Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:22:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708536.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_SRR1708536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708536.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:22:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,281,356
Mapped reads	23,711,124 / 97.65%
Unmapped reads	570,232 / 2.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	700 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	327,075 / 1.35%
Duplication rate	1.36%
Clipped reads	294,407 / 1.21%

2.2. ACGT Content

Number/percentage of A's	367,046,150 / 31.04%
Number/percentage of C's	222,180,320 / 18.79%
Number/percentage of T's	367,252,879 / 31.05%
Number/percentage of G's	226,154,937 / 19.12%
Number/percentage of N's	40,994 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	0.3821

Standard Deviation	0.7838

2.4. Mapping Quality

Mean Mapping Quality	46.62

2.5. Mismatches and indels

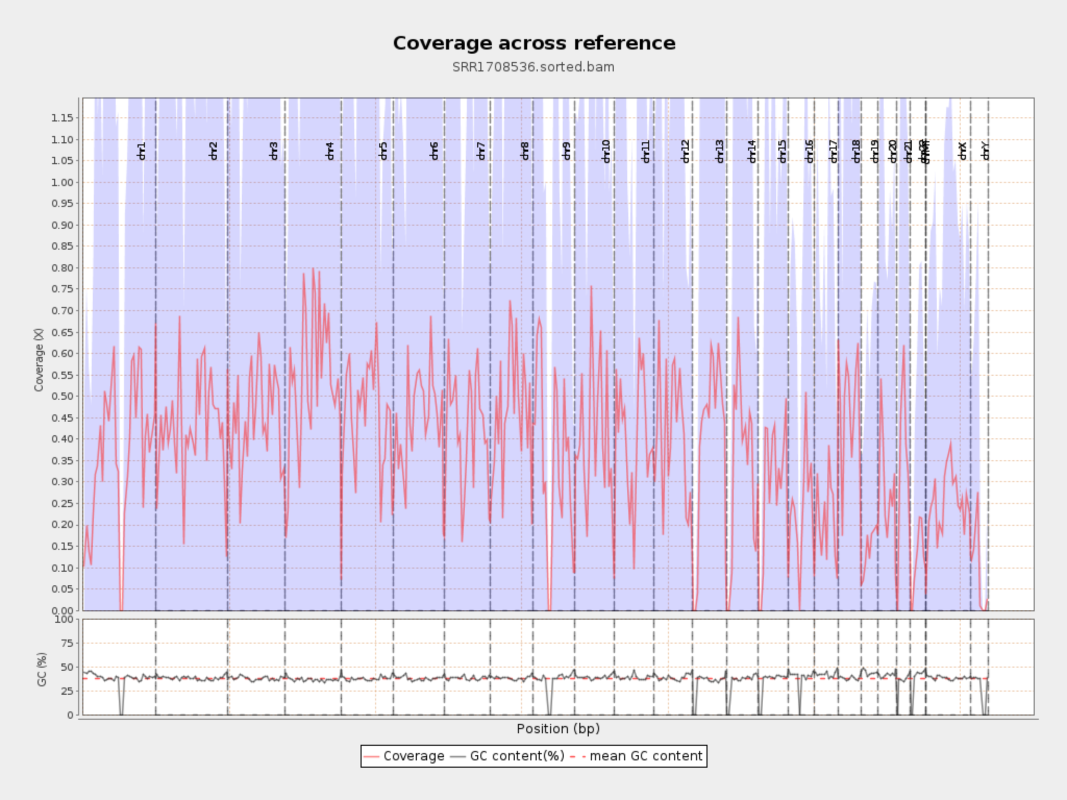
General error rate	0.2%
Mismatches	2,229,136
Insertions	70,254
Mapped reads with at least one insertion	0.3%
Deletions	62,947
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.15%

2.6. Chromosome stats

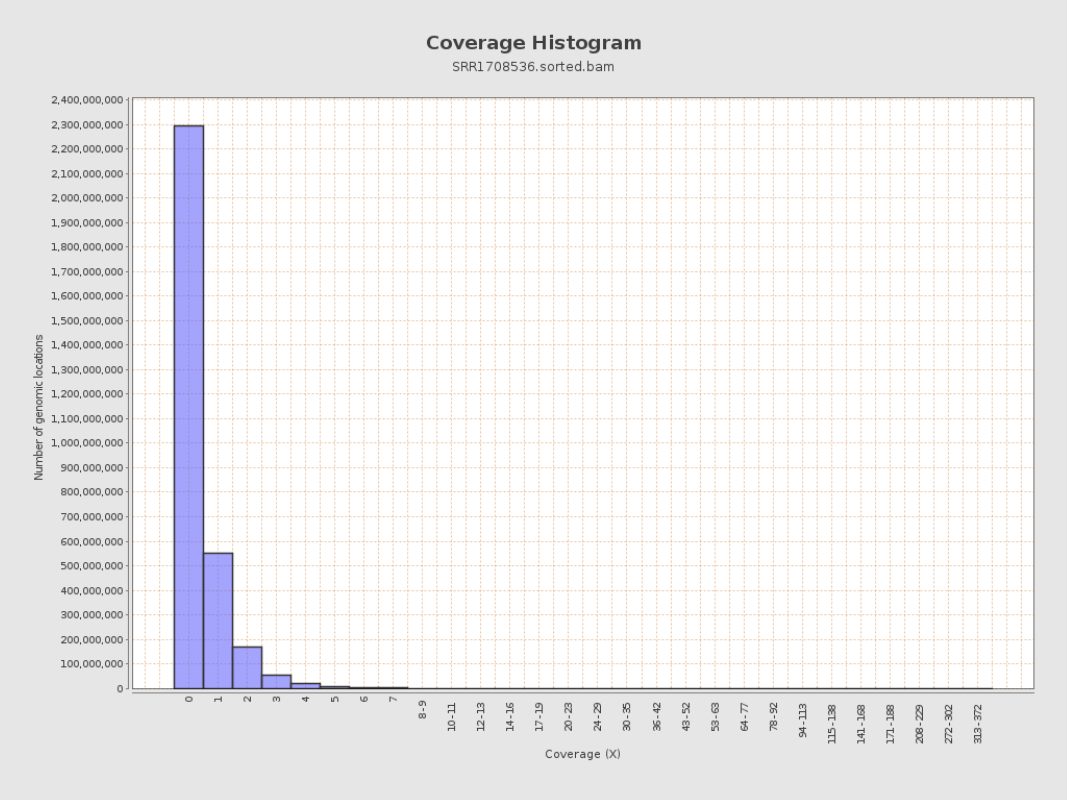
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	90421970	0.3628	0.778
chr2	243199373	103769190	0.4267	0.8197
chr3	198022430	89551548	0.4522	0.837
chr4	191154276	104520084	0.5468	0.9369
chr5	180915260	81873033	0.4525	0.8356
chr6	171115067	77772388	0.4545	0.8434
chr7	159138663	67204614	0.4223	0.8168

chr8	146364022	68414178	0.4674	0.8621
chr9	141213431	50748097	0.3594	0.7592
chr10	135534747	56034003	0.4134	0.8032
chr11	135006516	54469983	0.4035	0.8015
chr12	133851895	54523893	0.4073	0.803
chr13	115169878	47030481	0.4084	0.8106
chr14	107349540	36560327	0.3406	0.748
chr15	102531392	29853777	0.2912	0.6905
chr16	90354753	20860304	0.2309	0.5909
chr17	81195210	17781696	0.219	0.5826
chr18	78077248	36959936	0.4734	0.8528
chr19	59128983	8604600	0.1455	0.4537
chr20	63025520	18590302	0.295	0.6791
chr21	48129895	15765958	0.3276	0.7543
chr22	51304566	6182252	0.1205	0.42
chrMT	16571	650	0.0392	0.2068
chrX	155270560	39534262	0.2546	0.6125
chrY	59373566	5752267	0.0969	0.386

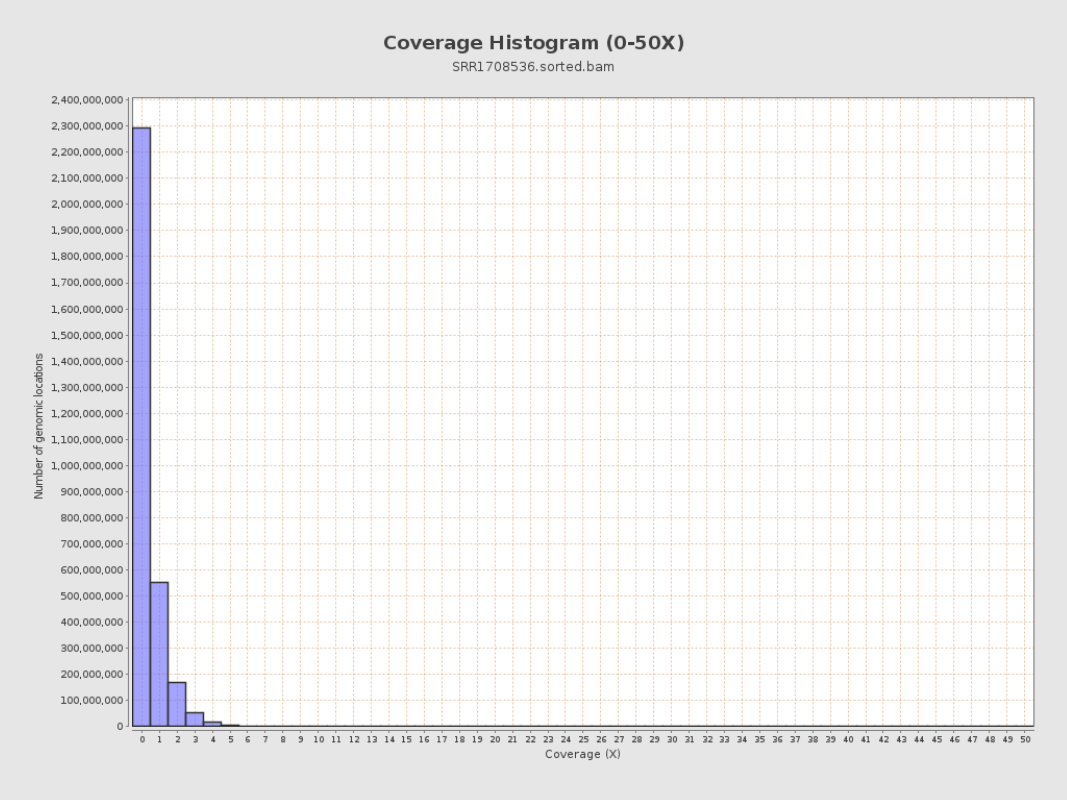
3. Results : Coverage across reference



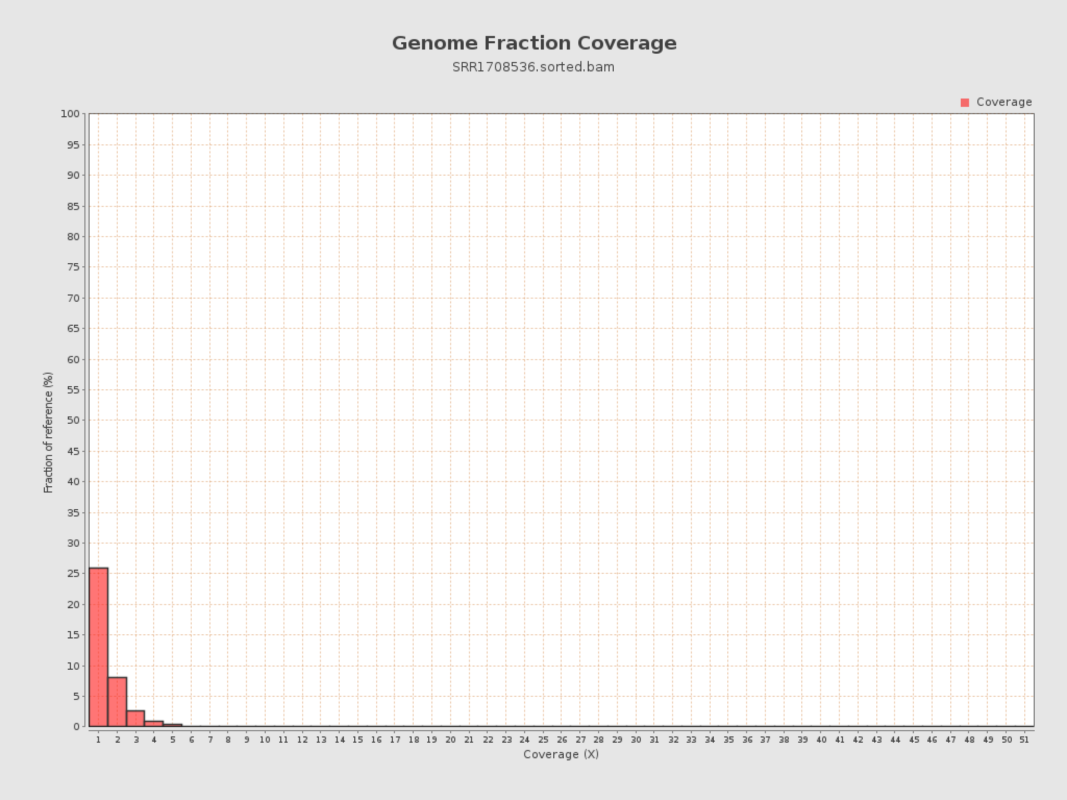
4. Results : Coverage Histogram



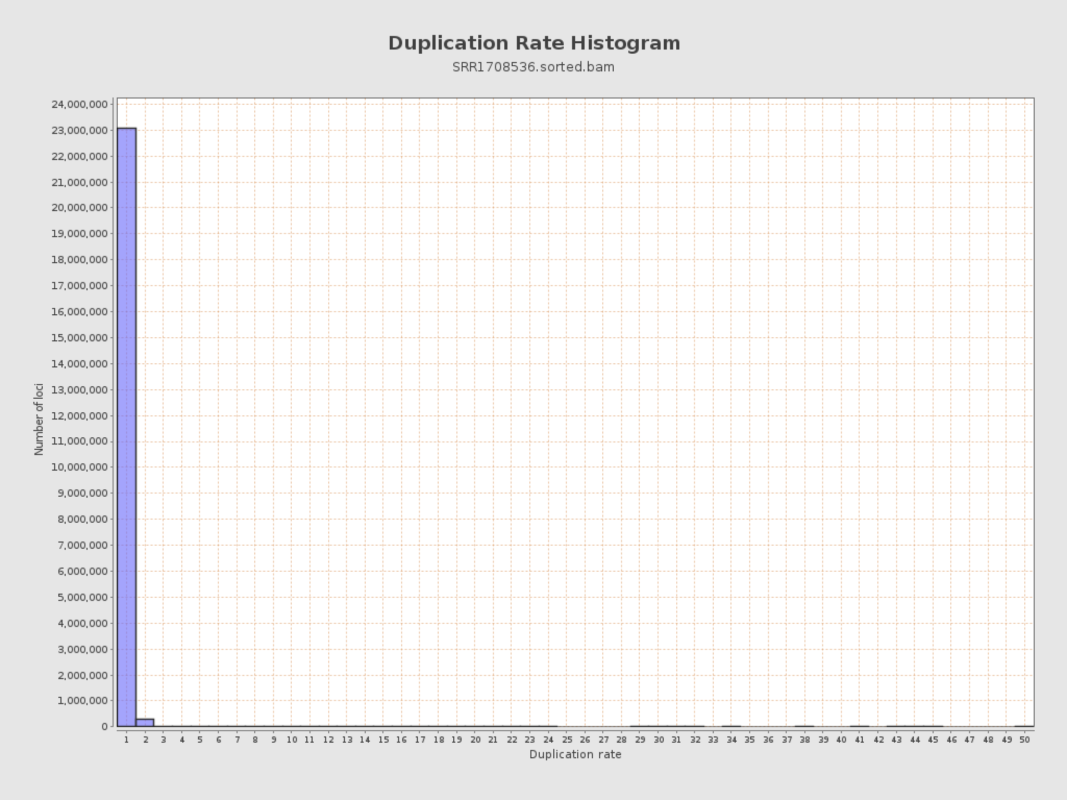
5. Results : Coverage Histogram (0-50X)



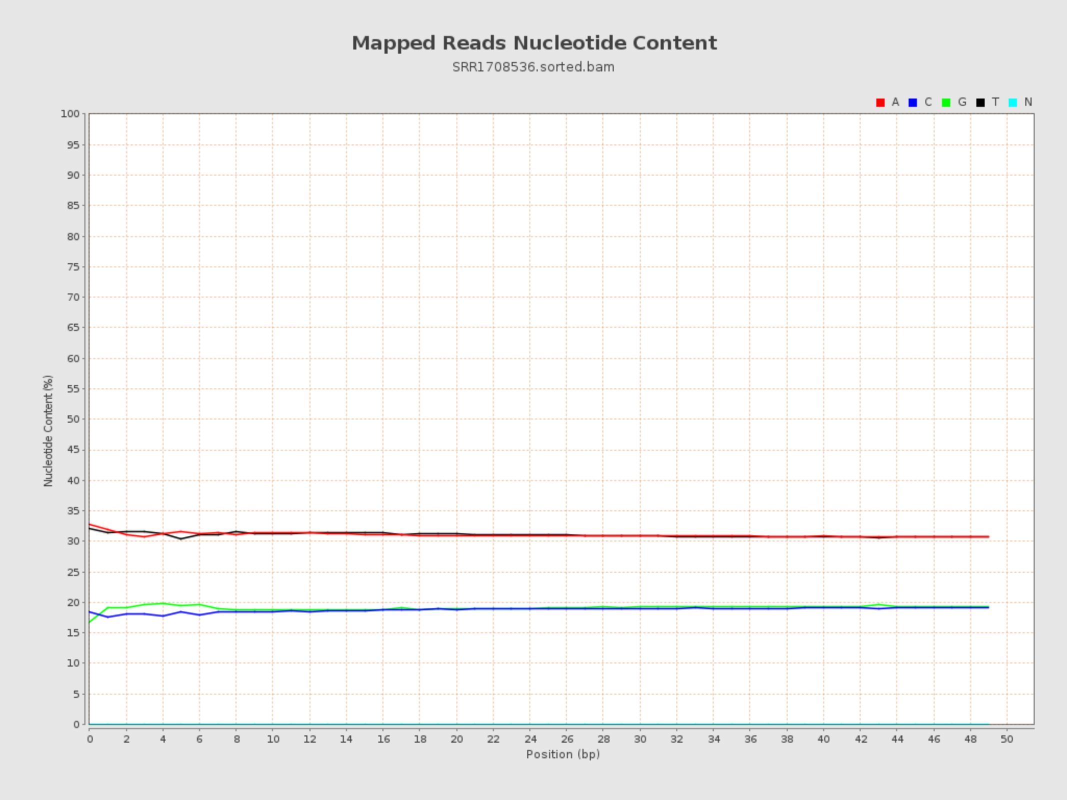
6. Results : Genome Fraction Coverage



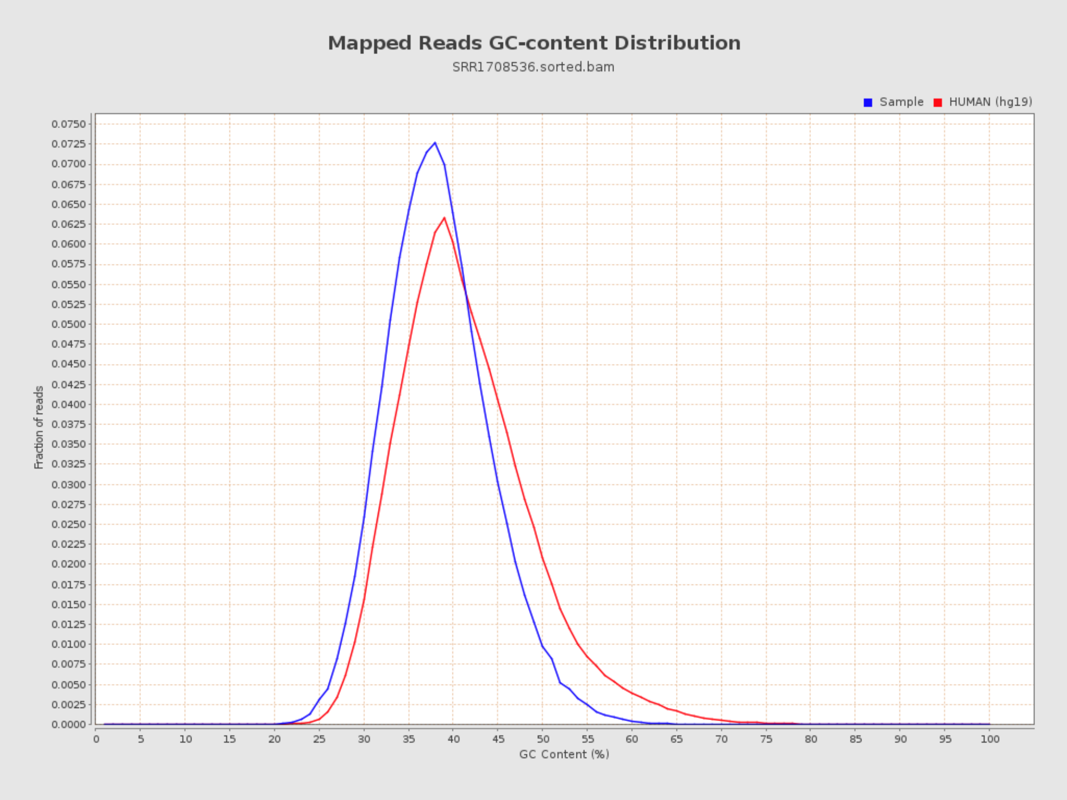
7. Results : Duplication Rate Histogram



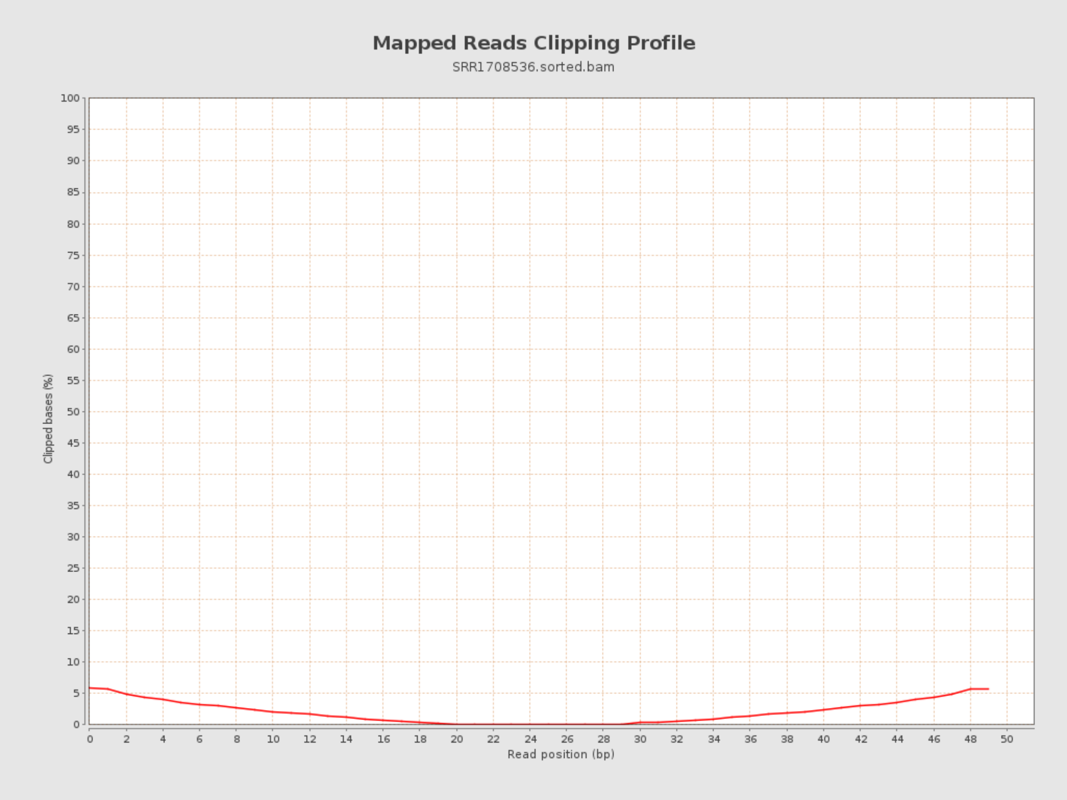
8. Results : Mapped Reads Nucleotide Content



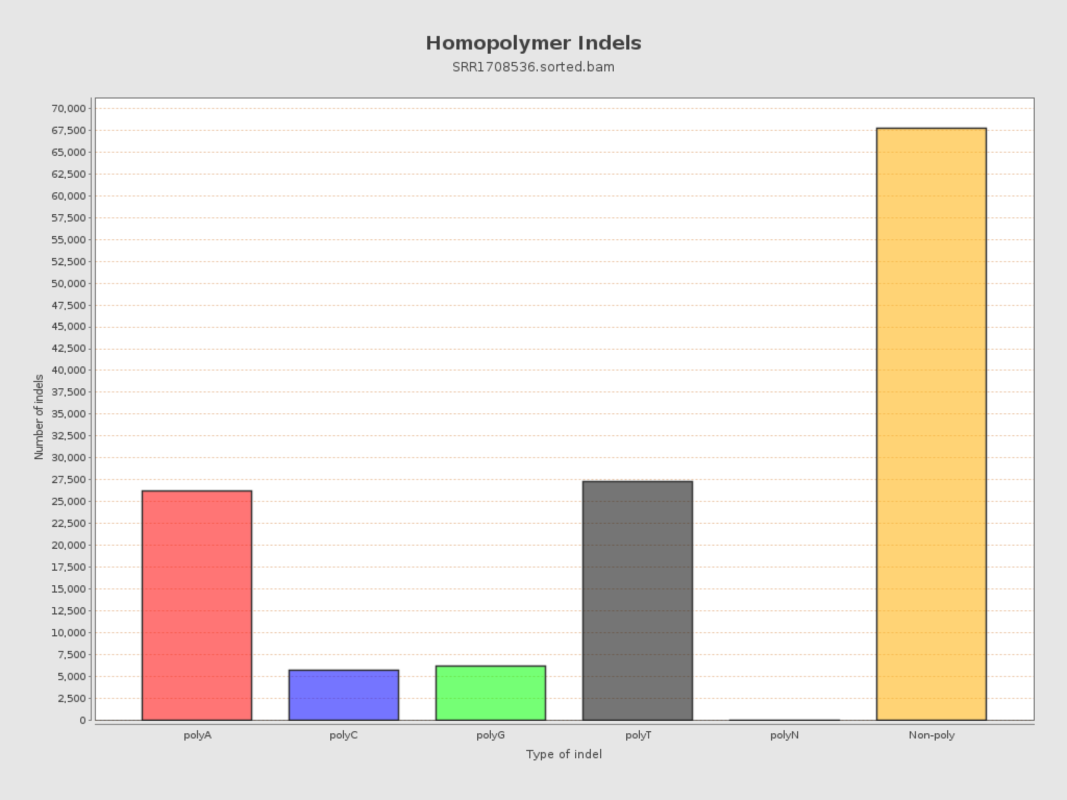
9. Results : Mapped Reads GC-content Distribution



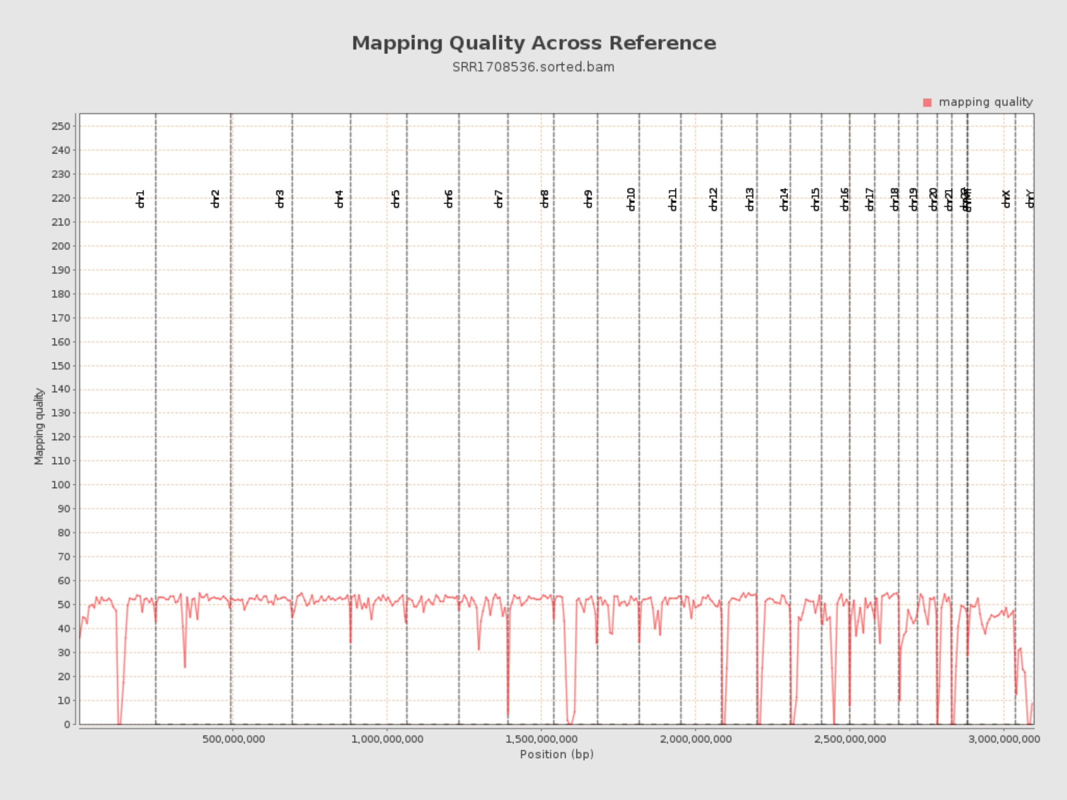
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram