

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 10:14:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472840.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_SRR3472840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 10:14:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,455,571
Mapped reads	2,154,684 / 87.75%
Unmapped reads	300,887 / 12.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,050 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	60,115 / 2.45%
Duplication rate	1.94%
Clipped reads	1,146,577 / 46.69%

2.2. ACGT Content

Number/percentage of A's	37,464,969 / 26.9%
Number/percentage of C's	28,448,189 / 20.43%
Number/percentage of T's	40,605,131 / 29.16%
Number/percentage of G's	32,750,370 / 23.52%
Number/percentage of N's	3,454 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.045

Standard Deviation	0.3437
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2.4. Mapping Quality

Mean Mapping Quality	43.5
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2.5. Mismatches and indels

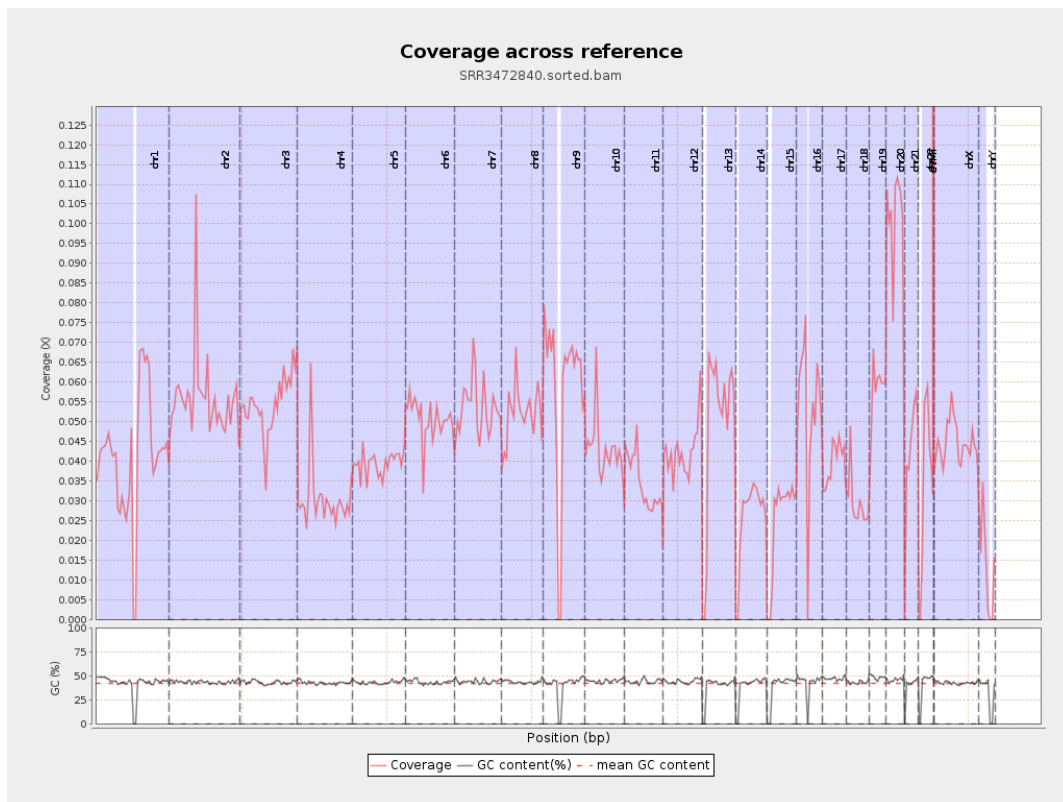
General error rate	0.84%
Mismatches	1,153,574
Insertions	10,738
Mapped reads with at least one insertion	0.49%
Deletions	29,457
Mapped reads with at least one deletion	1.35%
Homopolymer indels	44.38%

2.6. Chromosome stats

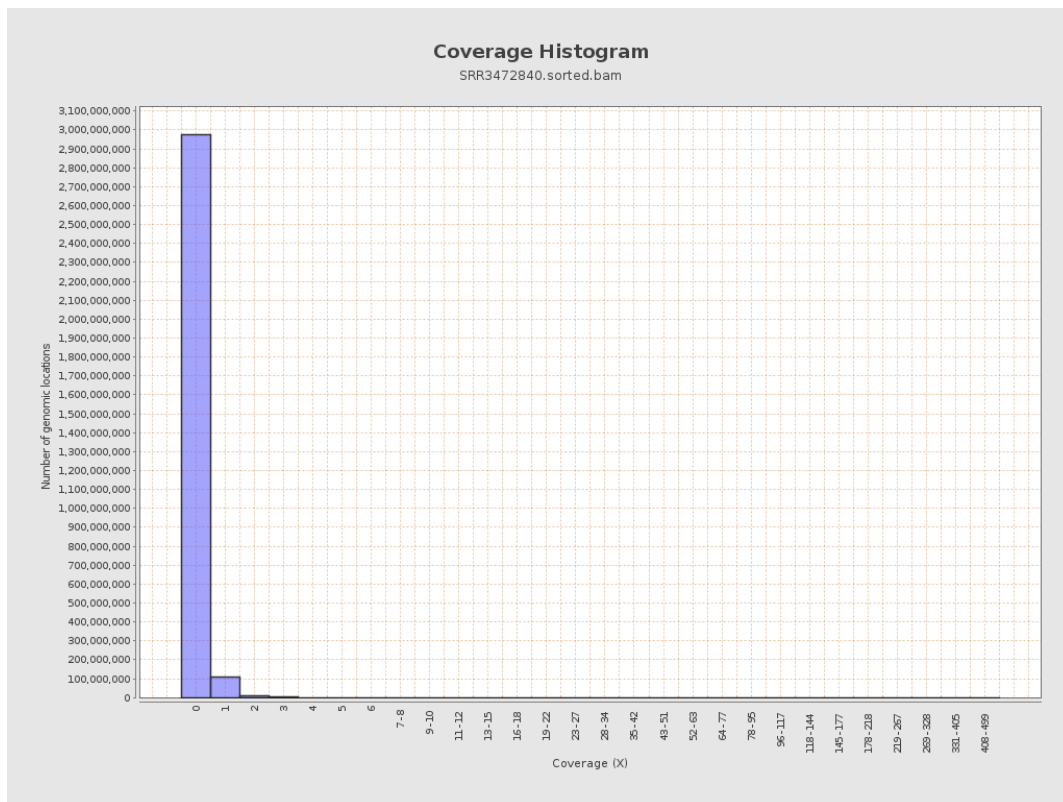
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10271644	0.0412	0.4433
chr2	243199373	13603161	0.0559	0.5294
chr3	198022430	10747065	0.0543	0.2568
chr4	191154276	5768715	0.0302	0.2376
chr5	180915260	7123618	0.0394	0.2197
chr6	171115067	8644193	0.0505	0.2613
chr7	159138663	8533523	0.0536	0.4187

chr8	146364022	7596621	0.0519	0.3241
chr9	141213431	8218124	0.0582	0.4077
chr10	135534747	5813886	0.0429	0.3463
chr11	135006516	4623652	0.0342	0.3122
chr12	133851895	5697786	0.0426	0.2386
chr13	115169878	5669589	0.0492	0.2526
chr14	107349540	2780495	0.0259	0.218
chr15	102531392	2577565	0.0251	0.1914
chr16	90354753	4839923	0.0536	0.2888
chr17	81195210	3236133	0.0399	0.2385
chr18	78077248	2326016	0.0298	0.6744
chr19	59128983	3435172	0.0581	0.3783
chr20	63025520	6329653	0.1004	0.368
chr21	48129895	2047548	0.0425	0.2696
chr22	51304566	1700808	0.0332	0.2163
chrMT	16571	24052	1.4515	1.5587
chrX	155270560	6930970	0.0446	0.2645
chrY	59373566	784884	0.0132	0.1954

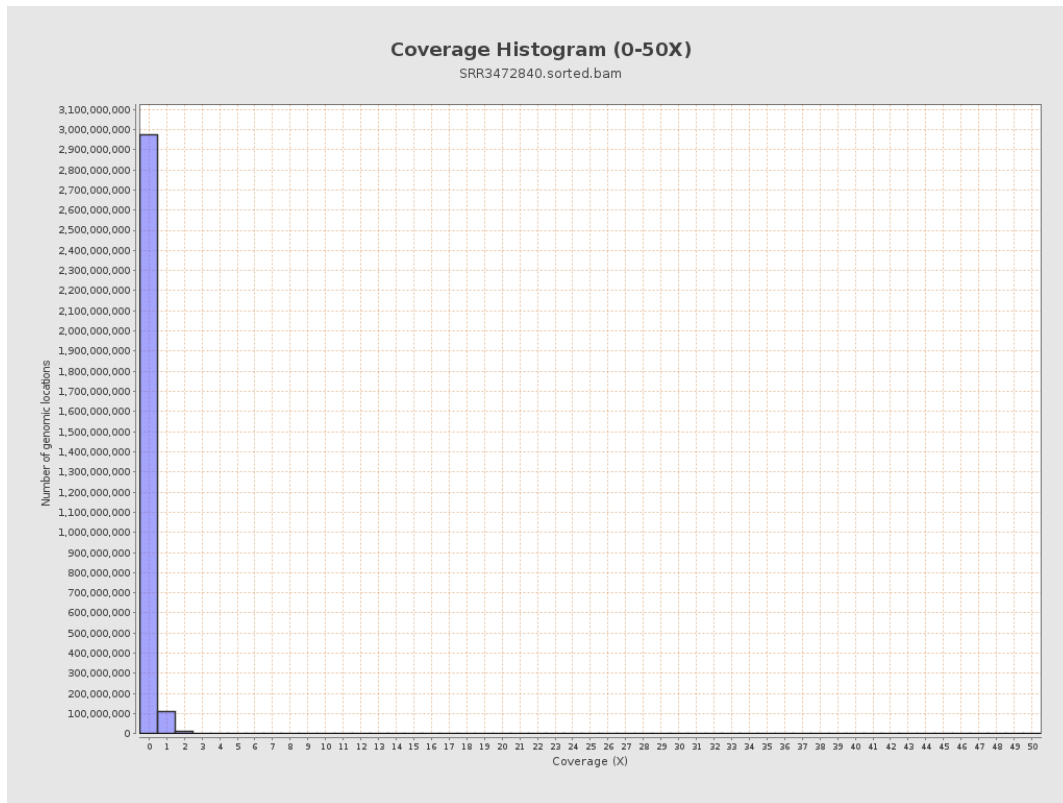
3. Results : Coverage across reference



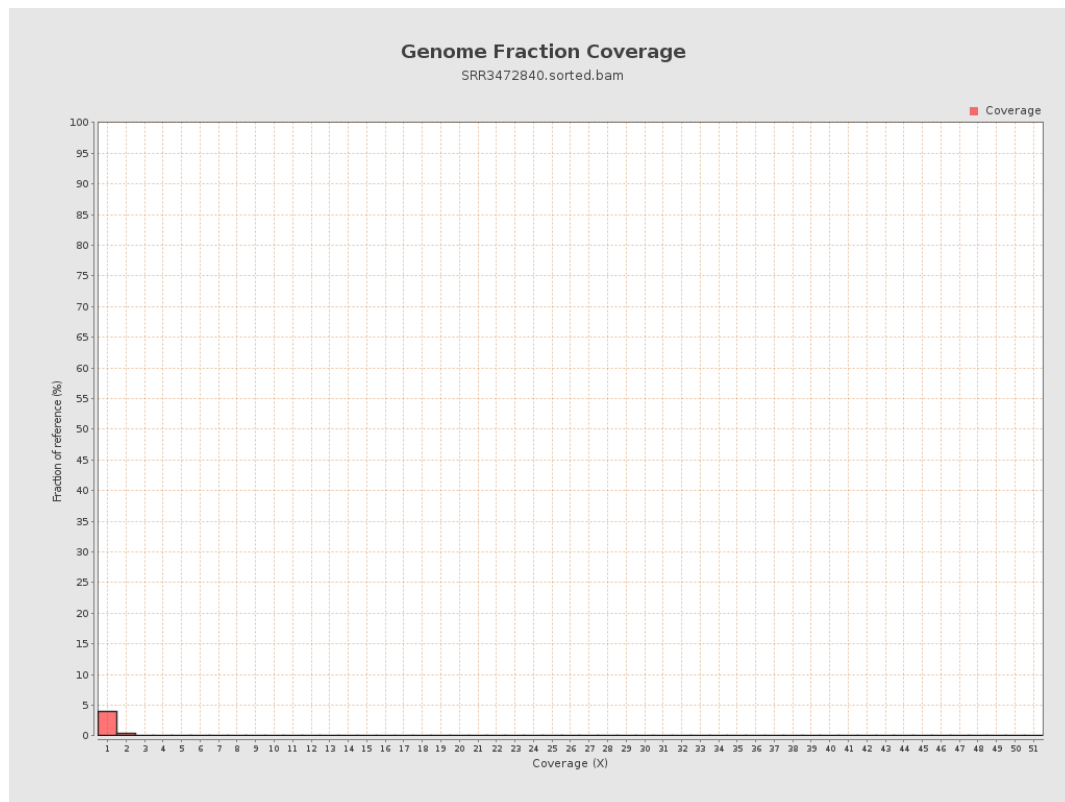
4. Results : Coverage Histogram



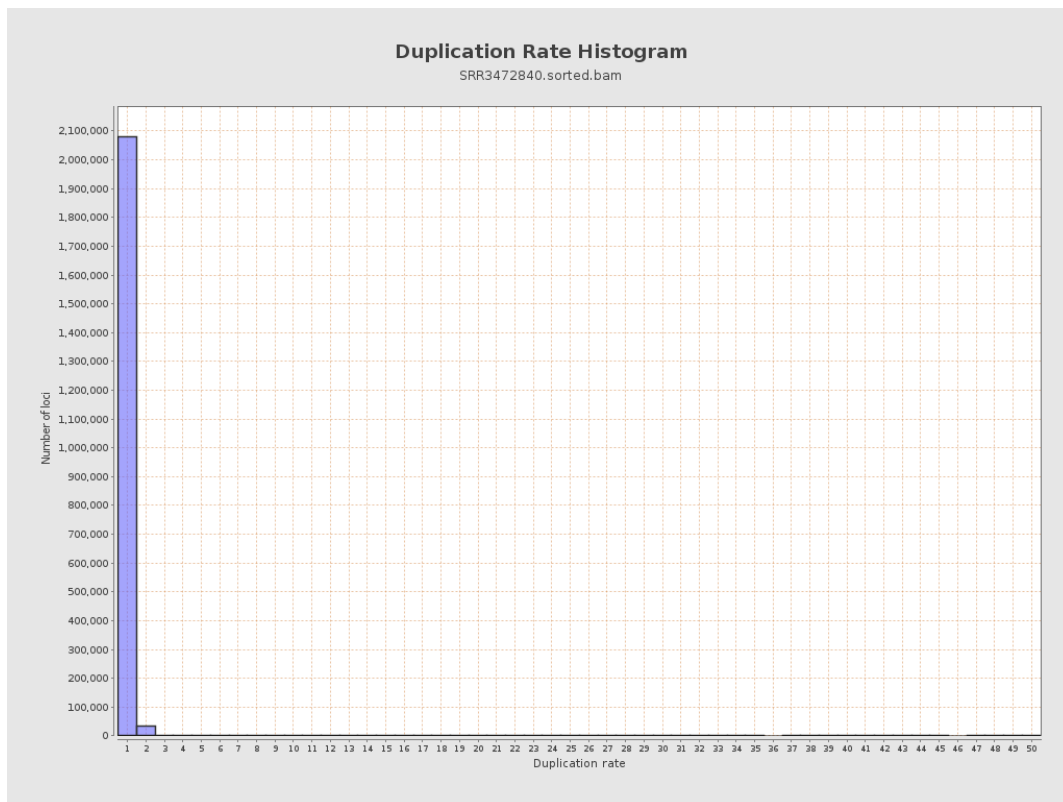
5. Results : Coverage Histogram (0-50X)



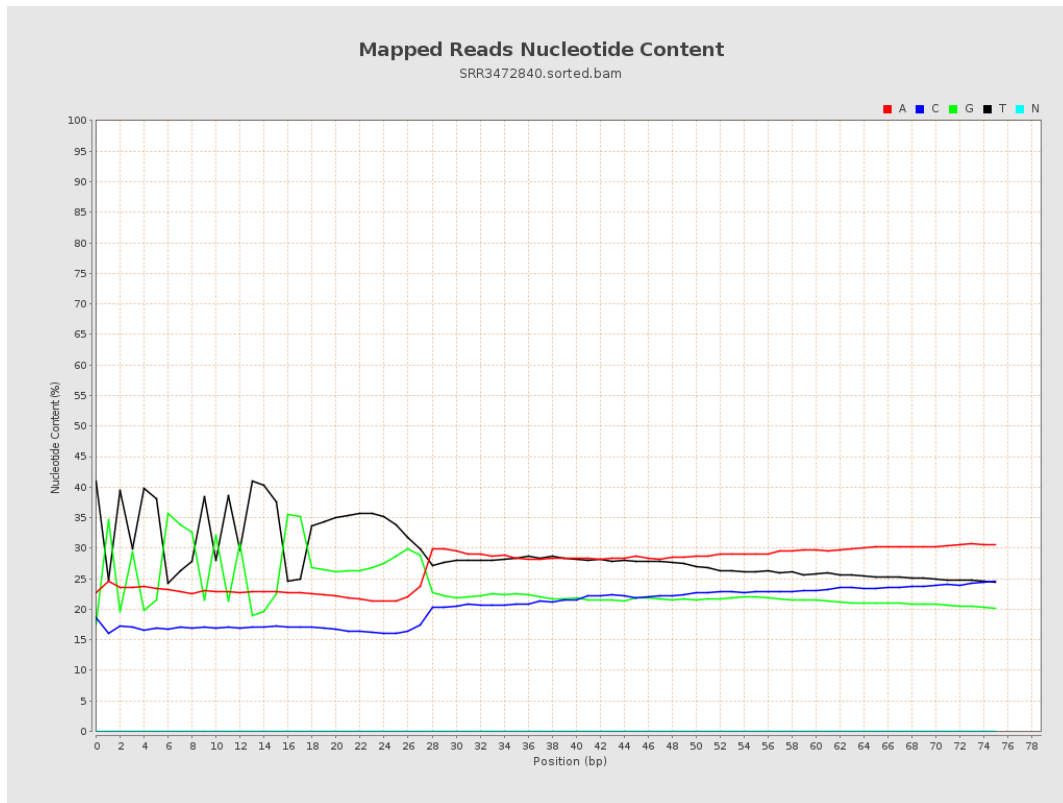
6. Results : Genome Fraction Coverage



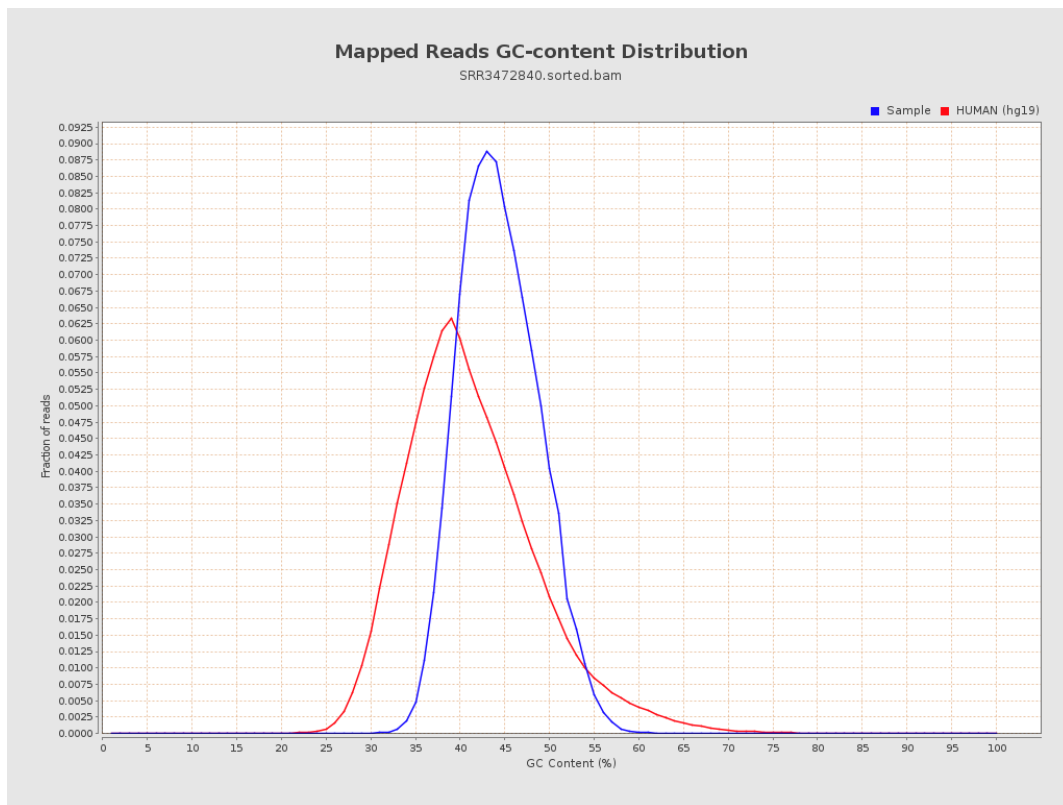
7. Results : Duplication Rate Histogram



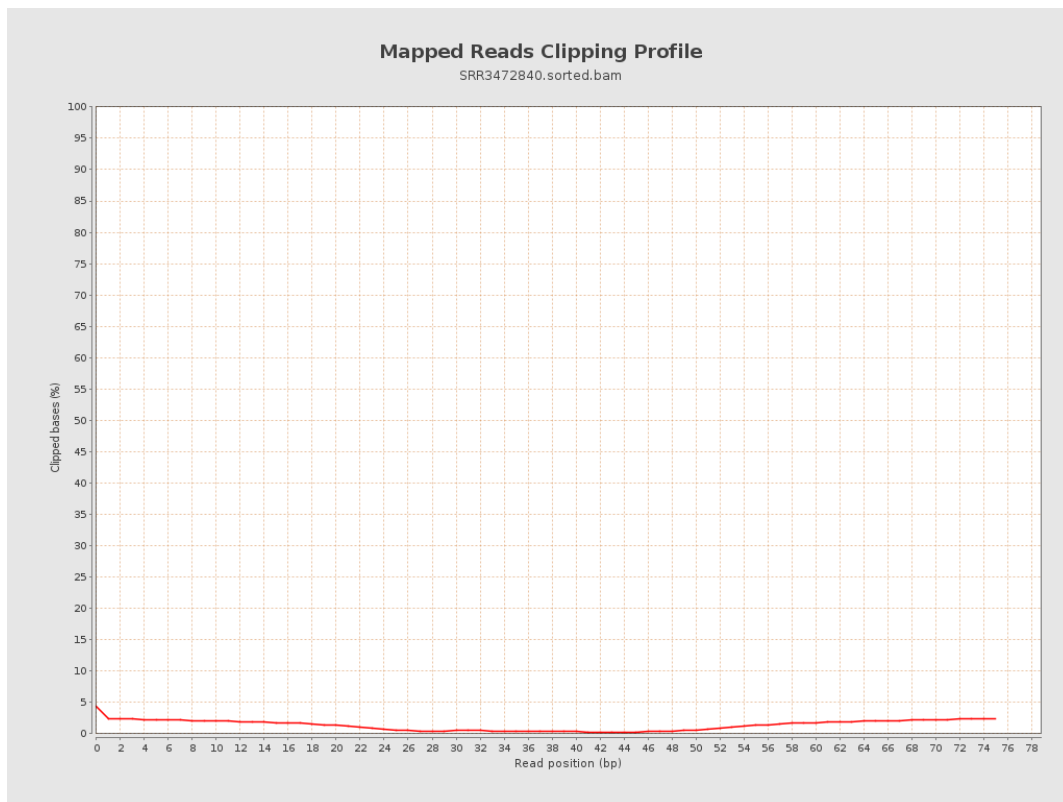
8. Results : Mapped Reads Nucleotide Content



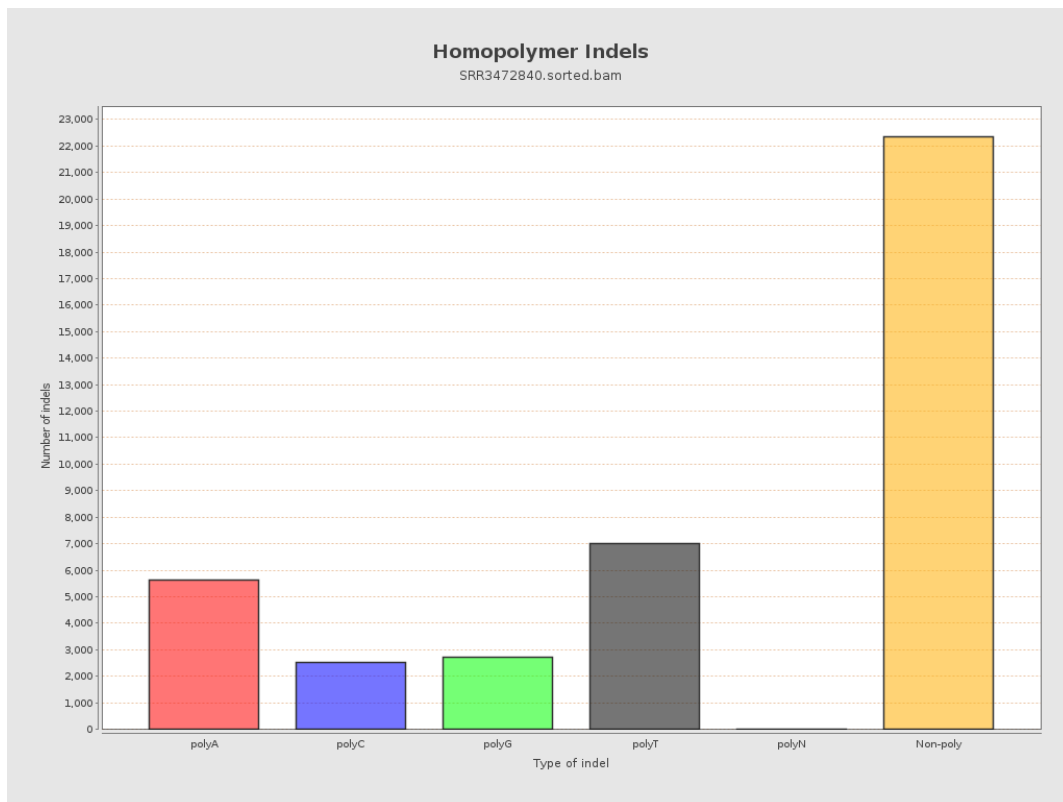
9. Results : Mapped Reads GC-content Distribution



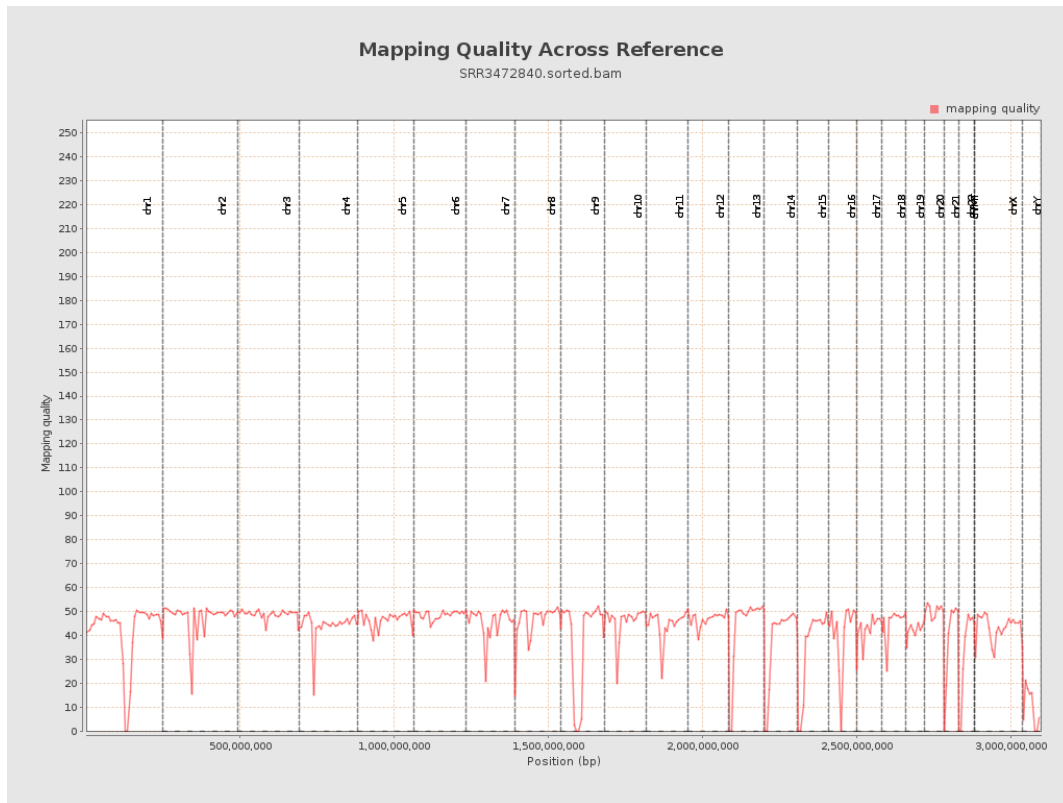
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

