

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 18:11:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472716.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_SRR3472716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472716_1.fastq.gz SRR3472716_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 18:11:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,551,674
Mapped reads	12,447,878 / 99.17%
Unmapped reads	103,796 / 0.83%
Mapped paired reads	12,447,878 / 99.17%
Mapped reads, first in pair	6,241,173 / 49.72%
Mapped reads, second in pair	6,206,705 / 49.45%
Mapped reads, both in pair	12,387,576 / 98.69%
Mapped reads, singletons	60,302 / 0.48%
Secondary alignments	0
Supplementary alignments	36,944 / 0.29%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	7,210,157 / 57.44%
Duplication rate	46.7%
Clipped reads	1,090,439 / 8.69%

2.2. ACGT Content

Number/percentage of A's	330,559,558 / 27.01%
Number/percentage of C's	283,147,083 / 23.14%
Number/percentage of T's	329,198,843 / 26.9%
Number/percentage of G's	280,610,193 / 22.93%
Number/percentage of N's	238,101 / 0.02%

GC Percentage	46.07%
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2.3. Coverage

Mean	0.3954
Standard Deviation	11.9701

2.4. Mapping Quality

Mean Mapping Quality	55.24
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2.5. Insert size

Mean	25,510.27
Standard Deviation	1,628,201.49
P25/Median/P75	163 / 230 / 311

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	7,023,456
Insertions	64,698
Mapped reads with at least one insertion	0.51%
Deletions	61,976
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.38%

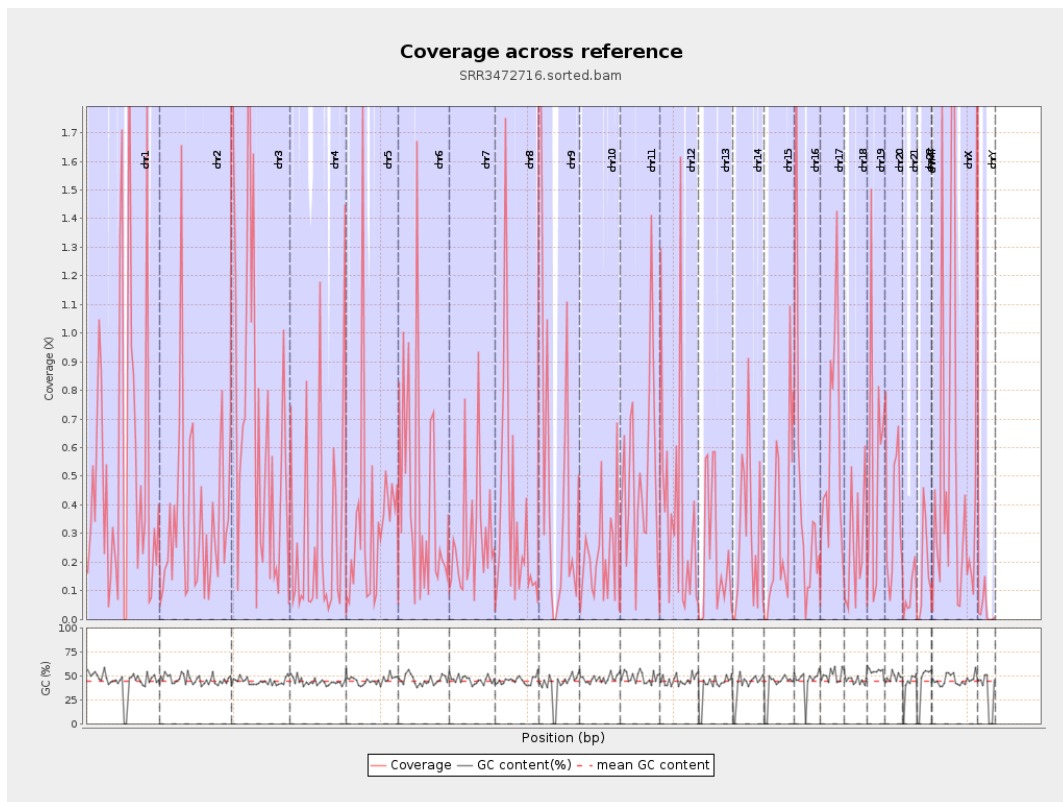
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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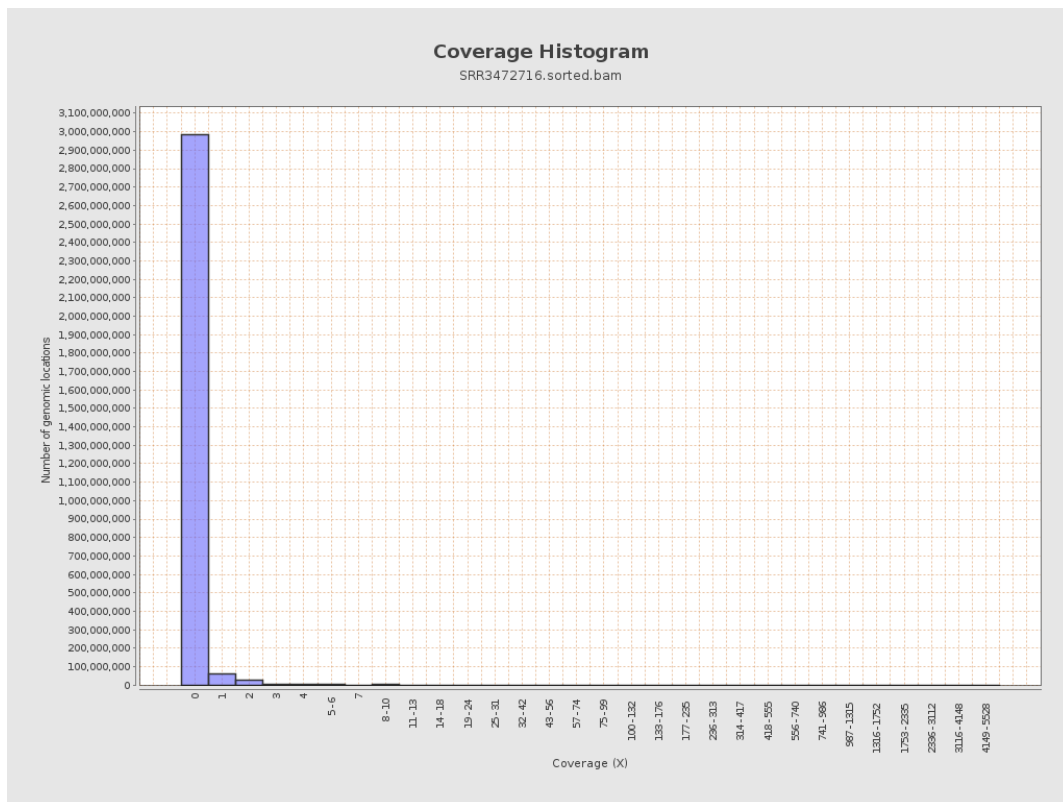
		bases	coverage	deviation
chr1	249250621	132963621	0.5335	15.4685
chr2	243199373	85158931	0.3502	11.3415
chr3	198022430	142035454	0.7173	14.6833
chr4	191154276	55640103	0.2911	9.9737
chr5	180915260	62415849	0.345	10.6028
chr6	171115067	71368141	0.4171	10.5939
chr7	159138663	45597938	0.2865	8.2688
chr8	146364022	51562790	0.3523	10.839
chr9	141213431	72466947	0.5132	15.792
chr10	135534747	30010922	0.2214	7.6627
chr11	135006516	67861686	0.5027	15.2547
chr12	133851895	53243353	0.3978	12.1821
chr13	115169878	26089523	0.2265	7.7137
chr14	107349540	30514825	0.2843	9.0467
chr15	102531392	31157972	0.3039	9.4092
chr16	90354753	38818499	0.4296	10.9405
chr17	81195210	48477446	0.597	14.5402
chr18	78077248	20234751	0.2592	8.6967
chr19	59128983	33530869	0.5671	12.0833
chr20	63025520	24493264	0.3886	10.9331
chr21	48129895	4470877	0.0929	3.0376
chr22	51304566	8810652	0.1717	4.4376
chrMT	16571	2173	0.1311	0.4298
chrX	155270560	85013809	0.5475	18.3562

chrY	59373566	1970073	0.0332	2.0473
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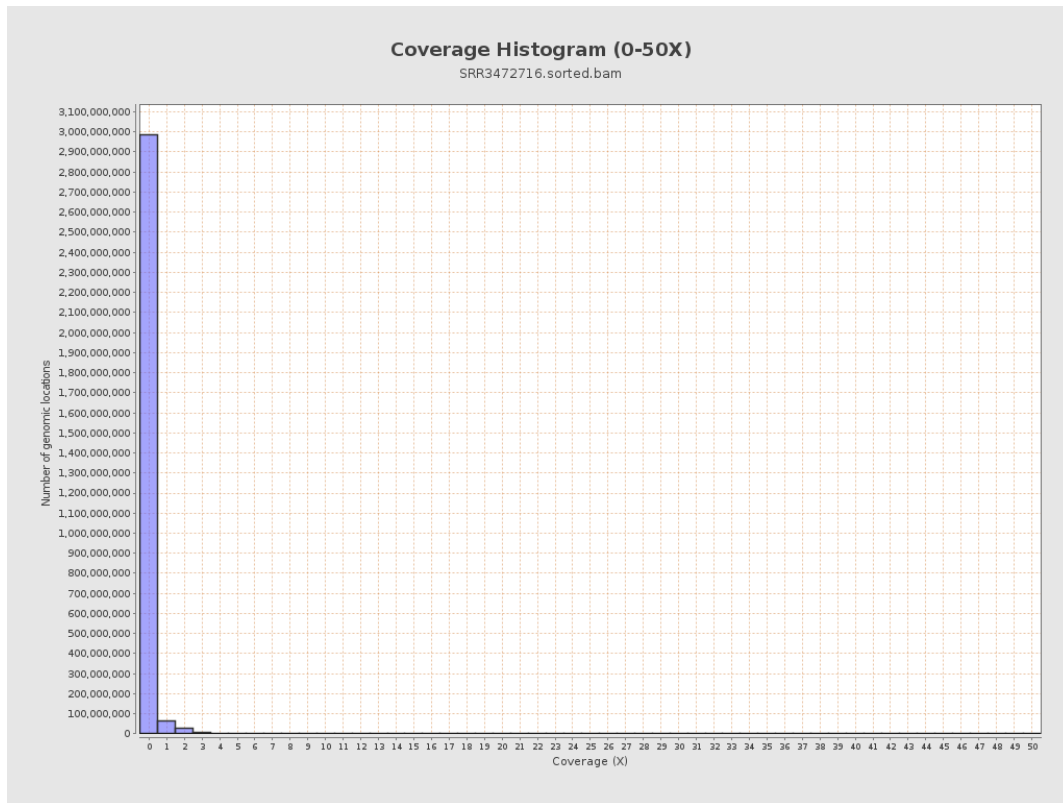
3. Results : Coverage across reference



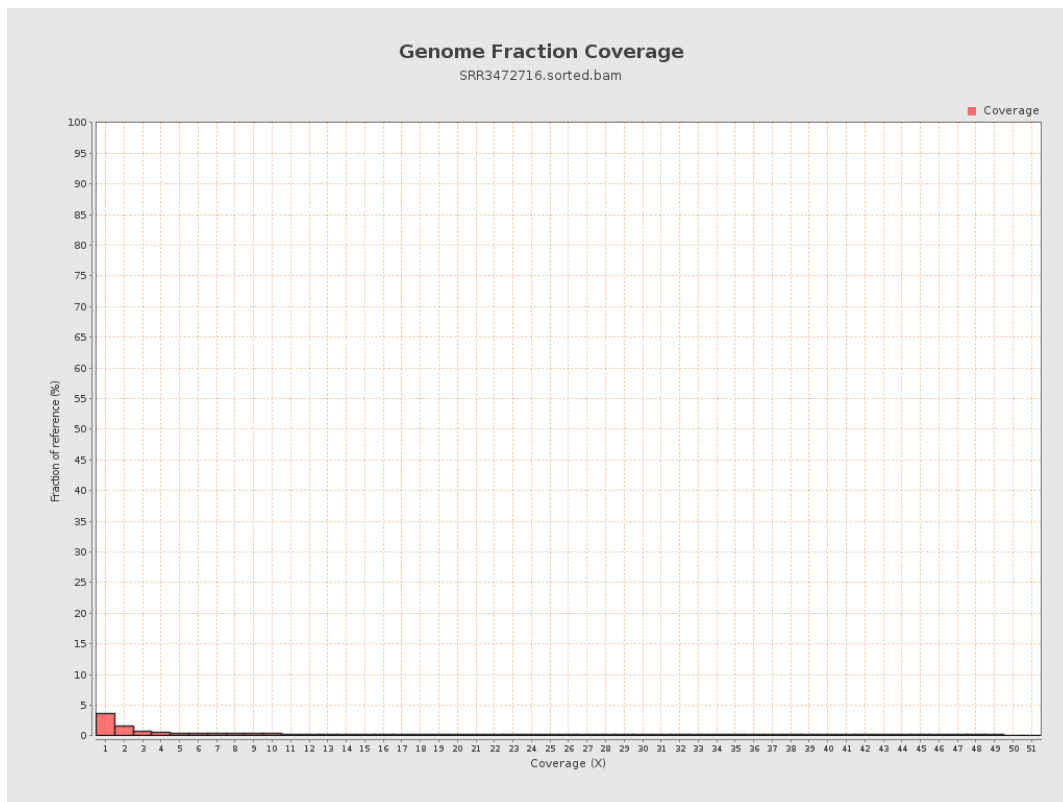
4. Results : Coverage Histogram



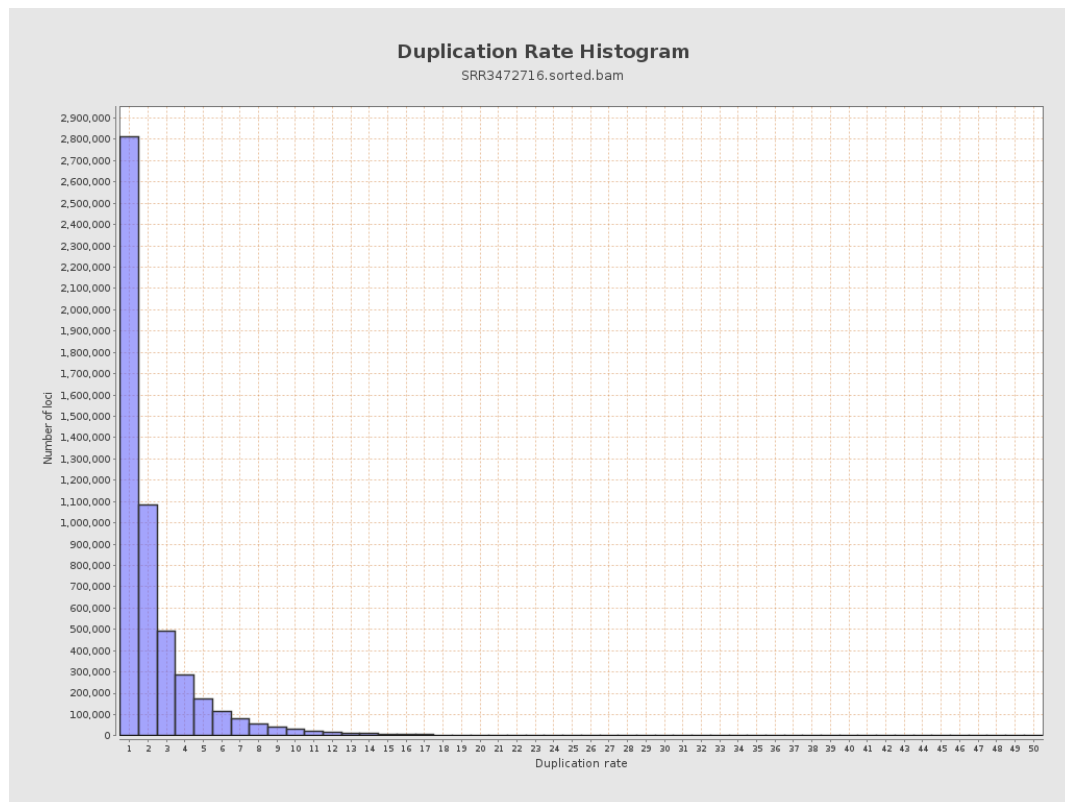
5. Results : Coverage Histogram (0-50X)



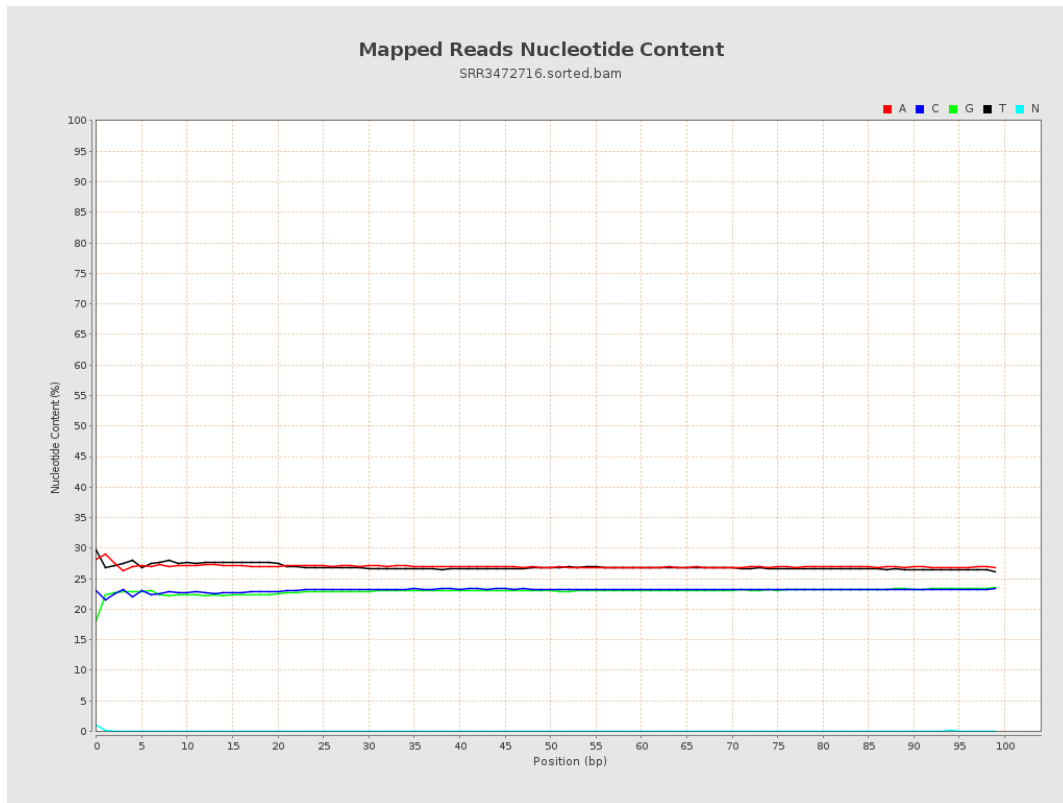
6. Results : Genome Fraction Coverage



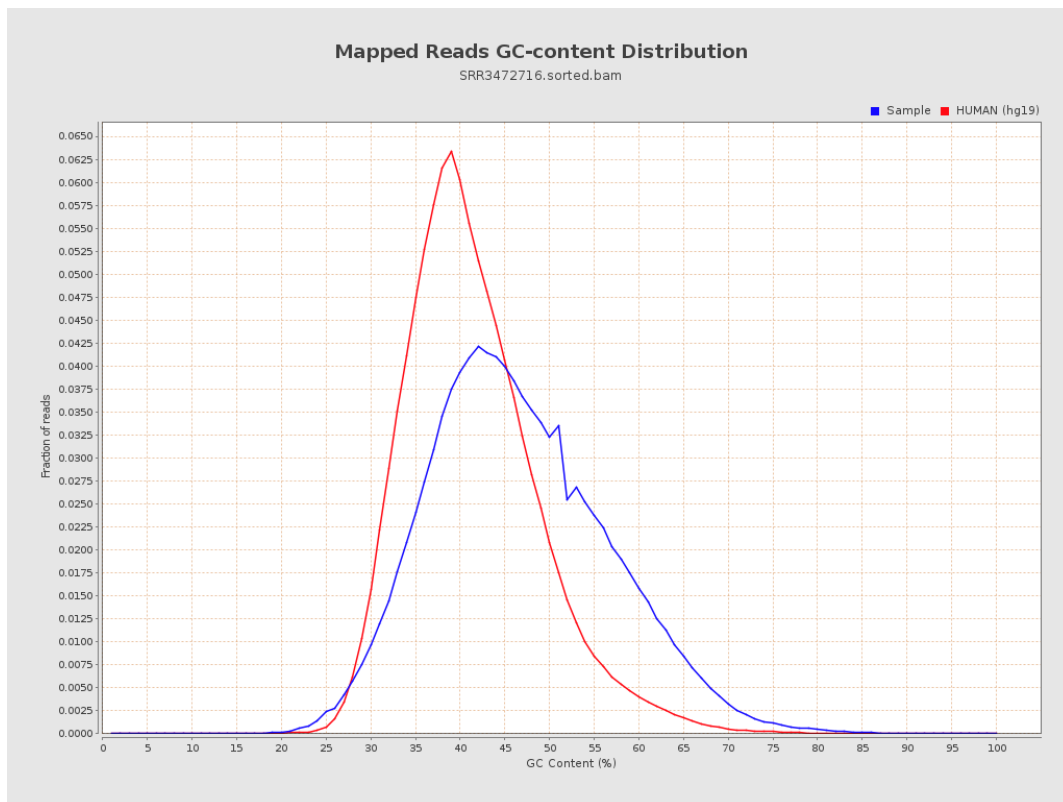
7. Results : Duplication Rate Histogram



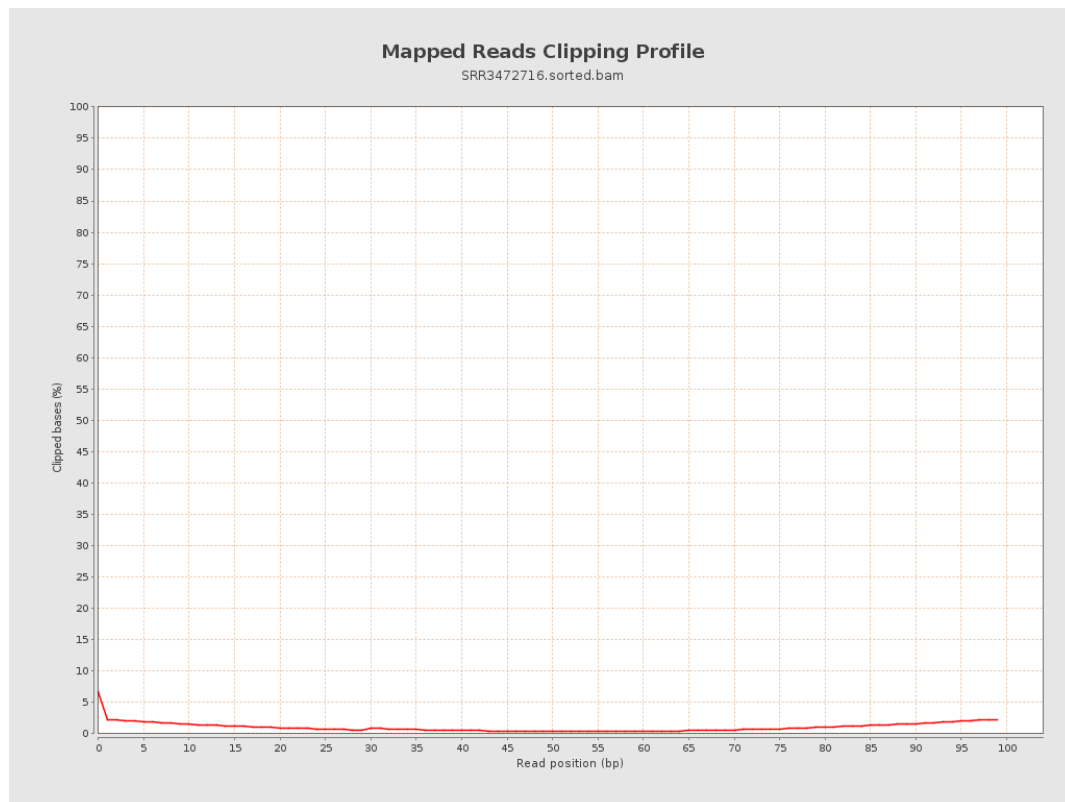
8. Results : Mapped Reads Nucleotide Content



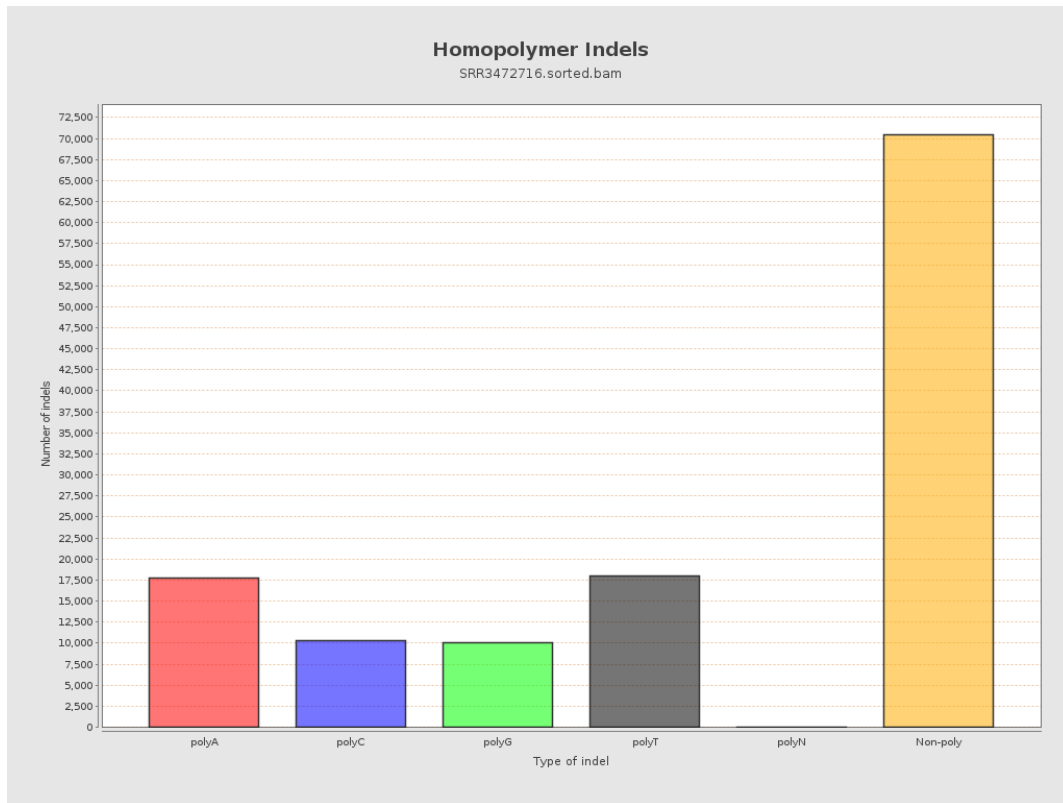
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



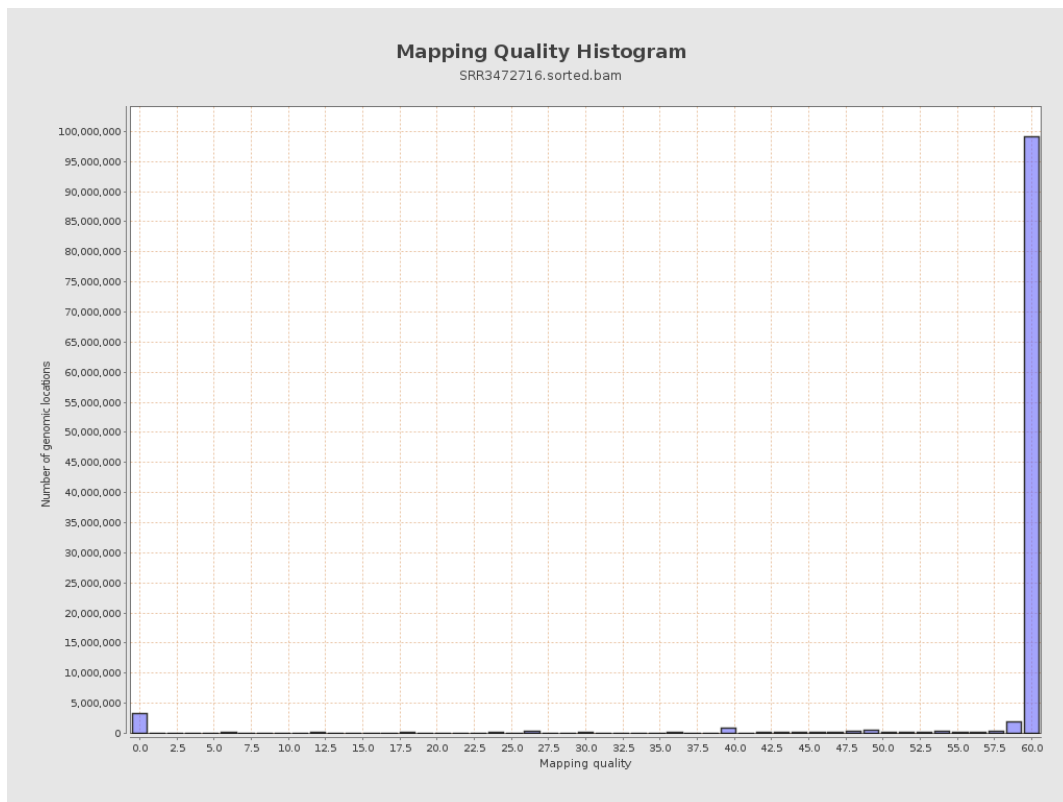
11. Results : Homopolymer Indels



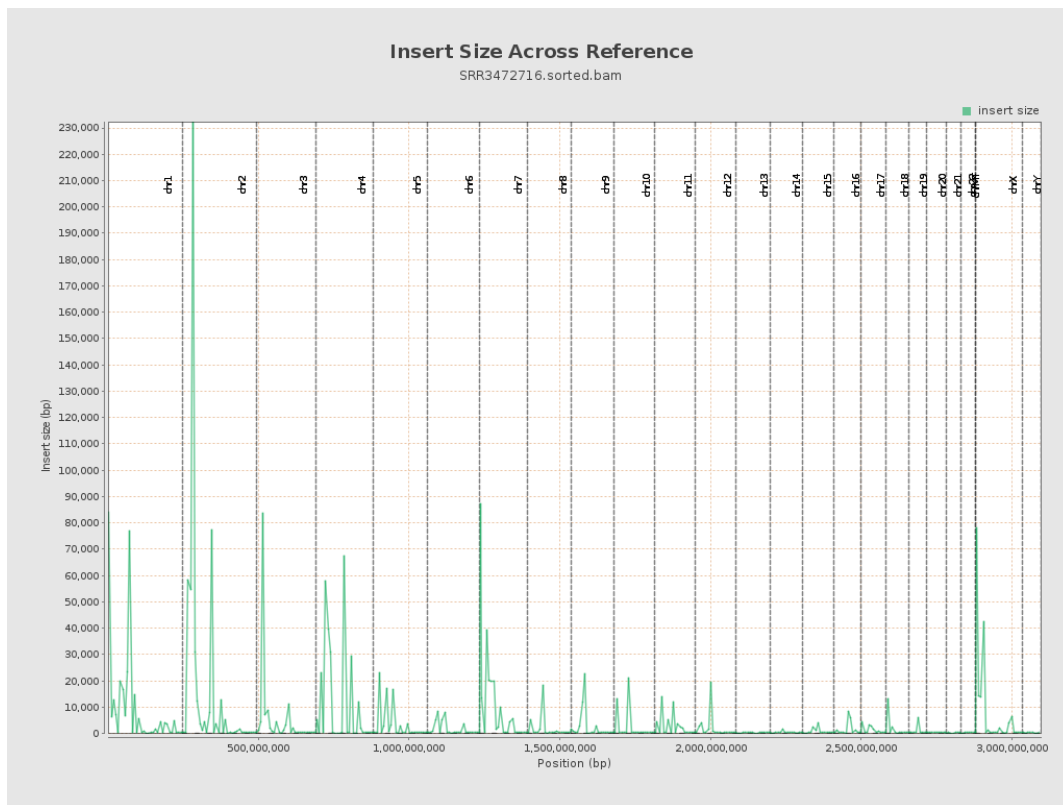
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

