Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:02:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708570.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_SRR1708570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:02:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,308,070
Mapped reads	3,540,733 / 82.19%
Unmapped reads	767,337 / 17.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	77 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,320 / 0.38%
Duplication rate	0.46%
Clipped reads	46,225 / 1.07%

2.2. ACGT Content

Number/percentage of A's	54,695,188 / 30.98%
Number/percentage of C's	33,534,446 / 18.99%
Number/percentage of T's	54,519,017 / 30.88%
Number/percentage of G's	33,822,068 / 19.15%
Number/percentage of N's	4,880 / 0%
GC Percentage	38.15%

2.3. Coverage

Mean	0.057

Standard Deviation	0.246

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

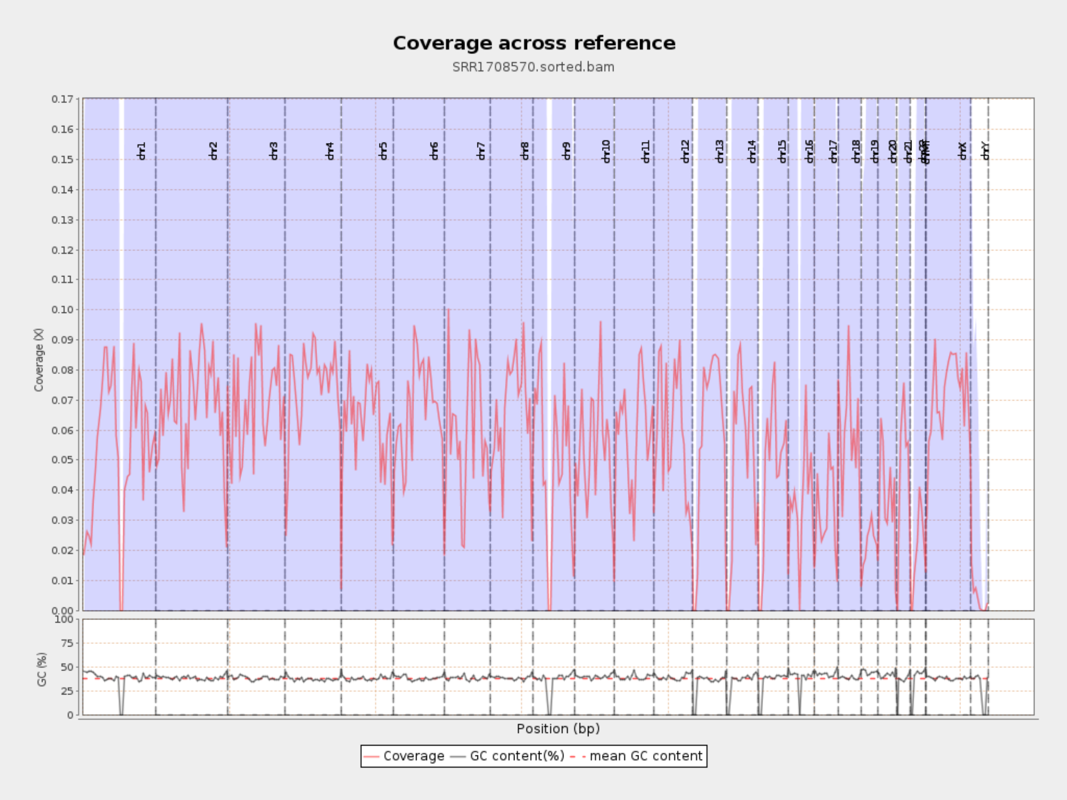
General error rate	0.16%
Mismatches	275,512
Insertions	11,731
Mapped reads with at least one insertion	0.33%
Deletions	9,302
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.86%

2.6. Chromosome stats

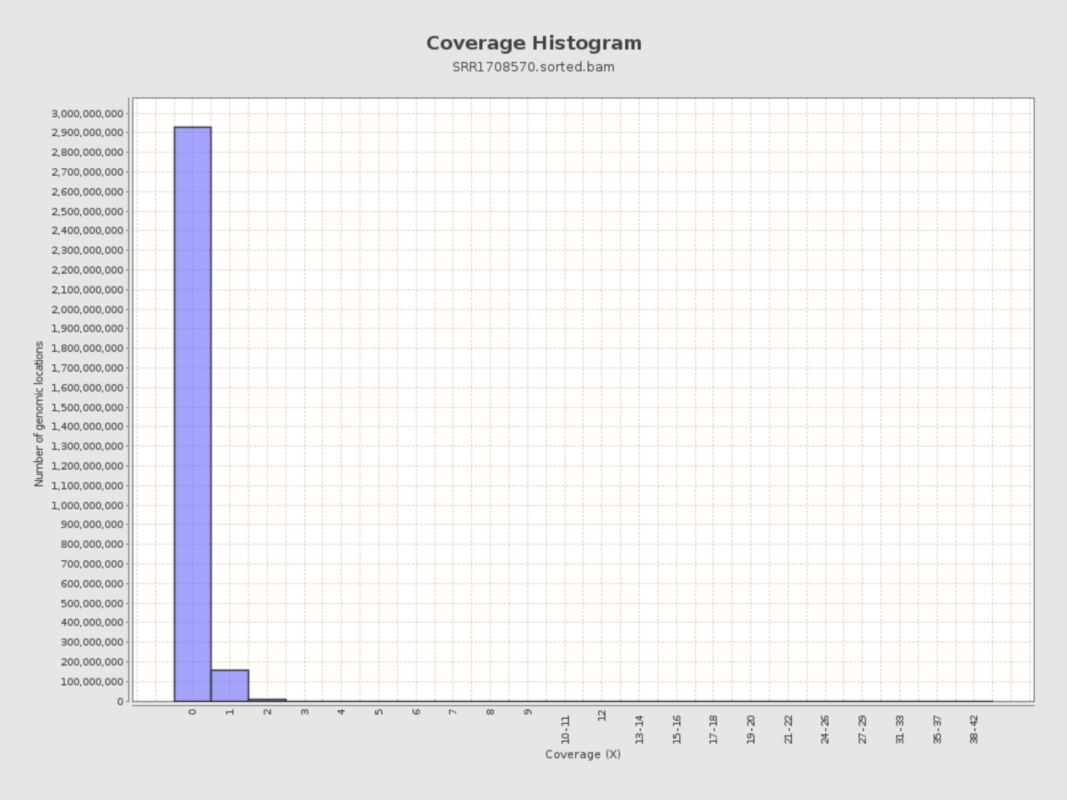
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13505631	0.0542	0.2405
chr2	243199373	16465766	0.0677	0.2671
chr3	198022430	13707797	0.0692	0.2699
chr4	191154276	14305202	0.0748	0.2803
chr5	180915260	11257842	0.0622	0.2557
chr6	171115067	11515774	0.0673	0.2662
chr7	159138663	9413159	0.0592	0.2503

chr8	146364022	9798222	0.0669	0.2653
chr9	141213431	7125819	0.0505	0.2321
chr10	135534747	7345104	0.0542	0.2388
chr11	135006516	7981167	0.0591	0.2508
chr12	133851895	7886855	0.0589	0.2498
chr13	115169878	6860167	0.0596	0.2513
chr14	107349540	5626277	0.0524	0.2368
chr15	102531392	4759501	0.0464	0.2224
chr16	90354753	3232635	0.0358	0.1942
chr17	81195210	2721958	0.0335	0.1889
chr18	78077248	4615589	0.0591	0.2496
chr19	59128983	1315731	0.0223	0.1522
chr20	63025520	2512931	0.0399	0.2055
chr21	48129895	2190461	0.0455	0.2218
chr22	51304566	1070155	0.0209	0.1481
chrMT	16571	499	0.0301	0.1765
chrX	155270560	11139039	0.0717	0.2755
chrY	59373566	237889	0.004	0.0658

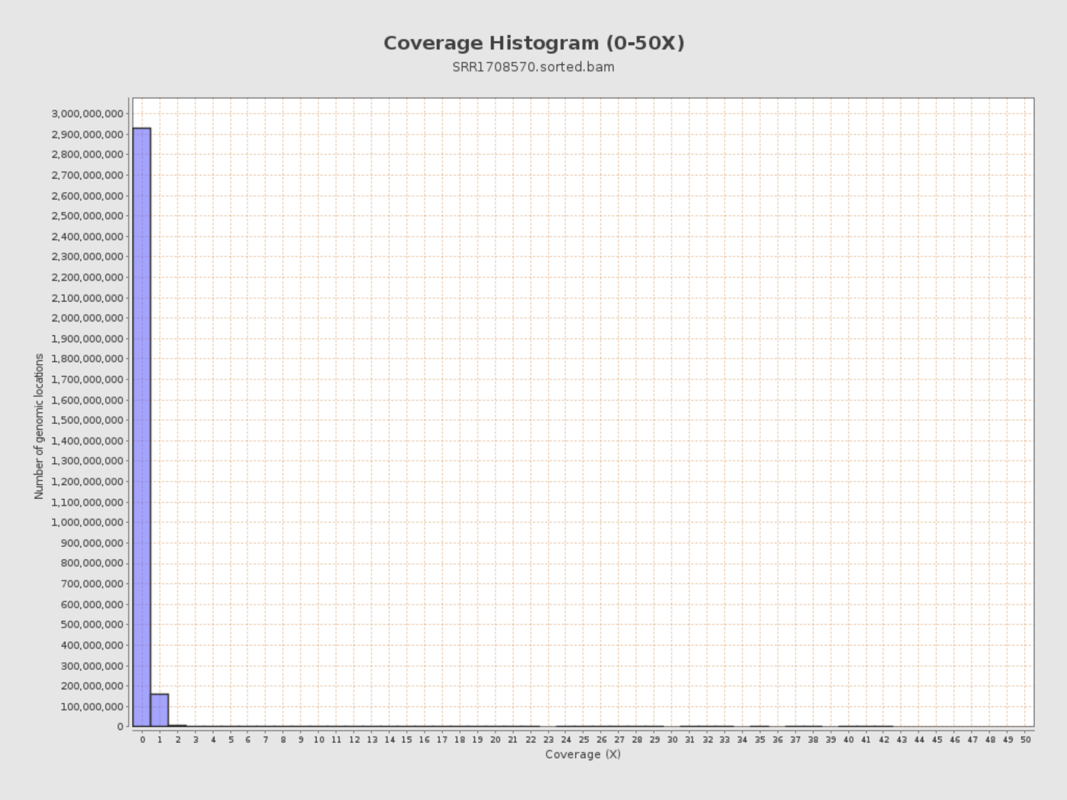
3. Results : Coverage across reference



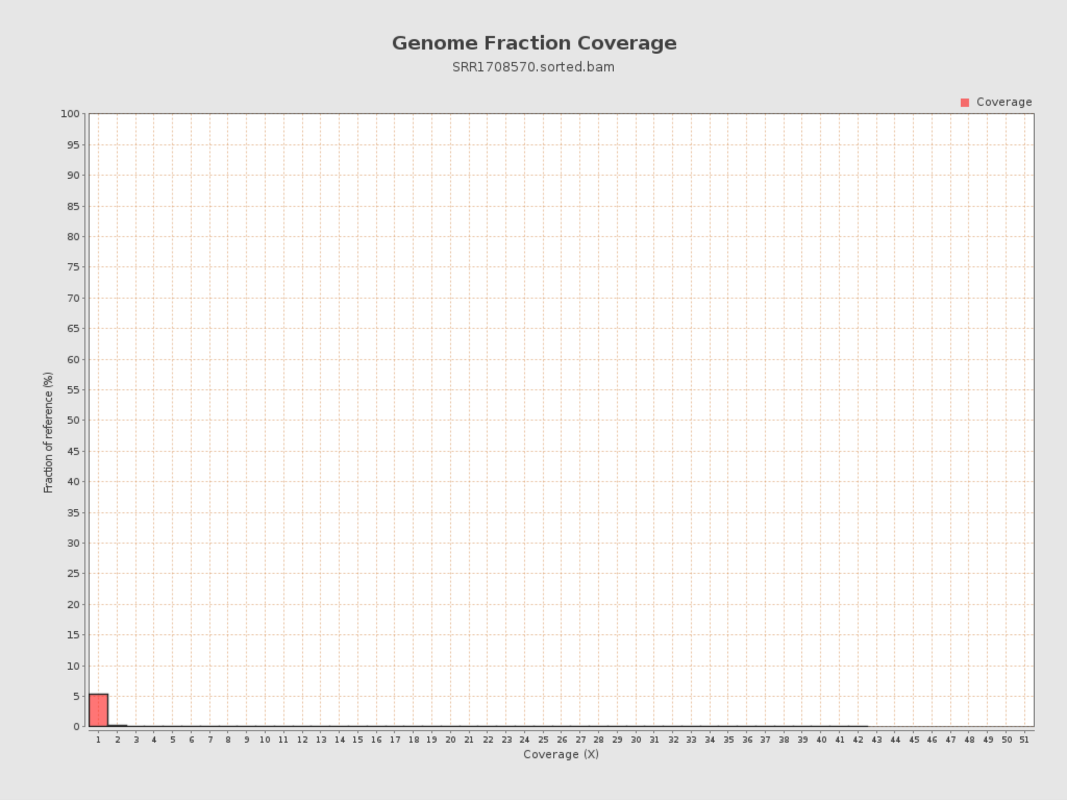
4. Results : Coverage Histogram



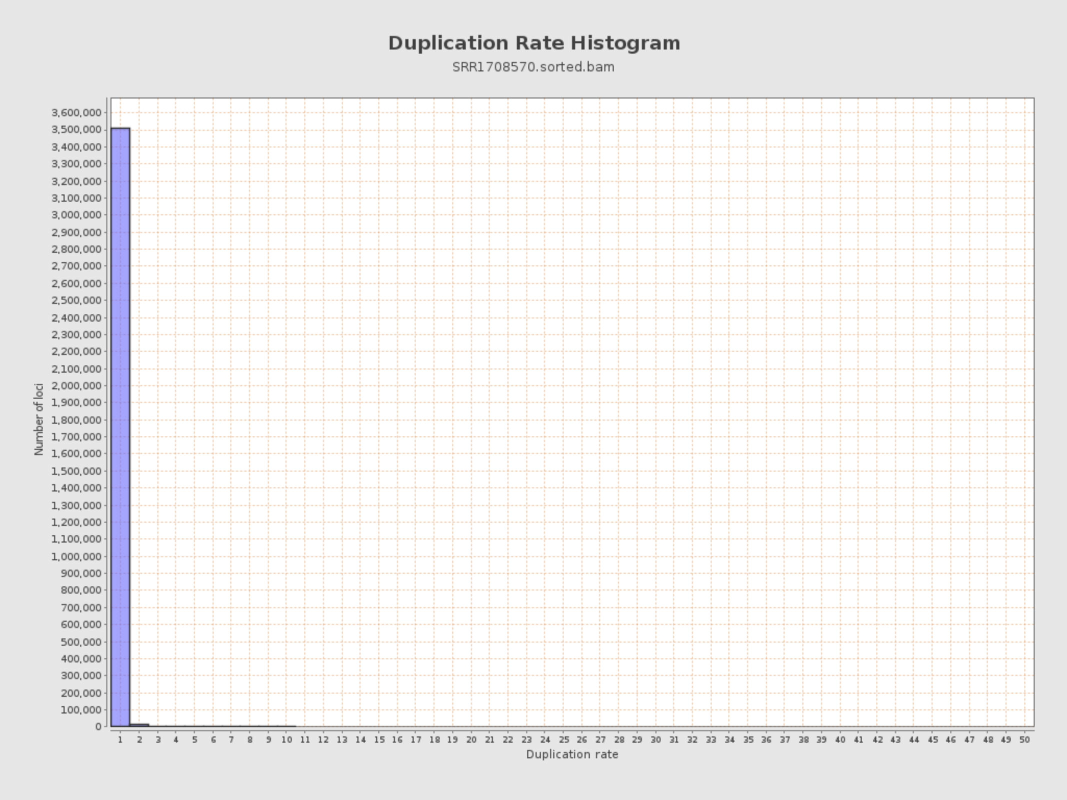
5. Results : Coverage Histogram (0-50X)



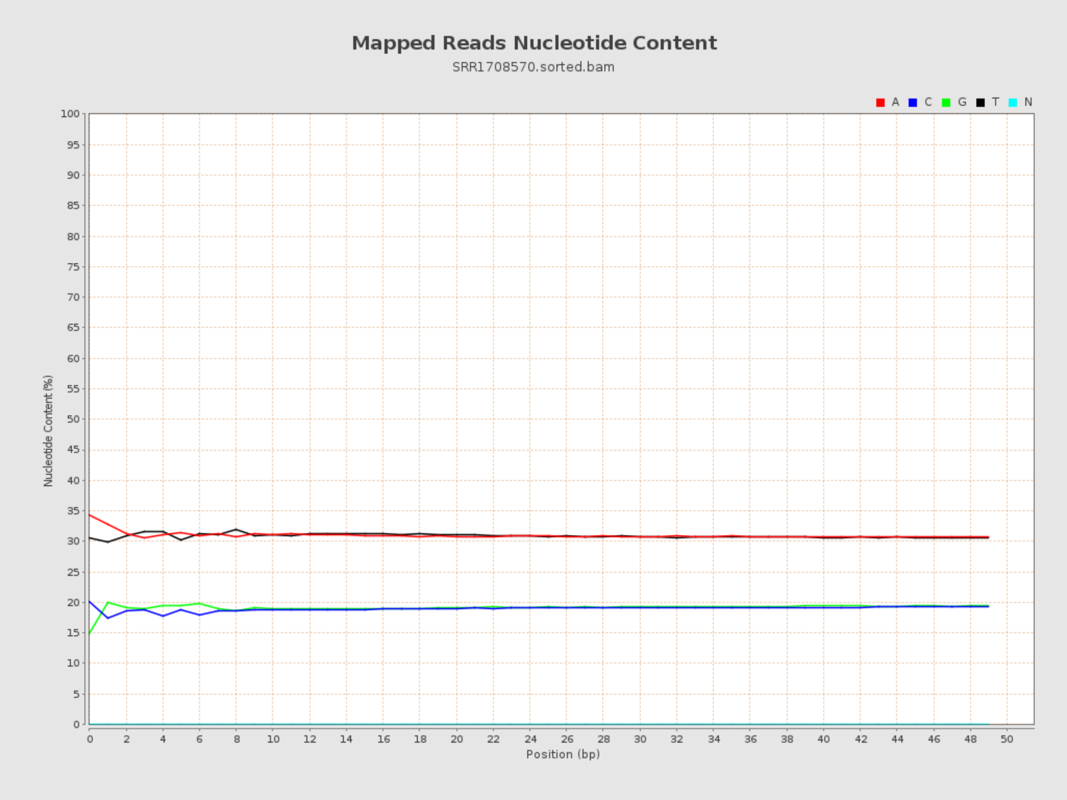
6. Results : Genome Fraction Coverage



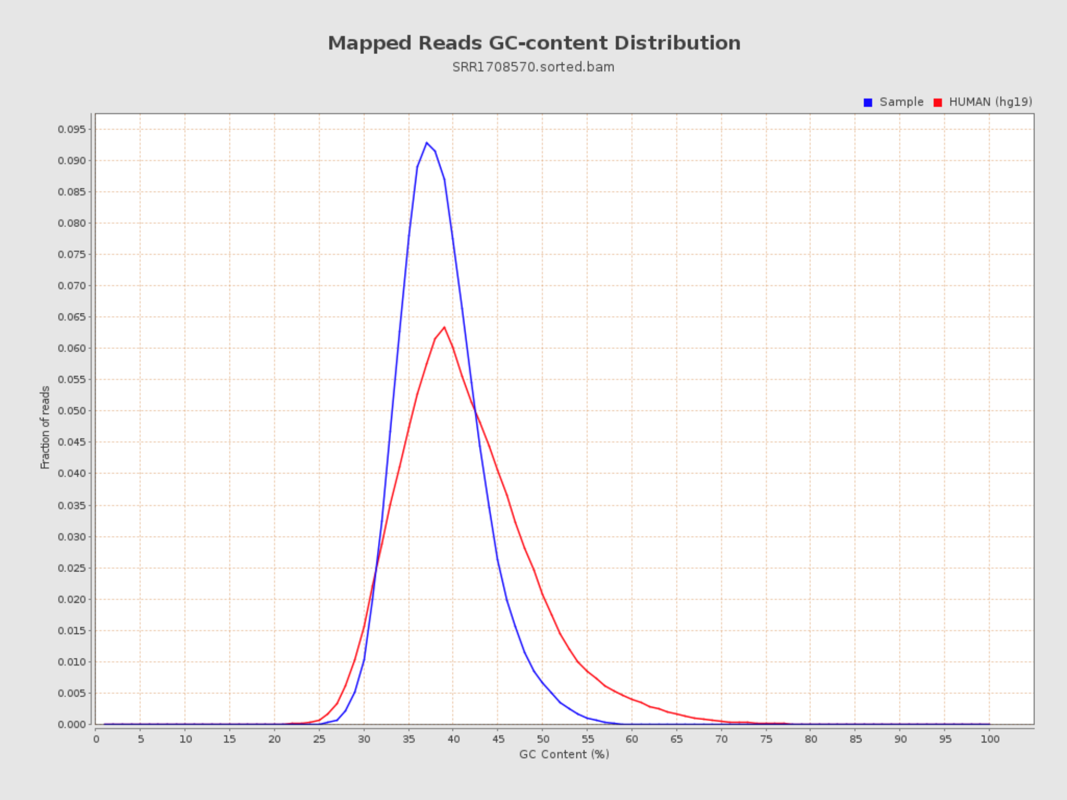
7. Results : Duplication Rate Histogram



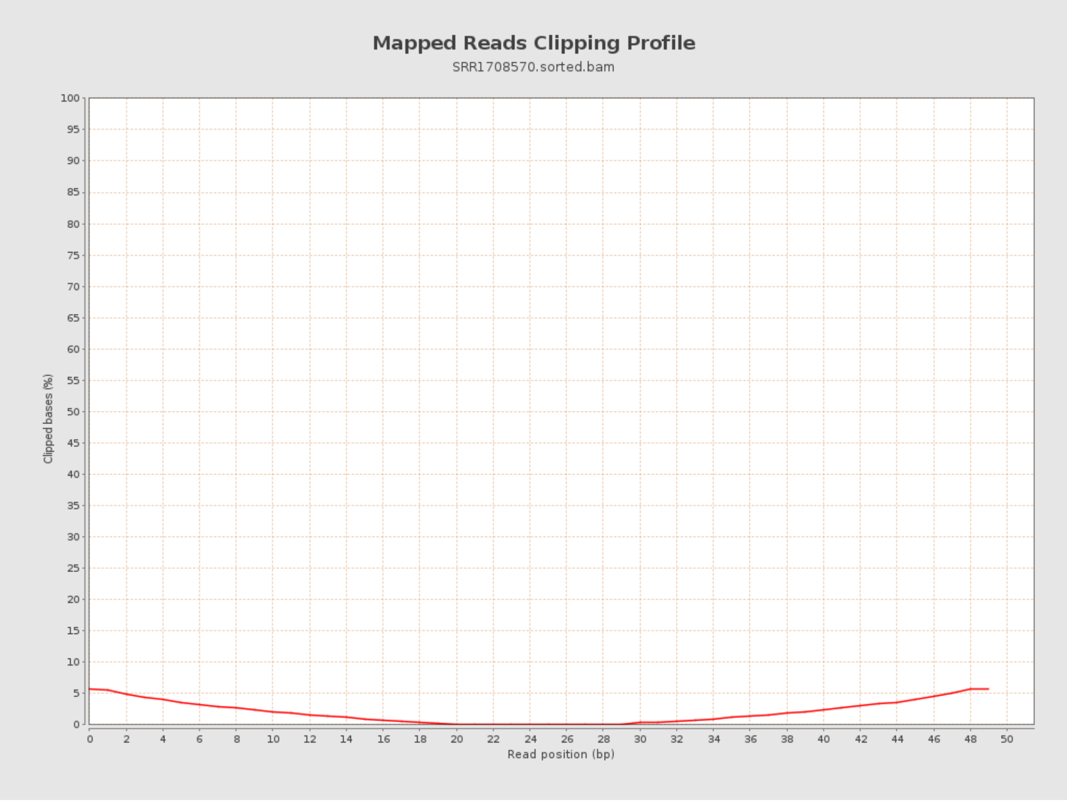
8. Results : Mapped Reads Nucleotide Content



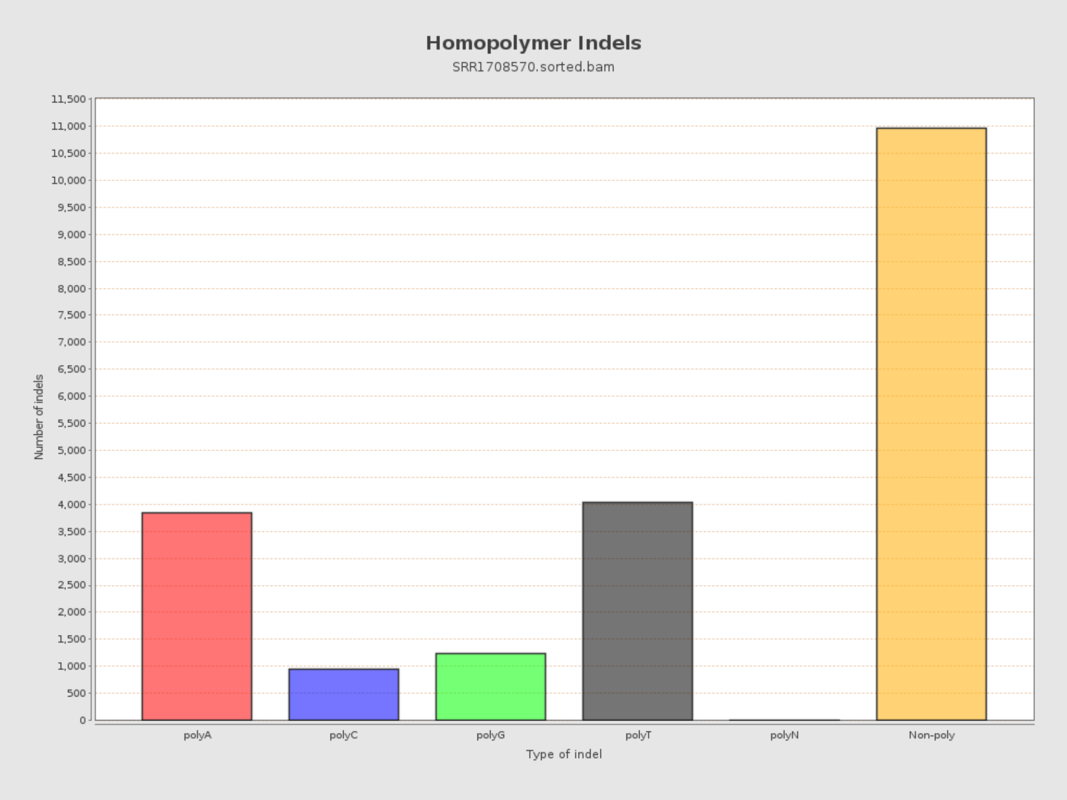
9. Results : Mapped Reads GC-content Distribution



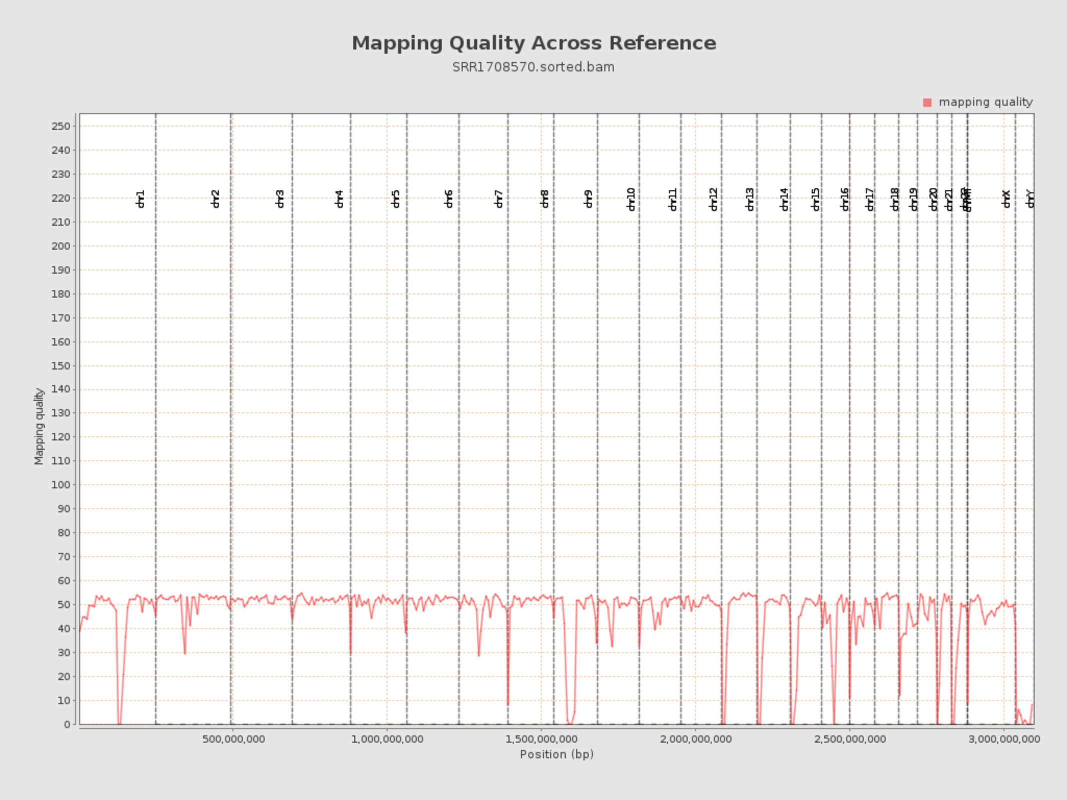
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram