Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004051.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_SRR6004051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,595,605
Mapped reads	1,705,921 / 65.72%
Unmapped reads	889,684 / 34.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,362 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	50,424 / 1.94%
Duplication rate	1.89%
Clipped reads	920,134 / 35.45%

2.2. ACGT Content

Number/percentage of A's	30,589,784 / 28.03%
Number/percentage of C's	20,926,142 / 19.17%
Number/percentage of T's	32,785,997 / 30.04%
Number/percentage of G's	24,831,011 / 22.75%
Number/percentage of N's	12,521 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0353

Standard Deviation	0.3311

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

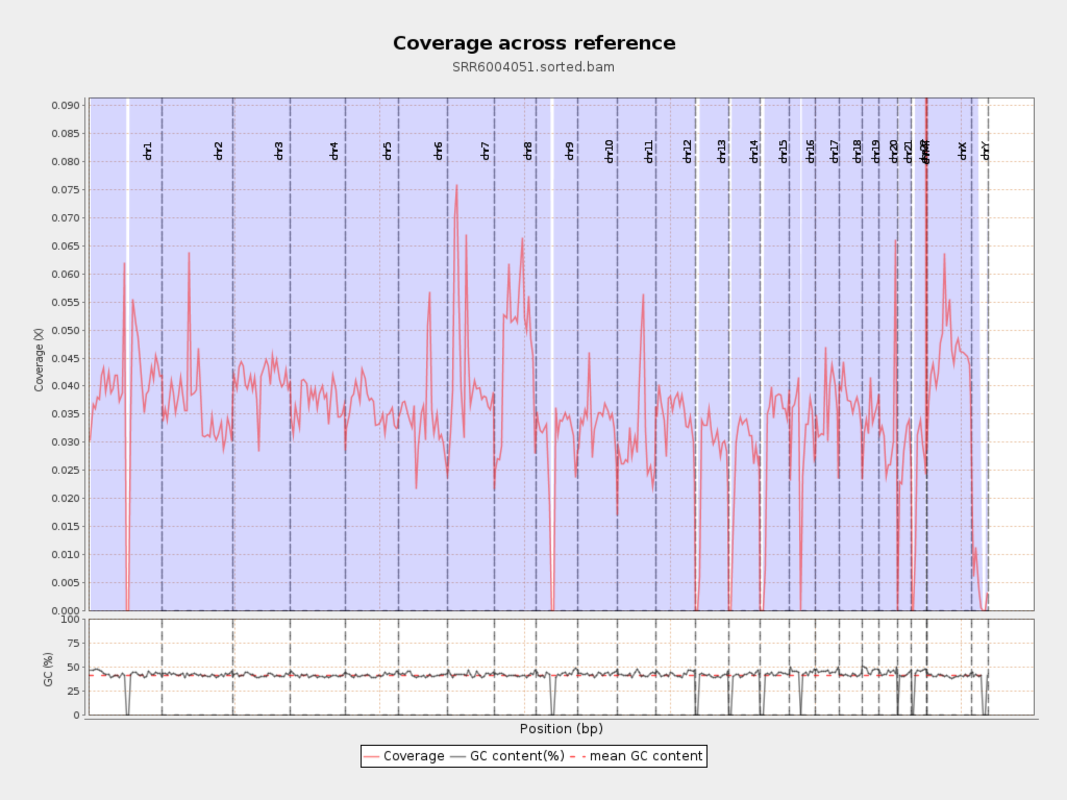
General error rate	0.79%
Mismatches	846,524
Insertions	8,579
Mapped reads with at least one insertion	0.5%
Deletions	28,228
Mapped reads with at least one deletion	1.63%
Homopolymer indels	43.99%

2.6. Chromosome stats

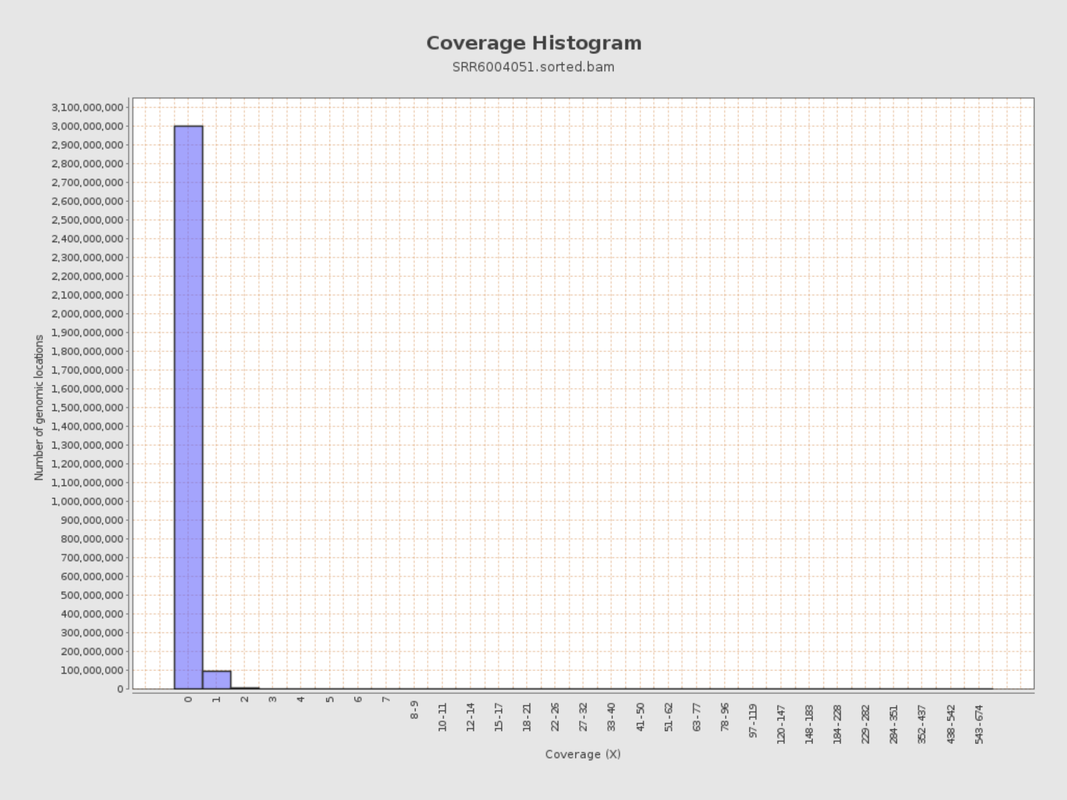
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9727762	0.039	0.5754
chr2	243199373	8796452	0.0362	0.3983
chr3	198022430	8169854	0.0413	0.2236
chr4	191154276	7111066	0.0372	0.2284
chr5	180915260	6559556	0.0363	0.2185
chr6	171115067	5910216	0.0345	0.2248
chr7	159138663	6889297	0.0433	0.5106

chr8	146364022	6843657	0.0468	0.3558
chr9	141213431	4007598	0.0284	0.3014
chr10	135534747	4632973	0.0342	0.269
chr11	135006516	4178662	0.031	0.2928
chr12	133851895	4708432	0.0352	0.212
chr13	115169878	3007069	0.0261	0.1779
chr14	107349540	2784697	0.0259	0.2032
chr15	102531392	3015676	0.0294	0.2184
chr16	90354753	2785389	0.0308	0.2115
chr17	81195210	2916216	0.0359	0.2265
chr18	78077248	2974260	0.0381	0.5251
chr19	59128983	2038944	0.0345	0.3815
chr20	63025520	2123514	0.0337	0.2394
chr21	48129895	1216091	0.0253	0.1916
chr22	51304566	1071554	0.0209	0.174
chrMT	16571	340369	20.54	14.1298
chrX	155270560	7115818	0.0458	0.274
chrY	59373566	269096	0.0045	0.0902

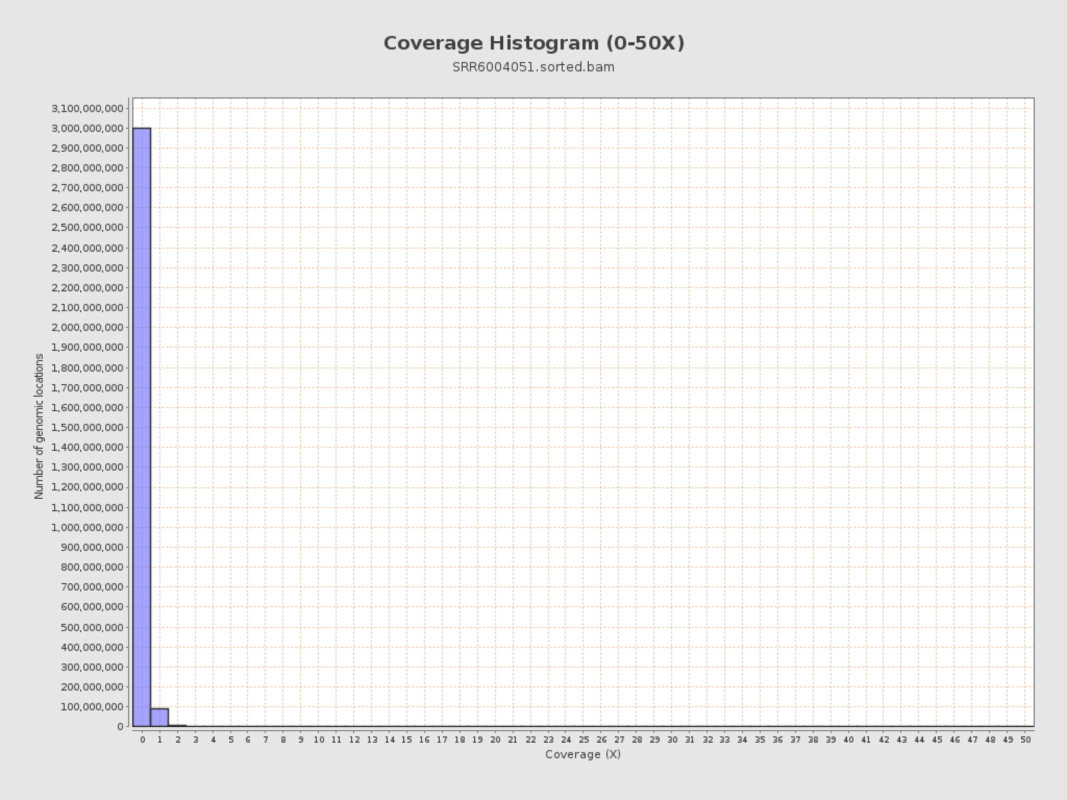
3. Results : Coverage across reference



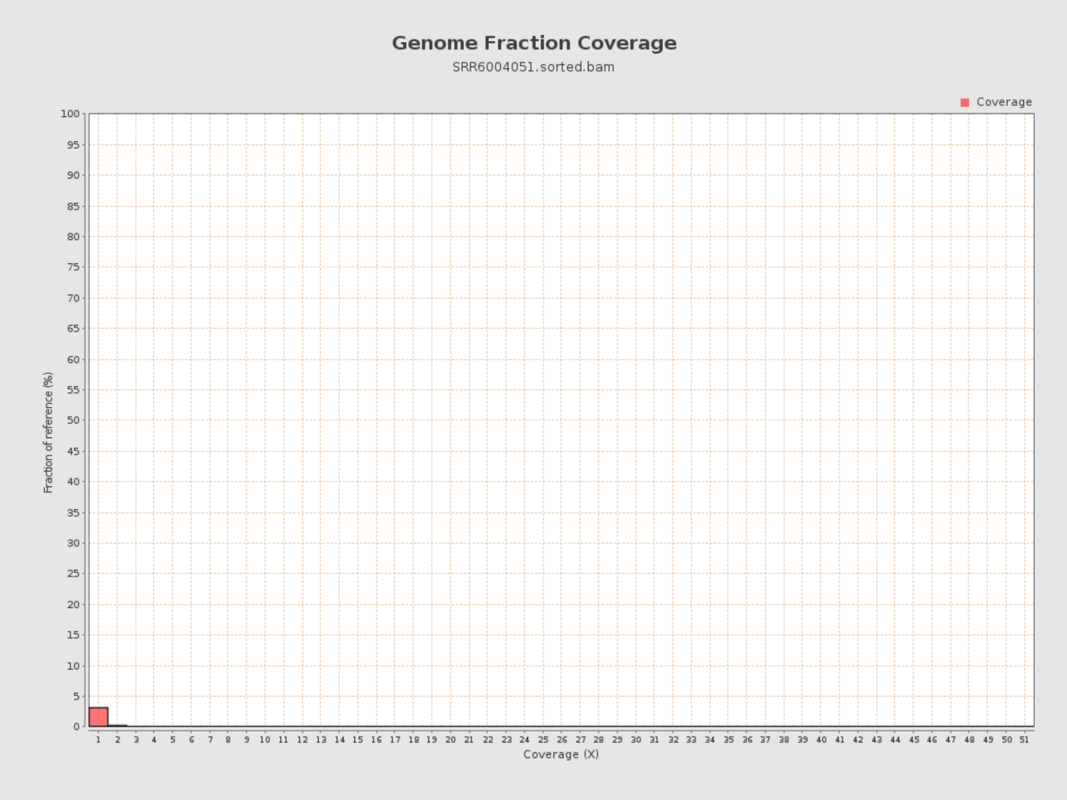
4. Results : Coverage Histogram



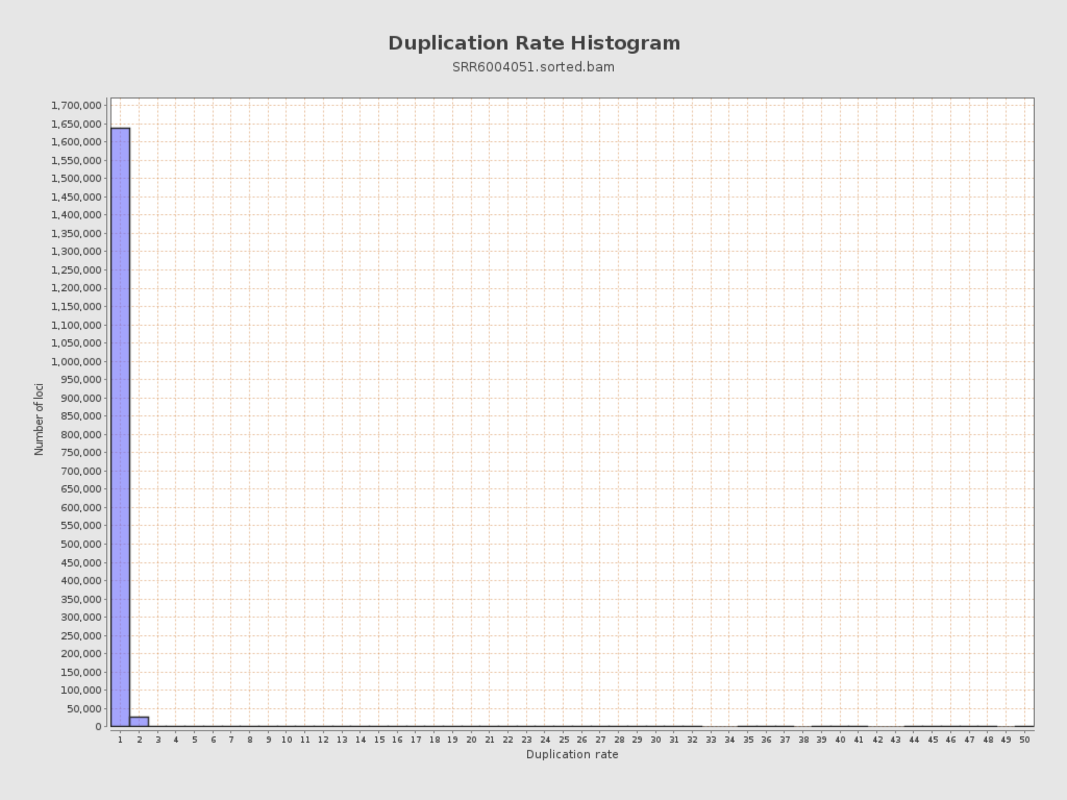
5. Results : Coverage Histogram (0-50X)



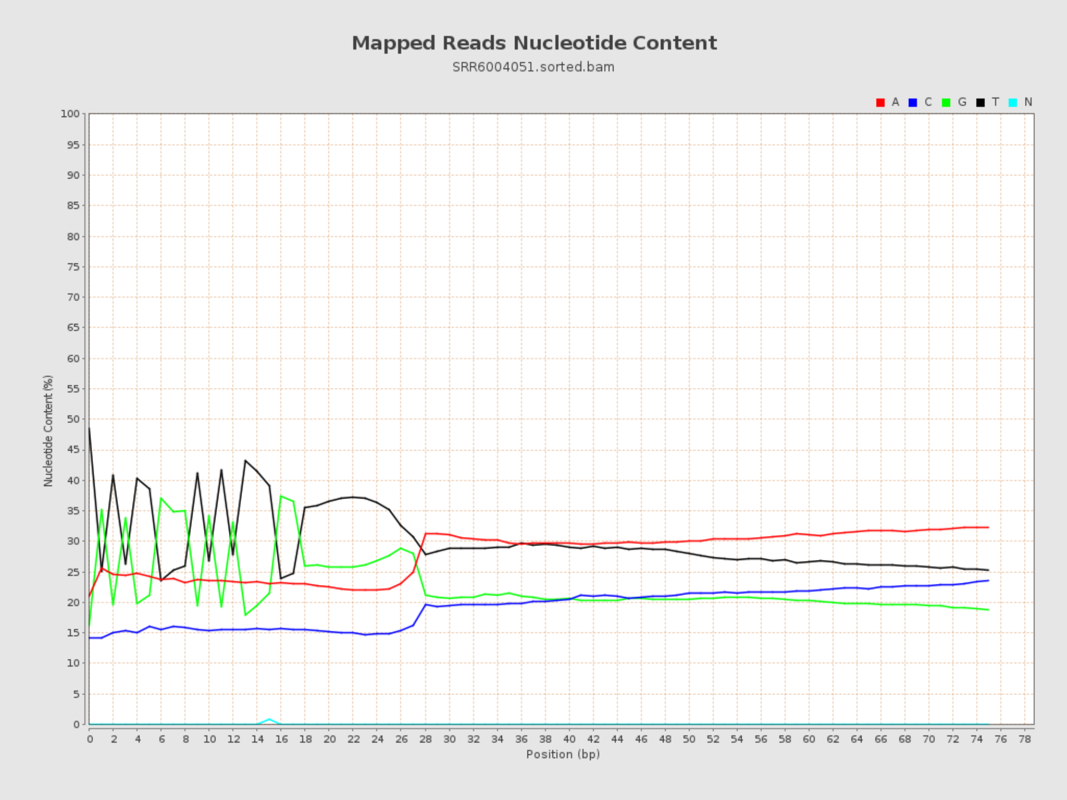
6. Results : Genome Fraction Coverage



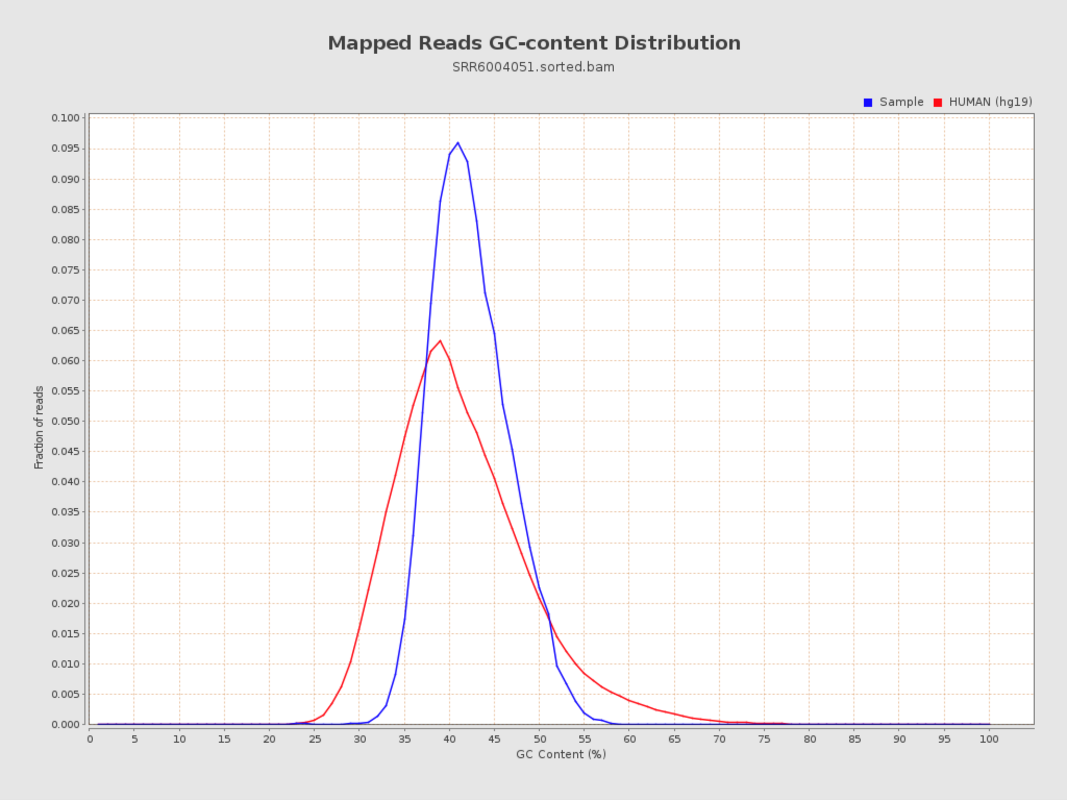
7. Results : Duplication Rate Histogram



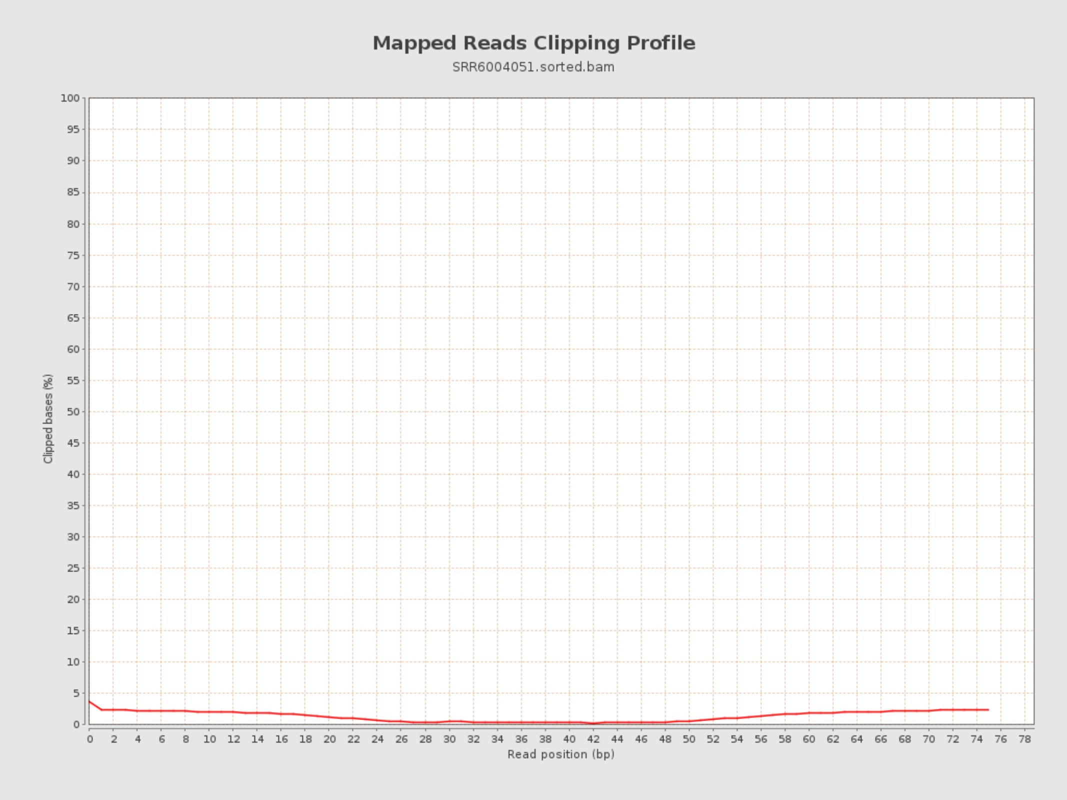
8. Results : Mapped Reads Nucleotide Content



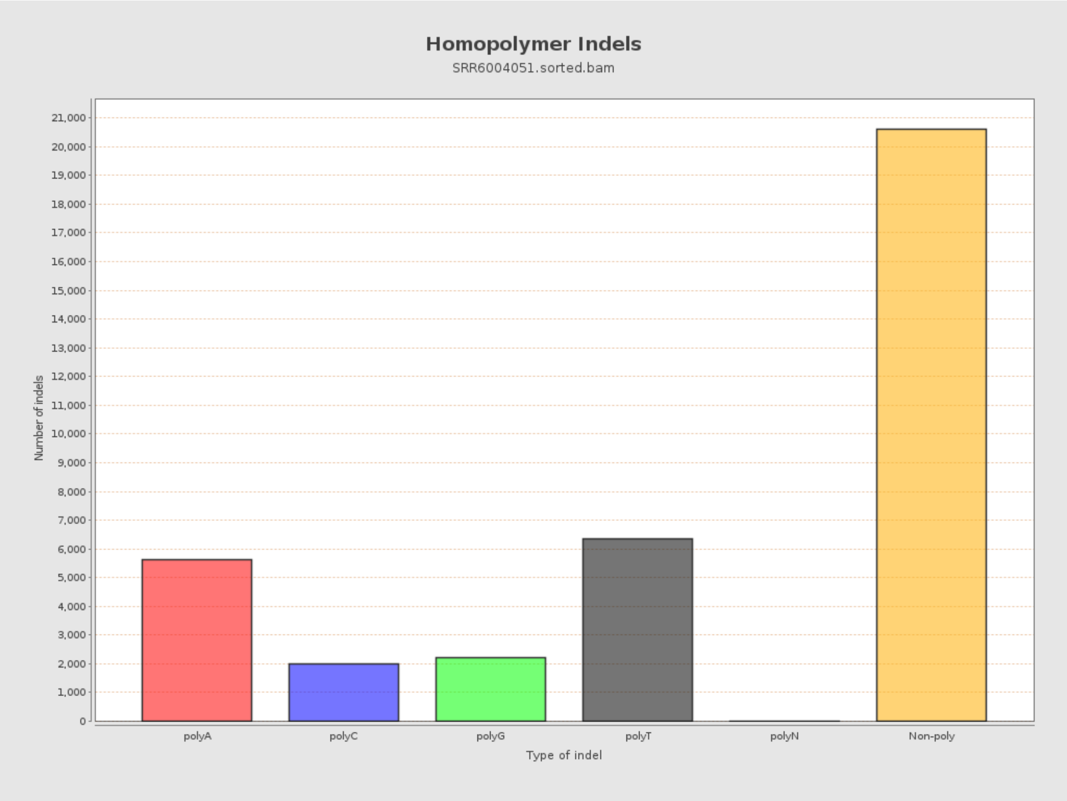
9. Results : Mapped Reads GC-content Distribution



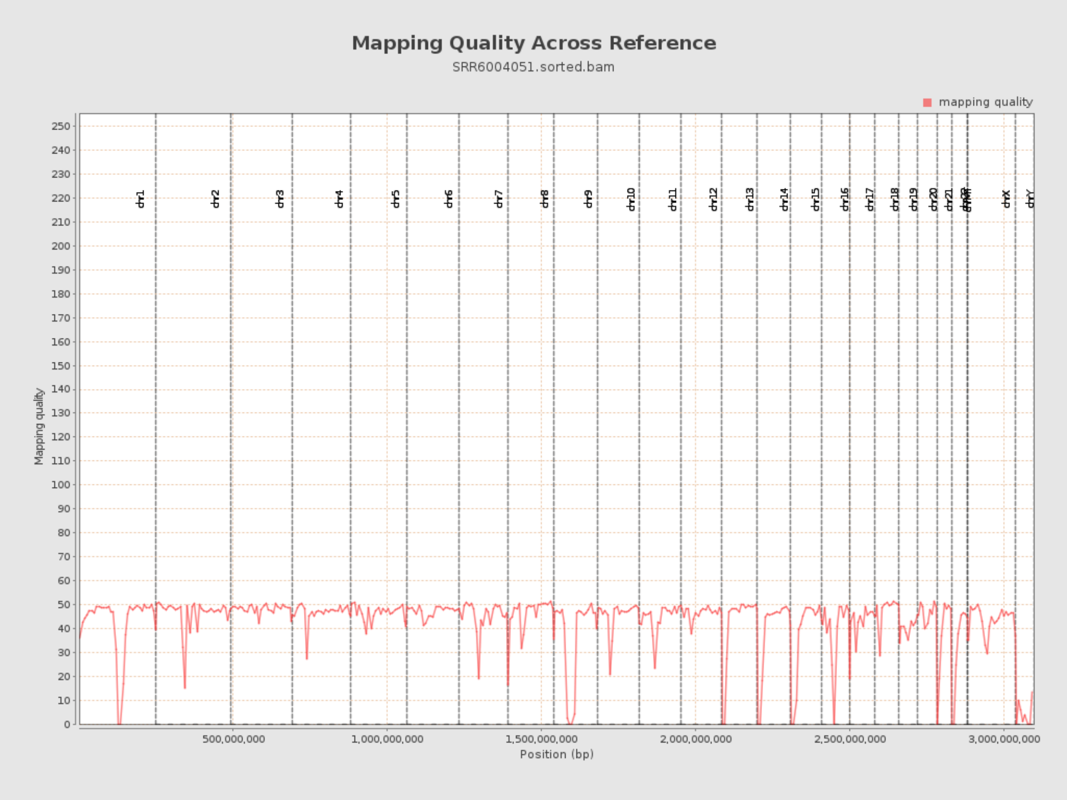
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram