Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:26:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708552.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_SRR1708552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708552.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:26:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,236,934
Mapped reads	3,484,882 / 82.25%
Unmapped reads	752,052 / 17.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	75 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,060 / 0.4%
Duplication rate	0.49%
Clipped reads	48,219 / 1.14%

2.2. ACGT Content

Number/percentage of A's	53,695,519 / 30.9%
Number/percentage of C's	33,094,507 / 19.05%
Number/percentage of T's	53,598,324 / 30.85%
Number/percentage of G's	33,366,289 / 19.2%
Number/percentage of N's	7,381 / 0%
GC Percentage	38.25%

2.3. Coverage

Mean	0.0561

Standard Deviation	0.2457

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

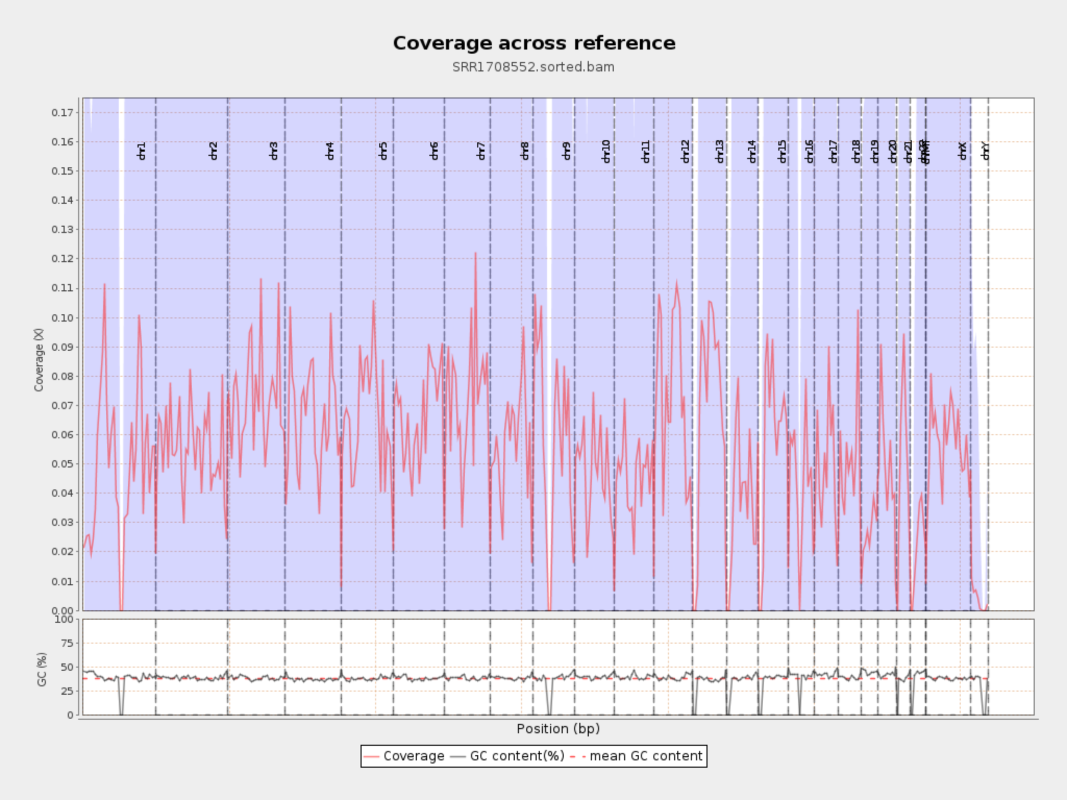
General error rate	0.17%
Mismatches	275,330
Insertions	11,477
Mapped reads with at least one insertion	0.33%
Deletions	9,204
Mapped reads with at least one deletion	0.26%
Homopolymer indels	46.93%

2.6. Chromosome stats

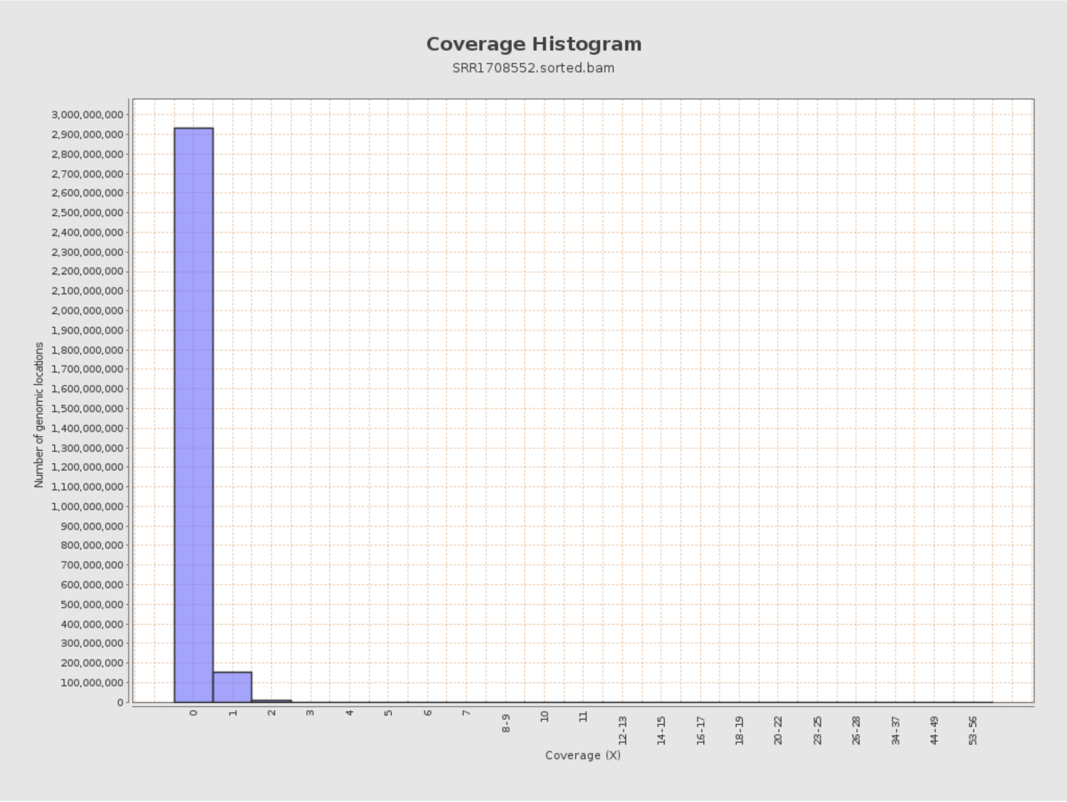
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12304157	0.0494	0.2313
chr2	243199373	13482923	0.0554	0.2433
chr3	198022430	14376734	0.0726	0.2781
chr4	191154276	12612340	0.066	0.2655
chr5	180915260	11736393	0.0649	0.2629
chr6	171115067	11486346	0.0671	0.2676
chr7	159138663	11273441	0.0708	0.2762

chr8	146364022	8362651	0.0571	0.2465
chr9	141213431	8353304	0.0592	0.2527
chr10	135534747	6507747	0.048	0.2259
chr11	135006516	6136437	0.0455	0.2205
chr12	133851895	9836972	0.0735	0.2814
chr13	115169878	8012468	0.0696	0.2741
chr14	107349540	4060903	0.0378	0.2019
chr15	102531392	5914678	0.0577	0.2503
chr16	90354753	3771346	0.0417	0.2113
chr17	81195210	4100691	0.0505	0.2331
chr18	78077248	4047080	0.0518	0.2348
chr19	59128983	1600285	0.0271	0.169
chr20	63025520	3206834	0.0509	0.2334
chr21	48129895	2311941	0.048	0.229
chr22	51304566	1138334	0.0222	0.1529
chrMT	16571	150	0.0091	0.0947
chrX	155270560	8928751	0.0575	0.2483
chrY	59373566	214515	0.0036	0.0622

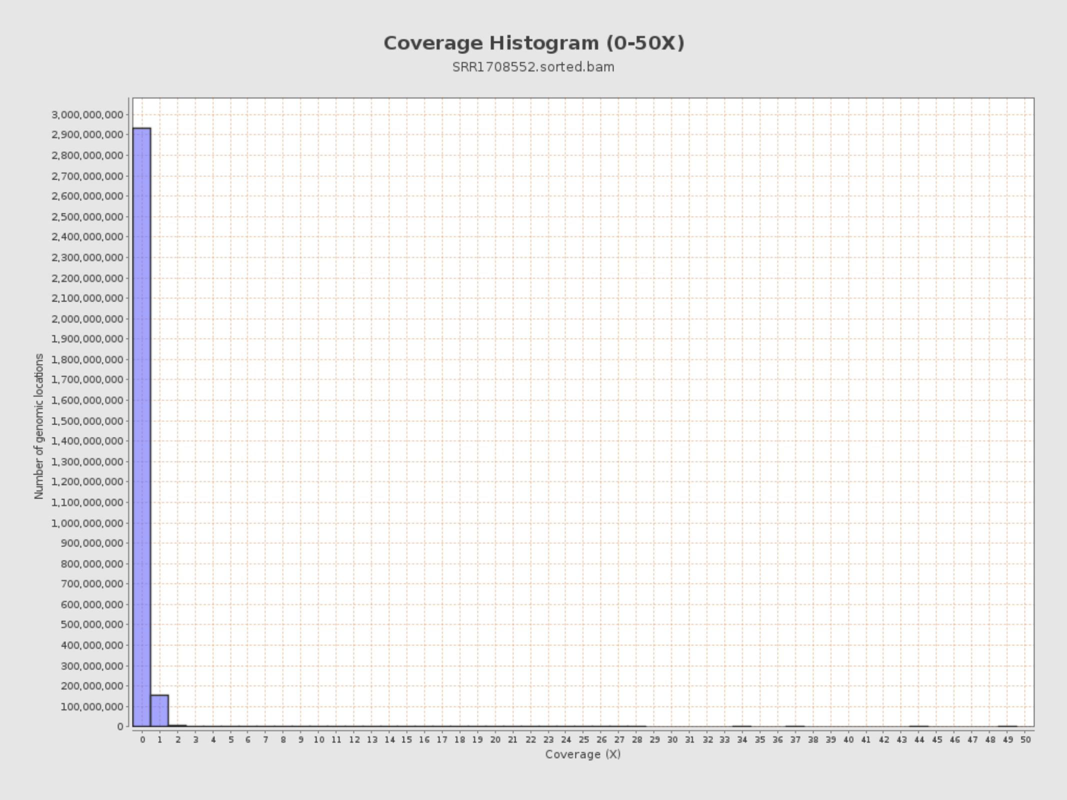
3. Results : Coverage across reference



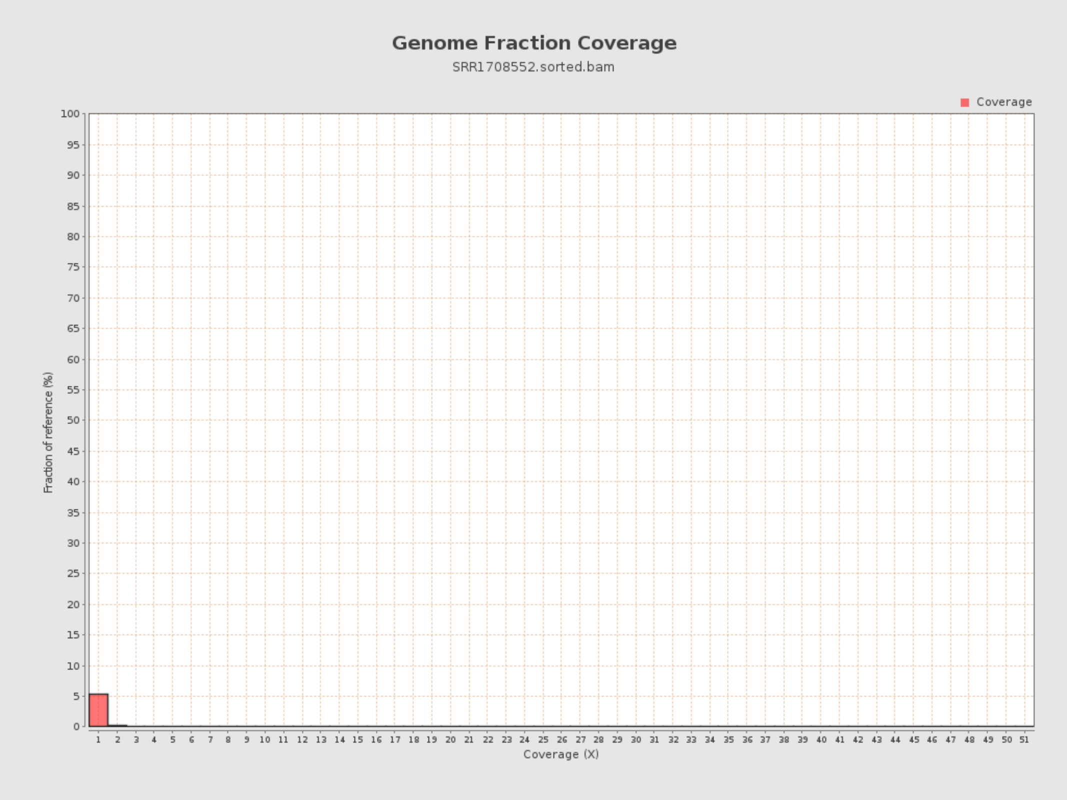
4. Results : Coverage Histogram



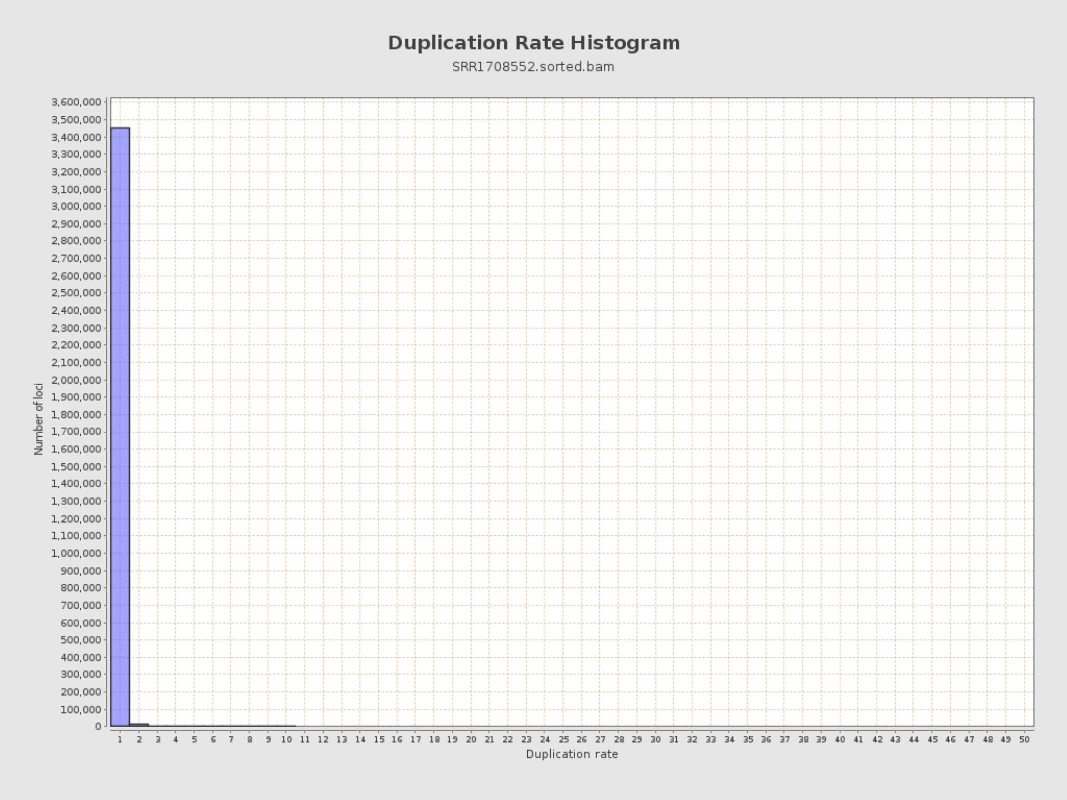
5. Results : Coverage Histogram (0-50X)



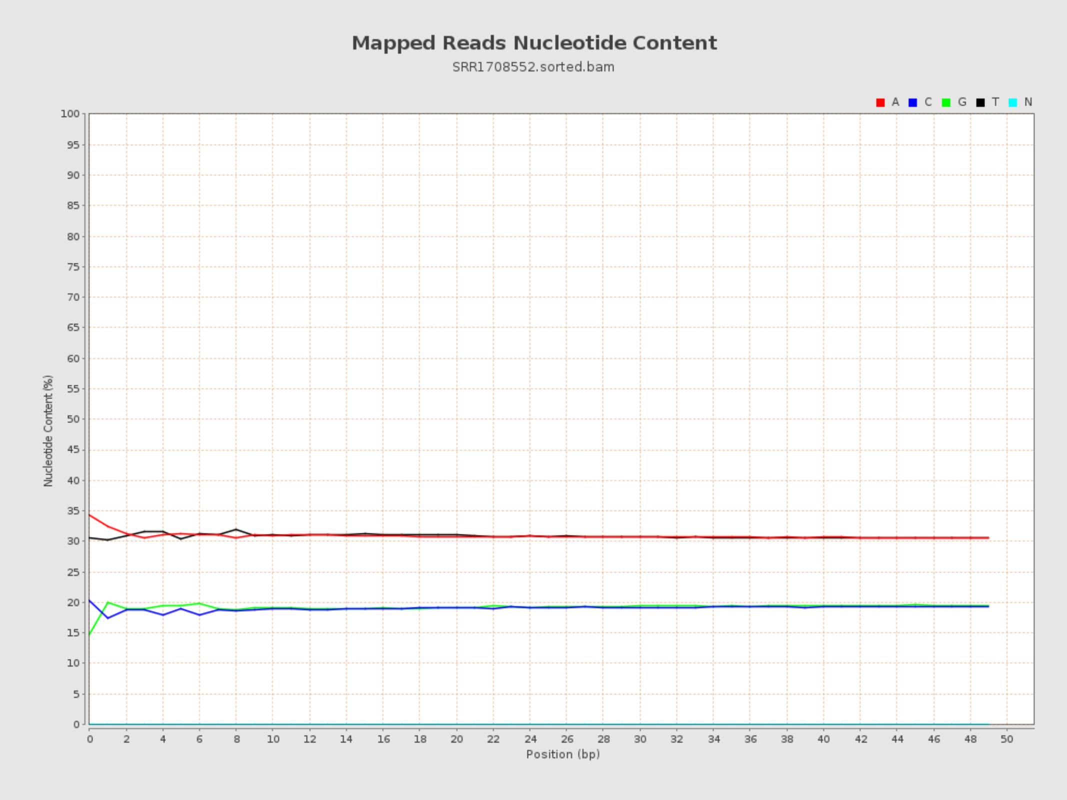
6. Results : Genome Fraction Coverage



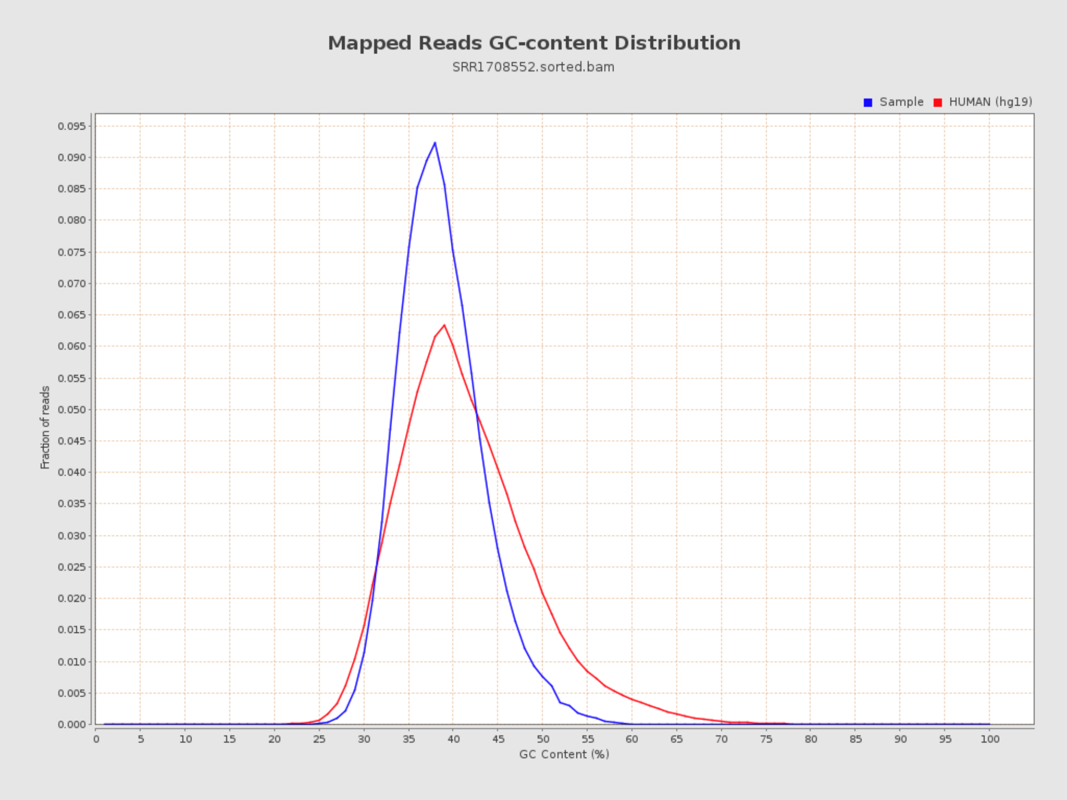
7. Results : Duplication Rate Histogram



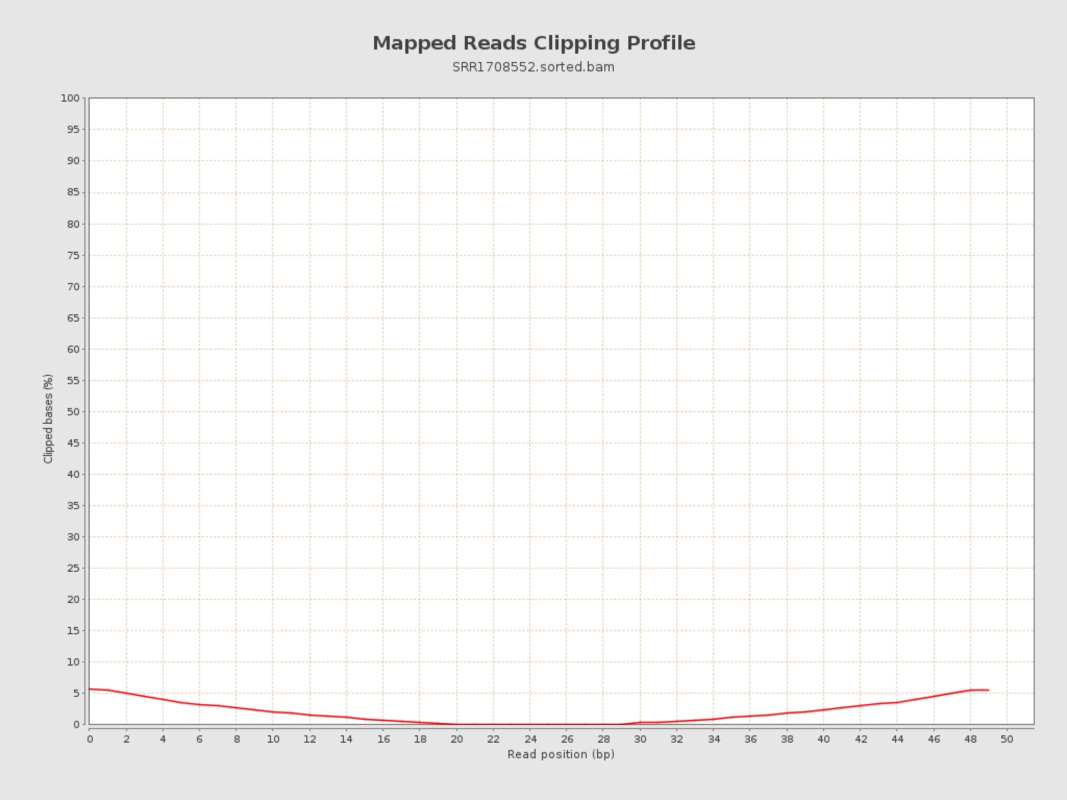
8. Results : Mapped Reads Nucleotide Content



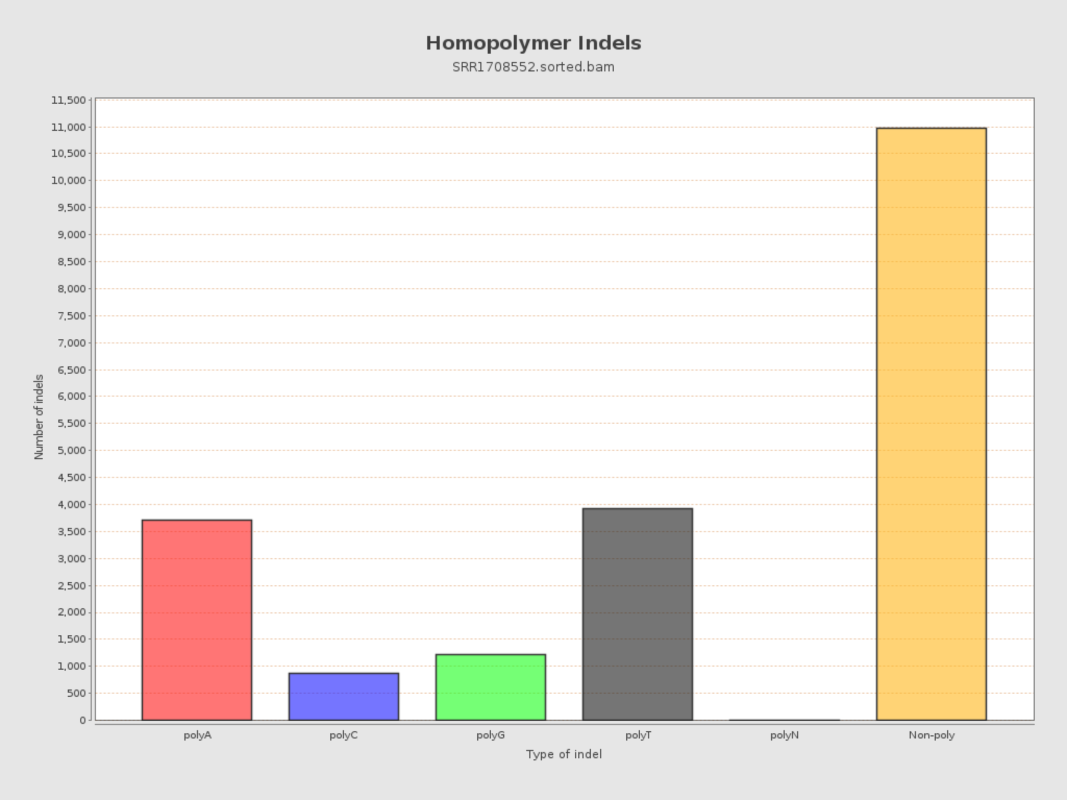
9. Results : Mapped Reads GC-content Distribution



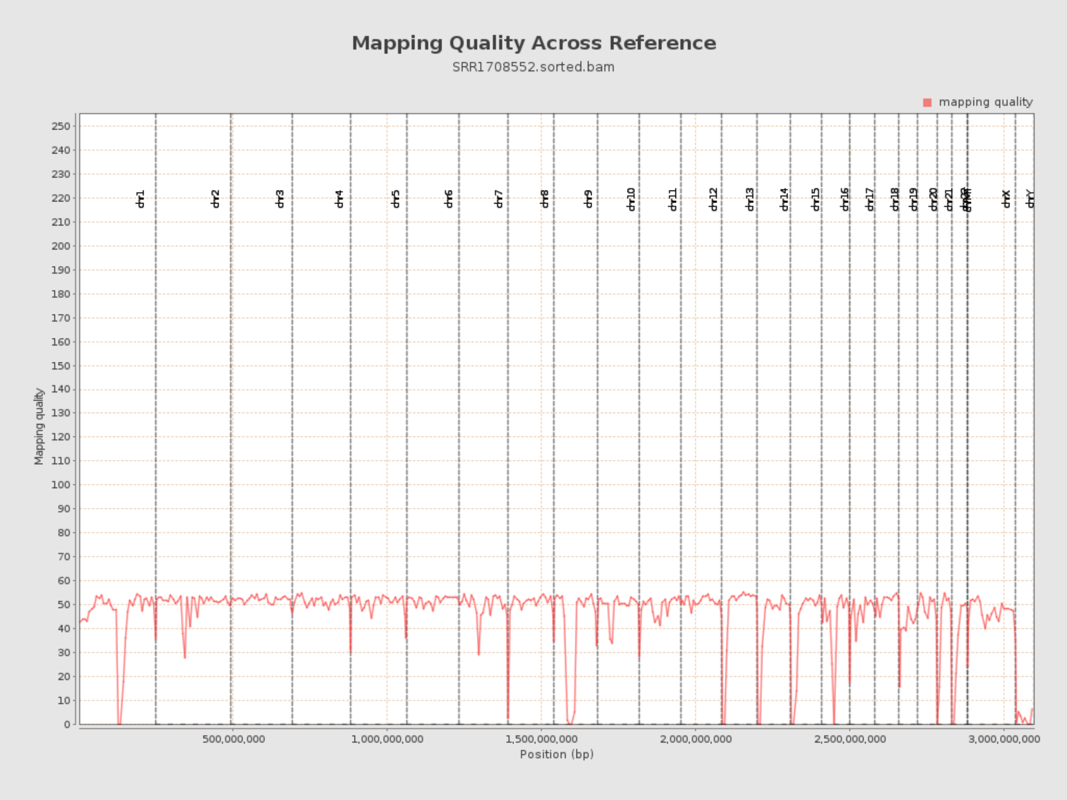
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram