Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:39:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080947.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_SRR3080947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080947.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:39:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,845,841
Mapped reads	2,527,078 / 88.8%
Unmapped reads	318,763 / 11.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,247 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	99,191 / 3.49%
Duplication rate	3.24%
Clipped reads	842,688 / 29.61%

2.2. ACGT Content

Number/percentage of A's	51,199,451 / 29.26%
Number/percentage of C's	30,988,432 / 17.71%
Number/percentage of T's	56,083,820 / 32.05%
Number/percentage of G's	35,835,975 / 20.48%
Number/percentage of N's	858,553 / 0.49%
GC Percentage	38.19%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.3967

2.4. Mapping Quality

Mean Mapping Quality	48.14

2.5. Mismatches and indels

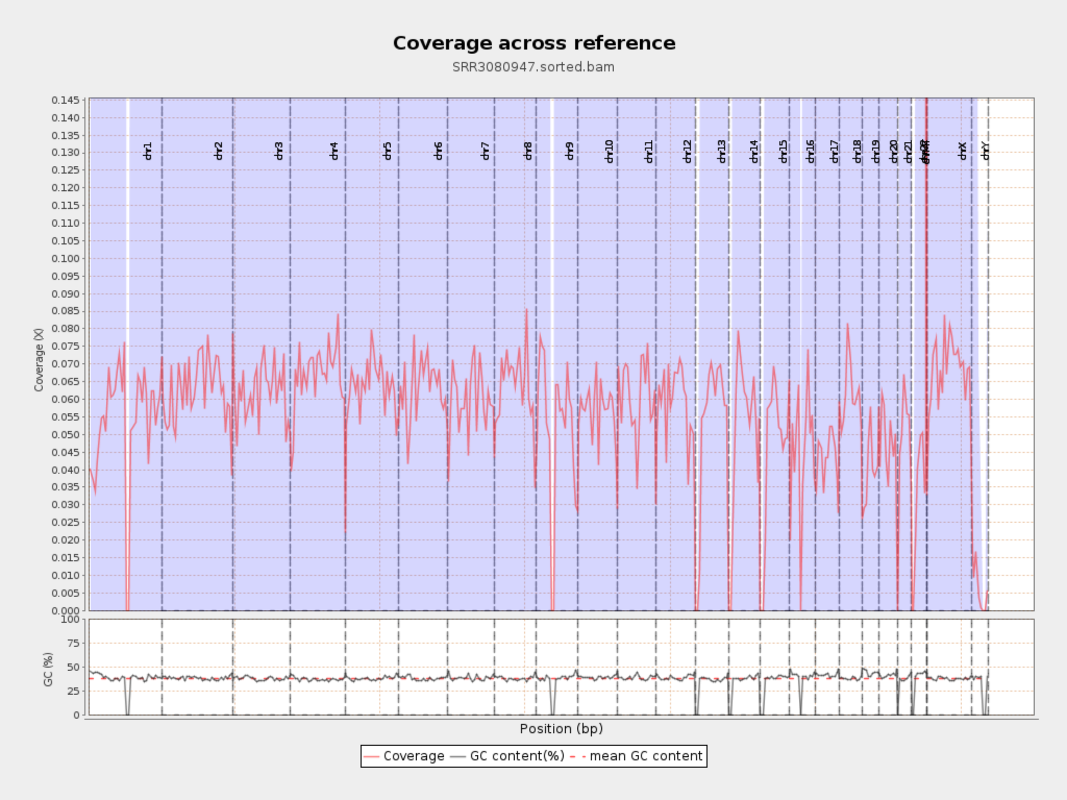
General error rate	1.14%
Mismatches	1,963,727
Insertions	13,386
Mapped reads with at least one insertion	0.53%
Deletions	37,924
Mapped reads with at least one deletion	1.49%
Homopolymer indels	50.47%

2.6. Chromosome stats

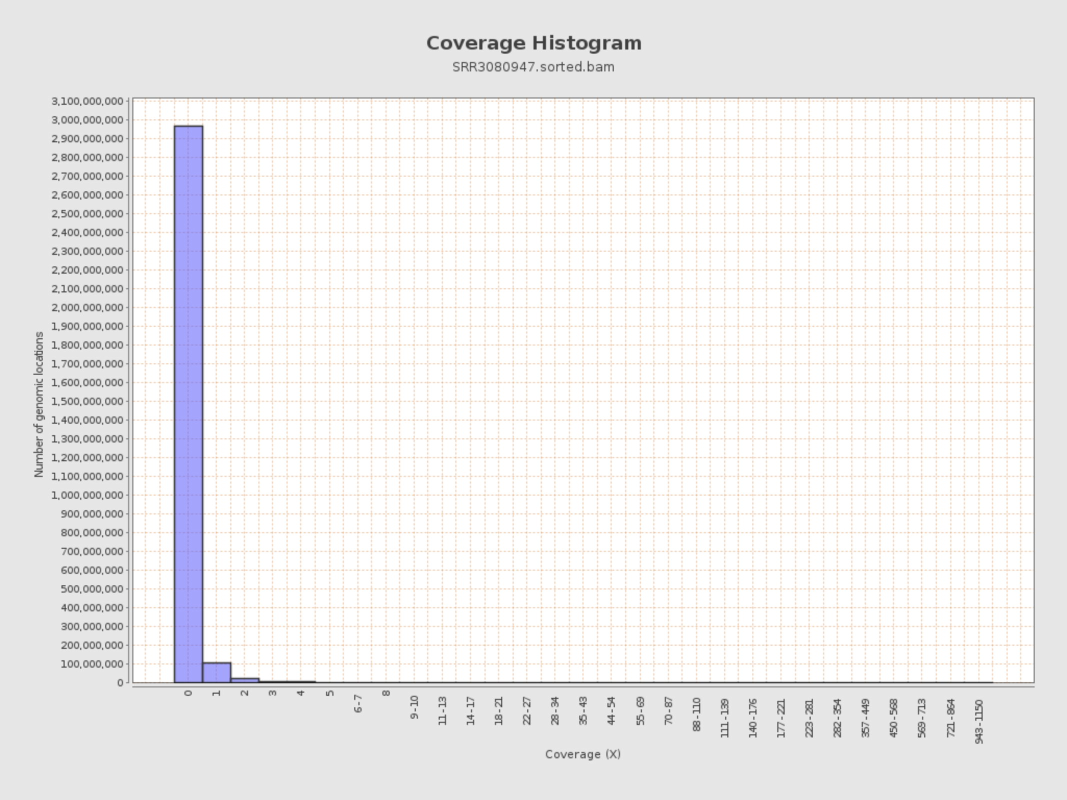
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13373173	0.0537	0.5884
chr2	243199373	15277494	0.0628	0.3835
chr3	198022430	12332448	0.0623	0.3149
chr4	191154276	12810315	0.067	0.3358
chr5	180915260	11612858	0.0642	0.3213
chr6	171115067	10814472	0.0632	0.3607
chr7	159138663	9603003	0.0603	0.4339

chr8	146364022	9322580	0.0637	0.7566
chr9	141213431	7395789	0.0524	0.3679
chr10	135534747	7791017	0.0575	0.3433
chr11	135006516	8156259	0.0604	0.3448
chr12	133851895	7886490	0.0589	0.3087
chr13	115169878	5963770	0.0518	0.2891
chr14	107349540	5473946	0.051	0.2957
chr15	102531392	4651188	0.0454	0.2685
chr16	90354753	4120778	0.0456	0.2796
chr17	81195210	3481893	0.0429	0.2804
chr18	78077248	4795966	0.0614	0.5506
chr19	59128983	2395539	0.0405	0.4211
chr20	63025520	2985127	0.0474	0.2805
chr21	48129895	2286795	0.0475	0.2891
chr22	51304566	1561291	0.0304	0.217
chrMT	16571	30340	1.8309	1.8693
chrX	155270560	10538487	0.0679	0.3462
chrY	59373566	367346	0.0062	0.1189

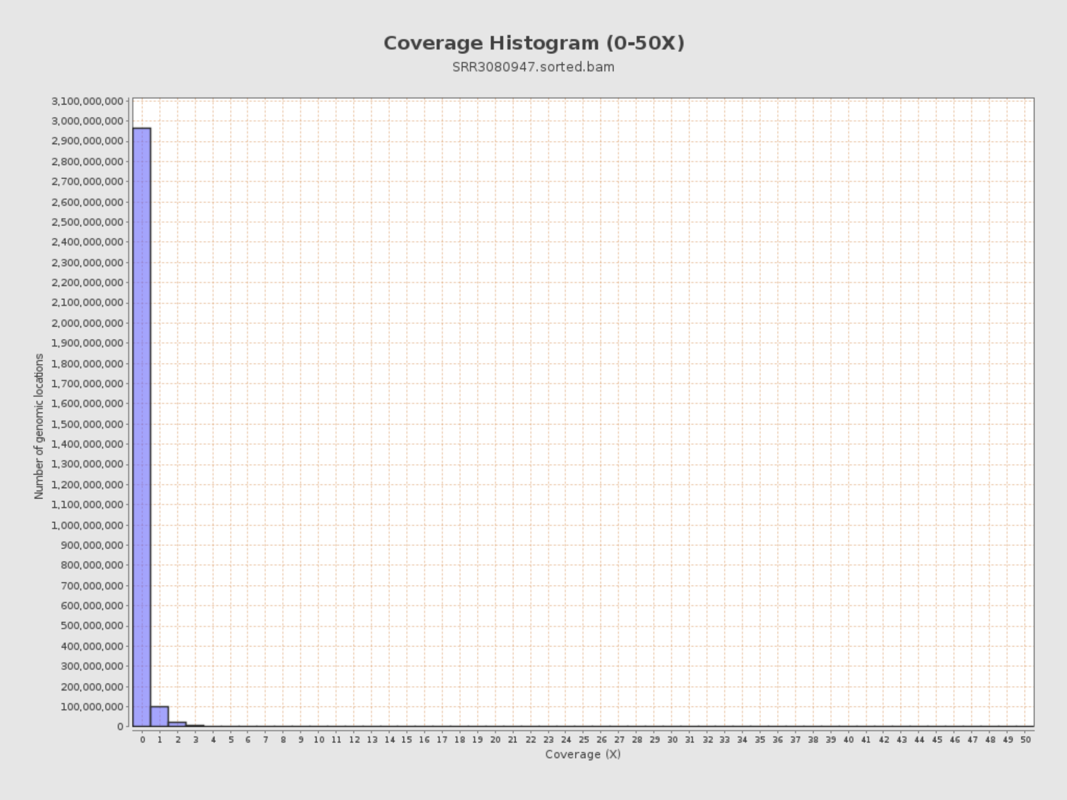
3. Results : Coverage across reference



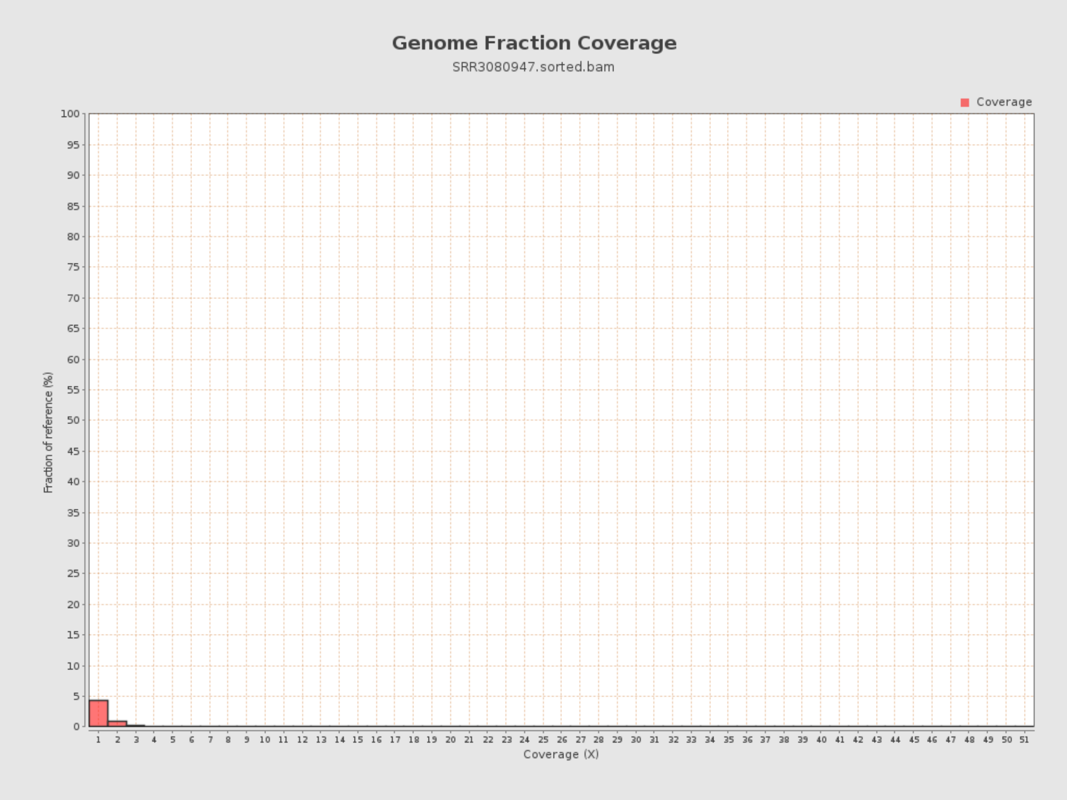
4. Results : Coverage Histogram



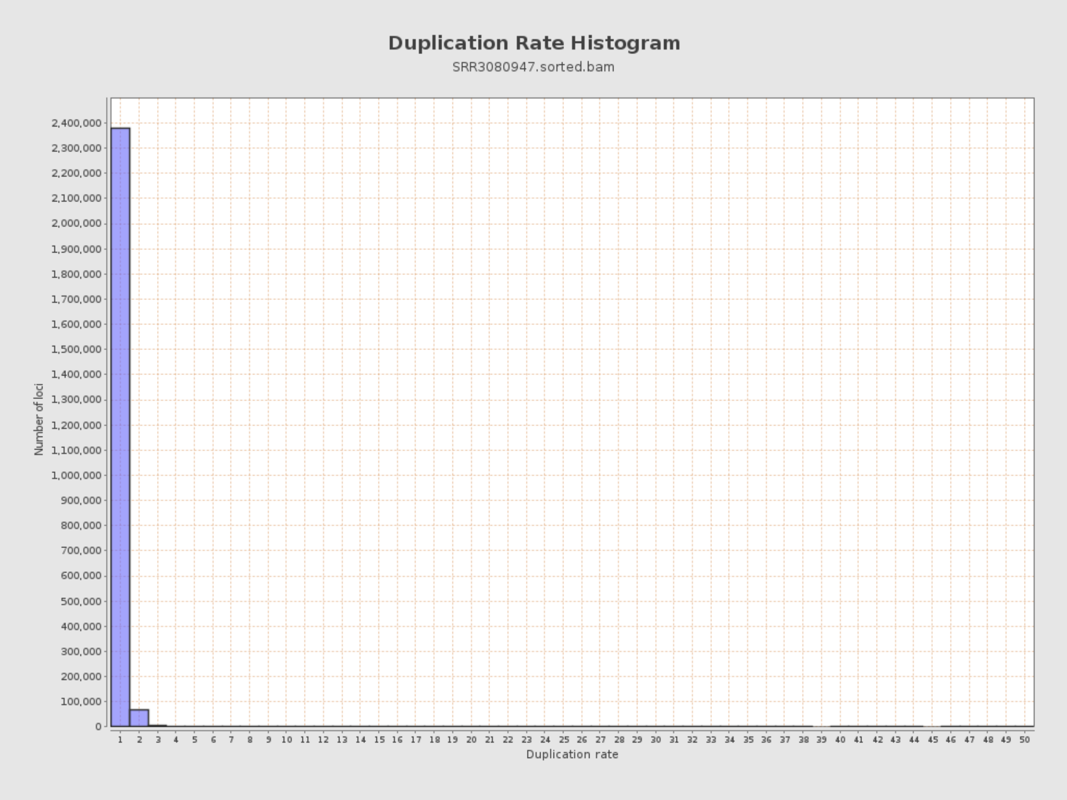
5. Results : Coverage Histogram (0-50X)



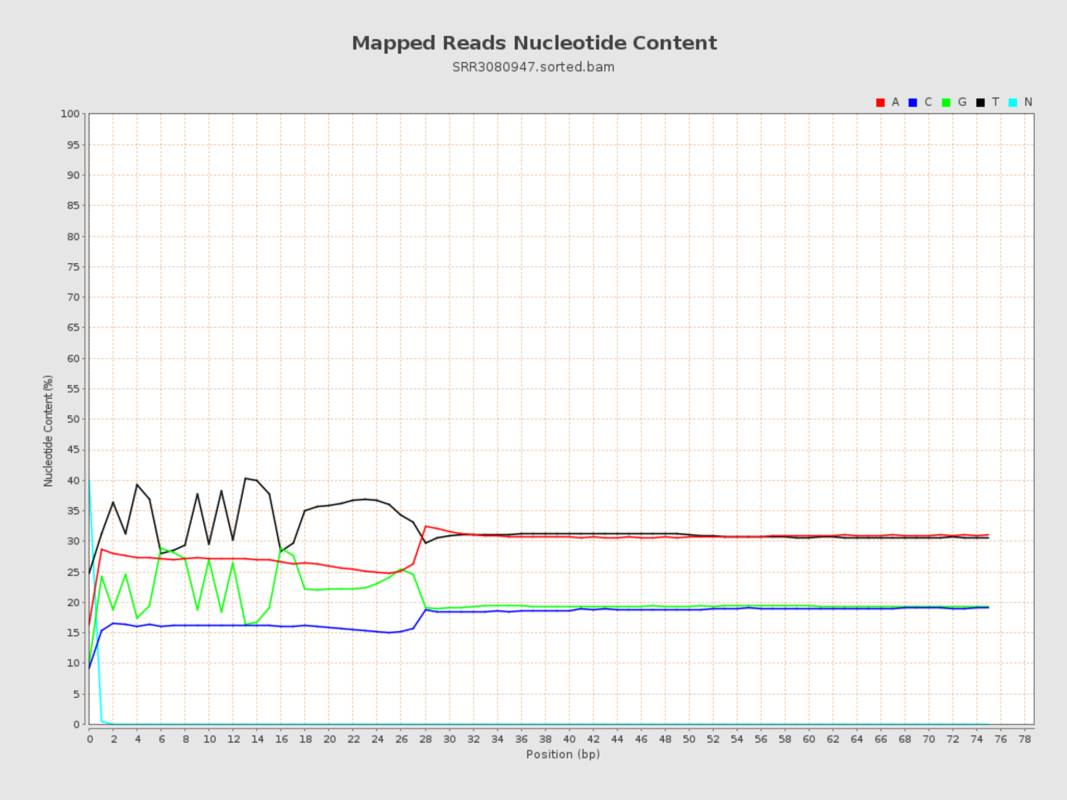
6. Results : Genome Fraction Coverage



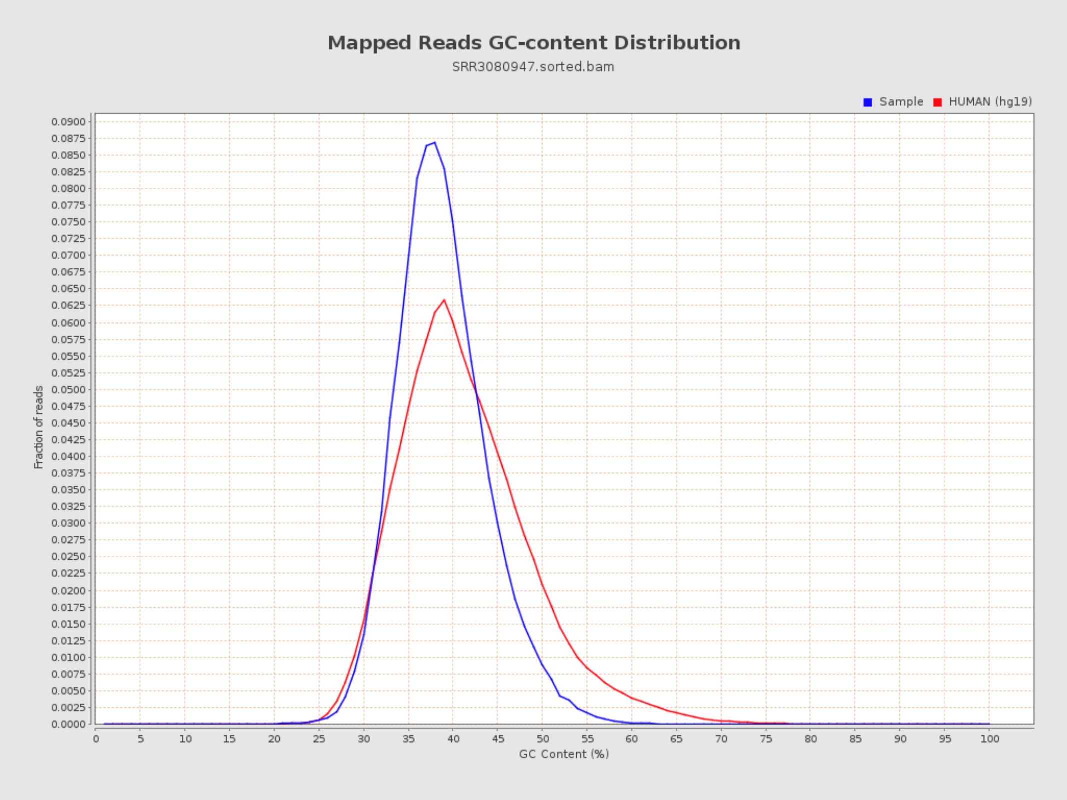
7. Results : Duplication Rate Histogram



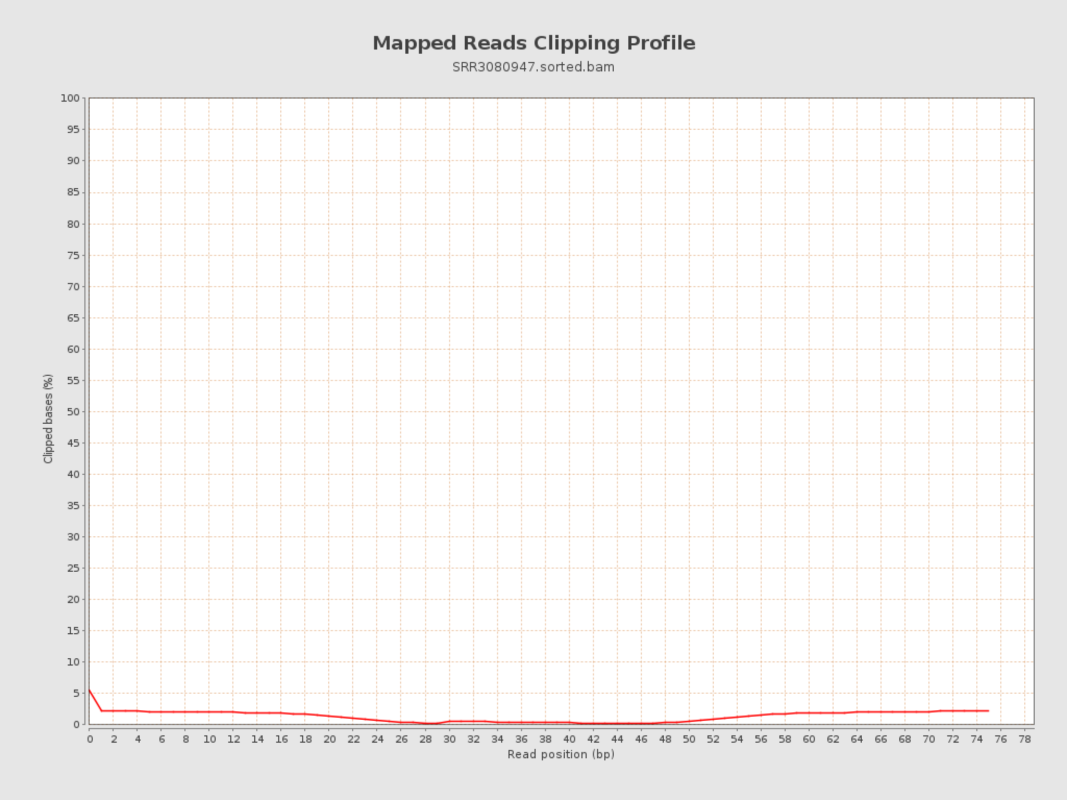
8. Results : Mapped Reads Nucleotide Content



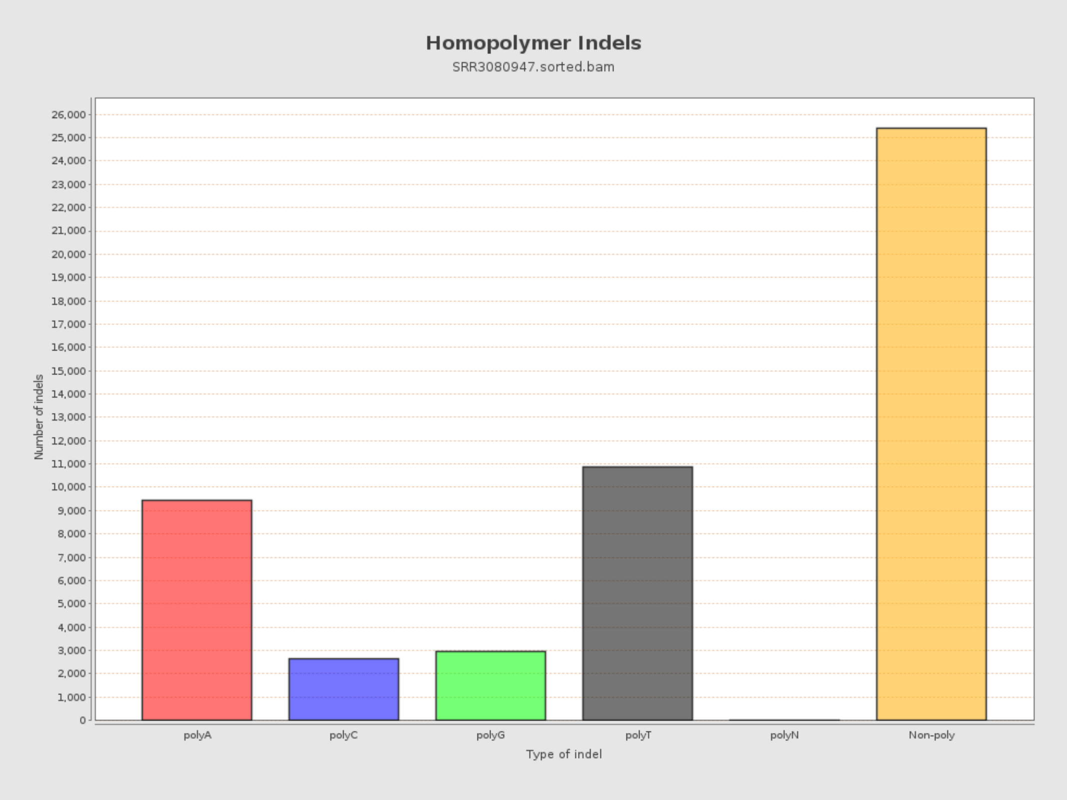
9. Results : Mapped Reads GC-content Distribution



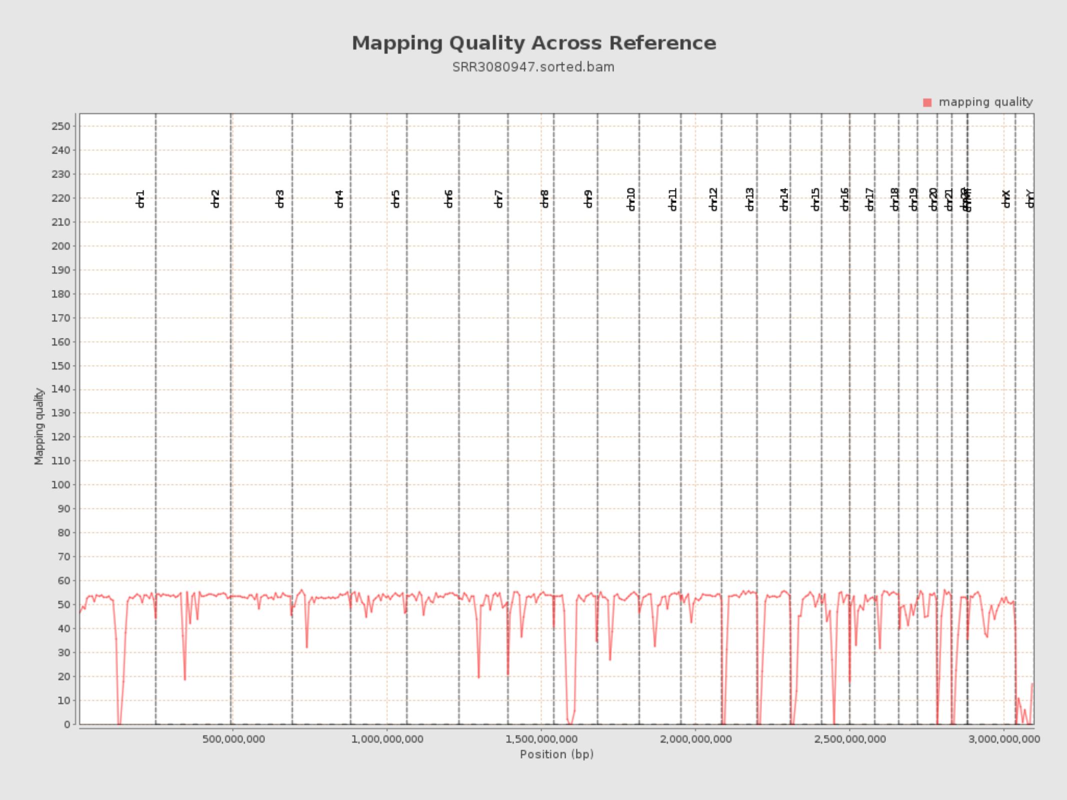
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram