Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230370.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_SRR6230370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230370.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:55:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,538,402
Mapped reads	4,241,262 / 93.45%
Unmapped reads	297,140 / 6.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,534 / 0.78%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	207,812 / 4.58%
Duplication rate	3.33%
Clipped reads	1,126,579 / 24.82%

2.2. ACGT Content

Number/percentage of A's	89,896,087 / 29.61%
Number/percentage of C's	61,954,984 / 20.41%
Number/percentage of T's	88,282,363 / 29.08%
Number/percentage of G's	63,274,145 / 20.84%
Number/percentage of N's	164,427 / 0.05%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0981

Standard Deviation	1.0025

2.4. Mapping Quality

Mean Mapping Quality	47.98

2.5. Mismatches and indels

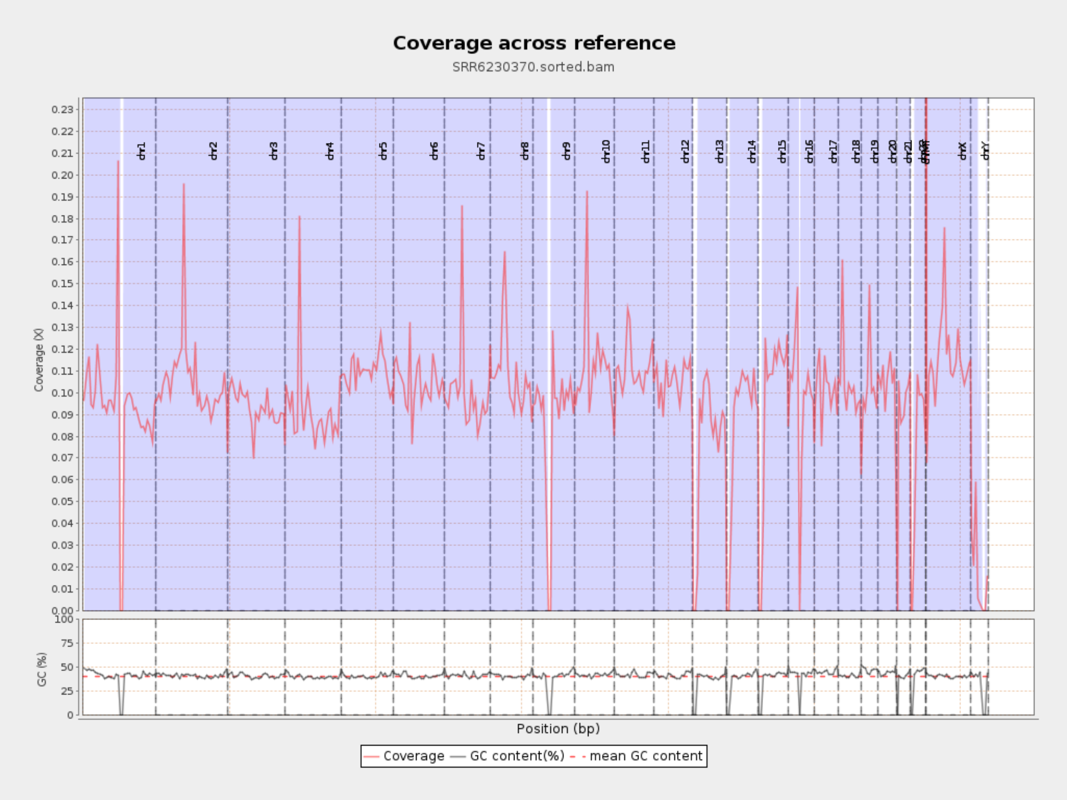
General error rate	0.91%
Mismatches	2,707,718
Insertions	27,175
Mapped reads with at least one insertion	0.64%
Deletions	86,193
Mapped reads with at least one deletion	2.01%
Homopolymer indels	46.39%

2.6. Chromosome stats

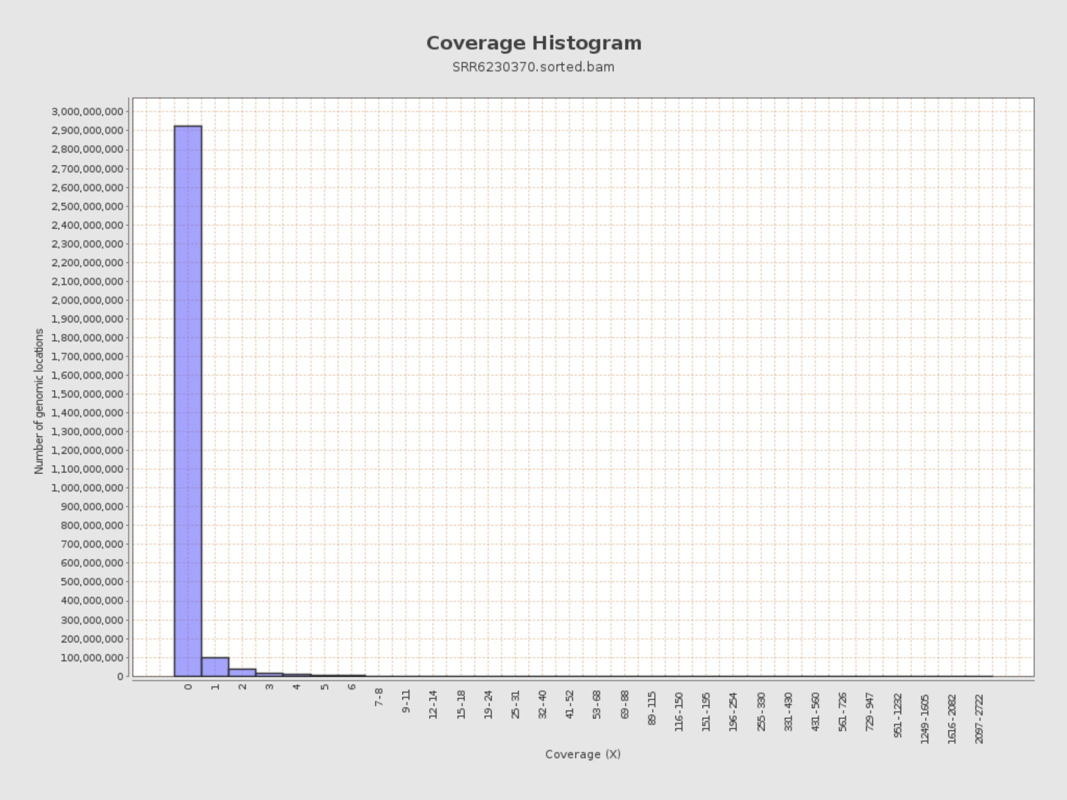
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23178537	0.093	2.1946
chr2	243199373	25790350	0.106	0.9591
chr3	198022430	18391333	0.0929	0.4755
chr4	191154276	17702511	0.0926	0.6022
chr5	180915260	19915886	0.1101	0.5255
chr6	171115067	17895951	0.1046	0.618
chr7	159138663	15944465	0.1002	1.1812

chr8	146364022	15851122	0.1083	1.1937
chr9	141213431	12247786	0.0867	0.8624
chr10	135534747	15208493	0.1122	0.9626
chr11	135006516	14977418	0.1109	0.8999
chr12	133851895	14145349	0.1057	0.5291
chr13	115169878	8734715	0.0758	0.4262
chr14	107349540	9192839	0.0856	0.524
chr15	102531392	9630871	0.0939	0.4773
chr16	90354753	8633986	0.0956	0.607
chr17	81195210	8291884	0.1021	0.6244
chr18	78077248	8211031	0.1052	1.8858
chr19	59128983	6117349	0.1035	1.3129
chr20	63025520	6630651	0.1052	0.5614
chr21	48129895	4292953	0.0892	0.5944
chr22	51304566	3538916	0.069	0.4043
chrMT	16571	280660	16.9368	12.7594
chrX	155270560	17923521	0.1154	0.6417
chrY	59373566	989747	0.0167	0.4862

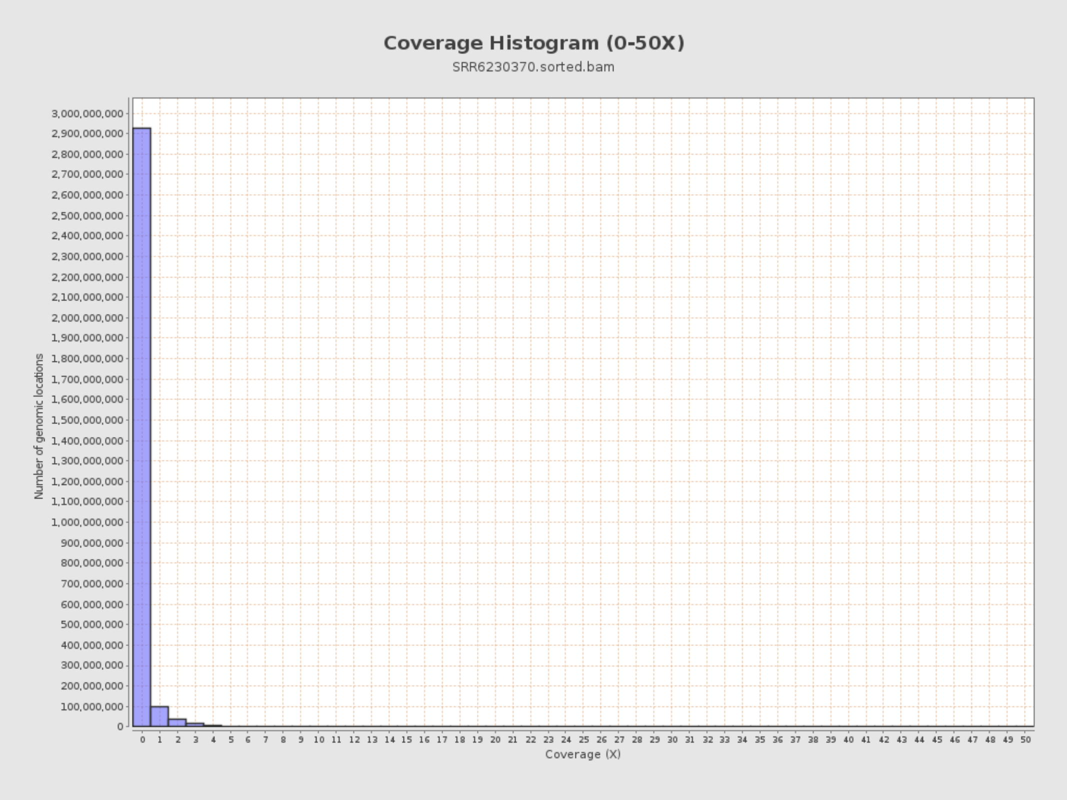
3. Results : Coverage across reference



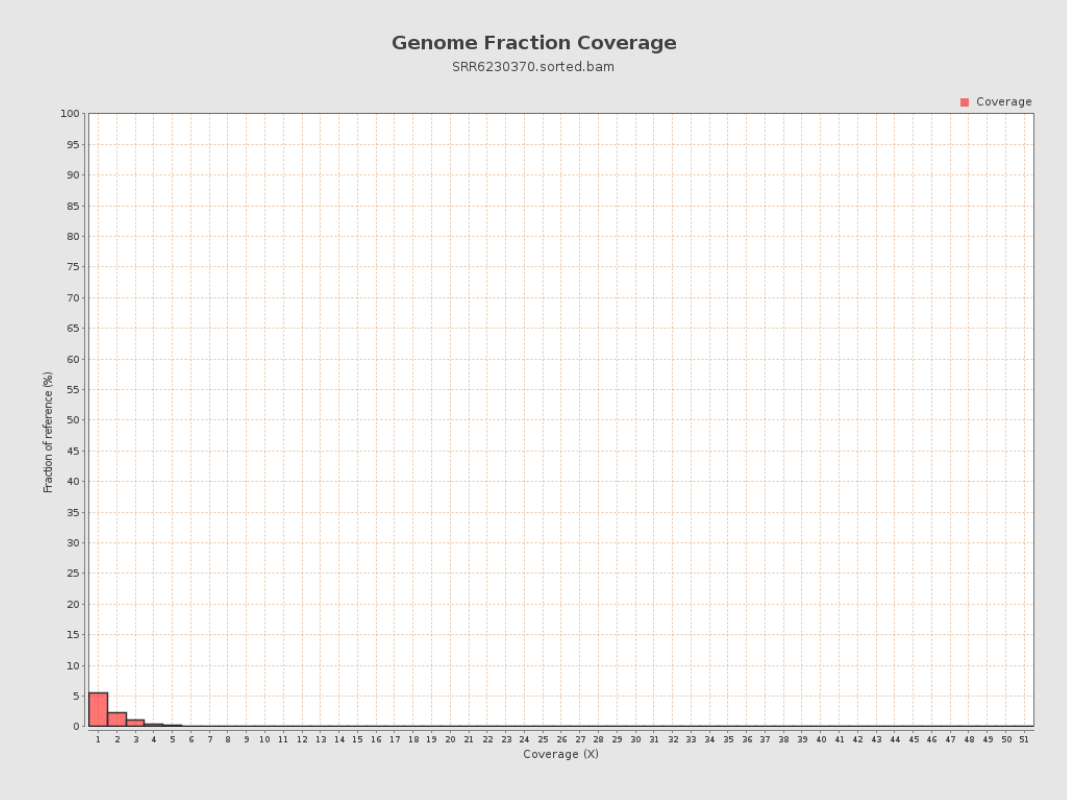
4. Results : Coverage Histogram



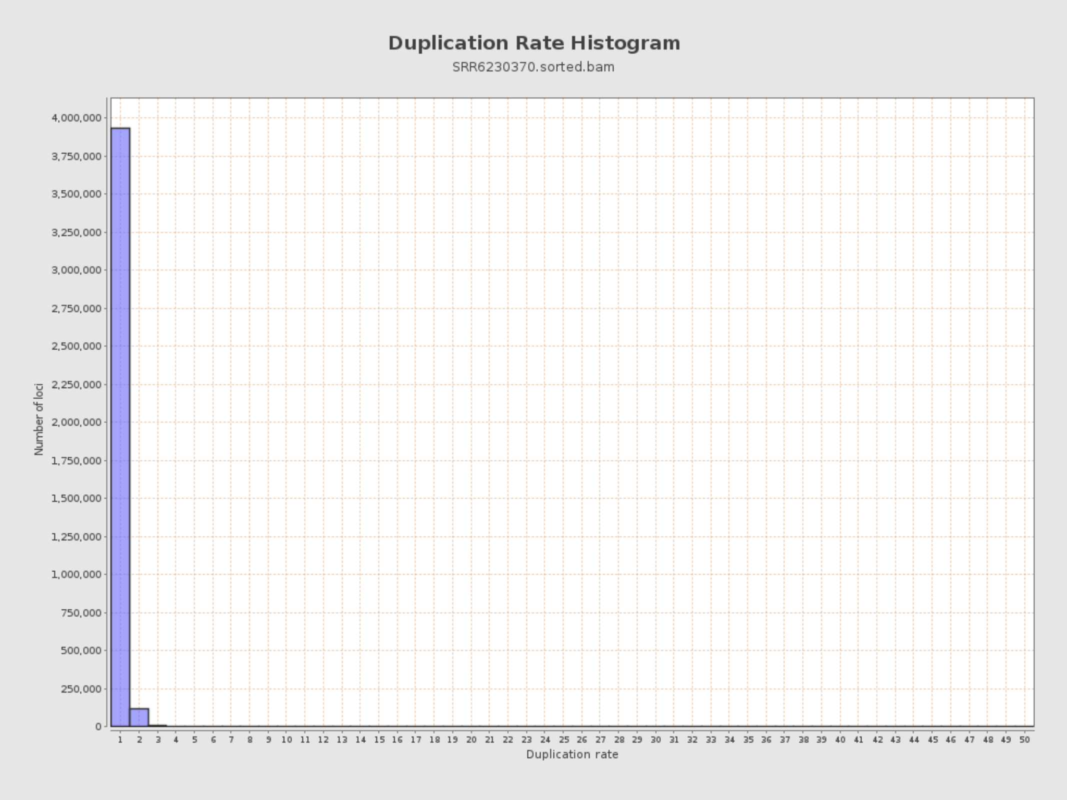
5. Results : Coverage Histogram (0-50X)



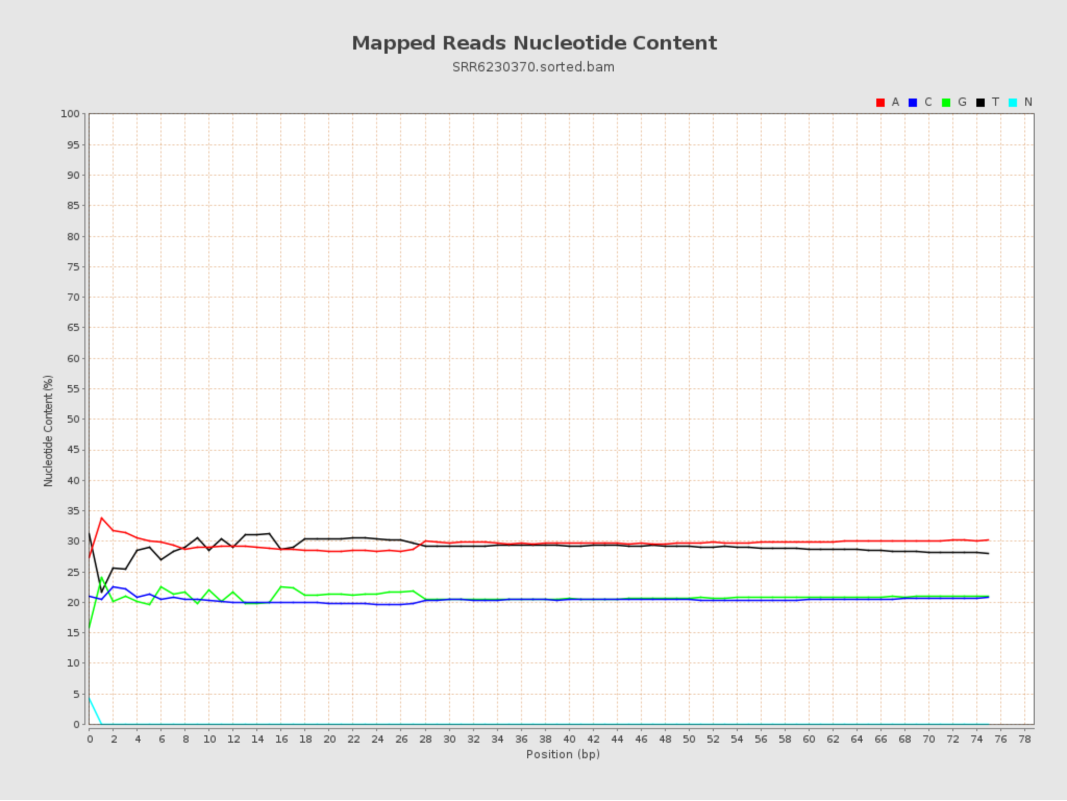
6. Results : Genome Fraction Coverage



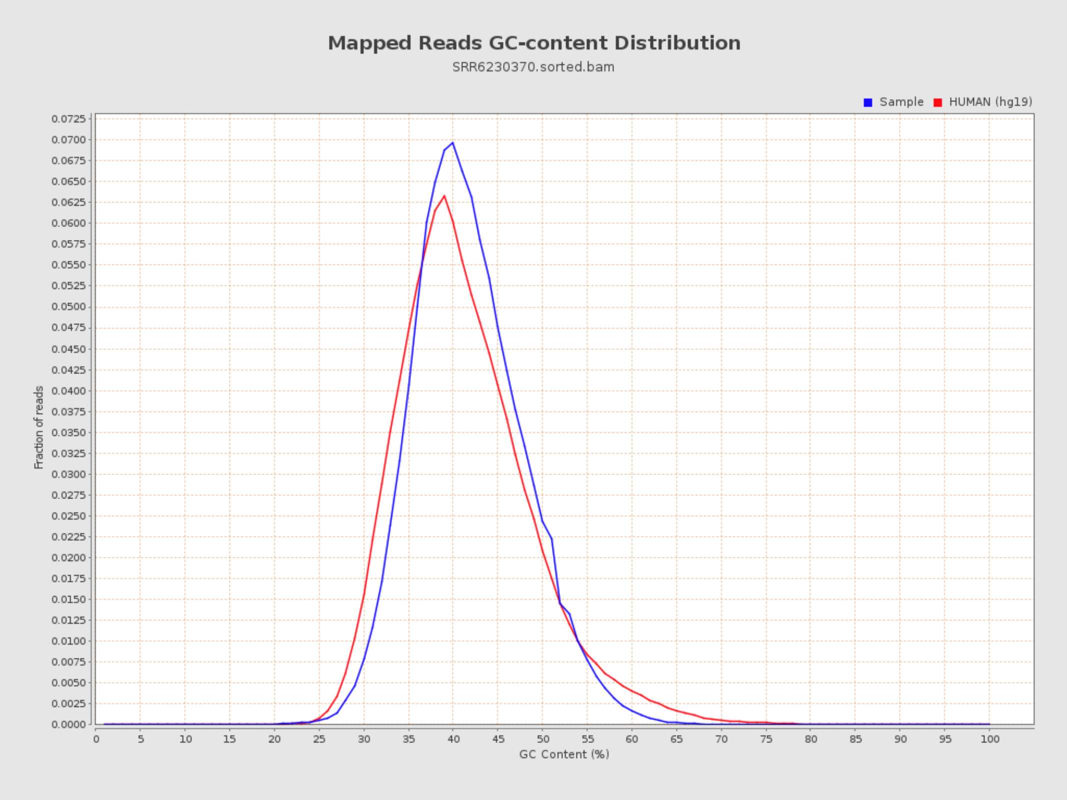
7. Results : Duplication Rate Histogram



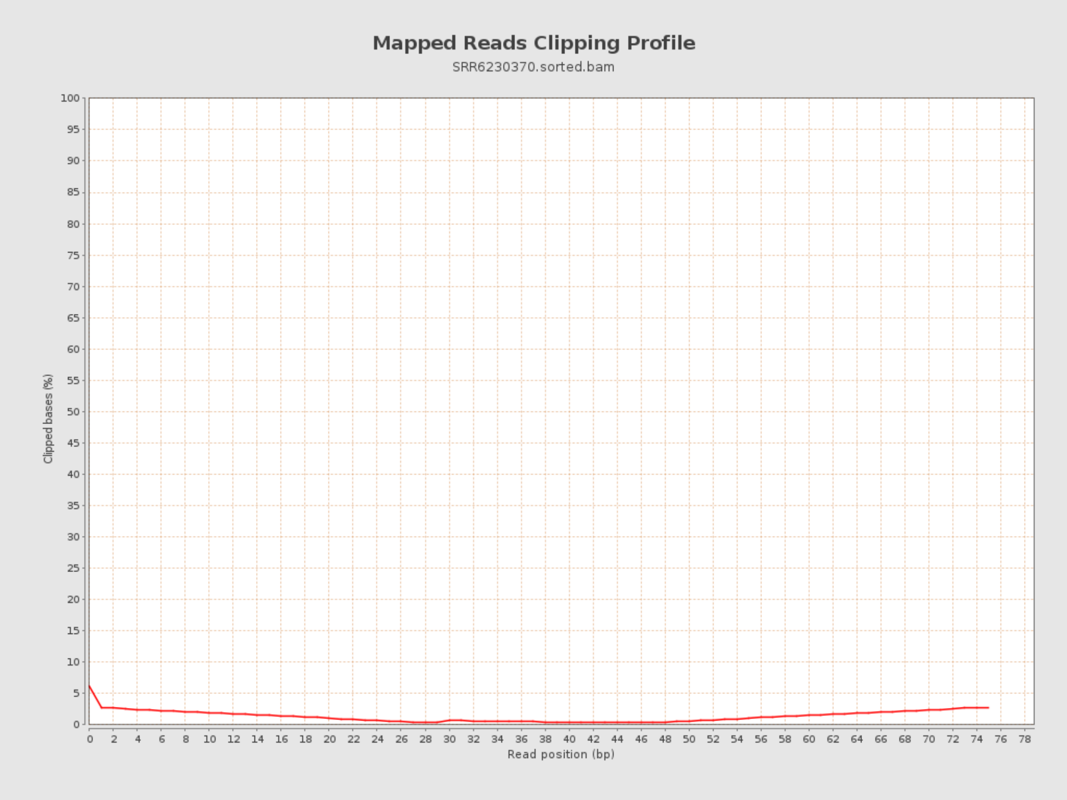
8. Results : Mapped Reads Nucleotide Content



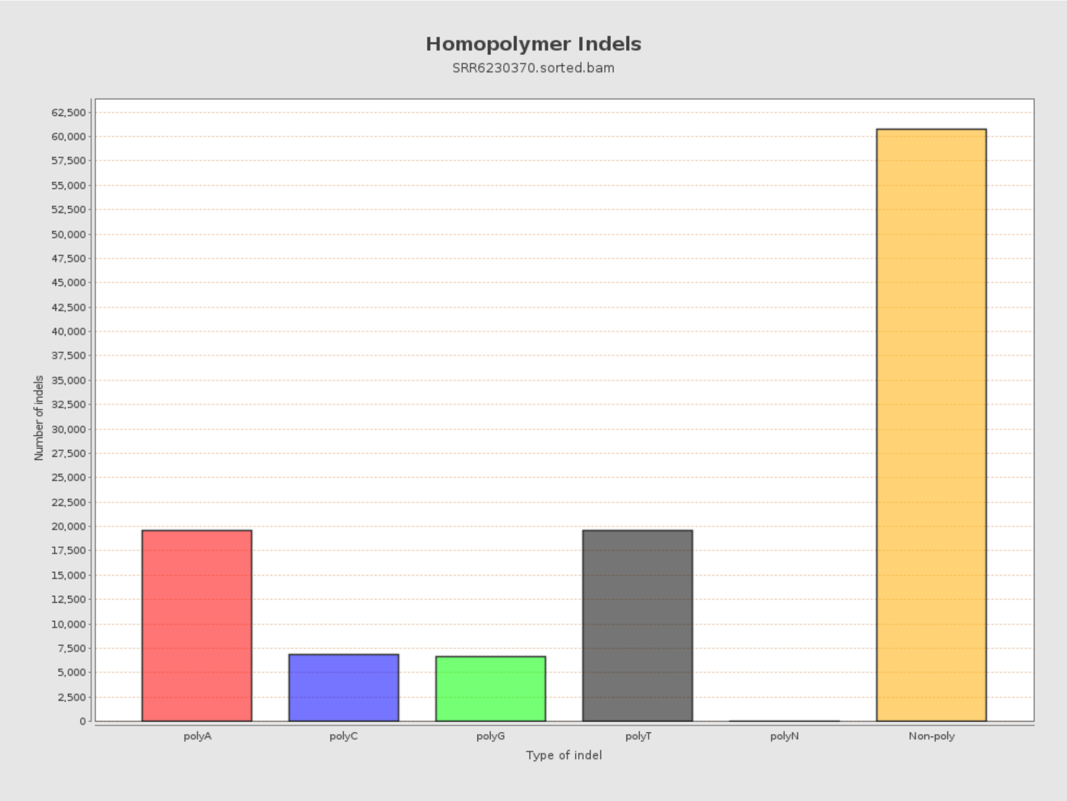
9. Results : Mapped Reads GC-content Distribution



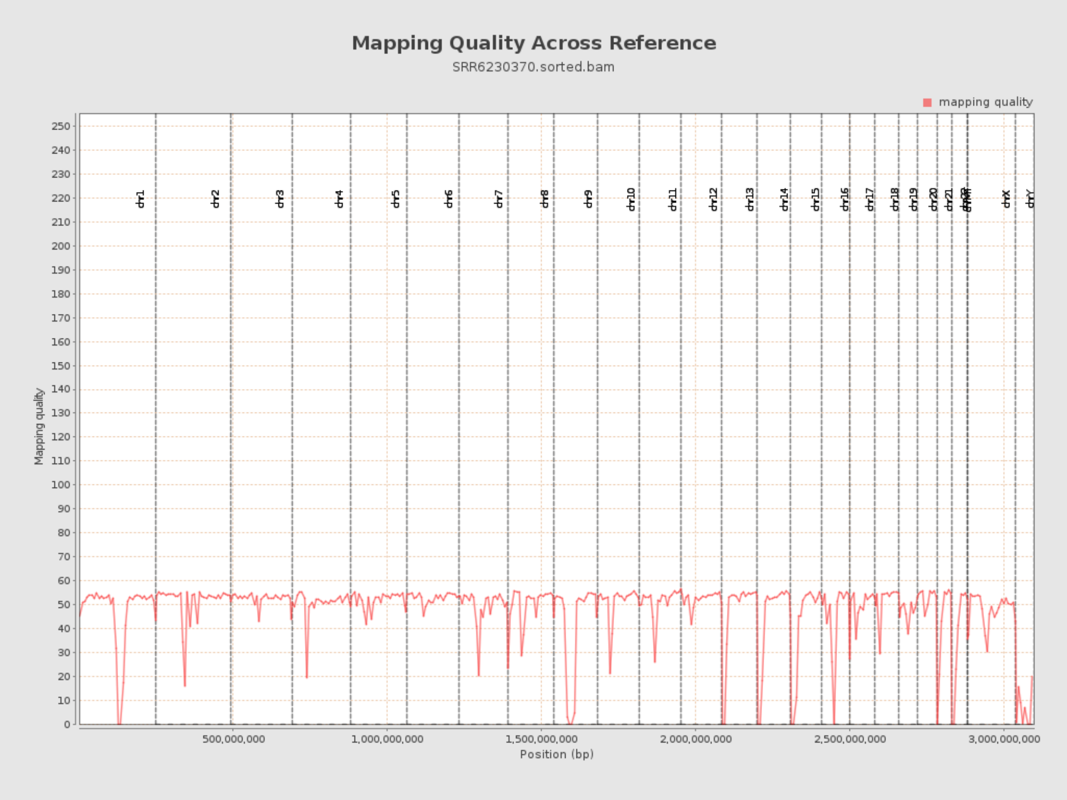
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram