

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/17 14:06:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954926.sorted.bam -c -nw 400 -hm 3
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1.2. Alignment

Command line:	bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\t PL:ILLUMINA\tSM:sample_SRR1954 926 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1954926_1.fastq.gz SRR1954926_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Tue Sep 17 14:06:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,300,504
Mapped reads	14,975,434 / 97.88%
Unmapped reads	325,070 / 2.12%
Mapped paired reads	14,975,434 / 97.88%
Mapped reads, first in pair	7,598,111 / 49.66%
Mapped reads, second in pair	7,377,323 / 48.22%
Mapped reads, both in pair	14,727,416 / 96.25%
Mapped reads, singletons	248,018 / 1.62%
Secondary alignments	0
Supplementary alignments	40,479 / 0.26%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	869,482 / 5.68%
Duplication rate	4.79%
Clipped reads	5,463,550 / 35.71%

2.2. ACGT Content

Number/percentage of A's	381,827,848 / 28.33%
Number/percentage of C's	259,158,742 / 19.23%
Number/percentage of T's	382,843,711 / 28.41%
Number/percentage of G's	323,839,769 / 24.03%
Number/percentage of N's	34,663 / 0%

GC Percentage	43.26%
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2.3. Coverage

Mean	0.4356
Standard Deviation	1.2924

2.4. Mapping Quality

Mean Mapping Quality	54.13
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2.5. Insert size

Mean	43,962.59
Standard Deviation	2,116,834.48
P25/Median/P75	305 / 319 / 333

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	10,387,956
Insertions	210,776
Mapped reads with at least one insertion	1.39%
Deletions	614,738
Mapped reads with at least one deletion	4.02%
Homopolymer indels	53.85%

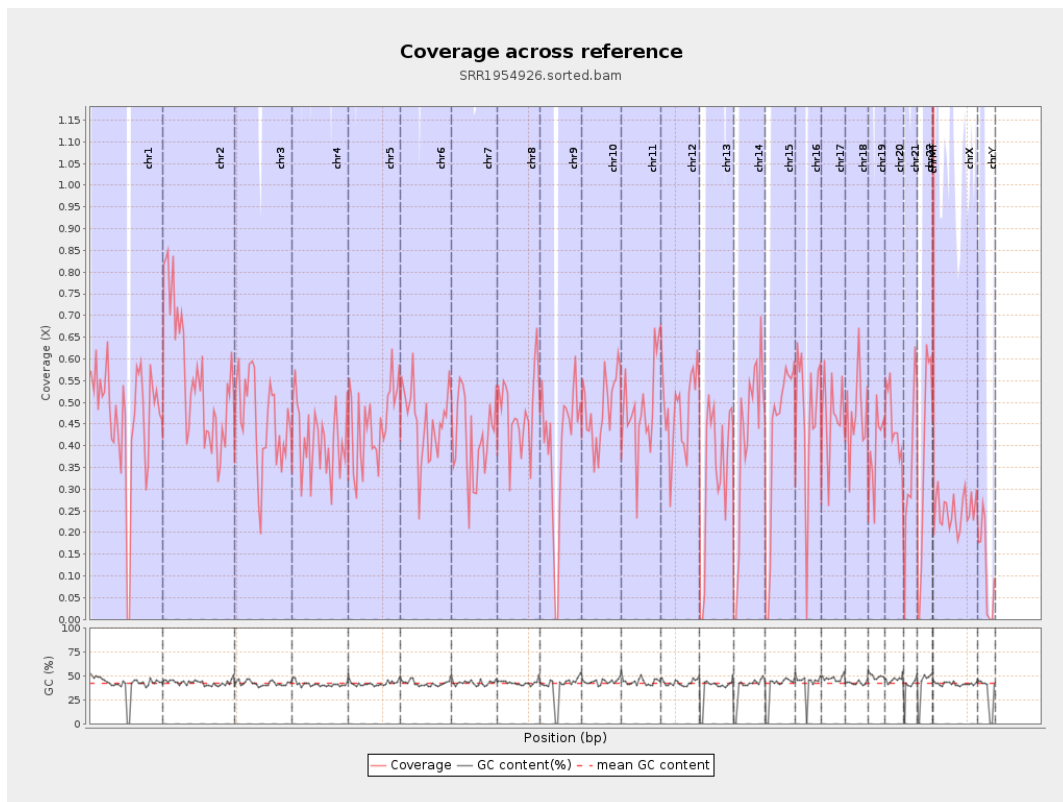
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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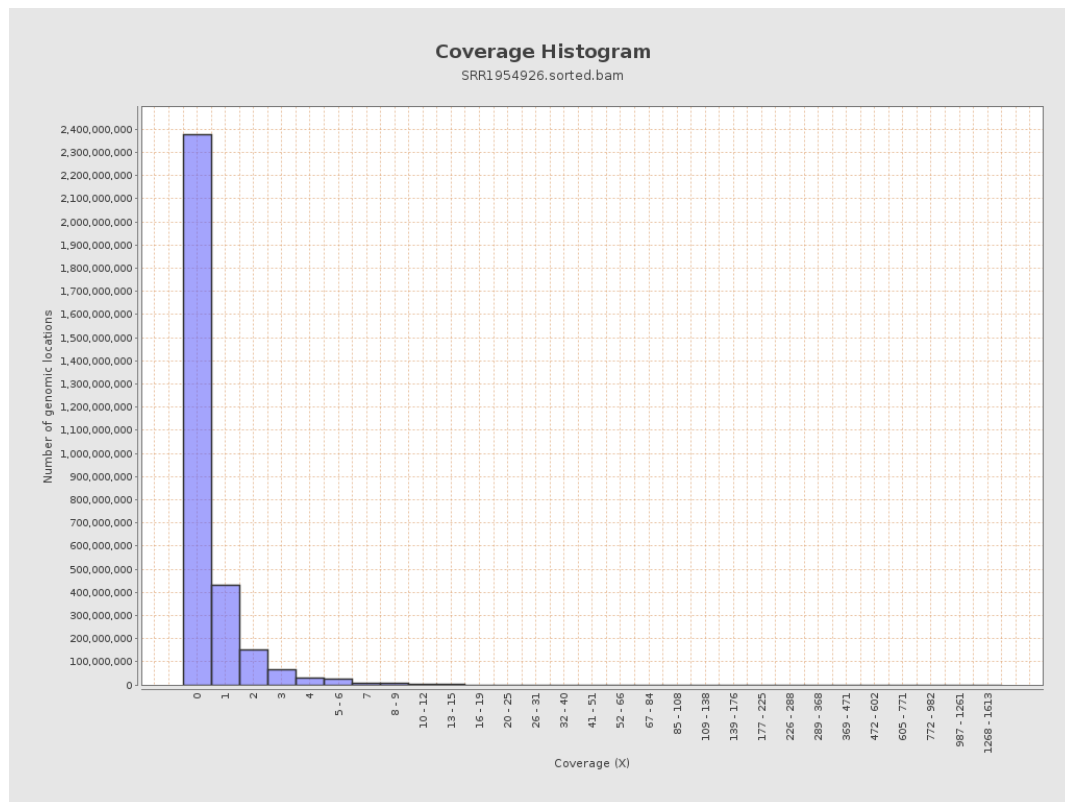
		bases	coverage	deviation
chr1	249250621	115951477	0.4652	1.3548
chr2	243199373	135403712	0.5568	2.1585
chr3	198022430	89676875	0.4529	1.1223
chr4	191154276	79314431	0.4149	1.1484
chr5	180915260	81870821	0.4525	1.1152
chr6	171115067	78102022	0.4564	1.1396
chr7	159138663	66472465	0.4177	1.0795
chr8	146364022	70119026	0.4791	1.2219
chr9	141213431	56251677	0.3983	1.3654
chr10	135534747	65779604	0.4853	1.2544
chr11	135006516	65540553	0.4855	1.3189
chr12	133851895	64992970	0.4856	1.1965
chr13	115169878	39227835	0.3406	0.9614
chr14	107349540	45217631	0.4212	1.1432
chr15	102531392	43097941	0.4203	1.1252
chr16	90354753	42223296	0.4673	1.4732
chr17	81195210	38402038	0.473	1.223
chr18	78077248	36589739	0.4686	1.4012
chr19	59128983	23245552	0.3931	1.1553
chr20	63025520	28219074	0.4477	1.1431
chr21	48129895	17411341	0.3618	1.4249
chr22	51304566	19393093	0.378	1.0964
chrMT	16571	272351	16.4354	12.6553
chrX	155270560	38744452	0.2495	0.7724

chrY	59373566	7038718	0.1185	0.8028
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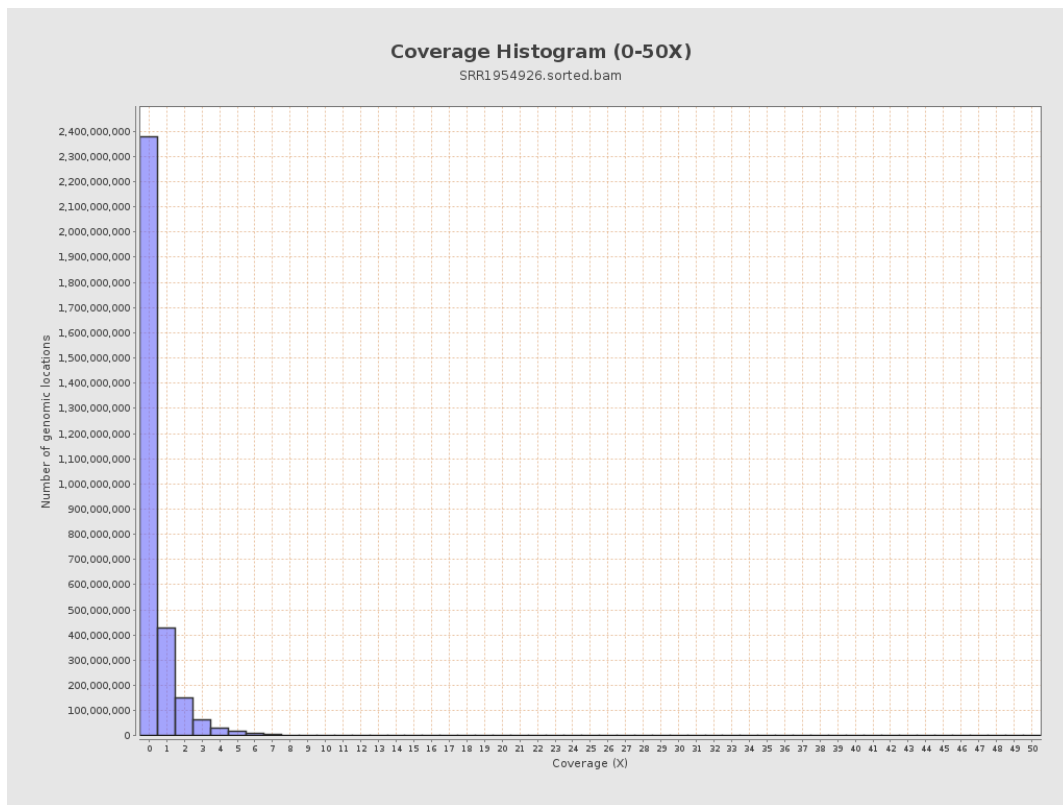
3. Results : Coverage across reference



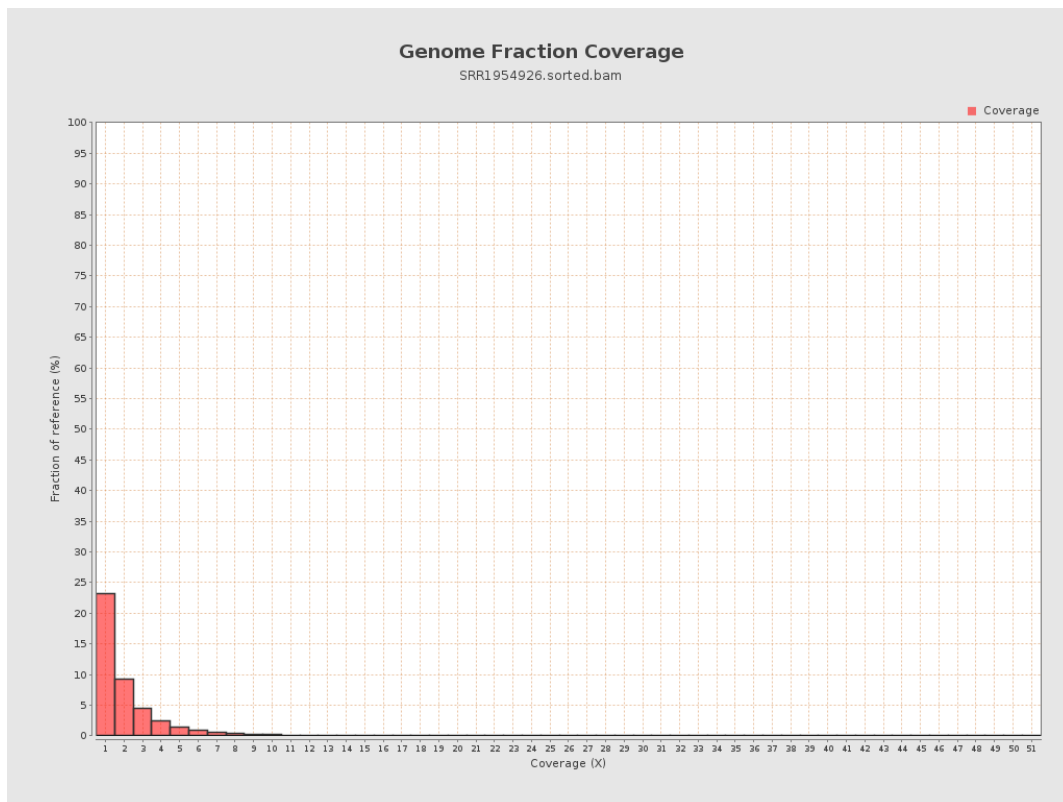
4. Results : Coverage Histogram



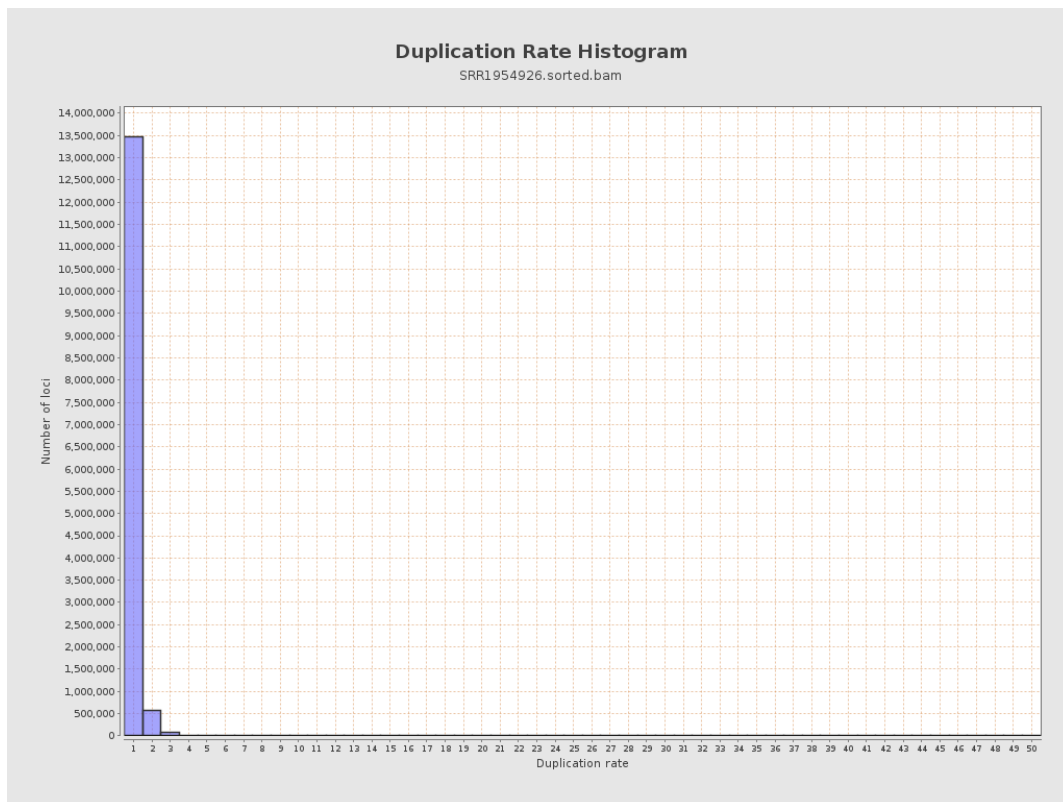
5. Results : Coverage Histogram (0-50X)



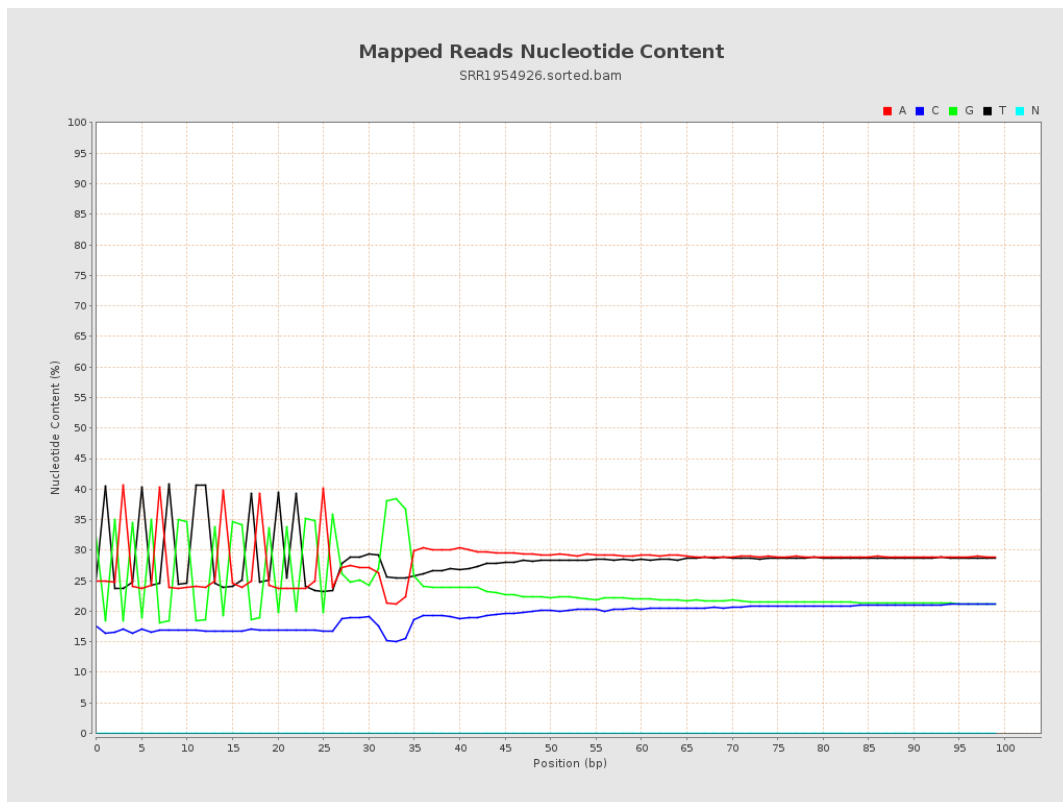
6. Results : Genome Fraction Coverage



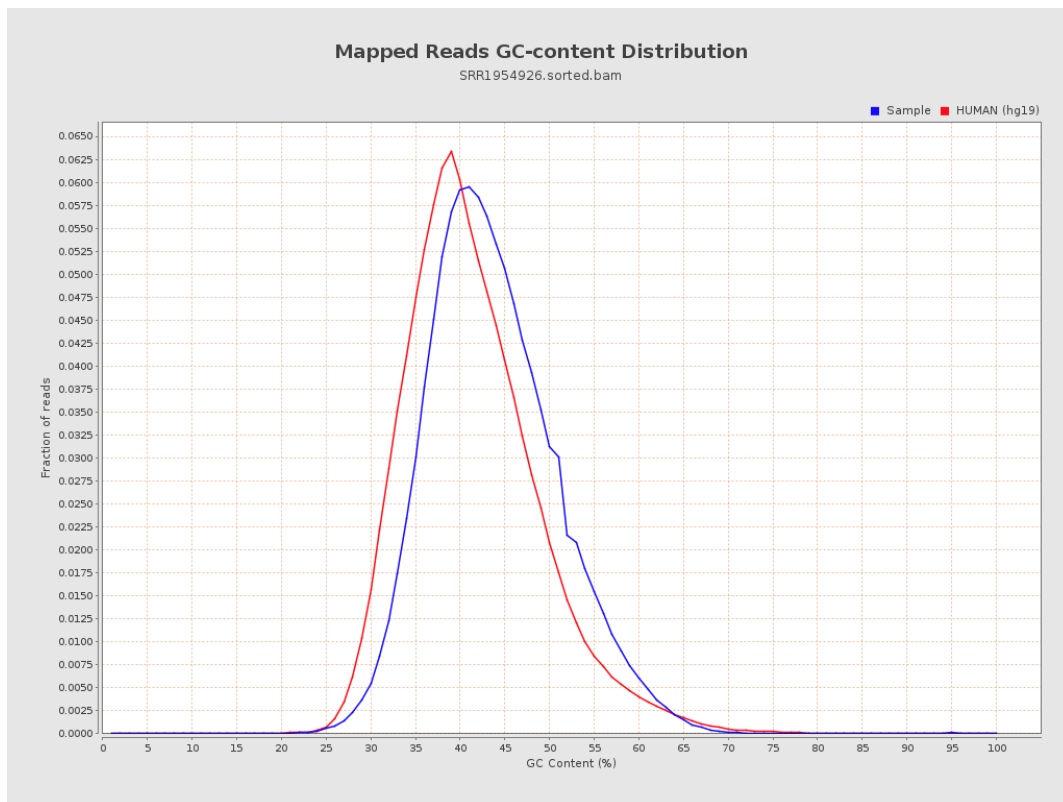
7. Results : Duplication Rate Histogram



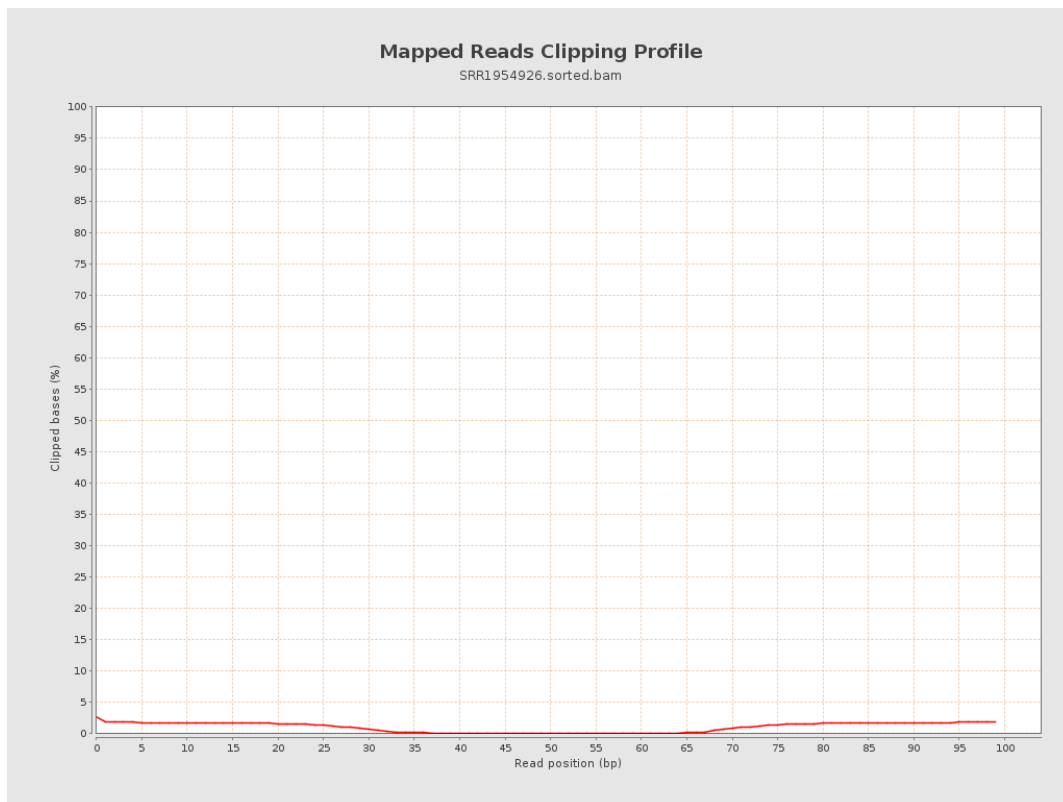
8. Results : Mapped Reads Nucleotide Content



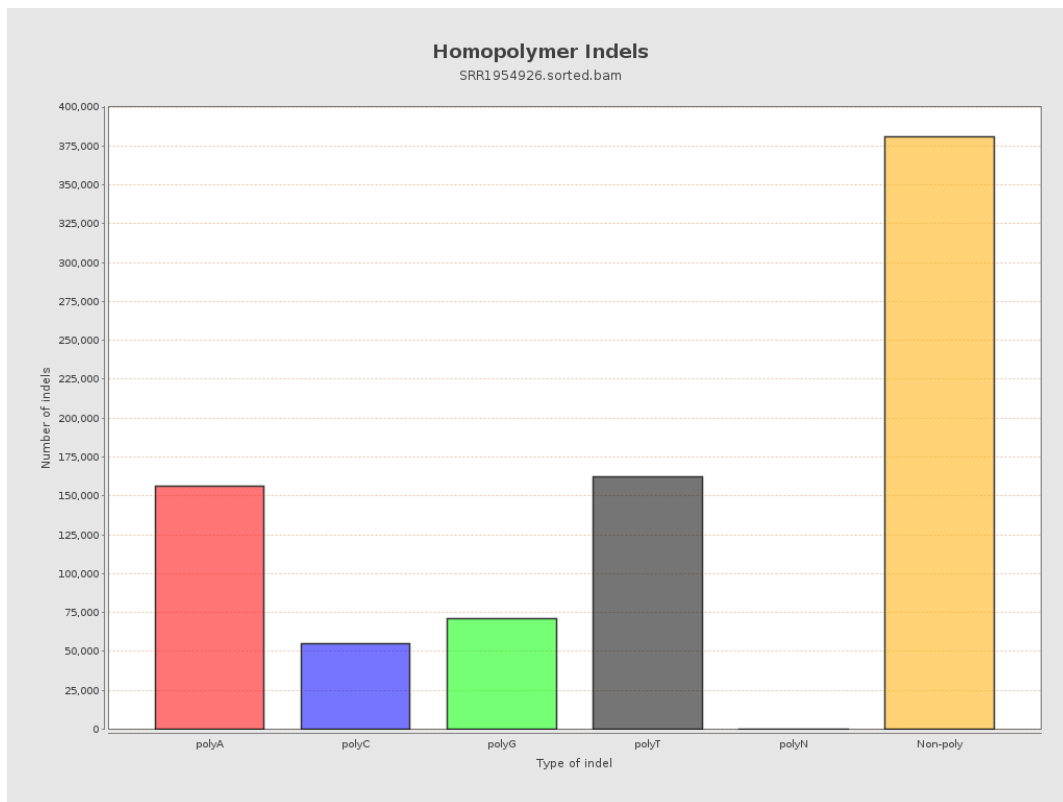
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



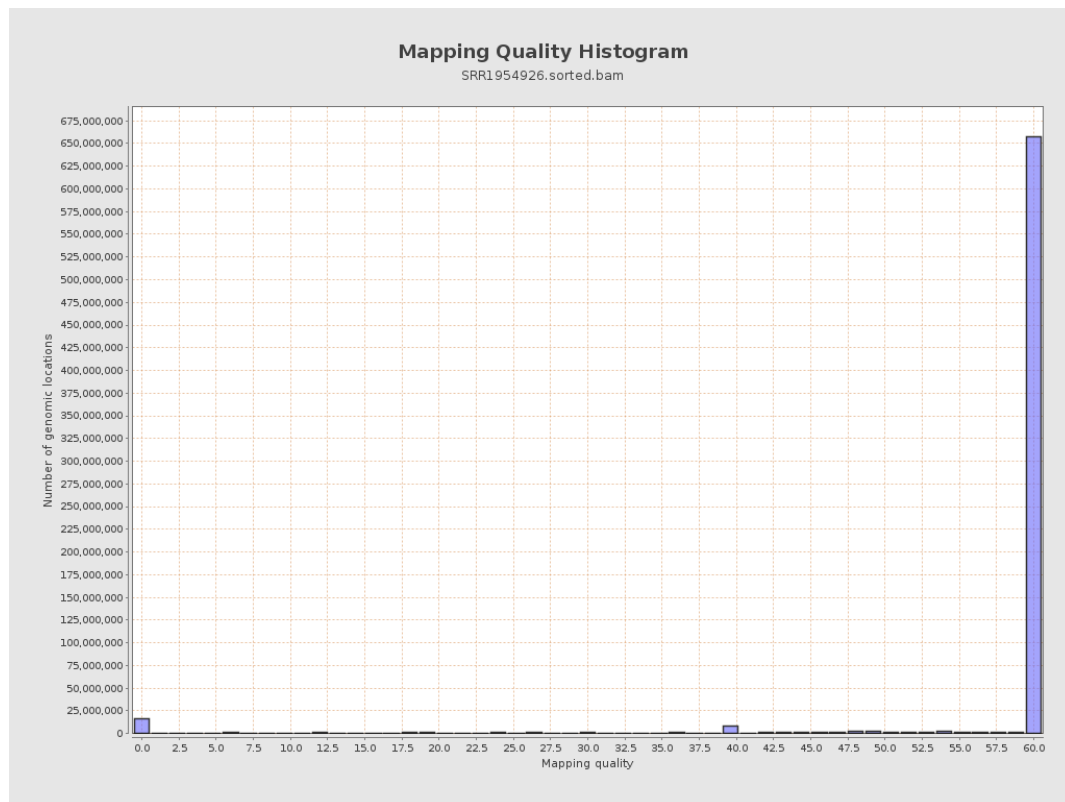
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



15. Results : Insert Size Histogram

