

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 00:39:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174042.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_SRR10174042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174042_1.fastq.gz SRR10174042_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 00:39:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,134,702
Mapped reads	4,037,406 / 97.65%
Unmapped reads	97,296 / 2.35%
Mapped paired reads	4,037,406 / 97.65%
Mapped reads, first in pair	2,018,669 / 48.82%
Mapped reads, second in pair	2,018,737 / 48.82%
Mapped reads, both in pair	3,971,978 / 96.06%
Mapped reads, singletons	65,428 / 1.58%
Secondary alignments	0
Supplementary alignments	419,627 / 10.15%
Read min/max/mean length	30 / 133 / 128.38
Duplicated reads (estimated)	3,146,748 / 76.11%
Duplication rate	64.64%
Clipped reads	1,592,001 / 38.5%

2.2. ACGT Content

Number/percentage of A's	145,337,370 / 30.33%
Number/percentage of C's	92,749,392 / 19.36%
Number/percentage of T's	145,024,877 / 30.27%
Number/percentage of G's	96,033,878 / 20.04%
Number/percentage of N's	6,222 / 0%

GC Percentage	39.4%
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2.3. Coverage

Mean	0.1549
Standard Deviation	2.3295

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	938,478.55
Standard Deviation	8,915,841.94
P25/Median/P75	144 / 199 / 283

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	4,751,660
Insertions	48,972
Mapped reads with at least one insertion	1.17%
Deletions	109,872
Mapped reads with at least one deletion	2.66%
Homopolymer indels	43.09%

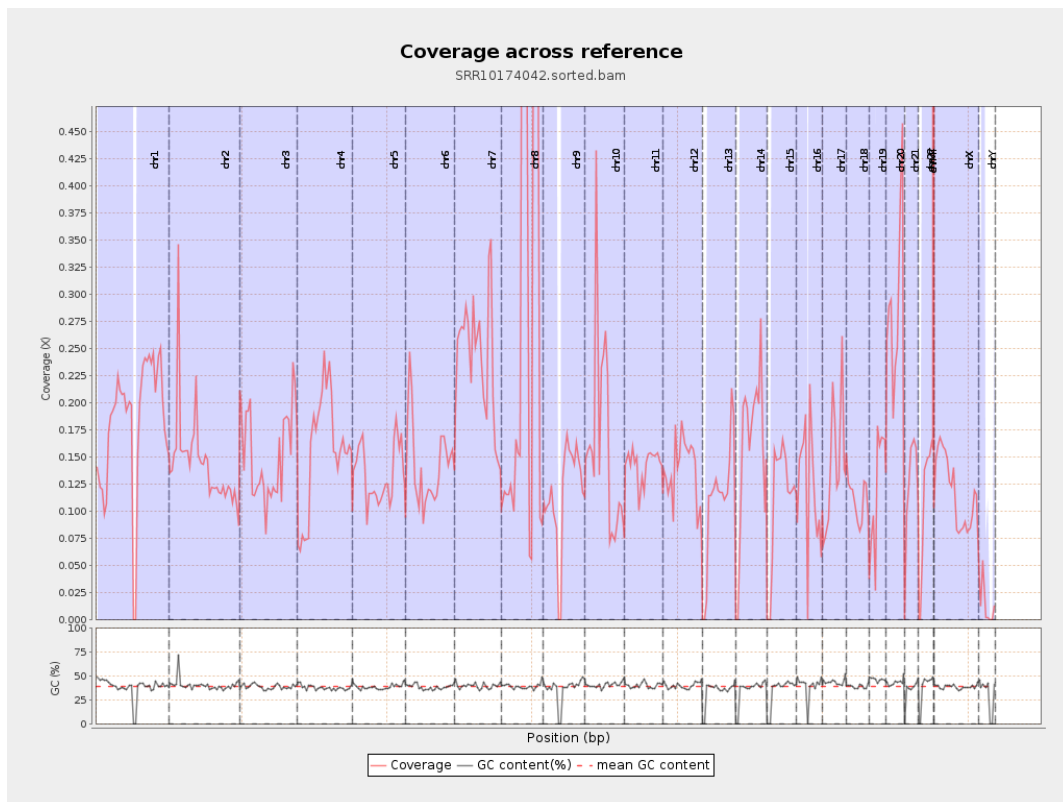
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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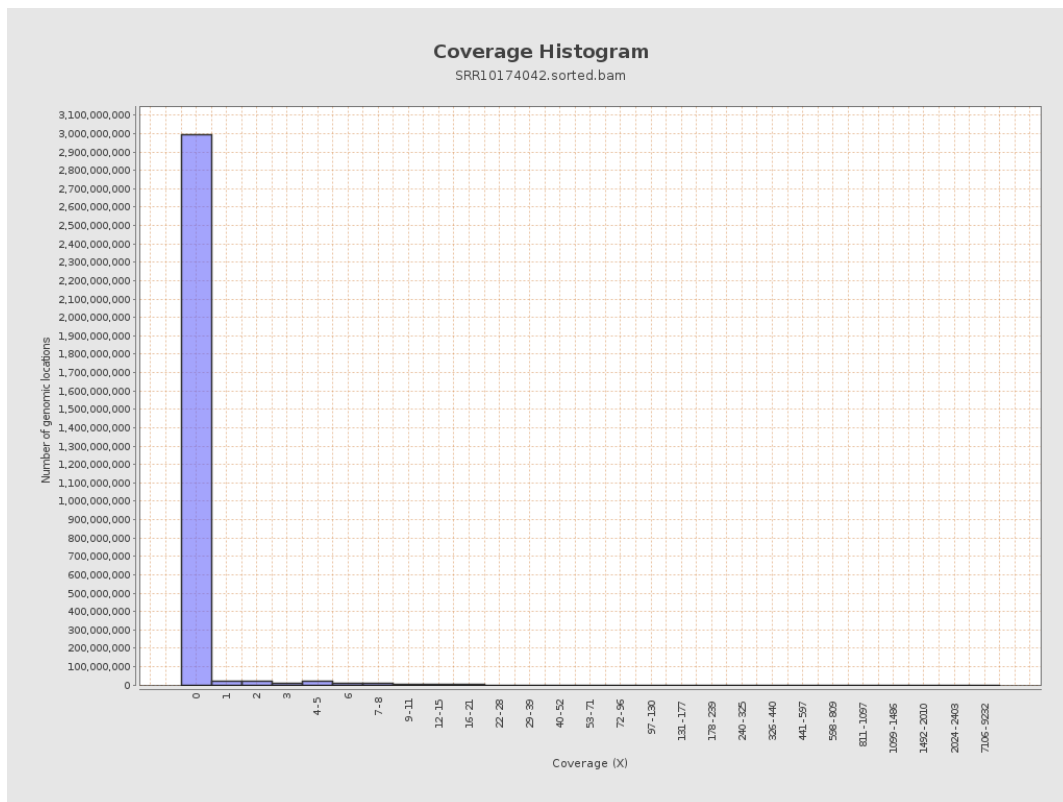
		bases	coverage	deviation
chr1	249250621	45192070	0.1813	1.4363
chr2	243199373	35141287	0.1445	6.5143
chr3	198022430	30103458	0.152	1.1464
chr4	191154276	29603602	0.1549	1.3427
chr5	180915260	24243893	0.134	1.0625
chr6	171115067	24003414	0.1403	1.1227
chr7	159138663	38709832	0.2432	2.4032
chr8	146364022	47282418	0.323	1.9441
chr9	141213431	16386198	0.116	1.1571
chr10	135534747	22041928	0.1626	3.3648
chr11	135006516	19142834	0.1418	1.1059
chr12	133851895	18570846	0.1387	1.0839
chr13	115169878	12783685	0.111	0.9765
chr14	107349540	16779989	0.1563	1.1491
chr15	102531392	11530972	0.1125	0.9649
chr16	90354753	10871916	0.1203	1.2625
chr17	81195210	11666311	0.1437	1.2108
chr18	78077248	8659465	0.1109	1.5225
chr19	59128983	7120264	0.1204	1.153
chr20	63025520	18208430	0.2889	1.5623
chr21	48129895	5958274	0.1238	1.0577
chr22	51304566	5429798	0.1058	0.8937
chrMT	16571	1045507	63.0926	56.9601
chrX	155270560	18157927	0.1169	0.9971

chrY	59373566	793673	0.0134	0.5833
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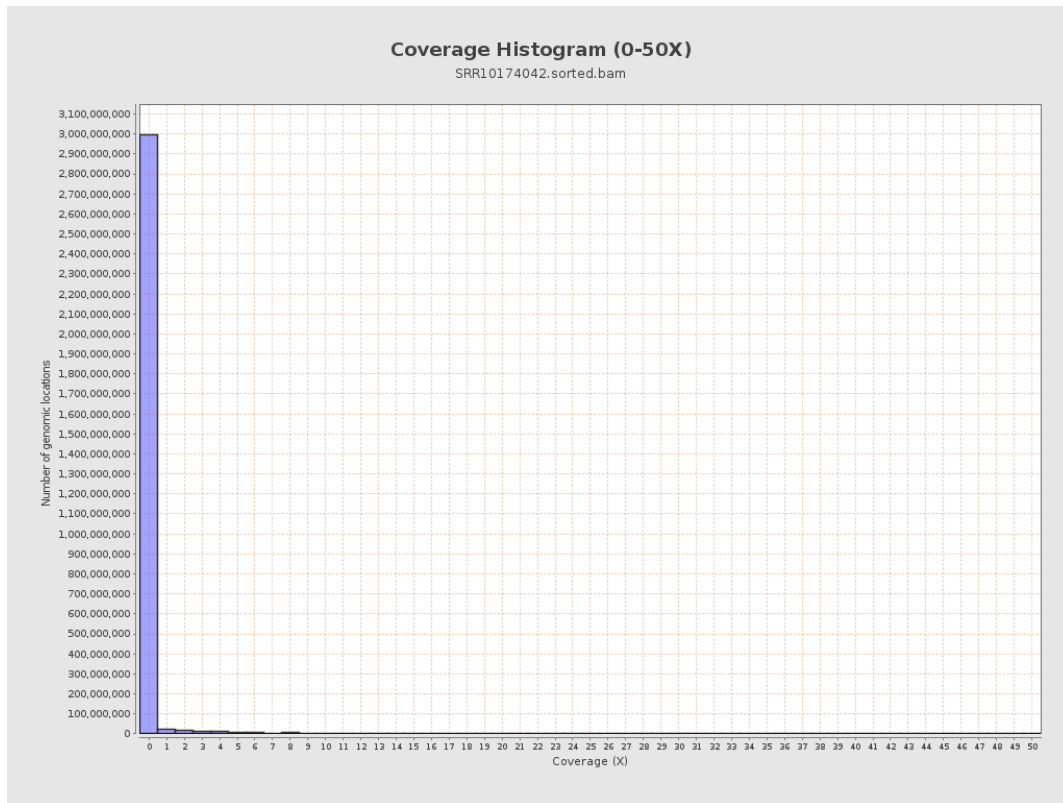
3. Results : Coverage across reference



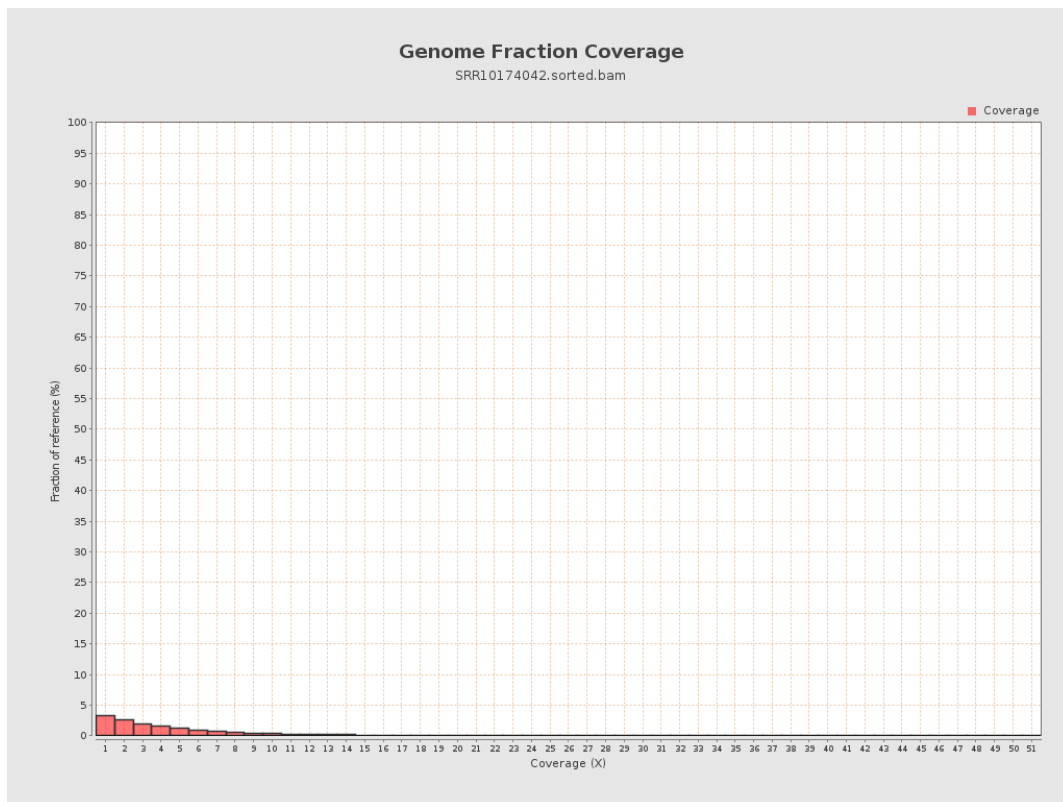
4. Results : Coverage Histogram



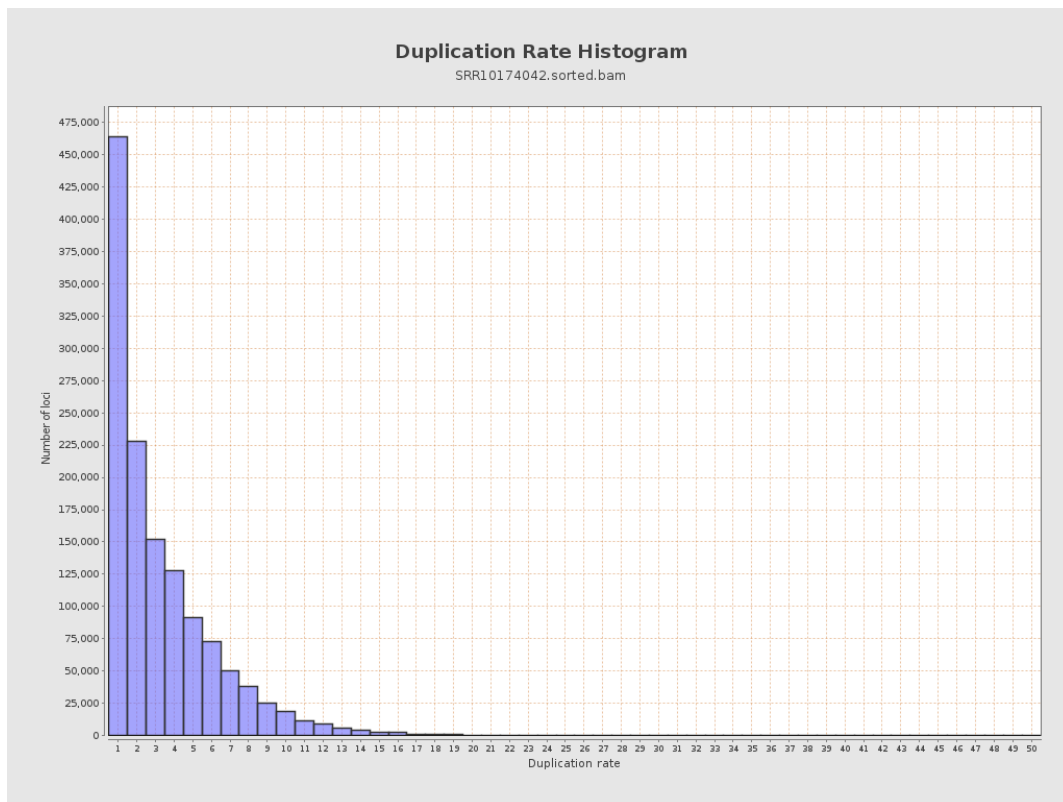
5. Results : Coverage Histogram (0-50X)



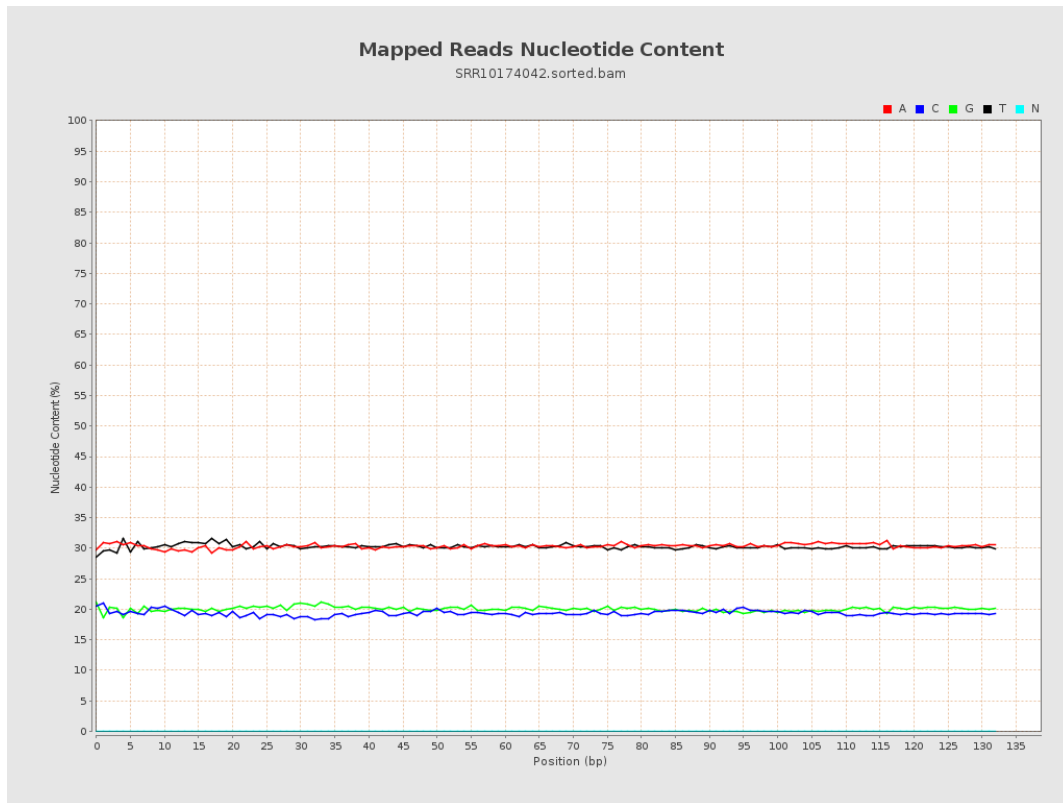
6. Results : Genome Fraction Coverage



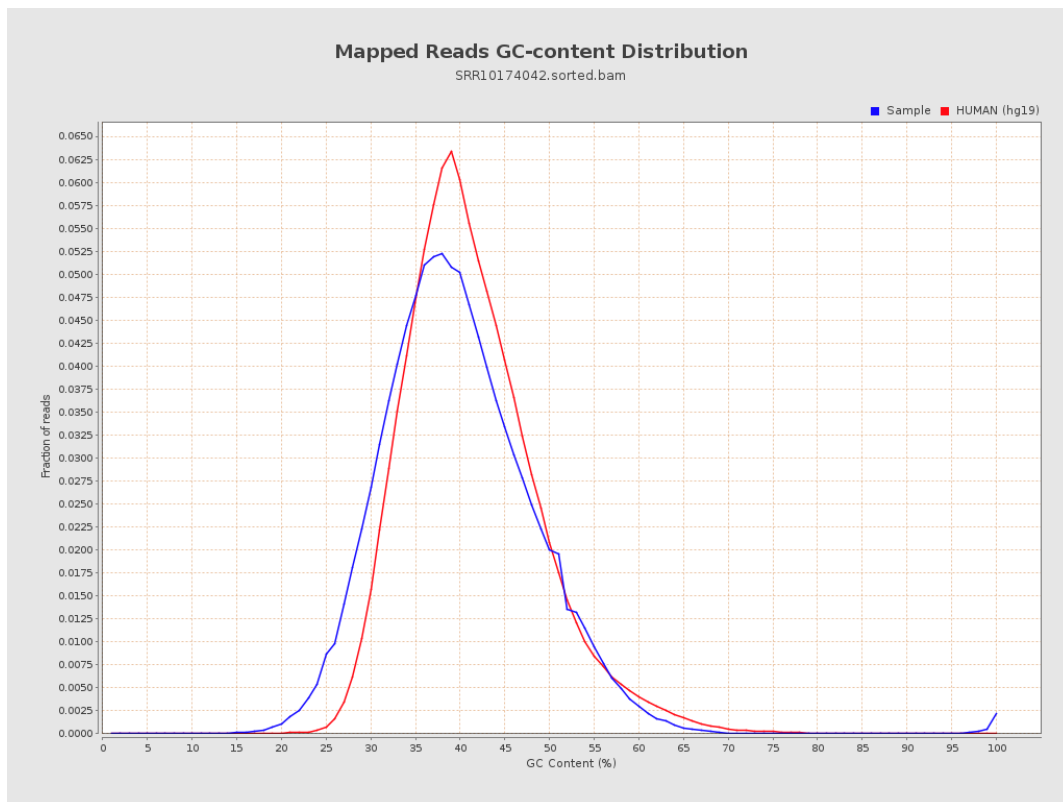
7. Results : Duplication Rate Histogram



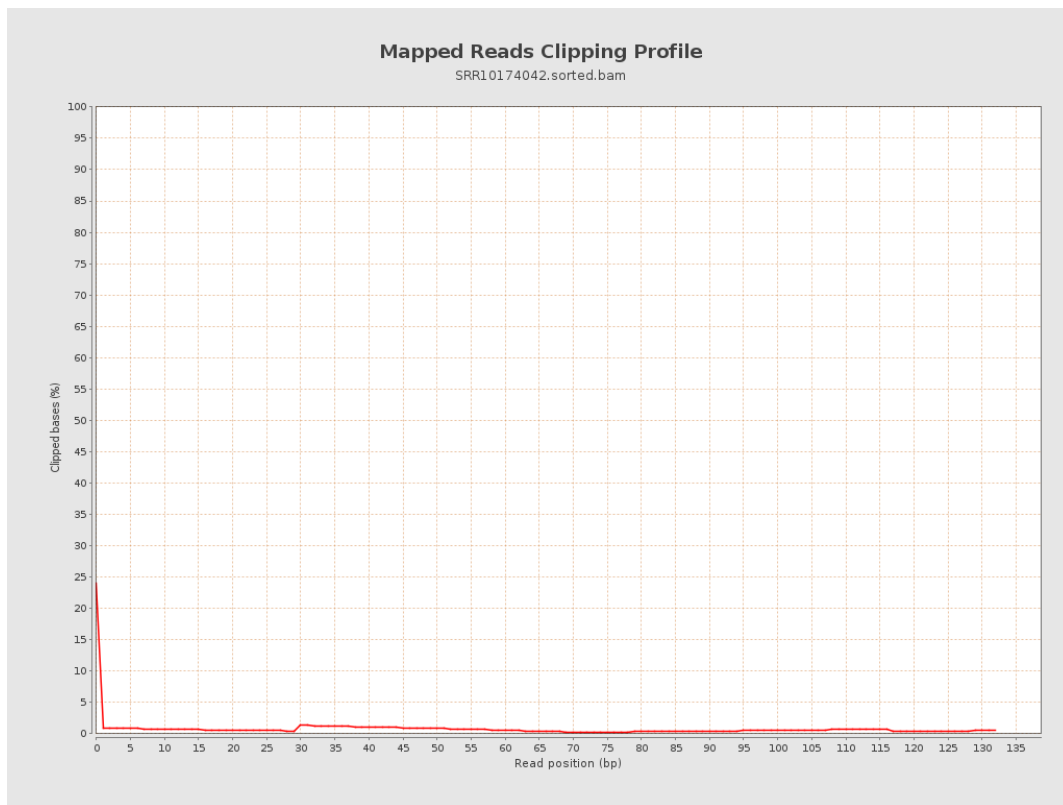
8. Results : Mapped Reads Nucleotide Content



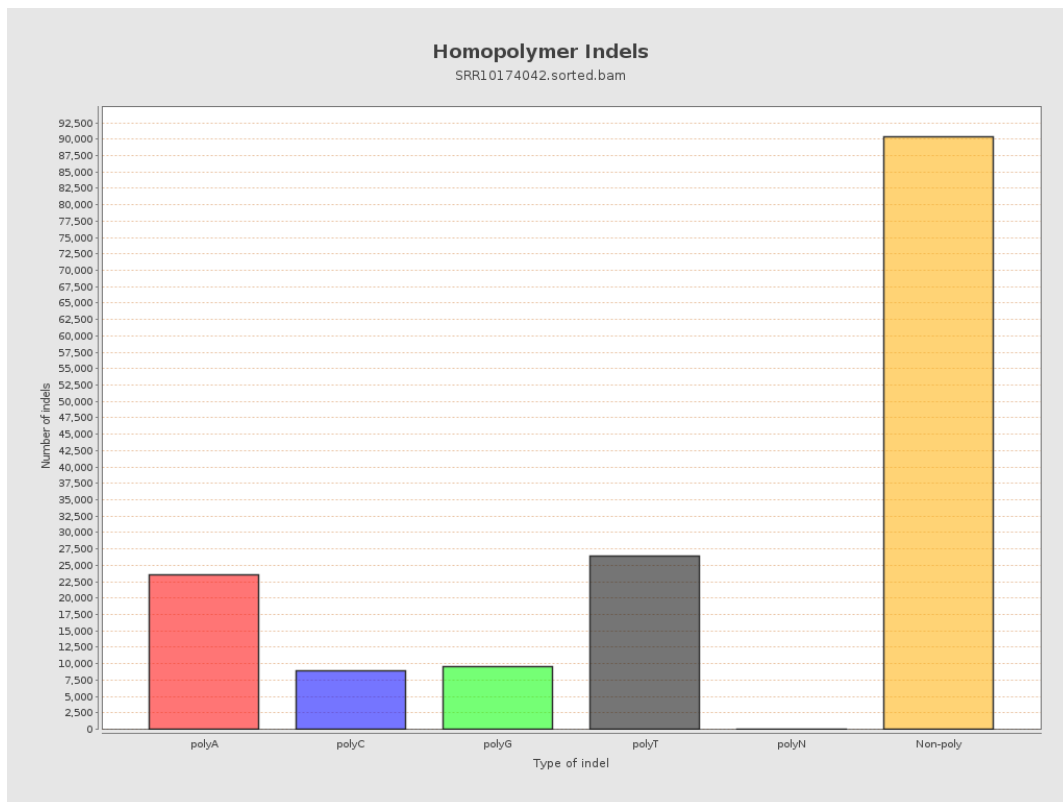
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



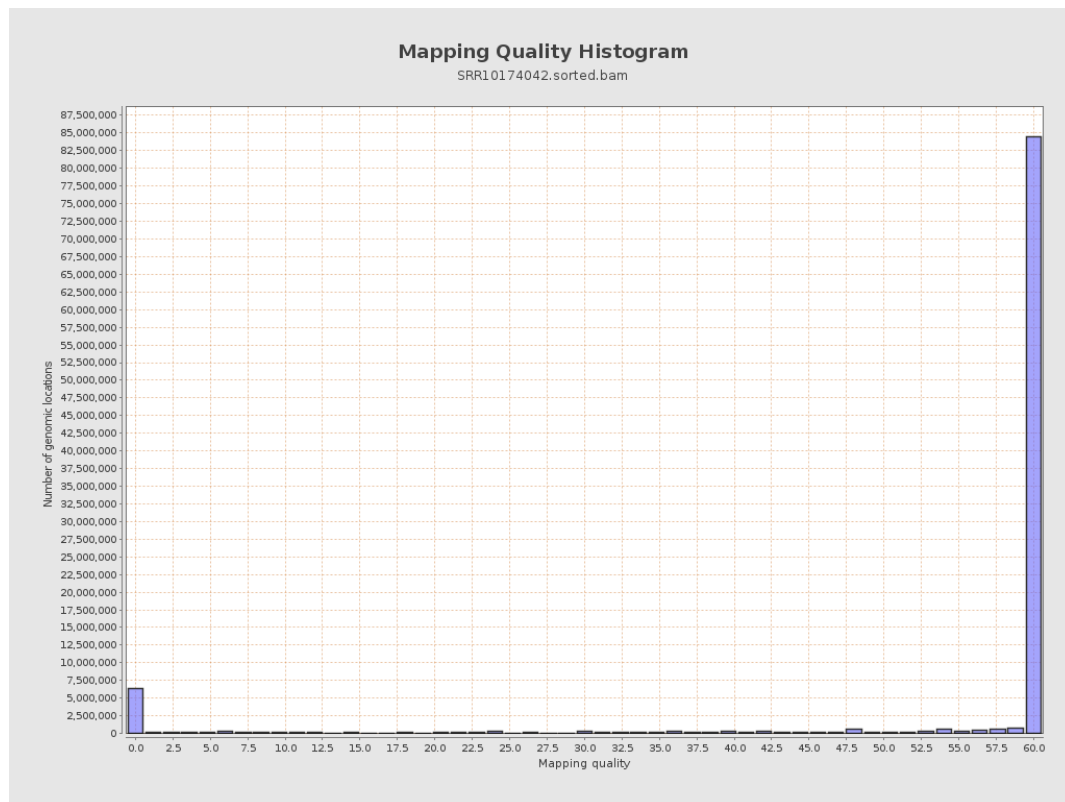
11. Results : Homopolymer Indels



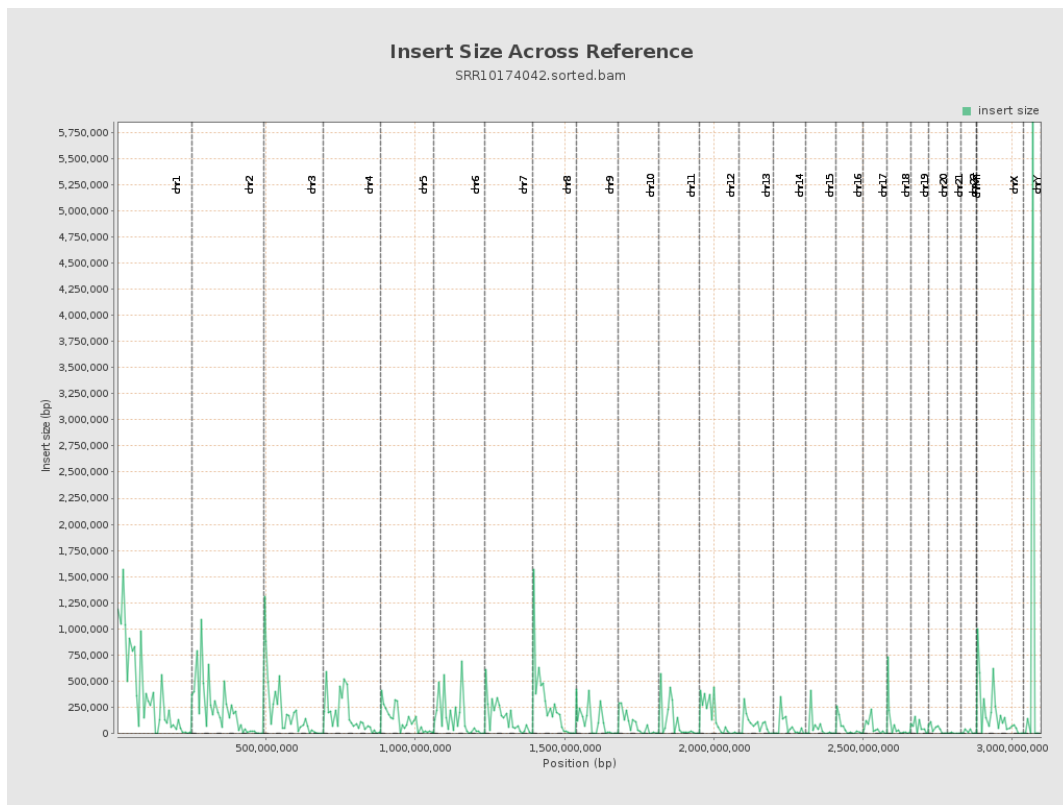
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

