

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 10:07:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472691.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_SRR3472691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472691_1.fastq.gz SRR3472691_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 10:07:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,619,410
Mapped reads	15,474,682 / 99.07%
Unmapped reads	144,728 / 0.93%
Mapped paired reads	15,474,682 / 99.07%
Mapped reads, first in pair	7,757,037 / 49.66%
Mapped reads, second in pair	7,717,645 / 49.41%
Mapped reads, both in pair	15,376,744 / 98.45%
Mapped reads, singletons	97,938 / 0.63%
Secondary alignments	0
Supplementary alignments	110,865 / 0.71%
Read min/max/mean length	30 / 101 / 99.88
Duplicated reads (estimated)	11,238,651 / 71.95%
Duplication rate	47.8%
Clipped reads	1,163,806 / 7.45%

2.2. ACGT Content

Number/percentage of A's	415,735,228 / 27.3%
Number/percentage of C's	347,645,417 / 22.83%
Number/percentage of T's	416,802,223 / 27.37%
Number/percentage of G's	342,549,200 / 22.49%
Number/percentage of N's	286,362 / 0.02%

GC Percentage	45.32%
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2.3. Coverage

Mean	0.492
Standard Deviation	32.4551

2.4. Mapping Quality

Mean Mapping Quality	54.5
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2.5. Insert size

Mean	28,678.24
Standard Deviation	1,667,699.86
P25/Median/P75	160 / 217 / 290

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,545,740
Insertions	93,850
Mapped reads with at least one insertion	0.6%
Deletions	71,639
Mapped reads with at least one deletion	0.45%
Homopolymer indels	47.62%

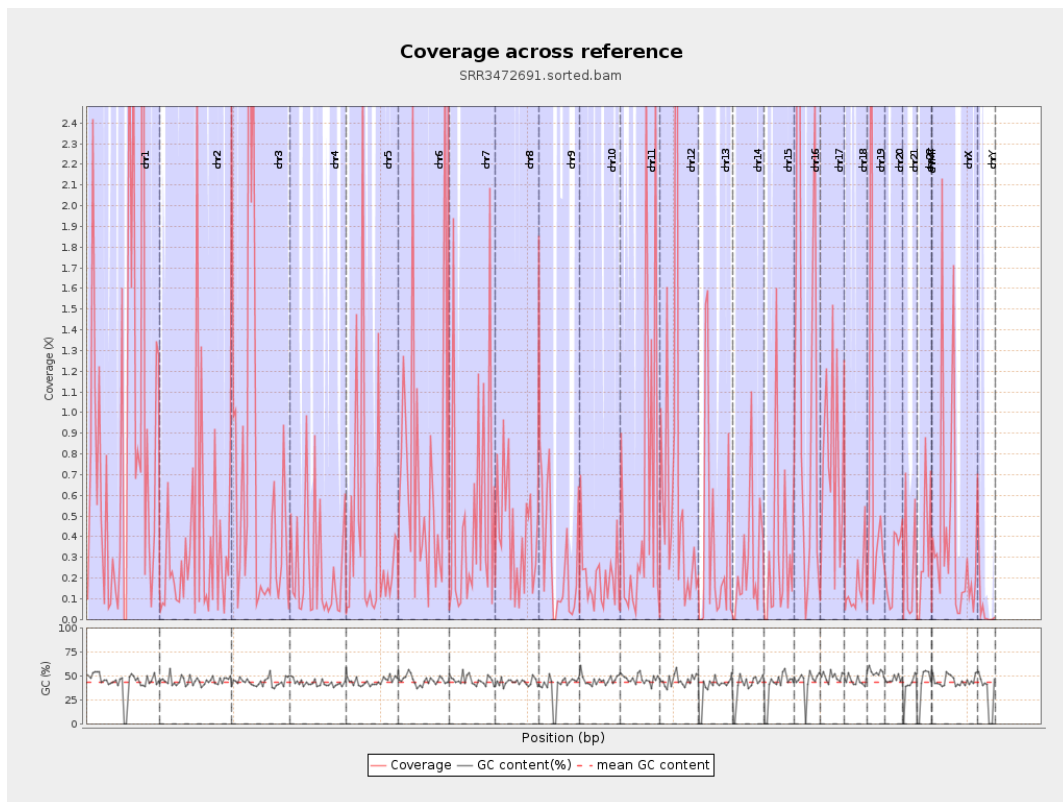
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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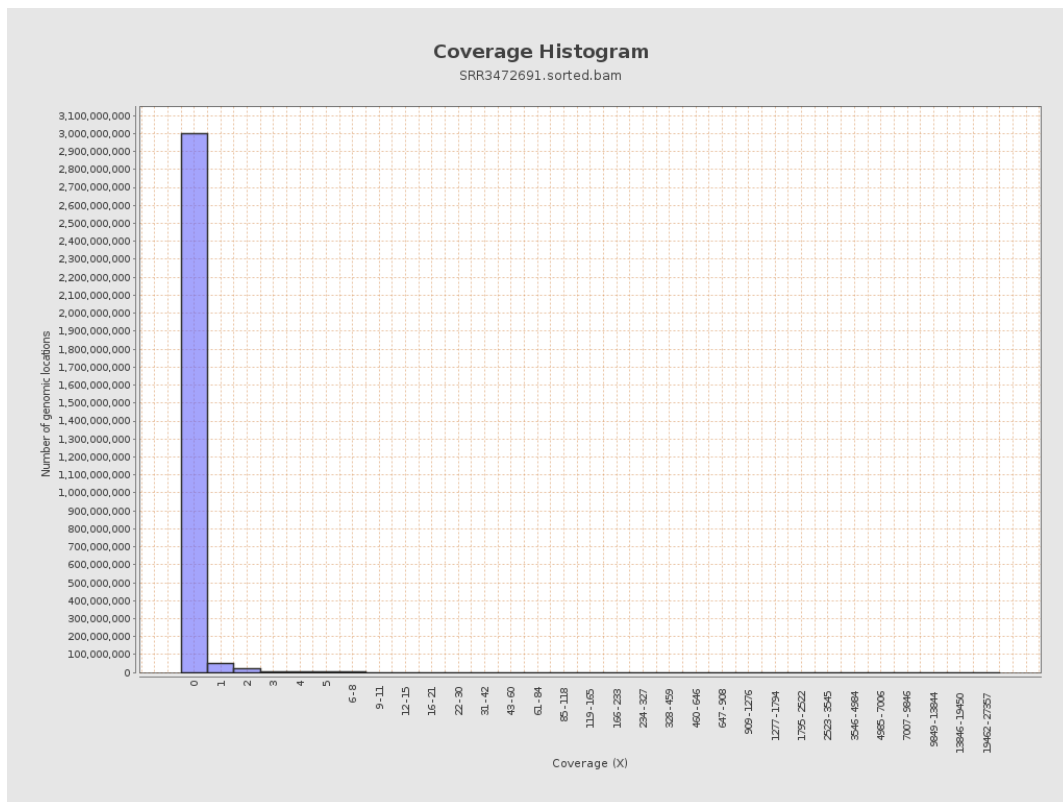
		bases	coverage	deviation
chr1	249250621	226028783	0.9068	49.7475
chr2	243199373	87589712	0.3602	32.9597
chr3	198022430	139595858	0.7049	33.3094
chr4	191154276	46053095	0.2409	12.4616
chr5	180915260	74593042	0.4123	22.2372
chr6	171115067	126851769	0.7413	32.1466
chr7	159138663	81313064	0.511	29.2829
chr8	146364022	61502645	0.4202	18.4783
chr9	141213431	43322076	0.3068	12.9574
chr10	135534747	27488136	0.2028	11.1739
chr11	135006516	76831605	0.5691	45.9105
chr12	133851895	95463717	0.7132	62.6193
chr13	115169878	42218802	0.3666	21.3549
chr14	107349540	28752773	0.2678	10.027
chr15	102531392	30854661	0.3009	16.0911
chr16	90354753	103305909	1.1433	76.1159
chr17	81195210	62321599	0.7676	26.2186
chr18	78077248	12666236	0.1622	7.5075
chr19	59128983	46828879	0.792	37.43
chr20	63025520	16955926	0.269	9.5643
chr21	48129895	11883114	0.2469	15.4978
chr22	51304566	17636240	0.3438	14.3837
chrMT	16571	3016	0.182	0.5259
chrX	155270560	60254988	0.3881	16.0755

chrY	59373566	2869561	0.0483	7.0056
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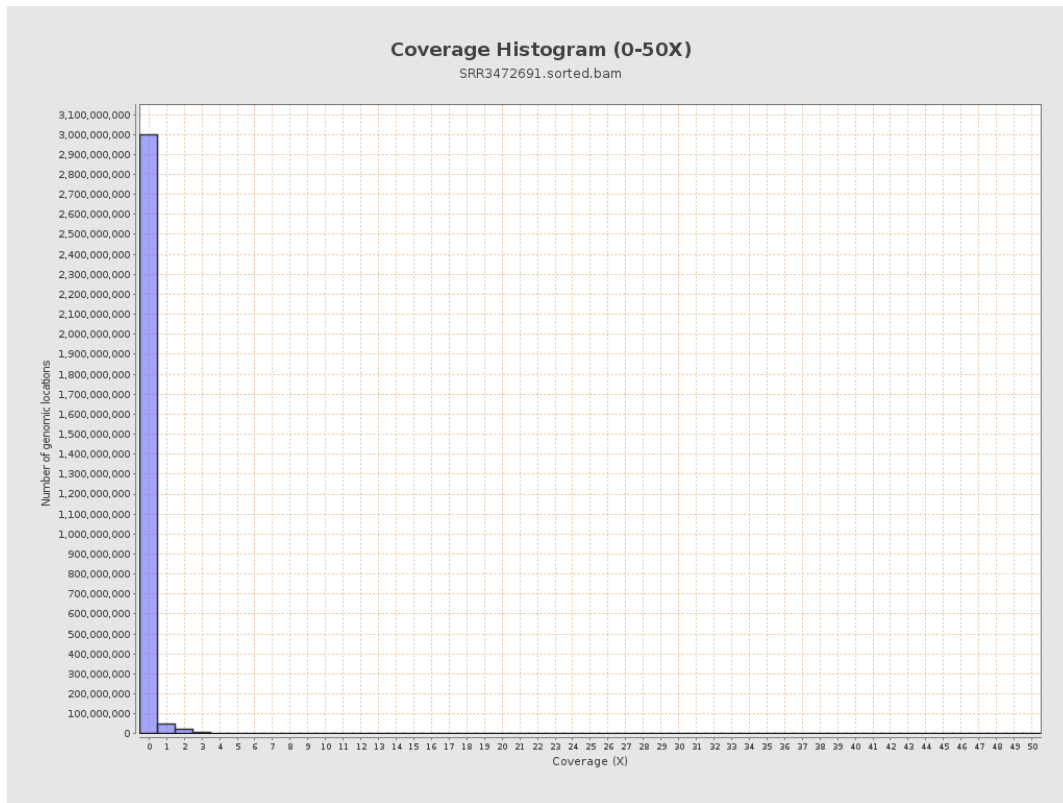
3. Results : Coverage across reference



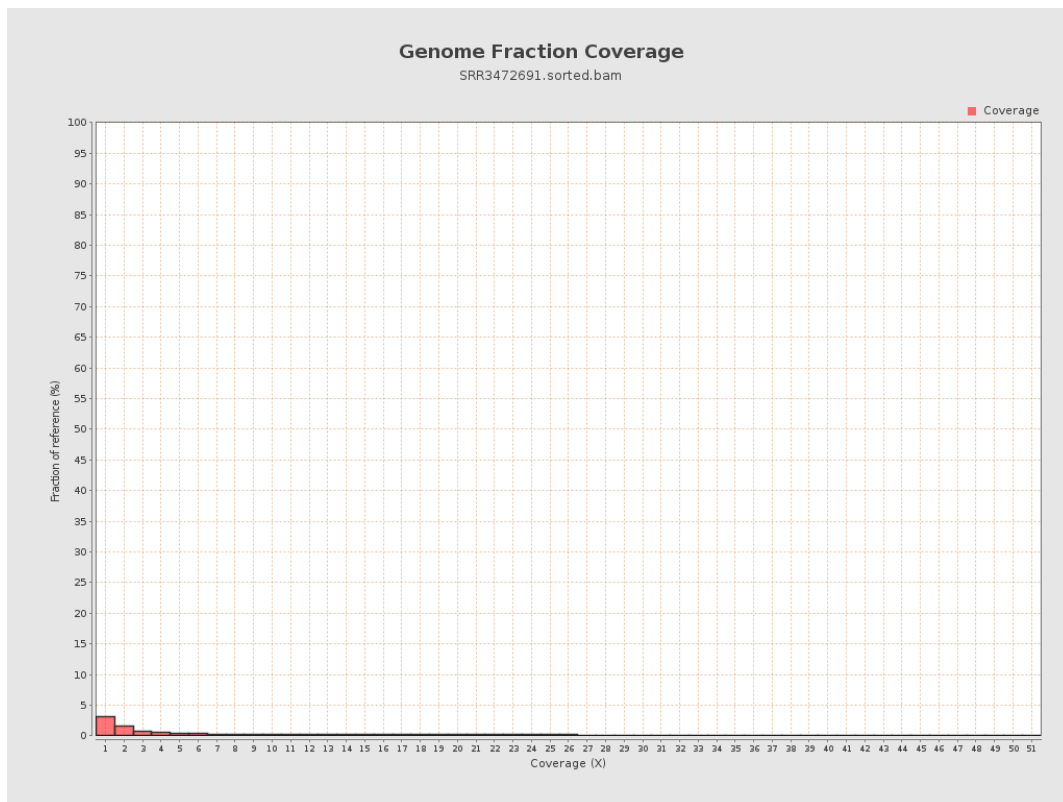
4. Results : Coverage Histogram



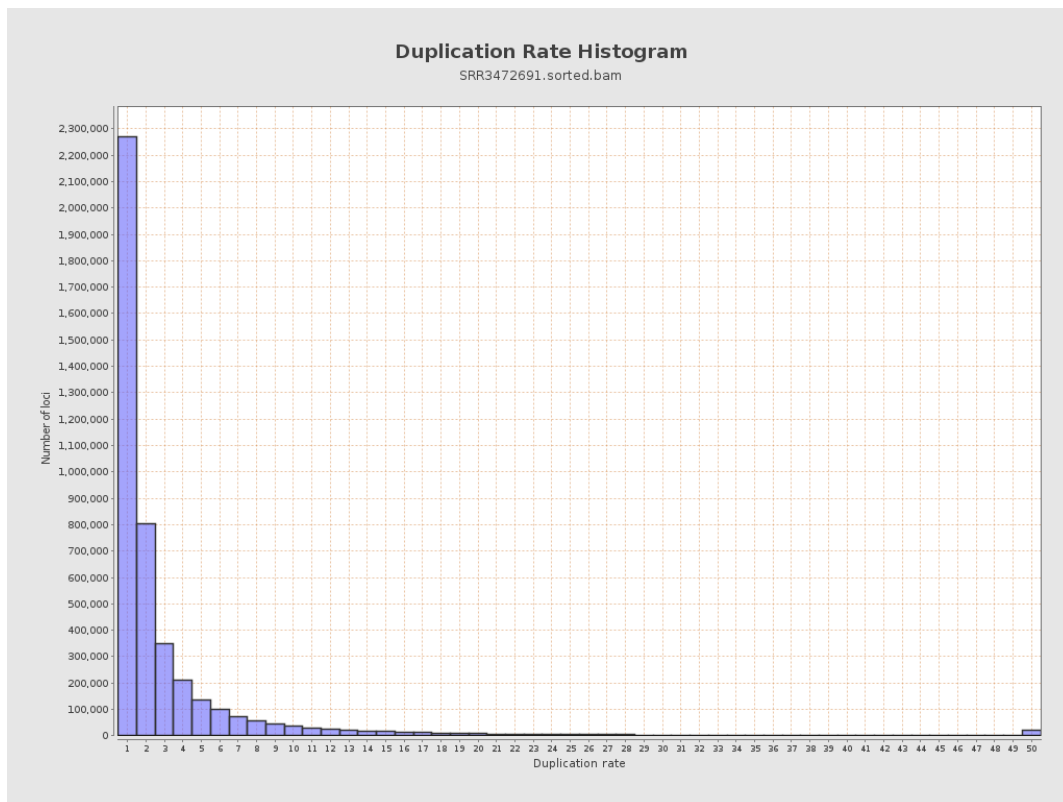
5. Results : Coverage Histogram (0-50X)



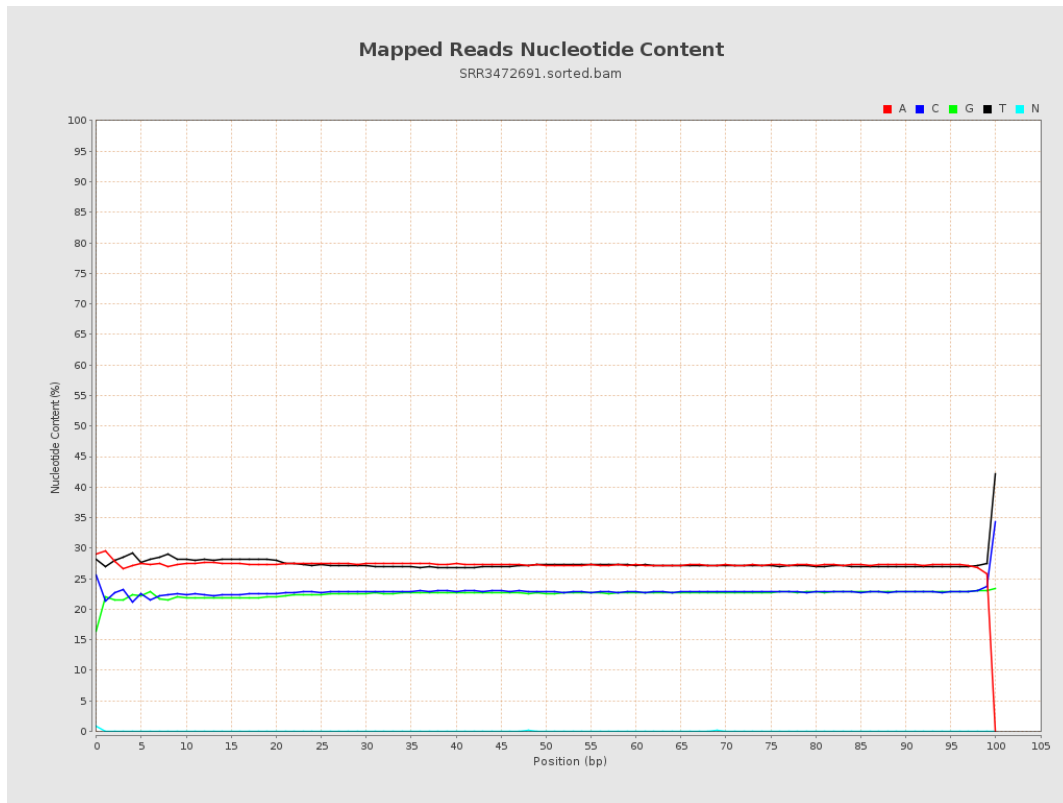
6. Results : Genome Fraction Coverage



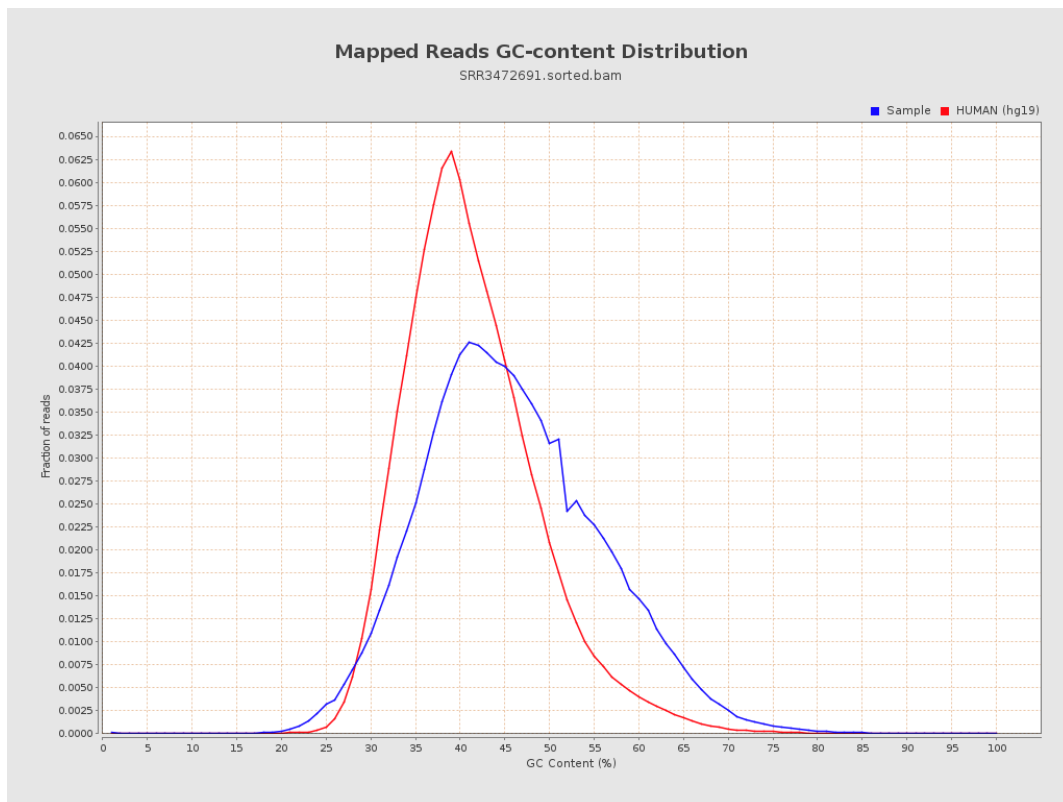
7. Results : Duplication Rate Histogram



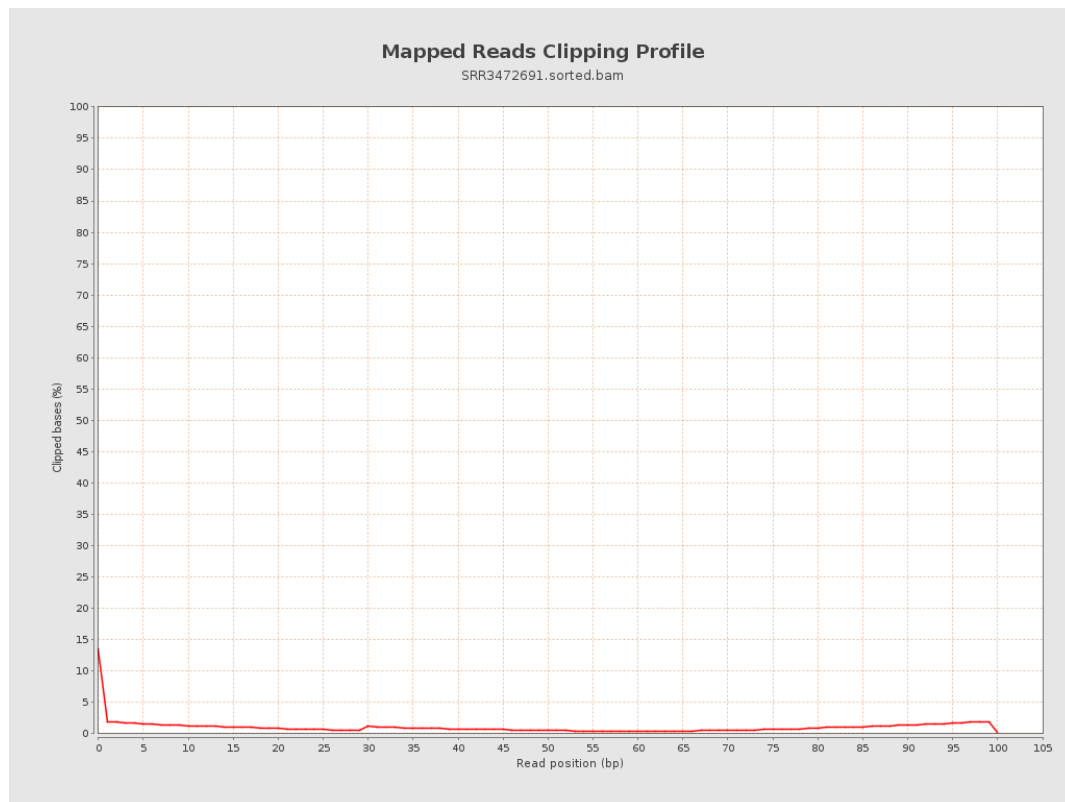
8. Results : Mapped Reads Nucleotide Content



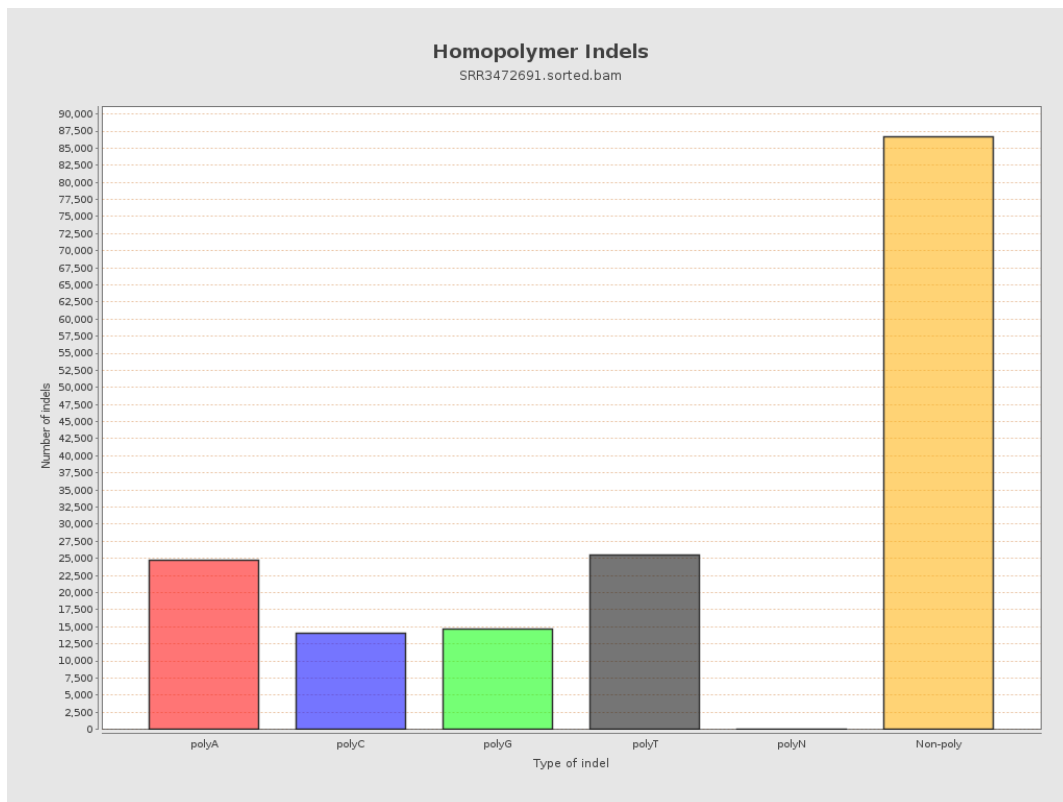
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



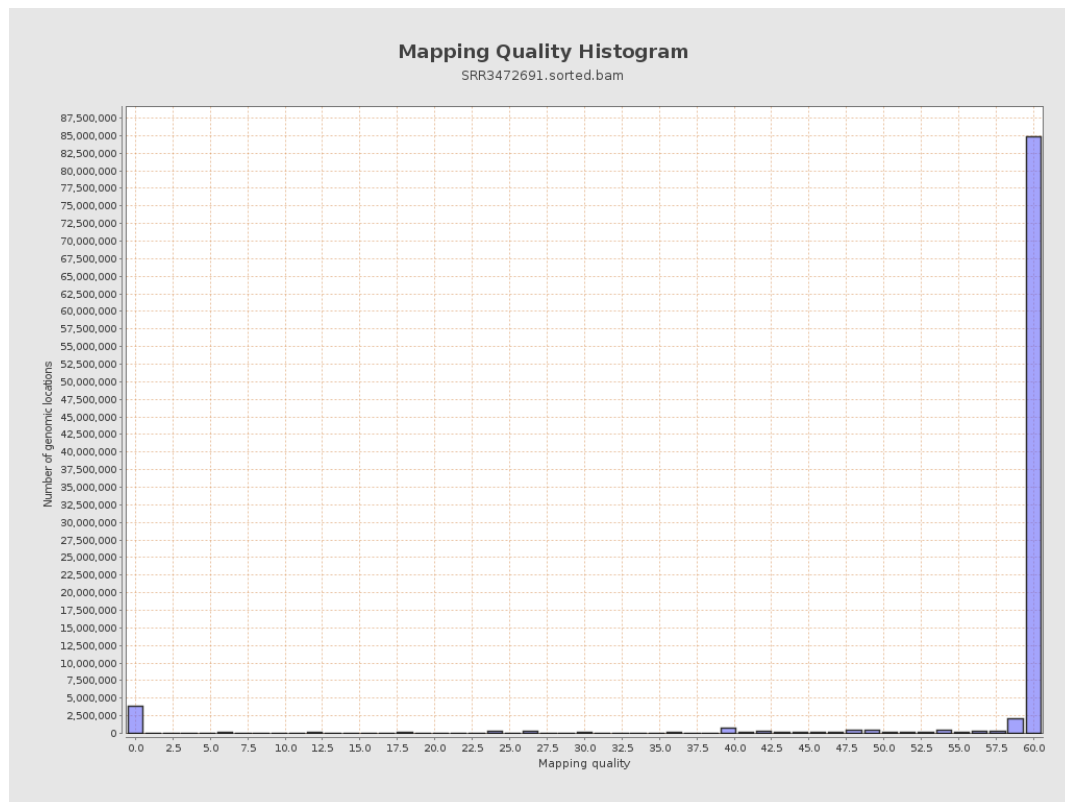
11. Results : Homopolymer Indels



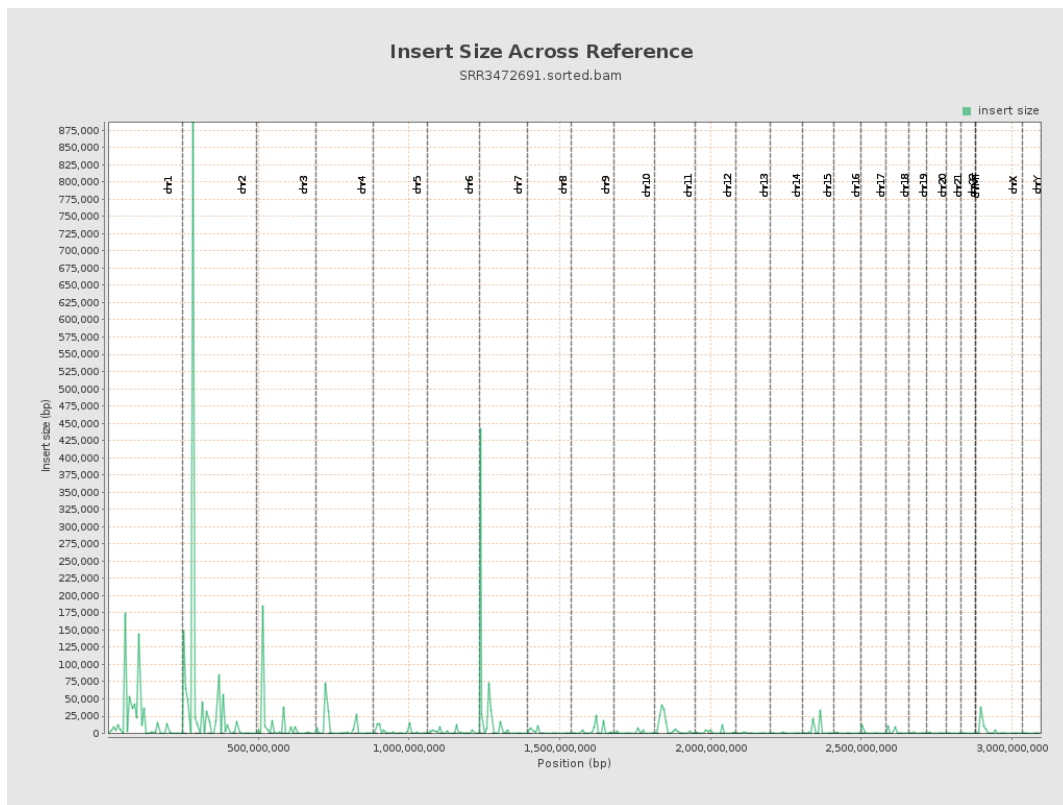
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

