Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:04:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081154.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_SRR3081154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:04:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,914,230
Mapped reads	2,630,994 / 90.28%
Unmapped reads	283,236 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,068 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	110,270 / 3.78%
Duplication rate	3.08%
Clipped reads	1,160,360 / 39.82%

2.2. ACGT Content

Number/percentage of A's	49,788,244 / 28.19%
Number/percentage of C's	32,711,036 / 18.52%
Number/percentage of T's	55,133,050 / 31.22%
Number/percentage of G's	38,921,800 / 22.04%
Number/percentage of N's	52,362 / 0.03%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.4998

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

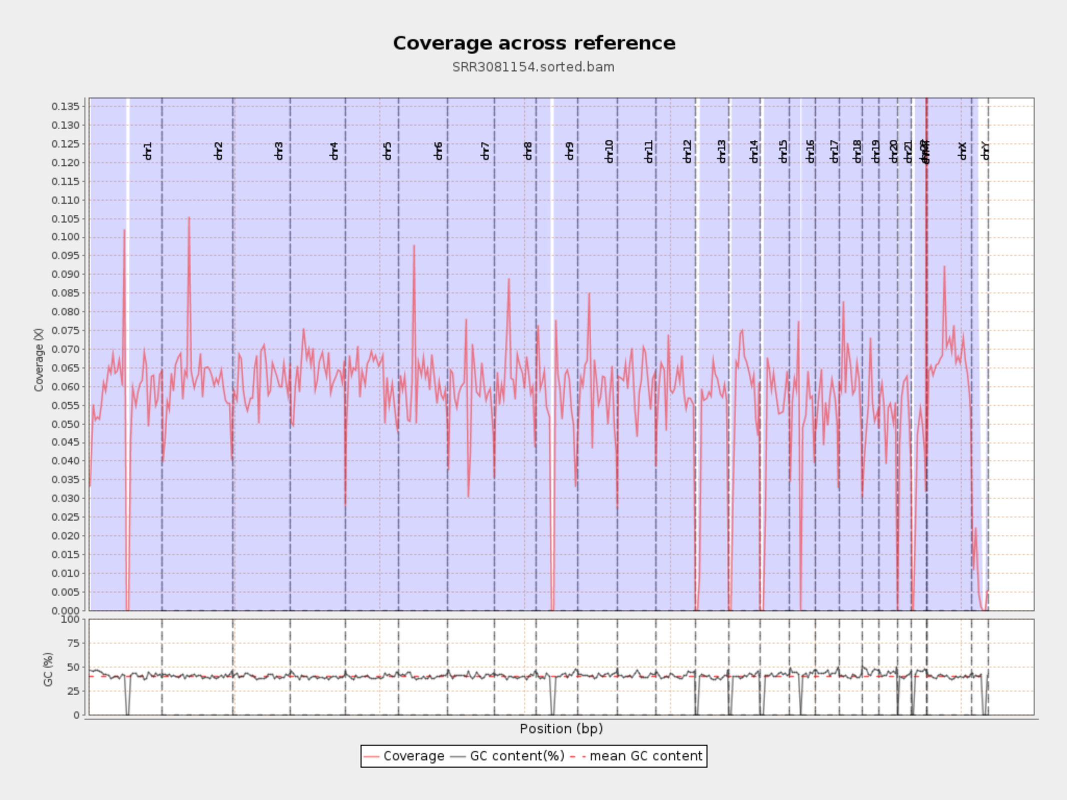
General error rate	0.86%
Mismatches	1,486,588
Insertions	13,926
Mapped reads with at least one insertion	0.53%
Deletions	41,498
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.94%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14021166	0.0563	0.9411
chr2	243199373	14962477	0.0615	0.6076
chr3	198022430	12170866	0.0615	0.2784
chr4	191154276	12203176	0.0638	0.3043
chr5	180915260	11225198	0.062	0.2849
chr6	171115067	10513475	0.0614	0.4183
chr7	159138663	9210219	0.0579	0.5676

chr8	146364022	9122362	0.0623	0.6649
chr9	141213431	7426771	0.0526	0.4851
chr10	135534747	8089159	0.0597	0.4045
chr11	135006516	8232025	0.061	0.4504
chr12	133851895	7919455	0.0592	0.2844
chr13	115169878	5647114	0.049	0.2496
chr14	107349540	5714379	0.0532	0.3018
chr15	102531392	4950057	0.0483	0.2627
chr16	90354753	4632280	0.0513	0.3204
chr17	81195210	4338713	0.0534	0.3161
chr18	78077248	4961377	0.0635	0.993
chr19	59128983	3107147	0.0525	0.6599
chr20	63025520	3263538	0.0518	0.2758
chr21	48129895	2329709	0.0484	0.2832
chr22	51304566	1726241	0.0336	0.2047
chrMT	16571	5634	0.34	0.6874
chrX	155270560	10463703	0.0674	0.3494
chrY	59373566	438269	0.0074	0.1519

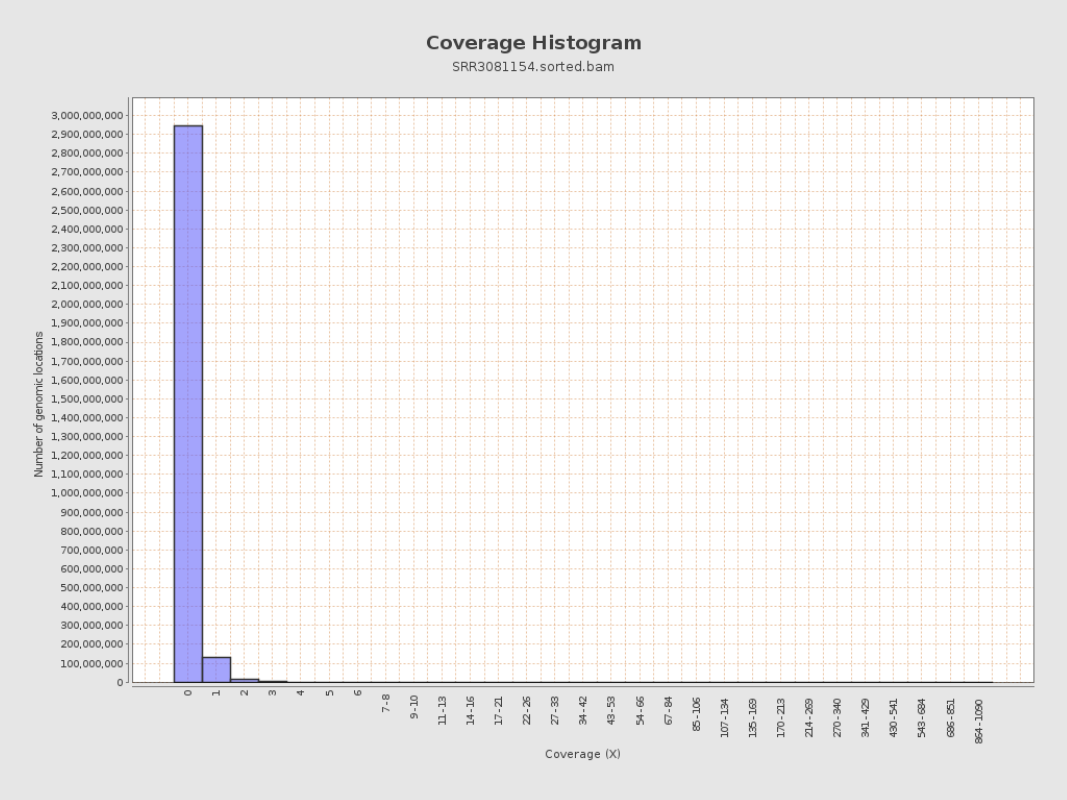
3. Results : Coverage across reference



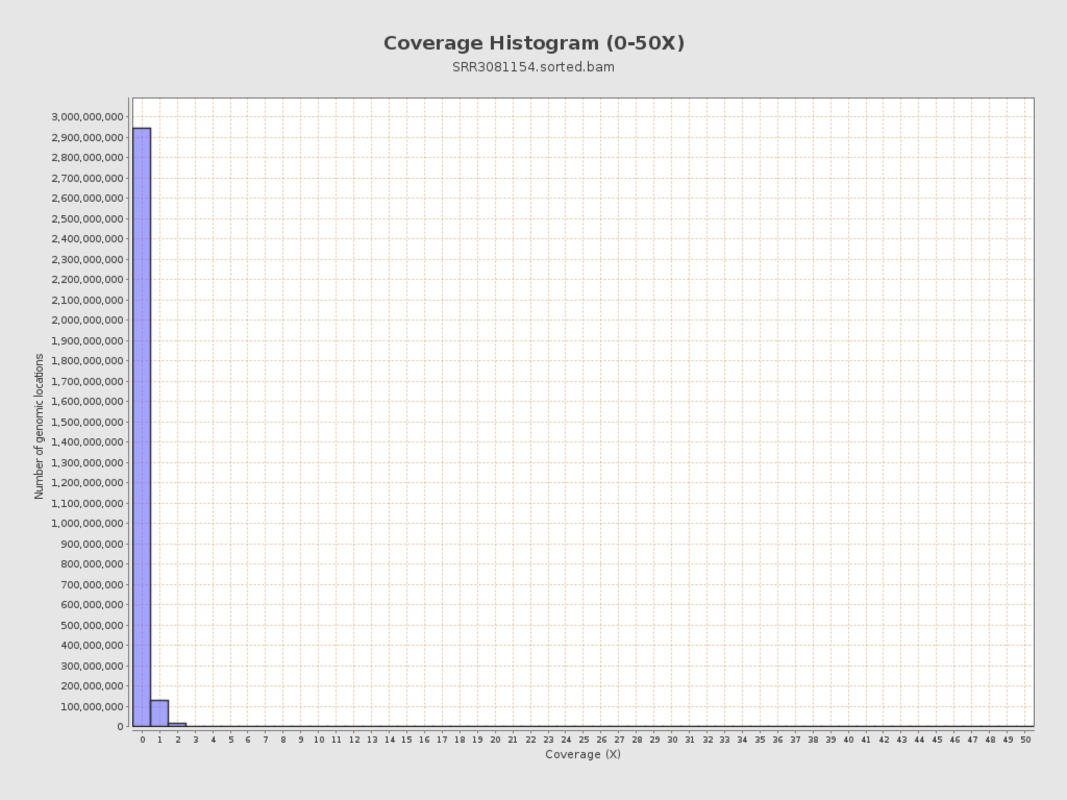
Coverage across reference

SRR3081154.sorted.bam

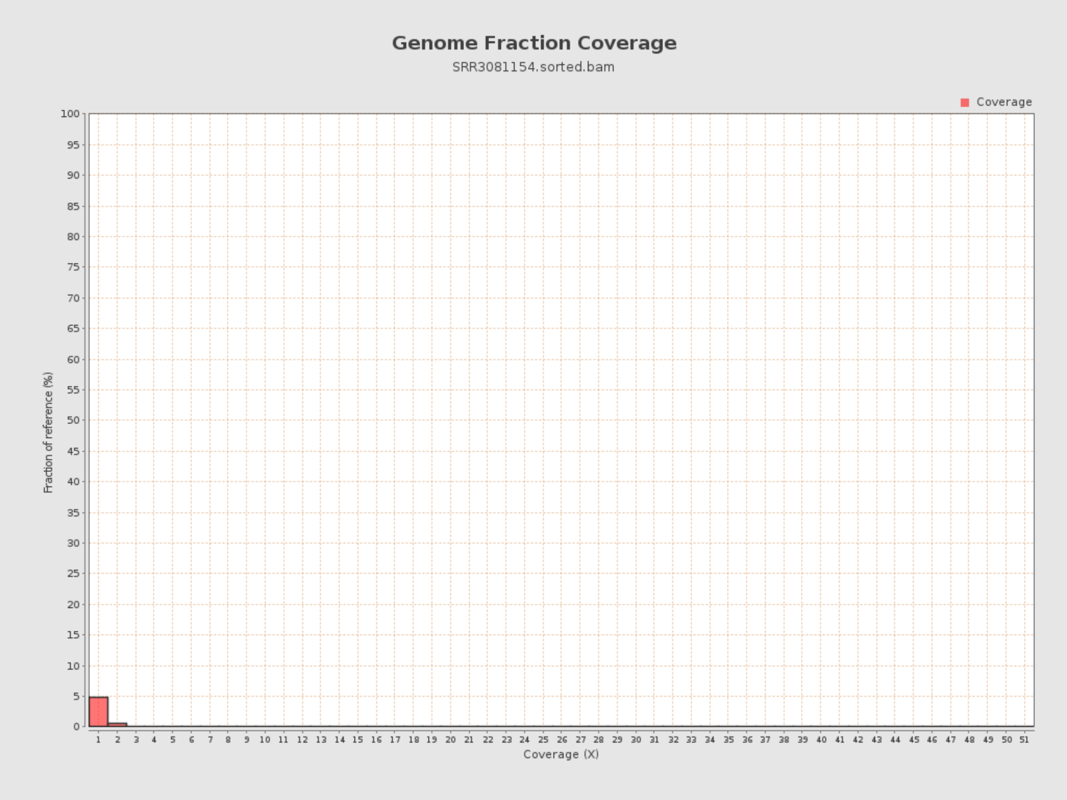
4. Results : Coverage Histogram



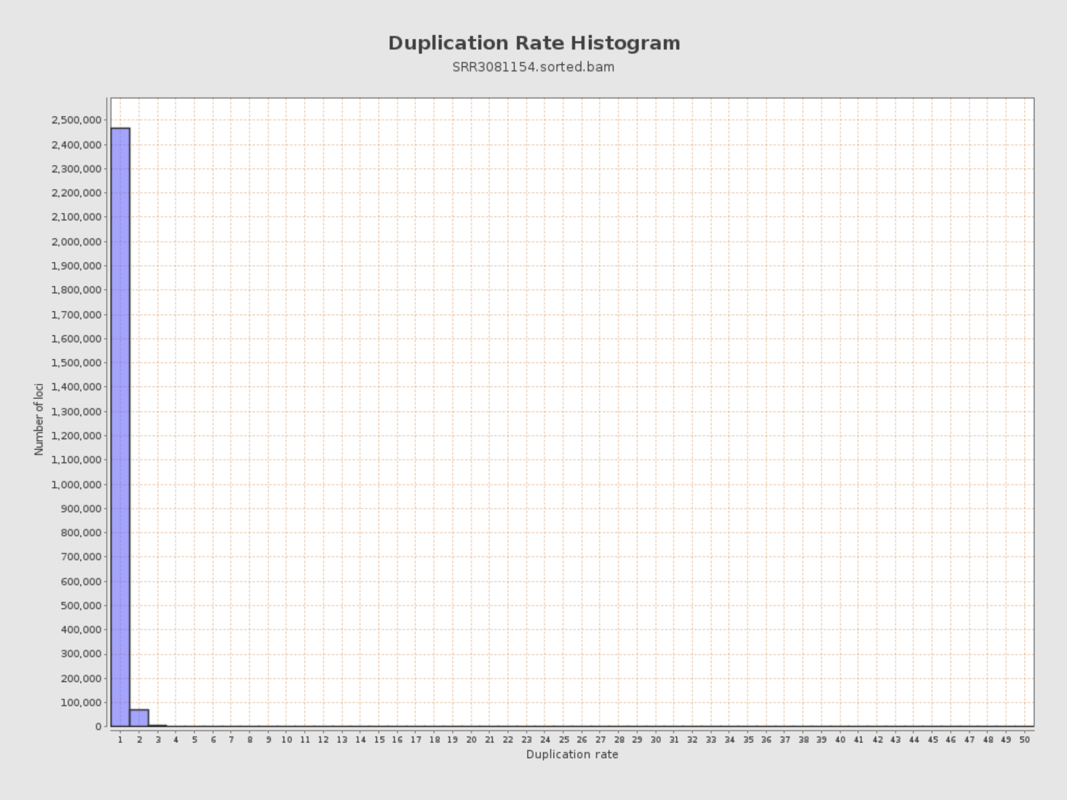
5. Results : Coverage Histogram (0-50X)



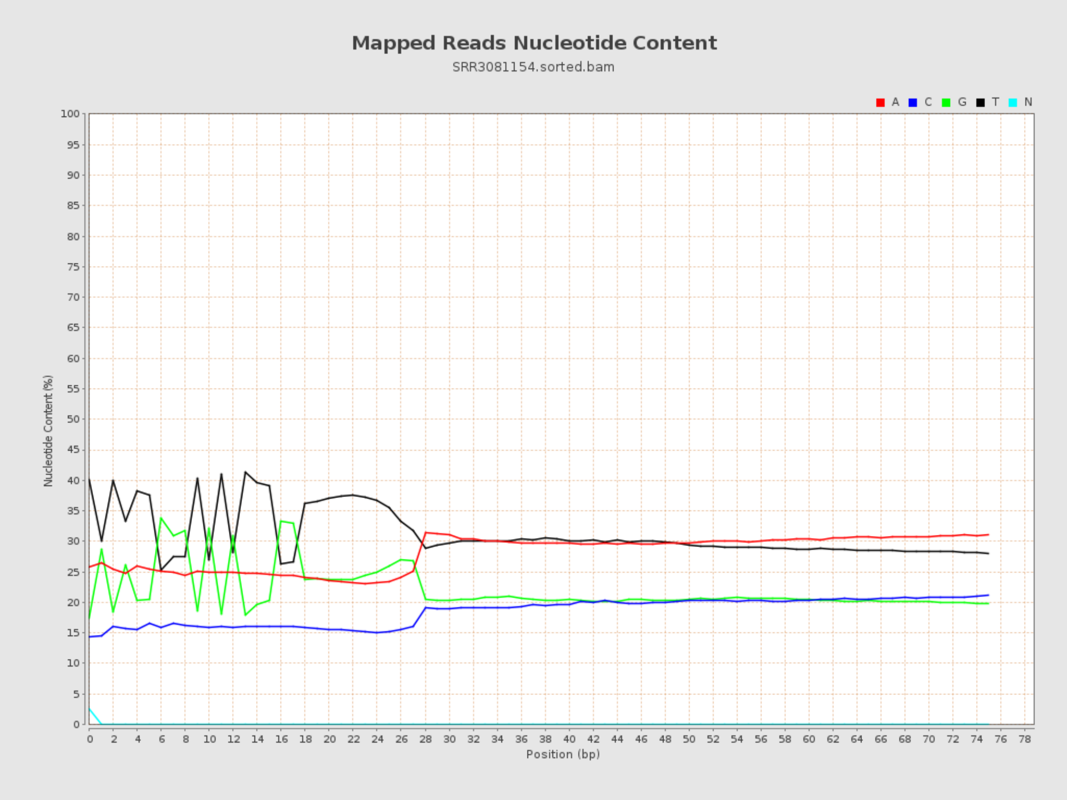
6. Results : Genome Fraction Coverage



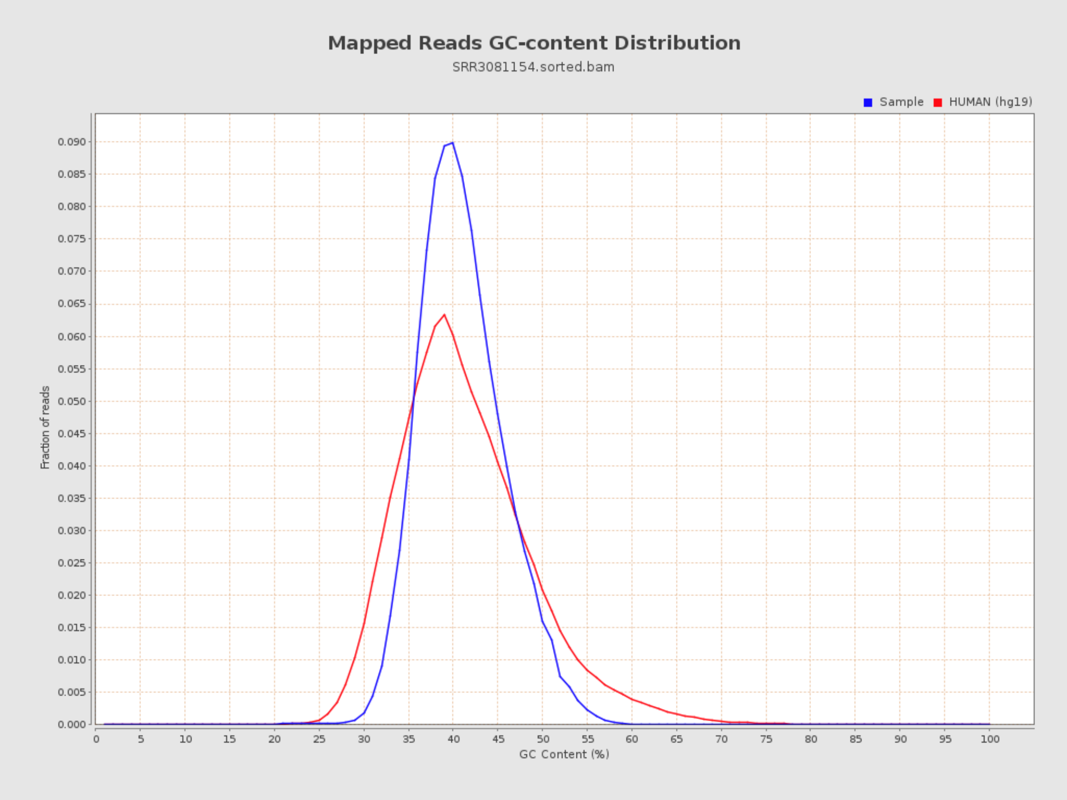
7. Results : Duplication Rate Histogram



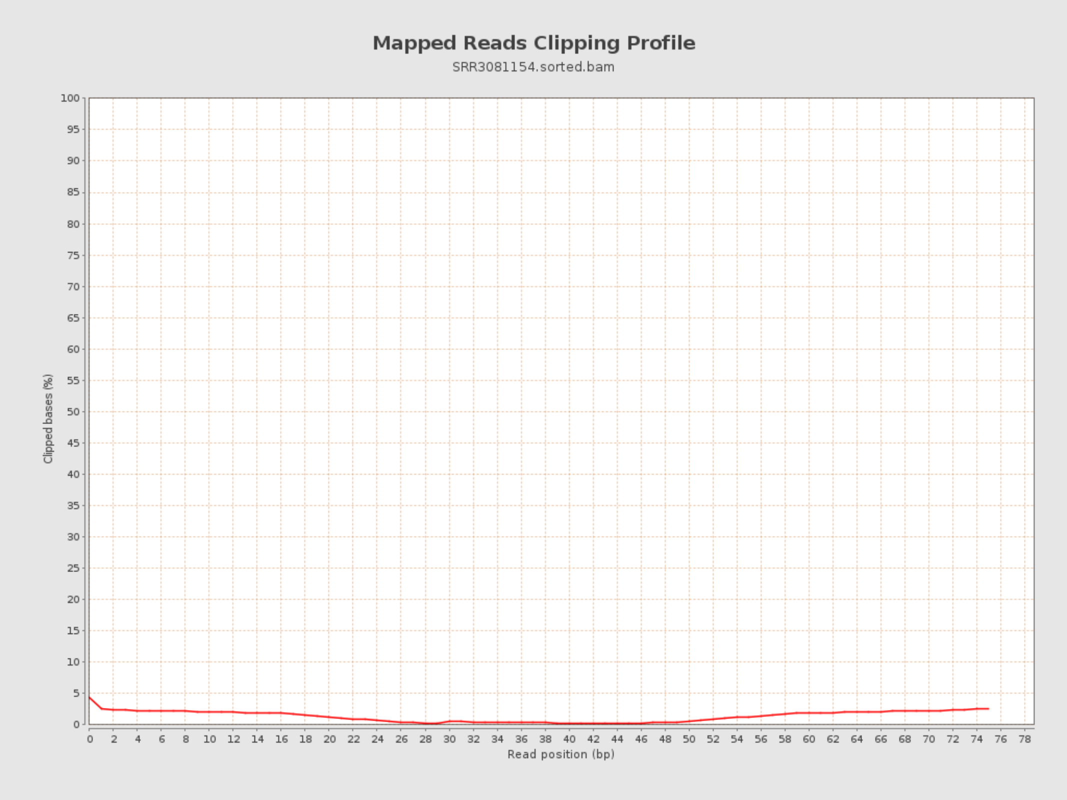
8. Results : Mapped Reads Nucleotide Content



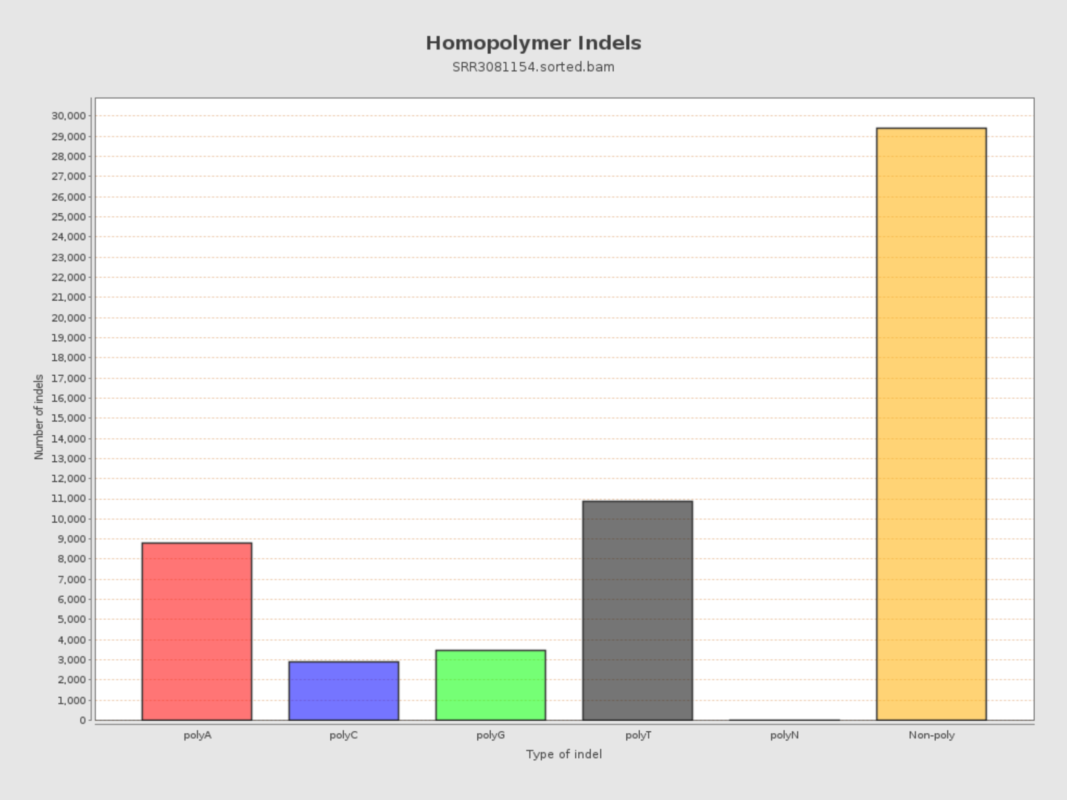
9. Results : Mapped Reads GC-content Distribution



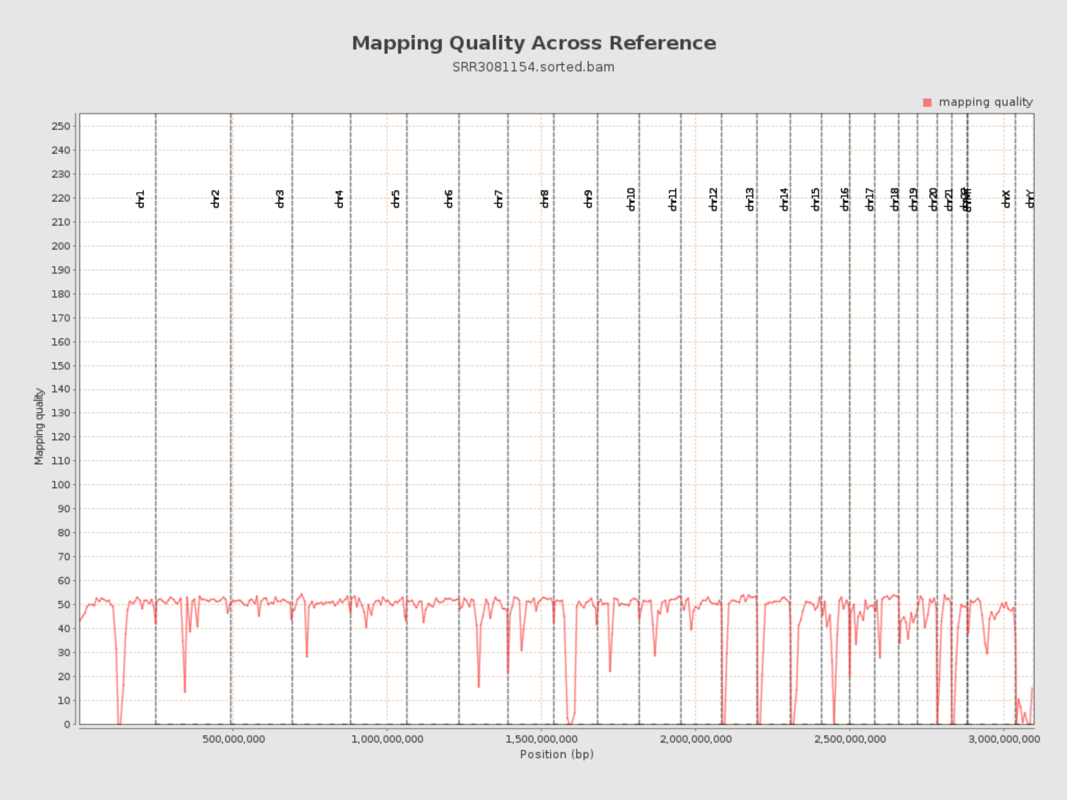
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram