

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 03:14:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926956.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR926956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926956_1.fastq.gz SRR926956_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 03:14:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,512,394
Mapped reads	14,106,414 / 97.2%
Unmapped reads	405,980 / 2.8%
Mapped paired reads	14,106,414 / 97.2%
Mapped reads, first in pair	7,041,663 / 48.52%
Mapped reads, second in pair	7,064,751 / 48.68%
Mapped reads, both in pair	13,870,952 / 95.58%
Mapped reads, singletons	235,462 / 1.62%
Secondary alignments	0
Supplementary alignments	543,318 / 3.74%
Read min/max/mean length	30 / 101 / 102.56
Duplicated reads (estimated)	1,062,656 / 7.32%
Duplication rate	6.22%
Clipped reads	6,861,315 / 47.28%

2.2. ACGT Content

Number/percentage of A's	361,418,584 / 28.15%
Number/percentage of C's	257,000,005 / 20.02%
Number/percentage of T's	366,773,036 / 28.57%
Number/percentage of G's	298,671,500 / 23.26%
Number/percentage of N's	51,714 / 0%

GC Percentage	43.28%
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2.3. Coverage

Mean	0.4151
Standard Deviation	1.5827

2.4. Mapping Quality

Mean Mapping Quality	51.98
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2.5. Insert size

Mean	459,440.34
Standard Deviation	6,809,803.02
P25/Median/P75	140 / 184 / 251

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	12,185,980
Insertions	221,438
Mapped reads with at least one insertion	1.54%
Deletions	652,016
Mapped reads with at least one deletion	4.5%
Homopolymer indels	51.76%

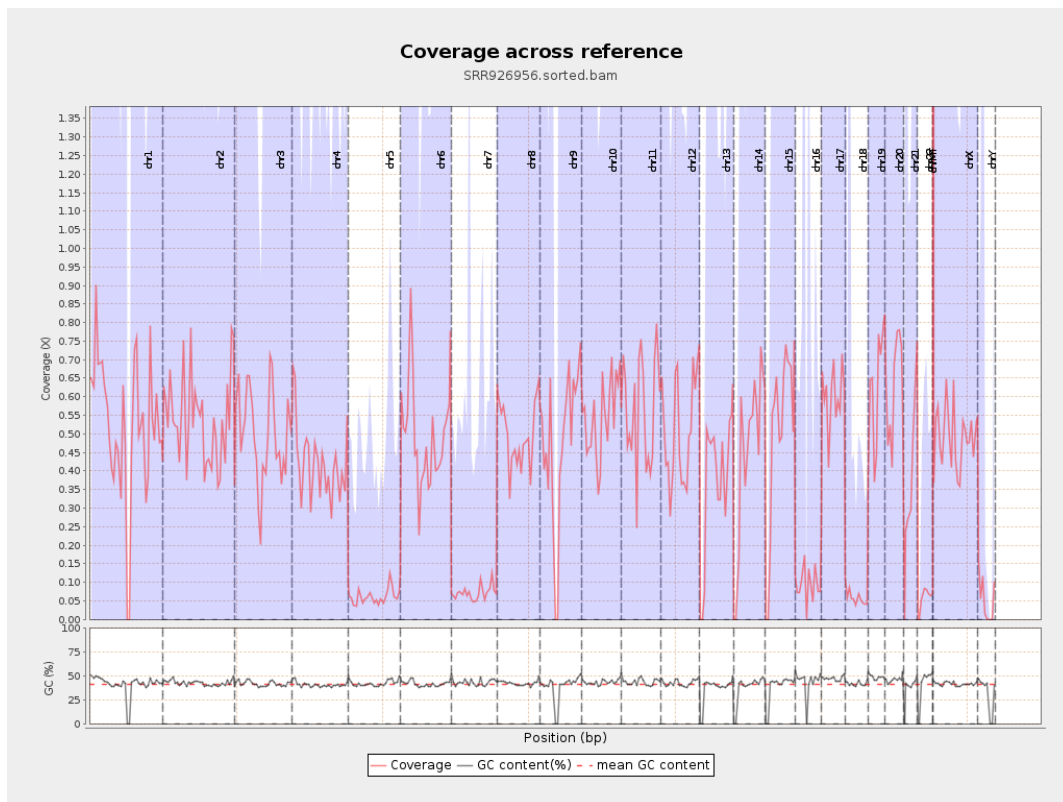
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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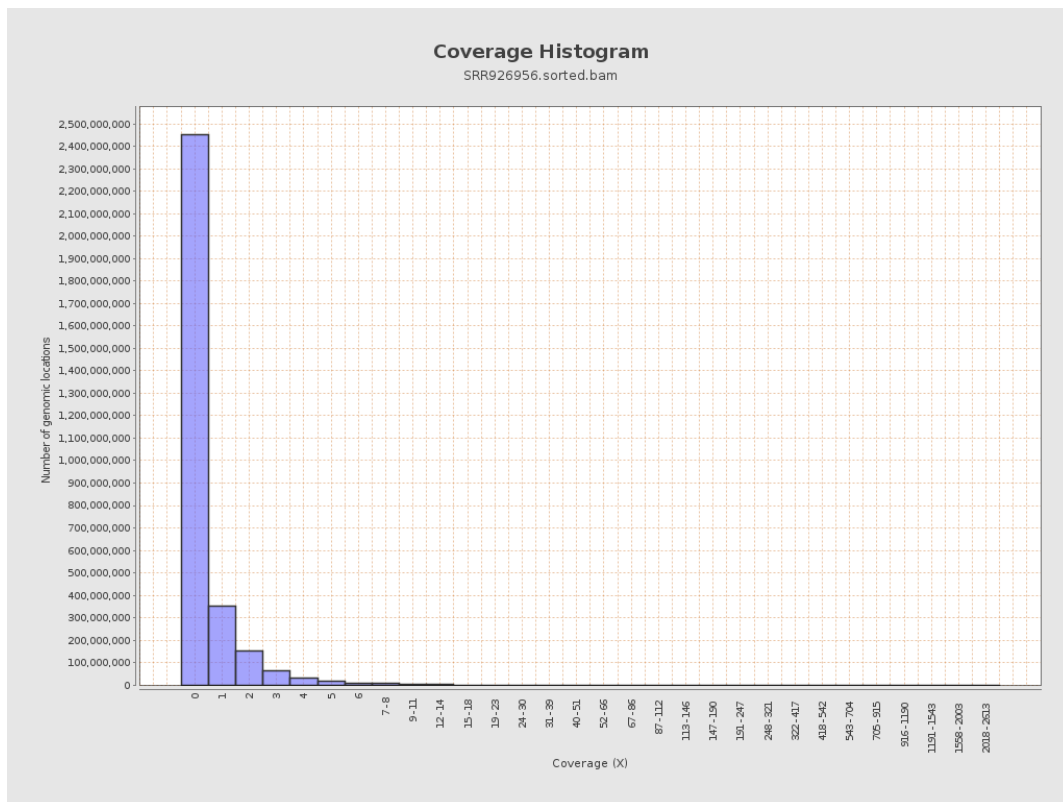
		bases	coverage	deviation
chr1	249250621	129667986	0.5202	1.8184
chr2	243199373	130876234	0.5381	2.9048
chr3	198022430	98301501	0.4964	1.1913
chr4	191154276	80039839	0.4187	1.5461
chr5	180915260	11349994	0.0627	0.4491
chr6	171115067	83934899	0.4905	1.2382
chr7	159138663	11450057	0.072	0.6216
chr8	146364022	72165518	0.4931	1.221
chr9	141213431	66823427	0.4732	1.5079
chr10	135534747	73570850	0.5428	2.6072
chr11	135006516	76067458	0.5634	1.4967
chr12	133851895	68465971	0.5115	1.3889
chr13	115169878	42741897	0.3711	1.0041
chr14	107349540	48704356	0.4537	1.1645
chr15	102531392	50518392	0.4927	1.238
chr16	90354753	8359027	0.0925	0.9797
chr17	81195210	49179333	0.6057	1.4774
chr18	78077248	4485084	0.0574	0.9897
chr19	59128983	36869624	0.6235	1.6394
chr20	63025520	39579938	0.628	1.5278
chr21	48129895	18488053	0.3841	1.5317
chr22	51304566	2857100	0.0557	0.4453
chrMT	16571	1146385	69.1802	73.5878
chrX	155270560	76140397	0.4904	1.198

chrY	59373566	3100723	0.0522	1.1466
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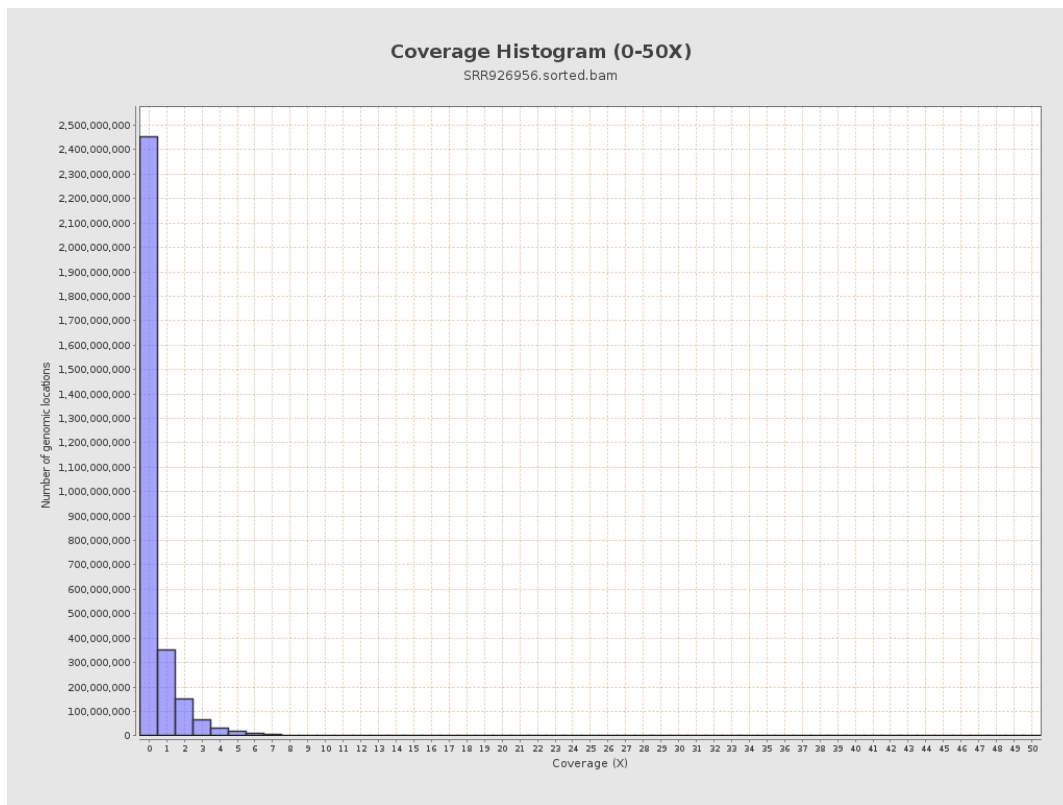
3. Results : Coverage across reference



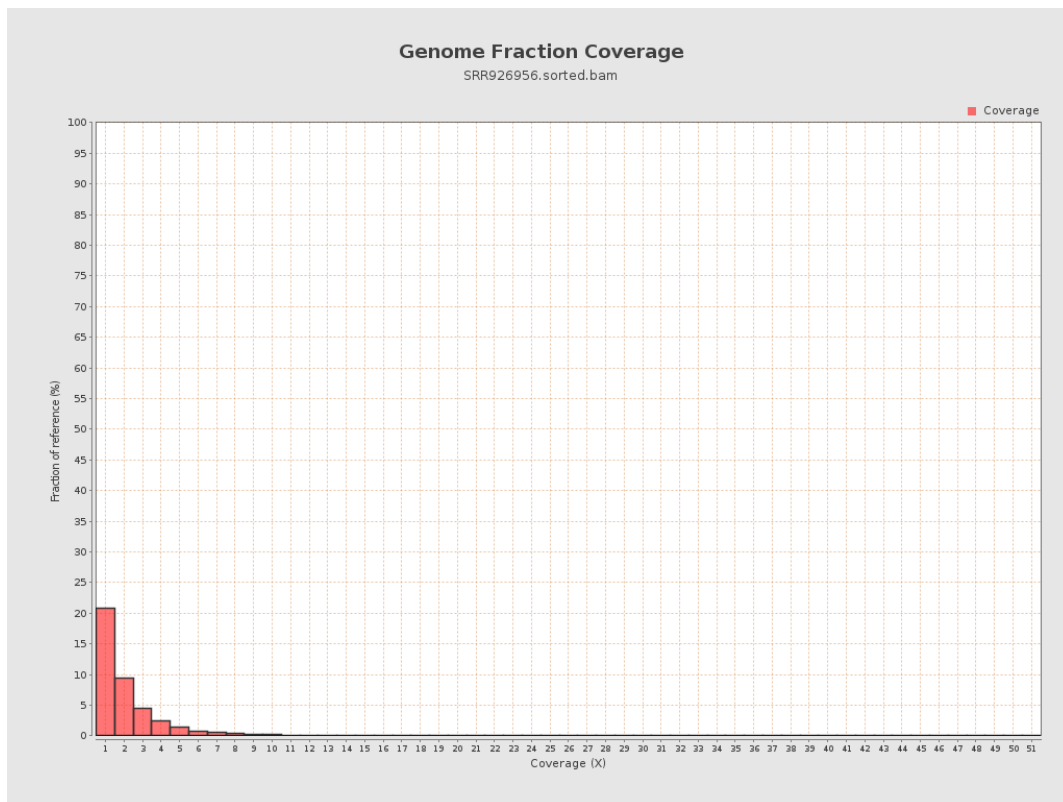
4. Results : Coverage Histogram



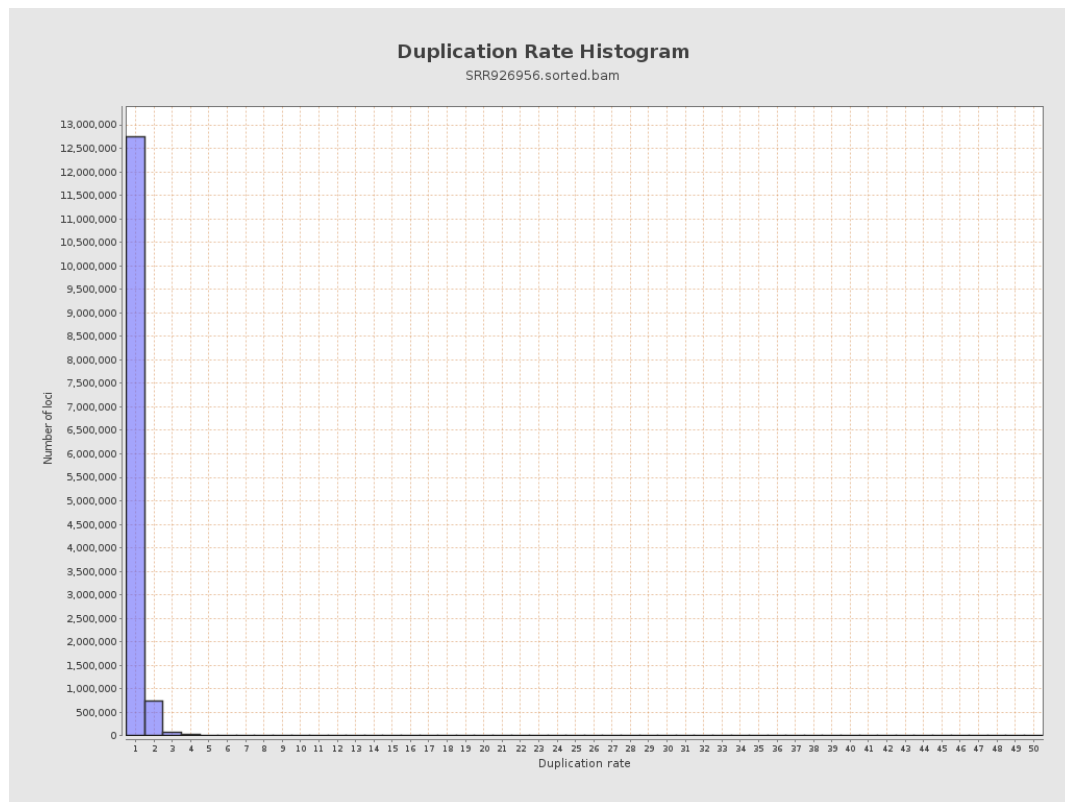
5. Results : Coverage Histogram (0-50X)



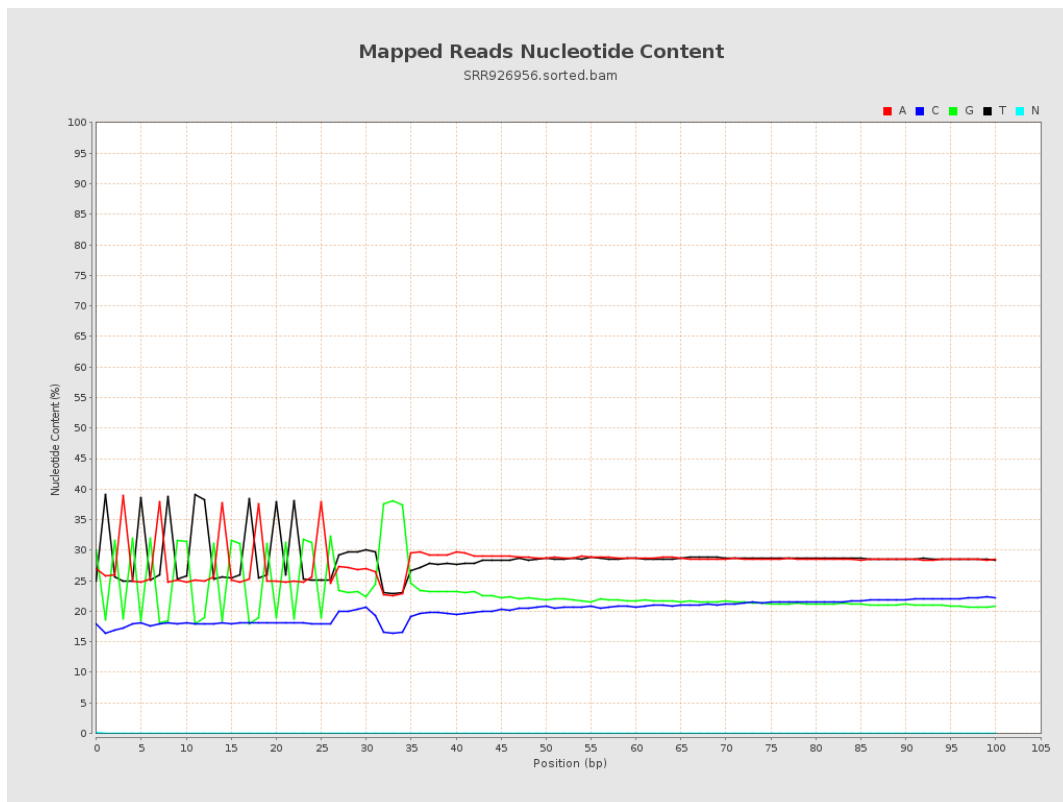
6. Results : Genome Fraction Coverage



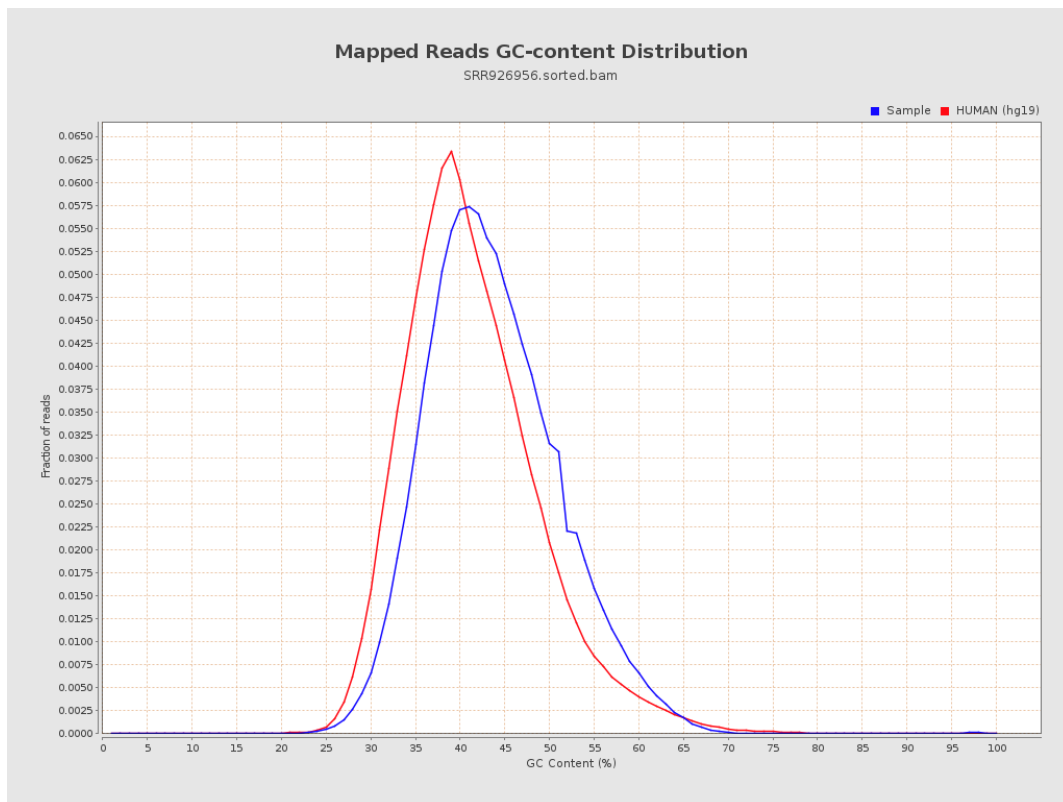
7. Results : Duplication Rate Histogram



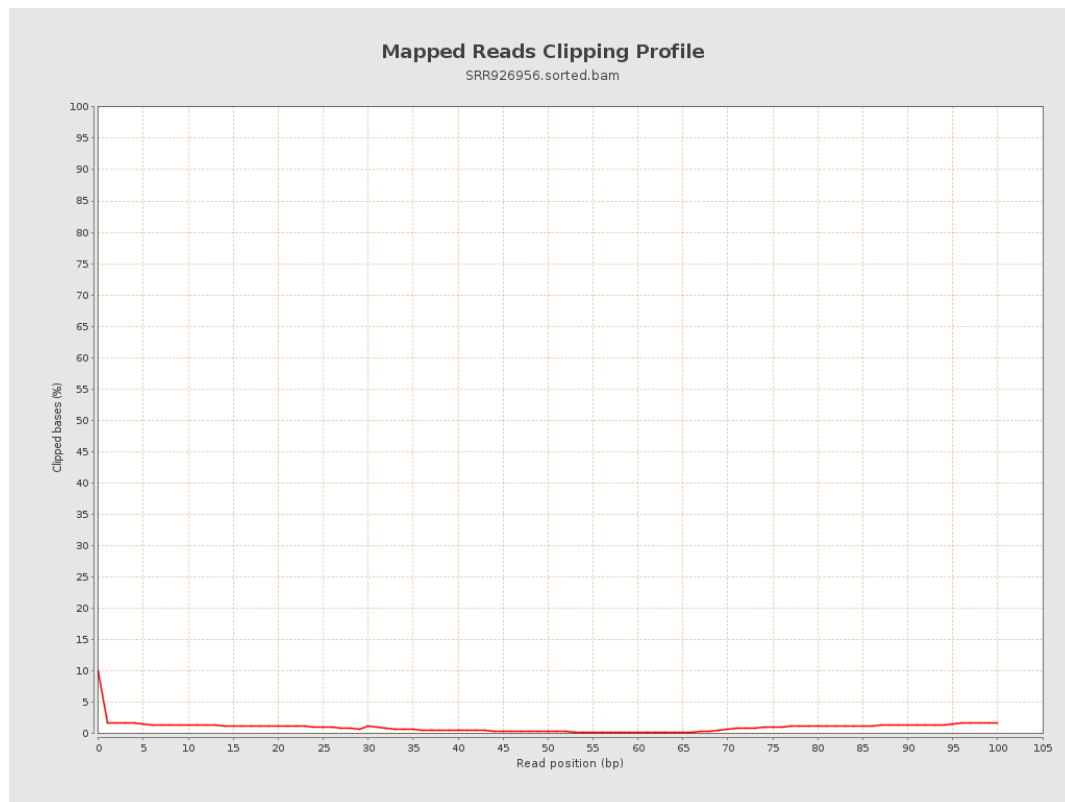
8. Results : Mapped Reads Nucleotide Content



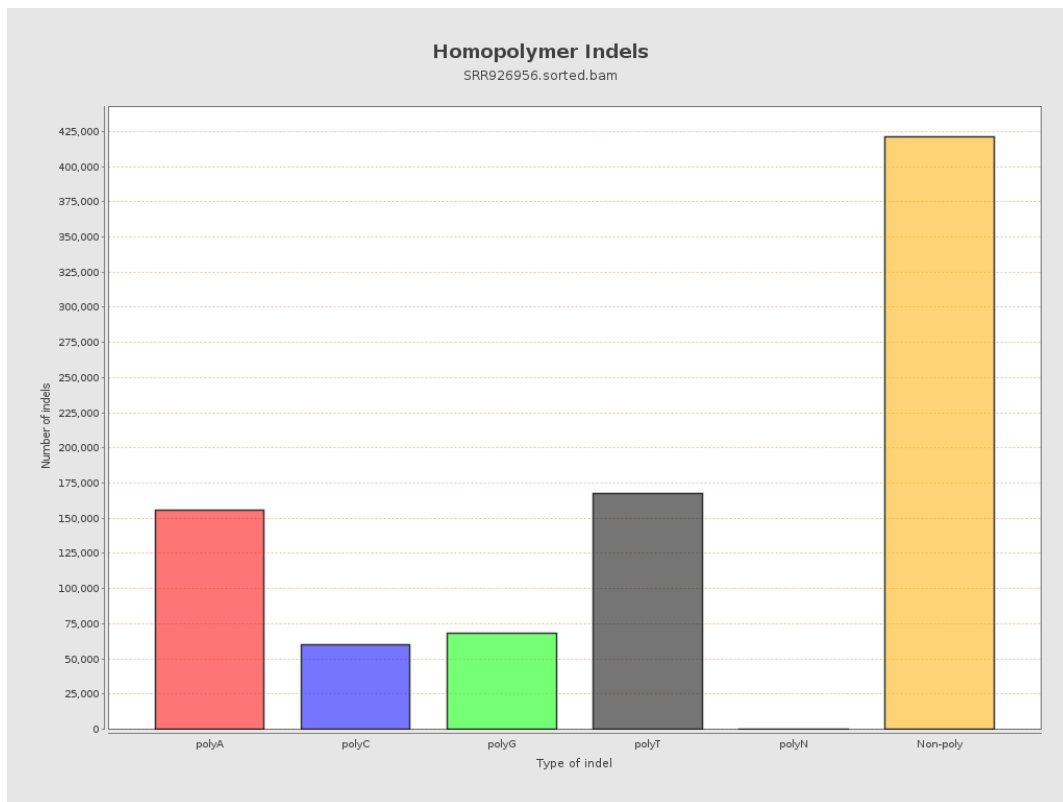
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



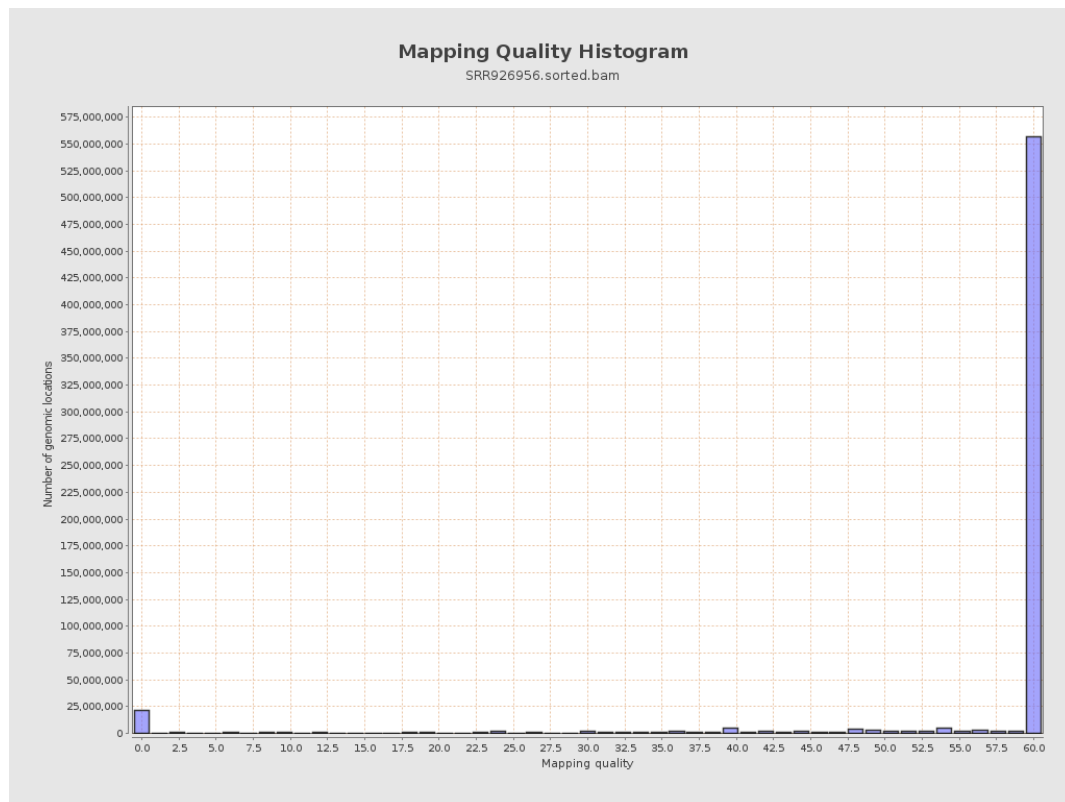
11. Results : Homopolymer Indels



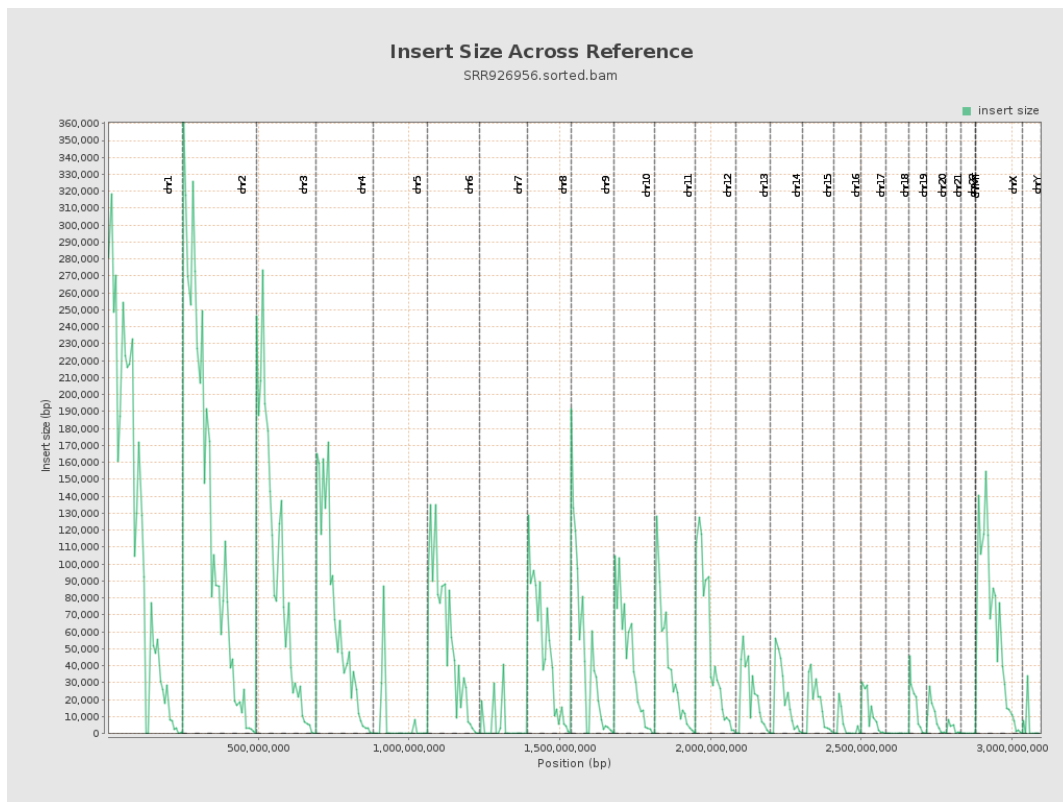
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

