

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:30:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173922.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_SRR10173922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173922_1.fastq.gz SRR10173922_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:30:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,928,340
Mapped reads	1,865,685 / 96.75%
Unmapped reads	62,655 / 3.25%
Mapped paired reads	1,865,685 / 96.75%
Mapped reads, first in pair	934,865 / 48.48%
Mapped reads, second in pair	930,820 / 48.27%
Mapped reads, both in pair	1,826,932 / 94.74%
Mapped reads, singletons	38,753 / 2.01%
Secondary alignments	0
Supplementary alignments	190,762 / 9.89%
Read min/max/mean length	30 / 133 / 128.39
Duplicated reads (estimated)	1,455,061 / 75.46%
Duplication rate	63.82%
Clipped reads	799,819 / 41.48%

2.2. ACGT Content

Number/percentage of A's	66,254,667 / 30.15%
Number/percentage of C's	42,900,268 / 19.52%
Number/percentage of T's	65,999,904 / 30.04%
Number/percentage of G's	44,582,904 / 20.29%
Number/percentage of N's	2,683 / 0%

GC Percentage	39.81%
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2.3. Coverage

Mean	0.071
Standard Deviation	1.2208

2.4. Mapping Quality

Mean Mapping Quality	52.81
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2.5. Insert size

Mean	1,230,829.65
Standard Deviation	10,529,691.61
P25/Median/P75	146 / 205 / 294

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	2,431,976
Insertions	26,974
Mapped reads with at least one insertion	1.38%
Deletions	49,976
Mapped reads with at least one deletion	2.6%
Homopolymer indels	42.57%

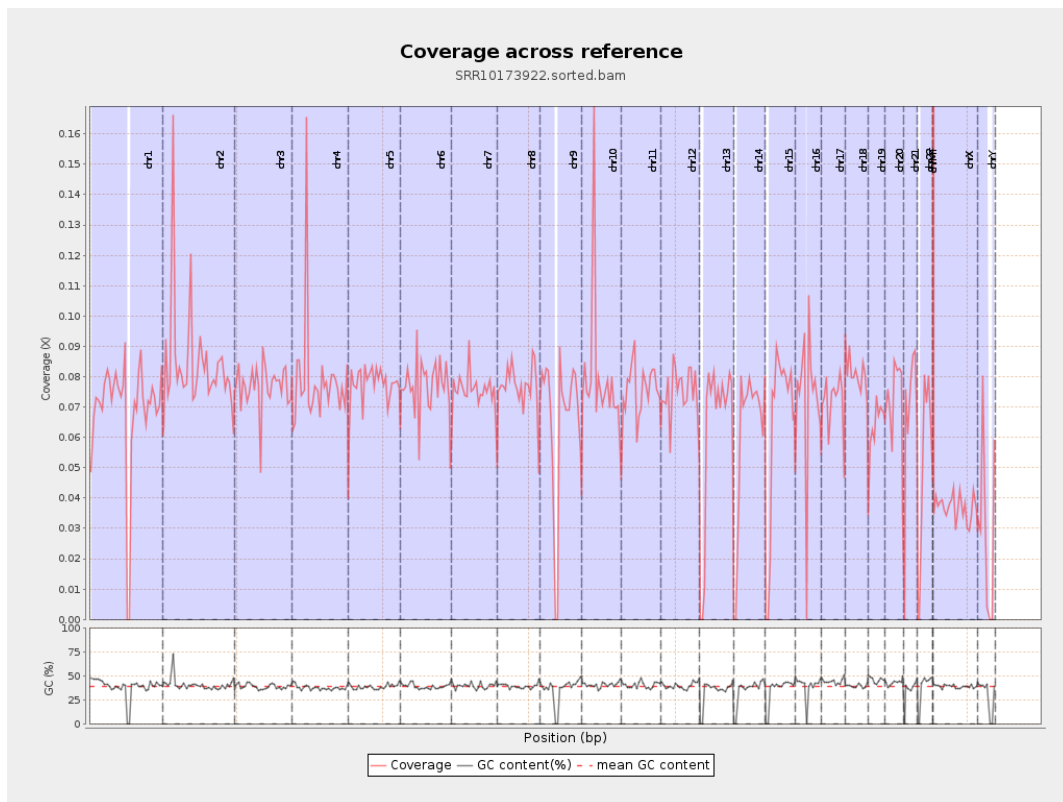
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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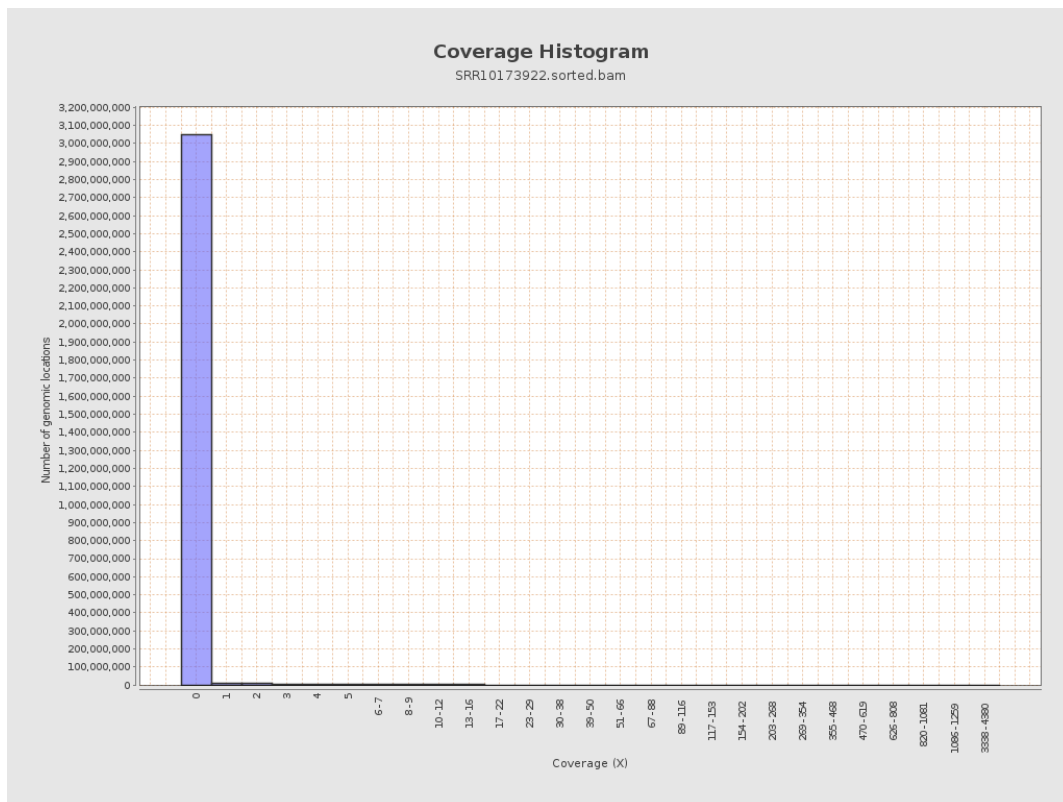
		bases	coverage	deviation
chr1	249250621	17223960	0.0691	0.9853
chr2	243199373	20481541	0.0842	3.1643
chr3	198022430	15204768	0.0768	0.8063
chr4	191154276	15078712	0.0789	1.0381
chr5	180915260	13991595	0.0773	0.8137
chr6	171115067	13132282	0.0767	0.8414
chr7	159138663	11972054	0.0752	0.9167
chr8	146364022	11216572	0.0766	1.0187
chr9	141213431	9324882	0.066	0.8962
chr10	135534747	10741439	0.0793	1.0955
chr11	135006516	10195069	0.0755	0.8093
chr12	133851895	10068765	0.0752	0.7968
chr13	115169878	7210236	0.0626	0.7314
chr14	107349540	6591212	0.0614	0.7135
chr15	102531392	6452032	0.0629	0.7175
chr16	90354753	6497317	0.0719	0.8482
chr17	81195210	5887922	0.0725	0.7948
chr18	78077248	6332214	0.0811	1.2211
chr19	59128983	3789558	0.0641	0.7806
chr20	63025520	4610122	0.0731	0.7902
chr21	48129895	3348205	0.0696	0.8935
chr22	51304566	2624063	0.0511	0.6537
chrMT	16571	394572	23.811	20.2131
chrX	155270560	5689809	0.0366	0.5436

chrY	59373566	1809090	0.0305	0.6619
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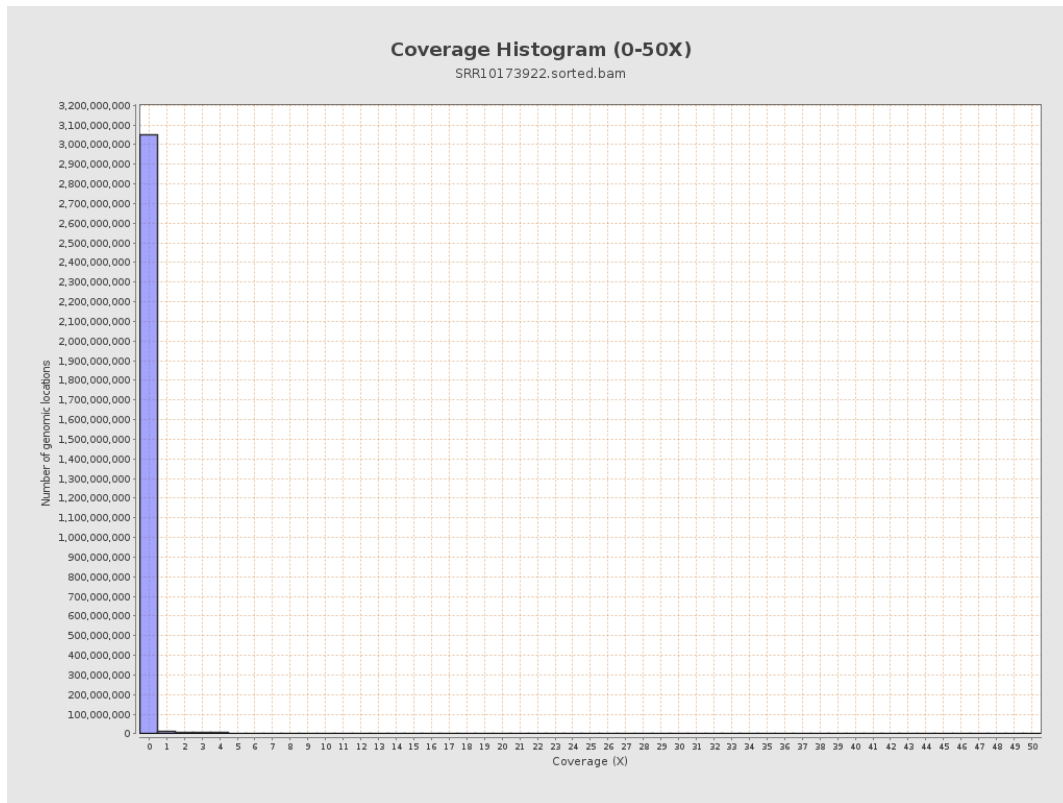
3. Results : Coverage across reference



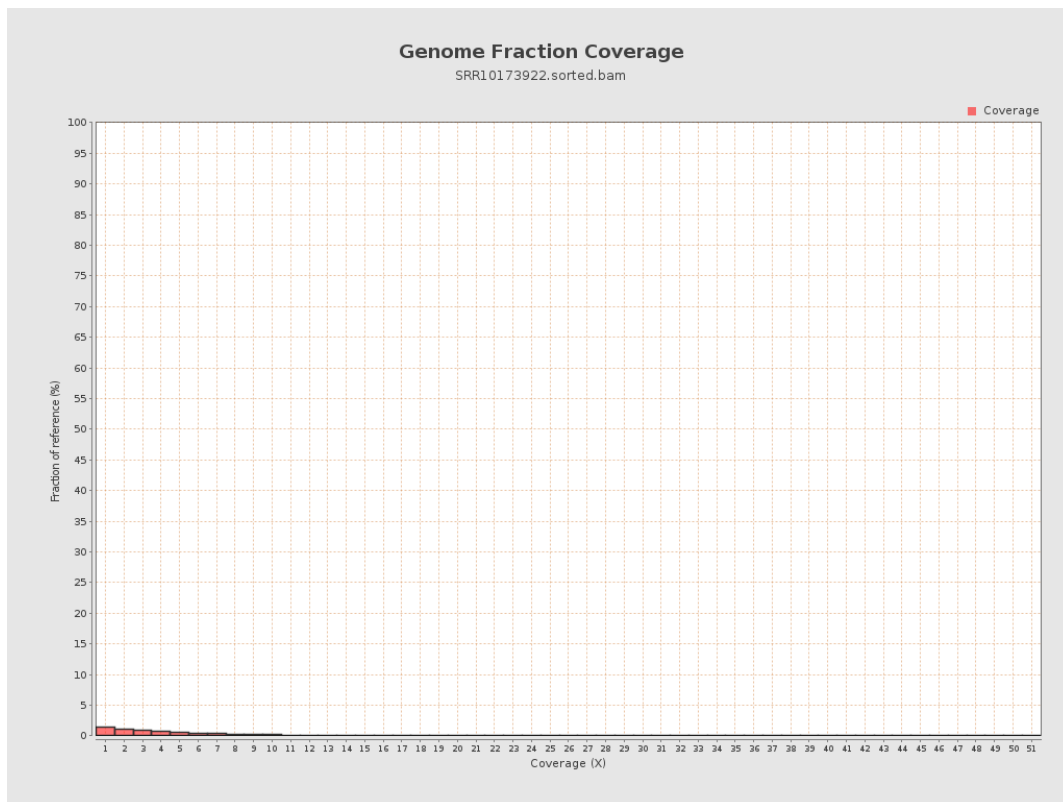
4. Results : Coverage Histogram



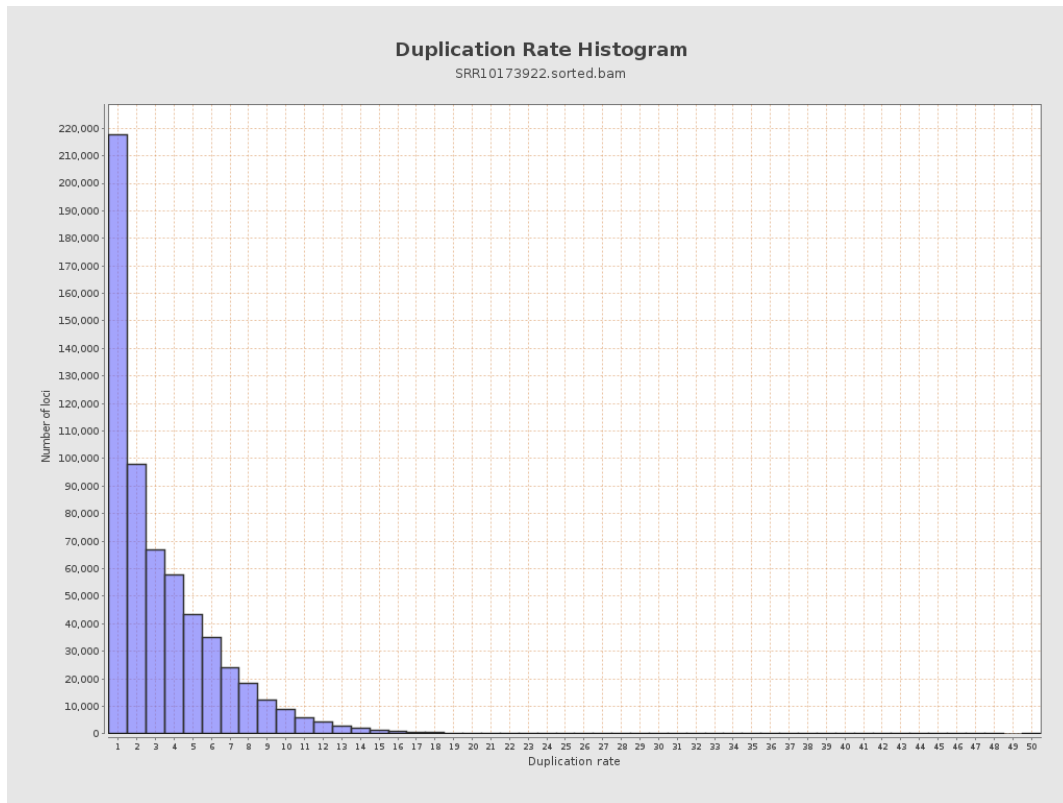
5. Results : Coverage Histogram (0-50X)



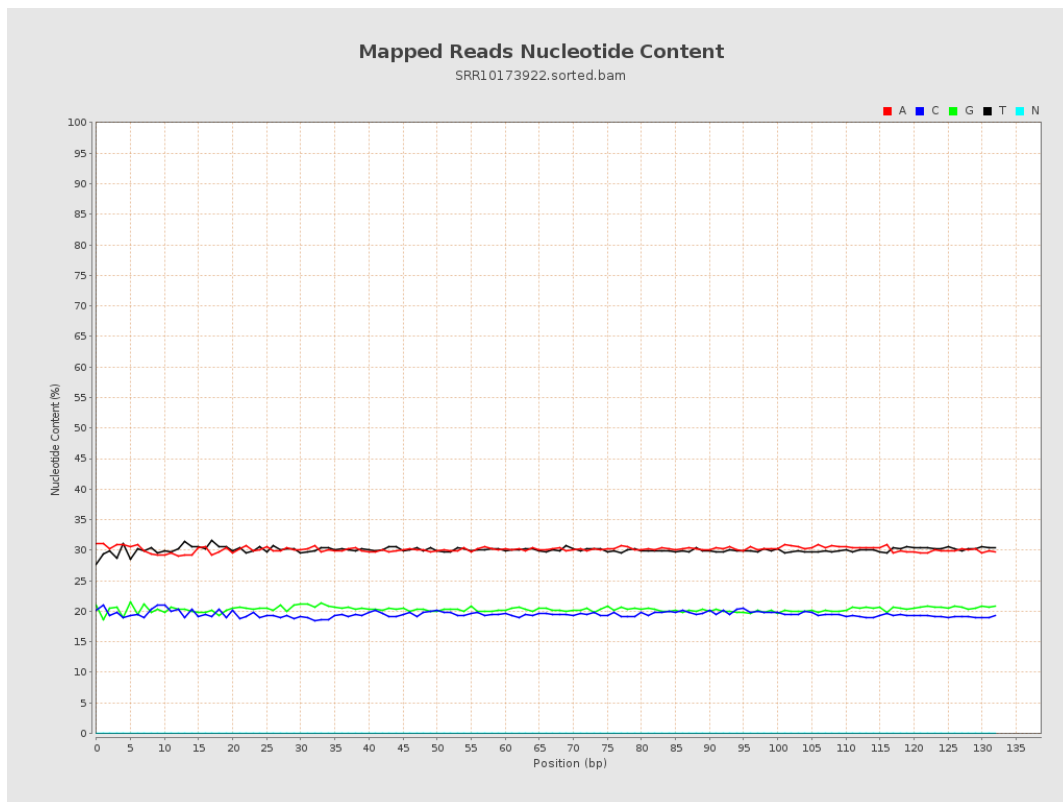
6. Results : Genome Fraction Coverage



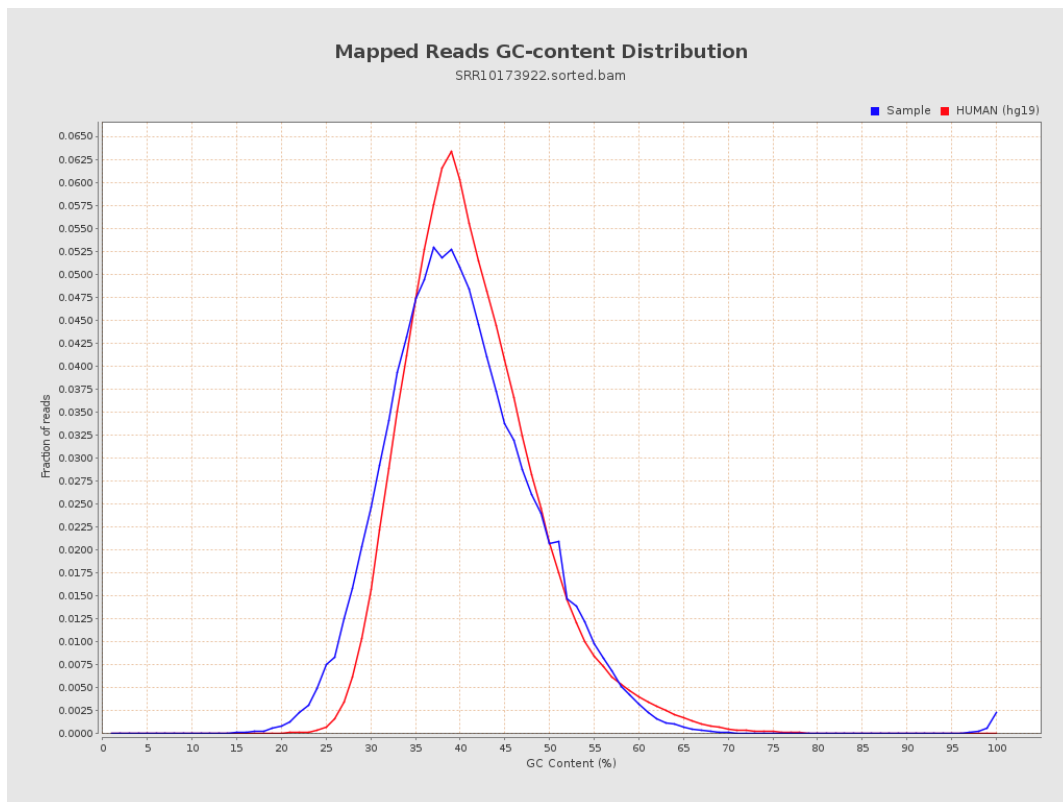
7. Results : Duplication Rate Histogram



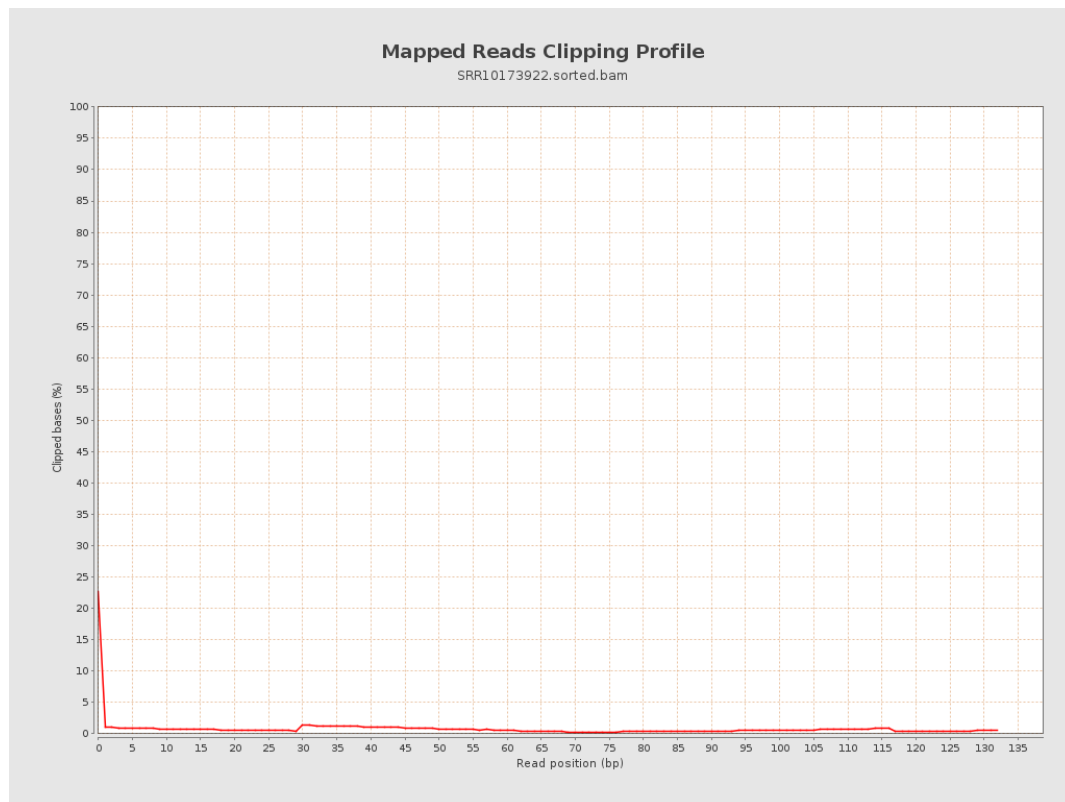
8. Results : Mapped Reads Nucleotide Content



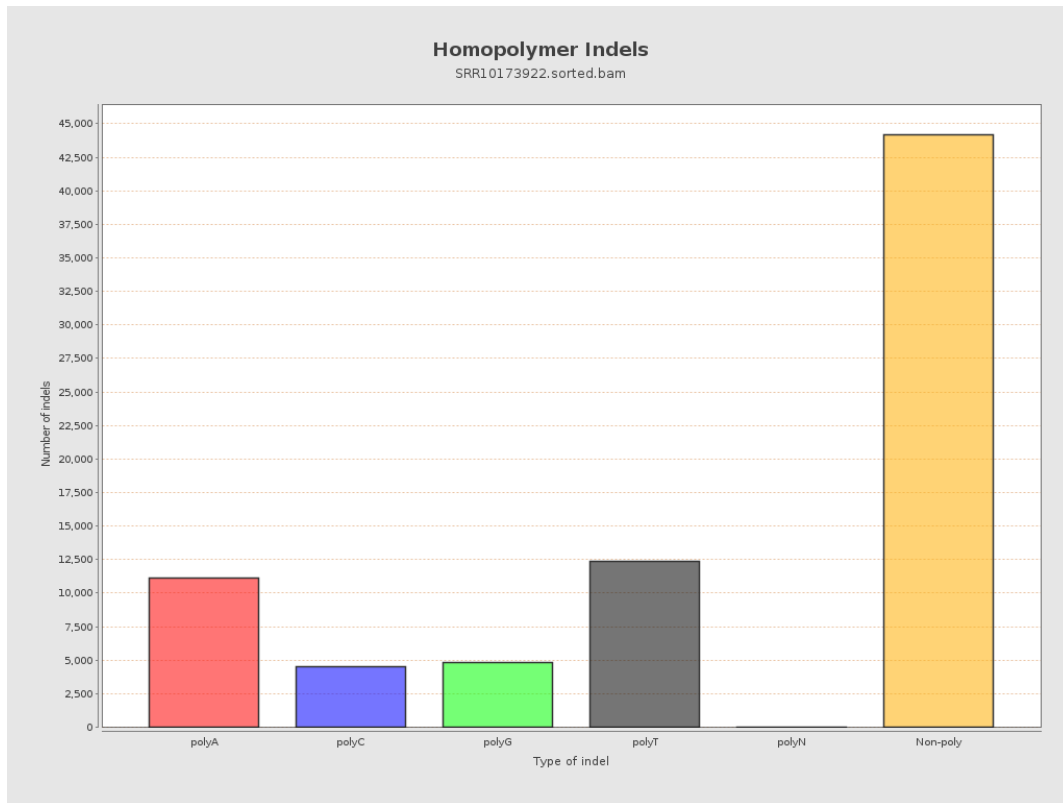
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



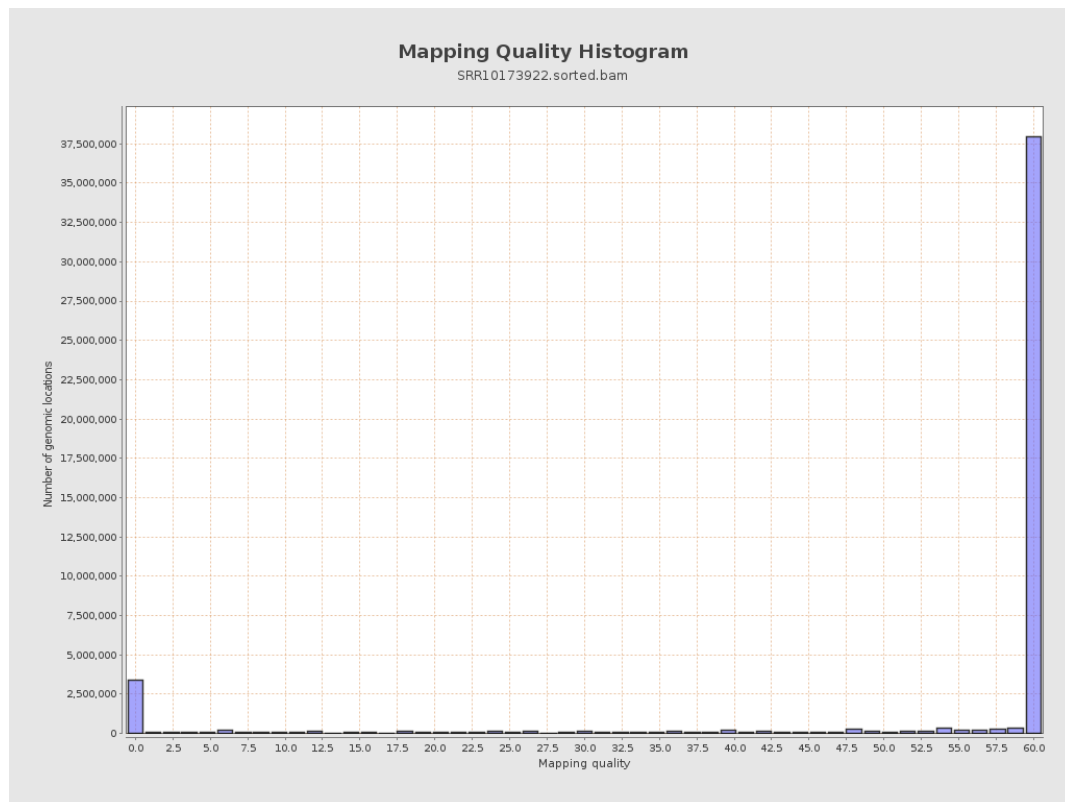
11. Results : Homopolymer Indels



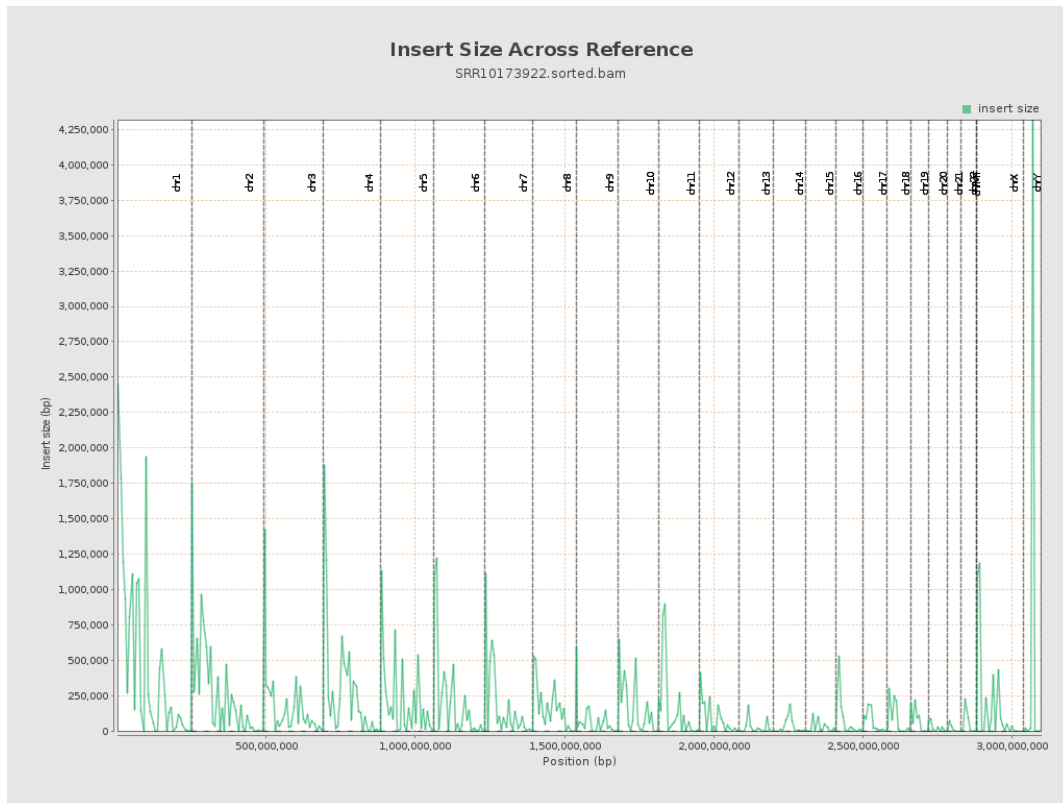
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

