

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:59:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173970.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_SRR10173970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173970_1.fastq.gz SRR10173970_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:59:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,854,794
Mapped reads	6,706,813 / 97.84%
Unmapped reads	147,981 / 2.16%
Mapped paired reads	6,706,813 / 97.84%
Mapped reads, first in pair	3,353,302 / 48.92%
Mapped reads, second in pair	3,353,511 / 48.92%
Mapped reads, both in pair	6,611,050 / 96.44%
Mapped reads, singletons	95,763 / 1.4%
Secondary alignments	0
Supplementary alignments	921,922 / 13.45%
Read min/max/mean length	30 / 133 / 125.93
Duplicated reads (estimated)	5,296,983 / 77.27%
Duplication rate	64.43%
Clipped reads	3,568,295 / 52.06%

2.2. ACGT Content

Number/percentage of A's	226,728,508 / 29.79%
Number/percentage of C's	151,541,384 / 19.91%
Number/percentage of T's	225,095,712 / 29.58%
Number/percentage of G's	157,683,973 / 20.72%
Number/percentage of N's	5,531 / 0%

GC Percentage	40.63%
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2.3. Coverage

Mean	0.246
Standard Deviation	4.0939

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	1,202,373.26
Standard Deviation	9,776,572.89
P25/Median/P75	106 / 157 / 244

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	6,514,294
Insertions	84,456
Mapped reads with at least one insertion	1.21%
Deletions	228,065
Mapped reads with at least one deletion	3.32%
Homopolymer indels	40.68%

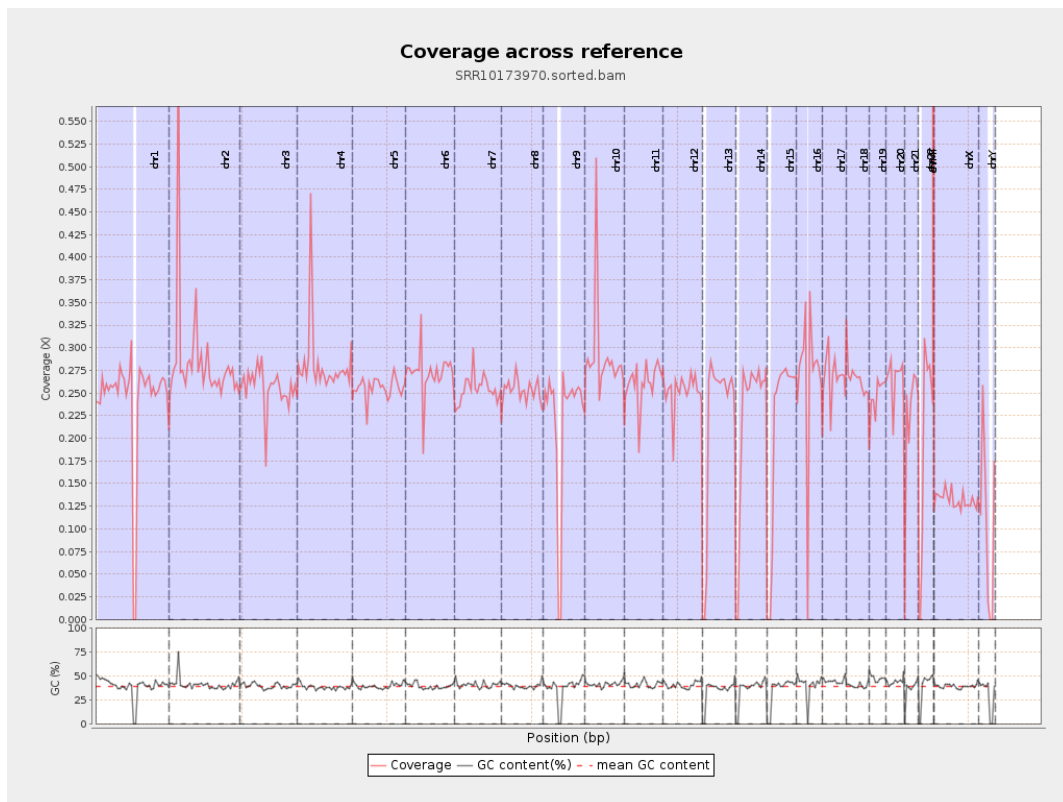
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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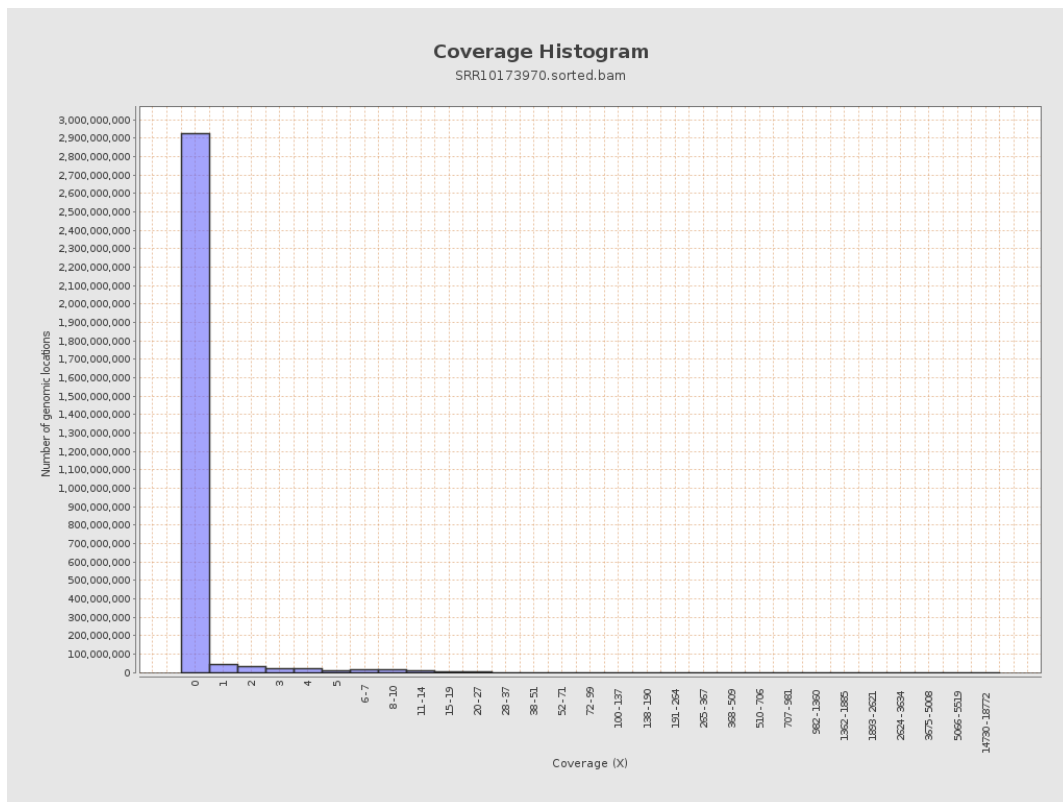
		bases	coverage	deviation
chr1	249250621	60708241	0.2436	2.2932
chr2	243199373	69800252	0.287	13.1161
chr3	198022430	50701970	0.256	1.4779
chr4	191154276	53687709	0.2809	2.1475
chr5	180915260	46328627	0.2561	1.4737
chr6	171115067	46498209	0.2717	1.8279
chr7	159138663	40506362	0.2545	2.0121
chr8	146364022	37071995	0.2533	2.4822
chr9	141213431	31078668	0.2201	1.8952
chr10	135534747	39313879	0.2901	2.6325
chr11	135006516	35234763	0.261	1.5361
chr12	133851895	33755468	0.2522	1.5046
chr13	115169878	25256726	0.2193	1.3636
chr14	107349540	23762915	0.2214	1.3758
chr15	102531392	21876890	0.2134	1.3754
chr16	90354753	24161614	0.2674	1.9219
chr17	81195210	21736661	0.2677	1.7041
chr18	78077248	20719292	0.2654	2.7459
chr19	59128983	14630695	0.2474	1.8048
chr20	63025520	16769138	0.2661	1.5847
chr21	48129895	10683473	0.222	1.8436
chr22	51304566	9872168	0.1924	1.5667
chrMT	16571	876300	52.8815	47.7442
chrX	155270560	20492671	0.132	1.0762

chrY	59373566	6071490	0.1023	1.6621
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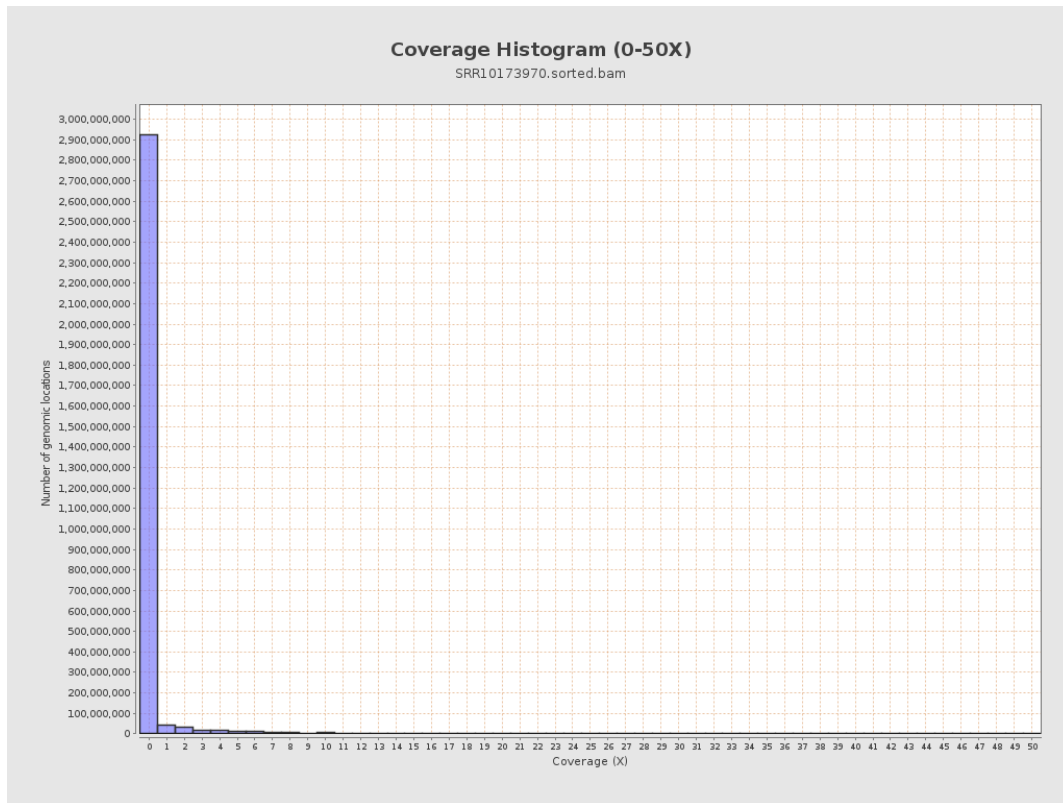
3. Results : Coverage across reference



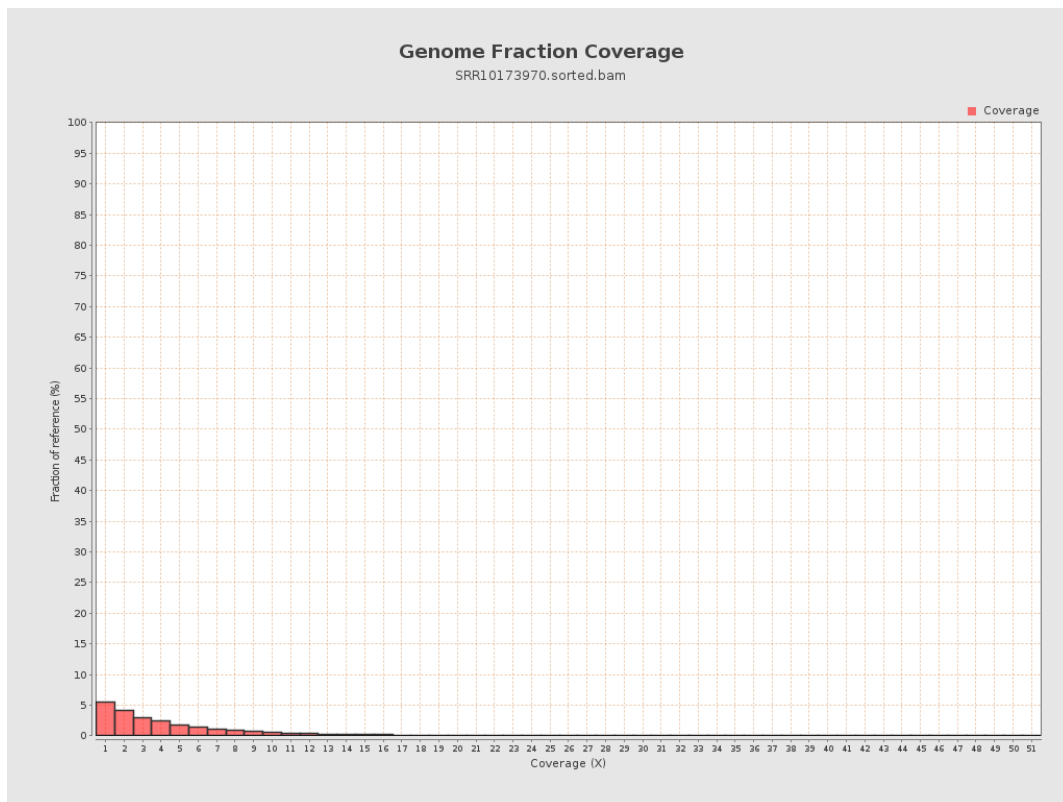
4. Results : Coverage Histogram



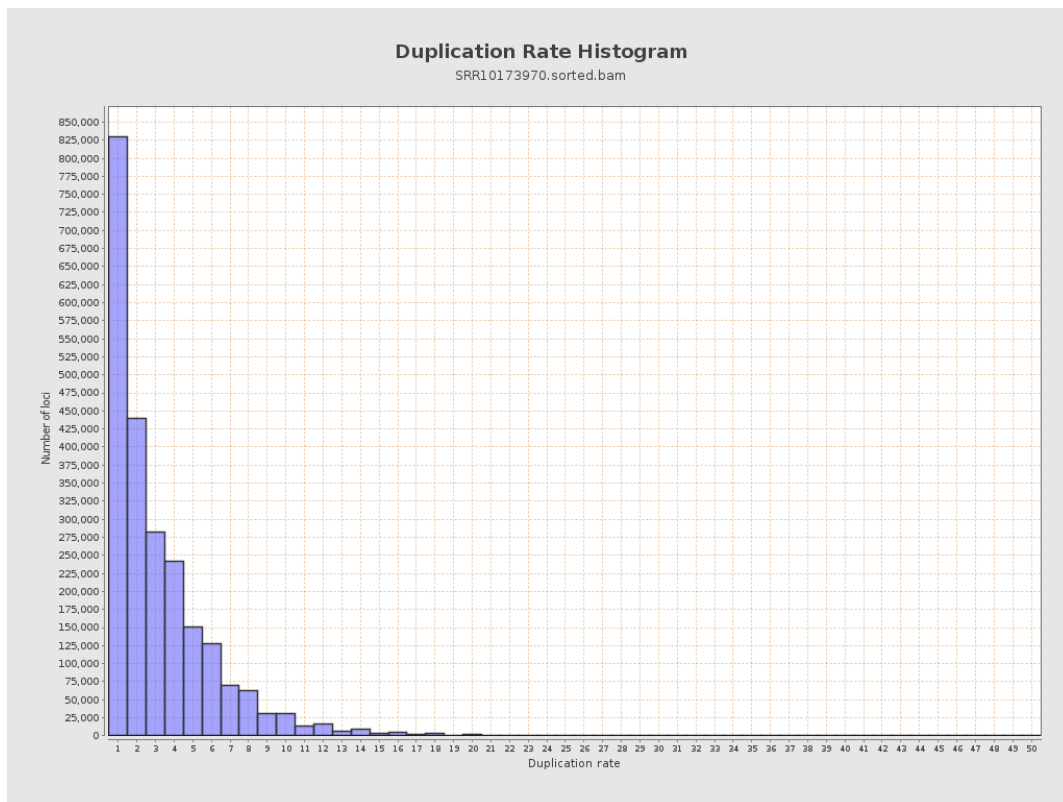
5. Results : Coverage Histogram (0-50X)



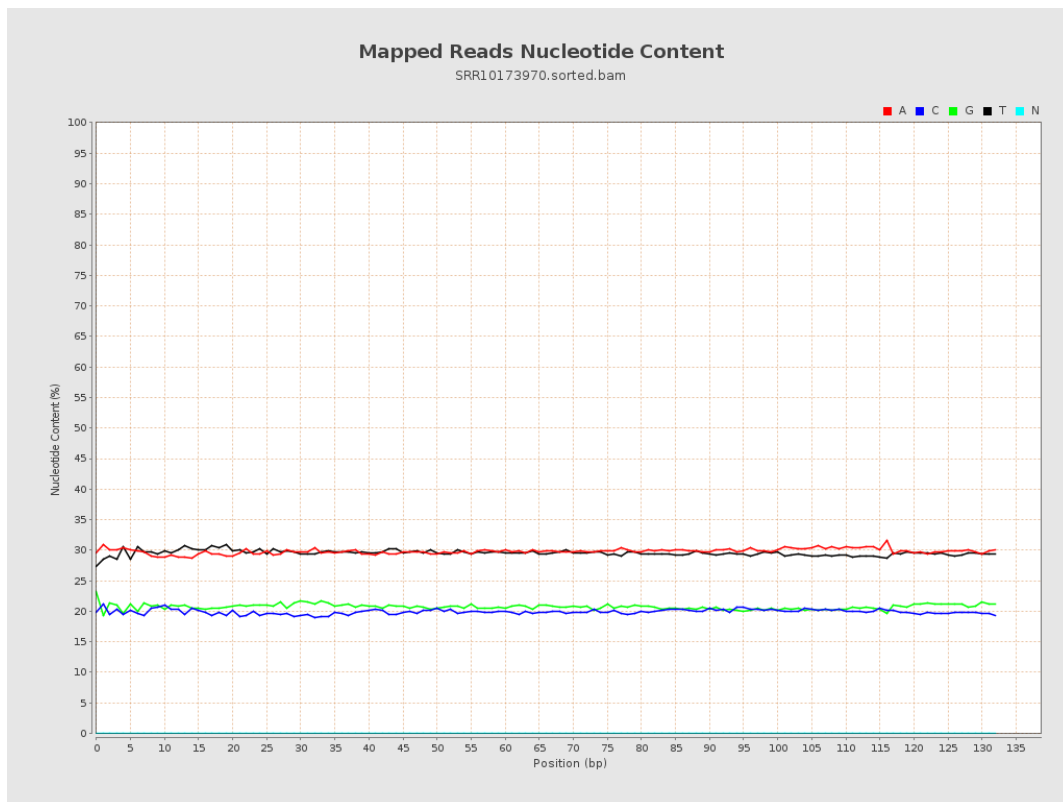
6. Results : Genome Fraction Coverage



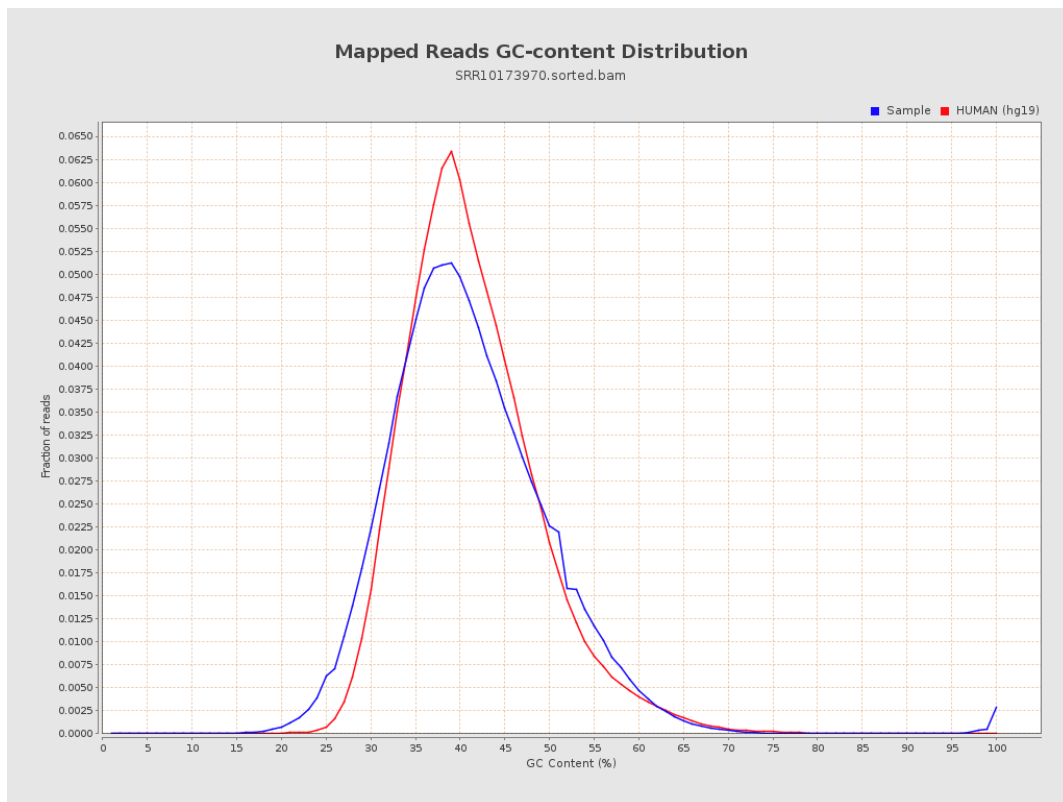
7. Results : Duplication Rate Histogram



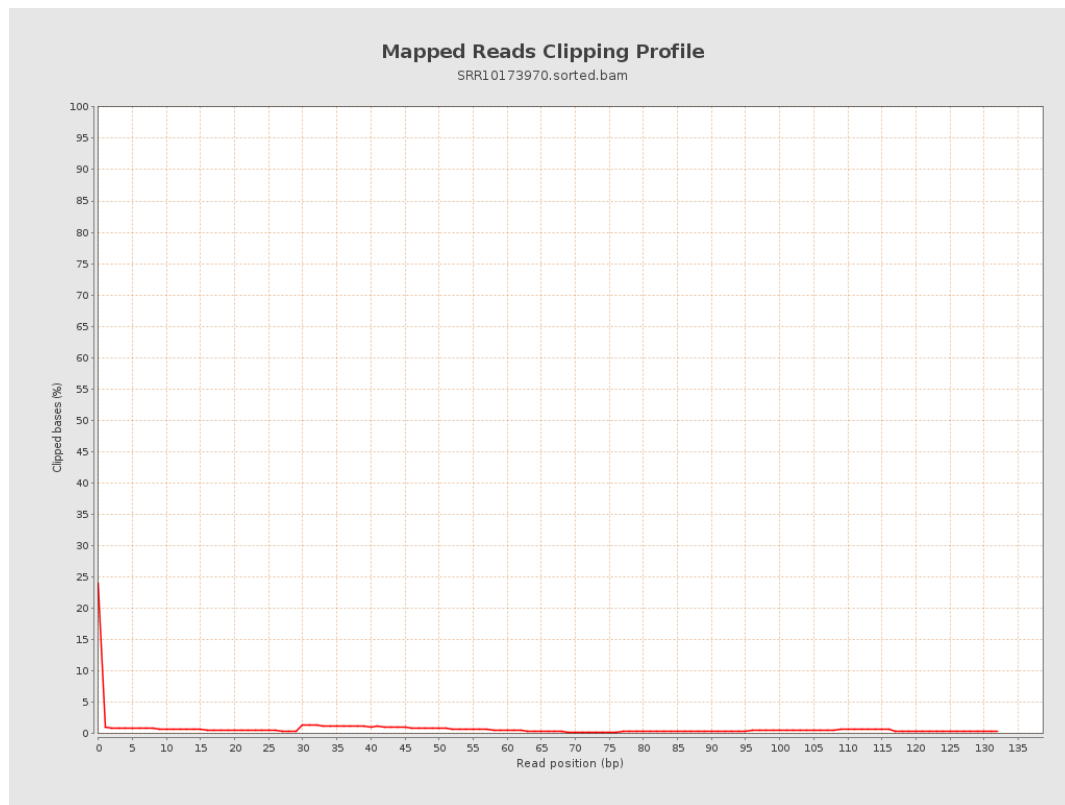
8. Results : Mapped Reads Nucleotide Content



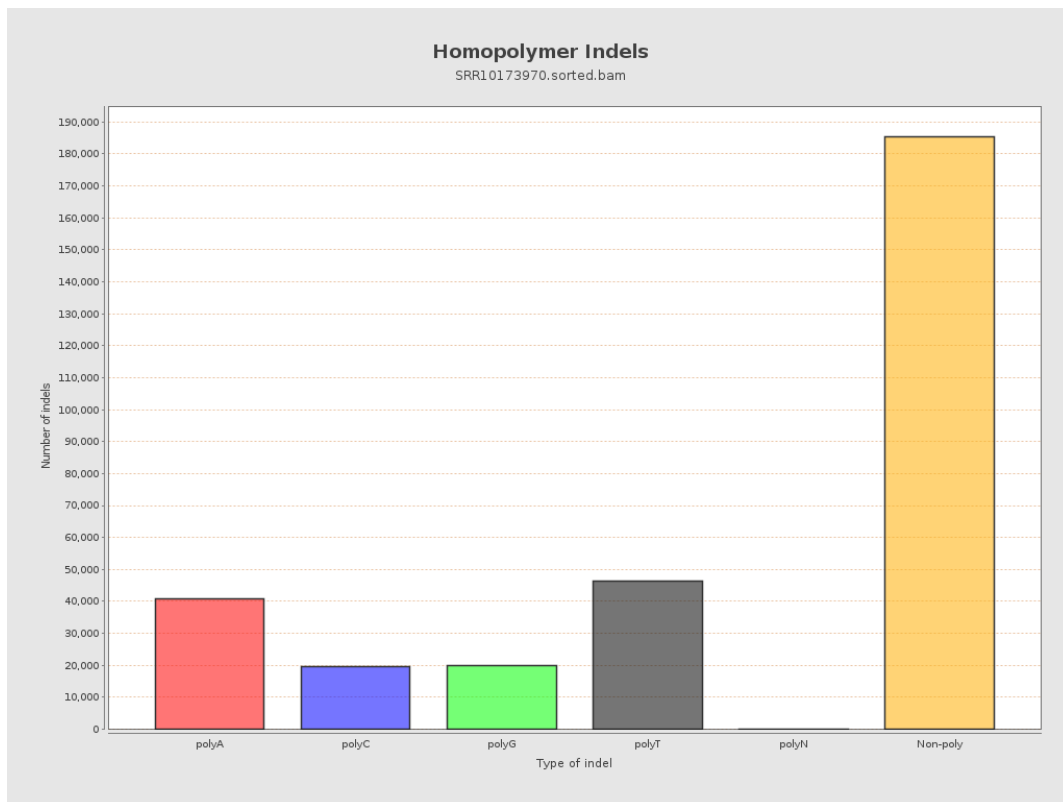
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



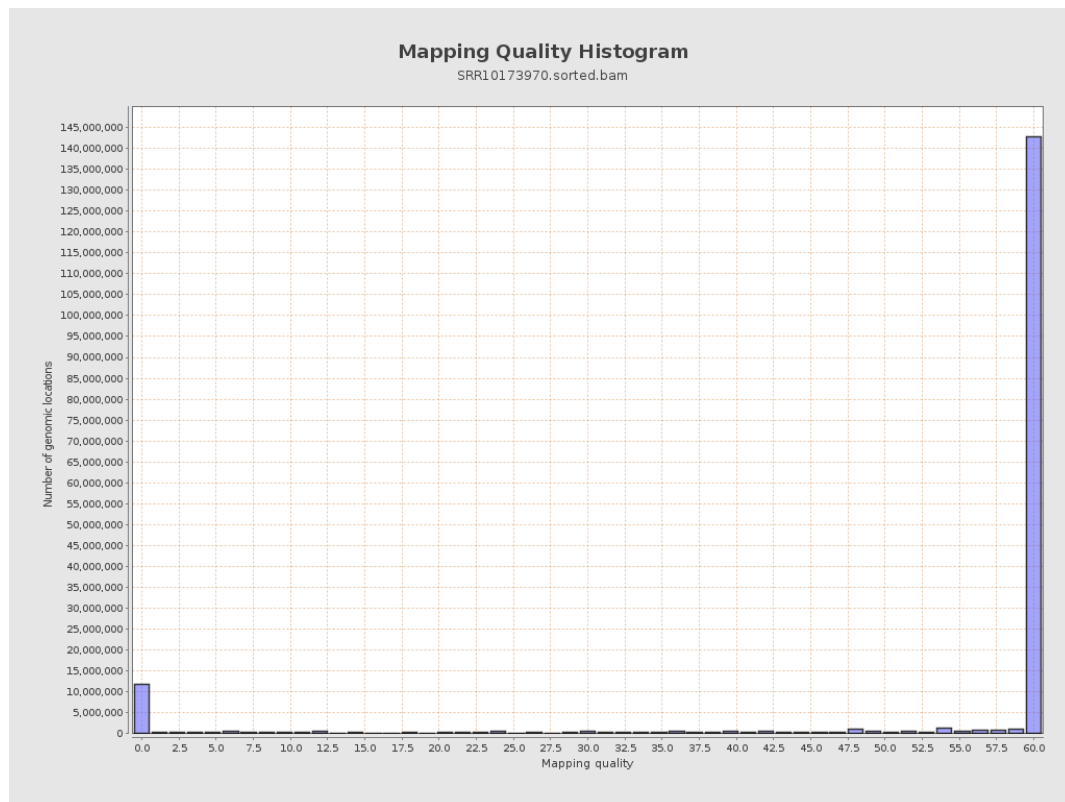
11. Results : Homopolymer Indels



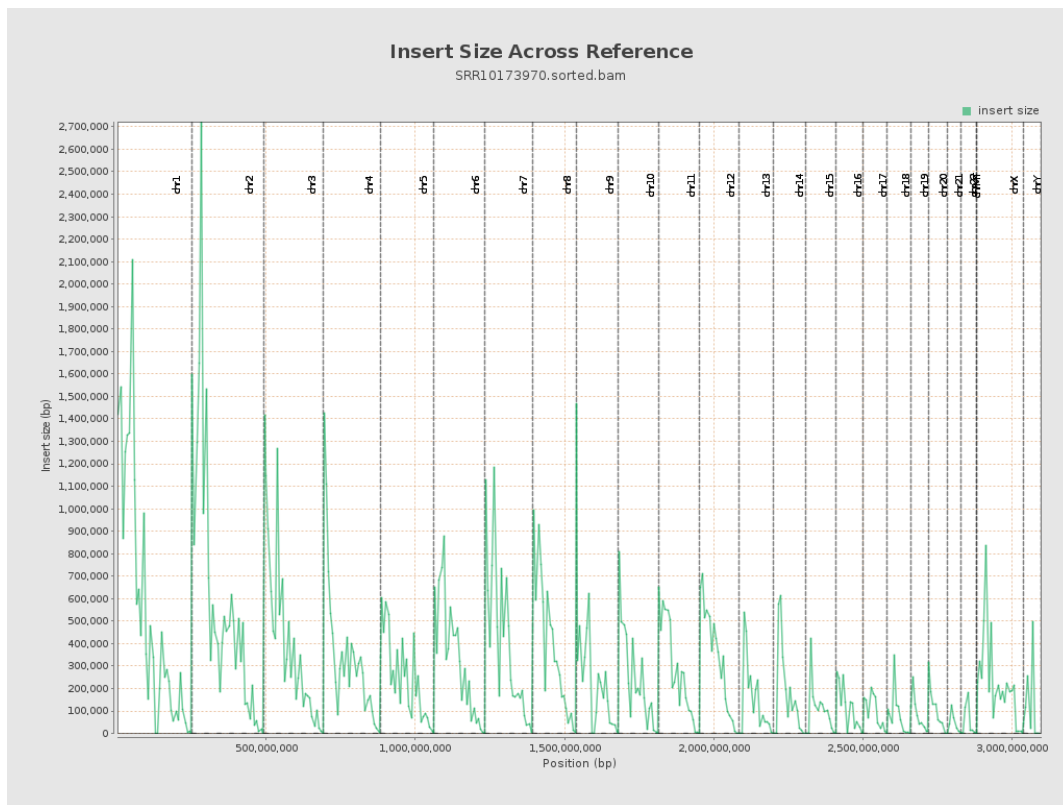
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

