Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:52:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240236.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_SRR6240236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:52:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,532,768
Mapped reads	2,027,994 / 80.07%
Unmapped reads	504,774 / 19.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,001 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	331,676 / 13.1%
Duplication rate	11.9%
Clipped reads	900,450 / 35.55%

2.2. ACGT Content

Number/percentage of A's	37,654,400 / 27.86%
Number/percentage of C's	24,702,406 / 18.28%
Number/percentage of T's	43,558,111 / 32.22%
Number/percentage of G's	29,204,003 / 21.61%
Number/percentage of N's	50,578 / 0.04%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0437

Standard Deviation	0.5327

2.4. Mapping Quality

Mean Mapping Quality	47.1

2.5. Mismatches and indels

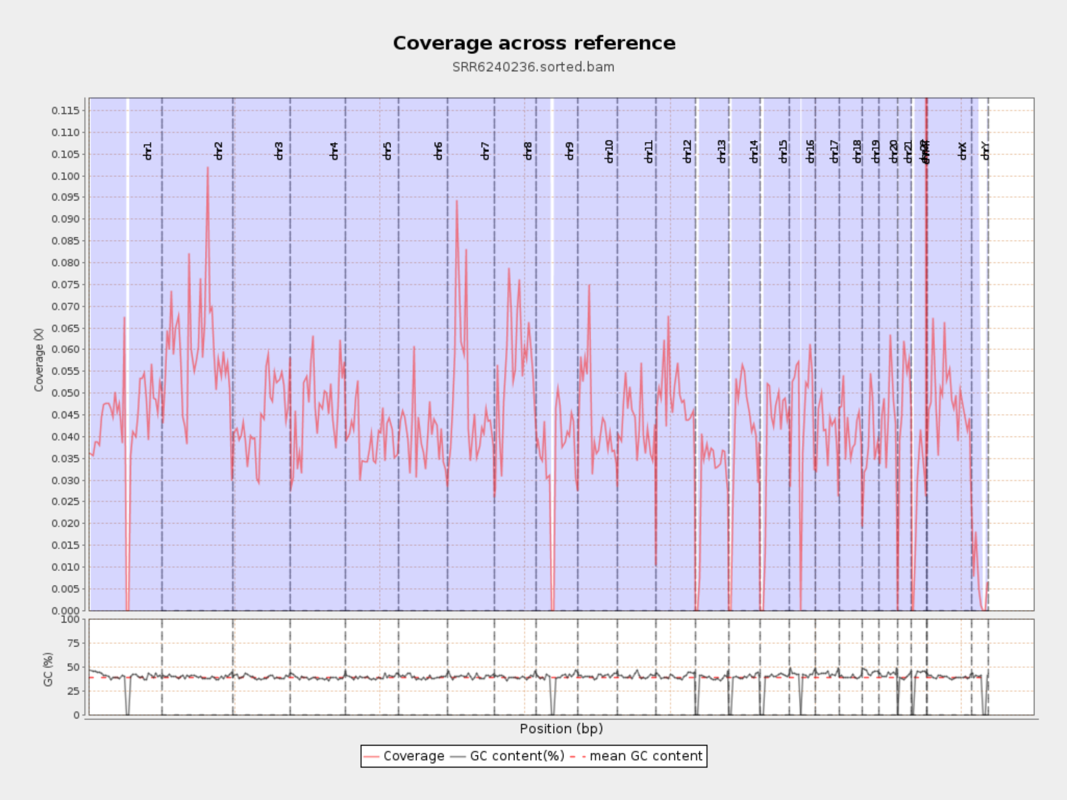
General error rate	0.87%
Mismatches	1,162,780
Insertions	9,889
Mapped reads with at least one insertion	0.48%
Deletions	37,400
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.12%

2.6. Chromosome stats

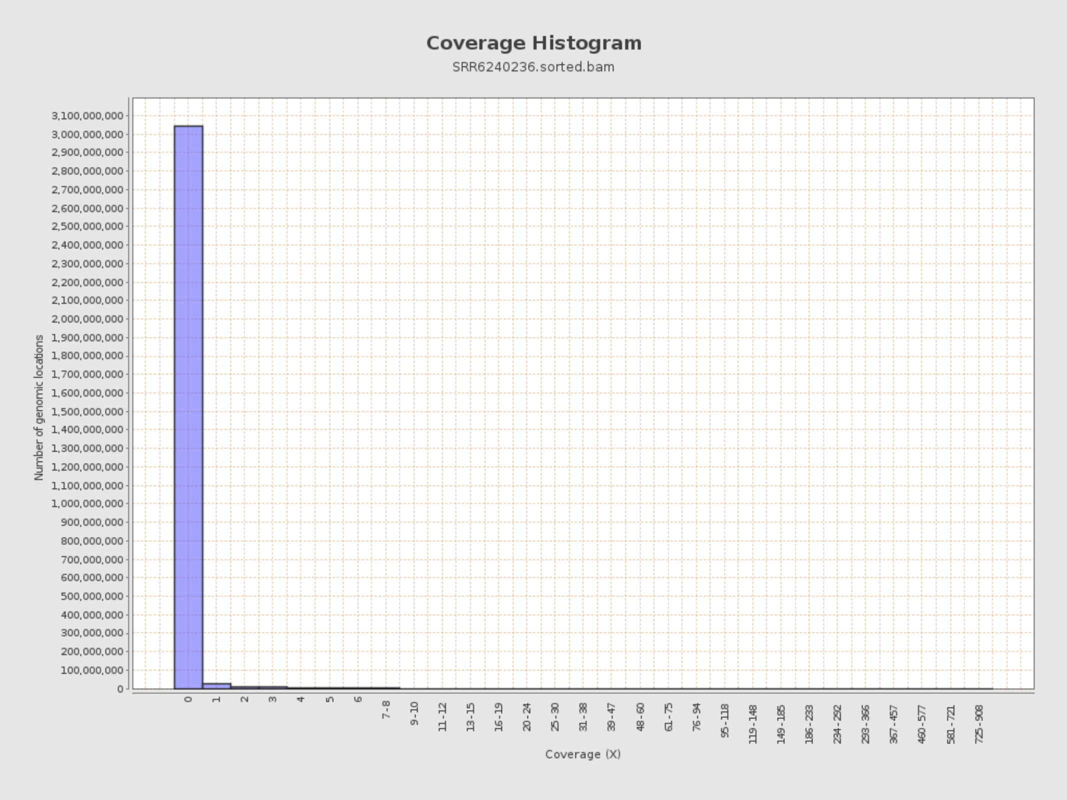
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10753278	0.0431	0.7943
chr2	243199373	14532424	0.0598	0.5905
chr3	198022430	8831923	0.0446	0.4339
chr4	191154276	8901094	0.0466	0.4521
chr5	180915260	7150060	0.0395	0.4132
chr6	171115067	6875556	0.0402	0.4467
chr7	159138663	7939140	0.0499	0.7548

chr8	146364022	8211559	0.0561	0.741
chr9	141213431	4982649	0.0353	0.4438
chr10	135534747	6046855	0.0446	0.506
chr11	135006516	5779424	0.0428	0.5016
chr12	133851895	6626970	0.0495	0.4891
chr13	115169878	3405611	0.0296	0.3557
chr14	107349540	4219371	0.0393	0.4134
chr15	102531392	3887145	0.0379	0.3961
chr16	90354753	4087680	0.0452	0.4385
chr17	81195210	3284679	0.0405	0.4257
chr18	78077248	3295828	0.0422	0.6623
chr19	59128983	2296214	0.0388	0.551
chr20	63025520	2793261	0.0443	0.4323
chr21	48129895	2231732	0.0464	0.4479
chr22	51304566	1230444	0.024	0.3091
chrMT	16571	21064	1.2711	2.0245
chrX	155270560	7473092	0.0481	0.4696
chrY	59373566	378500	0.0064	0.1486

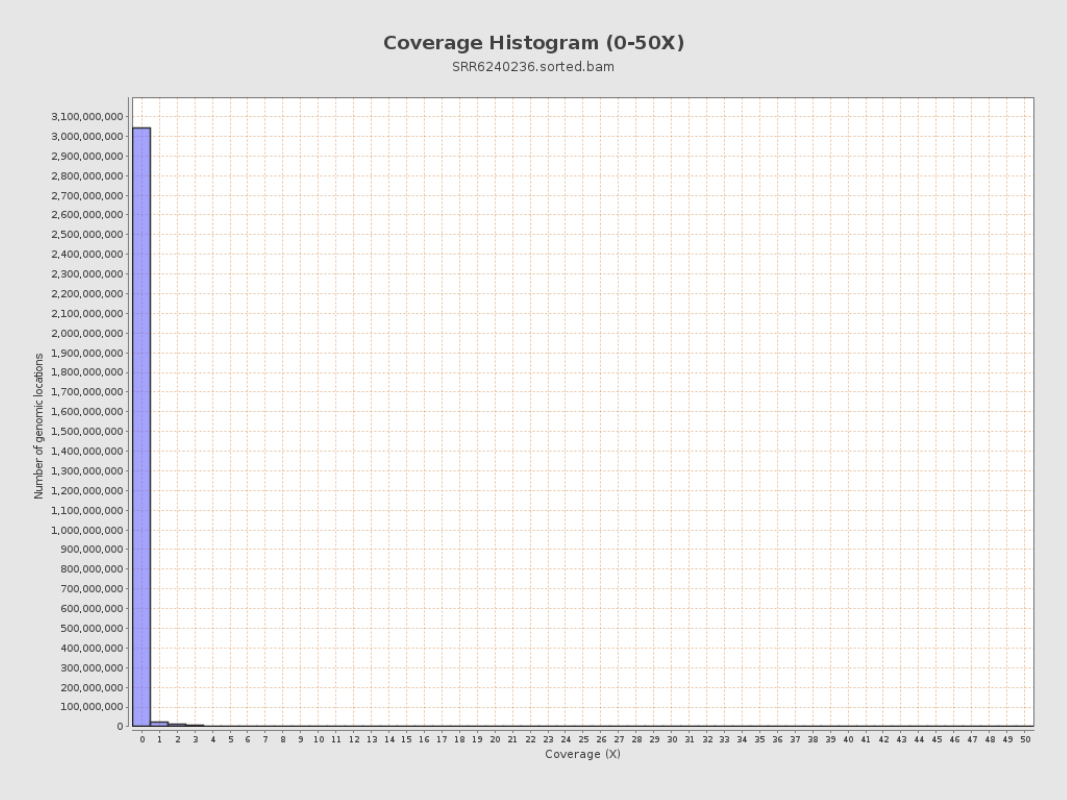
3. Results : Coverage across reference



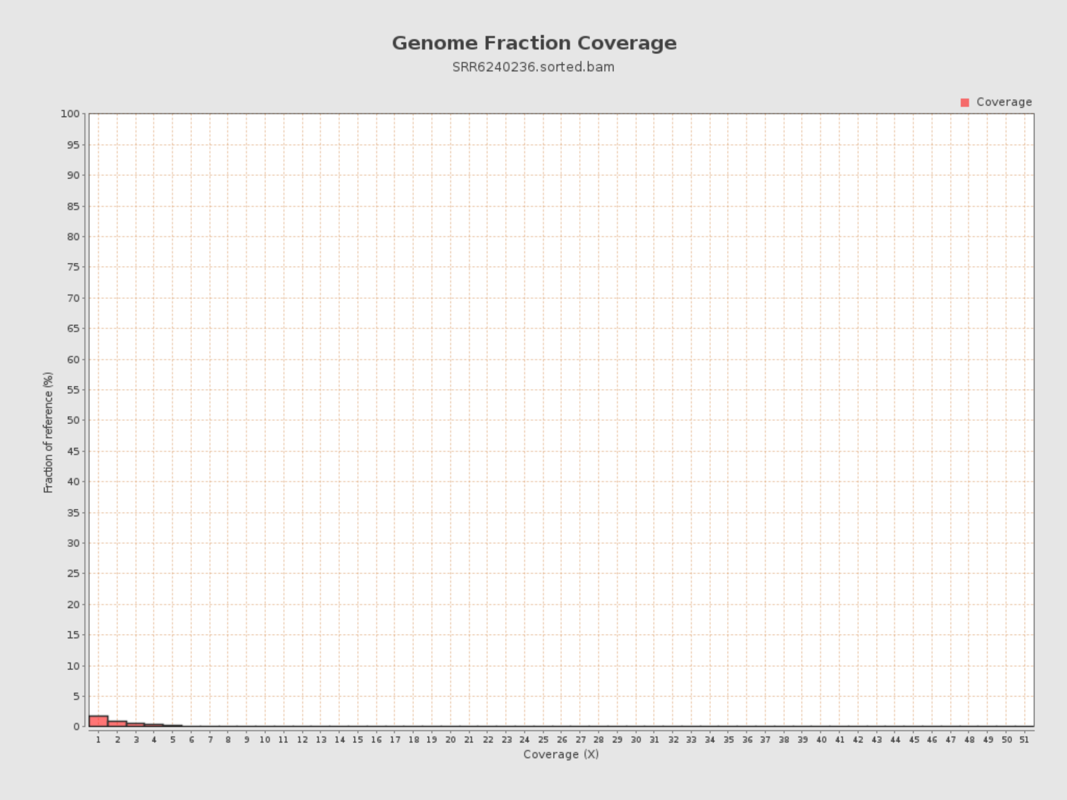
4. Results : Coverage Histogram



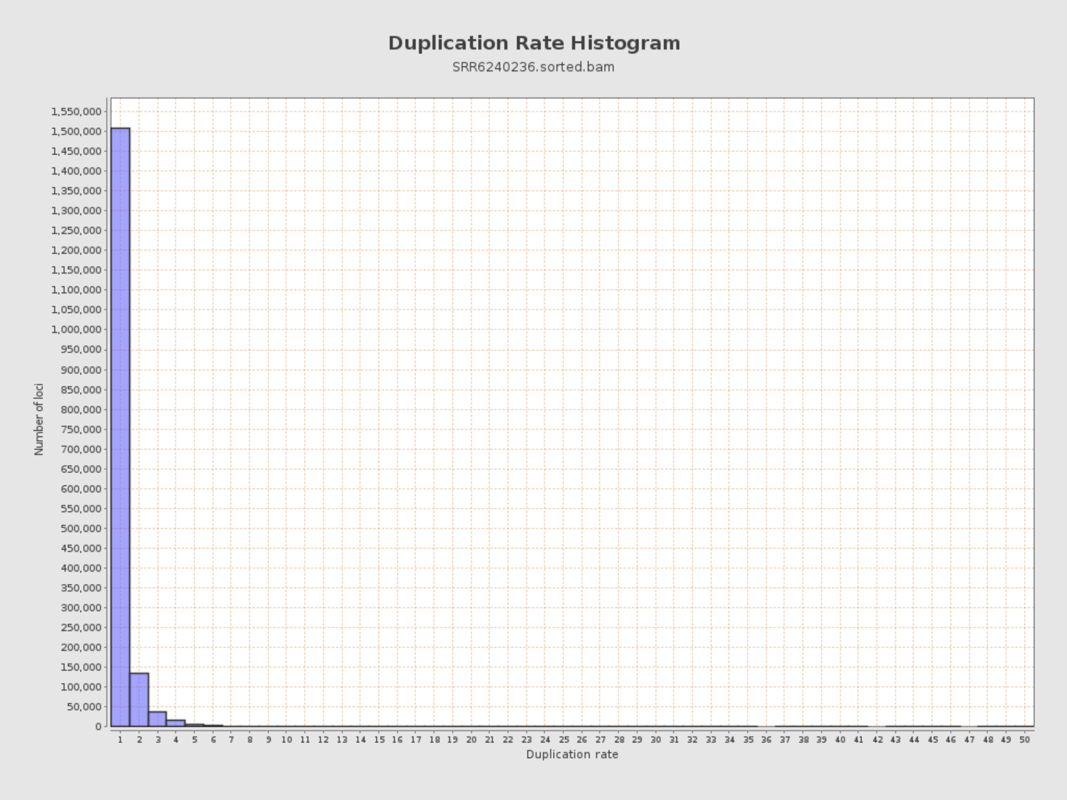
5. Results : Coverage Histogram (0-50X)



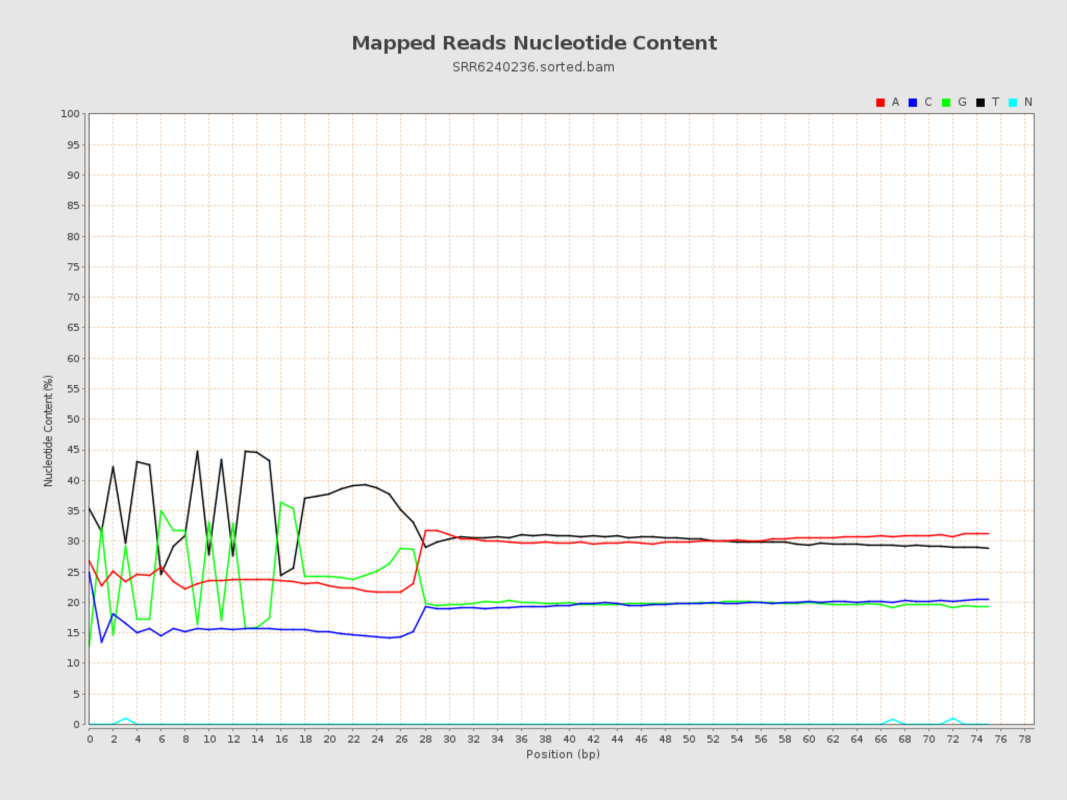
6. Results : Genome Fraction Coverage



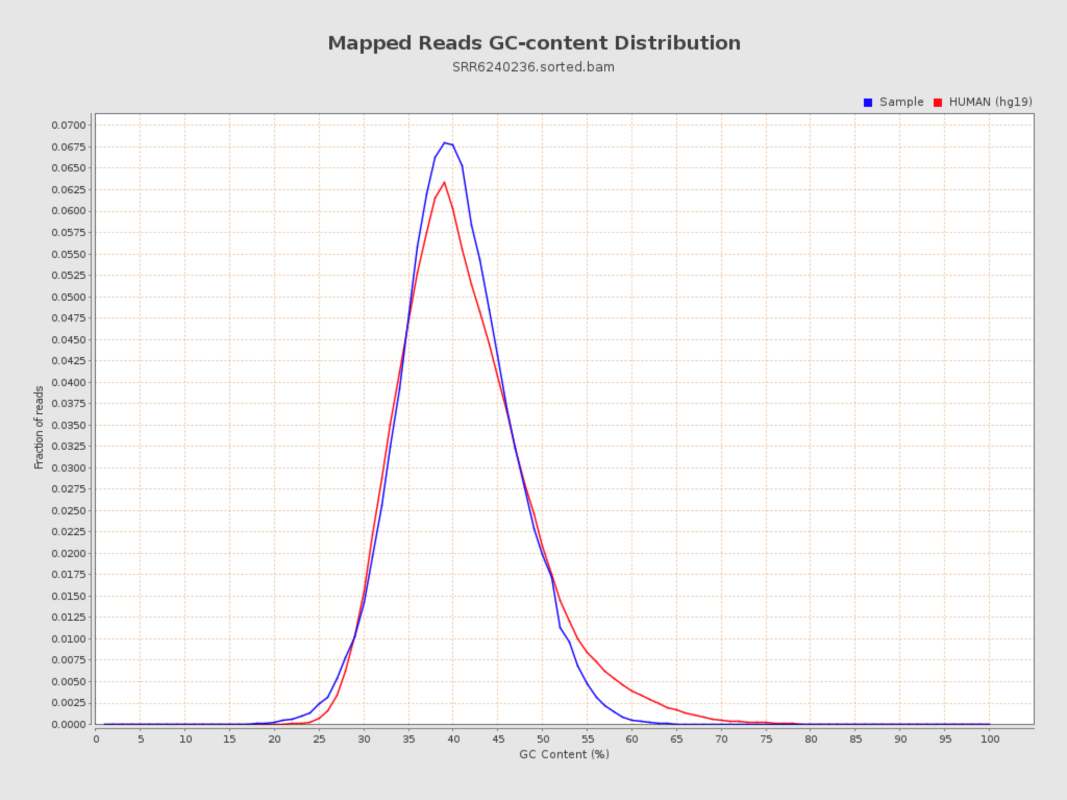
7. Results : Duplication Rate Histogram



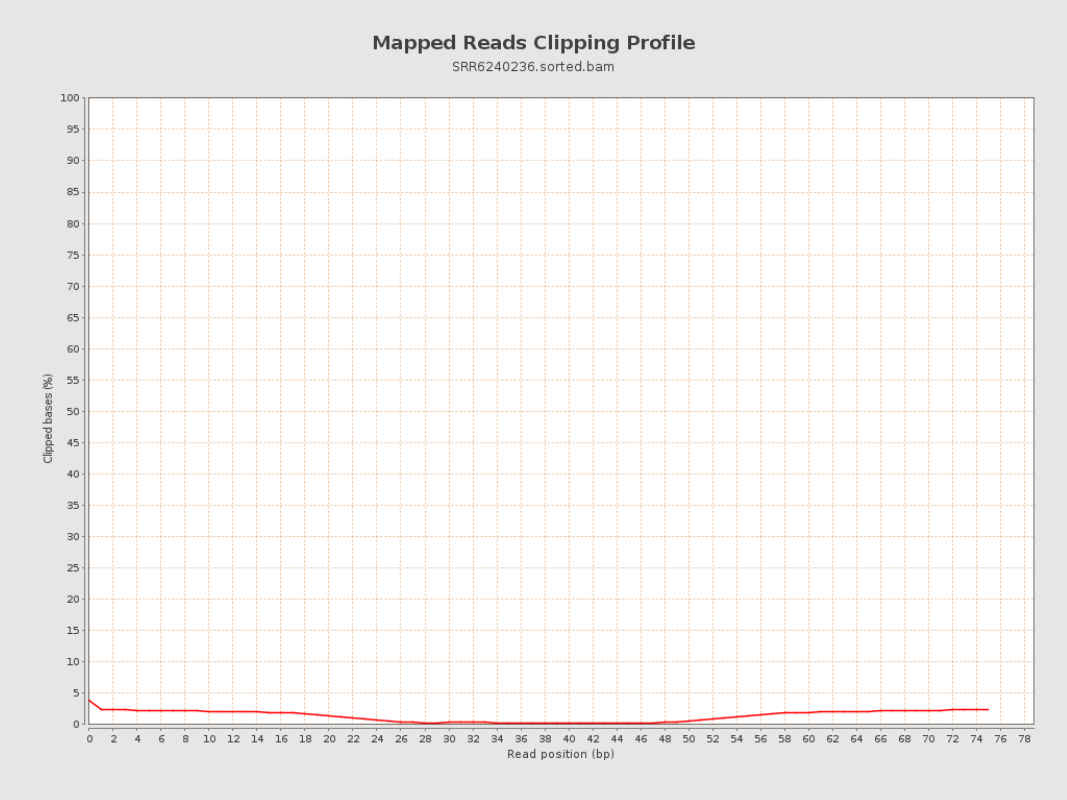
8. Results : Mapped Reads Nucleotide Content



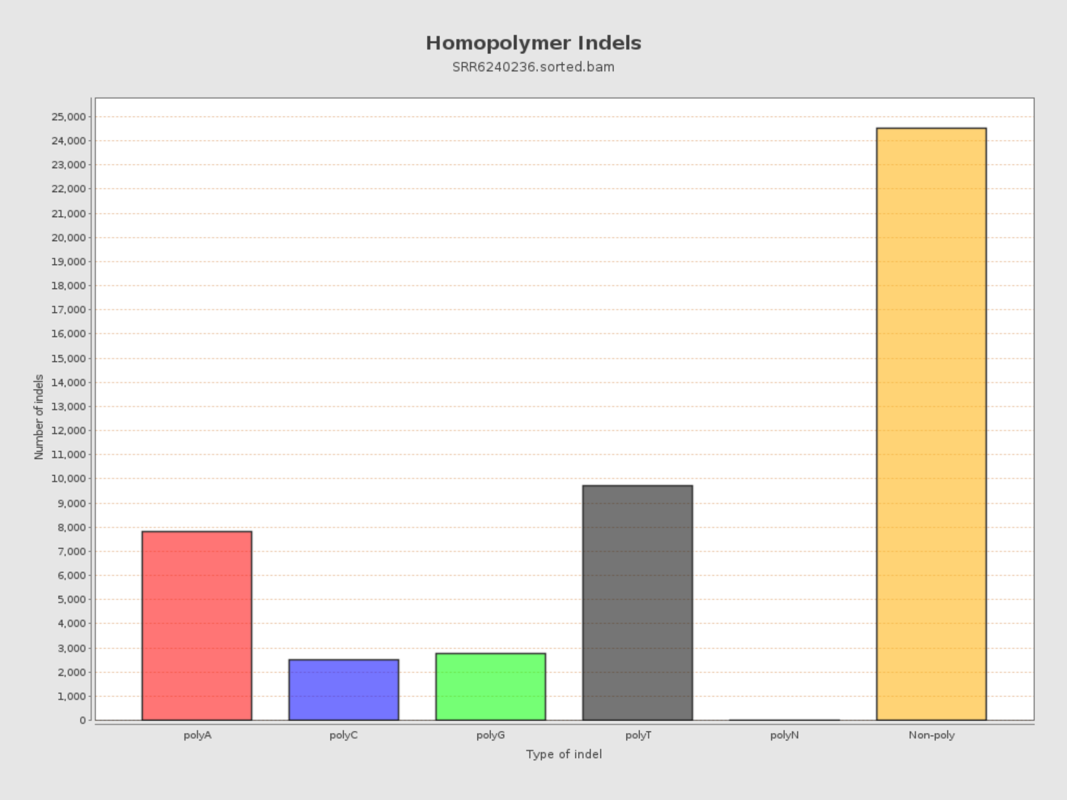
9. Results : Mapped Reads GC-content Distribution



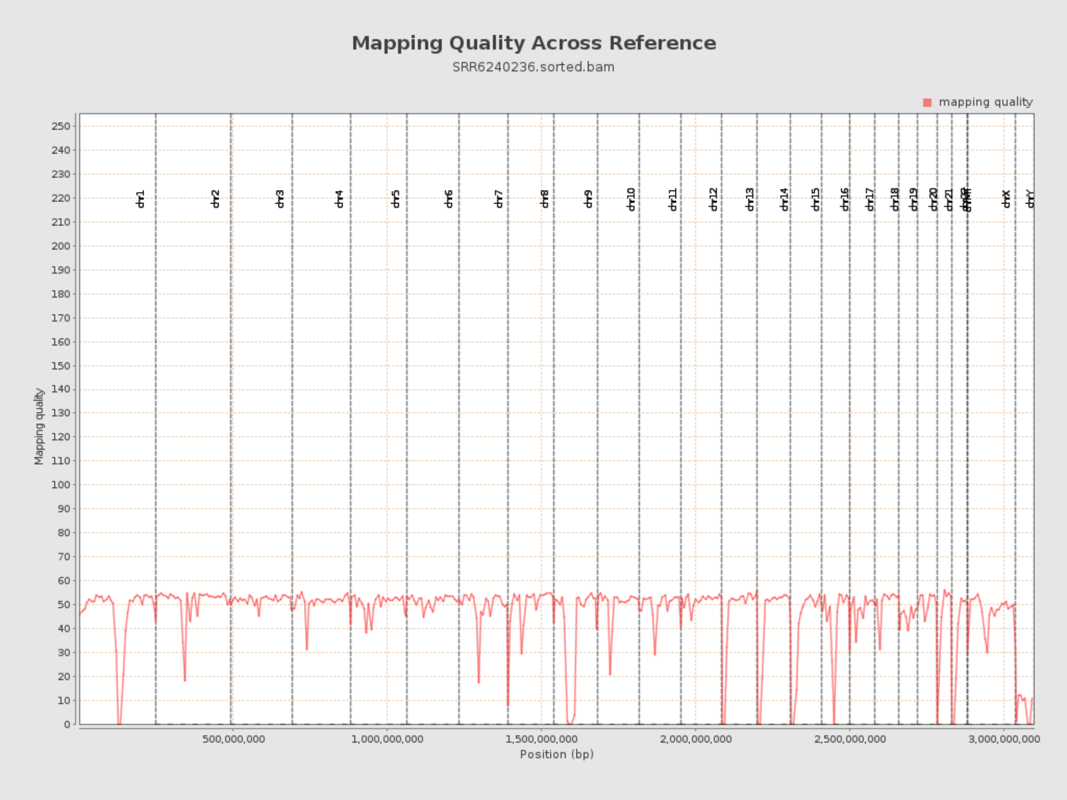
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram