Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:52:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708605.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_SRR1708605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:52:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,648,554
Mapped reads	5,464,795 / 96.75%
Unmapped reads	183,759 / 3.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	158 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	55,287 / 0.98%
Duplication rate	1.01%
Clipped reads	70,703 / 1.25%

2.2. ACGT Content

Number/percentage of A's	84,338,546 / 30.94%
Number/percentage of C's	51,757,326 / 18.99%
Number/percentage of T's	83,972,129 / 30.81%
Number/percentage of G's	52,490,298 / 19.26%
Number/percentage of N's	10,932 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	0.0881

Standard Deviation	0.3107

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

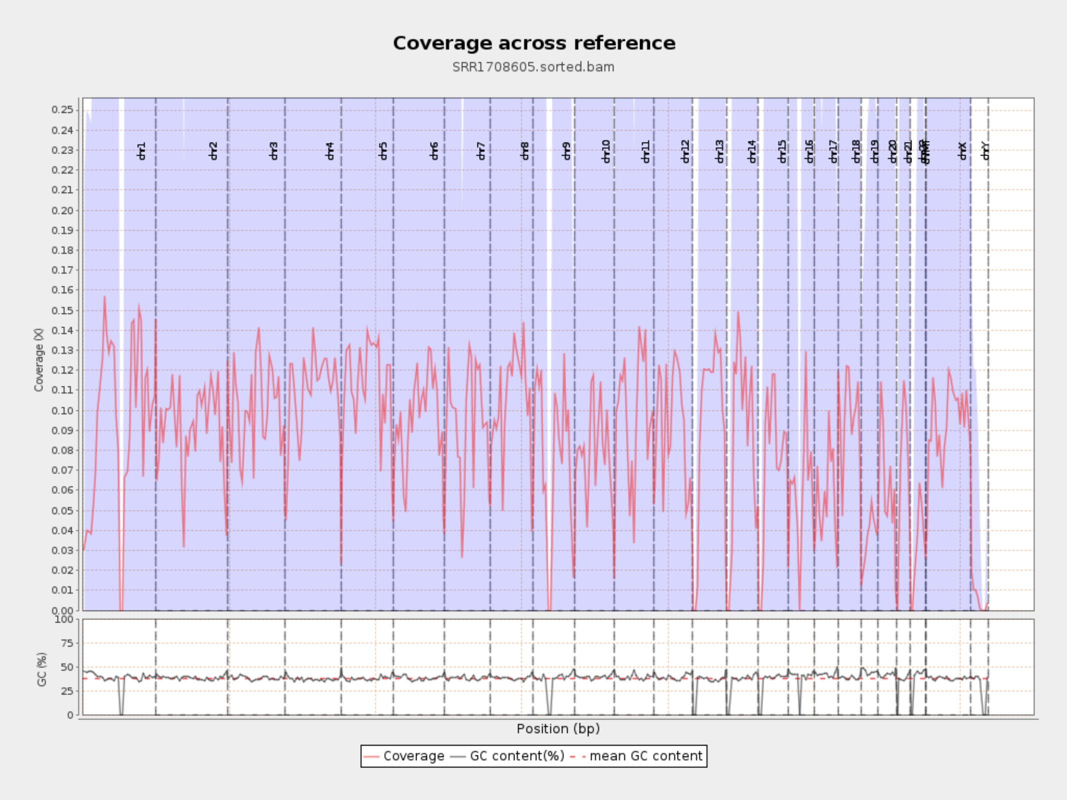
General error rate	0.15%
Mismatches	392,418
Insertions	17,041
Mapped reads with at least one insertion	0.31%
Deletions	13,881
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.64%

2.6. Chromosome stats

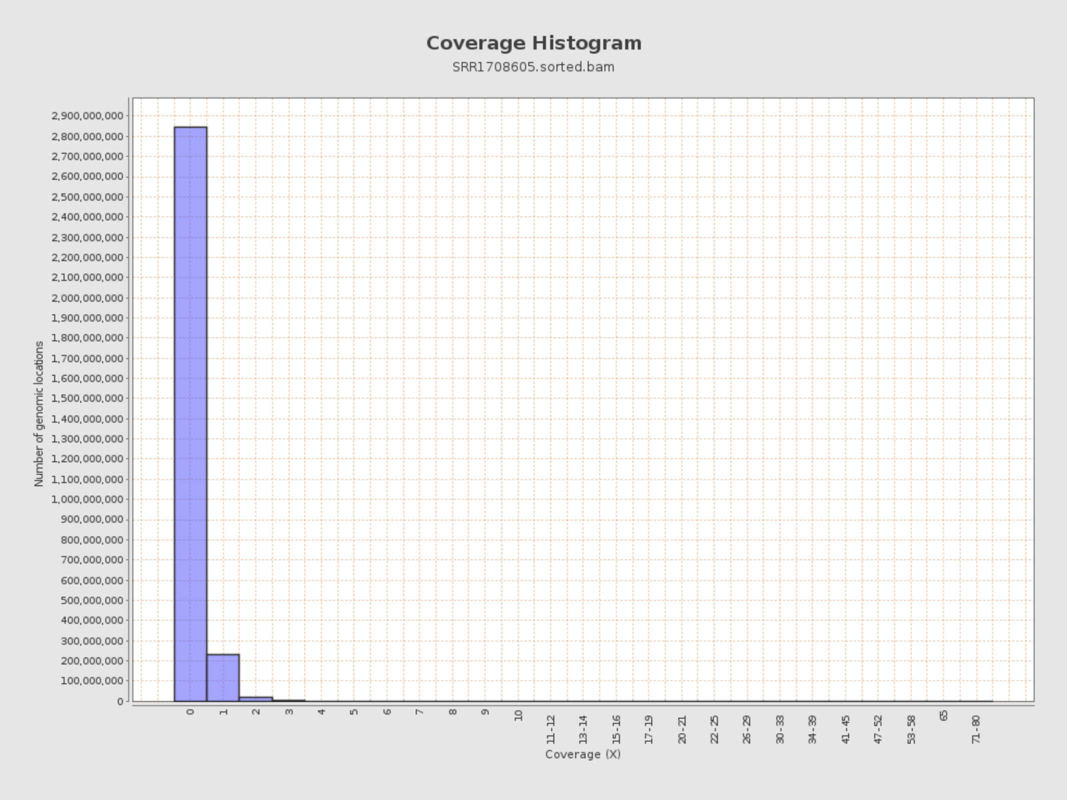
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23345673	0.0937	0.3236
chr2	243199373	22198828	0.0913	0.3142
chr3	198022430	20105599	0.1015	0.3317
chr4	191154276	20953313	0.1096	0.3441
chr5	180915260	20190662	0.1116	0.3476
chr6	171115067	16629191	0.0972	0.3249
chr7	159138663	14784690	0.0929	0.3185

chr8	146364022	15555615	0.1063	0.3401
chr9	141213431	10877319	0.077	0.2907
chr10	135534747	10915301	0.0805	0.2947
chr11	135006516	13174465	0.0976	0.3287
chr12	133851895	12344795	0.0922	0.3174
chr13	115169878	10805829	0.0938	0.3212
chr14	107349540	9356019	0.0872	0.3112
chr15	102531392	7489715	0.073	0.2843
chr16	90354753	5359854	0.0593	0.2546
chr17	81195210	4681738	0.0577	0.2515
chr18	78077248	7581447	0.0971	0.3236
chr19	59128983	2171081	0.0367	0.1983
chr20	63025520	4137148	0.0656	0.2674
chr21	48129895	3262034	0.0678	0.2747
chr22	51304566	1682882	0.0328	0.1888
chrMT	16571	545	0.0329	0.183
chrX	155270560	14643008	0.0943	0.3194
chrY	59373566	346295	0.0058	0.0809

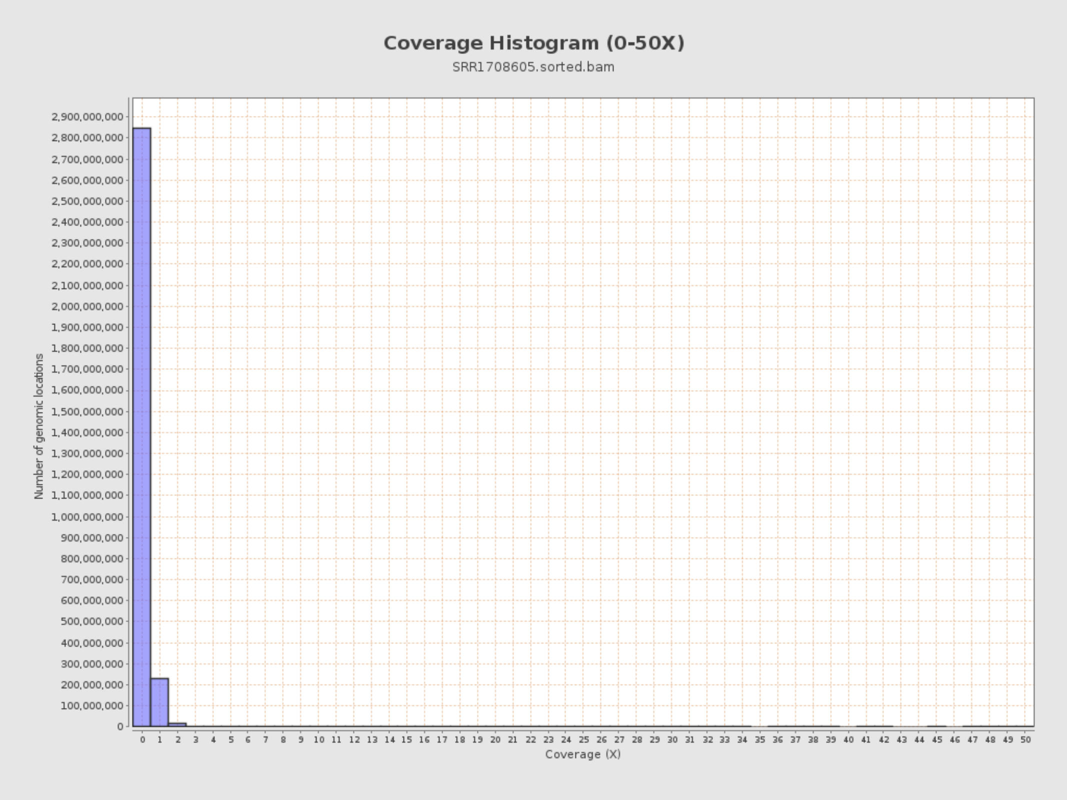
3. Results : Coverage across reference



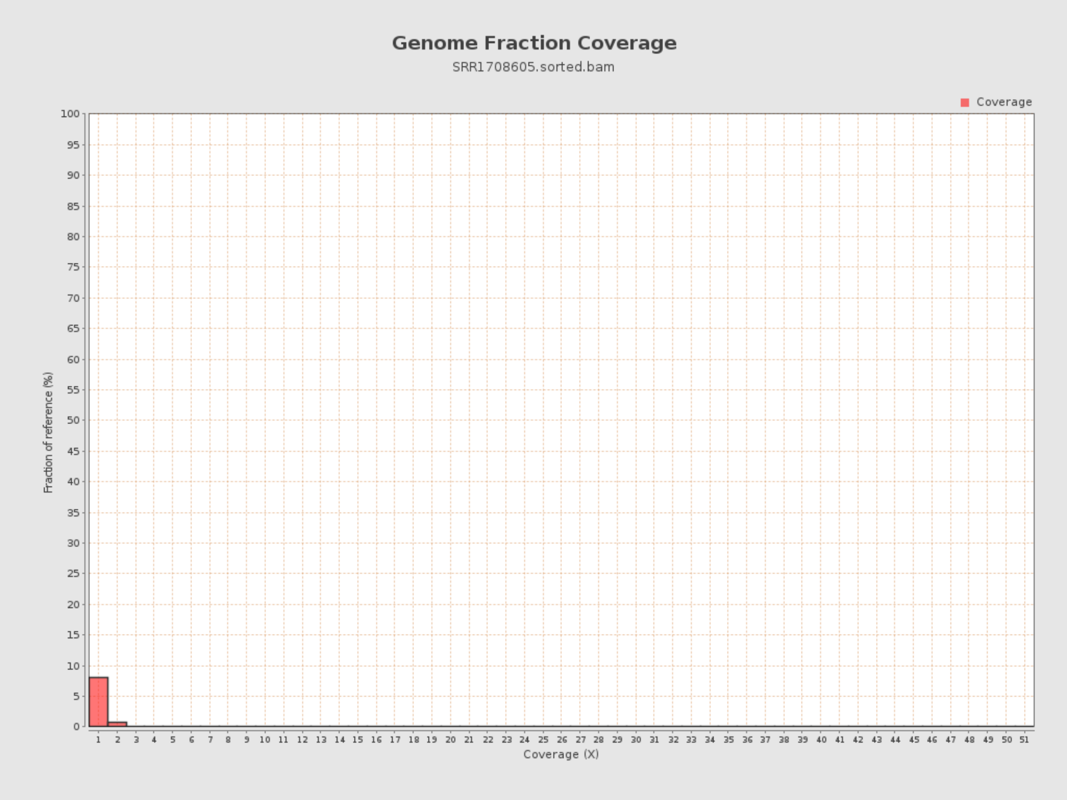
4. Results : Coverage Histogram



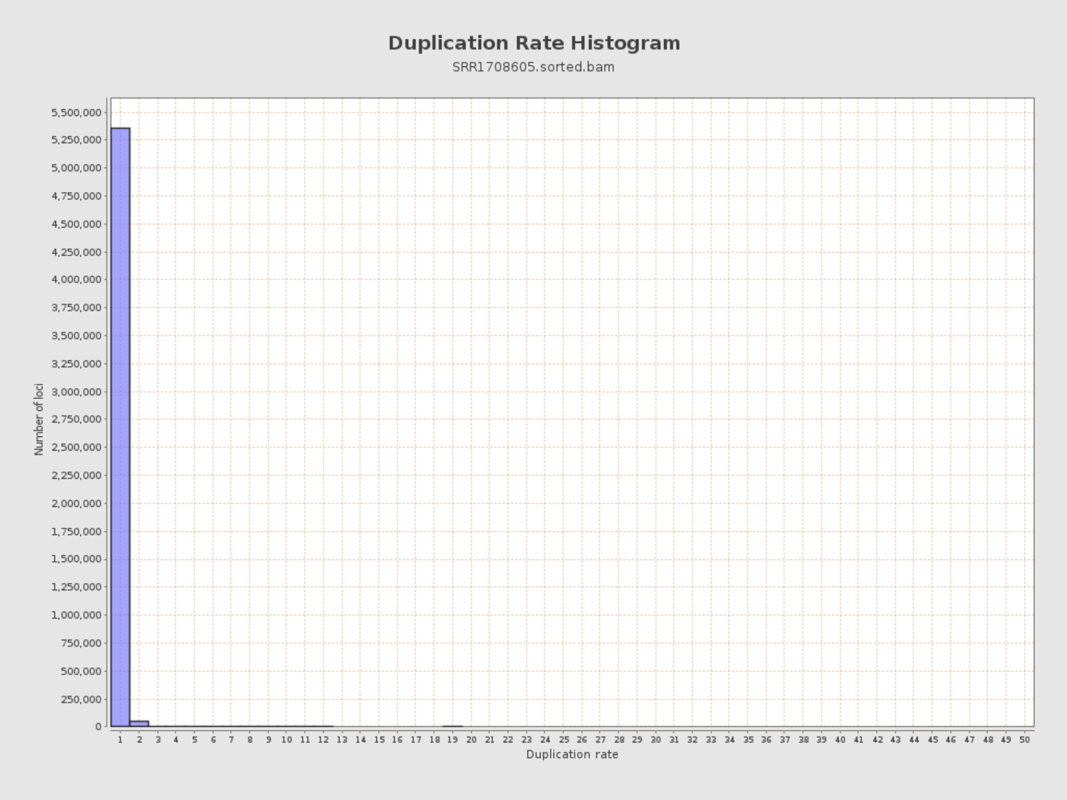
5. Results : Coverage Histogram (0-50X)



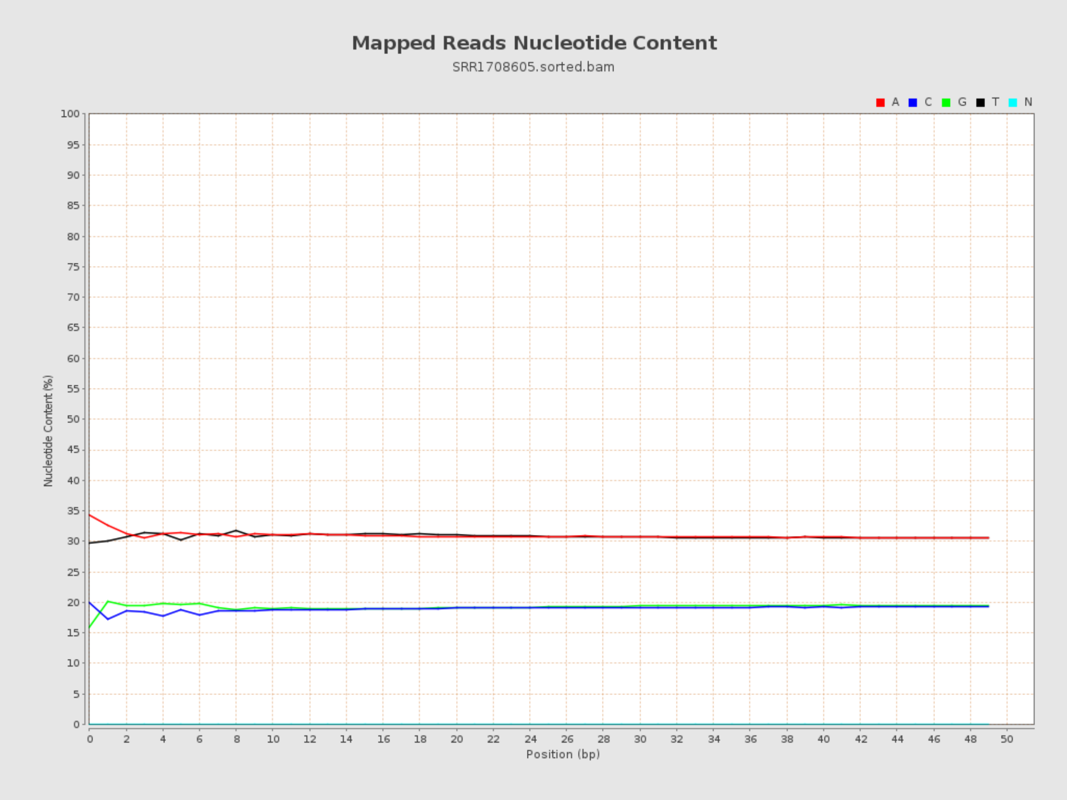
6. Results : Genome Fraction Coverage



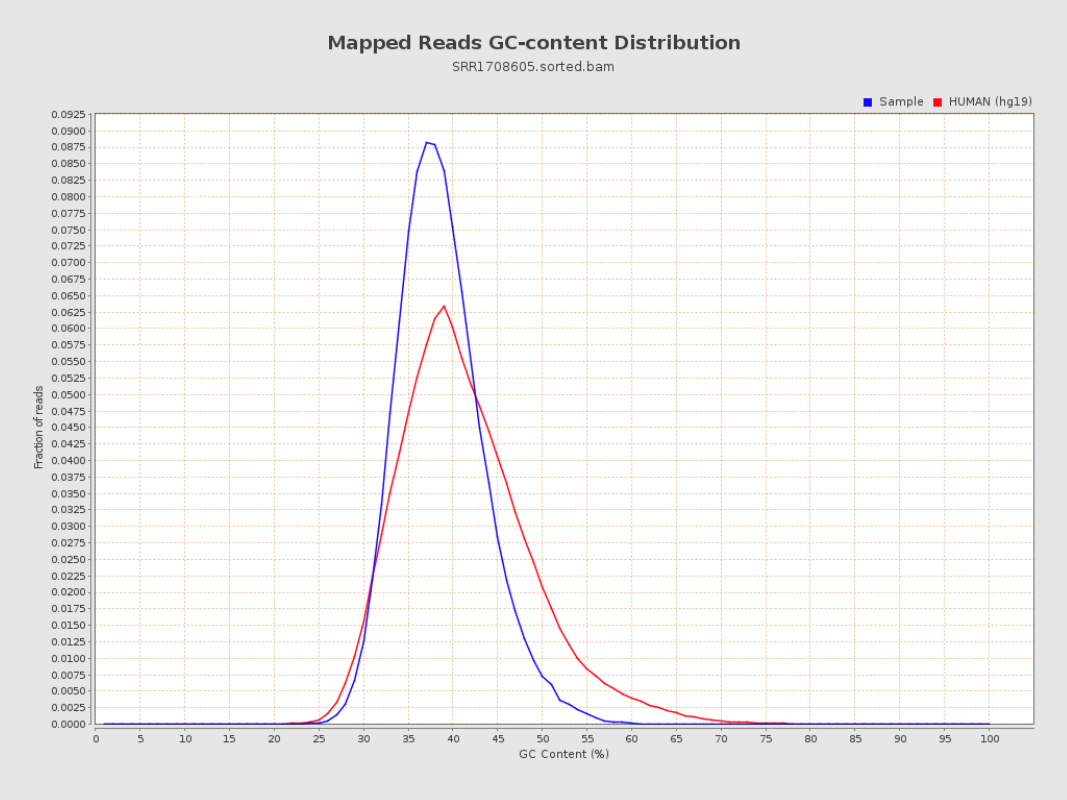
7. Results : Duplication Rate Histogram



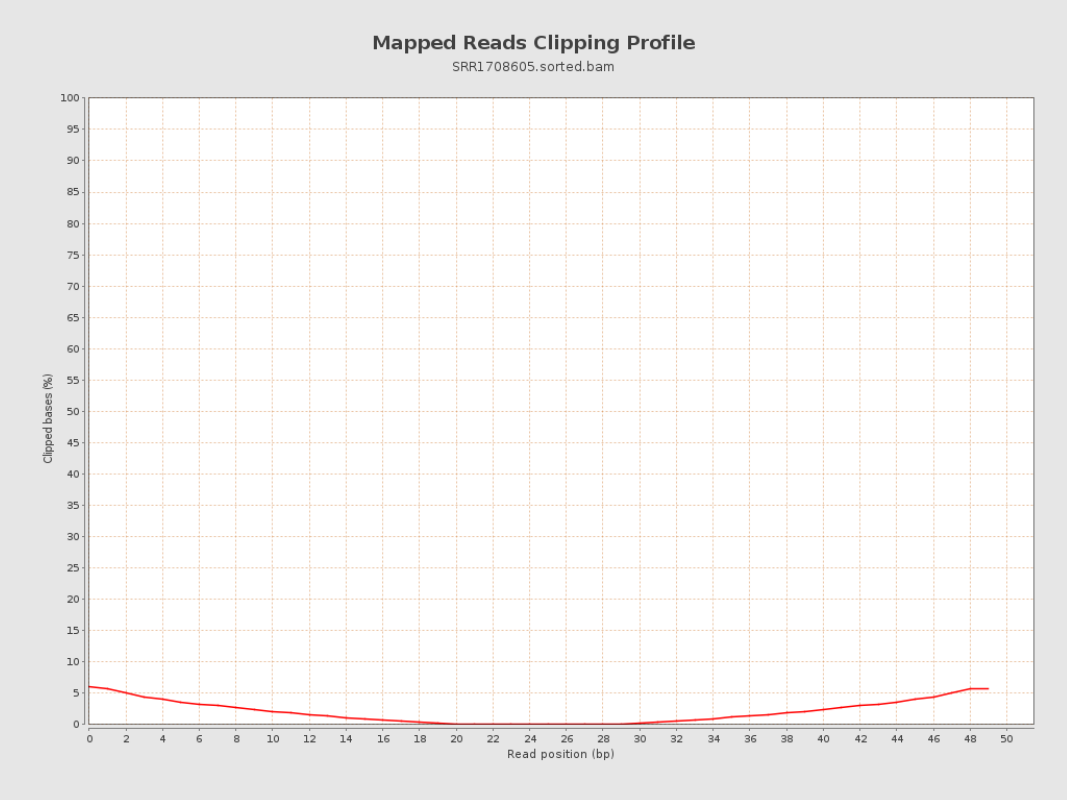
8. Results : Mapped Reads Nucleotide Content



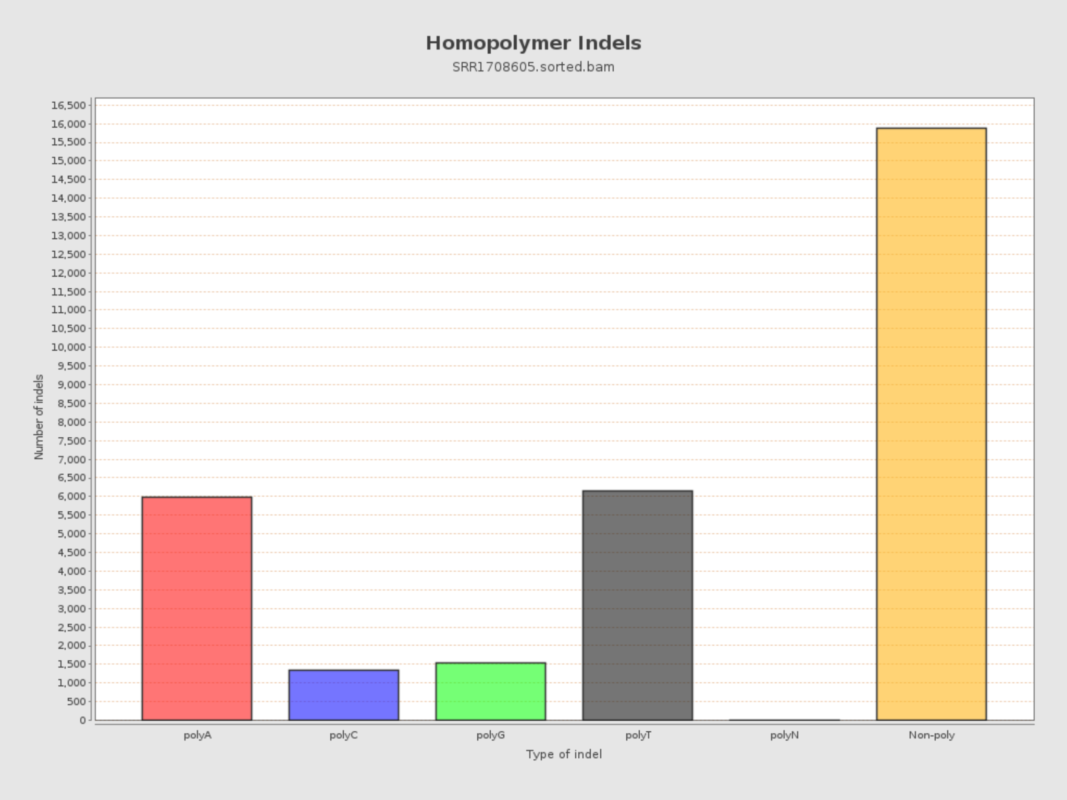
9. Results : Mapped Reads GC-content Distribution



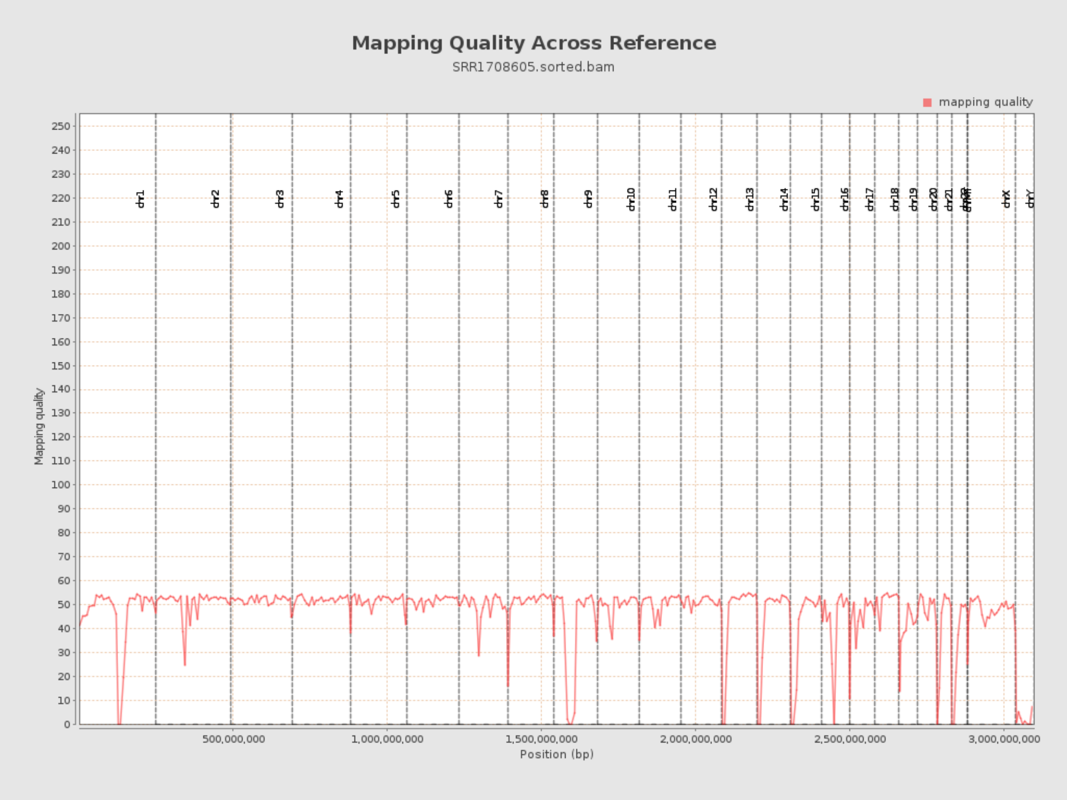
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram