Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:08:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081205.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_SRR3081205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:08:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,222,788
Mapped reads	6,506,789 / 79.13%
Unmapped reads	1,715,999 / 20.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,196 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	863,500 / 10.5%
Duplication rate	8.82%
Clipped reads	3,504,025 / 42.61%

2.2. ACGT Content

Number/percentage of A's	118,411,583 / 28.04%
Number/percentage of C's	84,994,667 / 20.13%
Number/percentage of T's	124,936,552 / 29.59%
Number/percentage of G's	93,647,230 / 22.18%
Number/percentage of N's	244,471 / 0.06%
GC Percentage	42.31%

2.3. Coverage

Mean	0.1364

Standard Deviation	1.4439

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

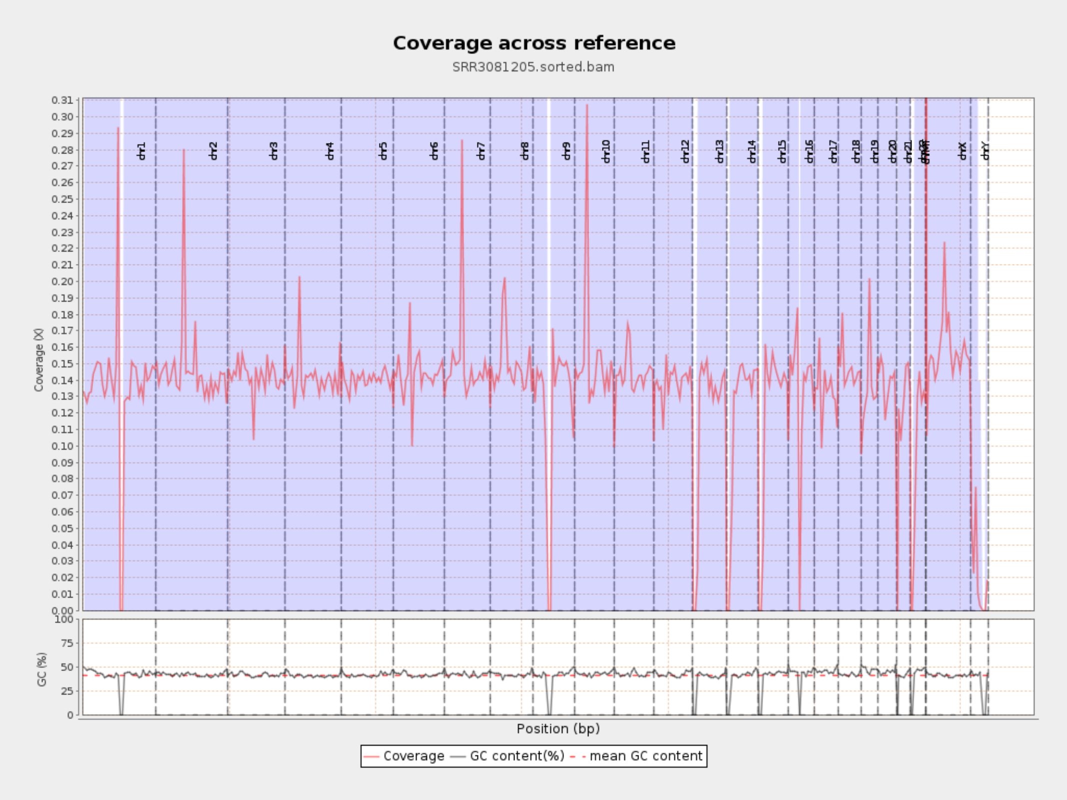
General error rate	1.05%
Mismatches	4,394,753
Insertions	30,355
Mapped reads with at least one insertion	0.46%
Deletions	80,513
Mapped reads with at least one deletion	1.22%
Homopolymer indels	43.38%

2.6. Chromosome stats

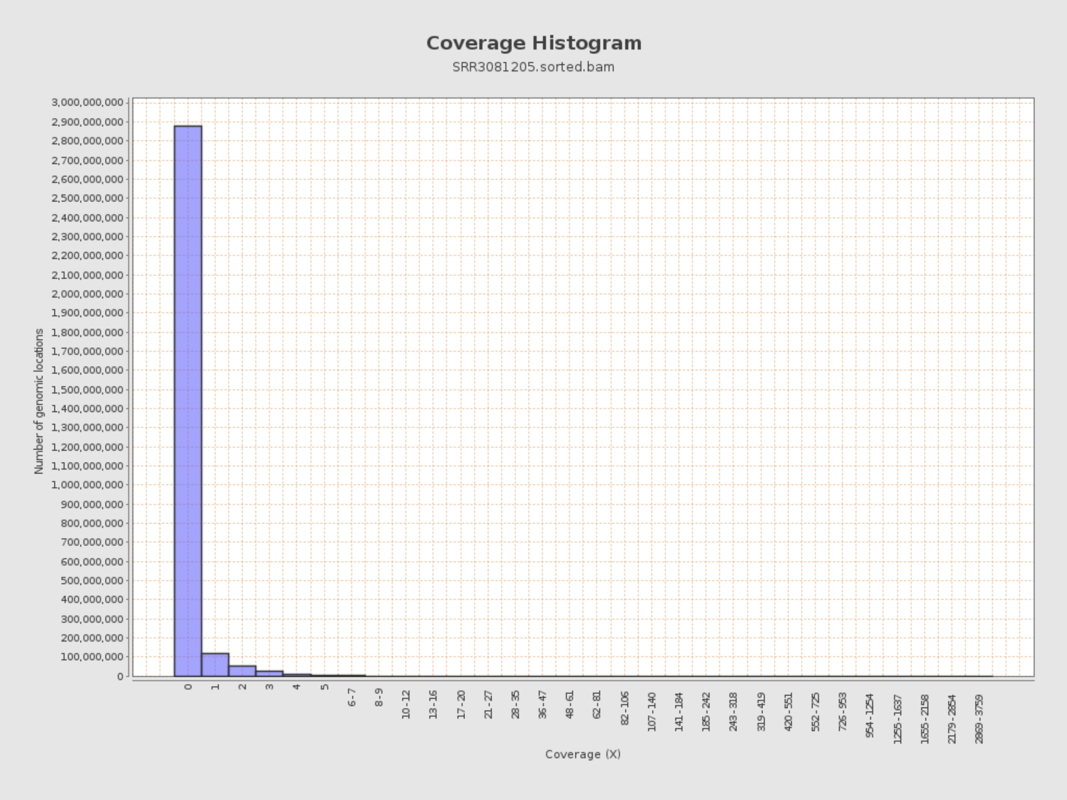
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33861450	0.1359	3.207
chr2	243199373	35652681	0.1466	1.1936
chr3	198022430	28117764	0.142	0.6339
chr4	191154276	27275657	0.1427	0.7426
chr5	180915260	25454251	0.1407	0.6397
chr6	171115067	24611728	0.1438	0.8477
chr7	159138663	23957843	0.1505	2.047

chr8	146364022	21832045	0.1492	2.2556
chr9	141213431	17652311	0.125	1.0544
chr10	135534747	20610795	0.1521	1.5321
chr11	135006516	19416955	0.1438	1.2246
chr12	133851895	18598687	0.1389	0.661
chr13	115169878	13373855	0.1161	0.5619
chr14	107349540	12662104	0.118	0.7825
chr15	102531392	11975732	0.1168	0.5659
chr16	90354753	11817565	0.1308	0.7078
chr17	81195210	10851176	0.1336	0.8191
chr18	78077248	11504346	0.1473	2.0681
chr19	59128983	8100871	0.137	2.1084
chr20	63025520	8732540	0.1386	0.6673
chr21	48129895	5709821	0.1186	0.7063
chr22	51304566	4731746	0.0922	0.5112
chrMT	16571	162816	9.8254	7.3681
chrX	155270560	24422054	0.1573	0.794
chrY	59373566	1273959	0.0215	0.5229

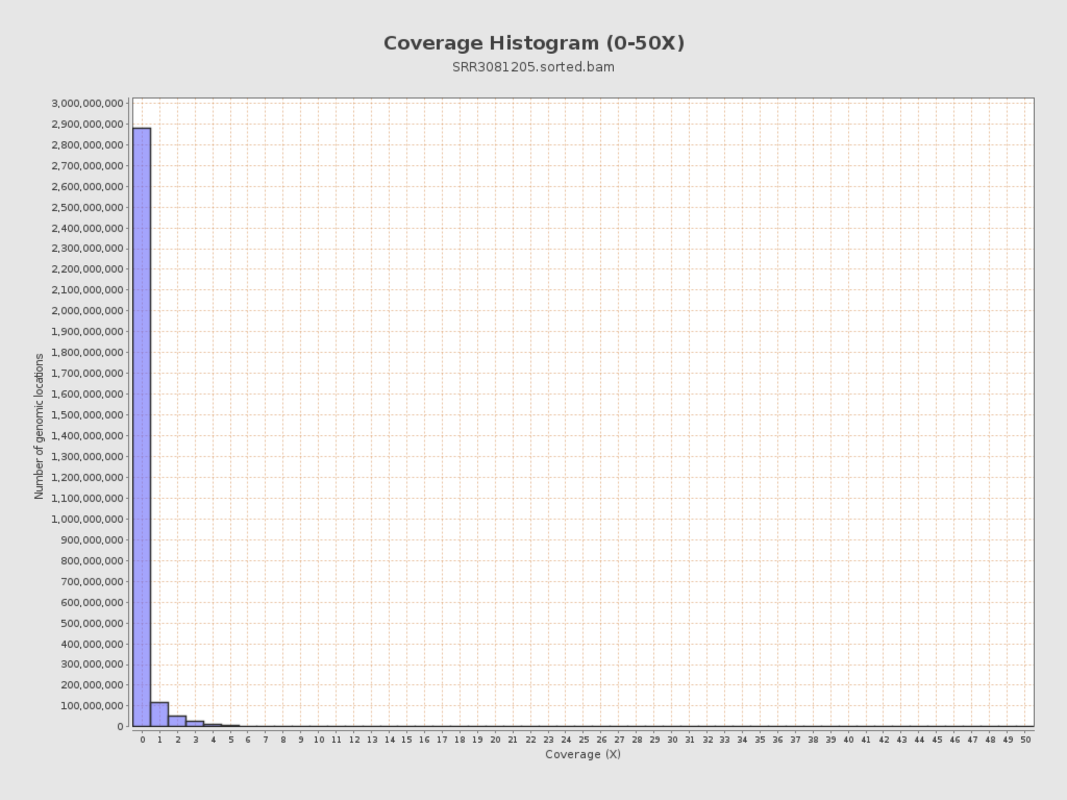
3. Results : Coverage across reference



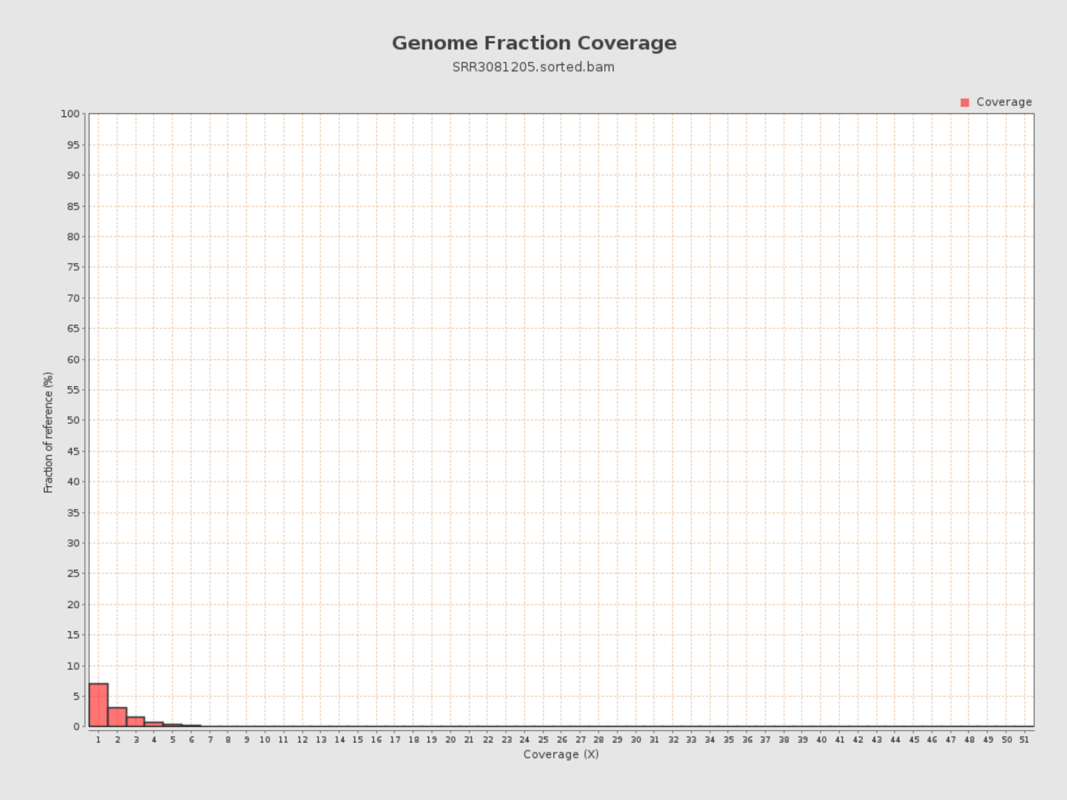
4. Results : Coverage Histogram



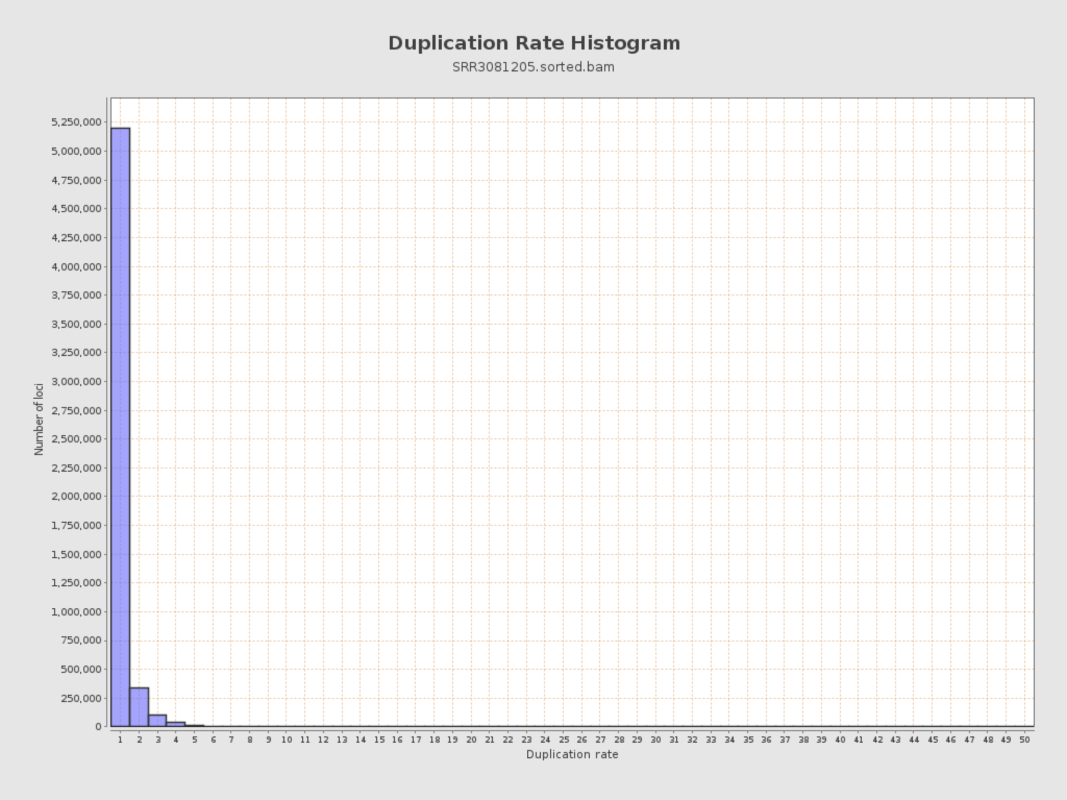
5. Results : Coverage Histogram (0-50X)



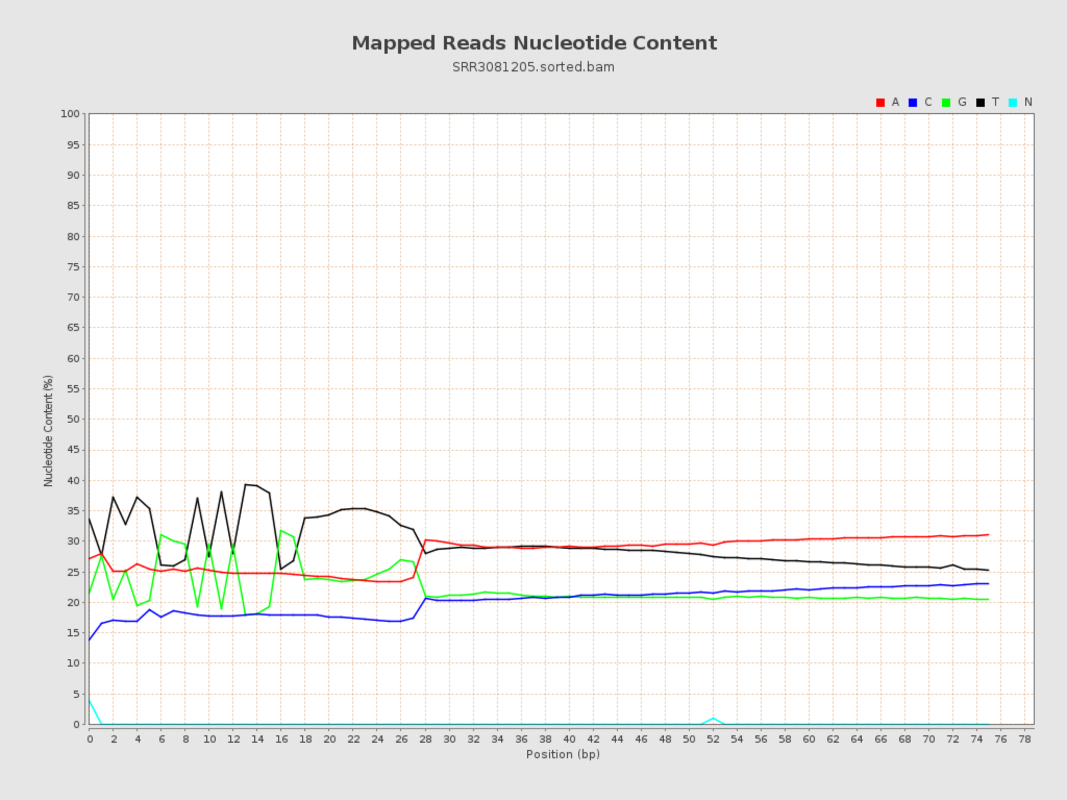
6. Results : Genome Fraction Coverage



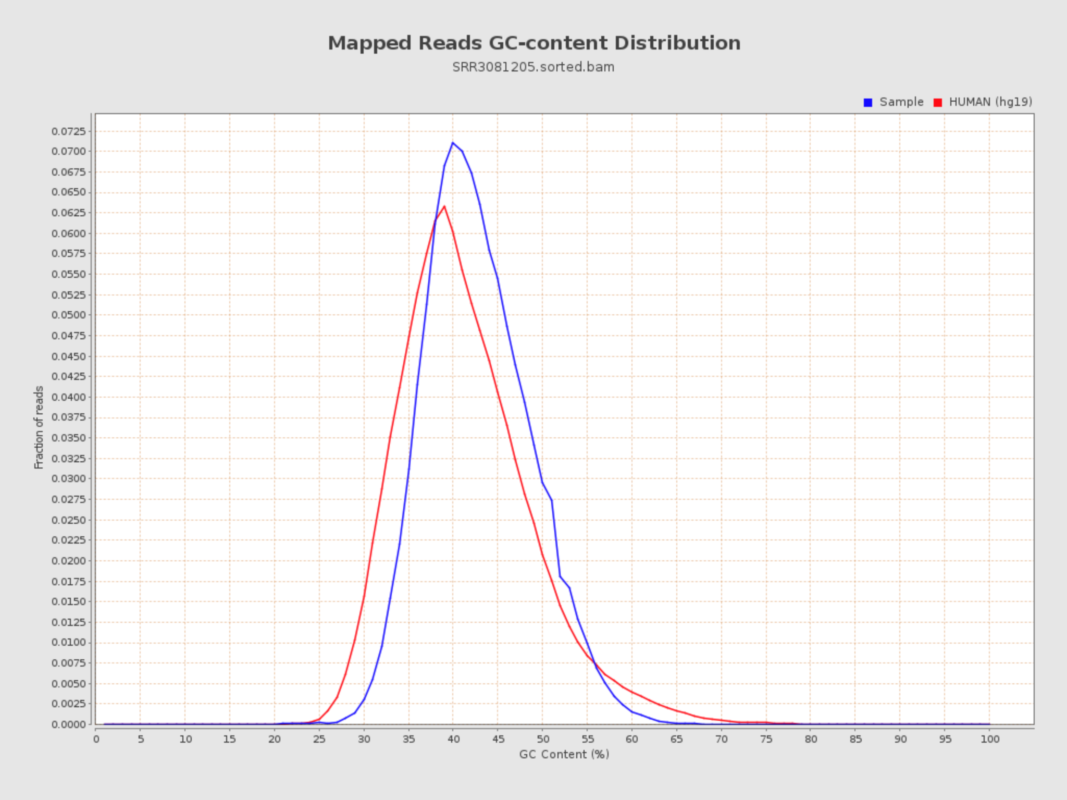
7. Results : Duplication Rate Histogram



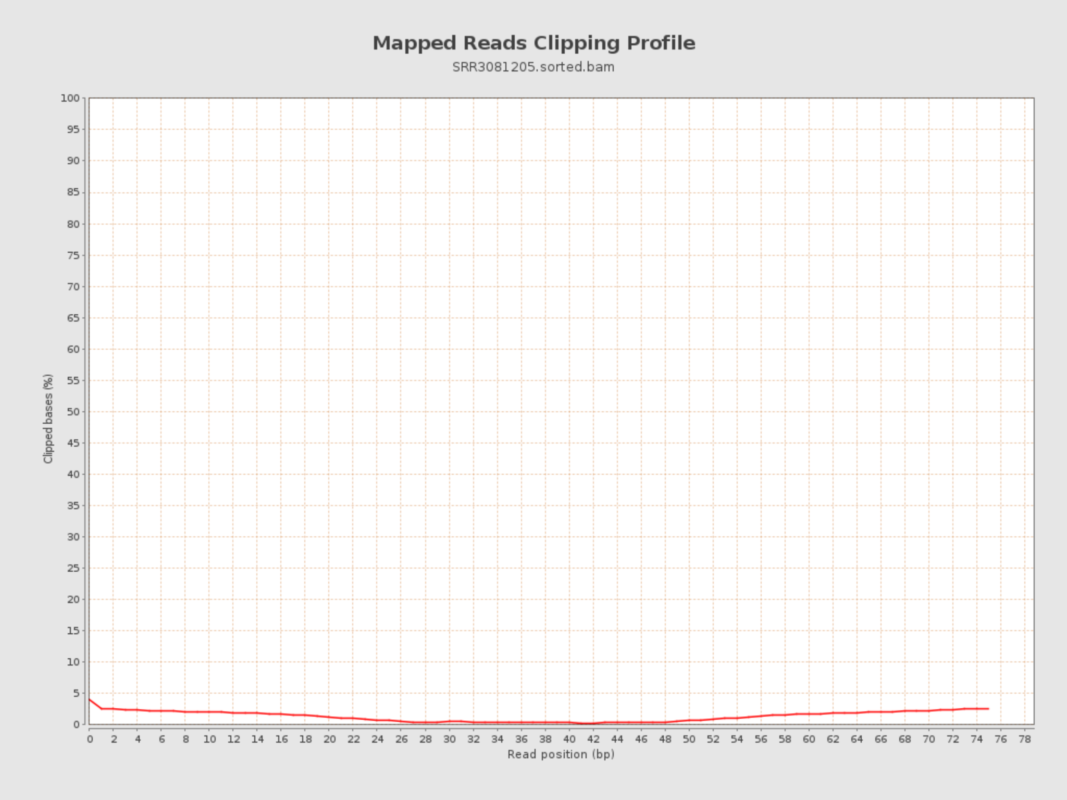
8. Results : Mapped Reads Nucleotide Content



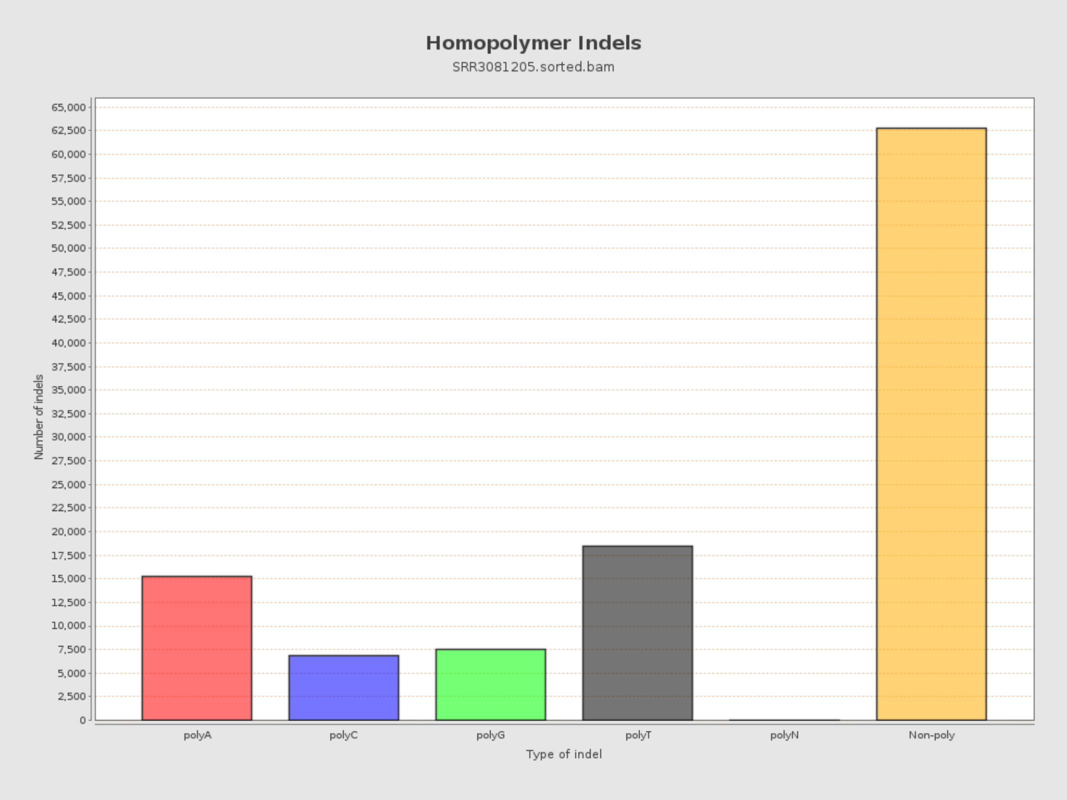
9. Results : Mapped Reads GC-content Distribution



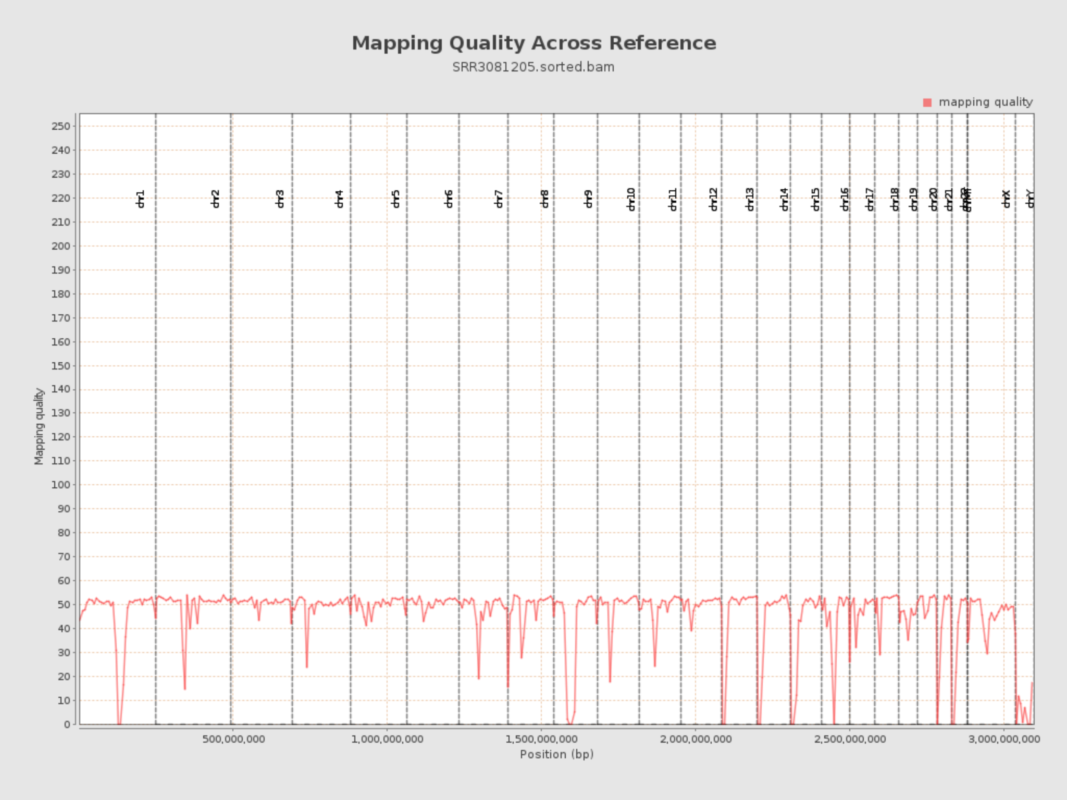
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram