Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:41:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240190.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_SRR6240190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:41:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,182,496
Mapped reads	1,725,392 / 79.06%
Unmapped reads	457,104 / 20.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,808 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	169,472 / 7.77%
Duplication rate	8.15%
Clipped reads	1,137,953 / 52.14%

2.2. ACGT Content

Number/percentage of A's	28,507,101 / 26.95%
Number/percentage of C's	18,155,742 / 17.17%
Number/percentage of T's	34,820,676 / 32.92%
Number/percentage of G's	24,260,012 / 22.94%
Number/percentage of N's	24,634 / 0.02%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.3378

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

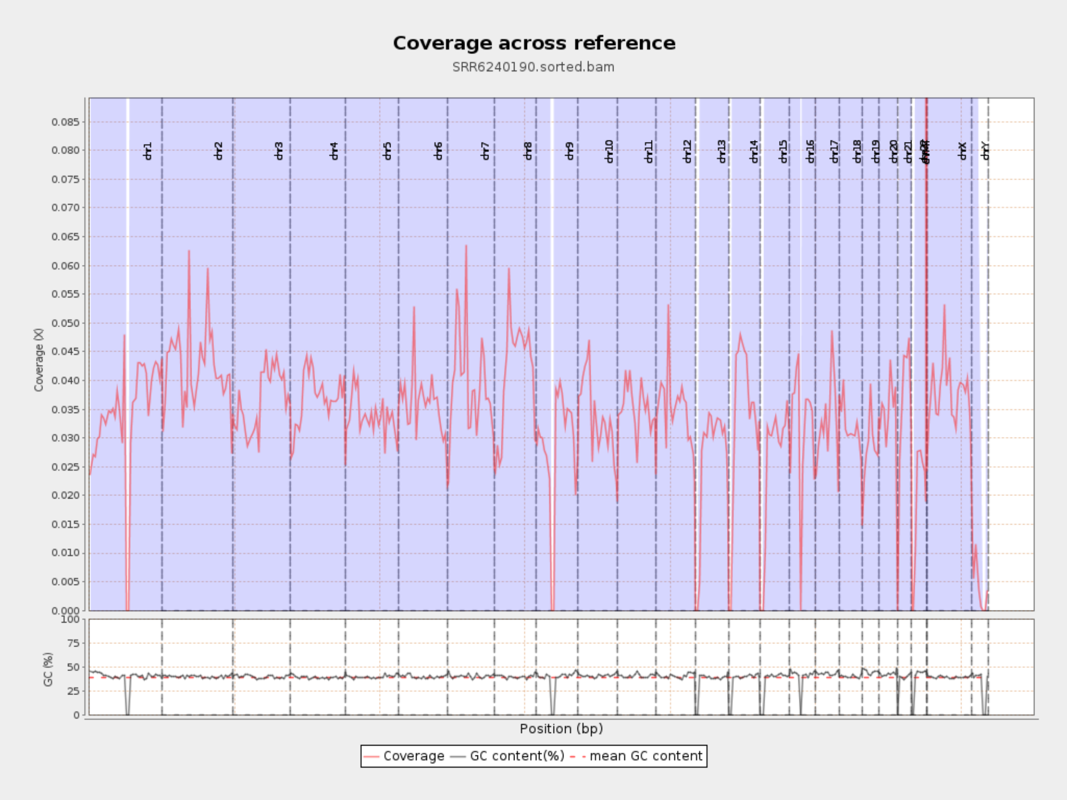
General error rate	0.97%
Mismatches	1,009,524
Insertions	7,533
Mapped reads with at least one insertion	0.43%
Deletions	35,507
Mapped reads with at least one deletion	2.04%
Homopolymer indels	49.76%

2.6. Chromosome stats

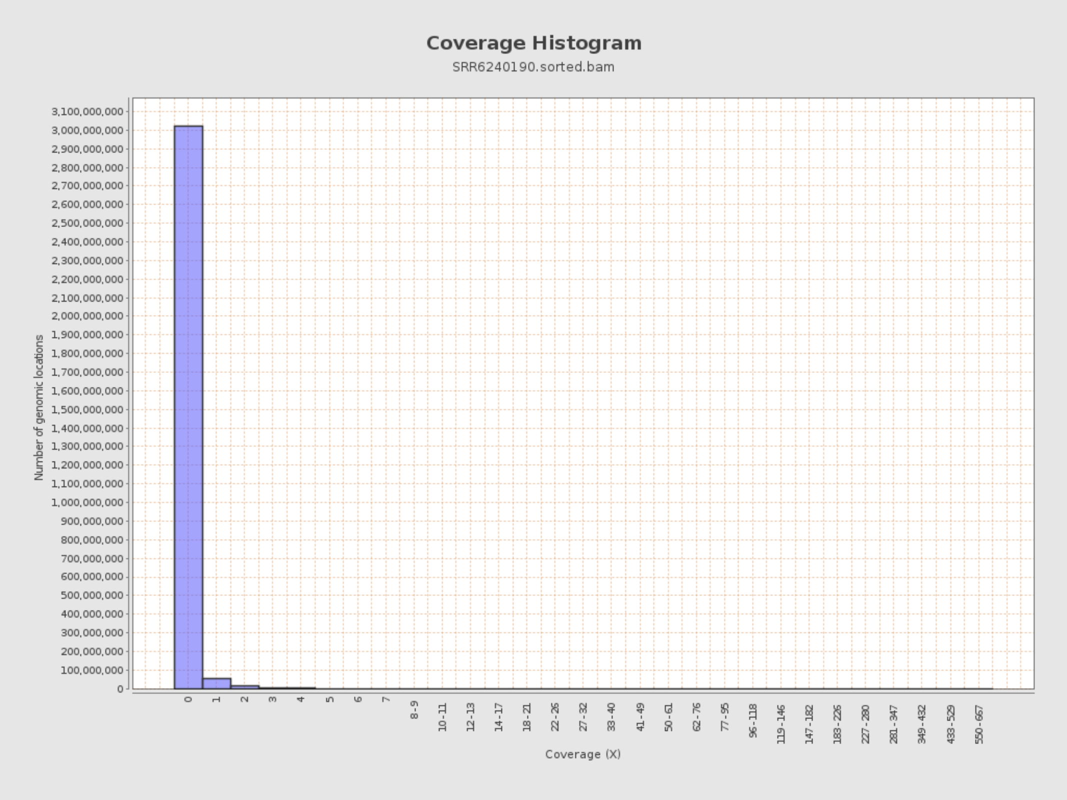
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8452763	0.0339	0.5006
chr2	243199373	10317682	0.0424	0.3997
chr3	198022430	7261818	0.0367	0.2541
chr4	191154276	7058197	0.0369	0.2623
chr5	180915260	6125246	0.0339	0.2454
chr6	171115067	6176280	0.0361	0.297
chr7	159138663	6360952	0.04	0.5415

chr8	146364022	6093225	0.0416	0.4795
chr9	141213431	3998529	0.0283	0.304
chr10	135534747	4614972	0.0341	0.2864
chr11	135006516	4739690	0.0351	0.3149
chr12	133851895	4739496	0.0354	0.2514
chr13	115169878	2986239	0.0259	0.213
chr14	107349540	3579173	0.0333	0.2503
chr15	102531392	2623591	0.0256	0.2194
chr16	90354753	2873943	0.0318	0.2431
chr17	81195210	2643320	0.0326	0.2532
chr18	78077248	2512955	0.0322	0.4767
chr19	59128983	1696073	0.0287	0.3344
chr20	63025520	2177713	0.0346	0.2512
chr21	48129895	1679435	0.0349	0.2558
chr22	51304566	933492	0.0182	0.171
chrMT	16571	72540	4.3775	4.4489
chrX	155270560	5861830	0.0378	0.2778
chrY	59373566	248100	0.0042	0.0939

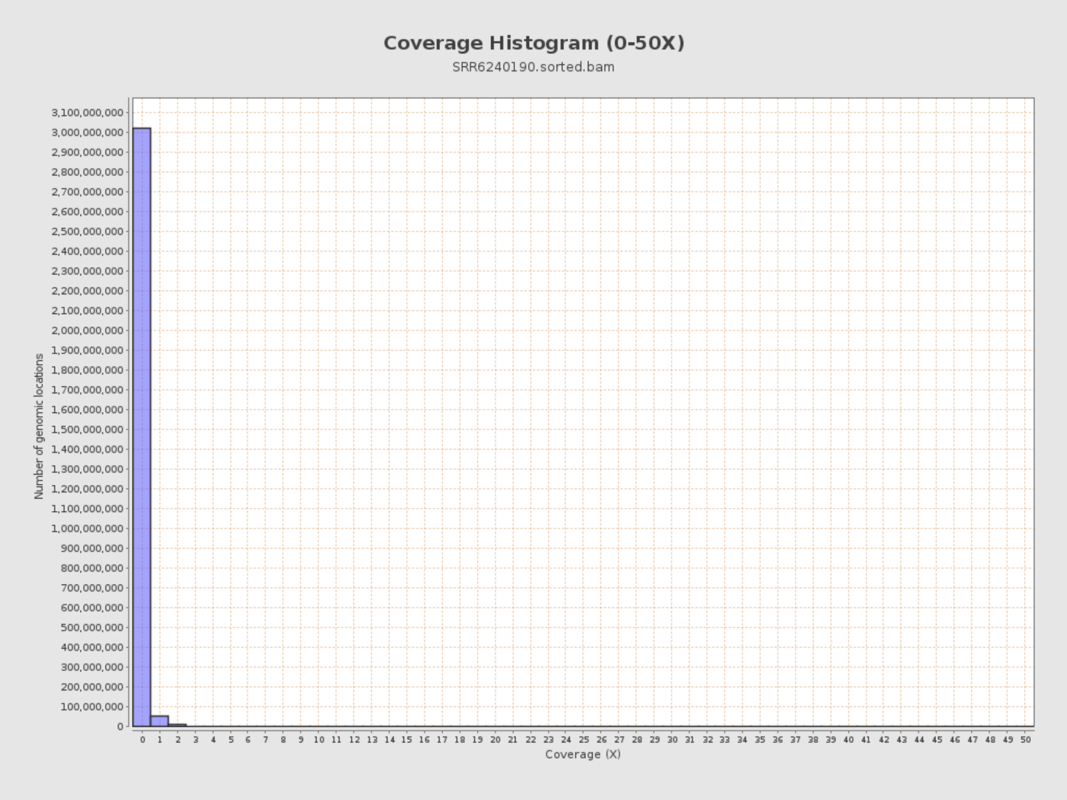
3. Results : Coverage across reference



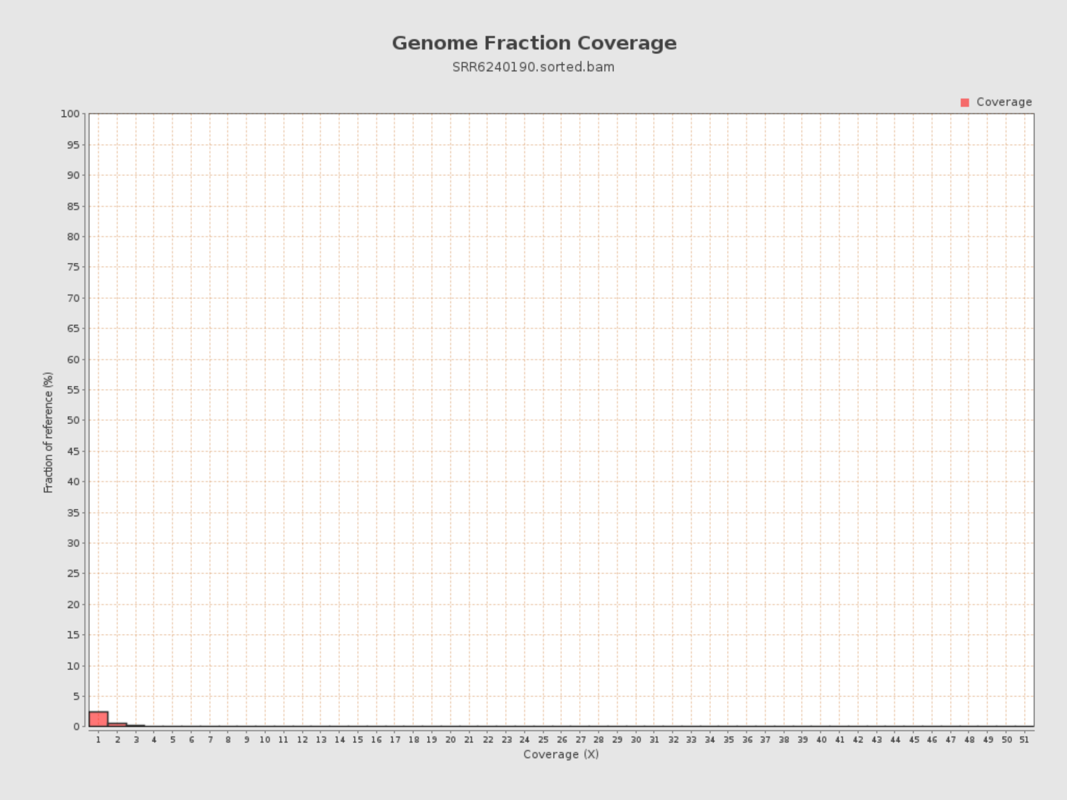
4. Results : Coverage Histogram



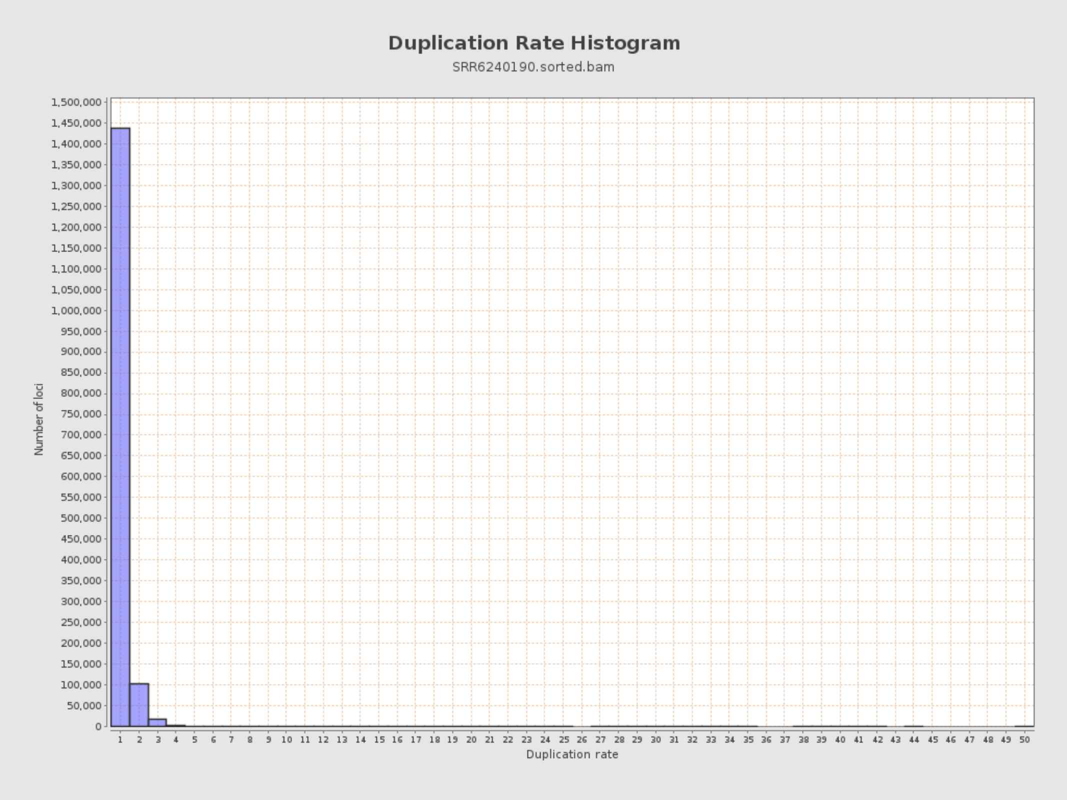
5. Results : Coverage Histogram (0-50X)



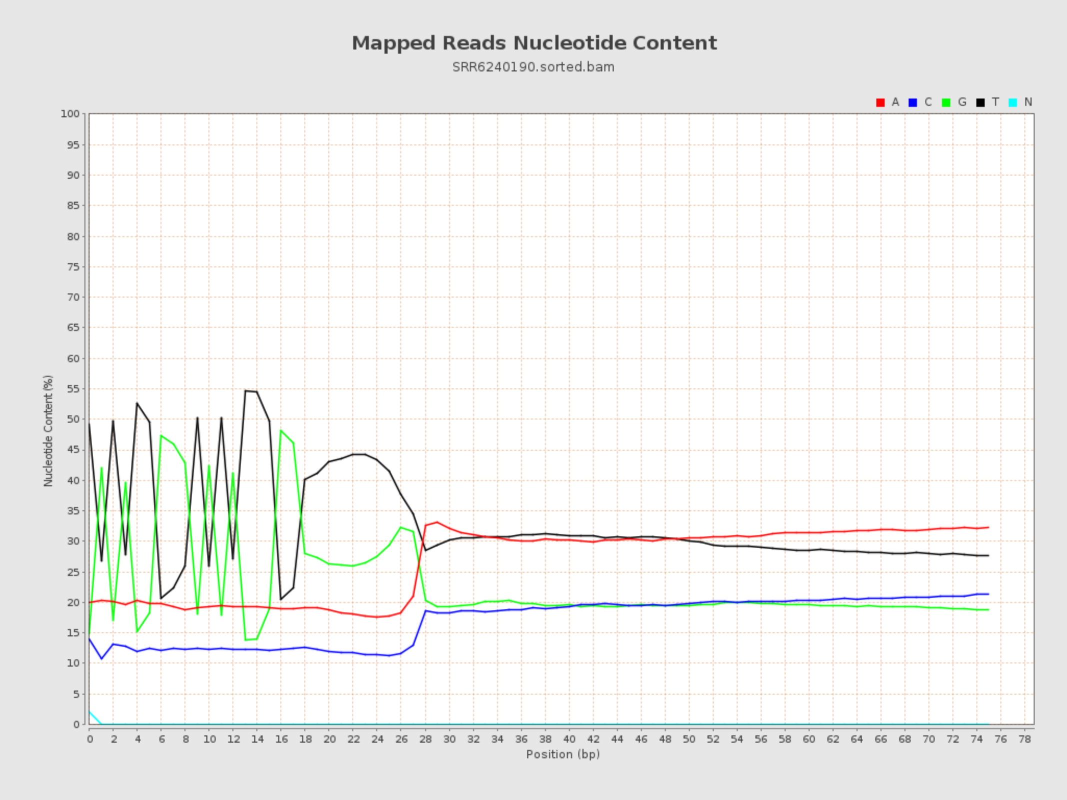
6. Results : Genome Fraction Coverage



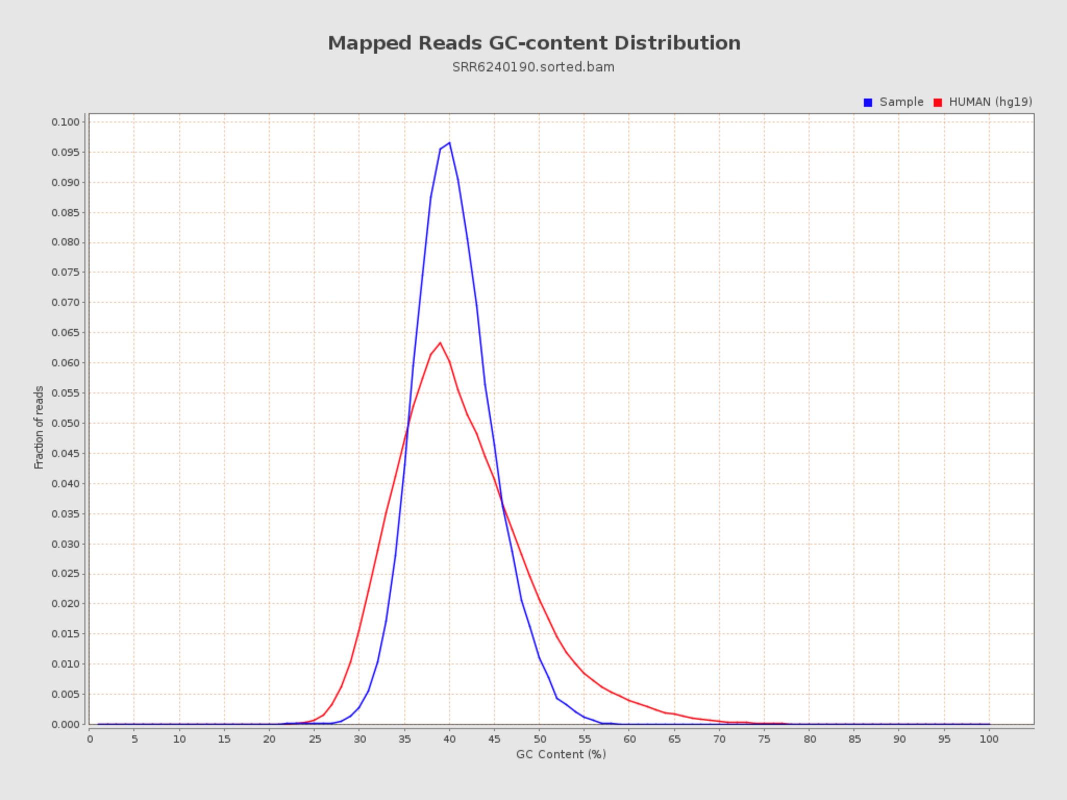
7. Results : Duplication Rate Histogram



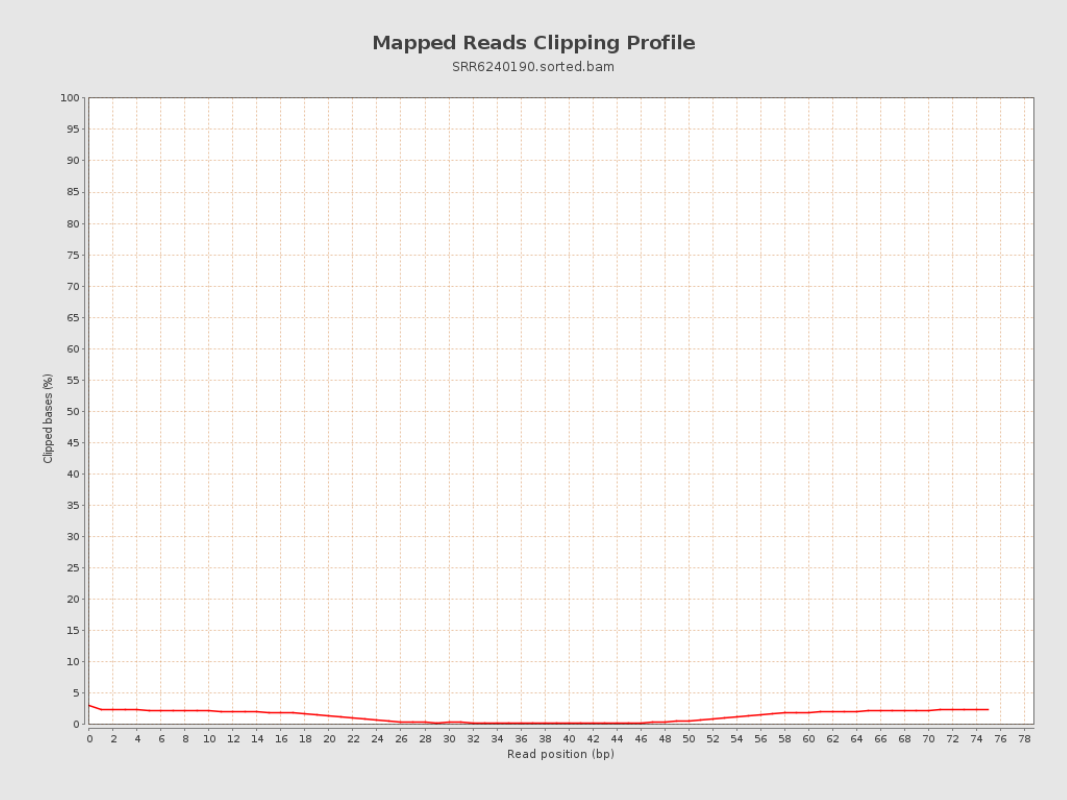
8. Results : Mapped Reads Nucleotide Content



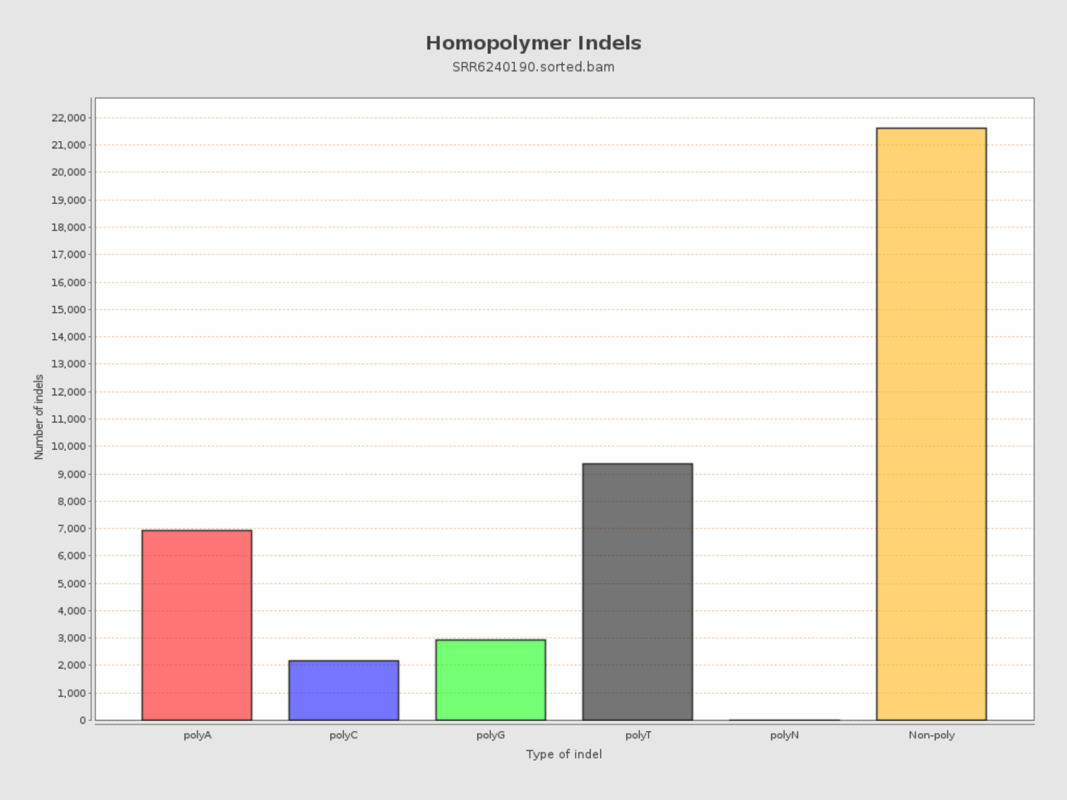
9. Results : Mapped Reads GC-content Distribution



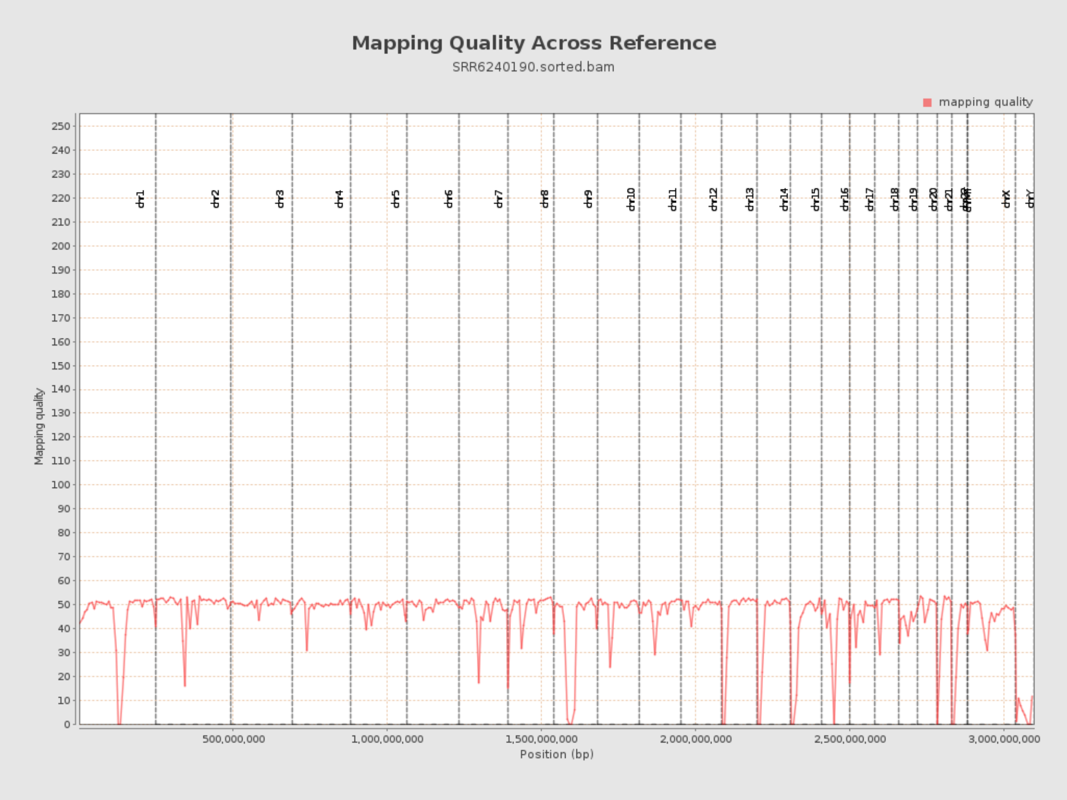
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram