

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:36:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524741.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_SRR10524741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:36:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,208,511
Mapped reads	2,016,157 / 91.29%
Unmapped reads	192,354 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,001 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	100,145 / 4.53%
Duplication rate	3.8%
Clipped reads	2,018,572 / 91.4%

2.2. ACGT Content

Number/percentage of A's	28,599,704 / 24.81%
Number/percentage of C's	22,333,066 / 19.37%
Number/percentage of T's	36,413,286 / 31.58%
Number/percentage of G's	27,933,710 / 24.23%
Number/percentage of N's	13,785 / 0.01%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.3113
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2.4. Mapping Quality

Mean Mapping Quality	44.4
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2.5. Mismatches and indels

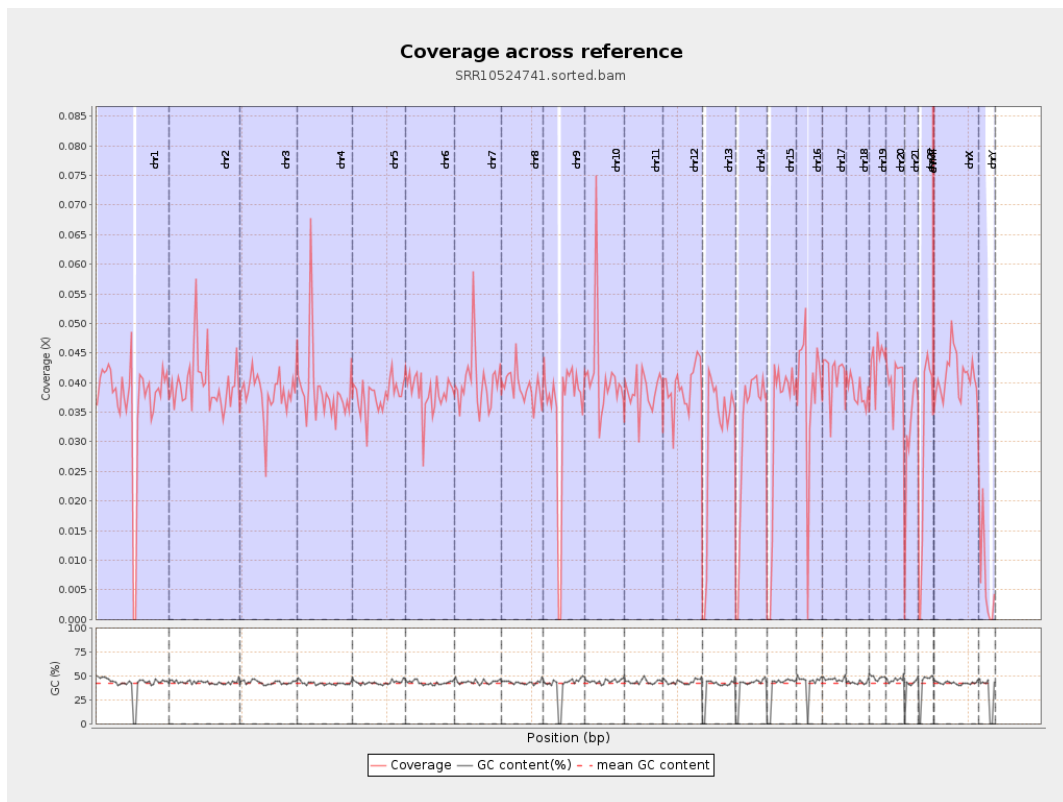
General error rate	0.52%
Mismatches	589,740
Insertions	7,565
Mapped reads with at least one insertion	0.37%
Deletions	23,515
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.74%

2.6. Chromosome stats

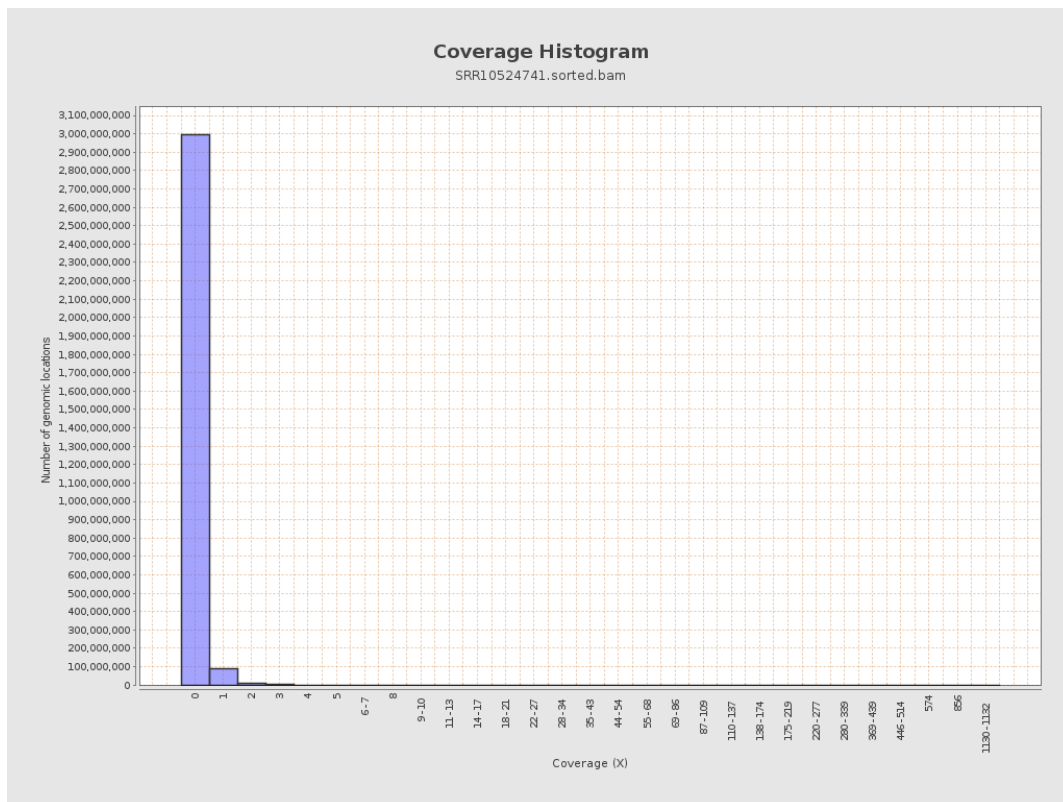
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9190365	0.0369	0.4216
chr2	243199373	9699032	0.0399	0.527
chr3	198022430	7549543	0.0381	0.2257
chr4	191154276	7366390	0.0385	0.2595
chr5	180915260	6833895	0.0378	0.2201
chr6	171115067	6551330	0.0383	0.2486
chr7	159138663	6399886	0.0402	0.3837

chr8	146364022	5740069	0.0392	0.283
chr9	141213431	4893478	0.0347	0.2633
chr10	135534747	5550588	0.041	0.3591
chr11	135006516	5184213	0.0384	0.2736
chr12	133851895	5262480	0.0393	0.2289
chr13	115169878	3536907	0.0307	0.1987
chr14	107349540	3441793	0.0321	0.2105
chr15	102531392	3326039	0.0324	0.2079
chr16	90354753	3509988	0.0388	0.2479
chr17	81195210	3346909	0.0412	0.2455
chr18	78077248	3012524	0.0386	0.4274
chr19	59128983	2582903	0.0437	0.3633
chr20	63025520	2541024	0.0403	0.2438
chr21	48129895	1528135	0.0318	0.2348
chr22	51304566	1488902	0.029	0.1962
chrMT	16571	34743	2.0966	1.996
chrX	155270560	6376873	0.0411	0.2506
chrY	59373566	383345	0.0065	0.169

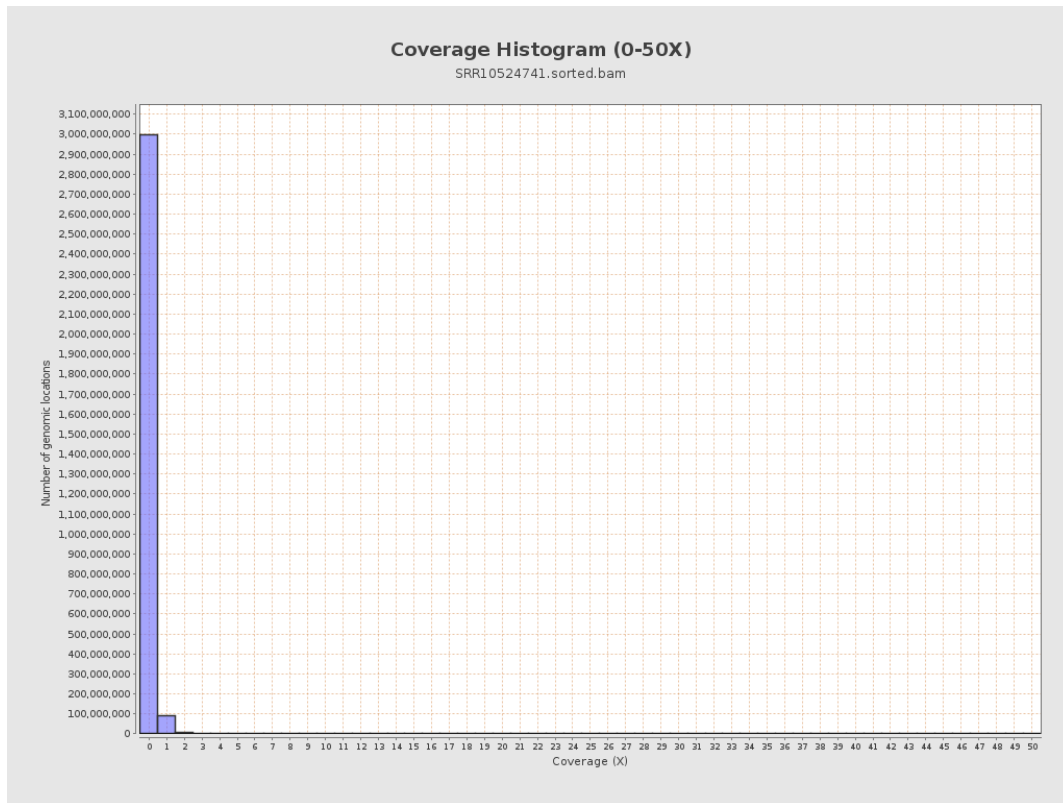
3. Results : Coverage across reference



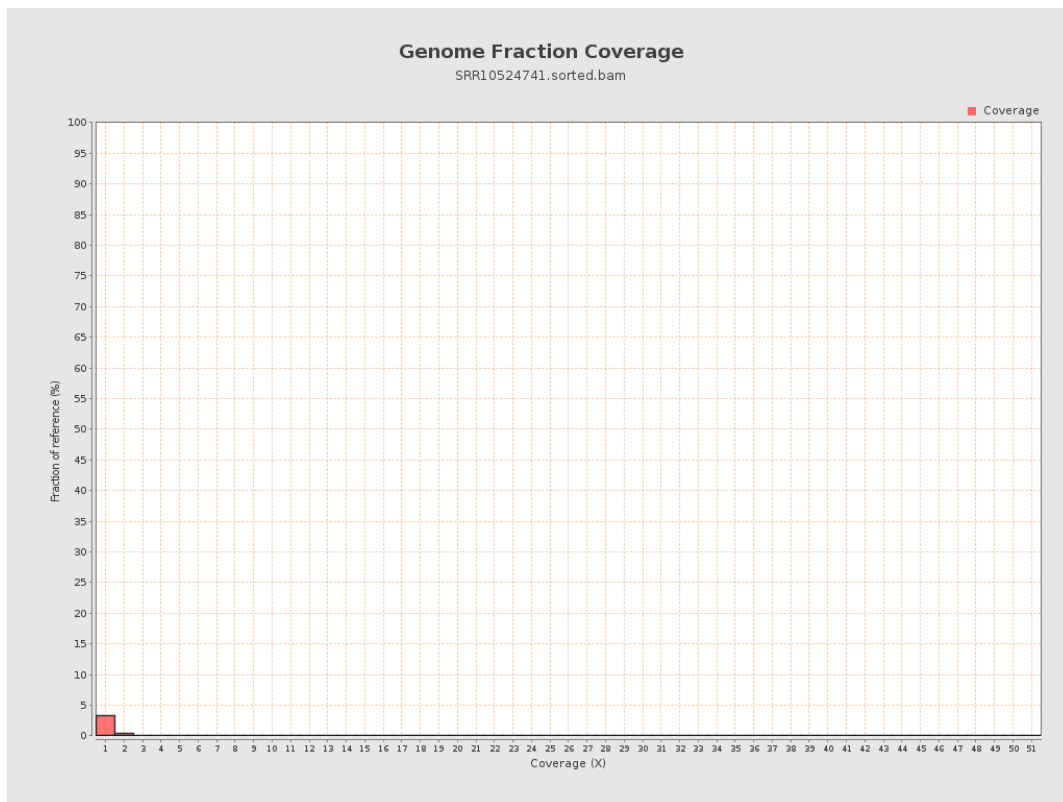
4. Results : Coverage Histogram



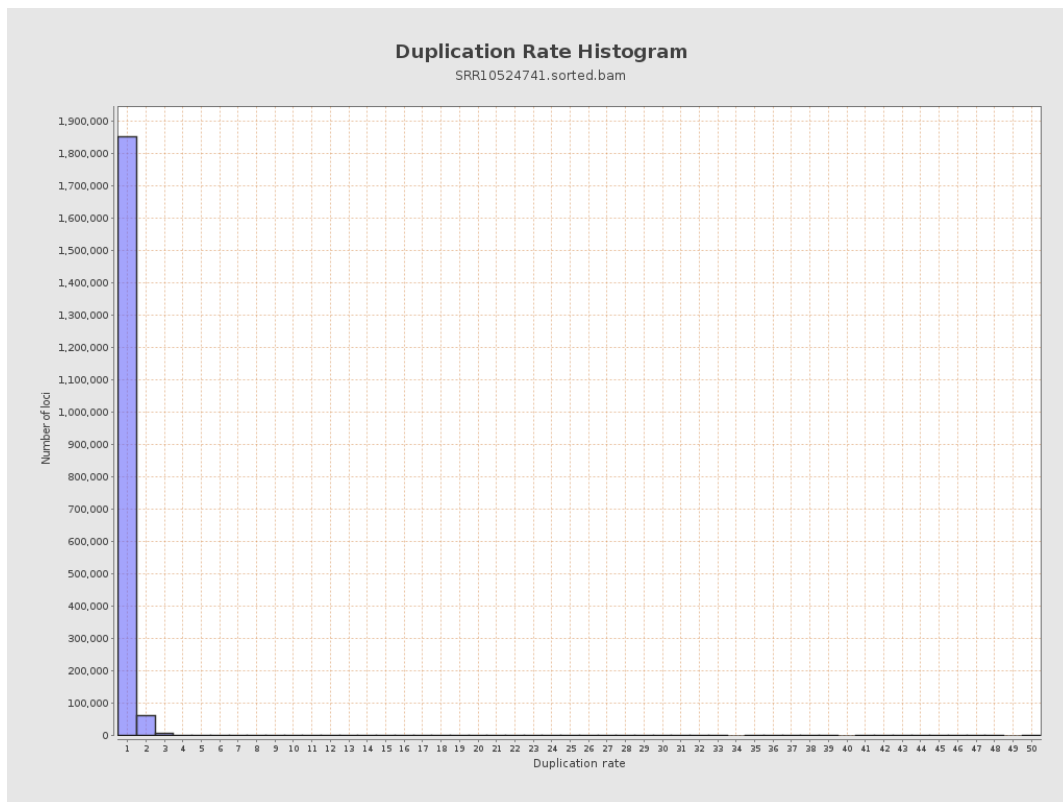
5. Results : Coverage Histogram (0-50X)



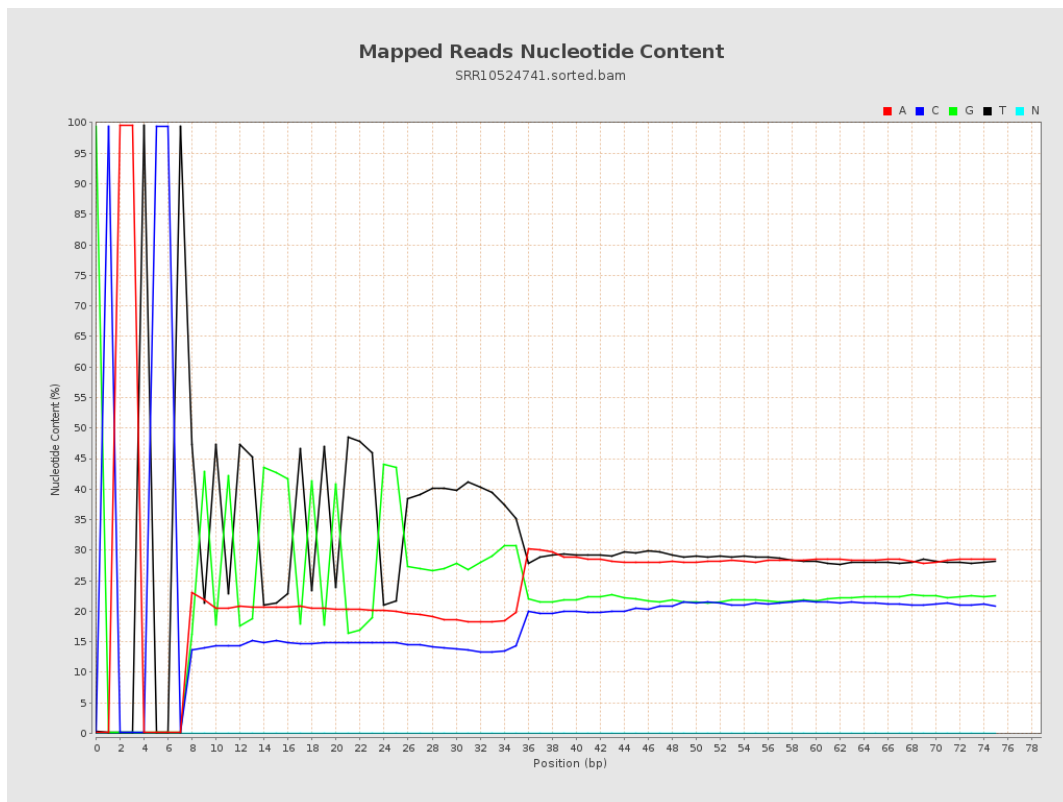
6. Results : Genome Fraction Coverage



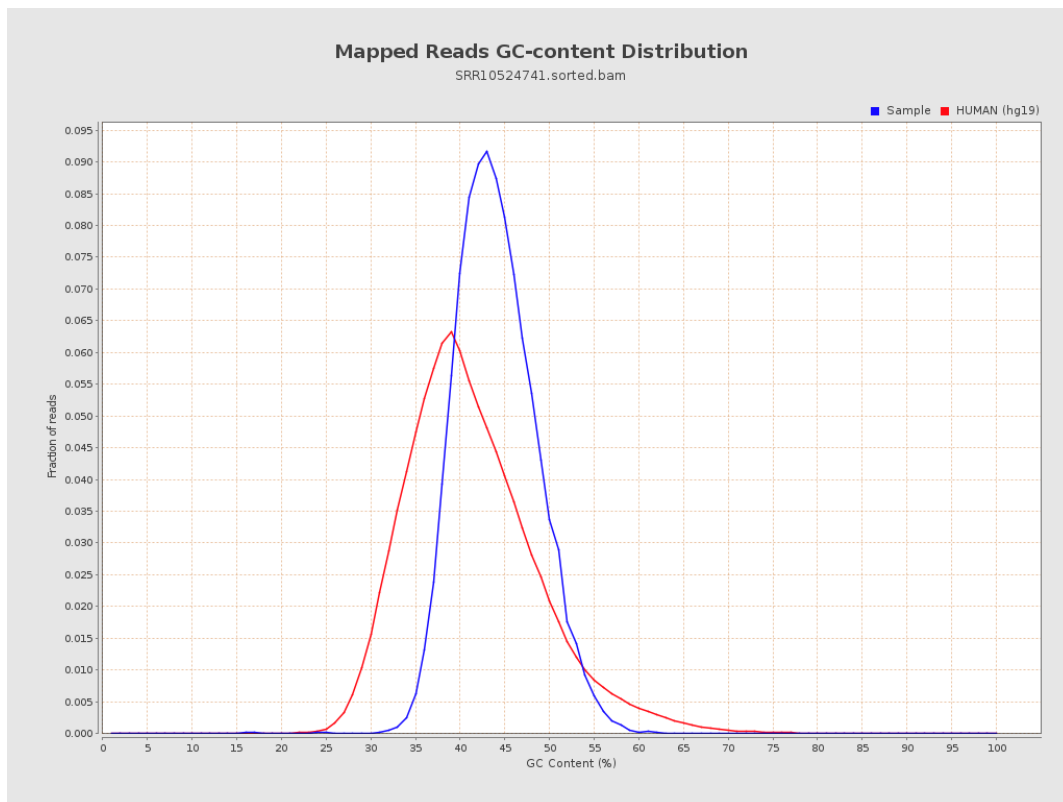
7. Results : Duplication Rate Histogram



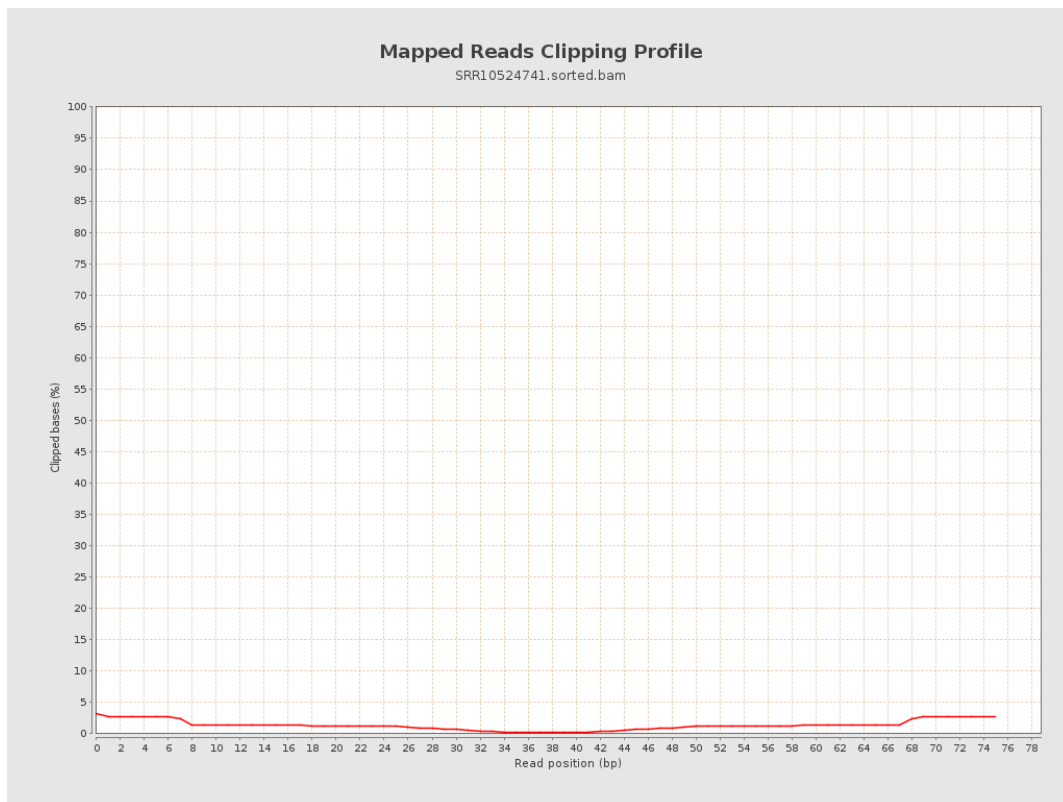
8. Results : Mapped Reads Nucleotide Content



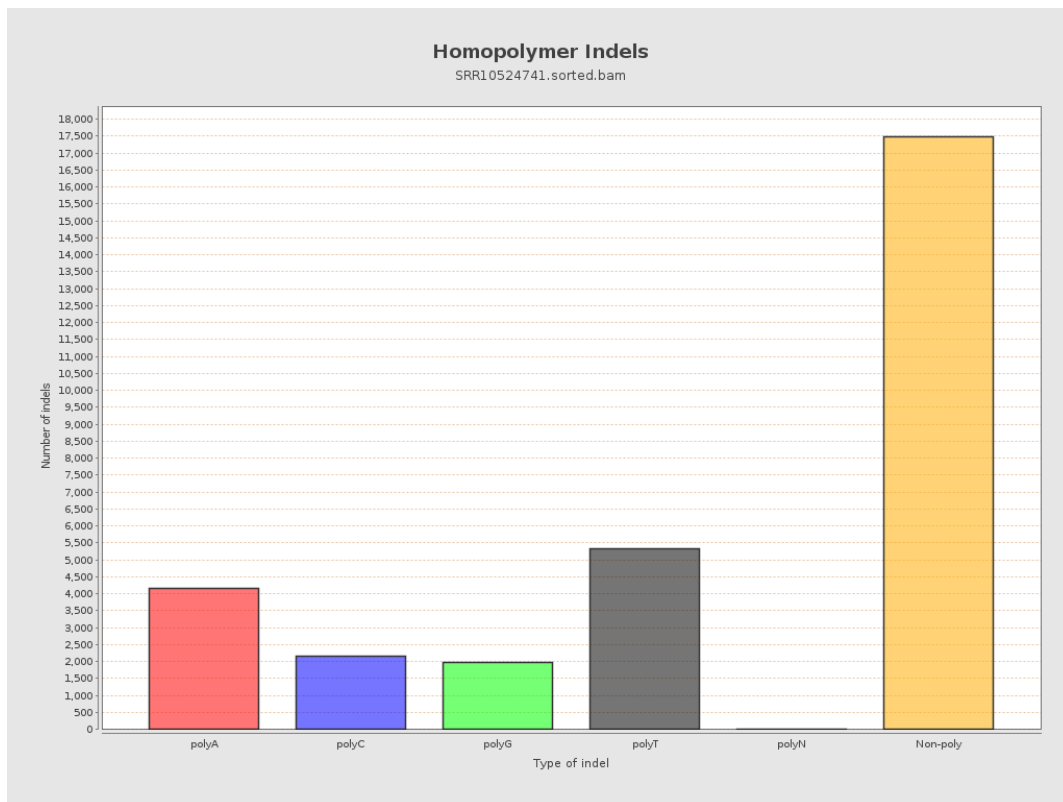
9. Results : Mapped Reads GC-content Distribution



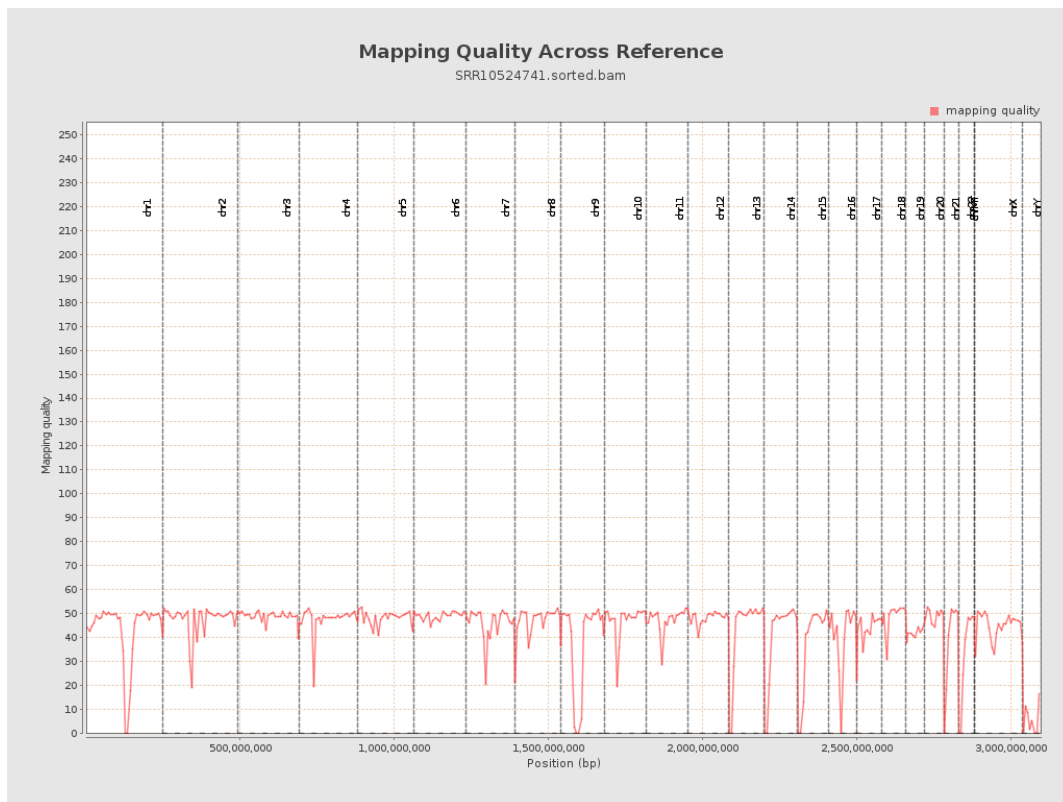
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

