

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 19:04:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472639.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_SRR3472639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472639_1.fastq.gz SRR3472639_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 19:04:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,381,364
Mapped reads	16,264,734 / 99.29%
Unmapped reads	116,630 / 0.71%
Mapped paired reads	16,264,734 / 99.29%
Mapped reads, first in pair	8,168,159 / 49.86%
Mapped reads, second in pair	8,096,575 / 49.43%
Mapped reads, both in pair	16,185,384 / 98.8%
Mapped reads, singletons	79,350 / 0.48%
Secondary alignments	0
Supplementary alignments	21,128 / 0.13%
Read min/max/mean length	30 / 101 / 99.49
Duplicated reads (estimated)	9,264,769 / 56.56%
Duplication rate	49.01%
Clipped reads	750,319 / 4.58%

2.2. ACGT Content

Number/percentage of A's	419,357,901 / 26.16%
Number/percentage of C's	381,783,640 / 23.82%
Number/percentage of T's	427,246,861 / 26.65%
Number/percentage of G's	374,158,071 / 23.34%
Number/percentage of N's	364,831 / 0.02%

GC Percentage	47.16%
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2.3. Coverage

Mean	0.5179
Standard Deviation	11.6688

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	16,622.54
Standard Deviation	1,326,314.66
P25/Median/P75	157 / 215 / 286

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	6,712,317
Insertions	66,726
Mapped reads with at least one insertion	0.4%
Deletions	80,804
Mapped reads with at least one deletion	0.49%
Homopolymer indels	43.23%

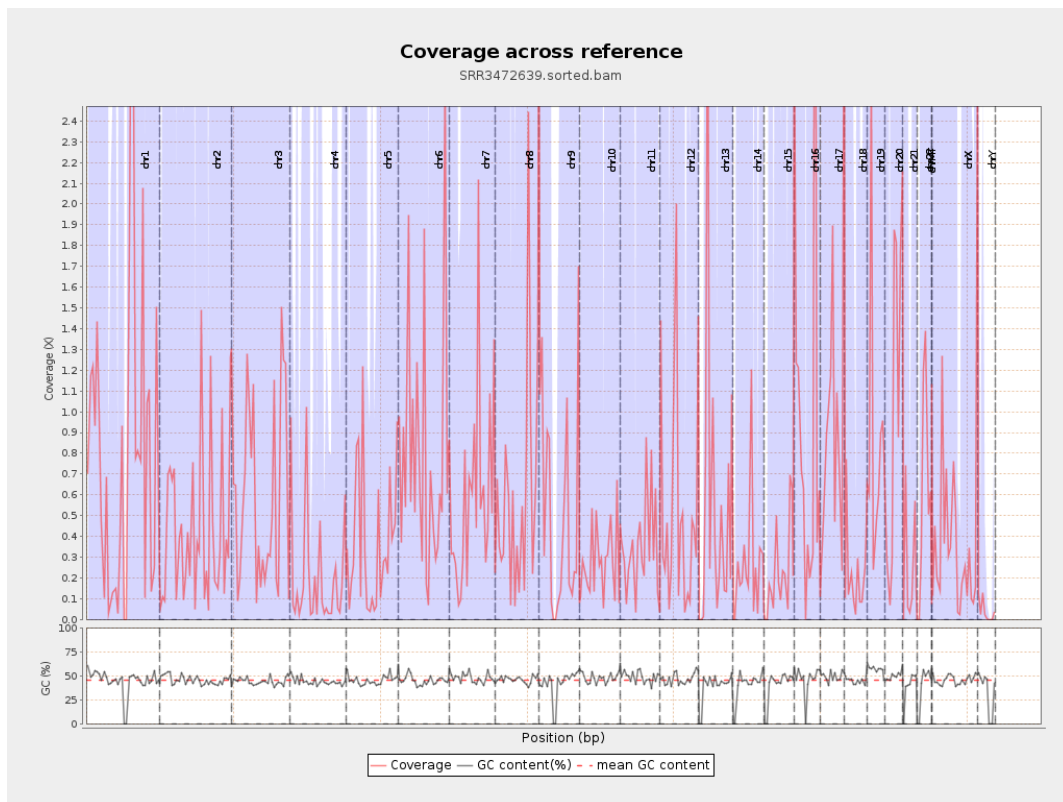
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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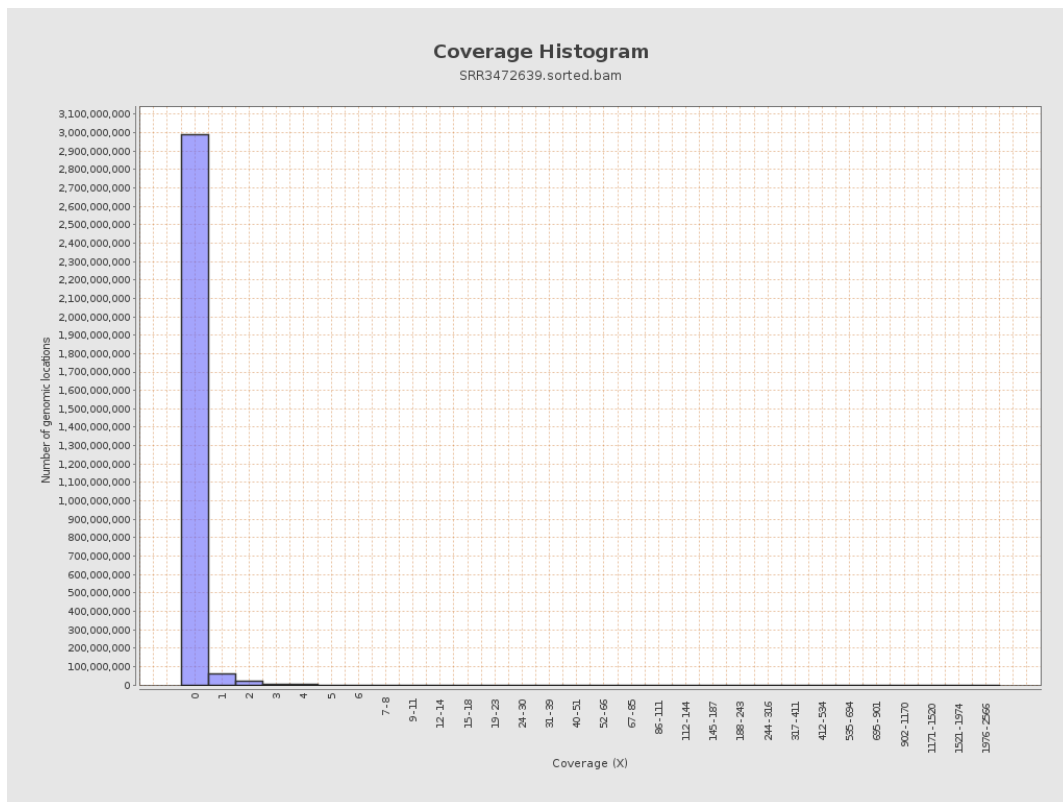
		bases	coverage	deviation
chr1	249250621	204506884	0.8205	16.0749
chr2	243199373	103199901	0.4243	9.9186
chr3	198022430	121243683	0.6123	11.8058
chr4	191154276	36785784	0.1924	5.6224
chr5	180915260	68301873	0.3775	8.9055
chr6	171115067	133970196	0.7829	14.2466
chr7	159138663	96107640	0.6039	13.1574
chr8	146364022	88250157	0.6029	12.7832
chr9	141213431	75780226	0.5366	10.1426
chr10	135534747	37726514	0.2784	7.2491
chr11	135006516	48213337	0.3571	7.8145
chr12	133851895	69718631	0.5209	9.4967
chr13	115169878	62370686	0.5416	15.5386
chr14	107349540	27272647	0.2541	5.9665
chr15	102531392	23500581	0.2292	5.566
chr16	90354753	92169971	1.0201	21.5522
chr17	81195210	76924450	0.9474	15.1571
chr18	78077248	17321638	0.2219	5.6786
chr19	59128983	53396863	0.9031	12.8614
chr20	63025520	63615975	1.0094	20.9633
chr21	48129895	12395840	0.2575	11.4941
chr22	51304566	31407391	0.6122	12.9754
chrMT	16571	18795	1.1342	1.4069
chrX	155270560	56683013	0.3651	6.3871

chrY	59373566	2237707	0.0377	1.2173
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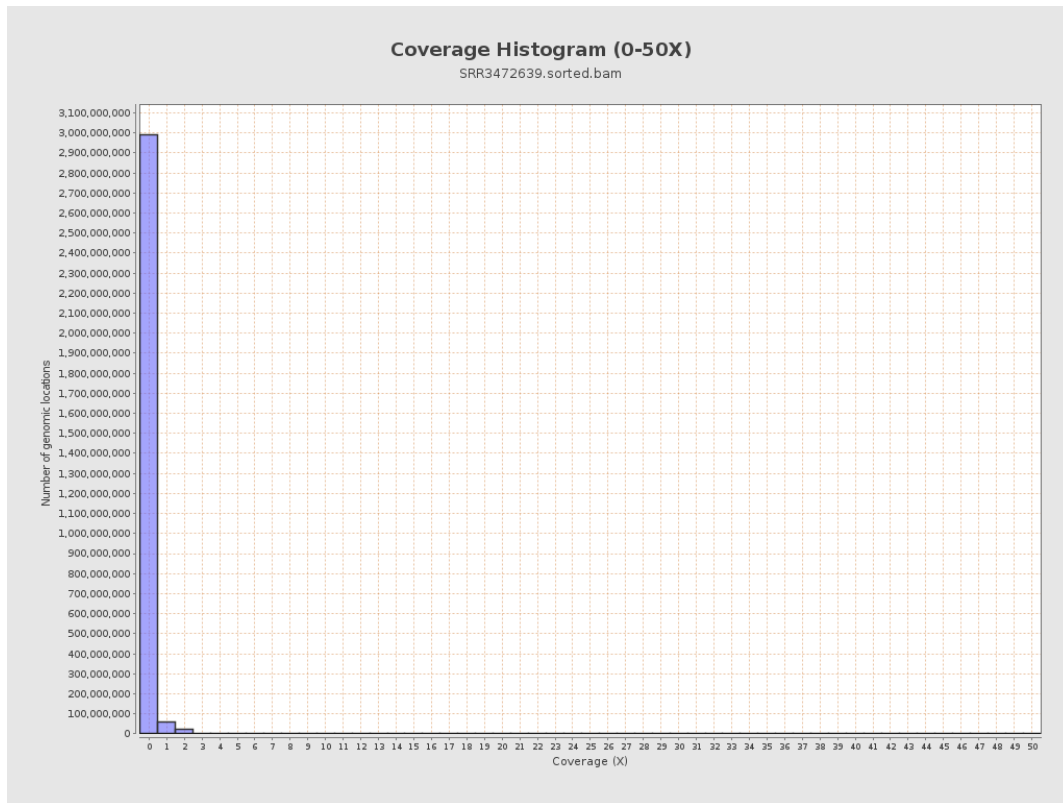
3. Results : Coverage across reference



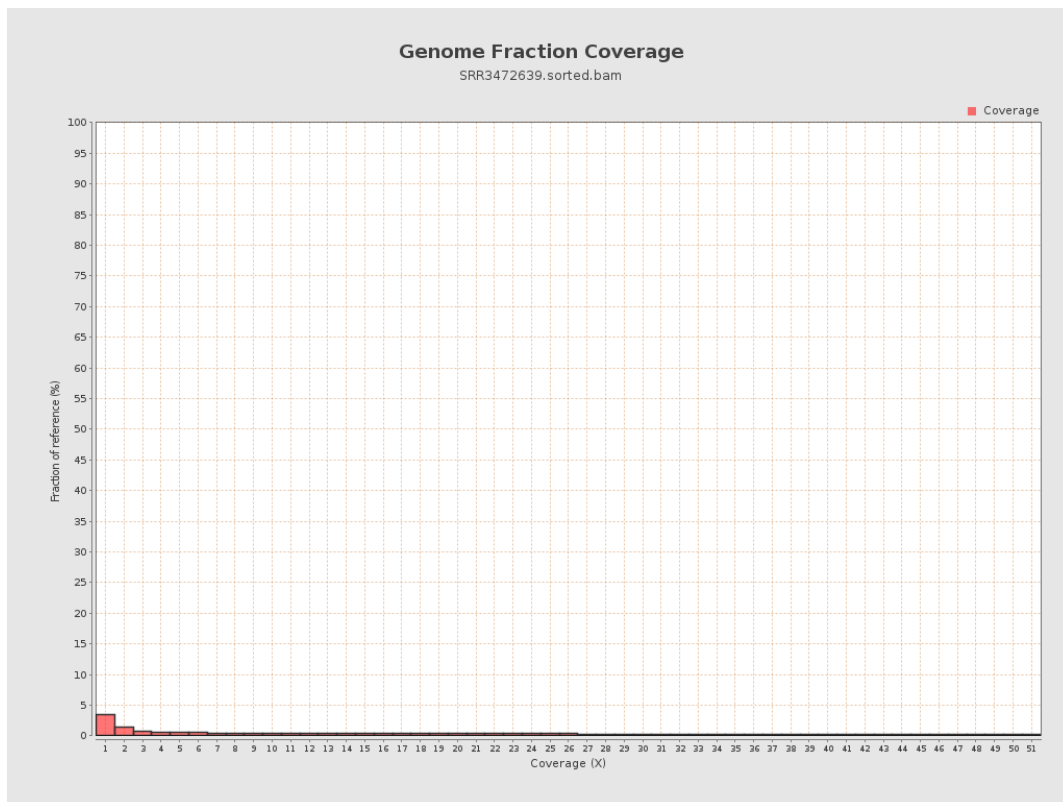
4. Results : Coverage Histogram



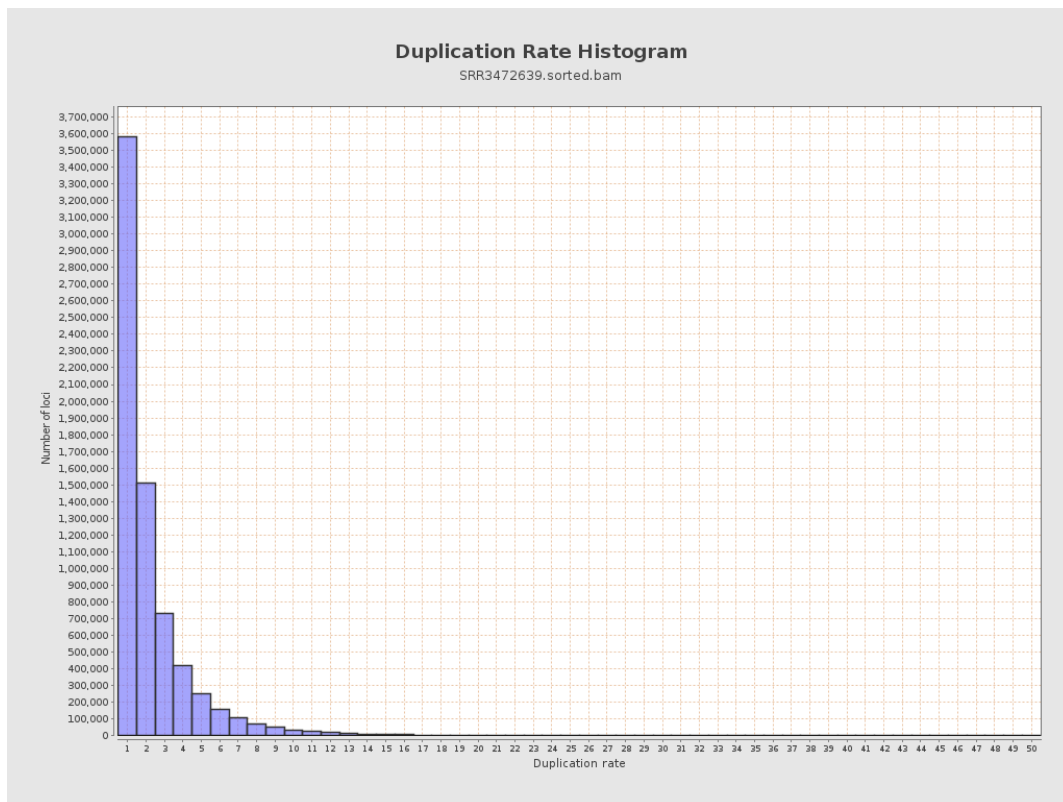
5. Results : Coverage Histogram (0-50X)



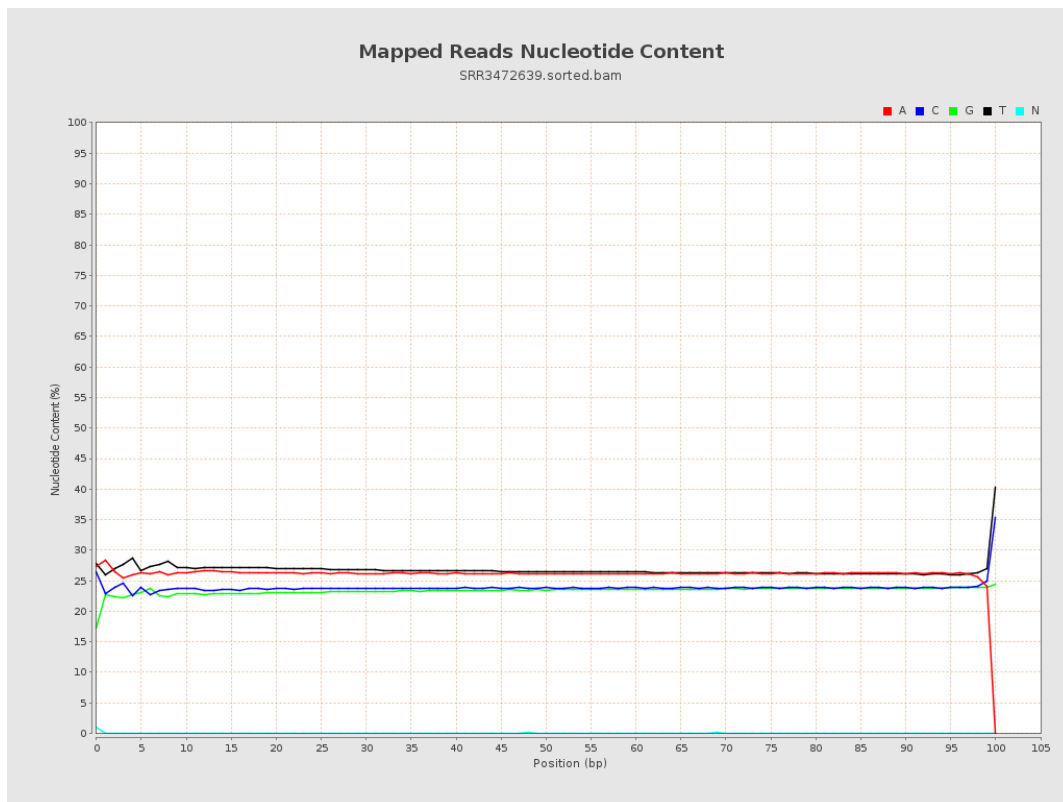
6. Results : Genome Fraction Coverage



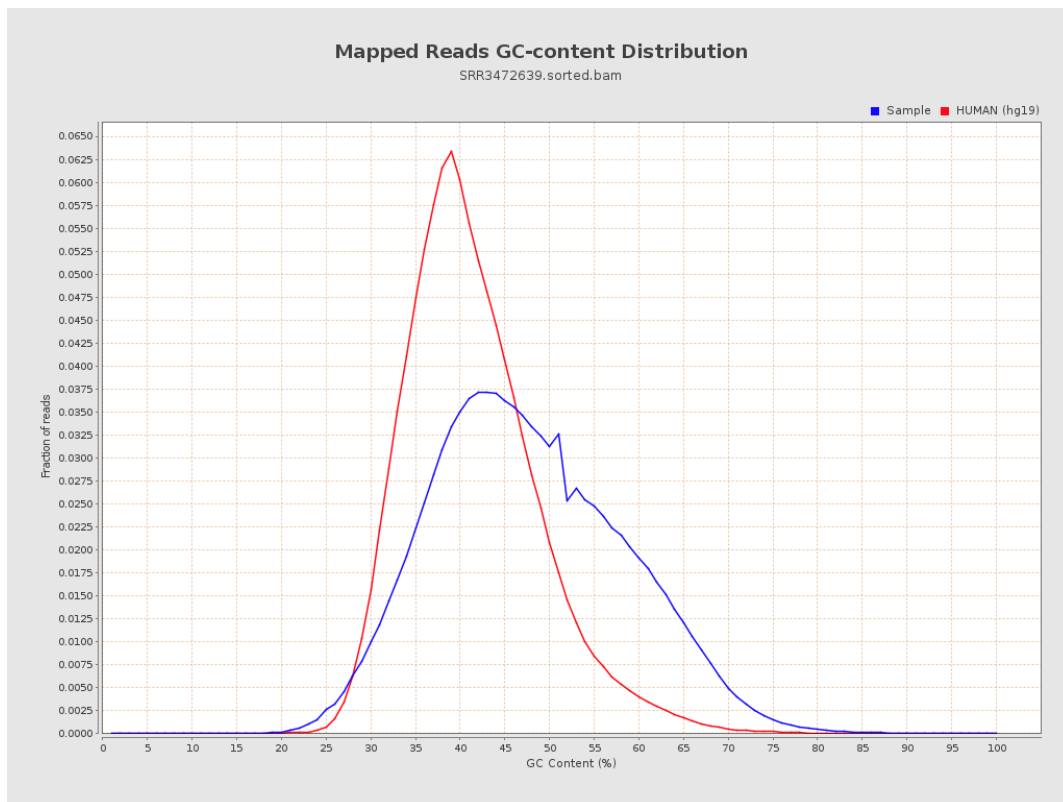
7. Results : Duplication Rate Histogram



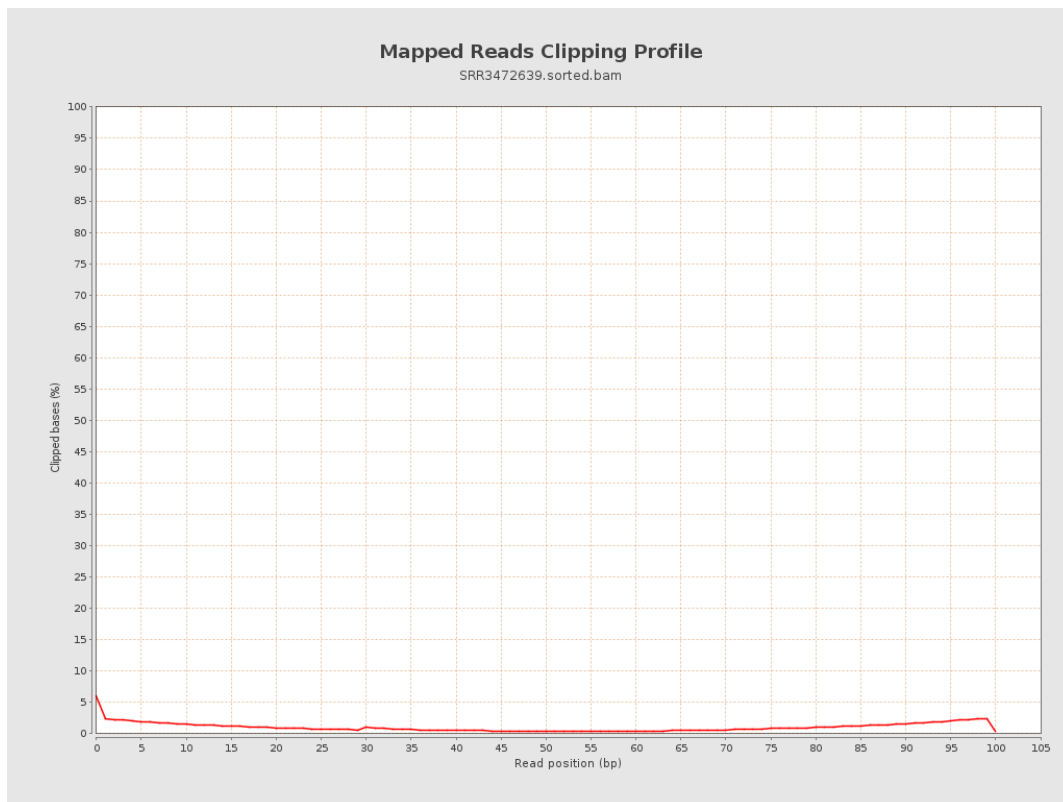
8. Results : Mapped Reads Nucleotide Content



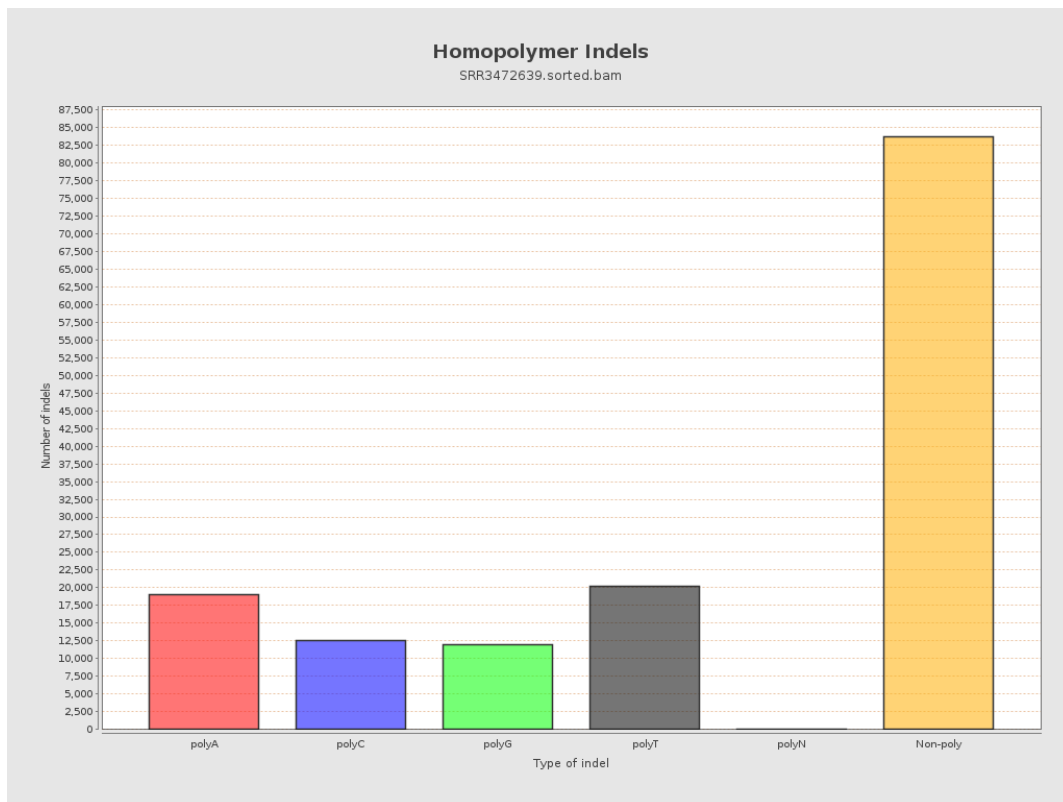
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



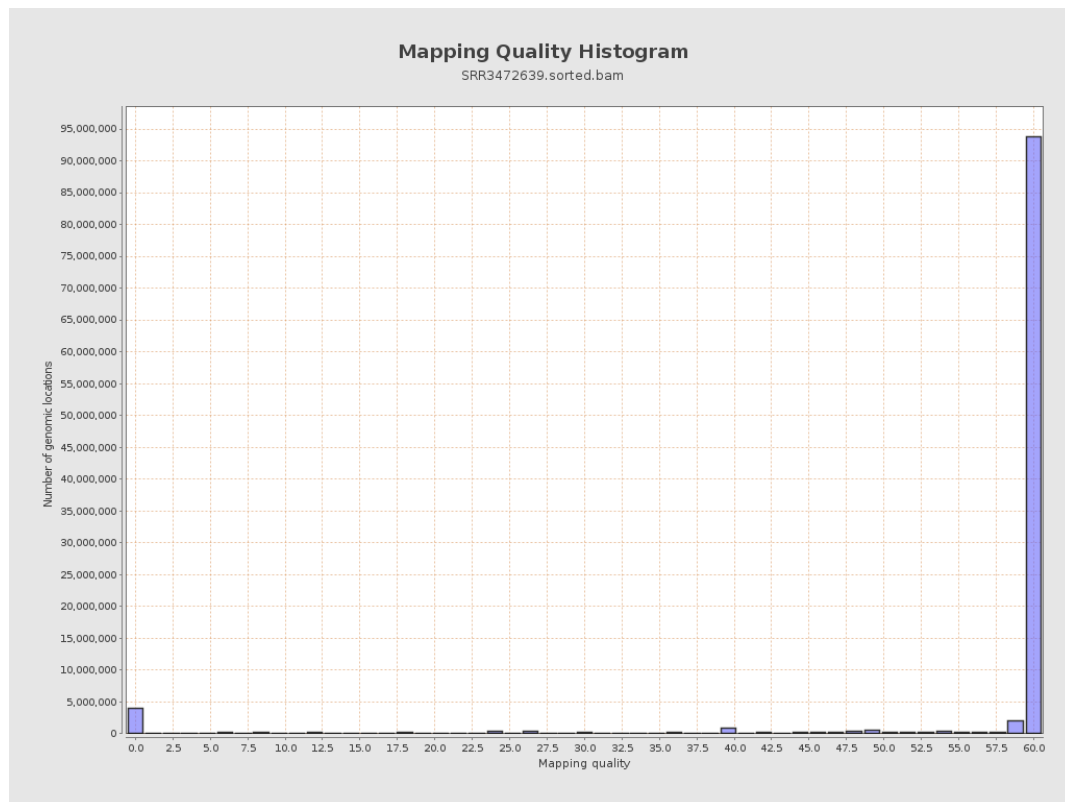
11. Results : Homopolymer Indels



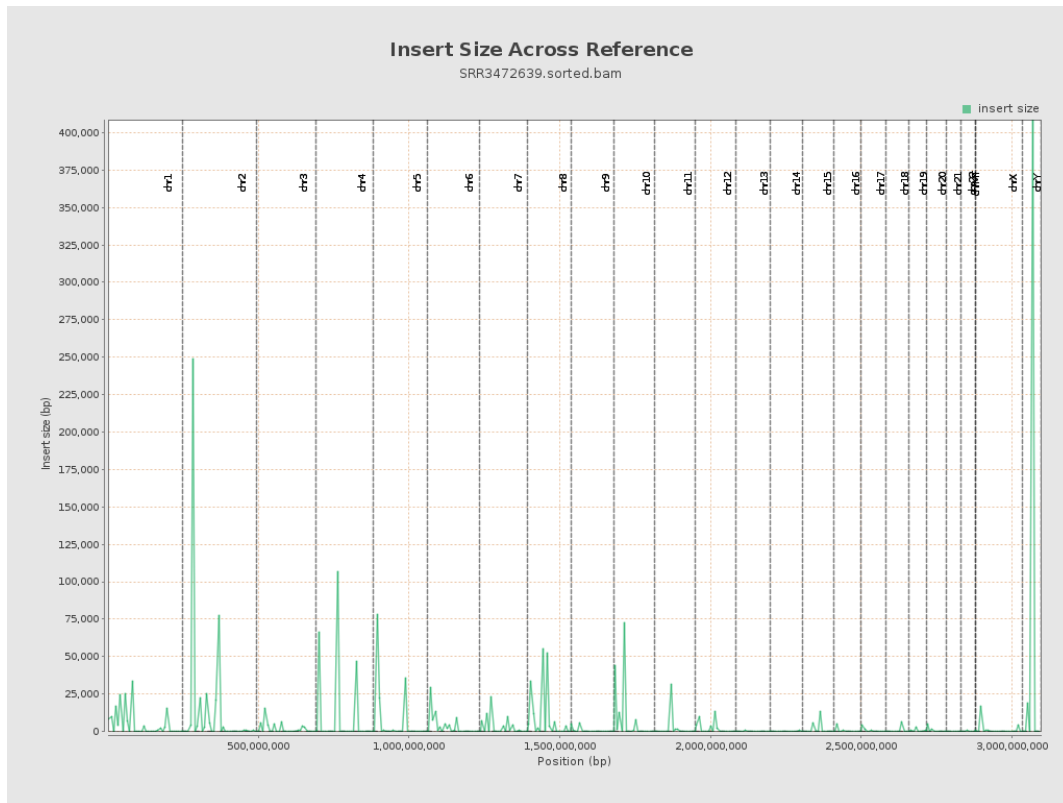
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

