

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 18:55:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472718.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_SRR3472718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472718_1.fastq.gz SRR3472718_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 18:55:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,734,234
Mapped reads	26,501,758 / 99.13%
Unmapped reads	232,476 / 0.87%
Mapped paired reads	26,501,758 / 99.13%
Mapped reads, first in pair	13,291,744 / 49.72%
Mapped reads, second in pair	13,210,014 / 49.41%
Mapped reads, both in pair	26,362,620 / 98.61%
Mapped reads, singletons	139,138 / 0.52%
Secondary alignments	0
Supplementary alignments	88,211 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	17,350,984 / 64.9%
Duplication rate	48.8%
Clipped reads	2,182,852 / 8.17%

2.2. ACGT Content

Number/percentage of A's	715,097,237 / 27.42%
Number/percentage of C's	592,446,920 / 22.72%
Number/percentage of T's	710,102,359 / 27.23%
Number/percentage of G's	589,707,488 / 22.61%
Number/percentage of N's	507,985 / 0.02%

GC Percentage	45.33%
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2.3. Coverage

Mean	0.8425
Standard Deviation	24.5876

2.4. Mapping Quality

Mean Mapping Quality	55.22
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2.5. Insert size

Mean	22,658.39
Standard Deviation	1,477,723.58
P25/Median/P75	170 / 240 / 324

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	15,735,547
Insertions	147,898
Mapped reads with at least one insertion	0.55%
Deletions	144,430
Mapped reads with at least one deletion	0.54%
Homopolymer indels	44.86%

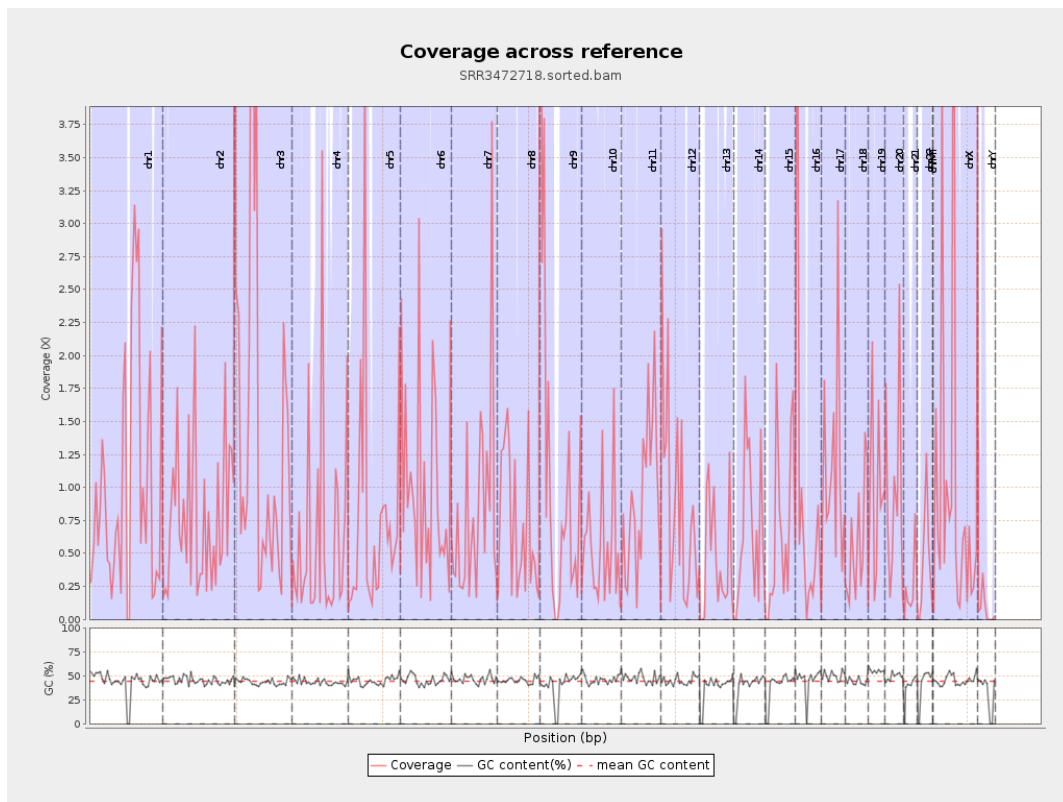
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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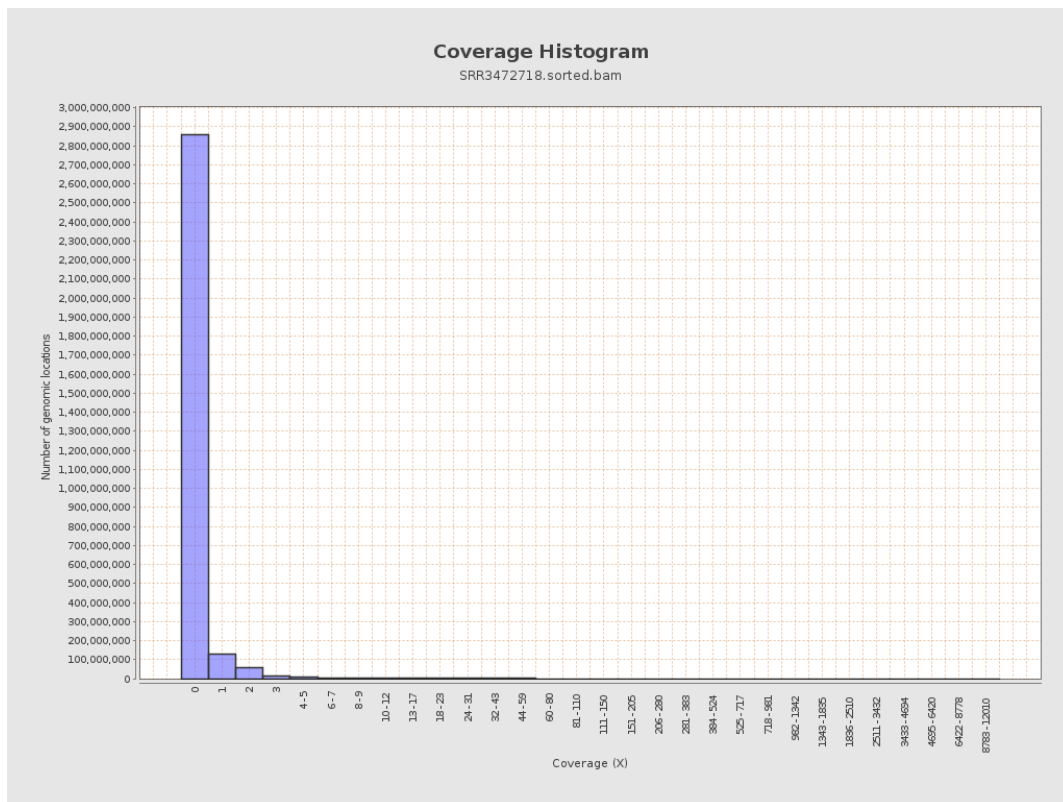
		bases	coverage	deviation
chr1	249250621	253972684	1.0189	30.6845
chr2	243199373	190362164	0.7827	22.841
chr3	198022430	306344637	1.547	32.396
chr4	191154276	121509568	0.6357	23.2582
chr5	180915260	140411818	0.7761	22.7064
chr6	171115067	167752363	0.9803	22.3921
chr7	159138663	131204343	0.8245	25.9279
chr8	146364022	104441176	0.7136	17.4219
chr9	141213431	139536984	0.9881	21.8533
chr10	135534747	76342653	0.5633	20.6374
chr11	135006516	123692218	0.9162	30.9411
chr12	133851895	121072461	0.9045	22.6757
chr13	115169878	52512396	0.456	15.1273
chr14	107349540	73018787	0.6802	21.3769
chr15	102531392	67030520	0.6538	18.1543
chr16	90354753	79286563	0.8775	21.3642
chr17	81195210	93939784	1.157	23.1755
chr18	78077248	43748361	0.5603	16.9407
chr19	59128983	57616682	0.9744	22.8864
chr20	63025520	59474711	0.9437	37.0802
chr21	48129895	11931348	0.2479	9.4637
chr22	51304566	23388296	0.4559	10.8058
chrMT	16571	3582	0.2162	0.5689
chrX	155270560	164737687	1.061	35.8763

chrY	59373566	4908508	0.0827	2.9322
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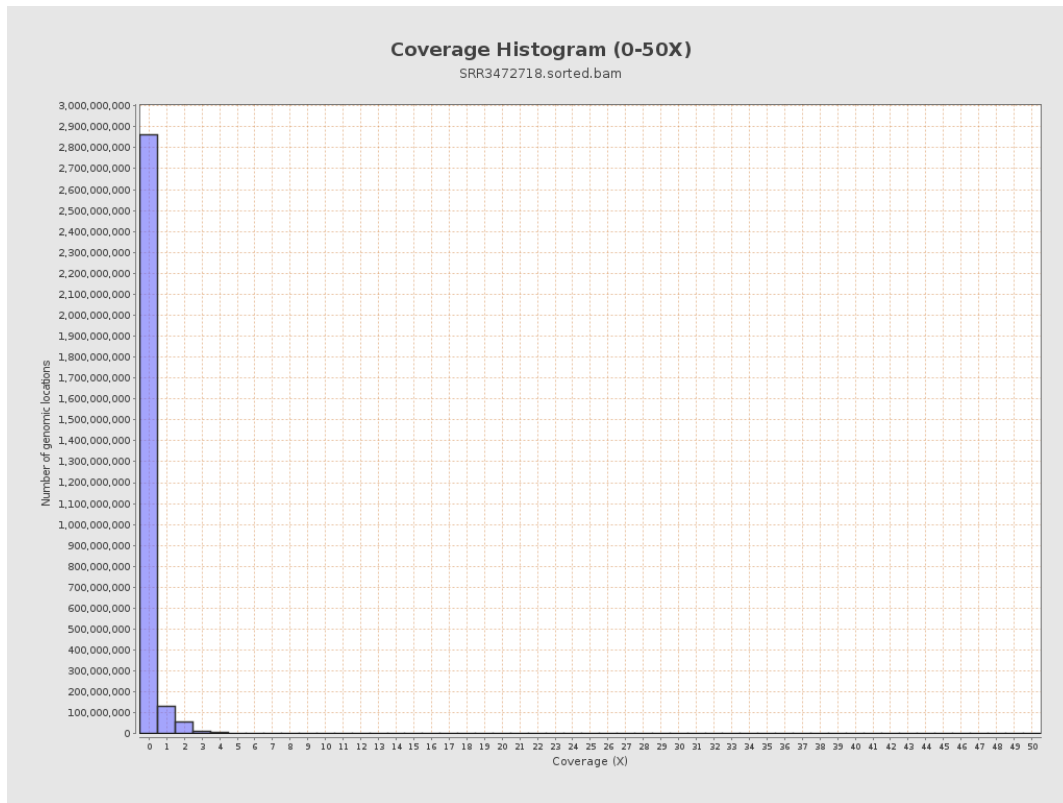
3. Results : Coverage across reference



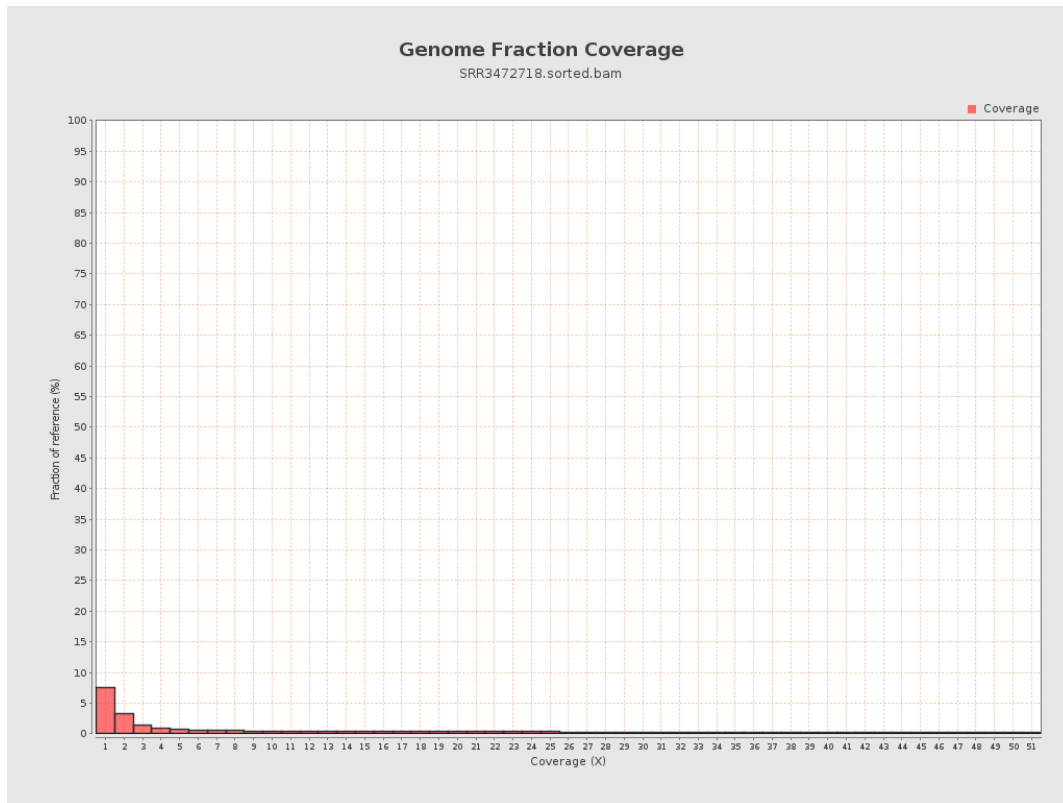
4. Results : Coverage Histogram



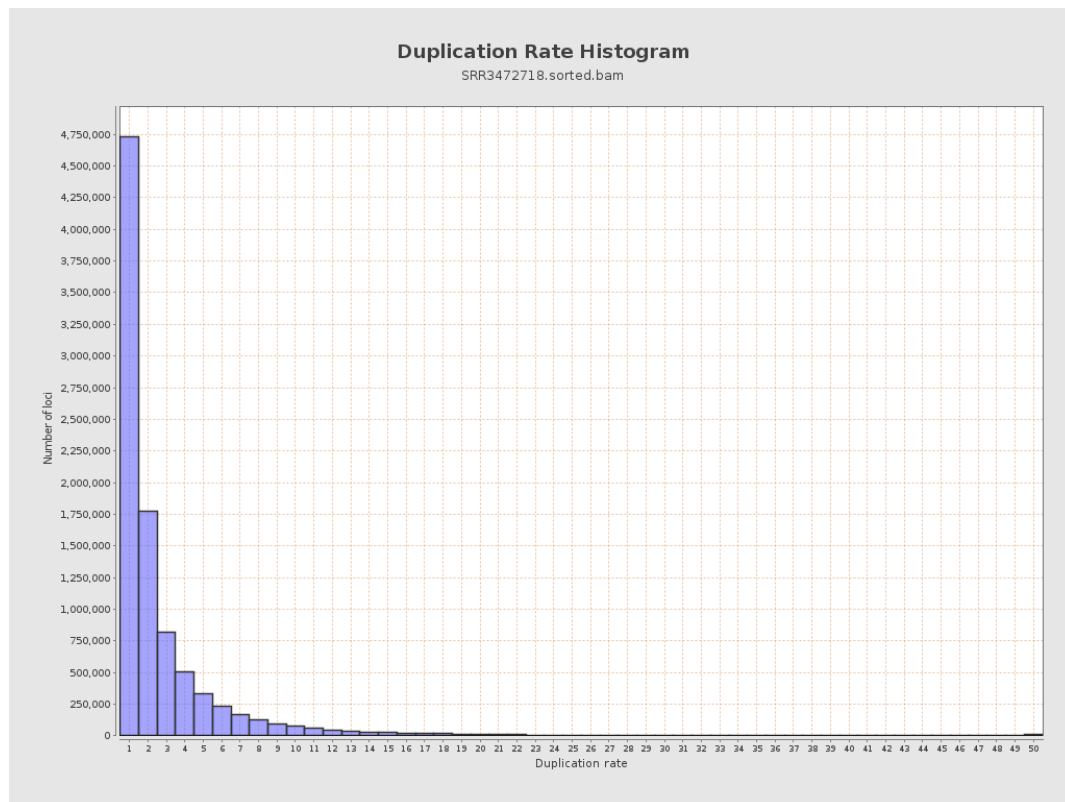
5. Results : Coverage Histogram (0-50X)



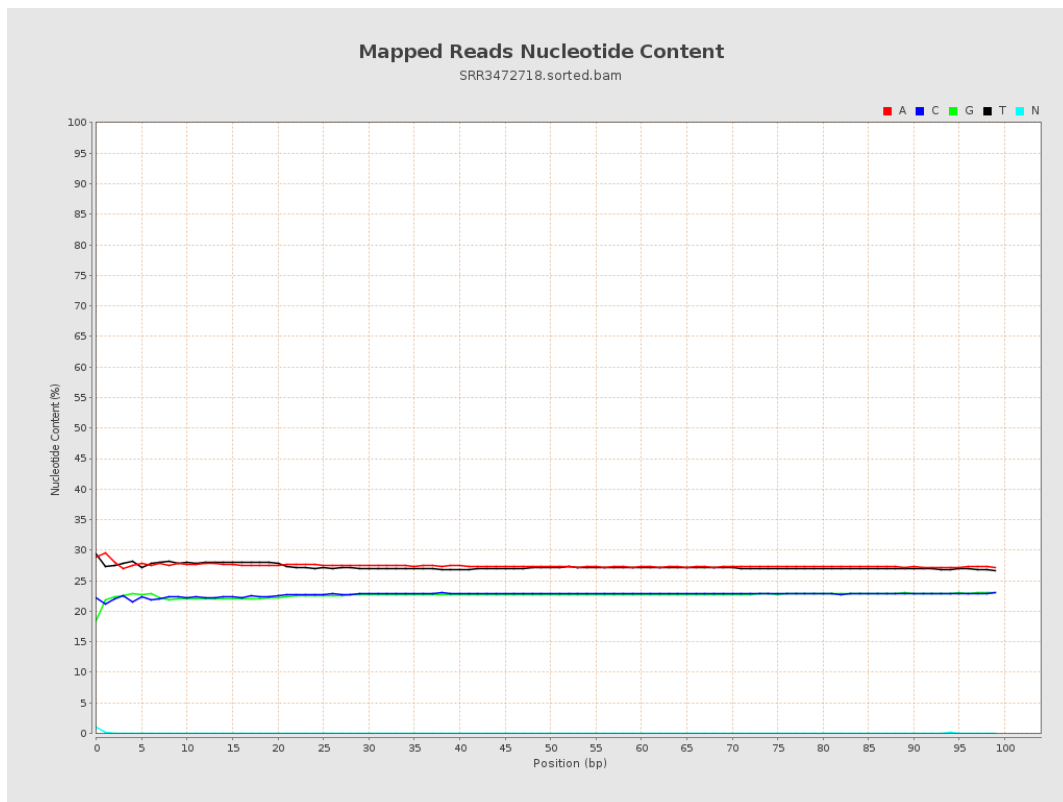
6. Results : Genome Fraction Coverage



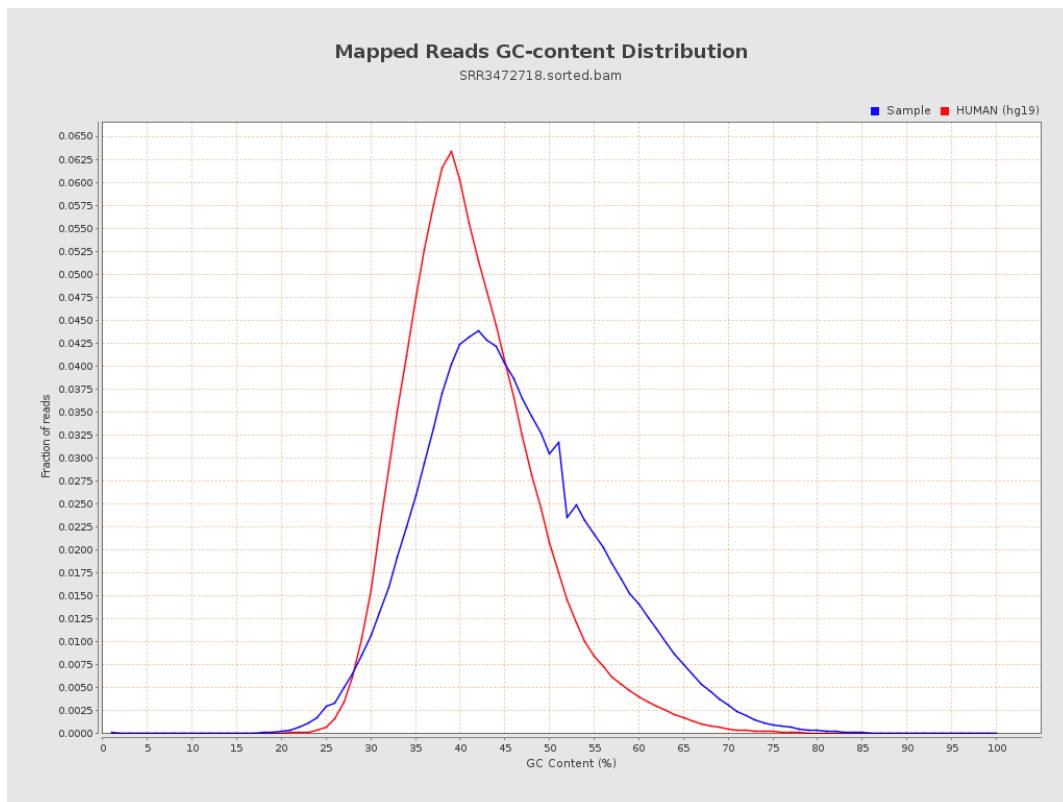
7. Results : Duplication Rate Histogram



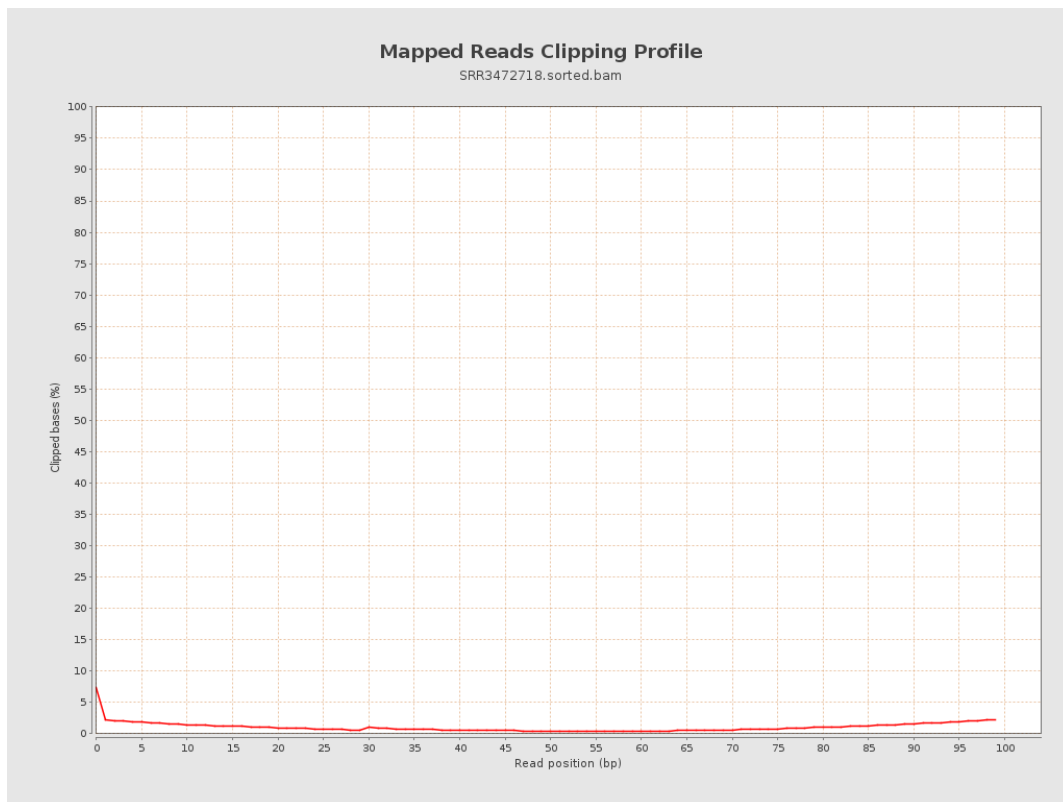
8. Results : Mapped Reads Nucleotide Content



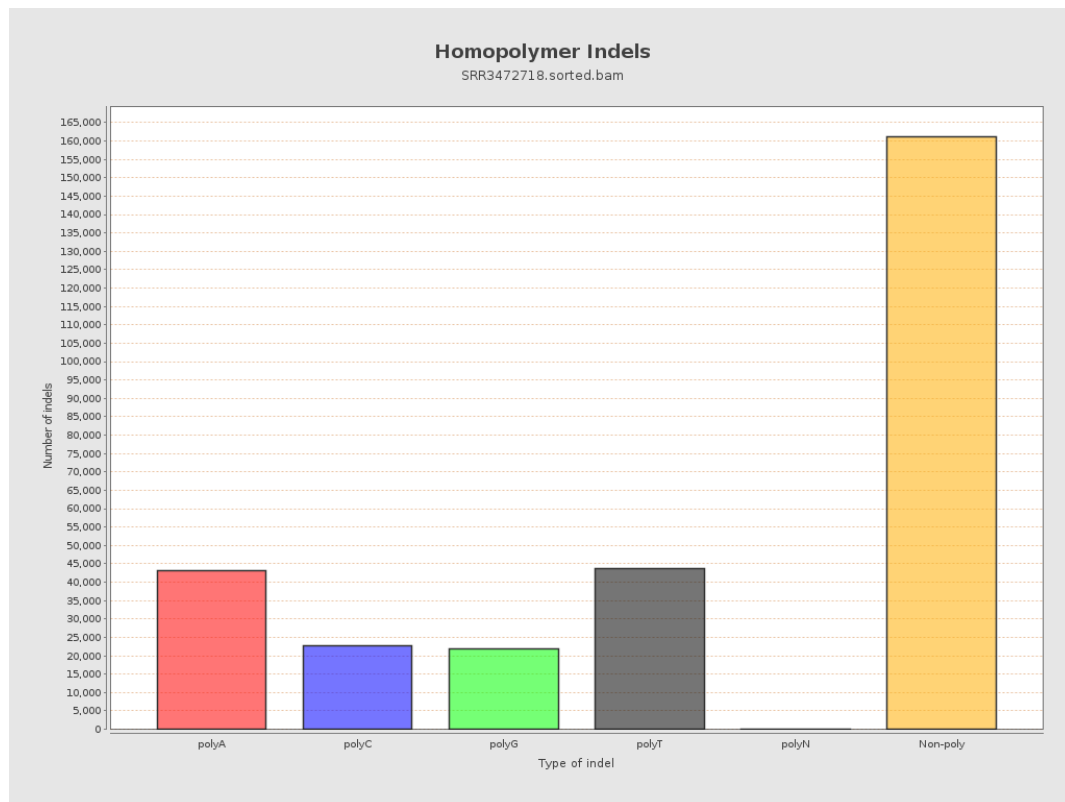
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



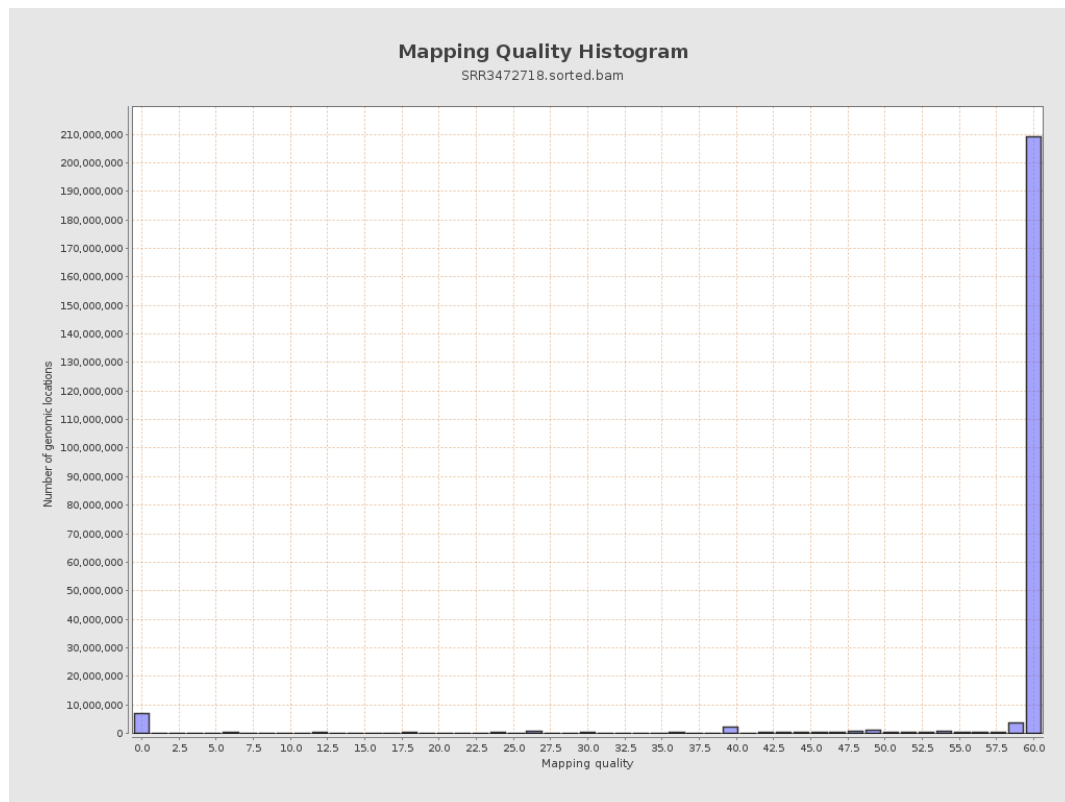
11. Results : Homopolymer Indels



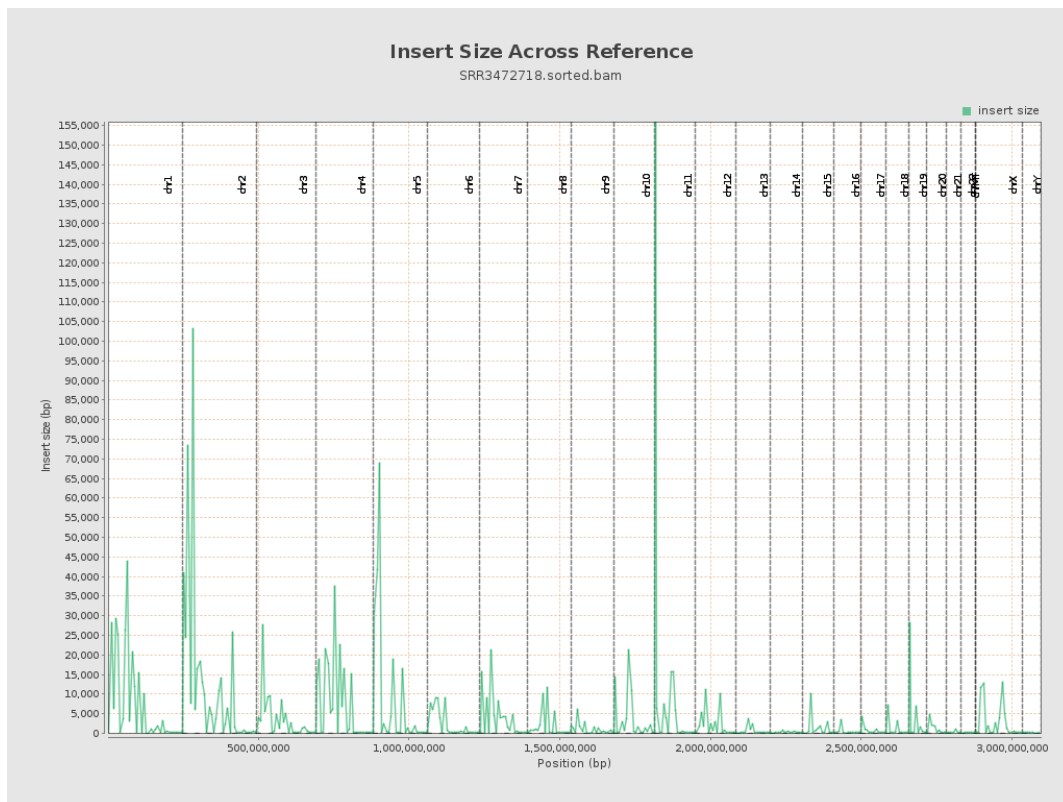
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

