Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708542.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_SRR1708542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708542.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:55:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,981,238
Mapped reads	22,150,289 / 96.38%
Unmapped reads	830,949 / 3.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	484 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	189,413 / 0.82%
Duplication rate	0.85%
Clipped reads	354,704 / 1.54%

2.2. ACGT Content

Number/percentage of A's	340,493,882 / 30.83%
Number/percentage of C's	210,139,630 / 19.02%
Number/percentage of T's	340,887,543 / 30.86%
Number/percentage of G's	212,582,182 / 19.25%
Number/percentage of N's	445,240 / 0.04%
GC Percentage	38.27%

2.3. Coverage

Mean	0.3568

Standard Deviation	0.6619

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

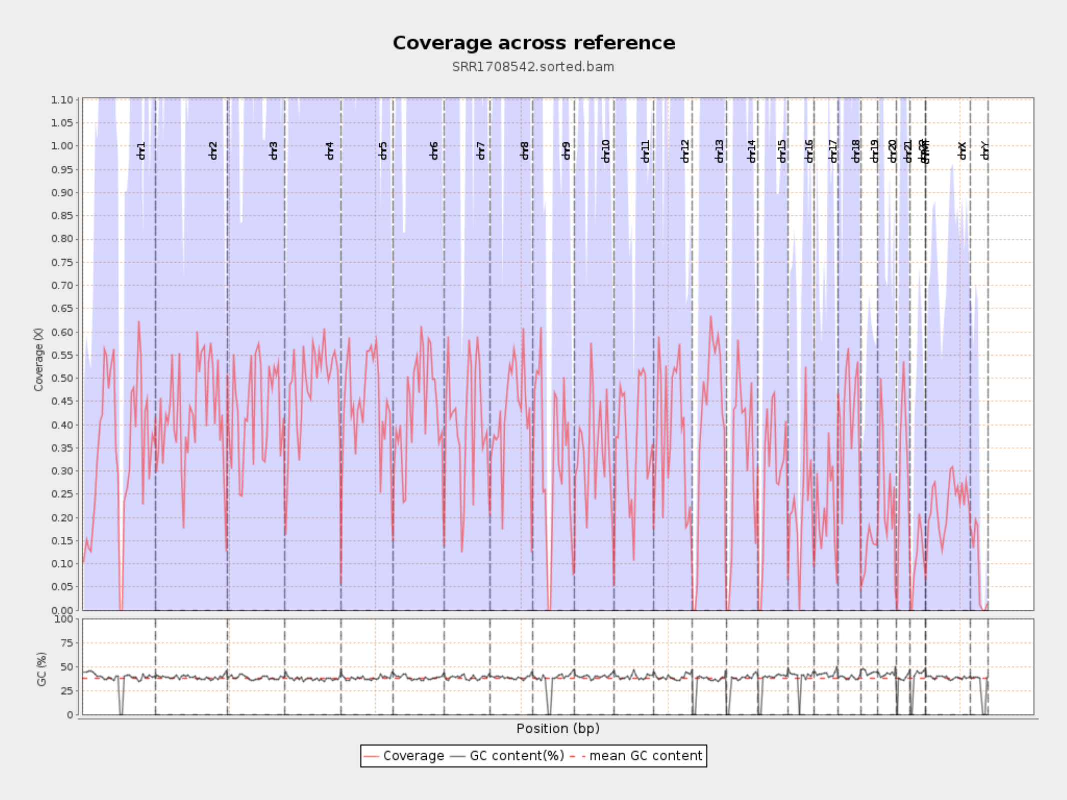
General error rate	0.36%
Mismatches	3,908,450
Insertions	57,278
Mapped reads with at least one insertion	0.26%
Deletions	55,906
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.05%

2.6. Chromosome stats

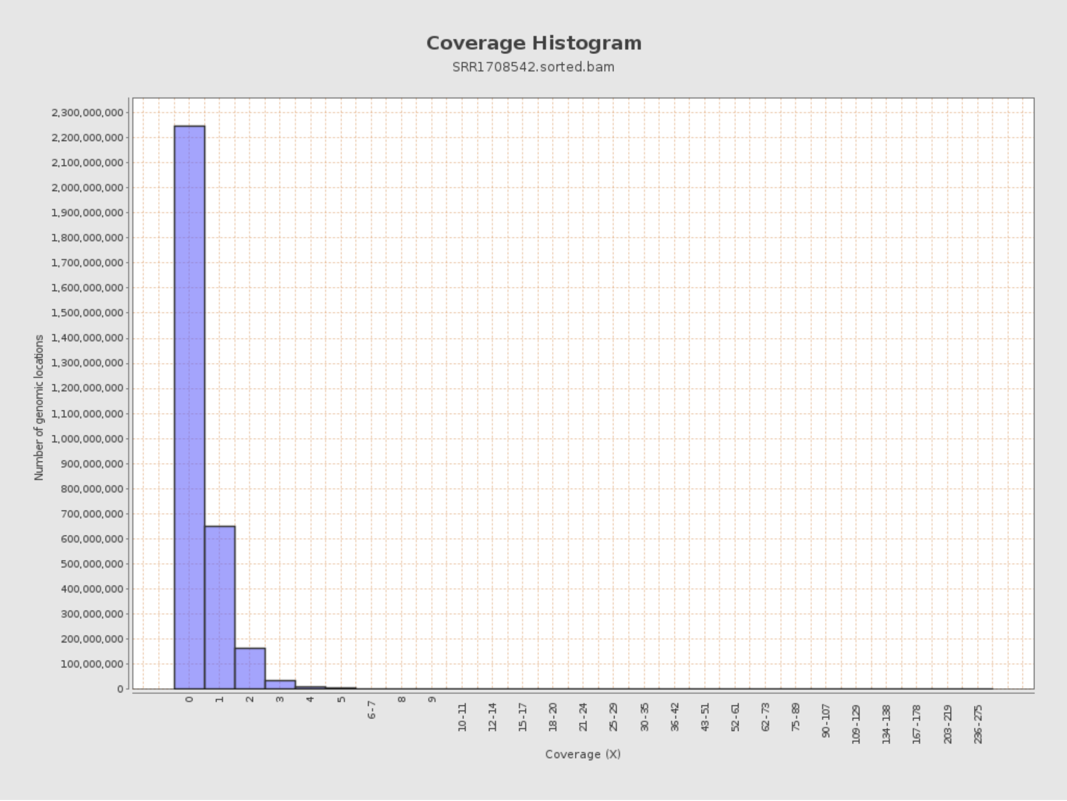
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	84698823	0.3398	0.6578
chr2	243199373	102430566	0.4212	0.7059
chr3	198022430	85559833	0.4321	0.7093
chr4	191154276	92173976	0.4822	0.7484
chr5	180915260	79240772	0.438	0.7157
chr6	171115067	74973790	0.4381	0.7191
chr7	159138663	63263562	0.3975	0.6951

chr8	146364022	61774277	0.4221	0.7051
chr9	141213431	46046787	0.3261	0.6403
chr10	135534747	47224616	0.3484	0.6408
chr11	135006516	49207676	0.3645	0.6684
chr12	133851895	51017678	0.3812	0.6815
chr13	115169878	46695631	0.4055	0.7074
chr14	107349540	35246528	0.3283	0.6419
chr15	102531392	29595916	0.2887	0.6065
chr16	90354753	19816256	0.2193	0.5195
chr17	81195210	17472951	0.2152	0.5188
chr18	78077248	33492364	0.429	0.7113
chr19	59128983	7638307	0.1292	0.3905
chr20	63025520	16867115	0.2676	0.575
chr21	48129895	14226302	0.2956	0.6293
chr22	51304566	5580595	0.1088	0.3646
chrMT	16571	1068	0.0644	0.2603
chrX	155270560	35357700	0.2277	0.5019
chrY	59373566	5038541	0.0849	0.3265

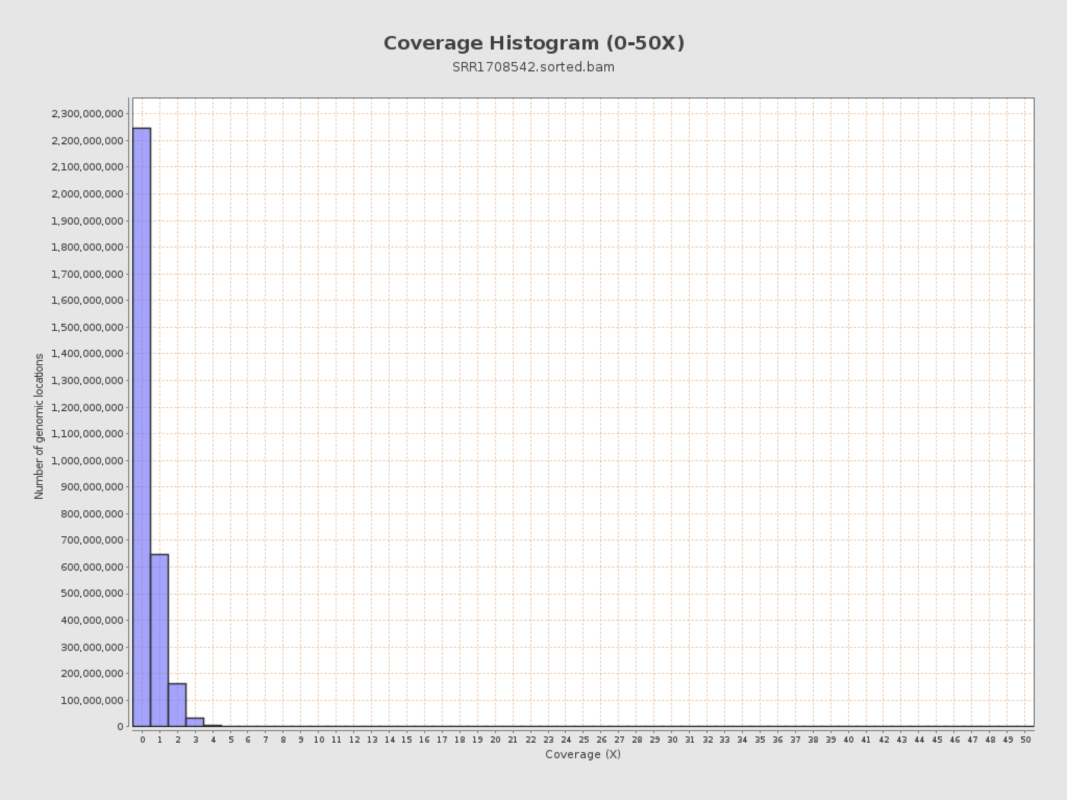
3. Results : Coverage across reference



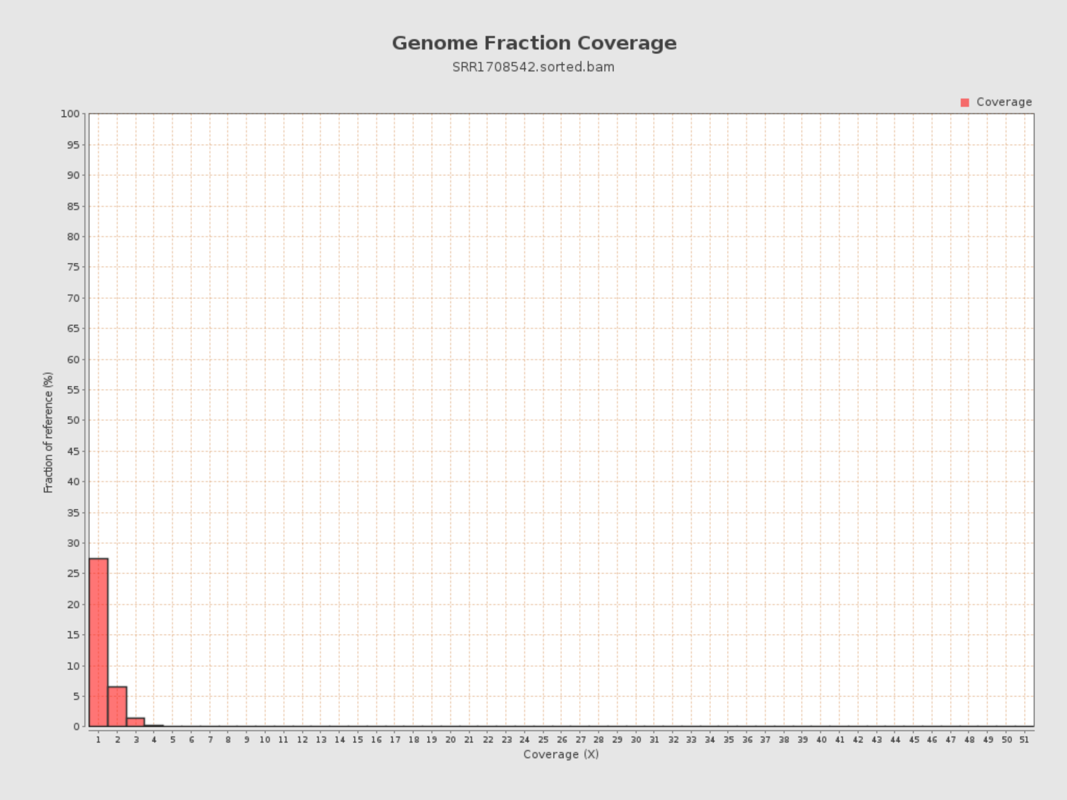
4. Results : Coverage Histogram



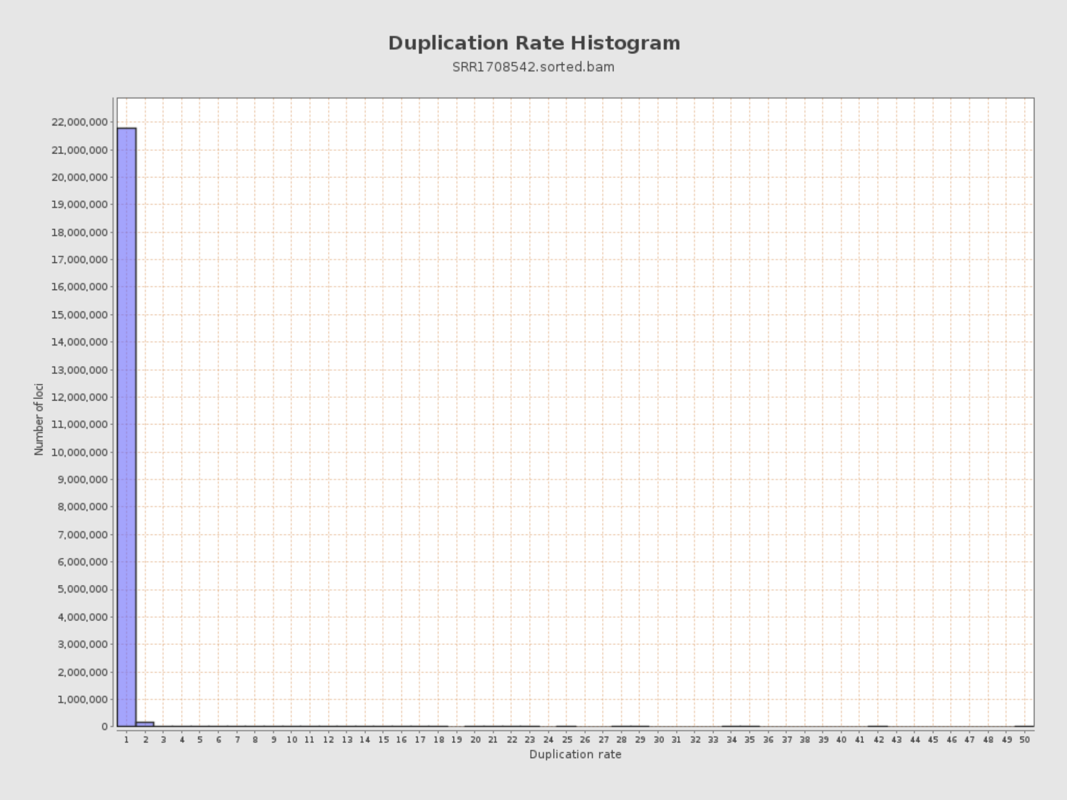
5. Results : Coverage Histogram (0-50X)



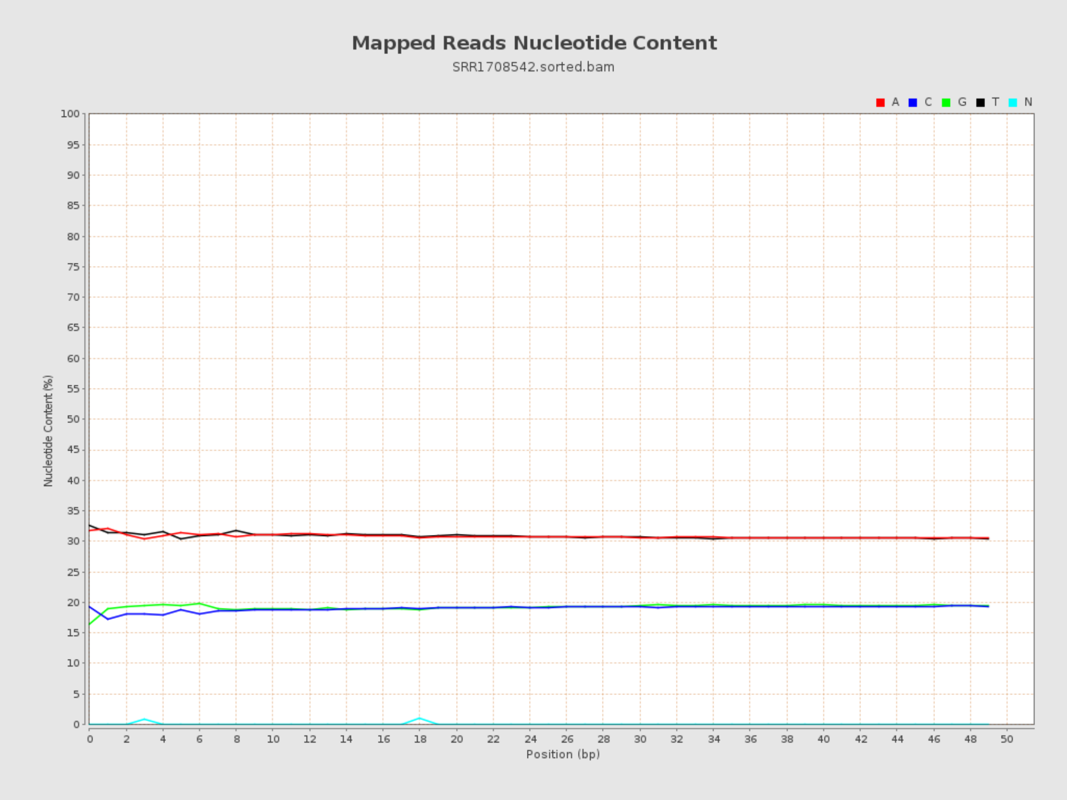
6. Results : Genome Fraction Coverage



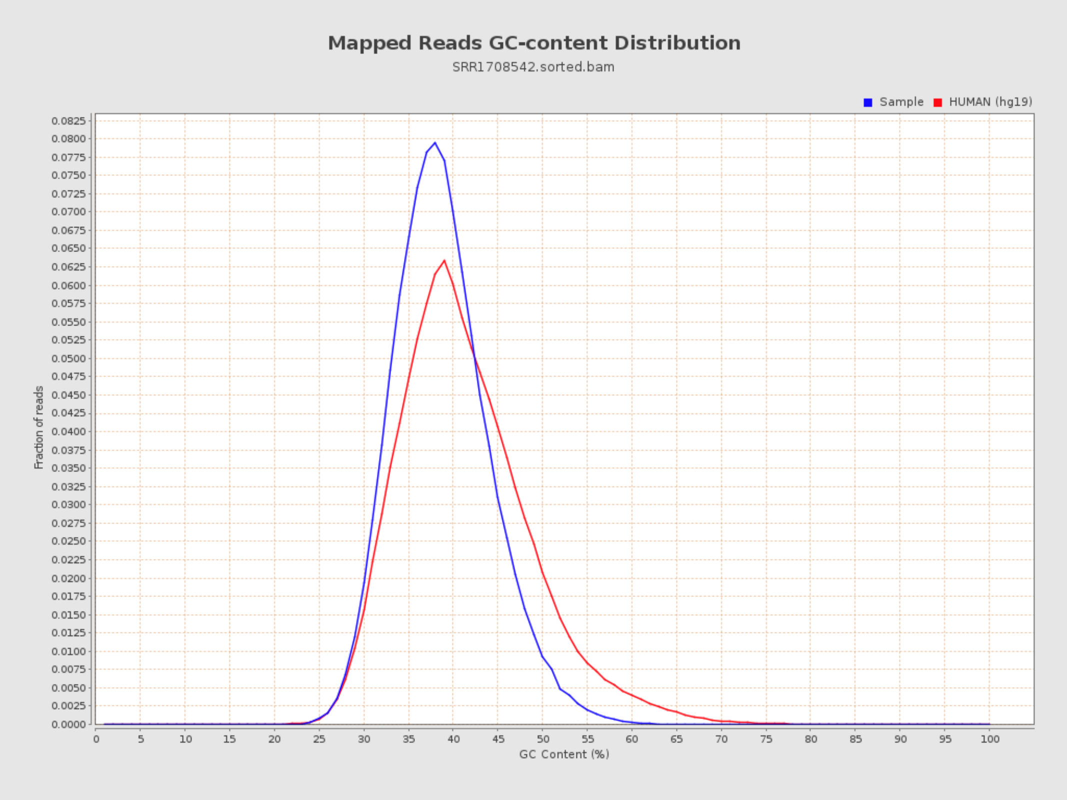
7. Results : Duplication Rate Histogram



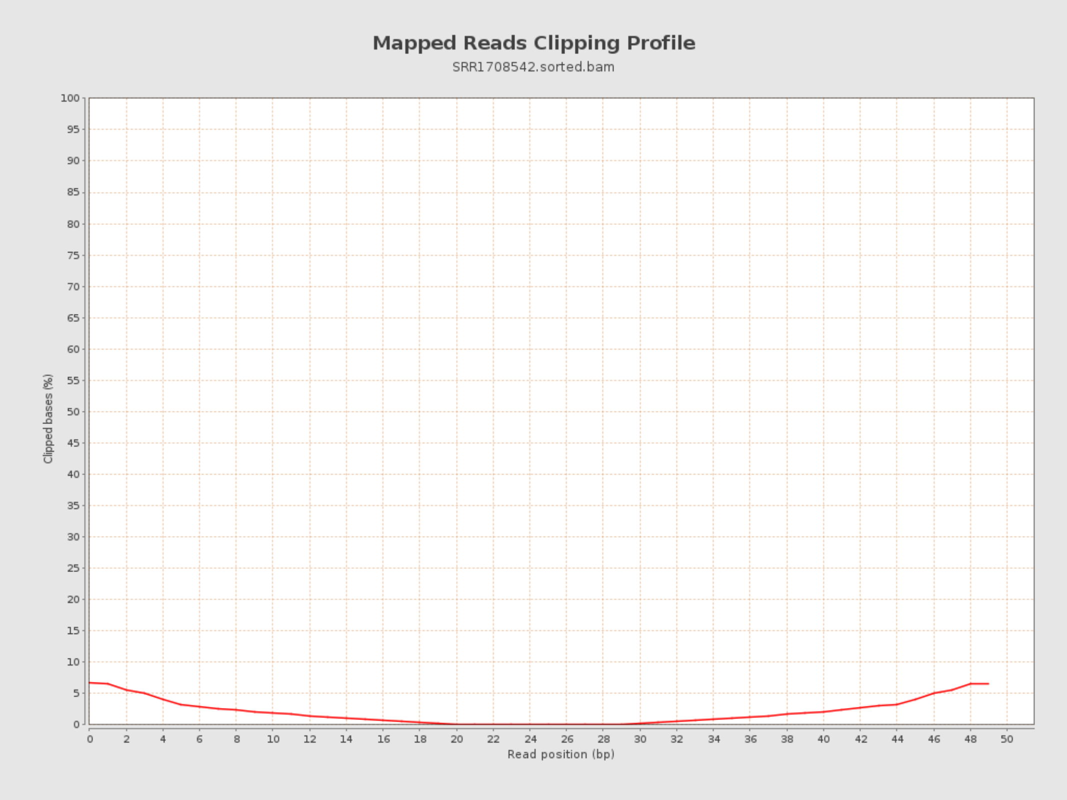
8. Results : Mapped Reads Nucleotide Content



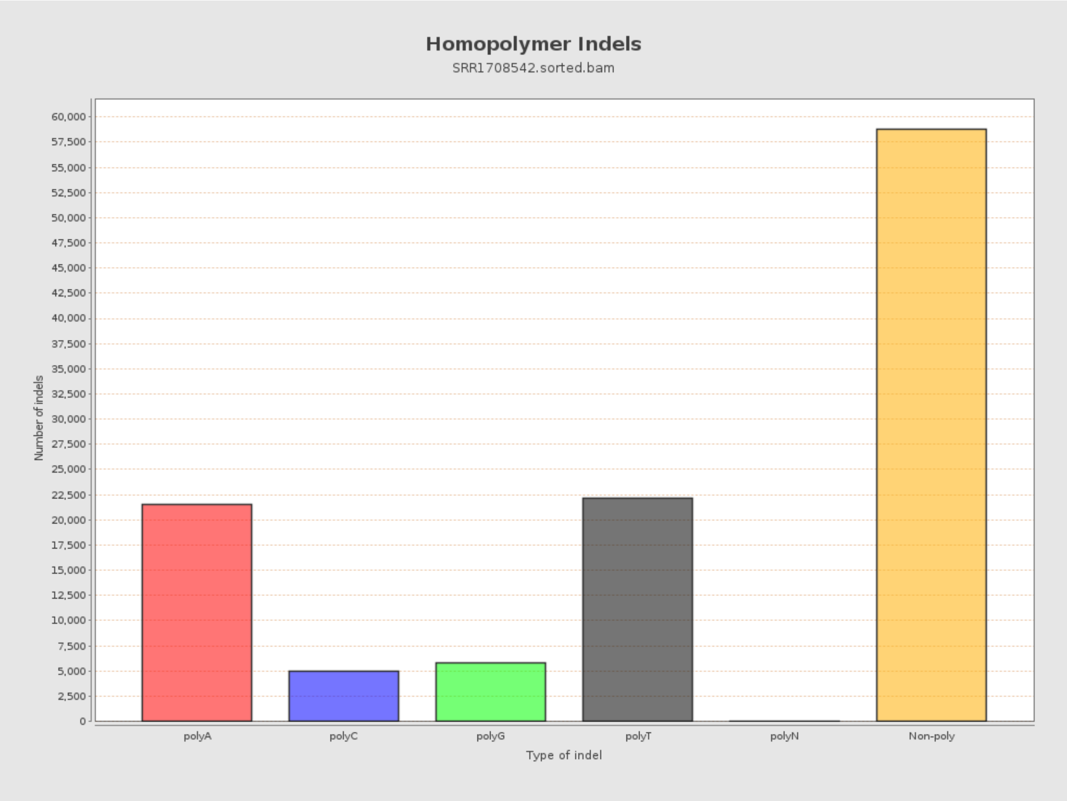
9. Results : Mapped Reads GC-content Distribution



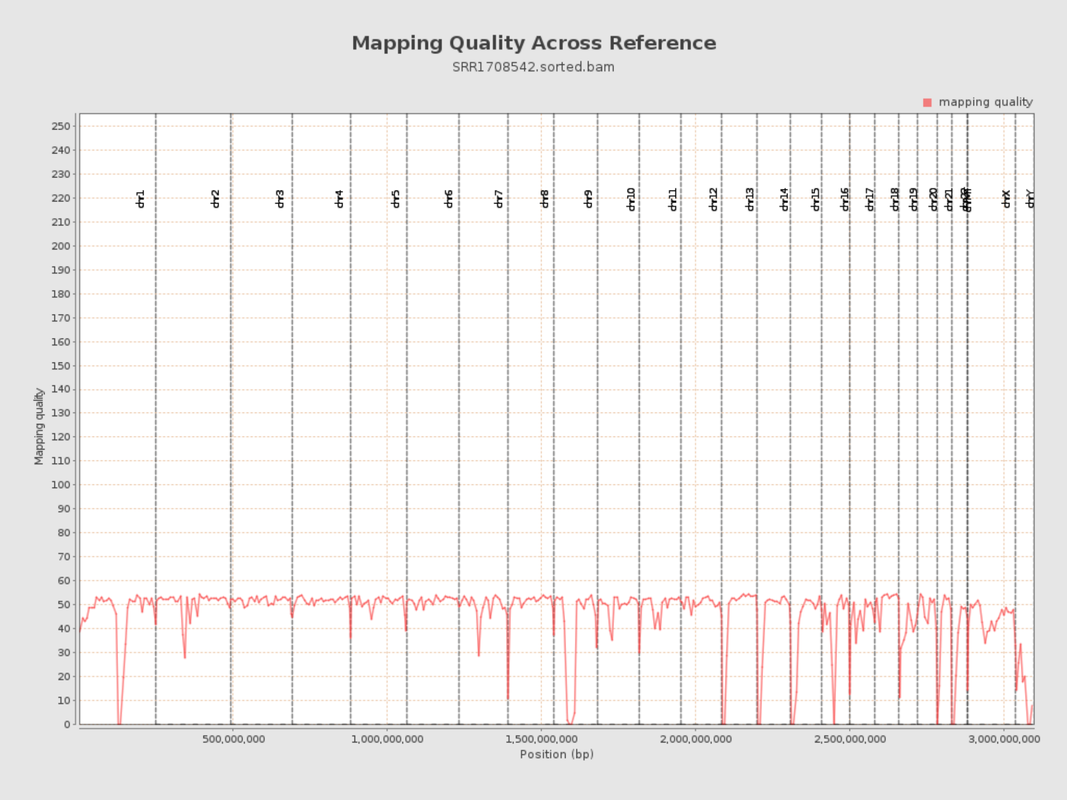
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram