

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:28:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174015.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_SRR10174015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174015_1.fastq.gz SRR10174015_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:28:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,544,476
Mapped reads	3,453,751 / 97.44%
Unmapped reads	90,725 / 2.56%
Mapped paired reads	3,453,751 / 97.44%
Mapped reads, first in pair	1,729,048 / 48.78%
Mapped reads, second in pair	1,724,703 / 48.66%
Mapped reads, both in pair	3,392,454 / 95.71%
Mapped reads, singletons	61,297 / 1.73%
Secondary alignments	0
Supplementary alignments	339,820 / 9.59%
Read min/max/mean length	30 / 133 / 128.22
Duplicated reads (estimated)	2,688,235 / 75.84%
Duplication rate	64.55%
Clipped reads	1,357,547 / 38.3%

2.2. ACGT Content

Number/percentage of A's	123,451,947 / 30.18%
Number/percentage of C's	79,961,720 / 19.55%
Number/percentage of T's	122,989,442 / 30.07%
Number/percentage of G's	82,663,923 / 20.21%
Number/percentage of N's	4,990 / 0%

GC Percentage	39.75%
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2.3. Coverage

Mean	0.1322
Standard Deviation	2.0121

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	904,564.2
Standard Deviation	8,788,752.18
P25/Median/P75	148 / 205 / 292

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	4,220,188
Insertions	42,498
Mapped reads with at least one insertion	1.19%
Deletions	89,317
Mapped reads with at least one deletion	2.52%
Homopolymer indels	43.47%

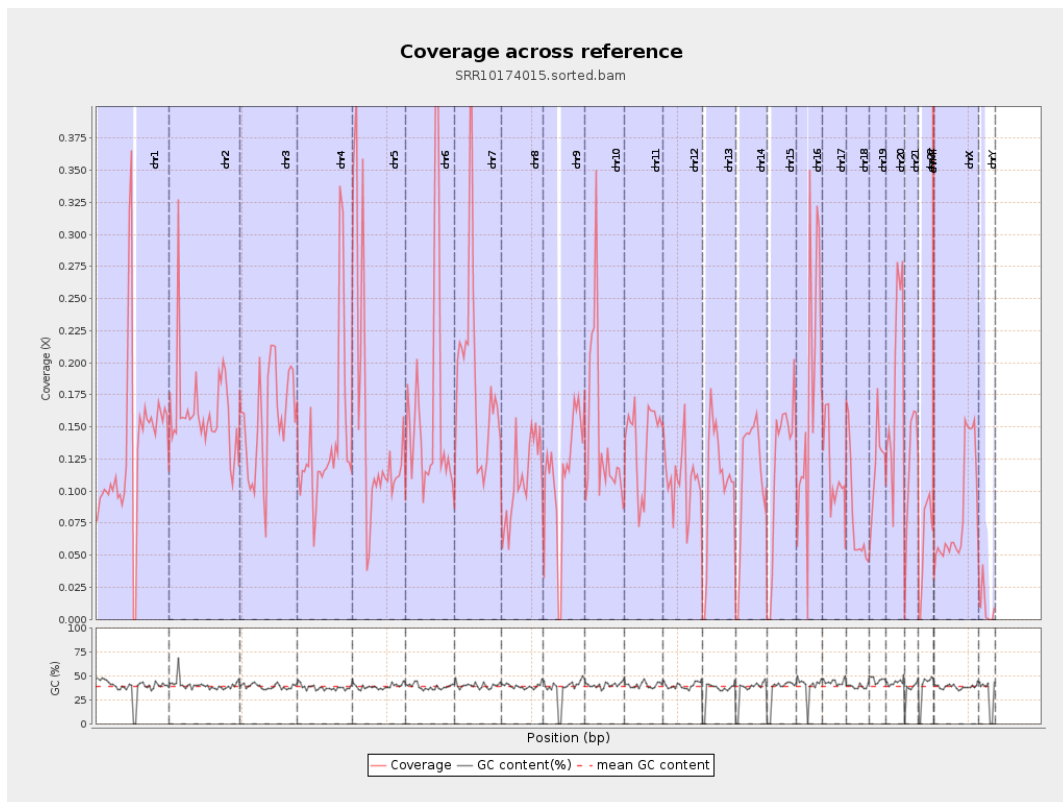
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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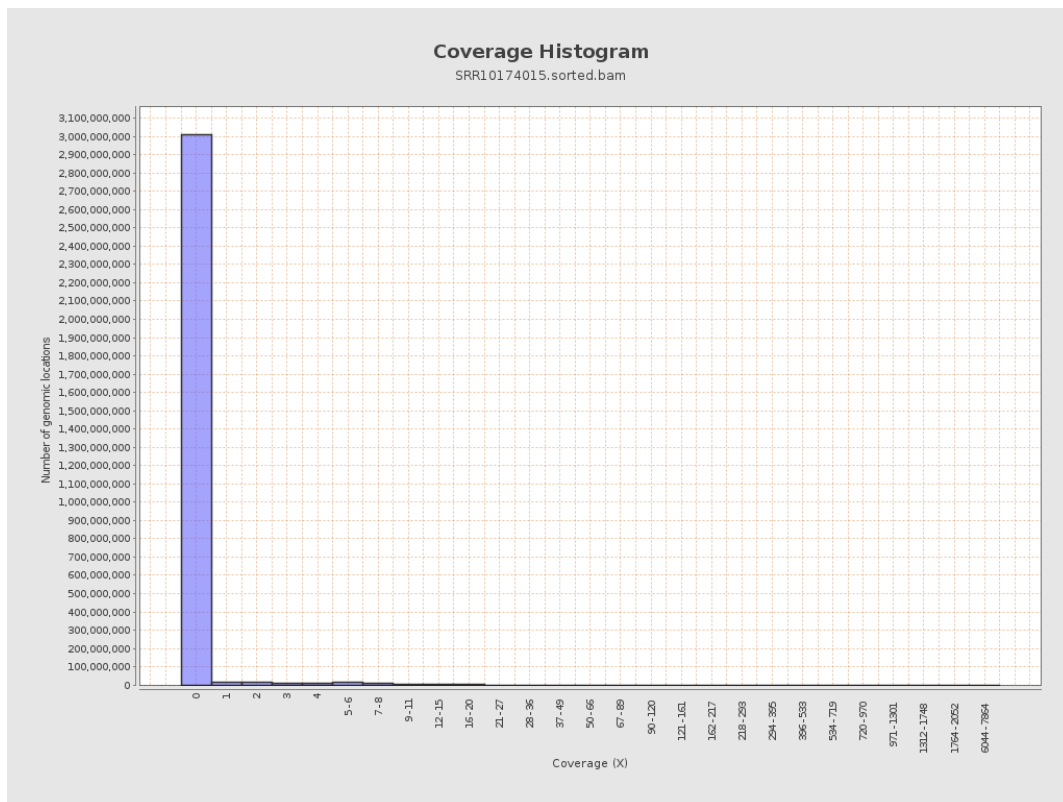
		bases	coverage	deviation
chr1	249250621	33020640	0.1325	1.7093
chr2	243199373	39228239	0.1613	5.572
chr3	198022430	30873682	0.1559	1.1494
chr4	191154276	25993809	0.136	1.2279
chr5	180915260	27262455	0.1507	1.1294
chr6	171115067	28602417	0.1672	1.2374
chr7	159138663	29467962	0.1852	1.9704
chr8	146364022	16068255	0.1098	1.0971
chr9	141213431	16504016	0.1169	1.1241
chr10	135534747	19398727	0.1431	2.1299
chr11	135006516	18823335	0.1394	1.1005
chr12	133851895	14515850	0.1084	0.9651
chr13	115169878	12130954	0.1053	0.9456
chr14	107349540	11879043	0.1107	0.965
chr15	102531392	12400067	0.1209	0.988
chr16	90354753	15716450	0.1739	1.6672
chr17	81195210	9092390	0.112	1.0078
chr18	78077248	6210720	0.0795	1.3163
chr19	59128983	7062750	0.1194	1.5793
chr20	63025520	11802113	0.1873	1.25
chr21	48129895	5706681	0.1186	1.0309
chr22	51304566	3135083	0.0611	0.674
chrMT	16571	1076438	64.9591	53.471
chrX	155270560	12779240	0.0823	0.8355

chrY	59373566	546756	0.0092	0.4957
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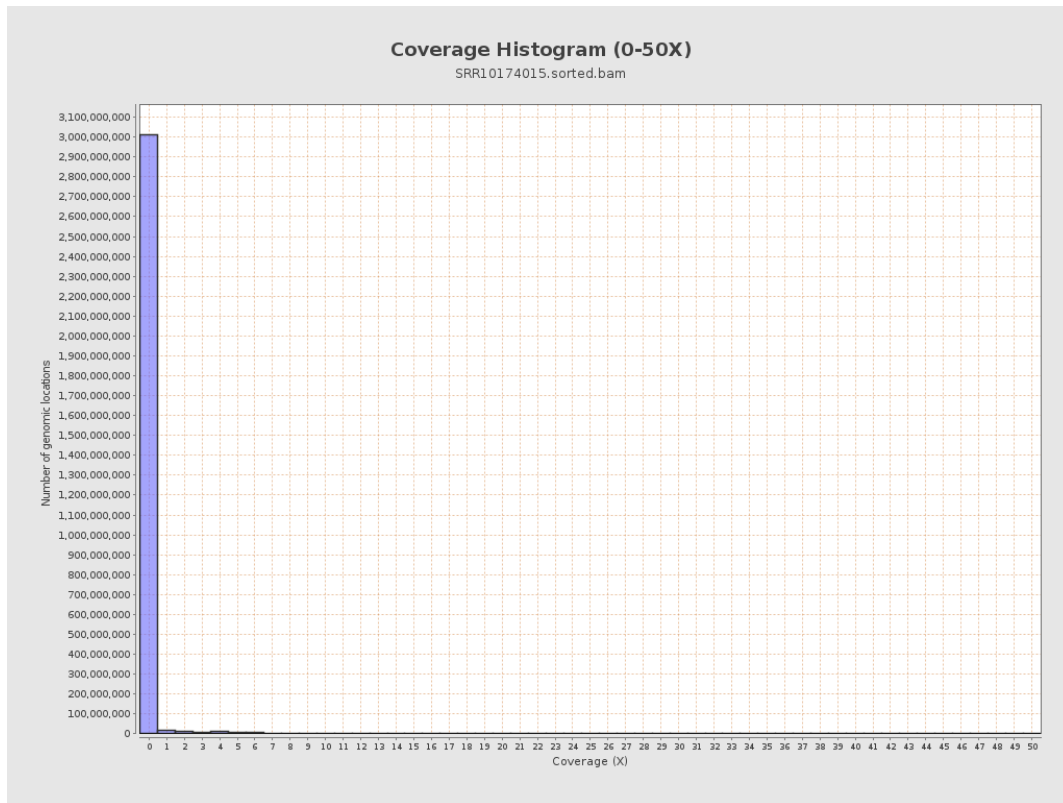
3. Results : Coverage across reference



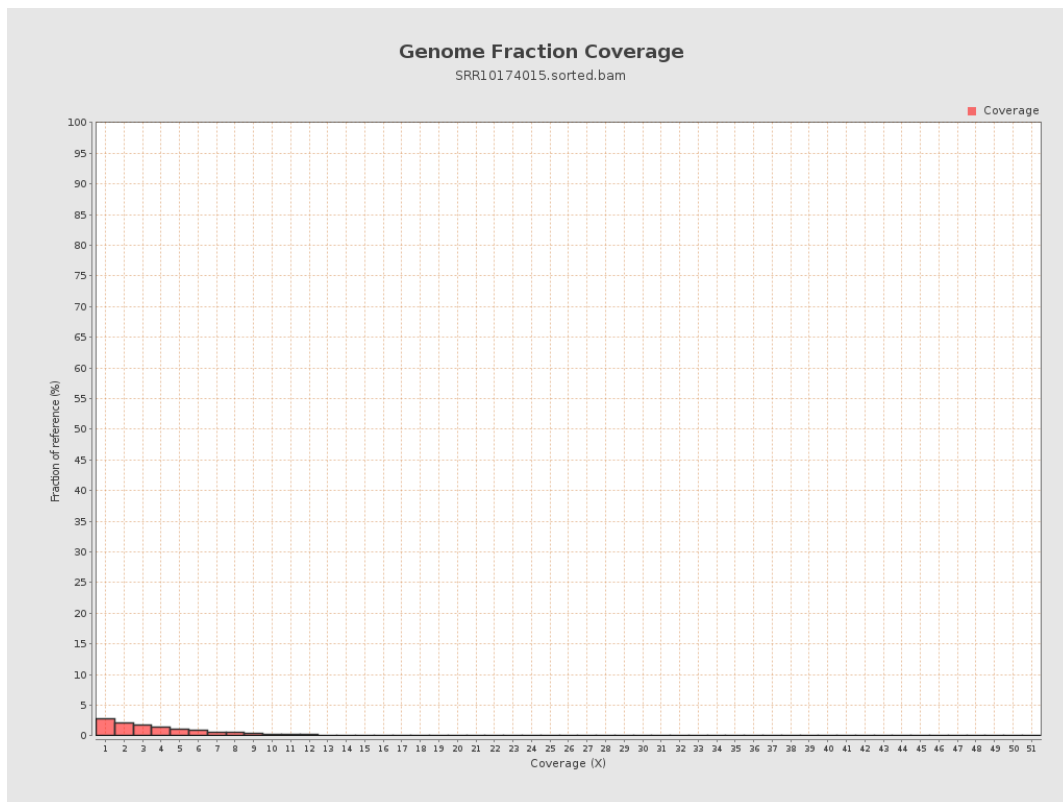
4. Results : Coverage Histogram



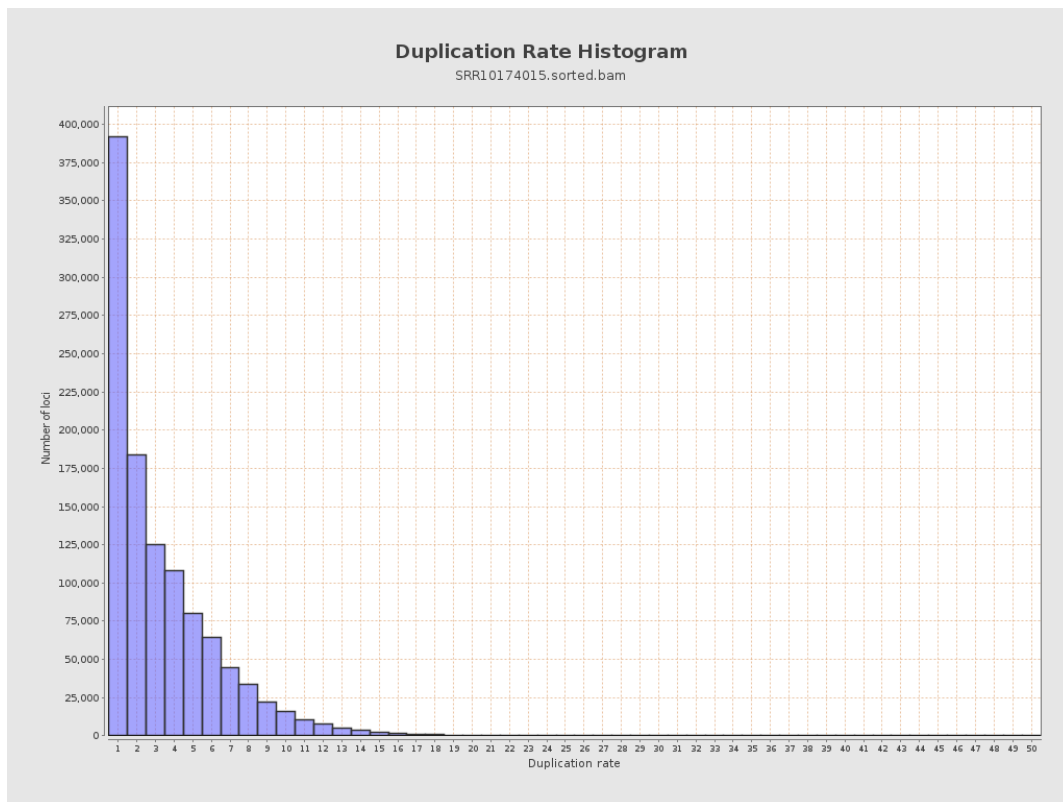
5. Results : Coverage Histogram (0-50X)



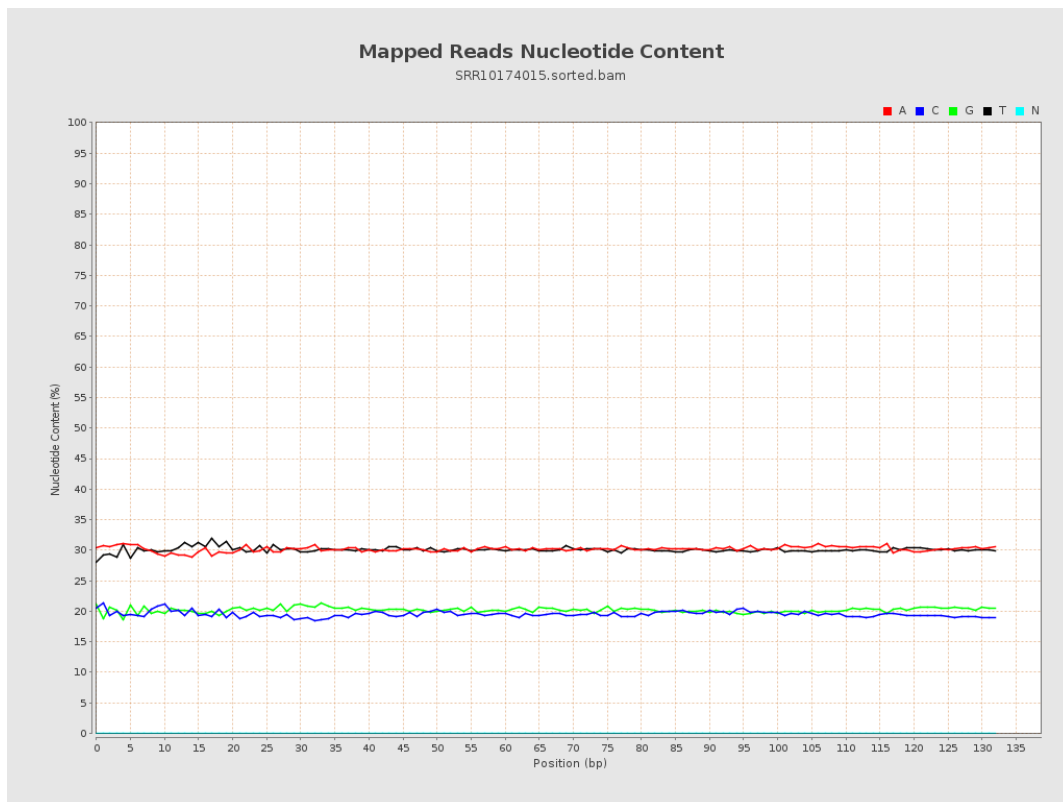
6. Results : Genome Fraction Coverage



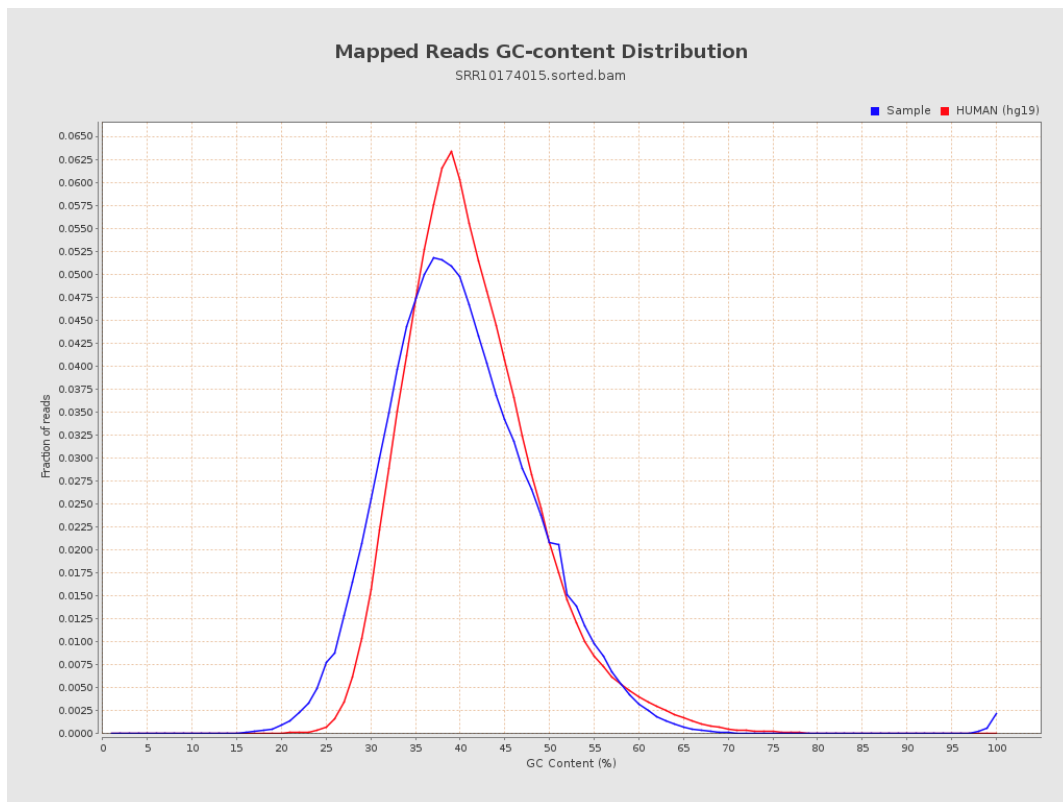
7. Results : Duplication Rate Histogram



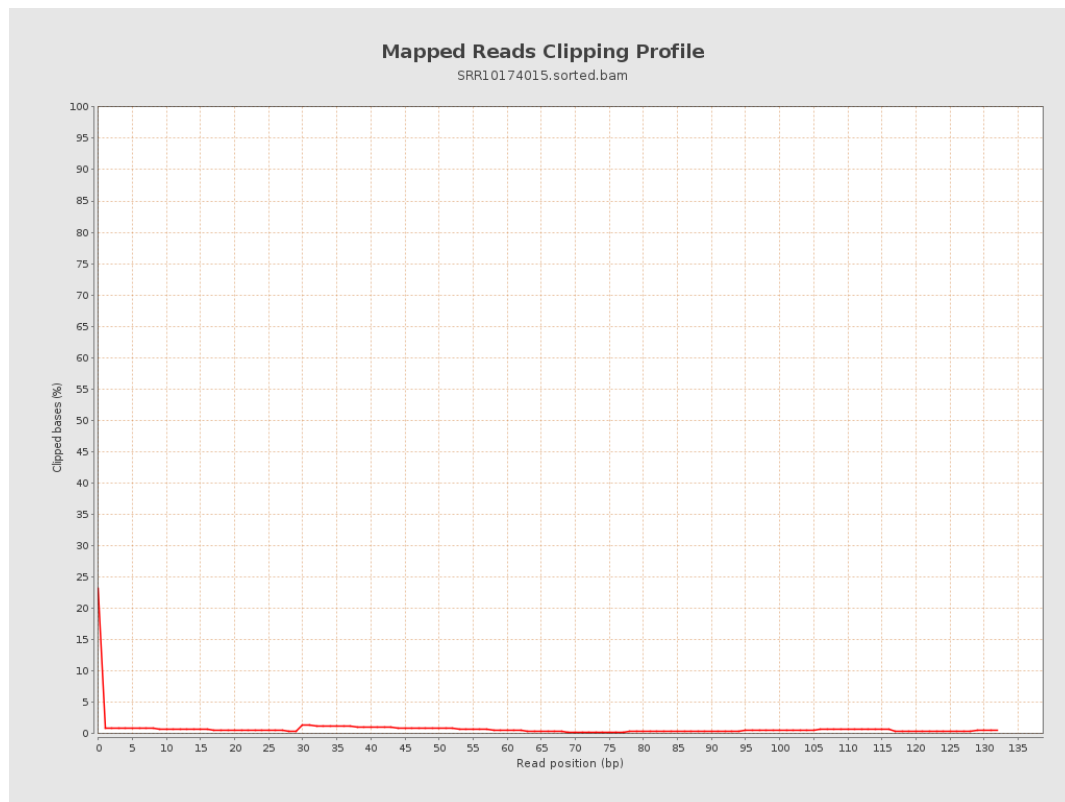
8. Results : Mapped Reads Nucleotide Content



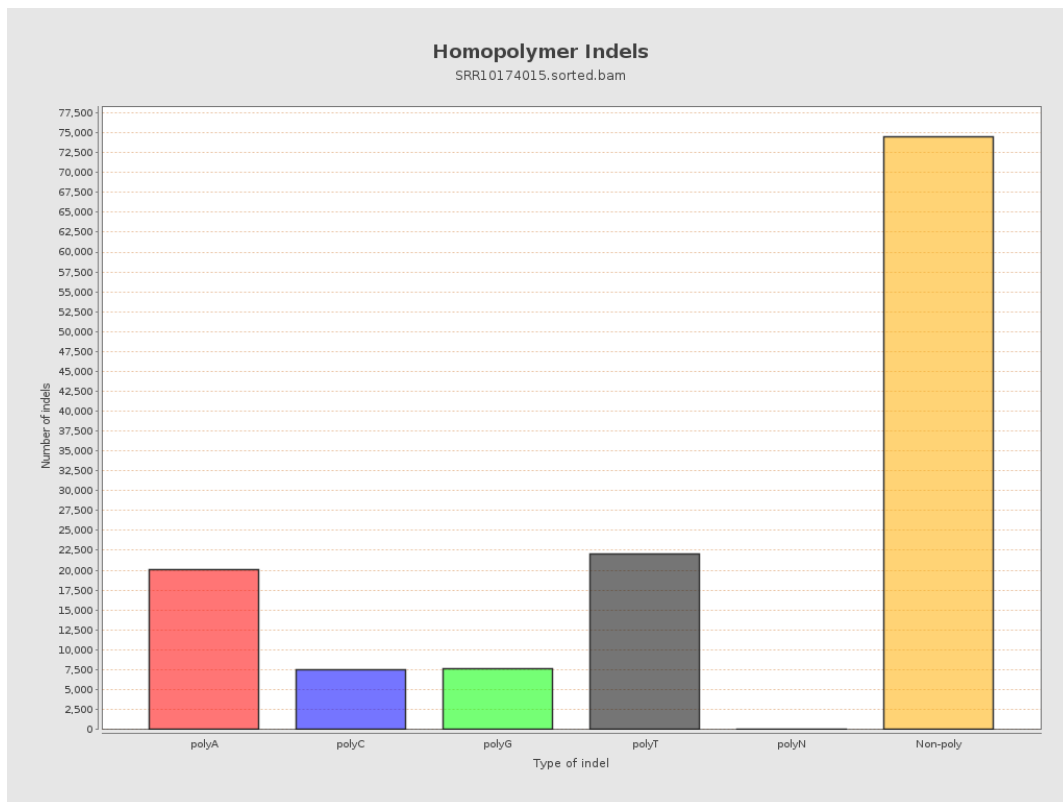
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



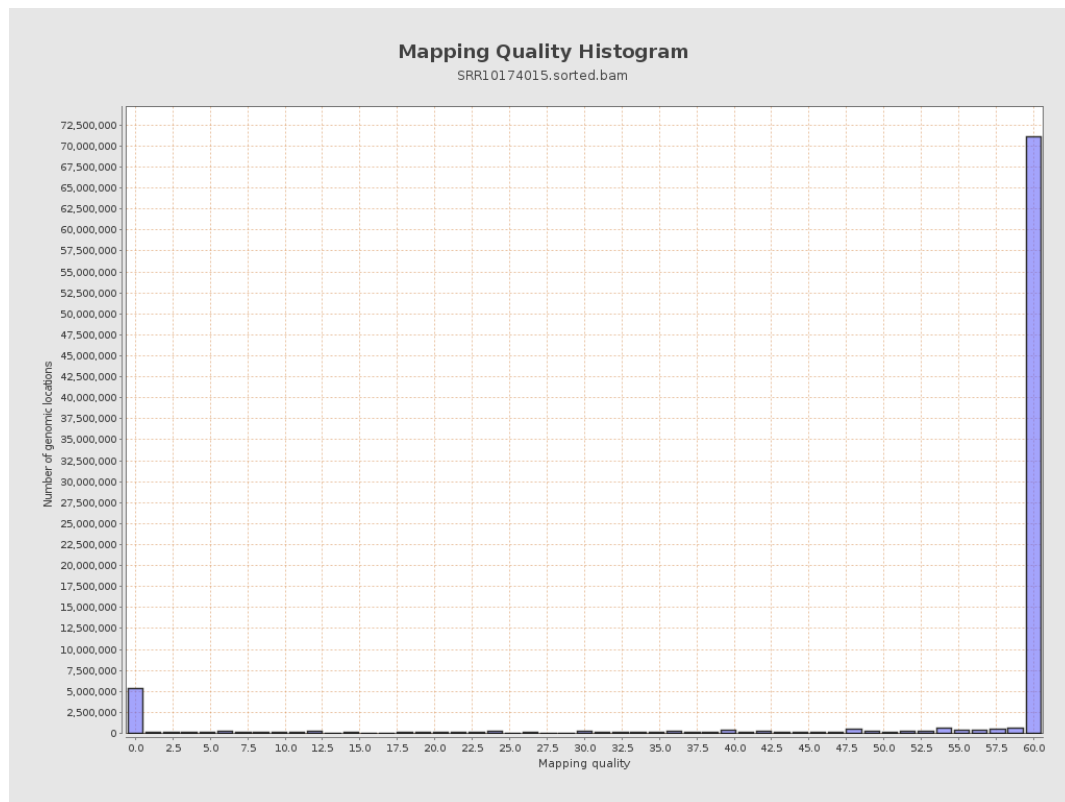
11. Results : Homopolymer Indels



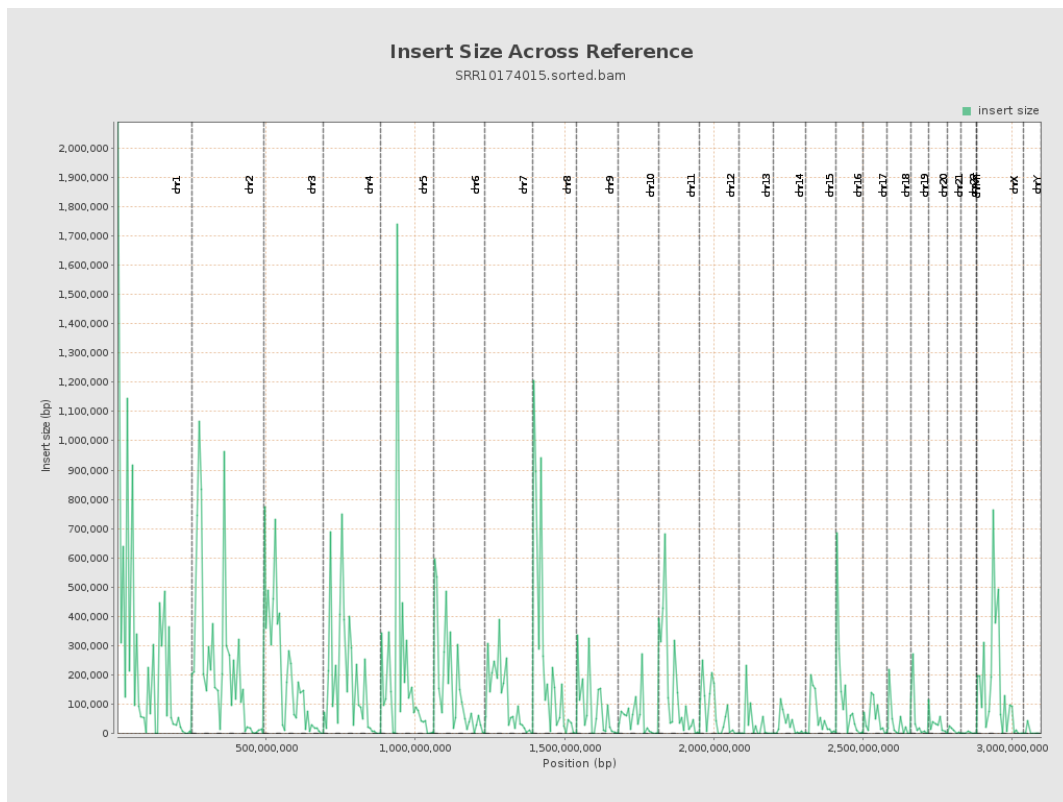
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

