Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:09:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234073.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_SRR6234073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,836,247
Mapped reads	4,556,365 / 94.21%
Unmapped reads	279,882 / 5.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,627 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	567,518 / 11.73%
Duplication rate	10.28%
Clipped reads	2,427,400 / 50.19%

2.2. ACGT Content

Number/percentage of A's	75,311,270 / 25.71%
Number/percentage of C's	52,990,134 / 18.09%
Number/percentage of T's	95,181,776 / 32.5%
Number/percentage of G's	69,398,050 / 23.69%
Number/percentage of N's	27,826 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0947

Standard Deviation	1.0234

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

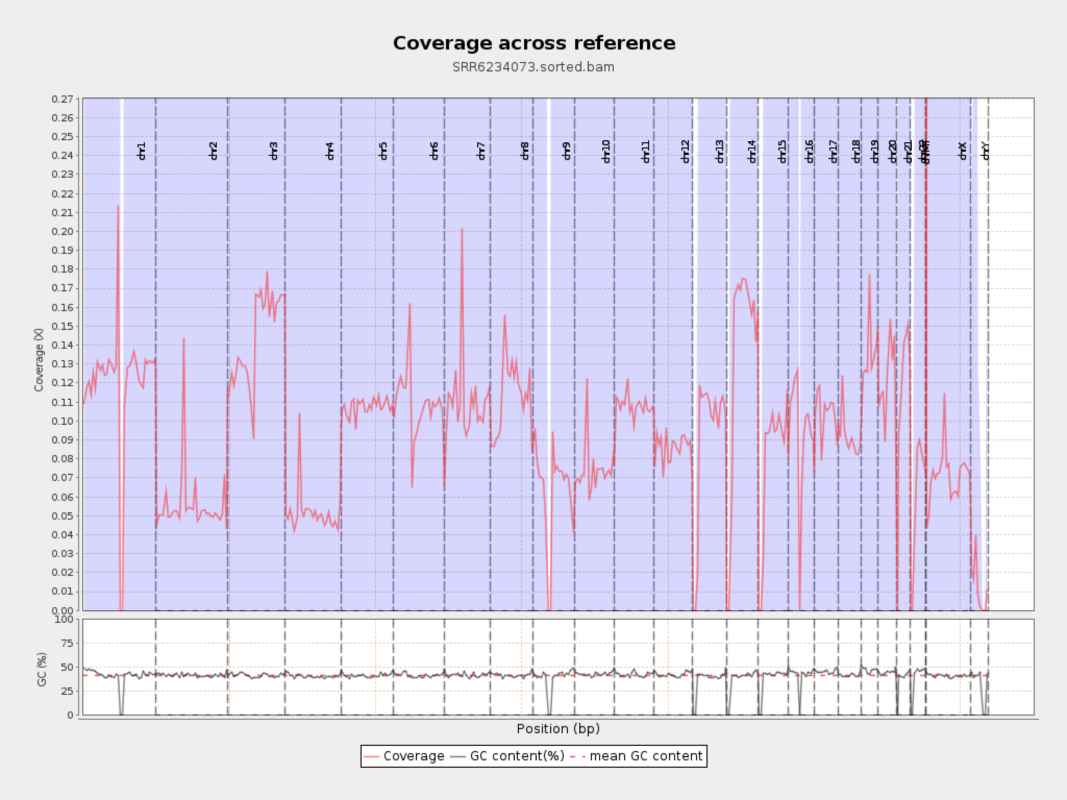
General error rate	0.56%
Mismatches	1,598,761
Insertions	18,873
Mapped reads with at least one insertion	0.41%
Deletions	63,361
Mapped reads with at least one deletion	1.38%
Homopolymer indels	44.34%

2.6. Chromosome stats

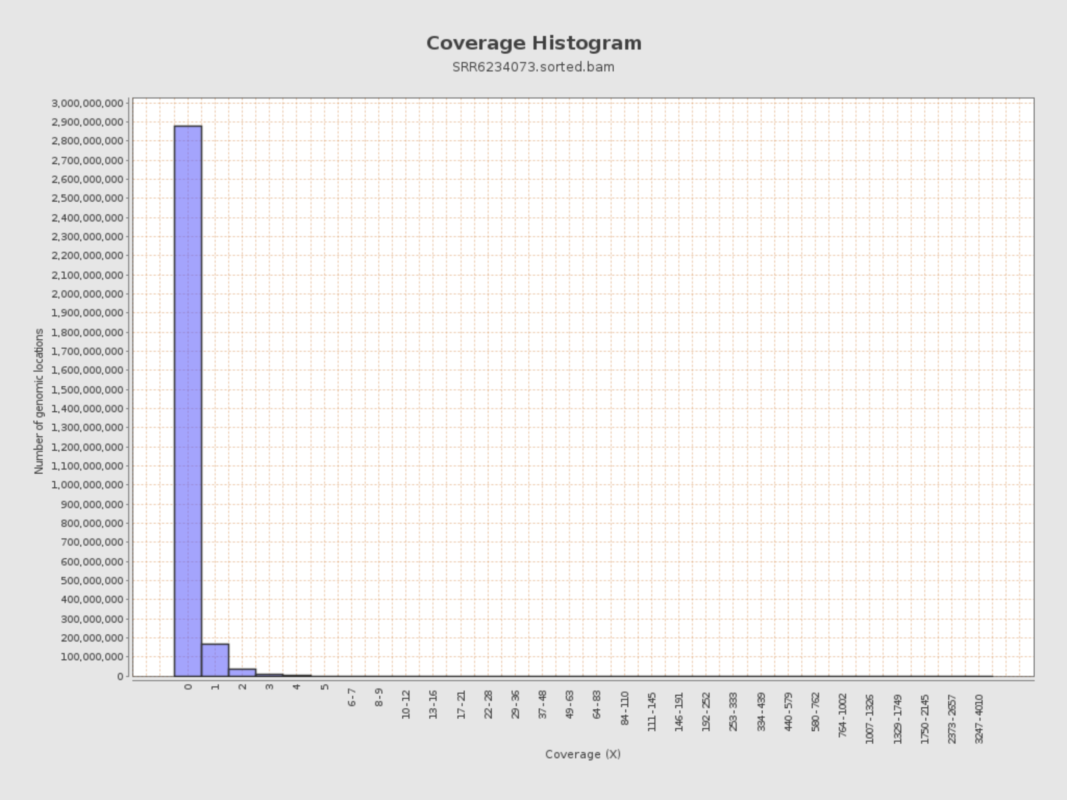
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30048923	0.1206	2.1357
chr2	243199373	13600834	0.0559	1.8236
chr3	198022430	28317820	0.143	0.494
chr4	191154276	9886080	0.0517	0.3692
chr5	180915260	19444925	0.1075	0.4347
chr6	171115067	18800740	0.1099	0.6944
chr7	159138663	17582302	0.1105	1.3506

chr8	146364022	16573850	0.1132	0.9916
chr9	141213431	8956224	0.0634	0.6171
chr10	135534747	9997490	0.0738	0.6524
chr11	135006516	14532785	0.1076	0.774
chr12	133851895	11537405	0.0862	0.3986
chr13	115169878	10489623	0.0911	0.4538
chr14	107349540	14692683	0.1369	0.5061
chr15	102531392	8031804	0.0783	0.4008
chr16	90354753	8307110	0.0919	0.4586
chr17	81195210	8530725	0.1051	0.5069
chr18	78077248	7193626	0.0921	1.5676
chr19	59128983	7993961	0.1352	1.1412
chr20	63025520	7683399	0.1219	0.488
chr21	48129895	5588963	0.1161	0.476
chr22	51304566	3037006	0.0592	0.3047
chrMT	16571	408517	24.6525	13.9346
chrX	155270560	11072765	0.0713	0.4441
chrY	59373566	709861	0.012	0.2651

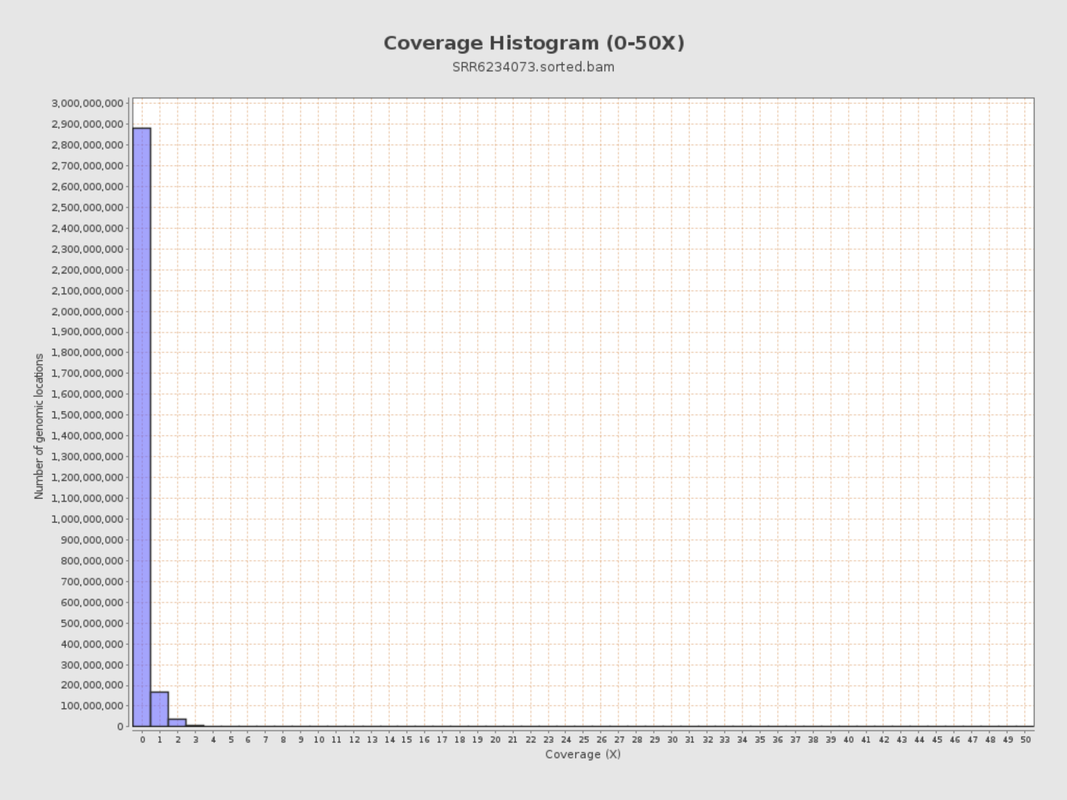
3. Results : Coverage across reference



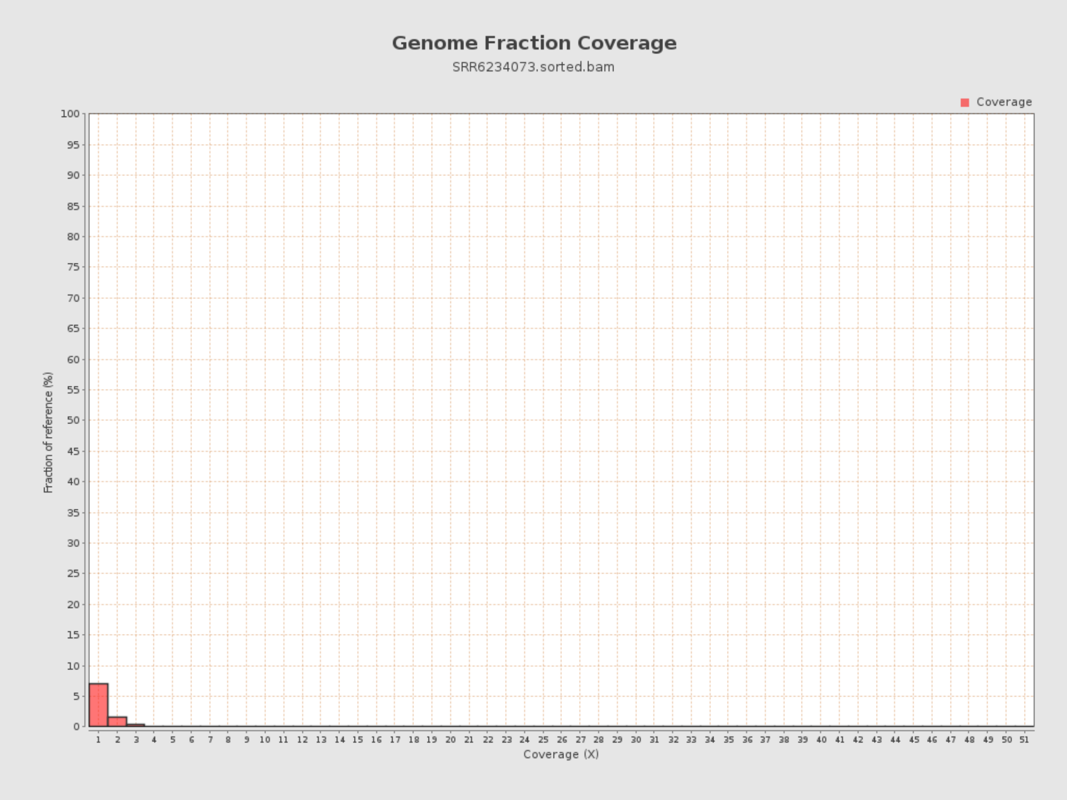
4. Results : Coverage Histogram



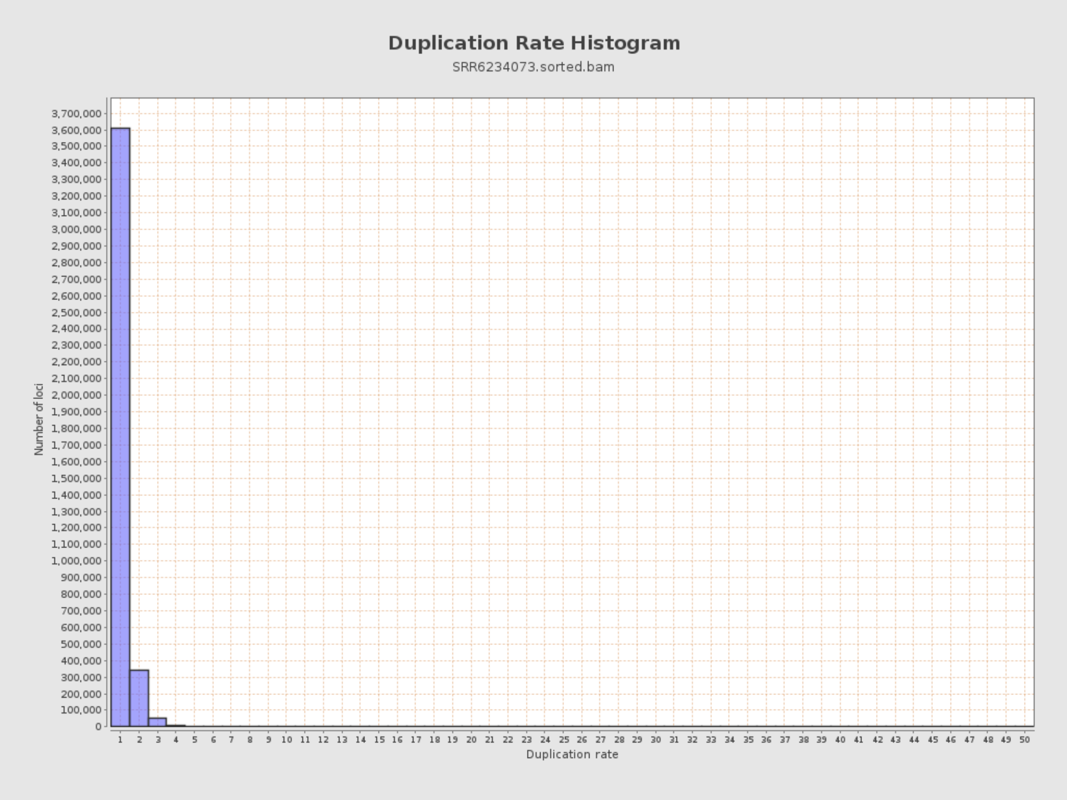
5. Results : Coverage Histogram (0-50X)



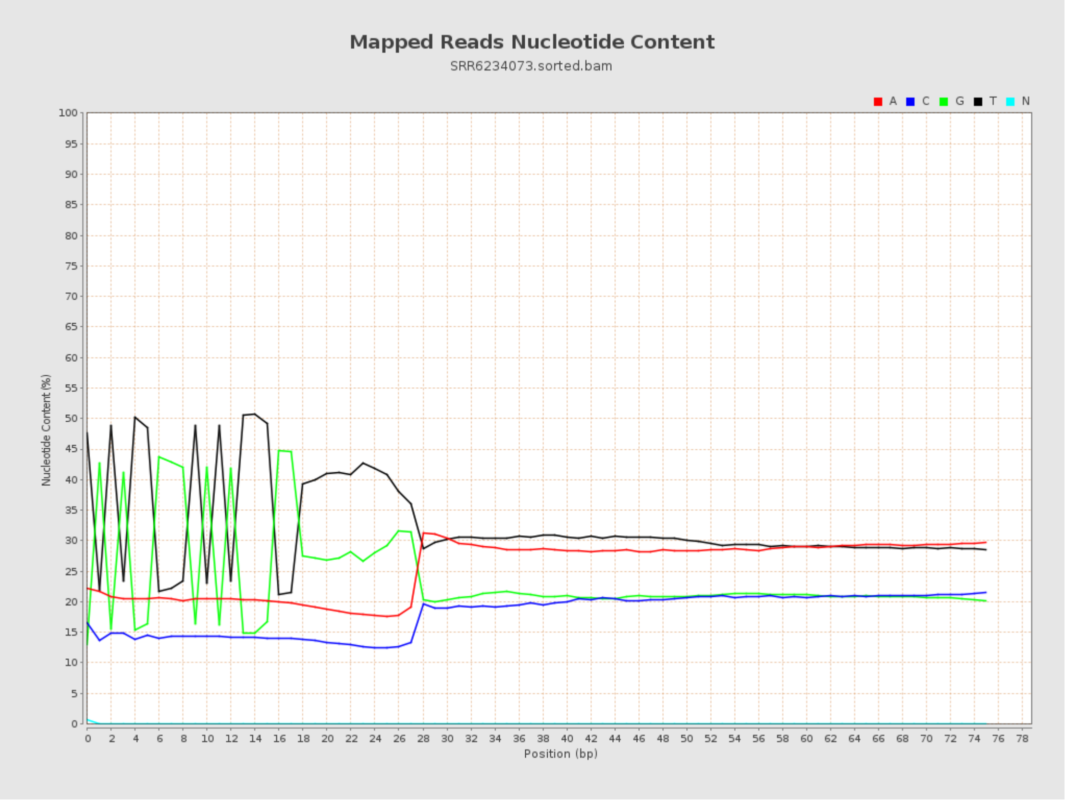
6. Results : Genome Fraction Coverage



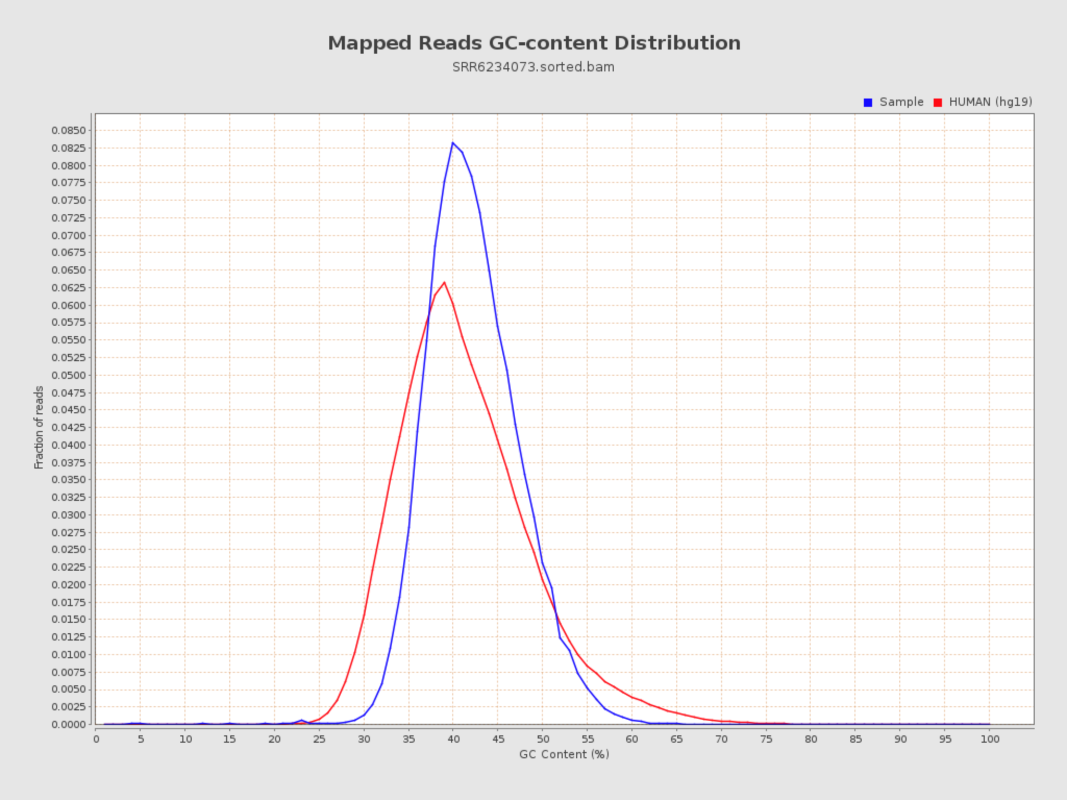
7. Results : Duplication Rate Histogram



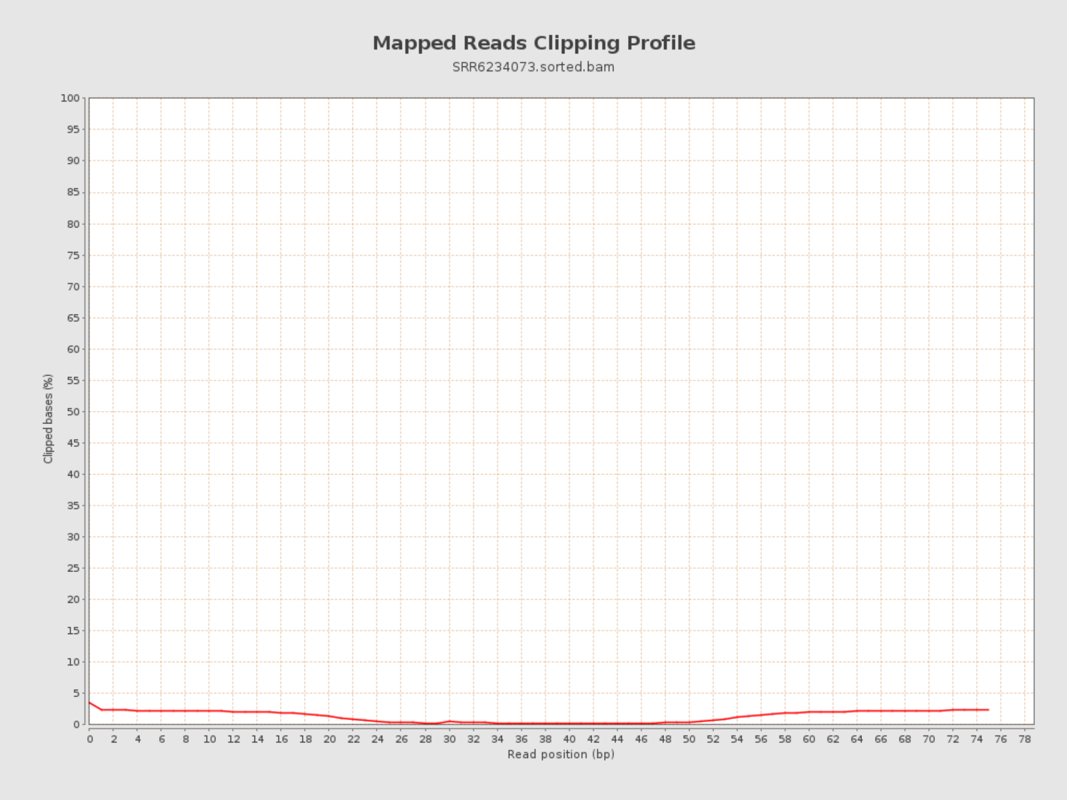
8. Results : Mapped Reads Nucleotide Content



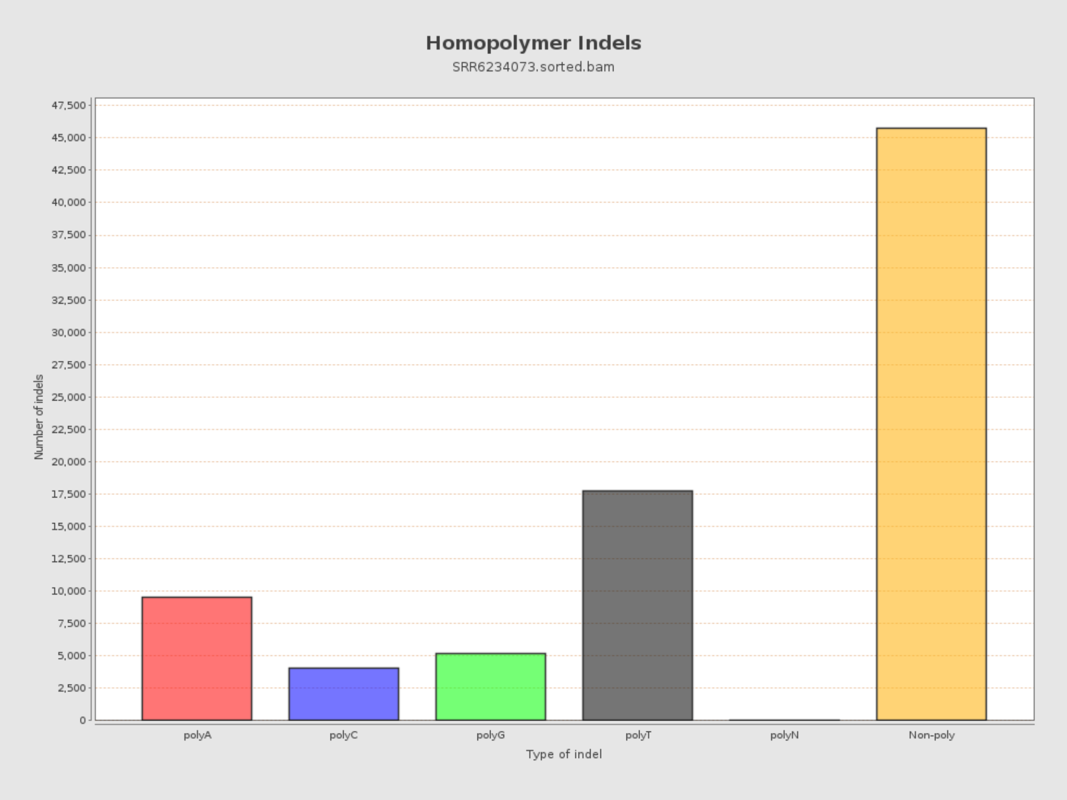
9. Results : Mapped Reads GC-content Distribution



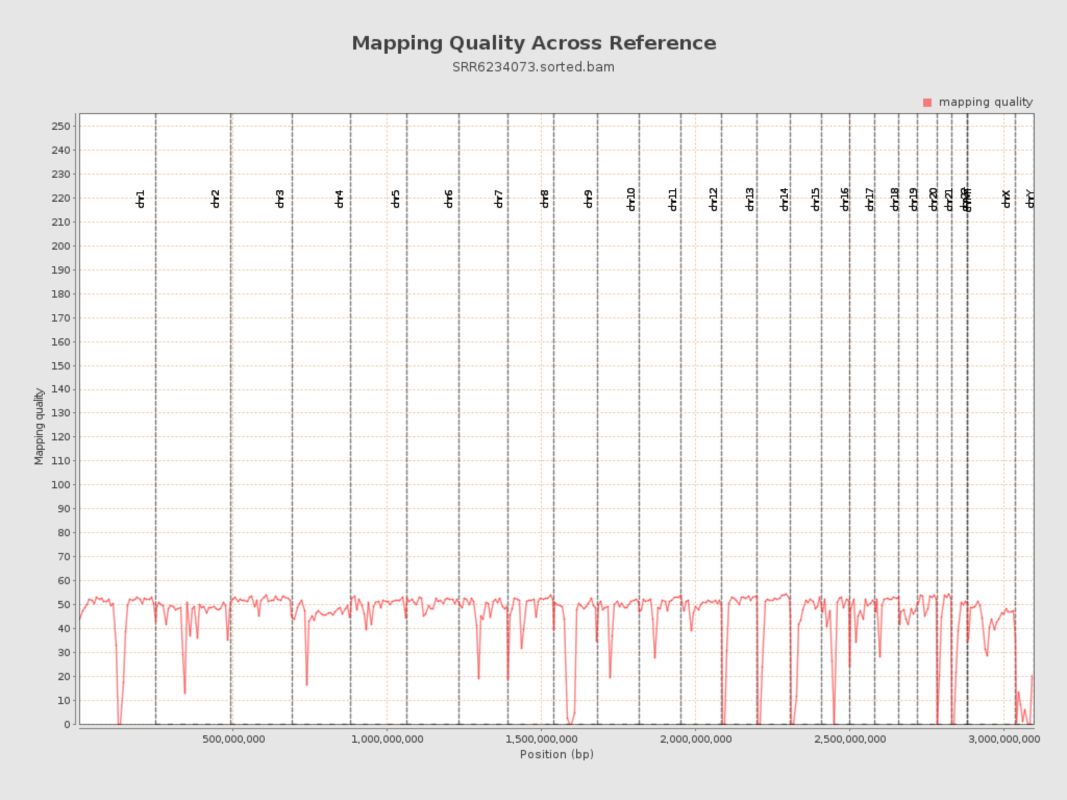
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram