Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 05:19:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR4012089.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_SRR4012089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR4012089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 05:19:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR4012089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	152,249,128
Mapped reads	142,853,692 / 93.83%
Unmapped reads	9,395,436 / 6.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,571 / 0.03%
Read min/max/mean length	30 / 60 / 55.87
Duplicated reads (estimated)	86,652,441 / 56.91%
Duplication rate	38.4%
Clipped reads	5,941,590 / 3.9%

2.2. ACGT Content

Number/percentage of A's	2,271,926,780 / 28.7%
Number/percentage of C's	1,496,716,223 / 18.9%
Number/percentage of T's	2,367,653,549 / 29.91%
Number/percentage of G's	1,780,687,250 / 22.49%
Number/percentage of N's	69,530 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	2.5582

Standard Deviation	25.4111

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

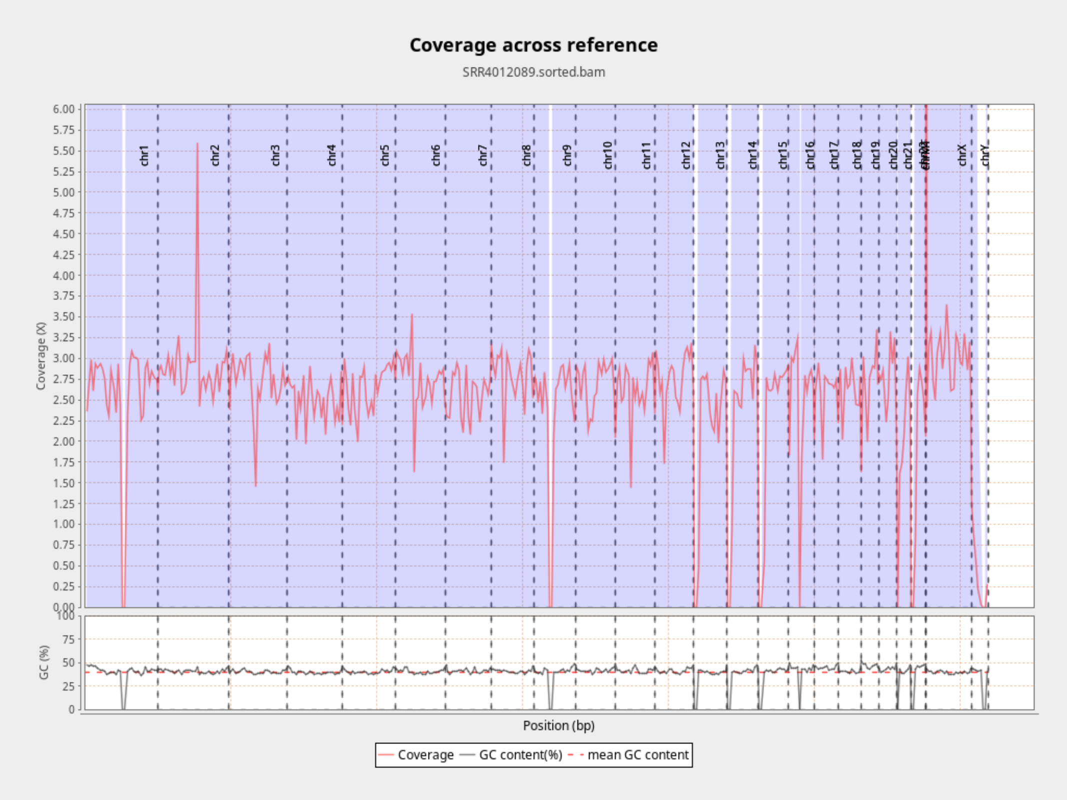
General error rate	0.42%
Mismatches	32,320,135
Insertions	562,668
Mapped reads with at least one insertion	0.39%
Deletions	1,288,057
Mapped reads with at least one deletion	0.9%
Homopolymer indels	43.37%

2.6. Chromosome stats

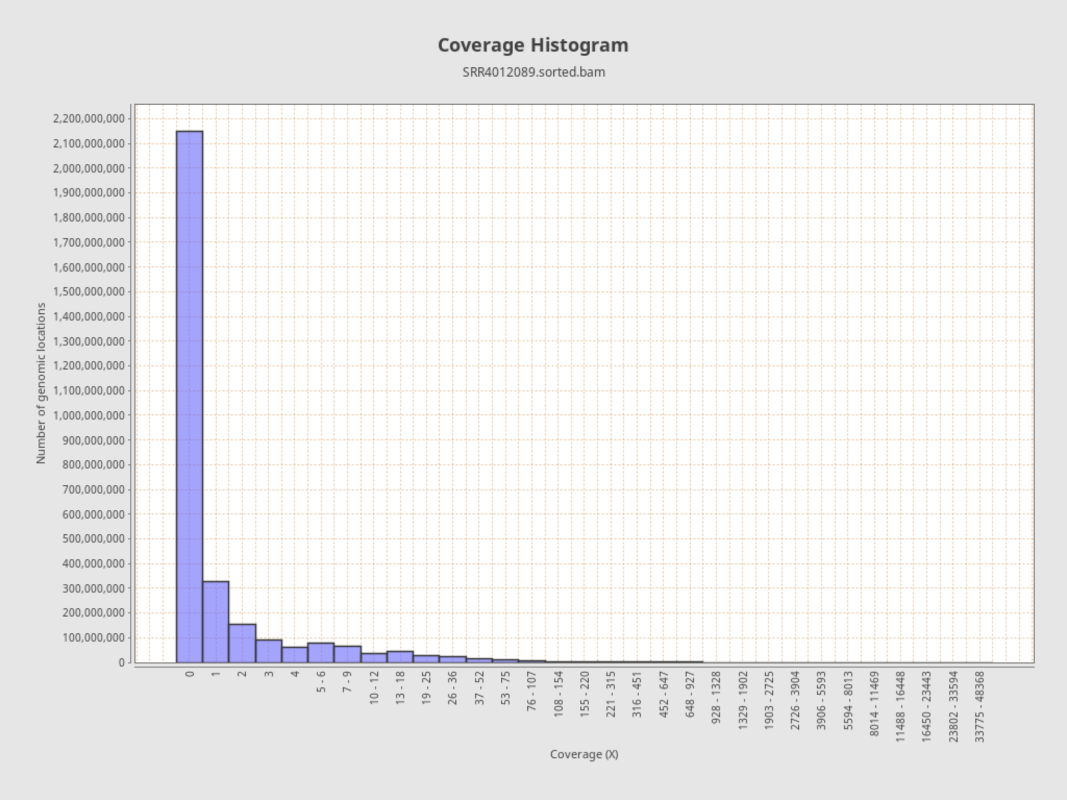
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	637351039	2.5571	16.3573
chr2	243199373	708240244	2.9122	50.381
chr3	198022430	538008850	2.7169	14.9578
chr4	191154276	477382893	2.4974	17.8833
chr5	180915260	480472344	2.6558	14.9198
chr6	171115067	470622443	2.7503	36.5956
chr7	159138663	406958722	2.5573	19.668

chr8	146364022	406902472	2.7801	17.9034
chr9	141213431	328950032	2.3295	25.0672
chr10	135534747	366489467	2.704	23.1236
chr11	135006516	353785619	2.6205	17.2537
chr12	133851895	368416711	2.7524	17.6088
chr13	115169878	242461128	2.1052	12.4525
chr14	107349540	243062678	2.2642	21.7361
chr15	102531392	223753936	2.1823	13.0606
chr16	90354753	225263334	2.4931	29.131
chr17	81195210	211133759	2.6003	13.7305
chr18	78077248	206938508	2.6504	27.367
chr19	59128983	161381911	2.7293	35.7665
chr20	63025520	176350542	2.7981	35.3767
chr21	48129895	97019364	2.0158	20.3539
chr22	51304566	93094487	1.8145	11.136
chrMT	16571	5229651	315.5905	1,191.4119
chrX	155270560	468426550	3.0168	19.6266
chrY	59373566	21729078	0.366	38.0446

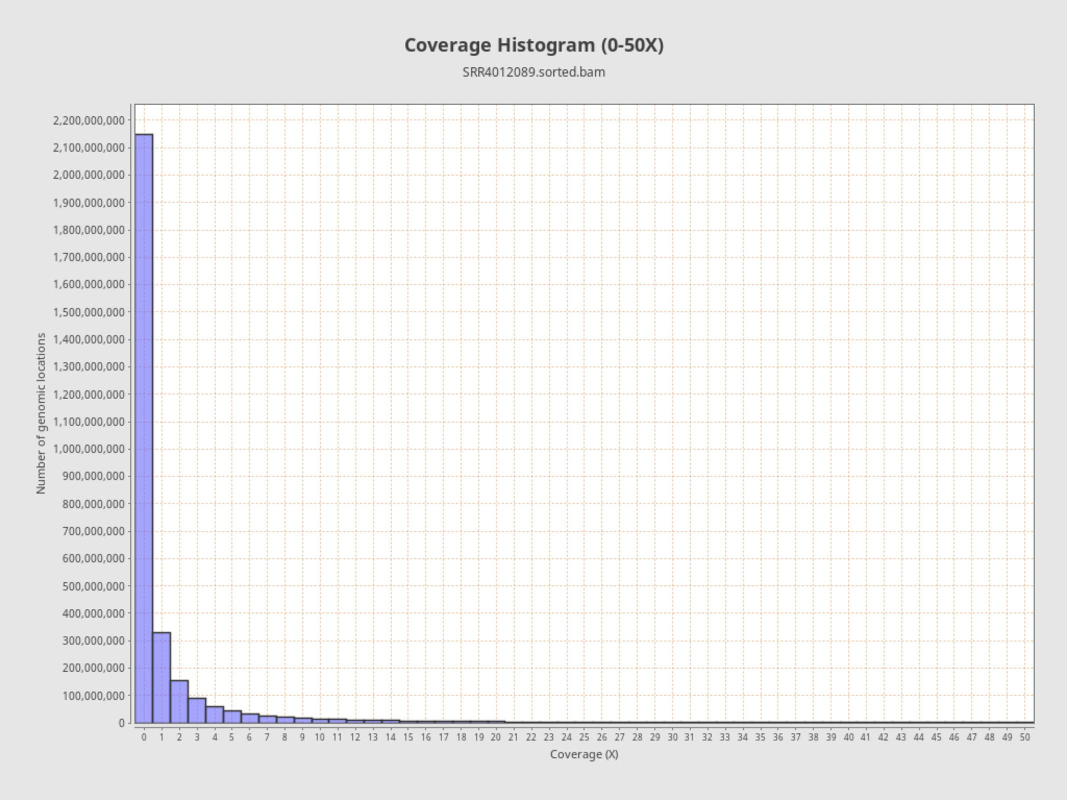
3. Results : Coverage across reference



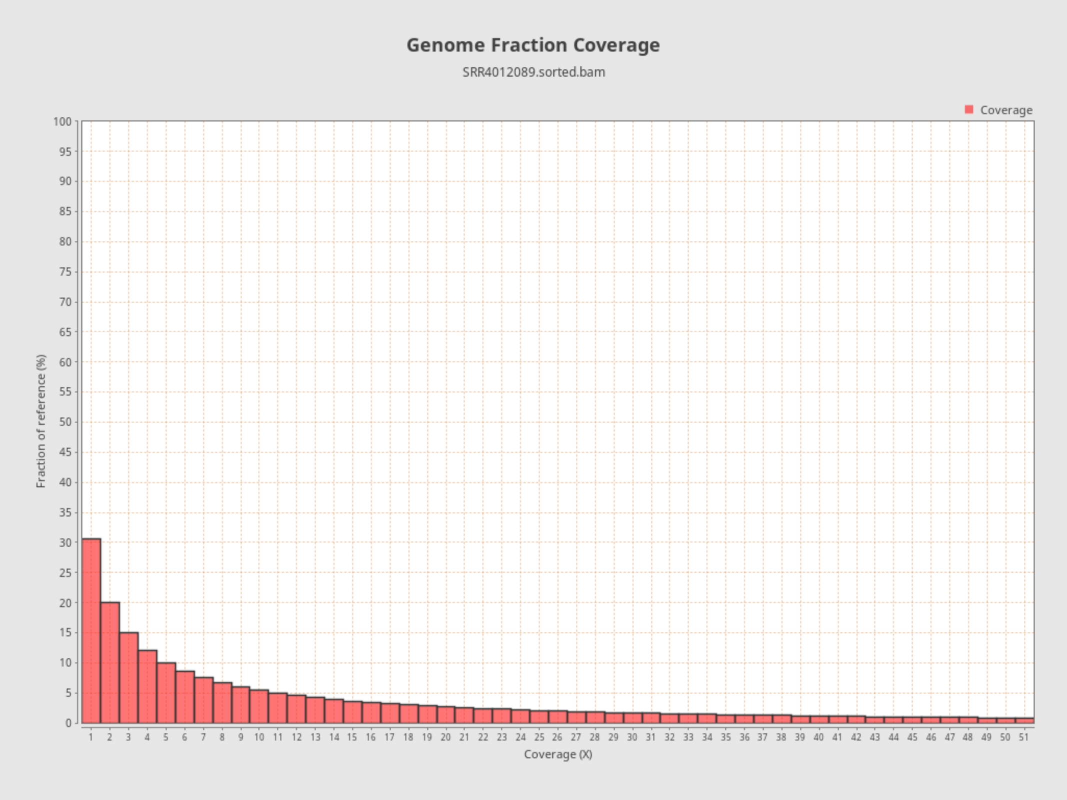
4. Results : Coverage Histogram



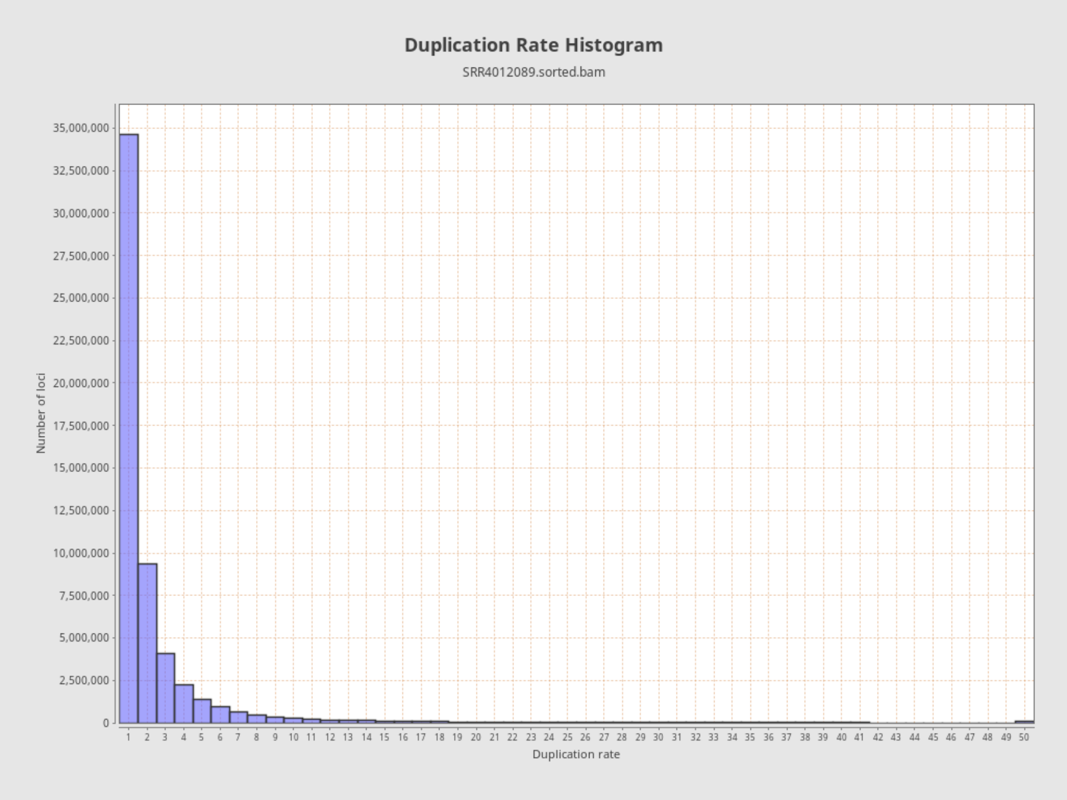
5. Results : Coverage Histogram (0-50X)



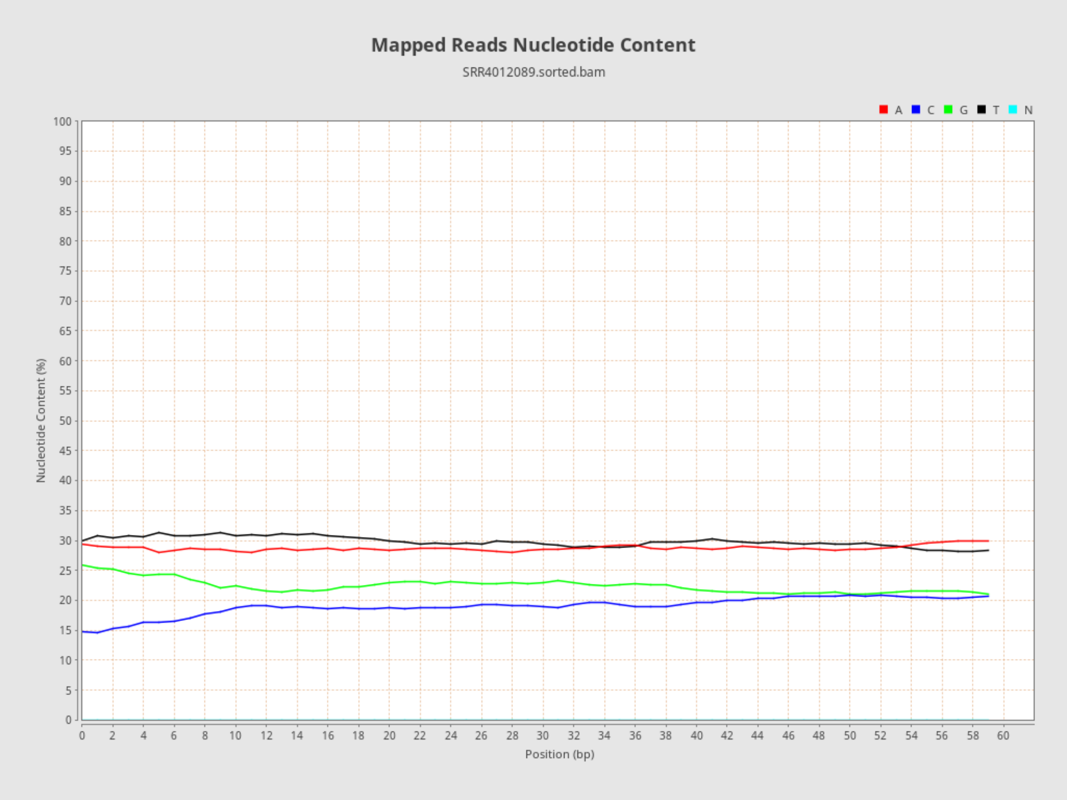
6. Results : Genome Fraction Coverage



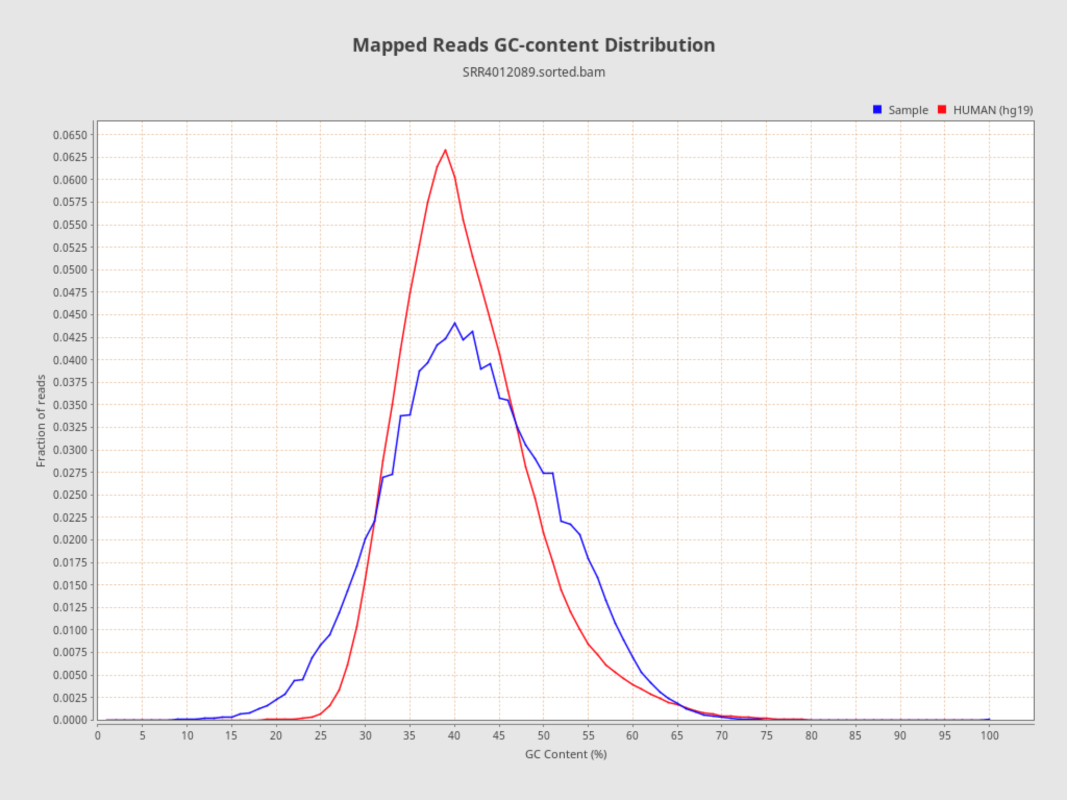
7. Results : Duplication Rate Histogram



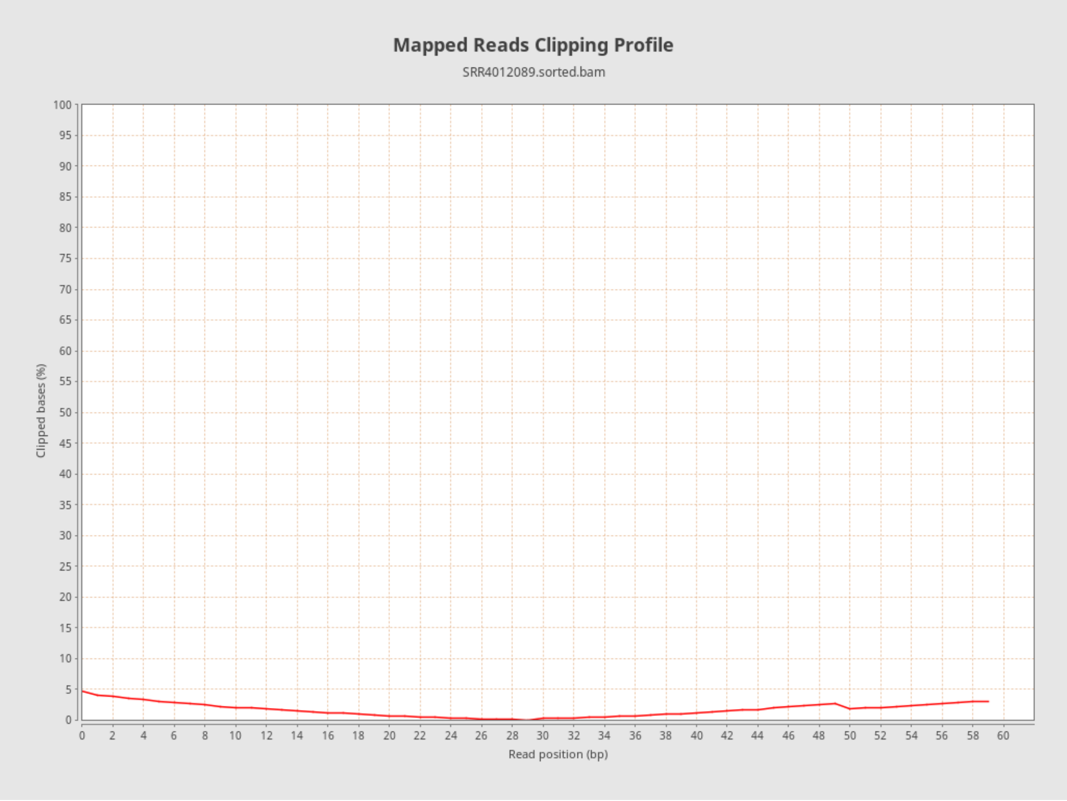
8. Results : Mapped Reads Nucleotide Content



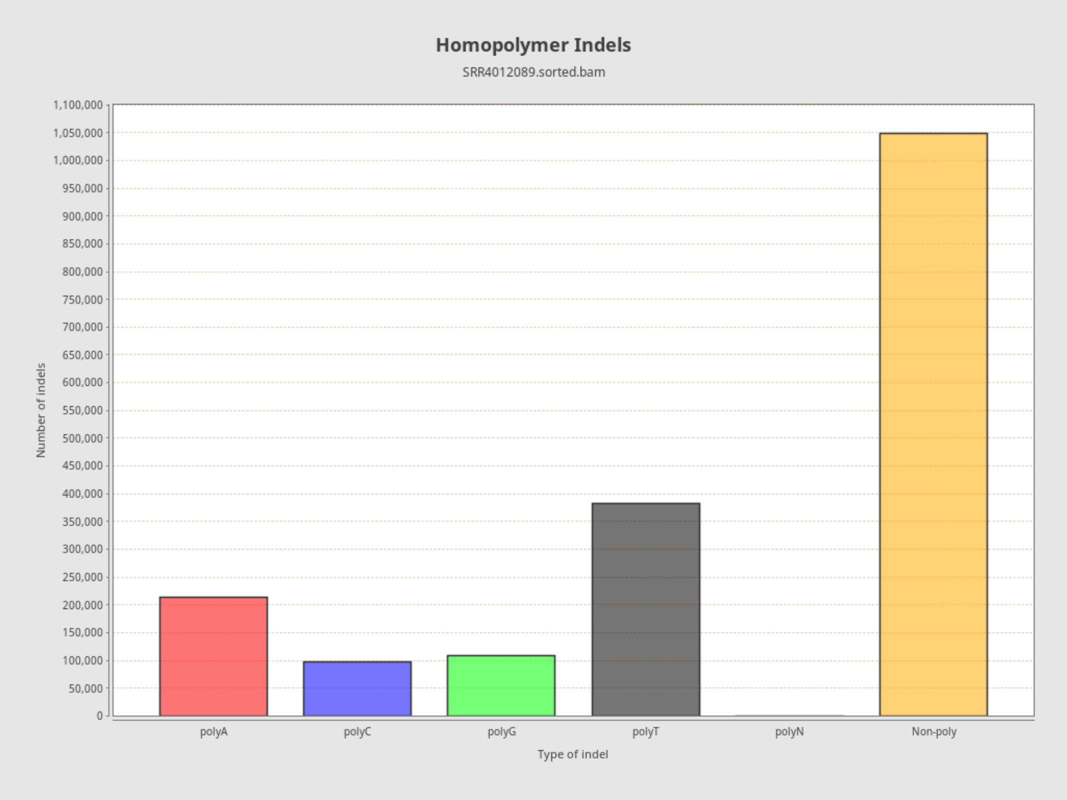
9. Results : Mapped Reads GC-content Distribution



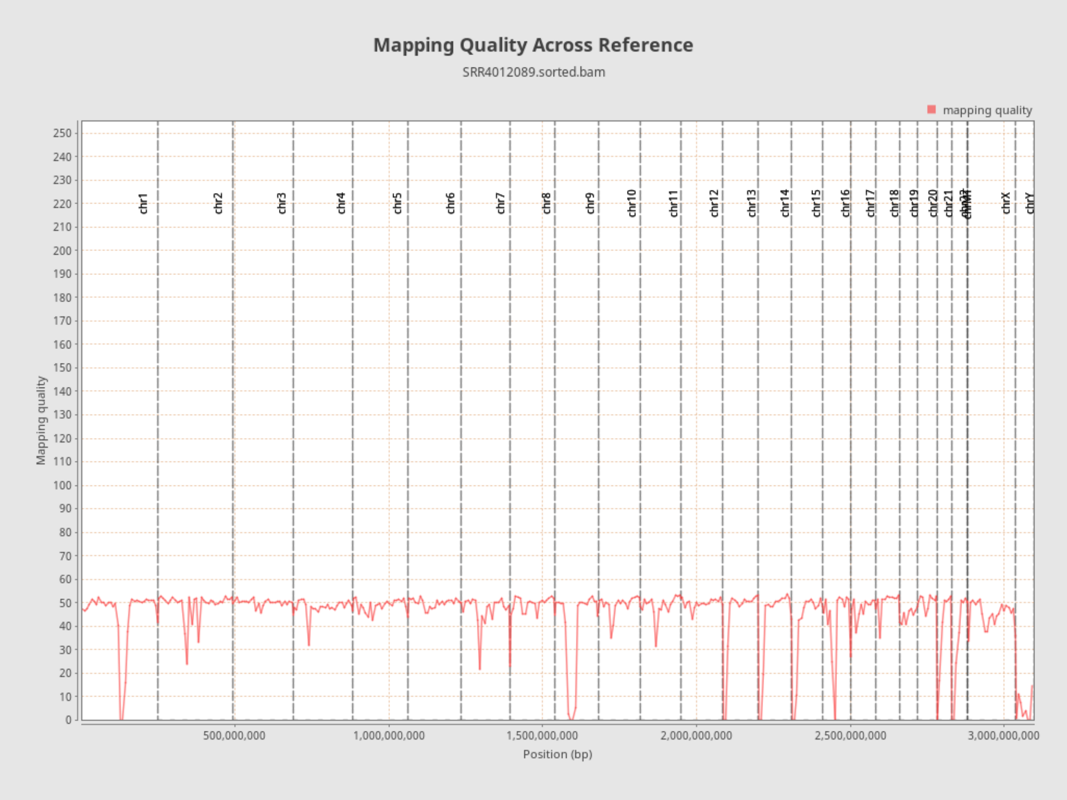
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram