Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:14:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234093.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_SRR6234093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:14:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,218,685
Mapped reads	5,892,307 / 94.75%
Unmapped reads	326,378 / 5.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,850 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	904,820 / 14.55%
Duplication rate	12.57%
Clipped reads	3,045,575 / 48.97%

2.2. ACGT Content

Number/percentage of A's	98,477,085 / 25.8%
Number/percentage of C's	69,434,256 / 18.19%
Number/percentage of T's	123,391,056 / 32.33%
Number/percentage of G's	90,300,983 / 23.66%
Number/percentage of N's	37,637 / 0.01%
GC Percentage	41.85%

2.3. Coverage

Mean	0.1233

Standard Deviation	1.2533

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

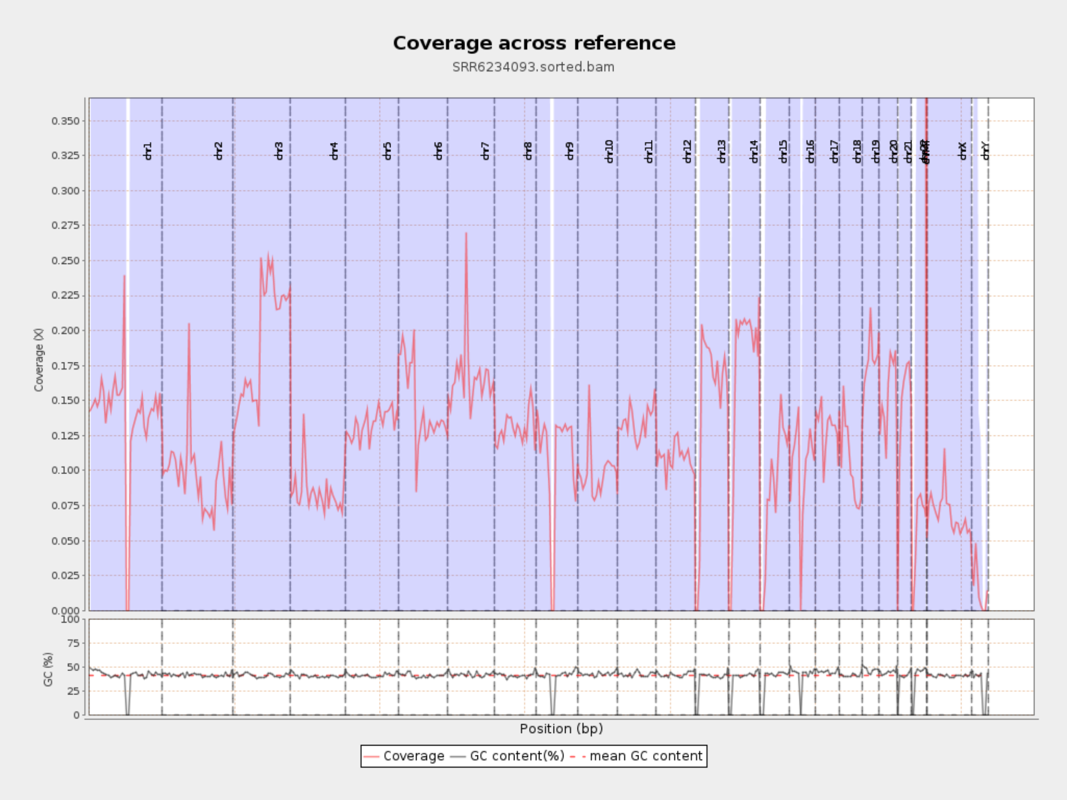
General error rate	0.55%
Mismatches	2,038,575
Insertions	25,302
Mapped reads with at least one insertion	0.43%
Deletions	82,296
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44.28%

2.6. Chromosome stats

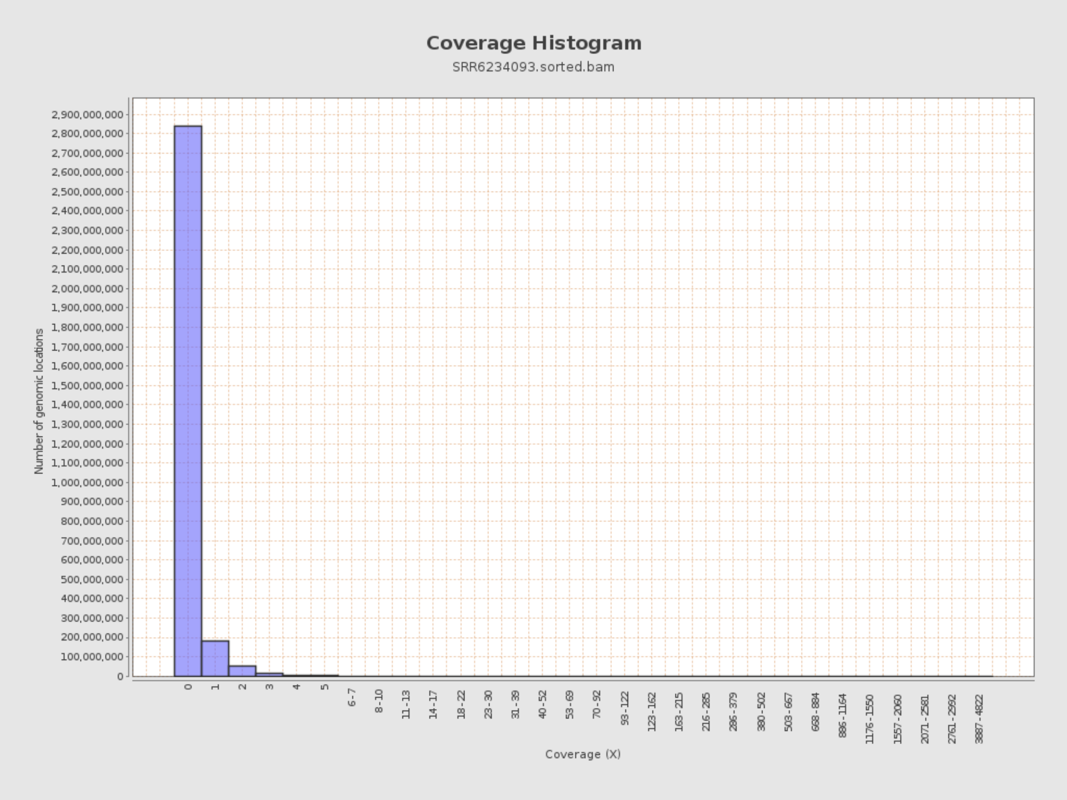
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34859279	0.1399	2.4395
chr2	243199373	23415432	0.0963	2.2255
chr3	198022430	37798348	0.1909	0.6153
chr4	191154276	16036348	0.0839	0.509
chr5	180915260	24124226	0.1333	0.5277
chr6	171115067	25114162	0.1468	0.8526
chr7	159138663	26668755	0.1676	1.7757

chr8	146364022	19136041	0.1307	1.4371
chr9	141213431	15222714	0.1078	0.8207
chr10	135534747	13268194	0.0979	0.8139
chr11	135006516	18047741	0.1337	1.0511
chr12	133851895	14594777	0.109	0.4895
chr13	115169878	16972033	0.1474	0.6076
chr14	107349540	17834233	0.1661	0.6355
chr15	102531392	8955602	0.0873	0.4618
chr16	90354753	9308227	0.103	0.581
chr17	81195210	10469339	0.1289	0.6364
chr18	78077248	8198625	0.105	1.9953
chr19	59128983	10609644	0.1794	1.3797
chr20	63025520	9665163	0.1534	0.6303
chr21	48129895	6786896	0.141	0.5769
chr22	51304566	2800537	0.0546	0.3124
chrMT	16571	326700	19.7152	12.8951
chrX	155270560	10731426	0.0691	0.541
chrY	59373566	839136	0.0141	0.3106

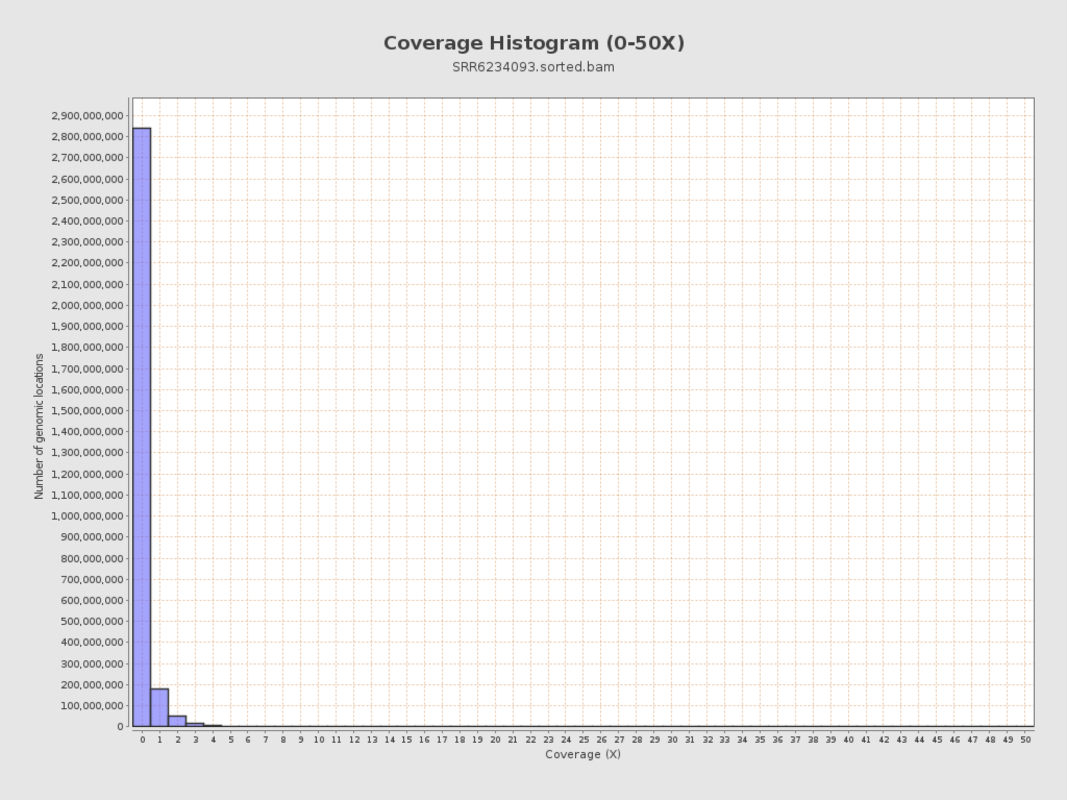
3. Results : Coverage across reference



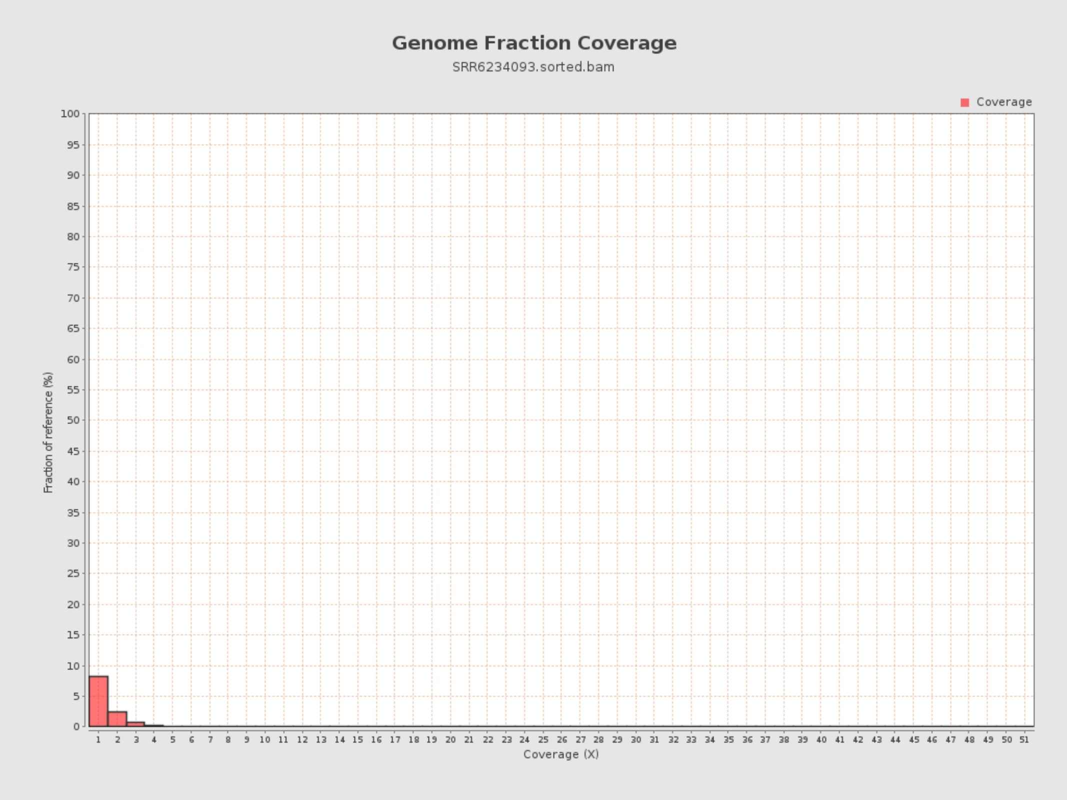
4. Results : Coverage Histogram



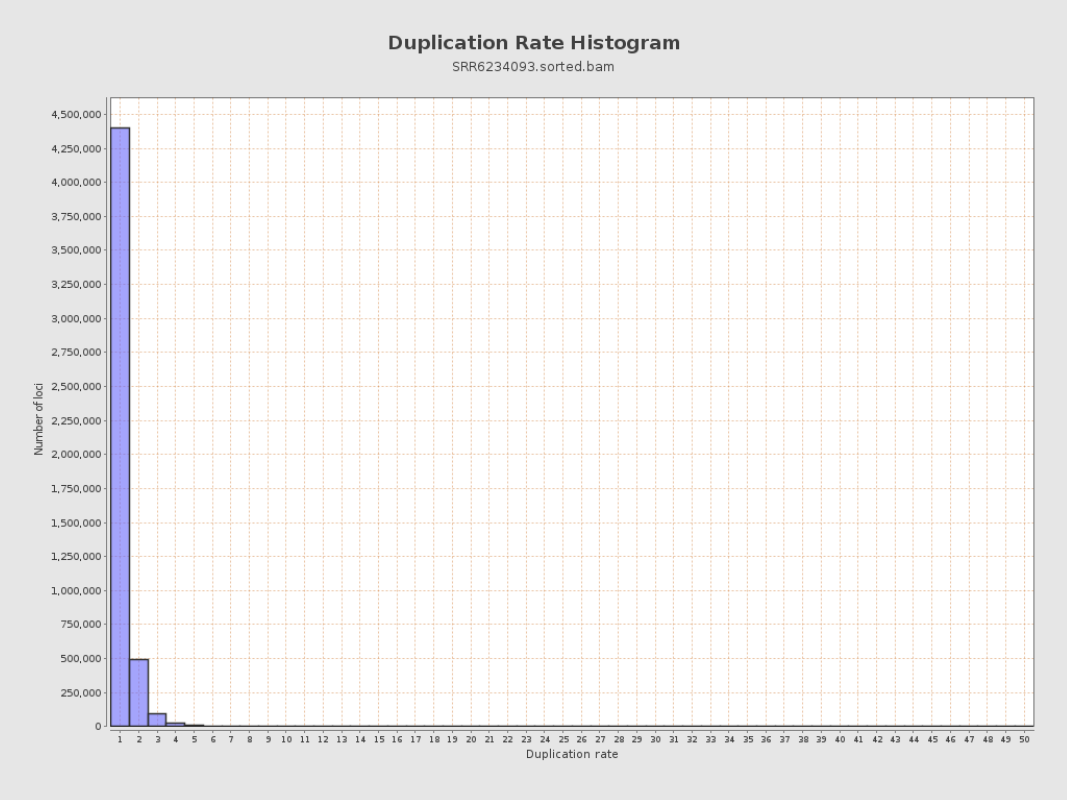
5. Results : Coverage Histogram (0-50X)



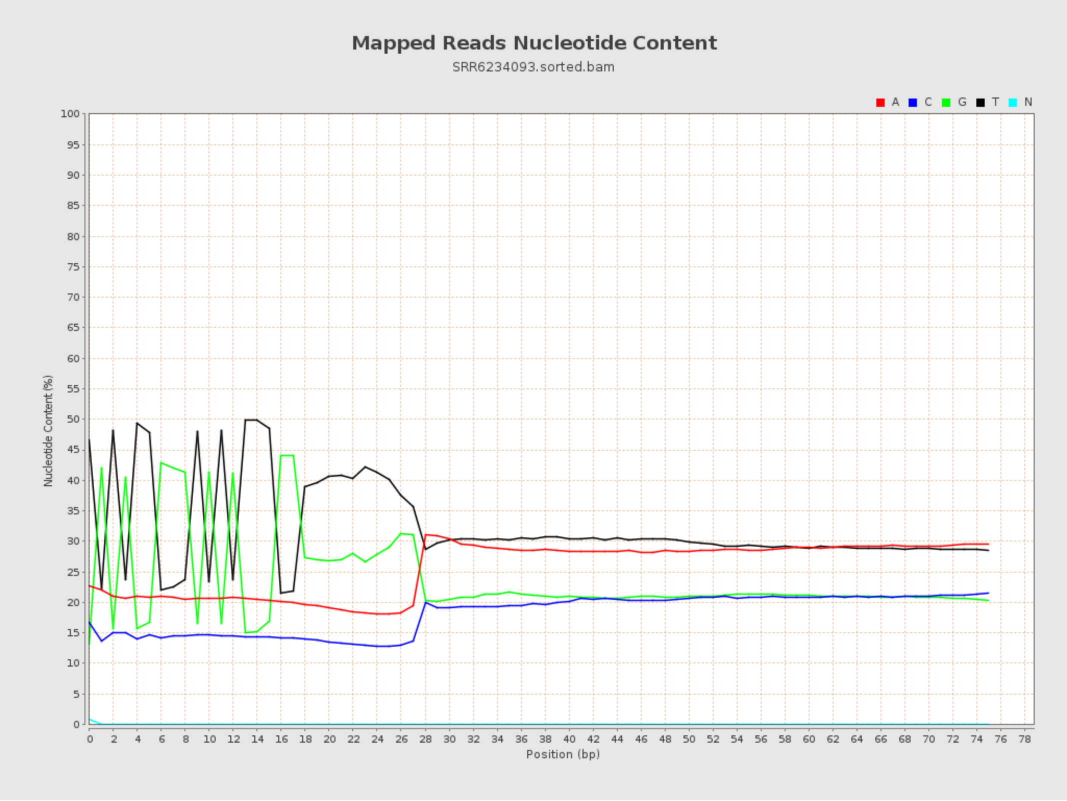
6. Results : Genome Fraction Coverage



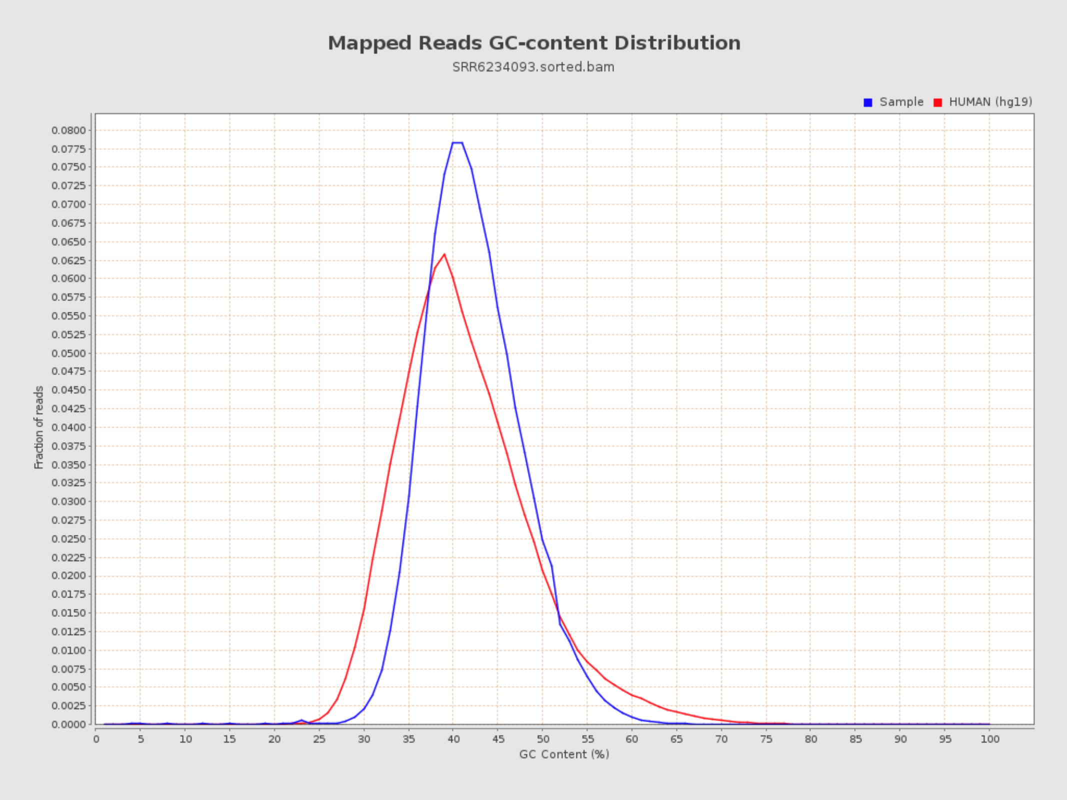
7. Results : Duplication Rate Histogram



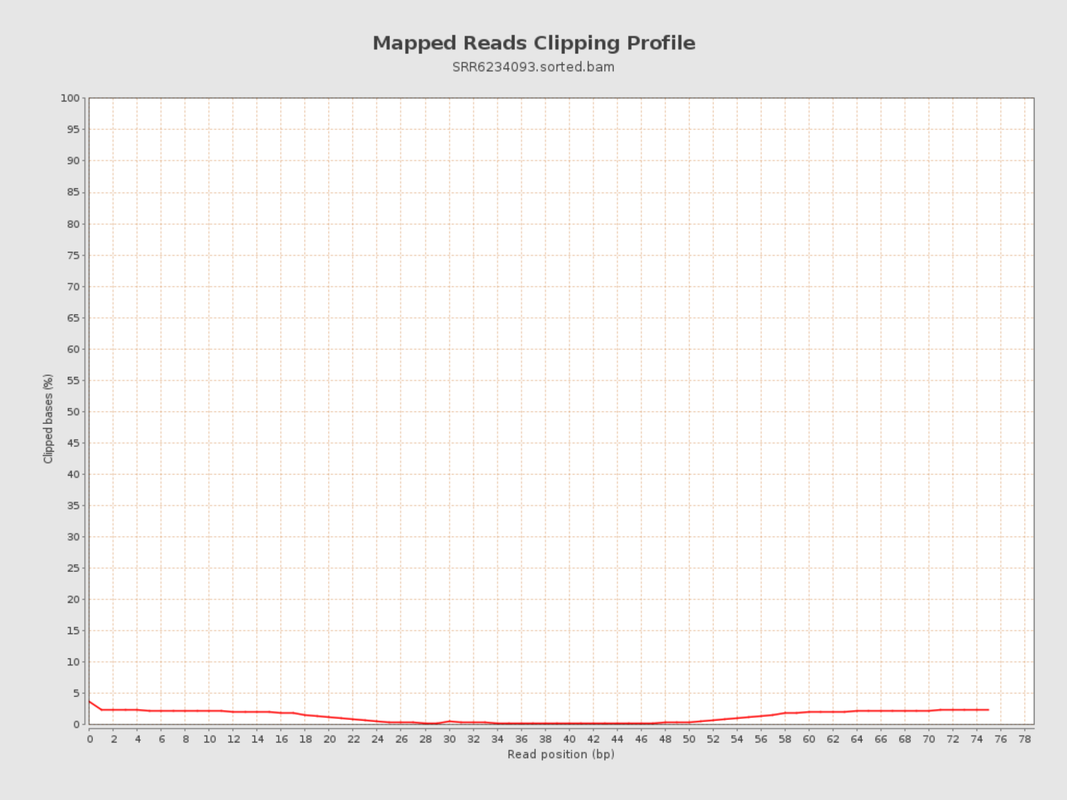
8. Results : Mapped Reads Nucleotide Content



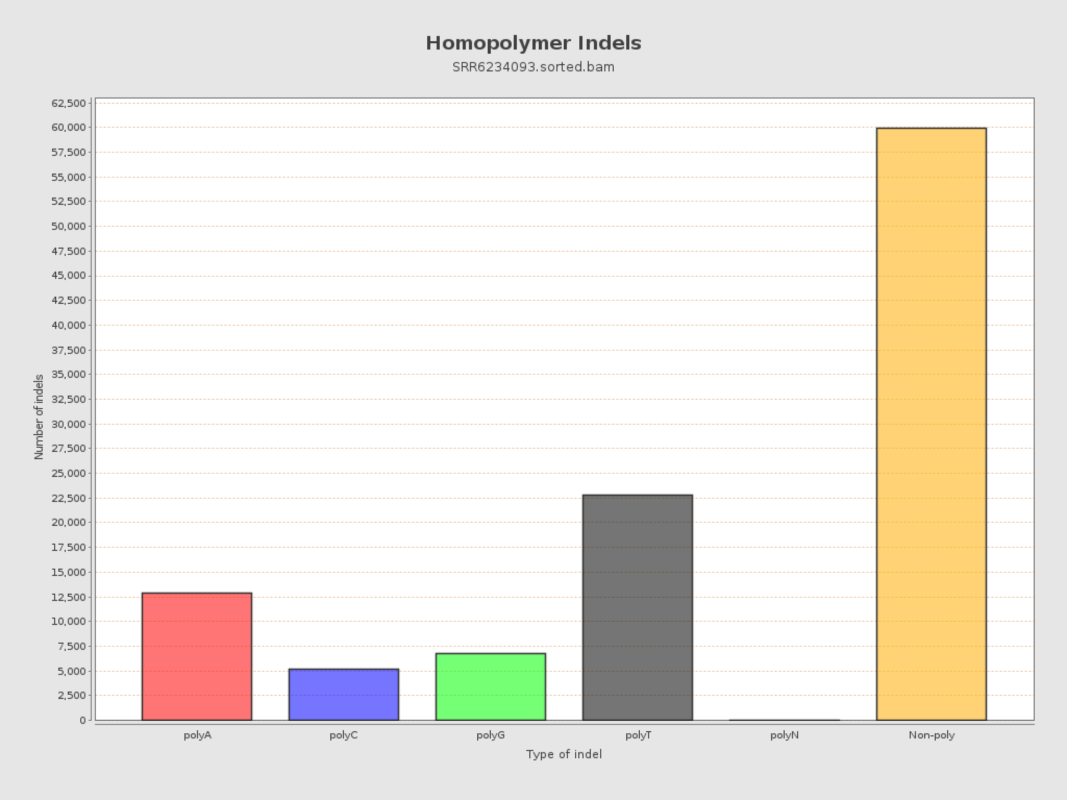
9. Results : Mapped Reads GC-content Distribution



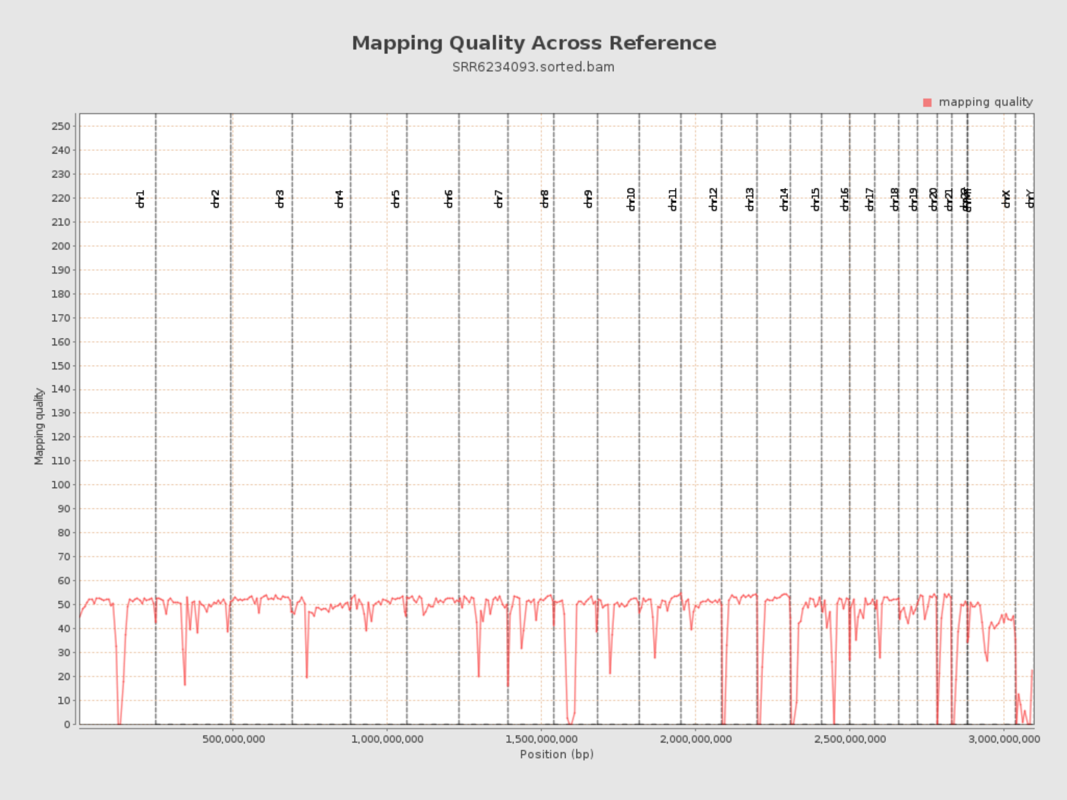
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram