Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:08:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708636.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_SRR1708636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:08:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,884,757
Mapped reads	4,629,665 / 94.78%
Unmapped reads	255,092 / 5.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	133 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	26,777 / 0.55%
Duplication rate	0.57%
Clipped reads	62,538 / 1.28%

2.2. ACGT Content

Number/percentage of A's	71,068,277 / 30.78%
Number/percentage of C's	44,148,595 / 19.12%
Number/percentage of T's	71,085,973 / 30.79%
Number/percentage of G's	44,571,287 / 19.3%
Number/percentage of N's	7,005 / 0%
GC Percentage	38.43%

2.3. Coverage

Mean	0.0746

Standard Deviation	0.296

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

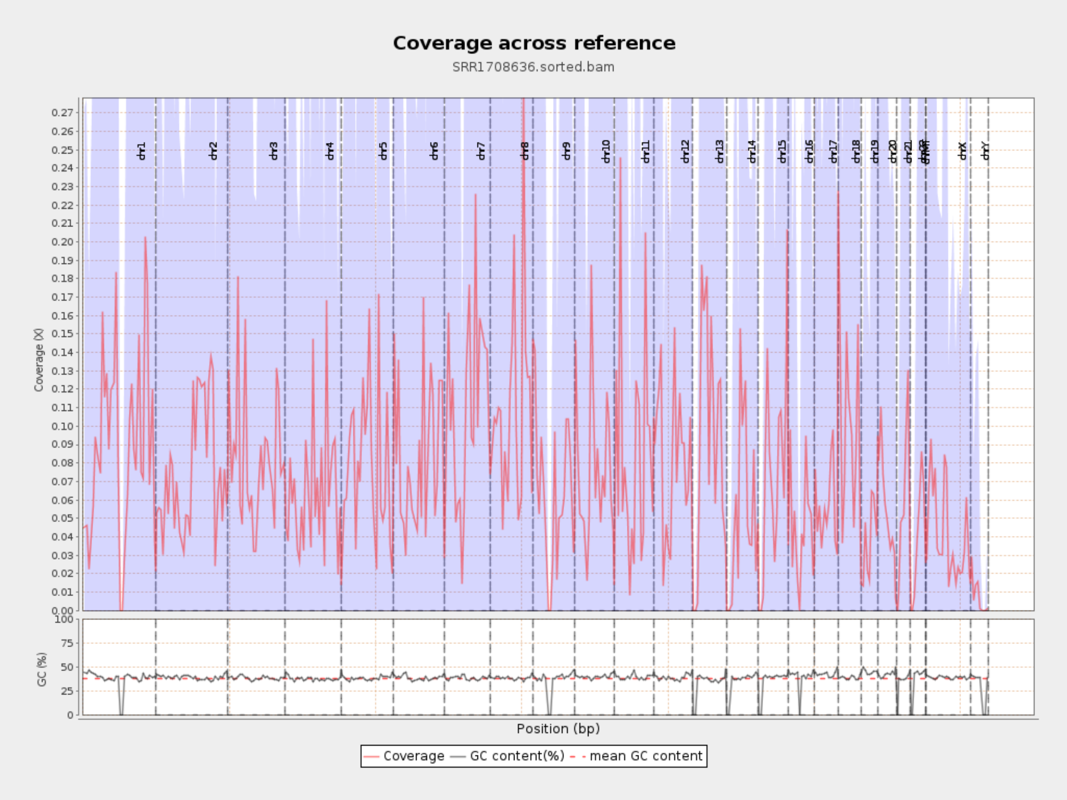
General error rate	0.17%
Mismatches	376,598
Insertions	15,968
Mapped reads with at least one insertion	0.34%
Deletions	13,375
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.7%

2.6. Chromosome stats

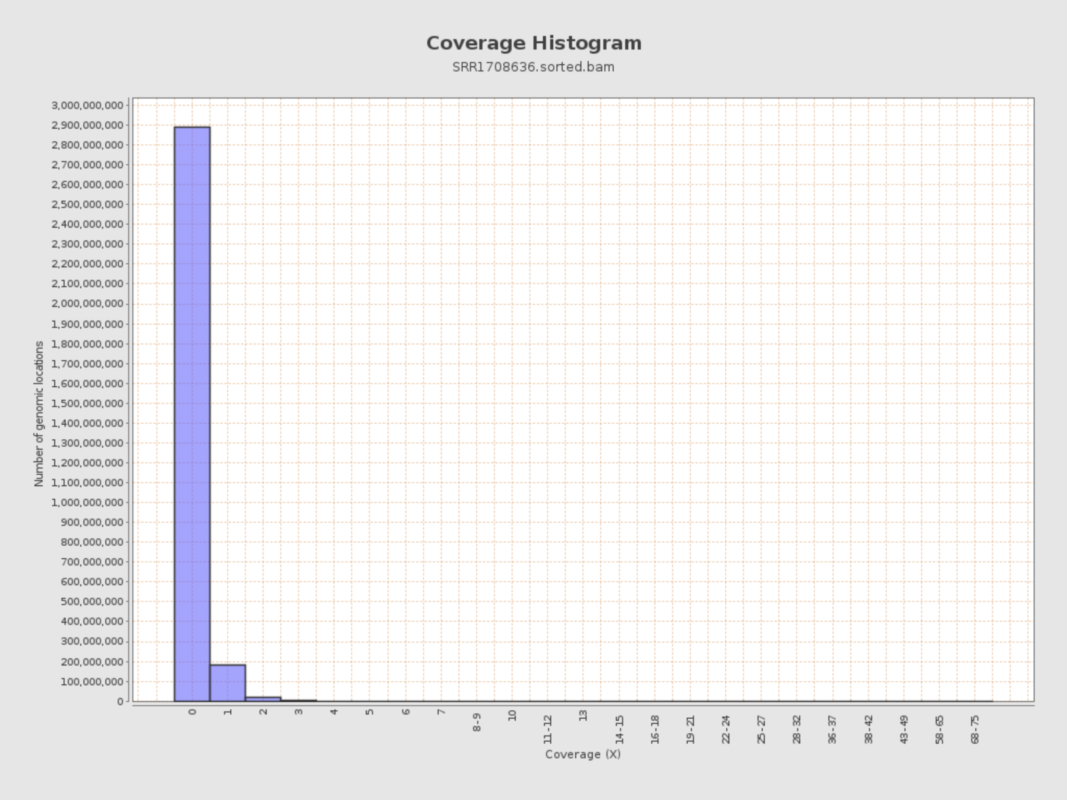
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22057402	0.0885	0.3249
chr2	243199373	18279304	0.0752	0.2933
chr3	198022430	16305138	0.0823	0.309
chr4	191154276	12481658	0.0653	0.274
chr5	180915260	14160216	0.0783	0.3031
chr6	171115067	14325044	0.0837	0.31
chr7	159138663	17277644	0.1086	0.3602

chr8	146364022	16326543	0.1115	0.364
chr9	141213431	8735749	0.0619	0.2655
chr10	135534747	10697901	0.0789	0.302
chr11	135006516	11350074	0.0841	0.3186
chr12	133851895	11093326	0.0829	0.3106
chr13	115169878	10654786	0.0925	0.3327
chr14	107349540	5680775	0.0529	0.249
chr15	102531392	7261779	0.0708	0.2889
chr16	90354753	4001457	0.0443	0.2236
chr17	81195210	4670813	0.0575	0.2562
chr18	78077248	7920883	0.1014	0.3438
chr19	59128983	2317270	0.0392	0.2098
chr20	63025520	3543164	0.0562	0.2529
chr21	48129895	2715464	0.0564	0.2574
chr22	51304566	2102930	0.041	0.2182
chrMT	16571	840	0.0507	0.2304
chrX	155270560	6502314	0.0419	0.219
chrY	59373566	441353	0.0074	0.092

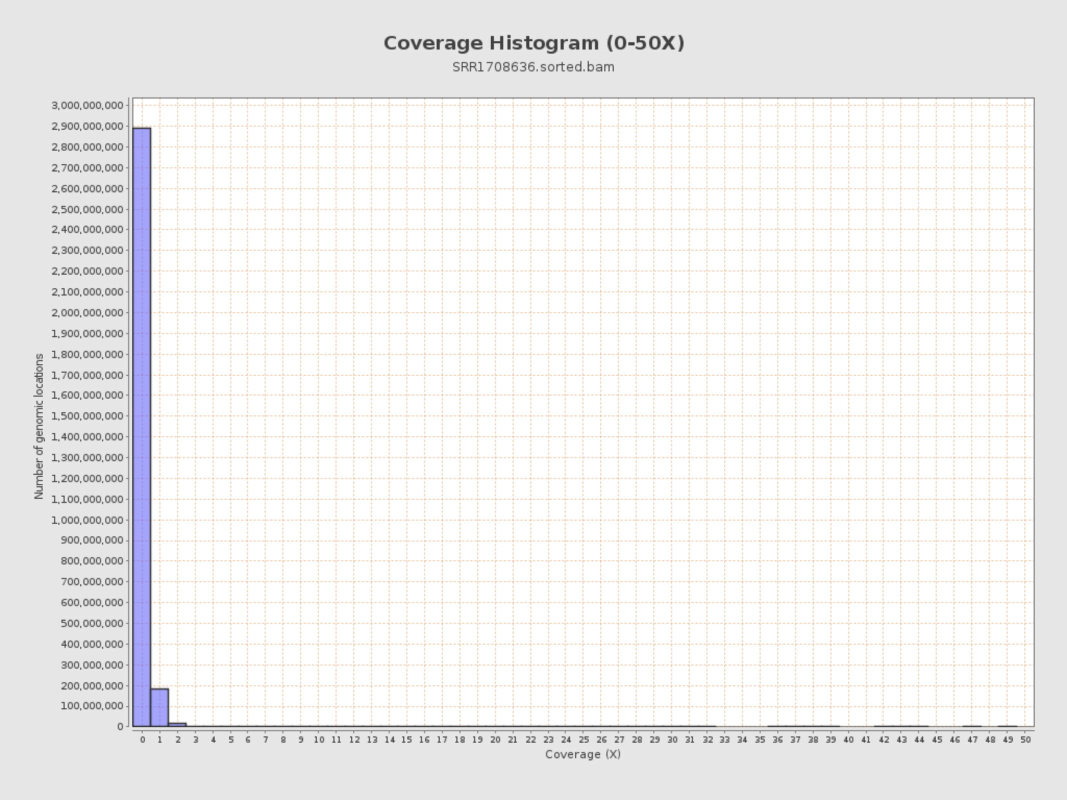
3. Results : Coverage across reference



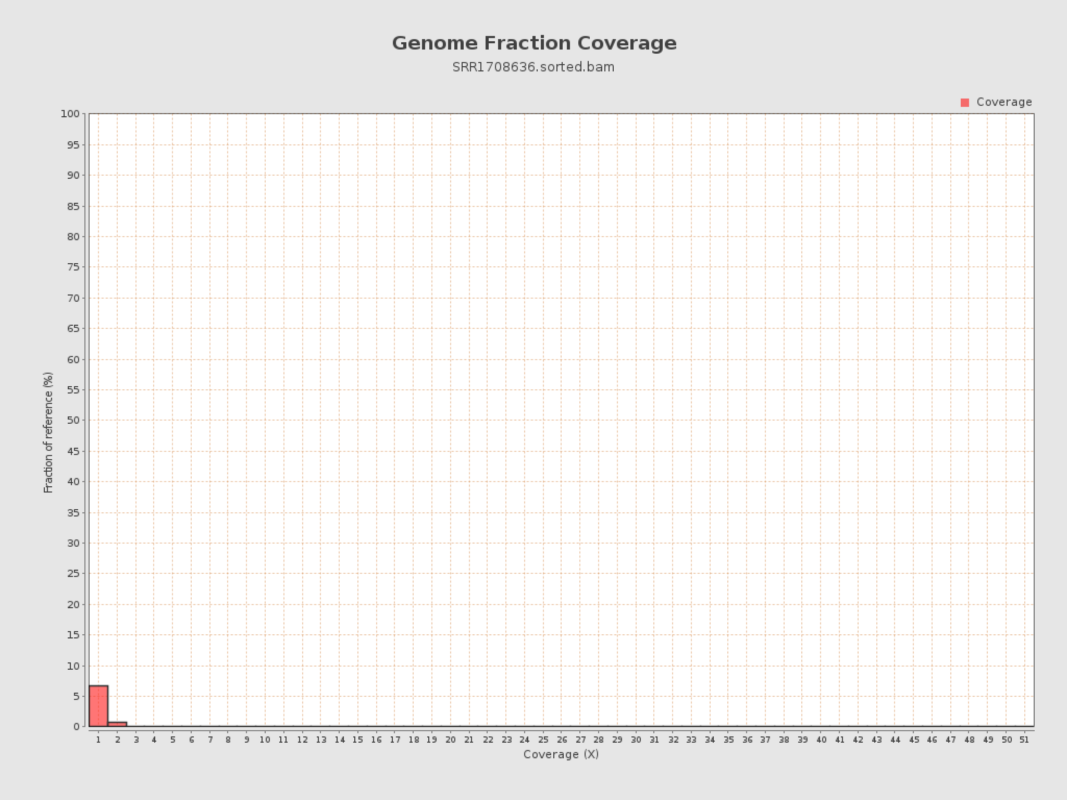
4. Results : Coverage Histogram



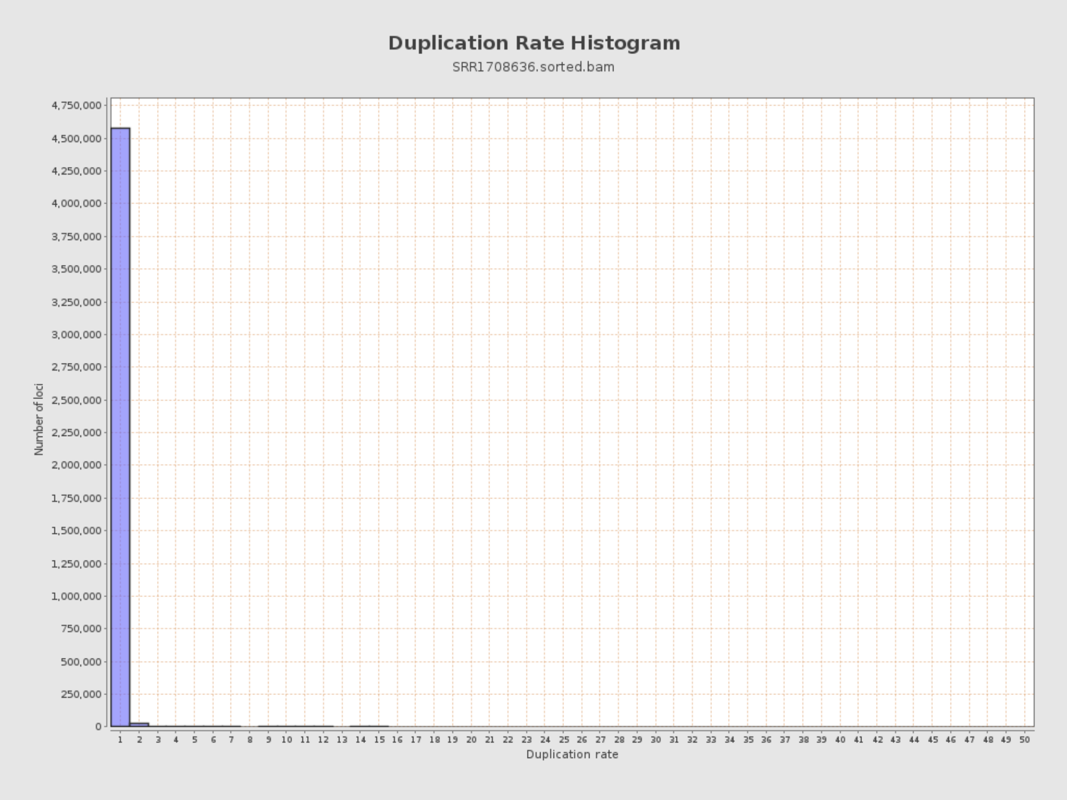
5. Results : Coverage Histogram (0-50X)



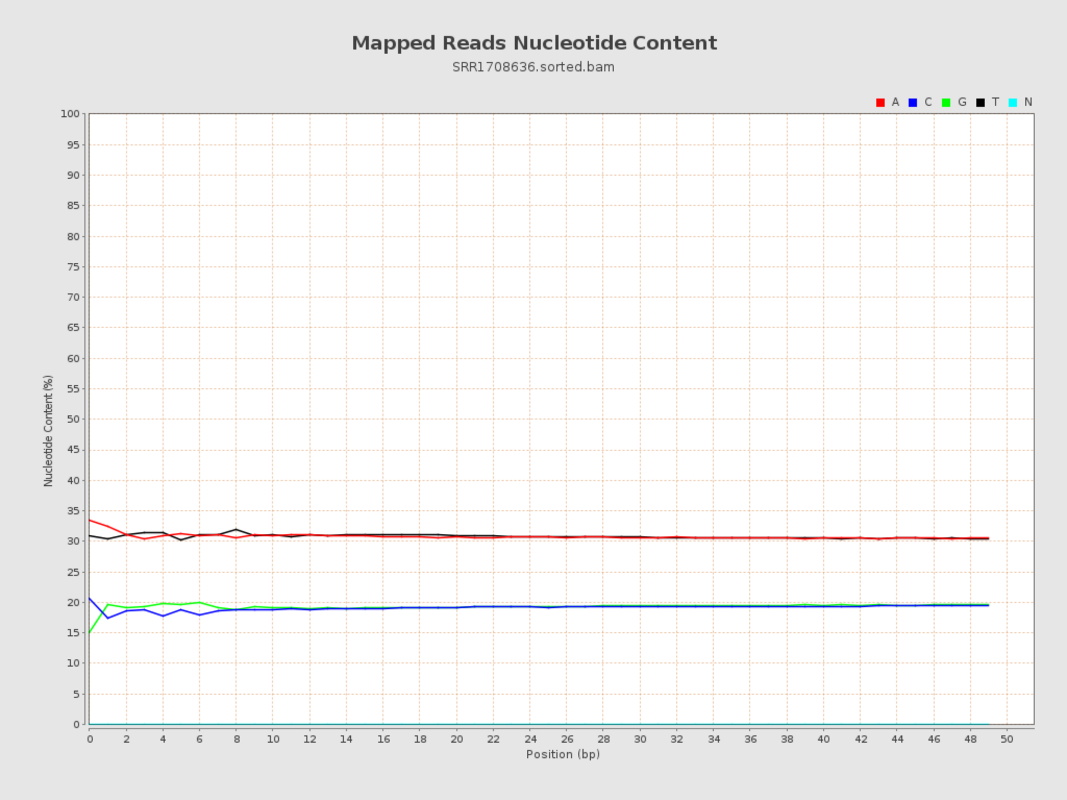
6. Results : Genome Fraction Coverage



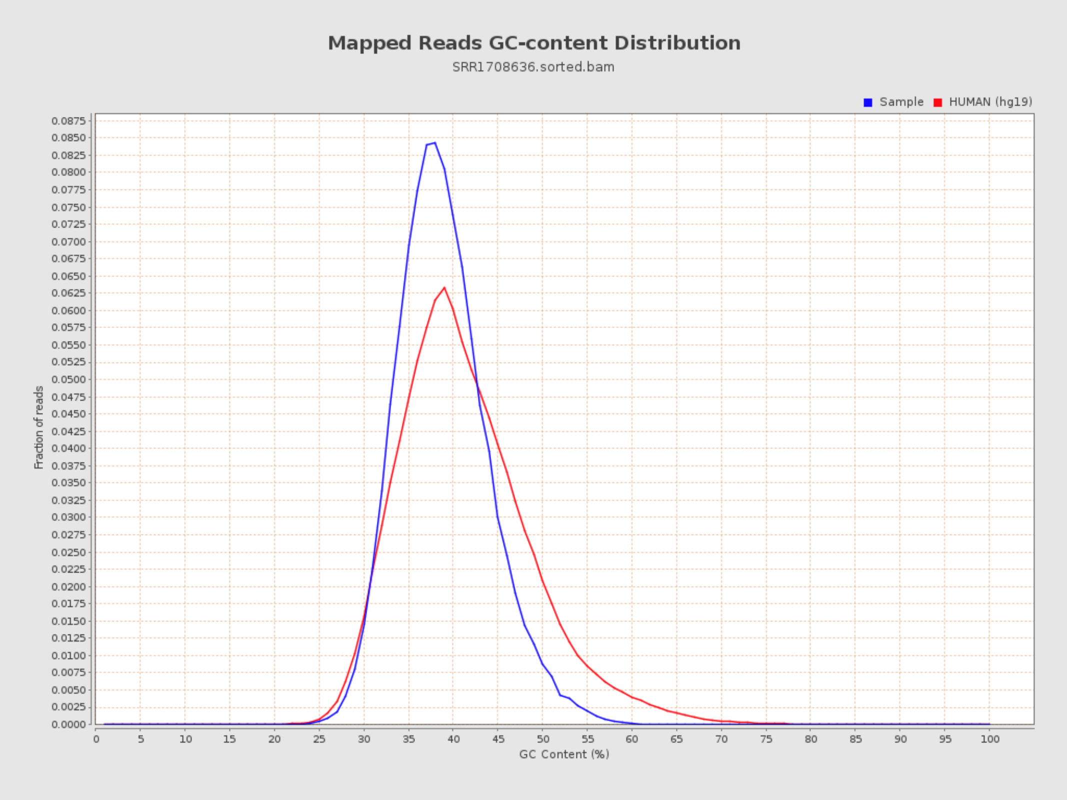
7. Results : Duplication Rate Histogram



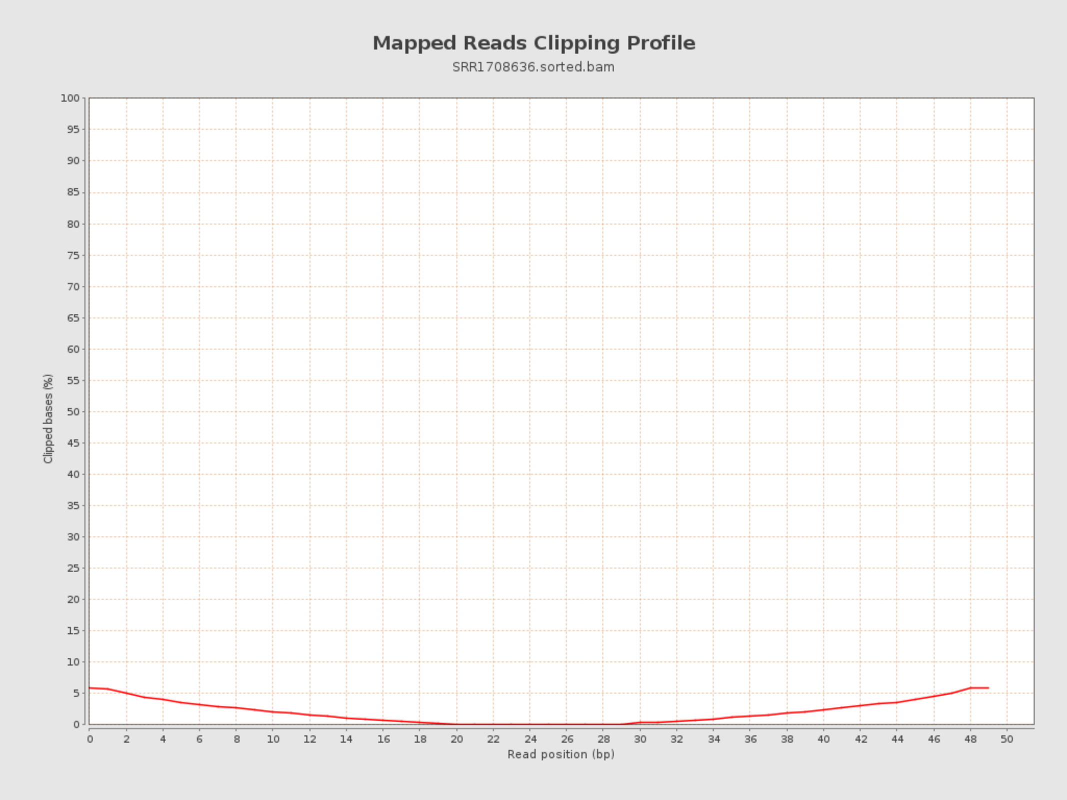
8. Results : Mapped Reads Nucleotide Content



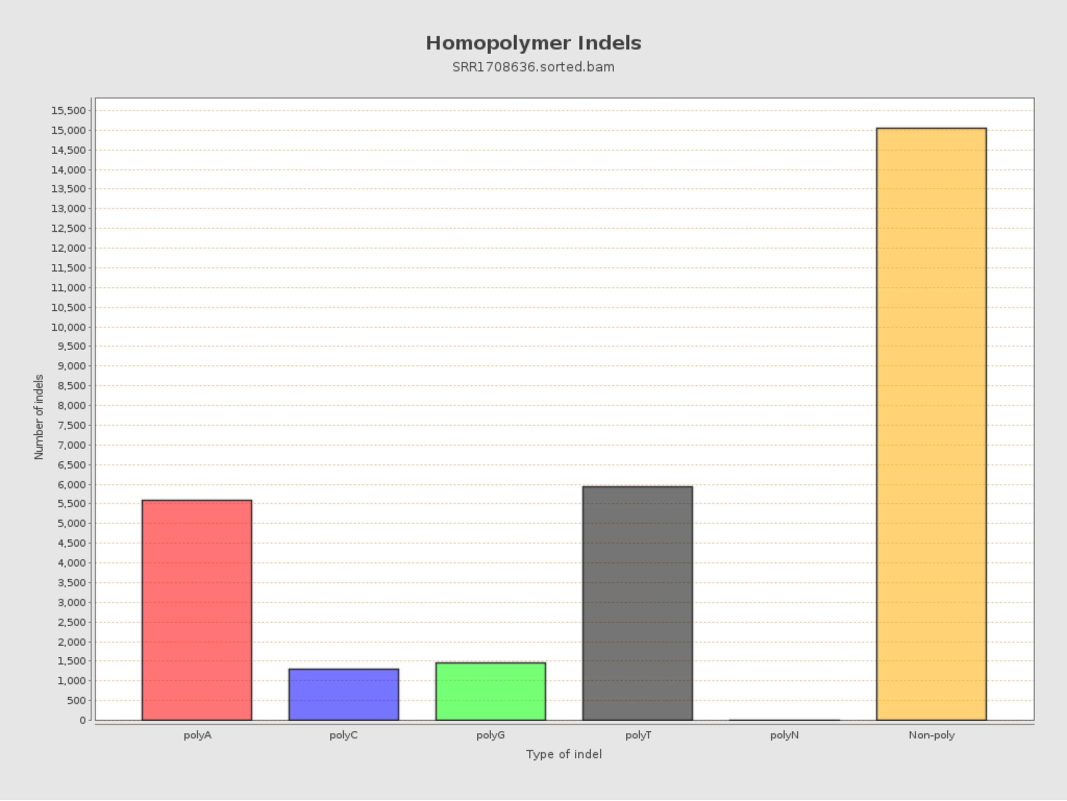
9. Results : Mapped Reads GC-content Distribution



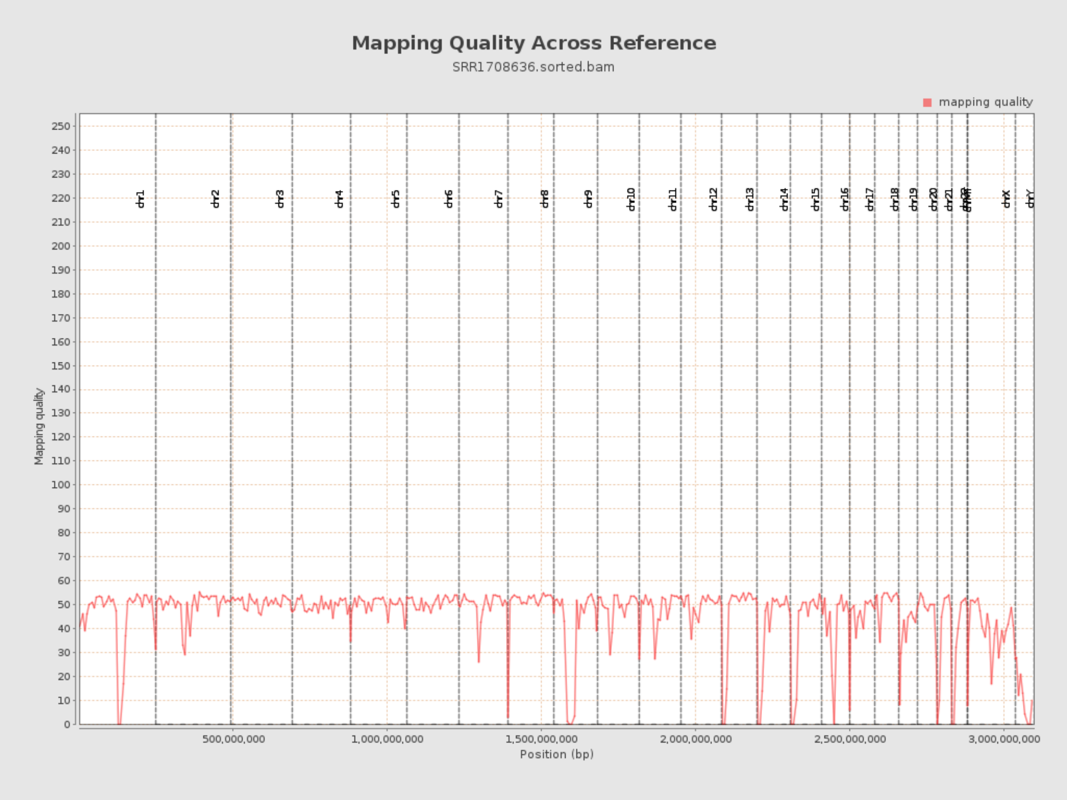
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram