Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:50:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081939.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_SRR3081939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081939.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:50:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,704,821
Mapped reads	2,471,470 / 91.37%
Unmapped reads	233,351 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,287 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	124,131 / 4.59%
Duplication rate	3.4%
Clipped reads	962,326 / 35.58%

2.2. ACGT Content

Number/percentage of A's	47,171,935 / 28.1%
Number/percentage of C's	31,131,942 / 18.55%
Number/percentage of T's	52,493,886 / 31.27%
Number/percentage of G's	37,038,591 / 22.07%
Number/percentage of N's	21,414 / 0.01%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0542

Standard Deviation	0.6104

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

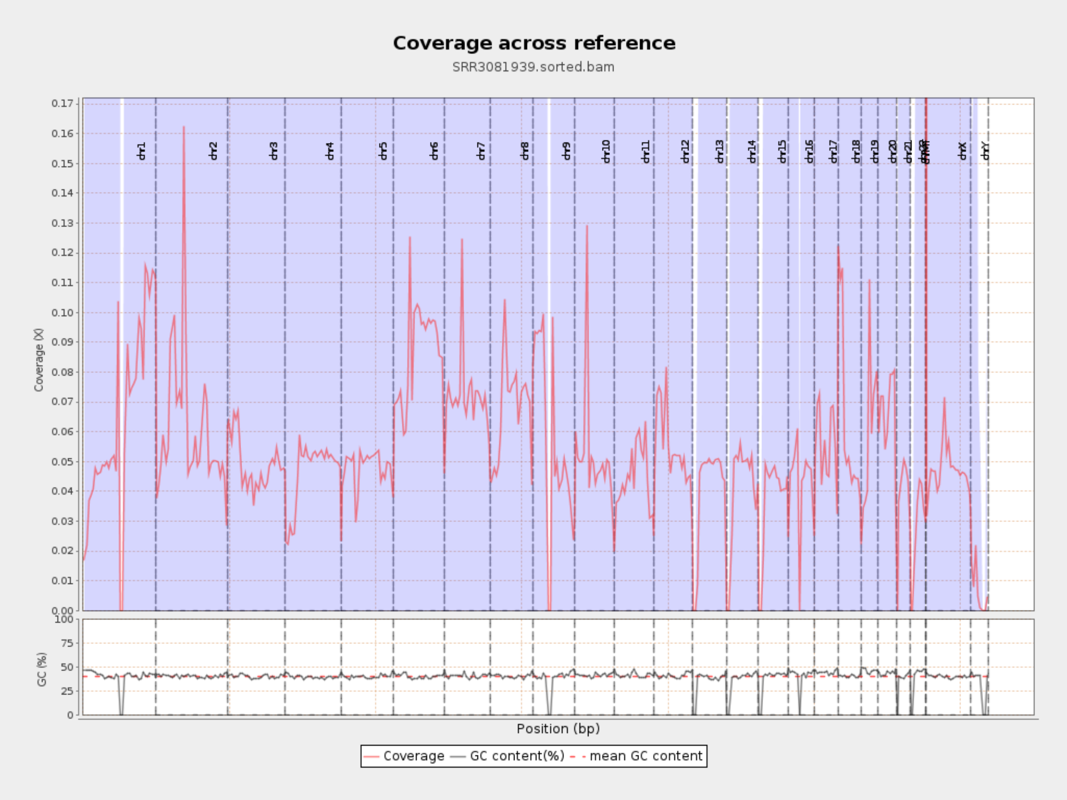
General error rate	0.81%
Mismatches	1,339,780
Insertions	12,799
Mapped reads with at least one insertion	0.51%
Deletions	34,824
Mapped reads with at least one deletion	1.39%
Homopolymer indels	46.86%

2.6. Chromosome stats

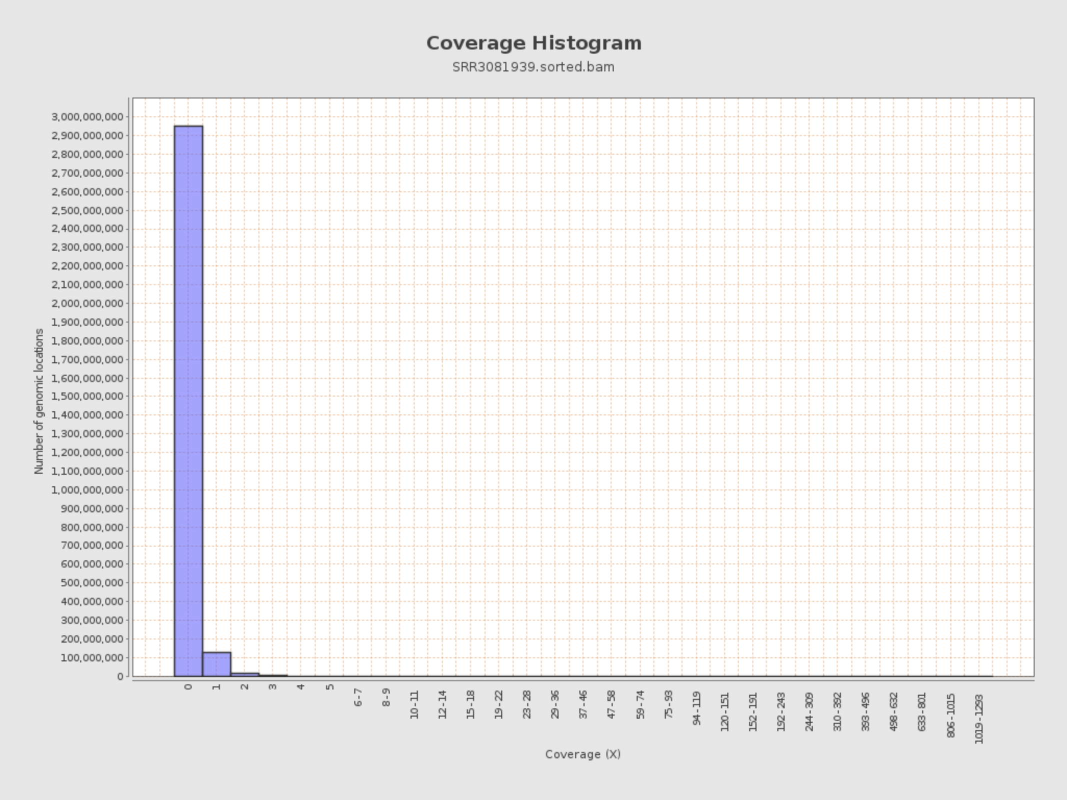
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15807129	0.0634	1.1497
chr2	243199373	15063584	0.0619	0.8795
chr3	198022430	9772104	0.0493	0.254
chr4	191154276	8906231	0.0466	0.2813
chr5	180915260	8617119	0.0476	0.2497
chr6	171115067	14879820	0.087	0.4817
chr7	159138663	11449800	0.0719	0.9192

chr8	146364022	9929223	0.0678	0.6836
chr9	141213431	7985348	0.0565	0.6814
chr10	135534747	7095209	0.0523	0.6158
chr11	135006516	6046590	0.0448	0.3972
chr12	133851895	7366198	0.055	0.2826
chr13	115169878	4624981	0.0402	0.2224
chr14	107349540	4374884	0.0408	0.2889
chr15	102531392	3723494	0.0363	0.2235
chr16	90354753	3799266	0.042	0.303
chr17	81195210	4588438	0.0565	0.3297
chr18	78077248	4929342	0.0631	1.0797
chr19	59128983	3573043	0.0604	0.8728
chr20	63025520	4299296	0.0682	0.311
chr21	48129895	1848531	0.0384	0.2665
chr22	51304566	1394141	0.0272	0.1814
chrMT	16571	96108	5.7998	3.6374
chrX	155270560	7355760	0.0474	0.3365
chrY	59373566	393689	0.0066	0.1917

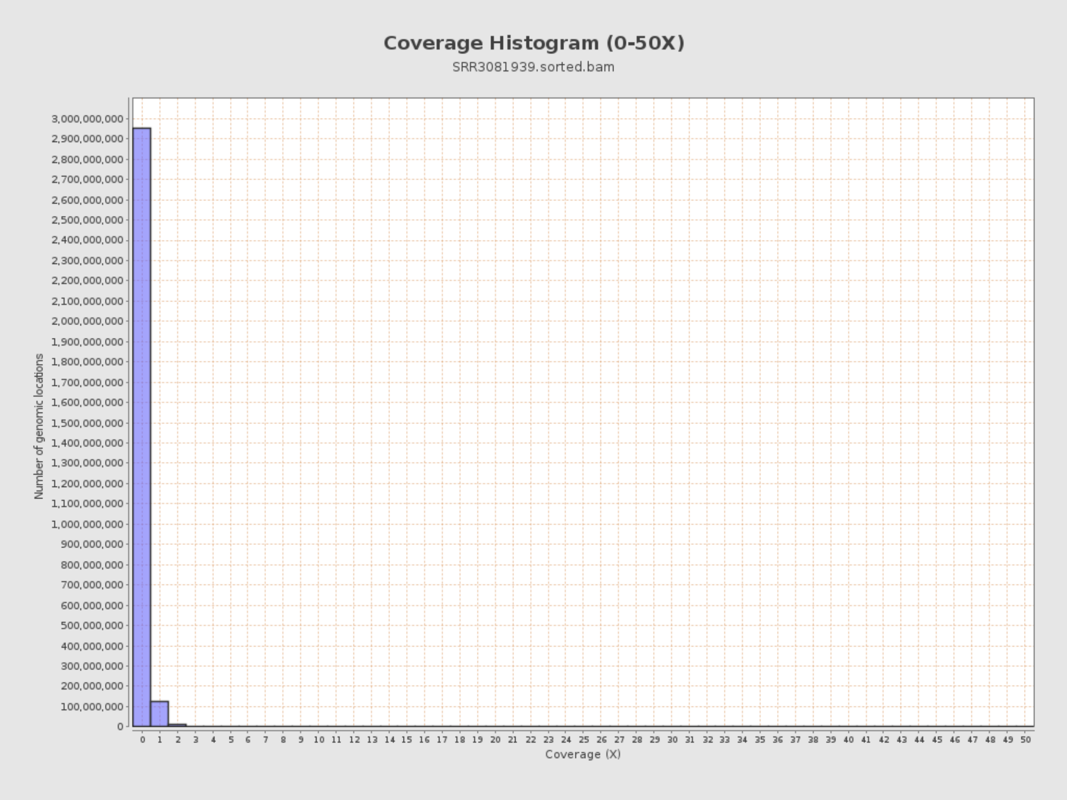
3. Results : Coverage across reference



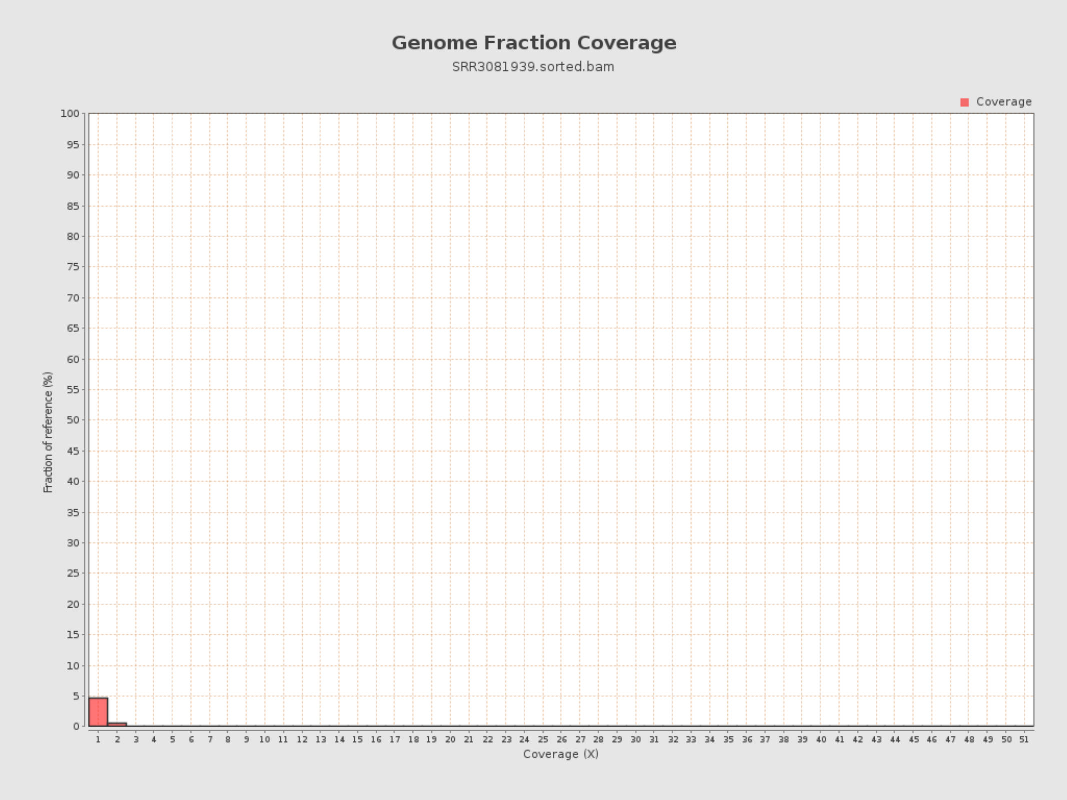
4. Results : Coverage Histogram



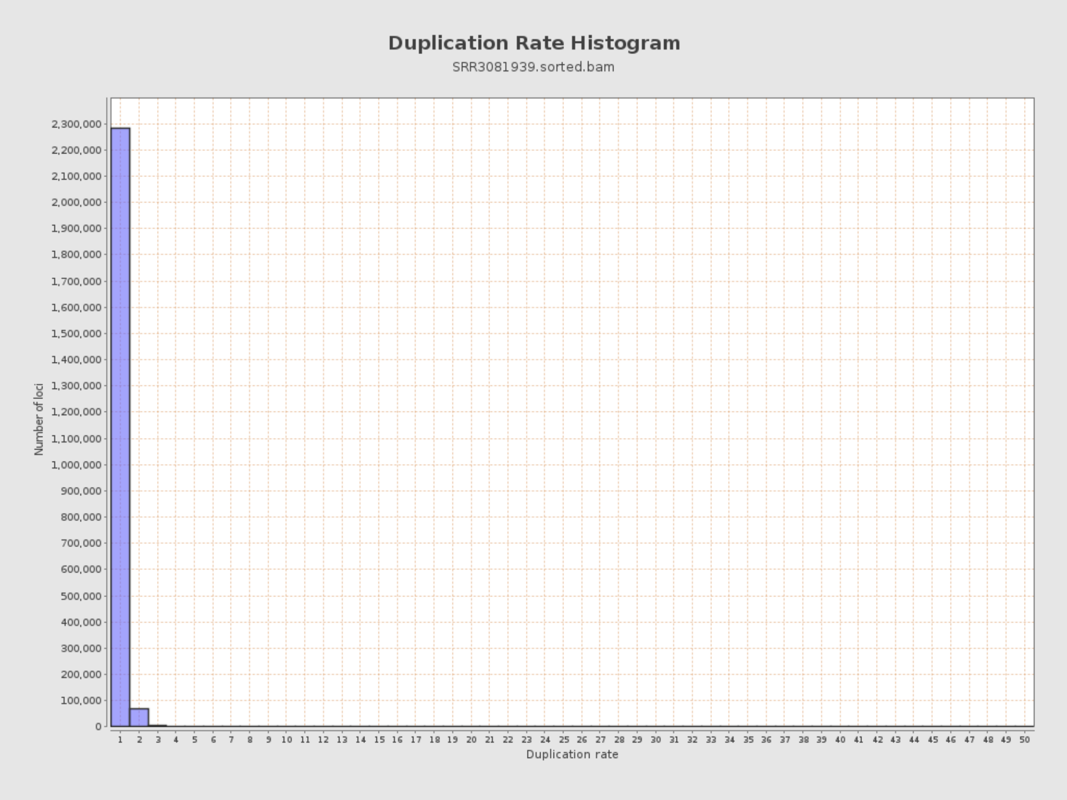
5. Results : Coverage Histogram (0-50X)



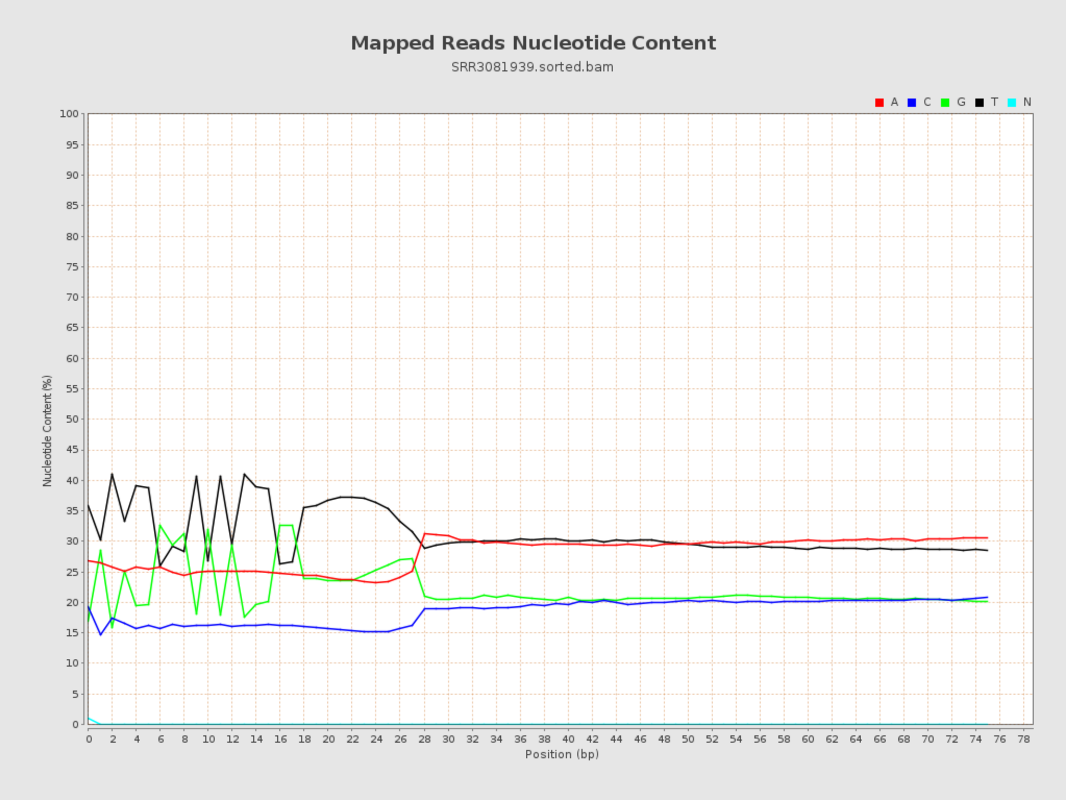
6. Results : Genome Fraction Coverage



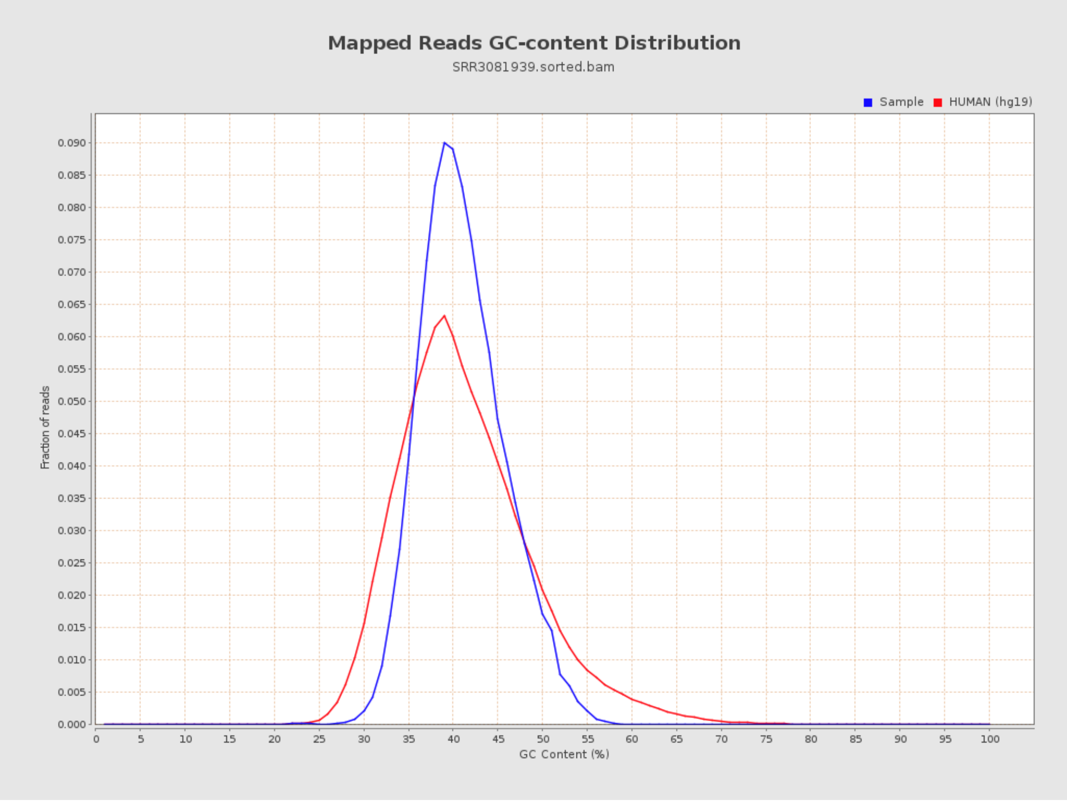
7. Results : Duplication Rate Histogram



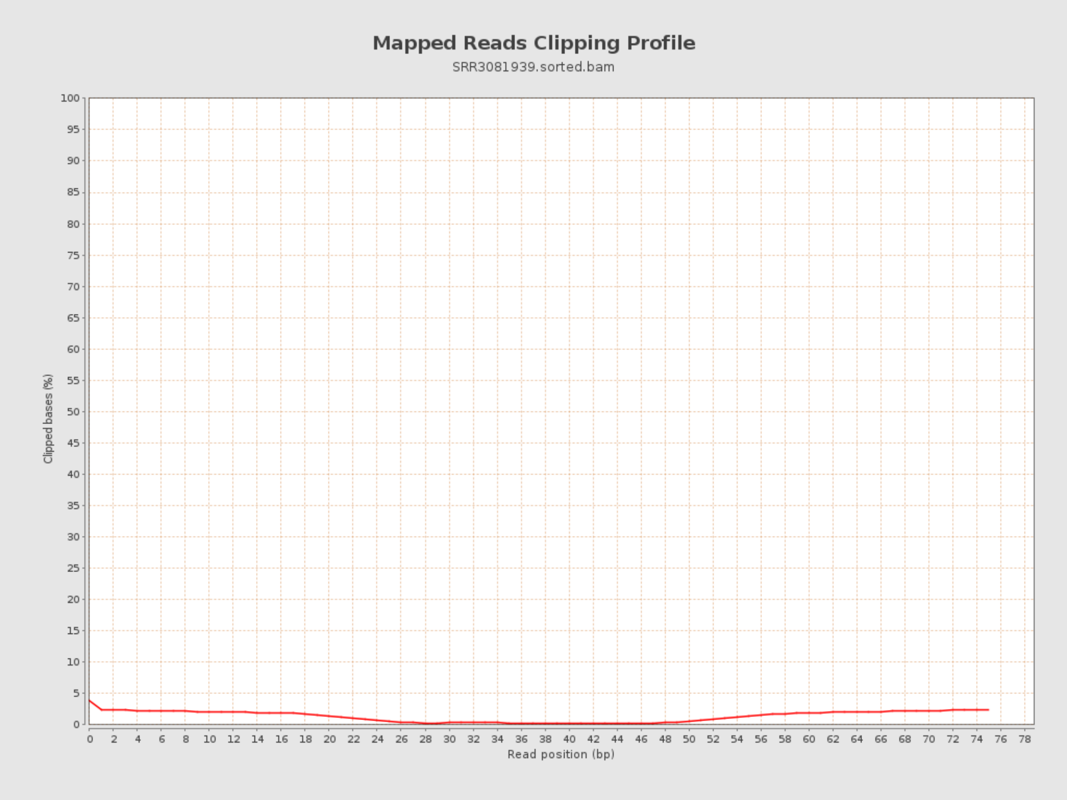
8. Results : Mapped Reads Nucleotide Content



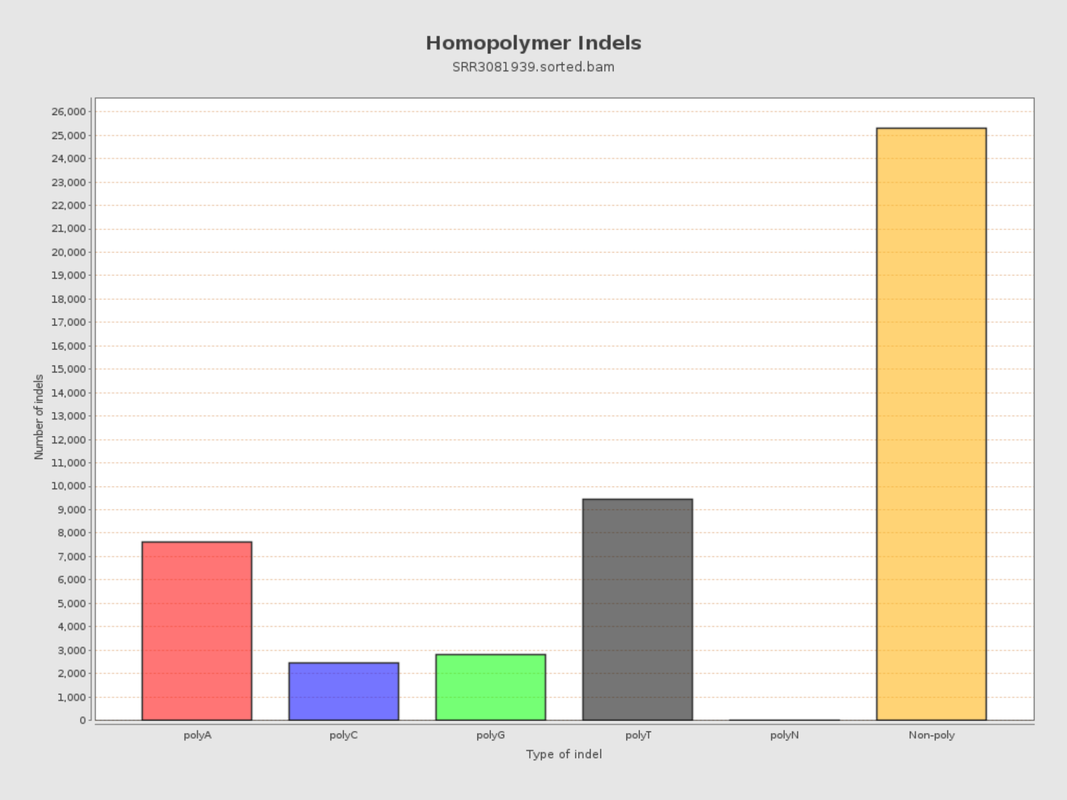
9. Results : Mapped Reads GC-content Distribution



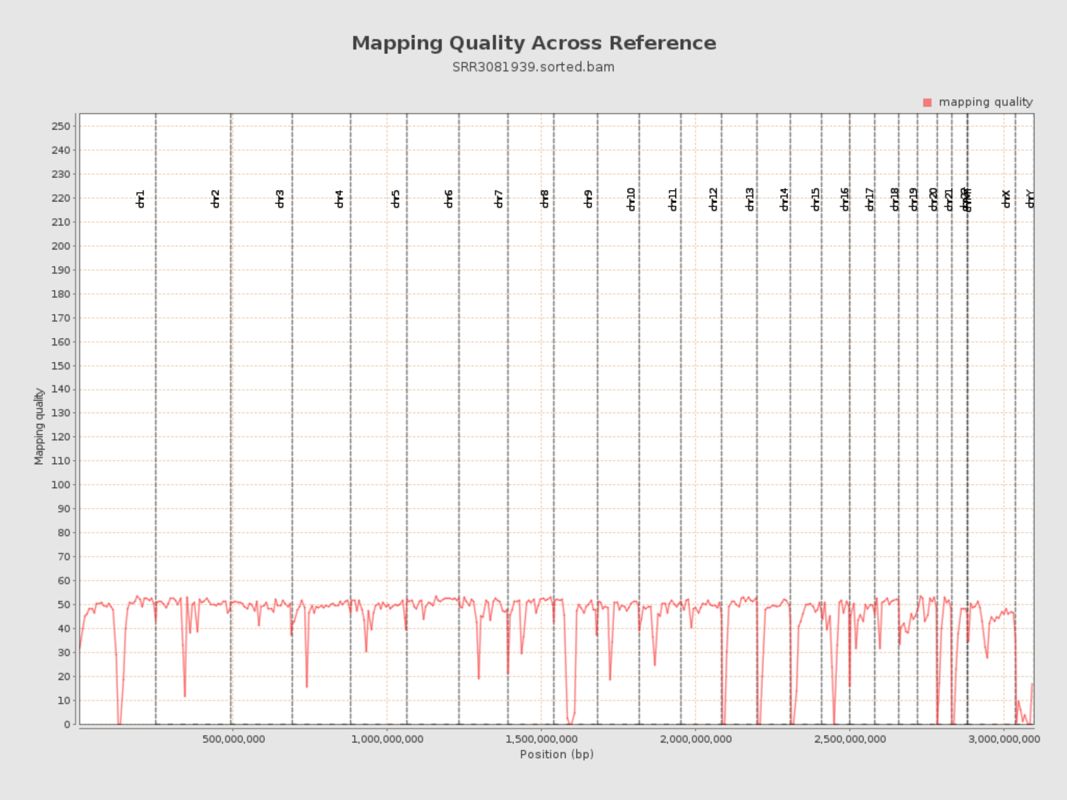
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram