Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:29:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081239.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_SRR3081239 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081239.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:29:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081239.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,681,005
Mapped reads	2,321,581 / 86.59%
Unmapped reads	359,424 / 13.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,571 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	147,755 / 5.51%
Duplication rate	5.29%
Clipped reads	1,333,473 / 49.74%

2.2. ACGT Content

Number/percentage of A's	42,965,386 / 28.84%
Number/percentage of C's	29,111,929 / 19.54%
Number/percentage of T's	45,186,831 / 30.33%
Number/percentage of G's	31,707,222 / 21.28%
Number/percentage of N's	18,386 / 0.01%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.3541

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

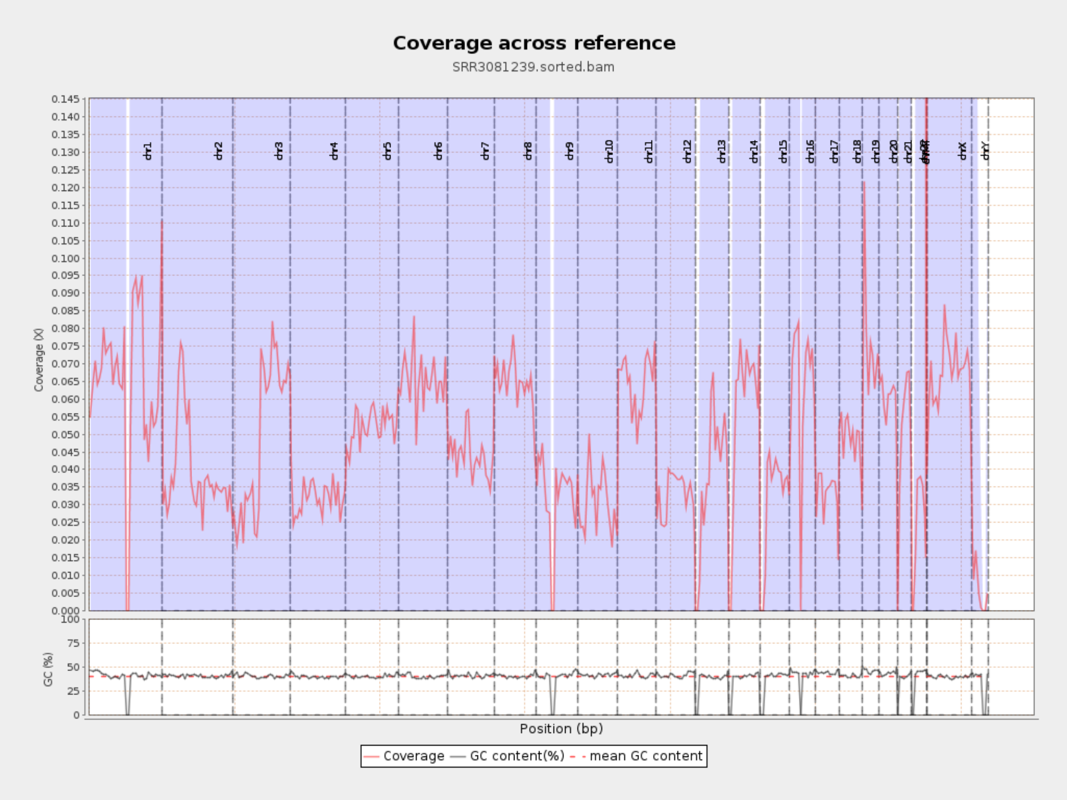
General error rate	0.93%
Mismatches	1,369,517
Insertions	11,573
Mapped reads with at least one insertion	0.49%
Deletions	34,143
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.62%

2.6. Chromosome stats

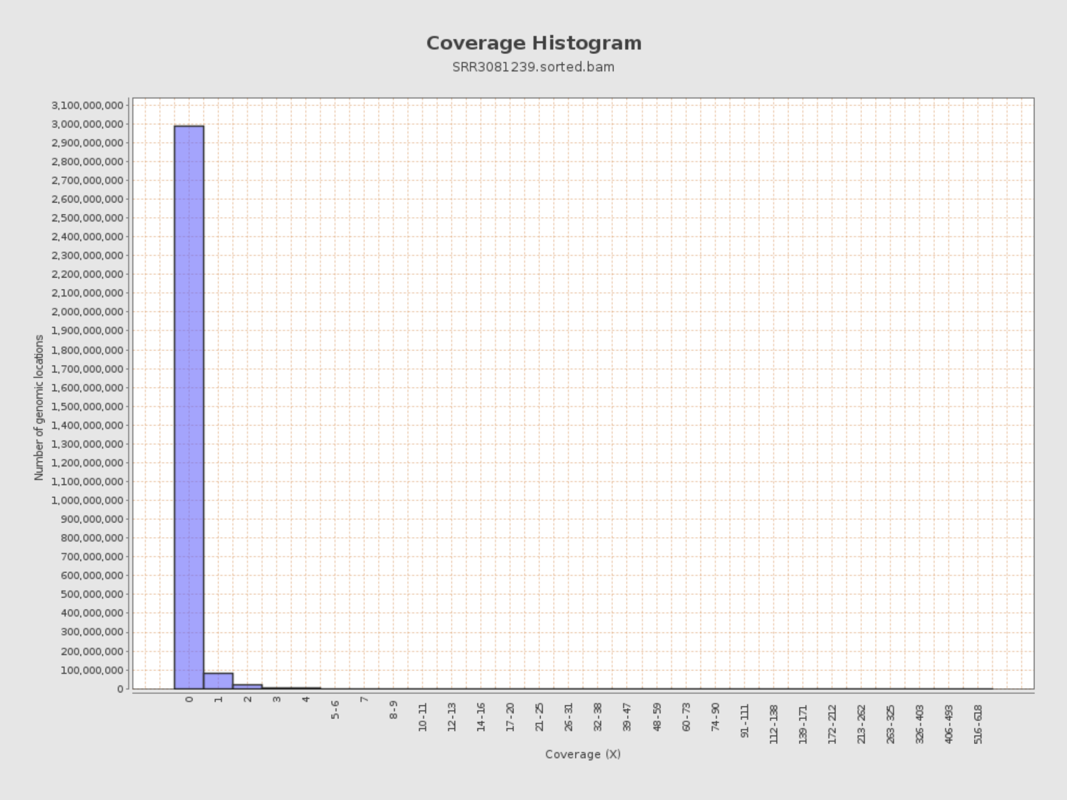
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16169145	0.0649	0.5629
chr2	243199373	9638820	0.0396	0.3821
chr3	198022430	9611684	0.0485	0.2879
chr4	191154276	6095845	0.0319	0.2355
chr5	180915260	9472343	0.0524	0.2982
chr6	171115067	11158743	0.0652	0.3639
chr7	159138663	6974906	0.0438	0.3435

chr8	146364022	9476424	0.0647	0.4981
chr9	141213431	4507169	0.0319	0.2785
chr10	135534747	4144127	0.0306	0.2919
chr11	135006516	8615759	0.0638	0.3855
chr12	133851895	4448220	0.0332	0.2377
chr13	115169878	4392572	0.0381	0.2561
chr14	107349540	5981666	0.0557	0.3154
chr15	102531392	3221572	0.0314	0.2401
chr16	90354753	5802643	0.0642	0.3355
chr17	81195210	2655560	0.0327	0.2484
chr18	78077248	3859917	0.0494	0.428
chr19	59128983	4458422	0.0754	0.4886
chr20	63025520	3804262	0.0604	0.3215
chr21	48129895	2396110	0.0498	0.298
chr22	51304566	1209255	0.0236	0.1926
chrMT	16571	111719	6.7418	5.6423
chrX	155270560	10465087	0.0674	0.3536
chrY	59373566	373578	0.0063	0.1124

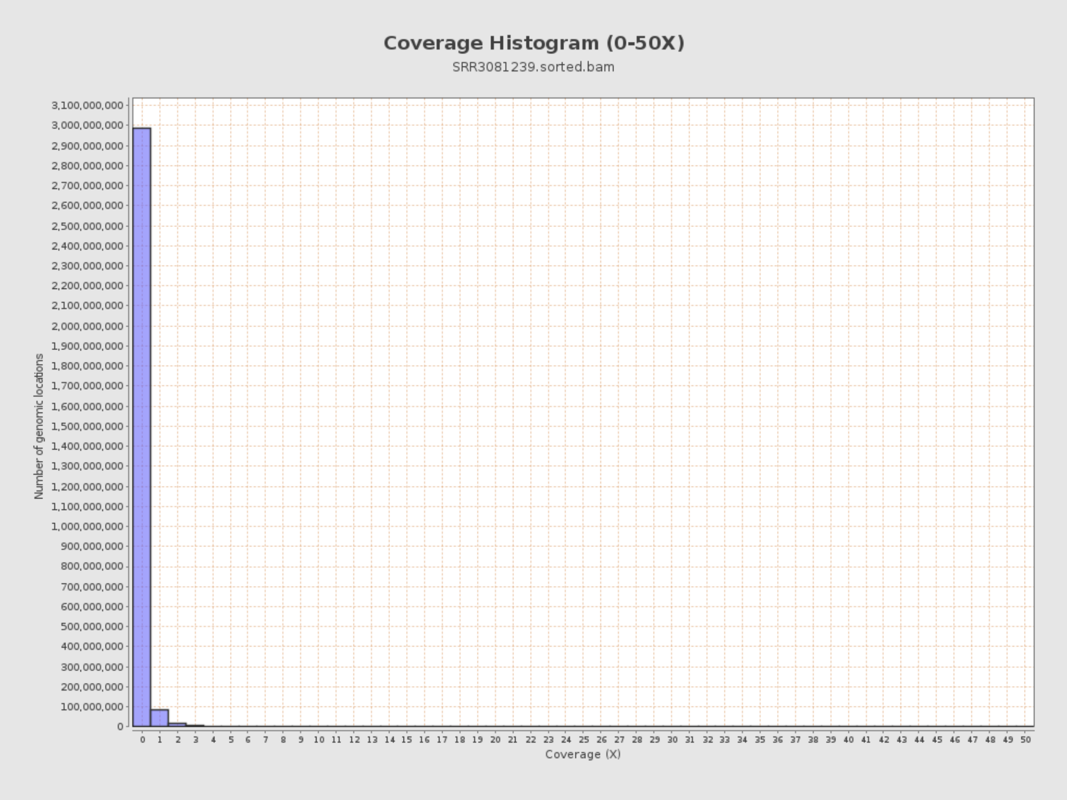
3. Results : Coverage across reference



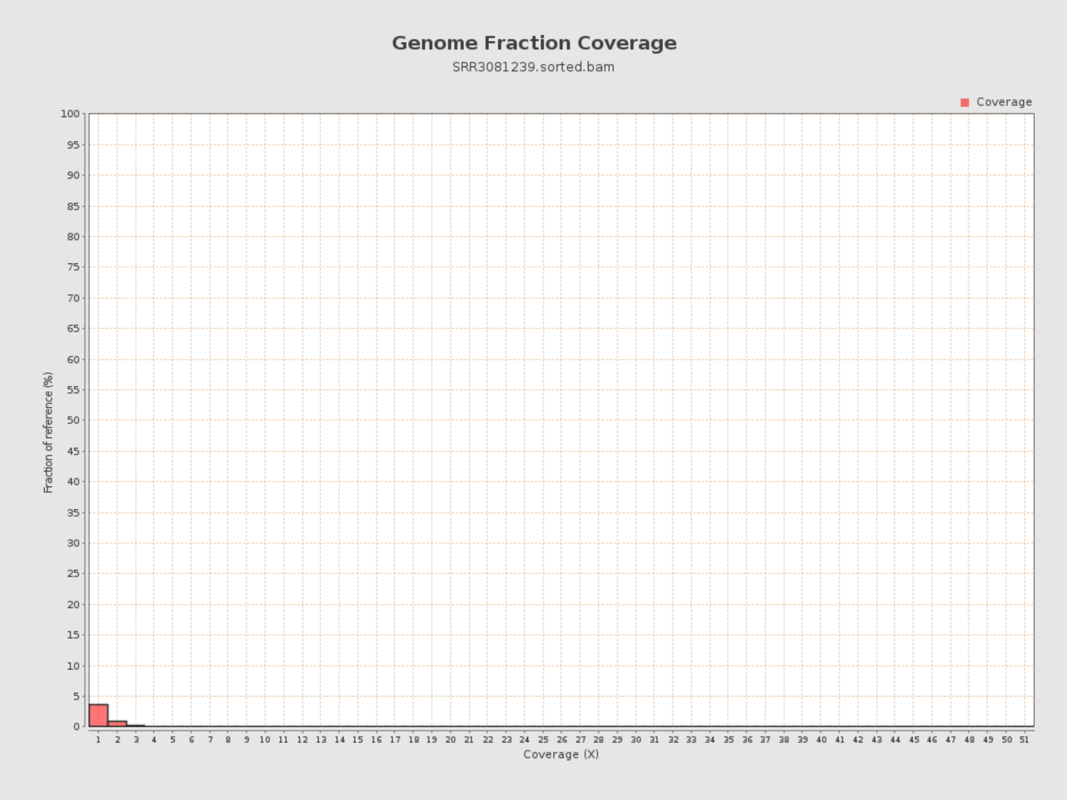
4. Results : Coverage Histogram



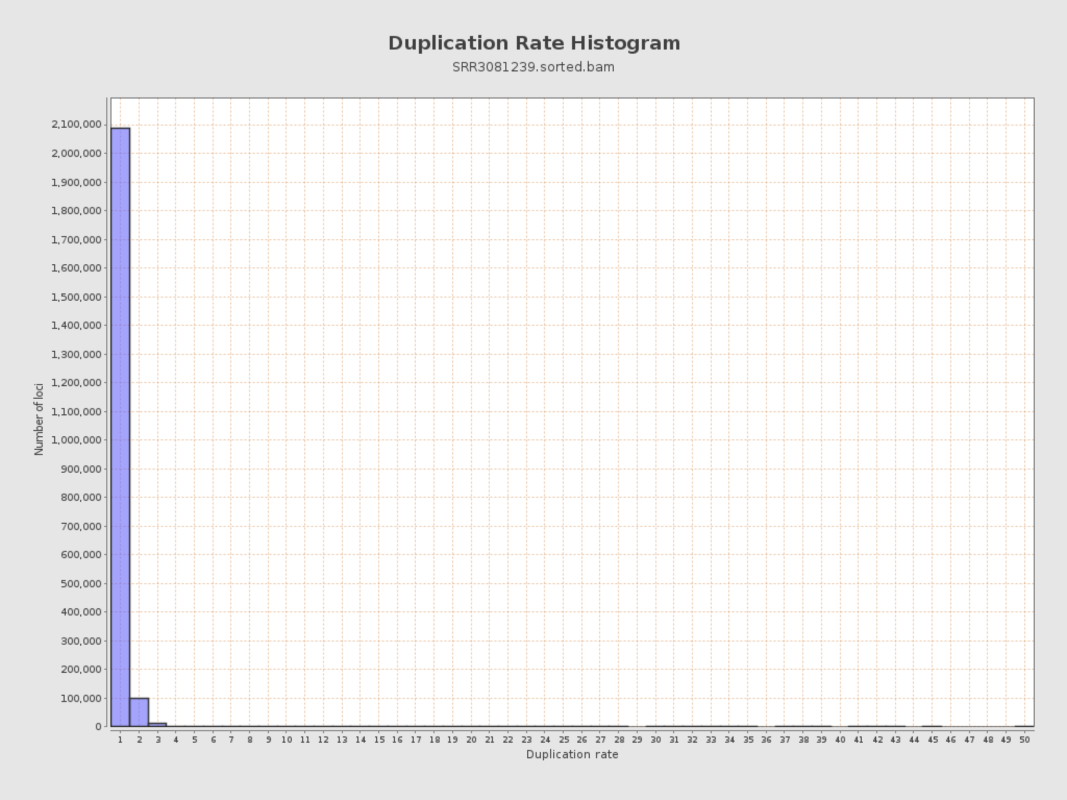
5. Results : Coverage Histogram (0-50X)



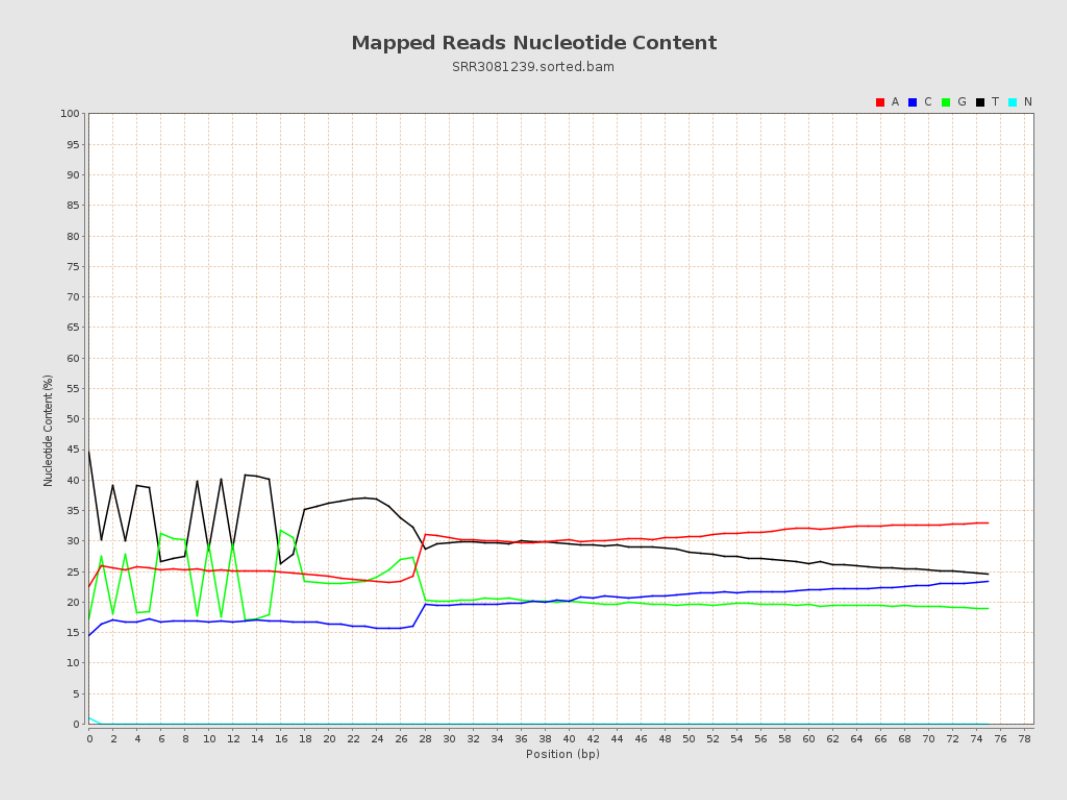
6. Results : Genome Fraction Coverage



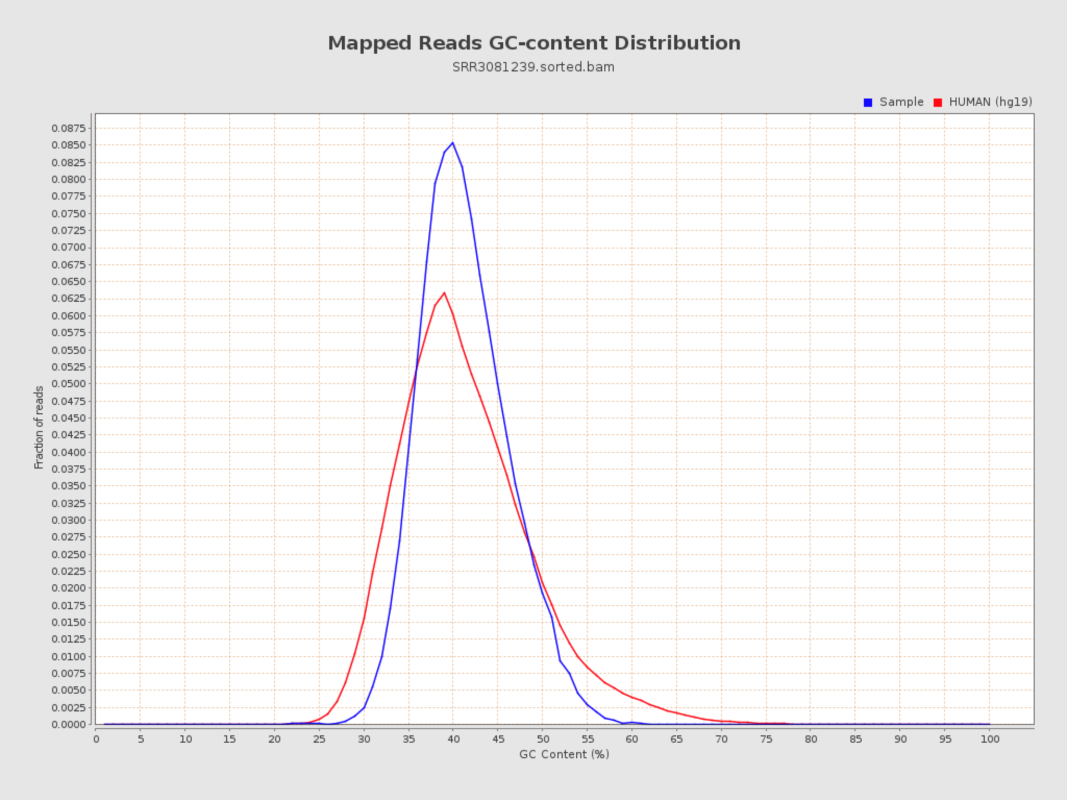
7. Results : Duplication Rate Histogram



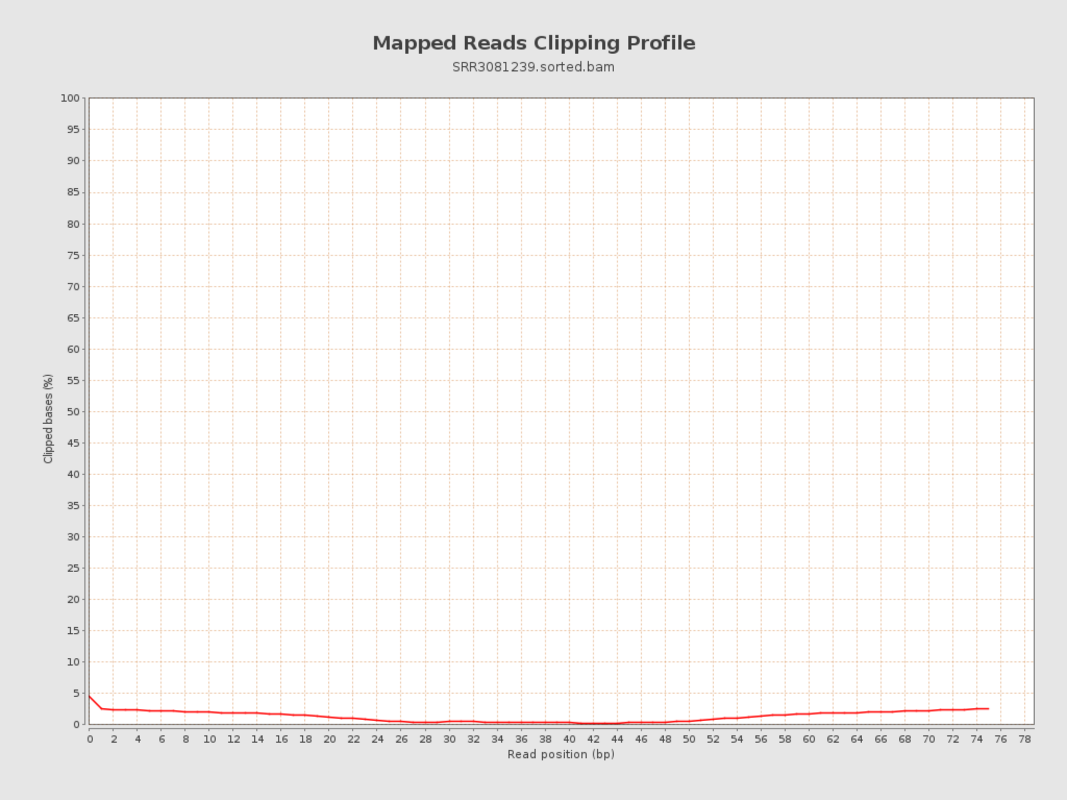
8. Results : Mapped Reads Nucleotide Content



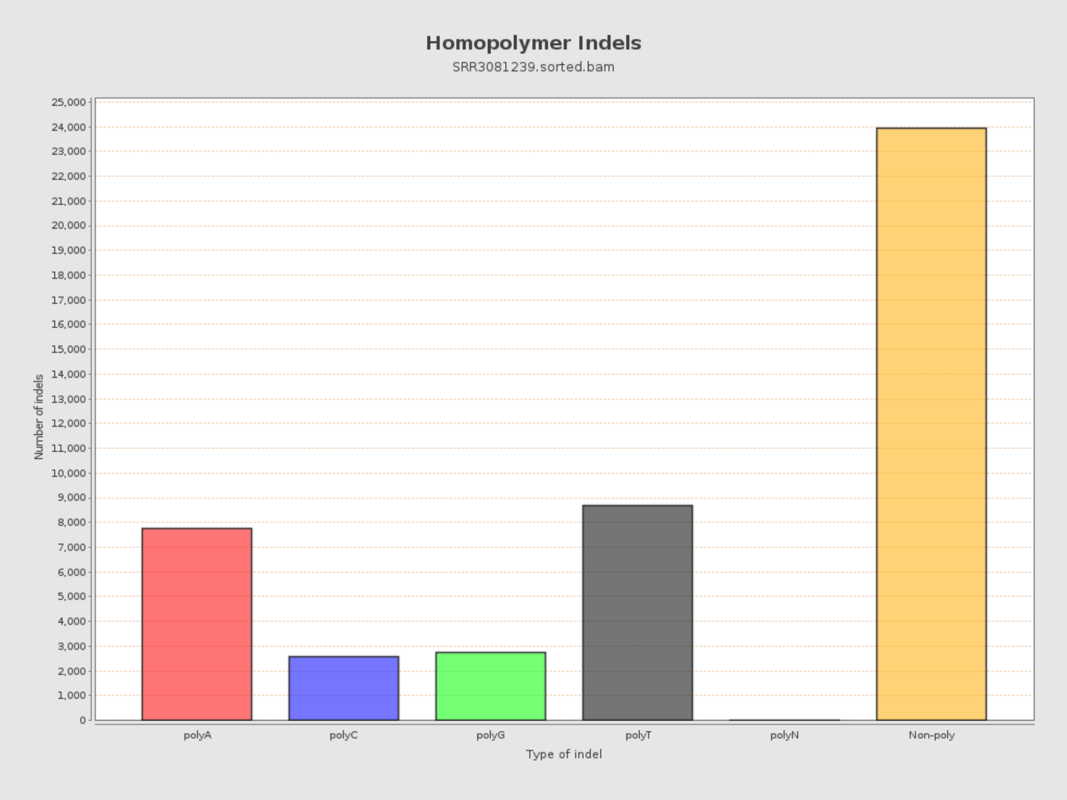
9. Results : Mapped Reads GC-content Distribution



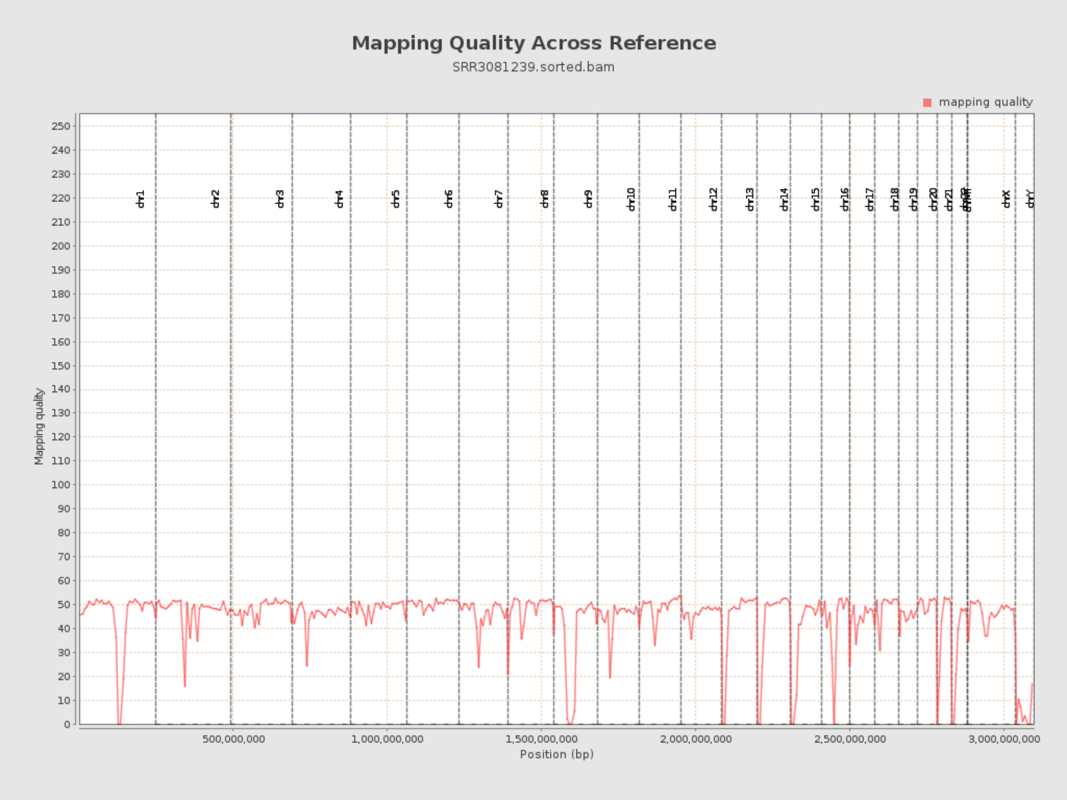
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram