Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:56:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708558.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_SRR1708558 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708558.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:56:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708558.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,306,302
Mapped reads	3,554,376 / 82.54%
Unmapped reads	751,926 / 17.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	91 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,356 / 0.38%
Duplication rate	0.46%
Clipped reads	48,636 / 1.13%

2.2. ACGT Content

Number/percentage of A's	54,918,761 / 30.99%
Number/percentage of C's	33,631,078 / 18.98%
Number/percentage of T's	54,720,677 / 30.87%
Number/percentage of G's	33,956,679 / 19.16%
Number/percentage of N's	7,818 / 0%
GC Percentage	38.13%

2.3. Coverage

Mean	0.0573

Standard Deviation	0.2463

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

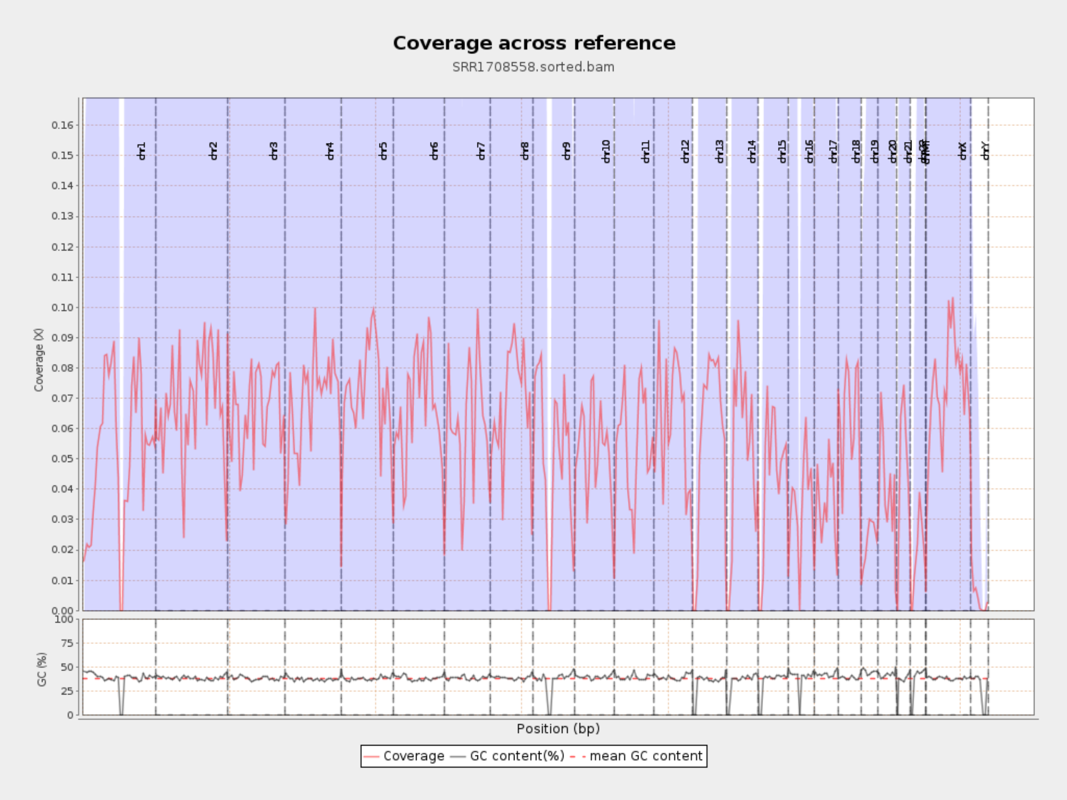
General error rate	0.17%
Mismatches	278,771
Insertions	11,956
Mapped reads with at least one insertion	0.34%
Deletions	9,461
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.39%

2.6. Chromosome stats

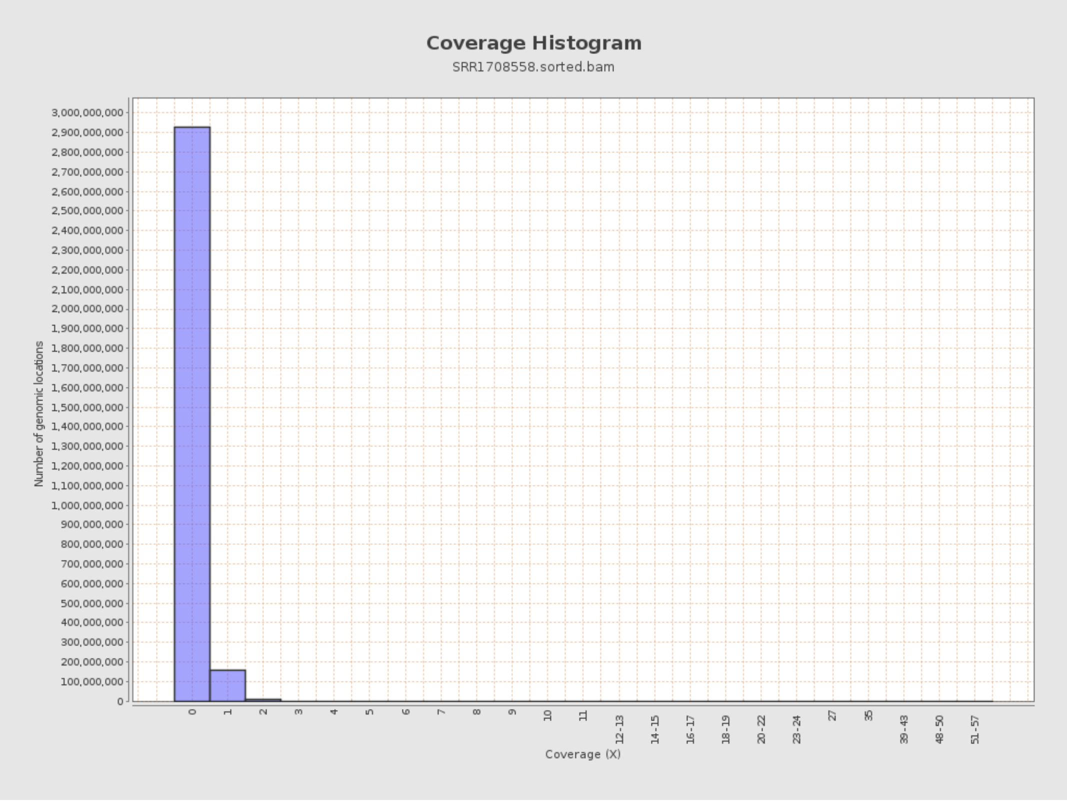
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13078280	0.0525	0.237
chr2	243199373	16538278	0.068	0.2678
chr3	198022430	13133259	0.0663	0.2636
chr4	191154276	13241021	0.0693	0.2696
chr5	180915260	12907156	0.0713	0.2735
chr6	171115067	11523427	0.0673	0.2661
chr7	159138663	9640681	0.0606	0.253

chr8	146364022	10045386	0.0686	0.2689
chr9	141213431	7292864	0.0516	0.234
chr10	135534747	7285136	0.0538	0.2374
chr11	135006516	7387156	0.0547	0.2404
chr12	133851895	8364619	0.0625	0.2568
chr13	115169878	6781818	0.0589	0.2498
chr14	107349540	5683477	0.0529	0.2377
chr15	102531392	4460127	0.0435	0.2149
chr16	90354753	3101130	0.0343	0.1901
chr17	81195210	2891795	0.0356	0.1945
chr18	78077248	5043443	0.0646	0.26
chr19	59128983	1372944	0.0232	0.1559
chr20	63025520	2627997	0.0417	0.2097
chr21	48129895	2149819	0.0447	0.2194
chr22	51304566	982149	0.0191	0.1416
chrMT	16571	100	0.006	0.0774
chrX	155270560	11462908	0.0738	0.2795
chrY	59373566	256272	0.0043	0.0681

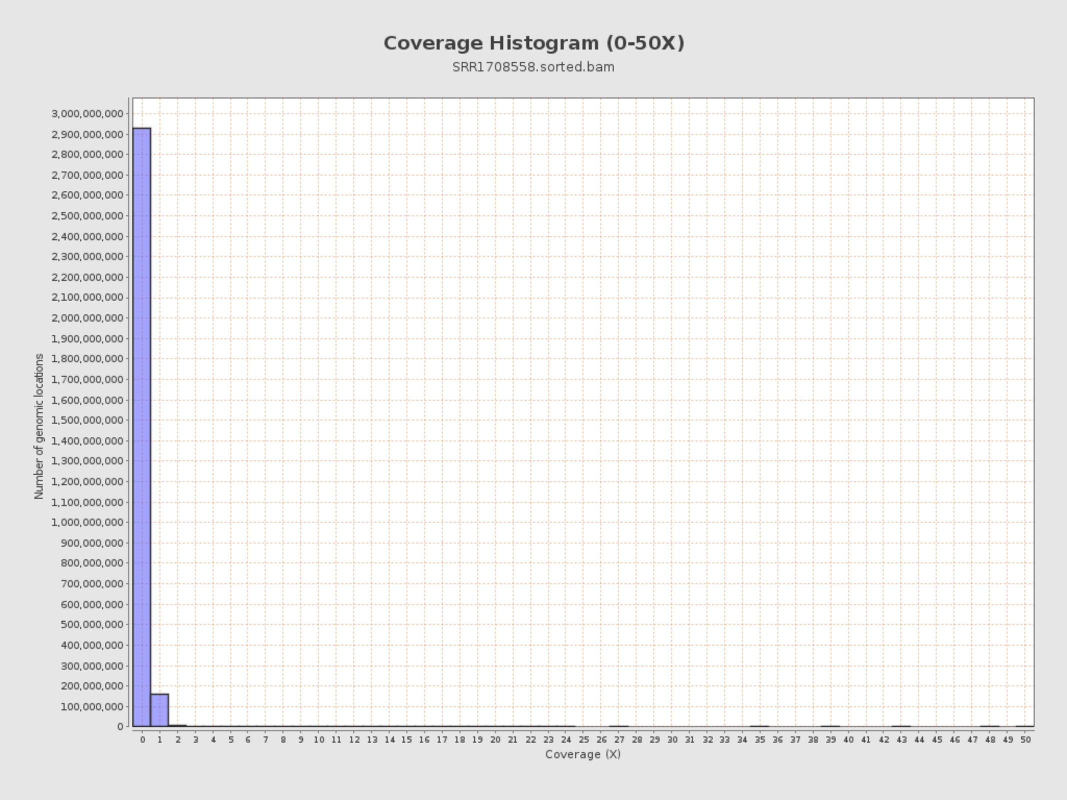
3. Results : Coverage across reference



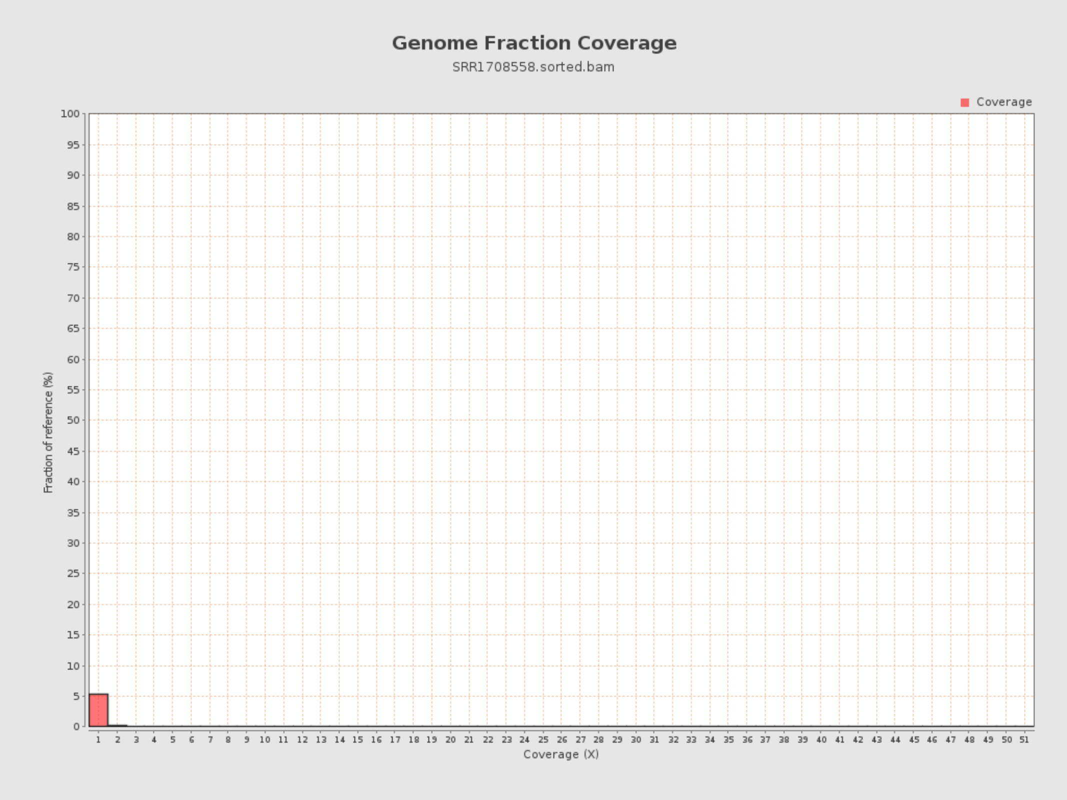
4. Results : Coverage Histogram



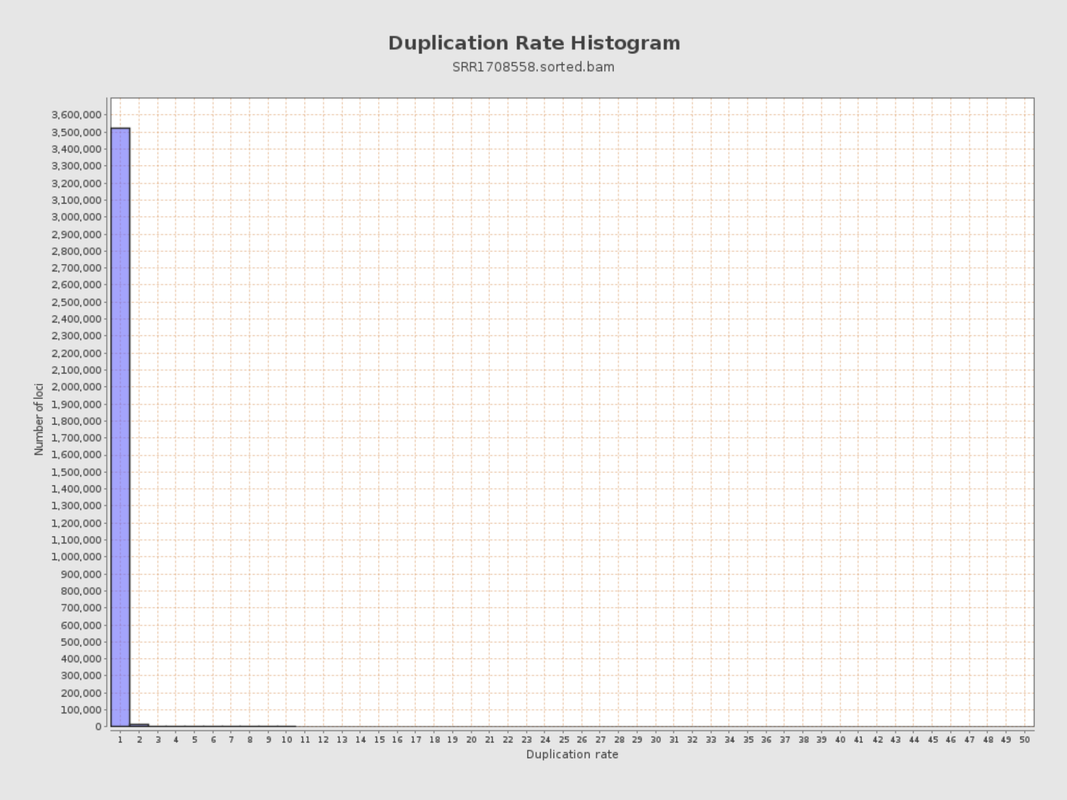
5. Results : Coverage Histogram (0-50X)



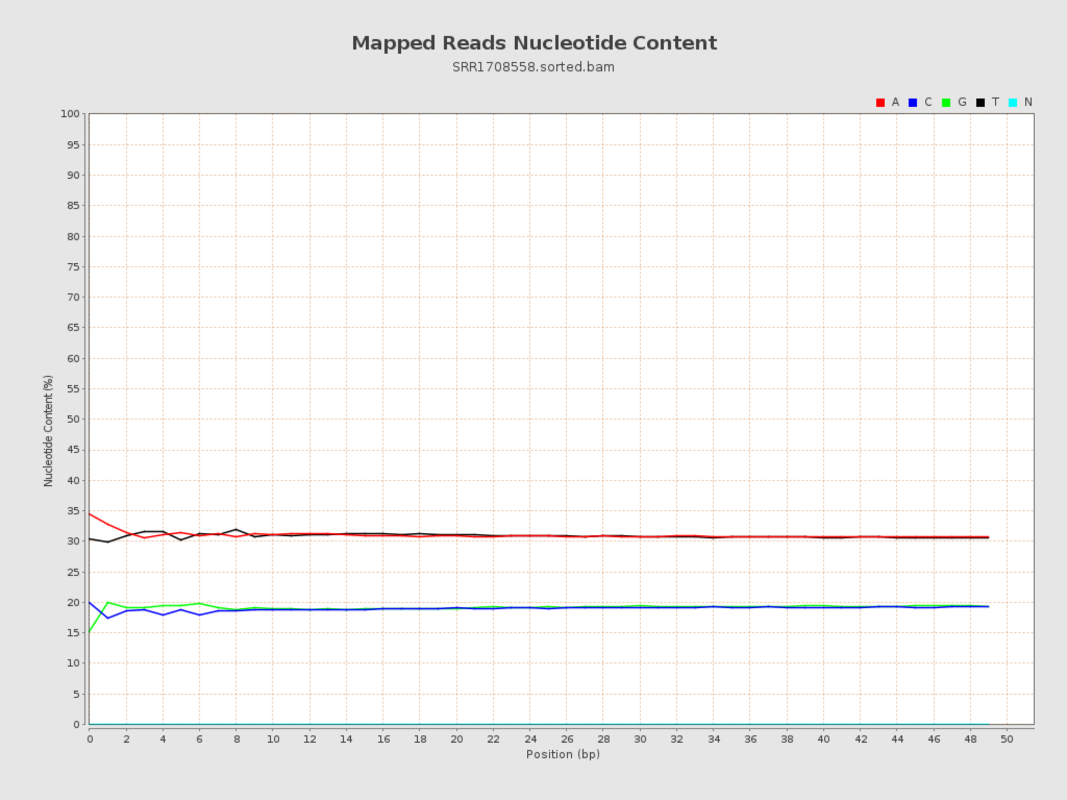
6. Results : Genome Fraction Coverage



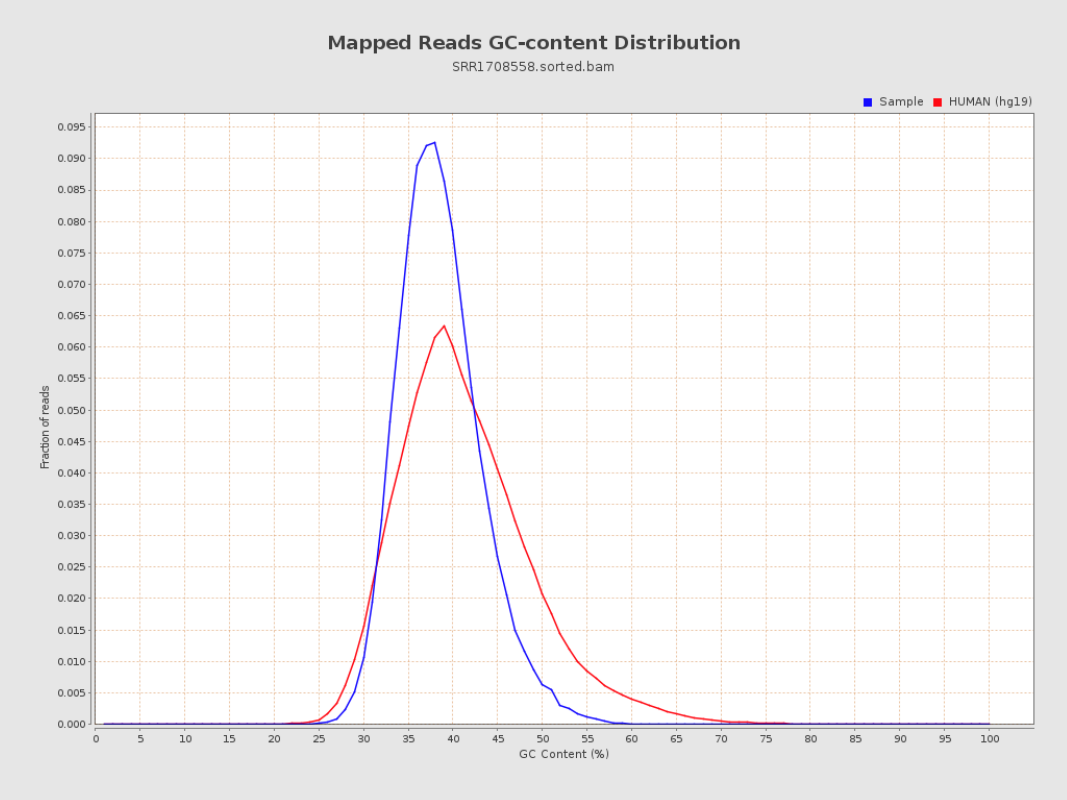
7. Results : Duplication Rate Histogram



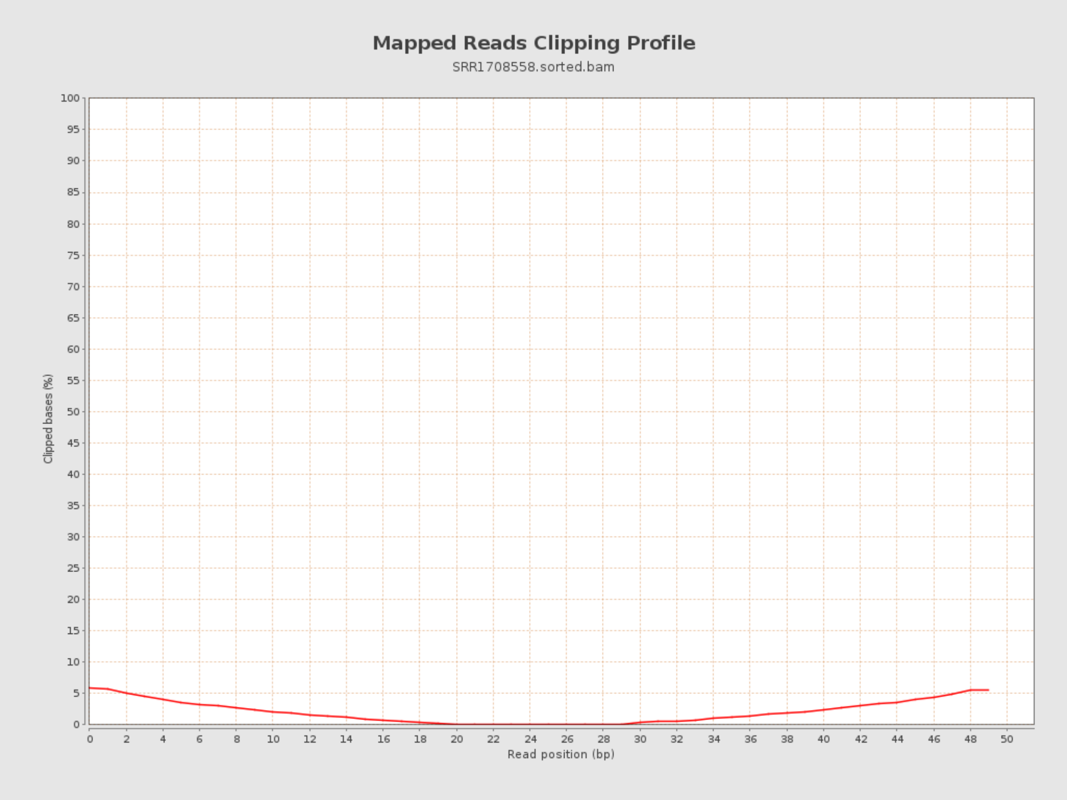
8. Results : Mapped Reads Nucleotide Content



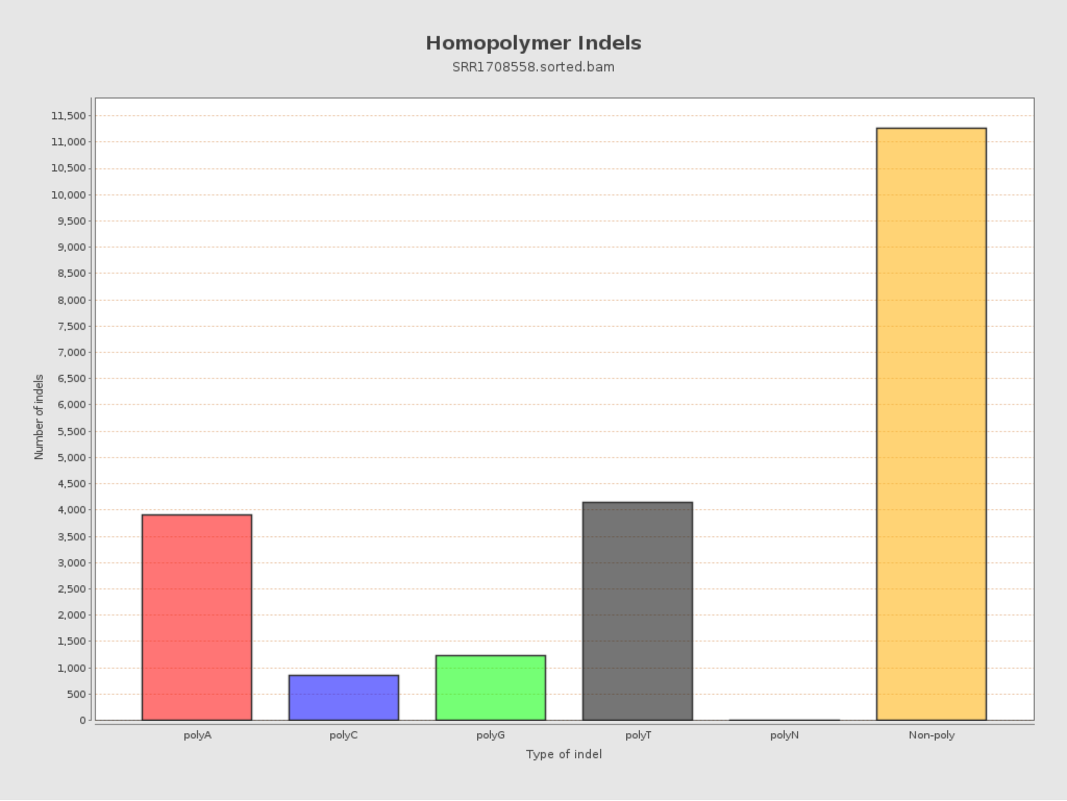
9. Results : Mapped Reads GC-content Distribution



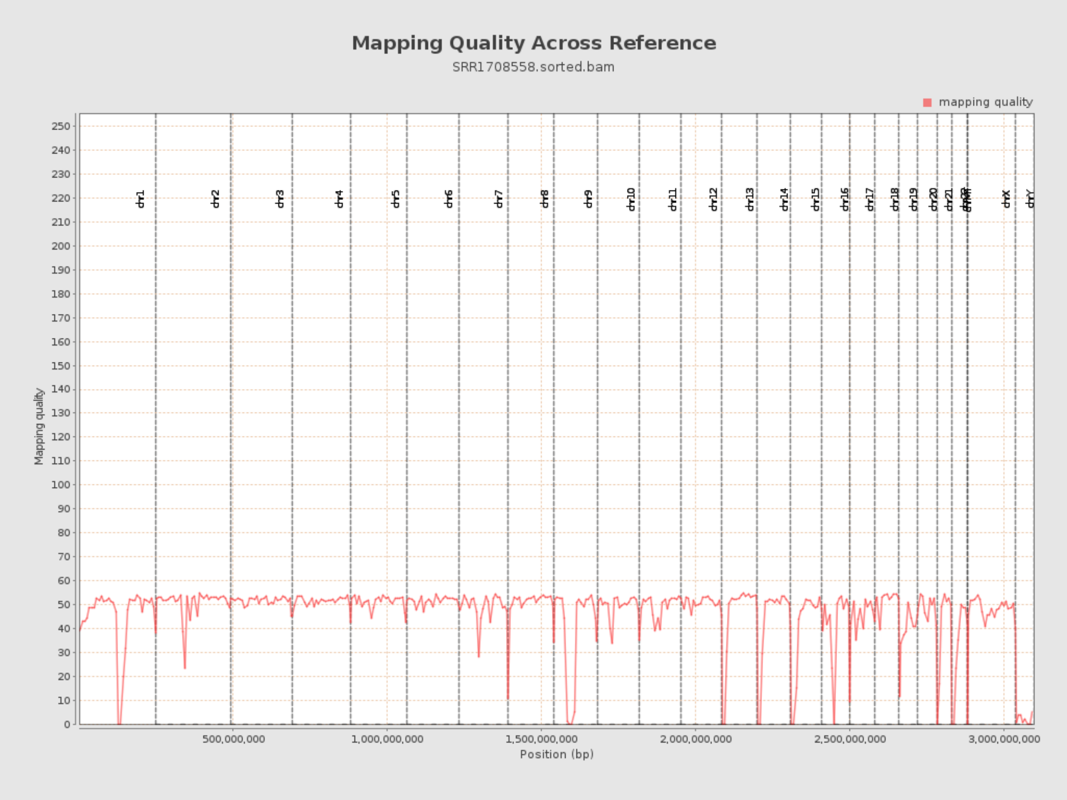
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram