

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:29:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695936.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_SRR1695936 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695936_1.fastq.gz SRR1695936_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 02:29:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,423,104
Mapped reads	10,398,667 / 91.03%
Unmapped reads	1,024,437 / 8.97%
Mapped paired reads	10,398,667 / 91.03%
Mapped reads, first in pair	5,273,766 / 46.17%
Mapped reads, second in pair	5,124,901 / 44.86%
Mapped reads, both in pair	10,019,476 / 87.71%
Mapped reads, singletons	379,191 / 3.32%
Secondary alignments	0
Supplementary alignments	20,353 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	1,139,468 / 9.98%
Duplication rate	7.69%
Clipped reads	6,105,233 / 53.45%

2.2. ACGT Content

Number/percentage of A's	225,438,606 / 25.39%
Number/percentage of C's	170,504,267 / 19.2%
Number/percentage of T's	263,481,690 / 29.67%
Number/percentage of G's	228,268,120 / 25.71%
Number/percentage of N's	300,920 / 0.03%

GC Percentage	44.91%
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2.3. Coverage

Mean	0.2869
Standard Deviation	2.6628

2.4. Mapping Quality

Mean Mapping Quality	53
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2.5. Insert size

Mean	63,287.46
Standard Deviation	2,384,995.23
P25/Median/P75	272 / 284 / 297

2.6. Mismatches and indels

General error rate	1.5%
Mismatches	13,192,830
Insertions	85,580
Mapped reads with at least one insertion	0.81%
Deletions	208,404
Mapped reads with at least one deletion	1.97%
Homopolymer indels	42.48%

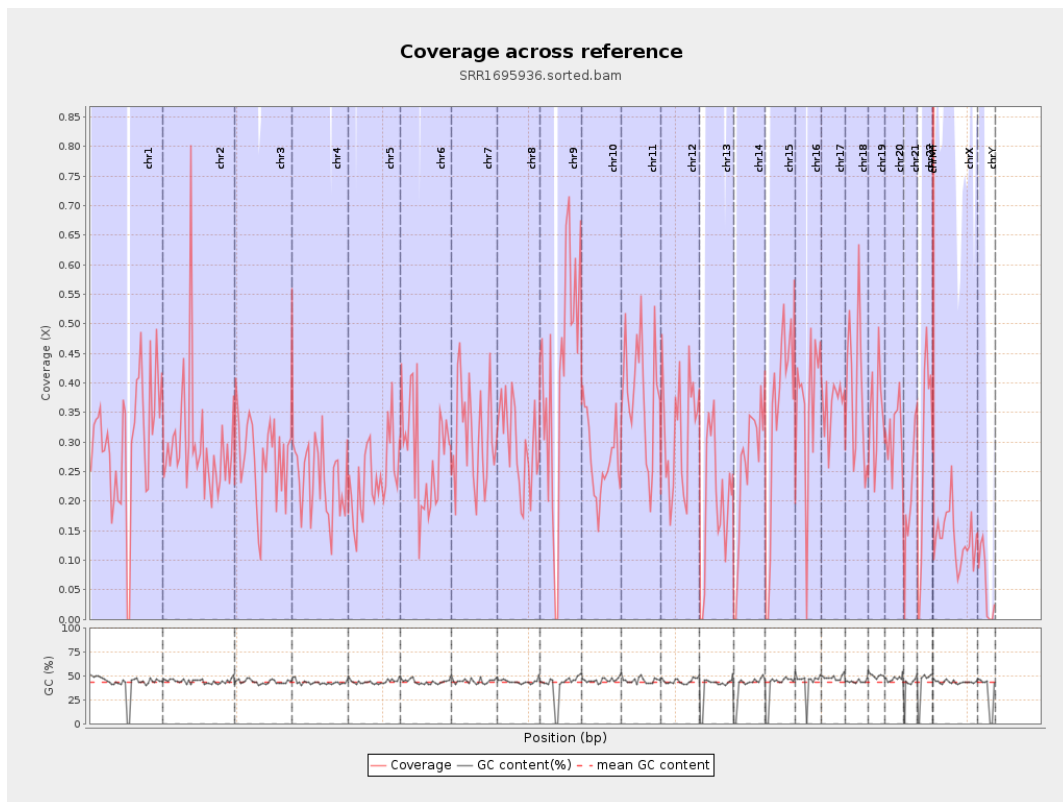
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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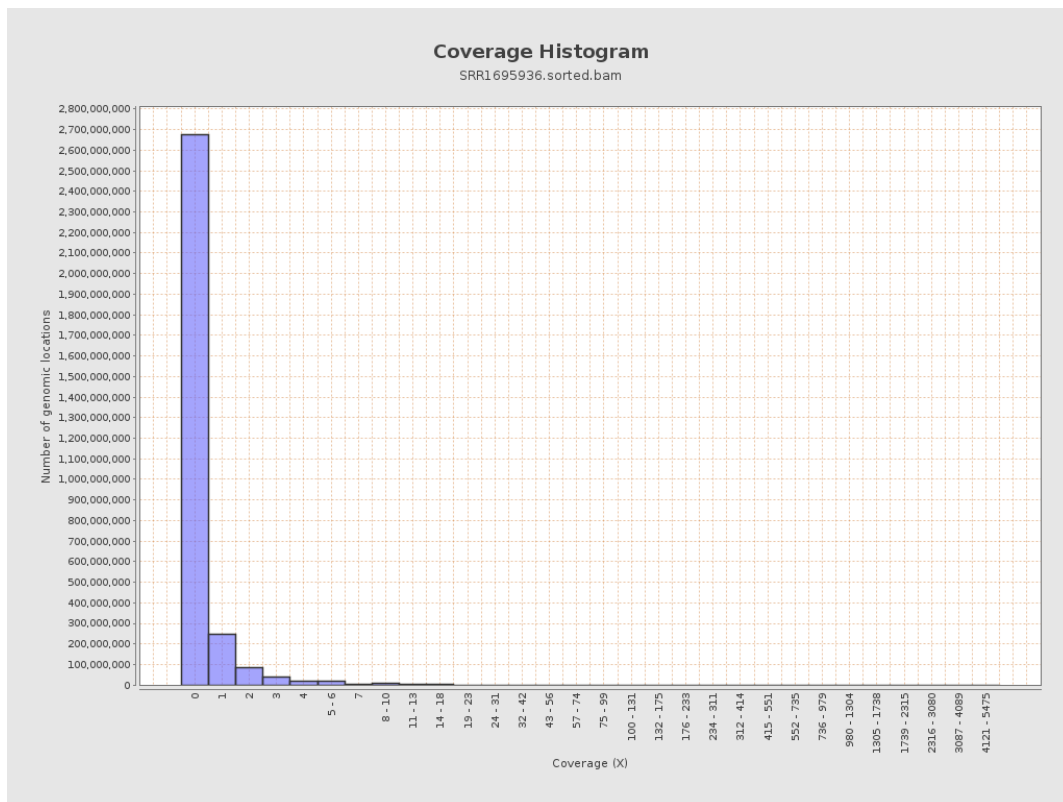
		bases	coverage	deviation
chr1	249250621	75131868	0.3014	1.7495
chr2	243199373	71752790	0.295	4.6657
chr3	198022430	54367492	0.2746	1.0565
chr4	191154276	45485324	0.238	1.1513
chr5	180915260	43878199	0.2425	1.1825
chr6	171115067	47430514	0.2772	2.7572
chr7	159138663	49018710	0.308	2.976
chr8	146364022	42784647	0.2923	2.1218
chr9	141213431	58452585	0.4139	3.5833
chr10	135534747	36915463	0.2724	1.1108
chr11	135006516	51519975	0.3816	5.6471
chr12	133851895	42976631	0.3211	1.3133
chr13	115169878	22676245	0.1969	0.8707
chr14	107349540	27632817	0.2574	1.5402
chr15	102531392	35225738	0.3436	1.2538
chr16	90354753	32671125	0.3616	1.8294
chr17	81195210	29689226	0.3657	1.5731
chr18	78077248	29841383	0.3822	5.4791
chr19	59128983	20533373	0.3473	1.382
chr20	63025520	19780130	0.3138	1.2074
chr21	48129895	10559635	0.2194	2.0096
chr22	51304566	14650235	0.2856	1.1422
chrMT	16571	269379	16.256	49.7094
chrX	155270560	21530224	0.1387	2.9646

chrY	59373566	3530696	0.0595	0.8157
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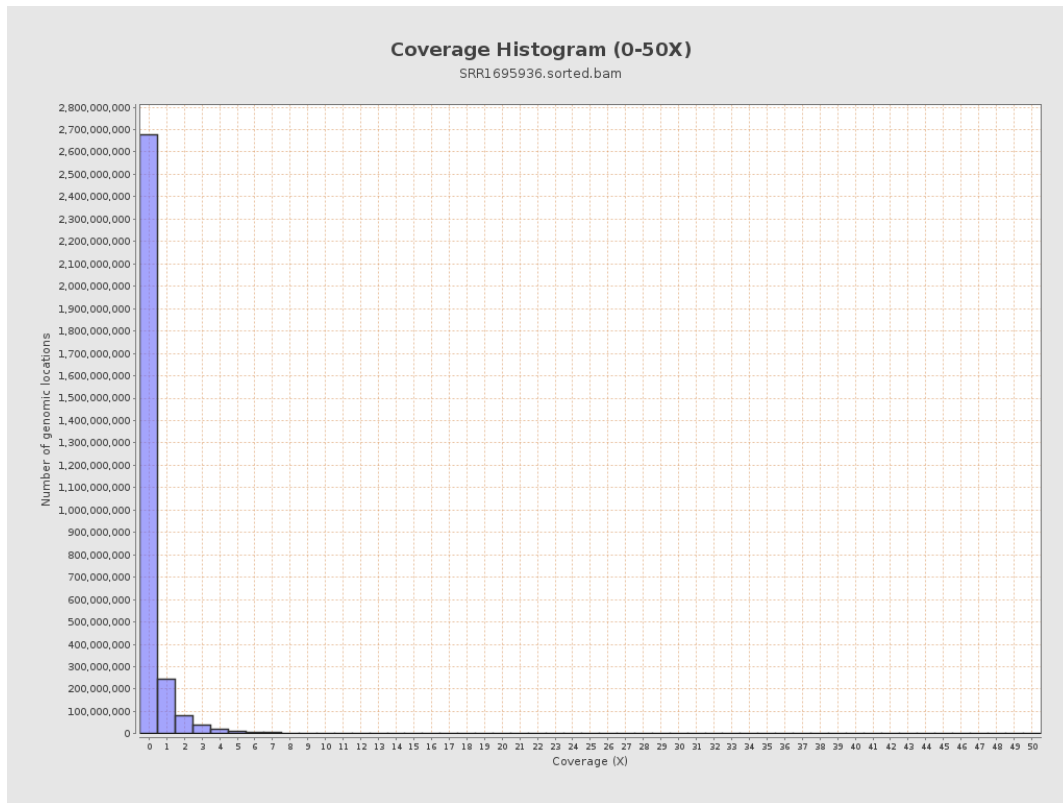
3. Results : Coverage across reference



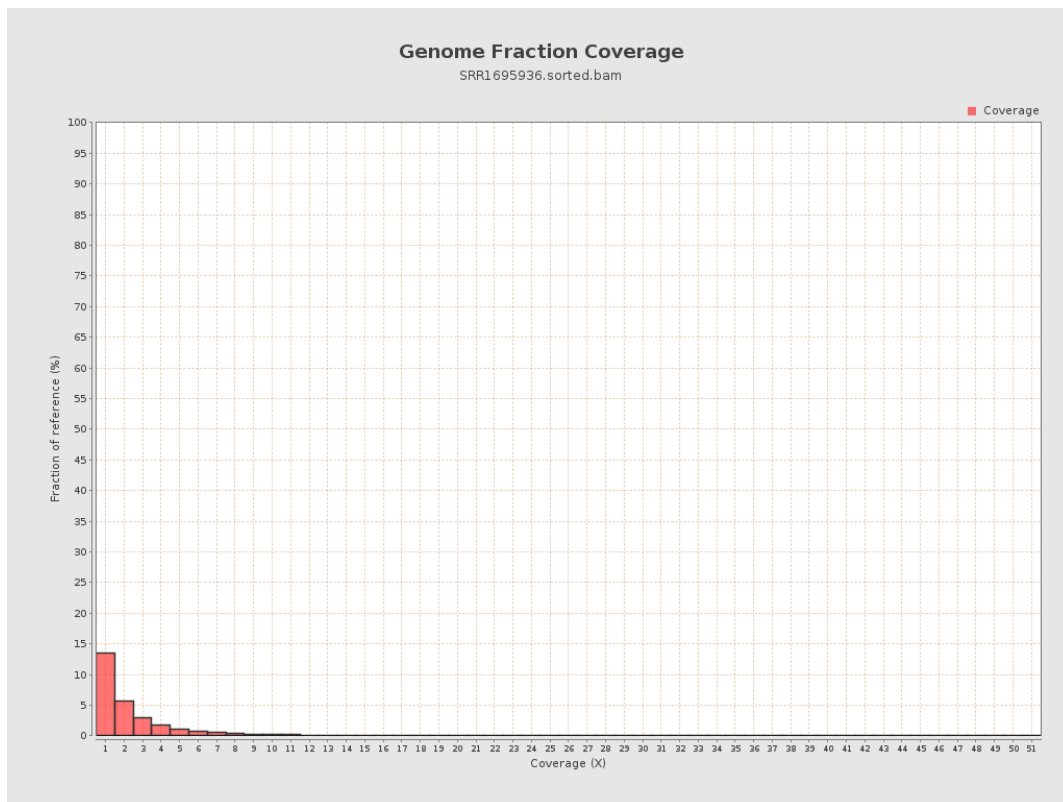
4. Results : Coverage Histogram



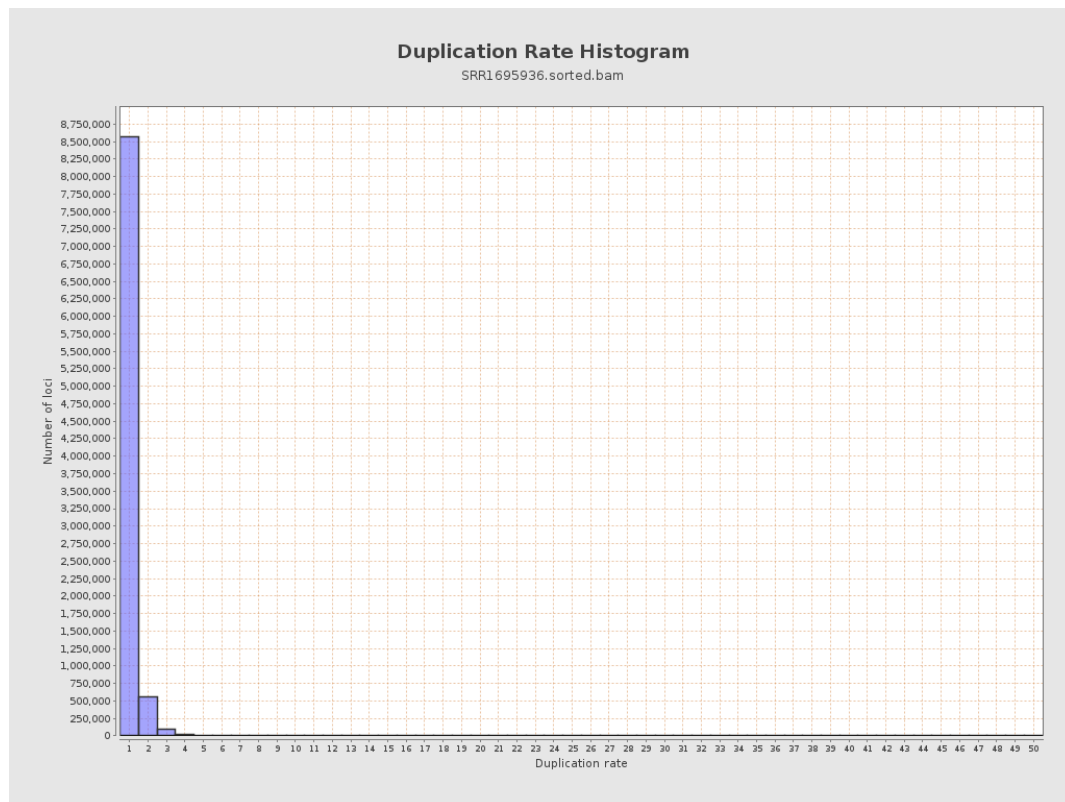
5. Results : Coverage Histogram (0-50X)



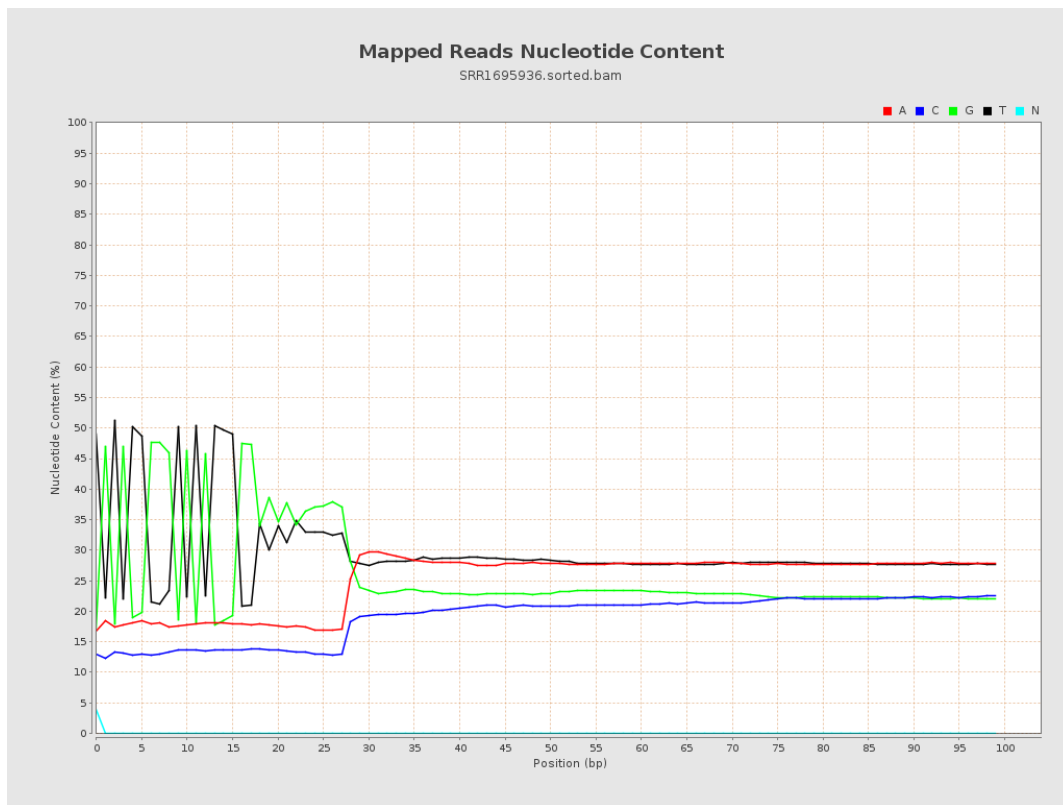
6. Results : Genome Fraction Coverage



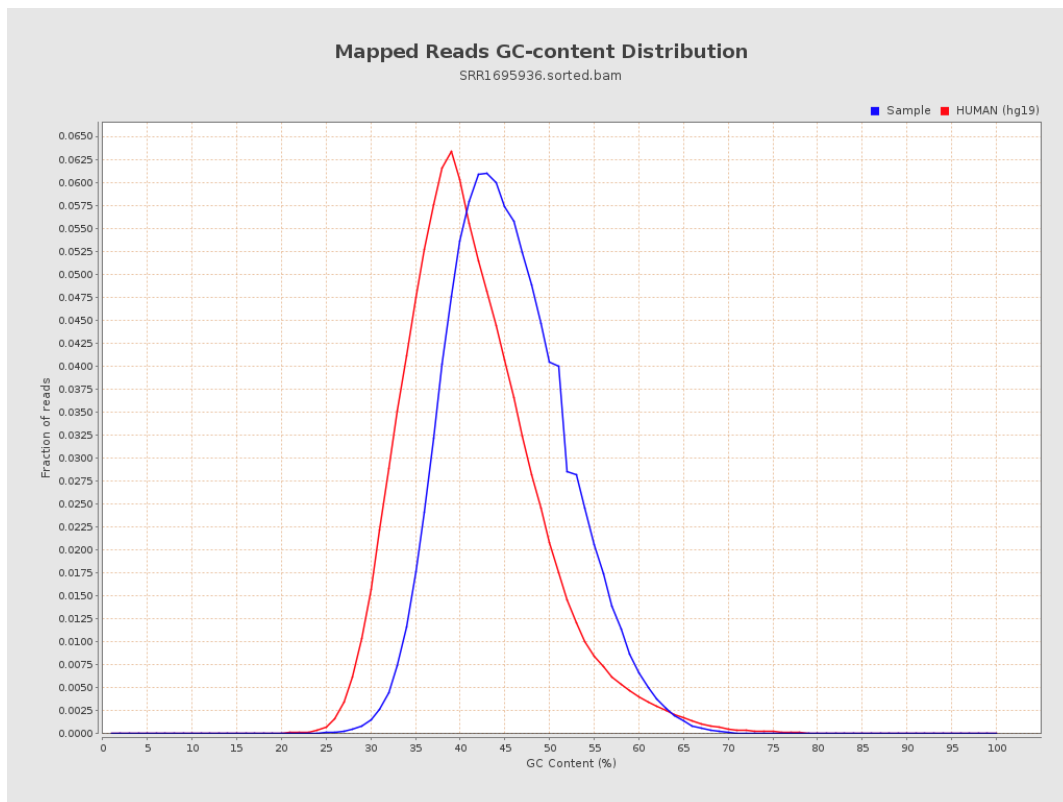
7. Results : Duplication Rate Histogram



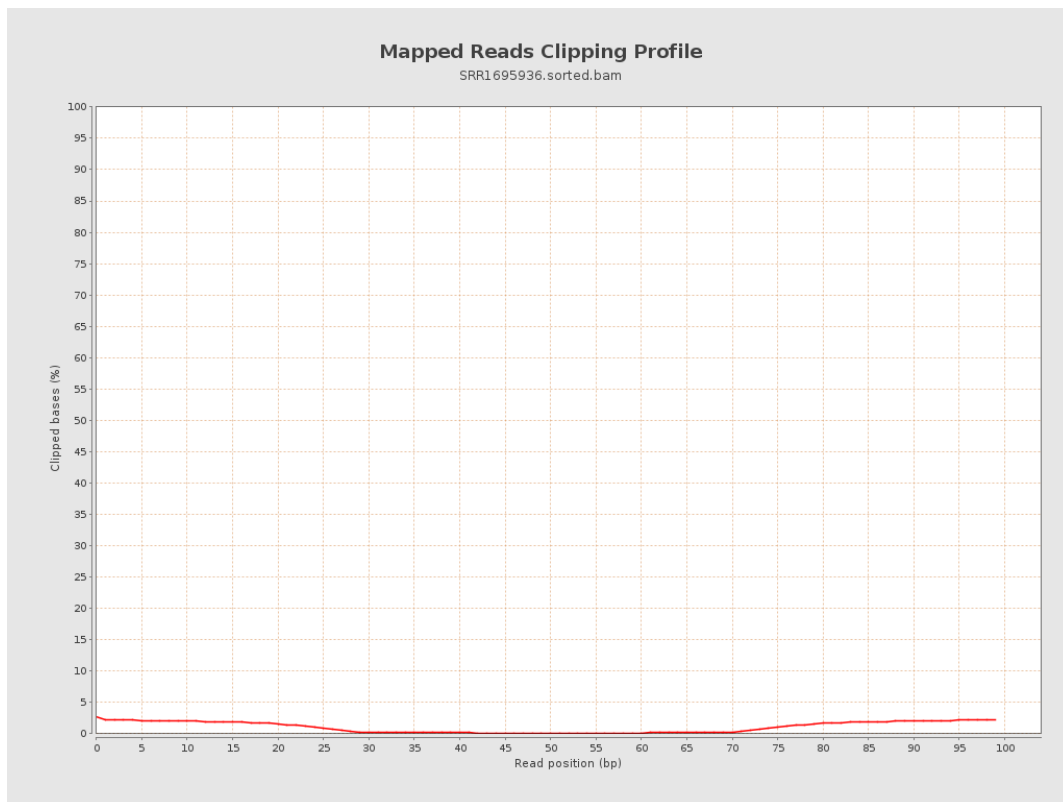
8. Results : Mapped Reads Nucleotide Content



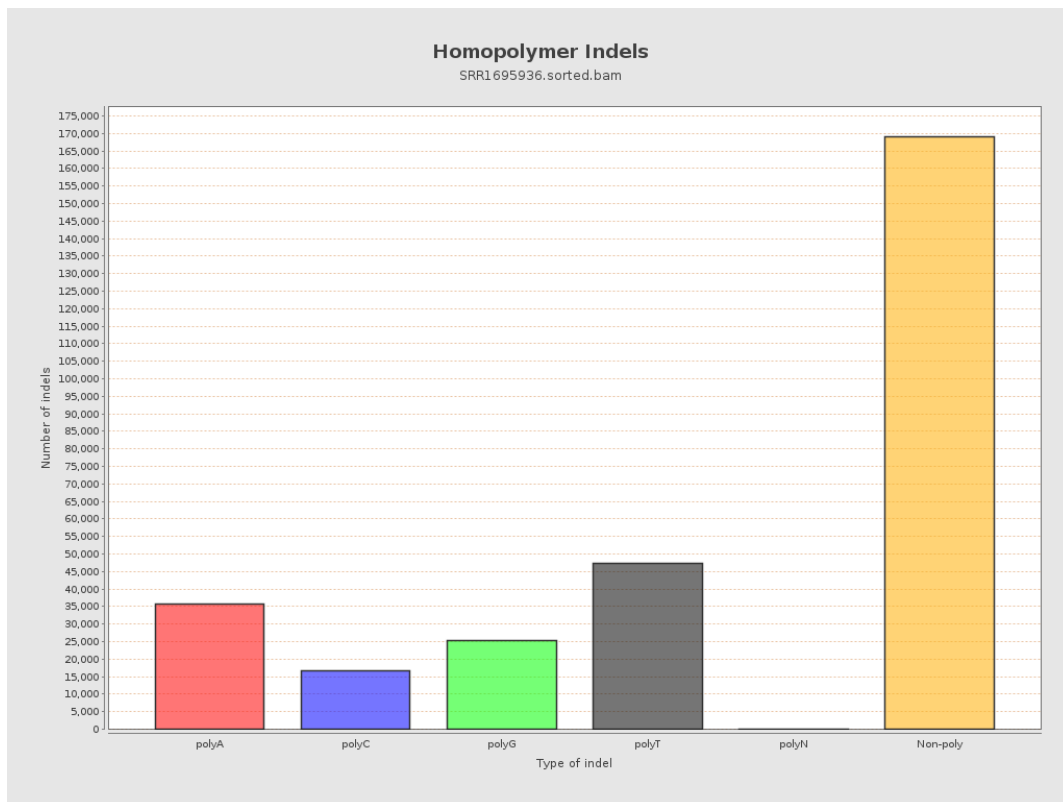
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



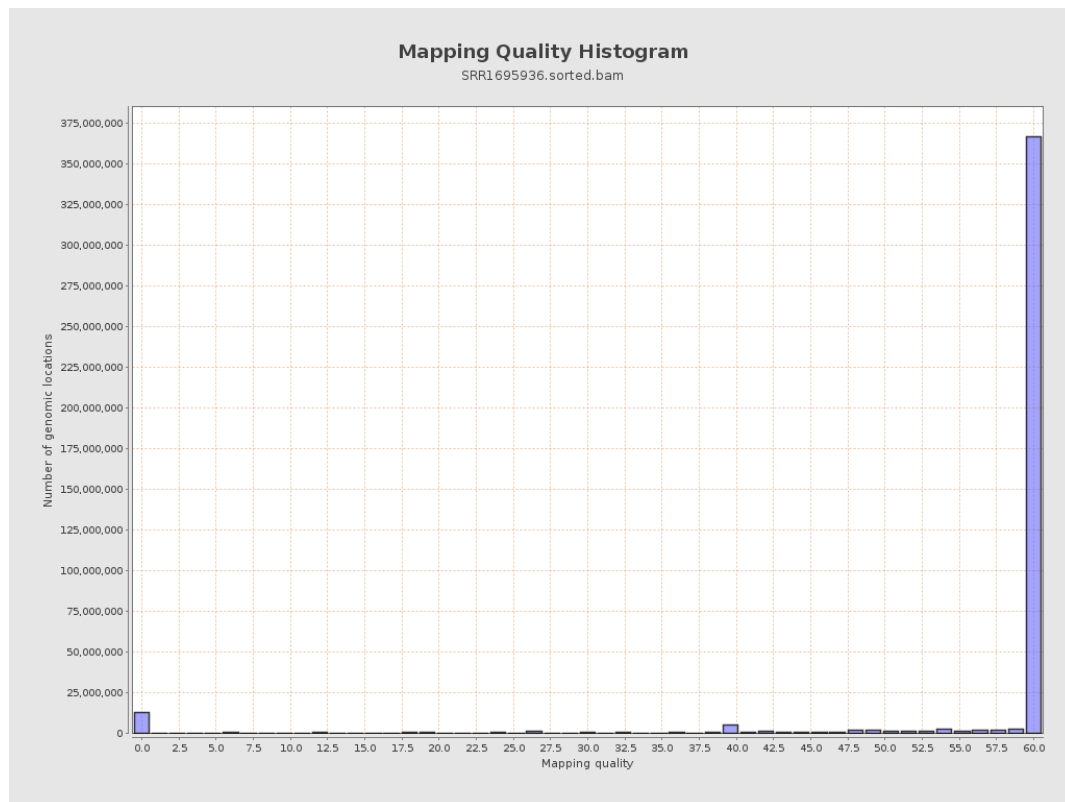
11. Results : Homopolymer Indels



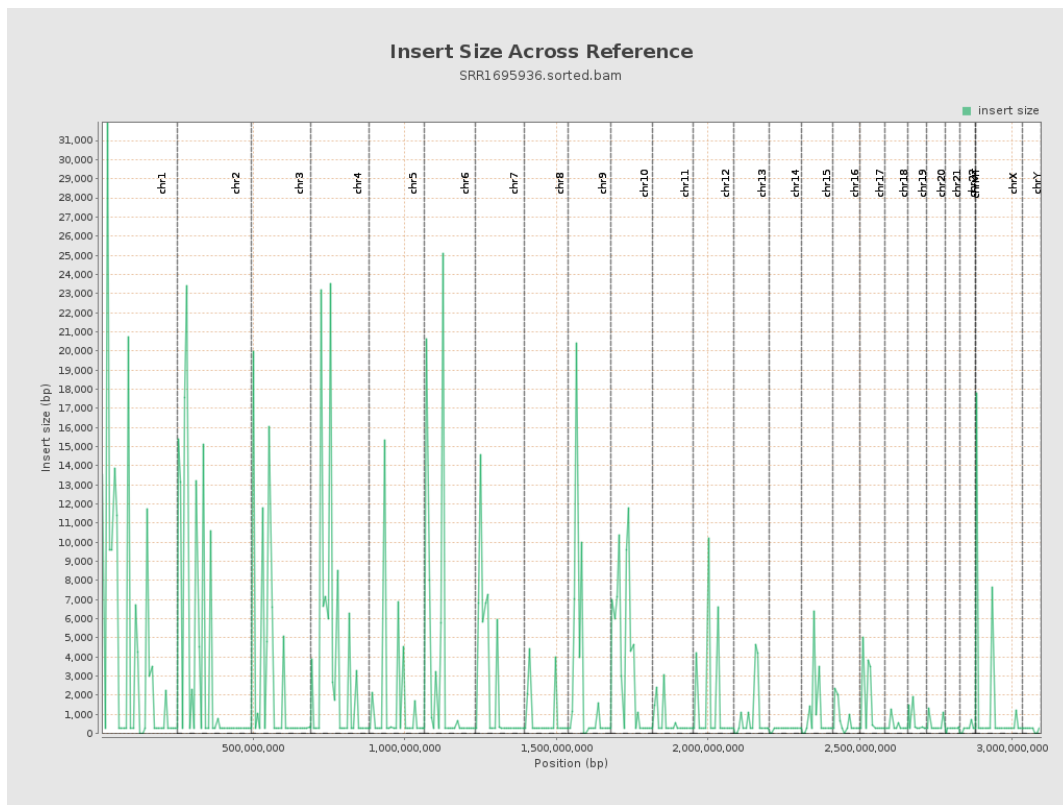
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

