

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 06:12:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472597.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_SRR3472597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472597_1.fastq.gz SRR3472597_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 06:12:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,134,244
Mapped reads	9,385,006 / 92.61%
Unmapped reads	749,238 / 7.39%
Mapped paired reads	9,385,006 / 92.61%
Mapped reads, first in pair	4,738,883 / 46.76%
Mapped reads, second in pair	4,646,123 / 45.85%
Mapped reads, both in pair	9,170,264 / 90.49%
Mapped reads, singletons	214,742 / 2.12%
Secondary alignments	0
Supplementary alignments	258,537 / 2.55%
Read min/max/mean length	30 / 100 / 100.99
Duplicated reads (estimated)	1,368,210 / 13.5%
Duplication rate	12.88%
Clipped reads	7,014,258 / 69.21%

2.2. ACGT Content

Number/percentage of A's	199,093,325 / 26.02%
Number/percentage of C's	153,024,402 / 20%
Number/percentage of T's	227,282,873 / 29.7%
Number/percentage of G's	185,266,517 / 24.21%
Number/percentage of N's	485,413 / 0.06%

GC Percentage	44.21%
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2.3. Coverage

Mean	0.2473
Standard Deviation	1.9726

2.4. Mapping Quality

Mean Mapping Quality	50.64
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2.5. Insert size

Mean	203,771.65
Standard Deviation	4,346,017.51
P25/Median/P75	91 / 129 / 178

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	8,847,800
Insertions	72,820
Mapped reads with at least one insertion	0.76%
Deletions	179,743
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.44%

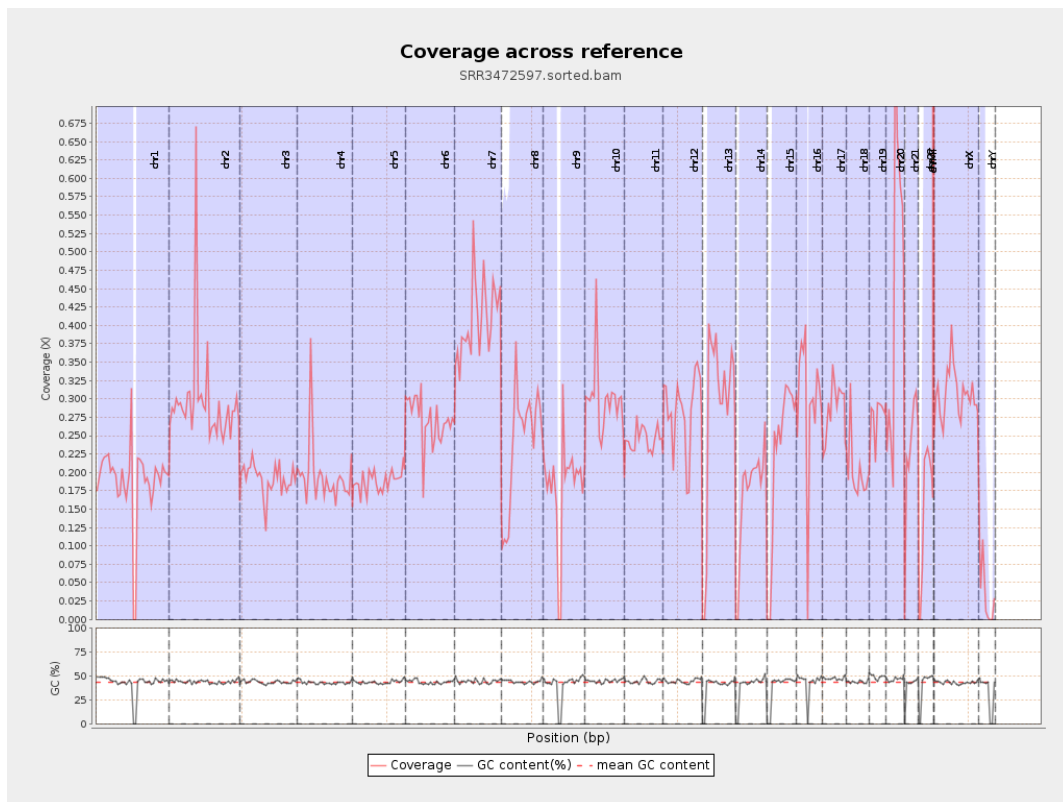
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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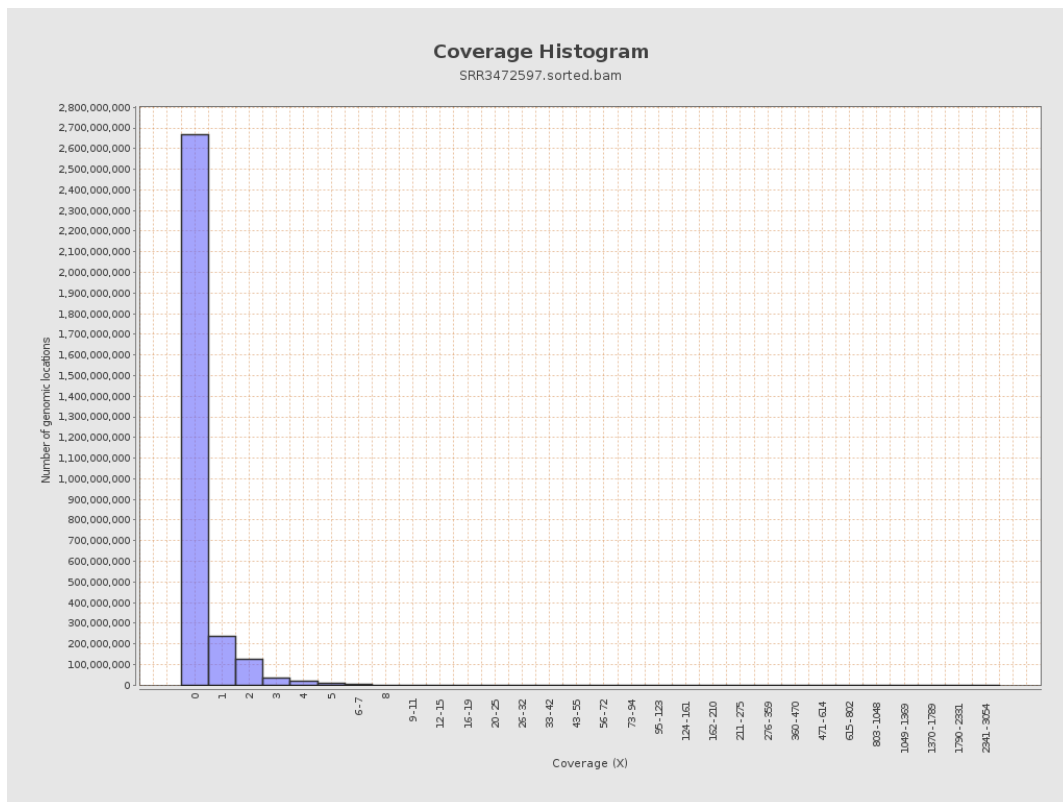
		bases	coverage	deviation
chr1	249250621	46826064	0.1879	2.5336
chr2	243199373	71921659	0.2957	3.0611
chr3	198022430	37810448	0.1909	0.6369
chr4	191154276	37001740	0.1936	1.1979
chr5	180915260	34056439	0.1882	0.6672
chr6	171115067	46354416	0.2709	1.1763
chr7	159138663	65197928	0.4097	3.5613
chr8	146364022	35180006	0.2404	1.7722
chr9	141213431	25306053	0.1792	2.3288
chr10	135534747	40488024	0.2987	2.1331
chr11	135006516	32939013	0.244	1.7672
chr12	133851895	37892710	0.2831	0.8234
chr13	115169878	32774230	0.2846	0.8241
chr14	107349540	18295183	0.1704	2.9306
chr15	102531392	23327078	0.2275	0.7275
chr16	90354753	26834748	0.297	1.3361
chr17	81195210	23391666	0.2881	1.5967
chr18	78077248	15749604	0.2017	3.5616
chr19	59128983	16221523	0.2743	1.8197
chr20	63025520	28658955	0.4547	1.268
chr21	48129895	11189225	0.2325	1.0234
chr22	51304566	7609626	0.1483	0.5722
chrMT	16571	755494	45.5913	25.7783
chrX	155270560	47683866	0.3071	1.1794

chrY	59373566	2027623	0.0342	1.0642
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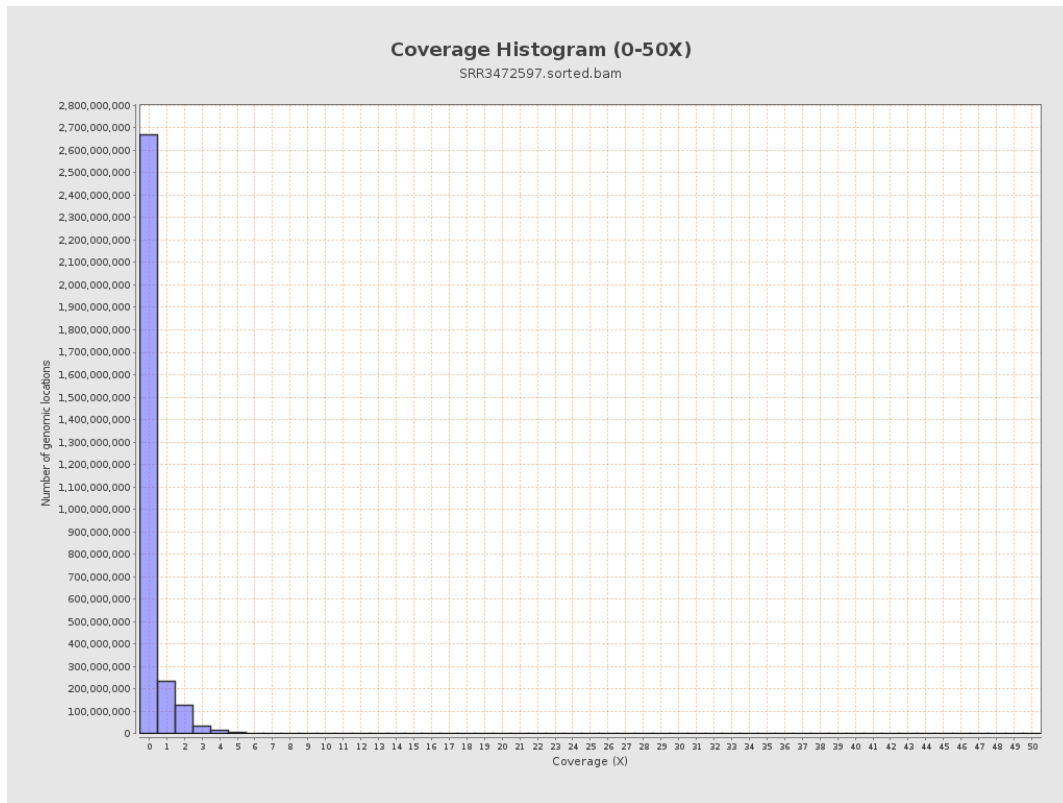
3. Results : Coverage across reference



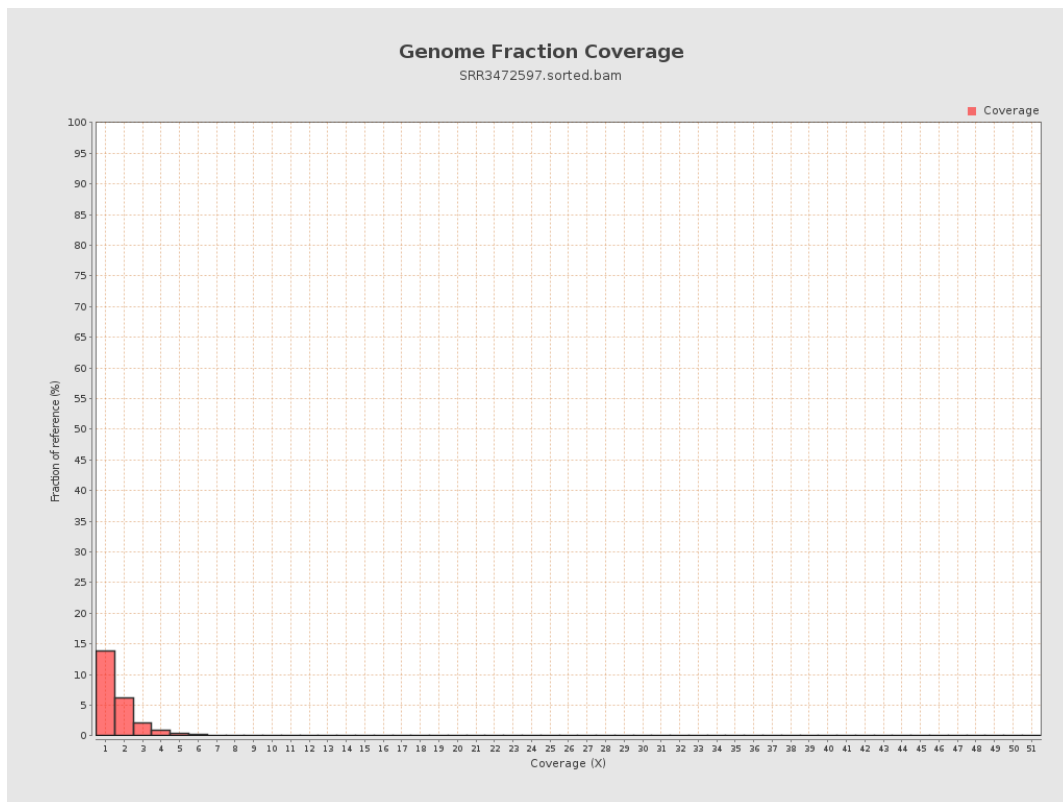
4. Results : Coverage Histogram



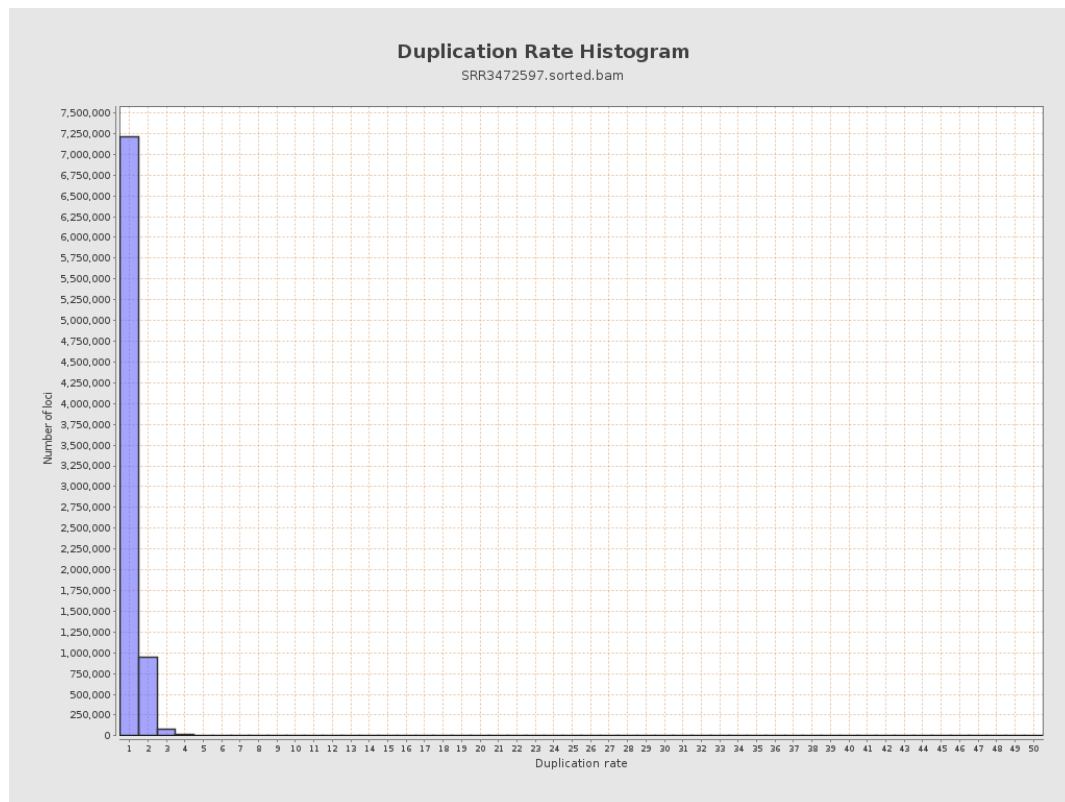
5. Results : Coverage Histogram (0-50X)



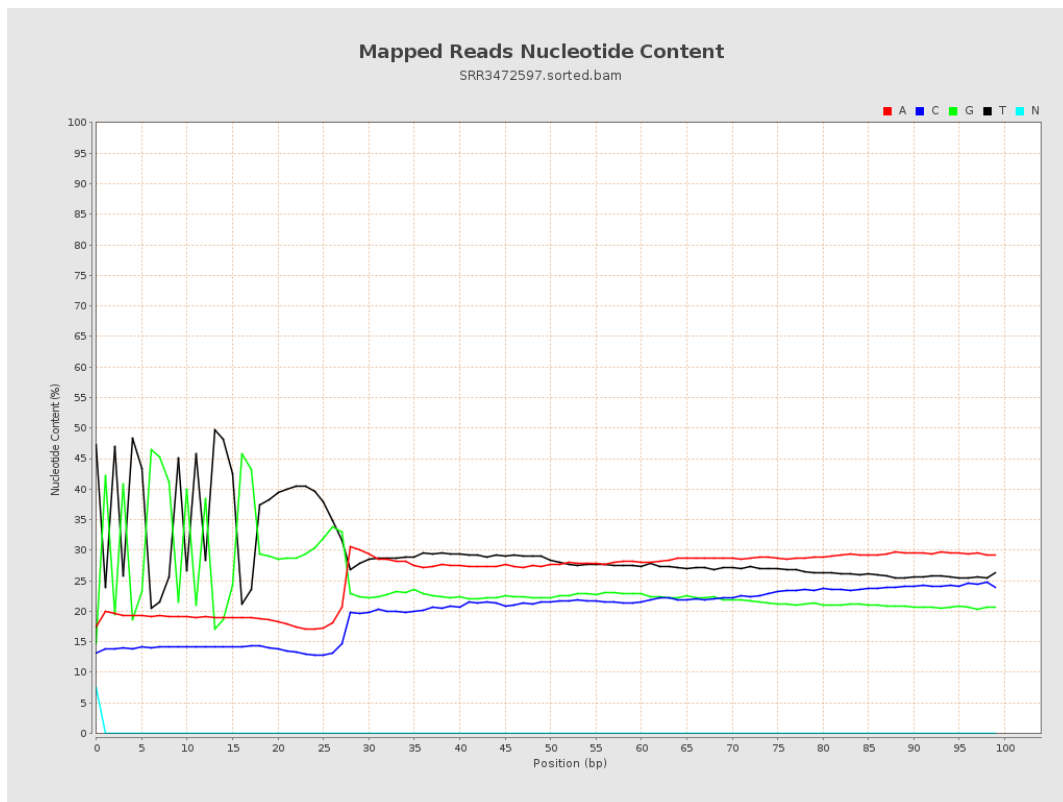
6. Results : Genome Fraction Coverage



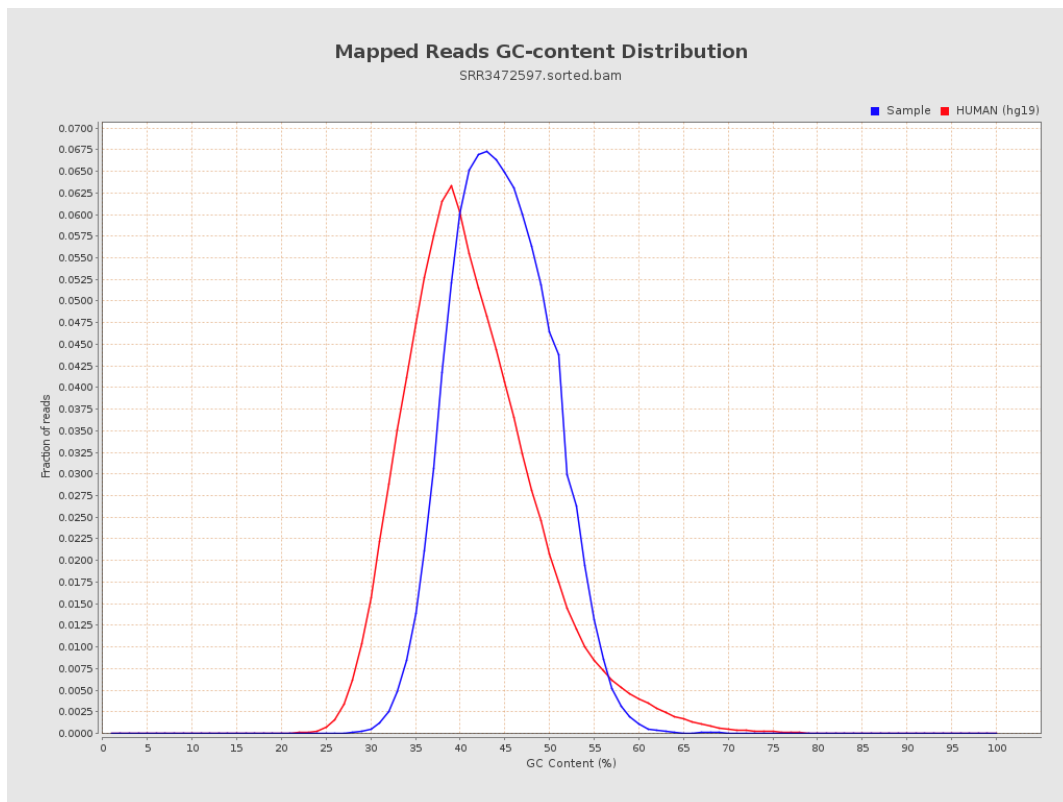
7. Results : Duplication Rate Histogram



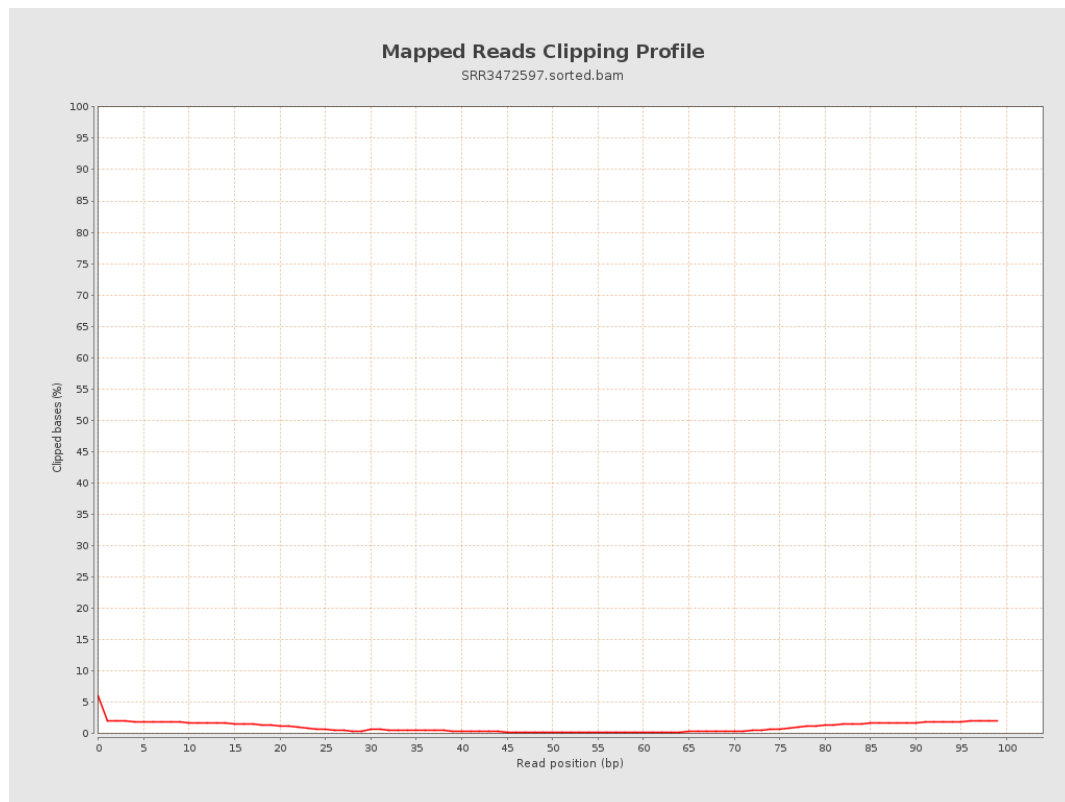
8. Results : Mapped Reads Nucleotide Content



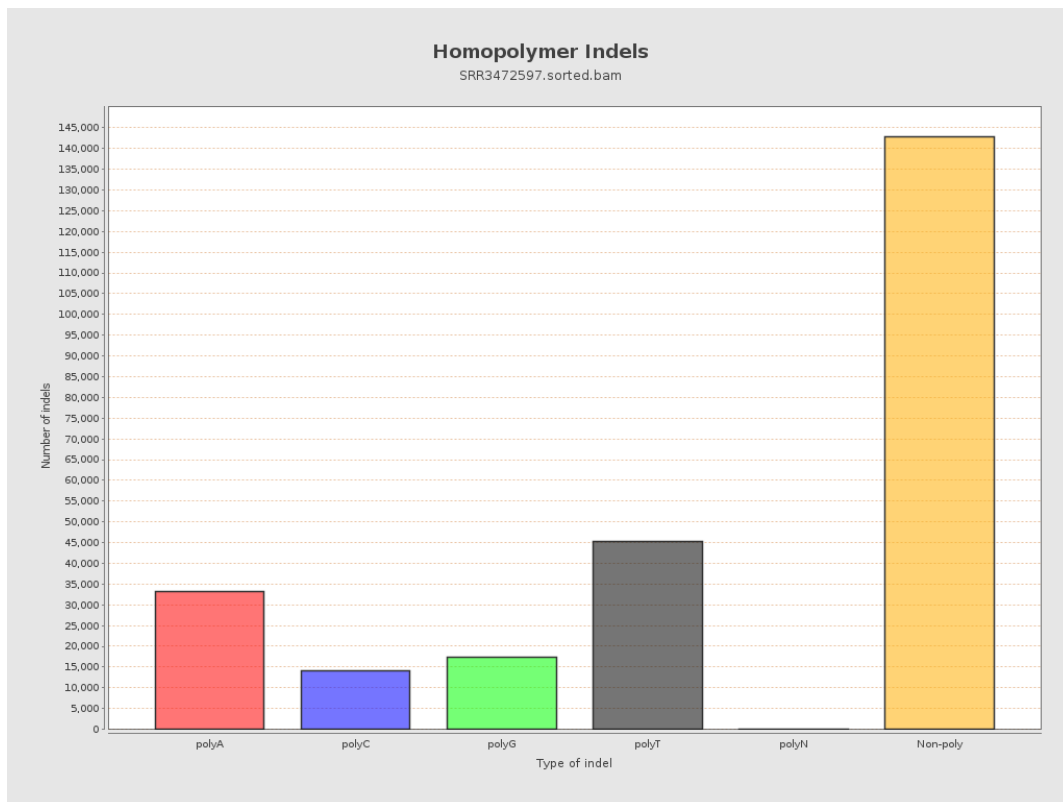
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



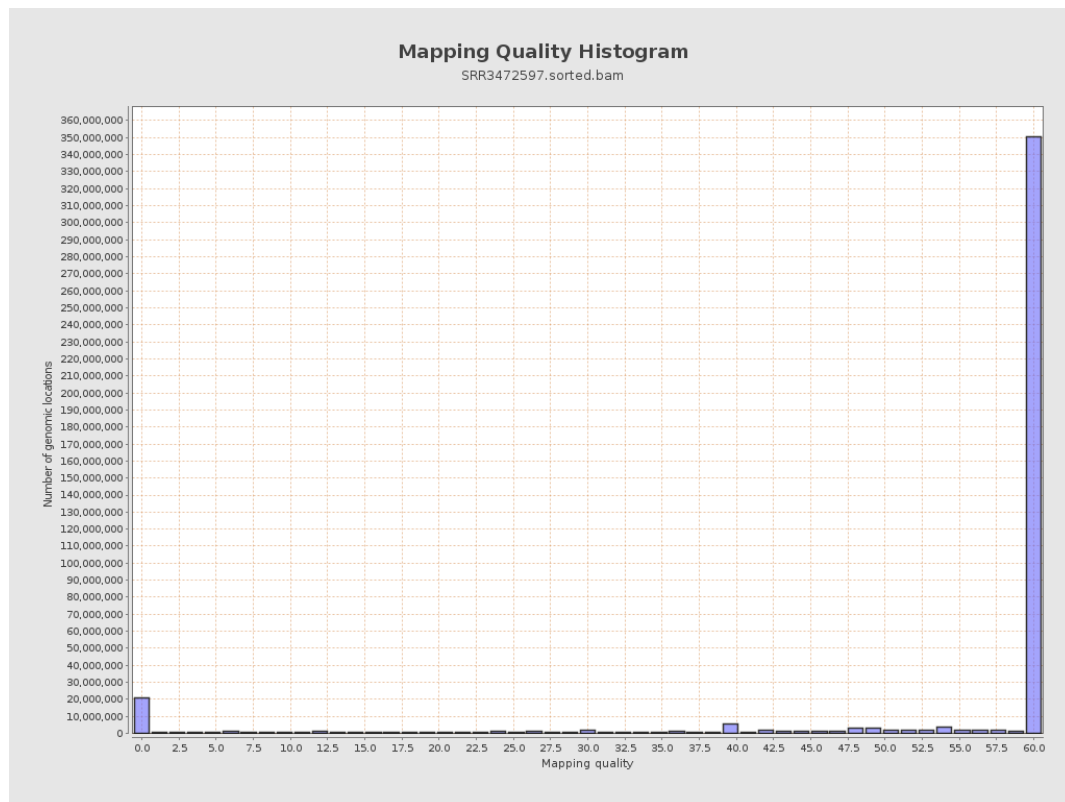
11. Results : Homopolymer Indels



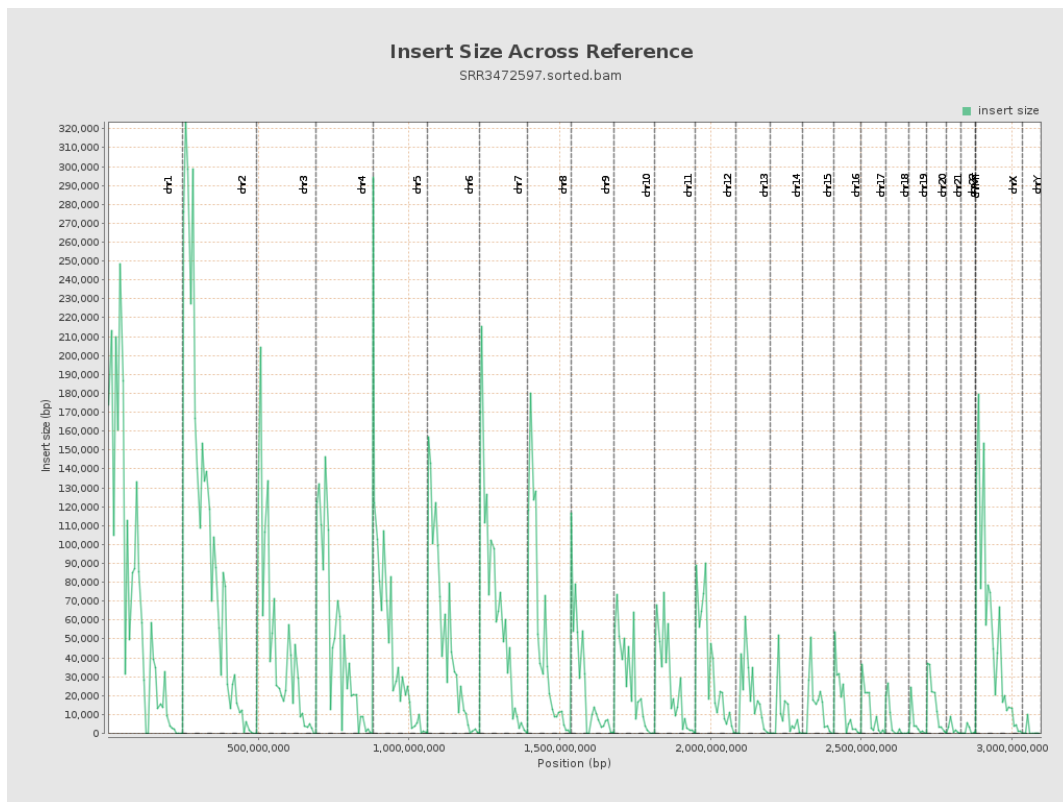
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

