Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:35:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231847.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_SRR6231847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:35:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,417,674
Mapped reads	2,319,291 / 52.5%
Unmapped reads	2,098,383 / 47.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,608 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	92,363 / 2.09%
Duplication rate	2.31%
Clipped reads	1,153,666 / 26.11%

2.2. ACGT Content

Number/percentage of A's	44,984,659 / 29.24%
Number/percentage of C's	31,997,113 / 20.8%
Number/percentage of T's	42,514,323 / 27.64%
Number/percentage of G's	34,323,734 / 22.31%
Number/percentage of N's	12,864 / 0.01%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0497

Standard Deviation	2.3256

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Mismatches and indels

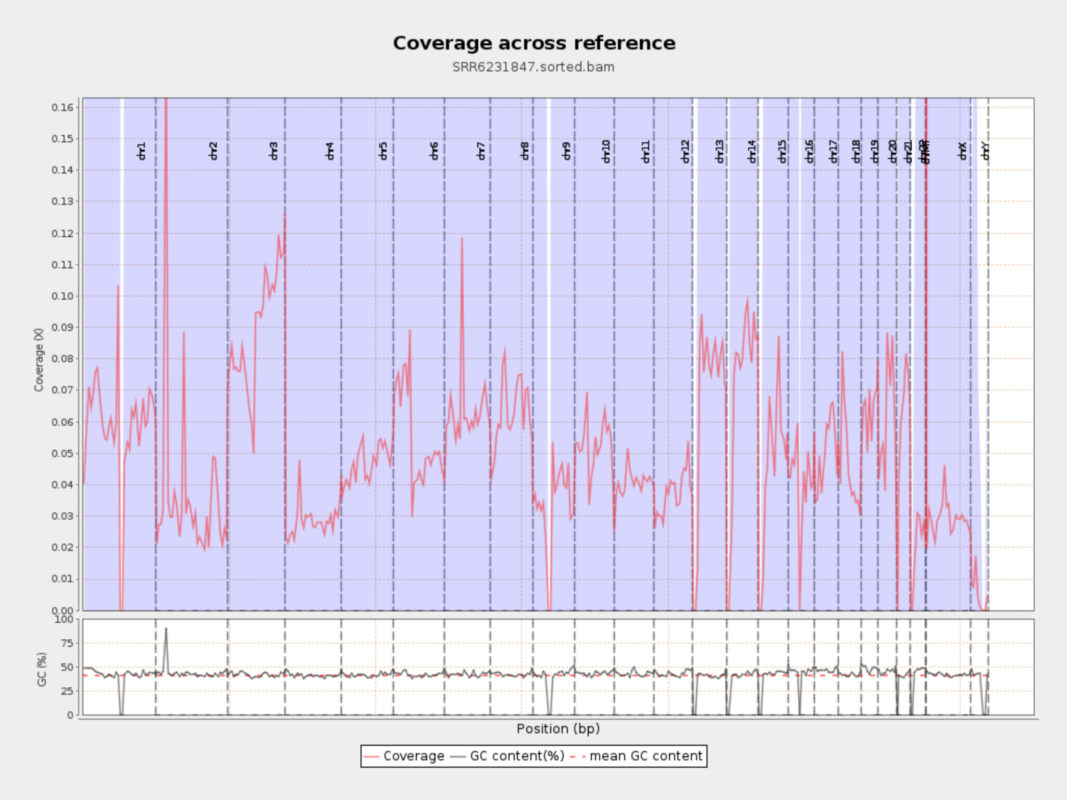
General error rate	0.6%
Mismatches	901,790
Insertions	11,090
Mapped reads with at least one insertion	0.47%
Deletions	37,699
Mapped reads with at least one deletion	1.61%
Homopolymer indels	44.51%

2.6. Chromosome stats

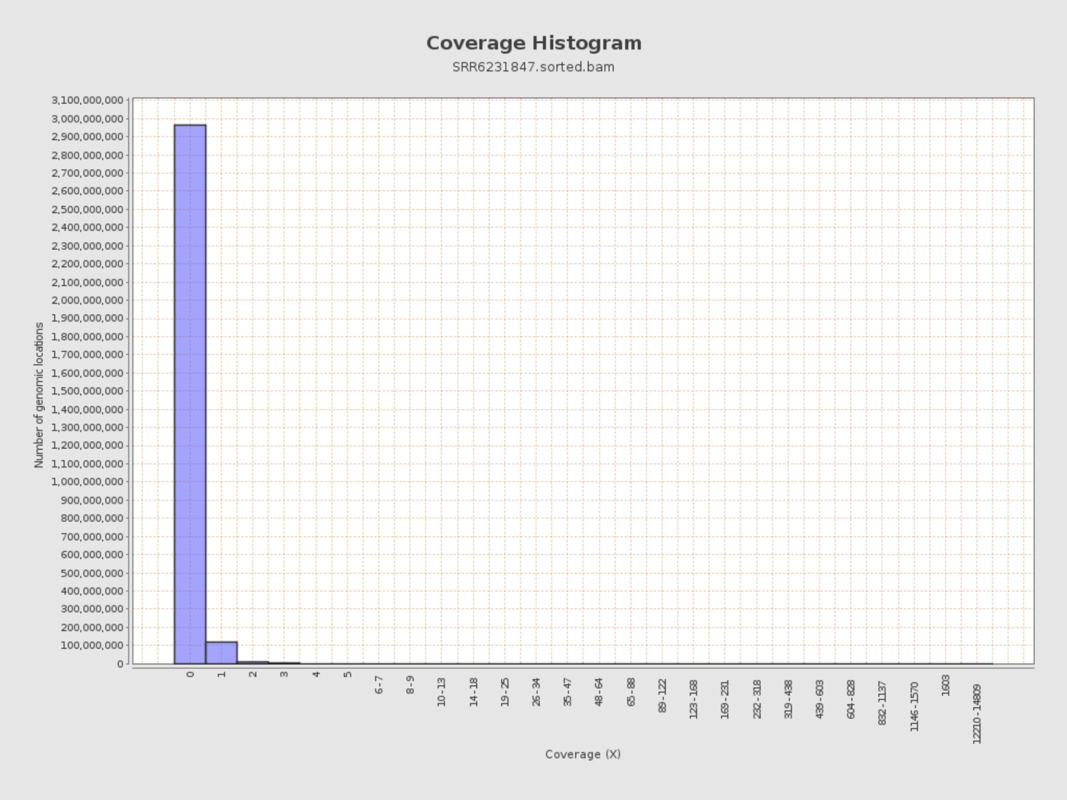
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14584154	0.0585	1.1402
chr2	243199373	8865102	0.0365	8.1044
chr3	198022430	17614125	0.089	0.3294
chr4	191154276	5450641	0.0285	0.199
chr5	180915260	8477035	0.0469	0.242
chr6	171115067	9432805	0.0551	0.3498
chr7	159138663	10129039	0.0636	0.8392

chr8	146364022	9211519	0.0629	0.5115
chr9	141213431	4724864	0.0335	0.3917
chr10	135534747	7151602	0.0528	0.4036
chr11	135006516	5500500	0.0407	0.3629
chr12	133851895	5009883	0.0374	0.2226
chr13	115169878	7795841	0.0677	0.2863
chr14	107349540	7528316	0.0701	0.3341
chr15	102531392	4599801	0.0449	0.234
chr16	90354753	3566984	0.0395	0.2977
chr17	81195210	4120061	0.0507	0.2867
chr18	78077248	3700044	0.0474	0.9938
chr19	59128983	3739134	0.0632	0.6569
chr20	63025520	3898156	0.0619	0.2914
chr21	48129895	2850615	0.0592	0.2834
chr22	51304566	1017337	0.0198	0.1528
chrMT	16571	62689	3.7831	2.8357
chrX	155270560	4552526	0.0293	0.2445
chrY	59373566	313712	0.0053	0.1216

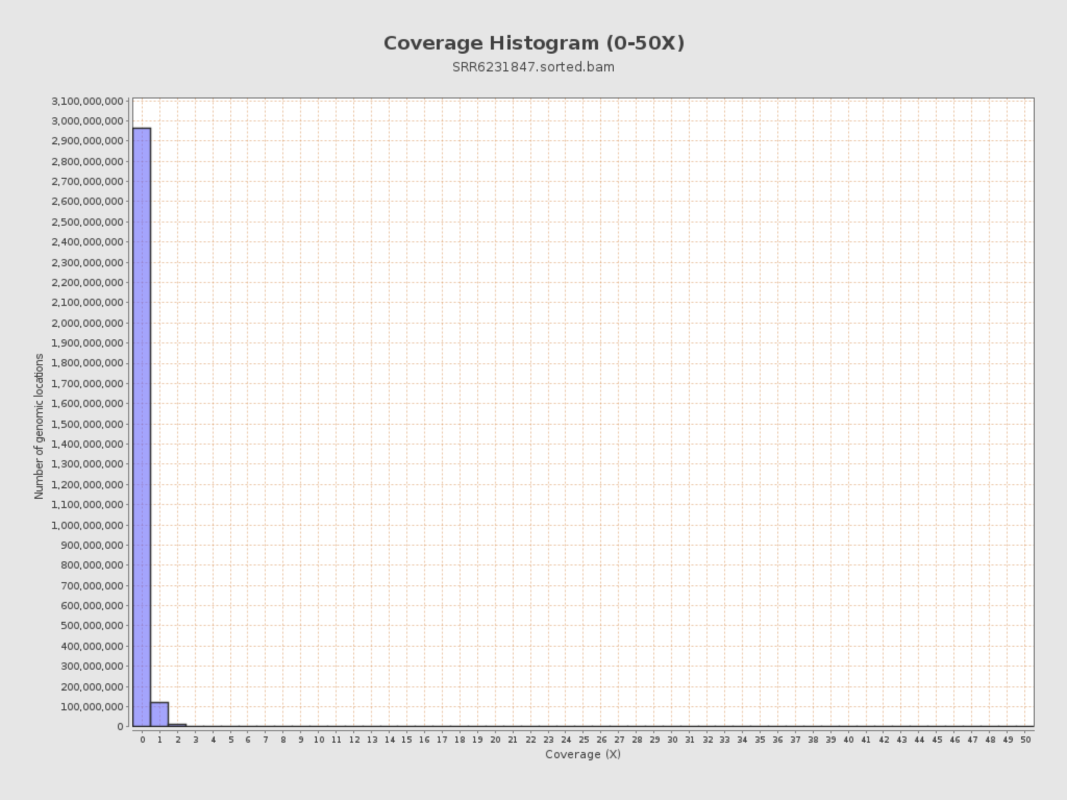
3. Results : Coverage across reference



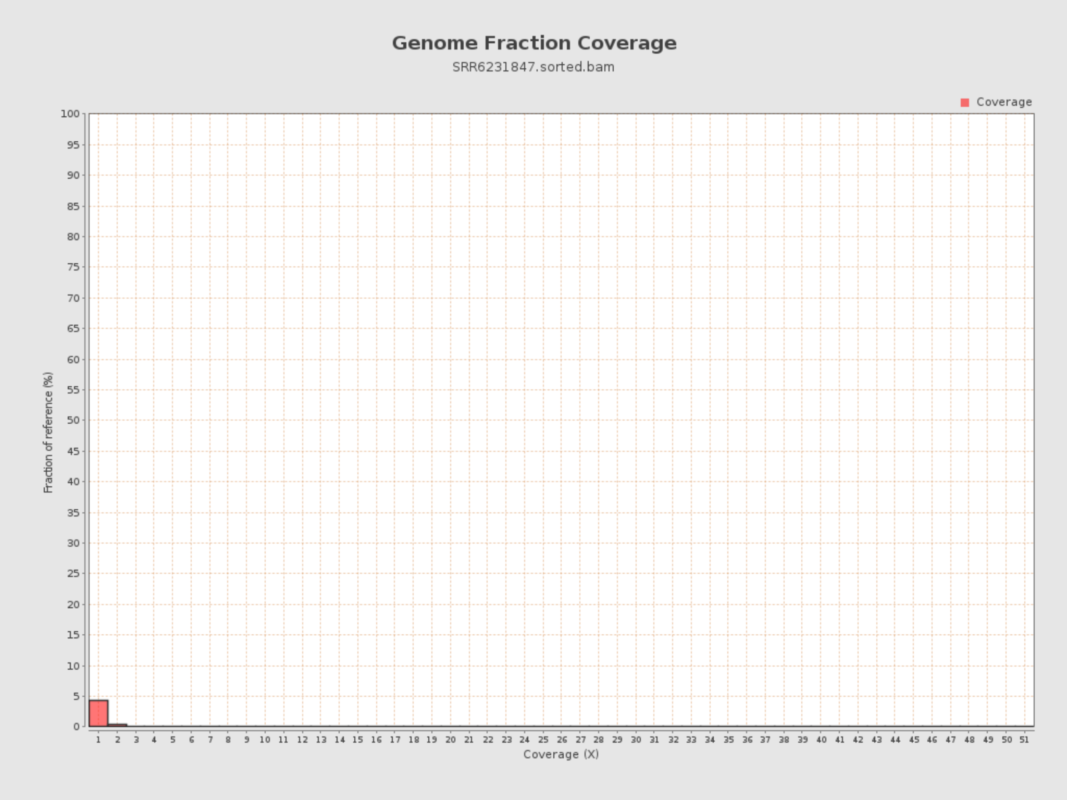
4. Results : Coverage Histogram



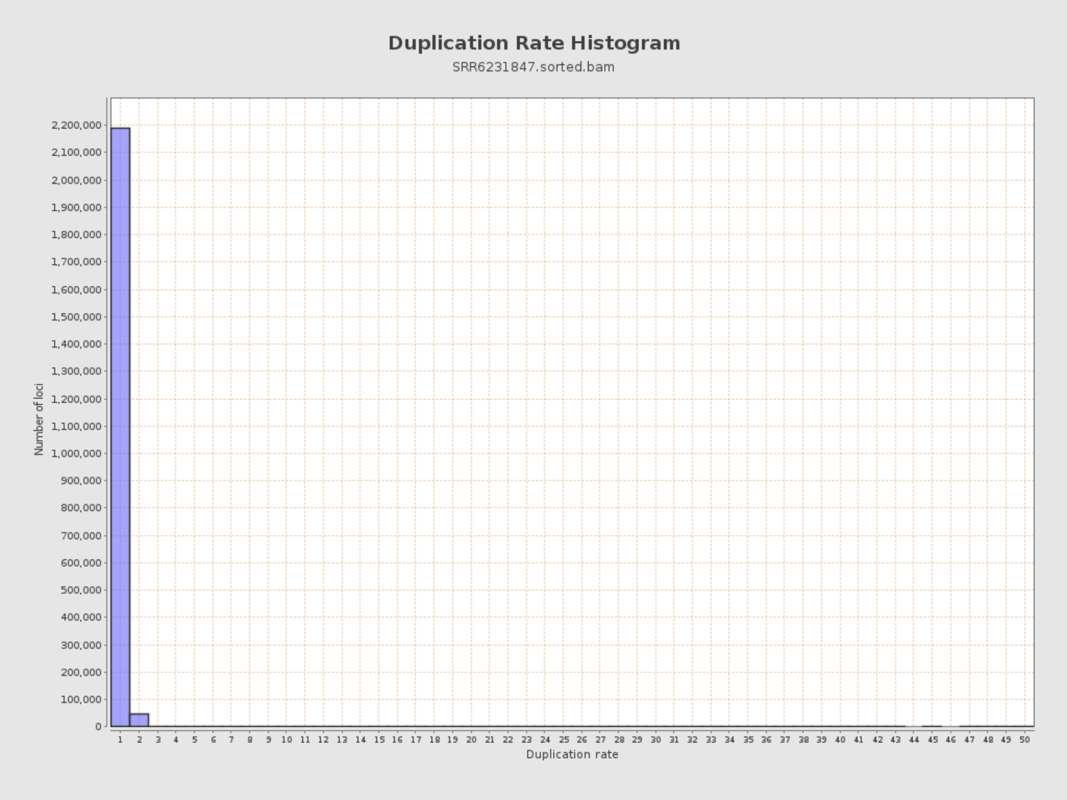
5. Results : Coverage Histogram (0-50X)



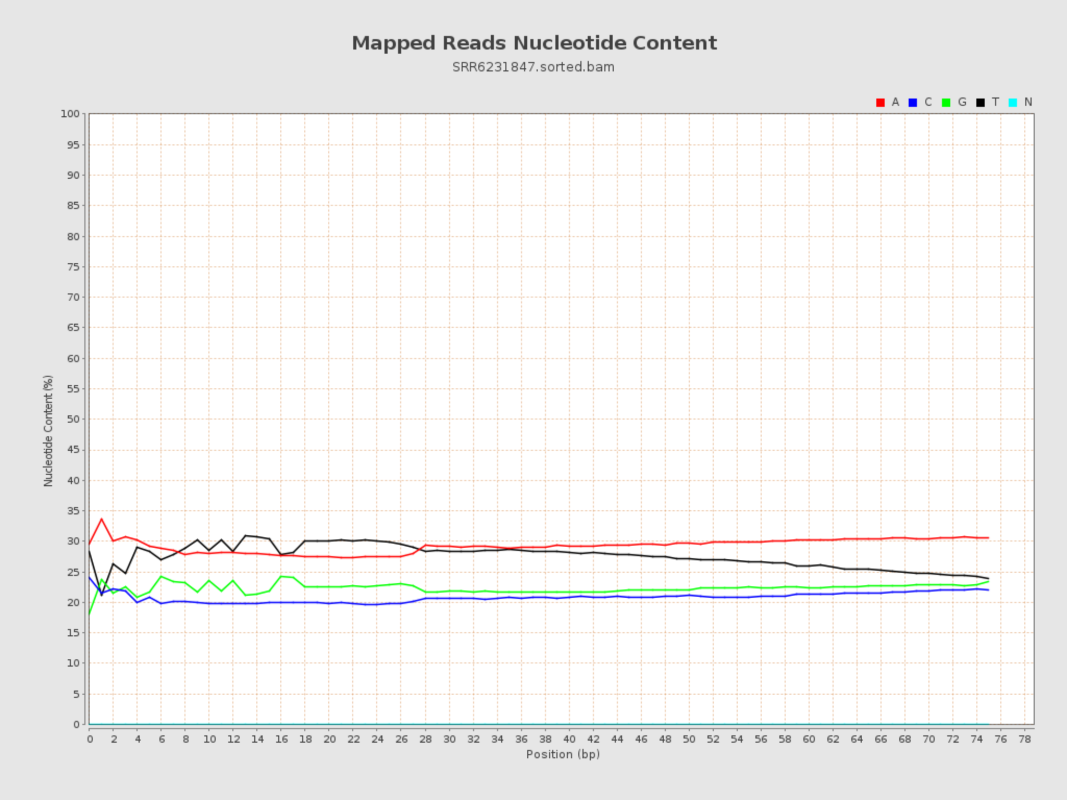
6. Results : Genome Fraction Coverage



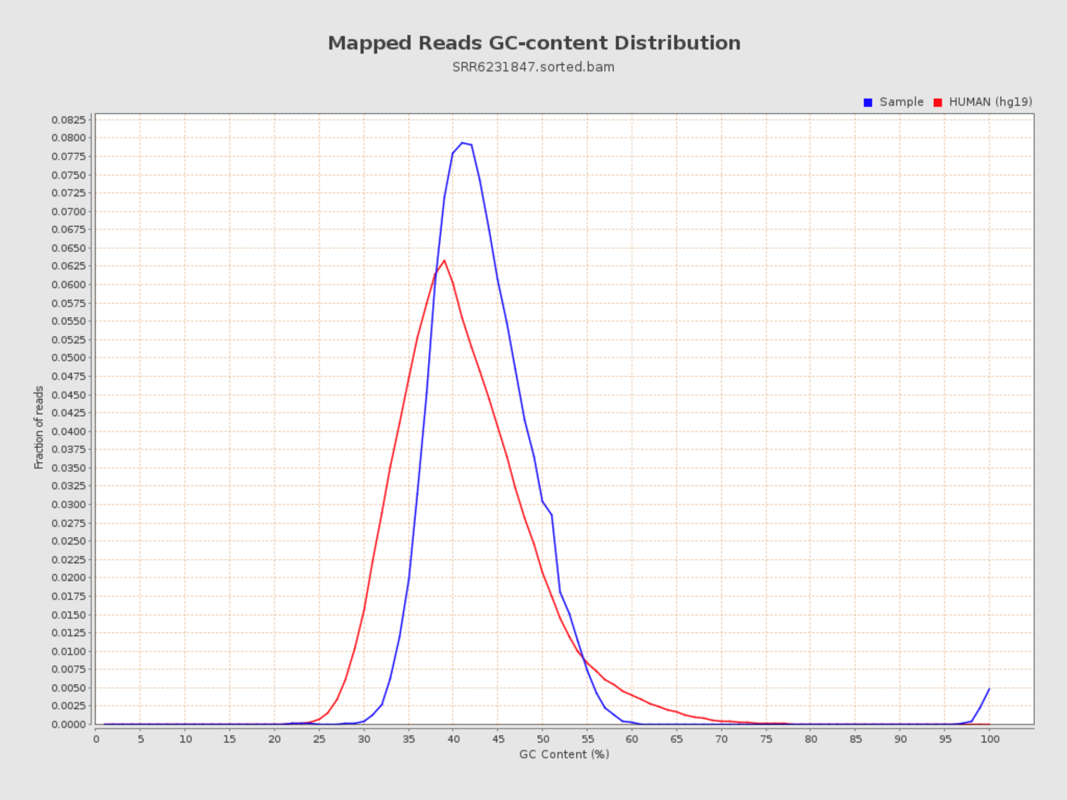
7. Results : Duplication Rate Histogram



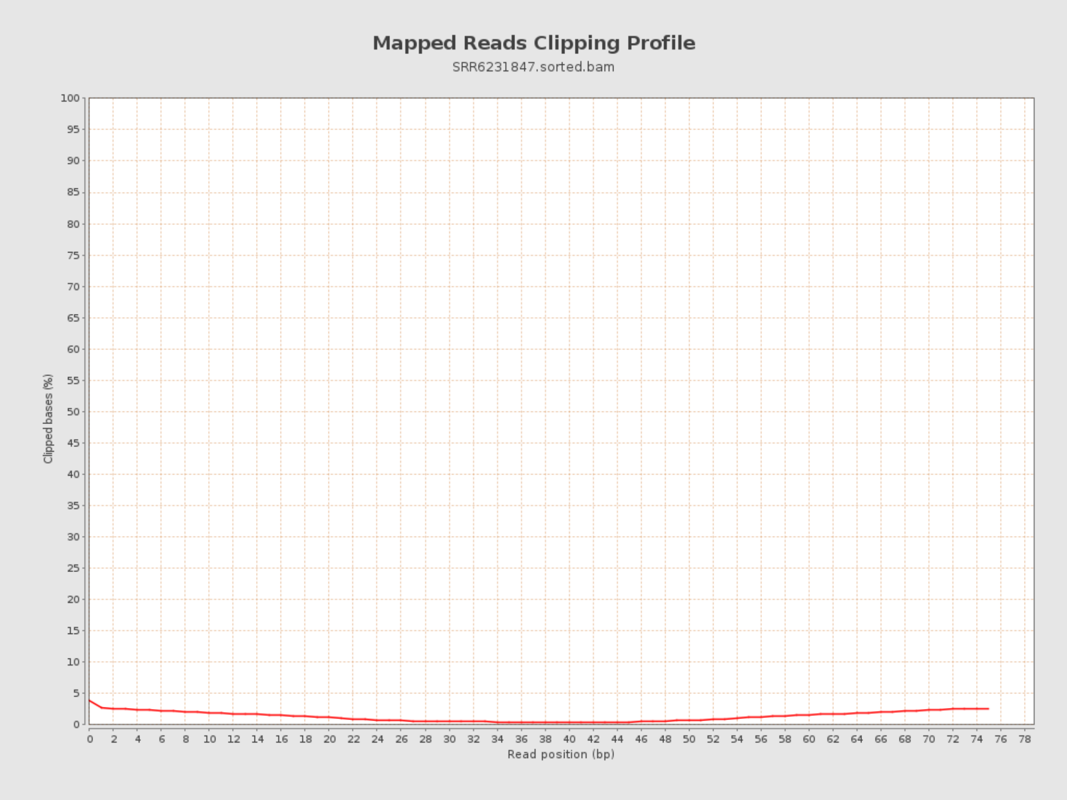
8. Results : Mapped Reads Nucleotide Content



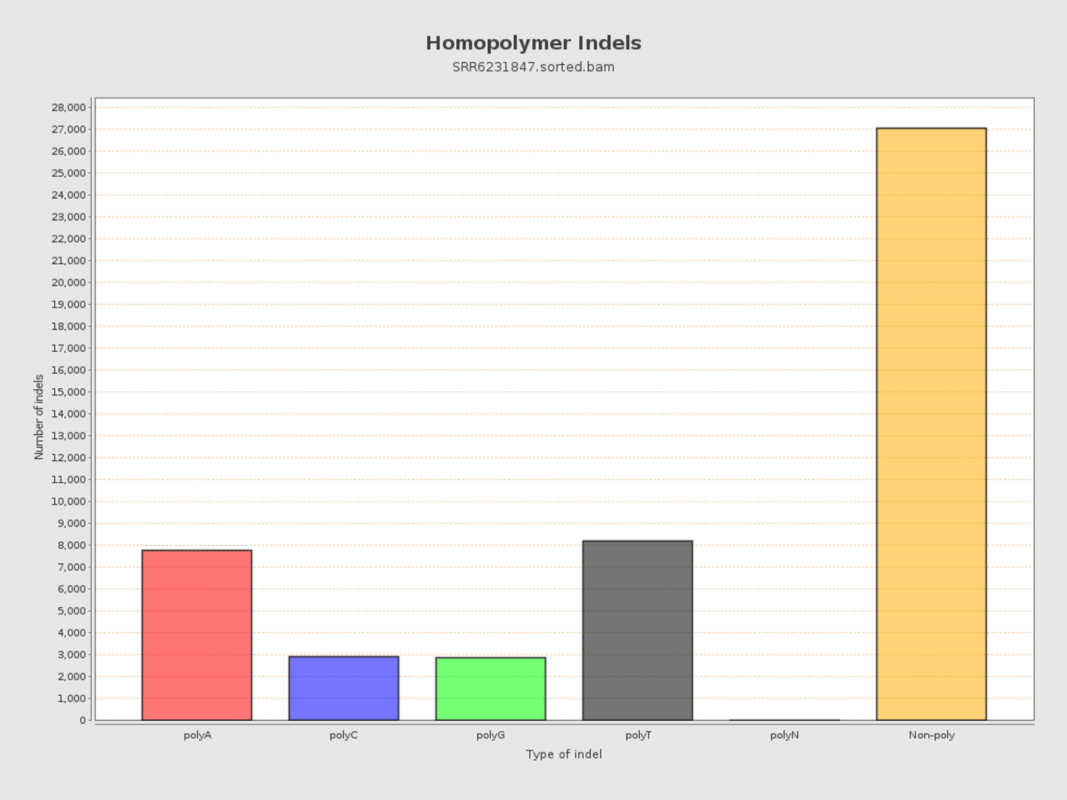
9. Results : Mapped Reads GC-content Distribution



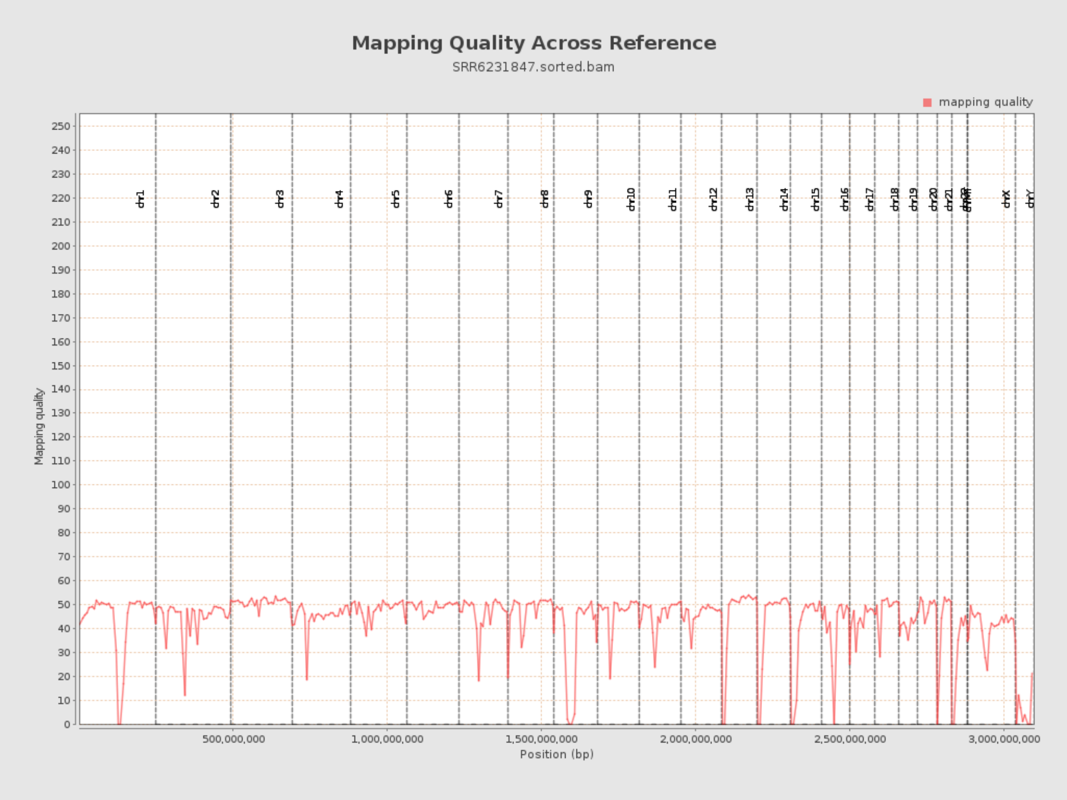
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram