

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 07:05:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472601.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_SRR3472601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472601_1.fastq.gz SRR3472601_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 07:05:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,564,728
Mapped reads	8,026,227 / 93.71%
Unmapped reads	538,501 / 6.29%
Mapped paired reads	8,026,227 / 93.71%
Mapped reads, first in pair	4,047,463 / 47.26%
Mapped reads, second in pair	3,978,764 / 46.46%
Mapped reads, both in pair	7,854,800 / 91.71%
Mapped reads, singletons	171,427 / 2%
Secondary alignments	0
Supplementary alignments	264,761 / 3.09%
Read min/max/mean length	30 / 100 / 101.21
Duplicated reads (estimated)	1,254,399 / 14.65%
Duplication rate	14%
Clipped reads	6,067,817 / 70.85%

2.2. ACGT Content

Number/percentage of A's	171,203,864 / 26.19%
Number/percentage of C's	130,436,744 / 19.95%
Number/percentage of T's	194,650,168 / 29.78%
Number/percentage of G's	156,995,754 / 24.02%
Number/percentage of N's	414,827 / 0.06%

GC Percentage	43.97%
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2.3. Coverage

Mean	0.2113
Standard Deviation	1.6968

2.4. Mapping Quality

Mean Mapping Quality	50.6
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2.5. Insert size

Mean	246,904.89
Standard Deviation	4,787,382.97
P25/Median/P75	88 / 127 / 177

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	7,464,137
Insertions	59,810
Mapped reads with at least one insertion	0.73%
Deletions	145,019
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.84%

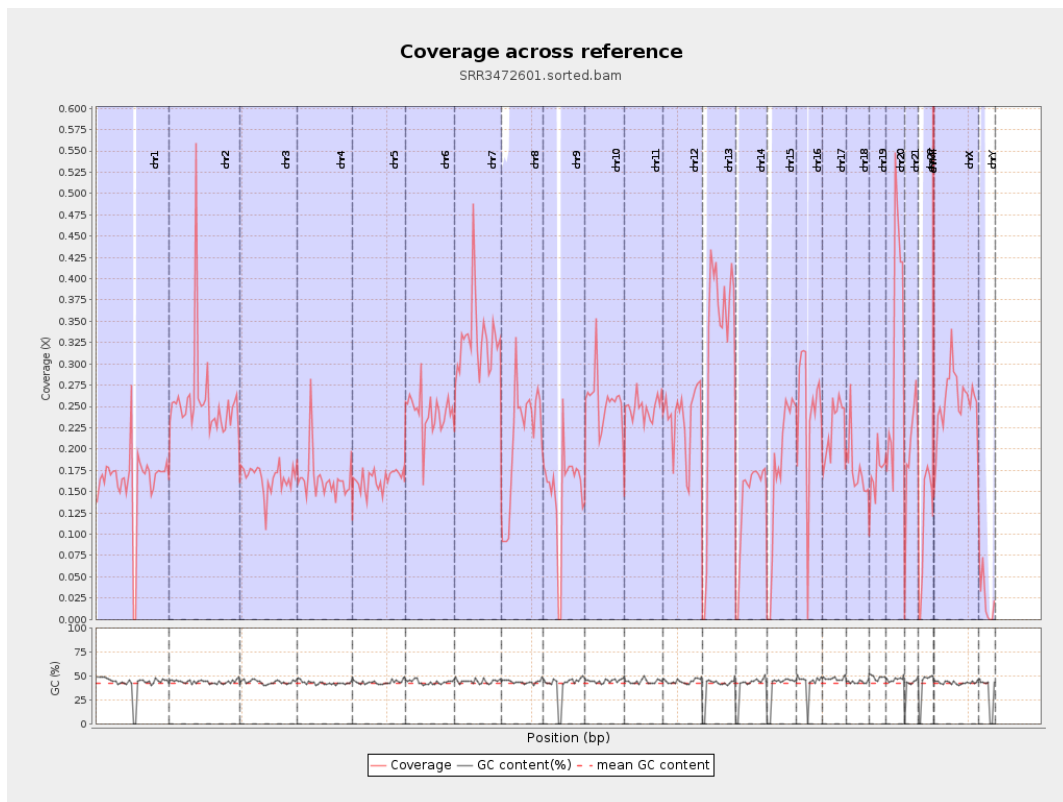
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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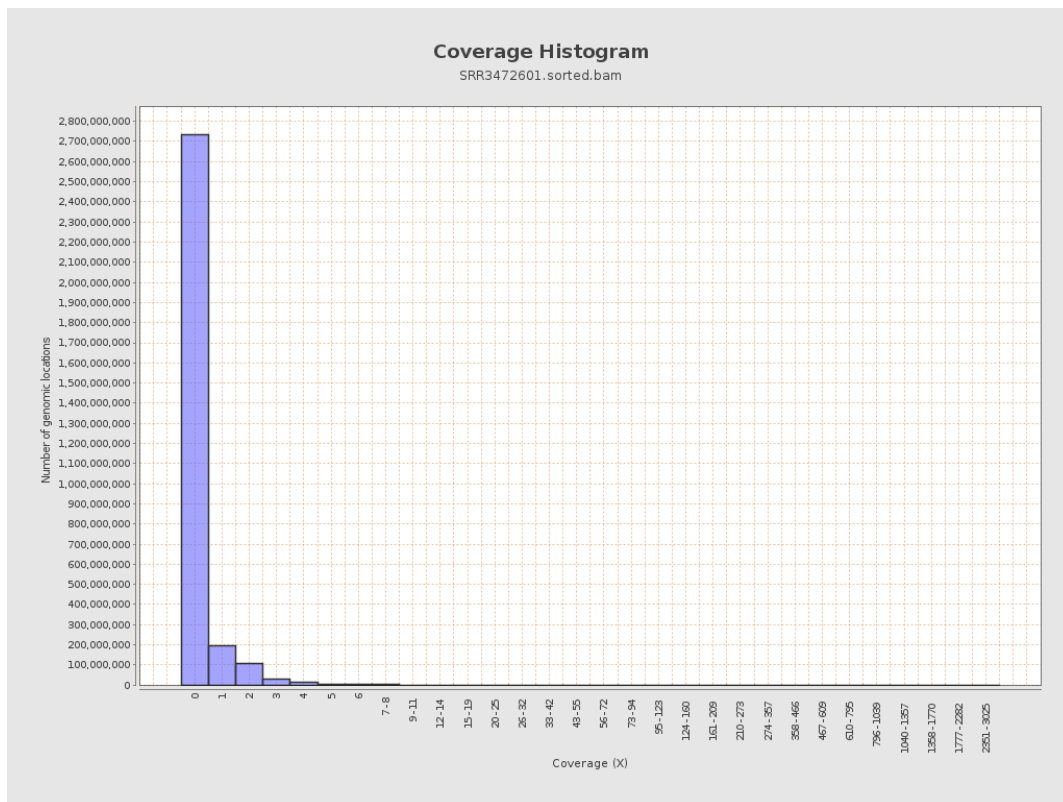
		bases	coverage	deviation
chr1	249250621	40289234	0.1616	2.1093
chr2	243199373	62297940	0.2562	2.6035
chr3	198022430	32881046	0.166	0.6072
chr4	191154276	31540669	0.165	0.8845
chr5	180915260	29659775	0.1639	0.623
chr6	171115067	41560150	0.2429	1.1266
chr7	159138663	52518402	0.33	3.4461
chr8	146364022	30802489	0.2105	1.5571
chr9	141213431	21332194	0.1511	1.875
chr10	135534747	34739161	0.2563	1.7491
chr11	135006516	33264565	0.2464	1.9514
chr12	133851895	31586060	0.236	0.7665
chr13	115169878	36325771	0.3154	0.9118
chr14	107349540	14986205	0.1396	1.4764
chr15	102531392	18211026	0.1776	0.651
chr16	90354753	22297166	0.2468	1.0522
chr17	81195210	18176112	0.2239	1.2175
chr18	78077248	13829576	0.1771	3.2492
chr19	59128983	10153963	0.1717	1.5521
chr20	63025520	20919880	0.3319	1.0183
chr21	48129895	9541379	0.1982	0.897
chr22	51304566	5843121	0.1139	0.5163
chrMT	16571	57682	3.4809	3.4166
chrX	155270560	39749663	0.256	1.0821

chrY	59373566	1409291	0.0237	0.644
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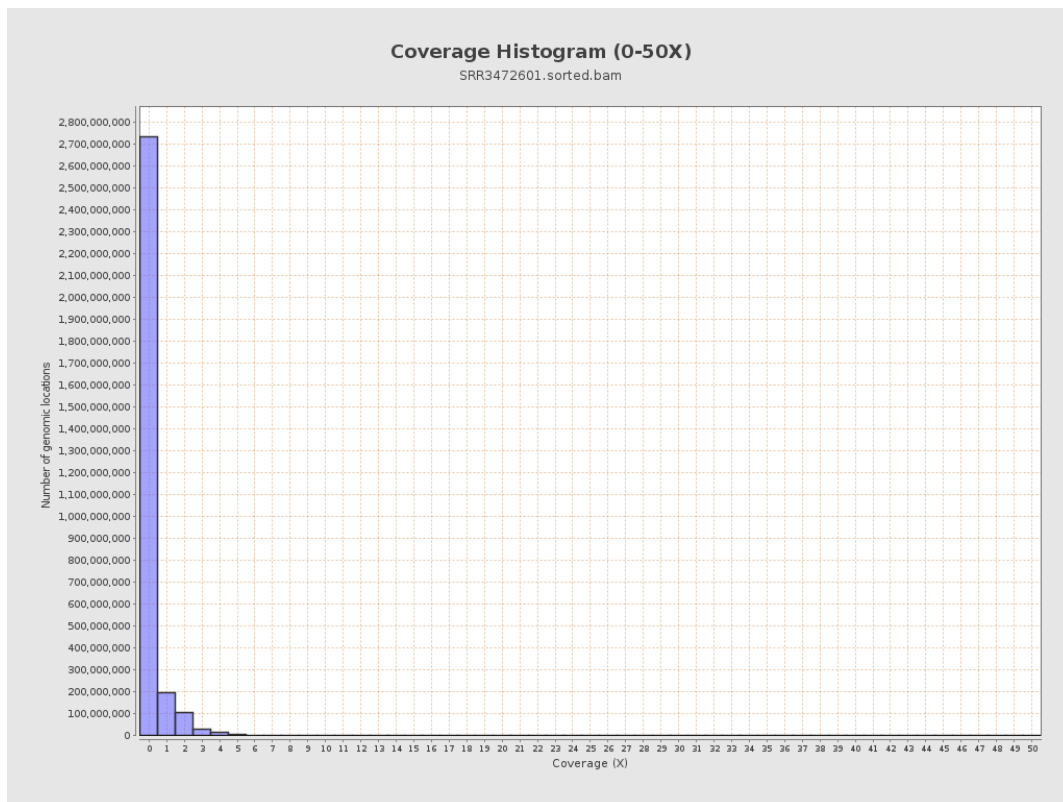
3. Results : Coverage across reference



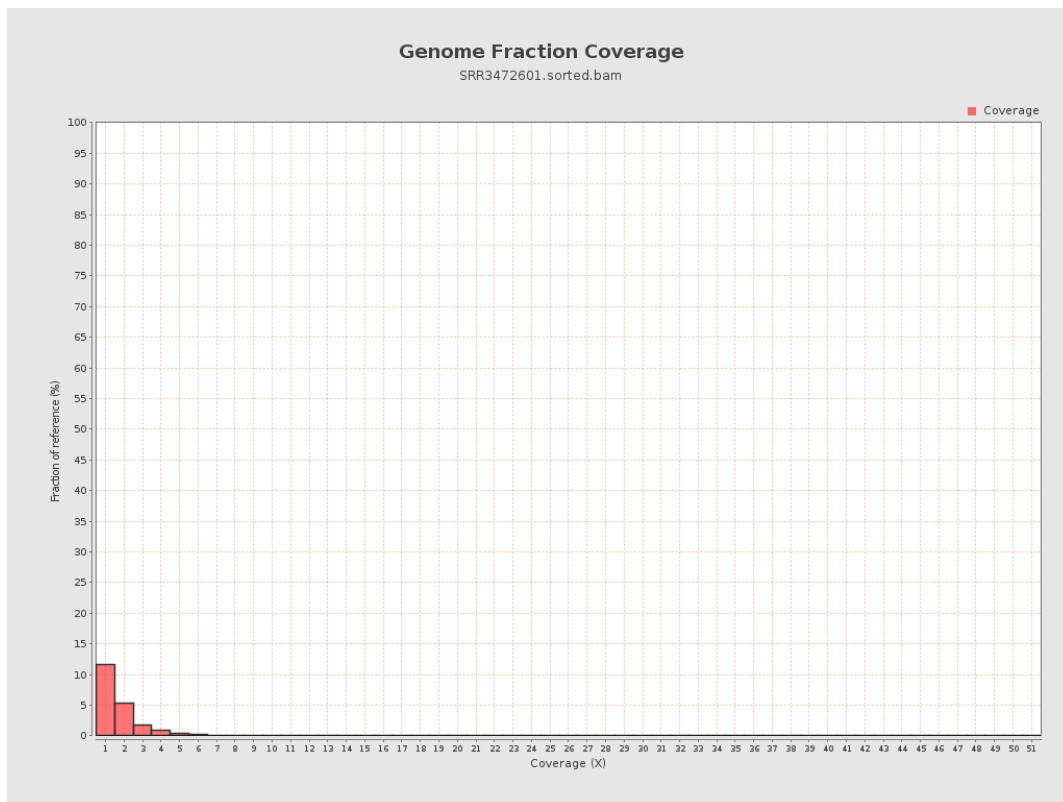
4. Results : Coverage Histogram



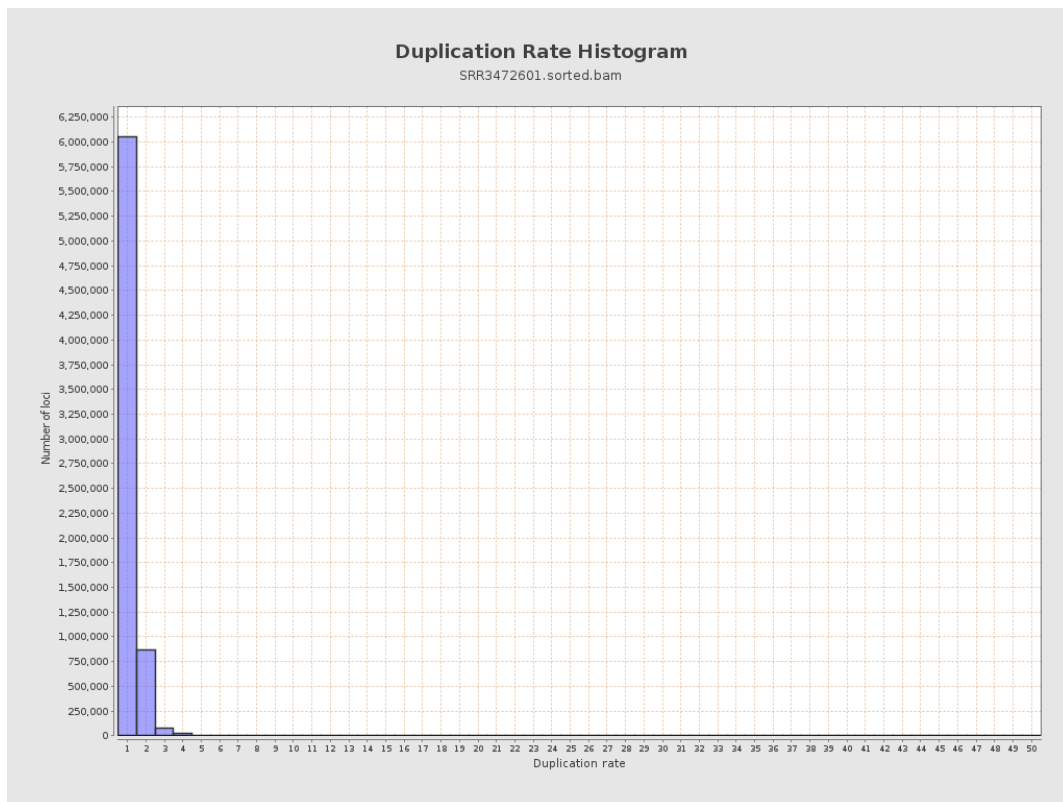
5. Results : Coverage Histogram (0-50X)



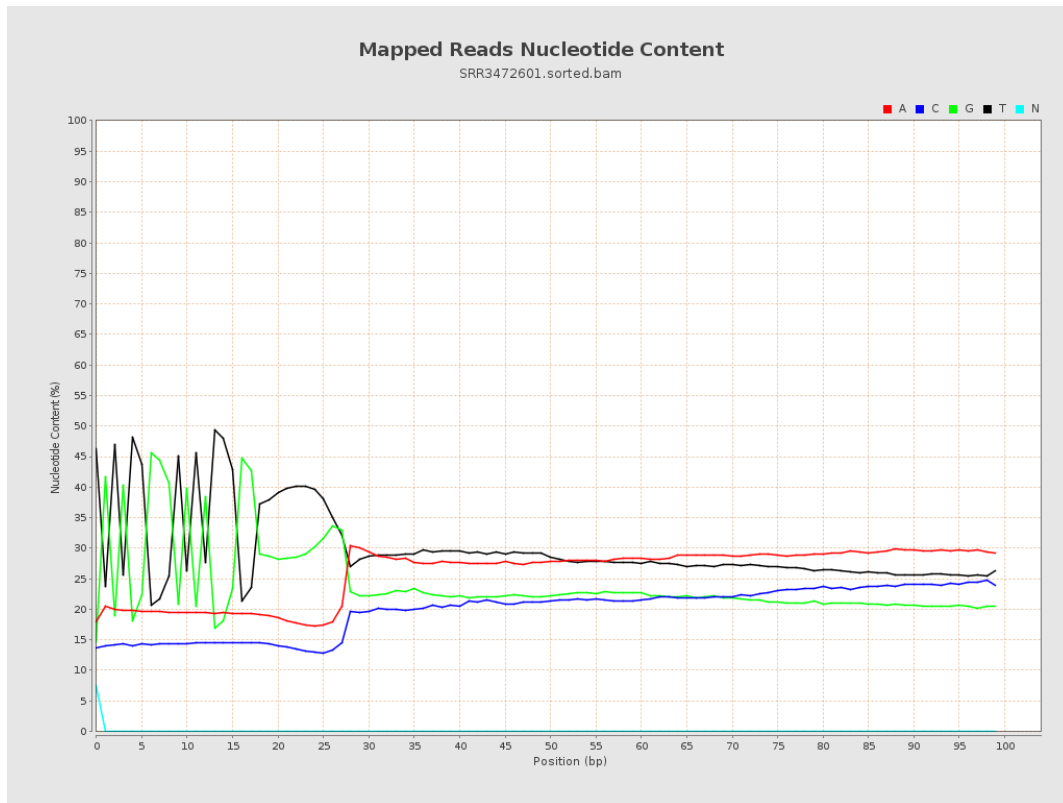
6. Results : Genome Fraction Coverage



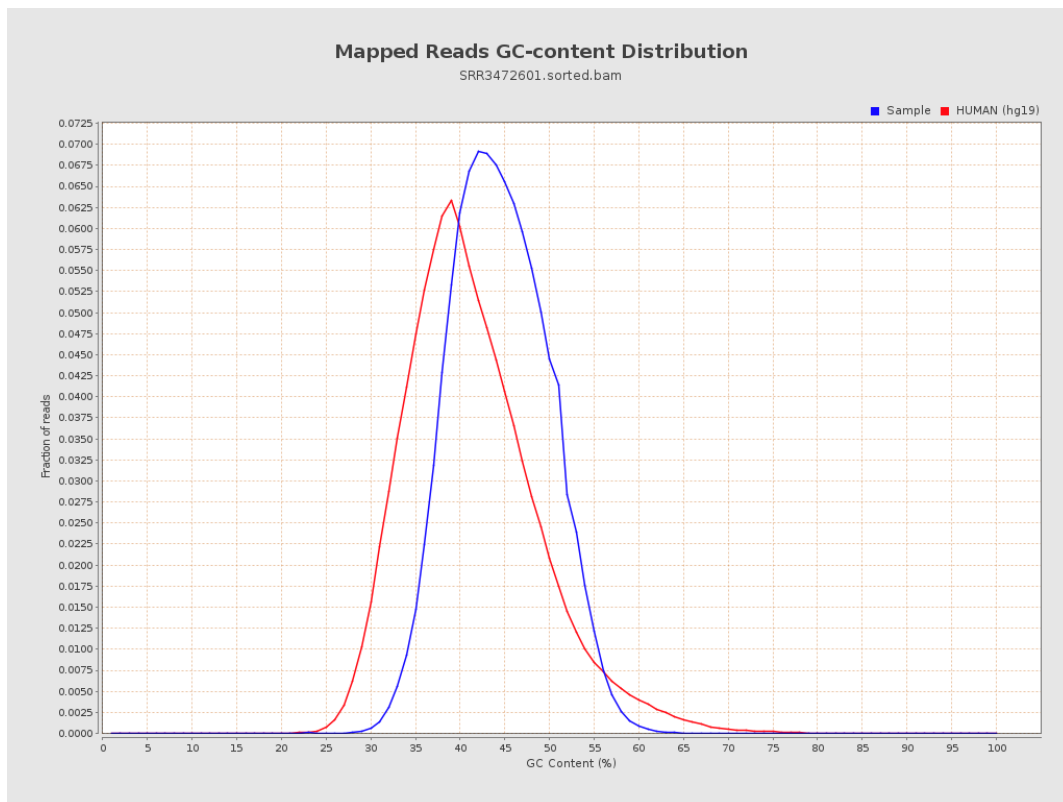
7. Results : Duplication Rate Histogram



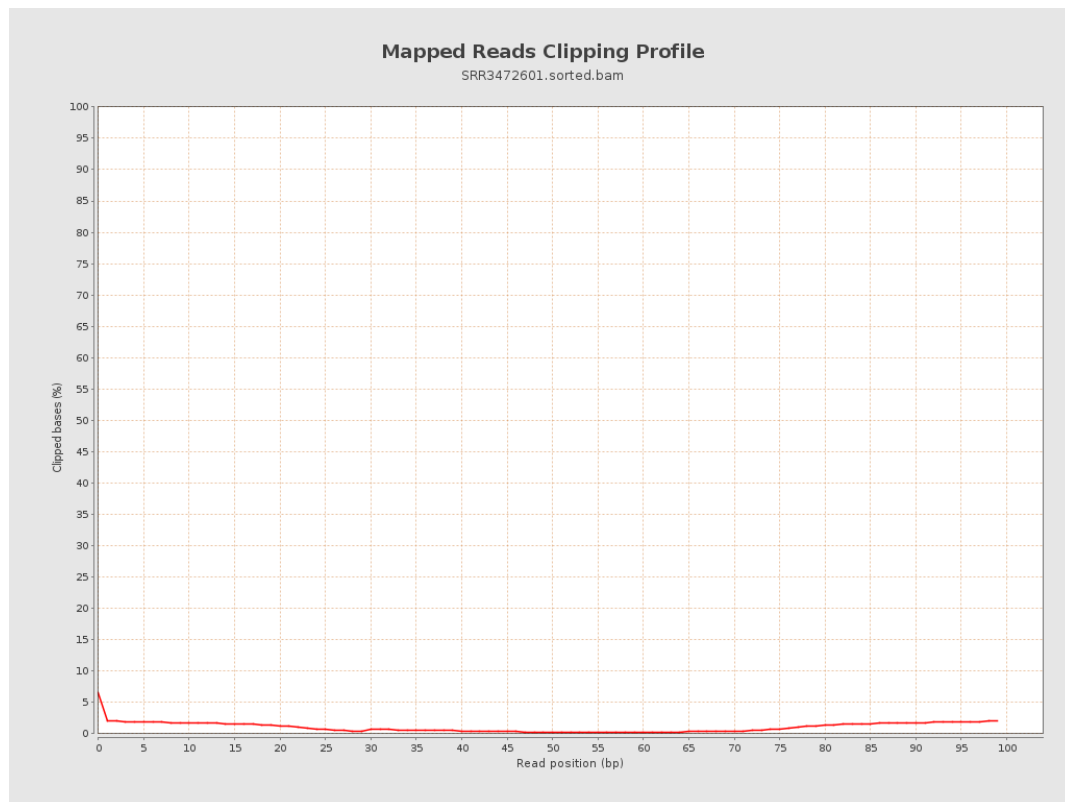
8. Results : Mapped Reads Nucleotide Content



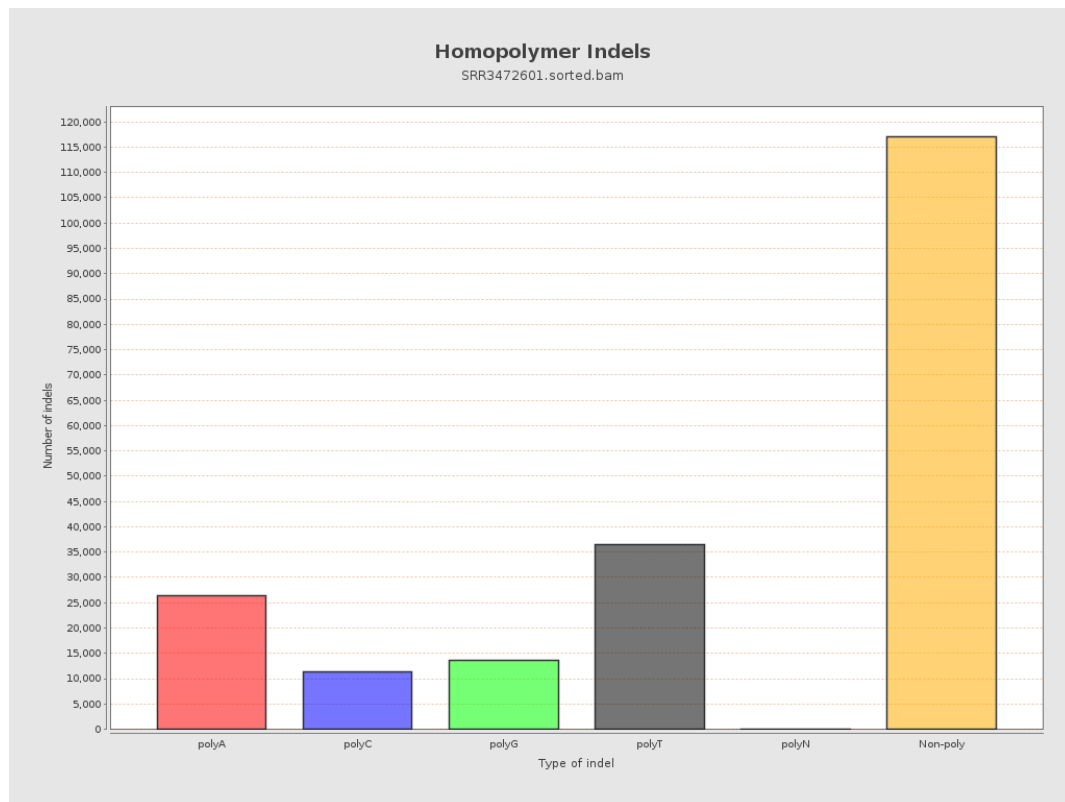
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



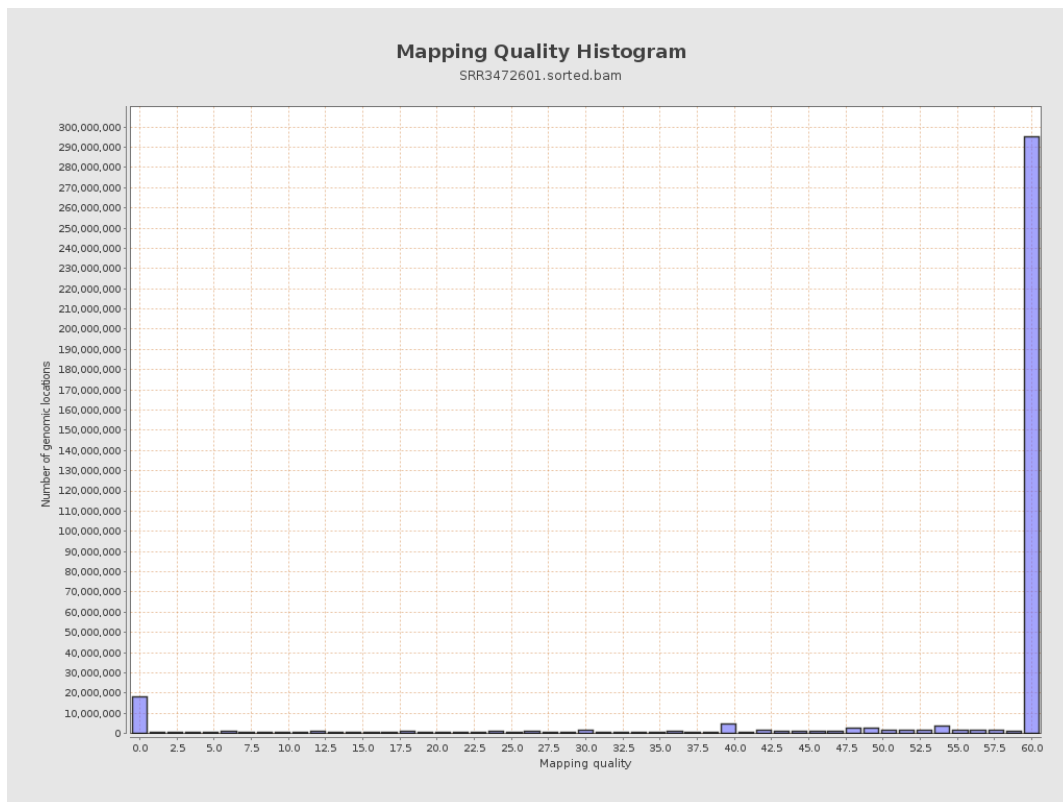
11. Results : Homopolymer Indels



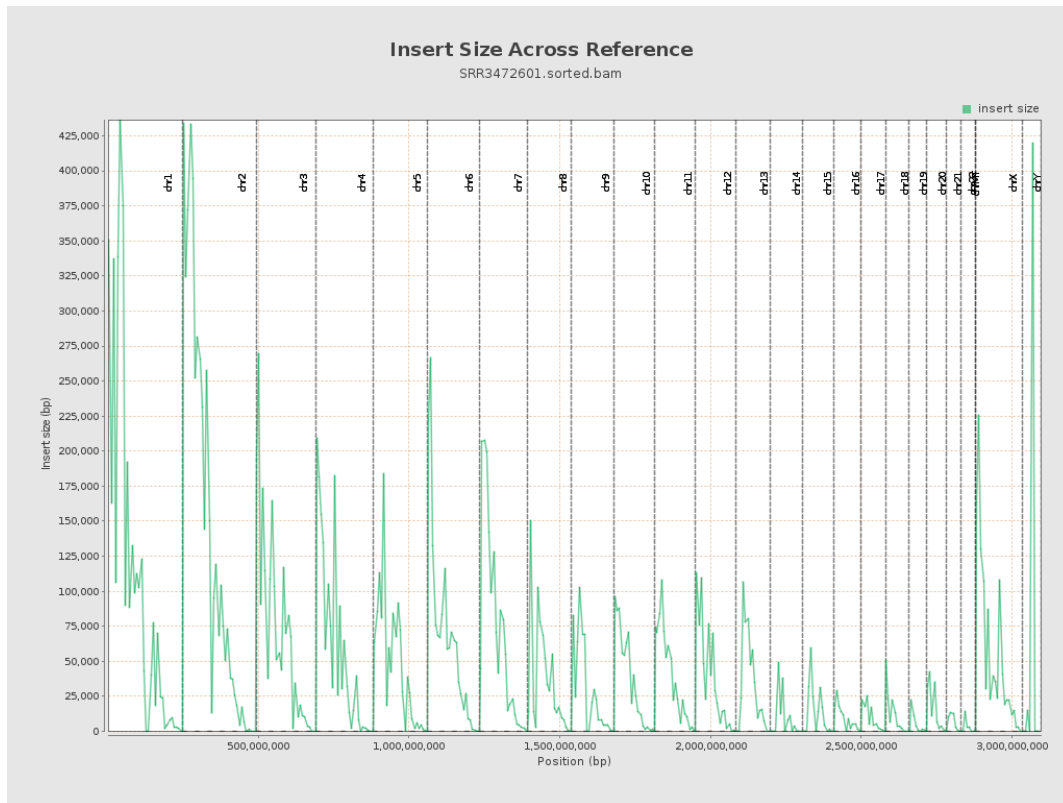
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

