

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:29:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173860.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_SRR10173860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173860_1.fastq.gz SRR10173860_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:29:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,573,148
Mapped reads	5,422,037 / 97.29%
Unmapped reads	151,111 / 2.71%
Mapped paired reads	5,422,037 / 97.29%
Mapped reads, first in pair	2,714,550 / 48.71%
Mapped reads, second in pair	2,707,487 / 48.58%
Mapped reads, both in pair	5,319,308 / 95.45%
Mapped reads, singletons	102,729 / 1.84%
Secondary alignments	0
Supplementary alignments	587,584 / 10.54%
Read min/max/mean length	30 / 133 / 128.21
Duplicated reads (estimated)	4,182,776 / 75.05%
Duplication rate	64.22%
Clipped reads	2,481,455 / 44.53%

2.2. ACGT Content

Number/percentage of A's	192,009,555 / 30.27%
Number/percentage of C's	122,985,320 / 19.39%
Number/percentage of T's	191,746,846 / 30.23%
Number/percentage of G's	127,515,267 / 20.1%
Number/percentage of N's	6,823 / 0%

GC Percentage	39.49%
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2.3. Coverage

Mean	0.205
Standard Deviation	3.154

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	926,639.03
Standard Deviation	8,344,212.49
P25/Median/P75	138 / 196 / 287

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	6,419,313
Insertions	66,854
Mapped reads with at least one insertion	1.19%
Deletions	147,406
Mapped reads with at least one deletion	2.65%
Homopolymer indels	42.69%

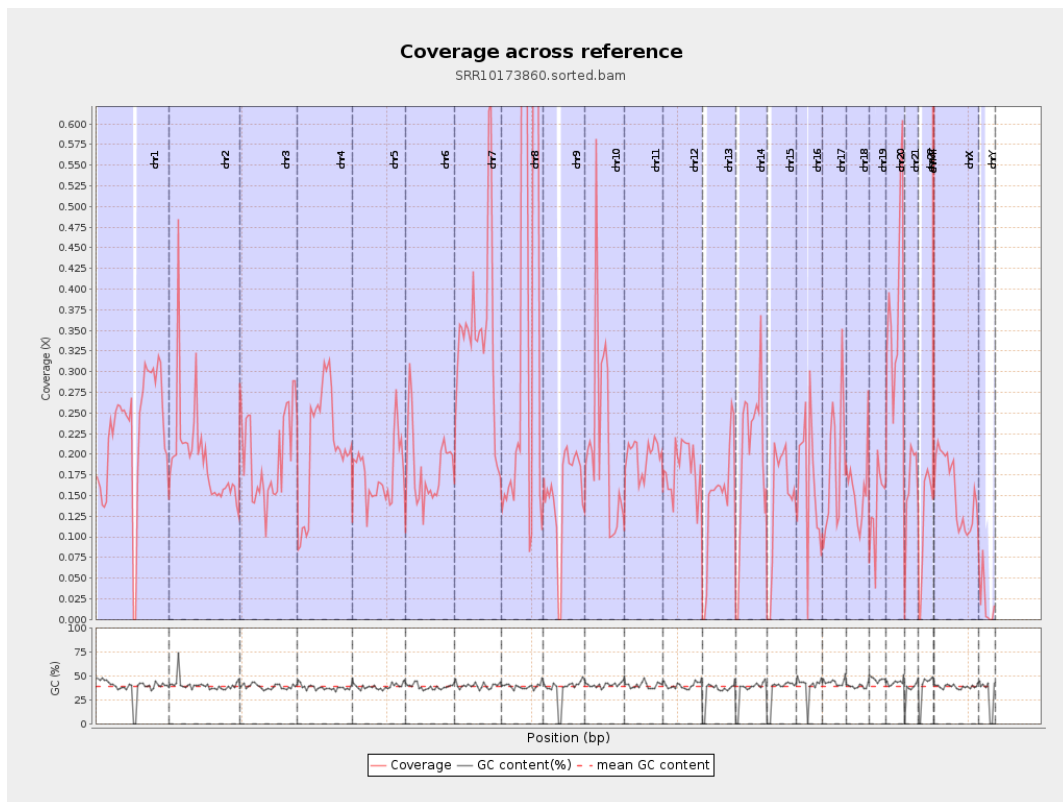
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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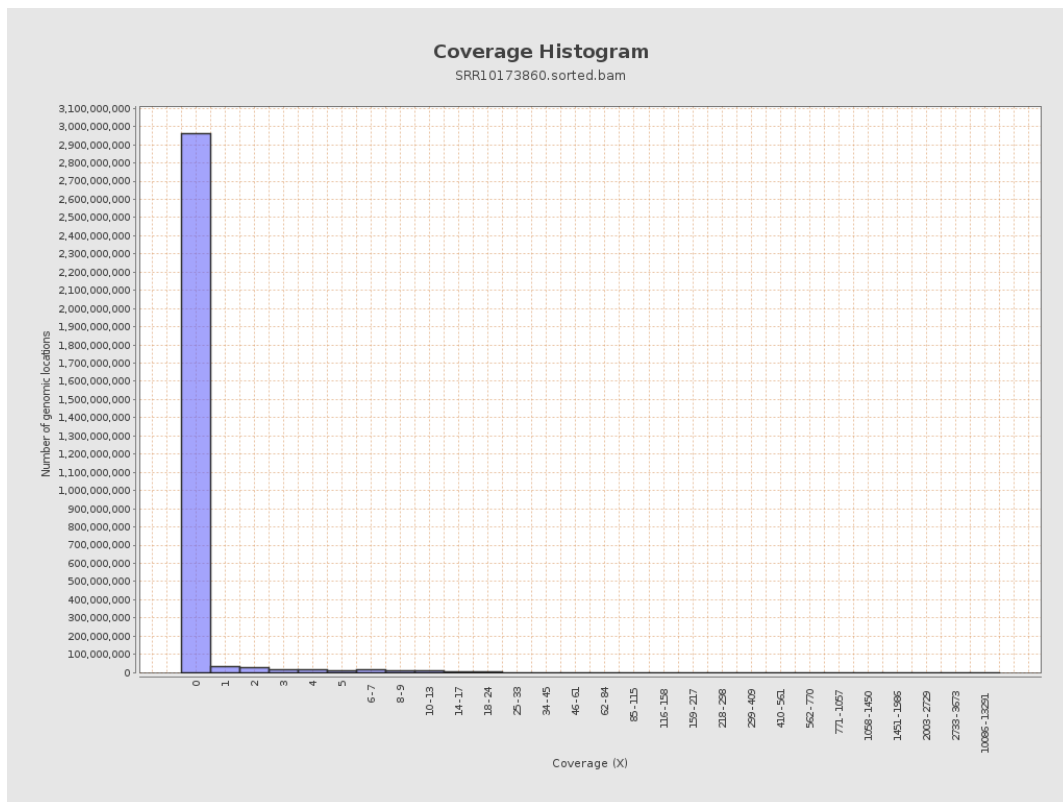
		bases	coverage	deviation
chr1	249250621	56467296	0.2265	1.8445
chr2	243199373	47403623	0.1949	9.2961
chr3	198022430	39308813	0.1985	1.2872
chr4	191154276	40042921	0.2095	1.6679
chr5	180915260	31846994	0.176	1.1833
chr6	171115067	31049435	0.1815	1.2631
chr7	159138663	55182074	0.3468	3.2423
chr8	146364022	63382605	0.433	2.358
chr9	141213431	21662459	0.1534	1.5164
chr10	135534747	29165108	0.2152	4.1207
chr11	135006516	26580854	0.1969	1.3378
chr12	133851895	24528303	0.1832	1.2122
chr13	115169878	16926831	0.147	1.0943
chr14	107349540	21500619	0.2003	1.2781
chr15	102531392	14947708	0.1458	1.0674
chr16	90354753	14861537	0.1645	1.5565
chr17	81195210	15085908	0.1858	1.3694
chr18	78077248	12129628	0.1554	2.0095
chr19	59128983	8205225	0.1388	1.3509
chr20	63025520	23799994	0.3776	1.7585
chr21	48129895	7696986	0.1599	1.2769
chr22	51304566	6076656	0.1184	0.9283
chrMT	16571	1459199	88.0574	63.6643
chrX	155270560	24126895	0.1554	1.1223

chrY	59373566	1194283	0.0201	0.8492
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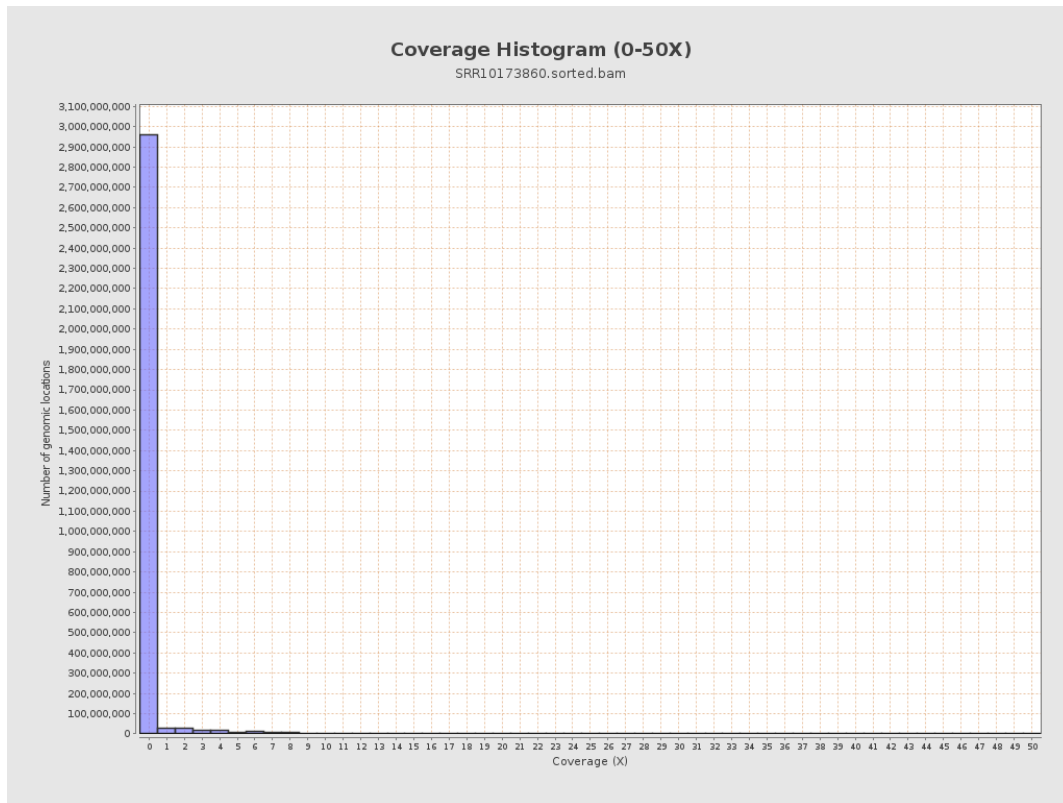
3. Results : Coverage across reference



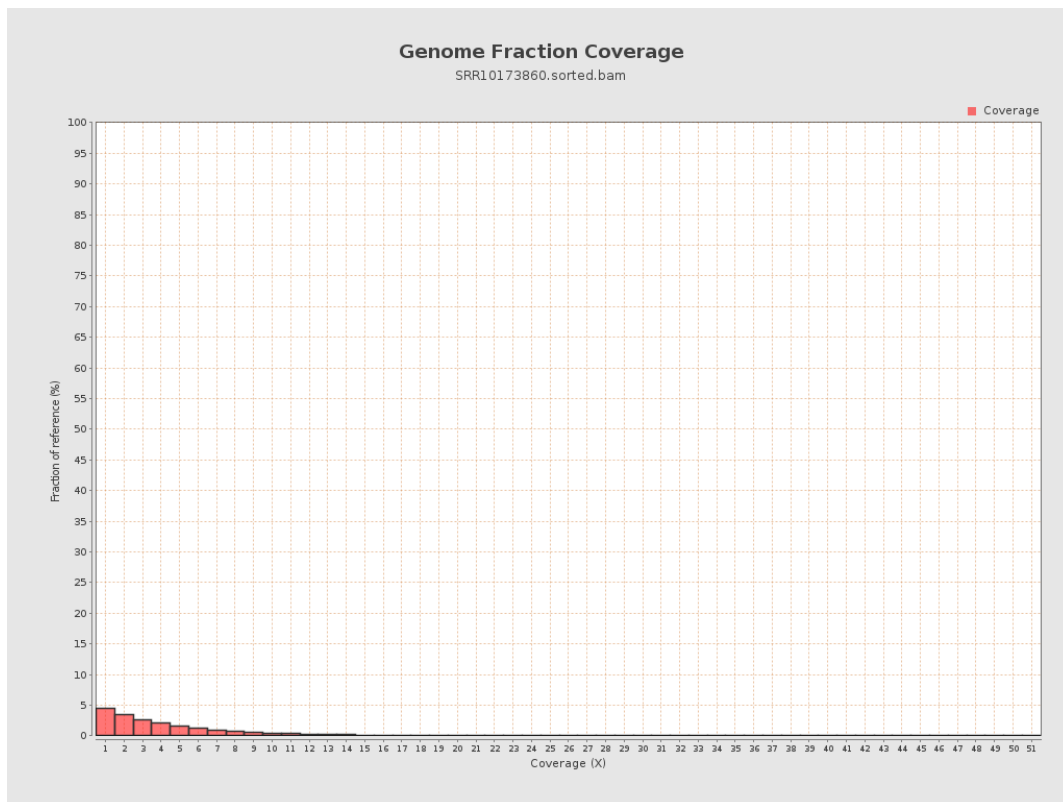
4. Results : Coverage Histogram



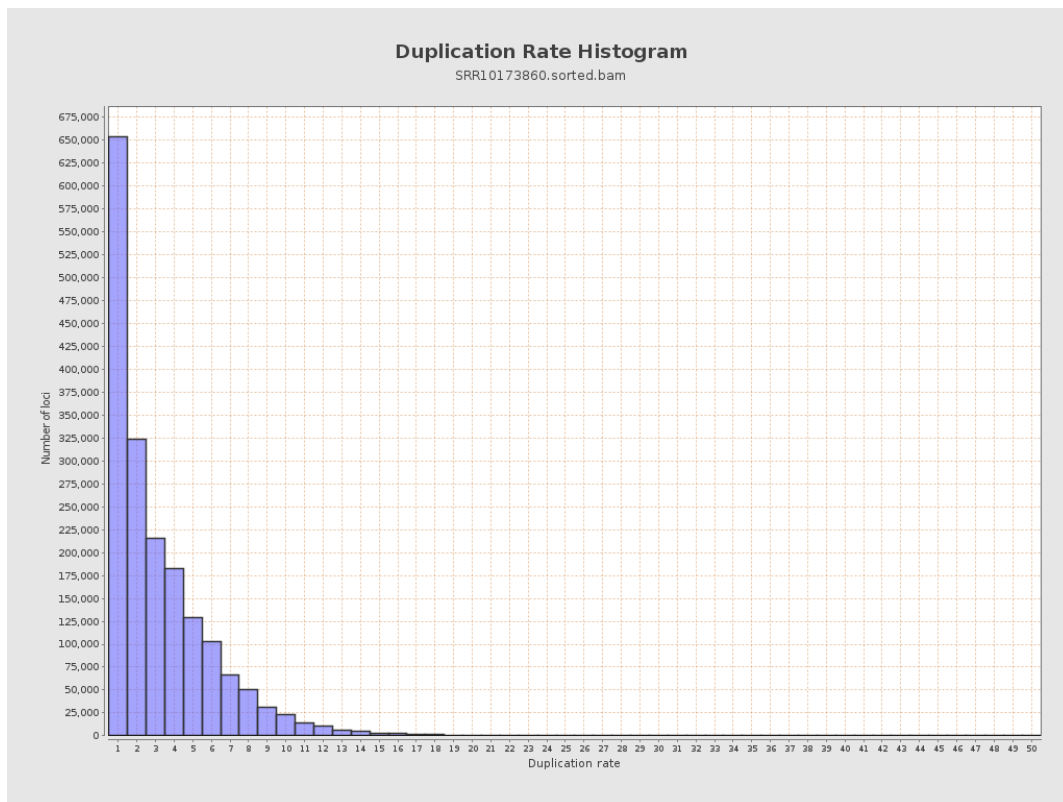
5. Results : Coverage Histogram (0-50X)



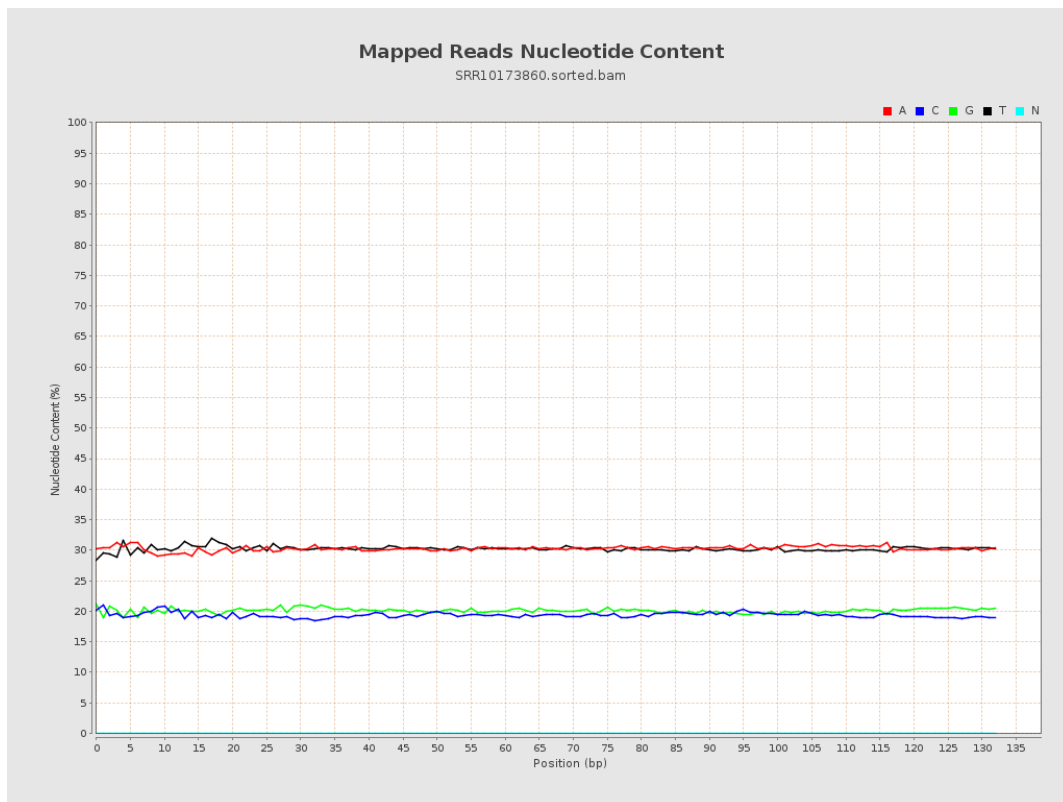
6. Results : Genome Fraction Coverage



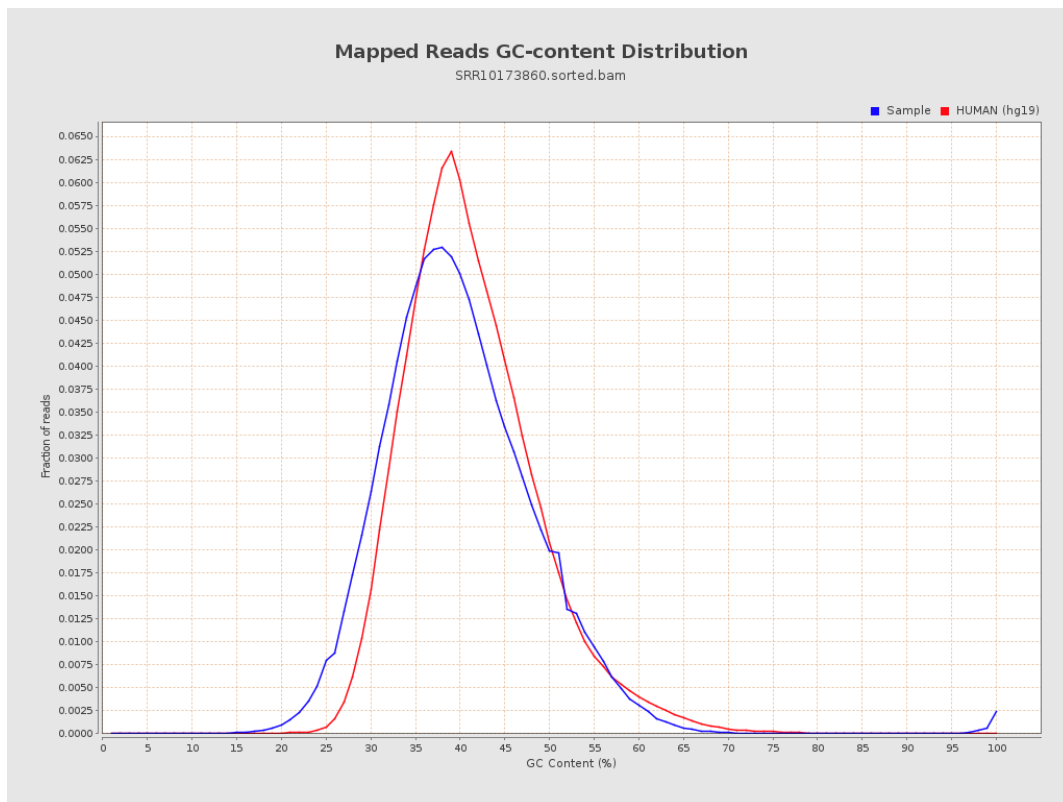
7. Results : Duplication Rate Histogram



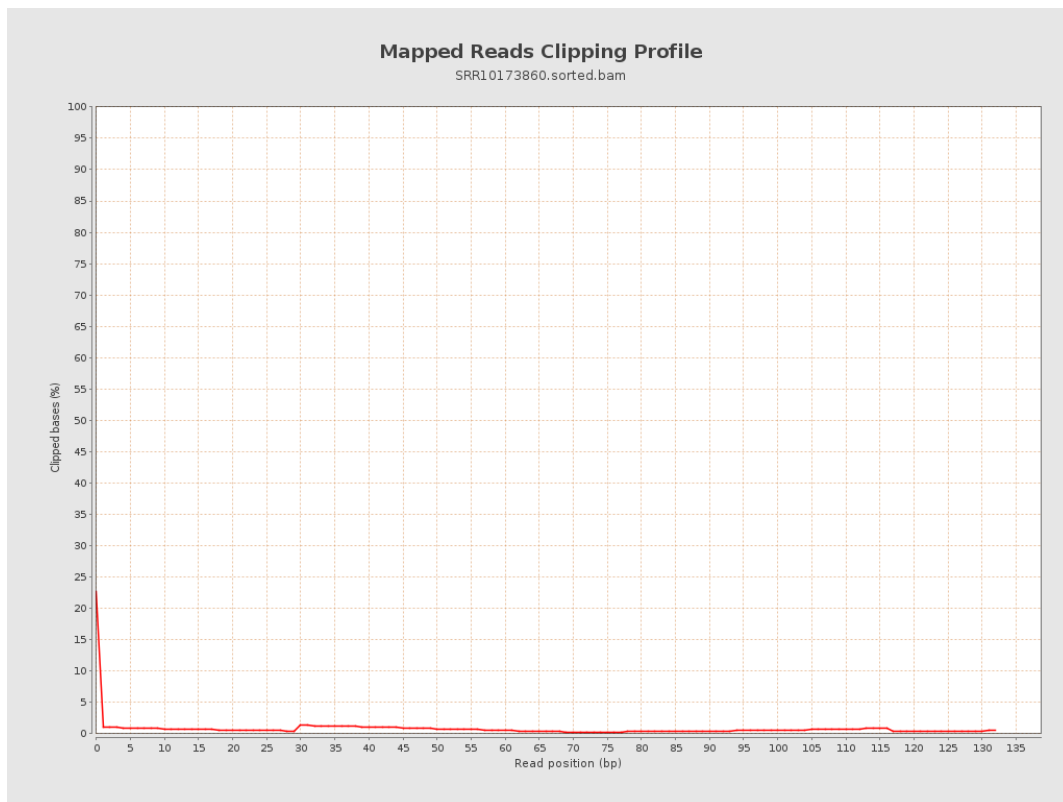
8. Results : Mapped Reads Nucleotide Content



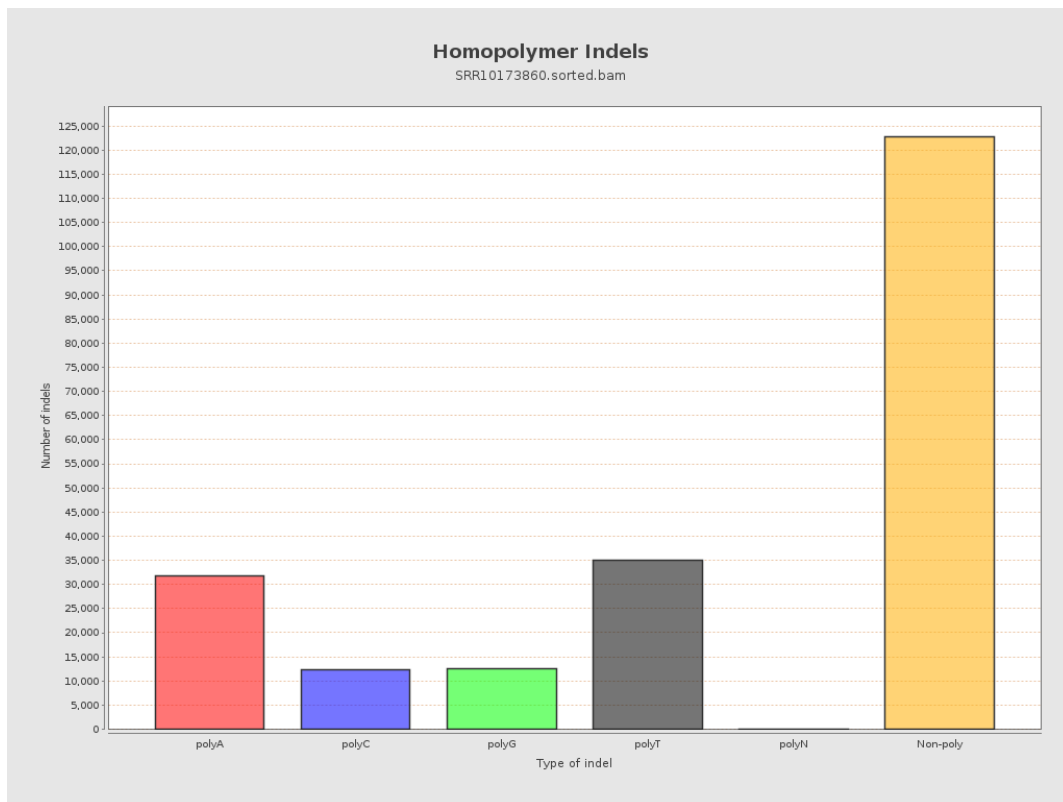
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



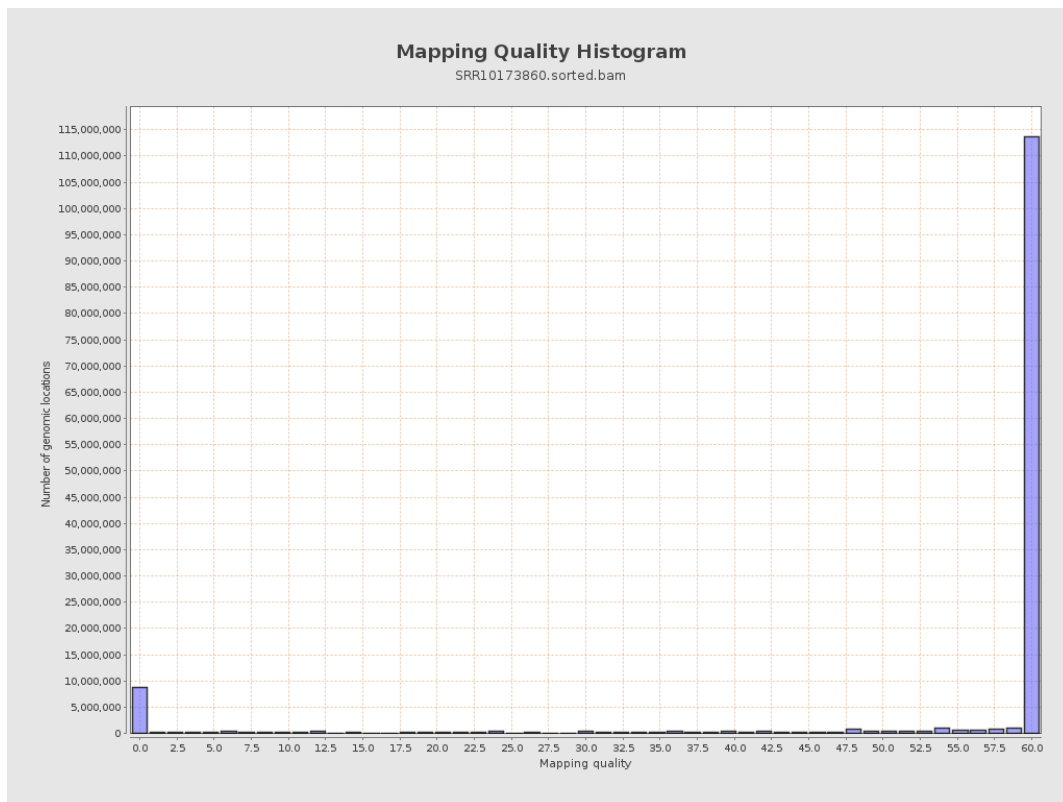
11. Results : Homopolymer Indels



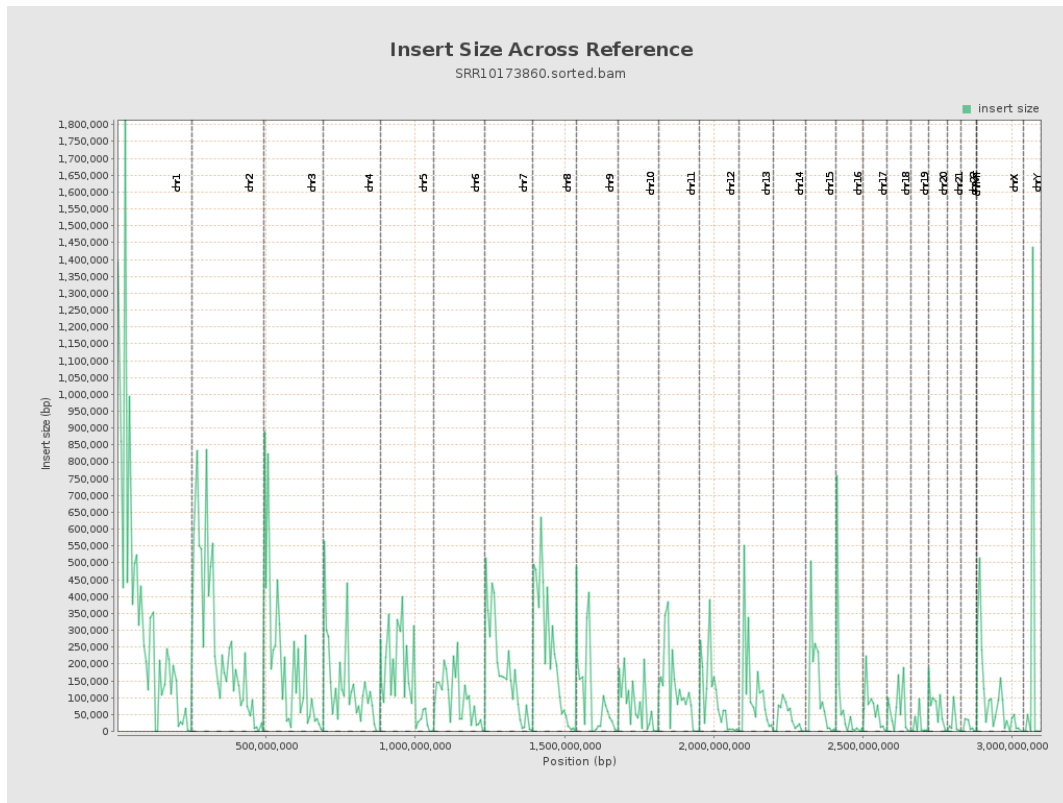
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

