

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 01:15:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472738.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_SRR3472738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472738_1.fastq.gz SRR3472738_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 01:15:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,540,284
Mapped reads	23,269,950 / 98.85%
Unmapped reads	270,334 / 1.15%
Mapped paired reads	23,269,950 / 98.85%
Mapped reads, first in pair	11,691,499 / 49.67%
Mapped reads, second in pair	11,578,451 / 49.19%
Mapped reads, both in pair	23,105,300 / 98.15%
Mapped reads, singletons	164,650 / 0.7%
Secondary alignments	0
Supplementary alignments	82,650 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	15,555,806 / 66.08%
Duplication rate	49.05%
Clipped reads	1,776,173 / 7.55%

2.2. ACGT Content

Number/percentage of A's	635,902,429 / 27.73%
Number/percentage of C's	513,968,001 / 22.41%
Number/percentage of T's	633,011,832 / 27.6%
Number/percentage of G's	510,106,282 / 22.24%
Number/percentage of N's	440,309 / 0.02%

GC Percentage	44.65%
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2.3. Coverage

Mean	0.741
Standard Deviation	24.1515

2.4. Mapping Quality

Mean Mapping Quality	55.35
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2.5. Insert size

Mean	23,194.51
Standard Deviation	1,504,337.96
P25/Median/P75	181 / 253 / 341

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	15,147,956
Insertions	146,084
Mapped reads with at least one insertion	0.62%
Deletions	138,582
Mapped reads with at least one deletion	0.59%
Homopolymer indels	45.26%

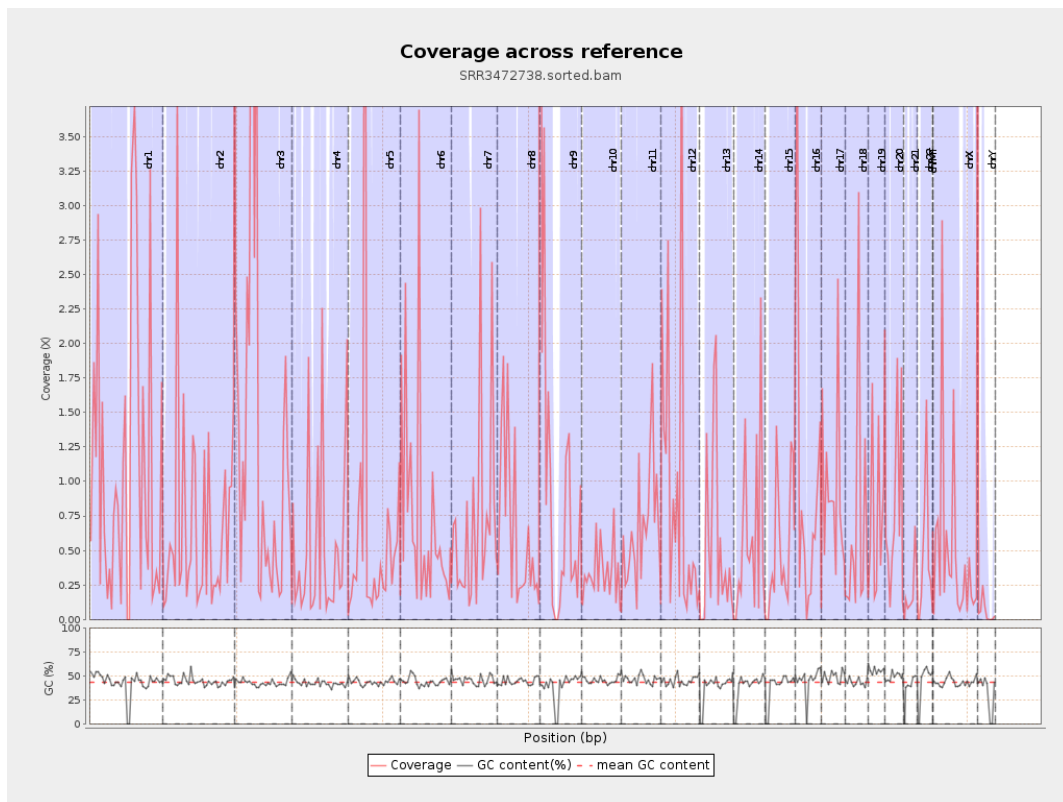
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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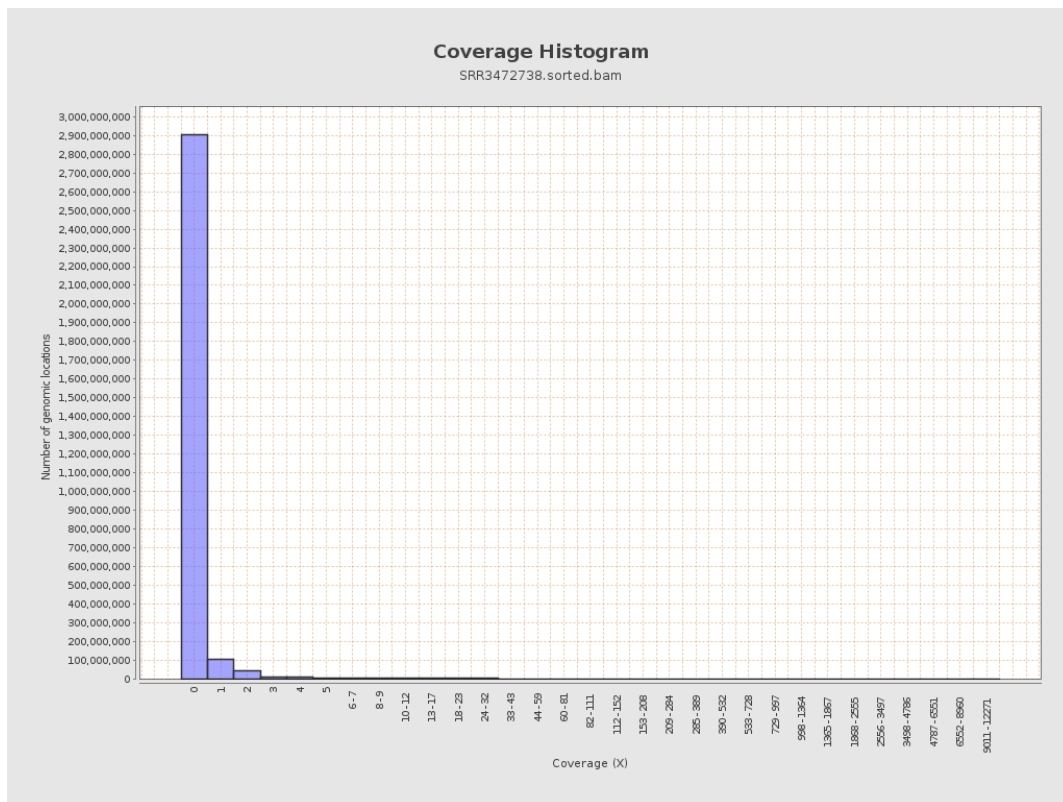
		bases	coverage	deviation
chr1	249250621	273453937	1.0971	33.376
chr2	243199373	160537932	0.6601	26.208
chr3	198022430	282010037	1.4241	31.2649
chr4	191154276	105186036	0.5503	20.8319
chr5	180915260	123306879	0.6816	25.8817
chr6	171115067	127639203	0.7459	18.2213
chr7	159138663	113814614	0.7152	20.8916
chr8	146364022	92193536	0.6299	22.4484
chr9	141213431	127860825	0.9054	23.1673
chr10	135534747	47067908	0.3473	11.3305
chr11	135006516	91050827	0.6744	19.3901
chr12	133851895	130740838	0.9768	32.9327
chr13	115169878	60801733	0.5279	23.5819
chr14	107349540	64946229	0.605	24.4804
chr15	102531392	50015877	0.4878	17.2832
chr16	90354753	87385030	0.9671	29.0768
chr17	81195210	78701981	0.9693	22.899
chr18	78077248	50418556	0.6458	32.6498
chr19	59128983	47180364	0.7979	19.8883
chr20	63025520	49956653	0.7926	20.5574
chr21	48129895	10357901	0.2152	8.0386
chr22	51304566	24853323	0.4844	16.7751
chrMT	16571	10660	0.6433	1.3674
chrX	155270560	90697459	0.5841	16.9979

chrY	59373566	3570432	0.0601	2.1395
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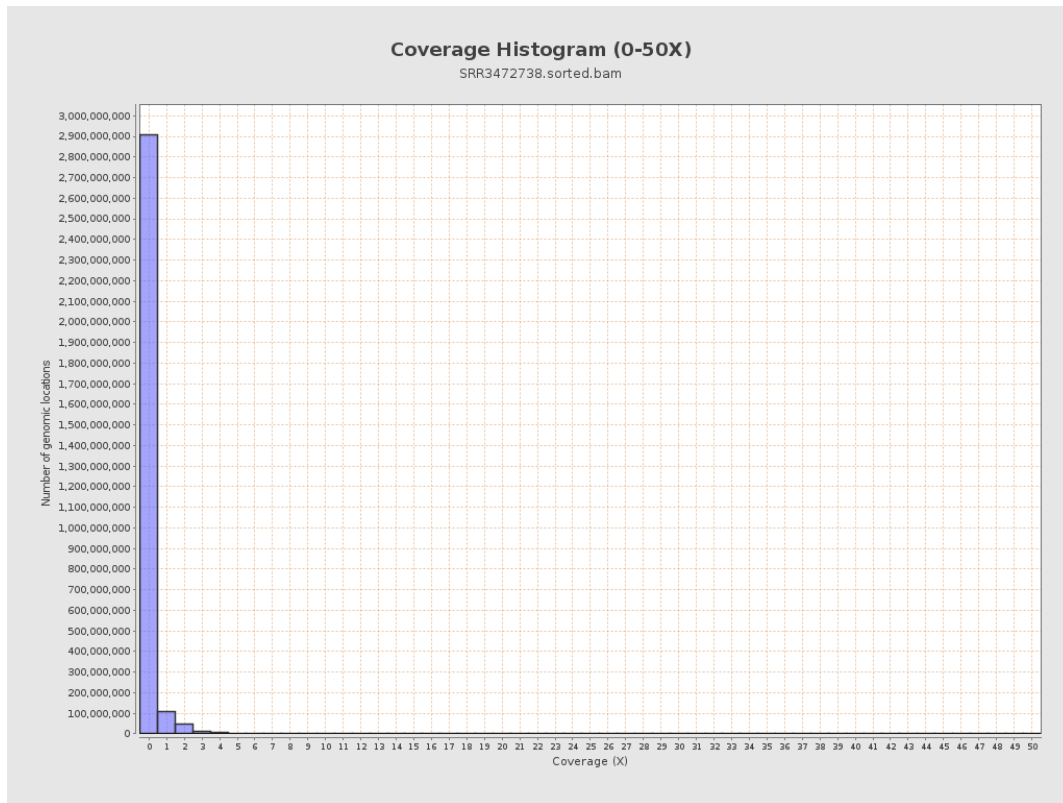
3. Results : Coverage across reference



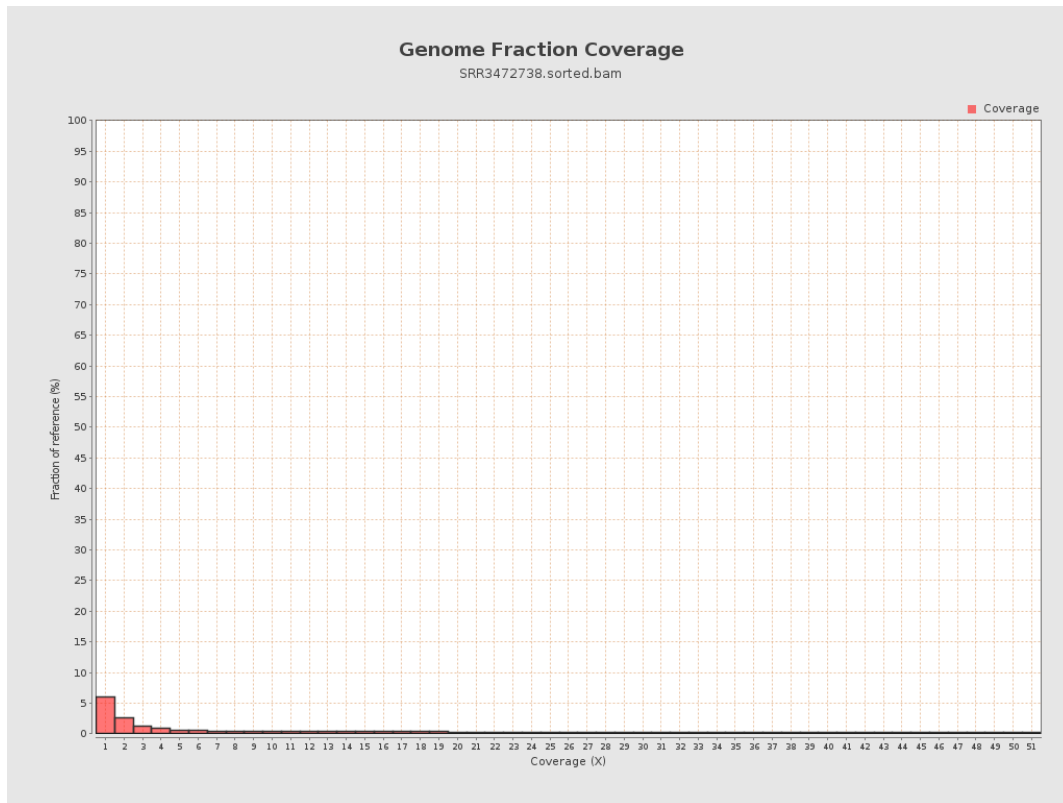
4. Results : Coverage Histogram



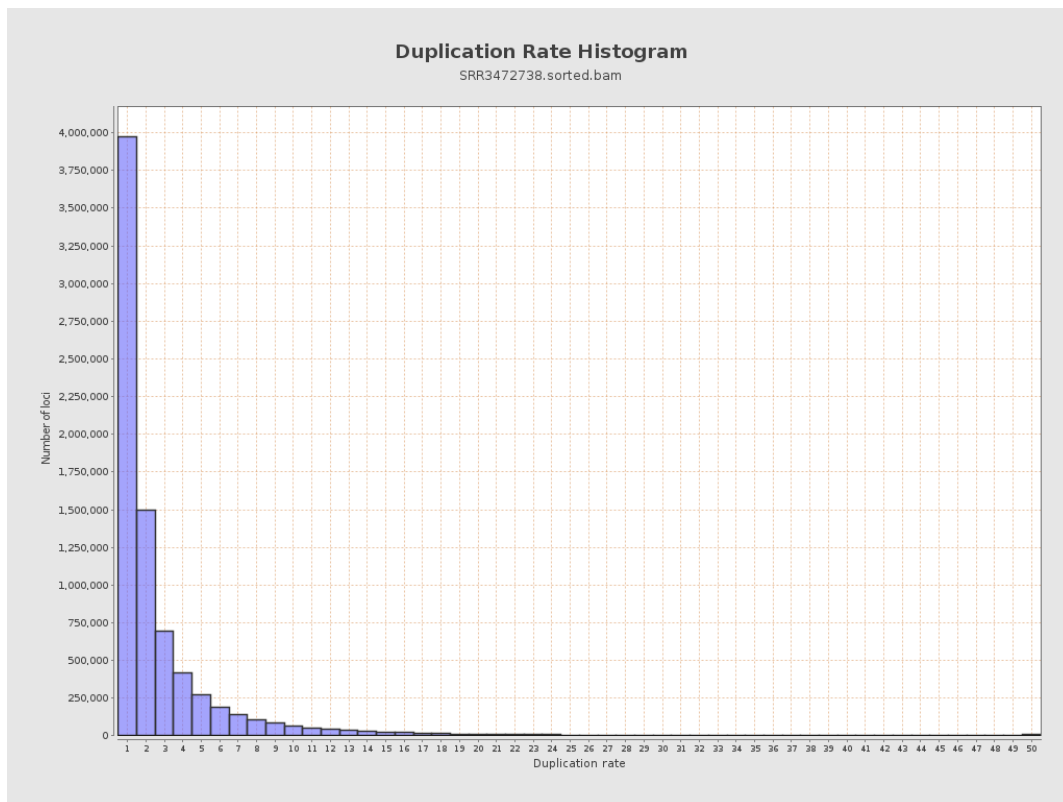
5. Results : Coverage Histogram (0-50X)



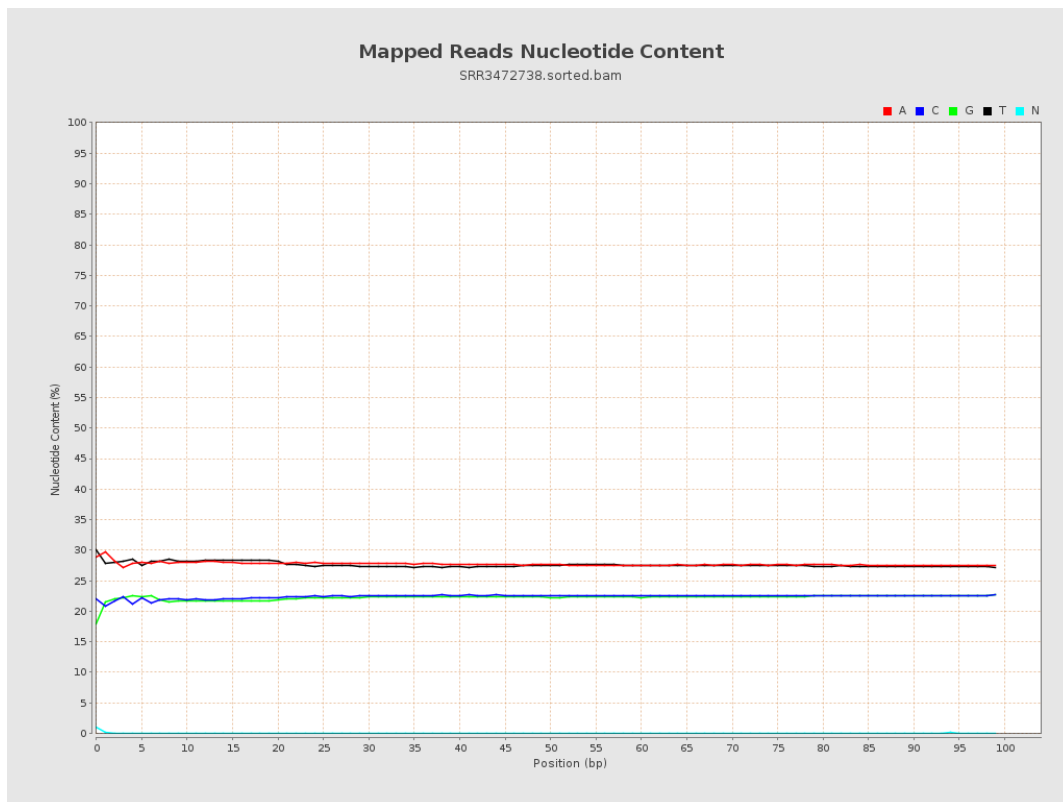
6. Results : Genome Fraction Coverage



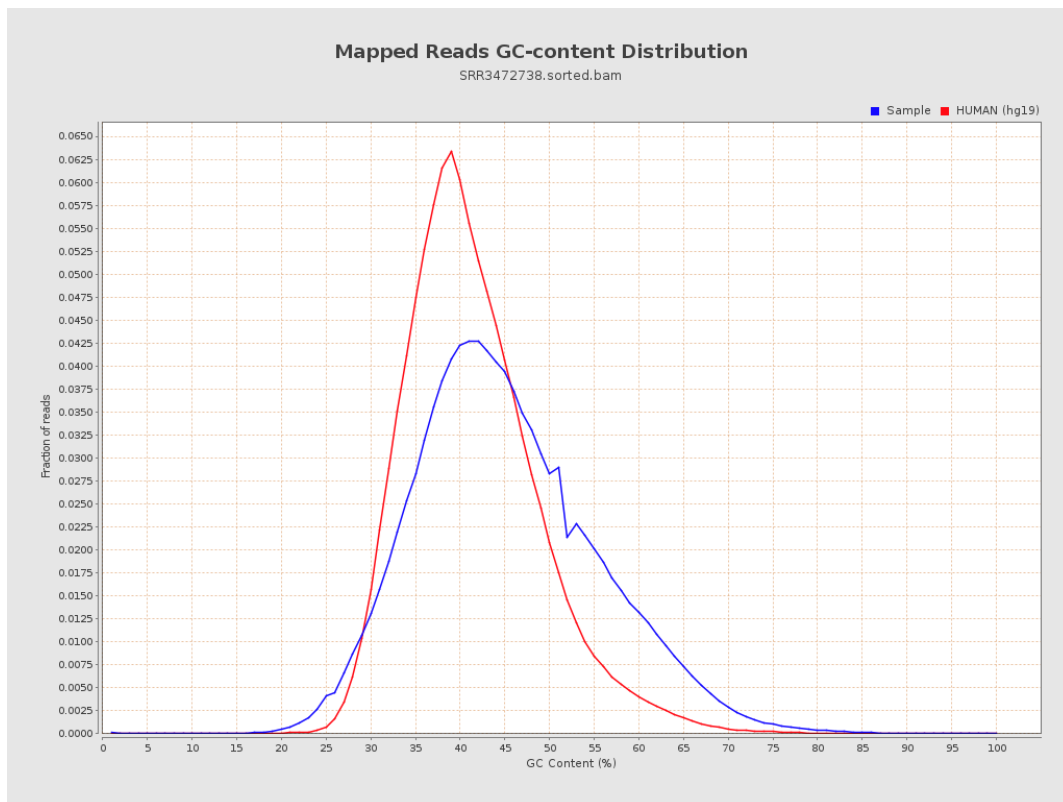
7. Results : Duplication Rate Histogram



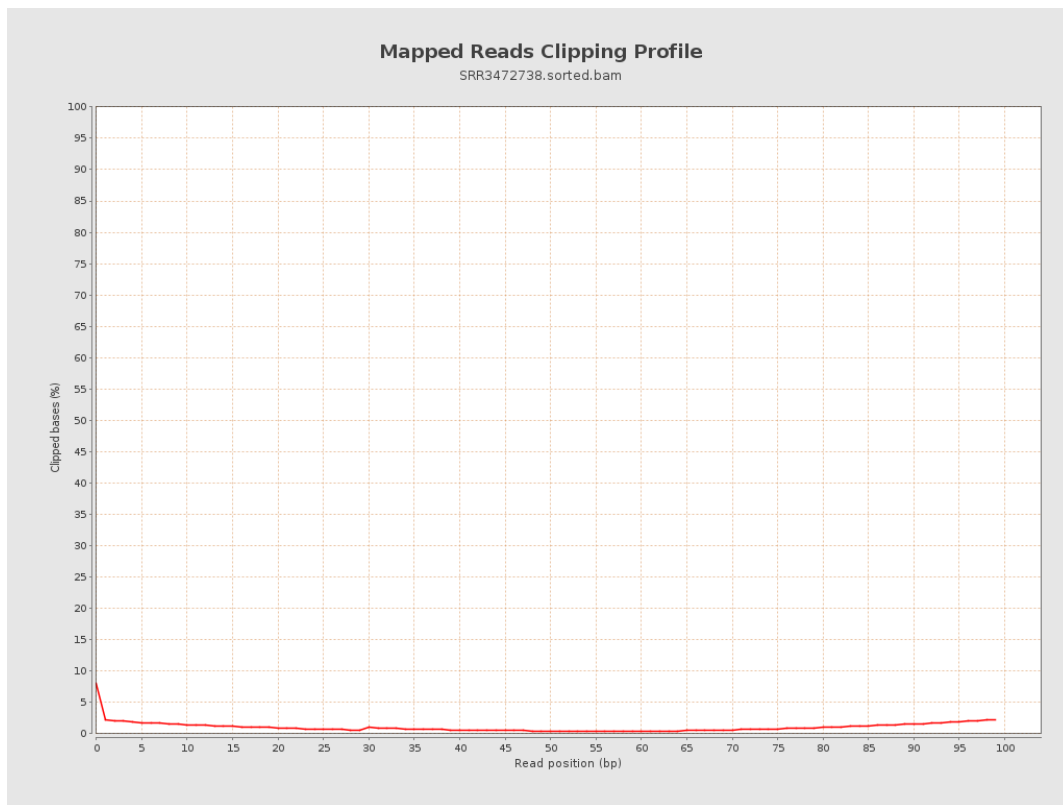
8. Results : Mapped Reads Nucleotide Content



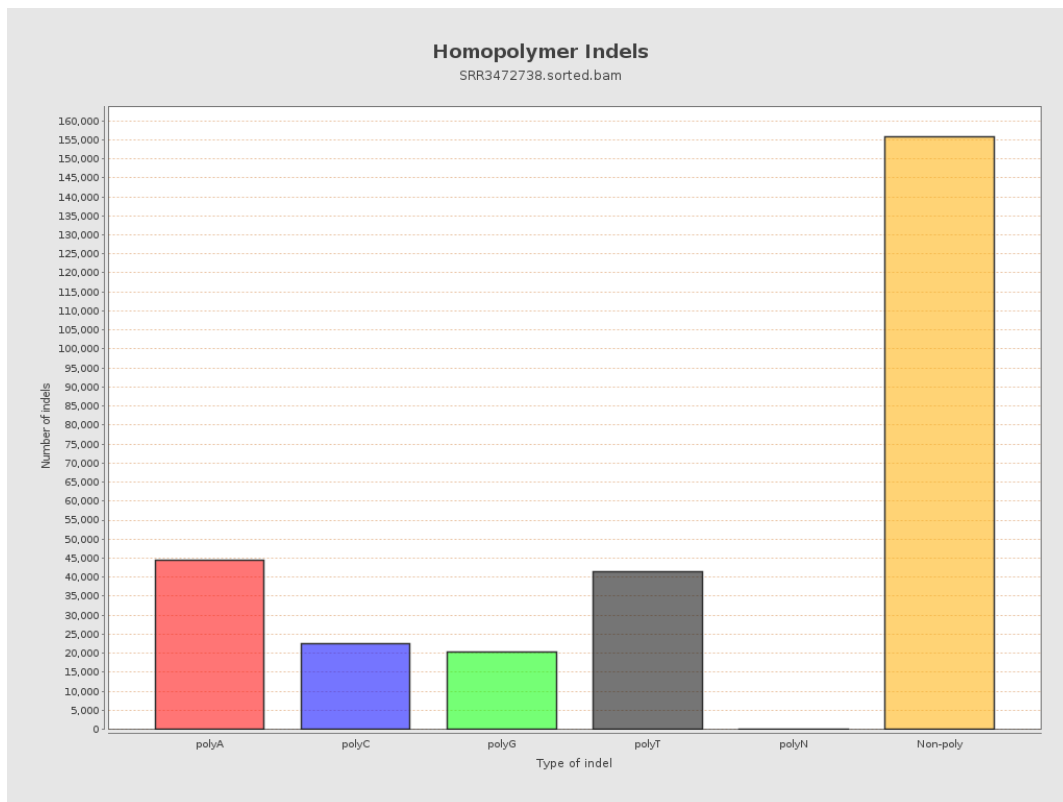
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



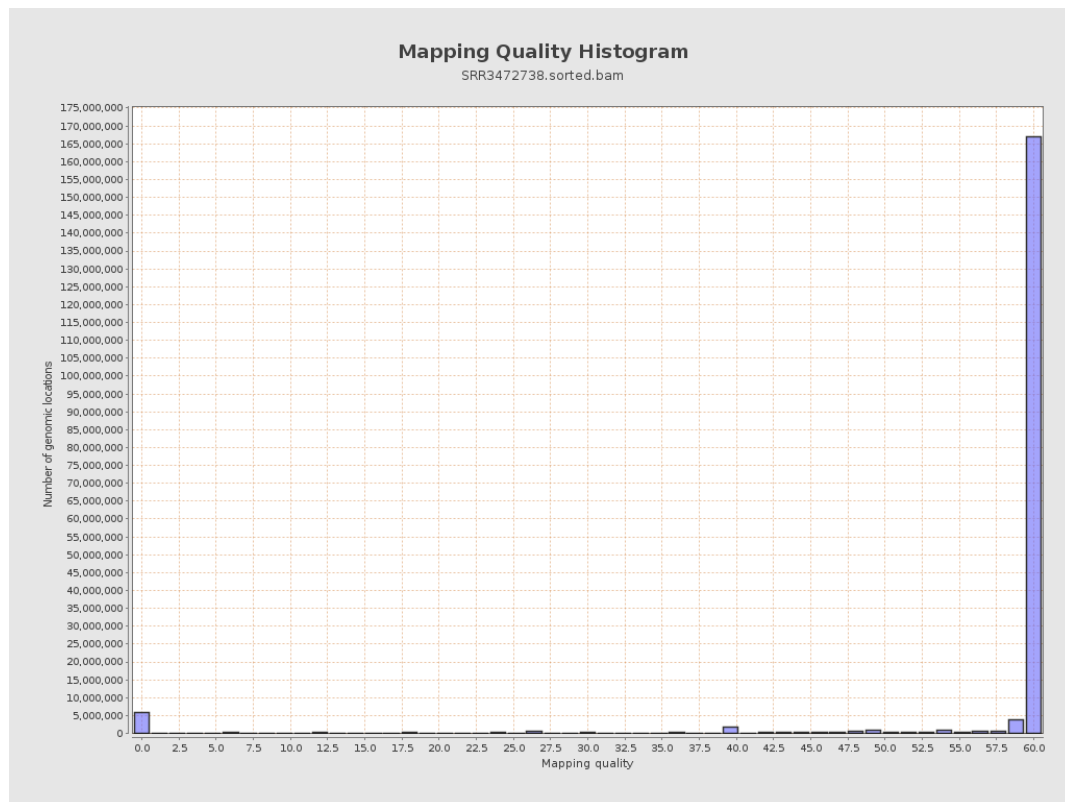
11. Results : Homopolymer Indels



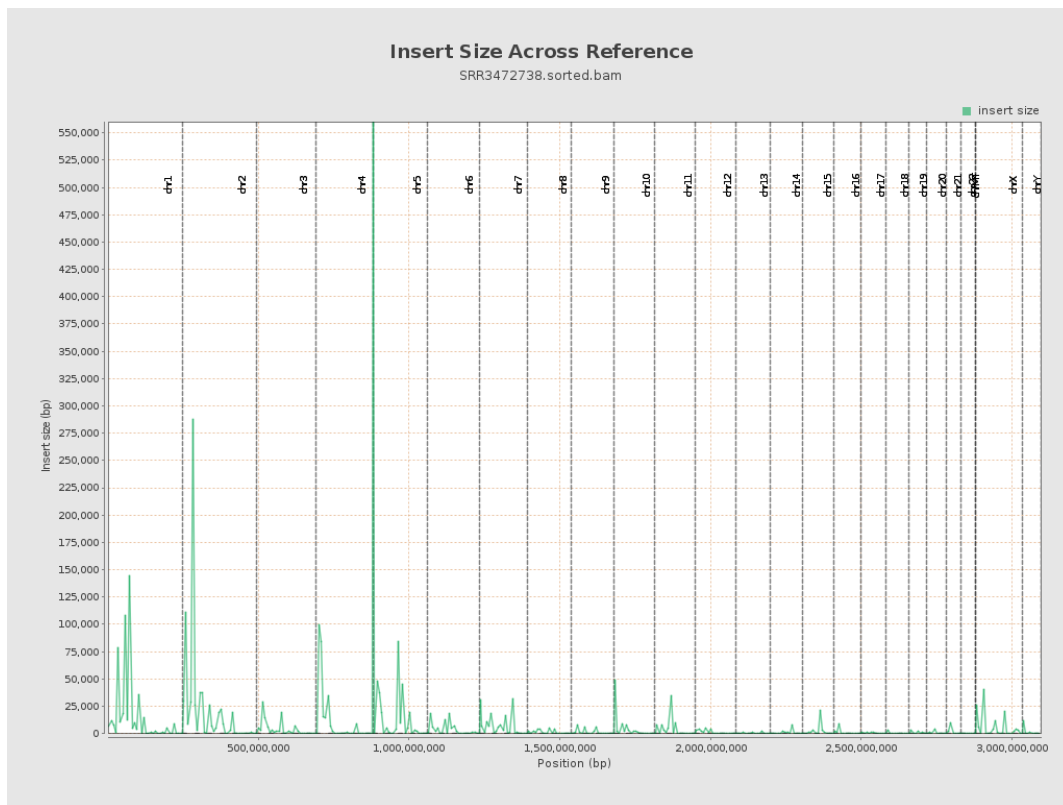
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

