Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:43:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708549.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_SRR1708549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708549.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:43:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,758,021
Mapped reads	3,929,831 / 82.59%
Unmapped reads	828,190 / 17.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	117 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	19,239 / 0.4%
Duplication rate	0.49%
Clipped reads	53,681 / 1.13%

2.2. ACGT Content

Number/percentage of A's	60,832,138 / 31.04%
Number/percentage of C's	37,097,824 / 18.93%
Number/percentage of T's	60,510,113 / 30.88%
Number/percentage of G's	37,506,197 / 19.14%
Number/percentage of N's	8,995 / 0%
GC Percentage	38.07%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.2598

2.4. Mapping Quality

Mean Mapping Quality	46.36

2.5. Mismatches and indels

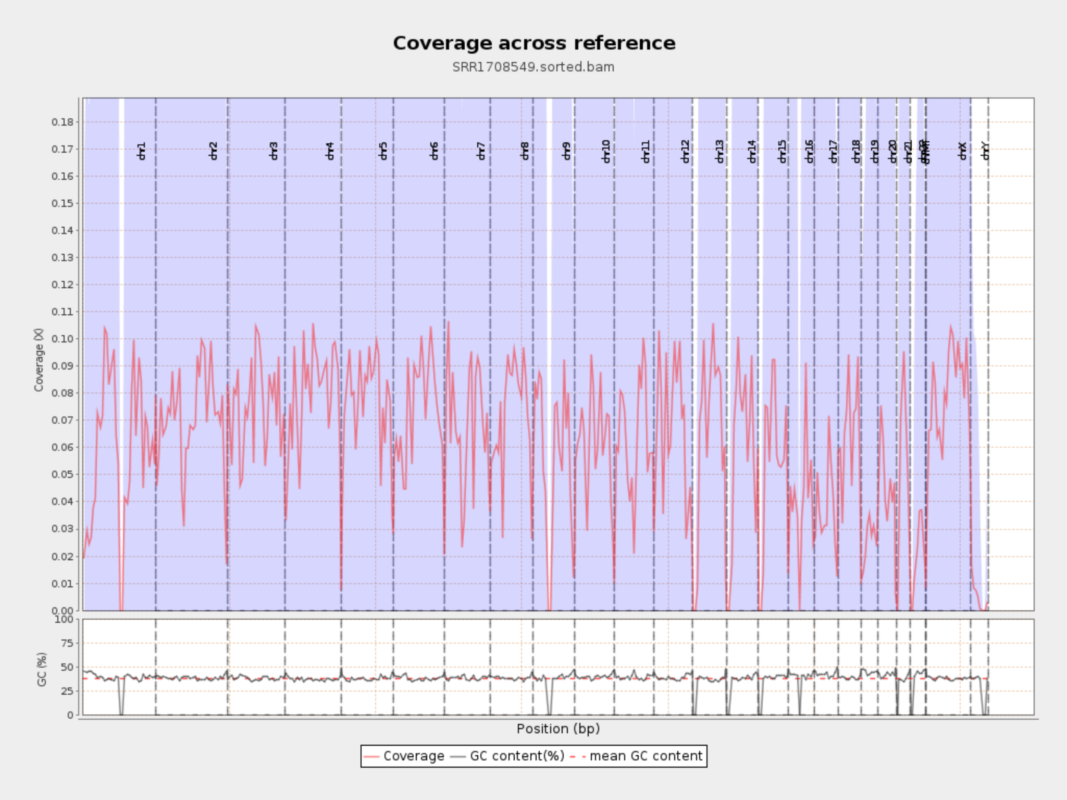
General error rate	0.17%
Mismatches	306,156
Insertions	13,204
Mapped reads with at least one insertion	0.34%
Deletions	10,508
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.43%

2.6. Chromosome stats

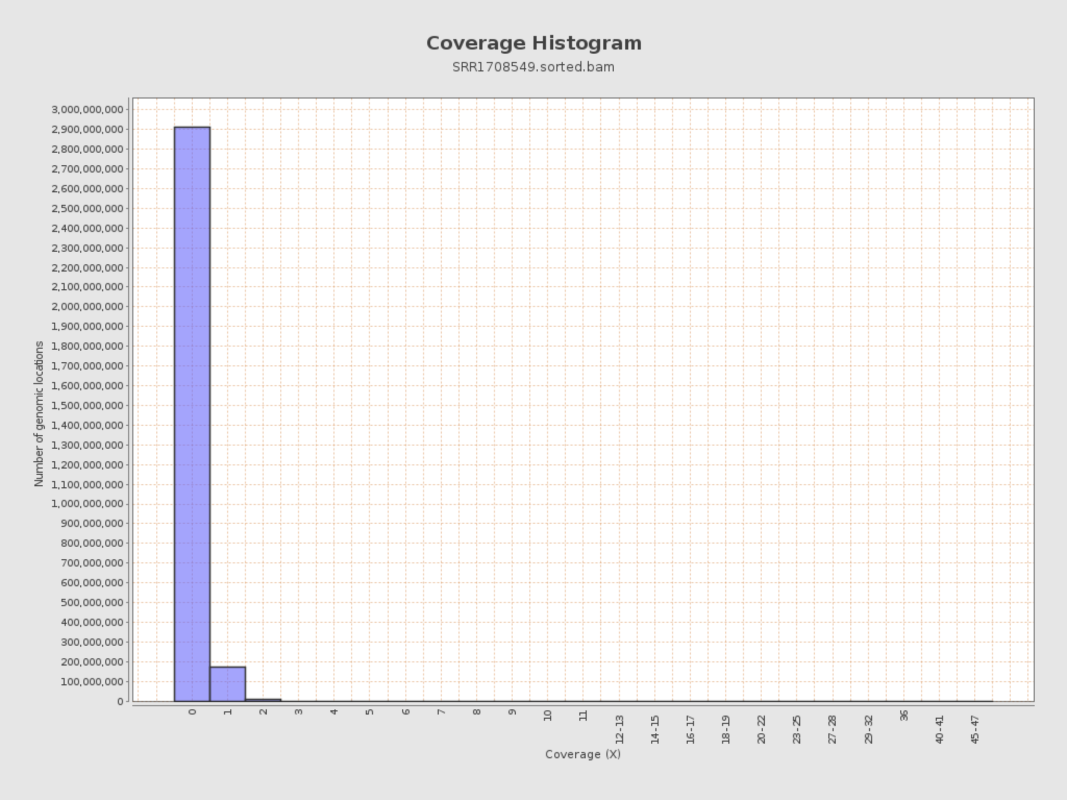
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14755115	0.0592	0.2521
chr2	243199373	17259415	0.071	0.274
chr3	198022430	14898061	0.0752	0.2821
chr4	191154276	15204979	0.0795	0.2895
chr5	180915260	13721590	0.0758	0.2829
chr6	171115067	12832858	0.075	0.2818
chr7	159138663	10771360	0.0677	0.2687

chr8	146364022	10624470	0.0726	0.2773
chr9	141213431	8003197	0.0567	0.2459
chr10	135534747	8514864	0.0628	0.2577
chr11	135006516	8488422	0.0629	0.2593
chr12	133851895	8990316	0.0672	0.2674
chr13	115169878	7461354	0.0648	0.2629
chr14	107349540	6304547	0.0587	0.2509
chr15	102531392	5547307	0.0541	0.2413
chr16	90354753	3583523	0.0397	0.2053
chr17	81195210	3140323	0.0387	0.2027
chr18	78077248	5148468	0.0659	0.2639
chr19	59128983	1529443	0.0259	0.1644
chr20	63025520	3001932	0.0476	0.2246
chr21	48129895	2457191	0.0511	0.2352
chr22	51304566	1053620	0.0205	0.1471
chrMT	16571	139	0.0084	0.0912
chrX	155270560	12407160	0.0799	0.292
chrY	59373566	273534	0.0046	0.0703

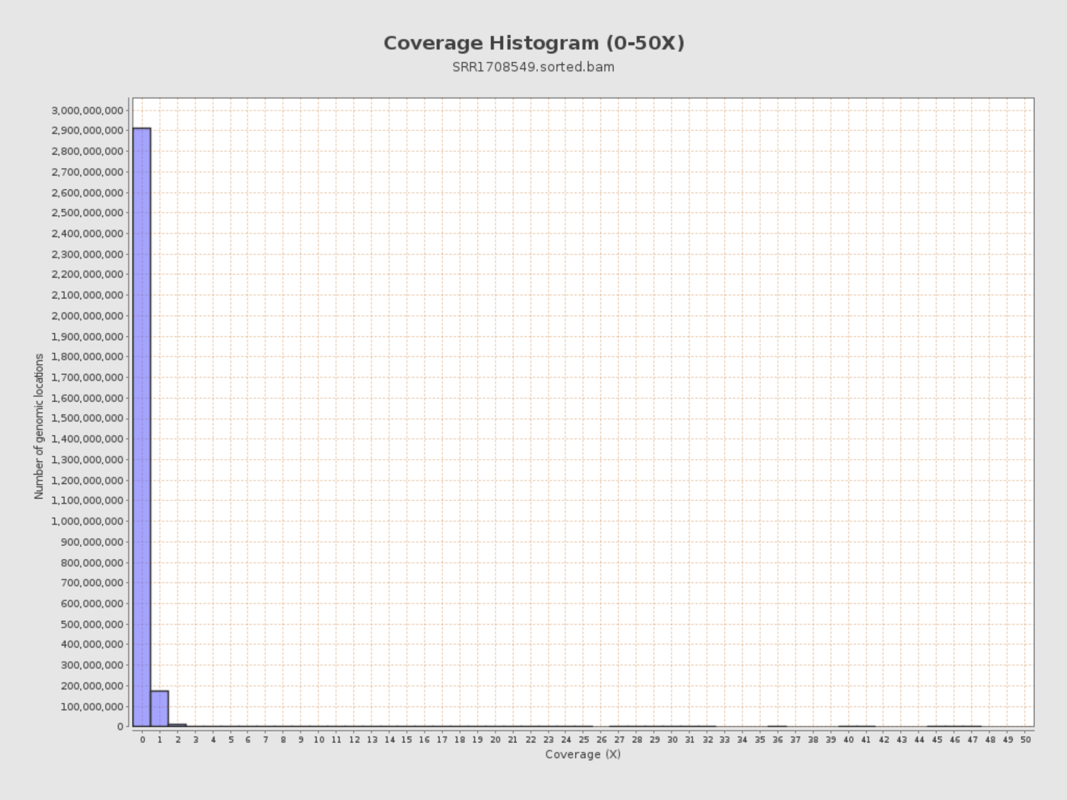
3. Results : Coverage across reference



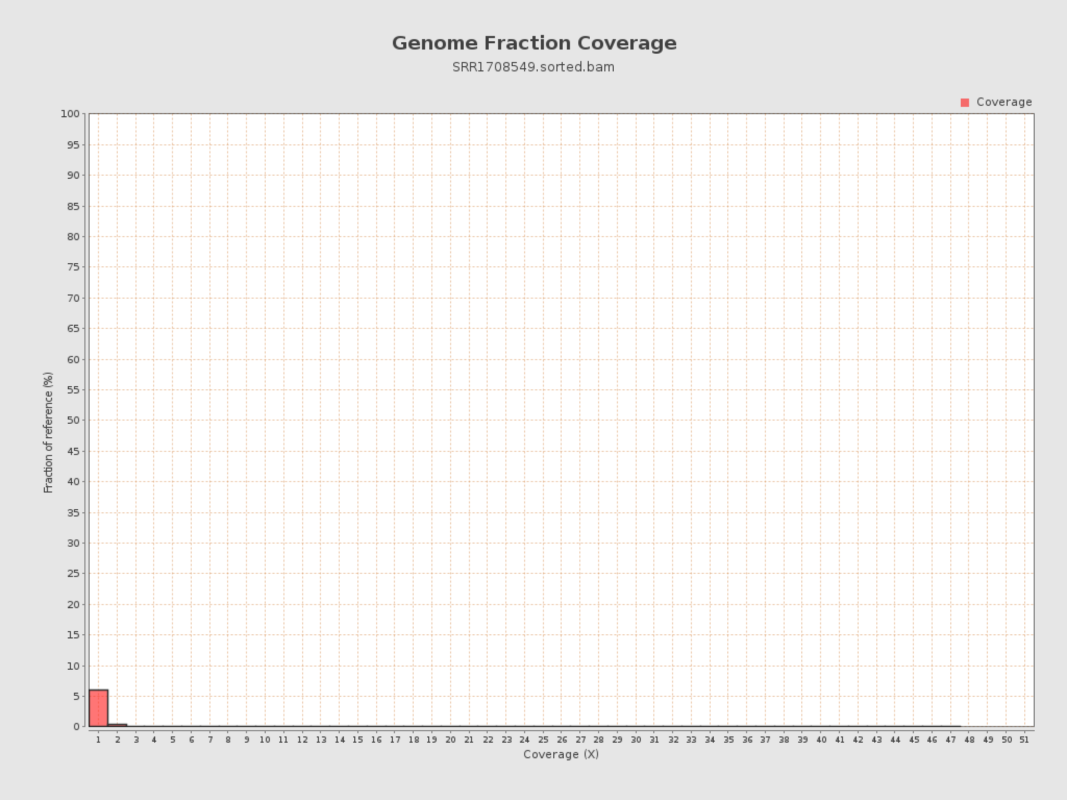
4. Results : Coverage Histogram



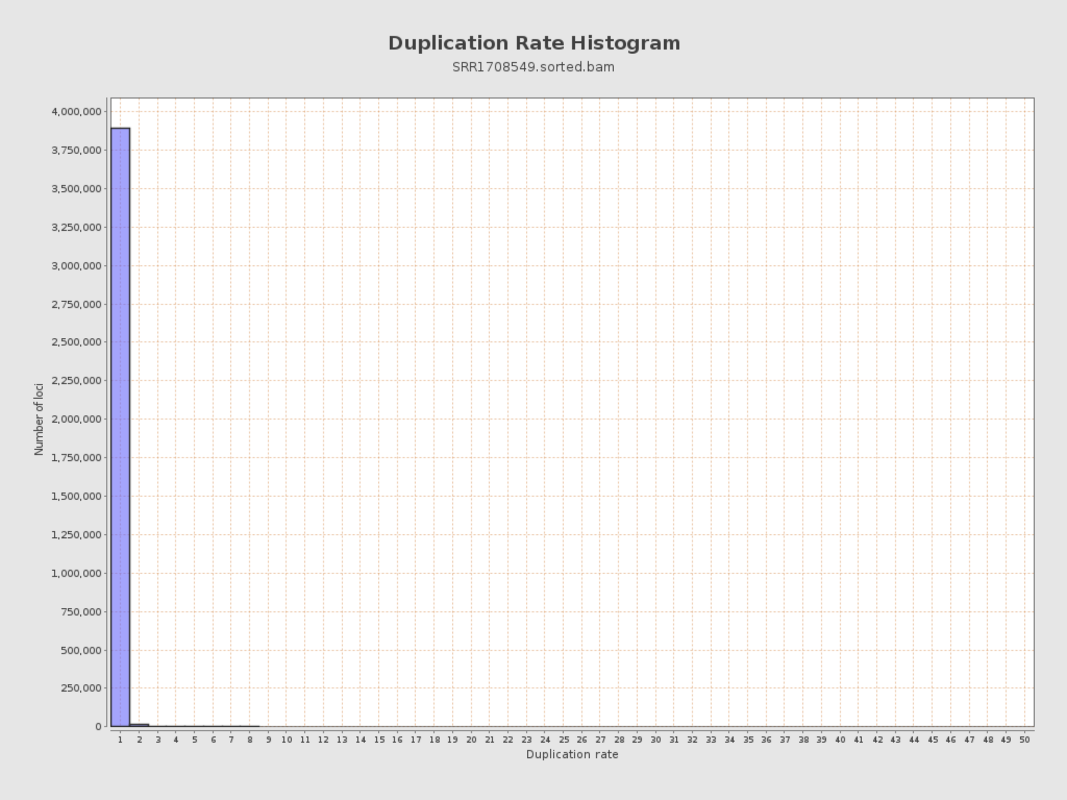
5. Results : Coverage Histogram (0-50X)



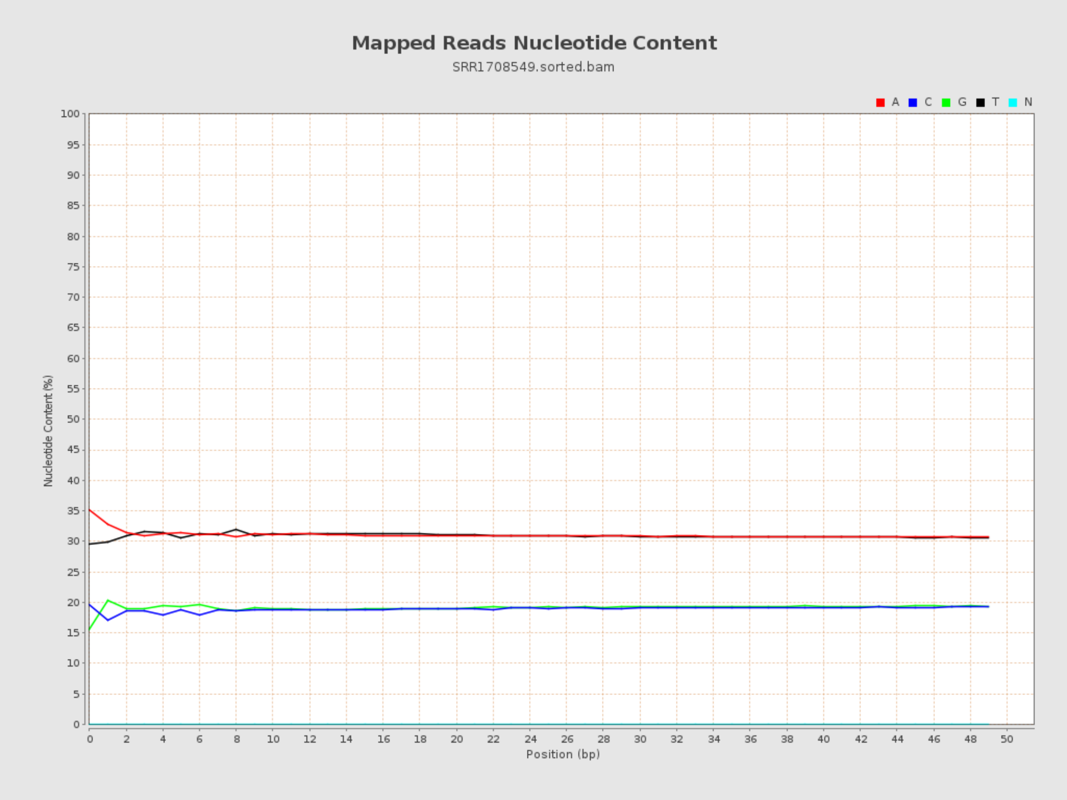
6. Results : Genome Fraction Coverage



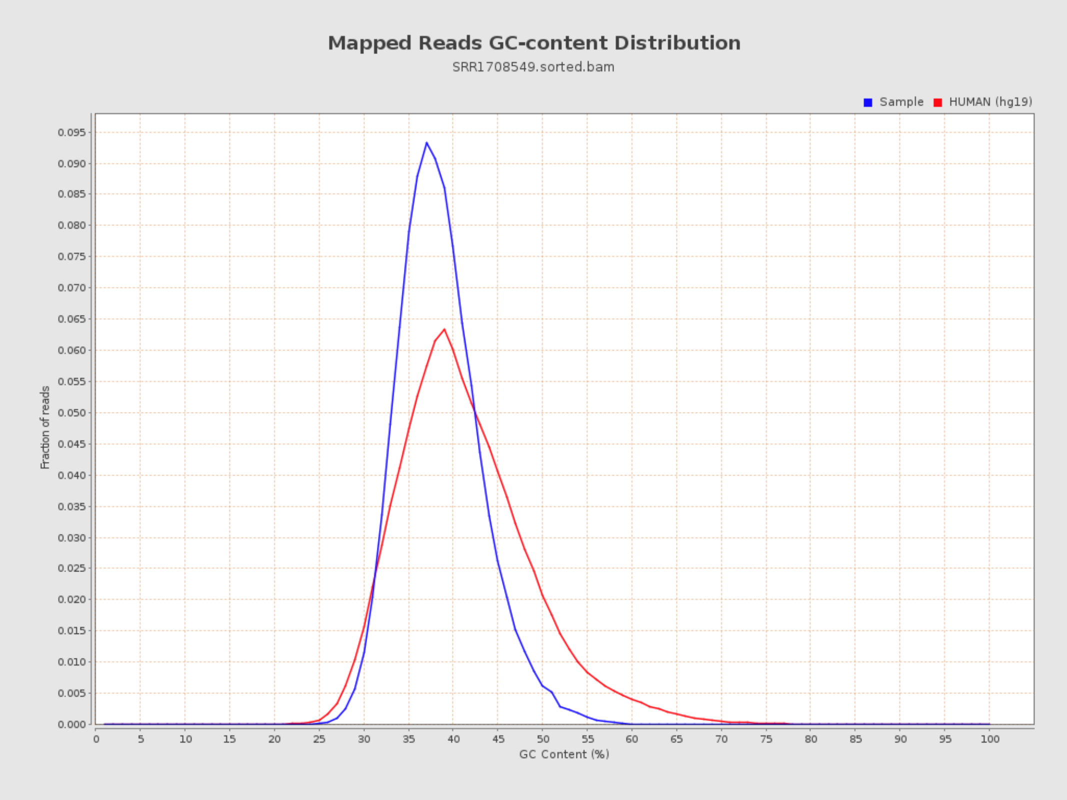
7. Results : Duplication Rate Histogram



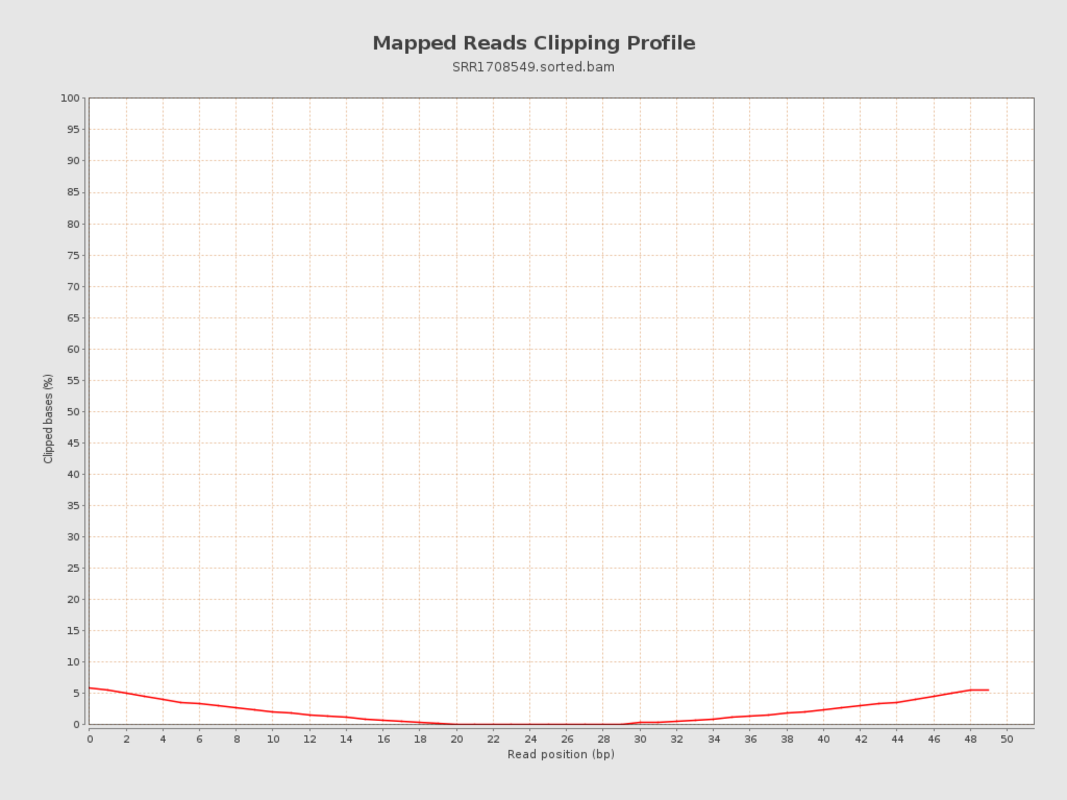
8. Results : Mapped Reads Nucleotide Content



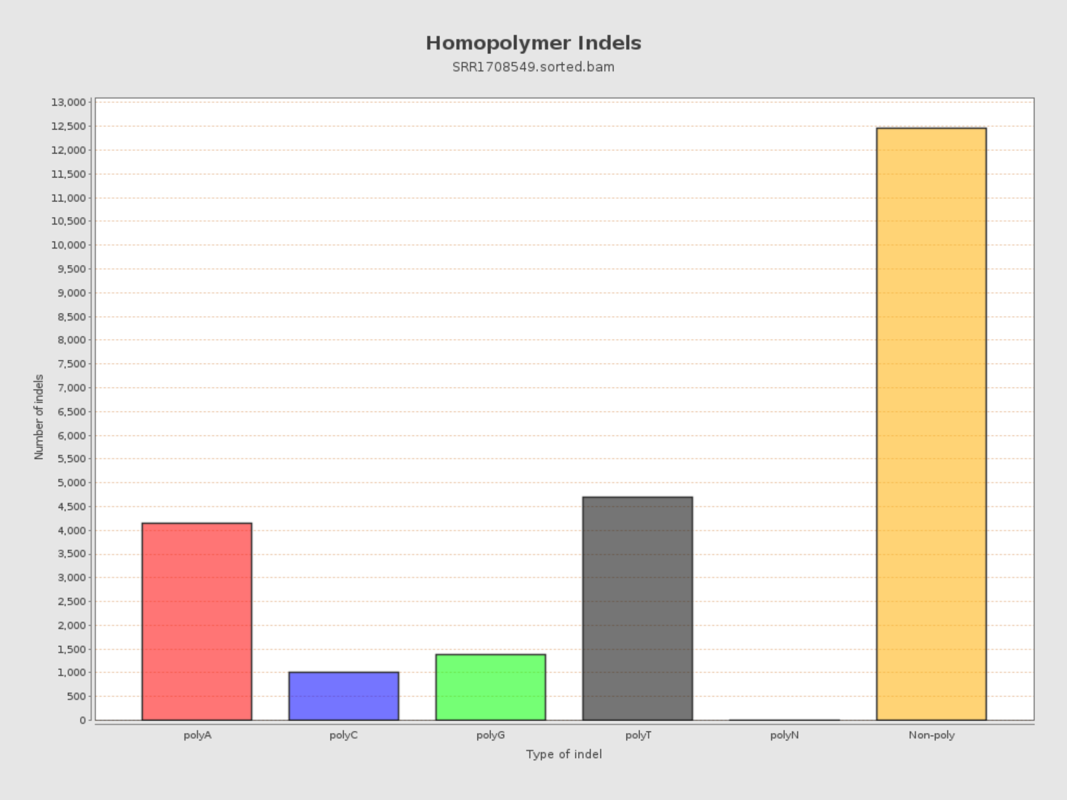
9. Results : Mapped Reads GC-content Distribution



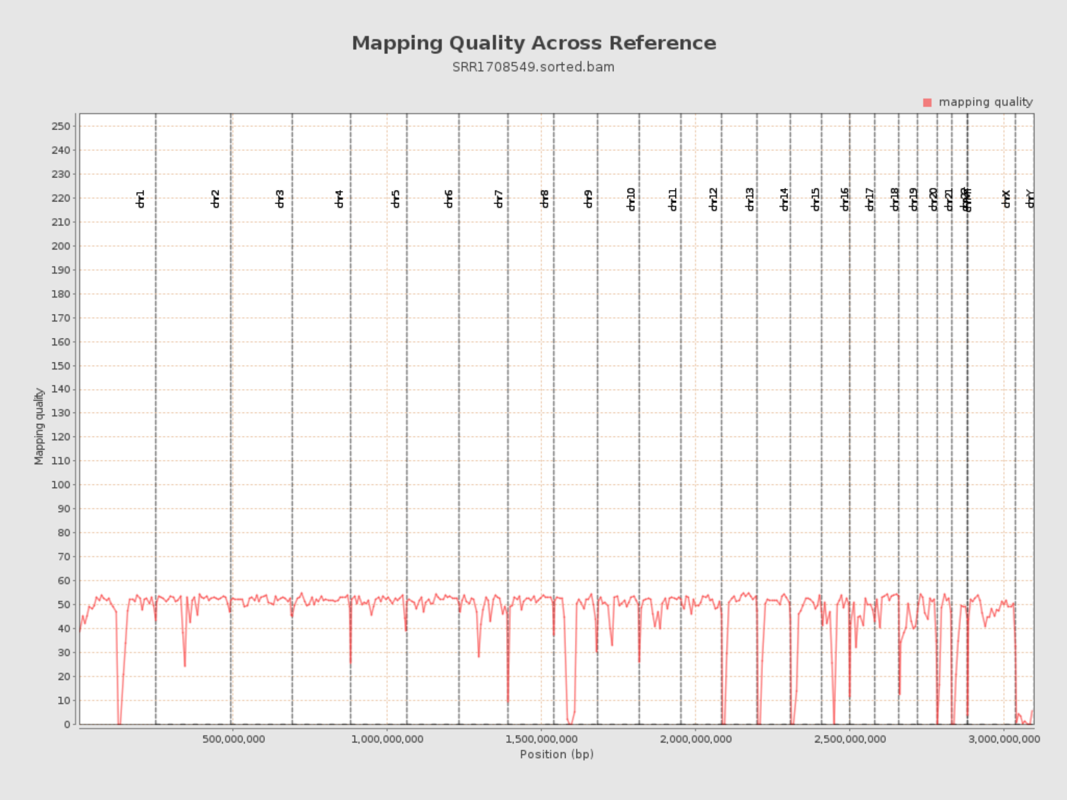
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram