Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080657.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_SRR3080657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080657.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:13:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,431,136
Mapped reads	1,288,838 / 90.06%
Unmapped reads	142,298 / 9.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,092 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	45,819 / 3.2%
Duplication rate	3.09%
Clipped reads	614,885 / 42.96%

2.2. ACGT Content

Number/percentage of A's	22,675,532 / 26.73%
Number/percentage of C's	15,695,156 / 18.5%
Number/percentage of T's	26,816,640 / 31.61%
Number/percentage of G's	19,647,729 / 23.16%
Number/percentage of N's	3,644 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.2218

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

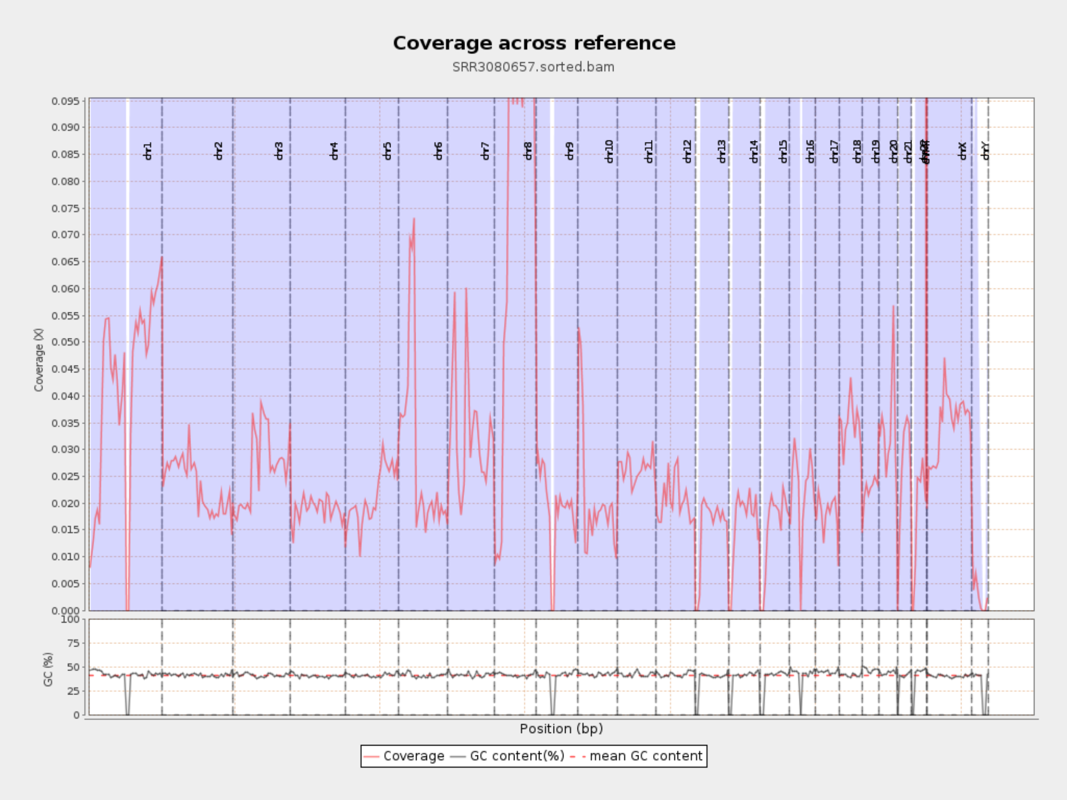
General error rate	0.7%
Mismatches	579,759
Insertions	6,101
Mapped reads with at least one insertion	0.47%
Deletions	19,658
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.89%

2.6. Chromosome stats

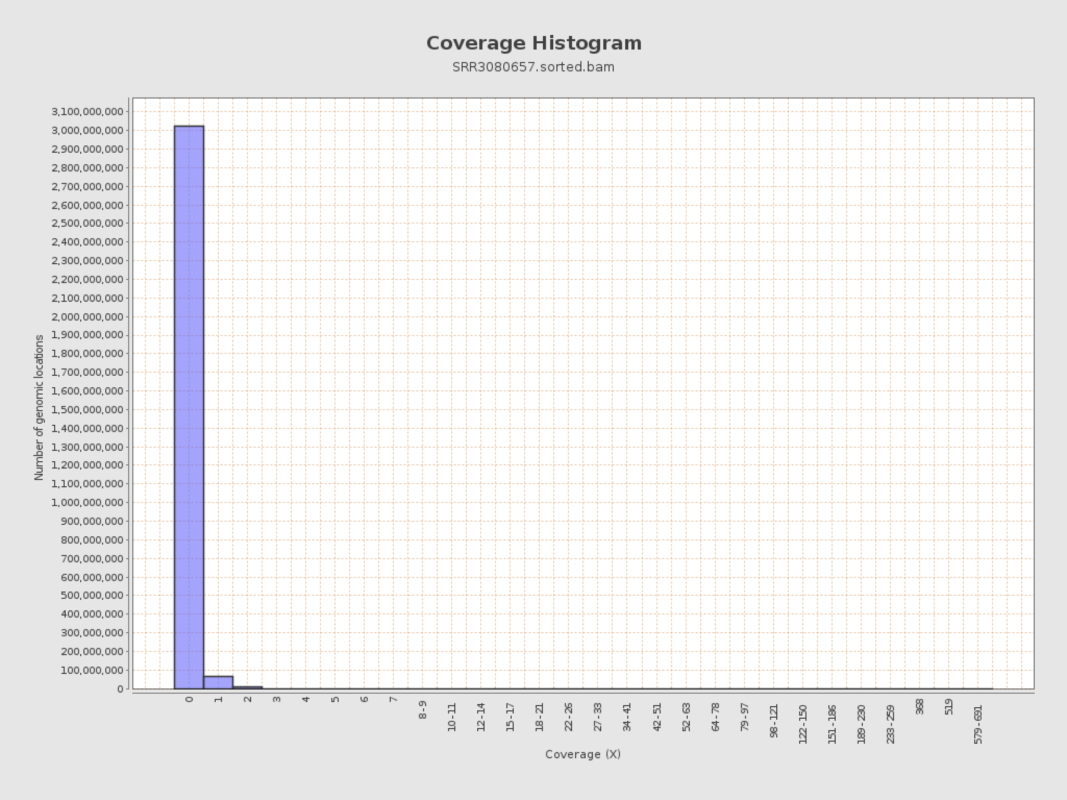
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10298500	0.0413	0.2519
chr2	243199373	5656036	0.0233	0.3385
chr3	198022430	5262469	0.0266	0.1807
chr4	191154276	3599910	0.0188	0.1561
chr5	180915260	3858996	0.0213	0.1619
chr6	171115067	5030429	0.0294	0.2261
chr7	159138663	5347852	0.0336	0.3589

chr8	146364022	11581670	0.0791	0.3419
chr9	141213431	2659518	0.0188	0.1703
chr10	135534747	2894161	0.0214	0.1682
chr11	135006516	3558606	0.0264	0.1868
chr12	133851895	2745588	0.0205	0.159
chr13	115169878	1743272	0.0151	0.137
chr14	107349540	1721809	0.016	0.141
chr15	102531392	1571036	0.0153	0.1504
chr16	90354753	2055831	0.0228	0.1705
chr17	81195210	1447936	0.0178	0.1496
chr18	78077248	2720584	0.0348	0.2351
chr19	59128983	1361145	0.023	0.1825
chr20	63025520	2114391	0.0335	0.2047
chr21	48129895	1231973	0.0256	0.1797
chr22	51304566	880160	0.0172	0.1441
chrMT	16571	10180	0.6143	0.9598
chrX	155270560	5345700	0.0344	0.2094
chrY	59373566	171908	0.0029	0.0664

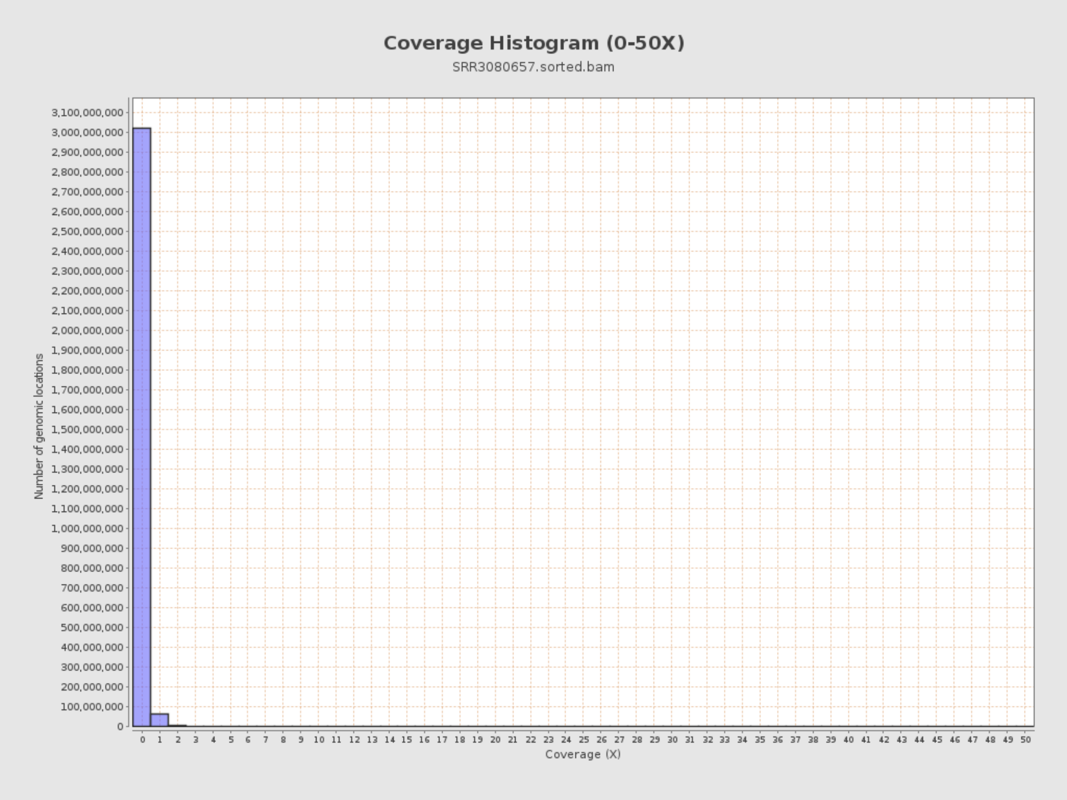
3. Results : Coverage across reference



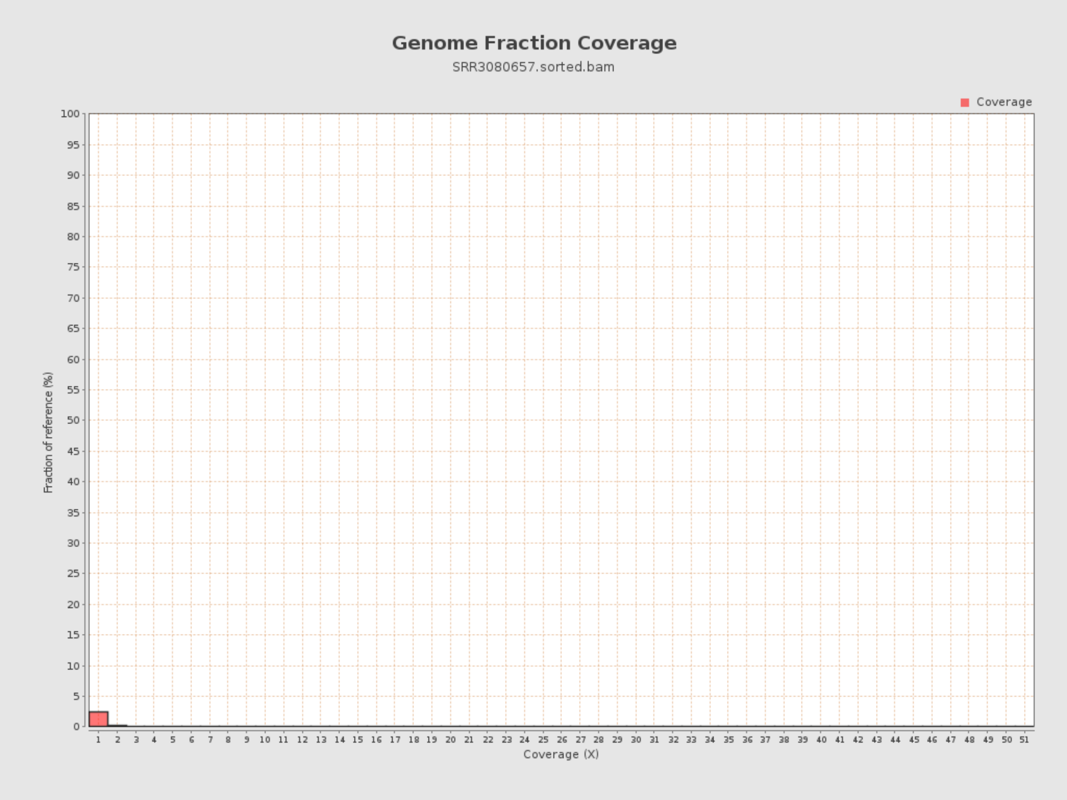
4. Results : Coverage Histogram



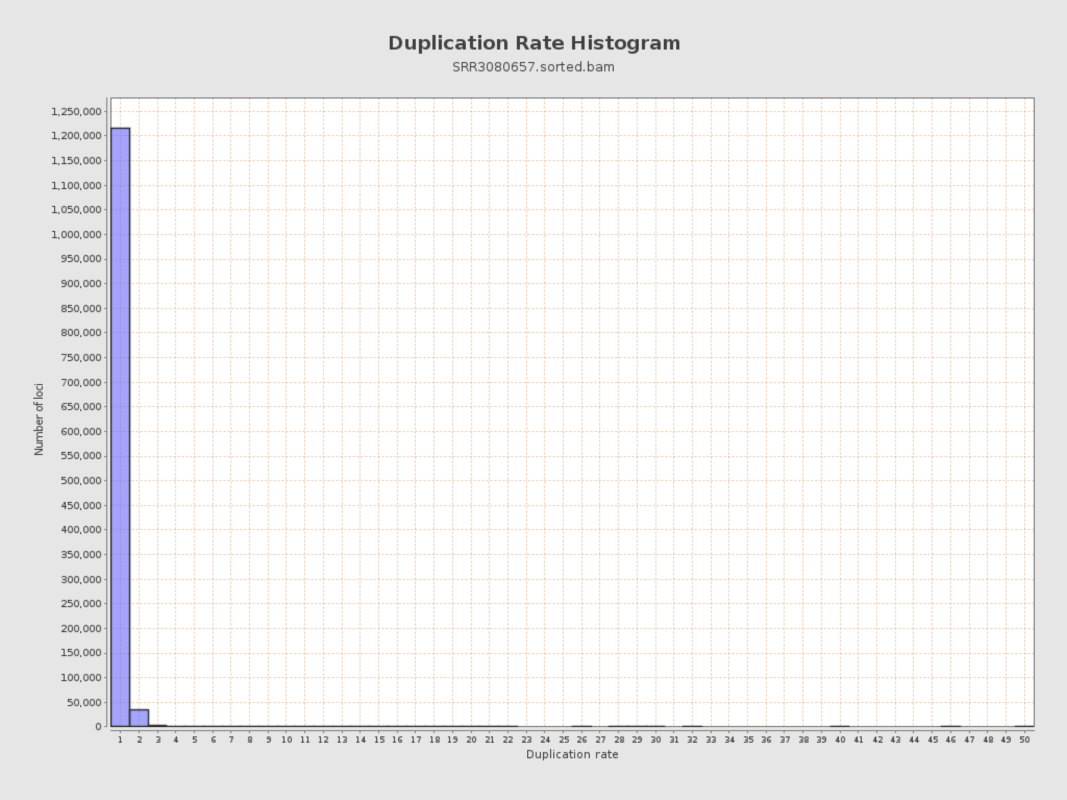
5. Results : Coverage Histogram (0-50X)



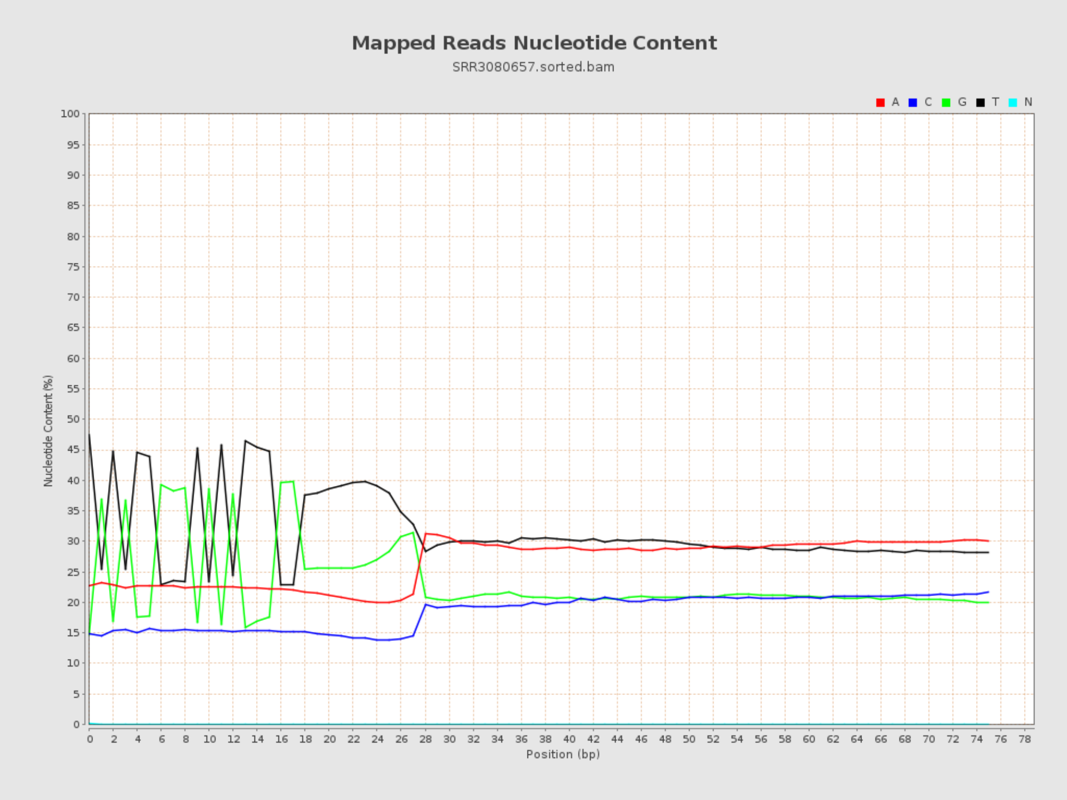
6. Results : Genome Fraction Coverage



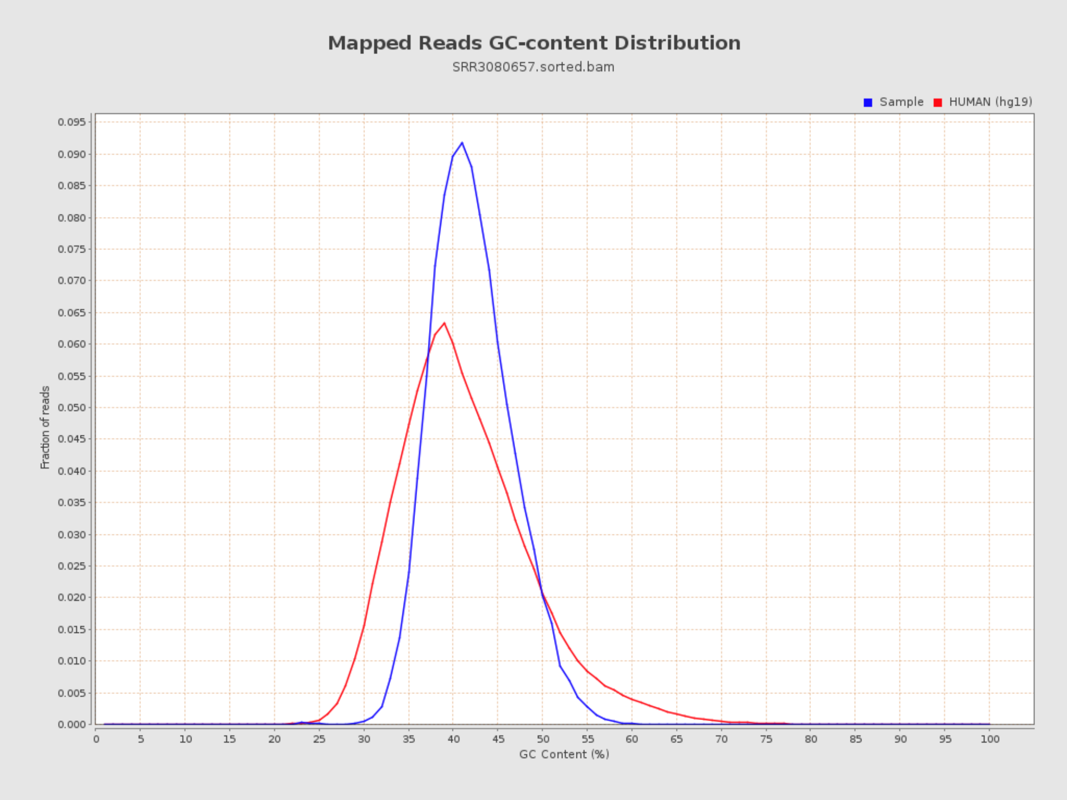
7. Results : Duplication Rate Histogram



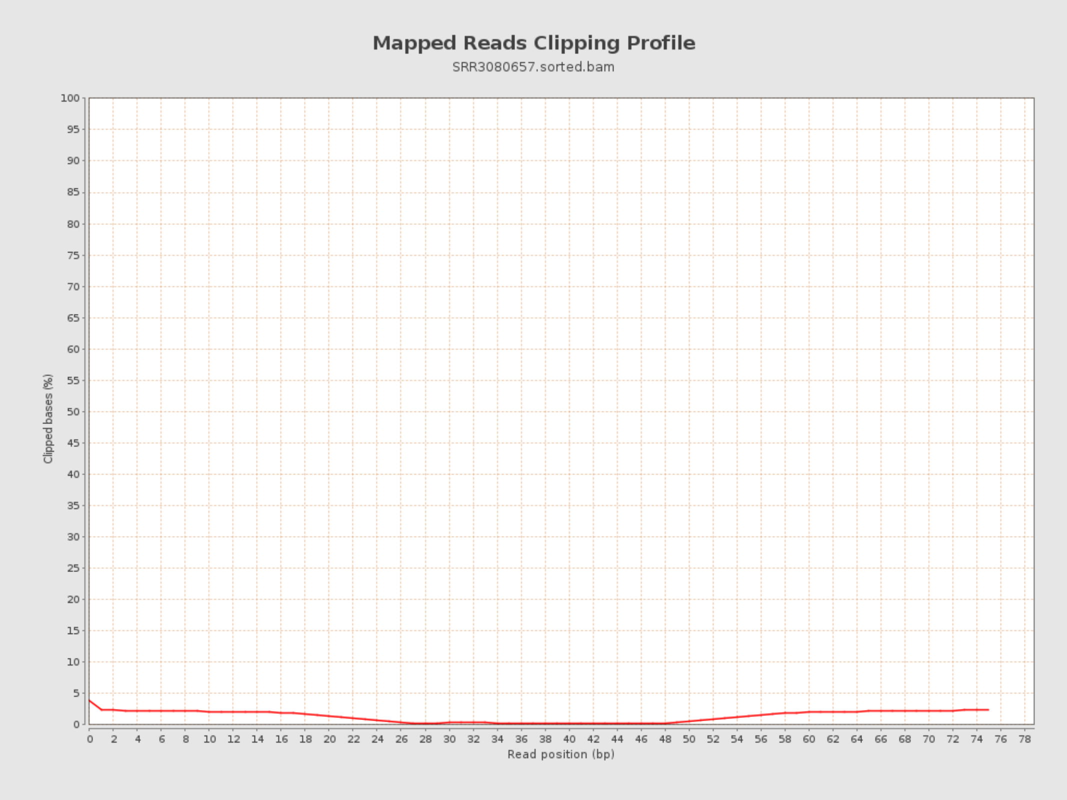
8. Results : Mapped Reads Nucleotide Content



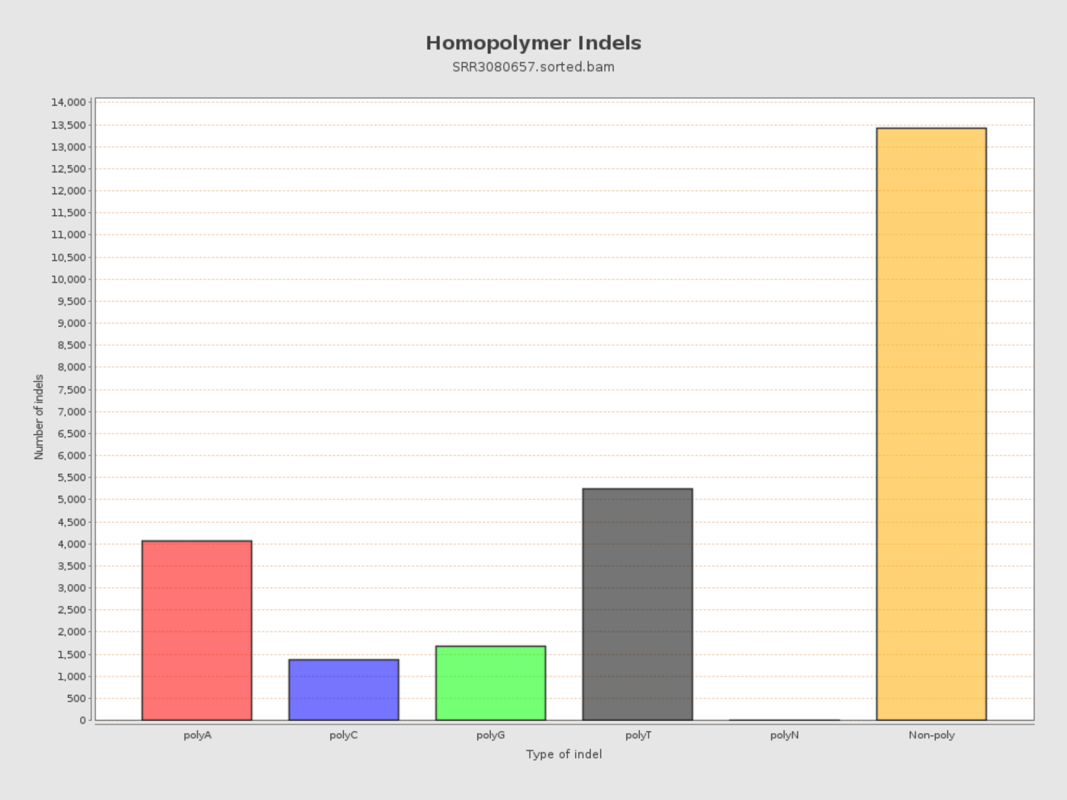
9. Results : Mapped Reads GC-content Distribution



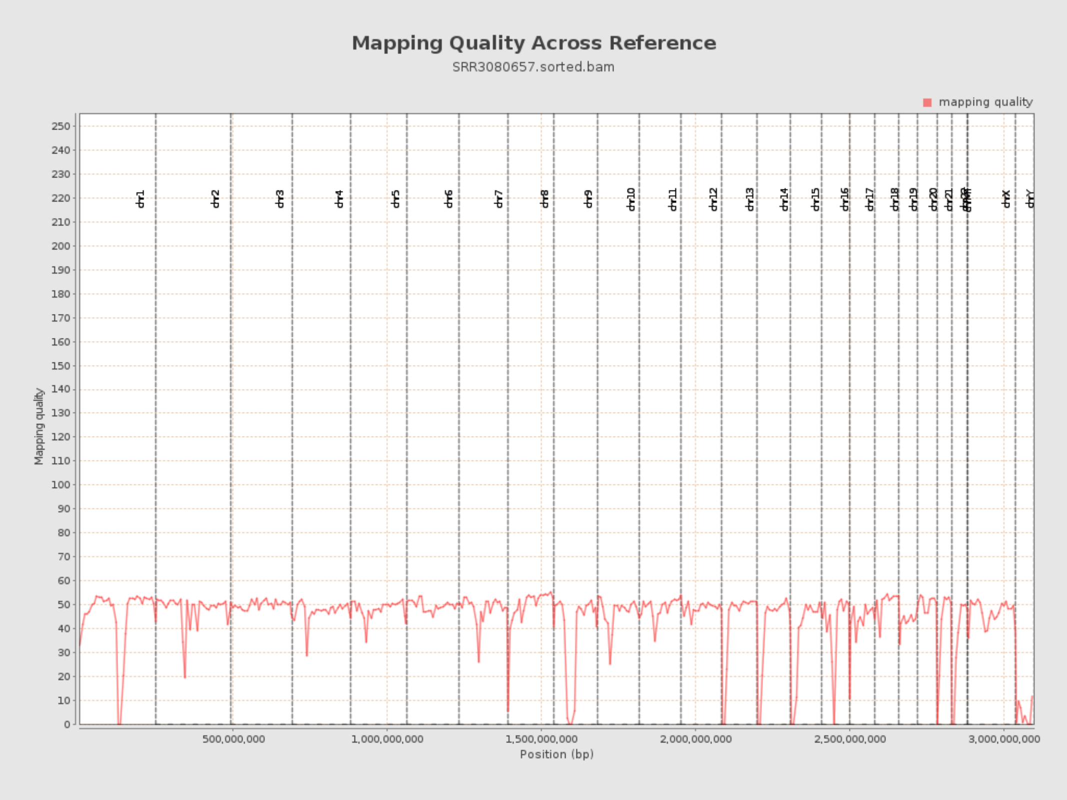
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram