Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234090.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_SRR6234090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,105,783
Mapped reads	1,392,727 / 66.14%
Unmapped reads	713,056 / 33.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,811 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	156,135 / 7.41%
Duplication rate	9.08%
Clipped reads	823,988 / 39.13%

2.2. ACGT Content

Number/percentage of A's	24,255,946 / 27.47%
Number/percentage of C's	16,448,108 / 18.63%
Number/percentage of T's	27,721,276 / 31.39%
Number/percentage of G's	19,868,539 / 22.5%
Number/percentage of N's	12,099 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.3023

2.4. Mapping Quality

Mean Mapping Quality	41.5

2.5. Mismatches and indels

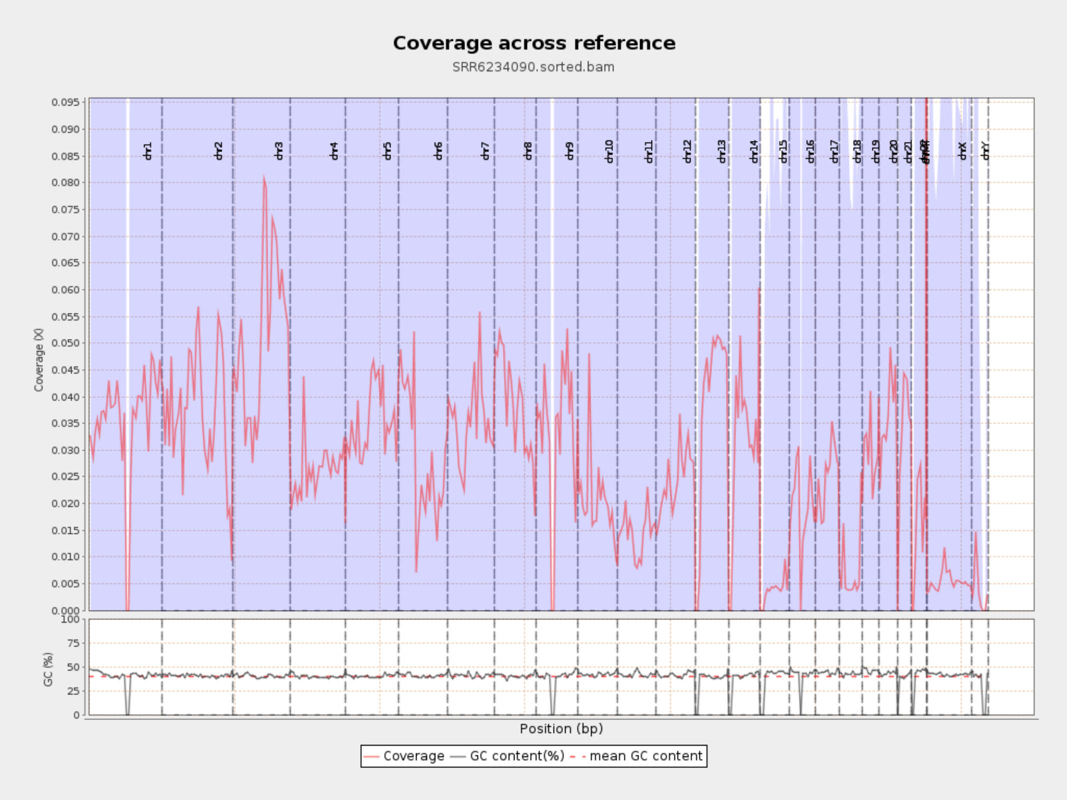
General error rate	0.91%
Mismatches	787,674
Insertions	6,977
Mapped reads with at least one insertion	0.5%
Deletions	32,329
Mapped reads with at least one deletion	2.28%
Homopolymer indels	42.79%

2.6. Chromosome stats

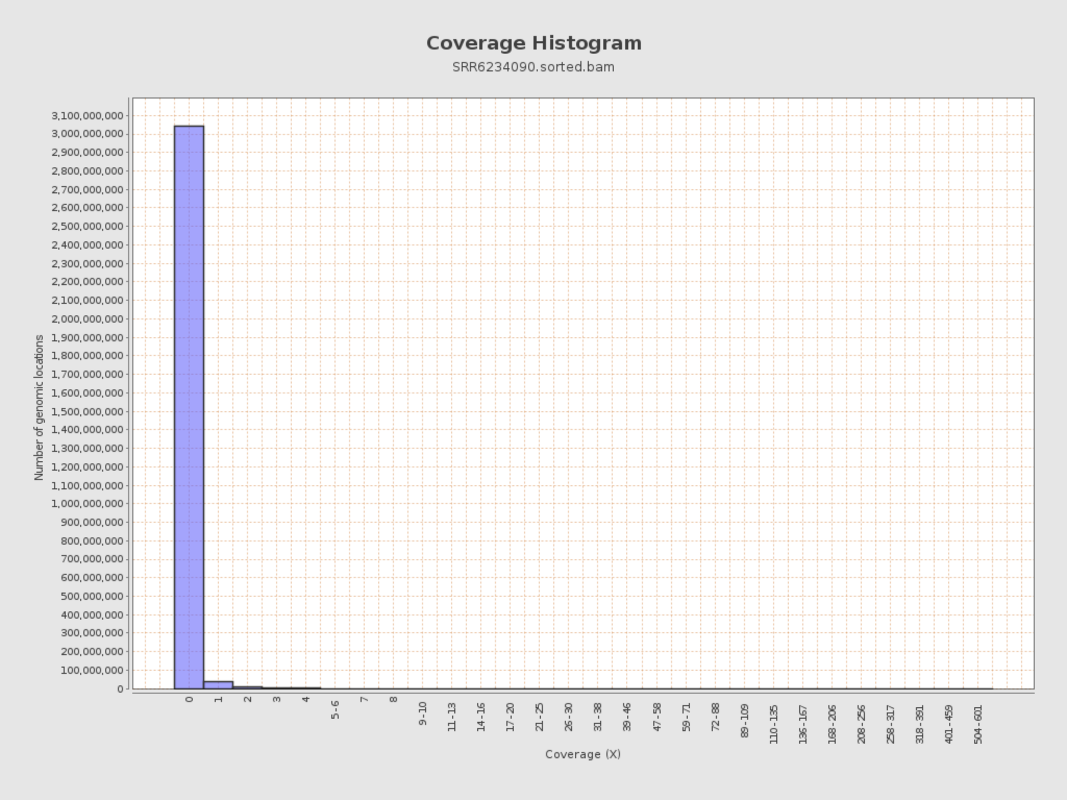
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8856993	0.0355	0.4234
chr2	243199373	9054572	0.0372	0.3893
chr3	198022430	10165544	0.0513	0.339
chr4	191154276	5014347	0.0262	0.2495
chr5	180915260	6390717	0.0353	0.2788
chr6	171115067	4923815	0.0288	0.2977
chr7	159138663	5649968	0.0355	0.3264

chr8	146364022	5618054	0.0384	0.4503
chr9	141213431	4640069	0.0329	0.2936
chr10	135534747	2798657	0.0206	0.2956
chr11	135006516	1949134	0.0144	0.185
chr12	133851895	3286395	0.0246	0.2352
chr13	115169878	4443032	0.0386	0.2968
chr14	107349540	3278483	0.0305	0.2687
chr15	102531392	415236	0.004	0.0861
chr16	90354753	1786361	0.0198	0.2149
chr17	81195210	2034215	0.0251	0.2346
chr18	78077248	543430	0.007	0.3211
chr19	59128983	1758977	0.0297	0.3125
chr20	63025520	2301603	0.0365	0.2902
chr21	48129895	1583025	0.0329	0.2736
chr22	51304566	758813	0.0148	0.1769
chrMT	16571	41079	2.479	2.7249
chrX	155270560	856906	0.0055	0.1057
chrY	59373566	212459	0.0036	0.1161

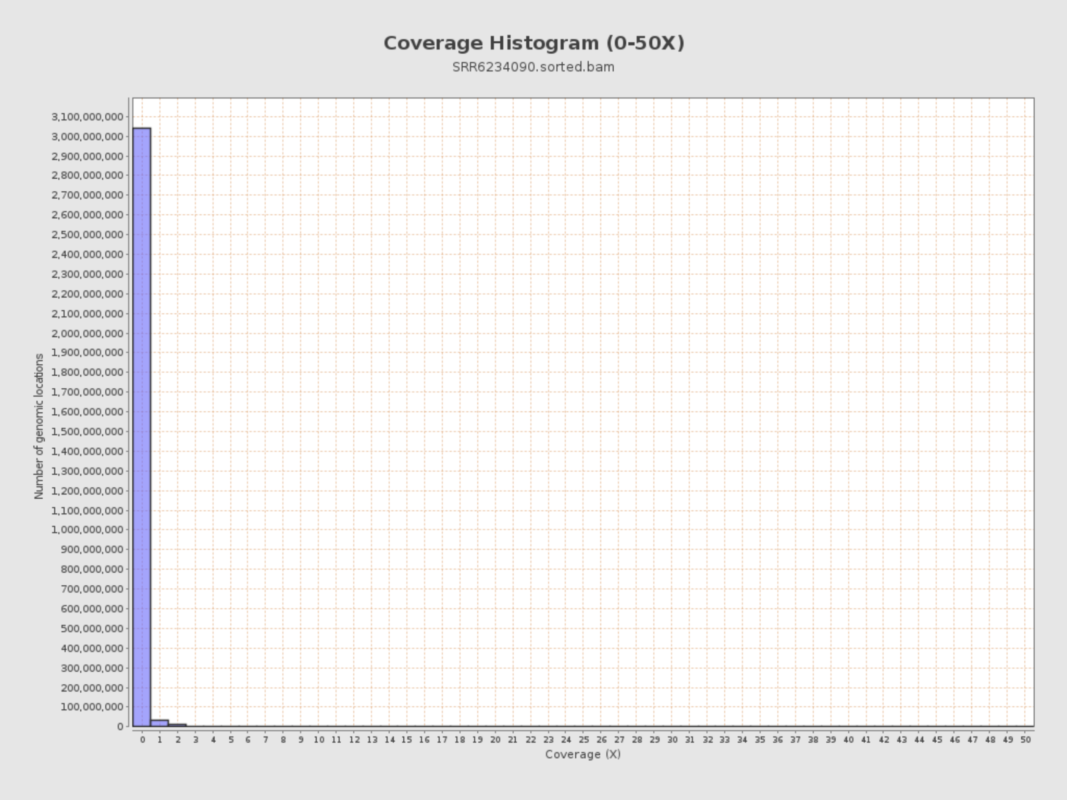
3. Results : Coverage across reference



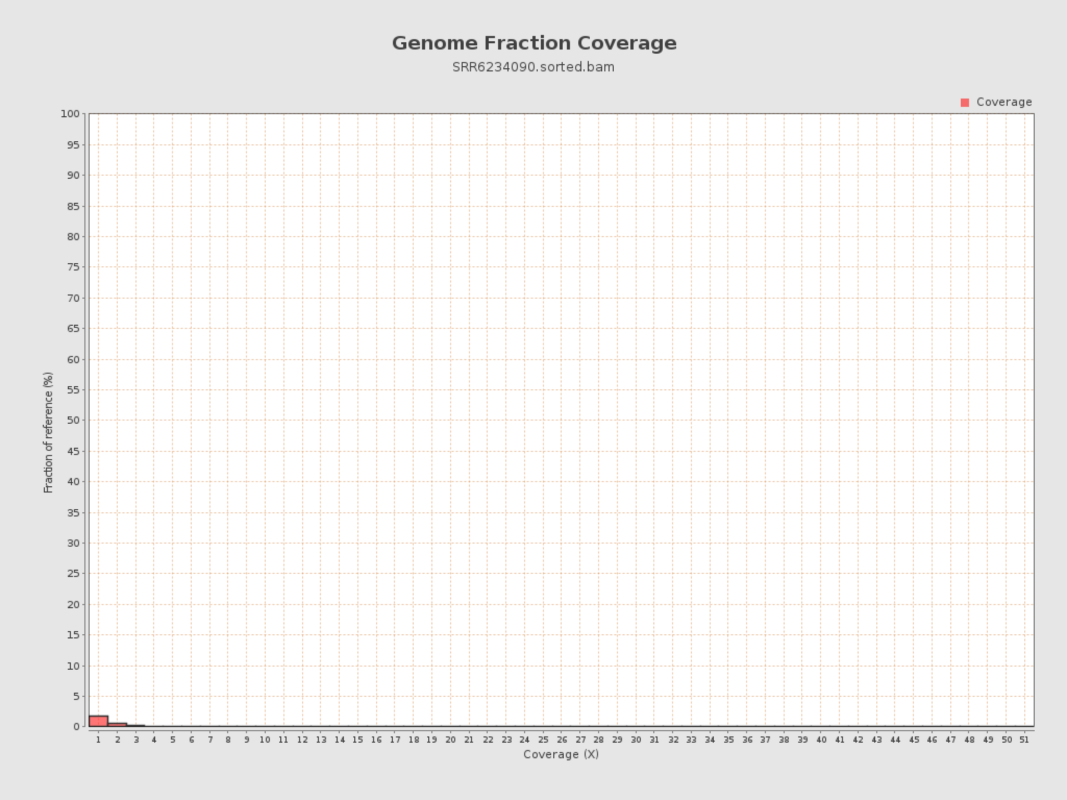
4. Results : Coverage Histogram



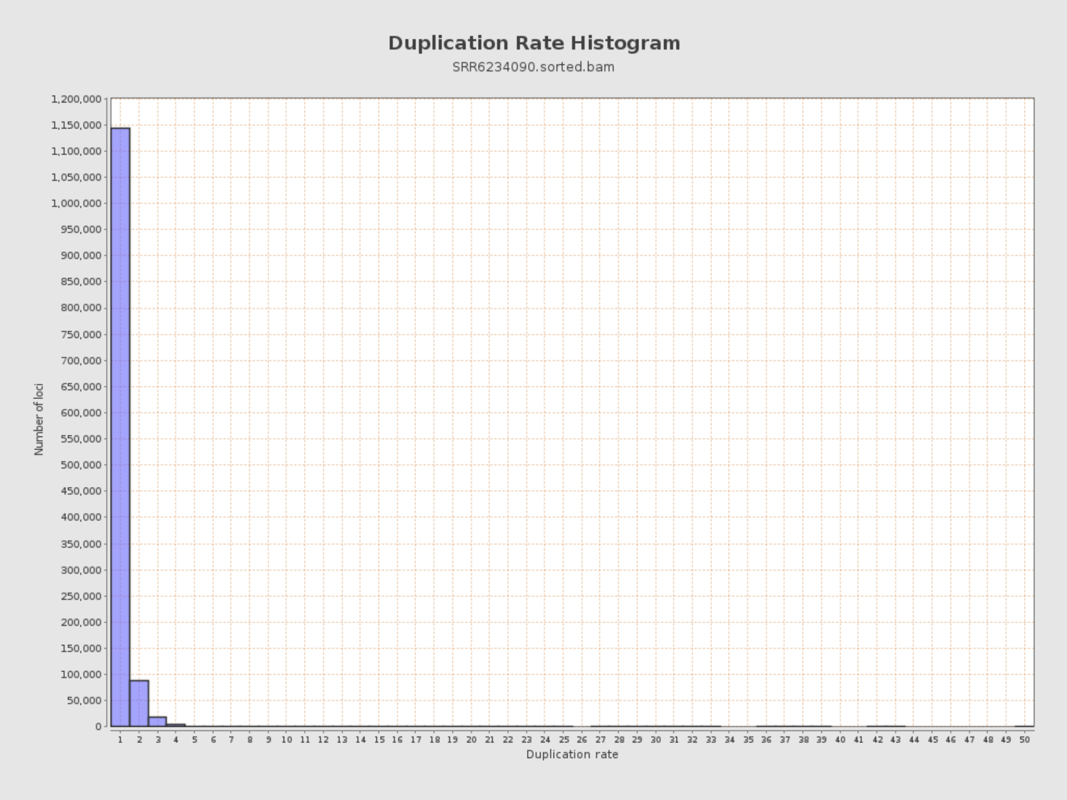
5. Results : Coverage Histogram (0-50X)



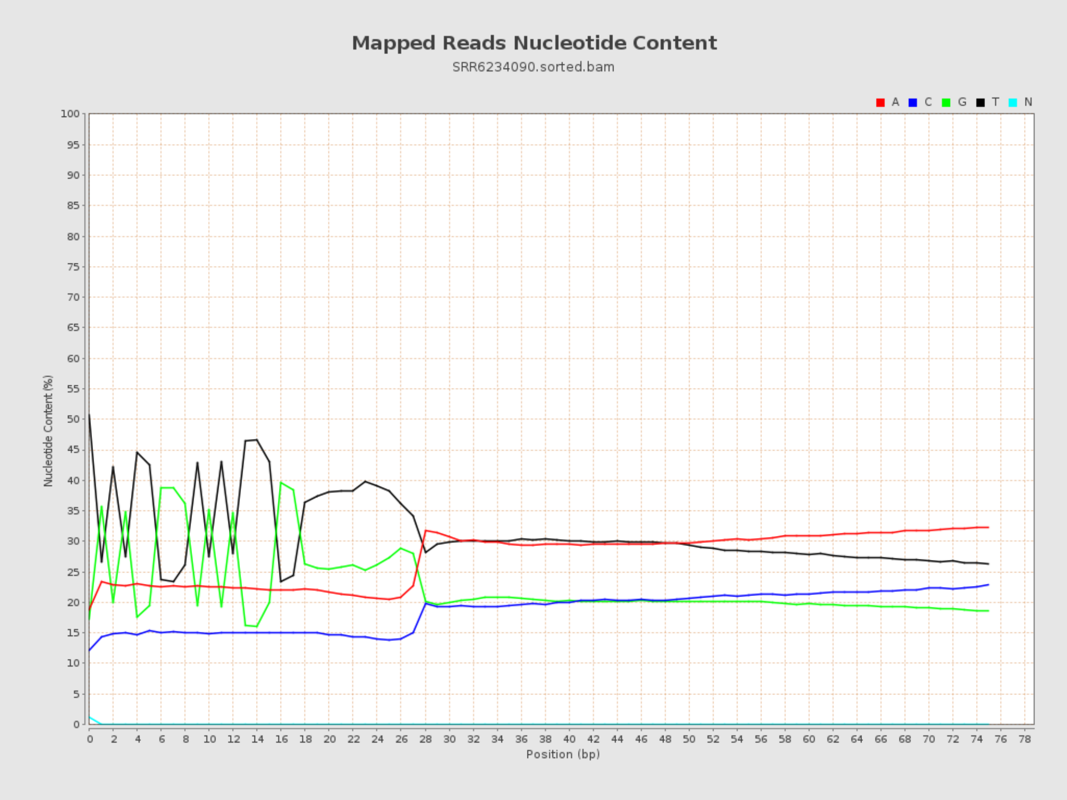
6. Results : Genome Fraction Coverage



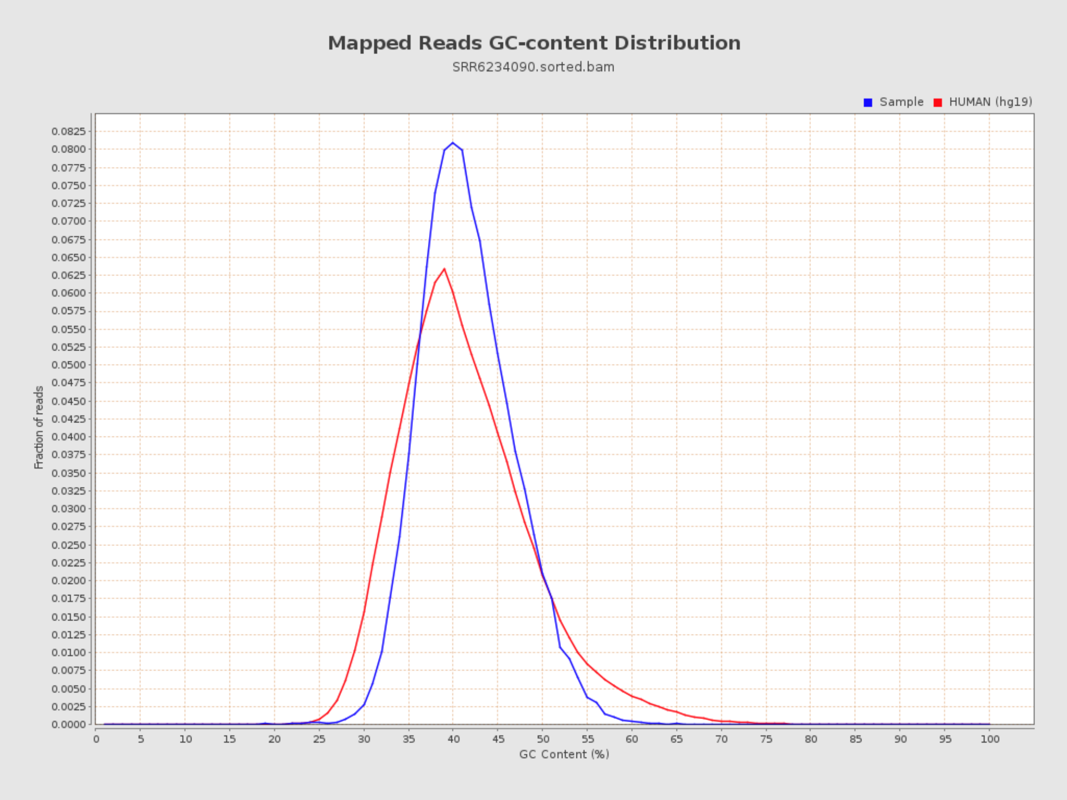
7. Results : Duplication Rate Histogram



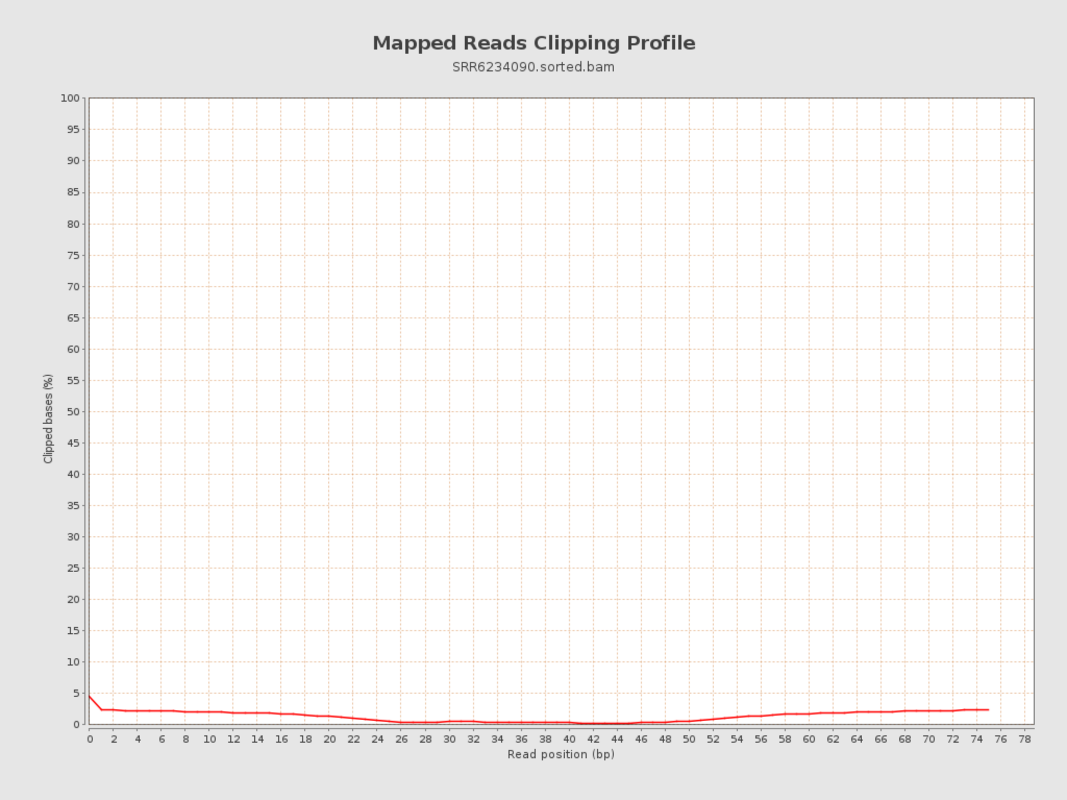
8. Results : Mapped Reads Nucleotide Content



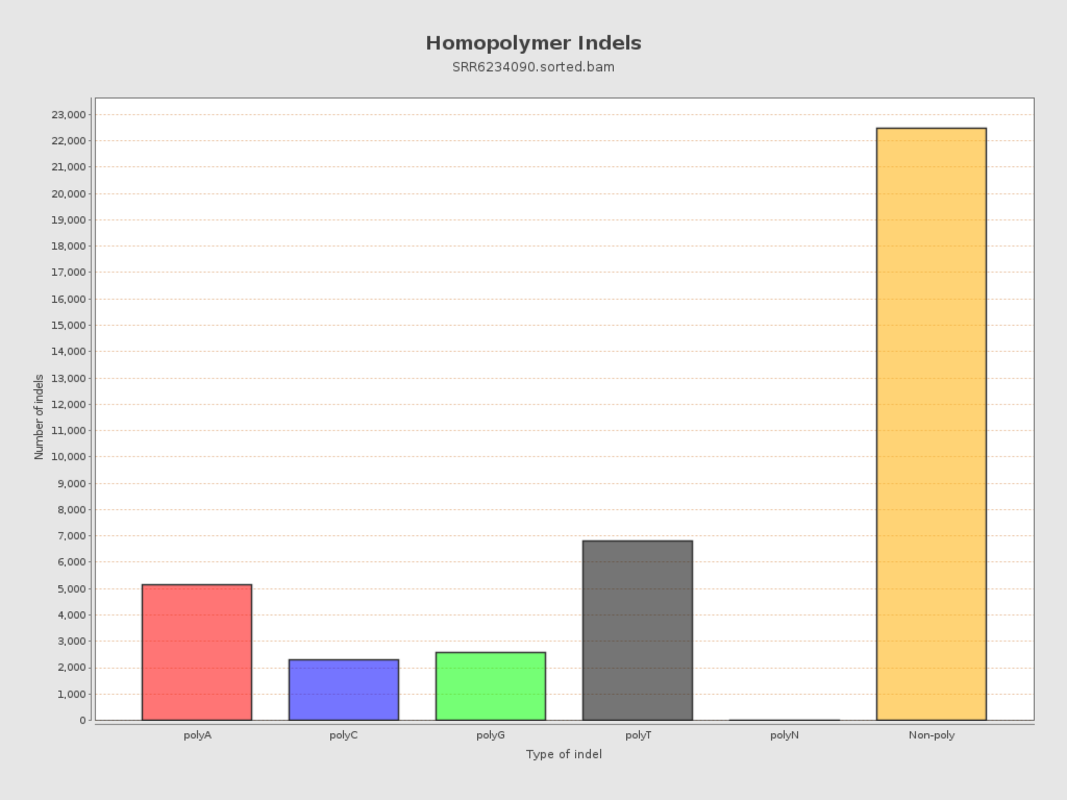
9. Results : Mapped Reads GC-content Distribution



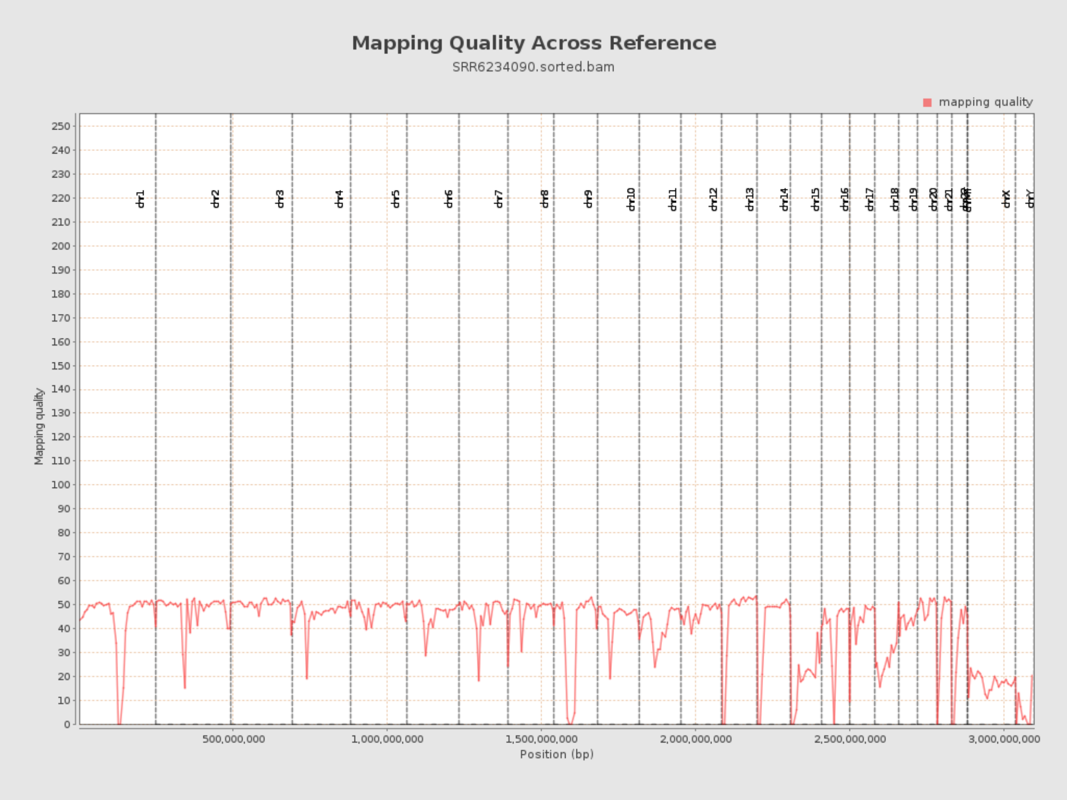
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram