Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:34:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240210.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_SRR6240210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:34:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,585,392
Mapped reads	2,676,897 / 74.66%
Unmapped reads	908,495 / 25.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,337 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	247,704 / 6.91%
Duplication rate	7.49%
Clipped reads	1,530,330 / 42.68%

2.2. ACGT Content

Number/percentage of A's	45,472,044 / 26.69%
Number/percentage of C's	31,887,677 / 18.71%
Number/percentage of T's	53,430,199 / 31.36%
Number/percentage of G's	39,591,297 / 23.23%
Number/percentage of N's	15,745 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0551

Standard Deviation	0.4861

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

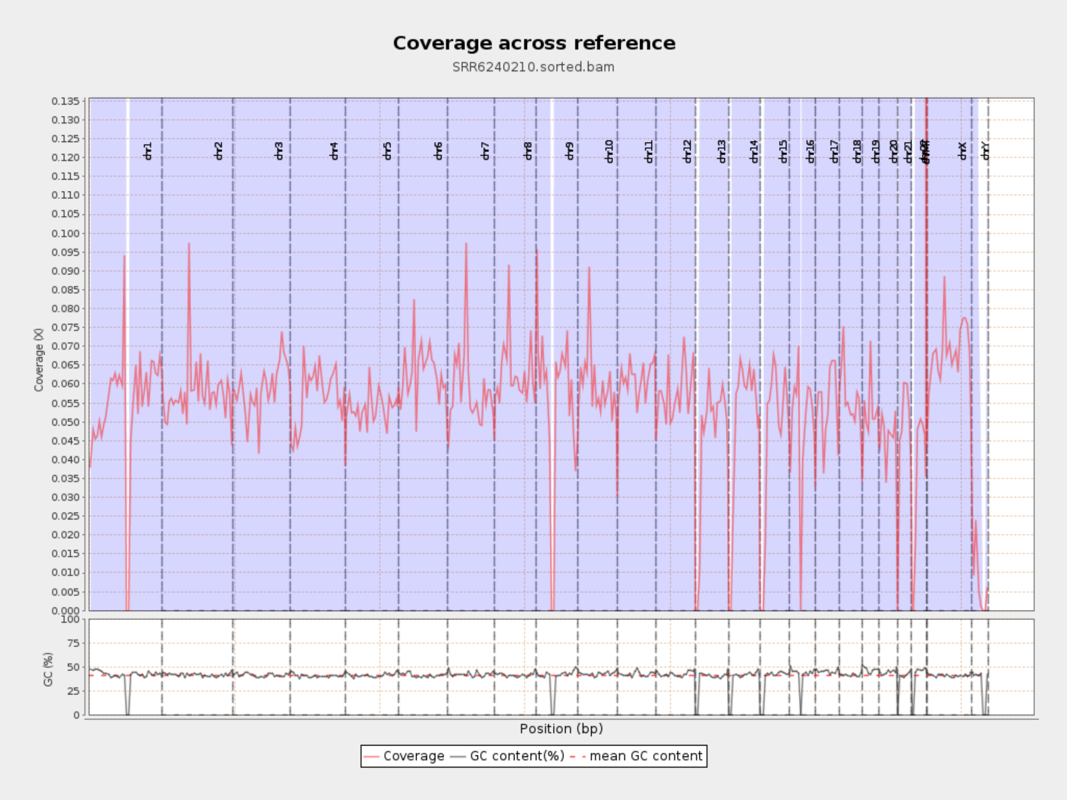
General error rate	0.85%
Mismatches	1,420,005
Insertions	11,086
Mapped reads with at least one insertion	0.41%
Deletions	41,722
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.32%

2.6. Chromosome stats

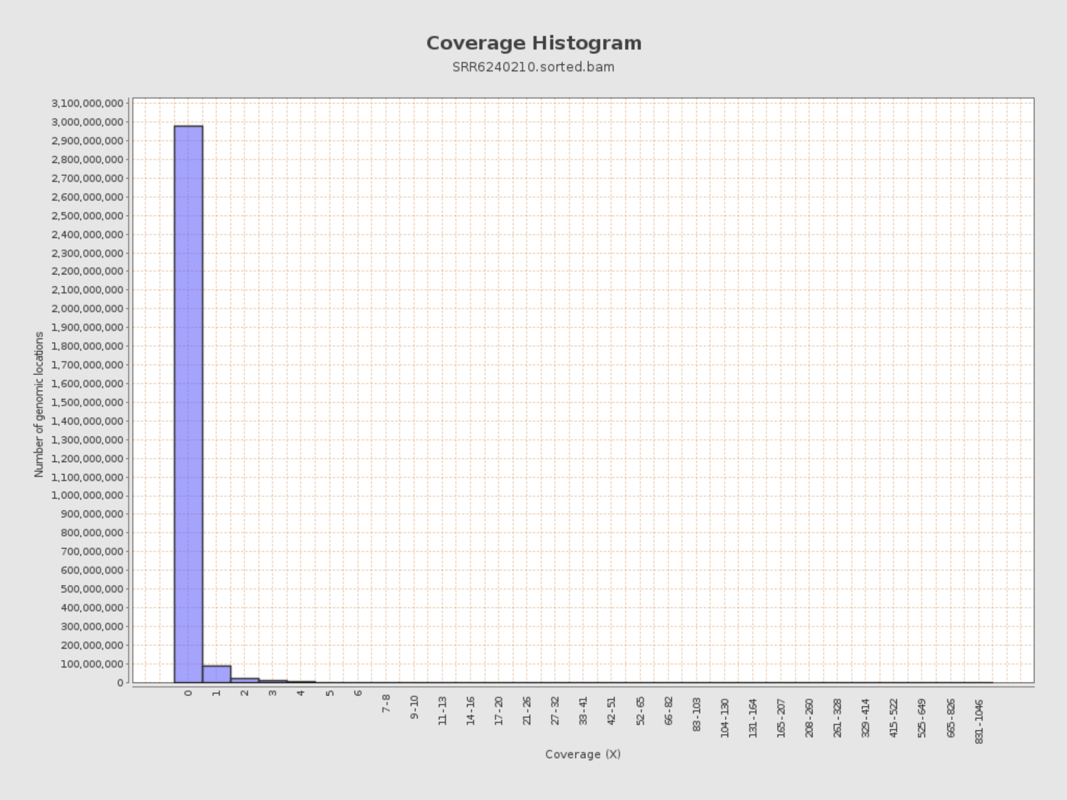
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13508457	0.0542	0.8648
chr2	243199373	14083048	0.0579	0.5795
chr3	198022430	11684693	0.059	0.3323
chr4	191154276	10822716	0.0566	0.3446
chr5	180915260	9698795	0.0536	0.3176
chr6	171115067	10734913	0.0627	0.3991
chr7	159138663	9420124	0.0592	0.6111

chr8	146364022	9202540	0.0629	0.5281
chr9	141213431	7597197	0.0538	0.4602
chr10	135534747	8151359	0.0601	0.4645
chr11	135006516	8190100	0.0607	0.4752
chr12	133851895	7739318	0.0578	0.3376
chr13	115169878	5157696	0.0448	0.2885
chr14	107349540	5342477	0.0498	0.3464
chr15	102531392	4712385	0.046	0.3094
chr16	90354753	4462576	0.0494	0.3464
chr17	81195210	4410089	0.0543	0.3654
chr18	78077248	4431462	0.0568	0.8115
chr19	59128983	3127951	0.0529	0.5849
chr20	63025520	2879747	0.0457	0.3066
chr21	48129895	2241703	0.0466	0.3184
chr22	51304566	1707605	0.0333	0.2467
chrMT	16571	126952	7.6611	5.6417
chrX	155270560	10580985	0.0681	0.403
chrY	59373566	454918	0.0077	0.1637

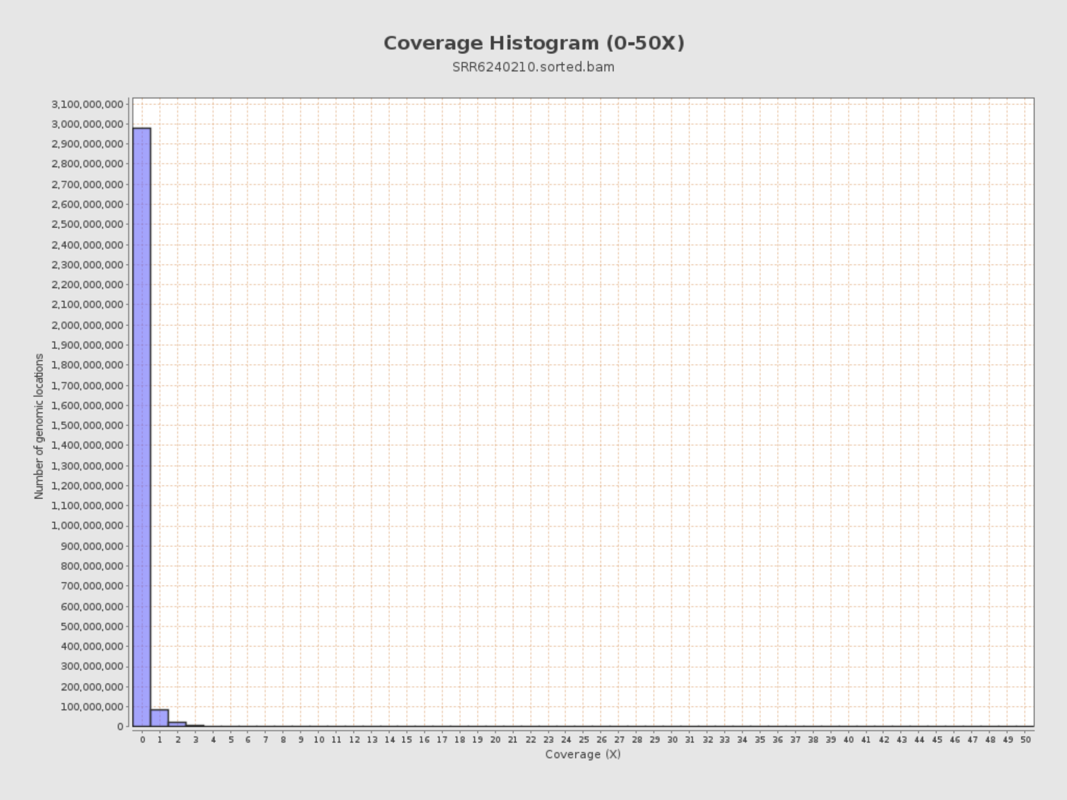
3. Results : Coverage across reference



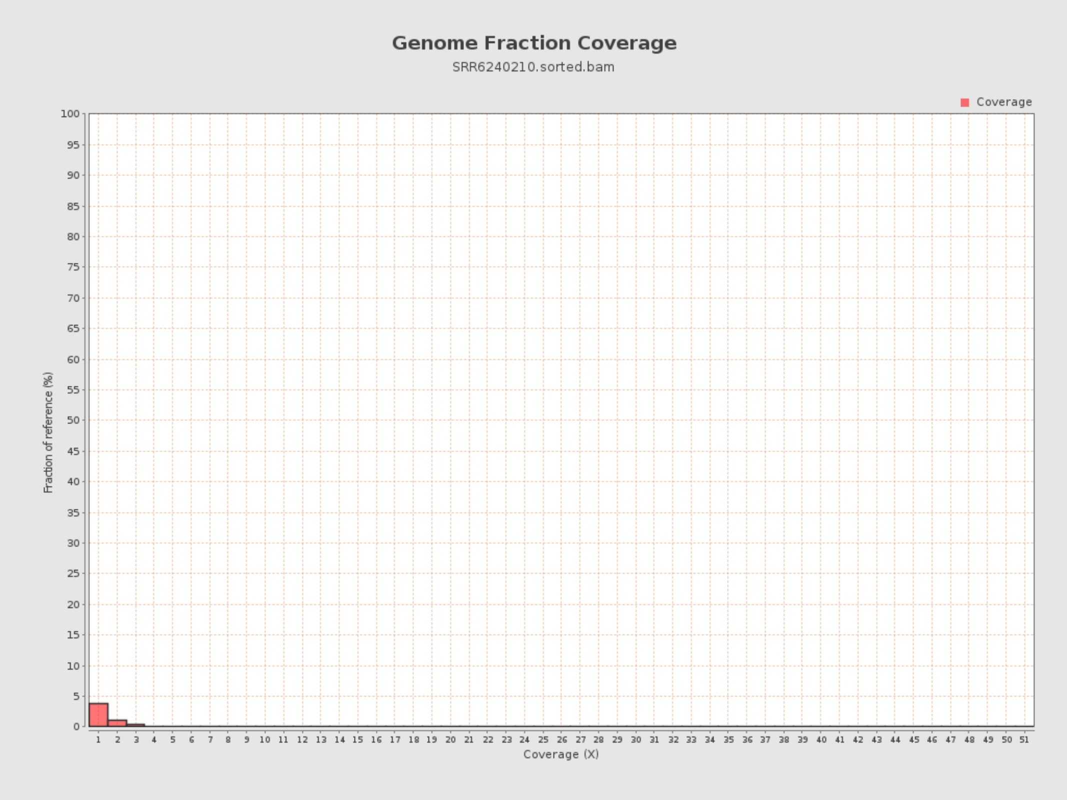
4. Results : Coverage Histogram



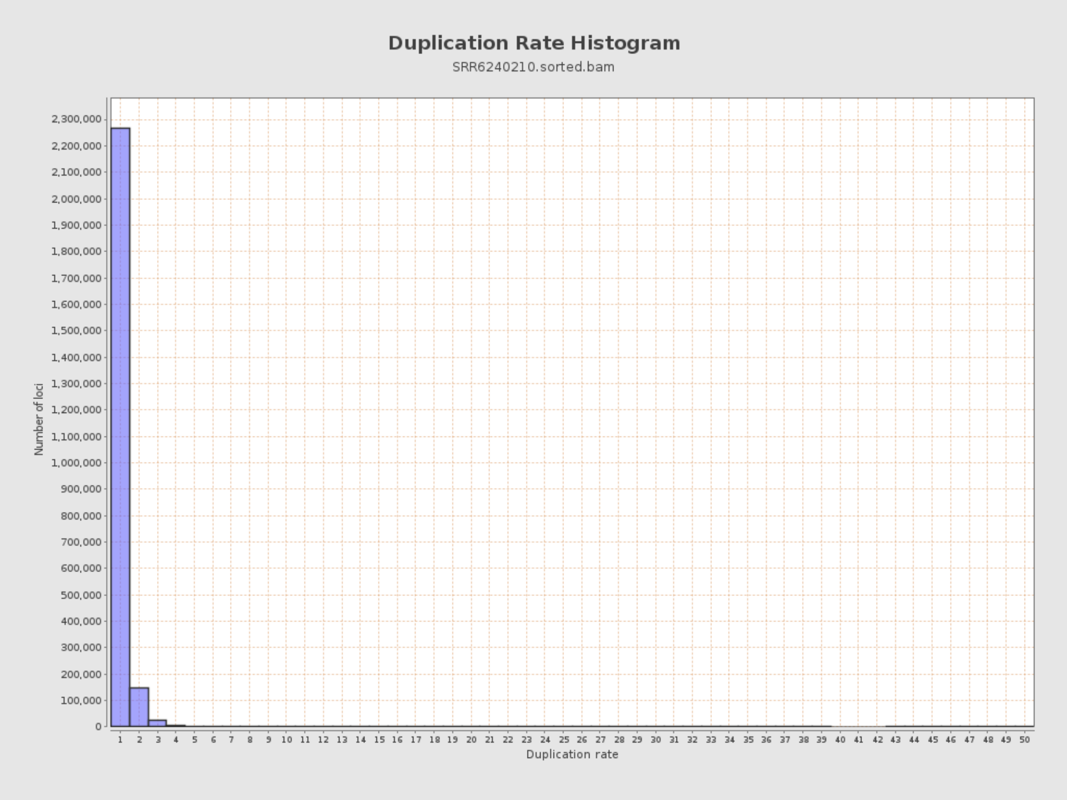
5. Results : Coverage Histogram (0-50X)



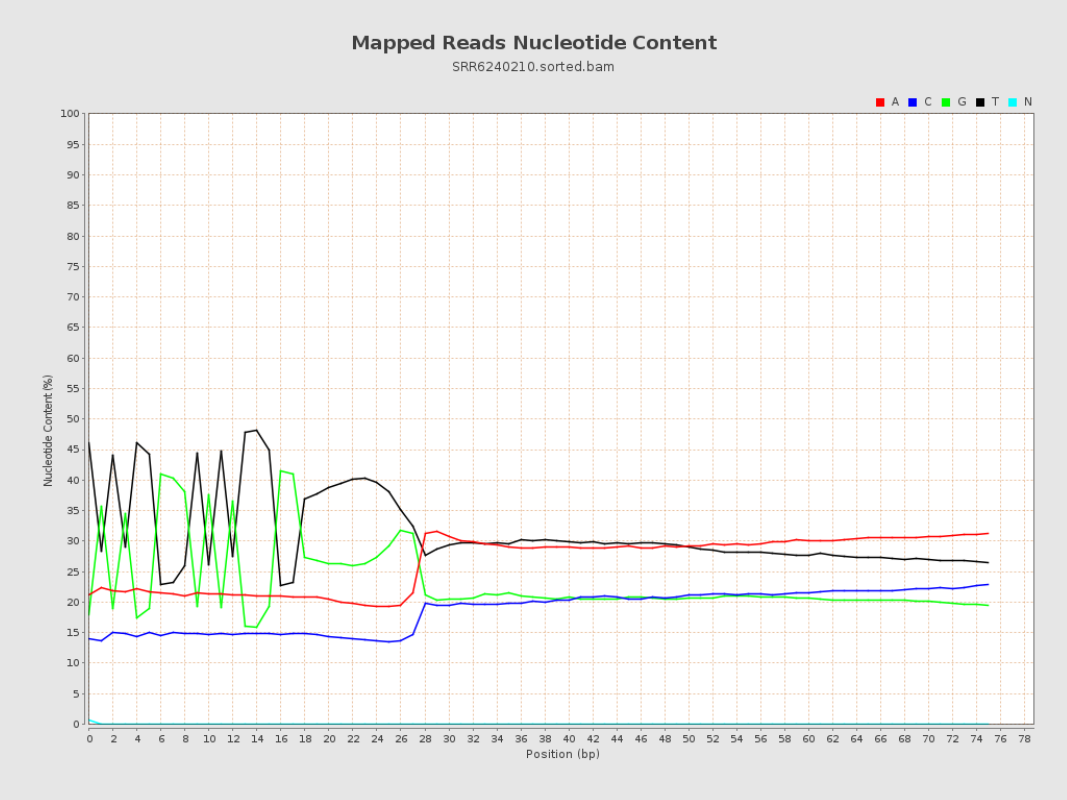
6. Results : Genome Fraction Coverage



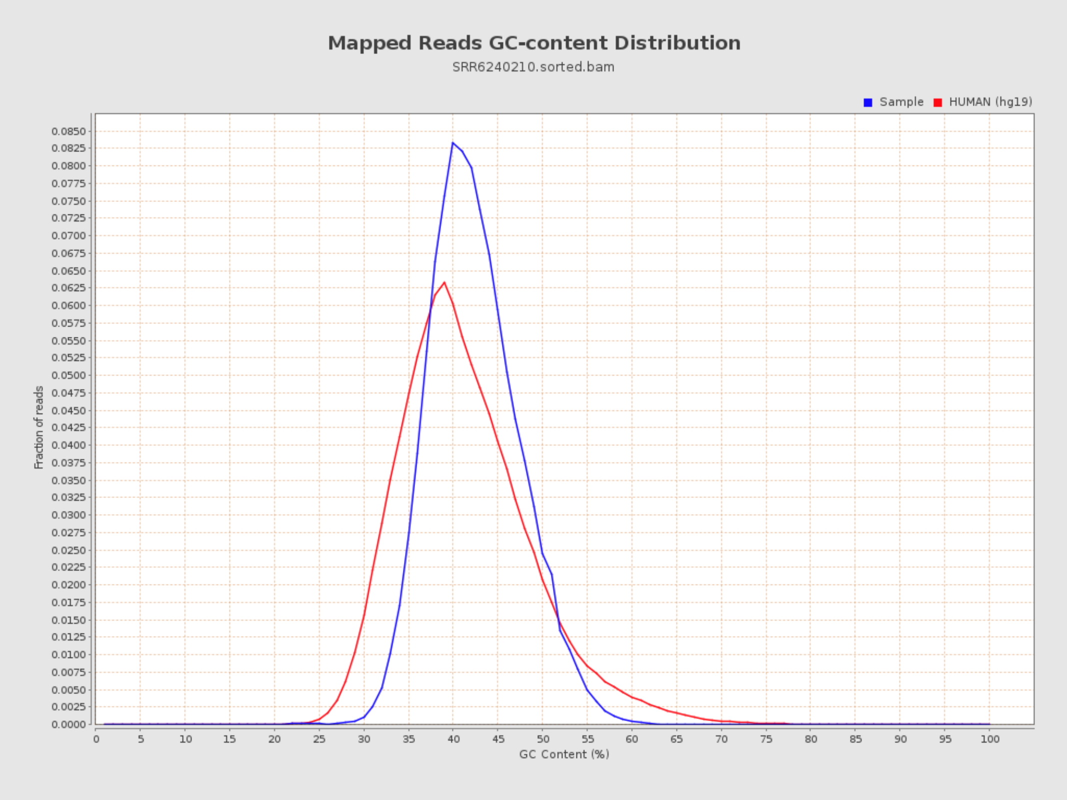
7. Results : Duplication Rate Histogram



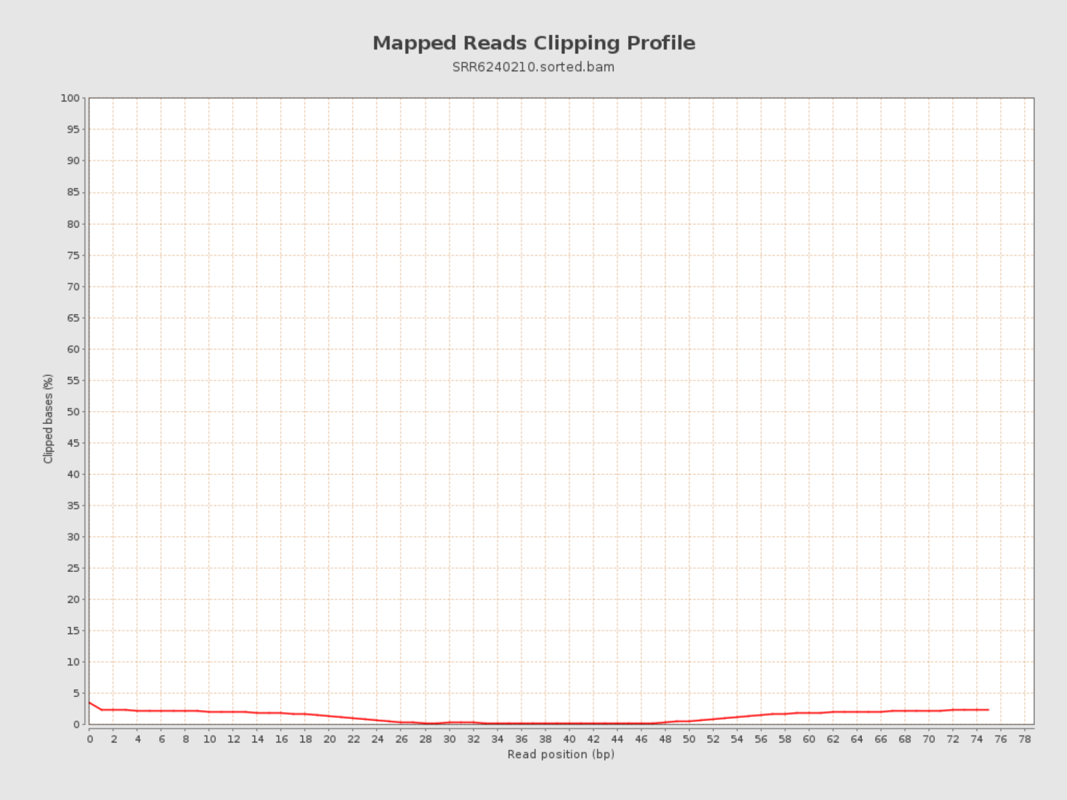
8. Results : Mapped Reads Nucleotide Content



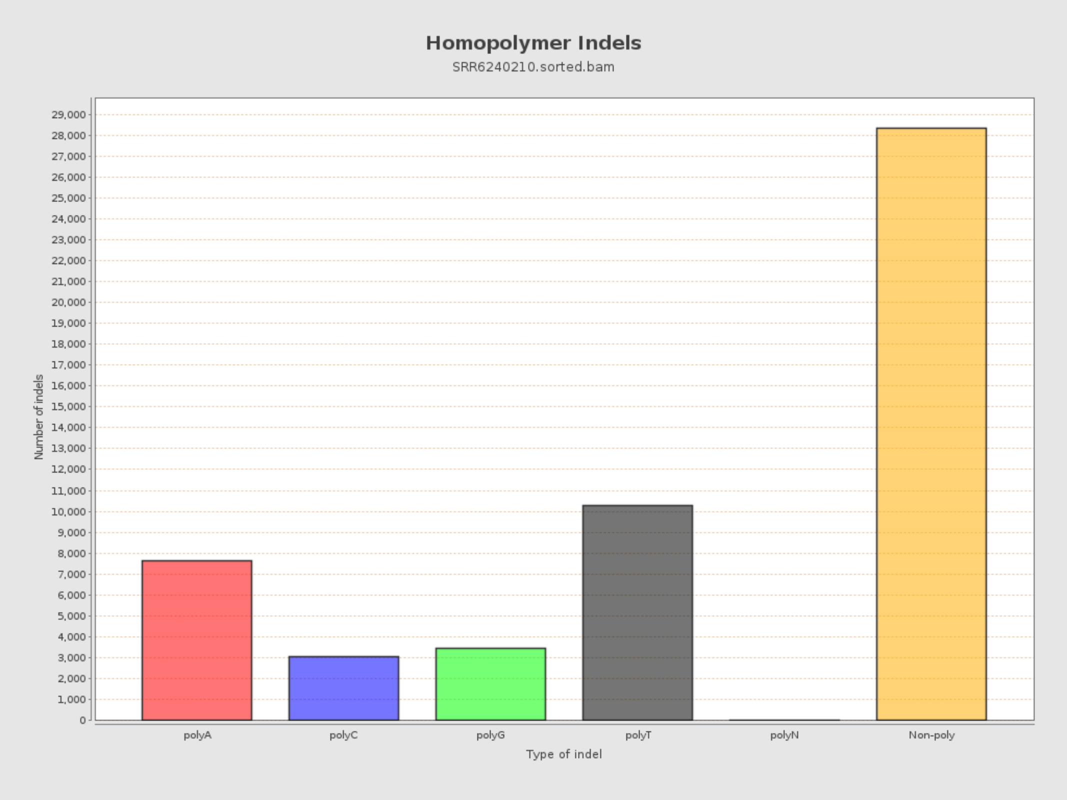
9. Results : Mapped Reads GC-content Distribution



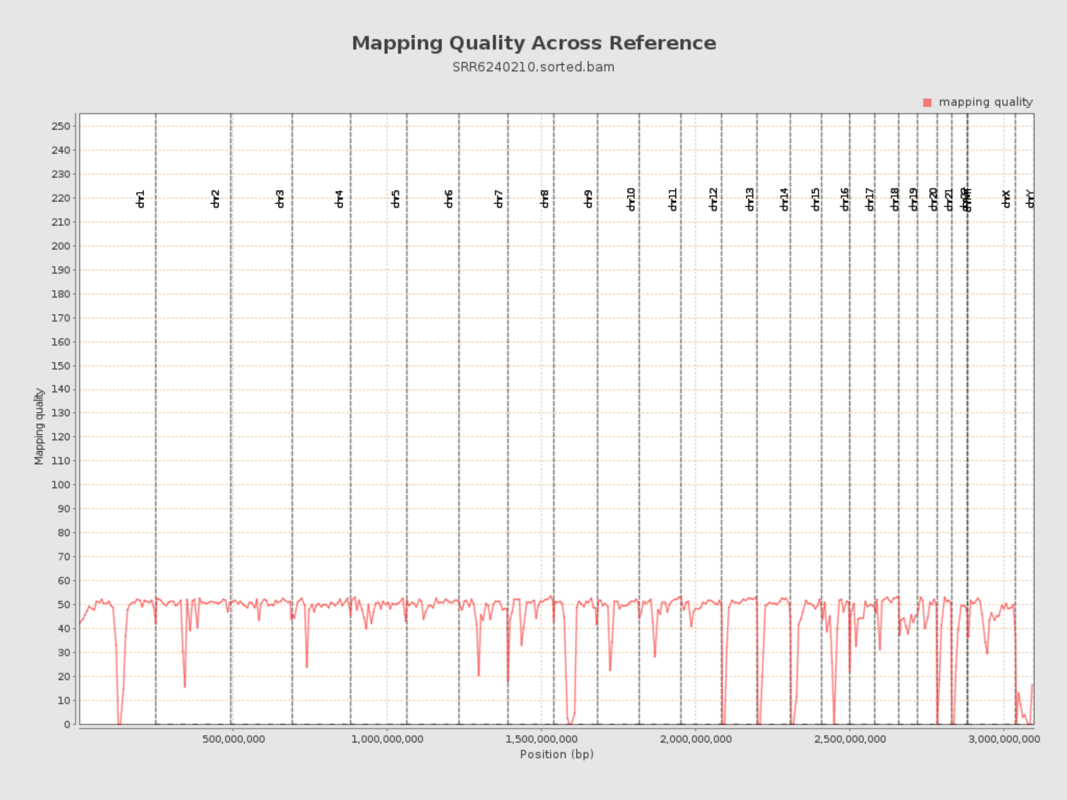
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram