Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:42:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081142.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_SRR3081142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:42:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,670,478
Mapped reads	2,369,005 / 88.71%
Unmapped reads	301,473 / 11.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,808 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	101,952 / 3.82%
Duplication rate	3.43%
Clipped reads	1,103,400 / 41.32%

2.2. ACGT Content

Number/percentage of A's	44,936,657 / 28.49%
Number/percentage of C's	29,410,160 / 18.65%
Number/percentage of T's	49,141,906 / 31.16%
Number/percentage of G's	34,180,269 / 21.67%
Number/percentage of N's	46,476 / 0.03%
GC Percentage	40.32%

2.3. Coverage

Mean	0.051

Standard Deviation	0.3936

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

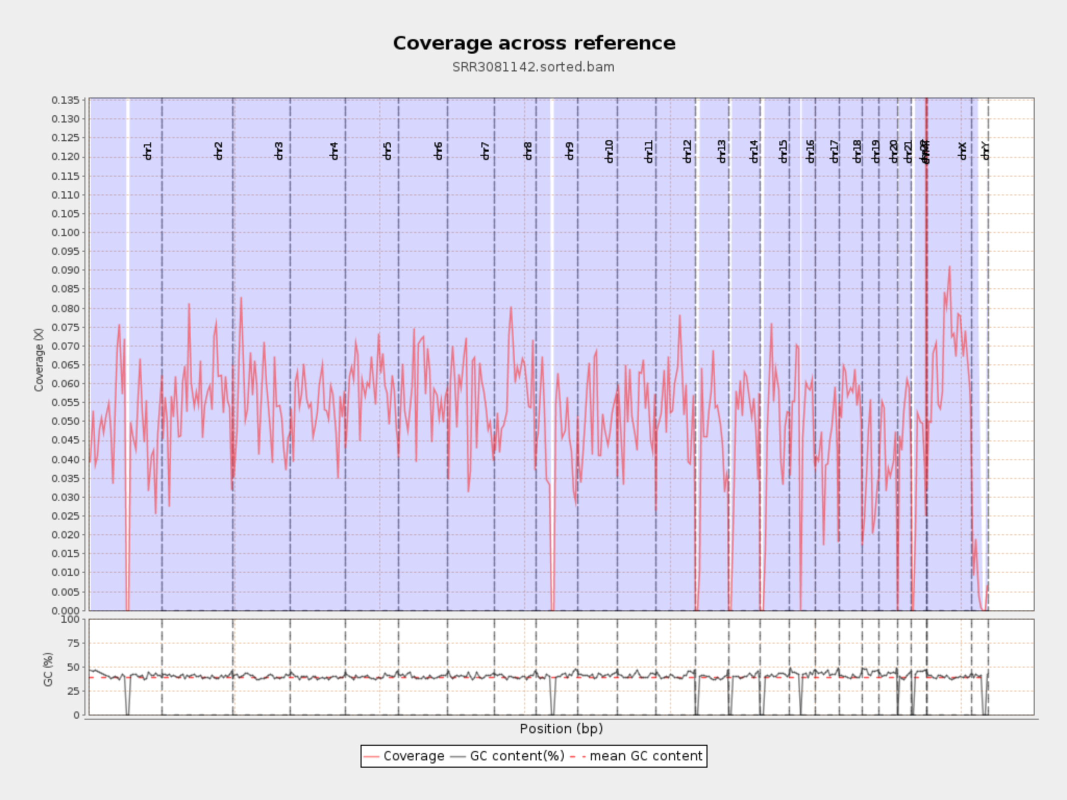
General error rate	0.85%
Mismatches	1,321,325
Insertions	12,010
Mapped reads with at least one insertion	0.5%
Deletions	35,277
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.1%

2.6. Chromosome stats

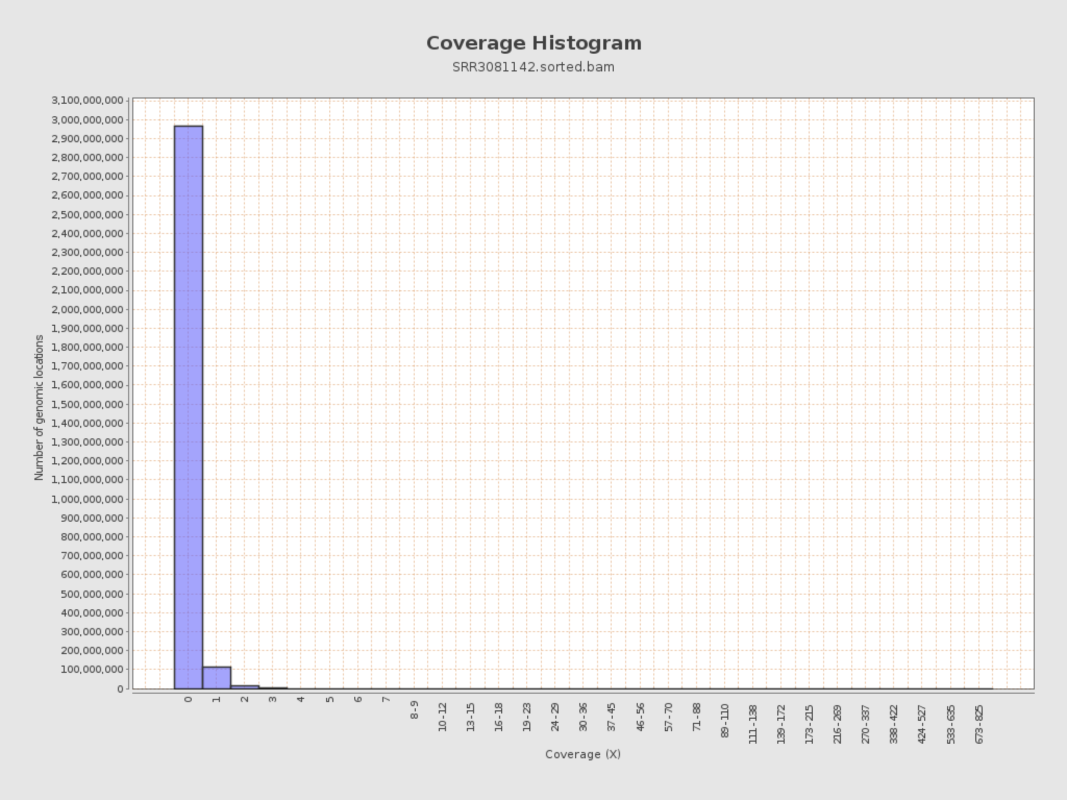
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11607238	0.0466	0.61
chr2	243199373	13710010	0.0564	0.4693
chr3	198022430	10905082	0.0551	0.2685
chr4	191154276	10331170	0.054	0.278
chr5	180915260	10765161	0.0595	0.2818
chr6	171115067	9871017	0.0577	0.3661
chr7	159138663	8832432	0.0555	0.5406

chr8	146364022	8534758	0.0583	0.5776
chr9	141213431	6002337	0.0425	0.3496
chr10	135534747	6802888	0.0502	0.3509
chr11	135006516	7132706	0.0528	0.3721
chr12	133851895	7413535	0.0554	0.2746
chr13	115169878	4825835	0.0419	0.2352
chr14	107349540	4804416	0.0448	0.2666
chr15	102531392	4437219	0.0433	0.2407
chr16	90354753	4630195	0.0512	0.2851
chr17	81195210	3291750	0.0405	0.2495
chr18	78077248	4541376	0.0582	0.6861
chr19	59128983	1985551	0.0336	0.4606
chr20	63025520	2661662	0.0422	0.2458
chr21	48129895	2221504	0.0462	0.2628
chr22	51304566	1664460	0.0324	0.2044
chrMT	16571	31302	1.889	1.693
chrX	155270560	10367720	0.0668	0.3249
chrY	59373566	401172	0.0068	0.1353

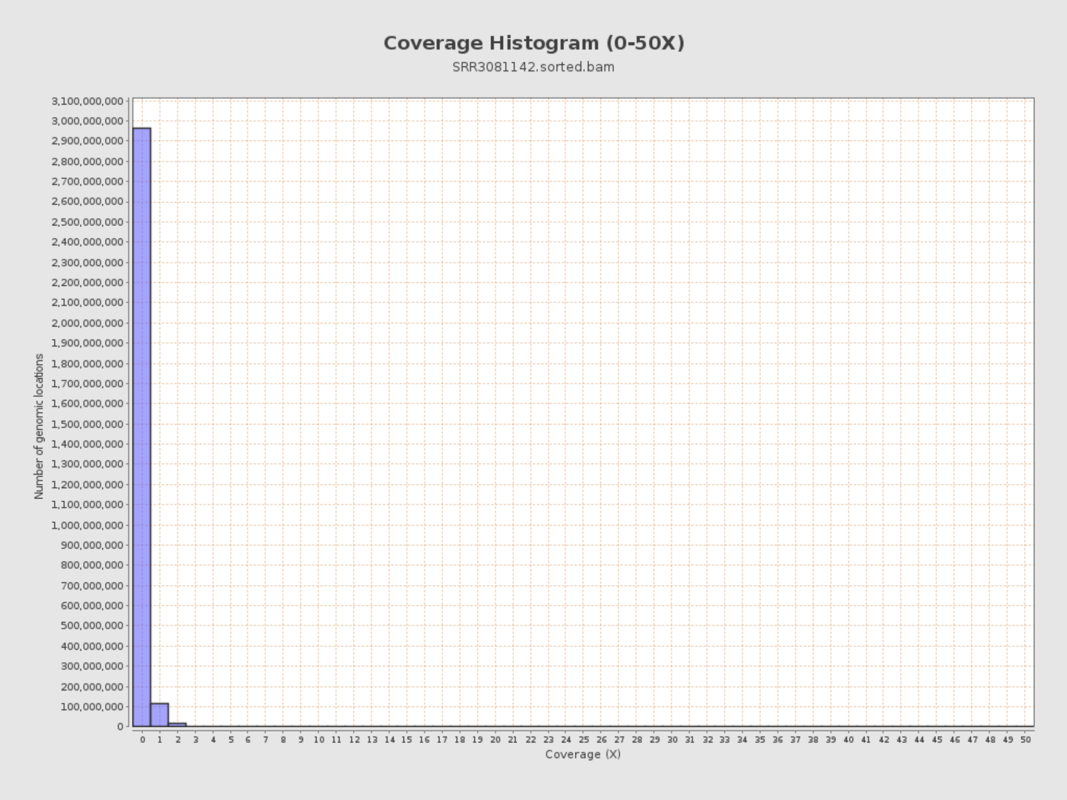
3. Results : Coverage across reference



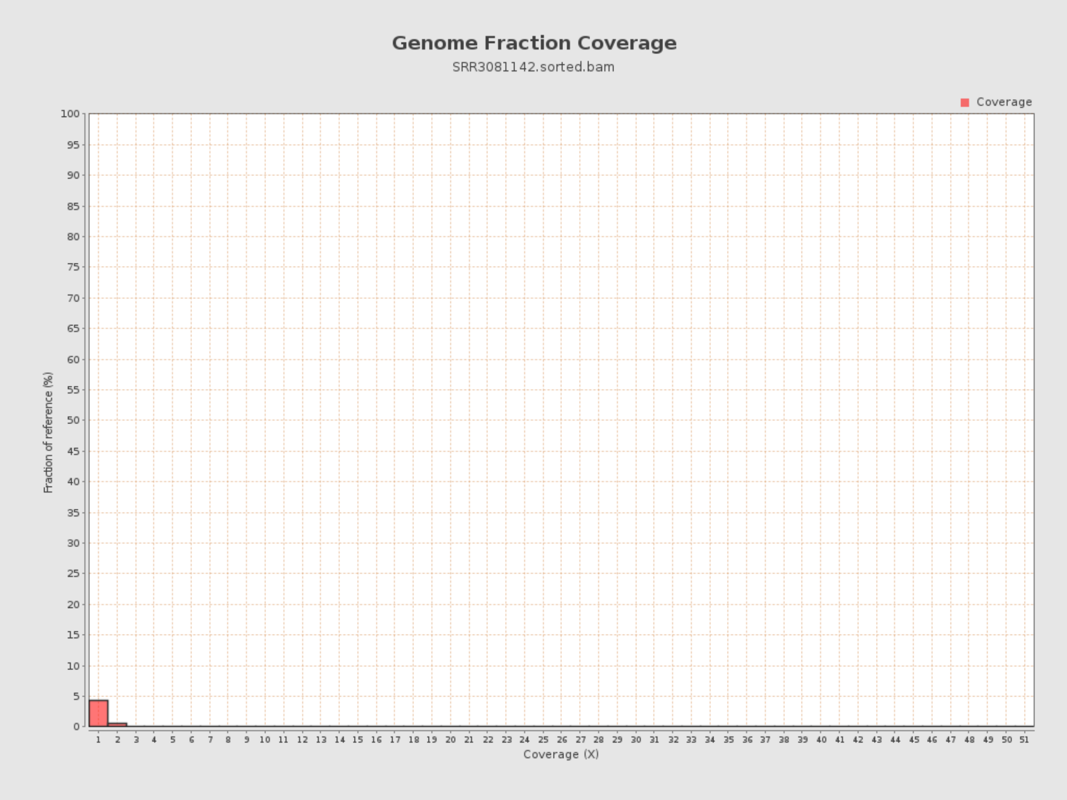
4. Results : Coverage Histogram



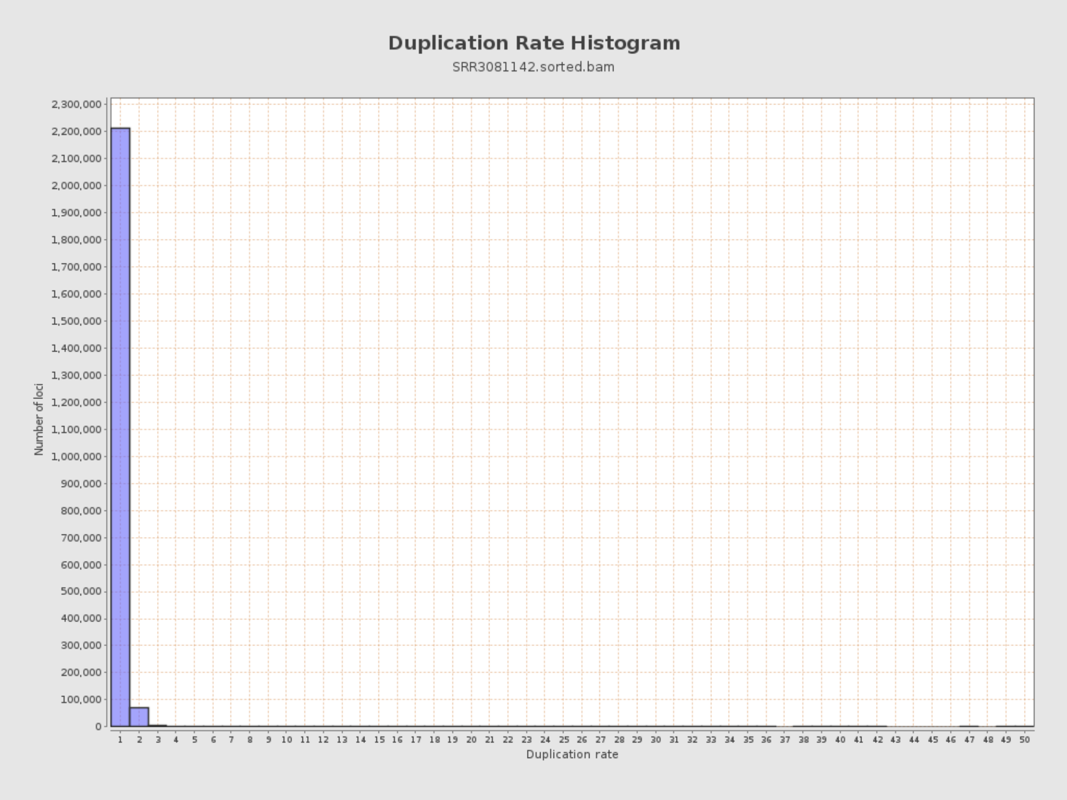
5. Results : Coverage Histogram (0-50X)



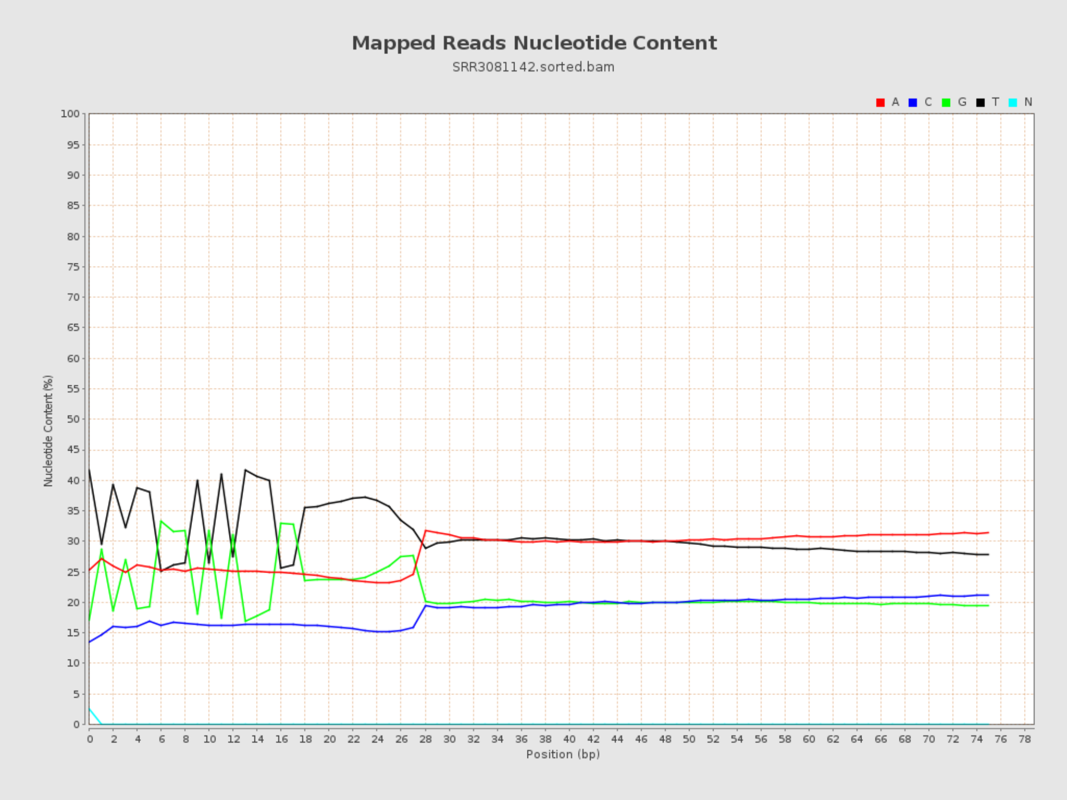
6. Results : Genome Fraction Coverage



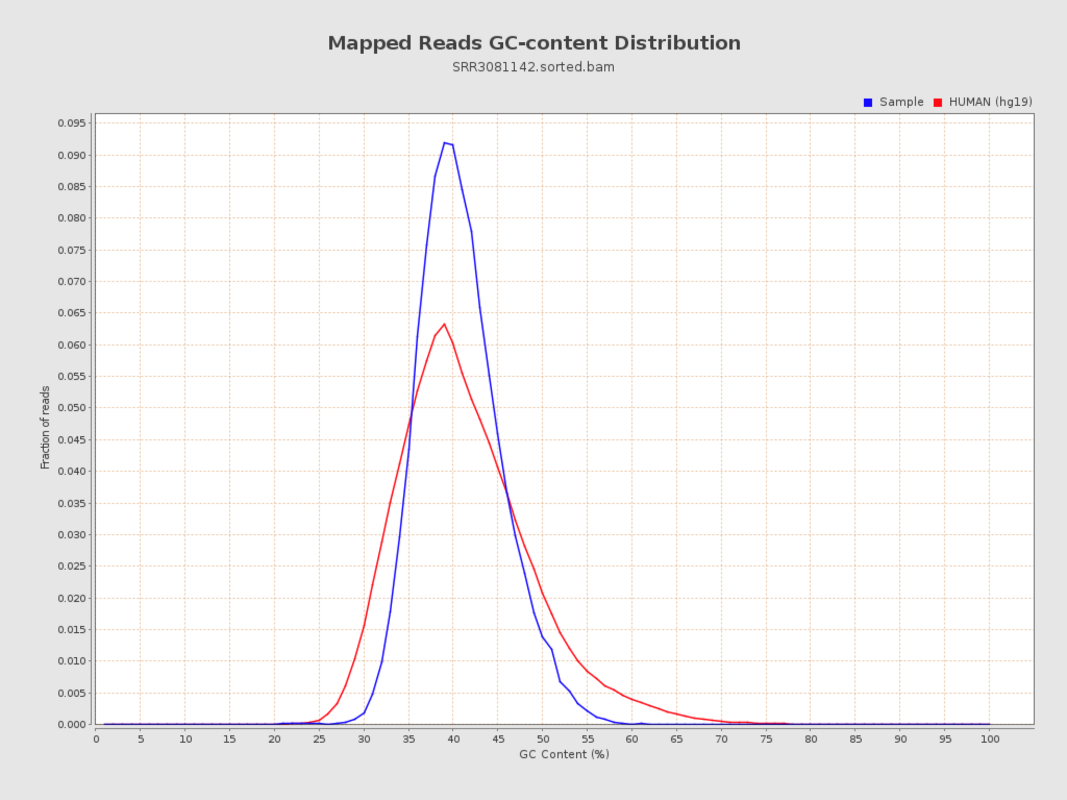
7. Results : Duplication Rate Histogram



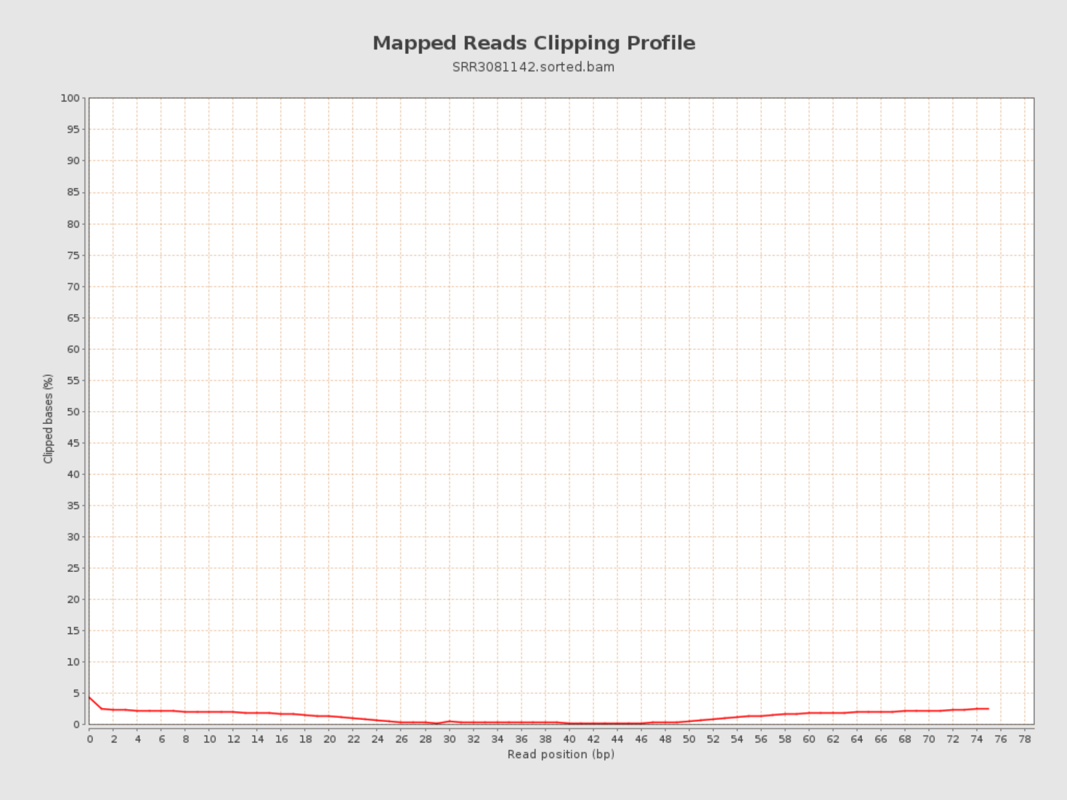
8. Results : Mapped Reads Nucleotide Content



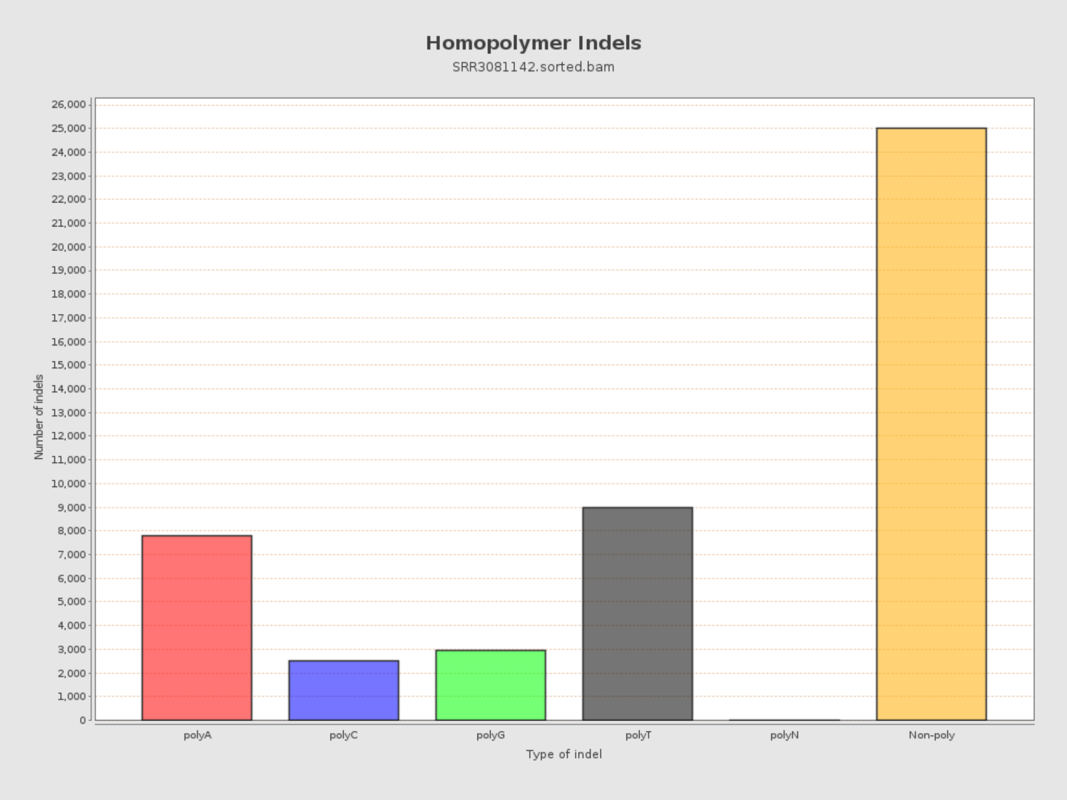
9. Results : Mapped Reads GC-content Distribution



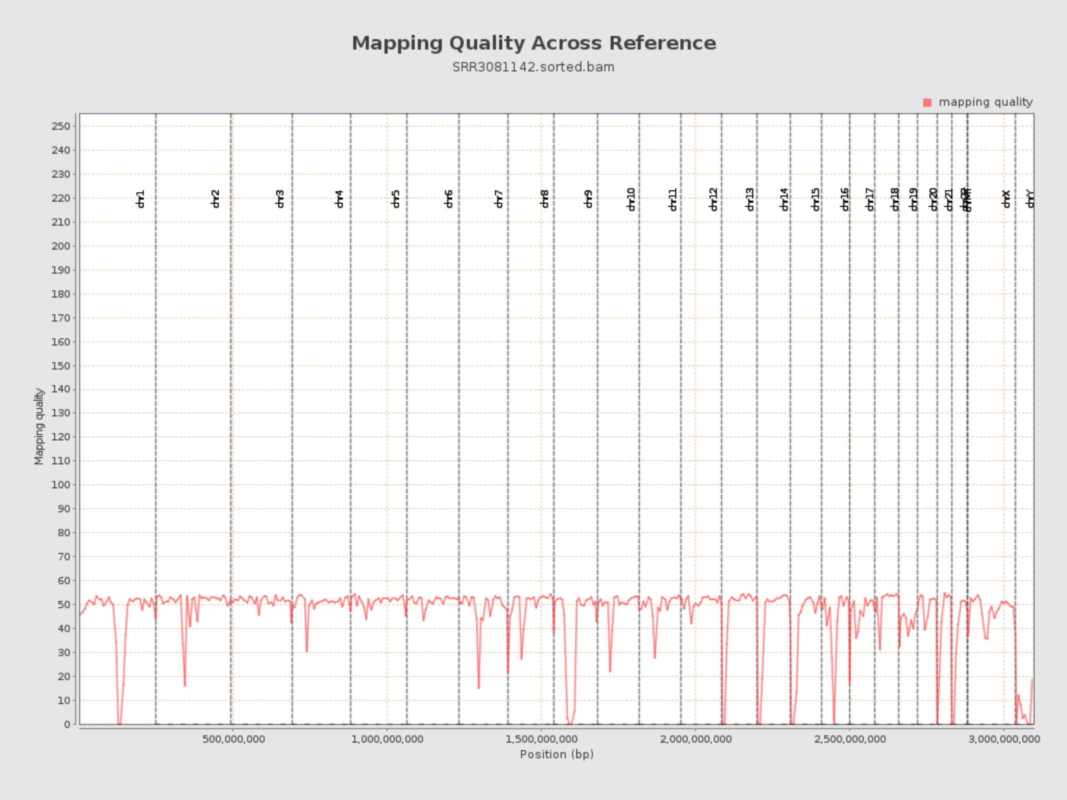
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram