Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:41:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708508.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_SRR1708508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708508.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:41:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,439,097
Mapped reads	2,341,245 / 68.08%
Unmapped reads	1,097,852 / 31.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	562 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	104,559 / 3.04%
Duplication rate	3.32%
Clipped reads	512,033 / 14.89%

2.2. ACGT Content

Number/percentage of A's	31,630,611 / 28.42%
Number/percentage of C's	20,580,374 / 18.49%
Number/percentage of T's	35,658,020 / 32.04%
Number/percentage of G's	23,414,204 / 21.04%
Number/percentage of N's	1,508 / 0%
GC Percentage	39.53%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3335

2.4. Mapping Quality

Mean Mapping Quality	40.29

2.5. Mismatches and indels

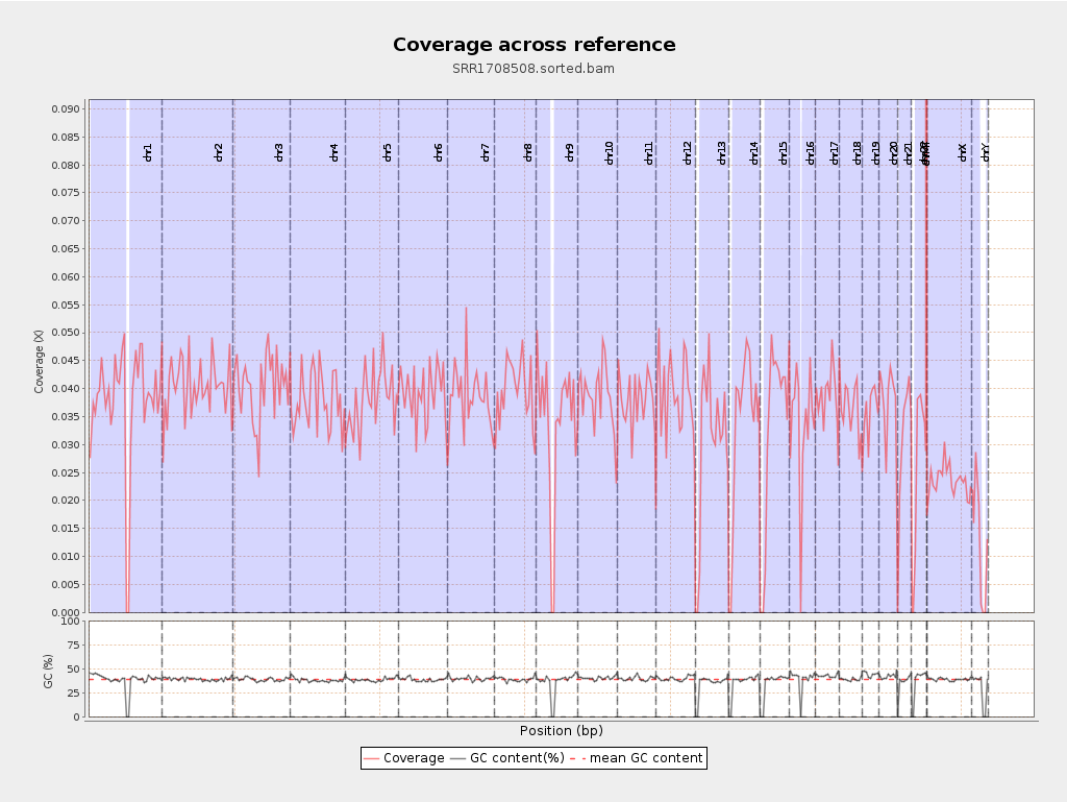
General error rate	0.5%
Mismatches	544,977
Insertions	5,956
Mapped reads with at least one insertion	0.25%
Deletions	17,616
Mapped reads with at least one deletion	0.75%
Homopolymer indels	48.29%

2.6. Chromosome stats

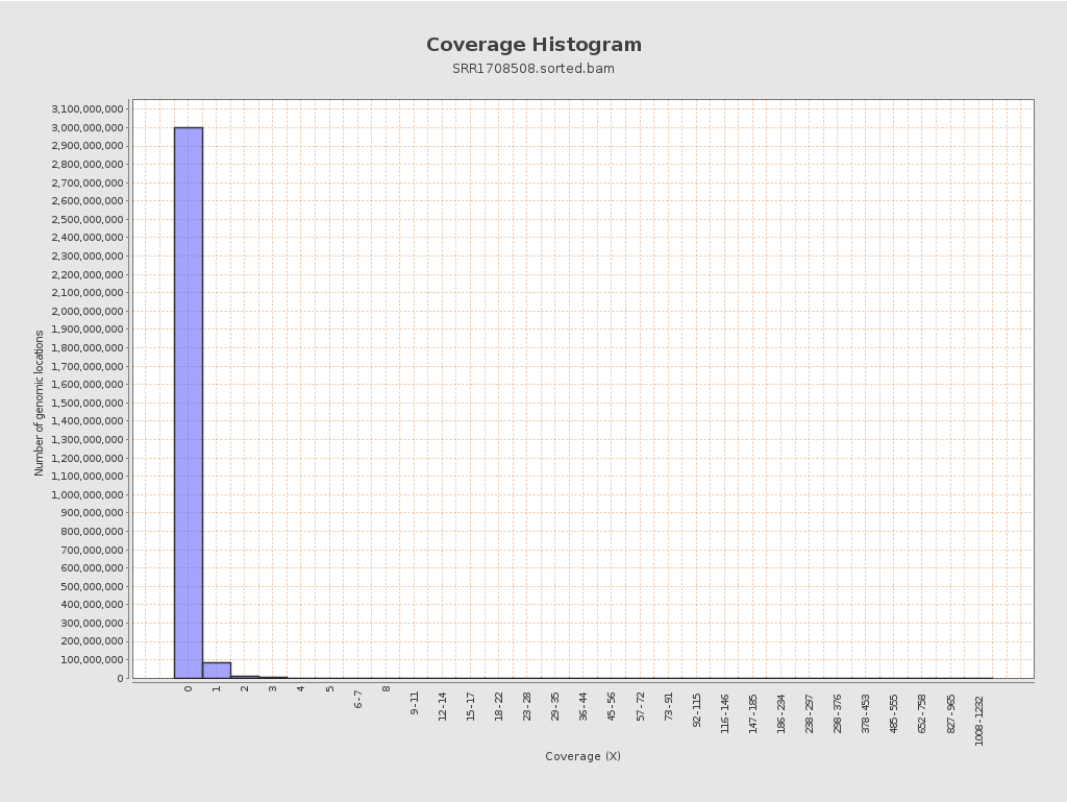
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9344378	0.0375	0.4561
chr2	243199373	9839246	0.0405	0.5595
chr3	198022430	7955816	0.0402	0.2403
chr4	191154276	7199441	0.0377	0.2388
chr5	180915260	6899938	0.0381	0.23
chr6	171115067	6689644	0.0391	0.3139
chr7	159138663	6184019	0.0389	0.3726

chr8	146364022	5775971	0.0395	0.5986
chr9	141213431	4682854	0.0332	0.2588
chr10	135534747	5242819	0.0387	0.2555
chr11	135006516	5092680	0.0377	0.2686
chr12	133851895	5260474	0.0393	0.2357
chr13	115169878	3461776	0.0301	0.2395
chr14	107349540	3572270	0.0333	0.2175
chr15	102531392	3363429	0.0328	0.2196
chr16	90354753	3019934	0.0334	0.218
chr17	81195210	3126677	0.0385	0.2439
chr18	78077248	2863649	0.0367	0.3288
chr19	59128983	2118308	0.0358	0.3367
chr20	63025520	2366253	0.0375	0.2303
chr21	48129895	1471080	0.0306	0.2199
chr22	51304566	1280602	0.025	0.1882
chrMT	16571	138204	8.3401	5.5693
chrX	155270560	3642279	0.0235	0.2012
chrY	59373566	719827	0.0121	0.1411

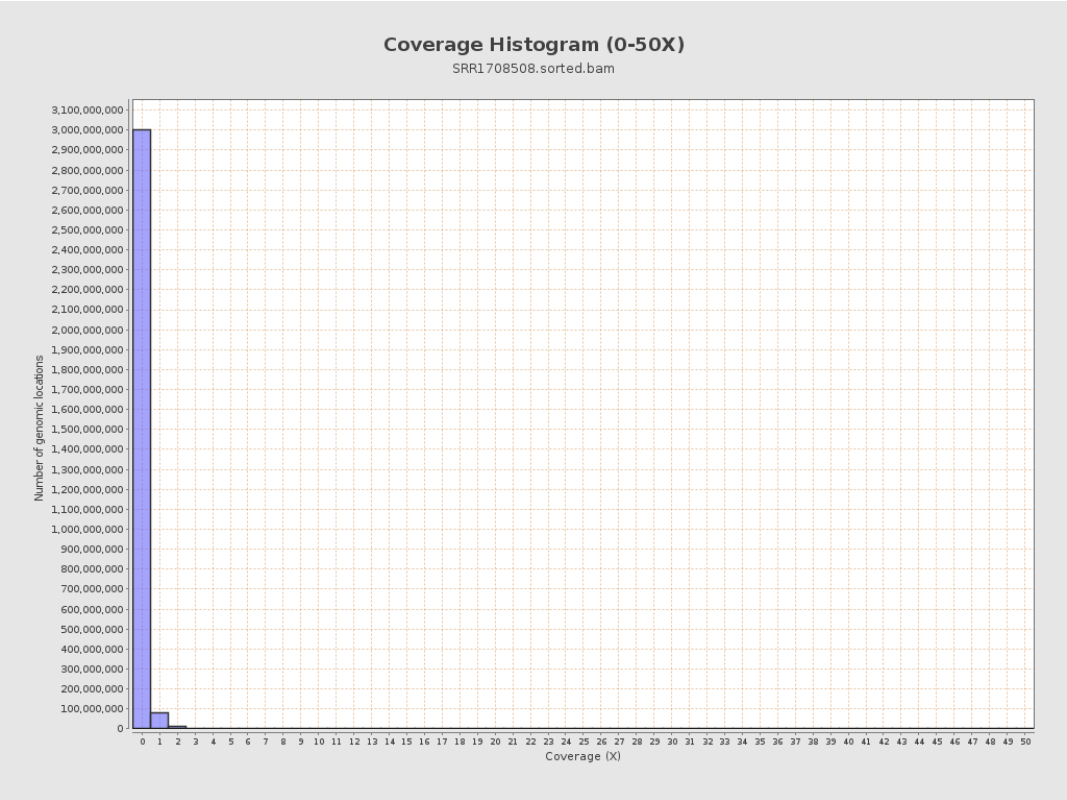
3. Results : Coverage across reference



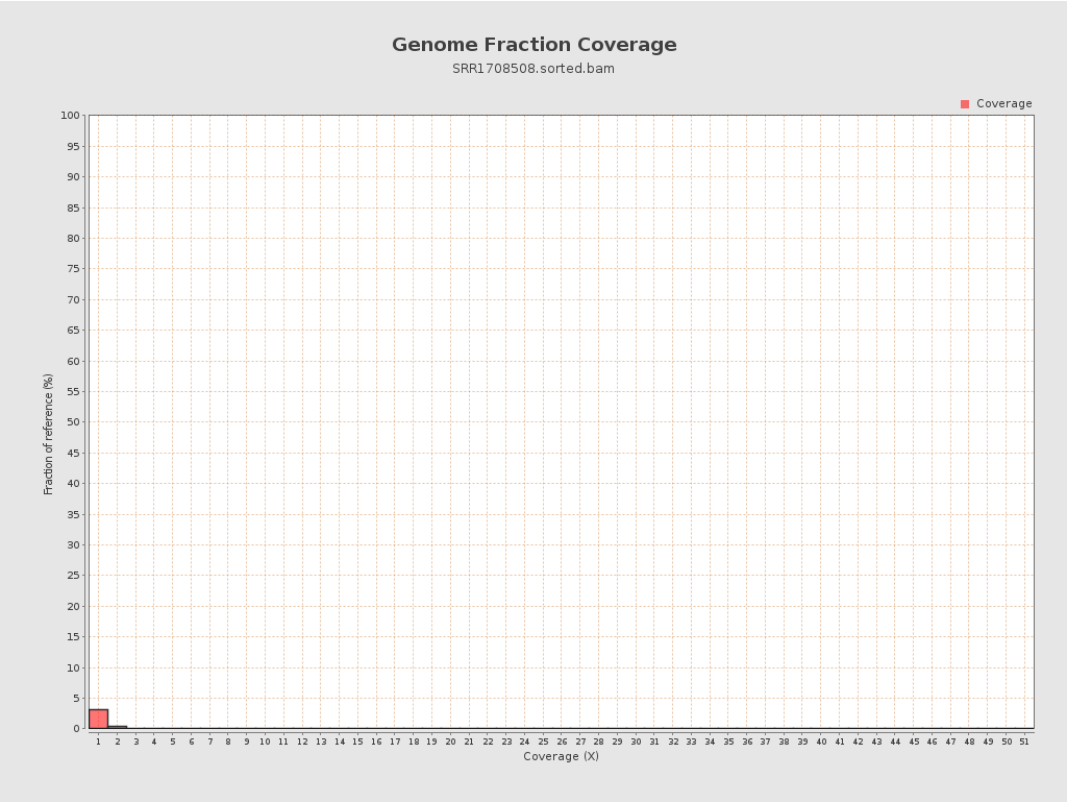
4. Results : Coverage Histogram



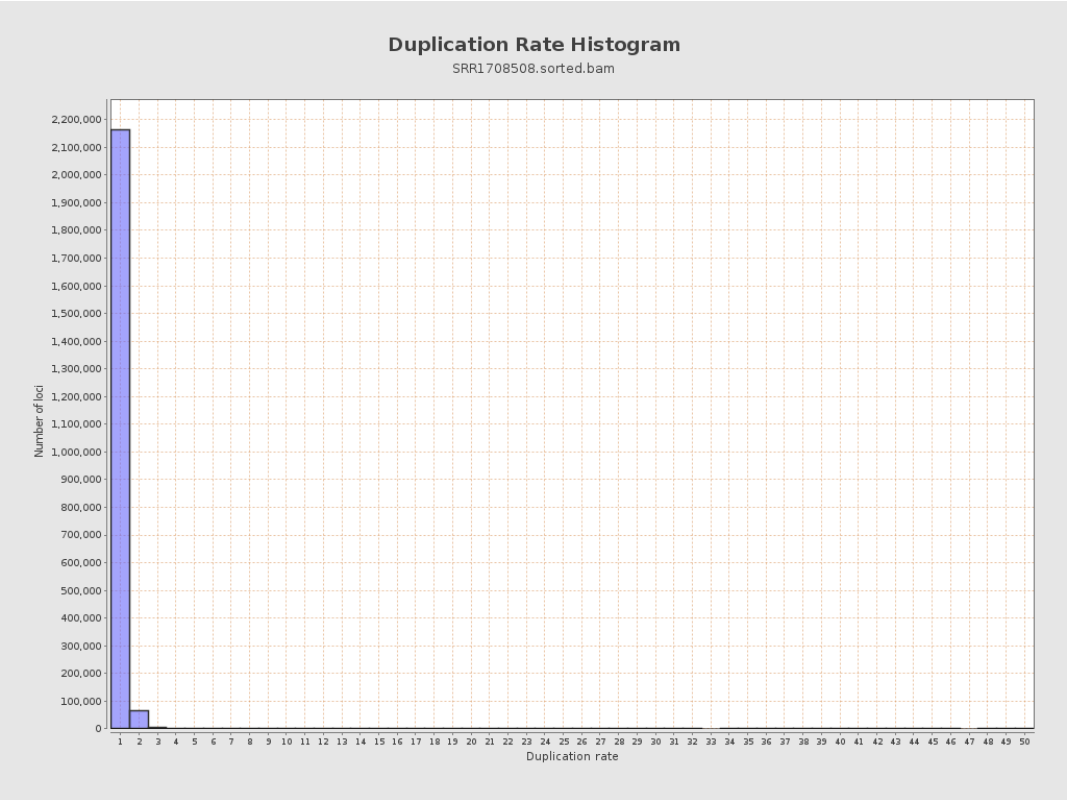
5. Results : Coverage Histogram (0-50X)



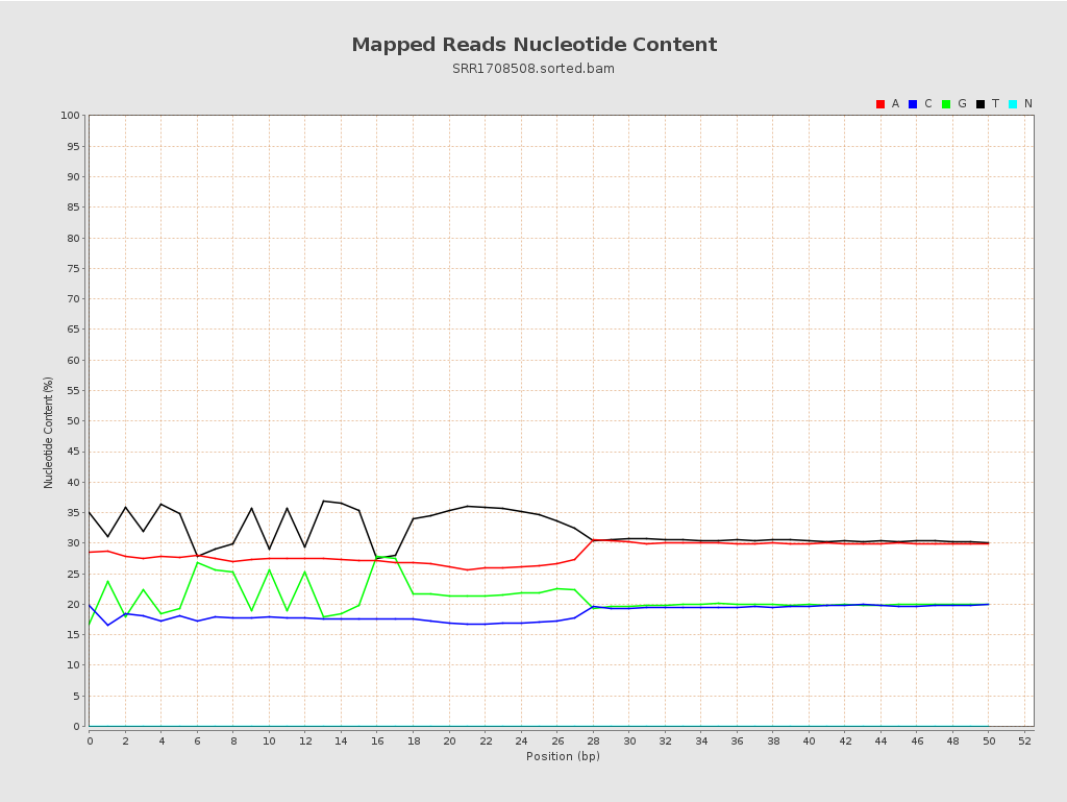
6. Results : Genome Fraction Coverage



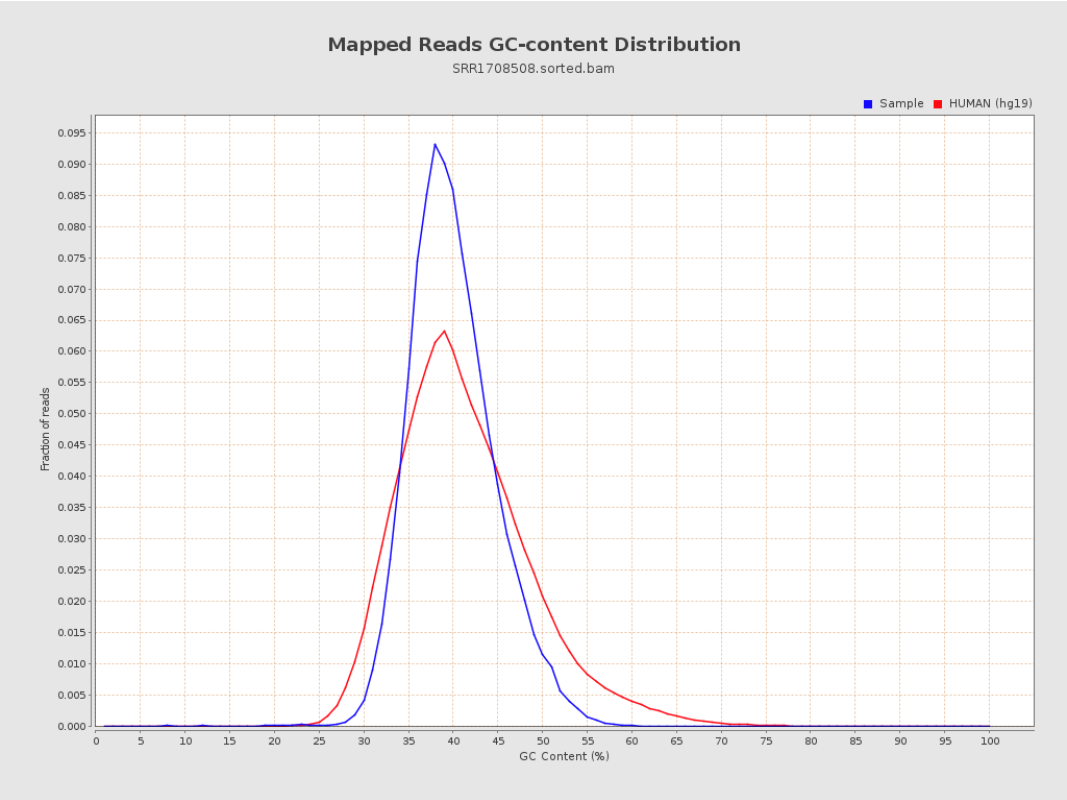
7. Results : Duplication Rate Histogram



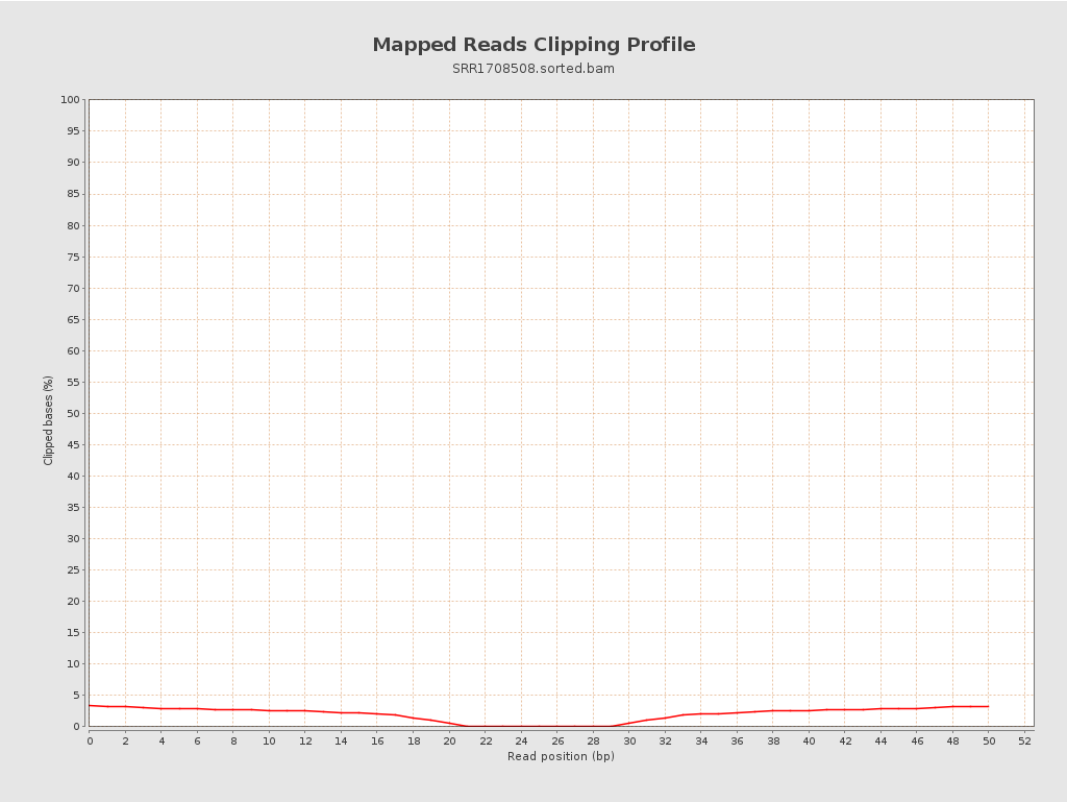
8. Results : Mapped Reads Nucleotide Content



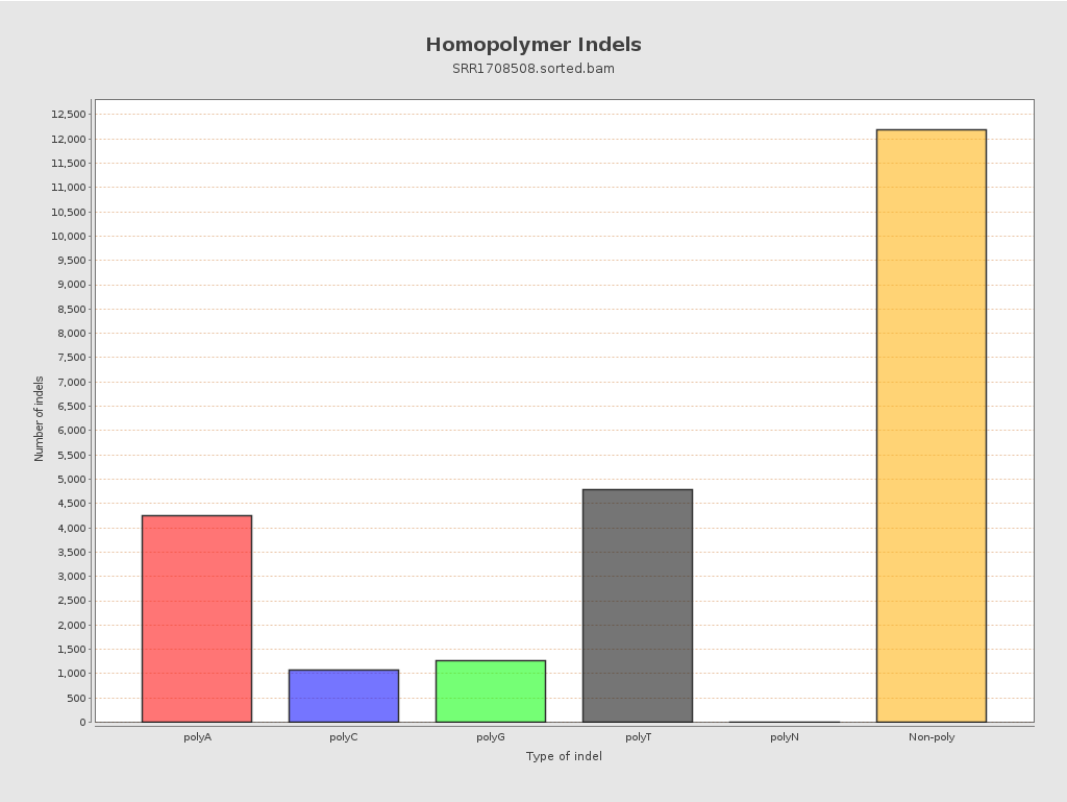
9. Results : Mapped Reads GC-content Distribution



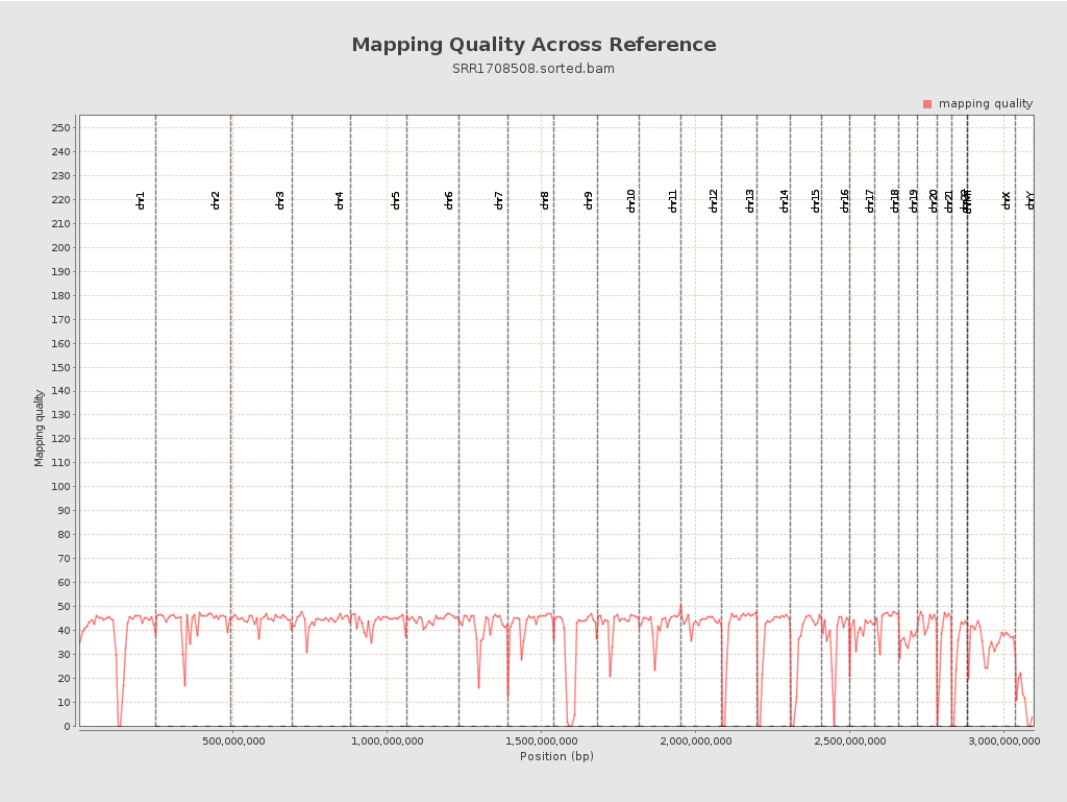
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram