Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:04:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081010.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_SRR3081010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:04:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,343,832
Mapped reads	2,740,570 / 81.96%
Unmapped reads	603,262 / 18.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,817 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	104,089 / 3.11%
Duplication rate	3.07%
Clipped reads	1,855,333 / 55.49%

2.2. ACGT Content

Number/percentage of A's	48,153,132 / 29.06%
Number/percentage of C's	33,953,044 / 20.49%
Number/percentage of T's	47,534,635 / 28.69%
Number/percentage of G's	36,065,252 / 21.76%
Number/percentage of N's	1,962 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.3571

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

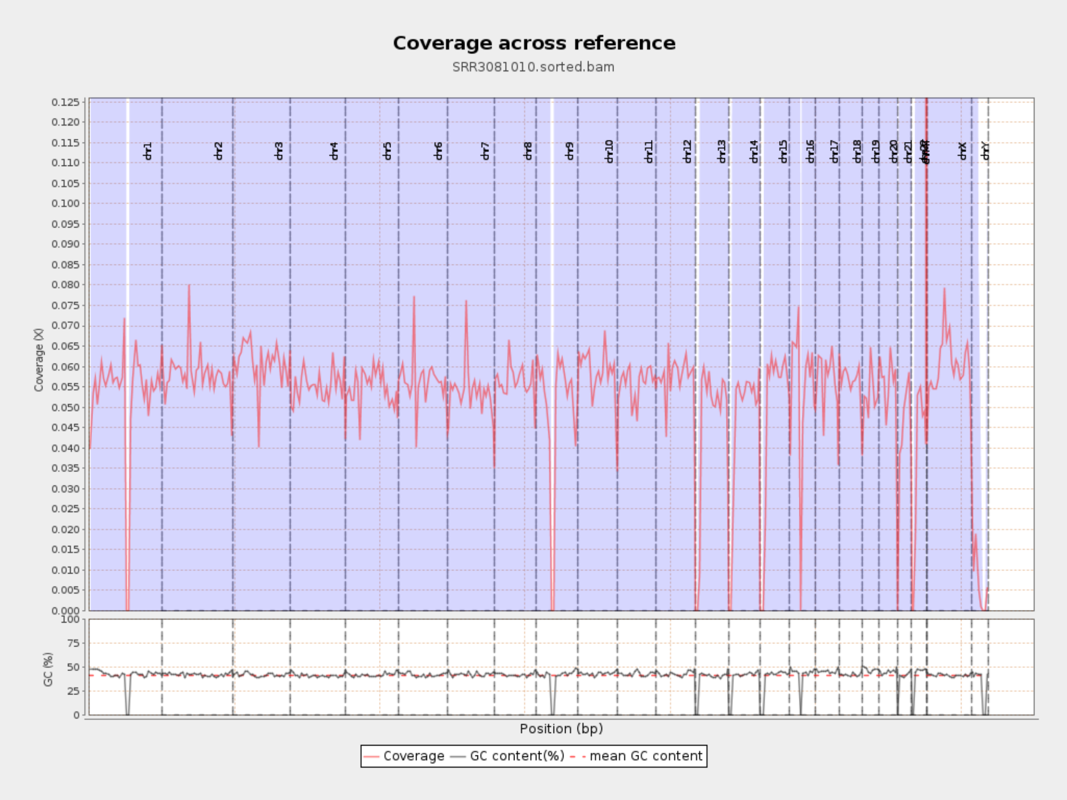
General error rate	0.76%
Mismatches	1,236,702
Insertions	11,048
Mapped reads with at least one insertion	0.4%
Deletions	30,411
Mapped reads with at least one deletion	1.1%
Homopolymer indels	45.49%

2.6. Chromosome stats

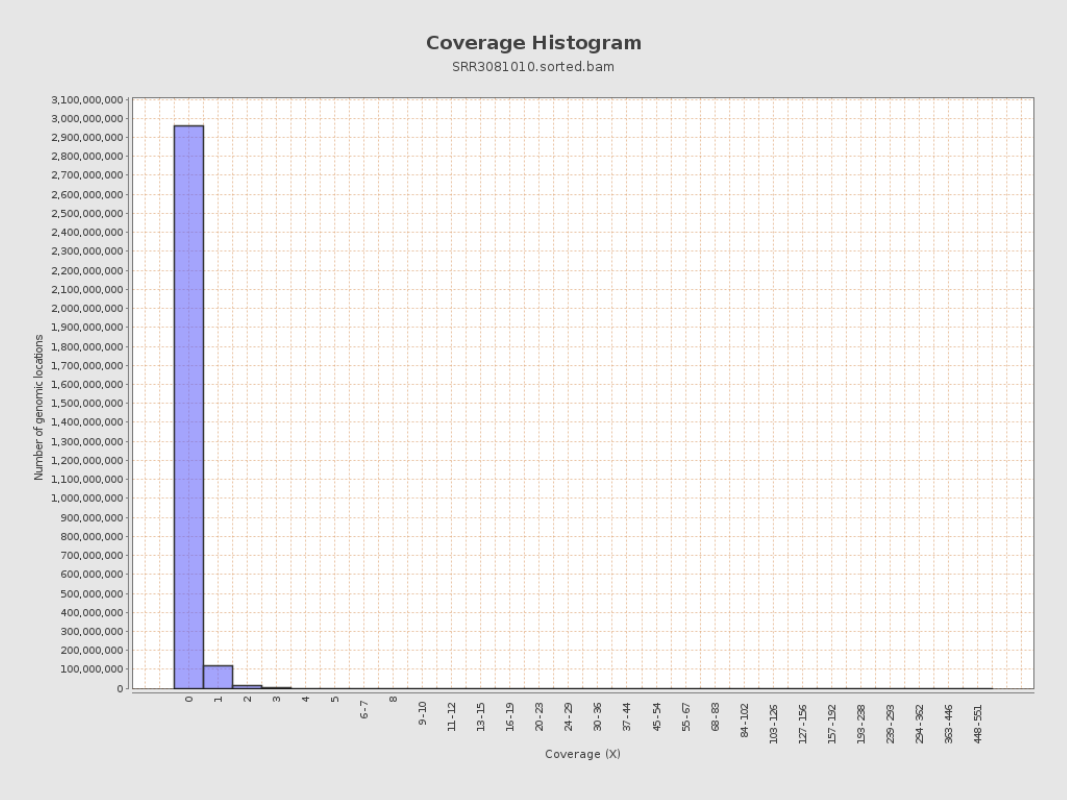
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13146692	0.0527	0.5214
chr2	243199373	14150702	0.0582	0.4111
chr3	198022430	12016413	0.0607	0.2879
chr4	191154276	10568942	0.0553	0.2858
chr5	180915260	9909234	0.0548	0.2741
chr6	171115067	9668093	0.0565	0.3492
chr7	159138663	8642153	0.0543	0.4764

chr8	146364022	8262940	0.0565	0.411
chr9	141213431	6889103	0.0488	0.343
chr10	135534747	8012377	0.0591	0.3406
chr11	135006516	7512603	0.0556	0.3212
chr12	133851895	7711516	0.0576	0.2859
chr13	115169878	5163207	0.0448	0.248
chr14	107349540	4832773	0.045	0.261
chr15	102531392	4924559	0.048	0.2732
chr16	90354753	4935530	0.0546	0.294
chr17	81195210	4556579	0.0561	0.308
chr18	78077248	4453662	0.057	0.5574
chr19	59128983	3150770	0.0533	0.4305
chr20	63025520	3500404	0.0555	0.2814
chr21	48129895	2063001	0.0429	0.2582
chr22	51304566	1802749	0.0351	0.2194
chrMT	16571	89605	5.4073	3.7487
chrX	155270560	9385953	0.0604	0.32
chrY	59373566	410540	0.0069	0.137

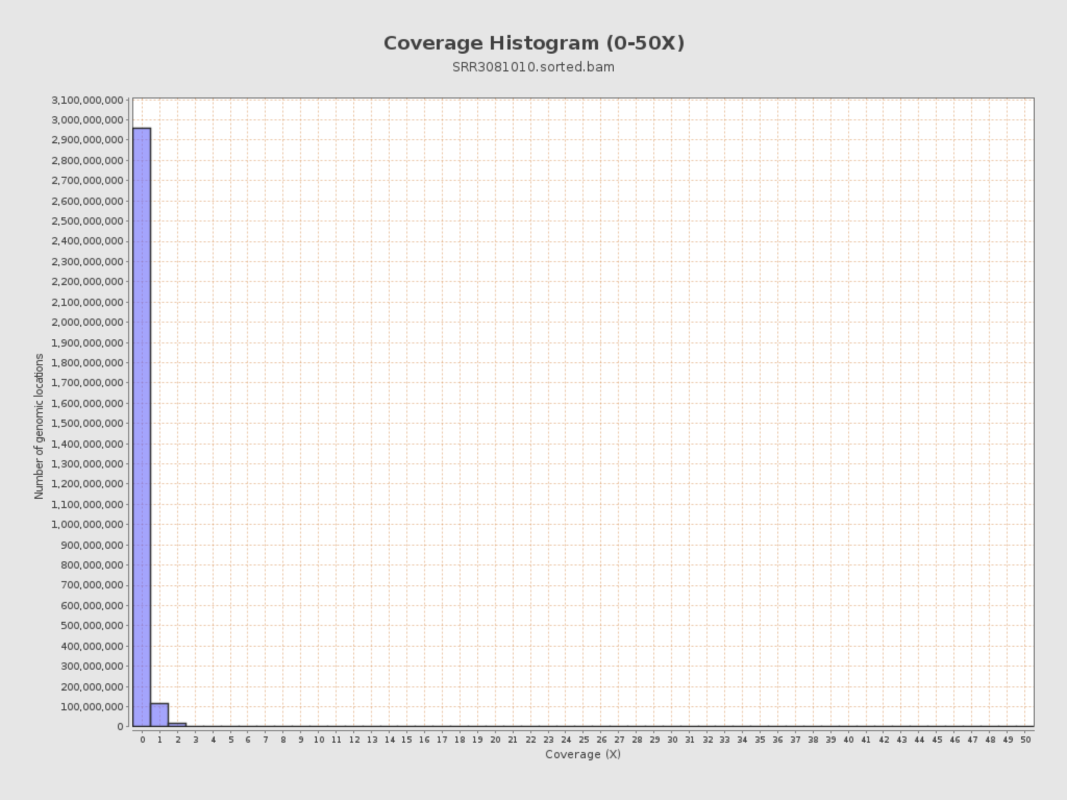
3. Results : Coverage across reference



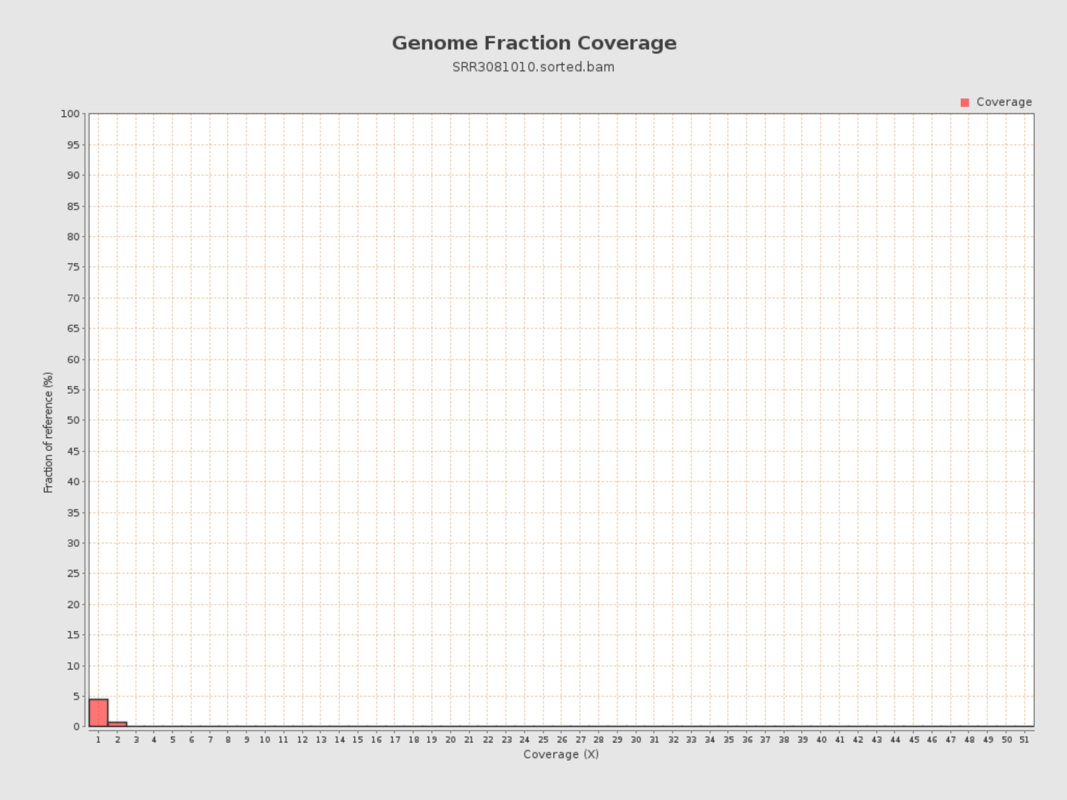
4. Results : Coverage Histogram



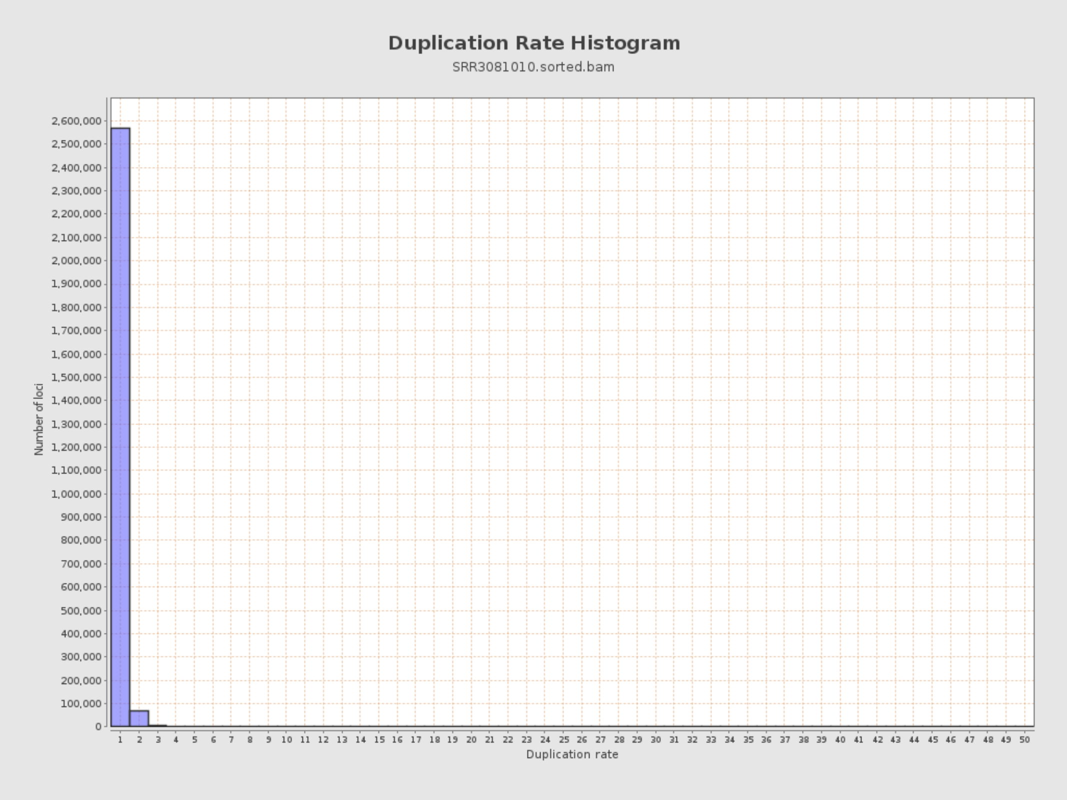
5. Results : Coverage Histogram (0-50X)



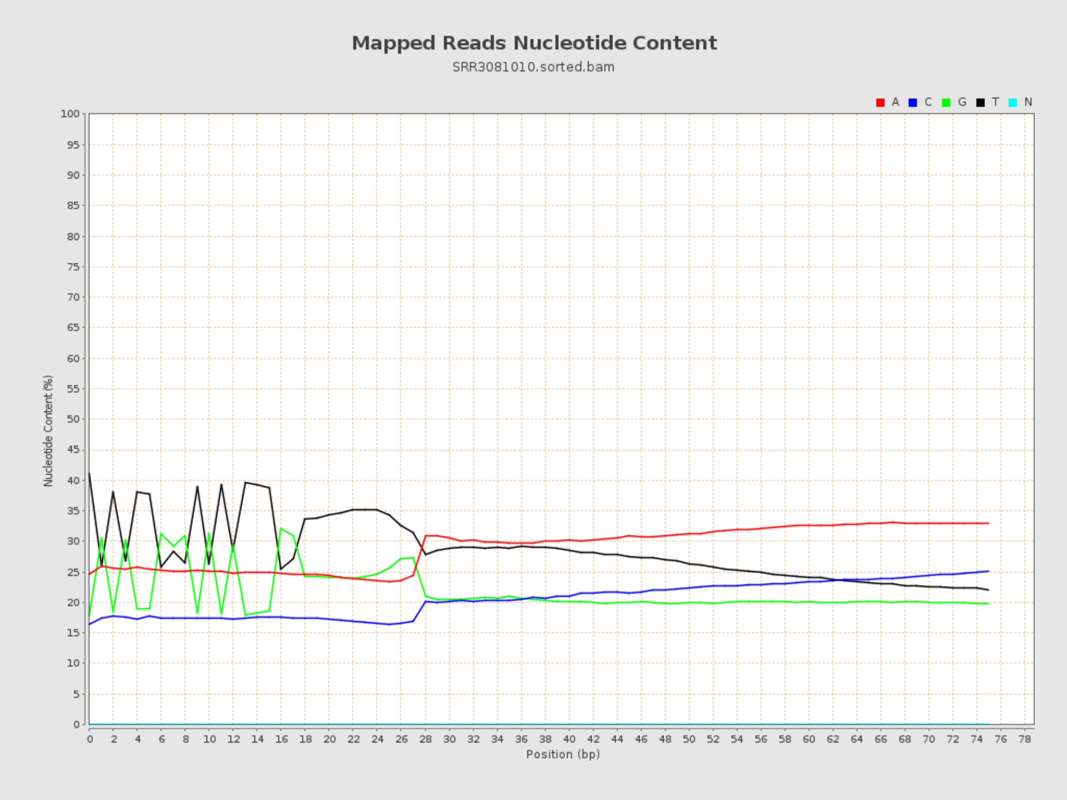
6. Results : Genome Fraction Coverage



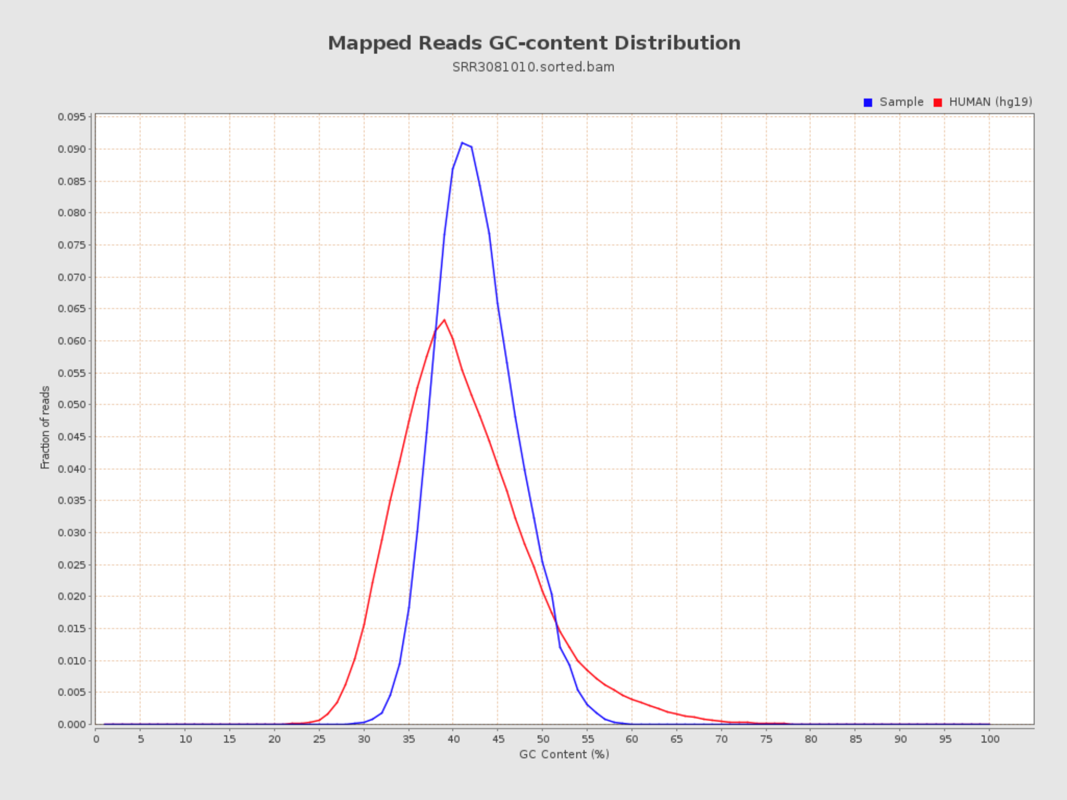
7. Results : Duplication Rate Histogram



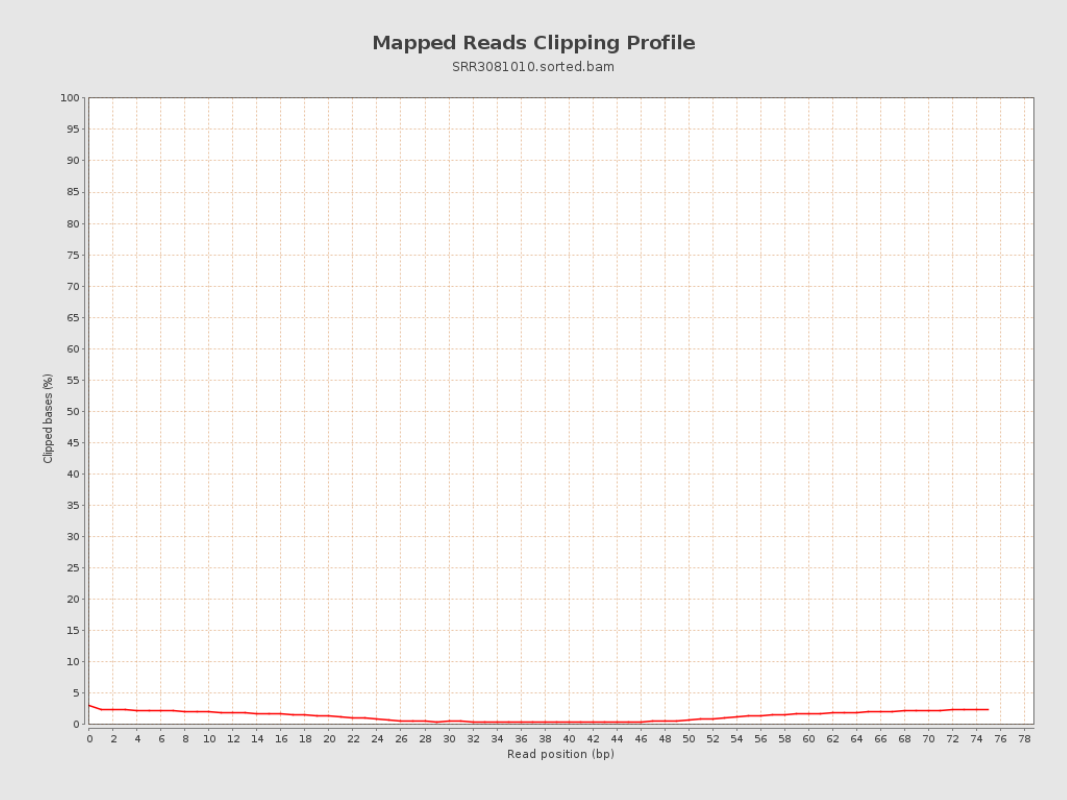
8. Results : Mapped Reads Nucleotide Content



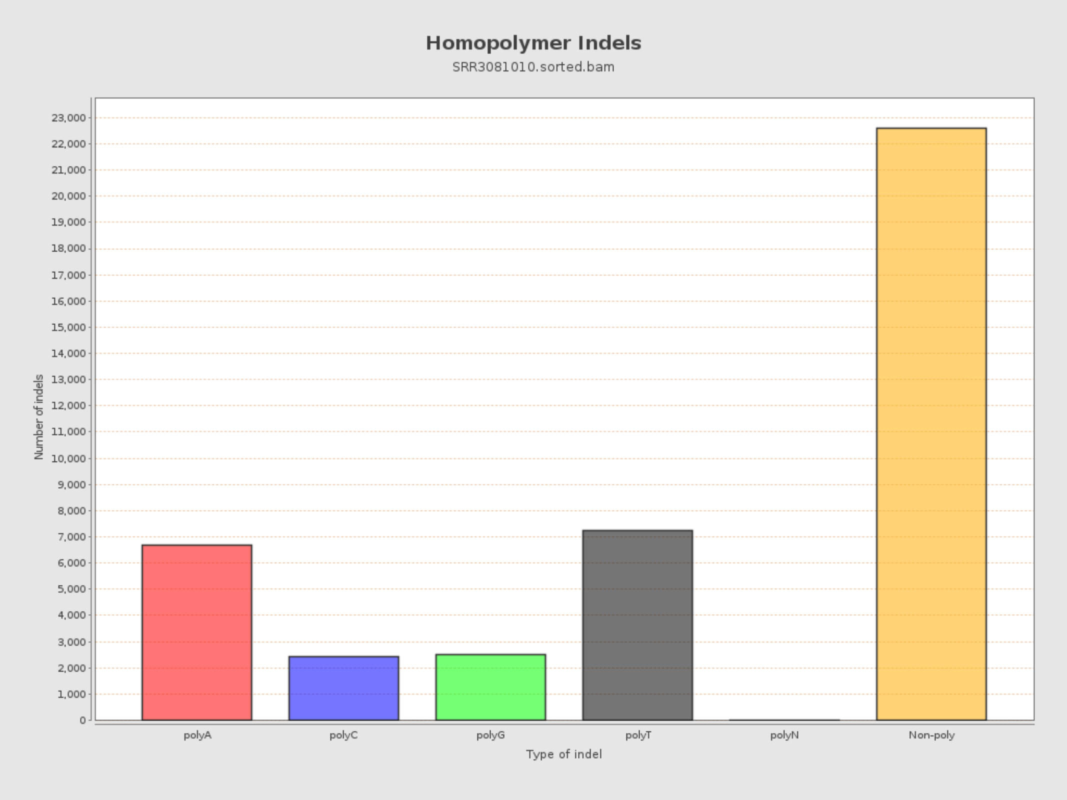
9. Results : Mapped Reads GC-content Distribution



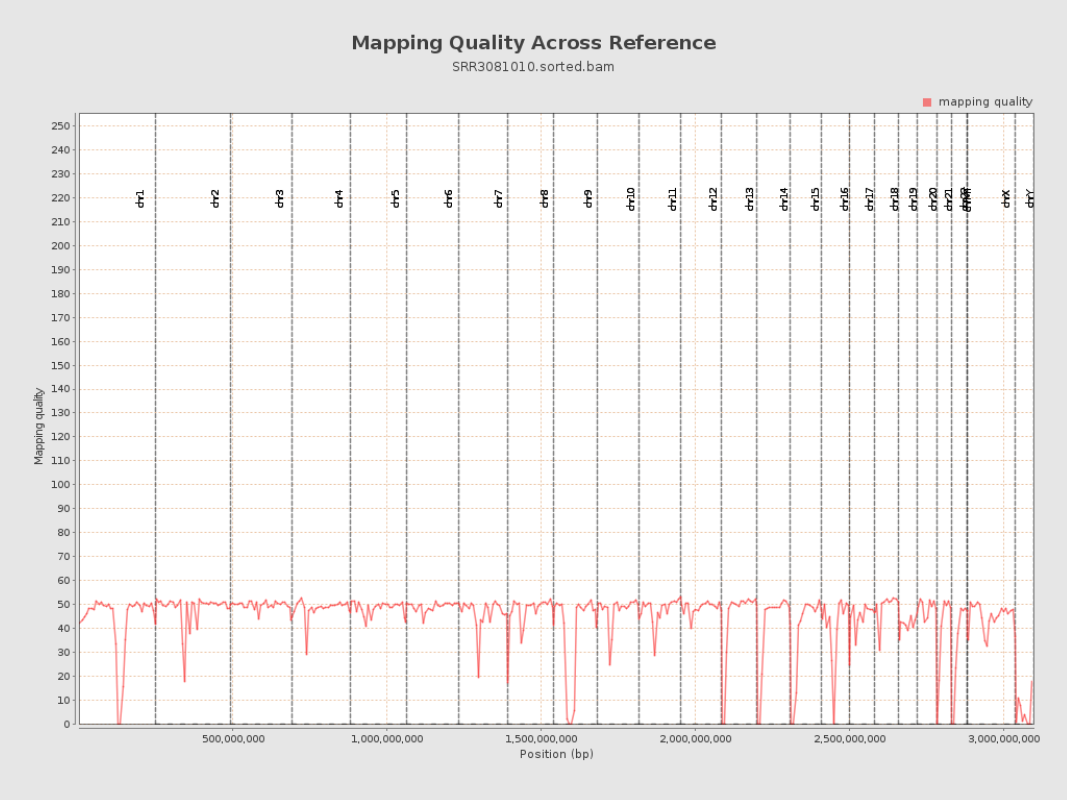
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram