Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:06:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231814.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_SRR6231814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:06:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,293,025
Mapped reads	4,914,725 / 92.85%
Unmapped reads	378,300 / 7.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,906 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	466,834 / 8.82%
Duplication rate	7.42%
Clipped reads	2,687,672 / 50.78%

2.2. ACGT Content

Number/percentage of A's	81,394,422 / 25.79%
Number/percentage of C's	57,384,233 / 18.18%
Number/percentage of T's	101,957,950 / 32.31%
Number/percentage of G's	74,745,724 / 23.68%
Number/percentage of N's	120,461 / 0.04%
GC Percentage	41.87%

2.3. Coverage

Mean	0.102

Standard Deviation	1.159

2.4. Mapping Quality

Mean Mapping Quality	42.75

2.5. Mismatches and indels

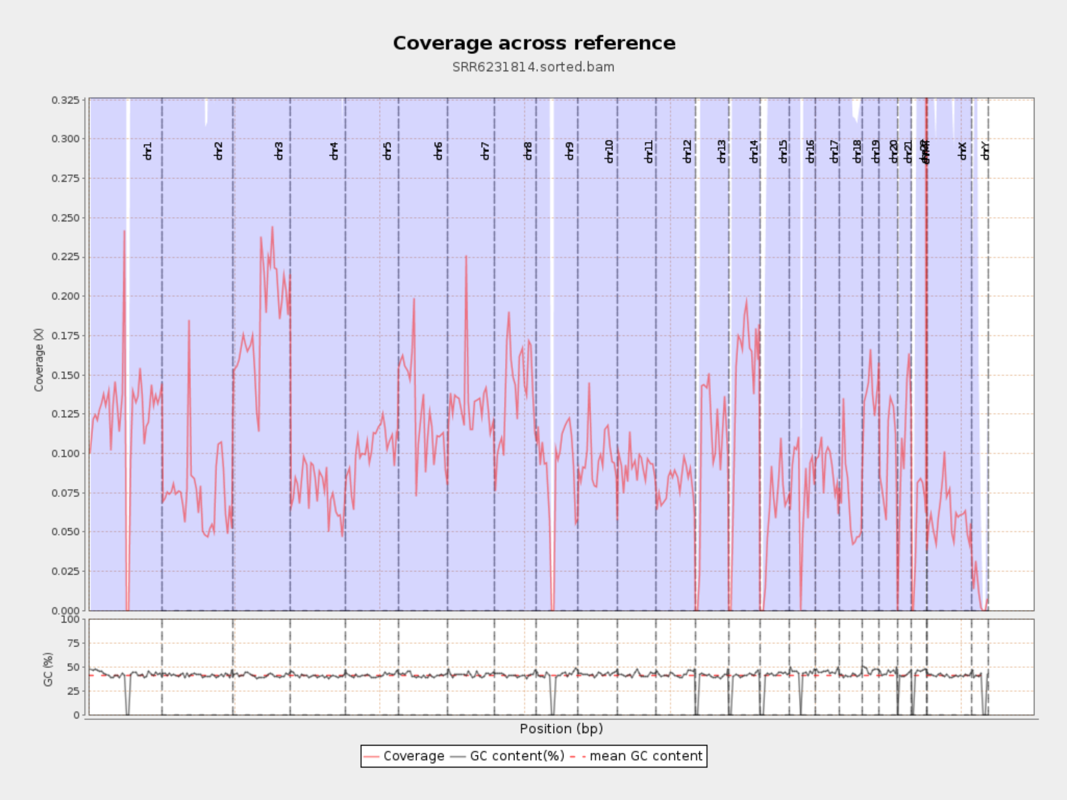
General error rate	0.65%
Mismatches	2,016,973
Insertions	21,087
Mapped reads with at least one insertion	0.43%
Deletions	71,521
Mapped reads with at least one deletion	1.44%
Homopolymer indels	43.82%

2.6. Chromosome stats

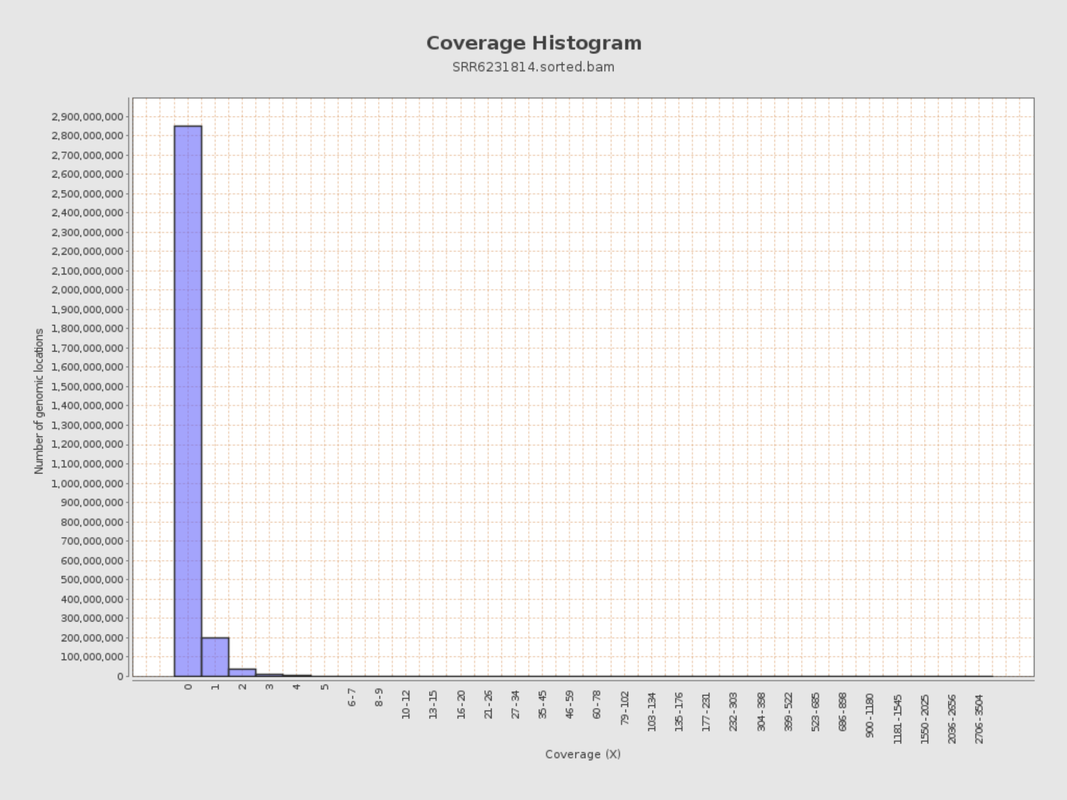
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30869114	0.1238	2.6361
chr2	243199373	18111573	0.0745	1.6903
chr3	198022430	36602535	0.1848	0.5461
chr4	191154276	14430578	0.0755	0.4122
chr5	180915260	18486877	0.1022	0.4243
chr6	171115067	21614829	0.1263	0.7496
chr7	159138663	21216576	0.1333	1.5673

chr8	146364022	20244570	0.1383	1.3119
chr9	141213431	12496855	0.0885	0.7446
chr10	135534747	13133971	0.0969	0.8585
chr11	135006516	12304948	0.0911	0.7612
chr12	133851895	10813816	0.0808	0.3944
chr13	115169878	11796767	0.1024	0.4434
chr14	107349540	15041623	0.1401	0.5387
chr15	102531392	6088609	0.0594	0.417
chr16	90354753	7169823	0.0794	0.503
chr17	81195210	7441637	0.0917	0.4797
chr18	78077248	5266125	0.0674	1.896
chr19	59128983	8239105	0.1393	1.4261
chr20	63025520	6144711	0.0975	0.4541
chr21	48129895	5050385	0.1049	0.4264
chr22	51304566	2824850	0.0551	0.283
chrMT	16571	365401	22.0506	12.477
chrX	155270560	9352890	0.0602	0.4715
chrY	59373566	617718	0.0104	0.2103

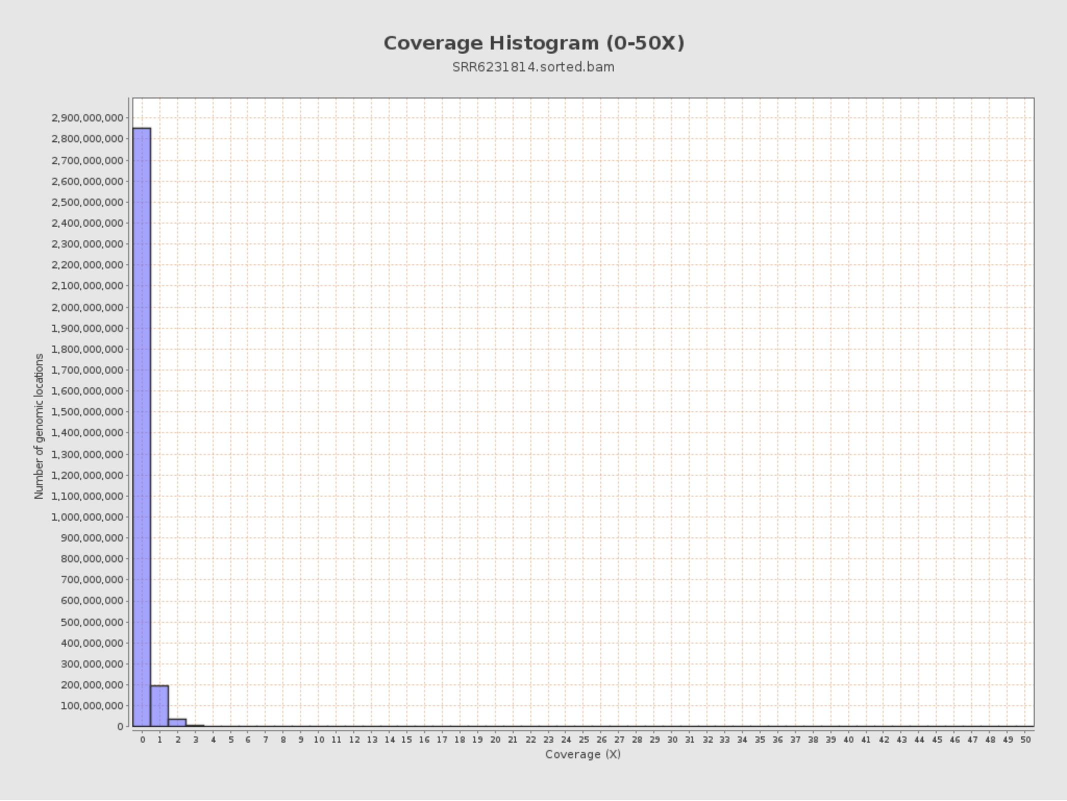
3. Results : Coverage across reference



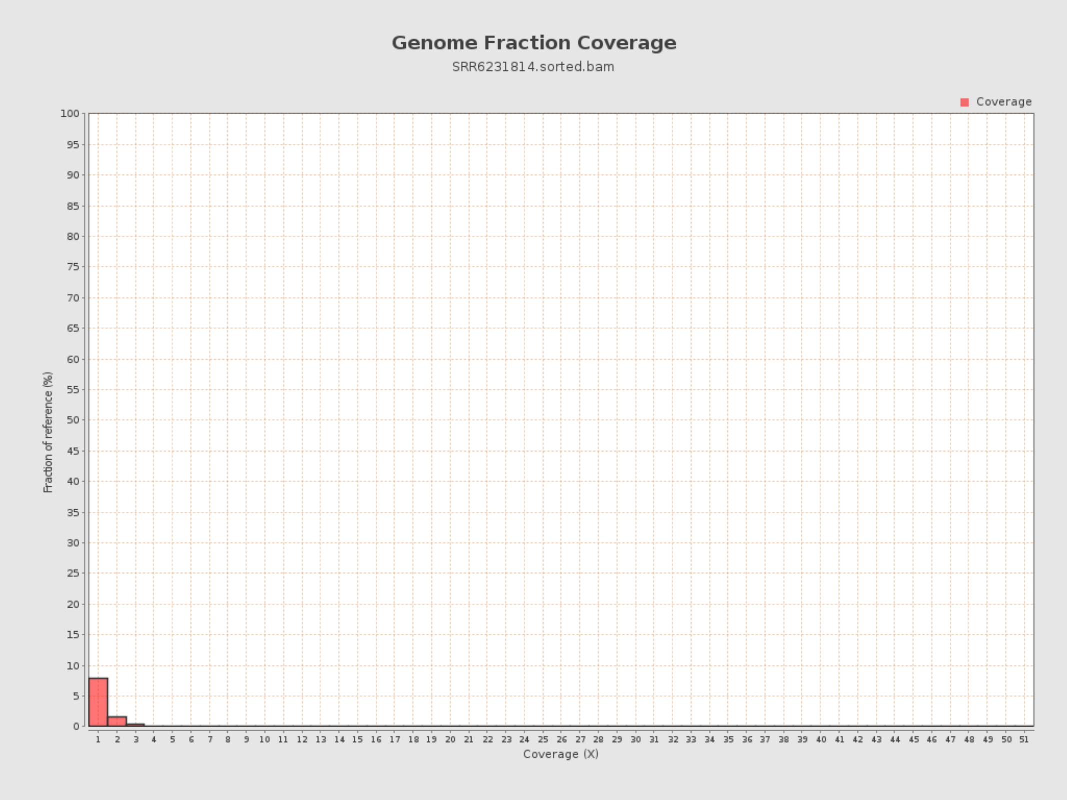
4. Results : Coverage Histogram



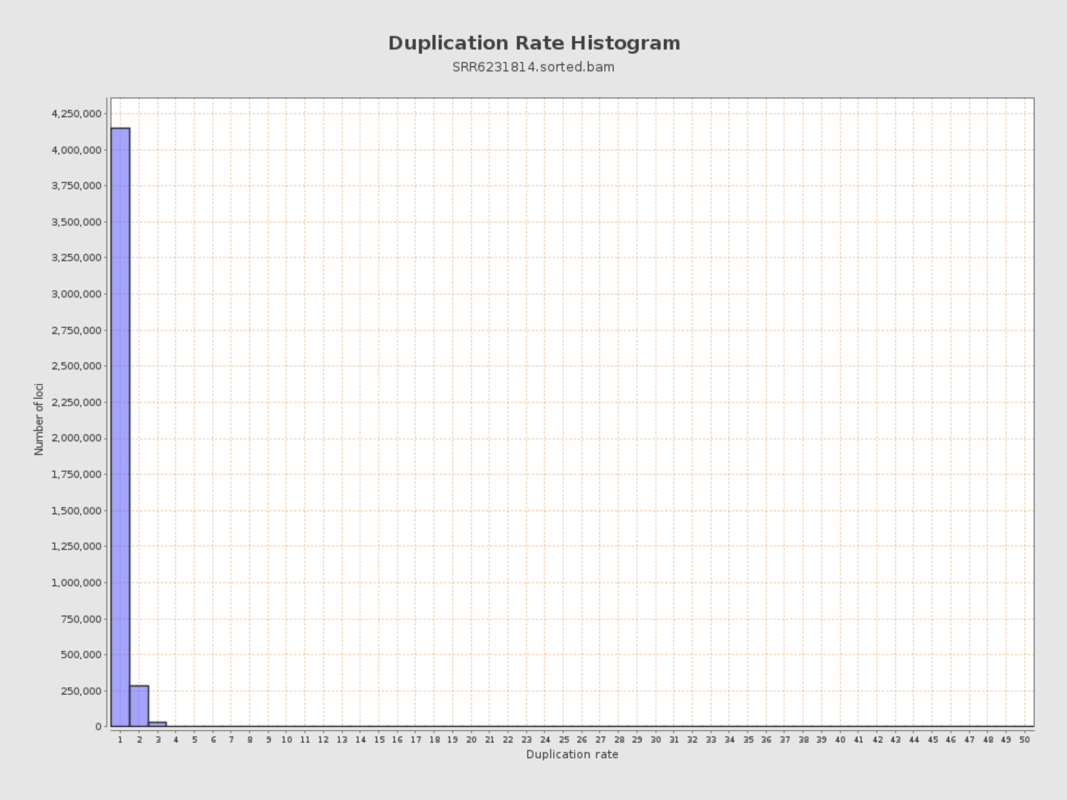
5. Results : Coverage Histogram (0-50X)



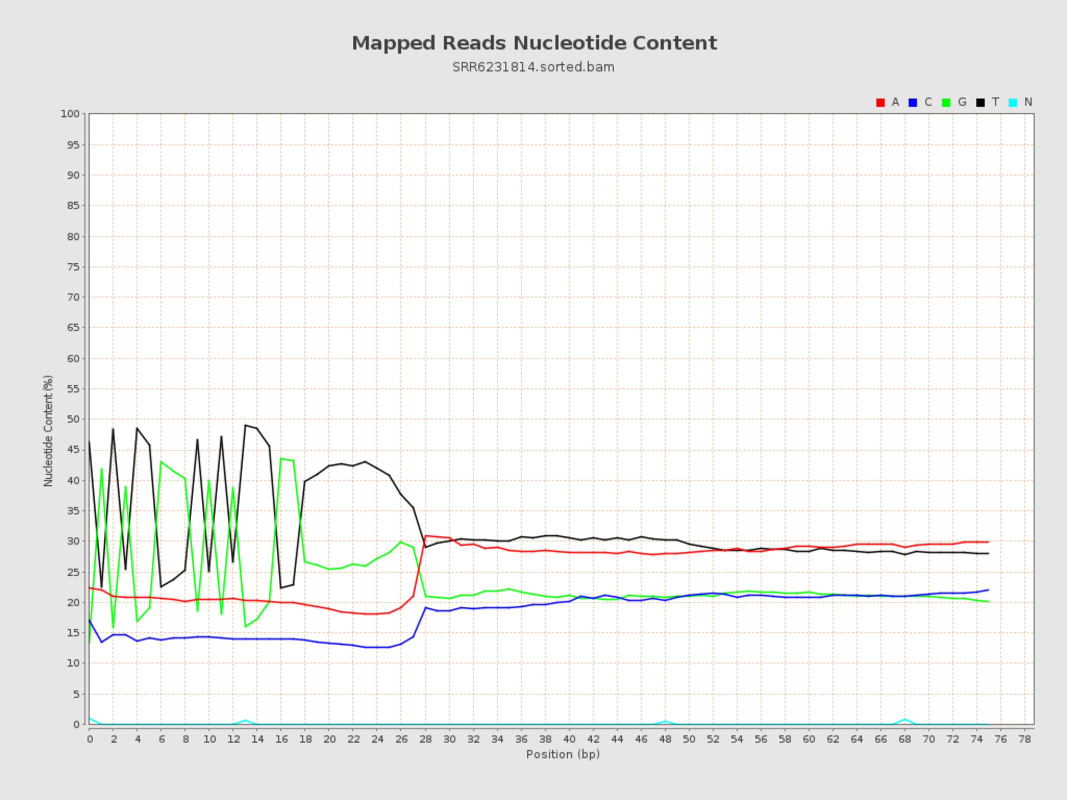
6. Results : Genome Fraction Coverage



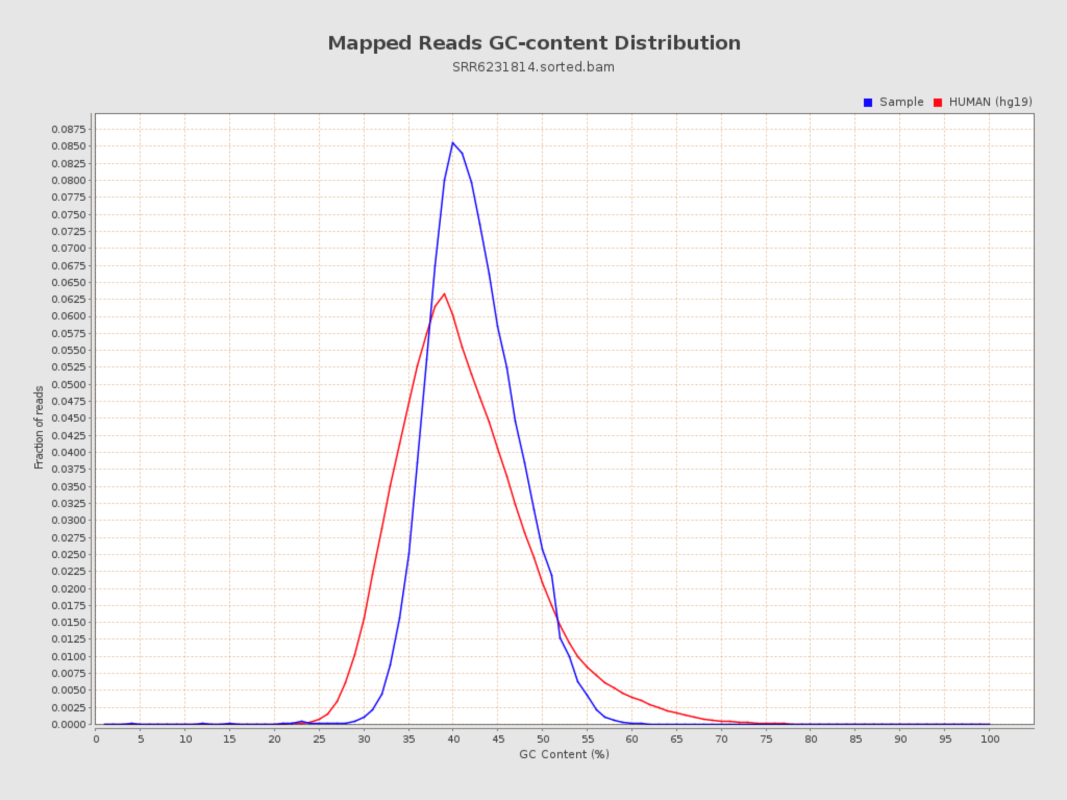
7. Results : Duplication Rate Histogram



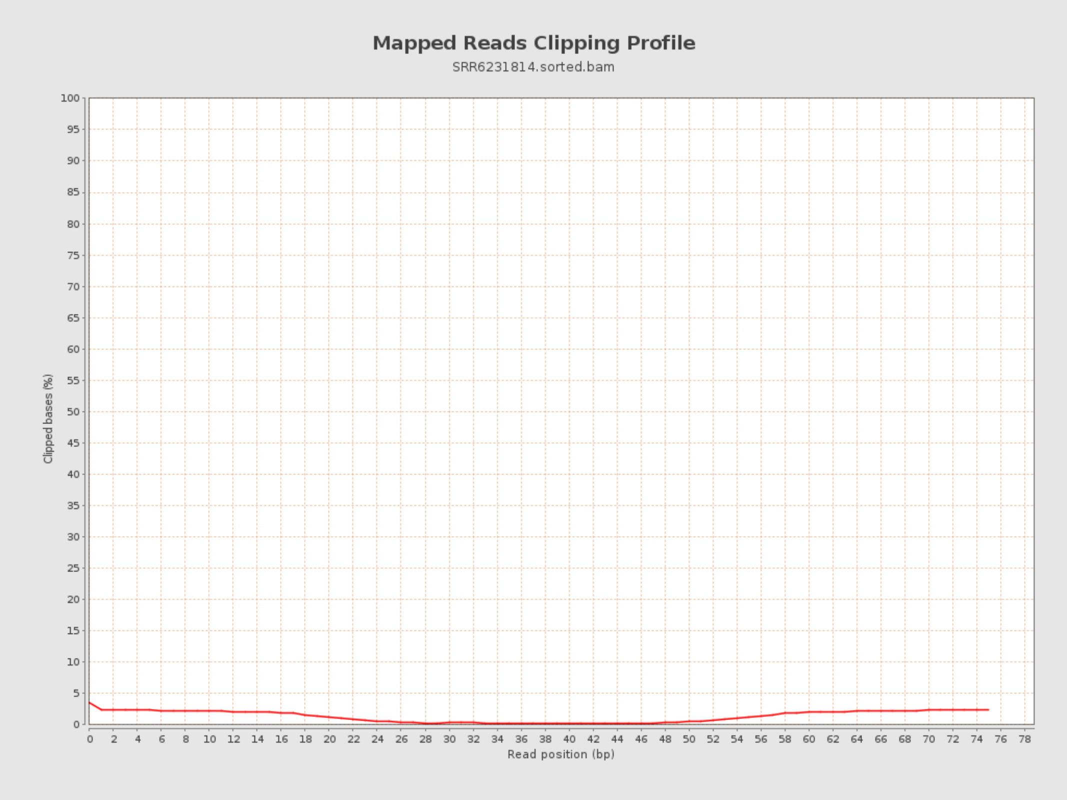
8. Results : Mapped Reads Nucleotide Content



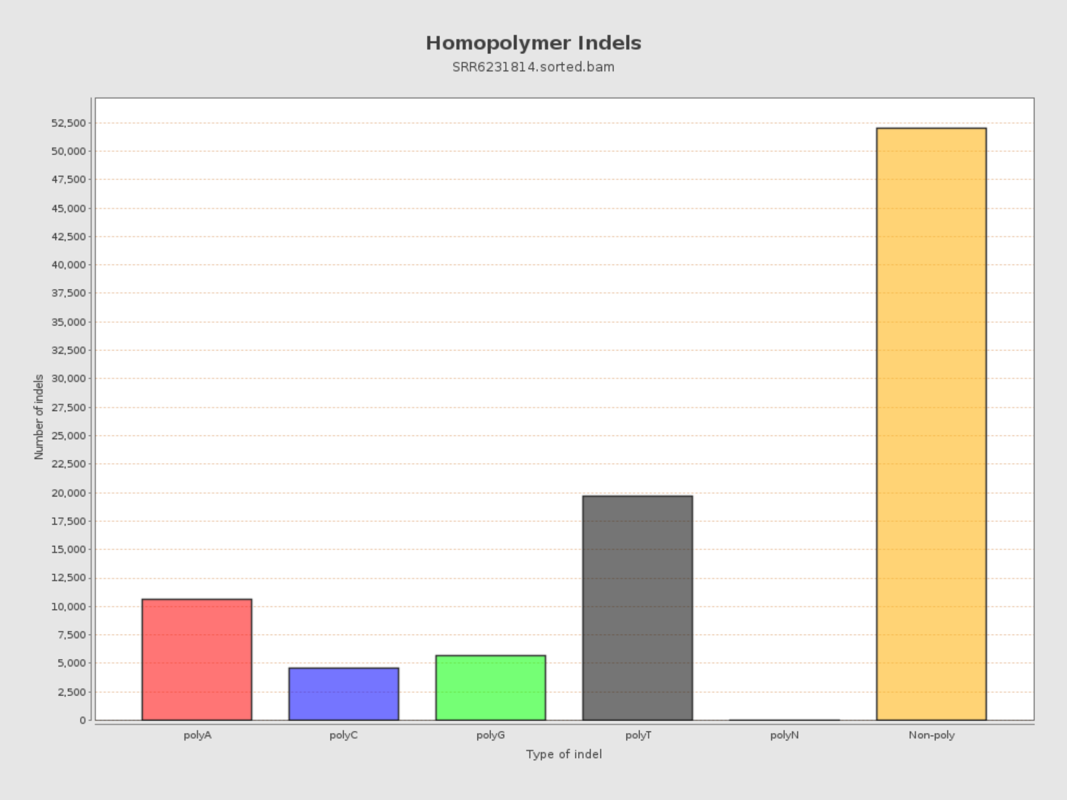
9. Results : Mapped Reads GC-content Distribution



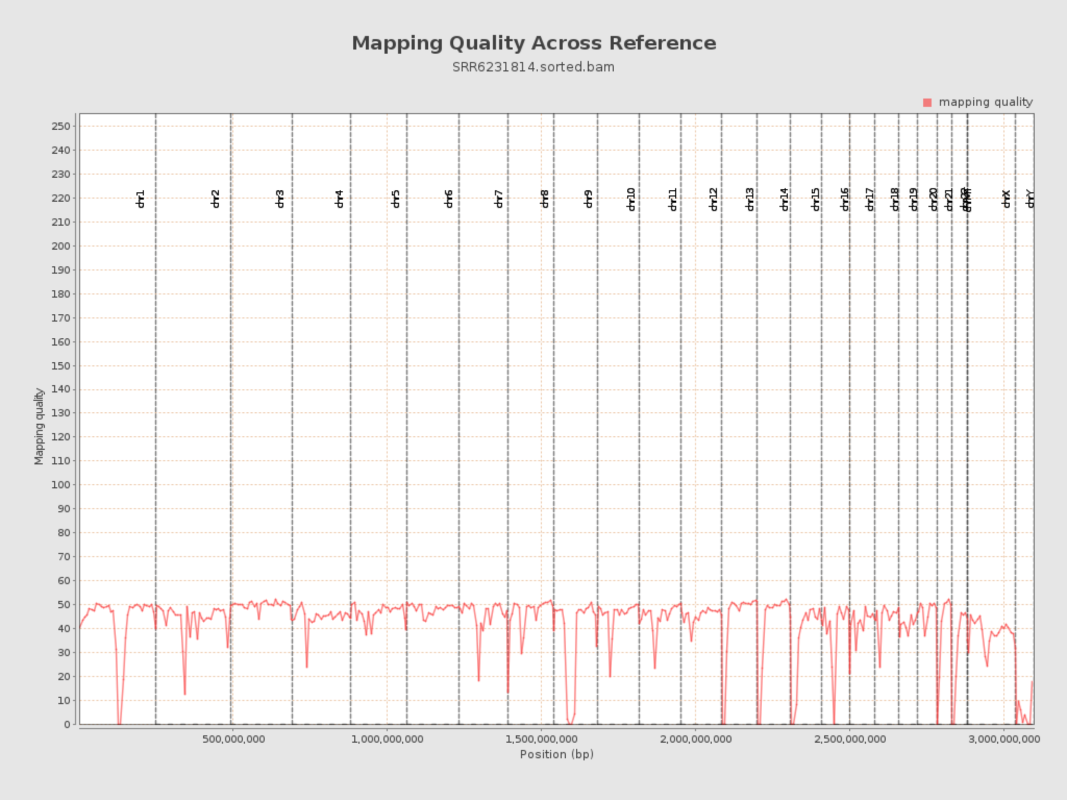
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram