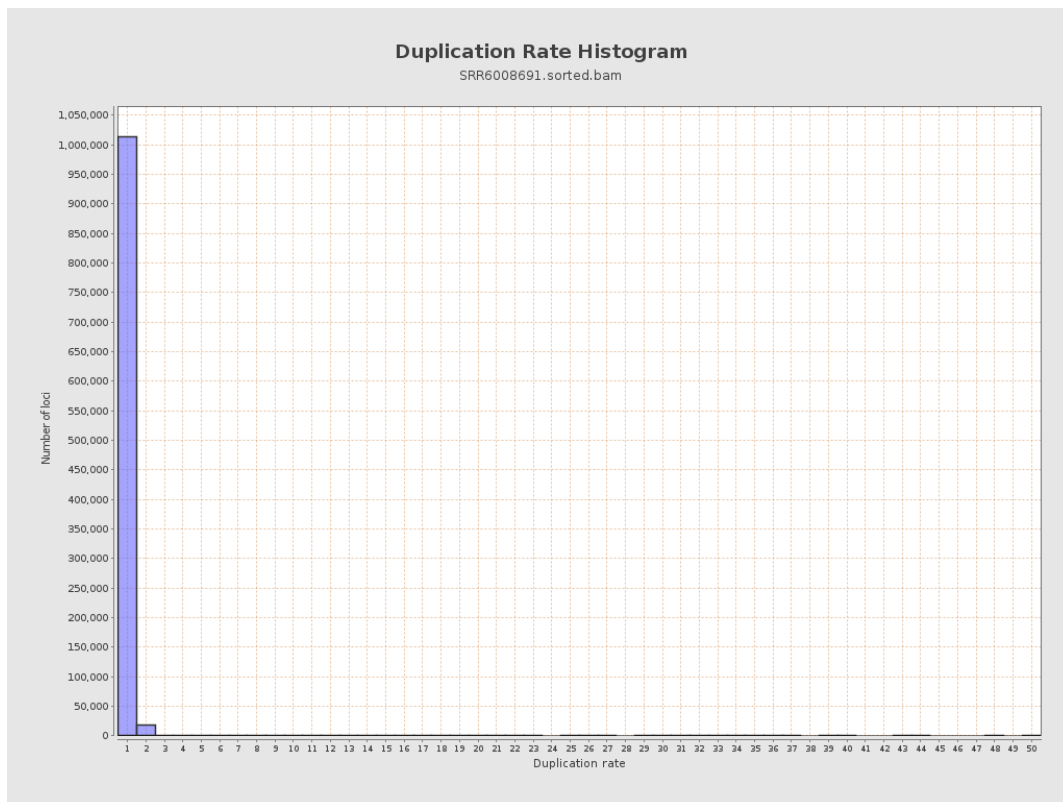
5. Results : Coverage Histogram (0-50X)



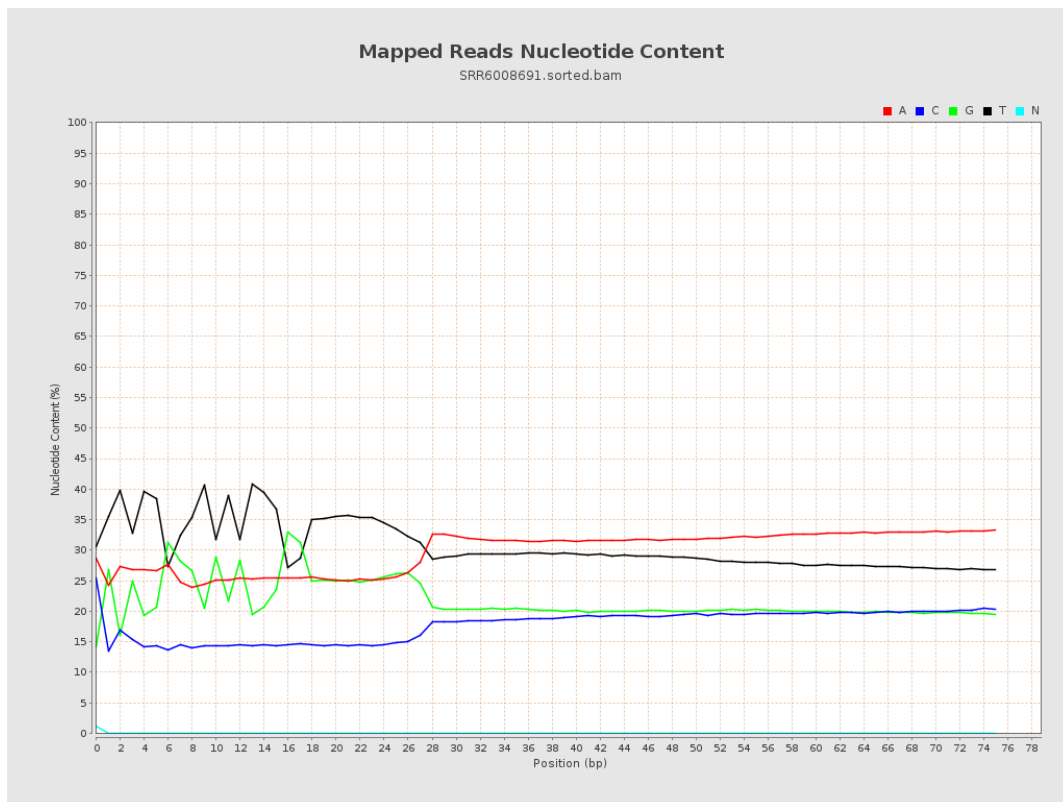
6. Results : Genome Fraction Coverage



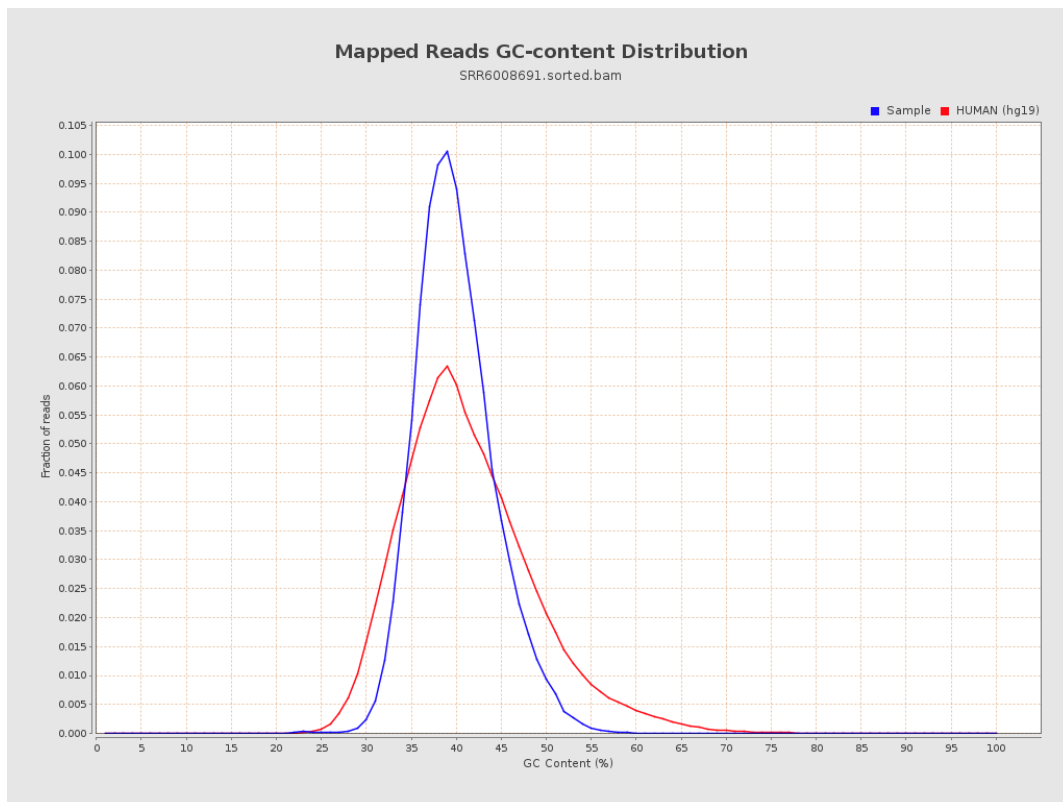
7. Results : Duplication Rate Histogram



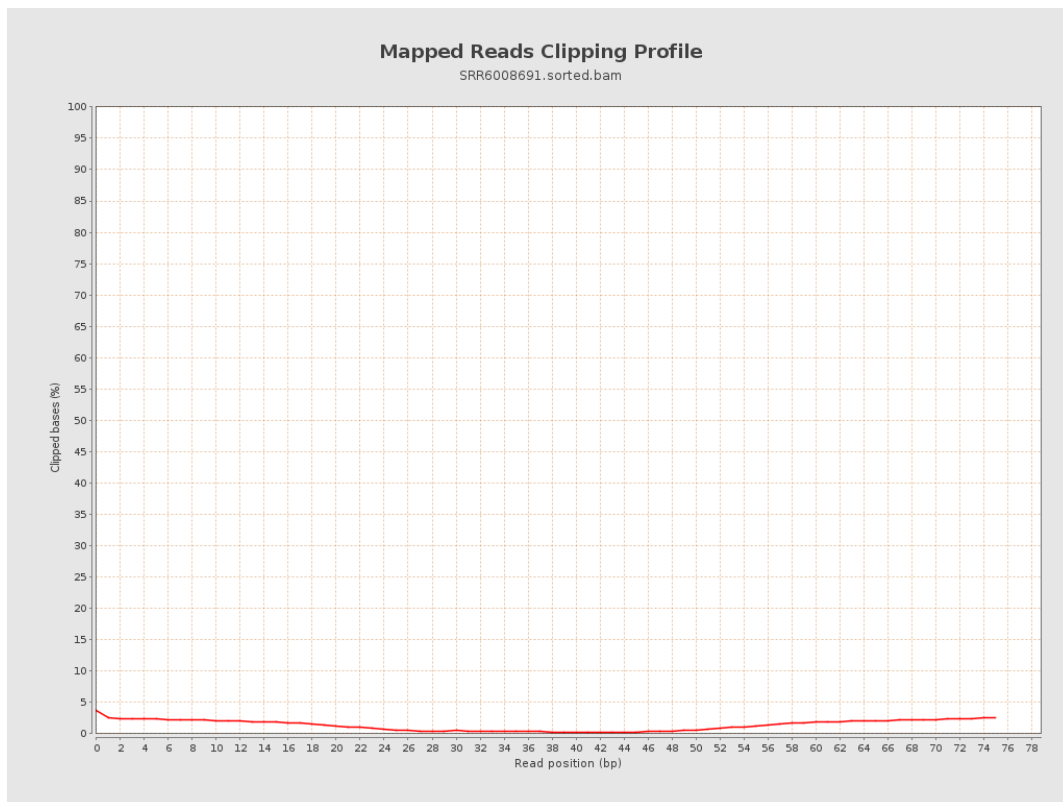
8. Results : Mapped Reads Nucleotide Content



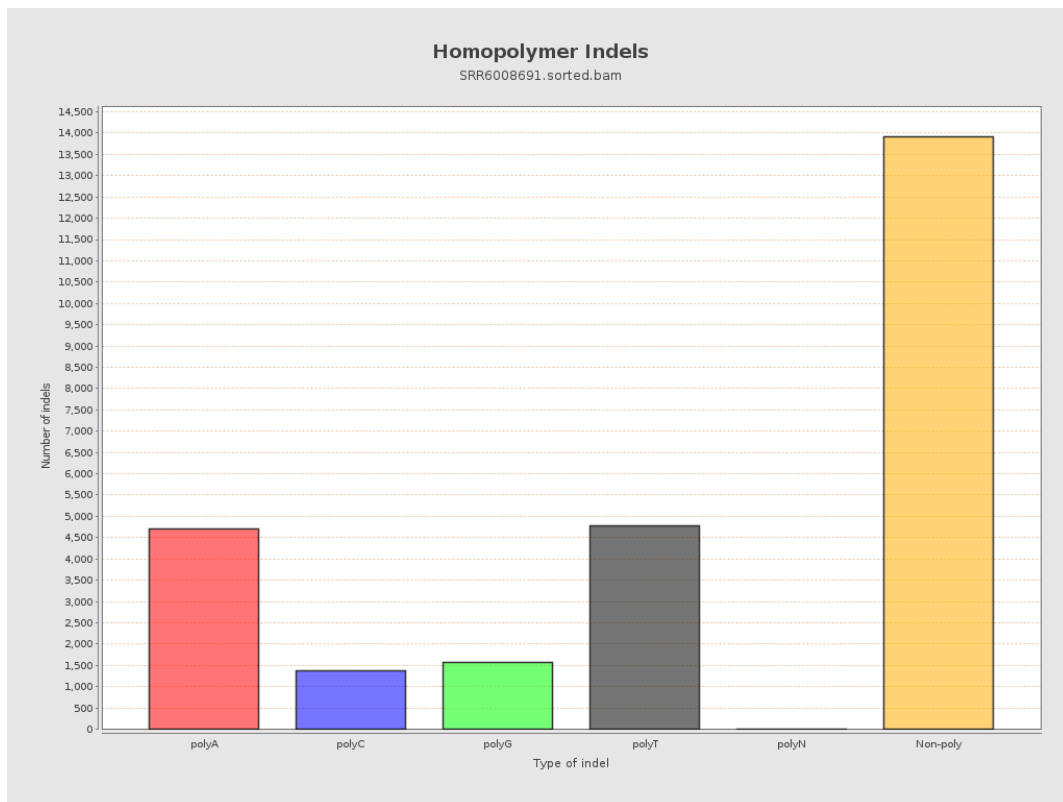
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

