

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695935.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_SRR1695935 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695935_1.fastq.gz SRR1695935_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 02:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,655,238
Mapped reads	10,610,595 / 91.04%
Unmapped reads	1,044,643 / 8.96%
Mapped paired reads	10,610,595 / 91.04%
Mapped reads, first in pair	5,365,537 / 46.04%
Mapped reads, second in pair	5,245,058 / 45%
Mapped reads, both in pair	10,222,882 / 87.71%
Mapped reads, singletons	387,713 / 3.33%
Secondary alignments	0
Supplementary alignments	25,976 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	1,118,558 / 9.6%
Duplication rate	6.65%
Clipped reads	6,726,052 / 57.71%

2.2. ACGT Content

Number/percentage of A's	227,316,233 / 25.43%
Number/percentage of C's	169,678,892 / 18.98%
Number/percentage of T's	267,635,341 / 29.94%
Number/percentage of G's	228,860,187 / 25.61%
Number/percentage of N's	290,504 / 0.03%

GC Percentage	44.59%
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2.3. Coverage

Mean	0.2888
Standard Deviation	3.6574

2.4. Mapping Quality

Mean Mapping Quality	52.47
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2.5. Insert size

Mean	65,403.89
Standard Deviation	2,454,365.62
P25/Median/P75	269 / 282 / 294

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	13,692,550
Insertions	90,200
Mapped reads with at least one insertion	0.84%
Deletions	215,401
Mapped reads with at least one deletion	2%
Homopolymer indels	41.53%

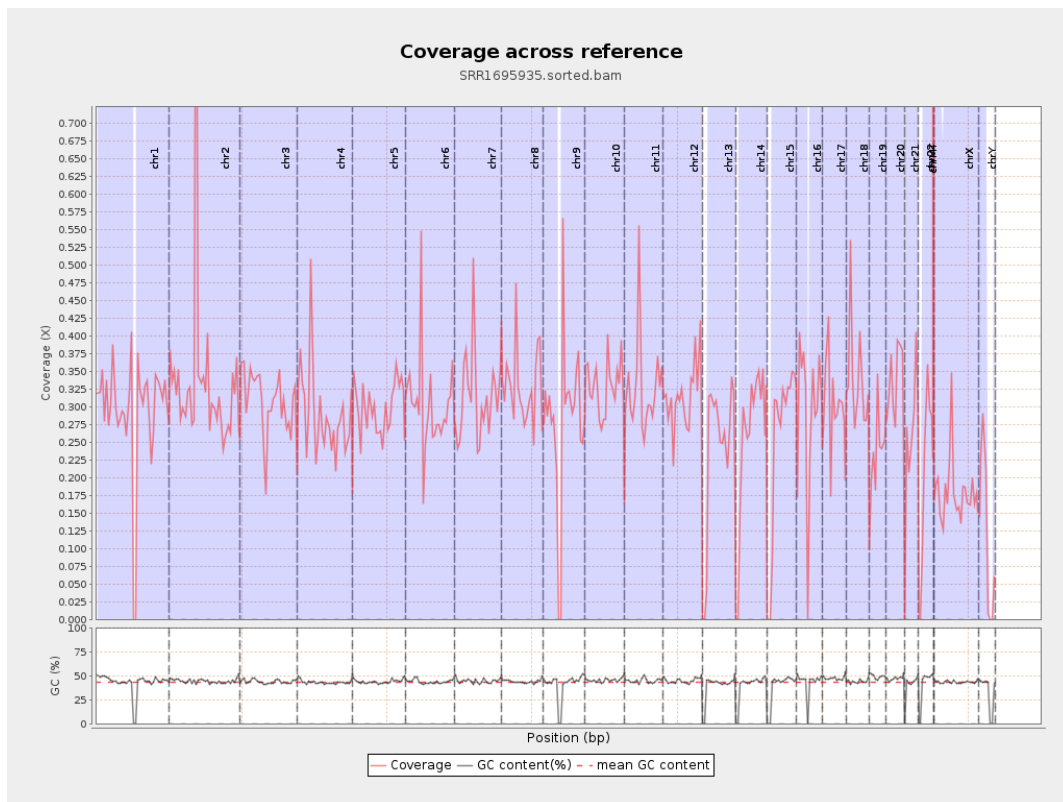
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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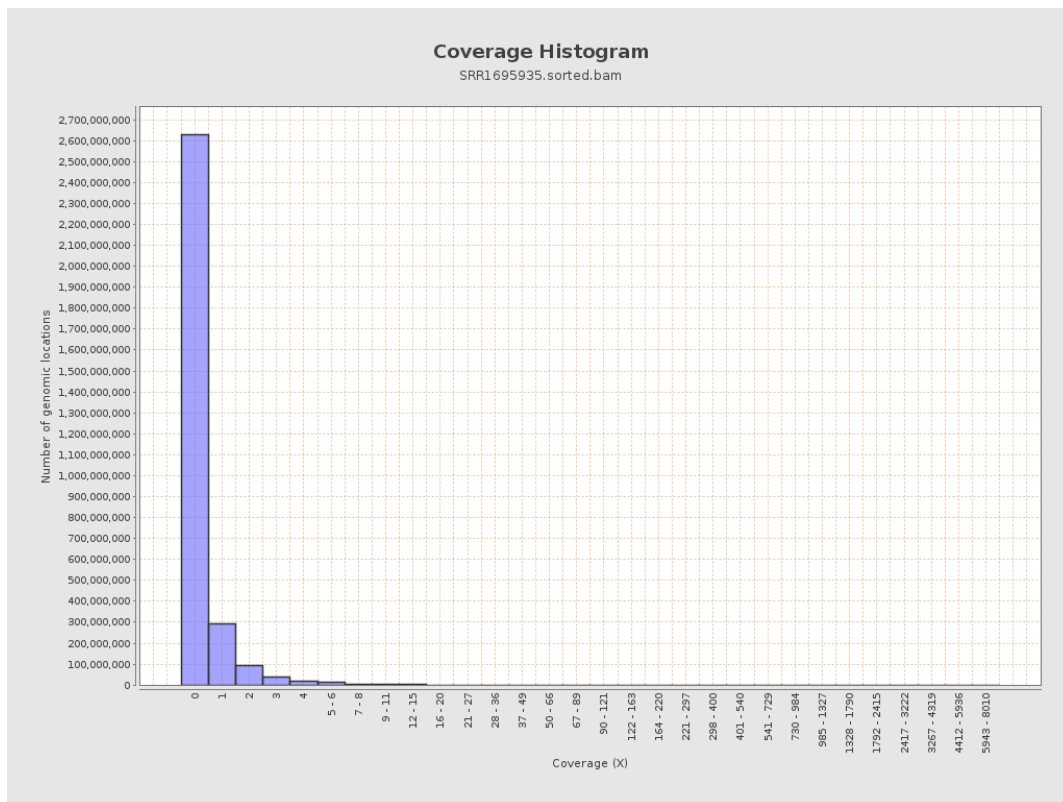
		bases	coverage	deviation
chr1	249250621	73019112	0.293	2.4885
chr2	243199373	81793552	0.3363	6.9859
chr3	198022430	60737497	0.3067	1.0191
chr4	191154276	54833086	0.2869	1.4824
chr5	180915260	53925056	0.2981	1.3905
chr6	171115067	51748064	0.3024	4.2733
chr7	159138663	49864979	0.3133	4.6031
chr8	146364022	48019379	0.3281	3.2627
chr9	141213431	39470694	0.2795	5.2016
chr10	135534747	44566076	0.3288	1.436
chr11	135006516	43217429	0.3201	6.5819
chr12	133851895	41861888	0.3127	1.3996
chr13	115169878	27267278	0.2368	0.8863
chr14	107349540	27344946	0.2547	1.9168
chr15	102531392	26046252	0.254	0.9455
chr16	90354753	26628132	0.2947	1.6314
chr17	81195210	24173770	0.2977	2.3865
chr18	78077248	26611095	0.3408	8.3104
chr19	59128983	14046038	0.2375	1.487
chr20	63025520	21064549	0.3342	1.2144
chr21	48129895	12324748	0.2561	3.0377
chr22	51304566	10384395	0.2024	0.8643
chrMT	16571	150782	9.0991	22.9394
chrX	155270560	28045293	0.1806	2.8736

chrY	59373566	6960480	0.1172	1.1583
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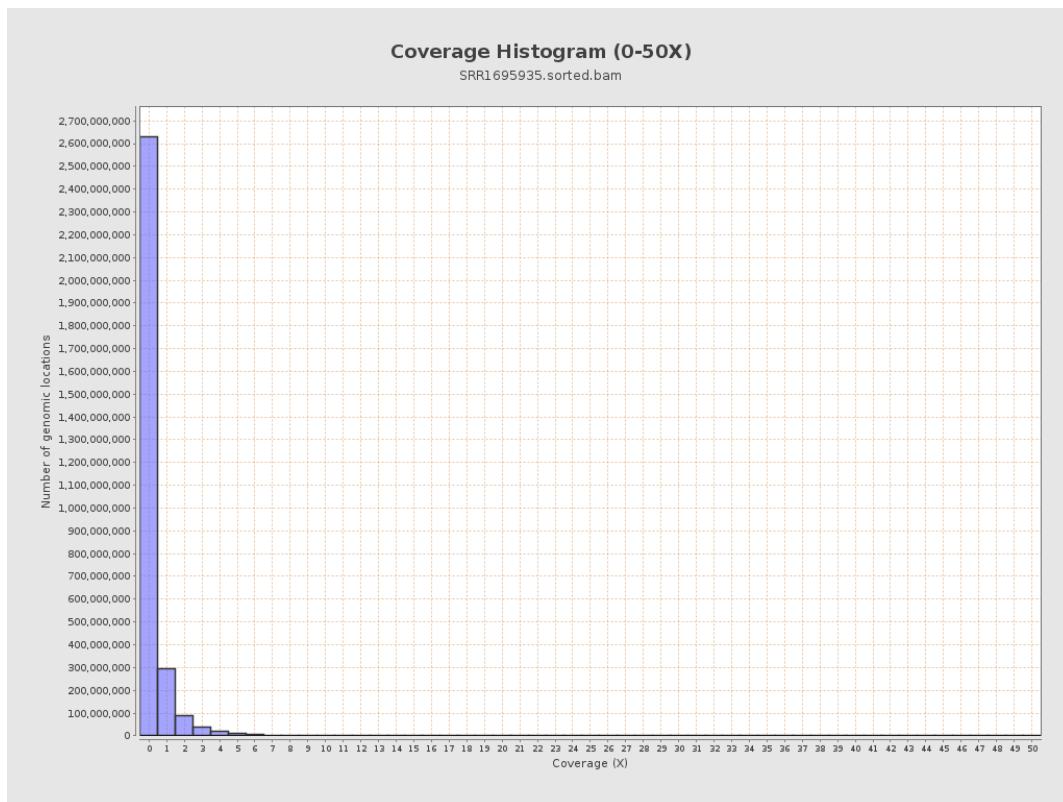
3. Results : Coverage across reference



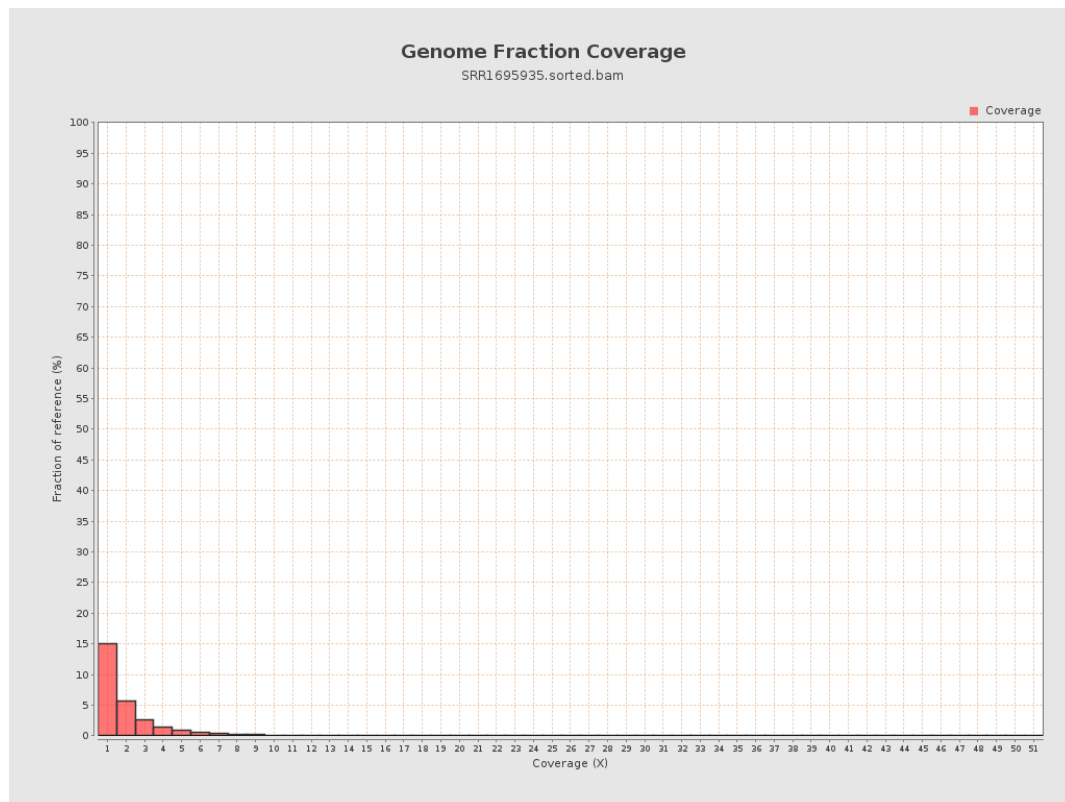
4. Results : Coverage Histogram



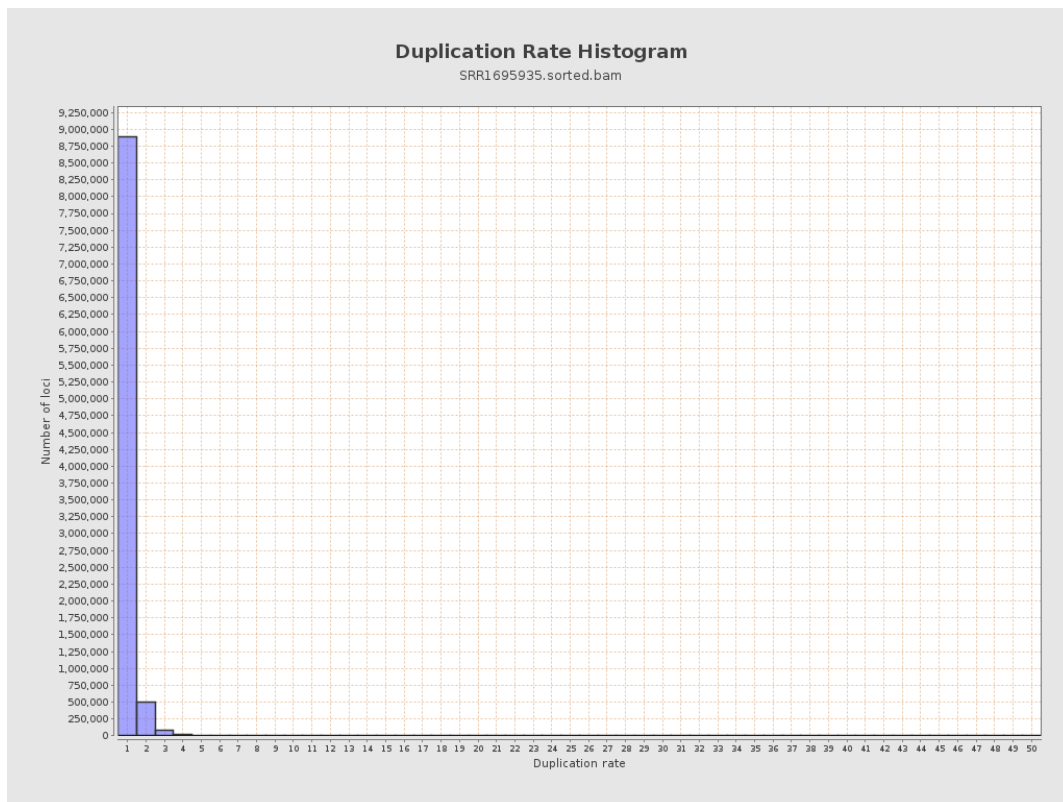
5. Results : Coverage Histogram (0-50X)



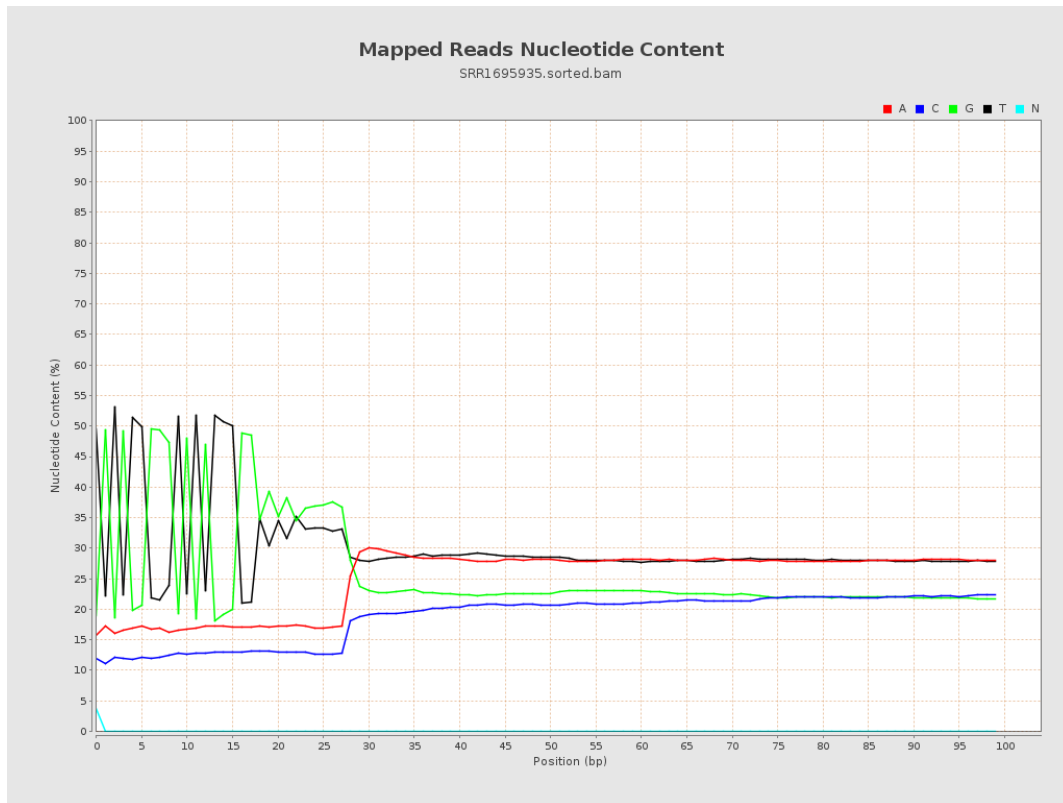
6. Results : Genome Fraction Coverage



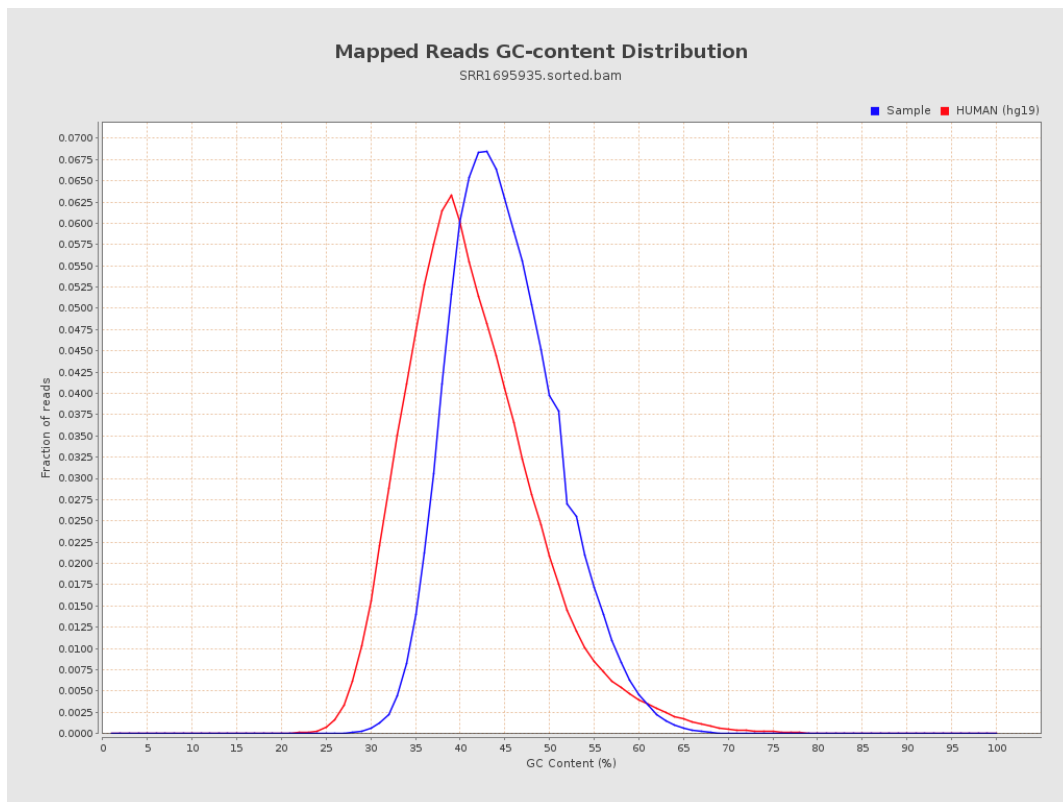
7. Results : Duplication Rate Histogram



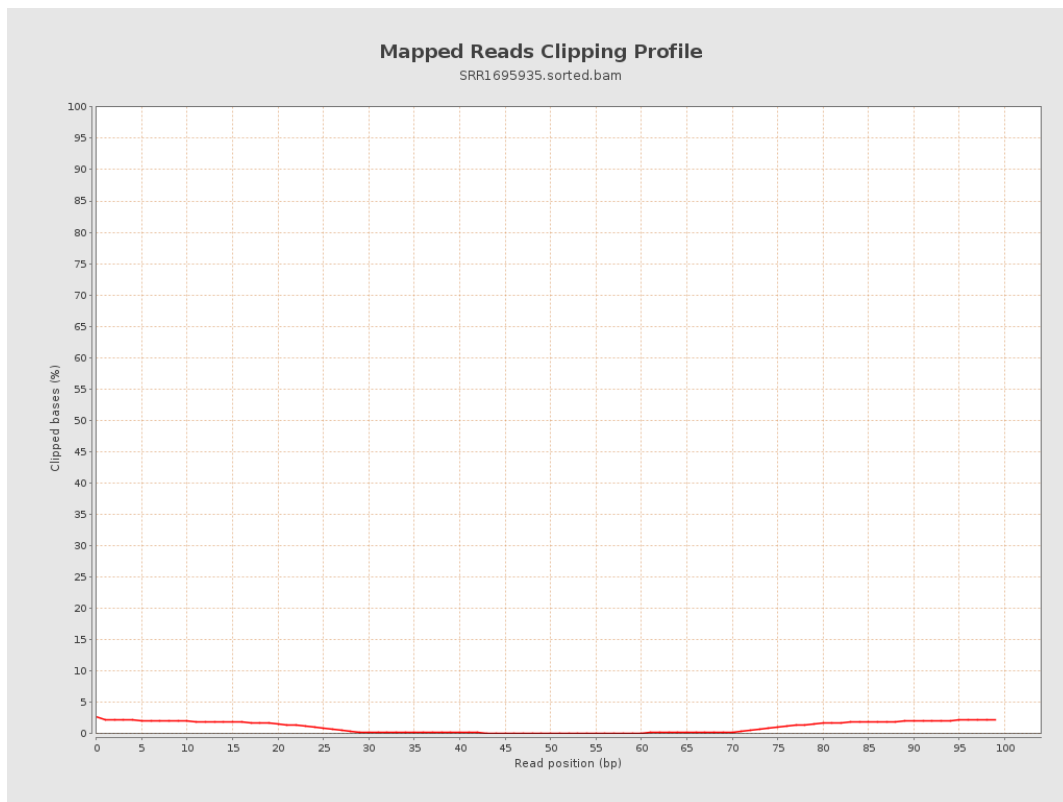
8. Results : Mapped Reads Nucleotide Content



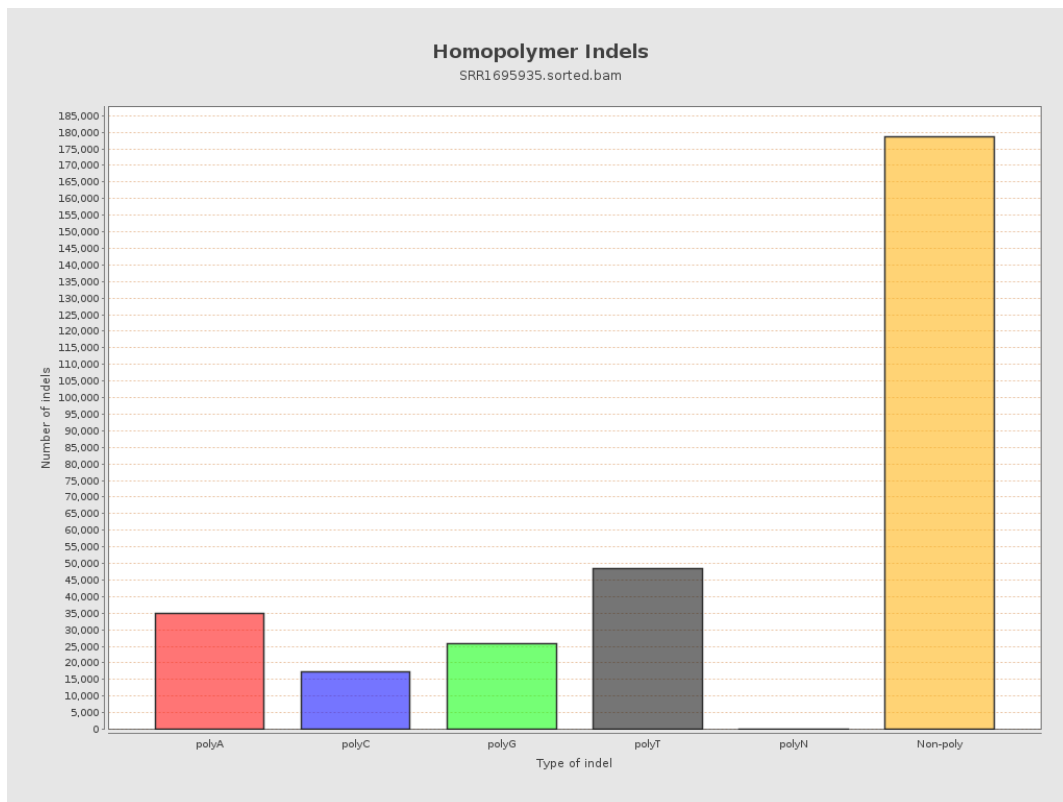
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



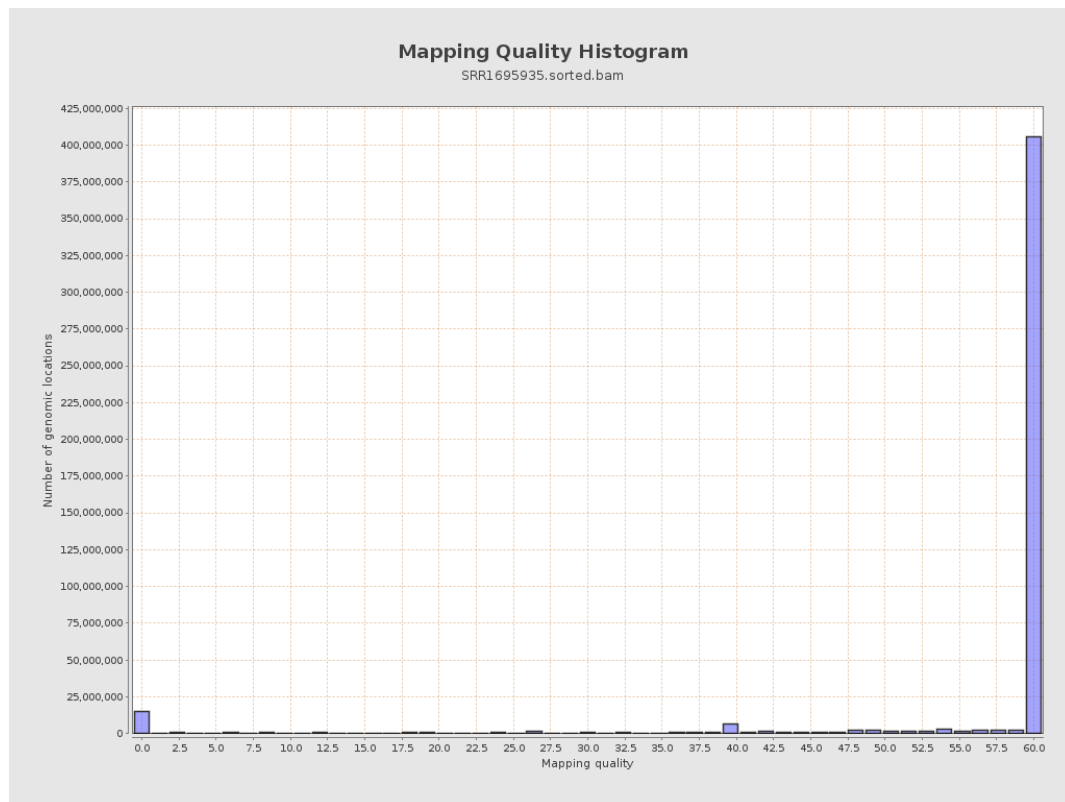
11. Results : Homopolymer Indels



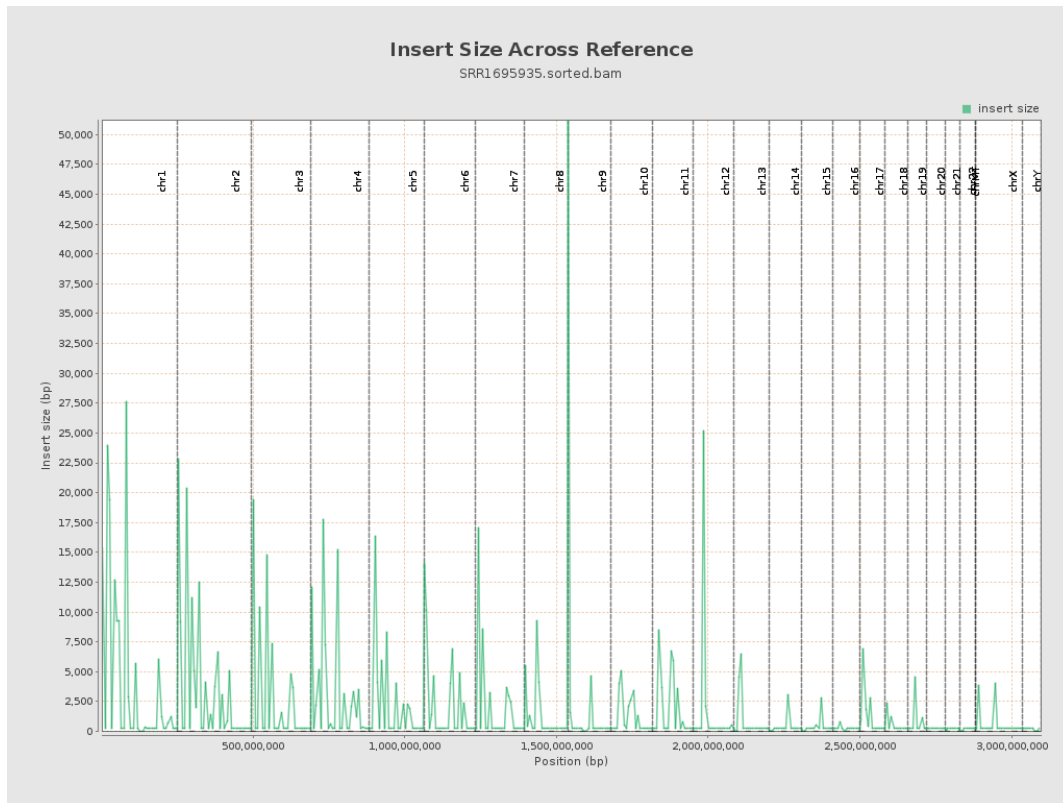
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

