

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 00:52:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174044.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_SRR10174044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174044_1.fastq.gz SRR10174044_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 00:52:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,241,540
Mapped reads	5,101,194 / 97.32%
Unmapped reads	140,346 / 2.68%
Mapped paired reads	5,101,194 / 97.32%
Mapped reads, first in pair	2,555,185 / 48.75%
Mapped reads, second in pair	2,546,009 / 48.57%
Mapped reads, both in pair	5,008,674 / 95.56%
Mapped reads, singletons	92,520 / 1.77%
Secondary alignments	0
Supplementary alignments	521,456 / 9.95%
Read min/max/mean length	30 / 133 / 128.3
Duplicated reads (estimated)	3,956,196 / 75.48%
Duplication rate	64.15%
Clipped reads	2,197,818 / 41.93%

2.2. ACGT Content

Number/percentage of A's	182,626,922 / 30.39%
Number/percentage of C's	115,792,490 / 19.27%
Number/percentage of T's	182,441,892 / 30.36%
Number/percentage of G's	120,151,875 / 19.99%
Number/percentage of N's	7,395 / 0%

GC Percentage	39.26%
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2.3. Coverage

Mean	0.1943
Standard Deviation	2.9172

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	763,230
Standard Deviation	7,841,107.12
P25/Median/P75	143 / 199 / 283

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	6,165,553
Insertions	64,026
Mapped reads with at least one insertion	1.21%
Deletions	147,155
Mapped reads with at least one deletion	2.81%
Homopolymer indels	42.59%

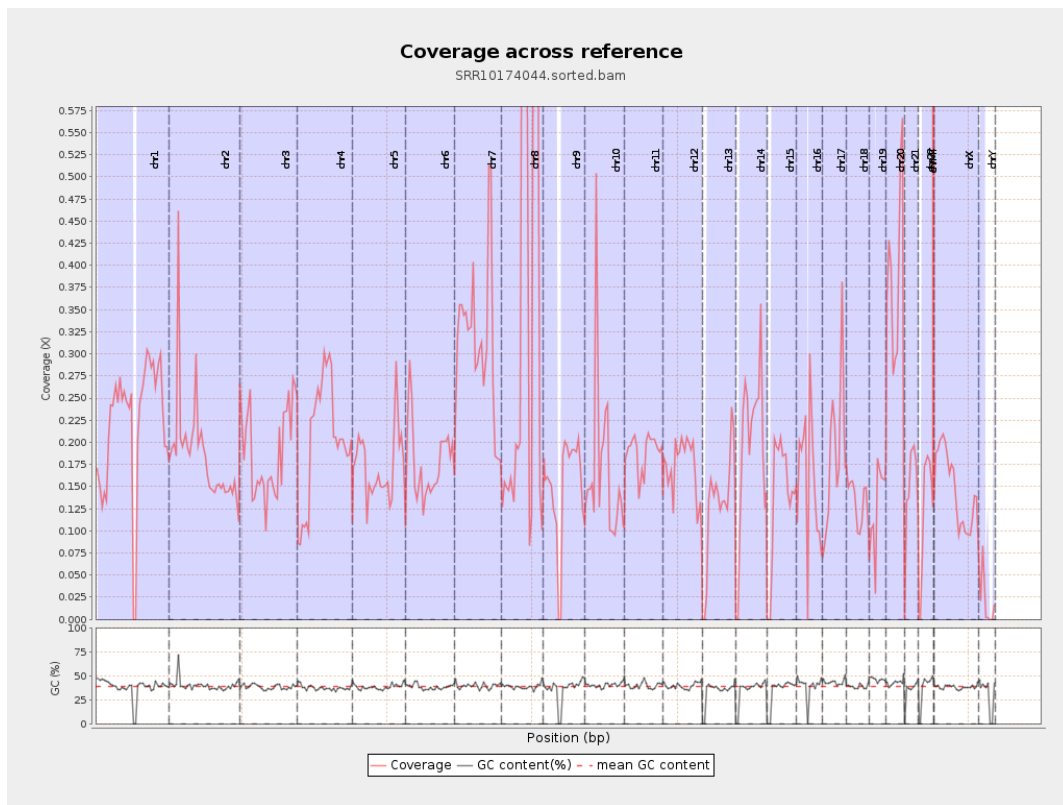
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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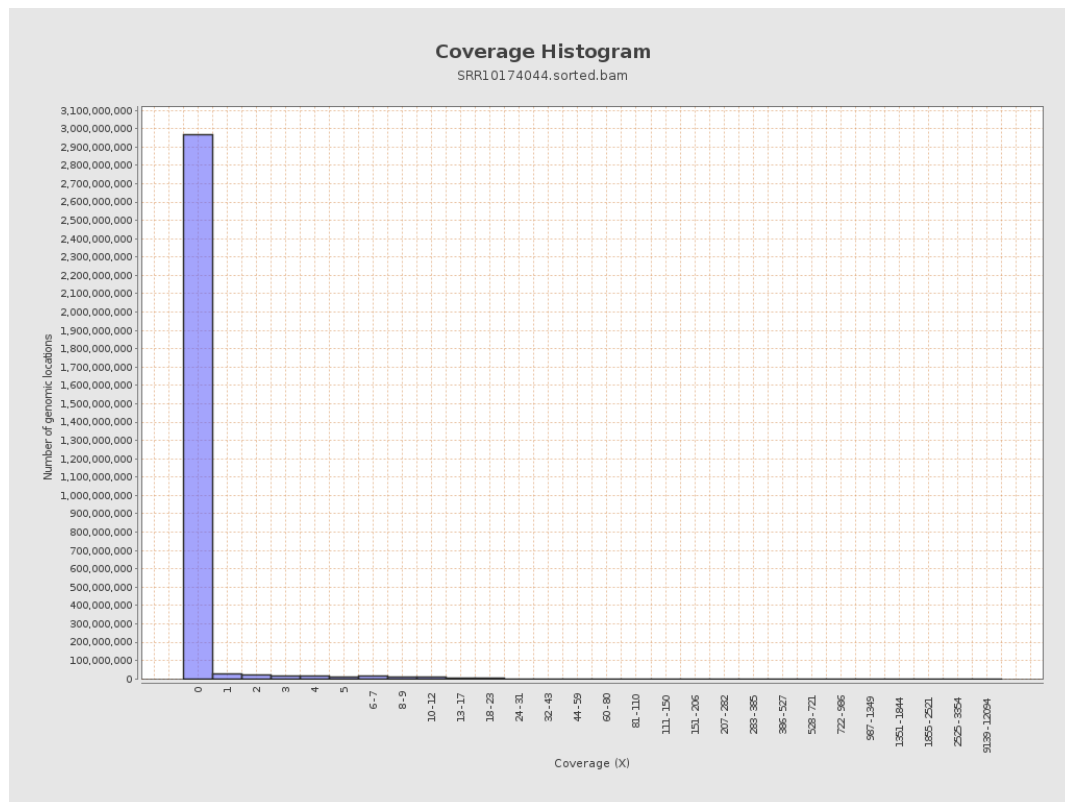
		bases	coverage	deviation
chr1	249250621	55195369	0.2214	1.7066
chr2	243199373	45180031	0.1858	8.4762
chr3	198022430	37673128	0.1902	1.2708
chr4	191154276	38651637	0.2022	1.6105
chr5	180915260	31299940	0.173	1.2014
chr6	171115067	30049465	0.1756	1.2678
chr7	159138663	50355825	0.3164	3.1495
chr8	146364022	60415896	0.4128	2.278
chr9	141213431	21147799	0.1498	1.4401
chr10	135534747	22806296	0.1683	3.7426
chr11	135006516	25440378	0.1884	1.2962
chr12	133851895	23213685	0.1734	1.2086
chr13	115169878	15006019	0.1303	1.0505
chr14	107349540	20895436	0.1946	1.2789
chr15	102531392	14370055	0.1402	1.0747
chr16	90354753	13966399	0.1546	1.5716
chr17	81195210	15242338	0.1877	1.362
chr18	78077248	10472959	0.1341	1.7748
chr19	59128983	7572217	0.1281	1.293
chr20	63025520	24162542	0.3834	1.8083
chr21	48129895	7059193	0.1467	1.2186
chr22	51304566	6148883	0.1199	0.9602
chrMT	16571	1145021	69.0979	52.6415
chrX	155270560	22725359	0.1464	1.1193

chrY	59373566	1185992	0.02	0.8351
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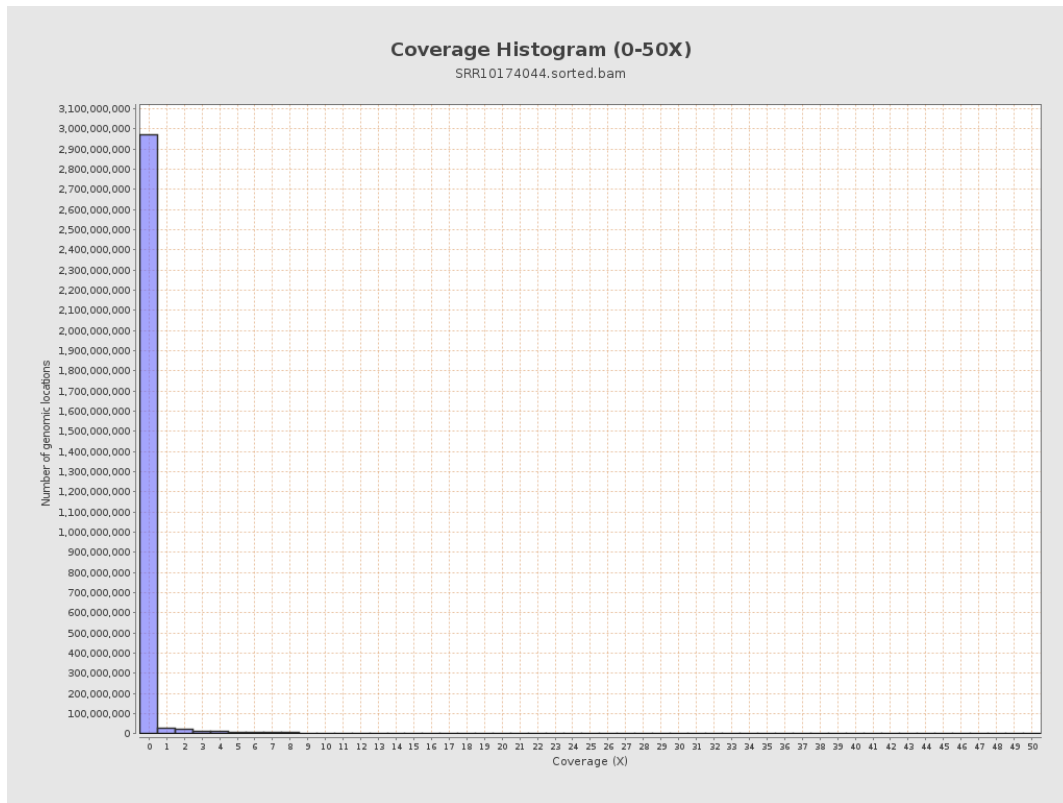
3. Results : Coverage across reference



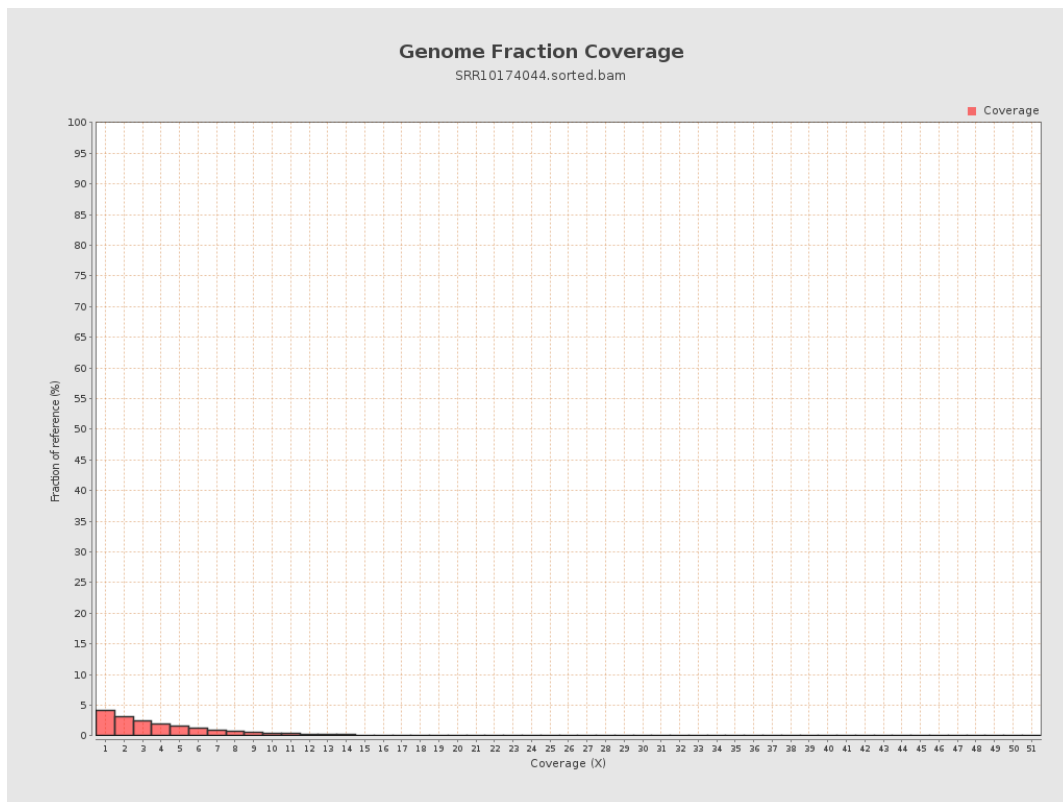
4. Results : Coverage Histogram



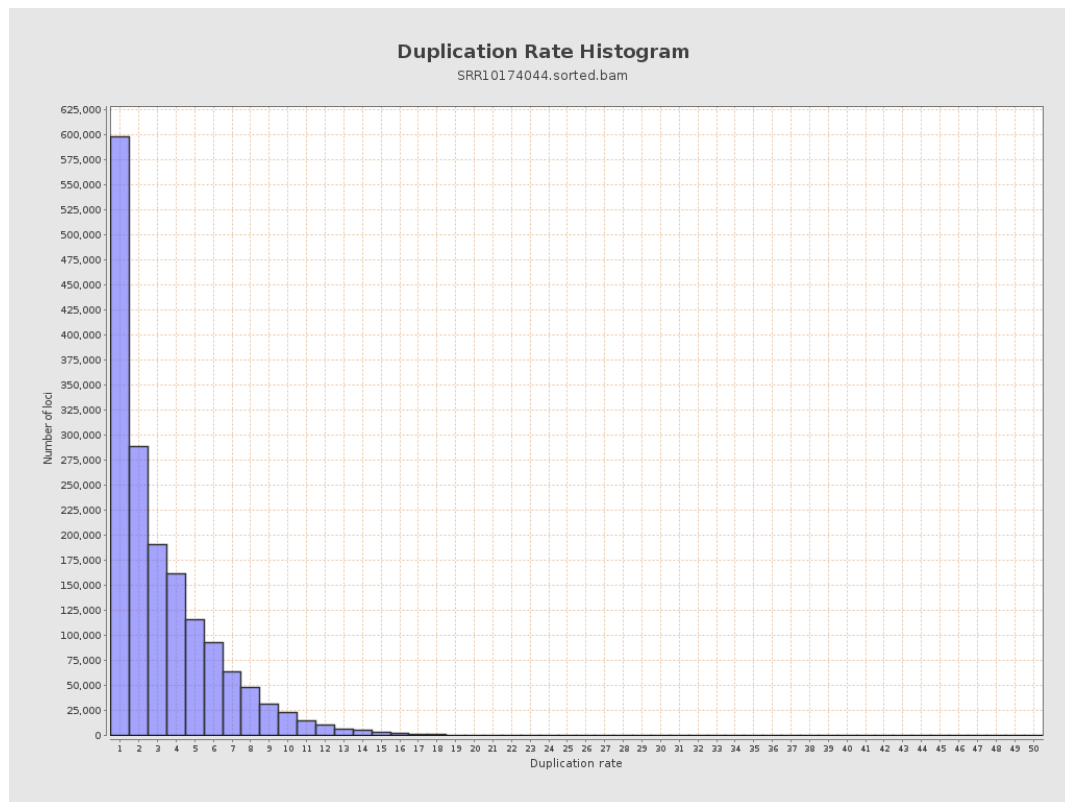
5. Results : Coverage Histogram (0-50X)



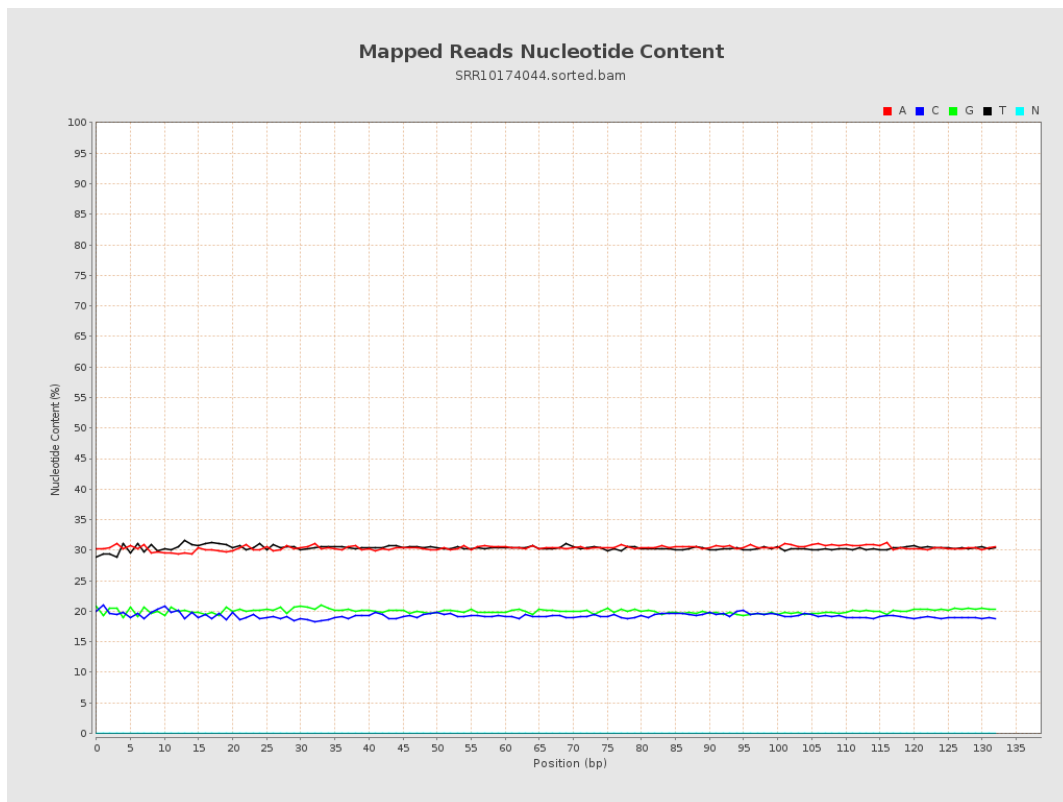
6. Results : Genome Fraction Coverage



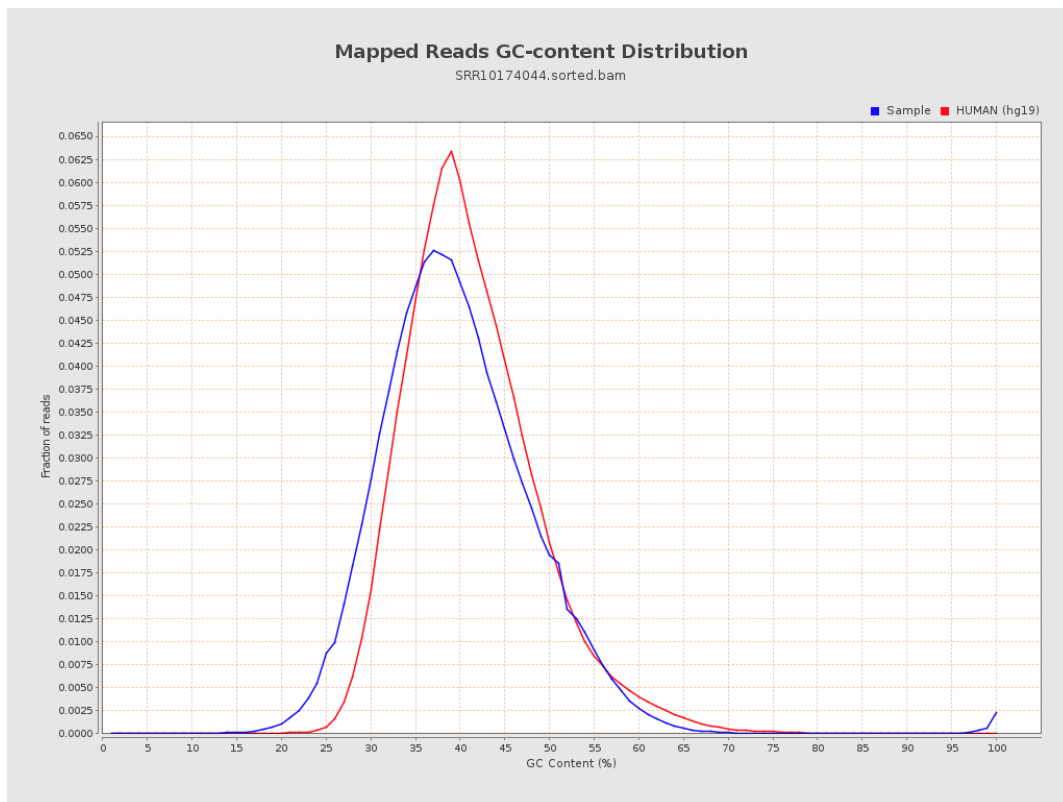
7. Results : Duplication Rate Histogram



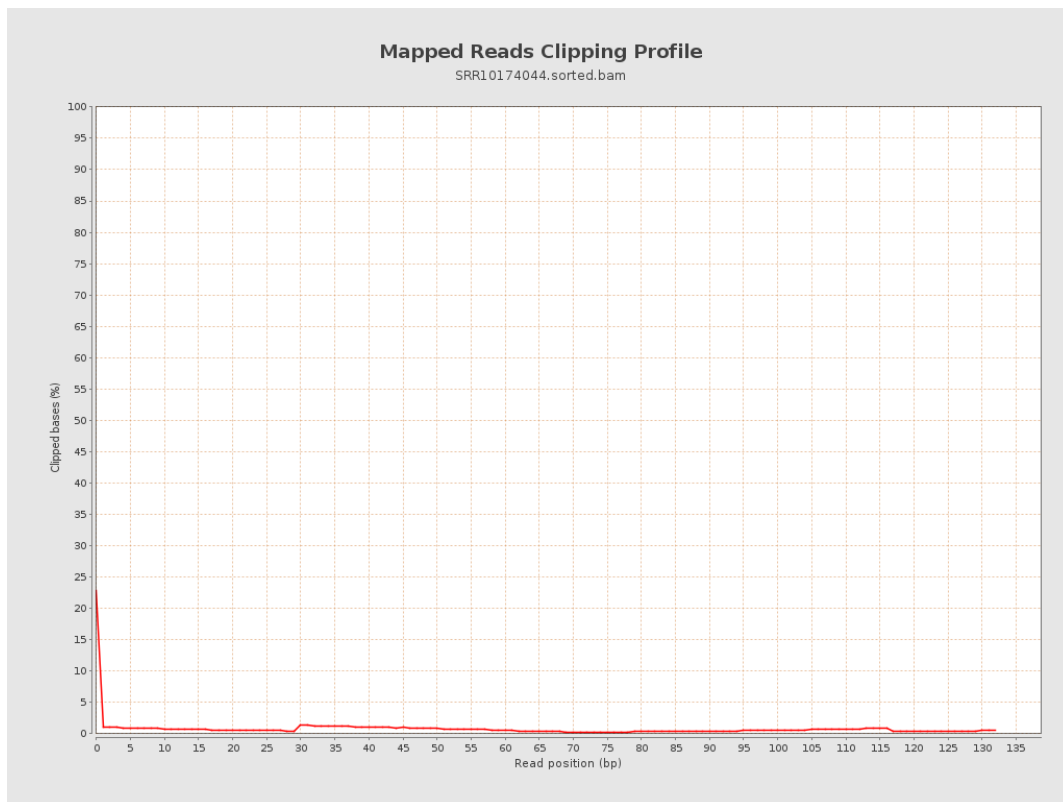
8. Results : Mapped Reads Nucleotide Content



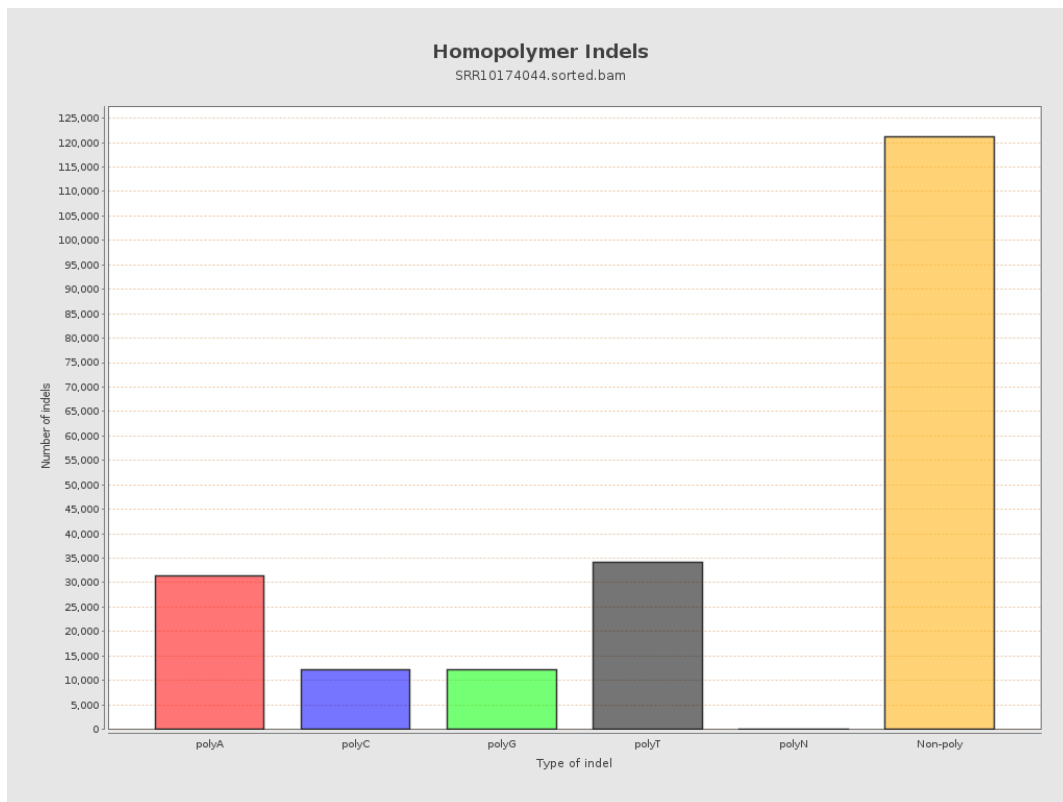
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



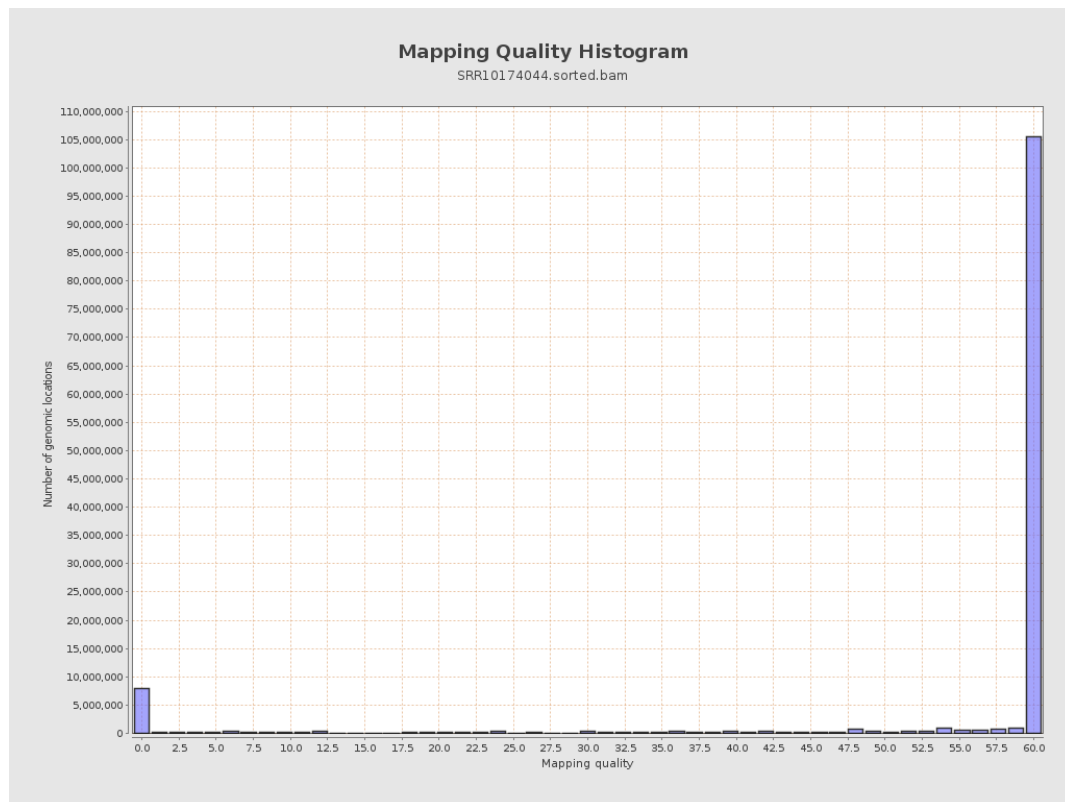
11. Results : Homopolymer Indels



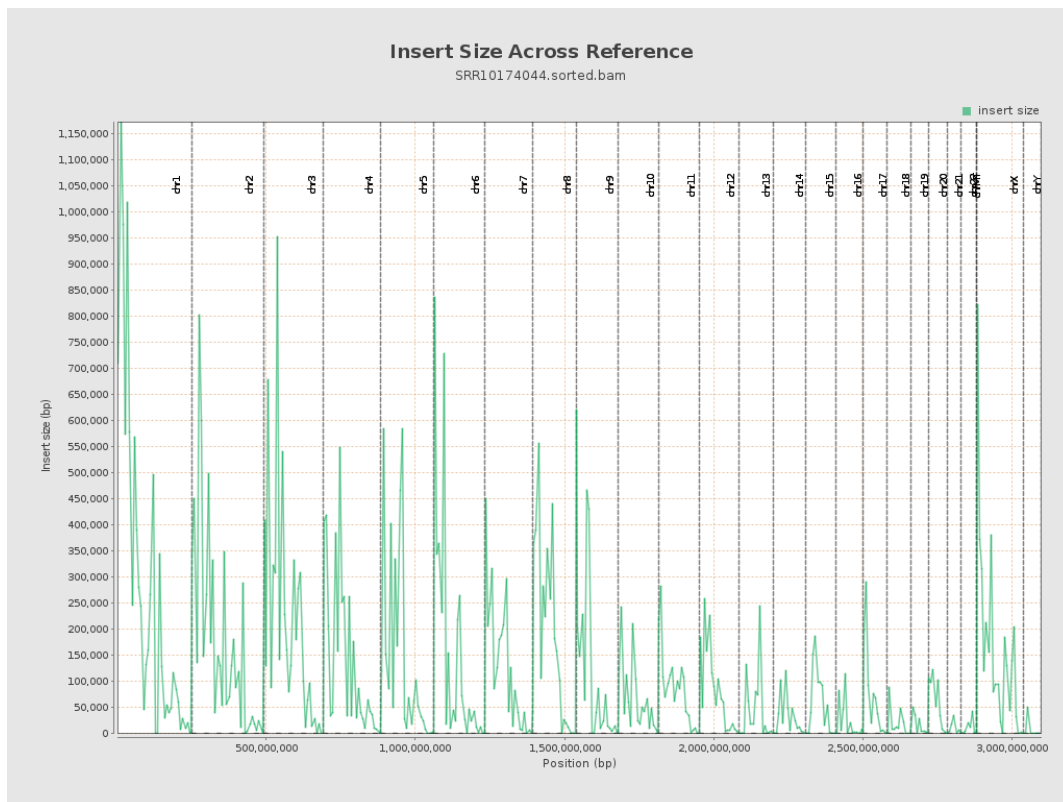
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

