Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081204.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_SRR3081204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:59:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,557,201
Mapped reads	4,616,944 / 83.08%
Unmapped reads	940,257 / 16.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,078 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	657,683 / 11.83%
Duplication rate	9.81%
Clipped reads	2,003,836 / 36.06%

2.2. ACGT Content

Number/percentage of A's	85,298,819 / 27.48%
Number/percentage of C's	60,797,768 / 19.59%
Number/percentage of T's	94,950,632 / 30.59%
Number/percentage of G's	69,151,641 / 22.28%
Number/percentage of N's	182,353 / 0.06%
GC Percentage	41.87%

2.3. Coverage

Mean	0.1003

Standard Deviation	1.0538

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

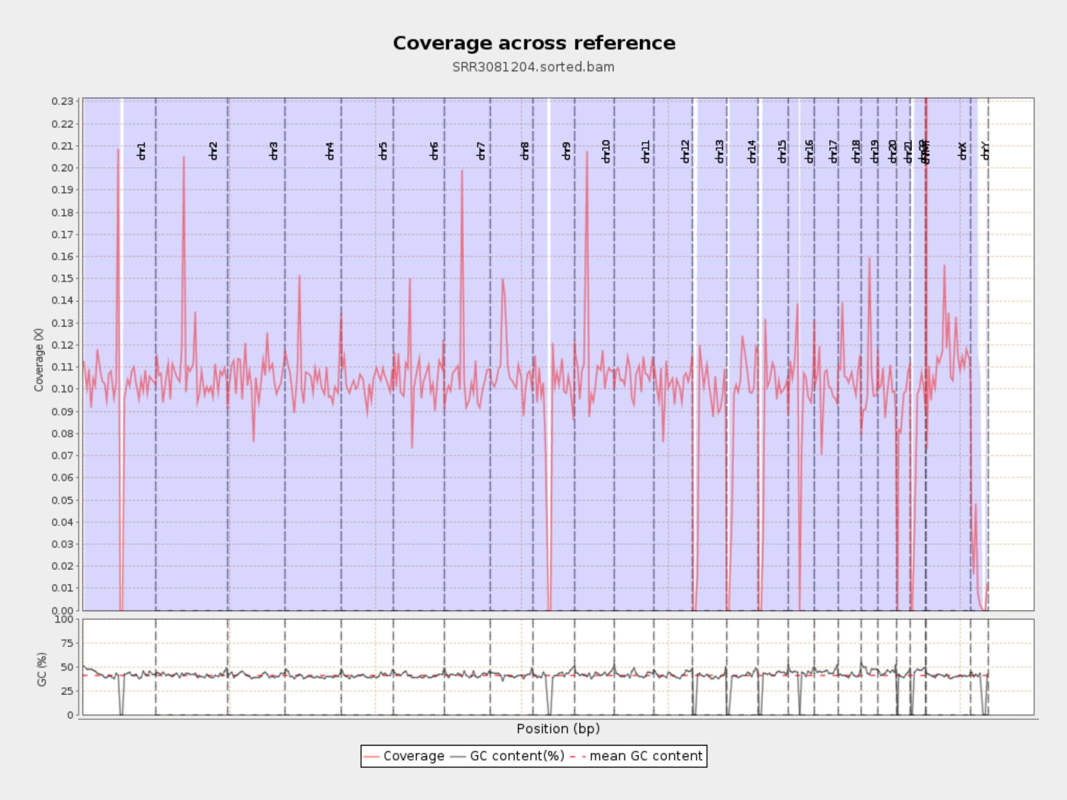
General error rate	1.04%
Mismatches	3,168,098
Insertions	23,633
Mapped reads with at least one insertion	0.51%
Deletions	62,074
Mapped reads with at least one deletion	1.33%
Homopolymer indels	45.58%

2.6. Chromosome stats

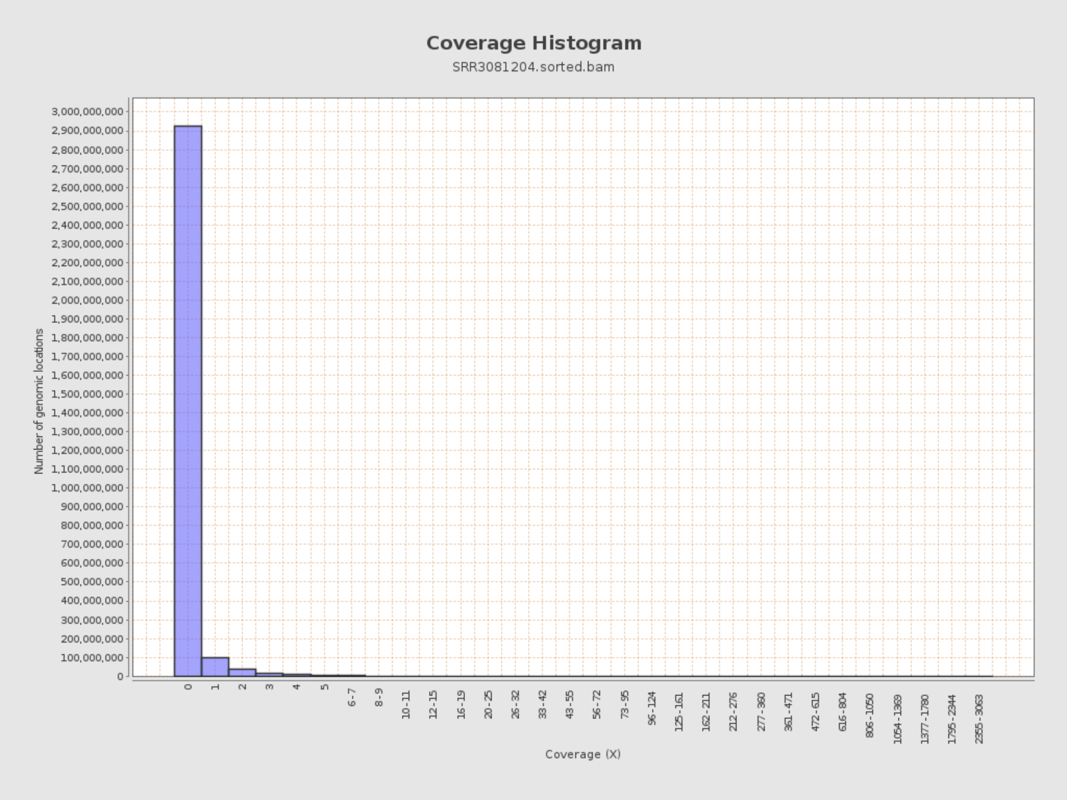
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25019660	0.1004	2.1648
chr2	243199373	26499434	0.109	0.9041
chr3	198022430	20855454	0.1053	0.5256
chr4	191154276	20139623	0.1054	0.577
chr5	180915260	18716489	0.1035	0.5248
chr6	171115067	18156321	0.1061	0.6887
chr7	159138663	16949783	0.1065	1.4086

chr8	146364022	15916061	0.1087	1.8515
chr9	141213431	12826468	0.0908	0.8462
chr10	135534747	15066422	0.1112	1.0573
chr11	135006516	14322177	0.1061	0.8457
chr12	133851895	13638465	0.1019	0.544
chr13	115169878	9750316	0.0847	0.4671
chr14	107349540	9472588	0.0882	0.6422
chr15	102531392	8755781	0.0854	0.4677
chr16	90354753	8645628	0.0957	0.5803
chr17	81195210	8165017	0.1006	0.622
chr18	78077248	8521492	0.1091	1.6723
chr19	59128983	6201011	0.1049	1.4537
chr20	63025520	6318743	0.1003	0.5398
chr21	48129895	4170756	0.0867	0.5436
chr22	51304566	3577858	0.0697	0.4335
chrMT	16571	327603	19.7697	11.7965
chrX	155270560	17592010	0.1133	0.6139
chrY	59373566	874479	0.0147	0.3666

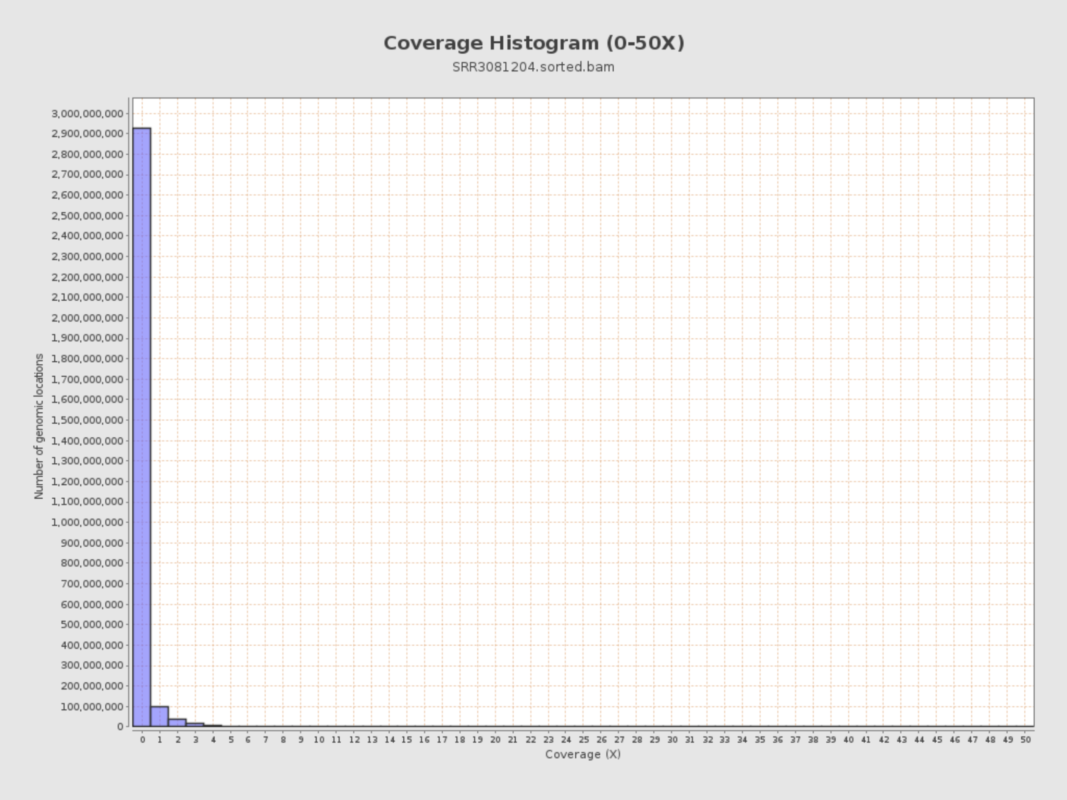
3. Results : Coverage across reference



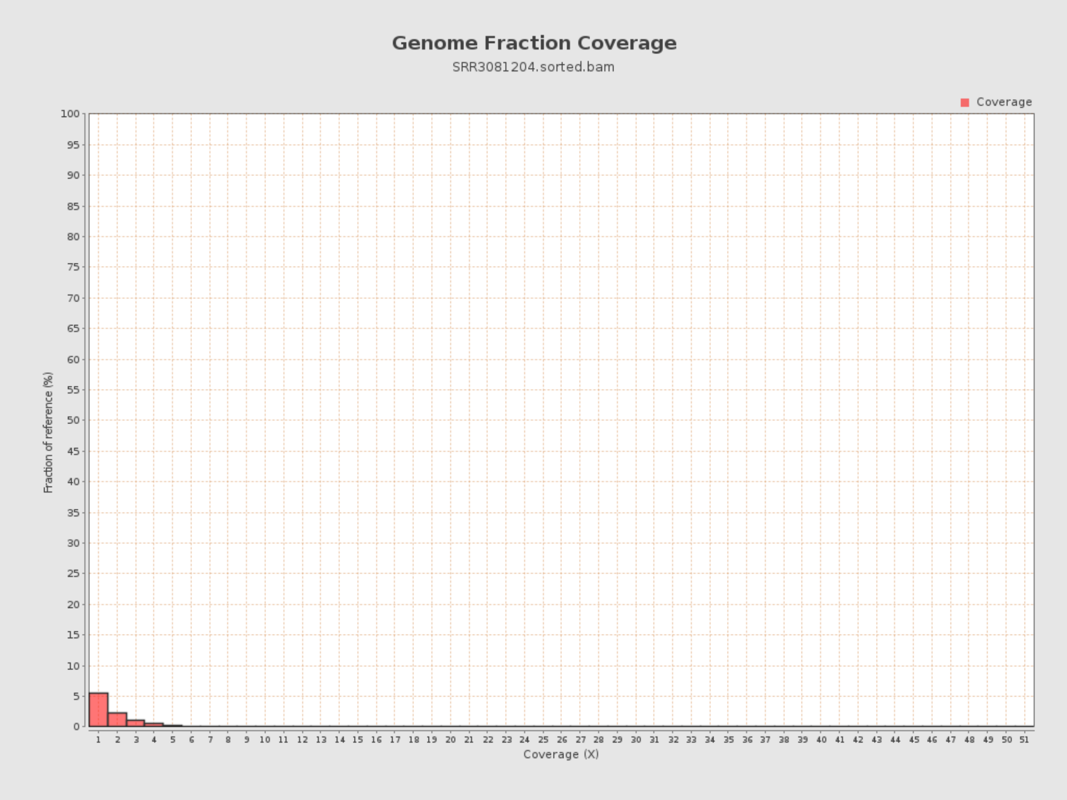
4. Results : Coverage Histogram



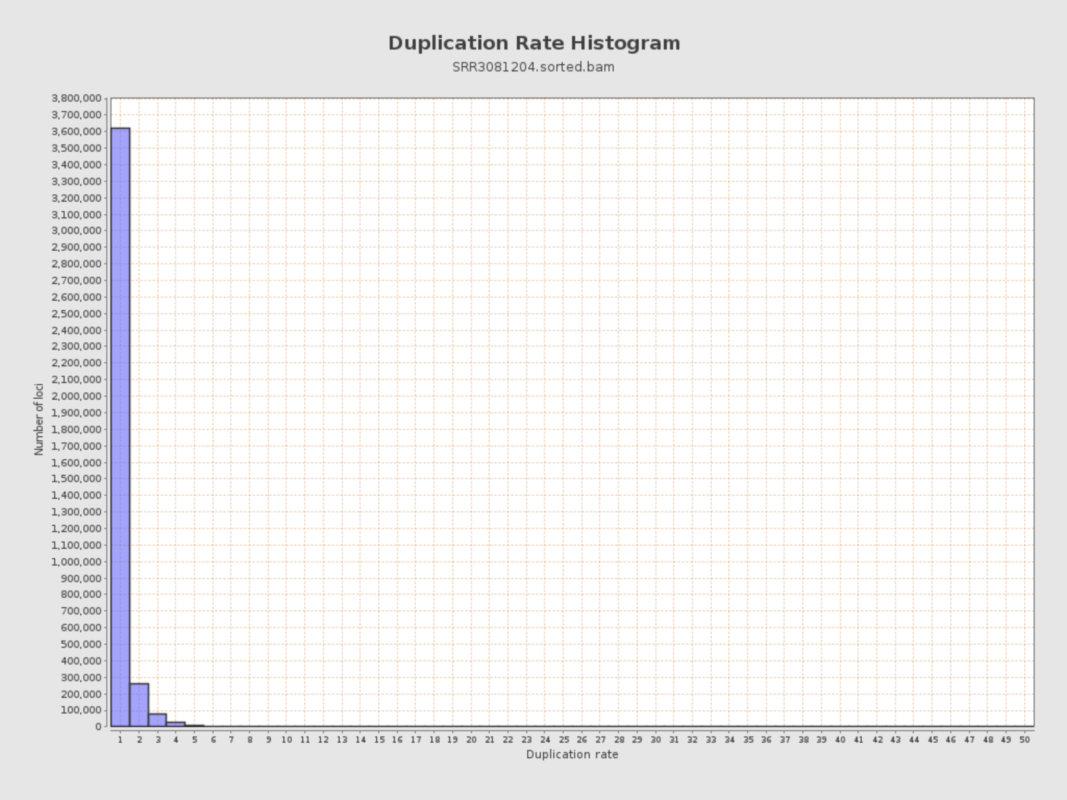
5. Results : Coverage Histogram (0-50X)



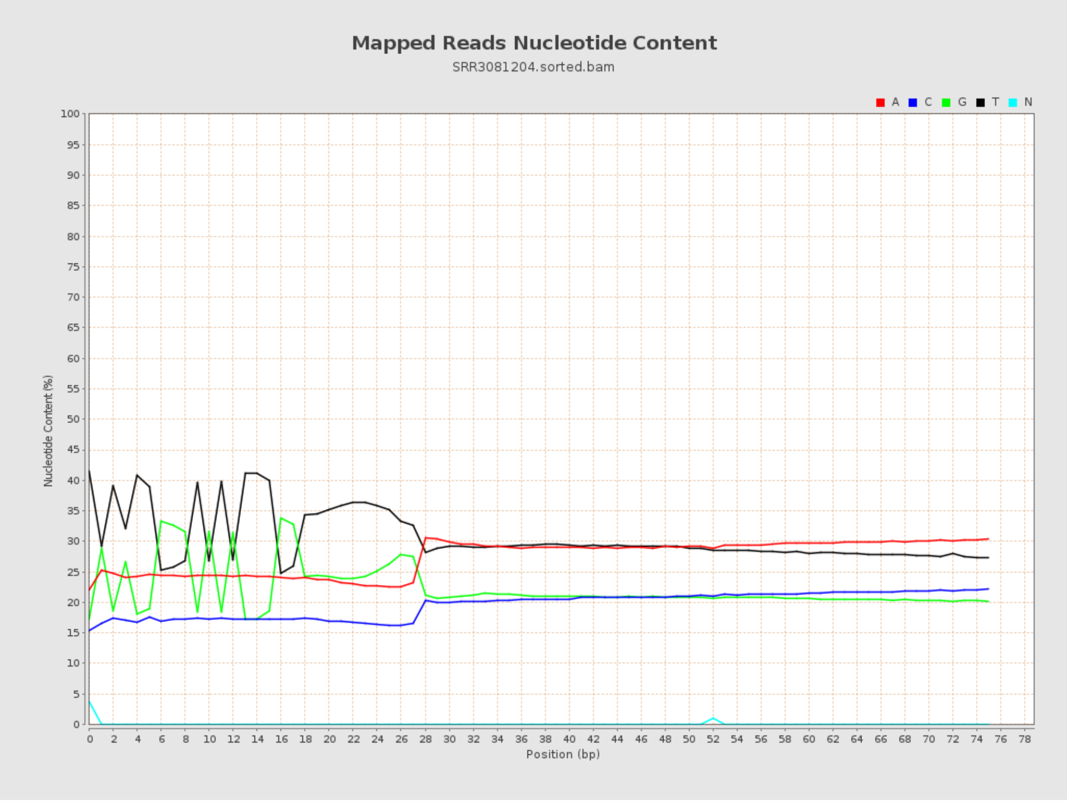
6. Results : Genome Fraction Coverage



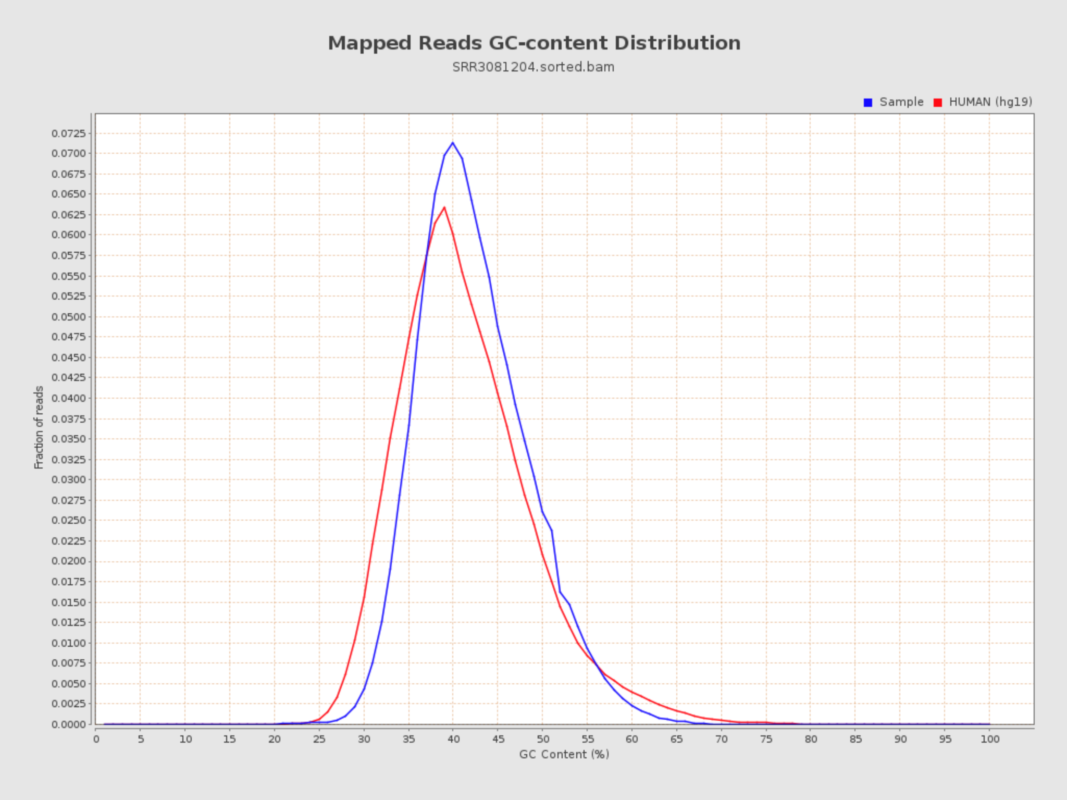
7. Results : Duplication Rate Histogram



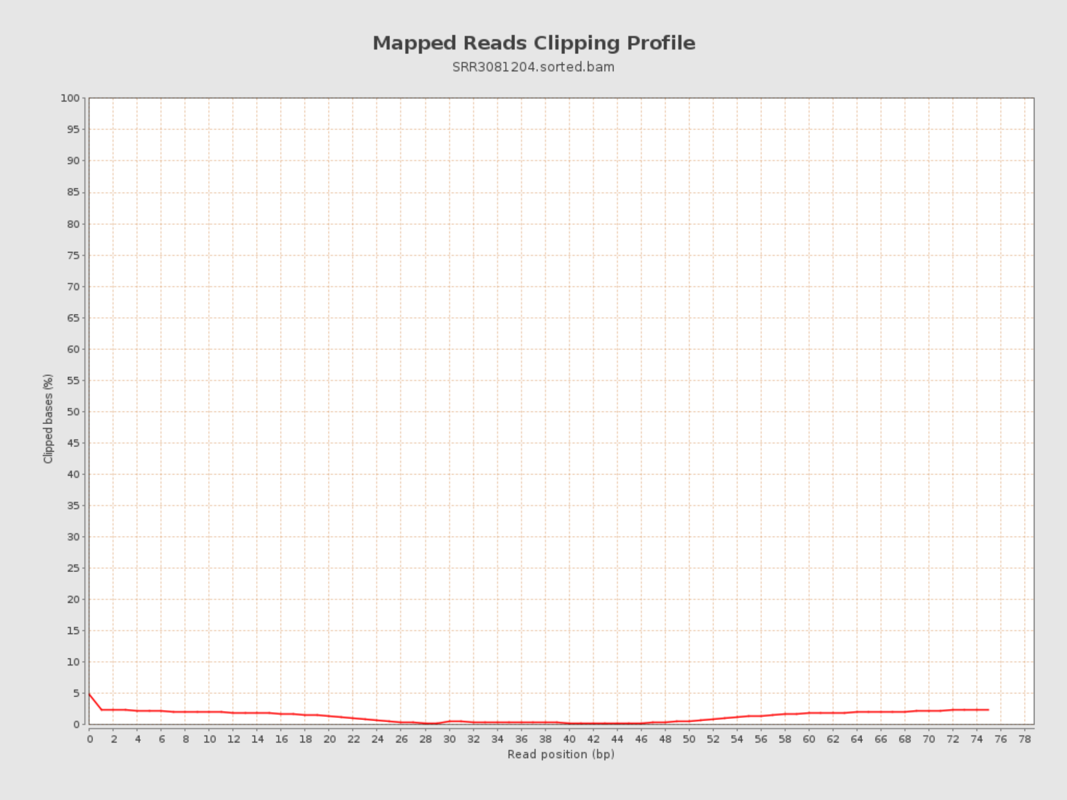
8. Results : Mapped Reads Nucleotide Content



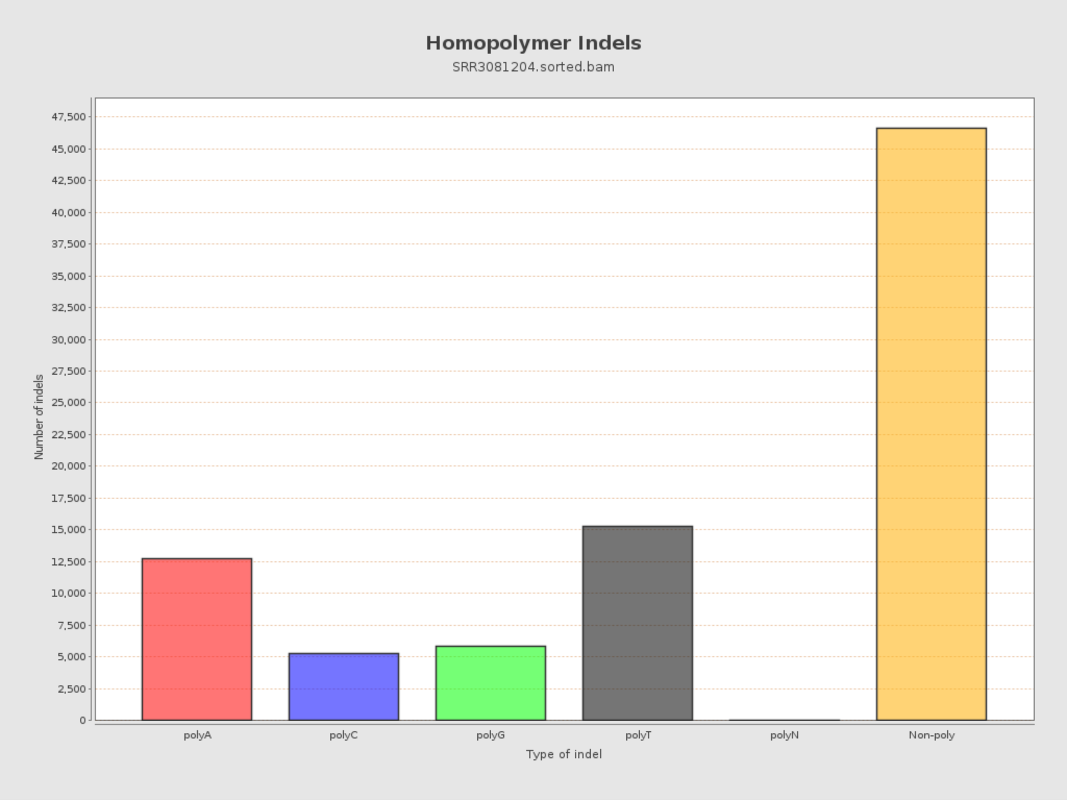
9. Results : Mapped Reads GC-content Distribution



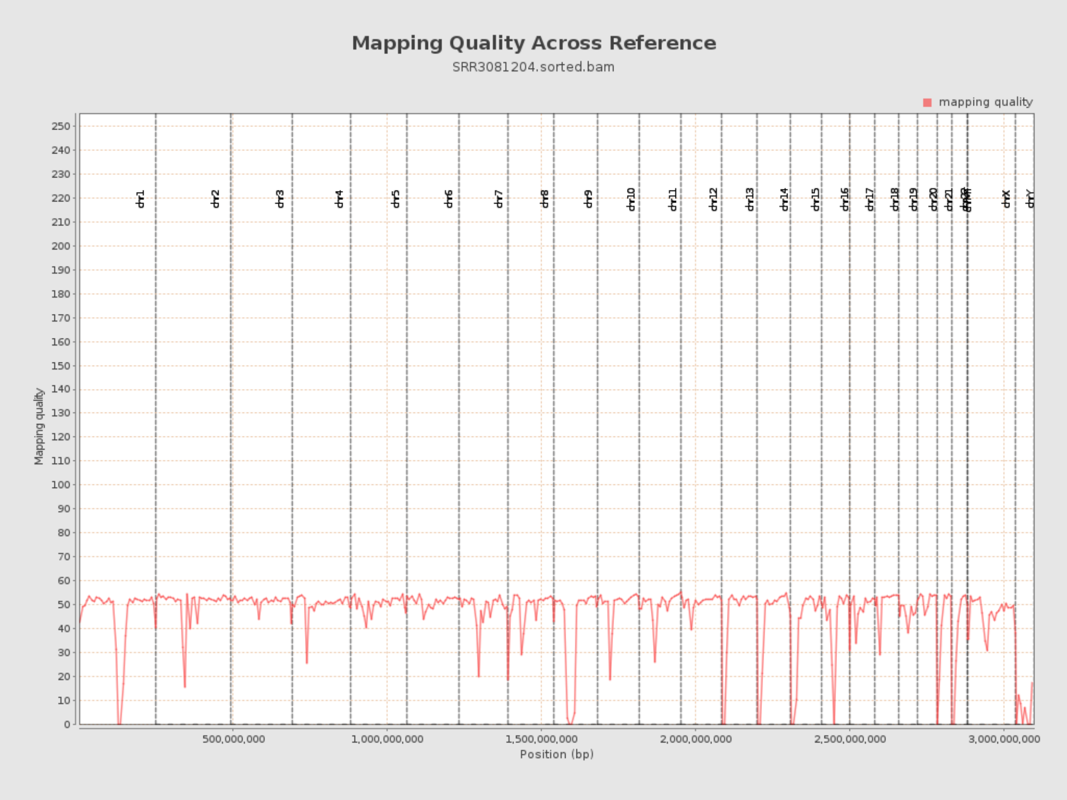
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram