Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:46:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708604.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_SRR1708604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:46:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,638,125
Mapped reads	4,551,113 / 98.12%
Unmapped reads	87,012 / 1.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	121 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	44,112 / 0.95%
Duplication rate	0.97%
Clipped reads	59,782 / 1.29%

2.2. ACGT Content

Number/percentage of A's	70,270,500 / 30.96%
Number/percentage of C's	43,086,516 / 18.98%
Number/percentage of T's	69,999,733 / 30.84%
Number/percentage of G's	43,624,003 / 19.22%
Number/percentage of N's	8,125 / 0%
GC Percentage	38.2%

2.3. Coverage

Mean	0.0733

Standard Deviation	0.2822

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

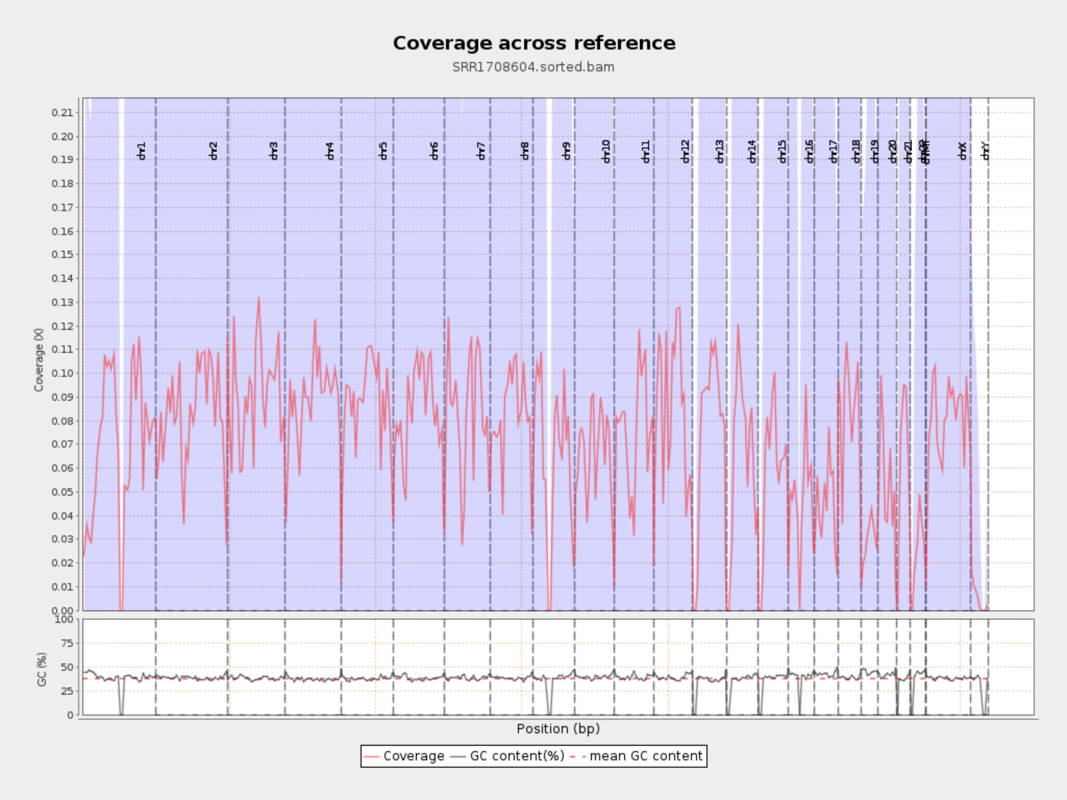
General error rate	0.15%
Mismatches	332,540
Insertions	14,256
Mapped reads with at least one insertion	0.31%
Deletions	11,506
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.23%

2.6. Chromosome stats

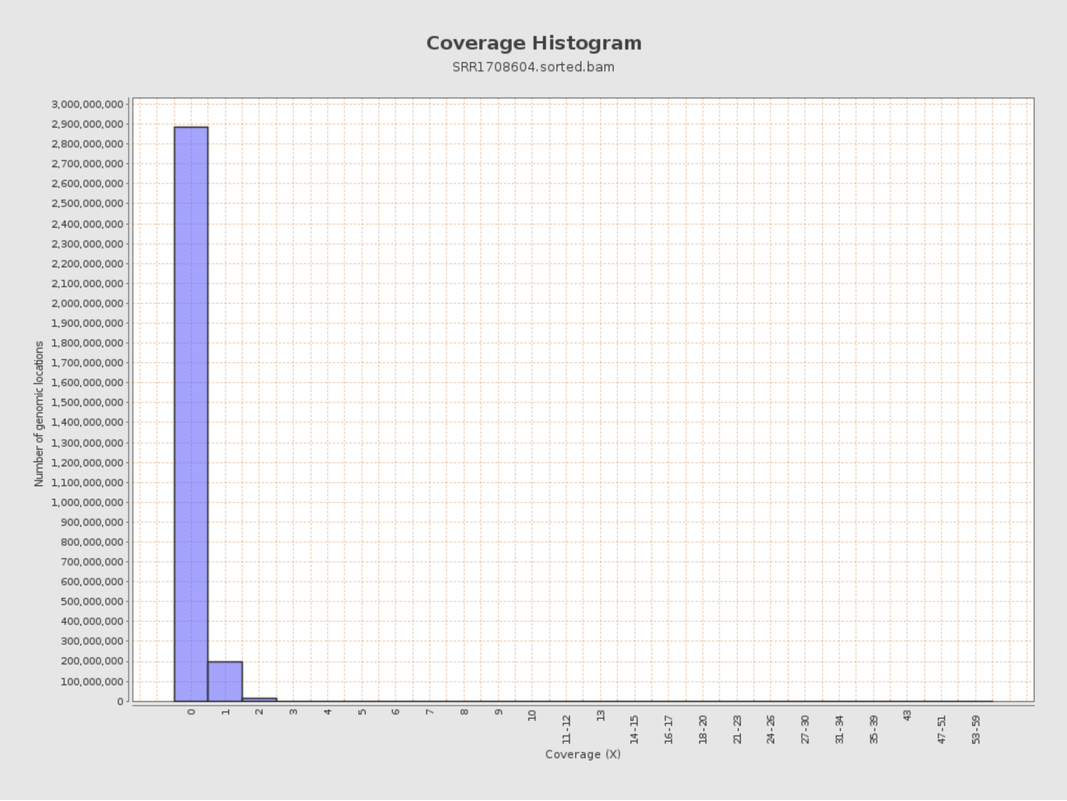
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17500308	0.0702	0.2776
chr2	243199373	20173680	0.083	0.2987
chr3	198022430	18182949	0.0918	0.3147
chr4	191154276	17027891	0.0891	0.3088
chr5	180915260	15744527	0.087	0.3062
chr6	171115067	14570283	0.0851	0.3025
chr7	159138663	13144350	0.0826	0.2993

chr8	146364022	12129793	0.0829	0.2986
chr9	141213431	9318437	0.066	0.2683
chr10	135534747	9086200	0.067	0.2682
chr11	135006516	10139225	0.0751	0.2859
chr12	133851895	11442477	0.0855	0.3047
chr13	115169878	8674110	0.0753	0.2859
chr14	107349540	6978470	0.065	0.2661
chr15	102531392	5945947	0.058	0.2514
chr16	90354753	4144990	0.0459	0.2225
chr17	81195210	3723560	0.0459	0.2225
chr18	78077248	6696849	0.0858	0.3031
chr19	59128983	1790533	0.0303	0.1796
chr20	63025520	3488730	0.0554	0.246
chr21	48129895	2936629	0.061	0.26
chr22	51304566	1287145	0.0251	0.1644
chrMT	16571	150	0.0091	0.0947
chrX	155270560	12571449	0.081	0.2955
chrY	59373566	309961	0.0052	0.076

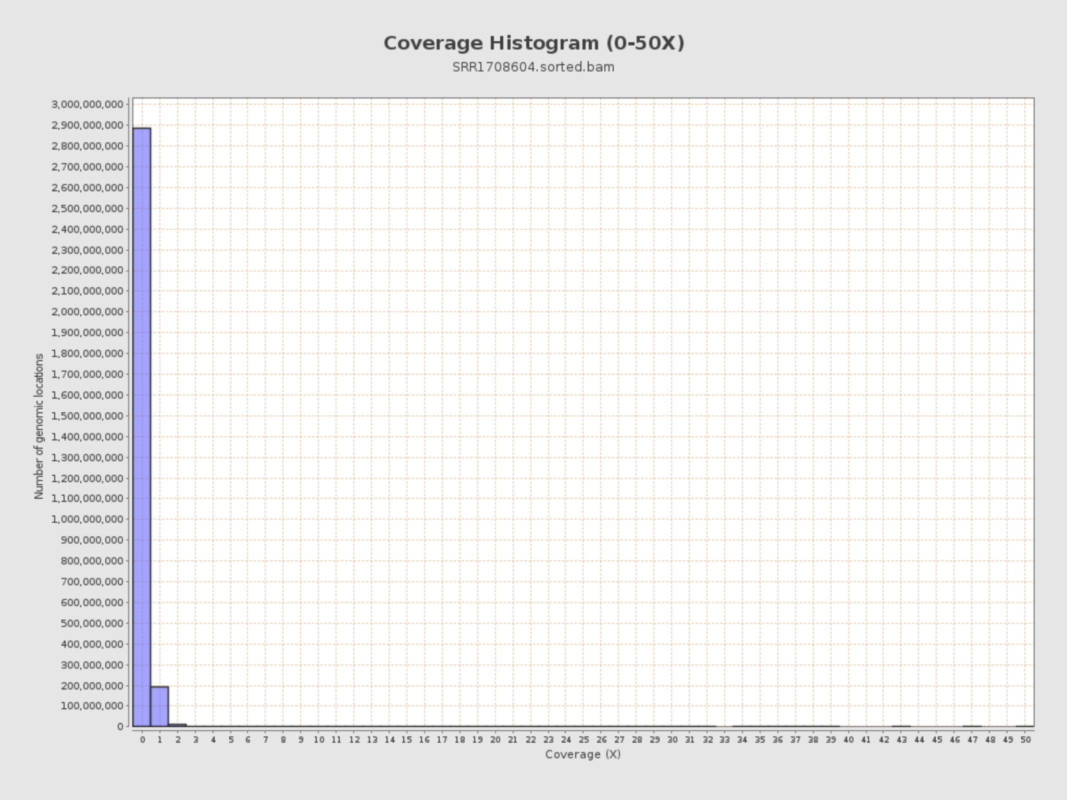
3. Results : Coverage across reference



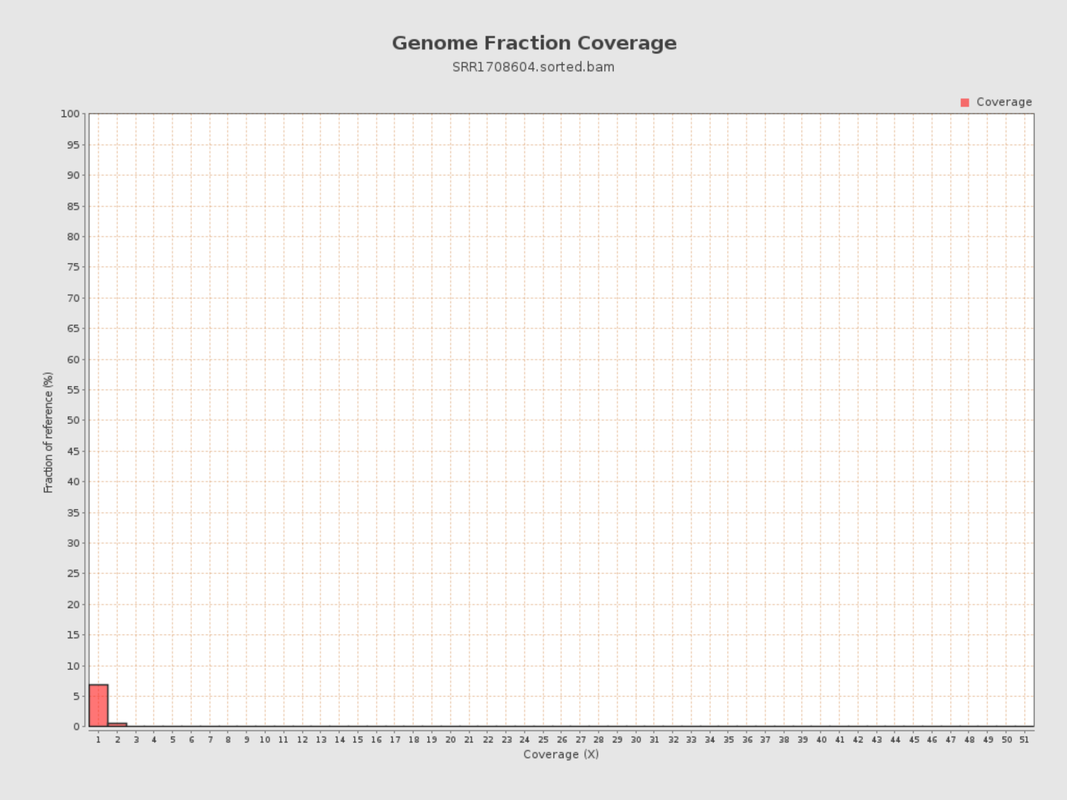
4. Results : Coverage Histogram



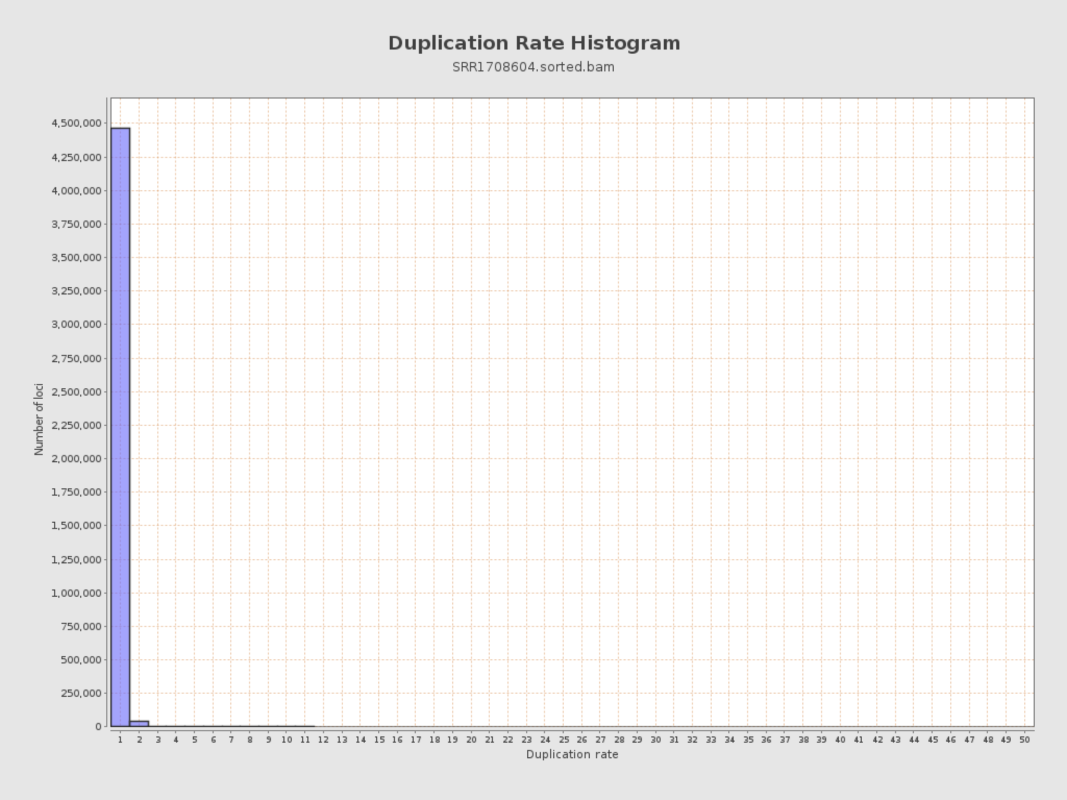
5. Results : Coverage Histogram (0-50X)



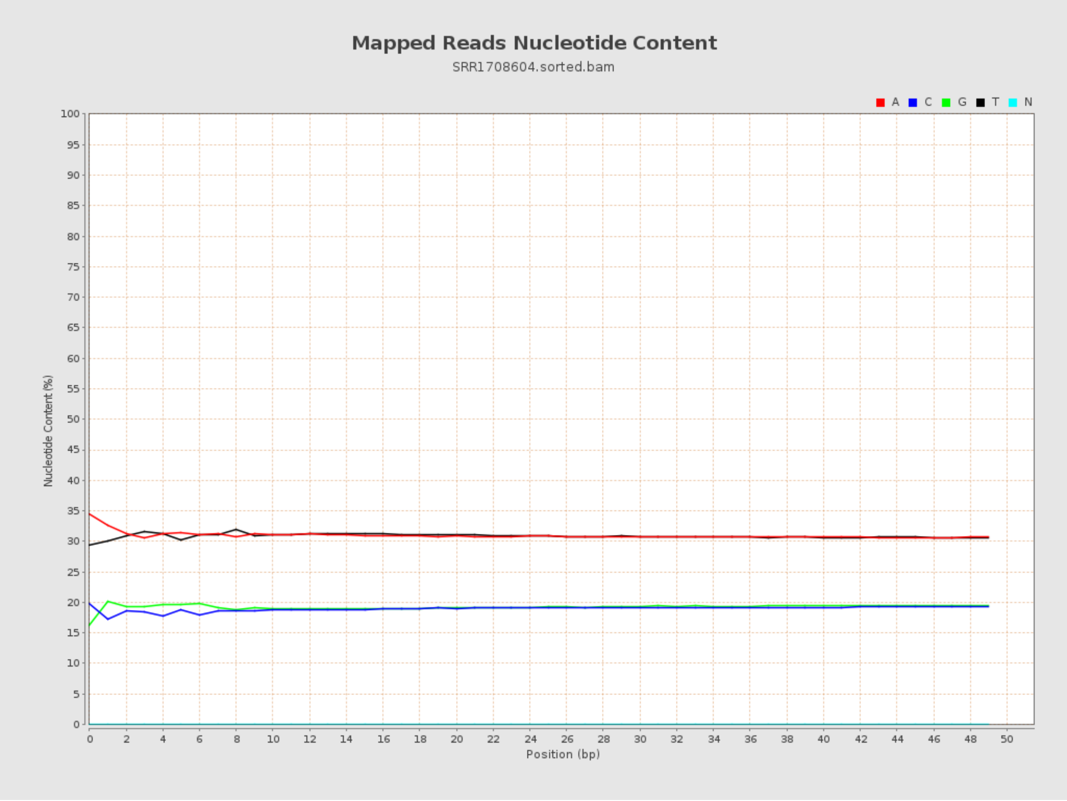
6. Results : Genome Fraction Coverage



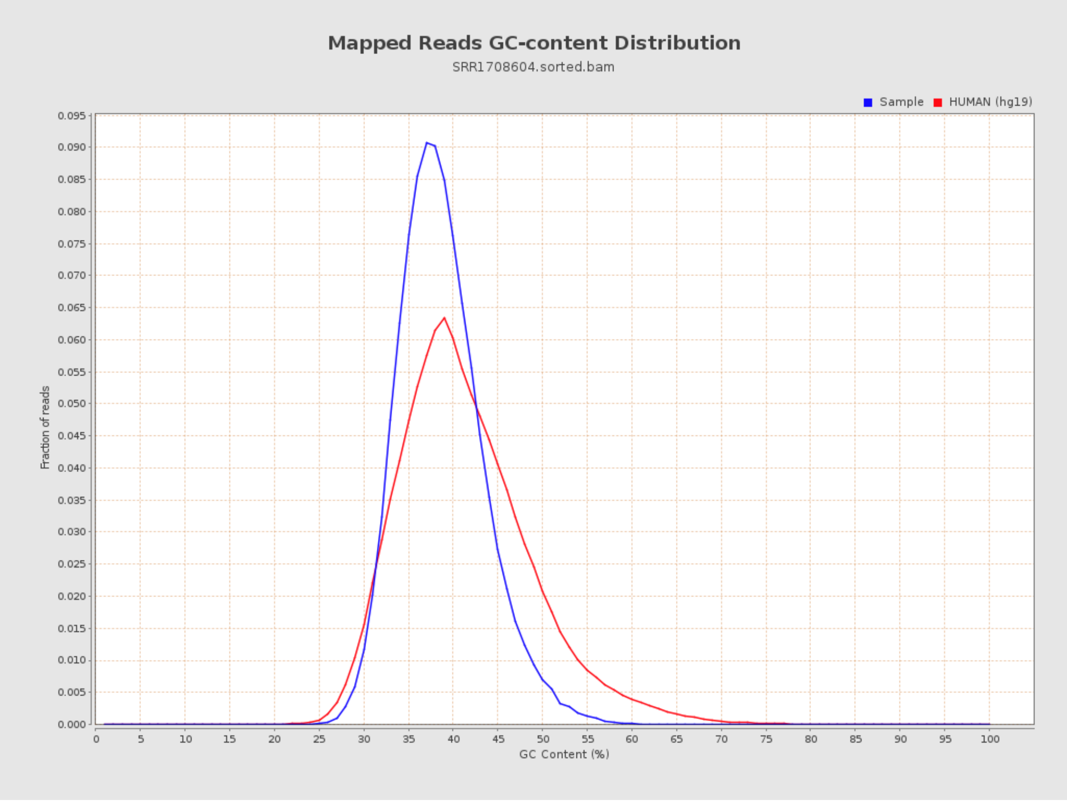
7. Results : Duplication Rate Histogram



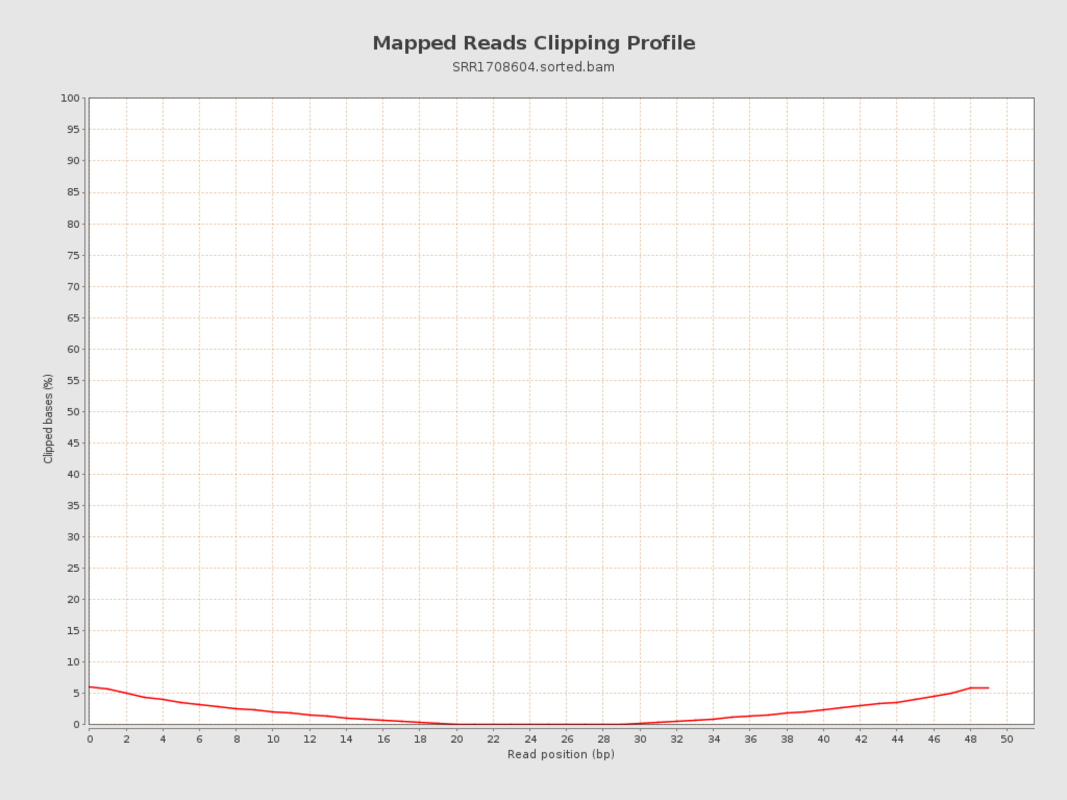
8. Results : Mapped Reads Nucleotide Content



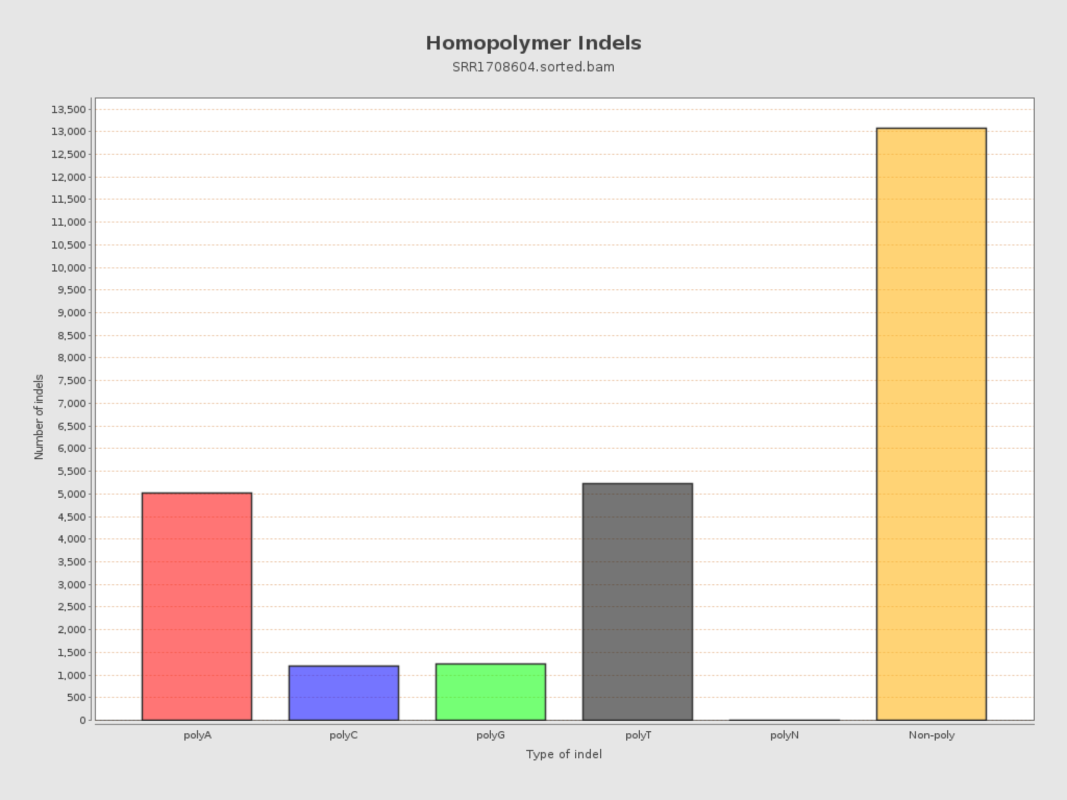
9. Results : Mapped Reads GC-content Distribution



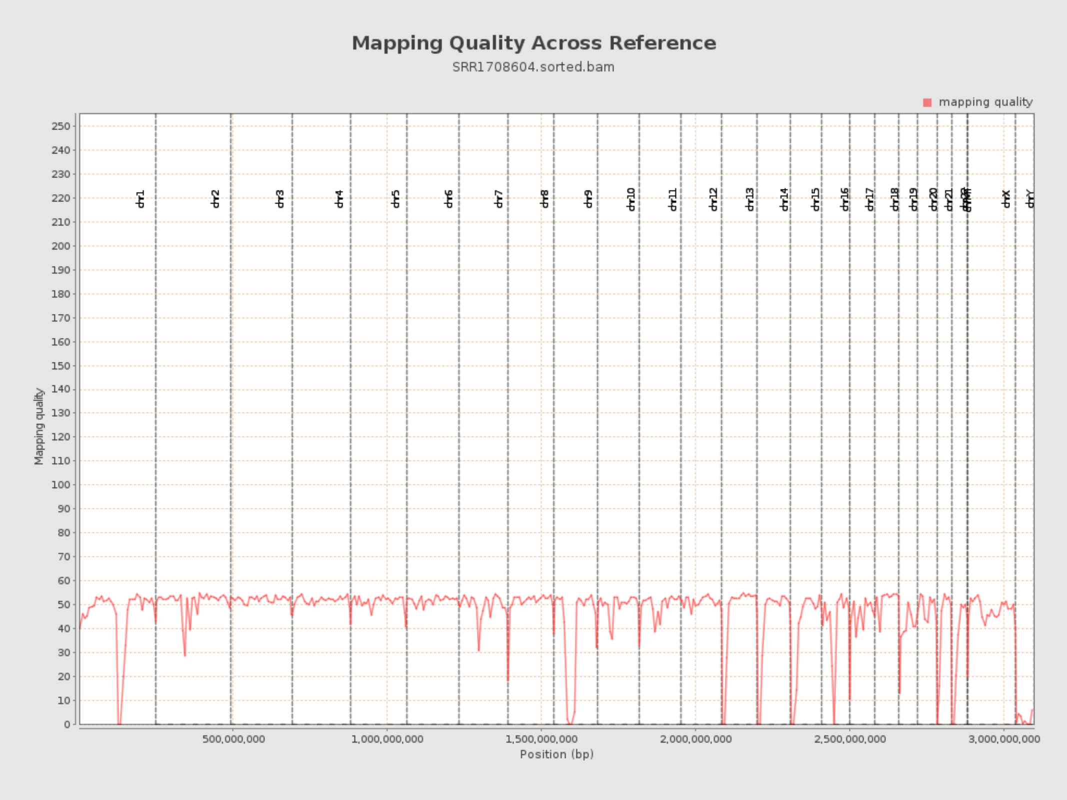
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram