Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:54:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008708.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_SRR6008708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:54:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,948,619
Mapped reads	1,394,275 / 71.55%
Unmapped reads	554,344 / 28.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,192 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	38,834 / 1.99%
Duplication rate	2.06%
Clipped reads	613,245 / 31.47%

2.2. ACGT Content

Number/percentage of A's	28,482,239 / 30.71%
Number/percentage of C's	15,724,608 / 16.95%
Number/percentage of T's	27,812,979 / 29.98%
Number/percentage of G's	20,717,314 / 22.33%
Number/percentage of N's	21,336 / 0.02%
GC Percentage	39.29%

2.3. Coverage

Mean	0.03

Standard Deviation	0.2352

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

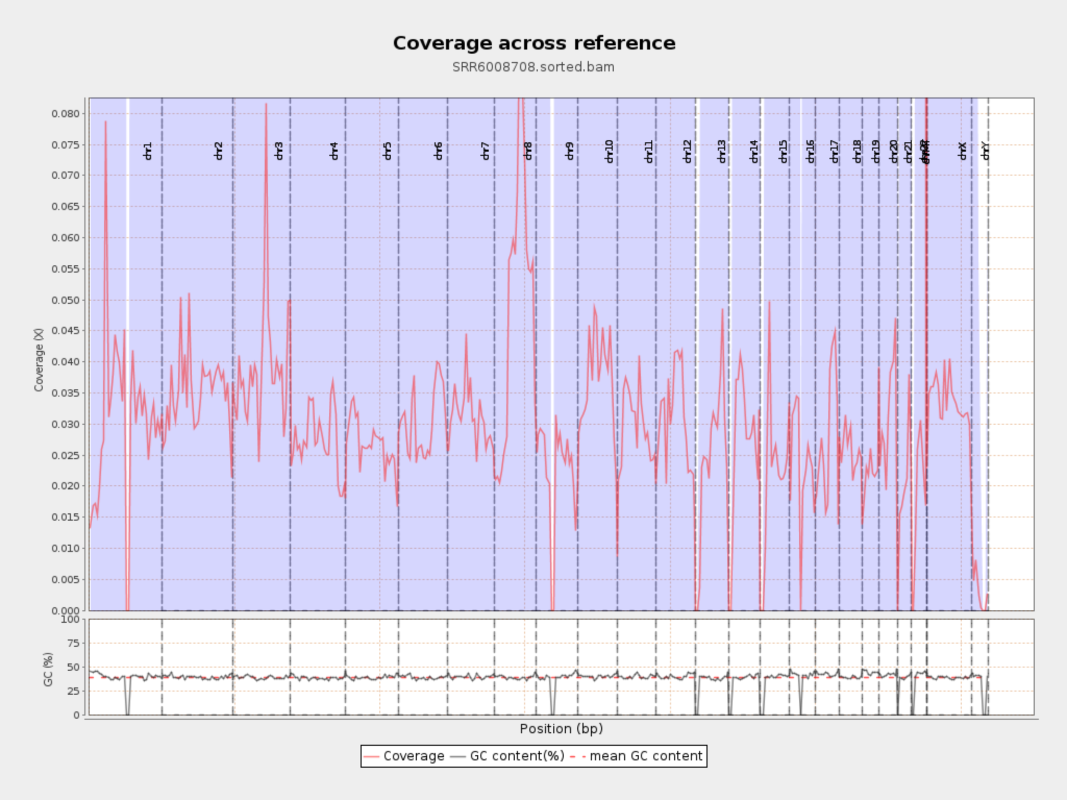
General error rate	0.96%
Mismatches	882,637
Insertions	7,036
Mapped reads with at least one insertion	0.5%
Deletions	29,461
Mapped reads with at least one deletion	2.09%
Homopolymer indels	48.22%

2.6. Chromosome stats

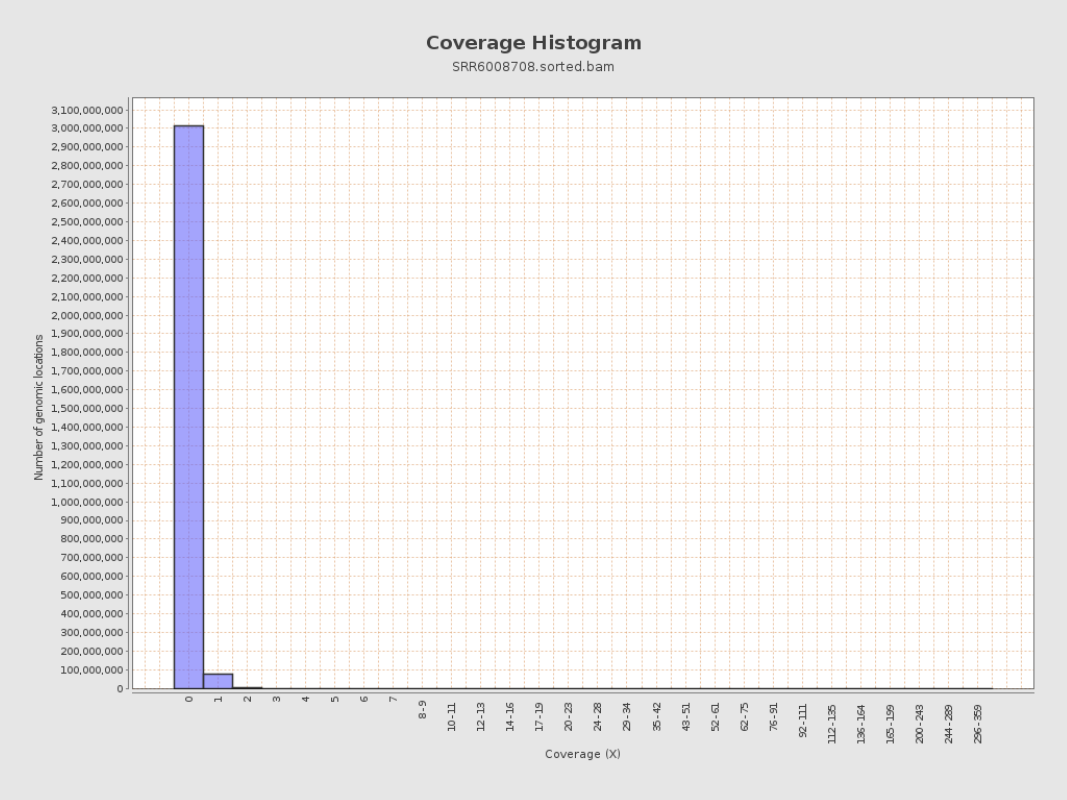
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7576421	0.0304	0.3215
chr2	243199373	8615750	0.0354	0.2889
chr3	198022430	7763393	0.0392	0.2198
chr4	191154276	5209607	0.0273	0.1822
chr5	180915260	4855315	0.0268	0.1794
chr6	171115067	5210342	0.0304	0.2071
chr7	159138663	5010548	0.0315	0.2971

chr8	146364022	7266180	0.0496	0.334
chr9	141213431	3148467	0.0223	0.2021
chr10	135534747	5096603	0.0376	0.2481
chr11	135006516	4008327	0.0297	0.2275
chr12	133851895	4148337	0.031	0.1953
chr13	115169878	2803861	0.0243	0.1741
chr14	107349540	2859482	0.0266	0.1842
chr15	102531392	2224955	0.0217	0.1645
chr16	90354753	2141100	0.0237	0.1805
chr17	81195210	2255233	0.0278	0.2002
chr18	78077248	2020101	0.0259	0.335
chr19	59128983	1325587	0.0224	0.2048
chr20	63025520	1989068	0.0316	0.1962
chr21	48129895	967321	0.0201	0.1603
chr22	51304566	898671	0.0175	0.144
chrMT	16571	21840	1.318	1.6555
chrX	155270560	5196187	0.0335	0.211
chrY	59373566	191878	0.0032	0.0745

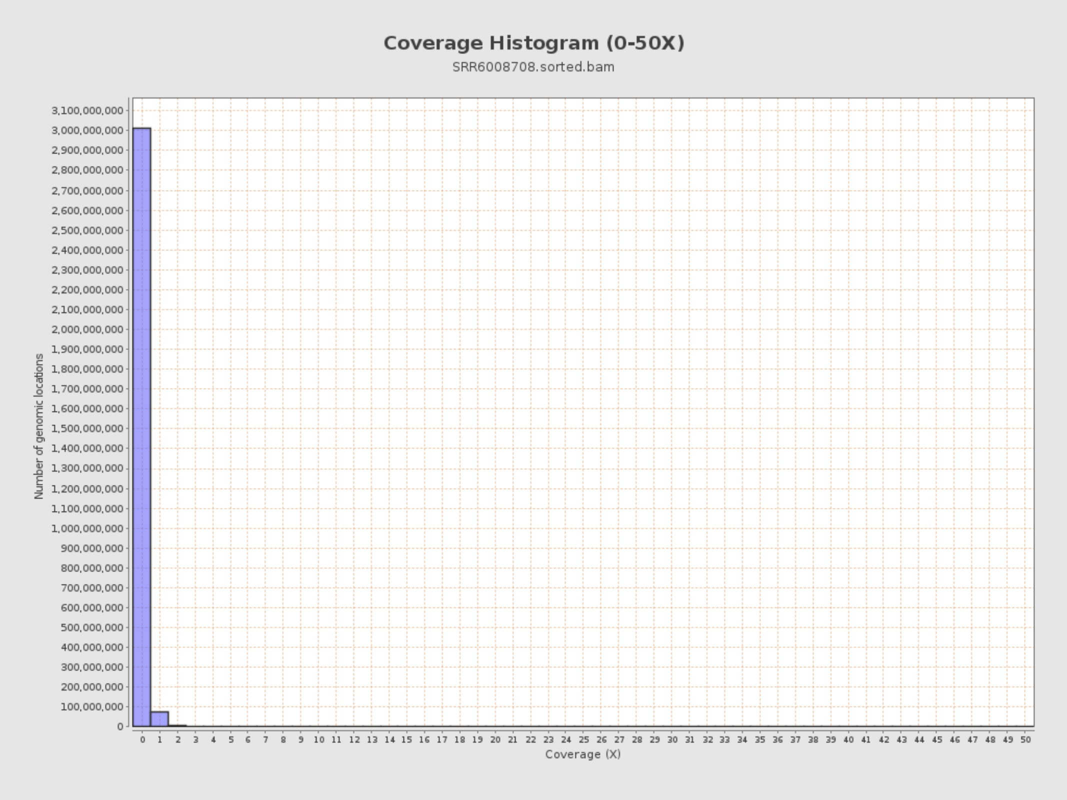
3. Results : Coverage across reference



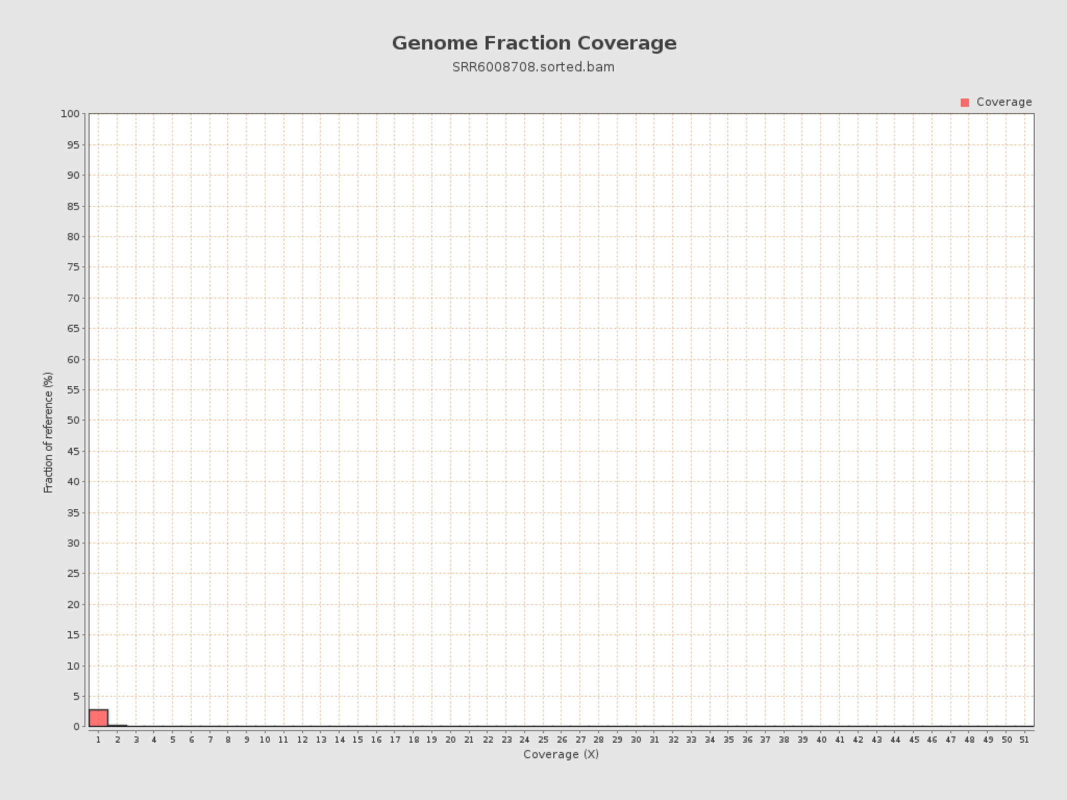
4. Results : Coverage Histogram



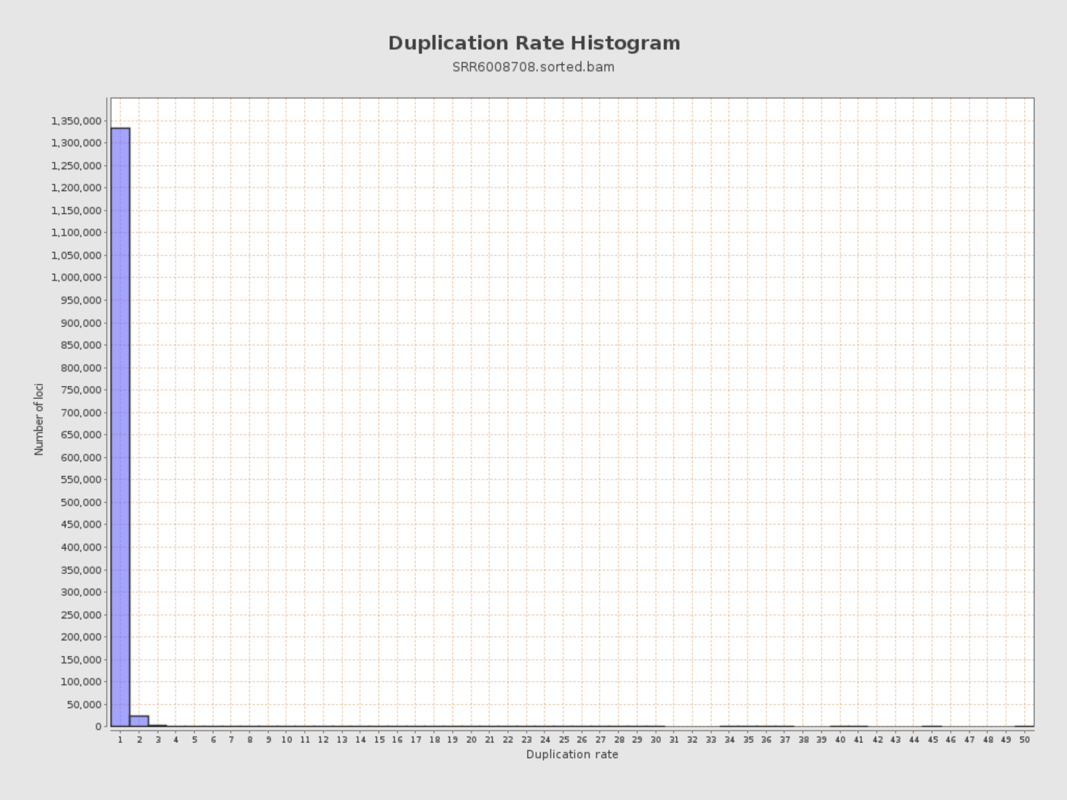
5. Results : Coverage Histogram (0-50X)



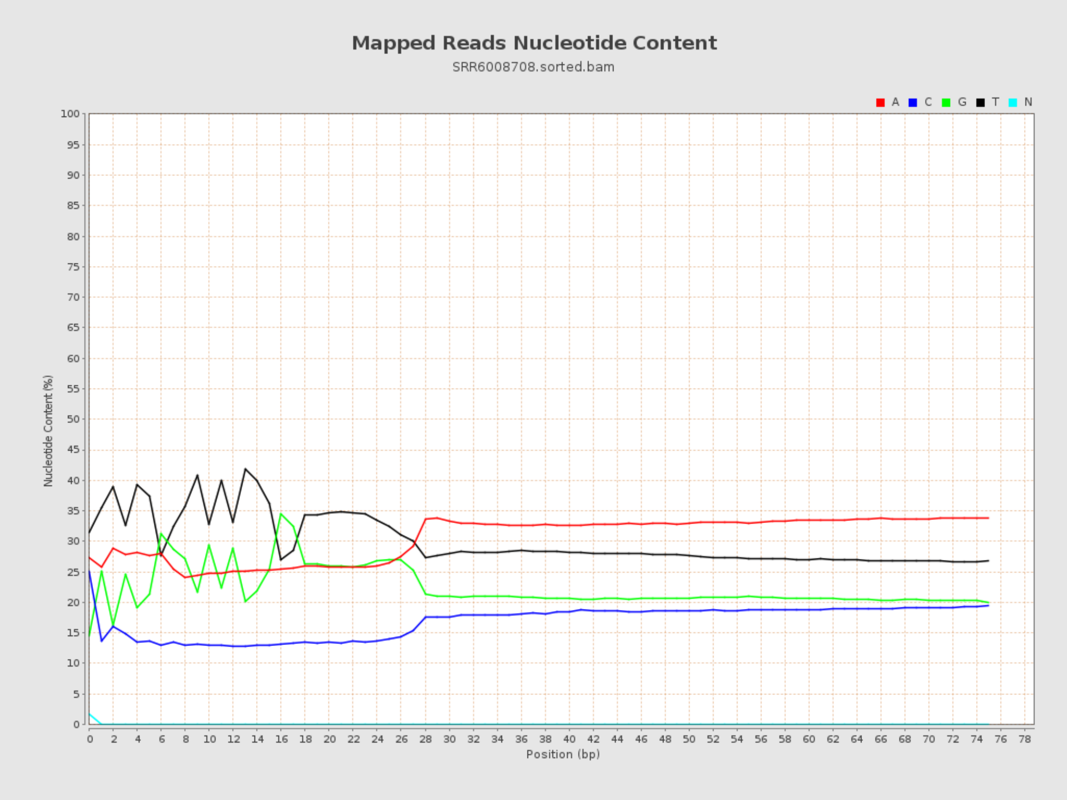
6. Results : Genome Fraction Coverage



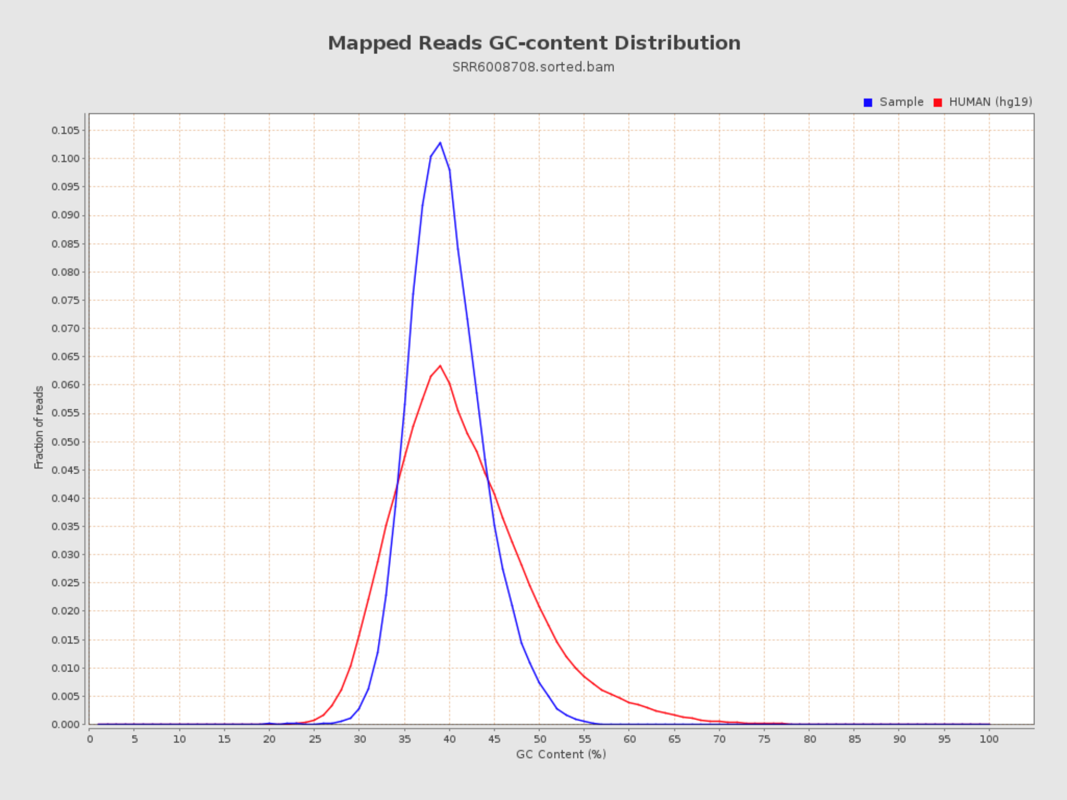
7. Results : Duplication Rate Histogram



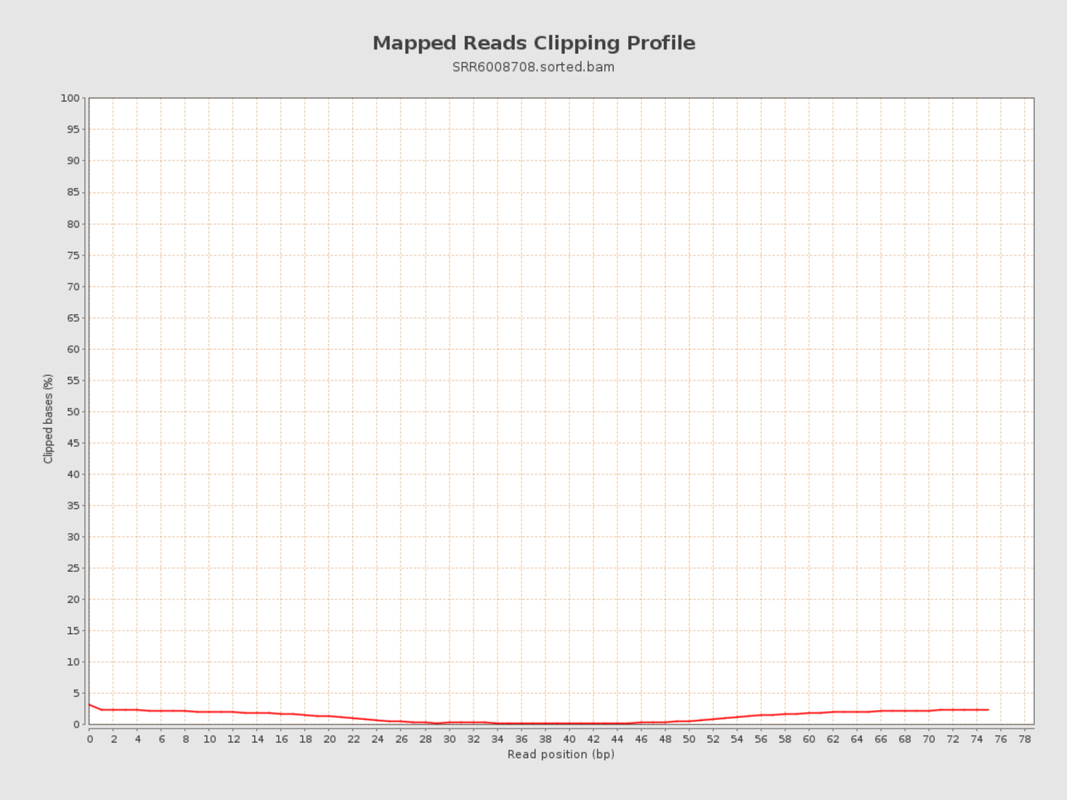
8. Results : Mapped Reads Nucleotide Content



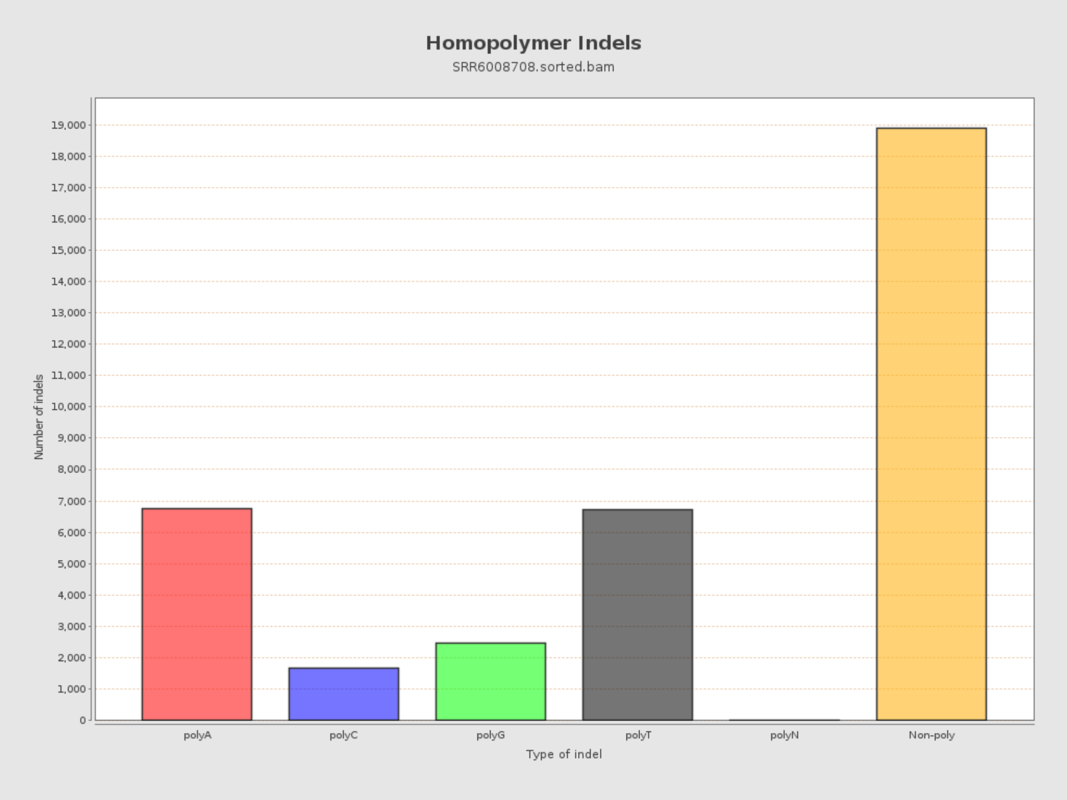
9. Results : Mapped Reads GC-content Distribution



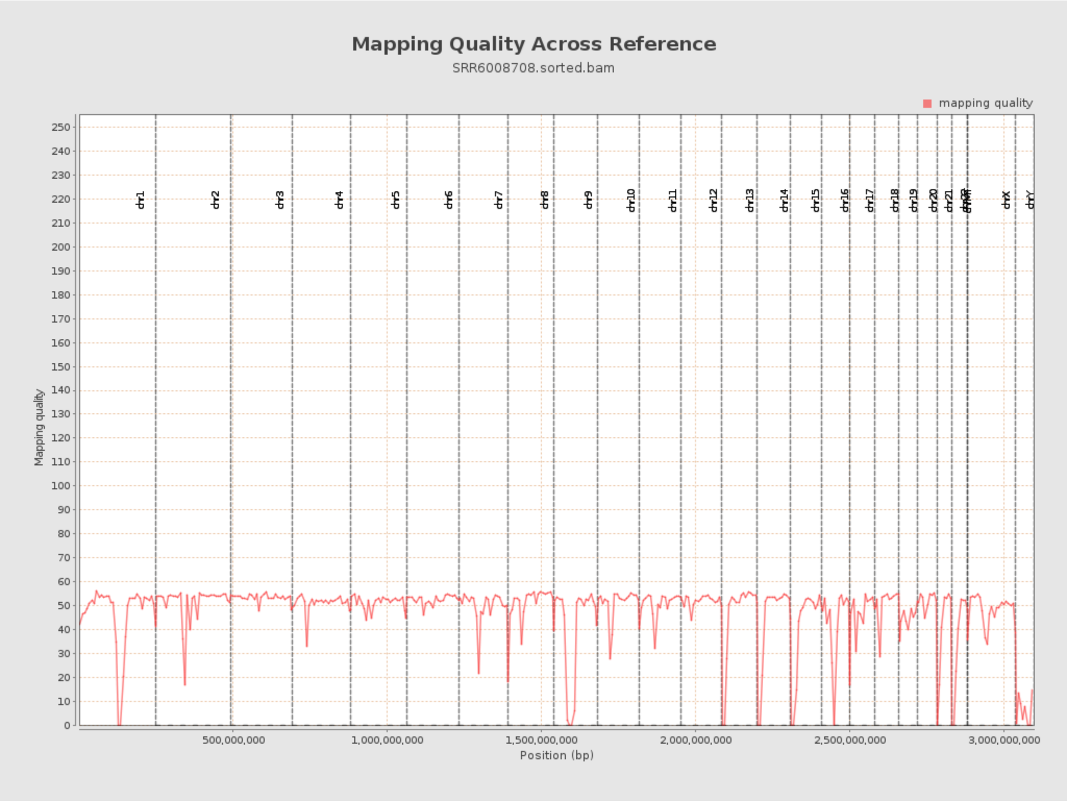
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram