Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:03:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080650.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_SRR3080650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:03:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,413,611
Mapped reads	1,276,180 / 90.28%
Unmapped reads	137,431 / 9.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,730 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	43,901 / 3.11%
Duplication rate	2.98%
Clipped reads	612,620 / 43.34%

2.2. ACGT Content

Number/percentage of A's	22,420,033 / 26.72%
Number/percentage of C's	15,491,024 / 18.46%
Number/percentage of T's	26,557,335 / 31.65%
Number/percentage of G's	19,439,162 / 23.17%
Number/percentage of N's	3,555 / 0%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2211

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

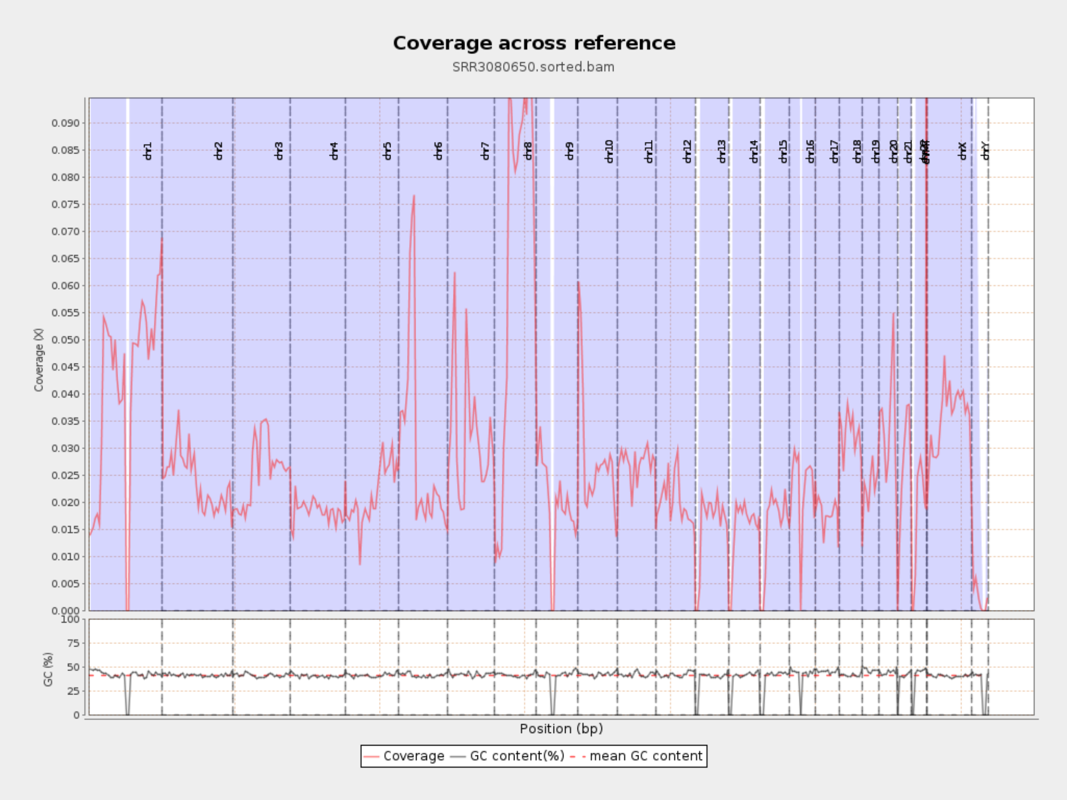
General error rate	0.7%
Mismatches	573,841
Insertions	6,193
Mapped reads with at least one insertion	0.48%
Deletions	19,488
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.97%

2.6. Chromosome stats

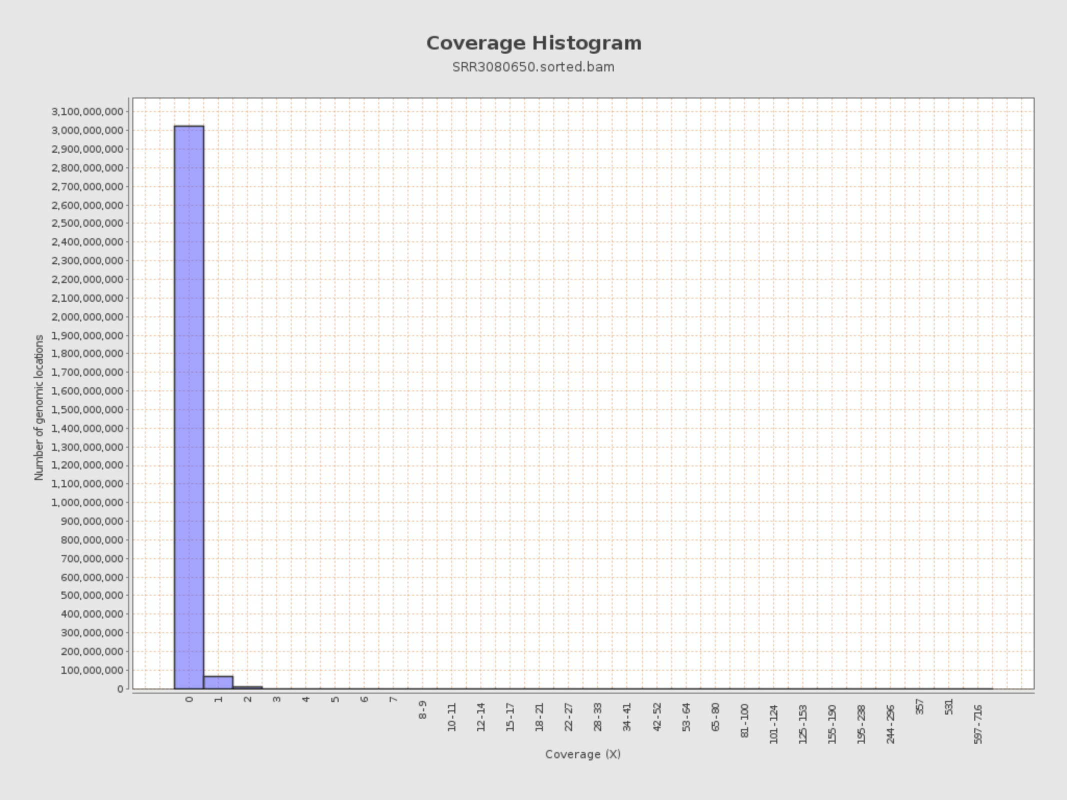
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10262000	0.0412	0.2534
chr2	243199373	5792632	0.0238	0.3409
chr3	198022430	5081591	0.0257	0.1763
chr4	191154276	3510062	0.0184	0.1526
chr5	180915260	3874957	0.0214	0.1613
chr6	171115067	5096773	0.0298	0.2297
chr7	159138663	5249472	0.033	0.3629

chr8	146364022	9823823	0.0671	0.3103
chr9	141213431	2750784	0.0195	0.1653
chr10	135534747	3873338	0.0286	0.1969
chr11	135006516	3651298	0.027	0.1912
chr12	133851895	2689466	0.0201	0.1574
chr13	115169878	1799746	0.0156	0.1401
chr14	107349540	1604062	0.0149	0.1357
chr15	102531392	1577870	0.0154	0.1463
chr16	90354753	2046978	0.0227	0.1694
chr17	81195210	1441848	0.0178	0.1493
chr18	78077248	2561709	0.0328	0.2402
chr19	59128983	1374596	0.0232	0.1802
chr20	63025520	2137045	0.0339	0.2056
chr21	48129895	1213589	0.0252	0.1775
chr22	51304566	846702	0.0165	0.1409
chrMT	16571	6336	0.3824	0.6882
chrX	155270560	5506346	0.0355	0.2149
chrY	59373566	169121	0.0028	0.0613

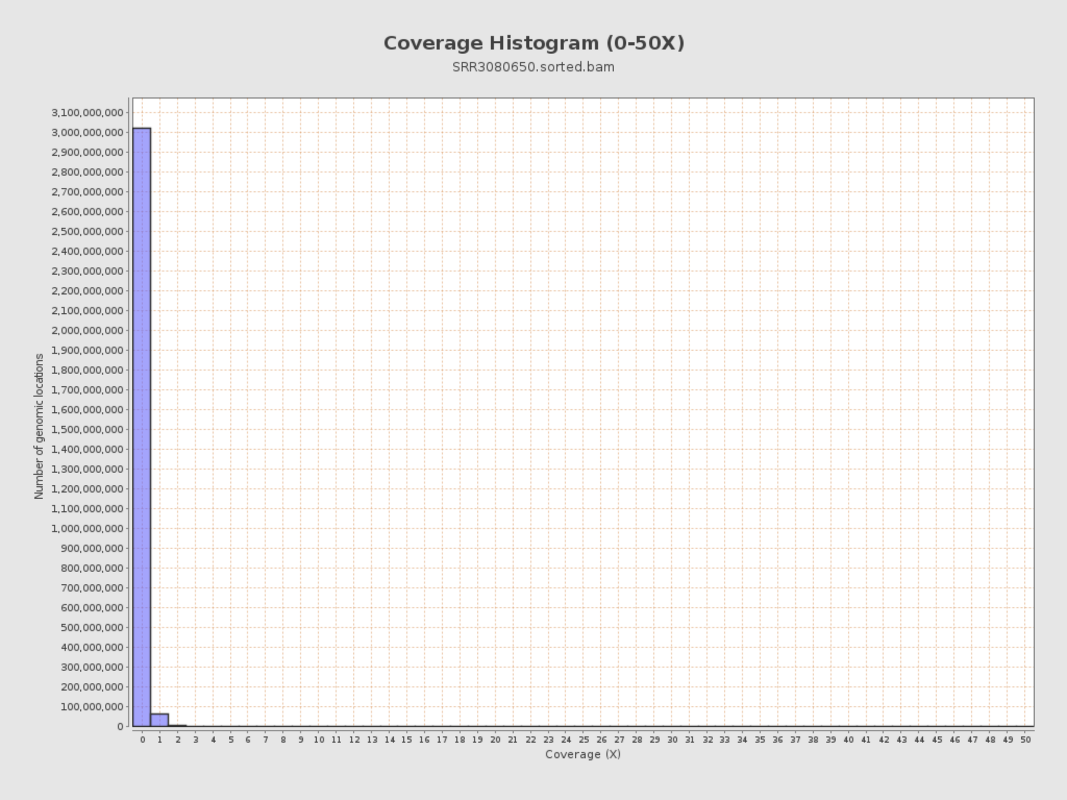
3. Results : Coverage across reference



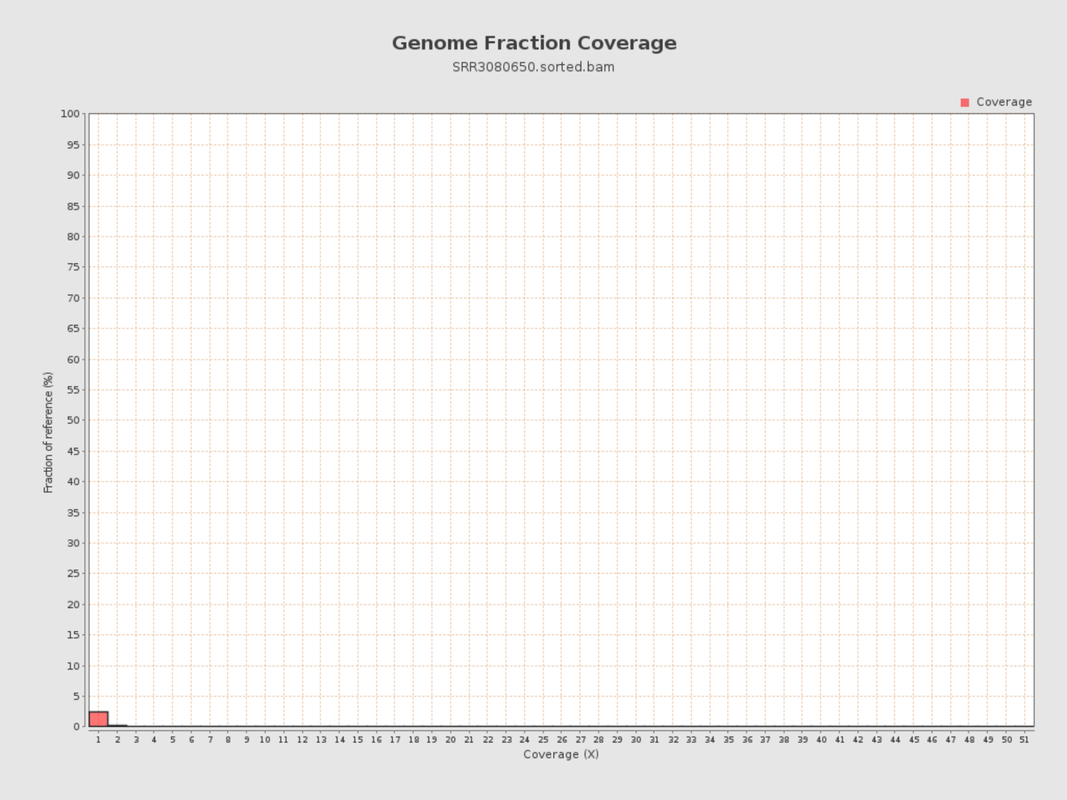
4. Results : Coverage Histogram



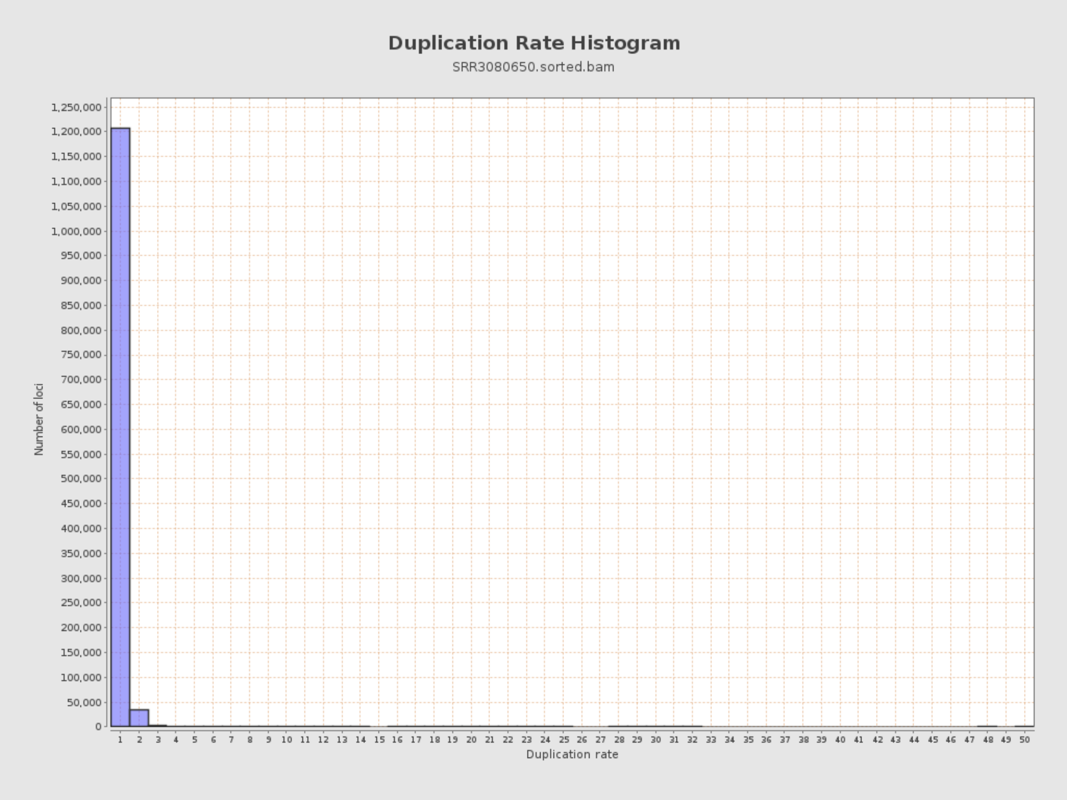
5. Results : Coverage Histogram (0-50X)



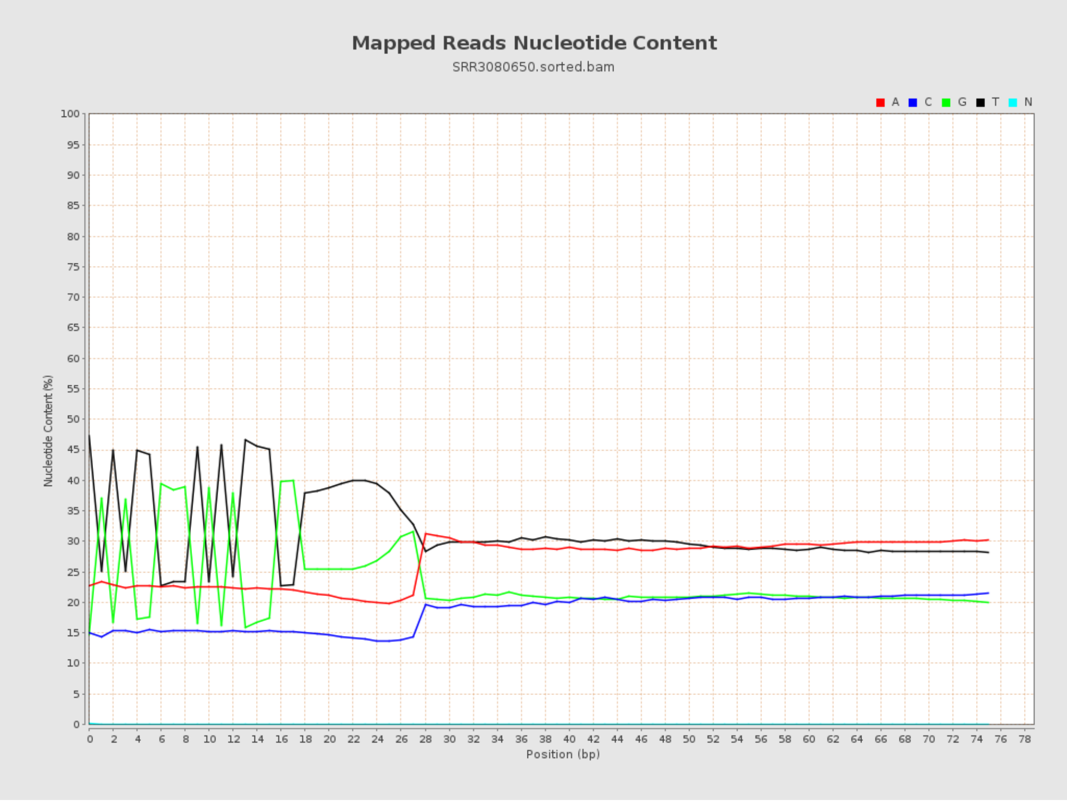
6. Results : Genome Fraction Coverage



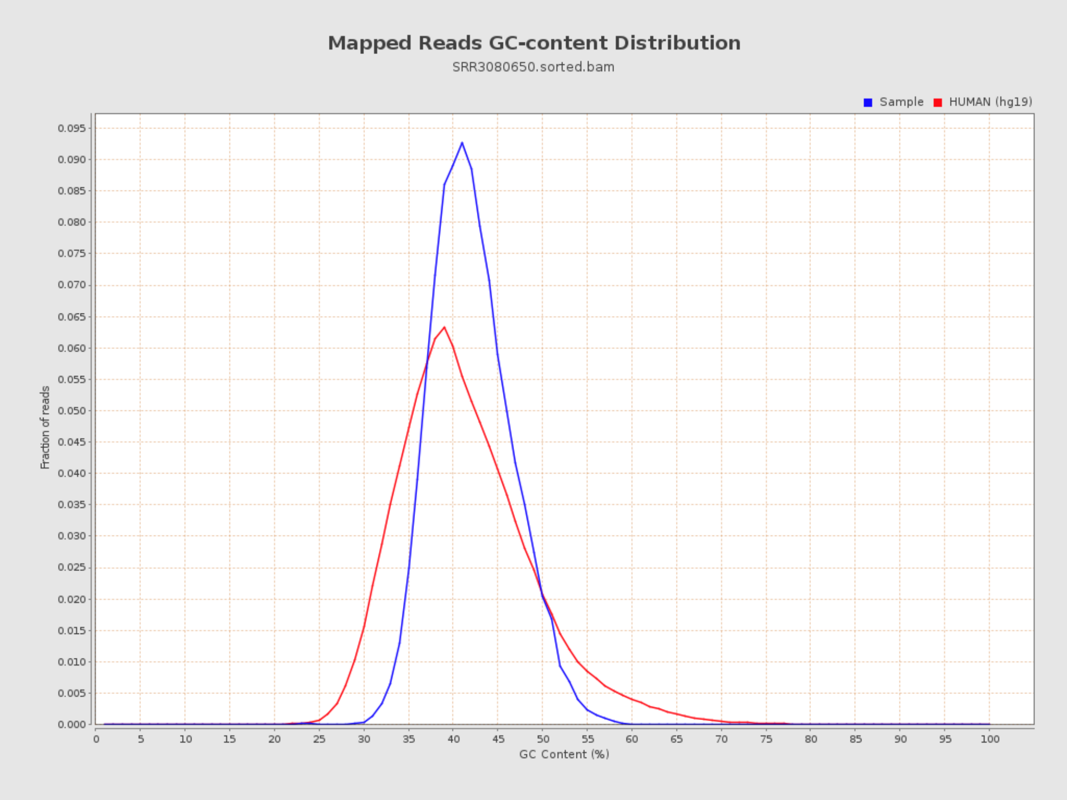
7. Results : Duplication Rate Histogram



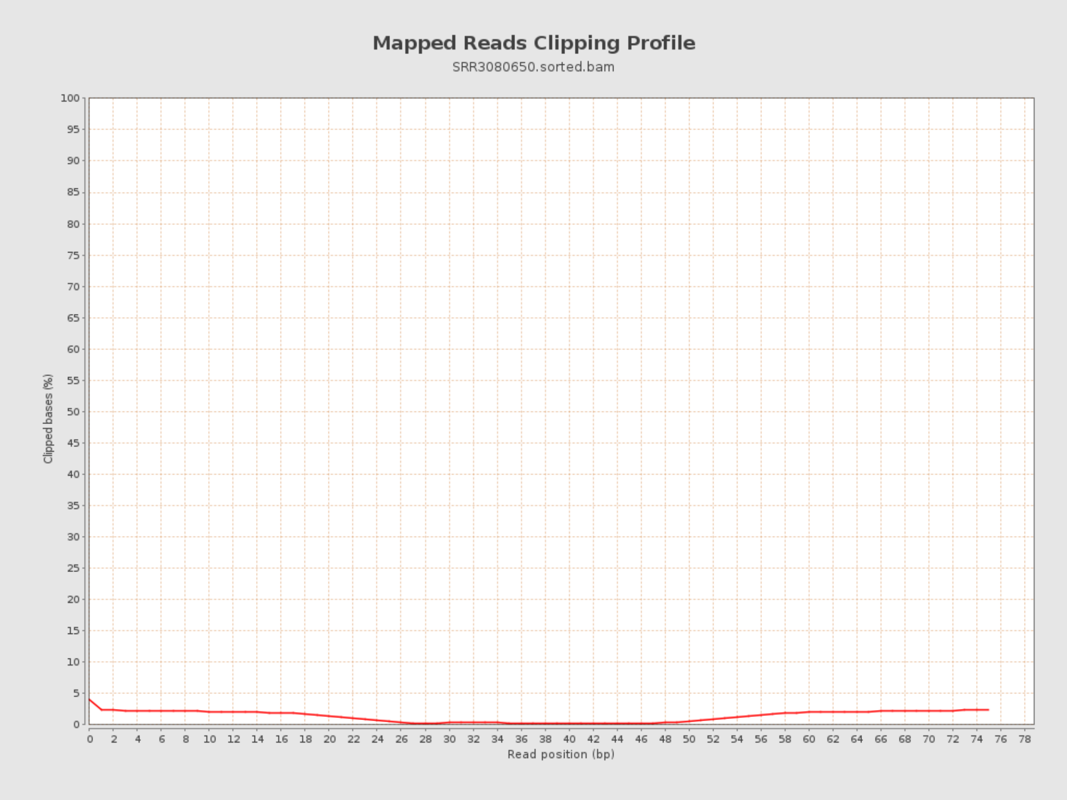
8. Results : Mapped Reads Nucleotide Content



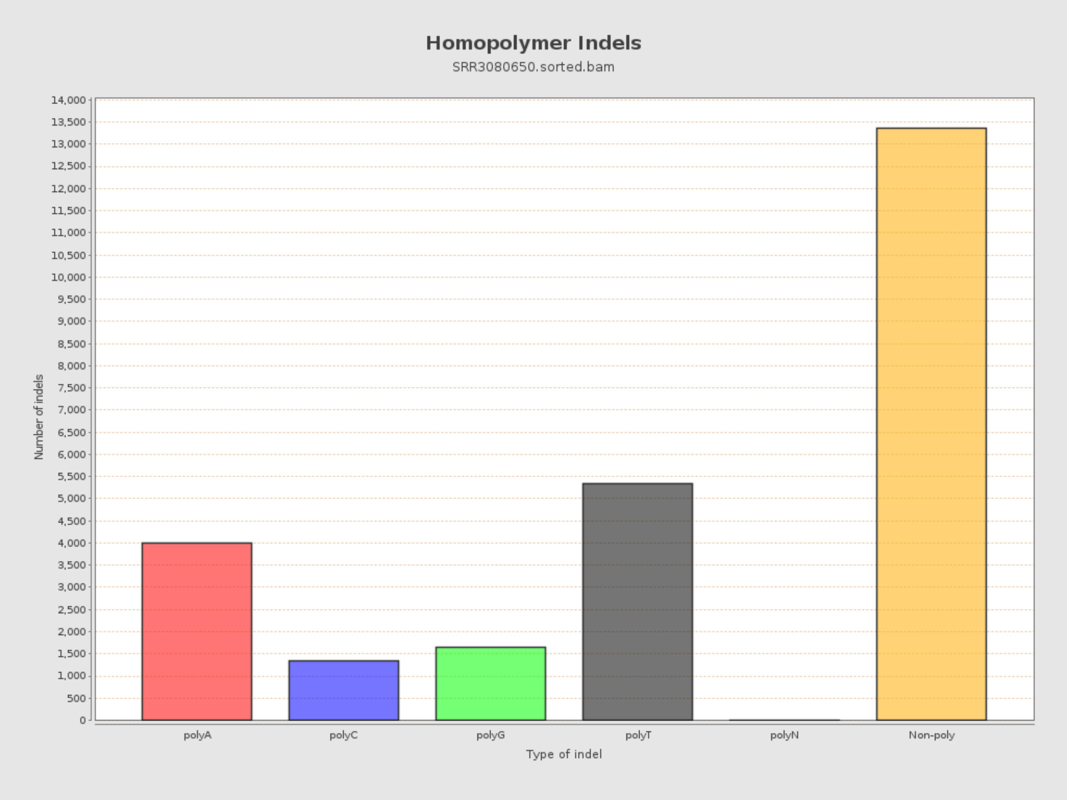
9. Results : Mapped Reads GC-content Distribution



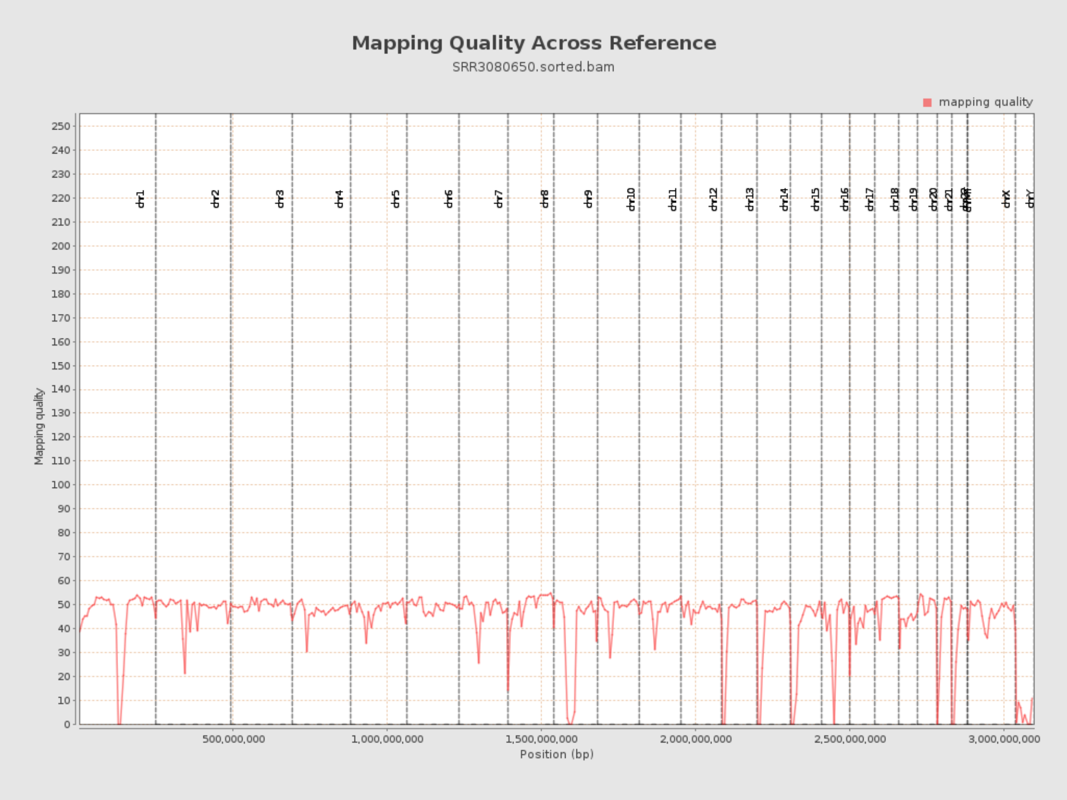
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram