Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:22:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234076.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_SRR6234076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:22:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,735,649
Mapped reads	4,477,923 / 94.56%
Unmapped reads	257,726 / 5.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,647 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	544,332 / 11.49%
Duplication rate	10.17%
Clipped reads	2,353,611 / 49.7%

2.2. ACGT Content

Number/percentage of A's	75,773,693 / 26.17%
Number/percentage of C's	52,867,660 / 18.26%
Number/percentage of T's	93,242,379 / 32.2%
Number/percentage of G's	67,645,068 / 23.36%
Number/percentage of N's	27,973 / 0.01%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0936

Standard Deviation	0.9316

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

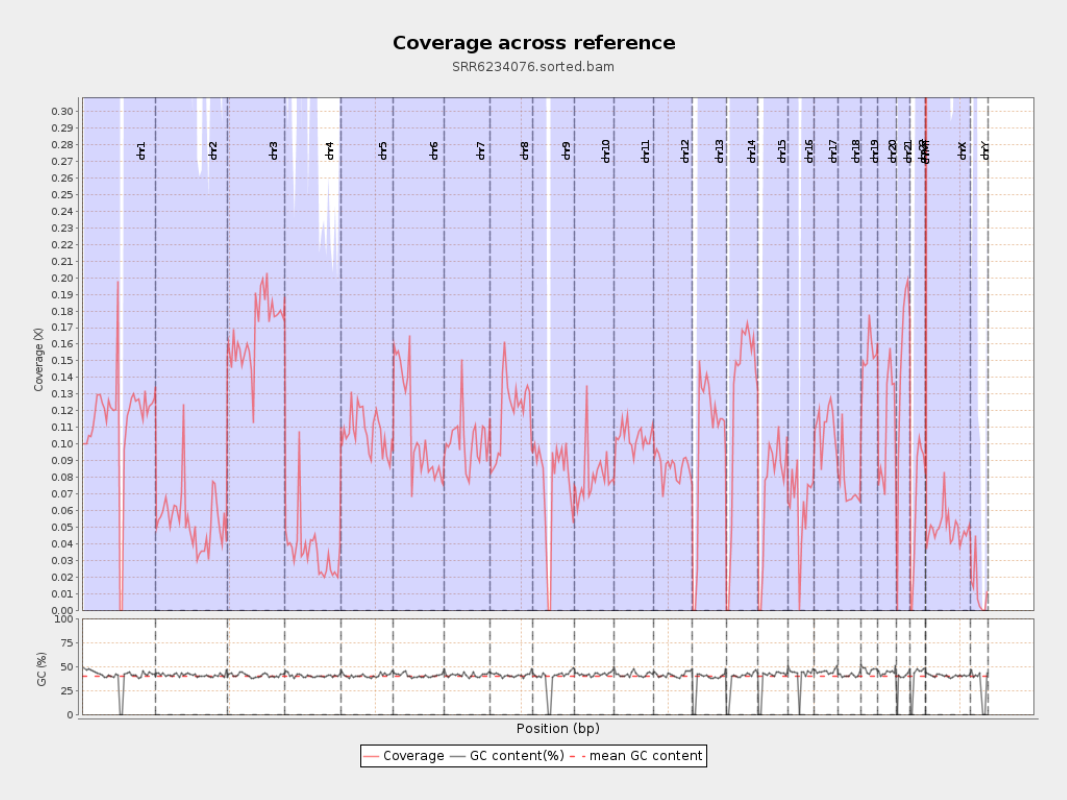
General error rate	0.56%
Mismatches	1,570,979
Insertions	19,753
Mapped reads with at least one insertion	0.44%
Deletions	63,681
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.7%

2.6. Chromosome stats

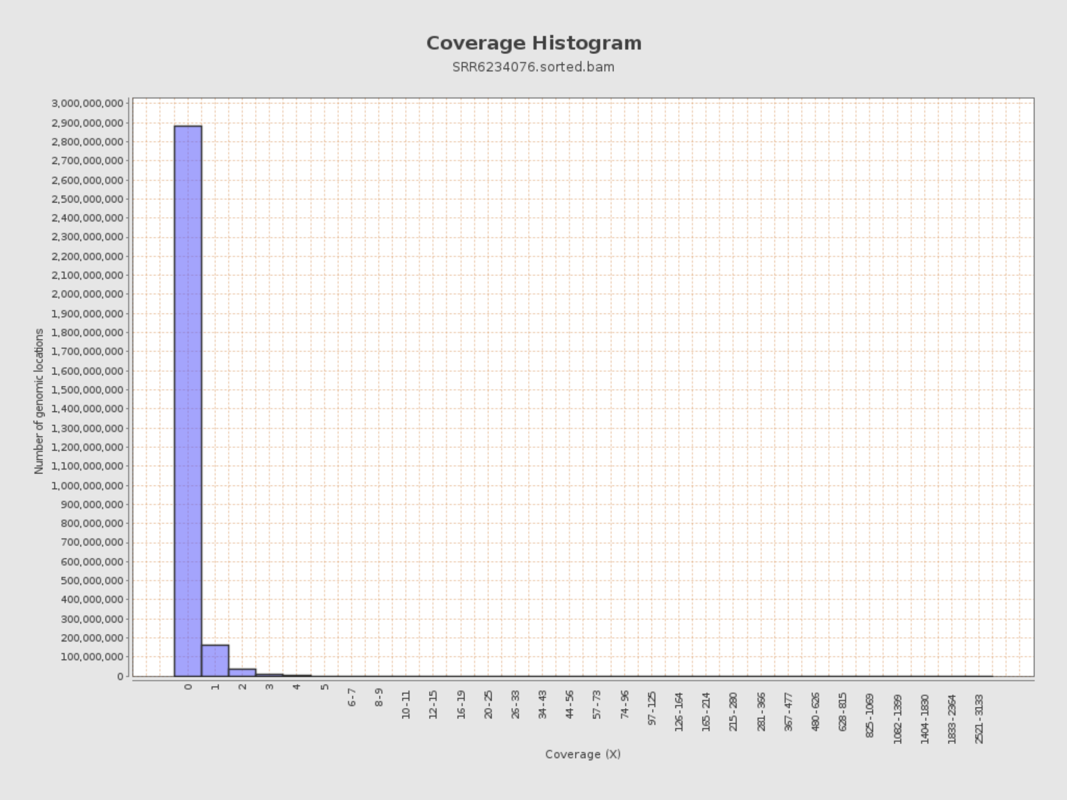
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28467690	0.1142	2.0105
chr2	243199373	13181475	0.0542	1.4628
chr3	198022430	33382464	0.1686	0.5348
chr4	191154276	6838770	0.0358	0.3554
chr5	180915260	19364332	0.107	0.4372
chr6	171115067	18537575	0.1083	0.6319
chr7	159138663	16255150	0.1021	0.9148

chr8	146364022	17332485	0.1184	1.1644
chr9	141213431	10808099	0.0765	0.5927
chr10	135534747	10855229	0.0801	0.7021
chr11	135006516	14002572	0.1037	0.7515
chr12	133851895	11608124	0.0867	0.3953
chr13	115169878	12027549	0.1044	0.46
chr14	107349540	13815213	0.1287	0.5072
chr15	102531392	7462099	0.0728	0.3706
chr16	90354753	5658609	0.0626	0.427
chr17	81195210	9084798	0.1119	0.5123
chr18	78077248	5855608	0.075	1.522
chr19	59128983	9091777	0.1538	1.0932
chr20	63025520	6932980	0.11	0.4894
chr21	48129895	7125665	0.1481	0.5405
chr22	51304566	3383567	0.066	0.3211
chrMT	16571	241058	14.547	9.7094
chrX	155270560	7654643	0.0493	0.405
chrY	59373566	700582	0.0118	0.3104

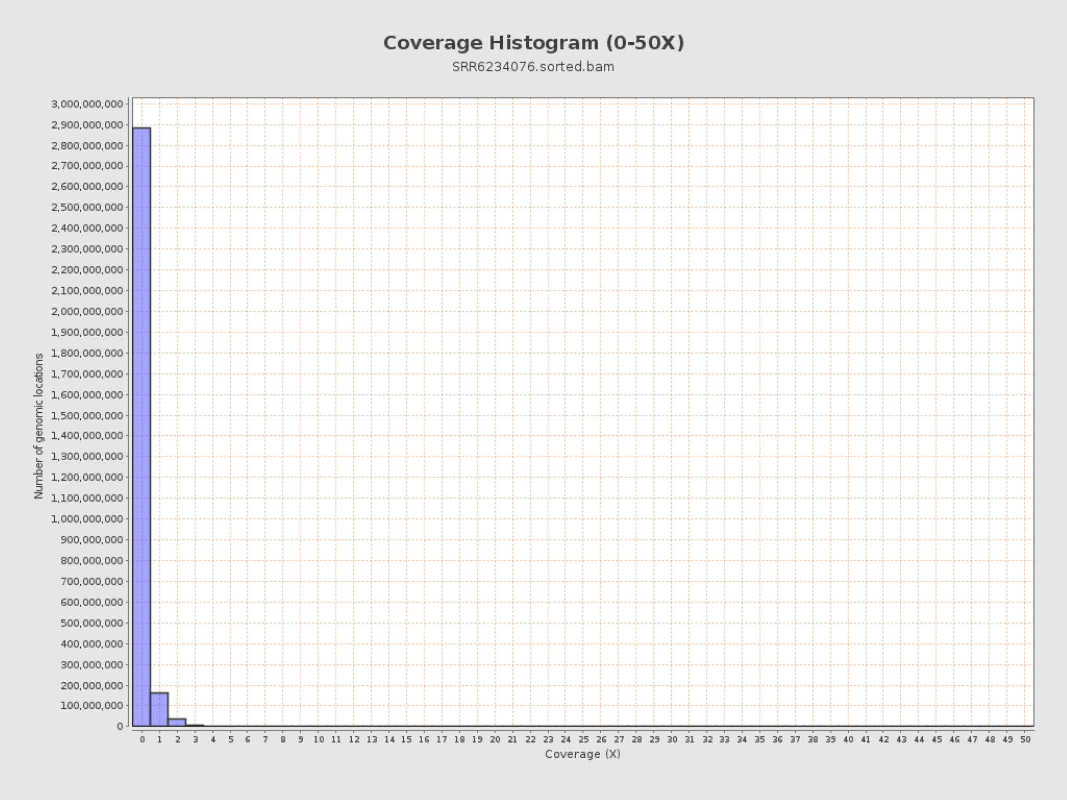
3. Results : Coverage across reference



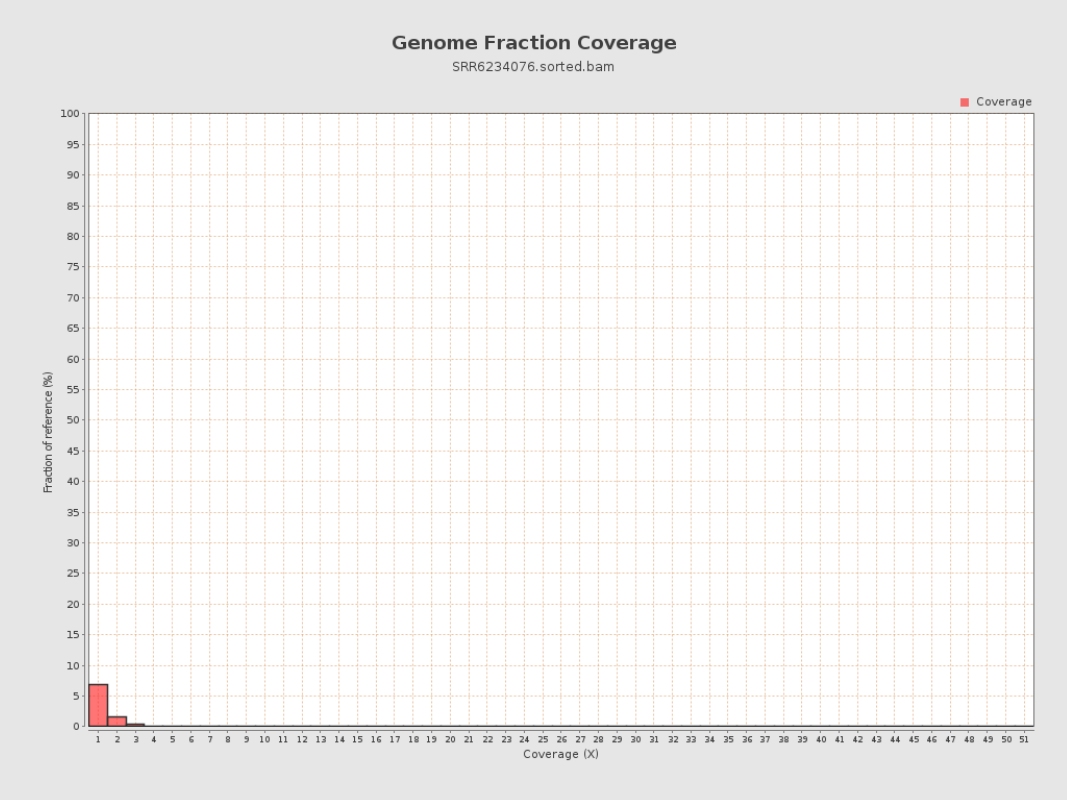
4. Results : Coverage Histogram



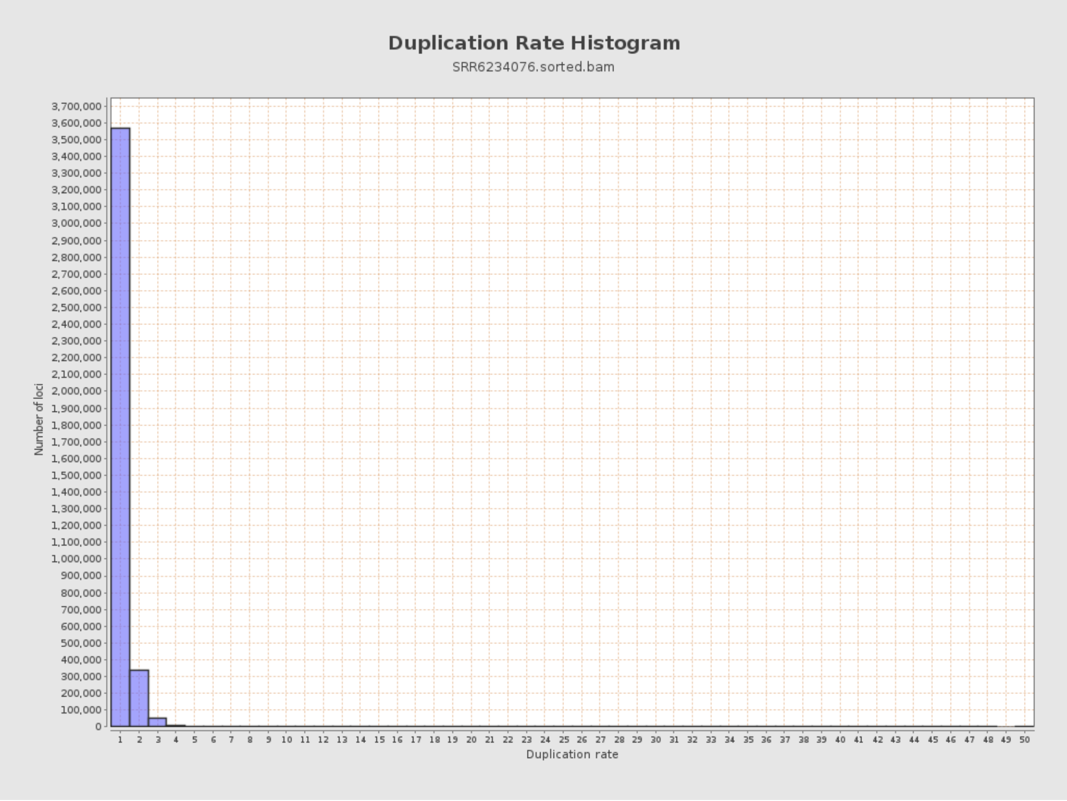
5. Results : Coverage Histogram (0-50X)



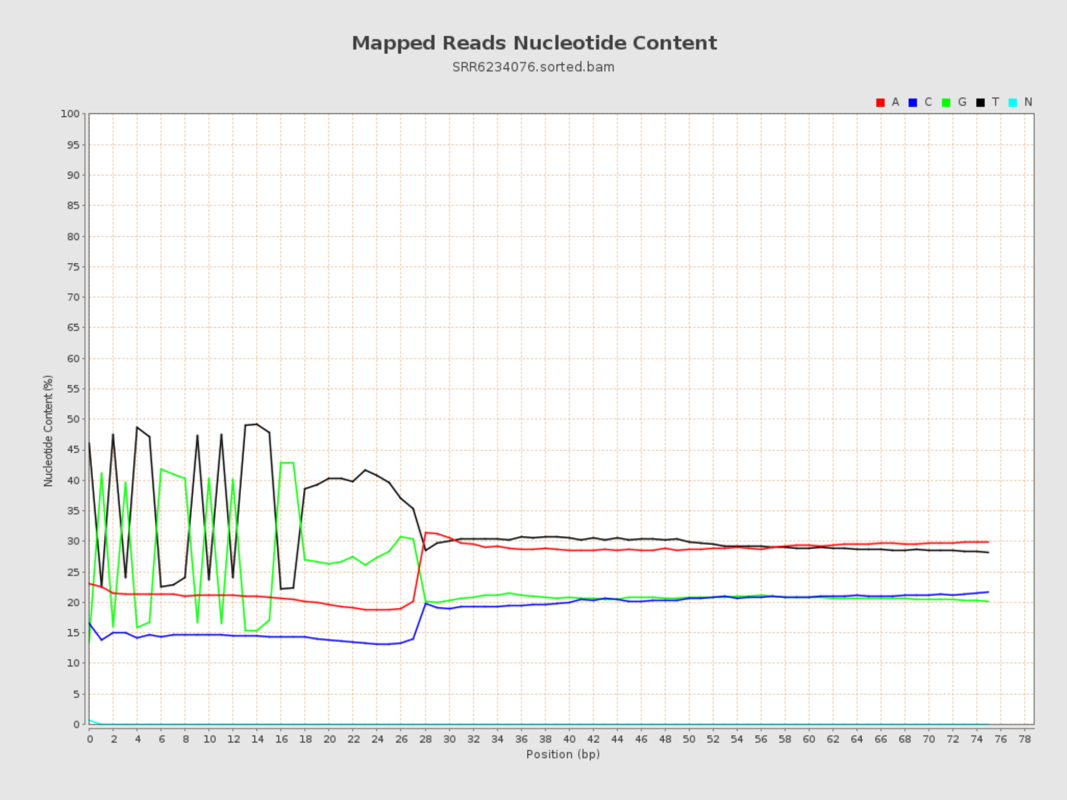
6. Results : Genome Fraction Coverage



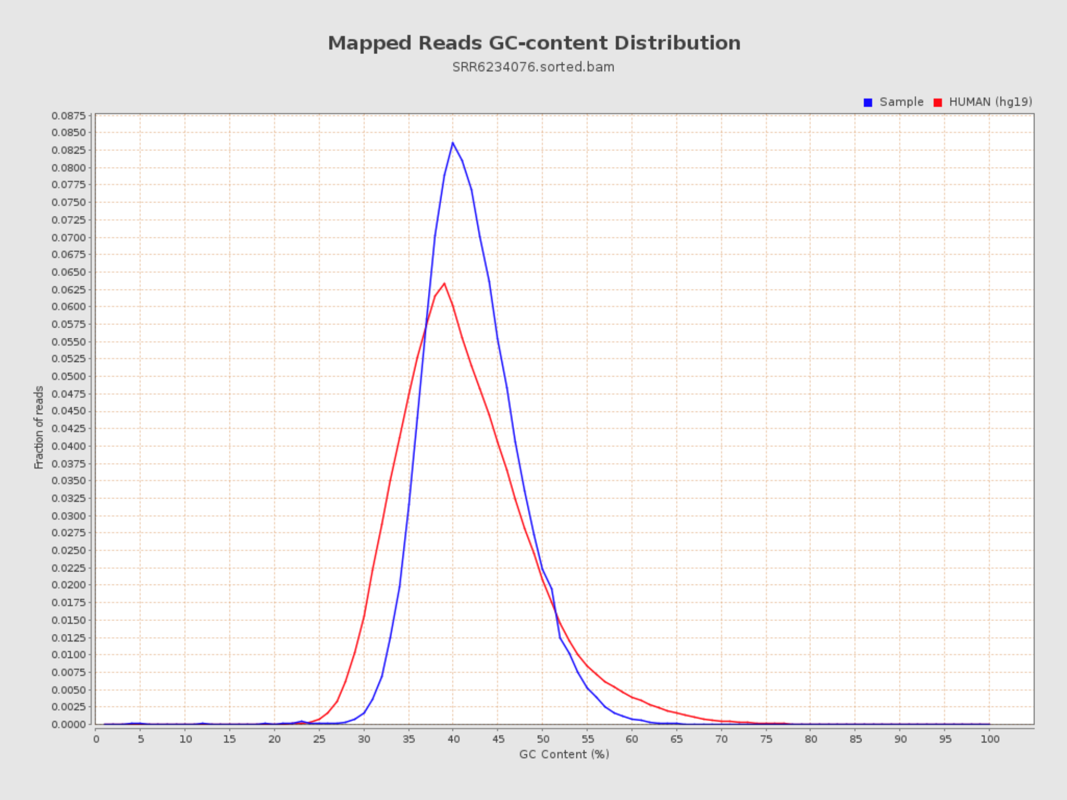
7. Results : Duplication Rate Histogram



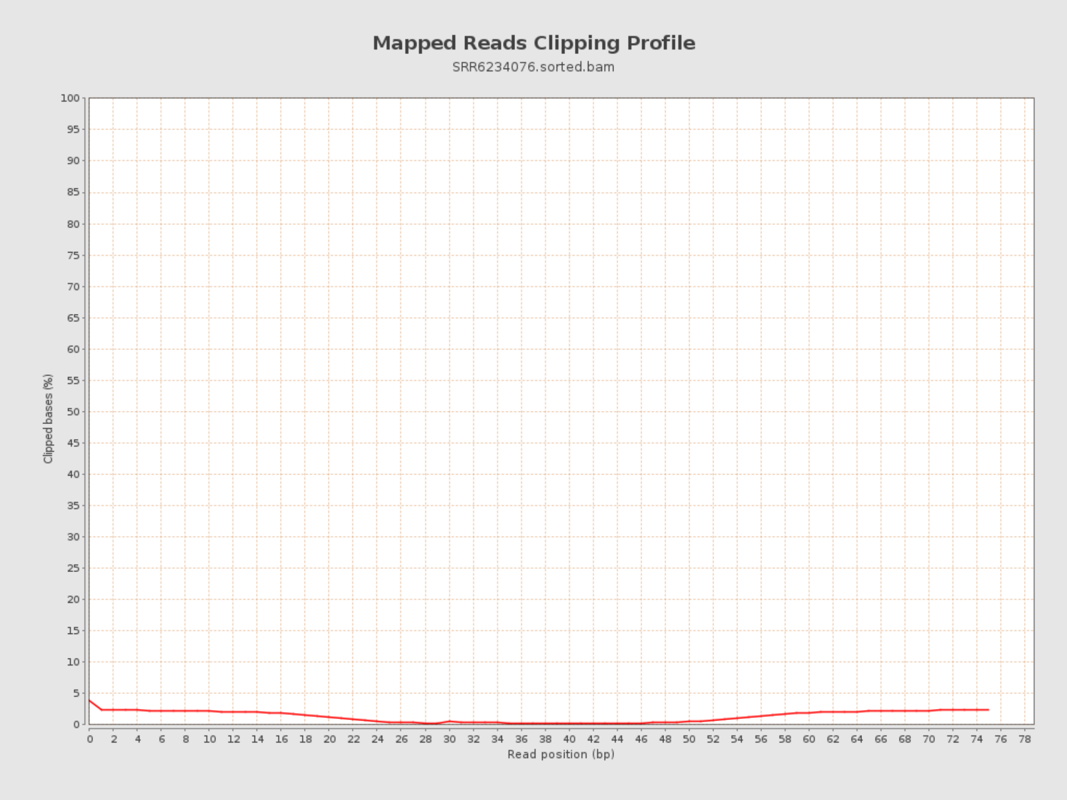
8. Results : Mapped Reads Nucleotide Content



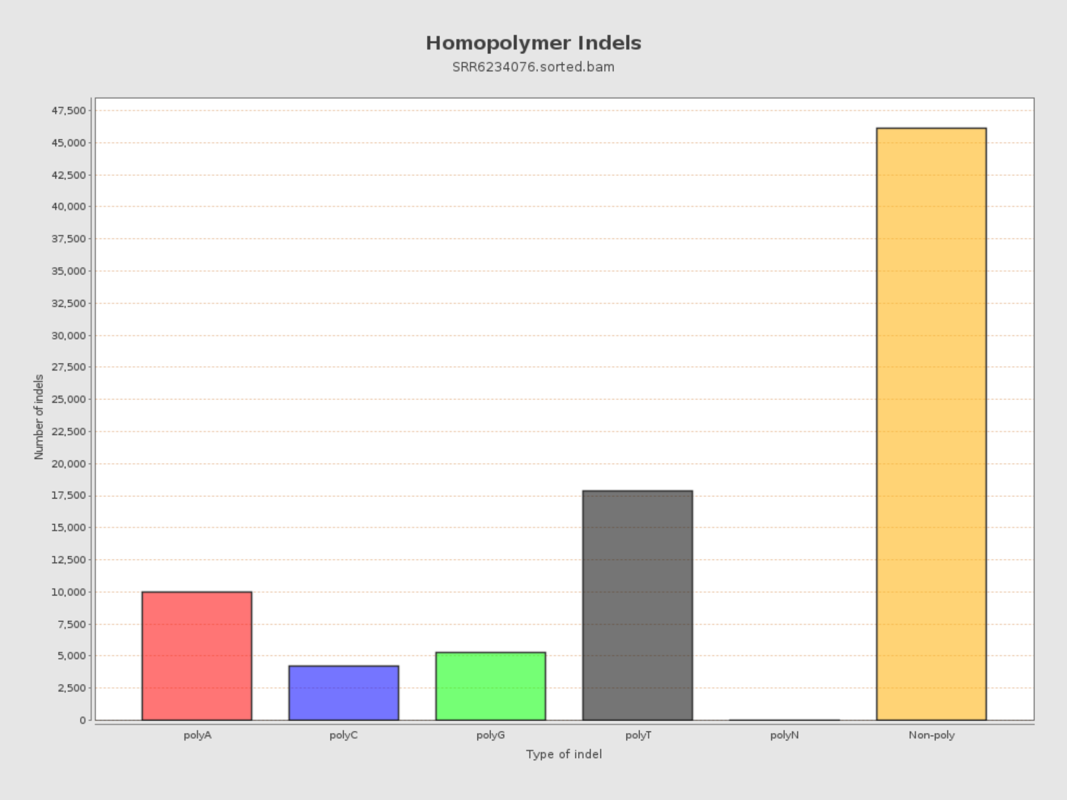
9. Results : Mapped Reads GC-content Distribution



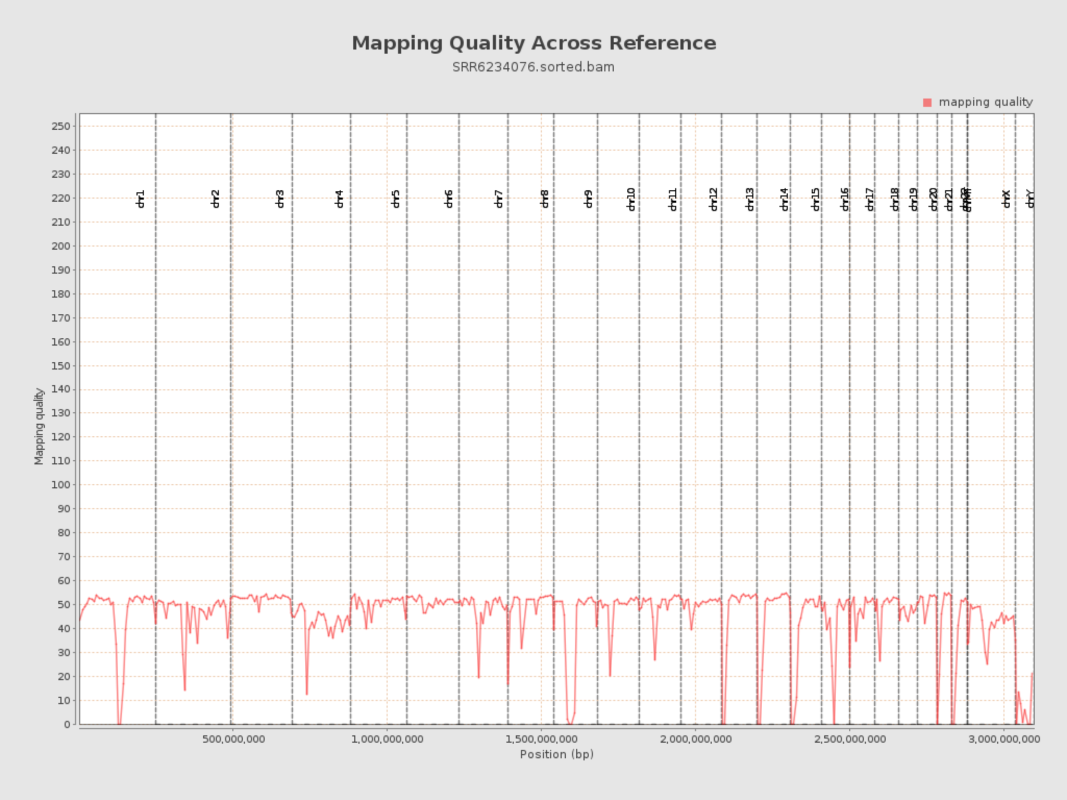
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram