

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 00:36:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695926.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_SRR1695926 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695926_1.fastq.gz SRR1695926_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 00:36:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,129,814
Mapped reads	12,096,889 / 92.13%
Unmapped reads	1,032,925 / 7.87%
Mapped paired reads	12,096,889 / 92.13%
Mapped reads, first in pair	6,092,983 / 46.41%
Mapped reads, second in pair	6,003,906 / 45.73%
Mapped reads, both in pair	11,495,058 / 87.55%
Mapped reads, singletons	601,831 / 4.58%
Secondary alignments	0
Supplementary alignments	297,558 / 2.27%
Read min/max/mean length	30 / 100 / 100.85
Duplicated reads (estimated)	2,799,076 / 21.32%
Duplication rate	14.5%
Clipped reads	8,078,754 / 61.53%

2.2. ACGT Content

Number/percentage of A's	275,246,700 / 27.03%
Number/percentage of C's	181,458,199 / 17.82%
Number/percentage of T's	330,088,130 / 32.42%
Number/percentage of G's	231,054,433 / 22.69%
Number/percentage of N's	332,976 / 0.03%

GC Percentage	40.51%
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2.3. Coverage

Mean	0.329
Standard Deviation	2.8998

2.4. Mapping Quality

Mean Mapping Quality	51.39
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2.5. Insert size

Mean	278,253.42
Standard Deviation	5,087,635.78
P25/Median/P75	277 / 296 / 308

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	12,711,754
Insertions	83,785
Mapped reads with at least one insertion	0.68%
Deletions	219,155
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.36%

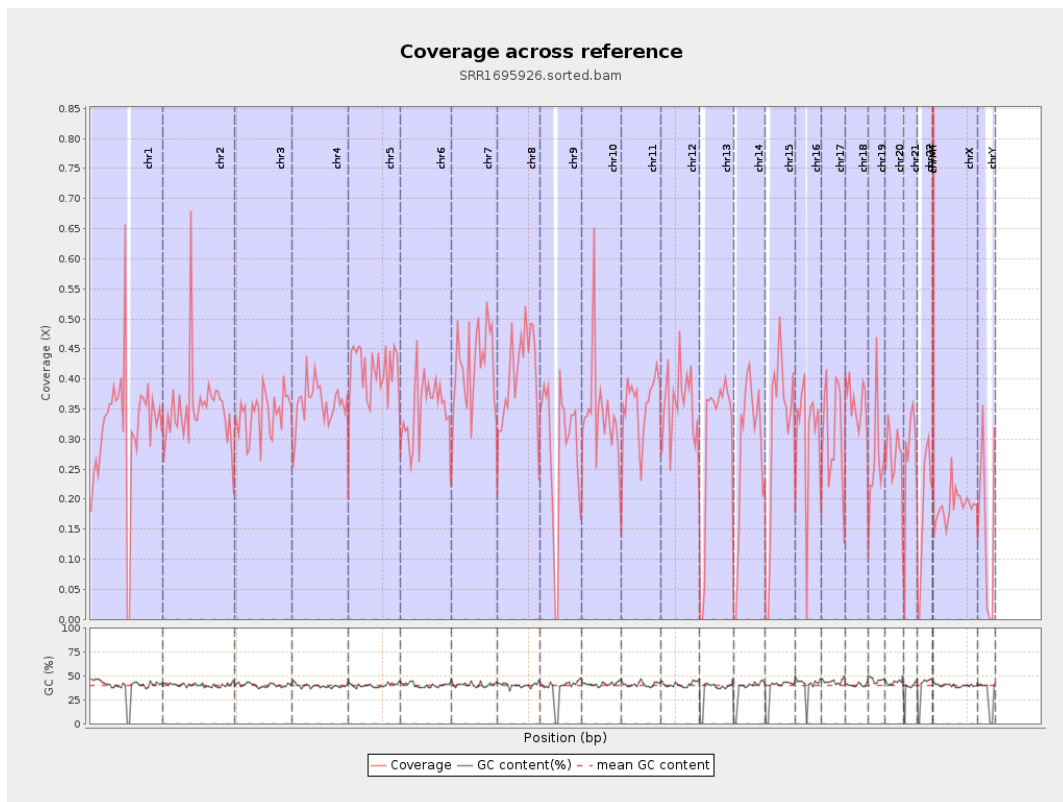
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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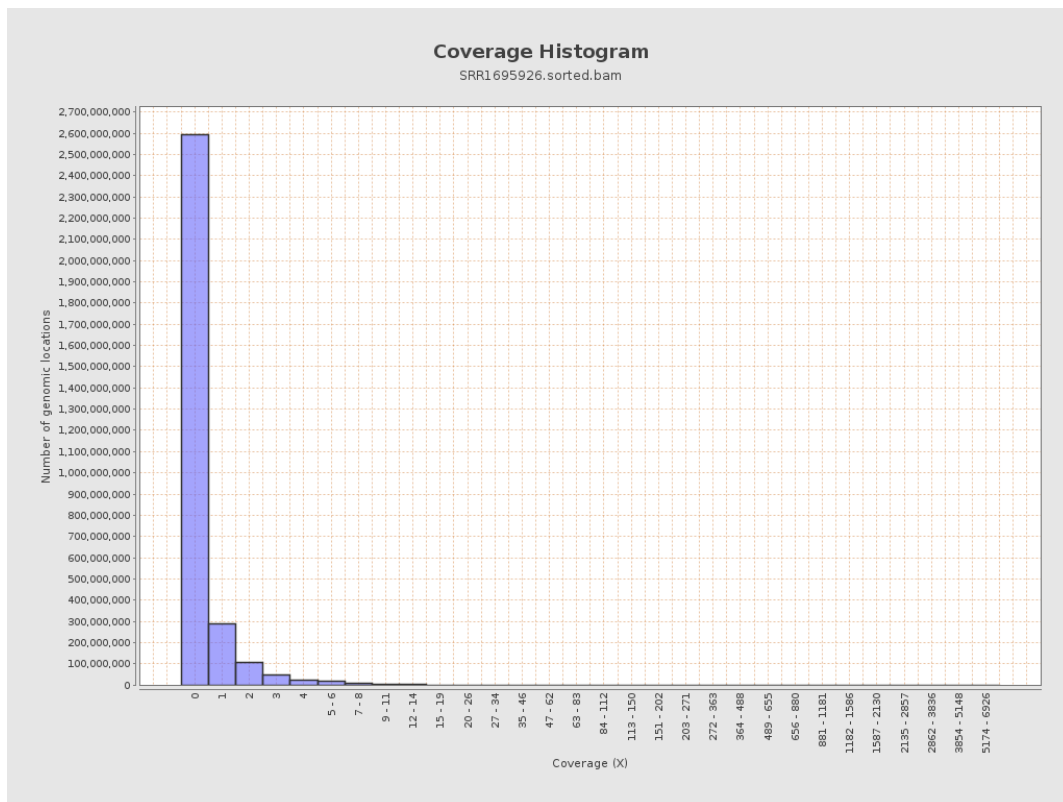
		bases	coverage	deviation
chr1	249250621	78959072	0.3168	6.2797
chr2	243199373	85043710	0.3497	3.1602
chr3	198022430	67718460	0.342	1.0635
chr4	191154276	68794875	0.3599	1.2787
chr5	180915260	74461665	0.4116	1.2583
chr6	171115067	59974612	0.3505	1.6868
chr7	159138663	66456233	0.4176	3.4074
chr8	146364022	59633453	0.4074	4.2942
chr9	141213431	40375275	0.2859	2.6065
chr10	135534747	46288877	0.3415	3.3417
chr11	135006516	48197812	0.357	2.2413
chr12	133851895	47891297	0.3578	1.1458
chr13	115169878	34856620	0.3027	1.0169
chr14	107349540	30587328	0.2849	1.2358
chr15	102531392	32014528	0.3122	1.0377
chr16	90354753	27159009	0.3006	1.2831
chr17	81195210	25435314	0.3133	1.7573
chr18	78077248	28228274	0.3615	4.5254
chr19	59128983	15957395	0.2699	4.3795
chr20	63025520	17265849	0.274	1.0488
chr21	48129895	13155920	0.2733	2.2667
chr22	51304566	9567875	0.1865	1.6265
chrMT	16571	1746080	105.3696	69.4952
chrX	155270560	29195016	0.188	1.0987

chrY	59373566	9611068	0.1619	1.5866
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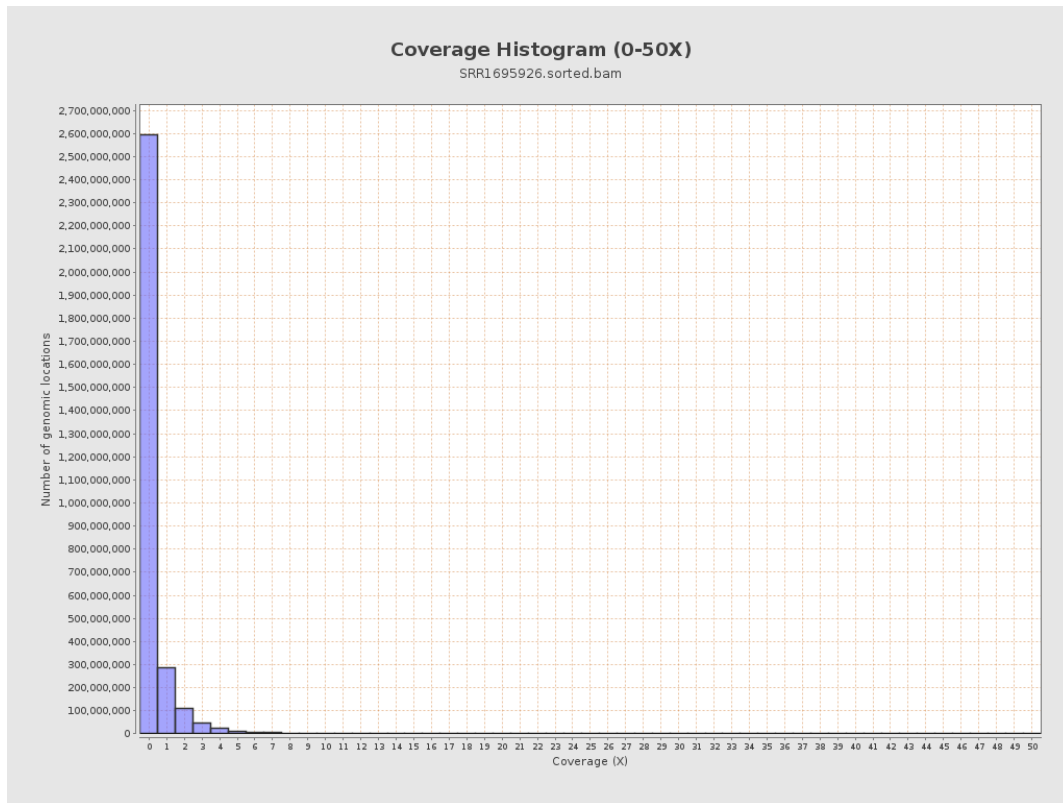
3. Results : Coverage across reference



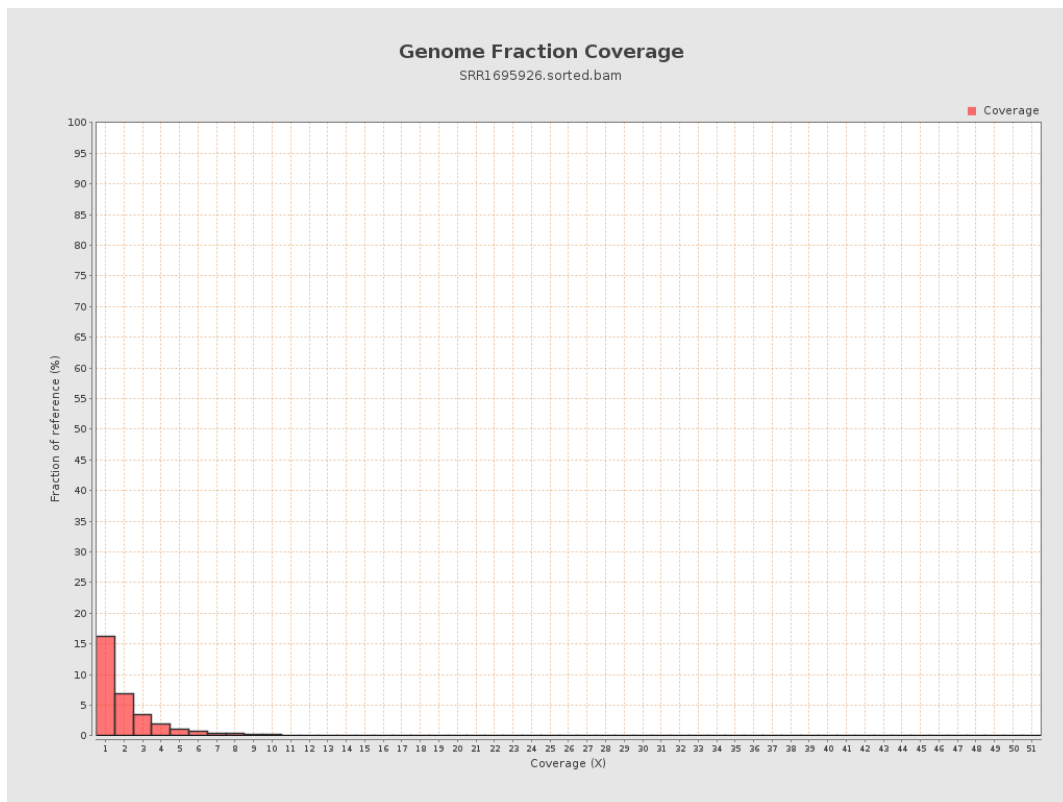
4. Results : Coverage Histogram



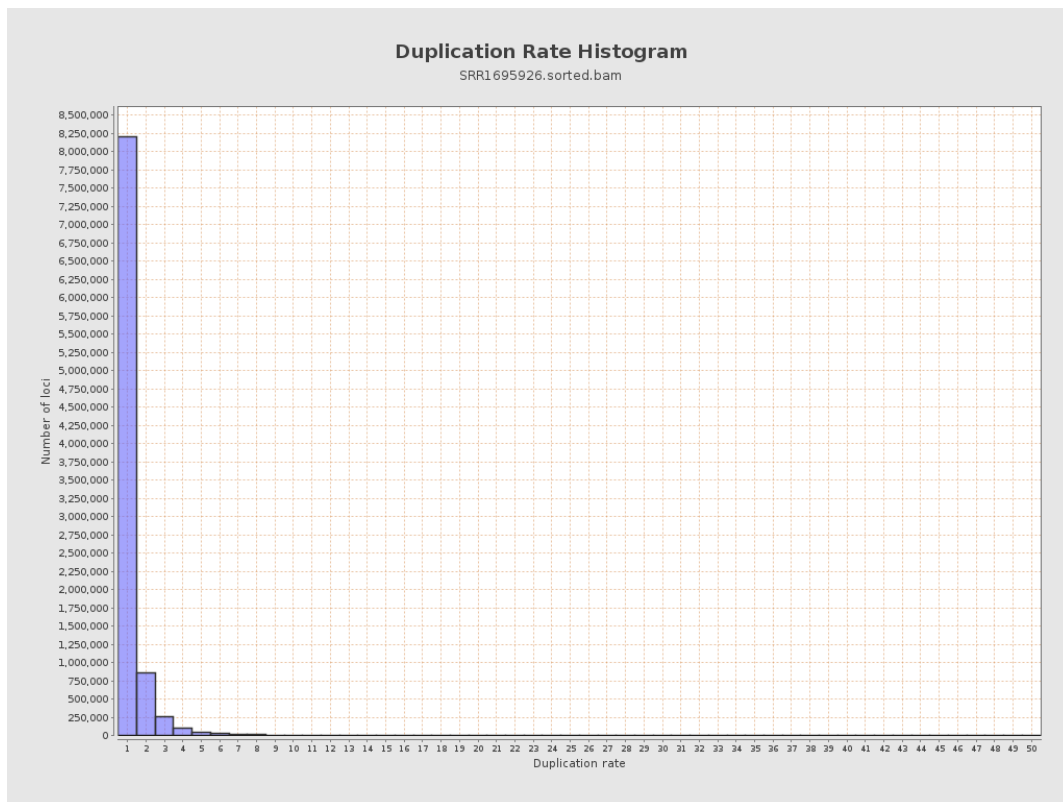
5. Results : Coverage Histogram (0-50X)



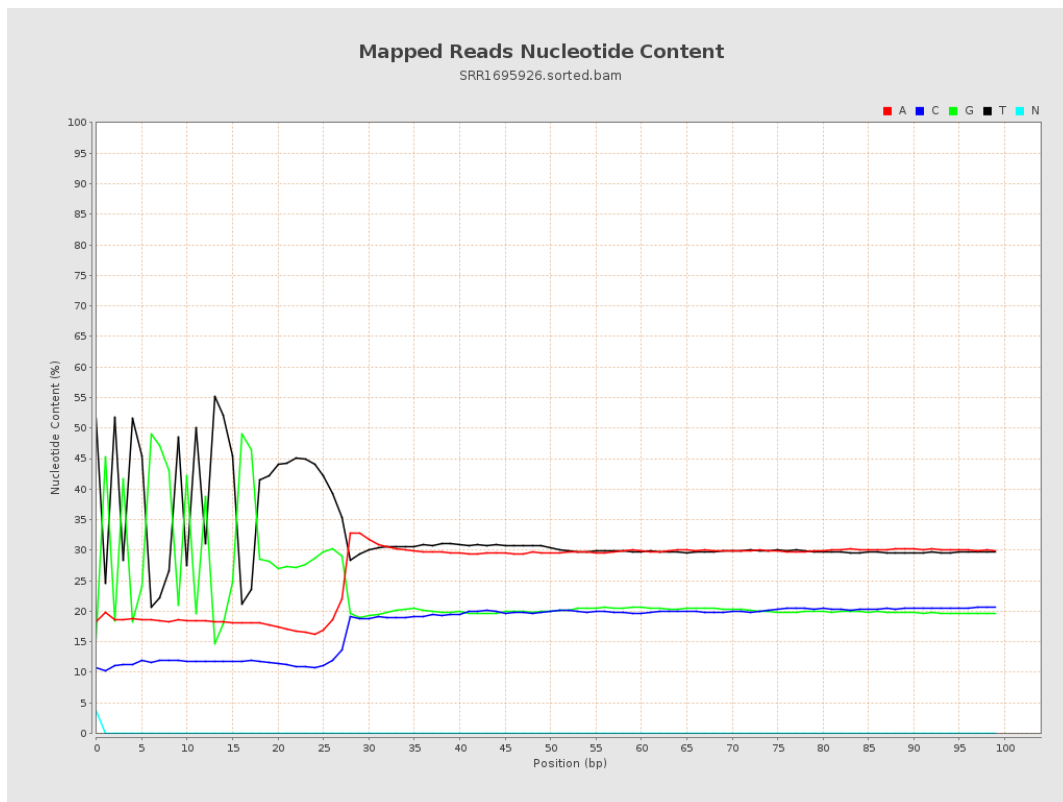
6. Results : Genome Fraction Coverage



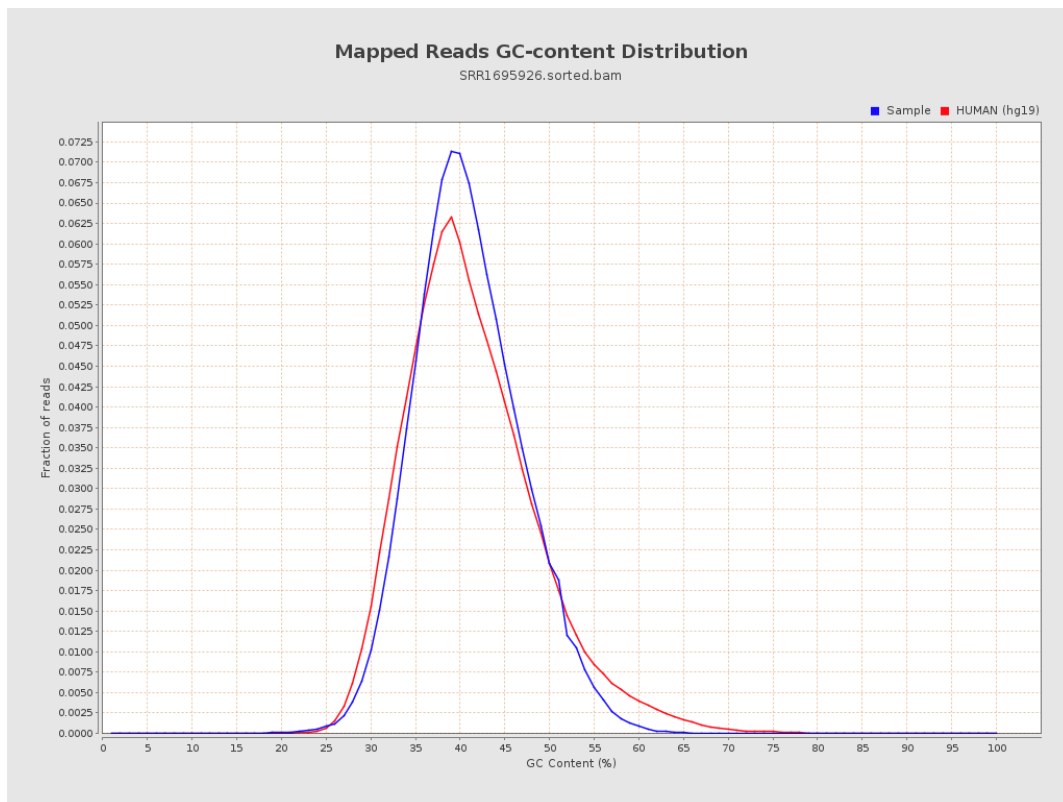
7. Results : Duplication Rate Histogram



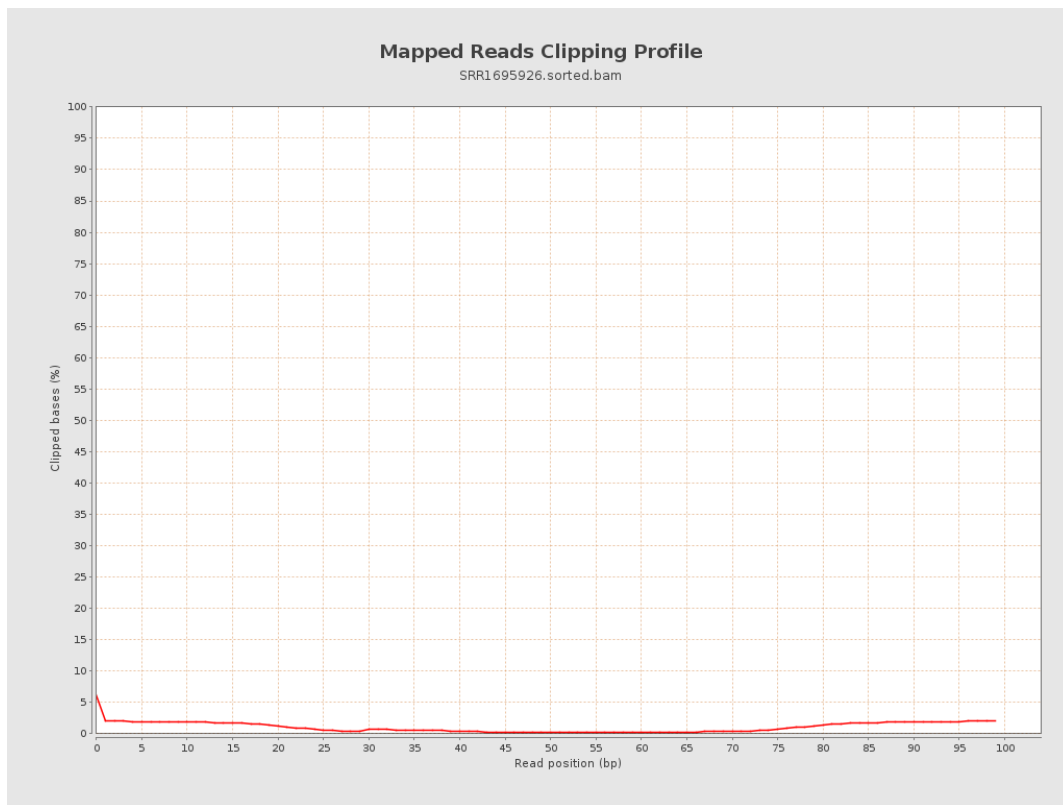
8. Results : Mapped Reads Nucleotide Content



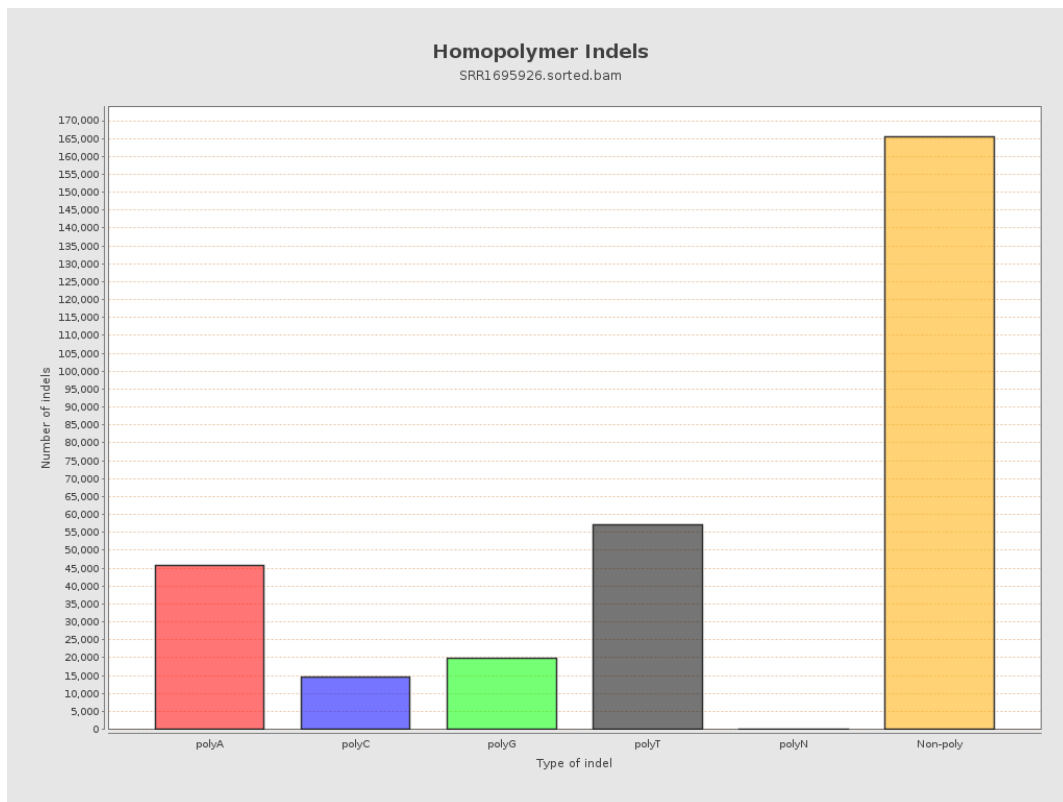
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



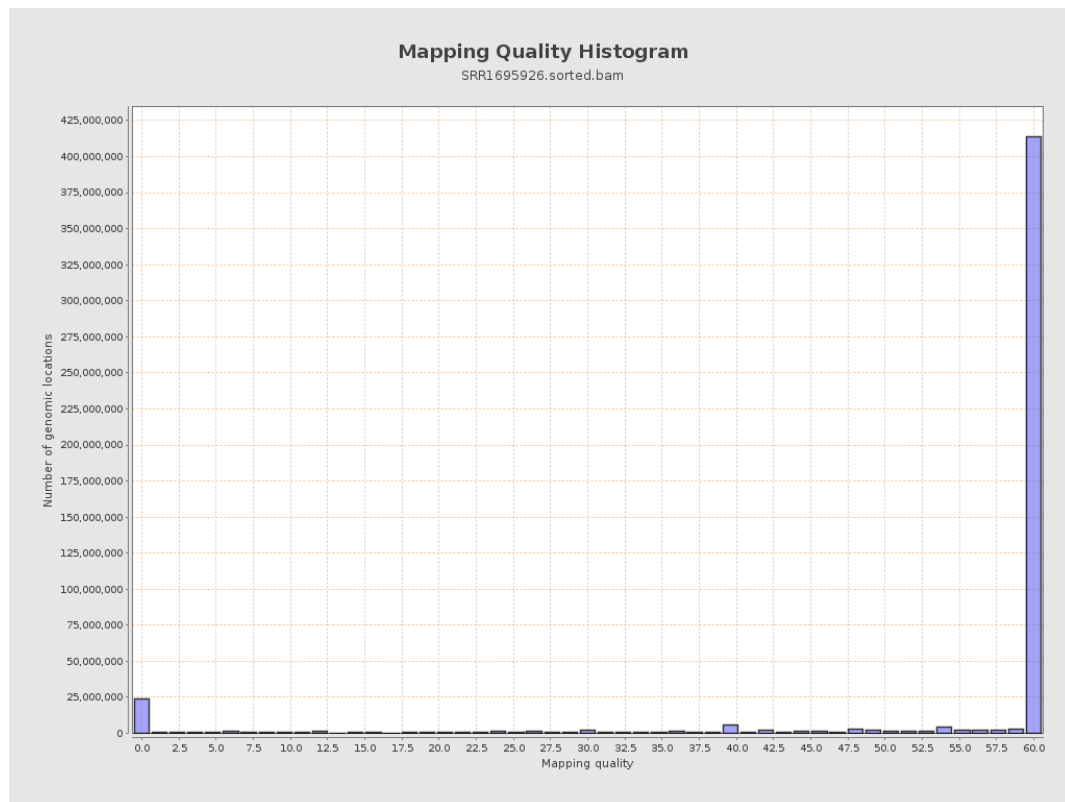
11. Results : Homopolymer Indels



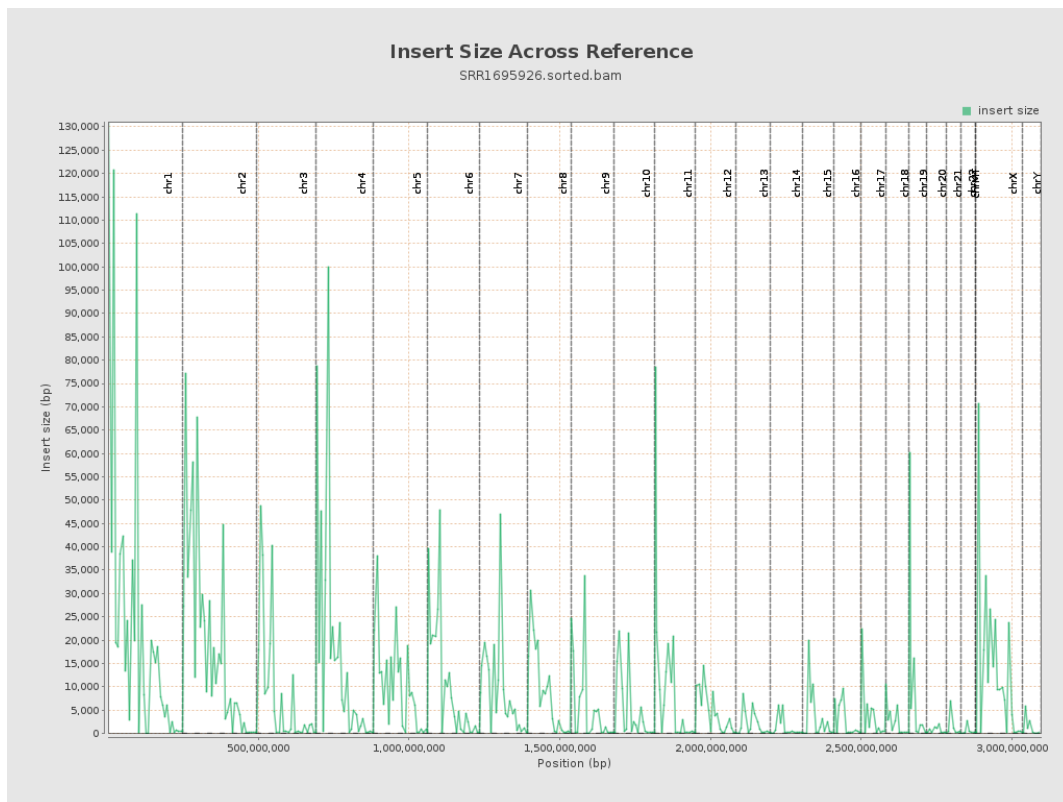
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

