Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081054.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_SRR3081054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,050,233
Mapped reads	1,617,098 / 78.87%
Unmapped reads	433,135 / 21.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,000 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	42,476 / 2.07%
Duplication rate	1.5%
Clipped reads	773,361 / 37.72%

2.2. ACGT Content

Number/percentage of A's	30,021,466 / 28.33%
Number/percentage of C's	20,740,015 / 19.57%
Number/percentage of T's	30,724,584 / 28.99%
Number/percentage of G's	24,479,707 / 23.1%
Number/percentage of N's	1,408 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.3642

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

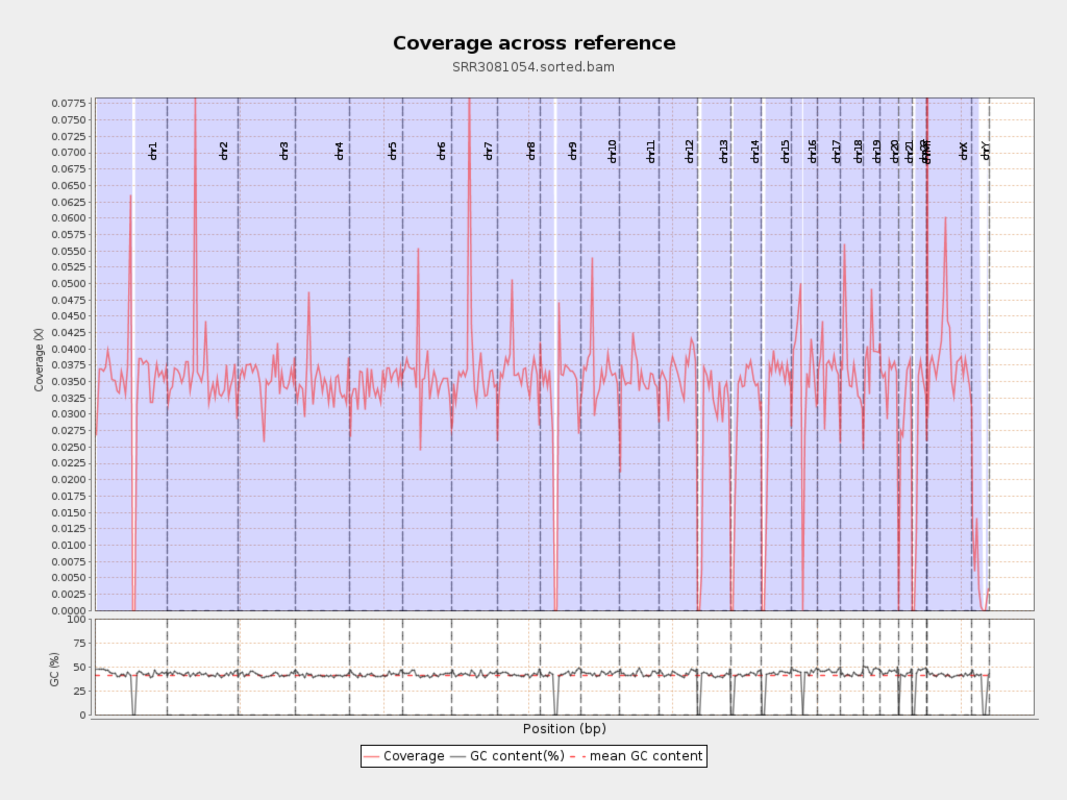
General error rate	0.8%
Mismatches	827,566
Insertions	8,241
Mapped reads with at least one insertion	0.5%
Deletions	19,615
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.06%

2.6. Chromosome stats

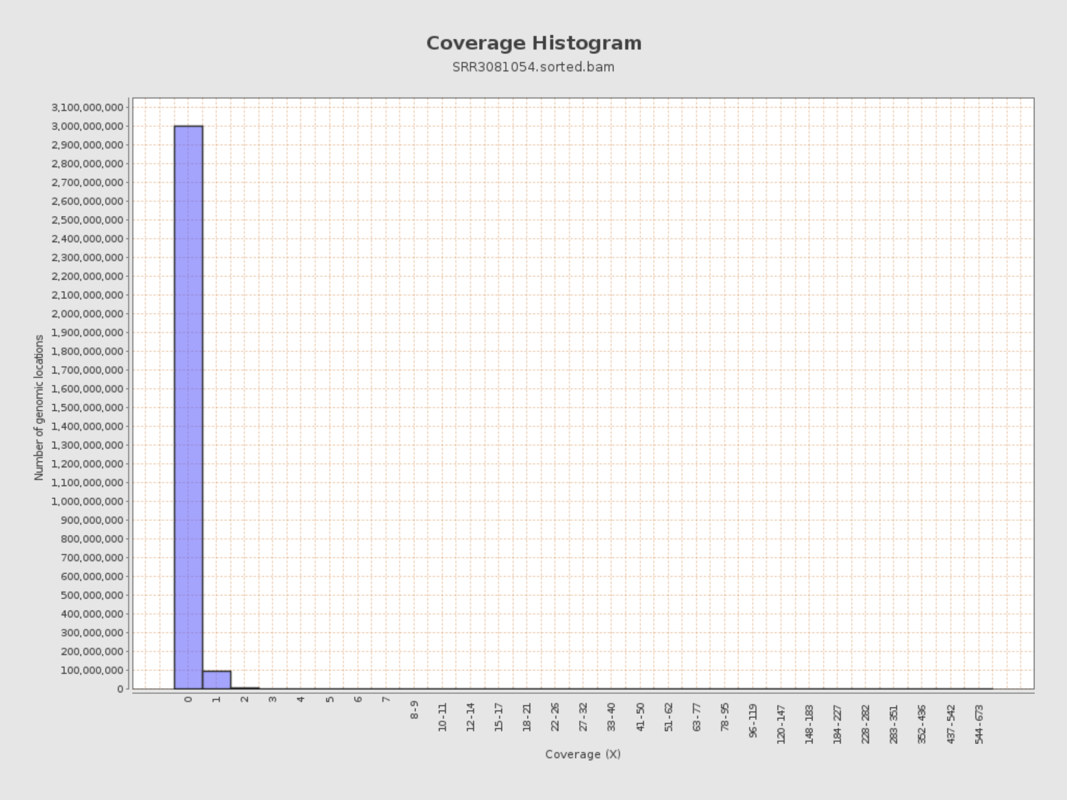
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8562180	0.0344	0.5853
chr2	243199373	8908814	0.0366	0.4373
chr3	198022430	7033273	0.0355	0.1973
chr4	191154276	6649665	0.0348	0.2122
chr5	180915260	6281515	0.0347	0.2005
chr6	171115067	6139750	0.0359	0.3007
chr7	159138663	5999380	0.0377	0.6697

chr8	146364022	5339534	0.0365	0.2917
chr9	141213431	4501751	0.0319	0.3641
chr10	135534747	4949473	0.0365	0.2945
chr11	135006516	4814300	0.0357	0.3601
chr12	133851895	4853166	0.0363	0.2063
chr13	115169878	3193840	0.0277	0.1746
chr14	107349540	3158888	0.0294	0.2235
chr15	102531392	3074844	0.03	0.2041
chr16	90354753	3114998	0.0345	0.2331
chr17	81195210	2974667	0.0366	0.252
chr18	78077248	2892642	0.037	0.7966
chr19	59128983	2321398	0.0393	0.4378
chr20	63025520	2216665	0.0352	0.2131
chr21	48129895	1395456	0.029	0.2054
chr22	51304566	1248595	0.0243	0.1641
chrMT	16571	26772	1.6156	1.6664
chrX	155270560	6070667	0.0391	0.2649
chrY	59373566	278948	0.0047	0.108

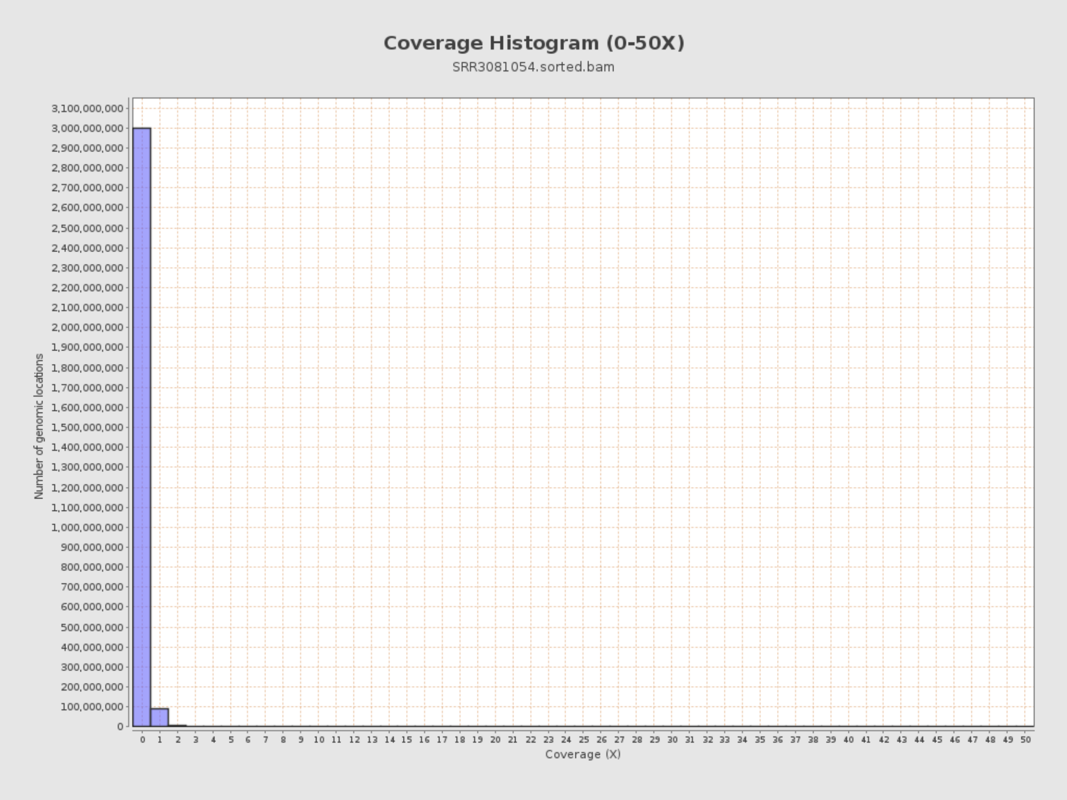
3. Results : Coverage across reference



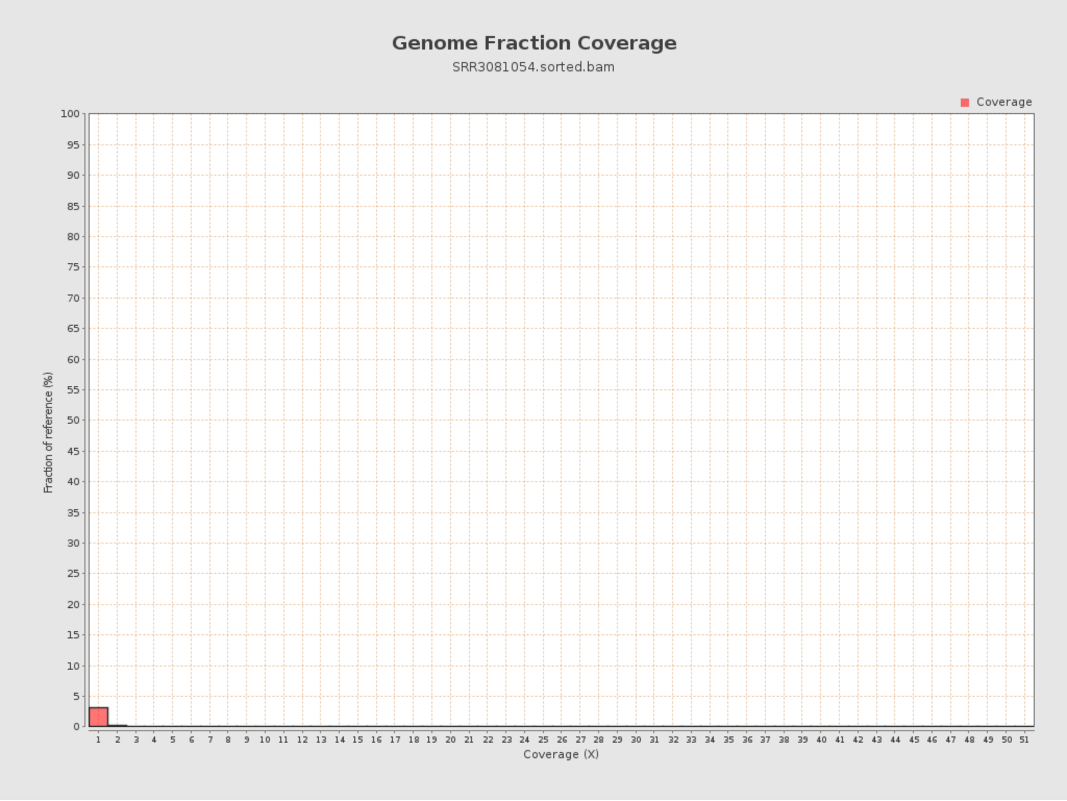
4. Results : Coverage Histogram



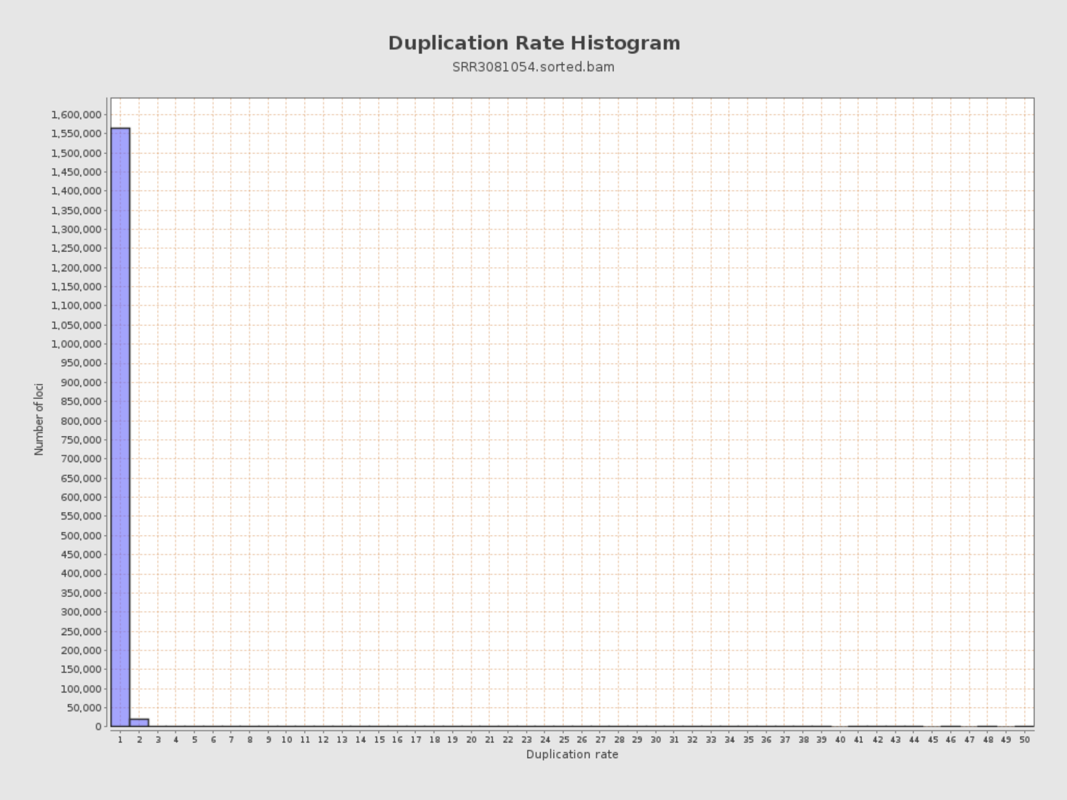
5. Results : Coverage Histogram (0-50X)



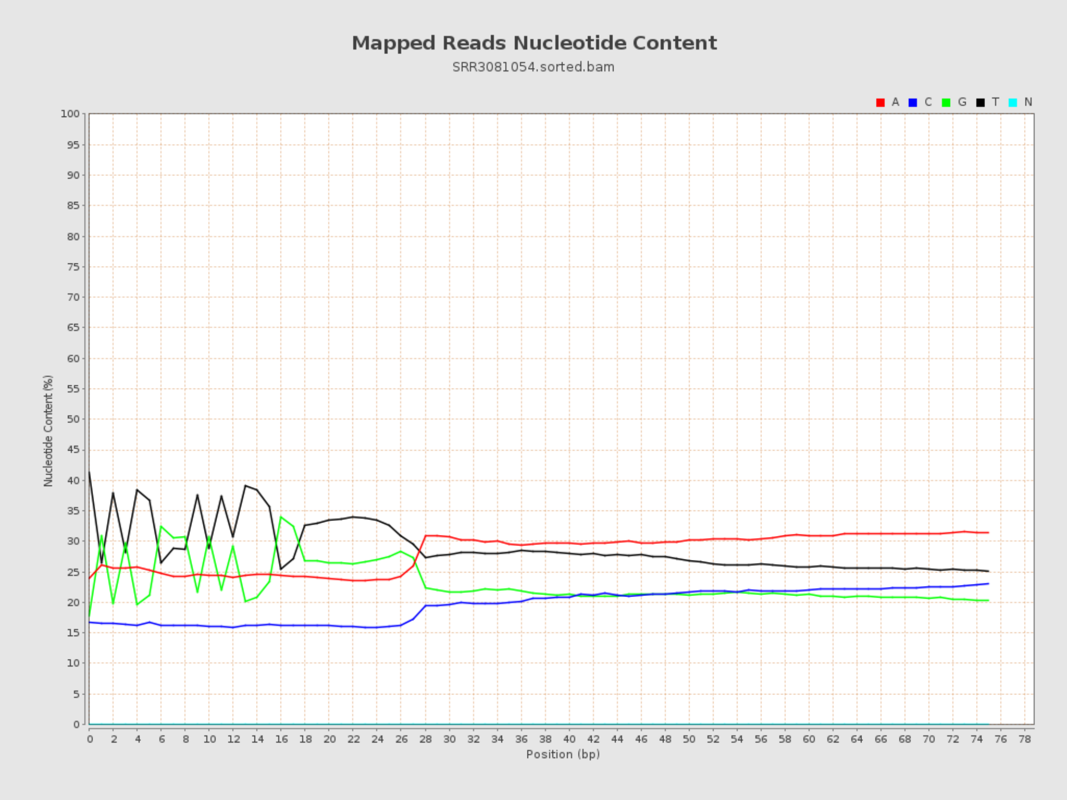
6. Results : Genome Fraction Coverage



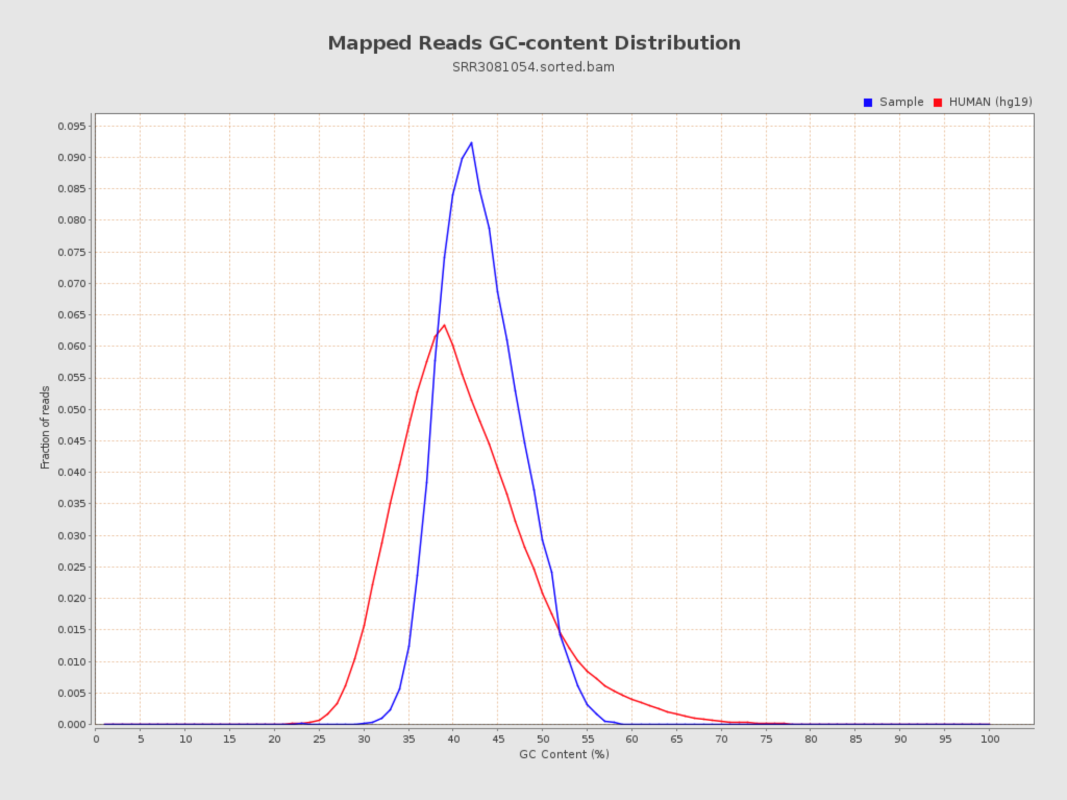
7. Results : Duplication Rate Histogram



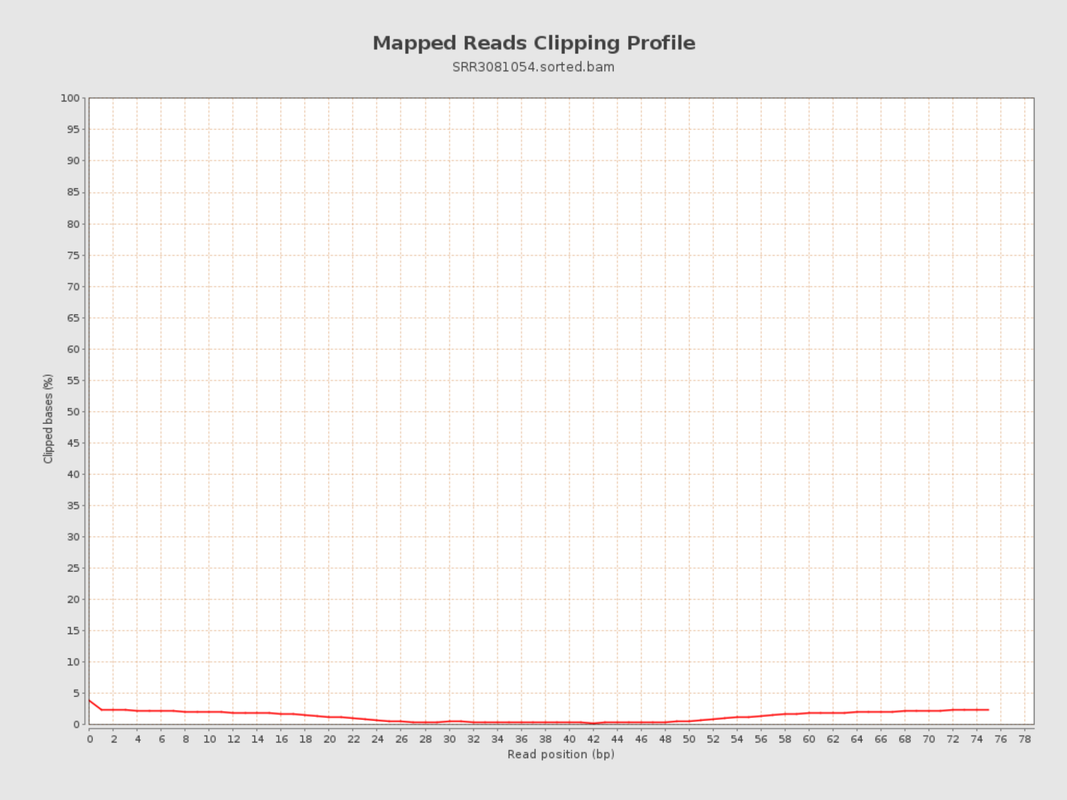
8. Results : Mapped Reads Nucleotide Content



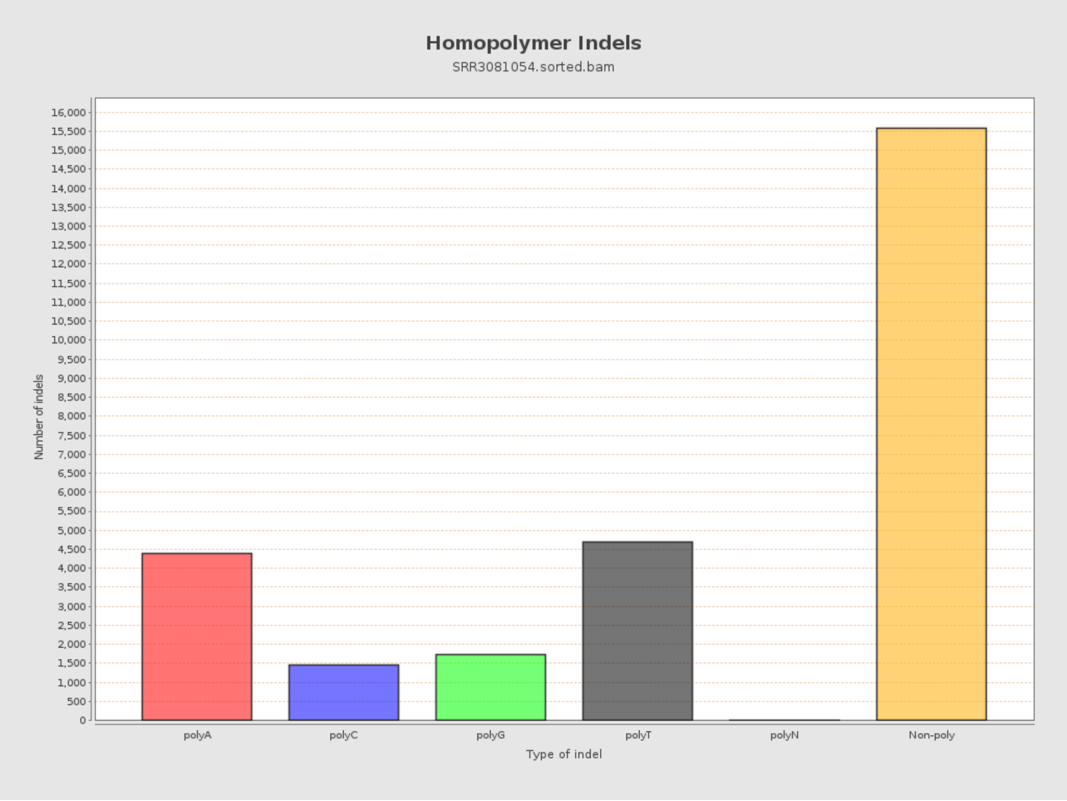
9. Results : Mapped Reads GC-content Distribution



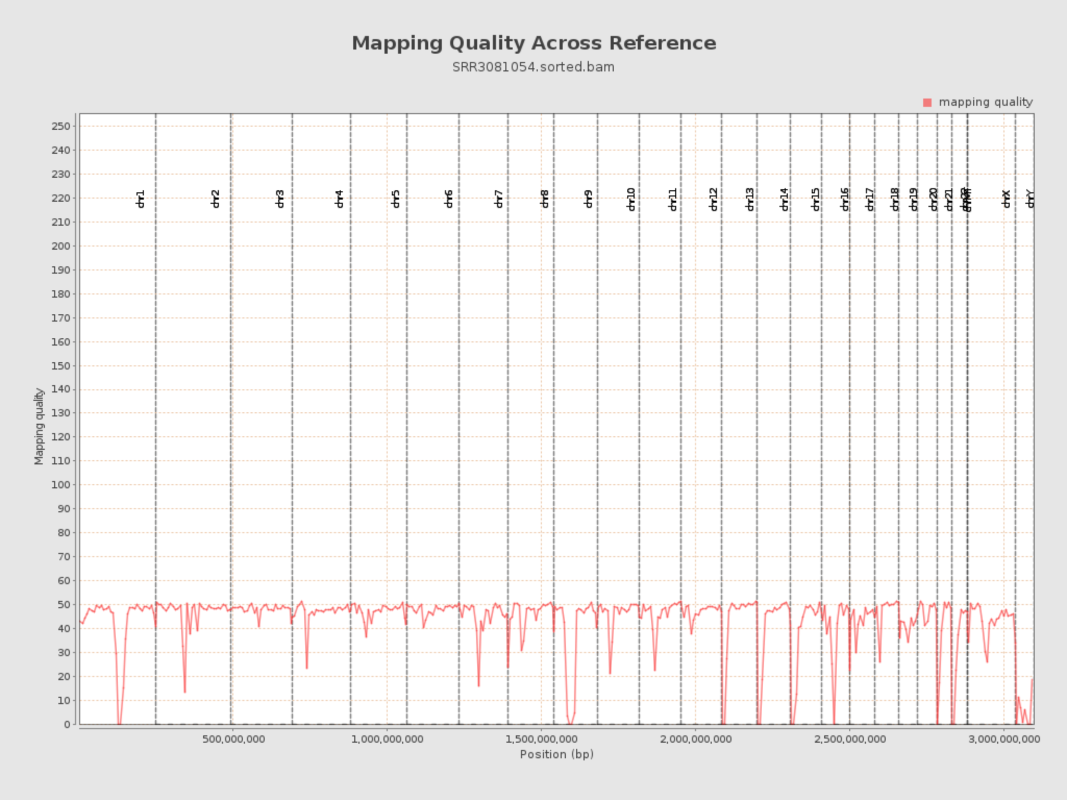
10. Results : Mapped Reads Clipping Profile



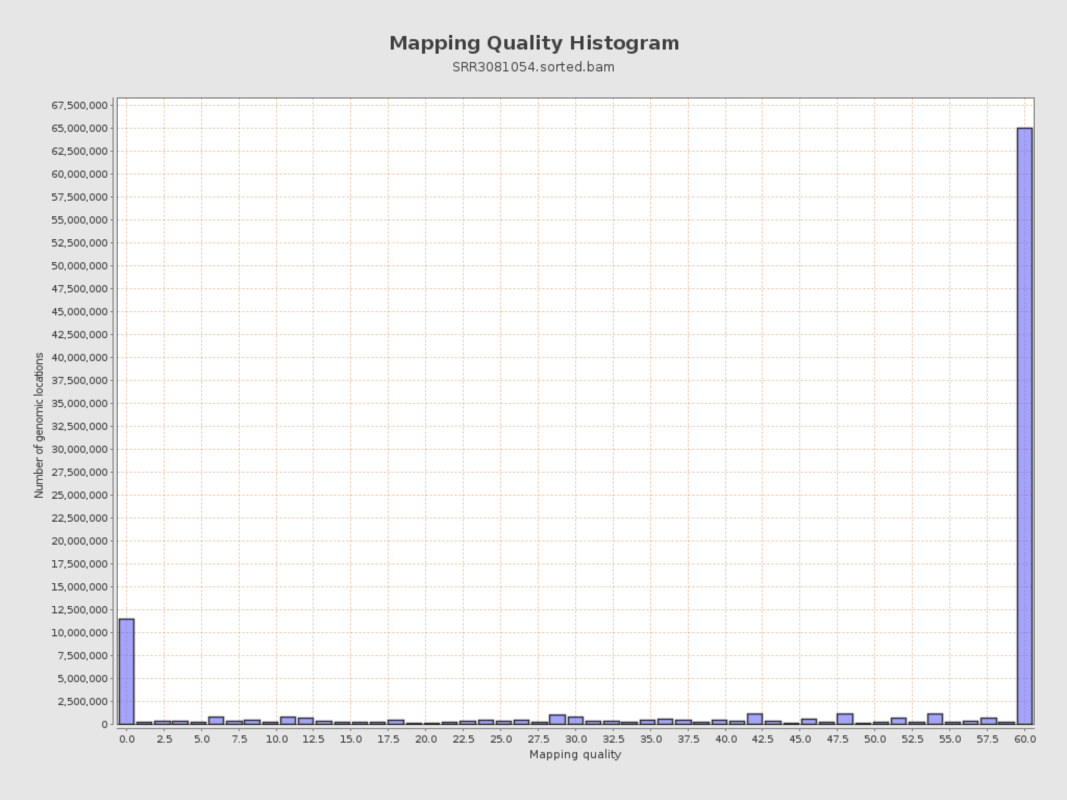
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



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