Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:21:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008672.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_SRR6008672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:21:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,071,087
Mapped reads	1,528,511 / 73.8%
Unmapped reads	542,576 / 26.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,997 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	123,865 / 5.98%
Duplication rate	6.31%
Clipped reads	1,094,967 / 52.87%

2.2. ACGT Content

Number/percentage of A's	23,978,438 / 26.11%
Number/percentage of C's	15,666,149 / 17.06%
Number/percentage of T's	29,450,088 / 32.07%
Number/percentage of G's	22,724,161 / 24.75%
Number/percentage of N's	14,503 / 0.02%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.2901

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

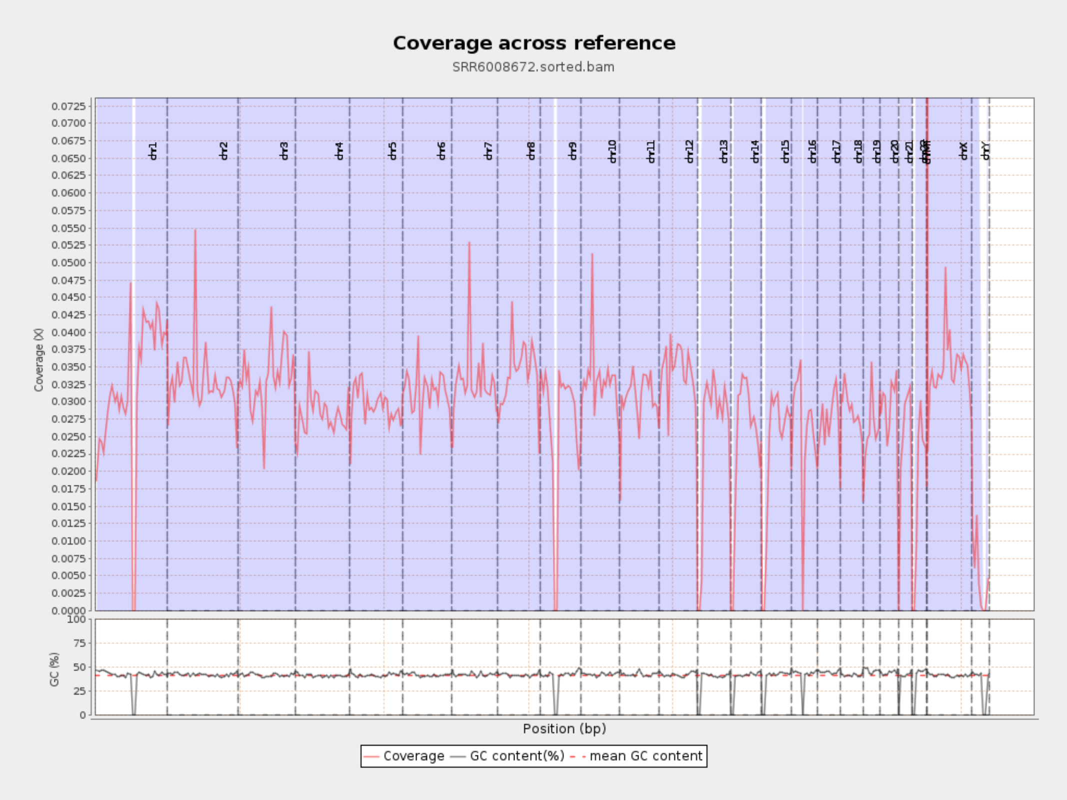
General error rate	1%
Mismatches	906,978
Insertions	7,269
Mapped reads with at least one insertion	0.47%
Deletions	35,895
Mapped reads with at least one deletion	2.32%
Homopolymer indels	48.74%

2.6. Chromosome stats

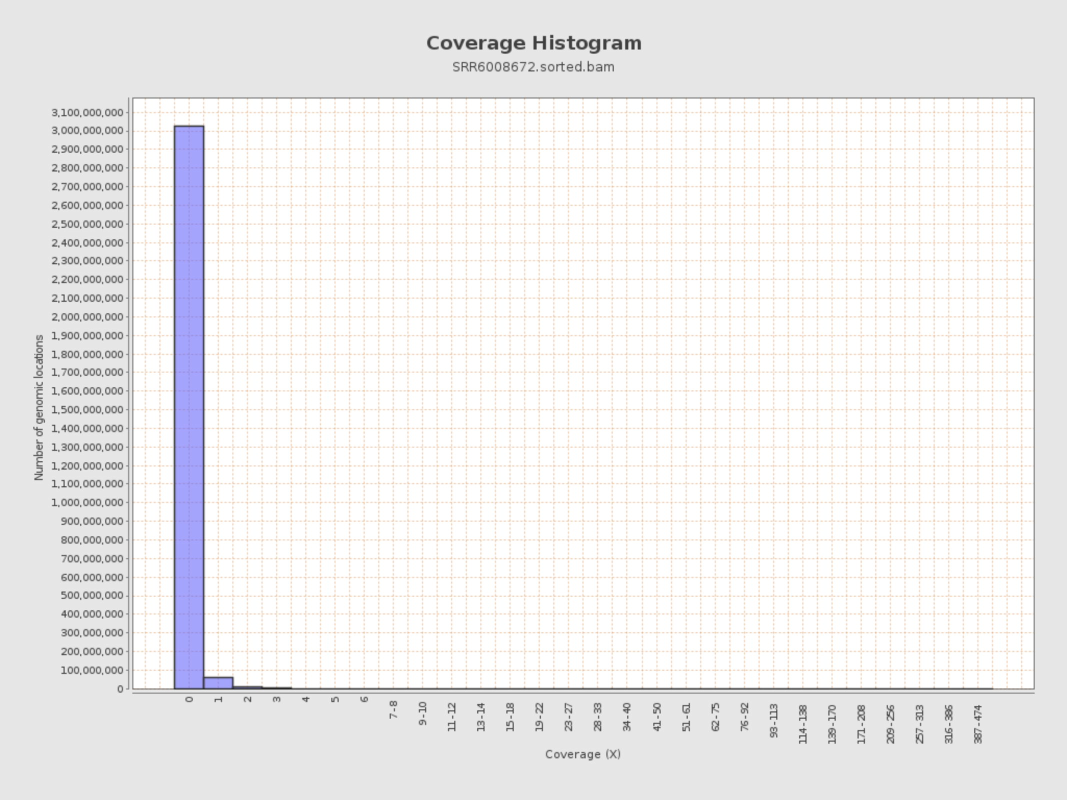
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7950776	0.0319	0.4079
chr2	243199373	8042581	0.0331	0.3481
chr3	198022430	6607454	0.0334	0.2384
chr4	191154276	5387012	0.0282	0.2199
chr5	180915260	5368686	0.0297	0.2181
chr6	171115067	5360434	0.0313	0.2683
chr7	159138663	5266857	0.0331	0.4285

chr8	146364022	4985561	0.0341	0.3036
chr9	141213431	3783899	0.0268	0.2852
chr10	135534747	4499354	0.0332	0.2981
chr11	135006516	4157038	0.0308	0.2913
chr12	133851895	4591084	0.0343	0.2428
chr13	115169878	2900402	0.0252	0.2077
chr14	107349540	2600425	0.0242	0.2115
chr15	102531392	2344078	0.0229	0.2051
chr16	90354753	2311540	0.0256	0.2288
chr17	81195210	2228629	0.0274	0.229
chr18	78077248	2254179	0.0289	0.4412
chr19	59128983	1553658	0.0263	0.2865
chr20	63025520	1845076	0.0293	0.2299
chr21	48129895	1177879	0.0245	0.2126
chr22	51304566	906942	0.0177	0.168
chrMT	16571	67671	4.0837	3.8049
chrX	155270560	5415888	0.0349	0.2702
chrY	59373566	281703	0.0047	0.1044

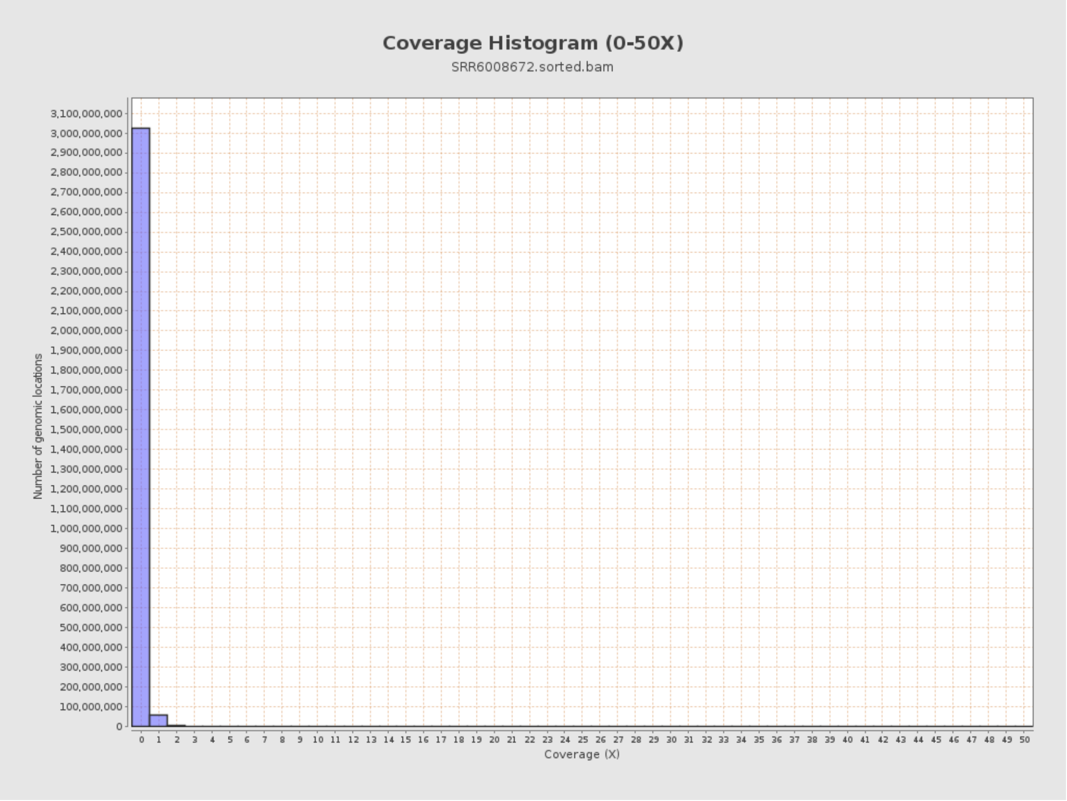
3. Results : Coverage across reference



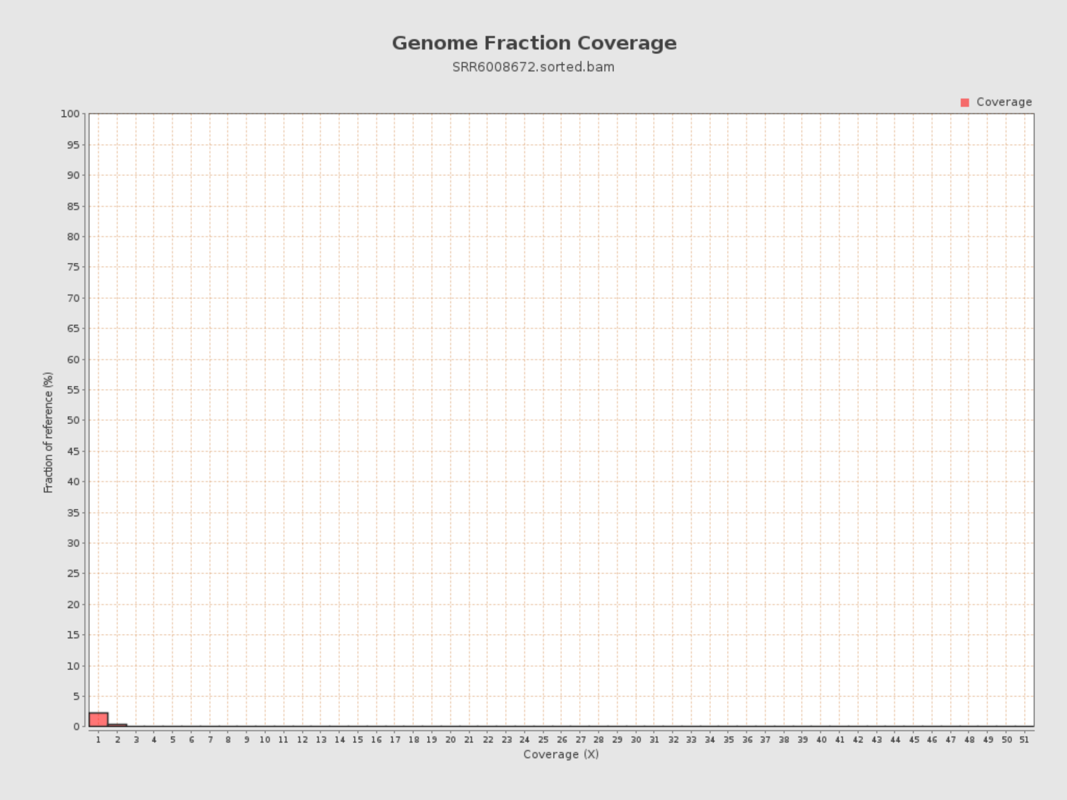
4. Results : Coverage Histogram



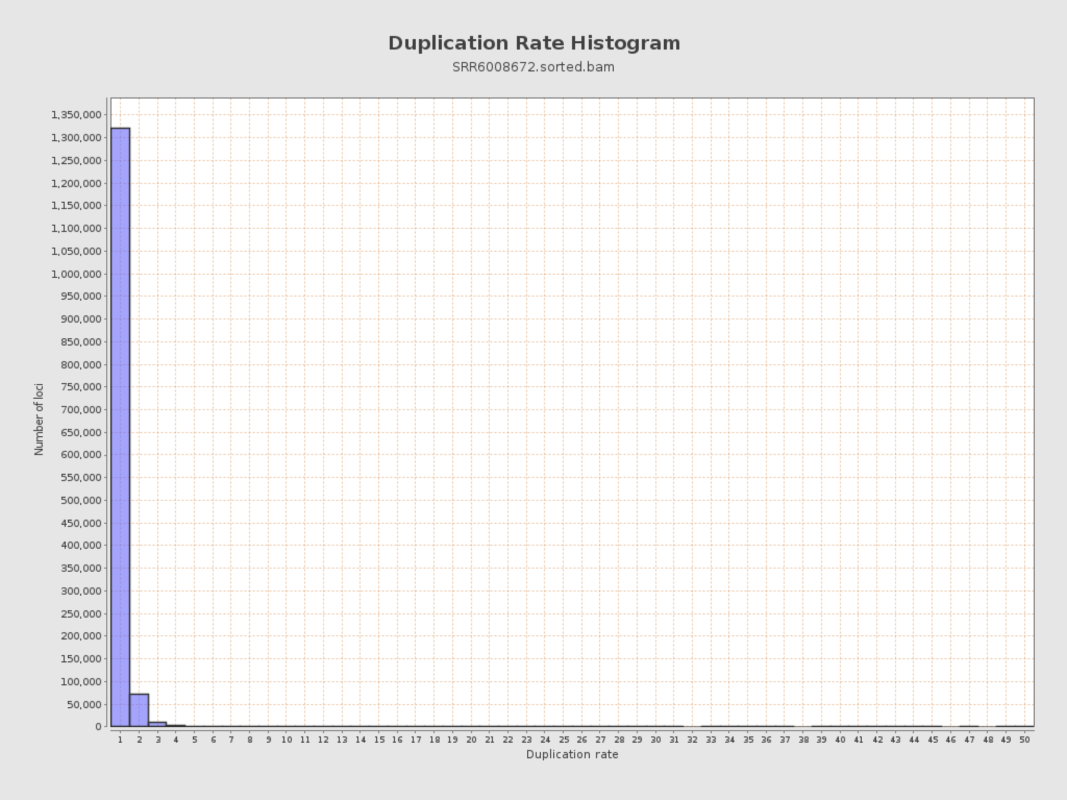
5. Results : Coverage Histogram (0-50X)



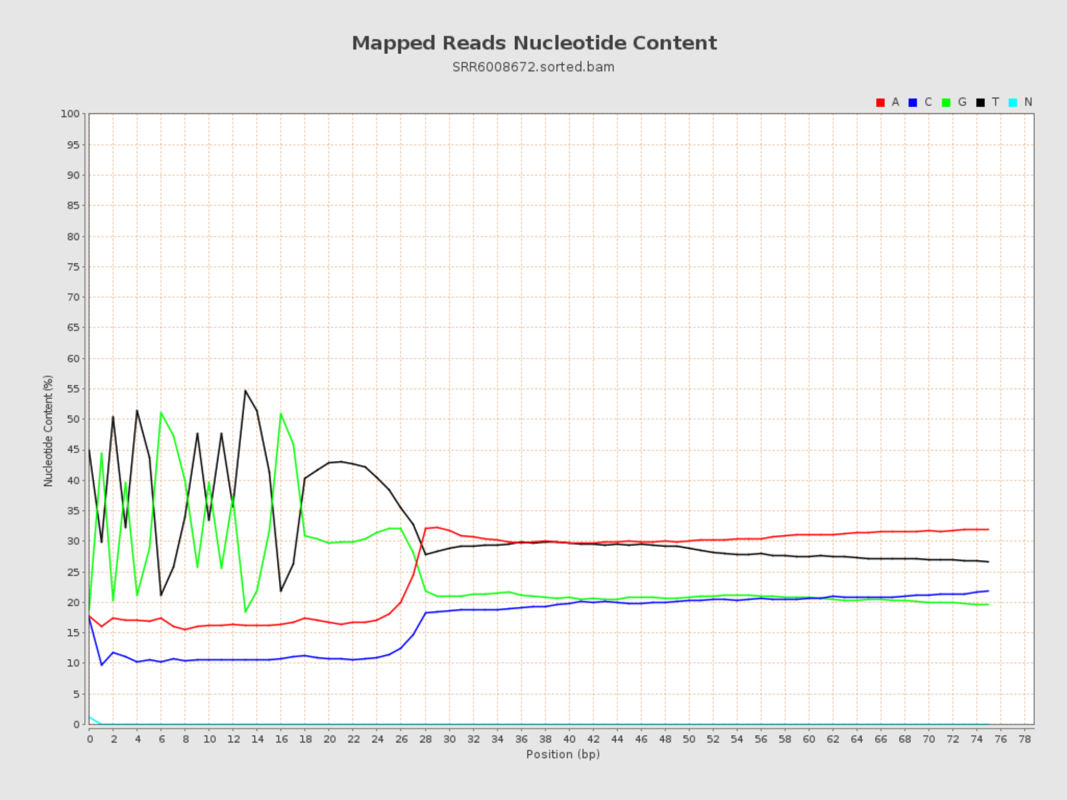
6. Results : Genome Fraction Coverage



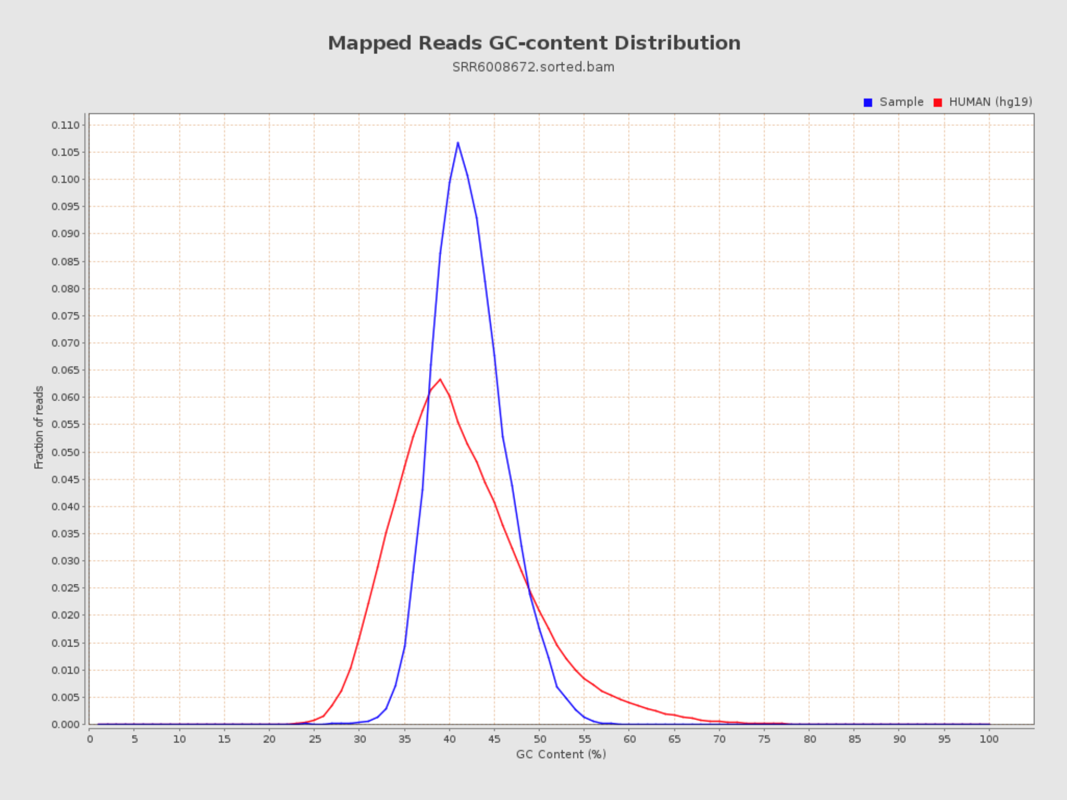
7. Results : Duplication Rate Histogram



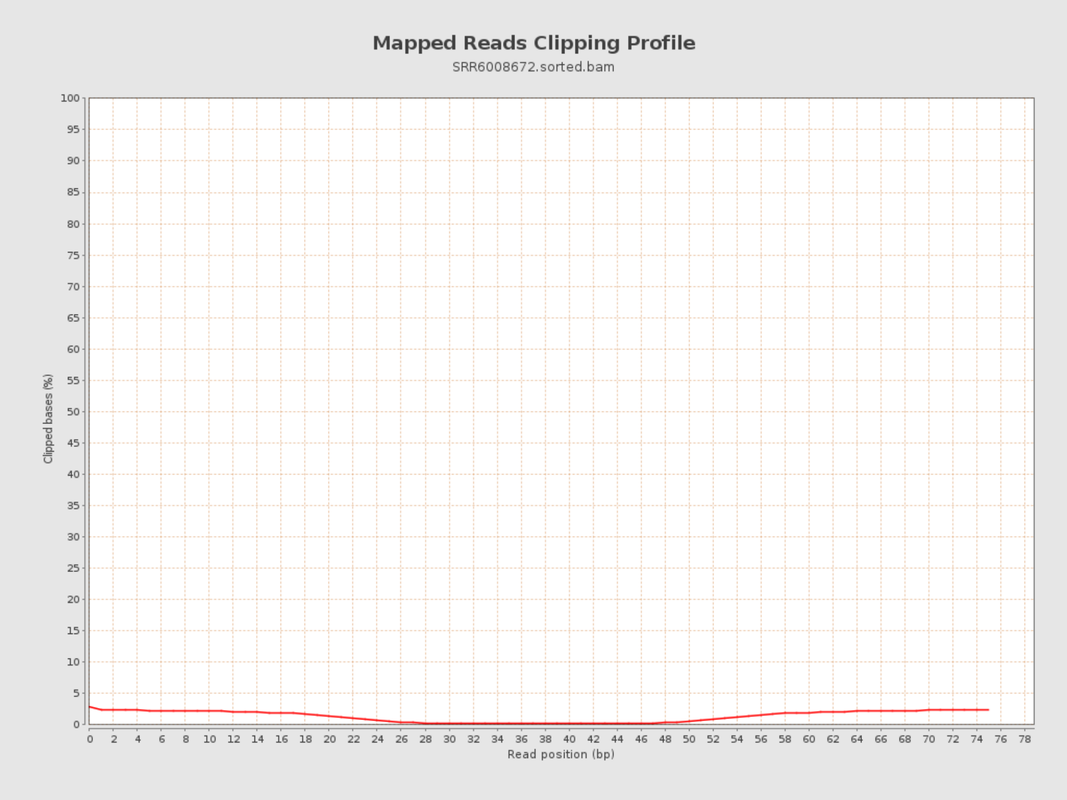
8. Results : Mapped Reads Nucleotide Content



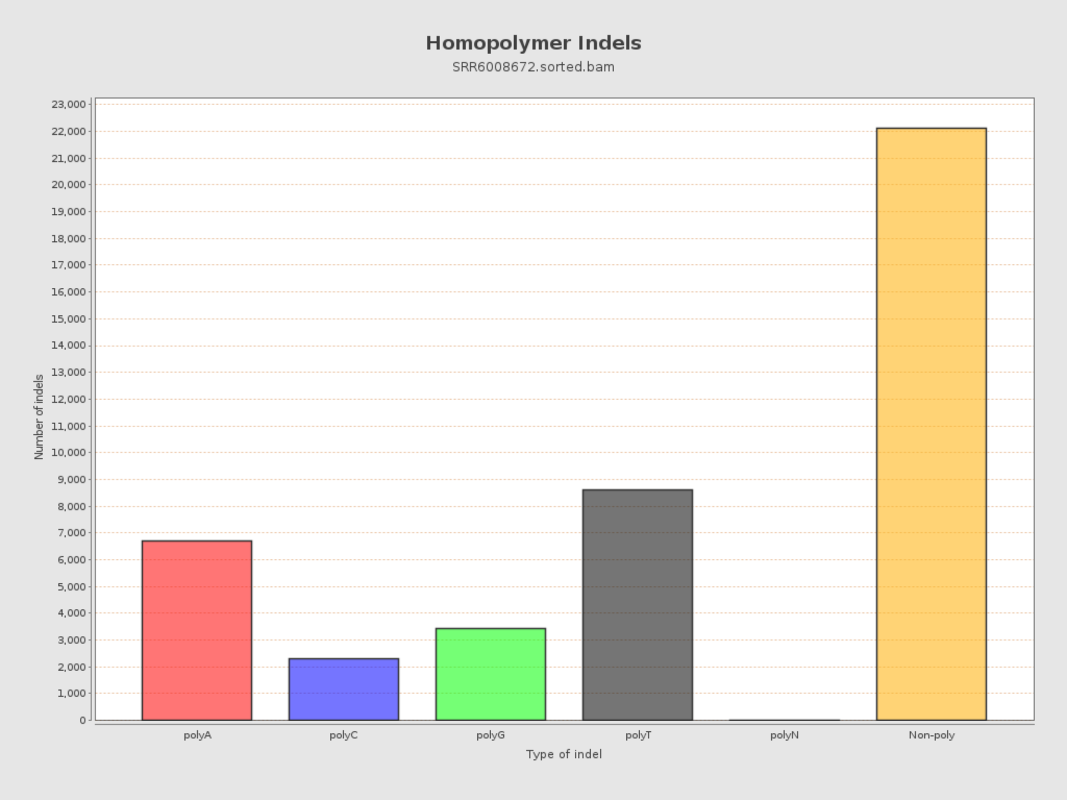
9. Results : Mapped Reads GC-content Distribution



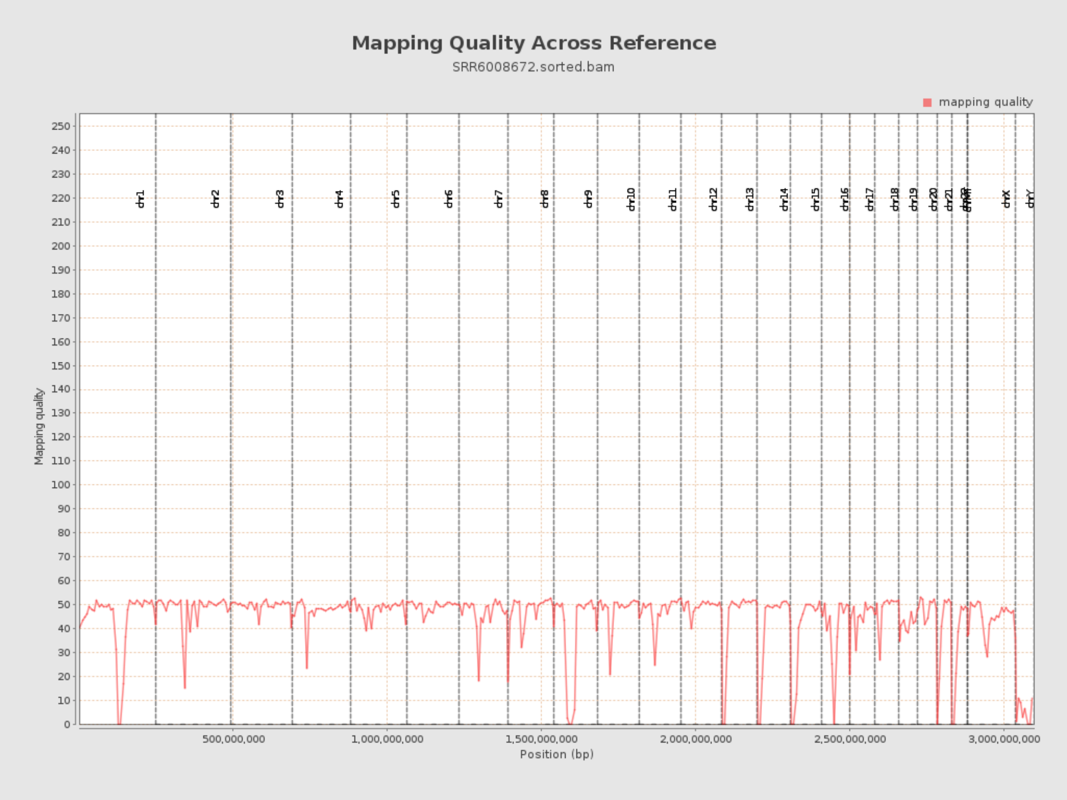
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram