Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:03:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230354.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_SRR6230354 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230354.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:03:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230354.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,013,673
Mapped reads	1,429,195 / 70.97%
Unmapped reads	584,478 / 29.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,094 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	116,153 / 5.77%
Duplication rate	6.89%
Clipped reads	1,028,621 / 51.08%

2.2. ACGT Content

Number/percentage of A's	21,372,165 / 24.9%
Number/percentage of C's	13,576,831 / 15.82%
Number/percentage of T's	29,732,131 / 34.64%
Number/percentage of G's	21,019,630 / 24.49%
Number/percentage of N's	141,313 / 0.16%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2631

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

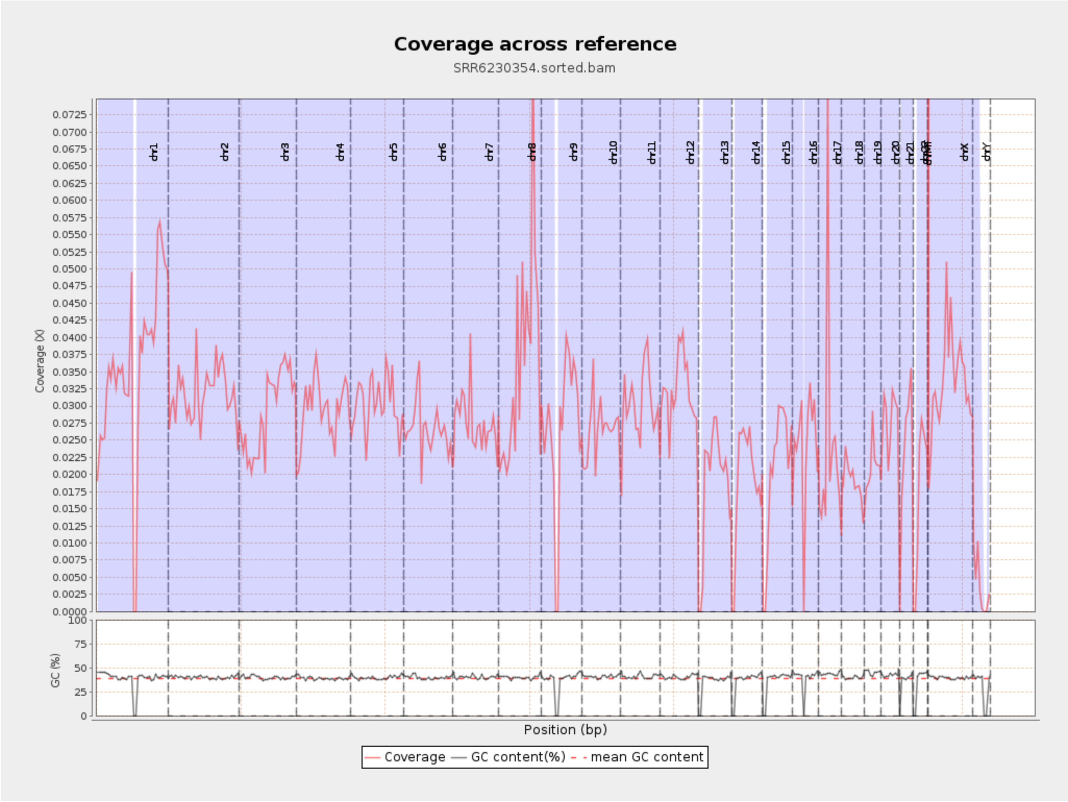
General error rate	0.97%
Mismatches	820,621
Insertions	7,101
Mapped reads with at least one insertion	0.49%
Deletions	29,002
Mapped reads with at least one deletion	2.01%
Homopolymer indels	50.48%

2.6. Chromosome stats

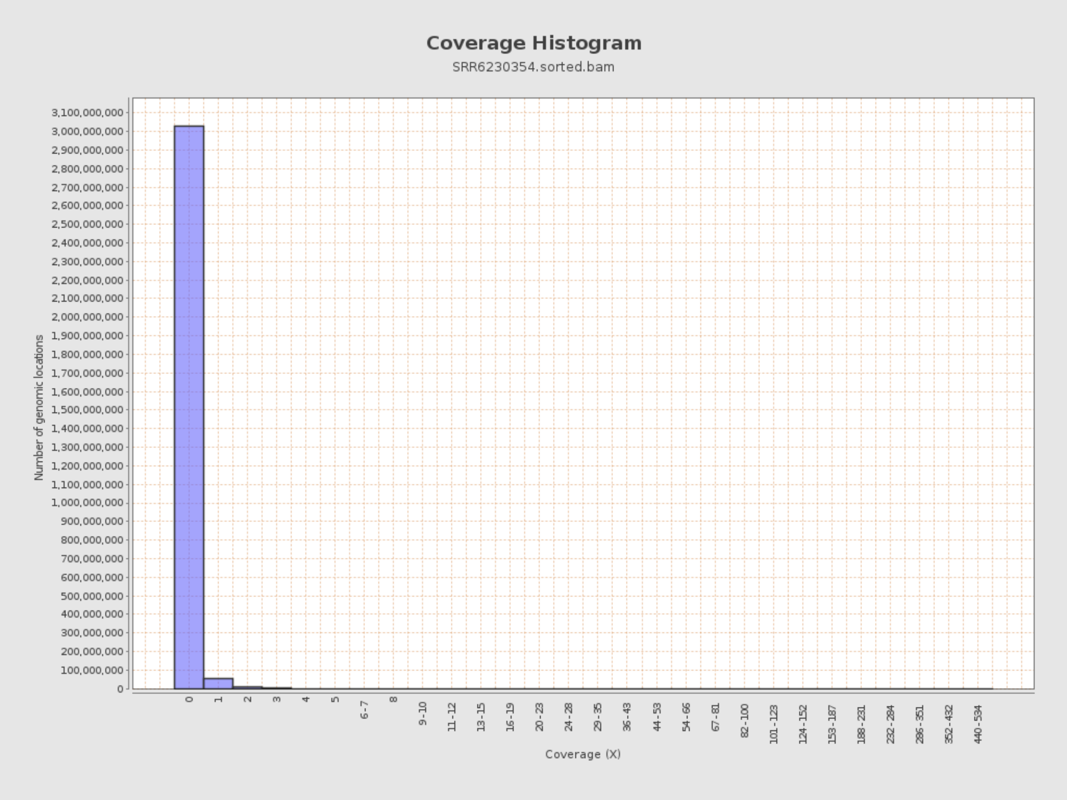
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8858329	0.0355	0.4211
chr2	243199373	7731703	0.0318	0.2899
chr3	198022430	5769548	0.0291	0.2055
chr4	191154276	5631617	0.0295	0.2144
chr5	180915260	5511493	0.0305	0.2112
chr6	171115067	4556846	0.0266	0.2354
chr7	159138663	4372105	0.0275	0.3359

chr8	146364022	5271467	0.036	0.3151
chr9	141213431	3797218	0.0269	0.279
chr10	135534747	3560075	0.0263	0.2396
chr11	135006516	4085277	0.0303	0.2471
chr12	133851895	4303342	0.0322	0.2204
chr13	115169878	2153399	0.0187	0.1636
chr14	107349540	2036663	0.019	0.1849
chr15	102531392	2089346	0.0204	0.1745
chr16	90354753	2156982	0.0239	0.1961
chr17	81195210	1946520	0.024	0.2046
chr18	78077248	1486614	0.019	0.358
chr19	59128983	1248214	0.0211	0.3128
chr20	63025520	1741411	0.0276	0.2056
chr21	48129895	1136933	0.0236	0.1912
chr22	51304566	890402	0.0174	0.155
chrMT	16571	80370	4.85	4.5562
chrX	155270560	5257844	0.0339	0.2475
chrY	59373566	212691	0.0036	0.0858

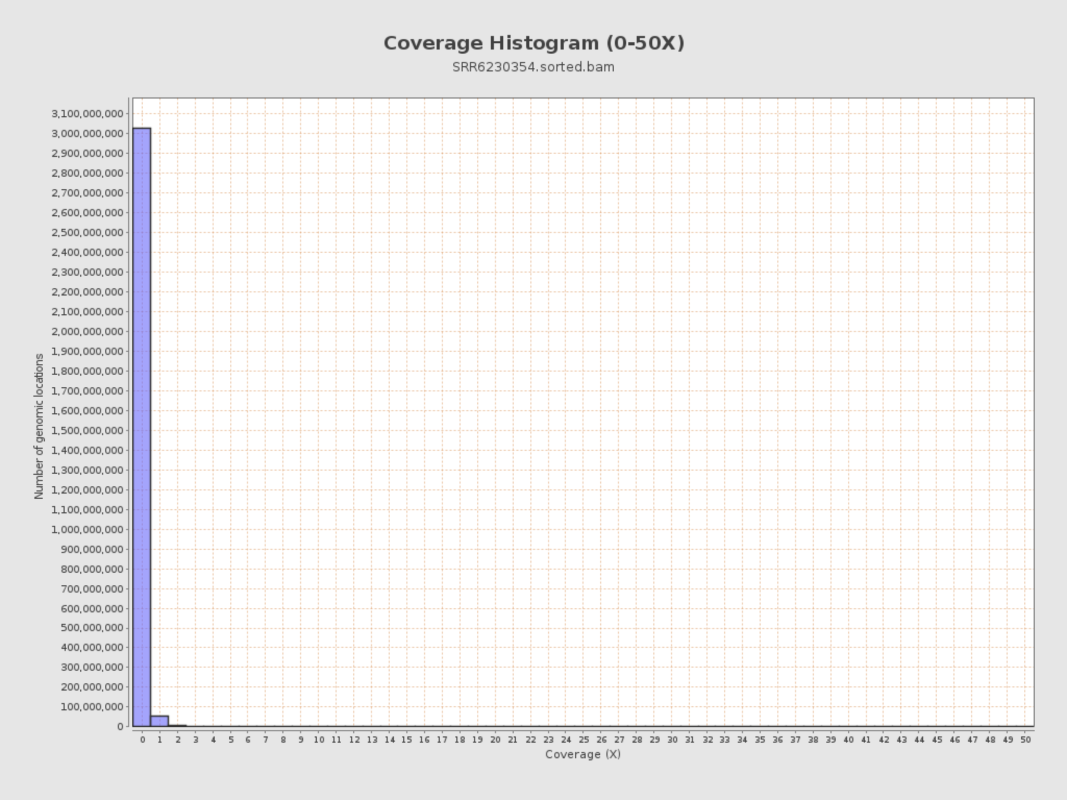
3. Results : Coverage across reference



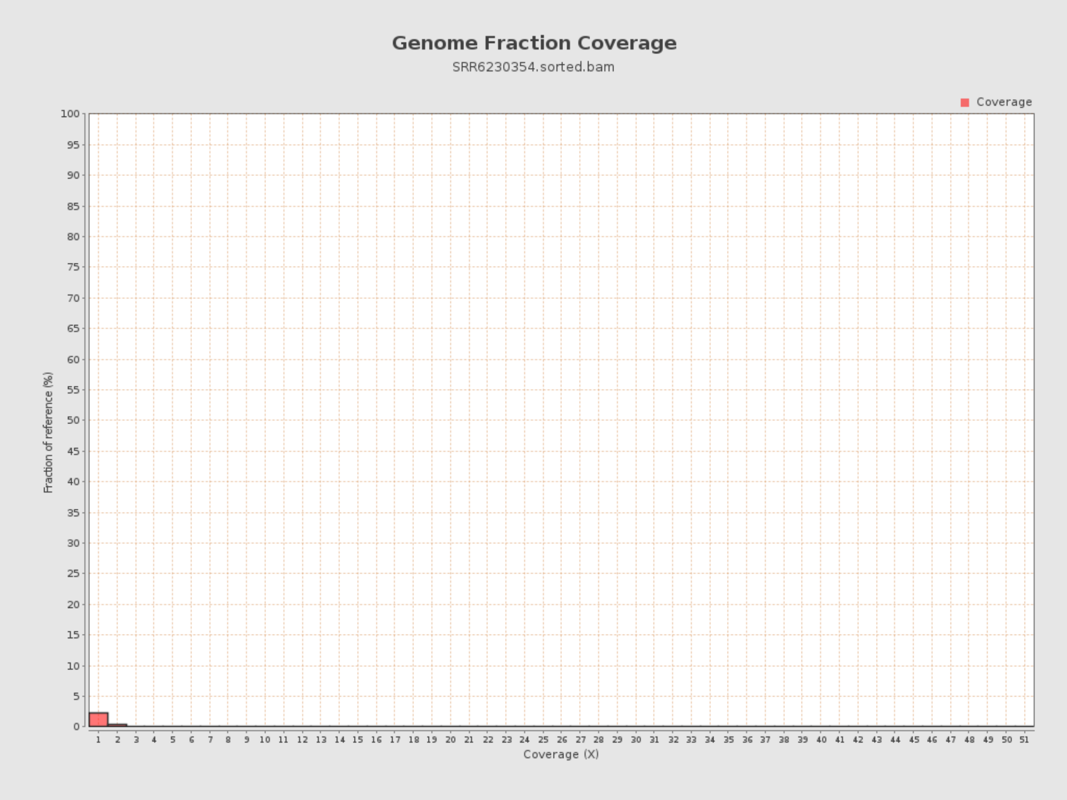
4. Results : Coverage Histogram



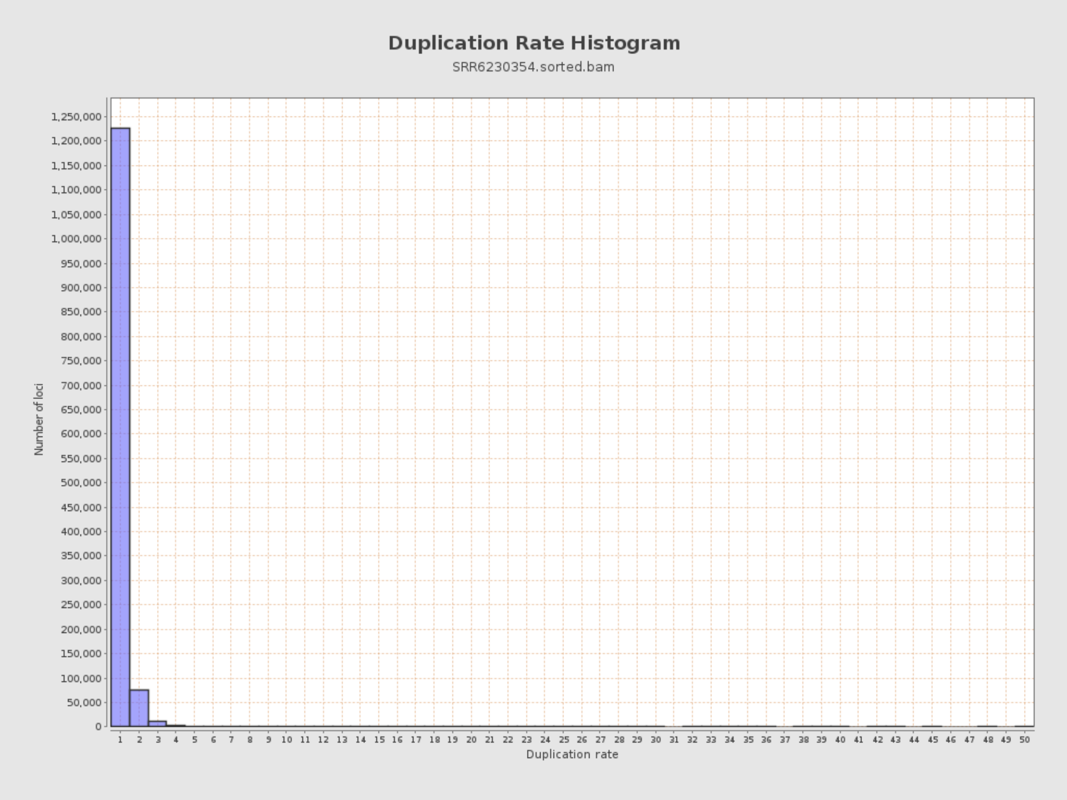
5. Results : Coverage Histogram (0-50X)



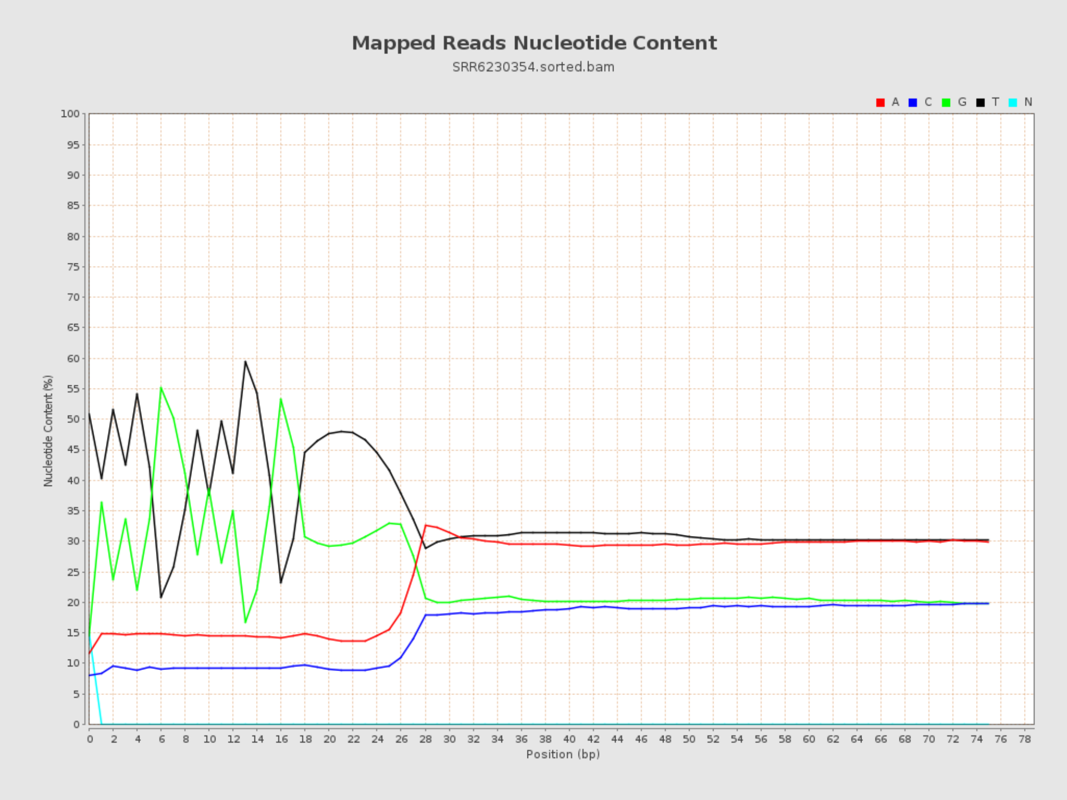
6. Results : Genome Fraction Coverage



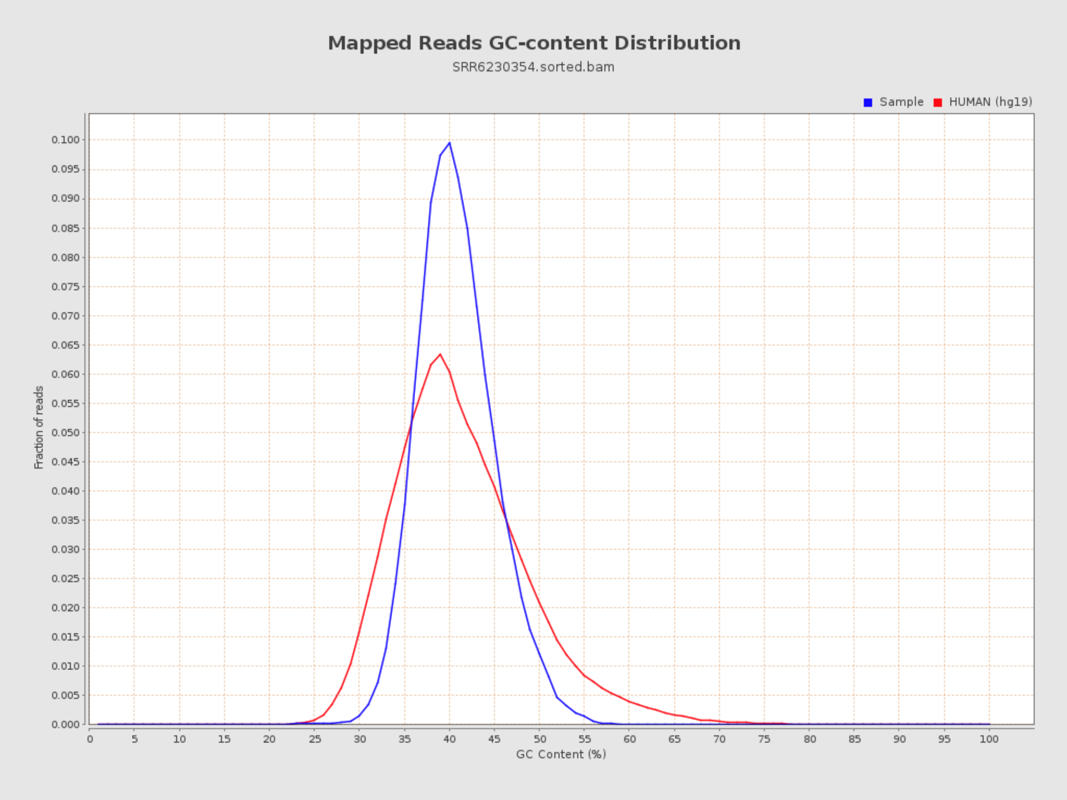
7. Results : Duplication Rate Histogram



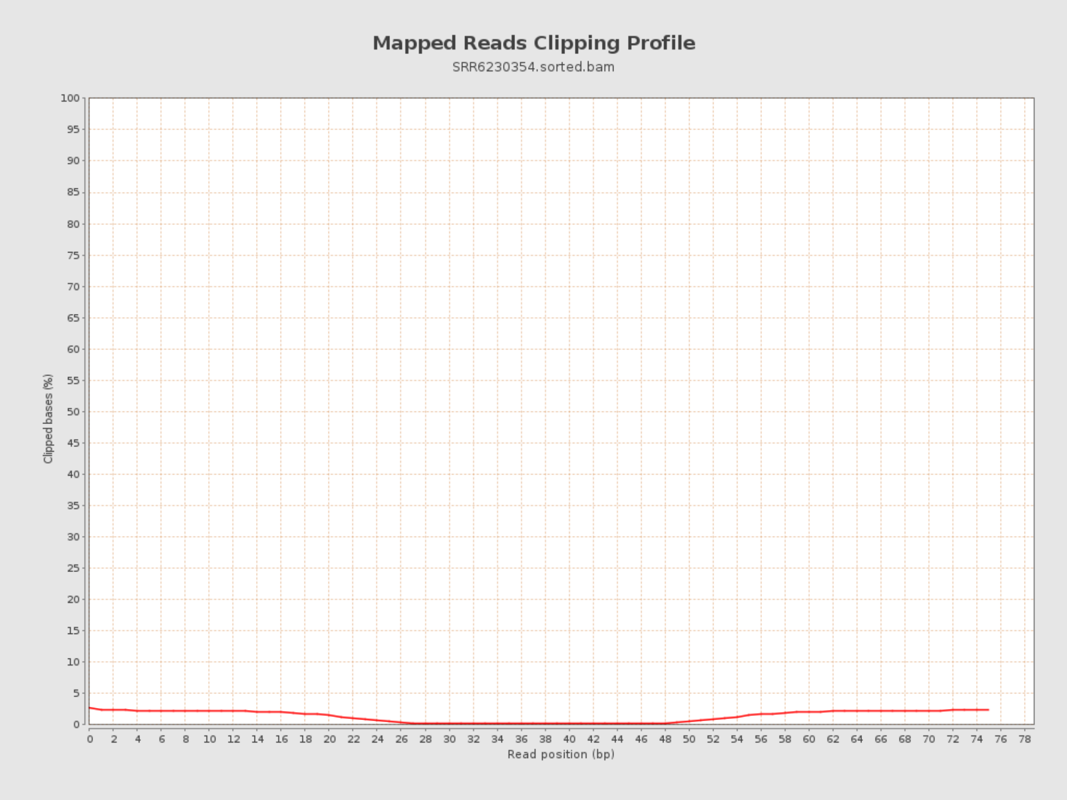
8. Results : Mapped Reads Nucleotide Content



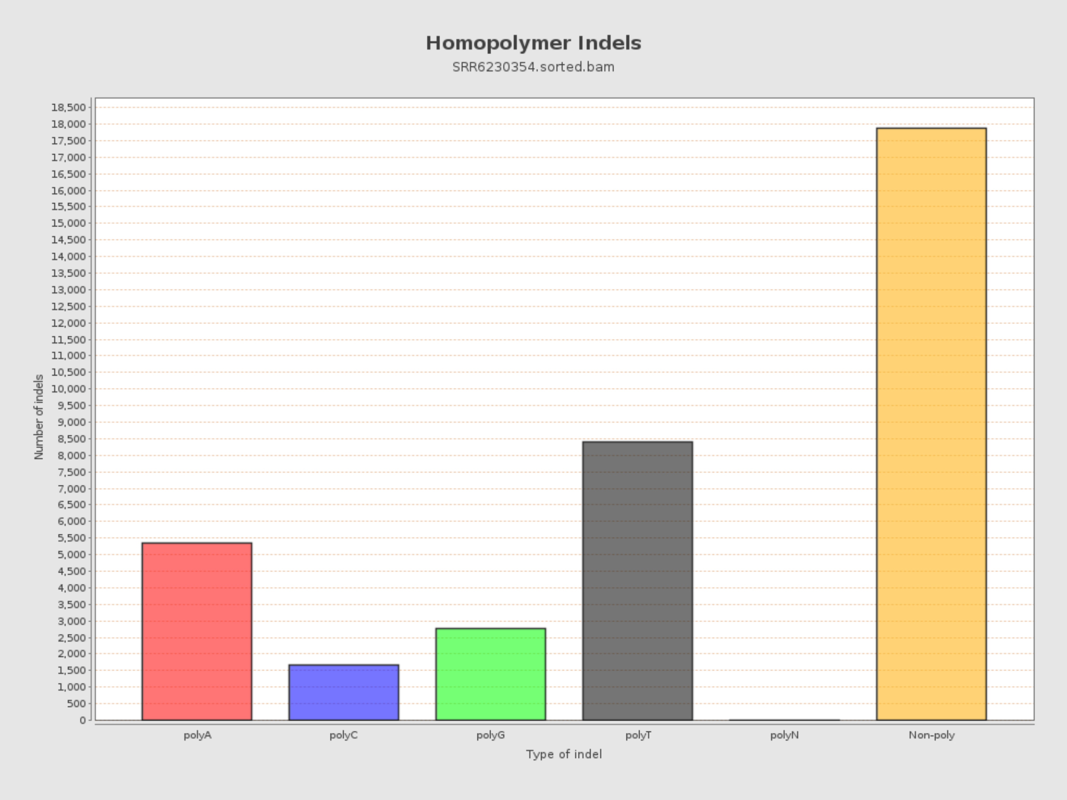
9. Results : Mapped Reads GC-content Distribution



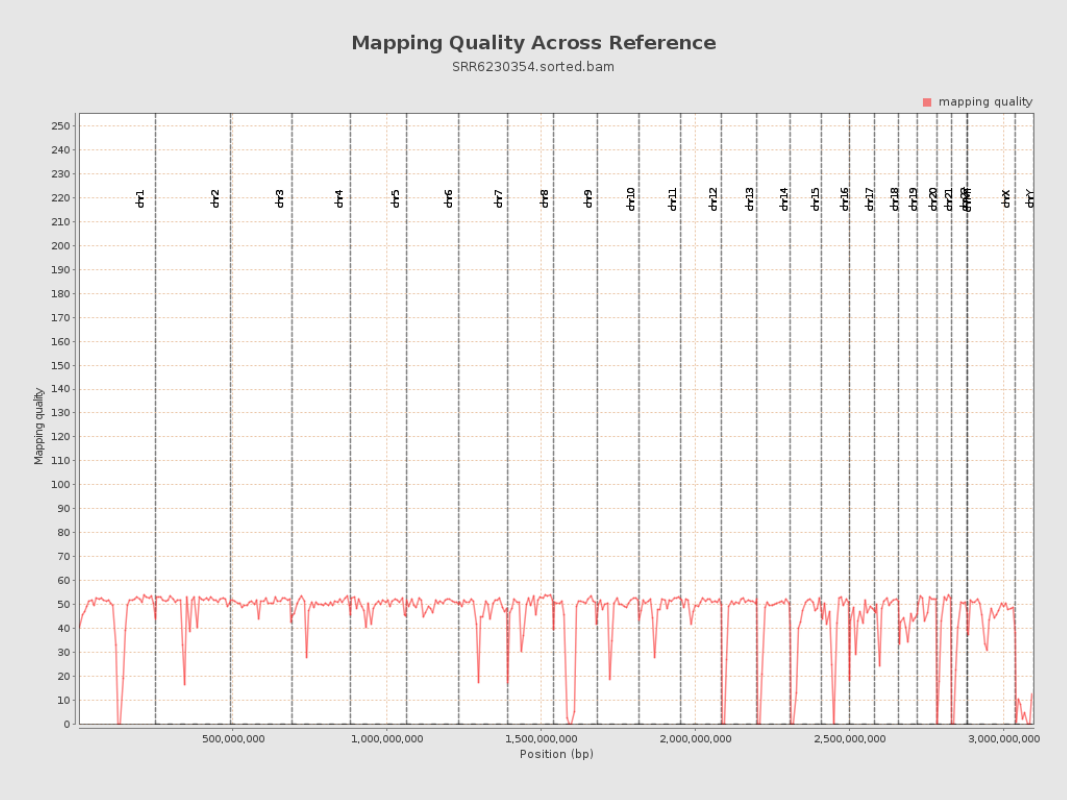
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram