Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:54:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231879.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_SRR6231879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231879.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:54:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,153,744
Mapped reads	988,185 / 85.65%
Unmapped reads	165,559 / 14.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,822 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	30,055 / 2.6%
Duplication rate	2.44%
Clipped reads	441,161 / 38.24%

2.2. ACGT Content

Number/percentage of A's	18,582,388 / 28.36%
Number/percentage of C's	11,503,410 / 17.55%
Number/percentage of T's	21,150,060 / 32.27%
Number/percentage of G's	14,291,947 / 21.81%
Number/percentage of N's	3,282 / 0.01%
GC Percentage	39.36%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2262

2.4. Mapping Quality

Mean Mapping Quality	46.46

2.5. Mismatches and indels

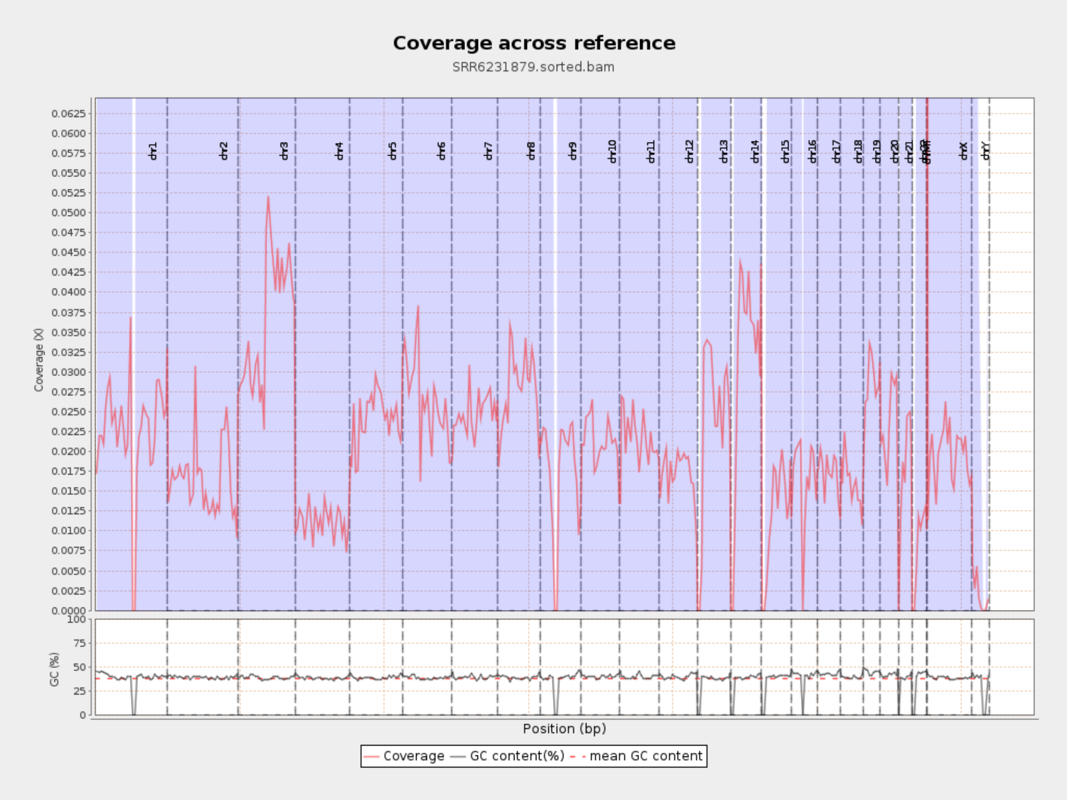
General error rate	0.75%
Mismatches	481,849
Insertions	4,722
Mapped reads with at least one insertion	0.48%
Deletions	19,925
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.8%

2.6. Chromosome stats

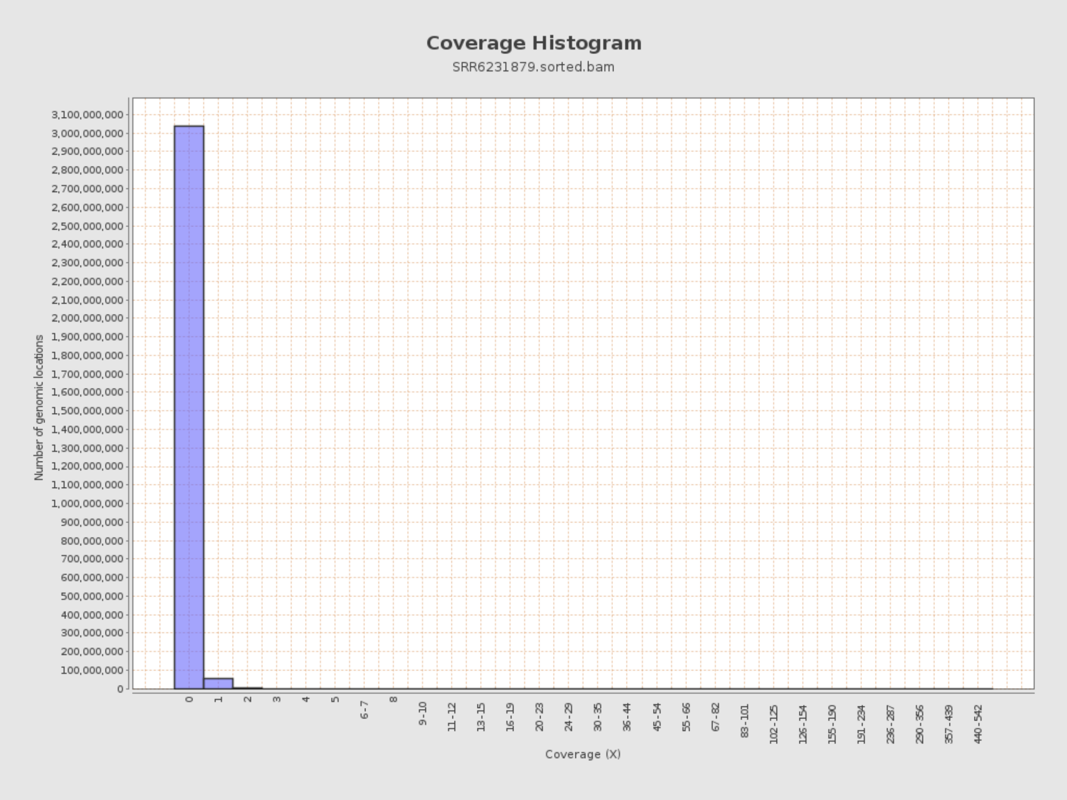
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5578527	0.0224	0.439
chr2	243199373	4020374	0.0165	0.2208
chr3	198022430	7264871	0.0367	0.2046
chr4	191154276	2124645	0.0111	0.1155
chr5	180915260	4372513	0.0242	0.1673
chr6	171115067	4561580	0.0267	0.2021
chr7	159138663	3933086	0.0247	0.2269

chr8	146364022	4095443	0.028	0.3741
chr9	141213431	2452216	0.0174	0.1727
chr10	135534747	2904871	0.0214	0.1871
chr11	135006516	2952555	0.0219	0.2114
chr12	133851895	2303763	0.0172	0.1415
chr13	115169878	2746011	0.0238	0.1648
chr14	107349540	3313547	0.0309	0.1926
chr15	102531392	1227813	0.012	0.12
chr16	90354753	1442578	0.016	0.1432
chr17	81195210	1405676	0.0173	0.149
chr18	78077248	1253346	0.0161	0.2636
chr19	59128983	1696902	0.0287	0.264
chr20	63025520	1464582	0.0232	0.1668
chr21	48129895	847385	0.0176	0.1436
chr22	51304566	422191	0.0082	0.0953
chrMT	16571	7419	0.4477	0.7528
chrX	155270560	3052927	0.0197	0.1589
chrY	59373566	120722	0.002	0.0522

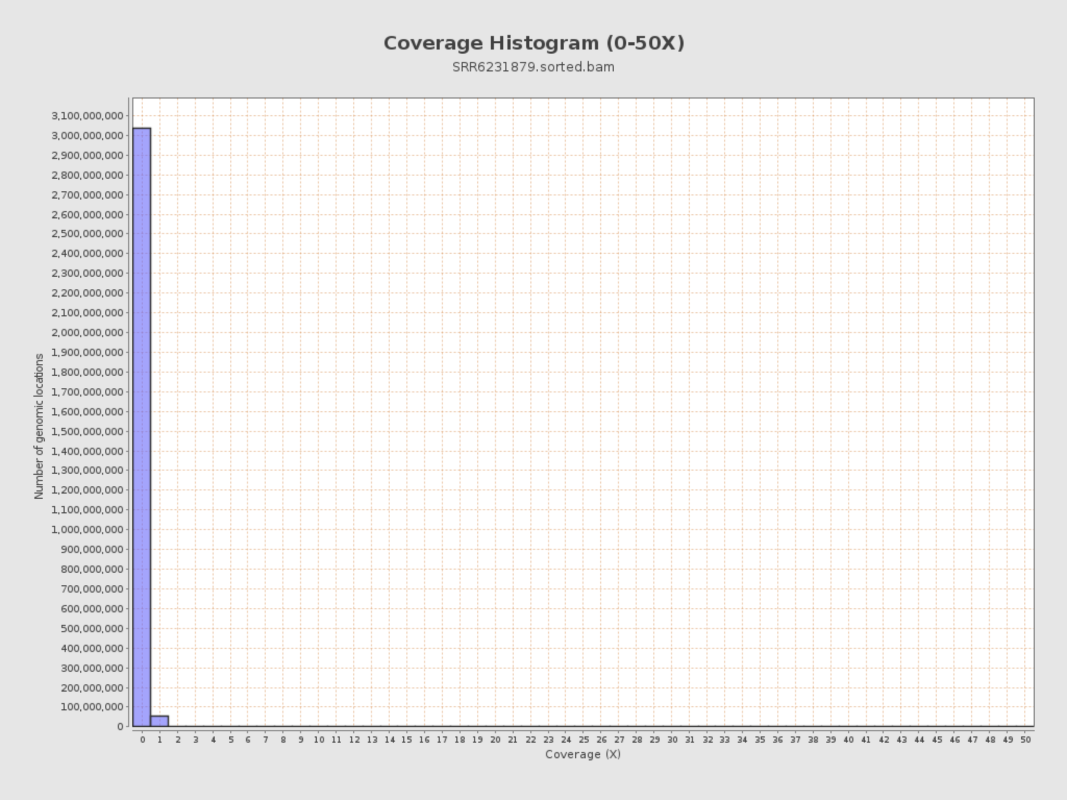
3. Results : Coverage across reference



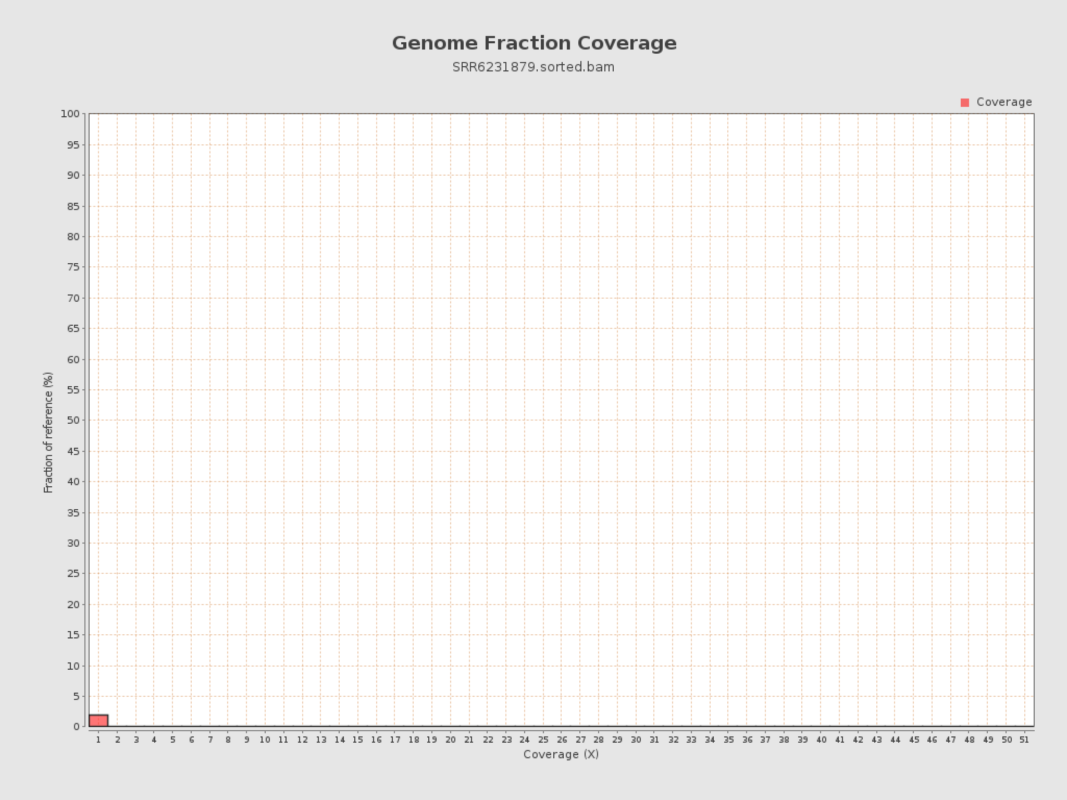
4. Results : Coverage Histogram



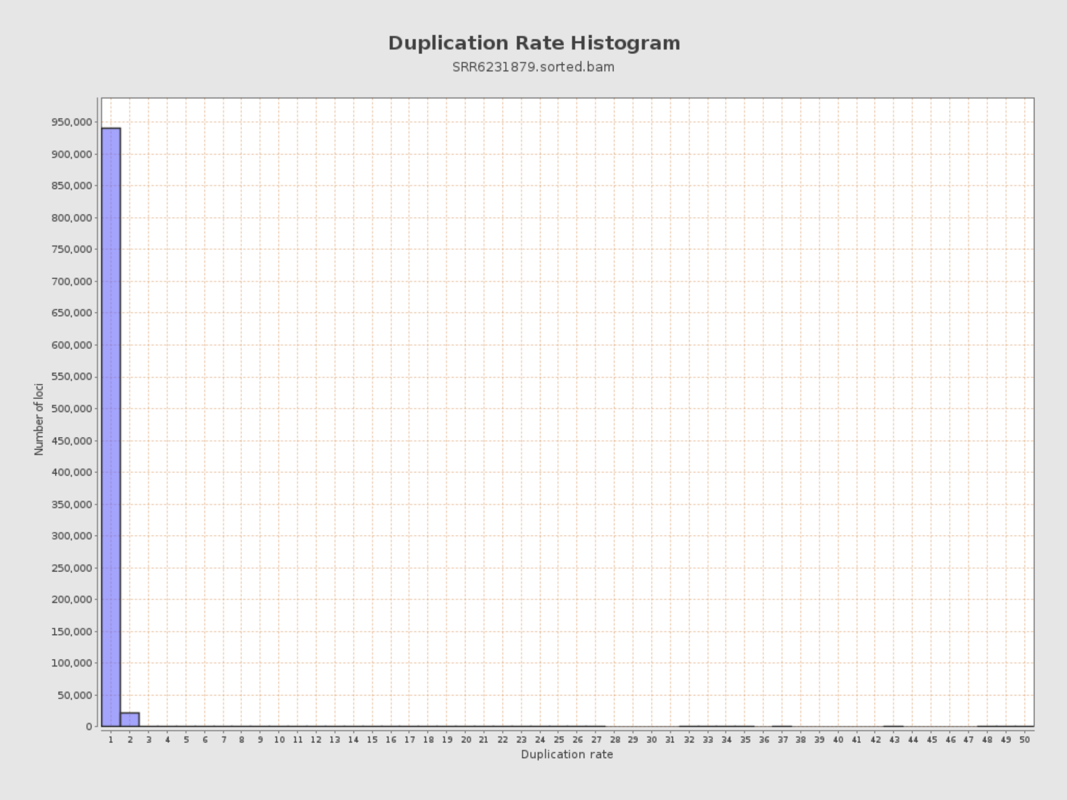
5. Results : Coverage Histogram (0-50X)



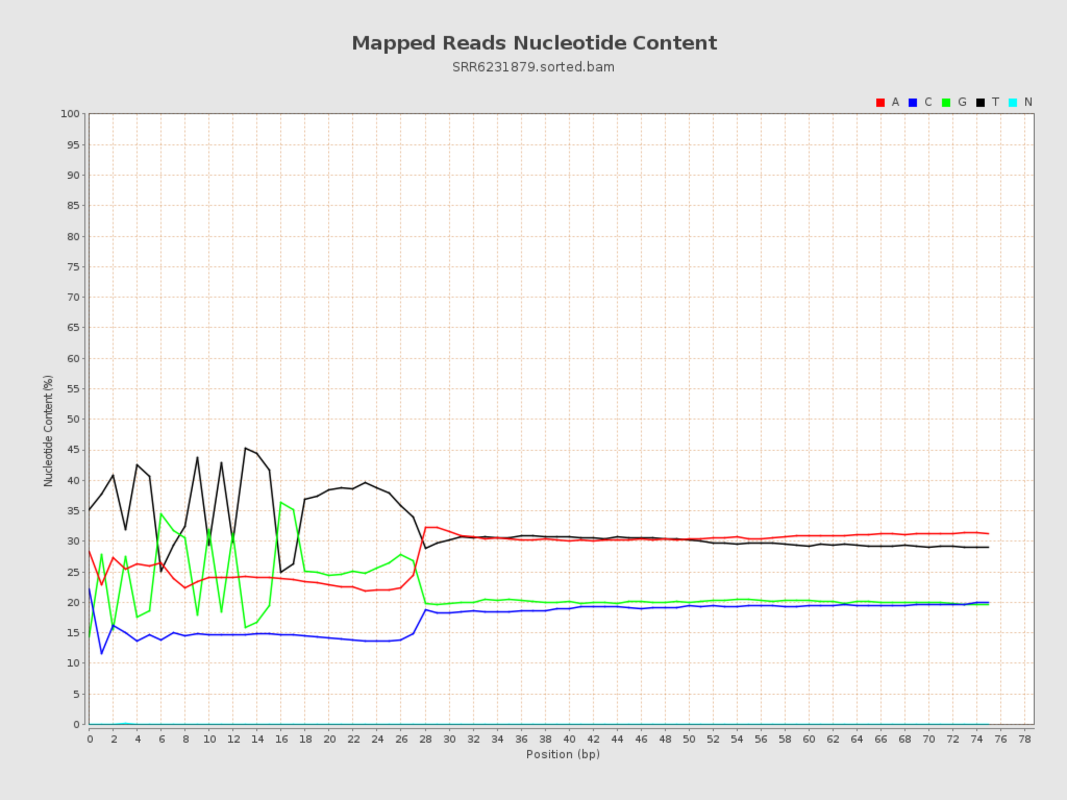
6. Results : Genome Fraction Coverage



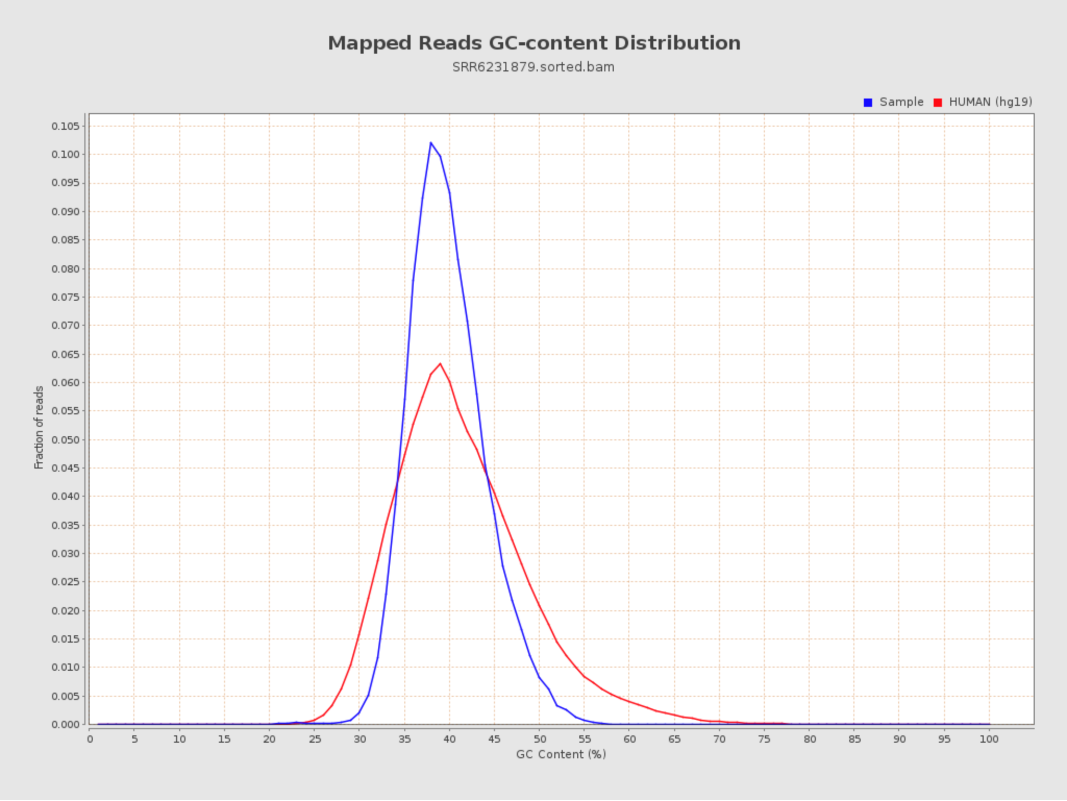
7. Results : Duplication Rate Histogram



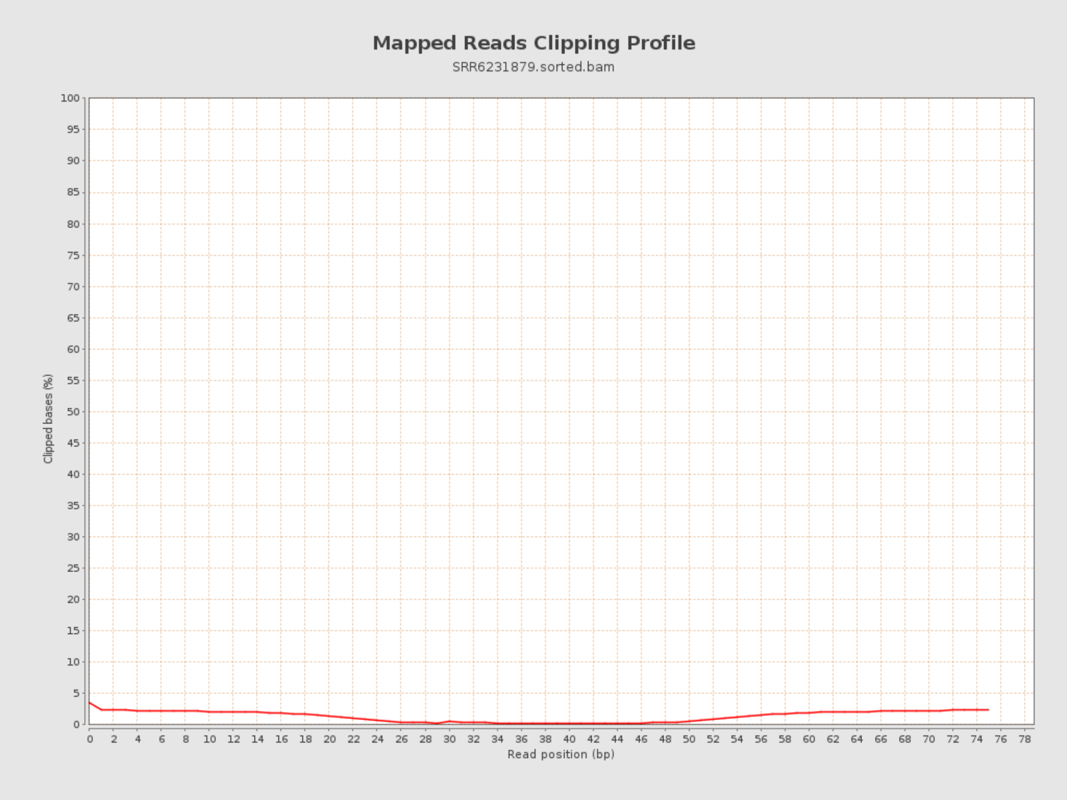
8. Results : Mapped Reads Nucleotide Content



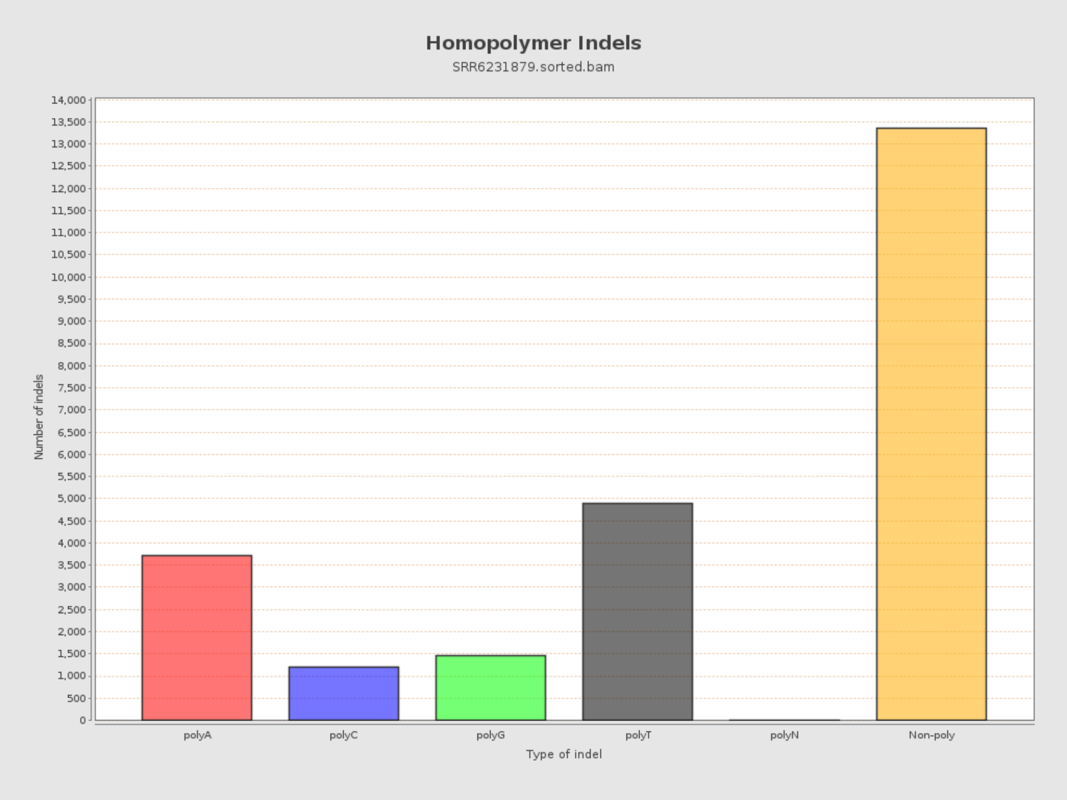
9. Results : Mapped Reads GC-content Distribution



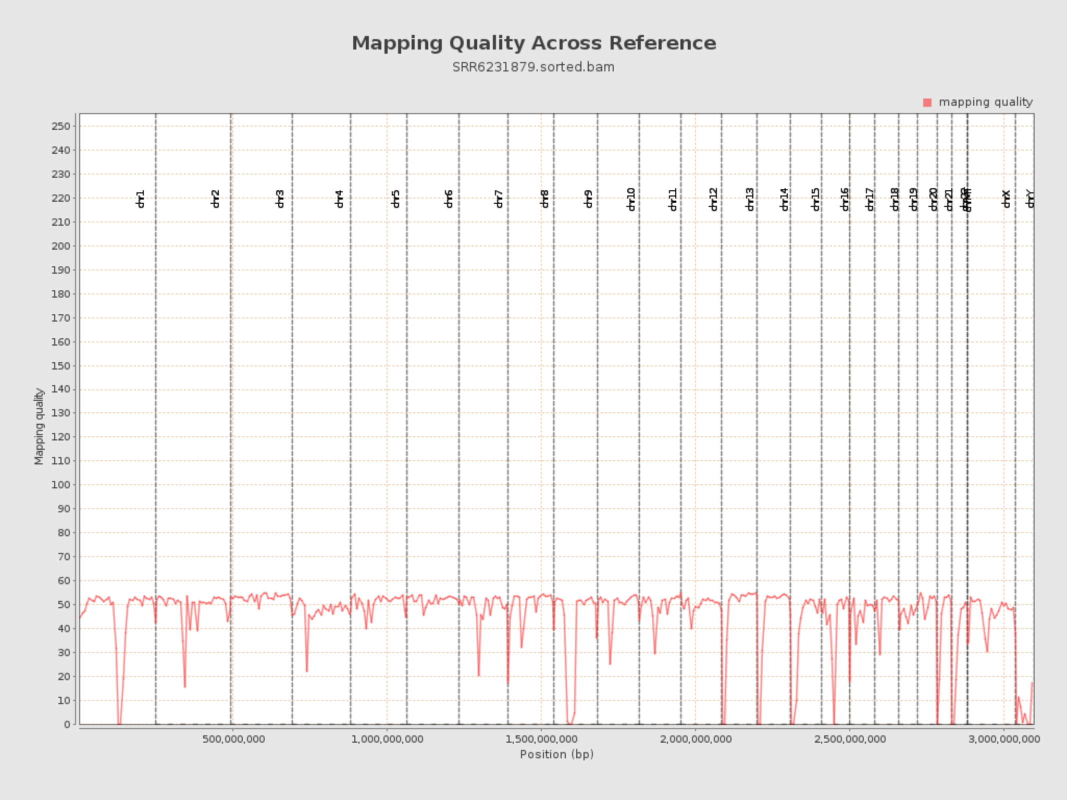
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram