Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230357.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_SRR6230357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230357.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	842,876
Mapped reads	763,483 / 90.58%
Unmapped reads	79,393 / 9.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,965 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	21,974 / 2.61%
Duplication rate	2.34%
Clipped reads	317,199 / 37.63%

2.2. ACGT Content

Number/percentage of A's	15,136,679 / 29.34%
Number/percentage of C's	9,358,051 / 18.14%
Number/percentage of T's	16,497,534 / 31.98%
Number/percentage of G's	10,574,159 / 20.49%
Number/percentage of N's	27,486 / 0.05%
GC Percentage	38.63%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.185

2.4. Mapping Quality

Mean Mapping Quality	47.45

2.5. Mismatches and indels

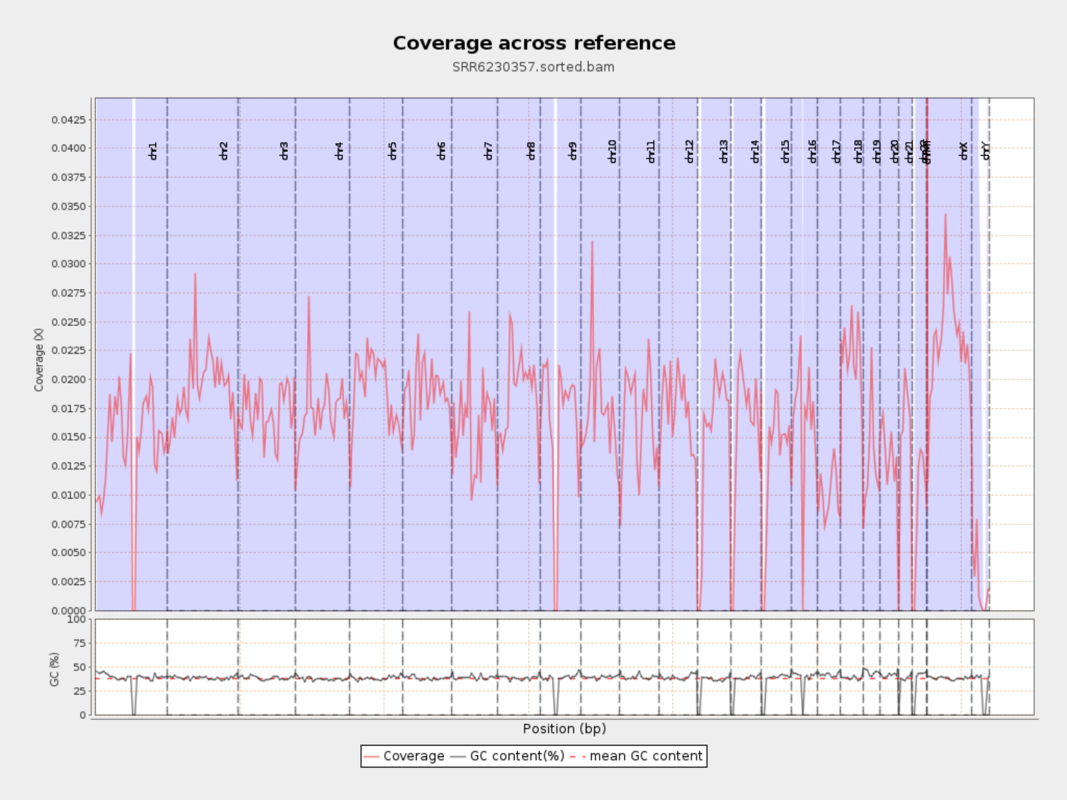
General error rate	0.9%
Mismatches	454,004
Insertions	4,601
Mapped reads with at least one insertion	0.6%
Deletions	15,447
Mapped reads with at least one deletion	2%
Homopolymer indels	46.65%

2.6. Chromosome stats

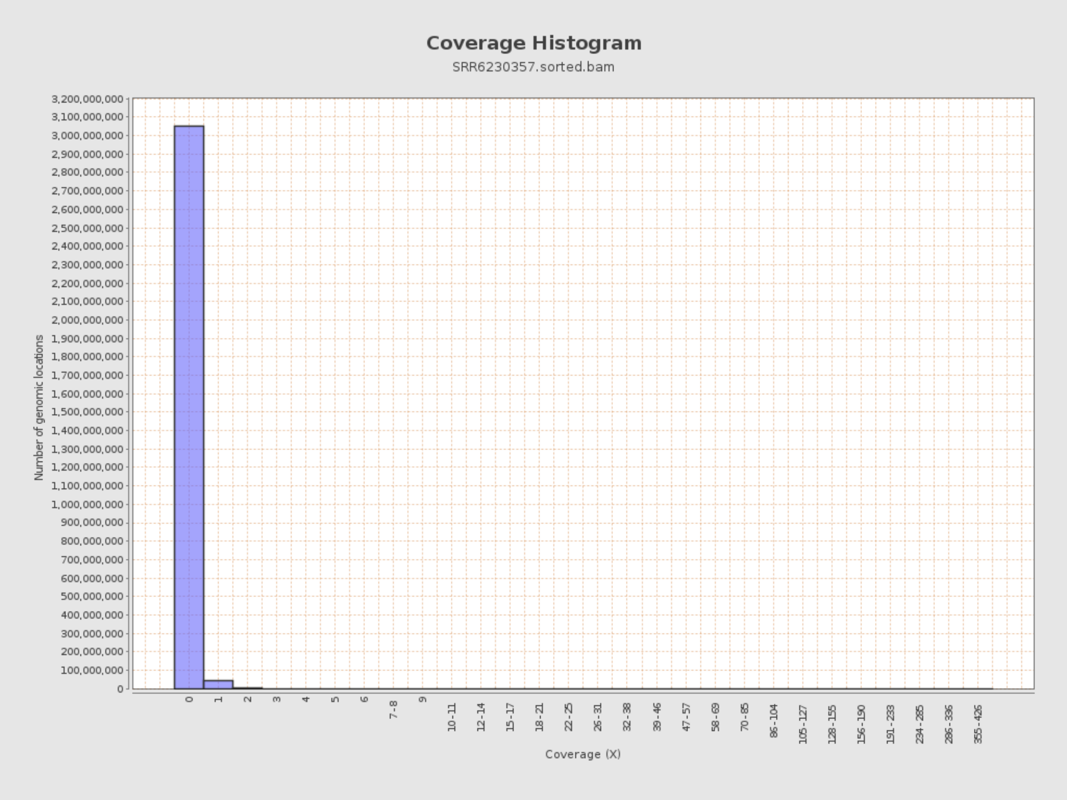
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3556196	0.0143	0.2724
chr2	243199373	4659507	0.0192	0.1883
chr3	198022430	3432831	0.0173	0.1433
chr4	191154276	3306557	0.0173	0.152
chr5	180915260	3497084	0.0193	0.151
chr6	171115067	3249523	0.019	0.1612
chr7	159138663	2554949	0.0161	0.1884

chr8	146364022	2775521	0.019	0.3167
chr9	141213431	2293626	0.0162	0.1782
chr10	135534747	2353361	0.0174	0.1964
chr11	135006516	2247847	0.0166	0.1659
chr12	133851895	2329905	0.0174	0.1441
chr13	115169878	1746021	0.0152	0.1334
chr14	107349540	1648539	0.0154	0.1397
chr15	102531392	1312683	0.0128	0.1222
chr16	90354753	1446998	0.016	0.1497
chr17	81195210	822736	0.0101	0.1126
chr18	78077248	1747972	0.0224	0.2978
chr19	59128983	780860	0.0132	0.1815
chr20	63025520	843714	0.0134	0.1269
chr21	48129895	725481	0.0151	0.1415
chr22	51304566	455804	0.0089	0.1015
chrMT	16571	1635	0.0987	0.3505
chrX	155270560	3690444	0.0238	0.1748
chrY	59373566	140014	0.0024	0.0749

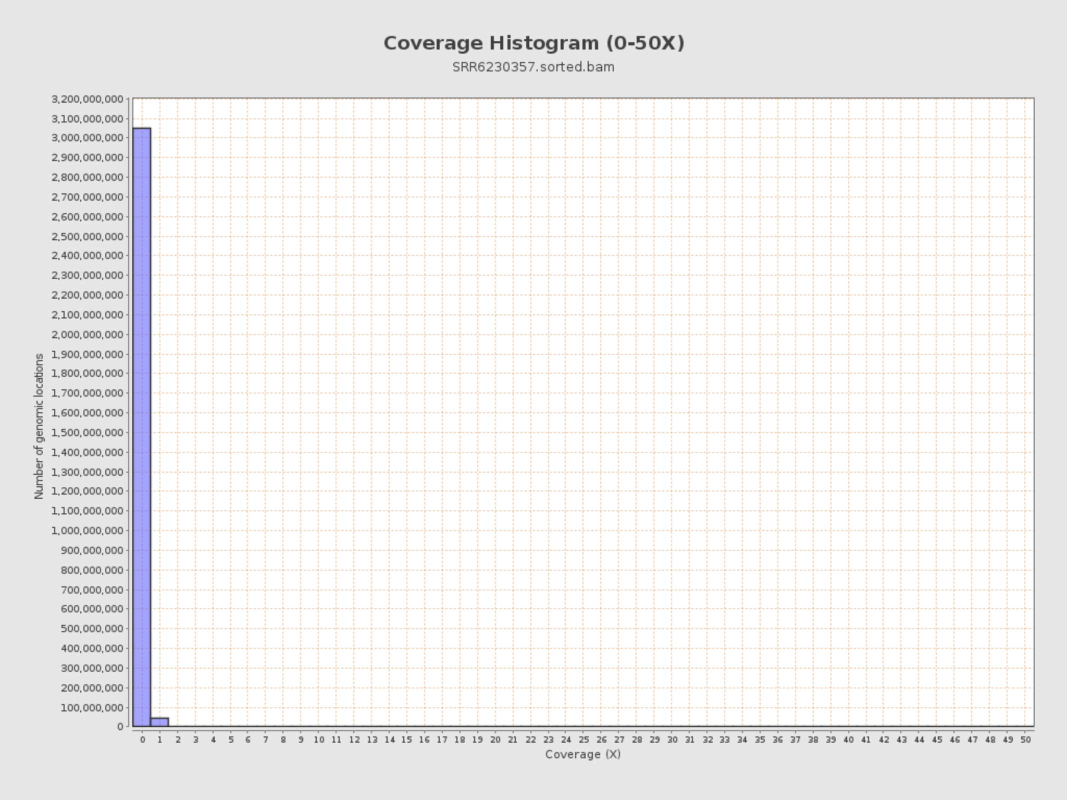
3. Results : Coverage across reference



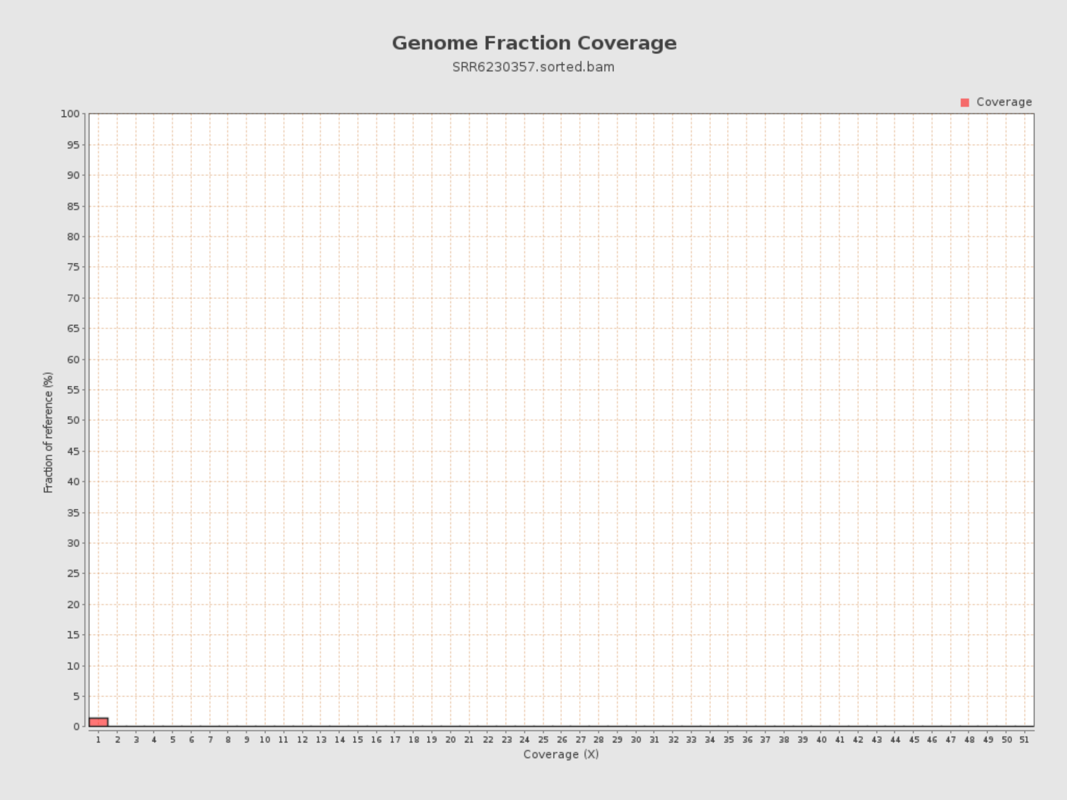
4. Results : Coverage Histogram



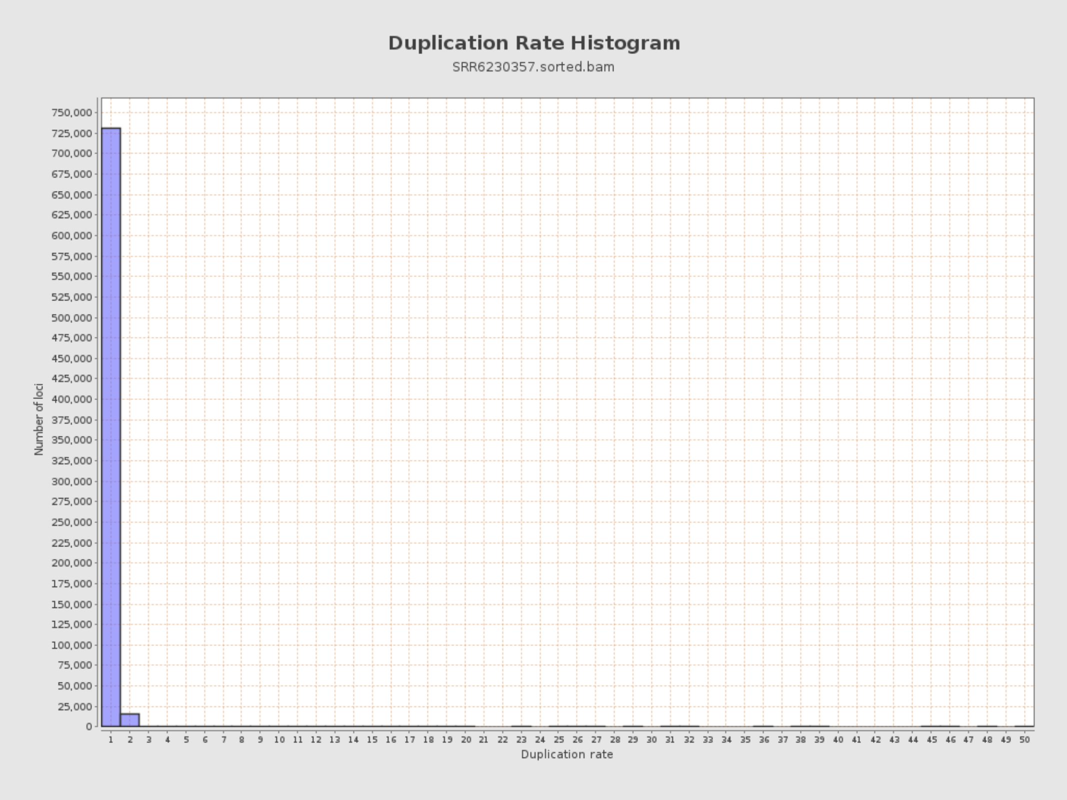
5. Results : Coverage Histogram (0-50X)



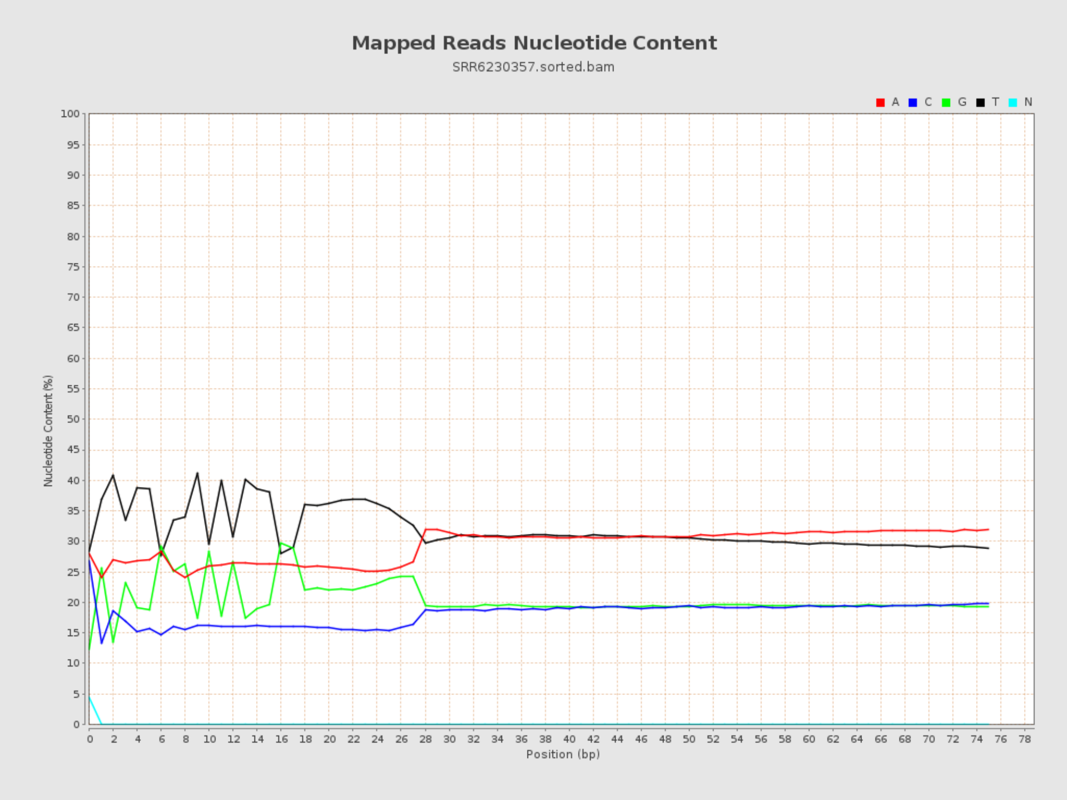
6. Results : Genome Fraction Coverage



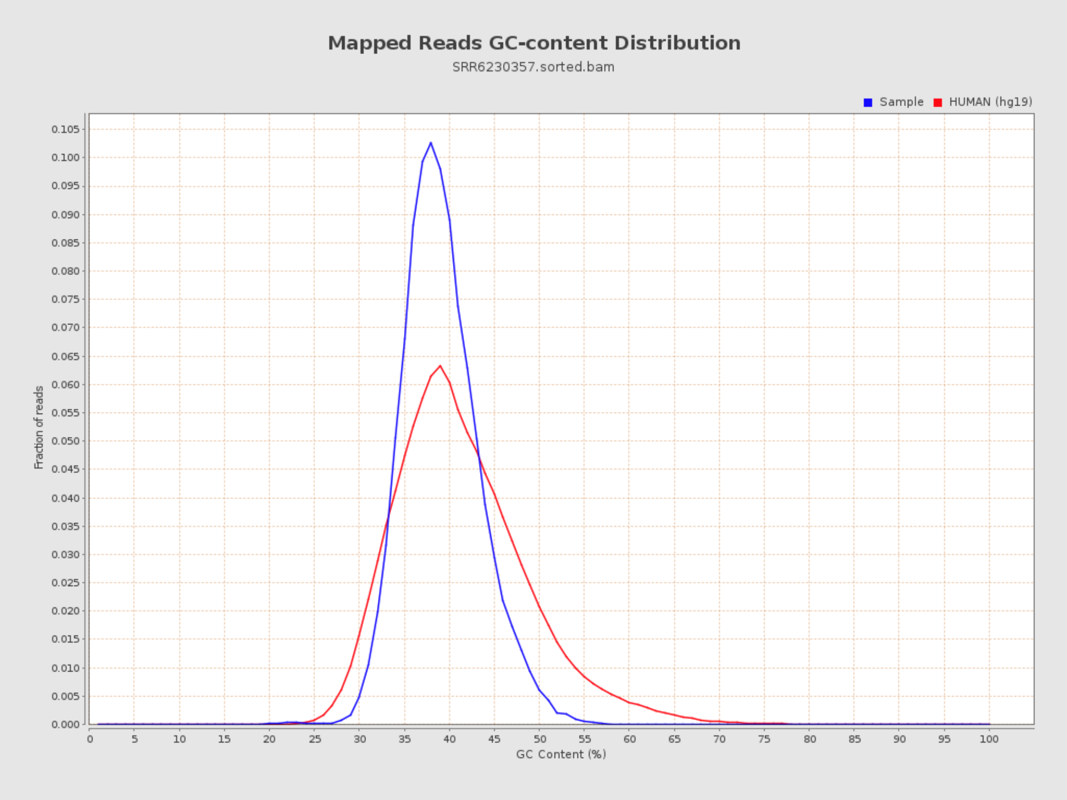
7. Results : Duplication Rate Histogram



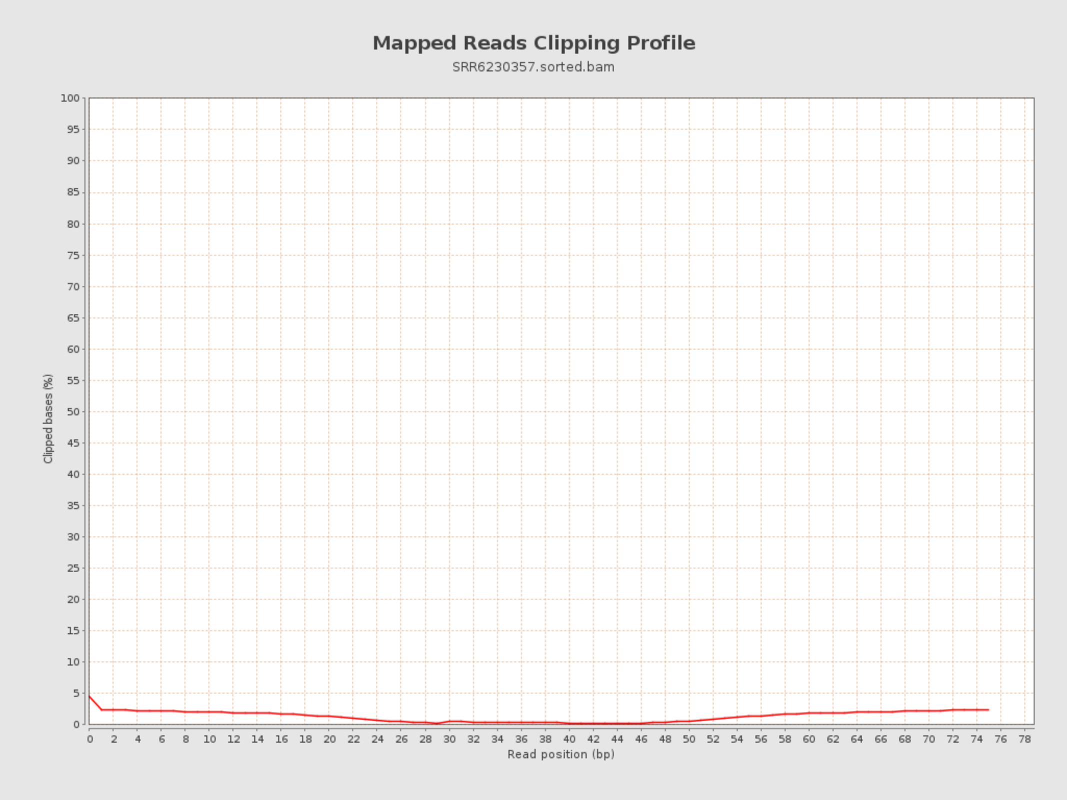
8. Results : Mapped Reads Nucleotide Content



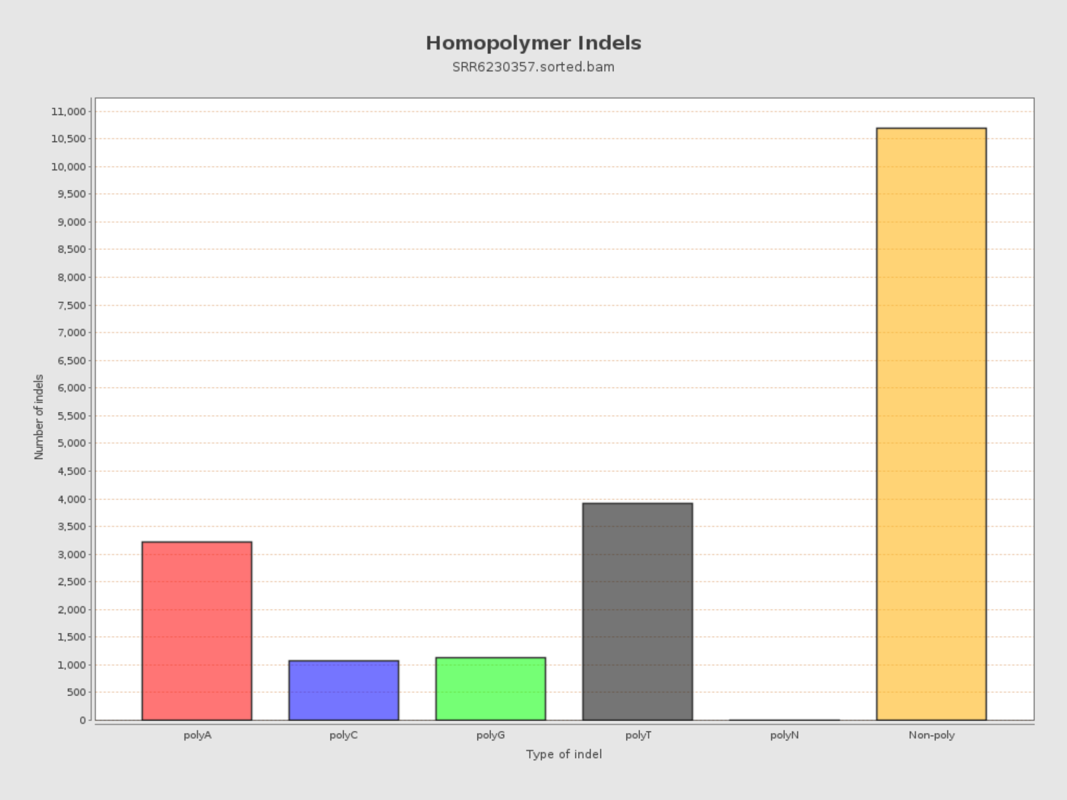
9. Results : Mapped Reads GC-content Distribution



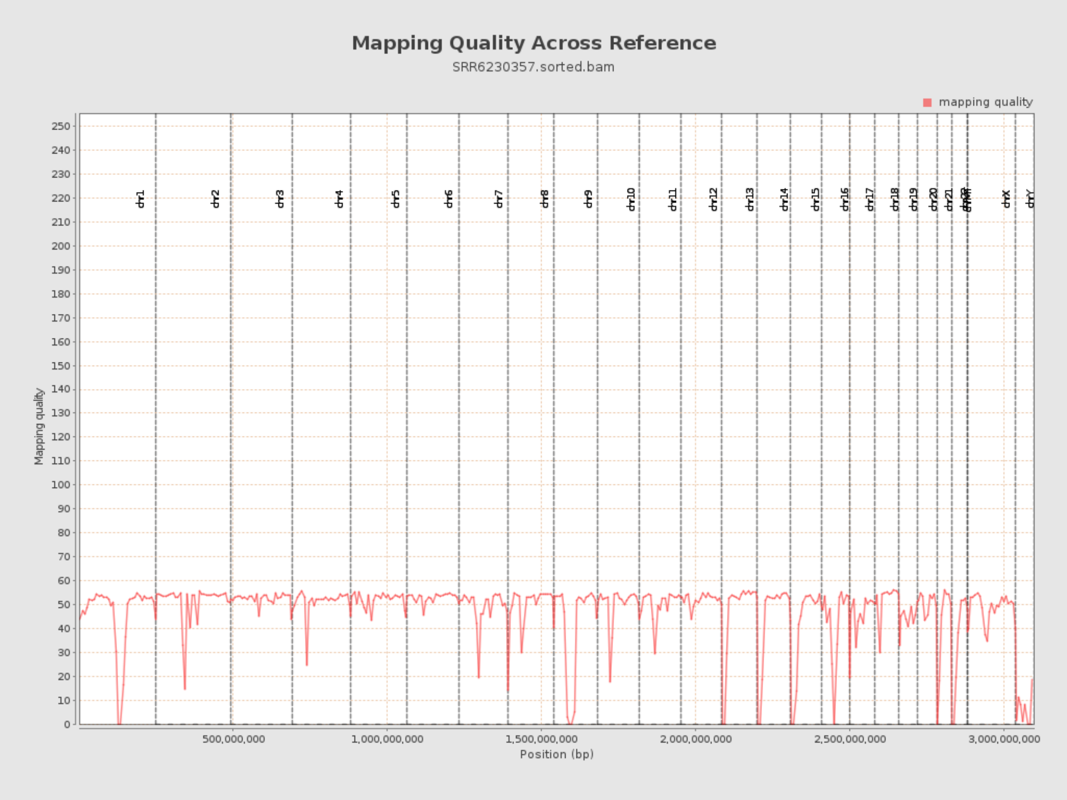
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram