Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:19:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708638.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_SRR1708638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:19:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,718,811
Mapped reads	3,427,646 / 92.17%
Unmapped reads	291,165 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	14,343 / 0.39%
Duplication rate	0.41%
Clipped reads	36,732 / 0.99%

2.2. ACGT Content

Number/percentage of A's	53,083,071 / 31.04%
Number/percentage of C's	32,340,156 / 18.91%
Number/percentage of T's	53,083,814 / 31.04%
Number/percentage of G's	32,514,493 / 19.01%
Number/percentage of N's	5,354 / 0%
GC Percentage	37.92%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.2417

2.4. Mapping Quality

Mean Mapping Quality	46.88

2.5. Mismatches and indels

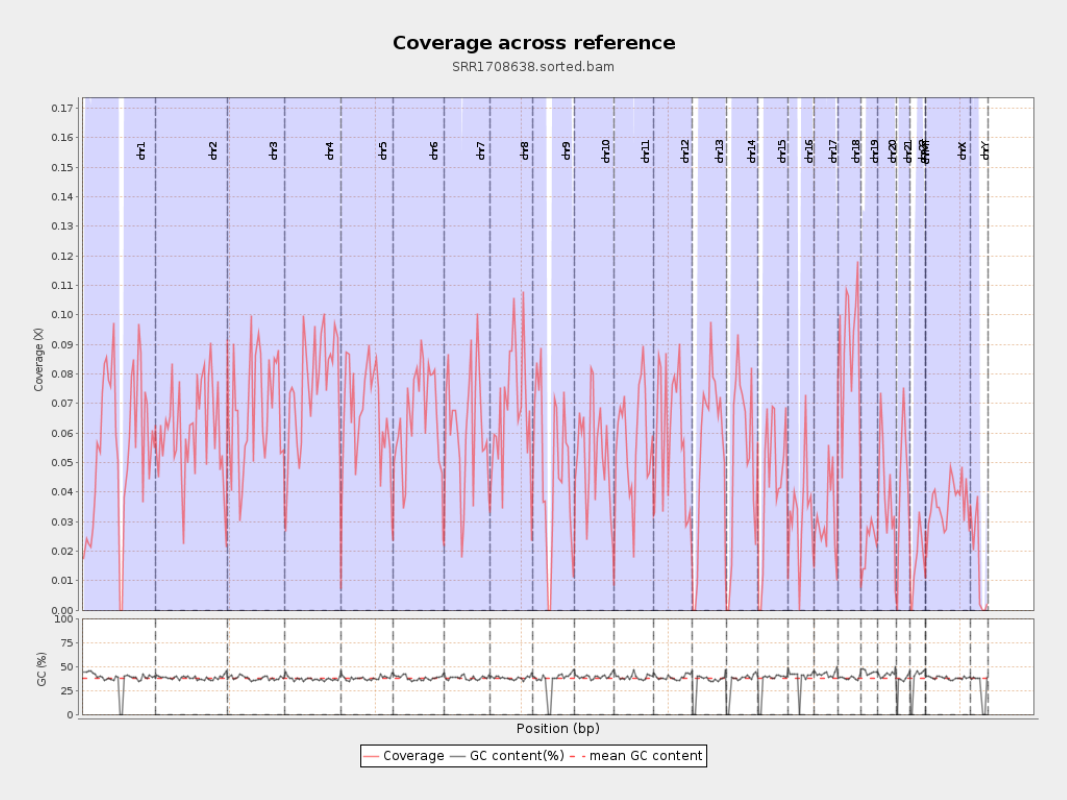
General error rate	0.17%
Mismatches	267,391
Insertions	11,437
Mapped reads with at least one insertion	0.33%
Deletions	9,605
Mapped reads with at least one deletion	0.28%
Homopolymer indels	48.79%

2.6. Chromosome stats

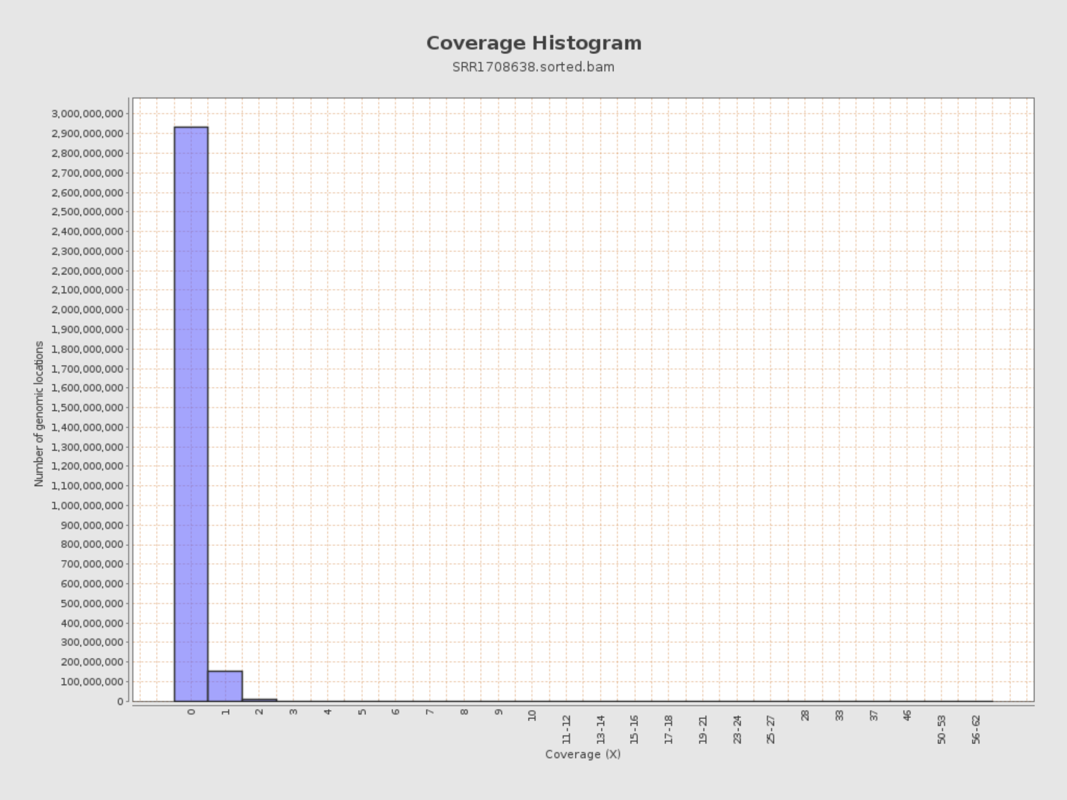
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13684602	0.0549	0.2425
chr2	243199373	14664464	0.0603	0.2512
chr3	198022430	13468639	0.068	0.2671
chr4	191154276	14503743	0.0759	0.2817
chr5	180915260	11900795	0.0658	0.2624
chr6	171115067	11280502	0.0659	0.2627
chr7	159138663	9659147	0.0607	0.2533

chr8	146364022	10016502	0.0684	0.268
chr9	141213431	6845293	0.0485	0.2265
chr10	135534747	7191960	0.0531	0.2358
chr11	135006516	7753865	0.0574	0.2463
chr12	133851895	7812029	0.0584	0.2482
chr13	115169878	6428858	0.0558	0.2426
chr14	107349540	5586031	0.052	0.2352
chr15	102531392	4426436	0.0432	0.2133
chr16	90354753	2935328	0.0325	0.1847
chr17	81195210	2580653	0.0318	0.1832
chr18	78077248	7025259	0.09	0.3092
chr19	59128983	1330637	0.0225	0.1529
chr20	63025520	2584567	0.041	0.2077
chr21	48129895	2013332	0.0418	0.2119
chr22	51304566	860711	0.0168	0.1324
chrMT	16571	450	0.0272	0.1801
chrX	155270560	5595414	0.036	0.1933
chrY	59373566	894113	0.0151	0.1263

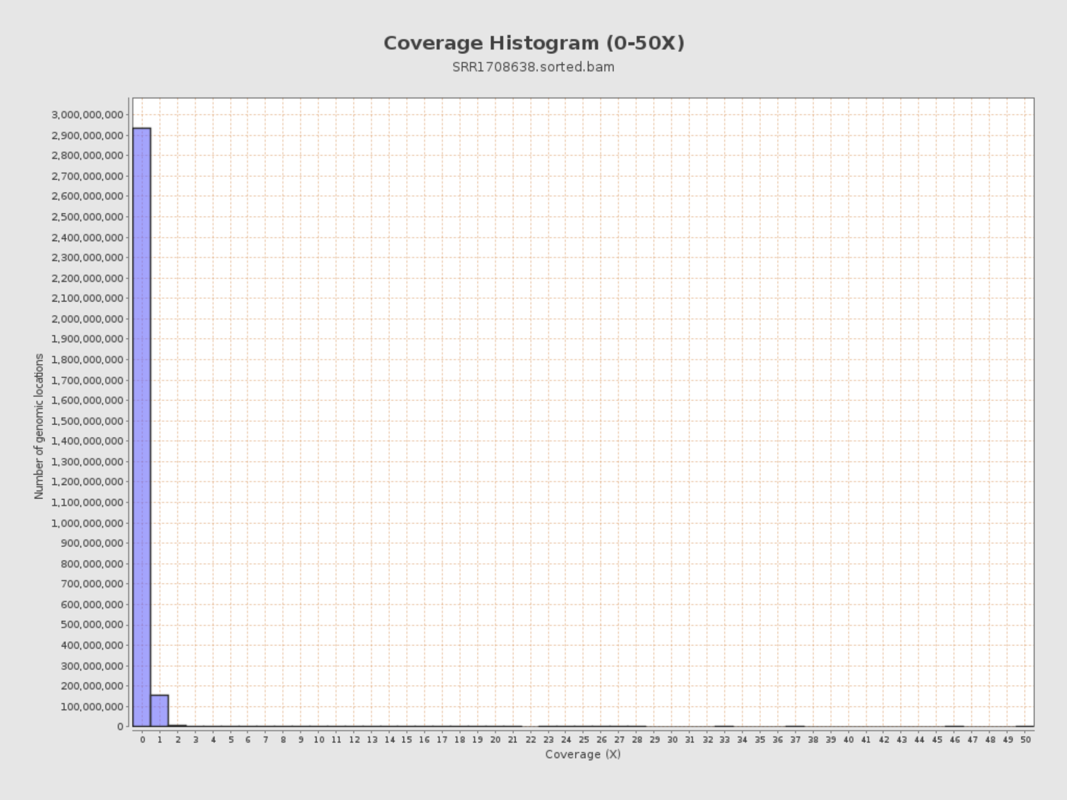
3. Results : Coverage across reference



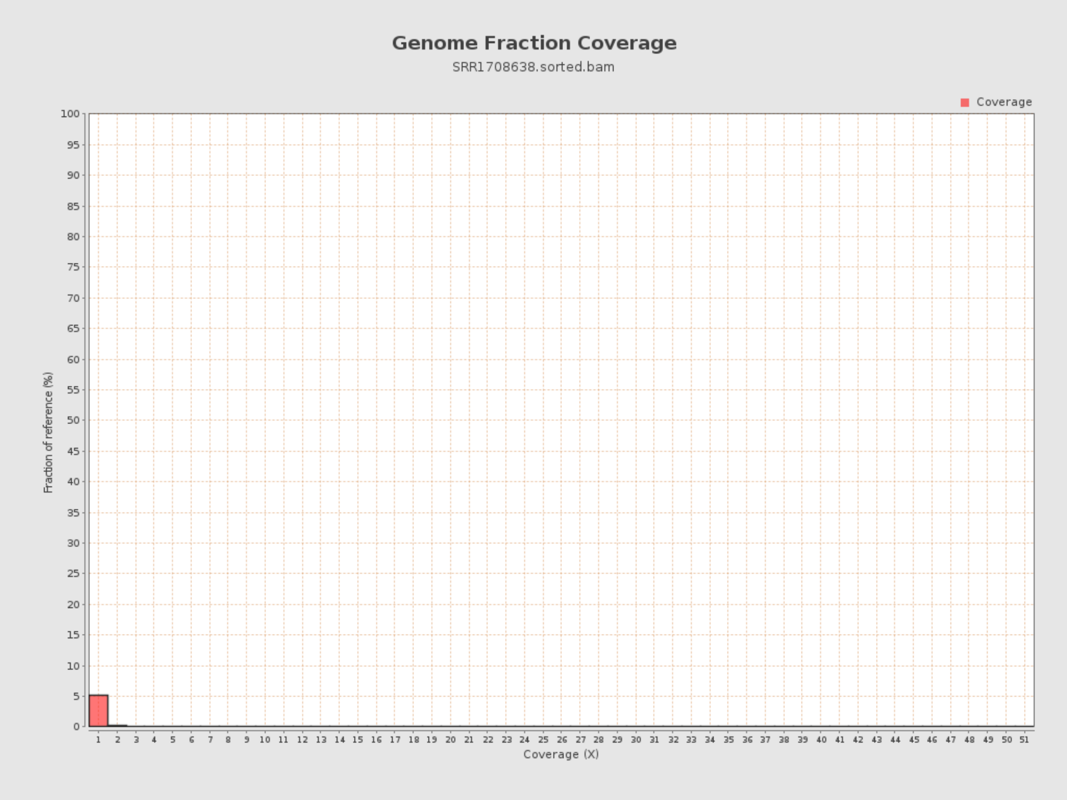
4. Results : Coverage Histogram



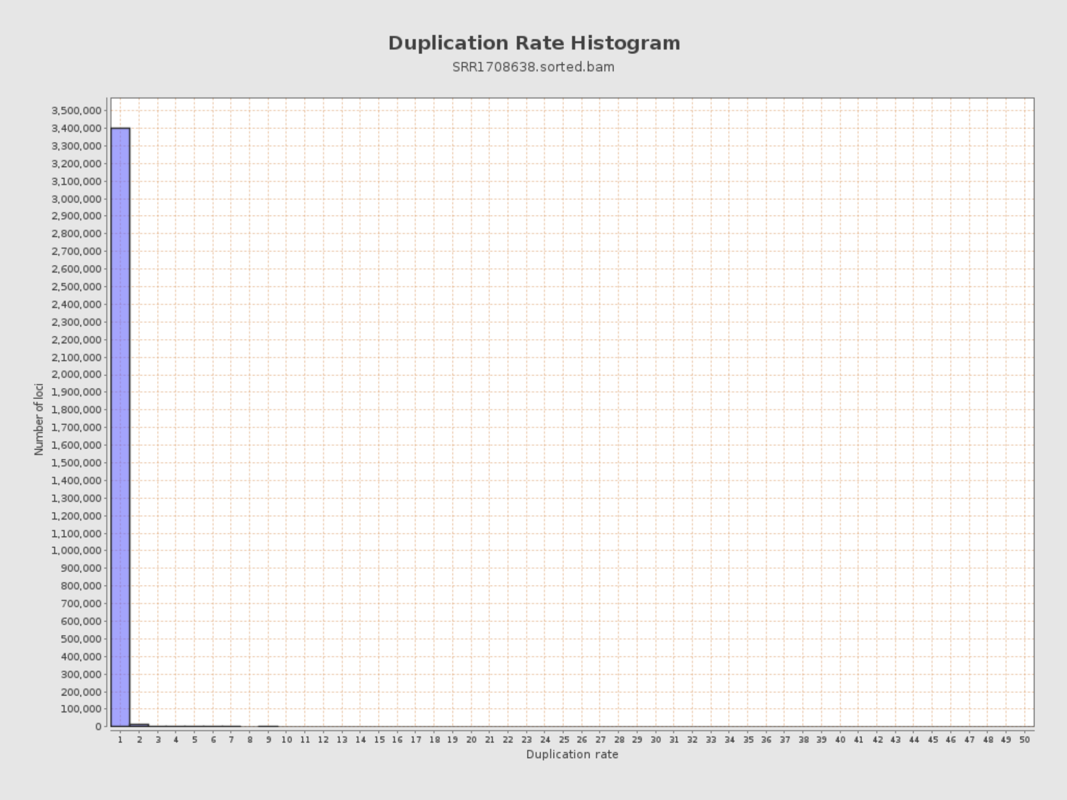
5. Results : Coverage Histogram (0-50X)



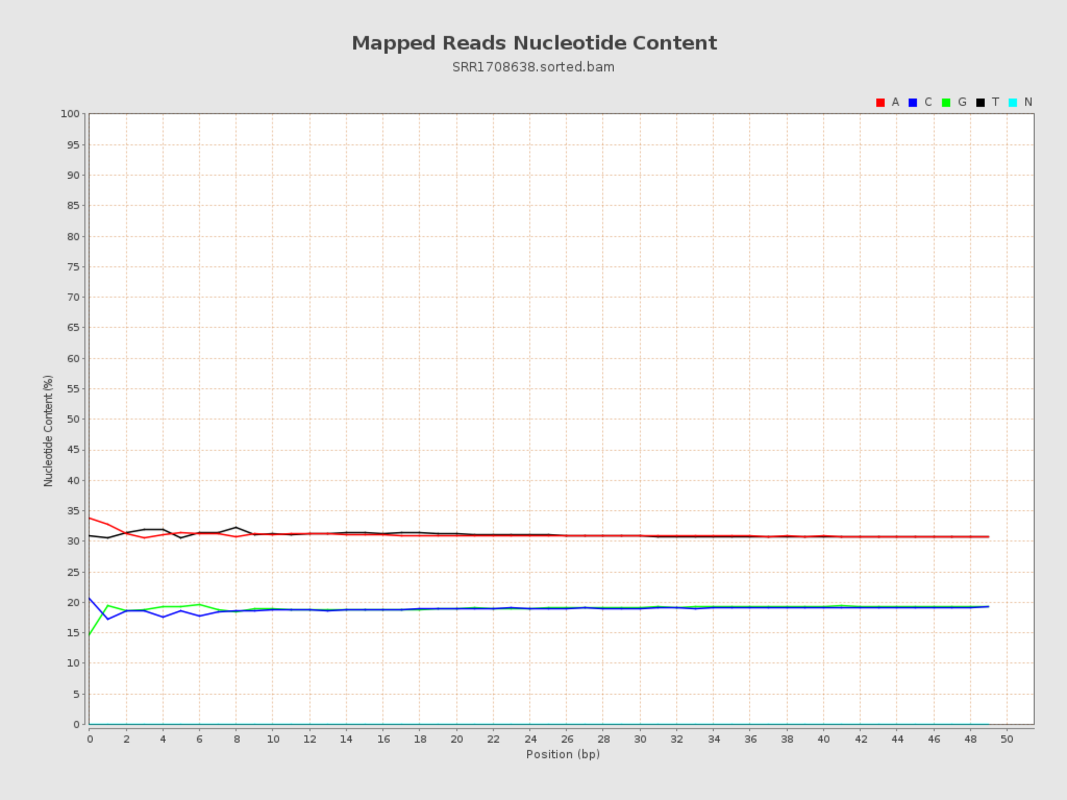
6. Results : Genome Fraction Coverage



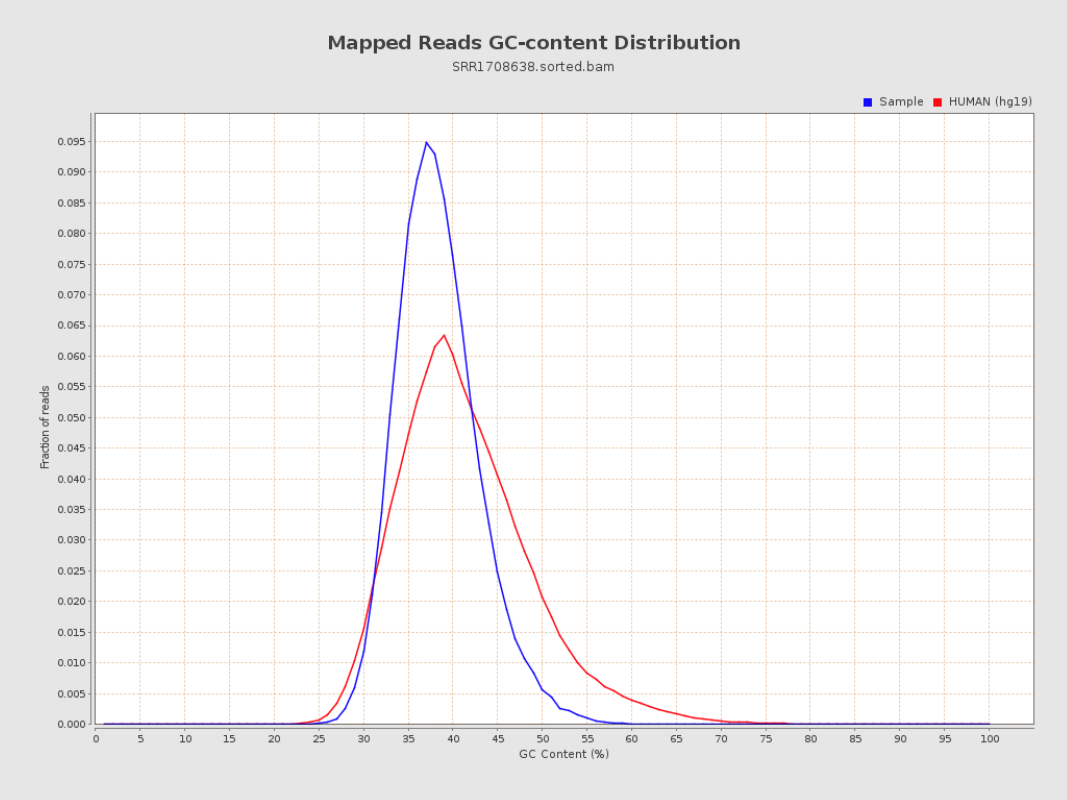
7. Results : Duplication Rate Histogram



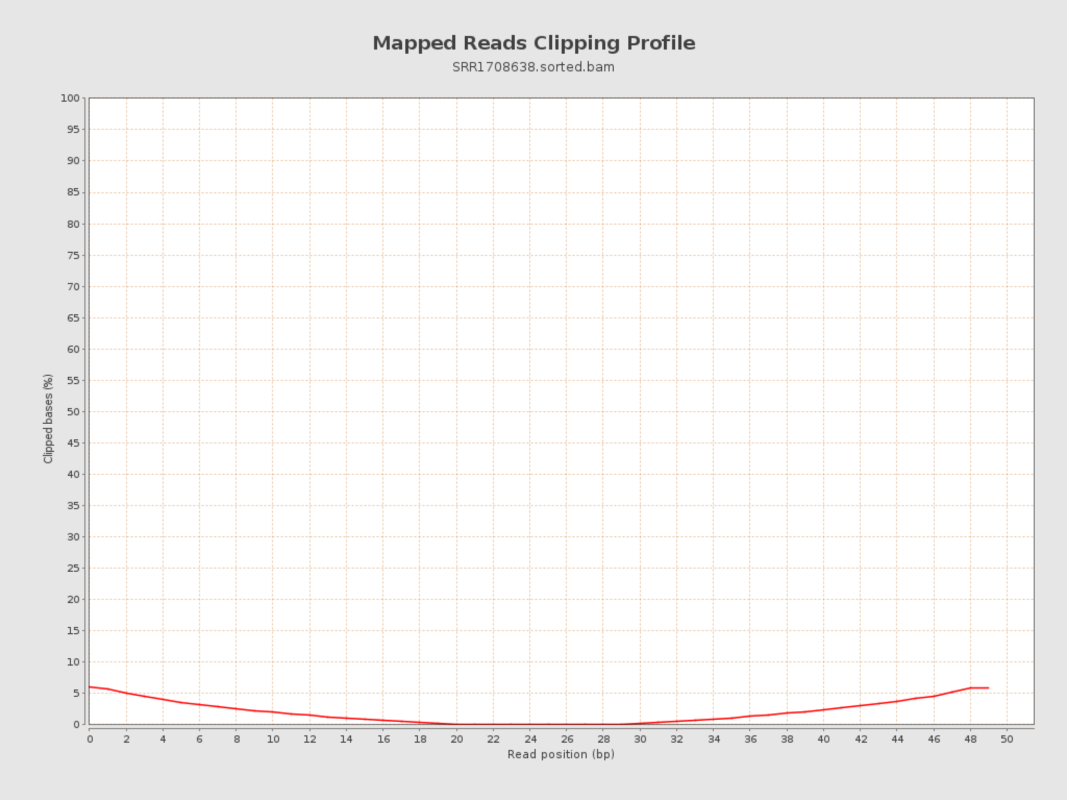
8. Results : Mapped Reads Nucleotide Content



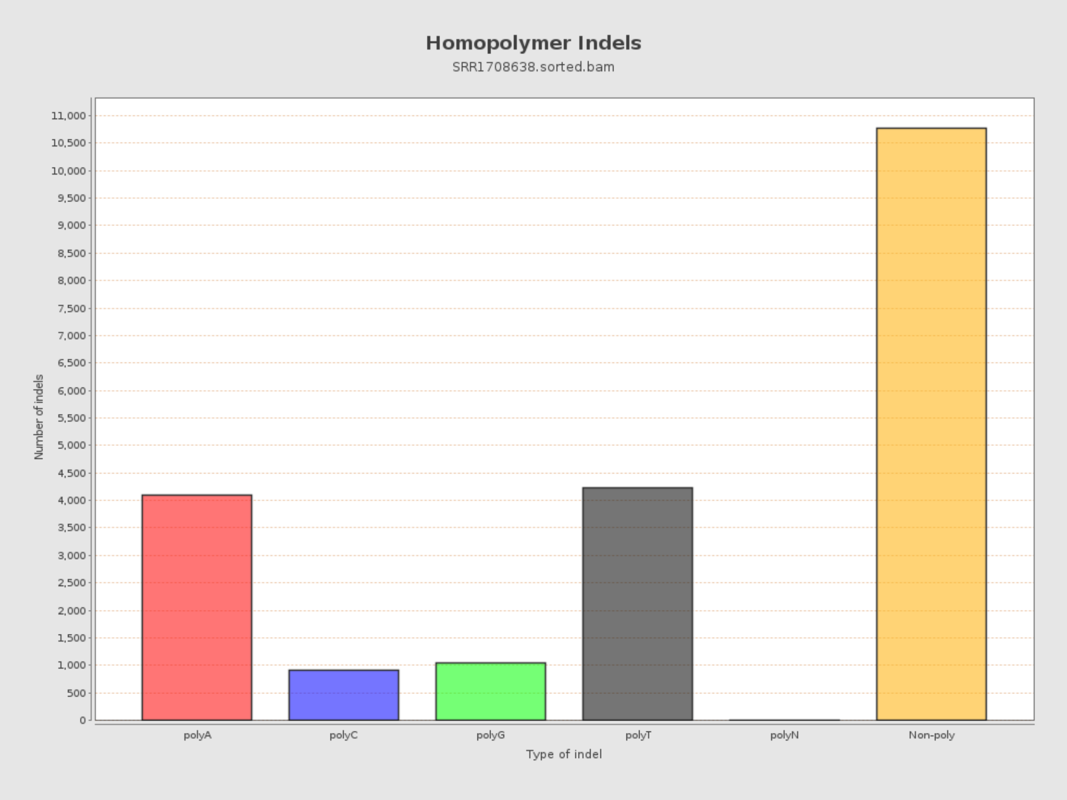
9. Results : Mapped Reads GC-content Distribution



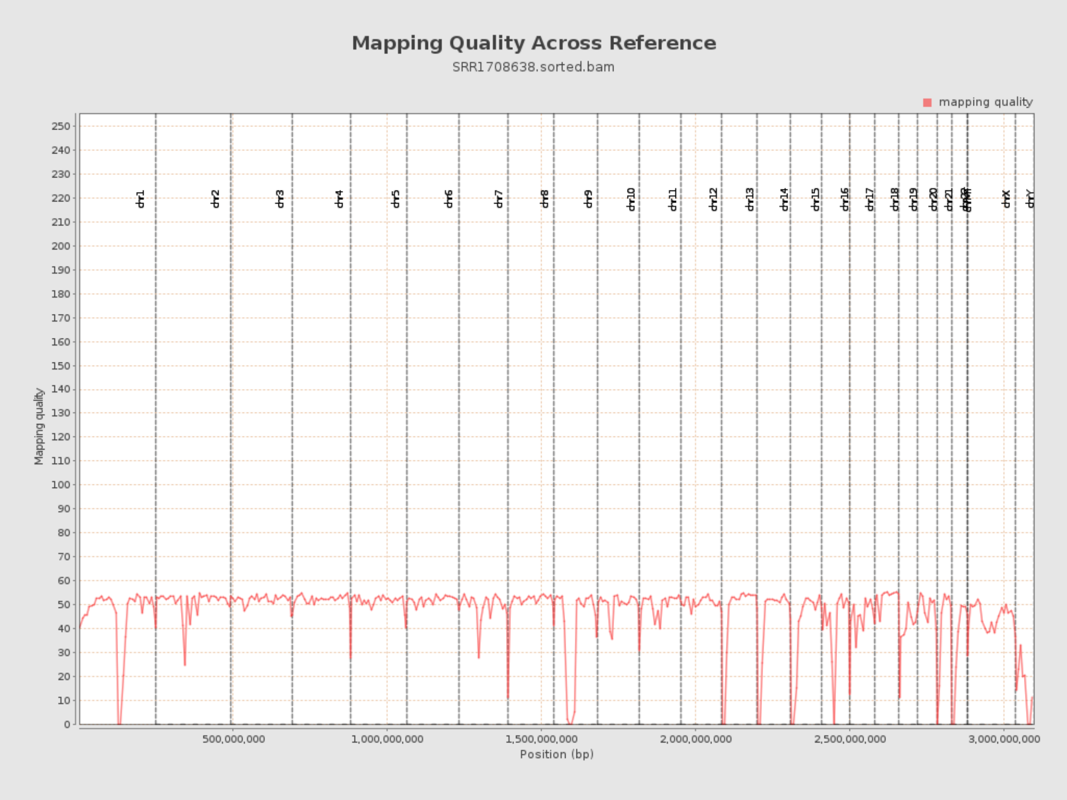
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram