

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 19:43:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472721.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_SRR3472721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472721_1.fastq.gz SRR3472721_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 19:43:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,995,982
Mapped reads	13,824,920 / 98.78%
Unmapped reads	171,062 / 1.22%
Mapped paired reads	13,824,920 / 98.78%
Mapped reads, first in pair	6,919,681 / 49.44%
Mapped reads, second in pair	6,905,239 / 49.34%
Mapped reads, both in pair	13,724,540 / 98.06%
Mapped reads, singletons	100,380 / 0.72%
Secondary alignments	0
Supplementary alignments	47,738 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,256,439 / 58.99%
Duplication rate	45.19%
Clipped reads	1,253,037 / 8.95%

2.2. ACGT Content

Number/percentage of A's	379,601,706 / 27.92%
Number/percentage of C's	306,110,813 / 22.51%
Number/percentage of T's	371,040,150 / 27.29%
Number/percentage of G's	302,600,555 / 22.26%
Number/percentage of N's	261,773 / 0.02%

GC Percentage	44.77%
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2.3. Coverage

Mean	0.4392
Standard Deviation	14.1378

2.4. Mapping Quality

Mean Mapping Quality	55.09
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2.5. Insert size

Mean	25,224.64
Standard Deviation	1,551,249.1
P25/Median/P75	166 / 228 / 305

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	11,050,932
Insertions	76,524
Mapped reads with at least one insertion	0.54%
Deletions	70,160
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.43%

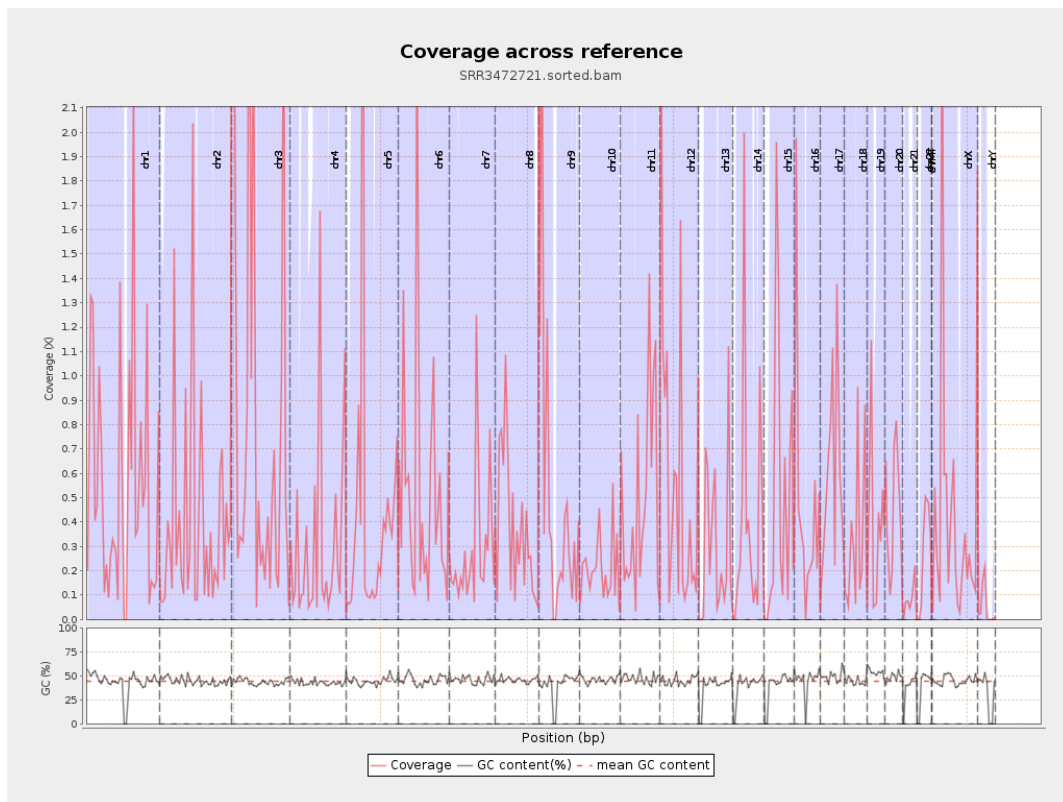
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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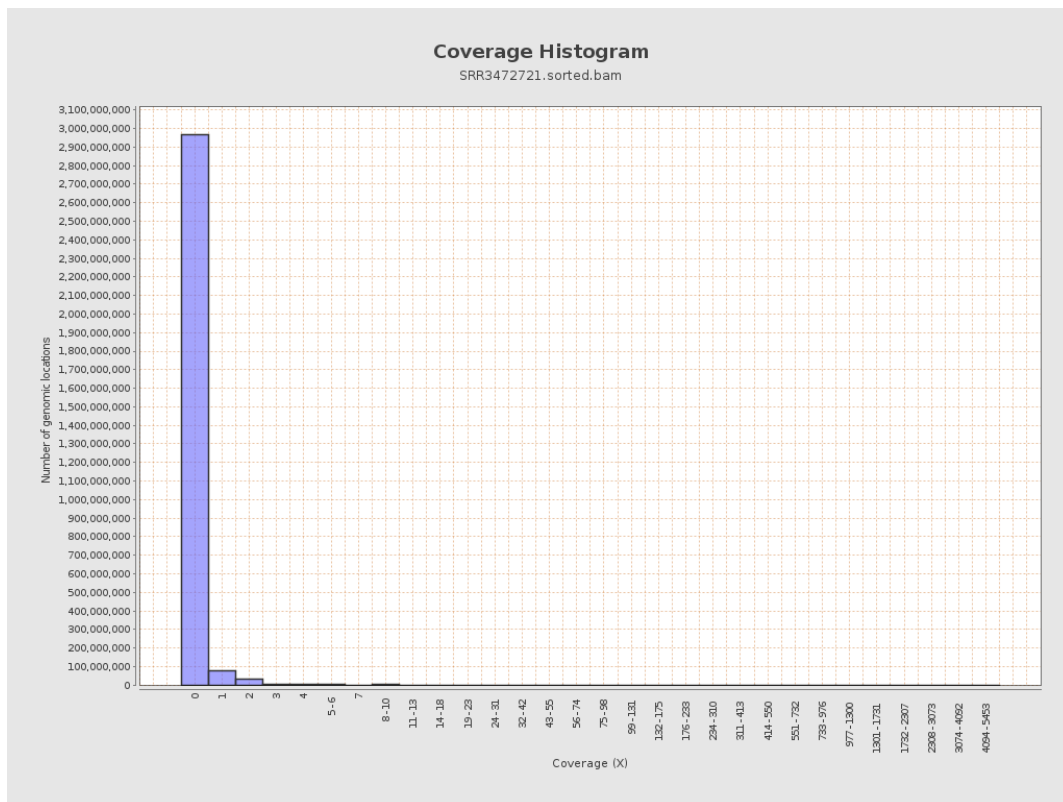
		bases	coverage	deviation
chr1	249250621	139478932	0.5596	16.7995
chr2	243199373	95500444	0.3927	15.9733
chr3	198022430	175093559	0.8842	21.5976
chr4	191154276	56514846	0.2957	12.4069
chr5	180915260	78327624	0.433	13.2707
chr6	171115067	87182450	0.5095	14.5275
chr7	159138663	47649274	0.2994	9.3027
chr8	146364022	54242422	0.3706	10.2783
chr9	141213431	70256224	0.4975	11.5071
chr10	135534747	28490253	0.2102	7.1689
chr11	135006516	65839743	0.4877	16.5778
chr12	133851895	81378966	0.608	18.3827
chr13	115169878	34722338	0.3015	13.1204
chr14	107349540	42228682	0.3934	13.7608
chr15	102531392	50245206	0.49	16.3987
chr16	90354753	39951368	0.4422	12.2326
chr17	81195210	48350437	0.5955	14.3833
chr18	78077248	25493120	0.3265	13.0582
chr19	59128983	24952365	0.422	10.1588
chr20	63025520	28708555	0.4555	13.7104
chr21	48129895	4086503	0.0849	3.272
chr22	51304566	13365579	0.2605	10.1087
chrMT	16571	3588	0.2165	0.7355
chrX	155270560	64403549	0.4148	12.273

chrY	59373566	3314465	0.0558	3.72
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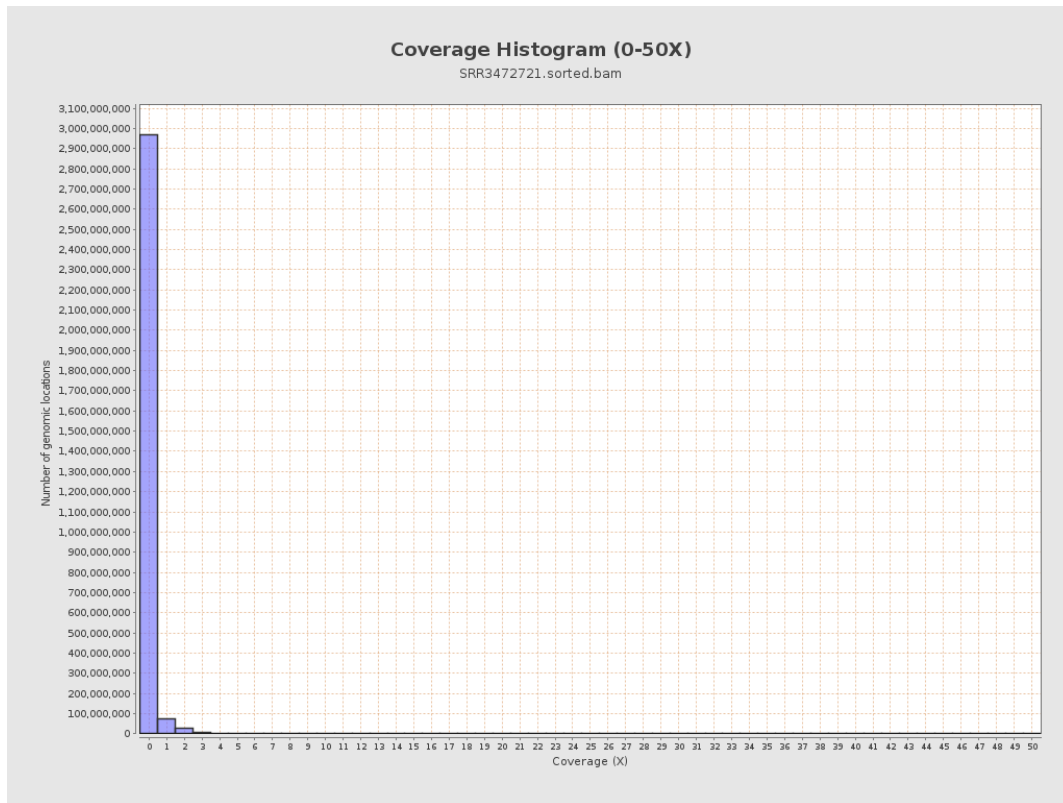
3. Results : Coverage across reference



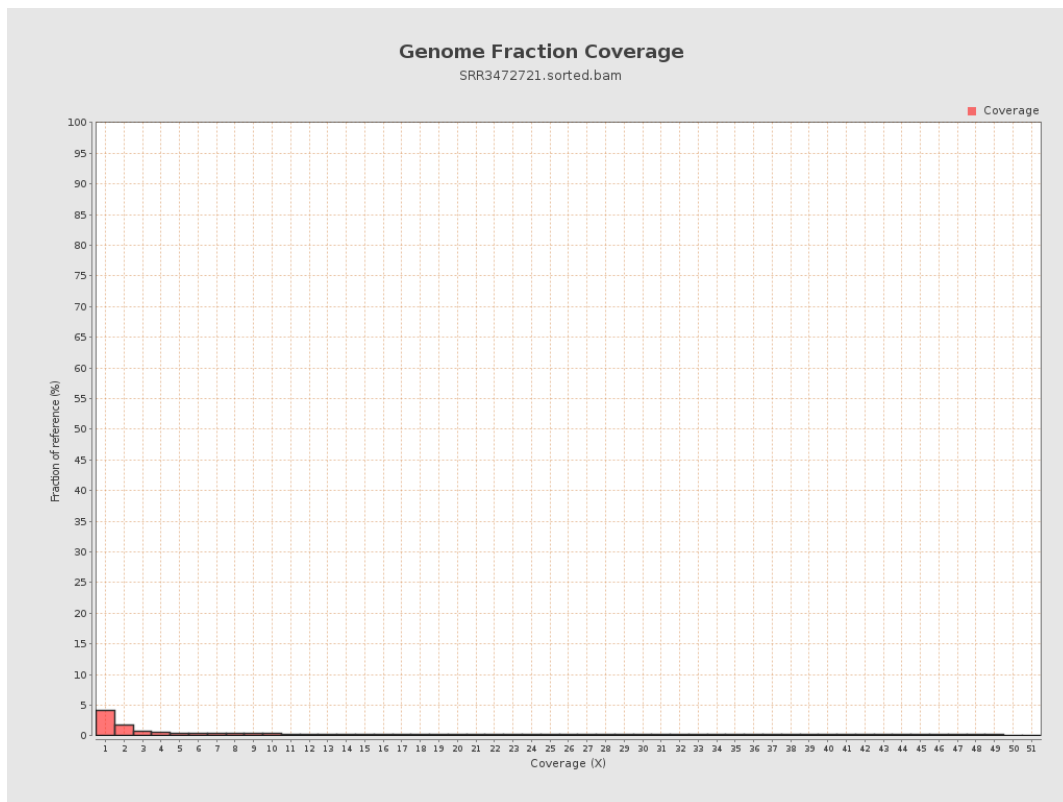
4. Results : Coverage Histogram



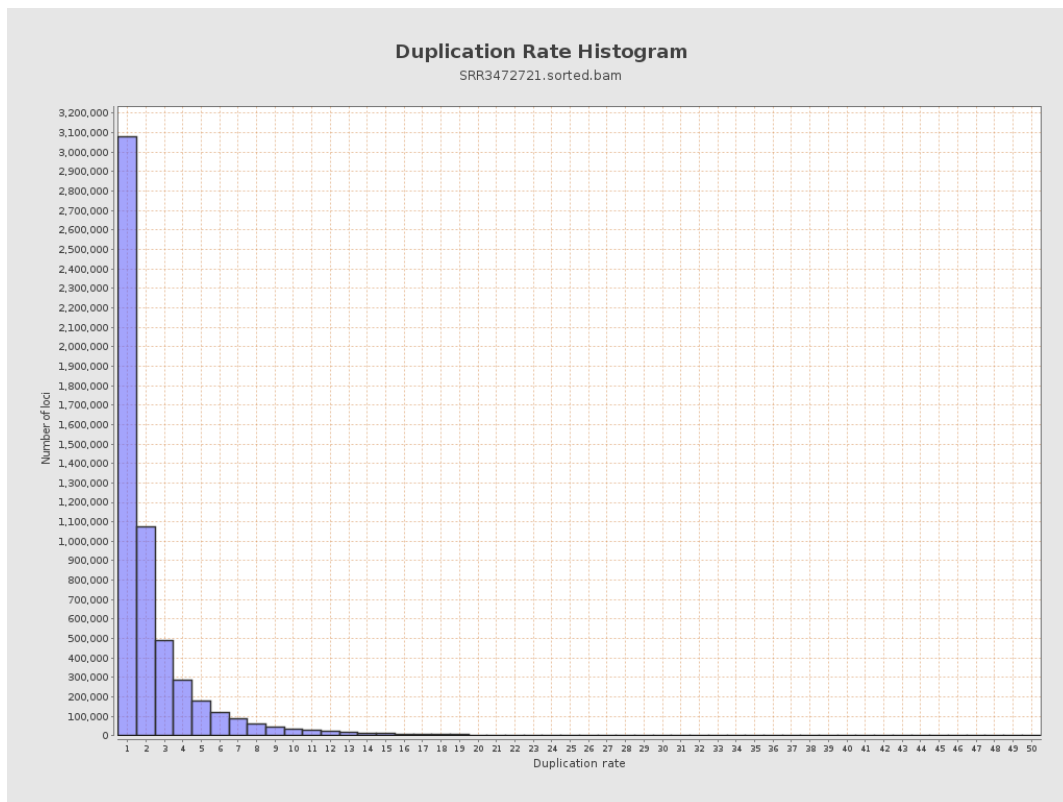
5. Results : Coverage Histogram (0-50X)



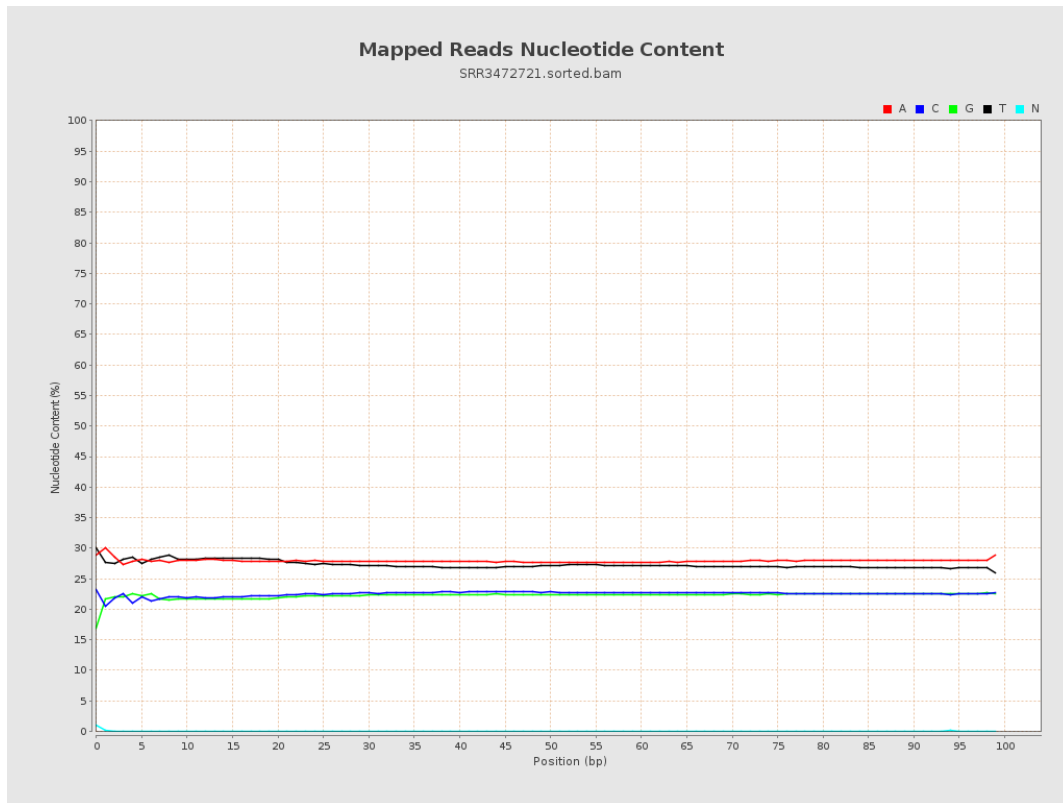
6. Results : Genome Fraction Coverage



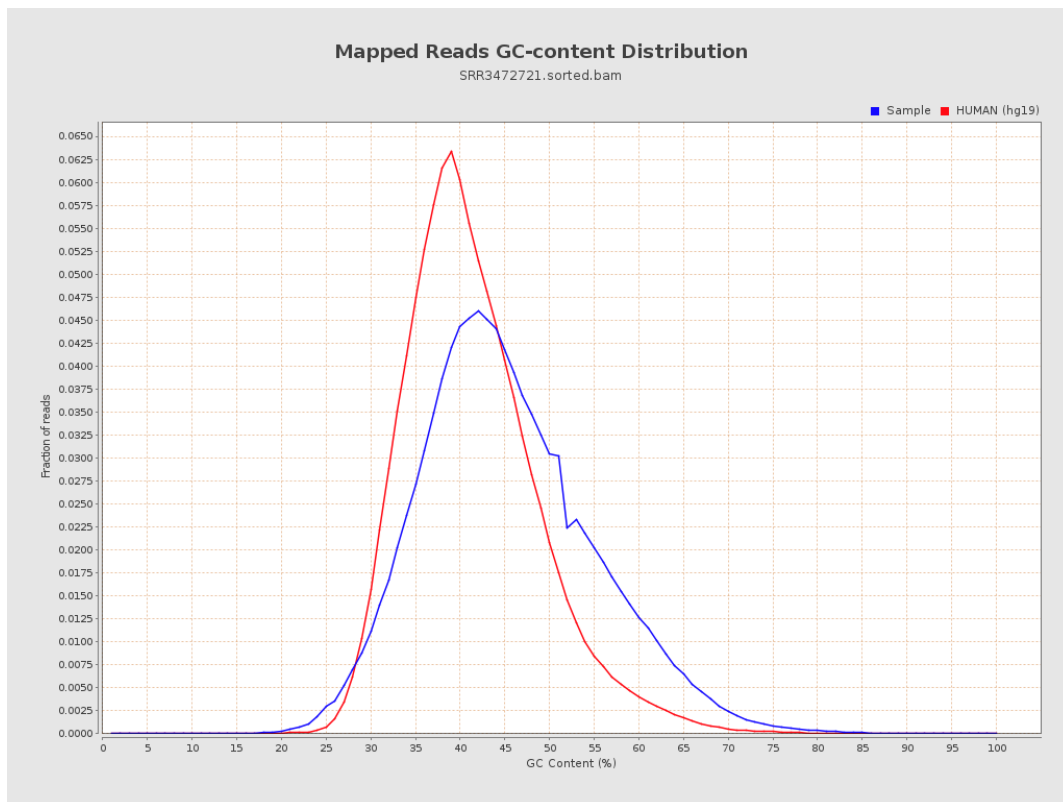
7. Results : Duplication Rate Histogram



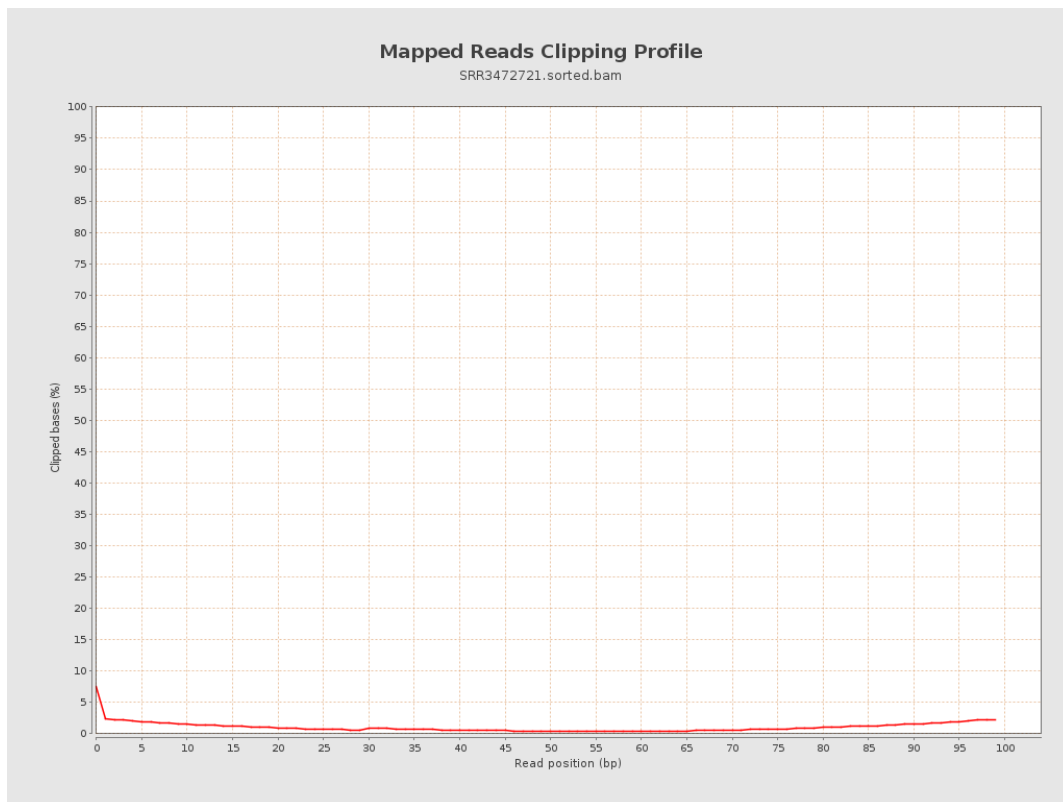
8. Results : Mapped Reads Nucleotide Content



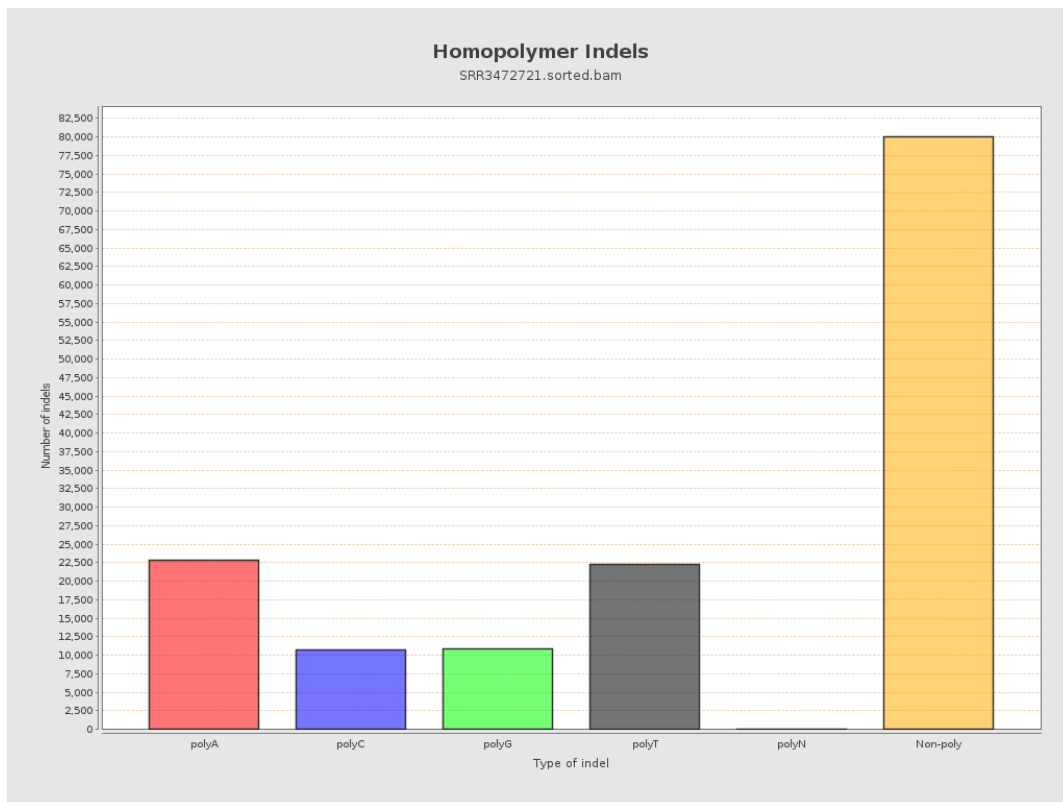
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



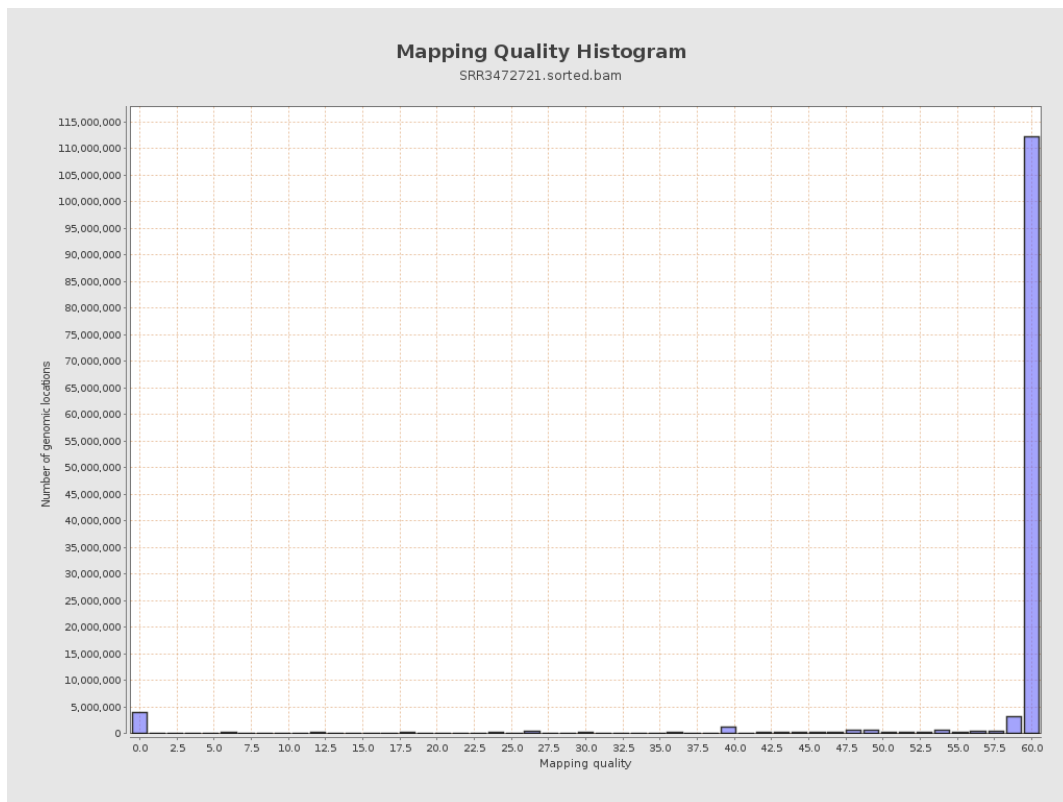
11. Results : Homopolymer Indels



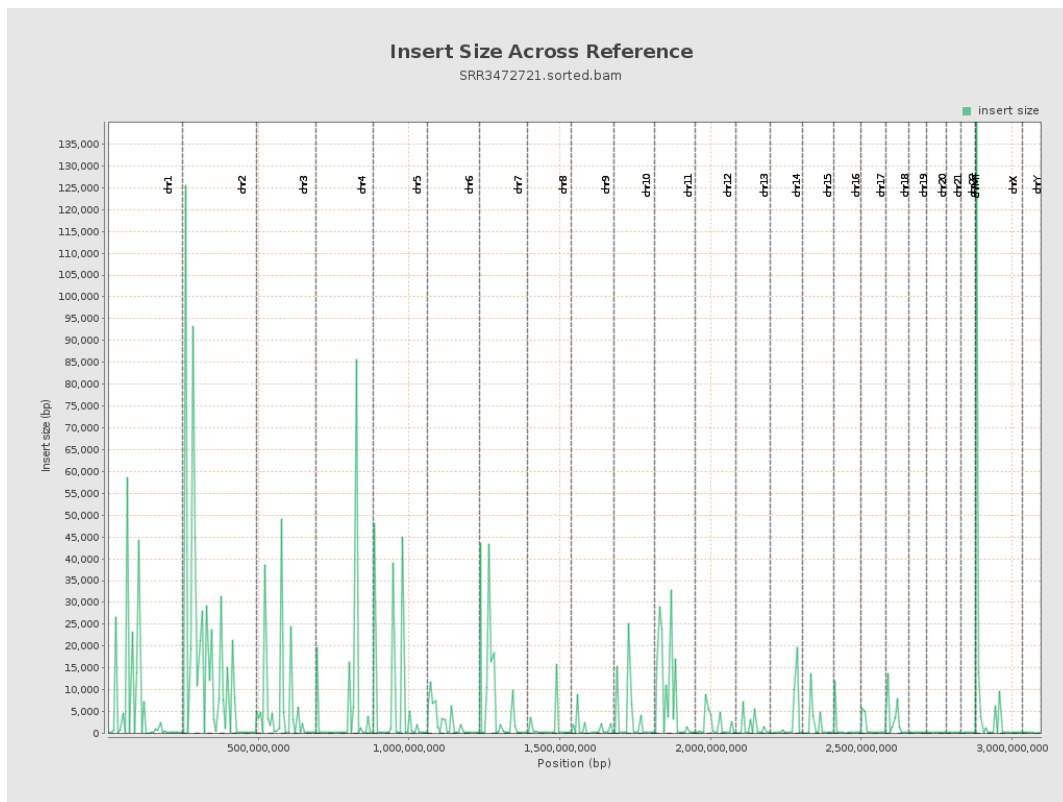
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

