Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:26:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240271.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_SRR6240271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:26:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,655,931
Mapped reads	2,196,323 / 82.7%
Unmapped reads	459,608 / 17.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,671 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	334,998 / 12.61%
Duplication rate	11.35%
Clipped reads	1,255,320 / 47.26%

2.2. ACGT Content

Number/percentage of A's	38,132,121 / 27.36%
Number/percentage of C's	25,509,542 / 18.31%
Number/percentage of T's	44,249,142 / 31.75%
Number/percentage of G's	31,429,139 / 22.55%
Number/percentage of N's	34,485 / 0.02%
GC Percentage	40.86%

2.3. Coverage

Mean	0.045

Standard Deviation	0.4572

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

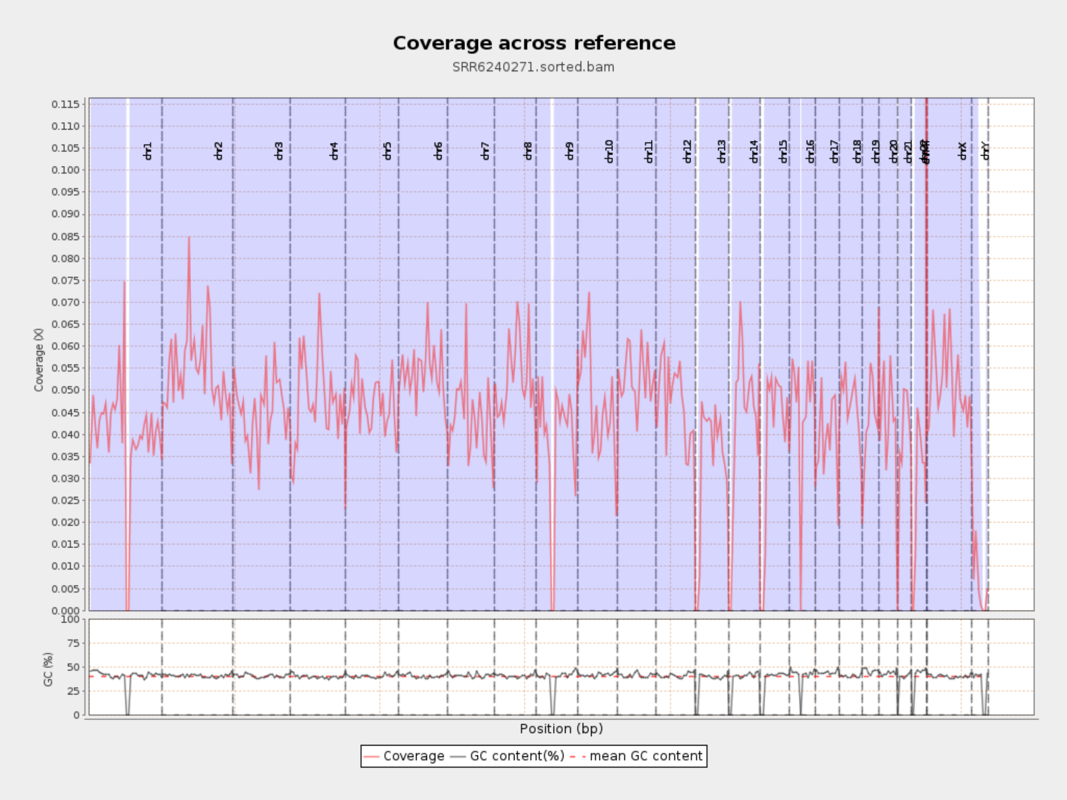
General error rate	0.8%
Mismatches	1,091,966
Insertions	9,584
Mapped reads with at least one insertion	0.43%
Deletions	30,631
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.4%

2.6. Chromosome stats

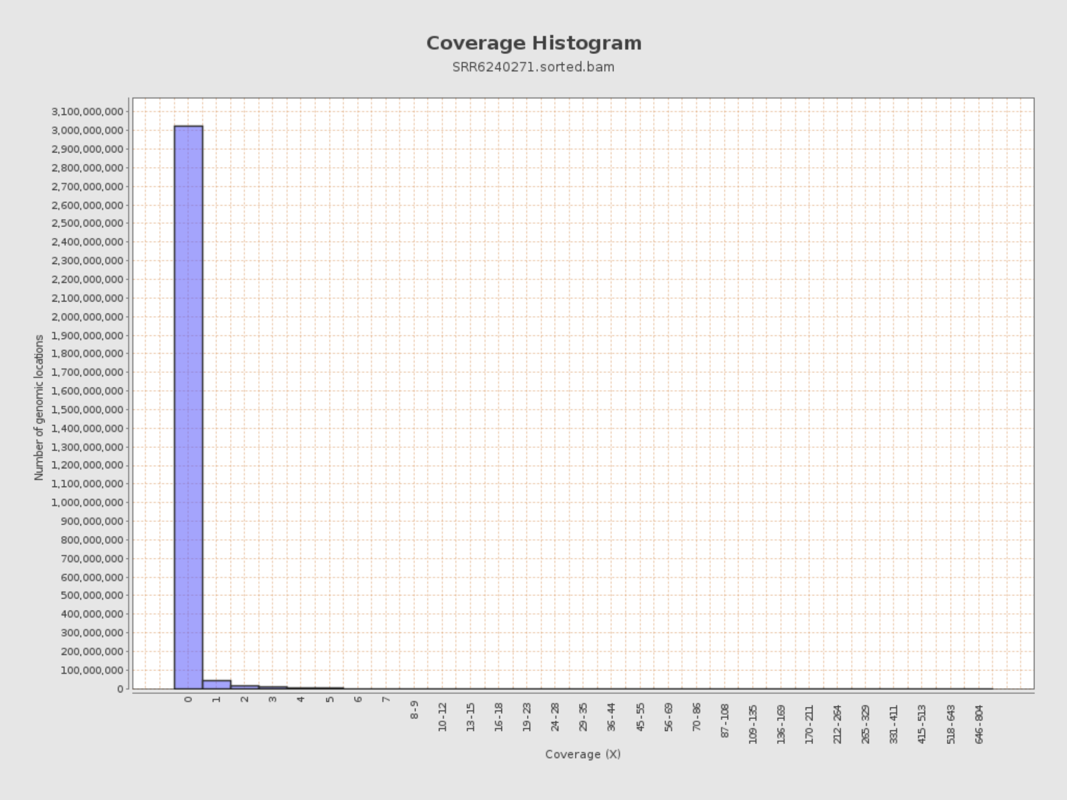
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10021722	0.0402	0.7242
chr2	243199373	13297935	0.0547	0.5755
chr3	198022430	8982426	0.0454	0.3627
chr4	191154276	9167638	0.048	0.3834
chr5	180915260	8434602	0.0466	0.363
chr6	171115067	9245122	0.054	0.4566
chr7	159138663	6944473	0.0436	0.4754

chr8	146364022	7785634	0.0532	0.5396
chr9	141213431	5435076	0.0385	0.399
chr10	135534747	6449079	0.0476	0.4681
chr11	135006516	7106569	0.0526	0.4213
chr12	133851895	6307139	0.0471	0.3725
chr13	115169878	3838163	0.0333	0.309
chr14	107349540	4540378	0.0423	0.3651
chr15	102531392	3935222	0.0384	0.3671
chr16	90354753	4157878	0.046	0.3705
chr17	81195210	3129988	0.0385	0.3393
chr18	78077248	3707086	0.0475	0.5966
chr19	59128983	2598803	0.044	0.5253
chr20	63025520	2756959	0.0437	0.3569
chr21	48129895	1826557	0.038	0.3329
chr22	51304566	1324699	0.0258	0.2648
chrMT	16571	33540	2.024	2.8476
chrX	155270560	7991666	0.0515	0.4043
chrY	59373566	387913	0.0065	0.1392

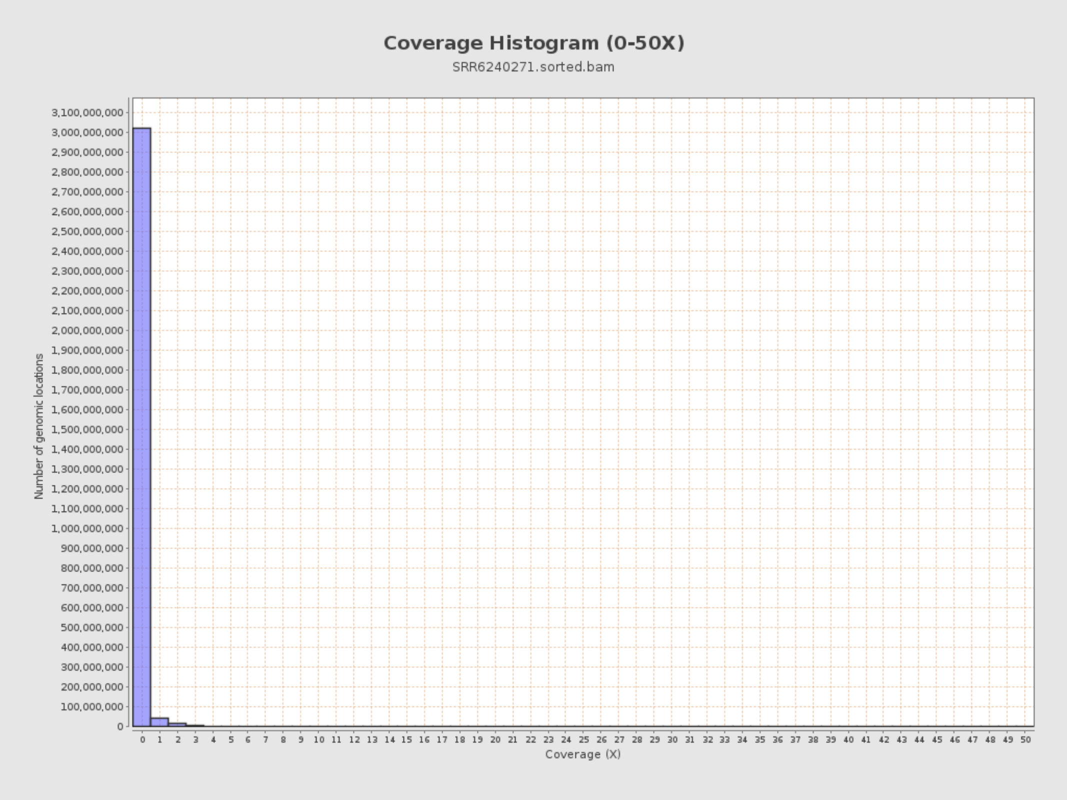
3. Results : Coverage across reference



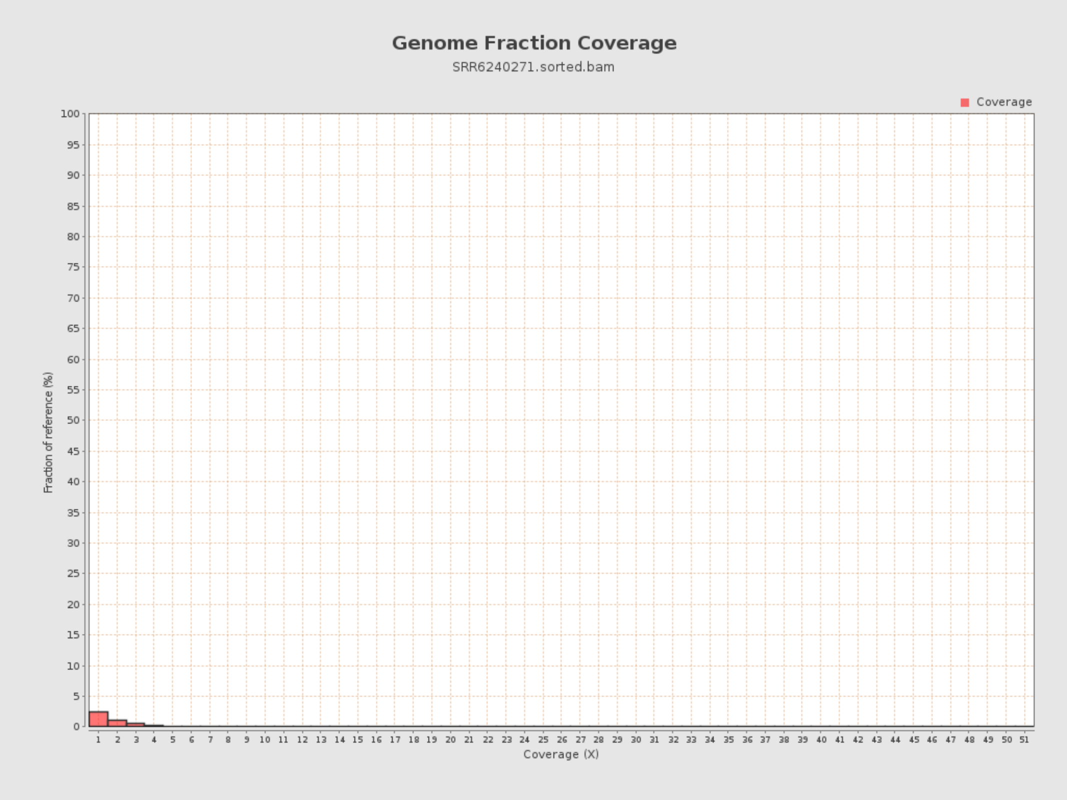
4. Results : Coverage Histogram



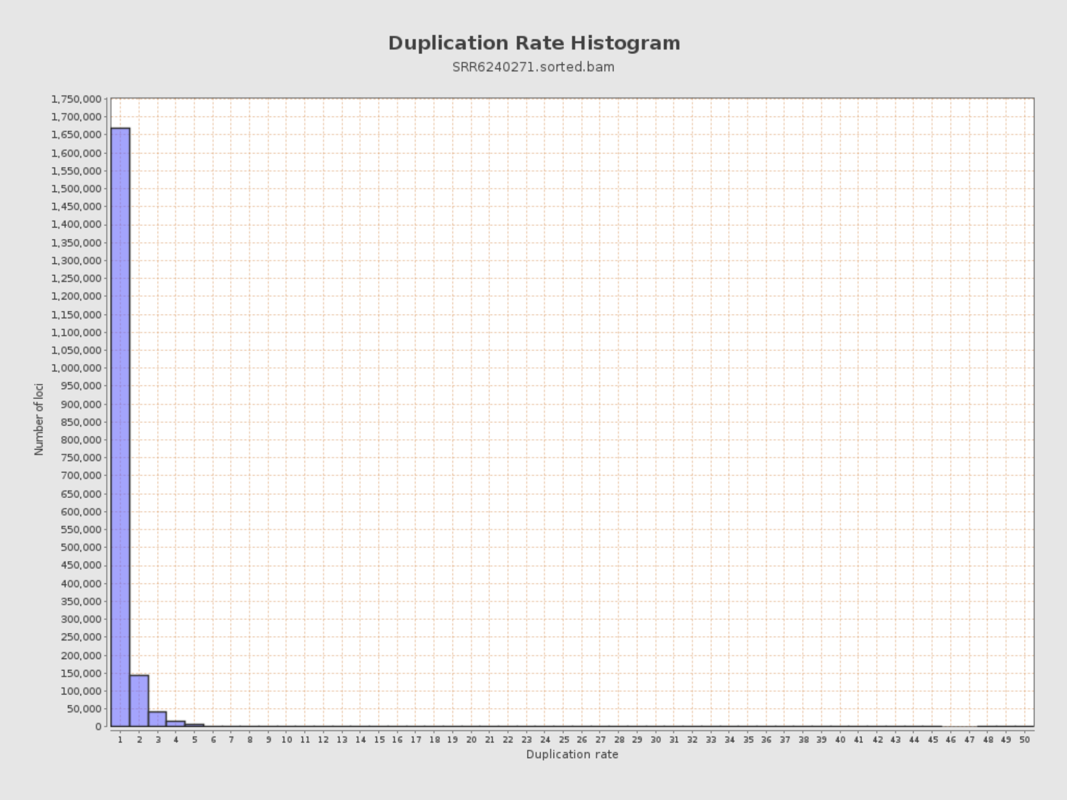
5. Results : Coverage Histogram (0-50X)



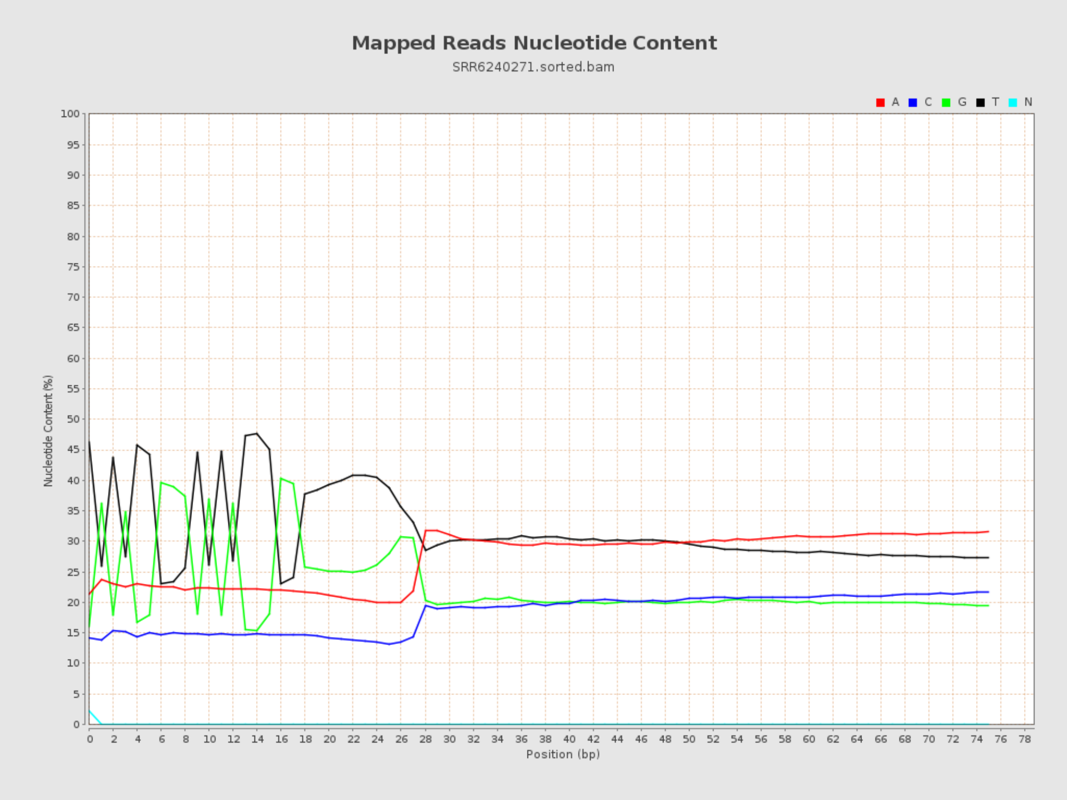
6. Results : Genome Fraction Coverage



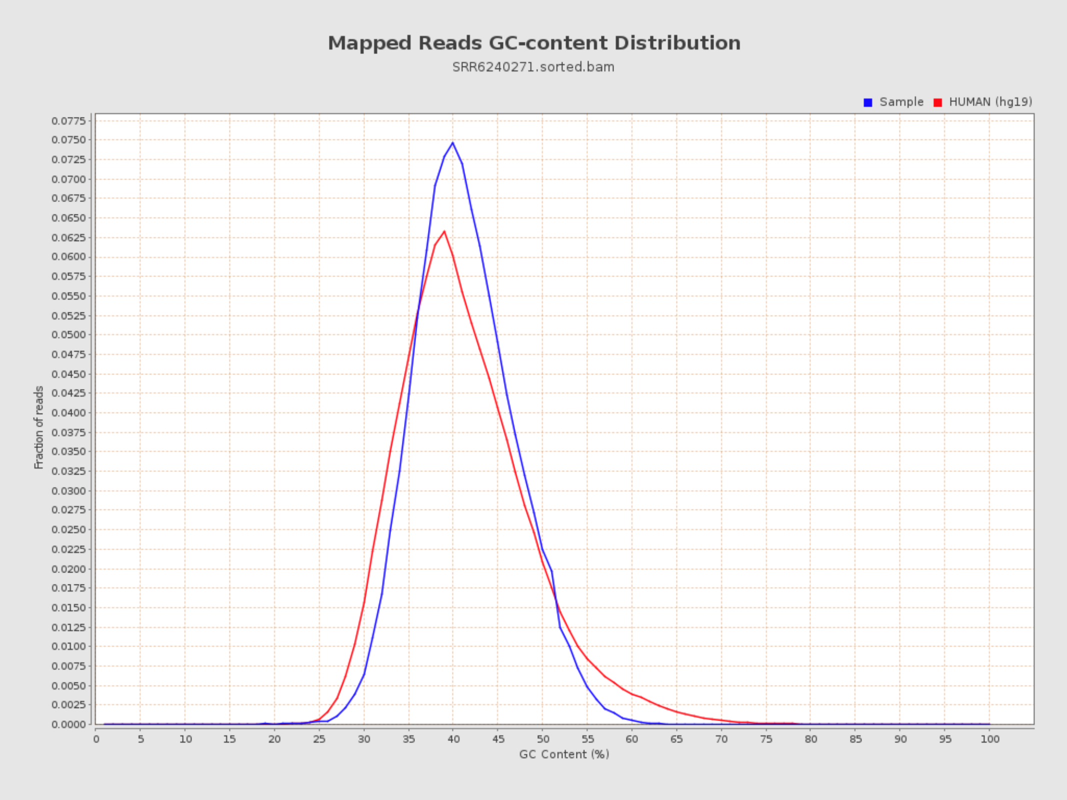
7. Results : Duplication Rate Histogram



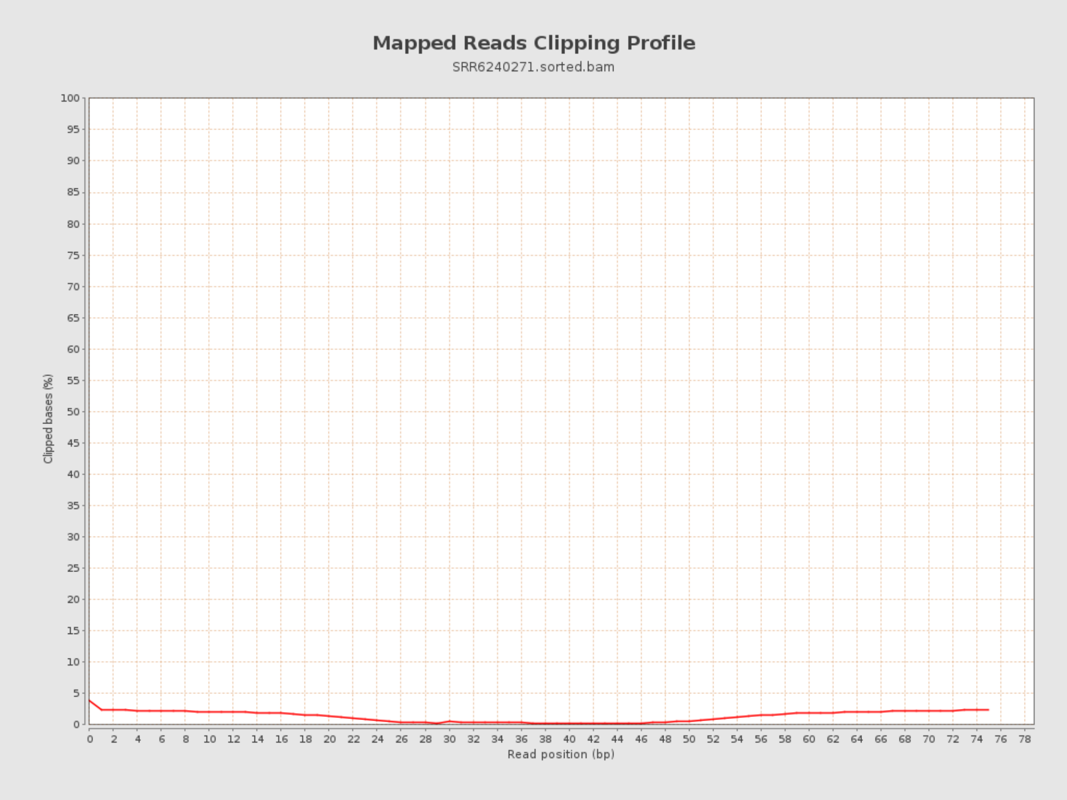
8. Results : Mapped Reads Nucleotide Content



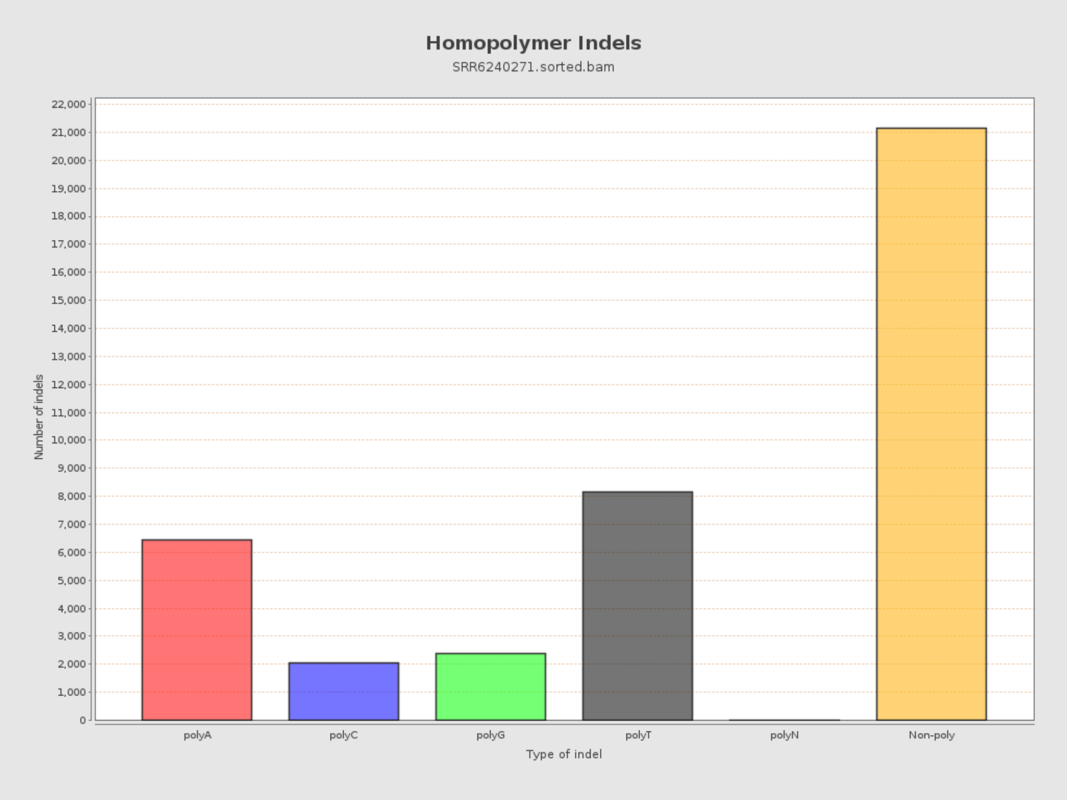
9. Results : Mapped Reads GC-content Distribution



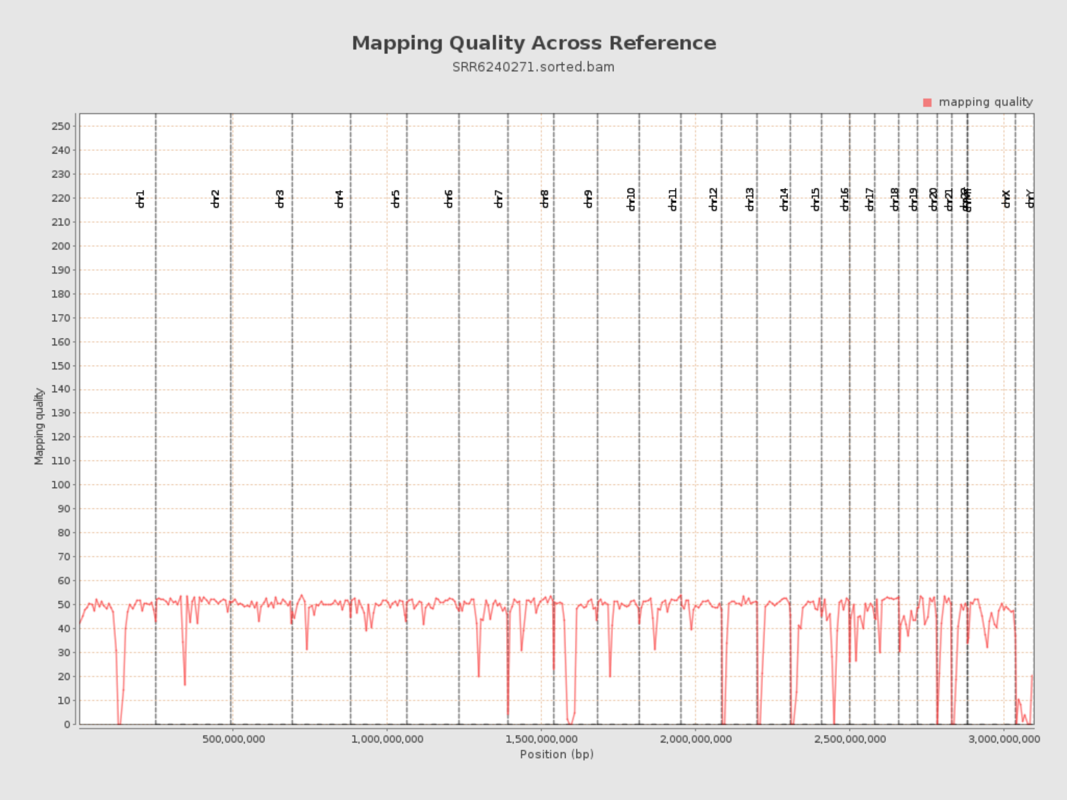
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram