Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:18:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234075.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_SRR6234075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:18:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,751,625
Mapped reads	3,514,070 / 93.67%
Unmapped reads	237,555 / 6.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,417 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	540,972 / 14.42%
Duplication rate	12.57%
Clipped reads	1,879,545 / 50.1%

2.2. ACGT Content

Number/percentage of A's	58,915,169 / 26.01%
Number/percentage of C's	40,573,082 / 17.92%
Number/percentage of T's	73,890,854 / 32.63%
Number/percentage of G's	53,070,137 / 23.43%
Number/percentage of N's	21,495 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0732

Standard Deviation	0.8479

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

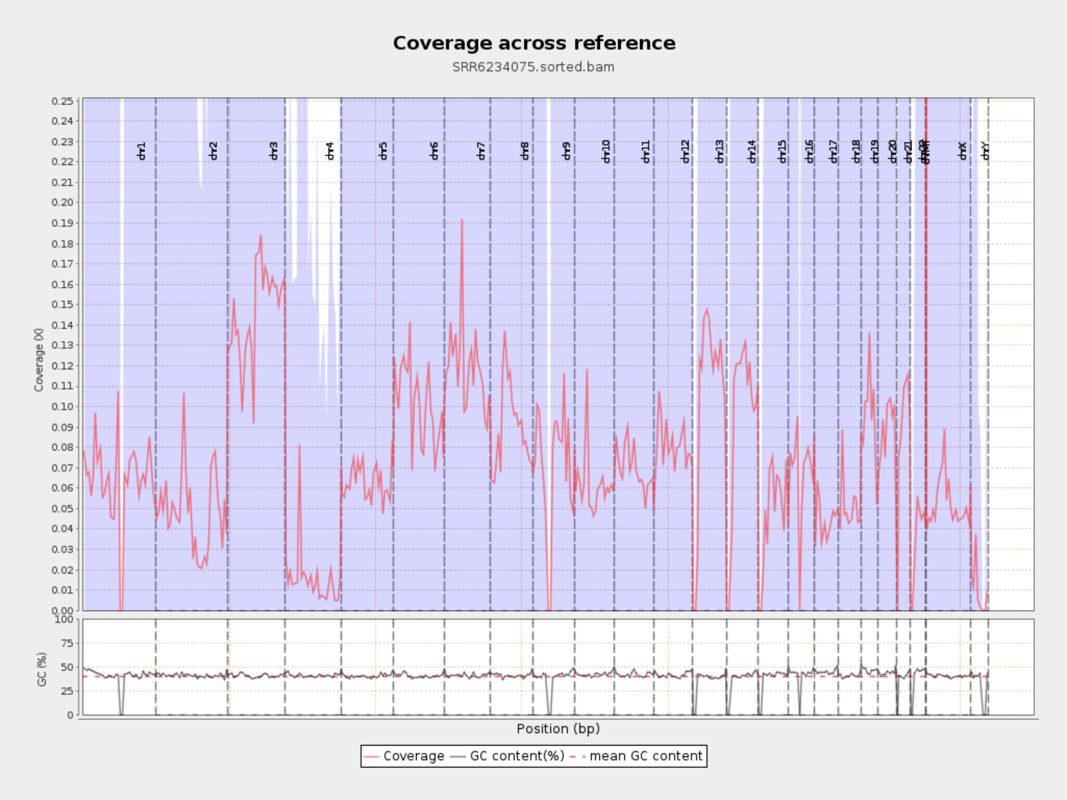
General error rate	0.57%
Mismatches	1,260,076
Insertions	15,728
Mapped reads with at least one insertion	0.44%
Deletions	49,710
Mapped reads with at least one deletion	1.4%
Homopolymer indels	43.9%

2.6. Chromosome stats

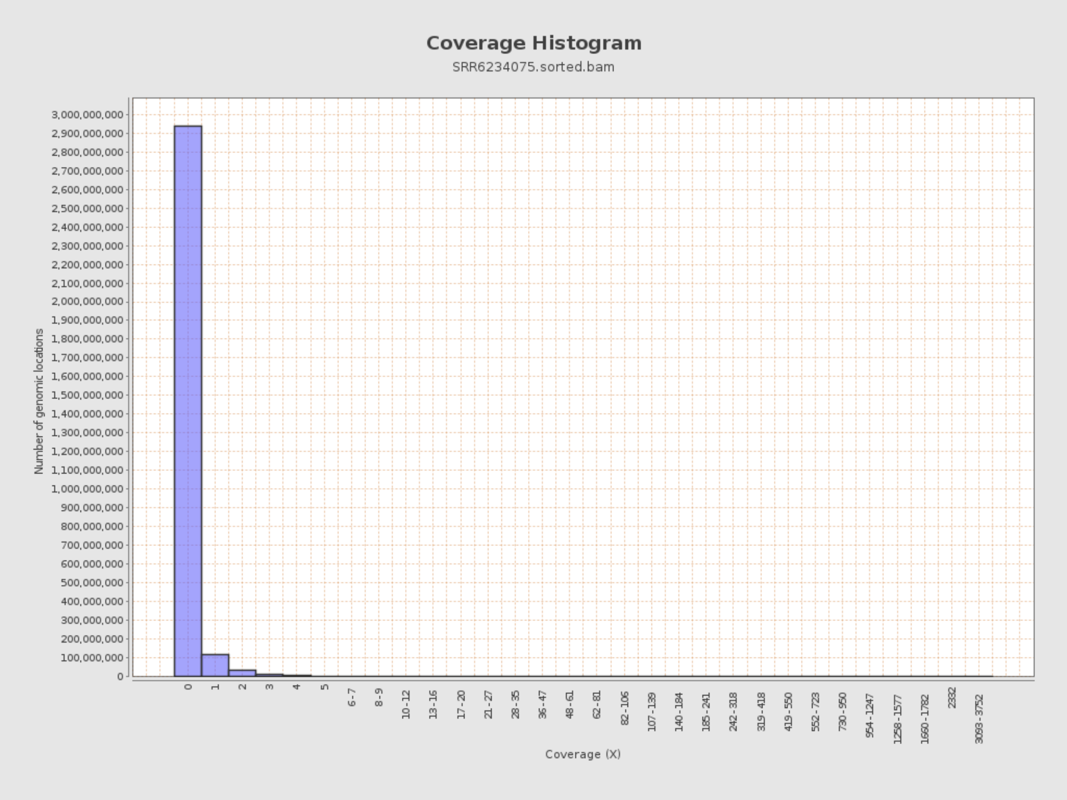
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15955112	0.064	1.1619
chr2	243199373	11820288	0.0486	1.7011
chr3	198022430	28949010	0.1462	0.529
chr4	191154276	3006570	0.0157	0.2971
chr5	180915260	11420971	0.0631	0.3543
chr6	171115067	17284464	0.101	0.6635
chr7	159138663	19054854	0.1197	1.3001

chr8	146364022	13185407	0.0901	1.152
chr9	141213431	9997484	0.0708	0.5342
chr10	135534747	8309050	0.0613	0.6813
chr11	135006516	9399612	0.0696	0.5485
chr12	133851895	10889941	0.0814	0.4009
chr13	115169878	12121383	0.1052	0.5012
chr14	107349540	10225548	0.0953	0.4597
chr15	102531392	4797642	0.0468	0.3378
chr16	90354753	5883880	0.0651	0.4374
chr17	81195210	3580962	0.0441	0.3501
chr18	78077248	3994173	0.0512	1.4772
chr19	59128983	5621036	0.0951	0.6919
chr20	63025520	5602309	0.0889	0.475
chr21	48129895	4299709	0.0893	0.4403
chr22	51304566	1778606	0.0347	0.2434
chrMT	16571	631257	38.0941	26.1023
chrX	155270560	8148968	0.0525	0.421
chrY	59373566	597989	0.0101	0.2872

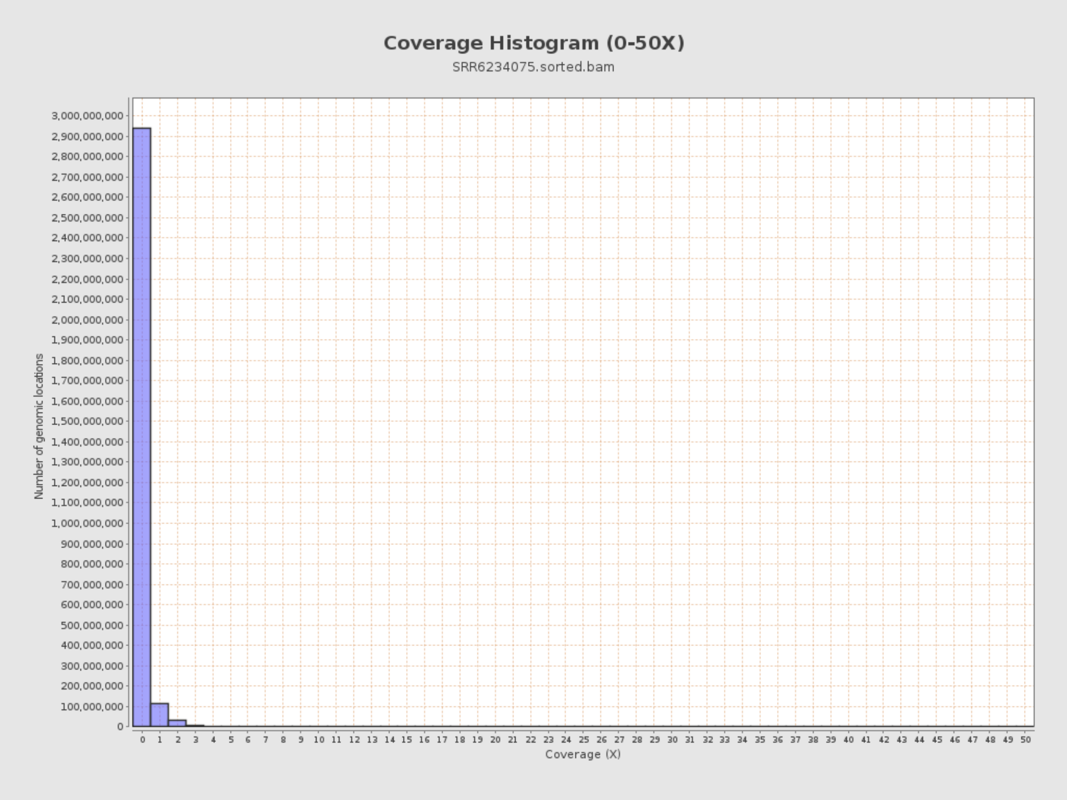
3. Results : Coverage across reference



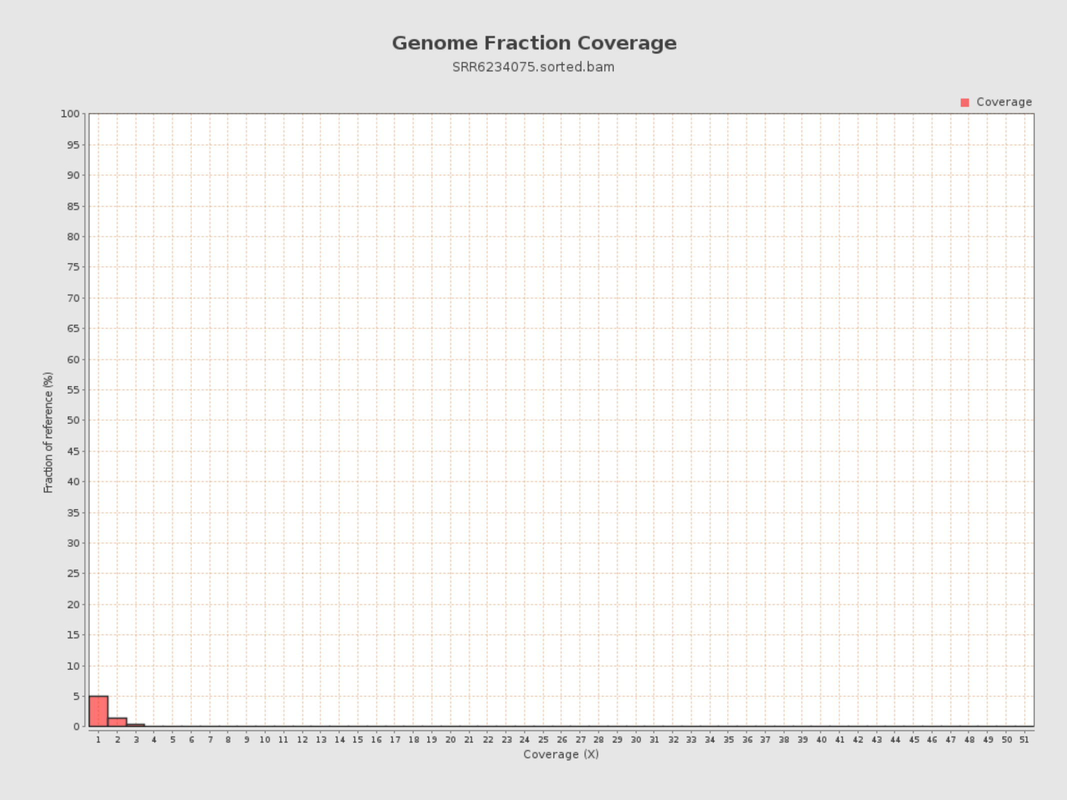
4. Results : Coverage Histogram



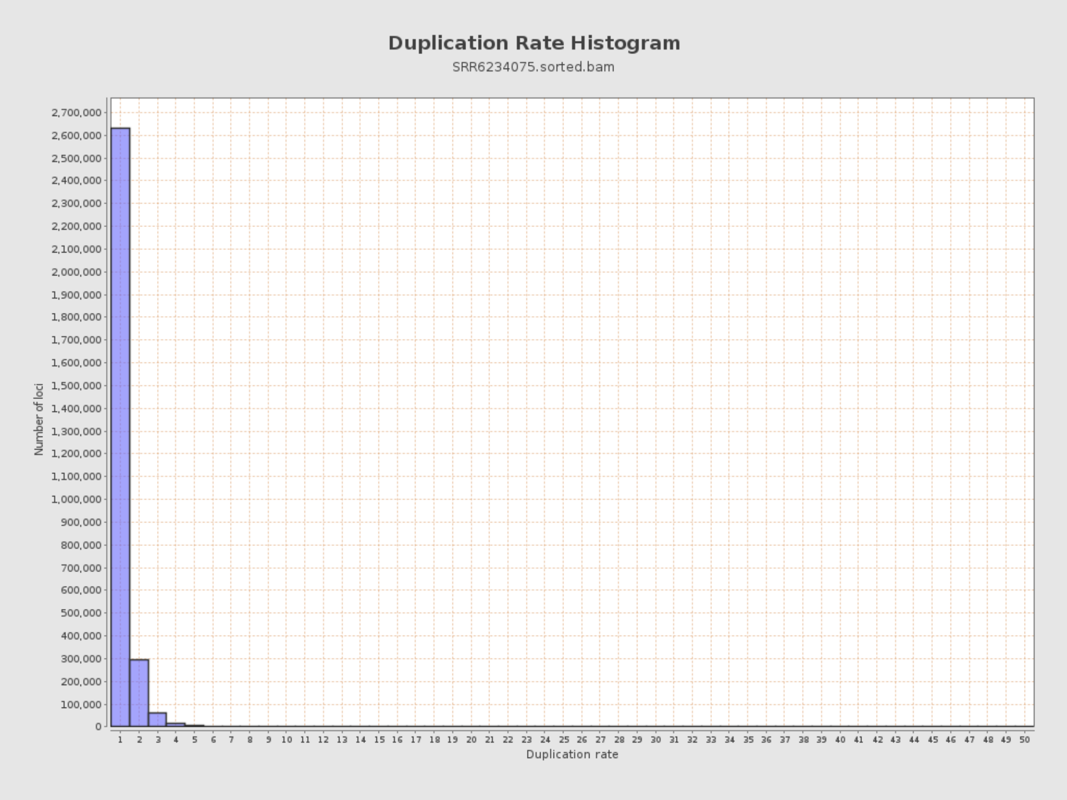
5. Results : Coverage Histogram (0-50X)



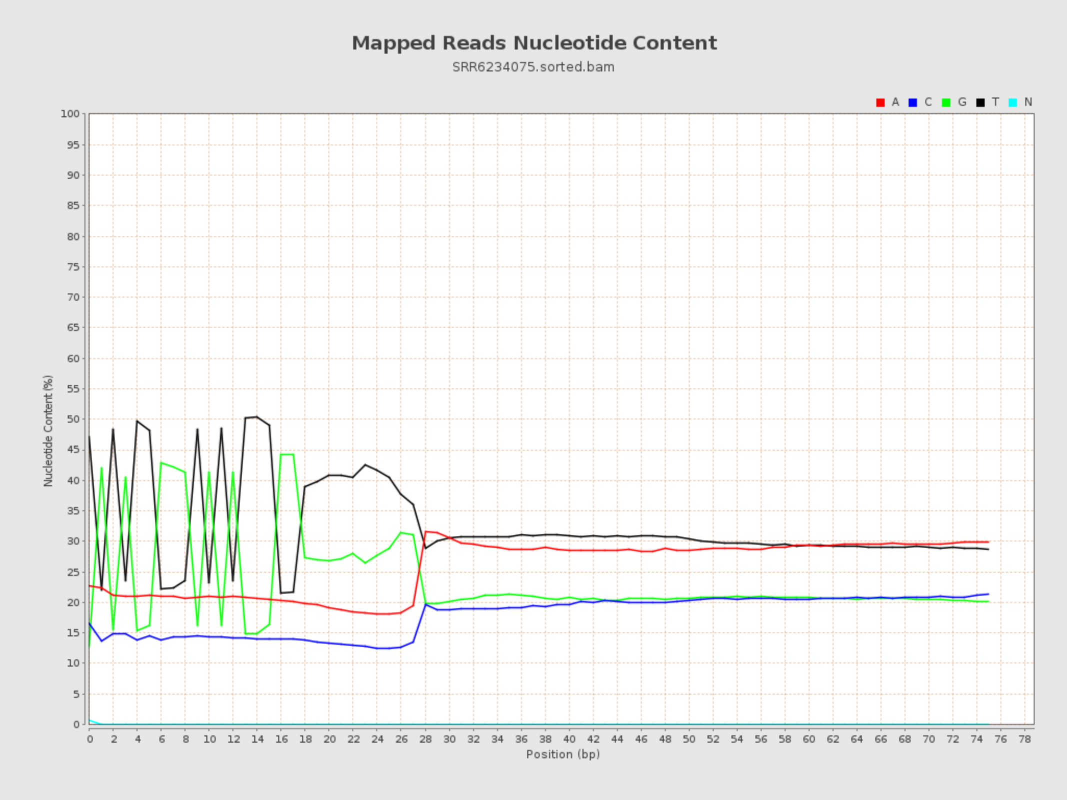
6. Results : Genome Fraction Coverage



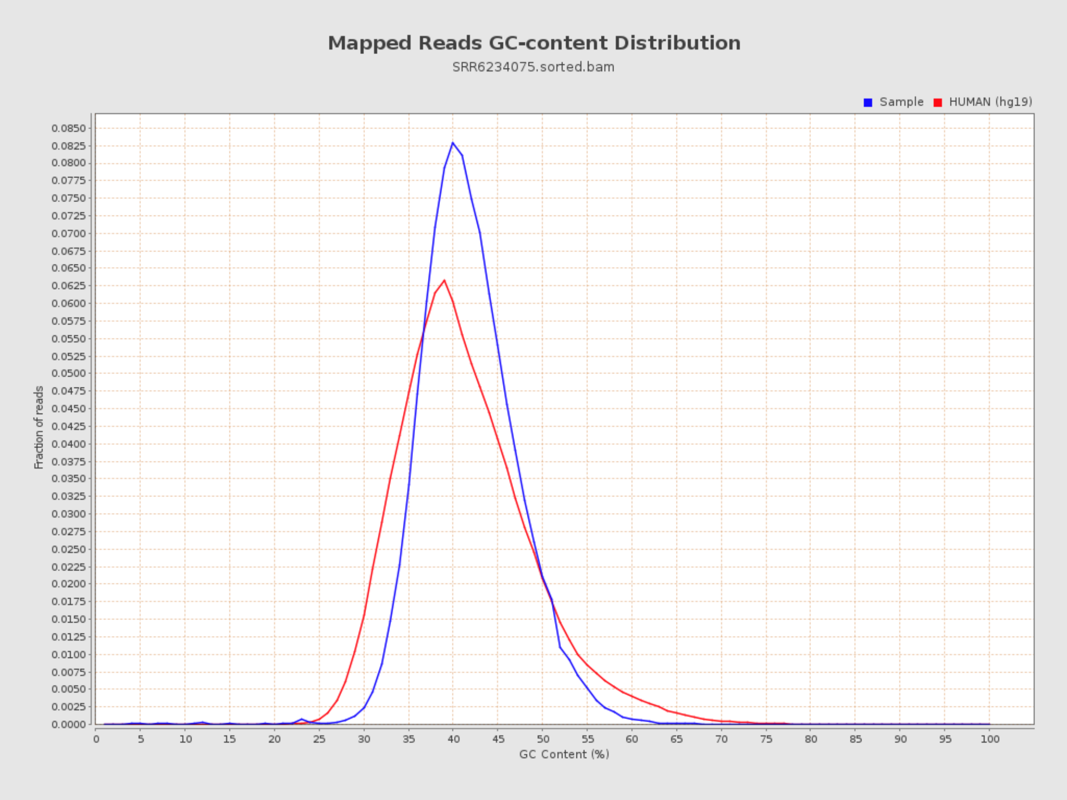
7. Results : Duplication Rate Histogram



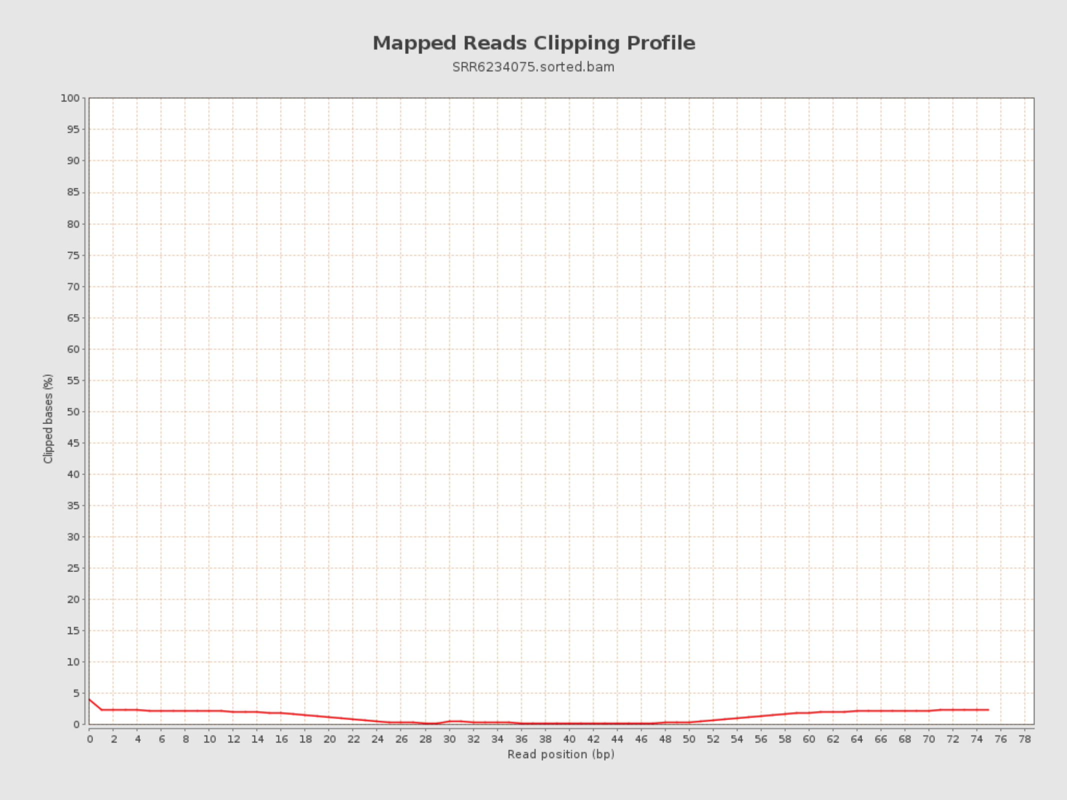
8. Results : Mapped Reads Nucleotide Content



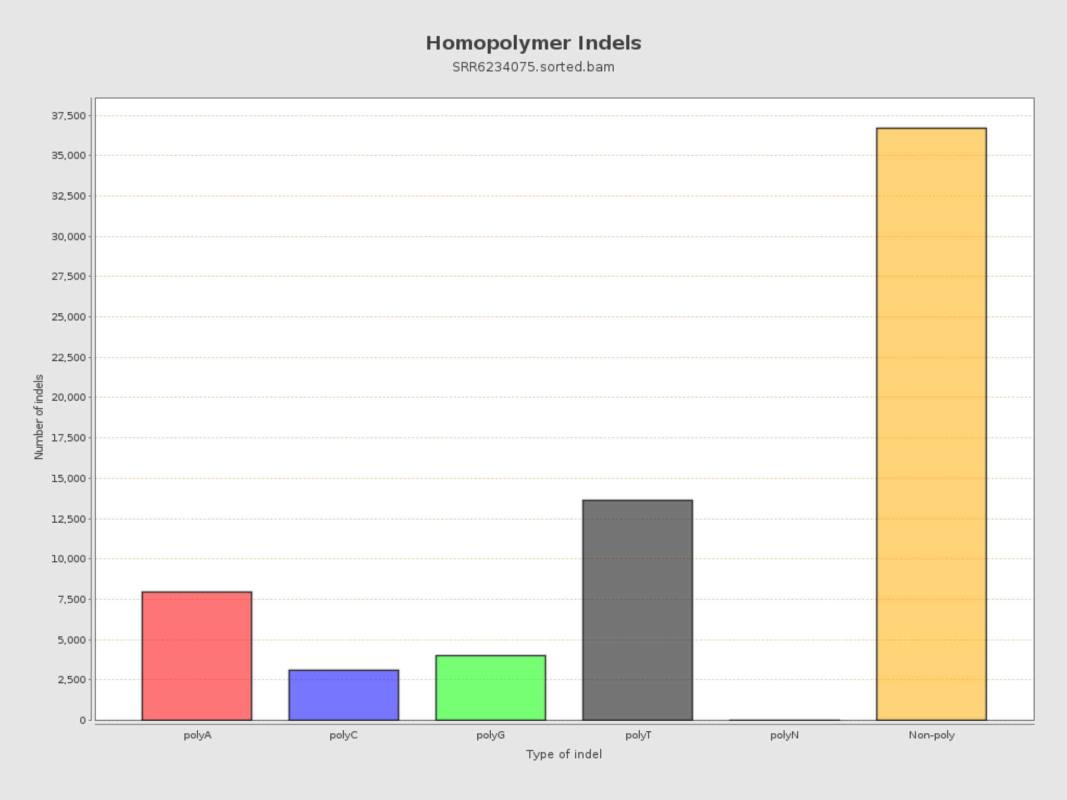
9. Results : Mapped Reads GC-content Distribution



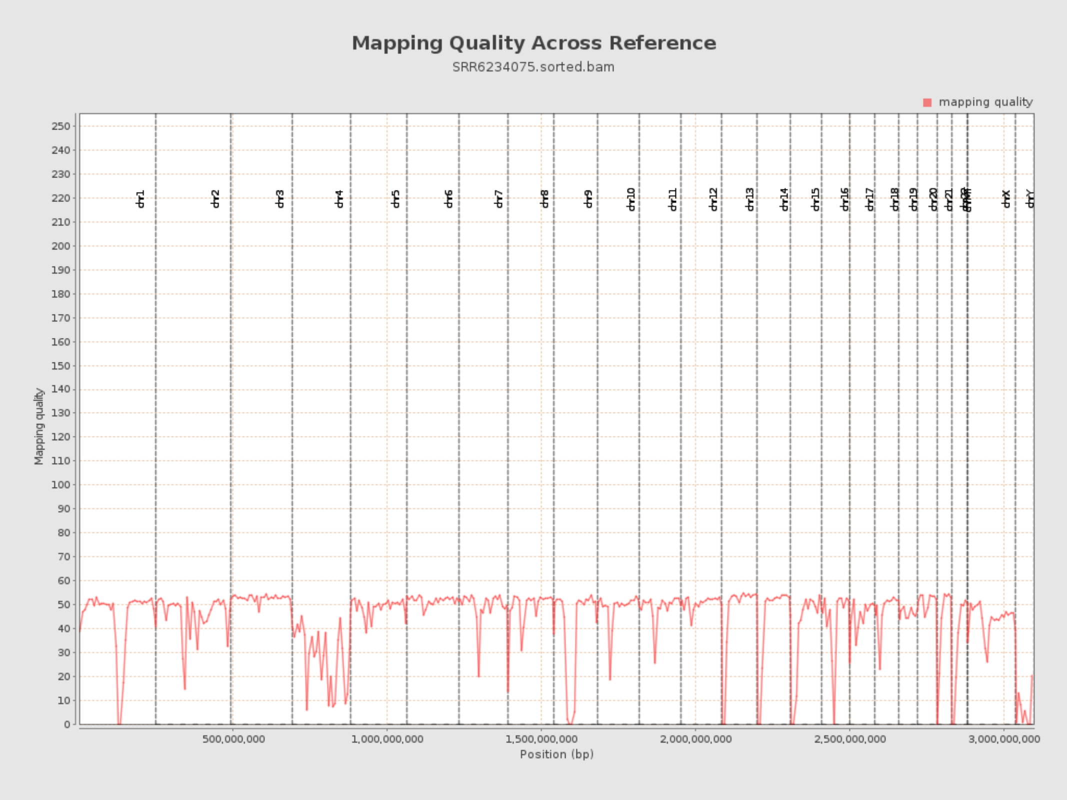
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram