Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:56:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082919.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_SRR3082919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:56:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,749,199
Mapped reads	3,223,643 / 85.98%
Unmapped reads	525,556 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,880 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	148,913 / 3.97%
Duplication rate	3.69%
Clipped reads	1,278,612 / 34.1%

2.2. ACGT Content

Number/percentage of A's	63,349,438 / 28.79%
Number/percentage of C's	40,091,697 / 18.22%
Number/percentage of T's	71,282,101 / 32.39%
Number/percentage of G's	45,331,531 / 20.6%
Number/percentage of N's	12,007 / 0.01%
GC Percentage	38.82%

2.3. Coverage

Mean	0.0711

Standard Deviation	0.5102

2.4. Mapping Quality

Mean Mapping Quality	47.25

2.5. Mismatches and indels

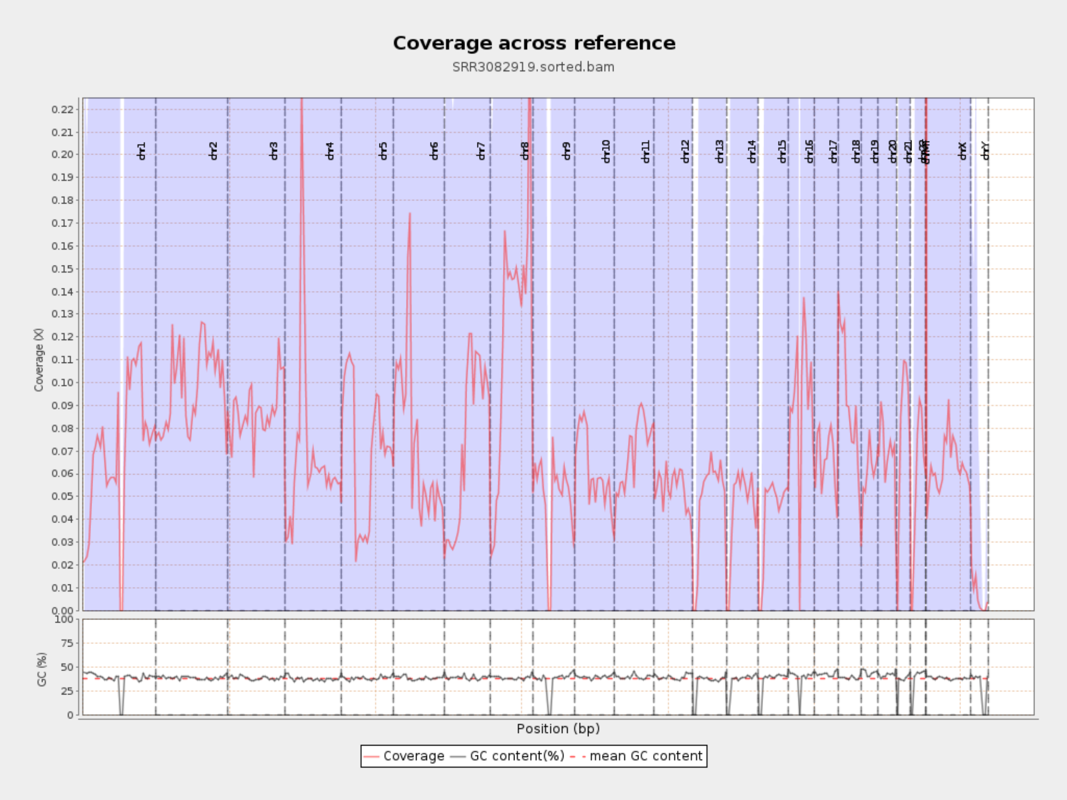
General error rate	0.9%
Mismatches	1,955,551
Insertions	17,980
Mapped reads with at least one insertion	0.55%
Deletions	49,785
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.3%

2.6. Chromosome stats

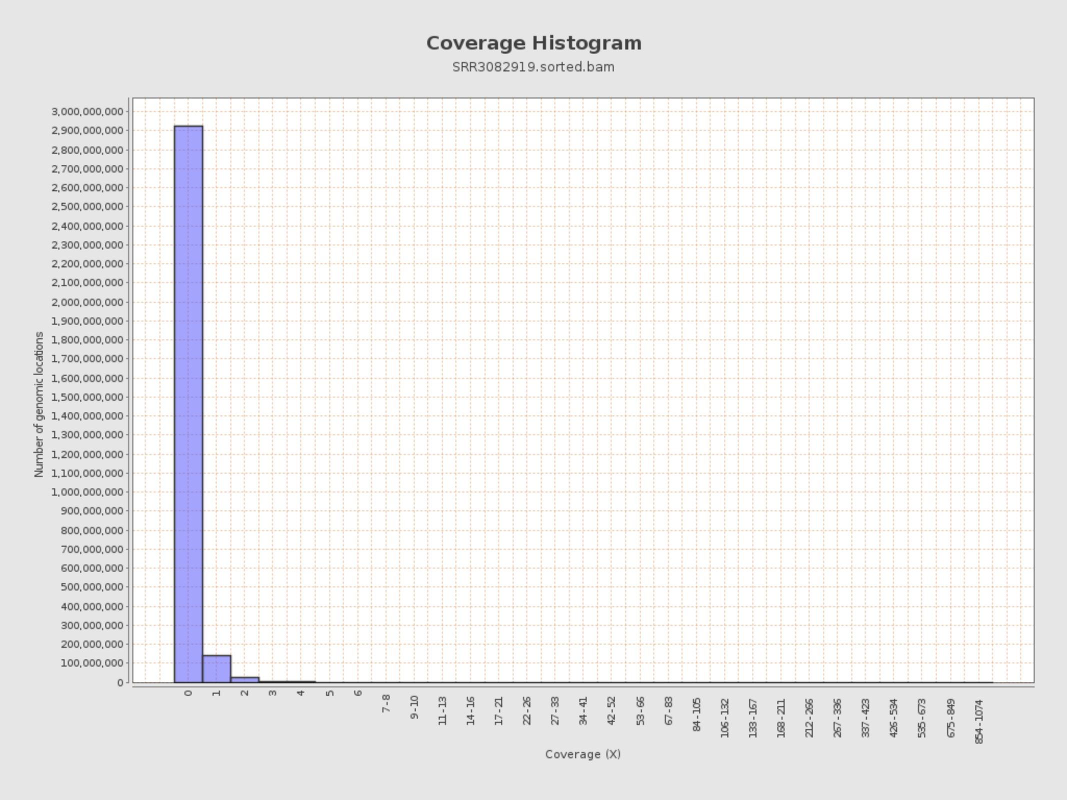
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17448790	0.07	0.9025
chr2	243199373	23976974	0.0986	0.6173
chr3	198022430	17289661	0.0873	0.3576
chr4	191154276	13347392	0.0698	0.3296
chr5	180915260	12651253	0.0699	0.3239
chr6	171115067	12790914	0.0748	0.4886
chr7	159138663	11789145	0.0741	0.4773

chr8	146364022	18225201	0.1245	0.8028
chr9	141213431	7036737	0.0498	0.455
chr10	135534747	8389186	0.0619	0.3912
chr11	135006516	9410875	0.0697	0.4351
chr12	133851895	7119684	0.0532	0.29
chr13	115169878	5547282	0.0482	0.2654
chr14	107349540	4870981	0.0454	0.2953
chr15	102531392	4232715	0.0413	0.2441
chr16	90354753	8192715	0.0907	0.4033
chr17	81195210	5432455	0.0669	0.3689
chr18	78077248	7306657	0.0936	0.9394
chr19	59128983	3607531	0.061	0.646
chr20	63025520	4454434	0.0707	0.3345
chr21	48129895	3705031	0.077	0.3486
chr22	51304566	2873593	0.056	0.2828
chrMT	16571	282785	17.0651	10.6019
chrX	155270560	9809326	0.0632	0.3431
chrY	59373566	360455	0.0061	0.1141

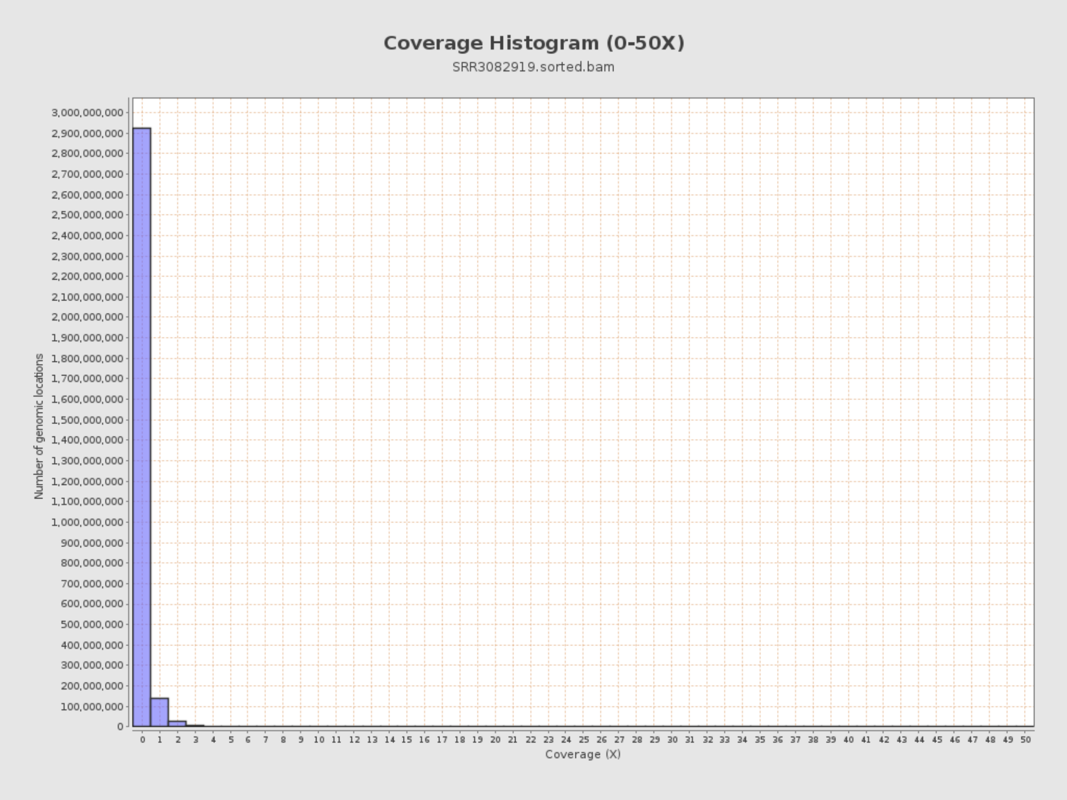
3. Results : Coverage across reference



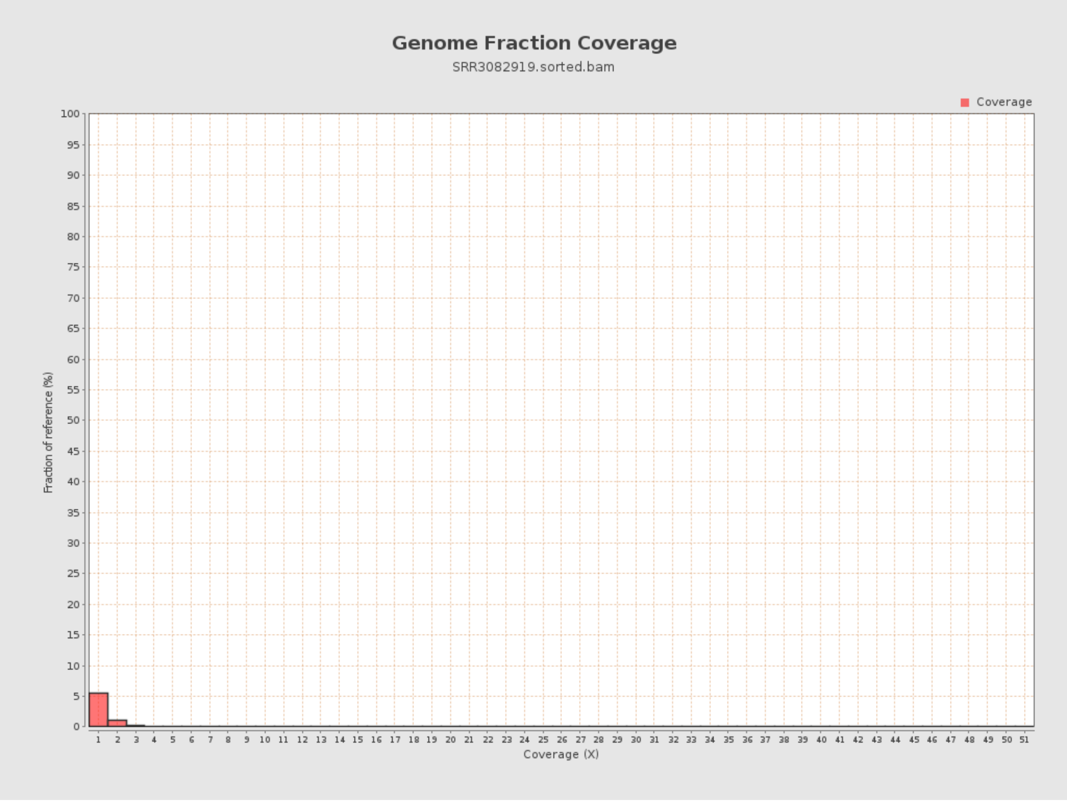
4. Results : Coverage Histogram



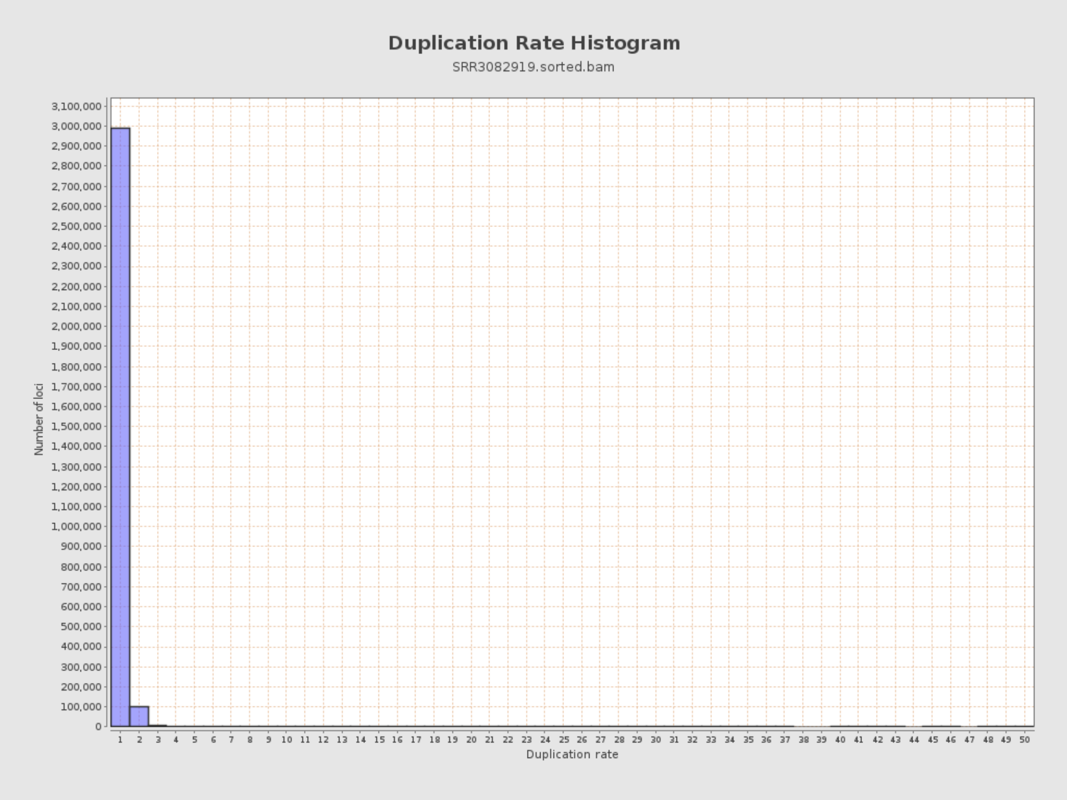
5. Results : Coverage Histogram (0-50X)



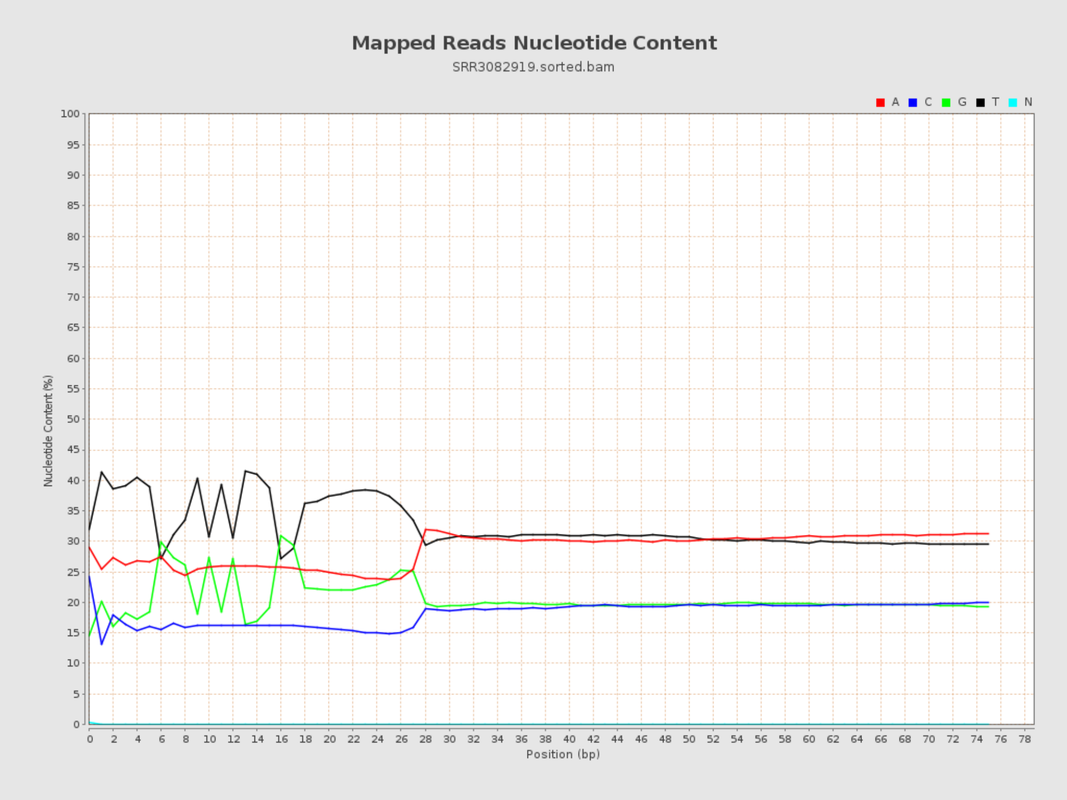
6. Results : Genome Fraction Coverage



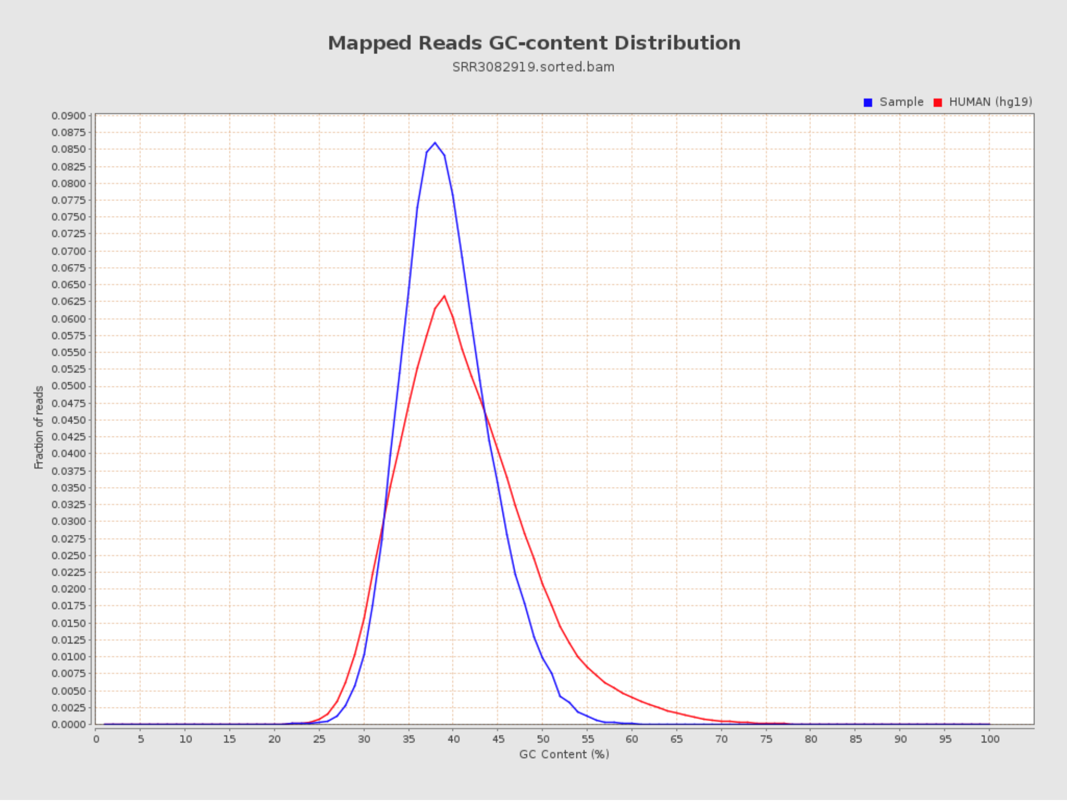
7. Results : Duplication Rate Histogram



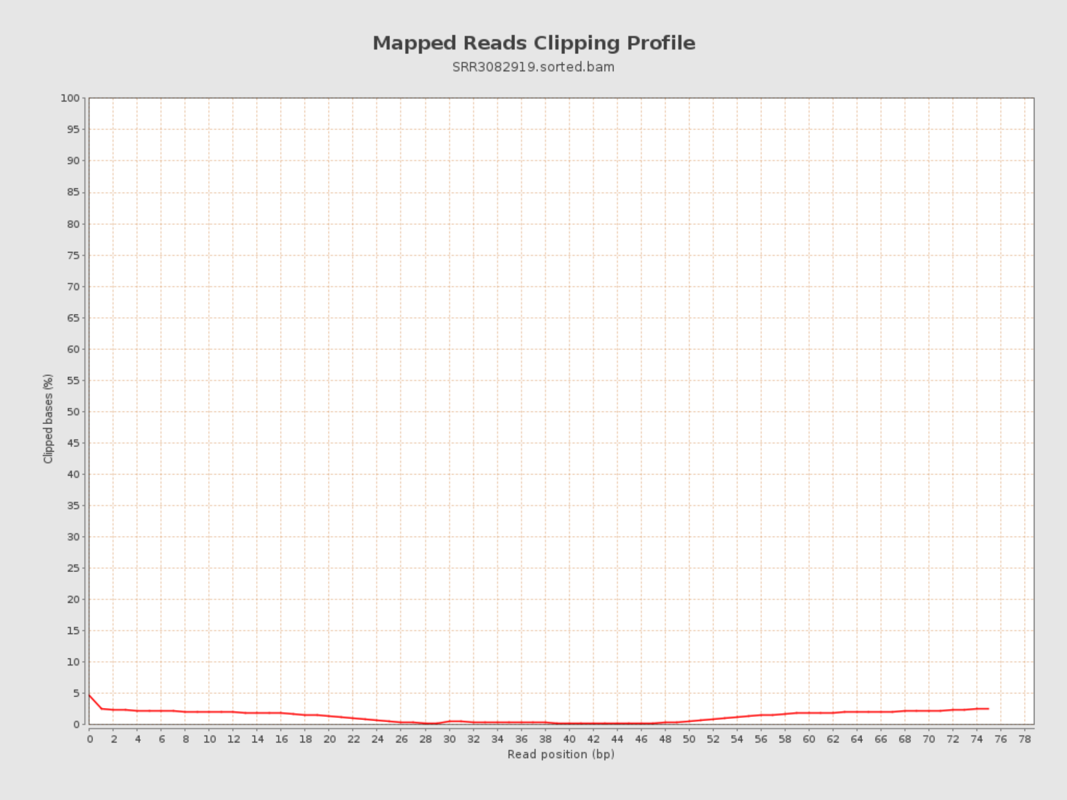
8. Results : Mapped Reads Nucleotide Content



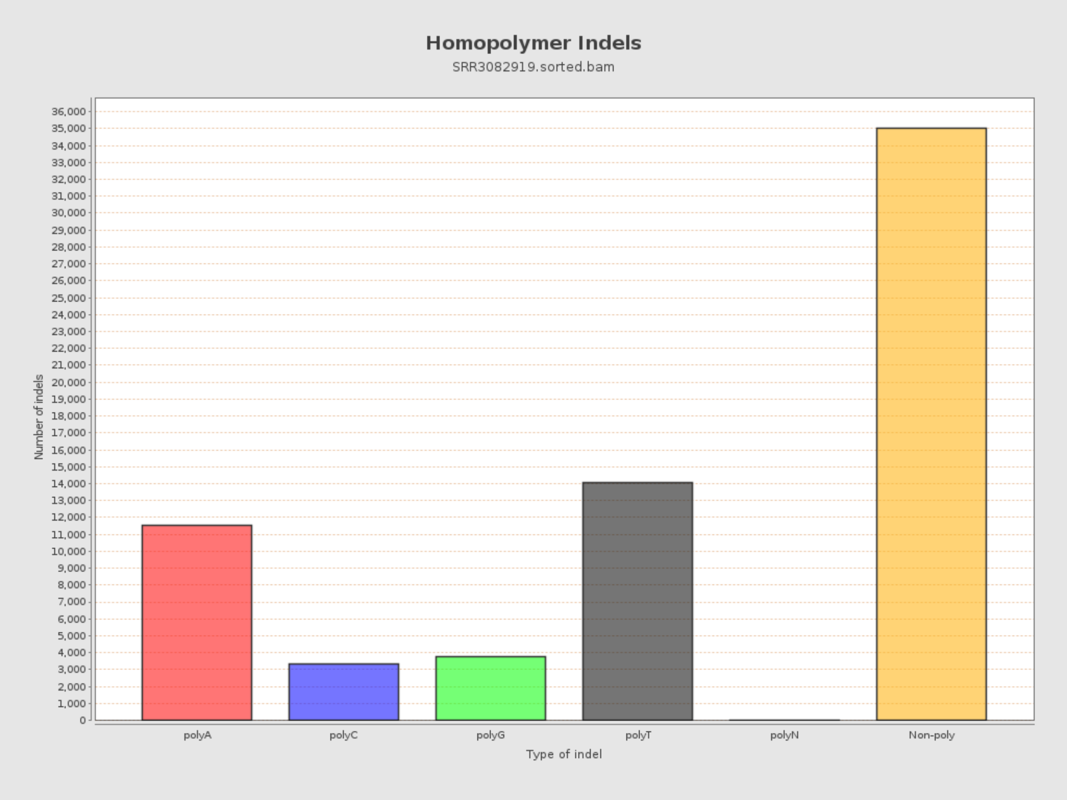
9. Results : Mapped Reads GC-content Distribution



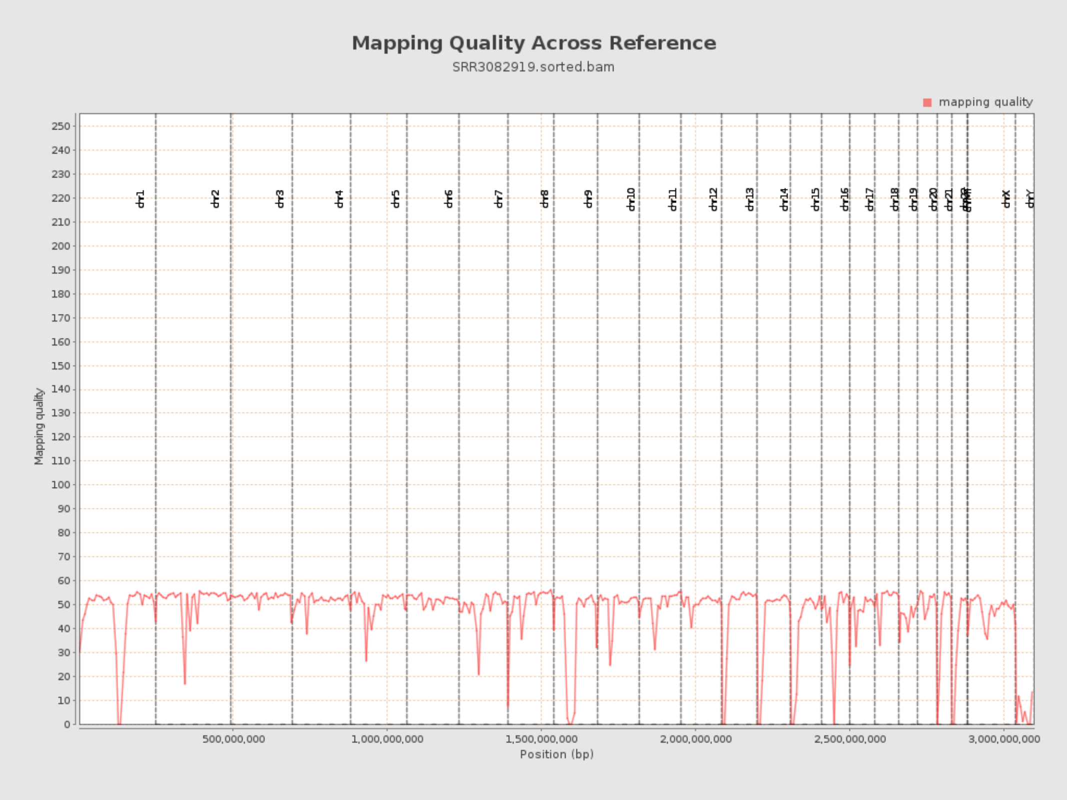
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram