Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:59:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081215.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_SRR3081215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:59:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,211,433
Mapped reads	1,936,186 / 87.55%
Unmapped reads	275,247 / 12.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,275 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	100,369 / 4.54%
Duplication rate	4.36%
Clipped reads	1,018,326 / 46.05%

2.2. ACGT Content

Number/percentage of A's	35,860,107 / 28.38%
Number/percentage of C's	24,649,535 / 19.51%
Number/percentage of T's	38,441,475 / 30.42%
Number/percentage of G's	27,403,431 / 21.69%
Number/percentage of N's	8,197 / 0.01%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3103

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

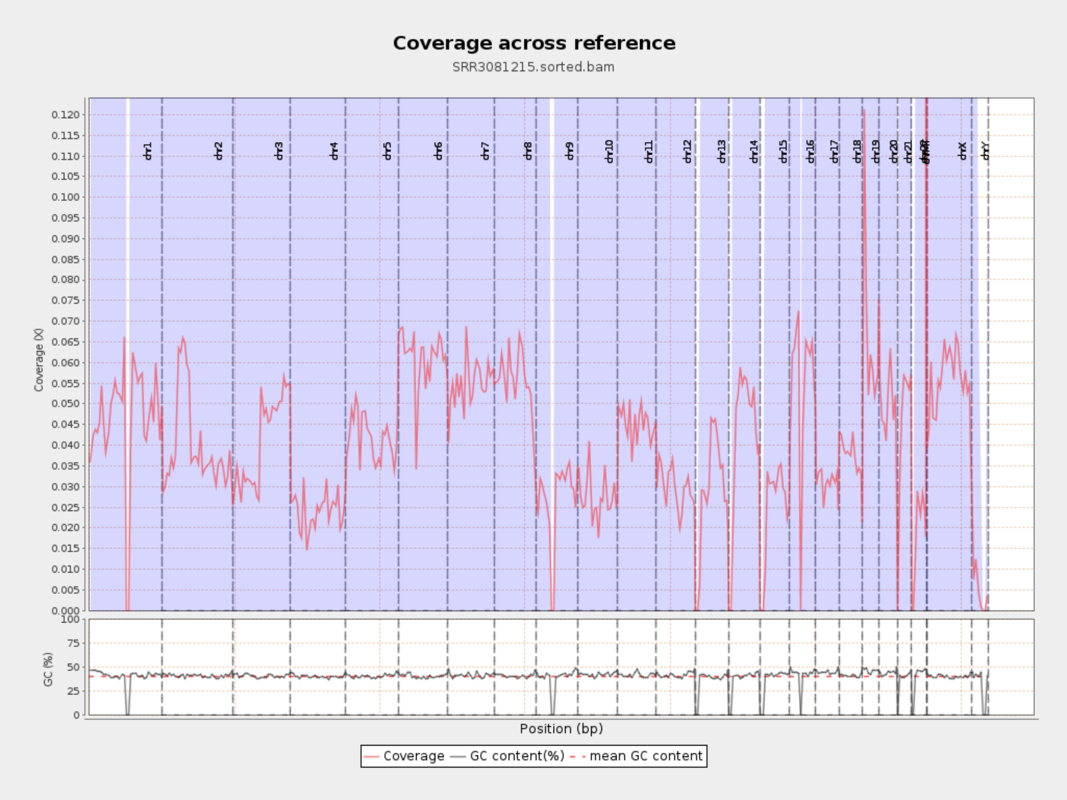
General error rate	0.89%
Mismatches	1,108,543
Insertions	9,370
Mapped reads with at least one insertion	0.48%
Deletions	28,389
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.68%

2.6. Chromosome stats

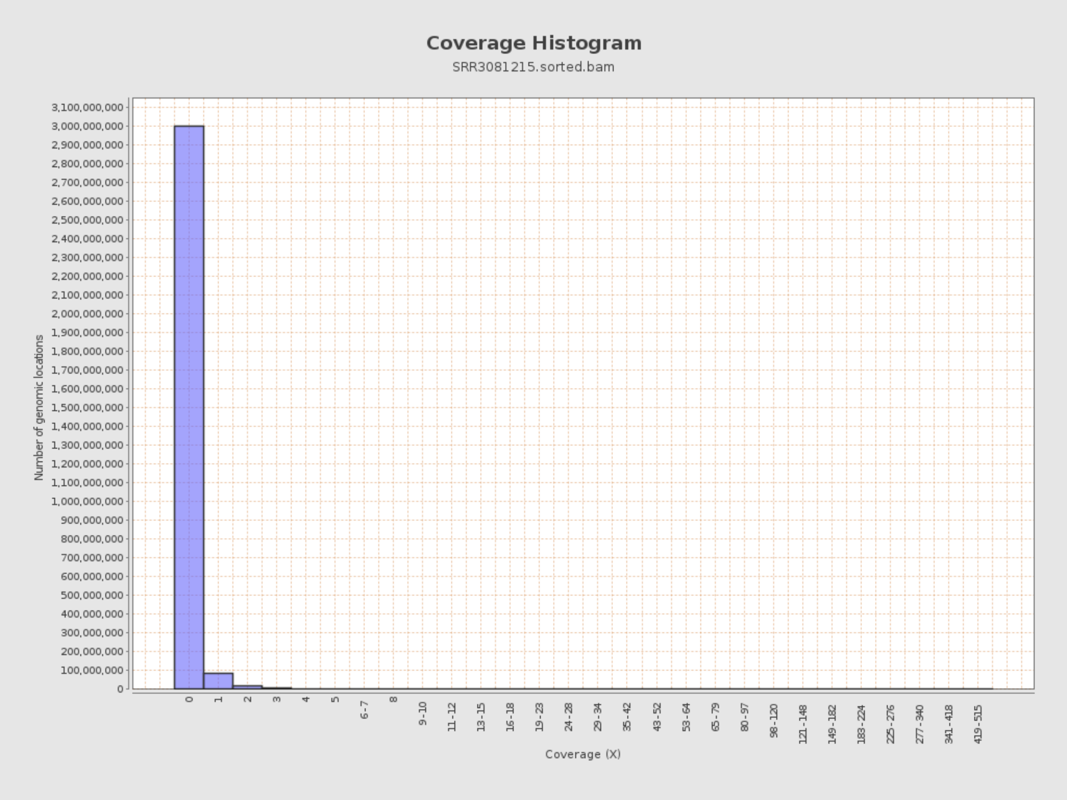
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11549726	0.0463	0.4852
chr2	243199373	9728638	0.04	0.3721
chr3	198022430	8047103	0.0406	0.2487
chr4	191154276	4583760	0.024	0.1925
chr5	180915260	7559851	0.0418	0.252
chr6	171115067	10457441	0.0611	0.3328
chr7	159138663	8763108	0.0551	0.4021

chr8	146364022	8118019	0.0555	0.3672
chr9	141213431	3764244	0.0267	0.2335
chr10	135534747	3698423	0.0273	0.2513
chr11	135006516	6066471	0.0449	0.3028
chr12	133851895	3985862	0.0298	0.2118
chr13	115169878	3310575	0.0287	0.2125
chr14	107349540	4545664	0.0423	0.2658
chr15	102531392	2507892	0.0245	0.2131
chr16	90354753	5024193	0.0556	0.2983
chr17	81195210	2510989	0.0309	0.2255
chr18	78077248	2980679	0.0382	0.3484
chr19	59128983	3913717	0.0662	0.4358
chr20	63025520	3102698	0.0492	0.2803
chr21	48129895	2181543	0.0453	0.2684
chr22	51304566	942375	0.0184	0.1636
chrMT	16571	56401	3.4036	2.9647
chrX	155270560	8681589	0.0559	0.3026
chrY	59373566	327800	0.0055	0.0986

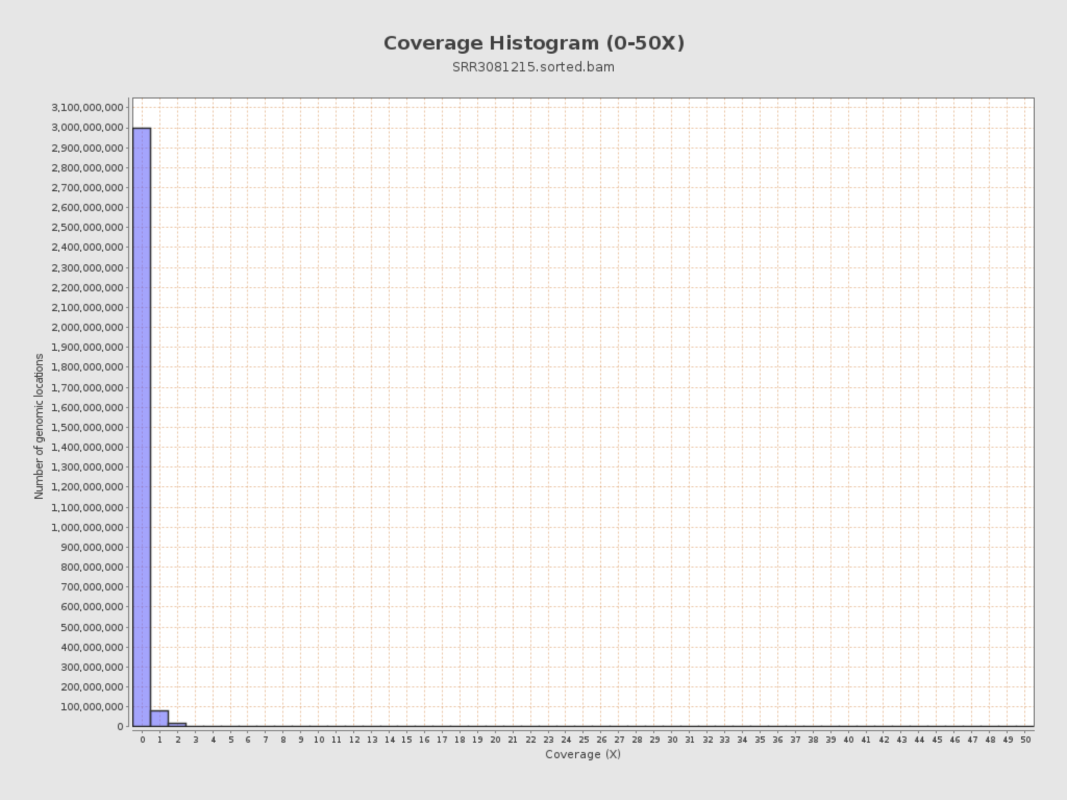
3. Results : Coverage across reference



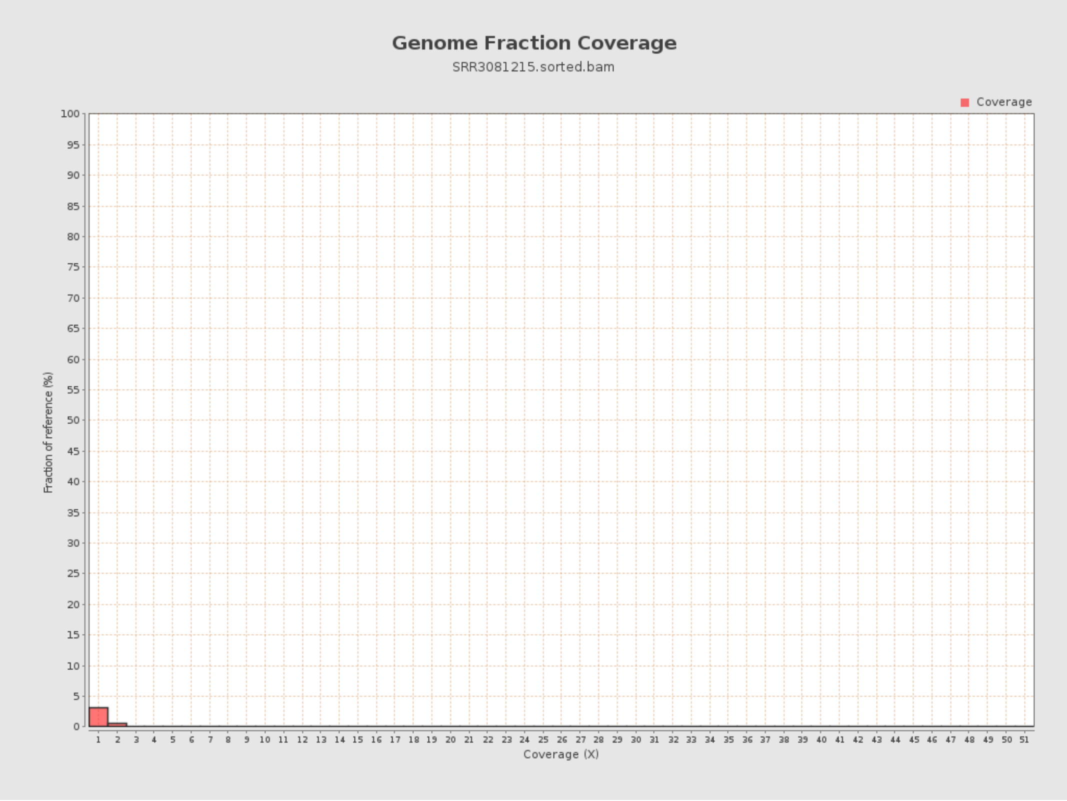
4. Results : Coverage Histogram



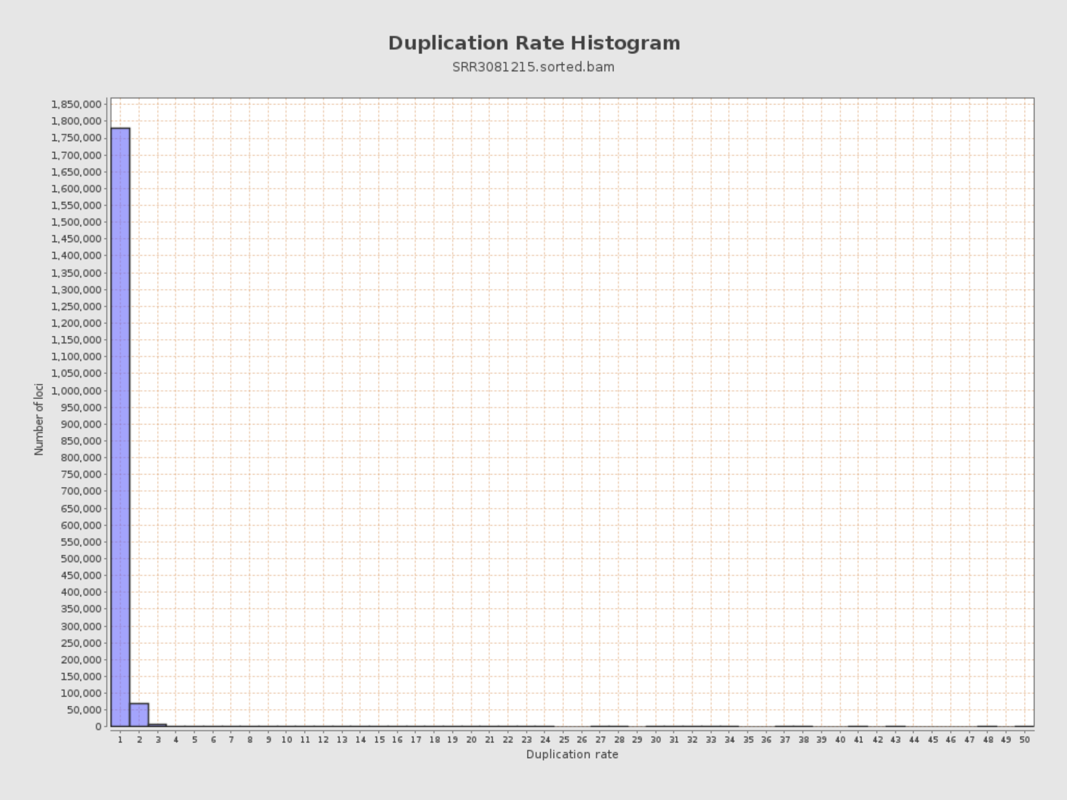
5. Results : Coverage Histogram (0-50X)



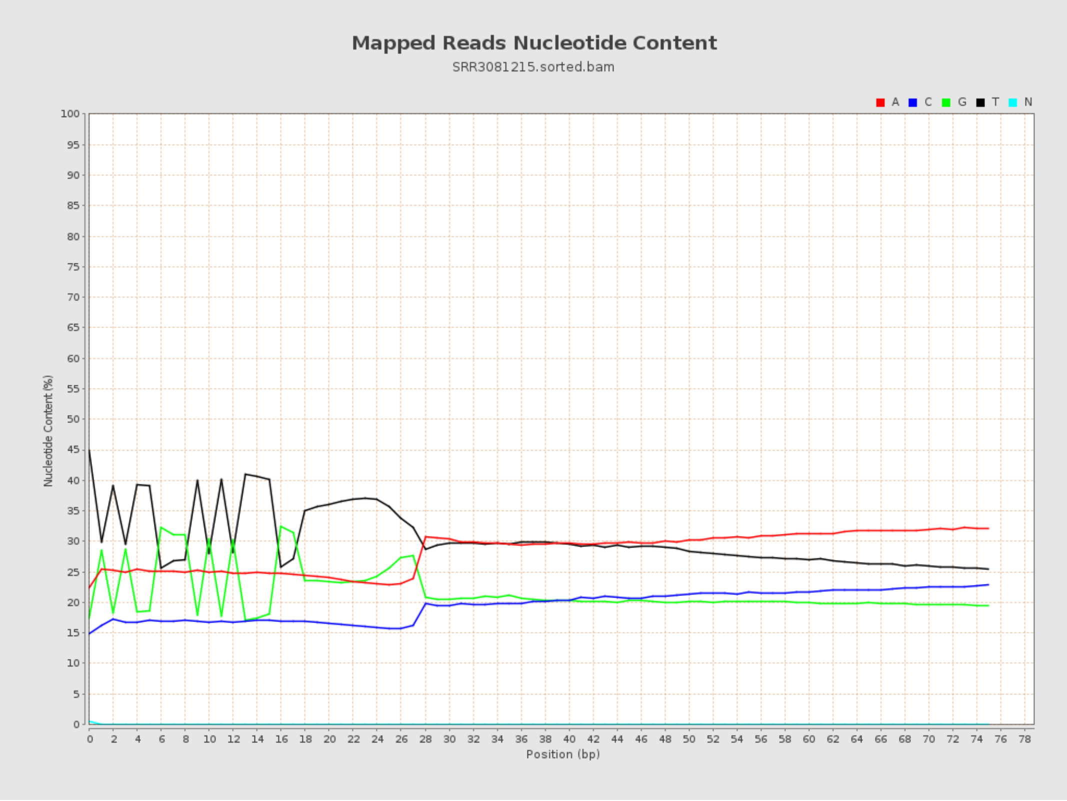
6. Results : Genome Fraction Coverage



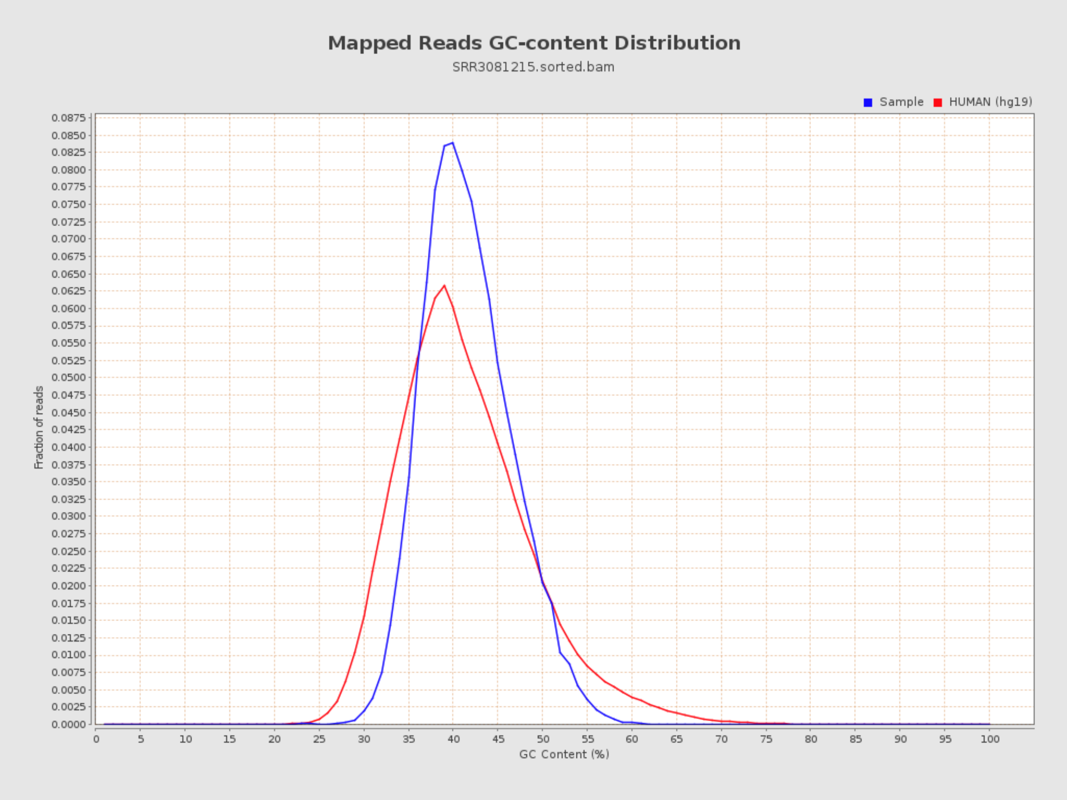
7. Results : Duplication Rate Histogram



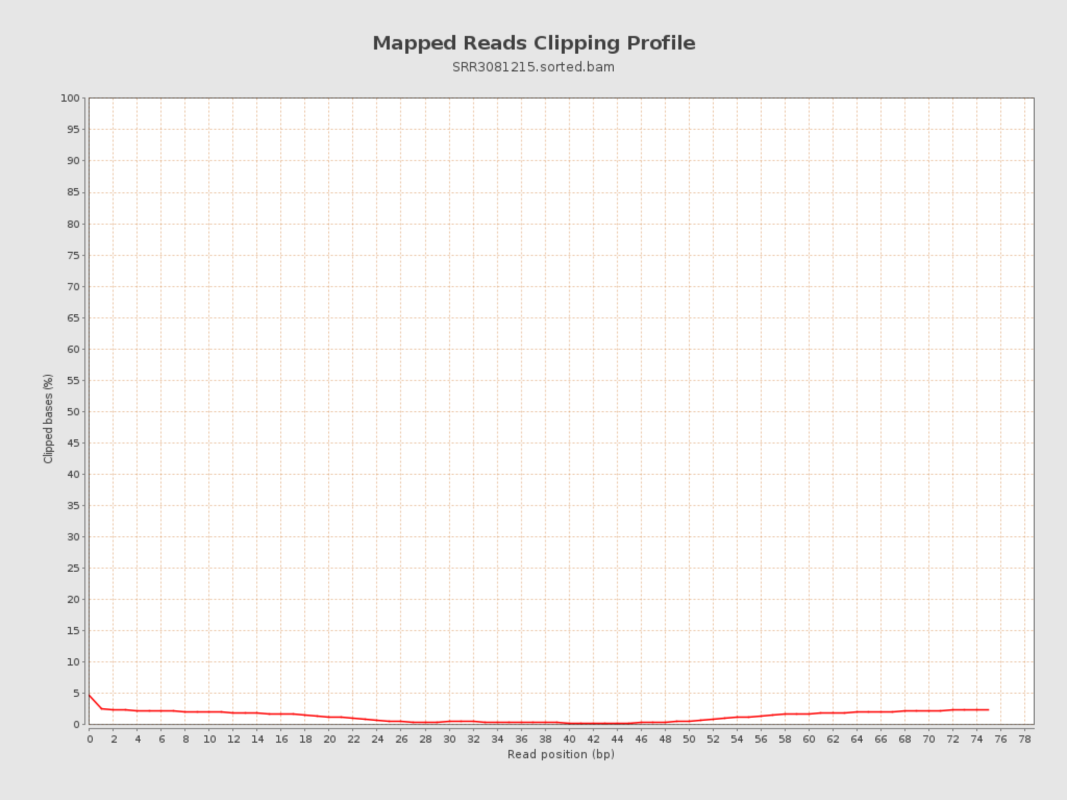
8. Results : Mapped Reads Nucleotide Content



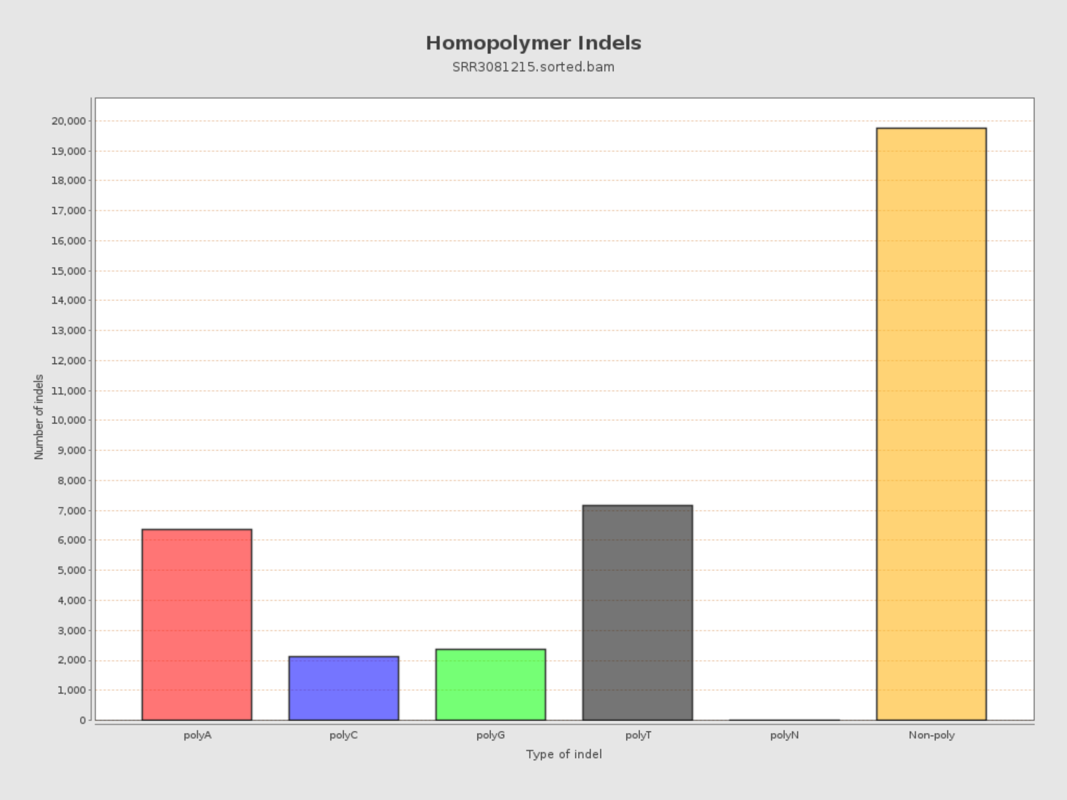
9. Results : Mapped Reads GC-content Distribution



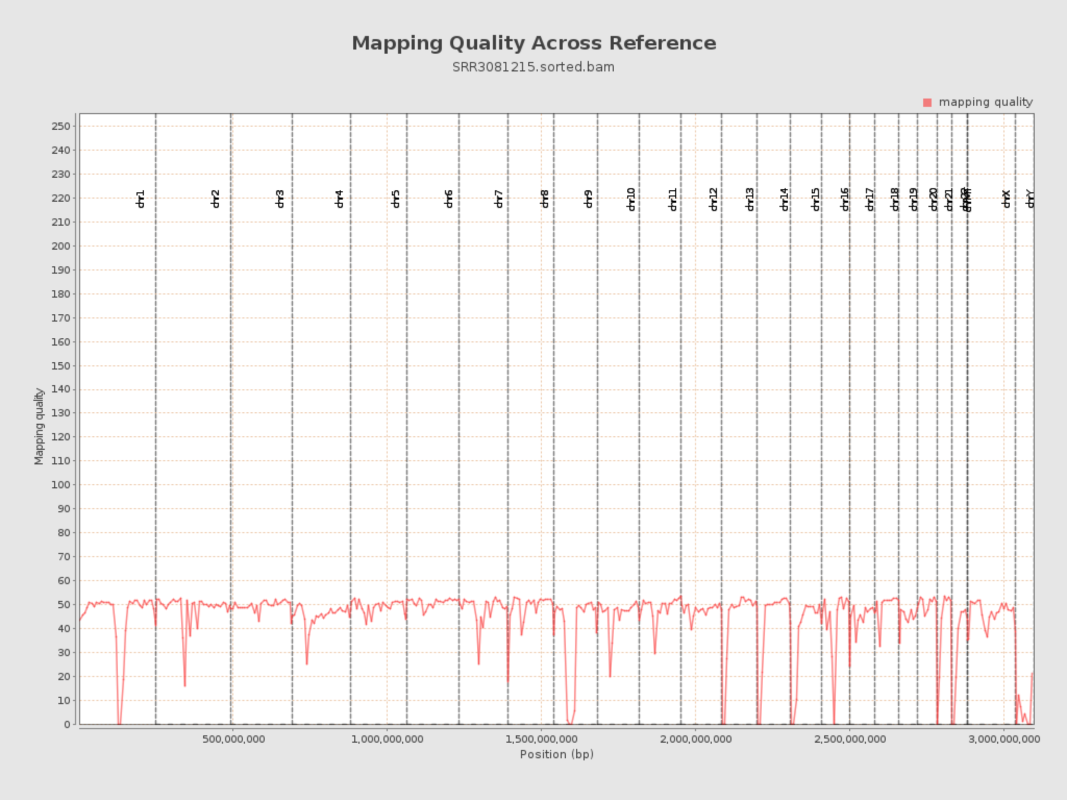
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram