

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:47:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124971.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_SRR3124971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124971_1.fastq.gz SRR3124971_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:47:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,735,672
Mapped reads	4,534,117 / 95.74%
Unmapped reads	201,555 / 4.26%
Mapped paired reads	4,534,117 / 95.74%
Mapped reads, first in pair	2,307,340 / 48.72%
Mapped reads, second in pair	2,226,777 / 47.02%
Mapped reads, both in pair	4,429,176 / 93.53%
Mapped reads, singletons	104,941 / 2.22%
Secondary alignments	0
Supplementary alignments	13,712 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	376,404 / 7.95%
Duplication rate	5.7%
Clipped reads	2,357,319 / 49.78%

2.2. ACGT Content

Number/percentage of A's	76,818,673 / 27.86%
Number/percentage of C's	48,441,478 / 17.57%
Number/percentage of T's	83,243,162 / 30.19%
Number/percentage of G's	67,221,724 / 24.38%
Number/percentage of N's	0 / 0%

GC Percentage	41.95%
---------------	--------

2.3. Coverage

Mean	0.0891
Standard Deviation	1.0191

2.4. Mapping Quality

Mean Mapping Quality	51.64
----------------------	-------

2.5. Insert size

Mean	73,487.51
Standard Deviation	2,619,448.44
P25/Median/P75	125 / 169 / 236

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,082,929
Insertions	33,703
Mapped reads with at least one insertion	0.74%
Deletions	86,617
Mapped reads with at least one deletion	1.89%
Homopolymer indels	47.16%

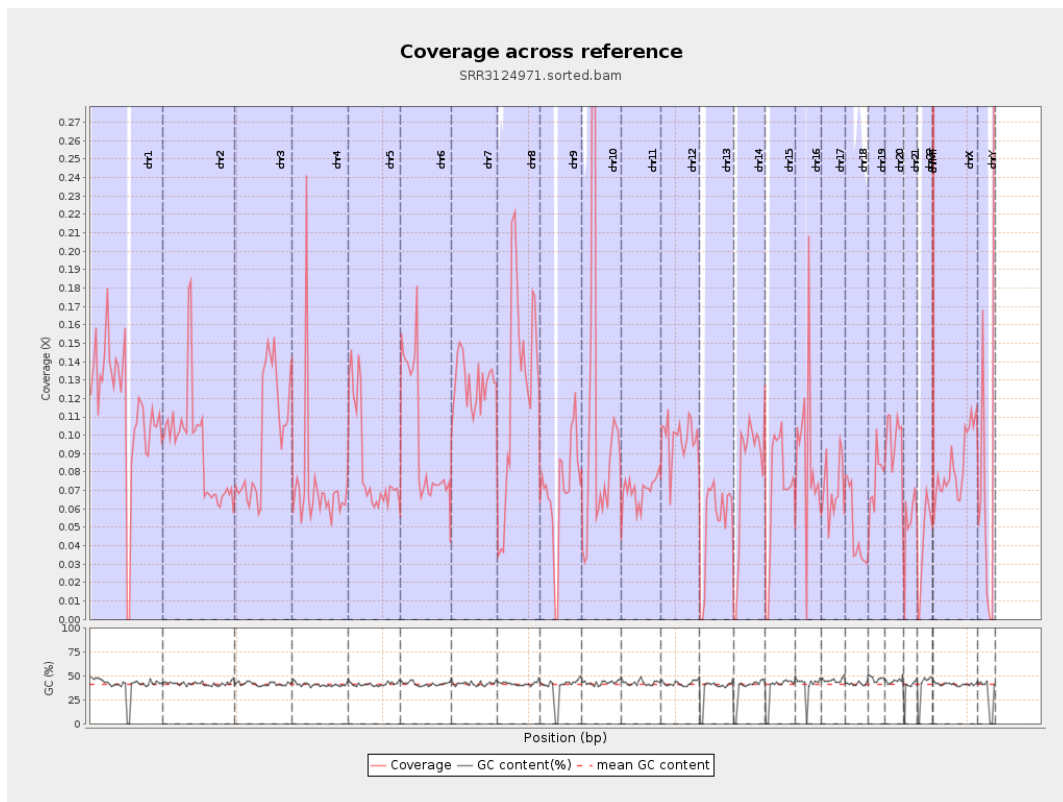
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

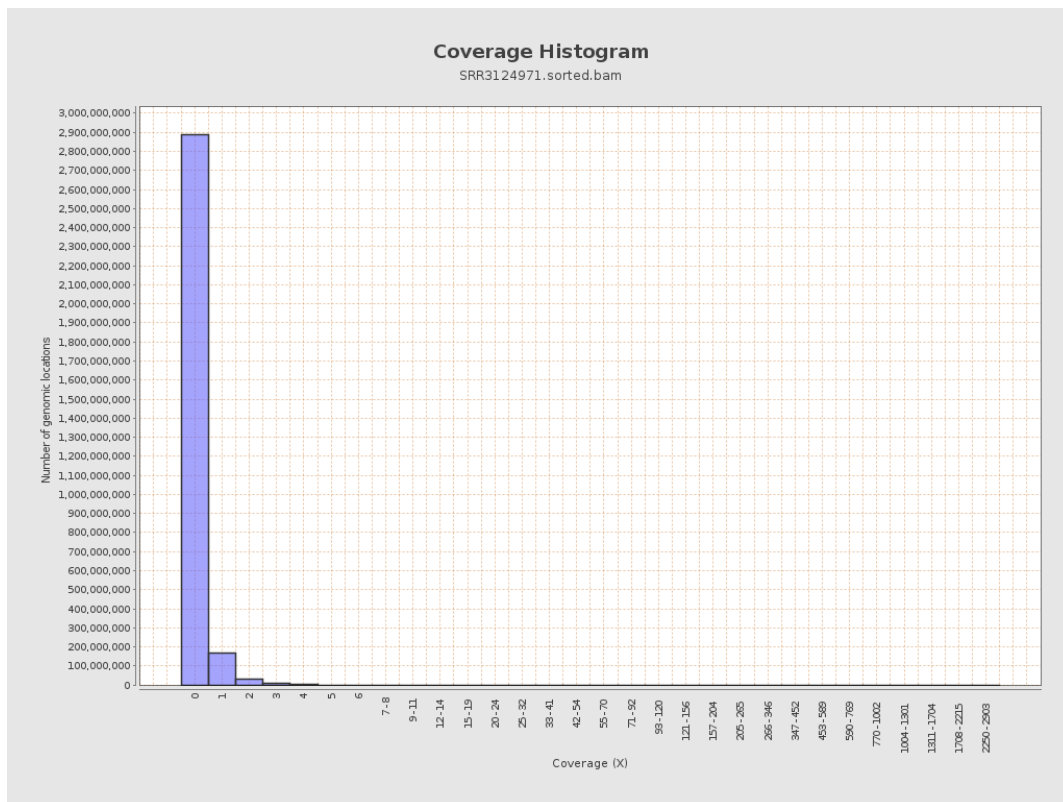
		bases	coverage	deviation
chr1	249250621	28689273	0.1151	0.7551
chr2	243199373	22557418	0.0928	0.909
chr3	198022430	19547766	0.0987	0.4538
chr4	191154276	13832135	0.0724	0.8189
chr5	180915260	15176172	0.0839	0.3655
chr6	171115067	16726933	0.0978	0.5718
chr7	159138663	20345907	0.1279	0.7633
chr8	146364022	18494459	0.1264	0.5179
chr9	141213431	10085173	0.0714	0.5229
chr10	135534747	14193468	0.1047	3.7557
chr11	135006516	9468267	0.0701	0.3879
chr12	133851895	13260254	0.0991	0.3884
chr13	115169878	6111531	0.0531	0.2748
chr14	107349540	8592293	0.08	0.3705
chr15	102531392	7156402	0.0698	0.3288
chr16	90354753	7866296	0.0871	1.0577
chr17	81195210	5792361	0.0713	0.6371
chr18	78077248	3786693	0.0485	0.6842
chr19	59128983	4480631	0.0758	0.5617
chr20	63025520	6203100	0.0984	0.4543
chr21	48129895	2592623	0.0539	0.4894
chr22	51304566	2159123	0.0421	0.2608
chrMT	16571	566992	34.2159	18.3917
chrX	155270560	13035926	0.084	0.4422

chrY	59373566	5140640	0.0866	1.7963
------	----------	---------	--------	--------

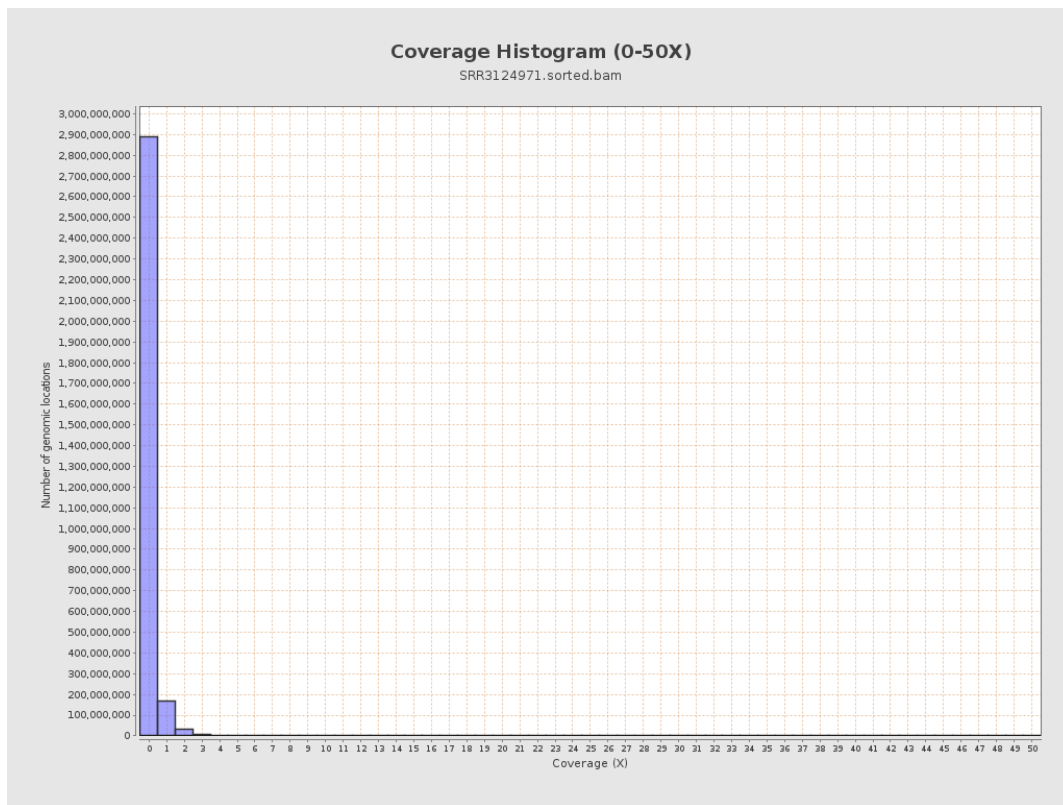
3. Results : Coverage across reference



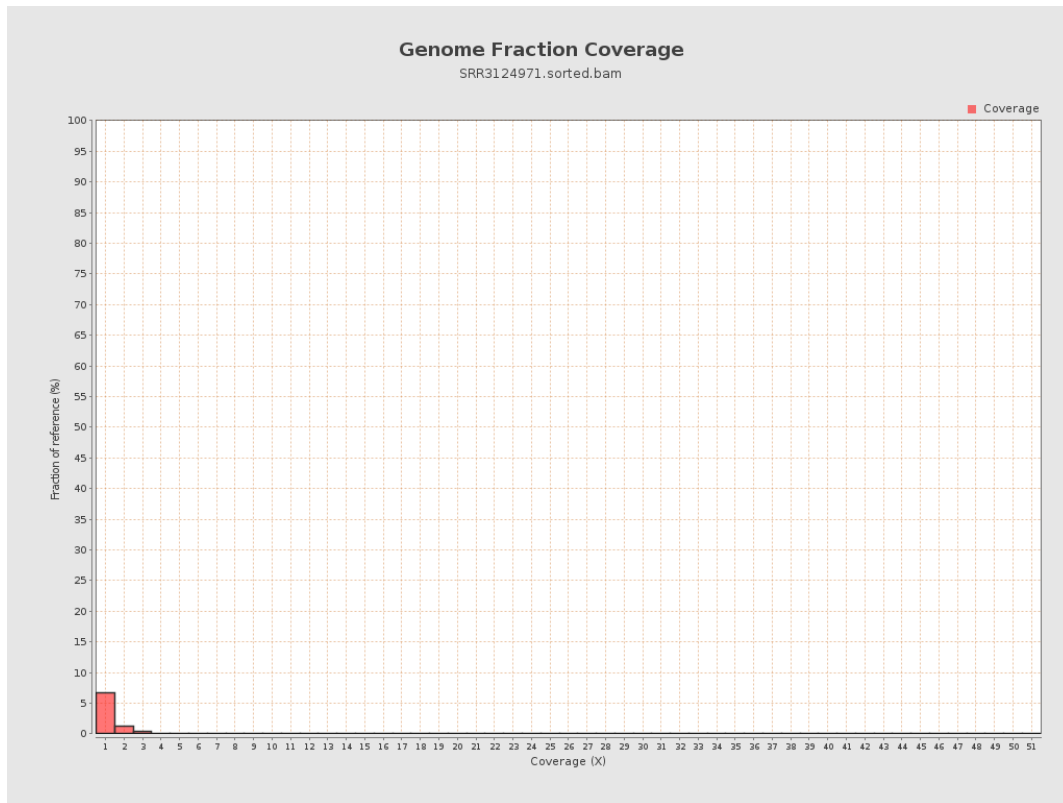
4. Results : Coverage Histogram



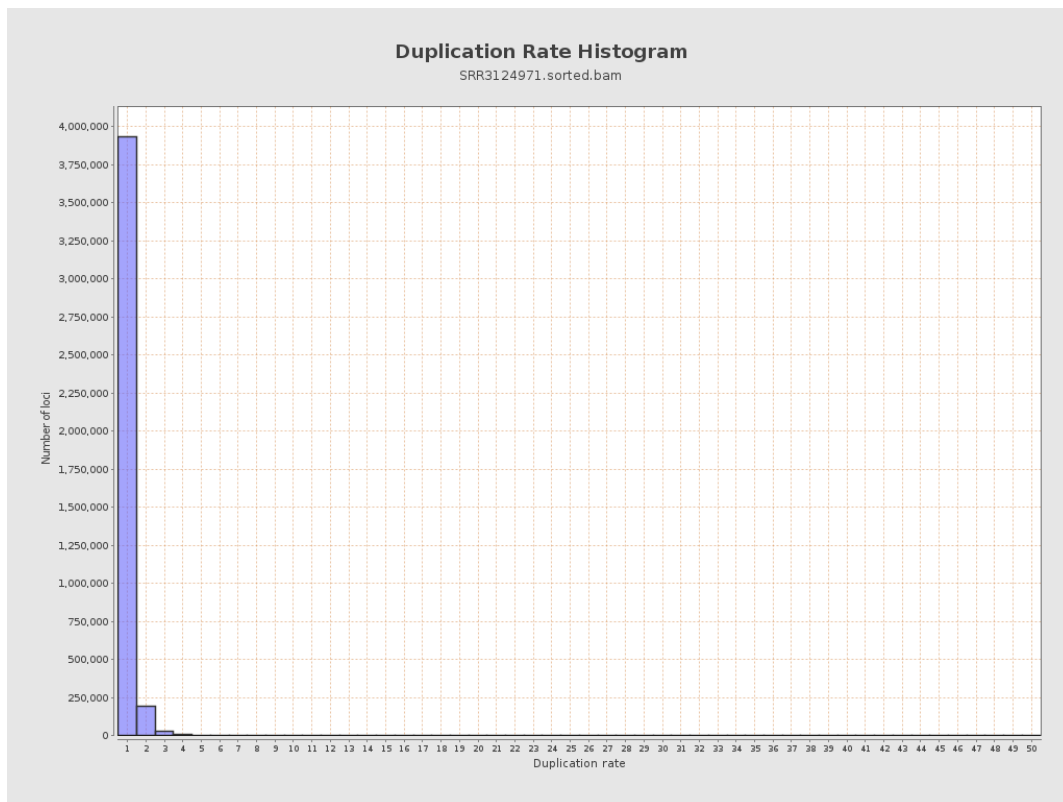
5. Results : Coverage Histogram (0-50X)



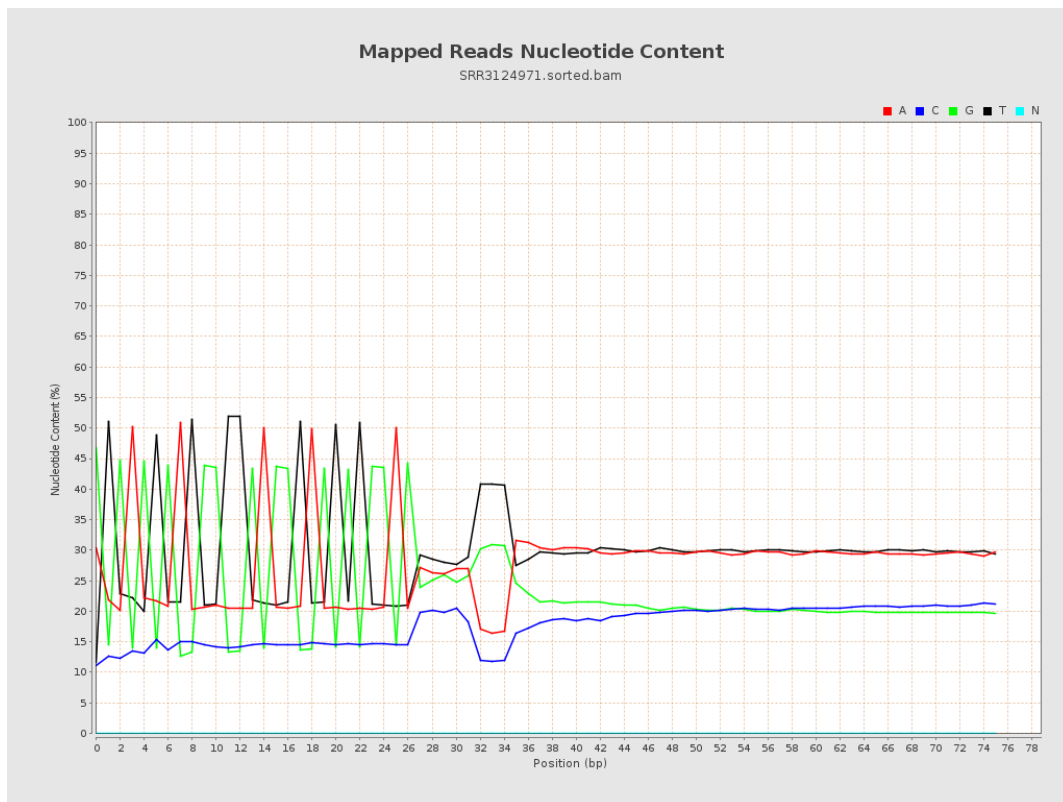
6. Results : Genome Fraction Coverage



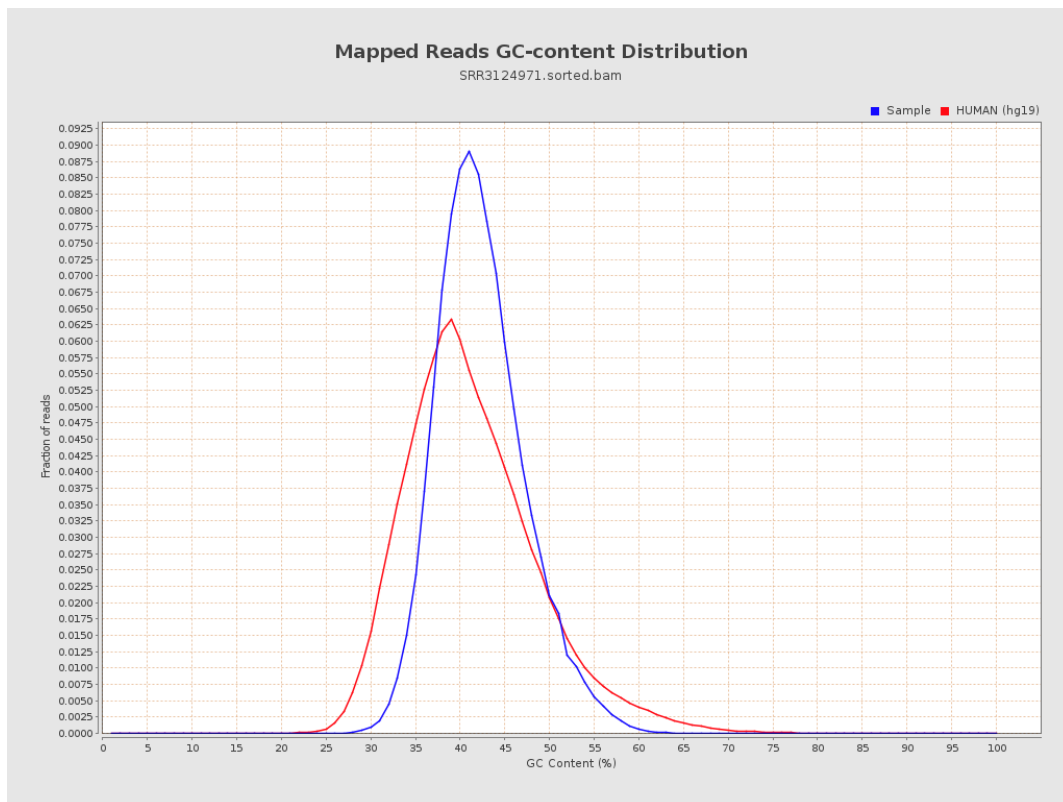
7. Results : Duplication Rate Histogram



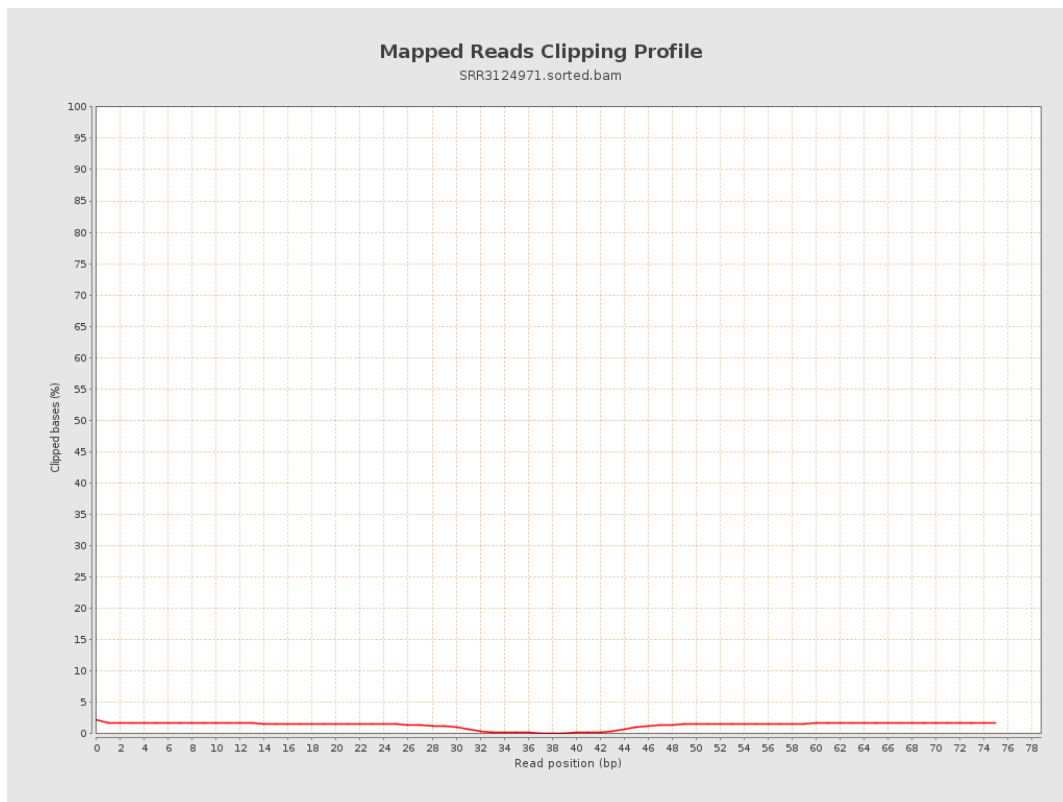
8. Results : Mapped Reads Nucleotide Content



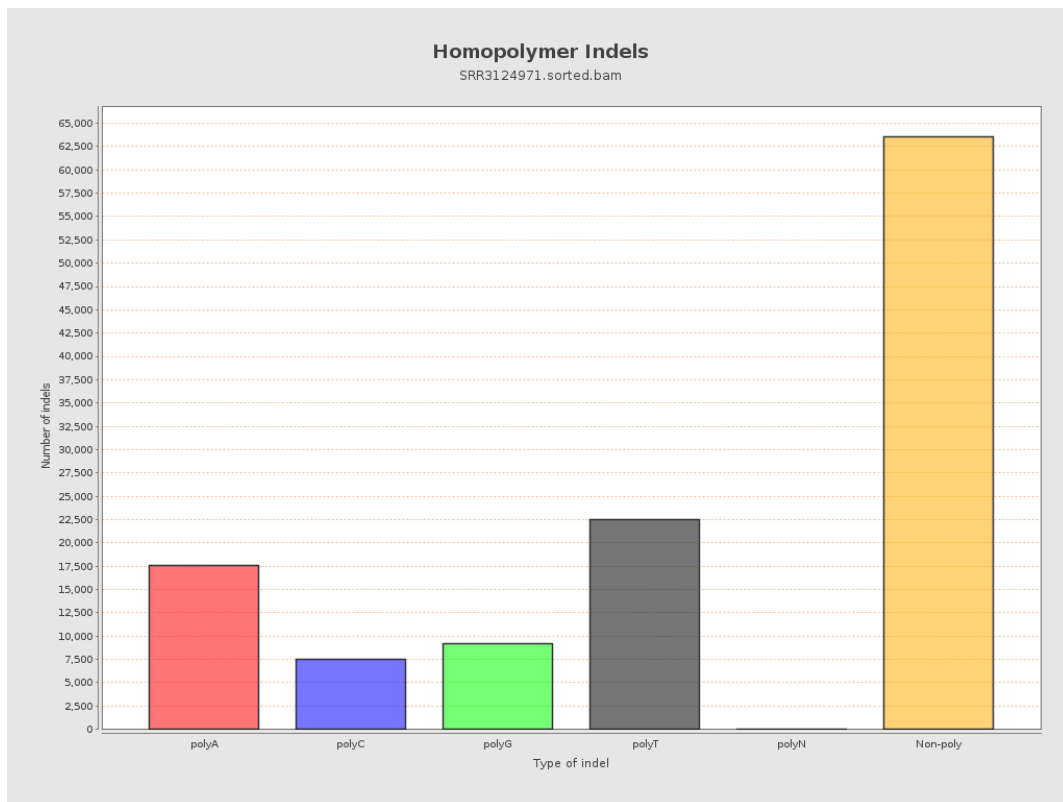
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



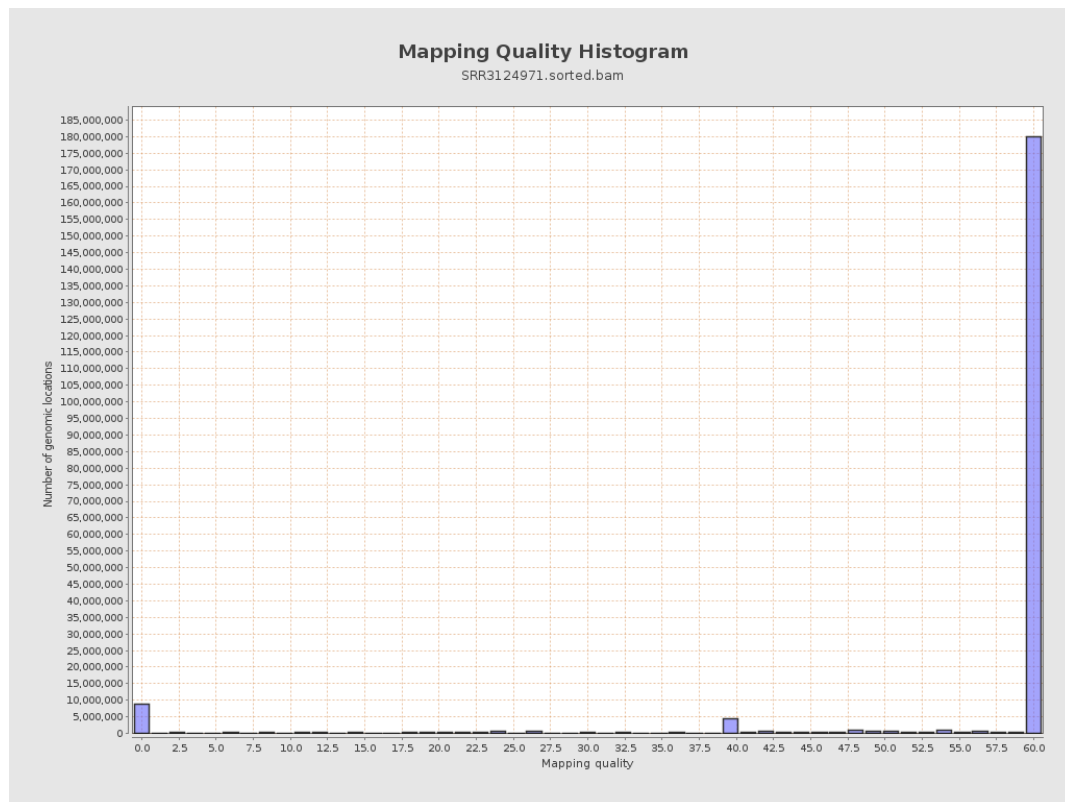
11. Results : Homopolymer Indels



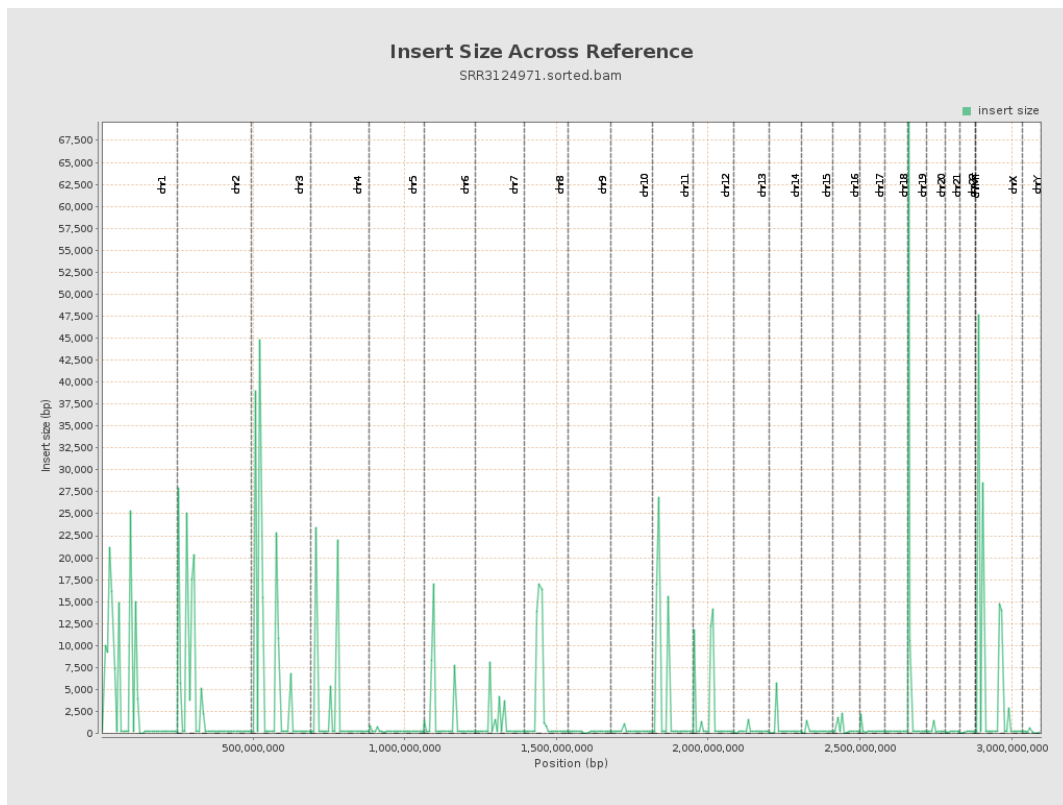
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

