Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:52:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080678.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_SRR3080678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:52:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,432,663
Mapped reads	1,314,091 / 91.72%
Unmapped reads	118,572 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,755 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	50,831 / 3.55%
Duplication rate	3.39%
Clipped reads	604,684 / 42.21%

2.2. ACGT Content

Number/percentage of A's	23,840,939 / 27.37%
Number/percentage of C's	15,900,832 / 18.26%
Number/percentage of T's	27,820,731 / 31.94%
Number/percentage of G's	19,527,152 / 22.42%
Number/percentage of N's	3,885 / 0%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.2235

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

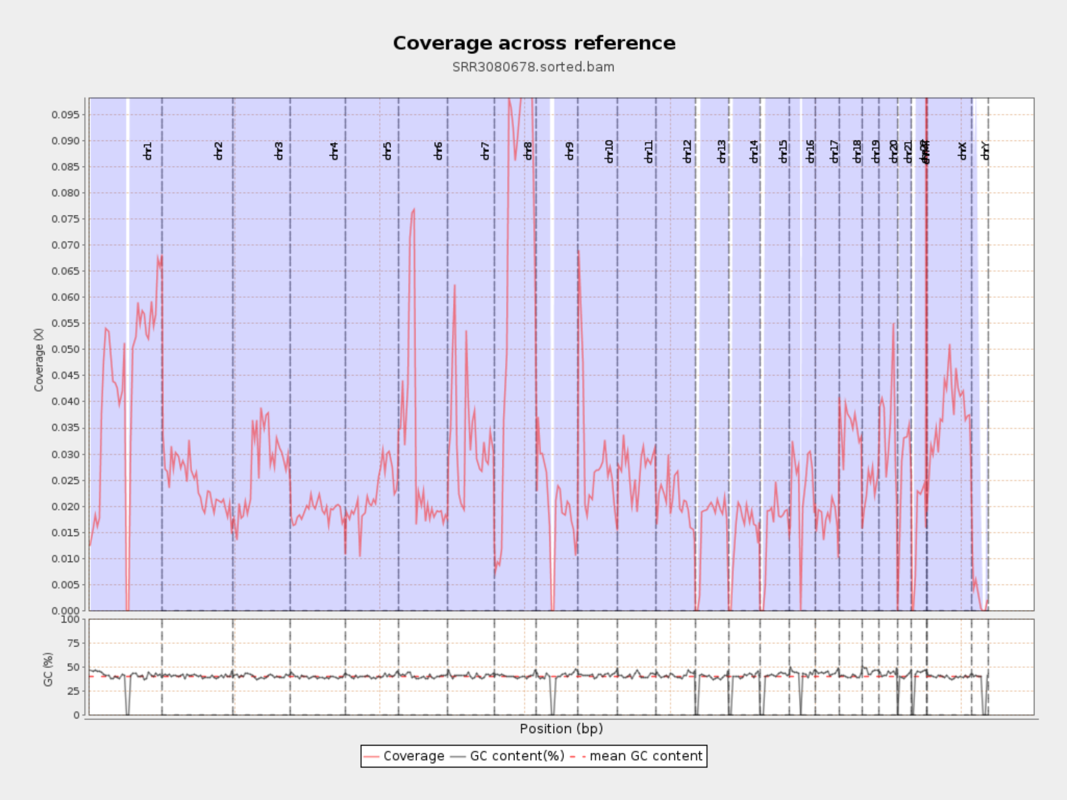
General error rate	0.69%
Mismatches	586,402
Insertions	6,571
Mapped reads with at least one insertion	0.5%
Deletions	19,884
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.74%

2.6. Chromosome stats

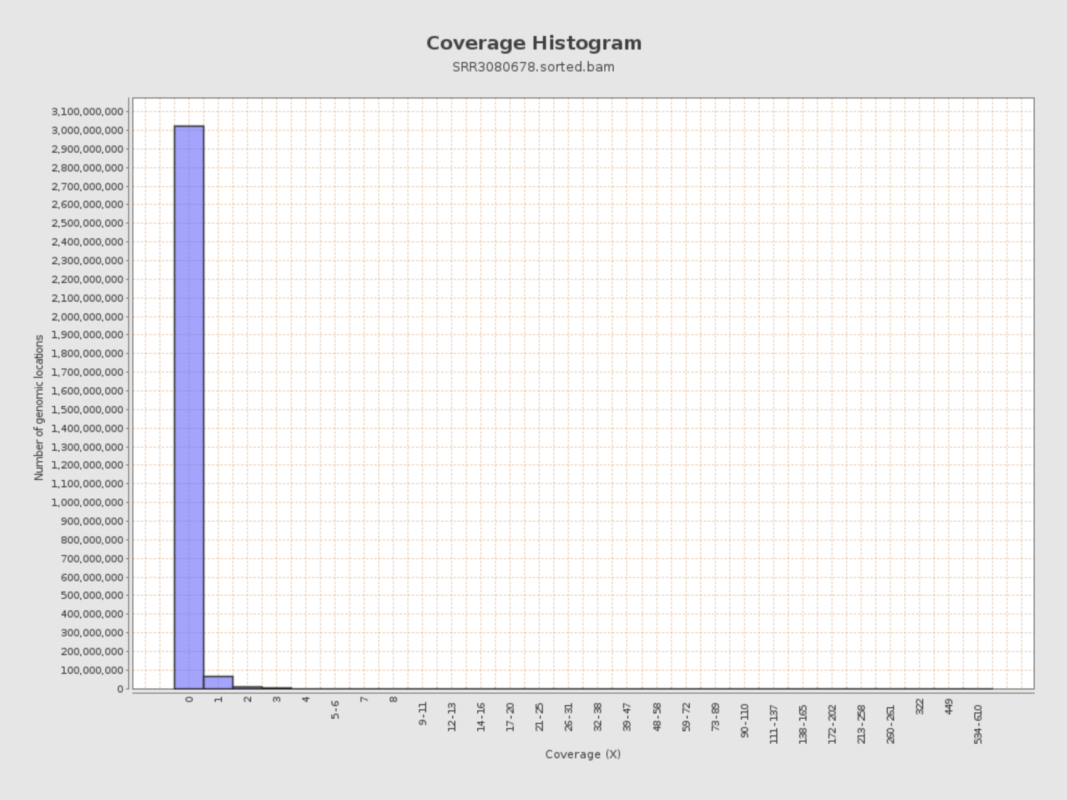
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10621846	0.0426	0.2668
chr2	243199373	5895522	0.0242	0.3167
chr3	198022430	5462833	0.0276	0.1869
chr4	191154276	3637597	0.019	0.158
chr5	180915260	4017992	0.0222	0.1664
chr6	171115067	5240897	0.0306	0.2297
chr7	159138663	5367153	0.0337	0.356

chr8	146364022	10475399	0.0716	0.3301
chr9	141213431	2804983	0.0199	0.174
chr10	135534747	4073279	0.0301	0.2034
chr11	135006516	3672041	0.0272	0.194
chr12	133851895	2816906	0.021	0.1636
chr13	115169878	1862055	0.0162	0.1431
chr14	107349540	1582620	0.0147	0.1367
chr15	102531392	1571189	0.0153	0.1473
chr16	90354753	2160814	0.0239	0.1762
chr17	81195210	1412472	0.0174	0.1505
chr18	78077248	2750265	0.0352	0.2458
chr19	59128983	1411287	0.0239	0.1919
chr20	63025520	2251059	0.0357	0.2148
chr21	48129895	1248323	0.0259	0.1822
chr22	51304566	802107	0.0156	0.1391
chrMT	16571	9463	0.5711	0.9497
chrX	155270560	5810827	0.0374	0.2225
chrY	59373566	166177	0.0028	0.0613

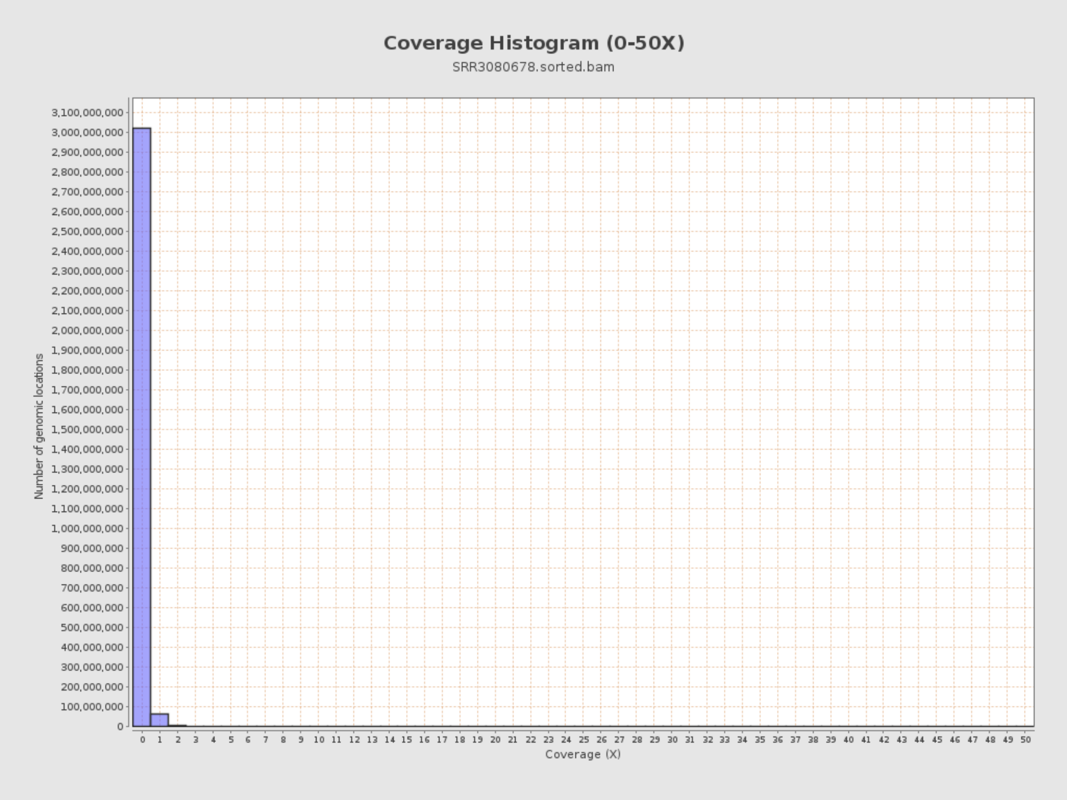
3. Results : Coverage across reference



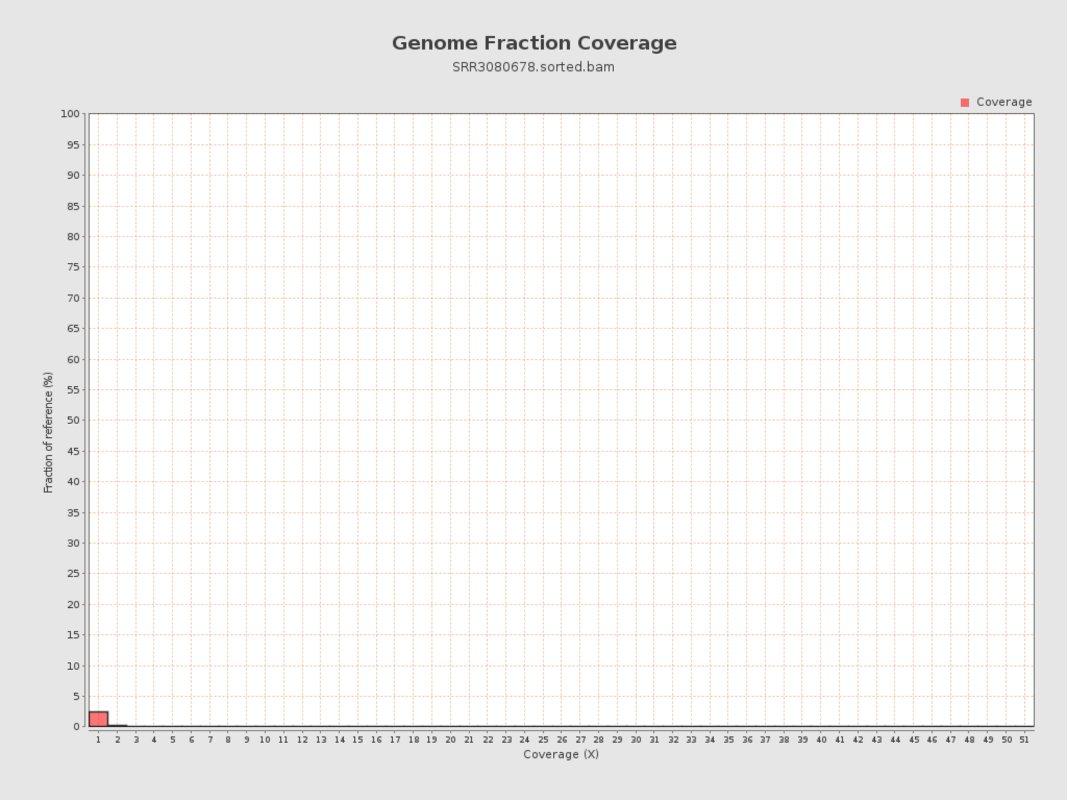
4. Results : Coverage Histogram



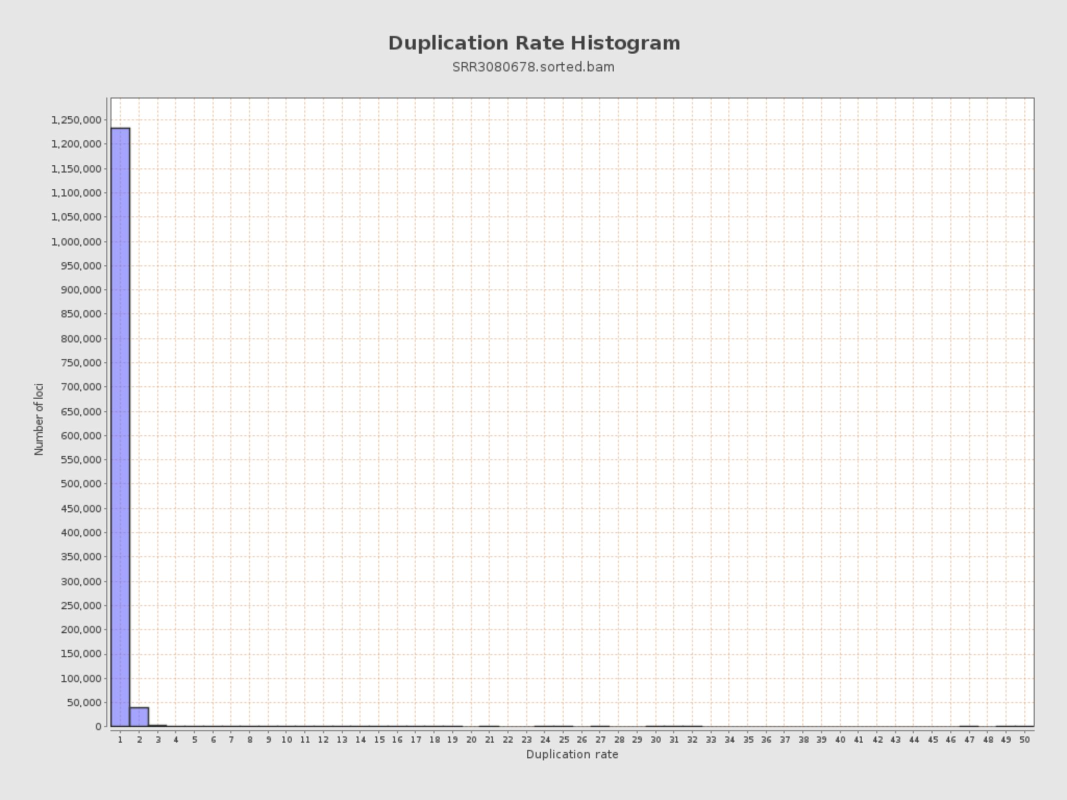
5. Results : Coverage Histogram (0-50X)



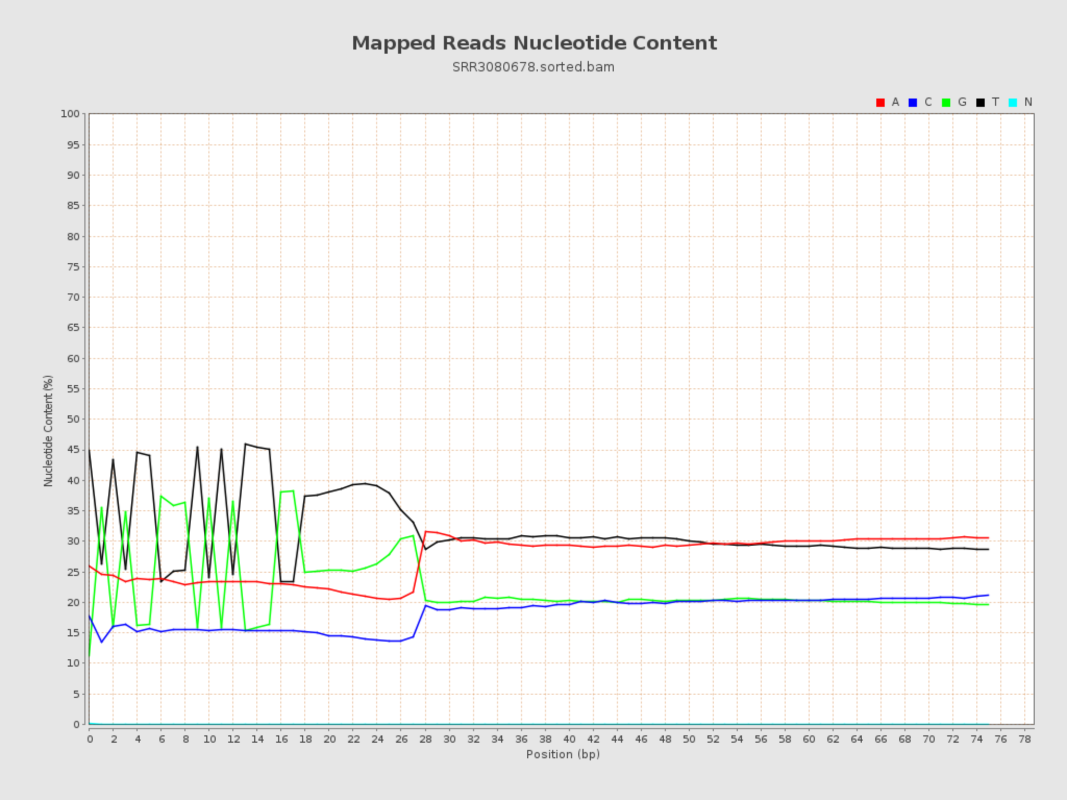
6. Results : Genome Fraction Coverage



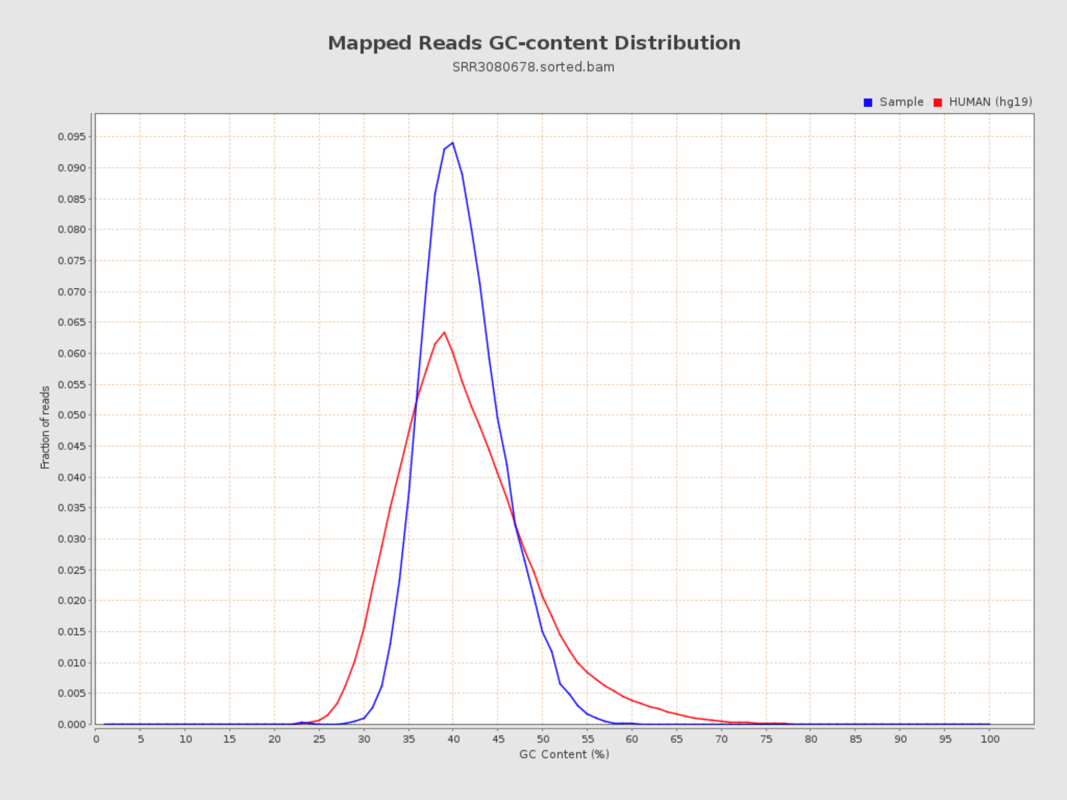
7. Results : Duplication Rate Histogram



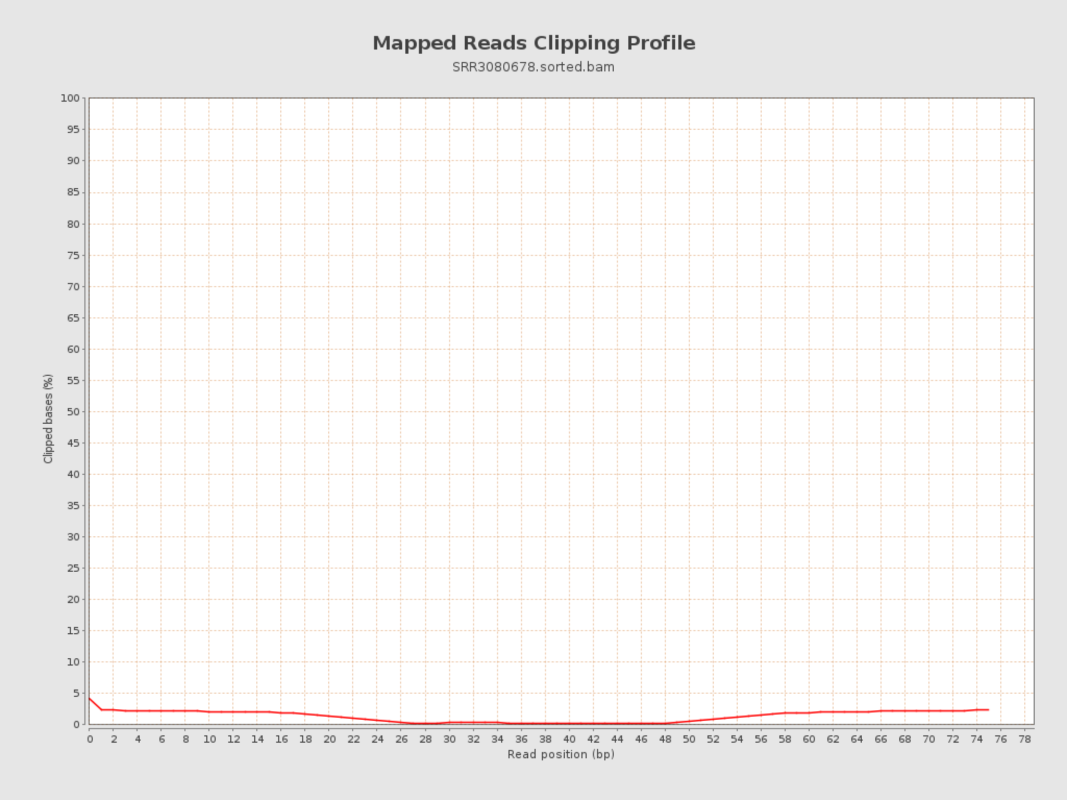
8. Results : Mapped Reads Nucleotide Content



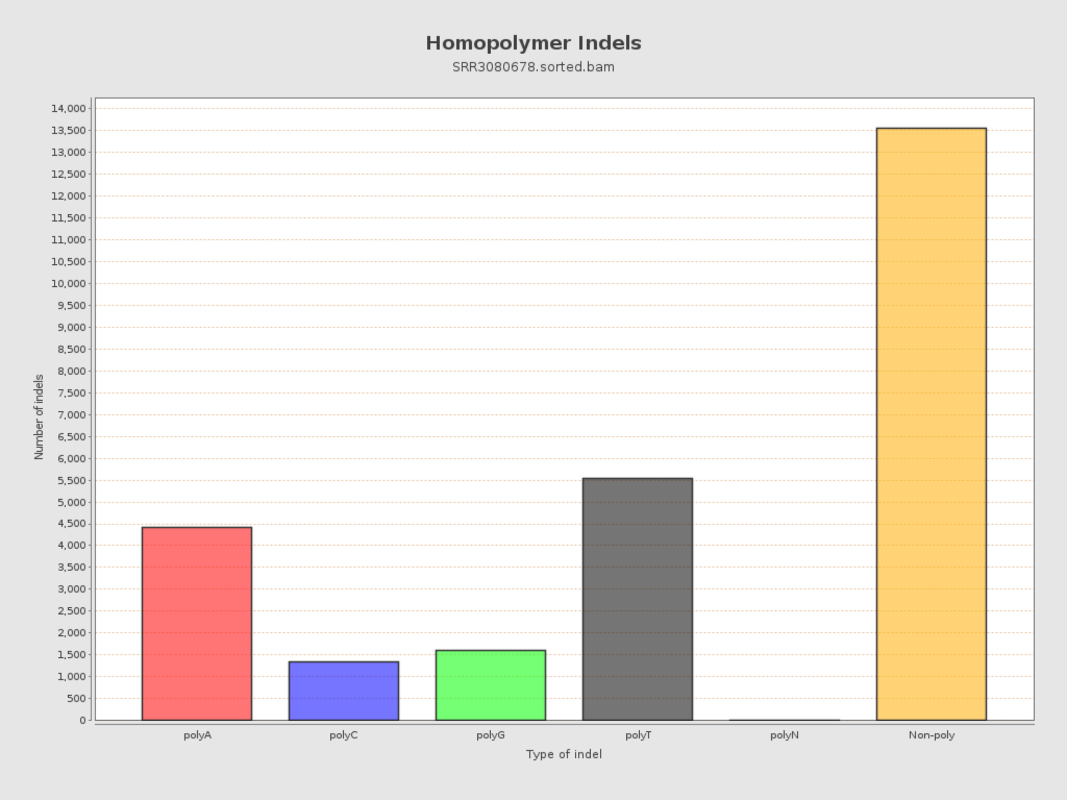
9. Results : Mapped Reads GC-content Distribution



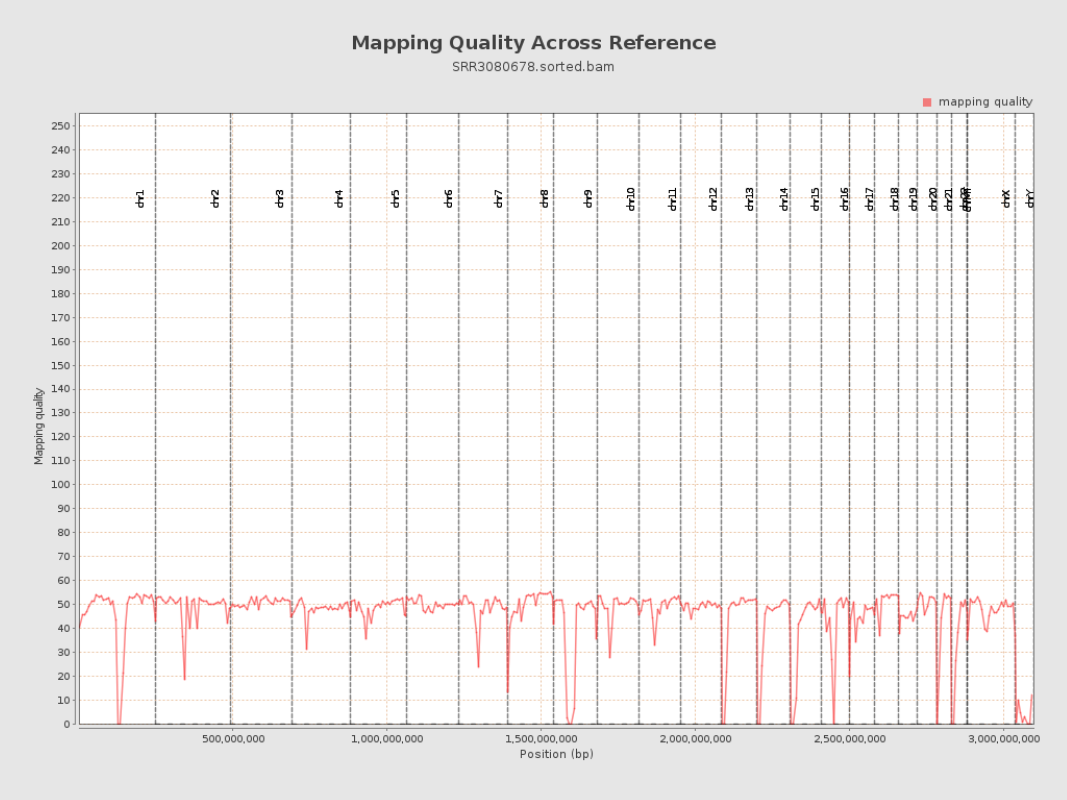
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram