Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:35:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708595.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_SRR1708595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:35:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,756,831
Mapped reads	4,682,432 / 98.44%
Unmapped reads	74,399 / 1.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	126 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	45,223 / 0.95%
Duplication rate	0.97%
Clipped reads	57,775 / 1.21%

2.2. ACGT Content

Number/percentage of A's	72,397,670 / 31%
Number/percentage of C's	44,262,116 / 18.95%
Number/percentage of T's	72,124,353 / 30.88%
Number/percentage of G's	44,785,002 / 19.17%
Number/percentage of N's	8,399 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0755

Standard Deviation	0.2859

2.4. Mapping Quality

Mean Mapping Quality	46.82

2.5. Mismatches and indels

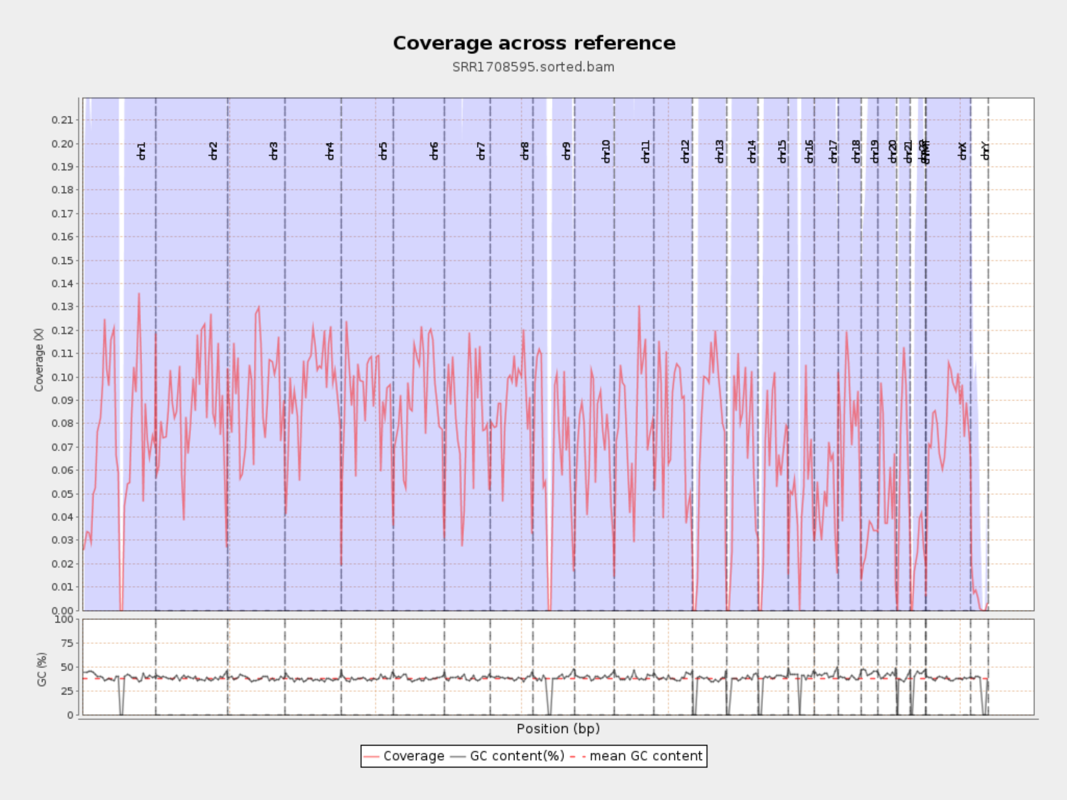
General error rate	0.15%
Mismatches	333,186
Insertions	14,517
Mapped reads with at least one insertion	0.31%
Deletions	11,553
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.6%

2.6. Chromosome stats

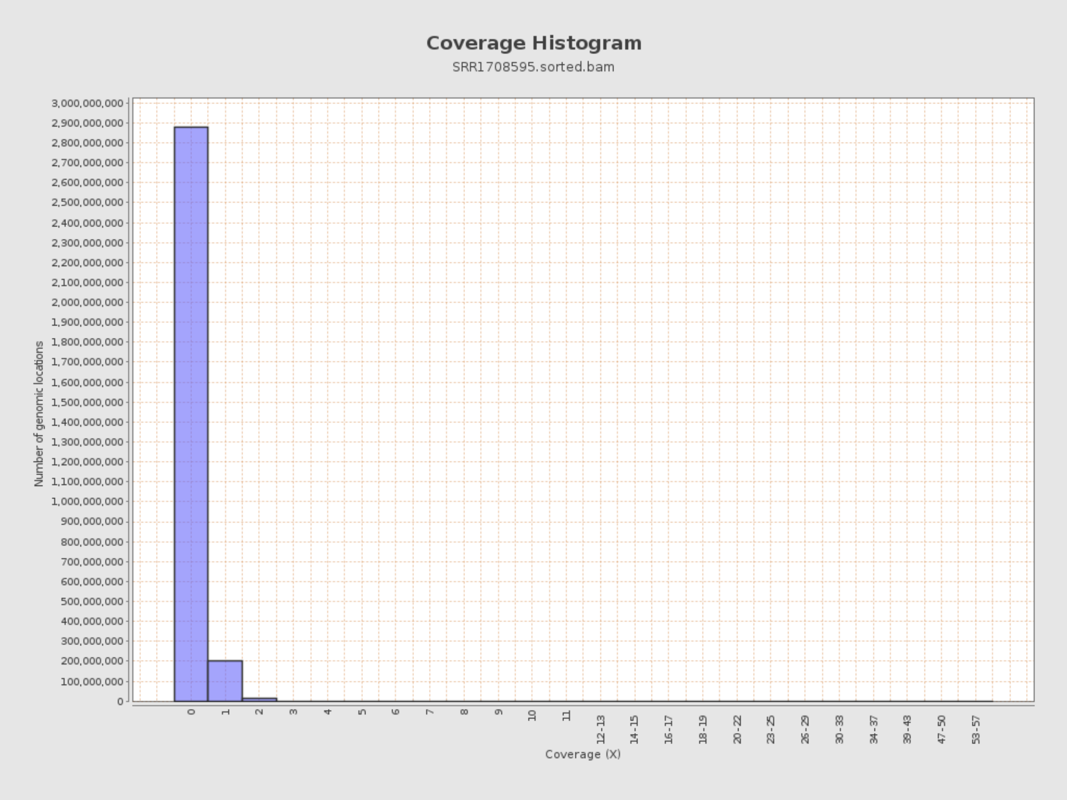
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17719136	0.0711	0.2793
chr2	243199373	20855626	0.0858	0.3044
chr3	198022430	18492266	0.0934	0.3166
chr4	191154276	18375818	0.0961	0.3206
chr5	180915260	16286107	0.09	0.3102
chr6	171115067	15648447	0.0914	0.3133
chr7	159138663	12769742	0.0802	0.2945

chr8	146364022	12890401	0.0881	0.3072
chr9	141213431	9641301	0.0683	0.2719
chr10	135534747	9898467	0.073	0.28
chr11	135006516	10907780	0.0808	0.2961
chr12	133851895	10425644	0.0779	0.2899
chr13	115169878	8890005	0.0772	0.2892
chr14	107349540	7248862	0.0675	0.2709
chr15	102531392	6207966	0.0605	0.2572
chr16	90354753	4397918	0.0487	0.2293
chr17	81195210	3852051	0.0474	0.2261
chr18	78077248	6538830	0.0837	0.2994
chr19	59128983	1773396	0.03	0.1785
chr20	63025520	3580026	0.0568	0.2478
chr21	48129895	3070756	0.0638	0.265
chr22	51304566	1196463	0.0233	0.158
chrMT	16571	100	0.006	0.0774
chrX	155270560	12630132	0.0813	0.2951
chrY	59373566	299848	0.0051	0.0744

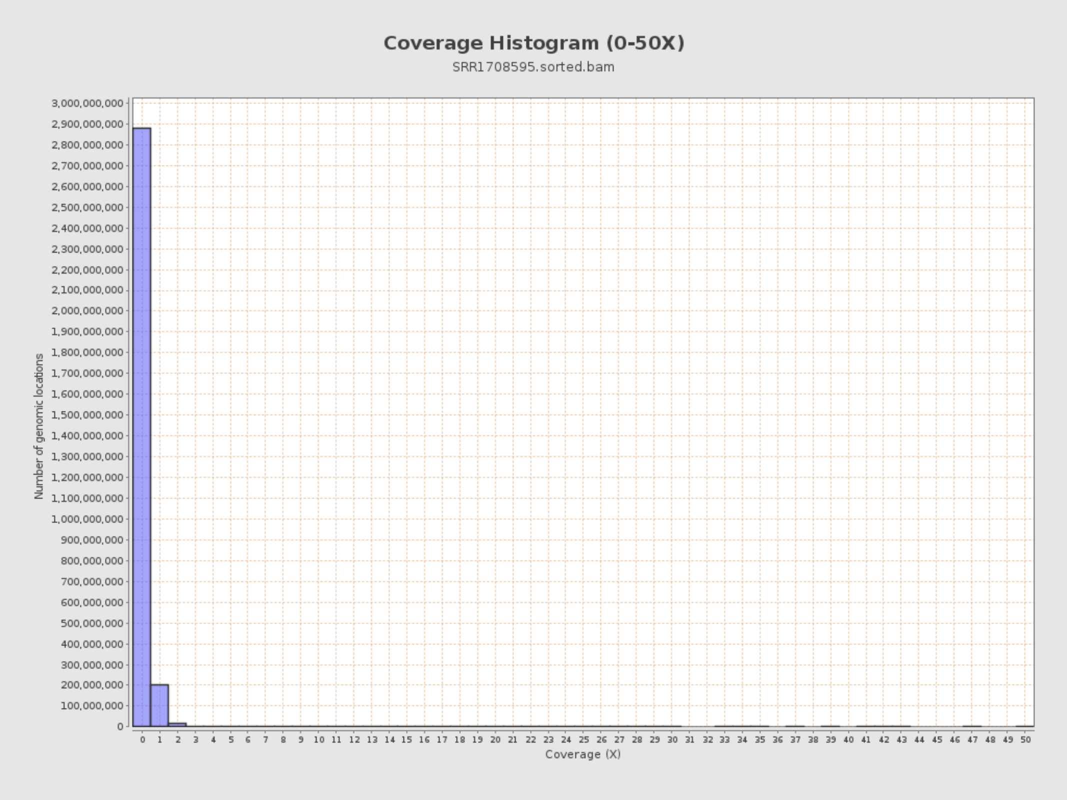
3. Results : Coverage across reference



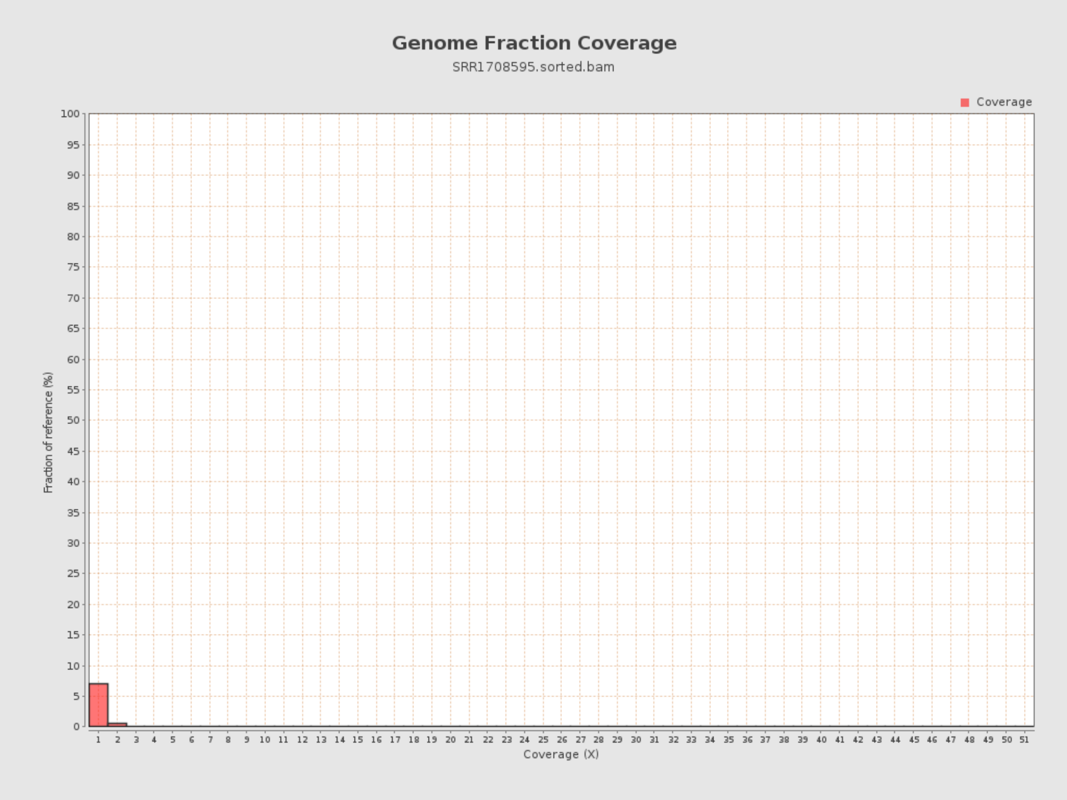
4. Results : Coverage Histogram



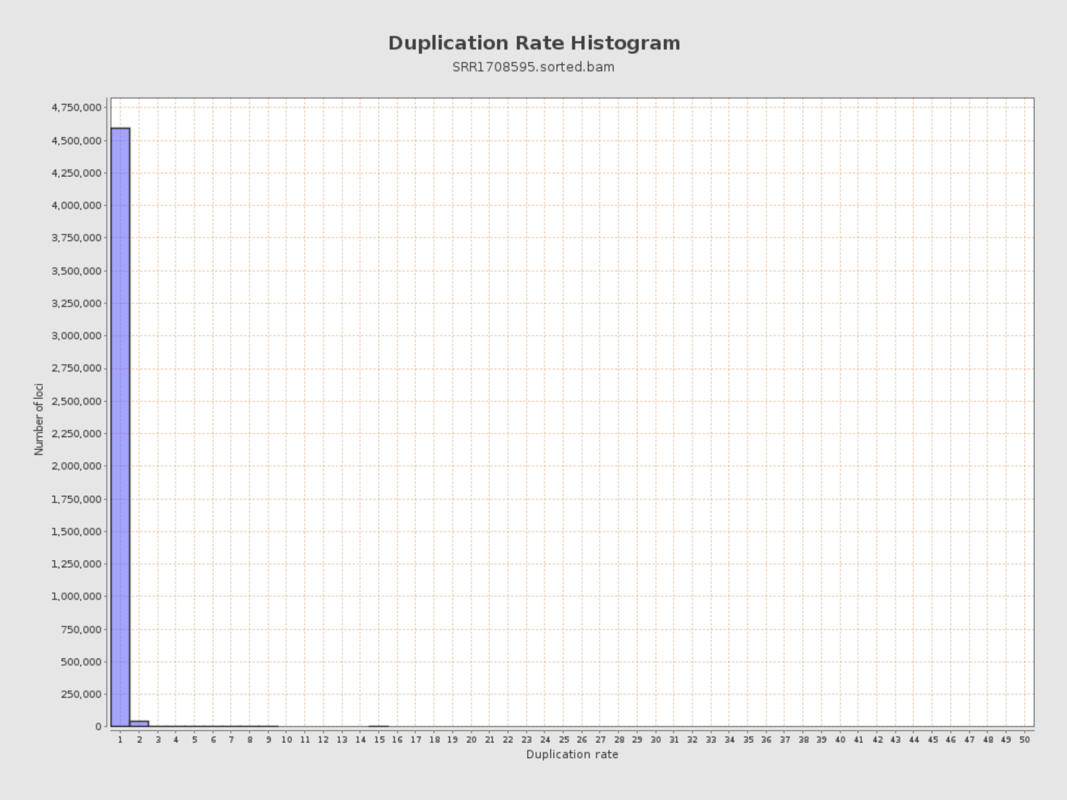
5. Results : Coverage Histogram (0-50X)



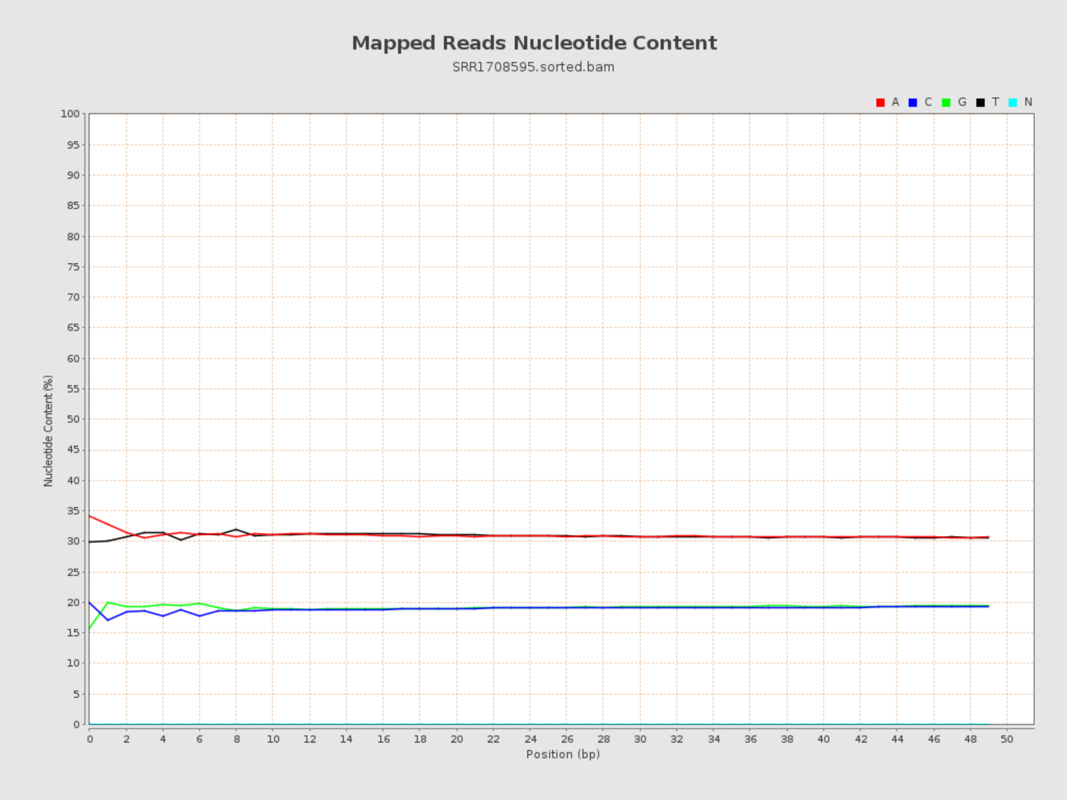
6. Results : Genome Fraction Coverage



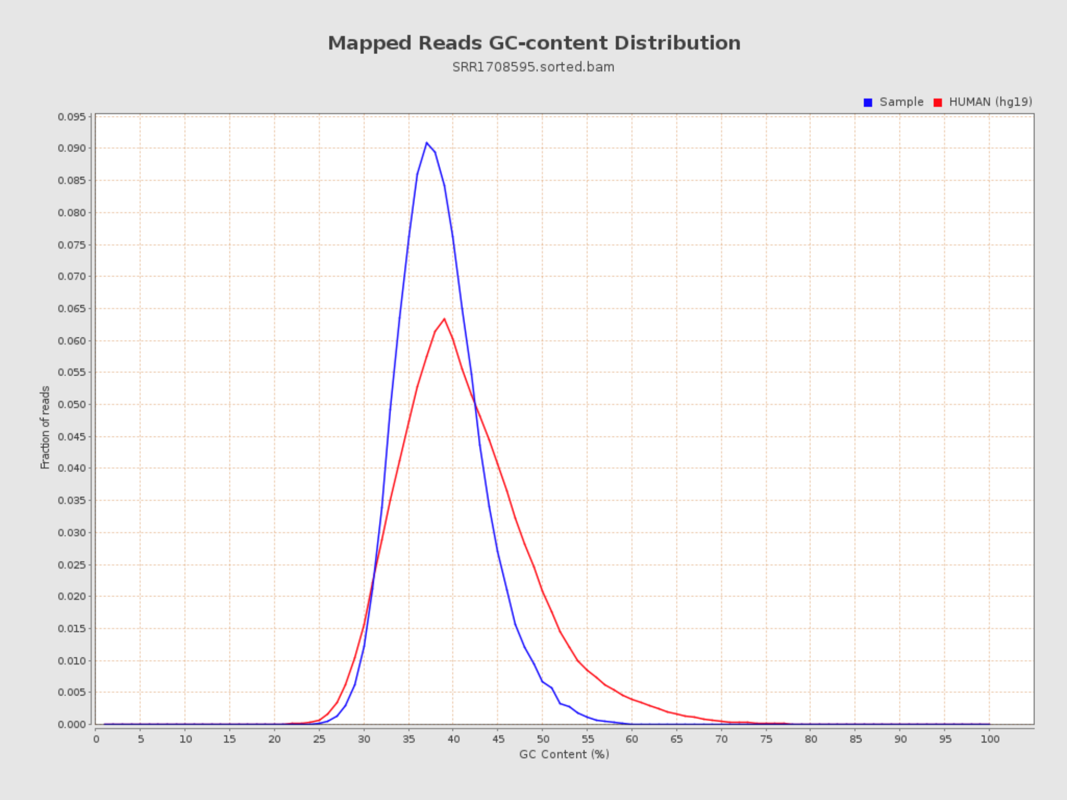
7. Results : Duplication Rate Histogram



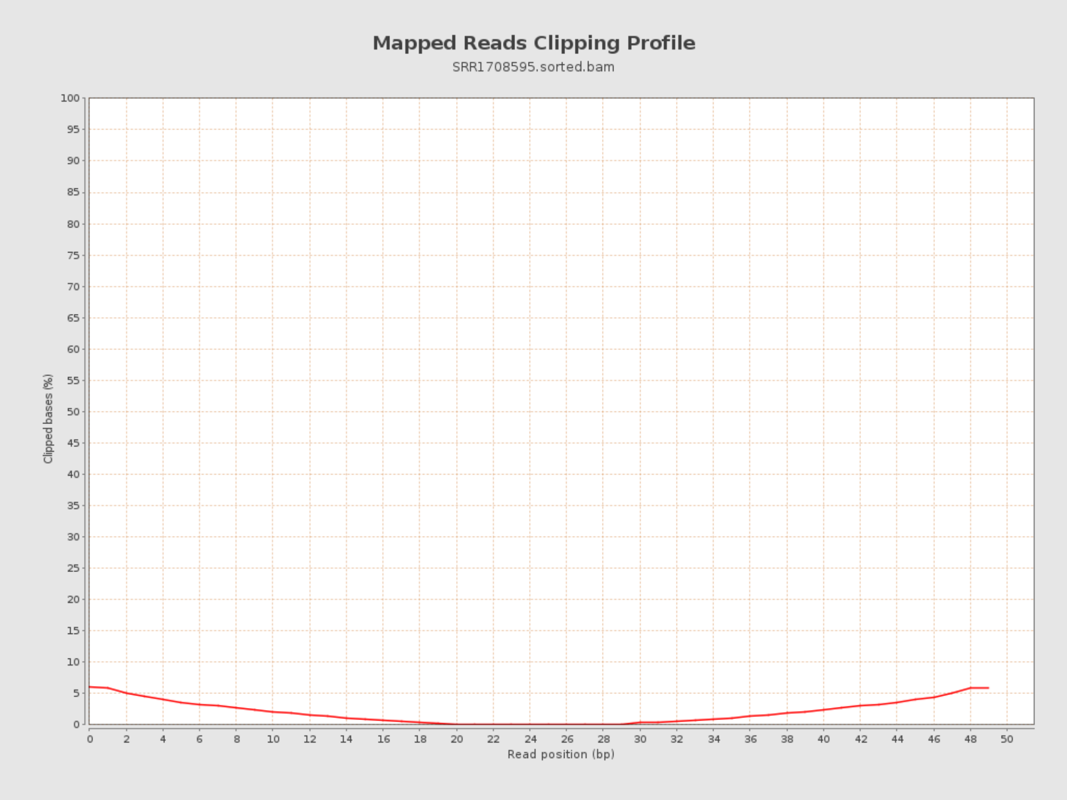
8. Results : Mapped Reads Nucleotide Content



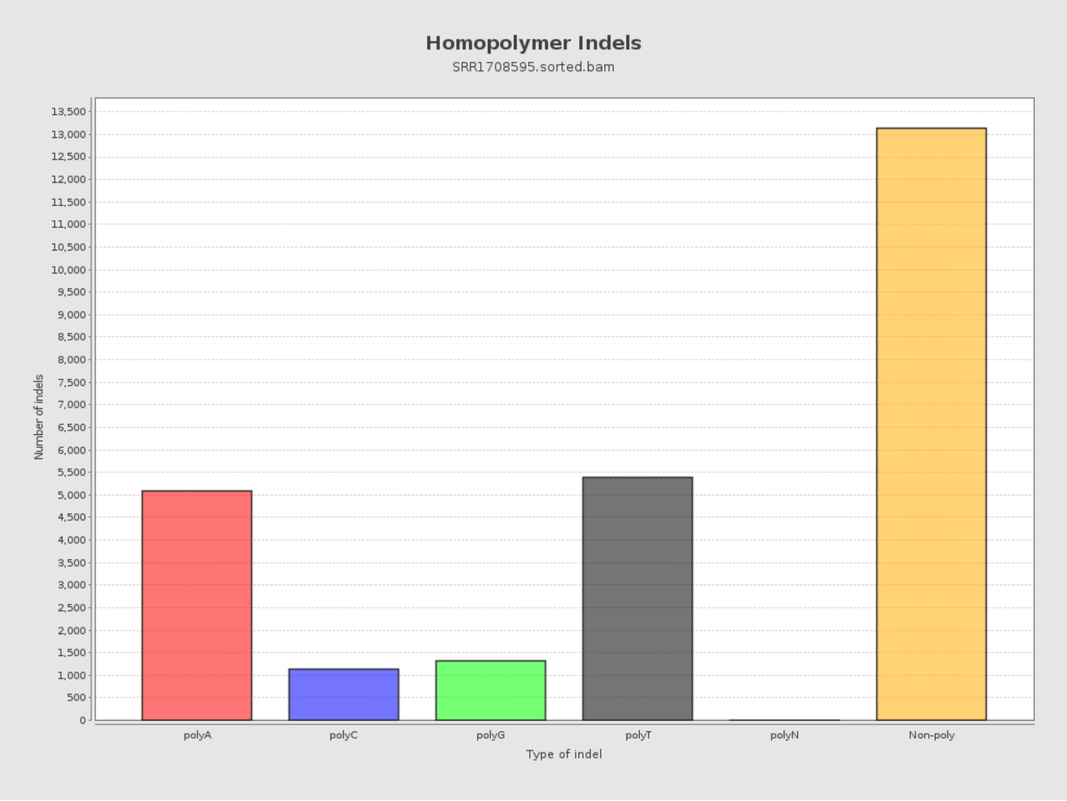
9. Results : Mapped Reads GC-content Distribution



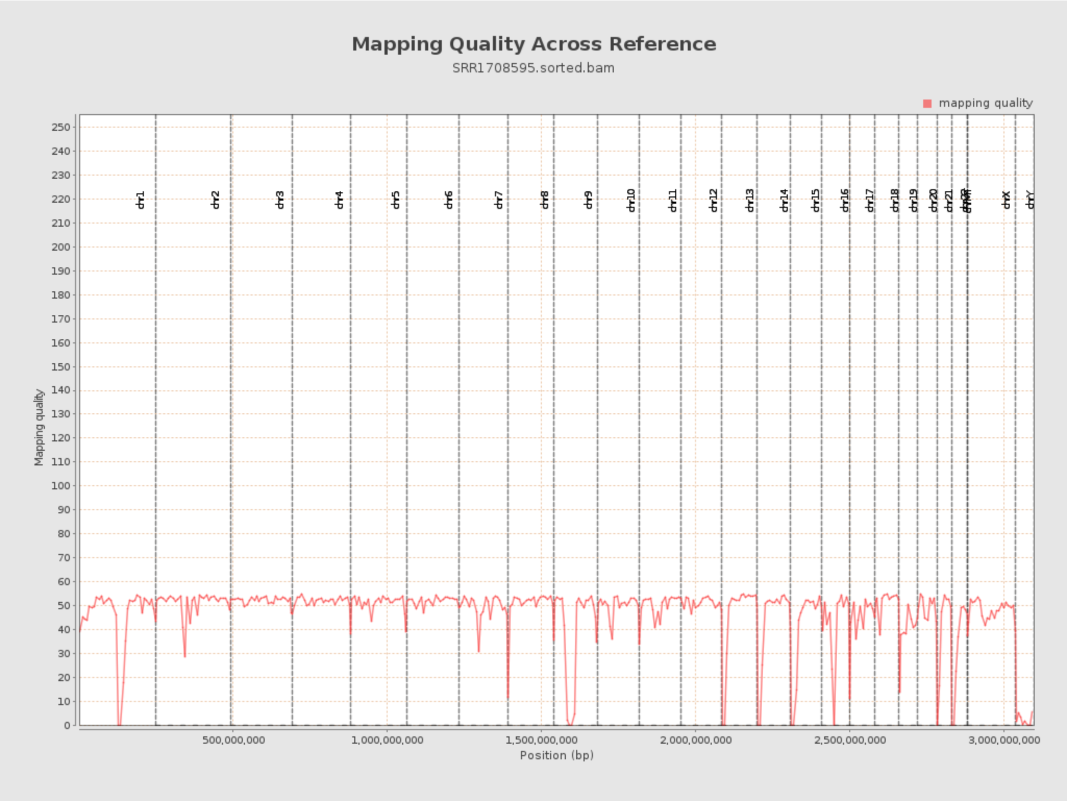
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram