Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081058.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_SRR3081058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:31:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,669,902
Mapped reads	2,431,911 / 91.09%
Unmapped reads	237,991 / 8.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,816 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	115,744 / 4.34%
Duplication rate	3.79%
Clipped reads	1,043,634 / 39.09%

2.2. ACGT Content

Number/percentage of A's	45,737,152 / 27.9%
Number/percentage of C's	30,814,681 / 18.8%
Number/percentage of T's	51,453,996 / 31.39%
Number/percentage of G's	35,913,701 / 21.91%
Number/percentage of N's	1,751 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.053

Standard Deviation	0.4128

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

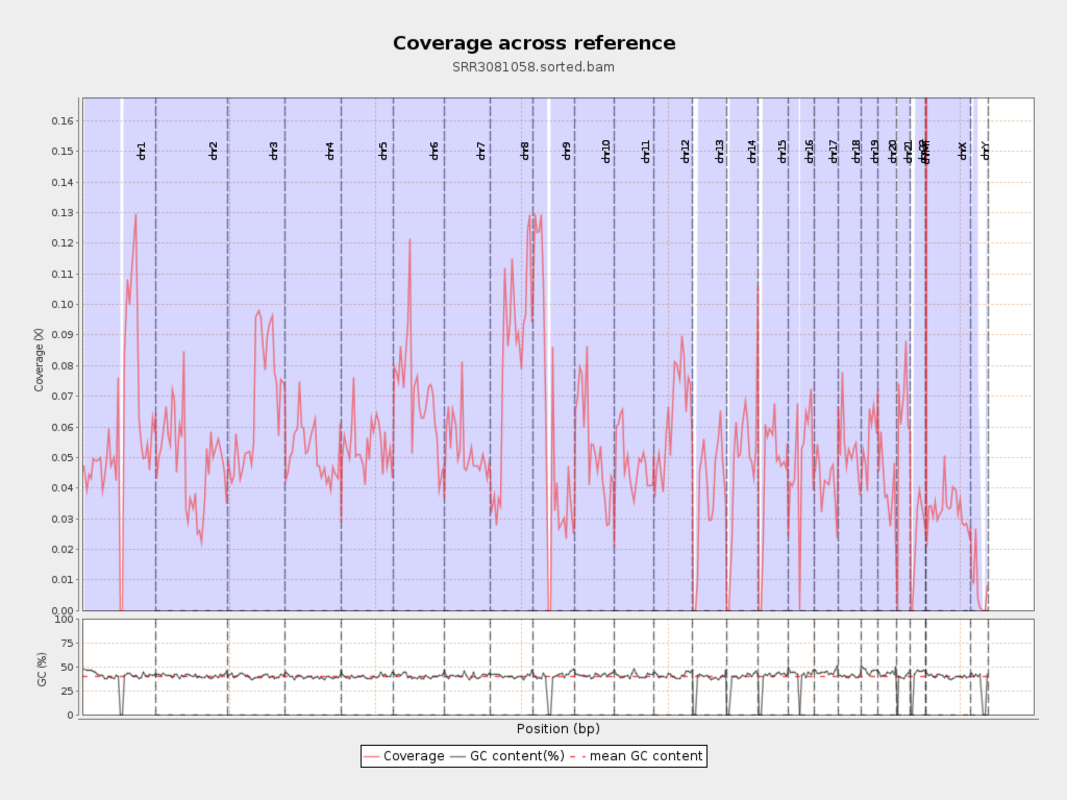
General error rate	0.92%
Mismatches	1,487,454
Insertions	13,024
Mapped reads with at least one insertion	0.53%
Deletions	36,848
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.85%

2.6. Chromosome stats

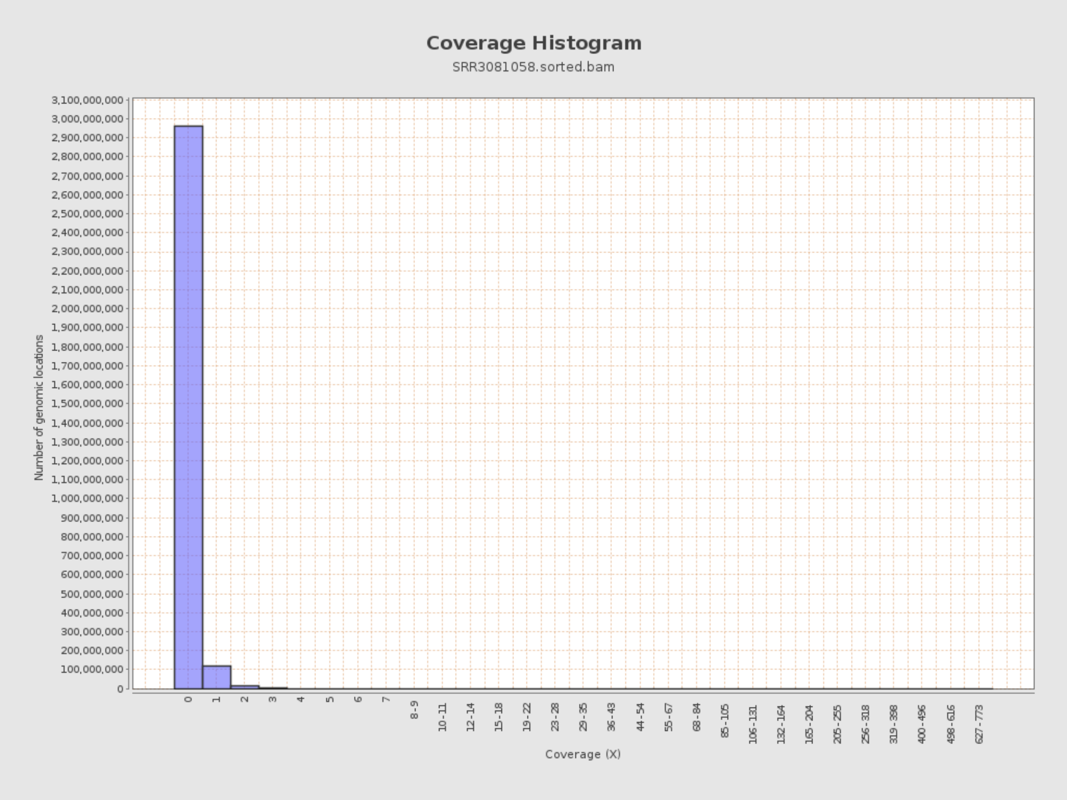
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14581245	0.0585	0.5964
chr2	243199373	11803140	0.0485	0.4576
chr3	198022430	13256277	0.0669	0.2992
chr4	191154276	9868876	0.0516	0.2847
chr5	180915260	9753748	0.0539	0.2715
chr6	171115067	12116764	0.0708	0.4544
chr7	159138663	8377285	0.0526	0.4972

chr8	146364022	11923460	0.0815	0.5016
chr9	141213431	8357531	0.0592	0.5102
chr10	135534747	7243514	0.0534	0.4194
chr11	135006516	6492055	0.0481	0.3139
chr12	133851895	8535539	0.0638	0.3055
chr13	115169878	4380898	0.038	0.2258
chr14	107349540	4925584	0.0459	0.3236
chr15	102531392	4551541	0.0444	0.2435
chr16	90354753	4303437	0.0476	0.333
chr17	81195210	3457608	0.0426	0.2453
chr18	78077248	4182378	0.0536	0.9311
chr19	59128983	3299899	0.0558	0.461
chr20	63025520	2599698	0.0412	0.2515
chr21	48129895	3035543	0.0631	0.3366
chr22	51304566	1224570	0.0239	0.1762
chrMT	16571	170580	10.2939	5.5438
chrX	155270560	5109331	0.0329	0.2457
chrY	59373566	431380	0.0073	0.1836

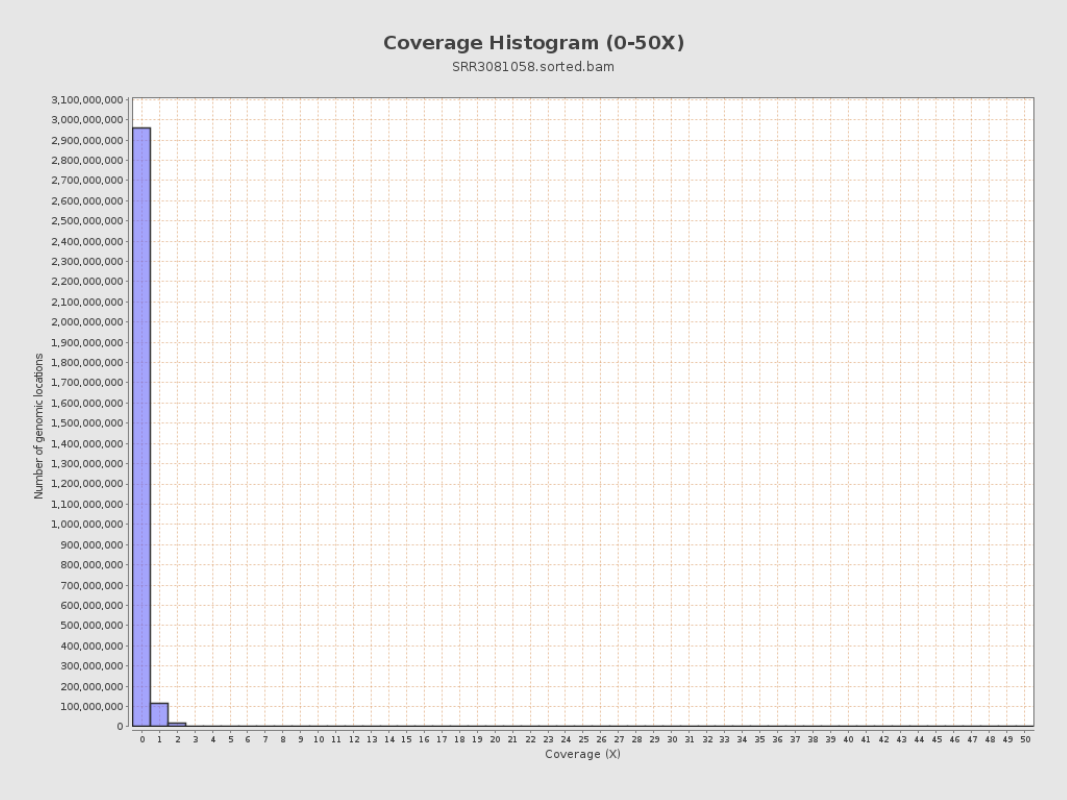
3. Results : Coverage across reference



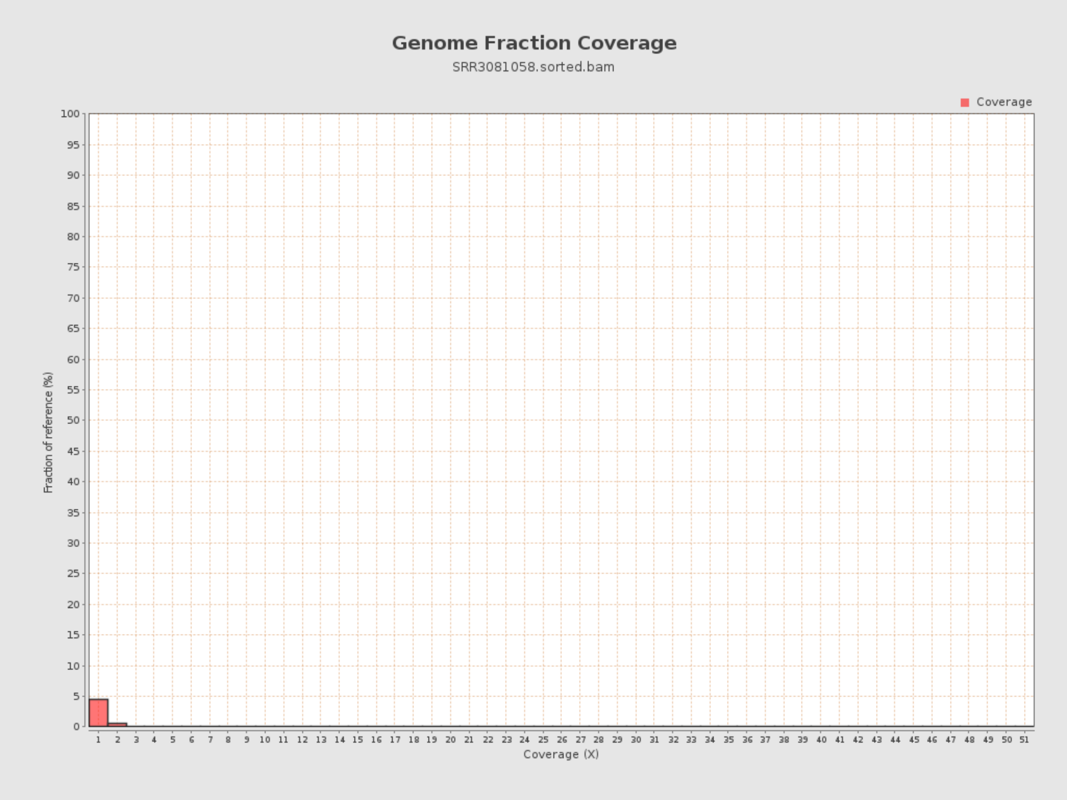
4. Results : Coverage Histogram



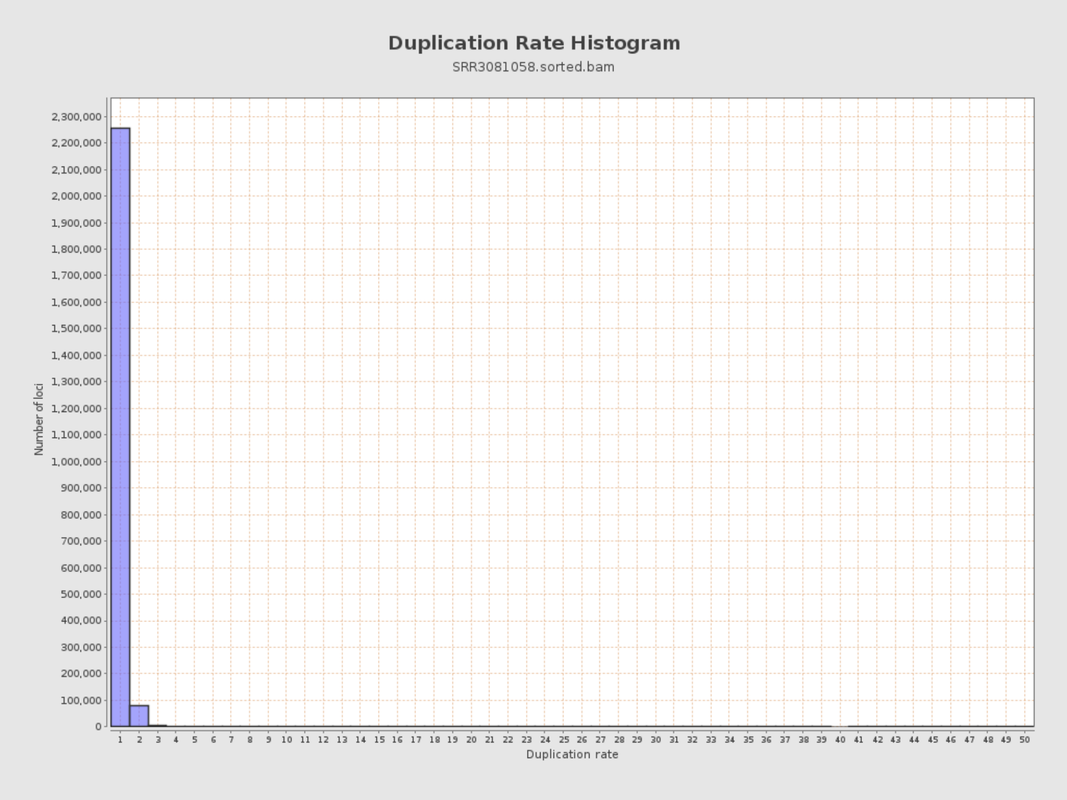
5. Results : Coverage Histogram (0-50X)



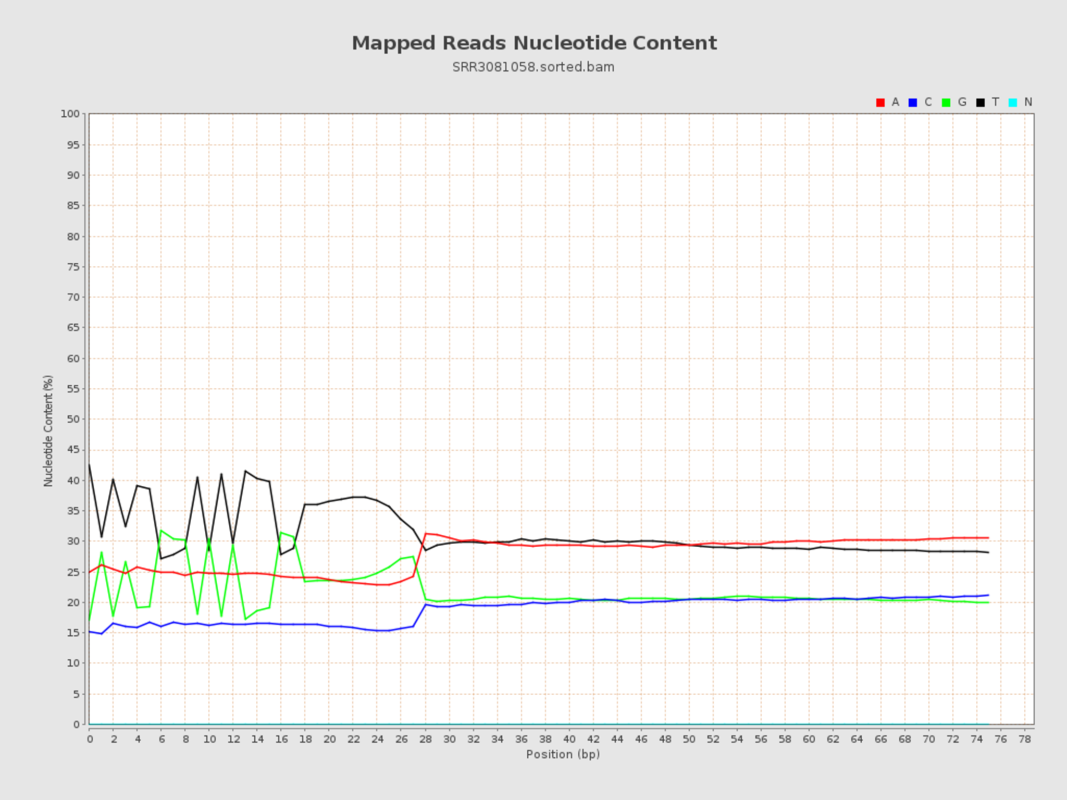
6. Results : Genome Fraction Coverage



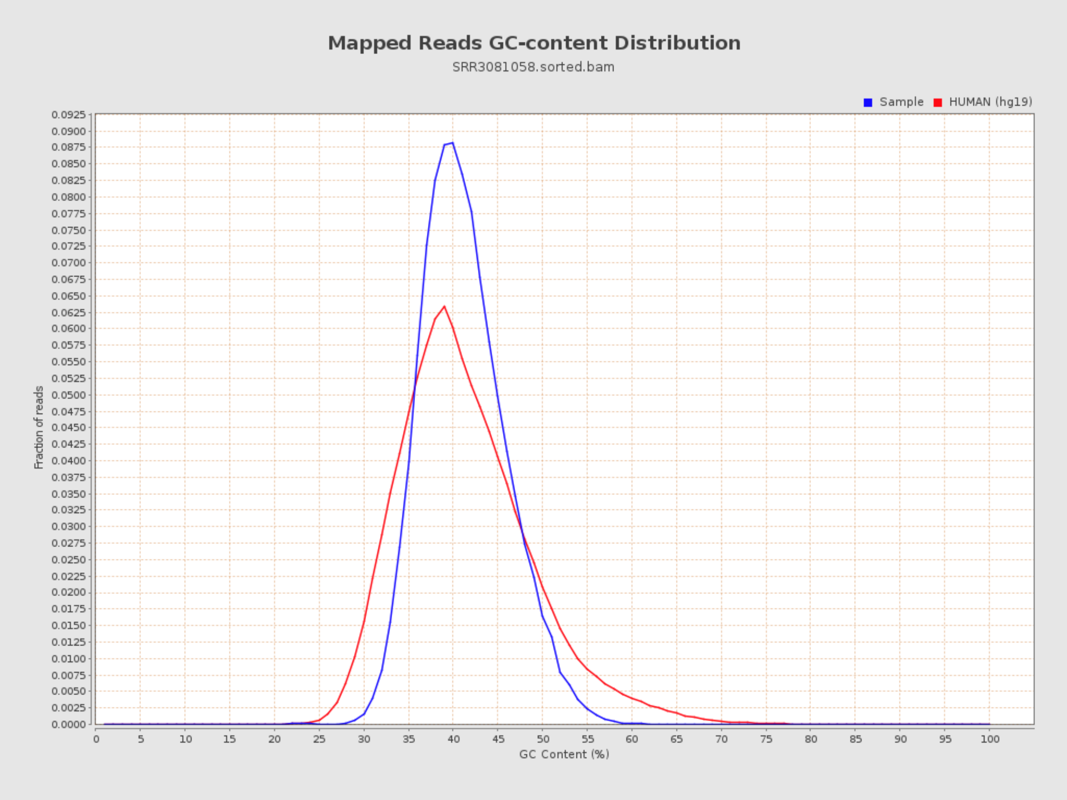
7. Results : Duplication Rate Histogram



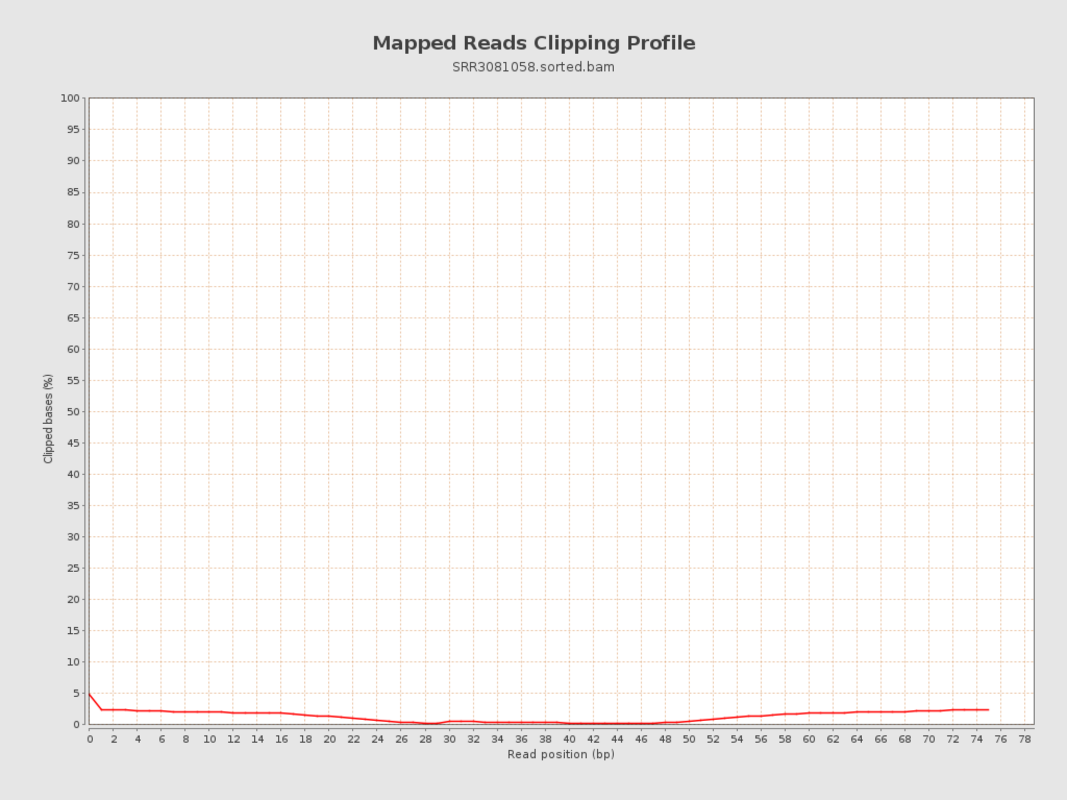
8. Results : Mapped Reads Nucleotide Content



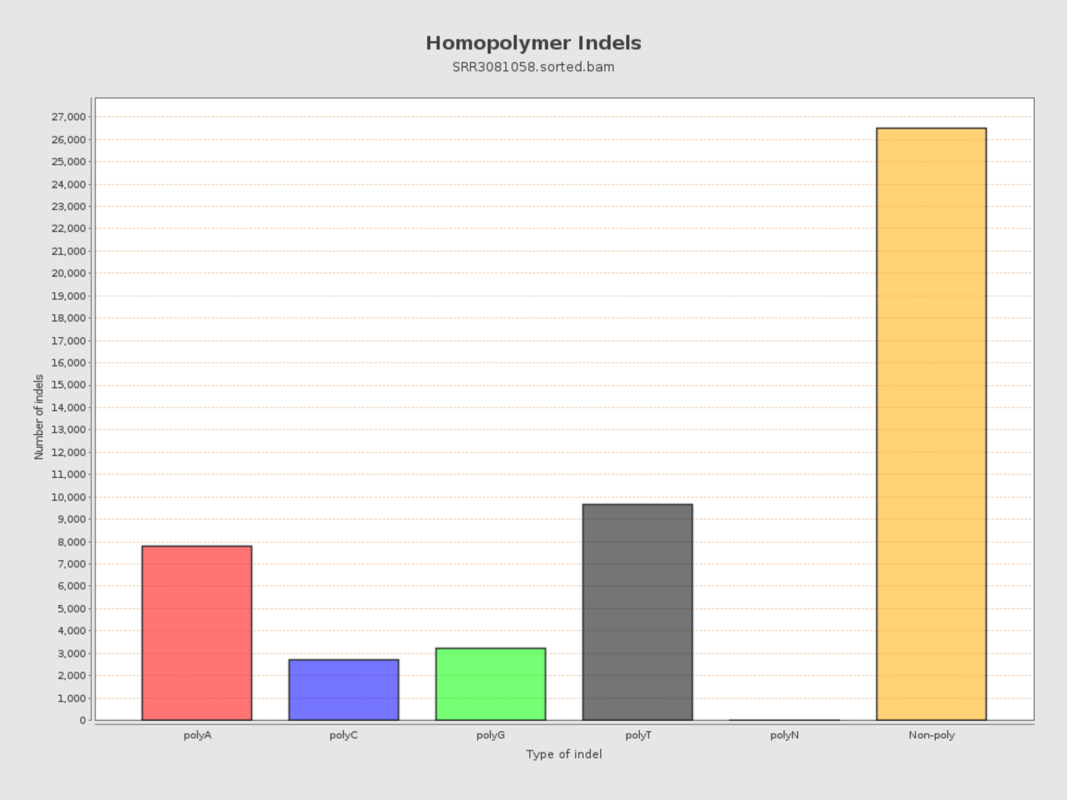
9. Results : Mapped Reads GC-content Distribution



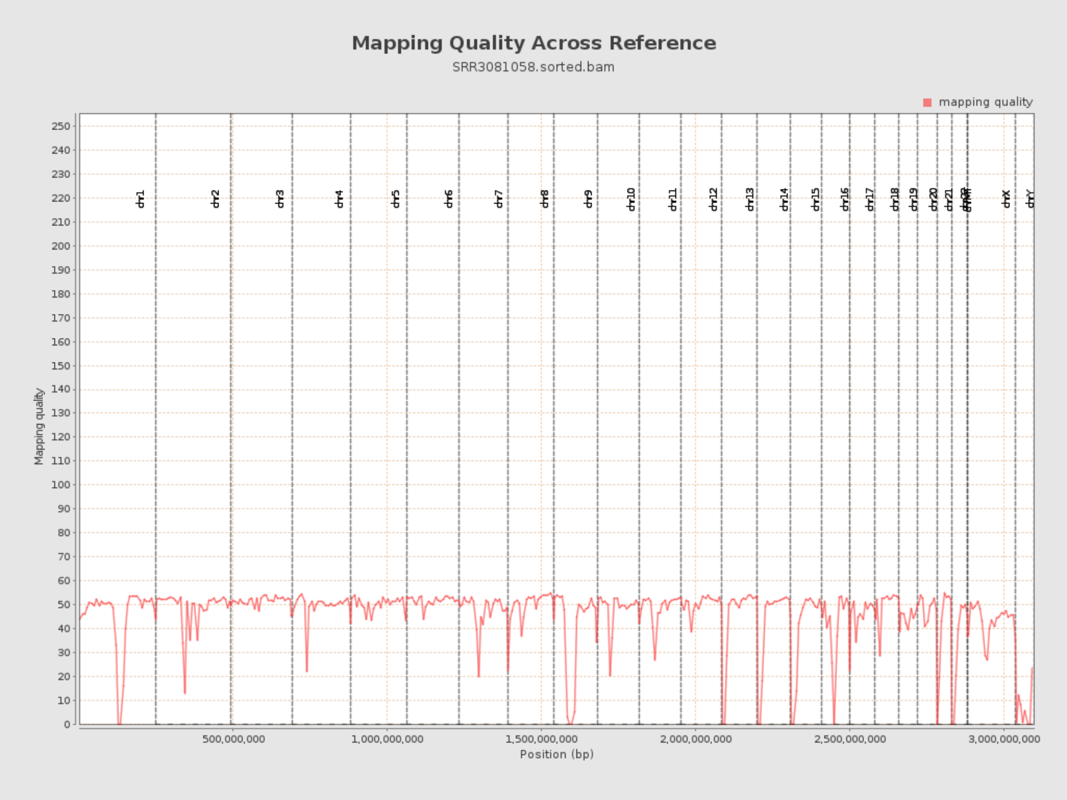
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram