

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 07:33:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695944.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695944 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695944_1.fastq.gz SRR1695944_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Fri Sep 13 07:33:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	422,994,434
Mapped reads	419,450,885 / 99.16%
Unmapped reads	3,543,549 / 0.84%
Mapped paired reads	419,450,885 / 99.16%
Mapped reads, first in pair	210,439,309 / 49.75%
Mapped reads, second in pair	209,011,576 / 49.41%
Mapped reads, both in pair	417,133,452 / 98.61%
Mapped reads, singletons	2,317,433 / 0.55%
Secondary alignments	0
Supplementary alignments	5,529,242 / 1.31%
Read min/max/mean length	30 / 100 / 100.54
Duplicated reads (estimated)	90,750,637 / 21.45%
Duplication rate	18.48%
Clipped reads	29,412,807 / 6.95%

2.2. ACGT Content

Number/percentage of A's	11,723,172,682 / 28.21%
Number/percentage of C's	8,968,537,852 / 21.58%
Number/percentage of T's	11,638,012,136 / 28%
Number/percentage of G's	9,232,075,510 / 22.21%
Number/percentage of N's	1,165,175 / 0%

GC Percentage	43.79%
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2.3. Coverage

Mean	13.4296
Standard Deviation	32.2252

2.4. Mapping Quality

Mean Mapping Quality	54.04
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2.5. Insert size

Mean	72,842.37
Standard Deviation	2,650,946.69
P25/Median/P75	307 / 315 / 323

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	183,809,845
Insertions	5,339,587
Mapped reads with at least one insertion	1.24%
Deletions	4,528,716
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.74%

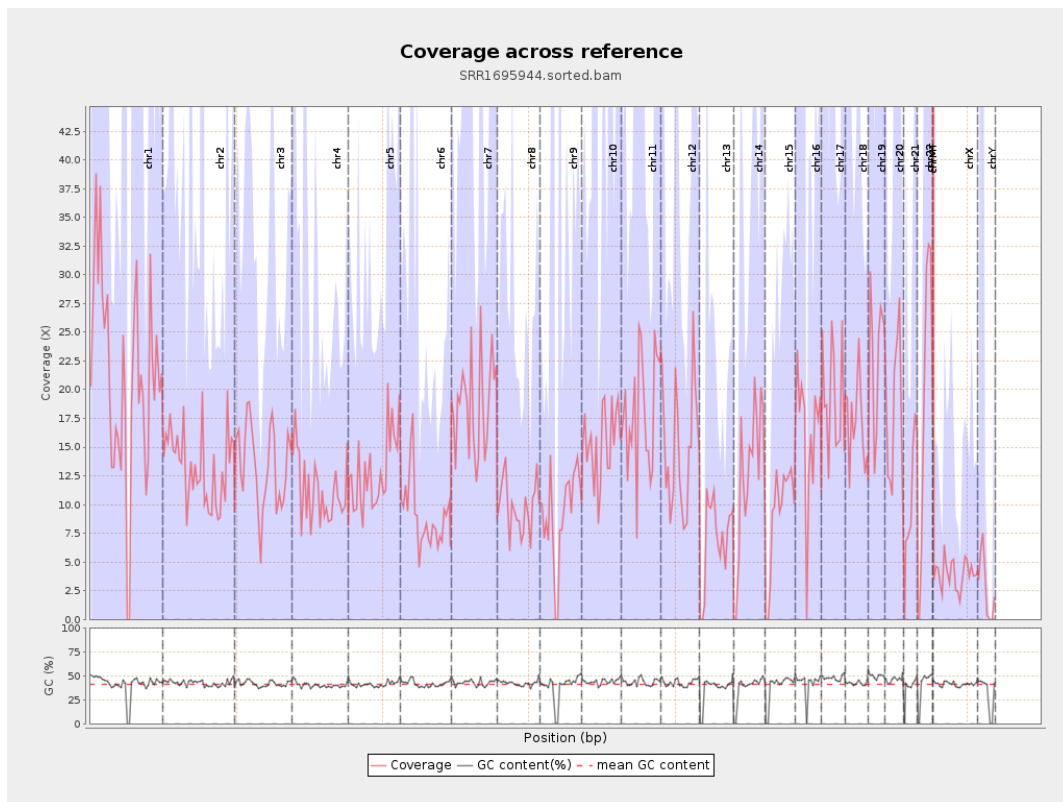
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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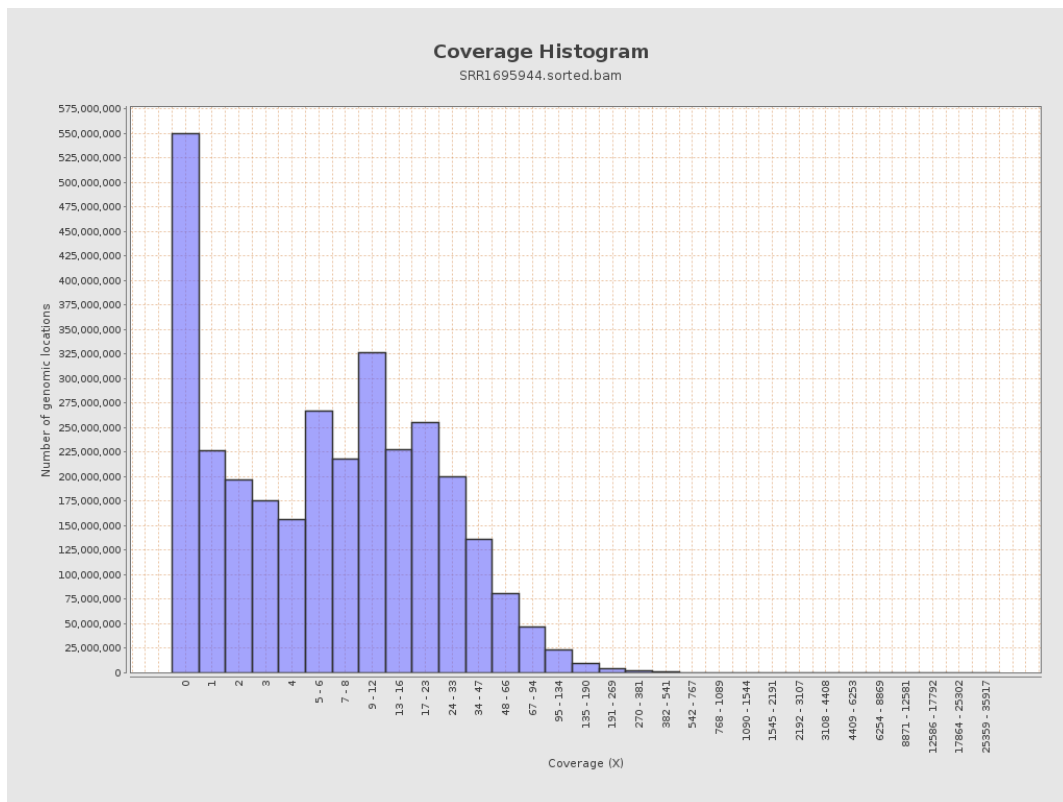
		bases	coverage	deviation
chr1	249250621	5248067421	21.0554	45.8898
chr2	243199373	3226356407	13.2663	43.9273
chr3	198022430	2636905966	13.3162	19.9987
chr4	191154276	2150403226	11.2496	20.3518
chr5	180915260	2334604976	12.9044	19.8374
chr6	171115067	1536714600	8.9806	19.8464
chr7	159138663	2999213121	18.8465	28.4578
chr8	146364022	1430280611	9.7721	18.8171
chr9	141213431	1290734266	9.1403	38.9296
chr10	135534747	2083028422	15.369	44.0333
chr11	135006516	2425187206	17.9635	29.541
chr12	133851895	2019665462	15.0888	25.2304
chr13	115169878	804120896	6.982	16.9739
chr14	107349540	1355416175	12.6262	26.7943
chr15	102531392	924608090	9.0178	17.711
chr16	90354753	1455744854	16.1114	40.9628
chr17	81195210	1568678391	19.3198	37.5595
chr18	78077248	1331571090	17.0545	48.4552
chr19	59128983	1335534086	22.5868	43.2393
chr20	63025520	1124255834	17.8381	29.1205
chr21	48129895	509178201	10.5793	24.4868
chr22	51304566	985751213	19.2137	43.3013
chrMT	16571	6580273	397.0957	137.4308
chrX	155270560	618458504	3.9831	12.2284

chrY	59373566	173020338	2.9141	37.7128
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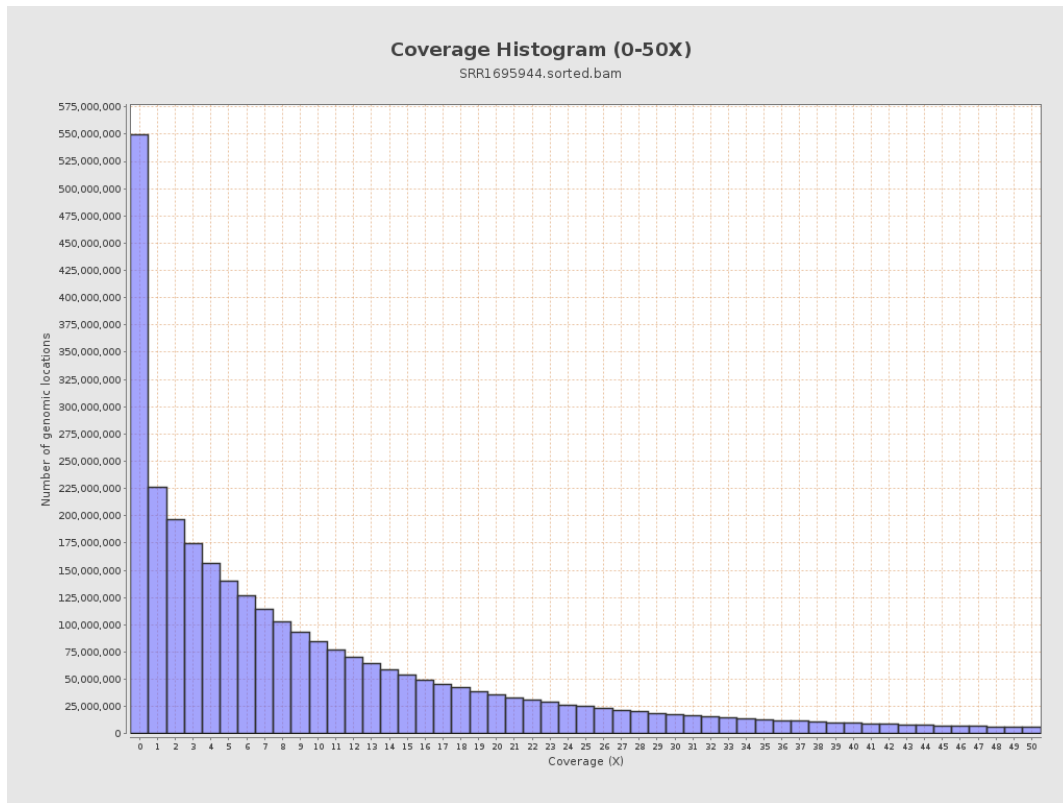
3. Results : Coverage across reference



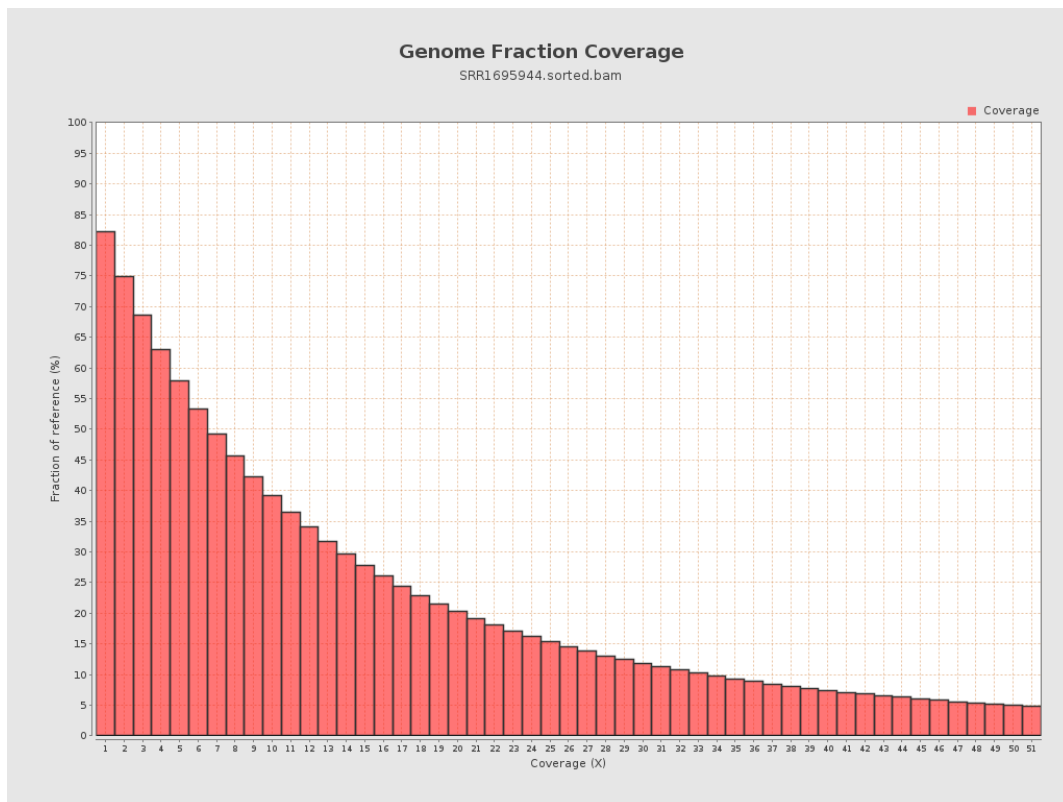
4. Results : Coverage Histogram



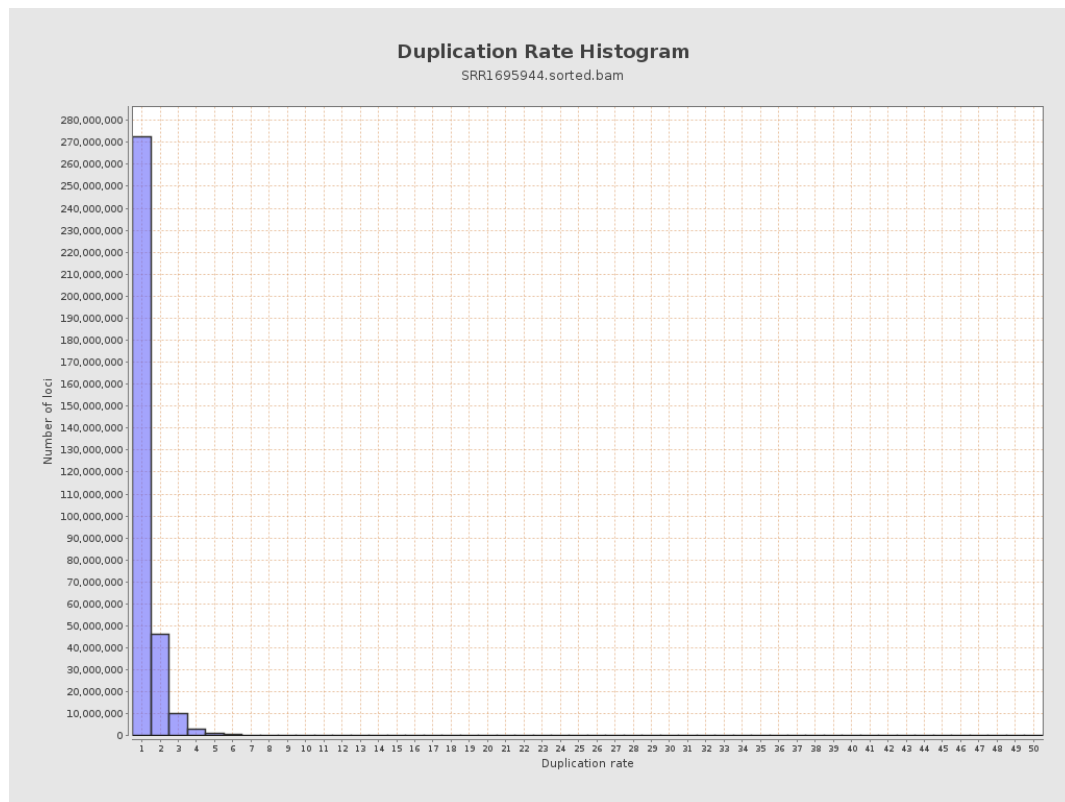
5. Results : Coverage Histogram (0-50X)



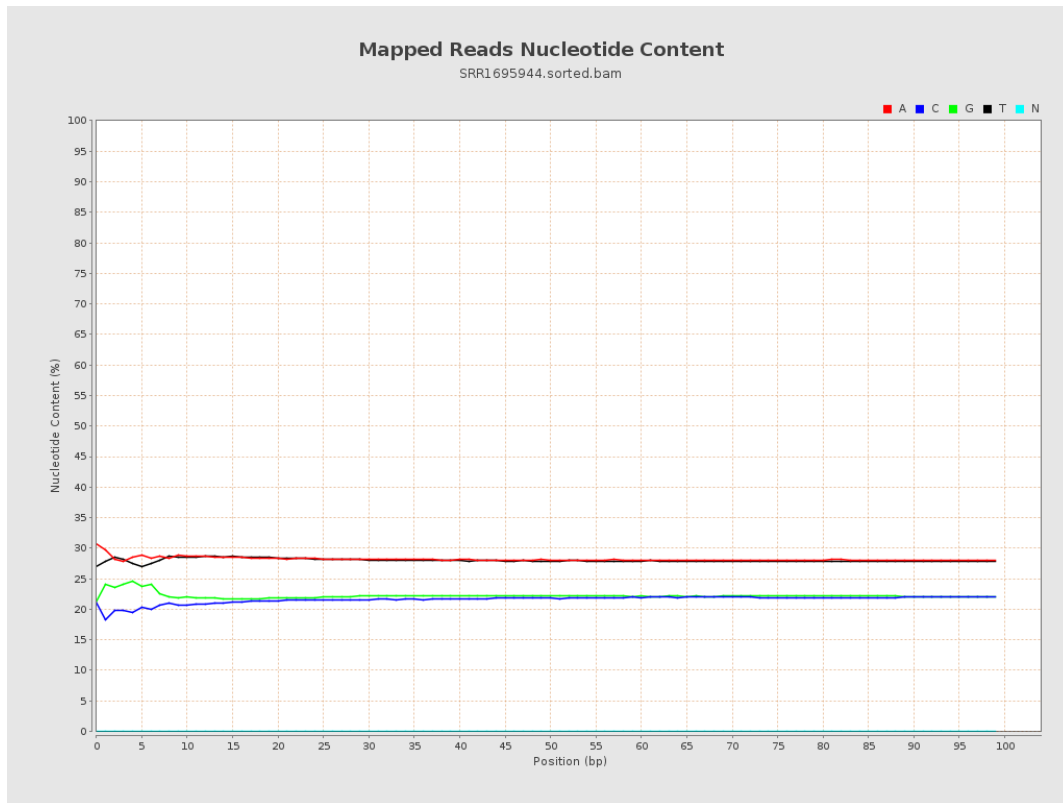
6. Results : Genome Fraction Coverage



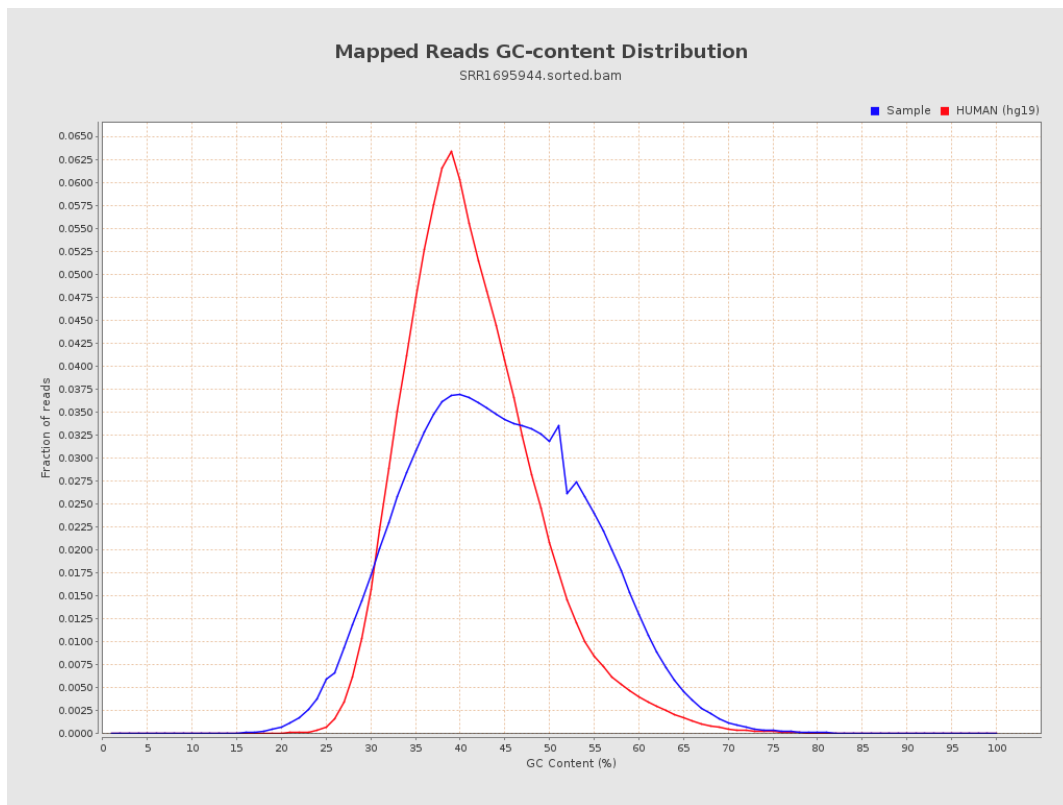
7. Results : Duplication Rate Histogram



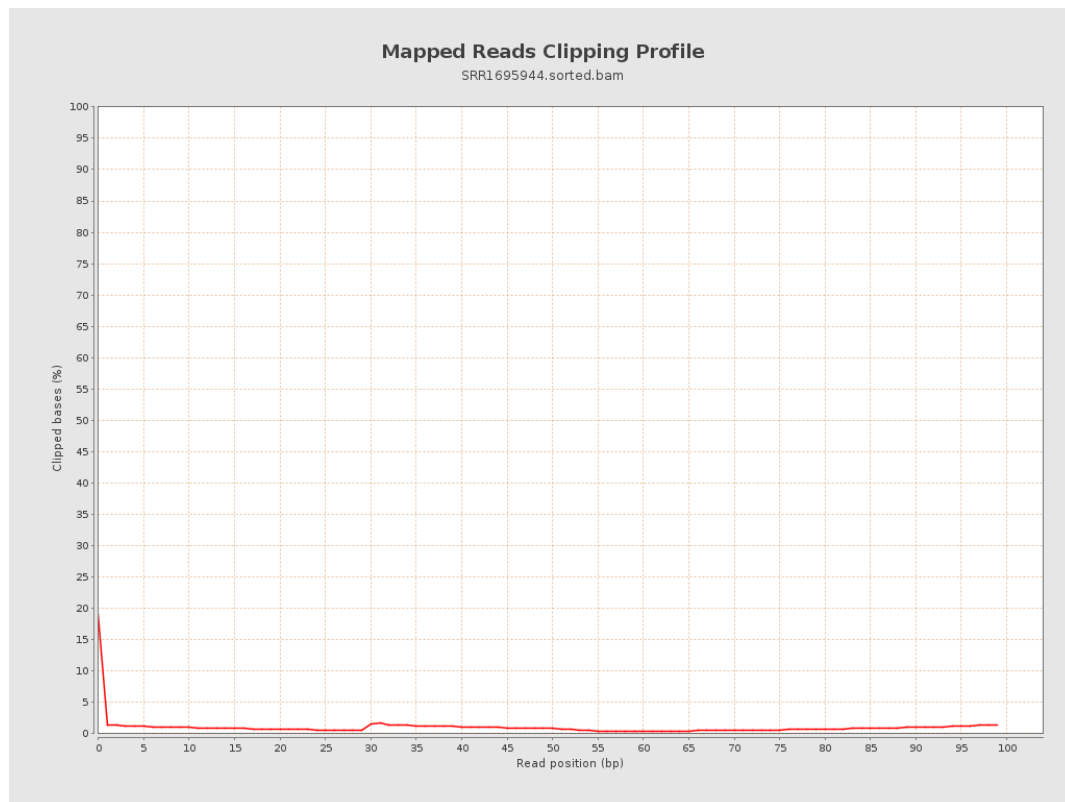
8. Results : Mapped Reads Nucleotide Content



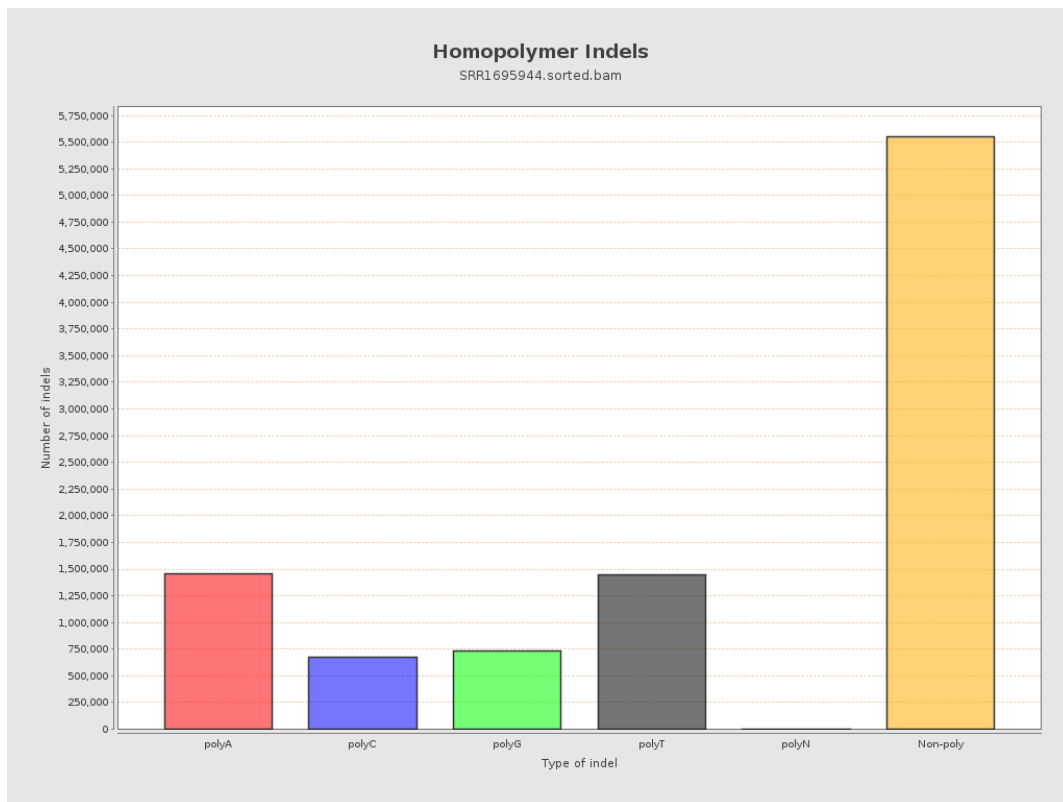
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



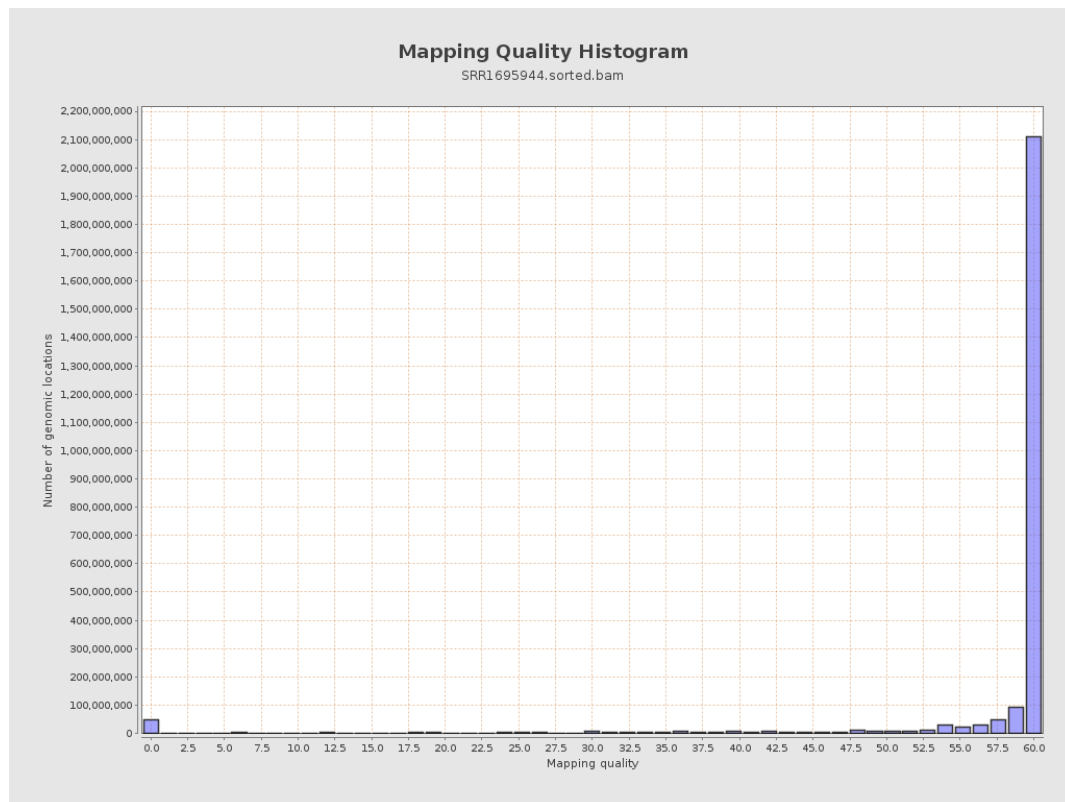
11. Results : Homopolymer Indels



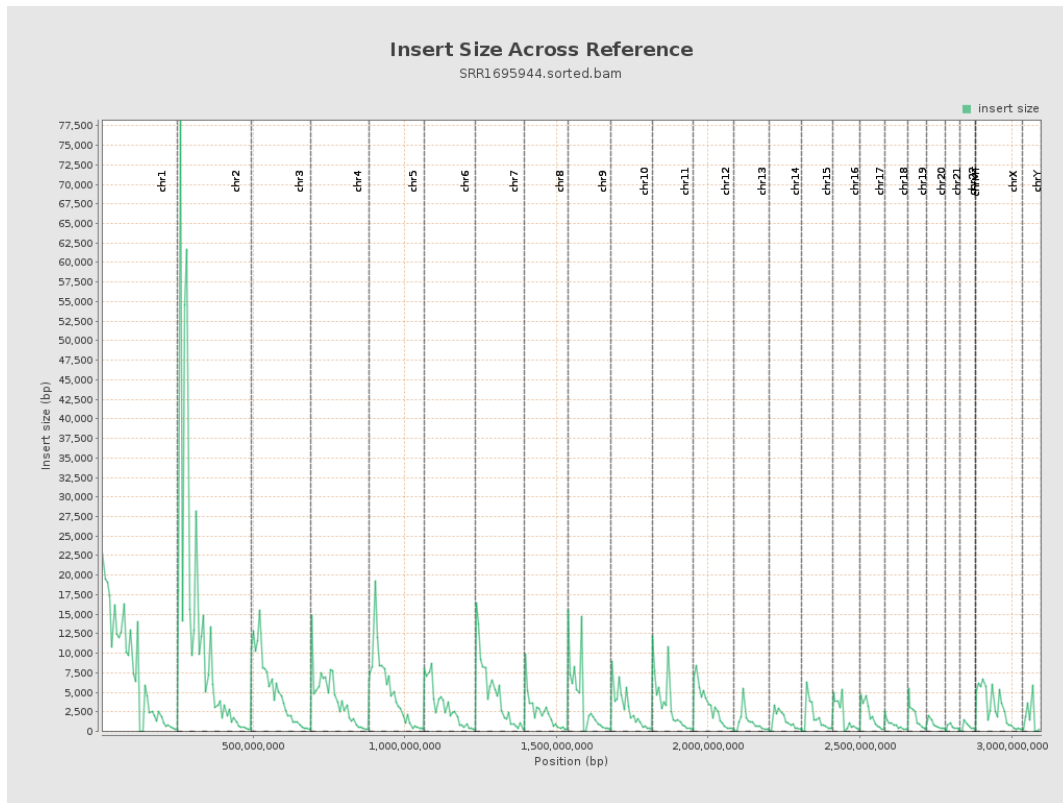
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

