

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 23:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695925.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_SRR1695925 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695925_1.fastq.gz SRR1695925_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 23:40:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	389,435,188
Mapped reads	387,273,556 / 99.44%
Unmapped reads	2,161,632 / 0.56%
Mapped paired reads	387,273,556 / 99.44%
Mapped reads, first in pair	194,293,272 / 49.89%
Mapped reads, second in pair	192,980,284 / 49.55%
Mapped reads, both in pair	385,676,322 / 99.03%
Mapped reads, singletons	1,597,234 / 0.41%
Secondary alignments	0
Supplementary alignments	3,437,146 / 0.88%
Read min/max/mean length	30 / 100 / 100.36
Duplicated reads (estimated)	66,103,190 / 16.97%
Duplication rate	16.11%
Clipped reads	18,064,296 / 4.64%

2.2. ACGT Content

Number/percentage of A's	11,628,037,642 / 30.21%
Number/percentage of C's	7,574,316,669 / 19.68%
Number/percentage of T's	11,624,237,184 / 30.2%
Number/percentage of G's	7,658,653,289 / 19.9%
Number/percentage of N's	6,726,002 / 0.02%

GC Percentage	39.57%
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2.3. Coverage

Mean	12.4365
Standard Deviation	16.6807

2.4. Mapping Quality

Mean Mapping Quality	54.51
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2.5. Insert size

Mean	41,688.75
Standard Deviation	1,945,246.4
P25/Median/P75	300 / 310 / 319

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	133,772,334
Insertions	2,636,694
Mapped reads with at least one insertion	0.67%
Deletions	3,506,014
Mapped reads with at least one deletion	0.89%
Homopolymer indels	46.39%

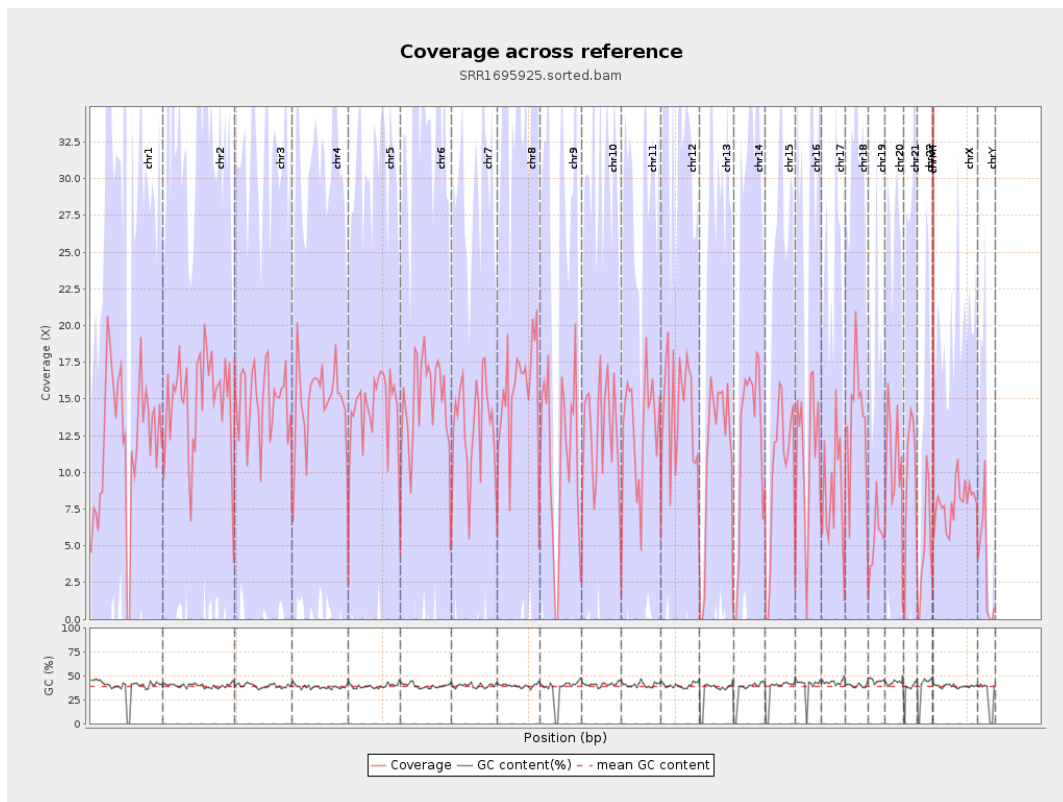
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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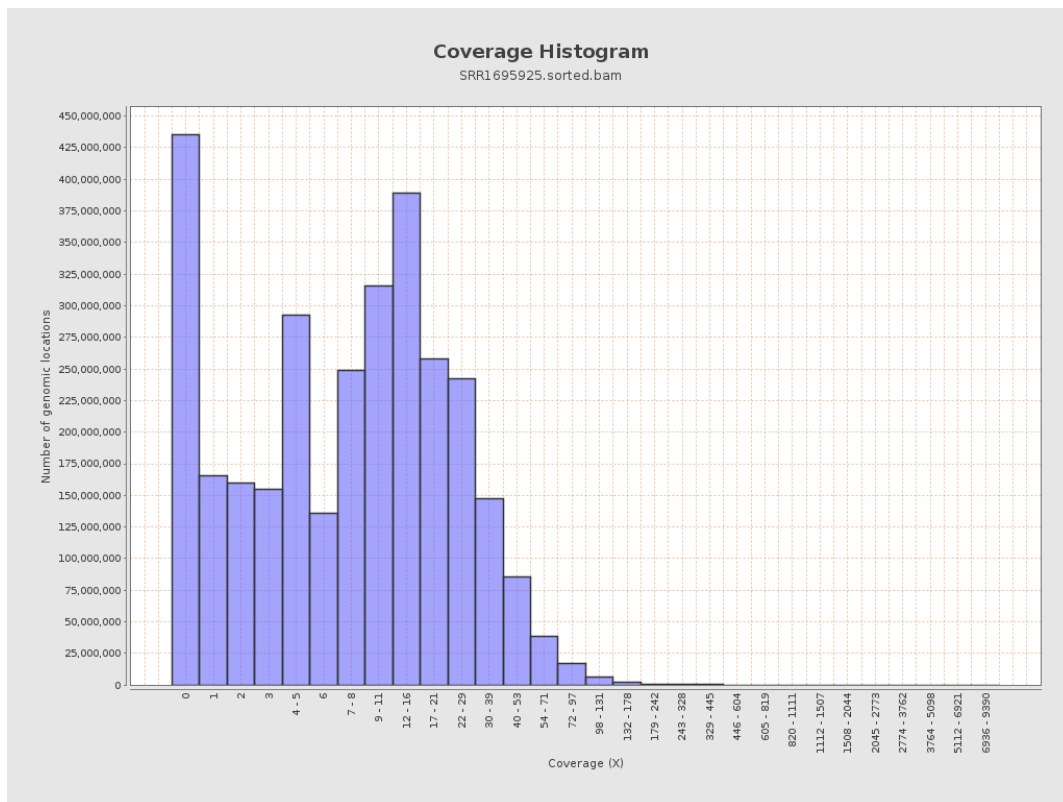
		bases	coverage	deviation
chr1	249250621	3019466097	12.1142	19.0728
chr2	243199373	3604789919	14.8224	17.132
chr3	198022430	2943864111	14.8663	16.1376
chr4	191154276	2849089320	14.9047	15.5087
chr5	180915260	2569643407	14.2036	15.7562
chr6	171115067	2575799810	15.053	18.4639
chr7	159138663	2071573939	13.0174	15.5952
chr8	146364022	2293618003	15.6706	19.2519
chr9	141213431	1556212774	11.0203	16.1823
chr10	135534747	1758043774	12.9712	17.091
chr11	135006516	1767359042	13.0909	15.574
chr12	133851895	1901651972	14.2071	18.0828
chr13	115169878	1303657800	11.3194	15.3657
chr14	107349540	1303420821	12.1418	16.5849
chr15	102531392	1030785140	10.0534	14.667
chr16	90354753	985188897	10.9036	18.4019
chr17	81195210	711082889	8.7577	14.8218
chr18	78077248	1065995959	13.6531	16.8877
chr19	59128983	327860156	5.5448	13.8123
chr20	63025520	684481862	10.8604	15.1365
chr21	48129895	465503053	9.6718	19.9155
chr22	51304566	260894681	5.0852	11.4179
chrMT	16571	1823668	110.0518	47.282
chrX	155270560	1233041465	7.9412	11.8247

chrY	59373566	214809691	3.6179	9.8141
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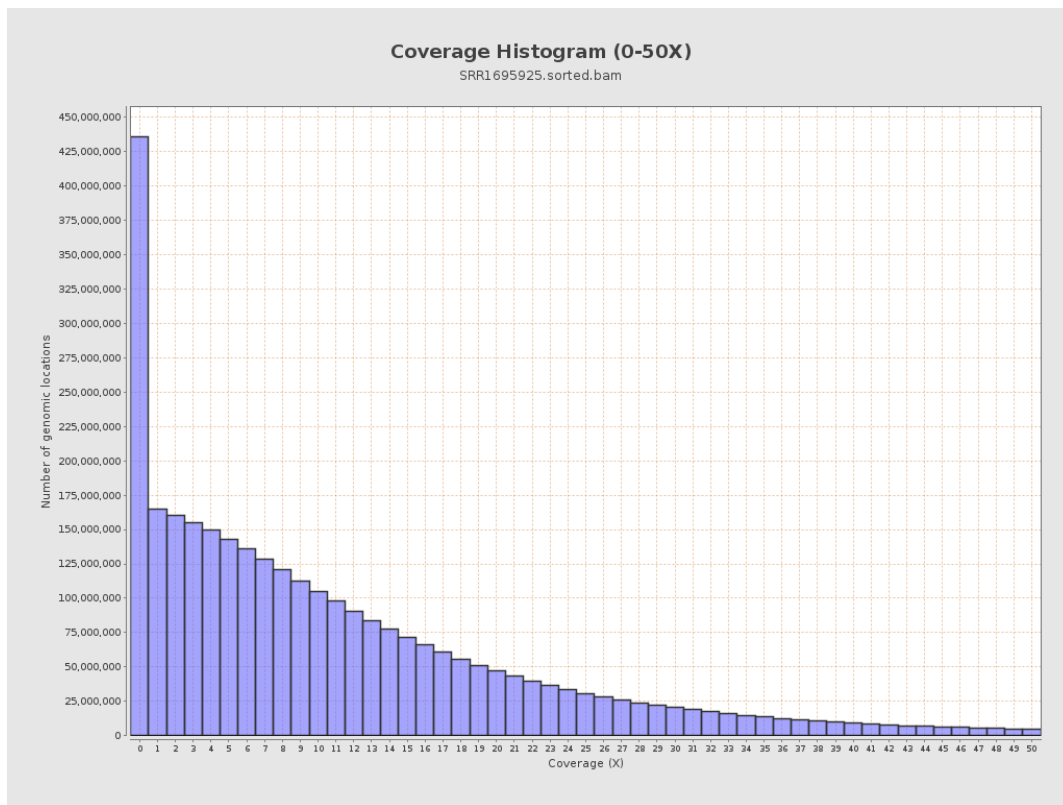
3. Results : Coverage across reference



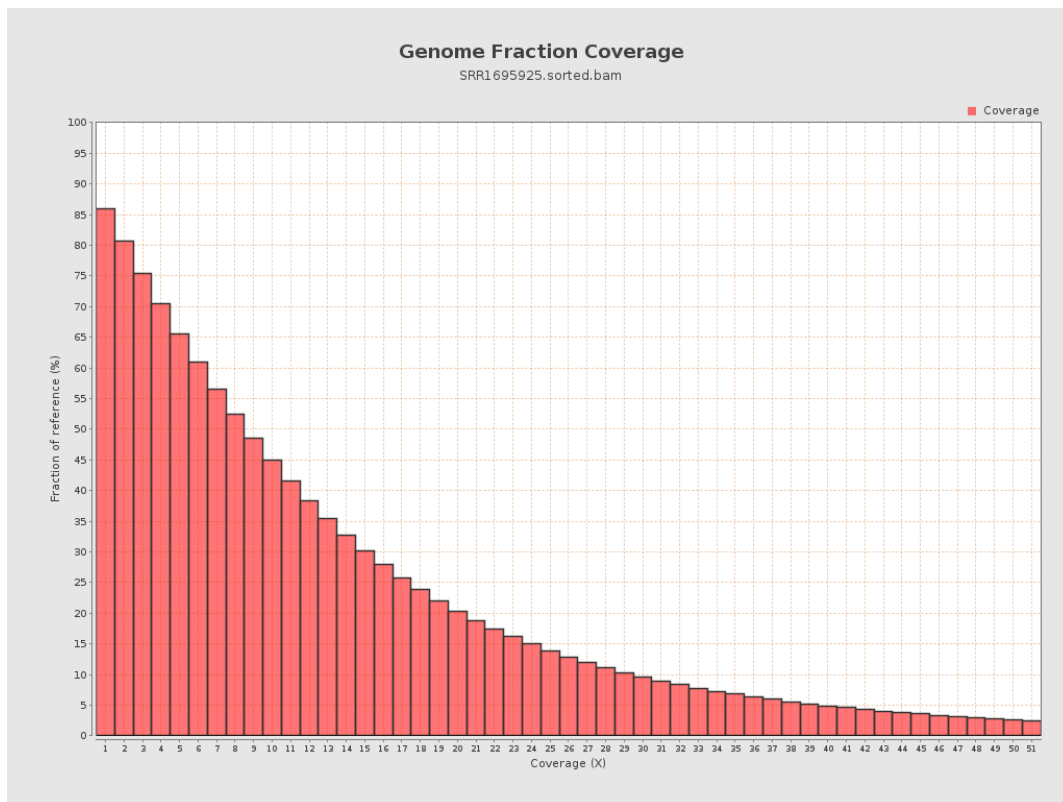
4. Results : Coverage Histogram



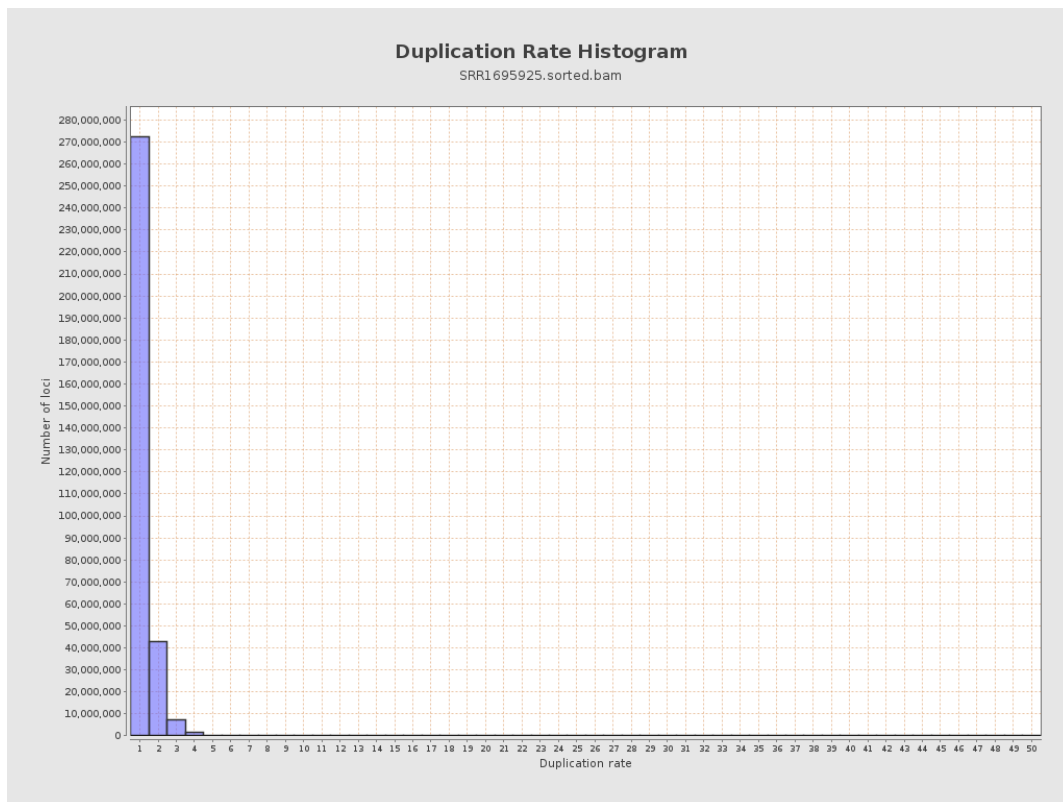
5. Results : Coverage Histogram (0-50X)



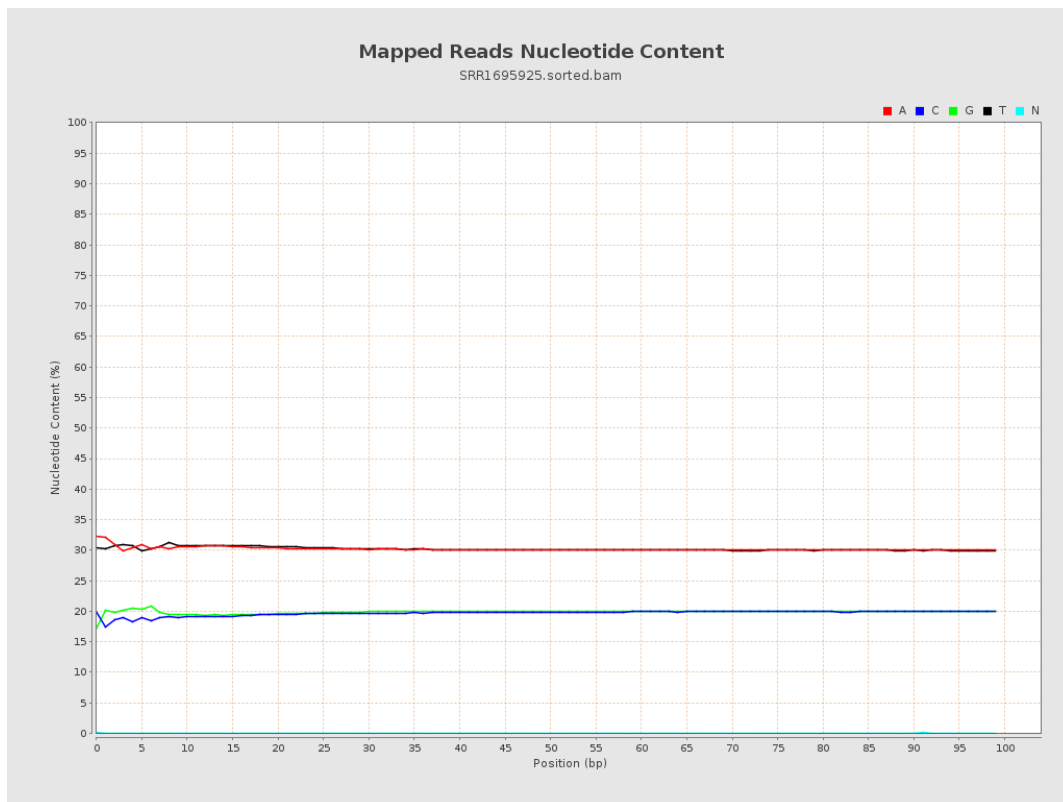
6. Results : Genome Fraction Coverage



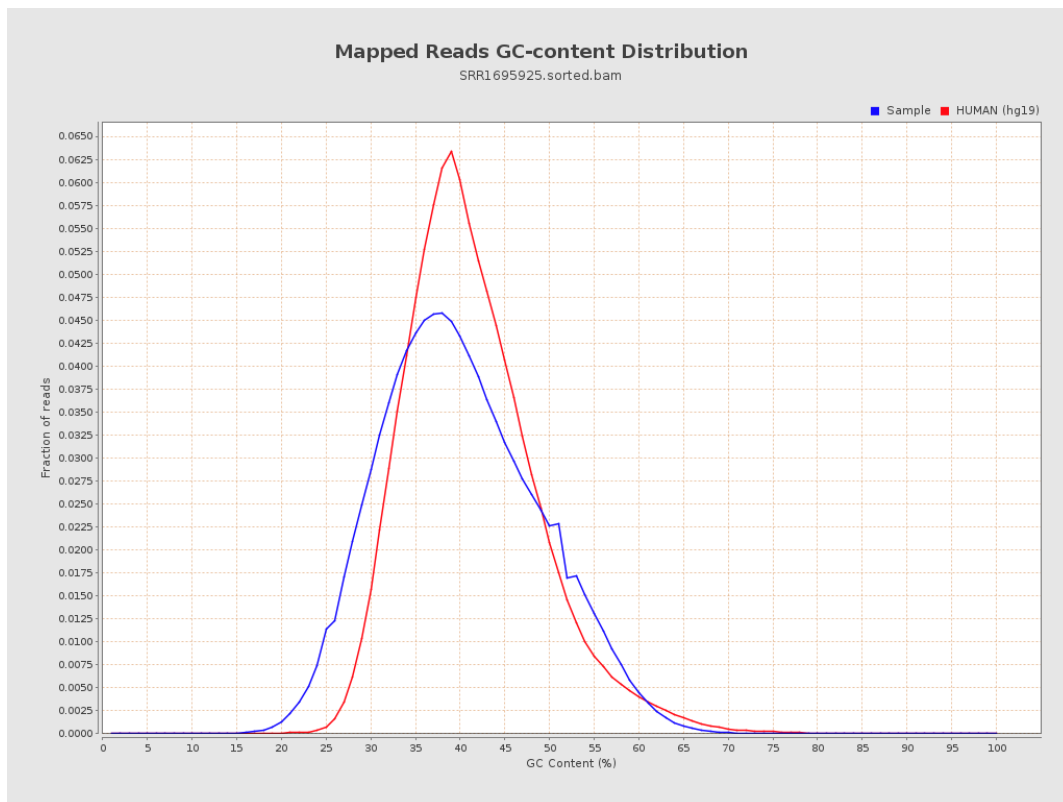
7. Results : Duplication Rate Histogram



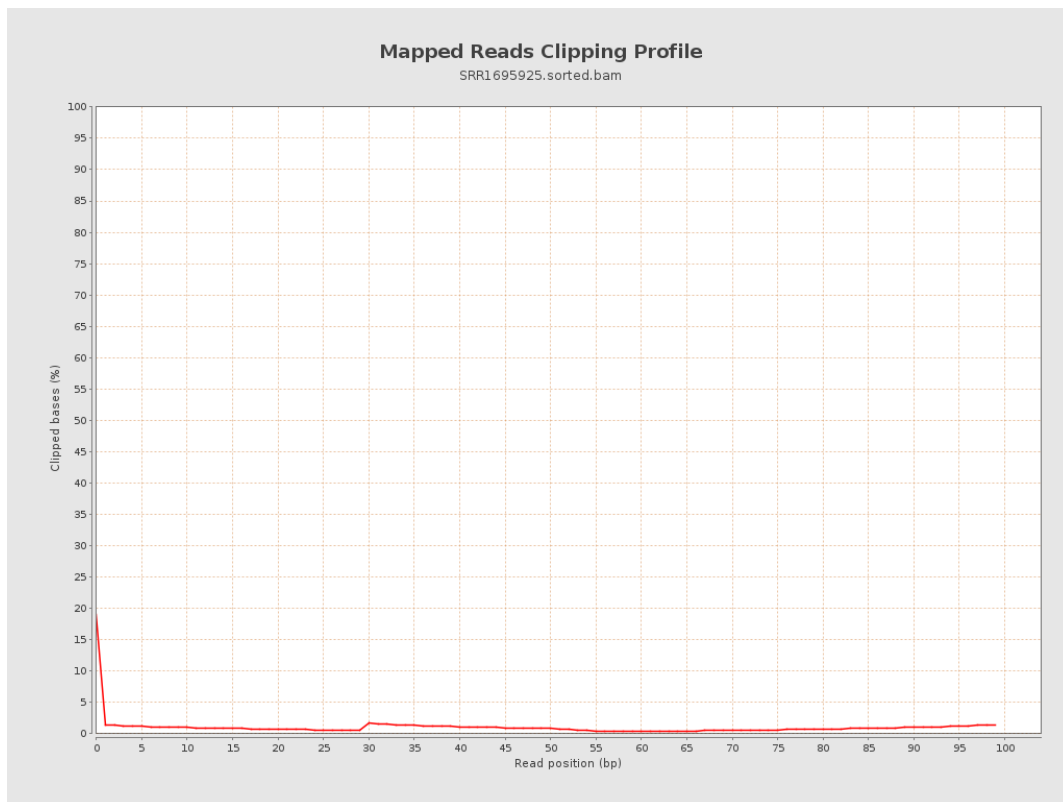
8. Results : Mapped Reads Nucleotide Content



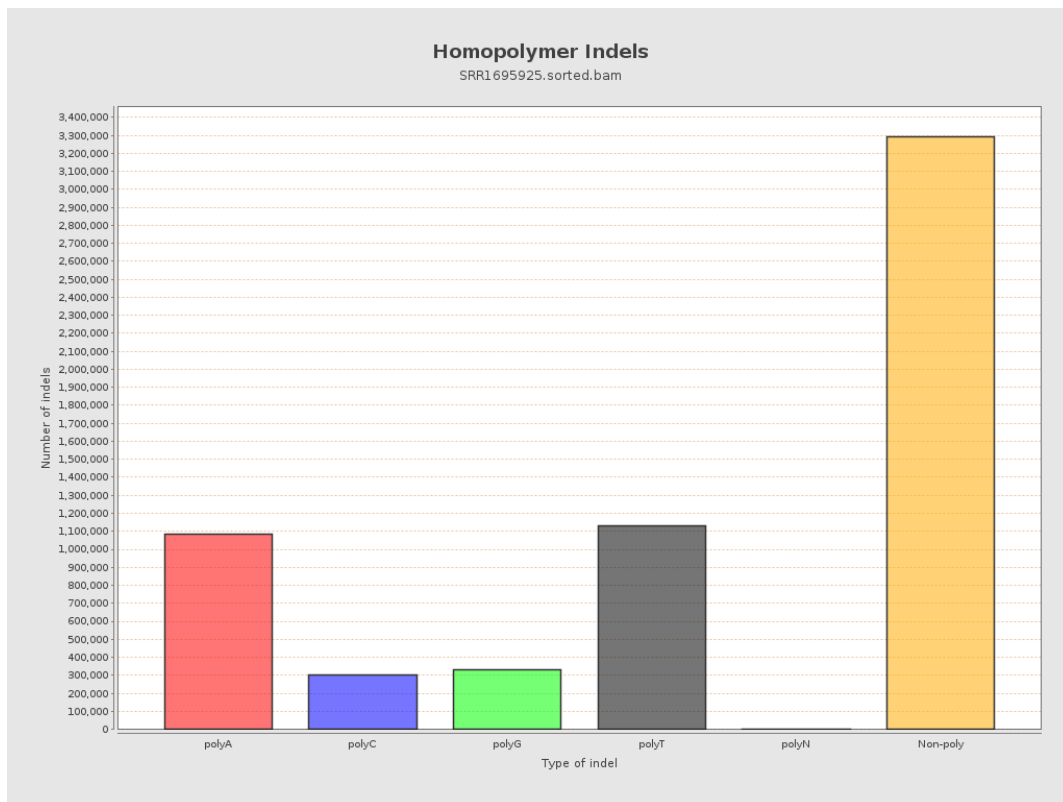
9. Results : Mapped Reads GC-content Distribution



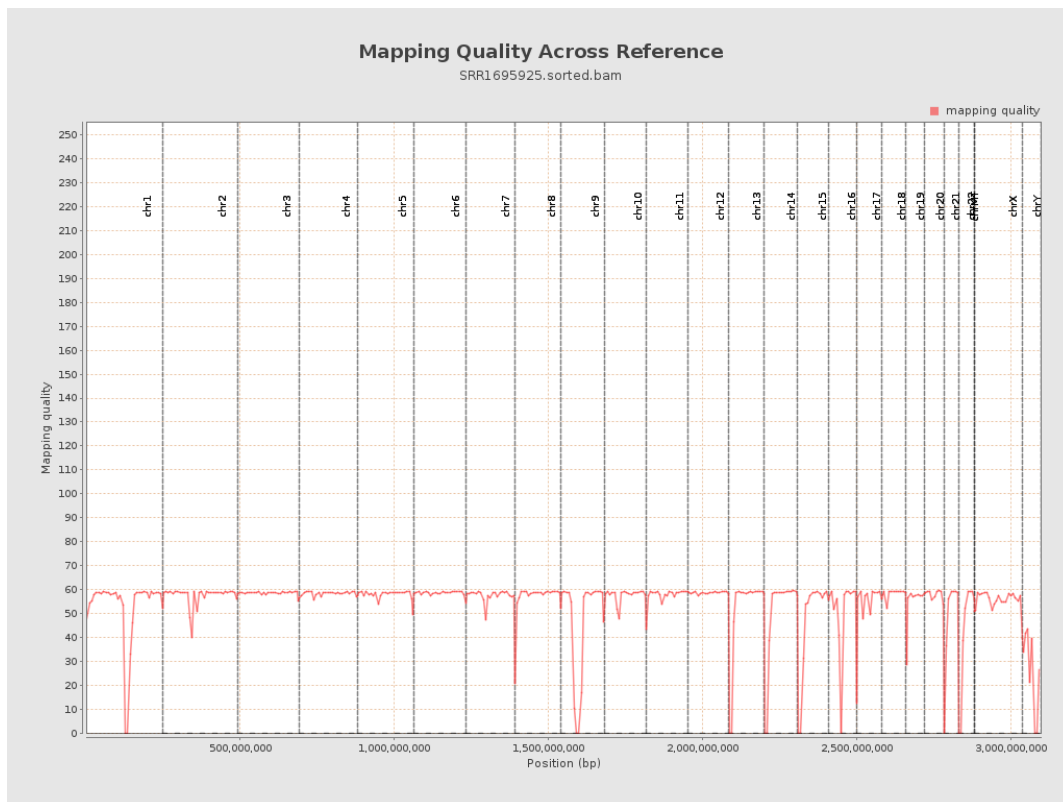
10. Results : Mapped Reads Clipping Profile



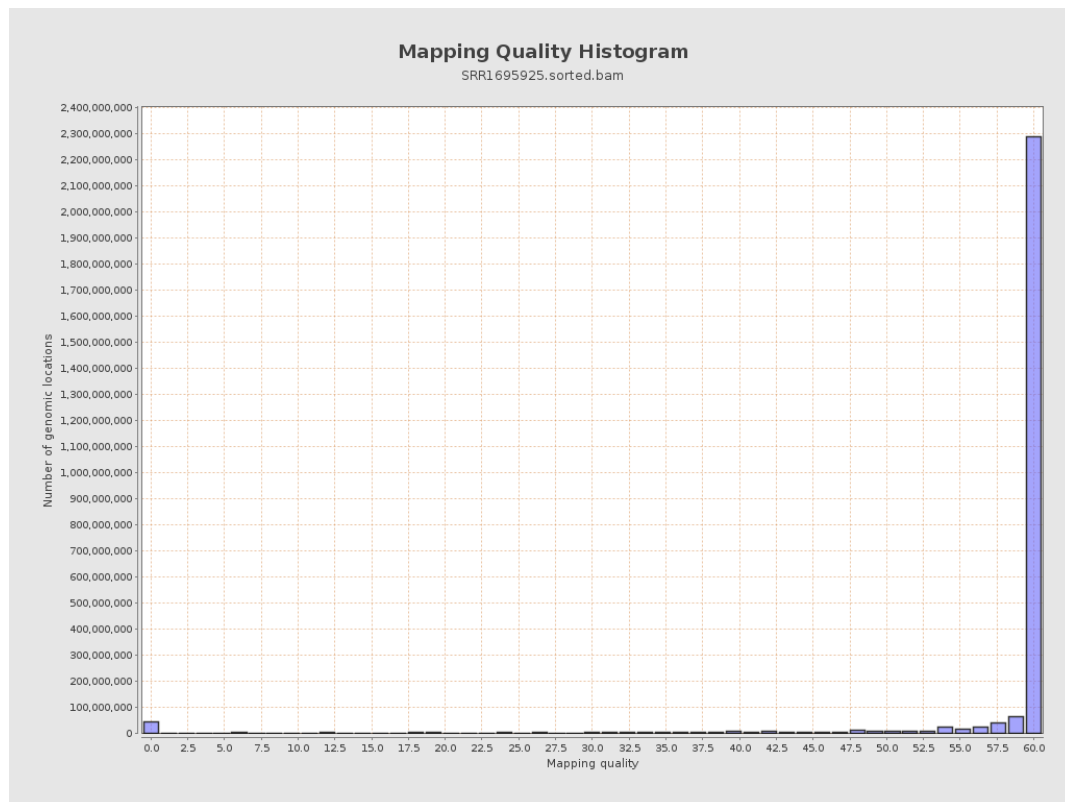
11. Results : Homopolymer Indels



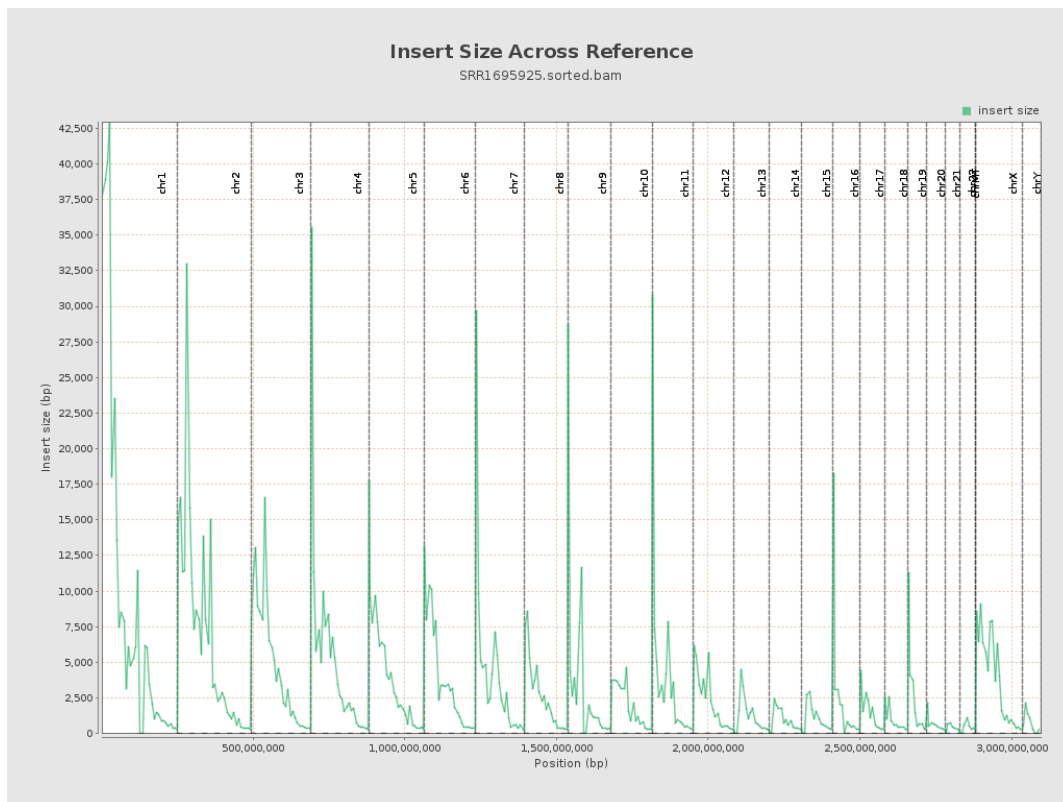
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

