Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:32:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081913.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_SRR3081913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081913.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:32:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,788,401
Mapped reads	2,541,285 / 91.14%
Unmapped reads	247,116 / 8.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,593 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	110,083 / 3.95%
Duplication rate	3.27%
Clipped reads	1,064,035 / 38.16%

2.2. ACGT Content

Number/percentage of A's	47,114,815 / 27.56%
Number/percentage of C's	32,834,806 / 19.2%
Number/percentage of T's	52,629,238 / 30.78%
Number/percentage of G's	38,394,953 / 22.46%
Number/percentage of N's	1,920 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.4699

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

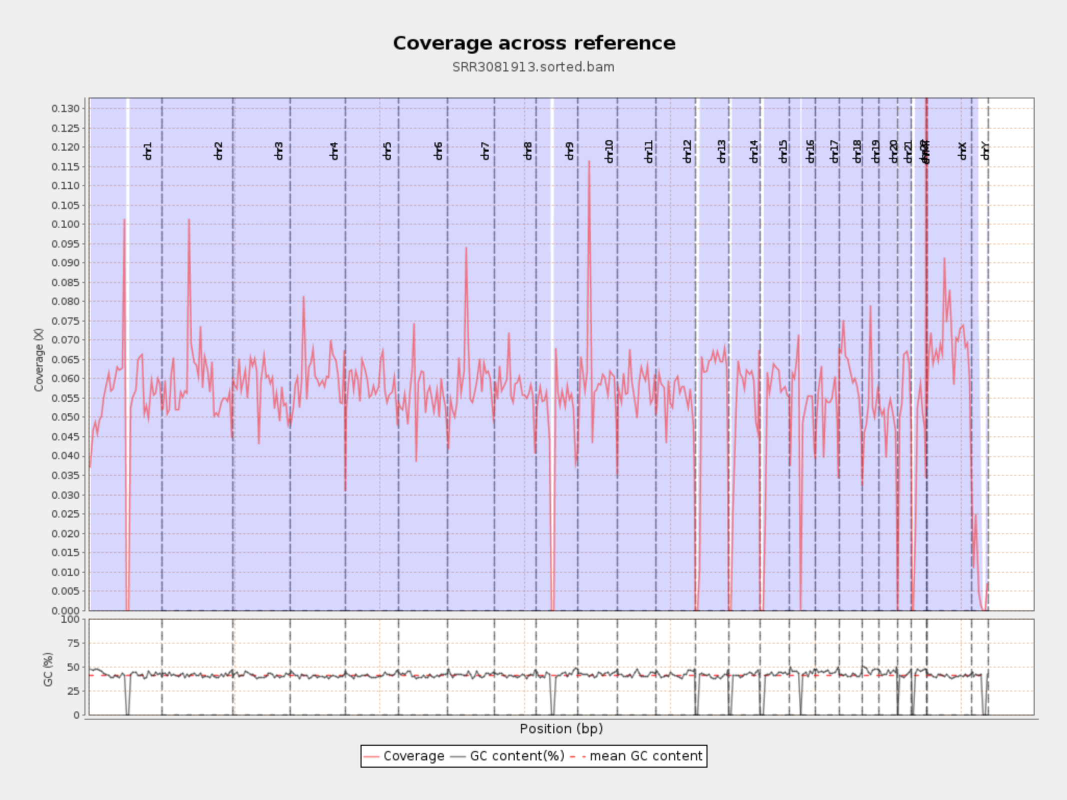
General error rate	0.83%
Mismatches	1,389,566
Insertions	12,009
Mapped reads with at least one insertion	0.47%
Deletions	34,475
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.08%

2.6. Chromosome stats

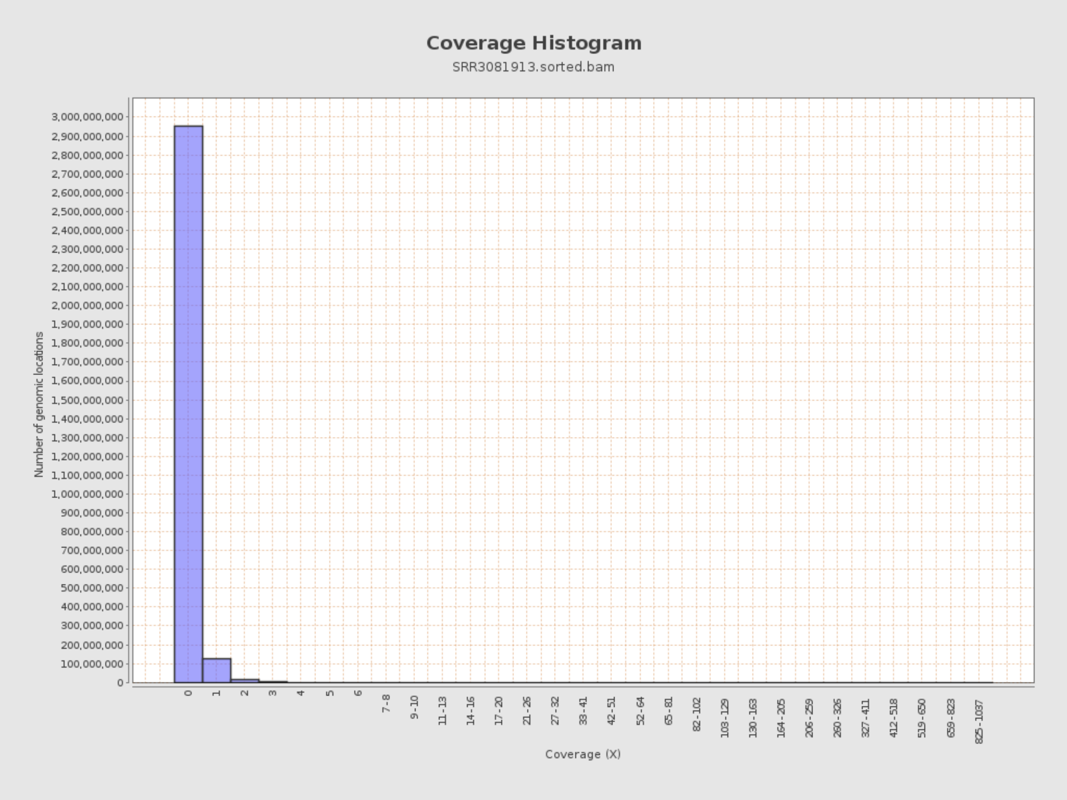
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13416559	0.0538	0.9234
chr2	243199373	14352948	0.059	0.524
chr3	198022430	11483862	0.058	0.2834
chr4	191154276	11612122	0.0607	0.3082
chr5	180915260	10567558	0.0584	0.2786
chr6	171115067	9502454	0.0555	0.3306
chr7	159138663	9469283	0.0595	0.5965

chr8	146364022	8401544	0.0574	0.5045
chr9	141213431	6809883	0.0482	0.3967
chr10	135534747	8302037	0.0613	0.5725
chr11	135006516	7806744	0.0578	0.4103
chr12	133851895	7385189	0.0552	0.2733
chr13	115169878	6180232	0.0537	0.2657
chr14	107349540	5188038	0.0483	0.2703
chr15	102531392	4949179	0.0483	0.2554
chr16	90354753	4590865	0.0508	0.312
chr17	81195210	4264547	0.0525	0.3052
chr18	78077248	4855501	0.0622	0.7906
chr19	59128983	3201468	0.0541	0.6396
chr20	63025520	3062762	0.0486	0.2651
chr21	48129895	2560651	0.0532	0.2926
chr22	51304566	1841058	0.0359	0.2164
chrMT	16571	16820	1.015	1.1526
chrX	155270560	10724892	0.0691	0.3481
chrY	59373566	491022	0.0083	0.1903

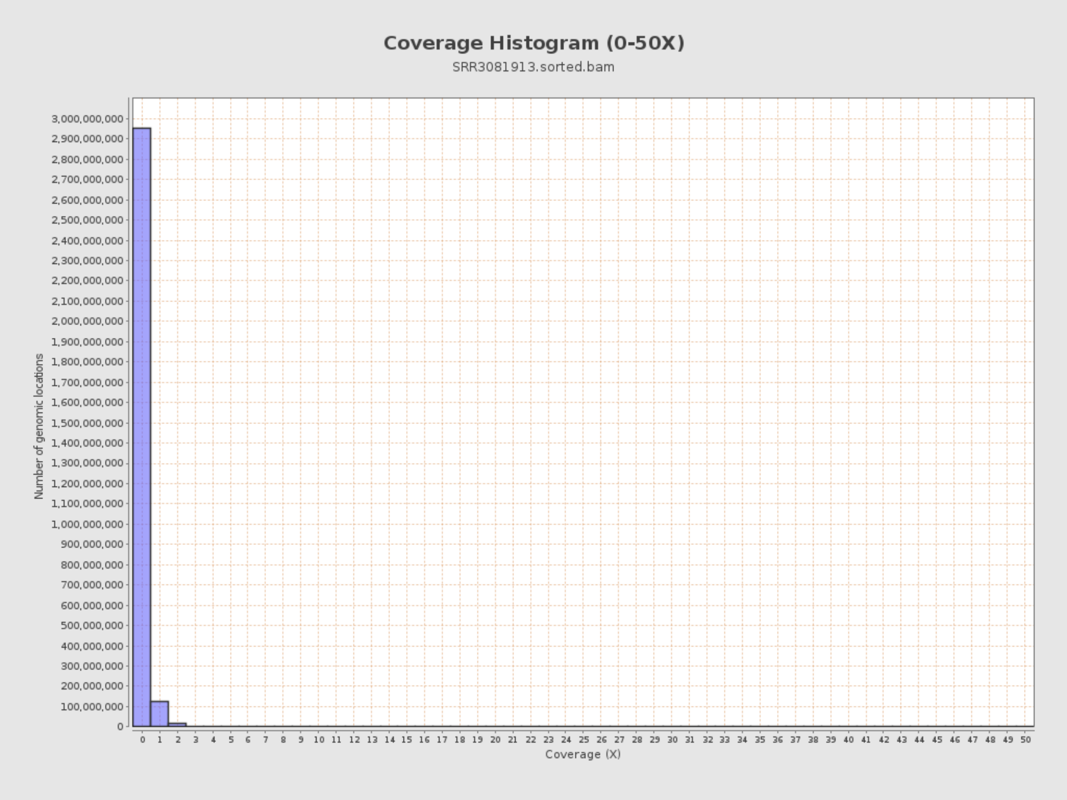
3. Results : Coverage across reference



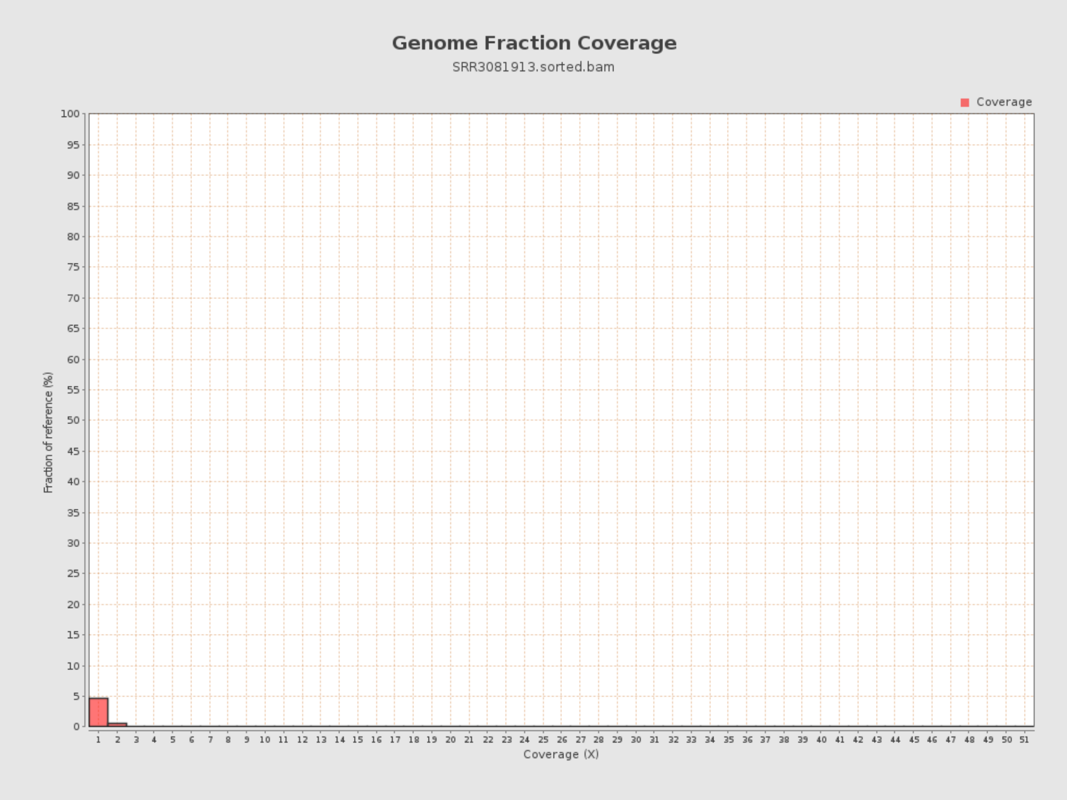
4. Results : Coverage Histogram



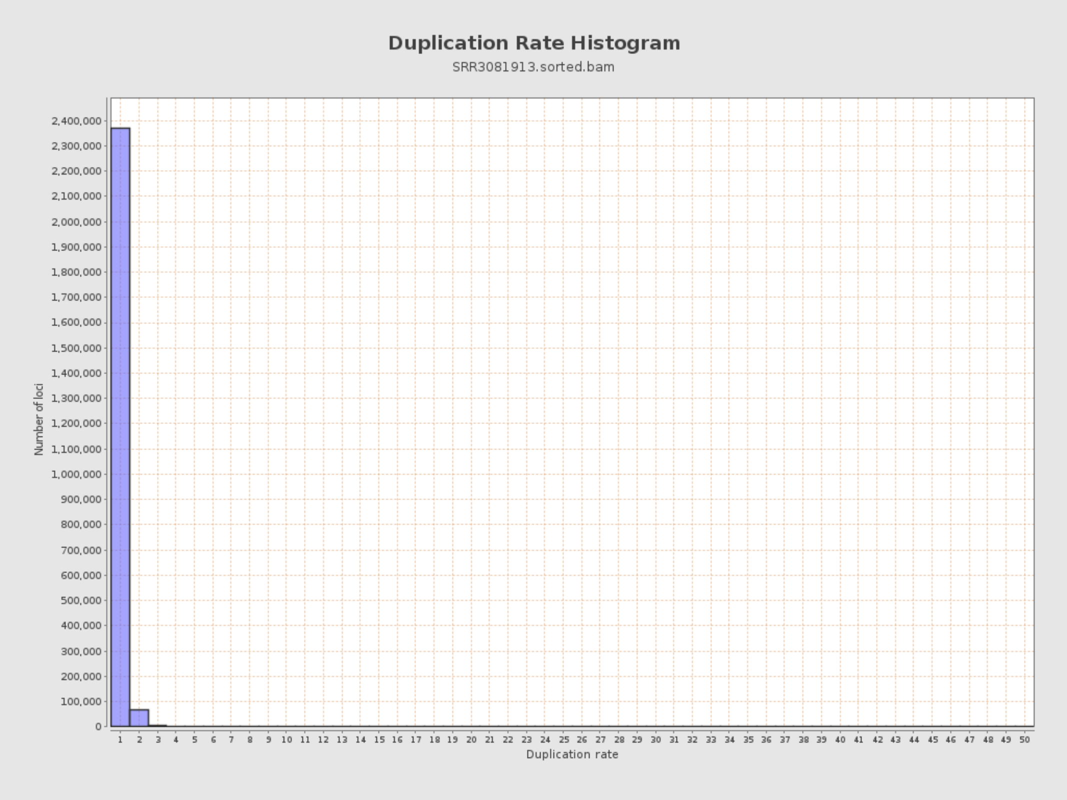
5. Results : Coverage Histogram (0-50X)



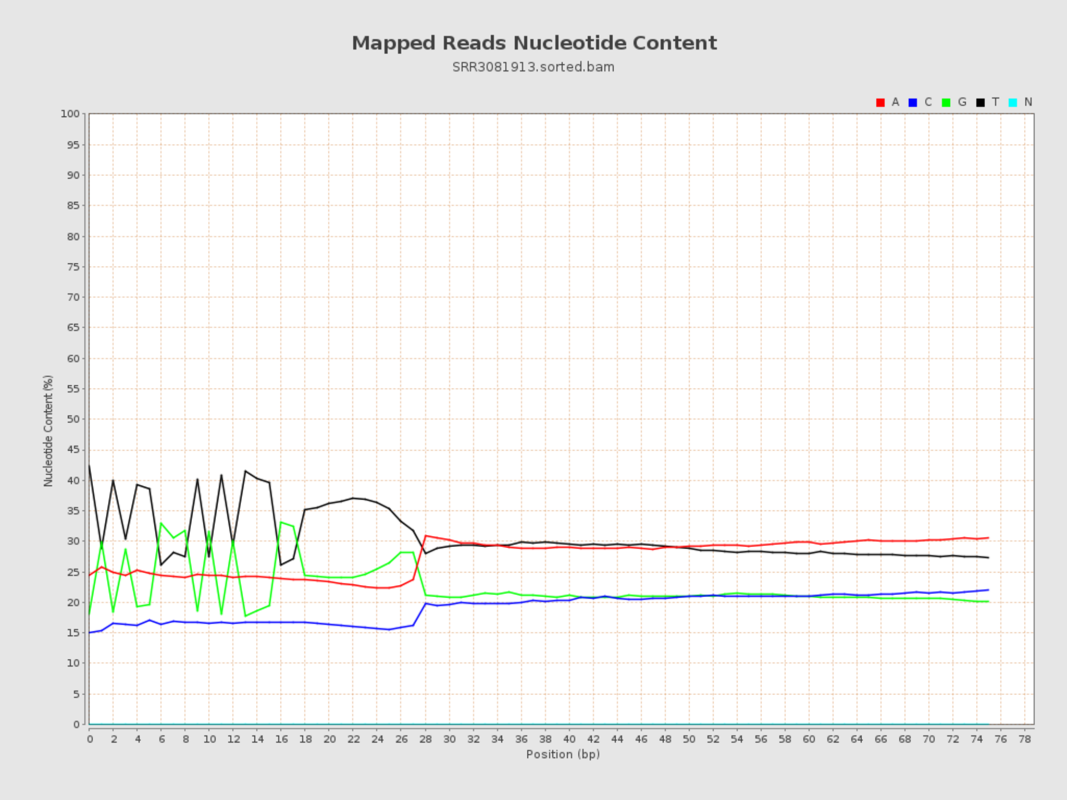
6. Results : Genome Fraction Coverage



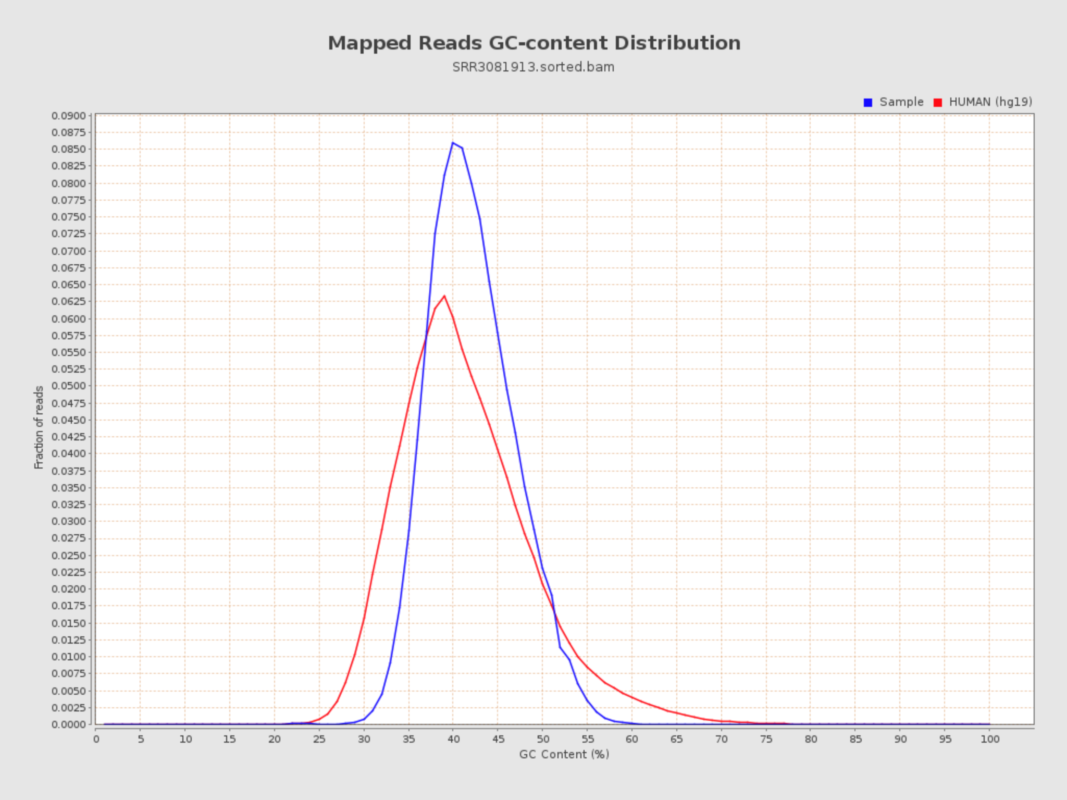
7. Results : Duplication Rate Histogram



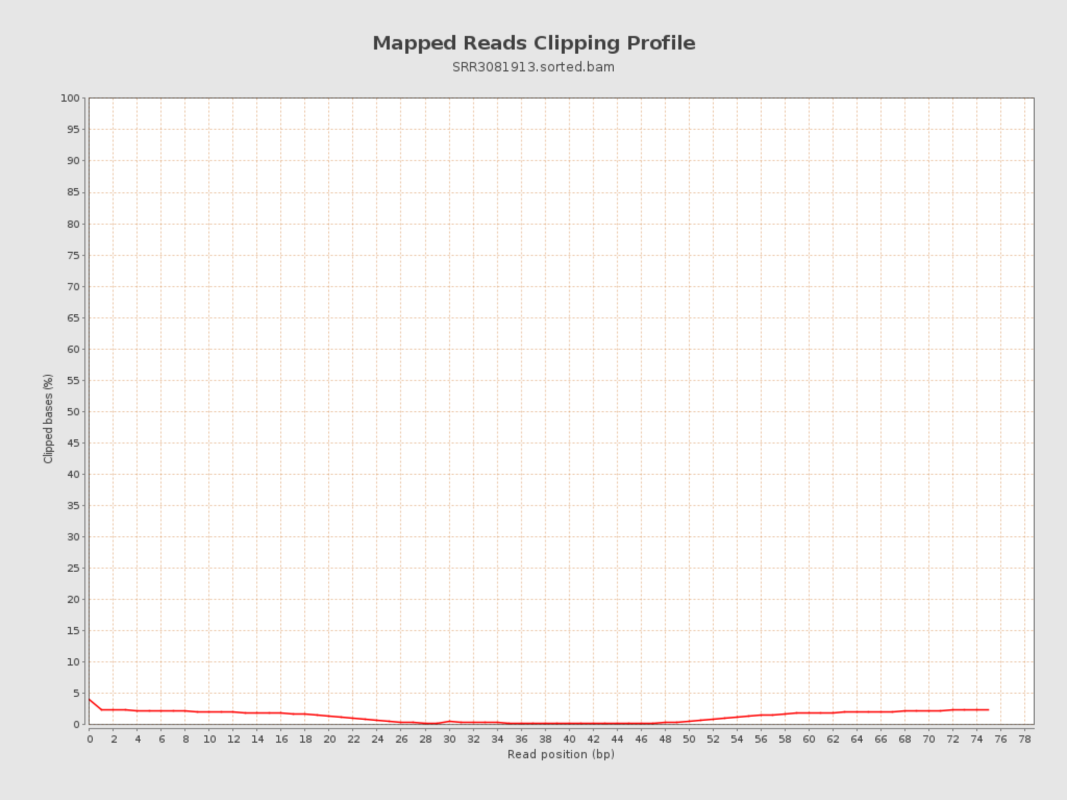
8. Results : Mapped Reads Nucleotide Content



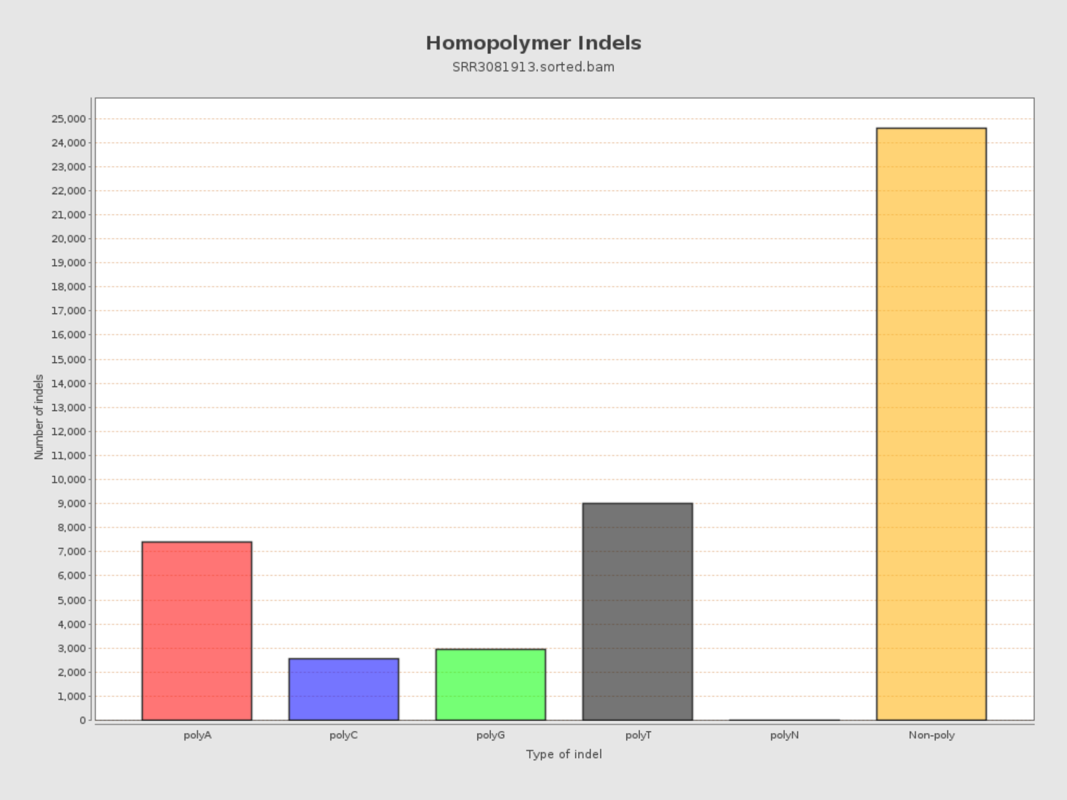
9. Results : Mapped Reads GC-content Distribution



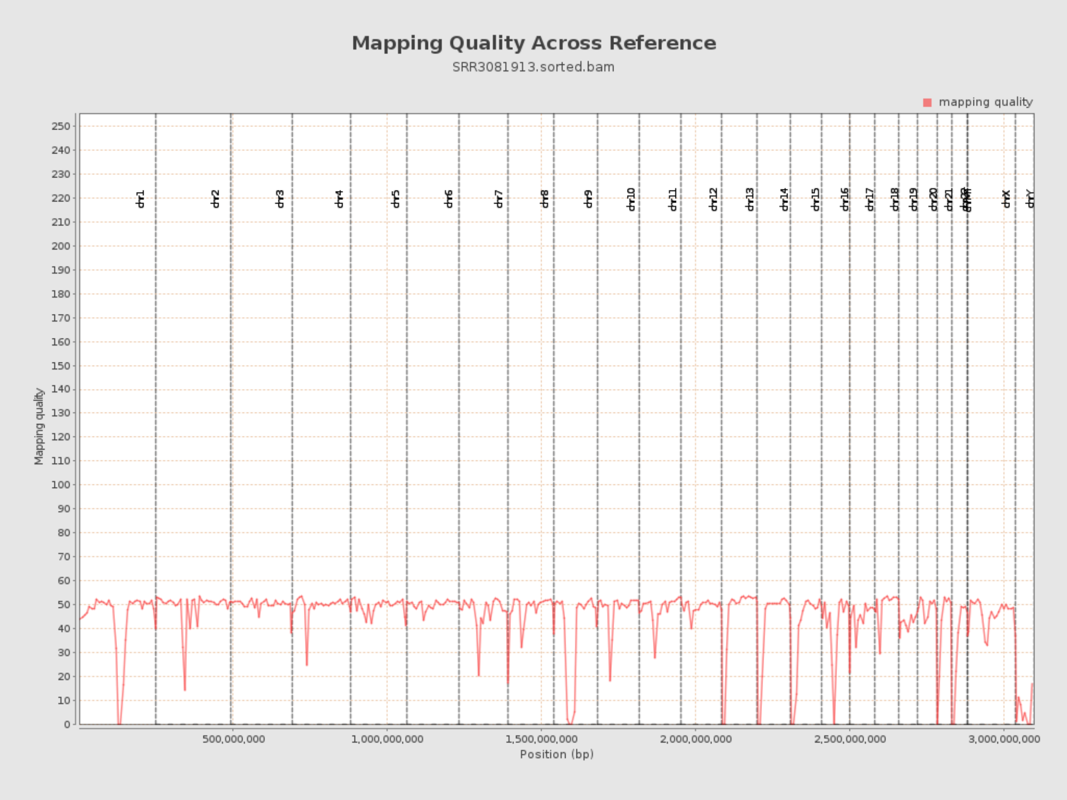
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram