Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:50:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081243.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_SRR3081243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:50:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,970,445
Mapped reads	1,740,111 / 88.31%
Unmapped reads	230,334 / 11.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,723 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	76,178 / 3.87%
Duplication rate	3.7%
Clipped reads	959,019 / 48.67%

2.2. ACGT Content

Number/percentage of A's	32,552,558 / 28.85%
Number/percentage of C's	21,554,414 / 19.1%
Number/percentage of T's	34,813,406 / 30.85%
Number/percentage of G's	23,913,131 / 21.19%
Number/percentage of N's	13,992 / 0.01%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.285

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

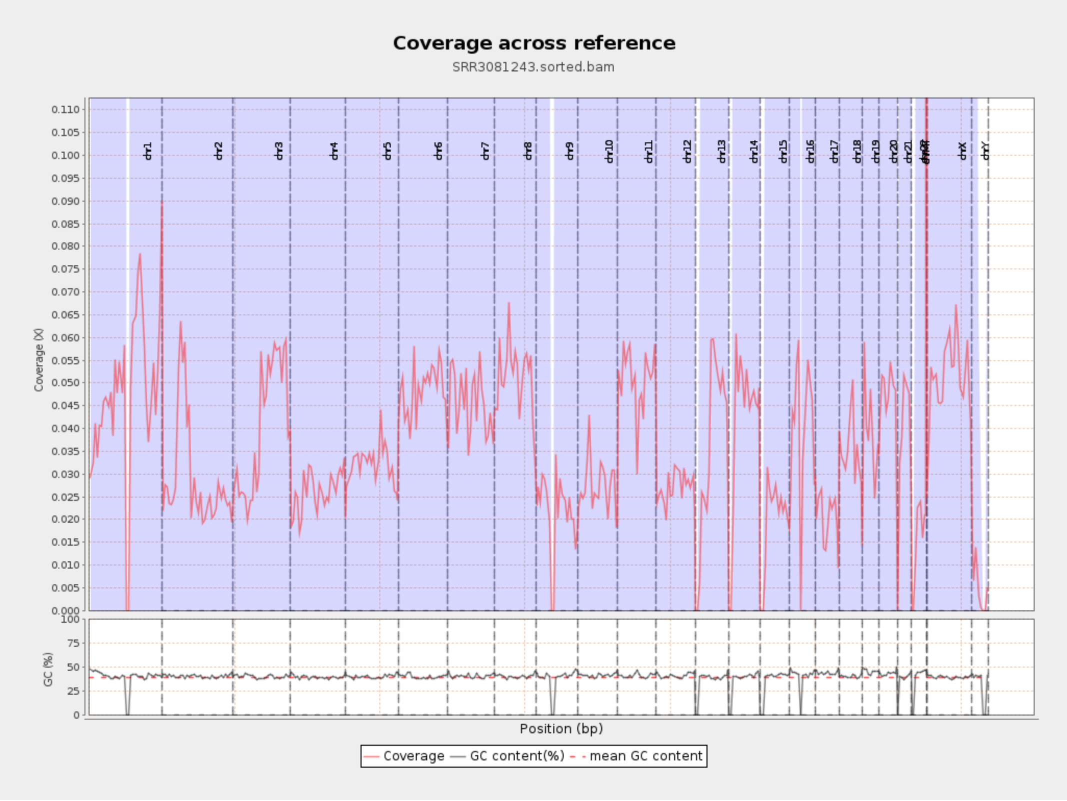
General error rate	0.91%
Mismatches	1,015,838
Insertions	8,580
Mapped reads with at least one insertion	0.49%
Deletions	26,428
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.21%

2.6. Chromosome stats

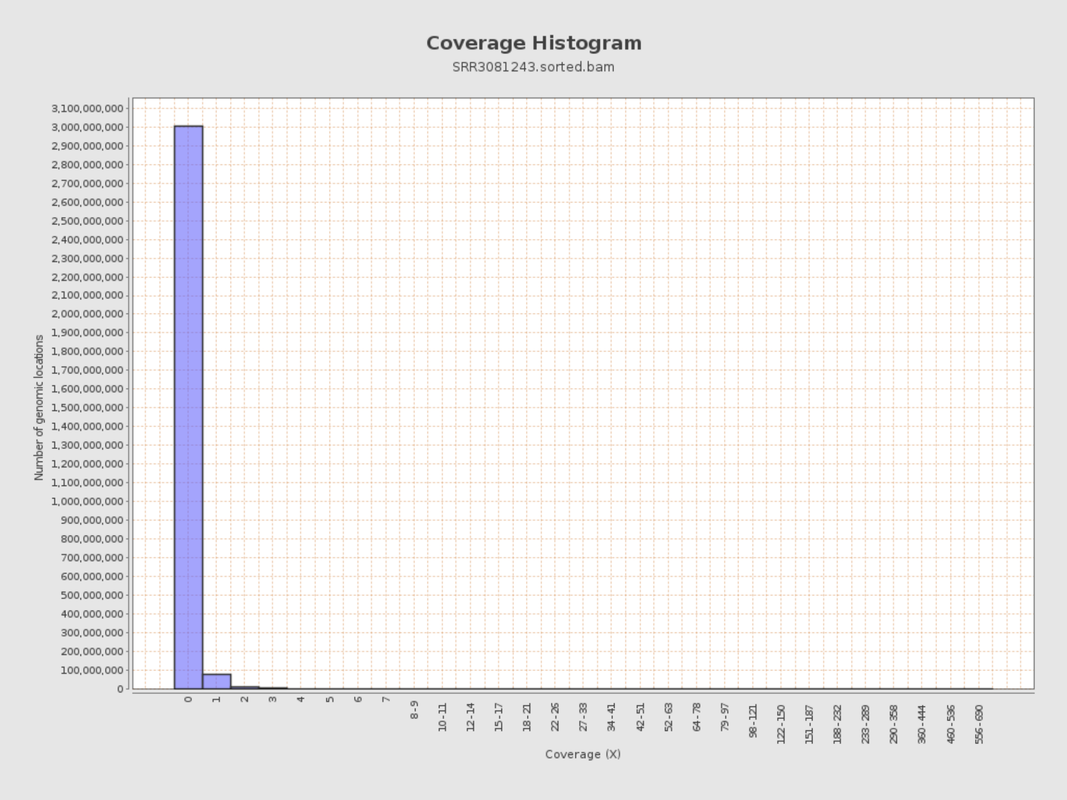
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11822390	0.0474	0.398
chr2	243199373	7139423	0.0294	0.2881
chr3	198022430	7956186	0.0402	0.2377
chr4	191154276	4995859	0.0261	0.197
chr5	180915260	5848132	0.0323	0.2113
chr6	171115067	8286440	0.0484	0.2721
chr7	159138663	7244587	0.0455	0.3319

chr8	146364022	7530237	0.0514	0.4945
chr9	141213431	3034913	0.0215	0.2122
chr10	135534747	3752977	0.0277	0.2633
chr11	135006516	6798681	0.0504	0.3646
chr12	133851895	3629320	0.0271	0.1932
chr13	115169878	4157306	0.0361	0.2258
chr14	107349540	4411164	0.0411	0.242
chr15	102531392	2047547	0.02	0.1741
chr16	90354753	3662304	0.0405	0.2424
chr17	81195210	1625704	0.02	0.1846
chr18	78077248	2785643	0.0357	0.35
chr19	59128983	2311820	0.0391	0.3307
chr20	63025520	2992101	0.0475	0.2583
chr21	48129895	1823541	0.0379	0.2358
chr22	51304566	765761	0.0149	0.1406
chrMT	16571	13504	0.8149	1.0778
chrX	155270560	7959245	0.0513	0.2796
chrY	59373566	296041	0.005	0.0974

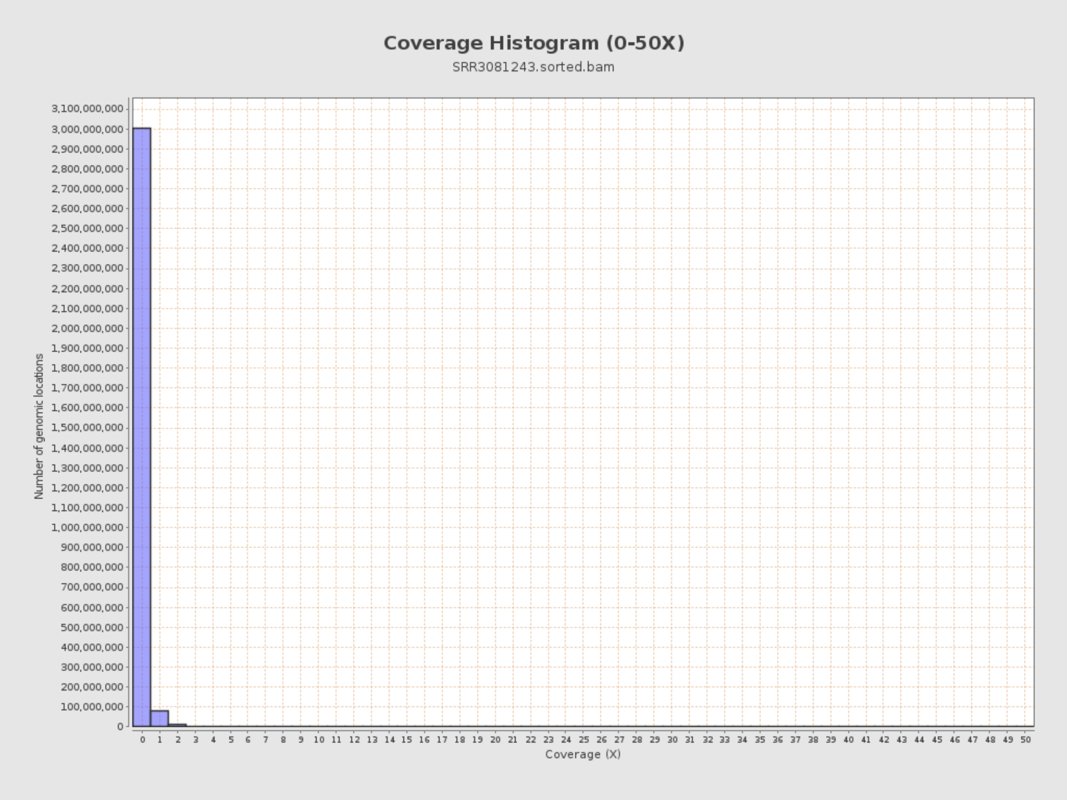
3. Results : Coverage across reference



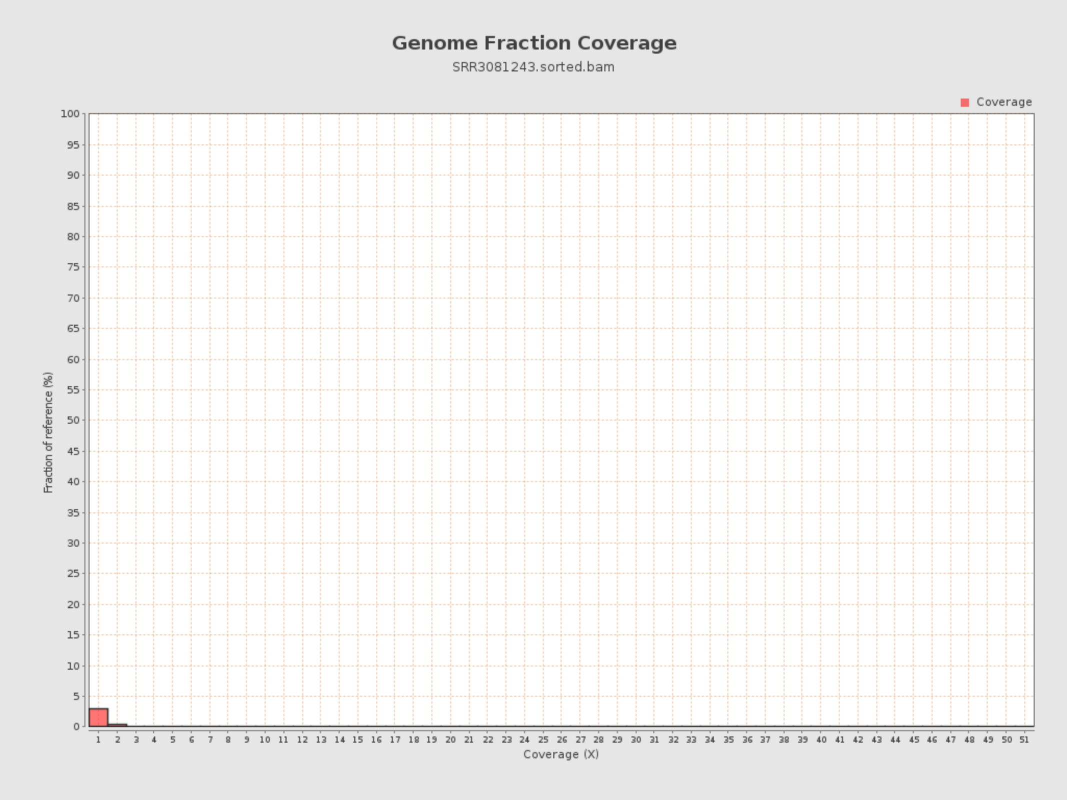
4. Results : Coverage Histogram



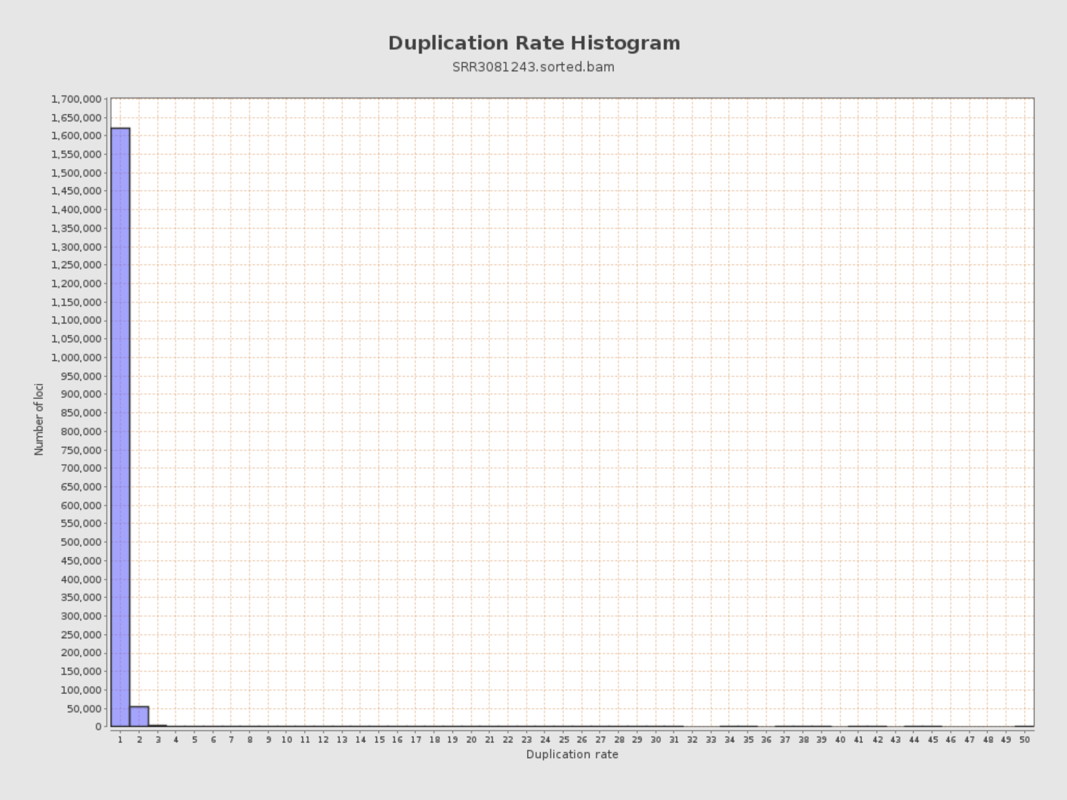
5. Results : Coverage Histogram (0-50X)



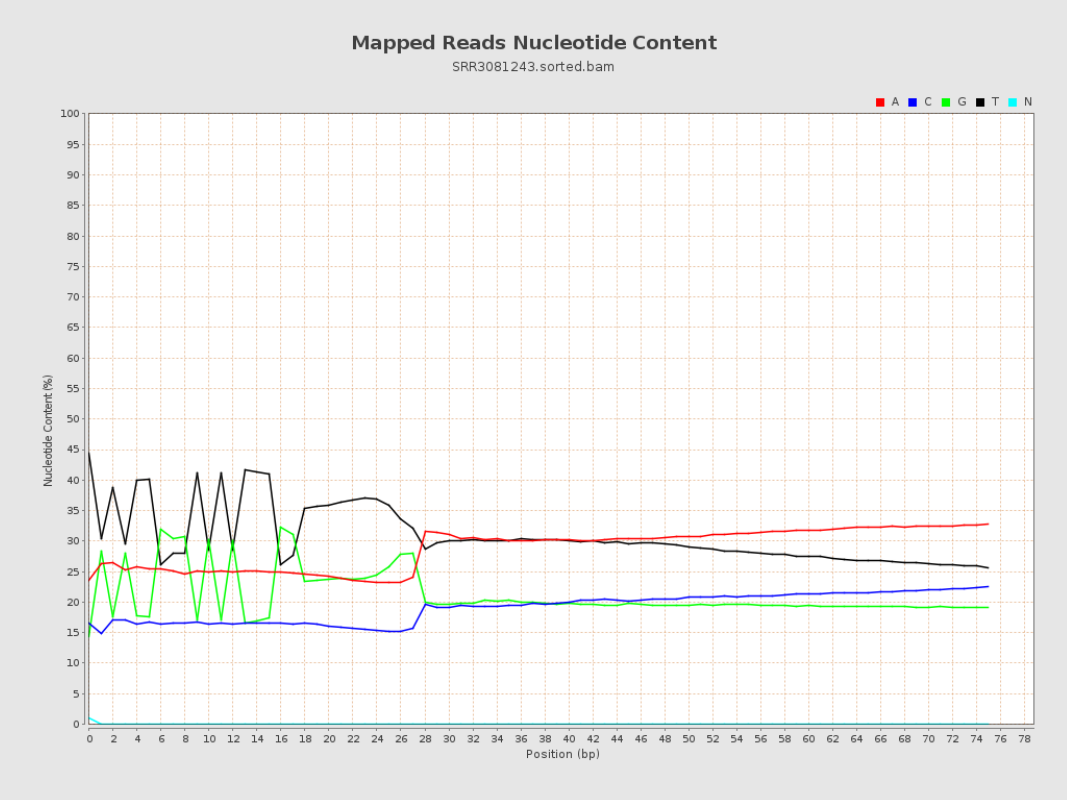
6. Results : Genome Fraction Coverage



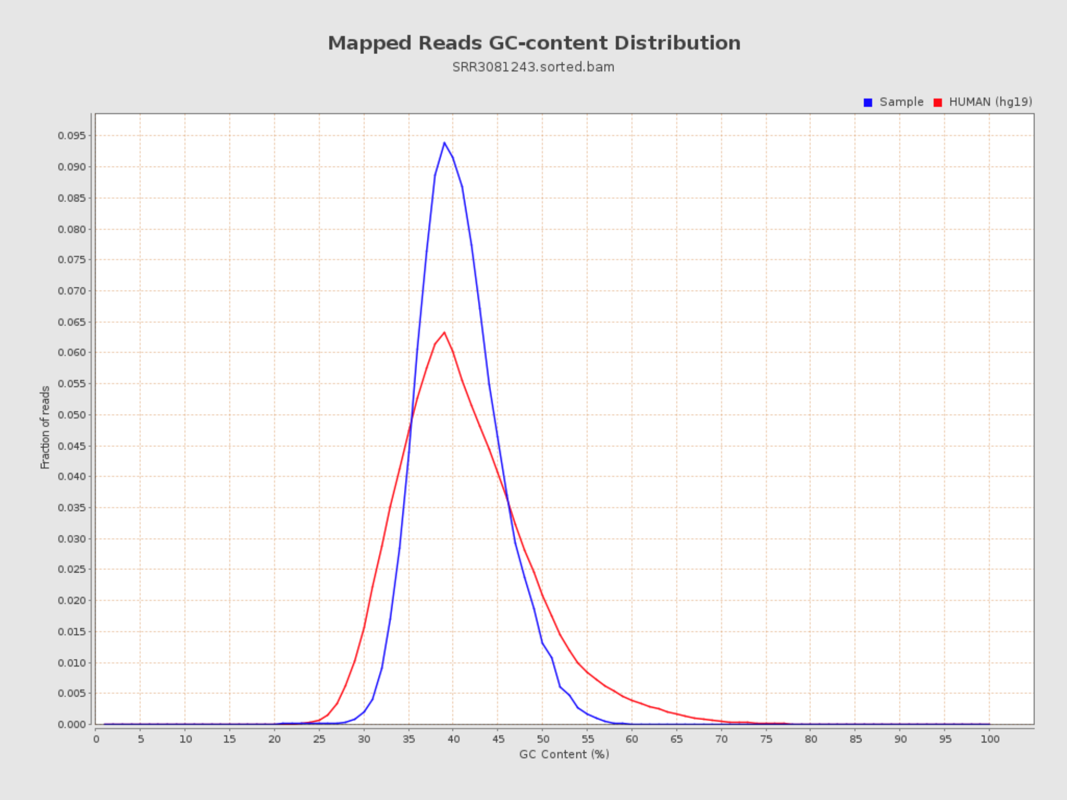
7. Results : Duplication Rate Histogram



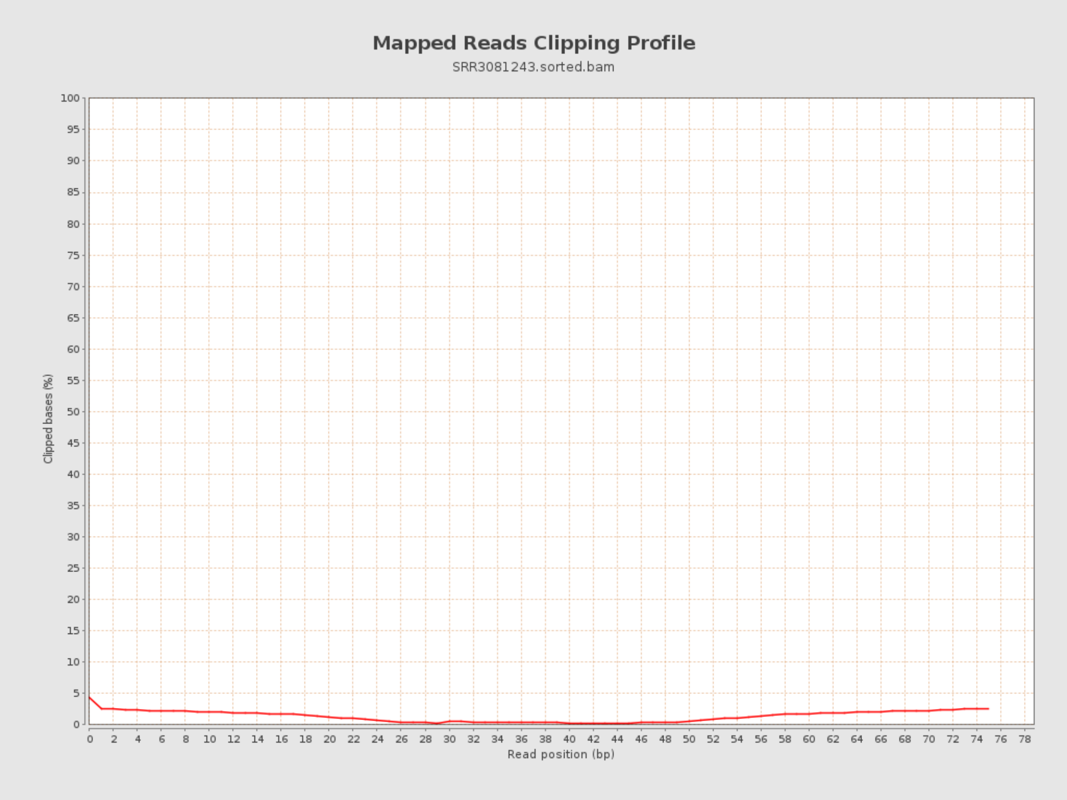
8. Results : Mapped Reads Nucleotide Content



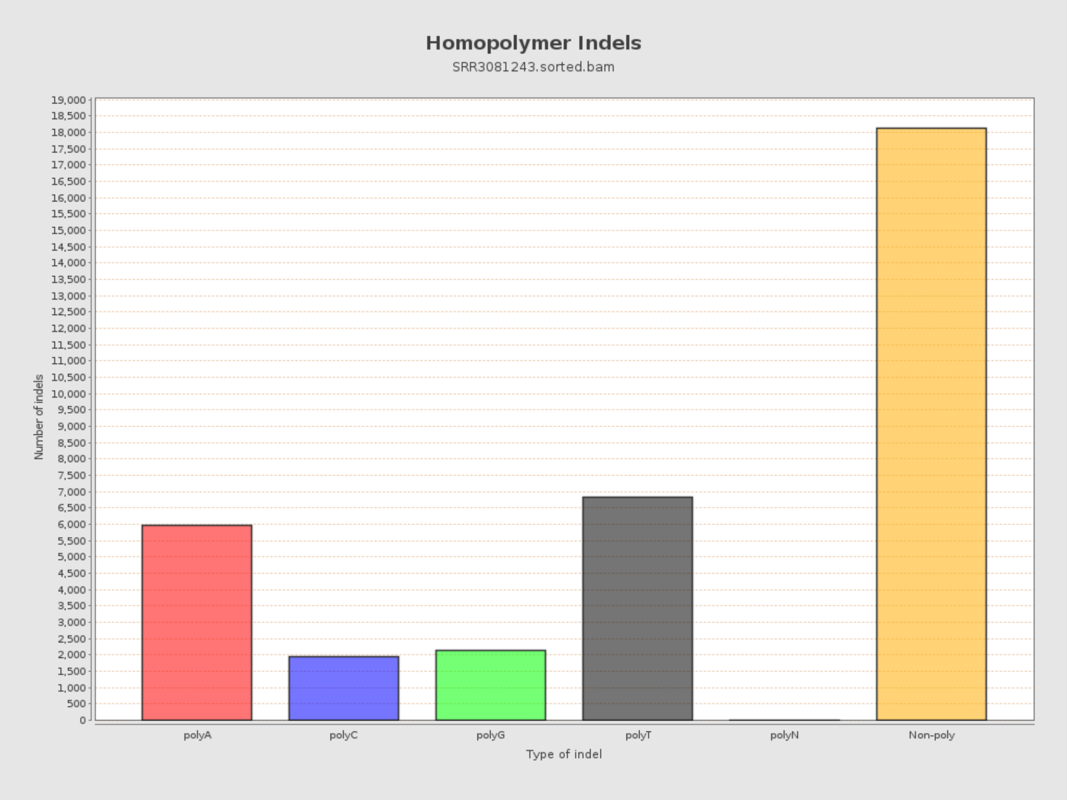
9. Results : Mapped Reads GC-content Distribution



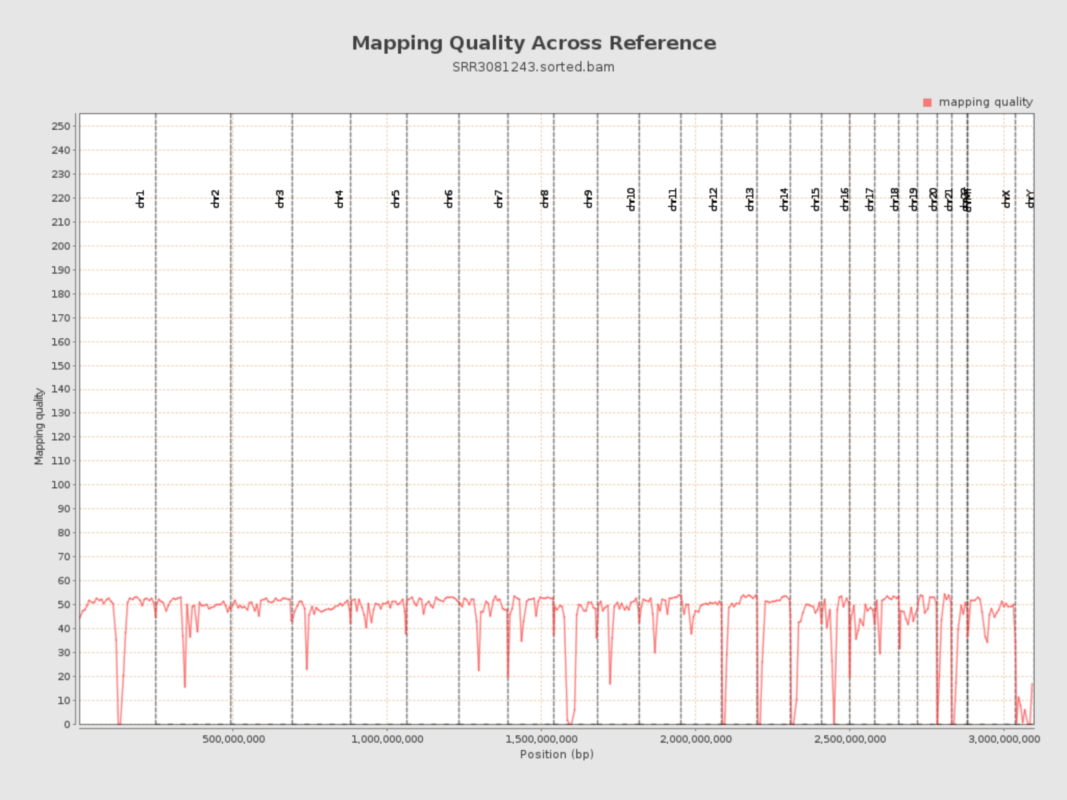
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram