

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 03:31:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472744.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_SRR3472744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472744_1.fastq.gz SRR3472744_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 03:31:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,725,626
Mapped reads	19,502,094 / 98.87%
Unmapped reads	223,532 / 1.13%
Mapped paired reads	19,502,094 / 98.87%
Mapped reads, first in pair	9,795,425 / 49.66%
Mapped reads, second in pair	9,706,669 / 49.21%
Mapped reads, both in pair	19,366,730 / 98.18%
Mapped reads, singletons	135,364 / 0.69%
Secondary alignments	0
Supplementary alignments	108,962 / 0.55%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	12,630,769 / 64.03%
Duplication rate	47.34%
Clipped reads	1,602,688 / 8.12%

2.2. ACGT Content

Number/percentage of A's	532,631,966 / 27.71%
Number/percentage of C's	431,037,933 / 22.43%
Number/percentage of T's	530,327,530 / 27.59%
Number/percentage of G's	427,551,976 / 22.25%
Number/percentage of N's	371,794 / 0.02%

GC Percentage	44.67%
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2.3. Coverage

Mean	0.6209
Standard Deviation	21.1604

2.4. Mapping Quality

Mean Mapping Quality	55.06
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2.5. Insert size

Mean	37,354.45
Standard Deviation	1,897,018.72
P25/Median/P75	178 / 250 / 339

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	12,459,646
Insertions	123,297
Mapped reads with at least one insertion	0.63%
Deletions	109,712
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.26%

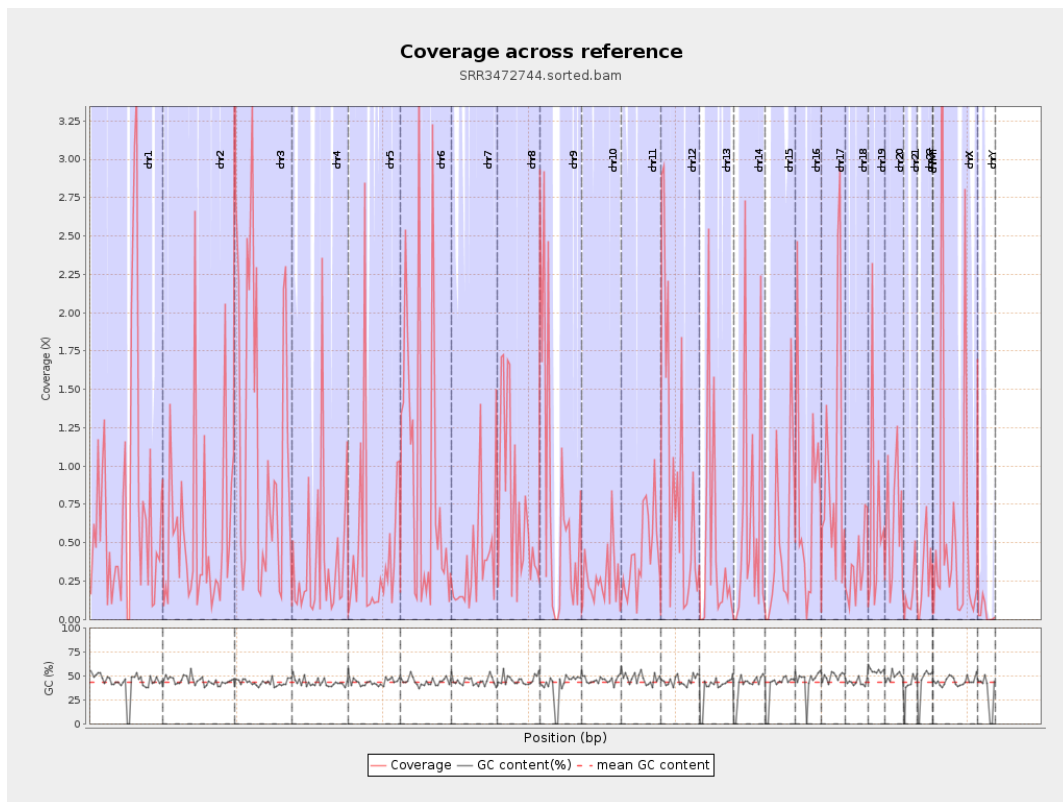
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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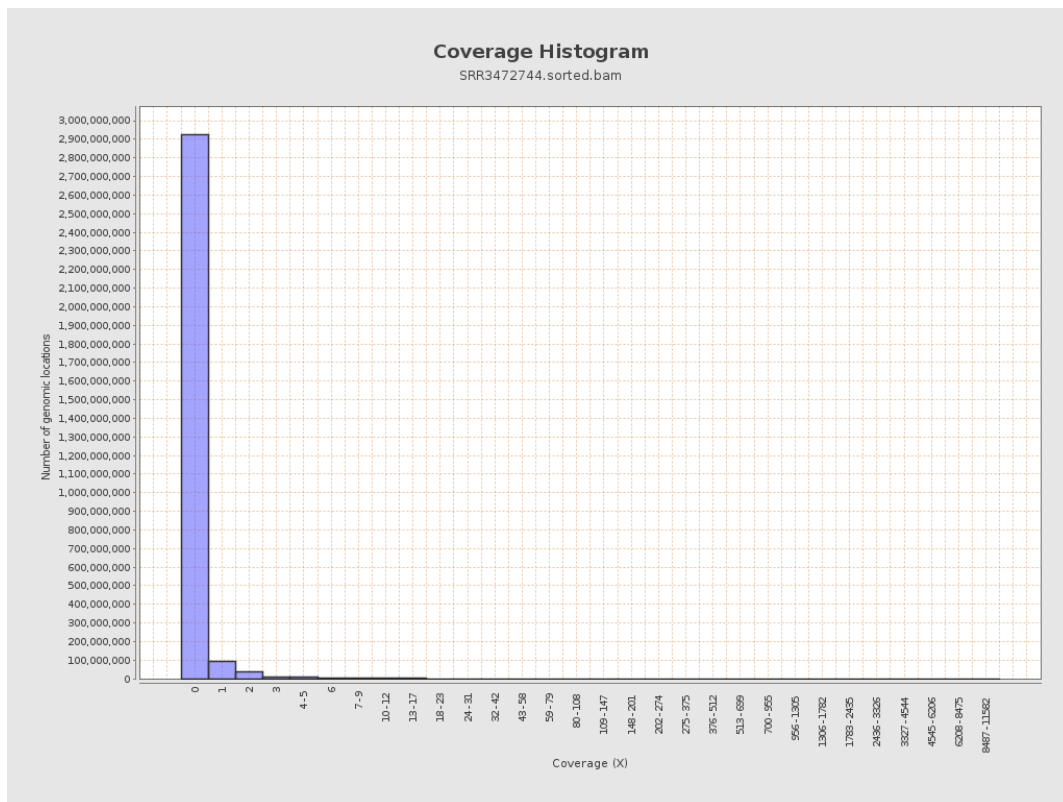
		bases	coverage	deviation
chr1	249250621	179296424	0.7193	23.1618
chr2	243199373	133685005	0.5497	16.1411
chr3	198022430	239368026	1.2088	28.087
chr4	191154276	75348022	0.3942	14.9254
chr5	180915260	80385866	0.4443	16.8462
chr6	171115067	159183647	0.9303	26.942
chr7	159138663	62792091	0.3946	16.1449
chr8	146364022	106401730	0.727	23.664
chr9	141213431	101985115	0.7222	20.3967
chr10	135534747	37397080	0.2759	8.3764
chr11	135006516	57053487	0.4226	11.5145
chr12	133851895	129955069	0.9709	32.1276
chr13	115169878	52129056	0.4526	19.1582
chr14	107349540	69254453	0.6451	36.0287
chr15	102531392	50033729	0.488	17.5321
chr16	90354753	67307138	0.7449	22.4216
chr17	81195210	86094064	1.0603	29.4745
chr18	78077248	26200044	0.3356	10.1791
chr19	59128983	39510660	0.6682	15.7426
chr20	63025520	41229653	0.6542	18.5512
chr21	48129895	8438154	0.1753	6.728
chr22	51304566	15663822	0.3053	9.4309
chrMT	16571	6084	0.3671	0.9925
chrX	155270560	100793668	0.6491	23.5687

chrY	59373566	2693019	0.0454	1.9095
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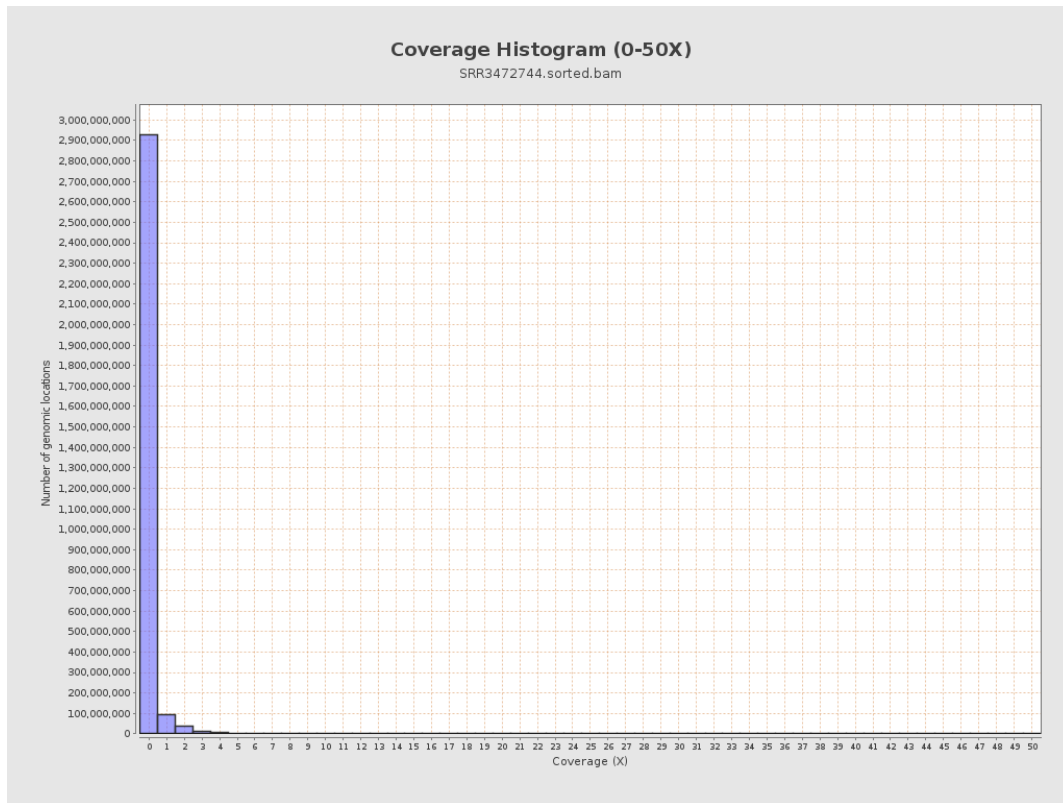
3. Results : Coverage across reference



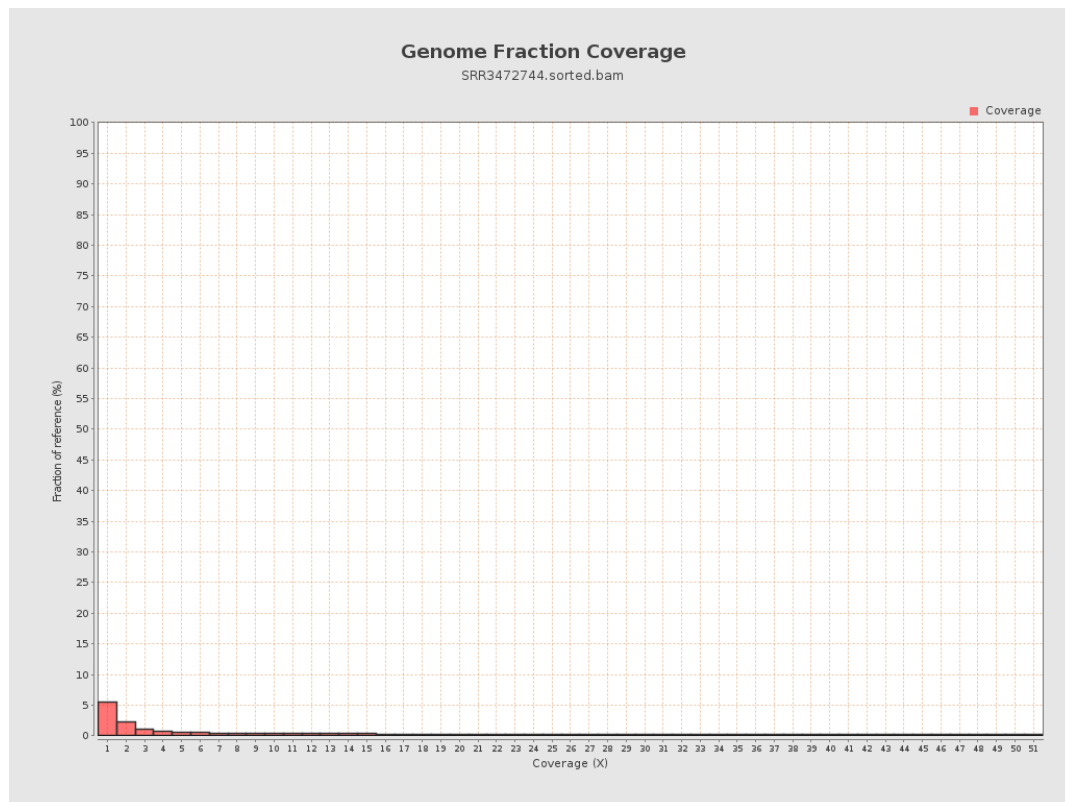
4. Results : Coverage Histogram



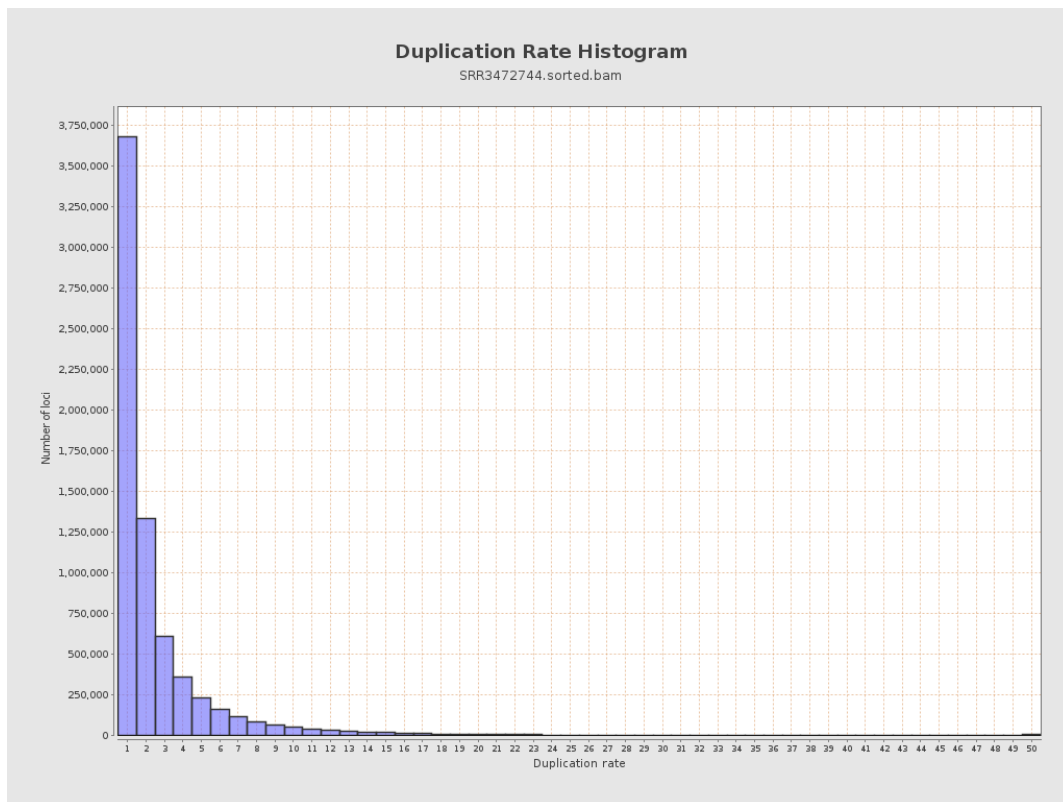
5. Results : Coverage Histogram (0-50X)



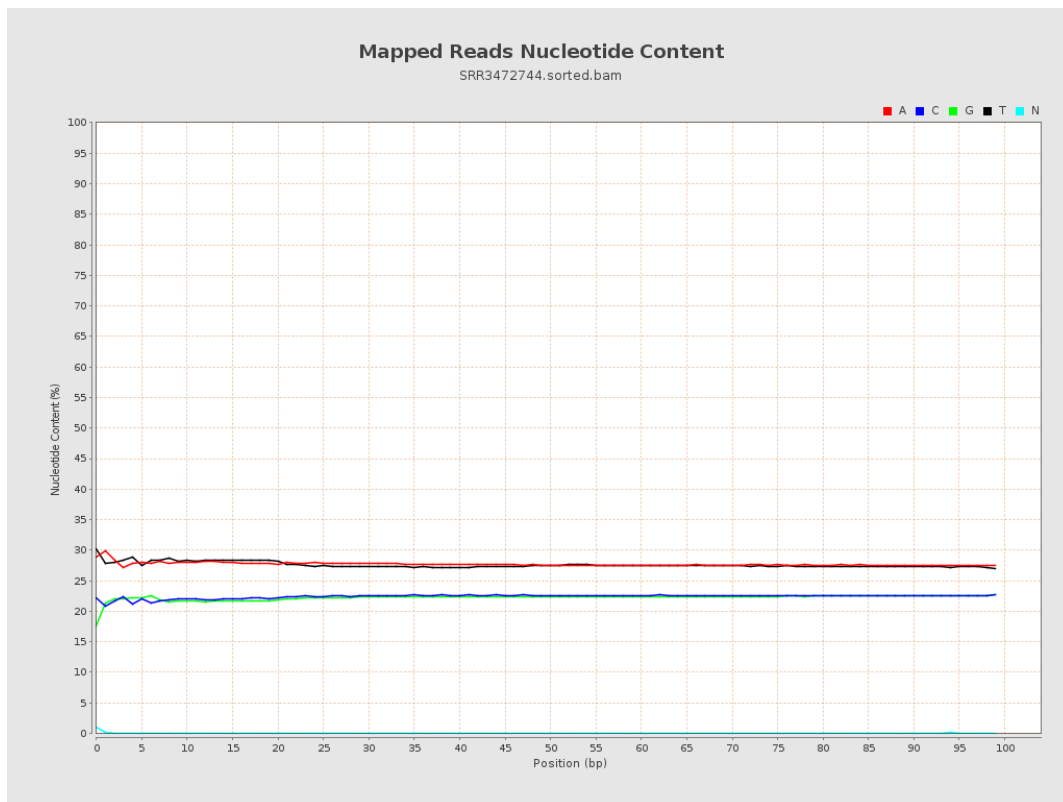
6. Results : Genome Fraction Coverage



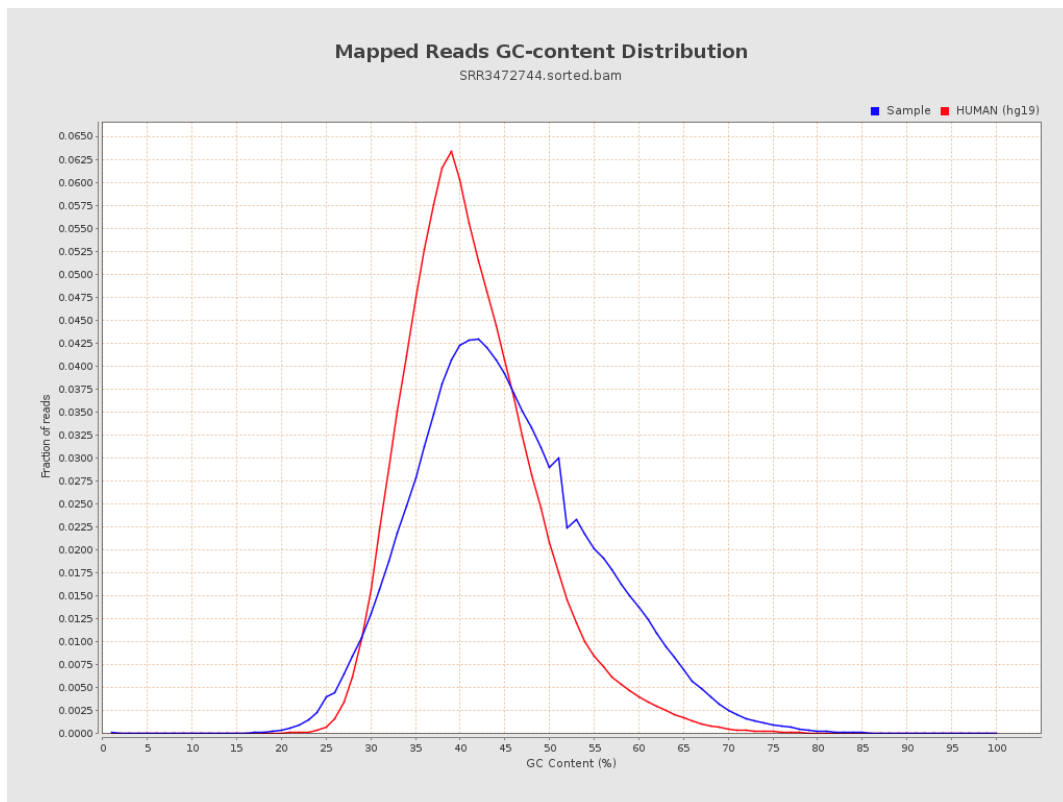
7. Results : Duplication Rate Histogram



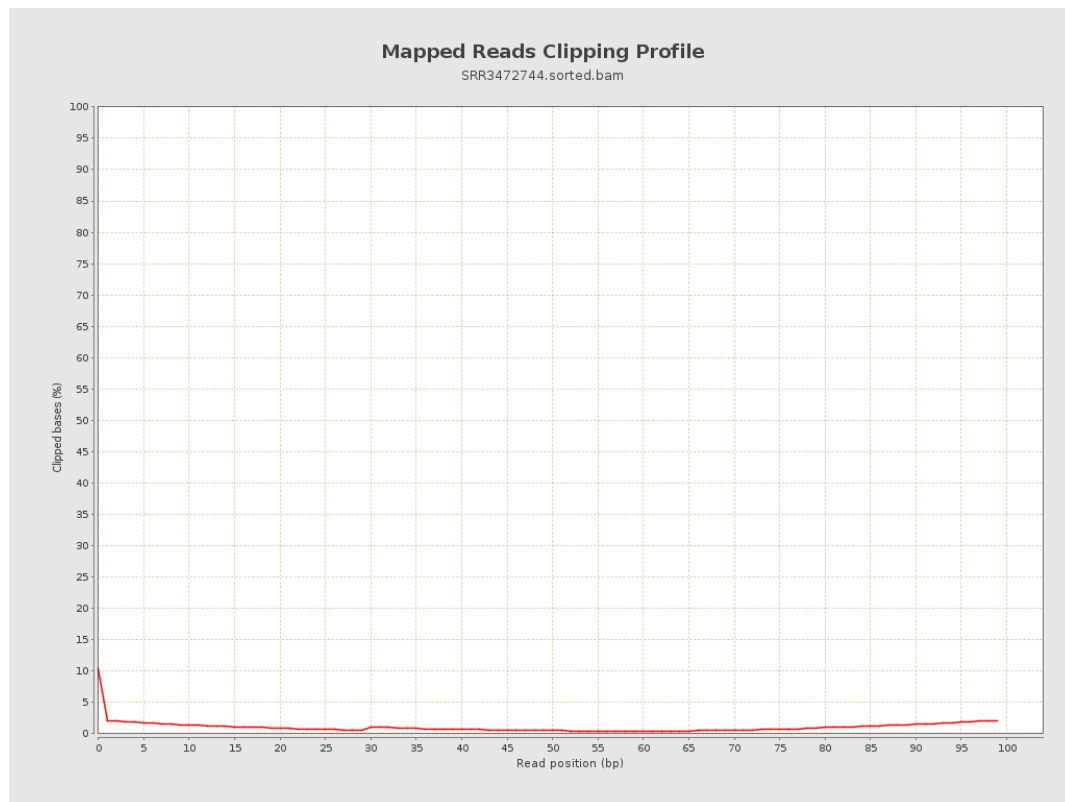
8. Results : Mapped Reads Nucleotide Content



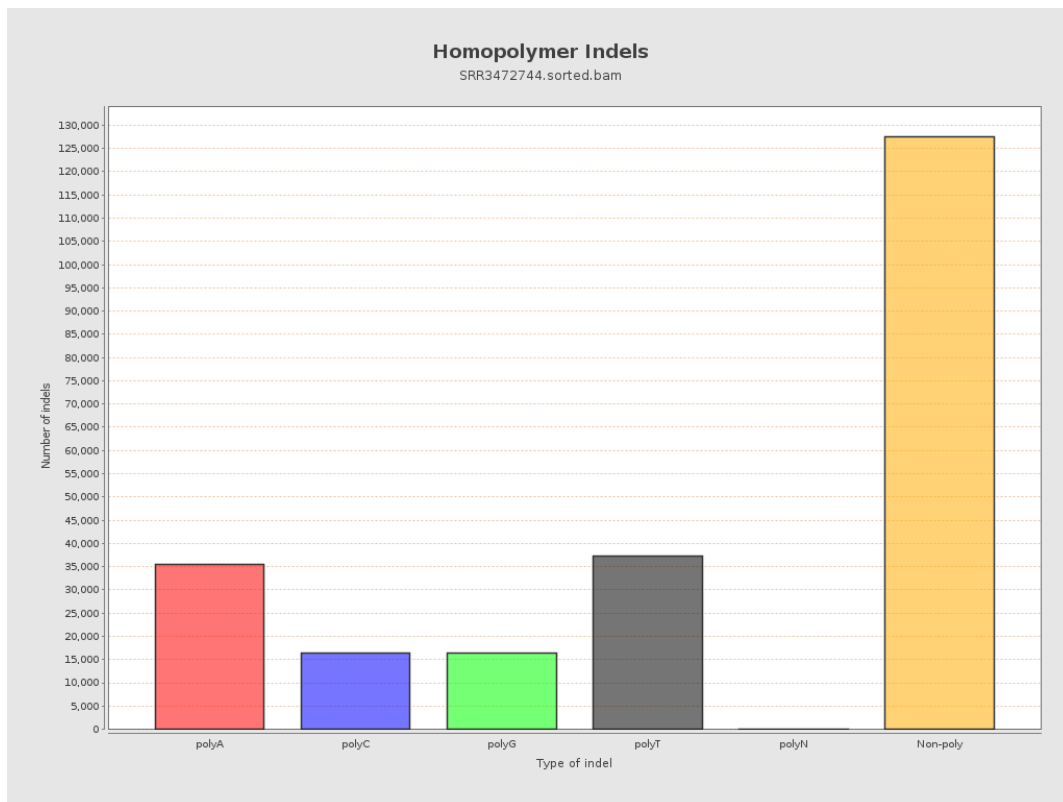
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



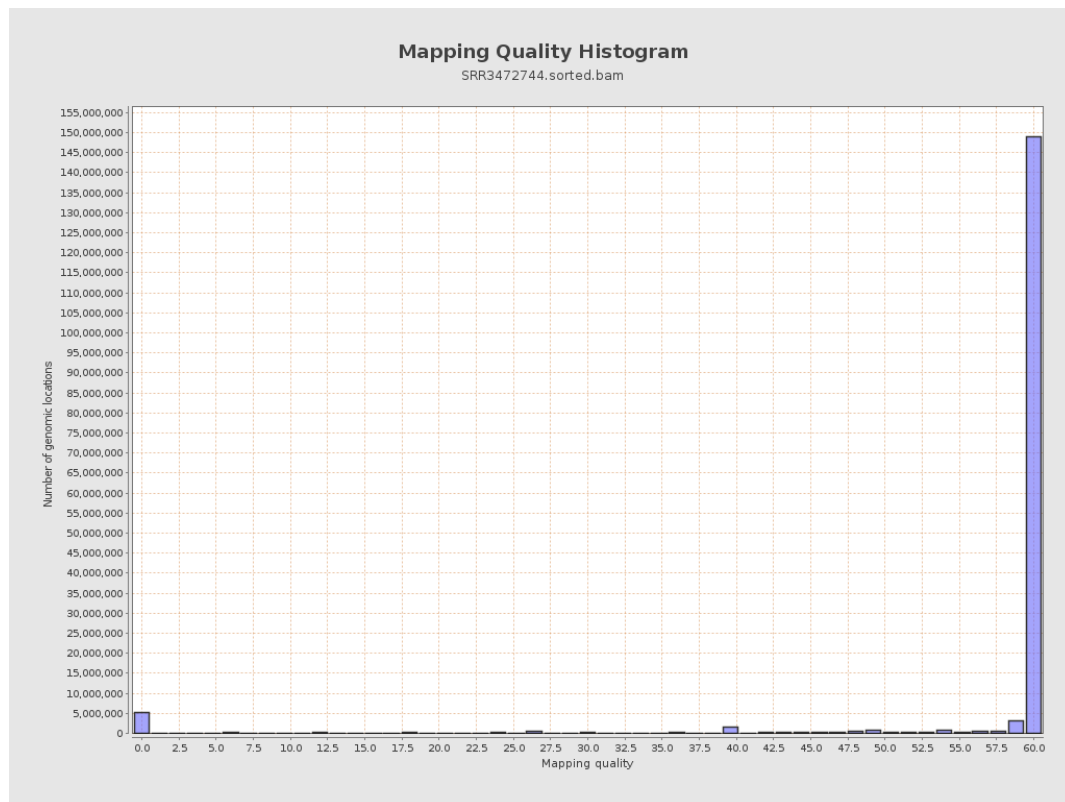
11. Results : Homopolymer Indels



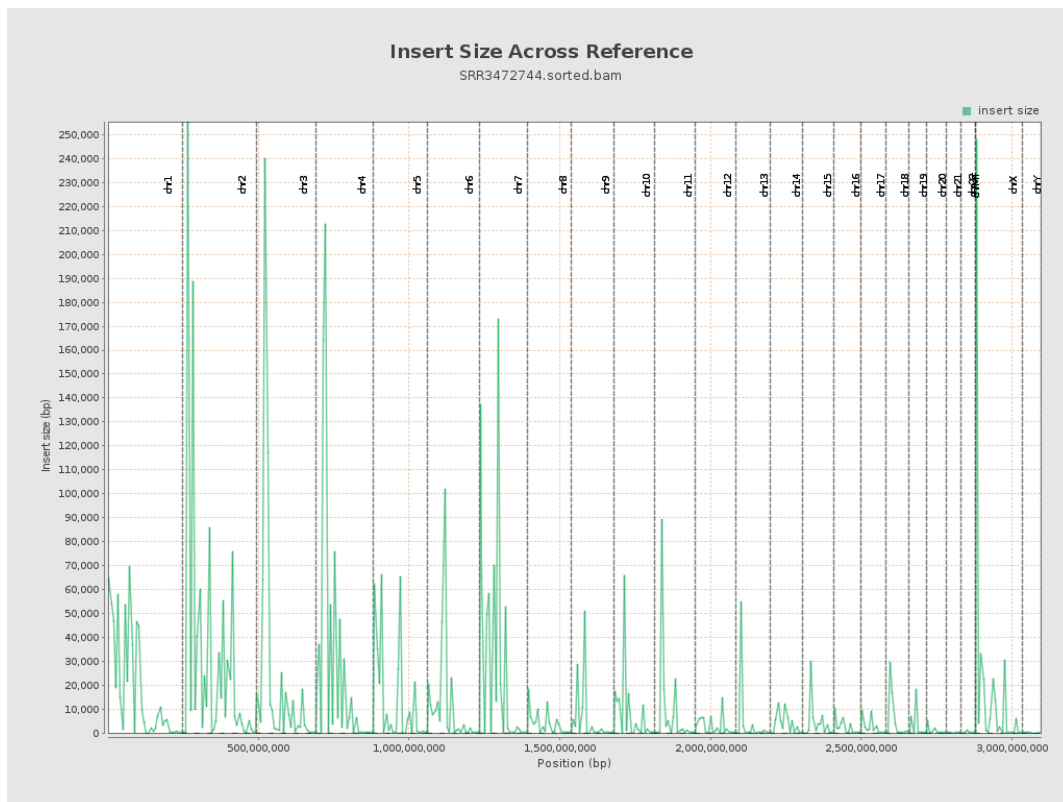
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

