Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:01:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080644.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_SRR3080644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:01:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,441,335
Mapped reads	1,301,148 / 90.27%
Unmapped reads	140,187 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,634 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	48,273 / 3.35%
Duplication rate	3.18%
Clipped reads	631,468 / 43.81%

2.2. ACGT Content

Number/percentage of A's	22,939,913 / 26.81%
Number/percentage of C's	15,974,947 / 18.67%
Number/percentage of T's	26,844,302 / 31.37%
Number/percentage of G's	19,809,152 / 23.15%
Number/percentage of N's	3,565 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2371

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

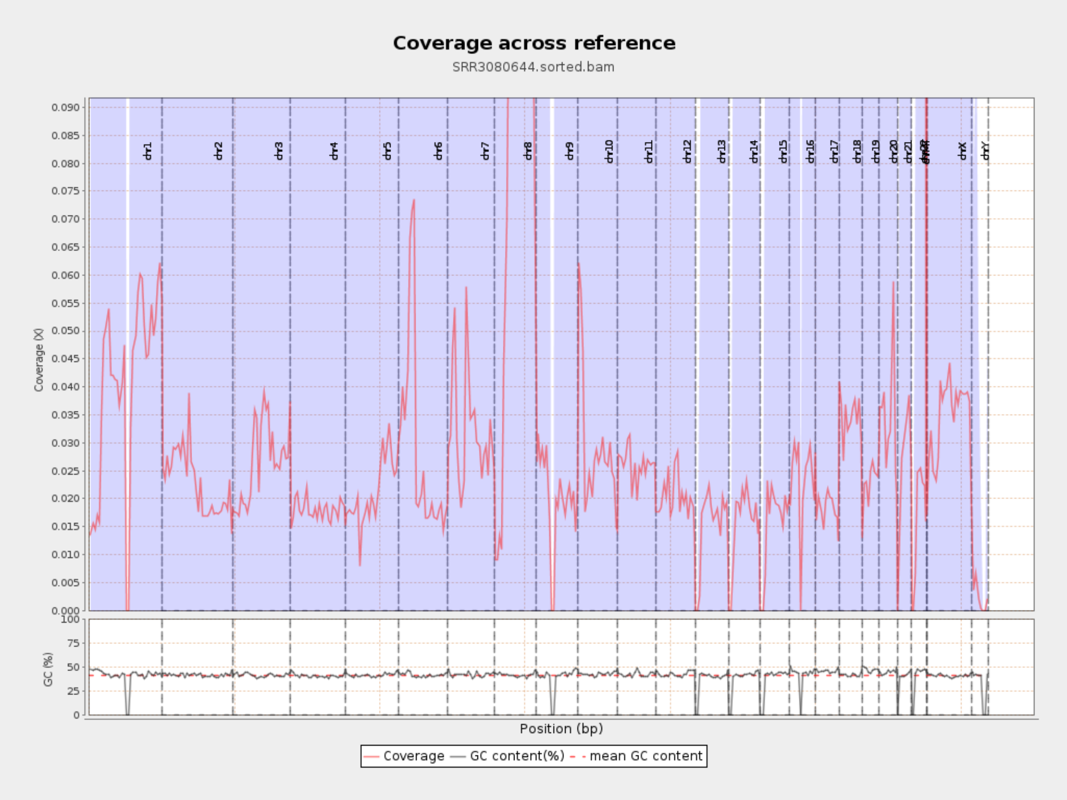
General error rate	0.7%
Mismatches	591,765
Insertions	6,414
Mapped reads with at least one insertion	0.49%
Deletions	20,106
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.29%

2.6. Chromosome stats

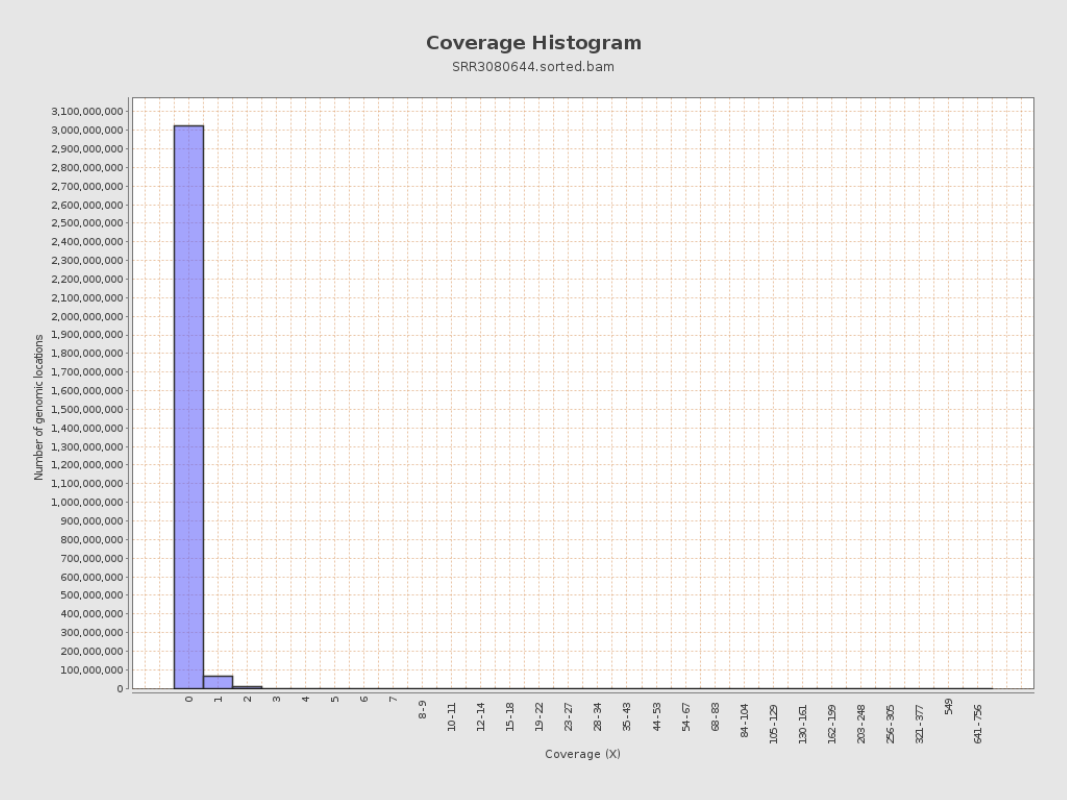
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9998100	0.0401	0.2671
chr2	243199373	5566061	0.0229	0.3686
chr3	198022430	5249325	0.0265	0.1812
chr4	191154276	3444843	0.018	0.1565
chr5	180915260	3833697	0.0212	0.1619
chr6	171115067	4991071	0.0292	0.2288
chr7	159138663	5251718	0.033	0.4401

chr8	146364022	11696307	0.0799	0.3493
chr9	141213431	2797866	0.0198	0.1773
chr10	135534747	4044140	0.0298	0.2039
chr11	135006516	3492970	0.0259	0.1898
chr12	133851895	2714758	0.0203	0.158
chr13	115169878	1754779	0.0152	0.1381
chr14	107349540	1659725	0.0155	0.1406
chr15	102531392	1599476	0.0156	0.1526
chr16	90354753	2114867	0.0234	0.1741
chr17	81195210	1473531	0.0181	0.154
chr18	78077248	2707267	0.0347	0.2391
chr19	59128983	1369485	0.0232	0.1906
chr20	63025520	2189288	0.0347	0.2112
chr21	48129895	1256311	0.0261	0.1827
chr22	51304566	820518	0.016	0.1394
chrMT	16571	17129	1.0337	1.252
chrX	155270560	5397855	0.0348	0.2136
chrY	59373566	162756	0.0027	0.0613

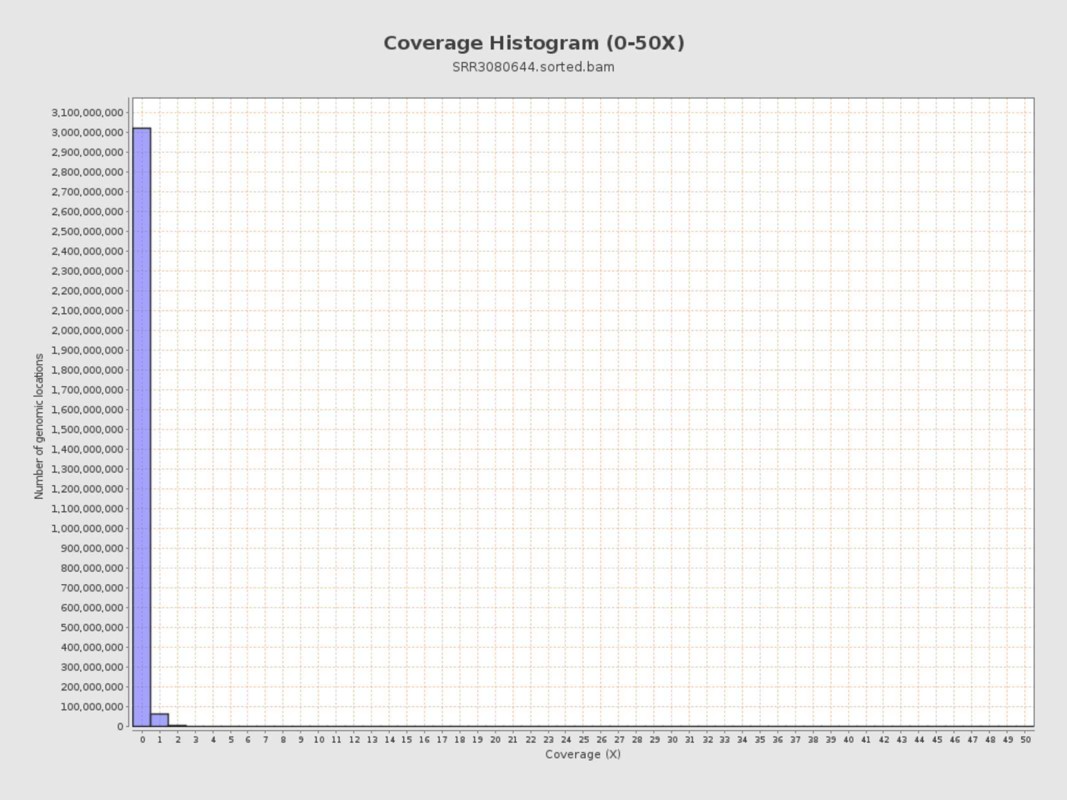
3. Results : Coverage across reference



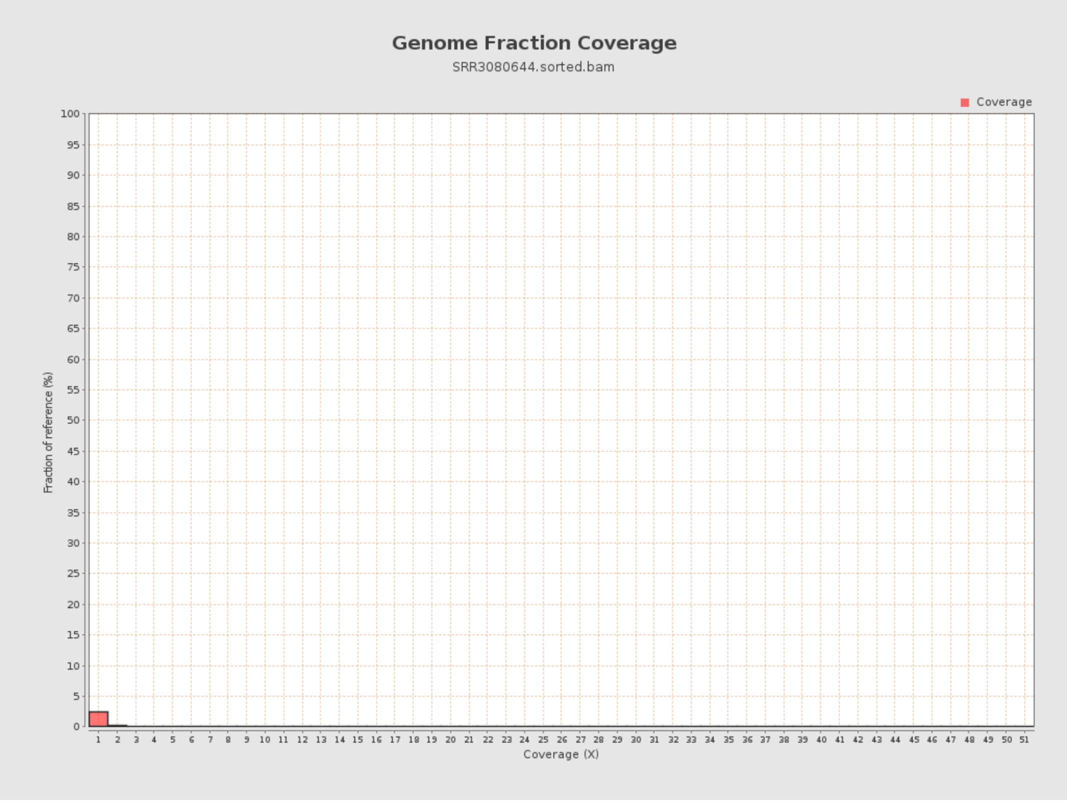
4. Results : Coverage Histogram



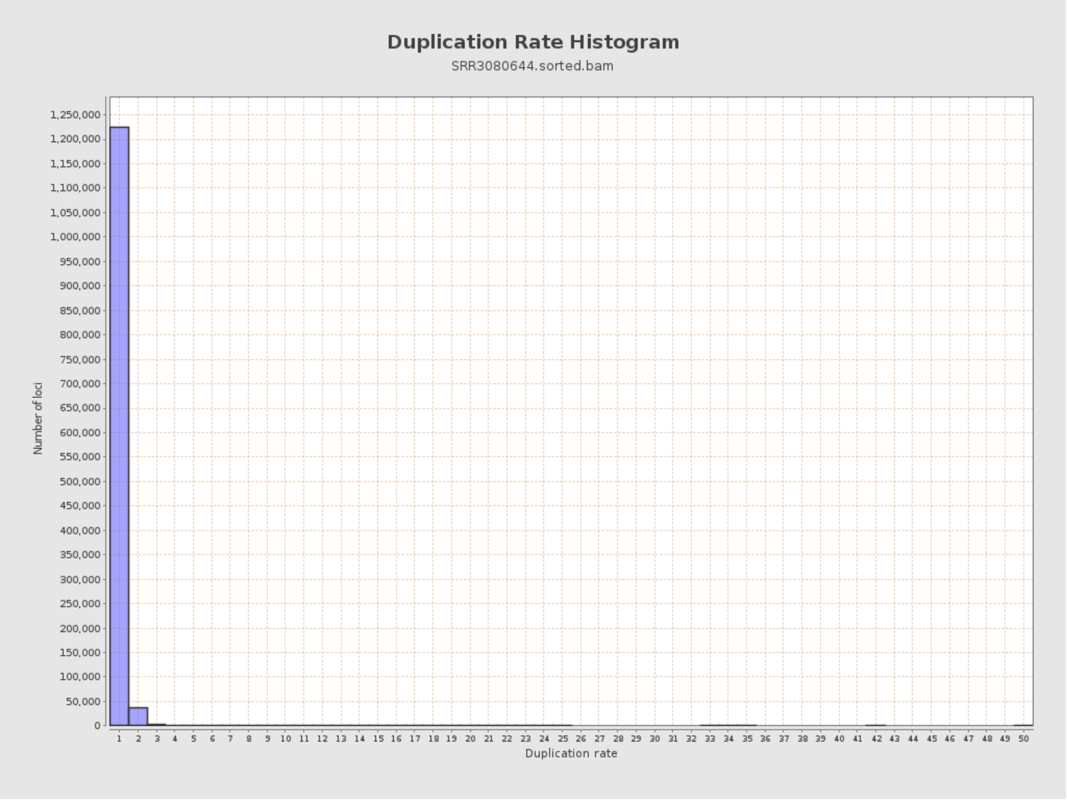
5. Results : Coverage Histogram (0-50X)



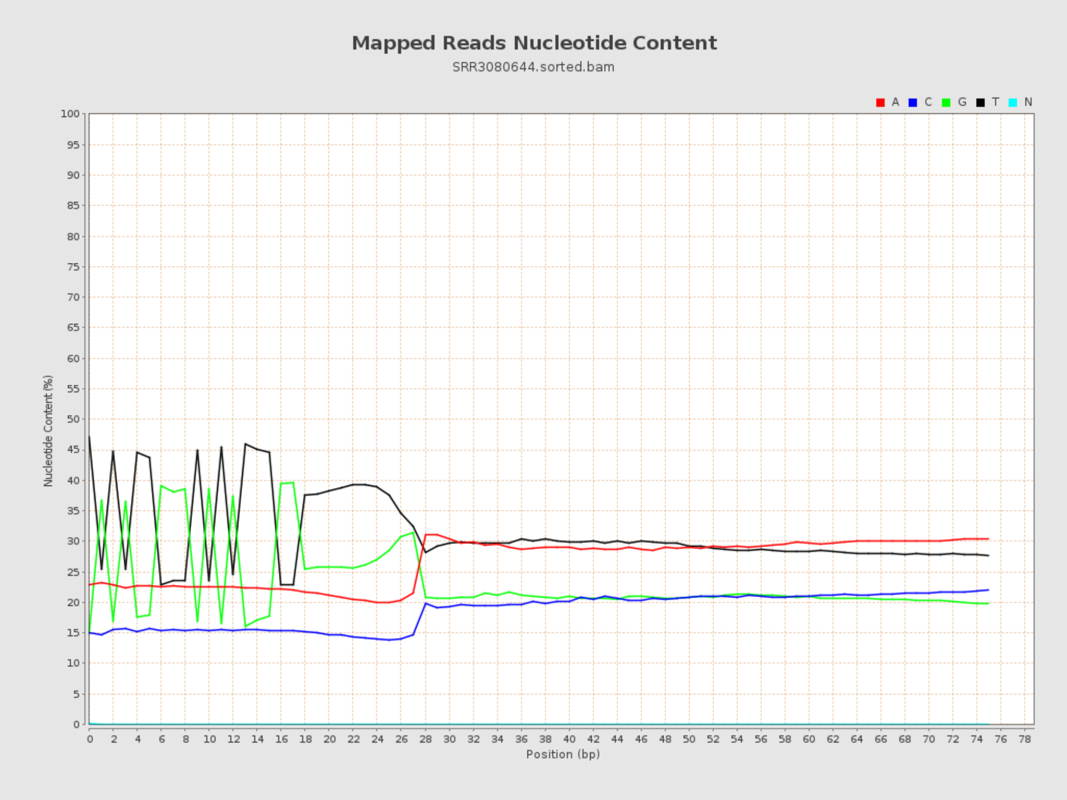
6. Results : Genome Fraction Coverage



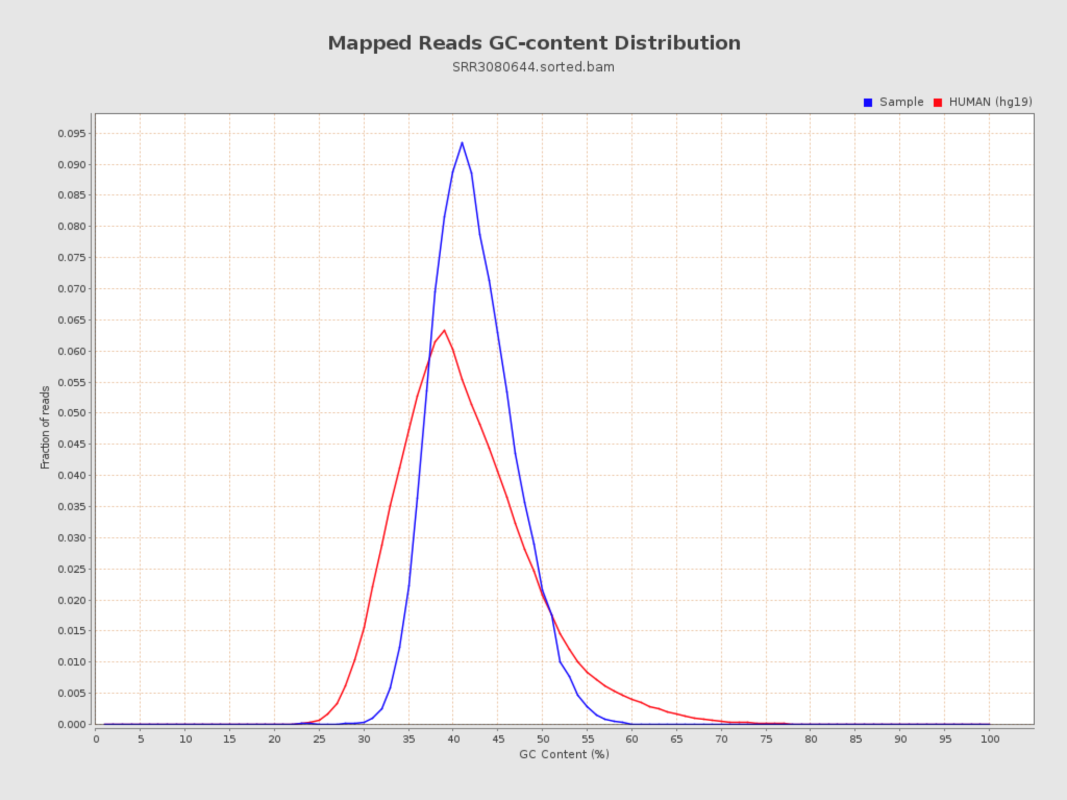
7. Results : Duplication Rate Histogram



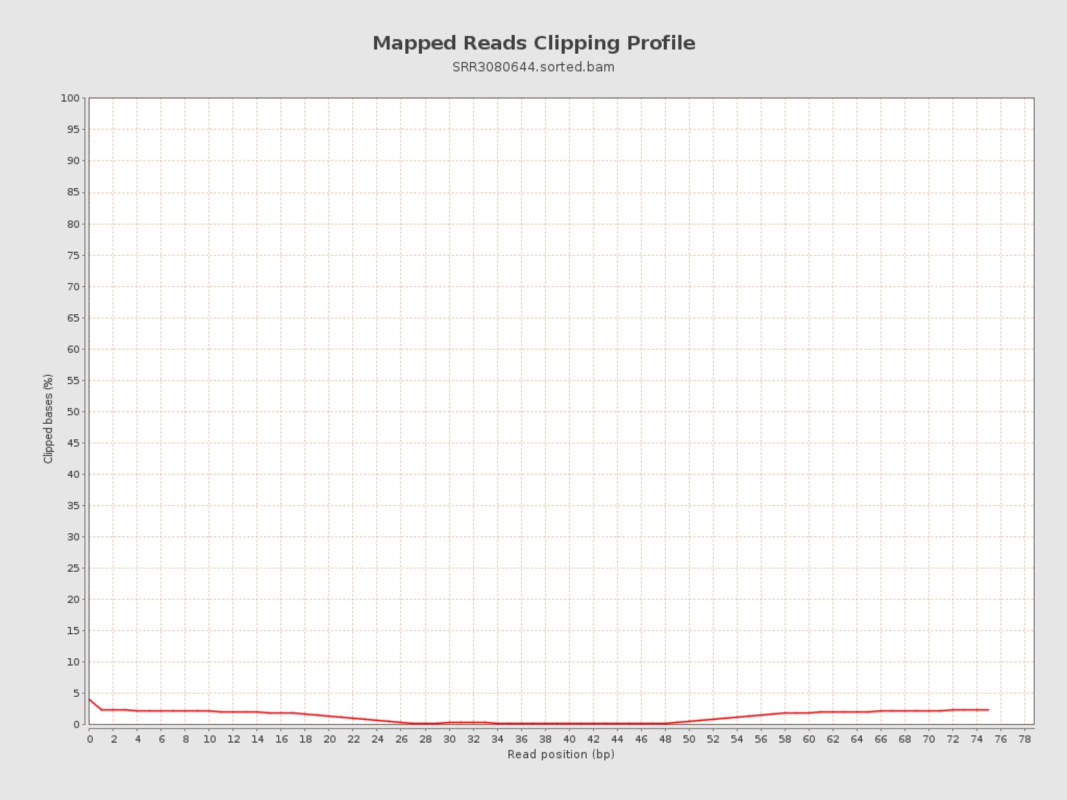
8. Results : Mapped Reads Nucleotide Content



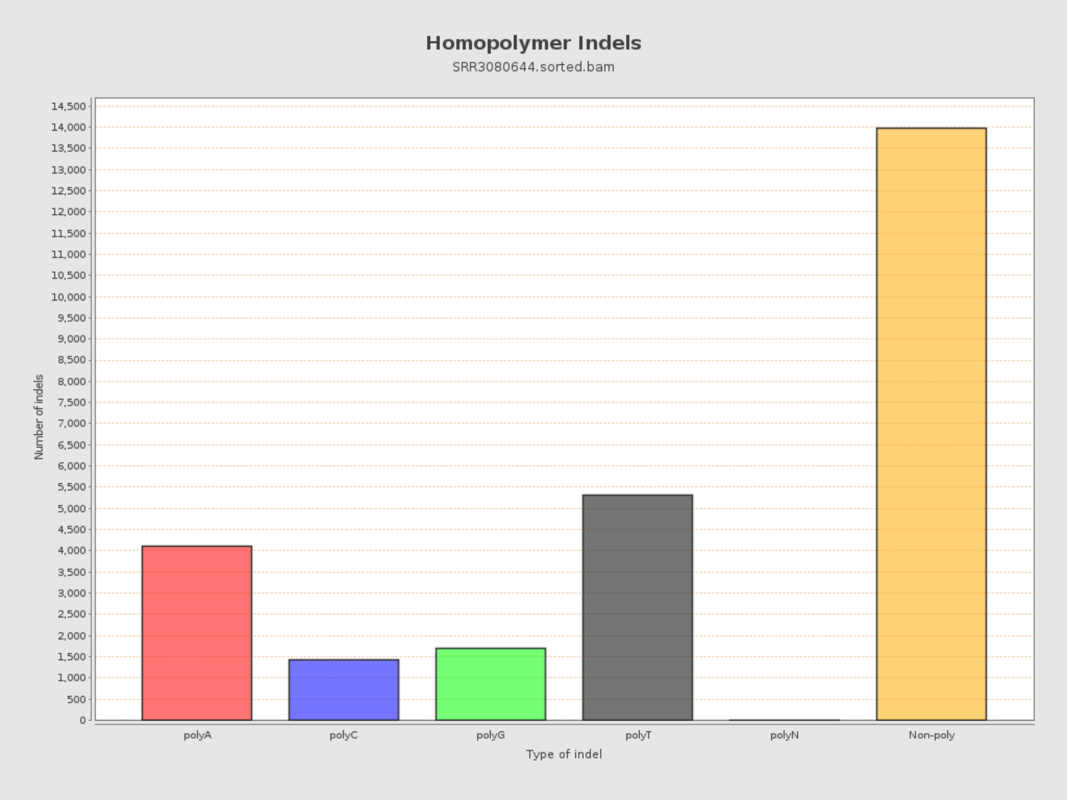
9. Results : Mapped Reads GC-content Distribution



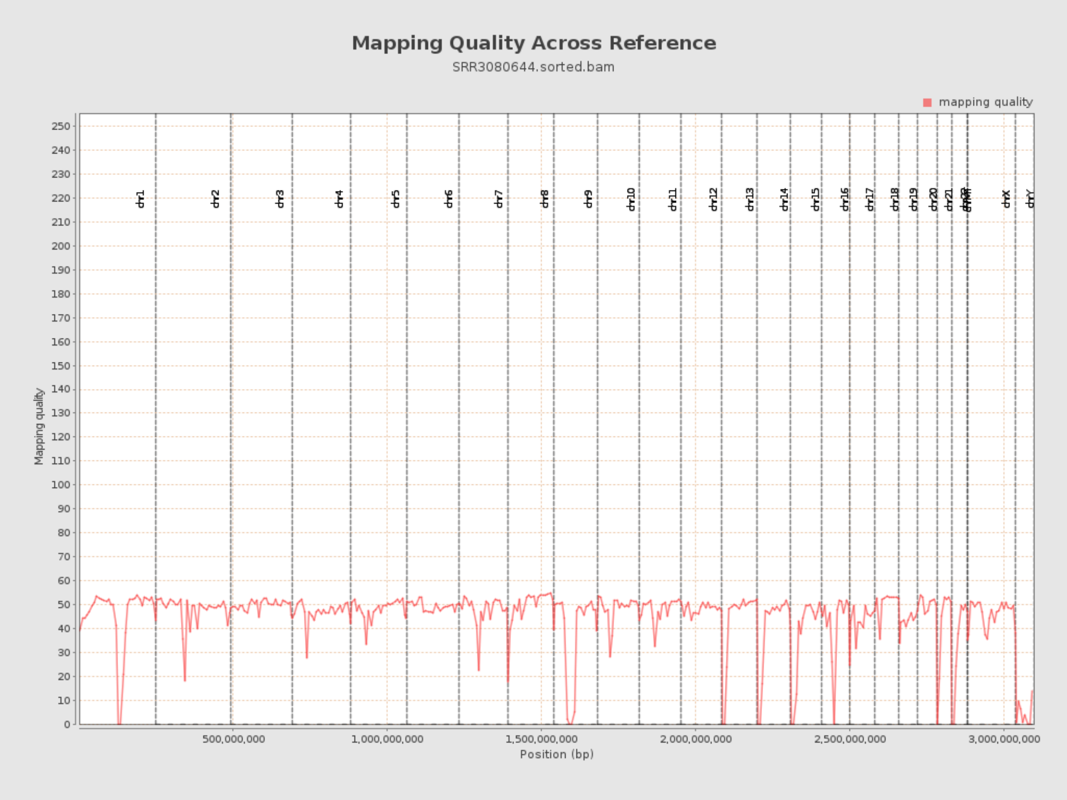
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram