Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:15:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708551.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_SRR1708551 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708551.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:15:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708551.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,165,495
Mapped reads	4,259,015 / 82.45%
Unmapped reads	906,480 / 17.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	137 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	21,537 / 0.42%
Duplication rate	0.5%
Clipped reads	58,947 / 1.14%

2.2. ACGT Content

Number/percentage of A's	65,975,510 / 31.07%
Number/percentage of C's	40,116,105 / 18.89%
Number/percentage of T's	65,703,744 / 30.94%
Number/percentage of G's	40,557,996 / 19.1%
Number/percentage of N's	7,666 / 0%
GC Percentage	37.99%

2.3. Coverage

Mean	0.0686

Standard Deviation	0.2748

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

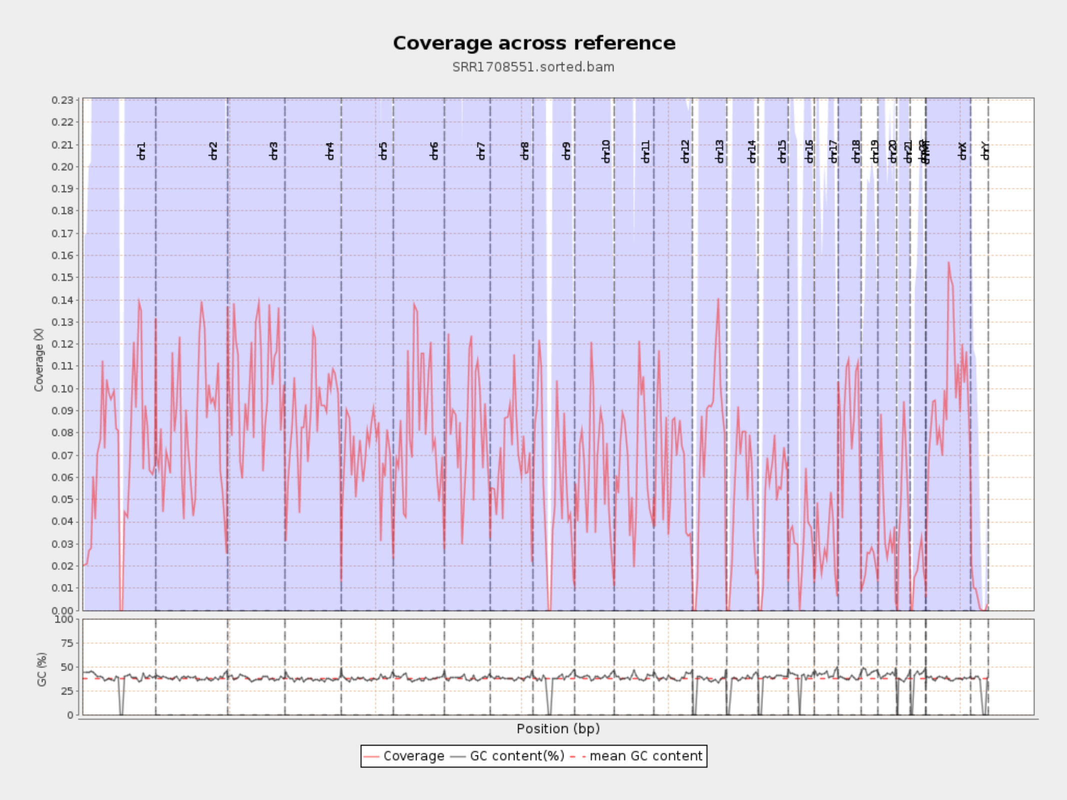
General error rate	0.17%
Mismatches	333,303
Insertions	14,336
Mapped reads with at least one insertion	0.34%
Deletions	11,325
Mapped reads with at least one deletion	0.26%
Homopolymer indels	47.48%

2.6. Chromosome stats

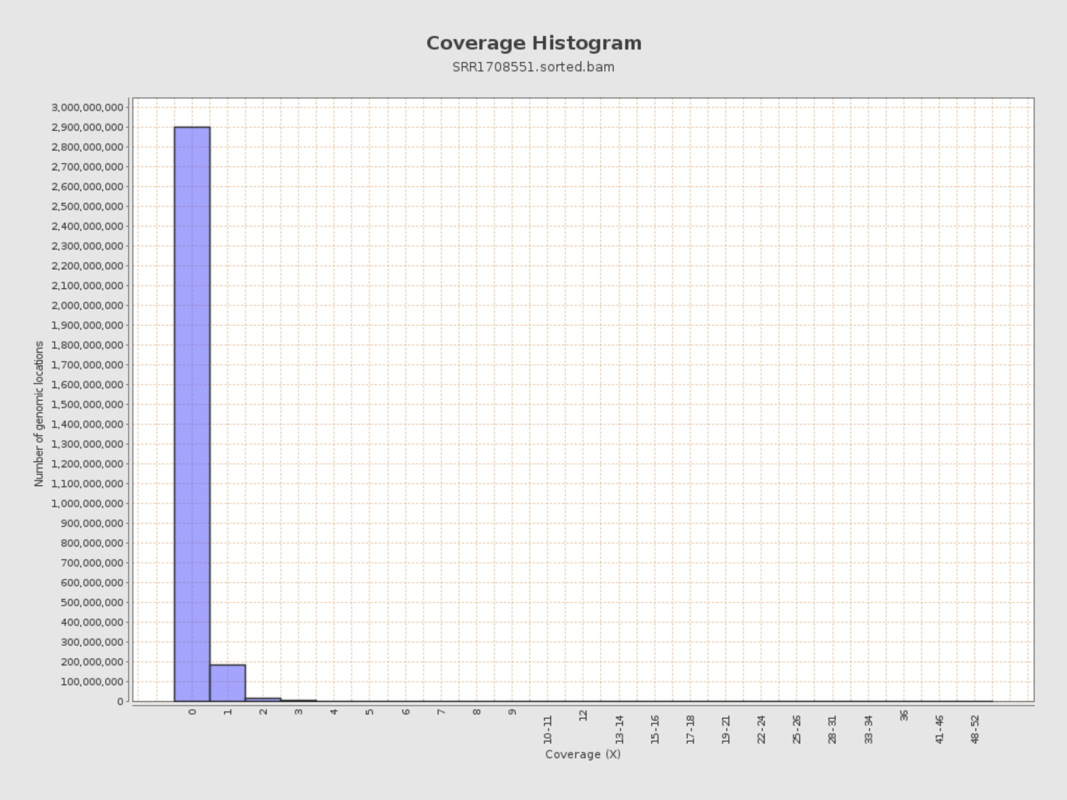
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17646305	0.0708	0.2802
chr2	243199373	19518252	0.0803	0.2962
chr3	198022430	20447580	0.1033	0.3356
chr4	191154276	16731046	0.0875	0.3083
chr5	180915260	12341336	0.0682	0.2715
chr6	171115067	14228182	0.0831	0.3013
chr7	159138663	12994961	0.0817	0.2981

chr8	146364022	10073701	0.0688	0.2737
chr9	141213431	8183789	0.058	0.2524
chr10	135534747	8689606	0.0641	0.2641
chr11	135006516	8779214	0.065	0.2676
chr12	133851895	8676988	0.0648	0.266
chr13	115169878	8708604	0.0756	0.2878
chr14	107349540	5519572	0.0514	0.2392
chr15	102531392	5123717	0.05	0.2339
chr16	90354753	2772312	0.0307	0.1812
chr17	81195210	2427904	0.0299	0.179
chr18	78077248	6986853	0.0895	0.3127
chr19	59128983	1223603	0.0207	0.1477
chr20	63025520	2522863	0.04	0.2089
chr21	48129895	2353144	0.0489	0.2325
chr22	51304566	876990	0.0171	0.1351
chrMT	16571	100	0.006	0.0774
chrX	155270560	15221551	0.098	0.3291
chrY	59373566	332060	0.0056	0.0786

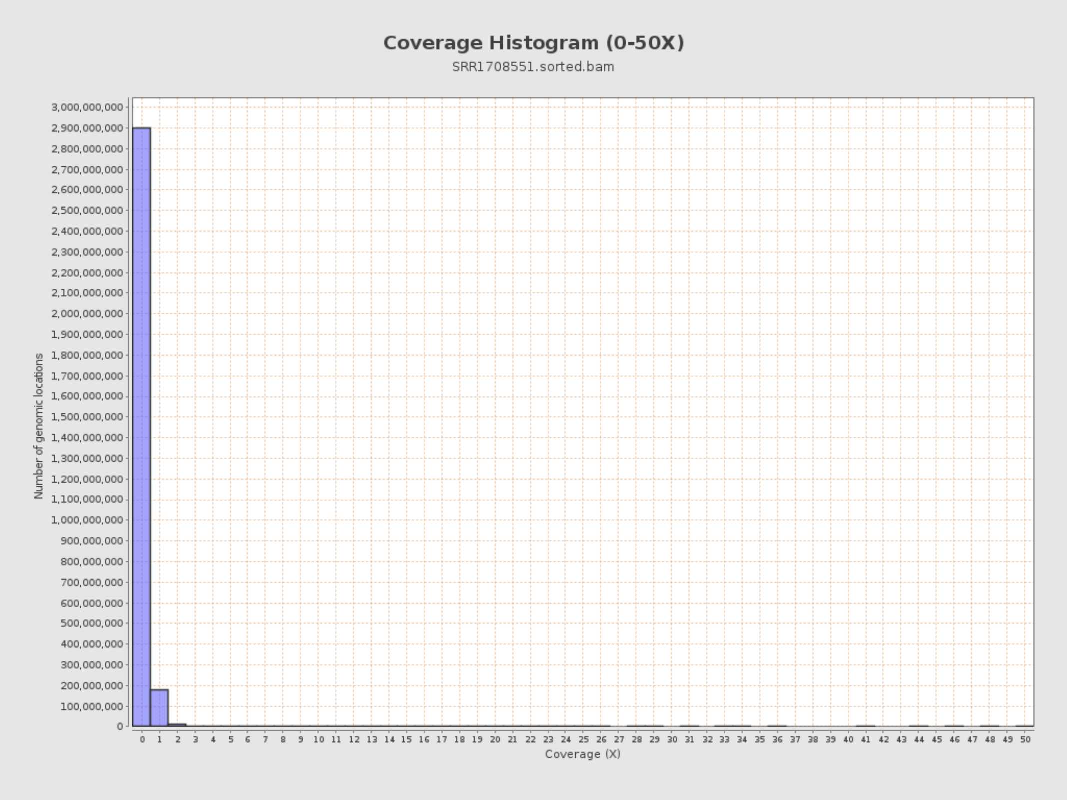
3. Results : Coverage across reference



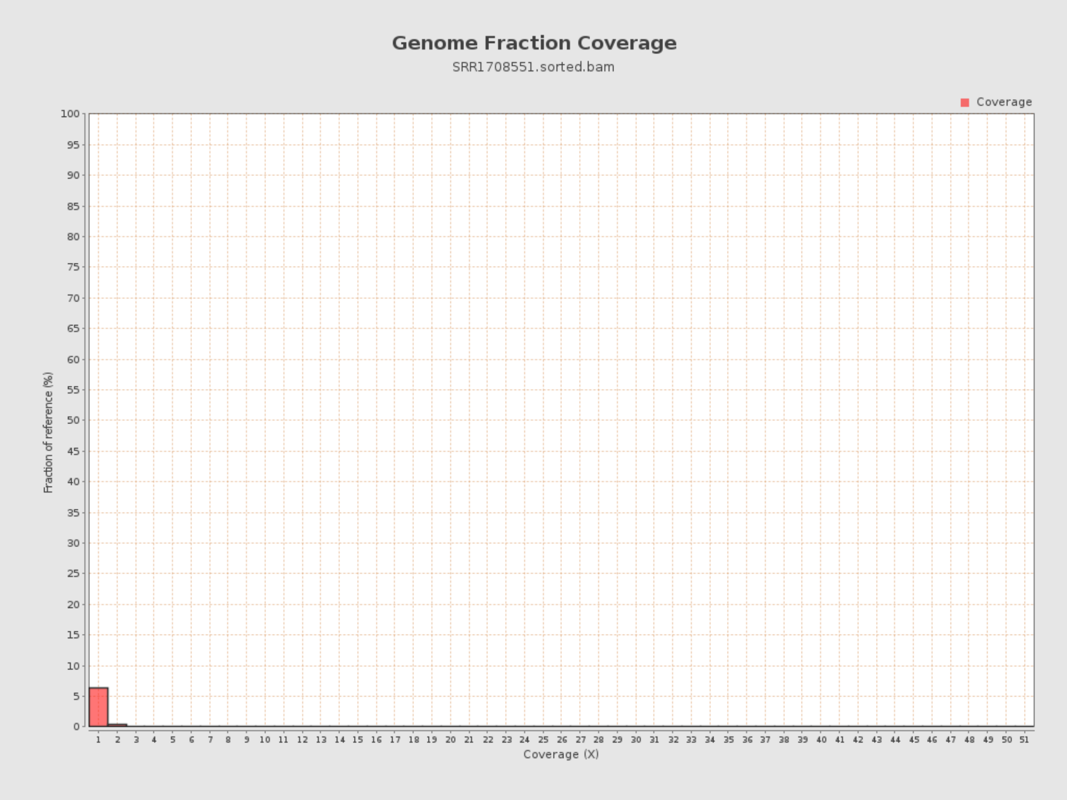
4. Results : Coverage Histogram



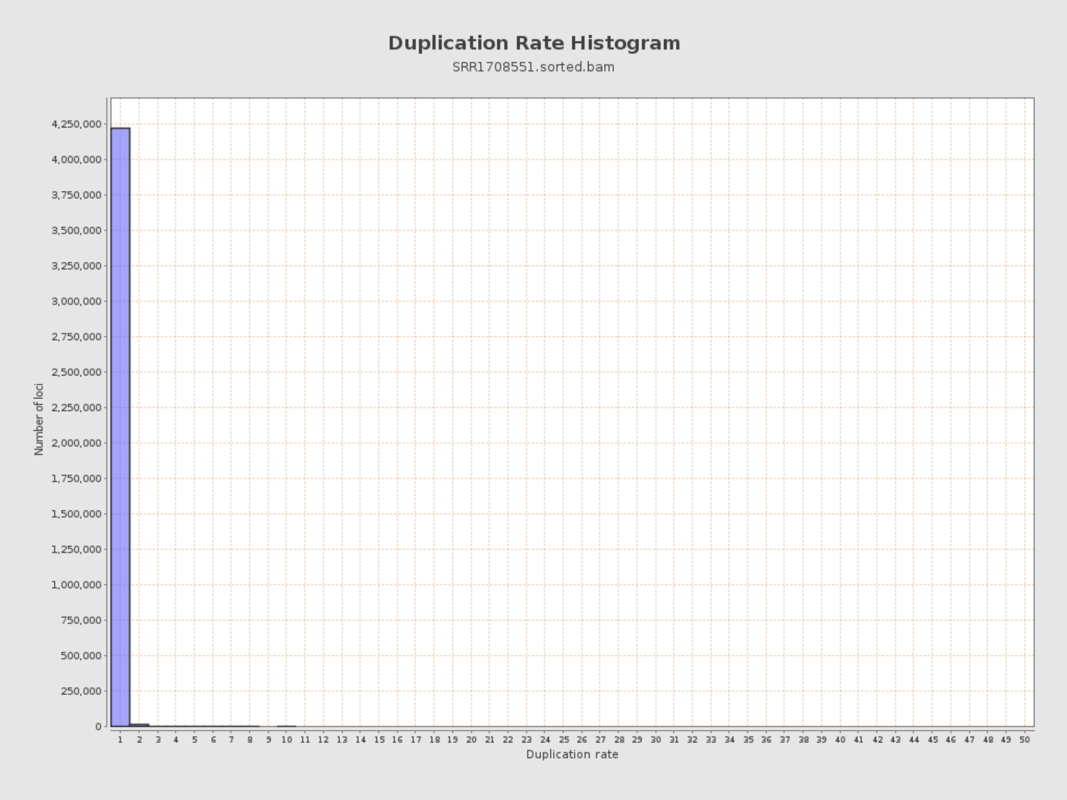
5. Results : Coverage Histogram (0-50X)



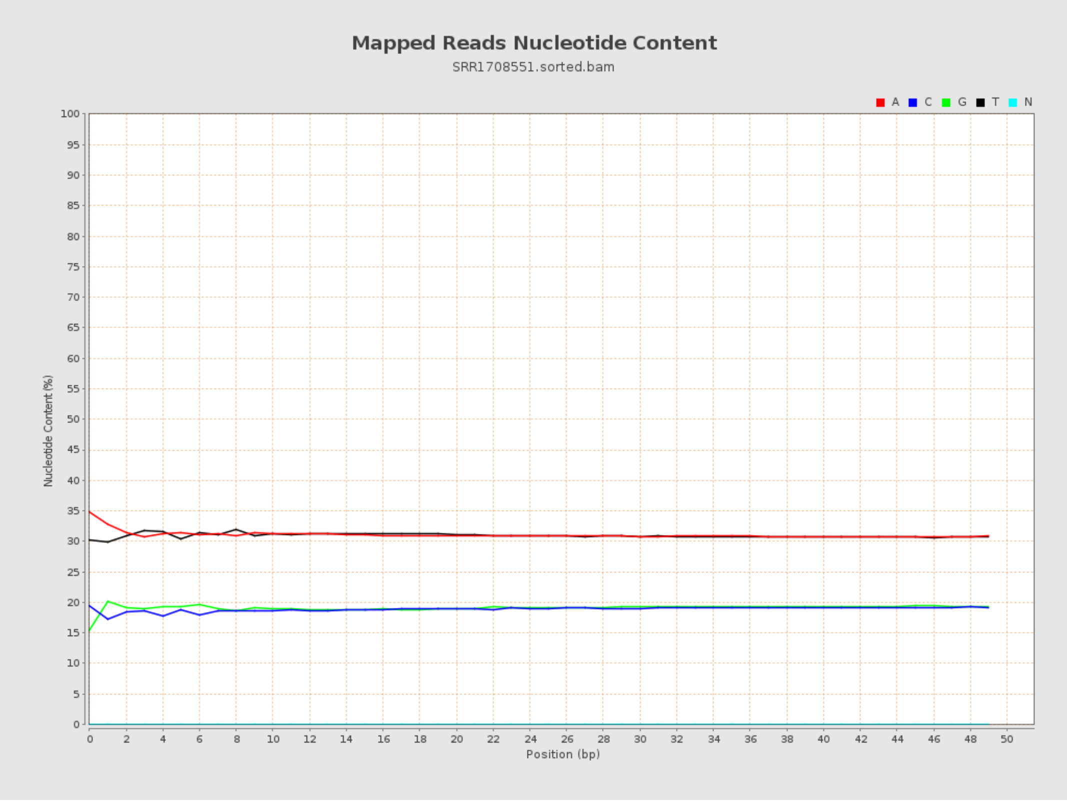
6. Results : Genome Fraction Coverage



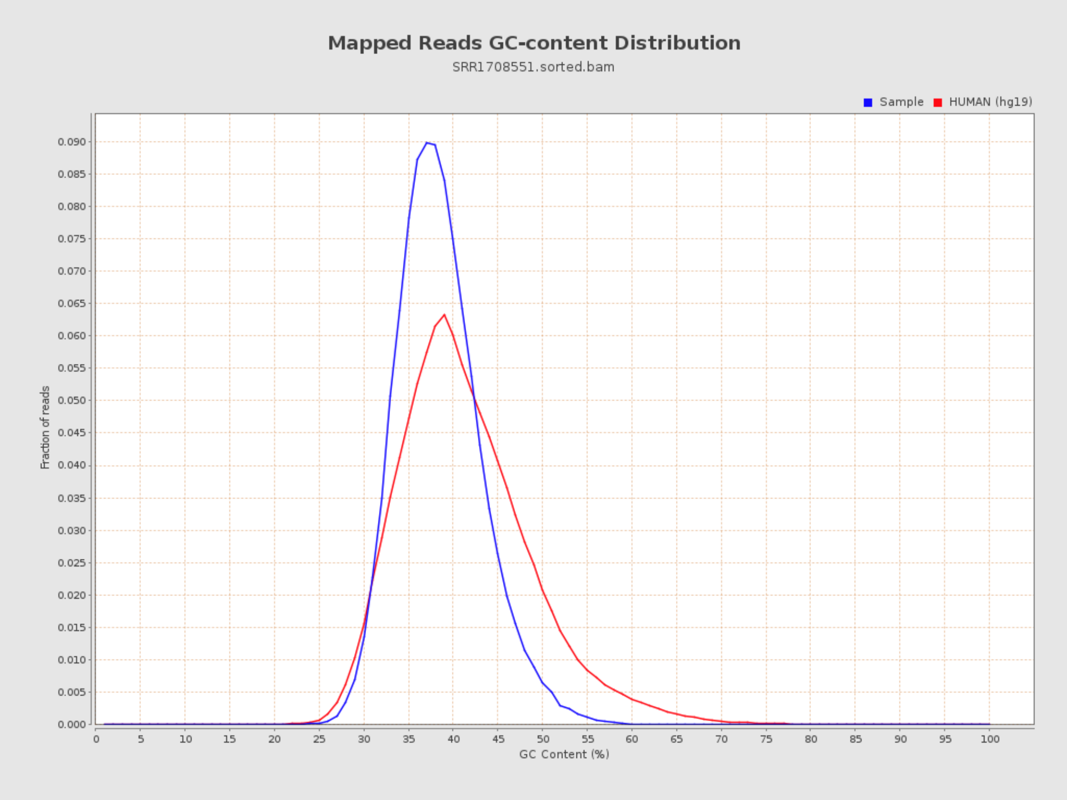
7. Results : Duplication Rate Histogram



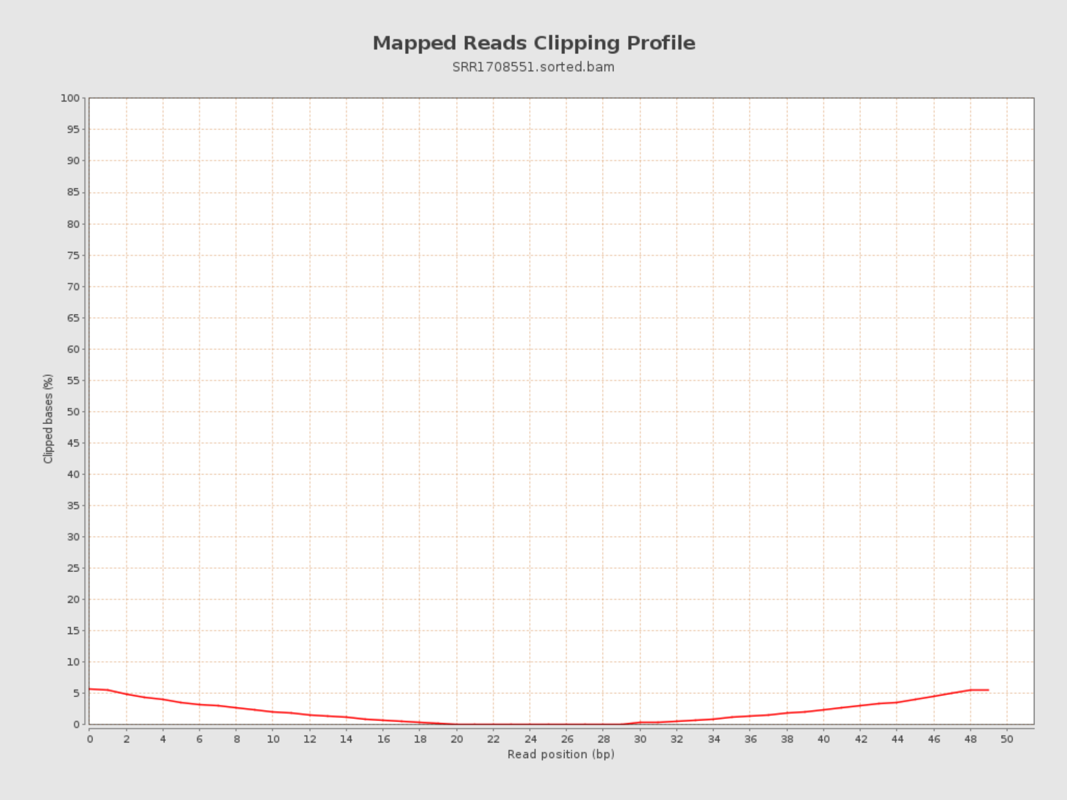
8. Results : Mapped Reads Nucleotide Content



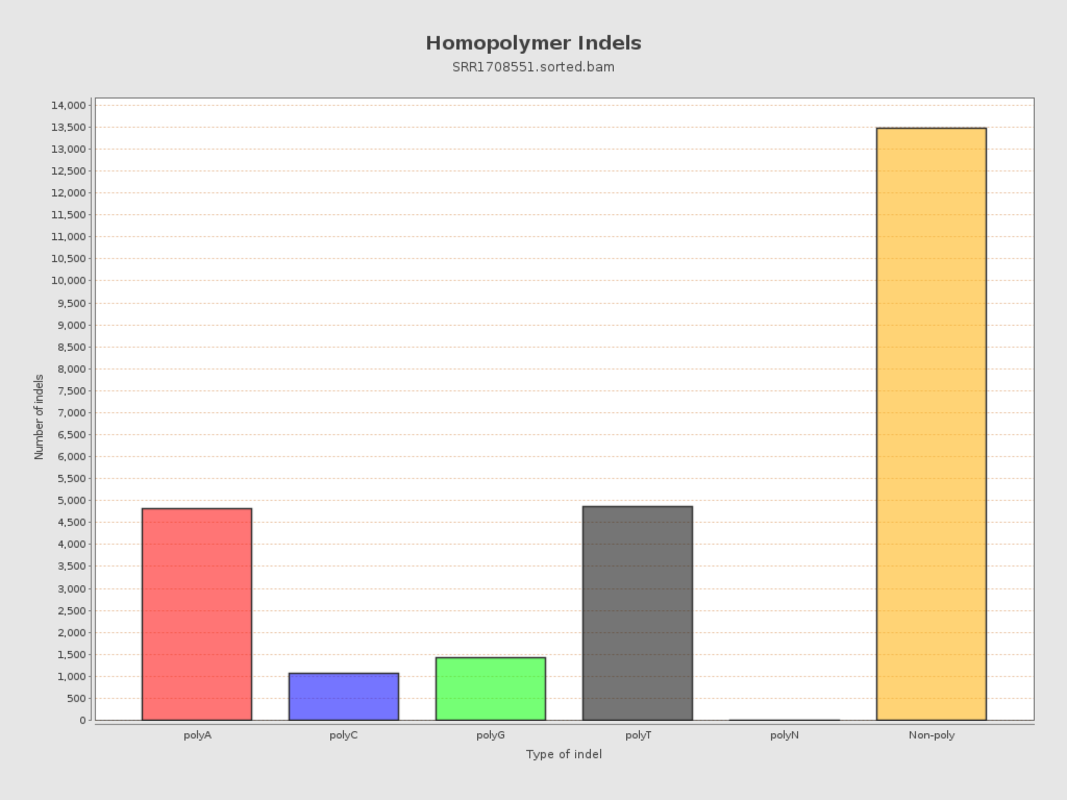
9. Results : Mapped Reads GC-content Distribution



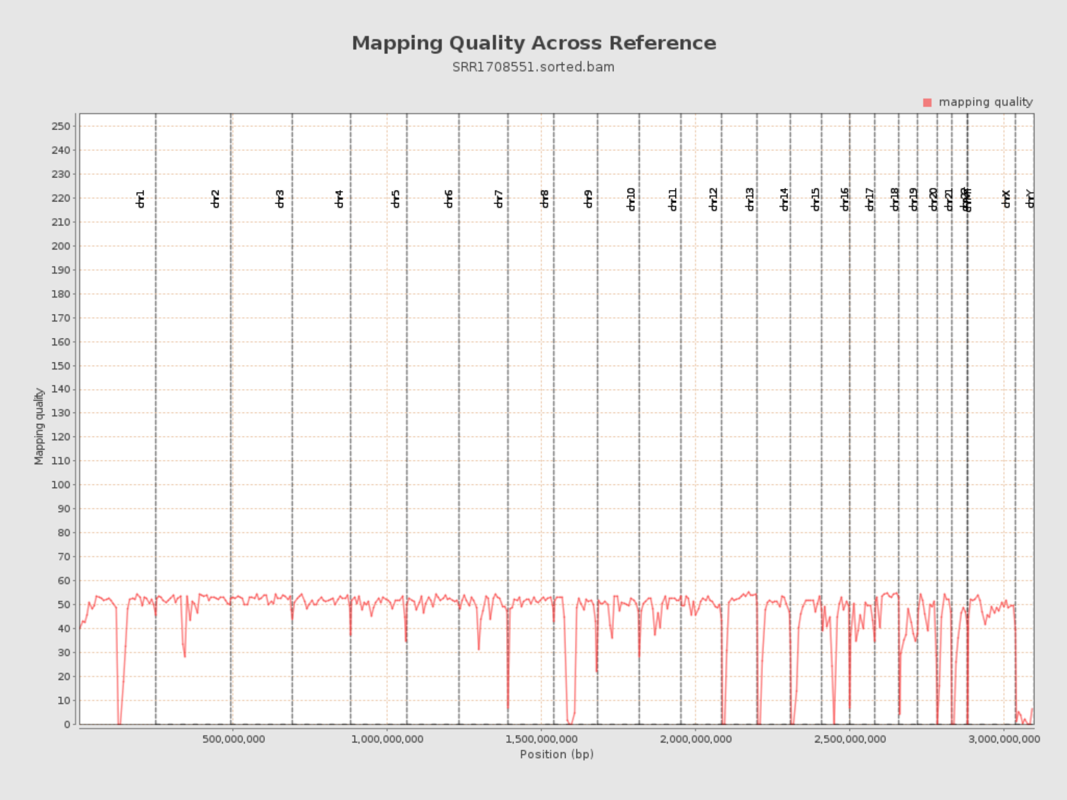
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram