Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:14:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008692.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_SRR6008692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008692.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,678,111
Mapped reads	1,150,859 / 68.58%
Unmapped reads	527,252 / 31.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,567 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	63,583 / 3.79%
Duplication rate	4.57%
Clipped reads	839,508 / 50.03%

2.2. ACGT Content

Number/percentage of A's	19,049,427 / 28.04%
Number/percentage of C's	11,809,222 / 17.38%
Number/percentage of T's	21,268,183 / 31.31%
Number/percentage of G's	15,779,817 / 23.23%
Number/percentage of N's	24,928 / 0.04%
GC Percentage	40.61%

2.3. Coverage

Mean	0.022

Standard Deviation	0.1977

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

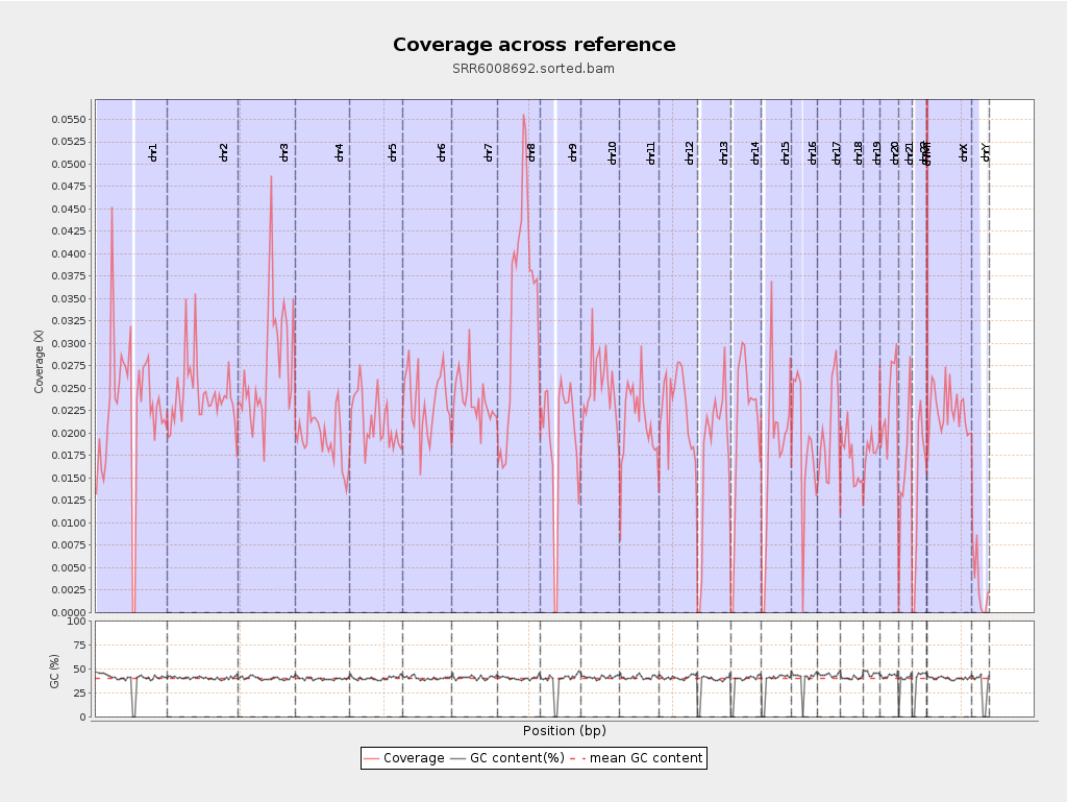
General error rate	1.03%
Mismatches	692,996
Insertions	5,464
Mapped reads with at least one insertion	0.47%
Deletions	28,330
Mapped reads with at least one deletion	2.43%
Homopolymer indels	48.34%

2.6. Chromosome stats

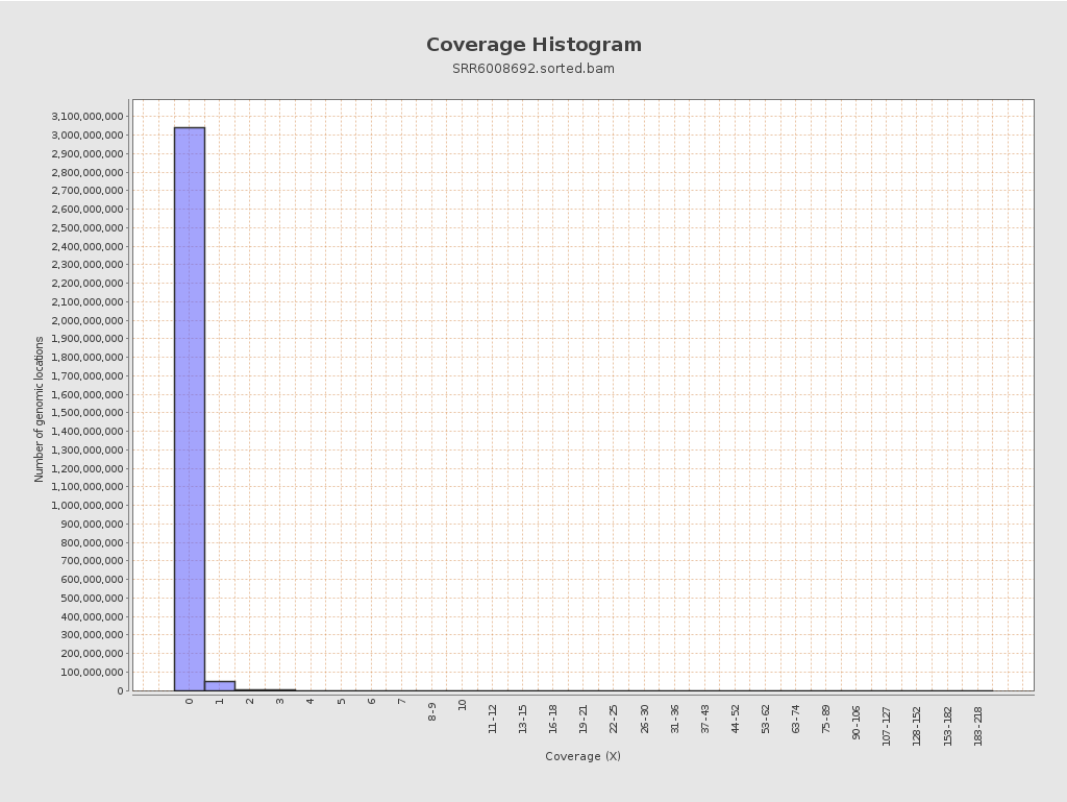
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5595883	0.0225	0.2399
chr2	243199373	5919304	0.0243	0.2317
chr3	198022430	5427333	0.0274	0.1978
chr4	191154276	3727465	0.0195	0.1678
chr5	180915260	3874407	0.0214	0.1739
chr6	171115067	4008234	0.0234	0.1936
chr7	159138663	3764230	0.0237	0.237

chr8	146364022	4989971	0.0341	0.2544
chr9	141213431	2734164	0.0194	0.1843
chr10	135534747	3375493	0.0249	0.2081
chr11	135006516	2893464	0.0214	0.1964
chr12	133851895	3062026	0.0229	0.181
chr13	115169878	2072027	0.018	0.1602
chr14	107349540	2239413	0.0209	0.1716
chr15	102531392	1852546	0.0181	0.1591
chr16	90354753	1673688	0.0185	0.1658
chr17	81195210	1650973	0.0203	0.1761
chr18	78077248	1332582	0.0171	0.226
chr19	59128983	1085148	0.0184	0.1866
chr20	63025520	1459684	0.0232	0.1834
chr21	48129895	795518	0.0165	0.1561
chr22	51304566	718586	0.014	0.1378
chrMT	16571	43175	2.6055	2.6477
chrX	155270560	3502608	0.0226	0.1847
chrY	59373566	177264	0.003	0.0746

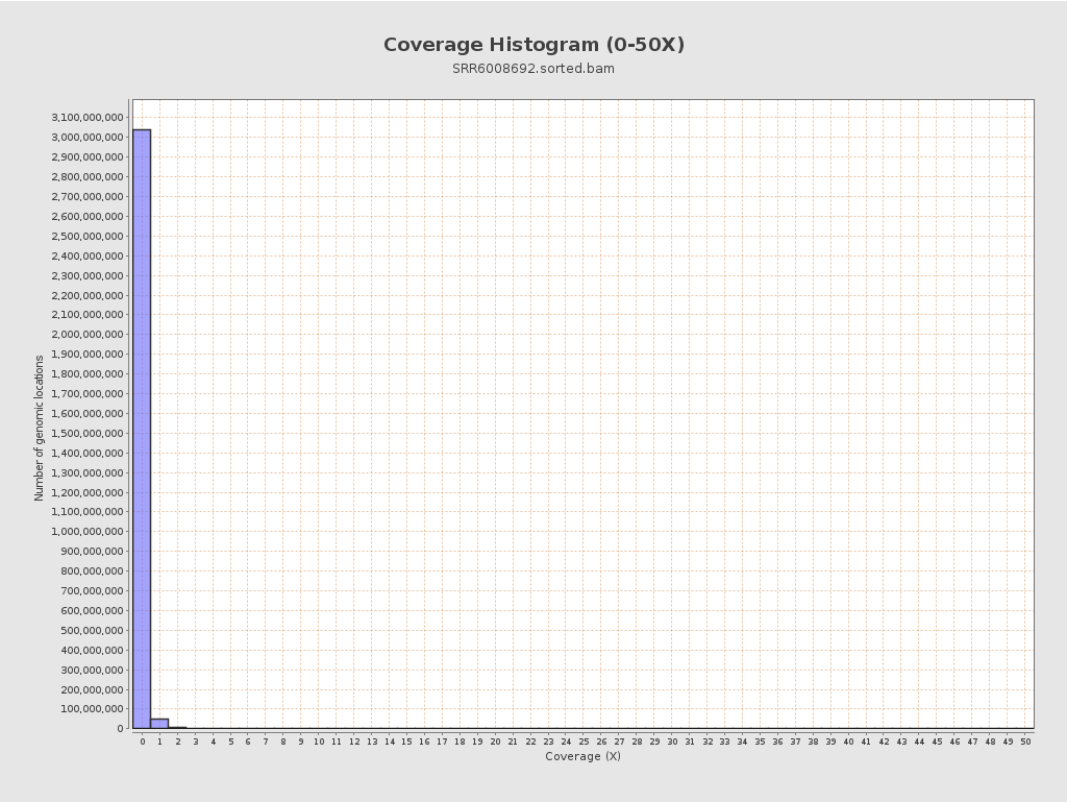
3. Results : Coverage across reference



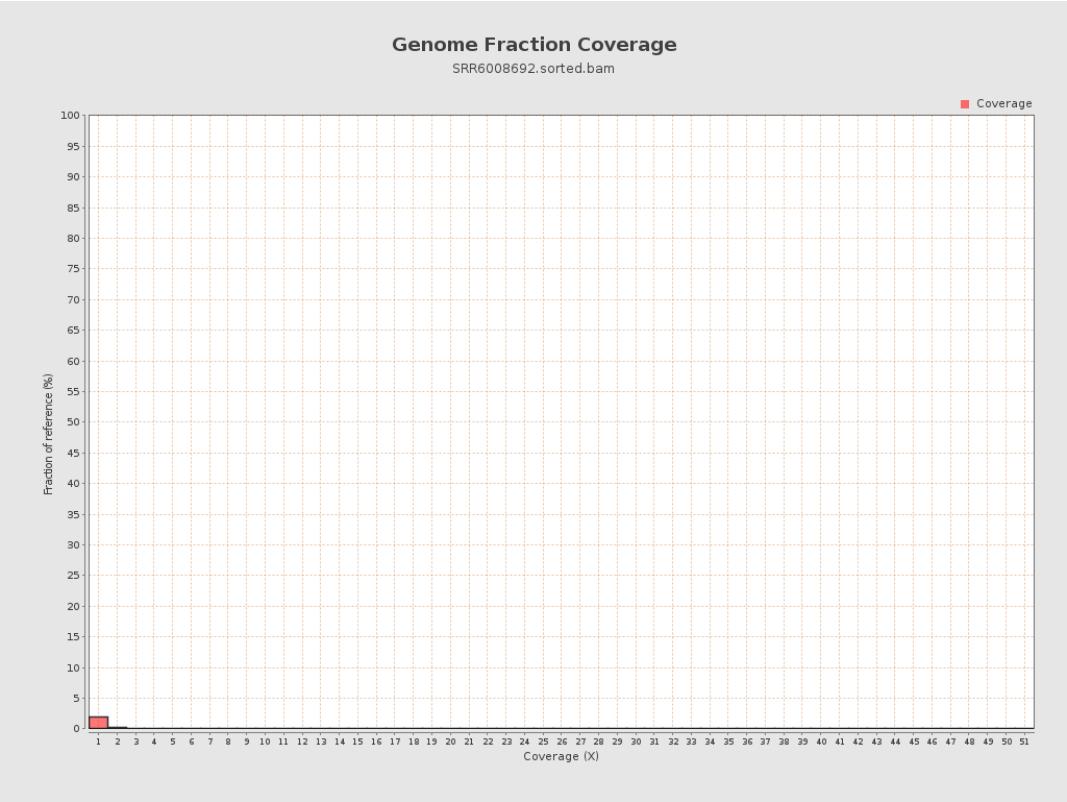
4. Results : Coverage Histogram



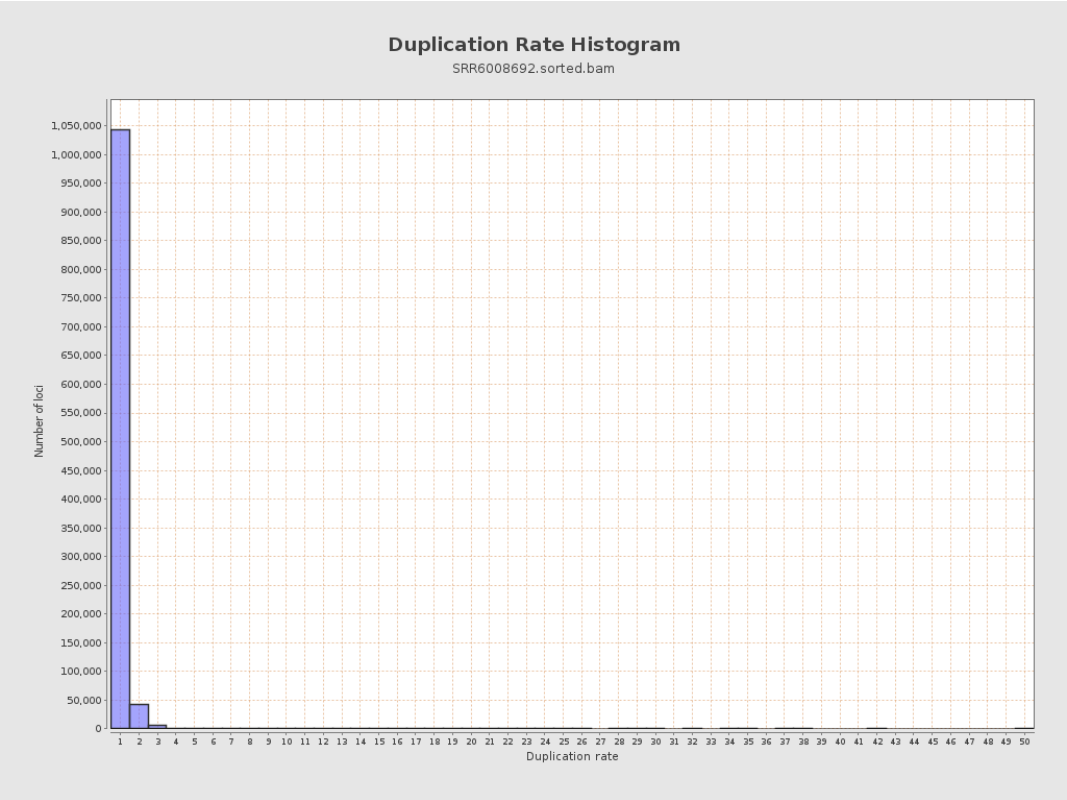
5. Results : Coverage Histogram (0-50X)



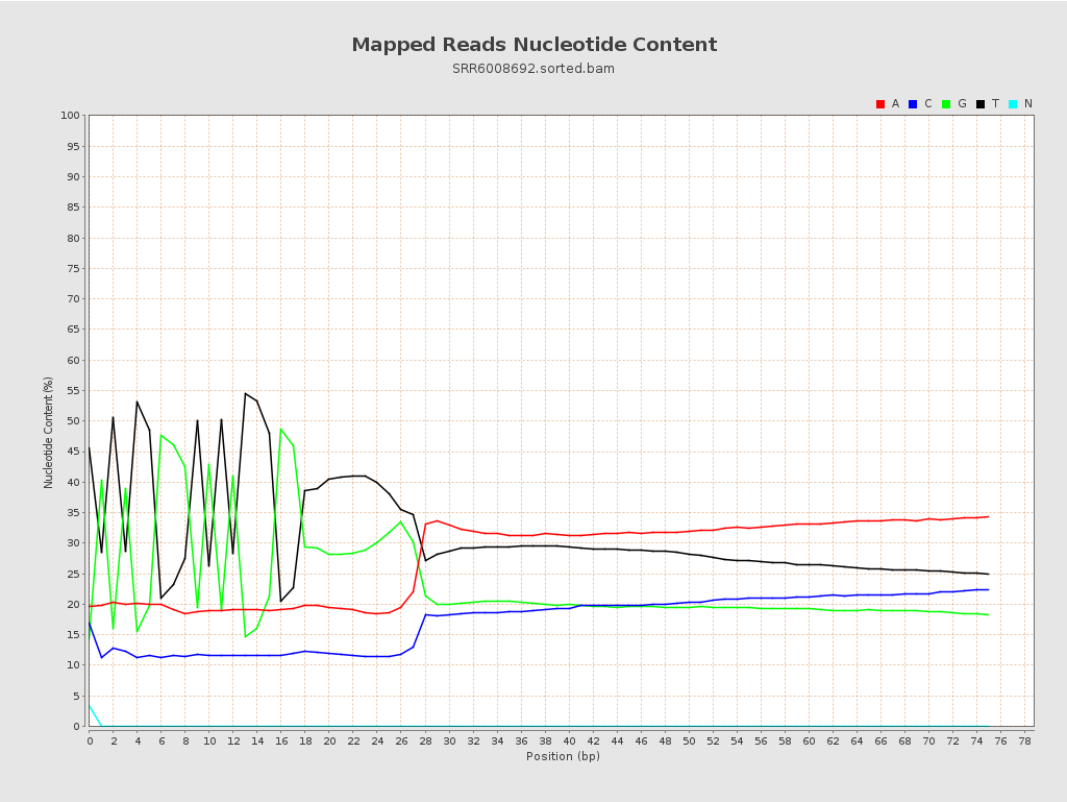
6. Results : Genome Fraction Coverage



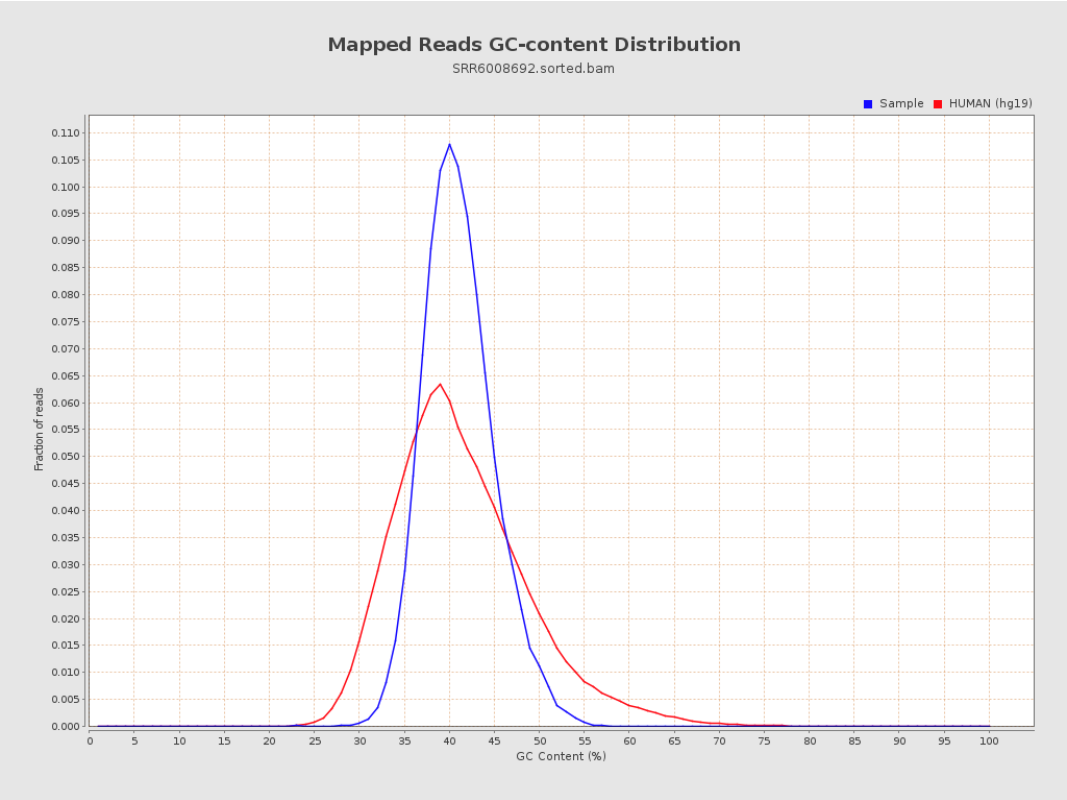
7. Results : Duplication Rate Histogram



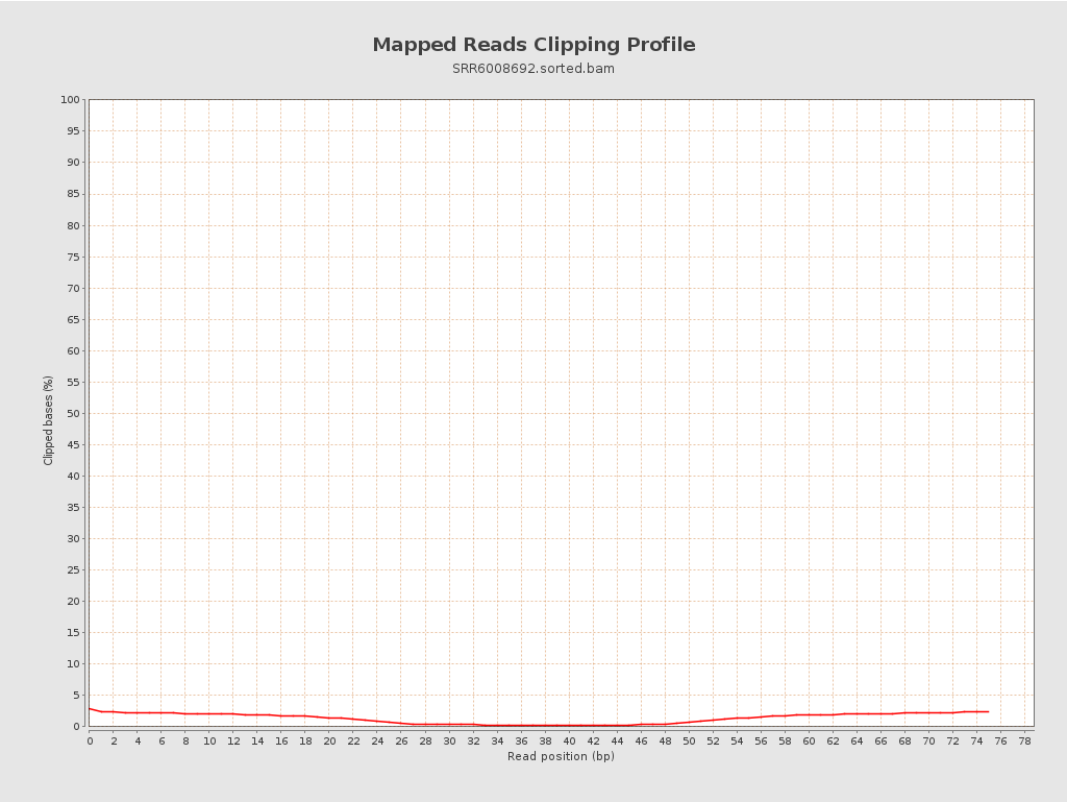
8. Results : Mapped Reads Nucleotide Content



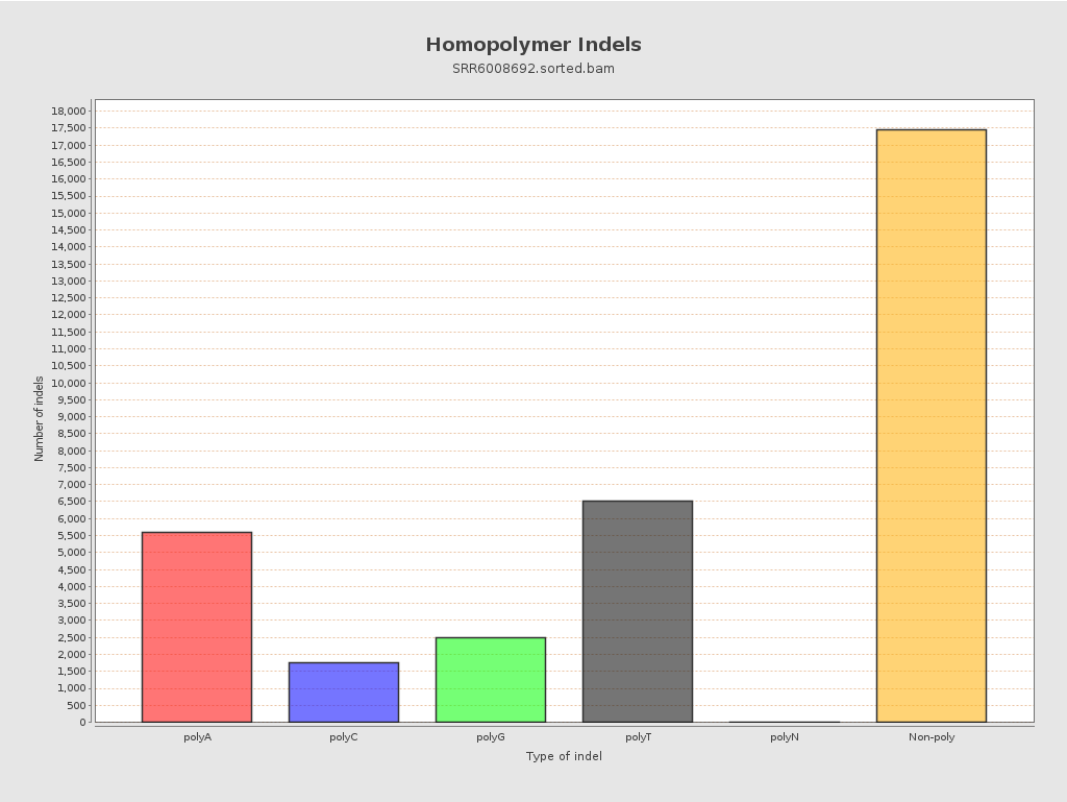
9. Results : Mapped Reads GC-content Distribution



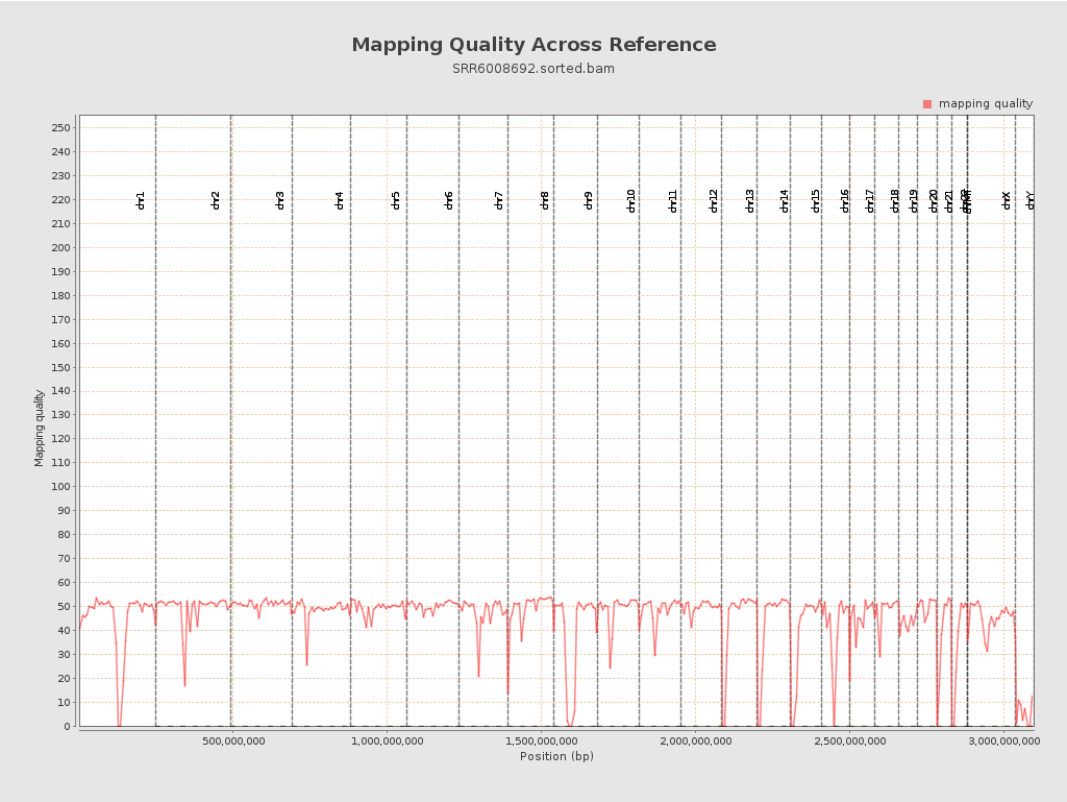
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram