Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:01:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708554.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_SRR1708554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708554.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:01:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,850,180
Mapped reads	3,168,086 / 82.28%
Unmapped reads	682,094 / 17.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	93 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,086 / 0.39%
Duplication rate	0.47%
Clipped reads	44,135 / 1.15%

2.2. ACGT Content

Number/percentage of A's	49,068,057 / 31.06%
Number/percentage of C's	29,889,679 / 18.92%
Number/percentage of T's	48,832,236 / 30.91%
Number/percentage of G's	30,169,447 / 19.1%
Number/percentage of N's	6,599 / 0%
GC Percentage	38.02%

2.3. Coverage

Mean	0.051

Standard Deviation	0.2329

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

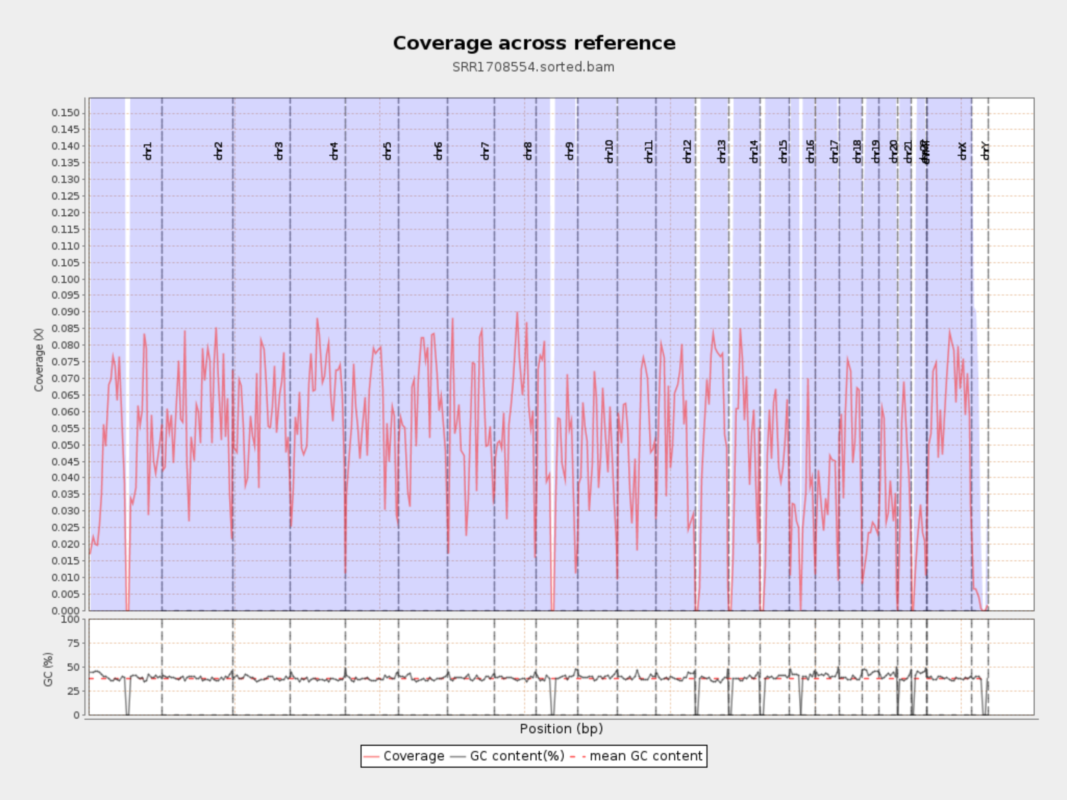
General error rate	0.17%
Mismatches	250,024
Insertions	10,524
Mapped reads with at least one insertion	0.33%
Deletions	8,620
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.16%

2.6. Chromosome stats

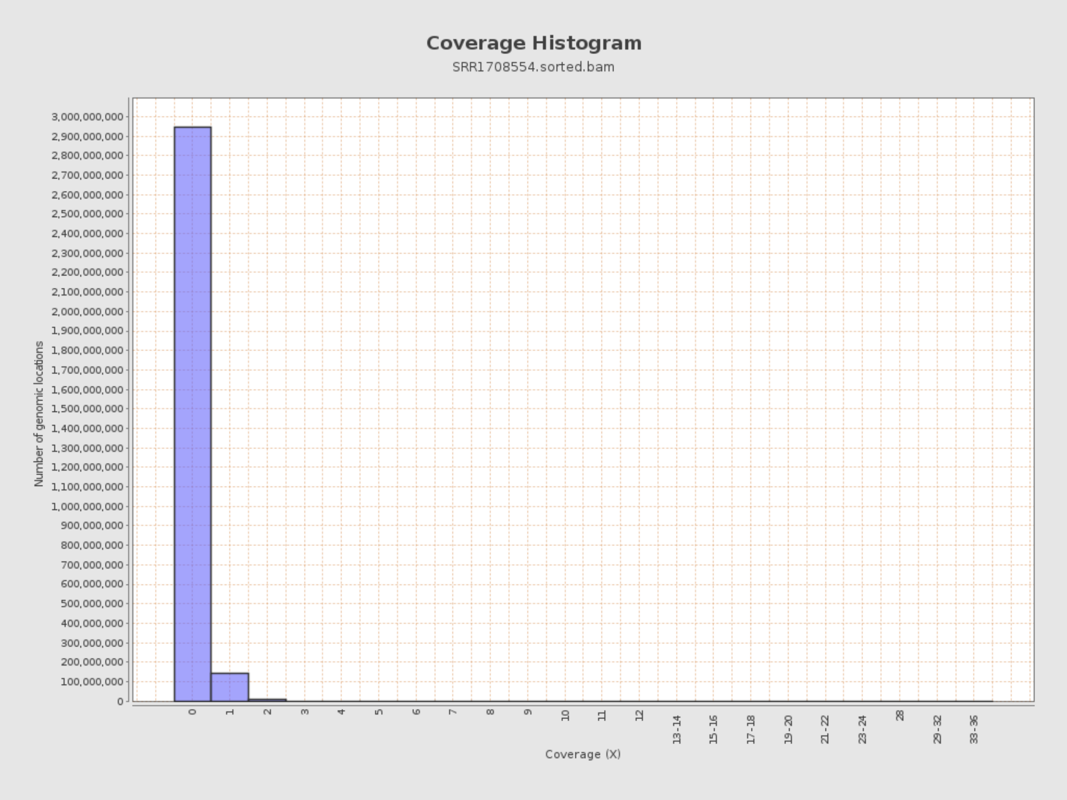
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11551605	0.0463	0.2228
chr2	243199373	14280009	0.0587	0.2493
chr3	198022430	11714868	0.0592	0.2497
chr4	191154276	12180571	0.0637	0.259
chr5	180915260	10461466	0.0578	0.2471
chr6	171115067	10675712	0.0624	0.2566
chr7	159138663	8929745	0.0561	0.244

chr8	146364022	8769658	0.0599	0.2519
chr9	141213431	6638861	0.047	0.2242
chr10	135534747	6622997	0.0489	0.2267
chr11	135006516	7022485	0.052	0.235
chr12	133851895	7265339	0.0543	0.2398
chr13	115169878	6248454	0.0543	0.2405
chr14	107349540	4978993	0.0464	0.2228
chr15	102531392	4253300	0.0415	0.2104
chr16	90354753	2705270	0.0299	0.1781
chr17	81195210	2677103	0.033	0.1868
chr18	78077248	4458054	0.0571	0.2453
chr19	59128983	1257599	0.0213	0.1492
chr20	63025520	2362944	0.0375	0.1993
chr21	48129895	1932374	0.0401	0.2076
chr22	51304566	866939	0.0169	0.133
chrMT	16571	248	0.015	0.1214
chrX	155270560	9897737	0.0637	0.26
chrY	59373566	228398	0.0038	0.0649

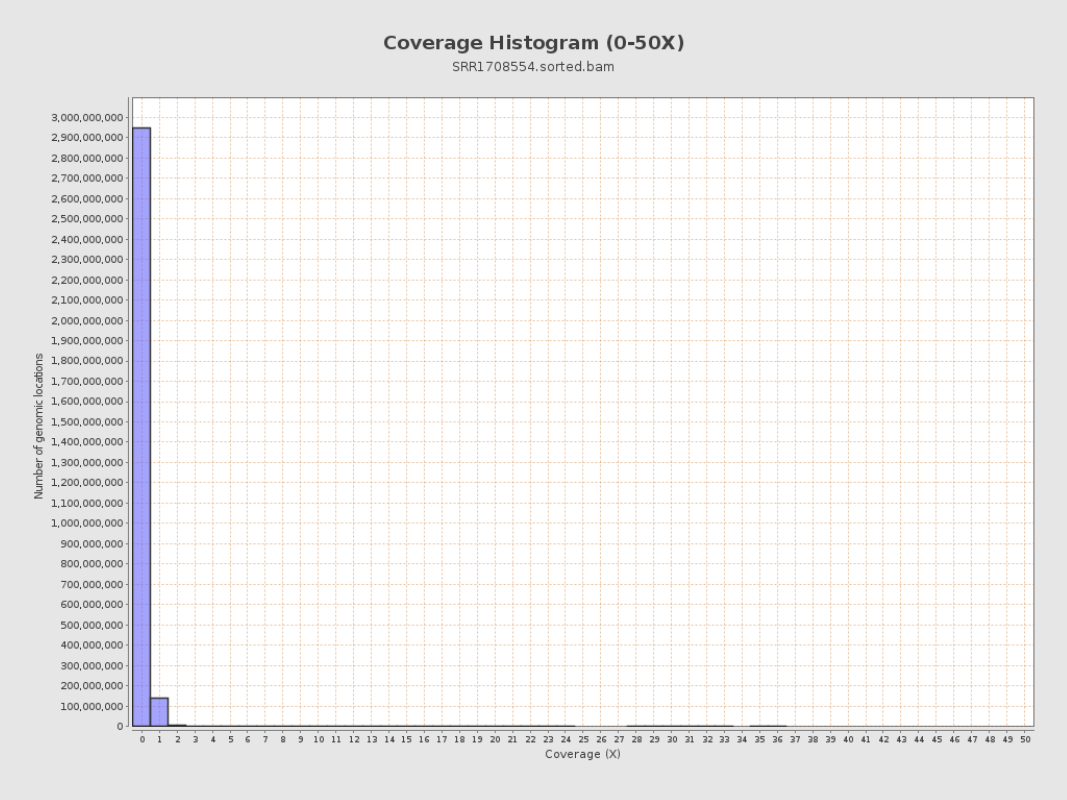
3. Results : Coverage across reference



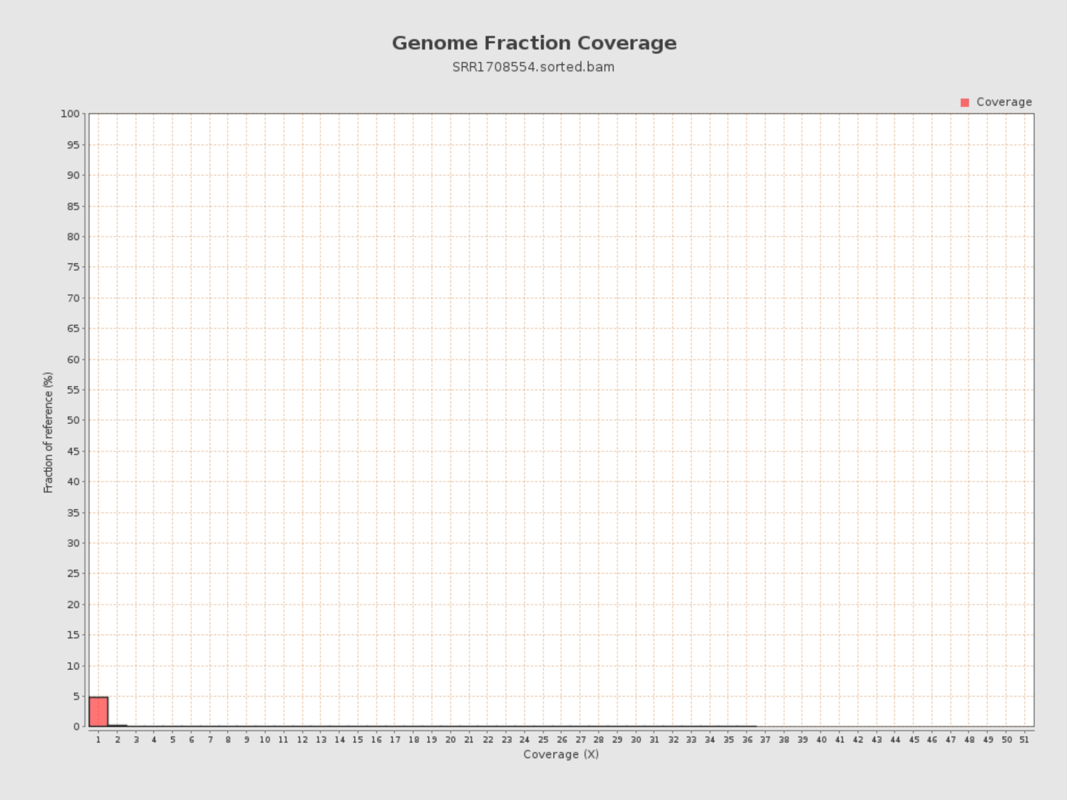
4. Results : Coverage Histogram



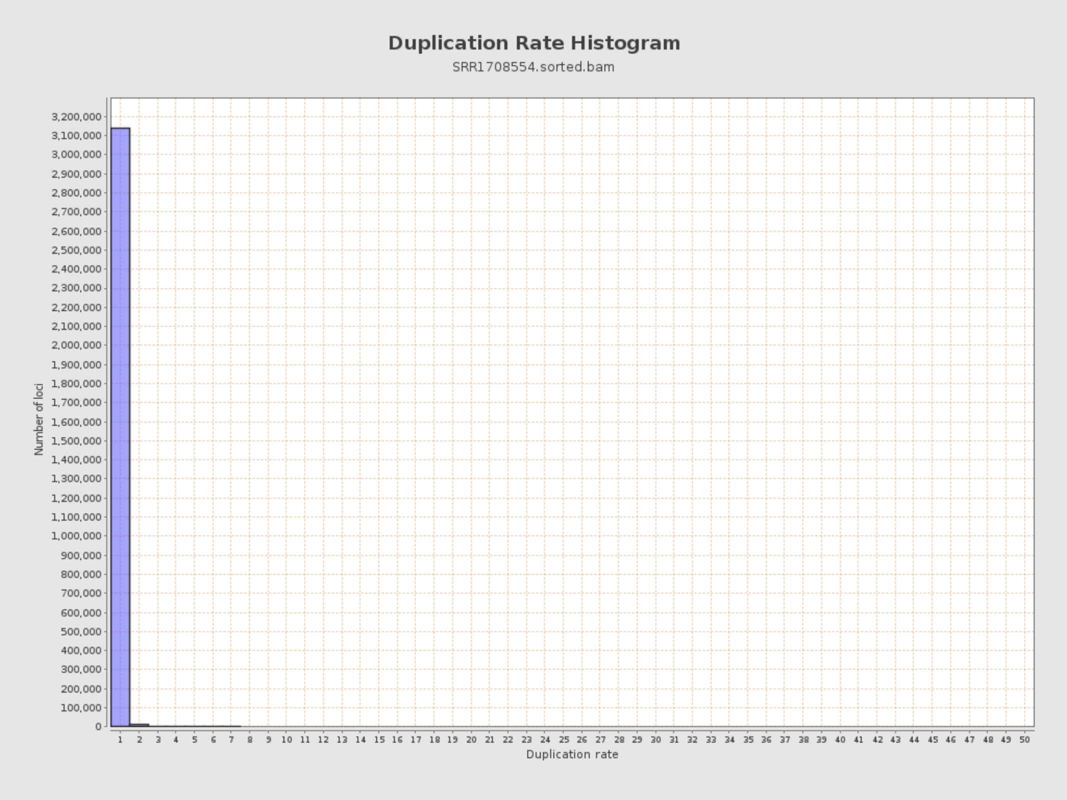
5. Results : Coverage Histogram (0-50X)



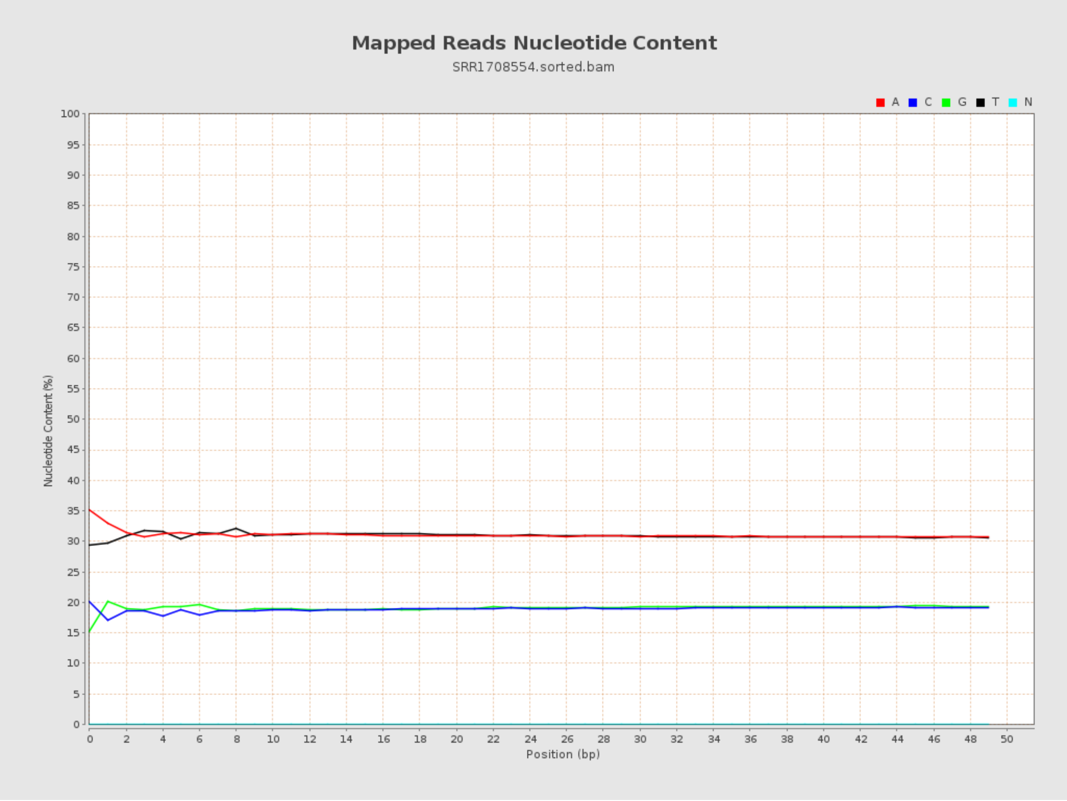
6. Results : Genome Fraction Coverage



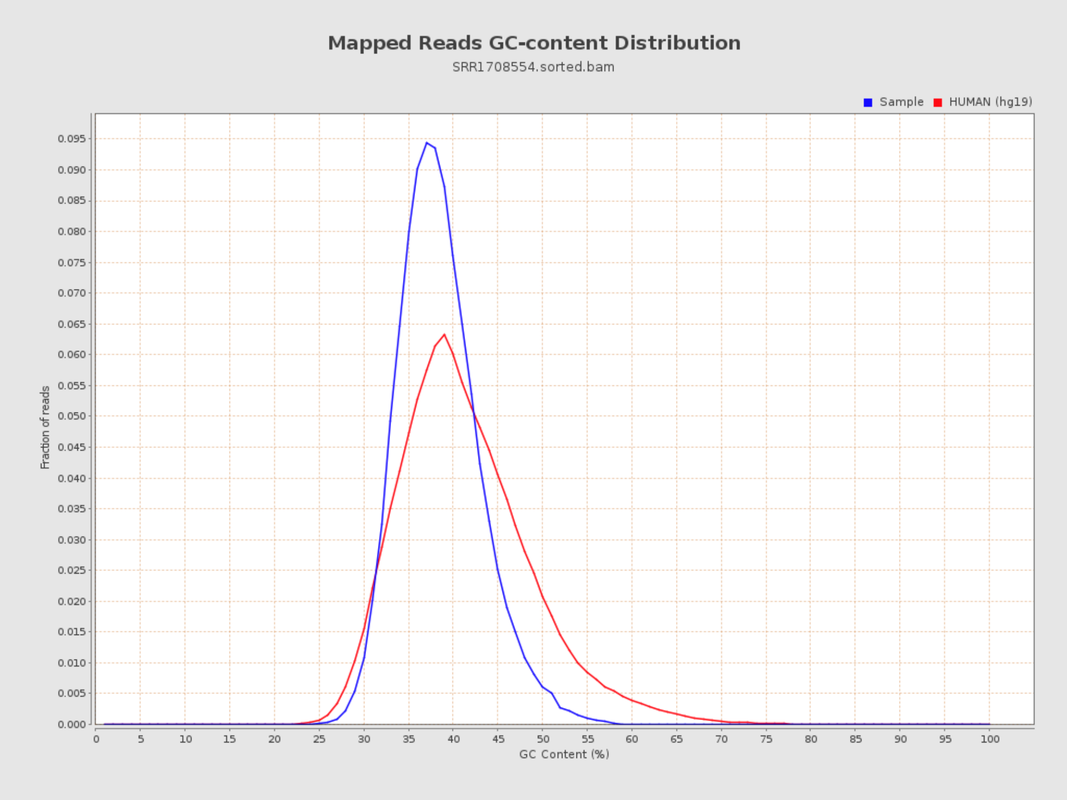
7. Results : Duplication Rate Histogram



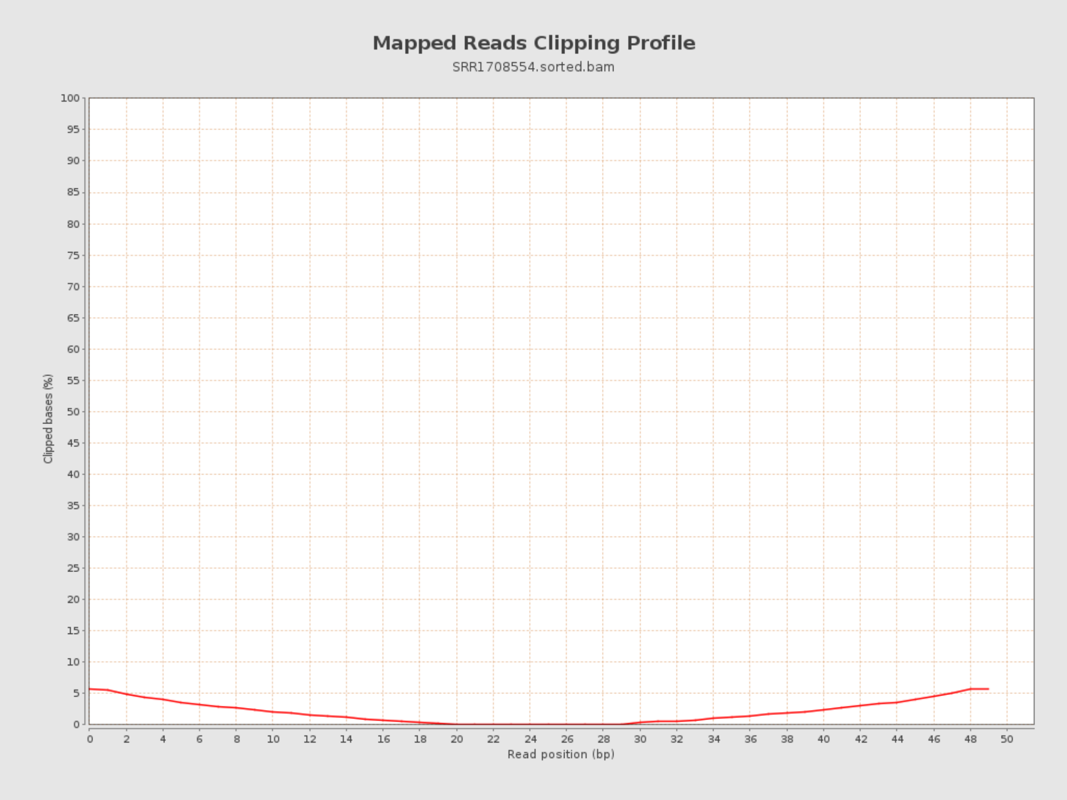
8. Results : Mapped Reads Nucleotide Content



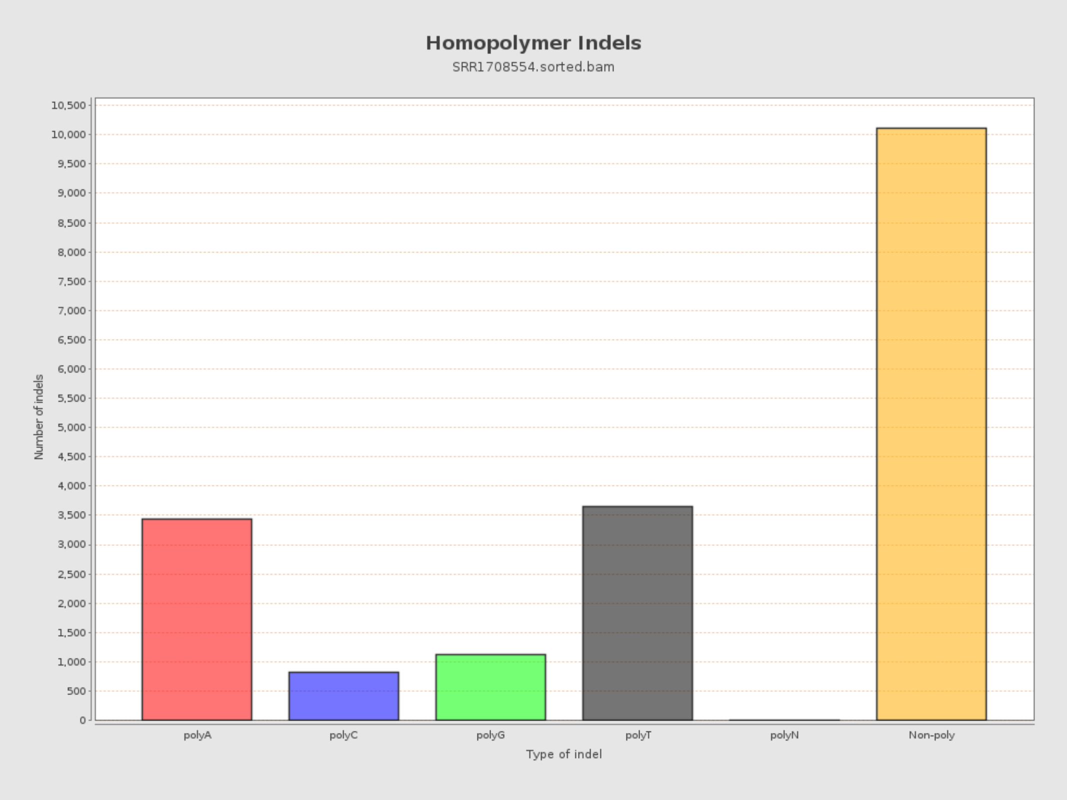
9. Results : Mapped Reads GC-content Distribution



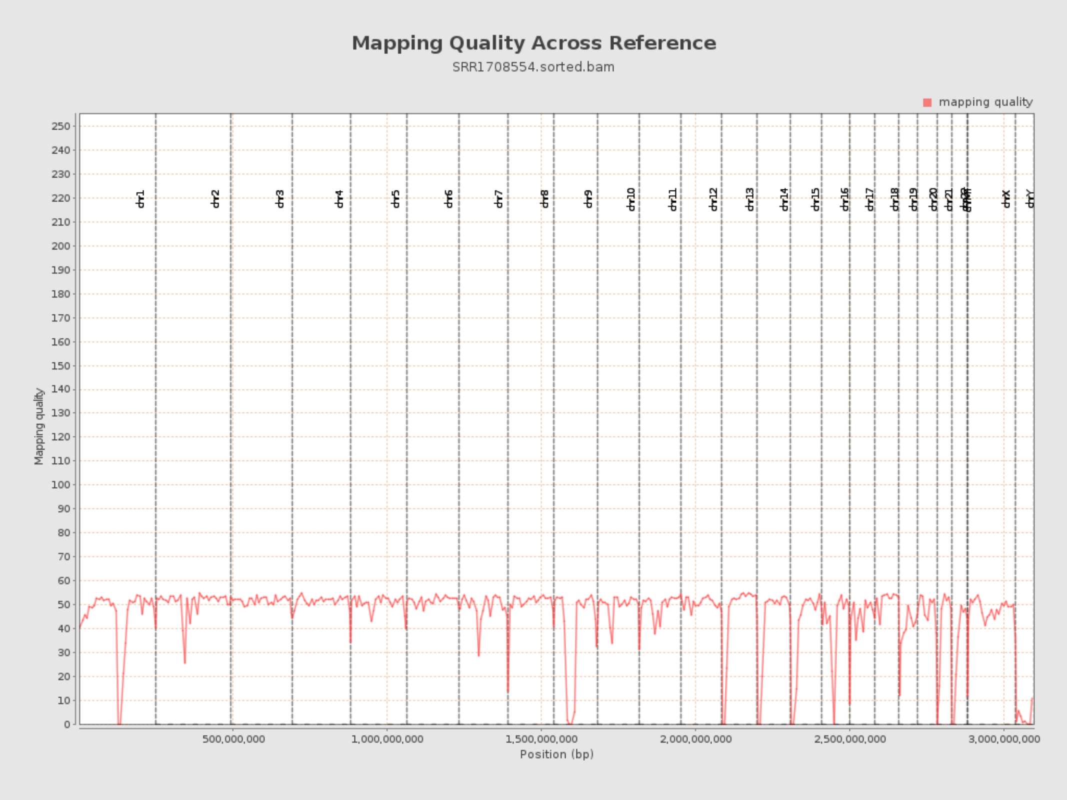
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram