Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:19:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708600.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_SRR1708600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:19:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,712,385
Mapped reads	4,600,302 / 97.62%
Unmapped reads	112,083 / 2.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	133 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	45,712 / 0.97%
Duplication rate	0.99%
Clipped reads	61,576 / 1.31%

2.2. ACGT Content

Number/percentage of A's	71,084,060 / 30.98%
Number/percentage of C's	43,470,982 / 18.95%
Number/percentage of T's	70,865,907 / 30.89%
Number/percentage of G's	44,006,250 / 19.18%
Number/percentage of N's	8,236 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	0.0741

Standard Deviation	0.2831

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

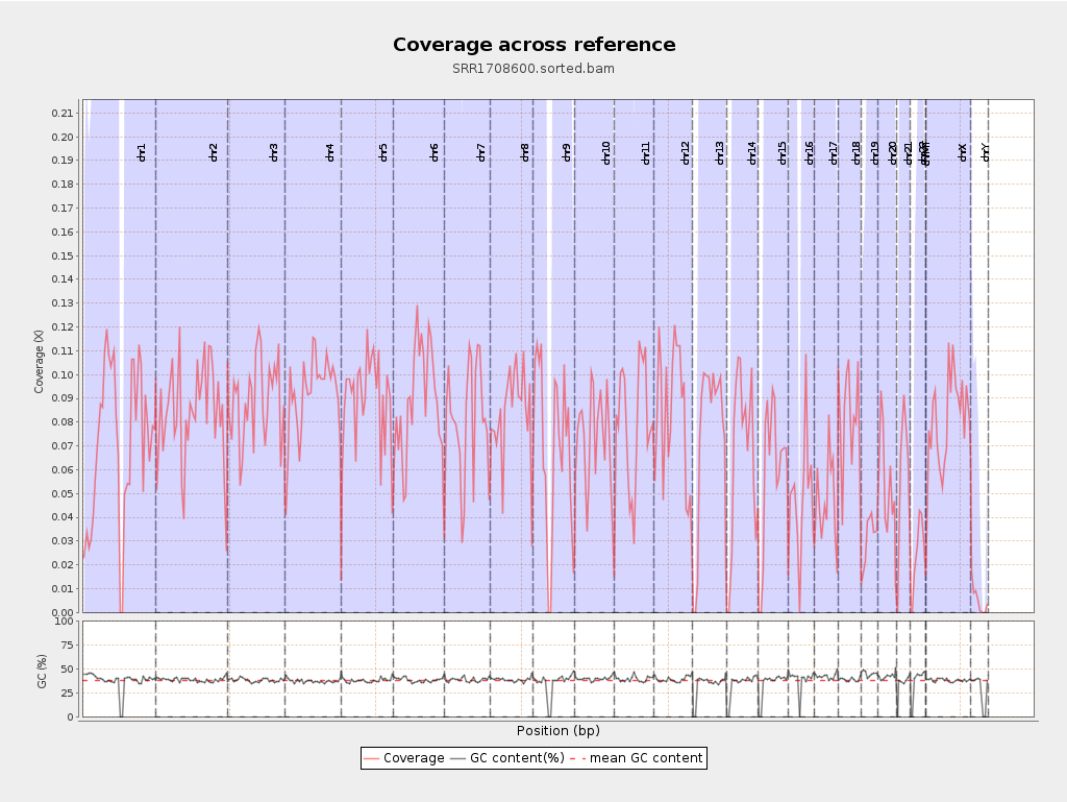
General error rate	0.15%
Mismatches	332,167
Insertions	14,382
Mapped reads with at least one insertion	0.31%
Deletions	11,345
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.67%

2.6. Chromosome stats

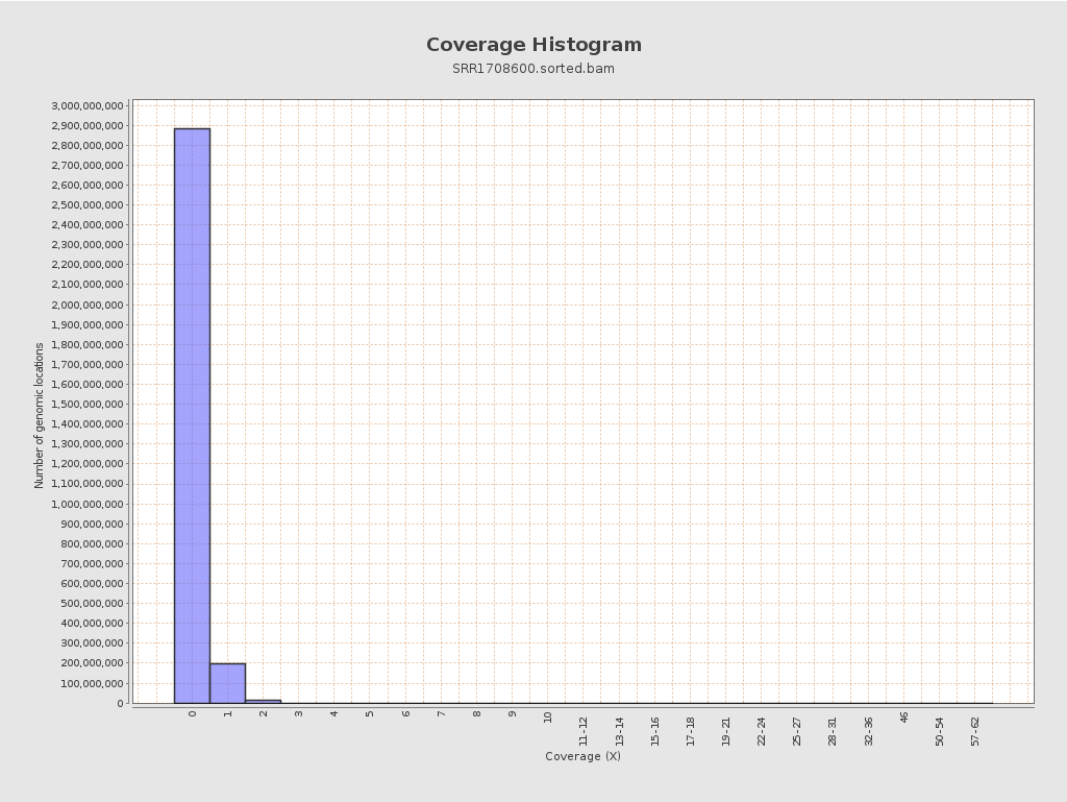
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17691441	0.071	0.2785
chr2	243199373	20394286	0.0839	0.2998
chr3	198022430	17628008	0.089	0.3089
chr4	191154276	17688106	0.0925	0.3141
chr5	180915260	16024368	0.0886	0.3081
chr6	171115067	15297659	0.0894	0.3095
chr7	159138663	12602795	0.0792	0.2921

chr8	146364022	12299716	0.084	0.2999
chr9	141213431	9798896	0.0694	0.2744
chr10	135534747	9953730	0.0734	0.2804
chr11	135006516	10664902	0.079	0.2929
chr12	133851895	11008873	0.0822	0.298
chr13	115169878	8598664	0.0747	0.284
chr14	107349540	7149891	0.0666	0.2697
chr15	102531392	6002781	0.0585	0.2528
chr16	90354753	4271682	0.0473	0.2259
chr17	81195210	3900688	0.048	0.229
chr18	78077248	6334163	0.0811	0.2949
chr19	59128983	1880431	0.0318	0.1838
chr20	63025520	3442443	0.0546	0.2419
chr21	48129895	2660339	0.0553	0.246
chr22	51304566	1268824	0.0247	0.1629
chrMT	16571	259	0.0156	0.124
chrX	155270560	12592209	0.0811	0.2952
chrY	59373566	299700	0.005	0.074

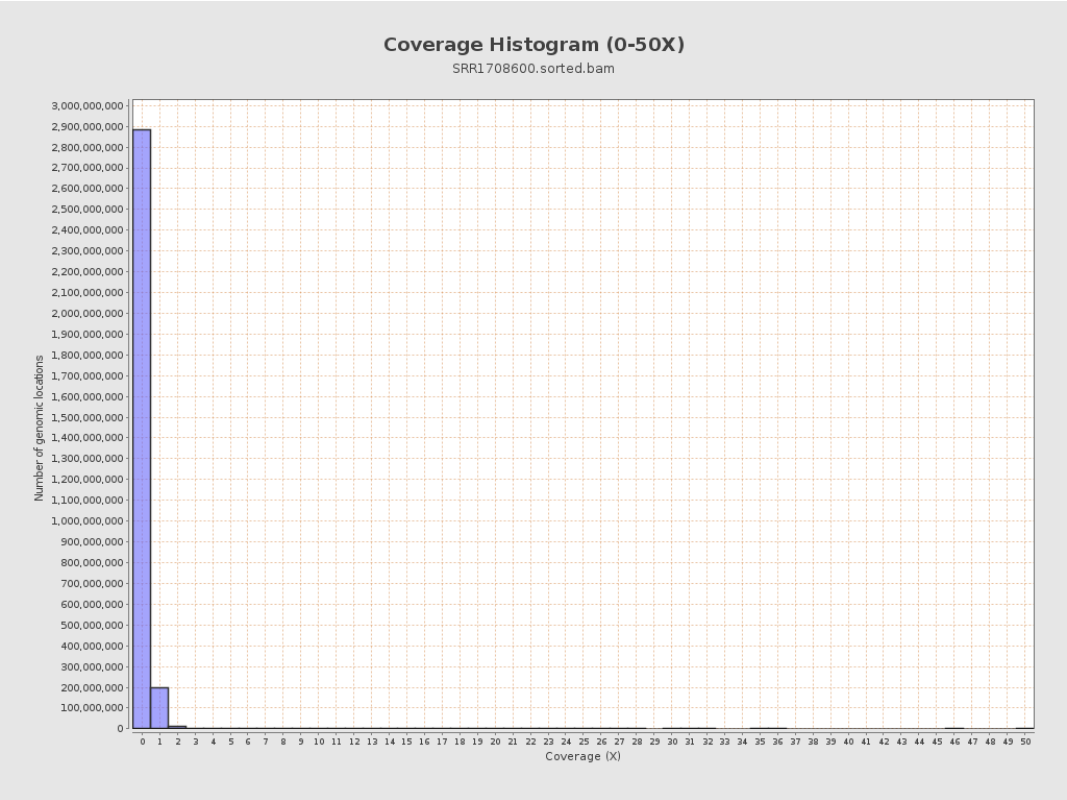
3. Results : Coverage across reference



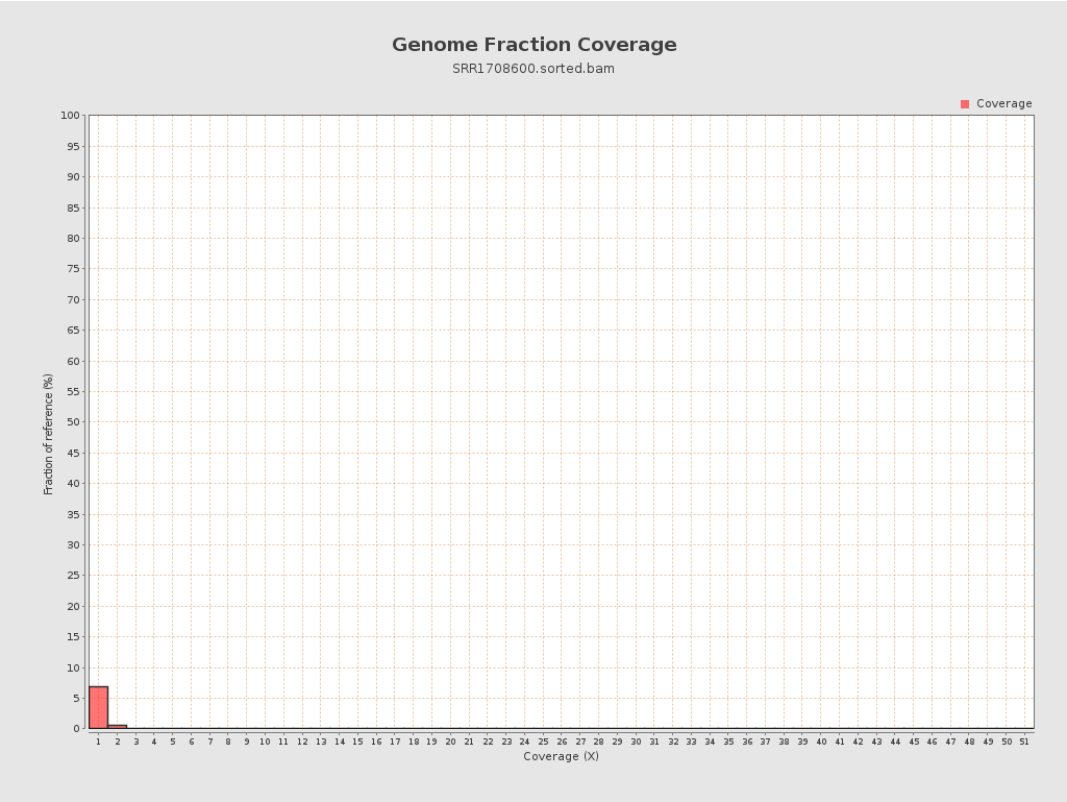
4. Results : Coverage Histogram



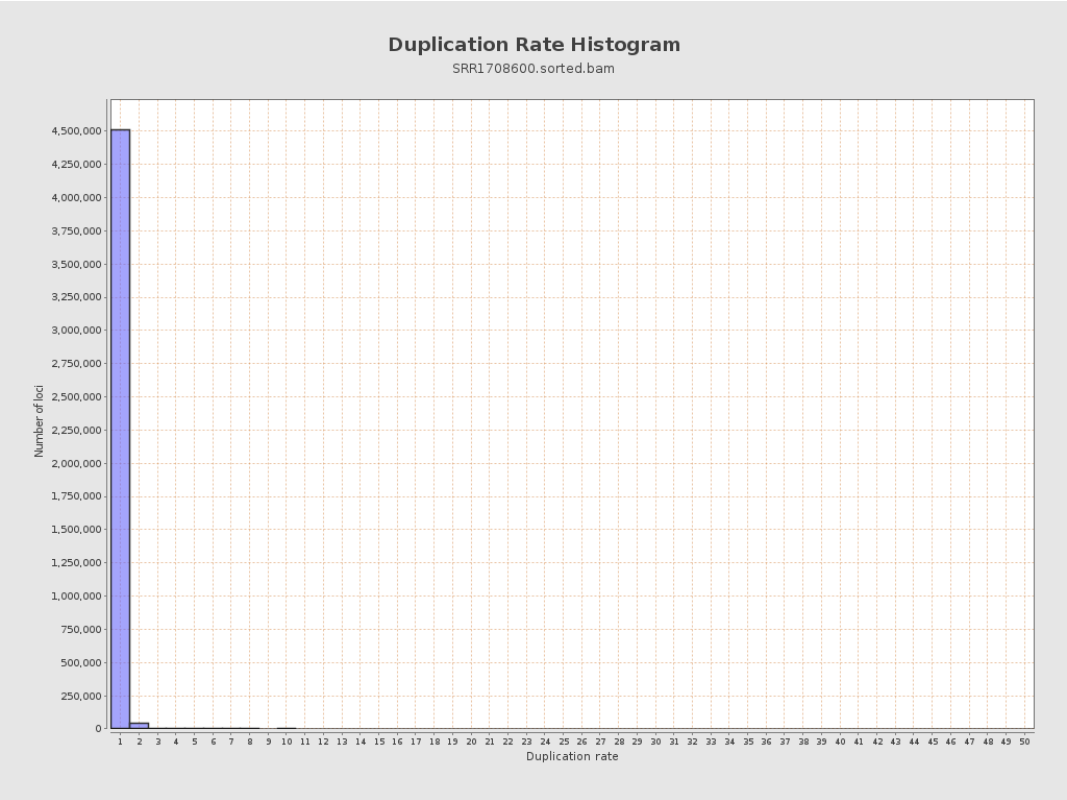
5. Results : Coverage Histogram (0-50X)



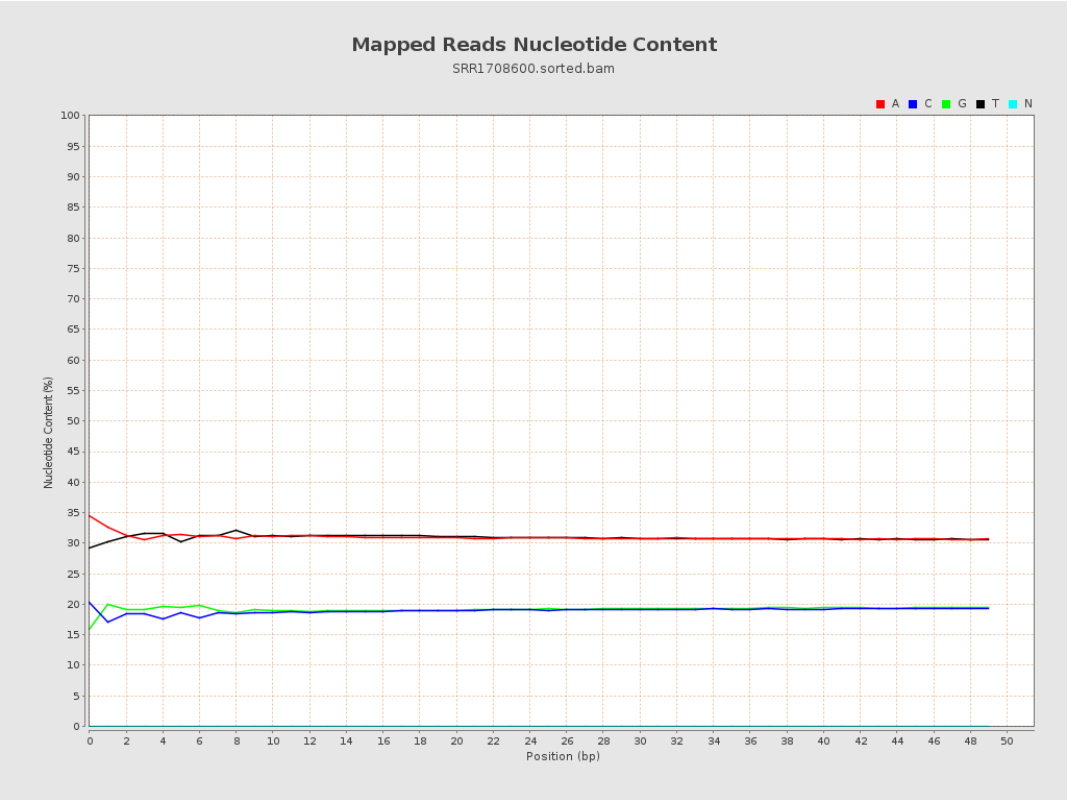
6. Results : Genome Fraction Coverage



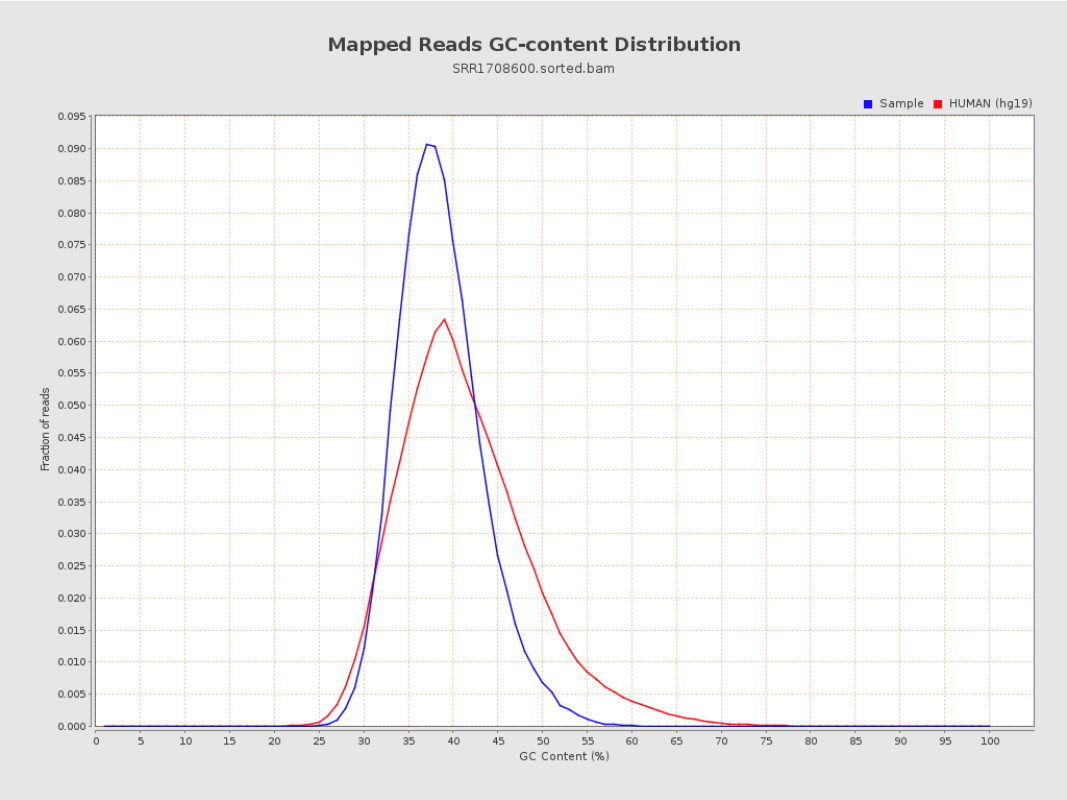
7. Results : Duplication Rate Histogram



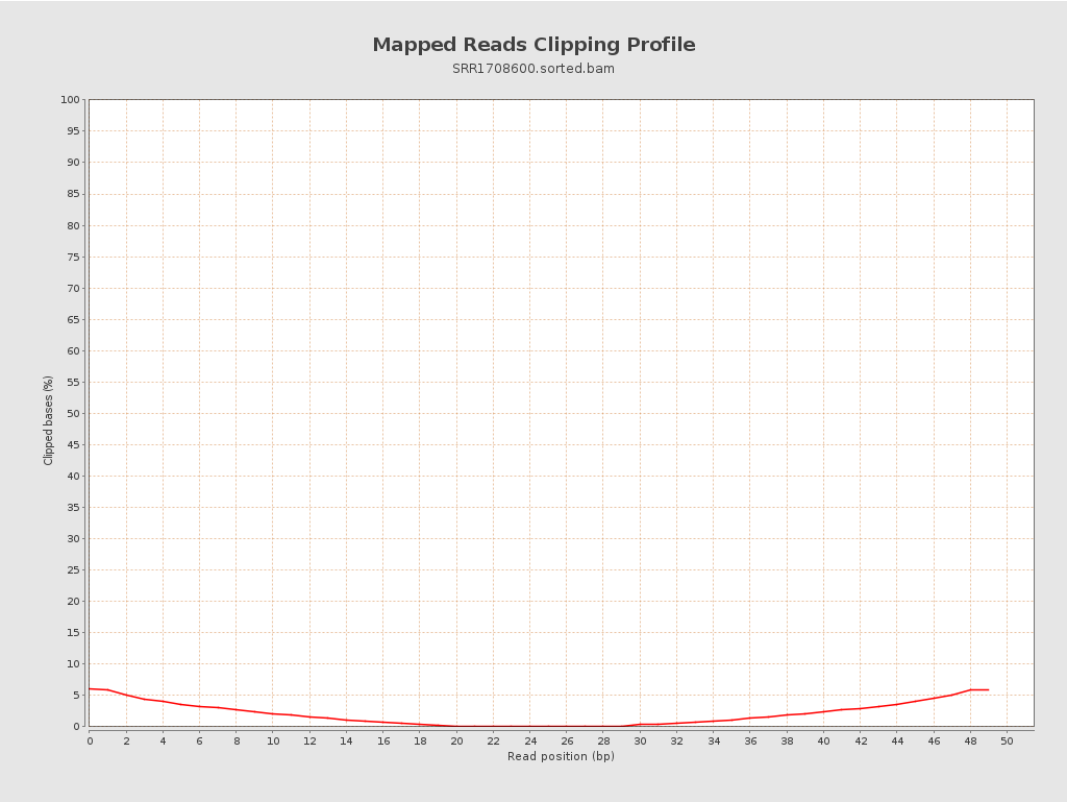
8. Results : Mapped Reads Nucleotide Content



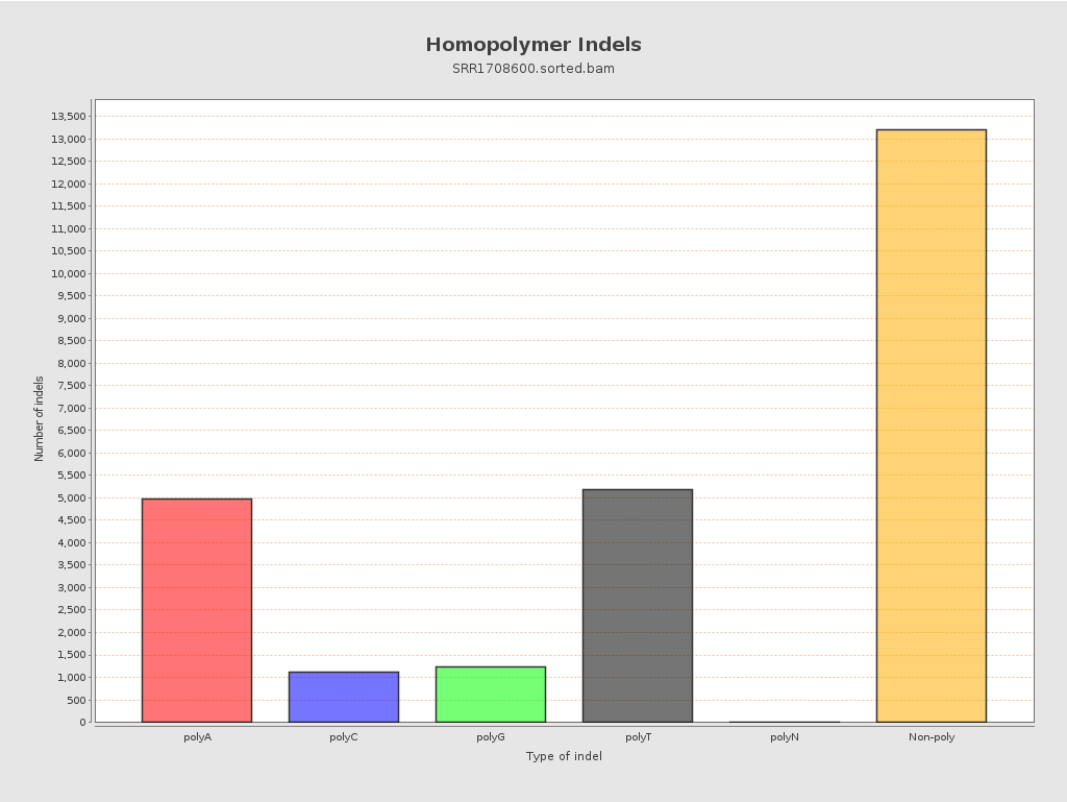
9. Results : Mapped Reads GC-content Distribution



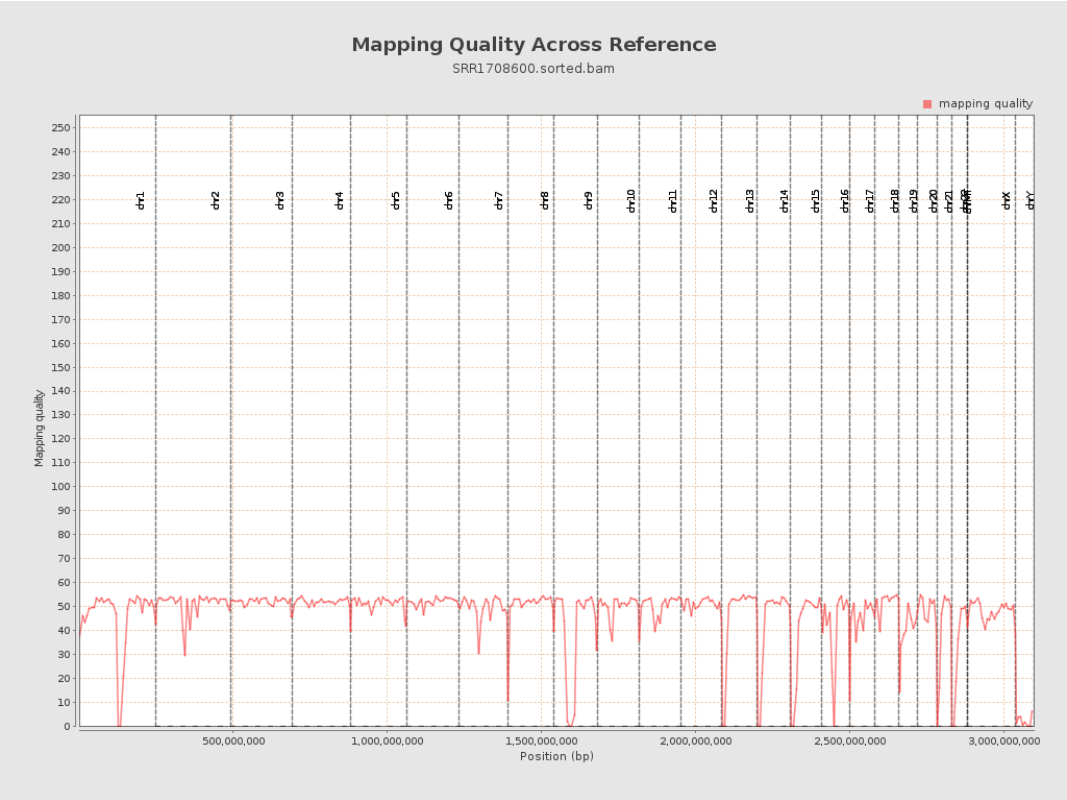
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram