Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:38:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004101.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_SRR6004101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:38:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,778,443
Mapped reads	3,096,510 / 81.95%
Unmapped reads	681,933 / 18.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,206 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	200,290 / 5.3%
Duplication rate	5.18%
Clipped reads	1,383,042 / 36.6%

2.2. ACGT Content

Number/percentage of A's	57,432,533 / 27.67%
Number/percentage of C's	38,219,220 / 18.41%
Number/percentage of T's	67,312,397 / 32.43%
Number/percentage of G's	44,557,448 / 21.47%
Number/percentage of N's	27,668 / 0.01%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0671

Standard Deviation	0.5659

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

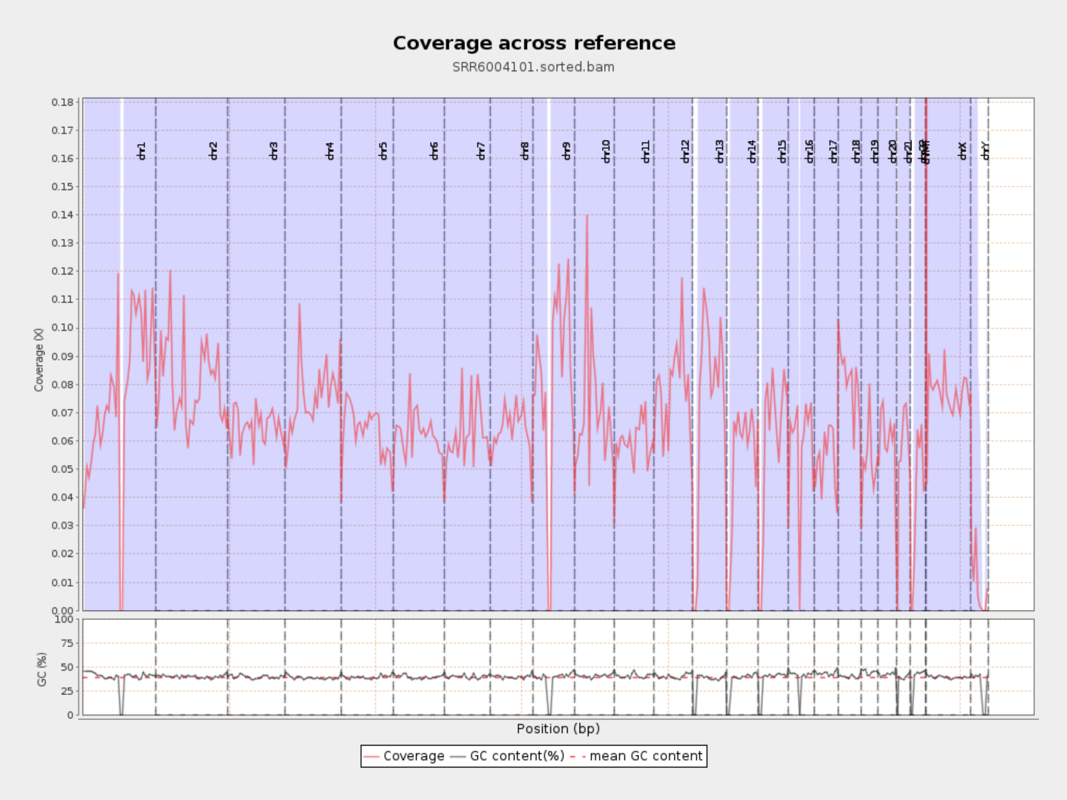
General error rate	0.95%
Mismatches	1,948,547
Insertions	17,018
Mapped reads with at least one insertion	0.54%
Deletions	50,049
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.07%

2.6. Chromosome stats

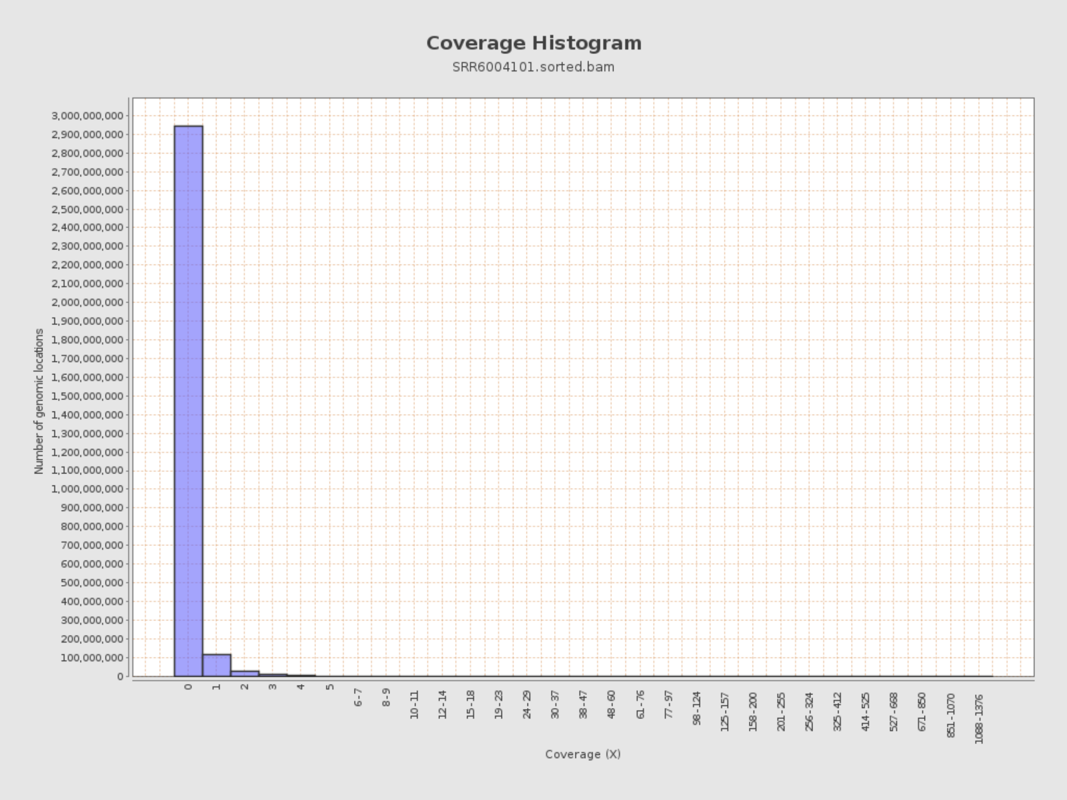
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18909400	0.0759	1.1696
chr2	243199373	19626021	0.0807	0.6301
chr3	198022430	12882442	0.0651	0.3497
chr4	191154276	14518425	0.076	0.3947
chr5	180915260	11448784	0.0633	0.3267
chr6	171115067	10732844	0.0627	0.4021
chr7	159138663	9929404	0.0624	0.5622

chr8	146364022	9343523	0.0638	0.6179
chr9	141213431	11735227	0.0831	0.53
chr10	135534747	9687184	0.0715	0.7407
chr11	135006516	8068493	0.0598	0.3983
chr12	133851895	10535714	0.0787	0.3726
chr13	115169878	8440810	0.0733	0.356
chr14	107349540	5647683	0.0526	0.3188
chr15	102531392	6018303	0.0587	0.3201
chr16	90354753	5132656	0.0568	0.3562
chr17	81195210	4381615	0.054	0.3332
chr18	78077248	6386321	0.0818	0.9007
chr19	59128983	3189360	0.0539	0.7078
chr20	63025520	3883378	0.0616	0.3389
chr21	48129895	2652400	0.0551	0.3463
chr22	51304566	2002536	0.039	0.254
chrMT	16571	55198	3.331	2.9377
chrX	155270560	11901912	0.0767	0.3881
chrY	59373566	521889	0.0088	0.2163

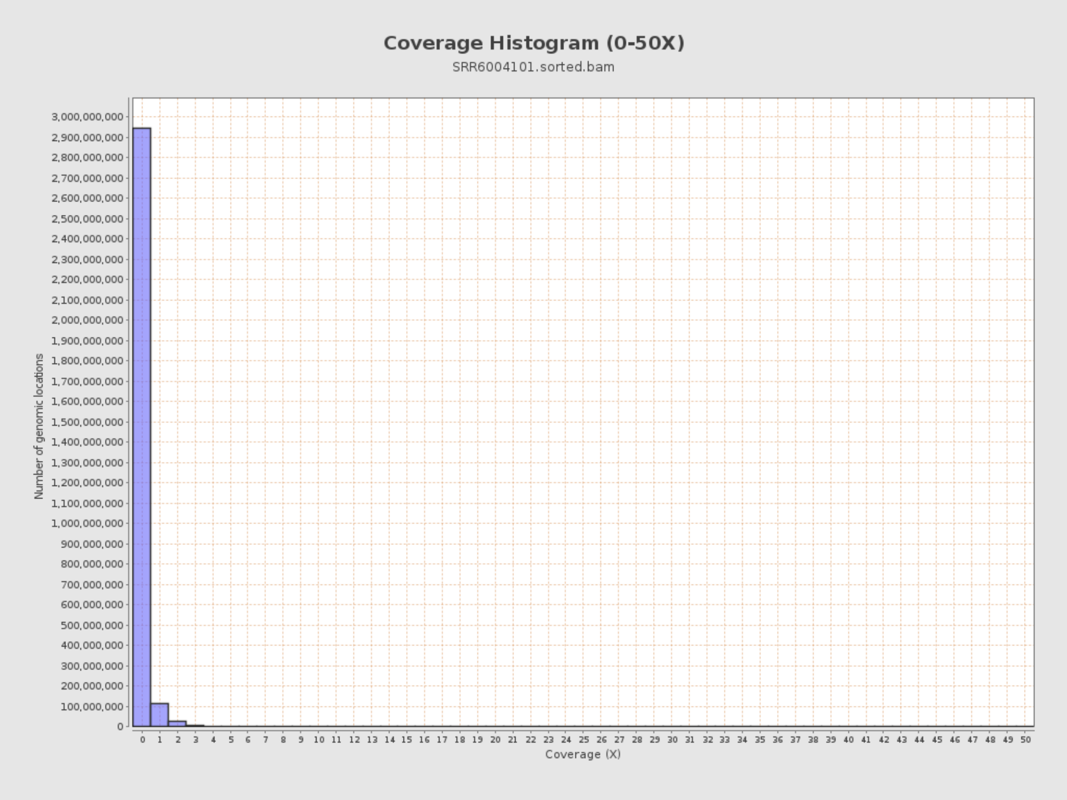
3. Results : Coverage across reference



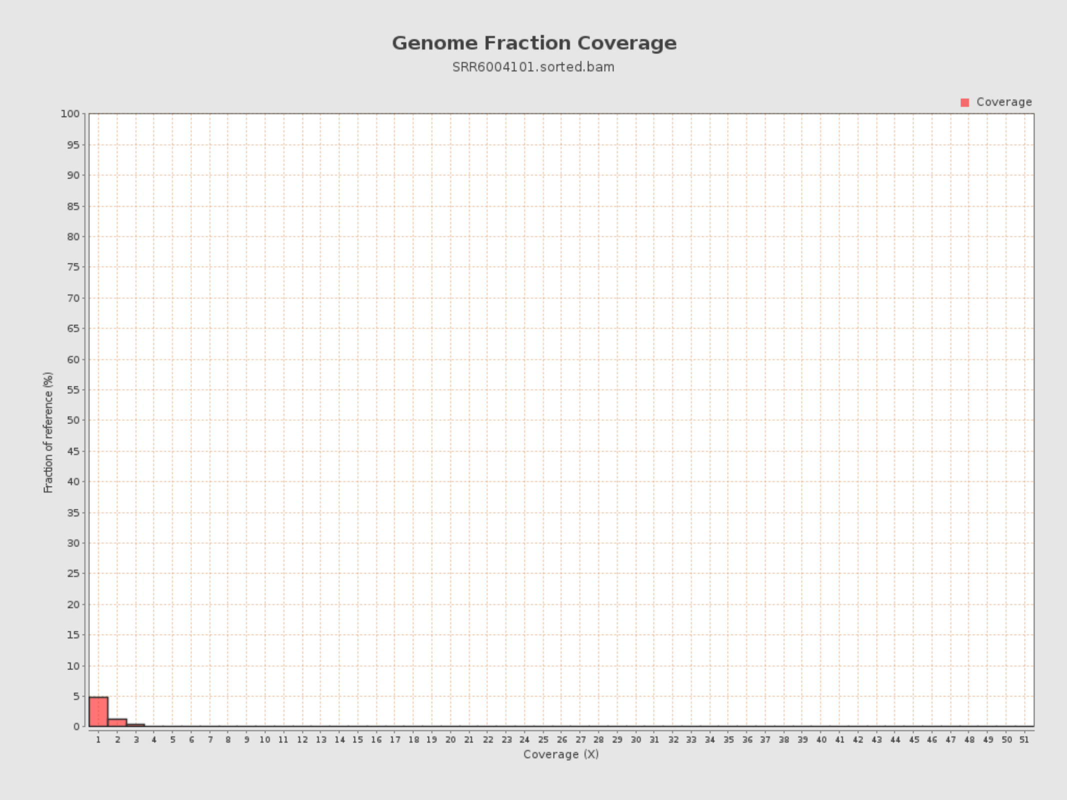
4. Results : Coverage Histogram



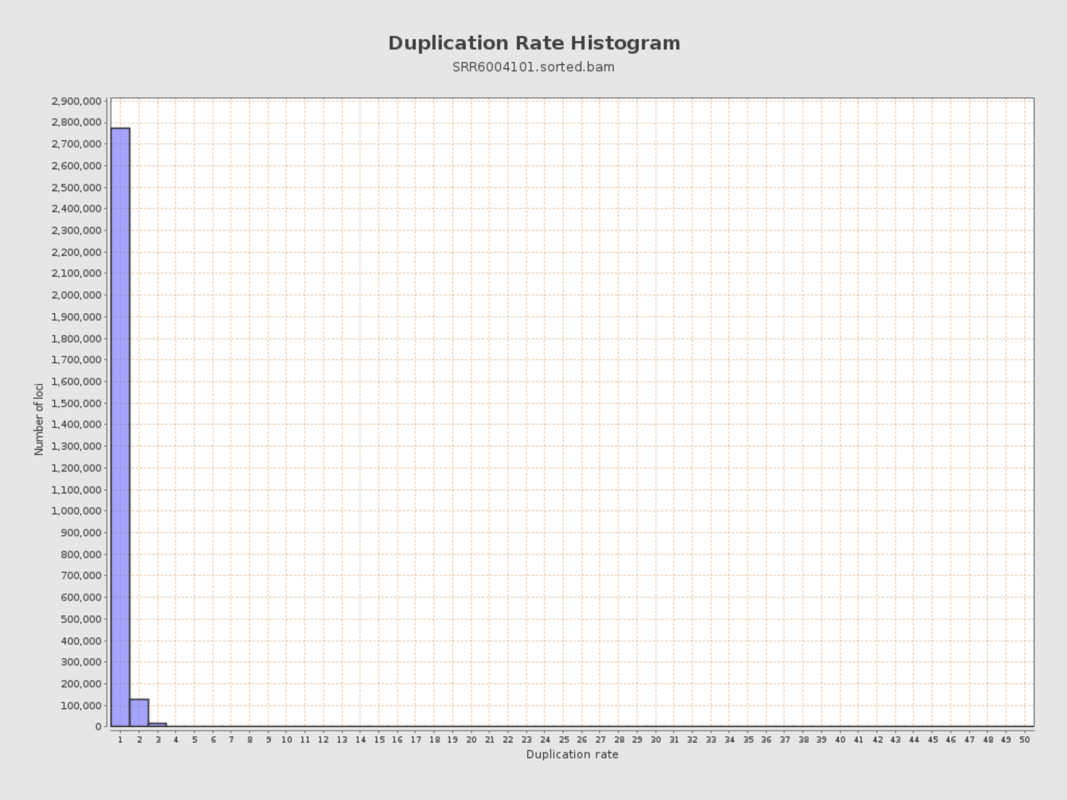
5. Results : Coverage Histogram (0-50X)



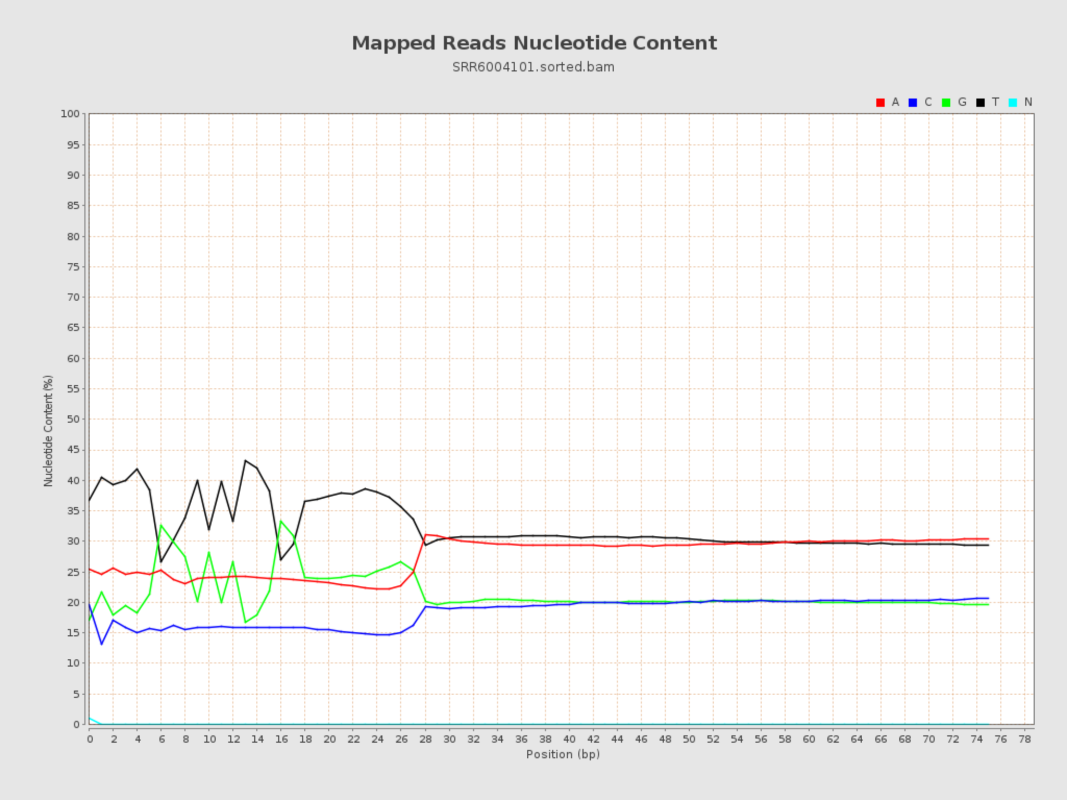
6. Results : Genome Fraction Coverage



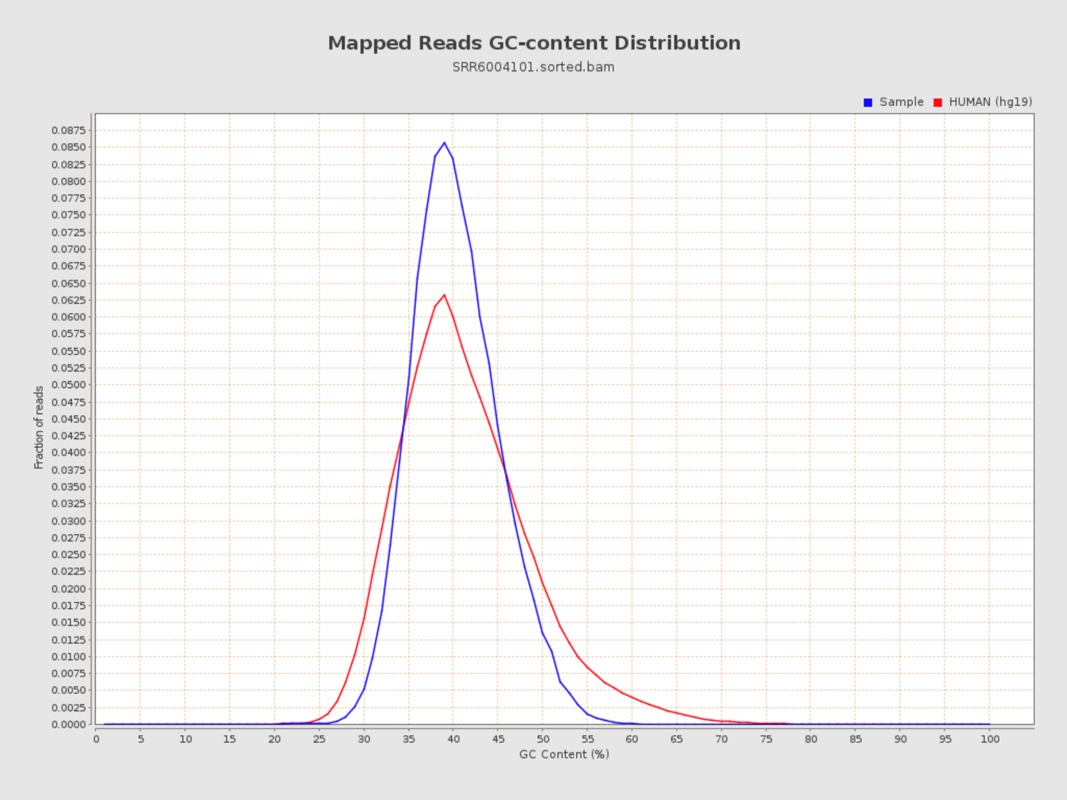
7. Results : Duplication Rate Histogram



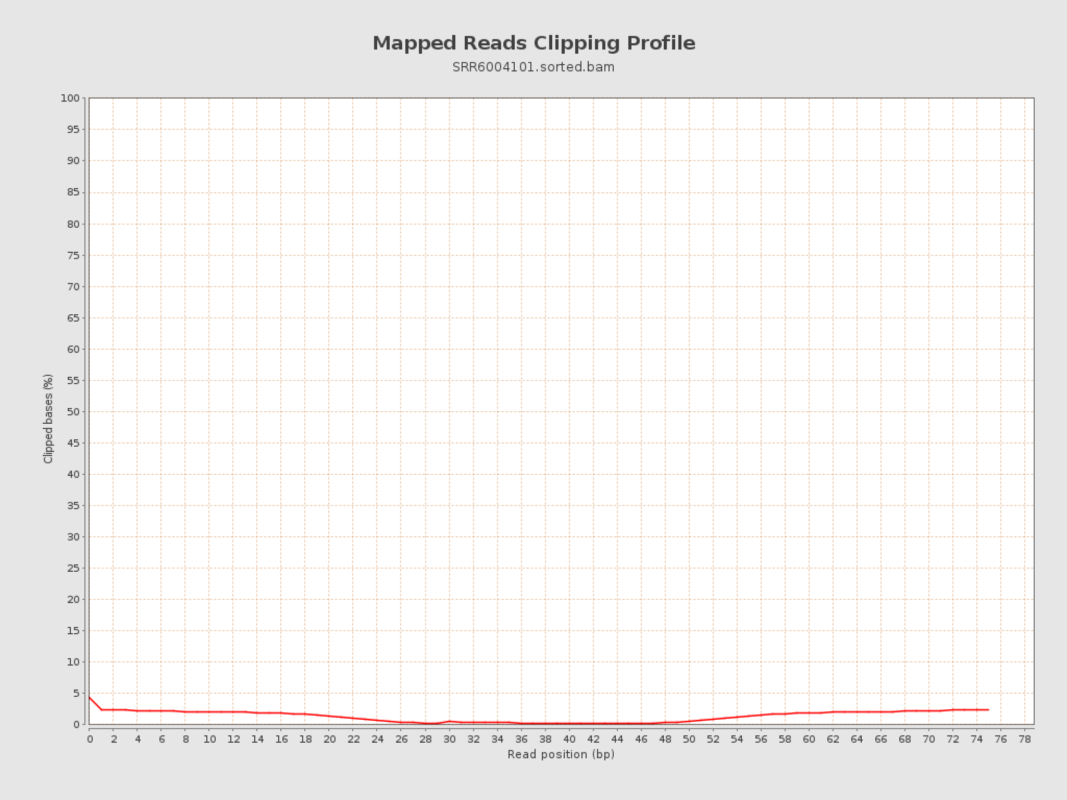
8. Results : Mapped Reads Nucleotide Content



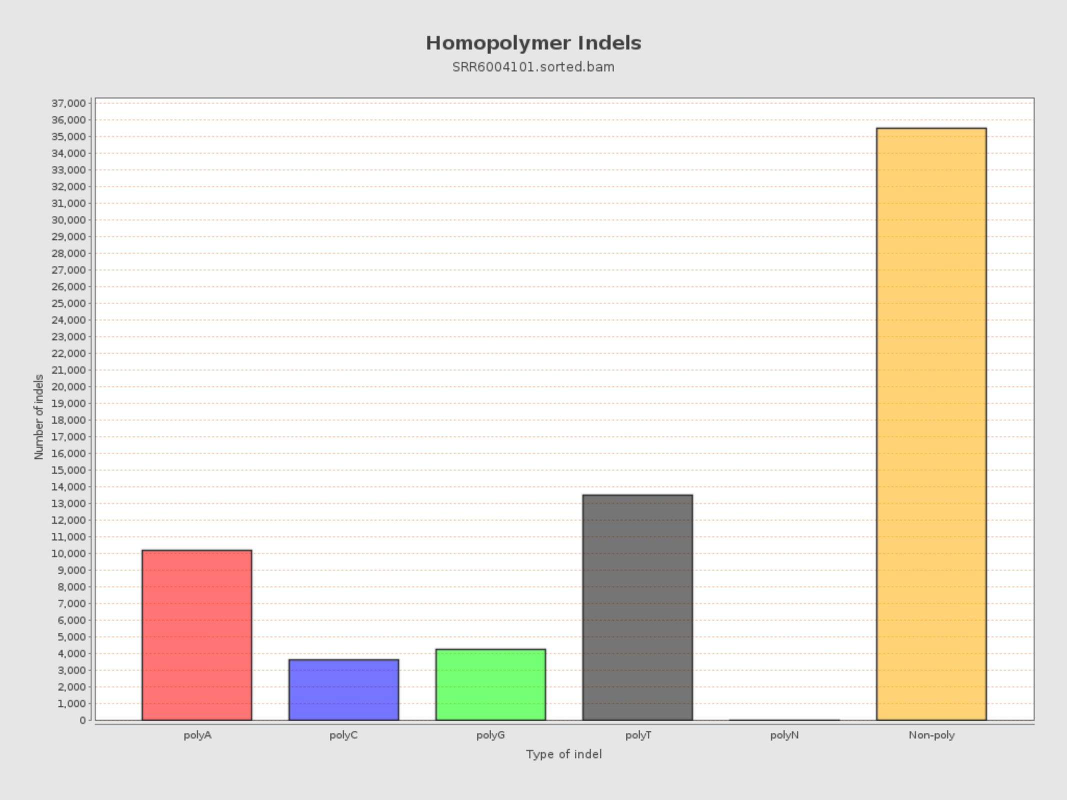
9. Results : Mapped Reads GC-content Distribution



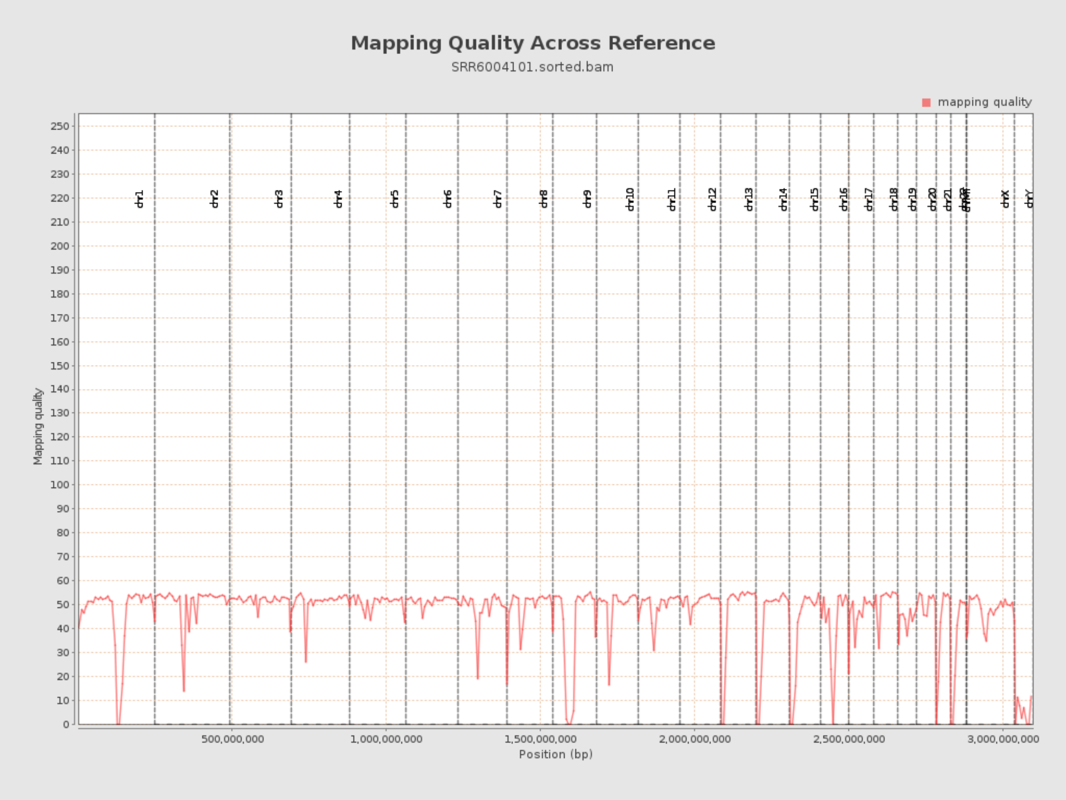
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram