

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:07:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716360.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_SRR9716360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716360.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:07:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,028,214
Mapped reads	914,144 / 88.91%
Unmapped reads	114,070 / 11.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,353 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	33,677 / 3.28%
Duplication rate	3.01%
Clipped reads	916,878 / 89.17%

2.2. ACGT Content

Number/percentage of A's	12,818,391 / 24.19%
Number/percentage of C's	10,728,167 / 20.25%
Number/percentage of T's	16,918,725 / 31.93%
Number/percentage of G's	12,518,096 / 23.63%
Number/percentage of N's	432 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.1729
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2.4. Mapping Quality

Mean Mapping Quality	44.71
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2.5. Mismatches and indels

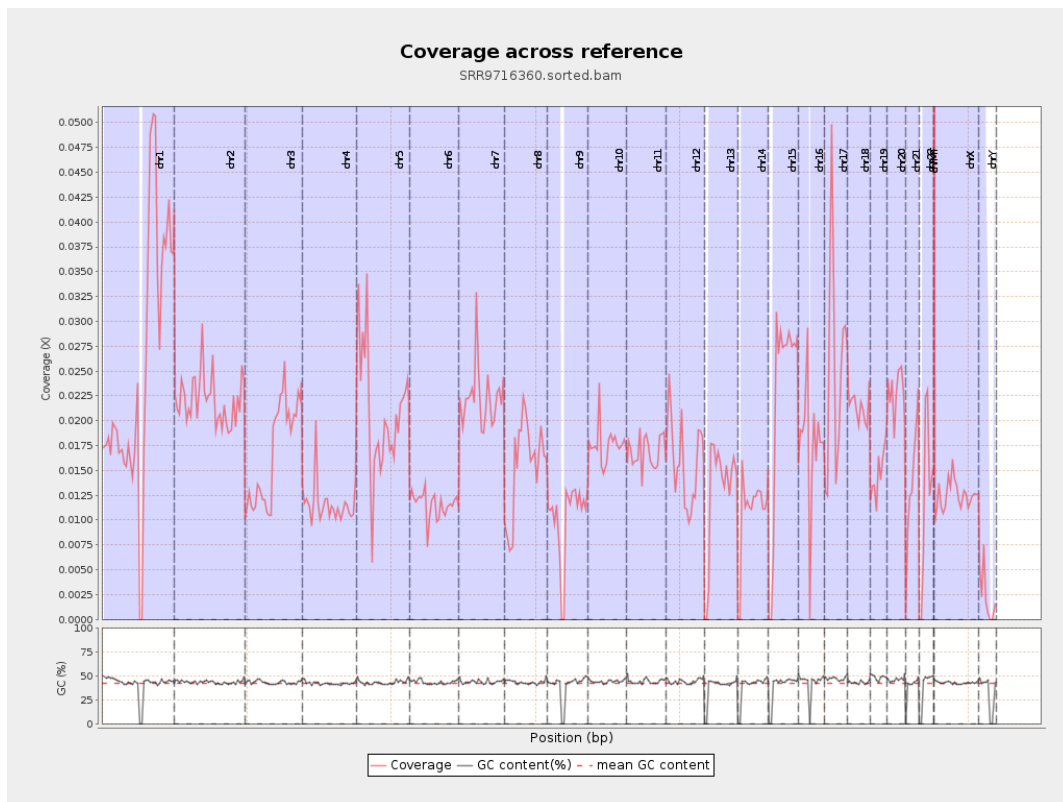
General error rate	0.5%
Mismatches	259,380
Insertions	3,783
Mapped reads with at least one insertion	0.41%
Deletions	9,171
Mapped reads with at least one deletion	1%
Homopolymer indels	42.41%

2.6. Chromosome stats

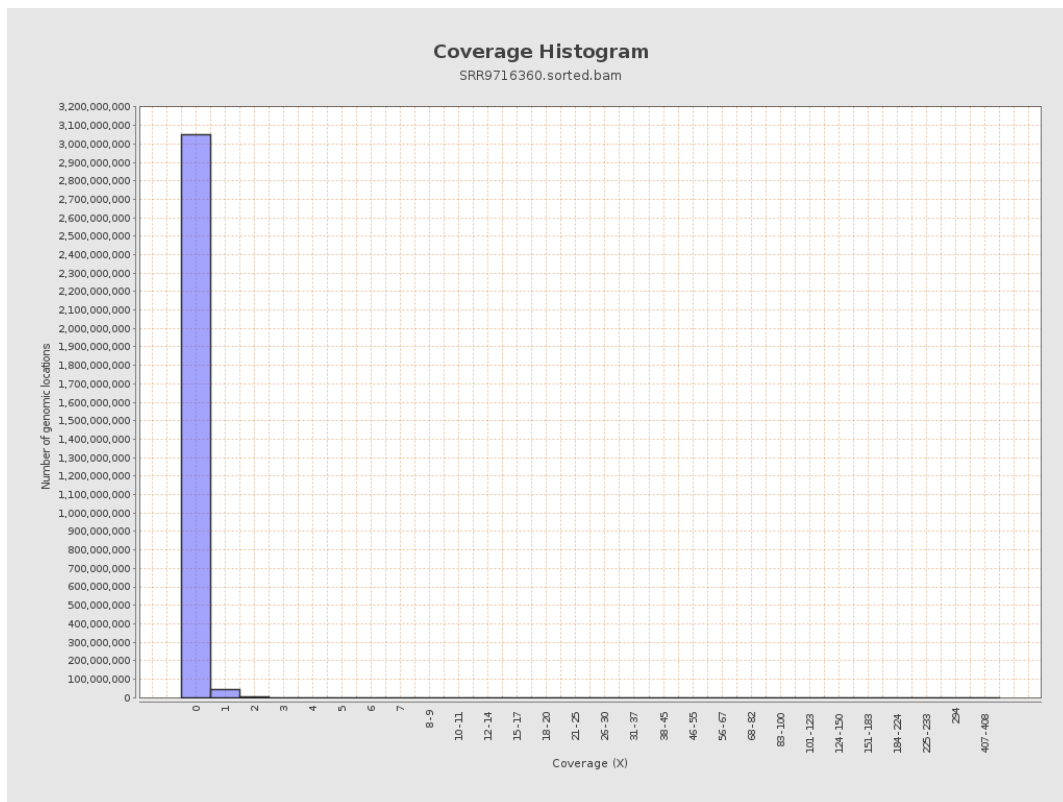
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6274436	0.0252	0.2438
chr2	243199373	5362486	0.022	0.2402
chr3	198022430	3310442	0.0167	0.1402
chr4	191154276	2223982	0.0116	0.128
chr5	180915260	3762604	0.0208	0.1568
chr6	171115067	1975132	0.0115	0.1232
chr7	159138663	3565044	0.0224	0.254

chr8	146364022	2291837	0.0157	0.155
chr9	141213431	1437928	0.0102	0.1317
chr10	135534747	2389830	0.0176	0.1635
chr11	135006516	2284037	0.0169	0.1627
chr12	133851895	2125046	0.0159	0.1371
chr13	115169878	1489303	0.0129	0.1225
chr14	107349540	1150841	0.0107	0.1147
chr15	102531392	2307307	0.0225	0.1637
chr16	90354753	1583073	0.0175	0.1483
chr17	81195210	2100304	0.0259	0.184
chr18	78077248	1660483	0.0213	0.247
chr19	59128983	871569	0.0147	0.1827
chr20	63025520	1440524	0.0229	0.1658
chr21	48129895	670014	0.0139	0.1338
chr22	51304566	643188	0.0125	0.1218
chrMT	16571	5629	0.3397	0.6562
chrX	155270560	1939872	0.0125	0.1289
chrY	59373566	133207	0.0022	0.072

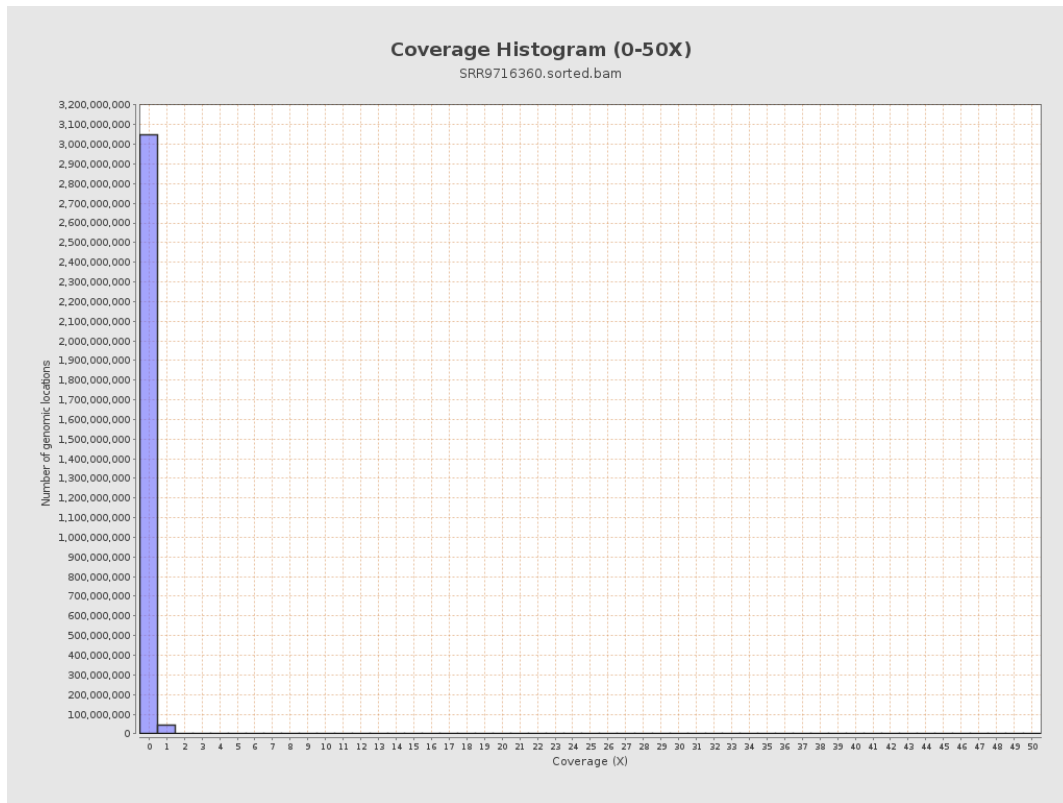
3. Results : Coverage across reference



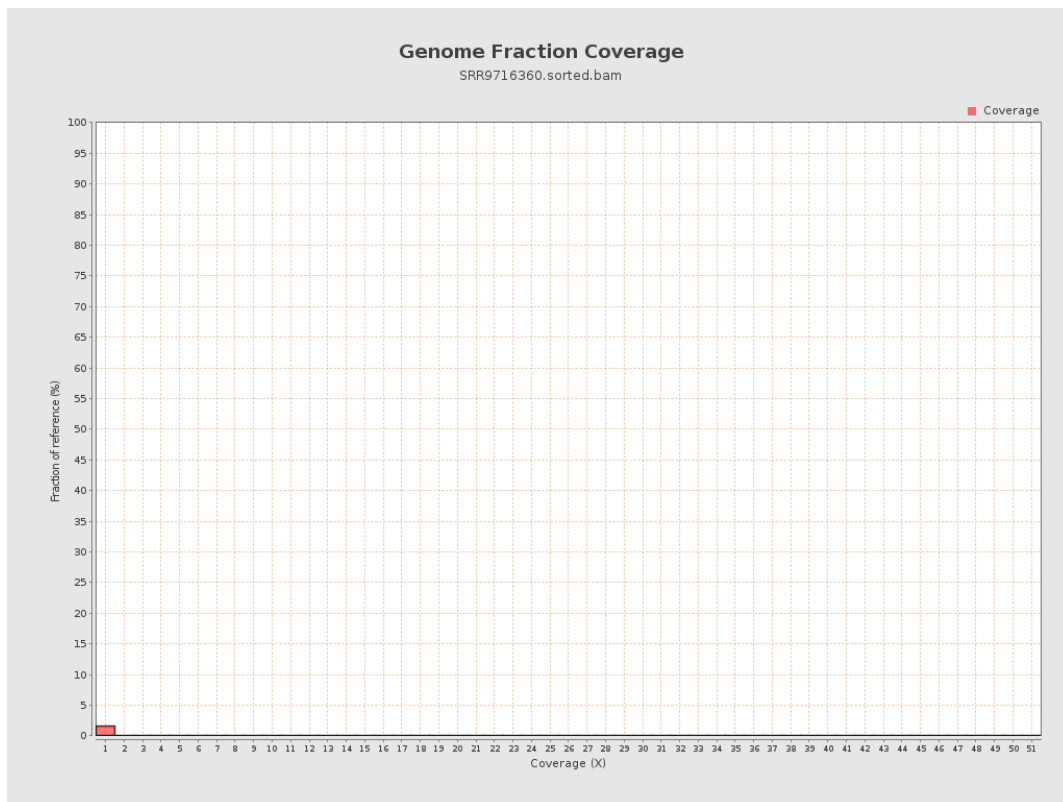
4. Results : Coverage Histogram



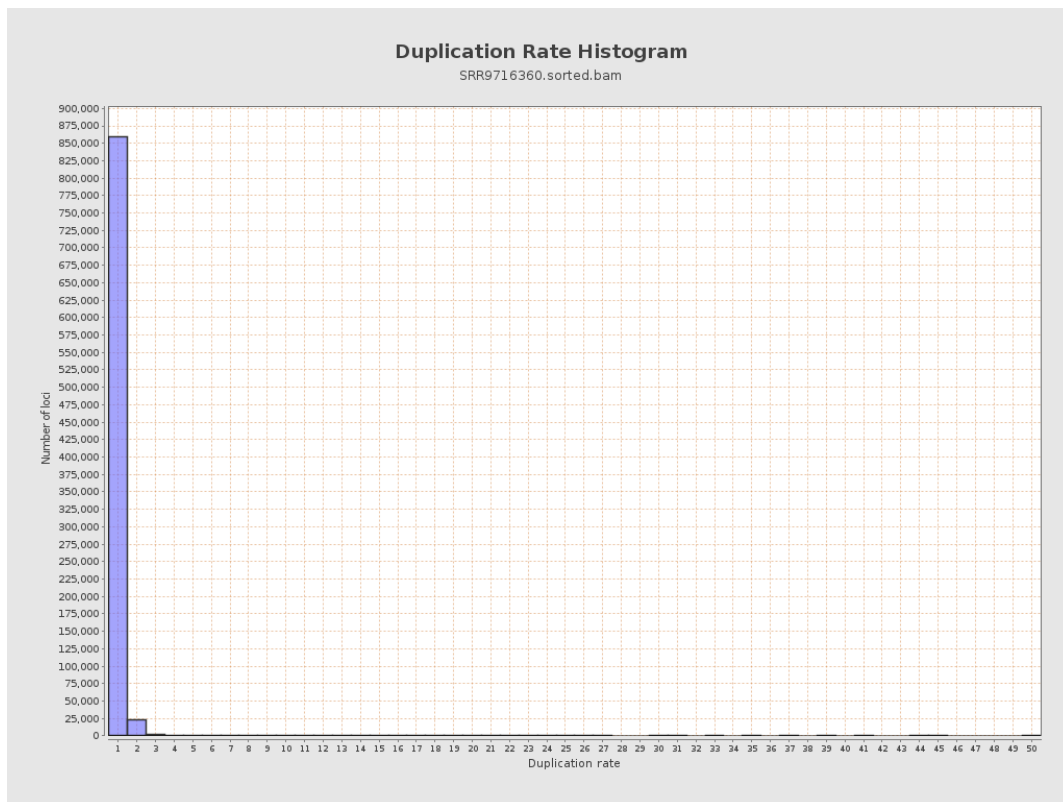
5. Results : Coverage Histogram (0-50X)



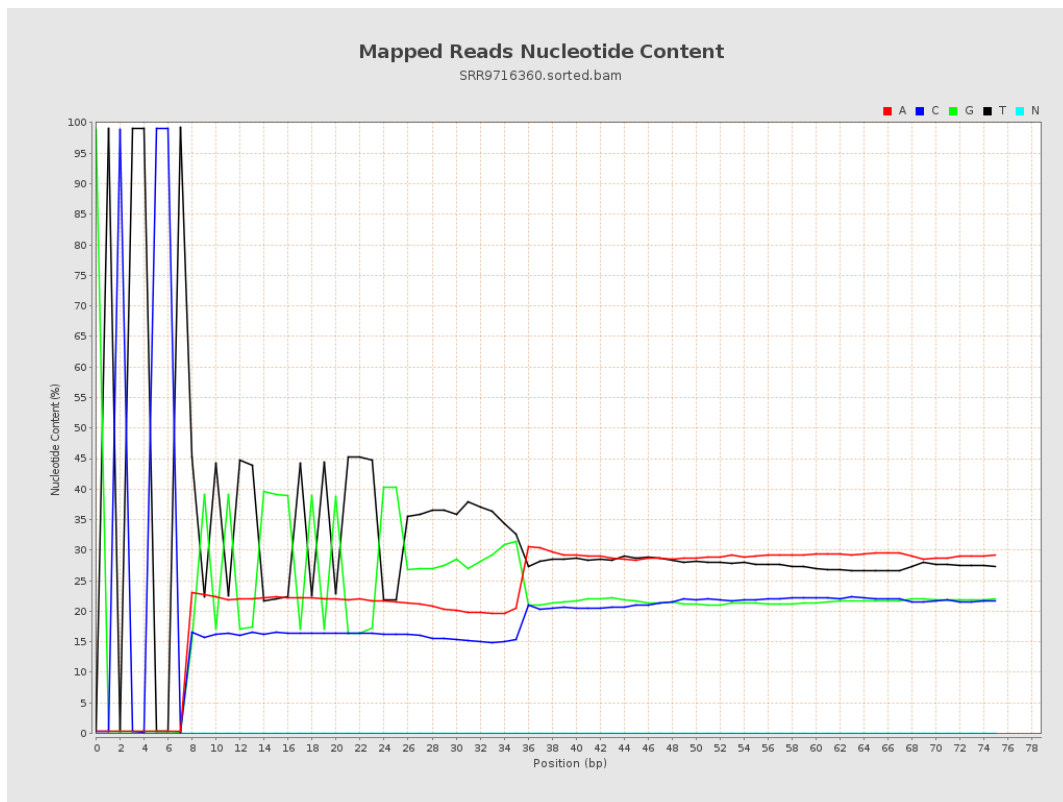
6. Results : Genome Fraction Coverage



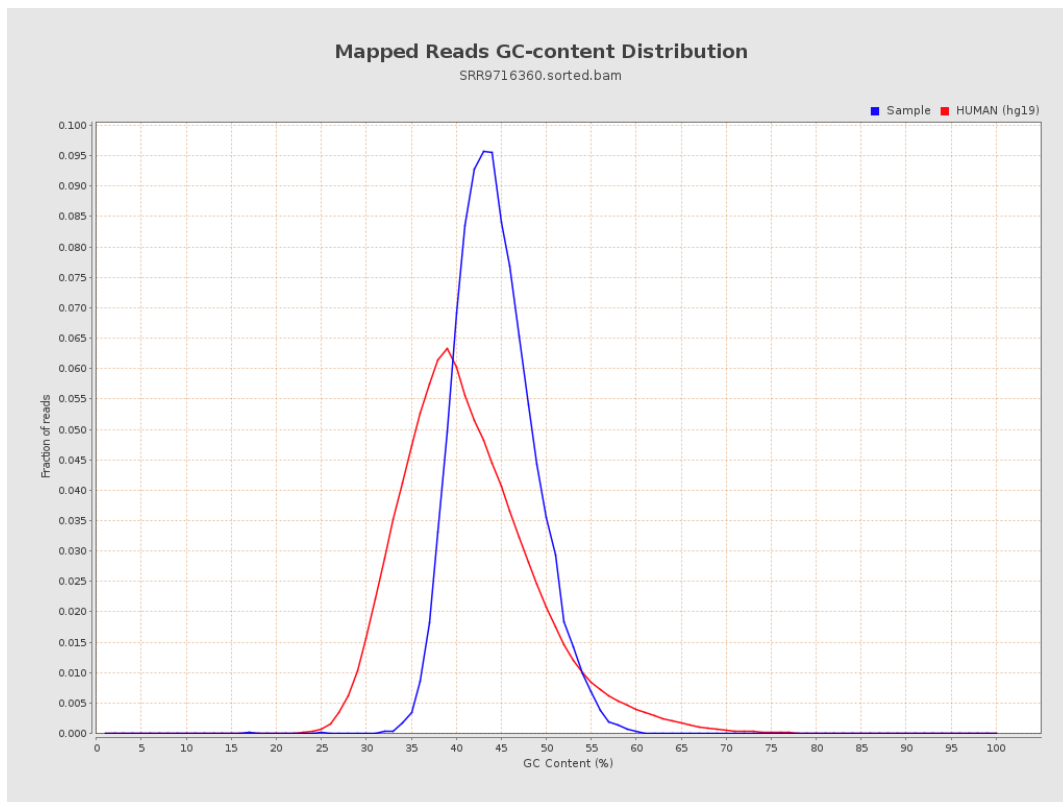
7. Results : Duplication Rate Histogram



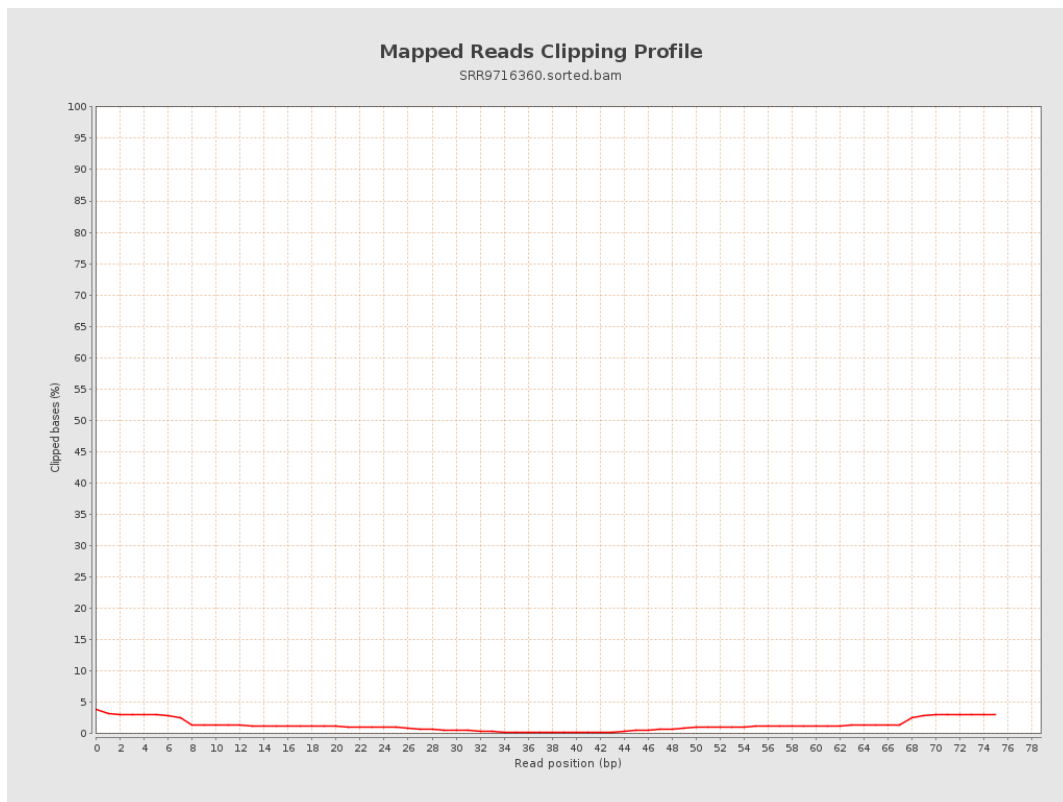
8. Results : Mapped Reads Nucleotide Content



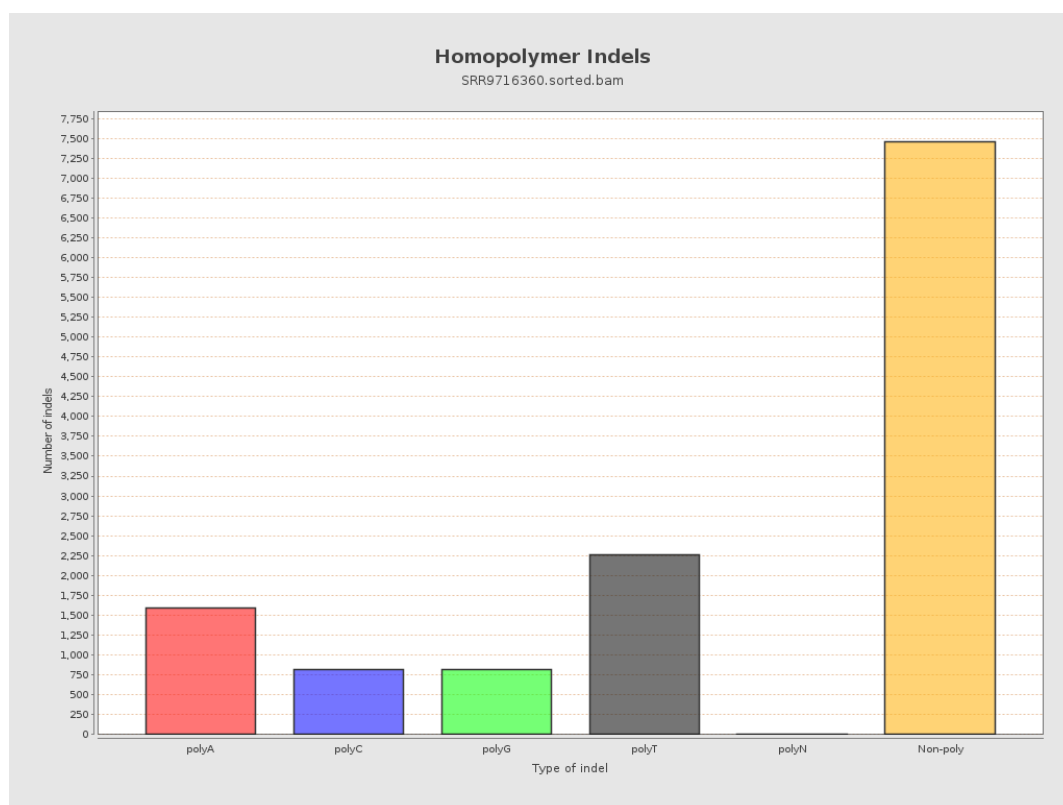
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

