Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:10:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240242.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_SRR6240242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:10:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,161,330
Mapped reads	1,860,827 / 86.1%
Unmapped reads	300,503 / 13.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,880 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	273,138 / 12.64%
Duplication rate	10.51%
Clipped reads	966,307 / 44.71%

2.2. ACGT Content

Number/percentage of A's	35,255,405 / 28.92%
Number/percentage of C's	22,449,785 / 18.42%
Number/percentage of T's	38,915,018 / 31.93%
Number/percentage of G's	25,262,239 / 20.72%
Number/percentage of N's	11,255 / 0.01%
GC Percentage	39.14%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.7059

2.4. Mapping Quality

Mean Mapping Quality	42.83

2.5. Mismatches and indels

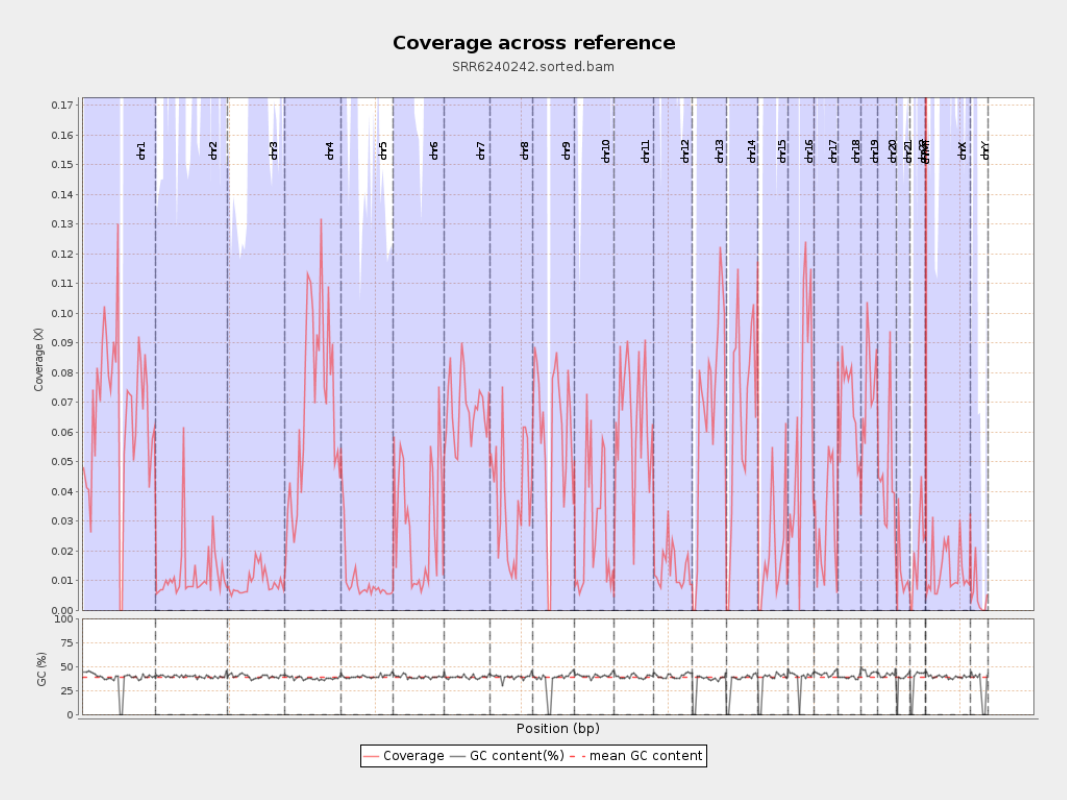
General error rate	0.89%
Mismatches	1,059,430
Insertions	9,942
Mapped reads with at least one insertion	0.53%
Deletions	35,115
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16491316	0.0662	1.4797
chr2	243199373	2997948	0.0123	0.4812
chr3	198022430	1878124	0.0095	0.1707
chr4	191154276	13067172	0.0684	0.5166
chr5	180915260	1871509	0.0103	0.1888
chr6	171115067	4876487	0.0285	0.3147
chr7	159138663	10794635	0.0678	0.6027

chr8	146364022	5393689	0.0369	1.4559
chr9	141213431	8425616	0.0597	0.6901
chr10	135534747	3691090	0.0272	0.4142
chr11	135006516	8685647	0.0643	0.6672
chr12	133851895	1908121	0.0143	0.2364
chr13	115169878	8011126	0.0696	0.503
chr14	107349540	7225956	0.0673	0.5376
chr15	102531392	2013577	0.0196	0.2604
chr16	90354753	5461420	0.0604	0.5219
chr17	81195210	2420789	0.0298	0.3418
chr18	78077248	5427011	0.0695	1.408
chr19	59128983	4436508	0.075	0.8818
chr20	63025520	2789629	0.0443	0.3948
chr21	48129895	608195	0.0126	0.2649
chr22	51304566	1011988	0.0197	0.2442
chrMT	16571	44891	2.709	3.4096
chrX	155270560	2118779	0.0136	0.2735
chrY	59373566	303932	0.0051	0.1878

3. Results : Coverage across reference



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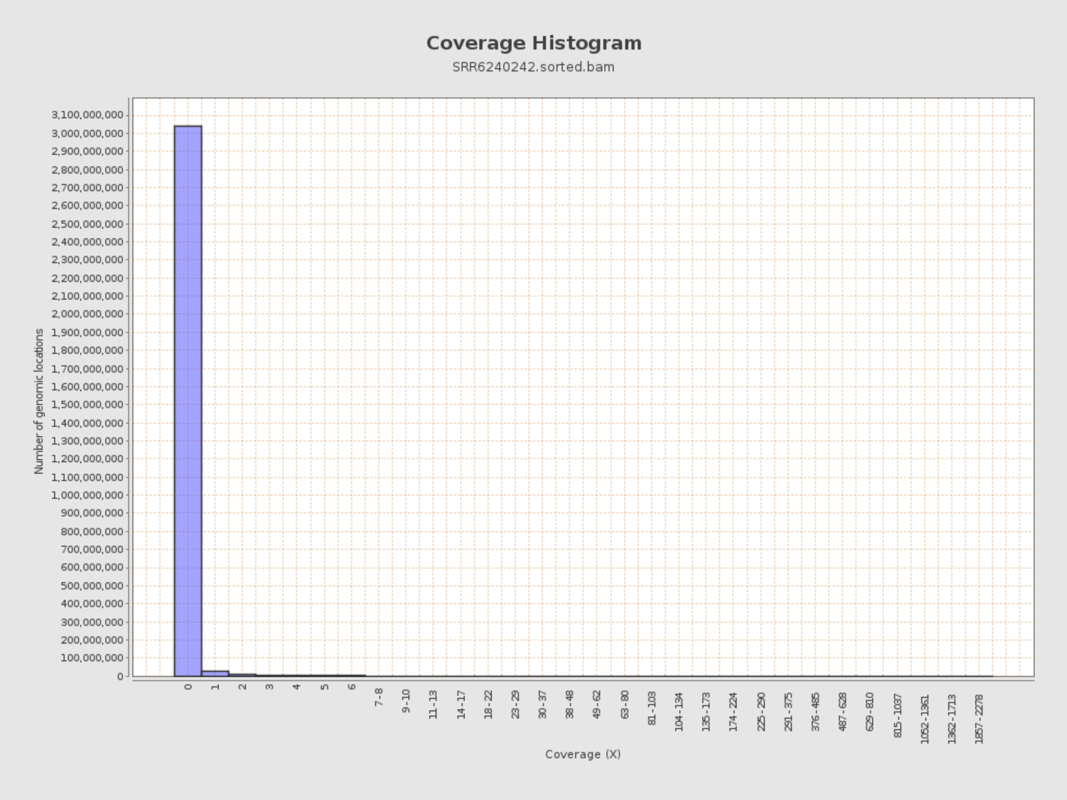
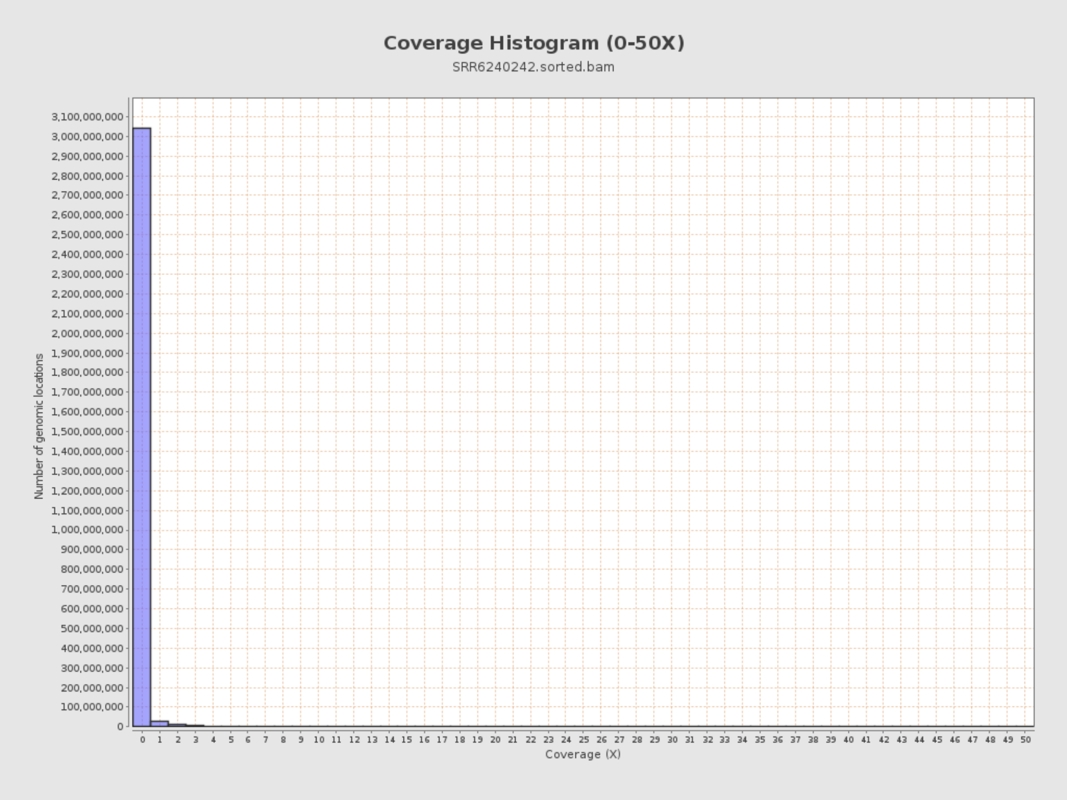
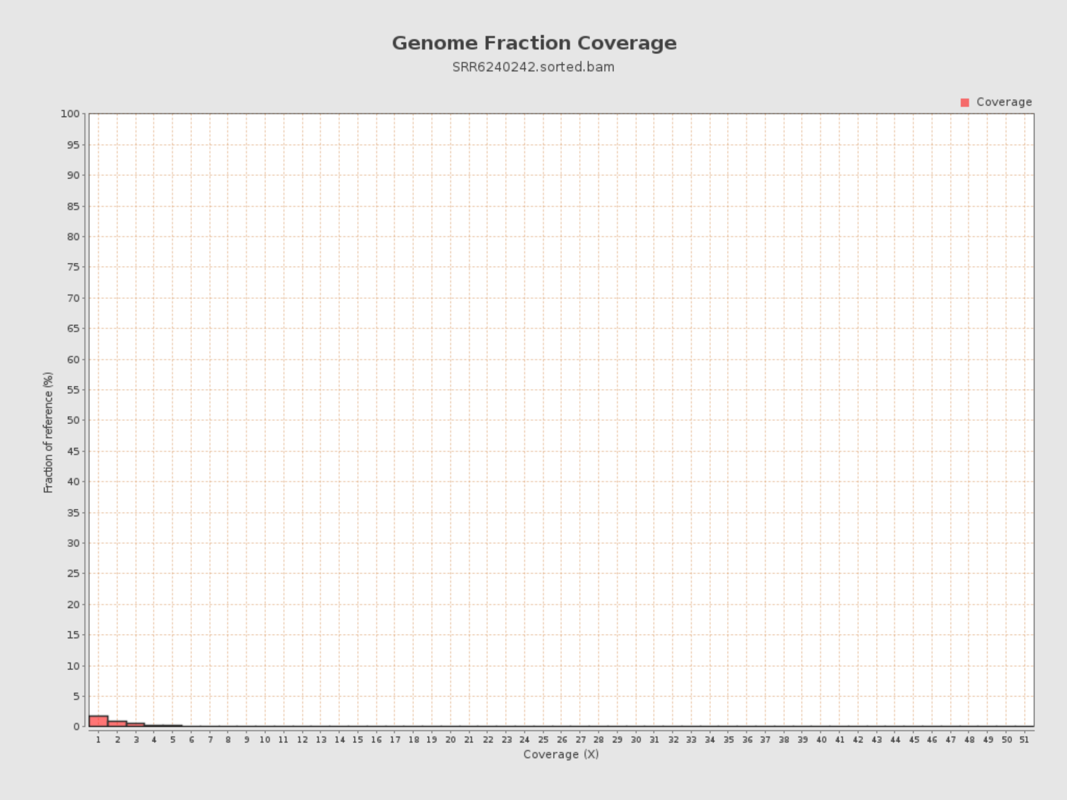
4. Results : Coverage Histogram



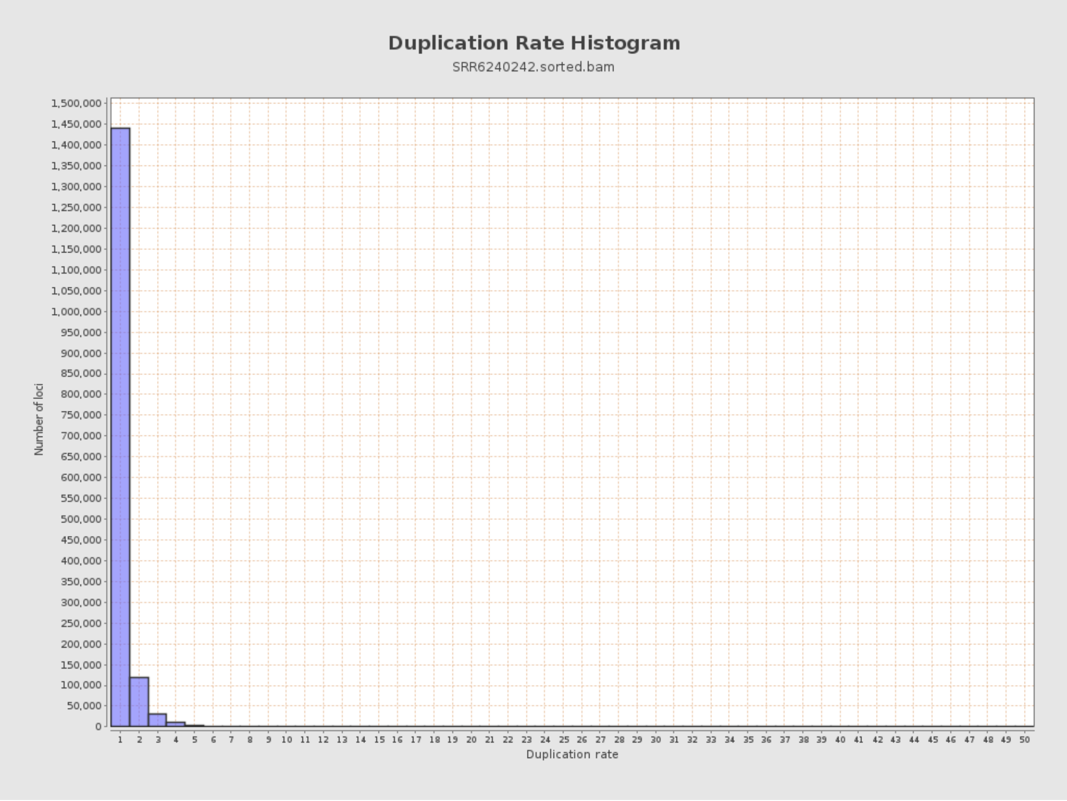
5. Results : Coverage Histogram (0-50X)



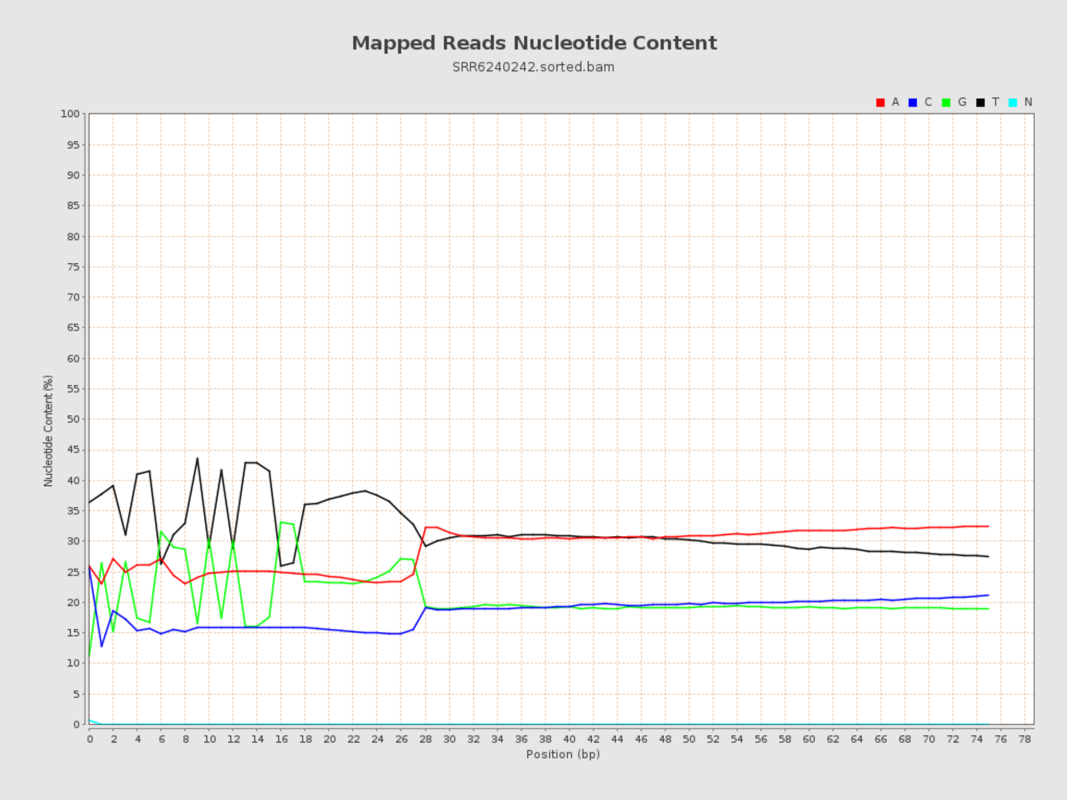
6. Results : Genome Fraction Coverage



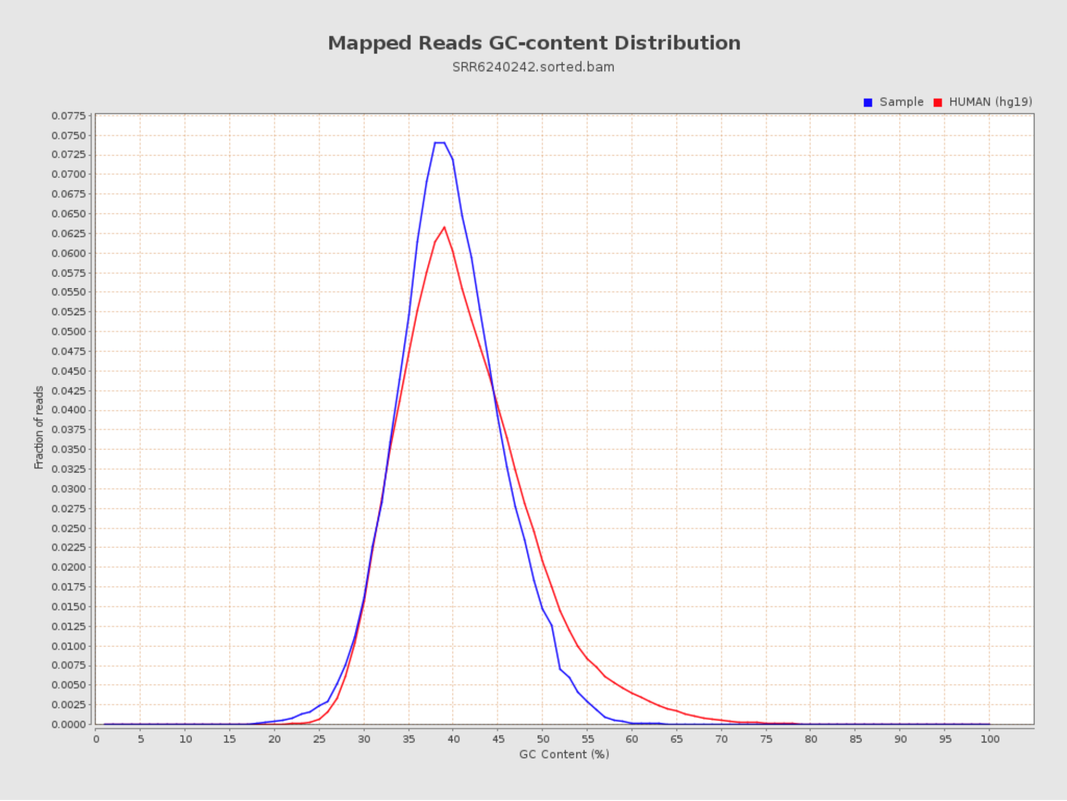
7. Results : Duplication Rate Histogram



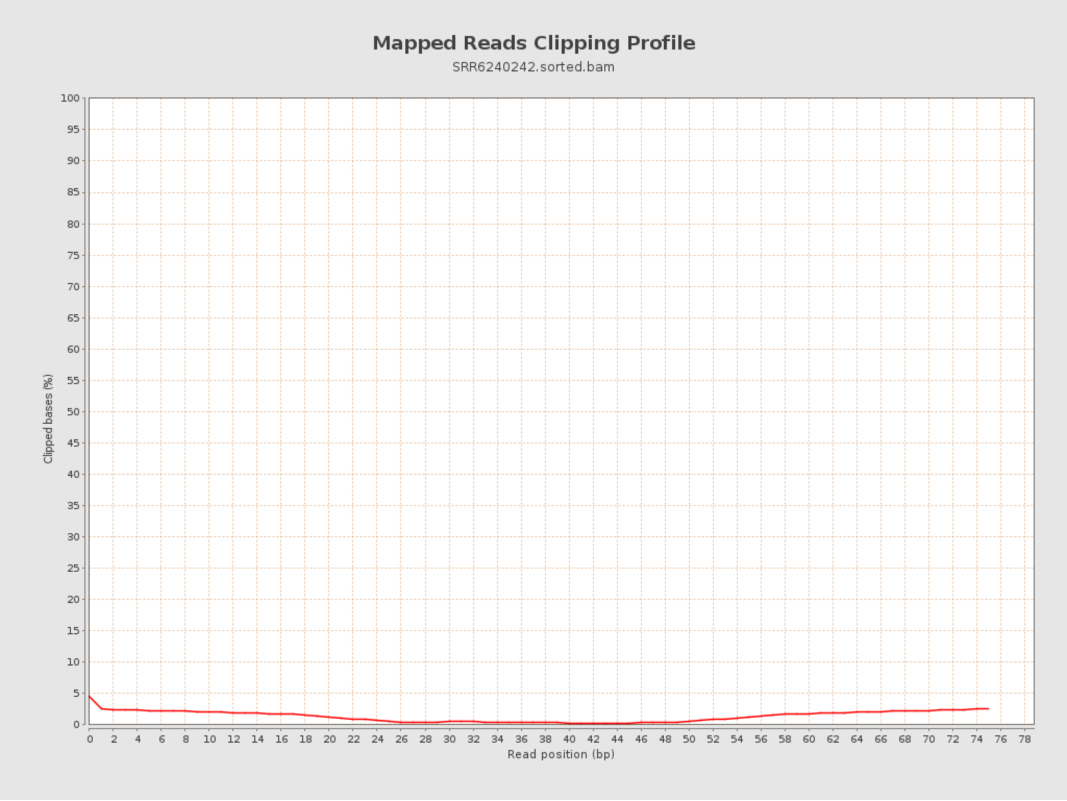
8. Results : Mapped Reads Nucleotide Content



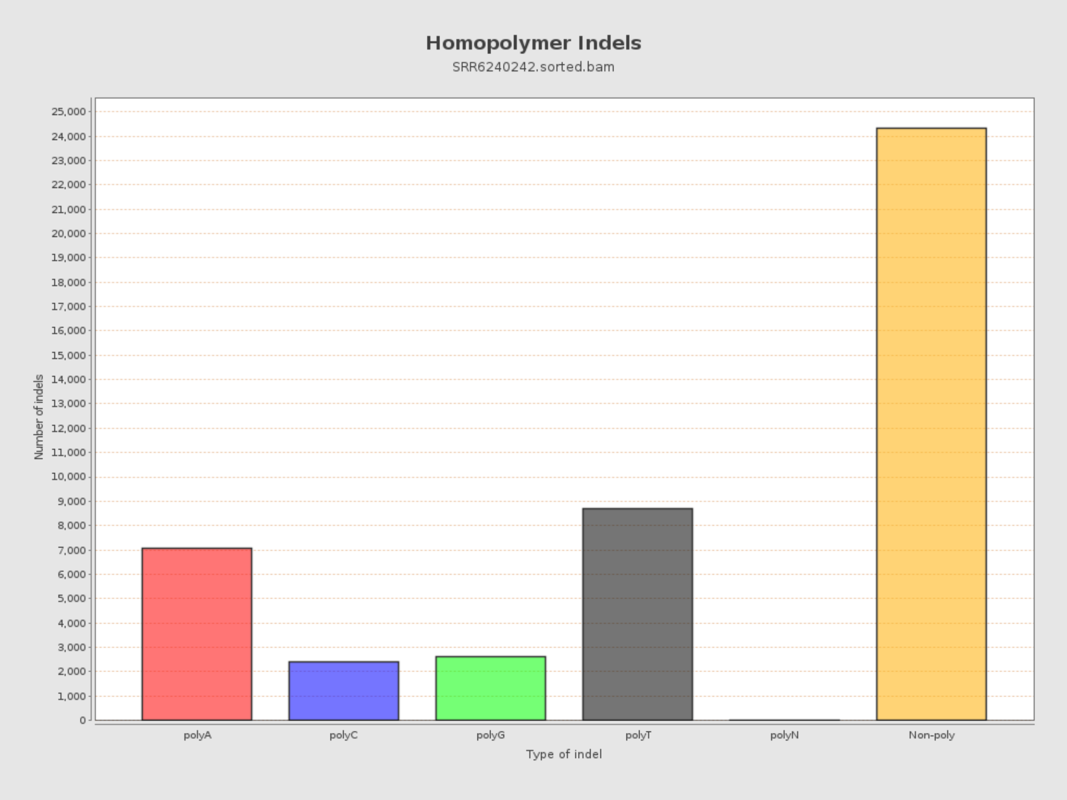
9. Results : Mapped Reads GC-content Distribution



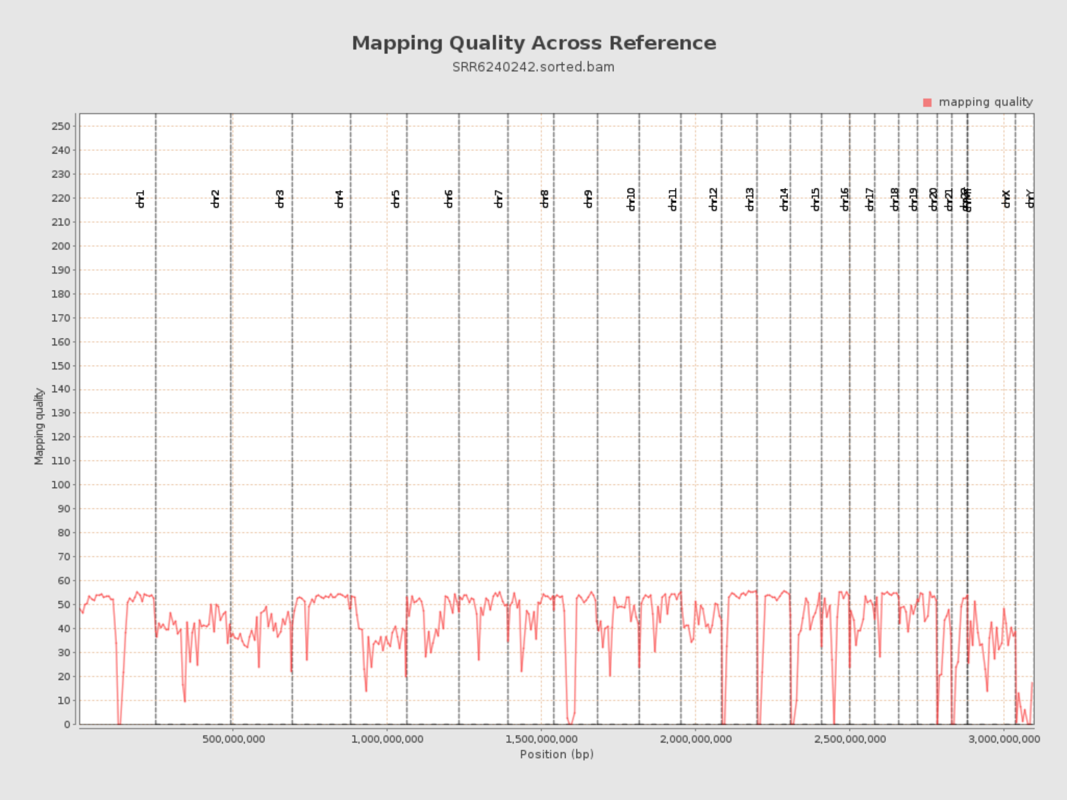
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram