Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:23:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234065.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_SRR6234065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:23:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,289,275
Mapped reads	4,967,784 / 93.92%
Unmapped reads	321,491 / 6.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,364 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	517,560 / 9.79%
Duplication rate	4.37%
Clipped reads	2,011,951 / 38.04%

2.2. ACGT Content

Number/percentage of A's	87,986,280 / 26.17%
Number/percentage of C's	60,653,520 / 18.04%
Number/percentage of T's	97,181,854 / 28.9%
Number/percentage of G's	90,349,514 / 26.87%
Number/percentage of N's	71,219 / 0.02%
GC Percentage	44.91%

2.3. Coverage

Mean	0.1087

Standard Deviation	37.3352

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

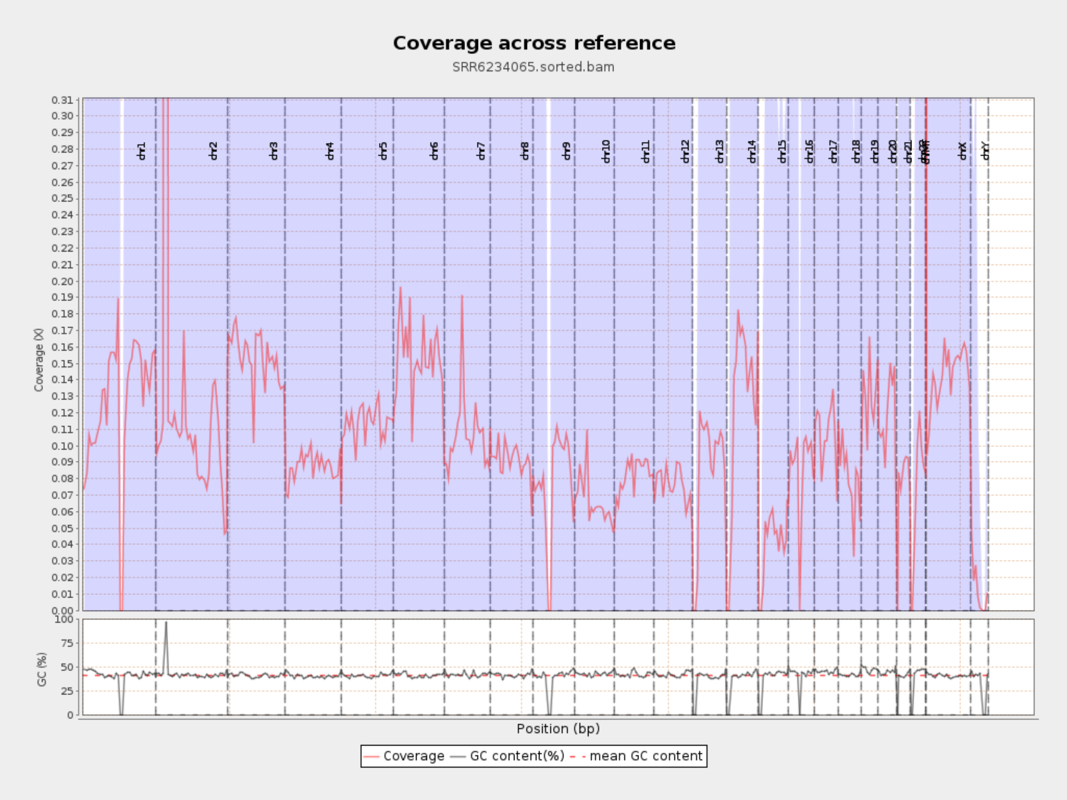
General error rate	0.64%
Mismatches	2,122,870
Insertions	22,250
Mapped reads with at least one insertion	0.44%
Deletions	71,744
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.74%

2.6. Chromosome stats

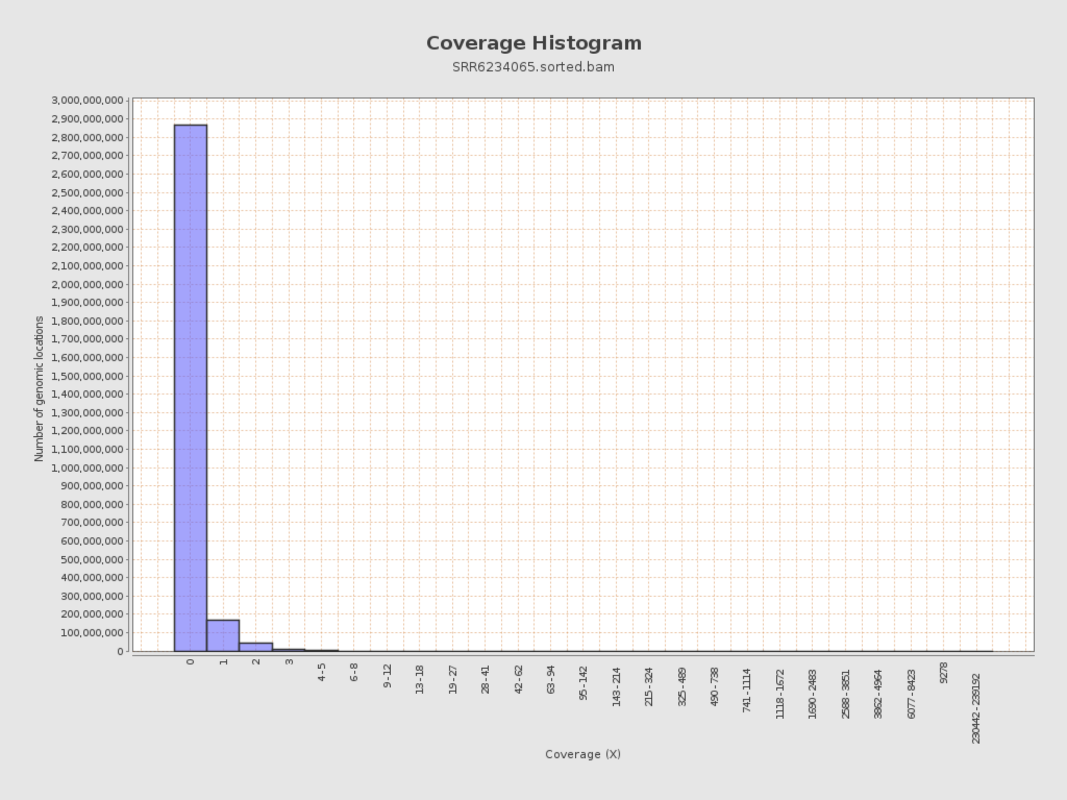
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31432937	0.1261	1.2737
chr2	243199373	43698918	0.1797	133.1783
chr3	198022430	30303272	0.153	0.5186
chr4	191154276	16769125	0.0877	0.4067
chr5	180915260	20553278	0.1136	0.4498
chr6	171115067	26351966	0.154	0.645
chr7	159138663	17065876	0.1072	1.3751

chr8	146364022	13347651	0.0912	0.9644
chr9	141213431	10983861	0.0778	0.6433
chr10	135534747	9018542	0.0665	0.5855
chr11	135006516	11080127	0.0821	0.7241
chr12	133851895	10199544	0.0762	0.377
chr13	115169878	9800576	0.0851	0.3829
chr14	107349540	13356411	0.1244	0.6918
chr15	102531392	4024001	0.0392	0.2667
chr16	90354753	7561576	0.0837	0.4476
chr17	81195210	8877219	0.1093	0.5122
chr18	78077248	6307541	0.0808	1.3754
chr19	59128983	7701900	0.1303	0.8673
chr20	63025520	7516375	0.1193	0.5021
chr21	48129895	3700320	0.0769	0.404
chr22	51304566	3617719	0.0705	0.3524
chrMT	16571	384663	23.213	16.3308
chrX	155270560	21949169	0.1414	0.5806
chrY	59373566	755970	0.0127	0.1801

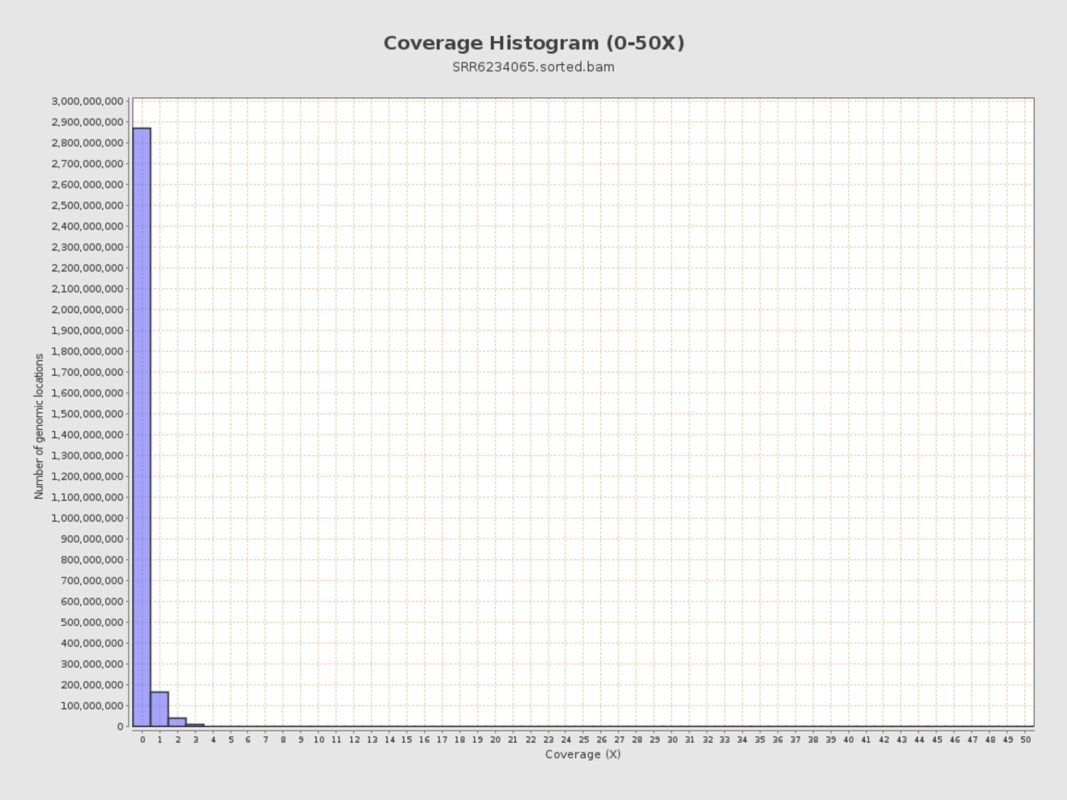
3. Results : Coverage across reference



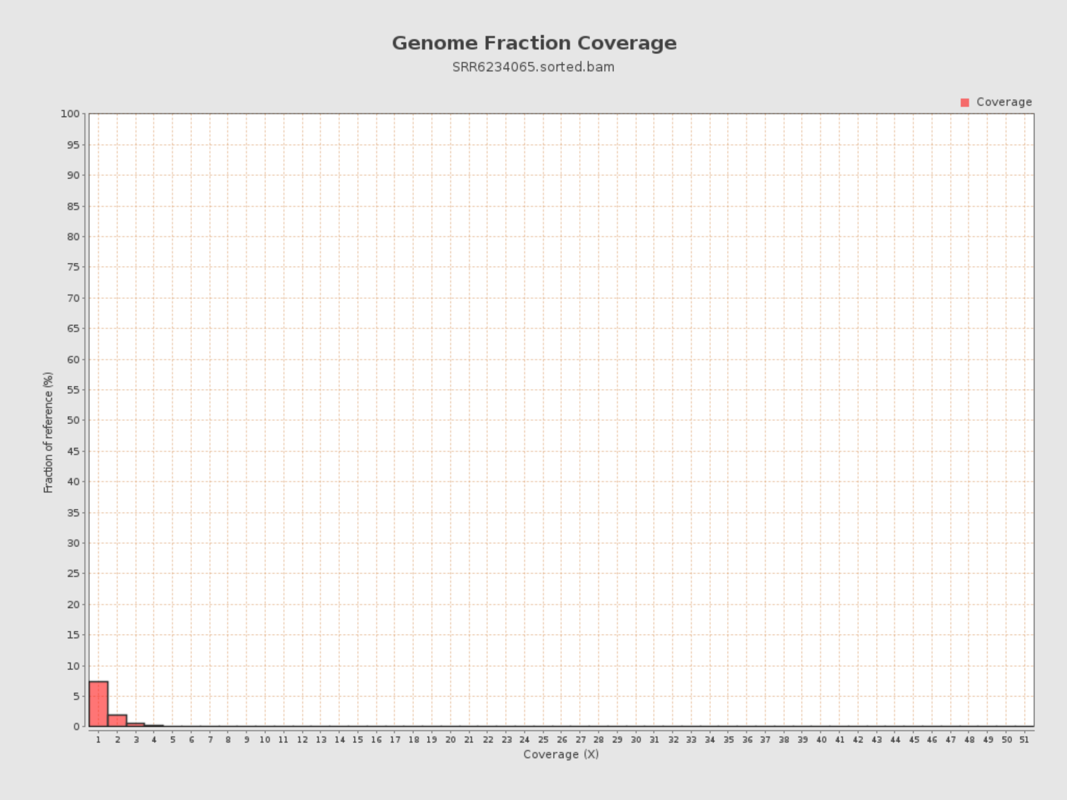
4. Results : Coverage Histogram



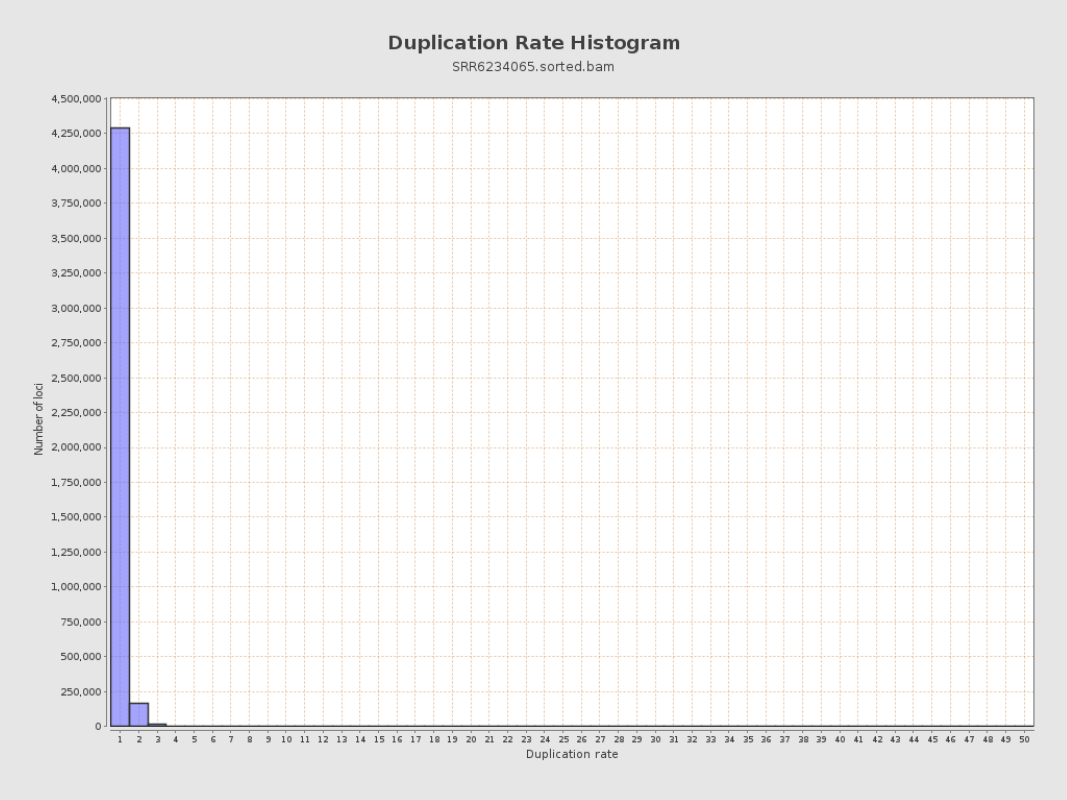
5. Results : Coverage Histogram (0-50X)



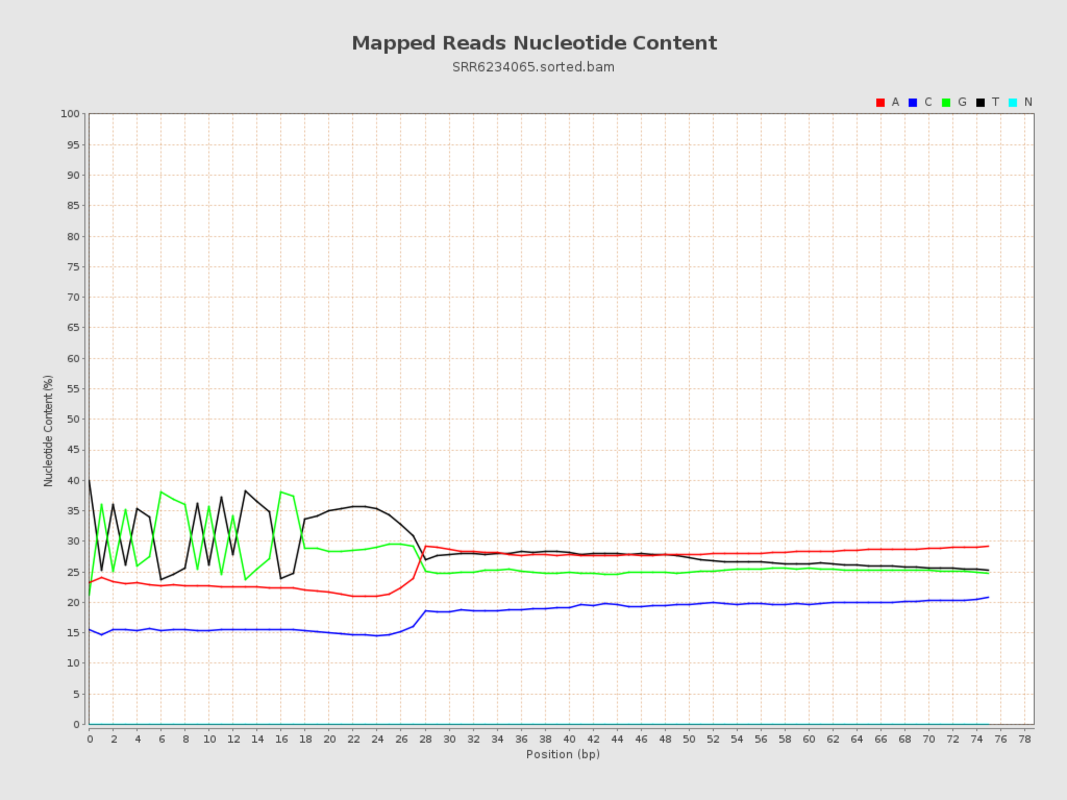
6. Results : Genome Fraction Coverage



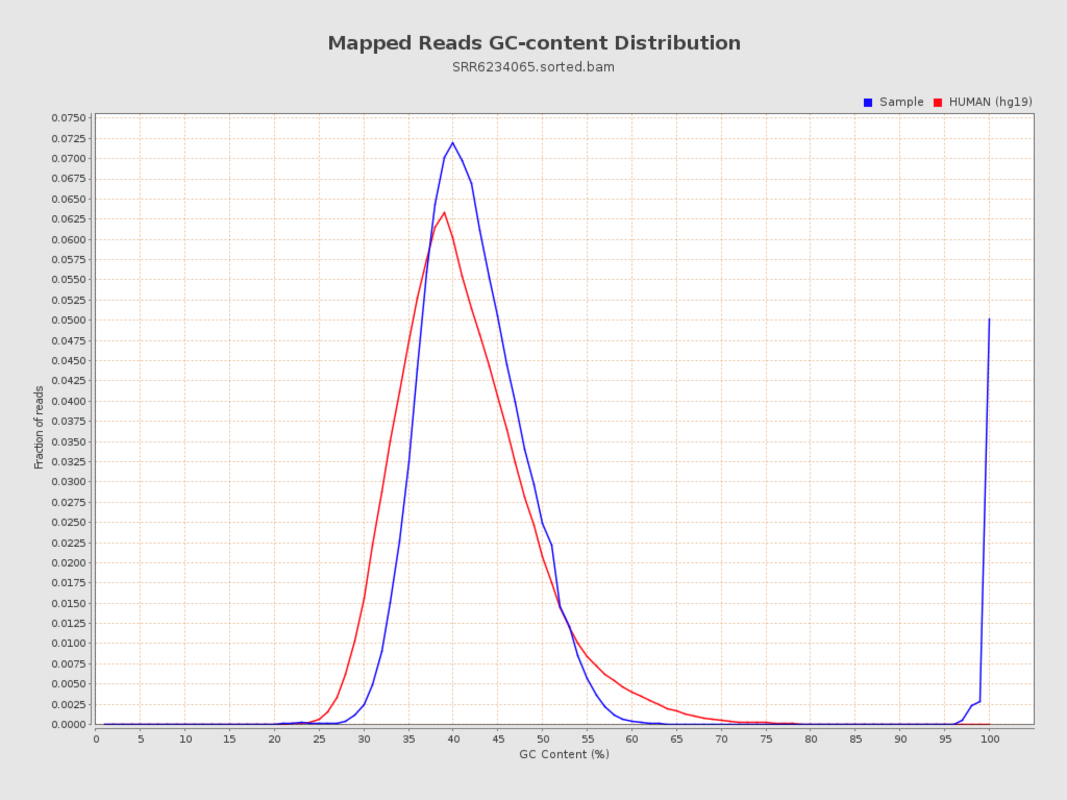
7. Results : Duplication Rate Histogram



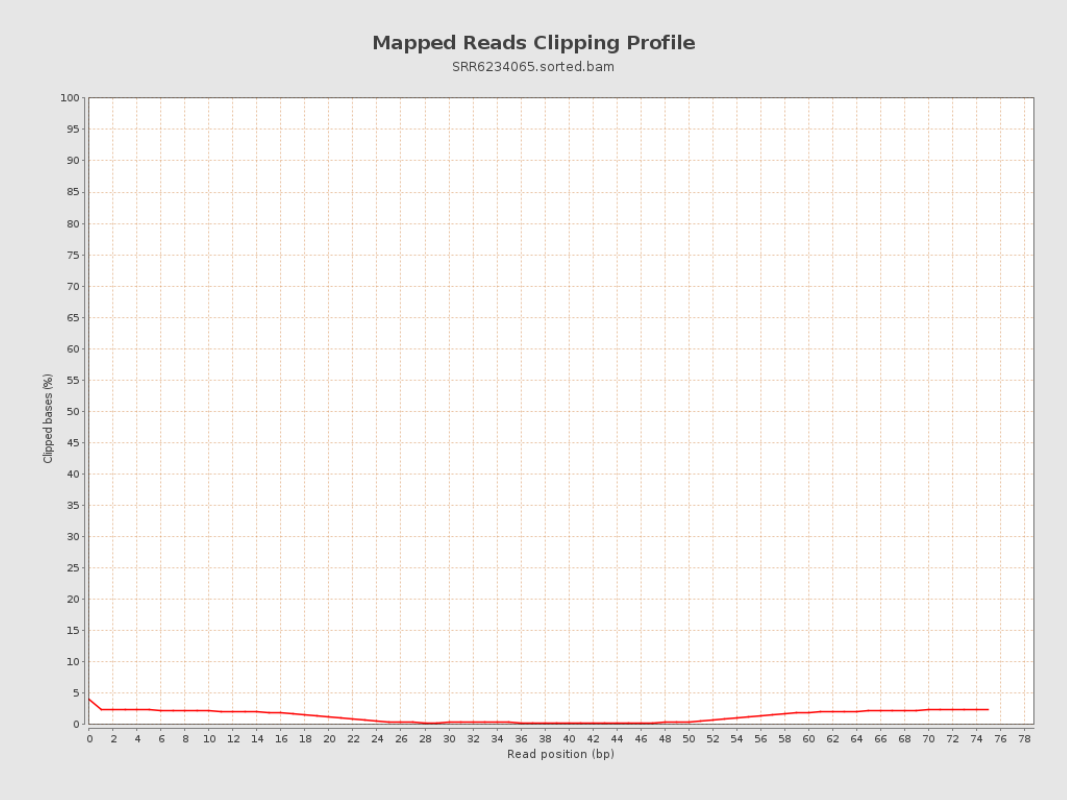
8. Results : Mapped Reads Nucleotide Content



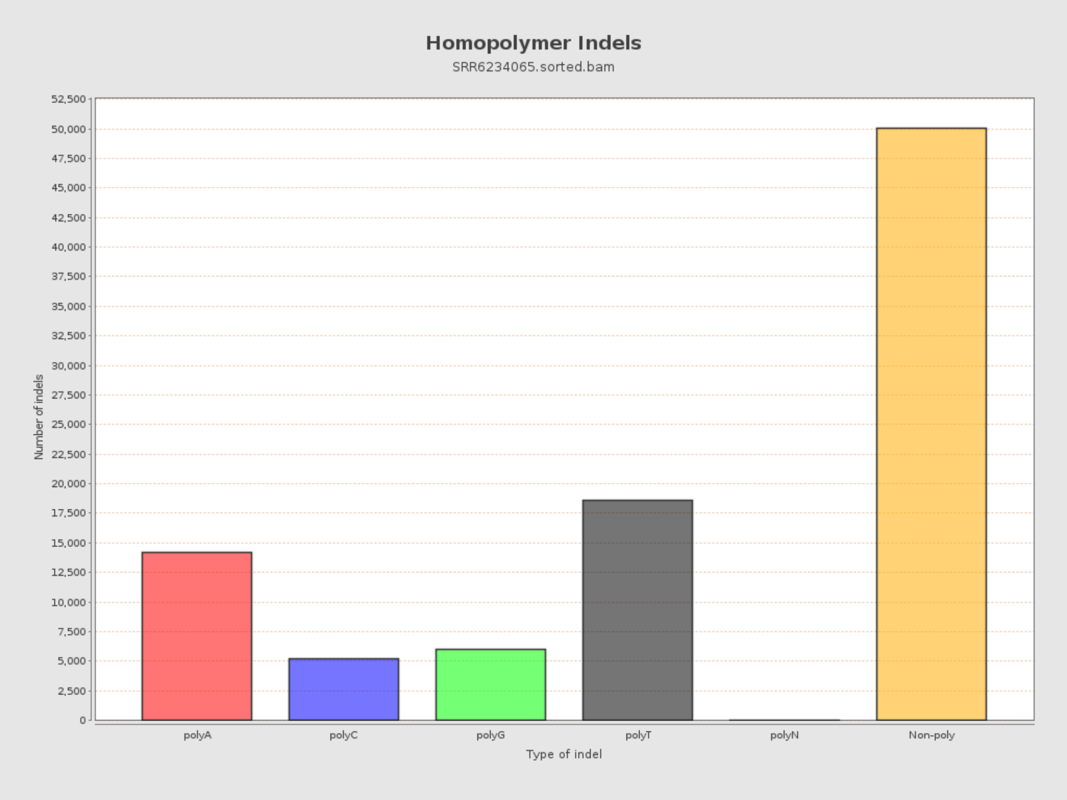
9. Results : Mapped Reads GC-content Distribution



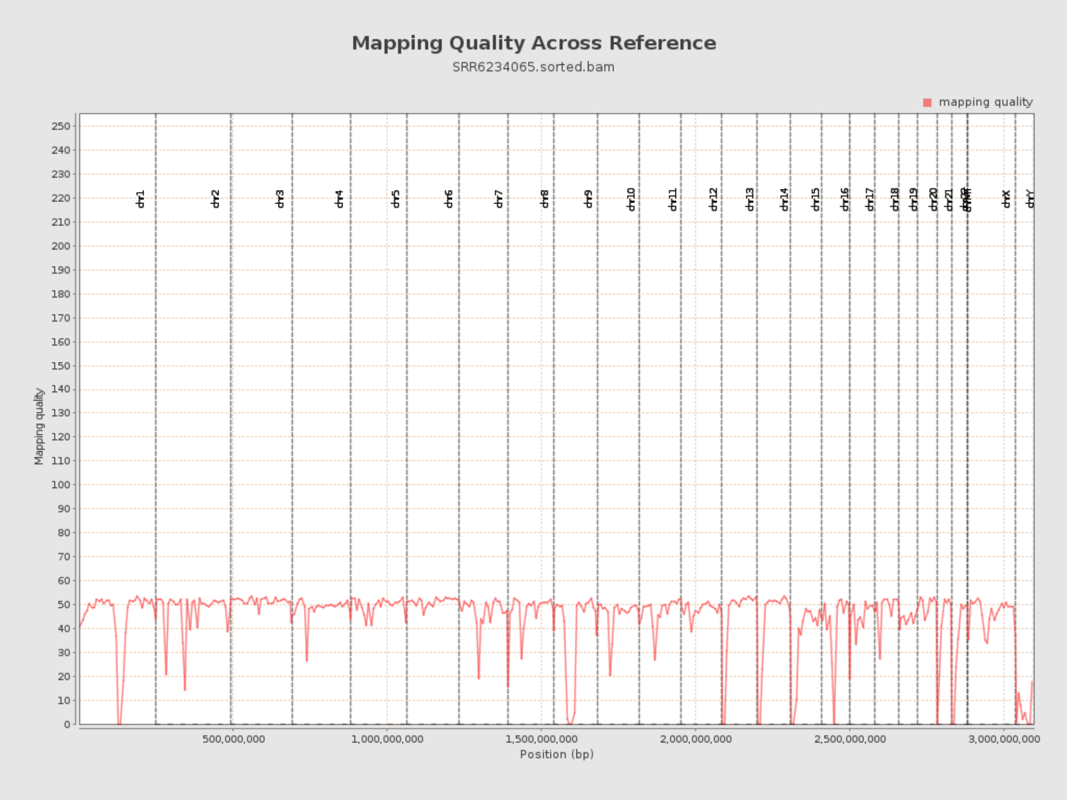
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram