Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:46:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230404.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_SRR6230404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230404.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:46:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	573,728
Mapped reads	505,035 / 88.03%
Unmapped reads	68,693 / 11.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,080 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	14,429 / 2.51%
Duplication rate	2.39%
Clipped reads	218,999 / 38.17%

2.2. ACGT Content

Number/percentage of A's	9,927,390 / 29.29%
Number/percentage of C's	6,003,990 / 17.72%
Number/percentage of T's	11,030,053 / 32.55%
Number/percentage of G's	6,909,817 / 20.39%
Number/percentage of N's	17,826 / 0.05%
GC Percentage	38.11%

2.3. Coverage

Mean	0.011

Standard Deviation	0.1385

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Mismatches and indels

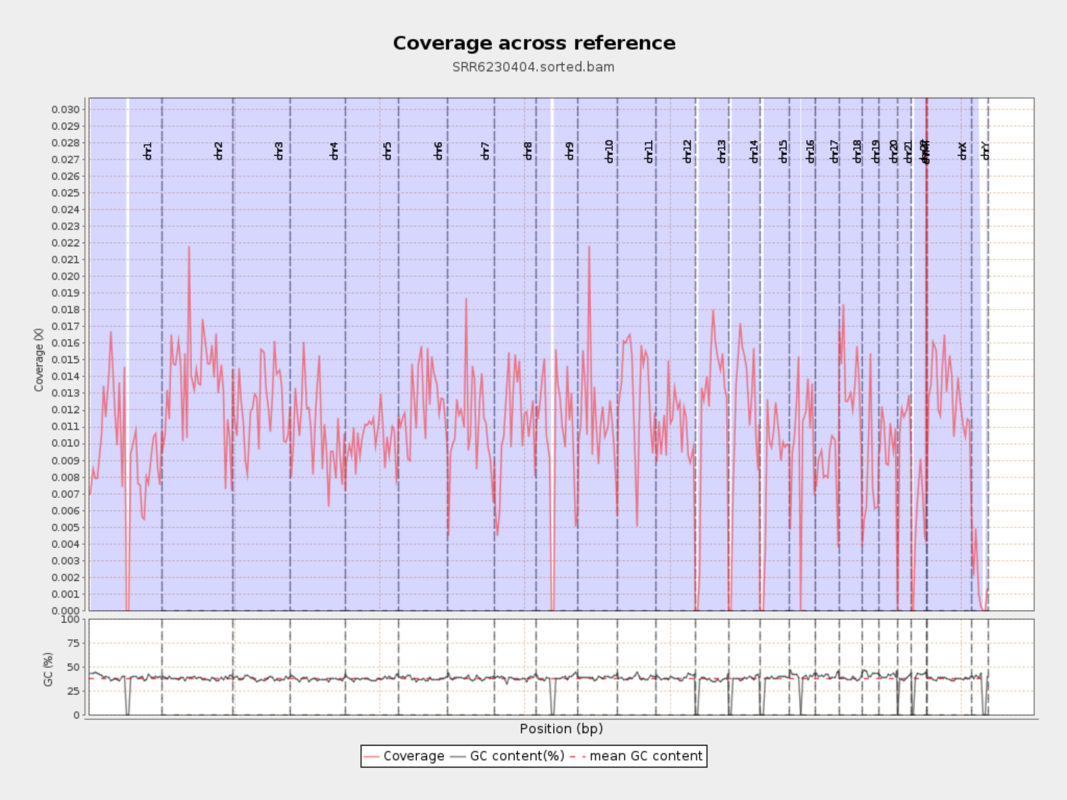
General error rate	0.9%
Mismatches	300,770
Insertions	2,888
Mapped reads with at least one insertion	0.57%
Deletions	10,165
Mapped reads with at least one deletion	1.99%
Homopolymer indels	47.23%

2.6. Chromosome stats

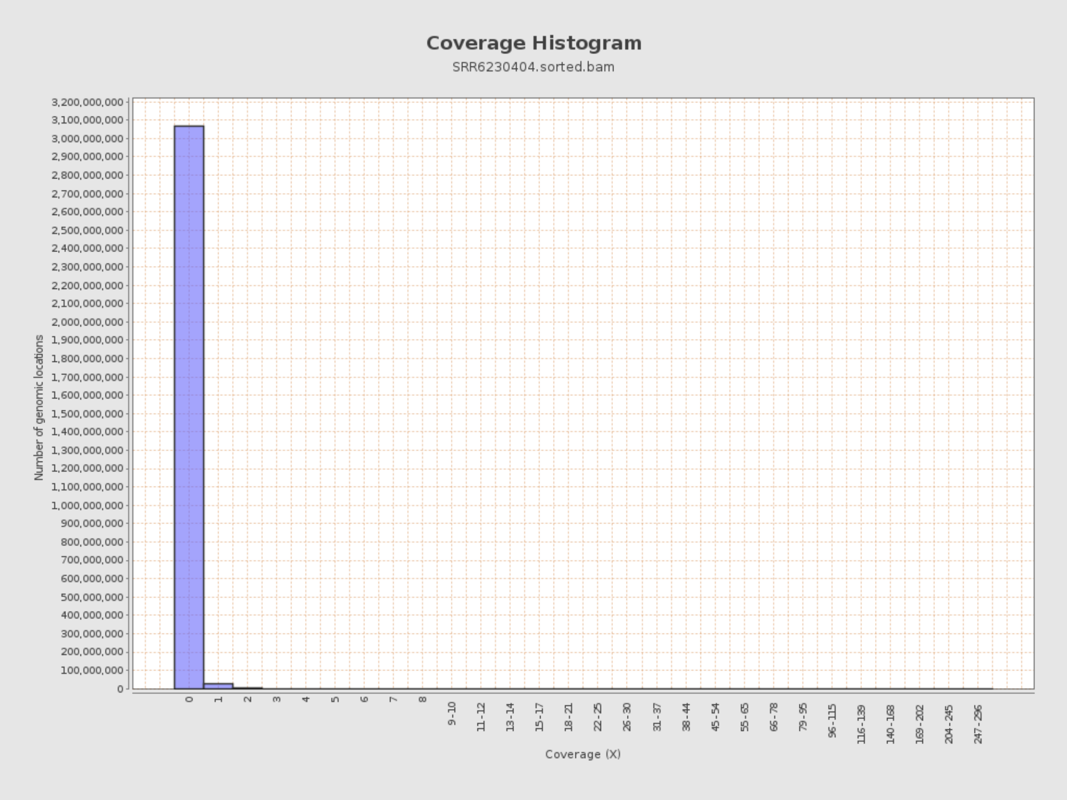
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2314517	0.0093	0.179
chr2	243199373	3334428	0.0137	0.1503
chr3	198022430	2431508	0.0123	0.1189
chr4	191154276	2040788	0.0107	0.113
chr5	180915260	1854796	0.0103	0.1082
chr6	171115067	2133711	0.0125	0.122
chr7	159138663	1782121	0.0112	0.1613

chr8	146364022	1607637	0.011	0.2164
chr9	141213431	1479334	0.0105	0.1352
chr10	135534747	1604404	0.0118	0.1369
chr11	135006516	1767368	0.0131	0.1401
chr12	133851895	1460653	0.0109	0.1127
chr13	115169878	1370083	0.0119	0.1166
chr14	107349540	1225983	0.0114	0.1168
chr15	102531392	871179	0.0085	0.0983
chr16	90354753	925568	0.0102	0.1185
chr17	81195210	682018	0.0084	0.1021
chr18	78077248	1085637	0.0139	0.2279
chr19	59128983	470299	0.008	0.1323
chr20	63025520	631356	0.01	0.1082
chr21	48129895	504557	0.0105	0.1133
chr22	51304566	252524	0.0049	0.0739
chrMT	16571	1254	0.0757	0.2693
chrX	155270560	1985312	0.0128	0.1262
chrY	59373566	88894	0.0015	0.0496

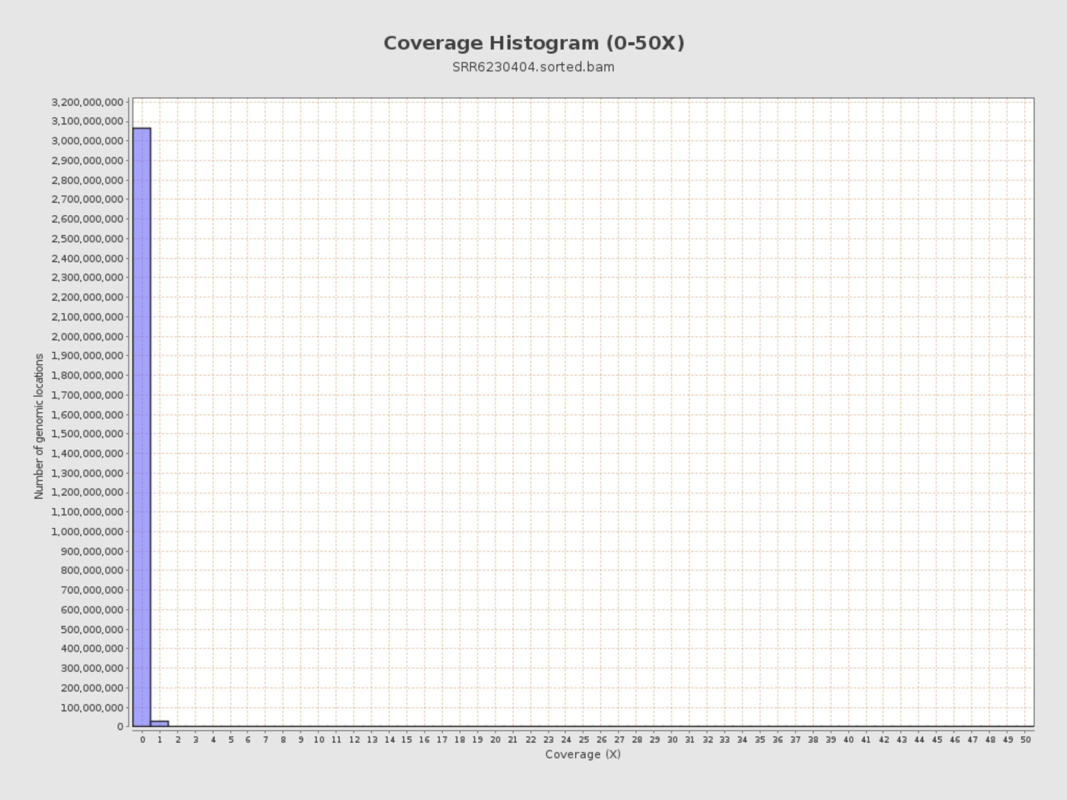
3. Results : Coverage across reference



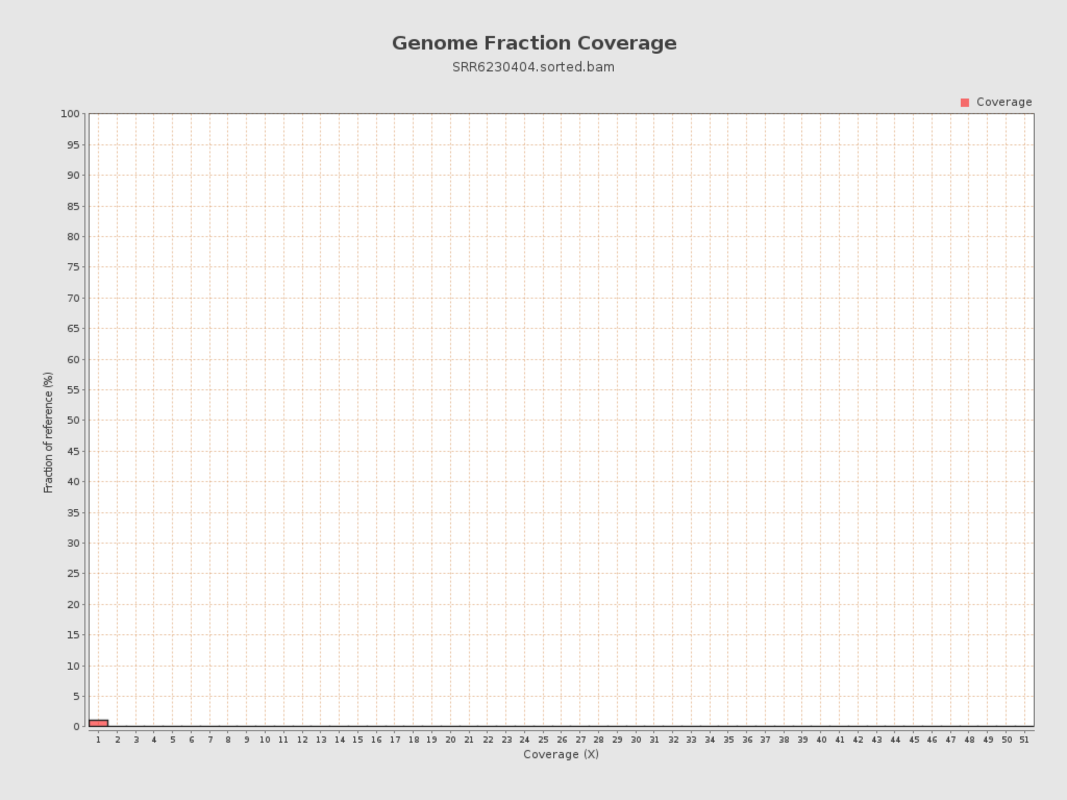
4. Results : Coverage Histogram



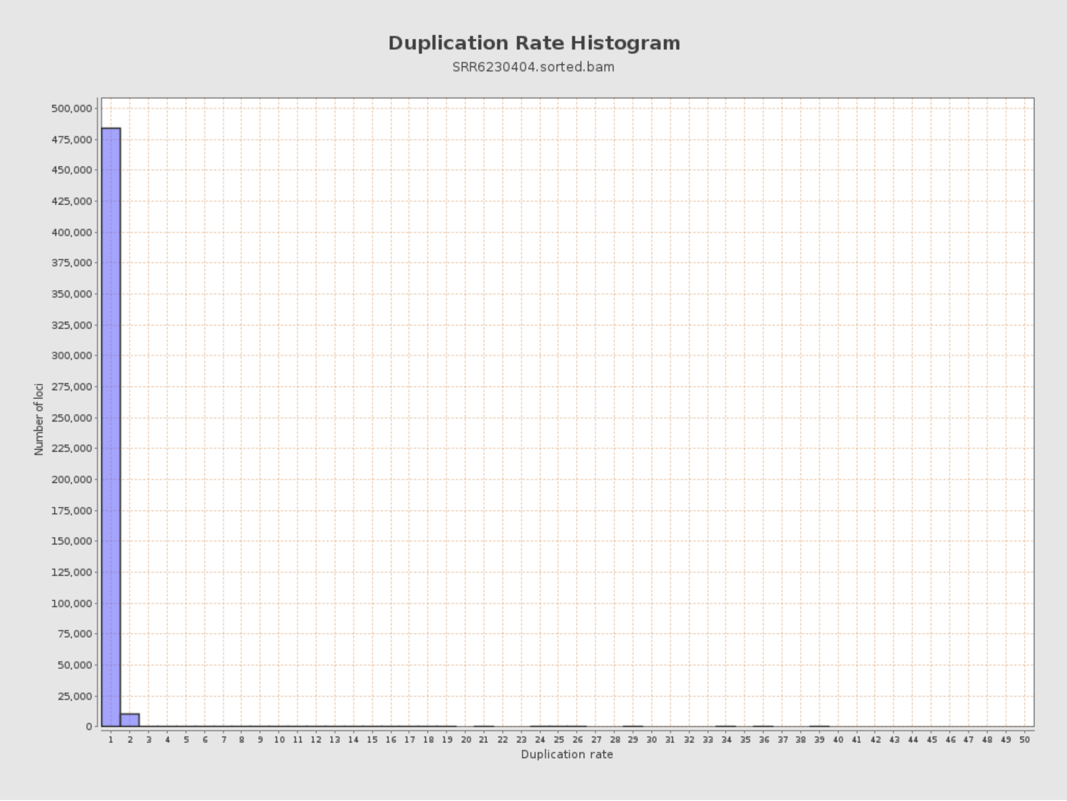
5. Results : Coverage Histogram (0-50X)



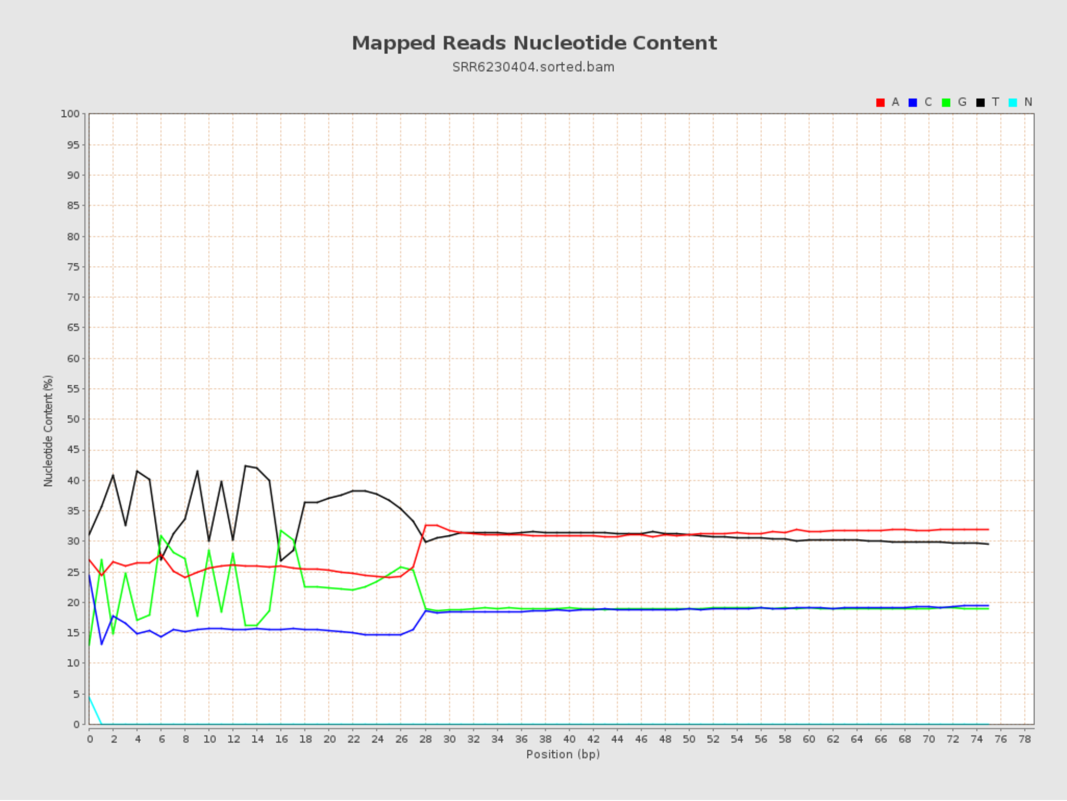
6. Results : Genome Fraction Coverage



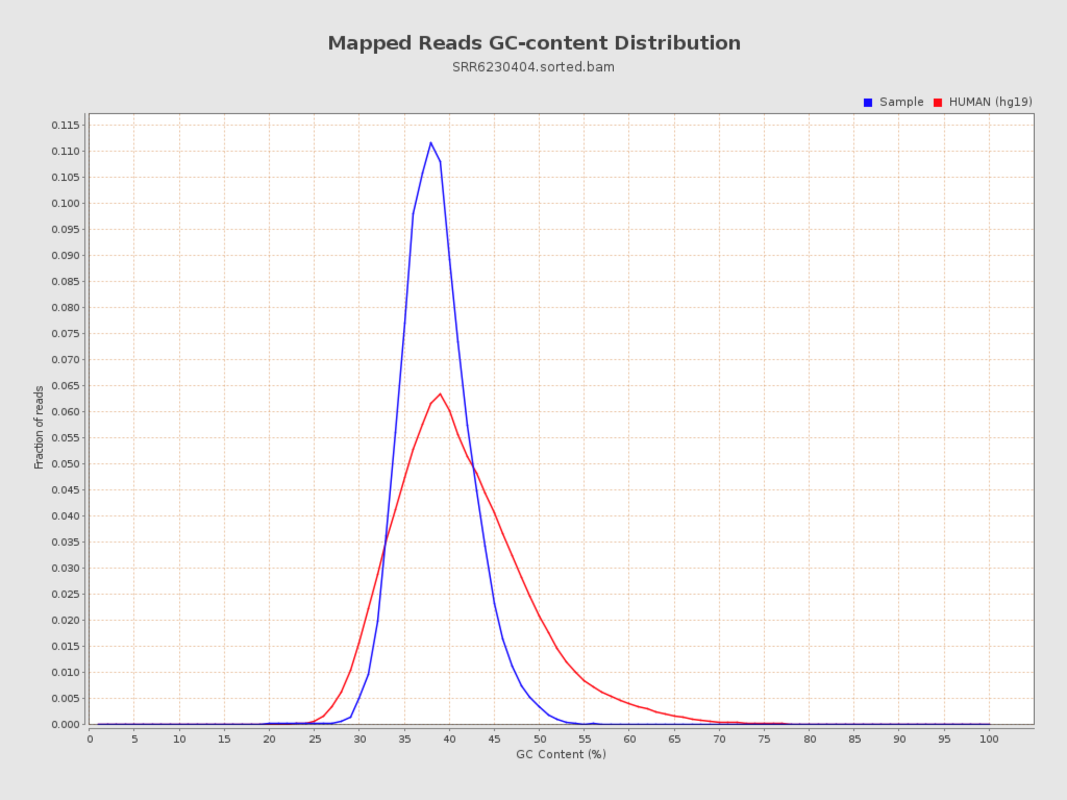
7. Results : Duplication Rate Histogram



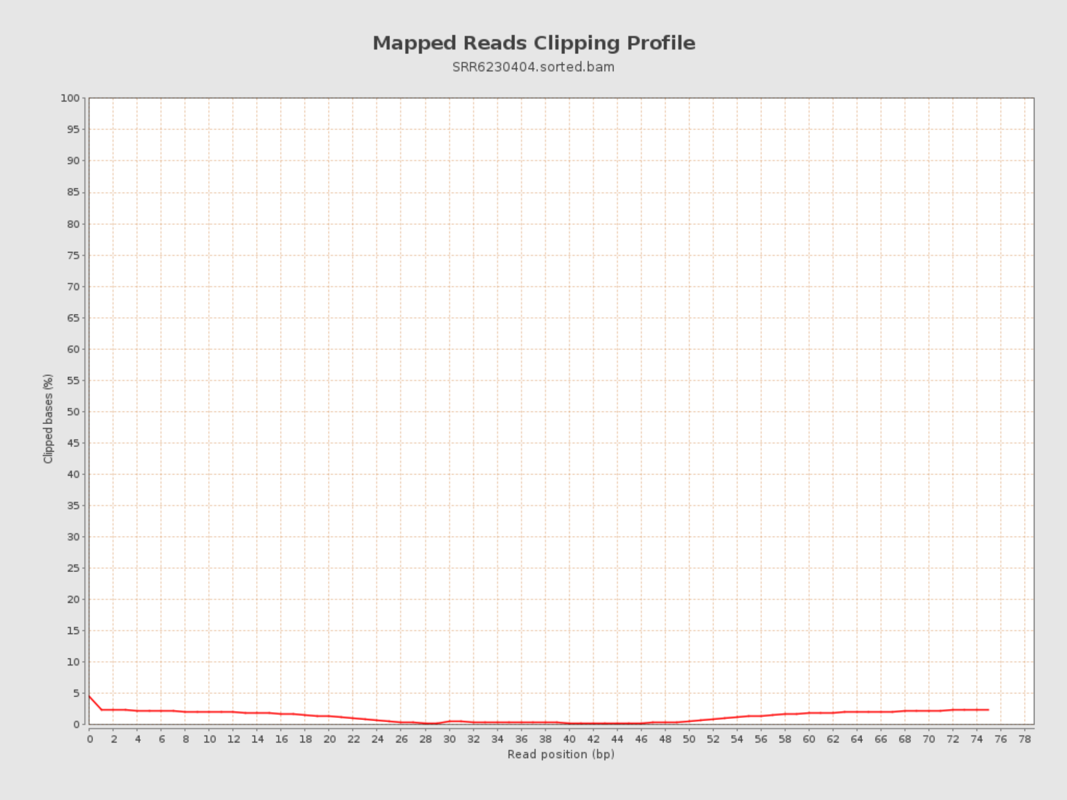
8. Results : Mapped Reads Nucleotide Content



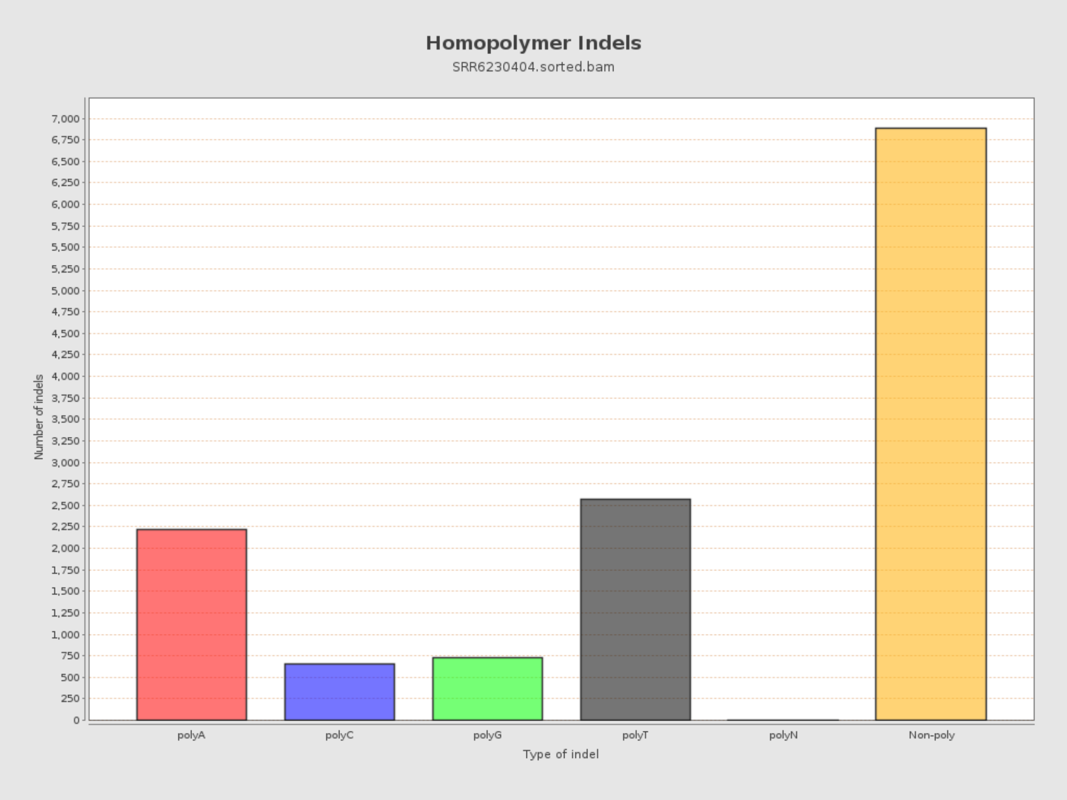
9. Results : Mapped Reads GC-content Distribution



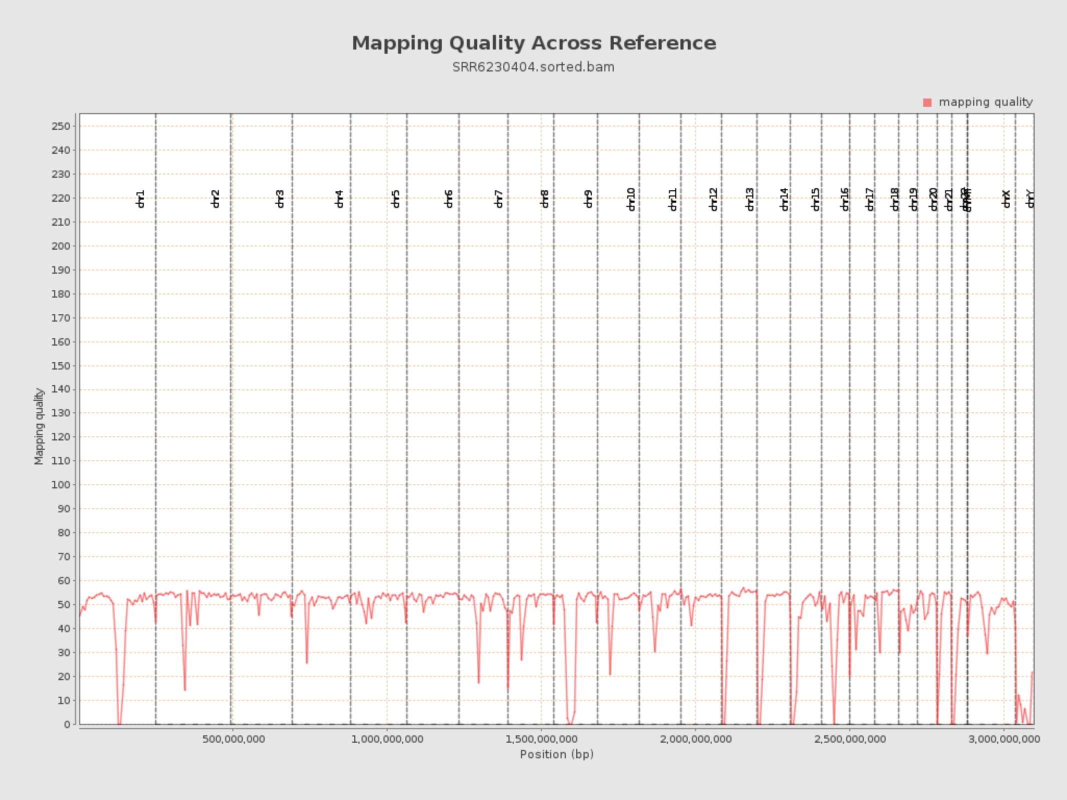
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram