Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:15:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081923.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_SRR3081923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:15:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,751,694
Mapped reads	2,483,040 / 90.24%
Unmapped reads	268,654 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,483 / 1.22%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	91,200 / 3.31%
Duplication rate	2.12%
Clipped reads	1,187,612 / 43.16%

2.2. ACGT Content

Number/percentage of A's	45,449,536 / 27.52%
Number/percentage of C's	32,361,649 / 19.6%
Number/percentage of T's	48,629,947 / 29.45%
Number/percentage of G's	38,680,801 / 23.43%
Number/percentage of N's	1,704 / 0%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0534

Standard Deviation	0.5984

2.4. Mapping Quality

Mean Mapping Quality	41.72

2.5. Mismatches and indels

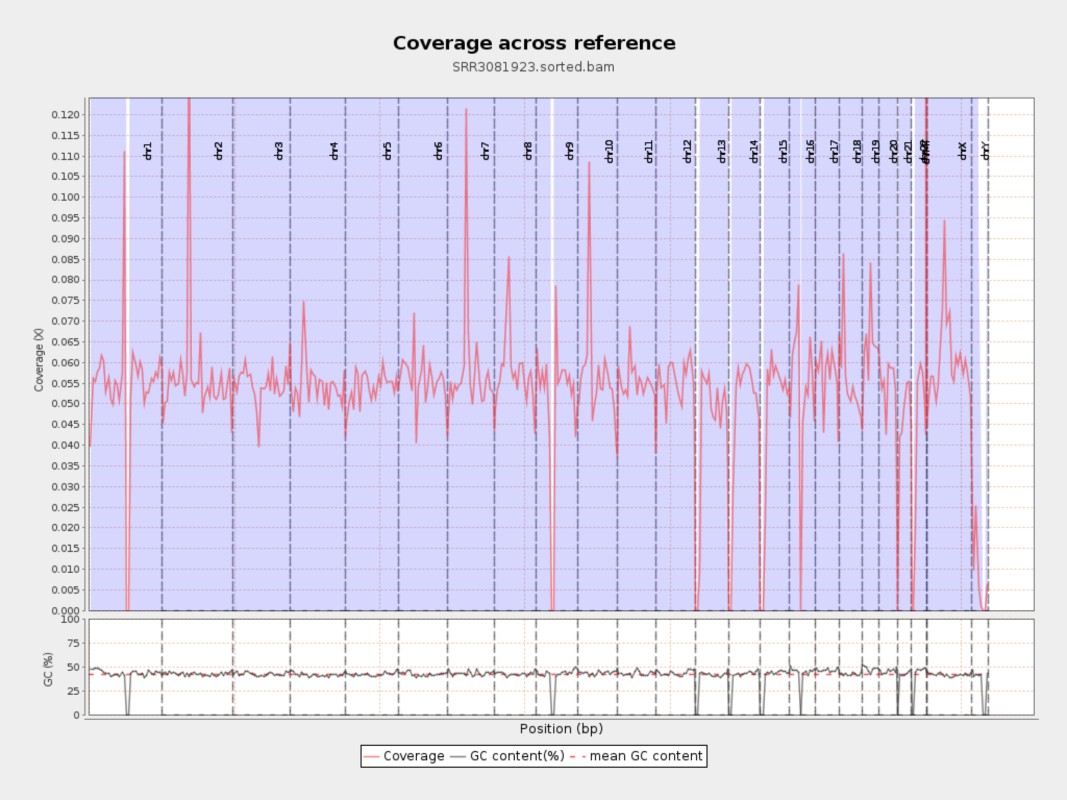
General error rate	0.89%
Mismatches	1,441,292
Insertions	14,758
Mapped reads with at least one insertion	0.59%
Deletions	34,943
Mapped reads with at least one deletion	1.39%
Homopolymer indels	43.05%

2.6. Chromosome stats

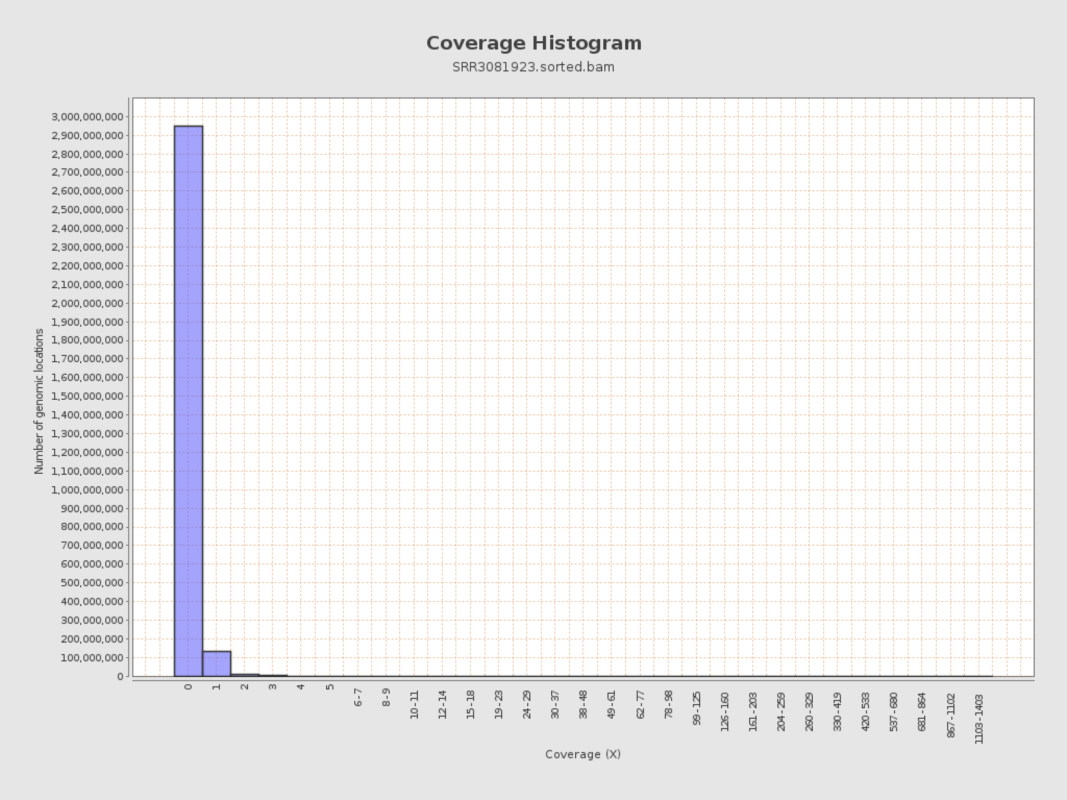
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13415938	0.0538	1.2149
chr2	243199373	13915585	0.0572	0.7765
chr3	198022430	10802654	0.0546	0.2593
chr4	191154276	10407217	0.0544	0.2883
chr5	180915260	9795535	0.0541	0.2582
chr6	171115067	9594570	0.0561	0.3379
chr7	159138663	9291047	0.0584	0.9113

chr8	146364022	8470132	0.0579	0.622
chr9	141213431	7023606	0.0497	0.5704
chr10	135534747	7766482	0.0573	0.5582
chr11	135006516	7442651	0.0551	0.4737
chr12	133851895	7467961	0.0558	0.2692
chr13	115169878	4928253	0.0428	0.2259
chr14	107349540	4997533	0.0466	0.3
chr15	102531392	4702787	0.0459	0.2618
chr16	90354753	4850655	0.0537	0.3251
chr17	81195210	4637322	0.0571	0.2995
chr18	78077248	4415842	0.0566	1.1145
chr19	59128983	3828205	0.0647	0.8902
chr20	63025520	3396481	0.0539	0.2688
chr21	48129895	2114119	0.0439	0.2696
chr22	51304566	1967661	0.0384	0.2125
chrMT	16571	27436	1.6557	1.7091
chrX	155270560	9427674	0.0607	0.3611
chrY	59373566	494971	0.0083	0.1922

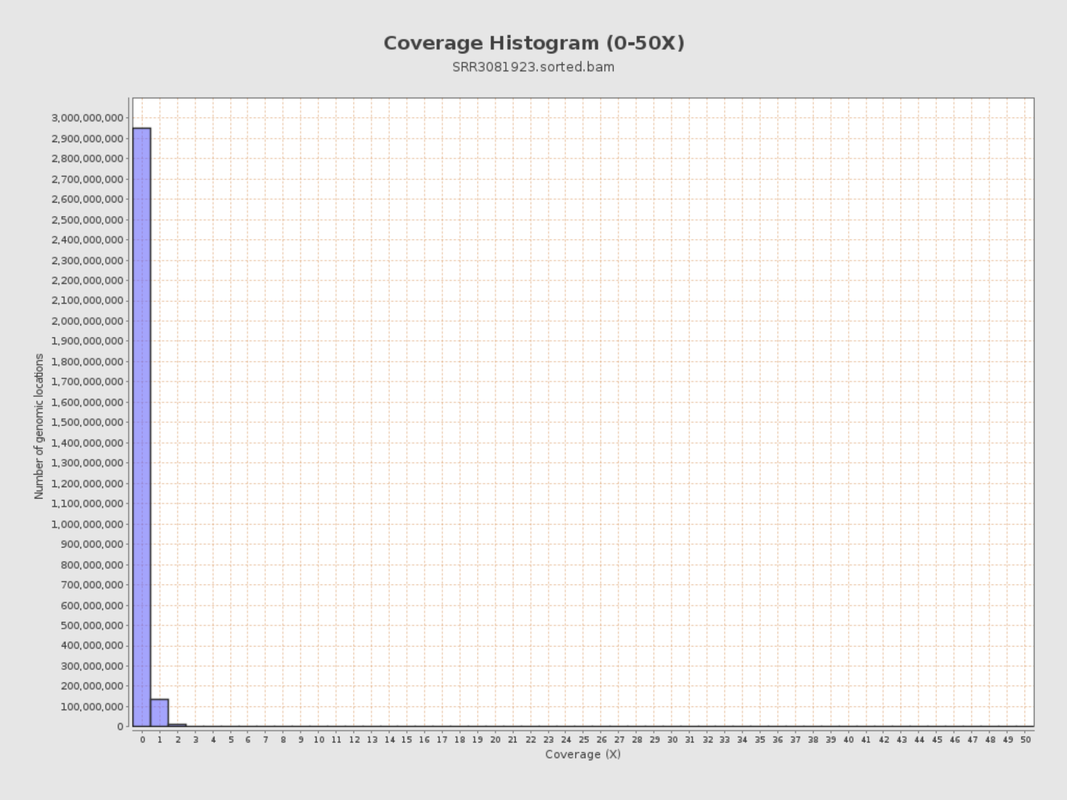
3. Results : Coverage across reference



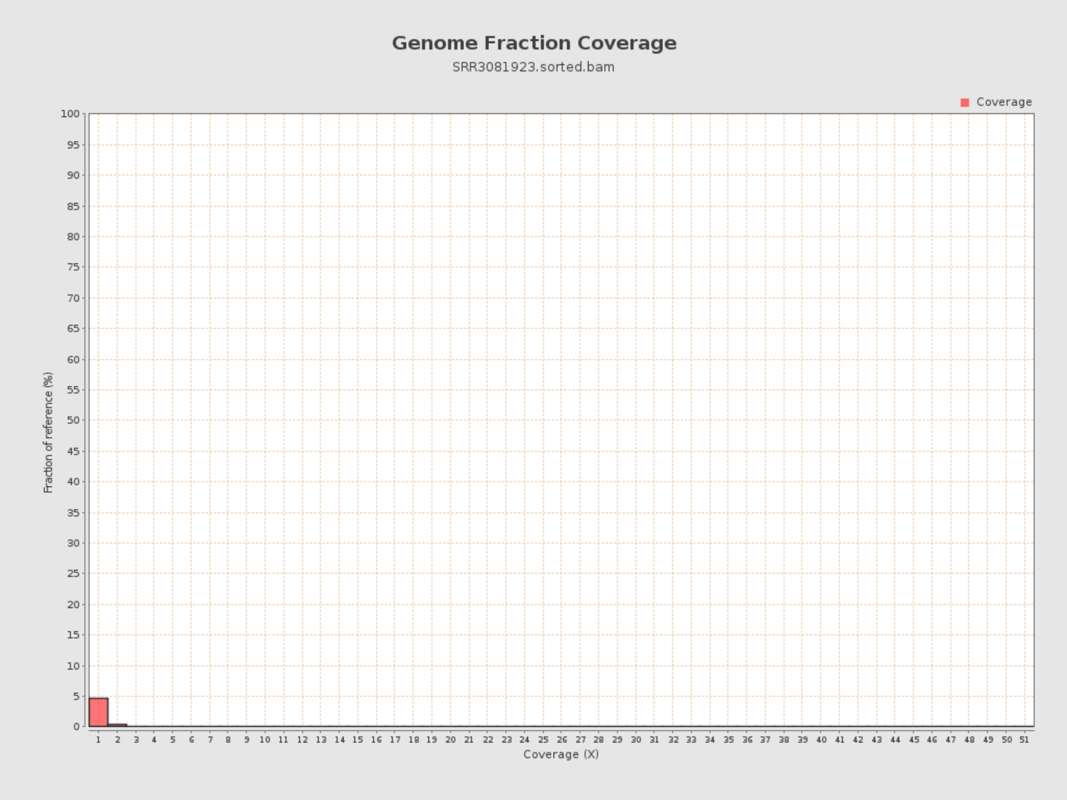
4. Results : Coverage Histogram



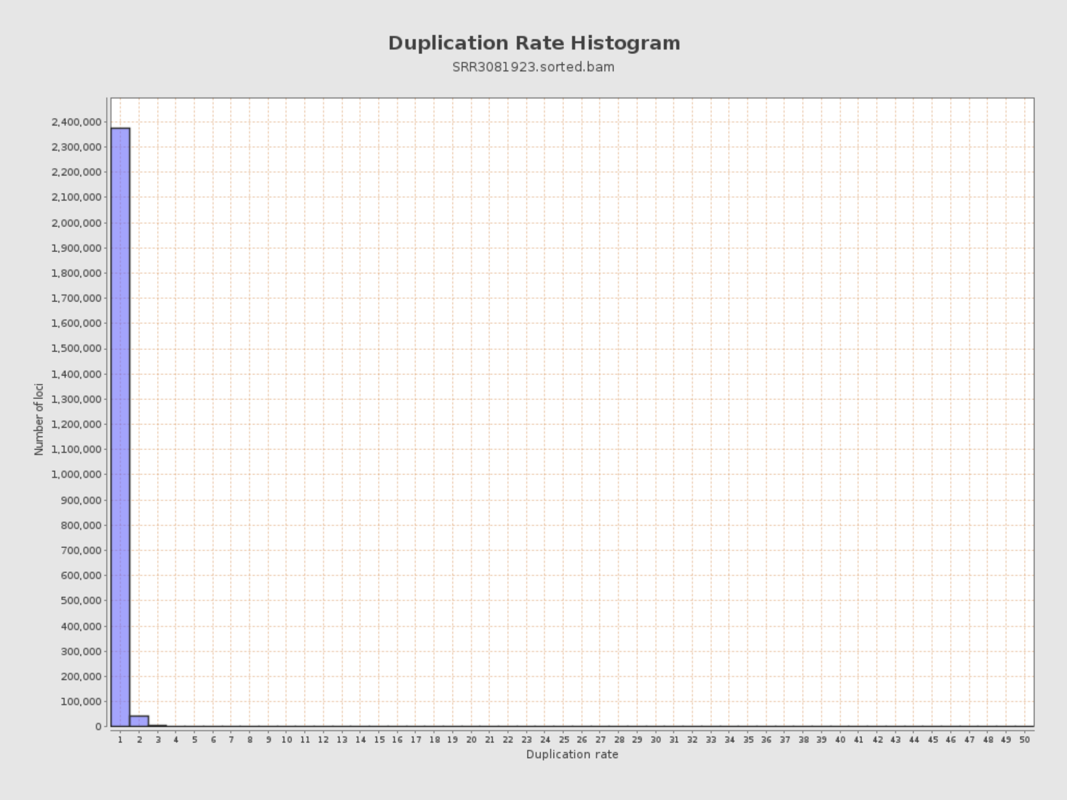
5. Results : Coverage Histogram (0-50X)



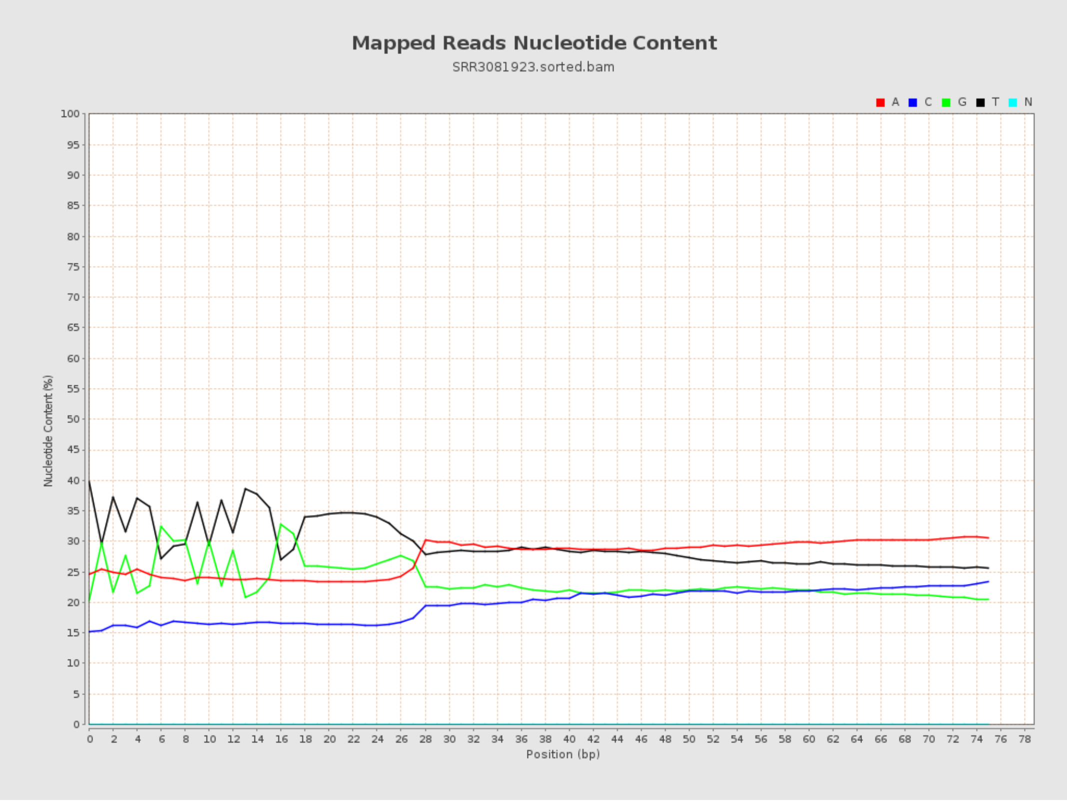
6. Results : Genome Fraction Coverage



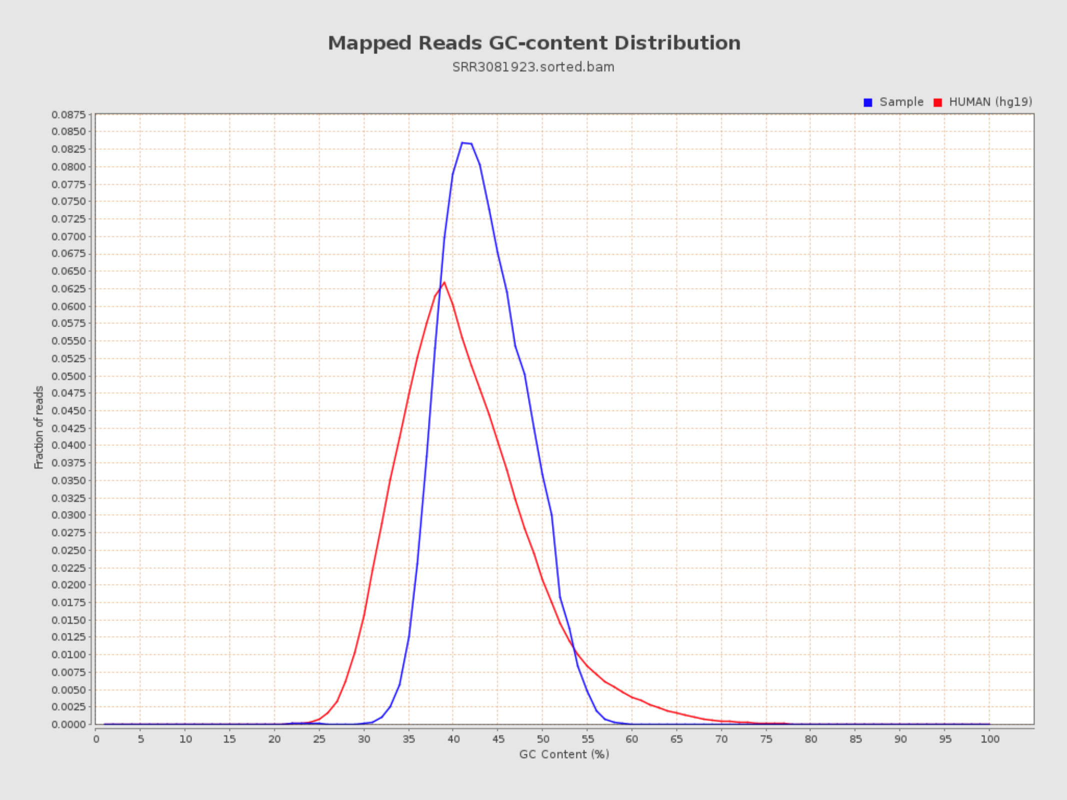
7. Results : Duplication Rate Histogram



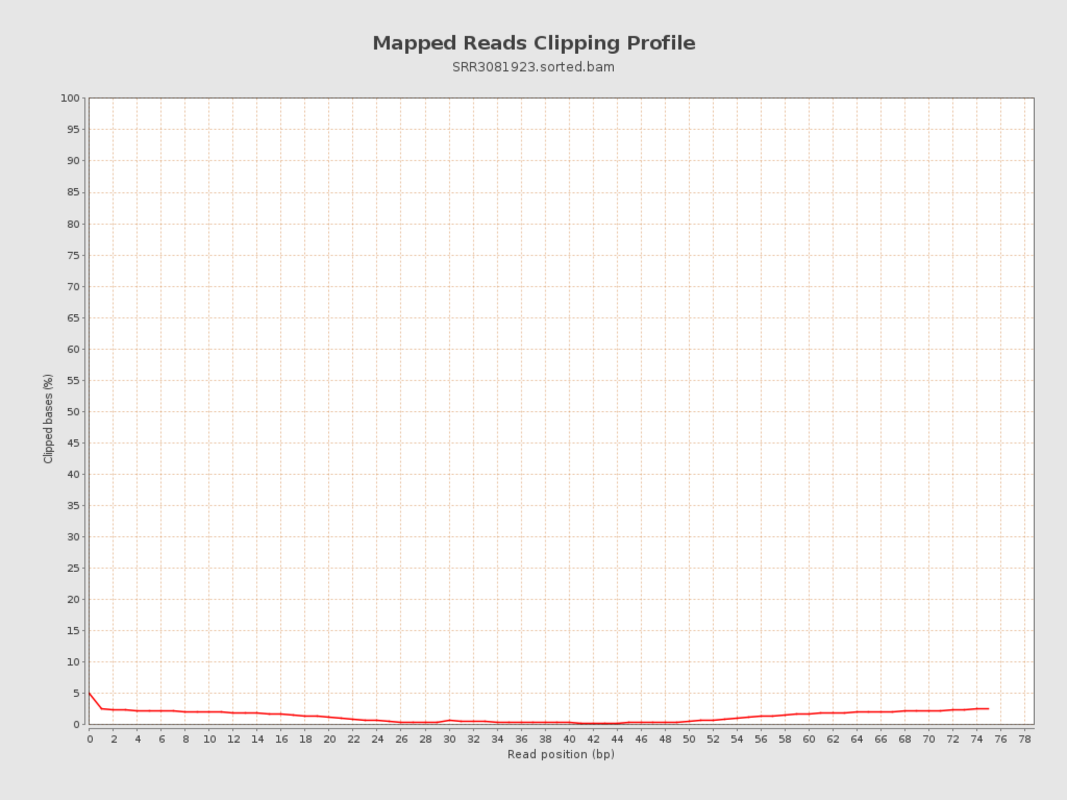
8. Results : Mapped Reads Nucleotide Content



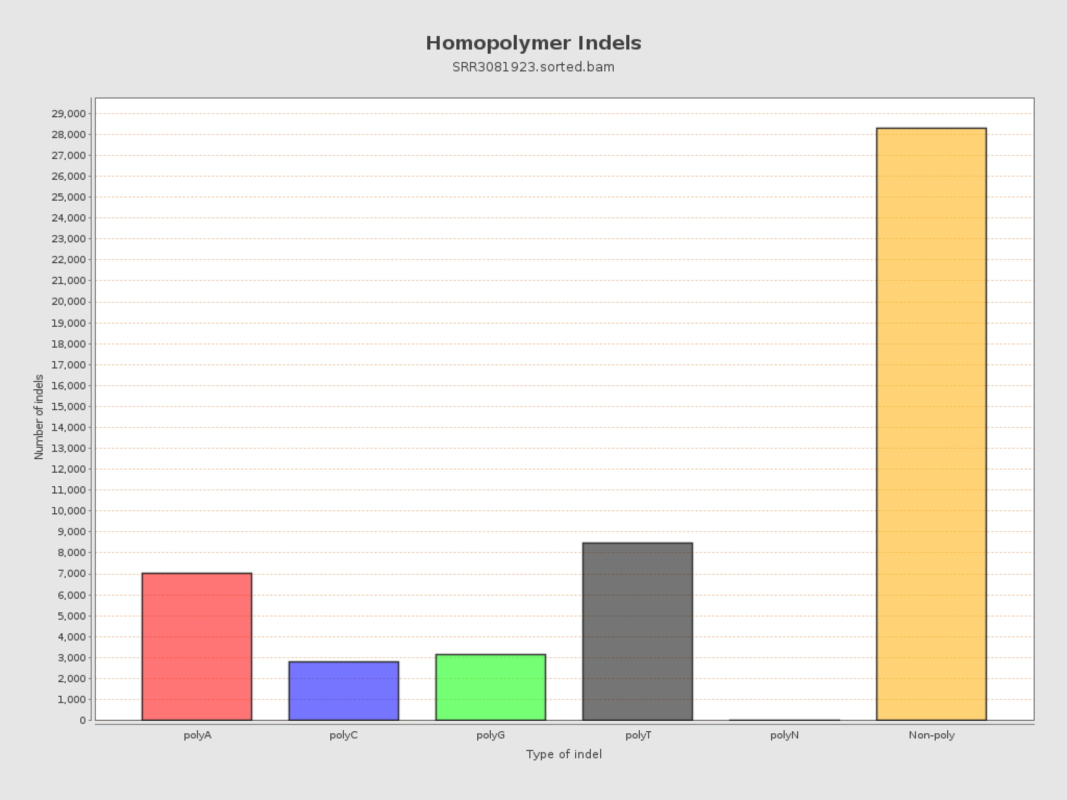
9. Results : Mapped Reads GC-content Distribution



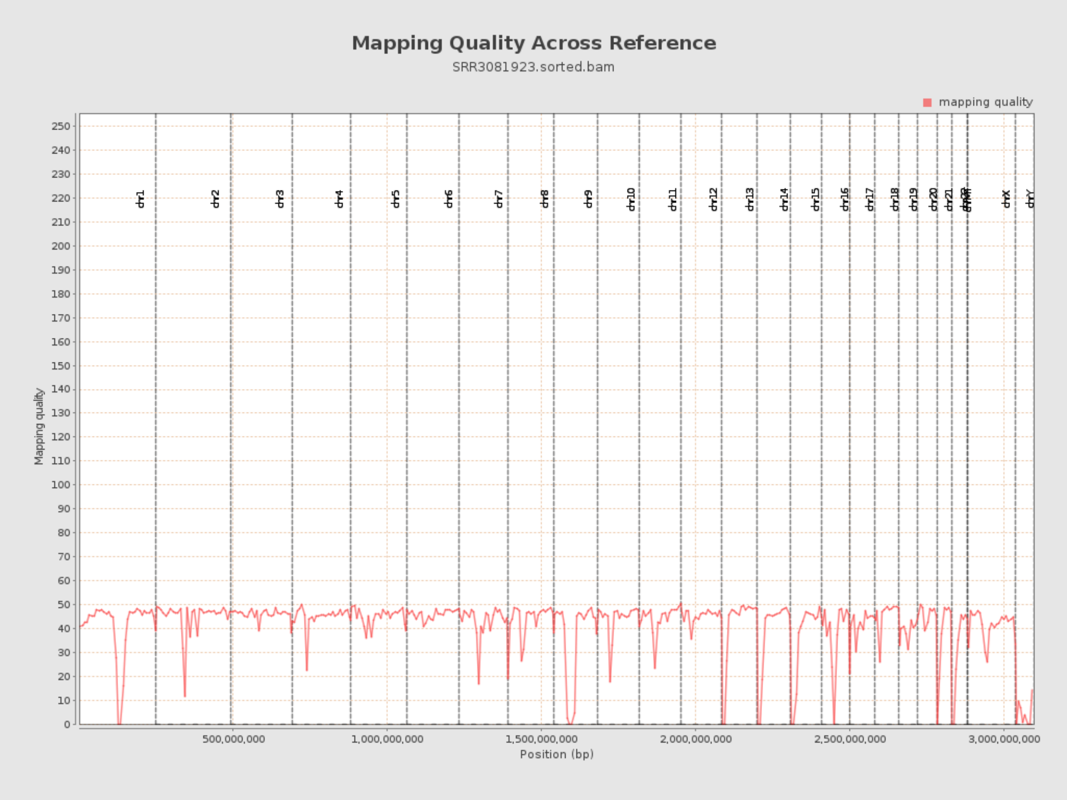
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram