Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:09:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708529.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_SRR1708529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:09:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,975,903
Mapped reads	2,682,121 / 67.46%
Unmapped reads	1,293,782 / 32.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,549 / 0.04%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	111,838 / 2.81%
Duplication rate	2.69%
Clipped reads	682,839 / 17.17%

2.2. ACGT Content

Number/percentage of A's	35,723,485 / 28.25%
Number/percentage of C's	23,205,254 / 18.35%
Number/percentage of T's	40,549,084 / 32.06%
Number/percentage of G's	26,987,994 / 21.34%
Number/percentage of N's	1,649 / 0%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.4337

2.4. Mapping Quality

Mean Mapping Quality	38.77

2.5. Mismatches and indels

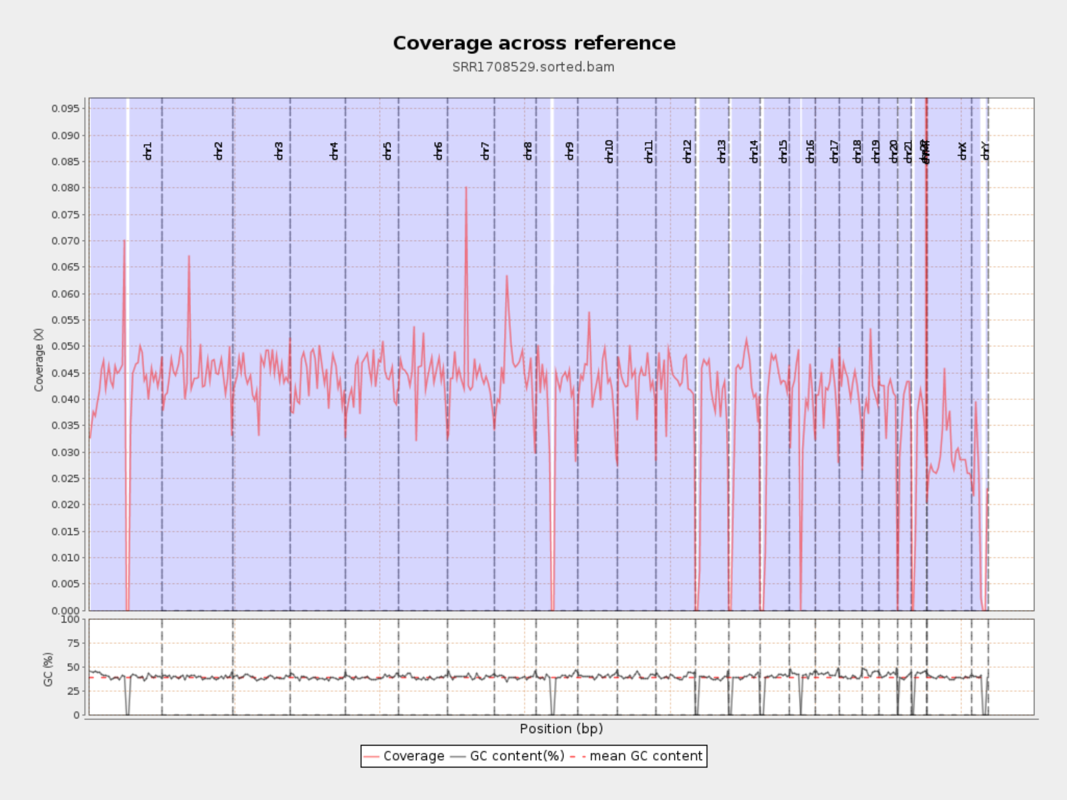
General error rate	0.55%
Mismatches	687,163
Insertions	7,700
Mapped reads with at least one insertion	0.29%
Deletions	20,694
Mapped reads with at least one deletion	0.77%
Homopolymer indels	47.04%

2.6. Chromosome stats

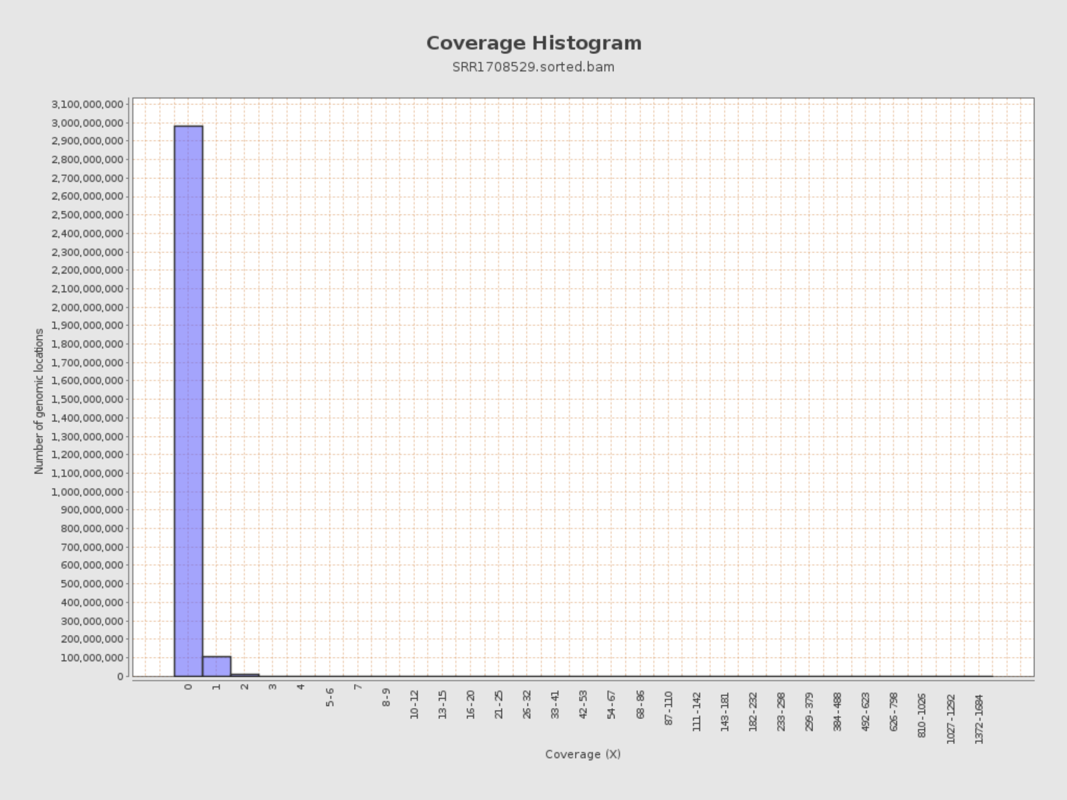
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10371798	0.0416	0.6706
chr2	243199373	11007250	0.0453	0.6536
chr3	198022430	8851868	0.0447	0.2469
chr4	191154276	8387291	0.0439	0.2635
chr5	180915260	7990427	0.0442	0.2418
chr6	171115067	7675334	0.0449	0.3466
chr7	159138663	7187598	0.0452	0.5394

chr8	146364022	6629675	0.0453	0.9268
chr9	141213431	5303462	0.0376	0.3054
chr10	135534747	5903399	0.0436	0.3022
chr11	135006516	5903723	0.0437	0.3707
chr12	133851895	5859566	0.0438	0.2441
chr13	115169878	4052023	0.0352	0.2678
chr14	107349540	3989686	0.0372	0.2364
chr15	102531392	3671620	0.0358	0.2293
chr16	90354753	3361262	0.0372	0.2341
chr17	81195210	3309042	0.0408	0.3006
chr18	78077248	3364018	0.0431	0.4907
chr19	59128983	2418215	0.0409	0.4698
chr20	63025520	2520414	0.04	0.2292
chr21	48129895	1655668	0.0344	0.2405
chr22	51304566	1347310	0.0263	0.1921
chrMT	16571	173859	10.4918	6.7949
chrX	155270560	4574996	0.0295	0.2452
chrY	59373566	989119	0.0167	0.1824

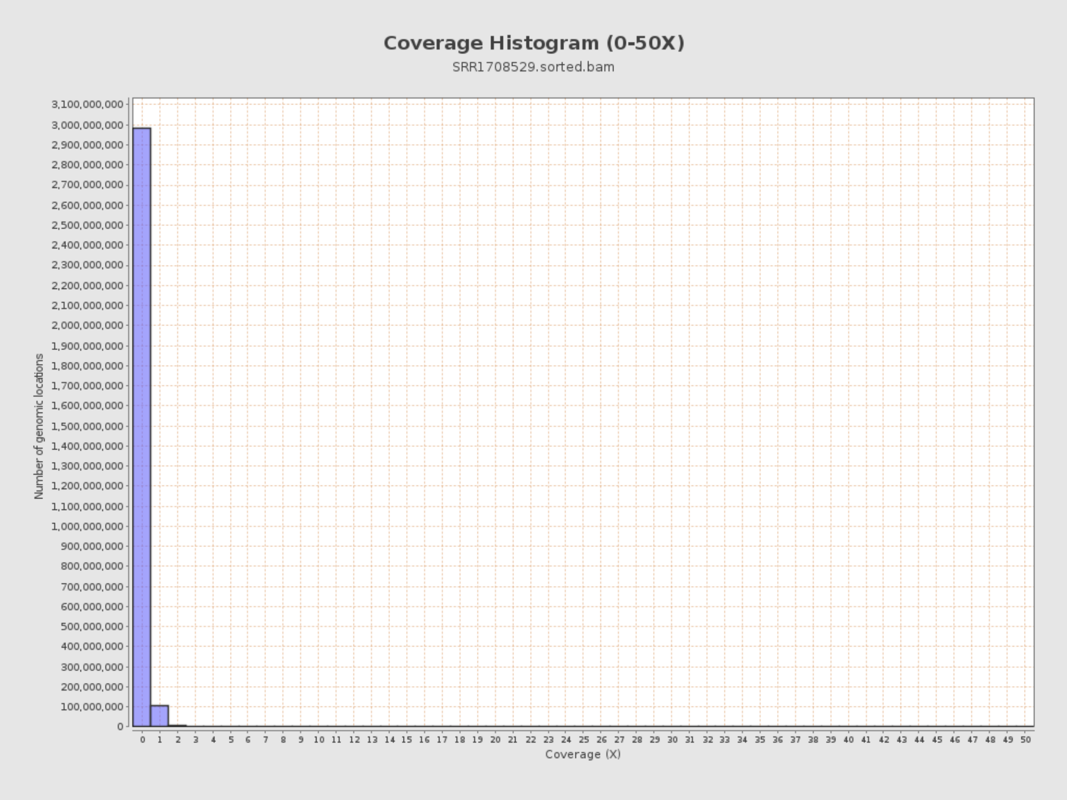
3. Results : Coverage across reference



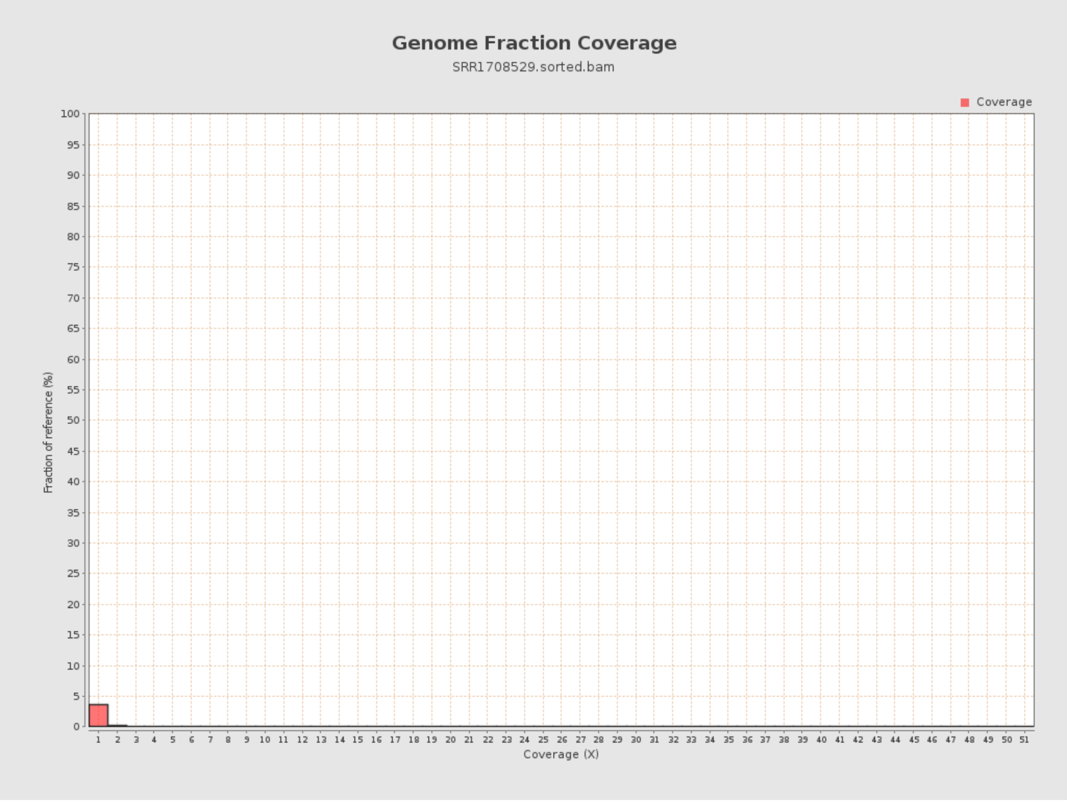
4. Results : Coverage Histogram



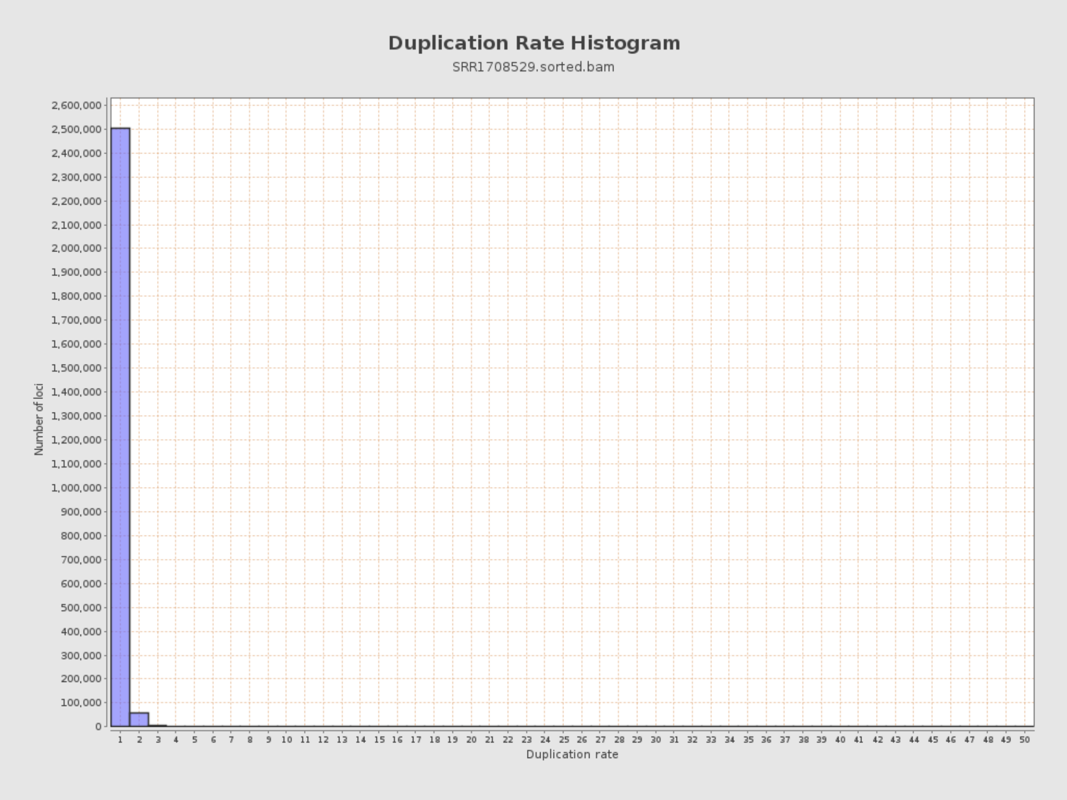
5. Results : Coverage Histogram (0-50X)



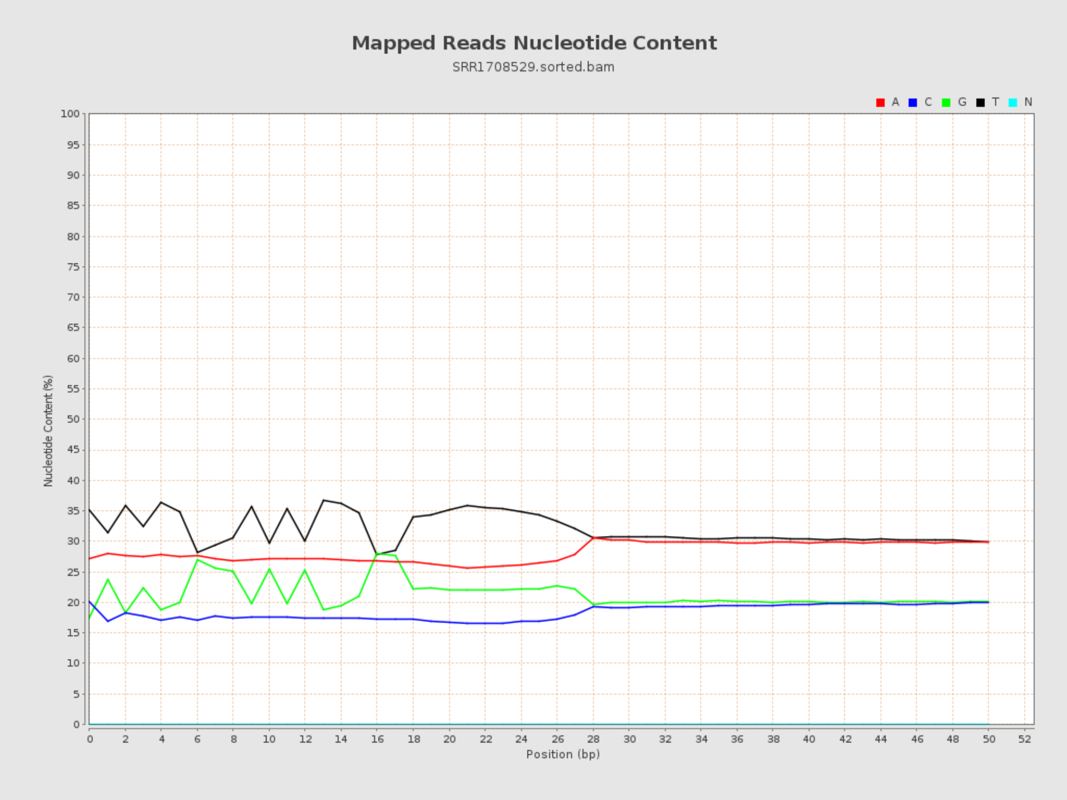
6. Results : Genome Fraction Coverage



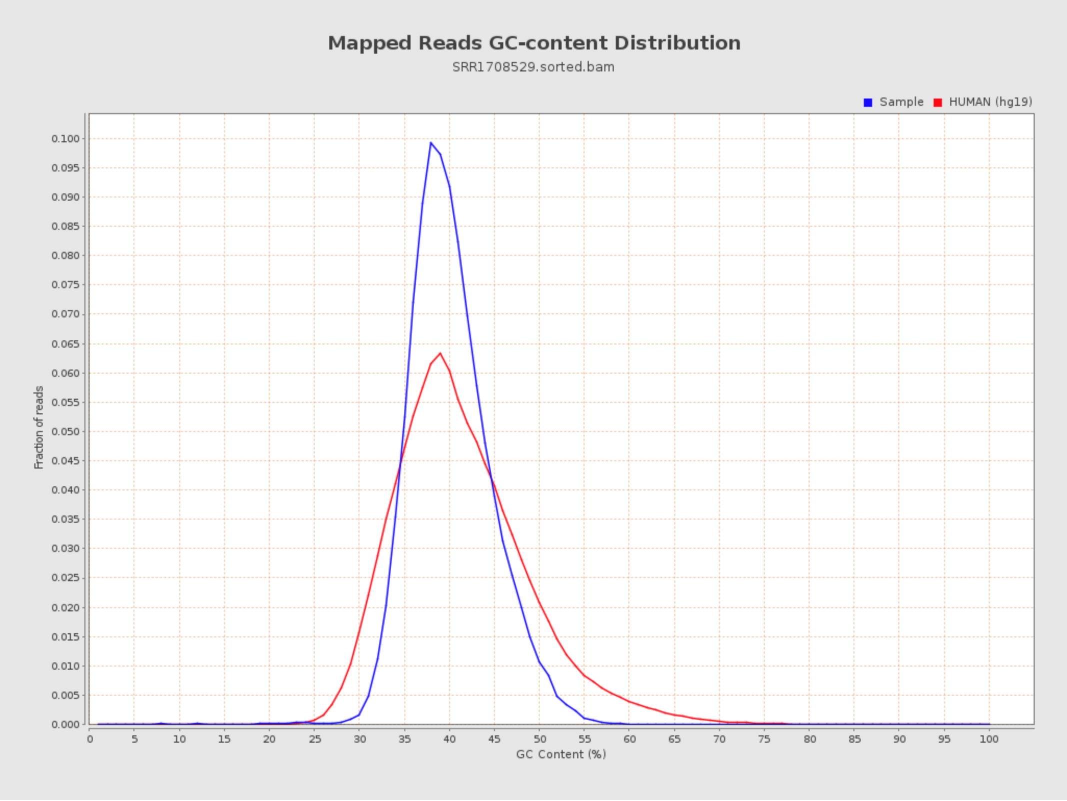
7. Results : Duplication Rate Histogram



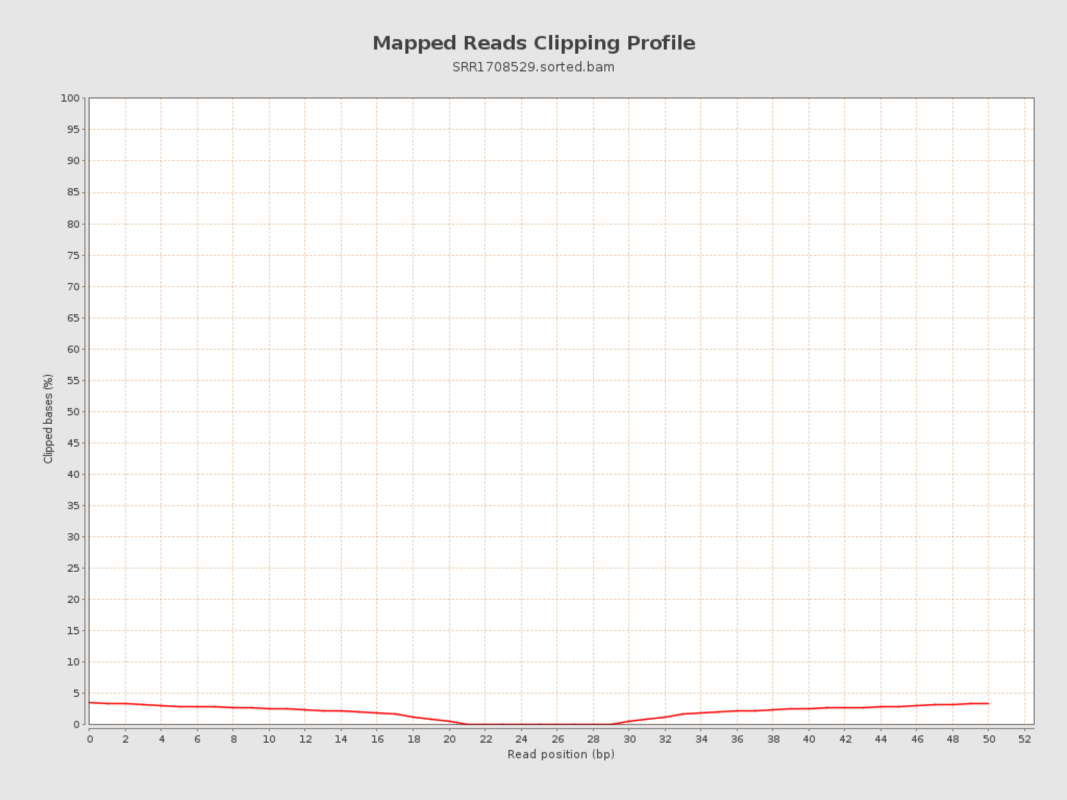
8. Results : Mapped Reads Nucleotide Content



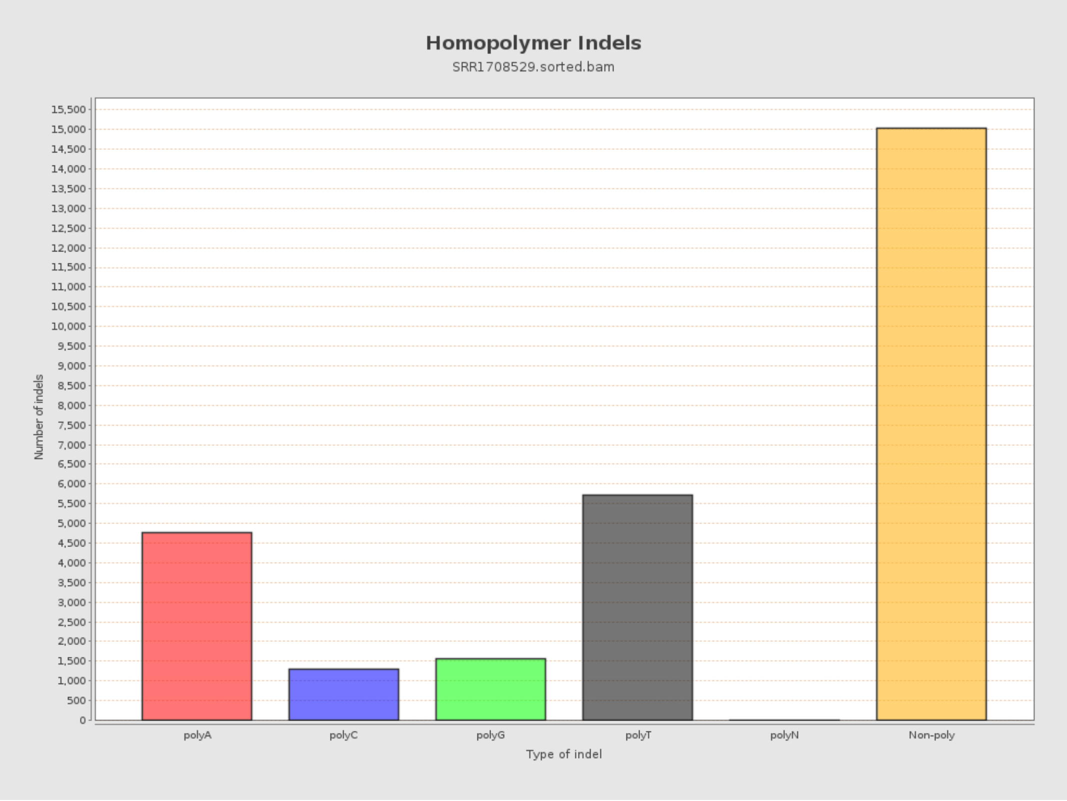
9. Results : Mapped Reads GC-content Distribution



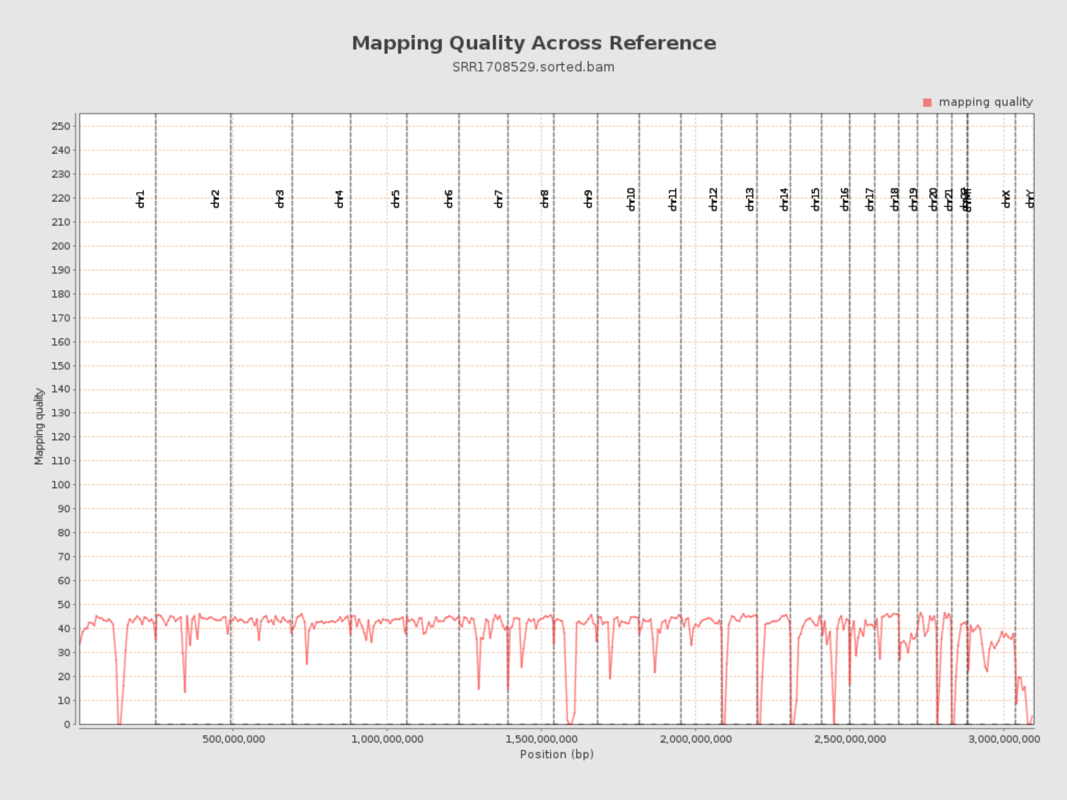
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram