Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:56:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081105.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_SRR3081105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:56:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,288,202
Mapped reads	2,108,158 / 92.13%
Unmapped reads	180,044 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,718 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	90,582 / 3.96%
Duplication rate	3.01%
Clipped reads	770,920 / 33.69%

2.2. ACGT Content

Number/percentage of A's	41,589,438 / 28.68%
Number/percentage of C's	27,127,136 / 18.71%
Number/percentage of T's	45,482,526 / 31.37%
Number/percentage of G's	30,793,499 / 21.24%
Number/percentage of N's	1,679 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.4731

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

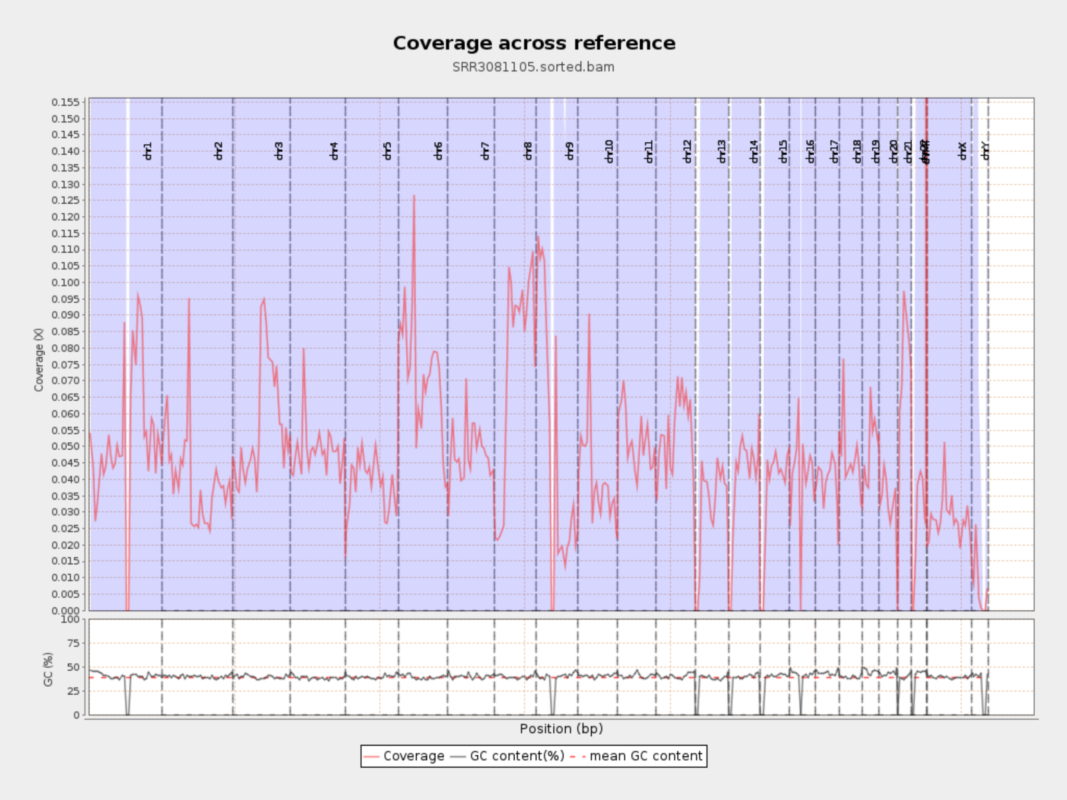
General error rate	0.93%
Mismatches	1,317,070
Insertions	12,601
Mapped reads with at least one insertion	0.59%
Deletions	34,299
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.26%

2.6. Chromosome stats

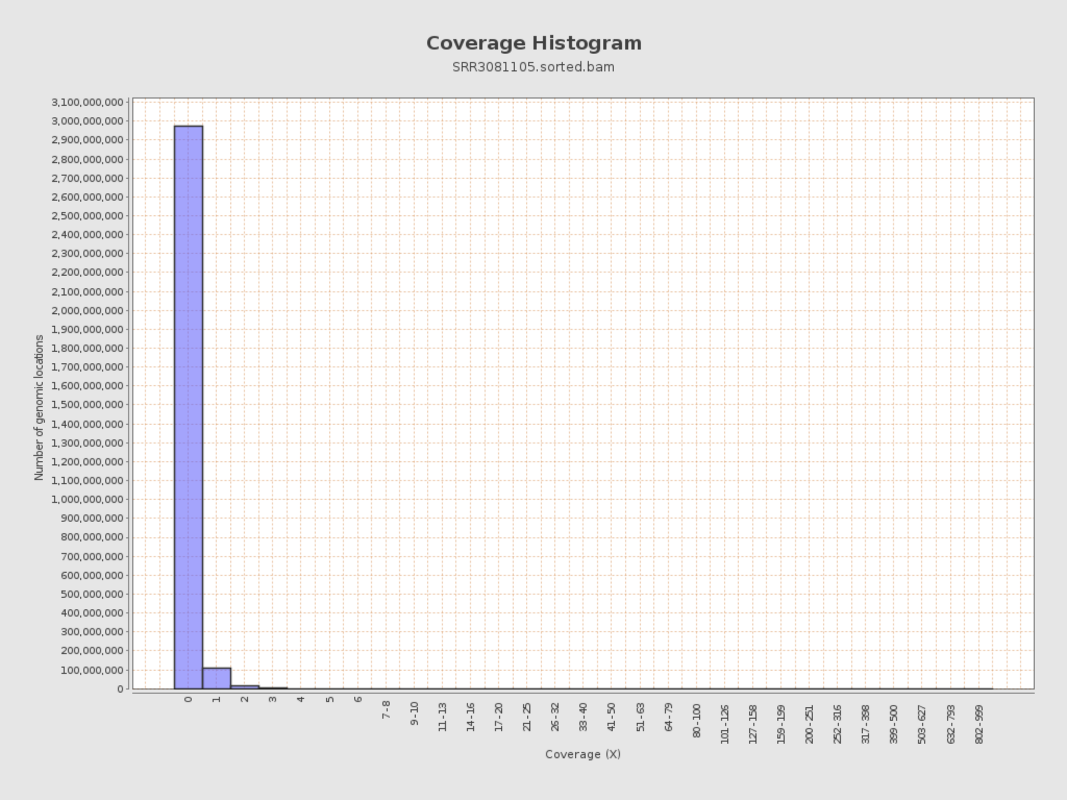
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12981032	0.0521	0.812
chr2	243199373	9827617	0.0404	0.4948
chr3	198022430	11295250	0.057	0.275
chr4	191154276	9349579	0.0489	0.2912
chr5	180915260	7034574	0.0389	0.2298
chr6	171115067	12453142	0.0728	0.5229
chr7	159138663	7694039	0.0483	0.4347

chr8	146364022	10928901	0.0747	0.5825
chr9	141213431	6737590	0.0477	0.5939
chr10	135534747	5598299	0.0413	0.4718
chr11	135006516	6946098	0.0515	0.3683
chr12	133851895	7209516	0.0539	0.2895
chr13	115169878	3646457	0.0317	0.1981
chr14	107349540	4205429	0.0392	0.3407
chr15	102531392	3683417	0.0359	0.2125
chr16	90354753	3689696	0.0408	0.3534
chr17	81195210	3197757	0.0394	0.2398
chr18	78077248	3705821	0.0475	1.1595
chr19	59128983	2934616	0.0496	0.5884
chr20	63025520	2161543	0.0343	0.2491
chr21	48129895	3428337	0.0712	0.3796
chr22	51304566	1321248	0.0258	0.1772
chrMT	16571	227738	13.7432	7.9912
chrX	155270560	4388555	0.0283	0.2485
chrY	59373566	405129	0.0068	0.202

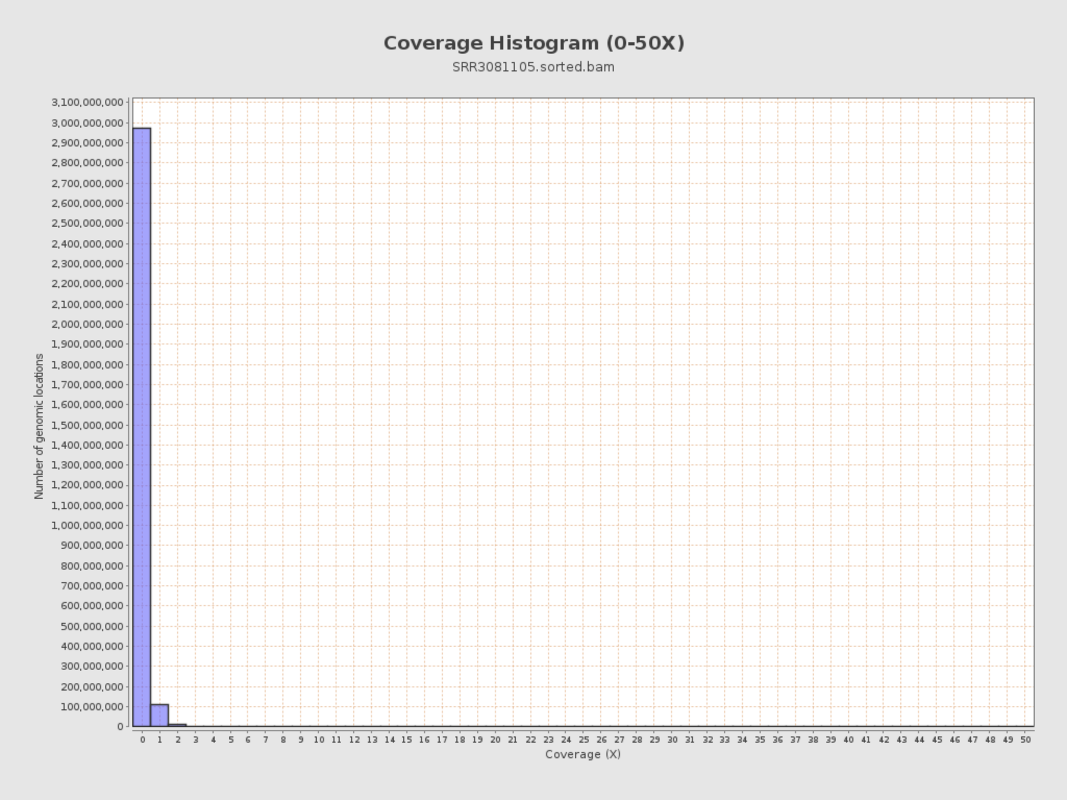
3. Results : Coverage across reference



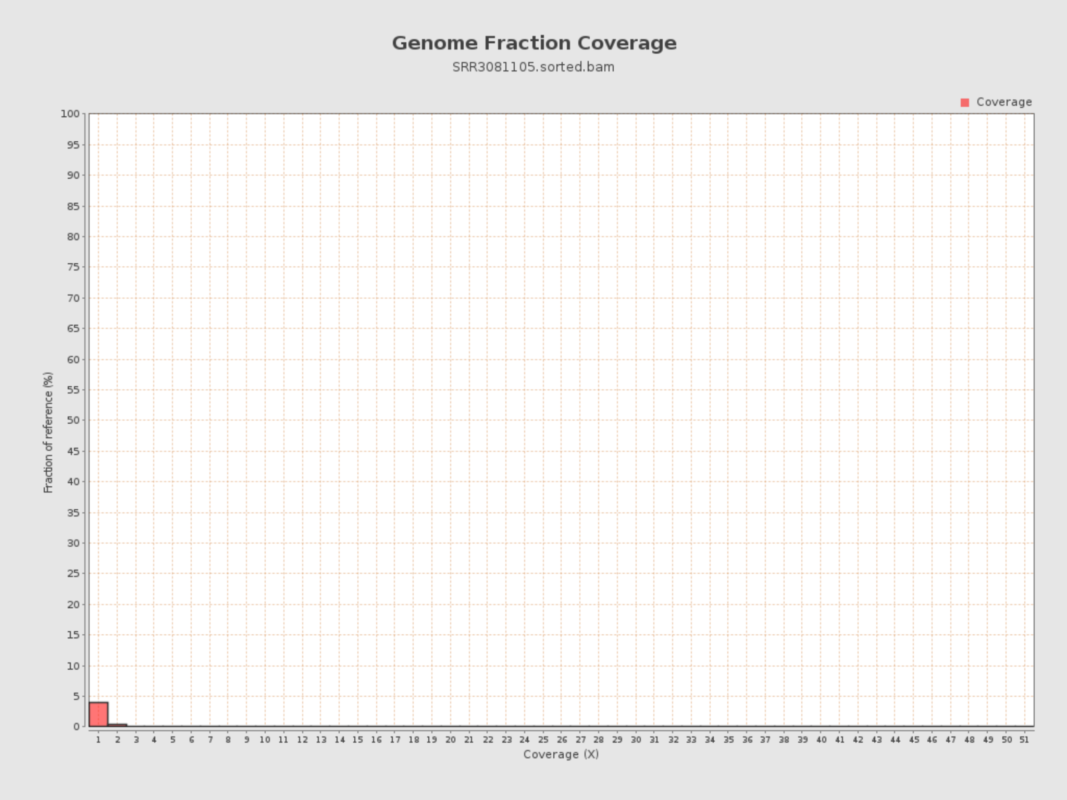
4. Results : Coverage Histogram



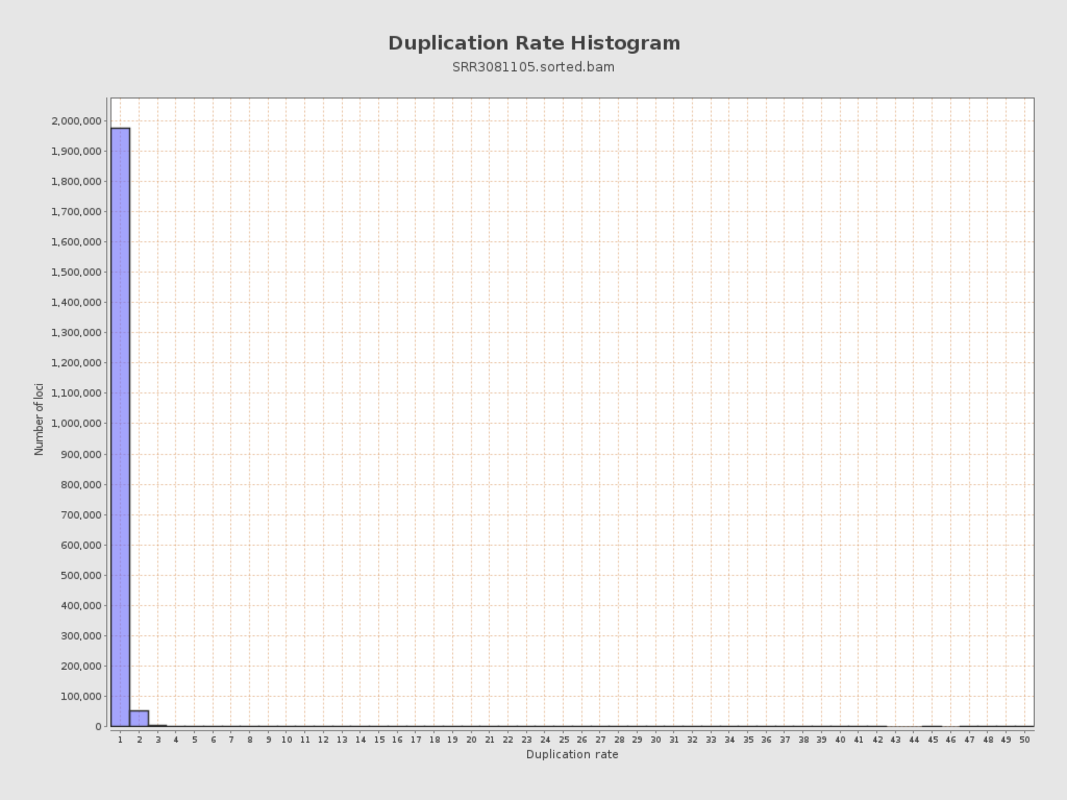
5. Results : Coverage Histogram (0-50X)



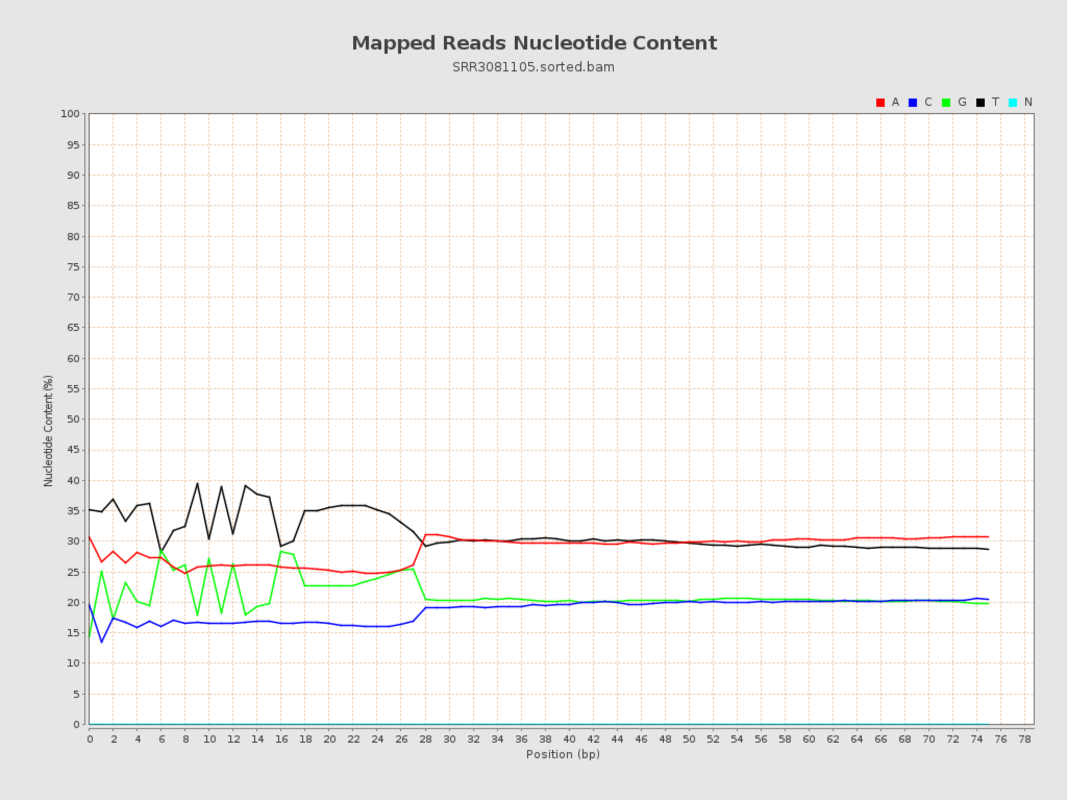
6. Results : Genome Fraction Coverage



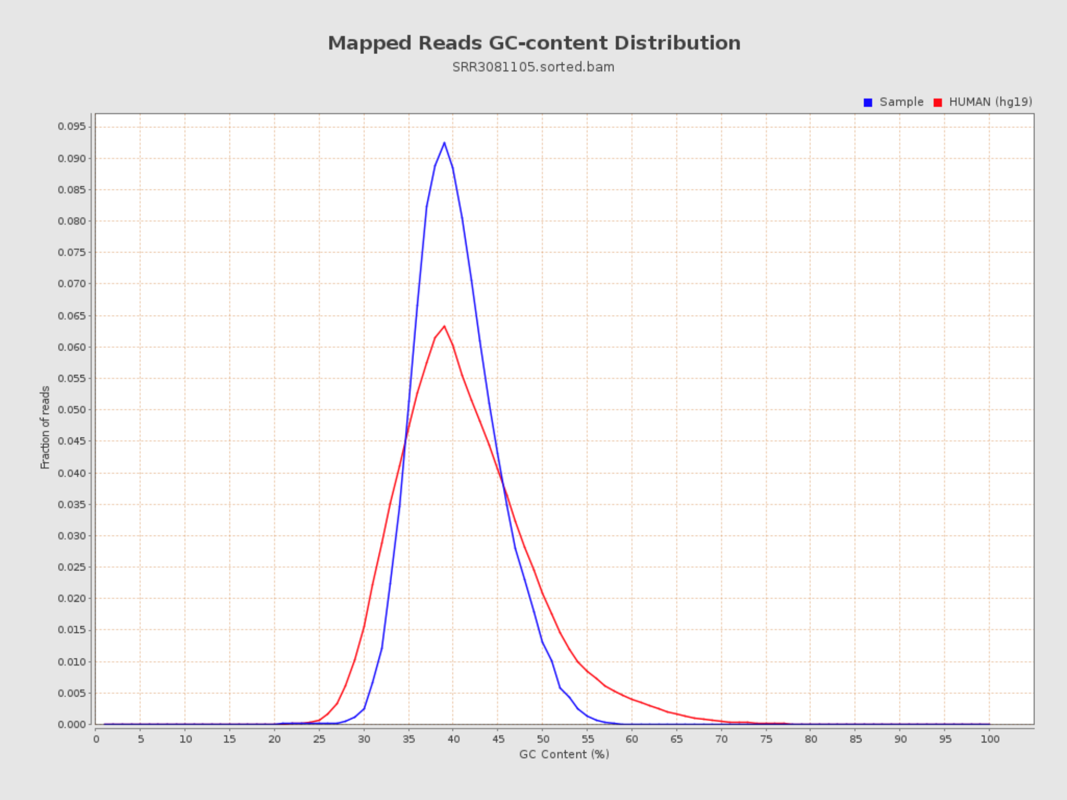
7. Results : Duplication Rate Histogram



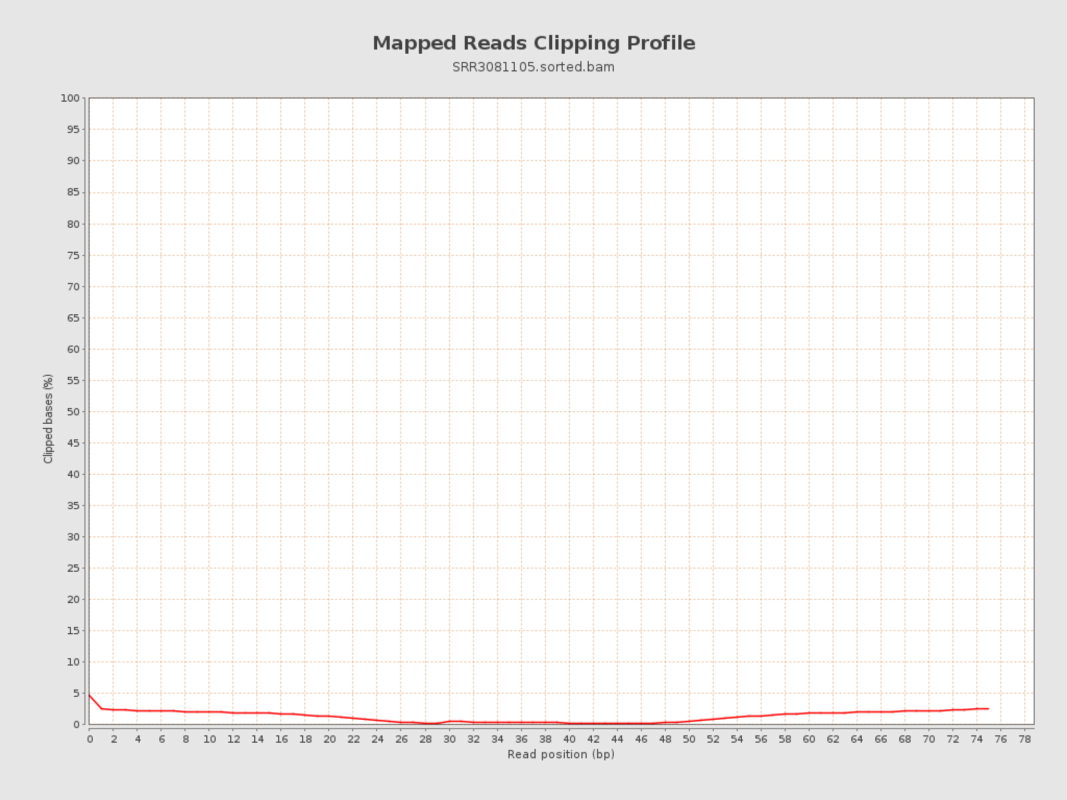
8. Results : Mapped Reads Nucleotide Content



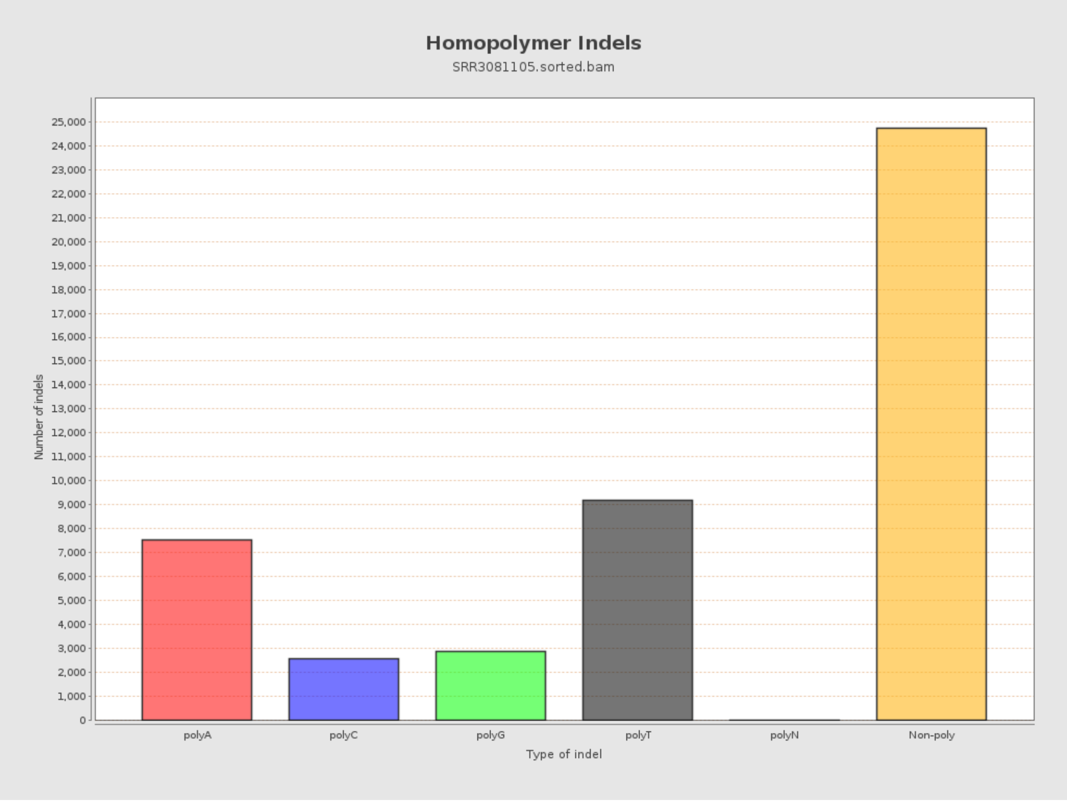
9. Results : Mapped Reads GC-content Distribution



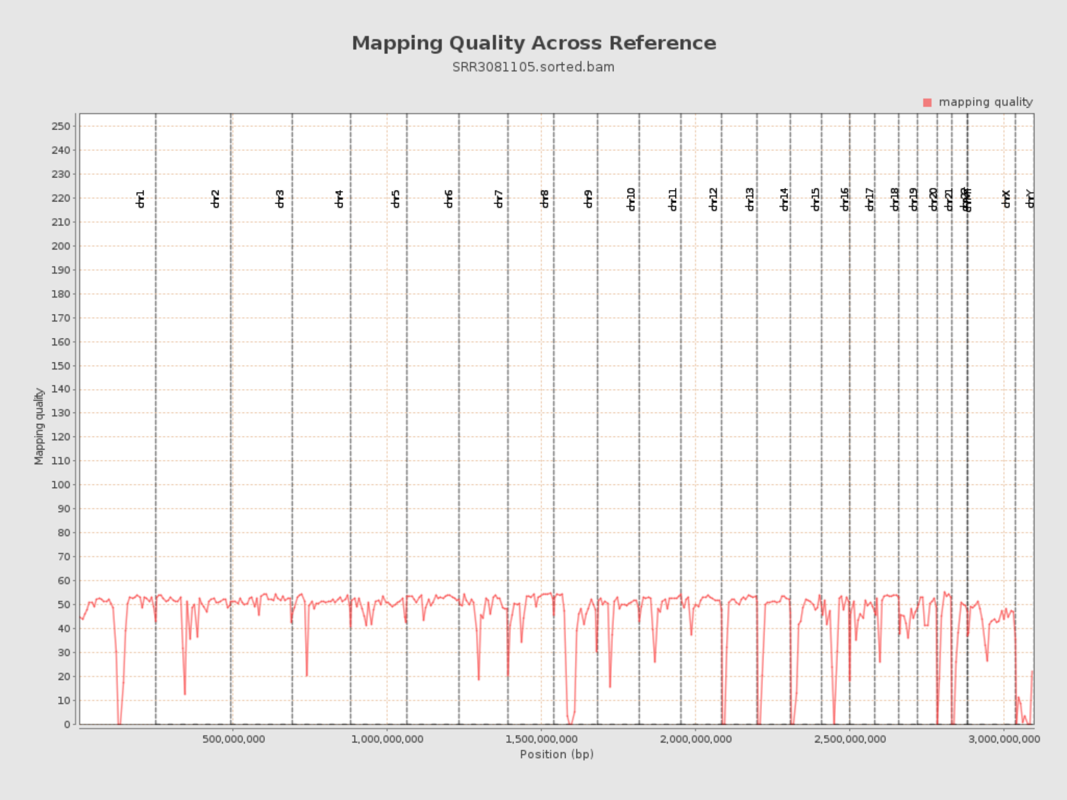
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram