Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:57:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081890.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_SRR3081890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081890.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:57:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,076,341
Mapped reads	2,800,234 / 91.02%
Unmapped reads	276,107 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,918 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	117,306 / 3.81%
Duplication rate	3.18%
Clipped reads	1,260,220 / 40.96%

2.2. ACGT Content

Number/percentage of A's	51,383,439 / 27.48%
Number/percentage of C's	36,557,578 / 19.55%
Number/percentage of T's	56,632,742 / 30.29%
Number/percentage of G's	42,401,977 / 22.68%
Number/percentage of N's	2,124 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.463

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

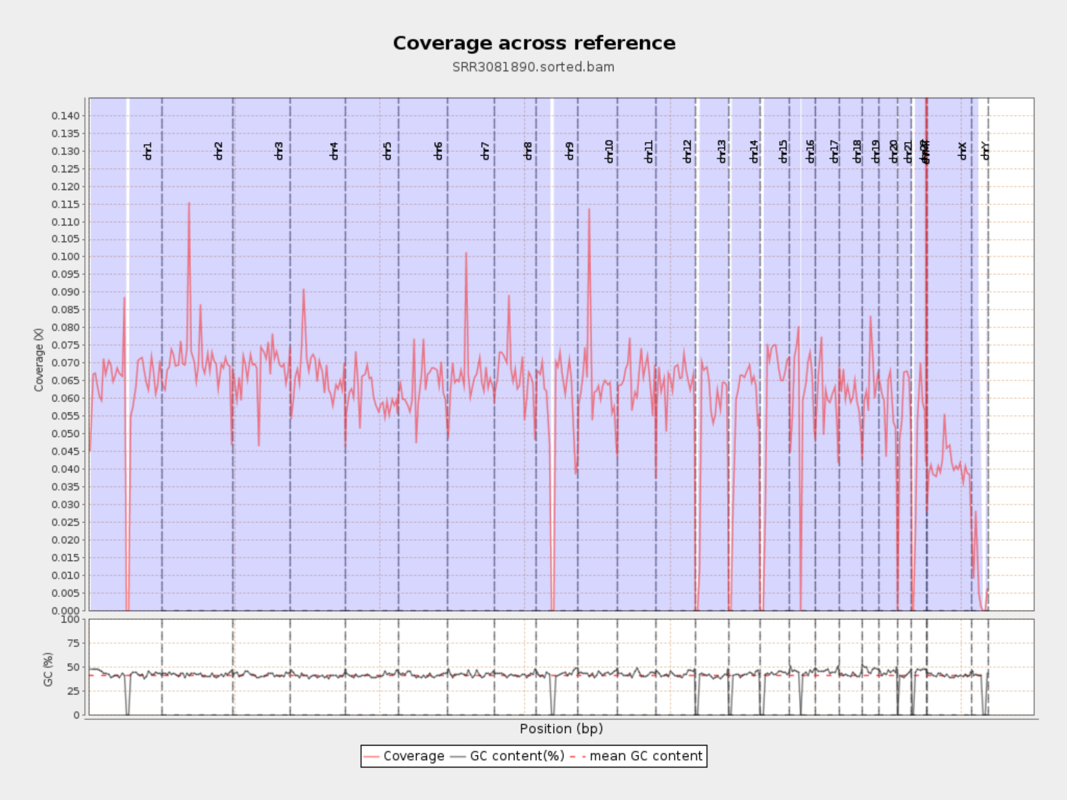
General error rate	0.85%
Mismatches	1,563,099
Insertions	13,773
Mapped reads with at least one insertion	0.49%
Deletions	37,807
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.03%

2.6. Chromosome stats

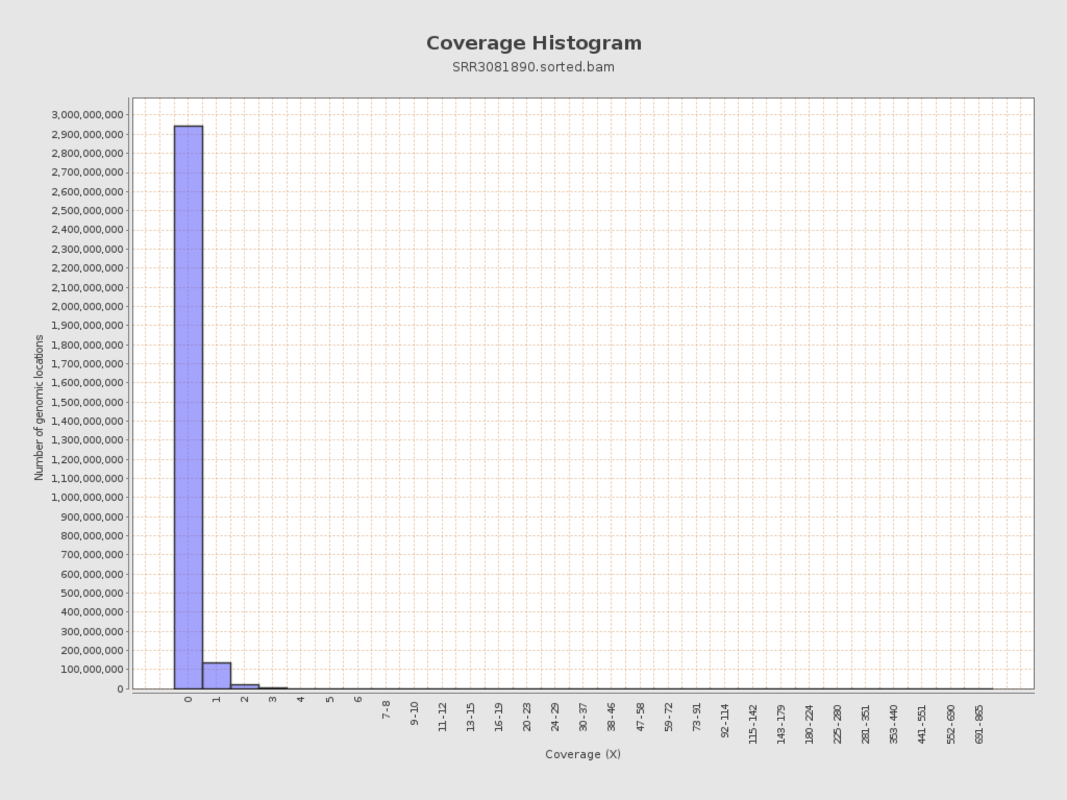
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15435410	0.0619	0.7907
chr2	243199373	17301974	0.0711	0.5884
chr3	198022430	13551044	0.0684	0.3075
chr4	191154276	12795443	0.0669	0.3409
chr5	180915260	11017085	0.0609	0.2873
chr6	171115067	10870569	0.0635	0.3265
chr7	159138663	10599180	0.0666	0.6475

chr8	146364022	9758914	0.0667	0.5284
chr9	141213431	7919355	0.0561	0.4195
chr10	135534747	8783151	0.0648	0.5517
chr11	135006516	8832961	0.0654	0.4159
chr12	133851895	8677775	0.0648	0.3001
chr13	115169878	5963794	0.0518	0.2636
chr14	107349540	5730843	0.0534	0.2878
chr15	102531392	5886382	0.0574	0.2848
chr16	90354753	5392065	0.0597	0.3402
chr17	81195210	4839765	0.0596	0.3309
chr18	78077248	4773063	0.0611	0.7601
chr19	59128983	3829929	0.0648	0.6241
chr20	63025520	3596048	0.0571	0.2873
chr21	48129895	2588064	0.0538	0.3048
chr22	51304566	2096718	0.0409	0.2352
chrMT	16571	29992	1.8099	1.592
chrX	155270560	6316565	0.0407	0.2775
chrY	59373566	459032	0.0077	0.2201

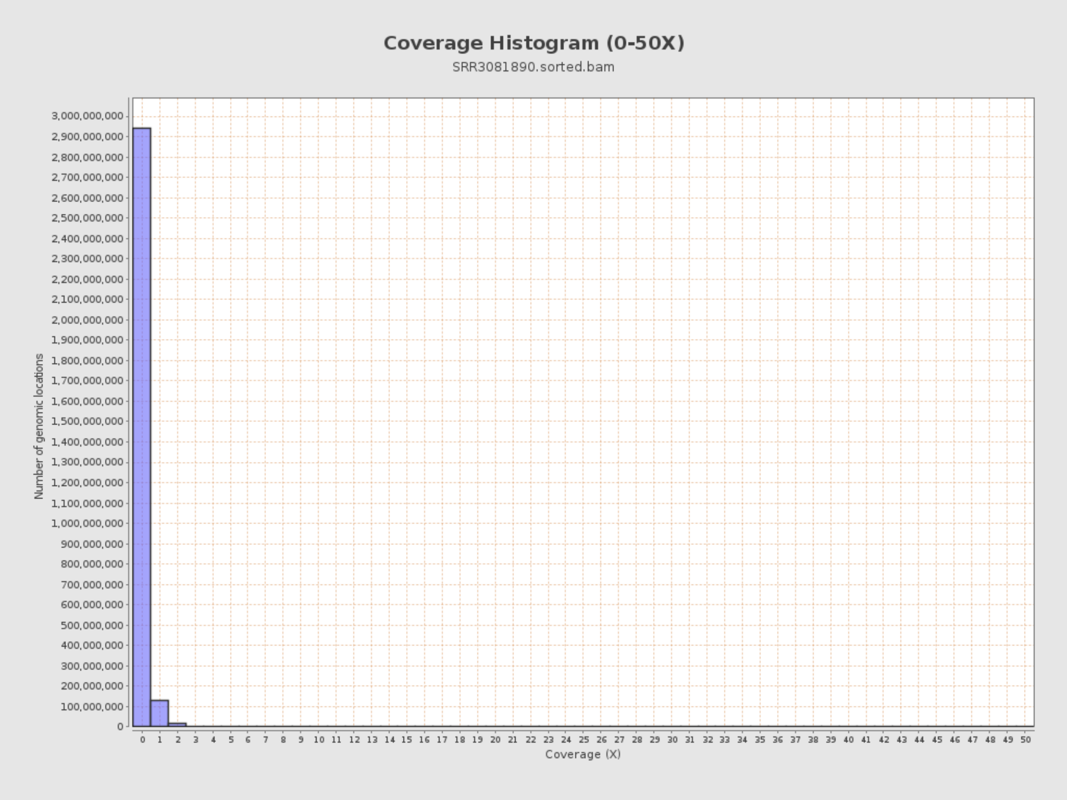
3. Results : Coverage across reference



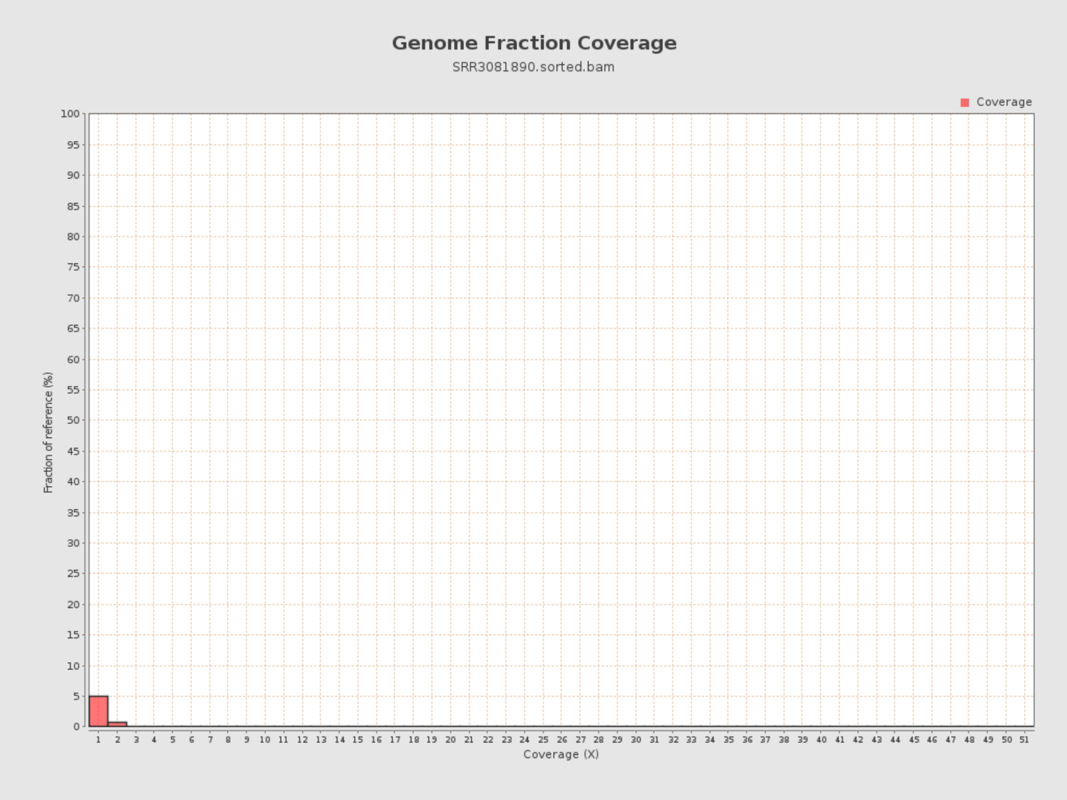
4. Results : Coverage Histogram



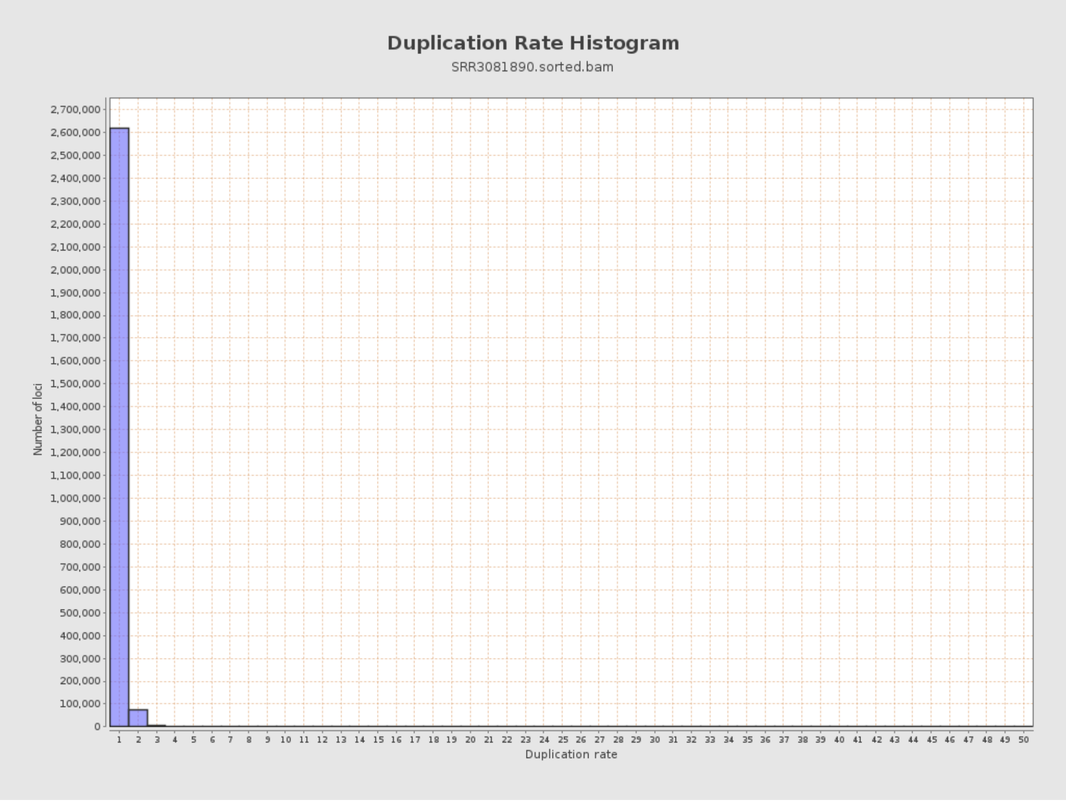
5. Results : Coverage Histogram (0-50X)



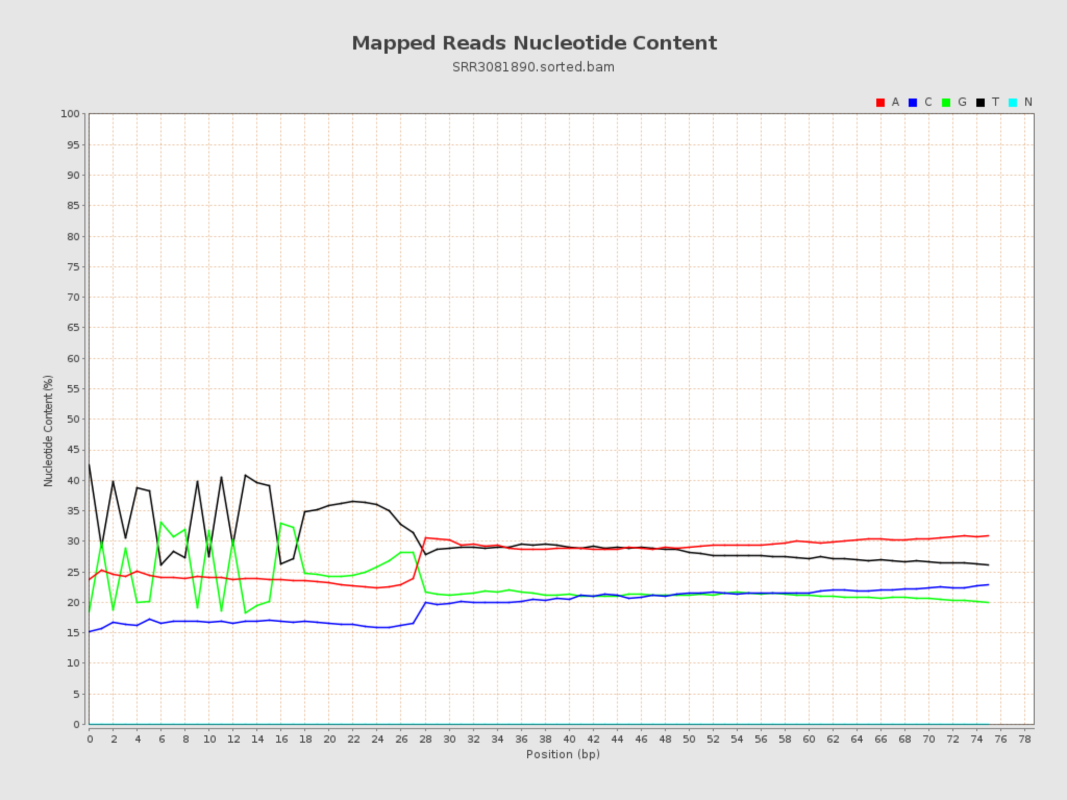
6. Results : Genome Fraction Coverage



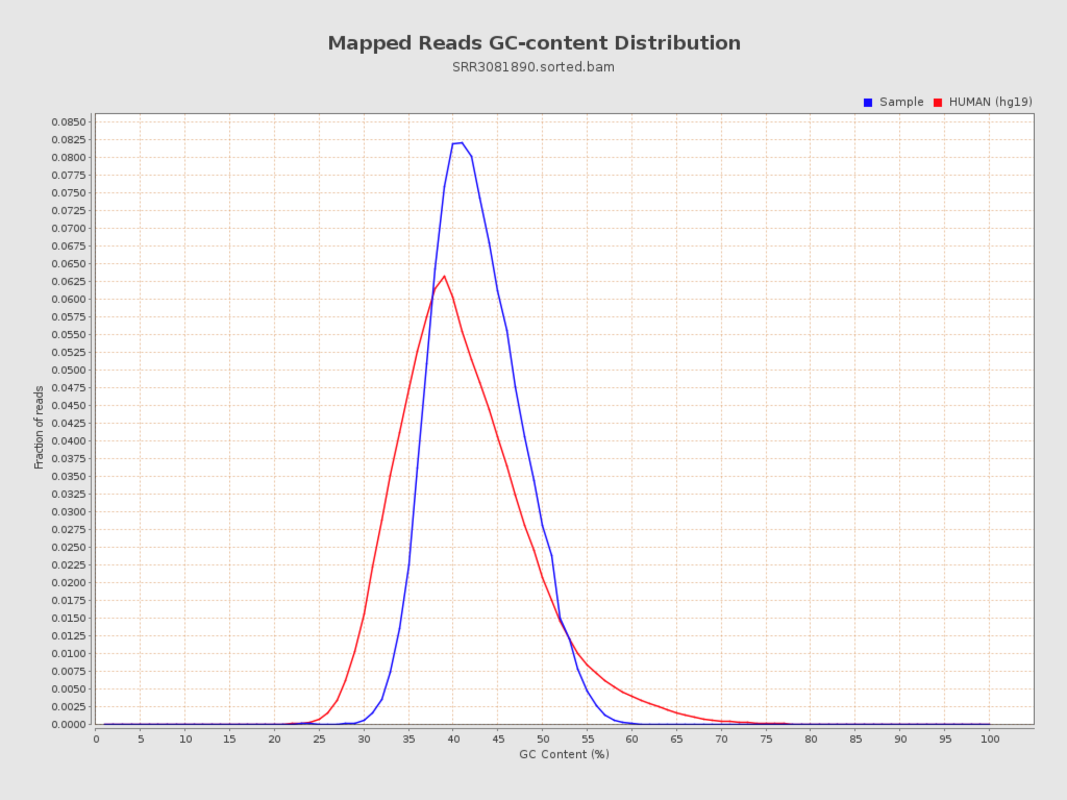
7. Results : Duplication Rate Histogram



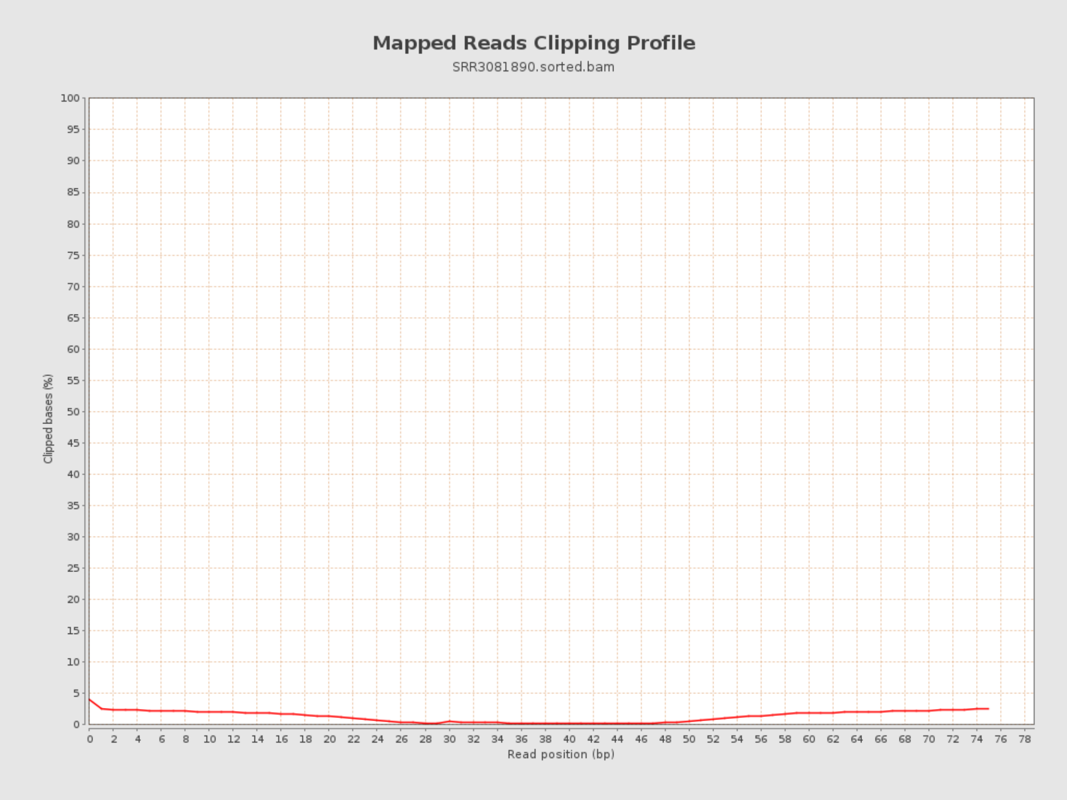
8. Results : Mapped Reads Nucleotide Content



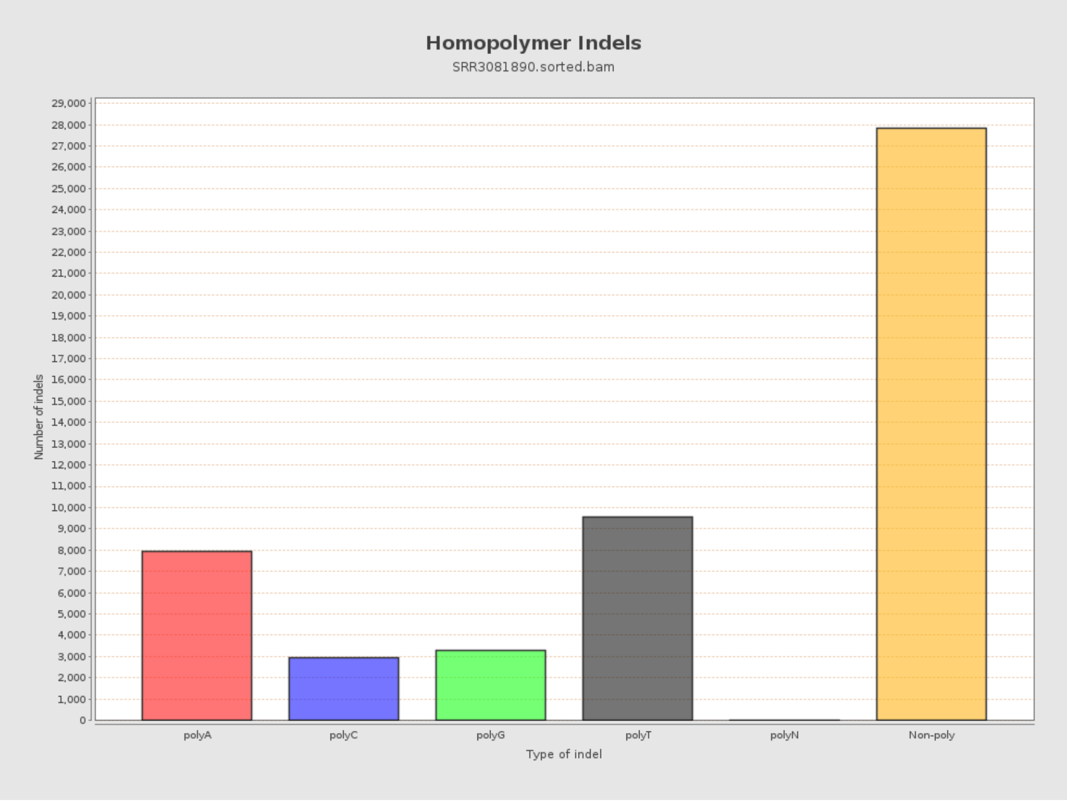
9. Results : Mapped Reads GC-content Distribution



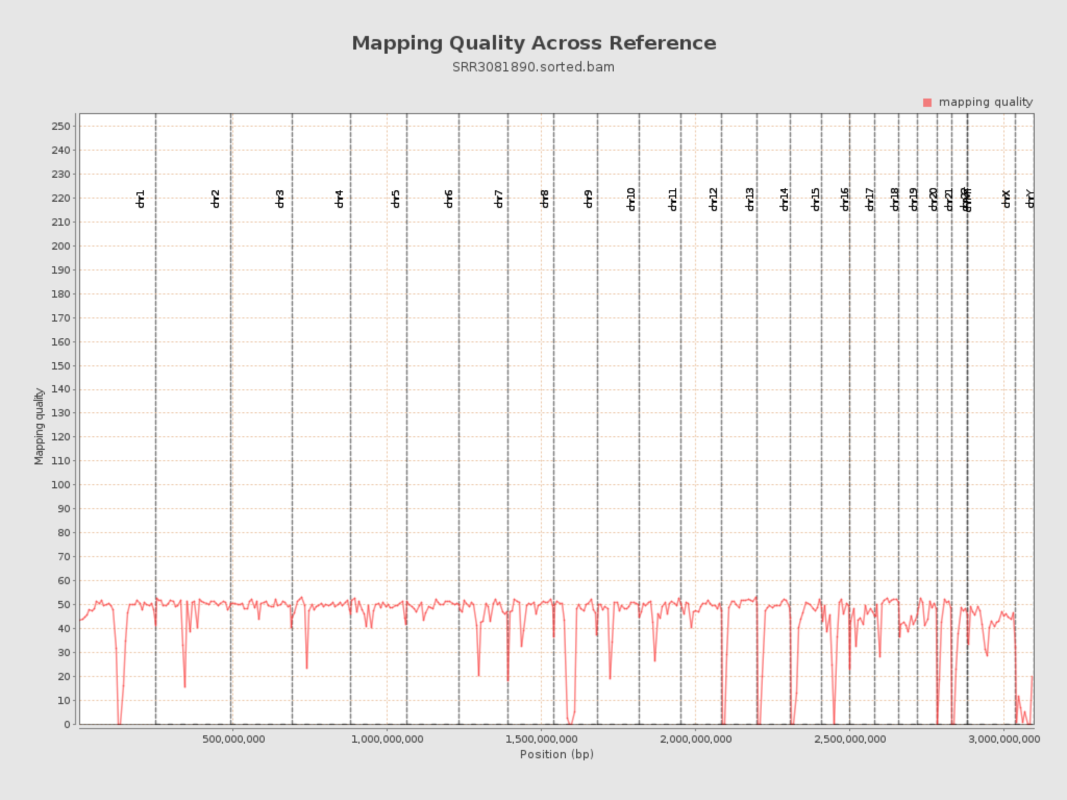
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram