Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:11:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080918.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_SRR3080918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:11:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,043,294
Mapped reads	2,730,775 / 89.73%
Unmapped reads	312,519 / 10.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,683 / 1.04%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	104,448 / 3.43%
Duplication rate	3.06%
Clipped reads	964,290 / 31.69%

2.2. ACGT Content

Number/percentage of A's	54,306,890 / 28.9%
Number/percentage of C's	33,416,891 / 17.78%
Number/percentage of T's	60,016,632 / 31.94%
Number/percentage of G's	39,272,714 / 20.9%
Number/percentage of N's	905,336 / 0.48%
GC Percentage	38.68%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.4252

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

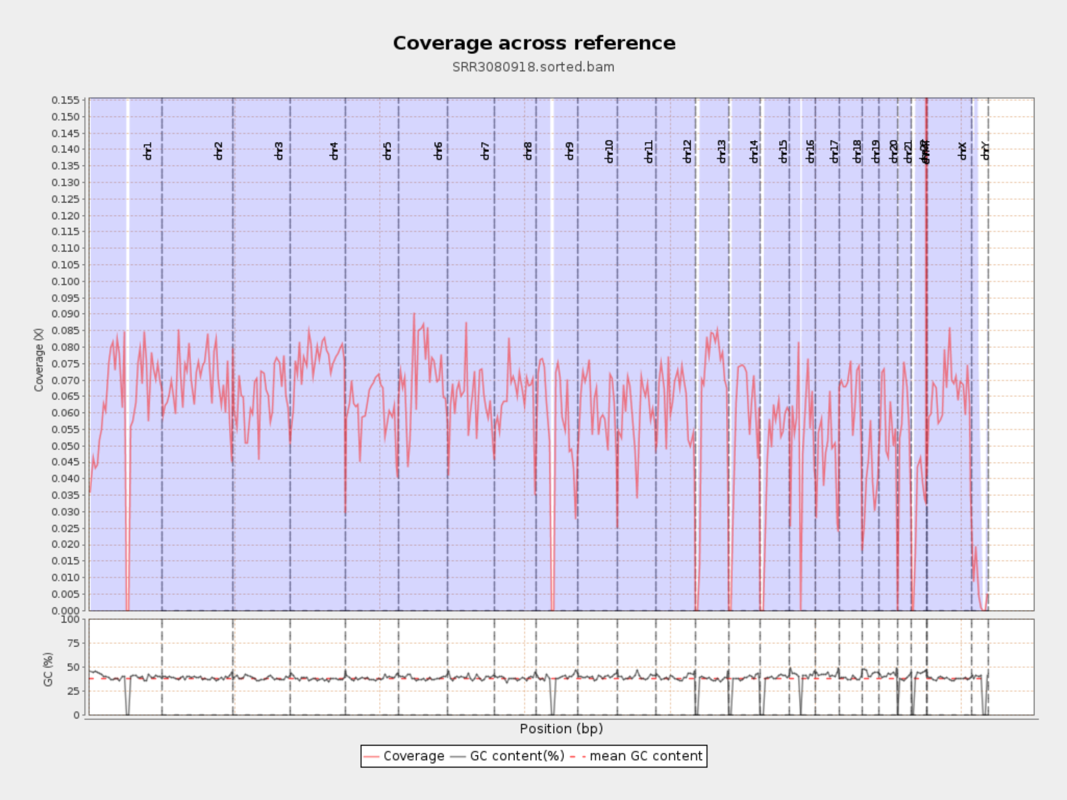
General error rate	1.14%
Mismatches	2,115,728
Insertions	14,083
Mapped reads with at least one insertion	0.51%
Deletions	41,556
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.84%

2.6. Chromosome stats

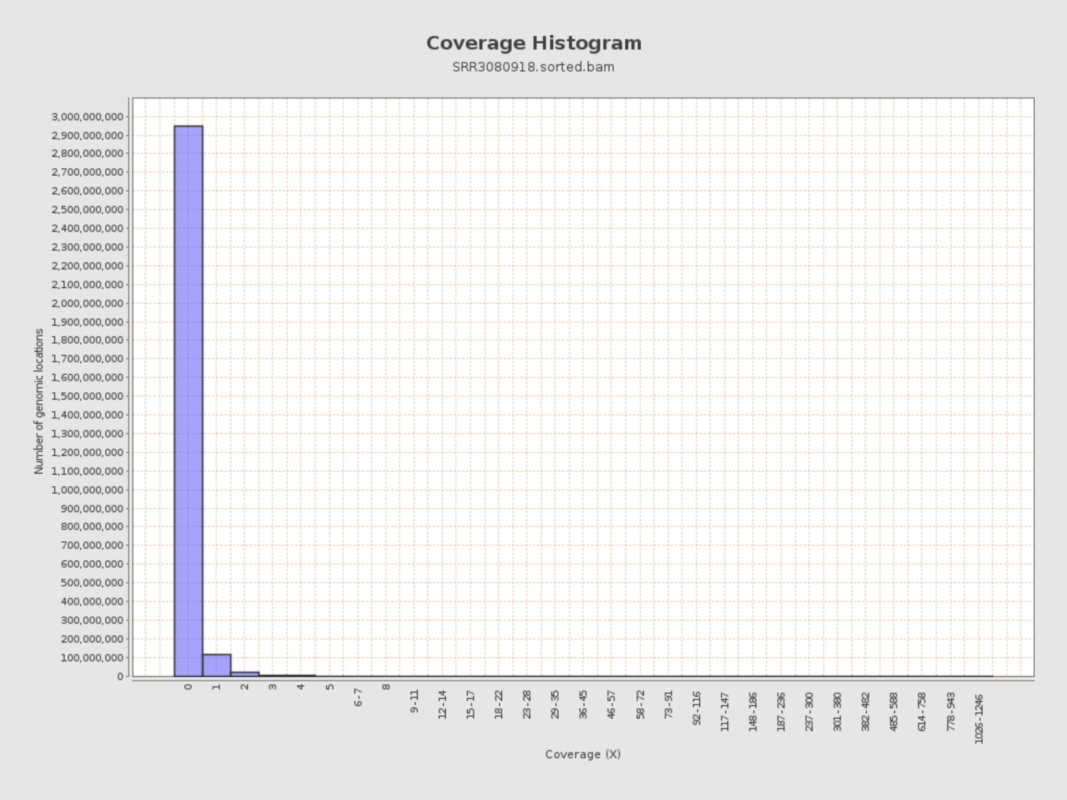
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15607276	0.0626	0.6004
chr2	243199373	16909716	0.0695	0.4125
chr3	198022430	12857298	0.0649	0.3112
chr4	191154276	14514130	0.0759	0.3461
chr5	180915260	11120230	0.0615	0.3044
chr6	171115067	12274639	0.0717	0.3994
chr7	159138663	10191583	0.064	0.5485

chr8	146364022	9499601	0.0649	0.8078
chr9	141213431	7721031	0.0547	0.4113
chr10	135534747	8520368	0.0629	0.3723
chr11	135006516	8002214	0.0593	0.3577
chr12	133851895	8502115	0.0635	0.3137
chr13	115169878	7363502	0.0639	0.31
chr14	107349540	5893770	0.0549	0.3069
chr15	102531392	4744387	0.0463	0.2631
chr16	90354753	4856914	0.0538	0.305
chr17	81195210	3737567	0.046	0.2912
chr18	78077248	5238064	0.0671	0.7213
chr19	59128983	2318324	0.0392	0.4361
chr20	63025520	3567674	0.0566	0.2979
chr21	48129895	2520509	0.0524	0.2998
chr22	51304566	1455785	0.0284	0.2009
chrMT	16571	28909	1.7446	1.6035
chrX	155270560	10162523	0.0655	0.3285
chrY	59373566	378537	0.0064	0.1327

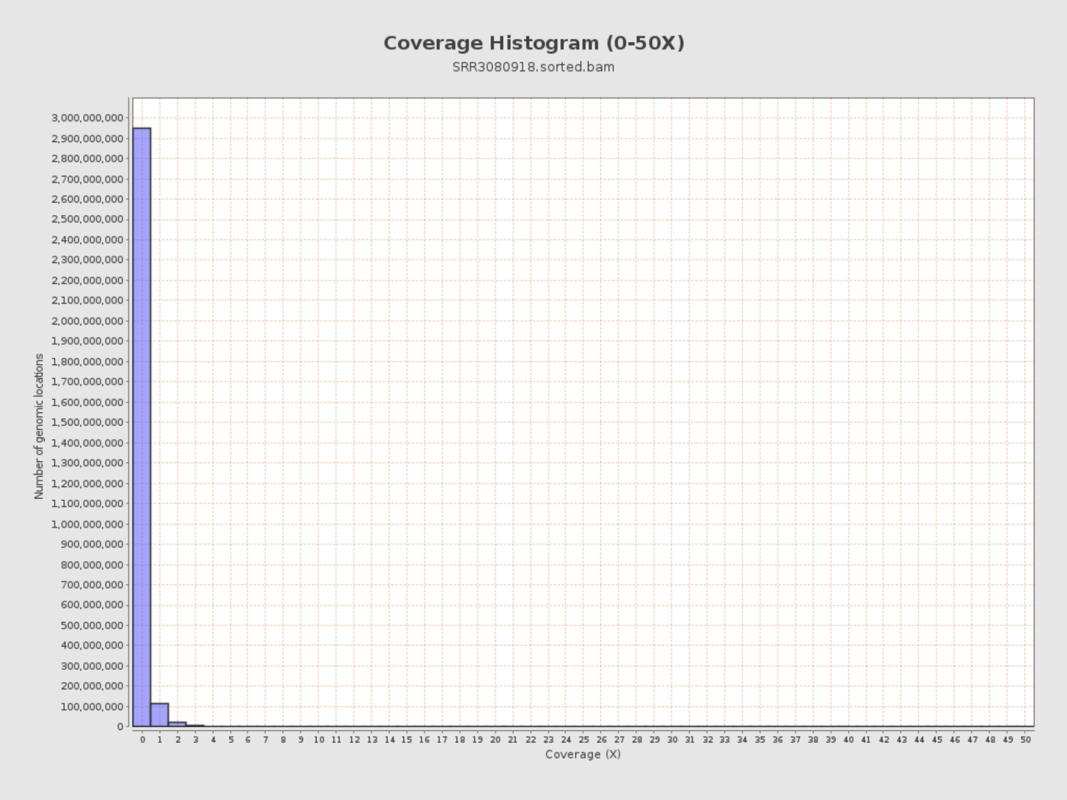
3. Results : Coverage across reference



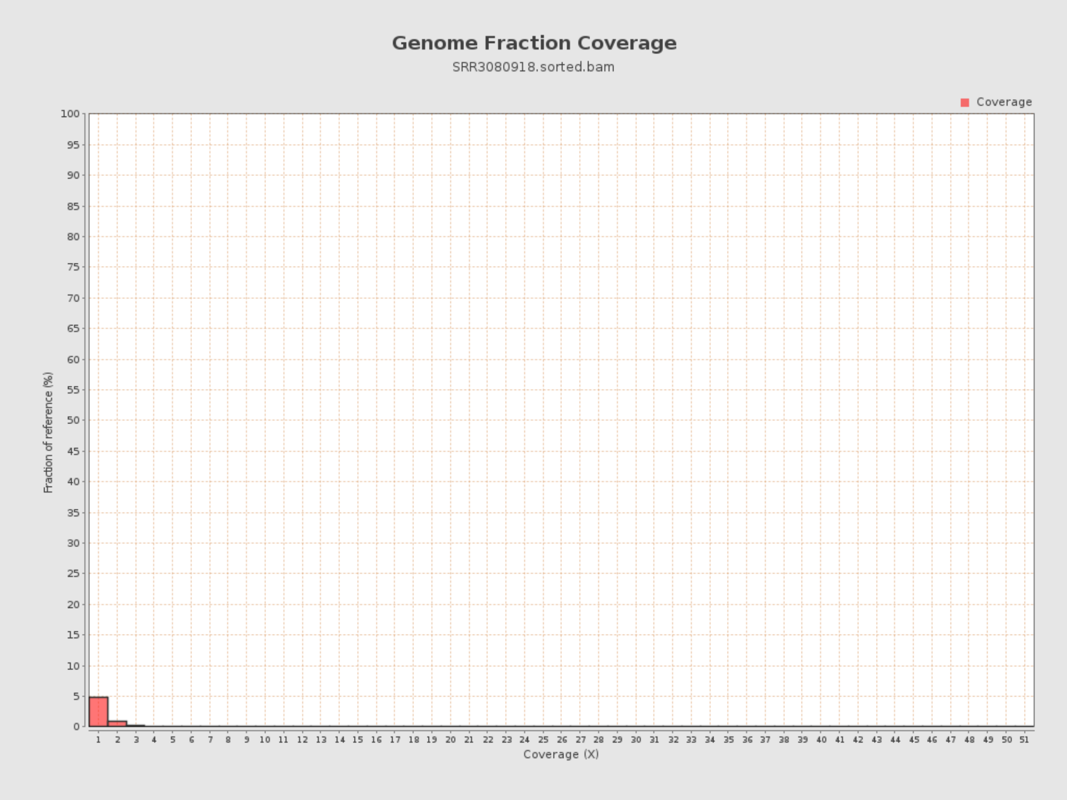
4. Results : Coverage Histogram



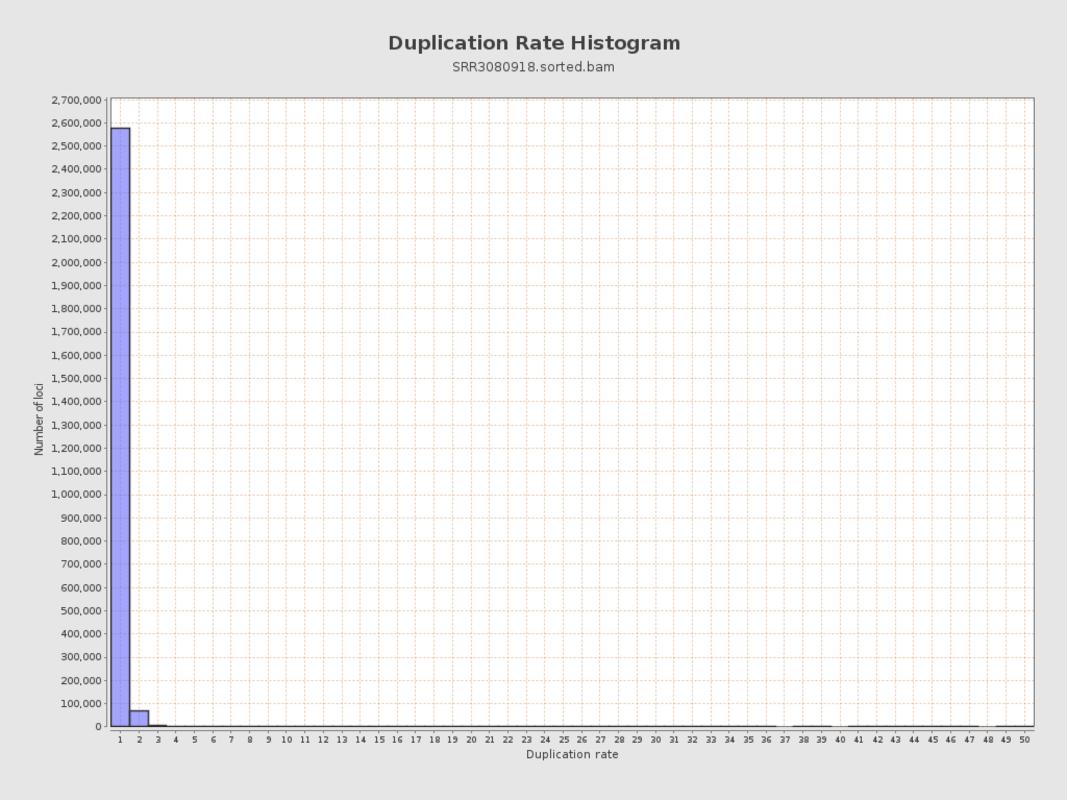
5. Results : Coverage Histogram (0-50X)



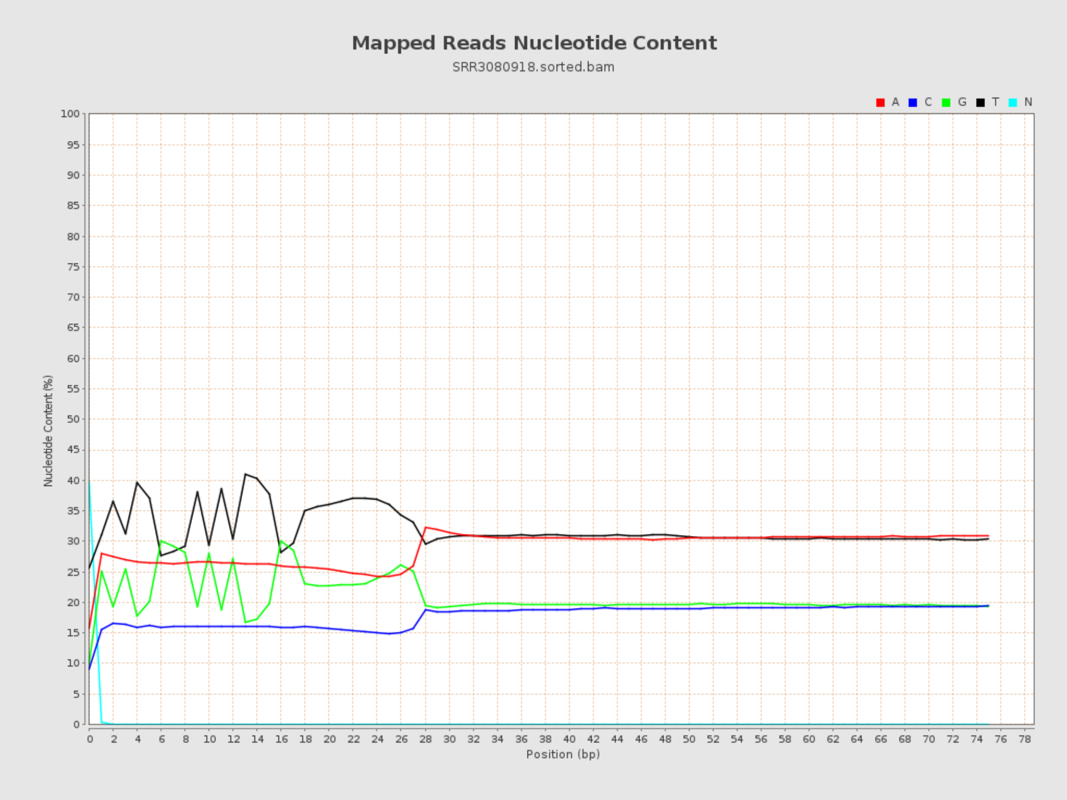
6. Results : Genome Fraction Coverage



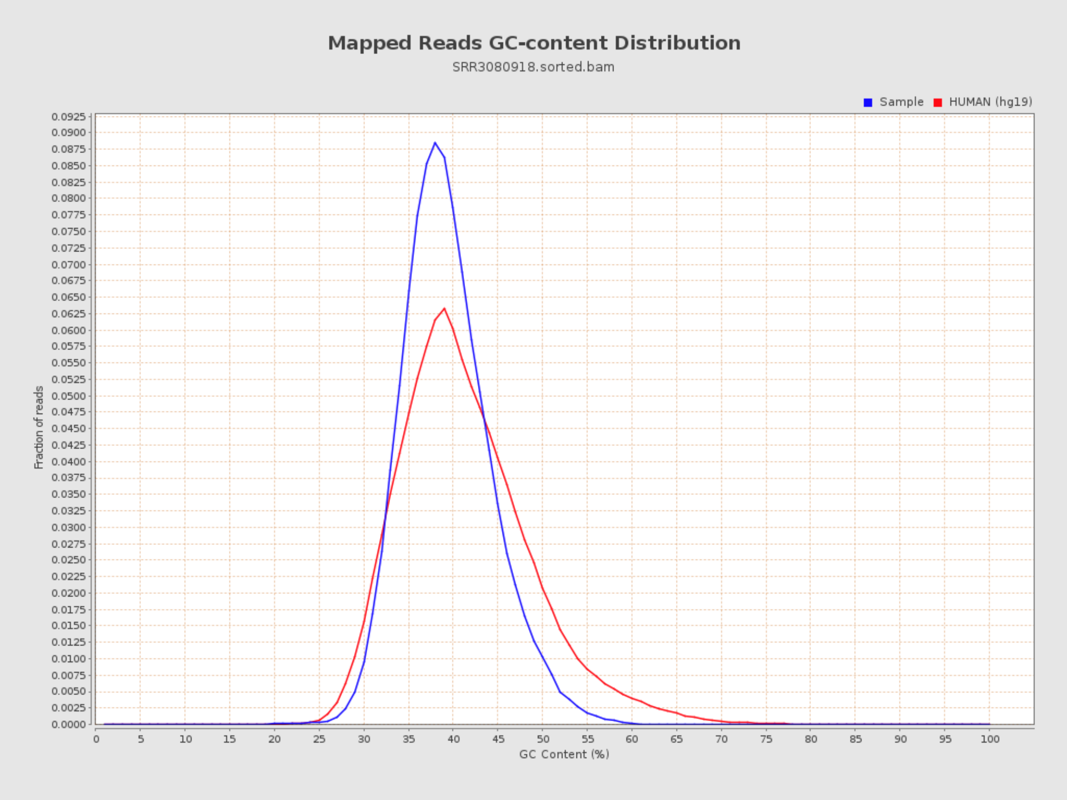
7. Results : Duplication Rate Histogram



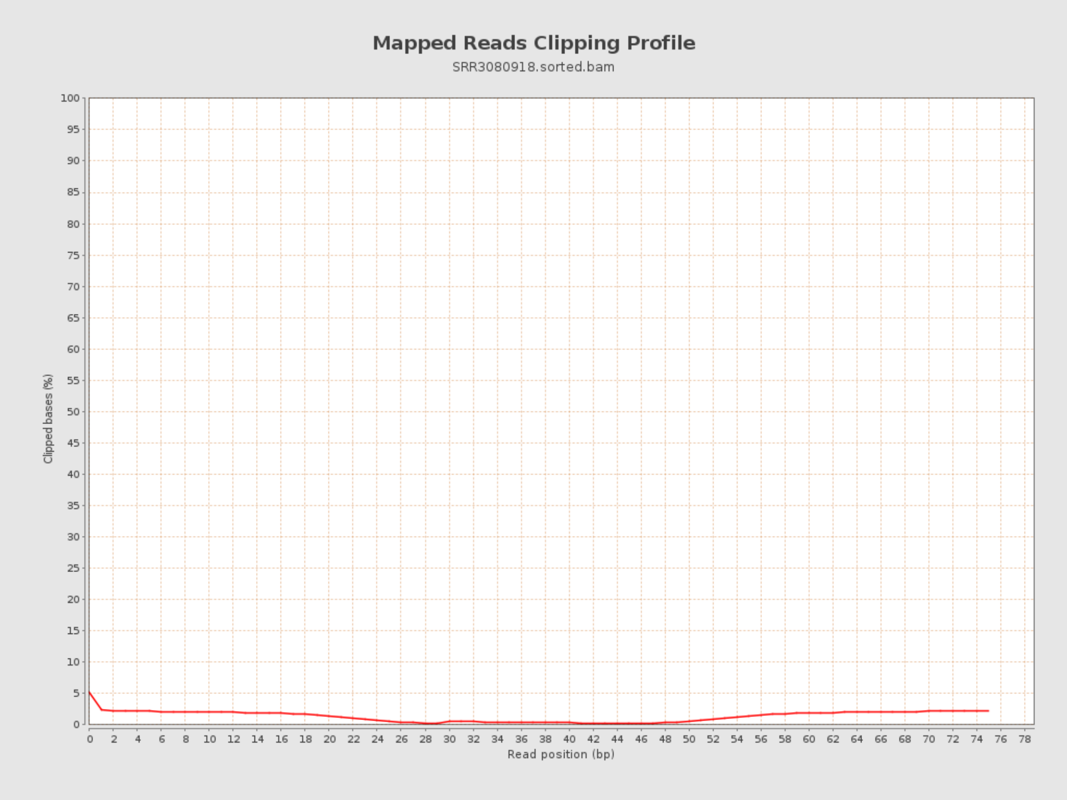
8. Results : Mapped Reads Nucleotide Content



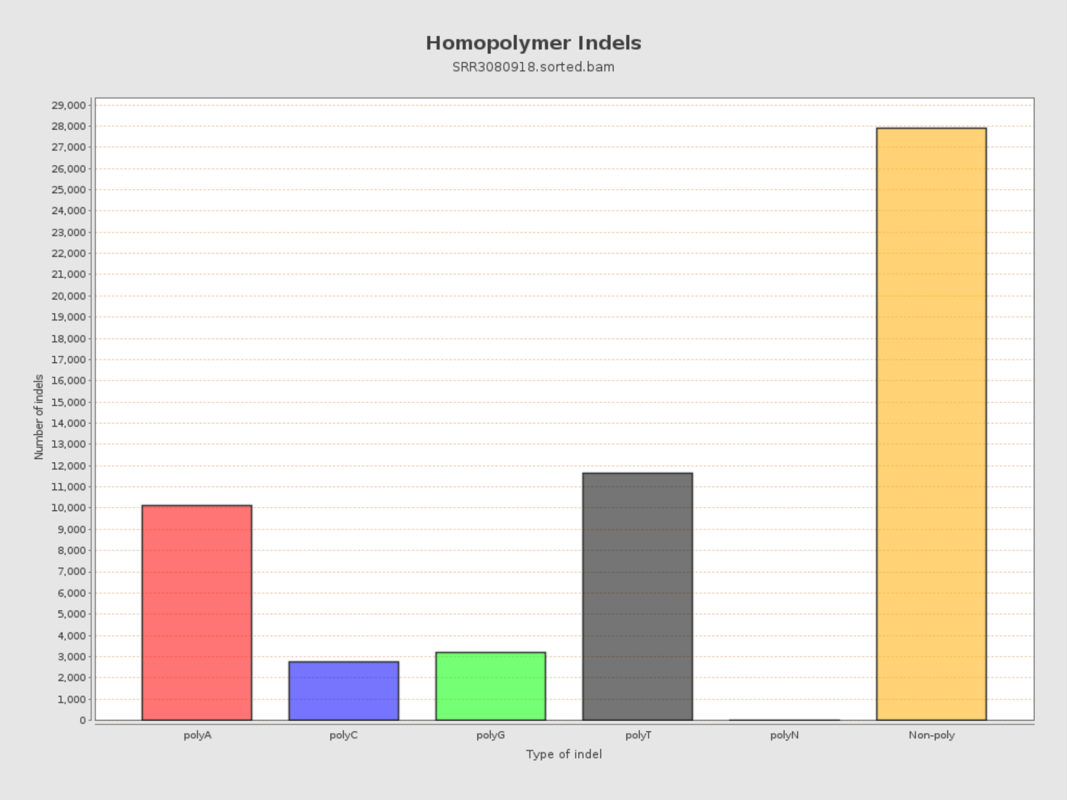
9. Results : Mapped Reads GC-content Distribution



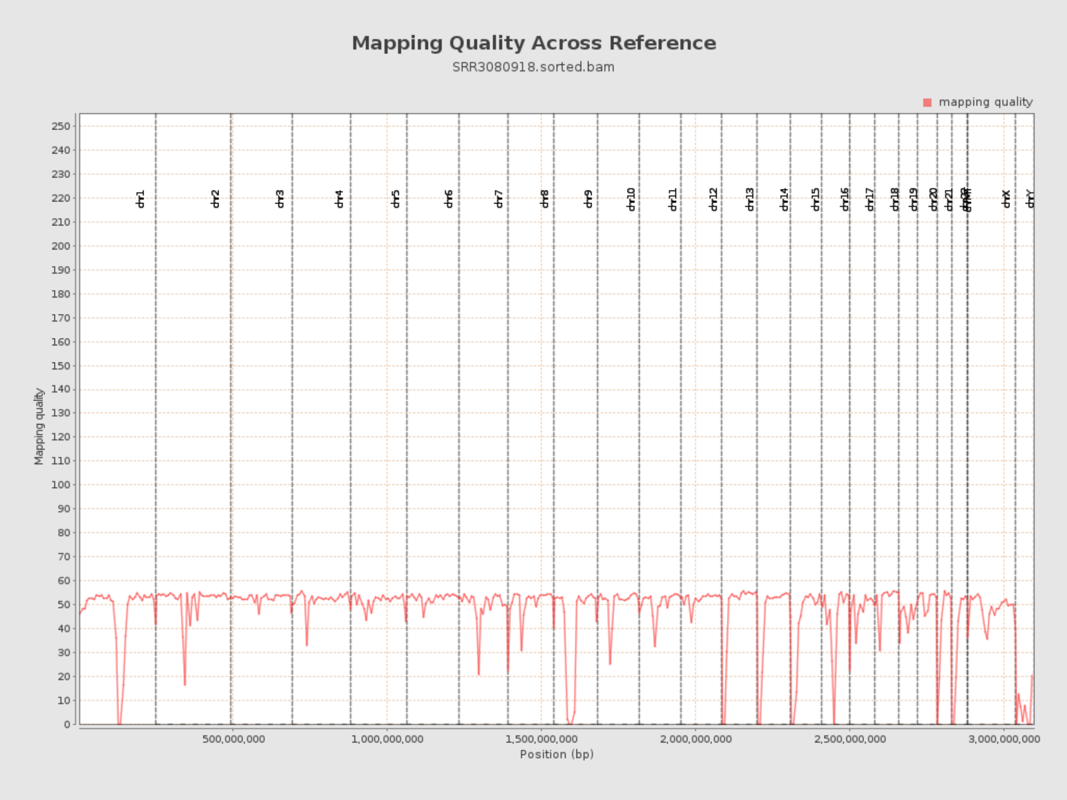
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram