Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:17:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525108.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_SRR10525108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:17:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	781,491
Mapped reads	689,760 / 88.26%
Unmapped reads	91,731 / 11.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,369 / 2.48%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	14,814 / 1.9%
Duplication rate	1.28%
Clipped reads	708,293 / 90.63%

2.2. ACGT Content

Number/percentage of A's	13,655,341 / 25.76%
Number/percentage of C's	10,251,326 / 19.34%
Number/percentage of T's	16,452,787 / 31.04%
Number/percentage of G's	12,640,987 / 23.85%
Number/percentage of N's	1,951 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.2013

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

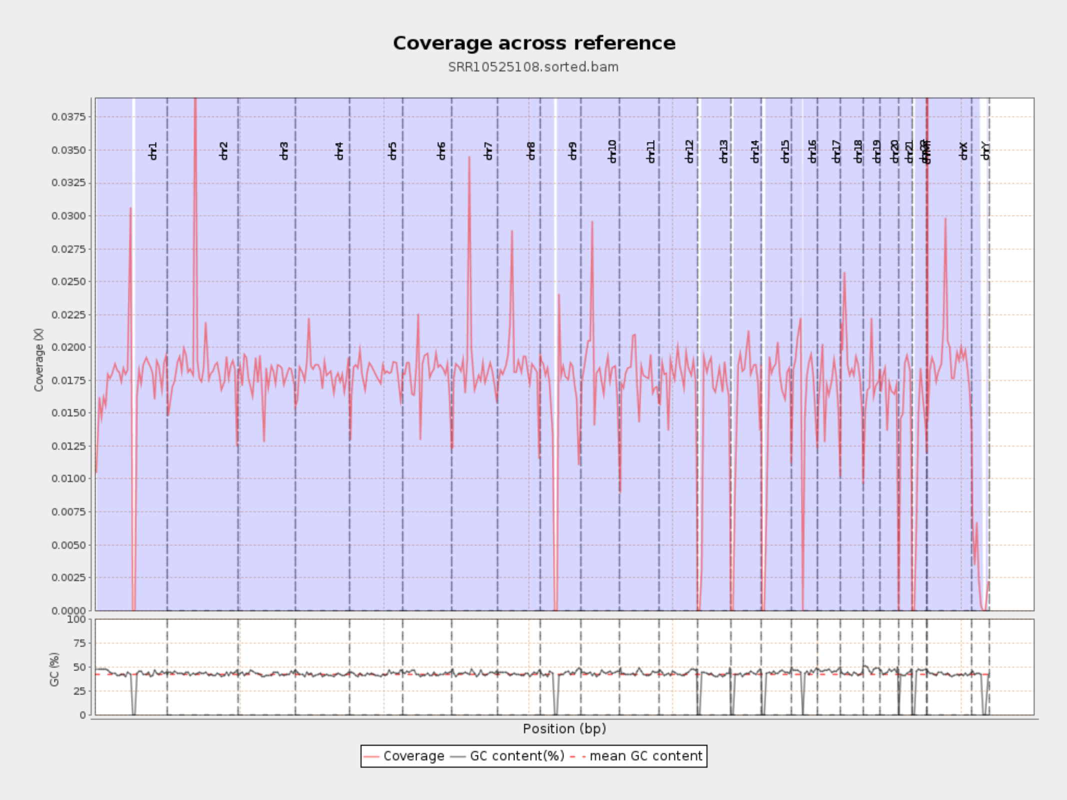
General error rate	0.76%
Mismatches	396,860
Insertions	4,506
Mapped reads with at least one insertion	0.64%
Deletions	12,086
Mapped reads with at least one deletion	1.73%
Homopolymer indels	42.94%

2.6. Chromosome stats

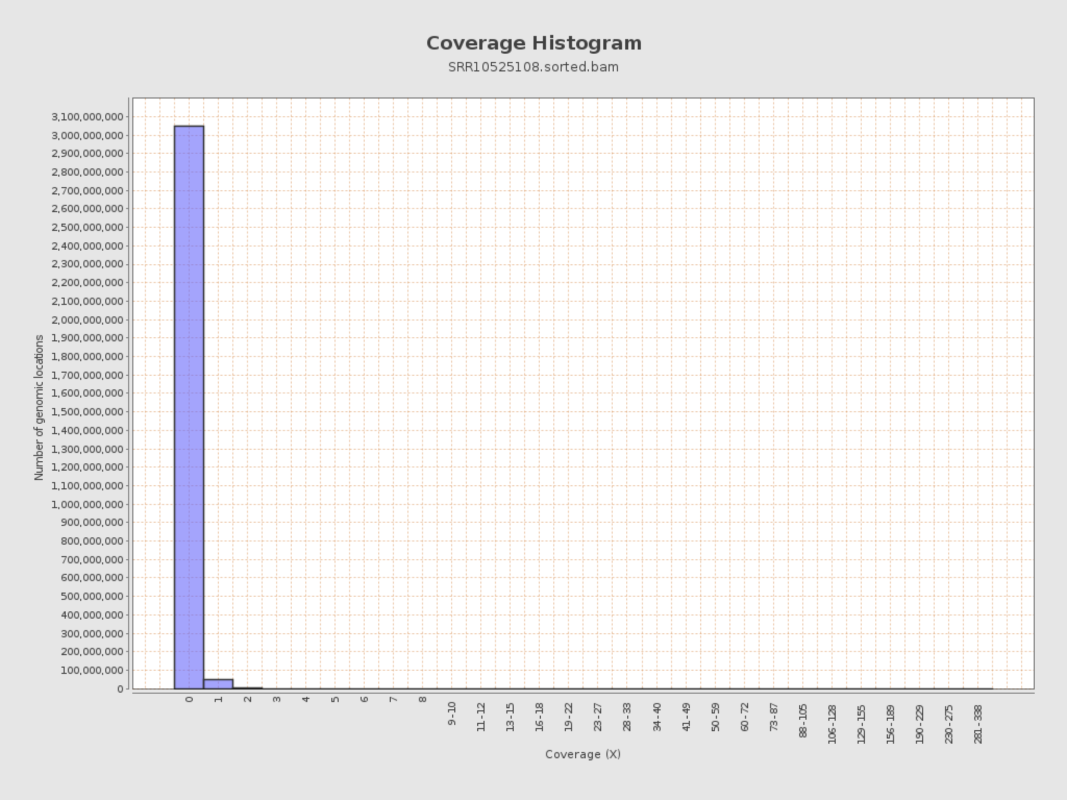
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4193299	0.0168	0.3005
chr2	243199373	4608755	0.019	0.2694
chr3	198022430	3529167	0.0178	0.1392
chr4	191154276	3447492	0.018	0.1434
chr5	180915260	3262237	0.018	0.1422
chr6	171115067	3098072	0.0181	0.1524
chr7	159138663	2963454	0.0186	0.2868

chr8	146364022	2753101	0.0188	0.2544
chr9	141213431	2218695	0.0157	0.1961
chr10	135534747	2503369	0.0185	0.1995
chr11	135006516	2389200	0.0177	0.2073
chr12	133851895	2386460	0.0178	0.1398
chr13	115169878	1700909	0.0148	0.1262
chr14	107349540	1657109	0.0154	0.1413
chr15	102531392	1513759	0.0148	0.1276
chr16	90354753	1472926	0.0163	0.1401
chr17	81195210	1352676	0.0167	0.1501
chr18	78077248	1495354	0.0192	0.3176
chr19	59128983	1009877	0.0171	0.2266
chr20	63025520	1030908	0.0164	0.1356
chr21	48129895	728256	0.0151	0.1333
chr22	51304566	565287	0.011	0.1098
chrMT	16571	6446	0.389	0.7415
chrX	155270560	2984918	0.0192	0.1795
chrY	59373566	151251	0.0025	0.0618

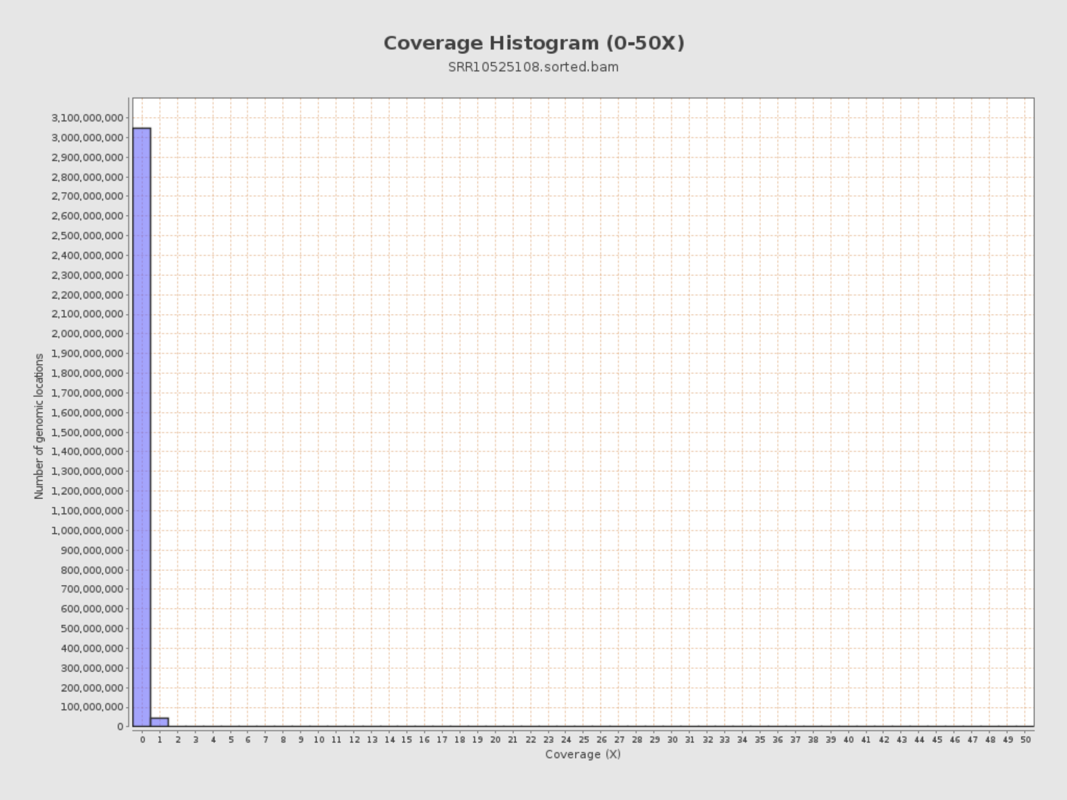
3. Results : Coverage across reference



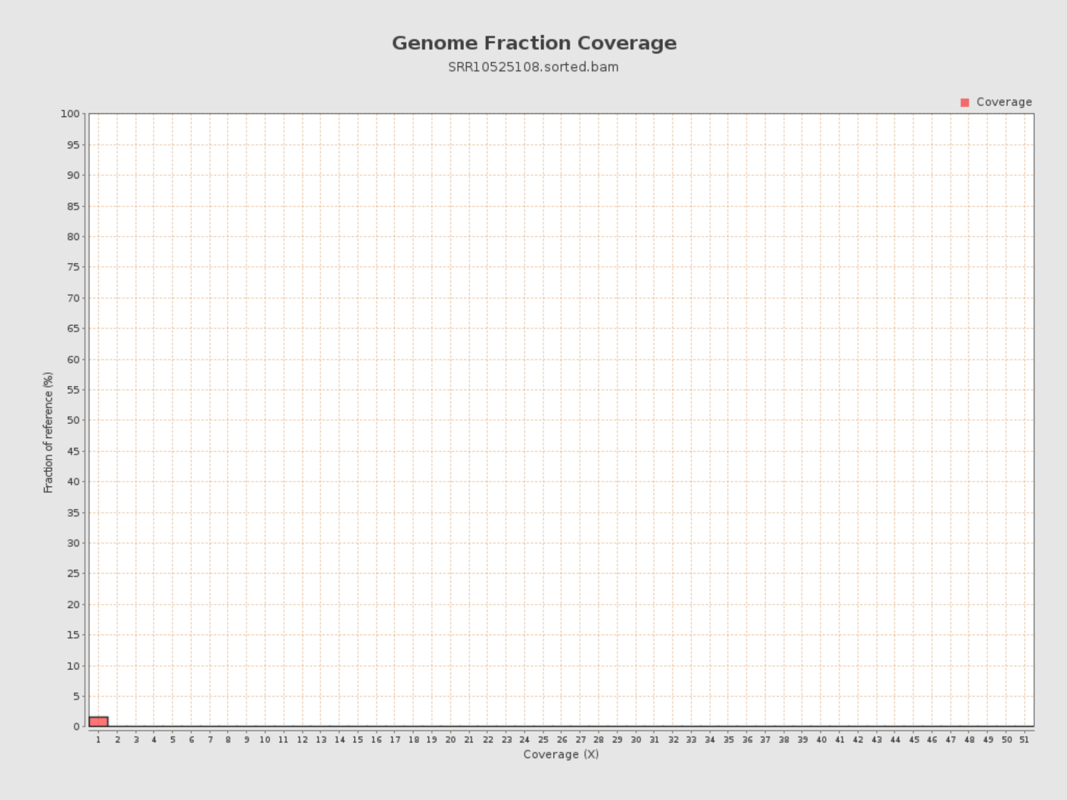
4. Results : Coverage Histogram



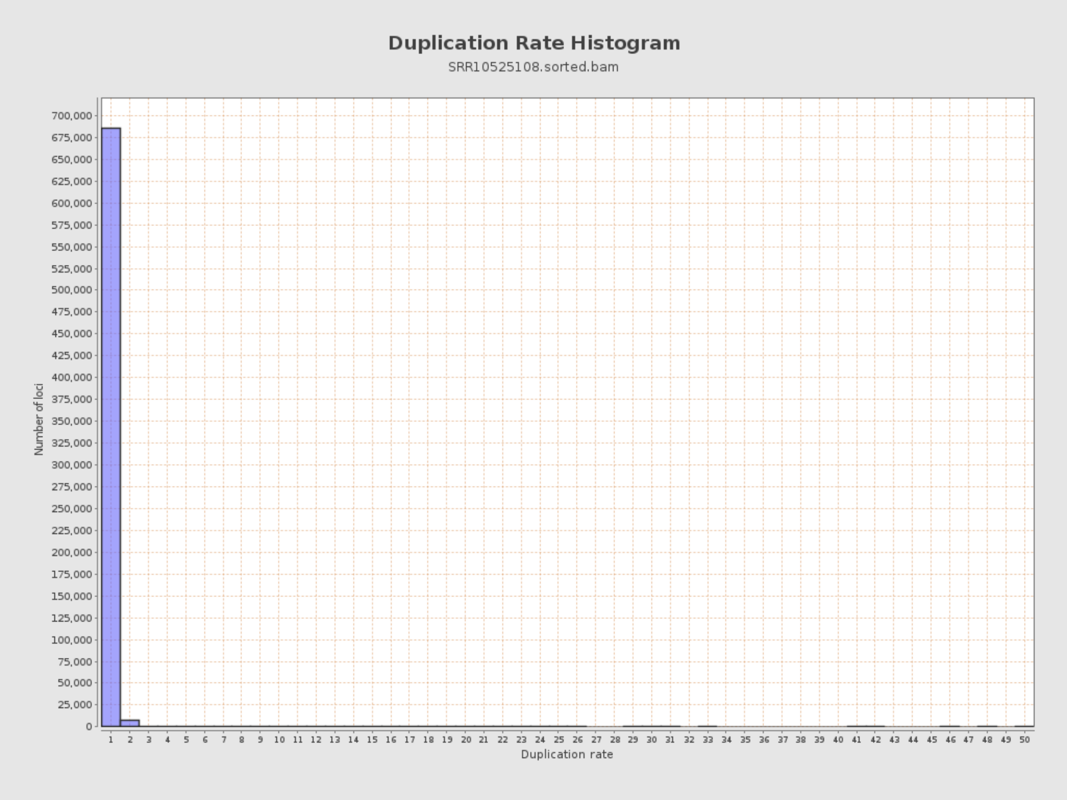
5. Results : Coverage Histogram (0-50X)



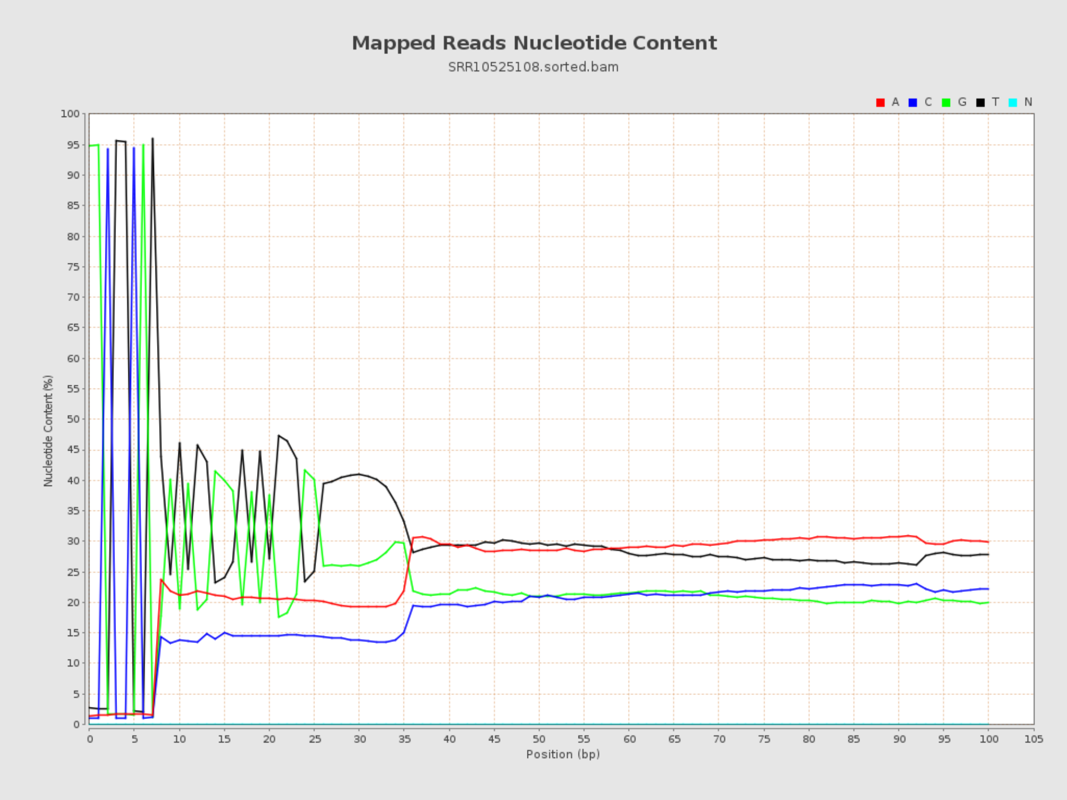
6. Results : Genome Fraction Coverage



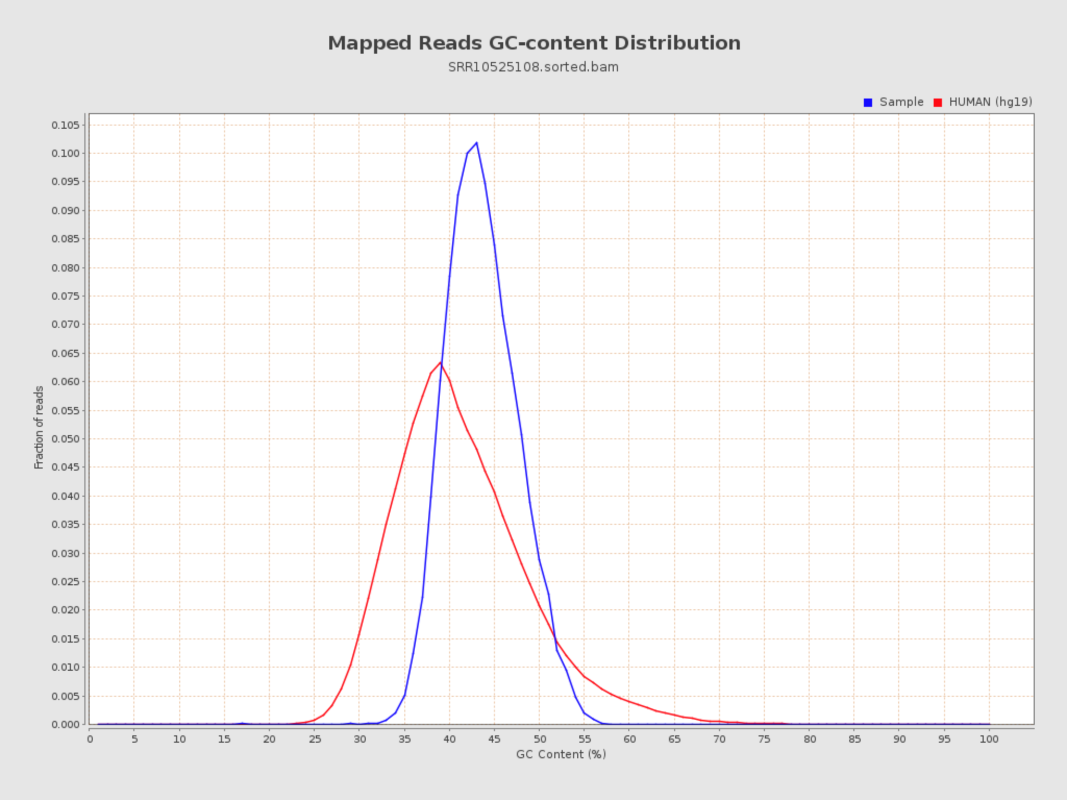
7. Results : Duplication Rate Histogram



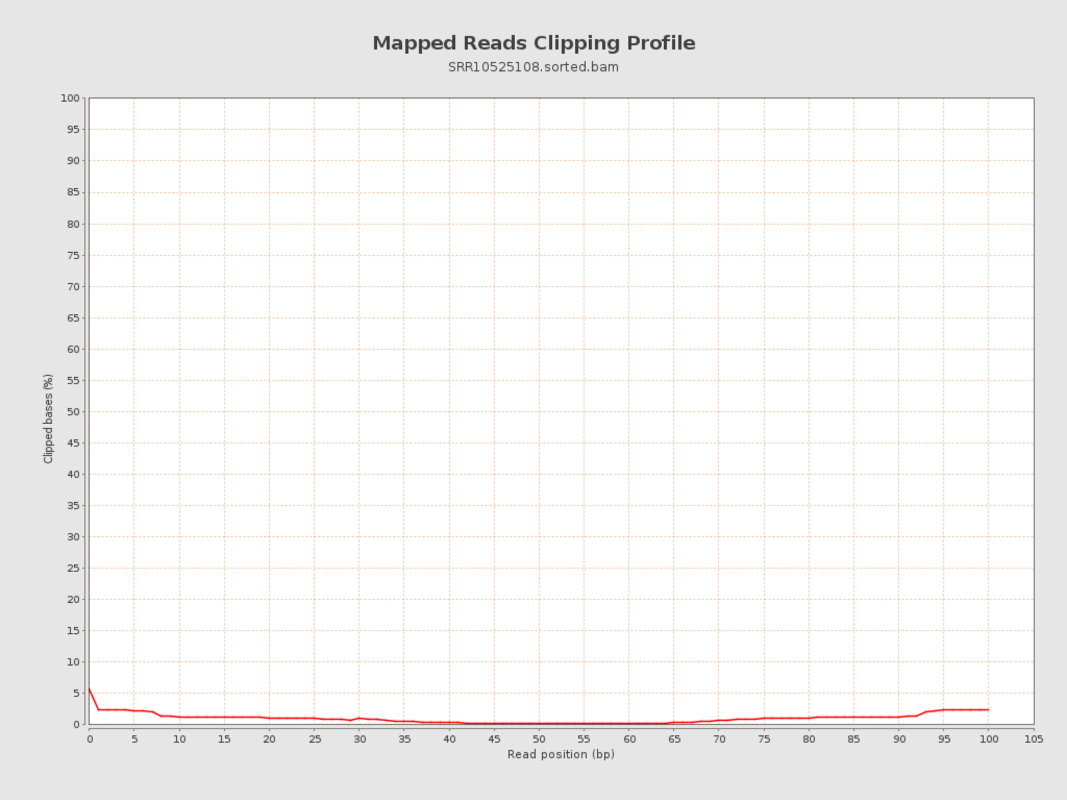
8. Results : Mapped Reads Nucleotide Content



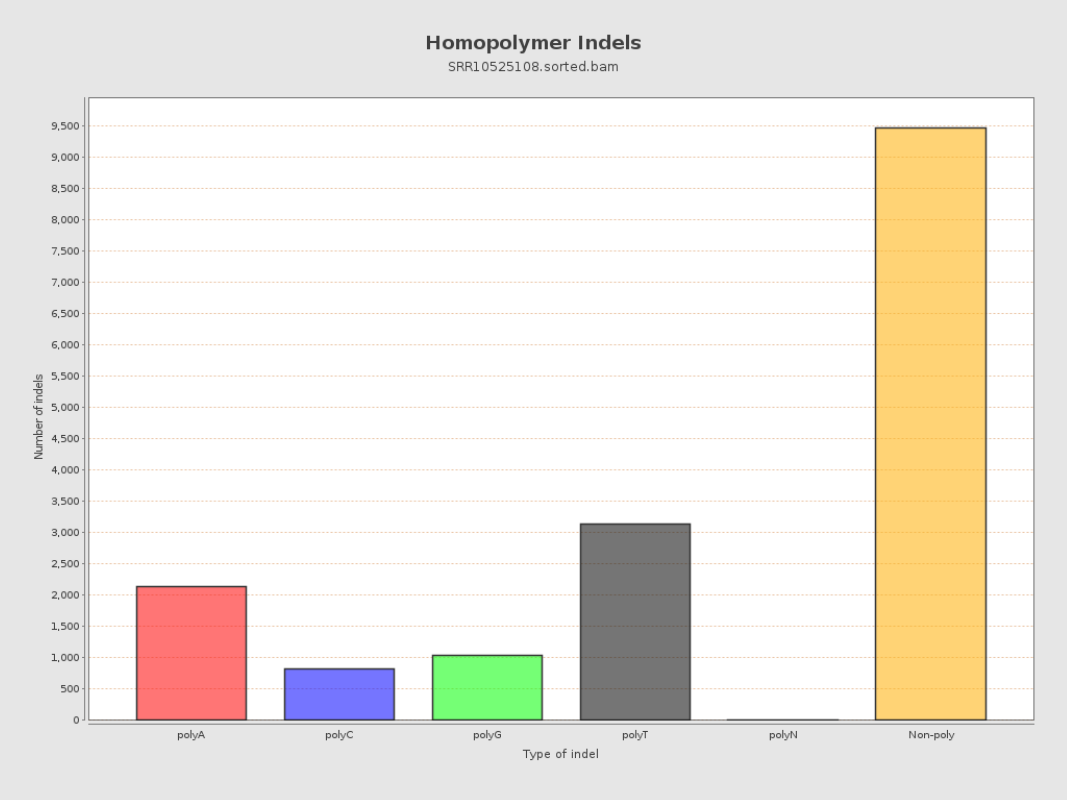
9. Results : Mapped Reads GC-content Distribution



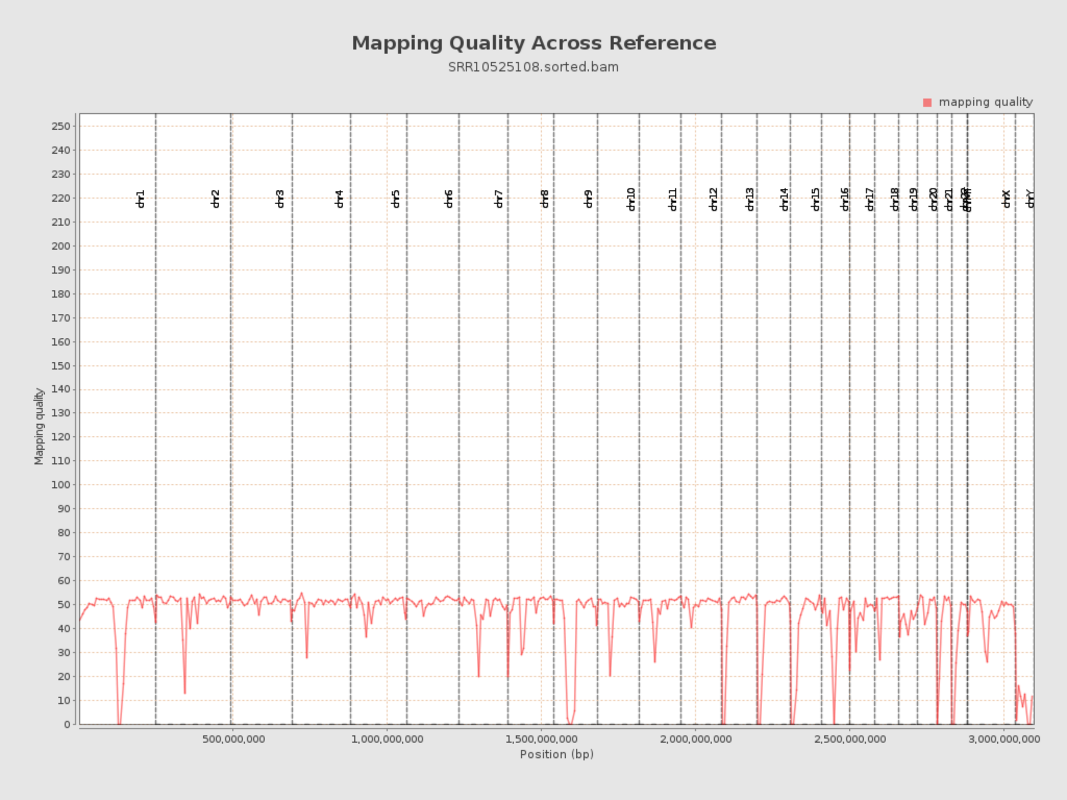
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram