Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:53:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708569.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_SRR1708569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708569.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:53:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,604,307
Mapped reads	3,773,094 / 81.95%
Unmapped reads	831,213 / 18.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	94 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	22,142 / 0.48%
Duplication rate	0.56%
Clipped reads	52,582 / 1.14%

2.2. ACGT Content

Number/percentage of A's	58,362,838 / 31.02%
Number/percentage of C's	35,636,724 / 18.94%
Number/percentage of T's	58,153,752 / 30.91%
Number/percentage of G's	35,964,343 / 19.12%
Number/percentage of N's	7,013 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	0.0608

Standard Deviation	0.27

2.4. Mapping Quality

Mean Mapping Quality	46.47

2.5. Mismatches and indels

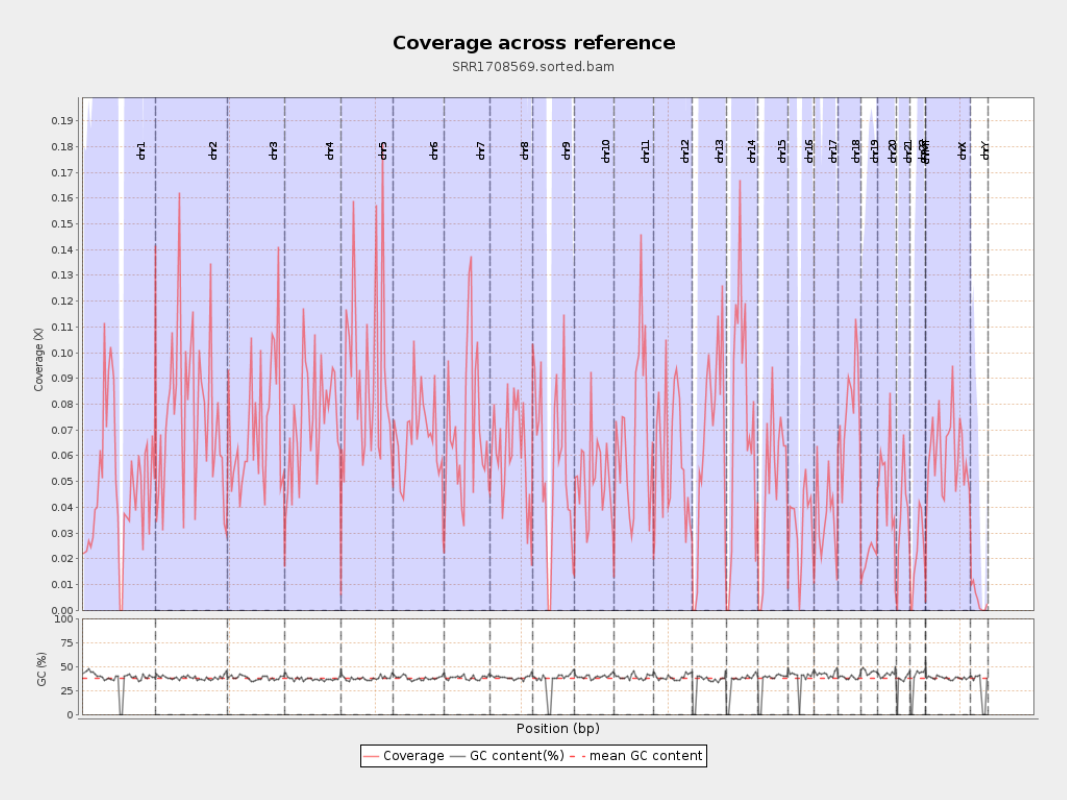
General error rate	0.17%
Mismatches	294,581
Insertions	12,962
Mapped reads with at least one insertion	0.34%
Deletions	10,068
Mapped reads with at least one deletion	0.27%
Homopolymer indels	48.02%

2.6. Chromosome stats

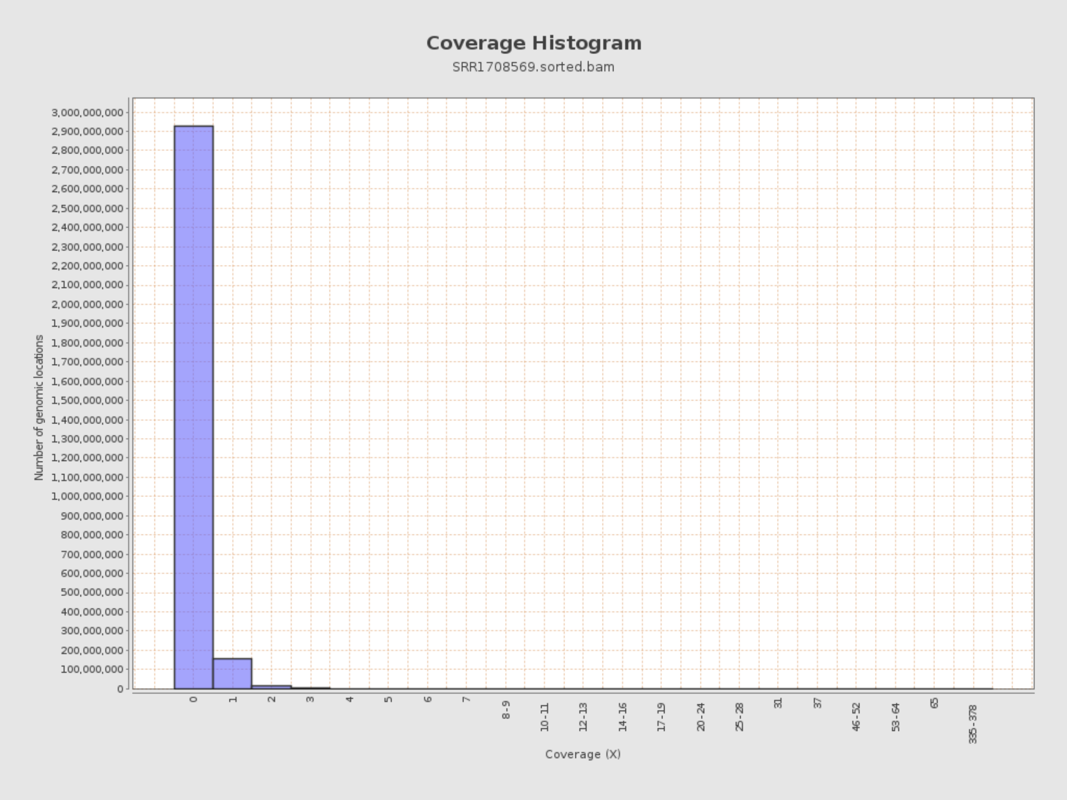
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12095834	0.0485	0.2351
chr2	243199373	18223173	0.0749	0.2951
chr3	198022430	13986927	0.0706	0.2838
chr4	191154276	14219430	0.0744	0.2907
chr5	180915260	16268999	0.0899	0.3234
chr6	171115067	11652864	0.0681	0.2767
chr7	159138663	11123683	0.0699	0.2839

chr8	146364022	8880626	0.0607	0.2615
chr9	141213431	7913365	0.056	0.2522
chr10	135534747	6997419	0.0516	0.2417
chr11	135006516	9220800	0.0683	0.3813
chr12	133851895	7983402	0.0596	0.2612
chr13	115169878	7631990	0.0663	0.2762
chr14	107349540	7958261	0.0741	0.3007
chr15	102531392	5017262	0.0489	0.2372
chr16	90354753	2930315	0.0324	0.1893
chr17	81195210	2944234	0.0363	0.201
chr18	78077248	6144520	0.0787	0.2997
chr19	59128983	1271608	0.0215	0.1522
chr20	63025520	3085481	0.049	0.2354
chr21	48129895	1744500	0.0362	0.2018
chr22	51304566	1147561	0.0224	0.1574
chrMT	16571	50	0.003	0.0548
chrX	155270560	9449278	0.0609	0.267
chrY	59373566	250090	0.0042	0.0683

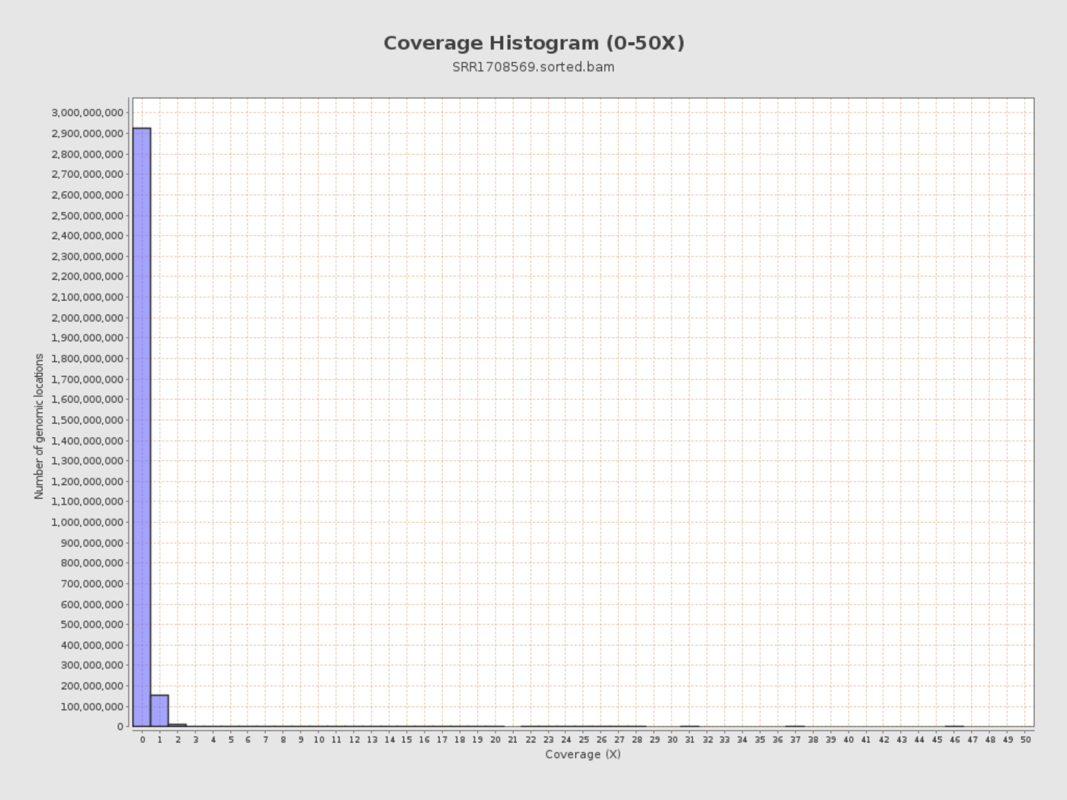
3. Results : Coverage across reference



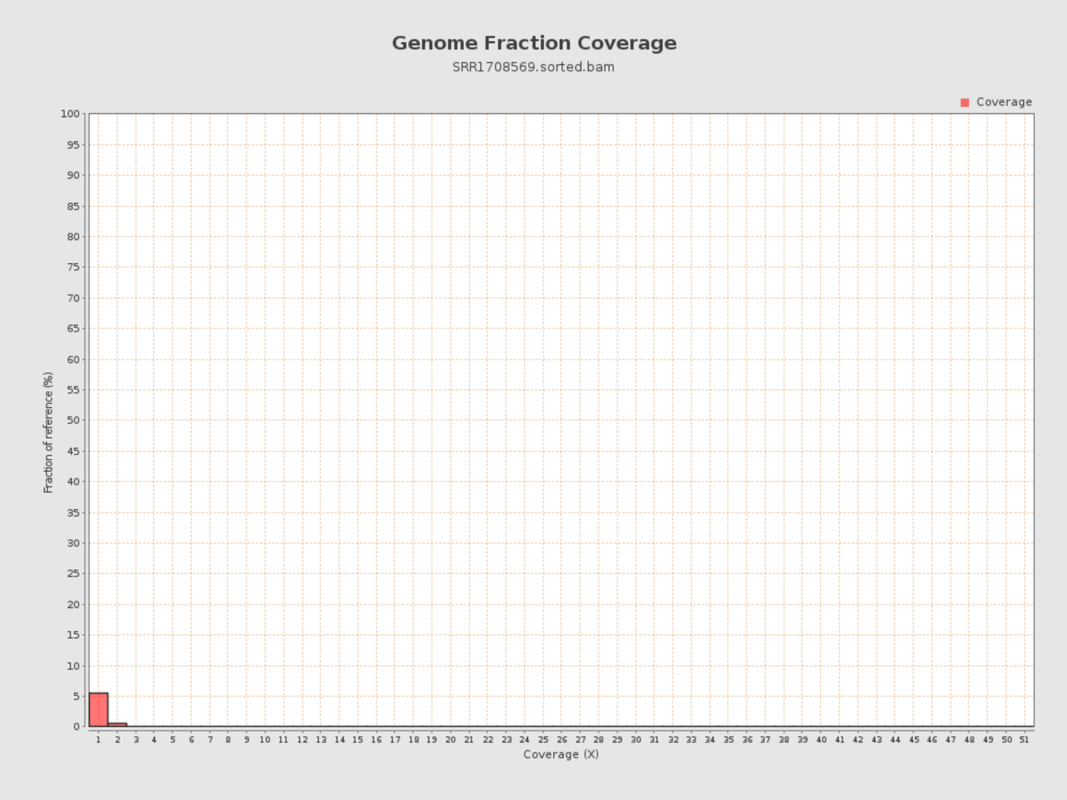
4. Results : Coverage Histogram



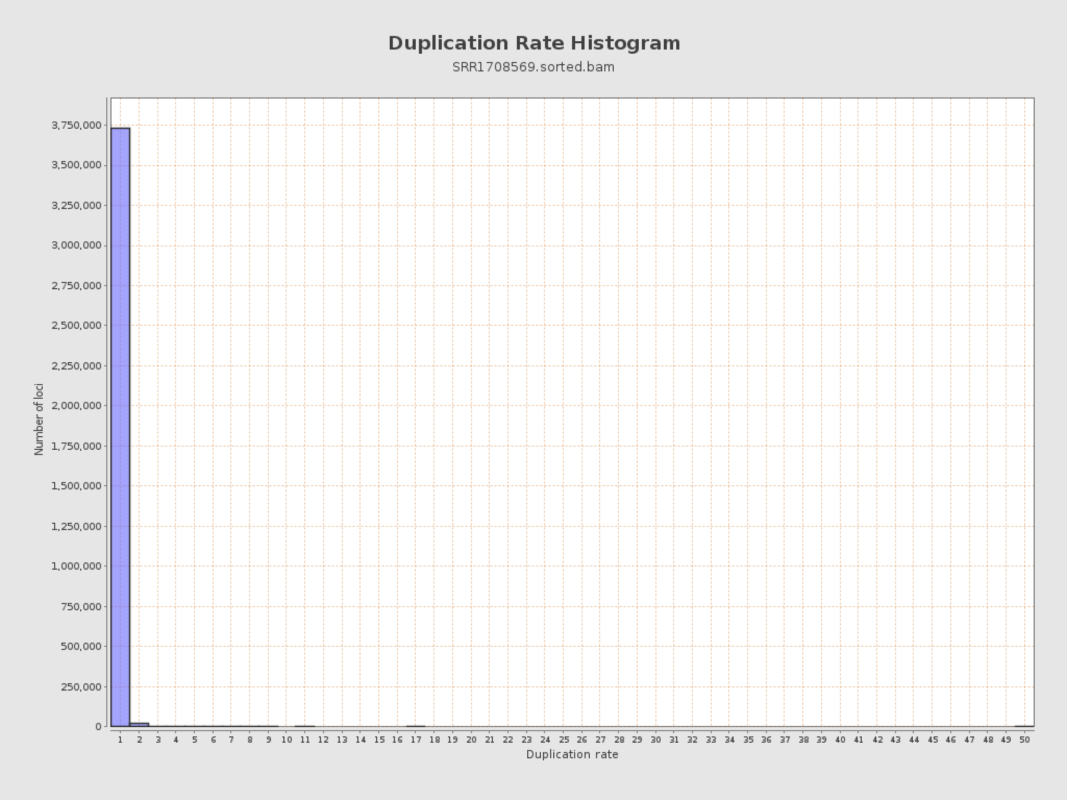
5. Results : Coverage Histogram (0-50X)



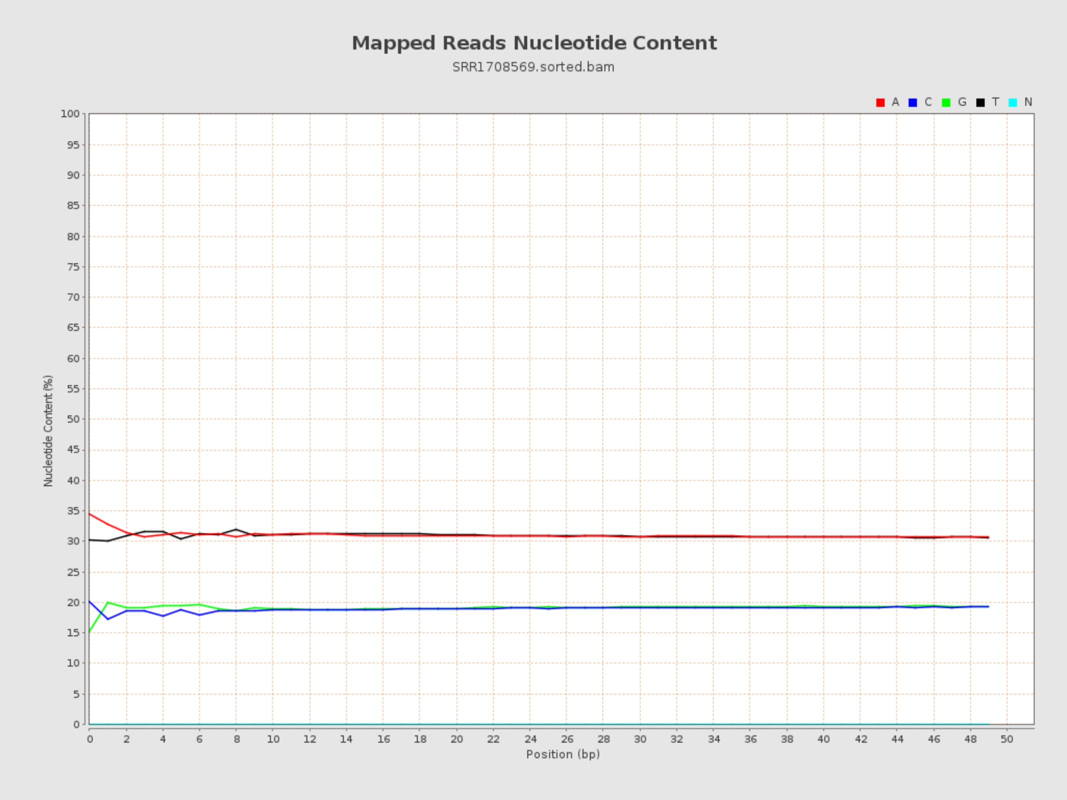
6. Results : Genome Fraction Coverage



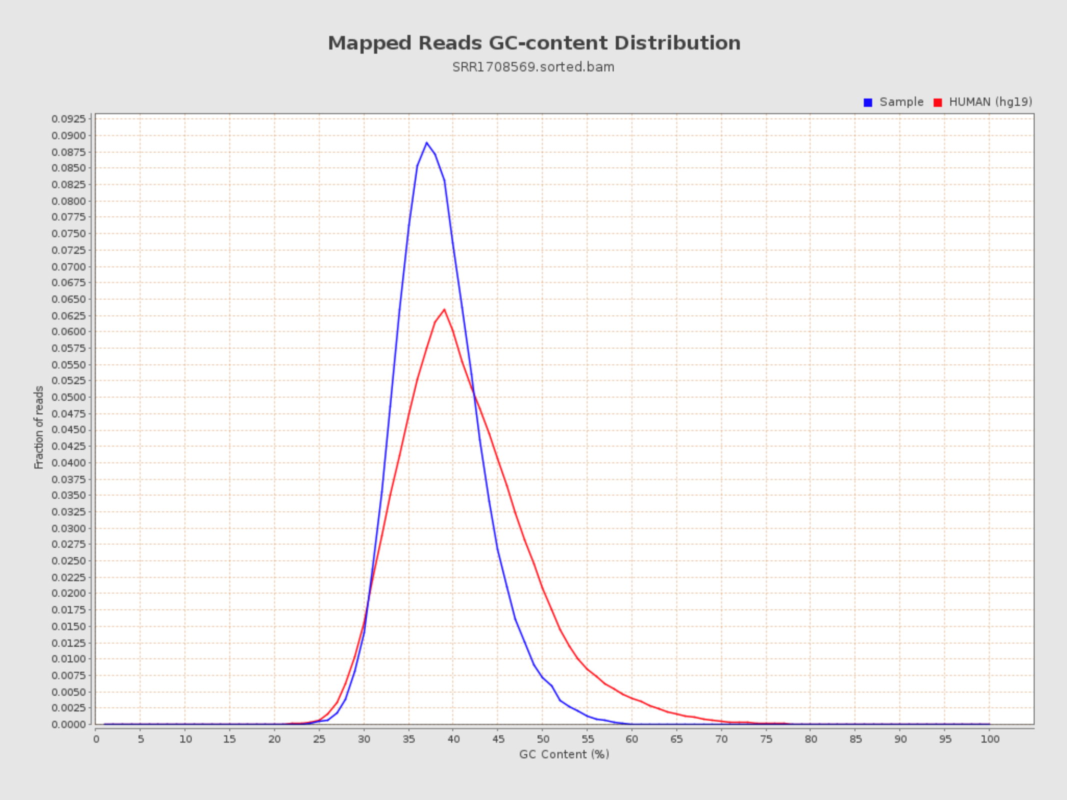
7. Results : Duplication Rate Histogram



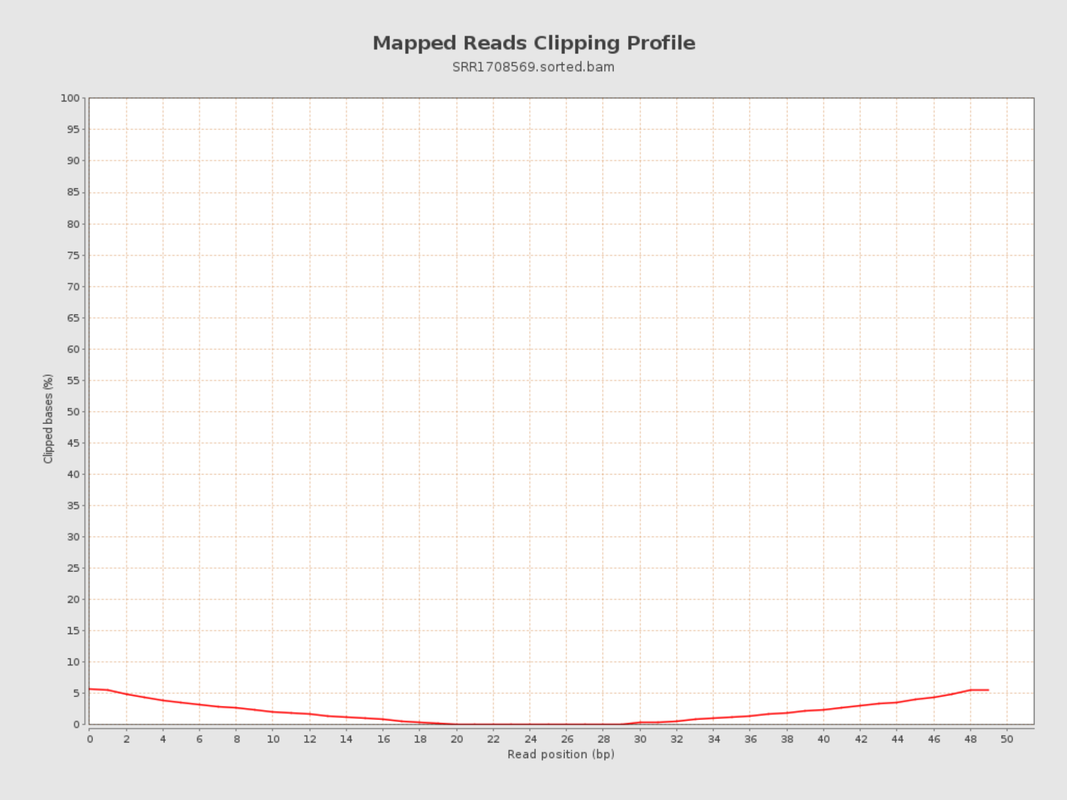
8. Results : Mapped Reads Nucleotide Content



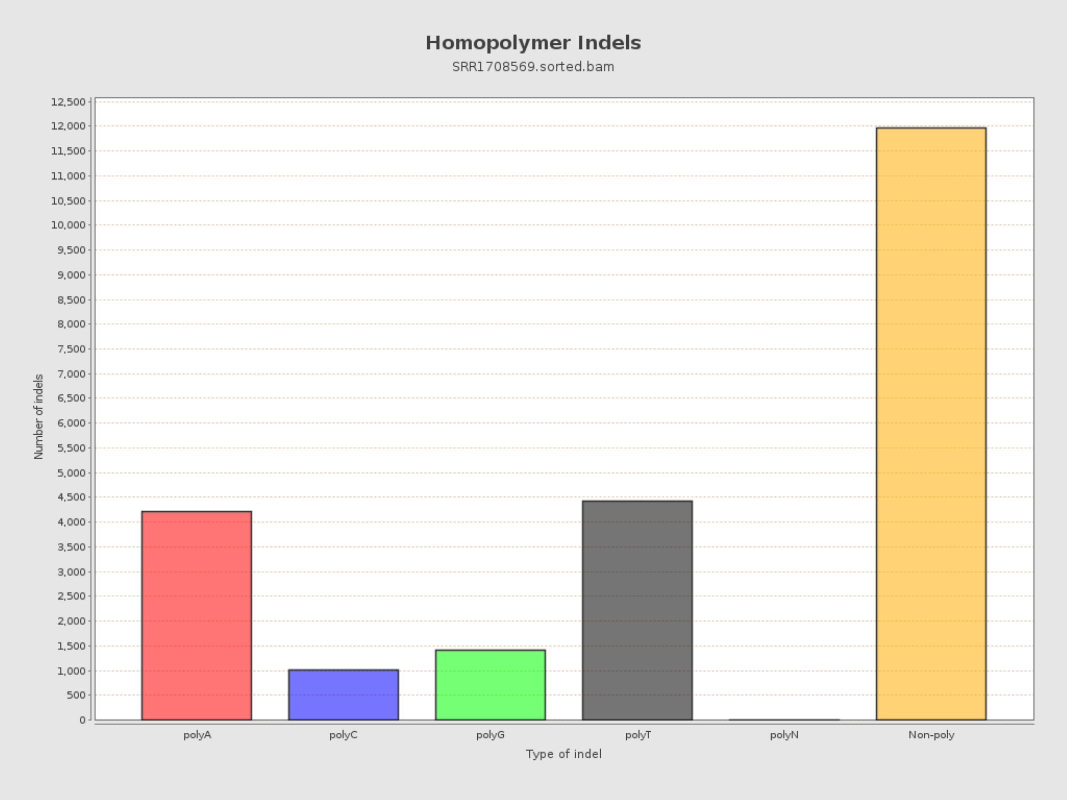
9. Results : Mapped Reads GC-content Distribution



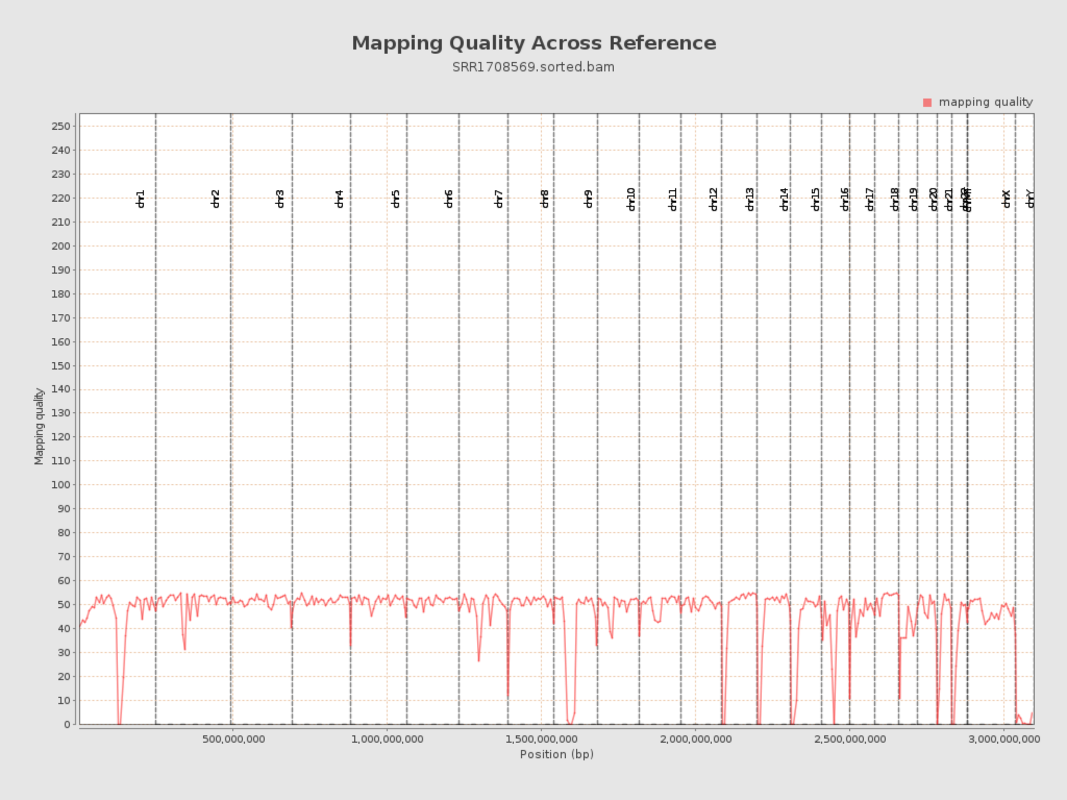
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram