Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:57:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234112.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_SRR6234112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:57:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	681,901
Mapped reads	460,674 / 67.56%
Unmapped reads	221,227 / 32.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,834 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	8,925 / 1.31%
Duplication rate	1.6%
Clipped reads	228,259 / 33.47%

2.2. ACGT Content

Number/percentage of A's	8,431,053 / 28.25%
Number/percentage of C's	5,077,990 / 17.01%
Number/percentage of T's	9,622,428 / 32.24%
Number/percentage of G's	6,710,921 / 22.48%
Number/percentage of N's	5,896 / 0.02%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0096

Standard Deviation	0.1196

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

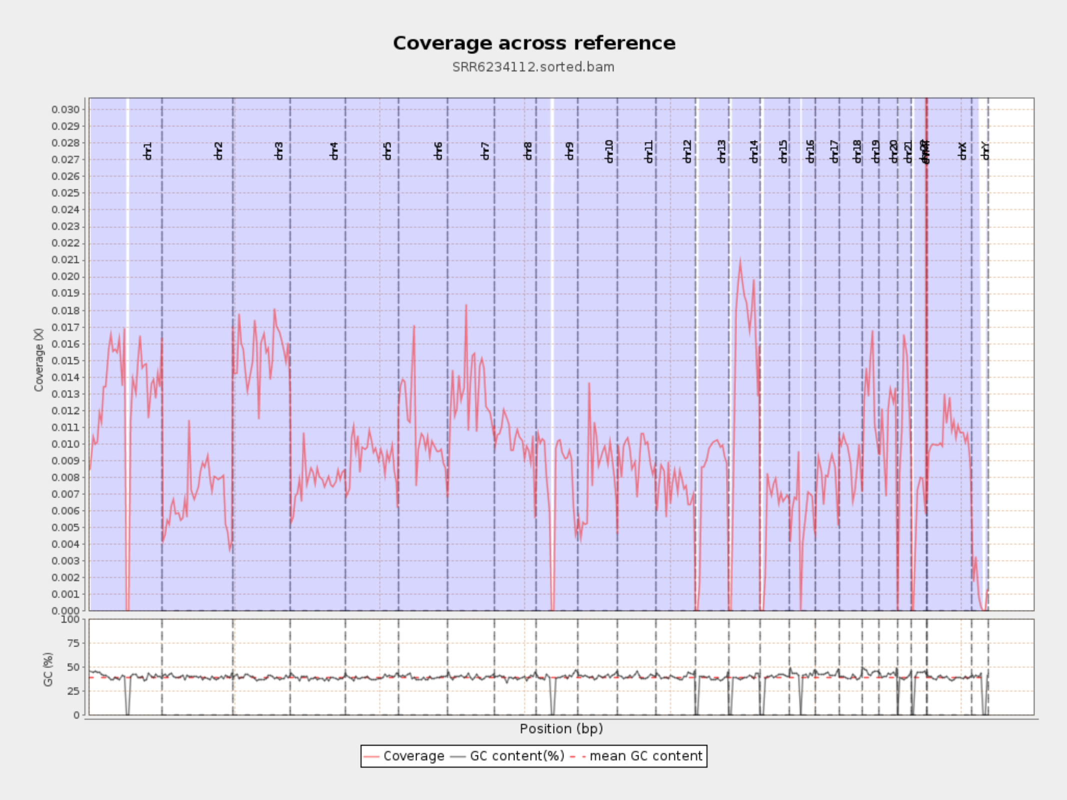
General error rate	0.92%
Mismatches	269,798
Insertions	2,367
Mapped reads with at least one insertion	0.51%
Deletions	7,276
Mapped reads with at least one deletion	1.57%
Homopolymer indels	46.86%

2.6. Chromosome stats

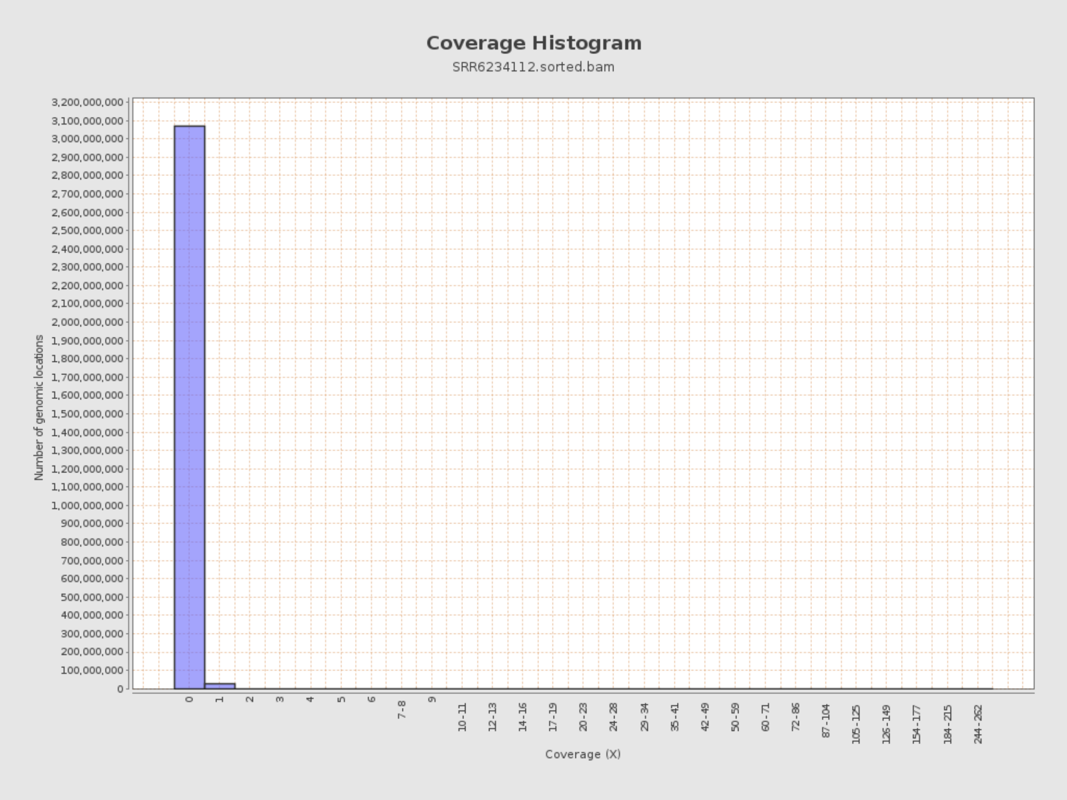
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3181847	0.0128	0.1689
chr2	243199373	1644347	0.0068	0.1079
chr3	198022430	3062626	0.0155	0.129
chr4	191154276	1480383	0.0077	0.092
chr5	180915260	1673233	0.0092	0.0996
chr6	171115067	1861666	0.0109	0.1149
chr7	159138663	2087899	0.0131	0.1527

chr8	146364022	1479304	0.0101	0.1884
chr9	141213431	1116514	0.0079	0.1006
chr10	135534747	1124813	0.0083	0.1083
chr11	135006516	1237182	0.0092	0.1053
chr12	133851895	981612	0.0073	0.0889
chr13	115169878	907012	0.0079	0.092
chr14	107349540	1605169	0.015	0.1279
chr15	102531392	590920	0.0058	0.0787
chr16	90354753	523593	0.0058	0.0822
chr17	81195210	638303	0.0079	0.0929
chr18	78077248	704453	0.009	0.1398
chr19	59128983	759814	0.0129	0.1359
chr20	63025520	685945	0.0109	0.1084
chr21	48129895	534394	0.0111	0.1107
chr22	51304566	269072	0.0052	0.0751
chrMT	16571	24483	1.4775	1.5643
chrX	155270560	1613663	0.0104	0.1074
chrY	59373566	72690	0.0012	0.0389

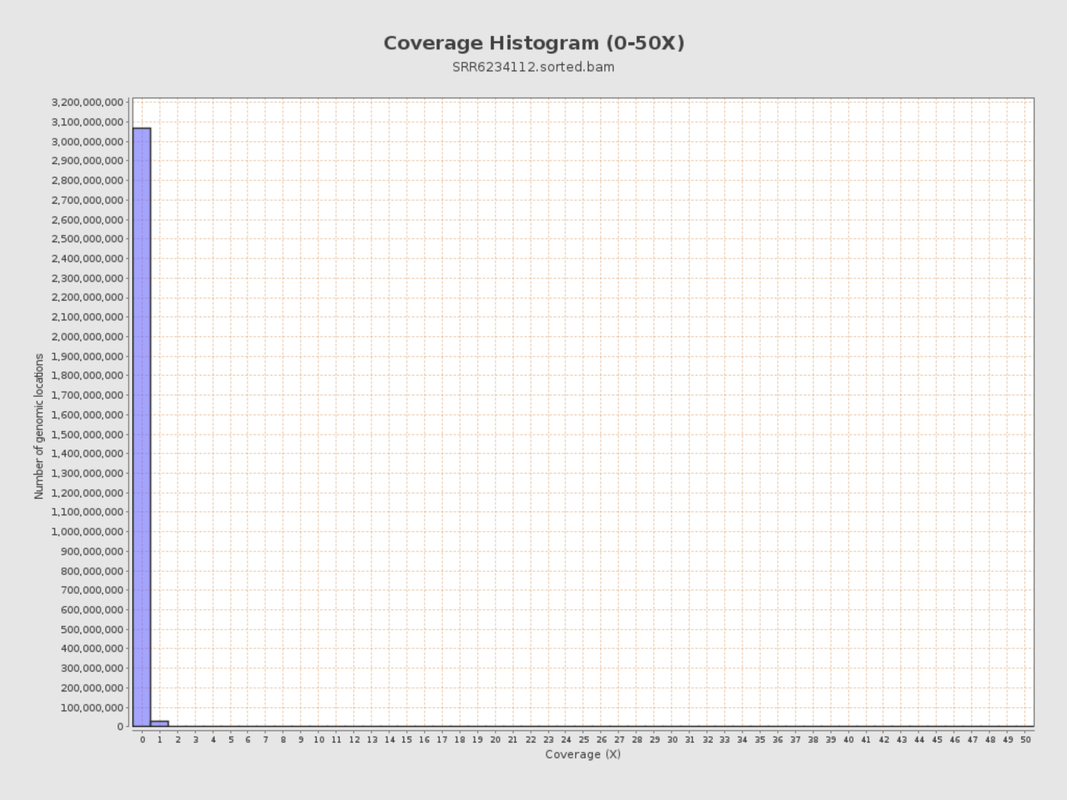
3. Results : Coverage across reference



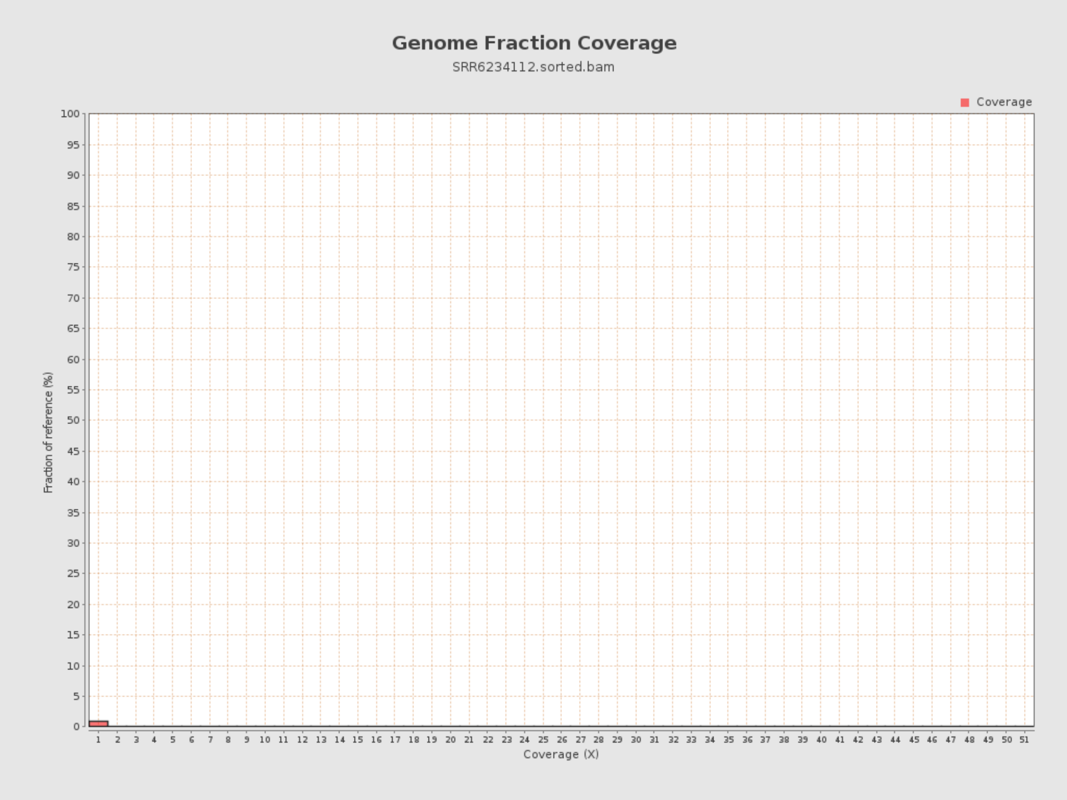
4. Results : Coverage Histogram



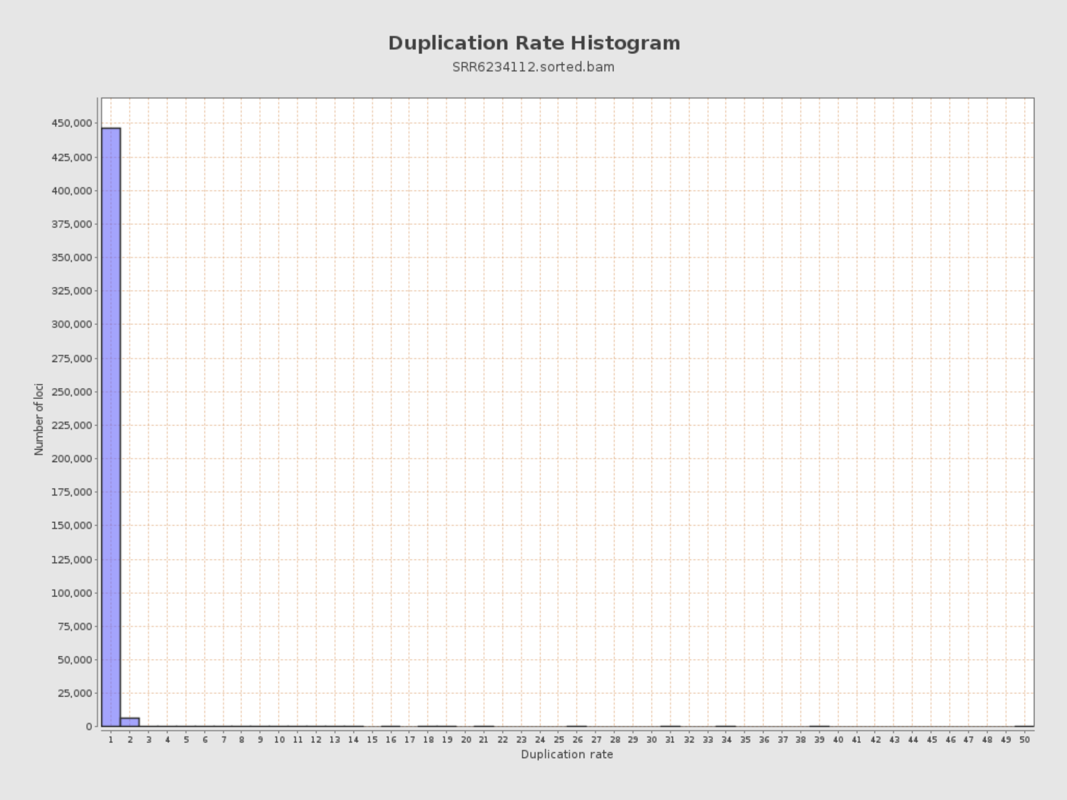
5. Results : Coverage Histogram (0-50X)



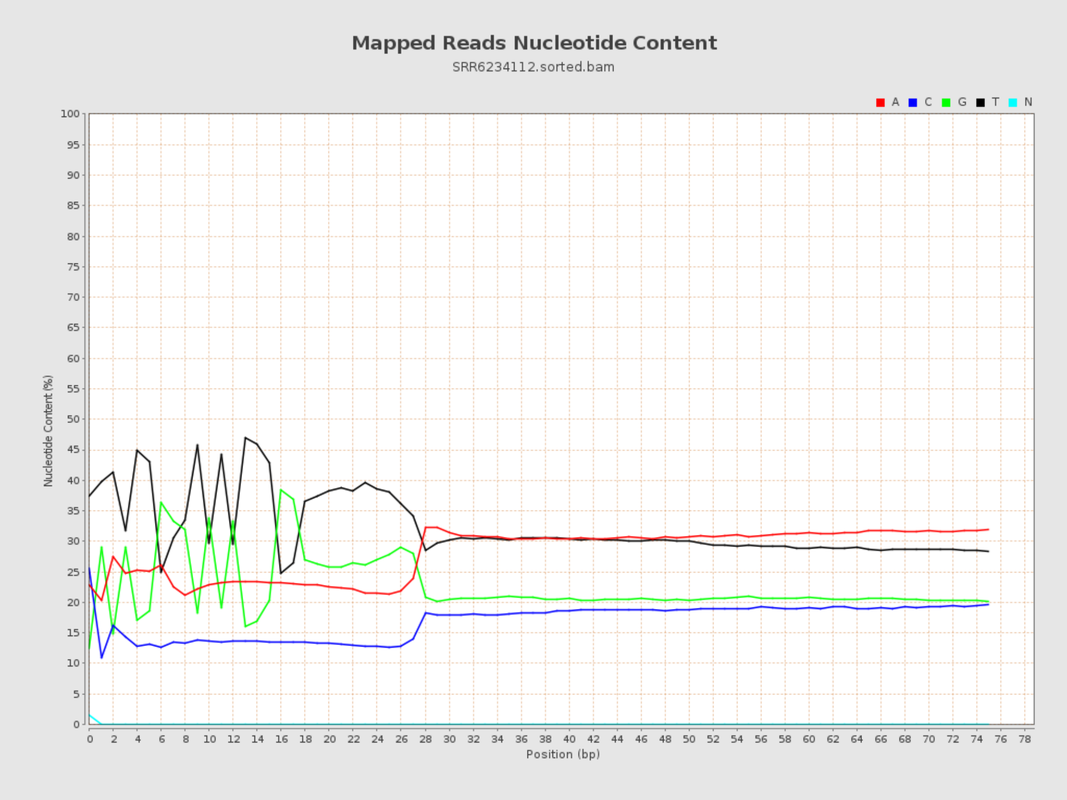
6. Results : Genome Fraction Coverage



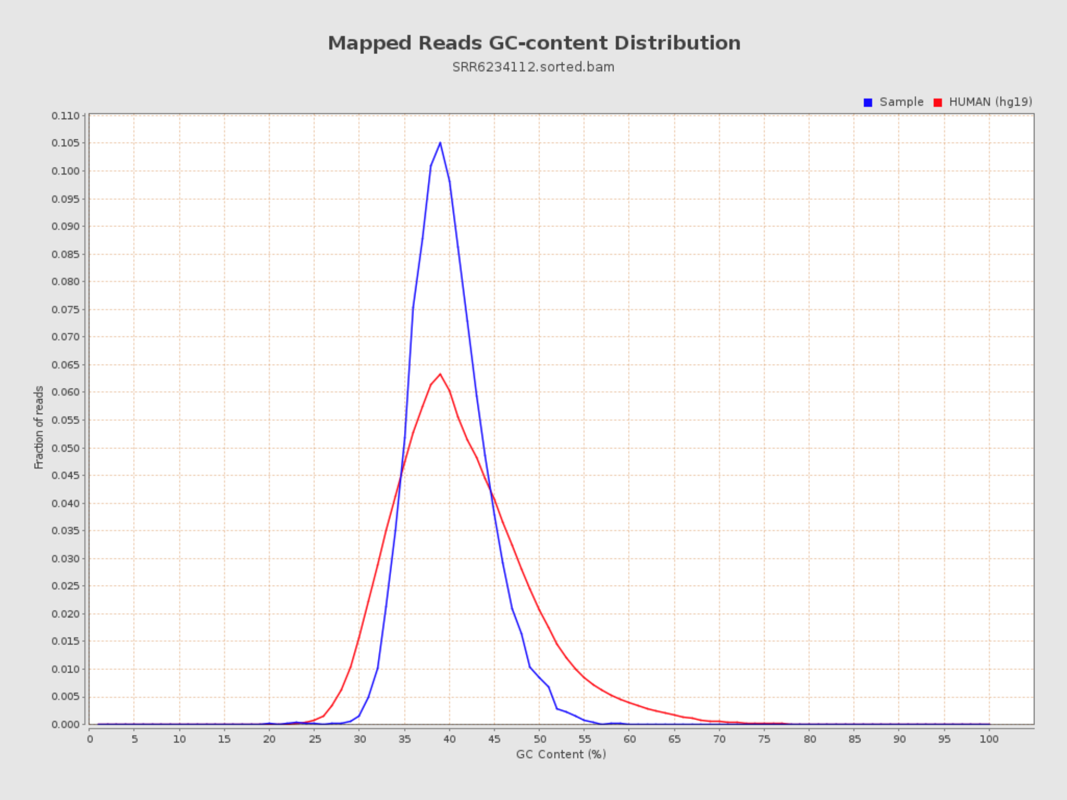
7. Results : Duplication Rate Histogram



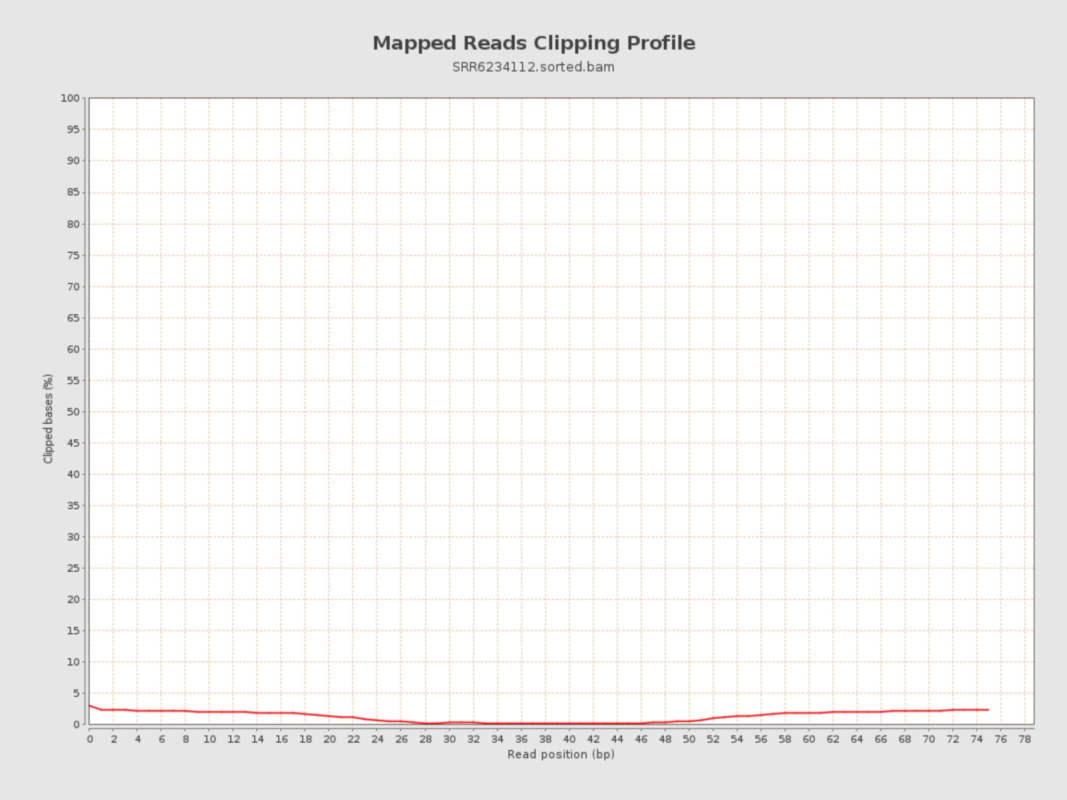
8. Results : Mapped Reads Nucleotide Content



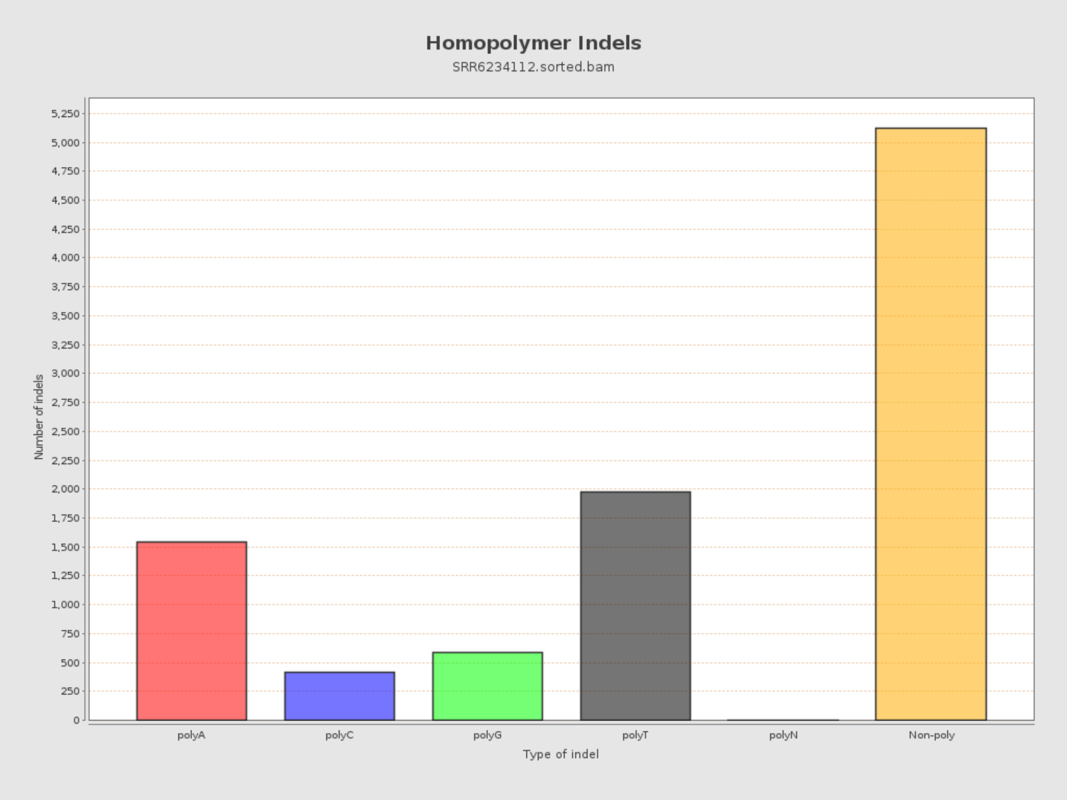
9. Results : Mapped Reads GC-content Distribution



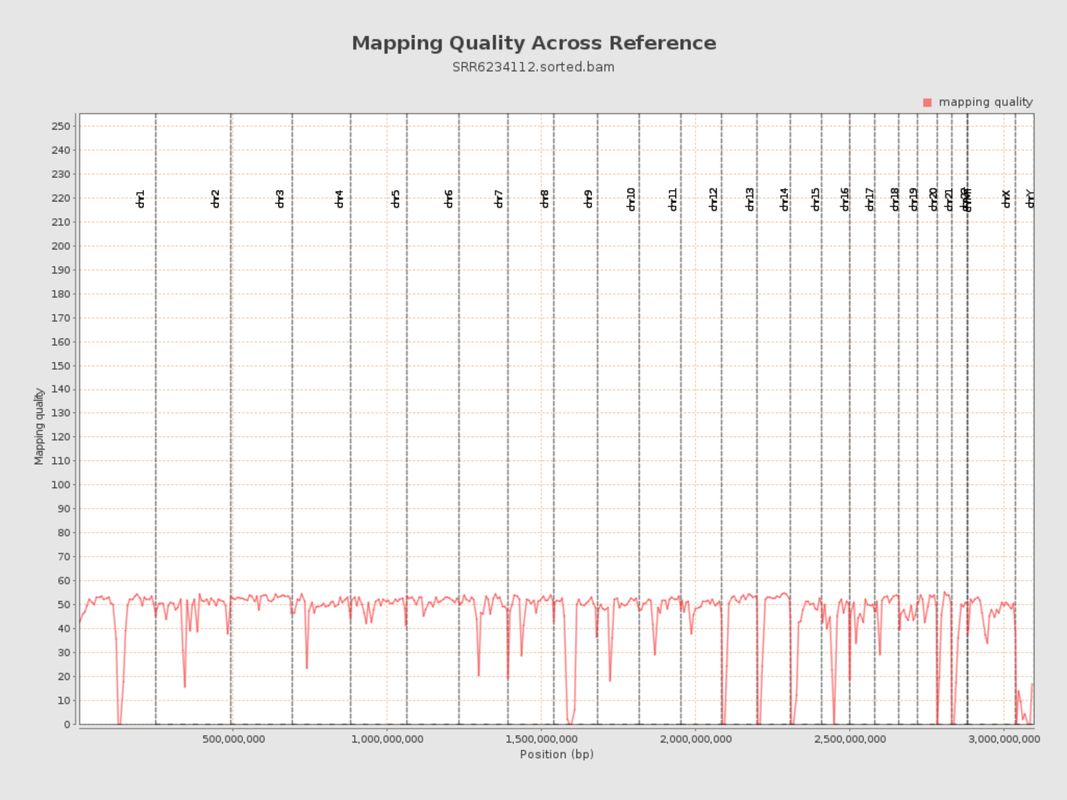
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram