Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:32:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080637.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_SRR3080637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:32:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,685,483
Mapped reads	2,303,359 / 85.77%
Unmapped reads	382,124 / 14.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,540 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	94,315 / 3.51%
Duplication rate	3.15%
Clipped reads	1,153,175 / 42.94%

2.2. ACGT Content

Number/percentage of A's	41,716,031 / 27.24%
Number/percentage of C's	27,471,215 / 17.94%
Number/percentage of T's	49,028,270 / 32.02%
Number/percentage of G's	34,782,010 / 22.72%
Number/percentage of N's	123,857 / 0.08%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0495

Standard Deviation	0.4493

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

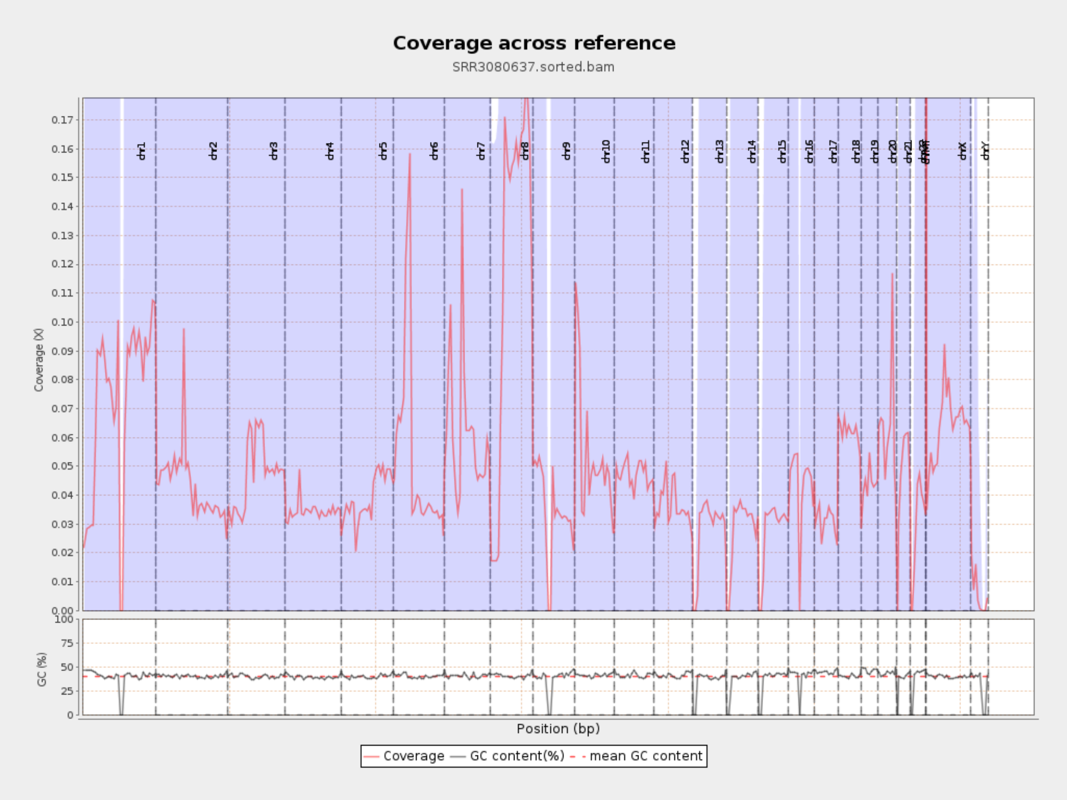
General error rate	0.92%
Mismatches	1,388,100
Insertions	13,439
Mapped reads with at least one insertion	0.58%
Deletions	36,545
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.13%

2.6. Chromosome stats

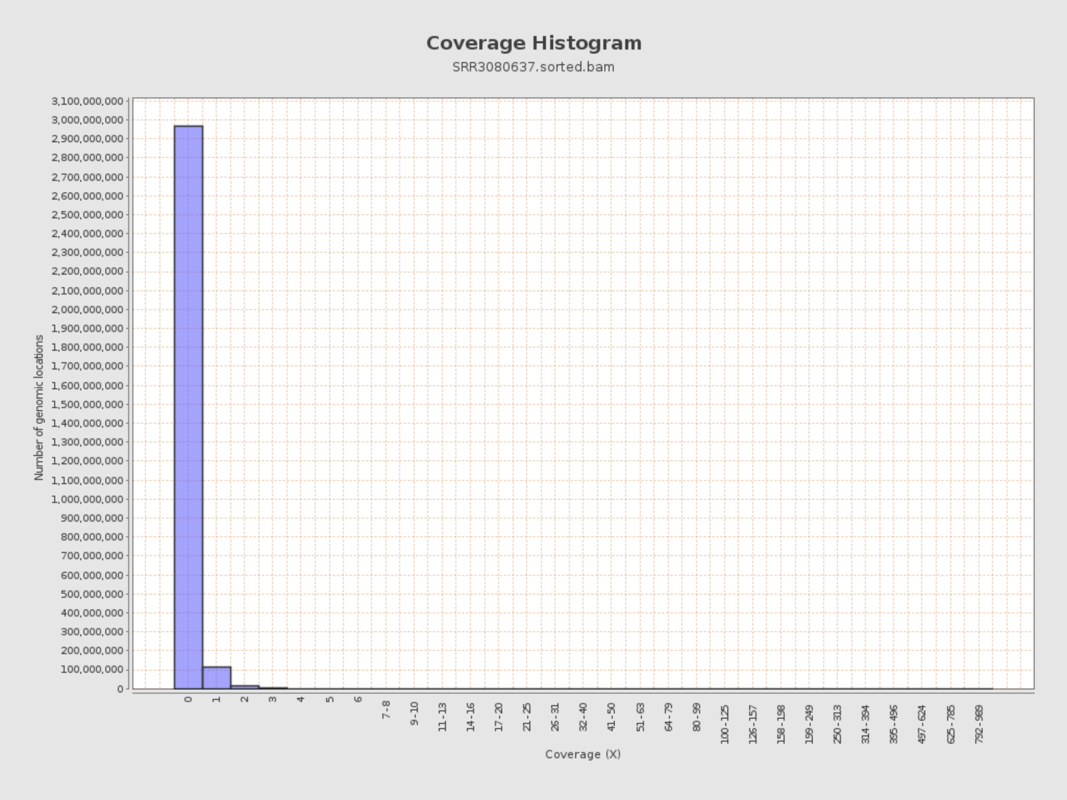
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18025531	0.0723	0.5855
chr2	243199373	10590615	0.0435	0.4702
chr3	198022430	9432707	0.0476	0.2457
chr4	191154276	6598243	0.0345	0.2213
chr5	180915260	7032880	0.0389	0.2206
chr6	171115067	9457650	0.0553	0.4172
chr7	159138663	9923772	0.0624	1.2215

chr8	146364022	17773333	0.1214	0.5541
chr9	141213431	4838134	0.0343	0.3595
chr10	135534747	7435398	0.0549	0.3804
chr11	135006516	6323730	0.0468	0.3207
chr12	133851895	4866153	0.0364	0.2164
chr13	115169878	3197096	0.0278	0.184
chr14	107349540	3030170	0.0282	0.2174
chr15	102531392	2742990	0.0268	0.1832
chr16	90354753	3831696	0.0424	0.2523
chr17	81195210	2545665	0.0314	0.2242
chr18	78077248	4860762	0.0623	0.5471
chr19	59128983	2598011	0.0439	0.4235
chr20	63025520	4078338	0.0647	0.2942
chr21	48129895	2227158	0.0463	0.2577
chr22	51304566	1493298	0.0291	0.1894
chrMT	16571	47915	2.8915	3.3475
chrX	155270560	9885407	0.0637	0.3215
chrY	59373566	344370	0.0058	0.1217

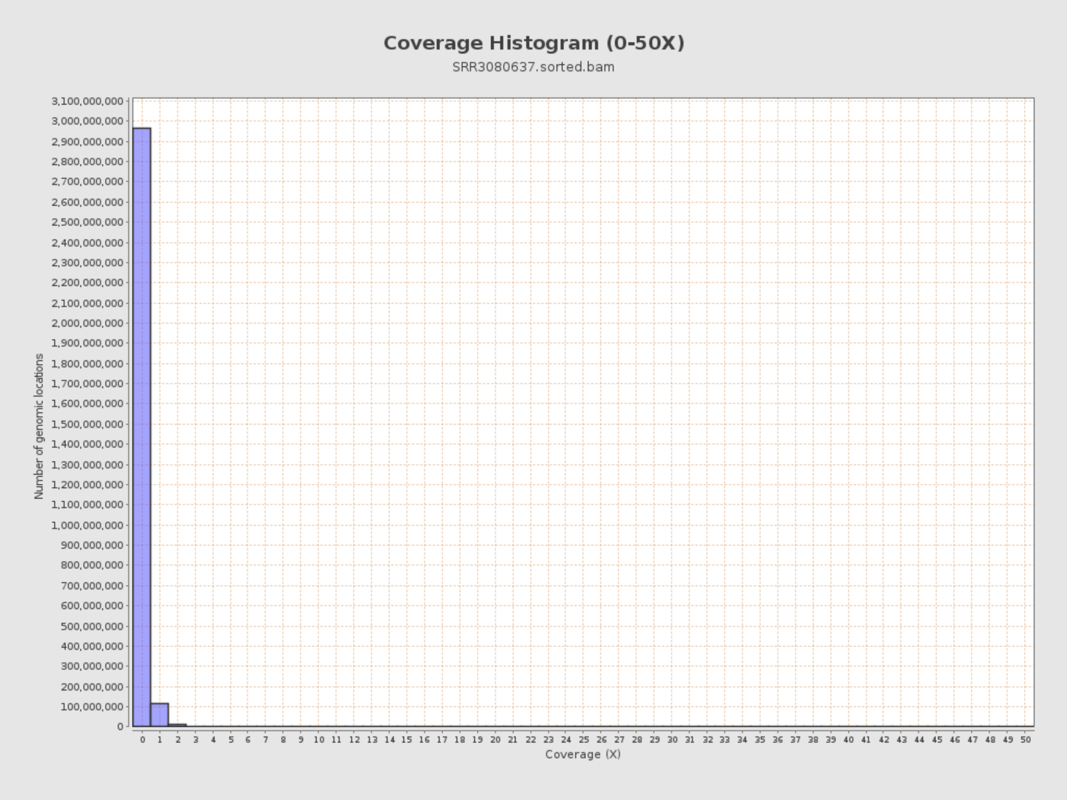
3. Results : Coverage across reference



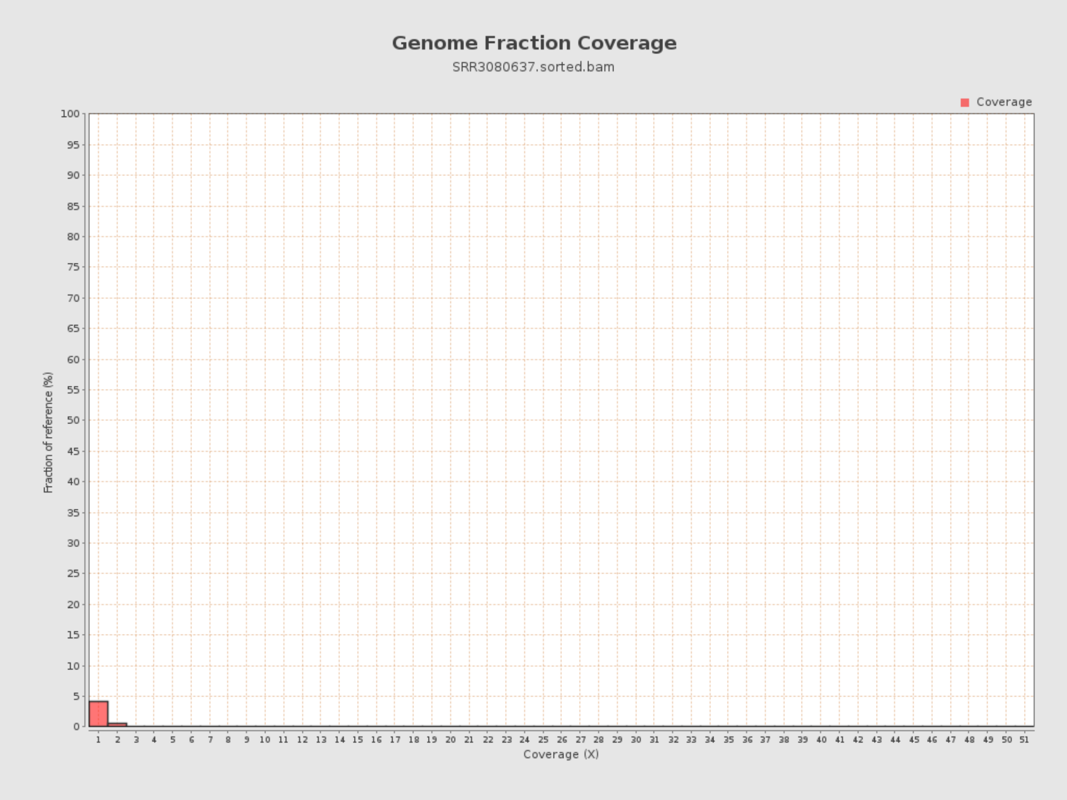
4. Results : Coverage Histogram



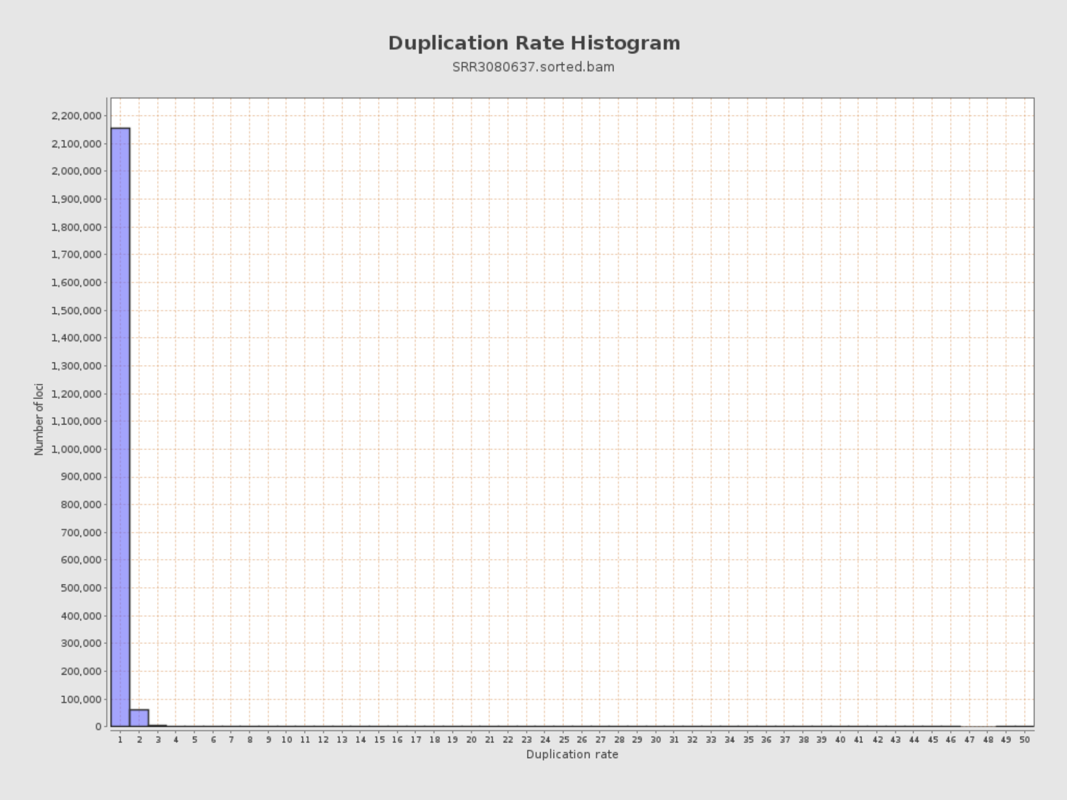
5. Results : Coverage Histogram (0-50X)



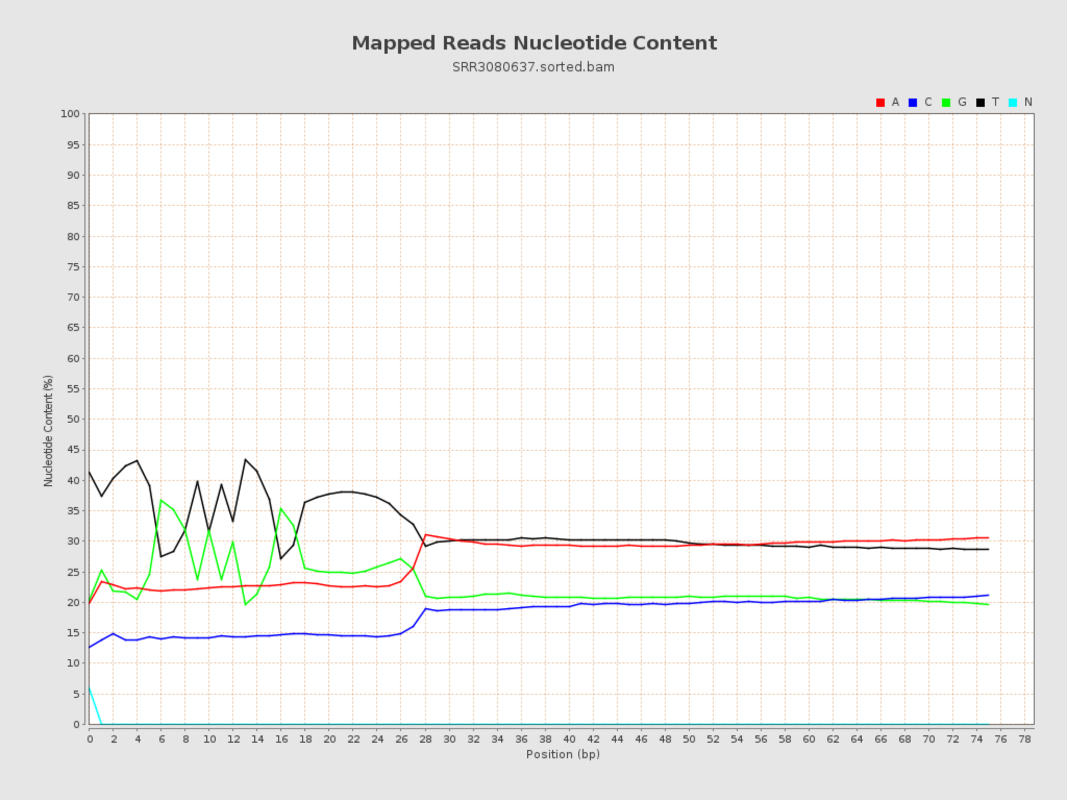
6. Results : Genome Fraction Coverage



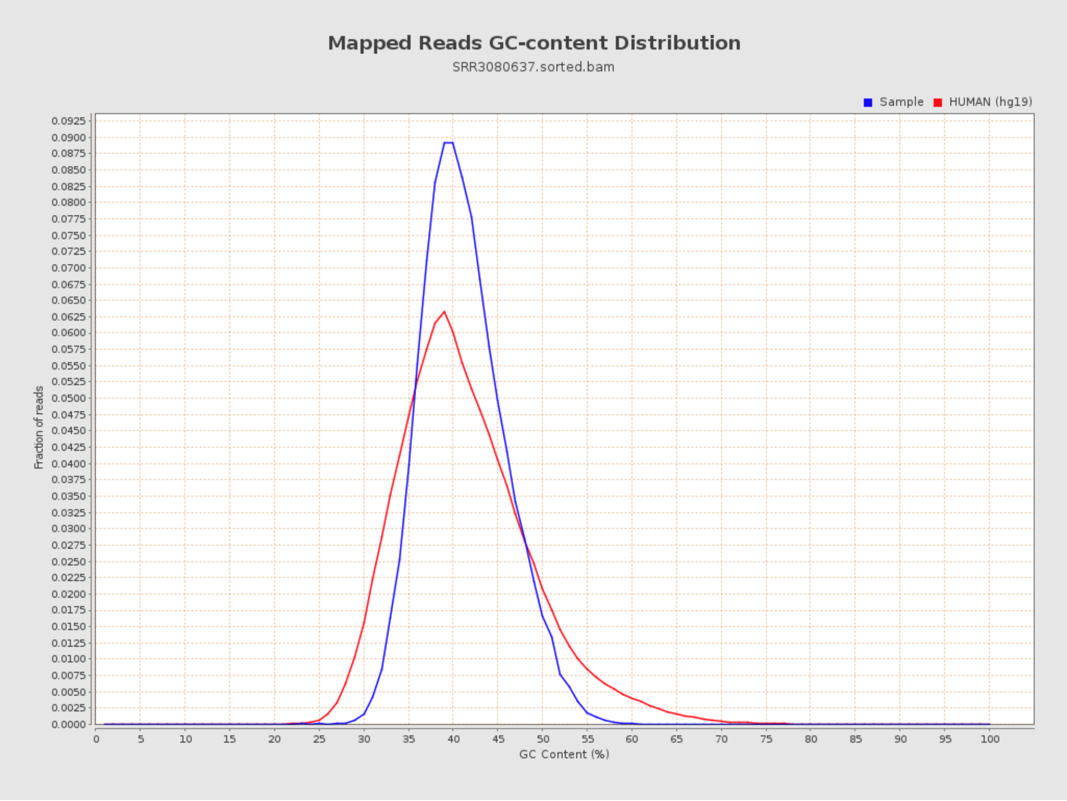
7. Results : Duplication Rate Histogram



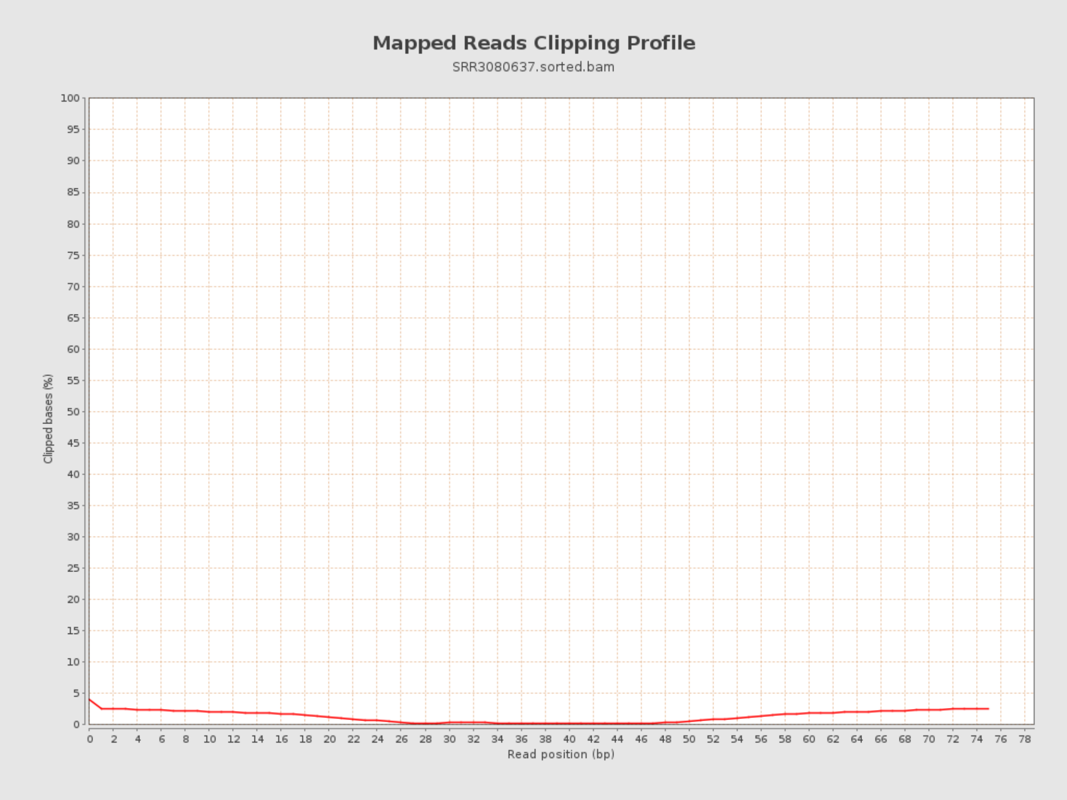
8. Results : Mapped Reads Nucleotide Content



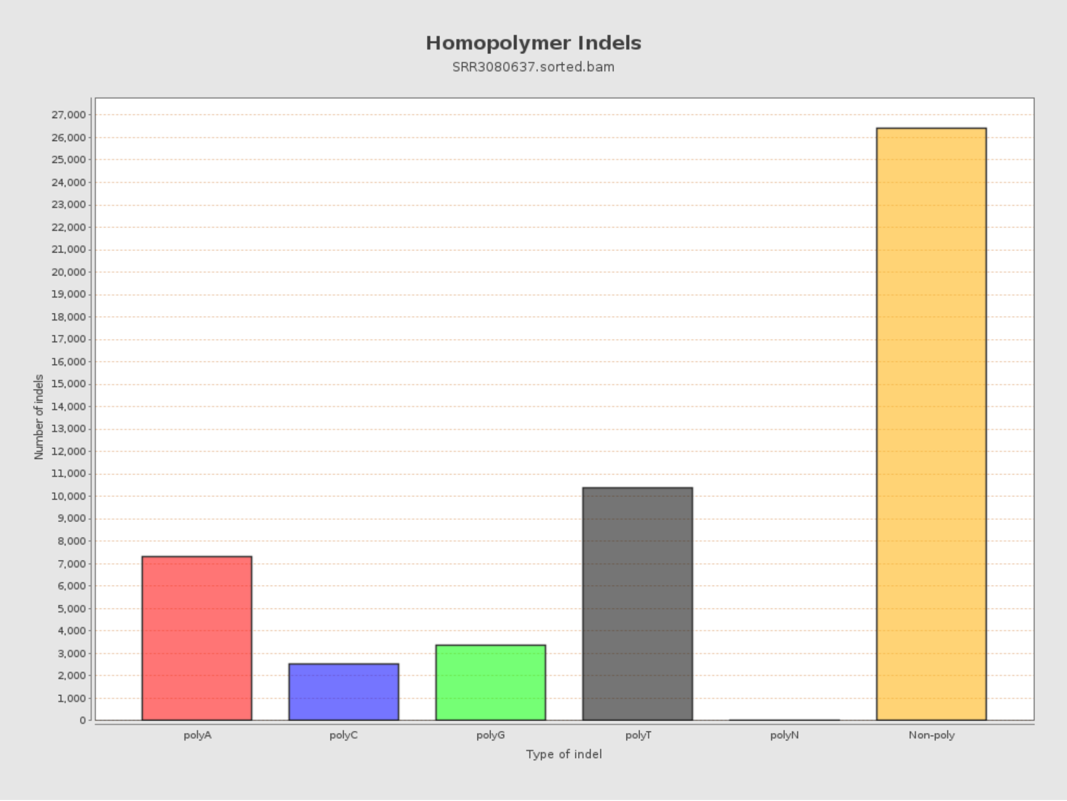
9. Results : Mapped Reads GC-content Distribution



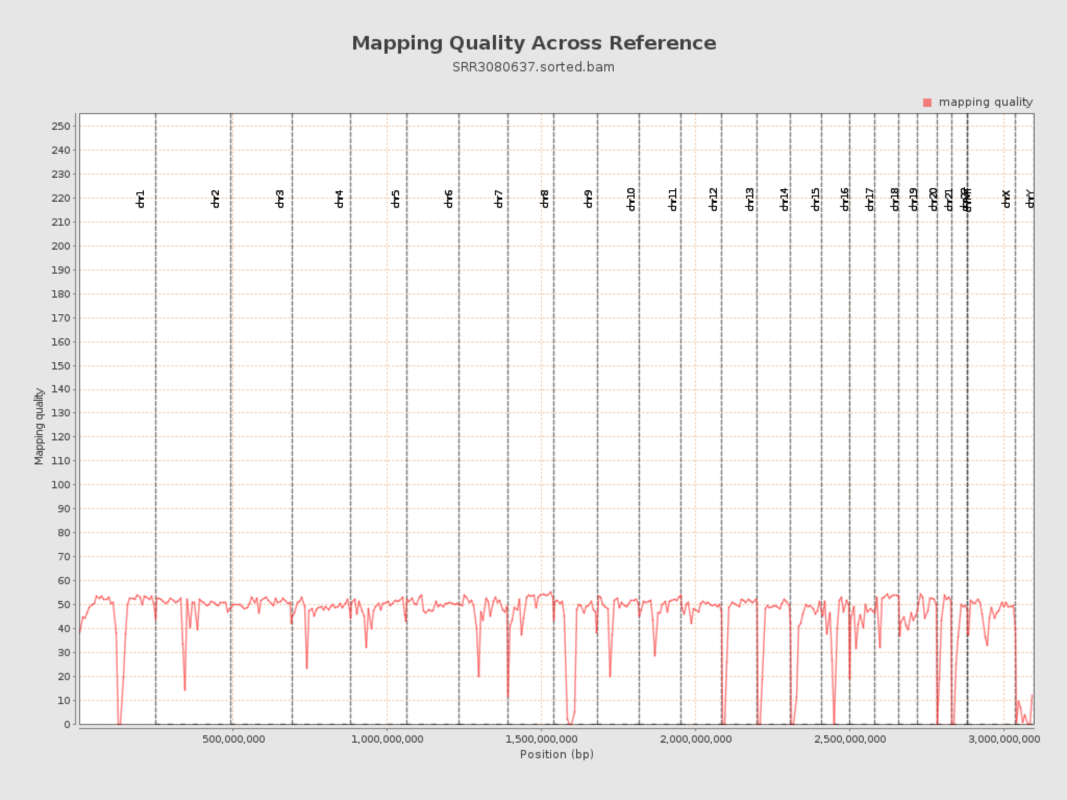
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram