Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:05:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080966.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_SRR3080966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080966.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:05:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,236,381
Mapped reads	6,484,026 / 89.6%
Unmapped reads	752,355 / 10.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	78,776 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	583,737 / 8.07%
Duplication rate	7.08%
Clipped reads	2,630,326 / 36.35%

2.2. ACGT Content

Number/percentage of A's	126,368,833 / 28.63%
Number/percentage of C's	79,568,164 / 18.03%
Number/percentage of T's	141,526,352 / 32.07%
Number/percentage of G's	92,999,494 / 21.07%
Number/percentage of N's	874,130 / 0.2%
GC Percentage	39.1%

2.3. Coverage

Mean	0.1426

Standard Deviation	0.8732

2.4. Mapping Quality

Mean Mapping Quality	47.18

2.5. Mismatches and indels

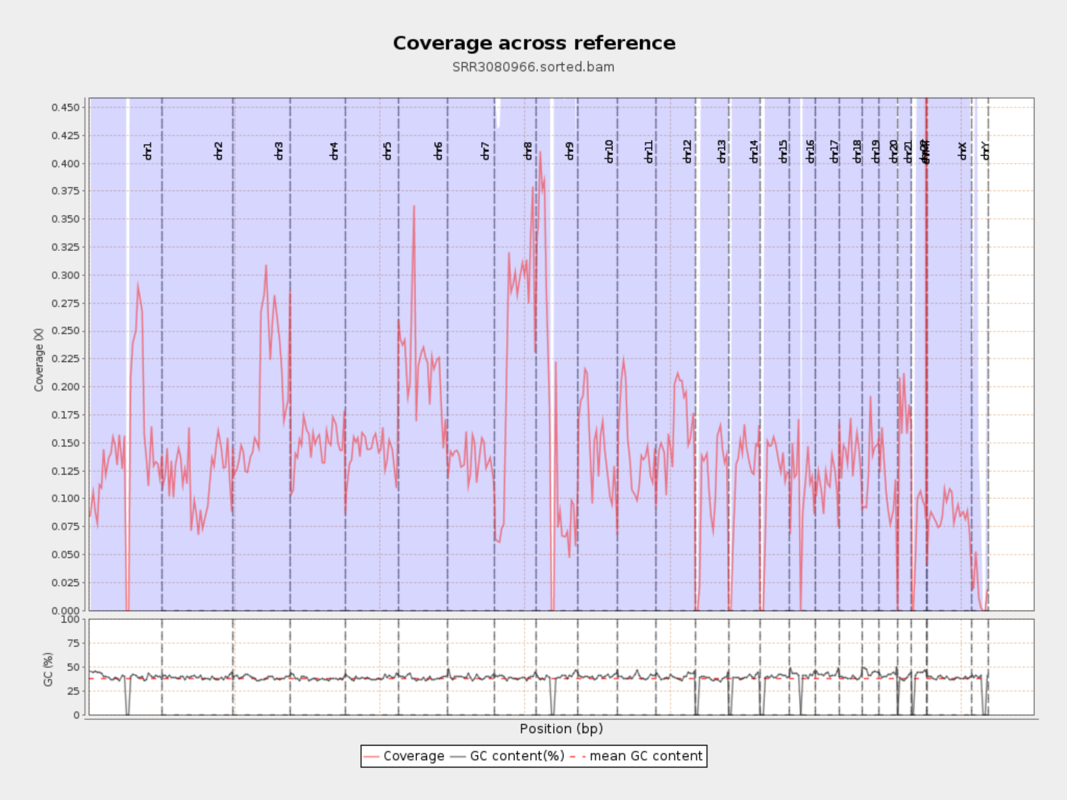
General error rate	1.02%
Mismatches	4,456,260
Insertions	34,815
Mapped reads with at least one insertion	0.53%
Deletions	97,514
Mapped reads with at least one deletion	1.49%
Homopolymer indels	49.23%

2.6. Chromosome stats

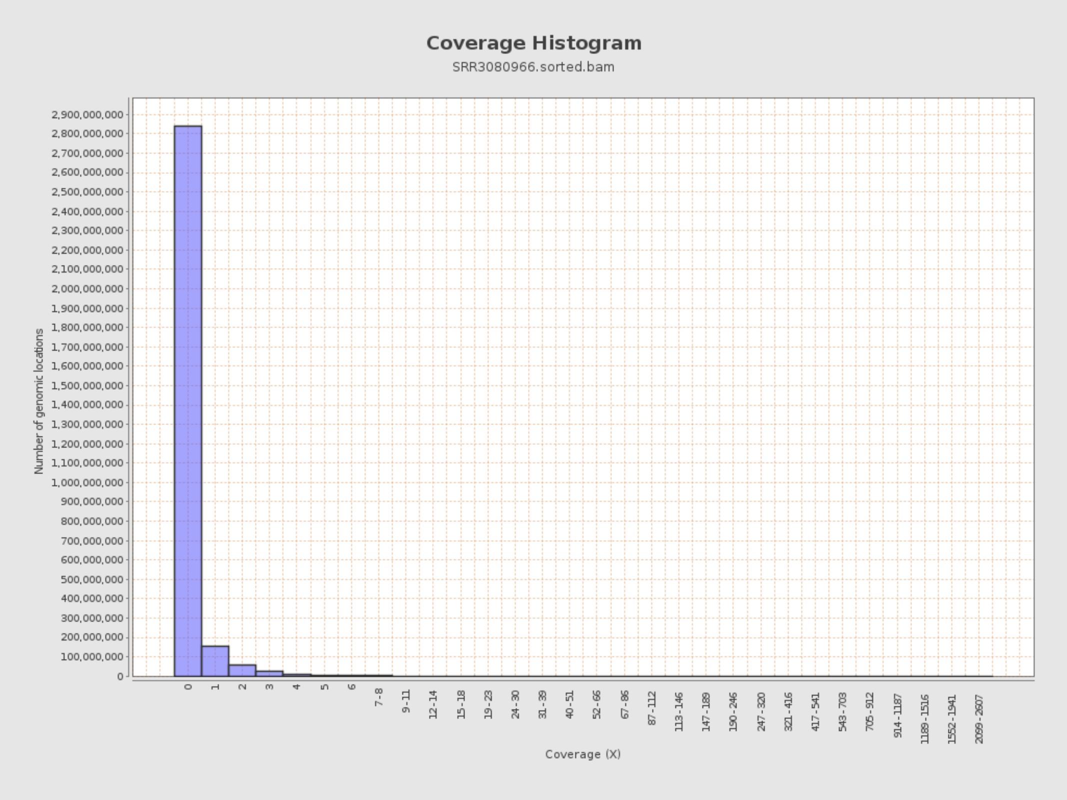
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35926805	0.1441	1.0149
chr2	243199373	28632460	0.1177	0.8118
chr3	198022430	38014546	0.192	0.688
chr4	191154276	28483939	0.149	0.6357
chr5	180915260	25720128	0.1422	0.5818
chr6	171115067	37803786	0.2209	1.1012
chr7	159138663	21743243	0.1366	0.8551

chr8	146364022	34540824	0.236	1.8174
chr9	141213431	22594385	0.16	1.0537
chr10	135534747	20298829	0.1498	0.7364
chr11	135006516	19190502	0.1421	0.7197
chr12	133851895	21822510	0.163	0.6551
chr13	115169878	12032408	0.1045	0.4977
chr14	107349540	12578418	0.1172	0.703
chr15	102531392	11597052	0.1131	0.5233
chr16	90354753	9952195	0.1101	0.6368
chr17	81195210	9072041	0.1117	0.5377
chr18	78077248	11070392	0.1418	1.6815
chr19	59128983	7779286	0.1316	0.9298
chr20	63025520	6896690	0.1094	0.5475
chr21	48129895	7944819	0.1651	0.7521
chr22	51304566	3598949	0.0701	0.3995
chrMT	16571	81014	4.8889	4.027
chrX	155270560	13216398	0.0851	0.5013
chrY	59373566	905989	0.0153	0.2949

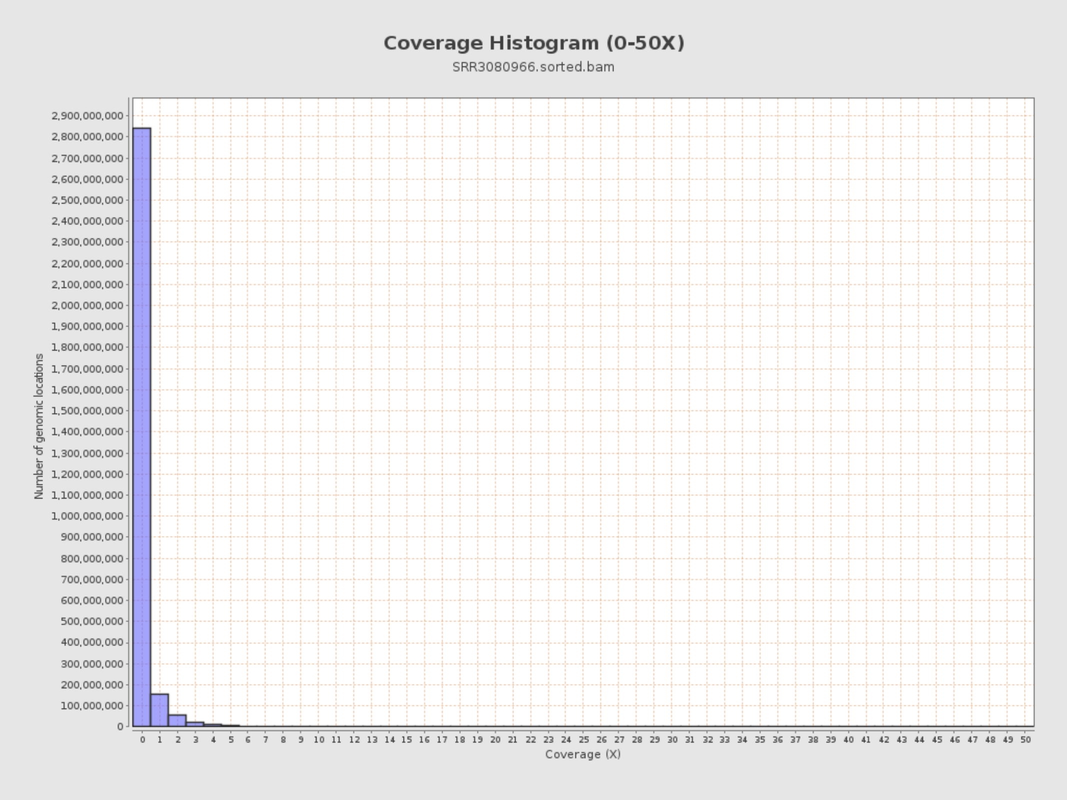
3. Results : Coverage across reference



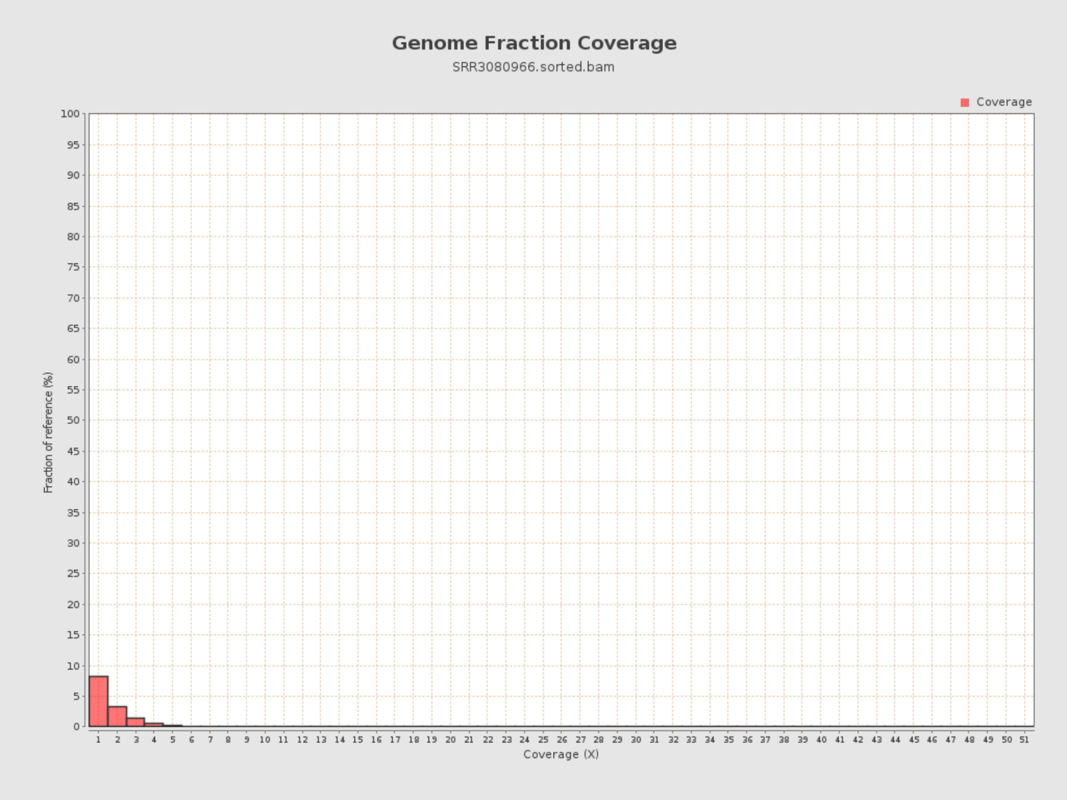
4. Results : Coverage Histogram



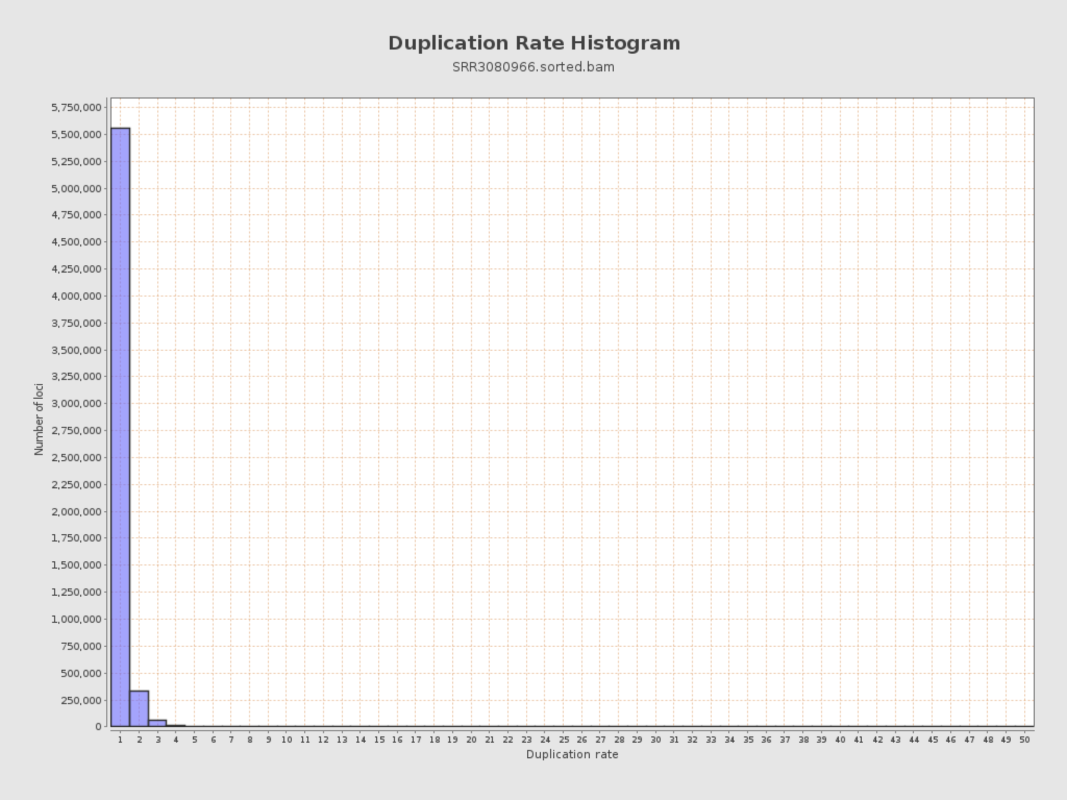
5. Results : Coverage Histogram (0-50X)



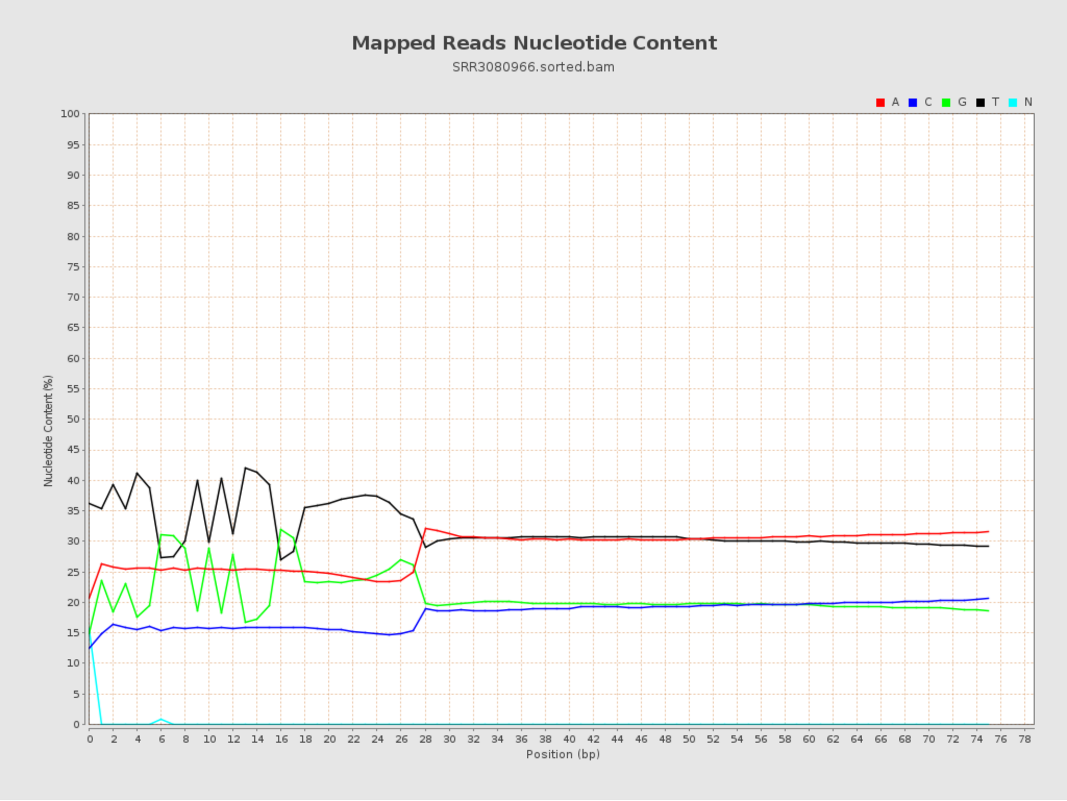
6. Results : Genome Fraction Coverage



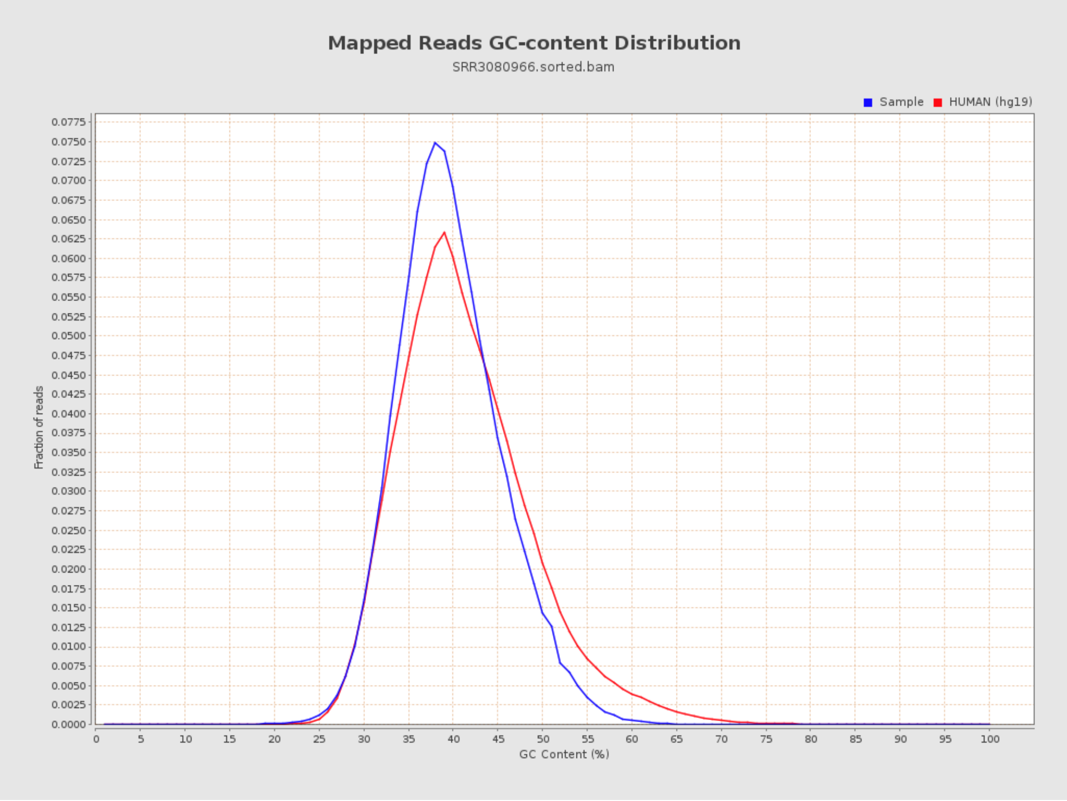
7. Results : Duplication Rate Histogram



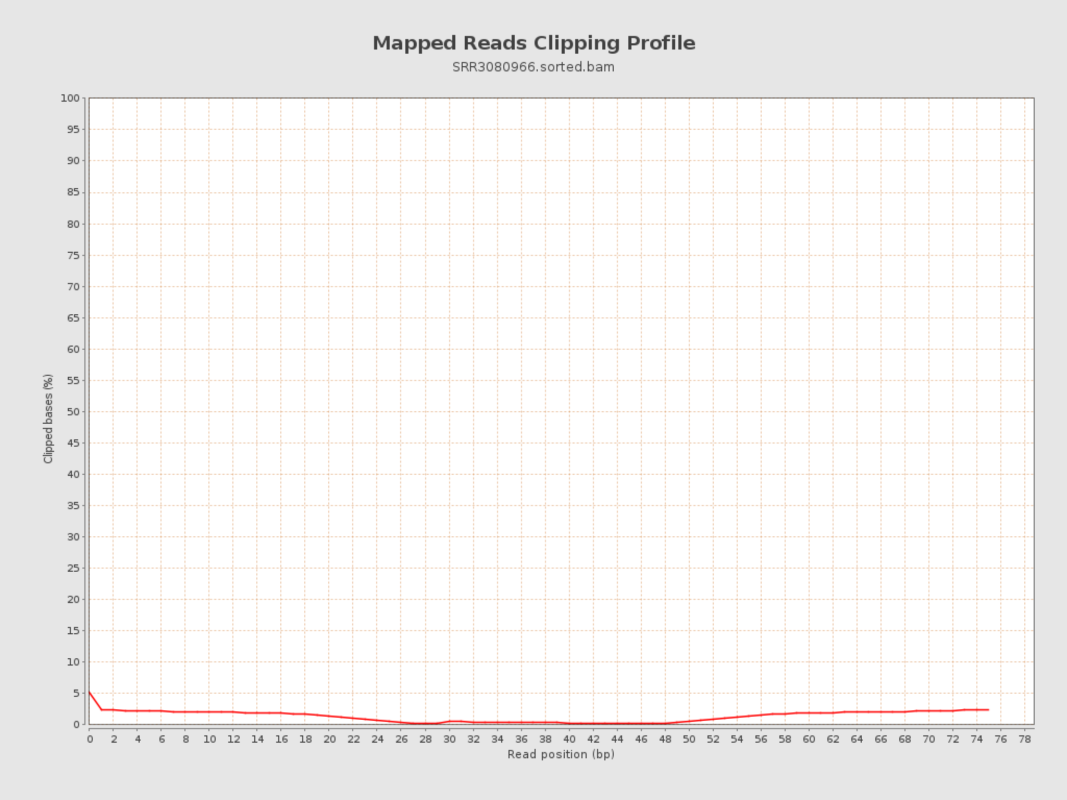
8. Results : Mapped Reads Nucleotide Content



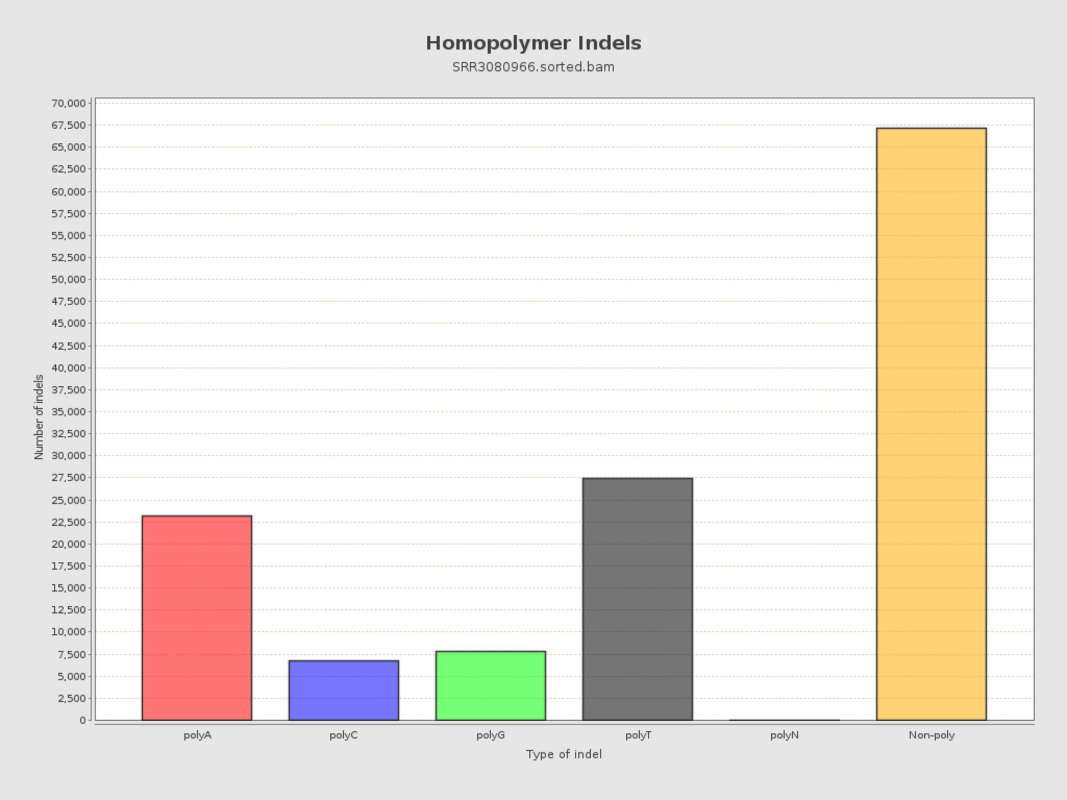
9. Results : Mapped Reads GC-content Distribution



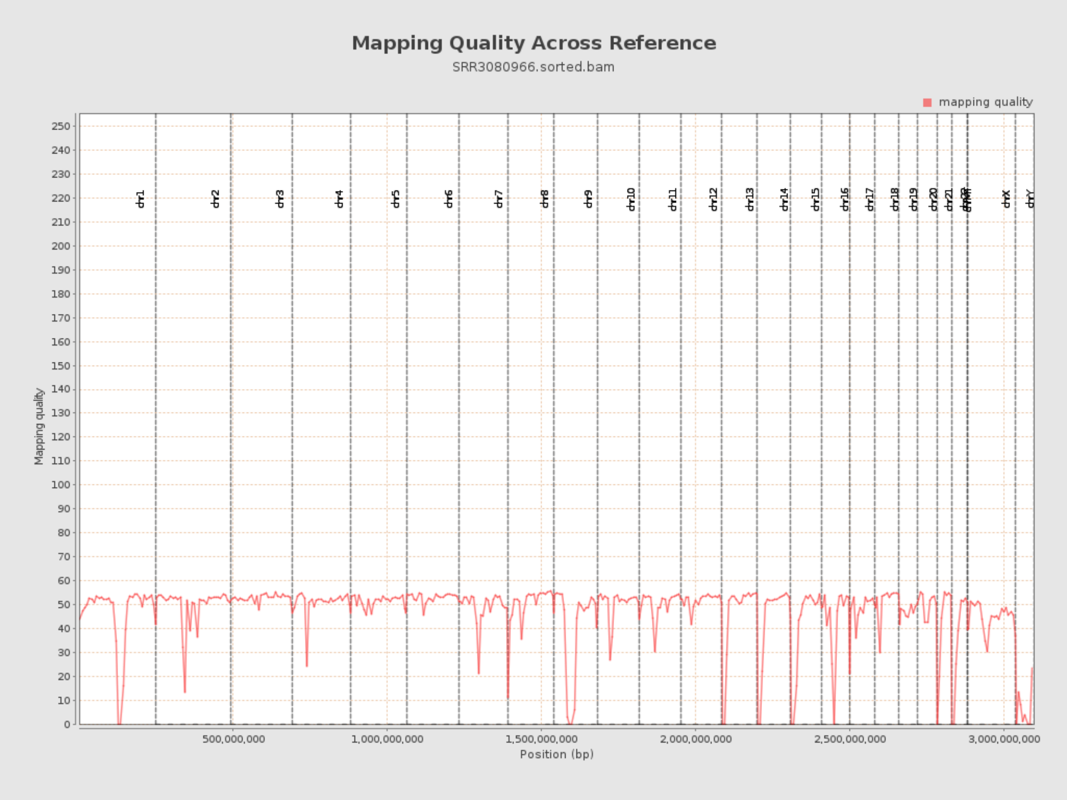
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram