Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:02:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081942.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_SRR3081942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081942.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:02:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,015,011
Mapped reads	2,789,444 / 92.52%
Unmapped reads	225,567 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,332 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	121,485 / 4.03%
Duplication rate	3.04%
Clipped reads	890,084 / 29.52%

2.2. ACGT Content

Number/percentage of A's	56,528,258 / 29.11%
Number/percentage of C's	36,193,150 / 18.64%
Number/percentage of T's	61,003,576 / 31.41%
Number/percentage of G's	40,436,529 / 20.82%
Number/percentage of N's	25,768 / 0.01%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0628

Standard Deviation	0.6248

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

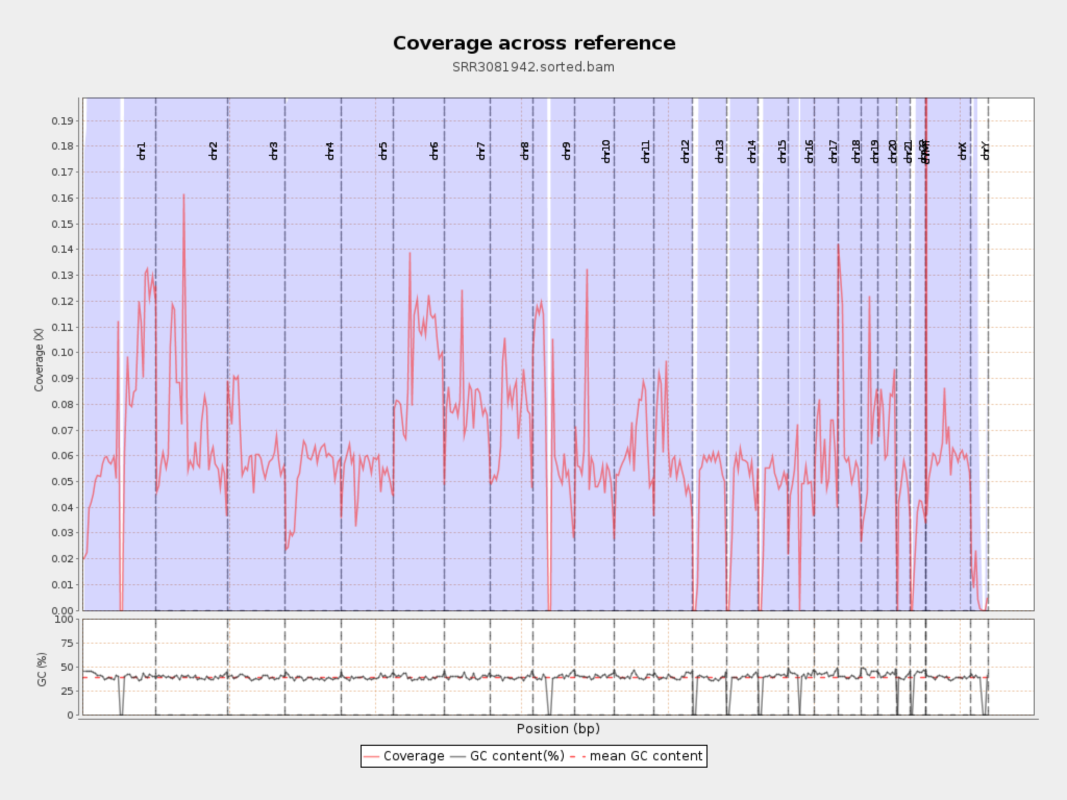
General error rate	0.8%
Mismatches	1,535,541
Insertions	14,344
Mapped reads with at least one insertion	0.51%
Deletions	47,994
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.28%

2.6. Chromosome stats

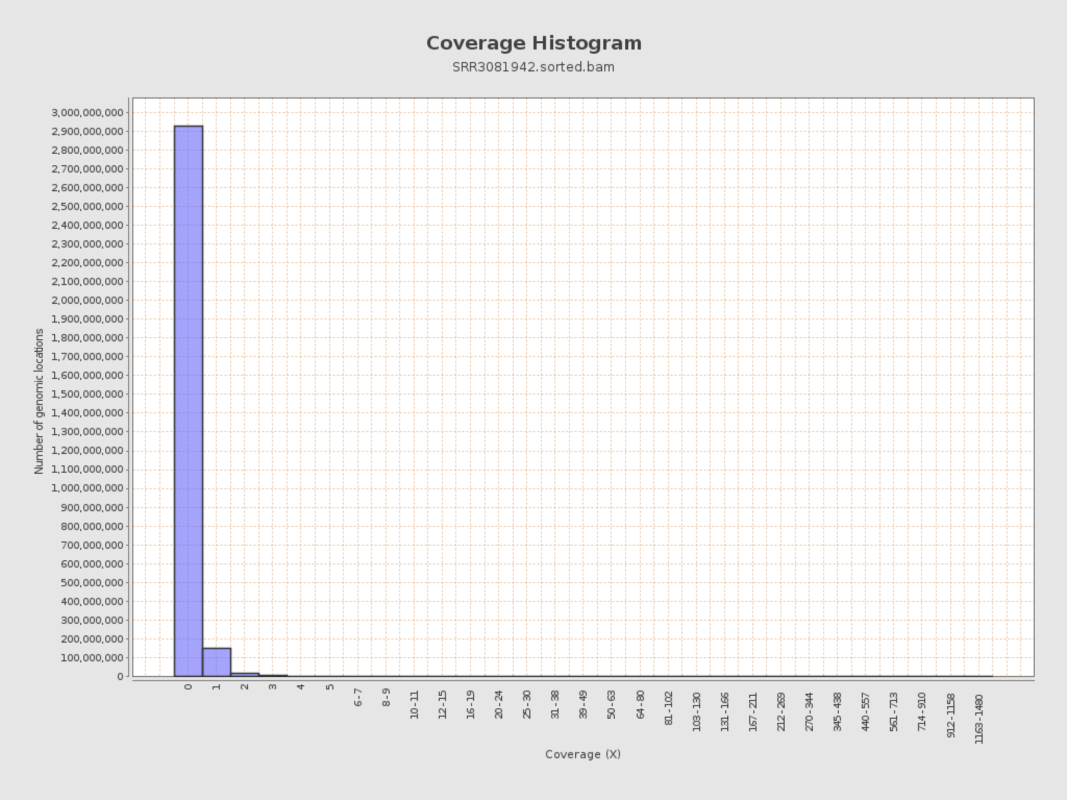
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17887313	0.0718	1.2835
chr2	243199373	17192838	0.0707	0.7619
chr3	198022430	12562976	0.0634	0.2864
chr4	191154276	10209233	0.0534	0.2803
chr5	180915260	9771529	0.054	0.2665
chr6	171115067	17077778	0.0998	0.4951
chr7	159138663	12680130	0.0797	0.8391

chr8	146364022	10972695	0.075	0.9103
chr9	141213431	9606286	0.068	0.6142
chr10	135534747	7874368	0.0581	0.6225
chr11	135006516	8602650	0.0637	0.4189
chr12	133851895	8289855	0.0619	0.2998
chr13	115169878	5454111	0.0474	0.2416
chr14	107349540	4939306	0.046	0.2878
chr15	102531392	4413897	0.043	0.2331
chr16	90354753	4070586	0.0451	0.3266
chr17	81195210	5095391	0.0628	0.3339
chr18	78077248	5672943	0.0727	0.9855
chr19	59128983	3873254	0.0655	0.8888
chr20	63025520	4747134	0.0753	0.3192
chr21	48129895	2101301	0.0437	0.2868
chr22	51304566	1441305	0.0281	0.1832
chrMT	16571	30294	1.8281	1.708
chrX	155270560	9291945	0.0598	0.3461
chrY	59373566	412438	0.0069	0.1743

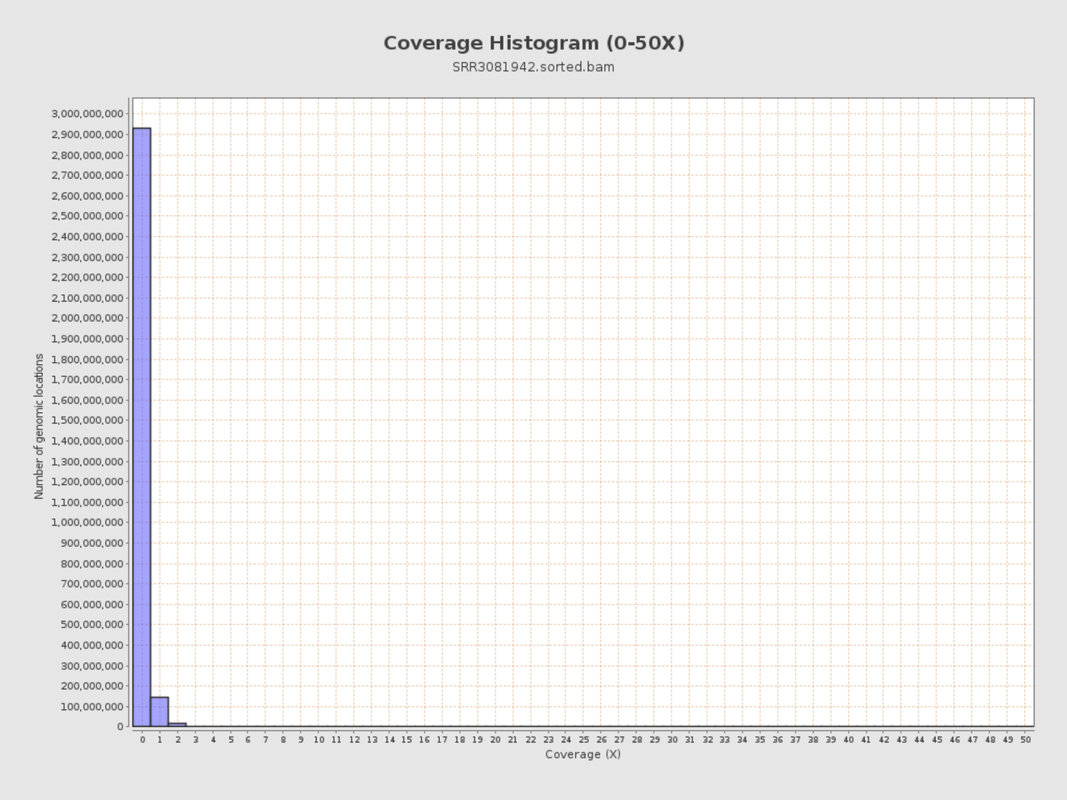
3. Results : Coverage across reference



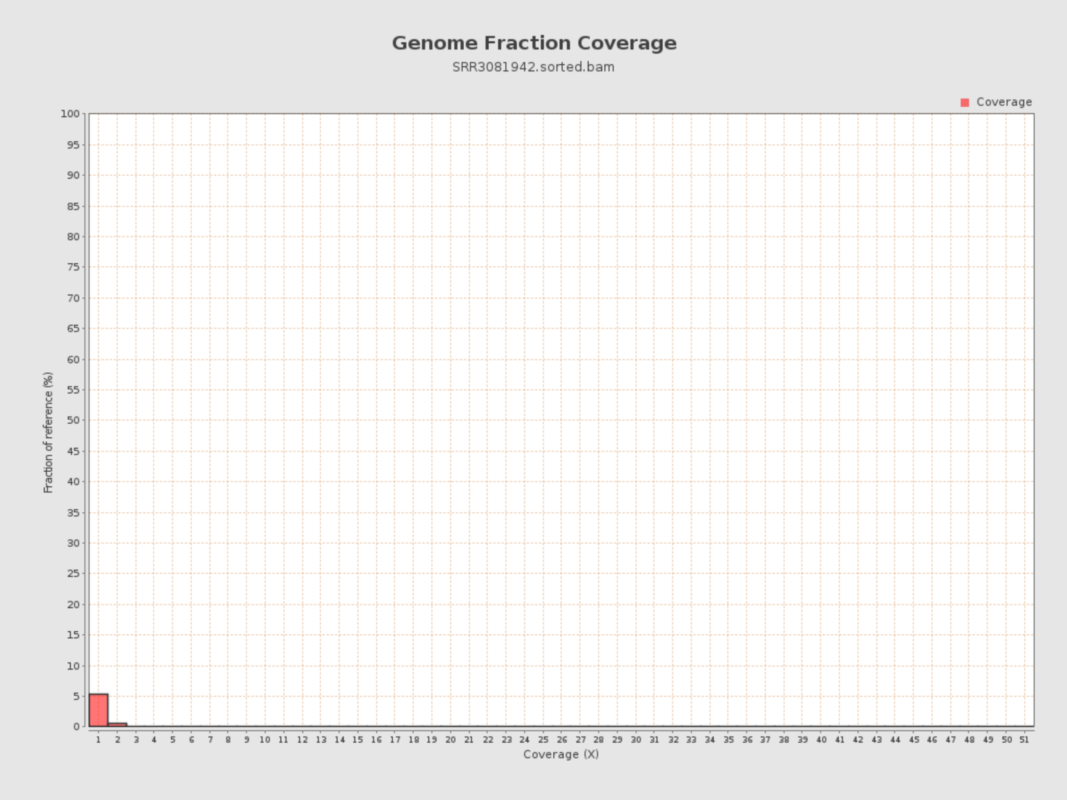
4. Results : Coverage Histogram



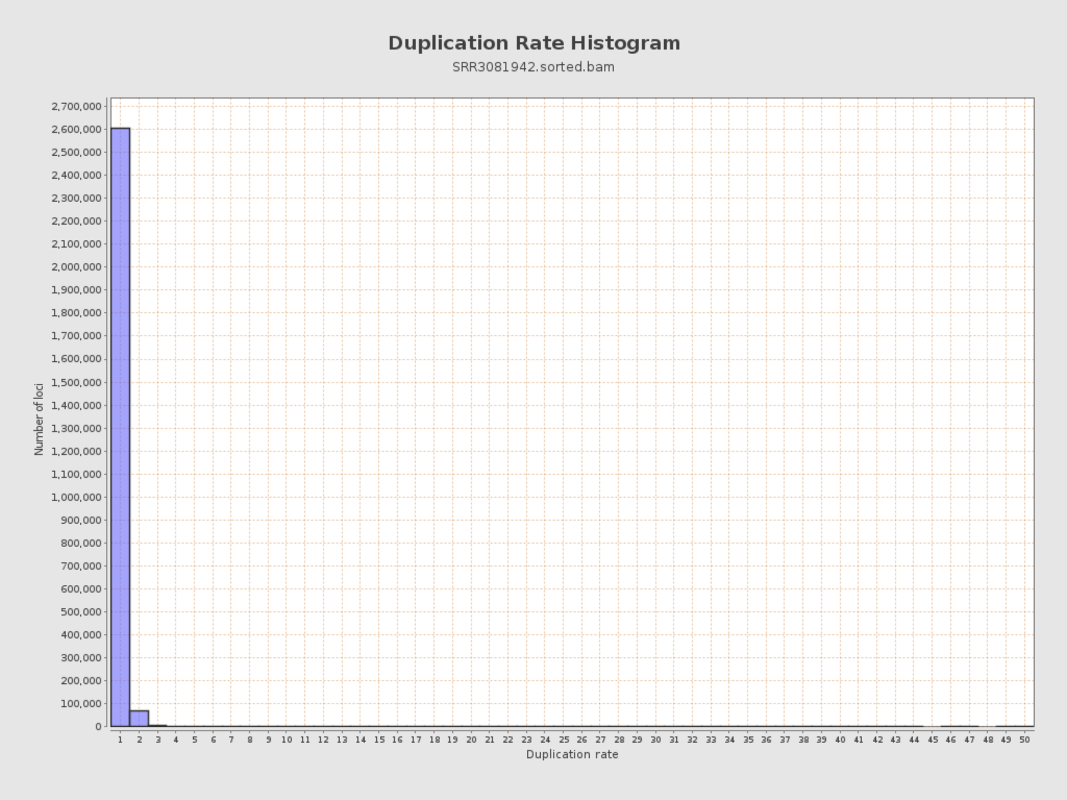
5. Results : Coverage Histogram (0-50X)



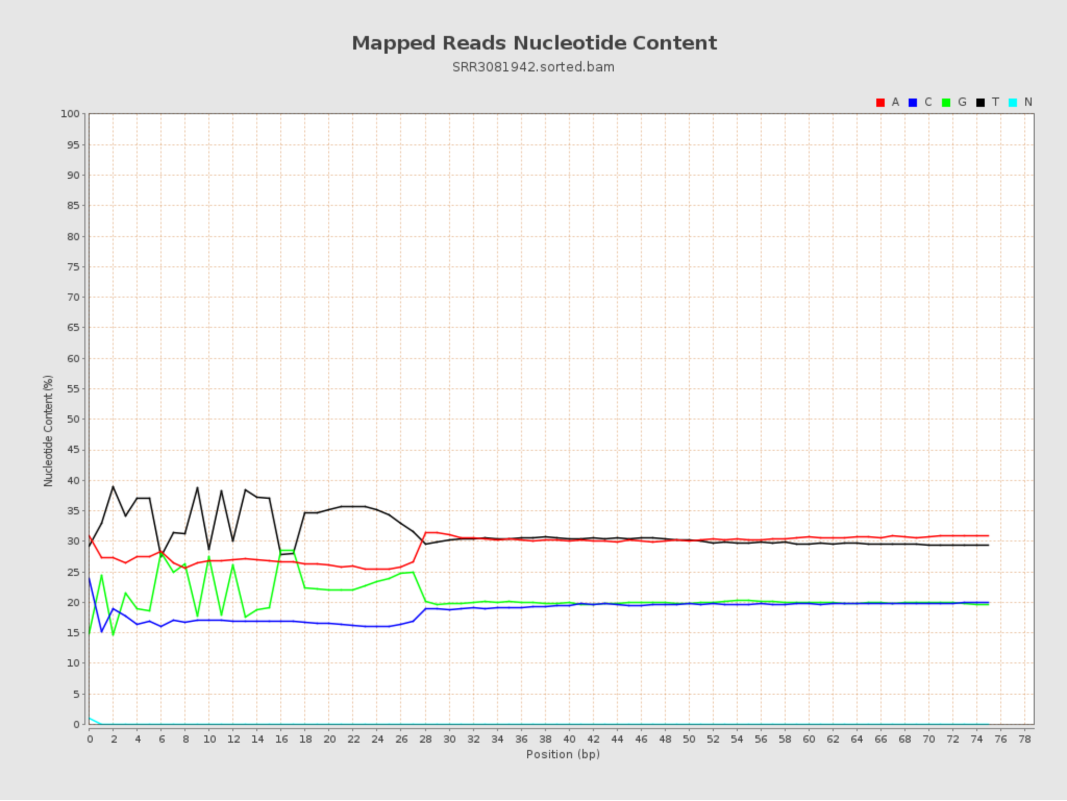
6. Results : Genome Fraction Coverage



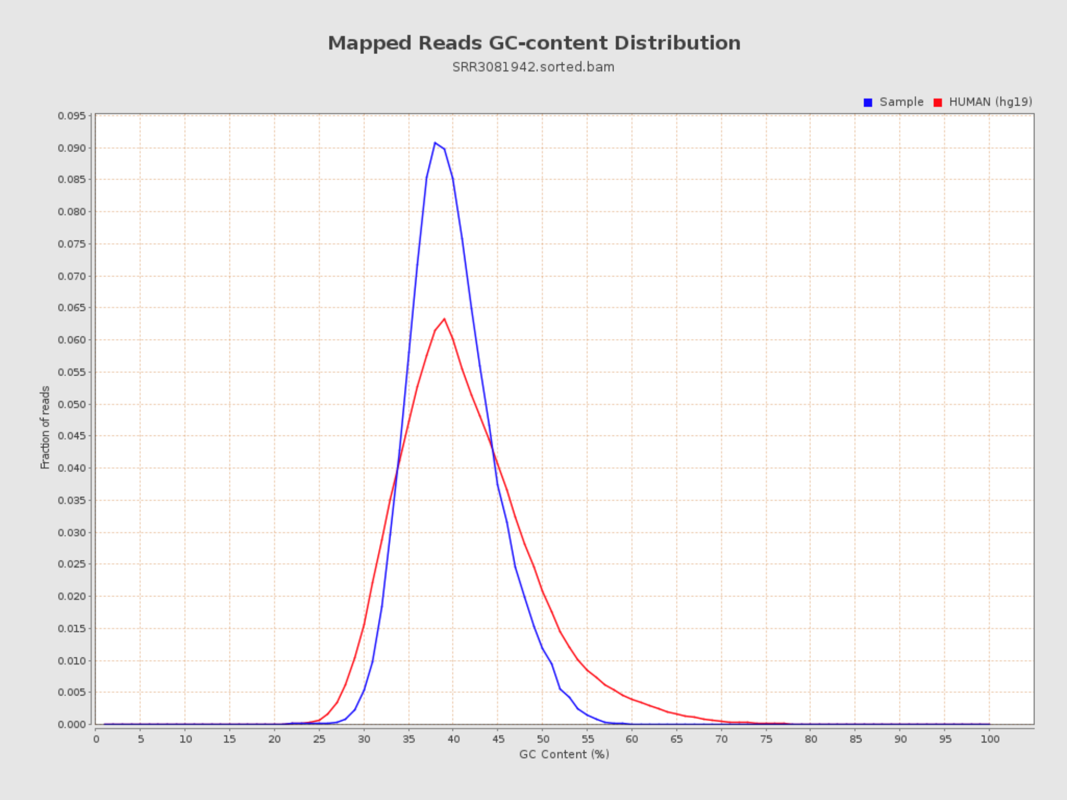
7. Results : Duplication Rate Histogram



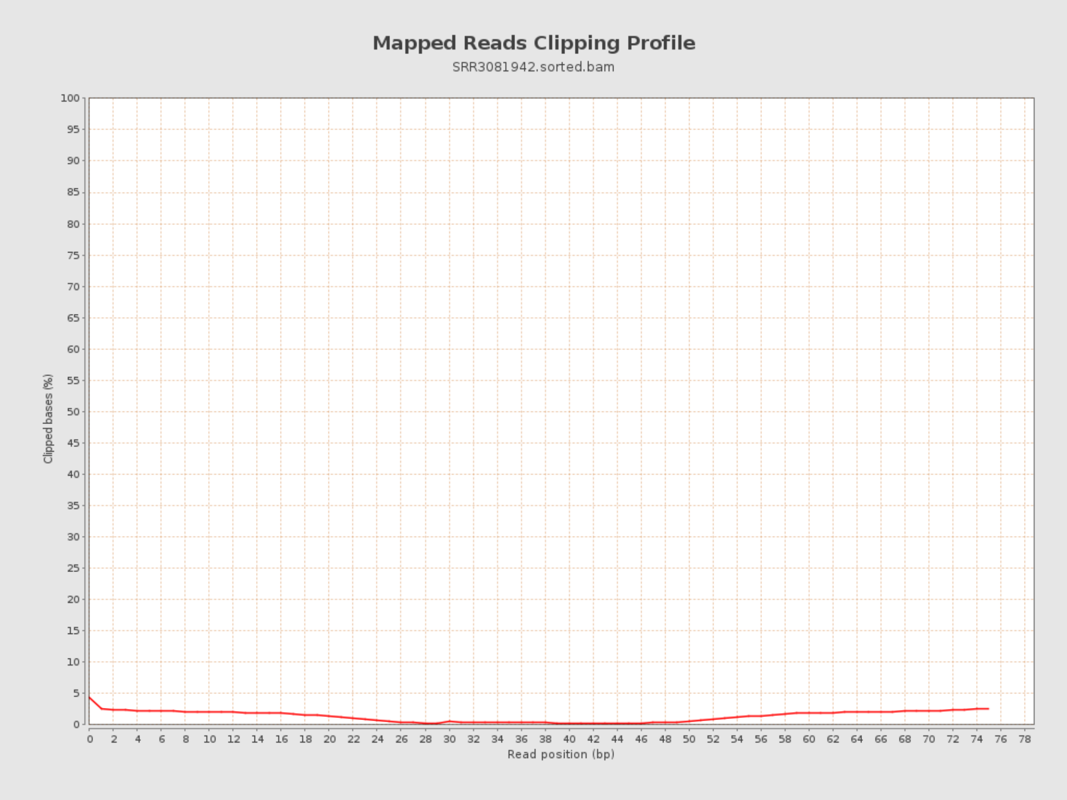
8. Results : Mapped Reads Nucleotide Content



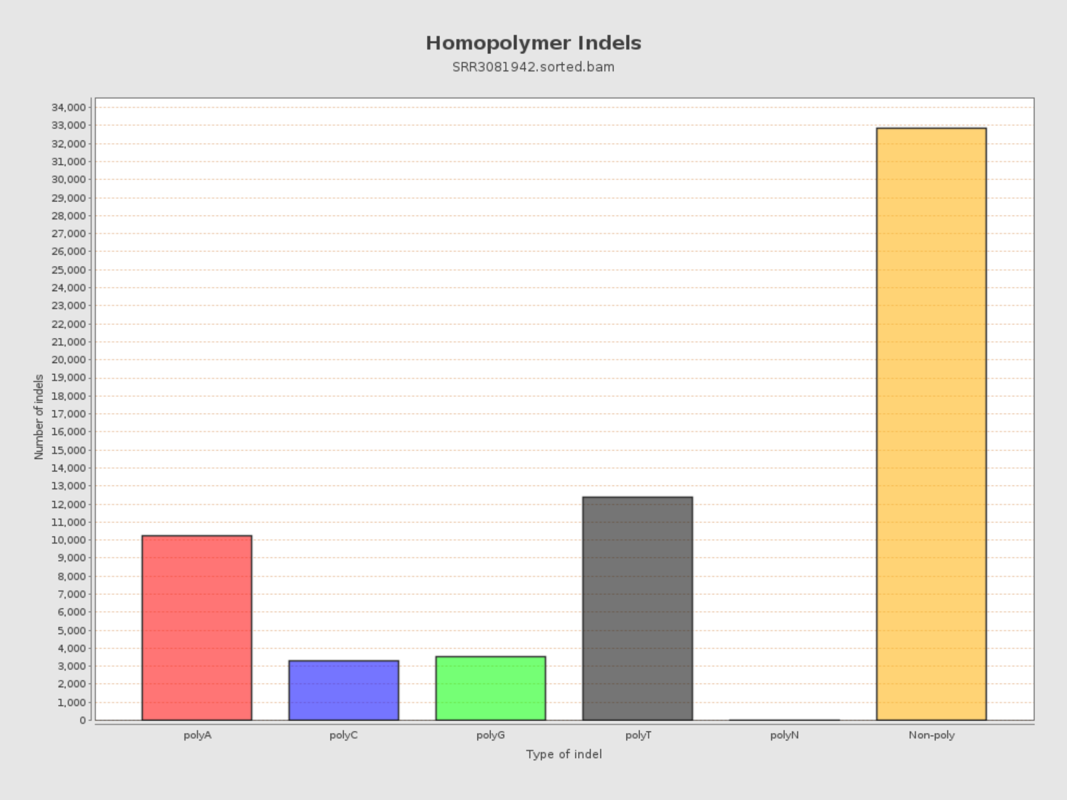
9. Results : Mapped Reads GC-content Distribution



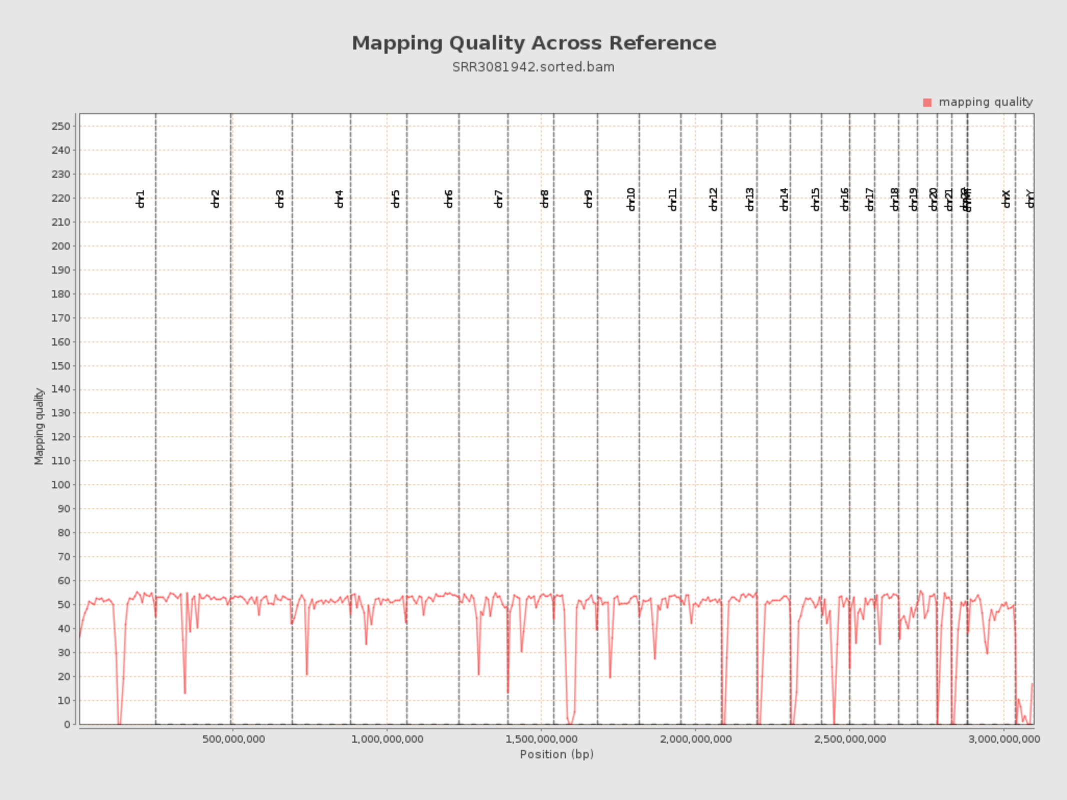
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram