Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:10:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004021.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_SRR6004021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:10:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,193,115
Mapped reads	2,713,725 / 84.99%
Unmapped reads	479,390 / 15.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,390 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	206,913 / 6.48%
Duplication rate	5.96%
Clipped reads	1,265,706 / 39.64%

2.2. ACGT Content

Number/percentage of A's	50,199,472 / 27.99%
Number/percentage of C's	32,462,965 / 18.1%
Number/percentage of T's	57,540,228 / 32.08%
Number/percentage of G's	39,058,667 / 21.78%
Number/percentage of N's	97,061 / 0.05%
GC Percentage	39.88%

2.3. Coverage

Mean	0.058

Standard Deviation	0.5625

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

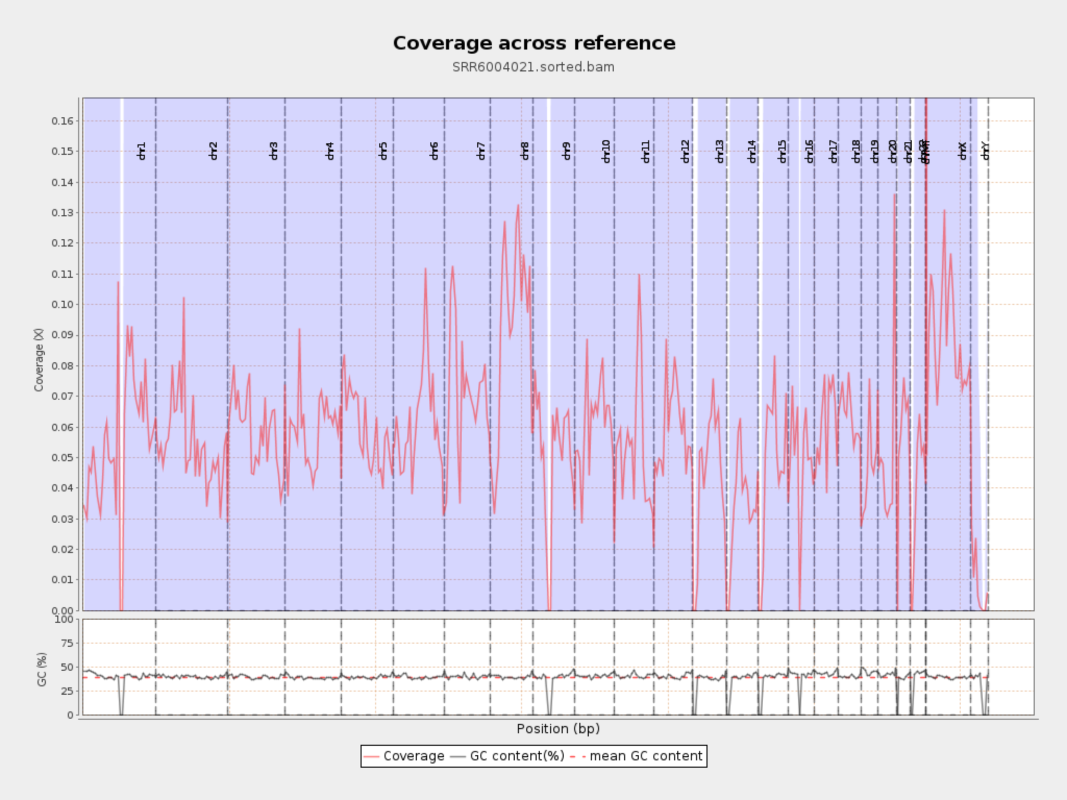
General error rate	0.9%
Mismatches	1,583,996
Insertions	13,612
Mapped reads with at least one insertion	0.5%
Deletions	62,399
Mapped reads with at least one deletion	2.27%
Homopolymer indels	44.98%

2.6. Chromosome stats

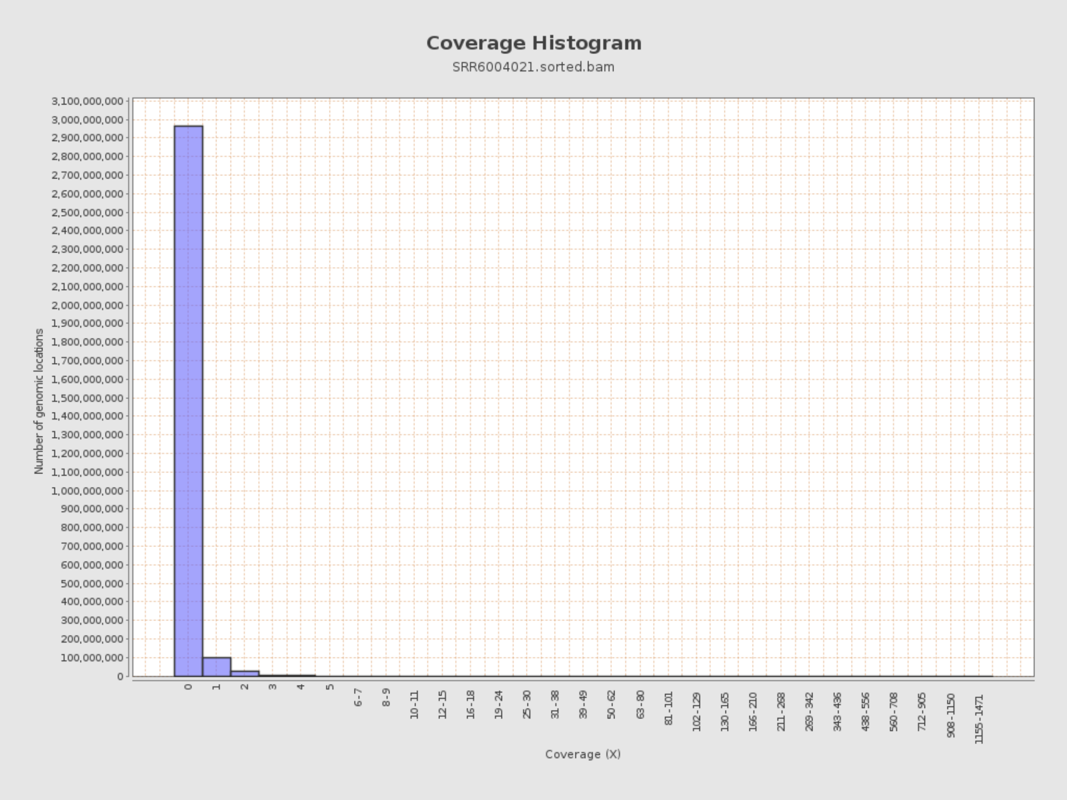
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13794772	0.0553	1.1351
chr2	243199373	13301945	0.0547	0.5437
chr3	198022430	11585483	0.0585	0.3133
chr4	191154276	11261451	0.0589	0.3388
chr5	180915260	10654973	0.0589	0.3231
chr6	171115067	10627060	0.0621	0.3792
chr7	159138663	11134236	0.07	0.6062

chr8	146364022	13473549	0.0921	0.9705
chr9	141213431	7231205	0.0512	0.496
chr10	135534747	8288269	0.0612	0.443
chr11	135006516	7158366	0.053	0.4354
chr12	133851895	8016330	0.0599	0.3357
chr13	115169878	5023598	0.0436	0.2722
chr14	107349540	3640025	0.0339	0.274
chr15	102531392	4809621	0.0469	0.285
chr16	90354753	4338151	0.048	0.332
chr17	81195210	4948252	0.0609	0.3485
chr18	78077248	5003094	0.0641	0.9911
chr19	59128983	2794524	0.0473	0.7083
chr20	63025520	3366974	0.0534	0.3141
chr21	48129895	2659879	0.0553	0.334
chr22	51304566	1974717	0.0385	0.2476
chrMT	16571	24645	1.4872	1.7702
chrX	155270560	13851581	0.0892	0.4749
chrY	59373566	501518	0.0084	0.1652

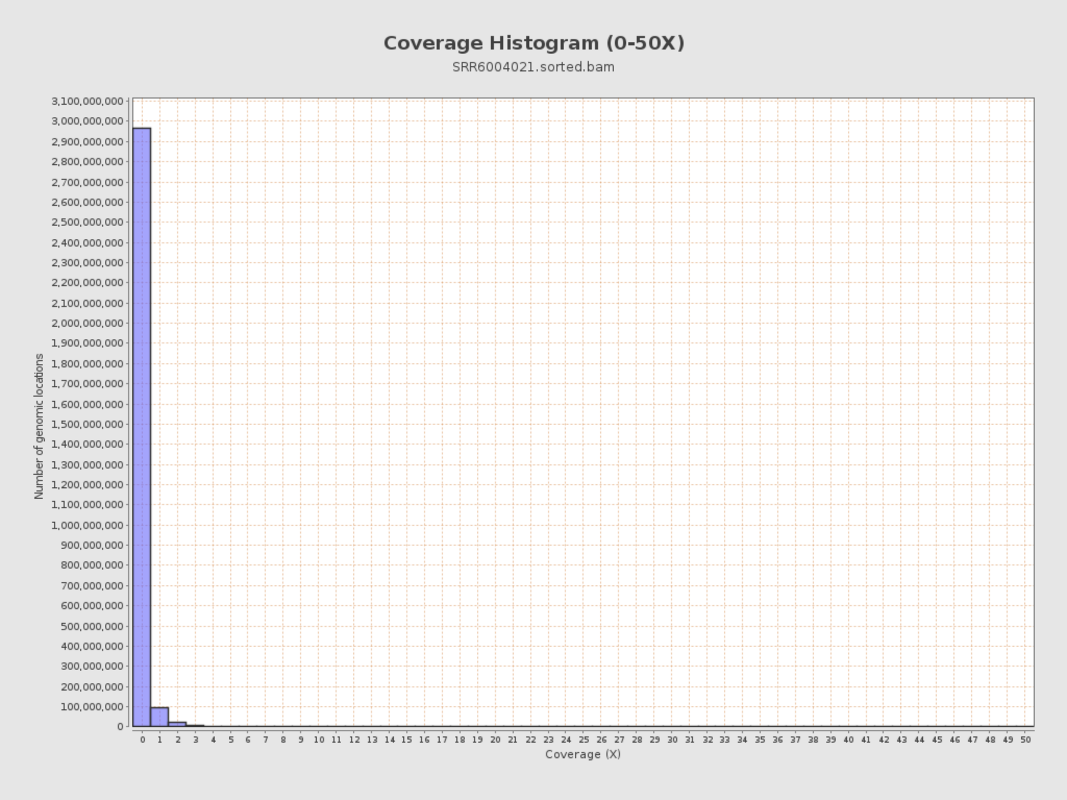
3. Results : Coverage across reference



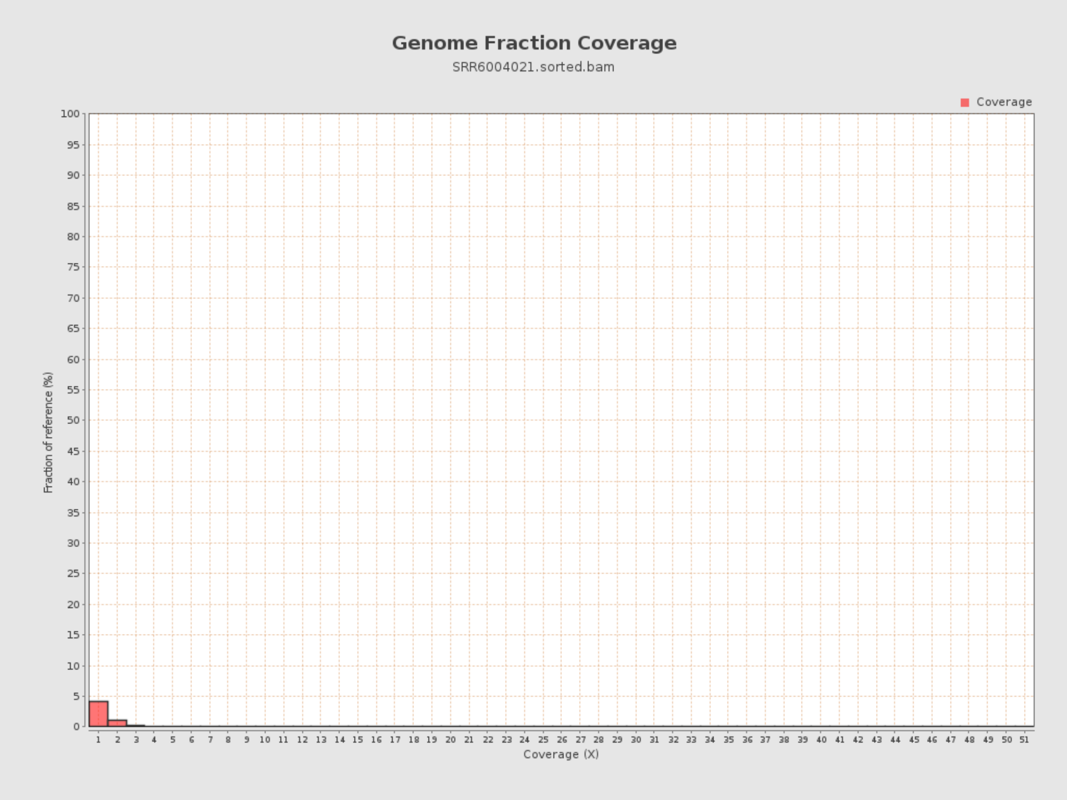
4. Results : Coverage Histogram



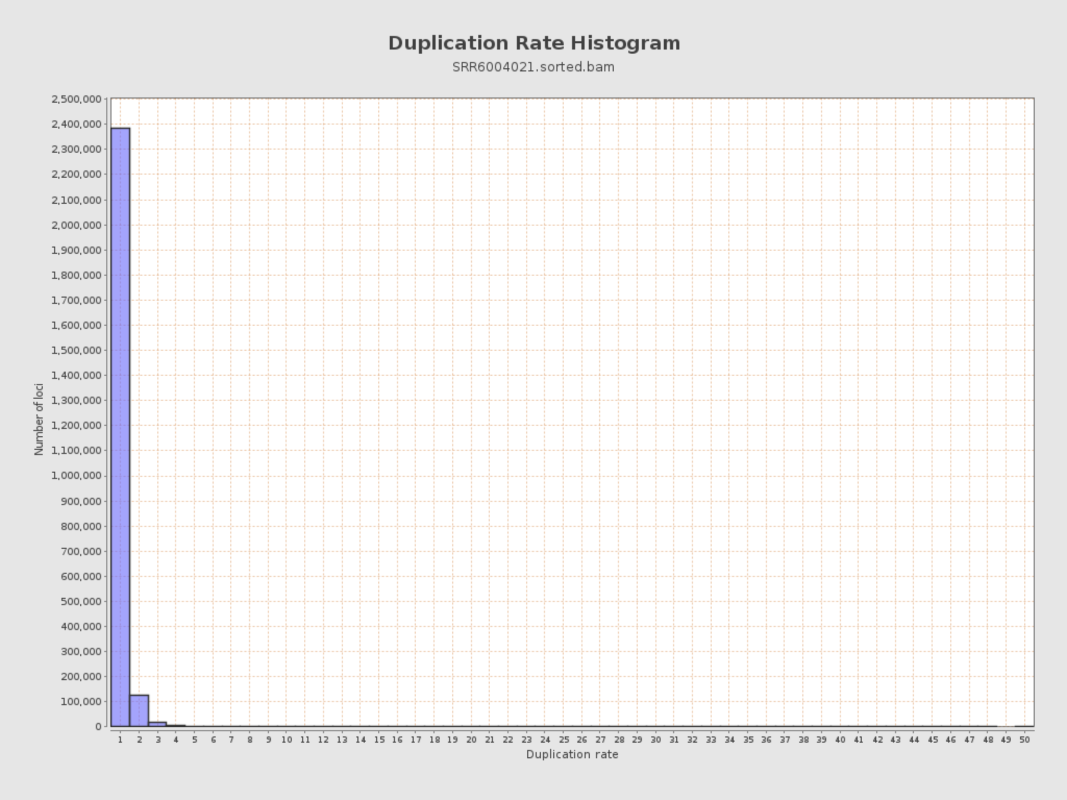
5. Results : Coverage Histogram (0-50X)



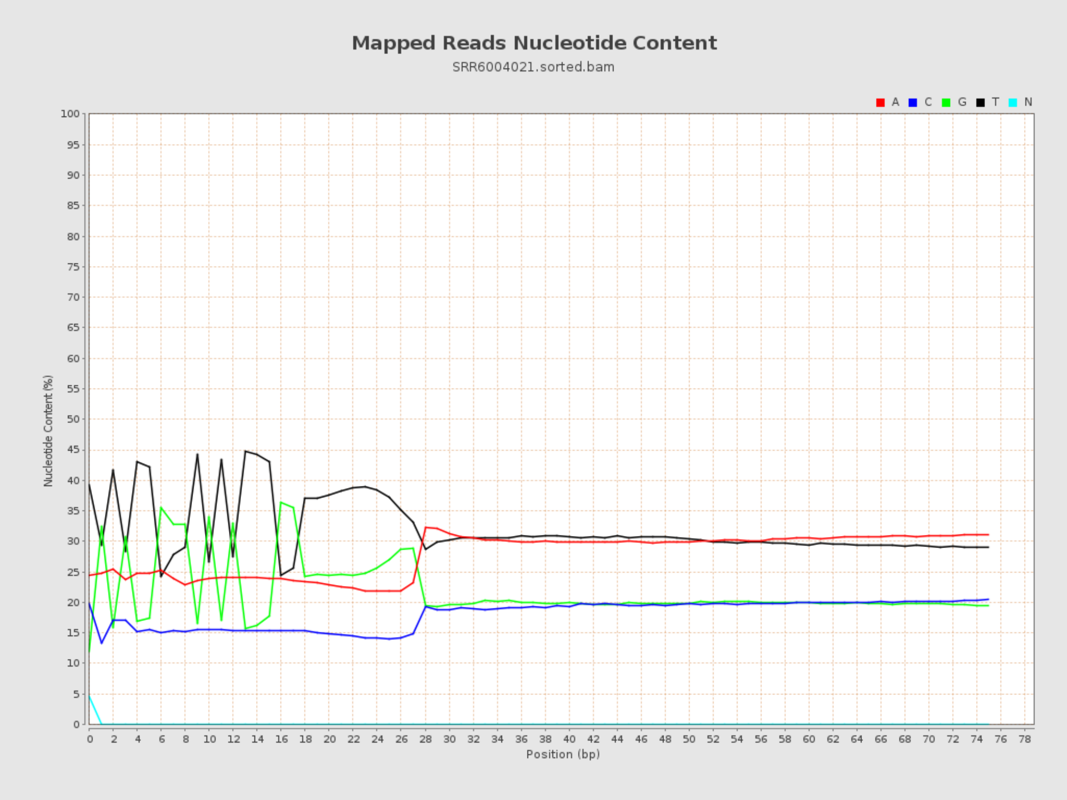
6. Results : Genome Fraction Coverage



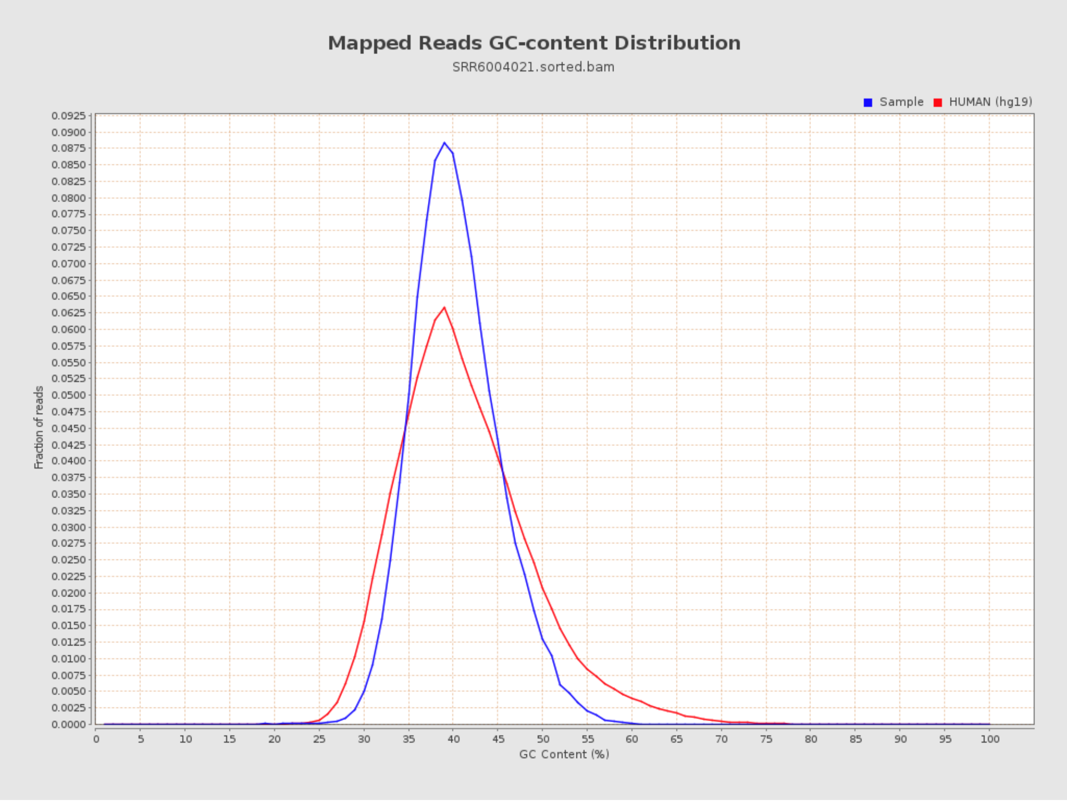
7. Results : Duplication Rate Histogram



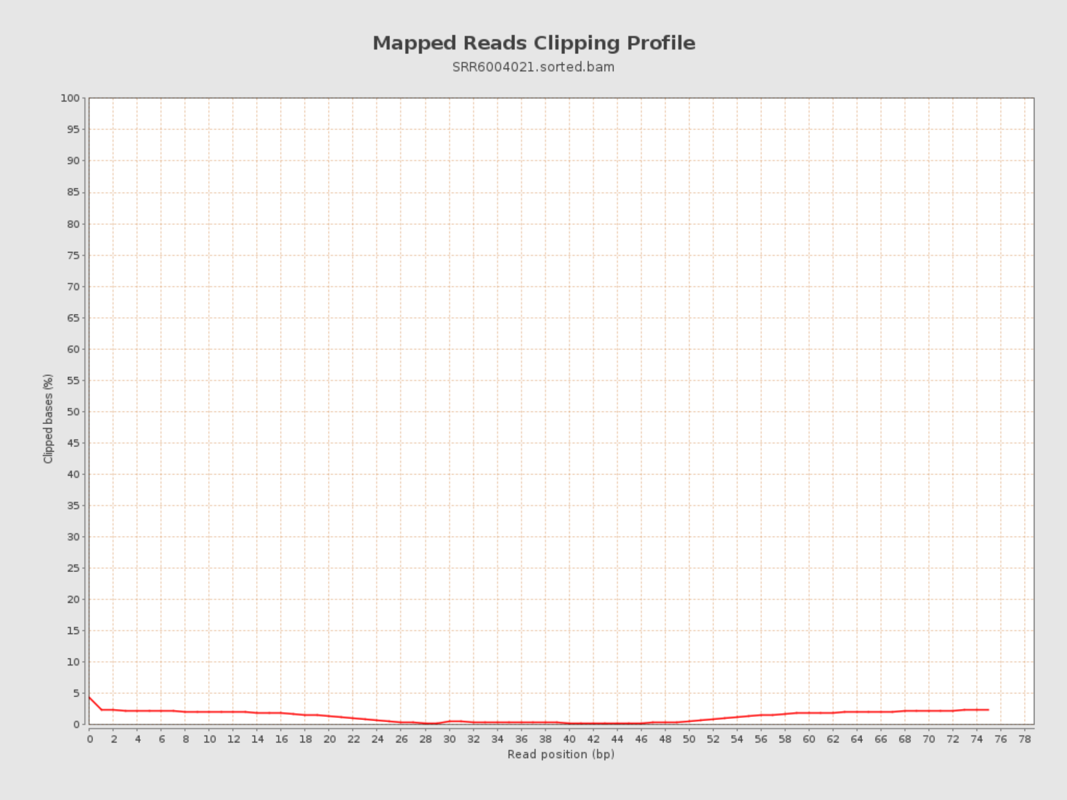
8. Results : Mapped Reads Nucleotide Content



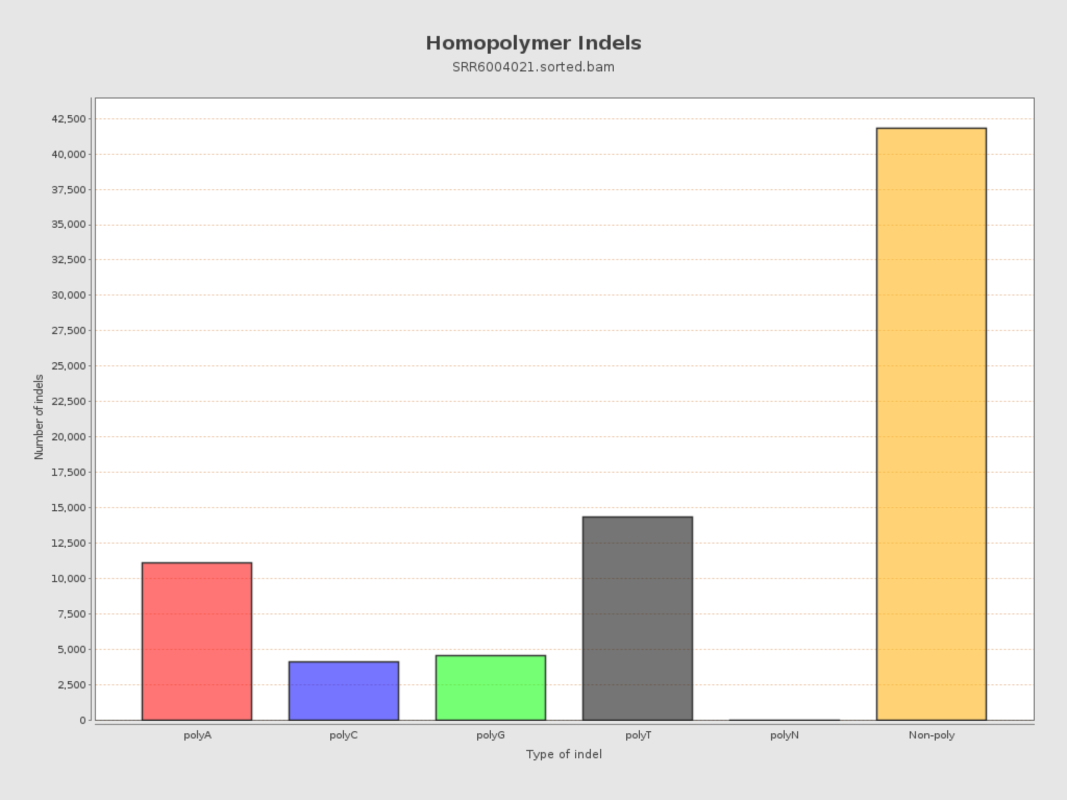
9. Results : Mapped Reads GC-content Distribution



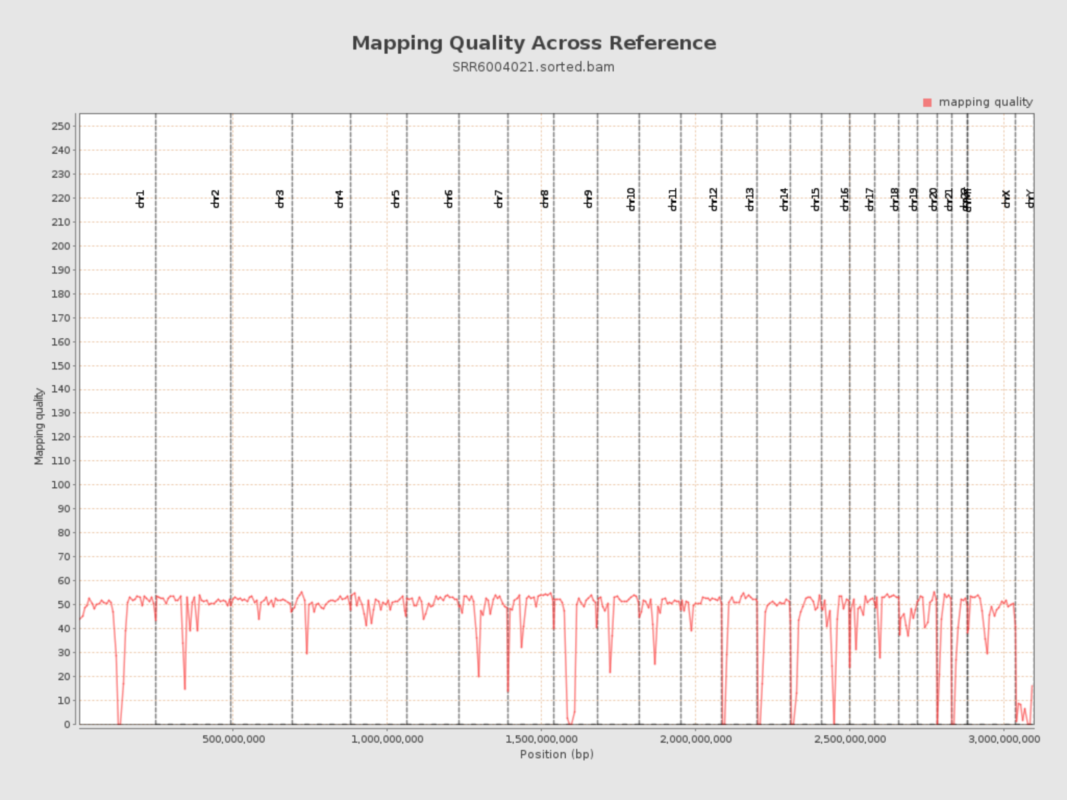
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram