Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:03:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081164.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_SRR3081164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:03:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,042,717
Mapped reads	1,835,983 / 89.88%
Unmapped reads	206,734 / 10.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,804 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	64,503 / 3.16%
Duplication rate	2.72%
Clipped reads	780,312 / 38.2%

2.2. ACGT Content

Number/percentage of A's	35,067,425 / 28.33%
Number/percentage of C's	22,864,826 / 18.47%
Number/percentage of T's	38,844,375 / 31.38%
Number/percentage of G's	26,957,002 / 21.78%
Number/percentage of N's	37,020 / 0.03%
GC Percentage	40.25%

2.3. Coverage

Mean	0.04

Standard Deviation	0.3357

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

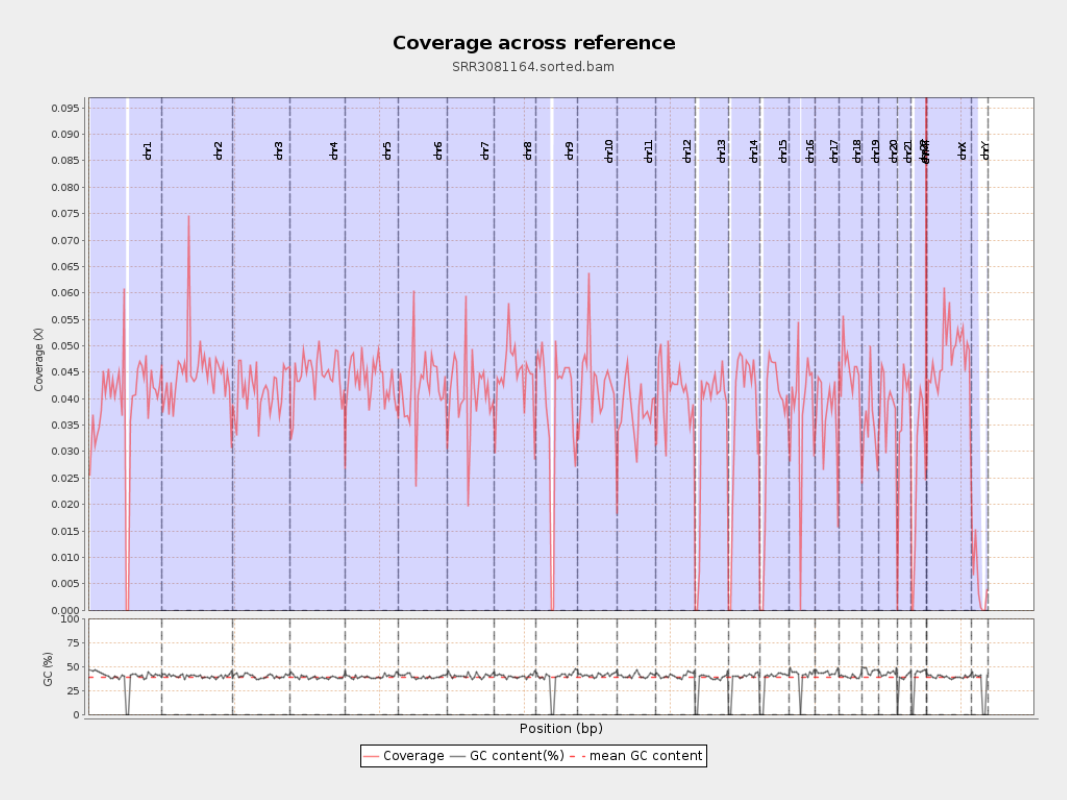
General error rate	0.85%
Mismatches	1,033,025
Insertions	10,047
Mapped reads with at least one insertion	0.54%
Deletions	28,349
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.09%

2.6. Chromosome stats

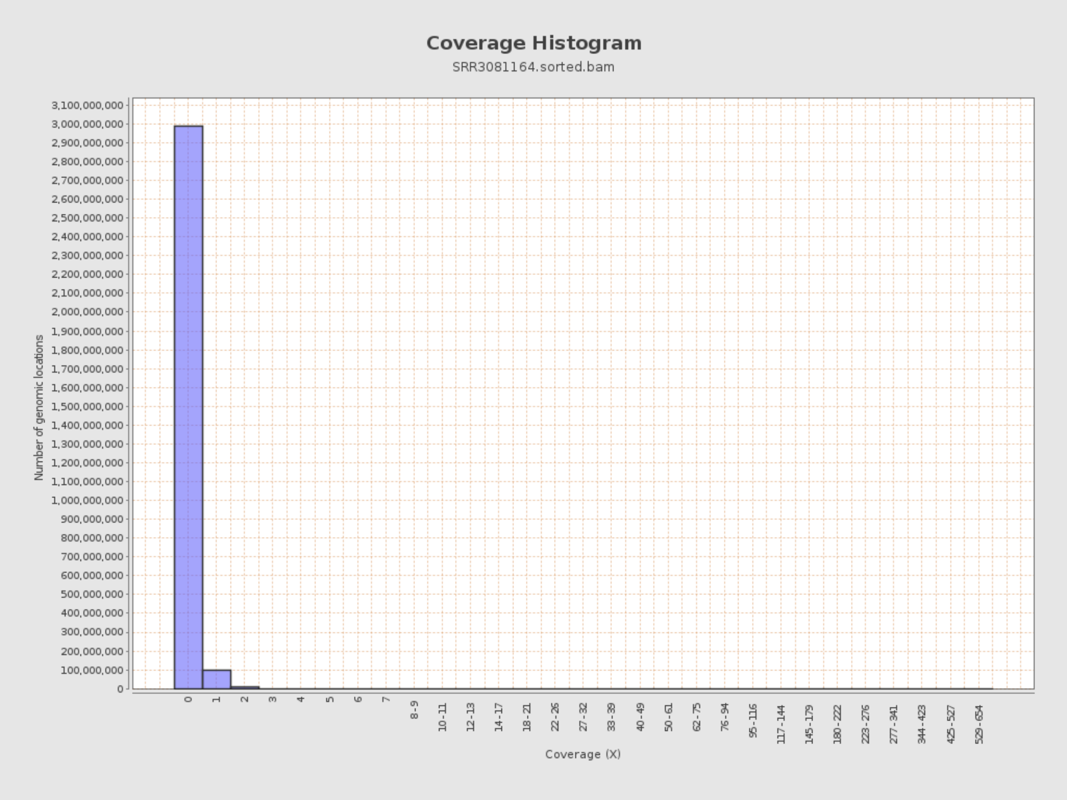
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9649784	0.0387	0.5342
chr2	243199373	10877309	0.0447	0.406
chr3	198022430	8246558	0.0416	0.2235
chr4	191154276	8453034	0.0442	0.2383
chr5	180915260	7863829	0.0435	0.2294
chr6	171115067	7193910	0.042	0.2757
chr7	159138663	6581084	0.0414	0.4396

chr8	146364022	6483177	0.0443	0.466
chr9	141213431	5396280	0.0382	0.344
chr10	135534747	5787593	0.0427	0.3119
chr11	135006516	5094036	0.0377	0.2775
chr12	133851895	5508429	0.0412	0.227
chr13	115169878	4037408	0.0351	0.2048
chr14	107349540	3953798	0.0368	0.2302
chr15	102531392	3555845	0.0347	0.2058
chr16	90354753	3418209	0.0378	0.2414
chr17	81195210	2967230	0.0365	0.2275
chr18	78077248	3515135	0.045	0.62
chr19	59128983	2092640	0.0354	0.4368
chr20	63025520	2444400	0.0388	0.2266
chr21	48129895	1713436	0.0356	0.2215
chr22	51304566	1285335	0.0251	0.1719
chrMT	16571	3506	0.2116	0.5083
chrX	155270560	7400669	0.0477	0.267
chrY	59373566	294197	0.005	0.1117

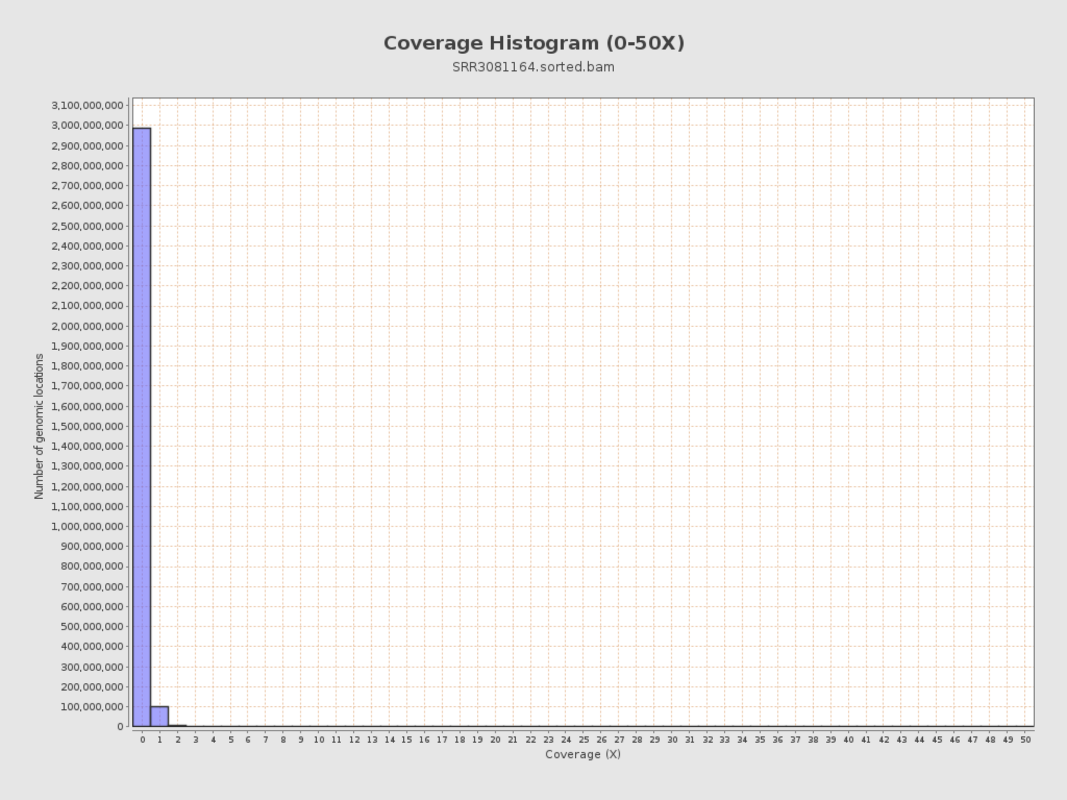
3. Results : Coverage across reference



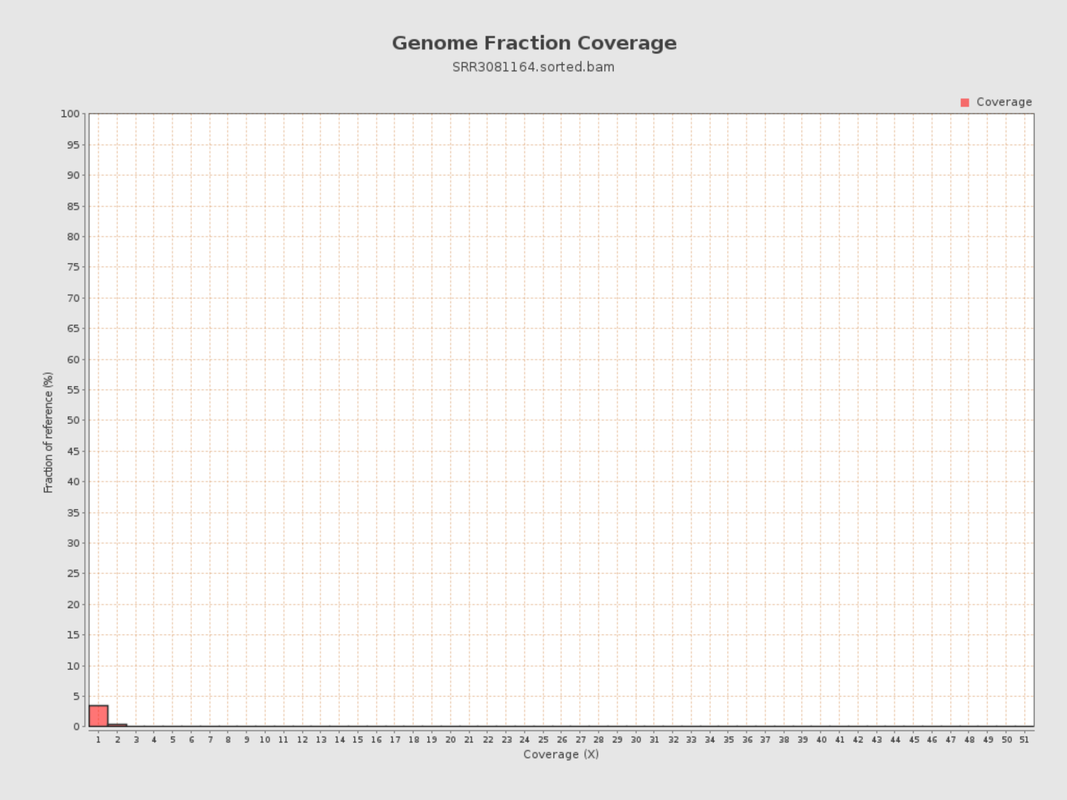
4. Results : Coverage Histogram



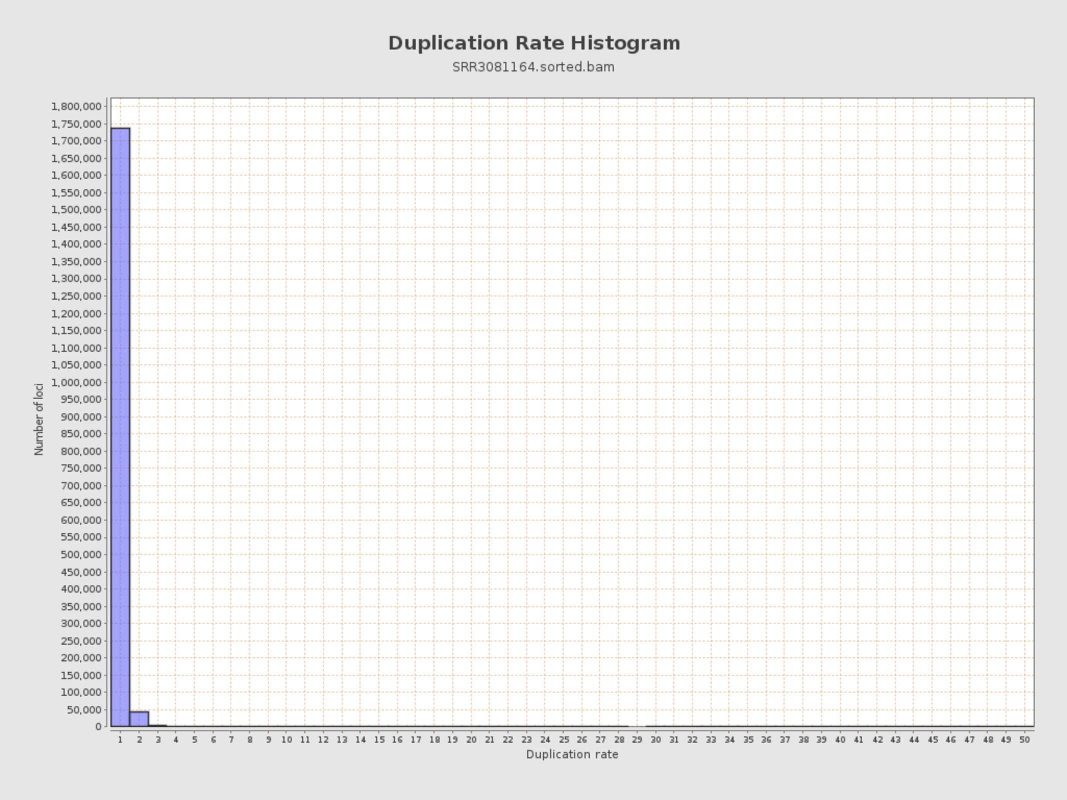
5. Results : Coverage Histogram (0-50X)



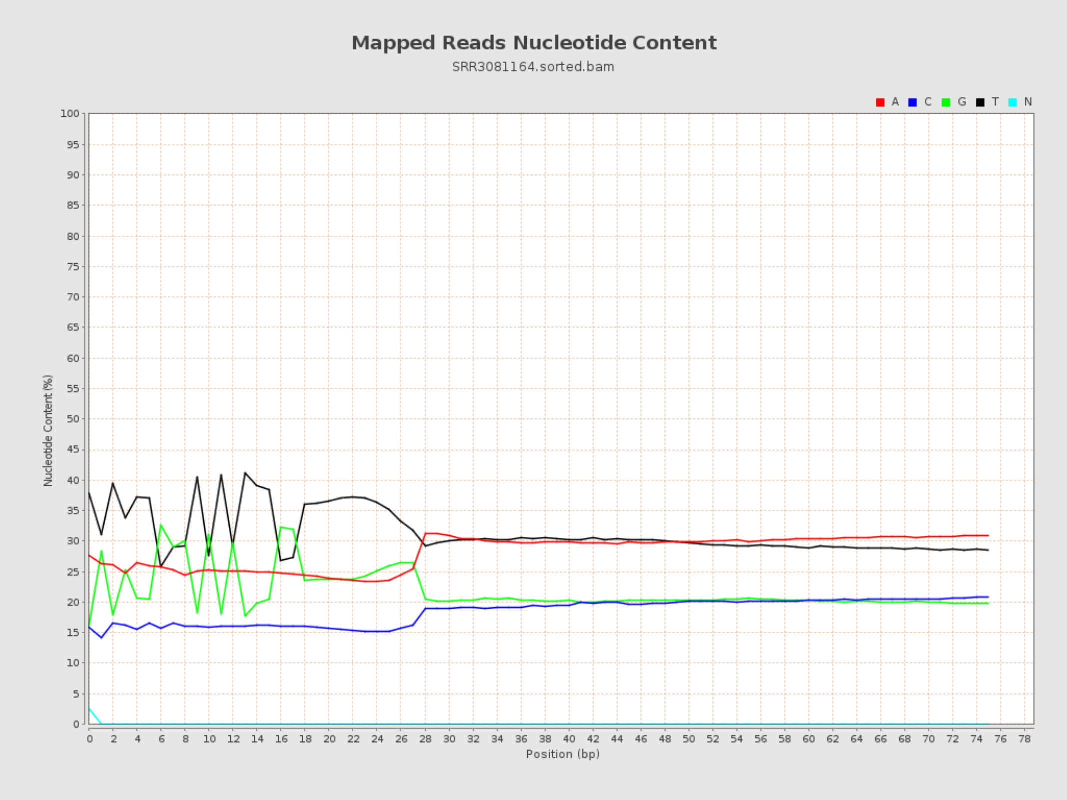
6. Results : Genome Fraction Coverage



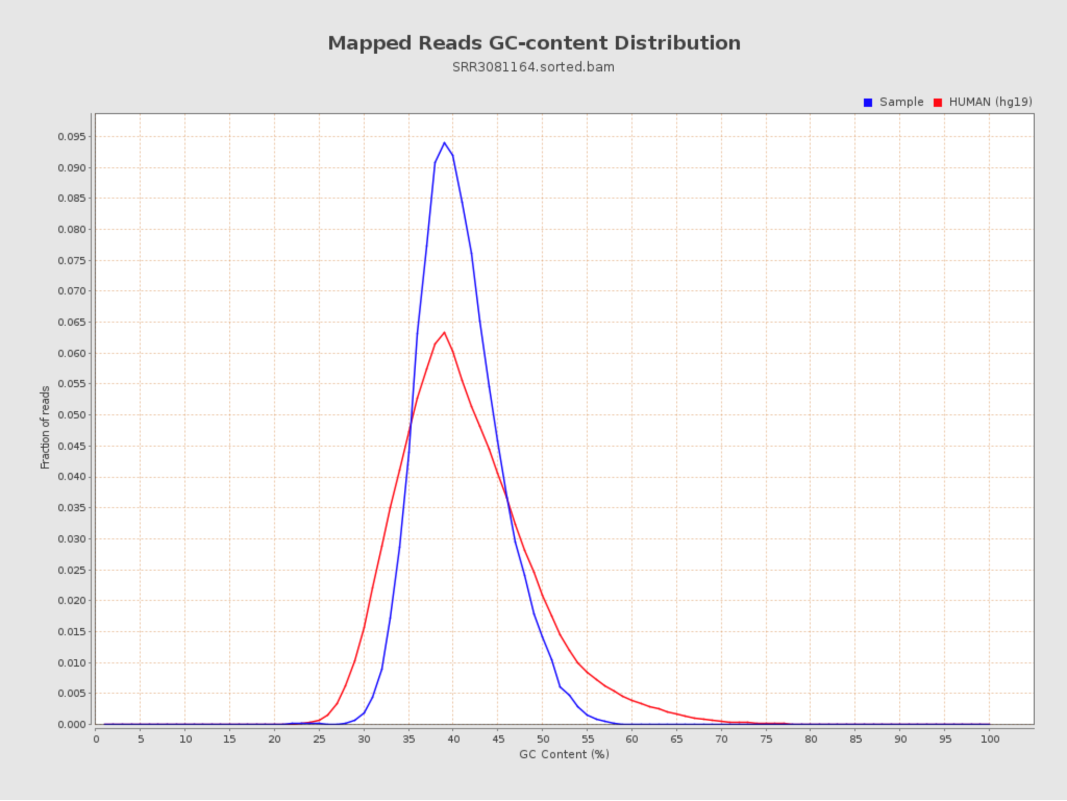
7. Results : Duplication Rate Histogram



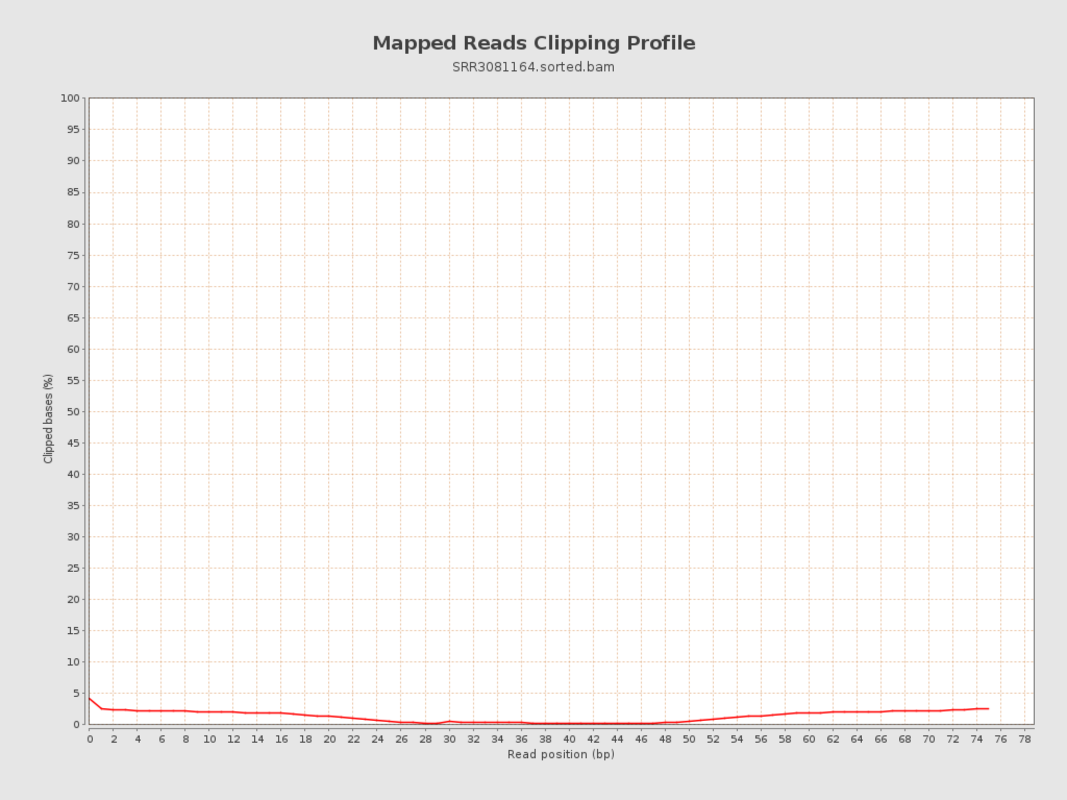
8. Results : Mapped Reads Nucleotide Content



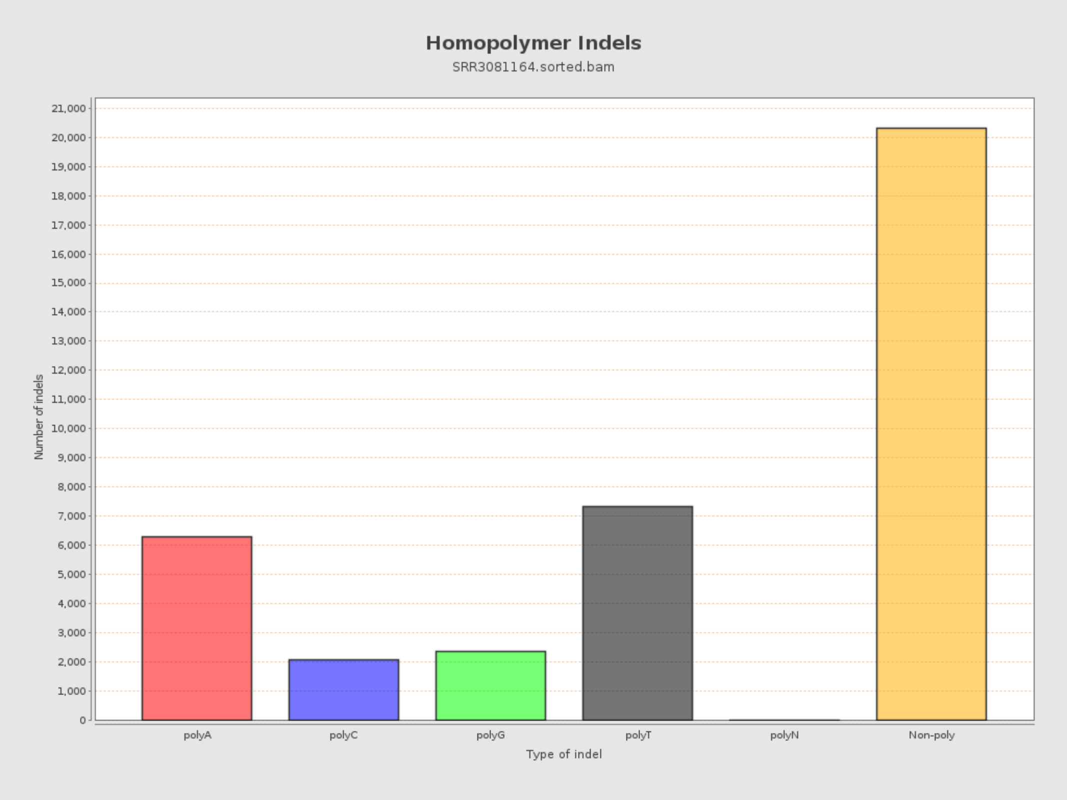
9. Results : Mapped Reads GC-content Distribution



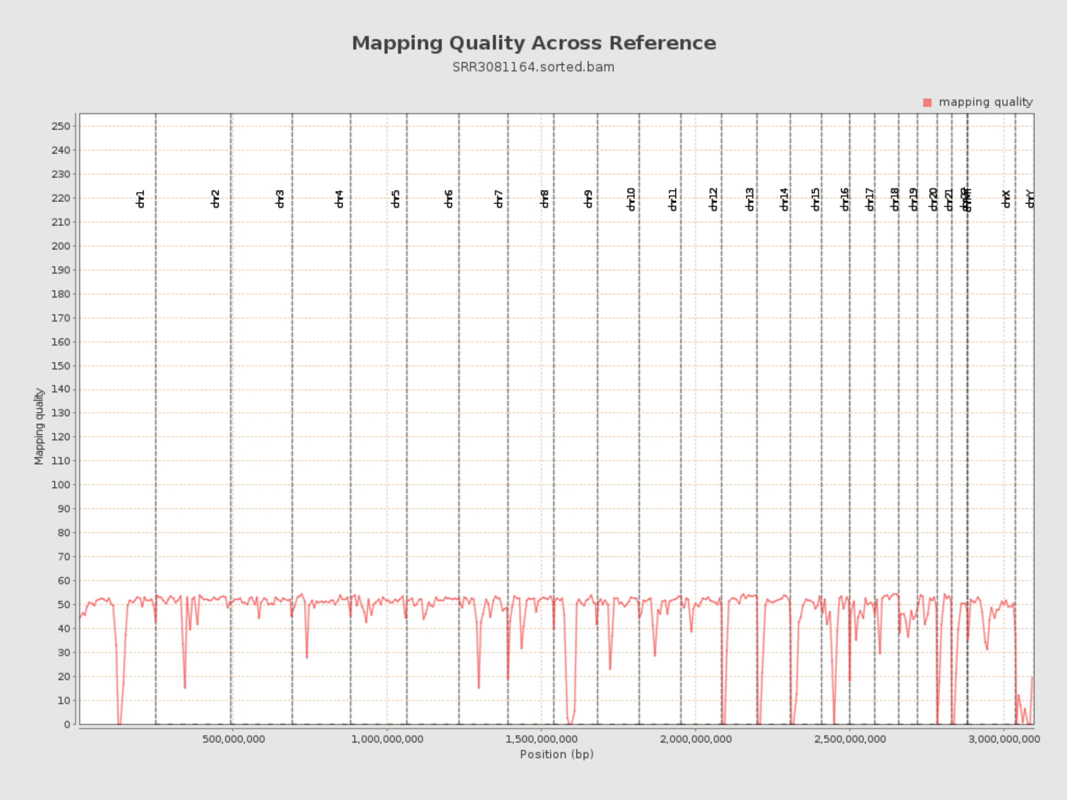
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram