Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:12:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013210.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_SRR6013210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:12:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,841,384
Mapped reads	2,474,770 / 87.1%
Unmapped reads	366,614 / 12.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,710 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	174,460 / 6.14%
Duplication rate	5.33%
Clipped reads	1,114,428 / 39.22%

2.2. ACGT Content

Number/percentage of A's	45,225,584 / 27.37%
Number/percentage of C's	30,604,081 / 18.52%
Number/percentage of T's	52,525,626 / 31.79%
Number/percentage of G's	36,817,776 / 22.29%
Number/percentage of N's	36,064 / 0.02%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0534

Standard Deviation	0.6344

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

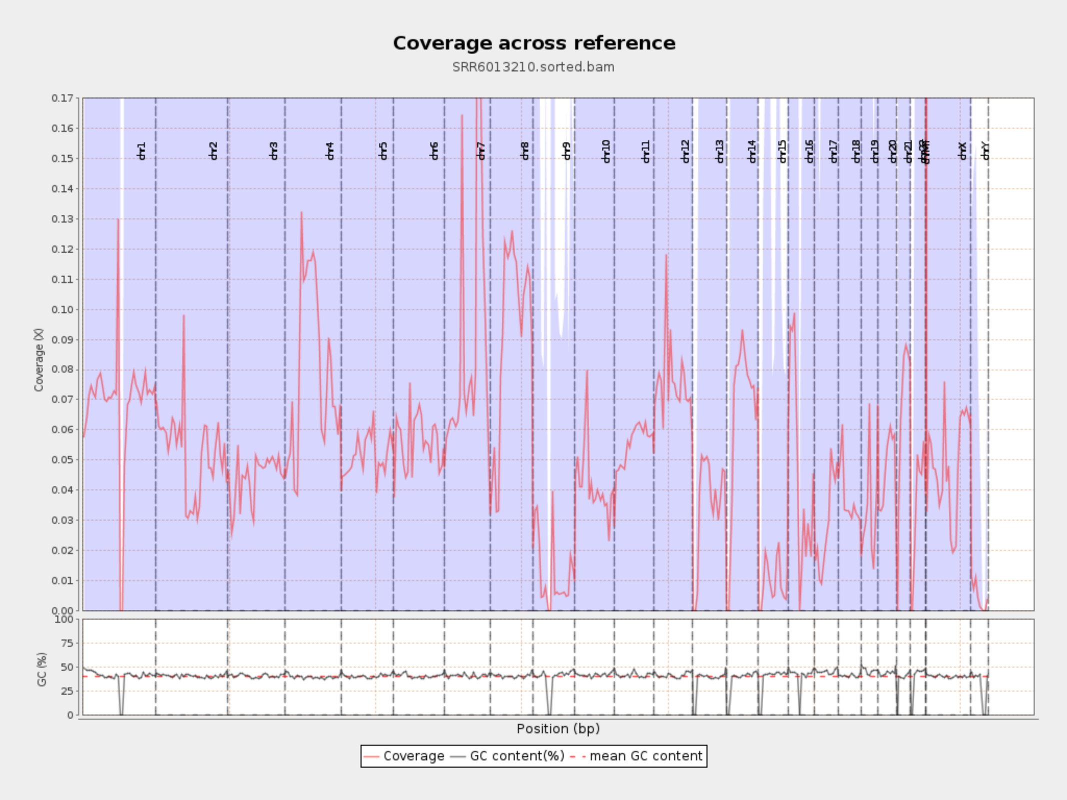
General error rate	0.83%
Mismatches	1,350,347
Insertions	11,178
Mapped reads with at least one insertion	0.45%
Deletions	36,974
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.78%

2.6. Chromosome stats

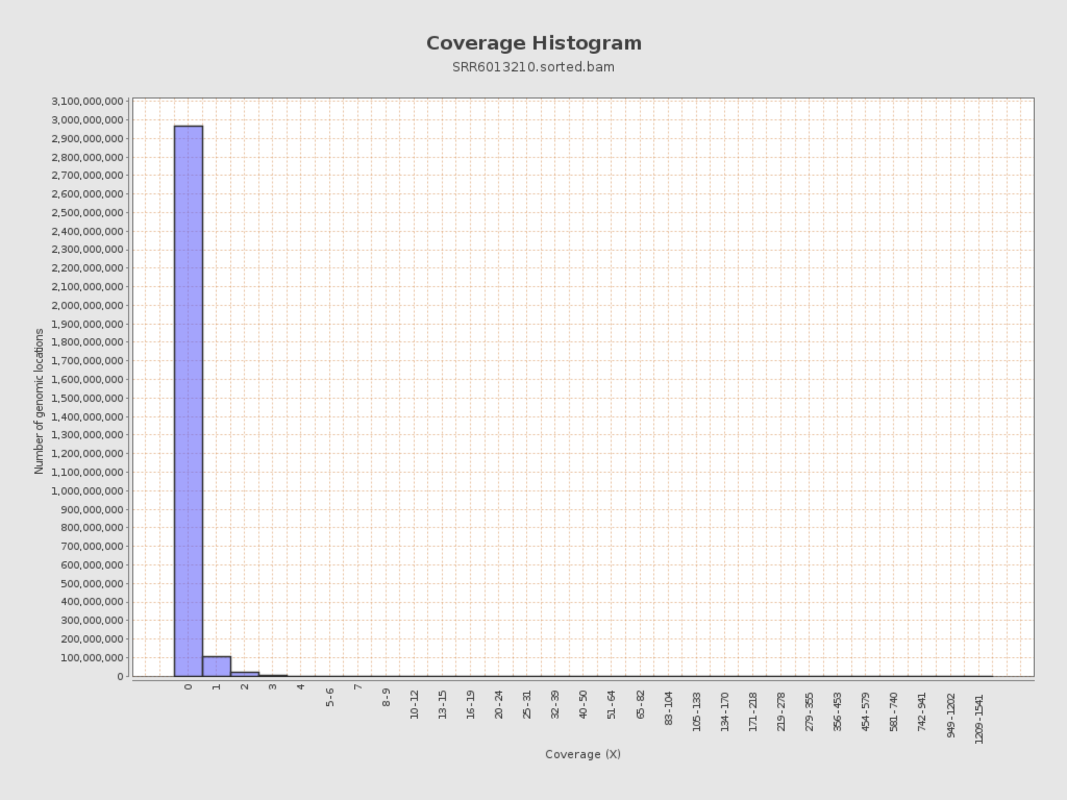
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17126589	0.0687	1.303
chr2	243199373	12703131	0.0522	0.6348
chr3	198022430	8751590	0.0442	0.2556
chr4	191154276	15506588	0.0811	0.359
chr5	180915260	9355084	0.0517	0.276
chr6	171115067	9626109	0.0563	0.3726
chr7	159138663	14312526	0.0899	1.3663

chr8	146364022	13626467	0.0931	0.7908
chr9	141213431	1711873	0.0121	0.374
chr10	135534747	5665954	0.0418	0.5377
chr11	135006516	7430755	0.055	0.3971
chr12	133851895	10206386	0.0763	0.3467
chr13	115169878	4058886	0.0352	0.2291
chr14	107349540	7051643	0.0657	0.3356
chr15	102531392	963019	0.0094	0.1218
chr16	90354753	4124892	0.0457	0.296
chr17	81195210	2320064	0.0286	0.2146
chr18	78077248	2943682	0.0377	0.8177
chr19	59128983	1990387	0.0337	0.9284
chr20	63025520	2975241	0.0472	0.2854
chr21	48129895	3150509	0.0655	0.3178
chr22	51304566	1759588	0.0343	0.2236
chrMT	16571	76325	4.6059	3.6084
chrX	155270560	7567132	0.0487	0.3097
chrY	59373566	267880	0.0045	0.0898

3. Results : Coverage across reference



4. Results : Coverage Histogram



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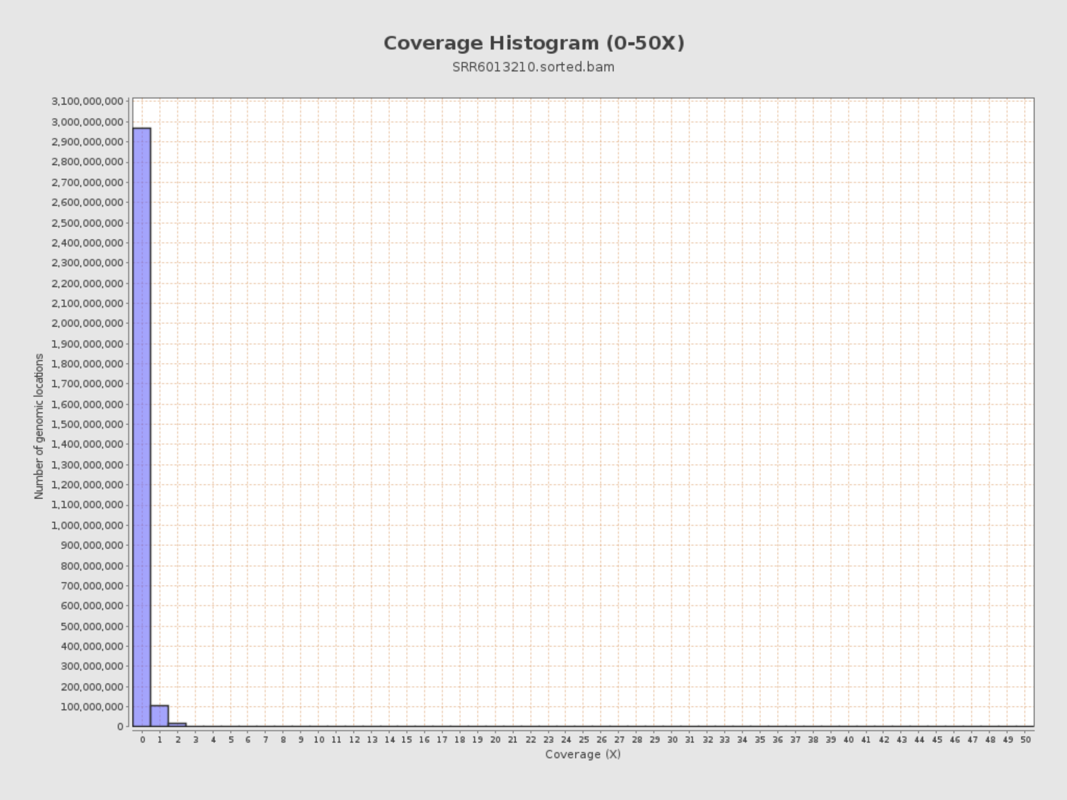
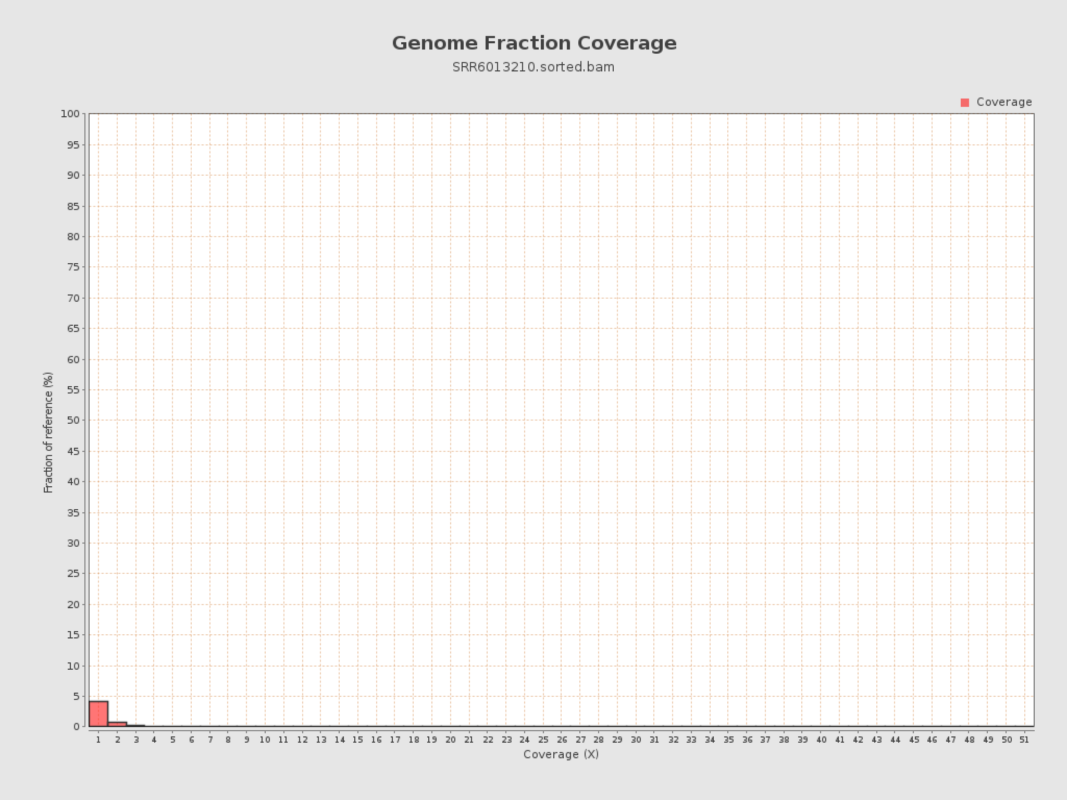
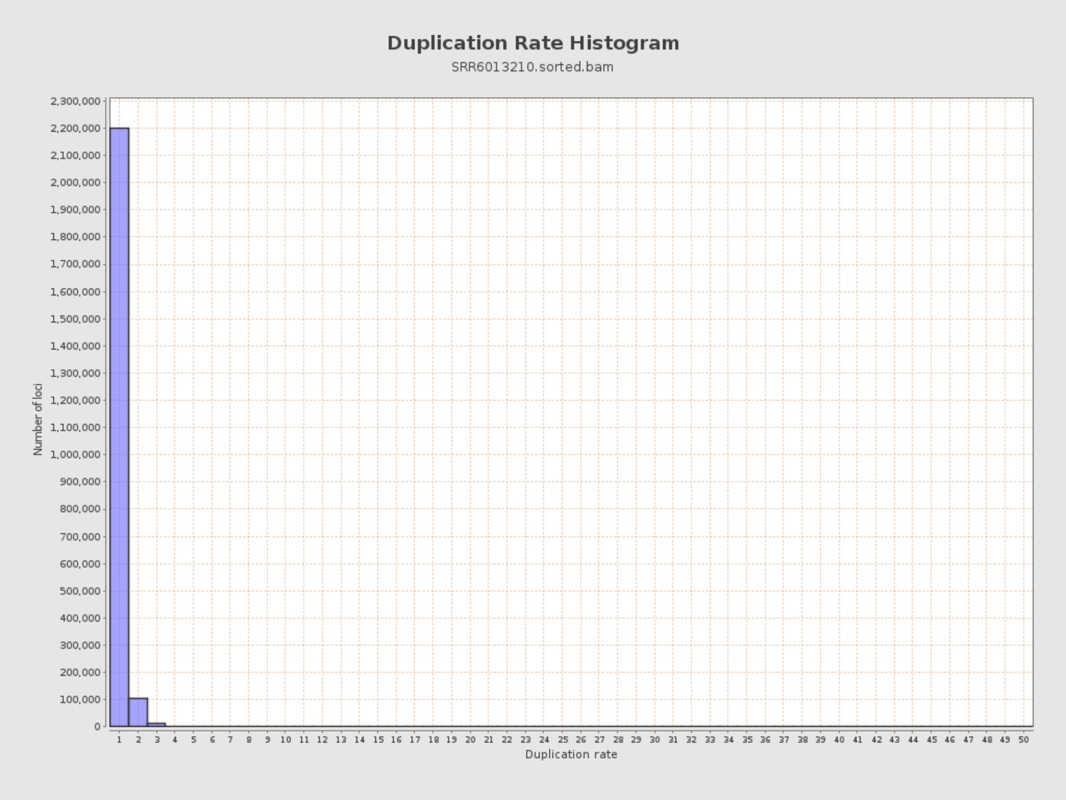
5. Results : Coverage Histogram (0-50X)



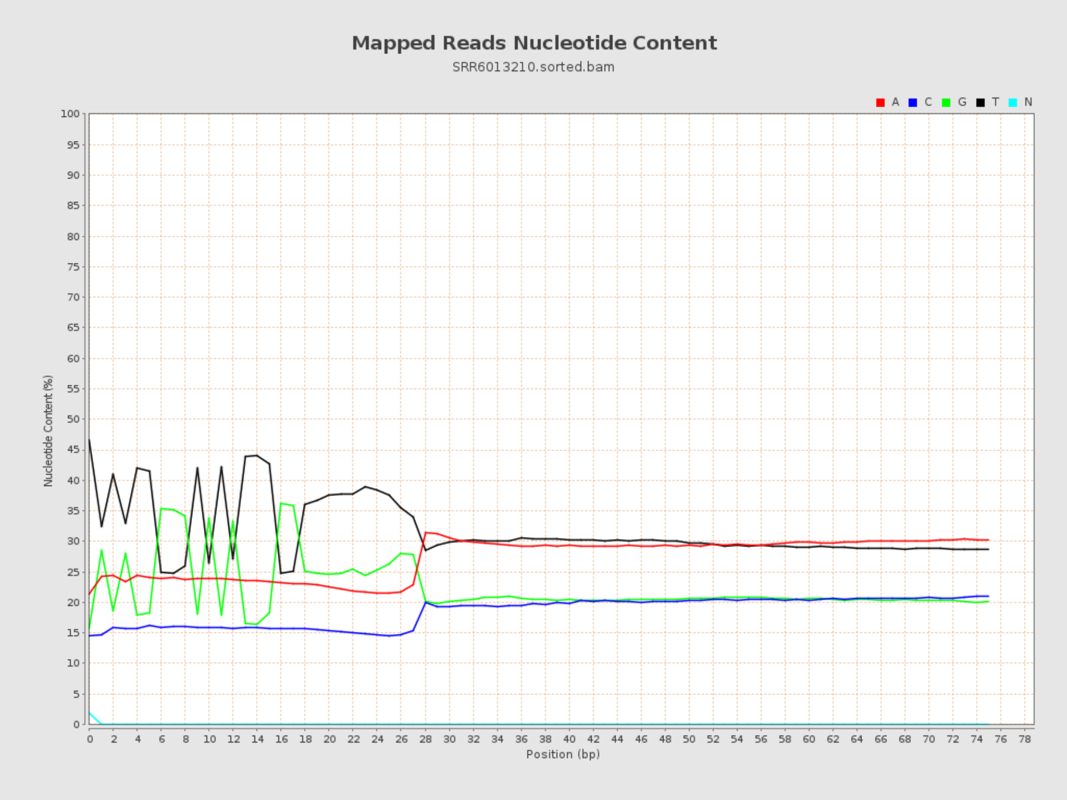
6. Results : Genome Fraction Coverage



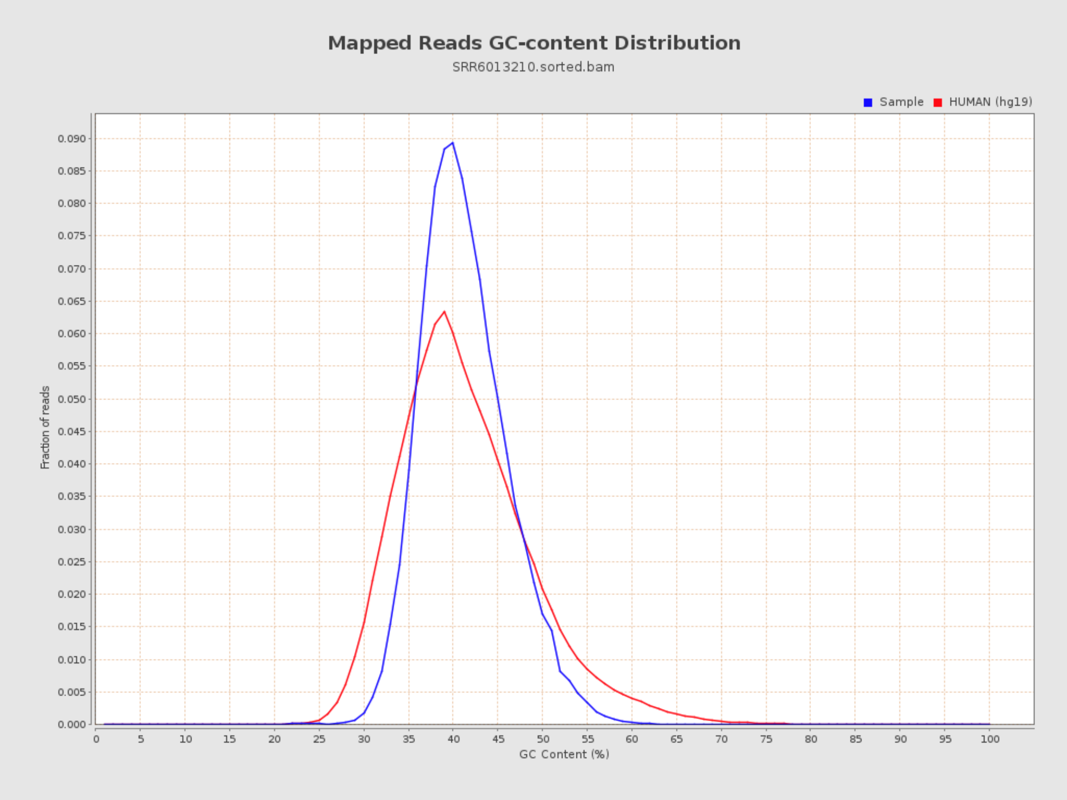
7. Results : Duplication Rate Histogram



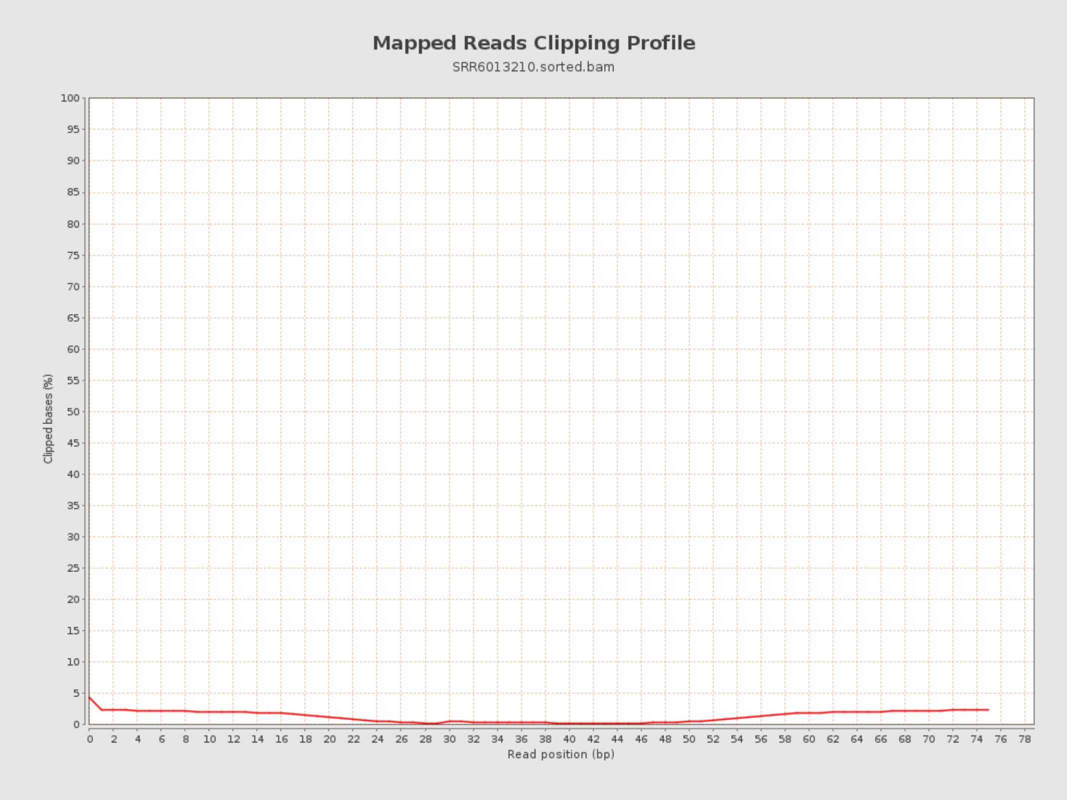
8. Results : Mapped Reads Nucleotide Content



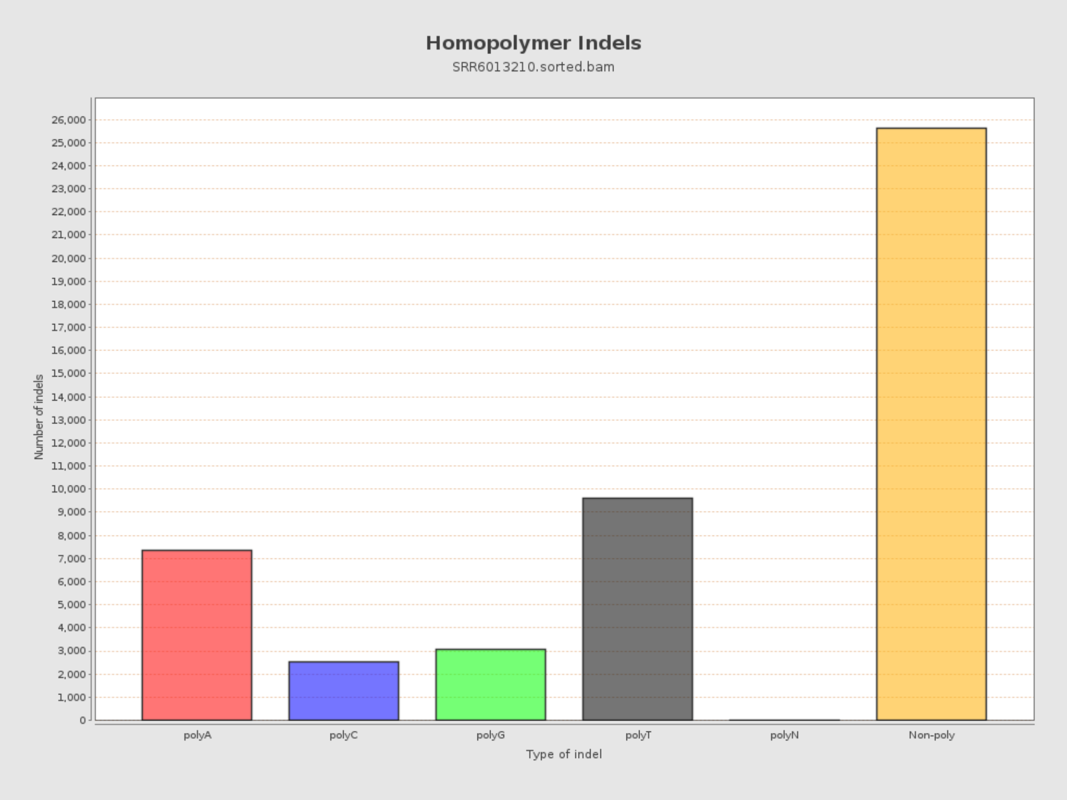
9. Results : Mapped Reads GC-content Distribution



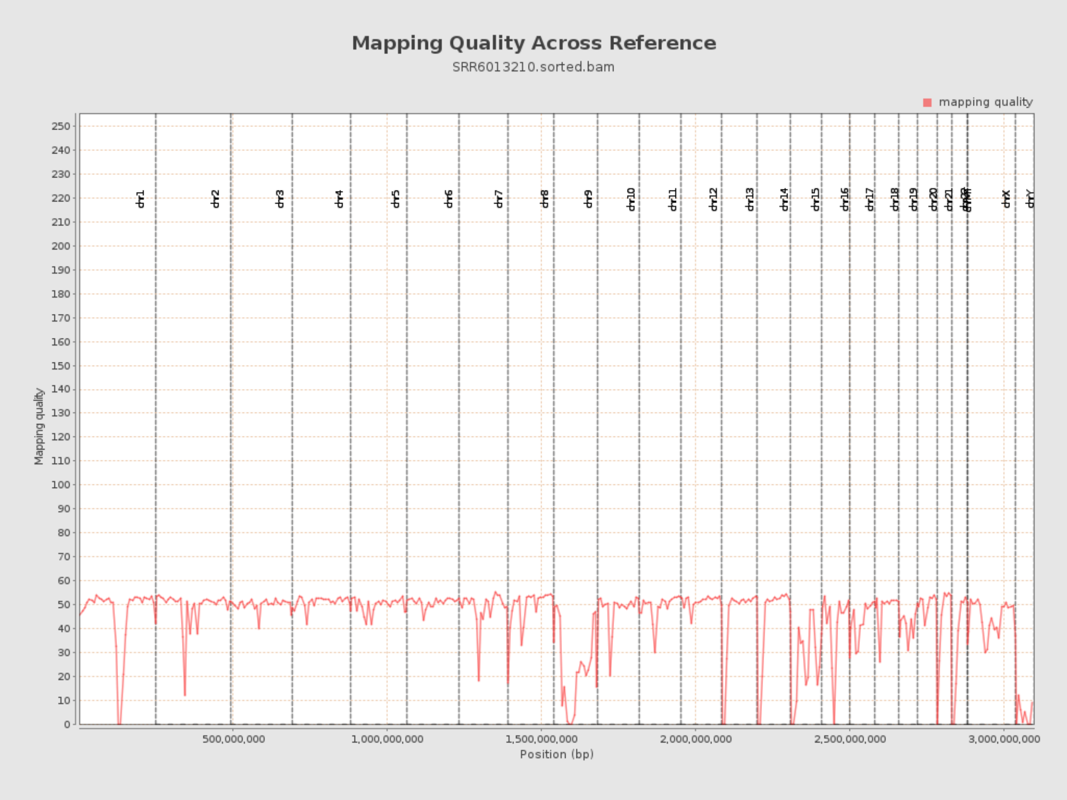
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram