Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708560.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_SRR1708560 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708560.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708560.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,062,949
Mapped reads	3,334,434 / 82.07%
Unmapped reads	728,515 / 17.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	114 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,321 / 0.38%
Duplication rate	0.46%
Clipped reads	46,264 / 1.14%

2.2. ACGT Content

Number/percentage of A's	51,546,449 / 31%
Number/percentage of C's	31,511,327 / 18.95%
Number/percentage of T's	51,366,203 / 30.9%
Number/percentage of G's	31,828,632 / 19.14%
Number/percentage of N's	6,723 / 0%
GC Percentage	38.1%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.2385

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

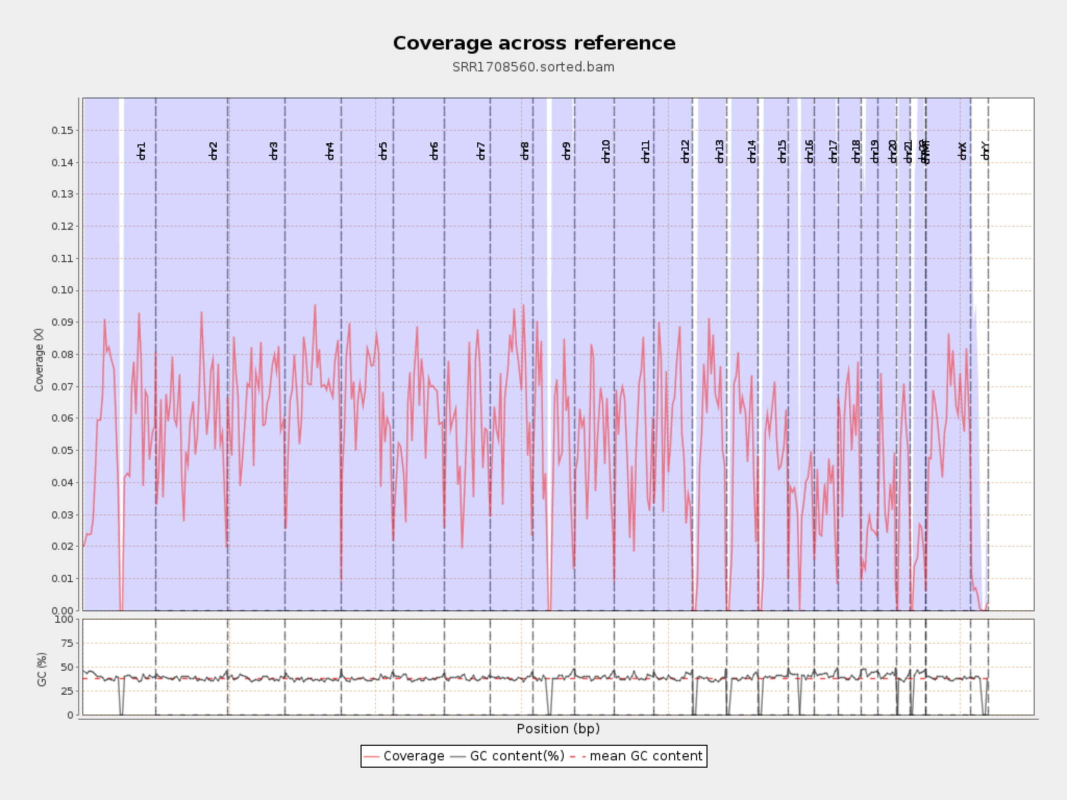
General error rate	0.17%
Mismatches	263,670
Insertions	11,468
Mapped reads with at least one insertion	0.34%
Deletions	9,049
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.41%

2.6. Chromosome stats

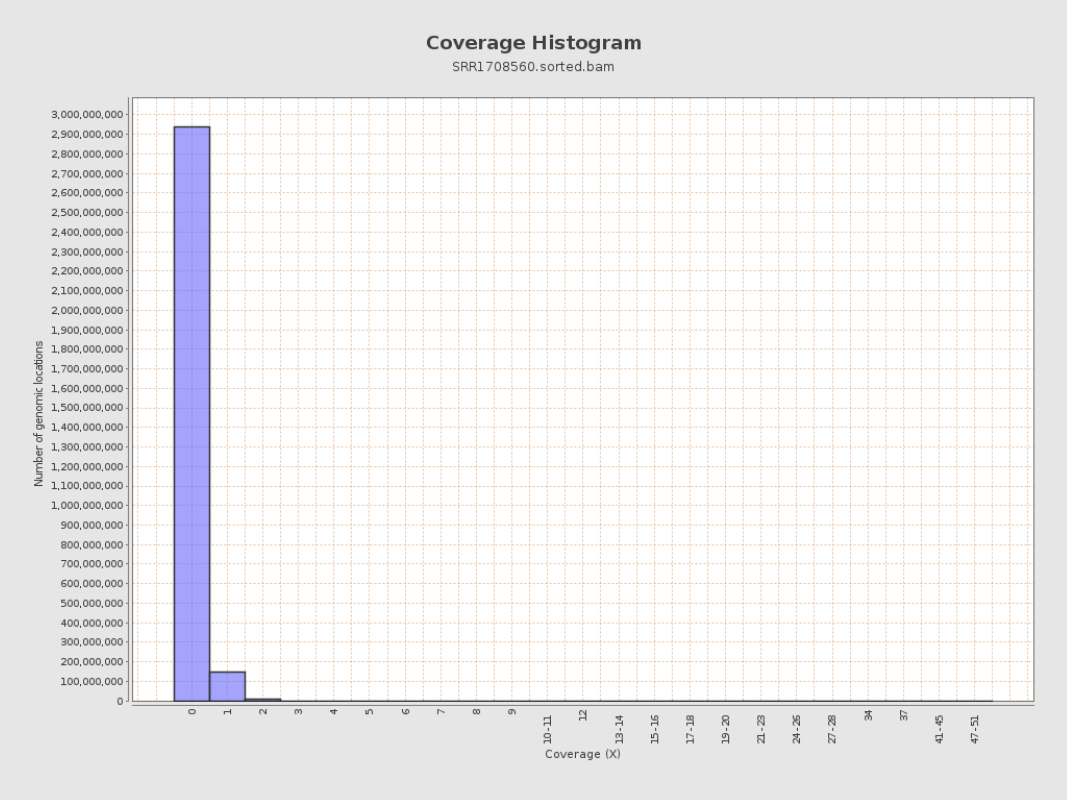
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13254024	0.0532	0.2385
chr2	243199373	14056728	0.0578	0.2465
chr3	198022430	13048383	0.0659	0.2631
chr4	191154276	13405773	0.0701	0.2716
chr5	180915260	11744706	0.0649	0.2612
chr6	171115067	10364193	0.0606	0.2527
chr7	159138663	8816066	0.0554	0.242

chr8	146364022	9722352	0.0664	0.2642
chr9	141213431	7193834	0.0509	0.2329
chr10	135534747	7300537	0.0539	0.2379
chr11	135006516	7203214	0.0534	0.2381
chr12	133851895	7463946	0.0558	0.2426
chr13	115169878	6241555	0.0542	0.2395
chr14	107349540	5291704	0.0493	0.2285
chr15	102531392	4604429	0.0449	0.2182
chr16	90354753	2873240	0.0318	0.183
chr17	81195210	2645742	0.0326	0.1853
chr18	78077248	4600346	0.0589	0.2487
chr19	59128983	1301911	0.022	0.1518
chr20	63025520	2577771	0.0409	0.2073
chr21	48129895	2071011	0.043	0.2148
chr22	51304566	807069	0.0157	0.1283
chrMT	16571	100	0.006	0.0774
chrX	155270560	9464081	0.061	0.2536
chrY	59373566	221961	0.0037	0.0634

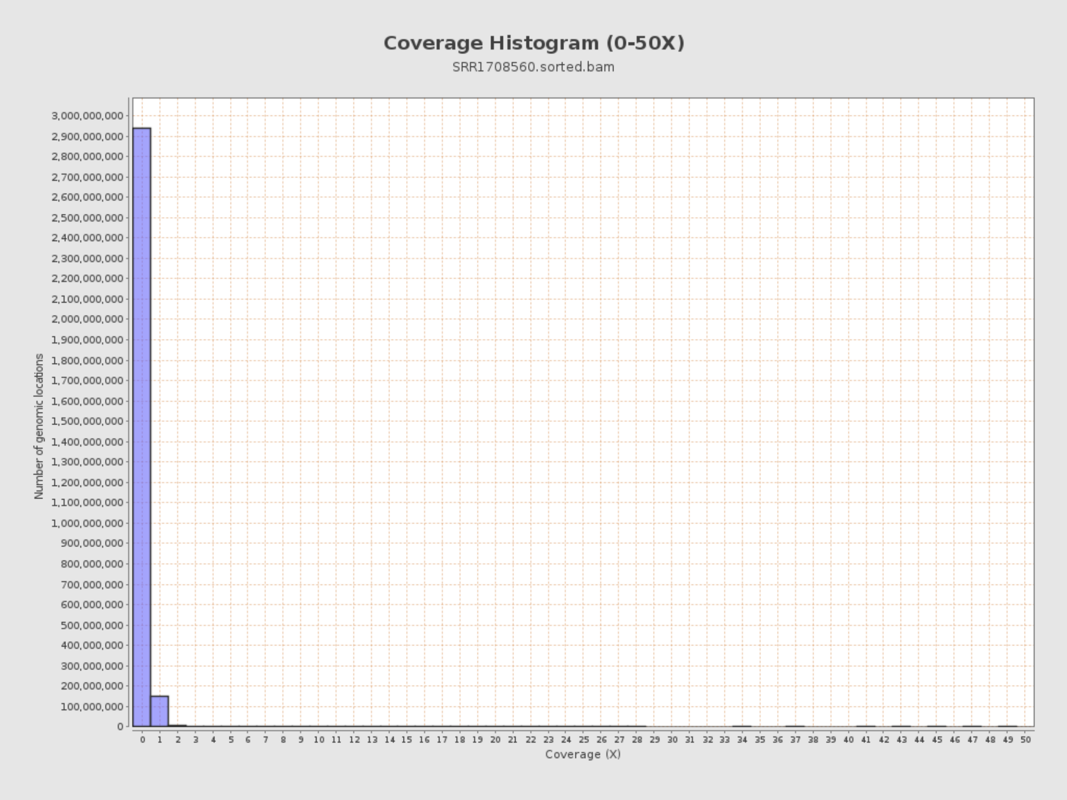
3. Results : Coverage across reference



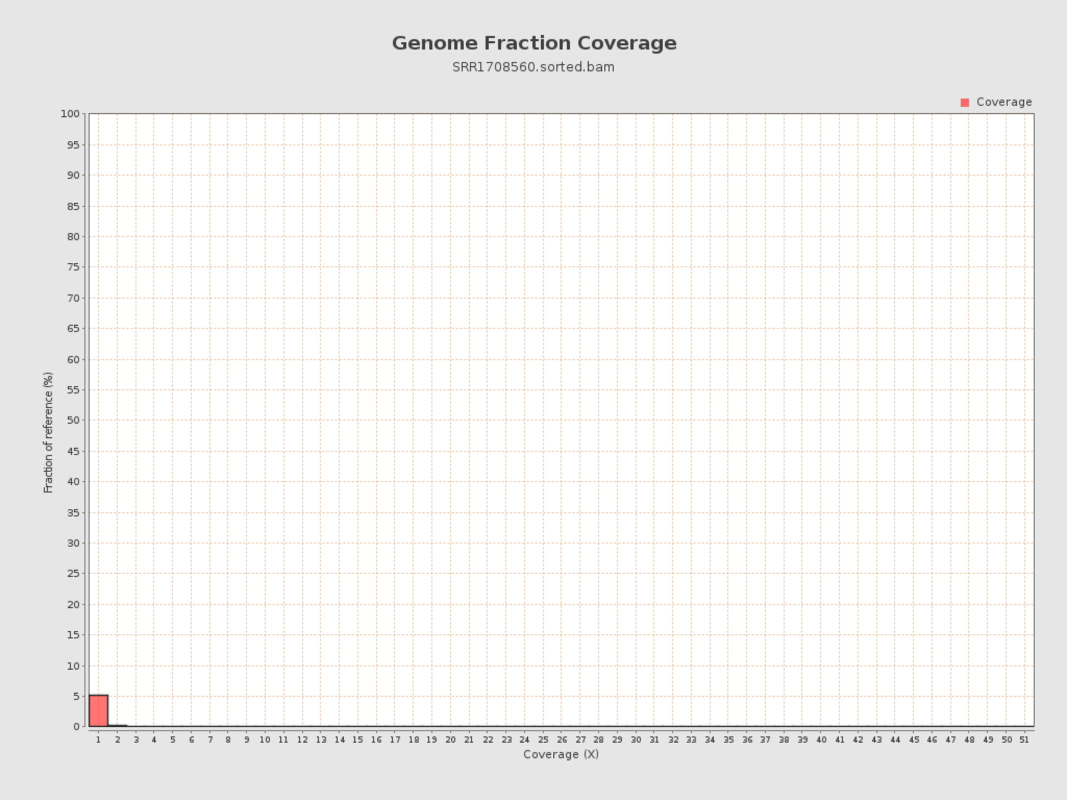
4. Results : Coverage Histogram



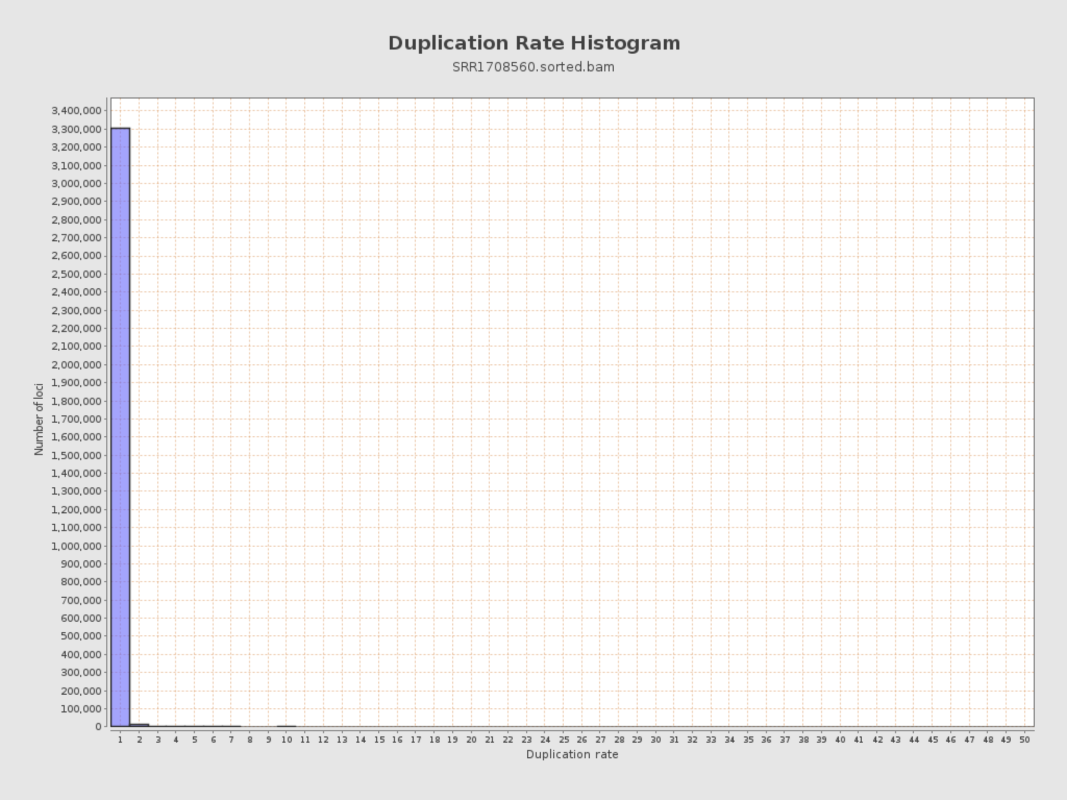
5. Results : Coverage Histogram (0-50X)



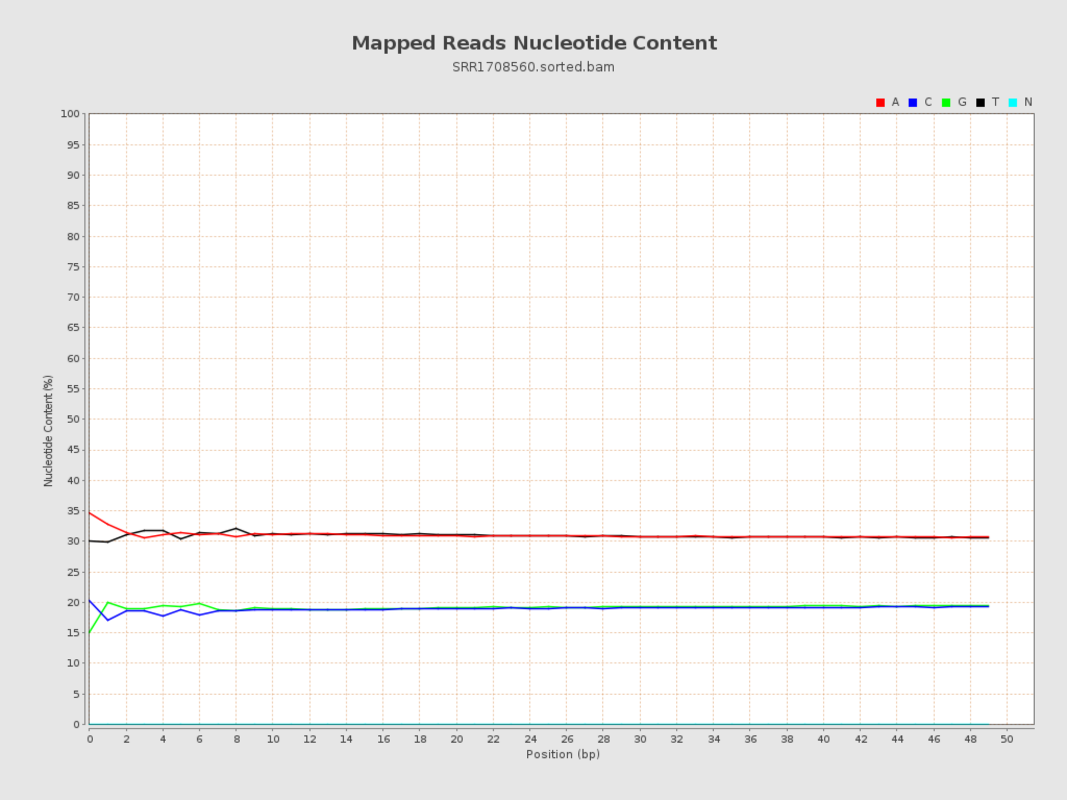
6. Results : Genome Fraction Coverage



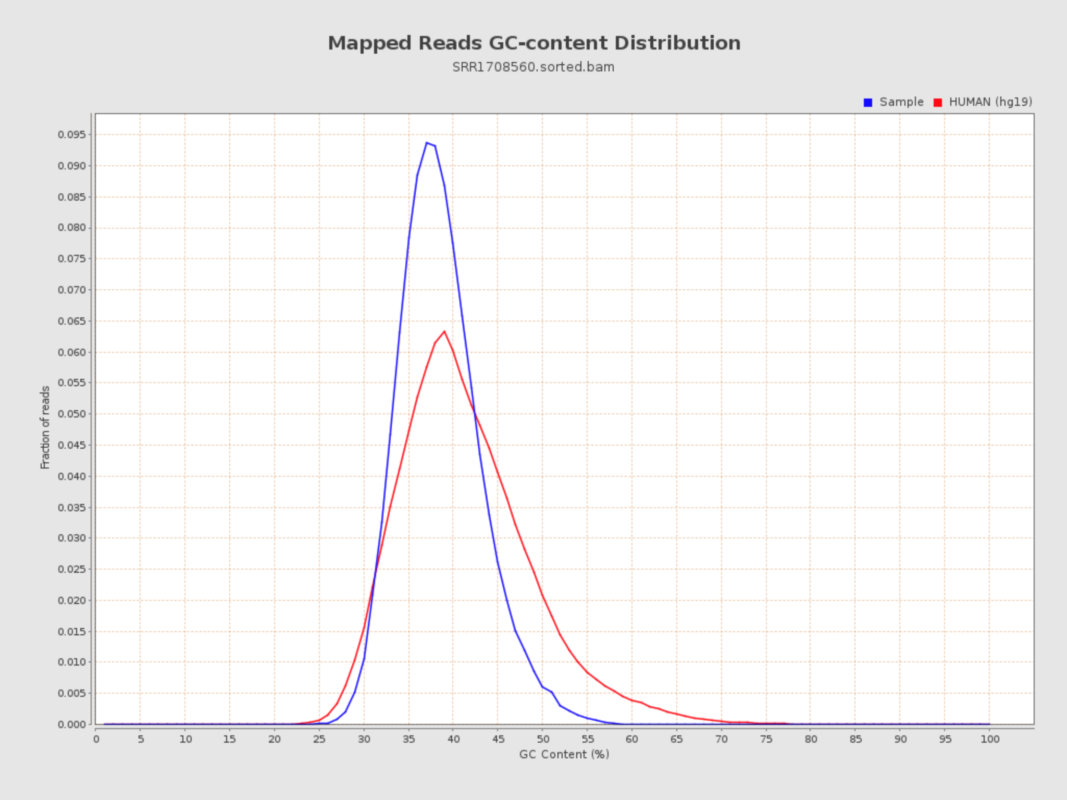
7. Results : Duplication Rate Histogram



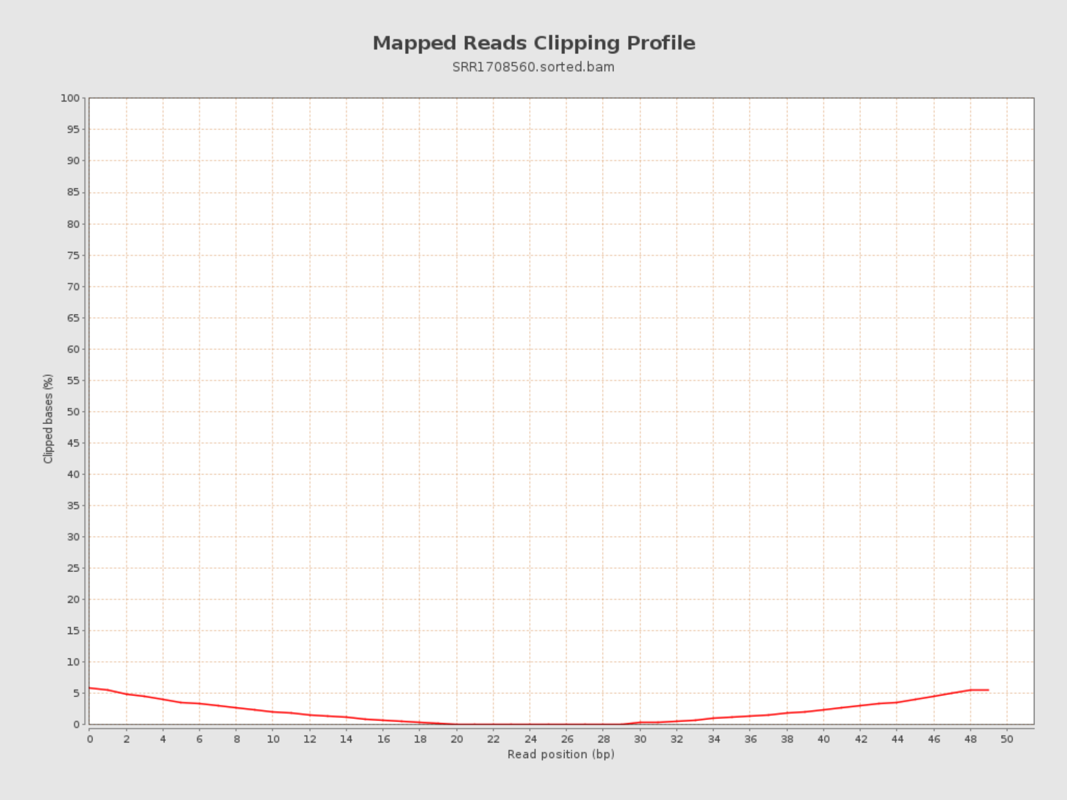
8. Results : Mapped Reads Nucleotide Content



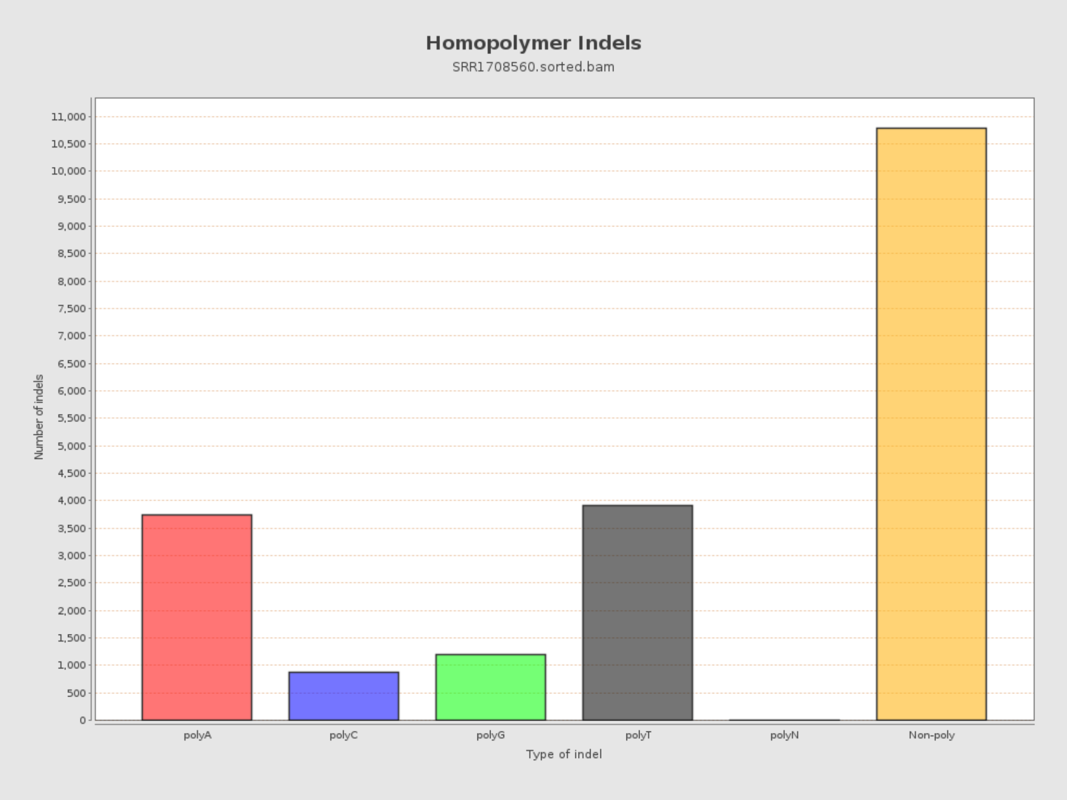
9. Results : Mapped Reads GC-content Distribution



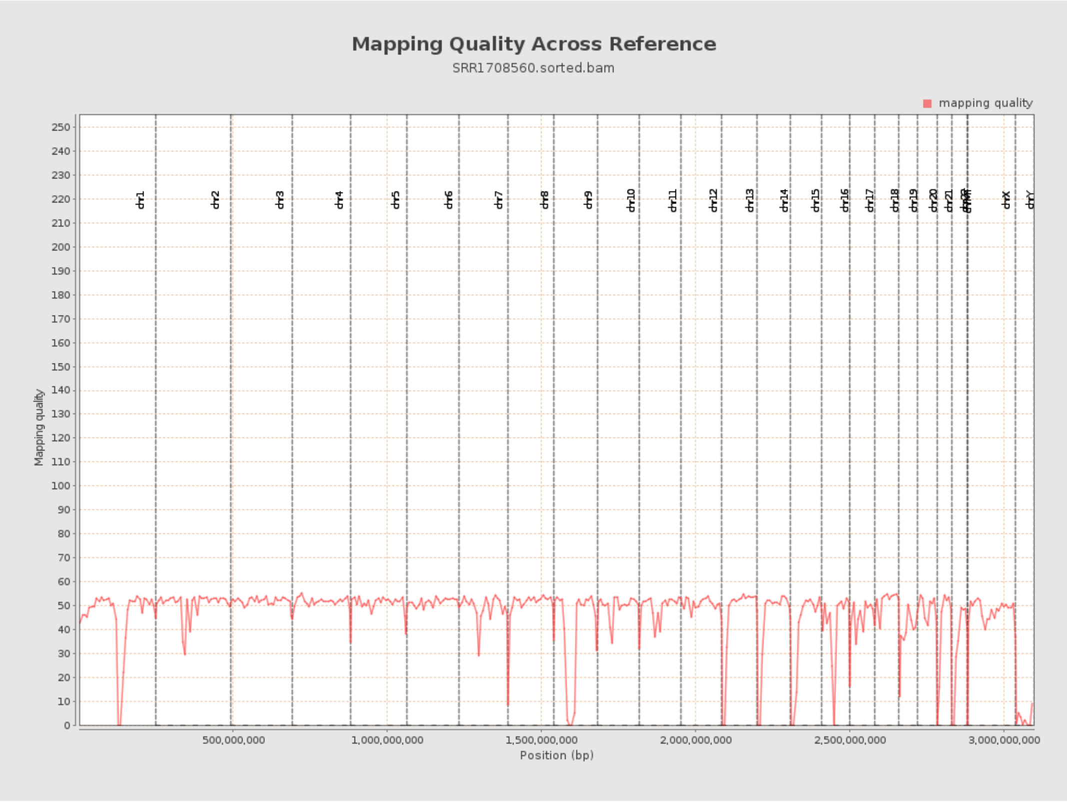
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram