Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:18:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708609.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_SRR1708609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:18:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,648,822
Mapped reads	4,393,286 / 94.5%
Unmapped reads	255,536 / 5.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	132 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	42,155 / 0.91%
Duplication rate	0.96%
Clipped reads	59,506 / 1.28%

2.2. ACGT Content

Number/percentage of A's	67,896,050 / 30.99%
Number/percentage of C's	41,554,836 / 18.97%
Number/percentage of T's	67,406,908 / 30.76%
Number/percentage of G's	42,237,793 / 19.28%
Number/percentage of N's	7,709 / 0%
GC Percentage	38.24%

2.3. Coverage

Mean	0.0708

Standard Deviation	0.2767

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

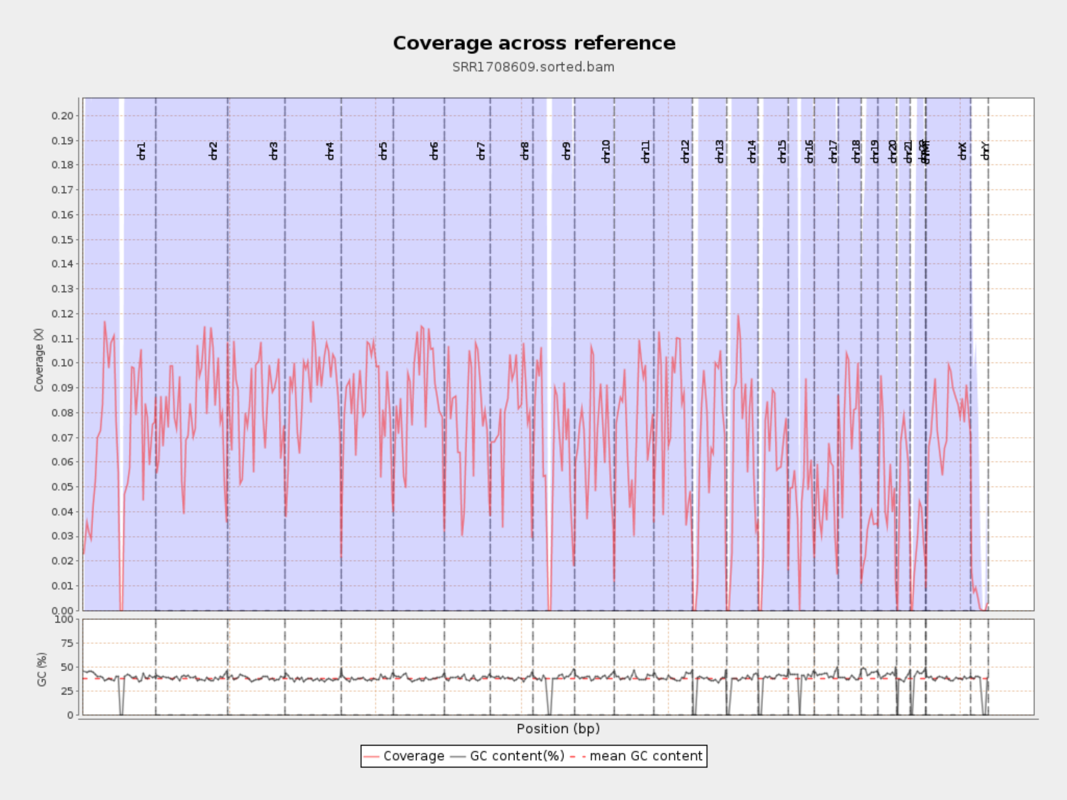
General error rate	0.16%
Mismatches	321,687
Insertions	13,762
Mapped reads with at least one insertion	0.31%
Deletions	10,945
Mapped reads with at least one deletion	0.25%
Homopolymer indels	49.08%

2.6. Chromosome stats

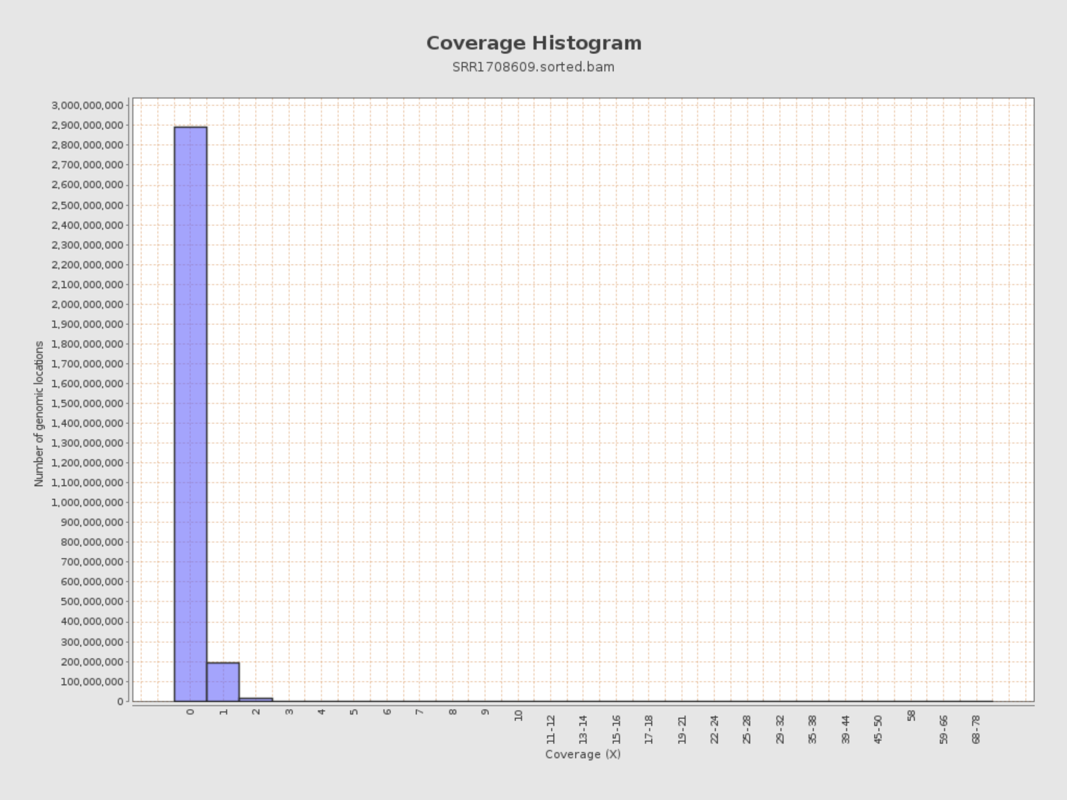
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16907652	0.0678	0.2742
chr2	243199373	19733212	0.0811	0.2973
chr3	198022430	16515851	0.0834	0.2982
chr4	191154276	17338250	0.0907	0.3107
chr5	180915260	15112472	0.0835	0.2984
chr6	171115067	15022585	0.0878	0.3064
chr7	159138663	12082717	0.0759	0.2858

chr8	146364022	11647581	0.0796	0.2915
chr9	141213431	9015973	0.0638	0.2628
chr10	135534747	9532681	0.0703	0.2745
chr11	135006516	10007947	0.0741	0.2841
chr12	133851895	10390077	0.0776	0.289
chr13	115169878	7517961	0.0653	0.2654
chr14	107349540	7178385	0.0669	0.2697
chr15	102531392	5943288	0.058	0.2509
chr16	90354753	4145217	0.0459	0.222
chr17	81195210	3633805	0.0448	0.2198
chr18	78077248	6176775	0.0791	0.2906
chr19	59128983	1807282	0.0306	0.1805
chr20	63025520	3424615	0.0543	0.2416
chr21	48129895	2472615	0.0514	0.237
chr22	51304566	1245352	0.0243	0.161
chrMT	16571	150	0.0091	0.0947
chrX	155270560	11992616	0.0772	0.2875
chrY	59373566	276878	0.0047	0.0713

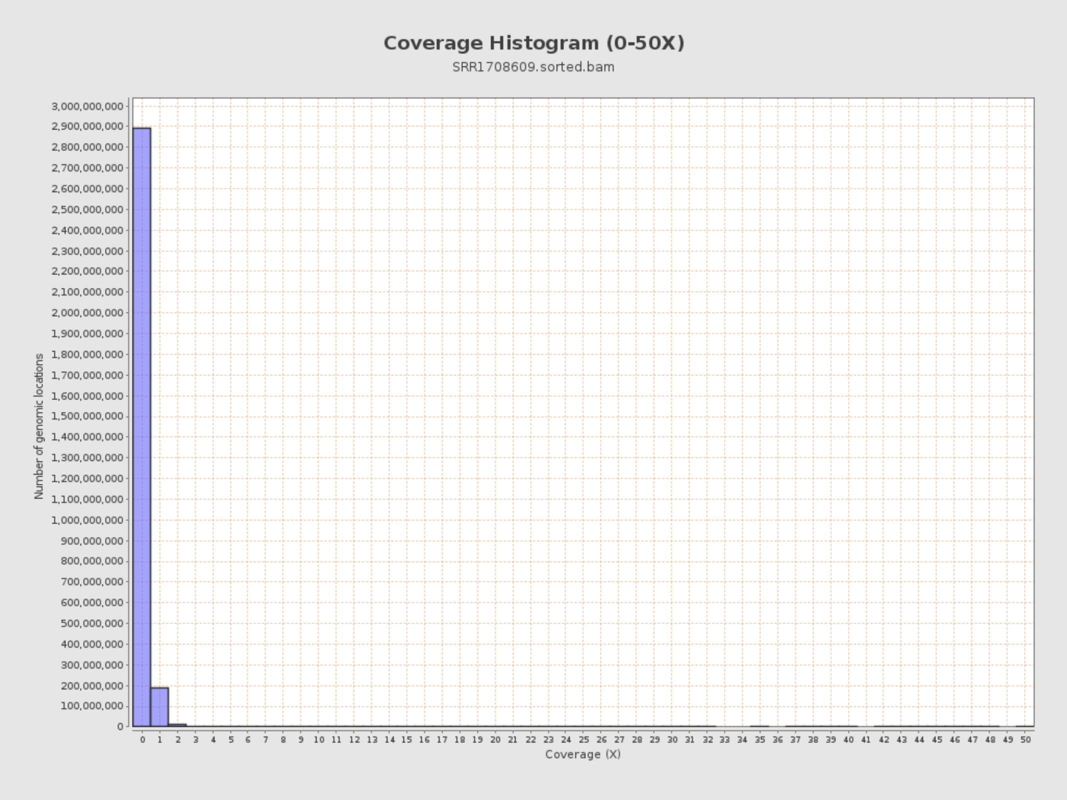
3. Results : Coverage across reference



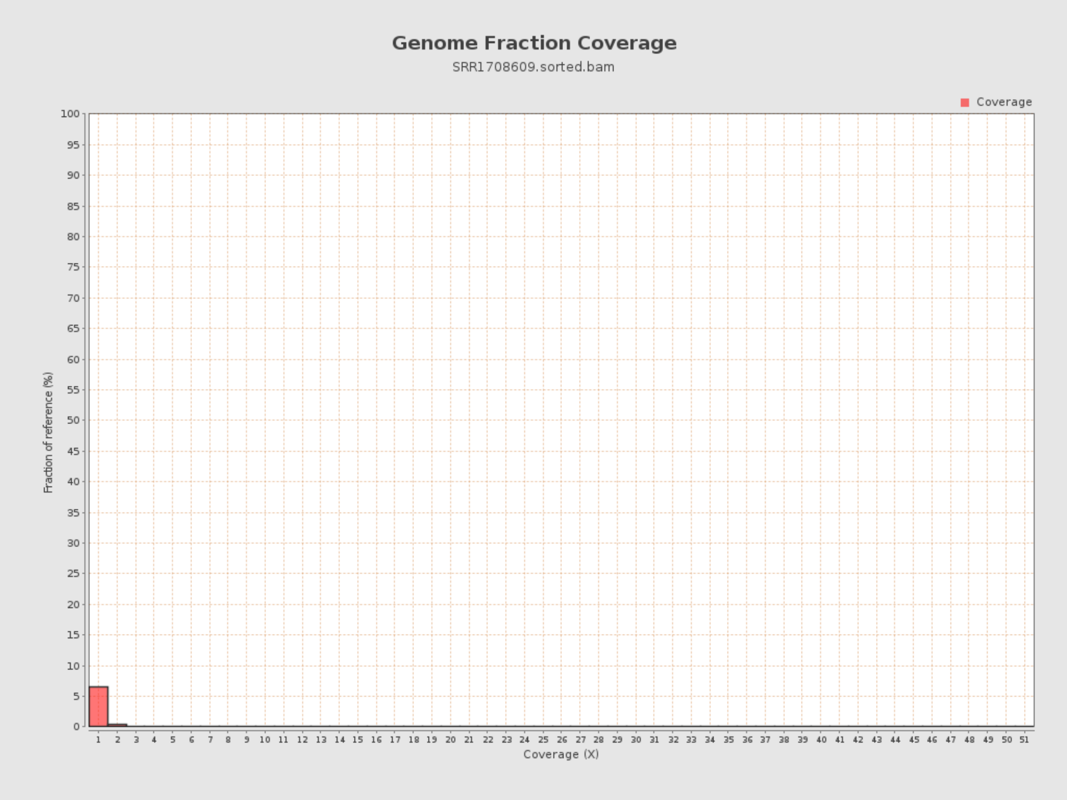
4. Results : Coverage Histogram



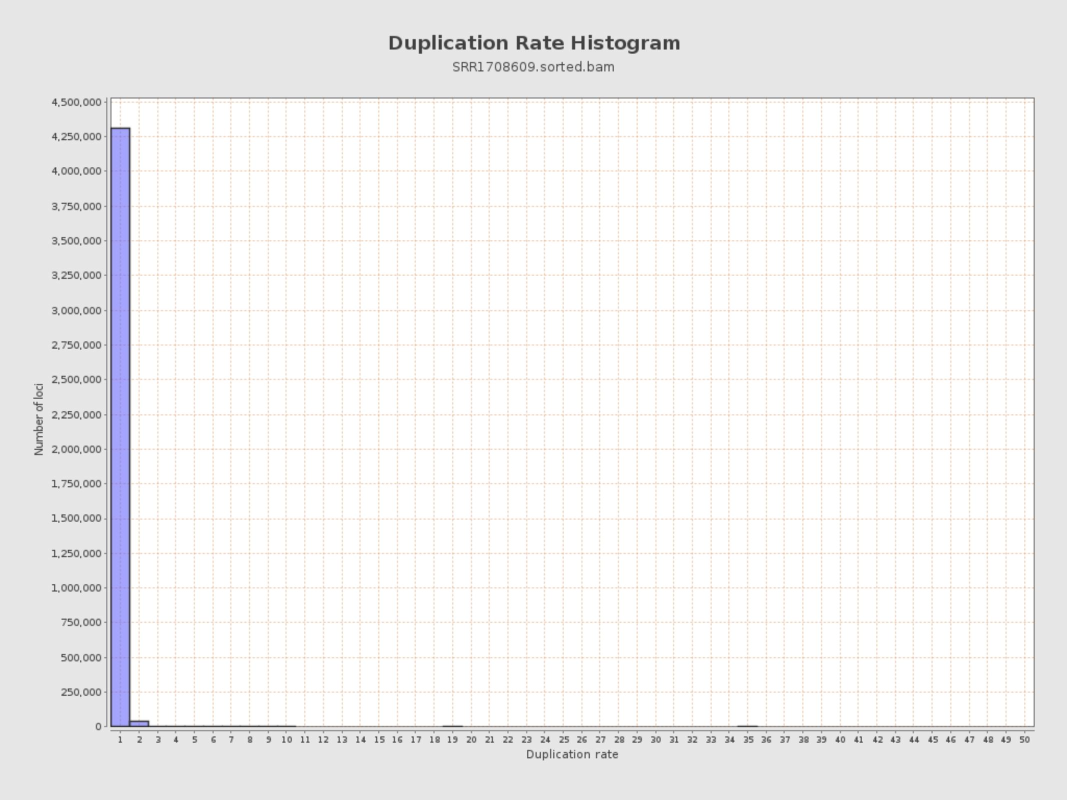
5. Results : Coverage Histogram (0-50X)



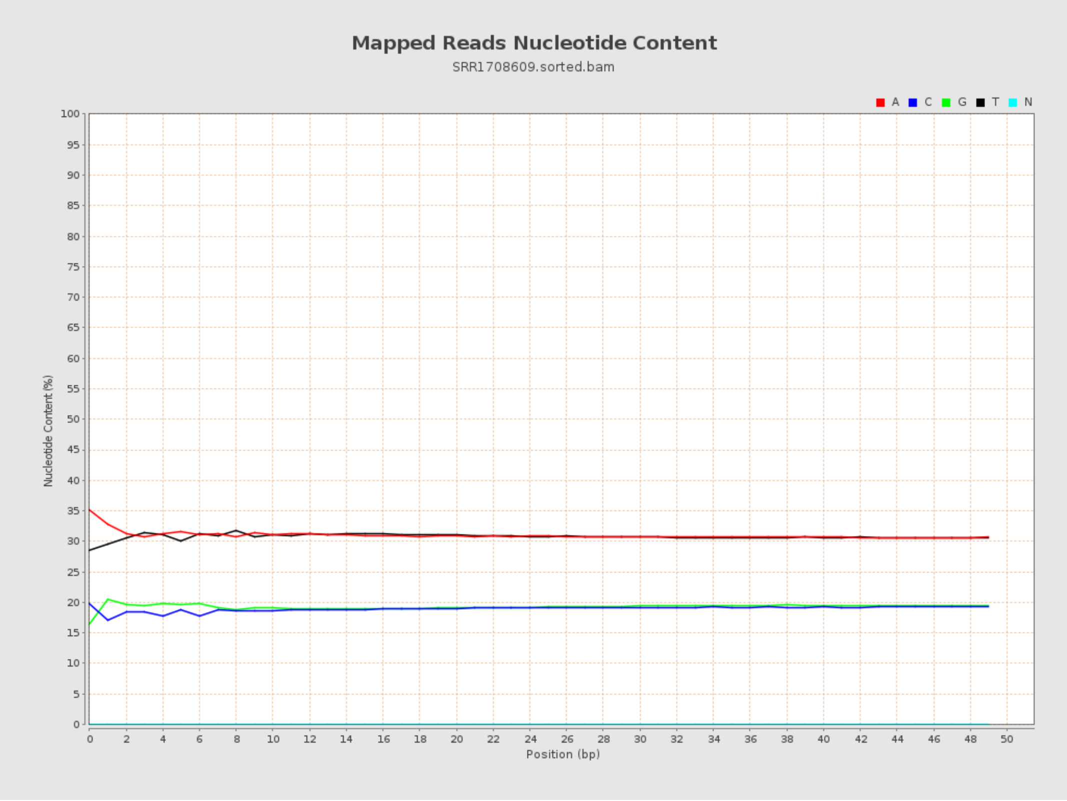
6. Results : Genome Fraction Coverage



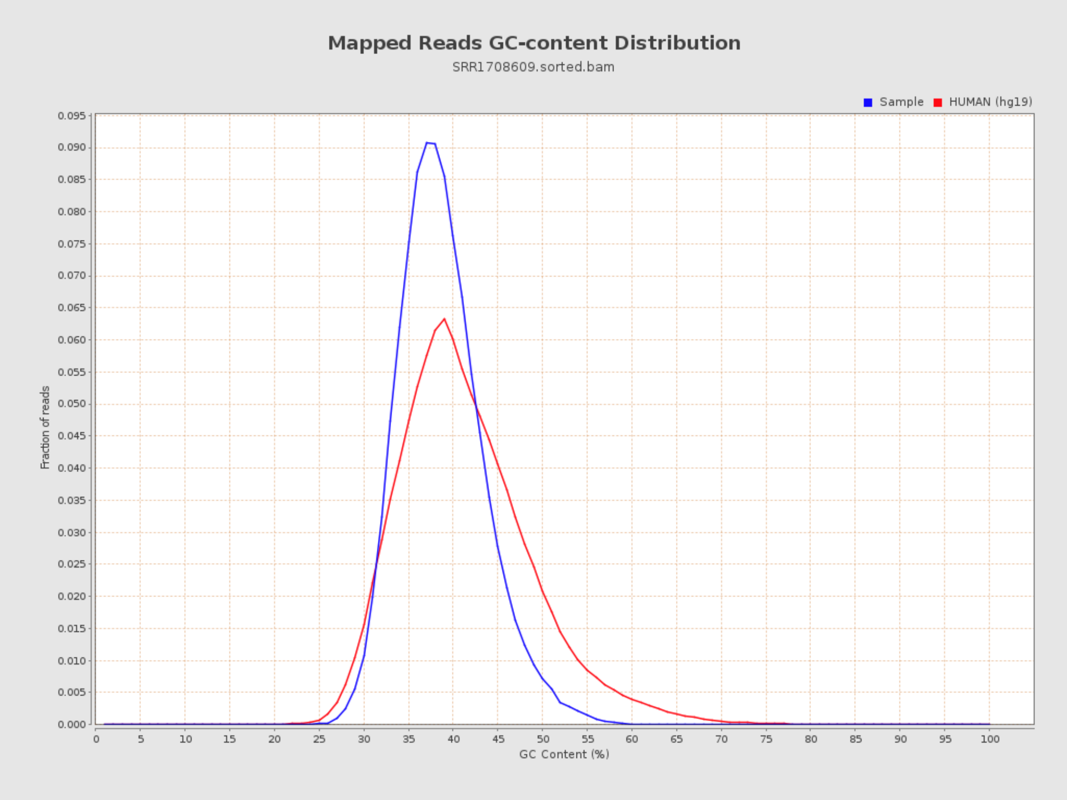
7. Results : Duplication Rate Histogram



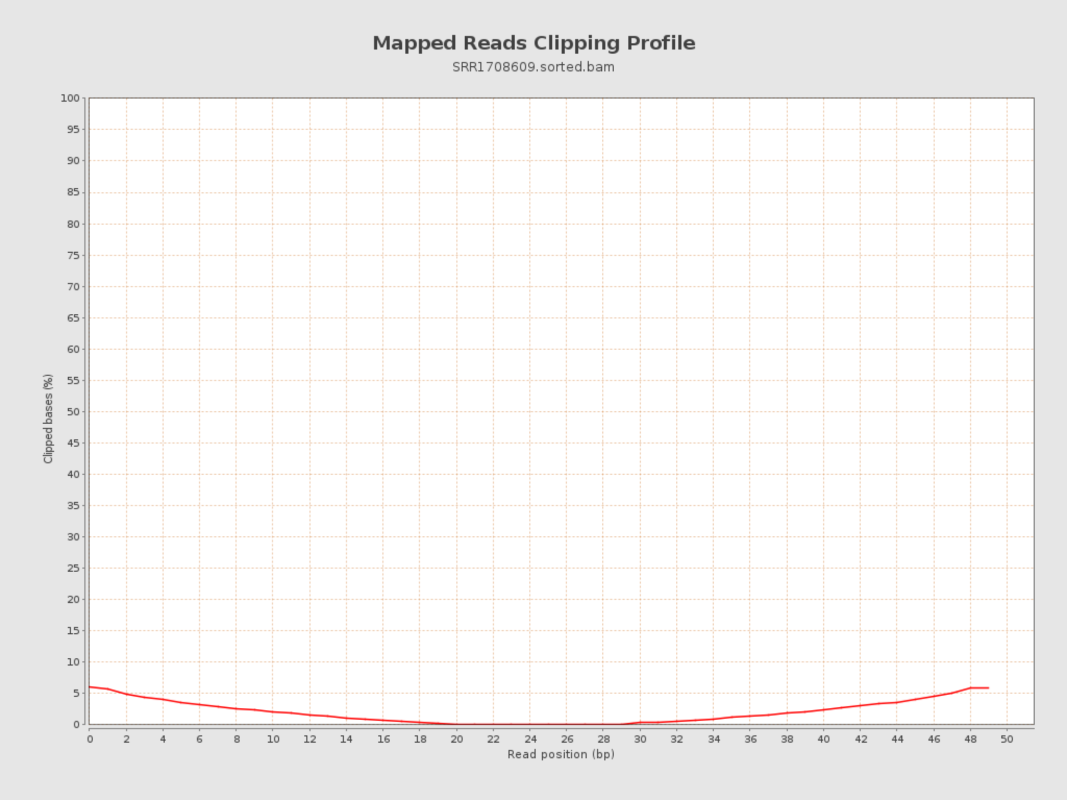
8. Results : Mapped Reads Nucleotide Content



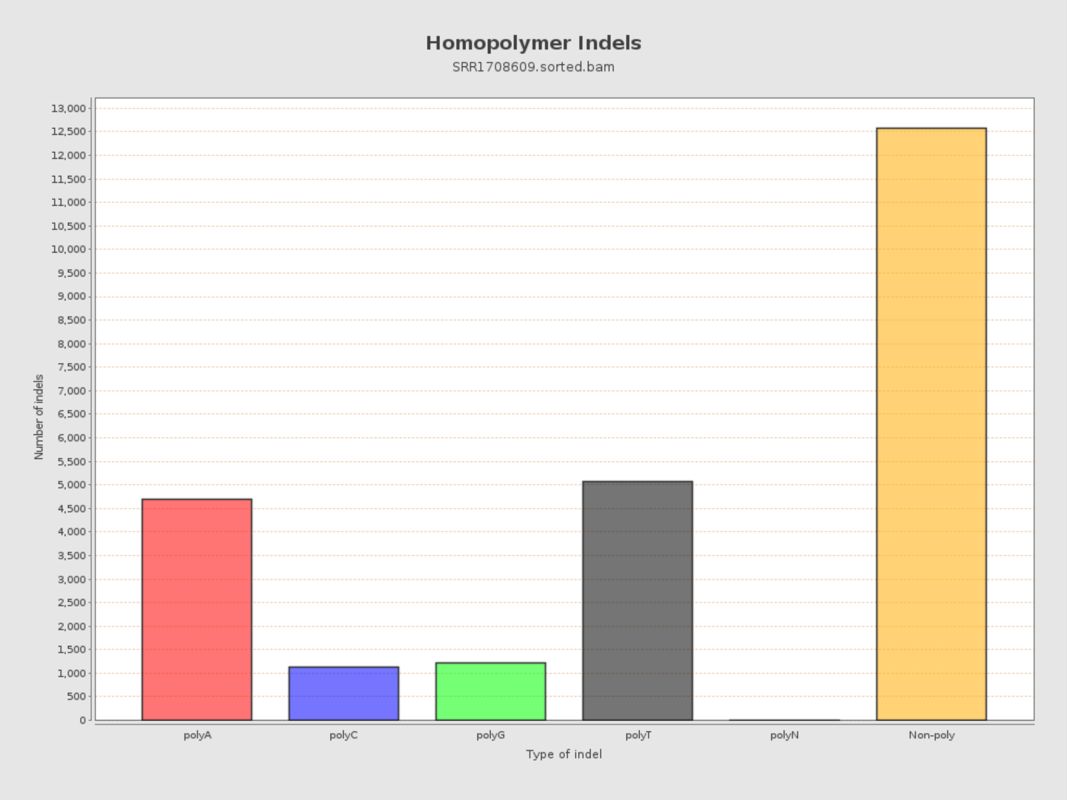
9. Results : Mapped Reads GC-content Distribution



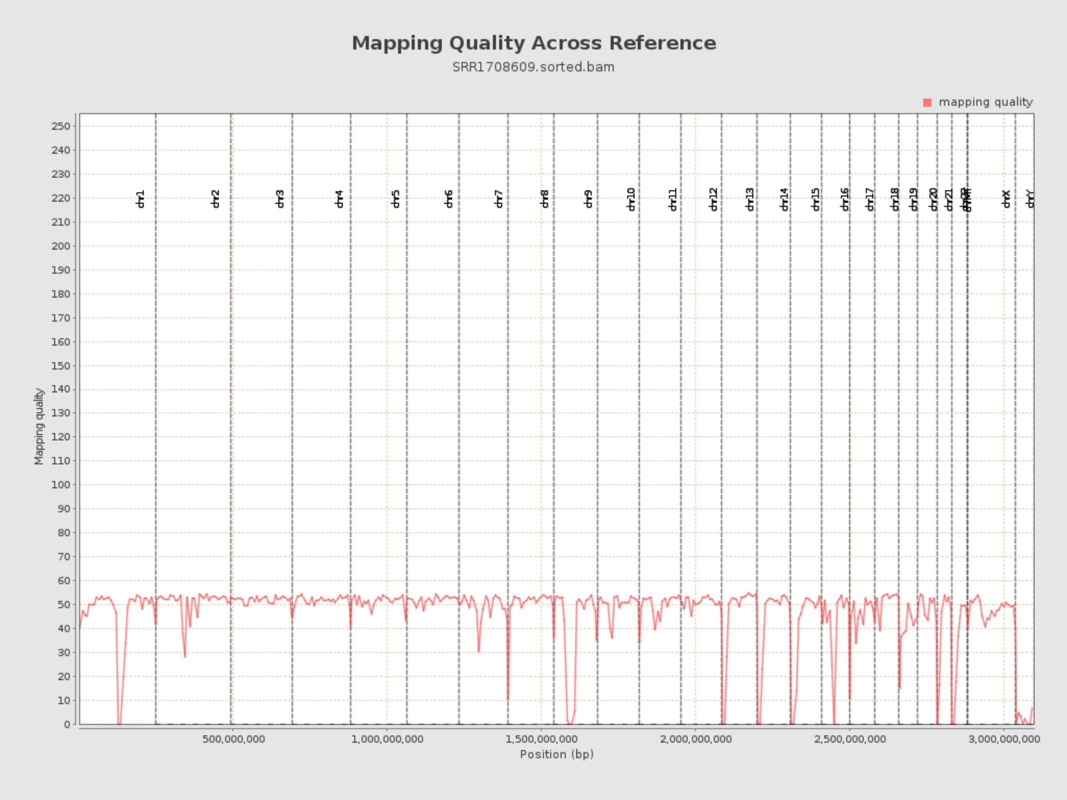
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram