Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:44:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008704.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_SRR6008704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008704.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:44:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,649,852
Mapped reads	1,252,773 / 75.93%
Unmapped reads	397,079 / 24.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,755 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	21,427 / 1.3%
Duplication rate	1.25%
Clipped reads	561,188 / 34.01%

2.2. ACGT Content

Number/percentage of A's	25,318,063 / 30.26%
Number/percentage of C's	14,592,978 / 17.44%
Number/percentage of T's	24,843,997 / 29.69%
Number/percentage of G's	18,892,980 / 22.58%
Number/percentage of N's	16,820 / 0.02%
GC Percentage	40.02%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2238

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

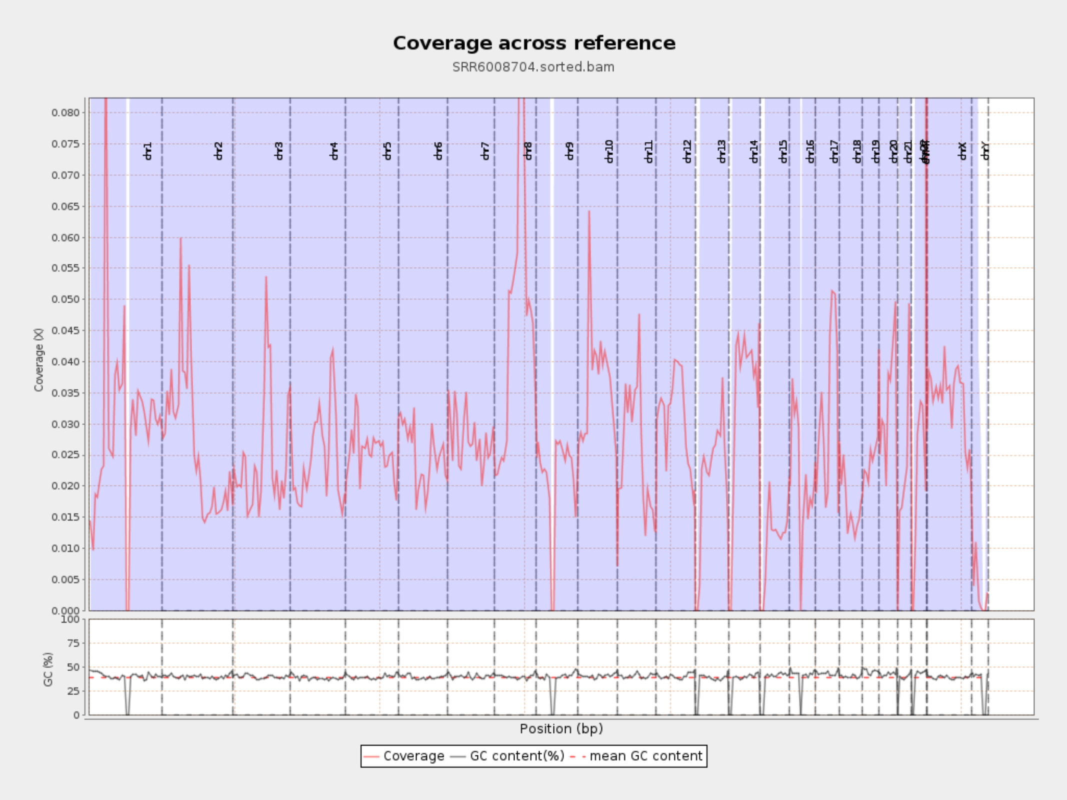
General error rate	0.92%
Mismatches	758,992
Insertions	5,885
Mapped reads with at least one insertion	0.47%
Deletions	27,115
Mapped reads with at least one deletion	2.14%
Homopolymer indels	44.77%

2.6. Chromosome stats

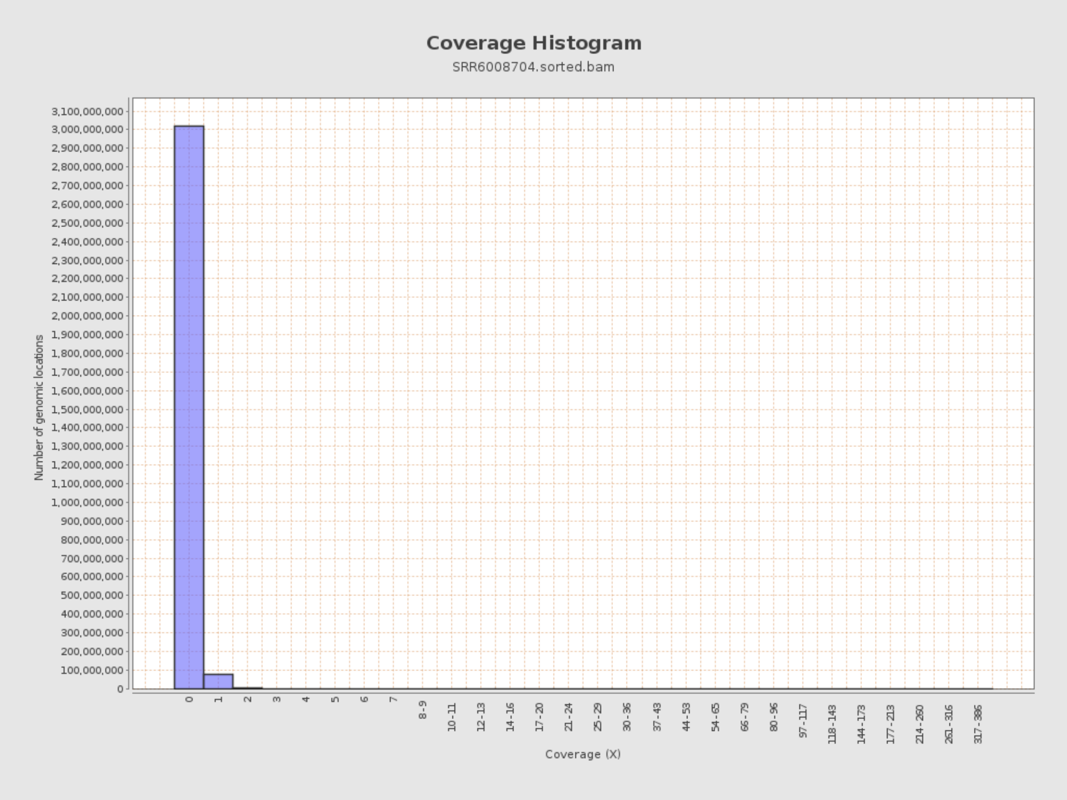
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7357821	0.0295	0.3625
chr2	243199373	6543080	0.0269	0.2551
chr3	198022430	4823176	0.0244	0.1665
chr4	191154276	4678405	0.0245	0.1656
chr5	180915260	4615753	0.0255	0.1648
chr6	171115067	4301774	0.0251	0.1786
chr7	159138663	4394128	0.0276	0.219

chr8	146364022	6999423	0.0478	0.2775
chr9	141213431	2986594	0.0211	0.1914
chr10	135534747	4949012	0.0365	0.3353
chr11	135006516	3471933	0.0257	0.2013
chr12	133851895	4197325	0.0314	0.184
chr13	115169878	2446717	0.0212	0.1497
chr14	107349540	3618444	0.0337	0.194
chr15	102531392	1157358	0.0113	0.1096
chr16	90354753	1948182	0.0216	0.1661
chr17	81195210	2626985	0.0324	0.2104
chr18	78077248	1323339	0.0169	0.3036
chr19	59128983	1446451	0.0245	0.2258
chr20	63025520	2157385	0.0342	0.1943
chr21	48129895	1111634	0.0231	0.1623
chr22	51304566	1046164	0.0204	0.1476
chrMT	16571	14243	0.8595	1.0366
chrX	155270560	5287381	0.0341	0.2037
chrY	59373566	207819	0.0035	0.0886

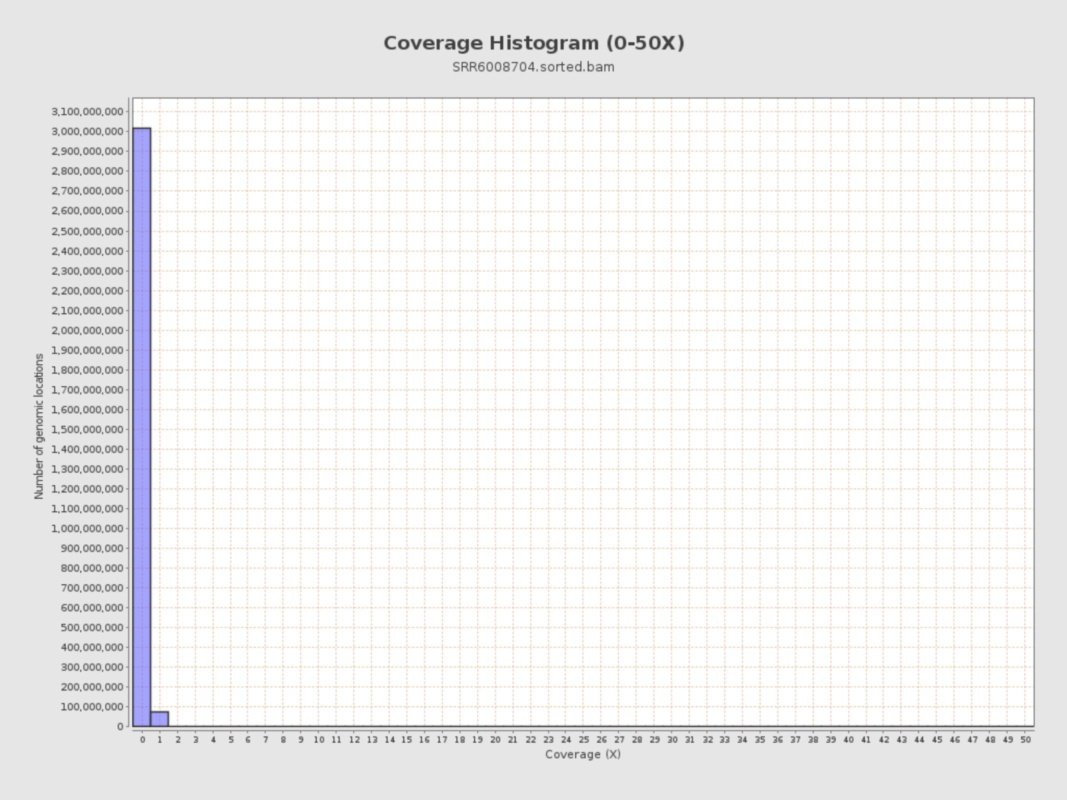
3. Results : Coverage across reference



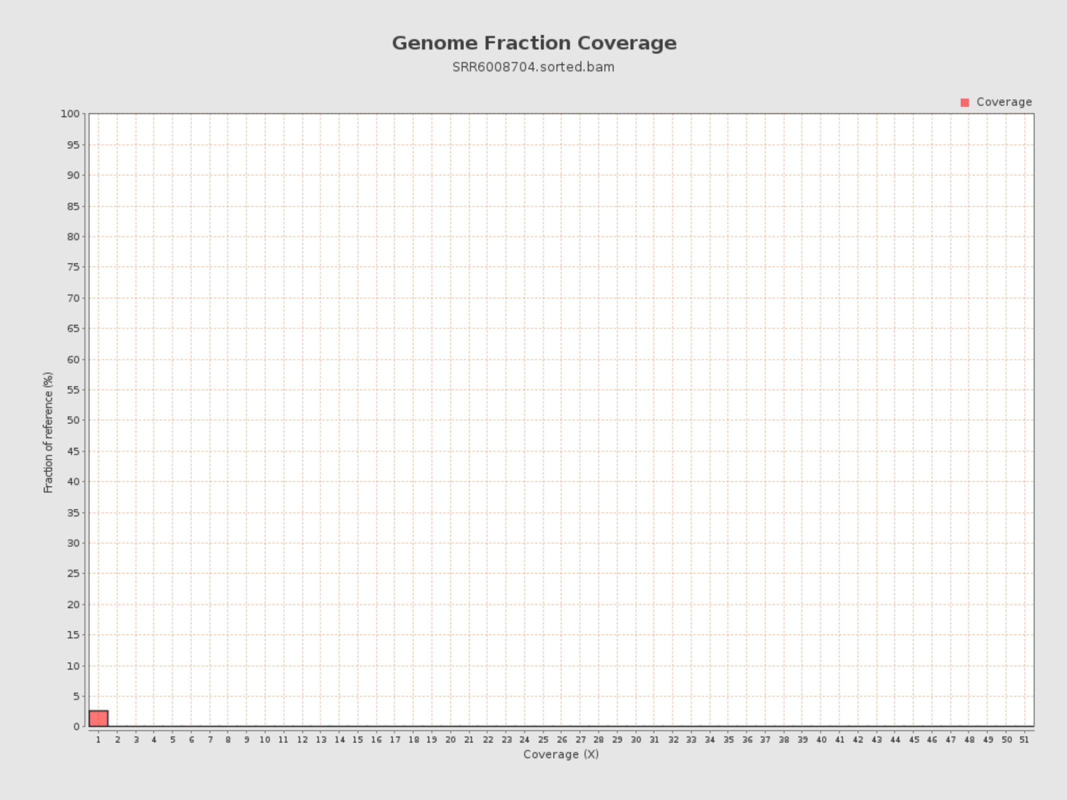
4. Results : Coverage Histogram



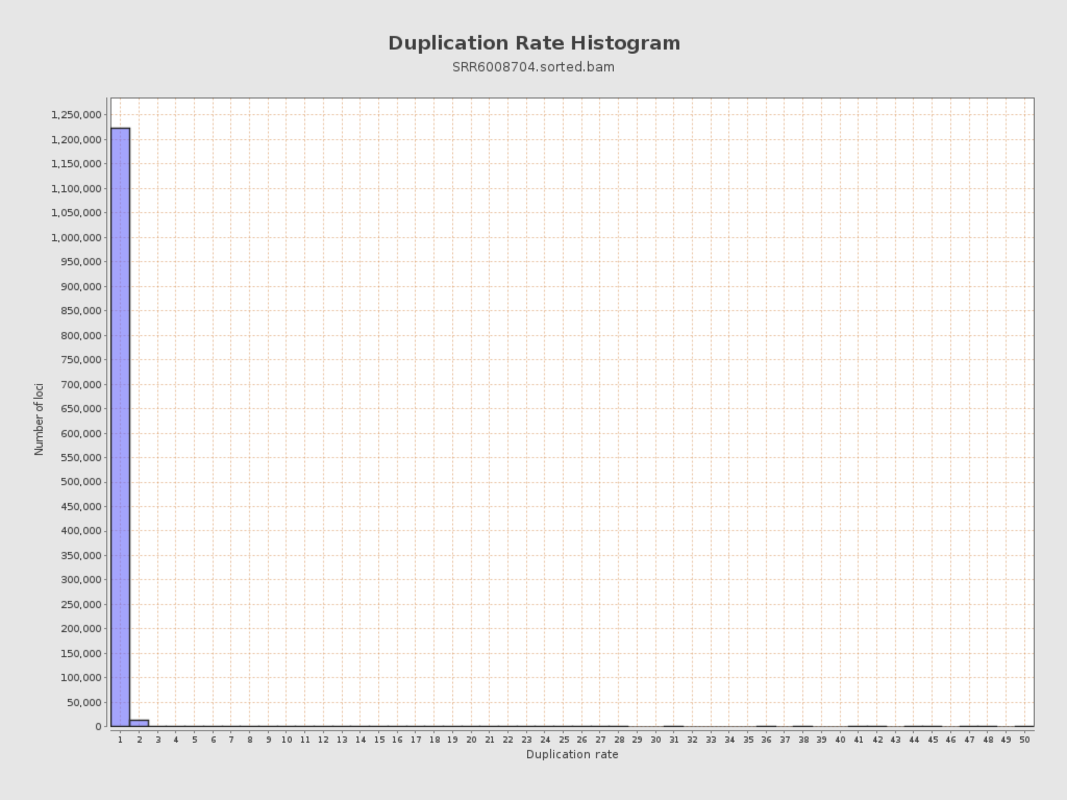
5. Results : Coverage Histogram (0-50X)



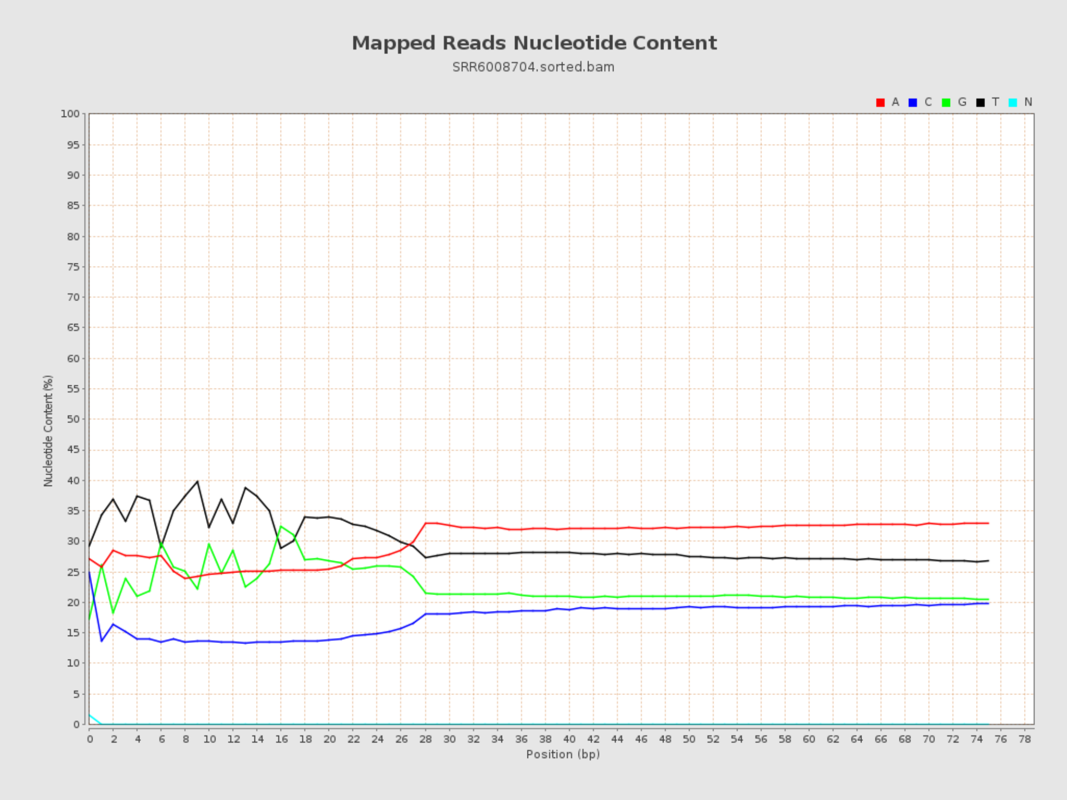
6. Results : Genome Fraction Coverage



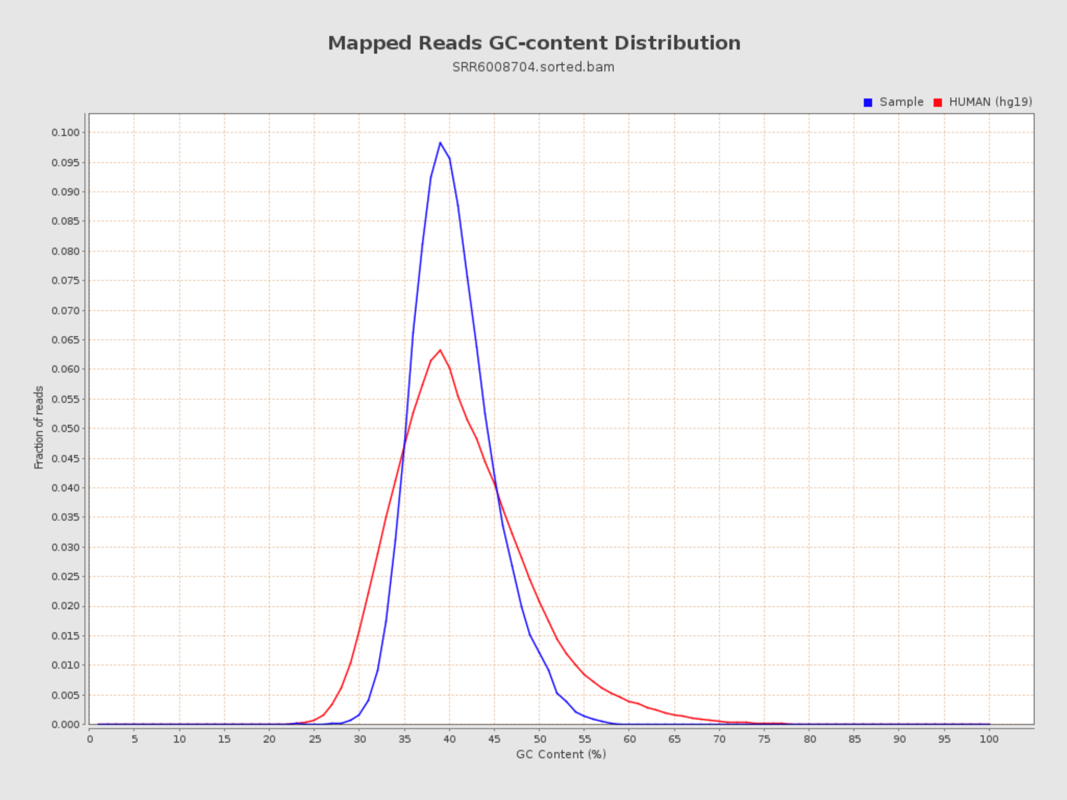
7. Results : Duplication Rate Histogram



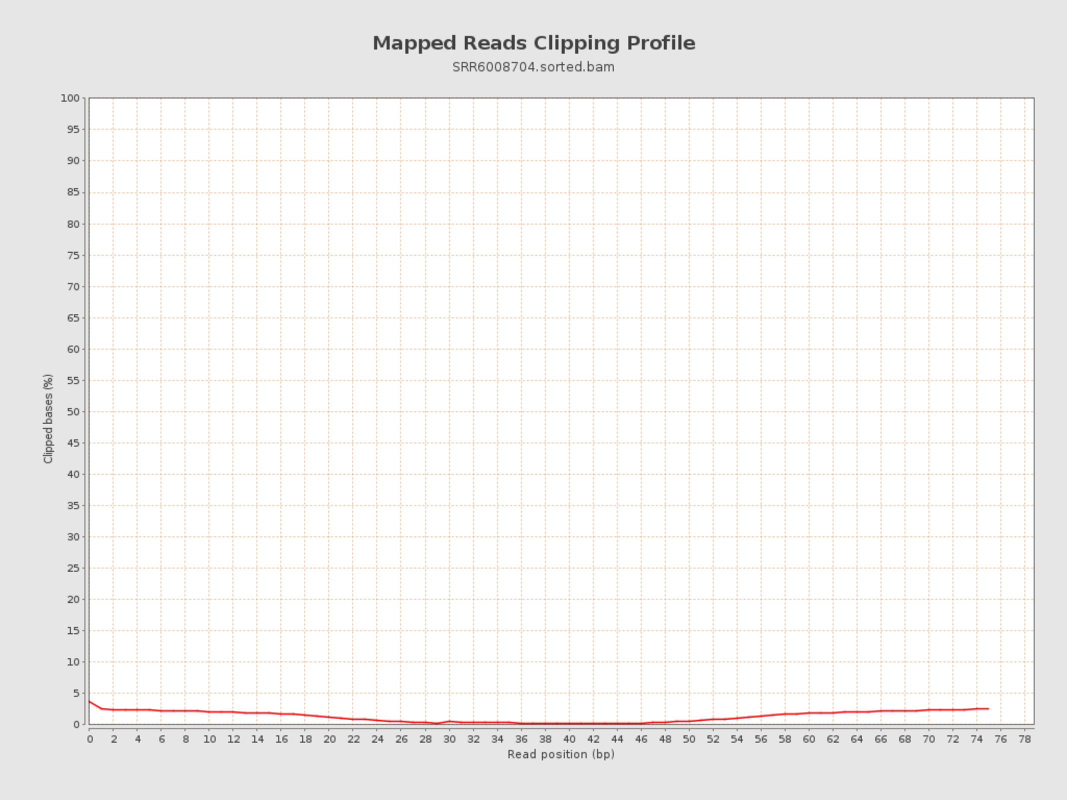
8. Results : Mapped Reads Nucleotide Content



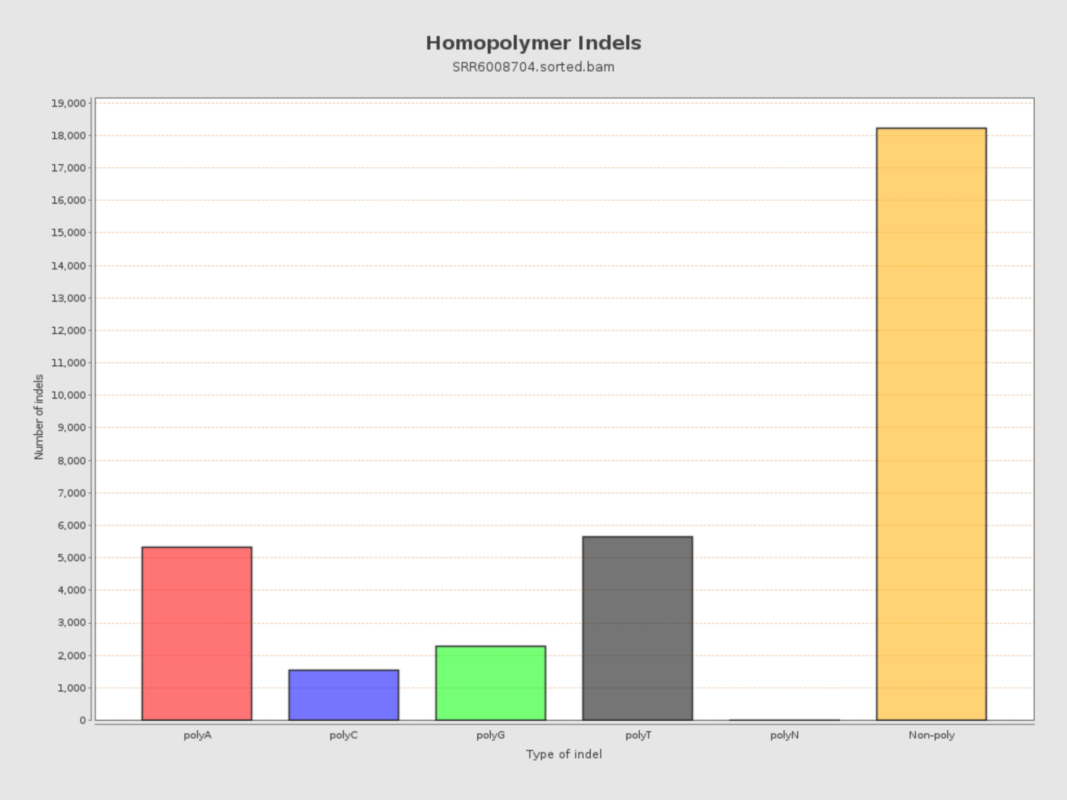
9. Results : Mapped Reads GC-content Distribution



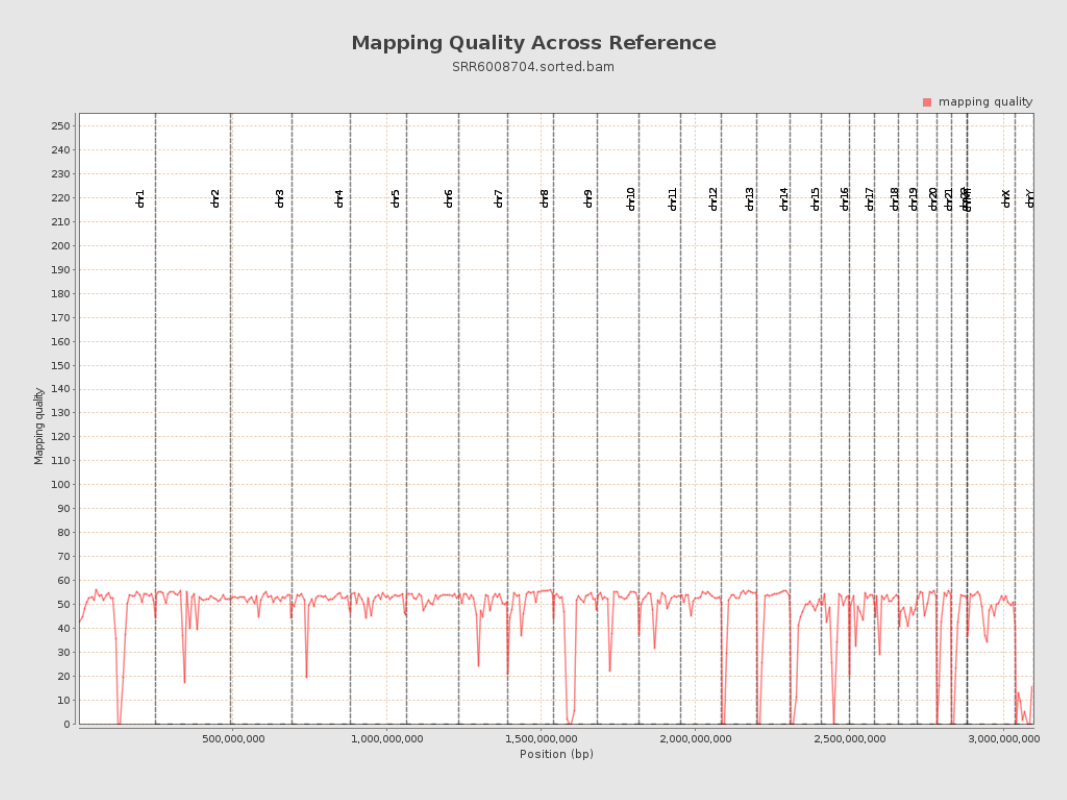
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram