Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:19:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234139.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_SRR6234139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:19:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,899
Mapped reads	1,702,454 / 88.12%
Unmapped reads	229,445 / 11.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,762 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	63,124 / 3.27%
Duplication rate	1.76%
Clipped reads	844,480 / 43.71%

2.2. ACGT Content

Number/percentage of A's	29,928,270 / 26.71%
Number/percentage of C's	21,476,980 / 19.17%
Number/percentage of T's	33,595,783 / 29.98%
Number/percentage of G's	27,034,824 / 24.12%
Number/percentage of N's	27,573 / 0.02%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.5581

2.4. Mapping Quality

Mean Mapping Quality	39.95

2.5. Mismatches and indels

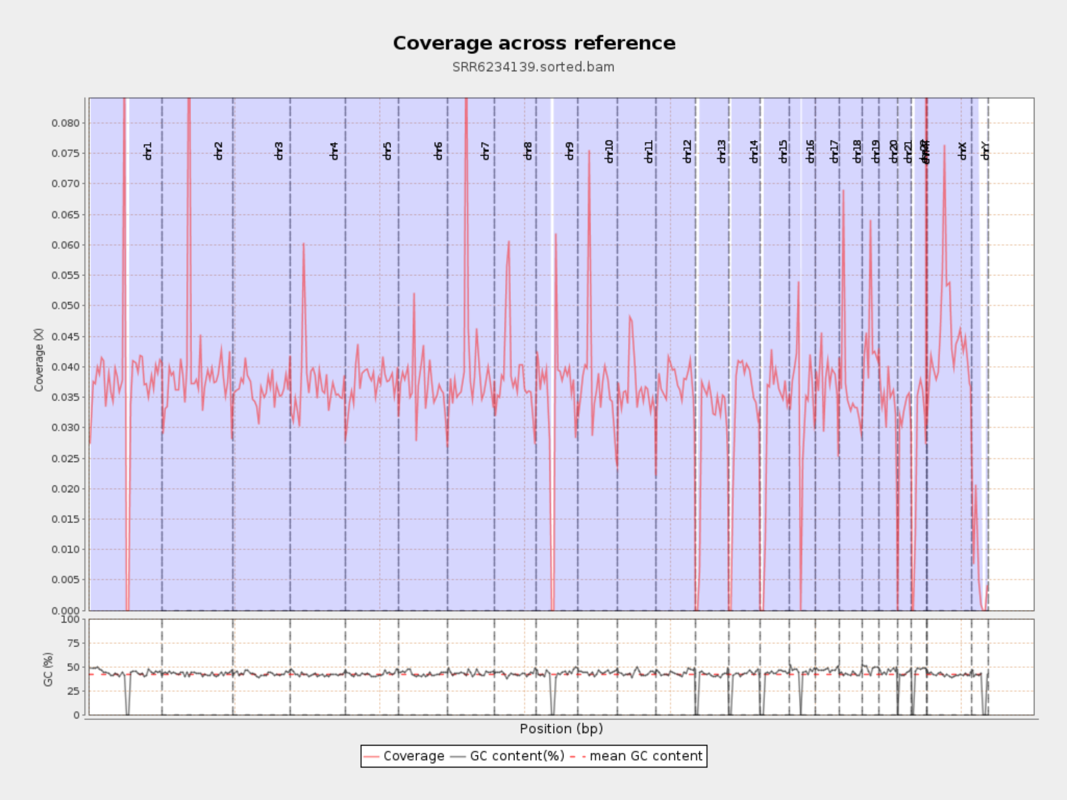
General error rate	0.85%
Mismatches	936,578
Insertions	9,788
Mapped reads with at least one insertion	0.57%
Deletions	25,997
Mapped reads with at least one deletion	1.51%
Homopolymer indels	44.27%

2.6. Chromosome stats

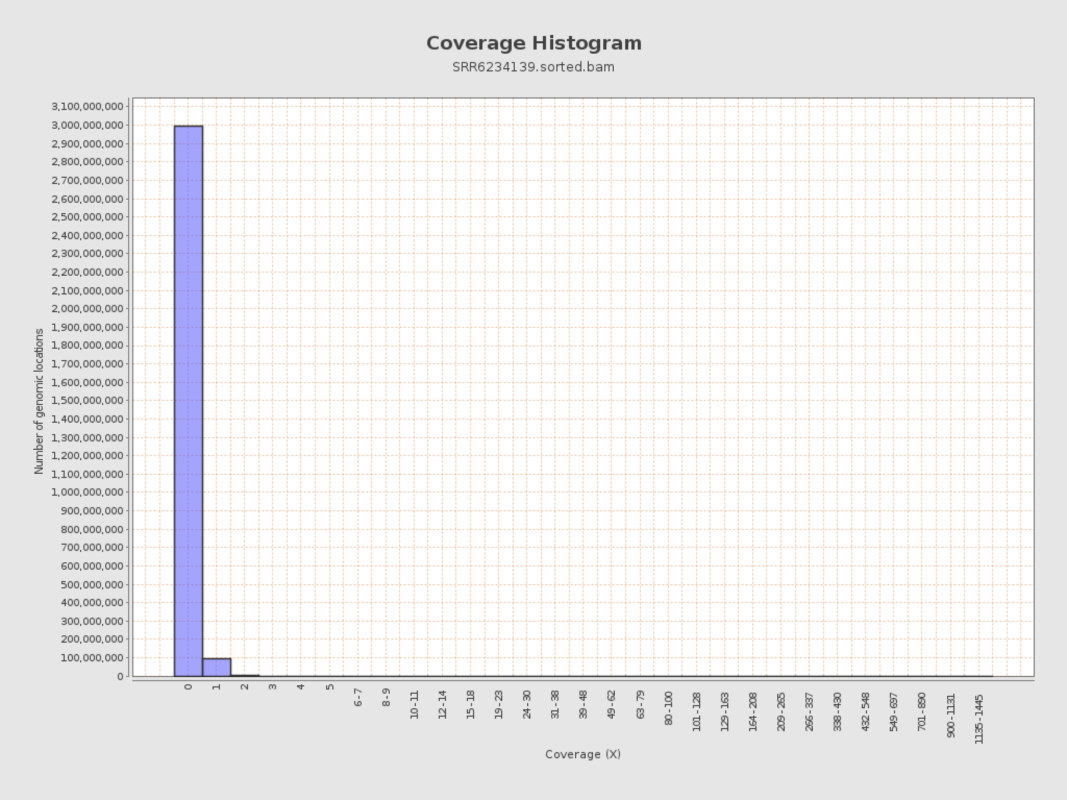
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9323256	0.0374	1.2573
chr2	243199373	9724164	0.04	0.6558
chr3	198022430	7203686	0.0364	0.2113
chr4	191154276	7068175	0.037	0.2564
chr5	180915260	6806316	0.0376	0.2169
chr6	171115067	6328710	0.037	0.2919
chr7	159138663	6467963	0.0406	0.8379

chr8	146364022	5624939	0.0384	0.5685
chr9	141213431	4875759	0.0345	0.4802
chr10	135534747	5103103	0.0377	0.4229
chr11	135006516	4920147	0.0364	0.4511
chr12	133851895	5005211	0.0374	0.2235
chr13	115169878	3307436	0.0287	0.1828
chr14	107349540	3419337	0.0319	0.2528
chr15	102531392	3067142	0.0299	0.2206
chr16	90354753	3098015	0.0343	0.2608
chr17	81195210	3030707	0.0373	0.2793
chr18	78077248	2935245	0.0376	0.9946
chr19	59128983	2621518	0.0443	0.8492
chr20	63025520	2163702	0.0343	0.2328
chr21	48129895	1428285	0.0297	0.2279
chr22	51304566	1244180	0.0243	0.1664
chrMT	16571	16159	0.9751	1.0209
chrX	155270560	6947379	0.0447	0.2986
chrY	59373566	377323	0.0064	0.1661

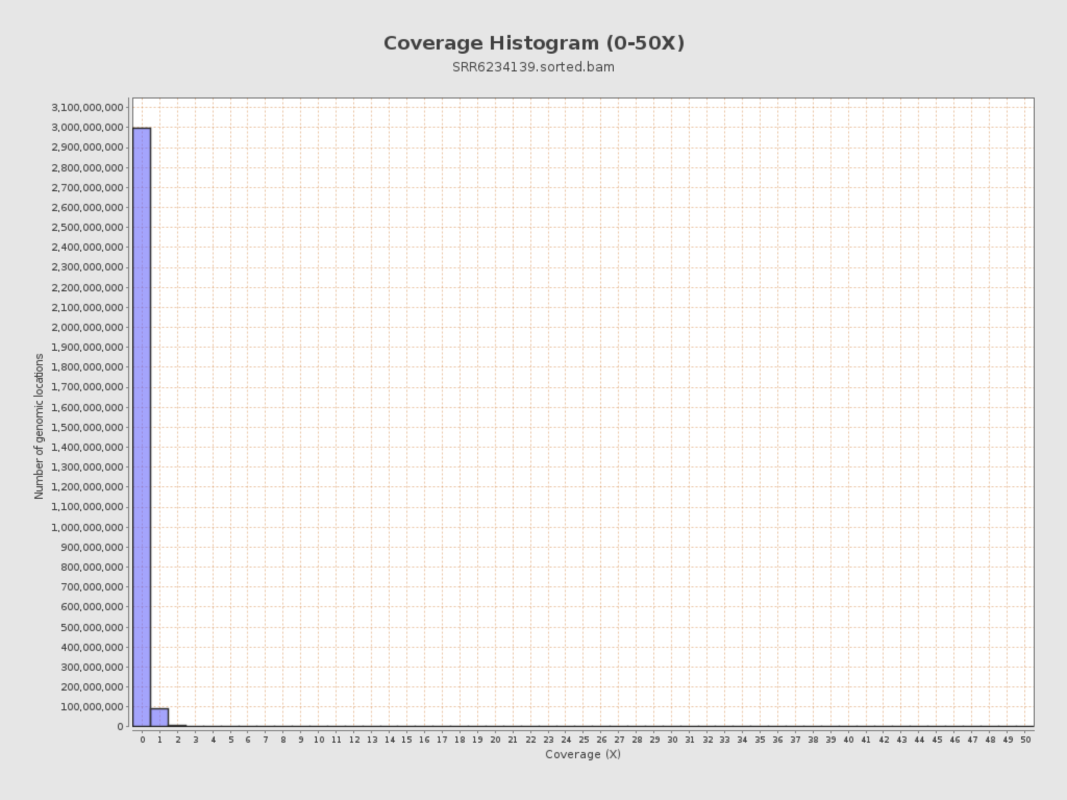
3. Results : Coverage across reference



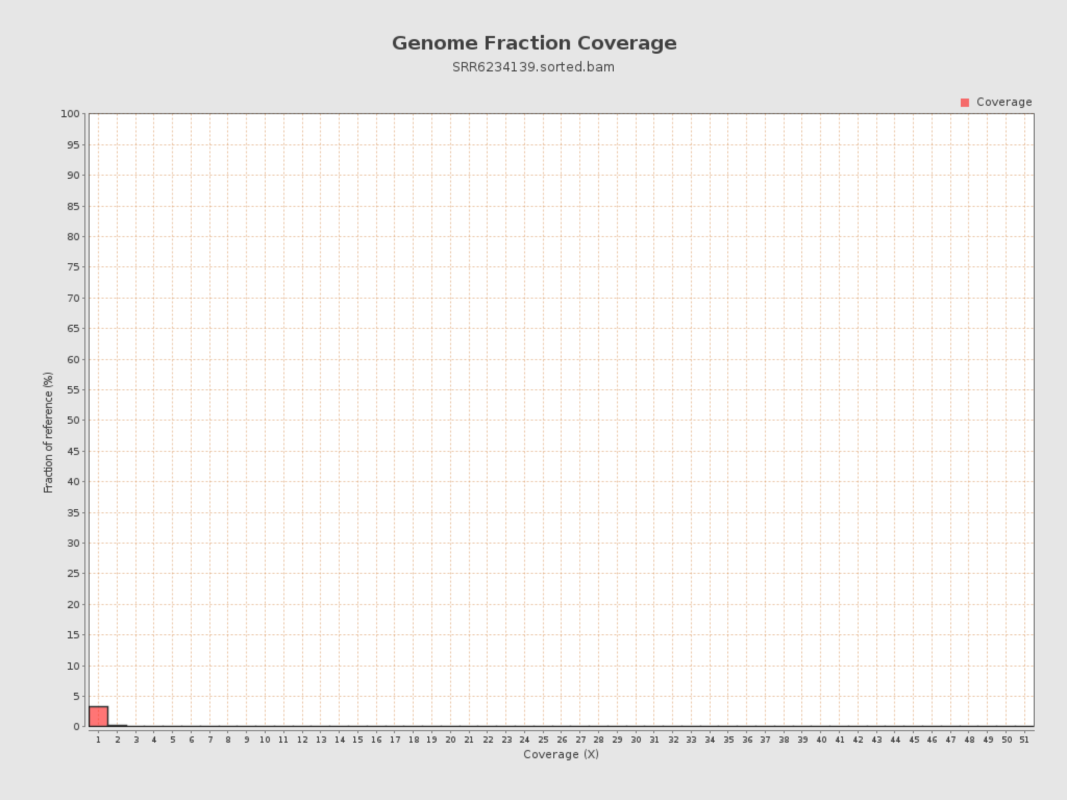
4. Results : Coverage Histogram



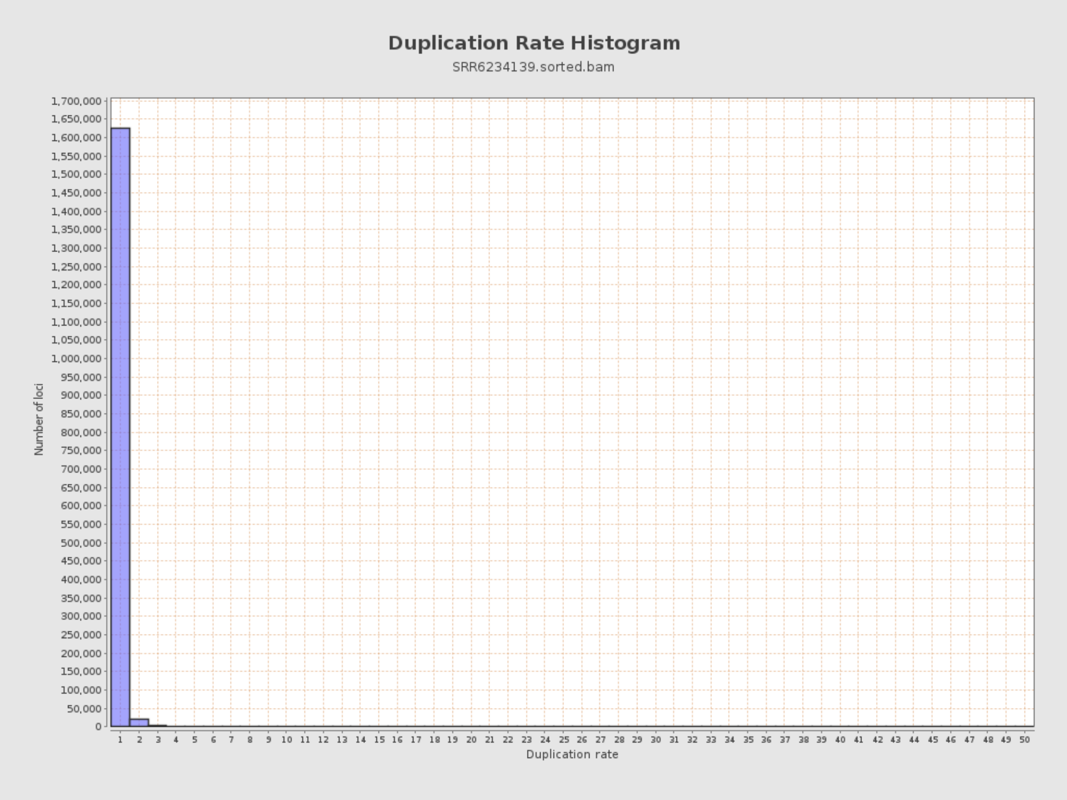
5. Results : Coverage Histogram (0-50X)



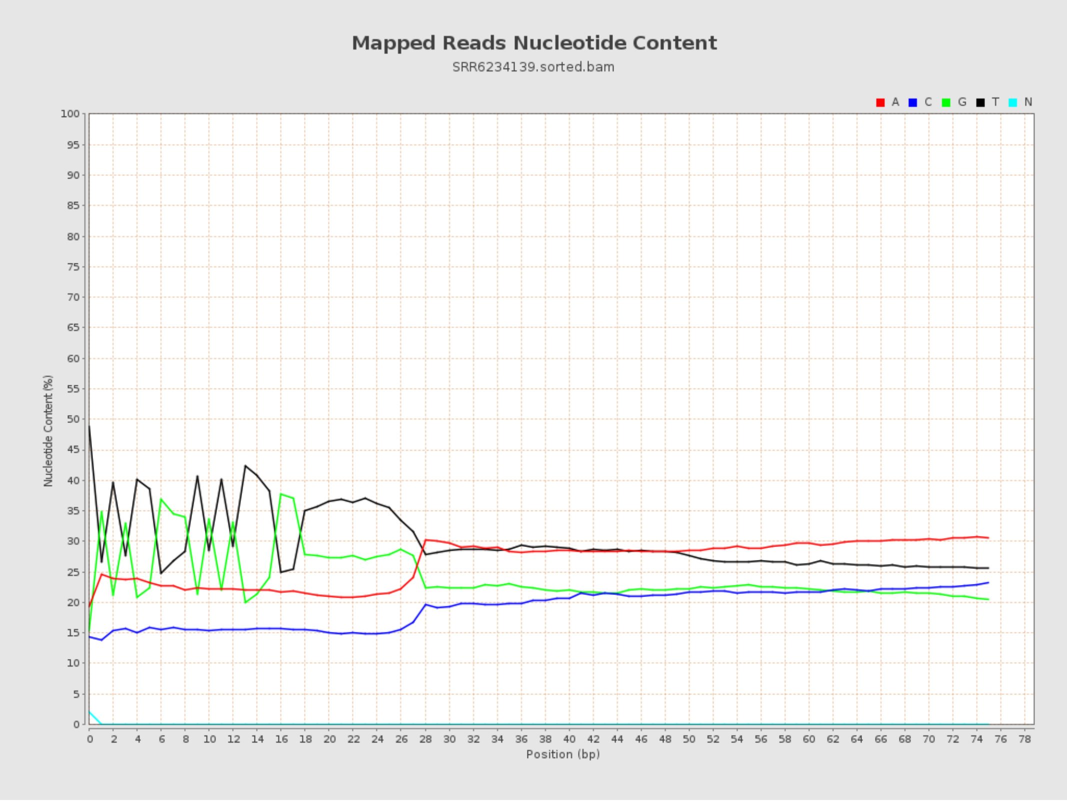
6. Results : Genome Fraction Coverage



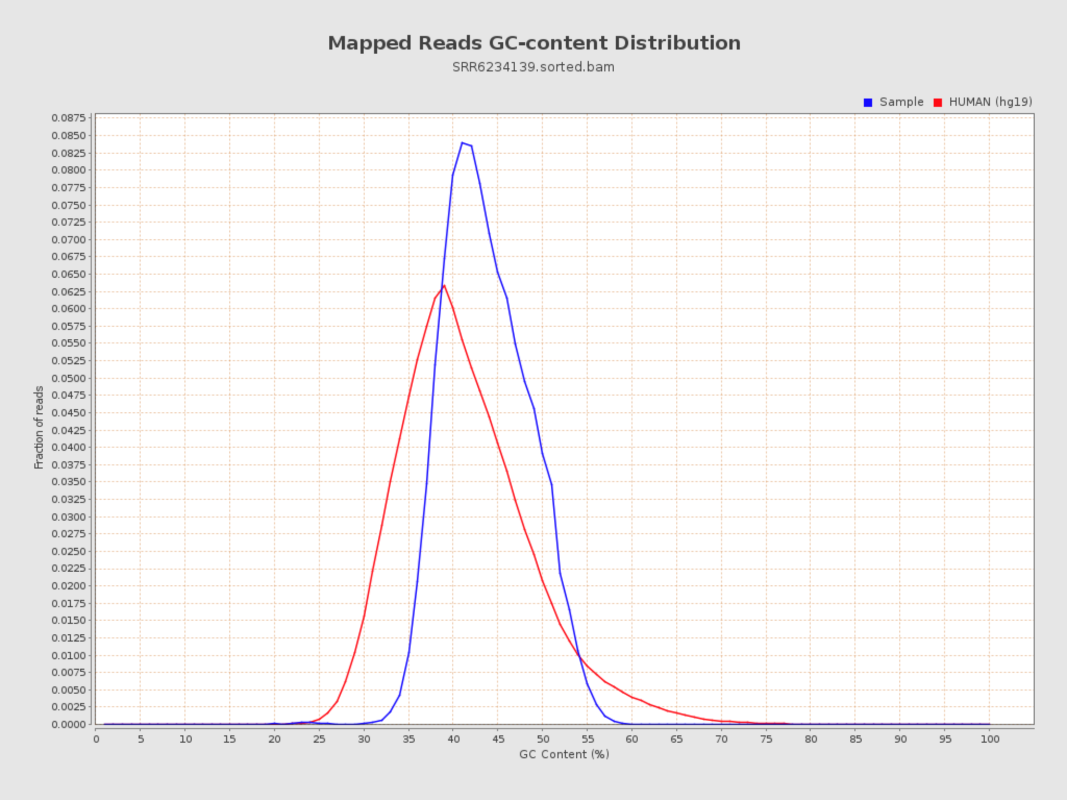
7. Results : Duplication Rate Histogram



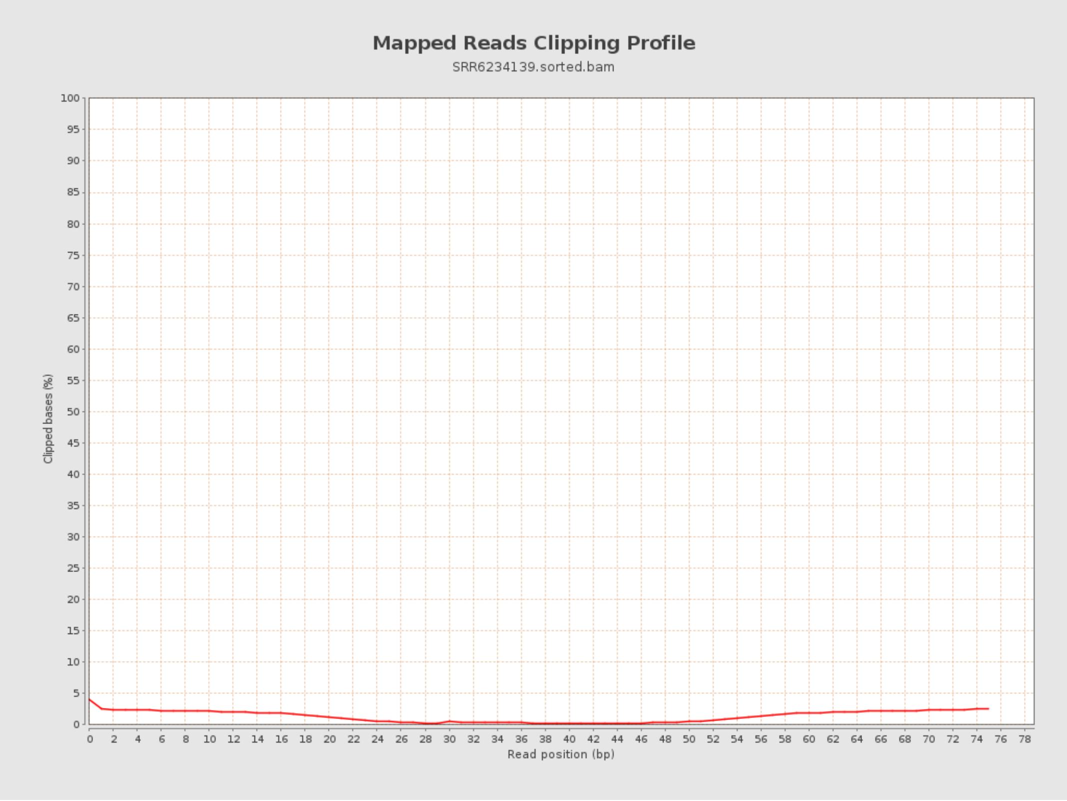
8. Results : Mapped Reads Nucleotide Content



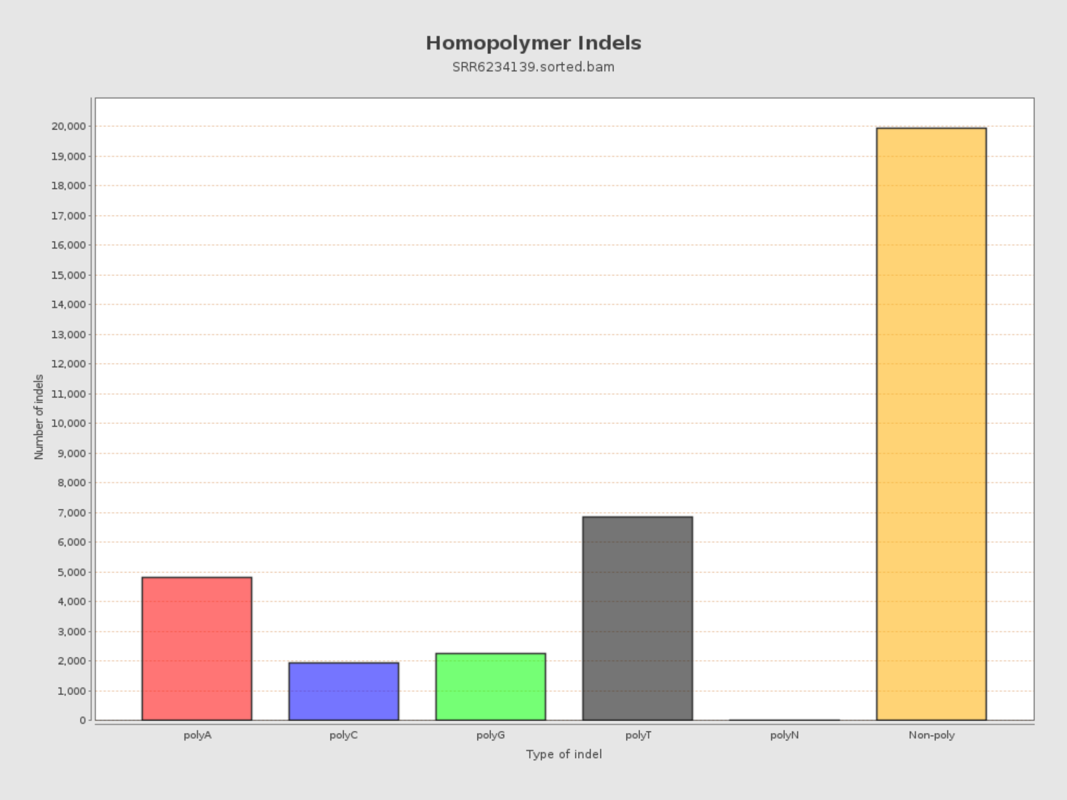
9. Results : Mapped Reads GC-content Distribution



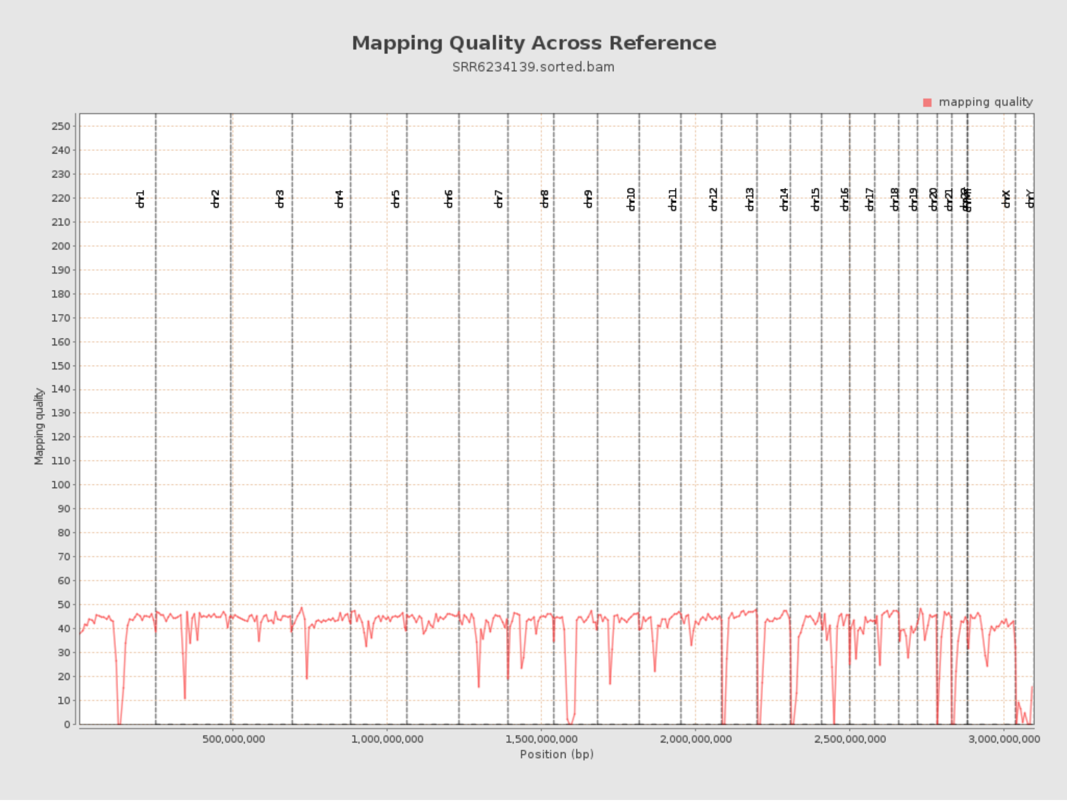
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram