Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:36:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708545.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_SRR1708545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708545.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:36:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,543,897
Mapped reads	19,814,361 / 96.45%
Unmapped reads	729,536 / 3.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	447 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	165,498 / 0.81%
Duplication rate	0.83%
Clipped reads	317,510 / 1.55%

2.2. ACGT Content

Number/percentage of A's	309,917,137 / 31.37%
Number/percentage of C's	182,955,269 / 18.52%
Number/percentage of T's	309,192,732 / 31.29%
Number/percentage of G's	185,566,242 / 18.78%
Number/percentage of N's	417,933 / 0.04%
GC Percentage	37.3%

2.3. Coverage

Mean	0.3192

Standard Deviation	0.6245

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

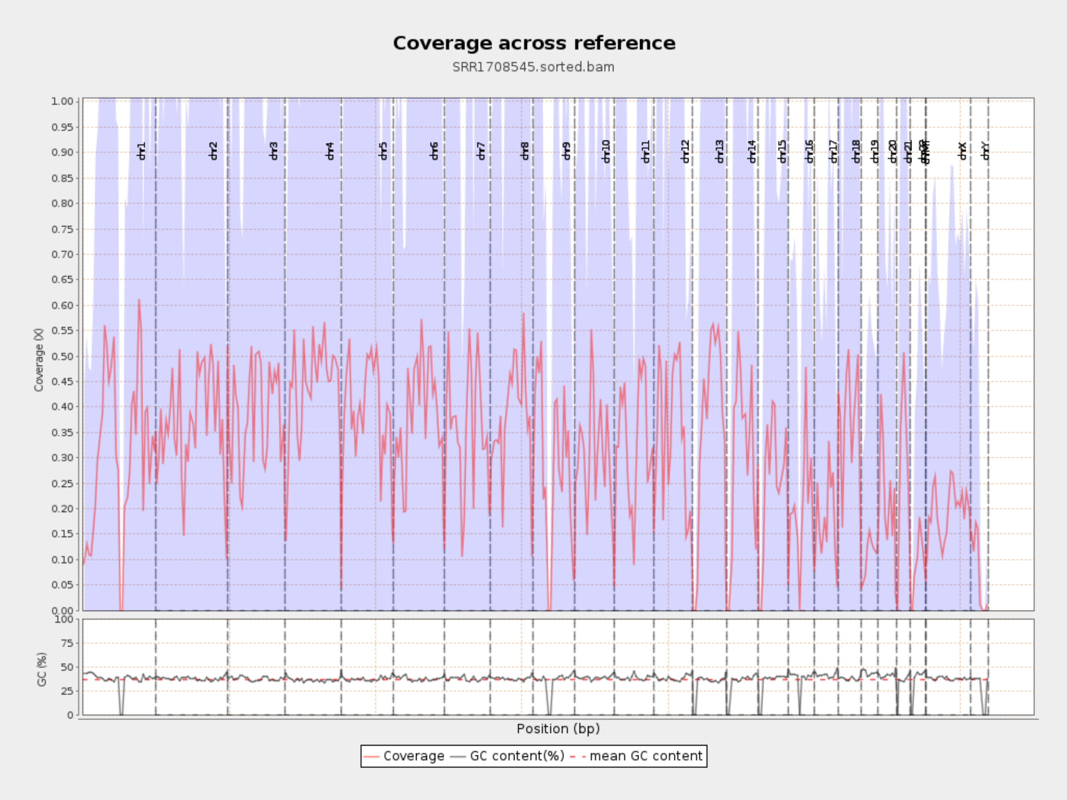
General error rate	0.36%
Mismatches	3,472,573
Insertions	55,306
Mapped reads with at least one insertion	0.28%
Deletions	51,704
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.36%

2.6. Chromosome stats

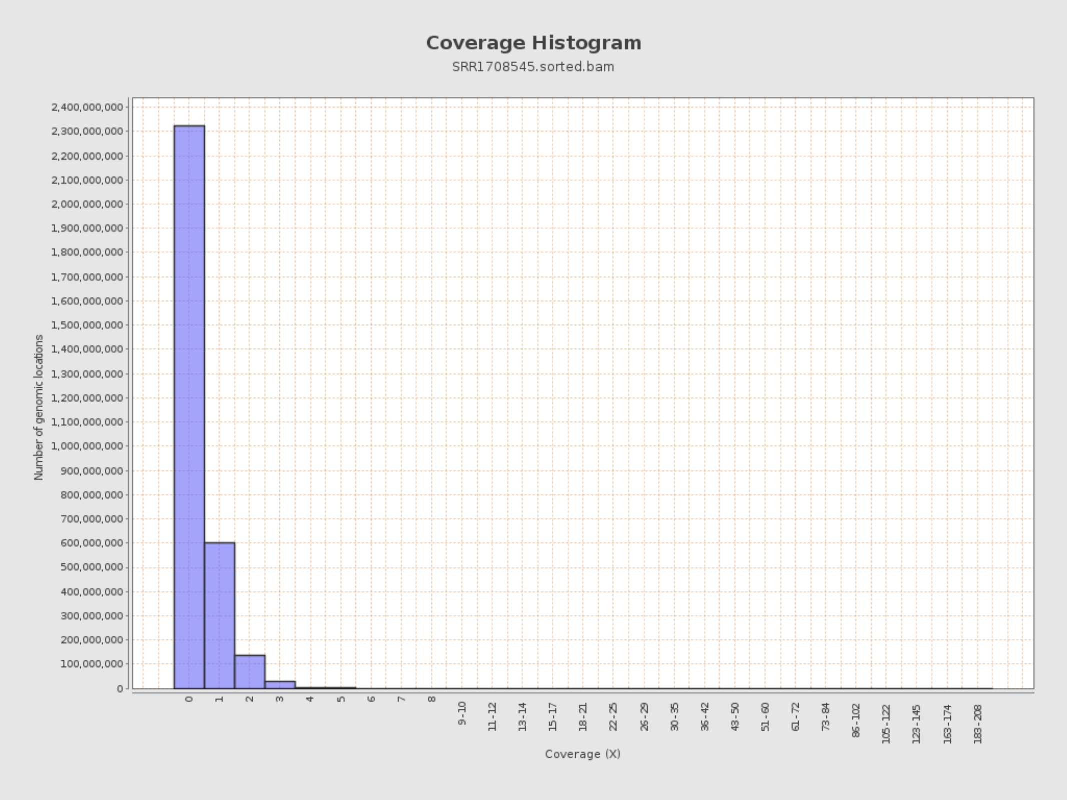
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	77163991	0.3096	0.626
chr2	243199373	89871948	0.3695	0.6594
chr3	198022430	76790159	0.3878	0.6723
chr4	191154276	83956154	0.4392	0.7139
chr5	180915260	70256603	0.3883	0.6721
chr6	171115067	66875054	0.3908	0.6774
chr7	159138663	56463134	0.3548	0.6555

chr8	146364022	55949105	0.3823	0.6705
chr9	141213431	40989735	0.2903	0.6006
chr10	135534747	42467137	0.3133	0.6085
chr11	135006516	44585866	0.3302	0.6357
chr12	133851895	46150250	0.3448	0.6466
chr13	115169878	42260683	0.3669	0.672
chr14	107349540	32404375	0.3019	0.6171
chr15	102531392	25650786	0.2502	0.5595
chr16	90354753	17809455	0.1971	0.4918
chr17	81195210	14904153	0.1836	0.4765
chr18	78077248	29744094	0.381	0.6708
chr19	59128983	6441954	0.1089	0.3562
chr20	63025520	14598308	0.2316	0.5334
chr21	48129895	13092226	0.272	0.6022
chr22	51304566	4799581	0.0936	0.3375
chrMT	16571	1982	0.1196	0.3574
chrX	155270560	30461612	0.1962	0.4646
chrY	59373566	4446636	0.0749	0.304

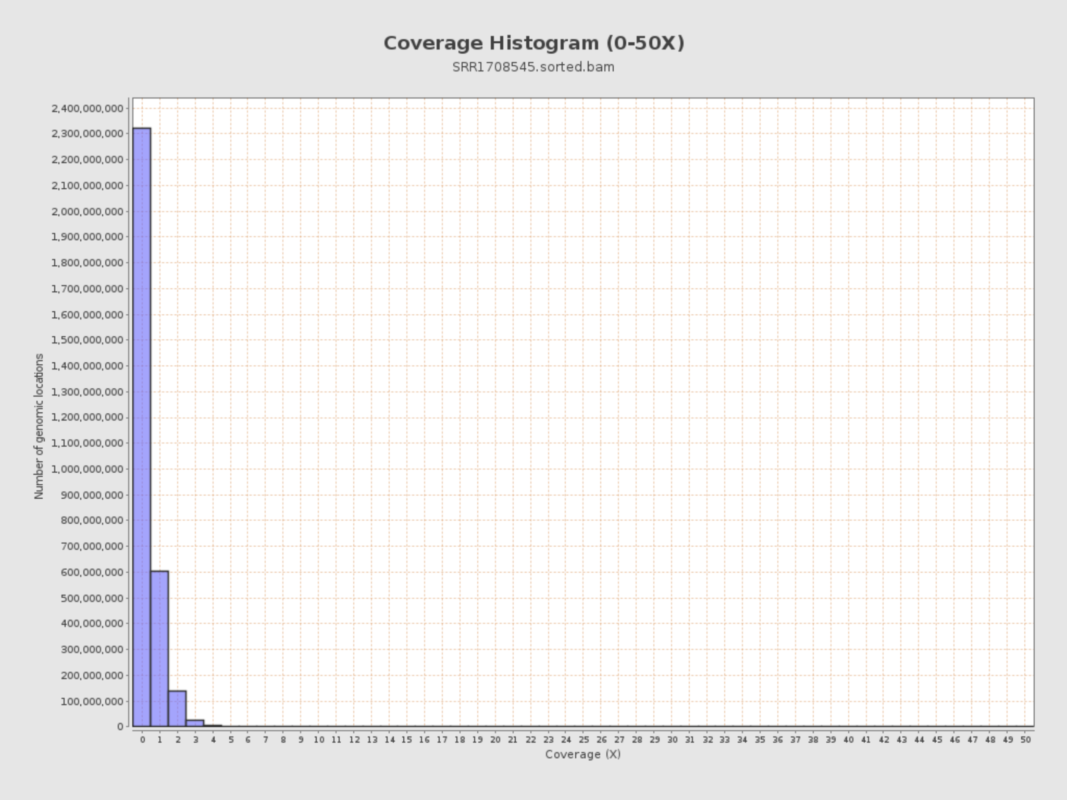
3. Results : Coverage across reference



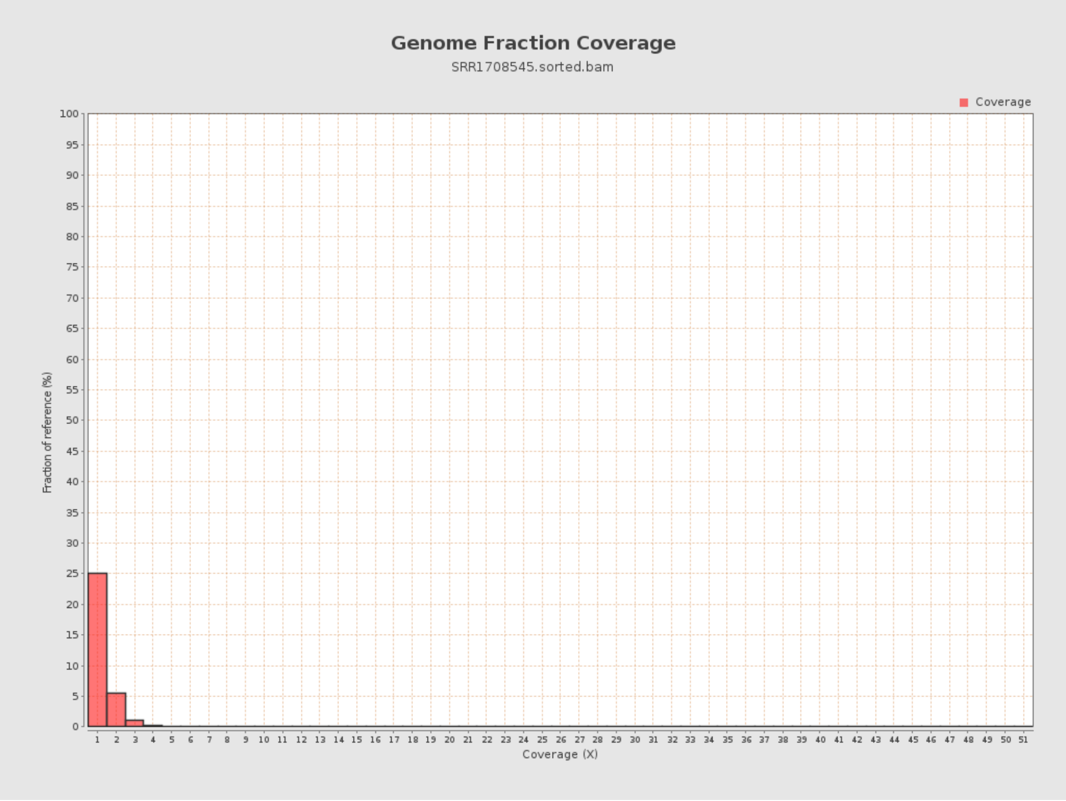
4. Results : Coverage Histogram



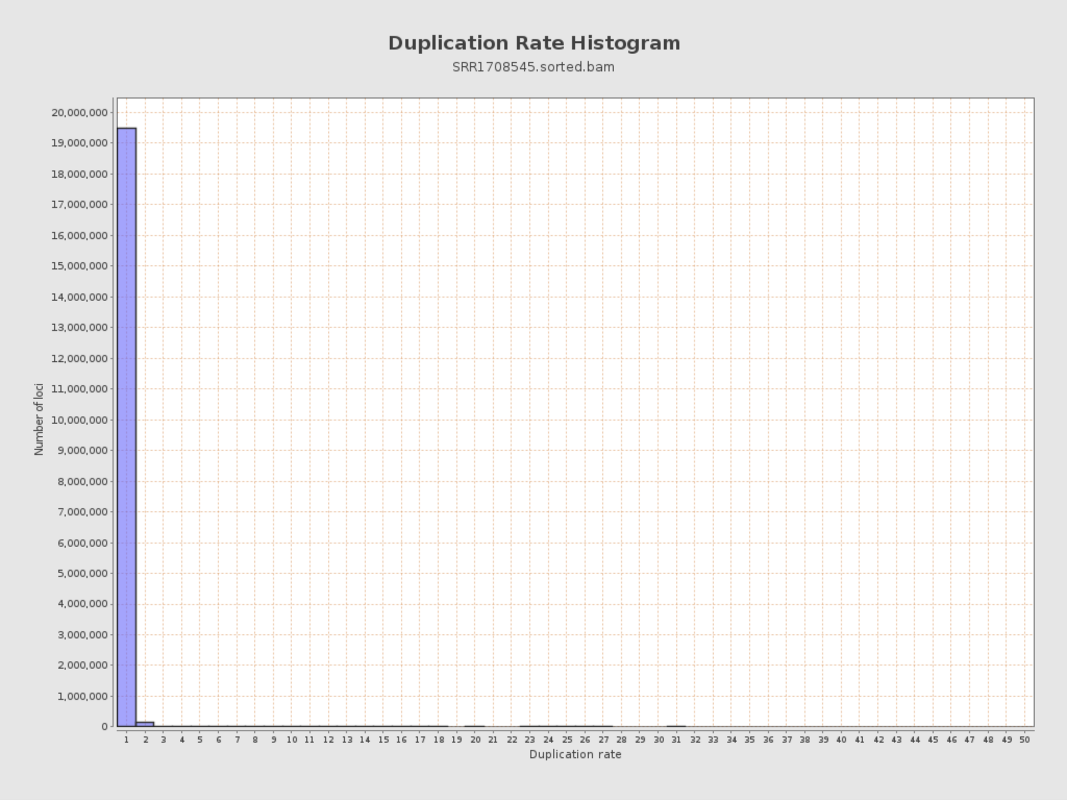
5. Results : Coverage Histogram (0-50X)



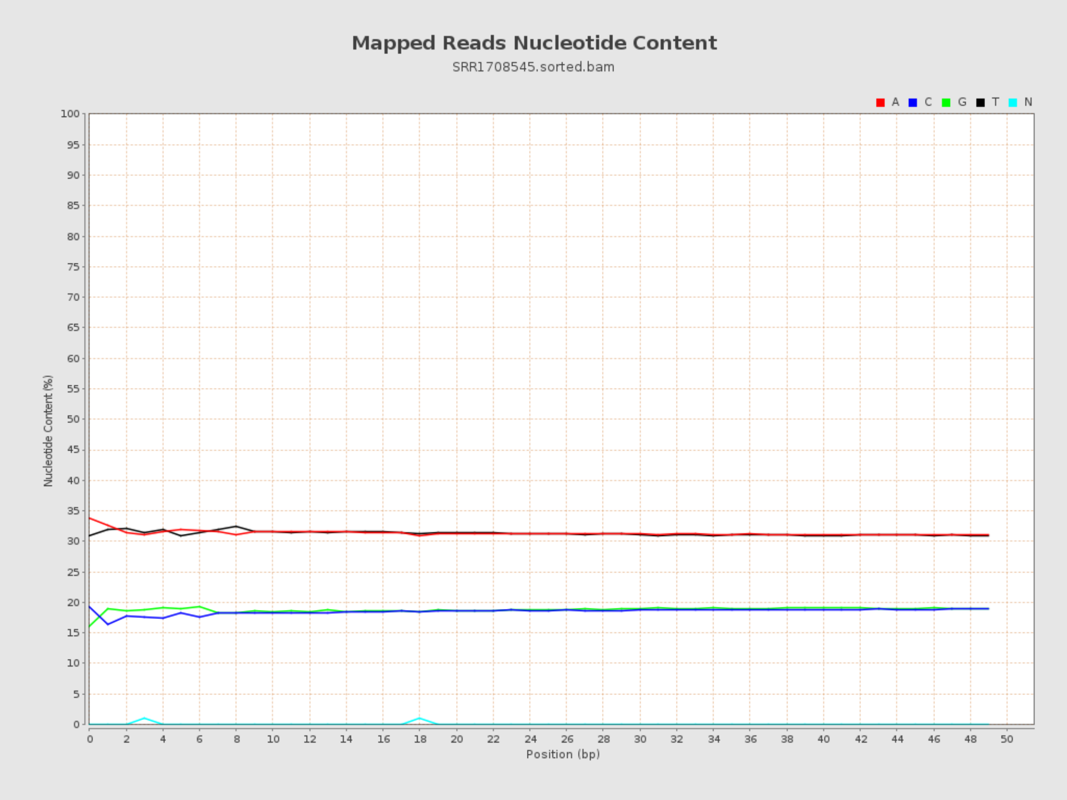
6. Results : Genome Fraction Coverage



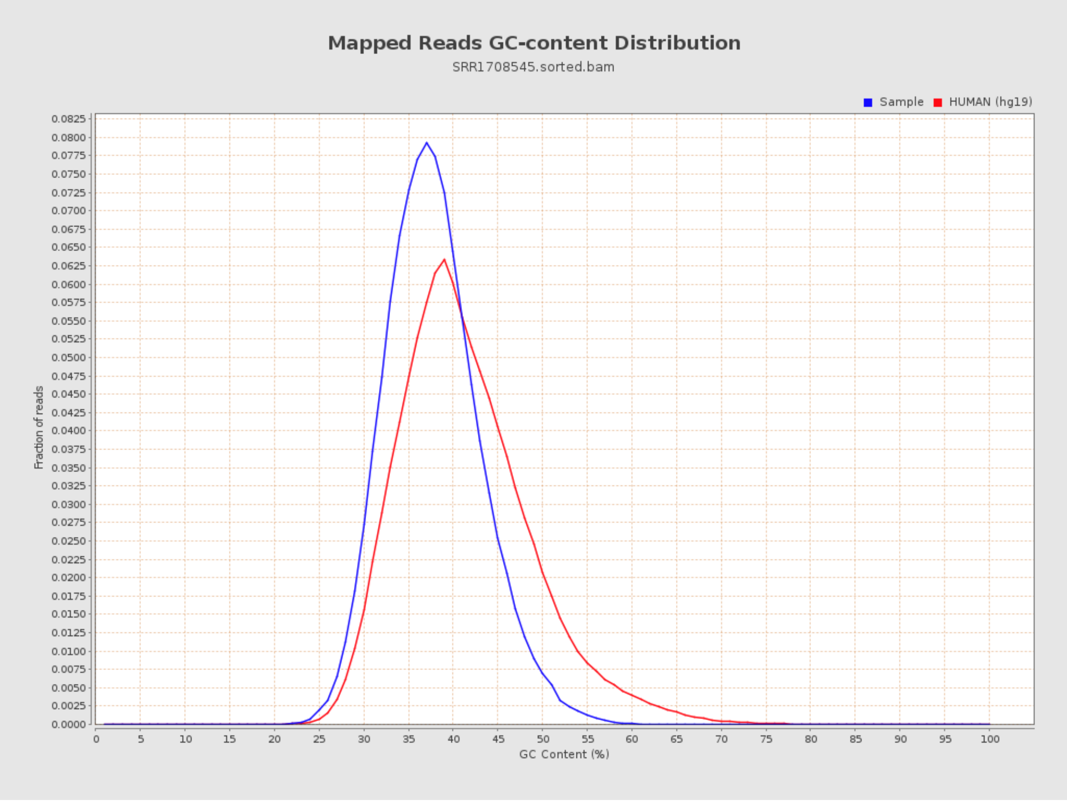
7. Results : Duplication Rate Histogram



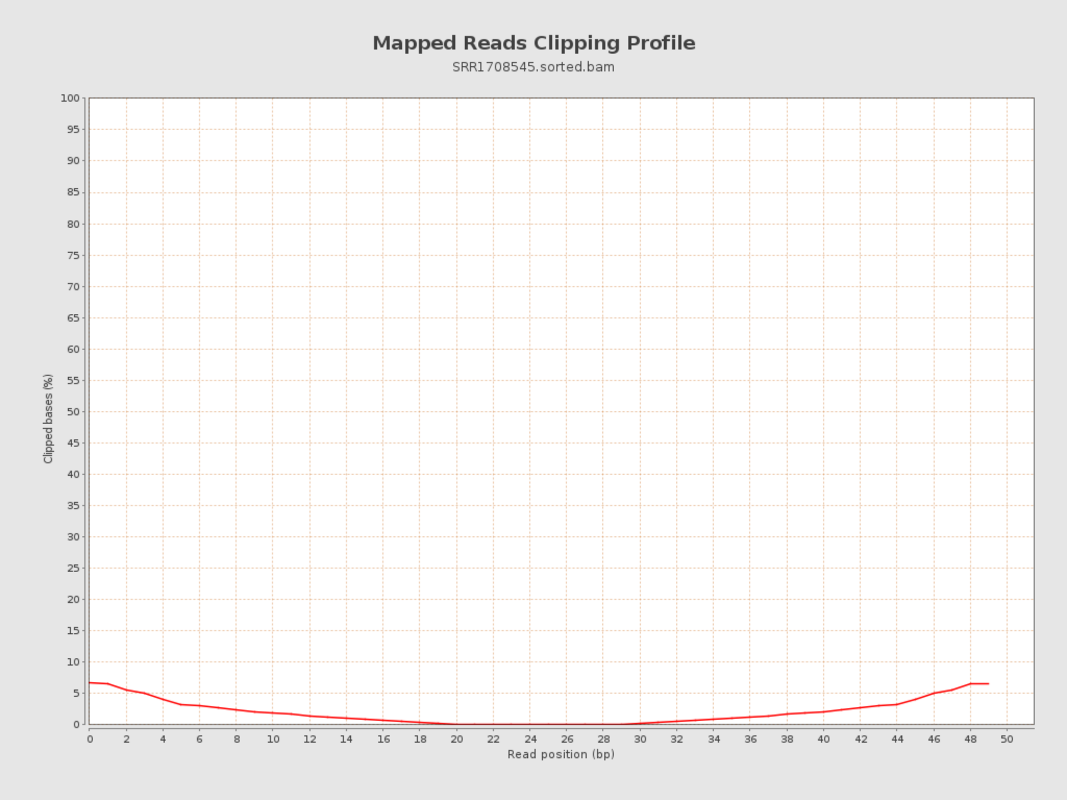
8. Results : Mapped Reads Nucleotide Content



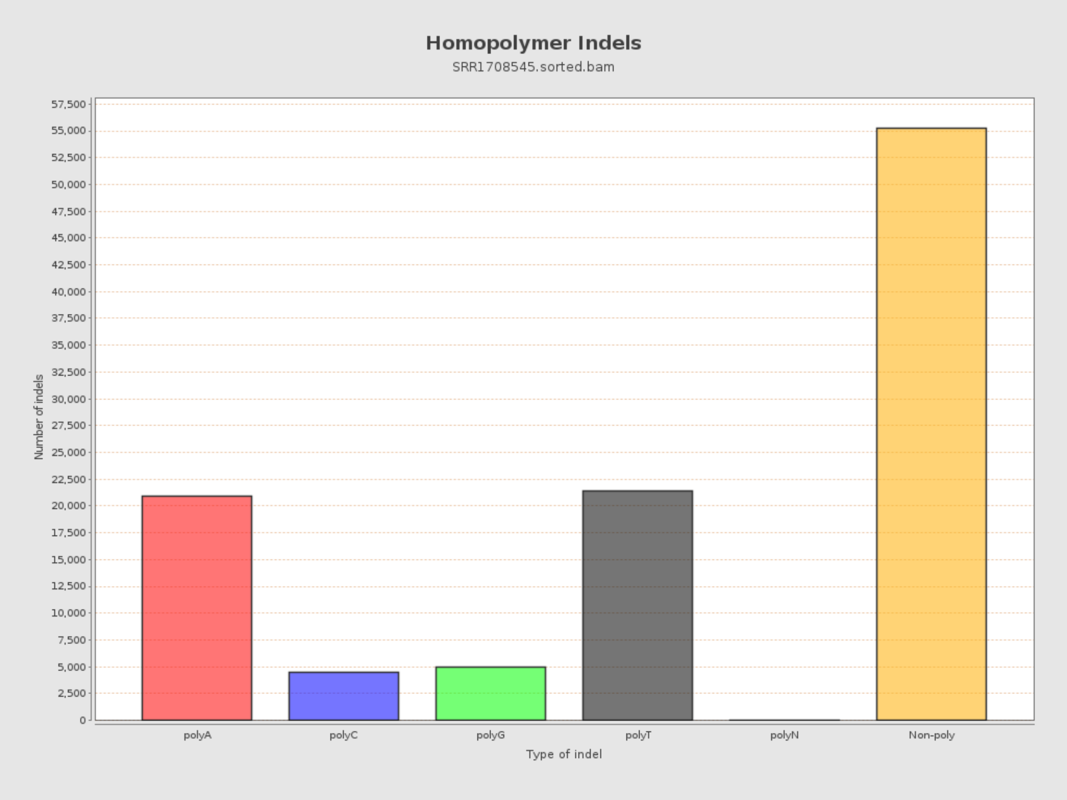
9. Results : Mapped Reads GC-content Distribution



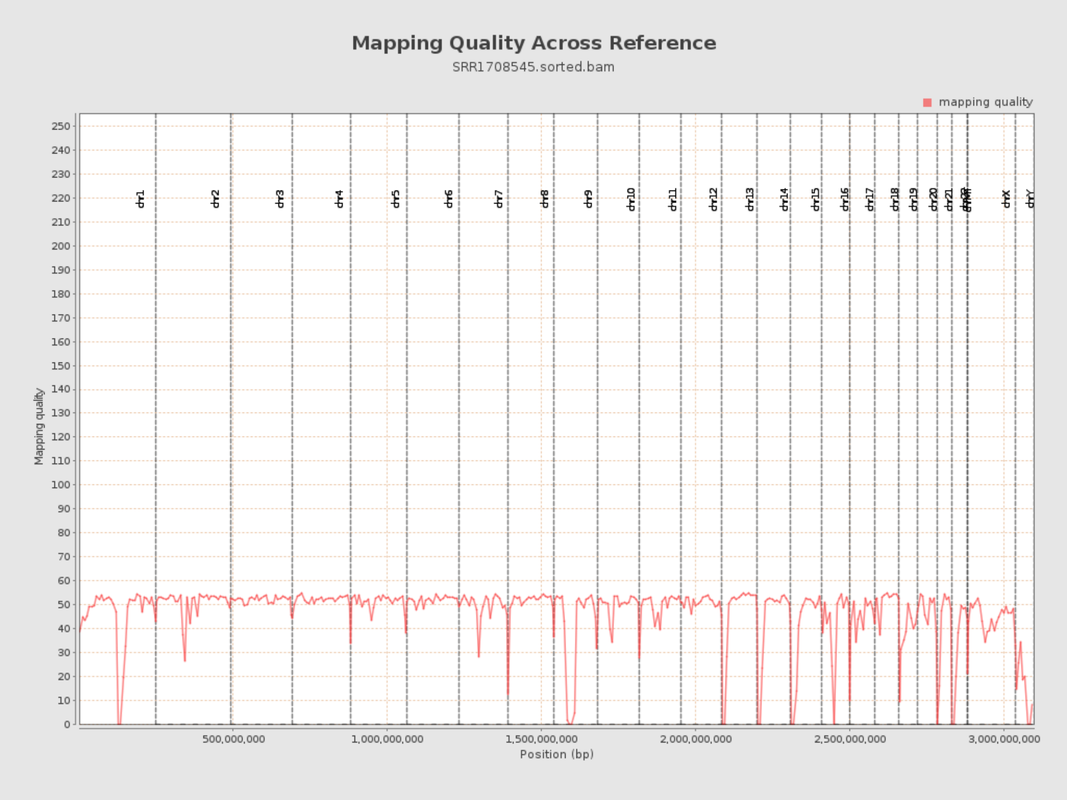
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram