

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:41:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524864.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_SRR10524864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524864.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:41:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,814,849
Mapped reads	1,680,062 / 92.57%
Unmapped reads	134,787 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,813 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	52,592 / 2.9%
Duplication rate	2.16%
Clipped reads	1,685,822 / 92.89%

2.2. ACGT Content

Number/percentage of A's	24,547,494 / 24.87%
Number/percentage of C's	18,070,142 / 18.31%
Number/percentage of T's	31,965,333 / 32.39%
Number/percentage of G's	24,098,673 / 24.42%
Number/percentage of N's	12,462 / 0.01%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.3091
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2.4. Mapping Quality

Mean Mapping Quality	45.51
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2.5. Mismatches and indels

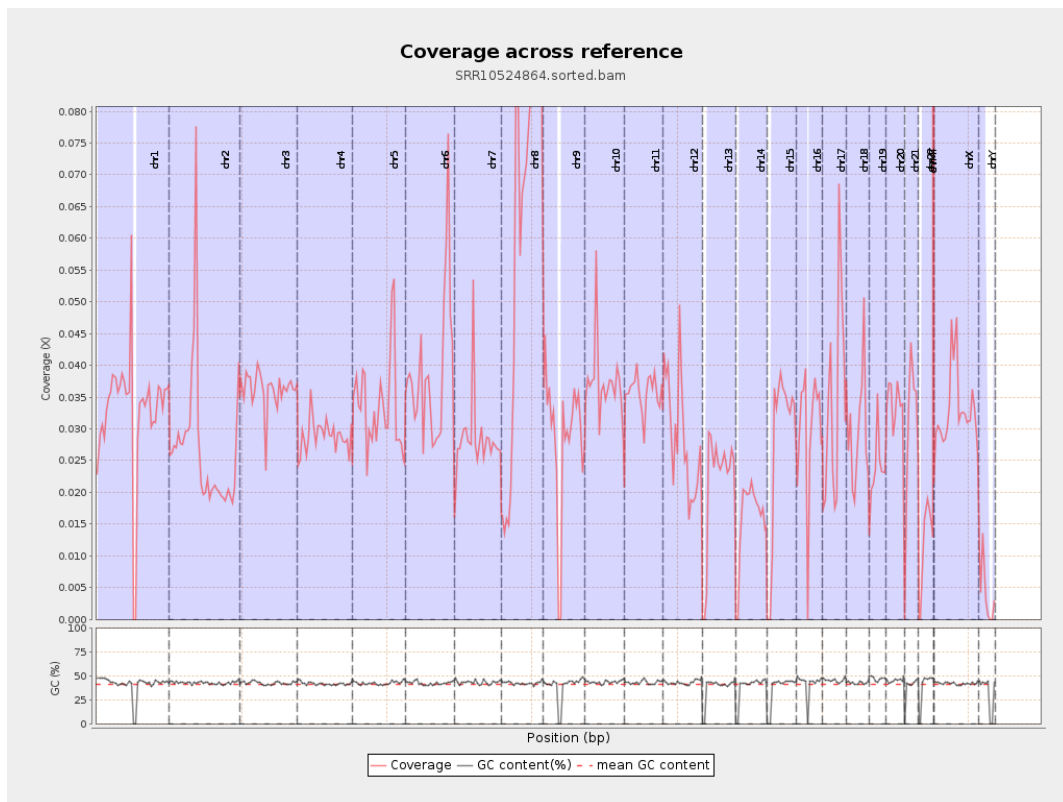
General error rate	0.49%
Mismatches	473,439
Insertions	5,754
Mapped reads with at least one insertion	0.34%
Deletions	18,597
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.01%

2.6. Chromosome stats

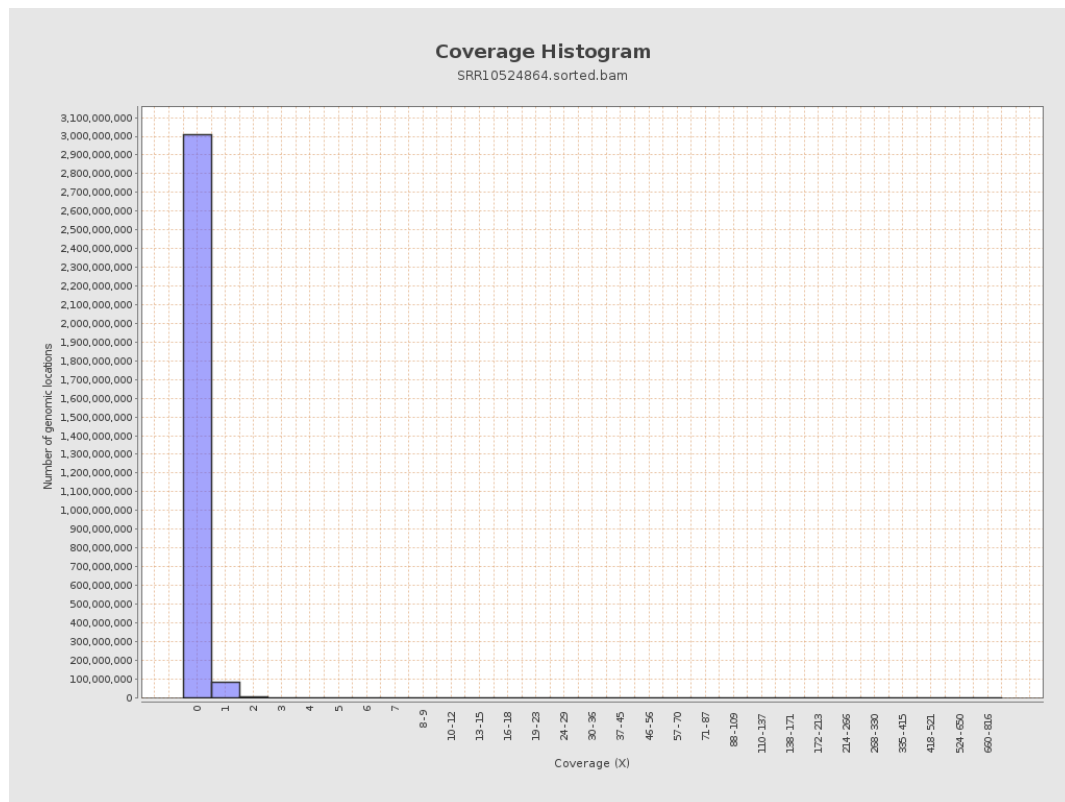
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8148853	0.0327	0.6254
chr2	243199373	6545081	0.0269	0.3064
chr3	198022430	7162731	0.0362	0.2032
chr4	191154276	5516531	0.0289	0.1937
chr5	180915260	6104961	0.0337	0.198
chr6	171115067	6560283	0.0383	0.2338
chr7	159138663	4565255	0.0287	0.4066

chr8	146364022	10664965	0.0729	0.4232
chr9	141213431	4038086	0.0286	0.2551
chr10	135534747	5046989	0.0372	0.288
chr11	135006516	4807505	0.0356	0.2733
chr12	133851895	3797355	0.0284	0.1873
chr13	115169878	2450019	0.0213	0.1569
chr14	107349540	1699034	0.0158	0.1473
chr15	102531392	2873353	0.028	0.1799
chr16	90354753	2726188	0.0302	0.1996
chr17	81195210	2714421	0.0334	0.2235
chr18	78077248	2356269	0.0302	0.4396
chr19	59128983	1427684	0.0241	0.4259
chr20	63025520	2109930	0.0335	0.1991
chr21	48129895	1443365	0.03	0.1985
chr22	51304566	602909	0.0118	0.1151
chrMT	16571	14760	0.8907	0.9593
chrX	155270560	5107187	0.0329	0.2261
chrY	59373566	239794	0.004	0.1014

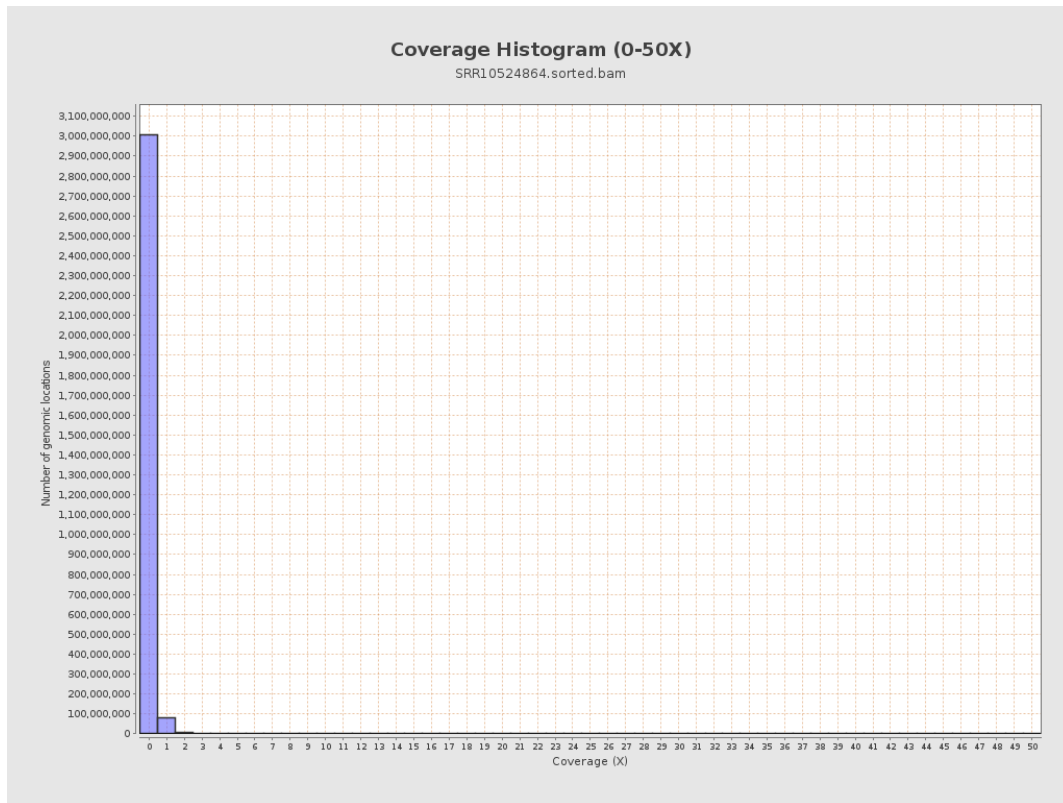
3. Results : Coverage across reference



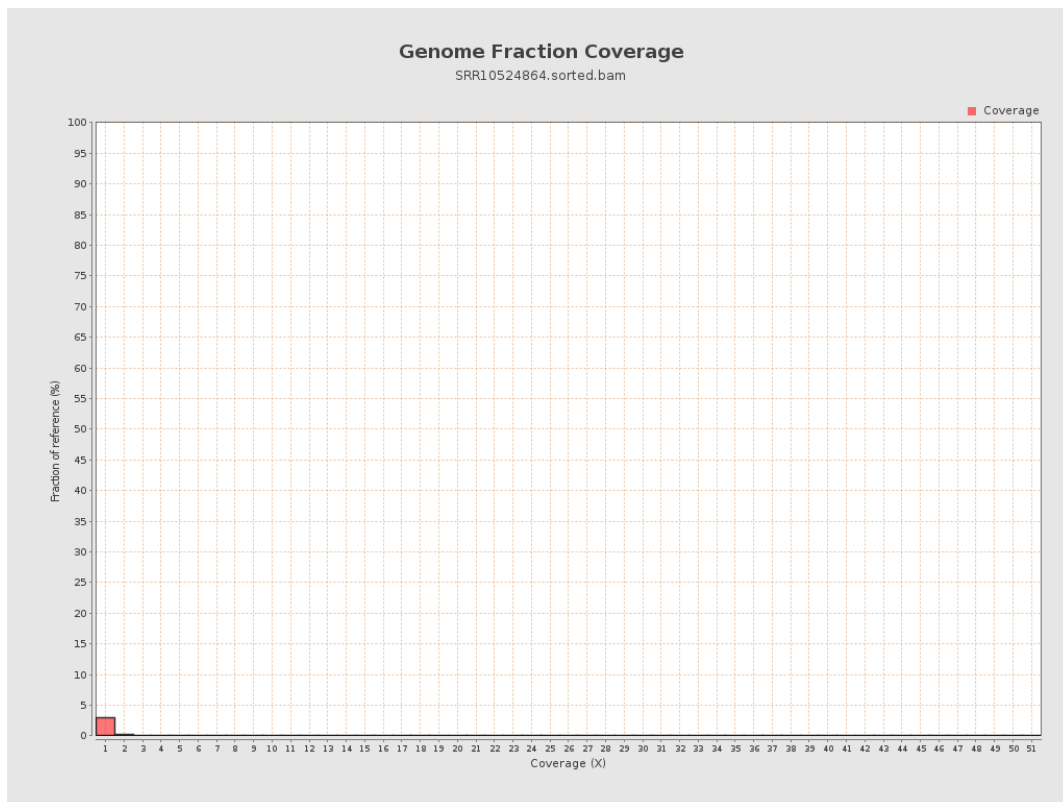
4. Results : Coverage Histogram



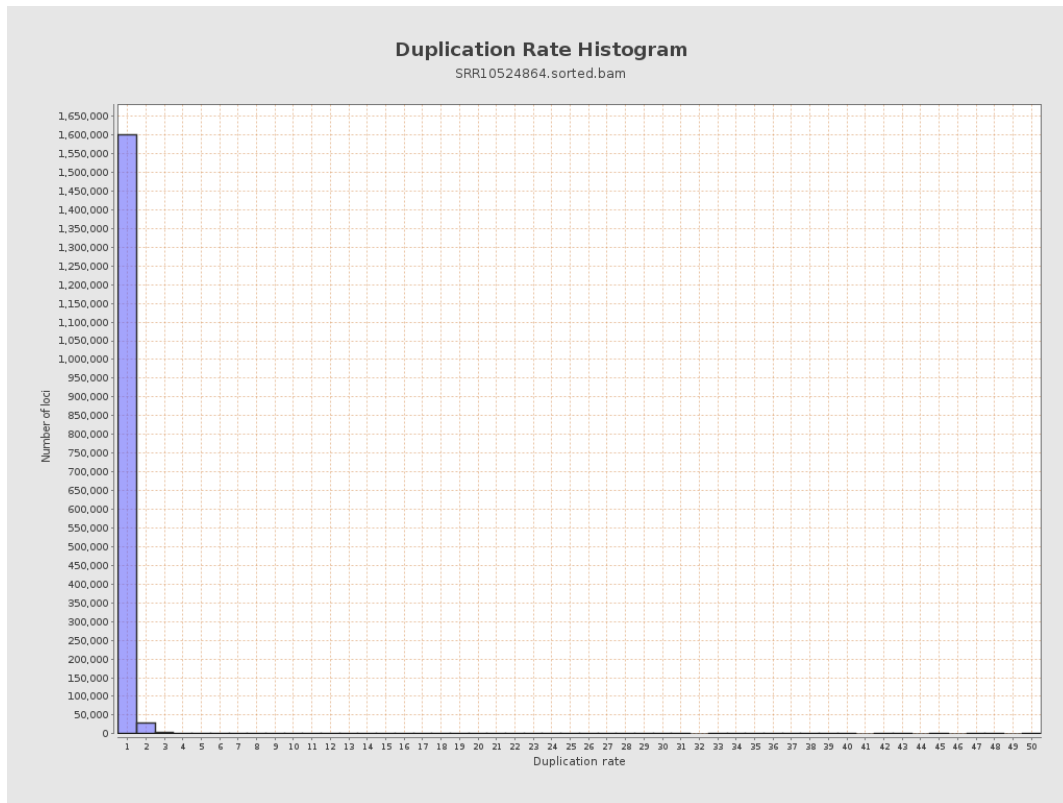
5. Results : Coverage Histogram (0-50X)



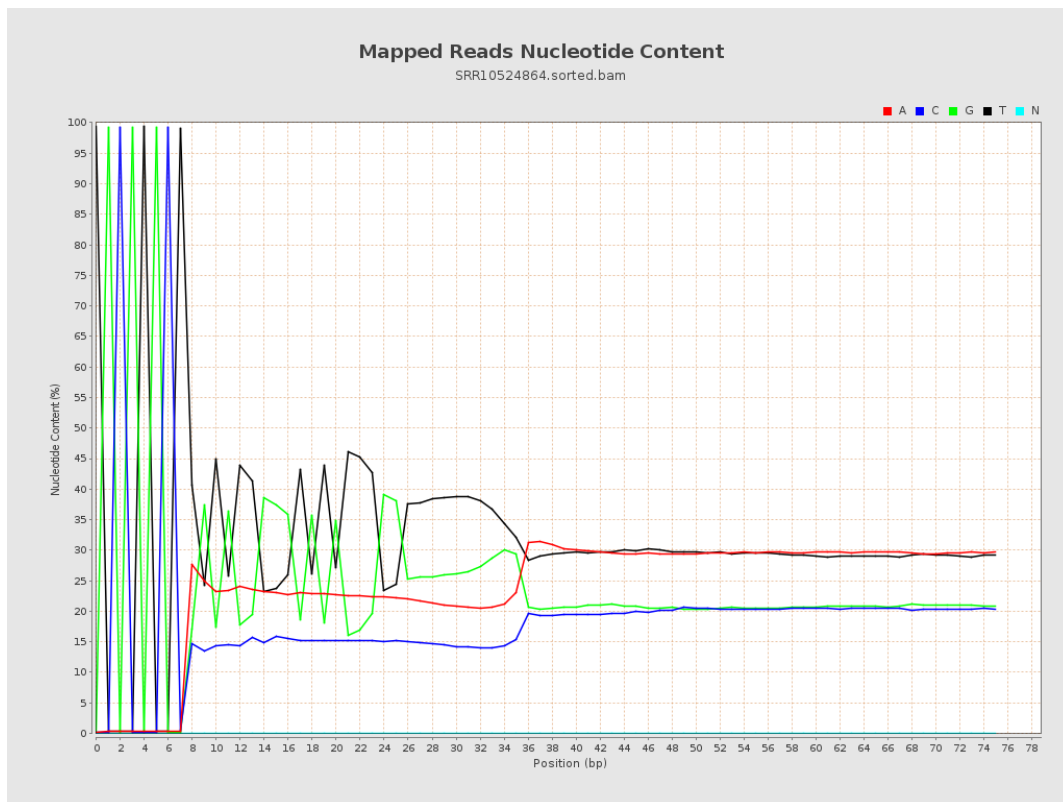
6. Results : Genome Fraction Coverage



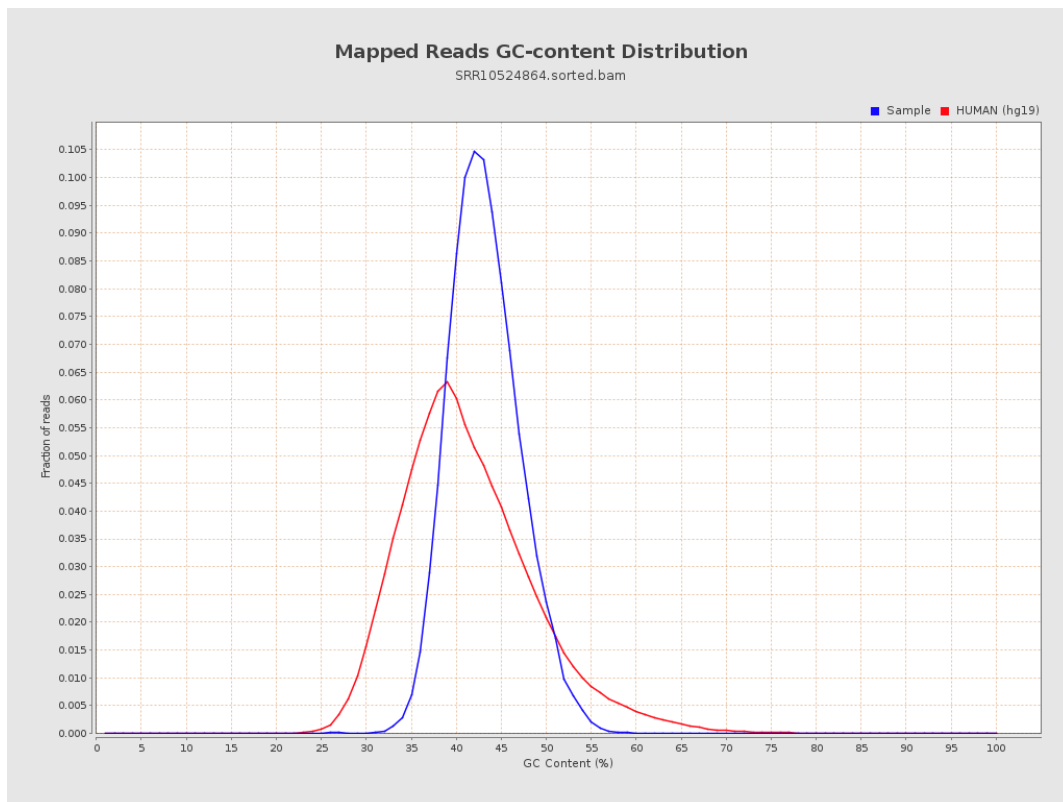
7. Results : Duplication Rate Histogram



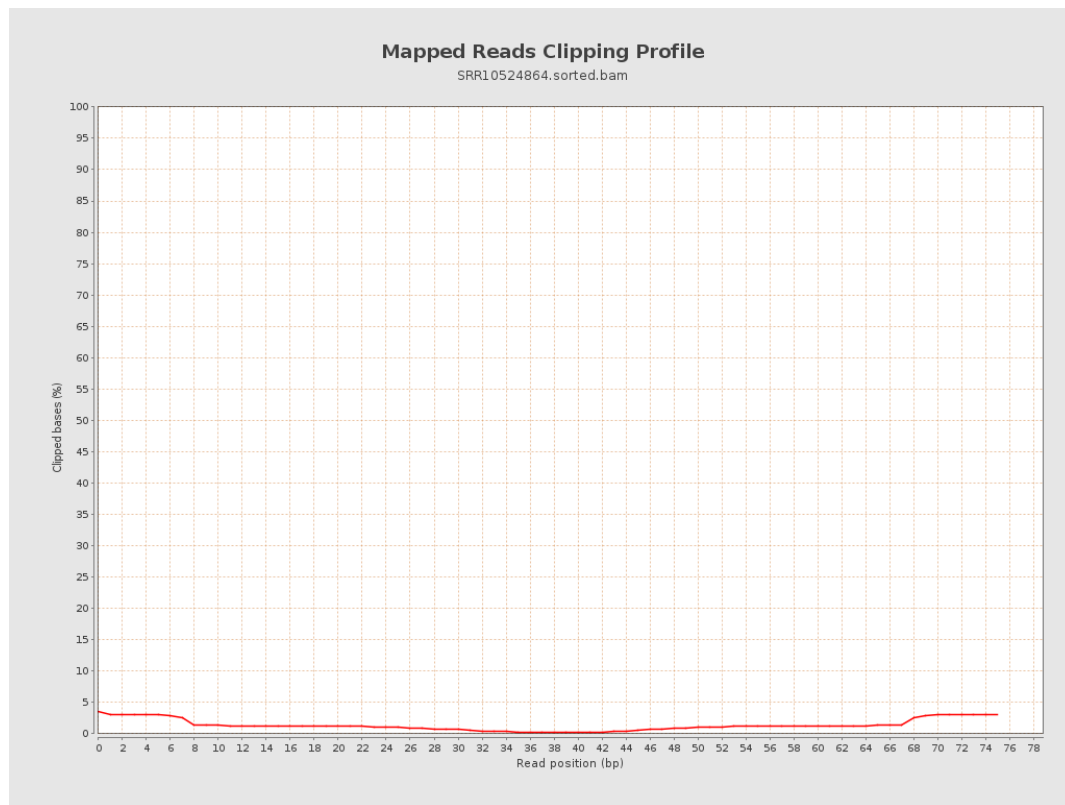
8. Results : Mapped Reads Nucleotide Content



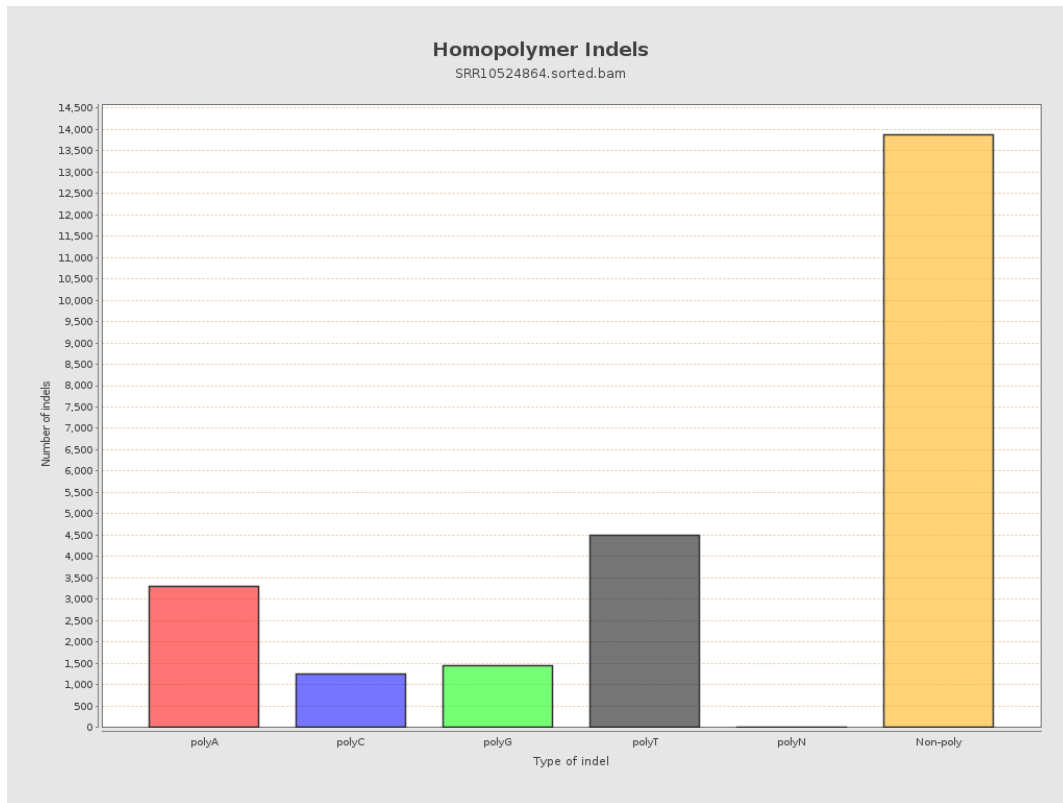
9. Results : Mapped Reads GC-content Distribution



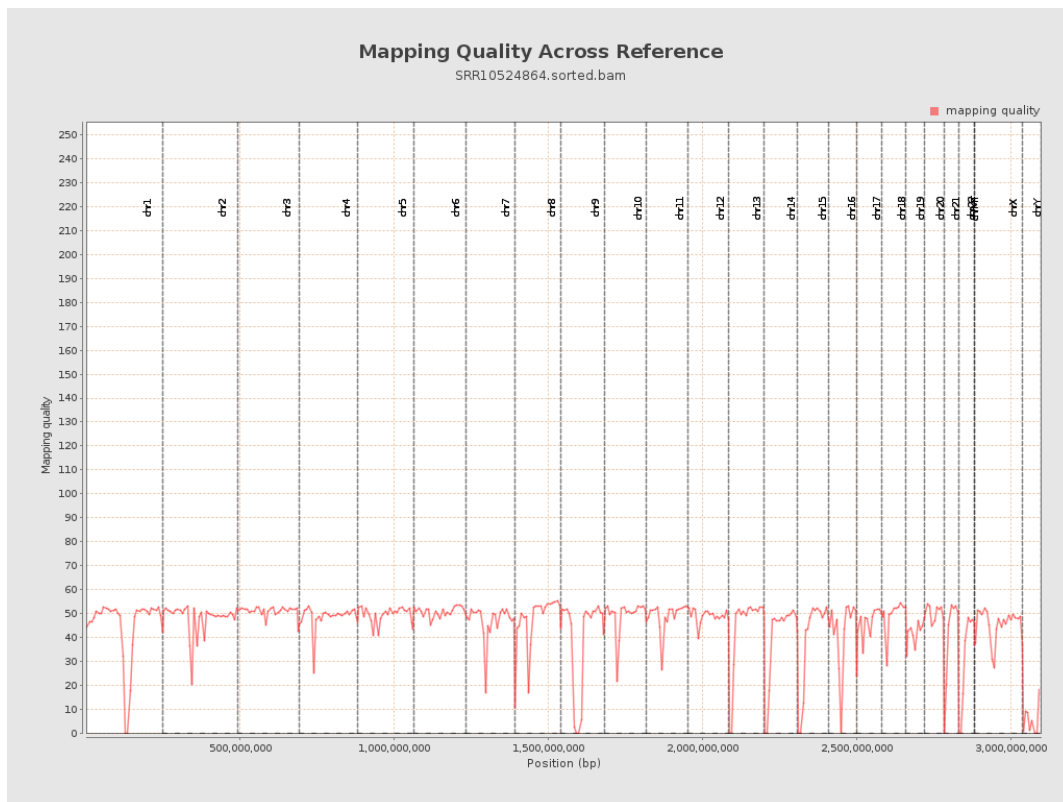
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

