Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:40:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004012.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_SRR6004012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:40:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,083,252
Mapped reads	2,757,149 / 89.42%
Unmapped reads	326,103 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,993 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	146,577 / 4.75%
Duplication rate	4.26%
Clipped reads	1,277,909 / 41.45%

2.2. ACGT Content

Number/percentage of A's	51,294,580 / 27.9%
Number/percentage of C's	35,101,304 / 19.09%
Number/percentage of T's	56,912,403 / 30.96%
Number/percentage of G's	40,492,905 / 22.03%
Number/percentage of N's	31,132 / 0.02%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0594

Standard Deviation	0.4695

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

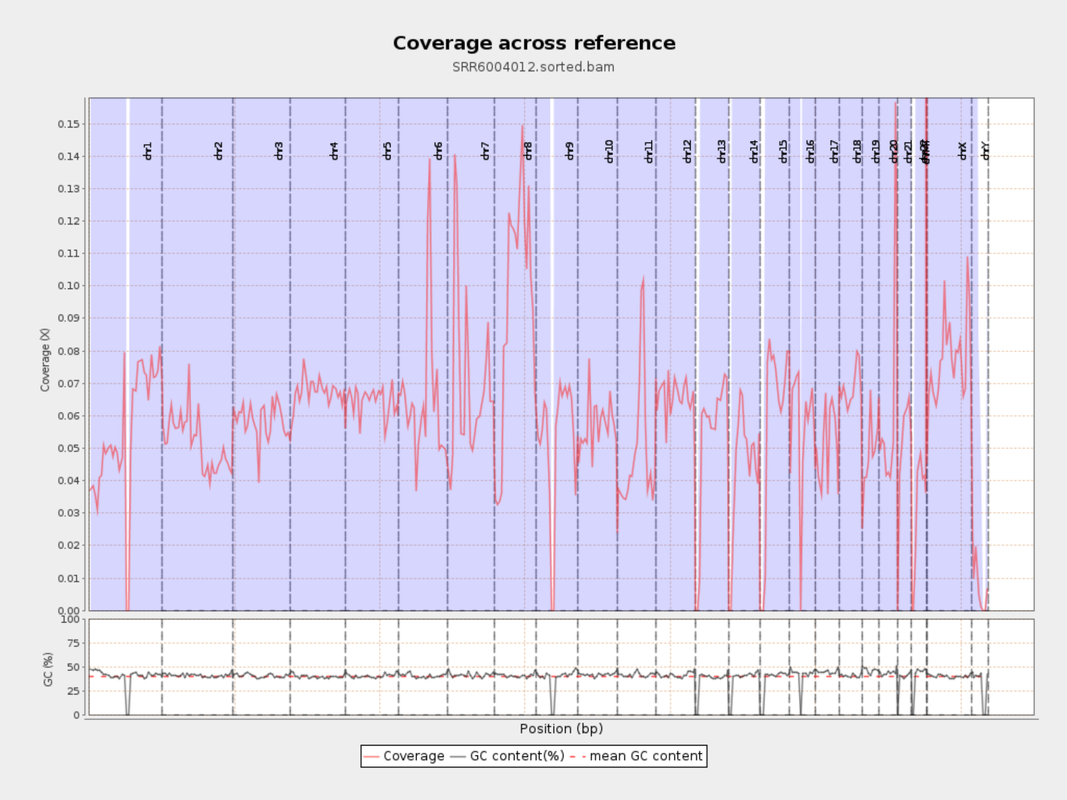
General error rate	0.87%
Mismatches	1,573,021
Insertions	12,734
Mapped reads with at least one insertion	0.46%
Deletions	40,348
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.45%

2.6. Chromosome stats

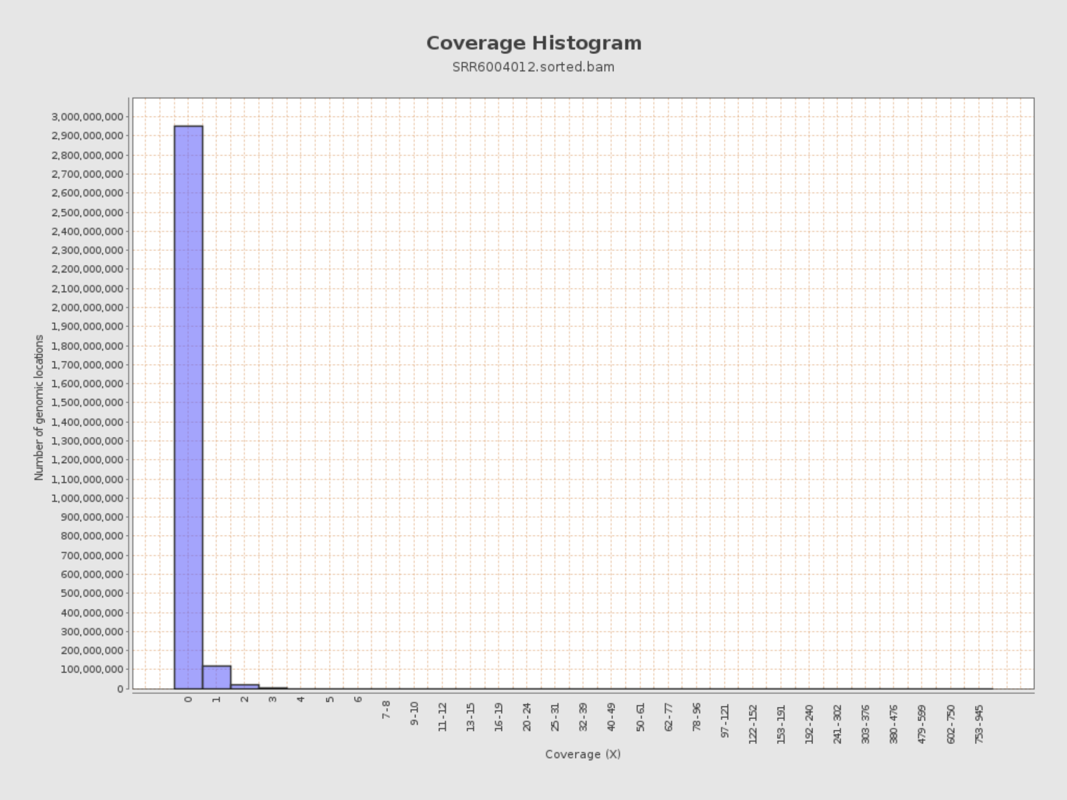
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13638867	0.0547	0.8579
chr2	243199373	12588064	0.0518	0.5047
chr3	198022430	11543402	0.0583	0.2893
chr4	191154276	12853615	0.0672	0.3307
chr5	180915260	11659630	0.0644	0.3061
chr6	171115067	11226640	0.0656	0.3414
chr7	159138663	11239216	0.0706	0.7265

chr8	146364022	13732872	0.0938	0.6221
chr9	141213431	7372230	0.0522	0.4098
chr10	135534747	7752763	0.0572	0.4009
chr11	135006516	6625455	0.0491	0.3626
chr12	133851895	8795478	0.0657	0.3157
chr13	115169878	6012032	0.0522	0.2901
chr14	107349540	4672282	0.0435	0.282
chr15	102531392	5968596	0.0582	0.294
chr16	90354753	5172276	0.0572	0.3127
chr17	81195210	4166447	0.0513	0.2956
chr18	78077248	5399211	0.0692	0.7526
chr19	59128983	2908800	0.0492	0.6071
chr20	63025520	4084202	0.0648	0.3237
chr21	48129895	2438554	0.0507	0.291
chr22	51304566	1540473	0.03	0.2029
chrMT	16571	25054	1.5119	1.6197
chrX	155270560	12034902	0.0775	0.374
chrY	59373566	450575	0.0076	0.139

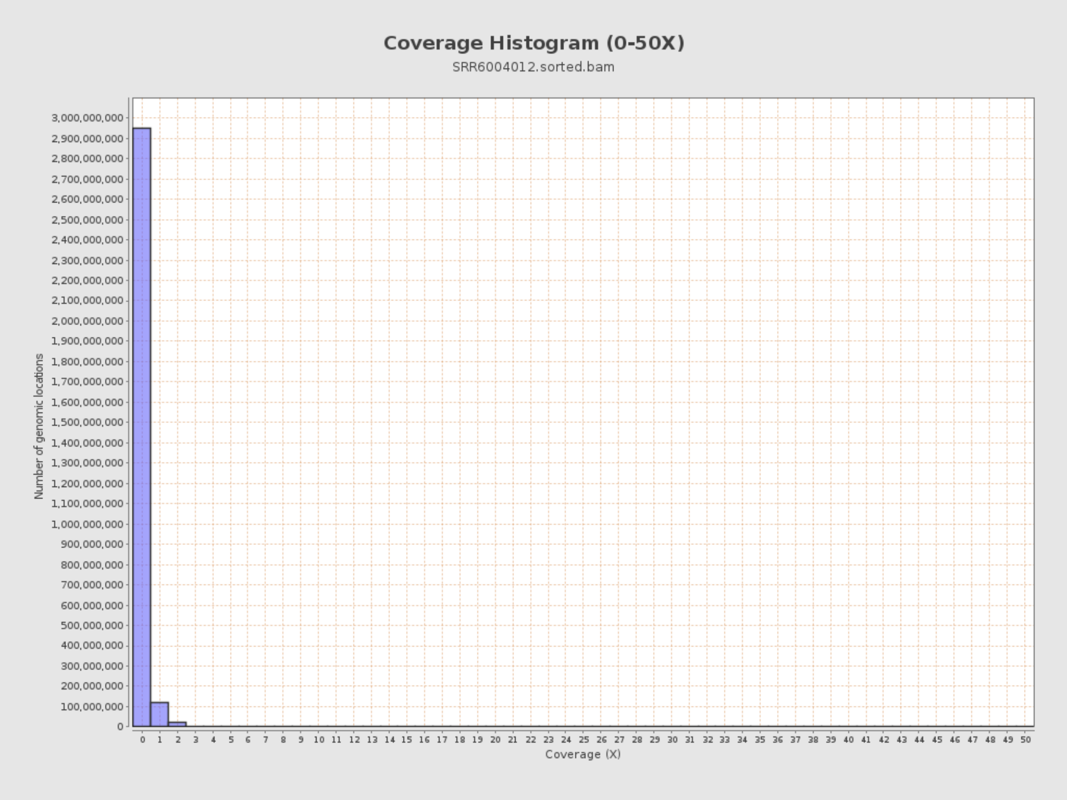
3. Results : Coverage across reference



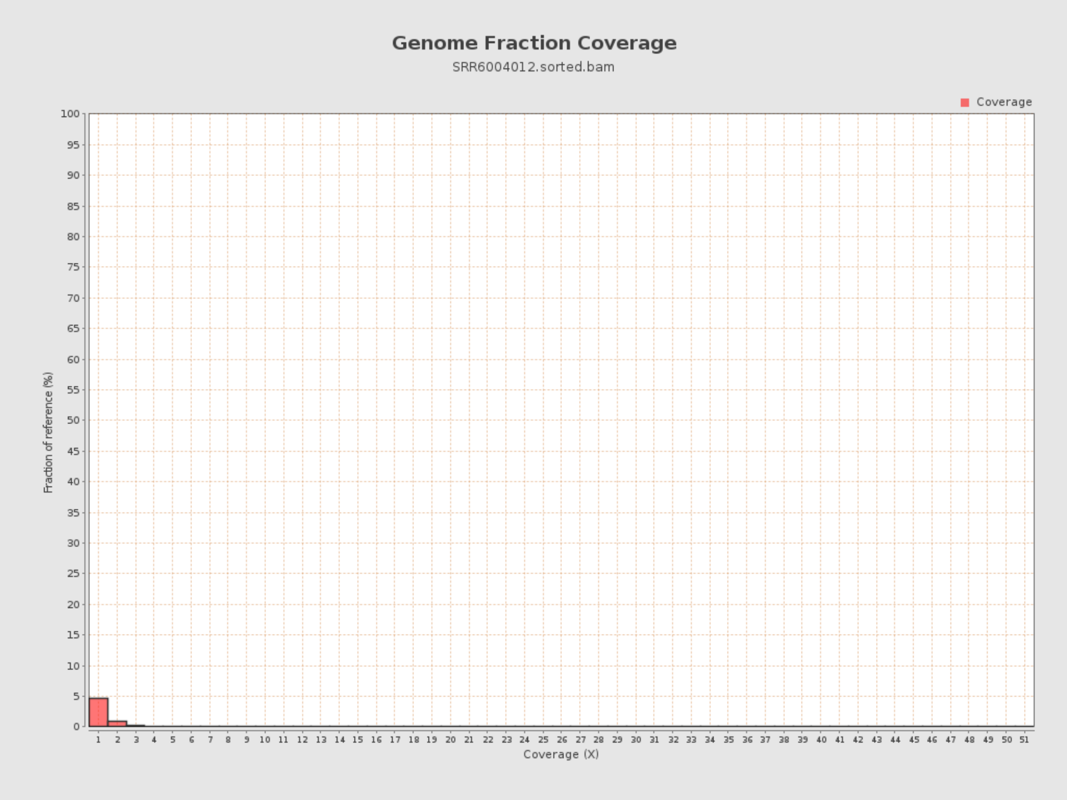
4. Results : Coverage Histogram



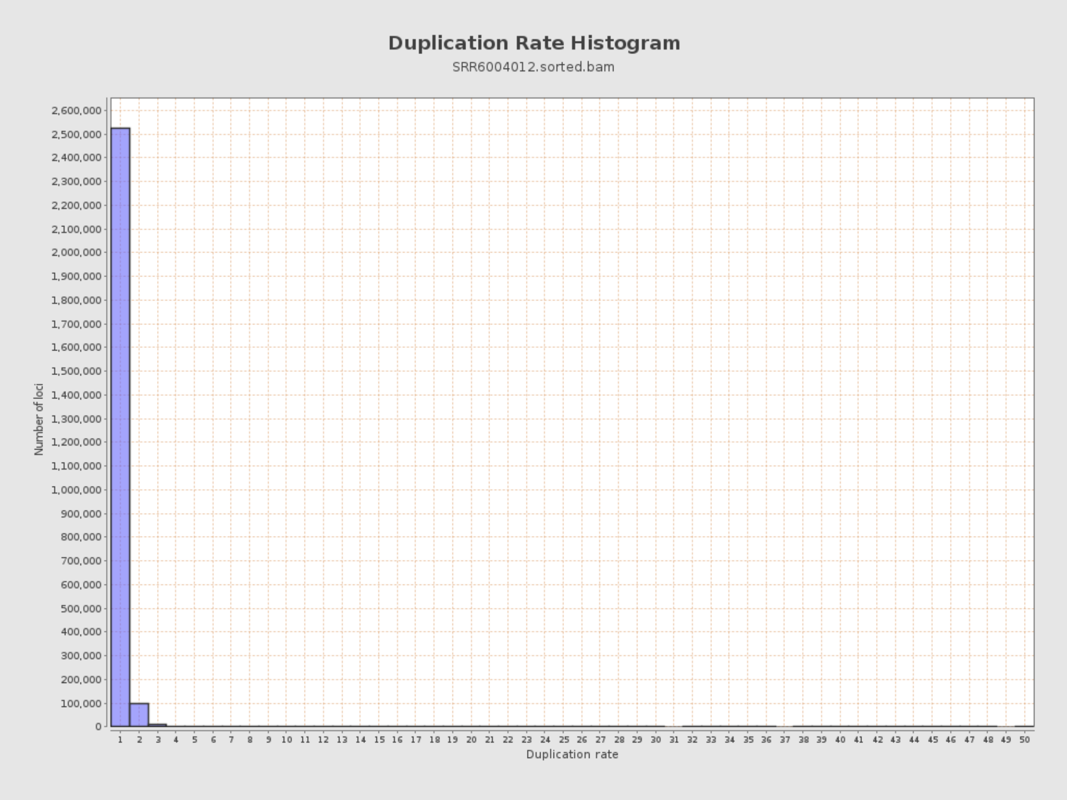
5. Results : Coverage Histogram (0-50X)



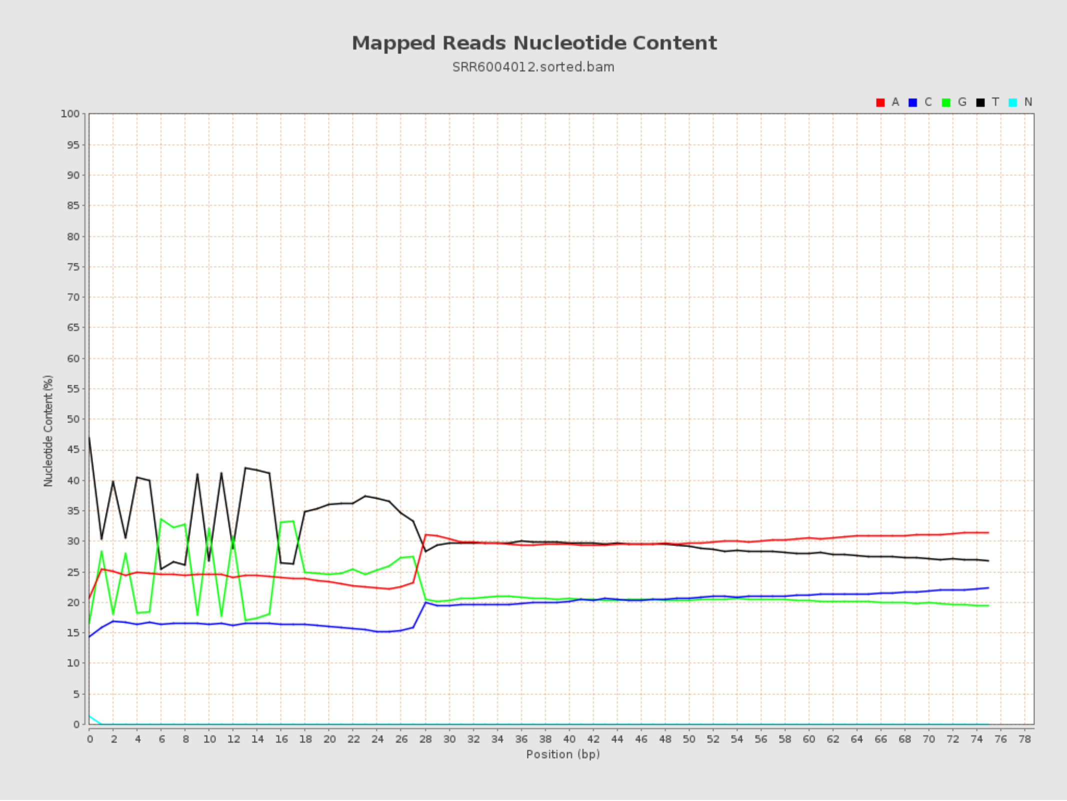
6. Results : Genome Fraction Coverage



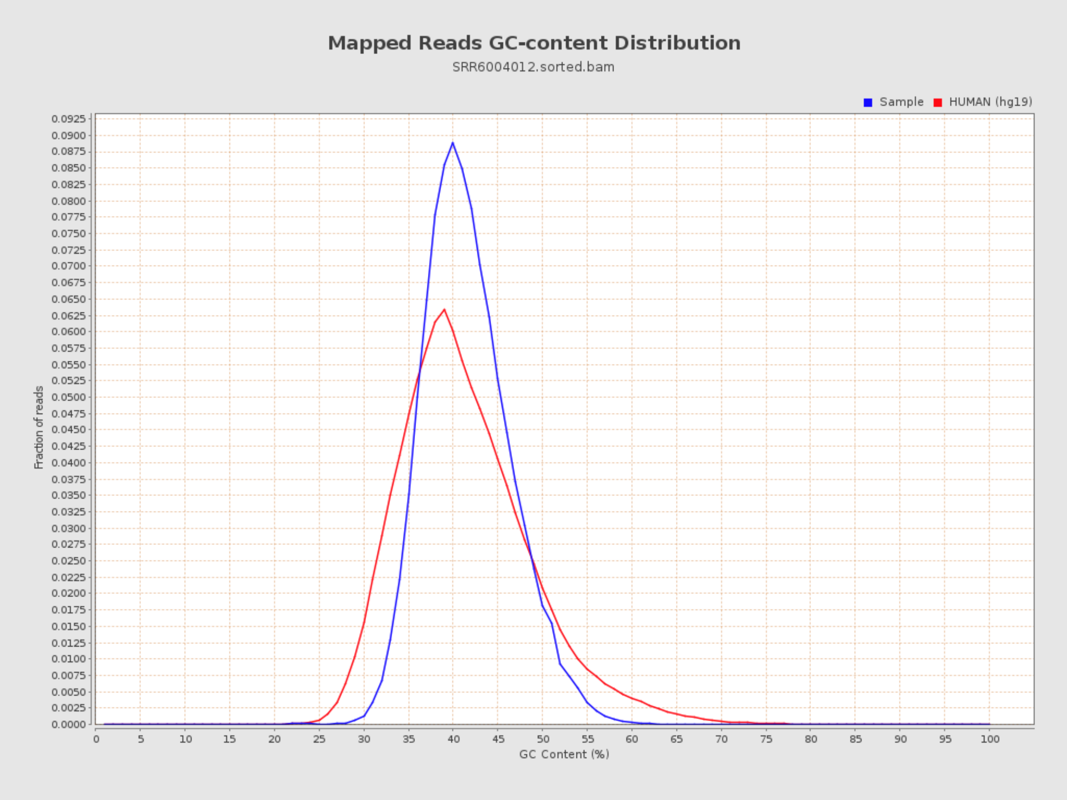
7. Results : Duplication Rate Histogram



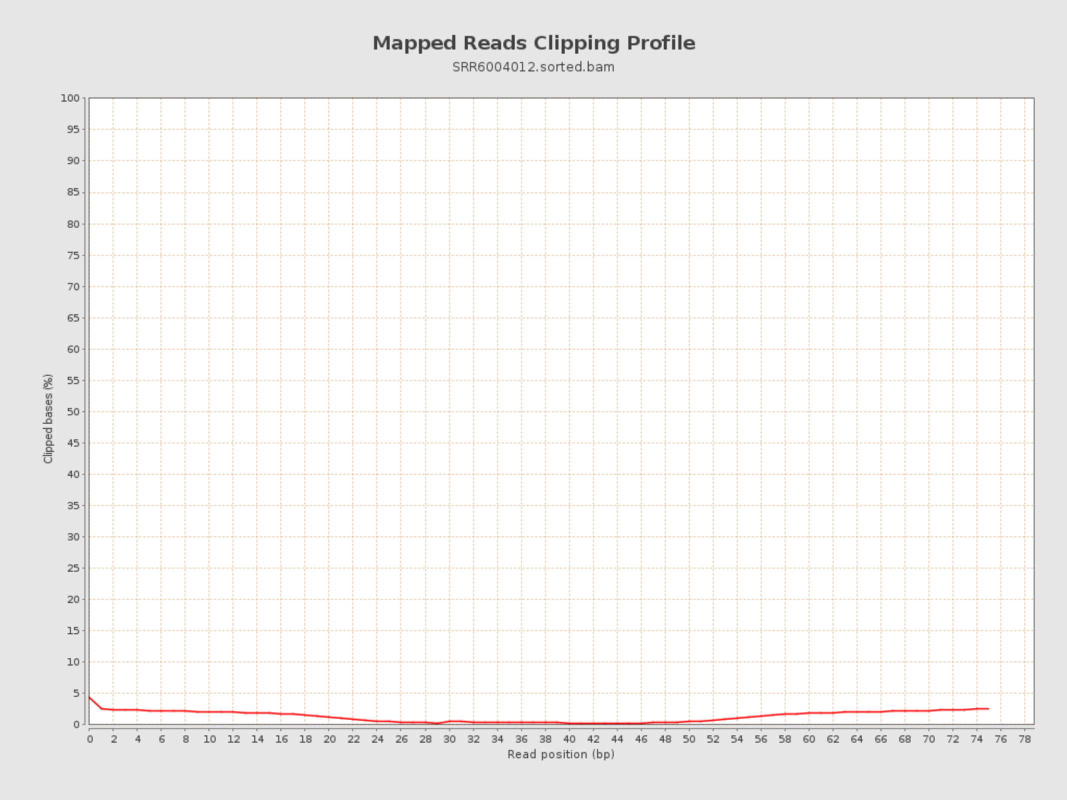
8. Results : Mapped Reads Nucleotide Content



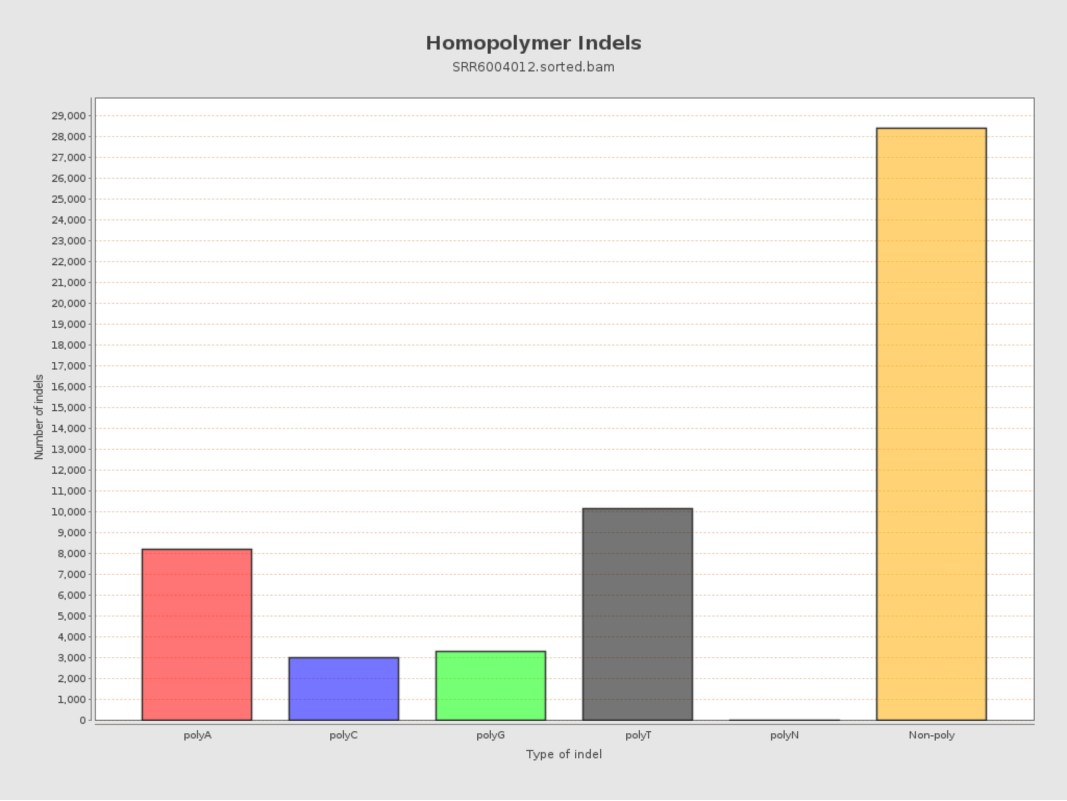
9. Results : Mapped Reads GC-content Distribution



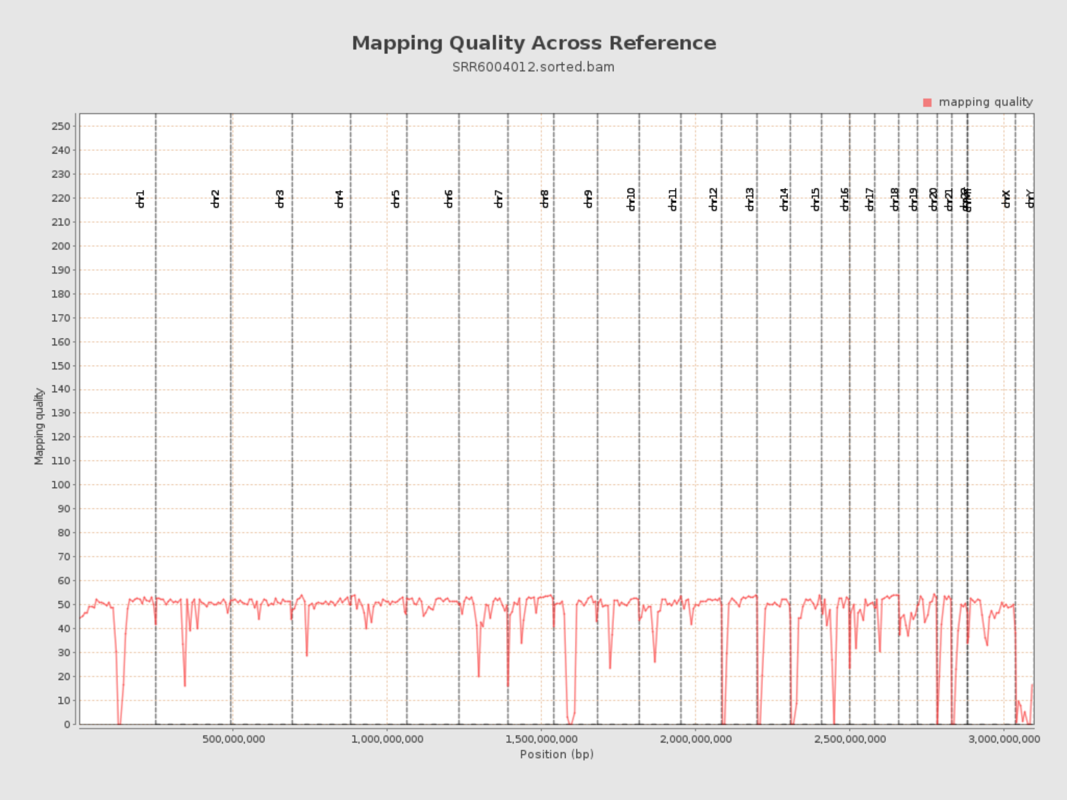
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram