Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:36:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234067.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_SRR6234067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:36:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,293,109
Mapped reads	5,919,797 / 94.07%
Unmapped reads	373,312 / 5.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,587 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	505,506 / 8.03%
Duplication rate	3.97%
Clipped reads	2,356,529 / 37.45%

2.2. ACGT Content

Number/percentage of A's	108,708,475 / 27.01%
Number/percentage of C's	75,249,020 / 18.69%
Number/percentage of T's	117,198,700 / 29.12%
Number/percentage of G's	101,281,449 / 25.16%
Number/percentage of N's	88,573 / 0.02%
GC Percentage	43.86%

2.3. Coverage

Mean	0.1301

Standard Deviation	28.6471

2.4. Mapping Quality

Mean Mapping Quality	42.98

2.5. Mismatches and indels

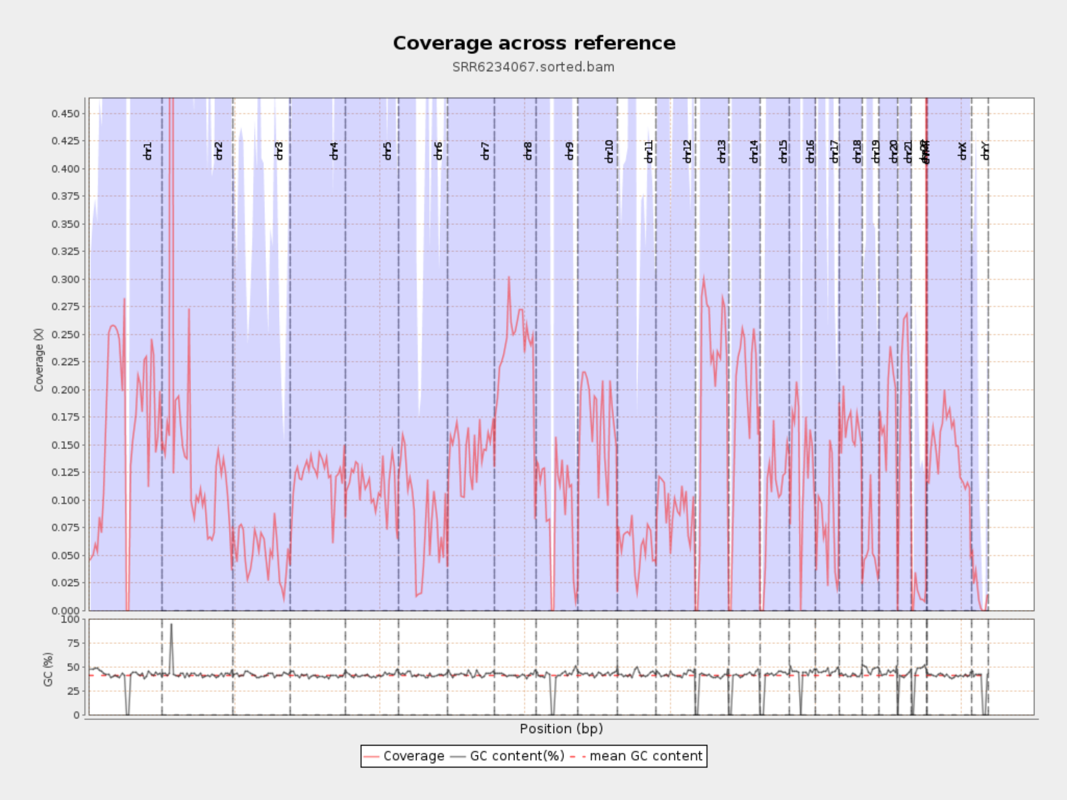
General error rate	0.66%
Mismatches	2,620,736
Insertions	27,438
Mapped reads with at least one insertion	0.46%
Deletions	86,645
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.14%

2.6. Chromosome stats

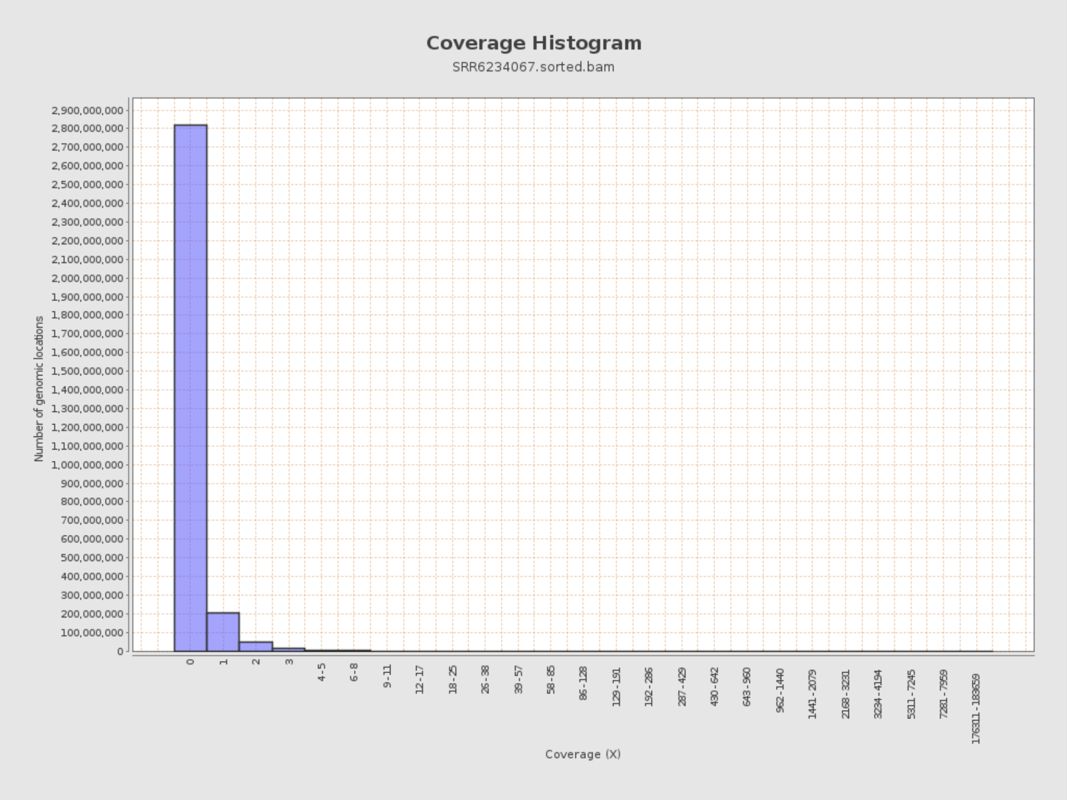
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40836811	0.1638	1.6211
chr2	243199373	45284573	0.1862	102.1594
chr3	198022430	10372922	0.0524	0.3089
chr4	191154276	23515170	0.123	0.4838
chr5	180915260	20297818	0.1122	0.4467
chr6	171115067	14307413	0.0836	0.4384
chr7	159138663	23025518	0.1447	0.9888

chr8	146364022	34596905	0.2364	1.3738
chr9	141213431	13134020	0.093	0.9728
chr10	135534747	23664235	0.1746	0.8069
chr11	135006516	7775031	0.0576	0.7082
chr12	133851895	12386148	0.0925	0.4325
chr13	115169878	24130715	0.2095	0.626
chr14	107349540	19578690	0.1824	0.8271
chr15	102531392	10442629	0.1018	0.4272
chr16	90354753	12422681	0.1375	0.6555
chr17	81195210	5928123	0.073	0.5064
chr18	78077248	13018528	0.1667	2.2118
chr19	59128983	3262798	0.0552	1.2238
chr20	63025520	11591516	0.1839	0.6607
chr21	48129895	9048997	0.188	0.6794
chr22	51304566	667643	0.013	0.1484
chrMT	16571	30931	1.8666	2.1521
chrX	155270560	22399462	0.1443	0.6528
chrY	59373566	945836	0.0159	0.2322

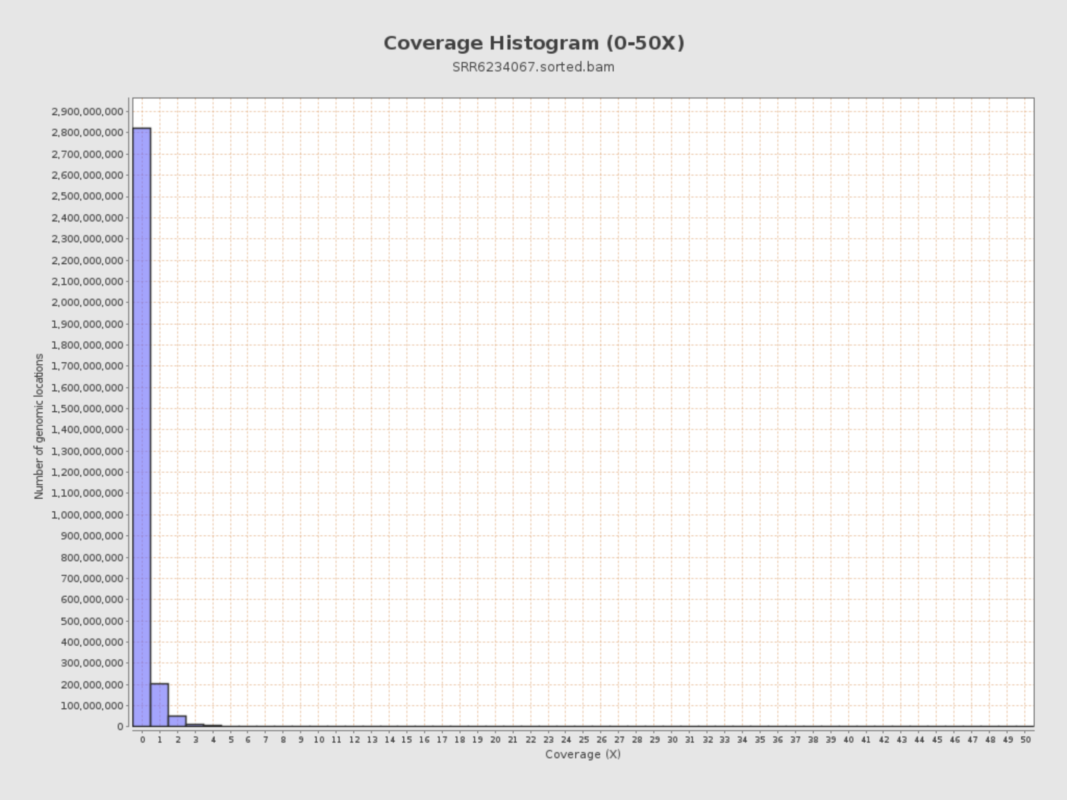
3. Results : Coverage across reference



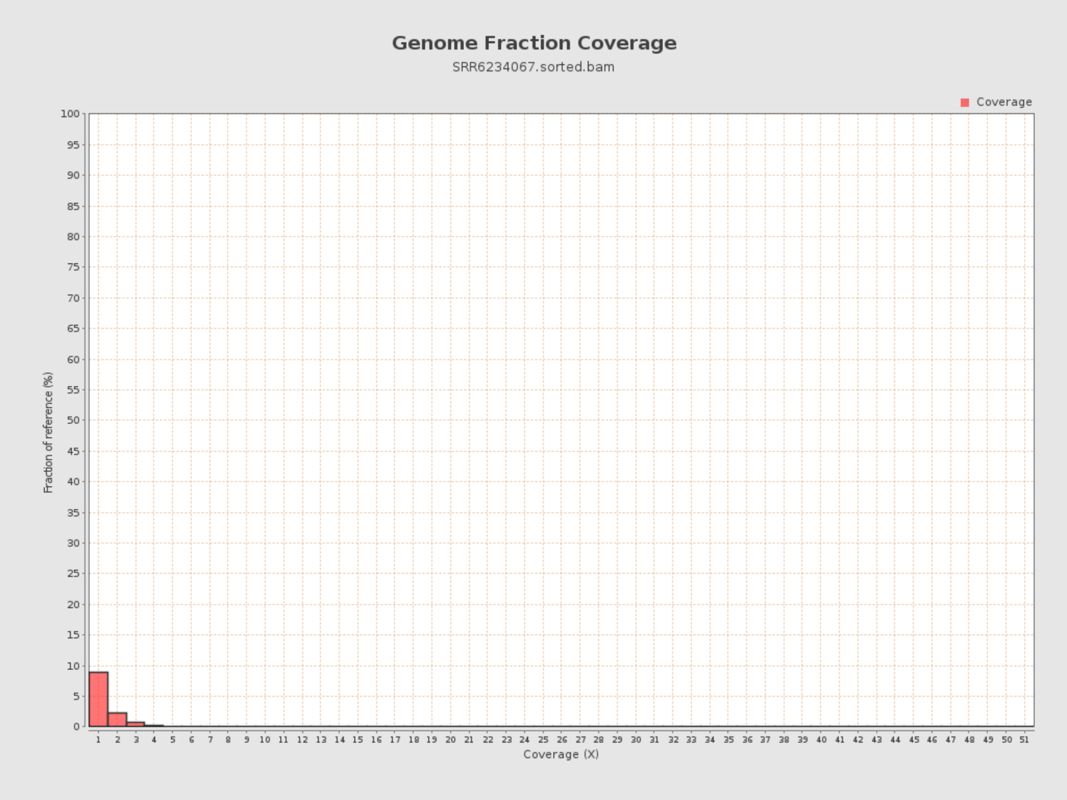
4. Results : Coverage Histogram



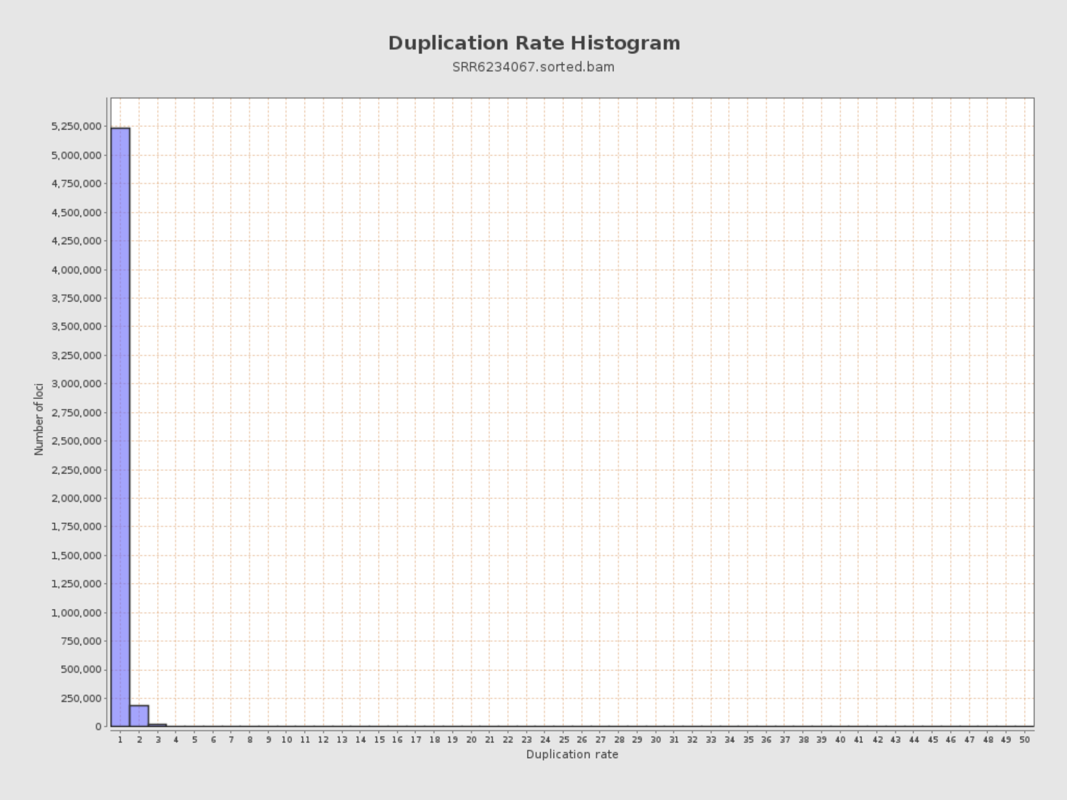
5. Results : Coverage Histogram (0-50X)



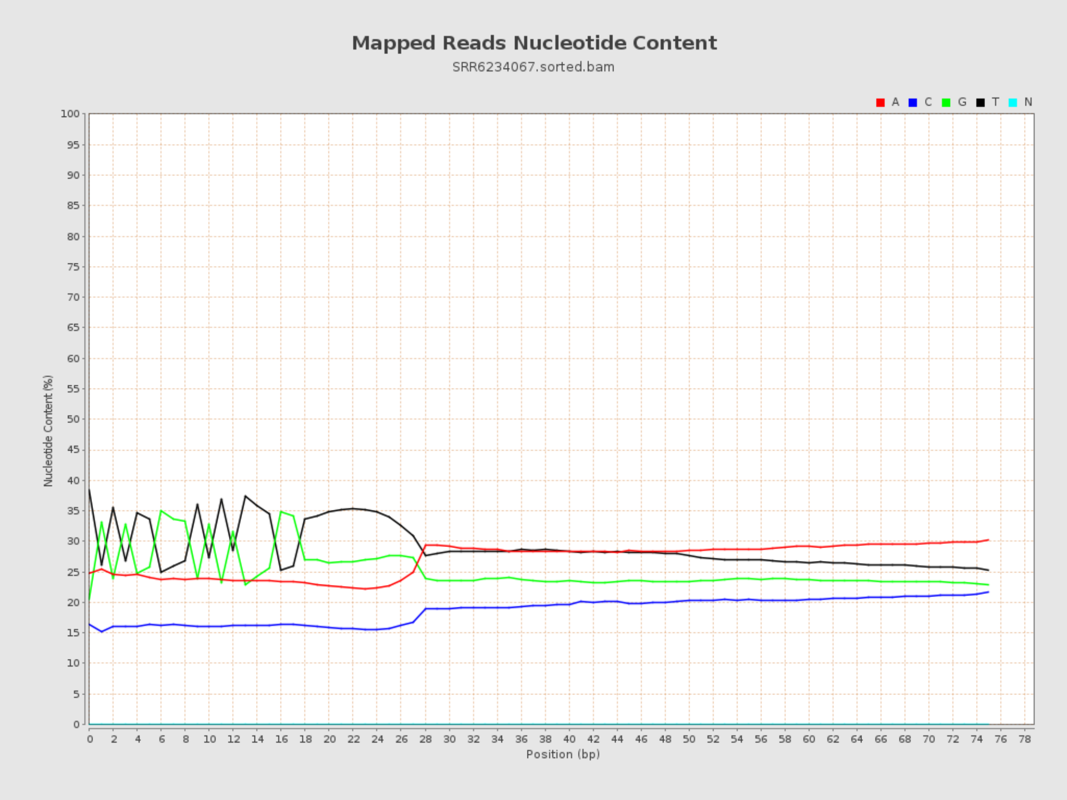
6. Results : Genome Fraction Coverage



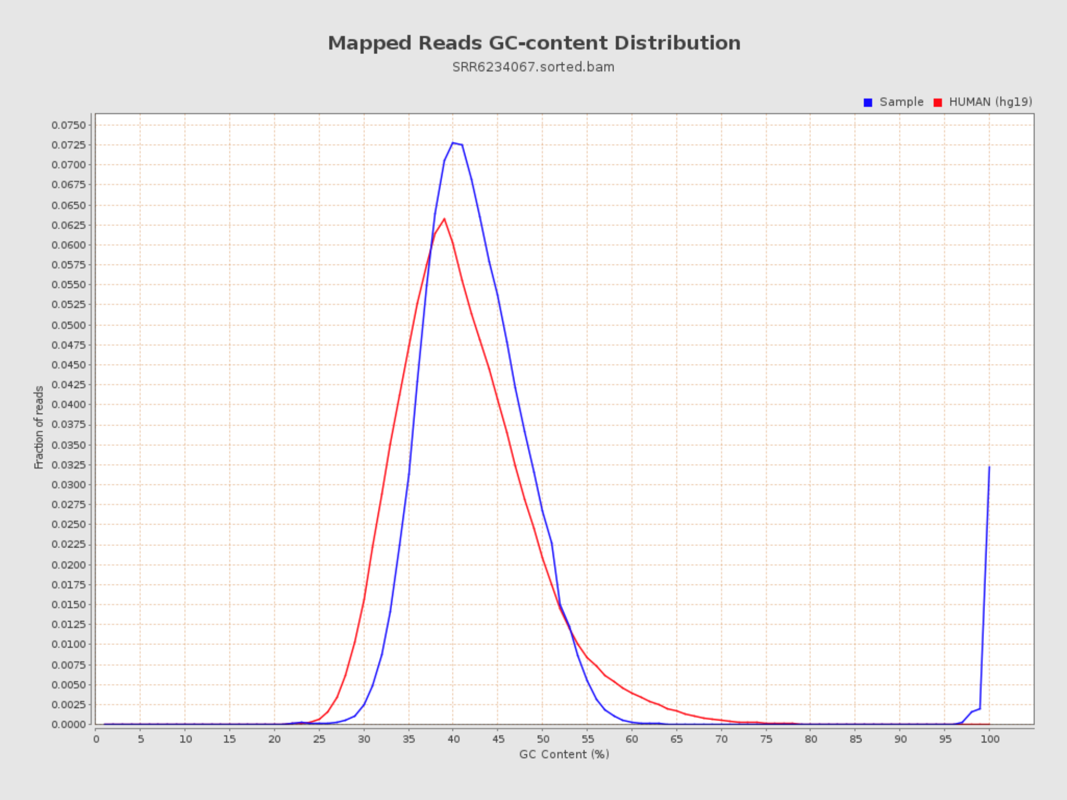
7. Results : Duplication Rate Histogram



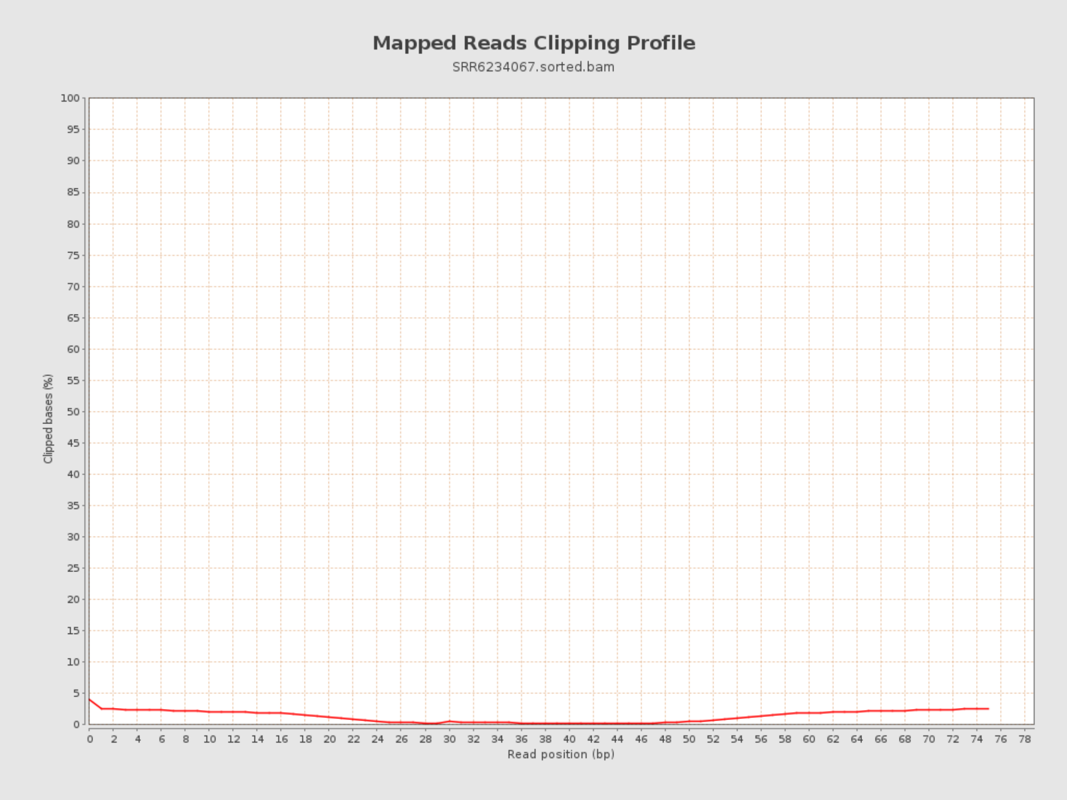
8. Results : Mapped Reads Nucleotide Content



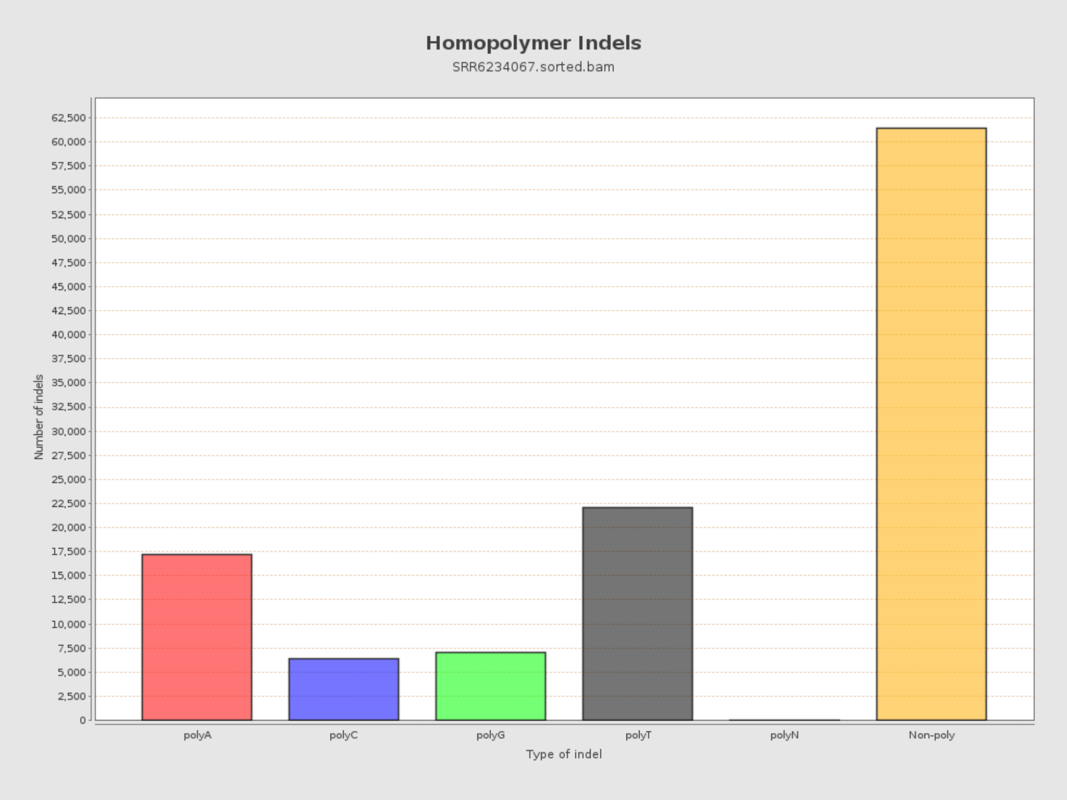
9. Results : Mapped Reads GC-content Distribution



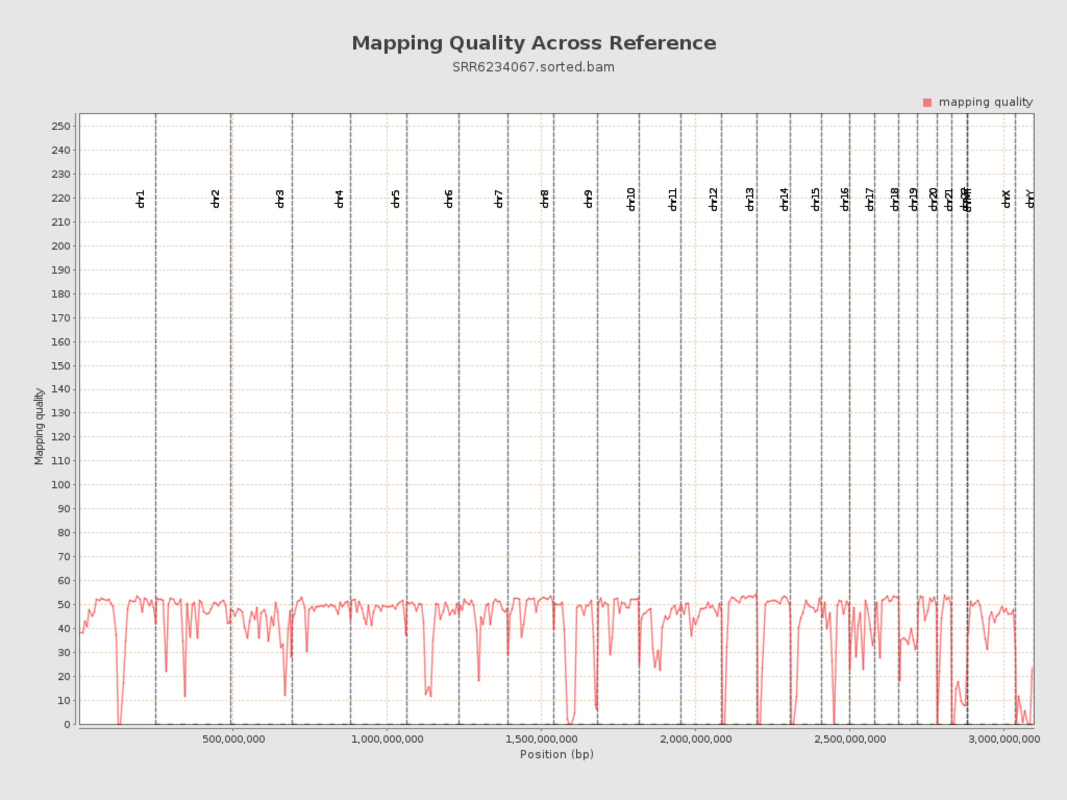
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram