Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:01:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234102.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_SRR6234102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:01:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,093,414
Mapped reads	4,814,782 / 94.53%
Unmapped reads	278,632 / 5.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,332 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	653,927 / 12.84%
Duplication rate	11.75%
Clipped reads	2,571,148 / 50.48%

2.2. ACGT Content

Number/percentage of A's	80,447,404 / 26.05%
Number/percentage of C's	55,818,208 / 18.08%
Number/percentage of T's	100,695,363 / 32.61%
Number/percentage of G's	71,814,716 / 23.26%
Number/percentage of N's	30,303 / 0.01%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0998

Standard Deviation	0.754

2.4. Mapping Quality

Mean Mapping Quality	37.88

2.5. Mismatches and indels

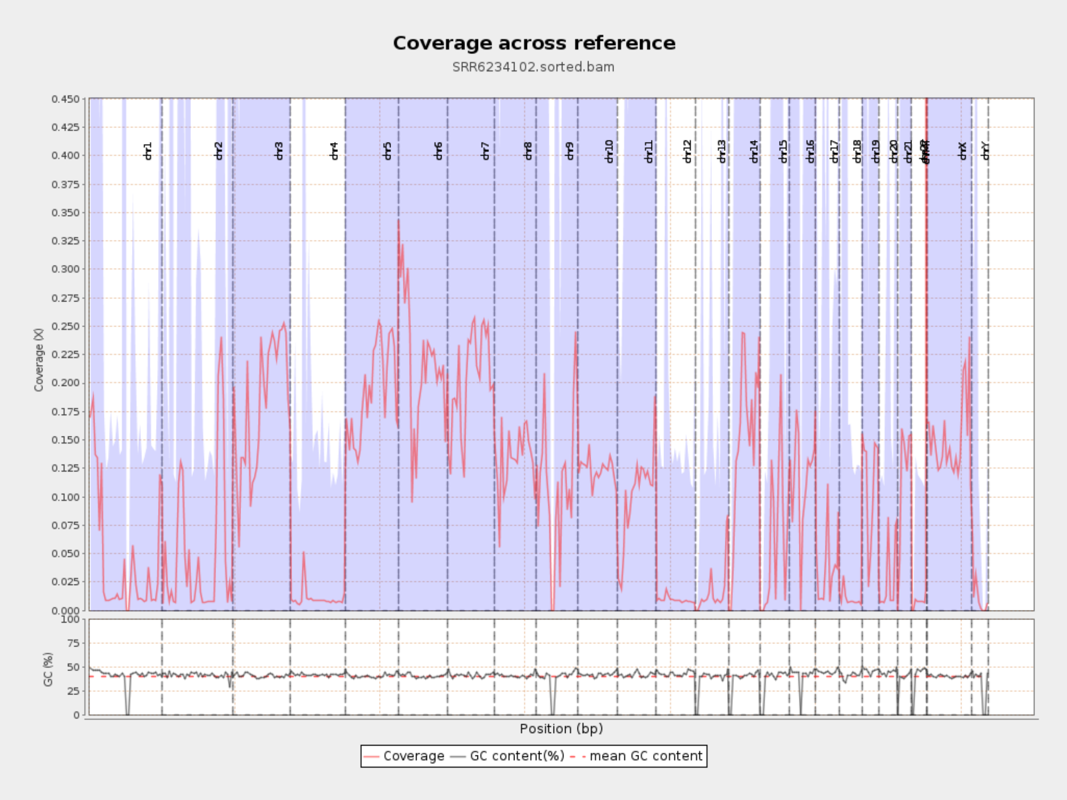
General error rate	0.52%
Mismatches	1,575,165
Insertions	18,285
Mapped reads with at least one insertion	0.38%
Deletions	72,667
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.04%

2.6. Chromosome stats

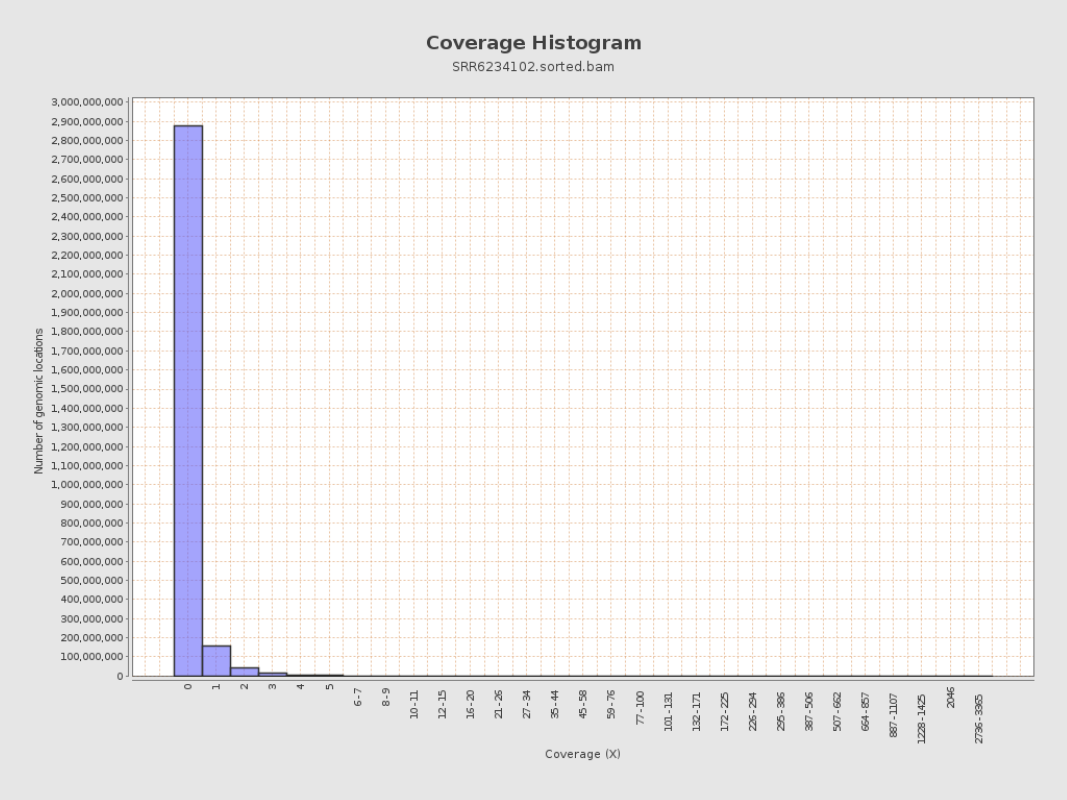
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10521372	0.0422	0.6998
chr2	243199373	12064925	0.0496	1.4848
chr3	198022430	35702682	0.1803	0.5557
chr4	191154276	1973997	0.0103	0.2461
chr5	180915260	34728479	0.192	0.5756
chr6	171115067	37530597	0.2193	0.9342
chr7	159138663	32873061	0.2066	1.4234

chr8	146364022	19509715	0.1333	0.6121
chr9	141213431	15237476	0.1079	0.4754
chr10	135534747	16807317	0.124	0.7782
chr11	135006516	13534442	0.1003	0.6035
chr12	133851895	1256500	0.0094	0.1878
chr13	115169878	1938138	0.0168	0.2686
chr14	107349540	15760676	0.1468	0.5021
chr15	102531392	6363537	0.0621	0.3695
chr16	90354753	10442782	0.1156	0.4596
chr17	81195210	3089900	0.0381	0.3138
chr18	78077248	830435	0.0106	0.7586
chr19	59128983	6119986	0.1035	0.8854
chr20	63025520	1851775	0.0294	0.2508
chr21	48129895	5626586	0.1169	0.4674
chr22	51304566	340757	0.0066	0.1017
chrMT	16571	476971	28.7835	15.34
chrX	155270560	23564969	0.1518	0.5951
chrY	59373566	785504	0.0132	0.2734

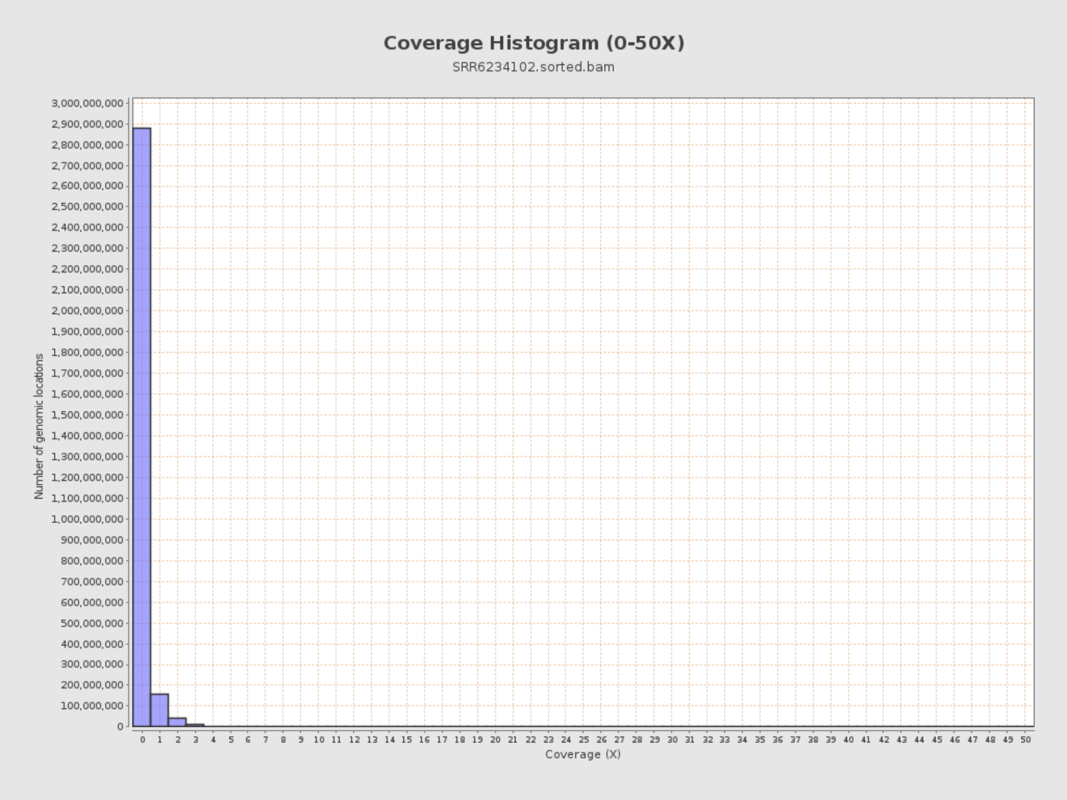
3. Results : Coverage across reference



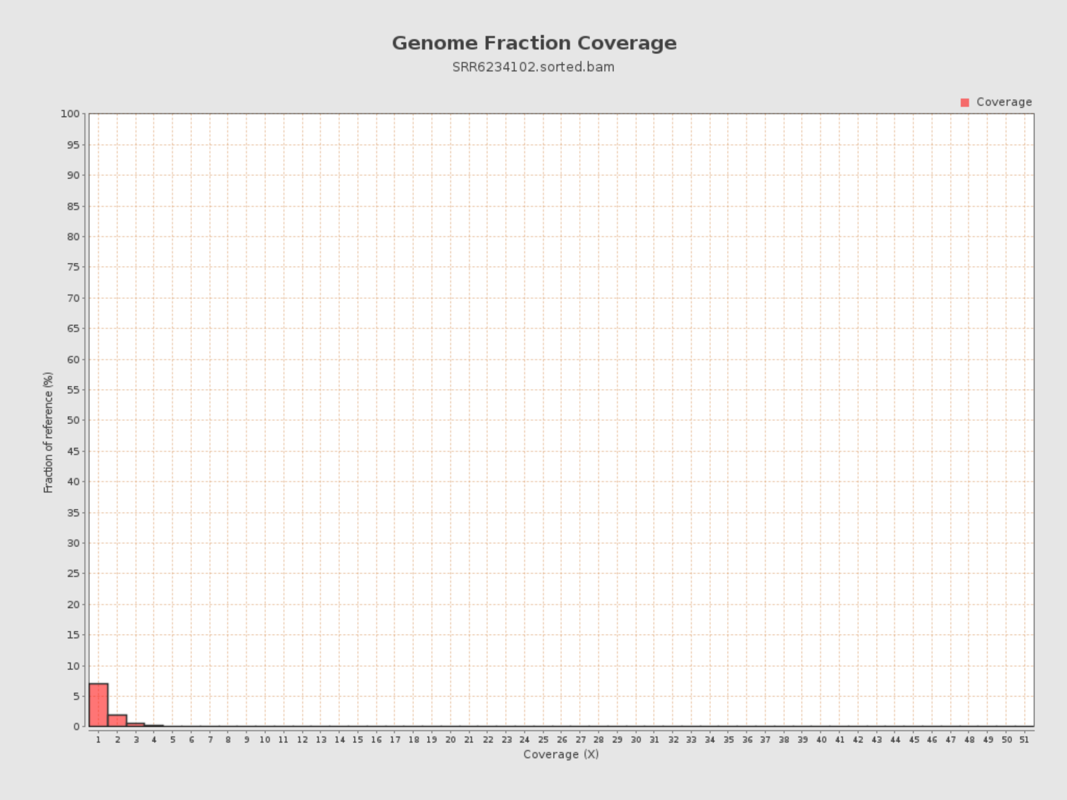
4. Results : Coverage Histogram



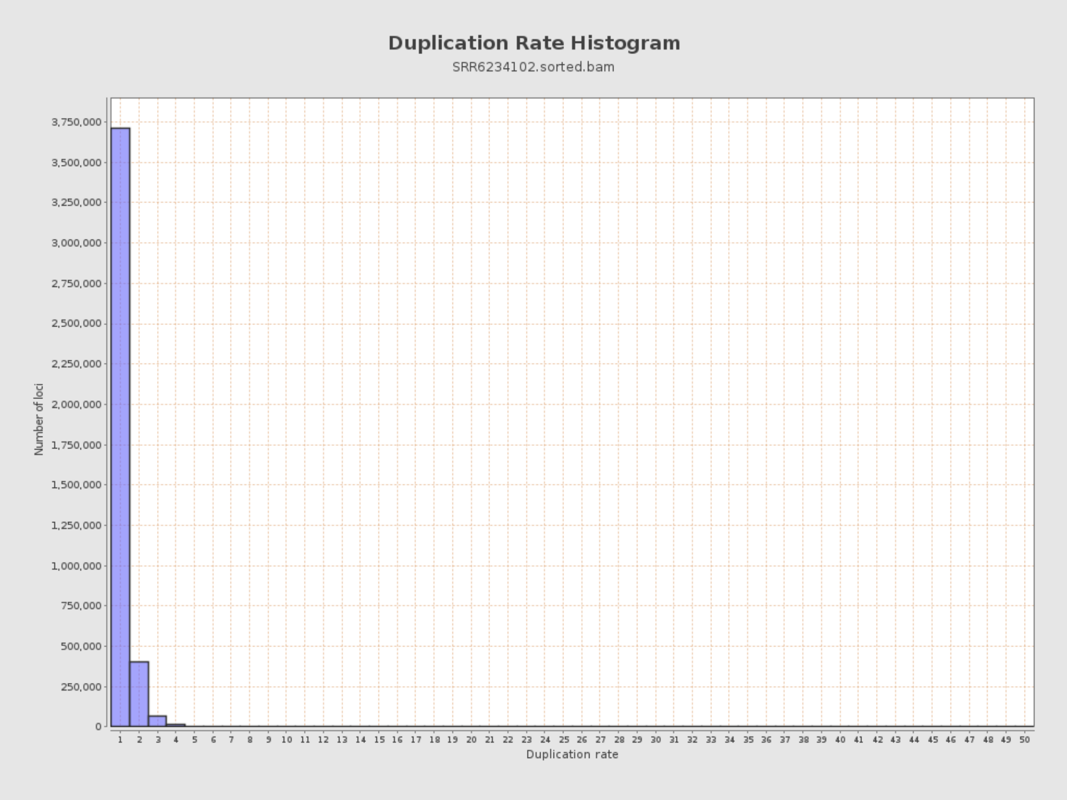
5. Results : Coverage Histogram (0-50X)



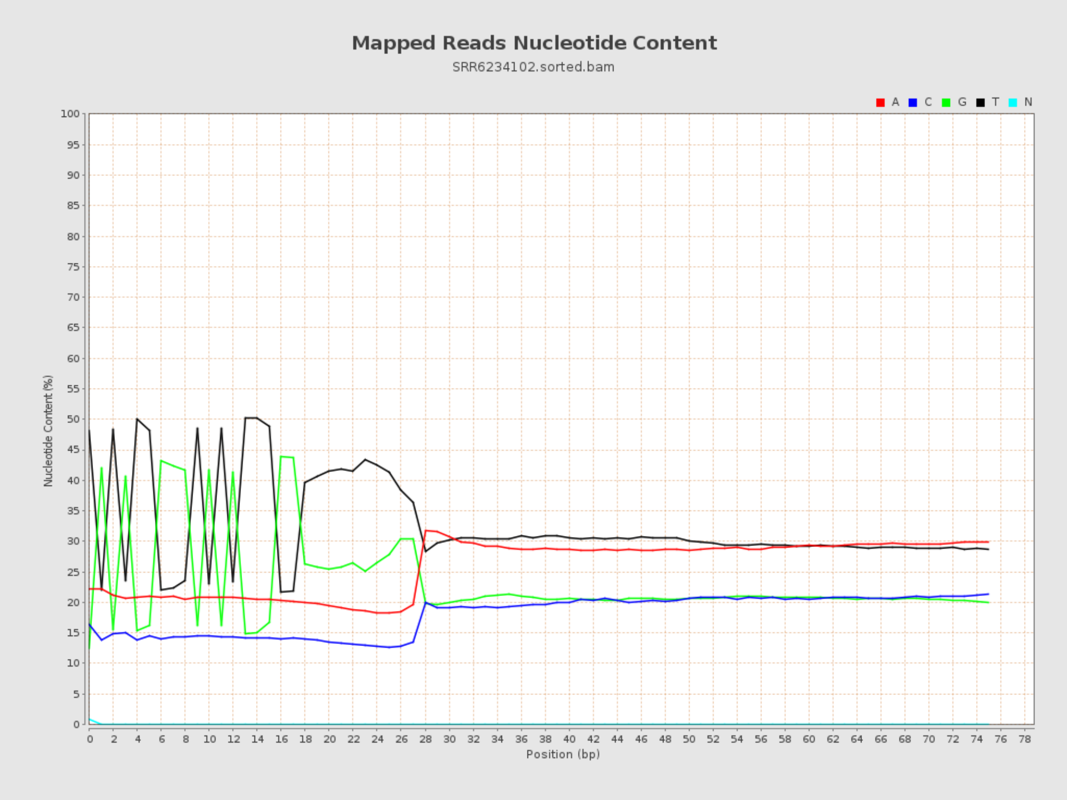
6. Results : Genome Fraction Coverage



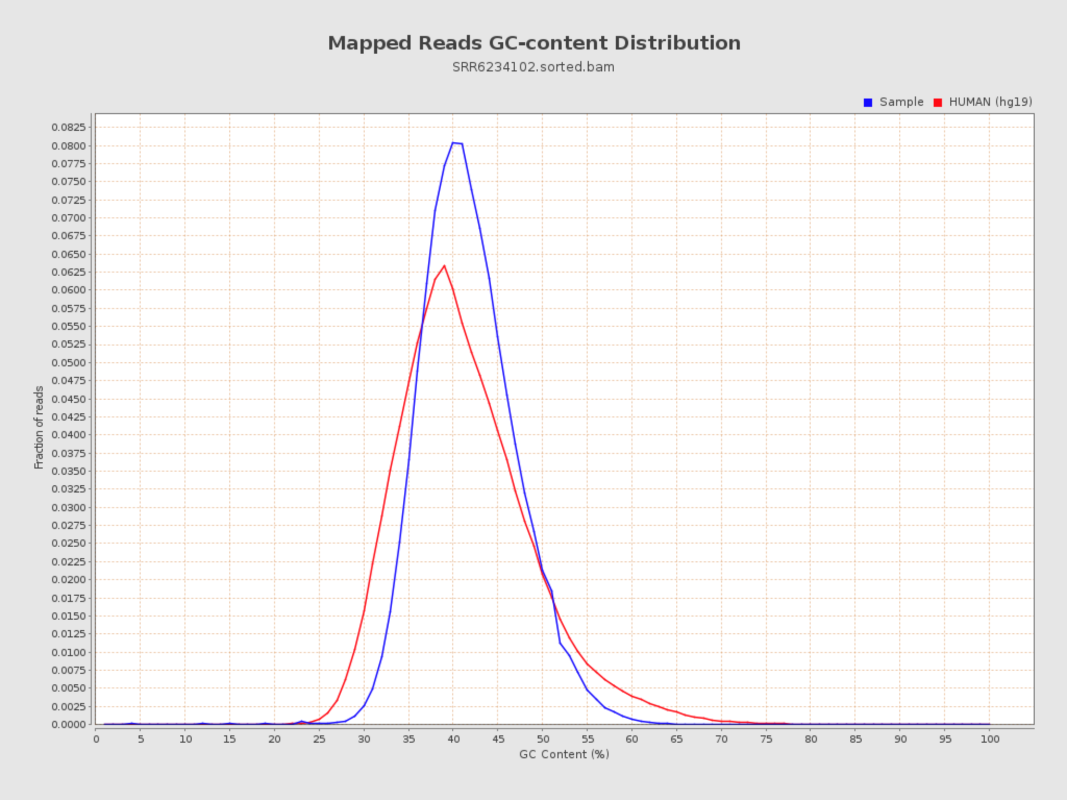
7. Results : Duplication Rate Histogram



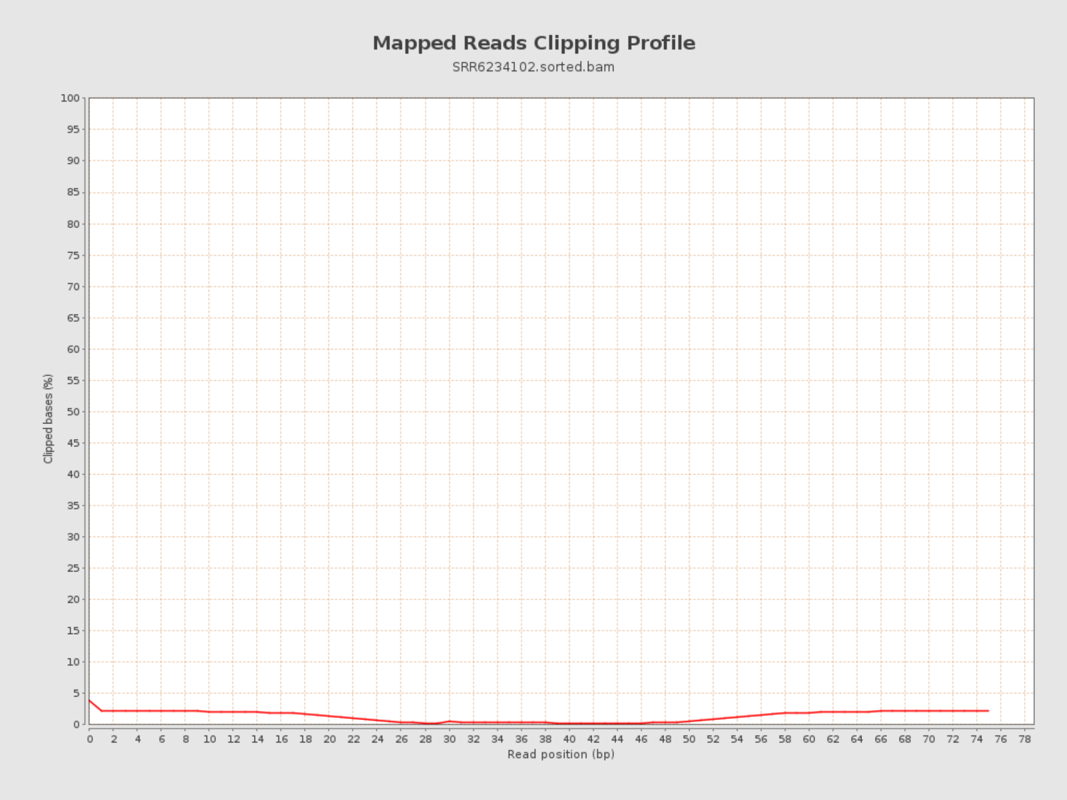
8. Results : Mapped Reads Nucleotide Content



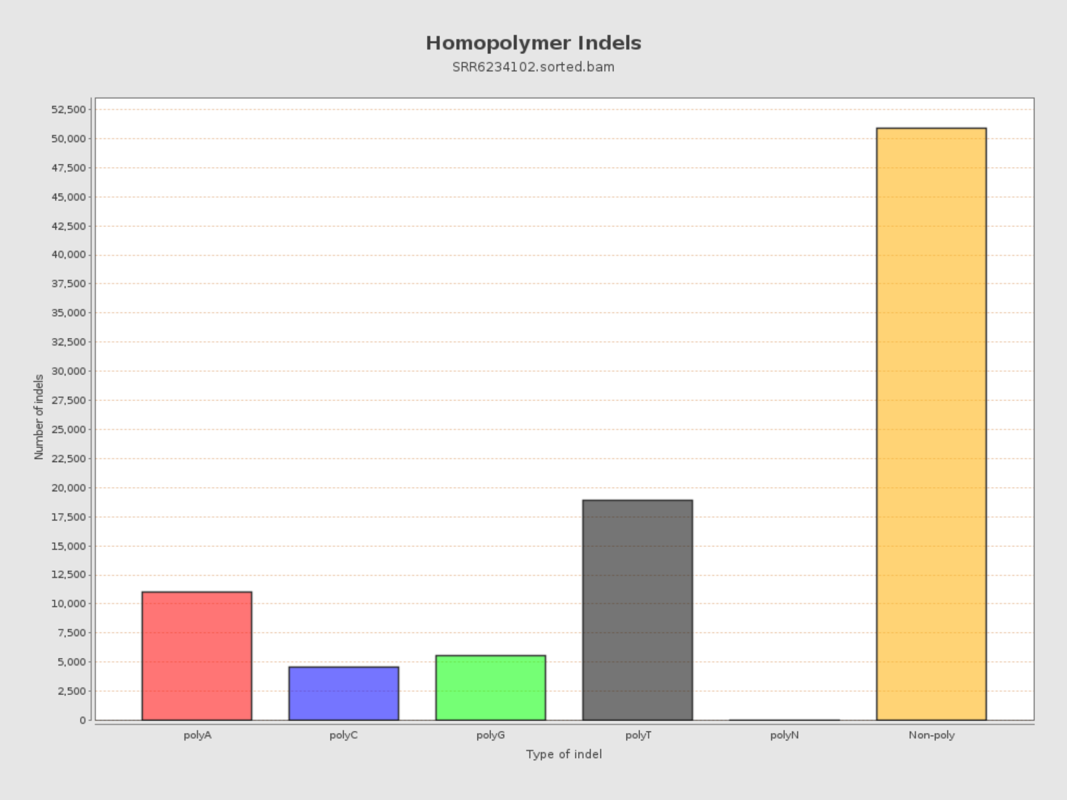
9. Results : Mapped Reads GC-content Distribution



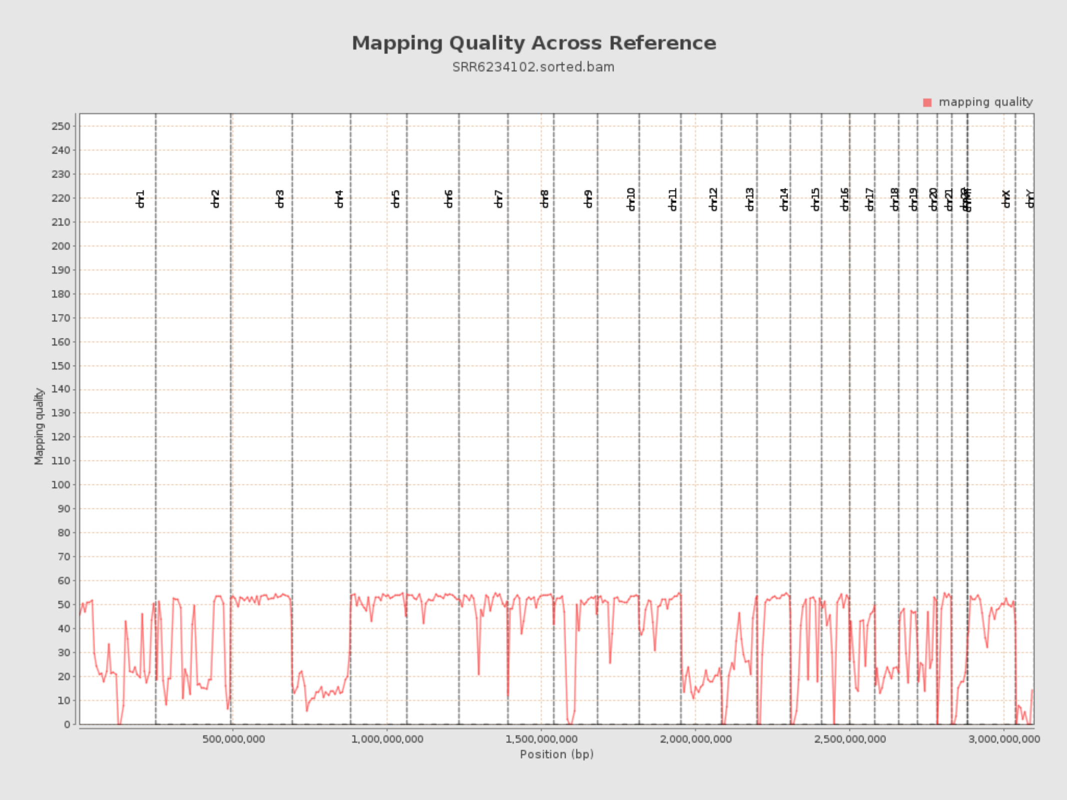
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram