Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:41:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081004.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_SRR3081004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:41:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,321,411
Mapped reads	2,860,023 / 86.11%
Unmapped reads	461,388 / 13.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,657 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	111,656 / 3.36%
Duplication rate	3.03%
Clipped reads	1,504,838 / 45.31%

2.2. ACGT Content

Number/percentage of A's	50,879,917 / 27.6%
Number/percentage of C's	37,122,461 / 20.14%
Number/percentage of T's	54,190,704 / 29.4%
Number/percentage of G's	42,123,272 / 22.85%
Number/percentage of N's	2,455 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.4273

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

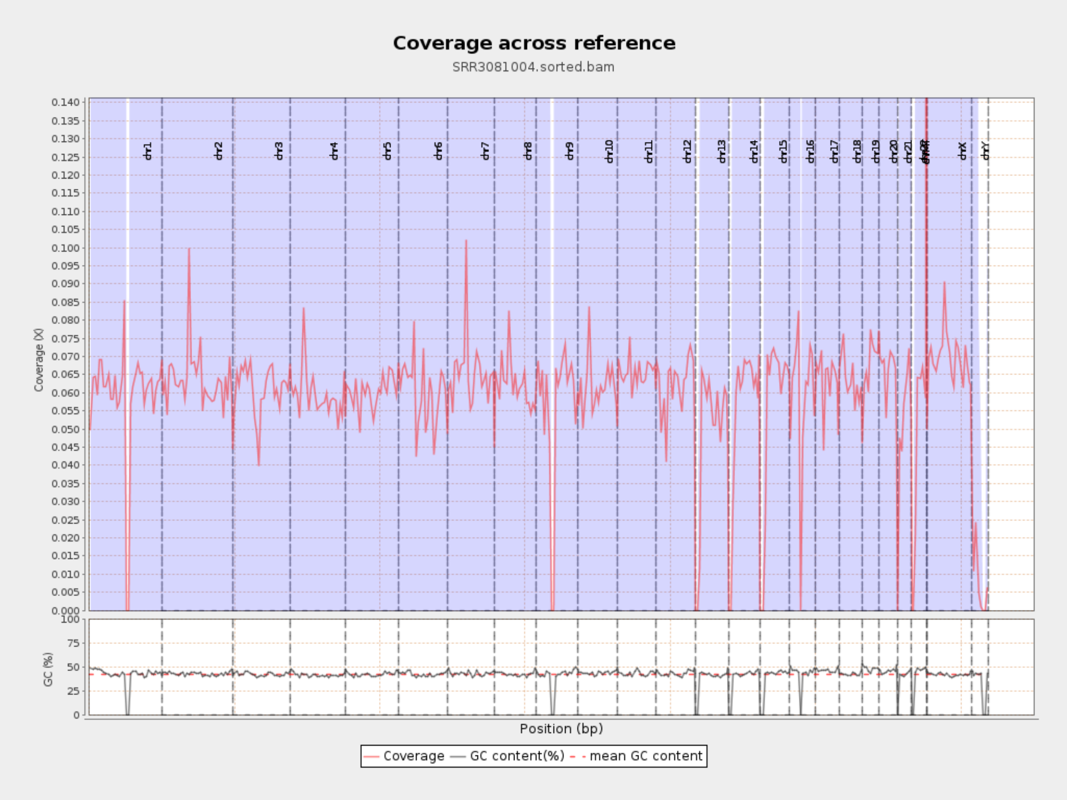
General error rate	0.76%
Mismatches	1,372,918
Insertions	12,738
Mapped reads with at least one insertion	0.44%
Deletions	37,672
Mapped reads with at least one deletion	1.3%
Homopolymer indels	46.3%

2.6. Chromosome stats

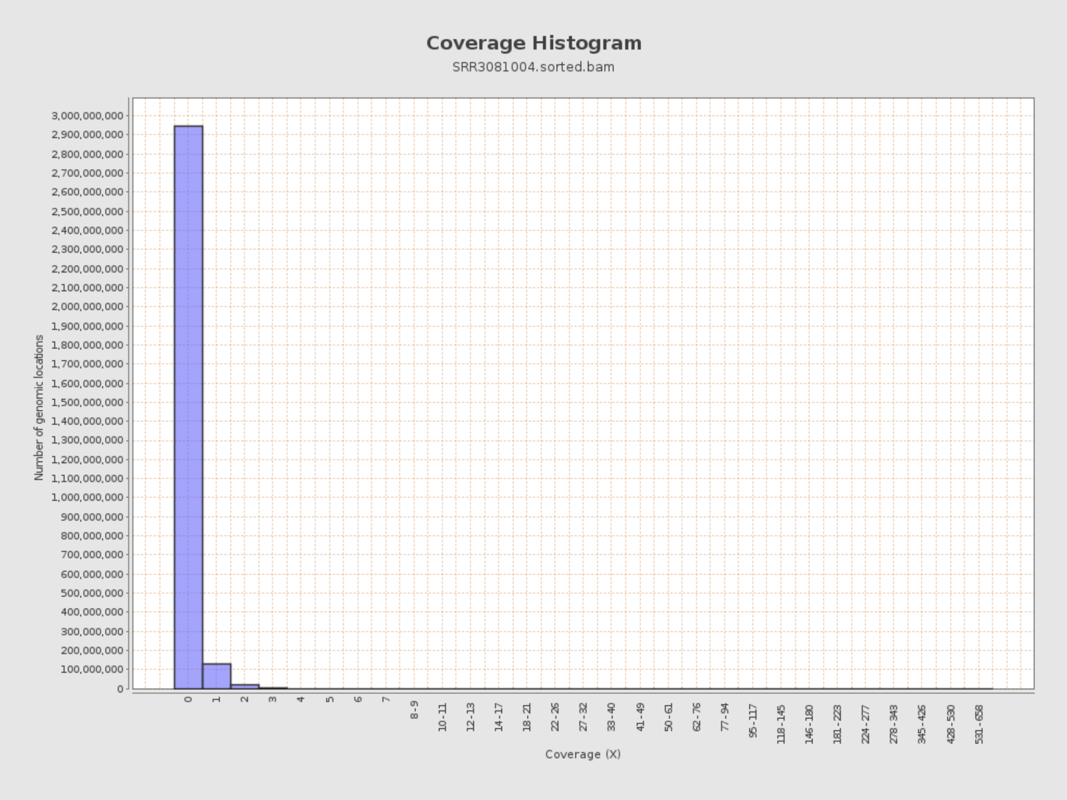
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14650598	0.0588	0.6212
chr2	243199373	15517667	0.0638	0.4793
chr3	198022430	12059835	0.0609	0.2878
chr4	191154276	11376878	0.0595	0.3157
chr5	180915260	10876122	0.0601	0.2885
chr6	171115067	10339963	0.0604	0.3747
chr7	159138663	10445107	0.0656	0.7755

chr8	146364022	9163112	0.0626	0.4048
chr9	141213431	7867848	0.0557	0.4004
chr10	135534747	8359448	0.0617	0.3891
chr11	135006516	8833923	0.0654	0.4221
chr12	133851895	8302588	0.062	0.2969
chr13	115169878	5556590	0.0482	0.2559
chr14	107349540	5791359	0.0539	0.2931
chr15	102531392	5603320	0.0546	0.2892
chr16	90354753	5343692	0.0591	0.322
chr17	81195210	5122538	0.0631	0.3428
chr18	78077248	5000743	0.064	0.7673
chr19	59128983	4016368	0.0679	0.5006
chr20	63025520	4141274	0.0657	0.3115
chr21	48129895	2474179	0.0514	0.3016
chr22	51304566	2260757	0.0441	0.2456
chrMT	16571	11873	0.7165	0.9723
chrX	155270560	10781667	0.0694	0.3513
chrY	59373566	487835	0.0082	0.1719

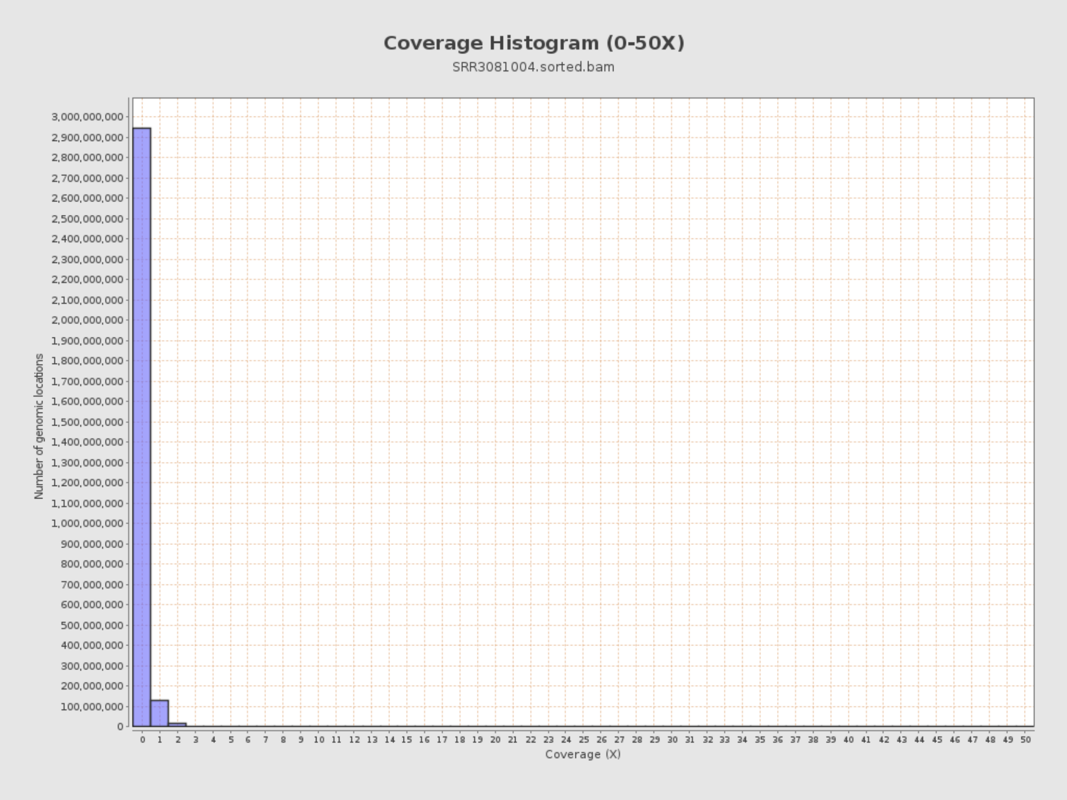
3. Results : Coverage across reference



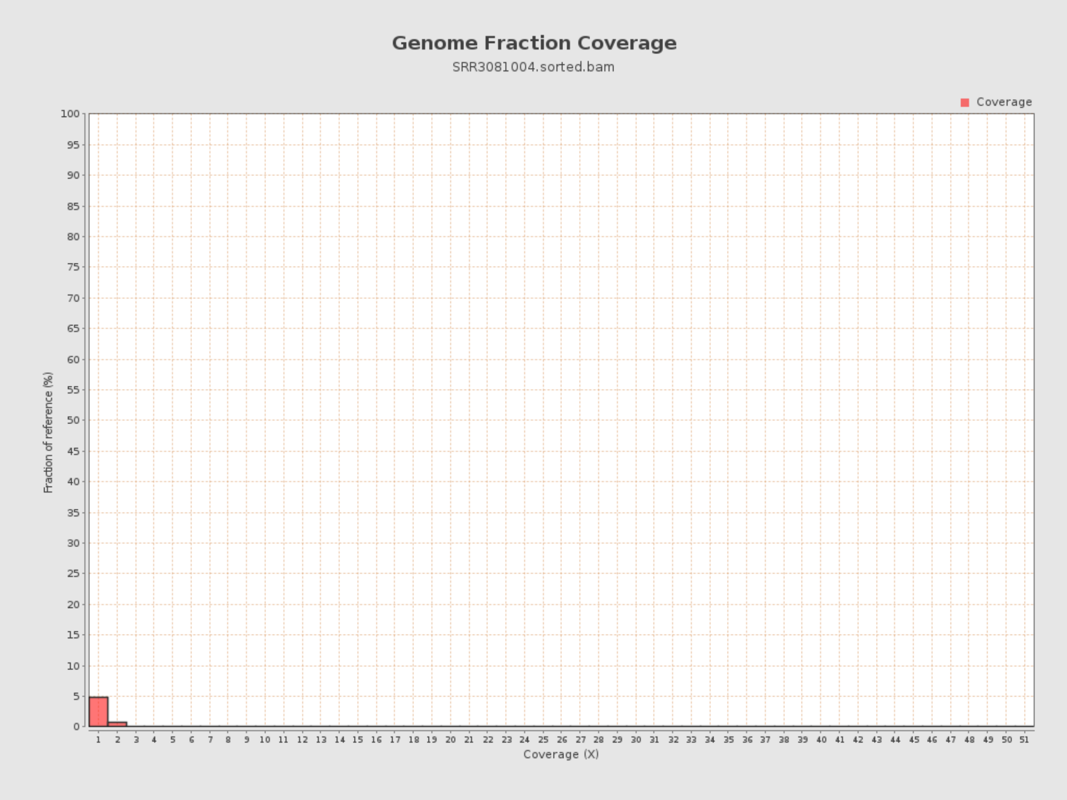
4. Results : Coverage Histogram



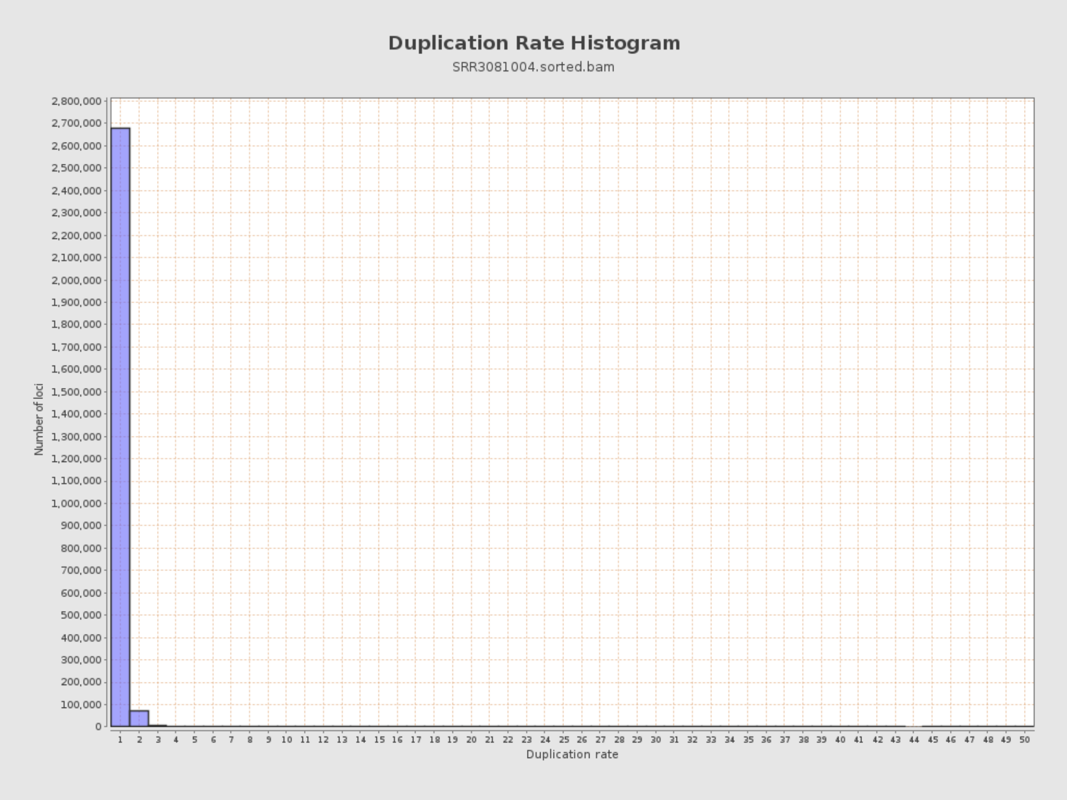
5. Results : Coverage Histogram (0-50X)



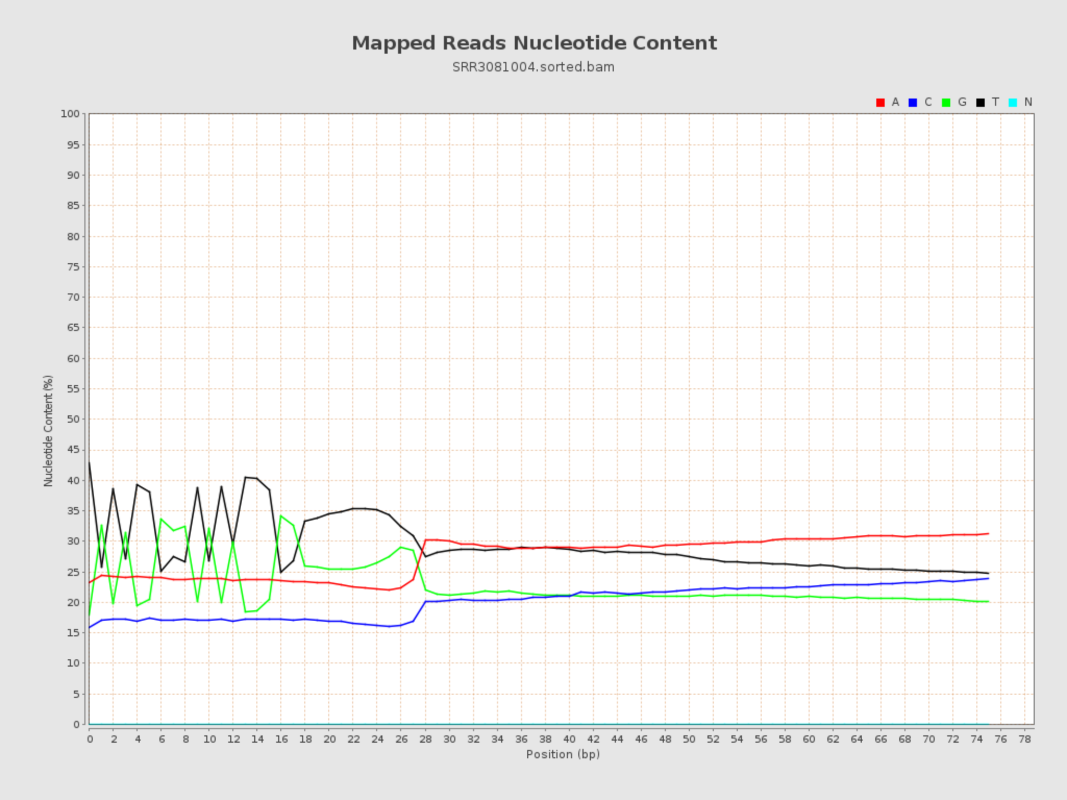
6. Results : Genome Fraction Coverage



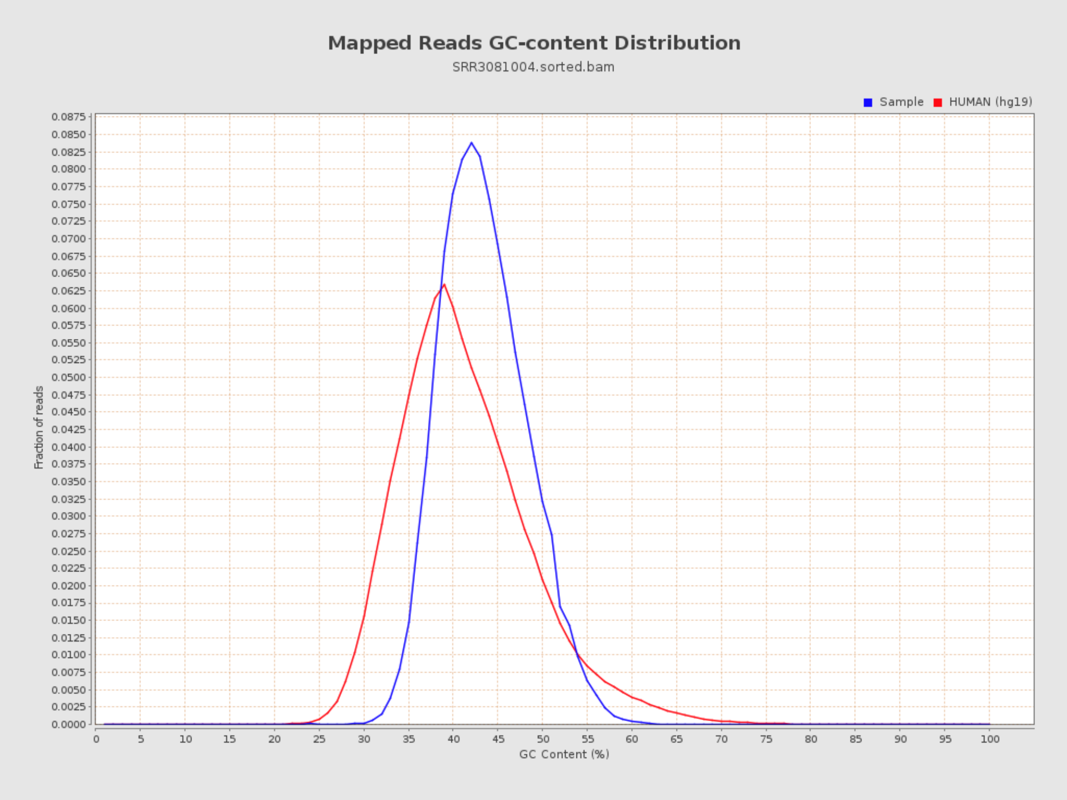
7. Results : Duplication Rate Histogram



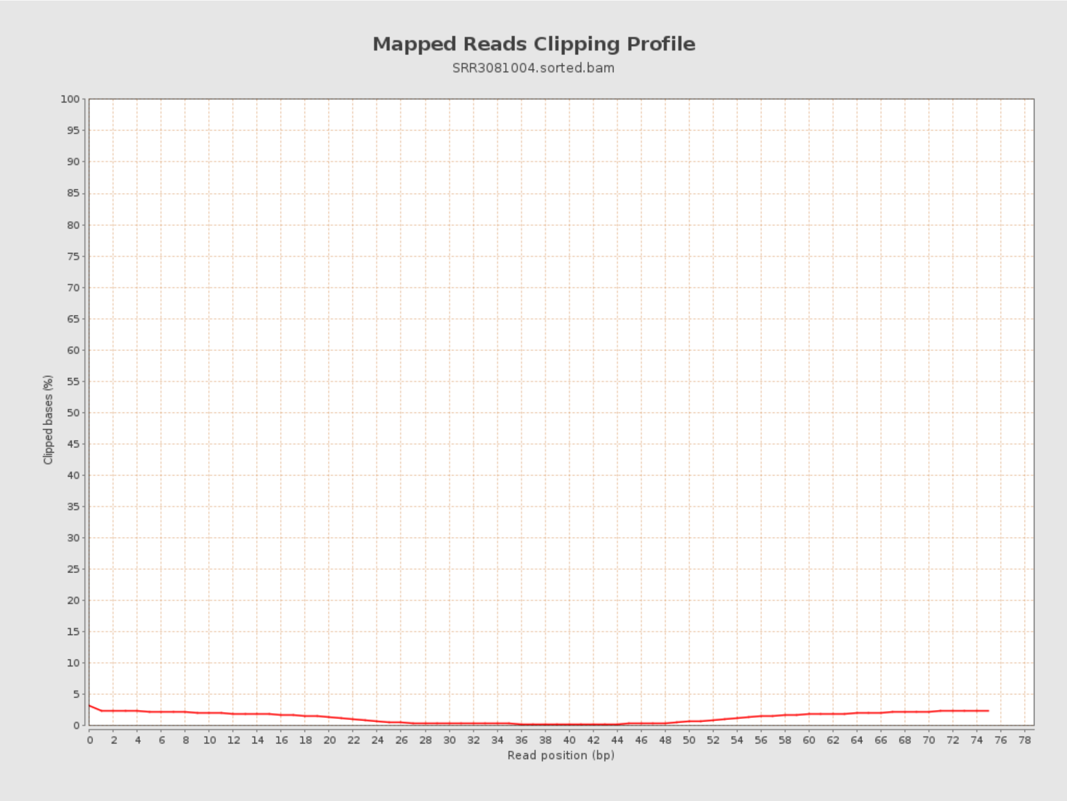
8. Results : Mapped Reads Nucleotide Content



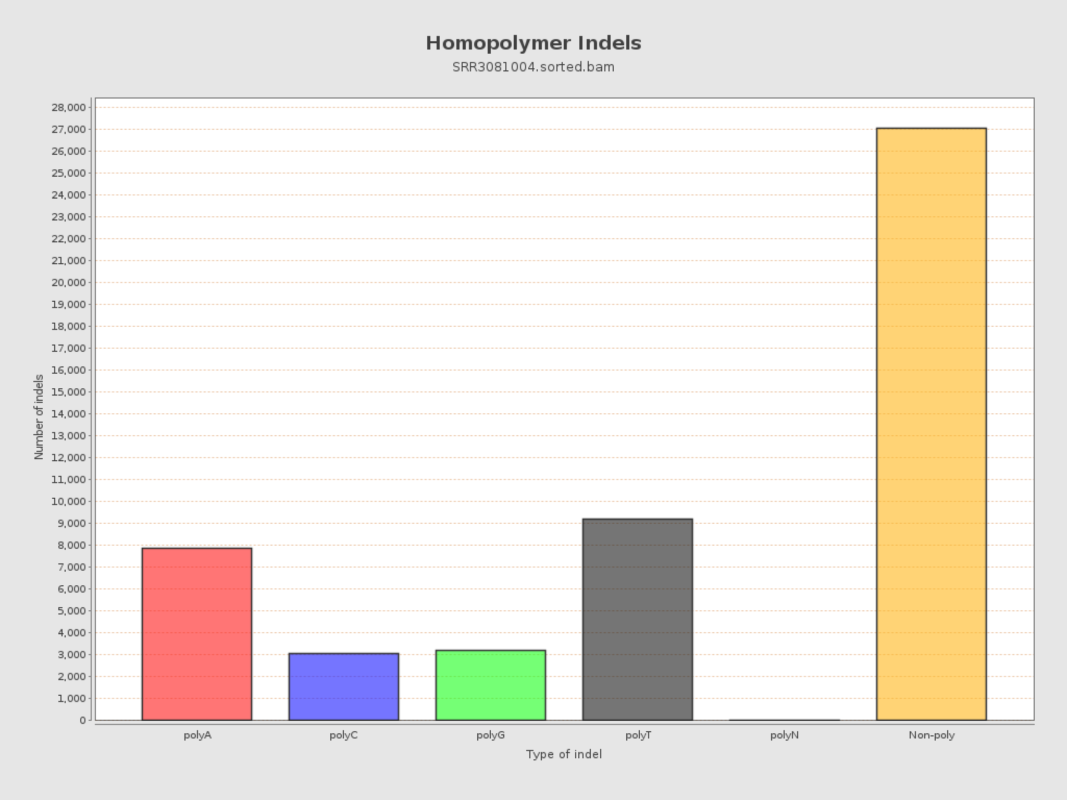
9. Results : Mapped Reads GC-content Distribution



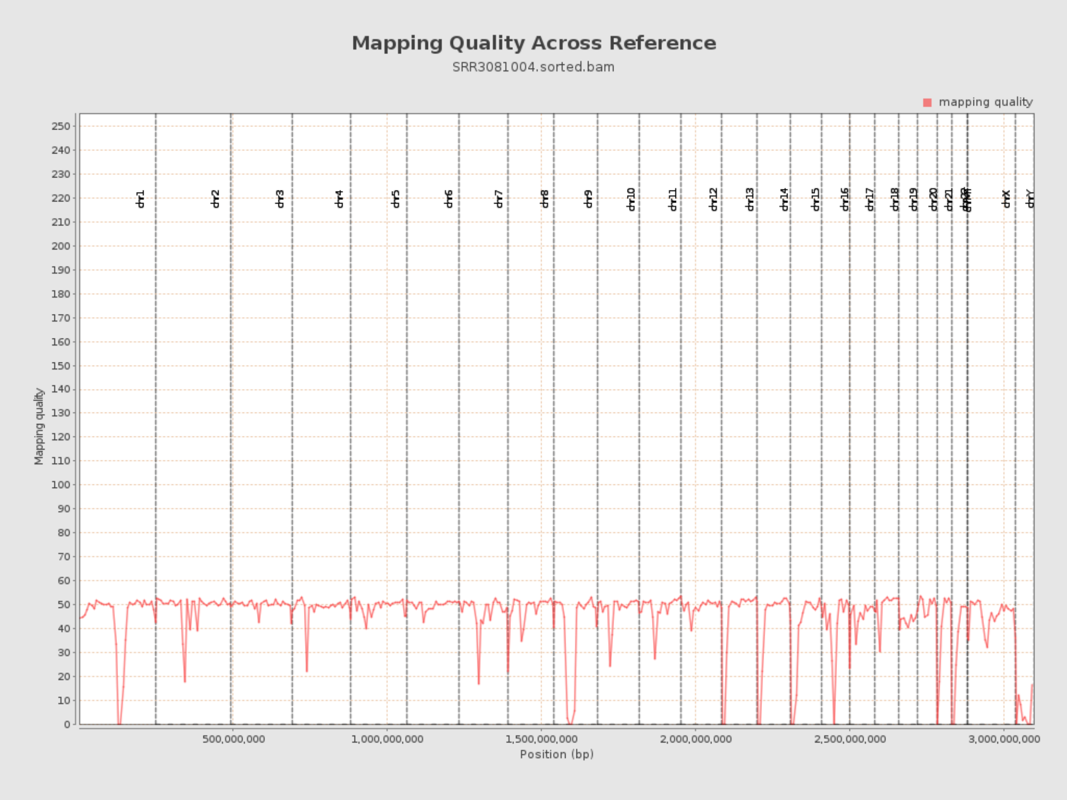
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram