Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:37:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081240.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_SRR3081240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:37:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,003
Mapped reads	1,953,042 / 88.41%
Unmapped reads	255,961 / 11.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,117 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	80,555 / 3.65%
Duplication rate	3.45%
Clipped reads	1,224,715 / 55.44%

2.2. ACGT Content

Number/percentage of A's	36,623,291 / 29.73%
Number/percentage of C's	23,978,129 / 19.46%
Number/percentage of T's	37,176,581 / 30.18%
Number/percentage of G's	25,414,360 / 20.63%
Number/percentage of N's	8,284 / 0.01%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.2917

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

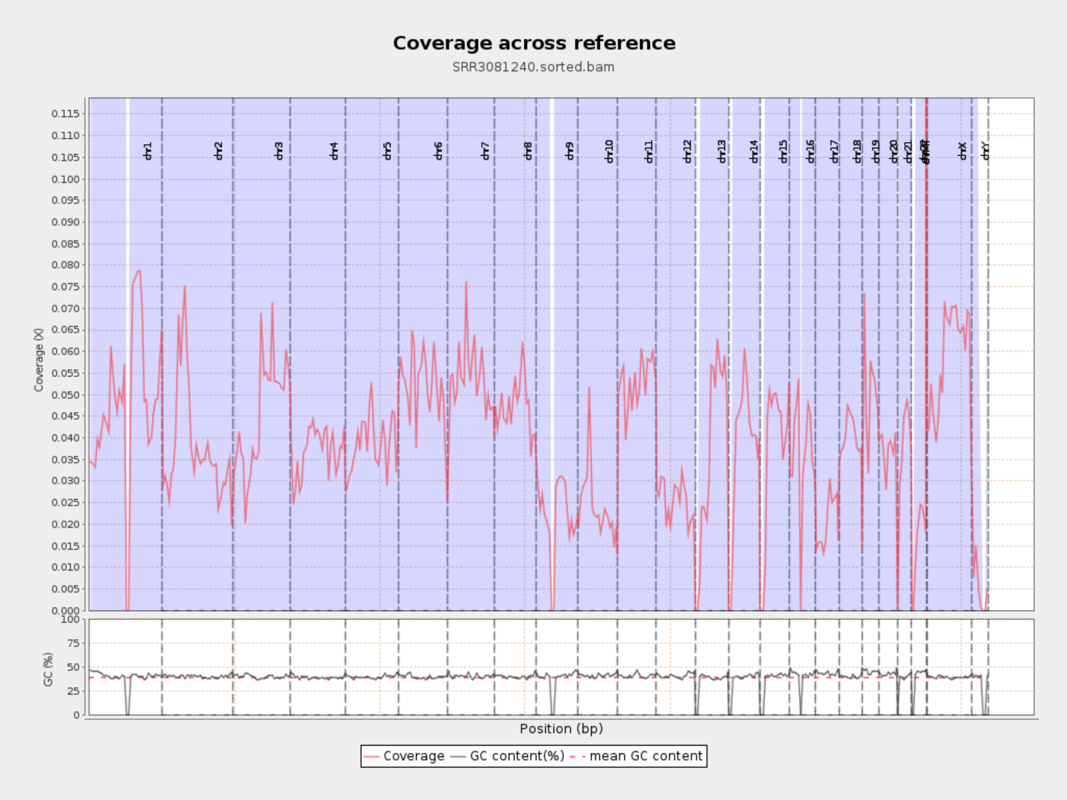
General error rate	0.91%
Mismatches	1,099,792
Insertions	9,362
Mapped reads with at least one insertion	0.48%
Deletions	27,622
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.3%

2.6. Chromosome stats

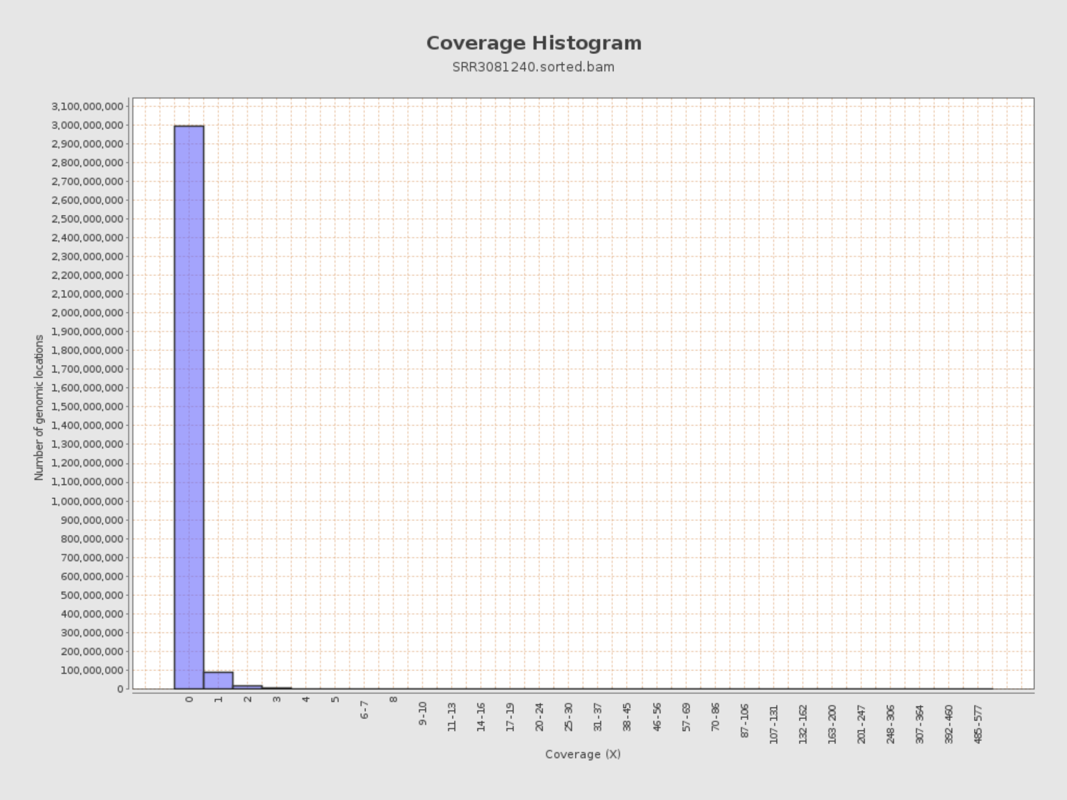
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11930970	0.0479	0.3824
chr2	243199373	9327513	0.0384	0.3118
chr3	198022430	8983900	0.0454	0.2517
chr4	191154276	7066974	0.037	0.2308
chr5	180915260	7005281	0.0387	0.2304
chr6	171115067	8893997	0.052	0.3008
chr7	159138663	8620489	0.0542	0.4368

chr8	146364022	6949875	0.0475	0.416
chr9	141213431	3063053	0.0217	0.1965
chr10	135534747	3286509	0.0242	0.28
chr11	135006516	7038103	0.0521	0.3421
chr12	133851895	3377851	0.0252	0.1878
chr13	115169878	4330102	0.0376	0.2295
chr14	107349540	4046385	0.0377	0.2338
chr15	102531392	3734451	0.0364	0.2391
chr16	90354753	3315508	0.0367	0.2317
chr17	81195210	1674297	0.0206	0.1886
chr18	78077248	3163937	0.0405	0.3117
chr19	59128983	2923064	0.0494	0.324
chr20	63025520	2304899	0.0366	0.225
chr21	48129895	1750563	0.0364	0.2295
chr22	51304566	794926	0.0155	0.1425
chrMT	16571	131399	7.9295	6.2222
chrX	155270560	9172593	0.0591	0.3029
chrY	59373566	358458	0.006	0.1115

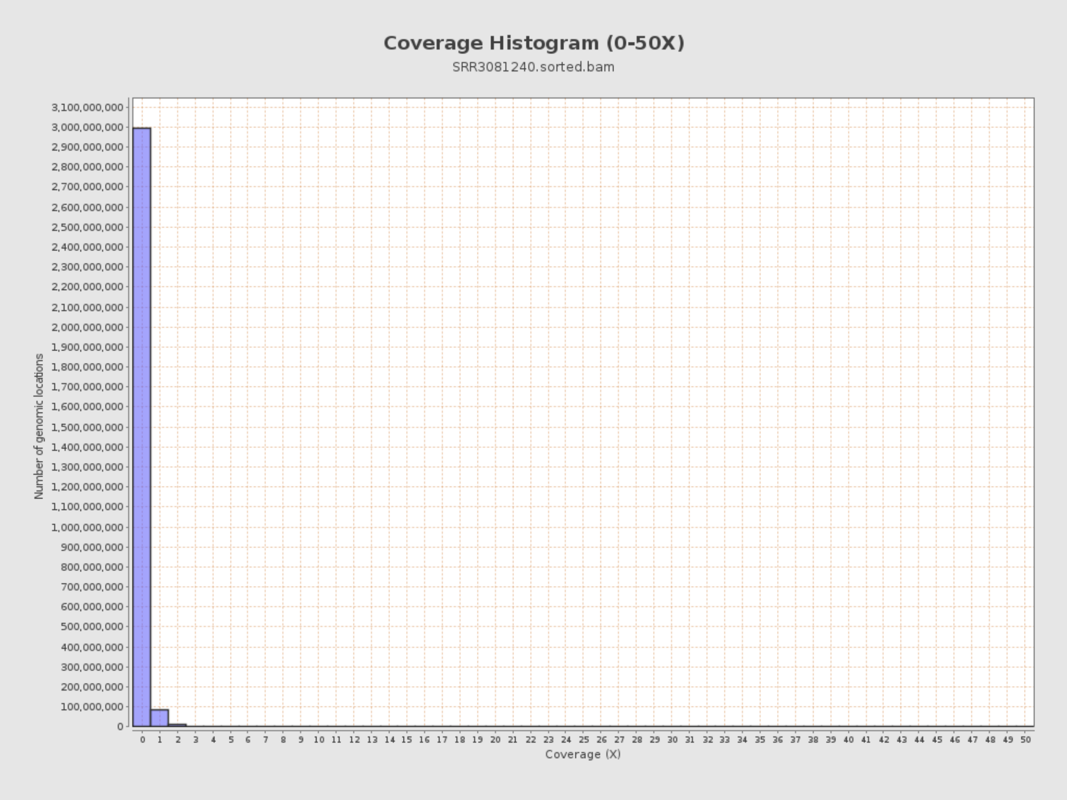
3. Results : Coverage across reference



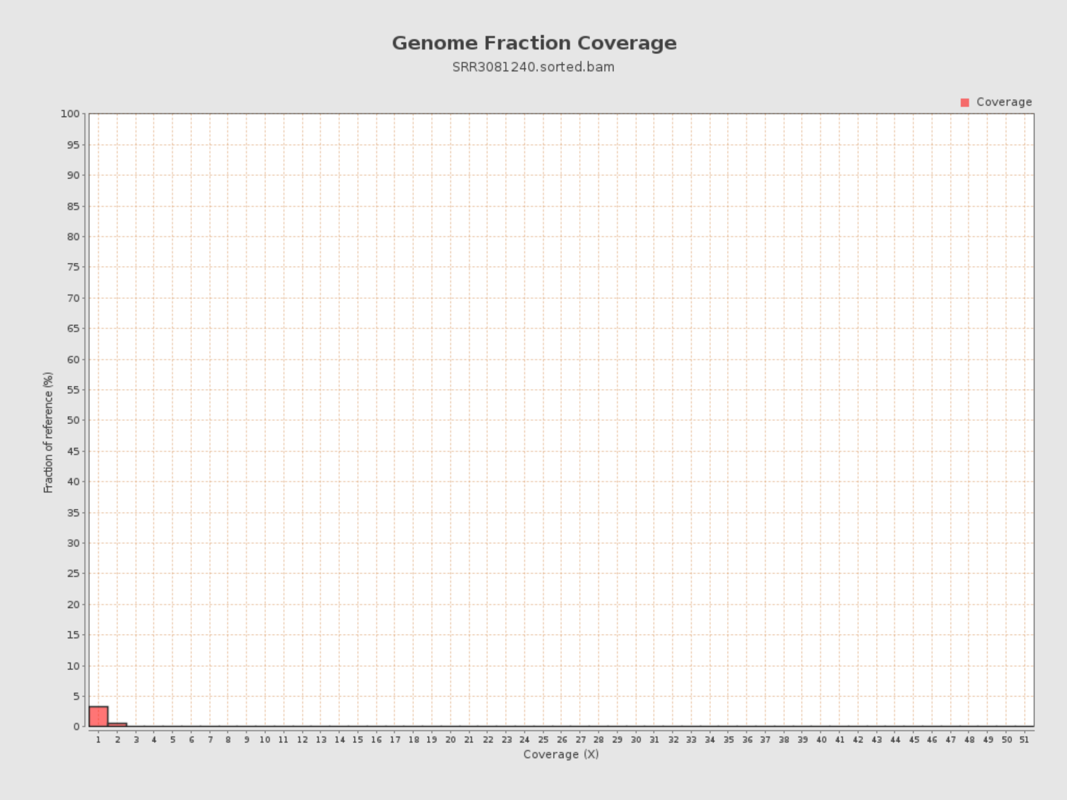
4. Results : Coverage Histogram



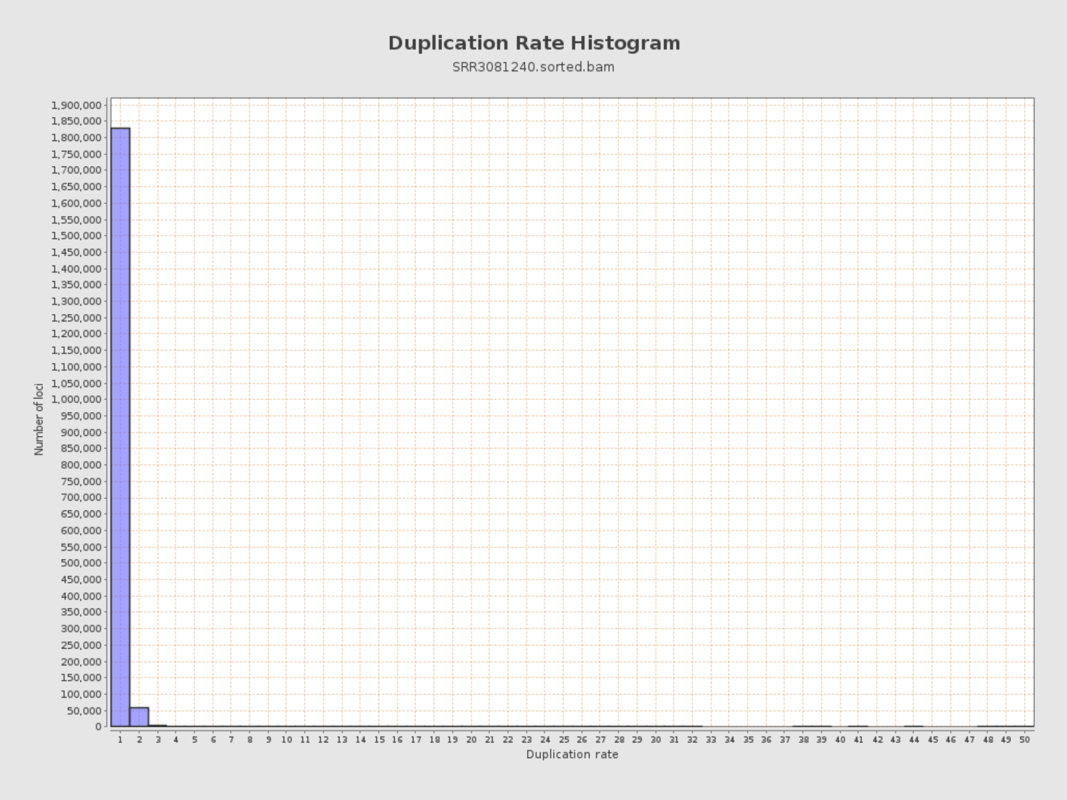
5. Results : Coverage Histogram (0-50X)



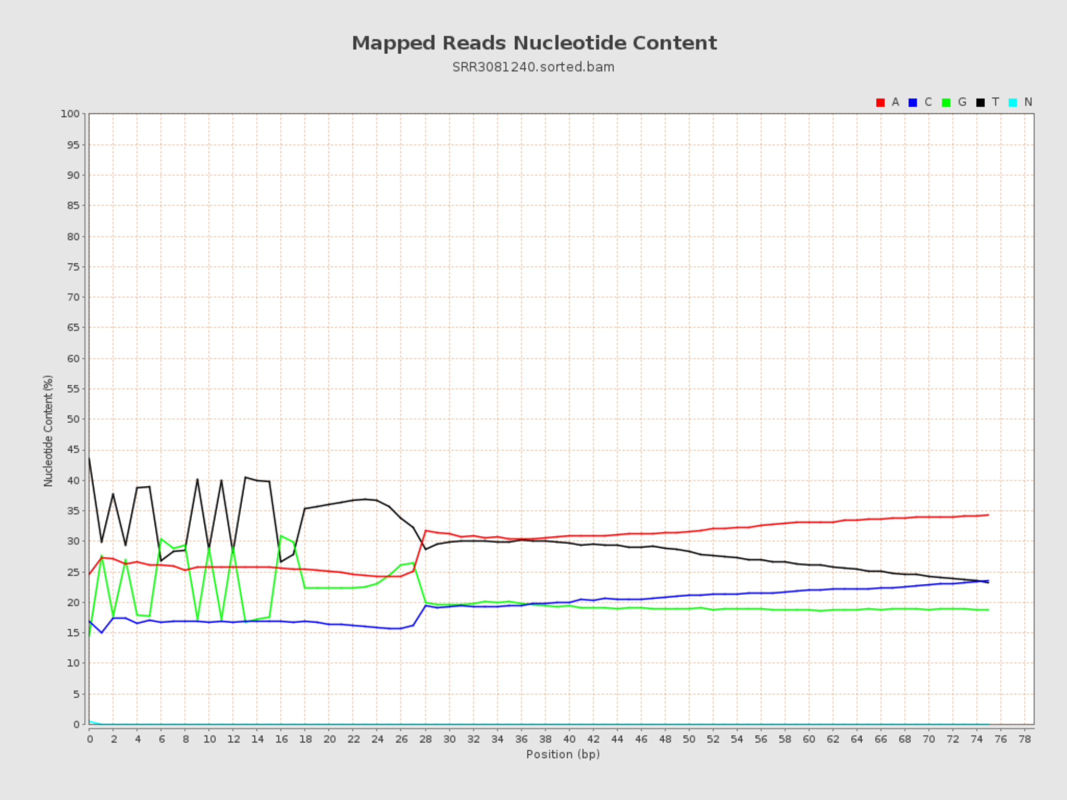
6. Results : Genome Fraction Coverage



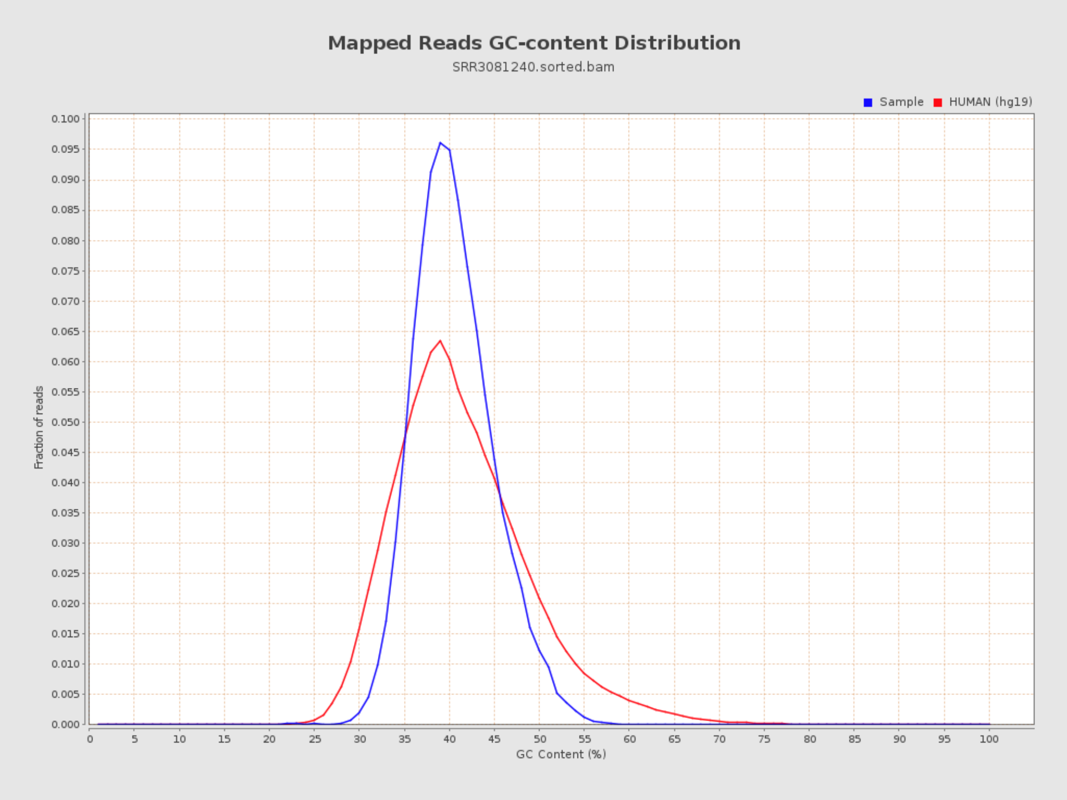
7. Results : Duplication Rate Histogram



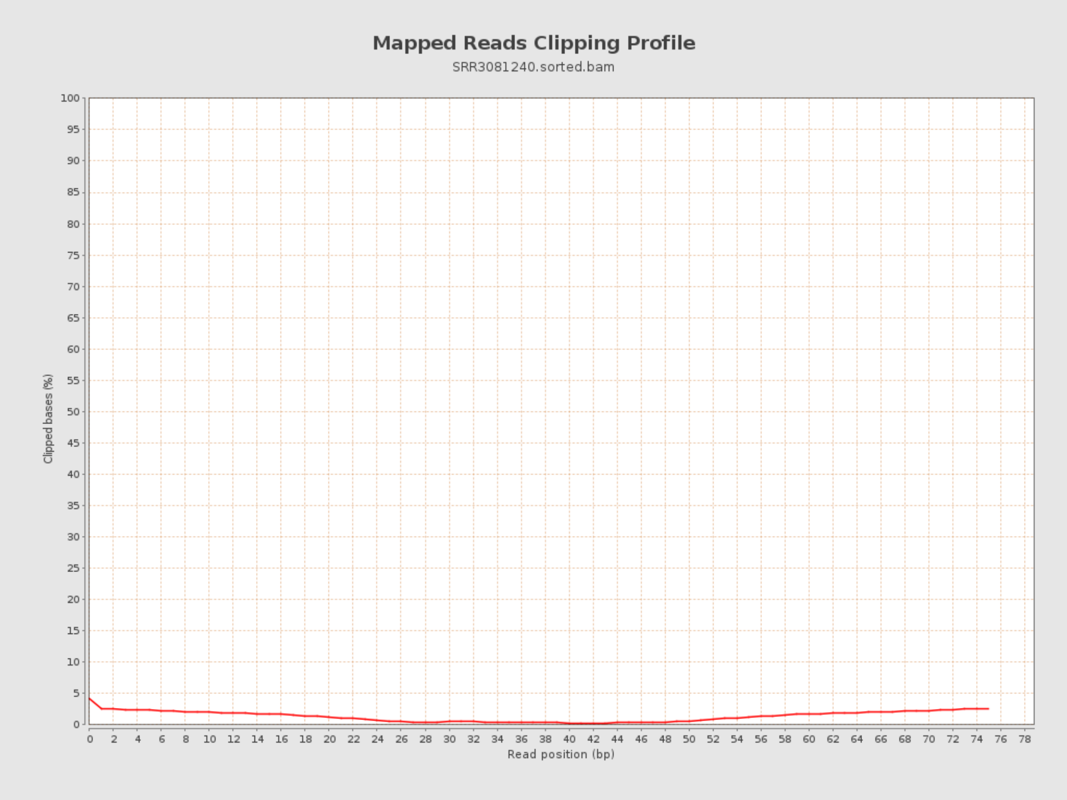
8. Results : Mapped Reads Nucleotide Content



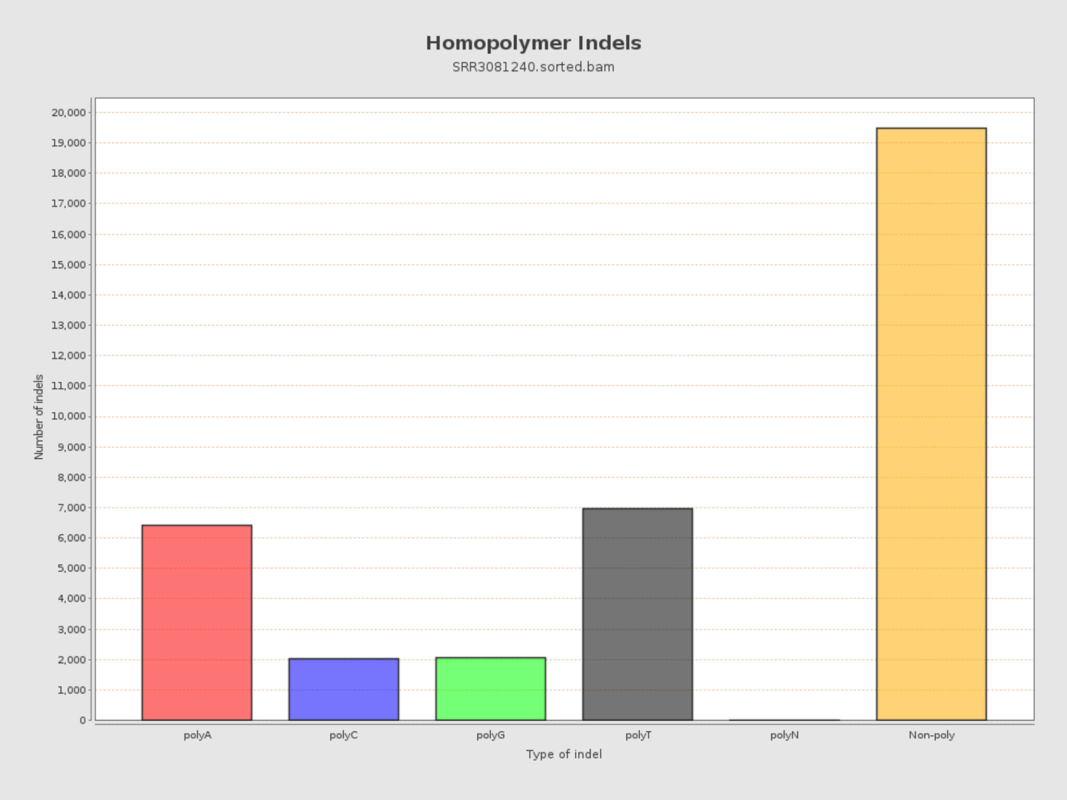
9. Results : Mapped Reads GC-content Distribution



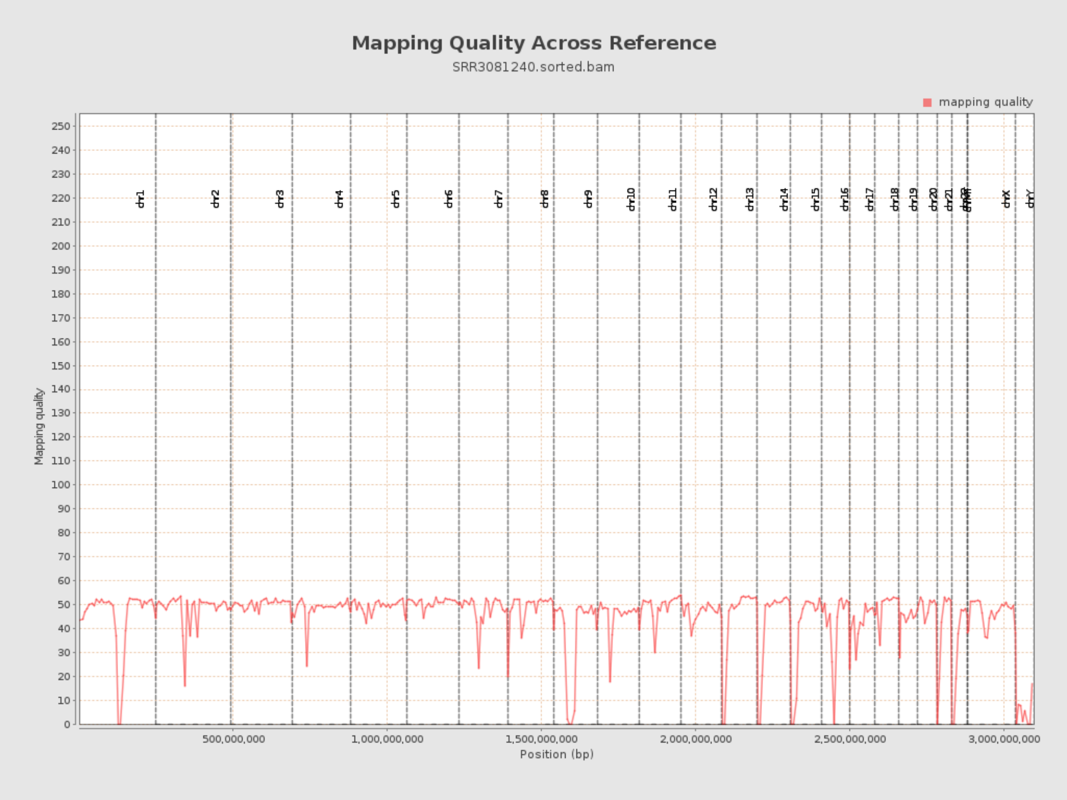
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram