Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:57:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708517.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_SRR1708517 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708517.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708517.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,123,733
Mapped reads	2,148,311 / 68.77%
Unmapped reads	975,422 / 31.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	414 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	110,836 / 3.55%
Duplication rate	4%
Clipped reads	424,955 / 13.6%

2.2. ACGT Content

Number/percentage of A's	29,824,862 / 28.98%
Number/percentage of C's	18,951,391 / 18.41%
Number/percentage of T's	33,133,847 / 32.19%
Number/percentage of G's	21,009,130 / 20.41%
Number/percentage of N's	1,402 / 0%
GC Percentage	38.83%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.3594

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

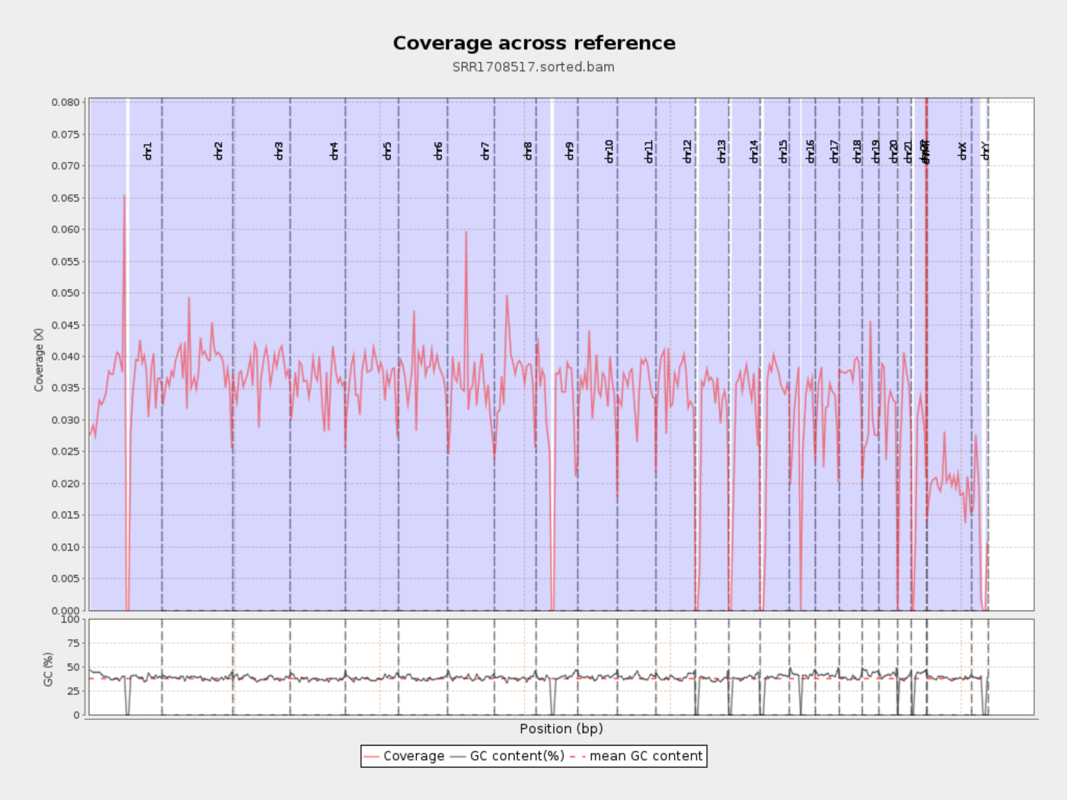
General error rate	0.49%
Mismatches	496,526
Insertions	4,860
Mapped reads with at least one insertion	0.23%
Deletions	12,341
Mapped reads with at least one deletion	0.57%
Homopolymer indels	49%

2.6. Chromosome stats

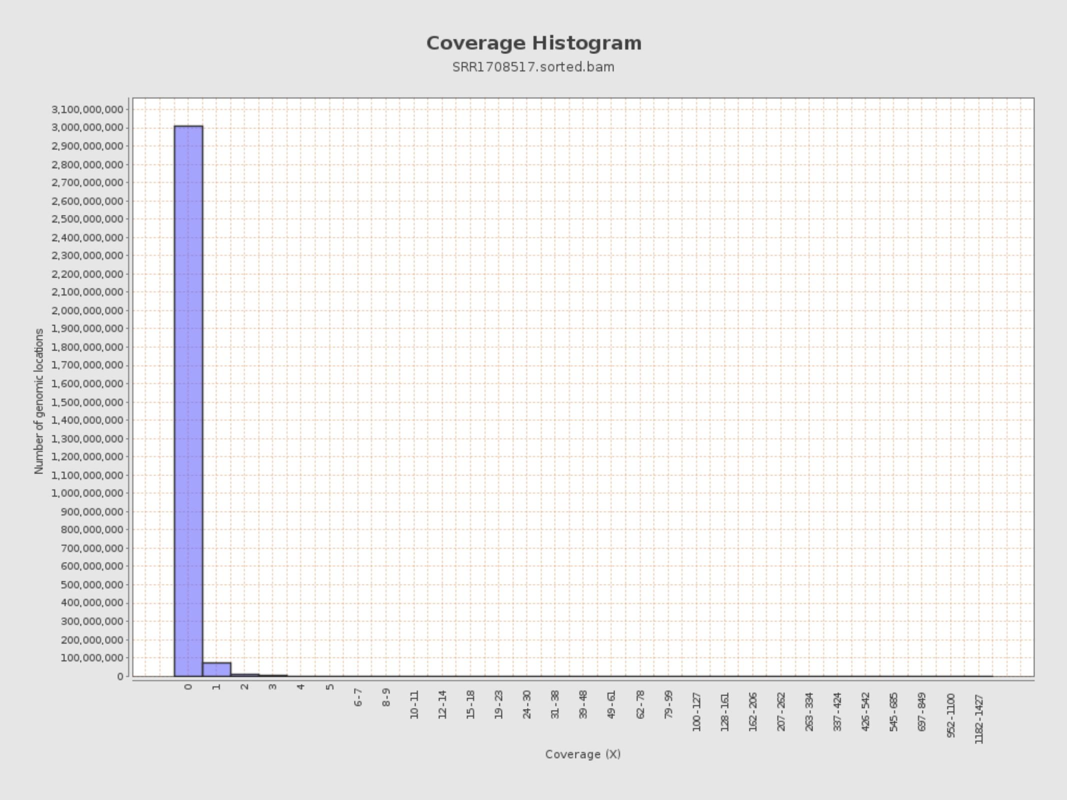
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8553461	0.0343	0.6751
chr2	243199373	9350897	0.0384	0.3014
chr3	198022430	7482875	0.0378	0.2289
chr4	191154276	6839383	0.0358	0.2255
chr5	180915260	6606940	0.0365	0.2252
chr6	171115067	6474508	0.0378	0.2737
chr7	159138663	5717129	0.0359	0.3967

chr8	146364022	5386947	0.0368	0.7911
chr9	141213431	4372193	0.031	0.2404
chr10	135534747	4825760	0.0356	0.2831
chr11	135006516	4720055	0.035	0.3173
chr12	133851895	4757385	0.0355	0.2232
chr13	115169878	3328621	0.0289	0.1998
chr14	107349540	3108655	0.029	0.204
chr15	102531392	3031549	0.0296	0.1997
chr16	90354753	2613644	0.0289	0.2045
chr17	81195210	2568176	0.0316	0.251
chr18	78077248	2944565	0.0377	0.4207
chr19	59128983	1752307	0.0296	0.459
chr20	63025520	2043084	0.0324	0.2105
chr21	48129895	1444068	0.03	0.2316
chr22	51304566	1076887	0.021	0.1877
chrMT	16571	208046	12.5548	9.5031
chrX	155270560	3053267	0.0197	0.1875
chrY	59373566	678895	0.0114	0.1317

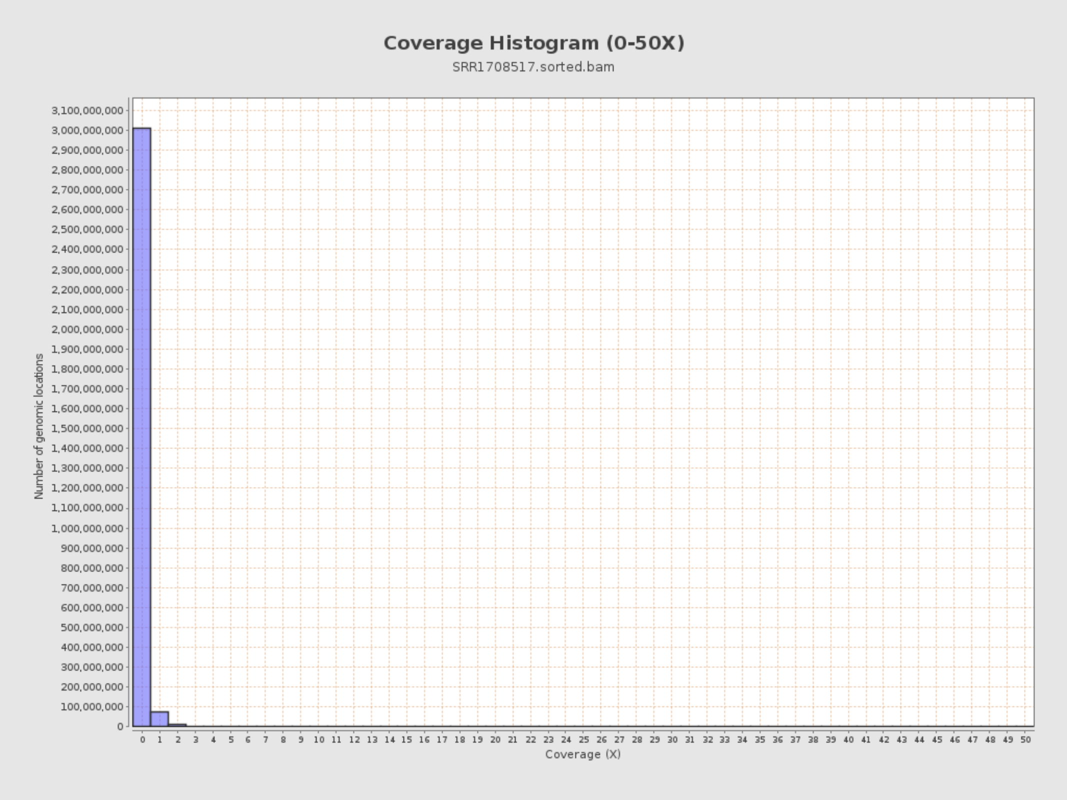
3. Results : Coverage across reference



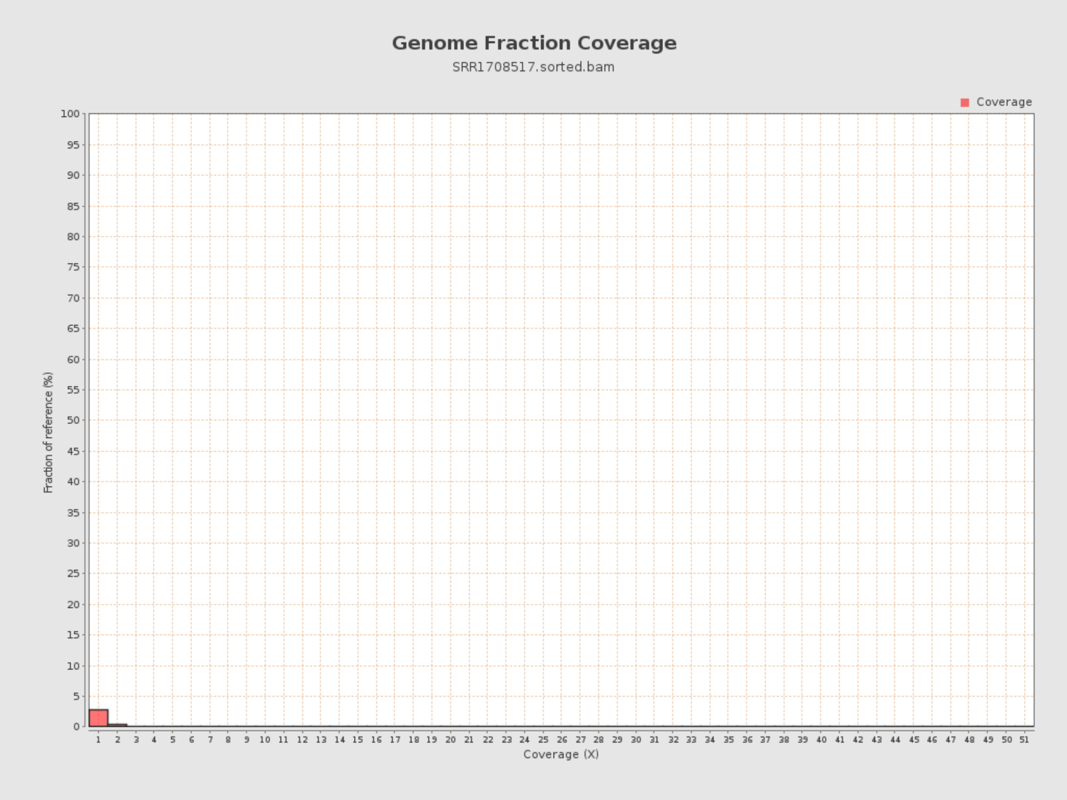
4. Results : Coverage Histogram



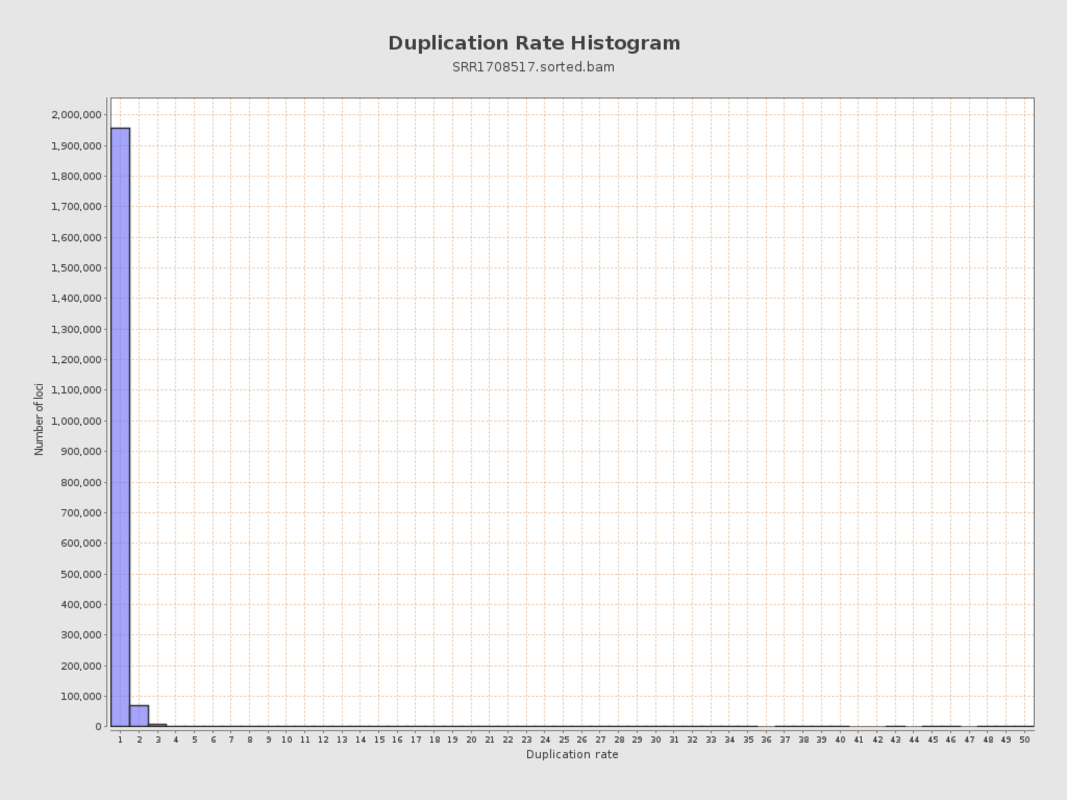
5. Results : Coverage Histogram (0-50X)



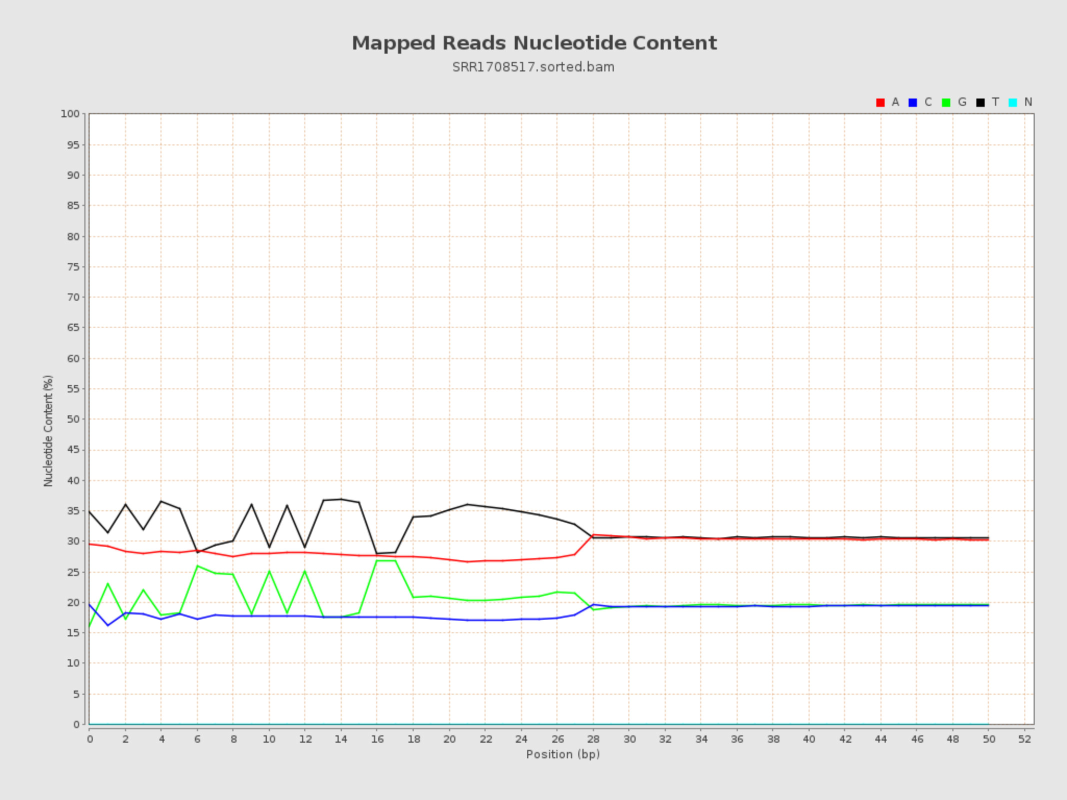
6. Results : Genome Fraction Coverage



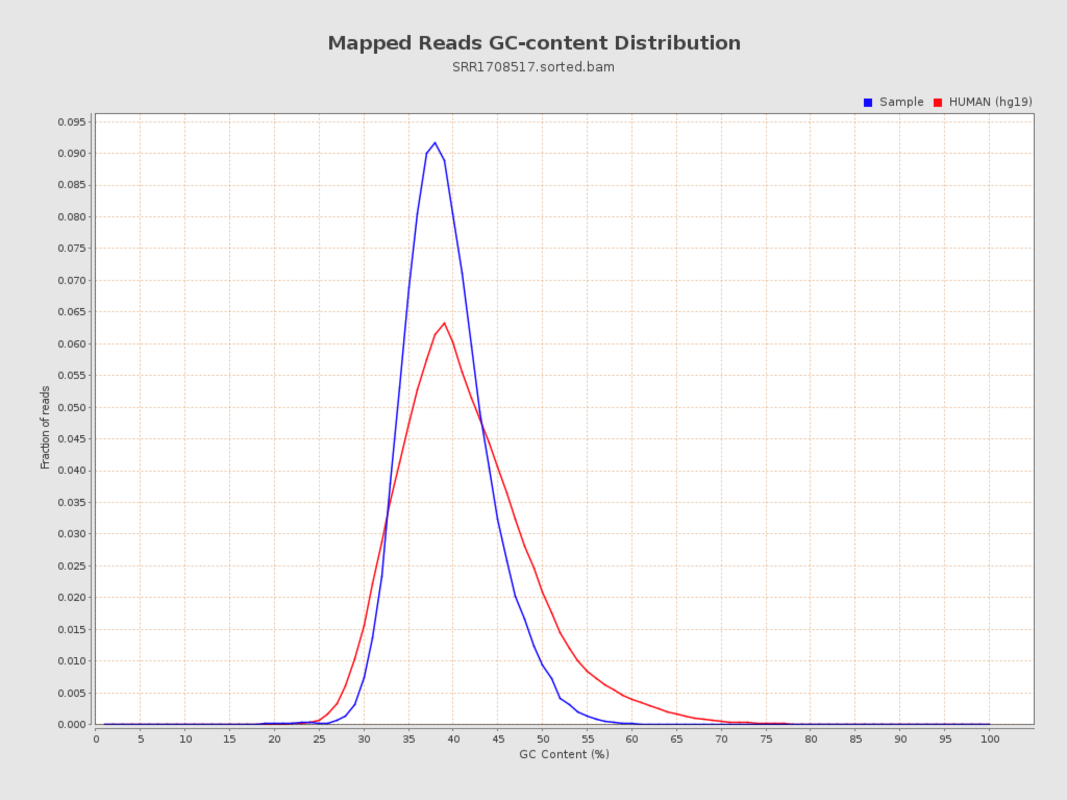
7. Results : Duplication Rate Histogram



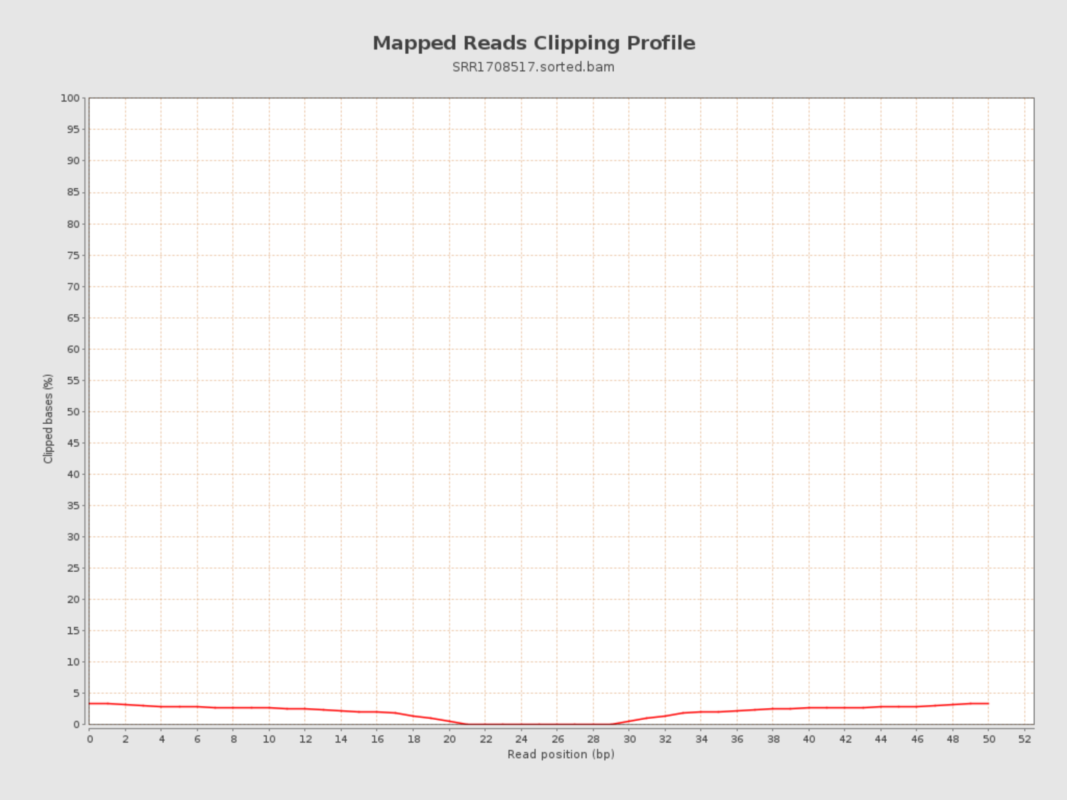
8. Results : Mapped Reads Nucleotide Content



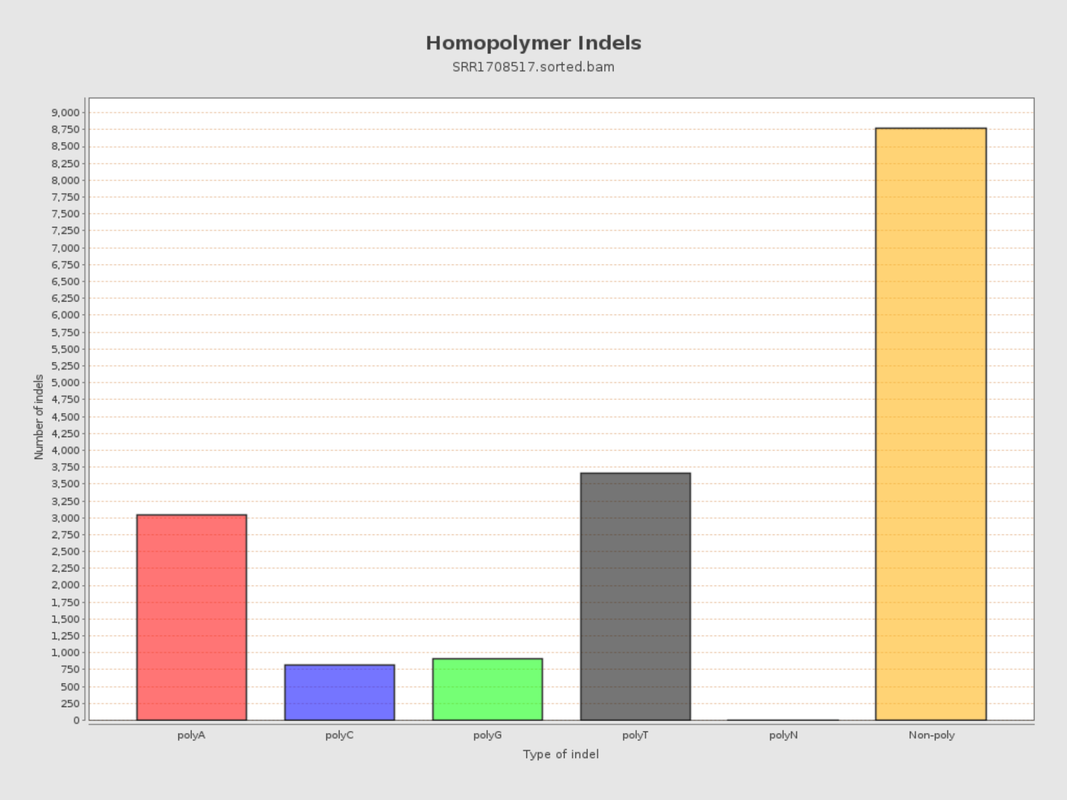
9. Results : Mapped Reads GC-content Distribution



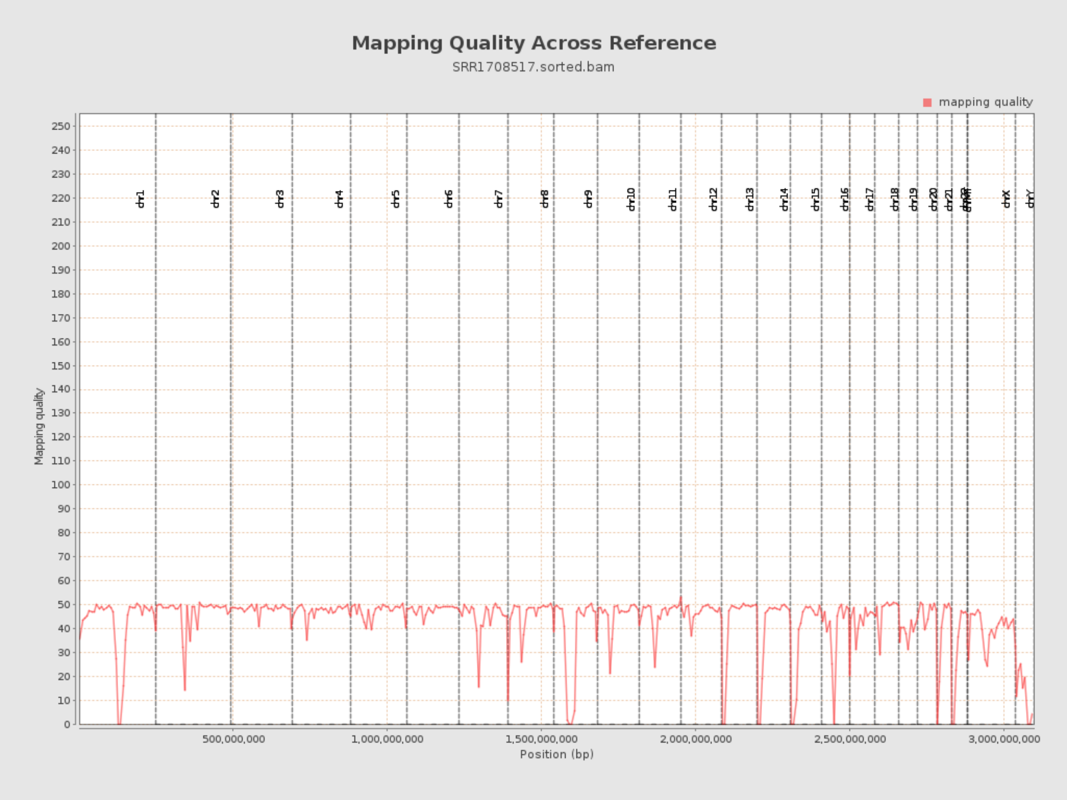
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram