Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231815.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_SRR6231815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:11:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,559,953
Mapped reads	4,188,698 / 91.86%
Unmapped reads	371,255 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,698 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	462,388 / 10.14%
Duplication rate	9.22%
Clipped reads	2,196,065 / 48.16%

2.2. ACGT Content

Number/percentage of A's	72,923,568 / 26.89%
Number/percentage of C's	48,852,422 / 18.01%
Number/percentage of T's	87,820,825 / 32.38%
Number/percentage of G's	61,526,583 / 22.68%
Number/percentage of N's	107,063 / 0.04%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0876

Standard Deviation	0.8891

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

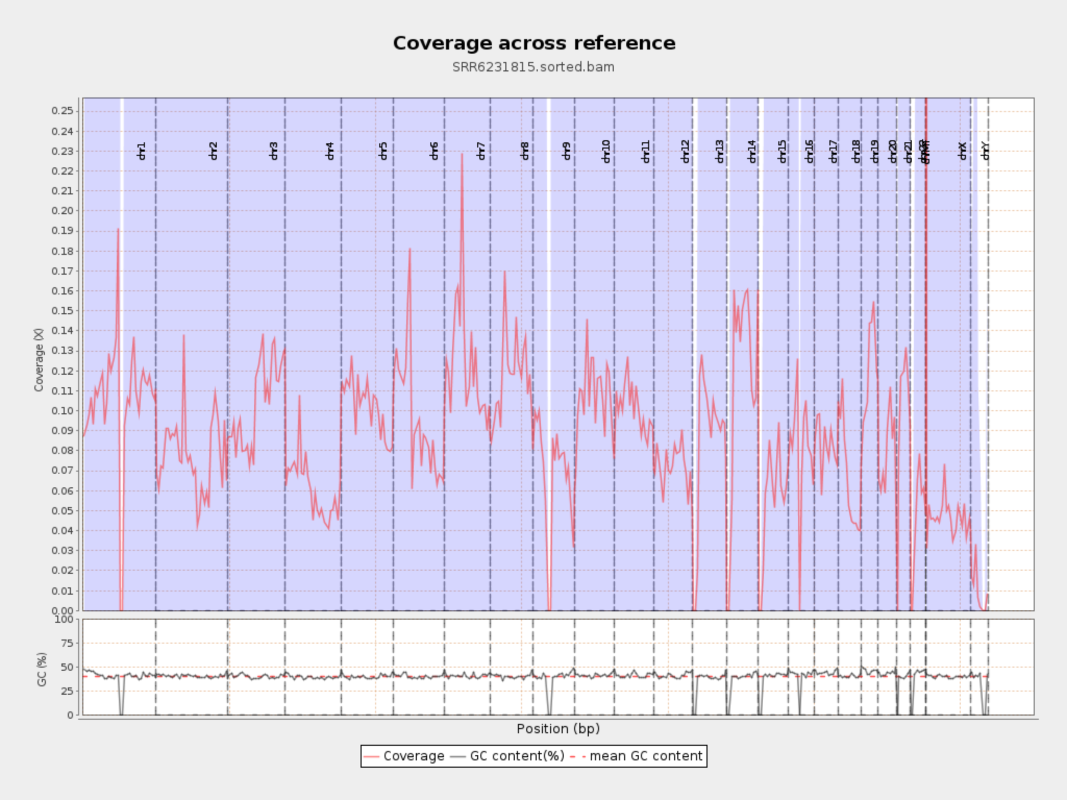
General error rate	0.63%
Mismatches	1,687,234
Insertions	18,204
Mapped reads with at least one insertion	0.43%
Deletions	61,001
Mapped reads with at least one deletion	1.44%
Homopolymer indels	45.01%

2.6. Chromosome stats

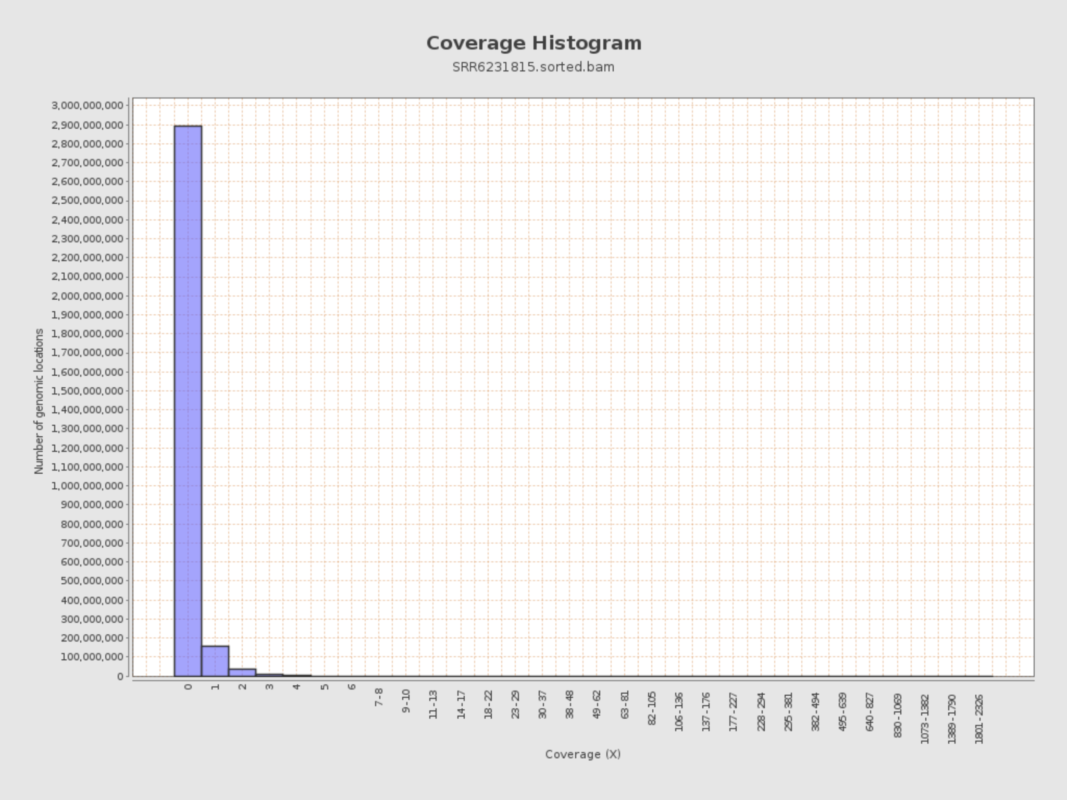
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26476465	0.1062	1.8063
chr2	243199373	18870832	0.0776	1.1596
chr3	198022430	20458370	0.1033	0.4094
chr4	191154276	11590059	0.0606	0.362
chr5	180915260	18485605	0.1022	0.4139
chr6	171115067	16587066	0.0969	0.6027
chr7	159138663	19824773	0.1246	1.5183

chr8	146364022	17250281	0.1179	1.3516
chr9	141213431	9560447	0.0677	0.529
chr10	135534747	14645290	0.1081	0.6355
chr11	135006516	13570423	0.1005	0.675
chr12	133851895	9689194	0.0724	0.3545
chr13	115169878	9813196	0.0852	0.4024
chr14	107349540	12330617	0.1149	0.4719
chr15	102531392	5540765	0.054	0.3346
chr16	90354753	7227897	0.08	0.4259
chr17	81195210	6777234	0.0835	0.4449
chr18	78077248	5183294	0.0664	1.3152
chr19	59128983	7106201	0.1202	1.1137
chr20	63025520	5018925	0.0796	0.4035
chr21	48129895	4797492	0.0997	0.4231
chr22	51304566	2354383	0.0459	0.2635
chrMT	16571	292997	17.6813	10.6346
chrX	155270560	7309153	0.0471	0.359
chrY	59373566	575299	0.0097	0.207

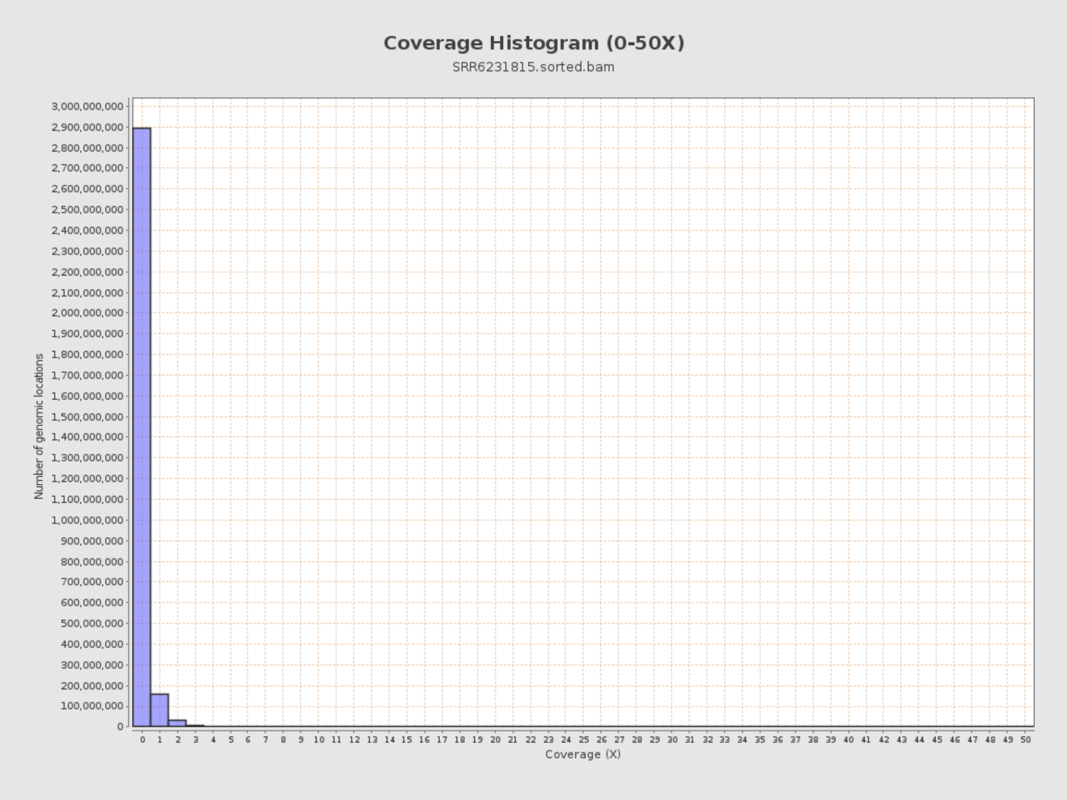
3. Results : Coverage across reference



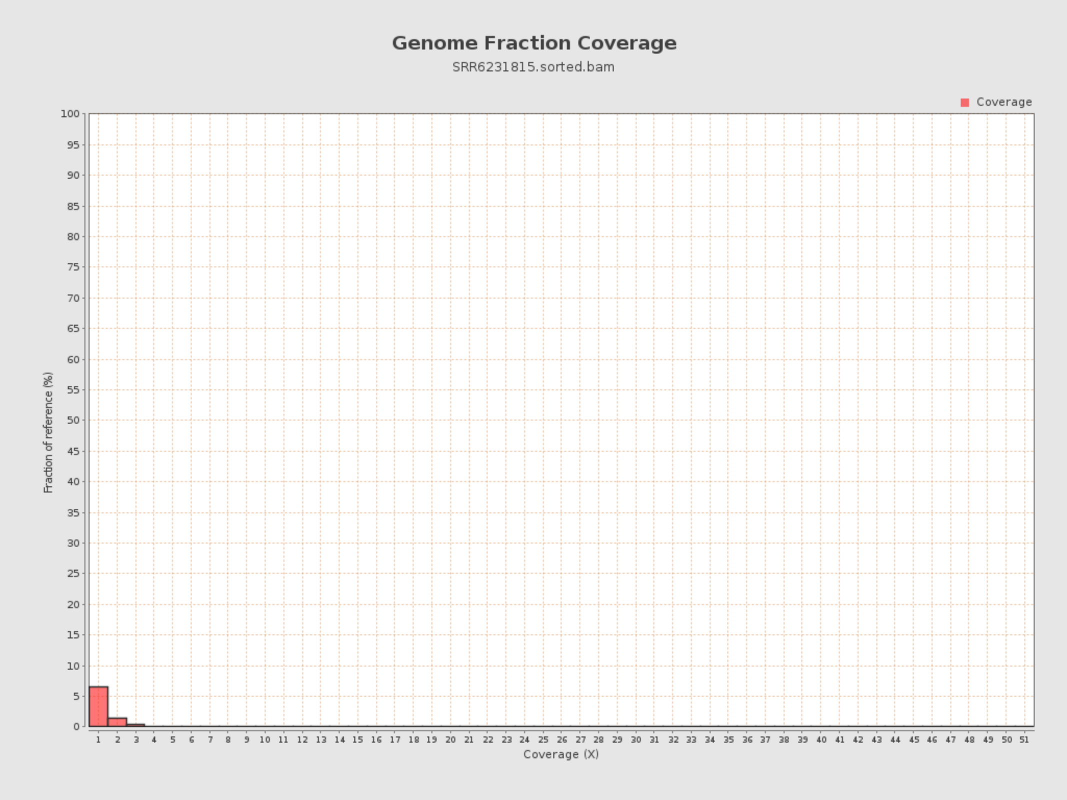
4. Results : Coverage Histogram



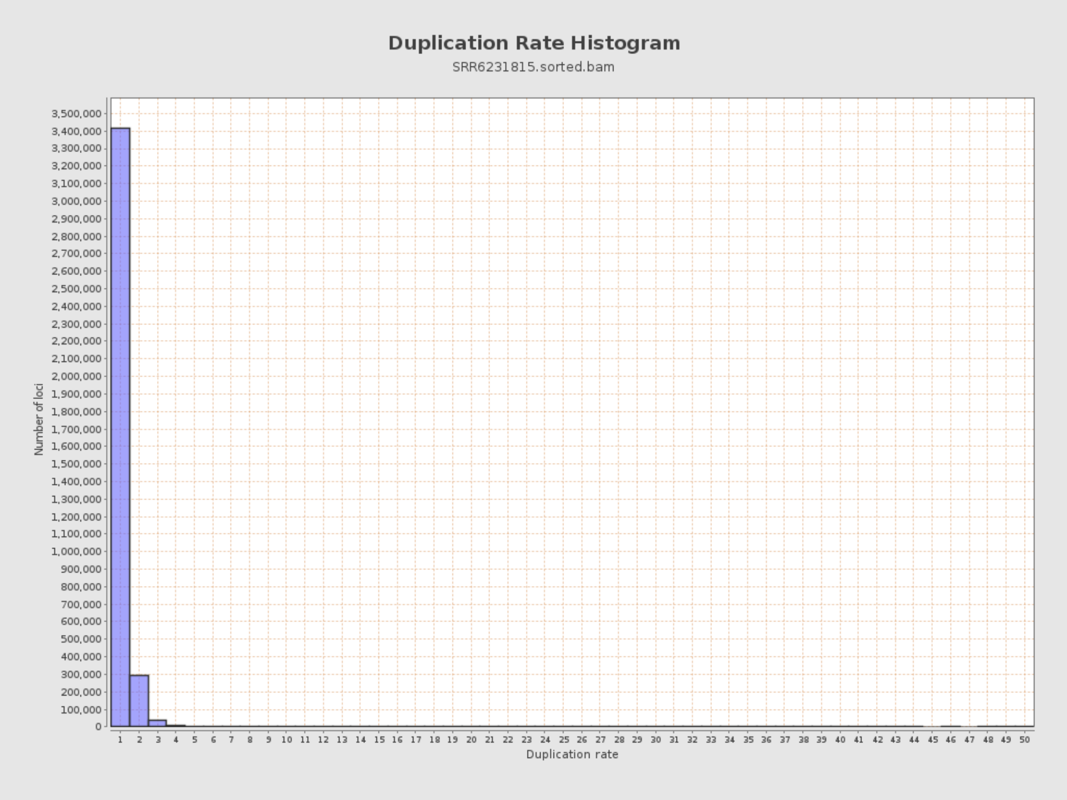
5. Results : Coverage Histogram (0-50X)



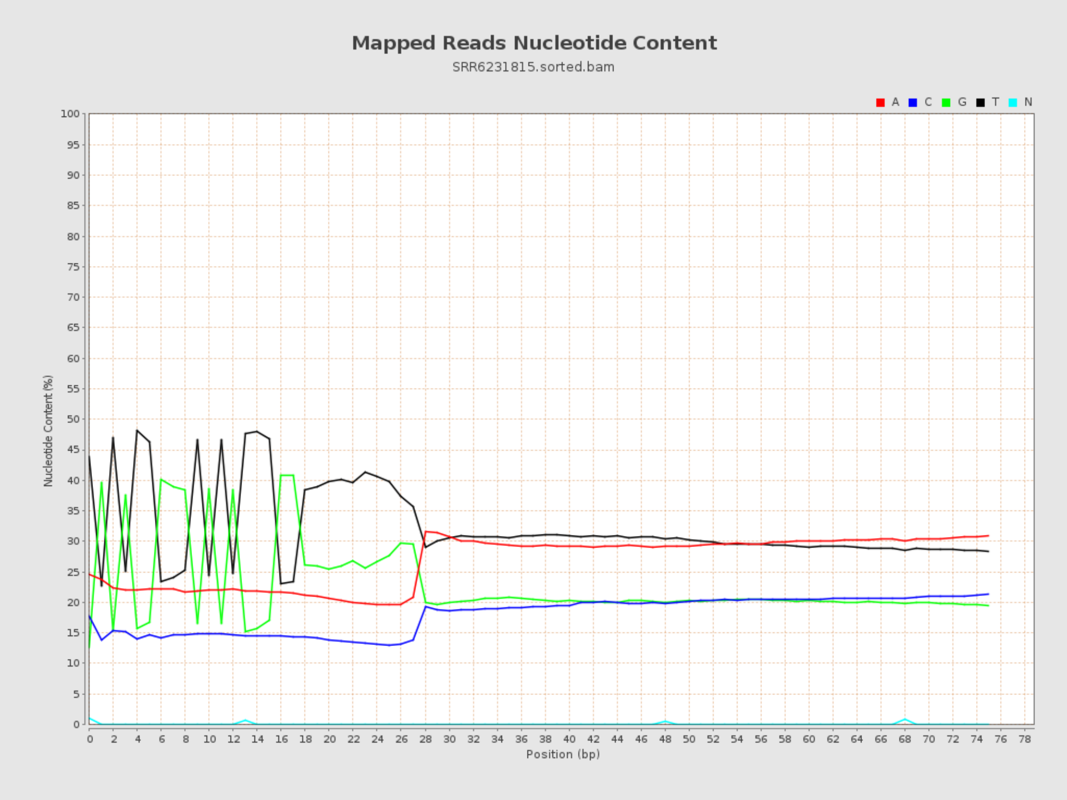
6. Results : Genome Fraction Coverage



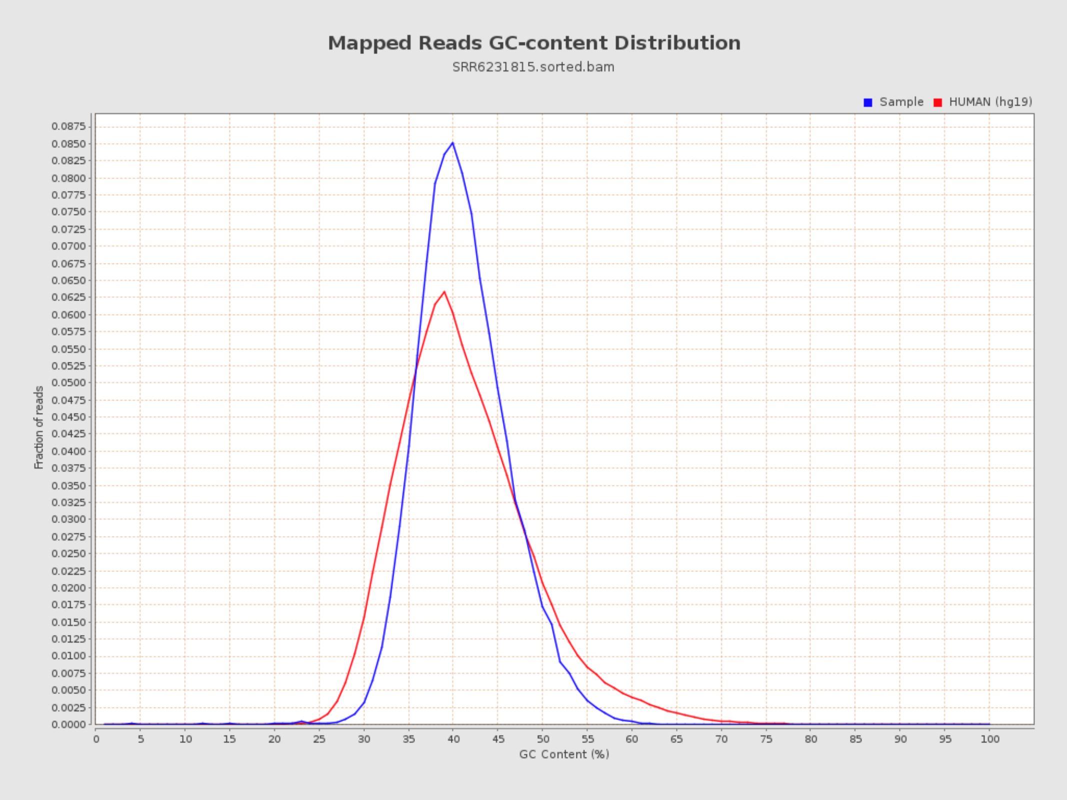
7. Results : Duplication Rate Histogram



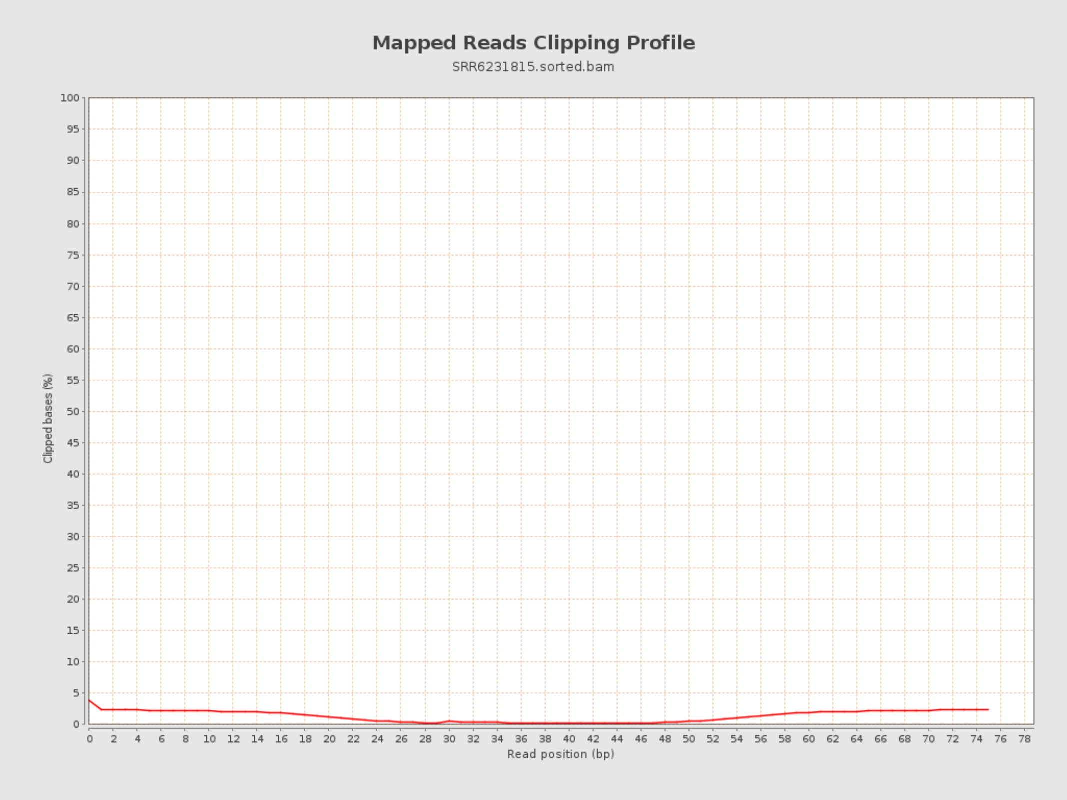
8. Results : Mapped Reads Nucleotide Content



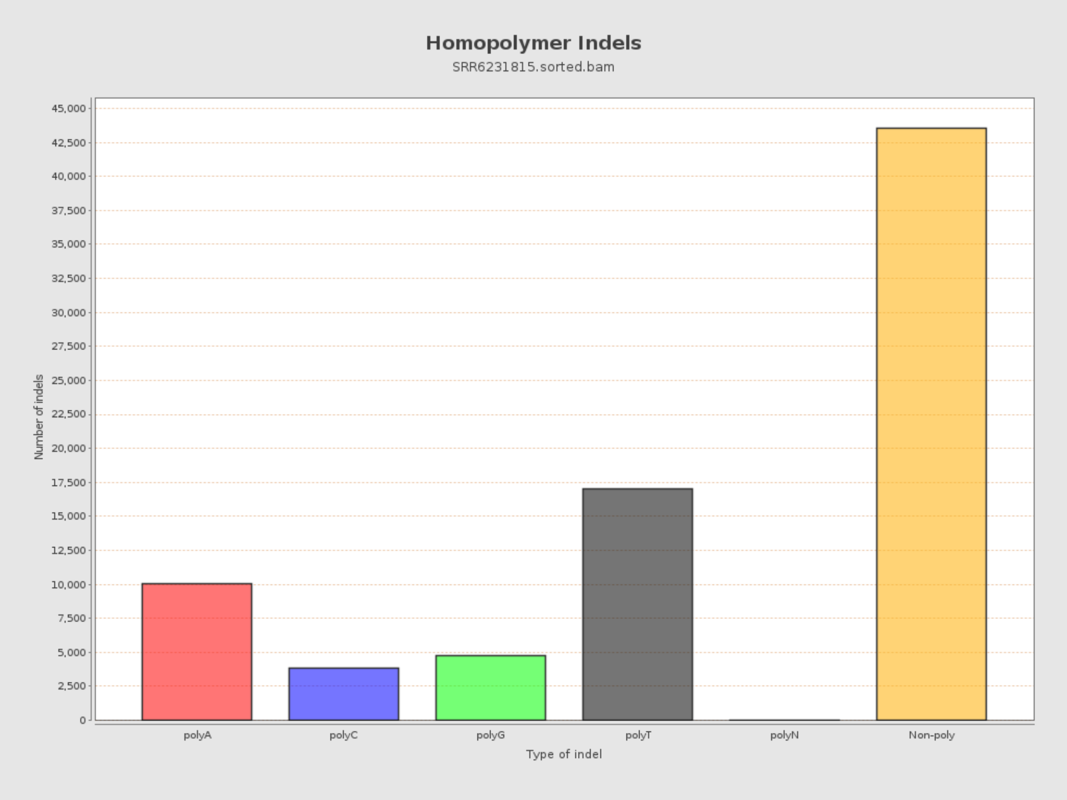
9. Results : Mapped Reads GC-content Distribution



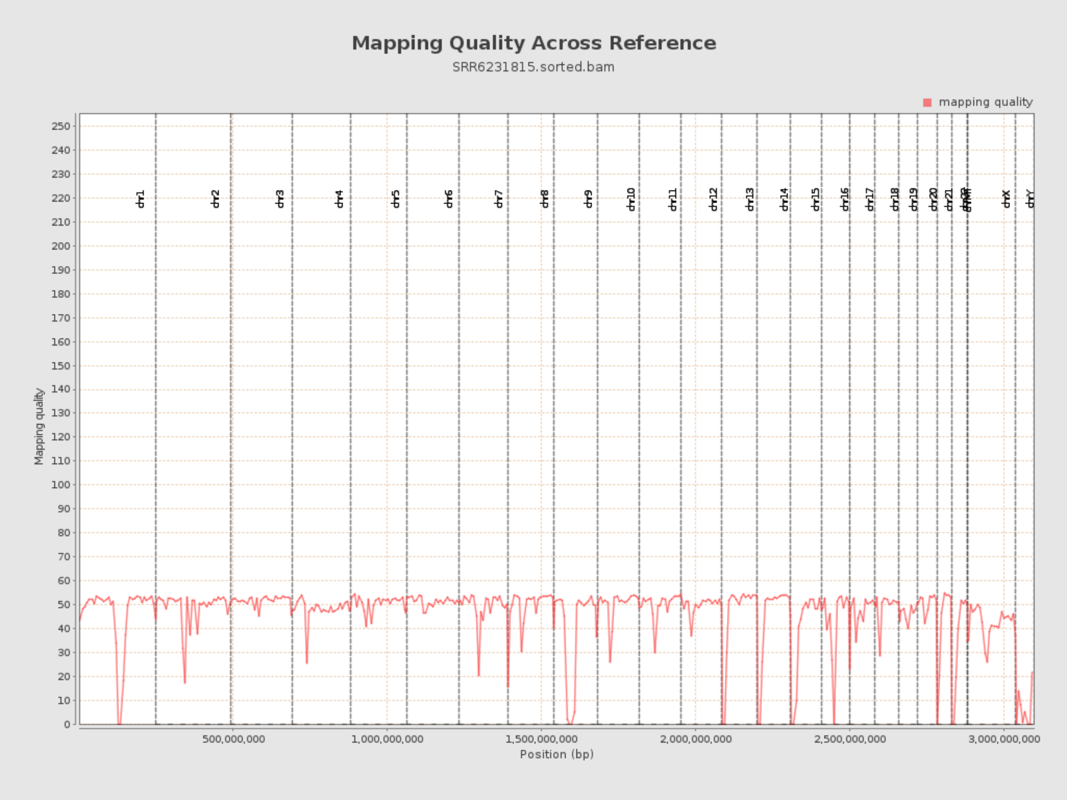
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram