

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:39:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173958.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_SRR10173958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173958_1.fastq.gz SRR10173958_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:39:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,666,182
Mapped reads	2,622,536 / 98.36%
Unmapped reads	43,646 / 1.64%
Mapped paired reads	2,622,536 / 98.36%
Mapped reads, first in pair	1,310,961 / 49.17%
Mapped reads, second in pair	1,311,575 / 49.19%
Mapped reads, both in pair	2,596,346 / 97.38%
Mapped reads, singletons	26,190 / 0.98%
Secondary alignments	0
Supplementary alignments	322,186 / 12.08%
Read min/max/mean length	30 / 133 / 123.9
Duplicated reads (estimated)	2,027,670 / 76.05%
Duplication rate	62.94%
Clipped reads	1,233,417 / 46.26%

2.2. ACGT Content

Number/percentage of A's	89,320,683 / 30.12%
Number/percentage of C's	58,371,203 / 19.68%
Number/percentage of T's	88,581,595 / 29.87%
Number/percentage of G's	60,301,183 / 20.33%
Number/percentage of N's	2,418 / 0%

GC Percentage	40.01%
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2.3. Coverage

Mean	0.0959
Standard Deviation	1.7656

2.4. Mapping Quality

Mean Mapping Quality	52.89
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2.5. Insert size

Mean	845,343.17
Standard Deviation	8,456,140.39
P25/Median/P75	102 / 145 / 214

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	2,338,155
Insertions	31,417
Mapped reads with at least one insertion	1.16%
Deletions	91,647
Mapped reads with at least one deletion	3.41%
Homopolymer indels	40.86%

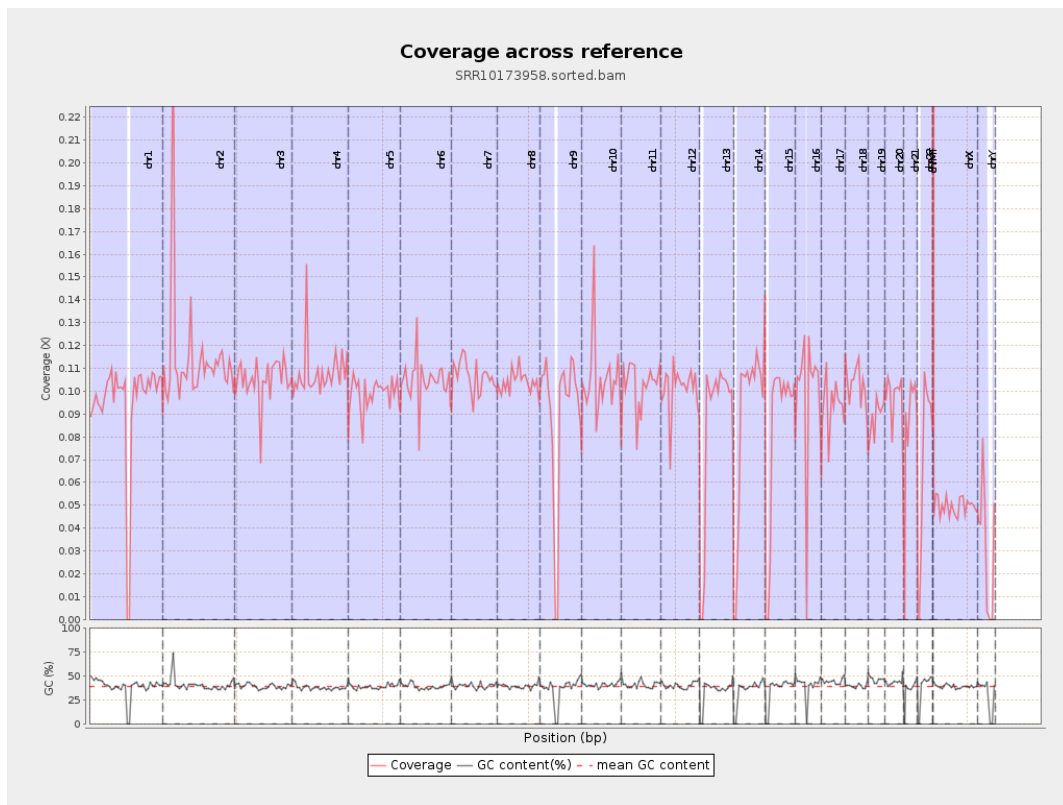
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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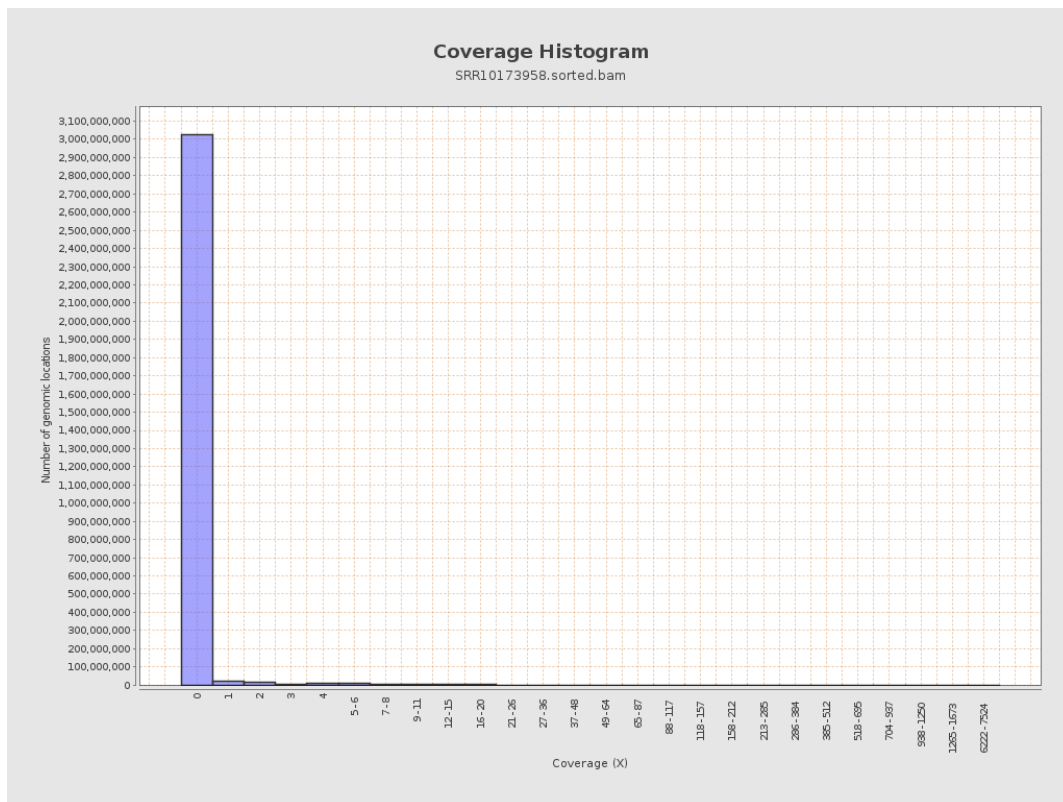
		bases	coverage	deviation
chr1	249250621	23596854	0.0947	0.9901
chr2	243199373	27705154	0.1139	5.3276
chr3	198022430	20839361	0.1052	0.9605
chr4	191154276	20665100	0.1081	1.0711
chr5	180915260	17874890	0.0988	0.9227
chr6	171115067	17943999	0.1049	1.0321
chr7	159138663	16882965	0.1061	1.0857
chr8	146364022	15226301	0.104	1.1877
chr9	141213431	12779090	0.0905	0.9894
chr10	135534747	14219820	0.1049	1.1833
chr11	135006516	13861060	0.1027	0.9681
chr12	133851895	13590793	0.1015	0.9492
chr13	115169878	9842390	0.0855	0.8639
chr14	107349540	9675402	0.0901	0.8984
chr15	102531392	8352337	0.0815	0.8216
chr16	90354753	8831883	0.0977	0.9973
chr17	81195210	7700426	0.0948	0.9385
chr18	78077248	8037408	0.1029	1.1394
chr19	59128983	5268862	0.0891	0.881
chr20	63025520	6164054	0.0978	0.9363
chr21	48129895	4098060	0.0851	0.9649
chr22	51304566	3531514	0.0688	0.8099
chrMT	16571	443393	26.7572	29.9408
chrX	155270560	7679295	0.0495	0.6424

chrY	59373566	1977831	0.0333	0.5788
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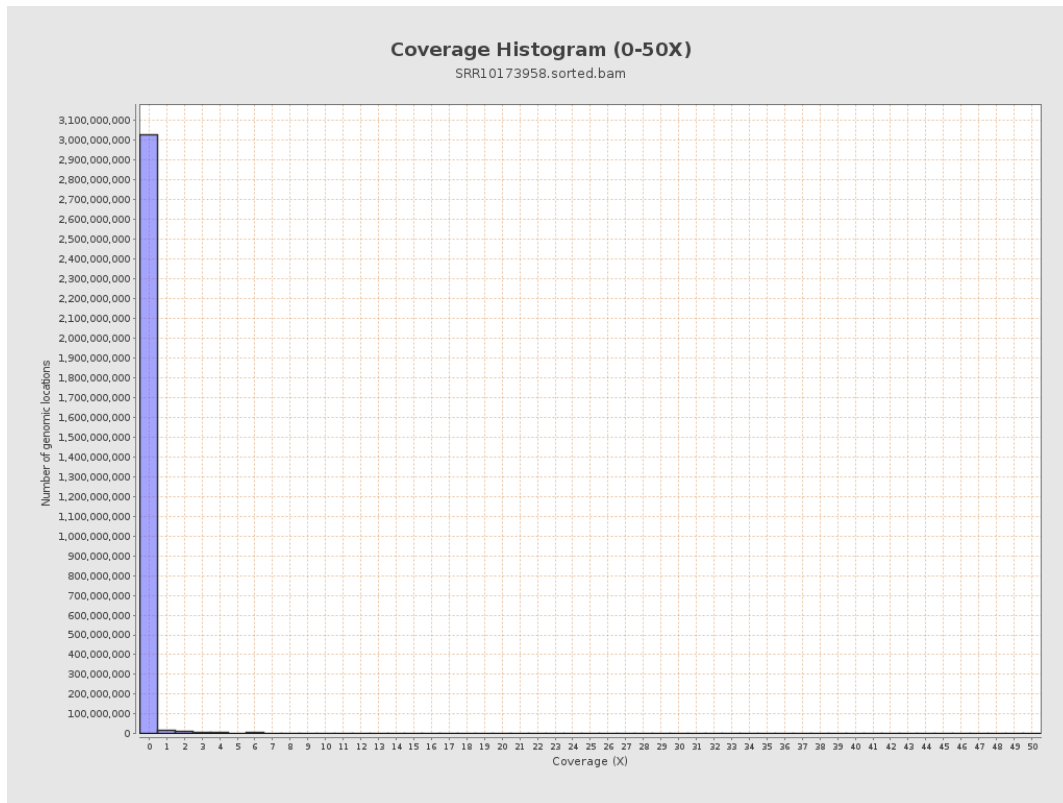
3. Results : Coverage across reference



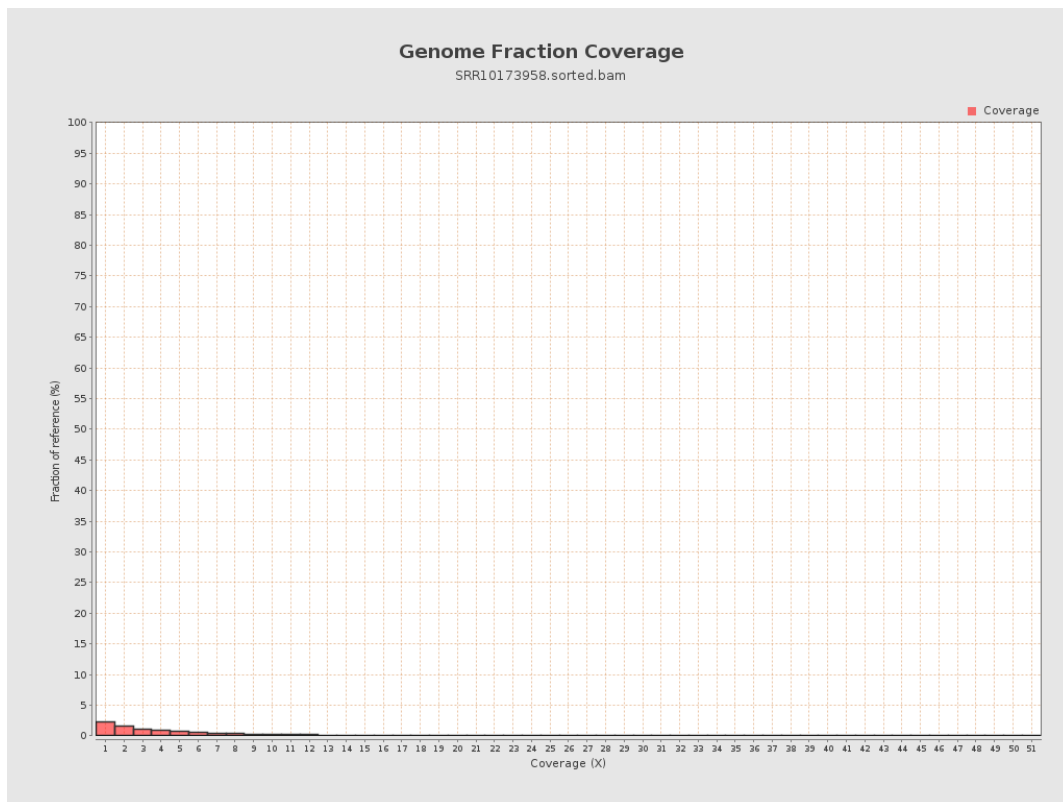
4. Results : Coverage Histogram



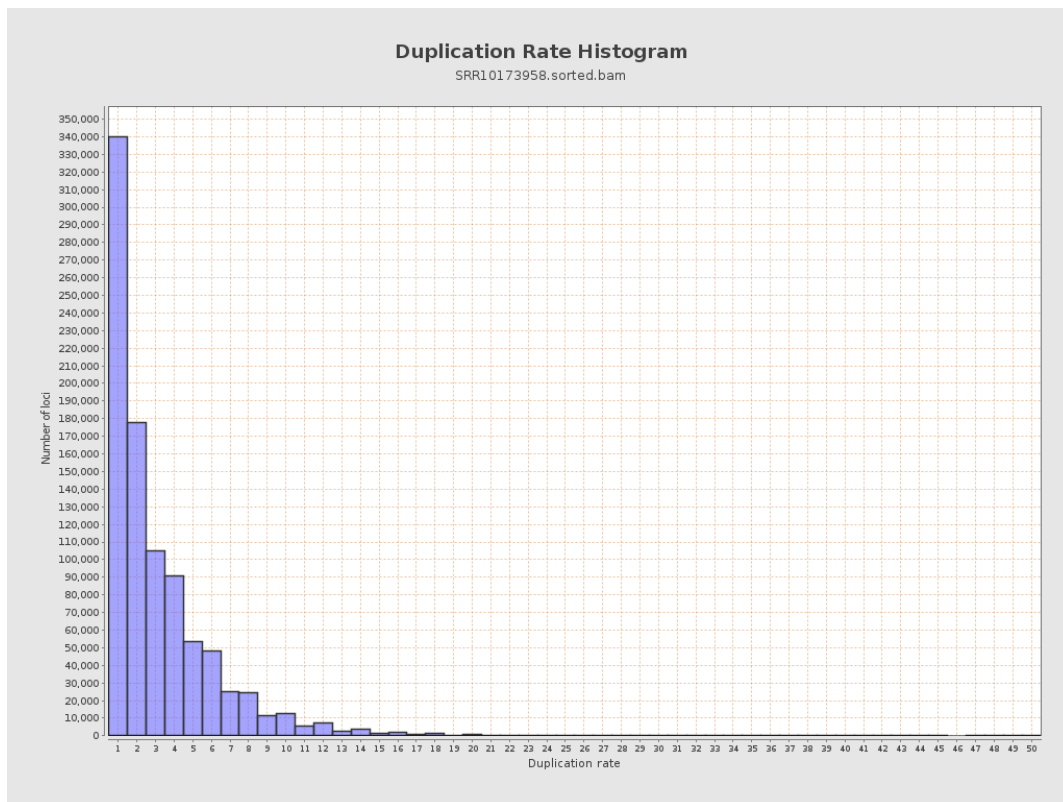
5. Results : Coverage Histogram (0-50X)



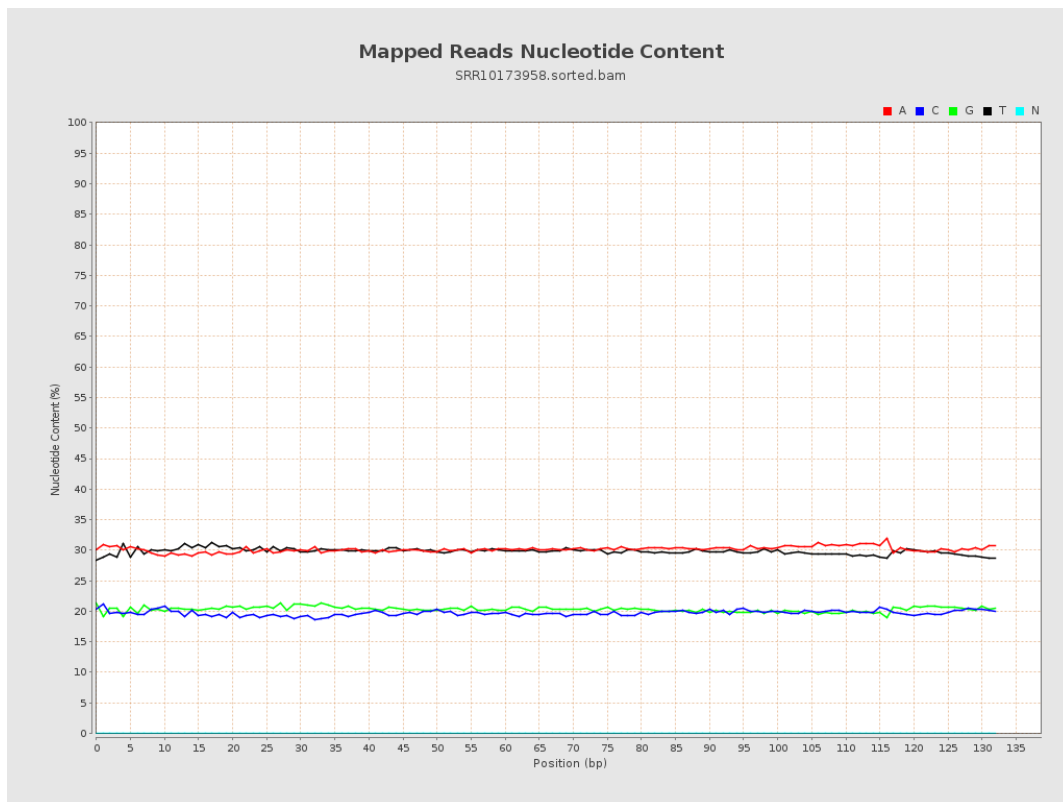
6. Results : Genome Fraction Coverage



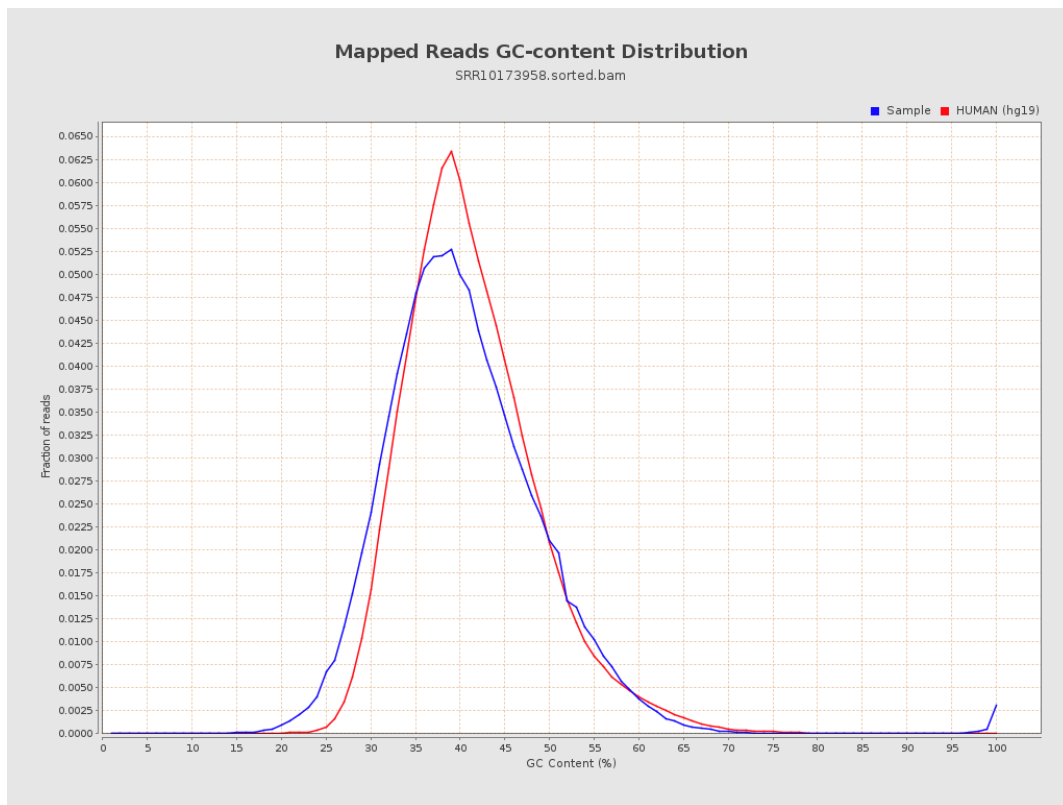
7. Results : Duplication Rate Histogram



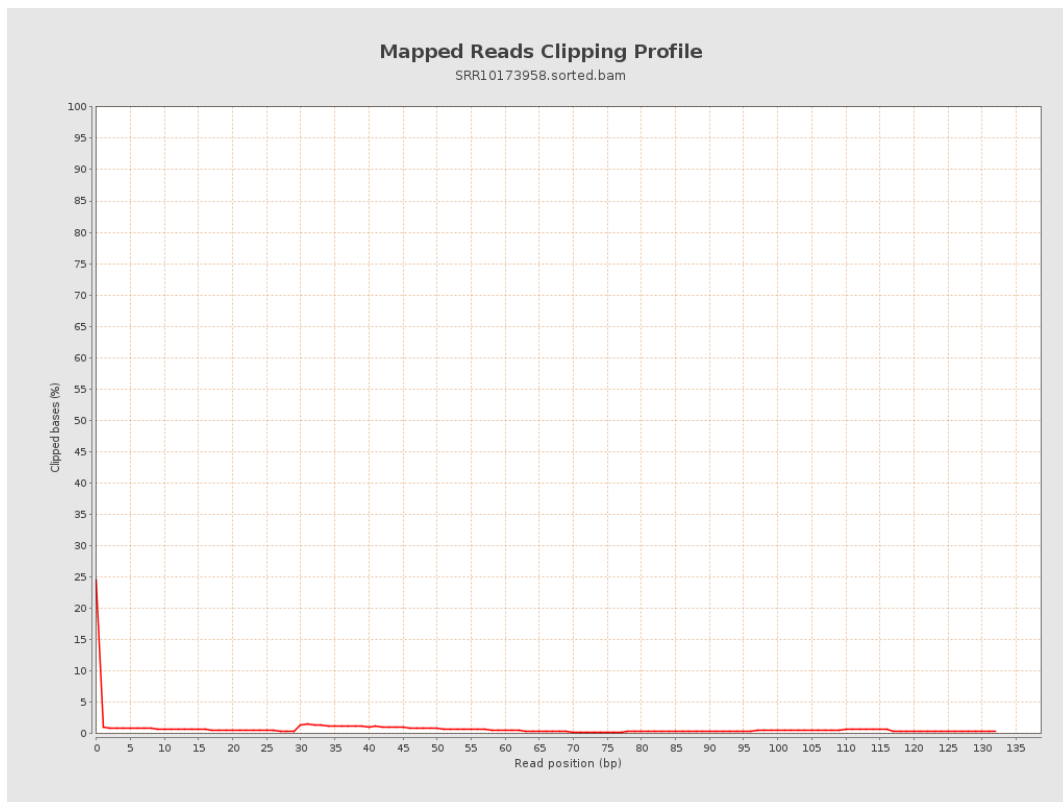
8. Results : Mapped Reads Nucleotide Content



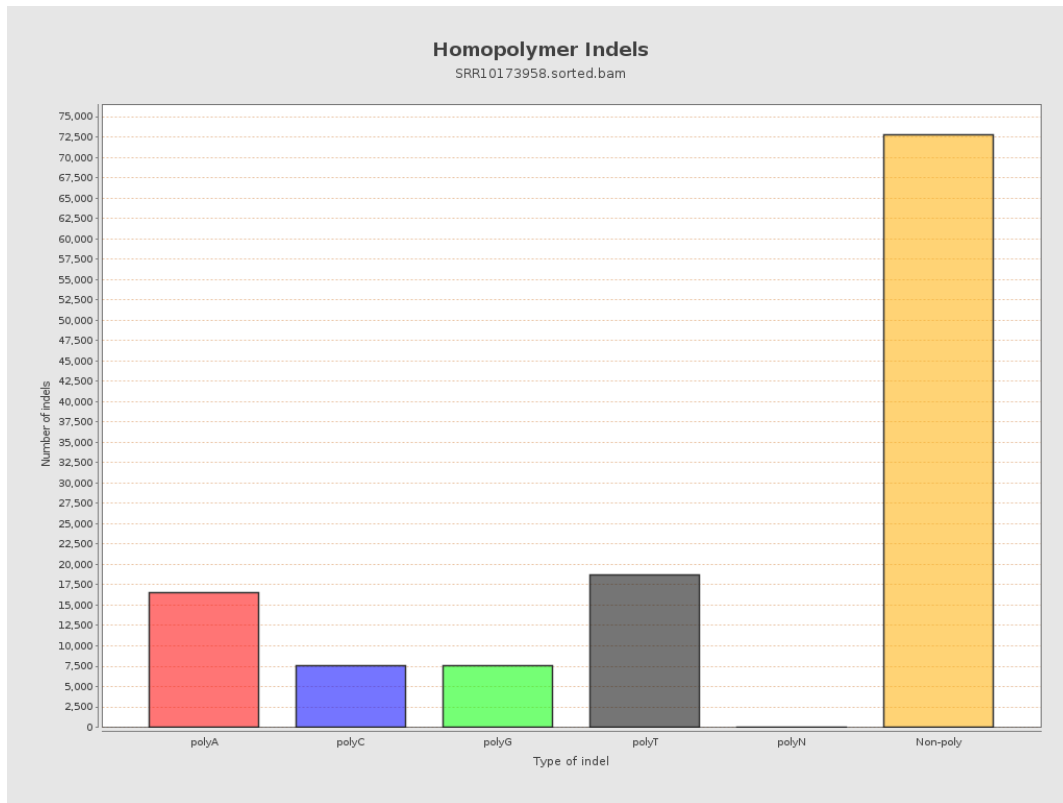
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



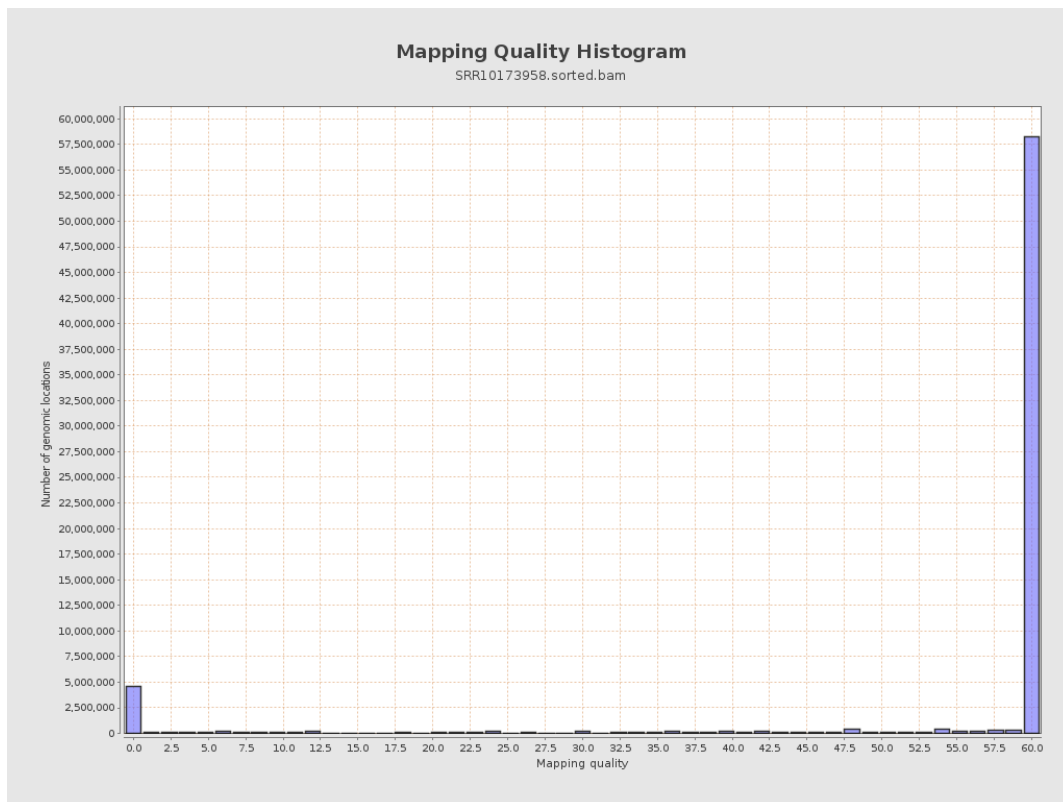
11. Results : Homopolymer Indels



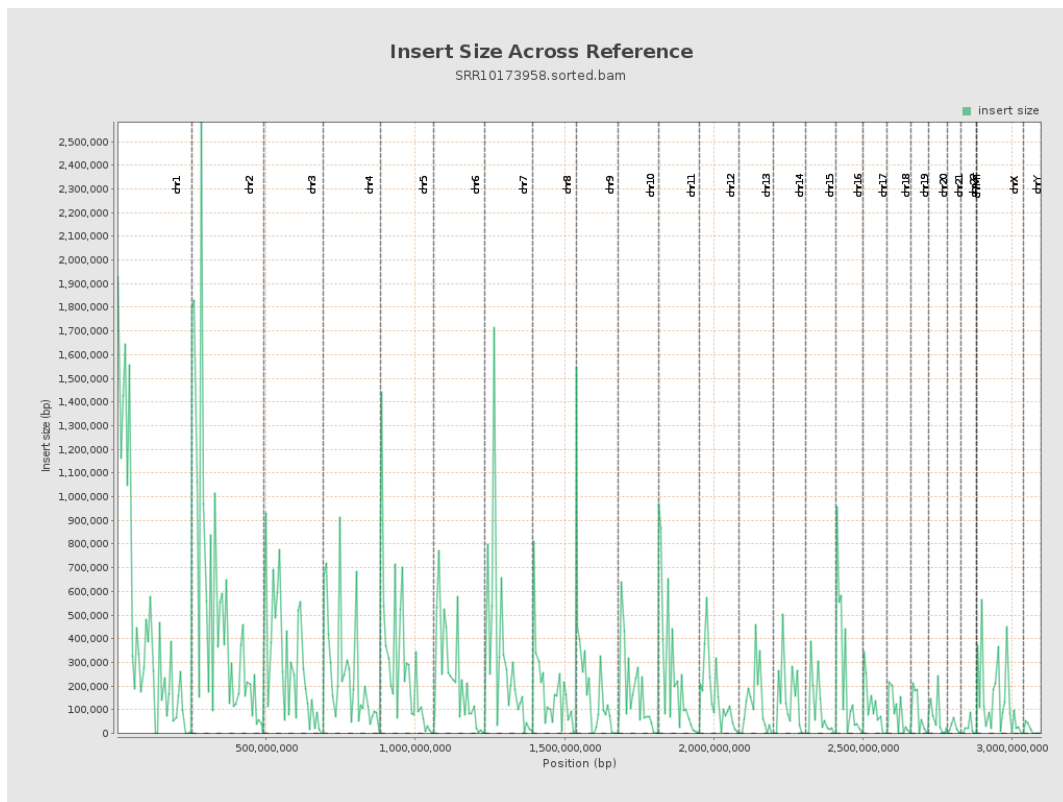
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

