

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:32:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472416.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_SRR3472416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472416_1.fastq.gz SRR3472416_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:32:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,935,924
Mapped reads	14,811,266 / 99.17%
Unmapped reads	124,658 / 0.83%
Mapped paired reads	14,811,266 / 99.17%
Mapped reads, first in pair	7,425,836 / 49.72%
Mapped reads, second in pair	7,385,430 / 49.45%
Mapped reads, both in pair	14,738,212 / 98.68%
Mapped reads, singletons	73,054 / 0.49%
Secondary alignments	0
Supplementary alignments	53,302 / 0.36%
Read min/max/mean length	30 / 100 / 99.22
Duplicated reads (estimated)	8,910,960 / 59.66%
Duplication rate	46.81%
Clipped reads	1,144,588 / 7.66%

2.2. ACGT Content

Number/percentage of A's	387,281,198 / 26.75%
Number/percentage of C's	337,679,461 / 23.33%
Number/percentage of T's	387,875,875 / 26.79%
Number/percentage of G's	334,636,447 / 23.12%
Number/percentage of N's	181,961 / 0.01%

GC Percentage	46.44%
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2.3. Coverage

Mean	0.4677
Standard Deviation	14.3399

2.4. Mapping Quality

Mean Mapping Quality	55.05
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2.5. Insert size

Mean	16,713.88
Standard Deviation	1,295,031.46
P25/Median/P75	147 / 207 / 279

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	7,708,331
Insertions	81,936
Mapped reads with at least one insertion	0.55%
Deletions	70,100
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.82%

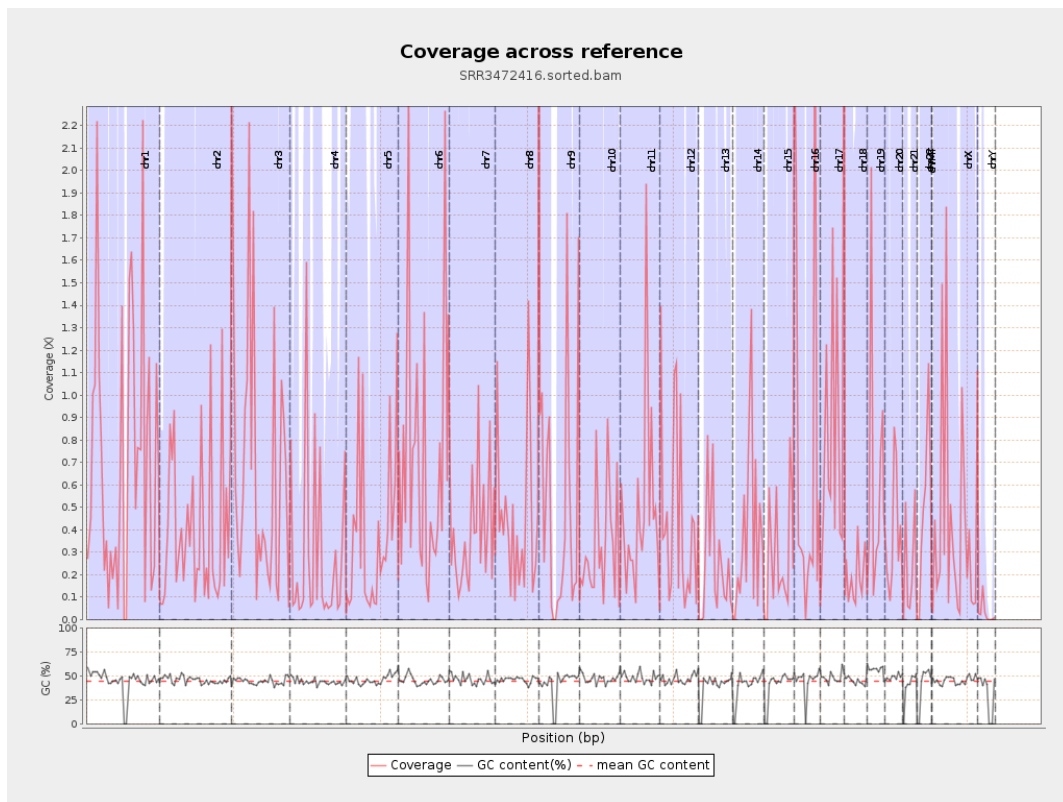
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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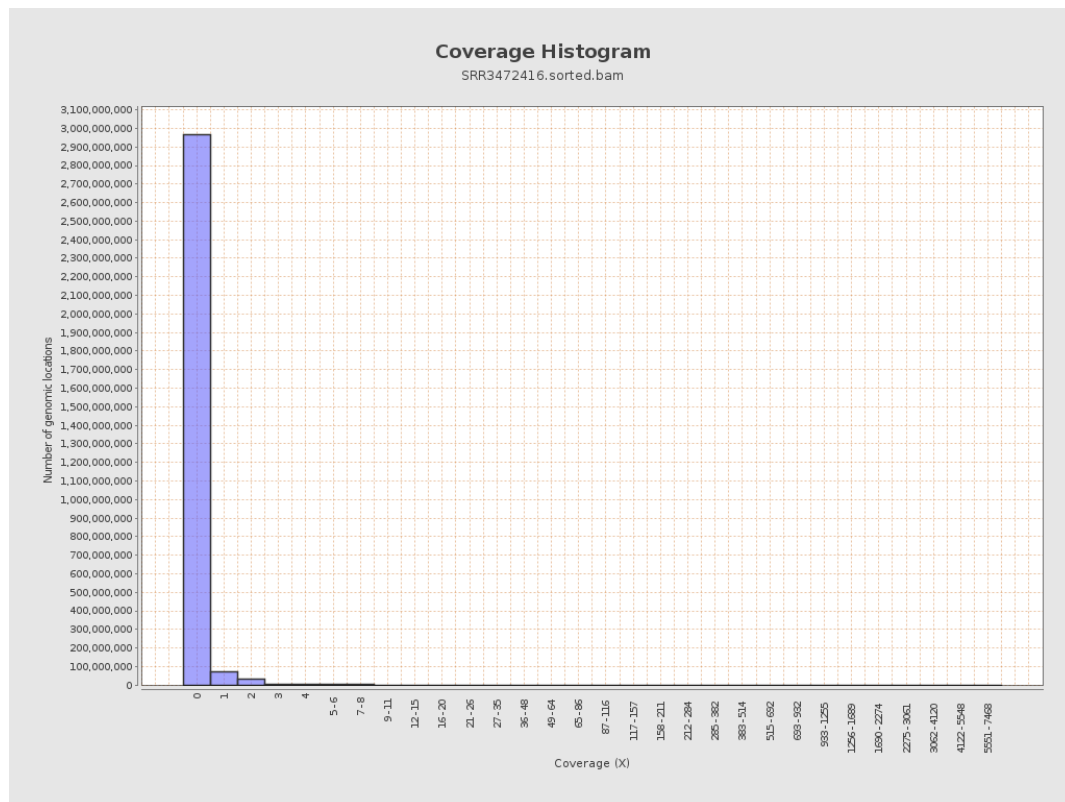
		bases	coverage	deviation
chr1	249250621	180541801	0.7243	20.2978
chr2	243199373	97662711	0.4016	13.1153
chr3	198022430	135940458	0.6865	16.7905
chr4	191154276	52924322	0.2769	11.5751
chr5	180915260	69827963	0.386	12.9163
chr6	171115067	121432836	0.7097	16.8082
chr7	159138663	63552704	0.3994	12.1608
chr8	146364022	67793635	0.4632	11.6968
chr9	141213431	74894607	0.5304	15.4957
chr10	135534747	43802993	0.3232	12.279
chr11	135006516	64794259	0.4799	18.3742
chr12	133851895	60387880	0.4512	11.4123
chr13	115169878	27741862	0.2409	8.1218
chr14	107349540	39393458	0.367	11.6891
chr15	102531392	29049235	0.2833	8.1962
chr16	90354753	69254688	0.7665	19.2209
chr17	81195210	69901959	0.8609	19.4215
chr18	78077248	15228551	0.195	5.6326
chr19	59128983	38631871	0.6533	14.1527
chr20	63025520	23888944	0.379	9.9718
chr21	48129895	11157645	0.2318	10.7419
chr22	51304566	24511030	0.4778	13.3247
chrMT	16571	1944	0.1173	0.3834
chrX	155270560	63667732	0.41	16.5546

chrY	59373566	1832287	0.0309	1.3401
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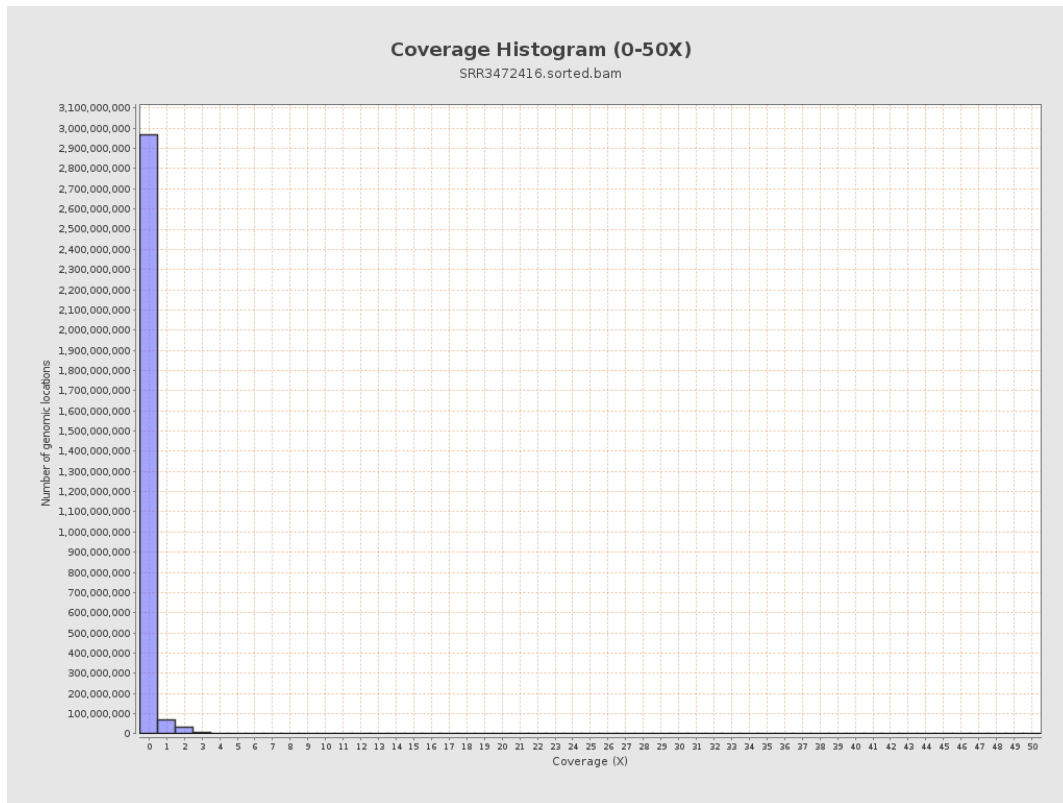
3. Results : Coverage across reference



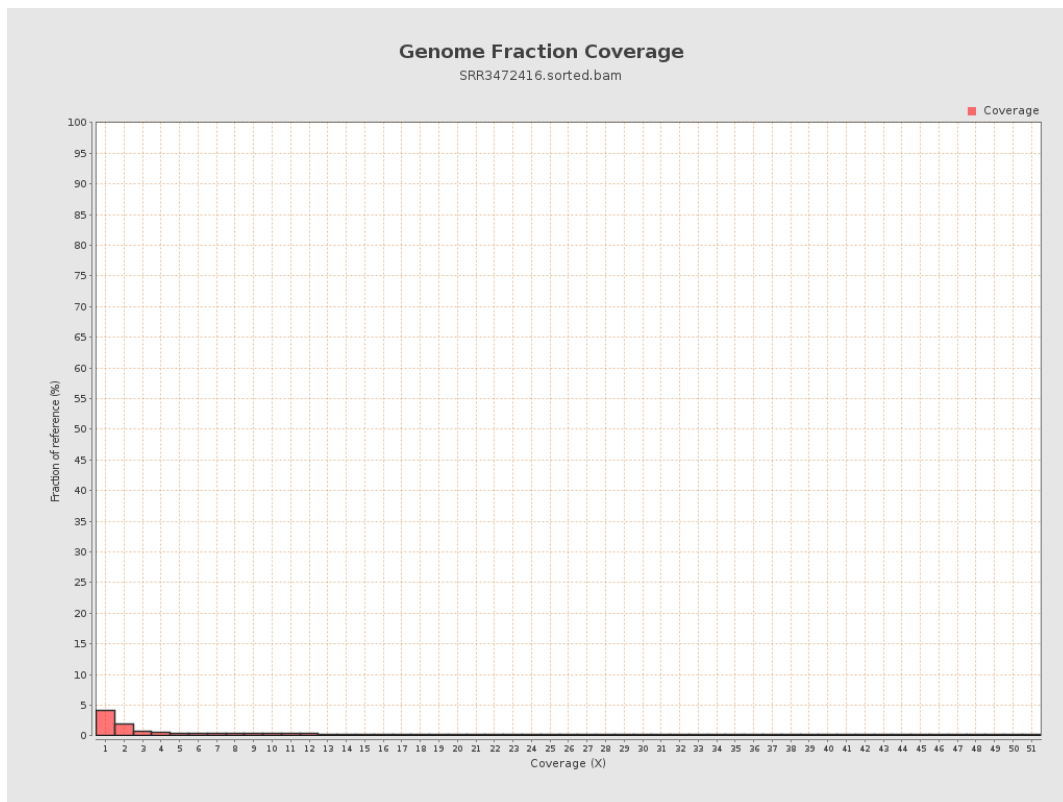
4. Results : Coverage Histogram



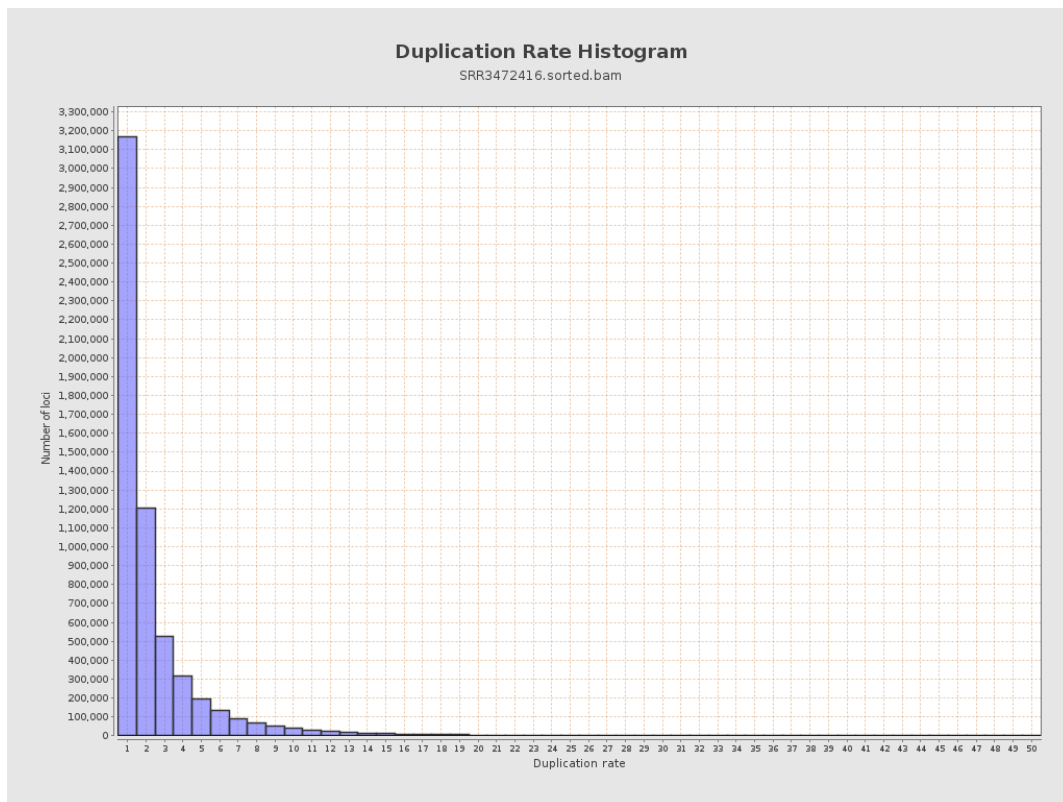
5. Results : Coverage Histogram (0-50X)



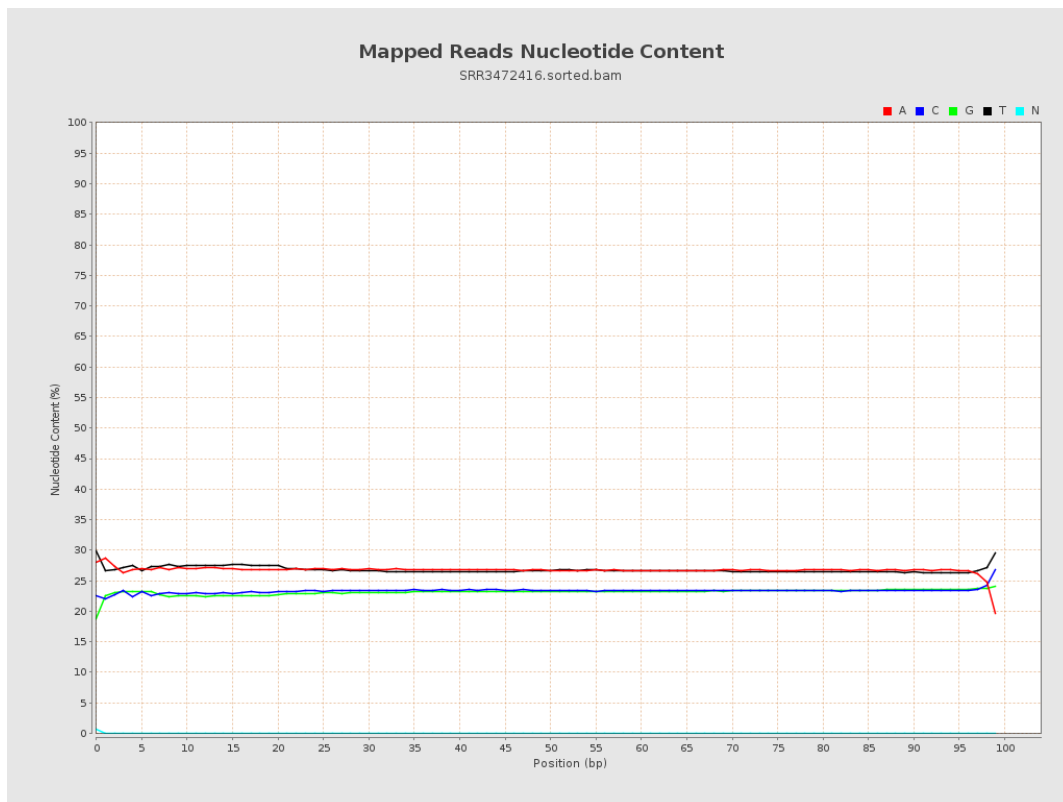
6. Results : Genome Fraction Coverage



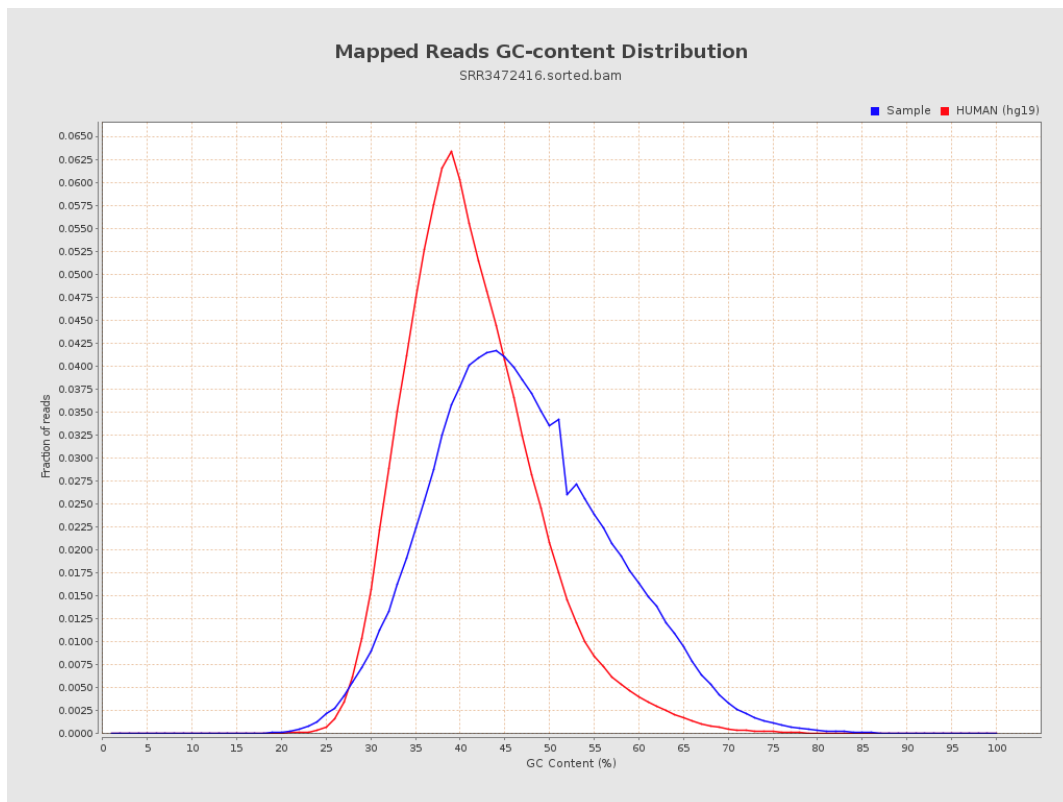
7. Results : Duplication Rate Histogram



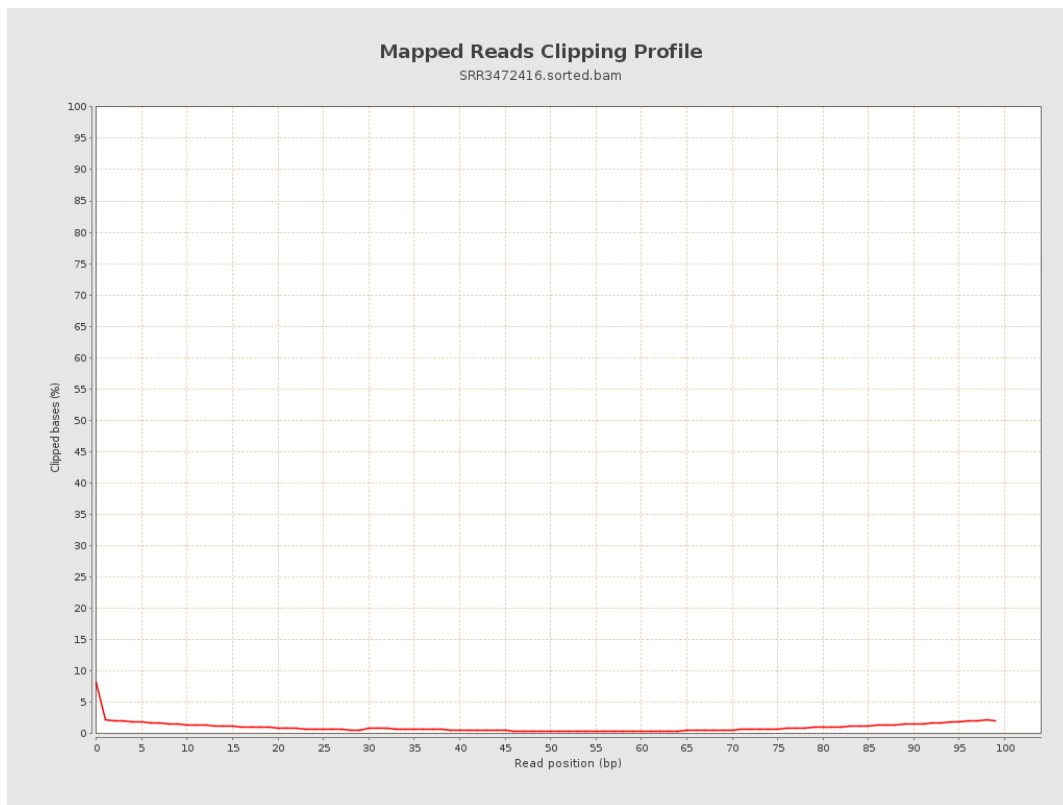
8. Results : Mapped Reads Nucleotide Content



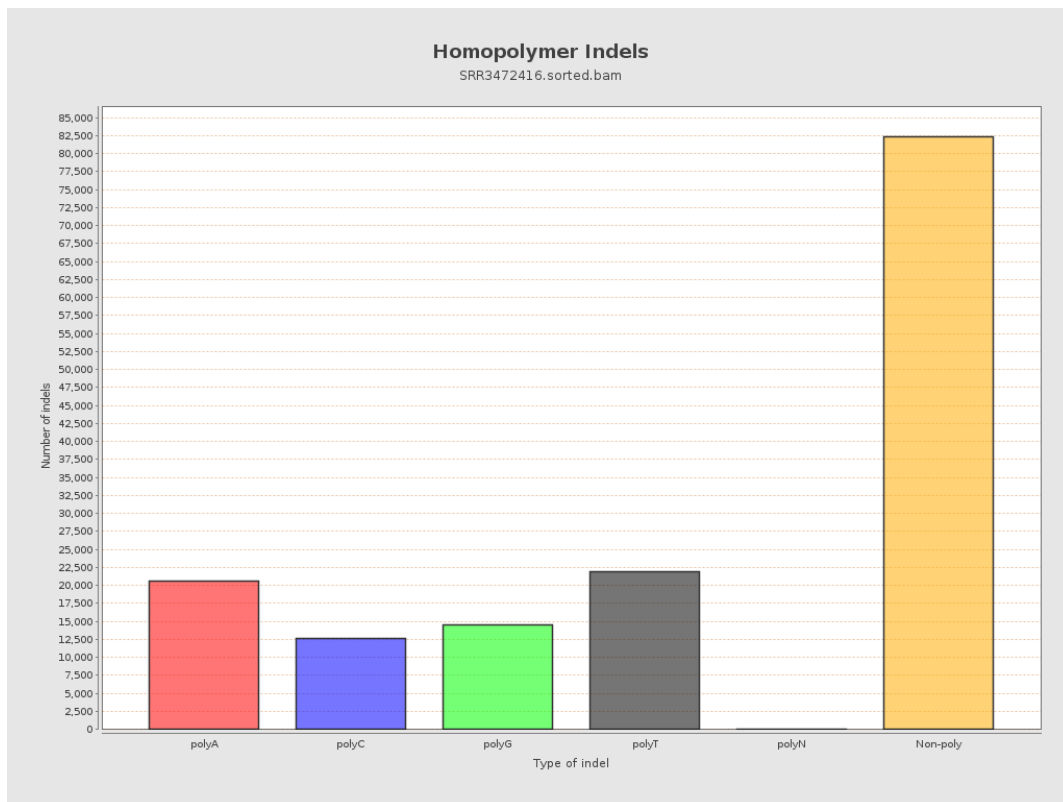
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



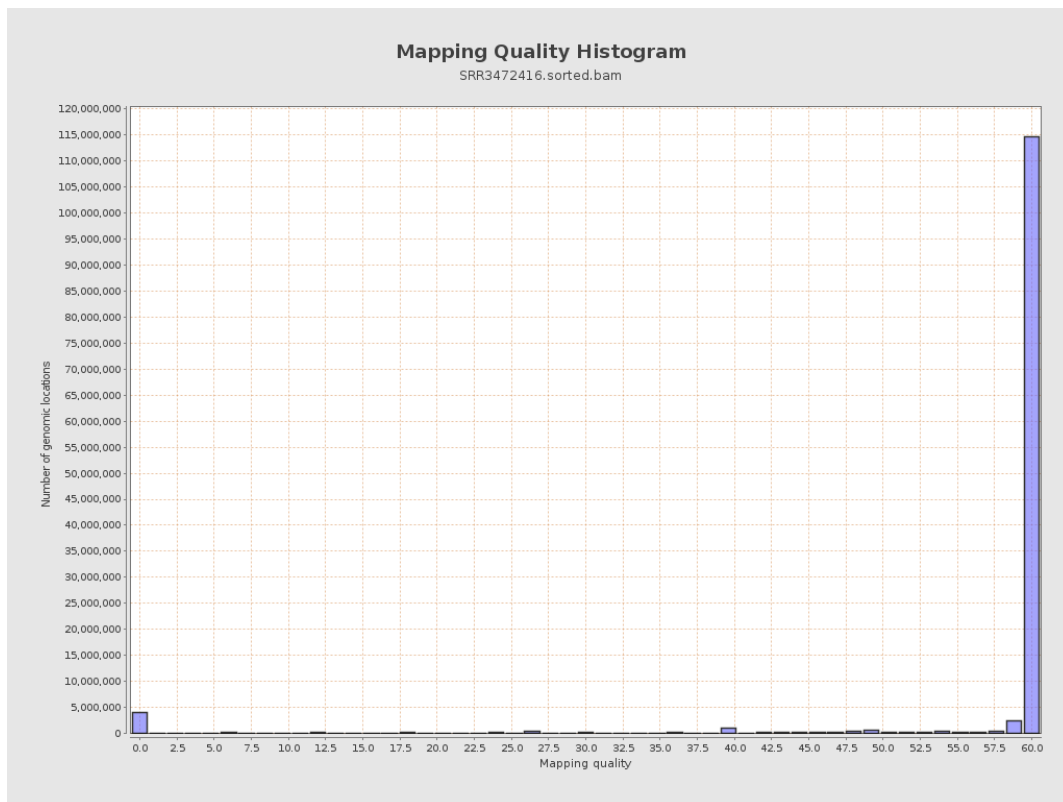
11. Results : Homopolymer Indels



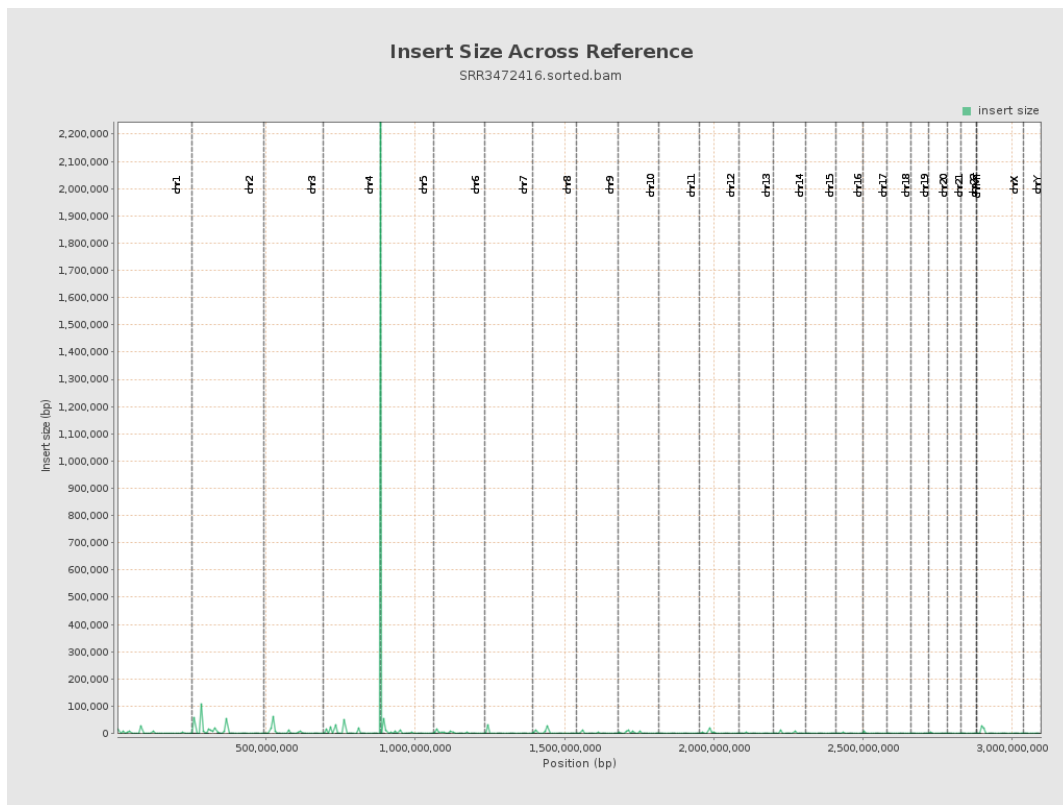
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

