

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:59:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174030.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_SRR10174030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174030_1.fastq.gz SRR10174030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:59:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,493,554
Mapped reads	2,429,013 / 97.41%
Unmapped reads	64,541 / 2.59%
Mapped paired reads	2,429,013 / 97.41%
Mapped reads, first in pair	1,215,842 / 48.76%
Mapped reads, second in pair	1,213,171 / 48.65%
Mapped reads, both in pair	2,386,396 / 95.7%
Mapped reads, singletons	42,617 / 1.71%
Secondary alignments	0
Supplementary alignments	252,717 / 10.13%
Read min/max/mean length	30 / 133 / 128.36
Duplicated reads (estimated)	1,812,235 / 72.68%
Duplication rate	62.16%
Clipped reads	1,066,248 / 42.76%

2.2. ACGT Content

Number/percentage of A's	86,406,811 / 30.23%
Number/percentage of C's	55,557,861 / 19.44%
Number/percentage of T's	86,287,425 / 30.19%
Number/percentage of G's	57,569,720 / 20.14%
Number/percentage of N's	3,021 / 0%

GC Percentage	39.58%
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2.3. Coverage

Mean	0.0924
Standard Deviation	1.5297

2.4. Mapping Quality

Mean Mapping Quality	52.56
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2.5. Insert size

Mean	748,563.69
Standard Deviation	8,059,455.63
P25/Median/P75	142 / 197 / 284

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	2,965,344
Insertions	30,940
Mapped reads with at least one insertion	1.23%
Deletions	72,221
Mapped reads with at least one deletion	2.9%
Homopolymer indels	42.52%

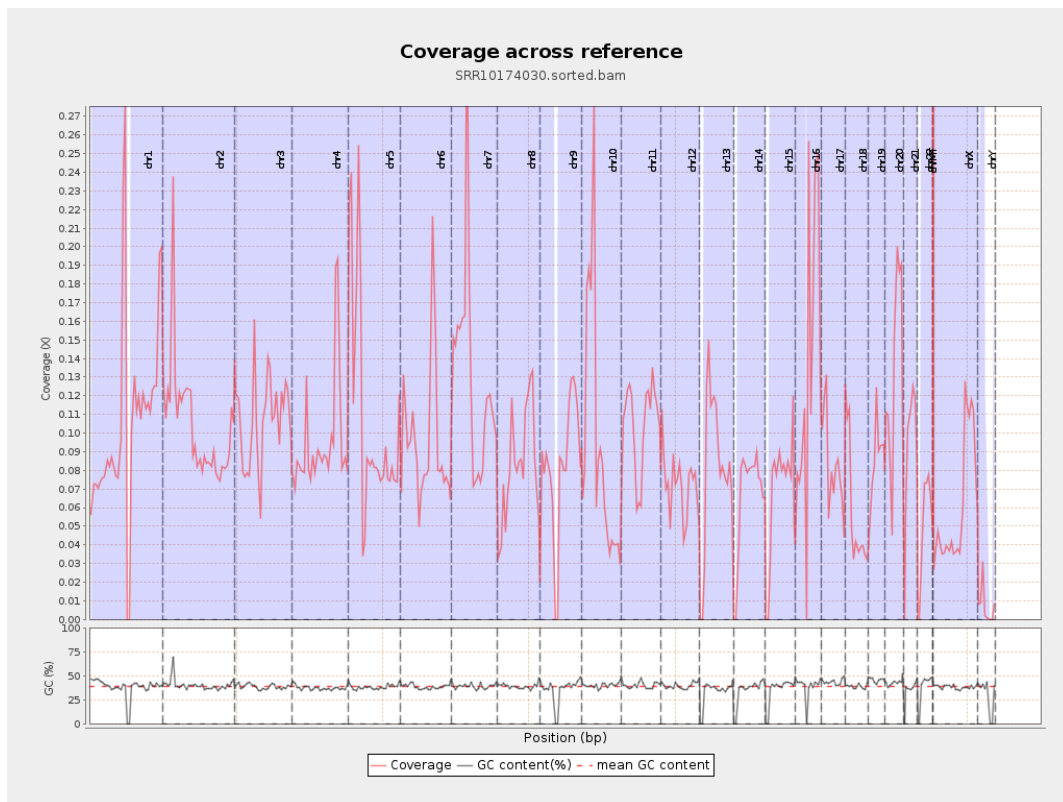
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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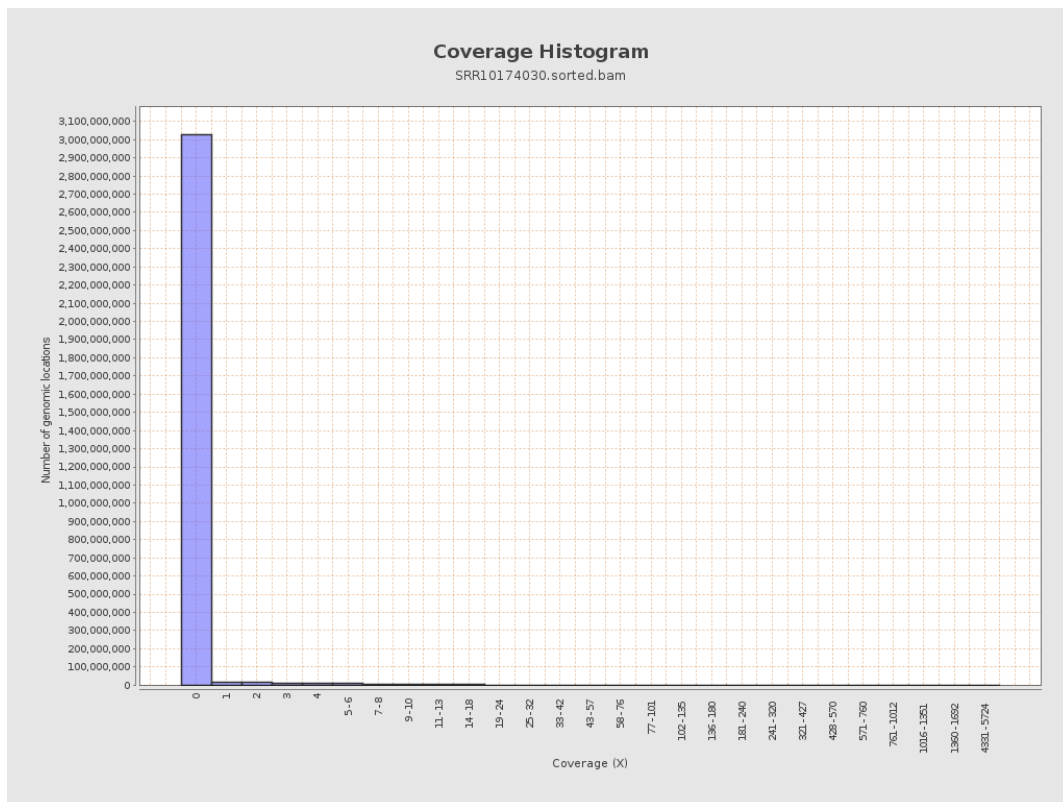
		bases	coverage	deviation
chr1	249250621	26509345	0.1064	1.3953
chr2	243199373	25152062	0.1034	4.0628
chr3	198022430	21167187	0.1069	0.9021
chr4	191154276	18375642	0.0961	0.9566
chr5	180915260	19765581	0.1093	0.9172
chr6	171115067	16450143	0.0961	0.8753
chr7	159138663	20689694	0.13	1.6495
chr8	146364022	12127507	0.0829	0.9405
chr9	141213431	11798814	0.0836	0.9238
chr10	135534747	12397281	0.0915	1.7168
chr11	135006516	14099313	0.1044	0.8959
chr12	133851895	9781212	0.0731	0.7358
chr13	115169878	9429476	0.0819	0.7914
chr14	107349540	7199001	0.0671	0.7099
chr15	102531392	6981328	0.0681	0.717
chr16	90354753	11863714	0.1313	1.3794
chr17	81195210	6829843	0.0841	0.8406
chr18	78077248	4437363	0.0568	1.2034
chr19	59128983	5021800	0.0849	1.3
chr20	63025520	8462843	0.1343	1.0071
chr21	48129895	4412780	0.0917	0.8432
chr22	51304566	2561398	0.0499	0.5888
chrMT	16571	695374	41.9633	32.7405
chrX	155270560	9356996	0.0603	0.6672

chrY	59373566	437523	0.0074	0.3418
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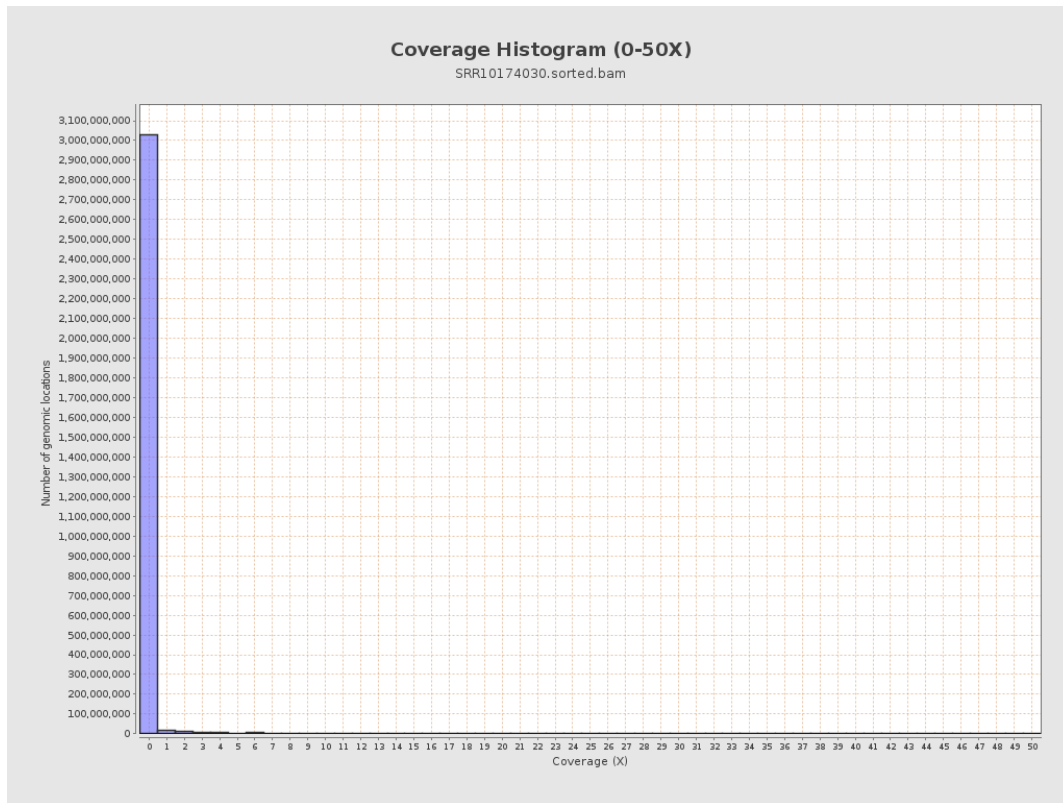
3. Results : Coverage across reference



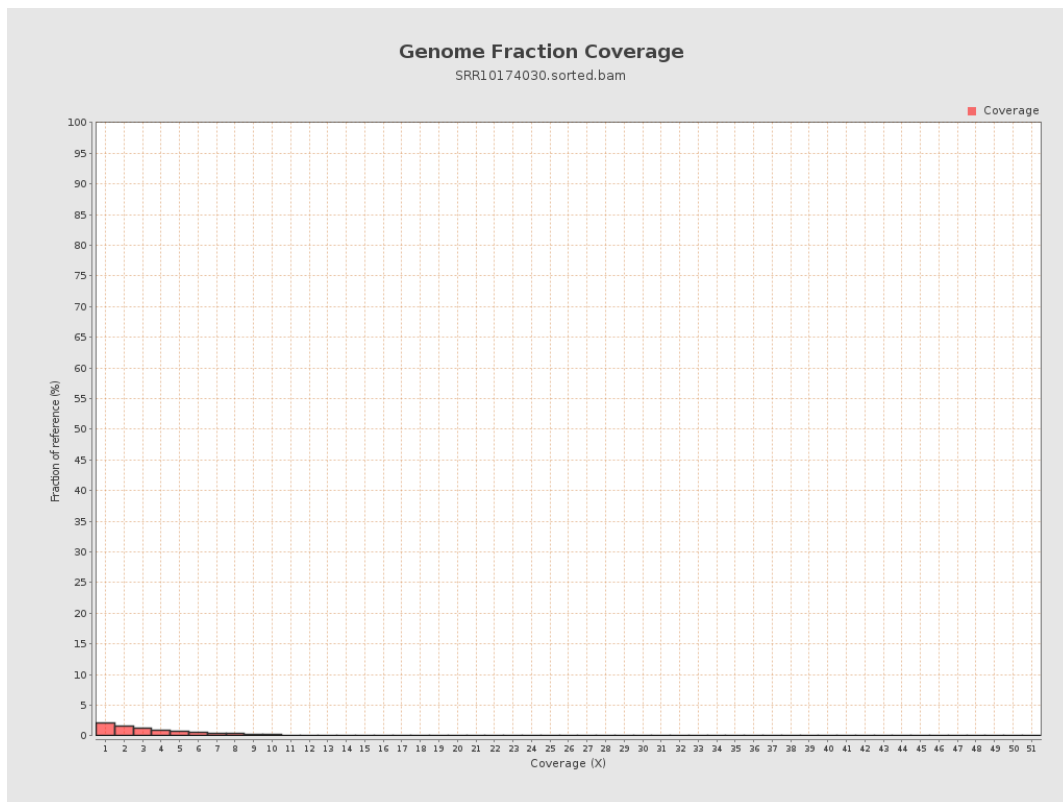
4. Results : Coverage Histogram



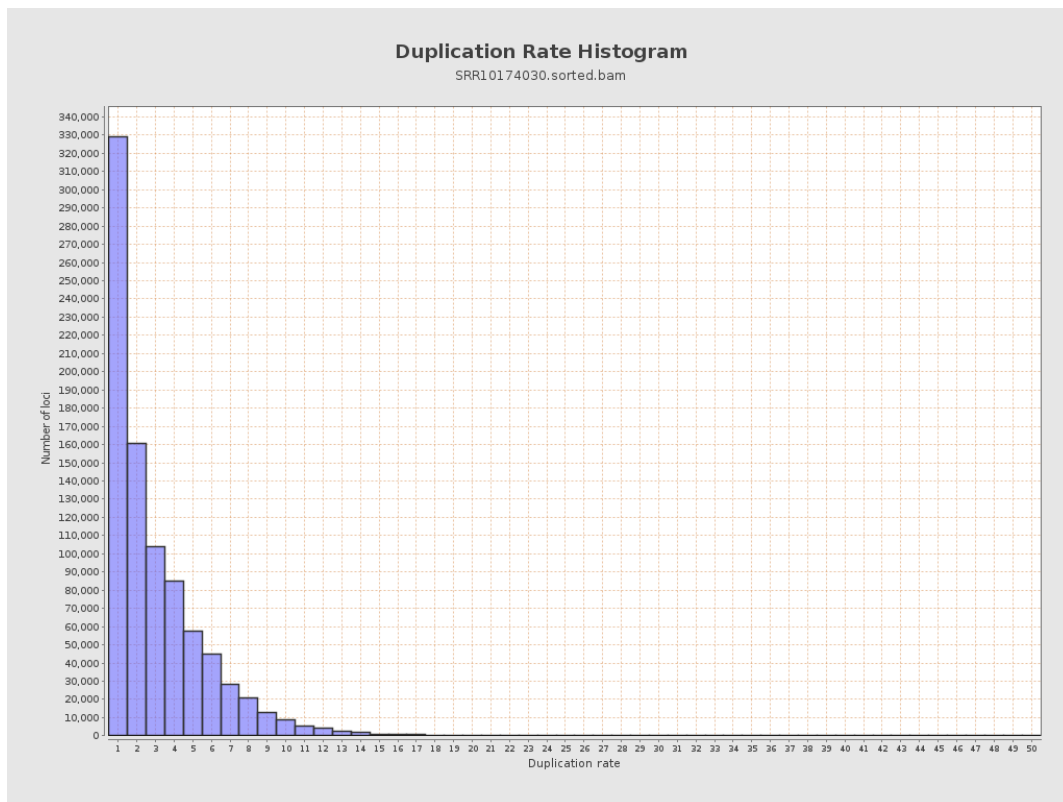
5. Results : Coverage Histogram (0-50X)



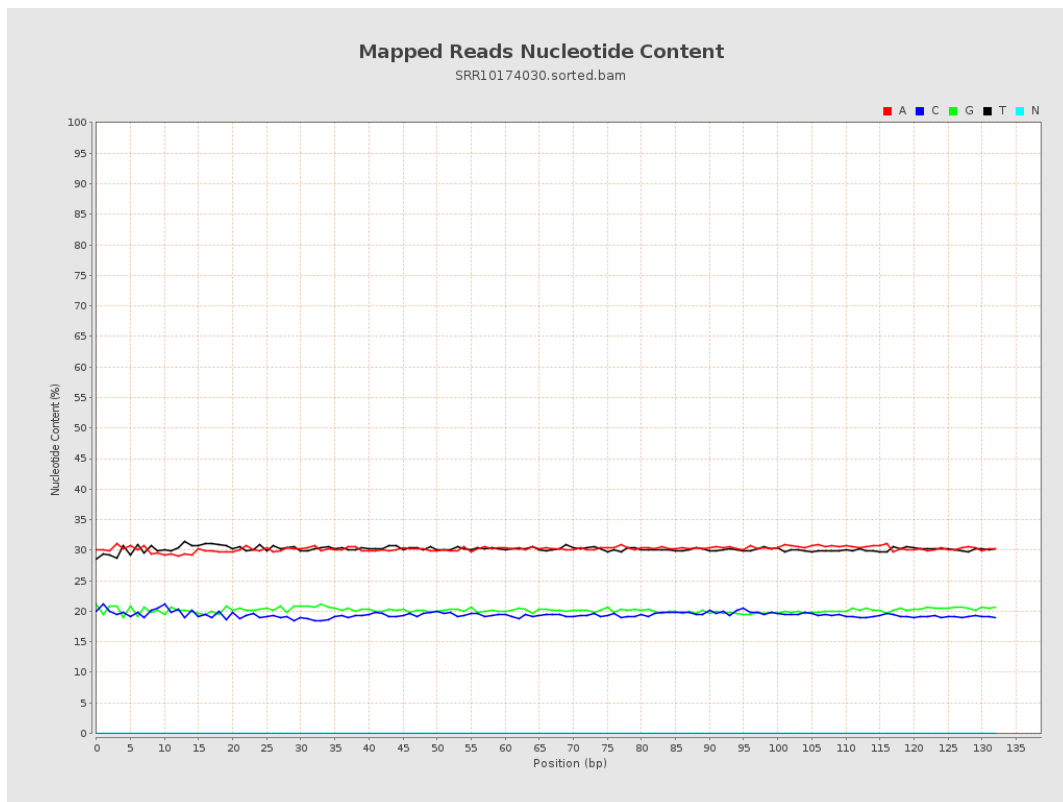
6. Results : Genome Fraction Coverage



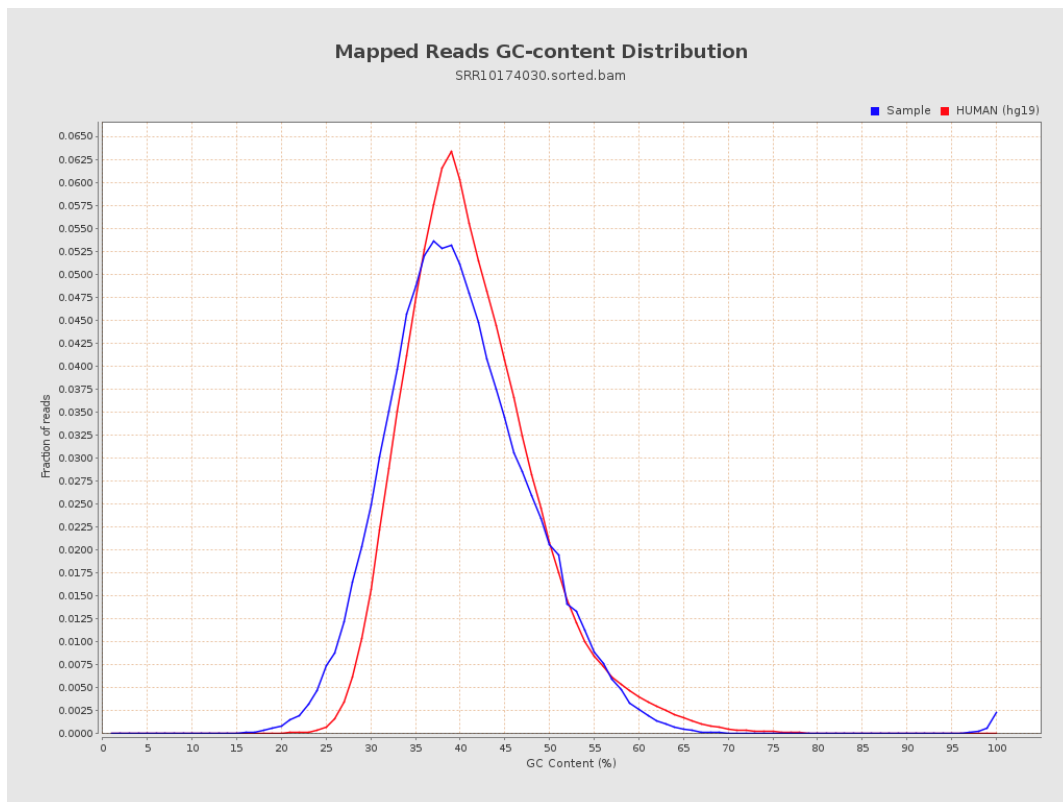
7. Results : Duplication Rate Histogram



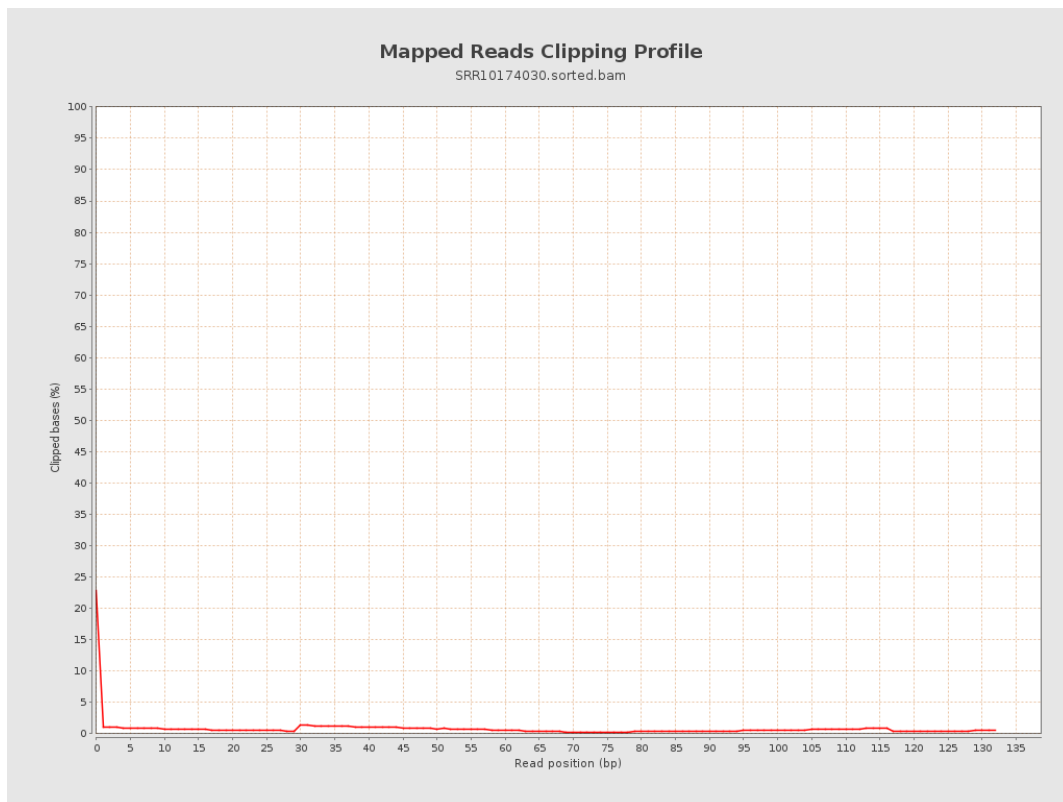
8. Results : Mapped Reads Nucleotide Content



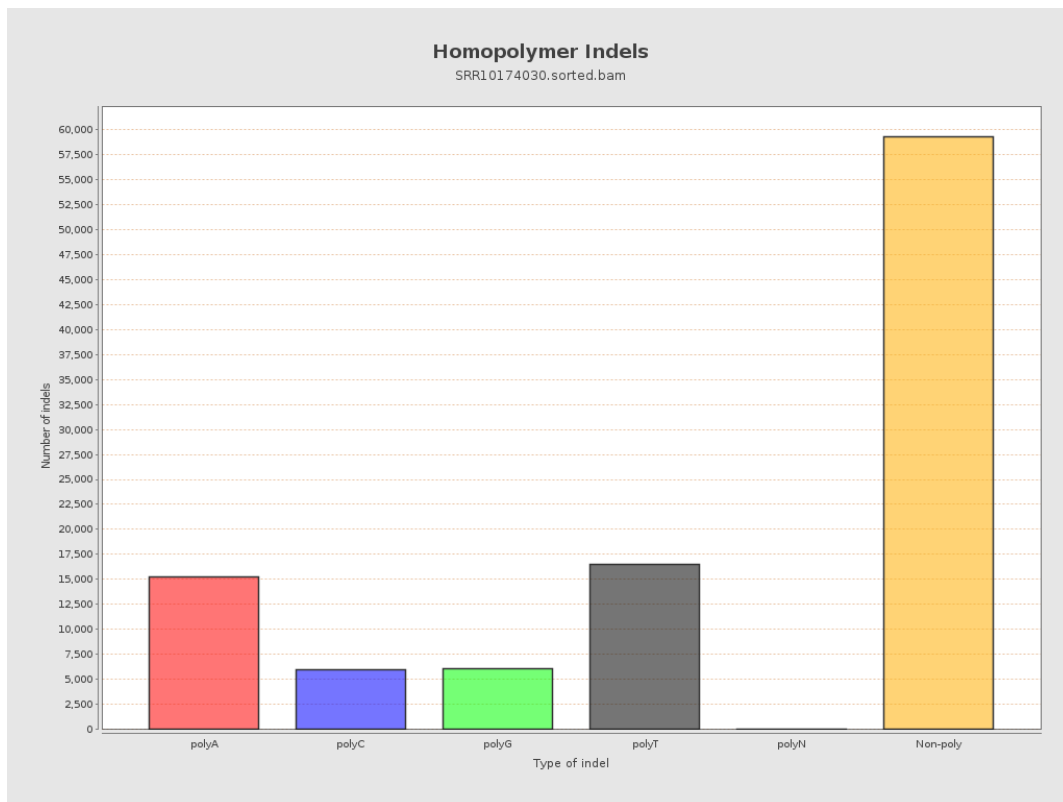
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



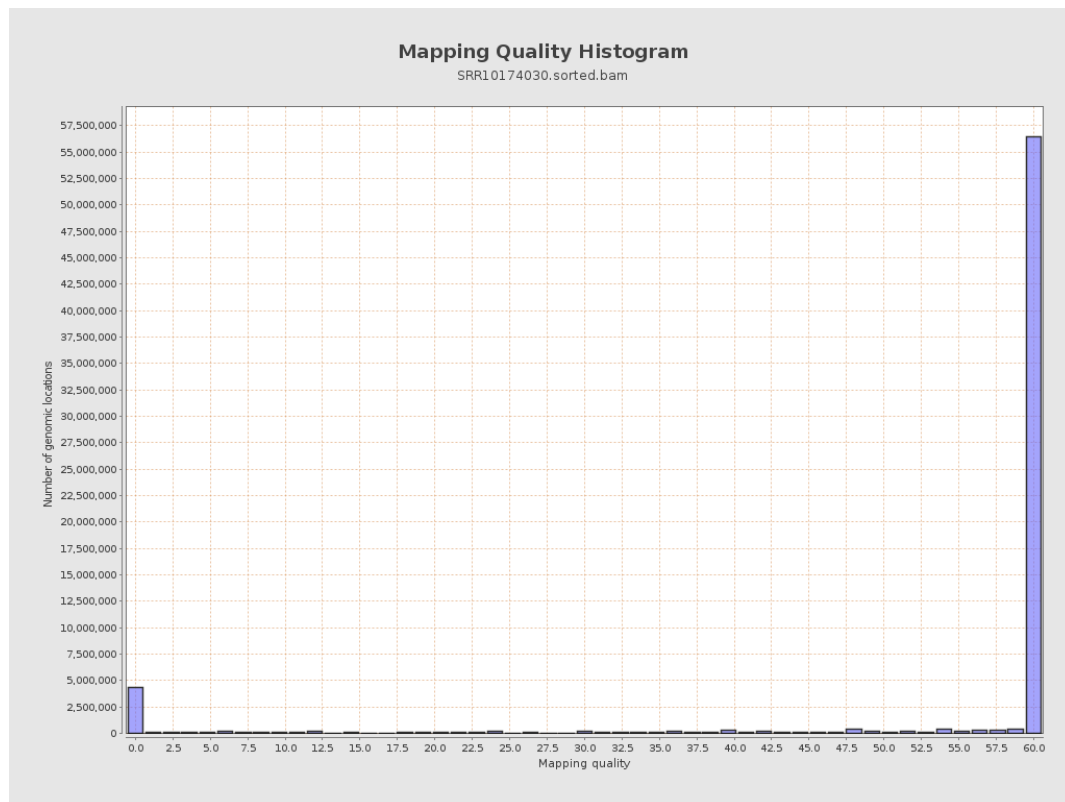
11. Results : Homopolymer Indels



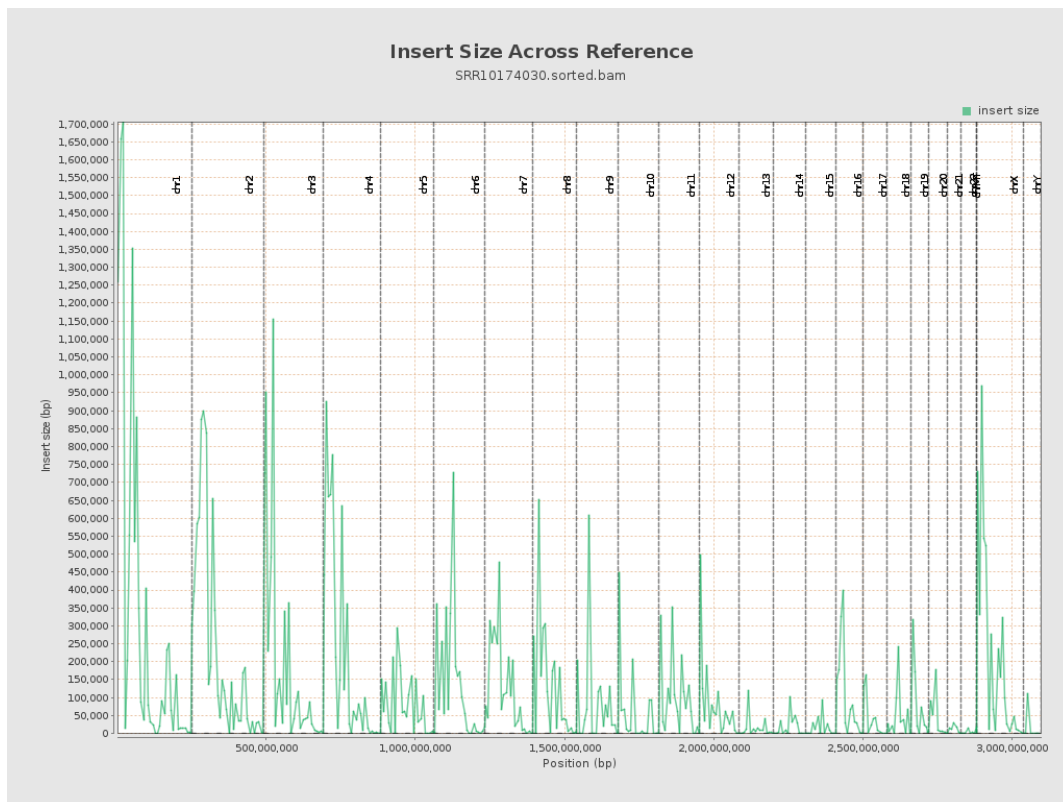
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

