Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:58:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708550.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_SRR1708550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708550.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:58:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708550.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,405,172
Mapped reads	3,616,408 / 82.09%
Unmapped reads	788,764 / 17.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	97 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,497 / 0.4%
Duplication rate	0.48%
Clipped reads	49,534 / 1.12%

2.2. ACGT Content

Number/percentage of A's	55,937,934 / 31.02%
Number/percentage of C's	34,193,275 / 18.96%
Number/percentage of T's	55,675,404 / 30.87%
Number/percentage of G's	34,512,240 / 19.14%
Number/percentage of N's	7,979 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	0.0583

Standard Deviation	0.2485

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

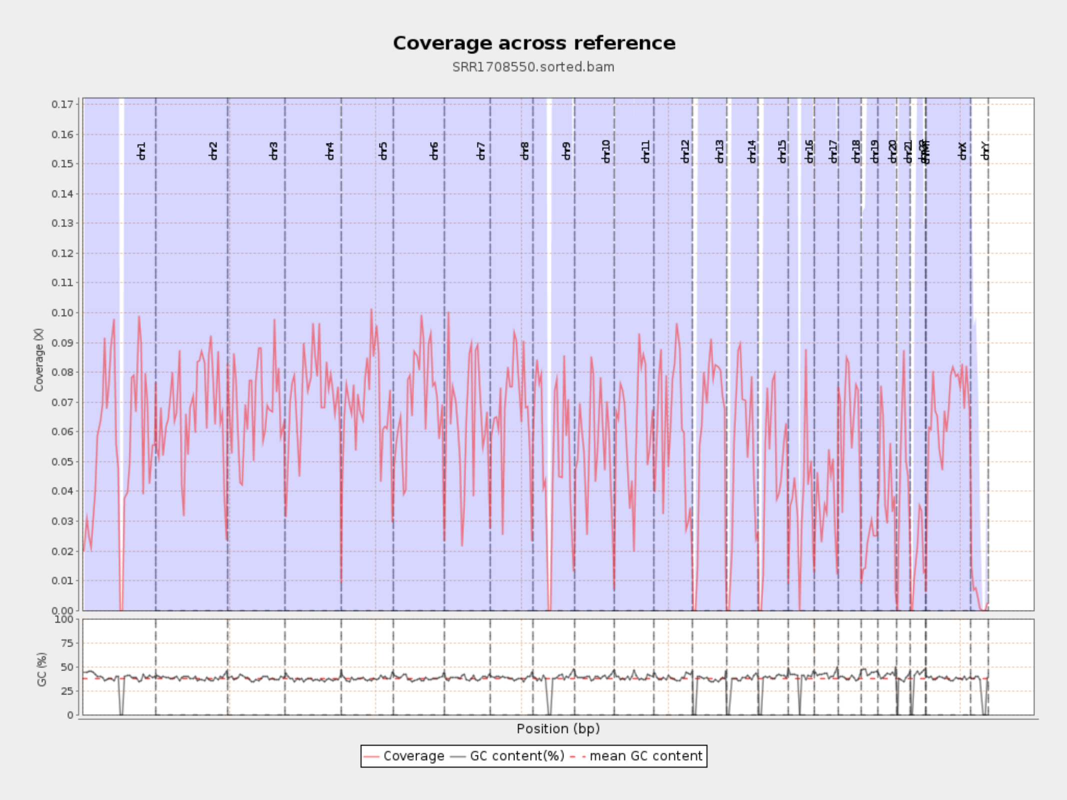
General error rate	0.17%
Mismatches	285,640
Insertions	12,230
Mapped reads with at least one insertion	0.34%
Deletions	9,717
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.1%

2.6. Chromosome stats

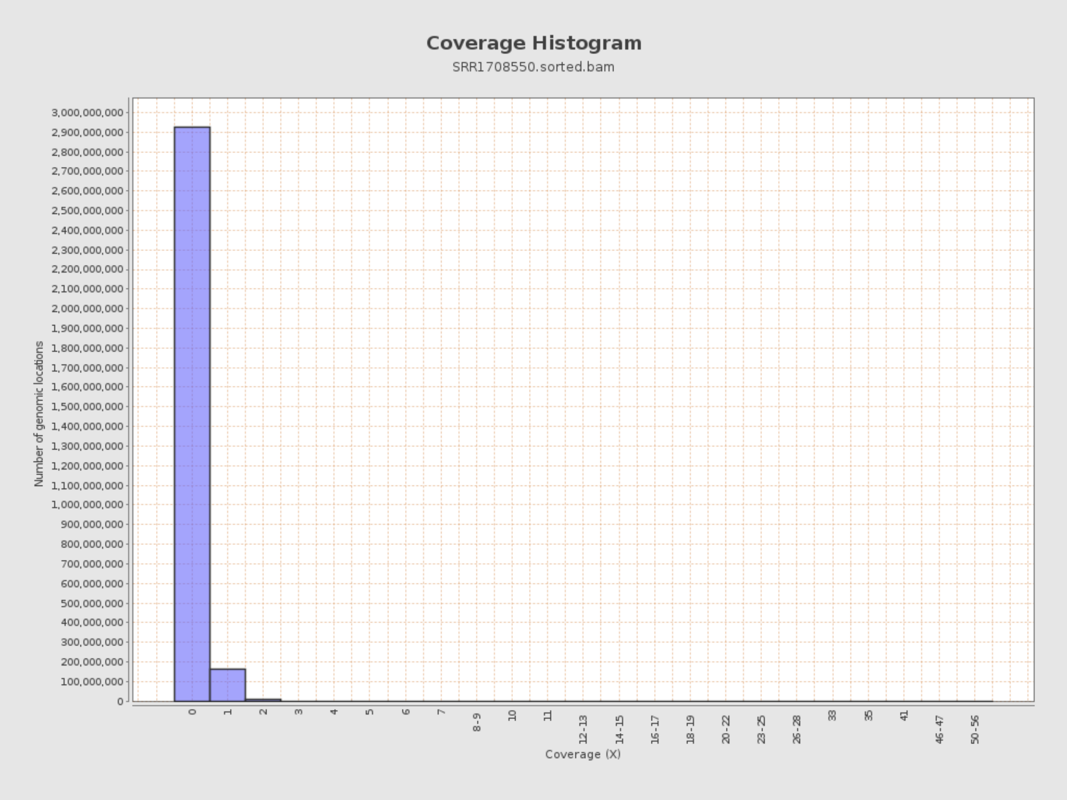
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13796647	0.0554	0.2436
chr2	243199373	16164462	0.0665	0.2645
chr3	198022430	13590577	0.0686	0.2685
chr4	191154276	13877745	0.0726	0.2762
chr5	180915260	12381358	0.0684	0.2684
chr6	171115067	12179920	0.0712	0.2737
chr7	159138663	10072634	0.0633	0.2587

chr8	146364022	9896359	0.0676	0.2667
chr9	141213431	7426331	0.0526	0.2365
chr10	135534747	7634232	0.0563	0.2433
chr11	135006516	8288195	0.0614	0.2553
chr12	133851895	8097381	0.0605	0.2537
chr13	115169878	7129073	0.0619	0.256
chr14	107349540	5673952	0.0529	0.237
chr15	102531392	4745692	0.0463	0.2222
chr16	90354753	3309383	0.0366	0.1964
chr17	81195210	2960574	0.0365	0.1962
chr18	78077248	5174047	0.0663	0.2636
chr19	59128983	1323737	0.0224	0.1529
chr20	63025520	2819812	0.0447	0.2181
chr21	48129895	2119394	0.044	0.2178
chr22	51304566	912203	0.0178	0.1366
chrMT	16571	100	0.006	0.0774
chrX	155270560	10523304	0.0678	0.2677
chrY	59373566	246358	0.0041	0.0671

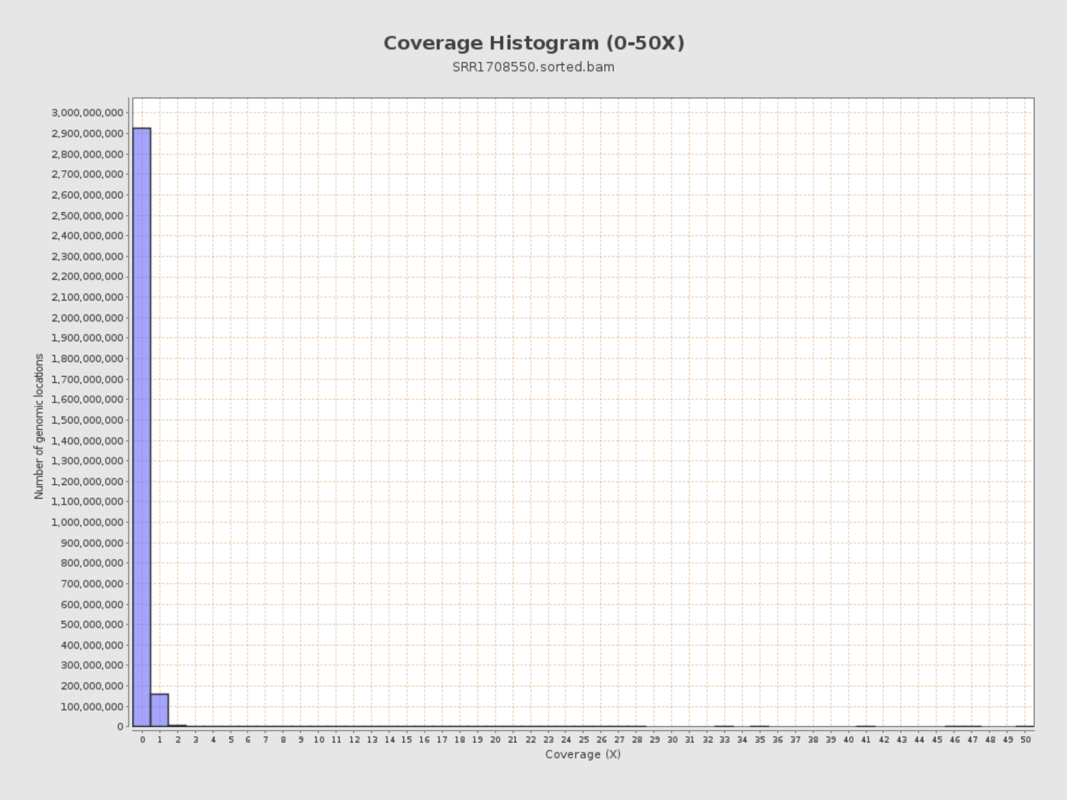
3. Results : Coverage across reference



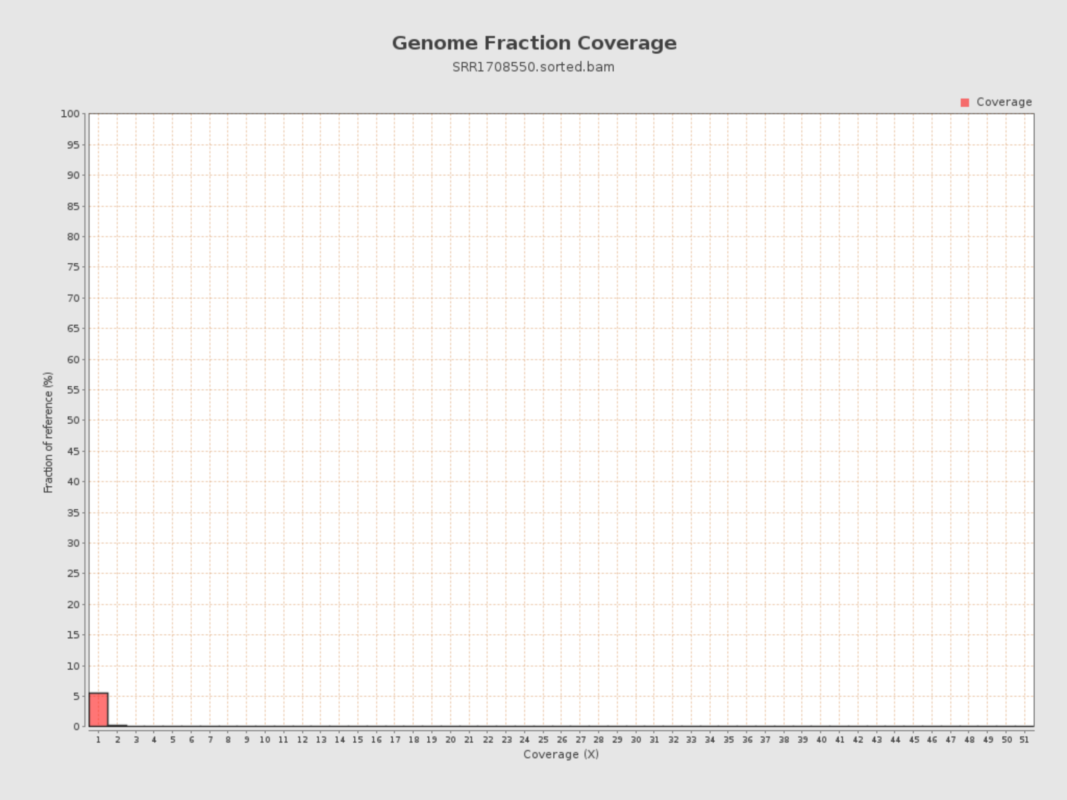
4. Results : Coverage Histogram



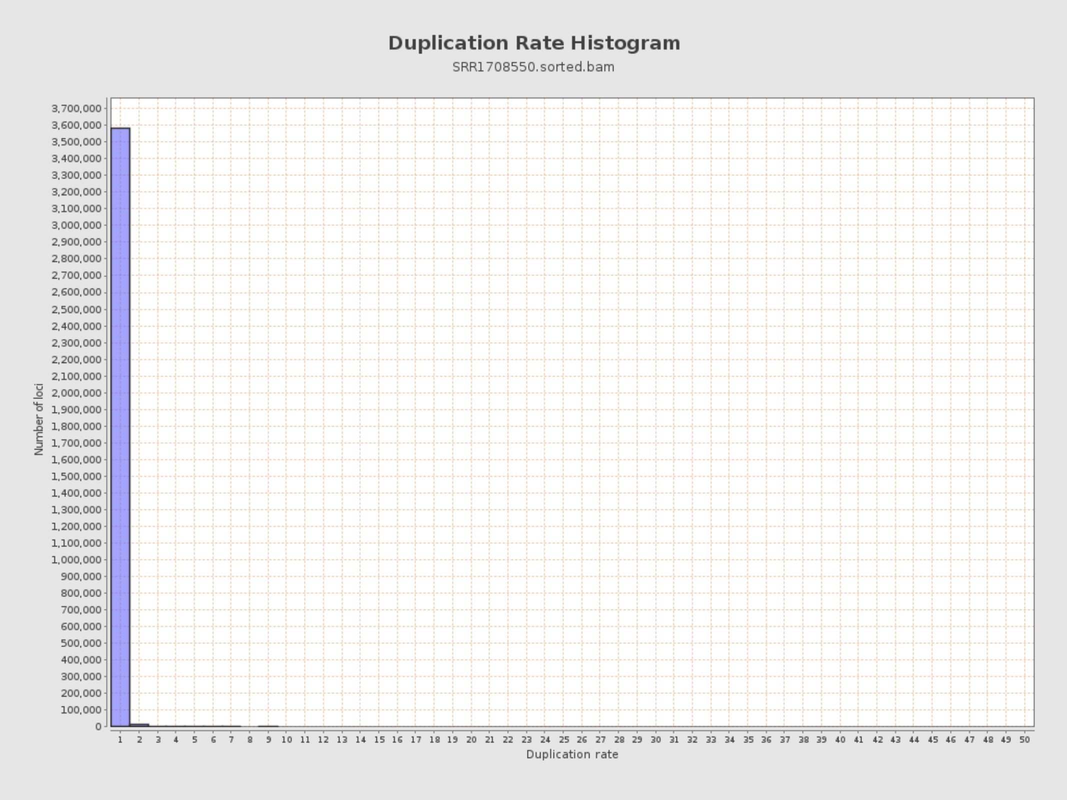
5. Results : Coverage Histogram (0-50X)



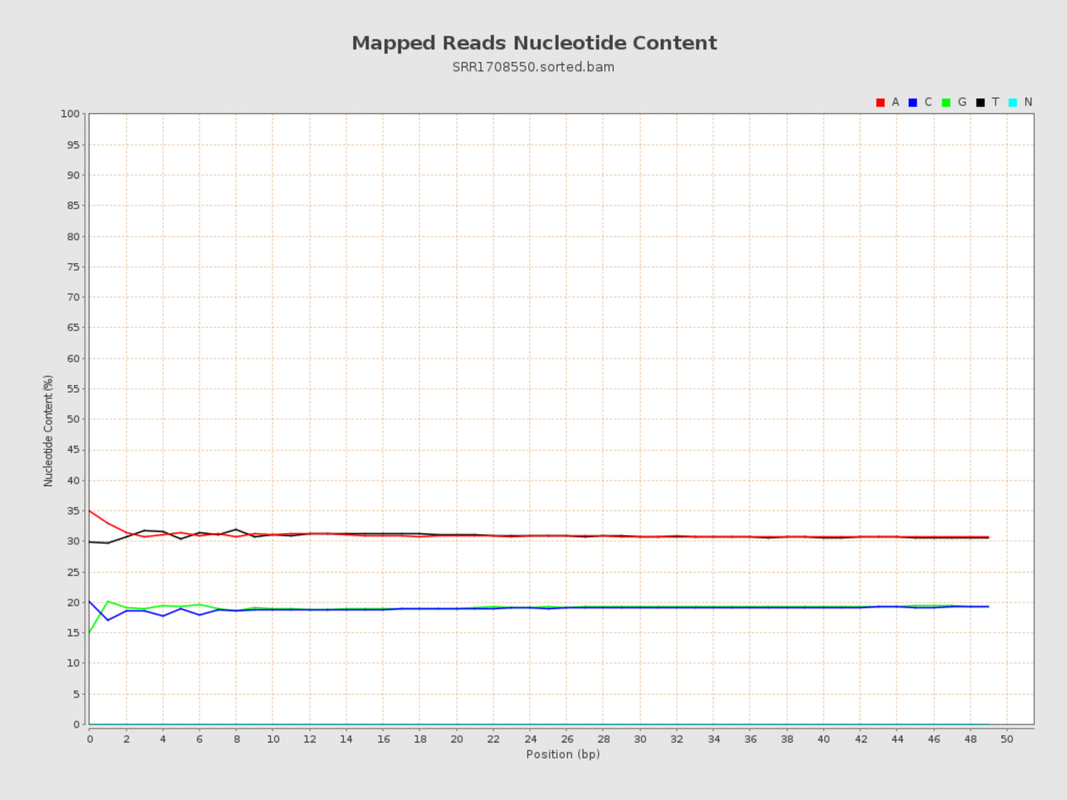
6. Results : Genome Fraction Coverage



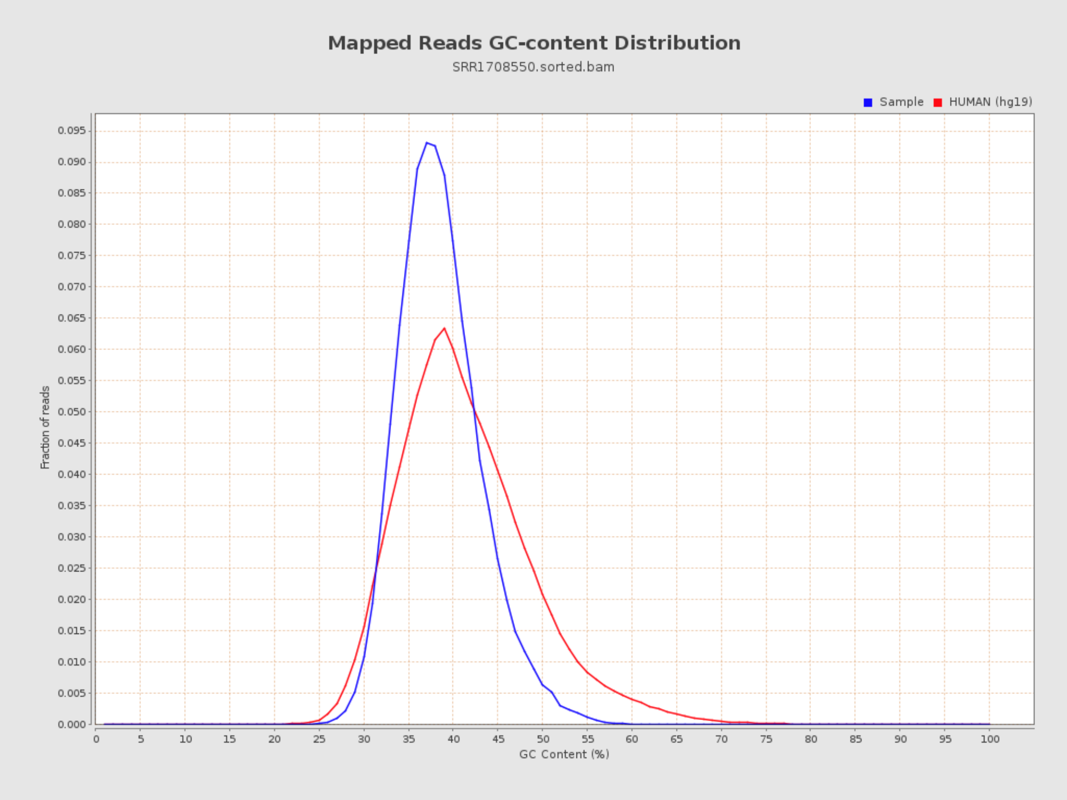
7. Results : Duplication Rate Histogram



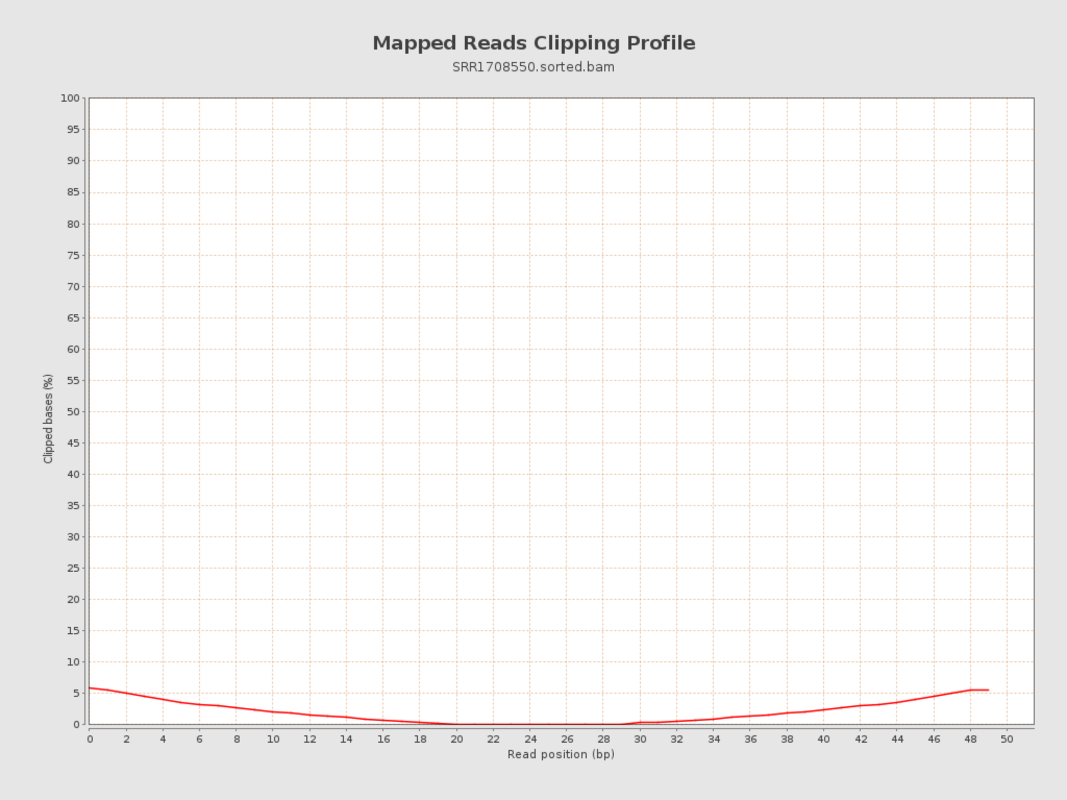
8. Results : Mapped Reads Nucleotide Content



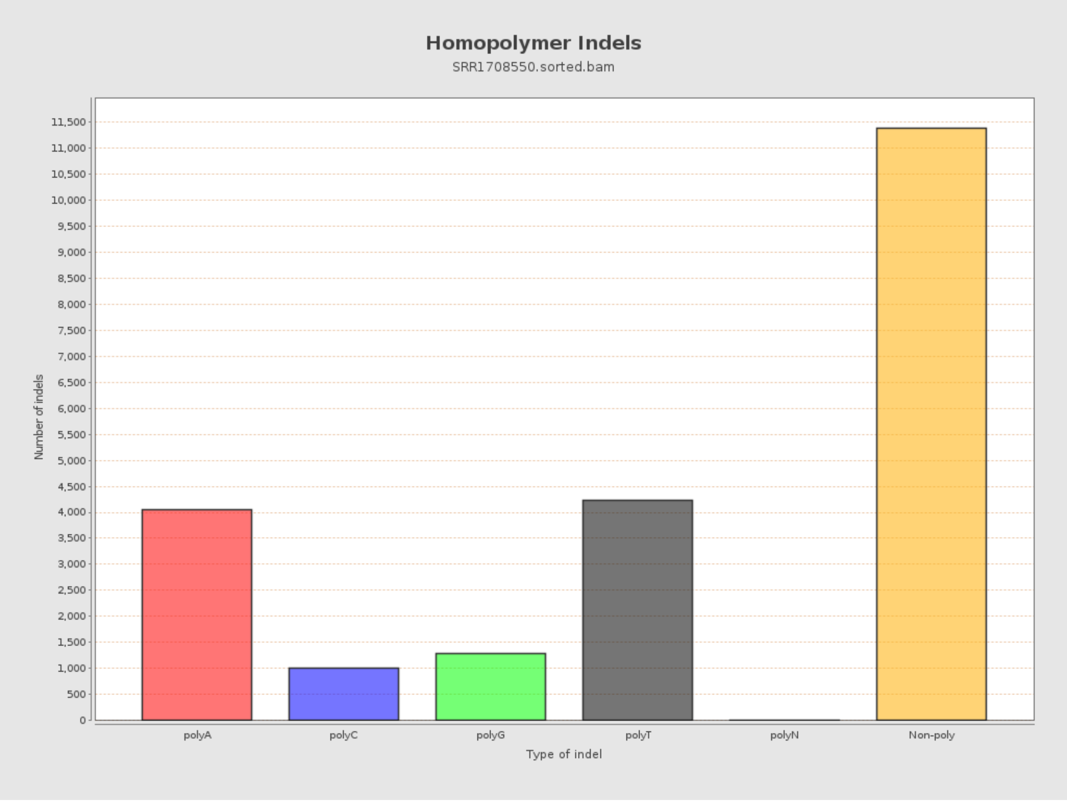
9. Results : Mapped Reads GC-content Distribution



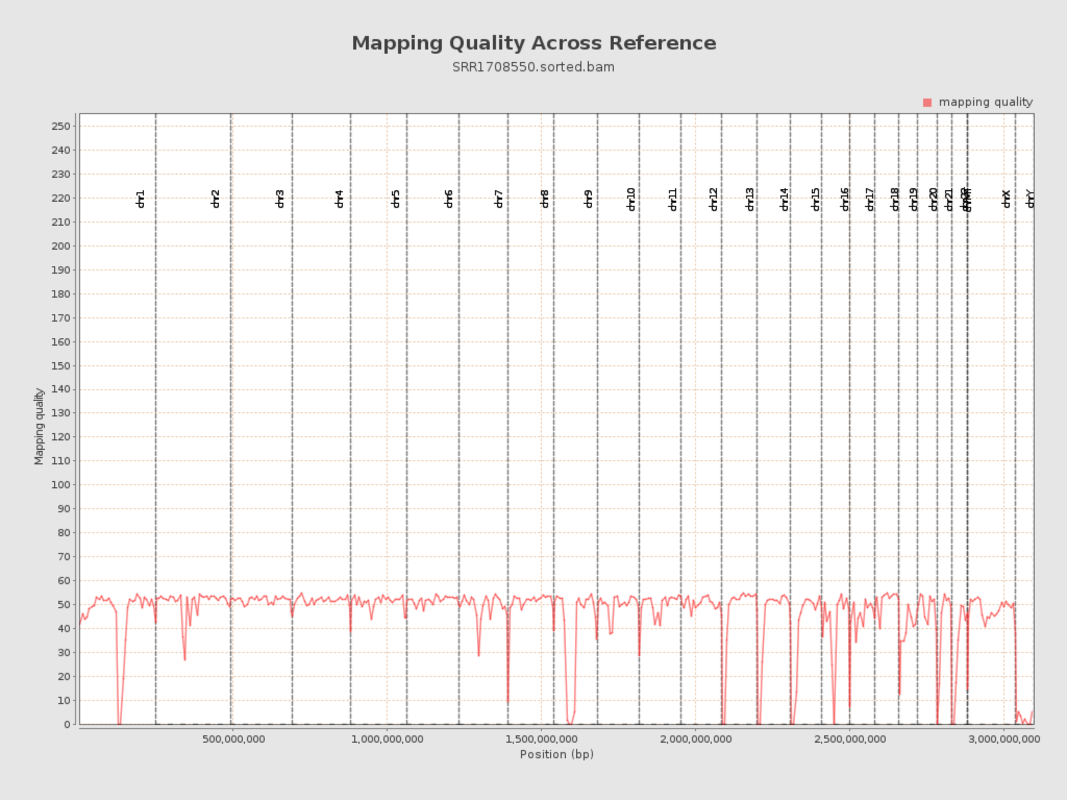
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram