

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:34:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695937.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_SRR1695937 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695937_1.fastq.gz SRR1695937_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 02:34:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,154,700
Mapped reads	10,366,013 / 92.93%
Unmapped reads	788,687 / 7.07%
Mapped paired reads	10,366,013 / 92.93%
Mapped reads, first in pair	5,254,596 / 47.11%
Mapped reads, second in pair	5,111,417 / 45.82%
Mapped reads, both in pair	9,988,310 / 89.54%
Mapped reads, singletons	377,703 / 3.39%
Secondary alignments	0
Supplementary alignments	18,643 / 0.17%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	1,093,981 / 9.81%
Duplication rate	7.1%
Clipped reads	6,049,683 / 54.23%

2.2. ACGT Content

Number/percentage of A's	225,934,102 / 25.45%
Number/percentage of C's	169,919,606 / 19.14%
Number/percentage of T's	263,729,661 / 29.7%
Number/percentage of G's	227,956,462 / 25.68%
Number/percentage of N's	298,760 / 0.03%

GC Percentage	44.81%
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2.3. Coverage

Mean	0.2869
Standard Deviation	3.284

2.4. Mapping Quality

Mean Mapping Quality	53.25
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2.5. Insert size

Mean	44,856.88
Standard Deviation	2,023,628.44
P25/Median/P75	282 / 292 / 301

2.6. Mismatches and indels

General error rate	1.52%
Mismatches	13,312,750
Insertions	87,781
Mapped reads with at least one insertion	0.84%
Deletions	202,328
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.16%

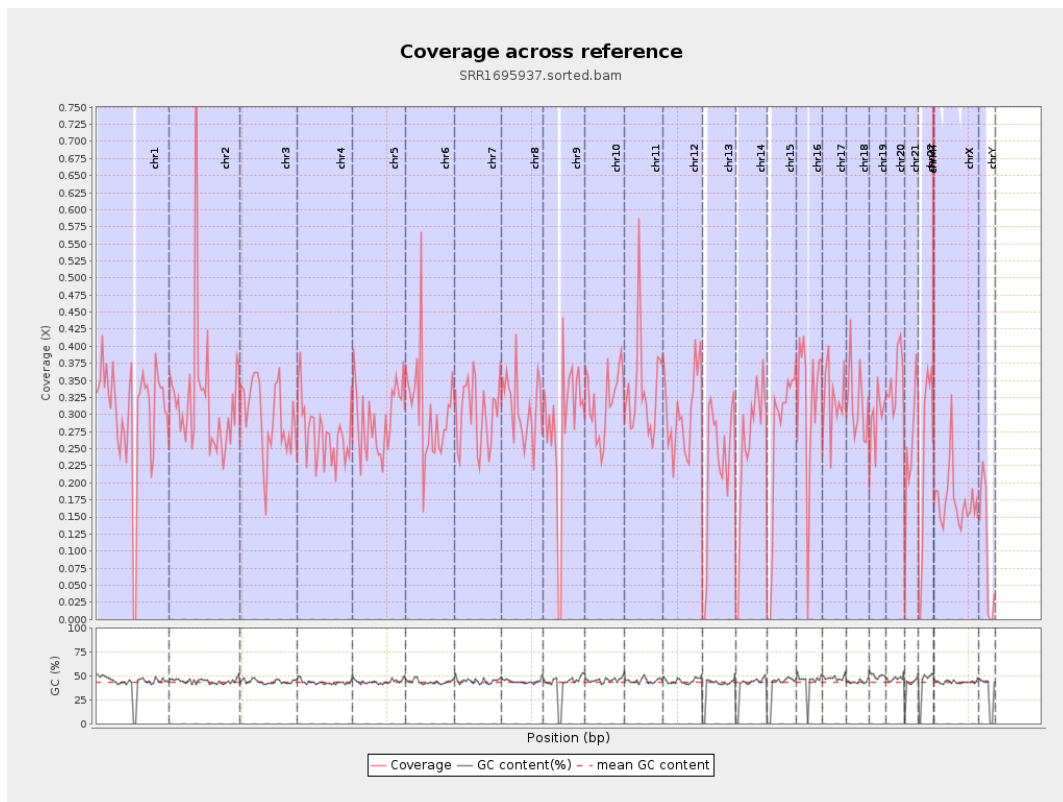
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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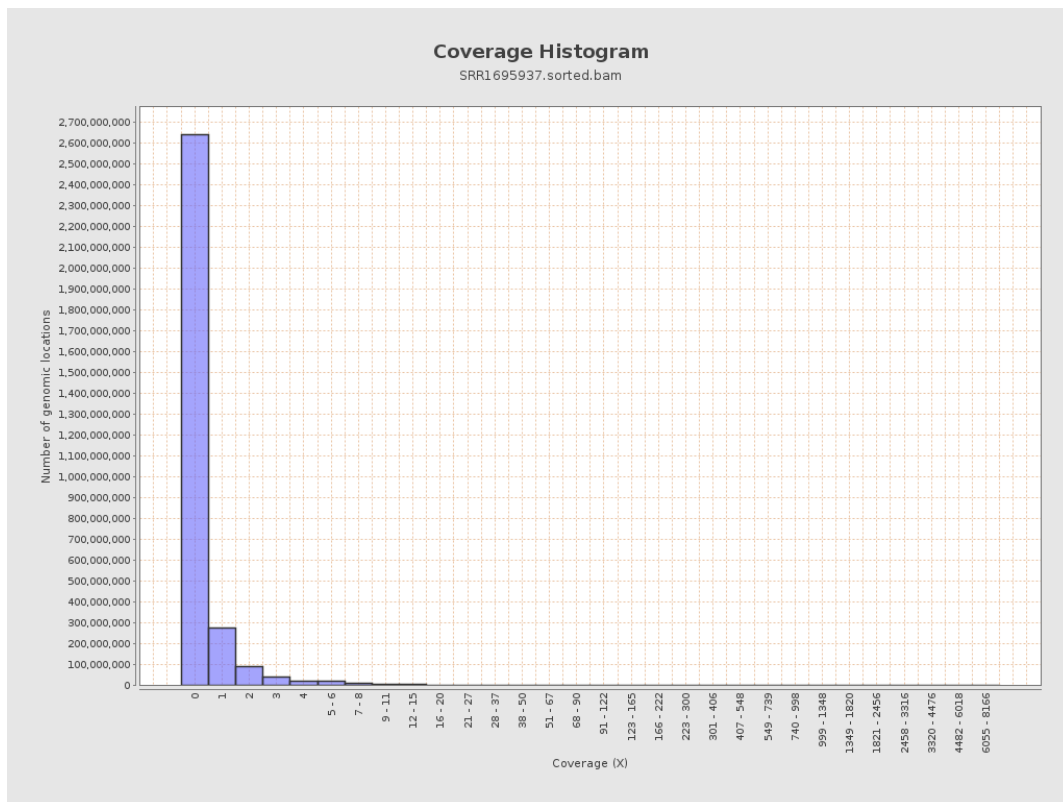
		bases	coverage	deviation
chr1	249250621	74957044	0.3007	2.0329
chr2	243199373	78520732	0.3229	6.2205
chr3	198022430	58622880	0.296	0.9984
chr4	191154276	51843764	0.2712	1.1175
chr5	180915260	52942030	0.2926	1.3279
chr6	171115067	52347464	0.3059	5.2446
chr7	159138663	47830393	0.3006	2.8676
chr8	146364022	45423937	0.3103	2.8409
chr9	141213431	39772126	0.2816	3.8499
chr10	135534747	43193225	0.3187	1.1427
chr11	135006516	44860964	0.3323	6.3828
chr12	133851895	40576583	0.3031	1.2813
chr13	115169878	25796439	0.224	0.861
chr14	107349540	27052507	0.252	1.6797
chr15	102531392	26999428	0.2633	0.9673
chr16	90354753	29147437	0.3226	1.8557
chr17	81195210	26183451	0.3225	1.7002
chr18	78077248	24860001	0.3184	6.7863
chr19	59128983	17591981	0.2975	1.1616
chr20	63025520	22033346	0.3496	1.1514
chr21	48129895	12227135	0.254	2.9104
chr22	51304566	12122067	0.2363	0.9415
chrMT	16571	71039	4.2869	11.9446
chrX	155270560	27291005	0.1758	3.3055

chrY	59373566	5873716	0.0989	0.971
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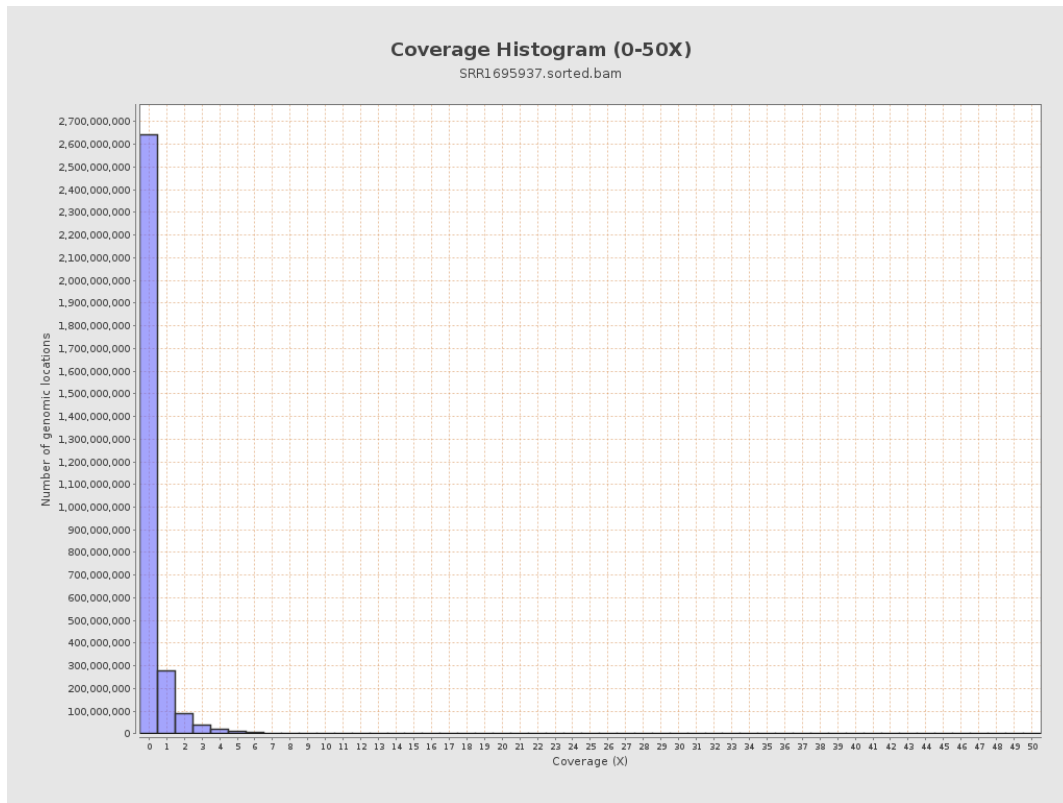
3. Results : Coverage across reference



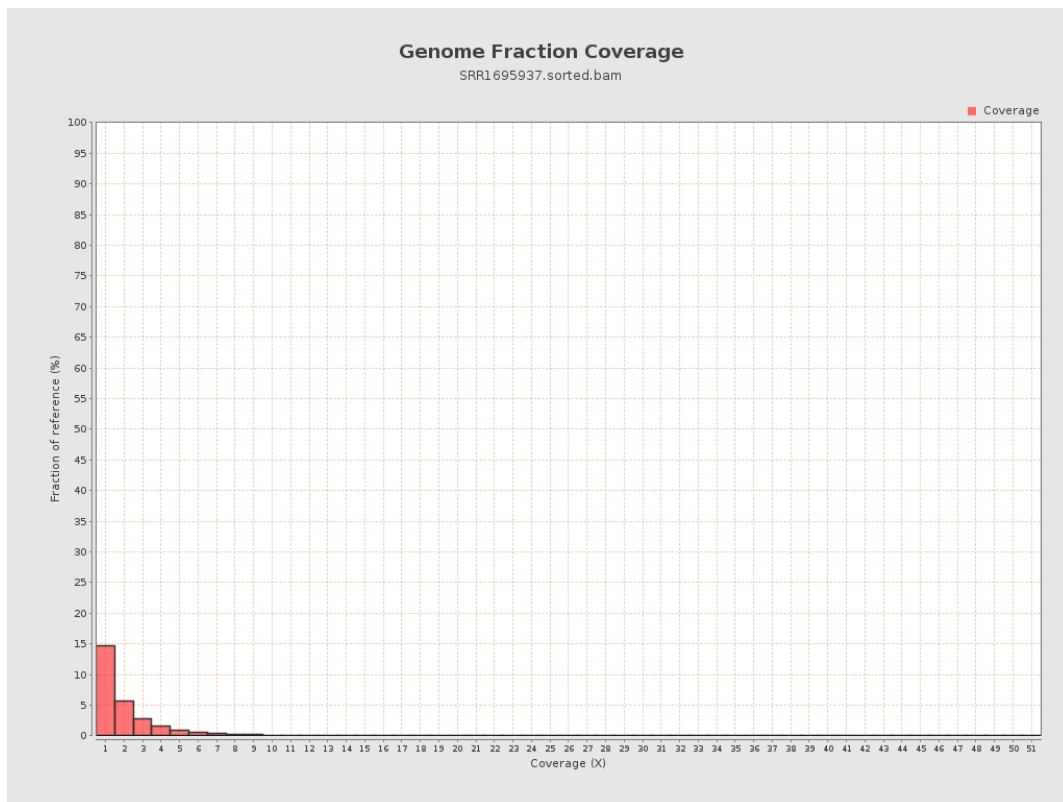
4. Results : Coverage Histogram



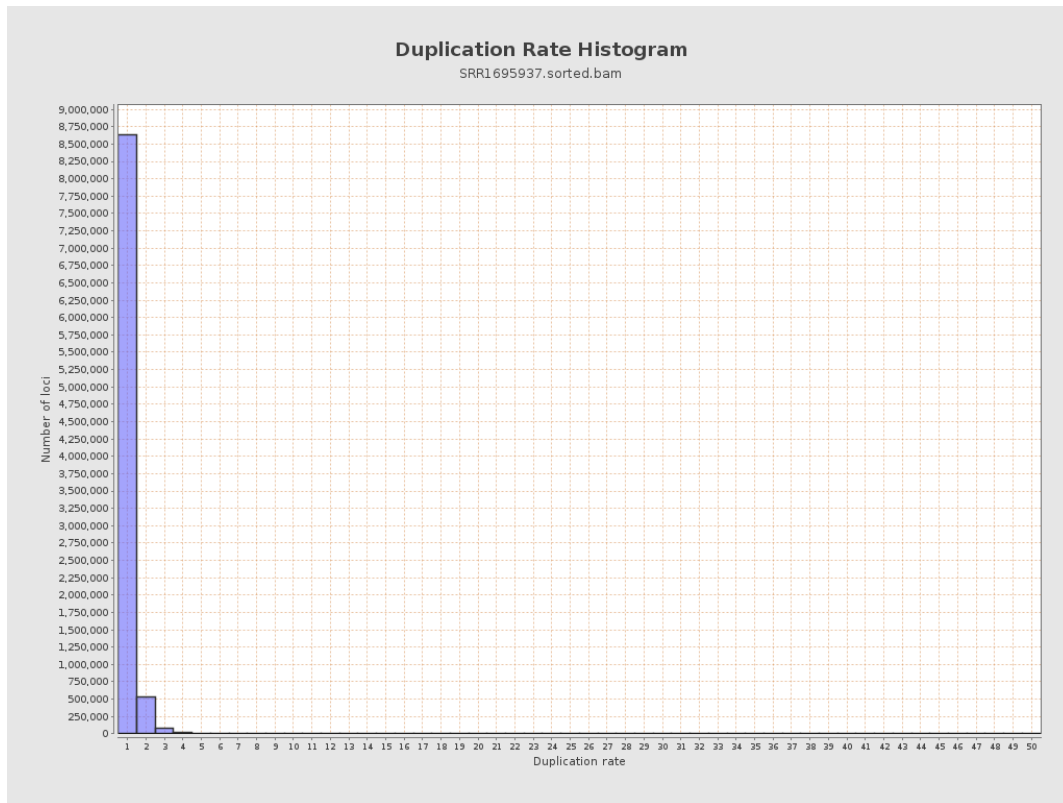
5. Results : Coverage Histogram (0-50X)



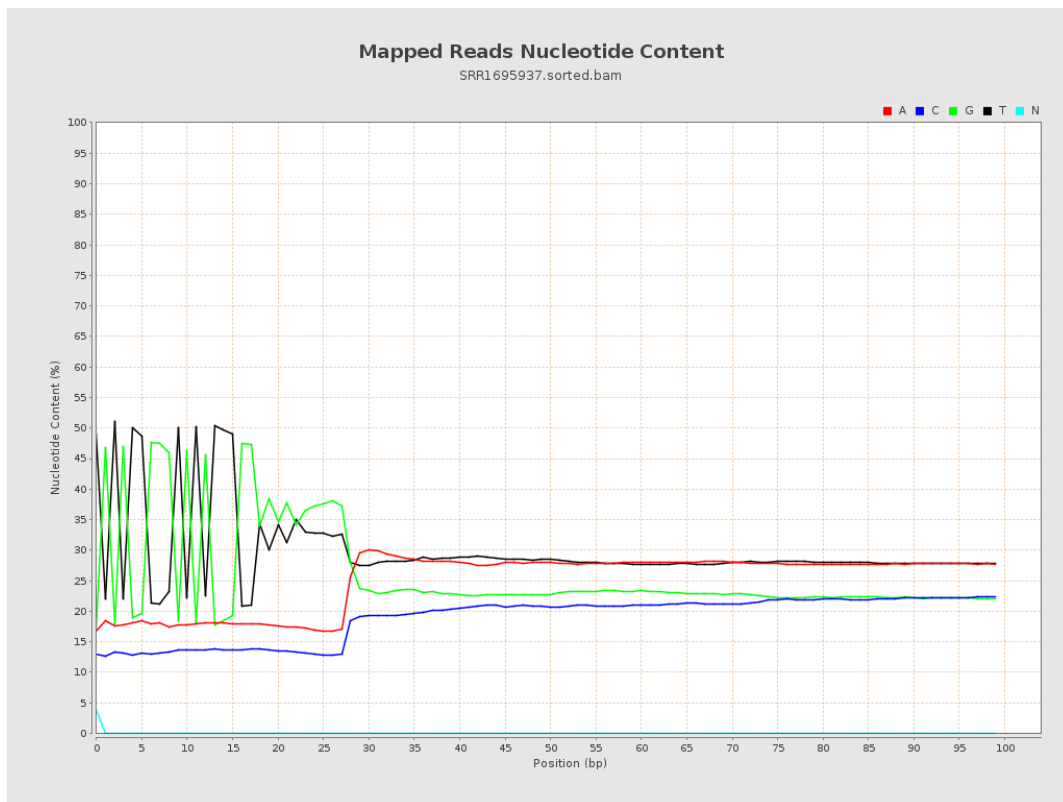
6. Results : Genome Fraction Coverage



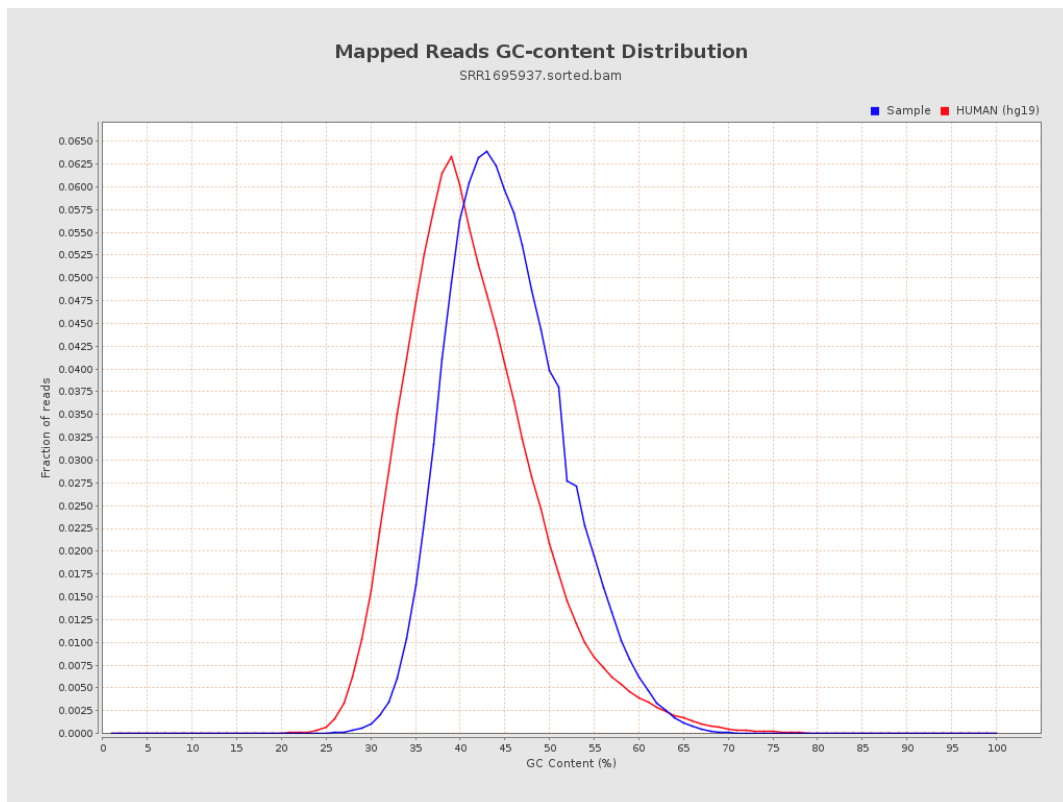
7. Results : Duplication Rate Histogram



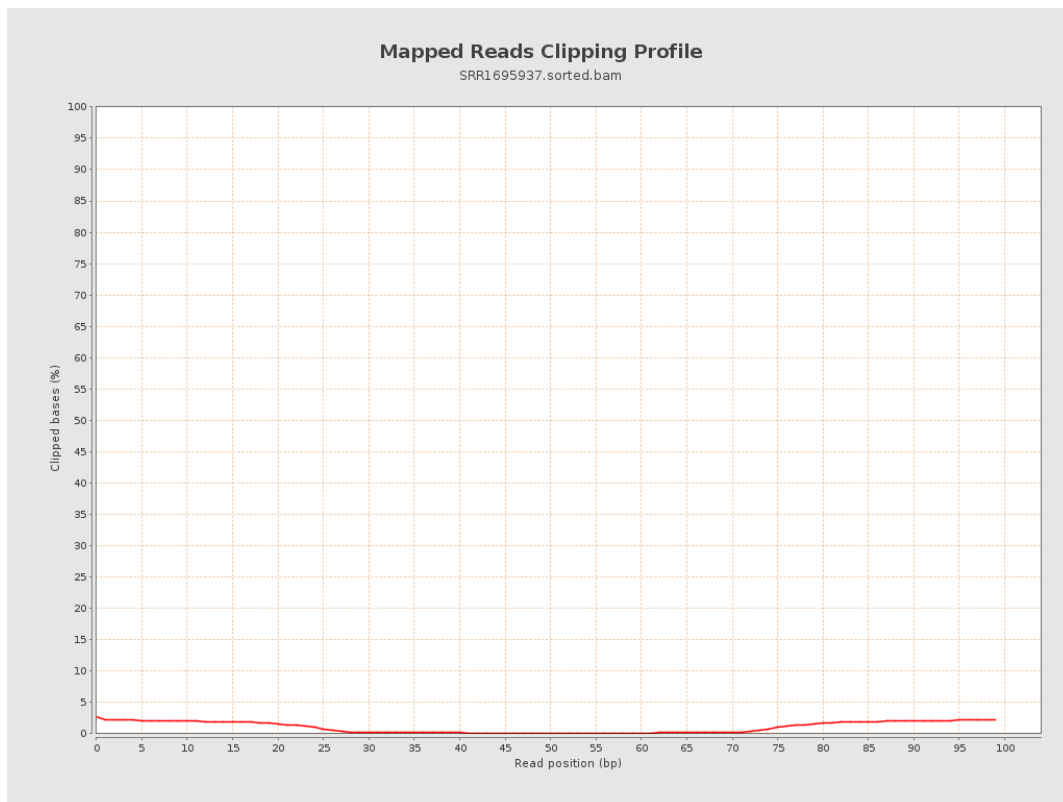
8. Results : Mapped Reads Nucleotide Content



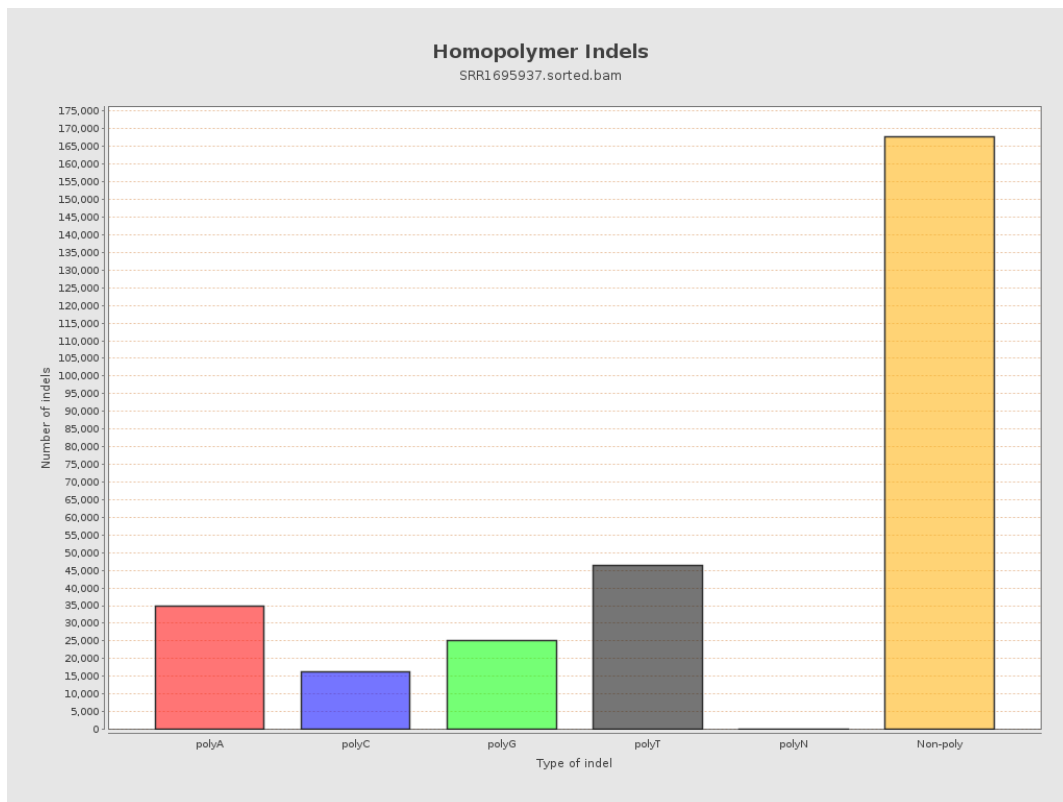
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



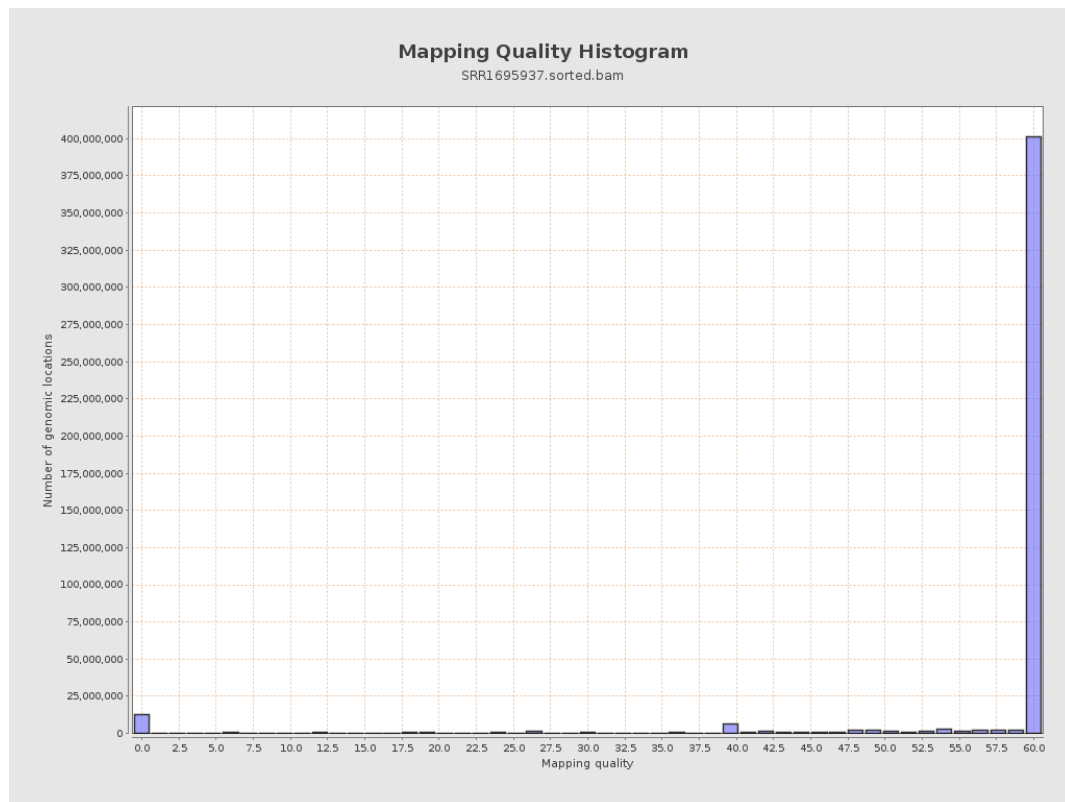
11. Results : Homopolymer Indels



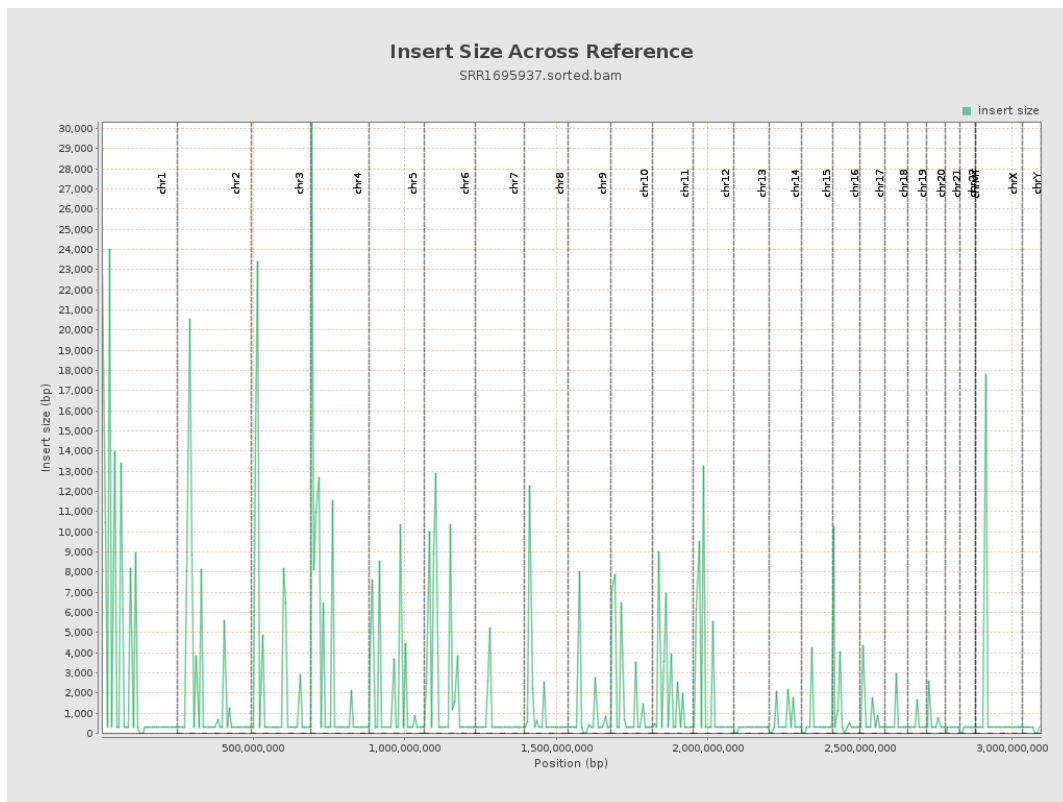
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

