Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:49:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240235.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_SRR6240235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:49:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,176,162
Mapped reads	2,535,687 / 79.83%
Unmapped reads	640,475 / 20.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,506 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	490,572 / 15.45%
Duplication rate	13.37%
Clipped reads	1,235,718 / 38.91%

2.2. ACGT Content

Number/percentage of A's	46,750,931 / 28.01%
Number/percentage of C's	30,494,393 / 18.27%
Number/percentage of T's	53,619,029 / 32.13%
Number/percentage of G's	35,966,257 / 21.55%
Number/percentage of N's	62,487 / 0.04%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0539

Standard Deviation	0.6271

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

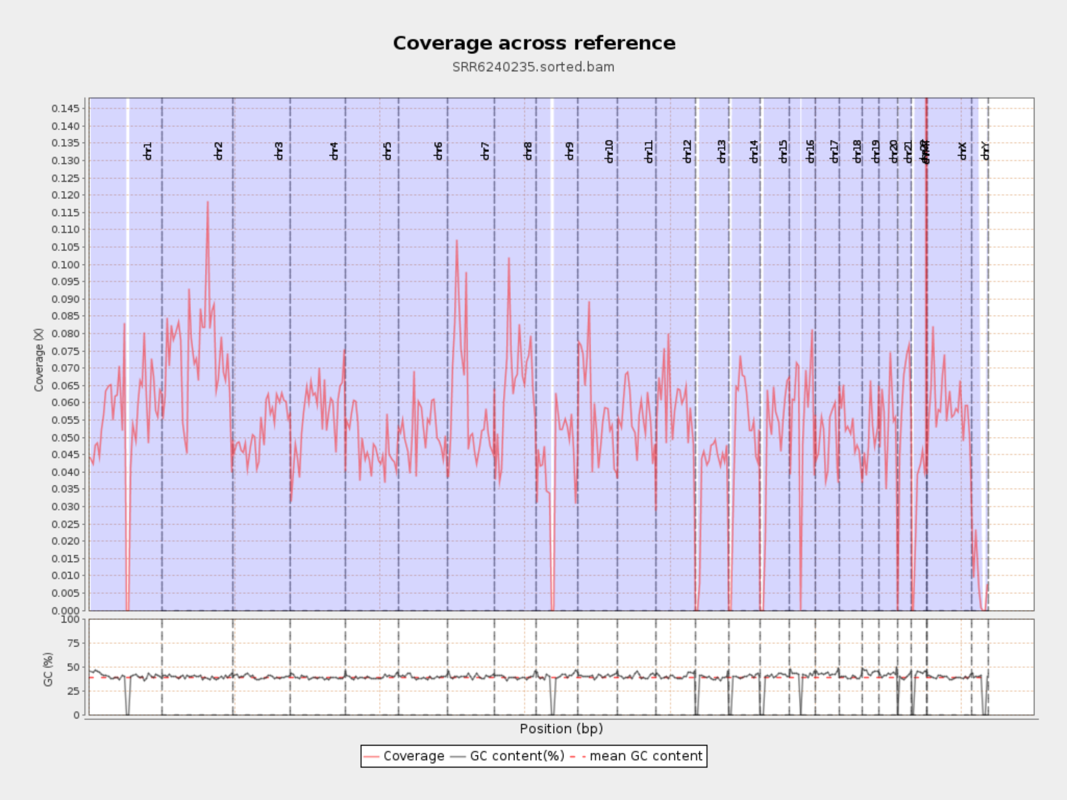
General error rate	0.88%
Mismatches	1,454,293
Insertions	12,238
Mapped reads with at least one insertion	0.48%
Deletions	46,023
Mapped reads with at least one deletion	1.79%
Homopolymer indels	48.4%

2.6. Chromosome stats

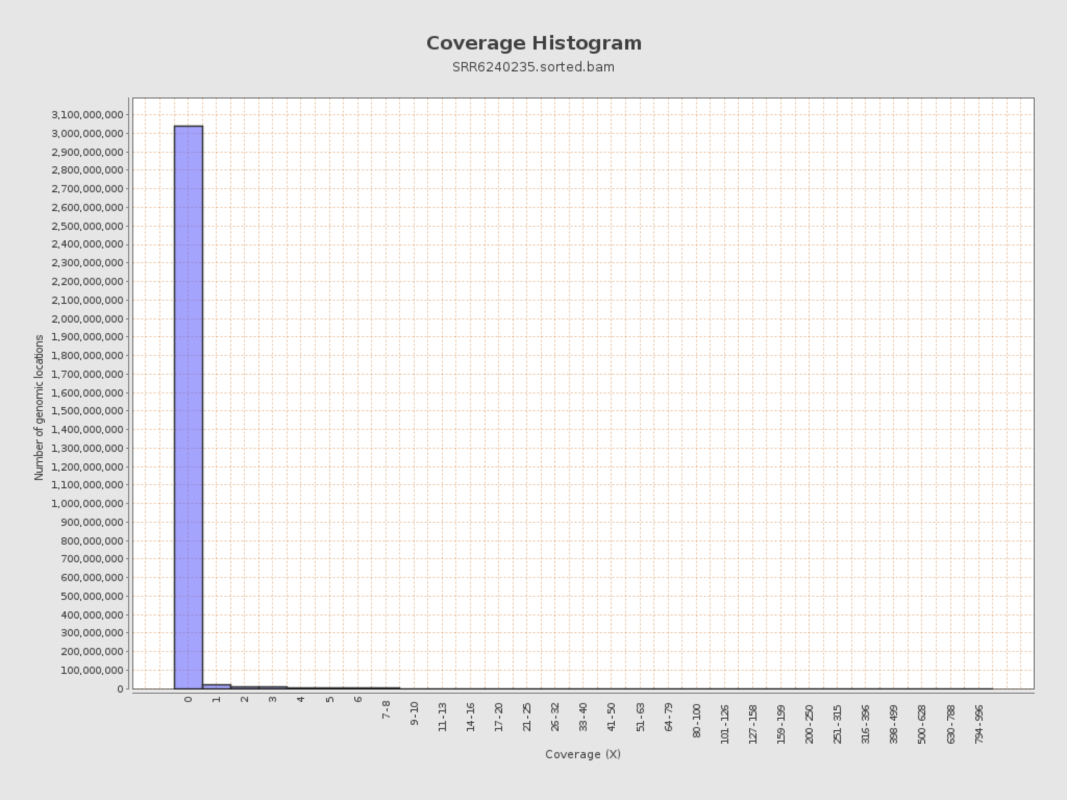
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13711153	0.055	0.8926
chr2	243199373	18010749	0.0741	0.7223
chr3	198022430	10412995	0.0526	0.513
chr4	191154276	10886382	0.057	0.5387
chr5	180915260	8580065	0.0474	0.4842
chr6	171115067	8844454	0.0517	0.5406
chr7	159138663	9705324	0.061	0.8363

chr8	146364022	9521937	0.0651	0.8309
chr9	141213431	5983151	0.0424	0.5348
chr10	135534747	7976133	0.0588	0.6578
chr11	135006516	7475418	0.0554	0.6394
chr12	133851895	7996491	0.0597	0.5452
chr13	115169878	4320209	0.0375	0.4399
chr14	107349540	5260729	0.049	0.5013
chr15	102531392	4799015	0.0468	0.4945
chr16	90354753	5081374	0.0562	0.5275
chr17	81195210	3929516	0.0484	0.494
chr18	78077248	4104015	0.0526	0.8203
chr19	59128983	2967384	0.0502	0.6342
chr20	63025520	3441120	0.0546	0.524
chr21	48129895	2765203	0.0575	0.5417
chr22	51304566	1528085	0.0298	0.3616
chrMT	16571	34039	2.0541	3.2907
chrX	155270560	9180578	0.0591	0.5623
chrY	59373566	457853	0.0077	0.1846

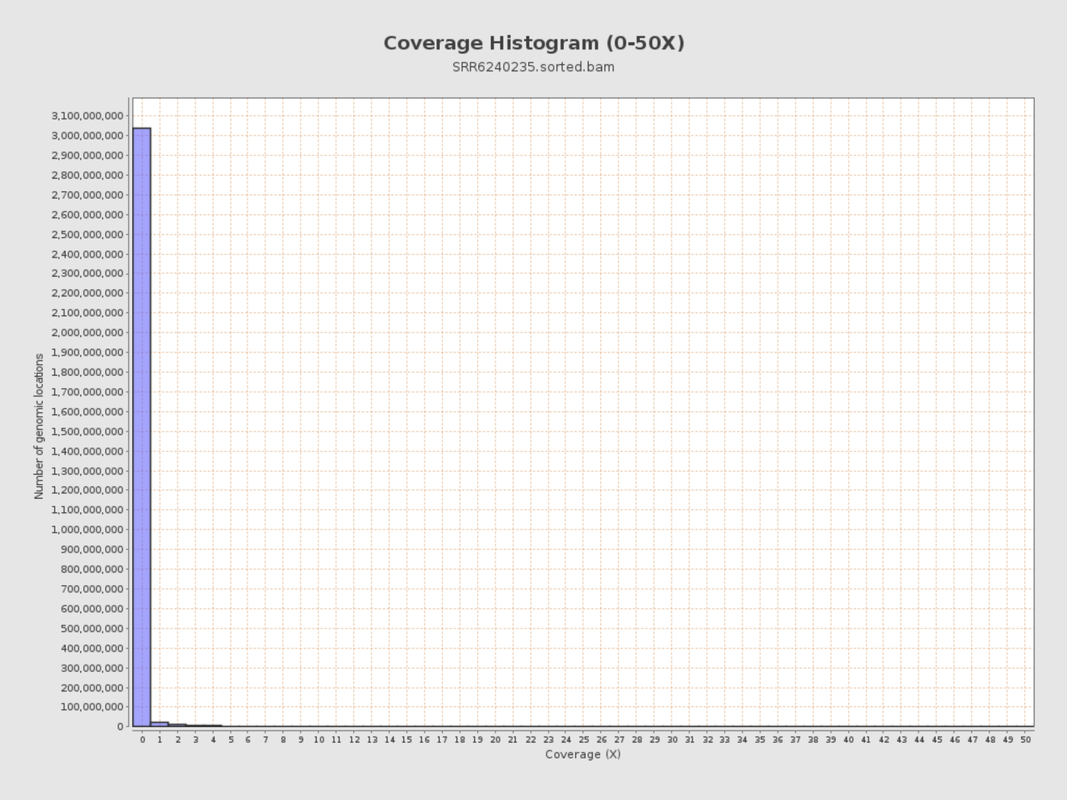
3. Results : Coverage across reference



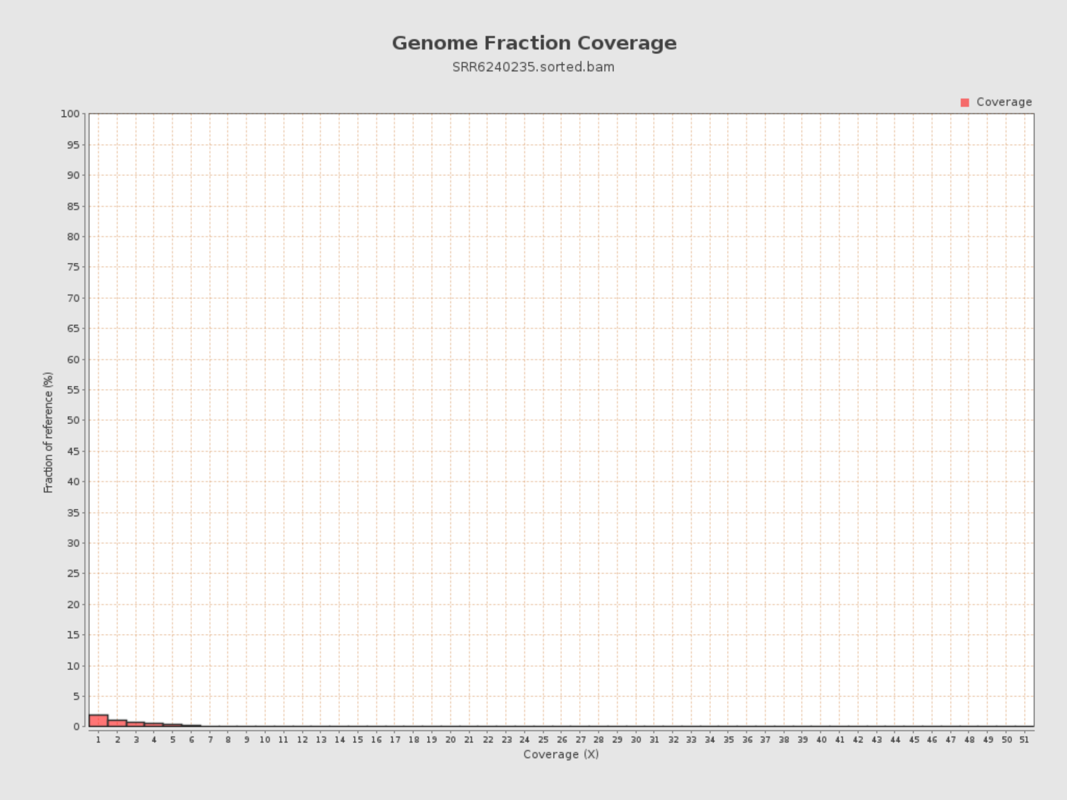
4. Results : Coverage Histogram



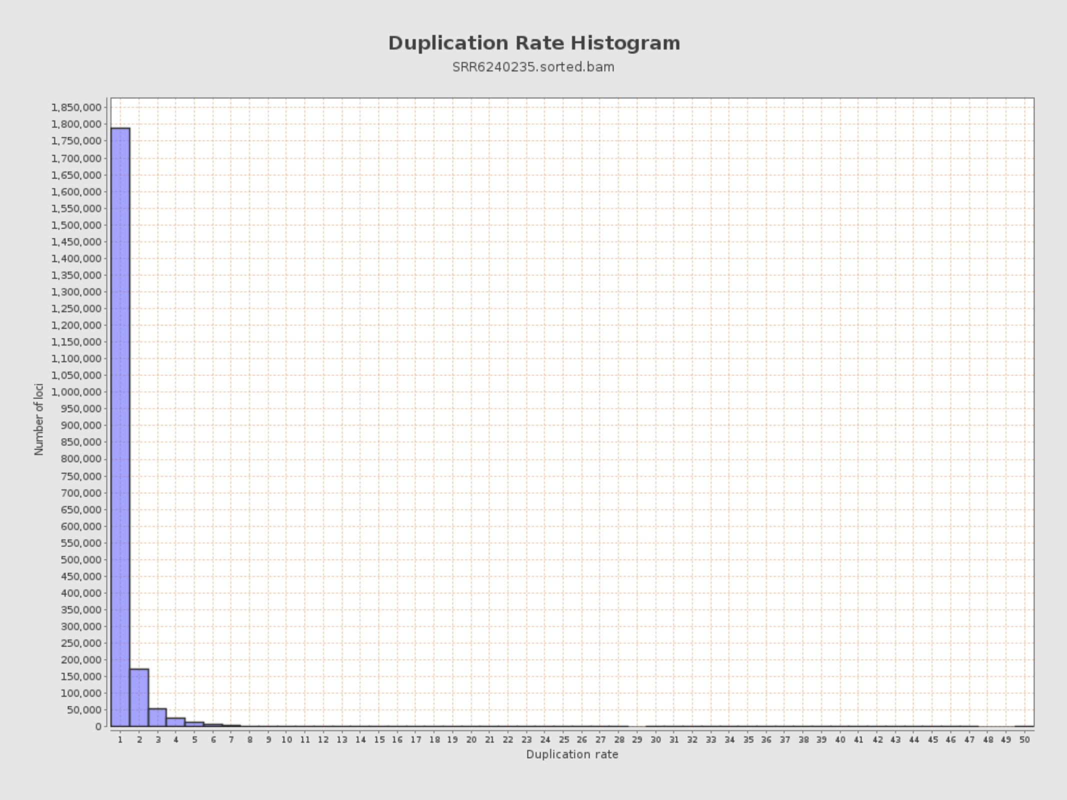
5. Results : Coverage Histogram (0-50X)



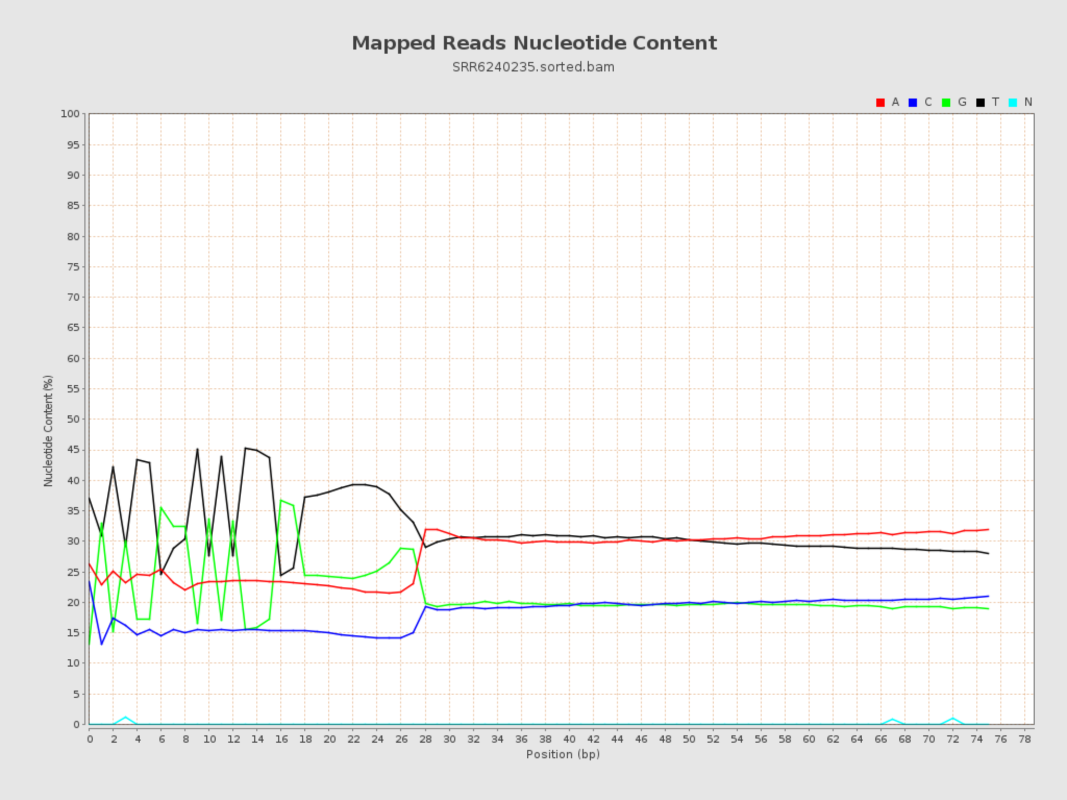
6. Results : Genome Fraction Coverage



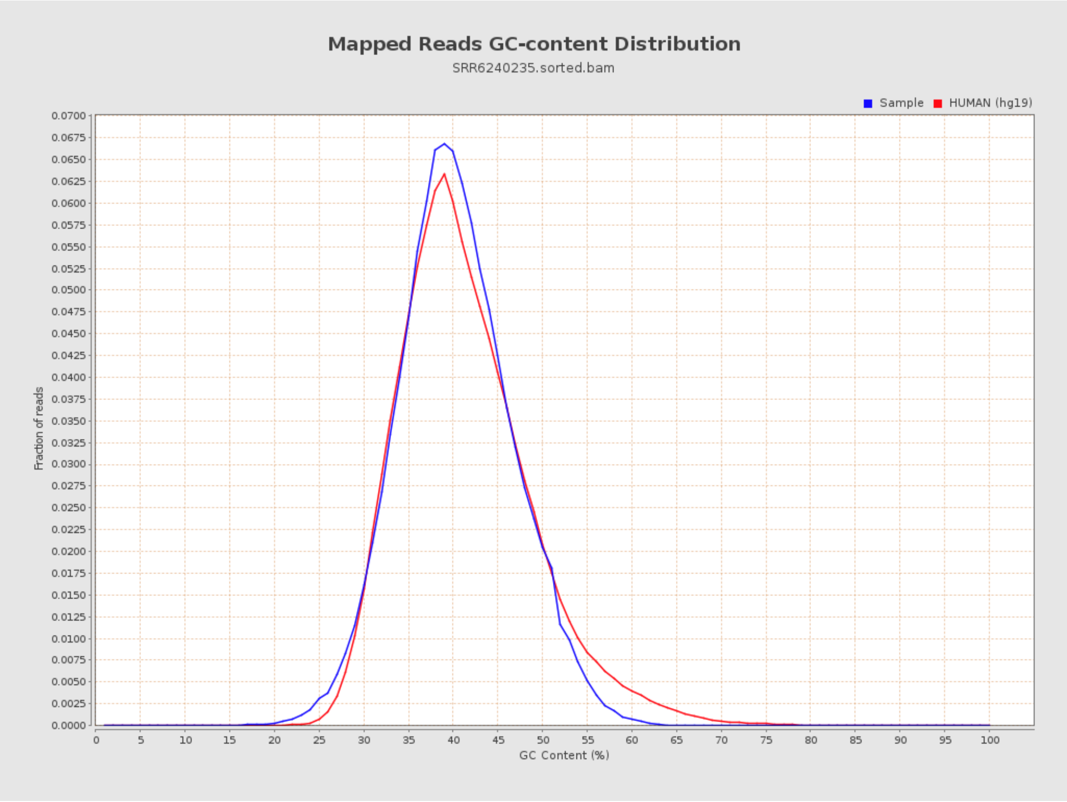
7. Results : Duplication Rate Histogram



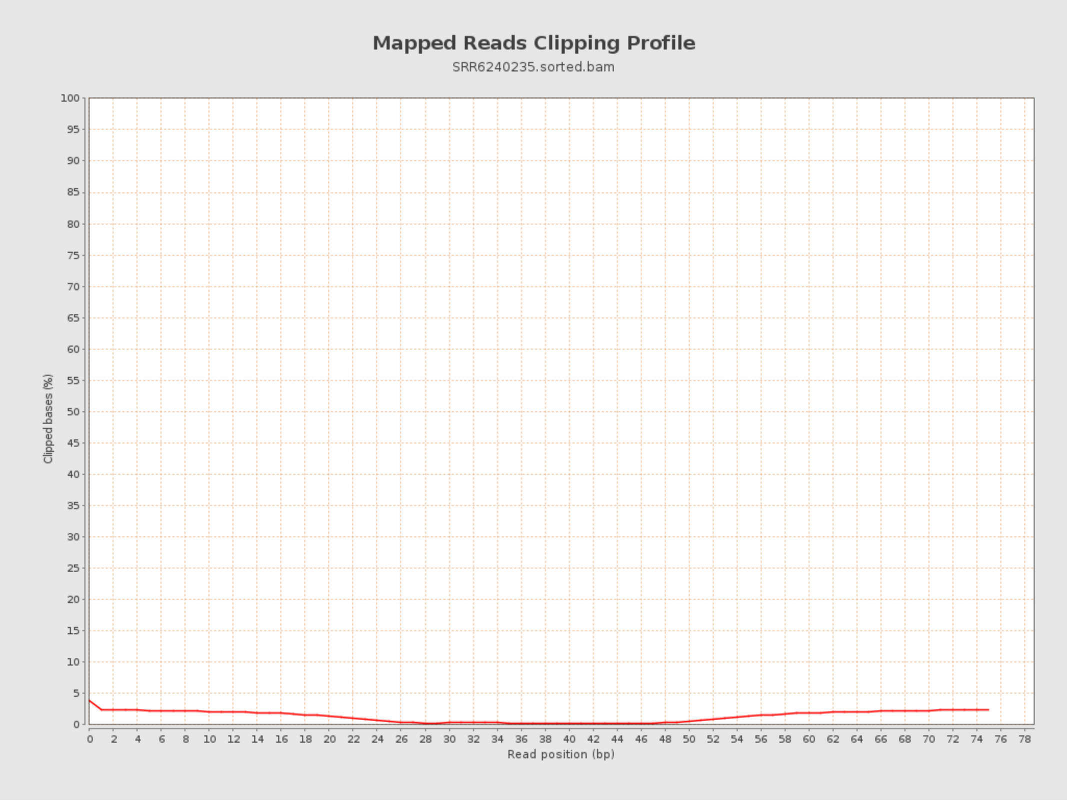
8. Results : Mapped Reads Nucleotide Content



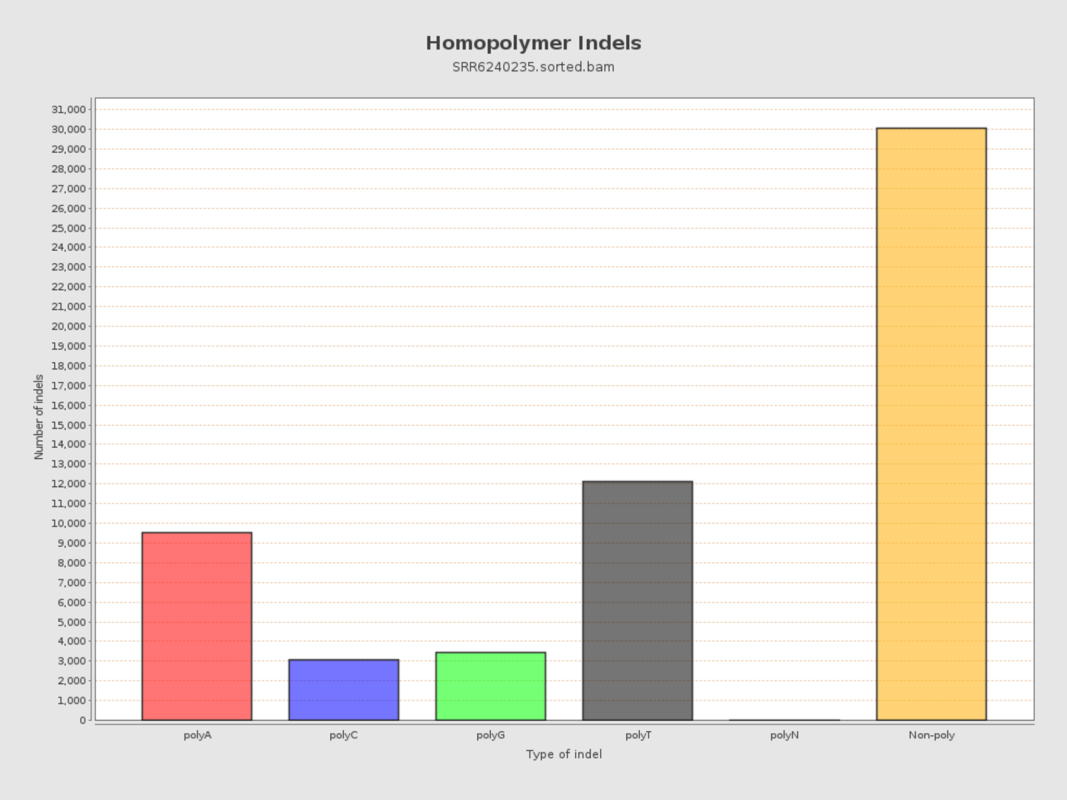
9. Results : Mapped Reads GC-content Distribution



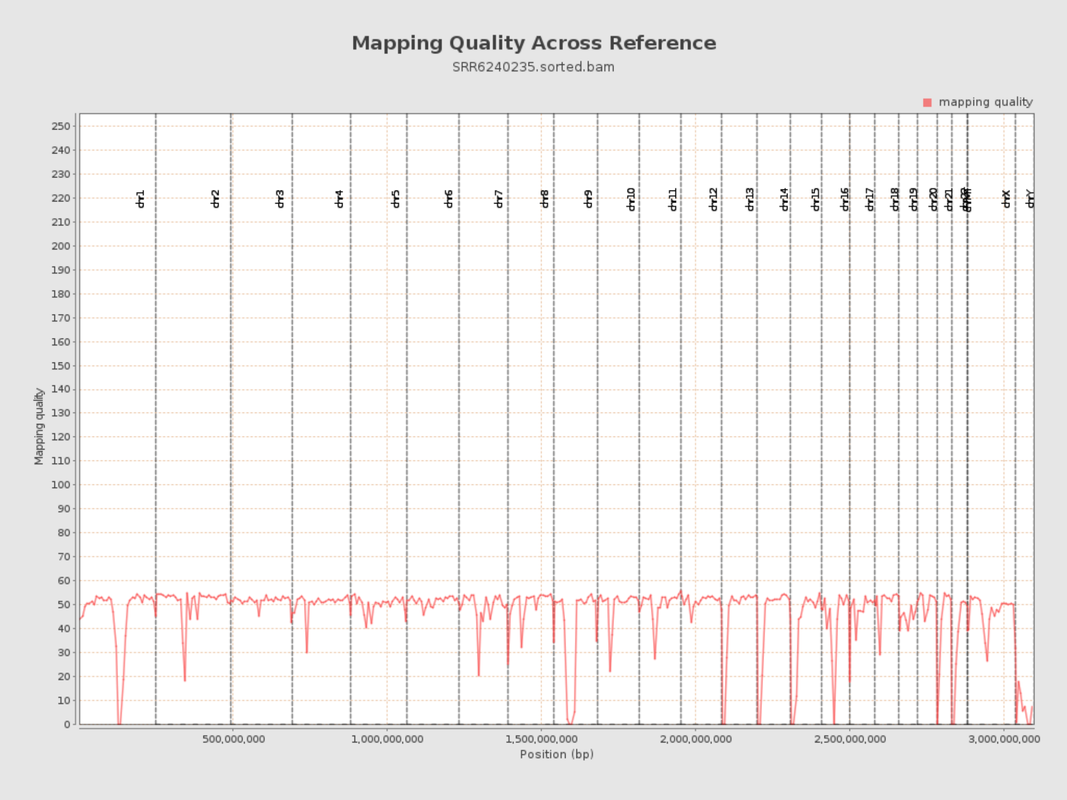
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram