

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:52:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472542.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_SRR3472542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472542_1.fastq.gz SRR3472542_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:52:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,719,678
Mapped reads	16,547,722 / 98.97%
Unmapped reads	171,956 / 1.03%
Mapped paired reads	16,547,722 / 98.97%
Mapped reads, first in pair	8,308,868 / 49.7%
Mapped reads, second in pair	8,238,854 / 49.28%
Mapped reads, both in pair	16,441,832 / 98.34%
Mapped reads, singletons	105,890 / 0.63%
Secondary alignments	0
Supplementary alignments	71,942 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,367,151 / 62.01%
Duplication rate	46.49%
Clipped reads	1,331,607 / 7.96%

2.2. ACGT Content

Number/percentage of A's	445,849,728 / 27.35%
Number/percentage of C's	372,178,834 / 22.83%
Number/percentage of T's	443,166,493 / 27.18%
Number/percentage of G's	368,982,855 / 22.63%
Number/percentage of N's	253,982 / 0.02%

GC Percentage	45.46%
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2.3. Coverage

Mean	0.5267
Standard Deviation	18.6815

2.4. Mapping Quality

Mean Mapping Quality	55.07
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2.5. Insert size

Mean	33,817.1
Standard Deviation	1,808,259.08
P25/Median/P75	171 / 238 / 319

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,807,012
Insertions	89,703
Mapped reads with at least one insertion	0.53%
Deletions	83,686
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.65%

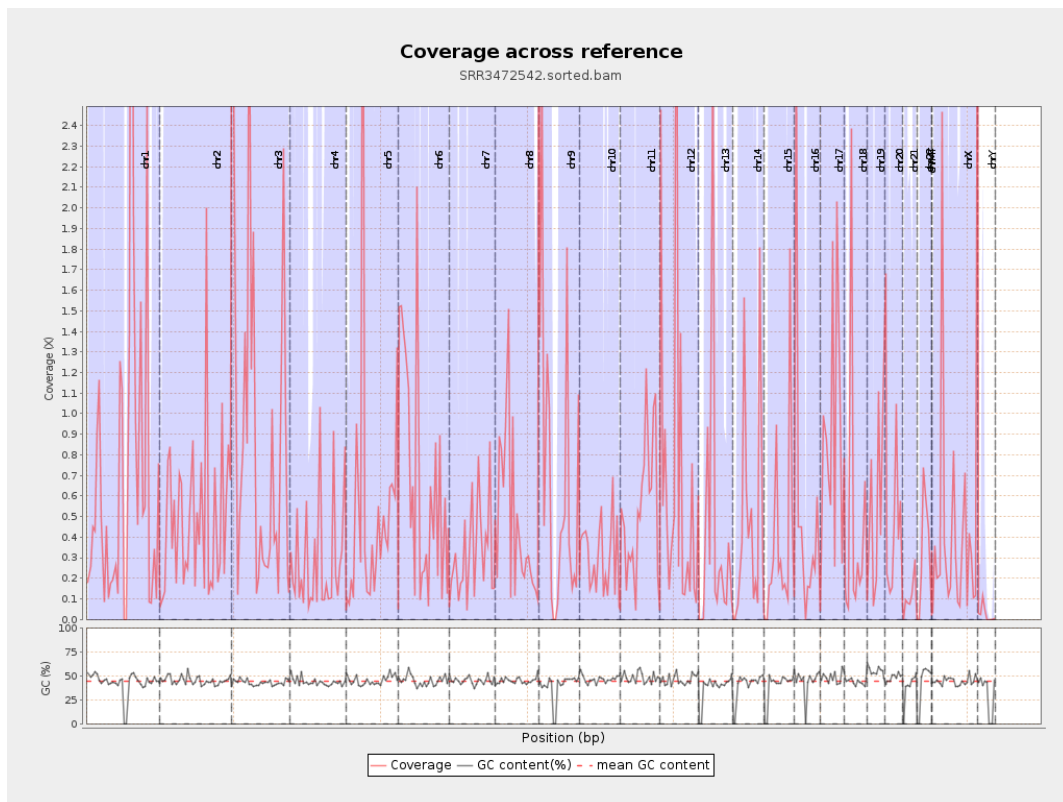
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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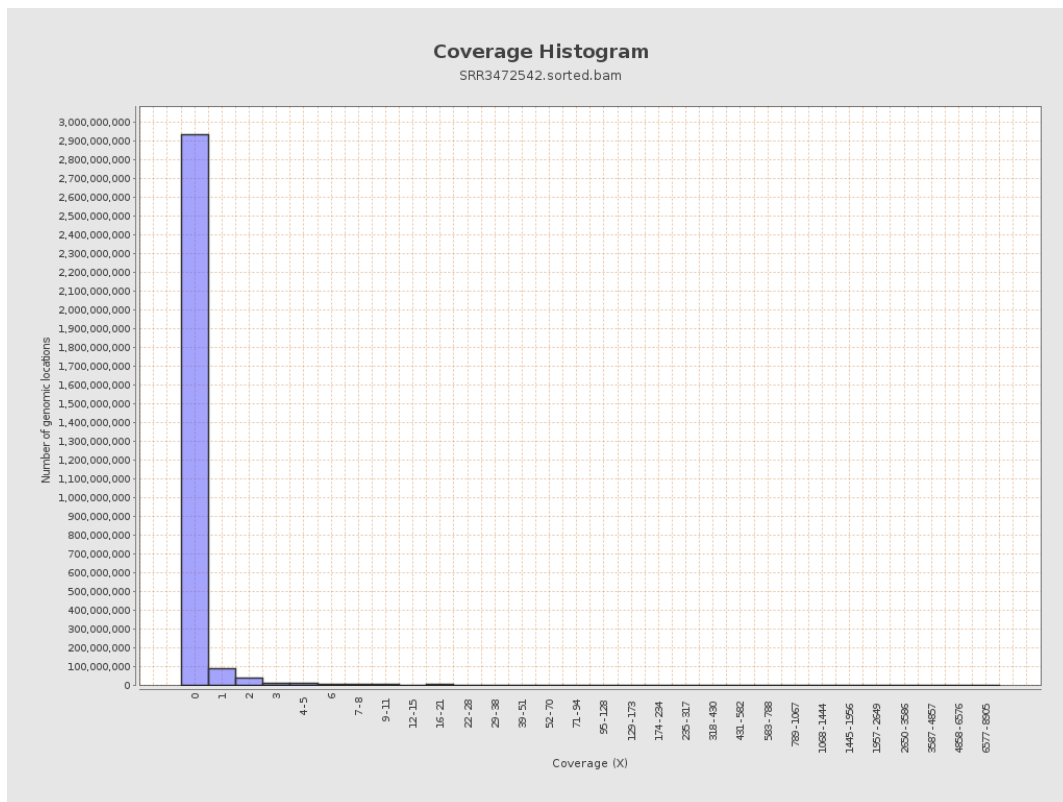
		bases	coverage	deviation
chr1	249250621	185830942	0.7456	29.4743
chr2	243199373	117795221	0.4844	18.2474
chr3	198022430	186249410	0.9405	21.1368
chr4	191154276	54222630	0.2837	9.8825
chr5	180915260	100610117	0.5561	19.0734
chr6	171115067	113736487	0.6647	20.1709
chr7	159138663	51439364	0.3232	8.5
chr8	146364022	68327883	0.4668	14.5892
chr9	141213431	97787122	0.6925	17.1907
chr10	135534747	42134465	0.3109	9.8453
chr11	135006516	72595846	0.5377	15.9957
chr12	133851895	98125165	0.7331	28.4667
chr13	115169878	46408699	0.403	17.0375
chr14	107349540	48349547	0.4504	23.5892
chr15	102531392	38418231	0.3747	12.5169
chr16	90354753	45061545	0.4987	12.6853
chr17	81195210	72138790	0.8885	21.698
chr18	78077248	34571227	0.4428	31.4549
chr19	59128983	33470602	0.5661	14.4128
chr20	63025520	32963101	0.523	13.8981
chr21	48129895	5565064	0.1156	4.3145
chr22	51304566	16770957	0.3269	12.5247
chrMT	16571	5484	0.3309	1.1562
chrX	155270560	66443292	0.4279	13.1792

chrY	59373566	1621583	0.0273	0.7635
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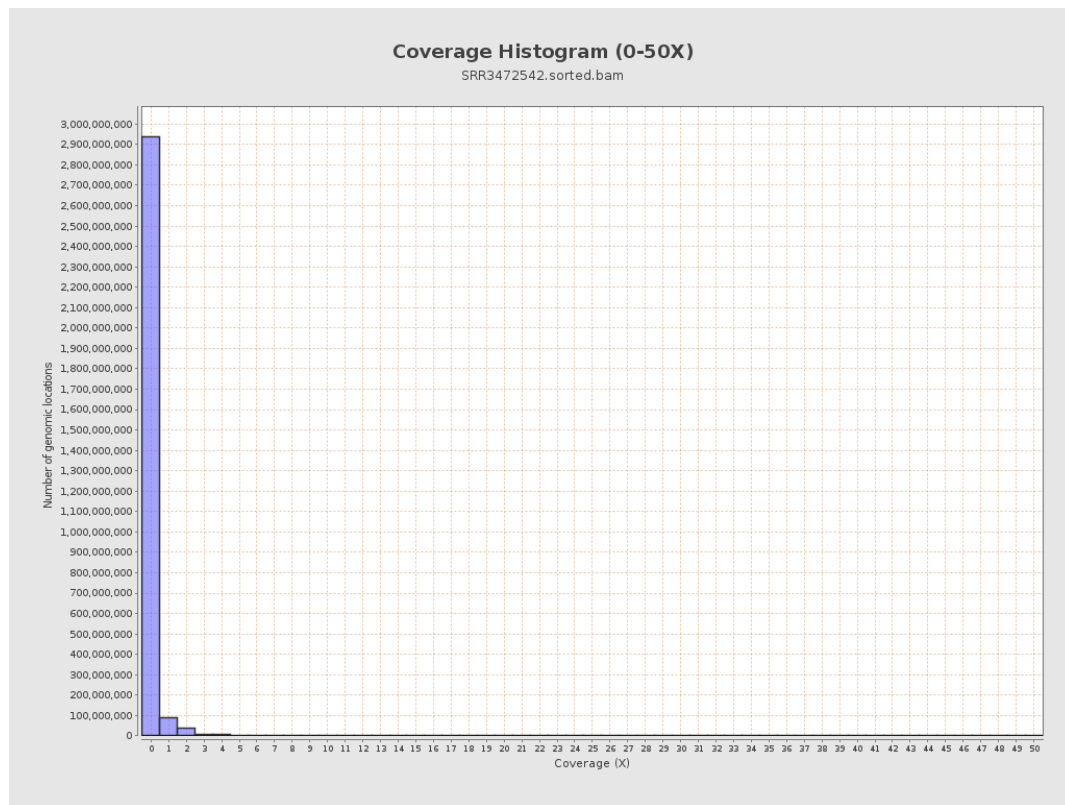
3. Results : Coverage across reference



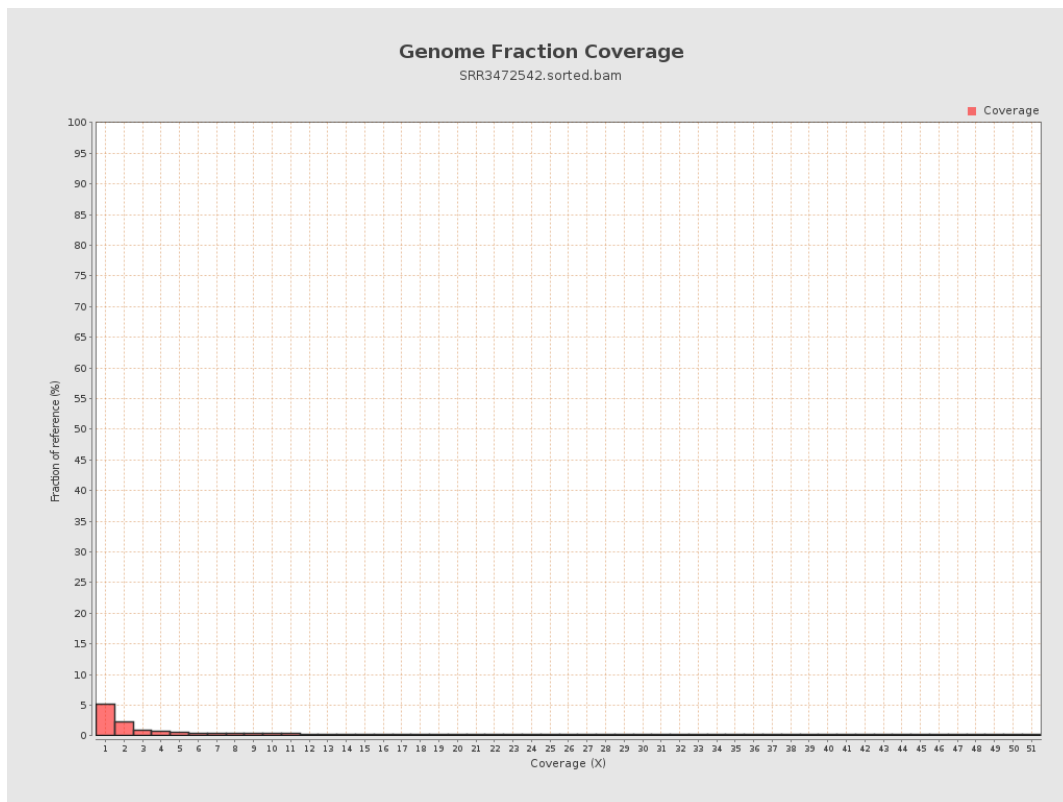
4. Results : Coverage Histogram



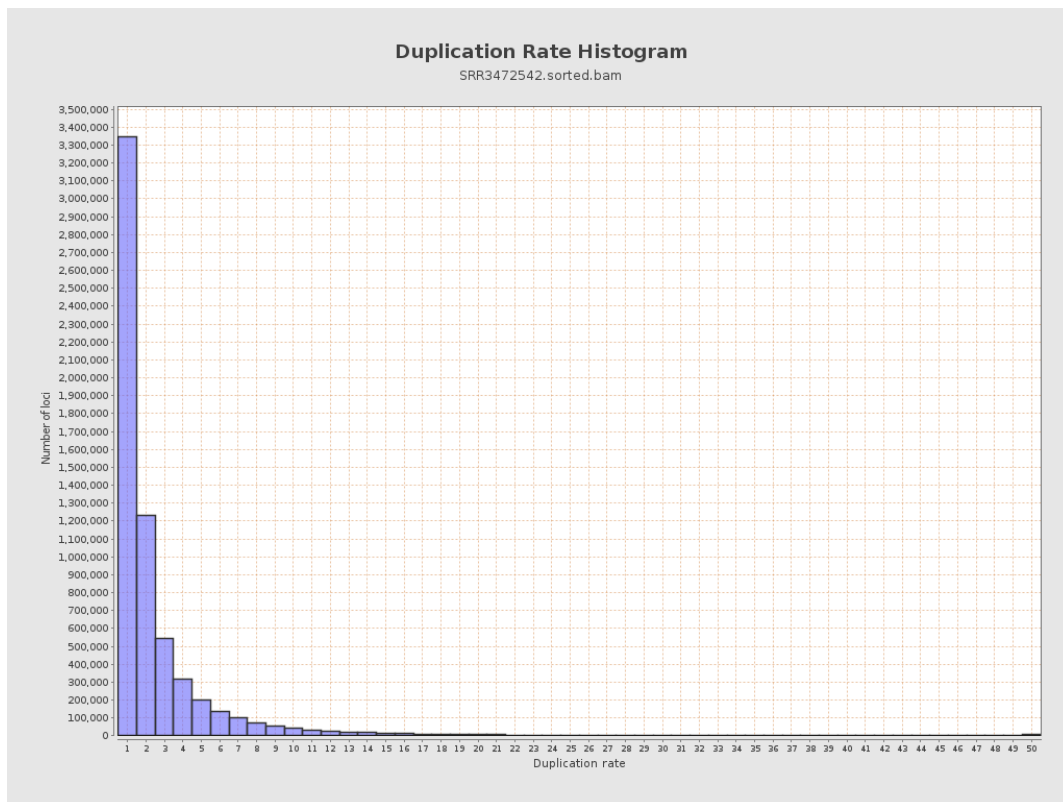
5. Results : Coverage Histogram (0-50X)



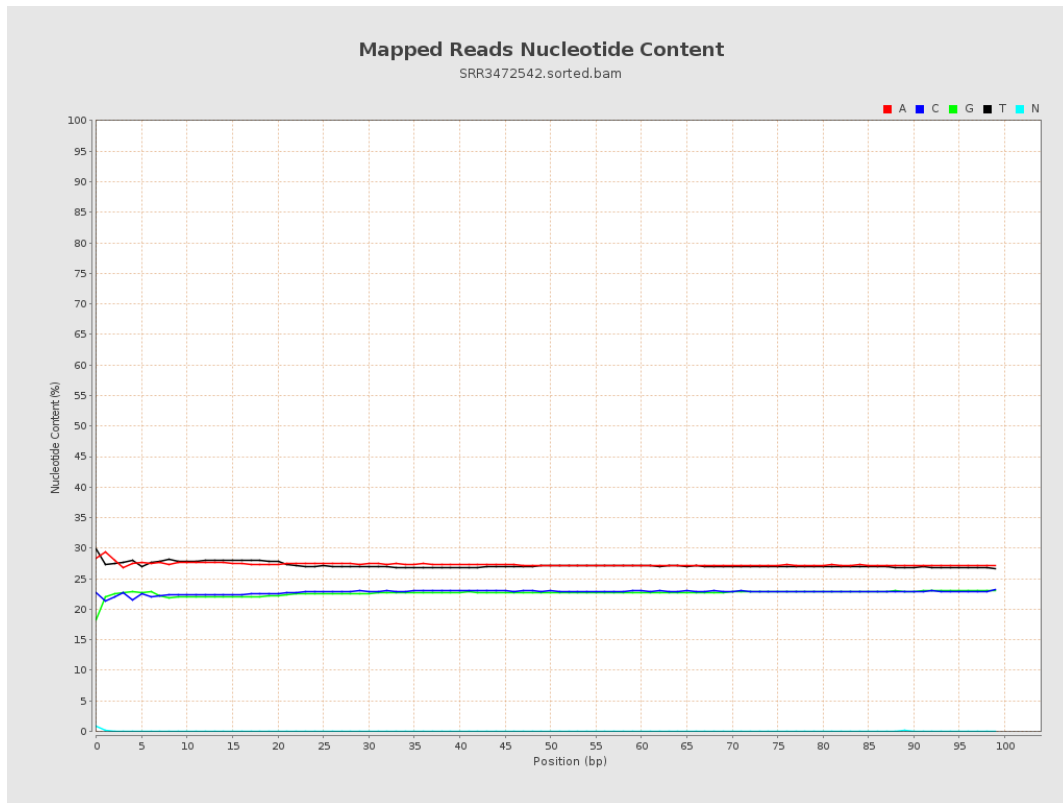
6. Results : Genome Fraction Coverage



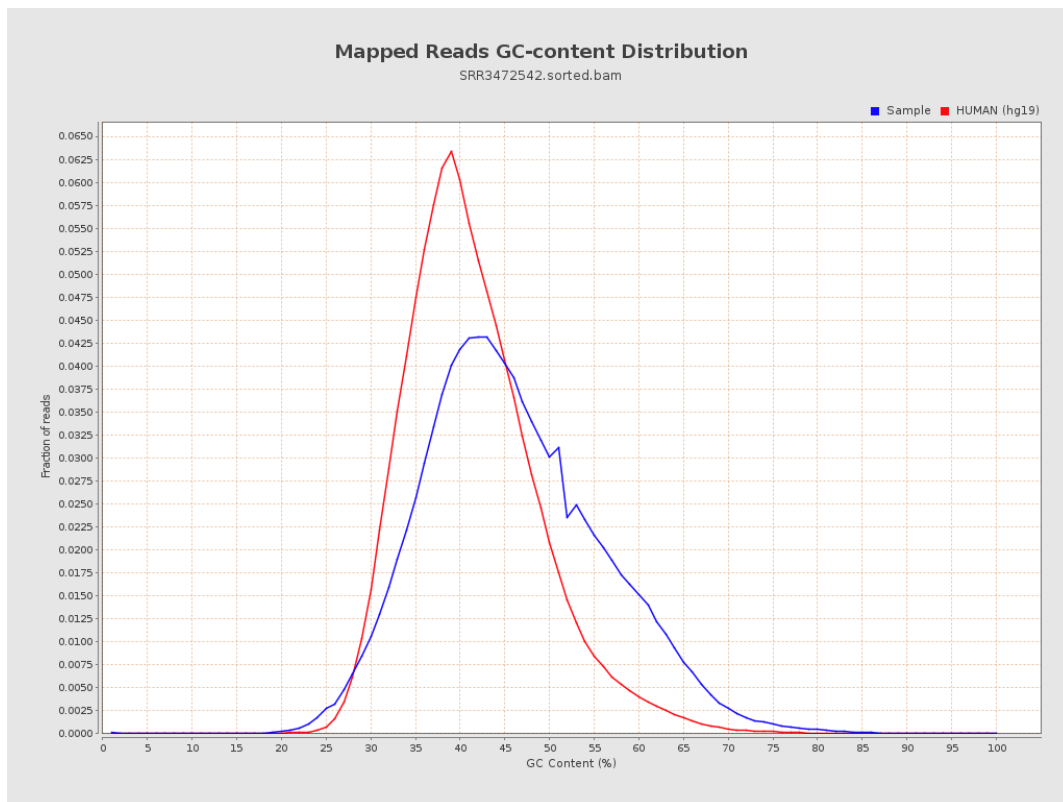
7. Results : Duplication Rate Histogram



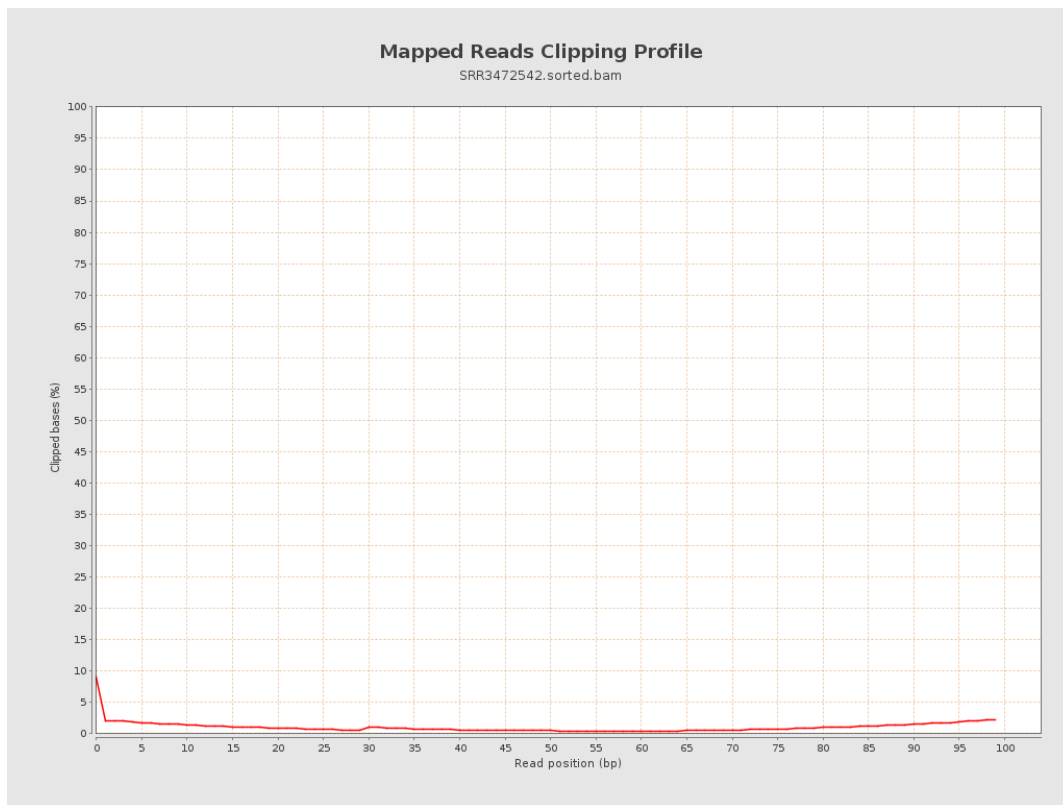
8. Results : Mapped Reads Nucleotide Content



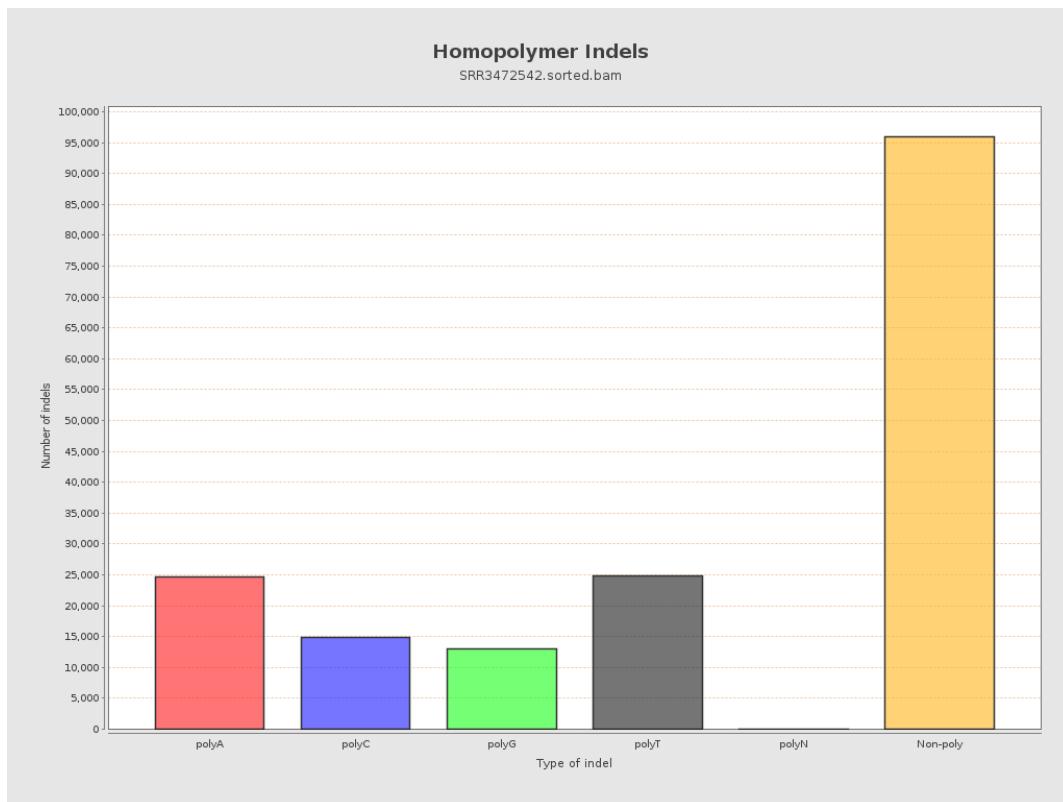
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



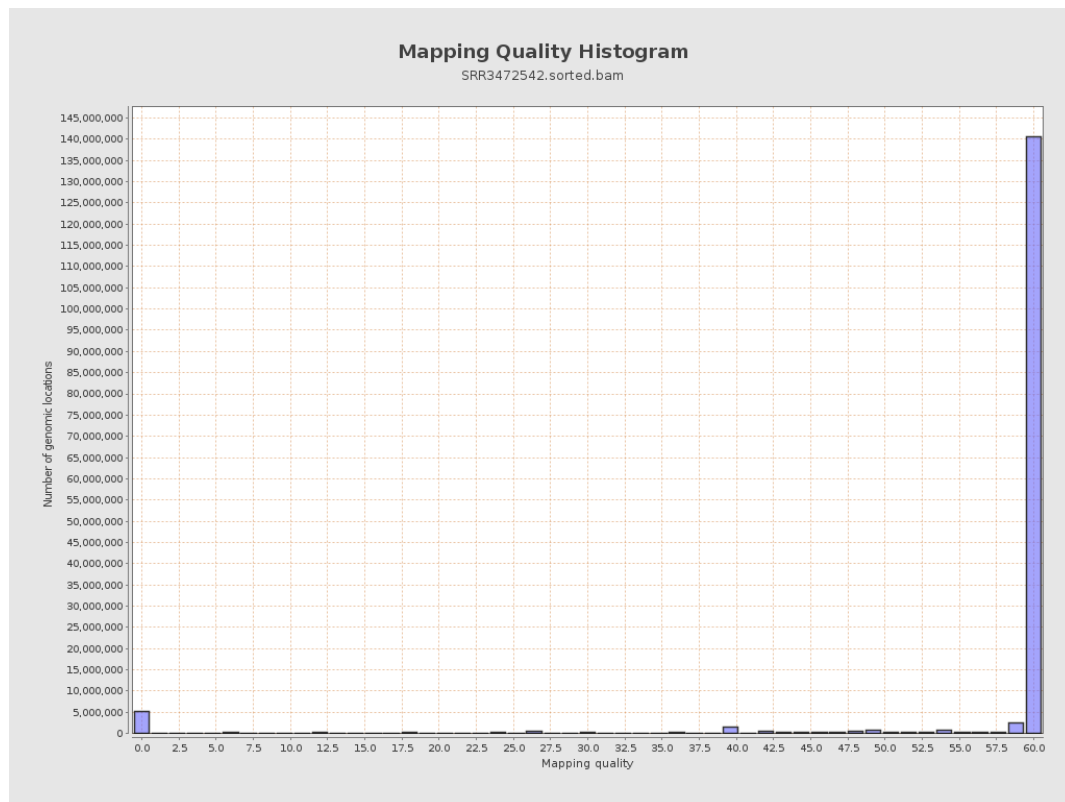
11. Results : Homopolymer Indels



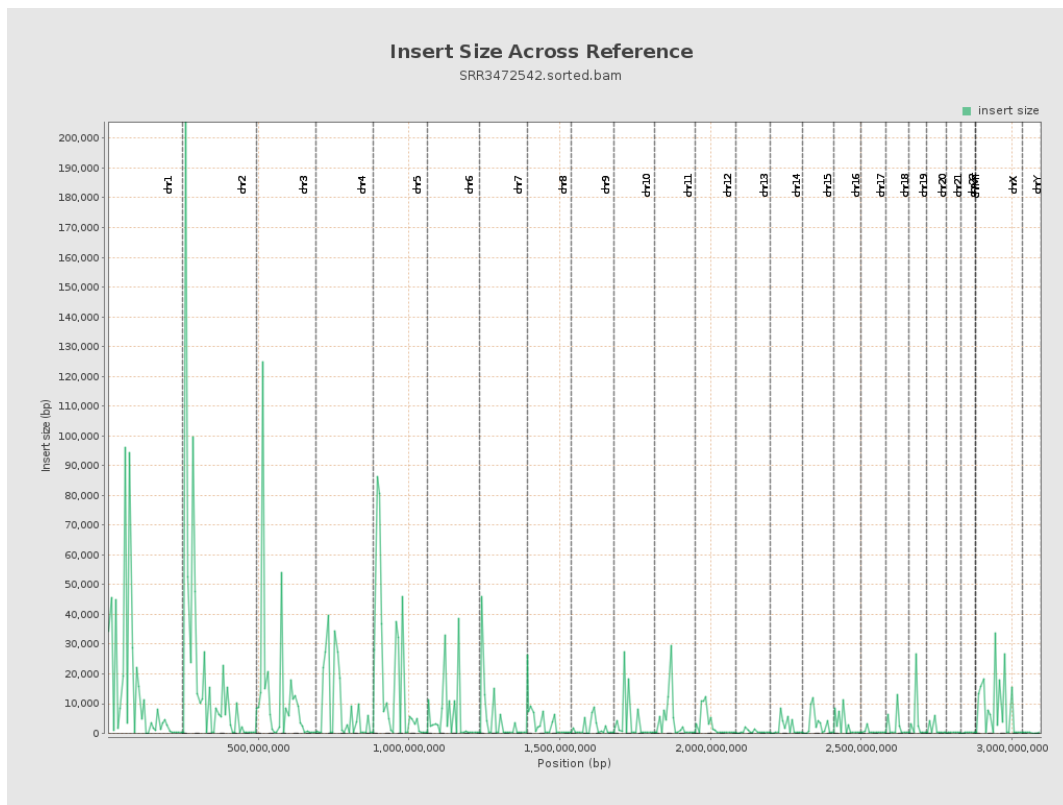
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

