Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:22:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084963.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_SRR3084963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:22:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,111,204
Mapped reads	2,816,778 / 90.54%
Unmapped reads	294,426 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,959 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	132,765 / 4.27%
Duplication rate	3.29%
Clipped reads	1,387,856 / 44.61%

2.2. ACGT Content

Number/percentage of A's	51,467,835 / 27.72%
Number/percentage of C's	34,287,810 / 18.47%
Number/percentage of T's	57,929,883 / 31.2%
Number/percentage of G's	41,959,434 / 22.6%
Number/percentage of N's	24,517 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.06

Standard Deviation	0.5958

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

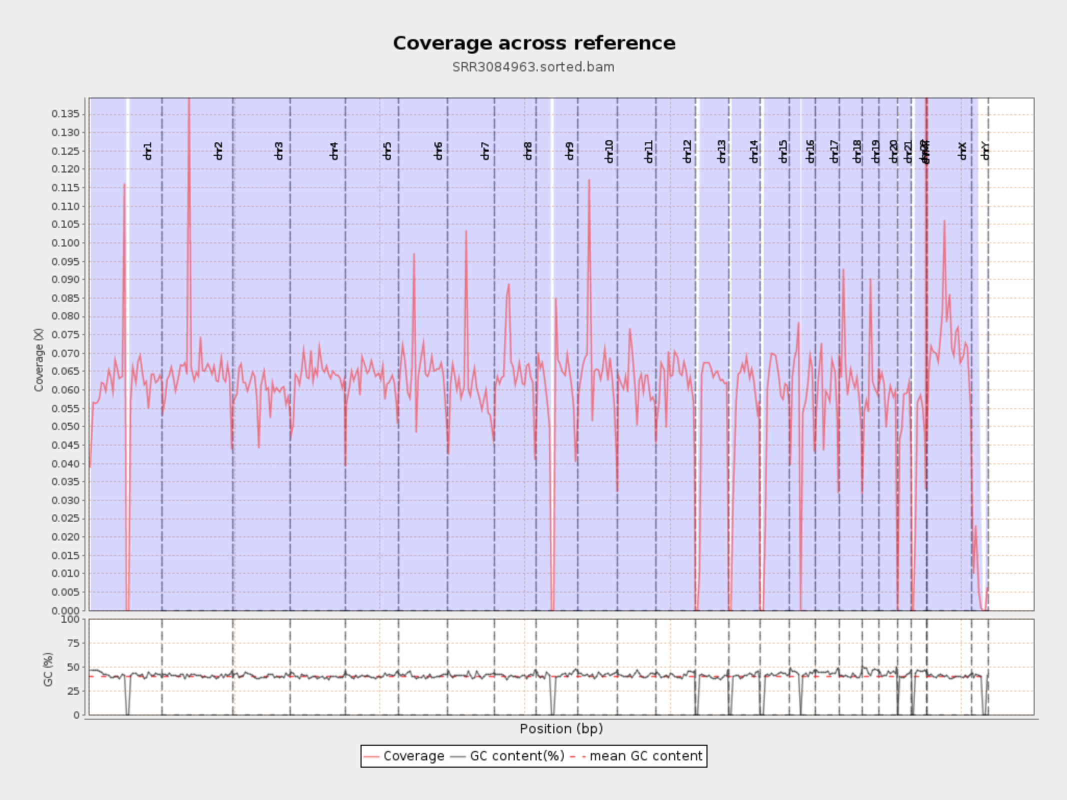
General error rate	0.86%
Mismatches	1,569,052
Insertions	14,798
Mapped reads with at least one insertion	0.52%
Deletions	42,611
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.29%

2.6. Chromosome stats

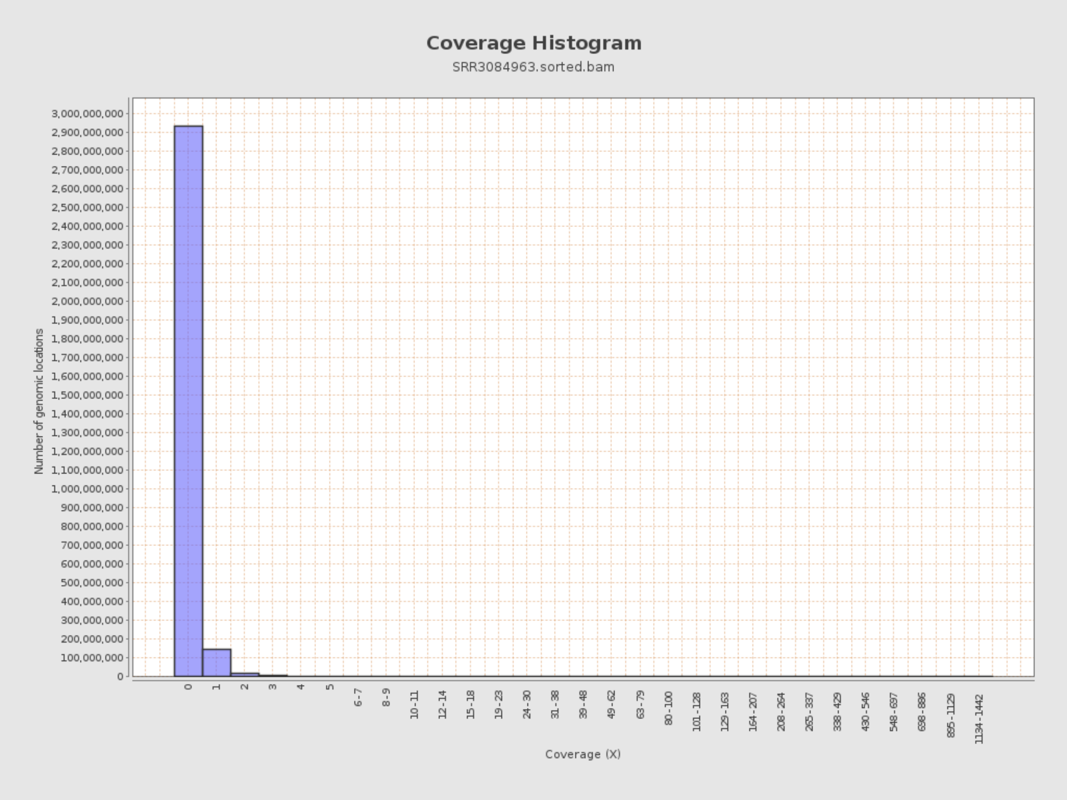
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14792974	0.0593	1.1717
chr2	243199373	16190902	0.0666	0.7574
chr3	198022430	11879506	0.06	0.2819
chr4	191154276	12172640	0.0637	0.3006
chr5	180915260	11393290	0.063	0.287
chr6	171115067	11215610	0.0655	0.4387
chr7	159138663	9689982	0.0609	0.5589

chr8	146364022	9552066	0.0653	0.8597
chr9	141213431	7982136	0.0565	0.5698
chr10	135534747	9002365	0.0664	0.5915
chr11	135006516	8283269	0.0614	0.55
chr12	133851895	8378868	0.0626	0.2961
chr13	115169878	6148556	0.0534	0.2588
chr14	107349540	5617142	0.0523	0.326
chr15	102531392	5273165	0.0514	0.2639
chr16	90354753	5107424	0.0565	0.338
chr17	81195210	4707167	0.058	0.3711
chr18	78077248	5071417	0.065	1.1452
chr19	59128983	3610254	0.0611	0.8526
chr20	63025520	3628714	0.0576	0.3002
chr21	48129895	2344438	0.0487	0.2901
chr22	51304566	1920656	0.0374	0.2148
chrMT	16571	26631	1.6071	1.5775
chrX	155270560	11284870	0.0727	0.4065
chrY	59373566	463921	0.0078	0.1541

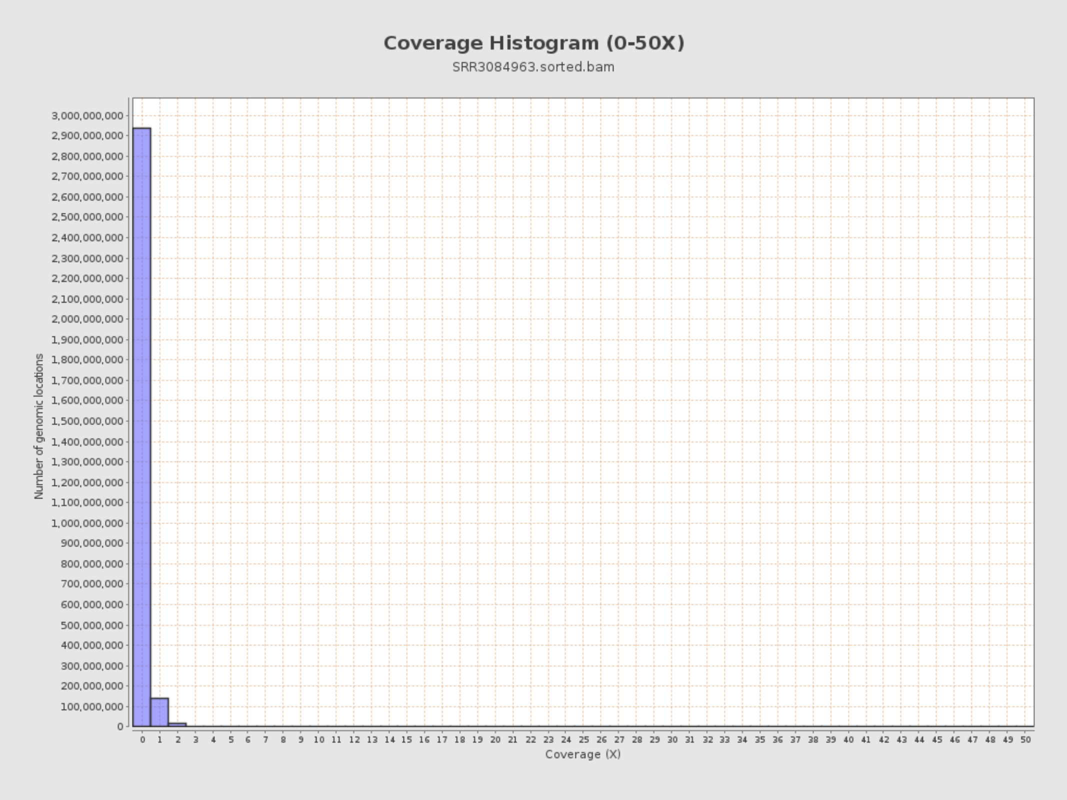
3. Results : Coverage across reference



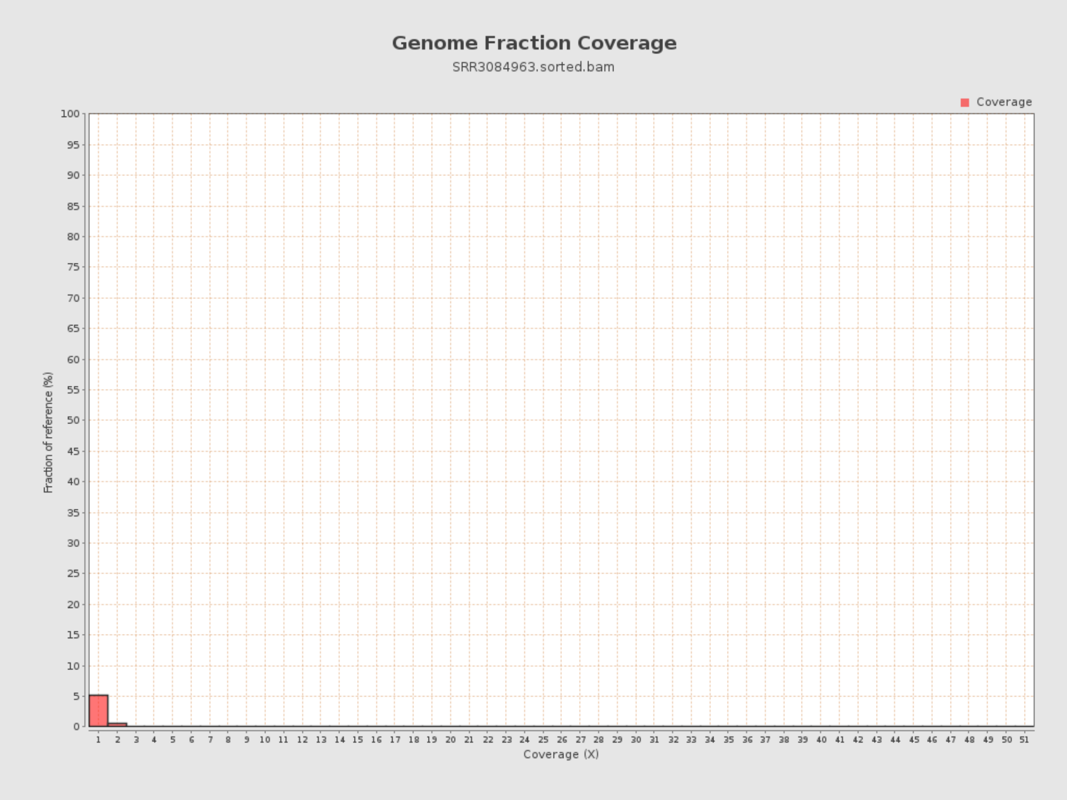
4. Results : Coverage Histogram



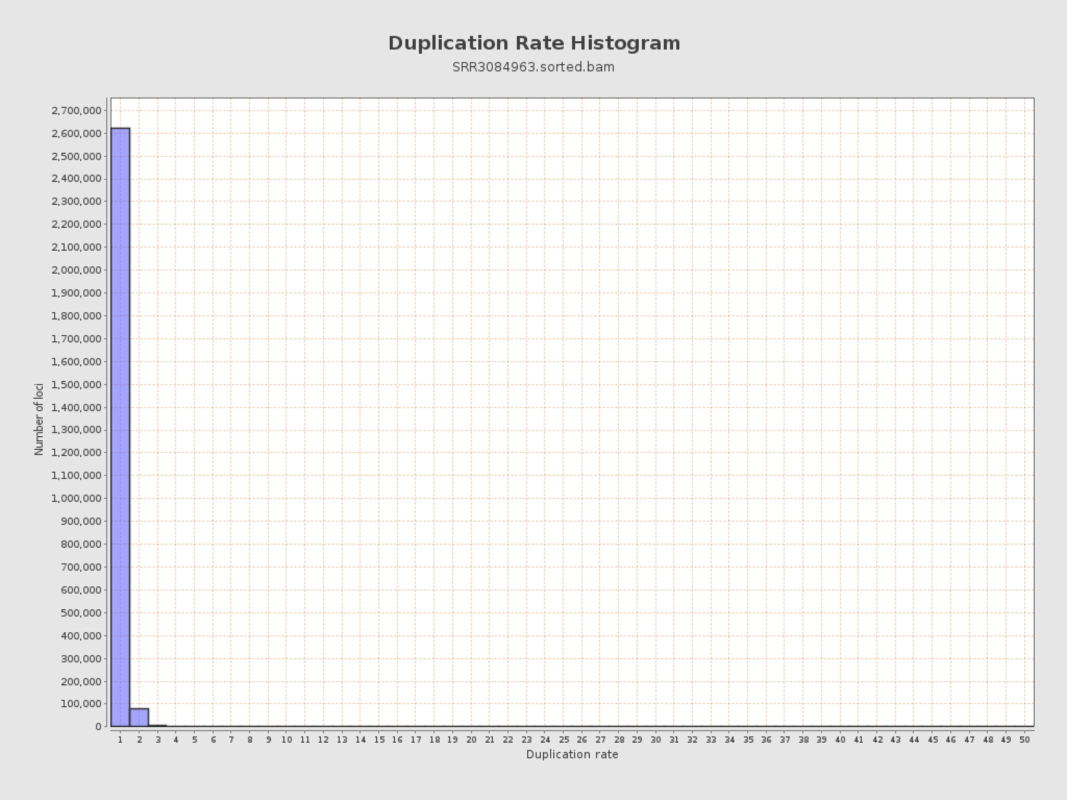
5. Results : Coverage Histogram (0-50X)



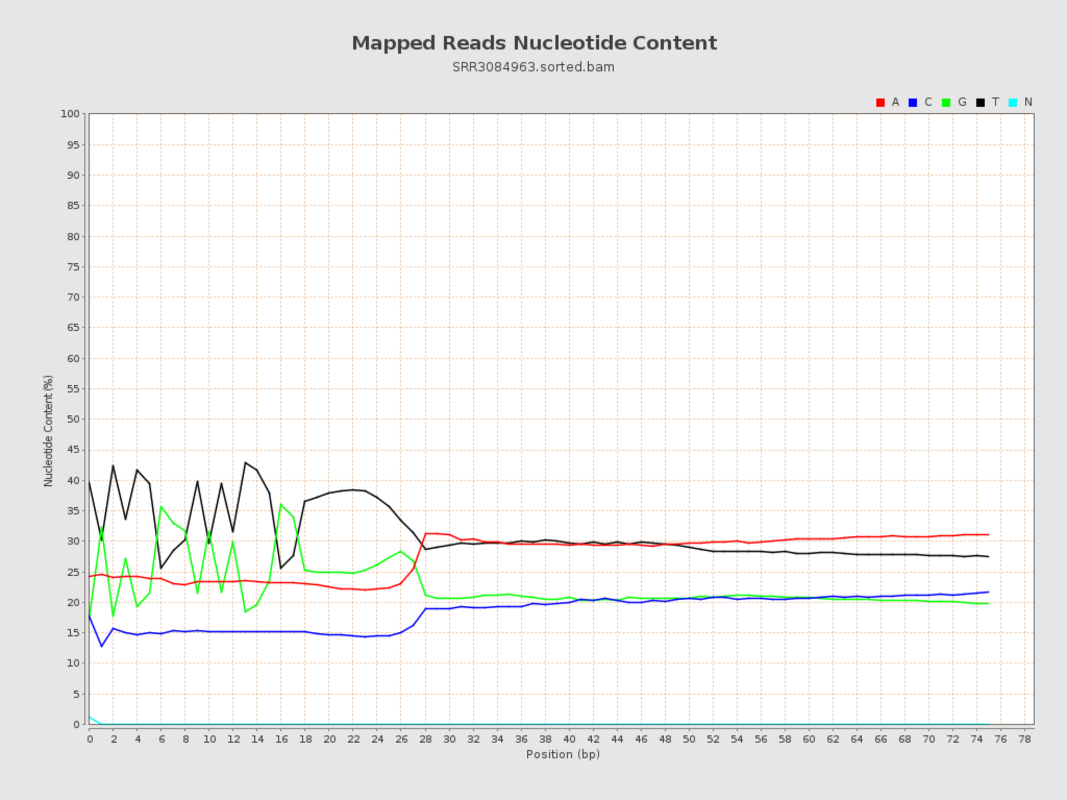
6. Results : Genome Fraction Coverage



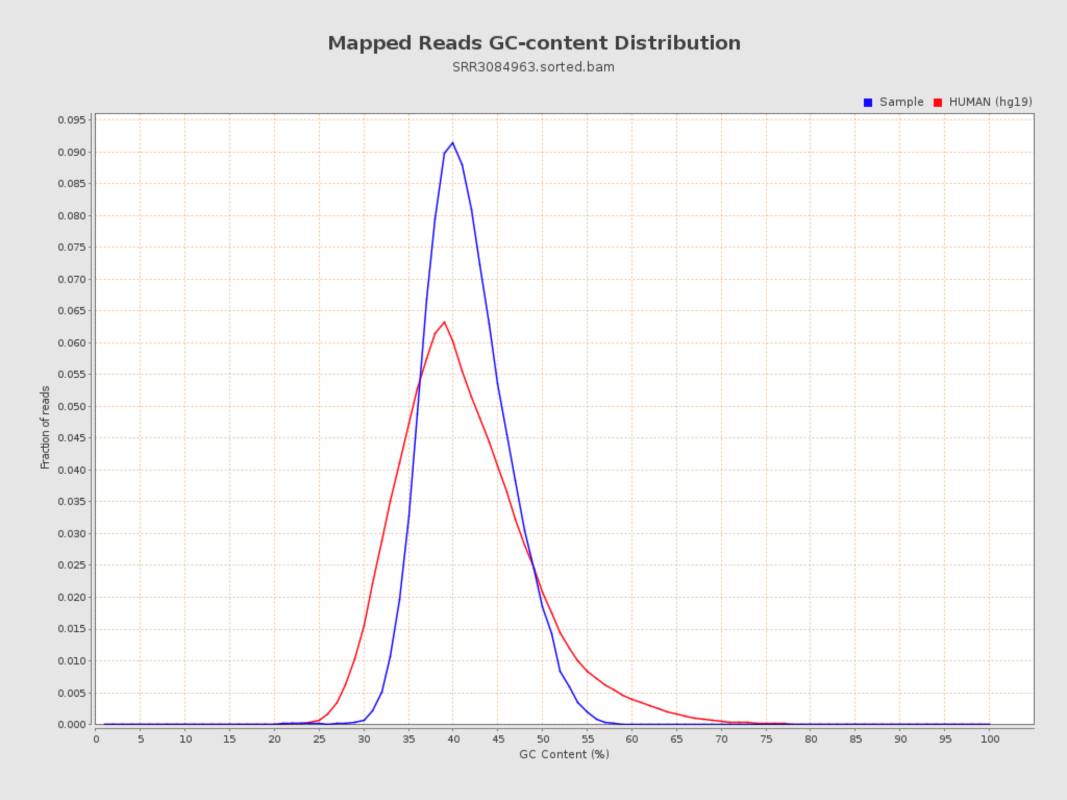
7. Results : Duplication Rate Histogram



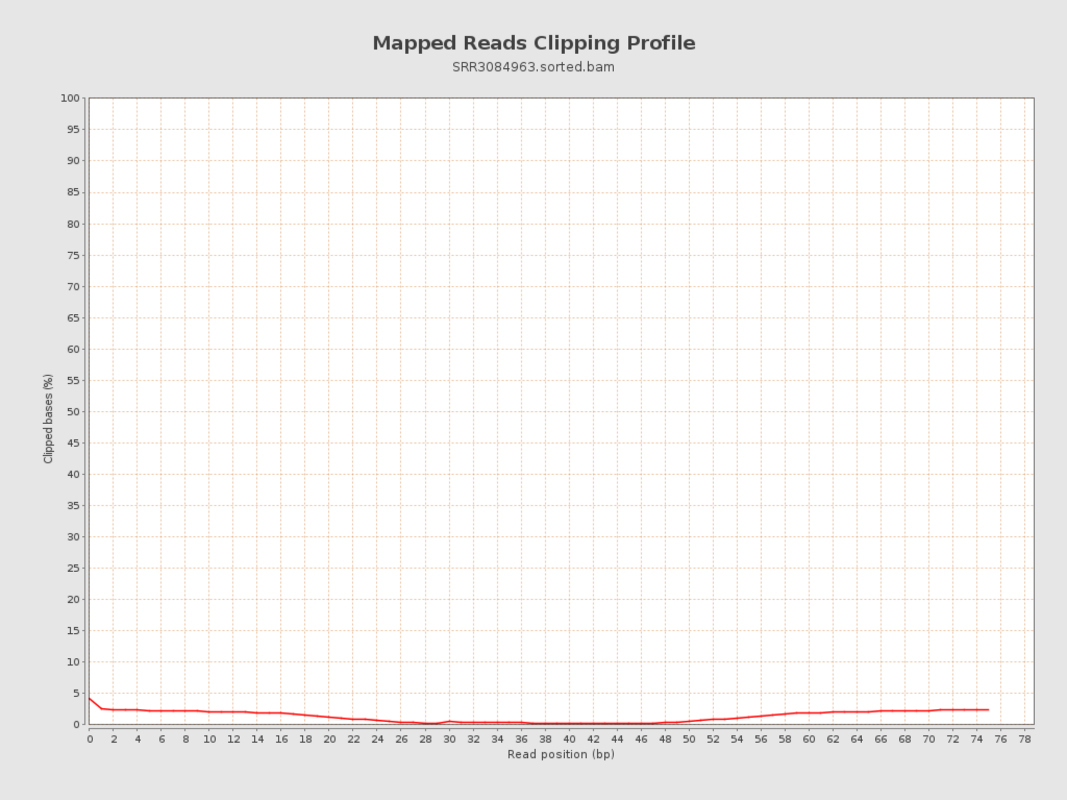
8. Results : Mapped Reads Nucleotide Content



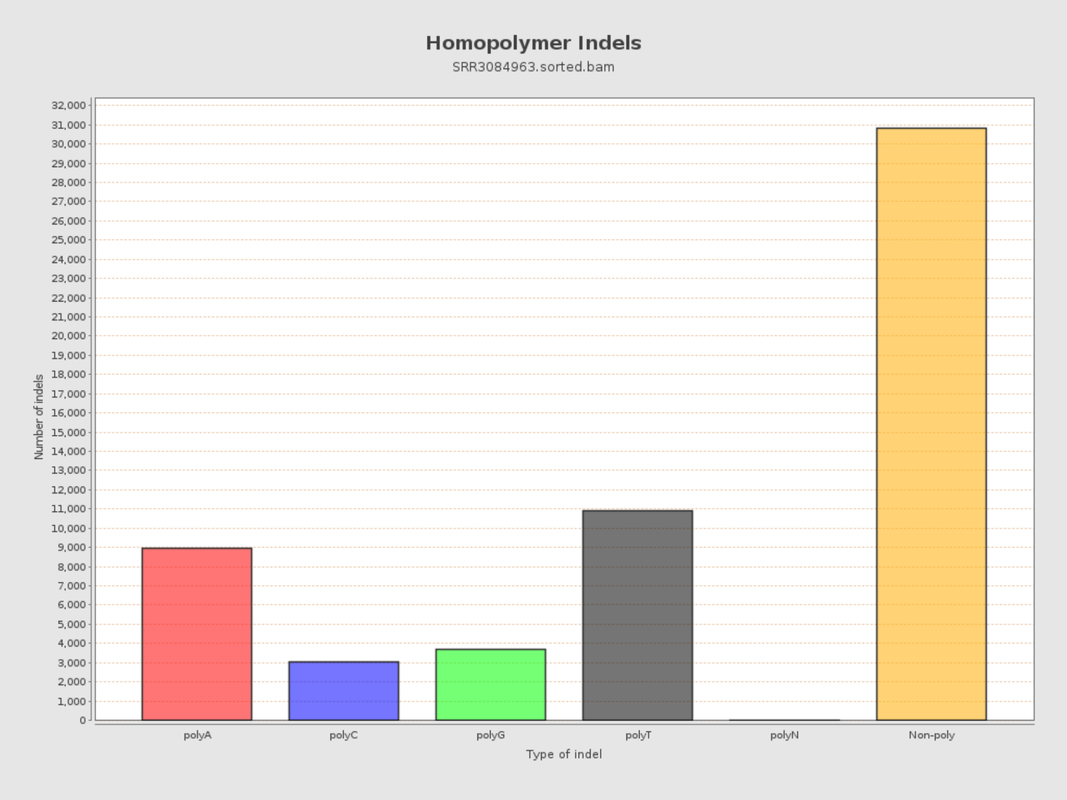
9. Results : Mapped Reads GC-content Distribution



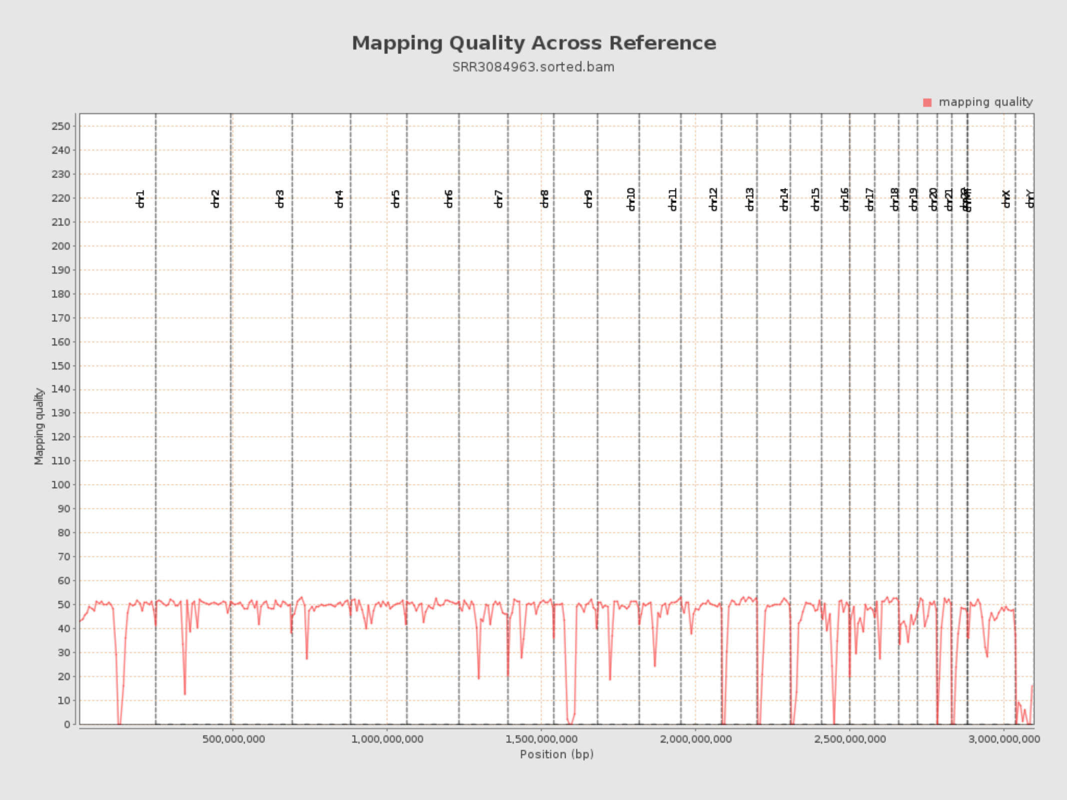
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram