

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:09:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008690.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_SRR6008690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008690.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:09:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008690.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,431,359
Mapped reads	981,258 / 68.55%
Unmapped reads	450,101 / 31.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,071 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	52,988 / 3.7%
Duplication rate	4.48%
Clipped reads	647,456 / 45.23%

2.2. ACGT Content

Number/percentage of A's	16,267,123 / 27.1%
Number/percentage of C's	10,924,965 / 18.2%
Number/percentage of T's	18,668,174 / 31.1%
Number/percentage of G's	14,152,951 / 23.58%
Number/percentage of N's	10,324 / 0.02%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.1991
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.27
----------------------	-------

2.5. Mismatches and indels

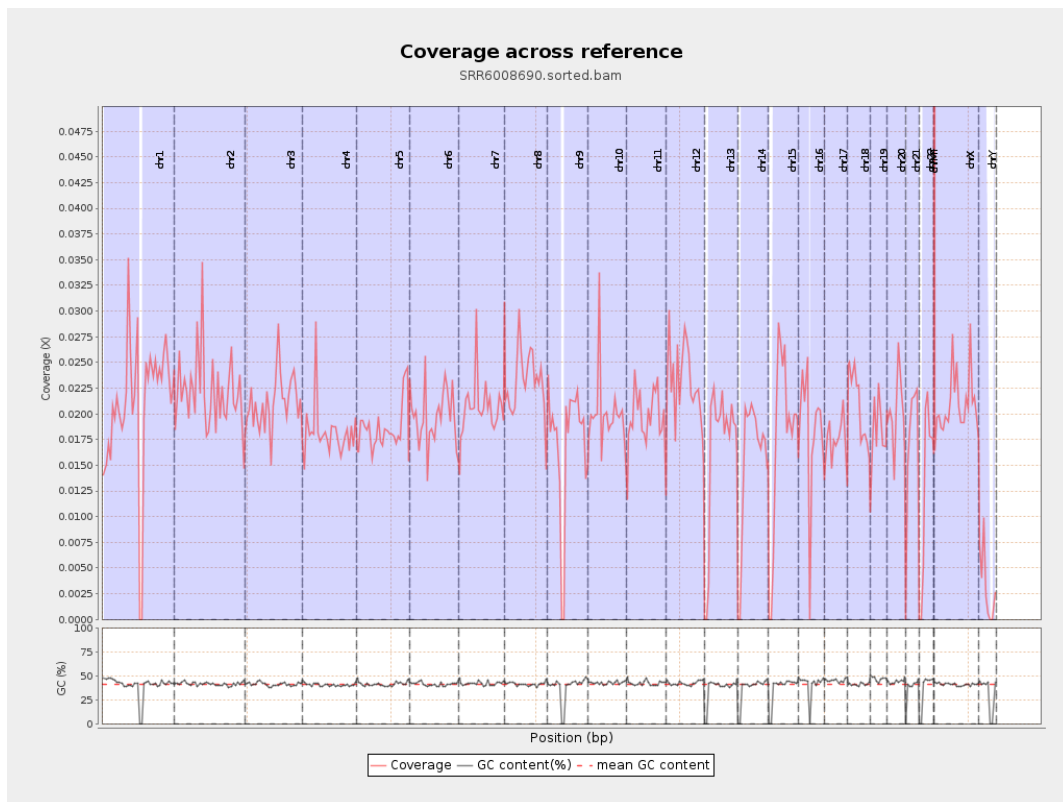
General error rate	1%
Mismatches	592,928
Insertions	5,233
Mapped reads with at least one insertion	0.53%
Deletions	23,392
Mapped reads with at least one deletion	2.35%
Homopolymer indels	48.35%

2.6. Chromosome stats

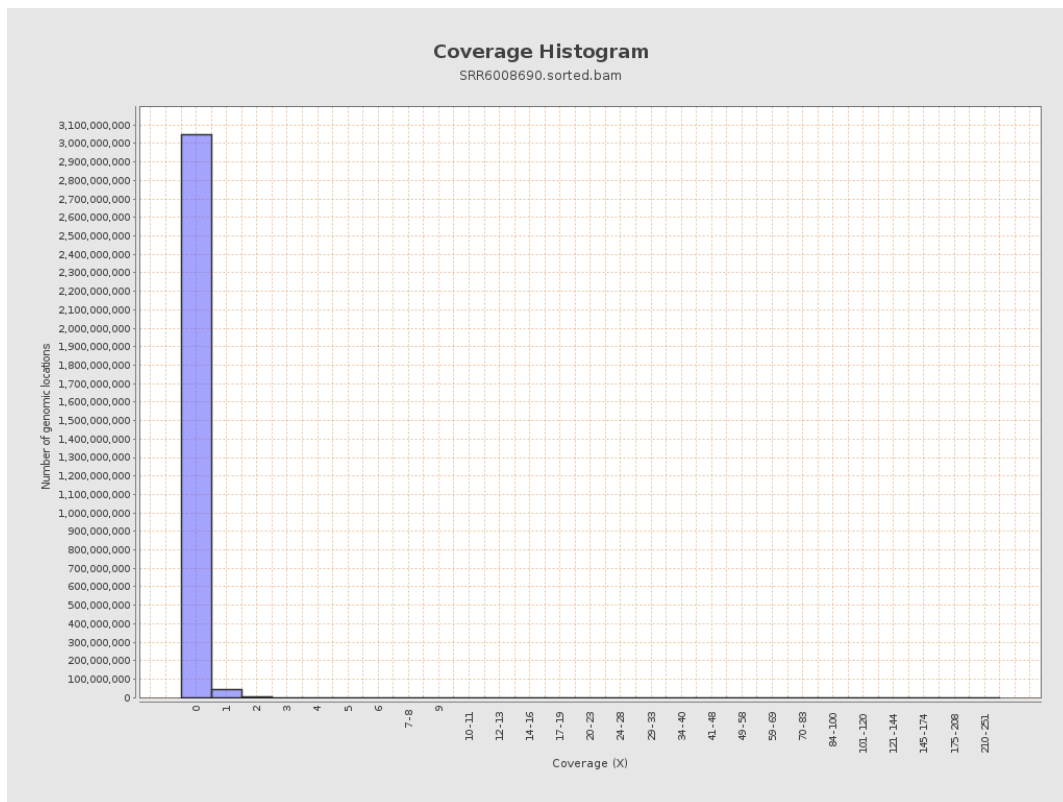
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5234952	0.021	0.258
chr2	243199373	5359975	0.022	0.2403
chr3	198022430	4171612	0.0211	0.173
chr4	191154276	3476481	0.0182	0.1639
chr5	180915260	3379832	0.0187	0.1617
chr6	171115067	3385265	0.0198	0.1816
chr7	159138663	3285353	0.0206	0.2552

chr8	146364022	3396207	0.0232	0.22
chr9	141213431	2423116	0.0172	0.19
chr10	135534747	2697733	0.0199	0.2057
chr11	135006516	2682783	0.0199	0.2012
chr12	133851895	3092050	0.0231	0.1823
chr13	115169878	1904555	0.0165	0.1559
chr14	107349540	1672444	0.0156	0.155
chr15	102531392	1834659	0.0179	0.1607
chr16	90354753	1645190	0.0182	0.1939
chr17	81195210	1418502	0.0175	0.167
chr18	78077248	1628684	0.0209	0.2863
chr19	59128983	1094613	0.0185	0.2085
chr20	63025520	1266860	0.0201	0.1702
chr21	48129895	838138	0.0174	0.162
chr22	51304566	678217	0.0132	0.1345
chrMT	16571	37165	2.2428	2.1291
chrX	155270560	3268460	0.0211	0.1827
chrY	59373566	188159	0.0032	0.0812

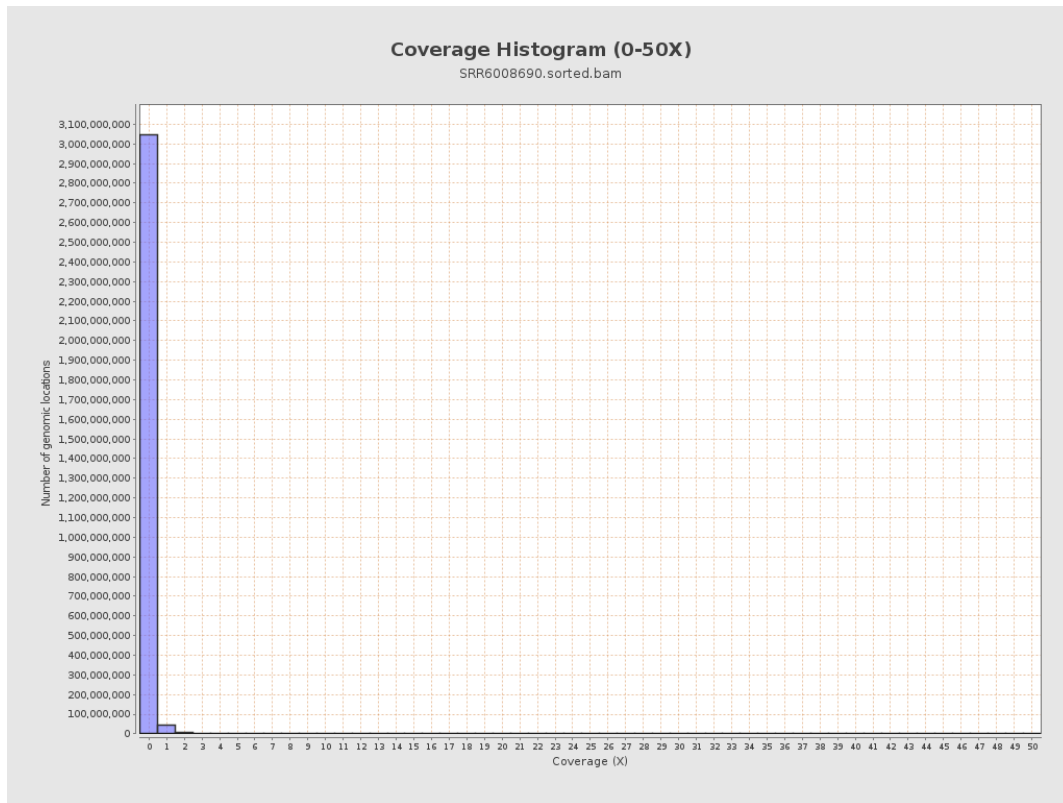
3. Results : Coverage across reference



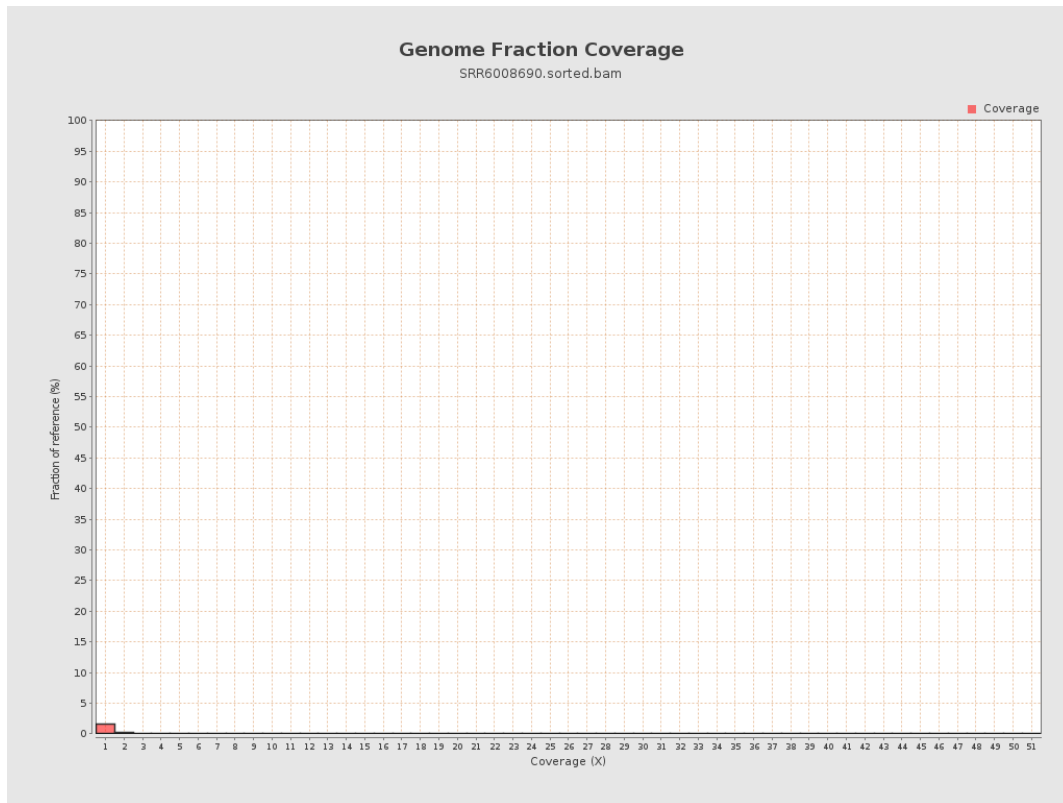
4. Results : Coverage Histogram



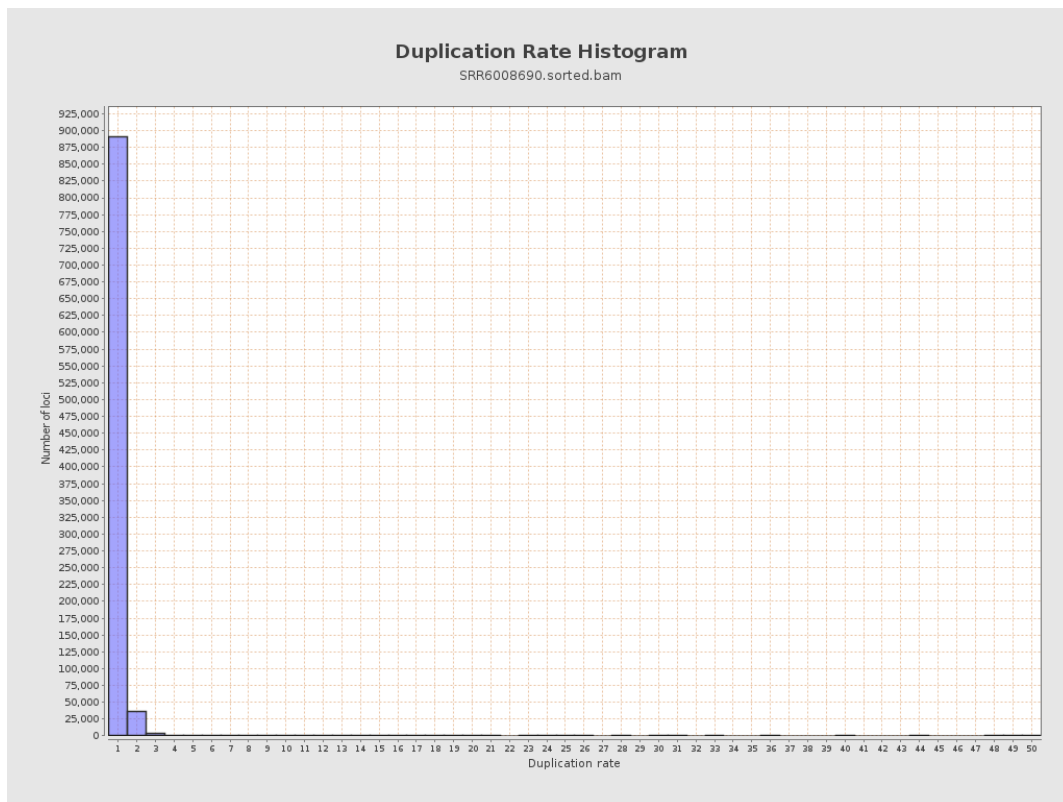
5. Results : Coverage Histogram (0-50X)



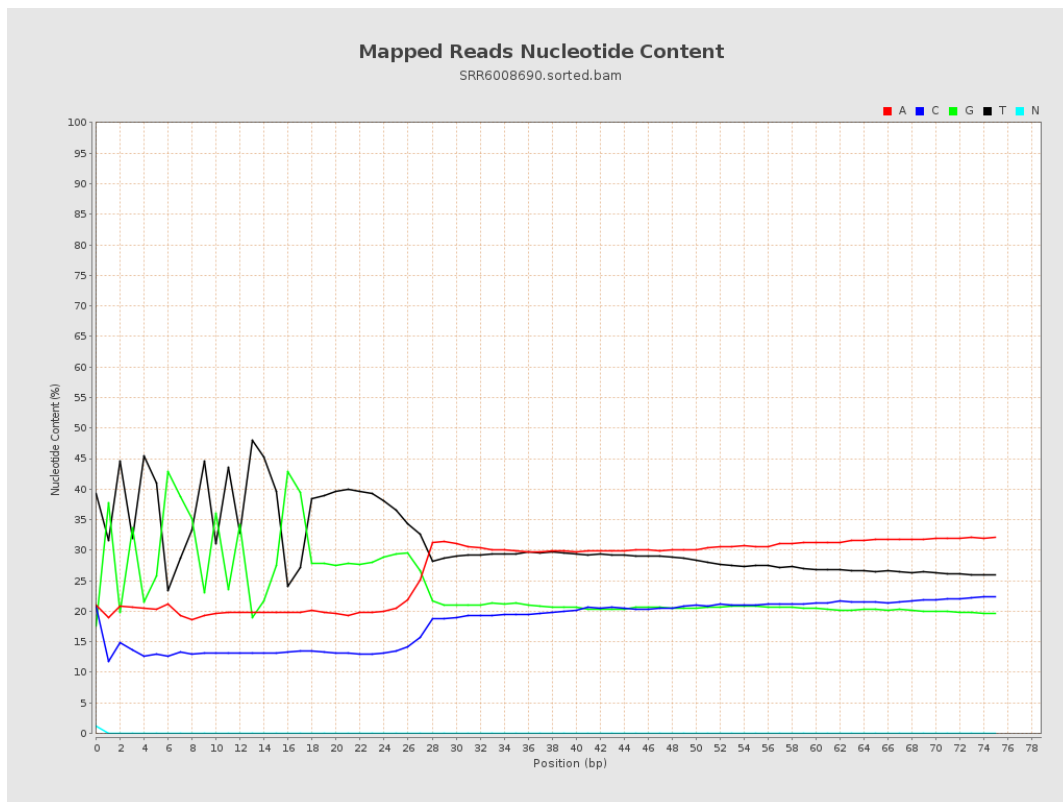
6. Results : Genome Fraction Coverage



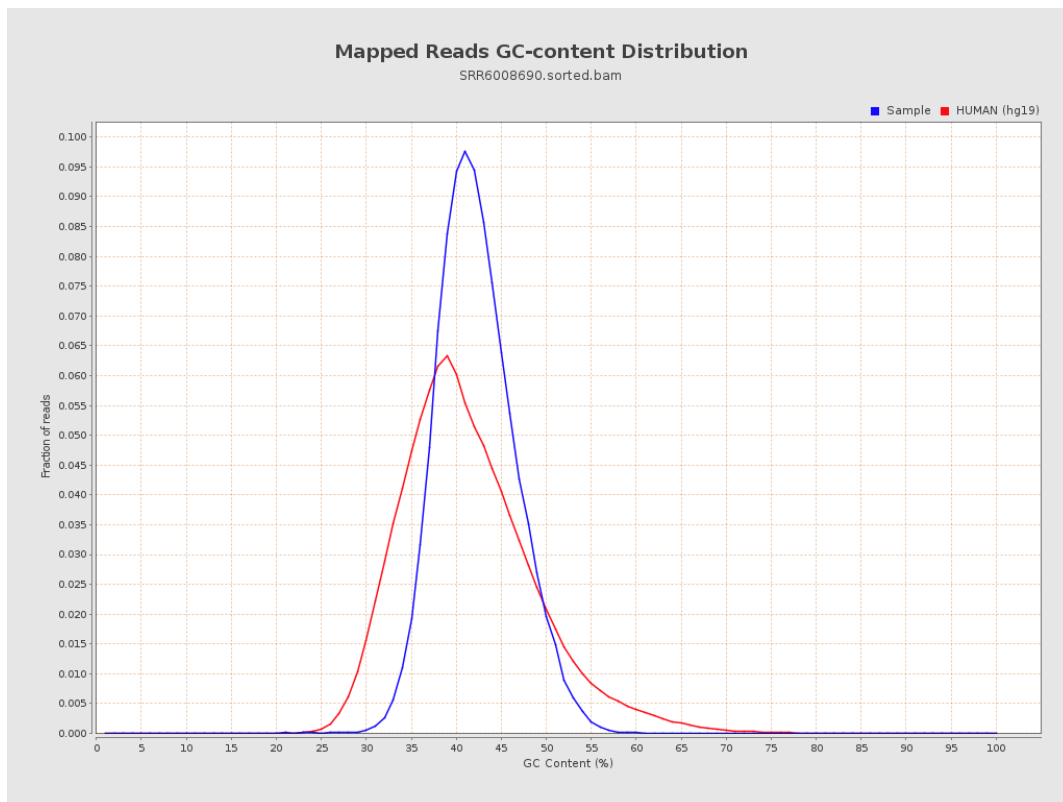
7. Results : Duplication Rate Histogram



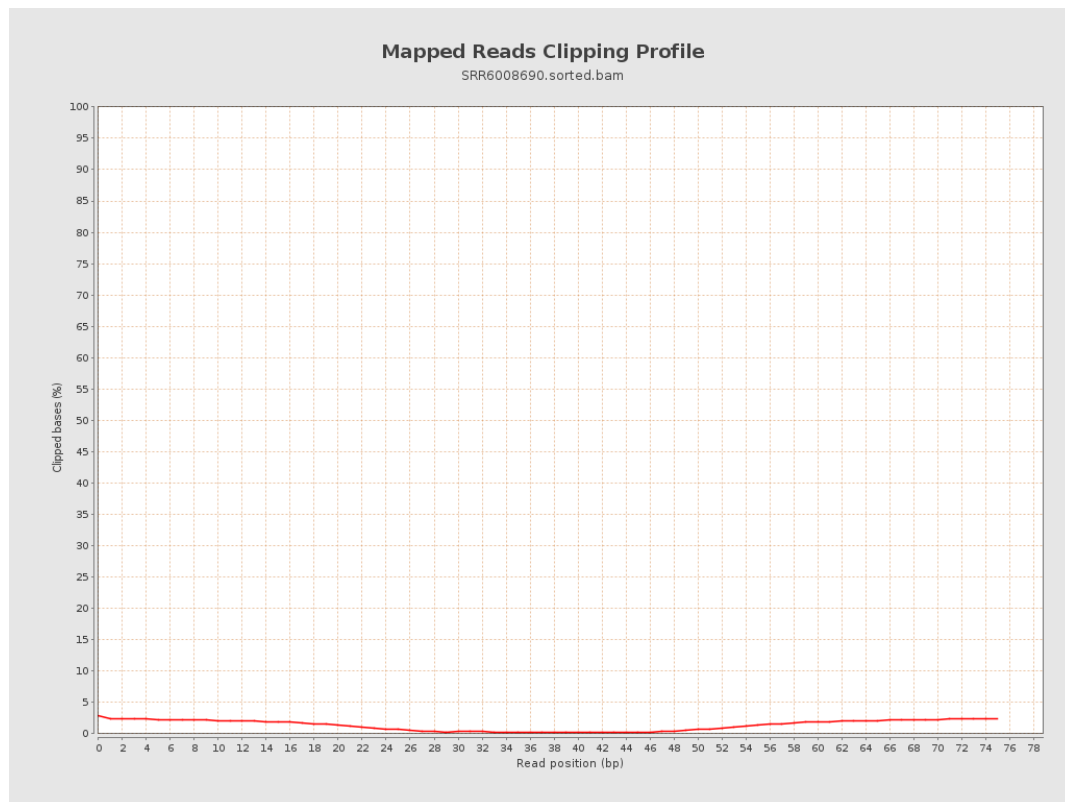
8. Results : Mapped Reads Nucleotide Content



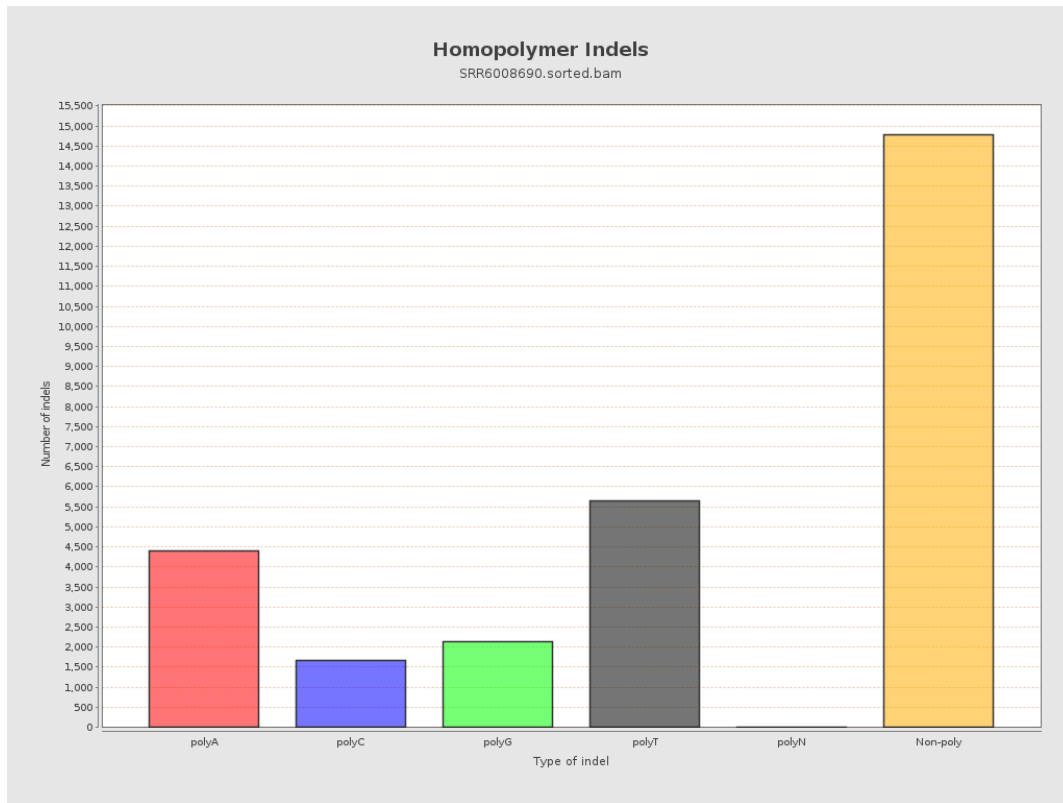
9. Results : Mapped Reads GC-content Distribution



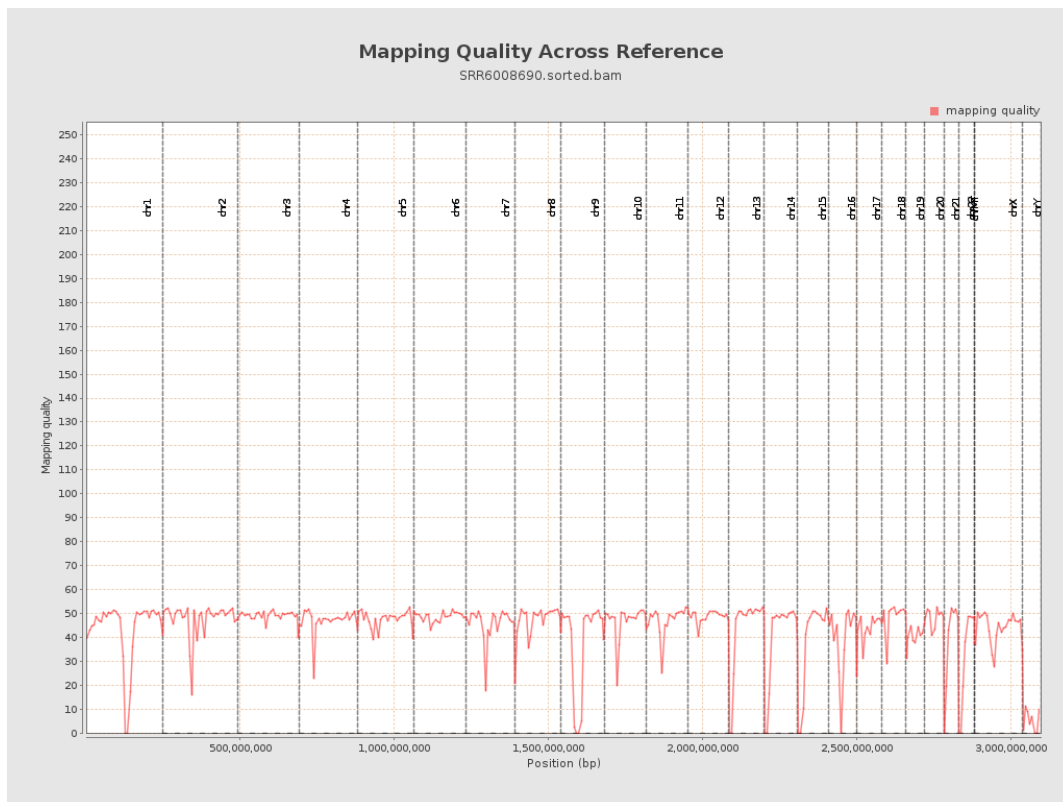
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

