

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:44:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173925.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_SRR10173925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173925_1.fastq.gz SRR10173925_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:44:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,643,304
Mapped reads	5,518,147 / 97.78%
Unmapped reads	125,157 / 2.22%
Mapped paired reads	5,518,147 / 97.78%
Mapped reads, first in pair	2,763,334 / 48.97%
Mapped reads, second in pair	2,754,813 / 48.82%
Mapped reads, both in pair	5,439,186 / 96.38%
Mapped reads, singletons	78,961 / 1.4%
Secondary alignments	0
Supplementary alignments	528,165 / 9.36%
Read min/max/mean length	30 / 133 / 128.14
Duplicated reads (estimated)	4,492,533 / 79.61%
Duplication rate	67.02%
Clipped reads	2,117,990 / 37.53%

2.2. ACGT Content

Number/percentage of A's	194,709,120 / 29.66%
Number/percentage of C's	131,575,906 / 20.05%
Number/percentage of T's	194,338,955 / 29.61%
Number/percentage of G's	135,743,604 / 20.68%
Number/percentage of N's	8,012 / 0%

GC Percentage	40.73%
---------------	--------

2.3. Coverage

Mean	0.2121
Standard Deviation	2.8755

2.4. Mapping Quality

Mean Mapping Quality	52.99
----------------------	-------

2.5. Insert size

Mean	918,933.59
Standard Deviation	8,910,298.34
P25/Median/P75	149 / 204 / 288

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	6,508,709
Insertions	64,093
Mapped reads with at least one insertion	1.13%
Deletions	155,391
Mapped reads with at least one deletion	2.76%
Homopolymer indels	43.66%

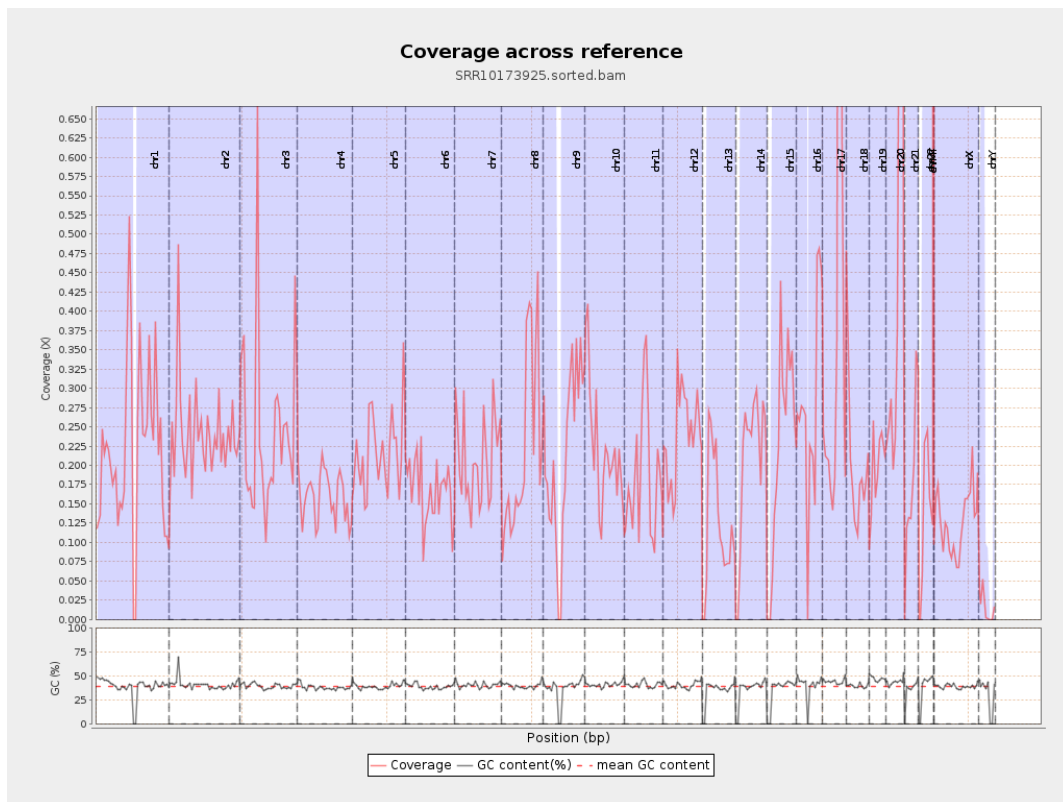
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

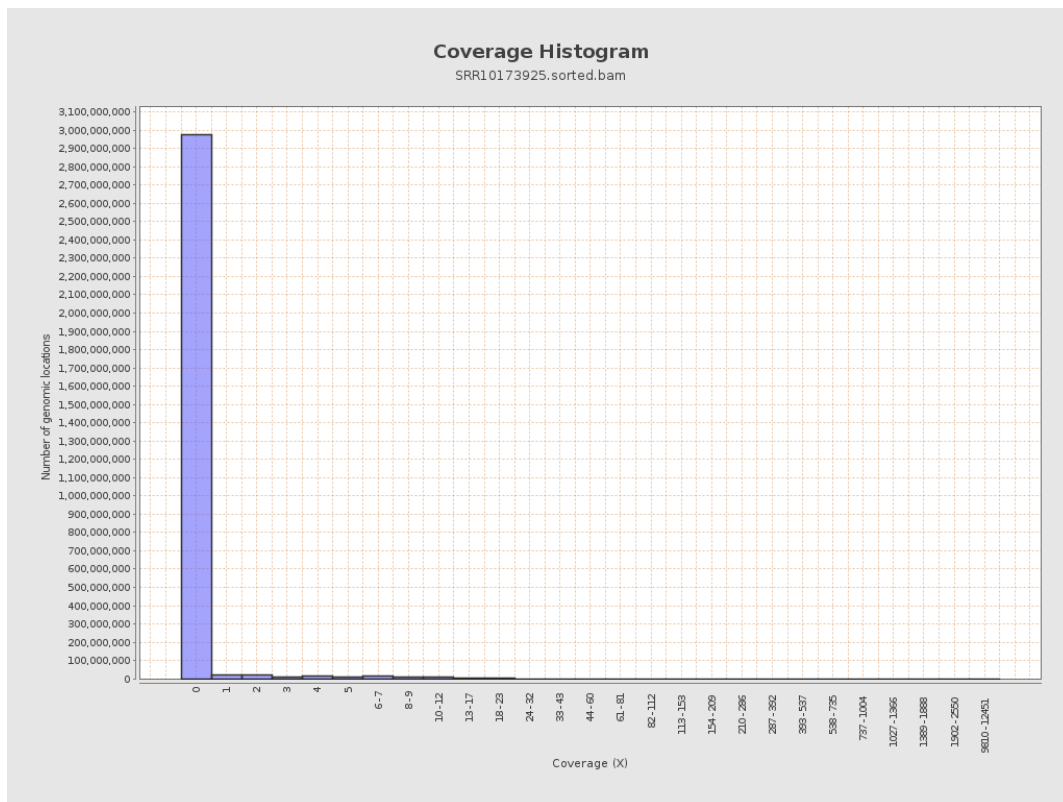
		bases	coverage	deviation
chr1	249250621	54247417	0.2176	1.7148
chr2	243199373	58741184	0.2415	8.7371
chr3	198022430	47730428	0.241	1.5693
chr4	191154276	30143980	0.1577	1.3455
chr5	180915260	39234711	0.2169	1.4452
chr6	171115067	28606811	0.1672	1.3928
chr7	159138663	33046784	0.2077	1.622
chr8	146364022	31926070	0.2181	1.6494
chr9	141213431	29289424	0.2074	1.5768
chr10	135534747	30062121	0.2218	2.0586
chr11	135006516	25299354	0.1874	1.3541
chr12	133851895	32106701	0.2399	1.5259
chr13	115169878	14077748	0.1222	1.0932
chr14	107349540	22305086	0.2078	1.4119
chr15	102531392	23126607	0.2256	1.4796
chr16	90354753	25244303	0.2794	1.7908
chr17	81195210	34303997	0.4225	2.2566
chr18	78077248	15581774	0.1996	1.7843
chr19	59128983	11763669	0.1989	1.5396
chr20	63025520	33578746	0.5328	2.5304
chr21	48129895	8832533	0.1835	1.3536
chr22	51304566	6674008	0.1301	1.0815
chrMT	16571	276808	16.7044	17.6851
chrX	155270560	19649540	0.1266	1.1027

chrY	59373566	895091	0.0151	0.5561
------	----------	--------	--------	--------

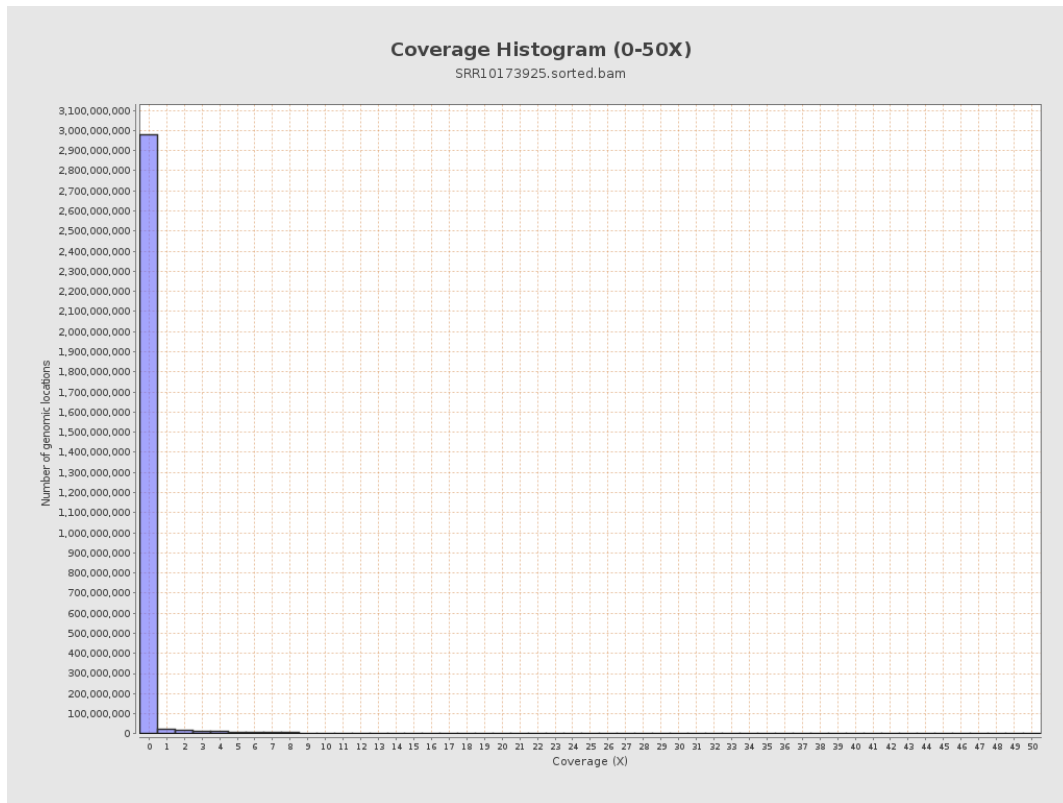
3. Results : Coverage across reference



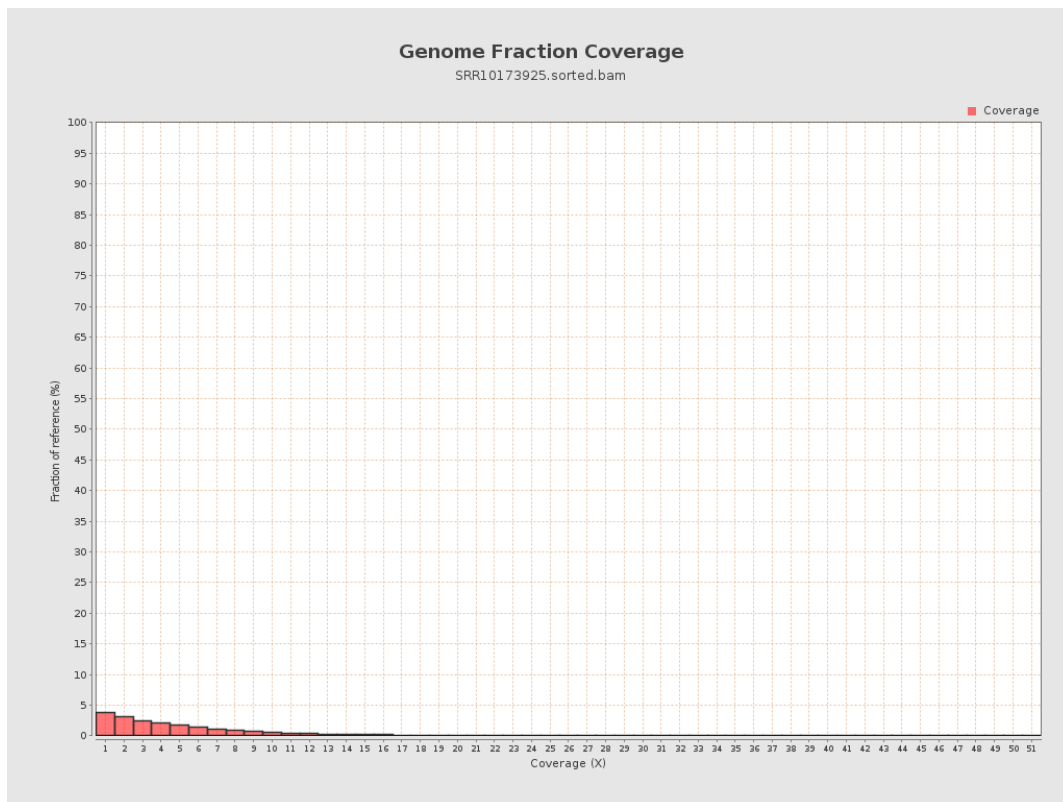
4. Results : Coverage Histogram



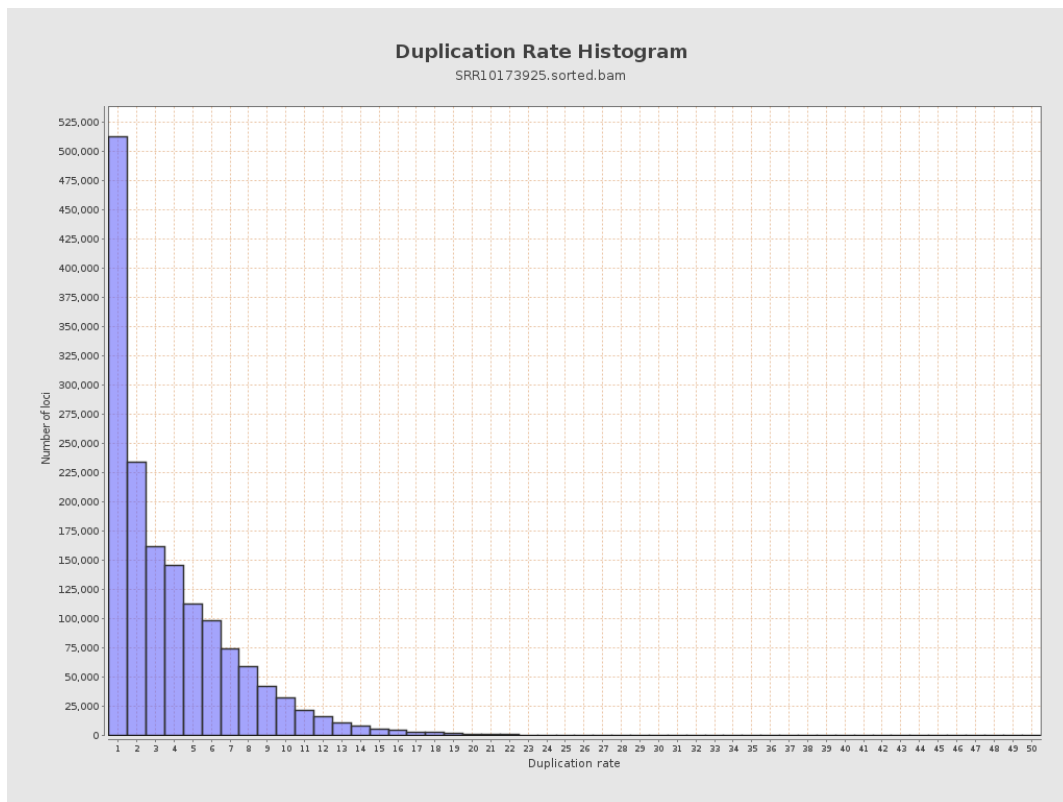
5. Results : Coverage Histogram (0-50X)



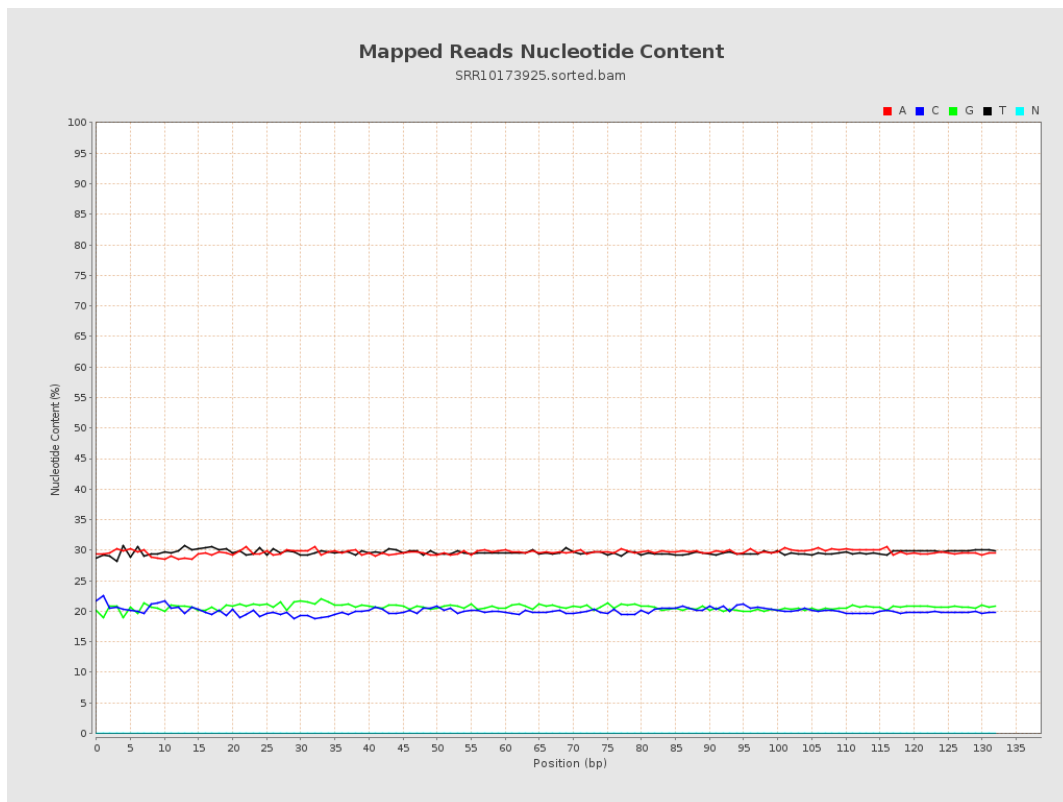
6. Results : Genome Fraction Coverage



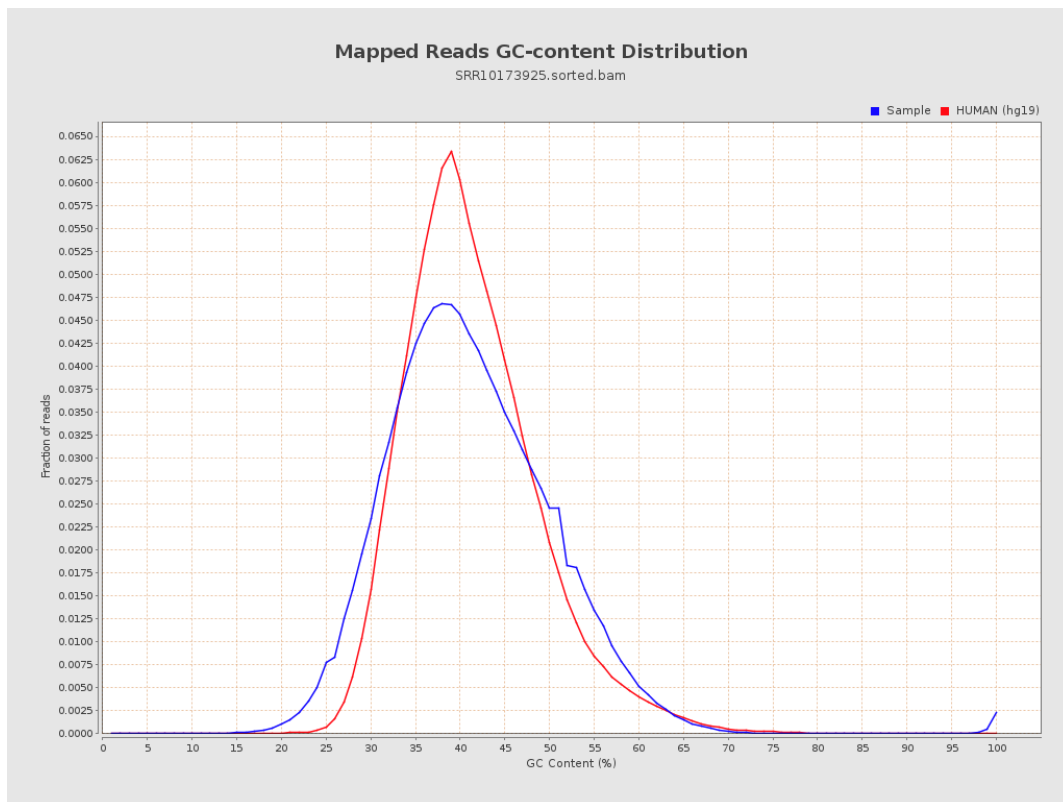
7. Results : Duplication Rate Histogram



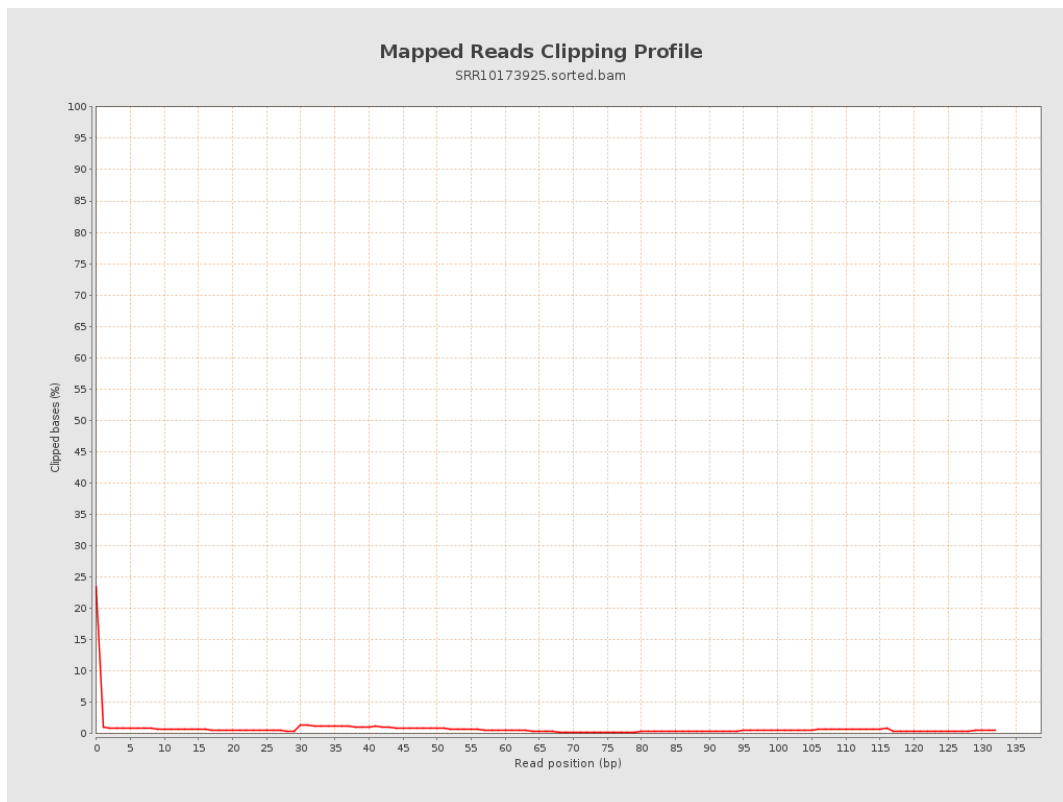
8. Results : Mapped Reads Nucleotide Content



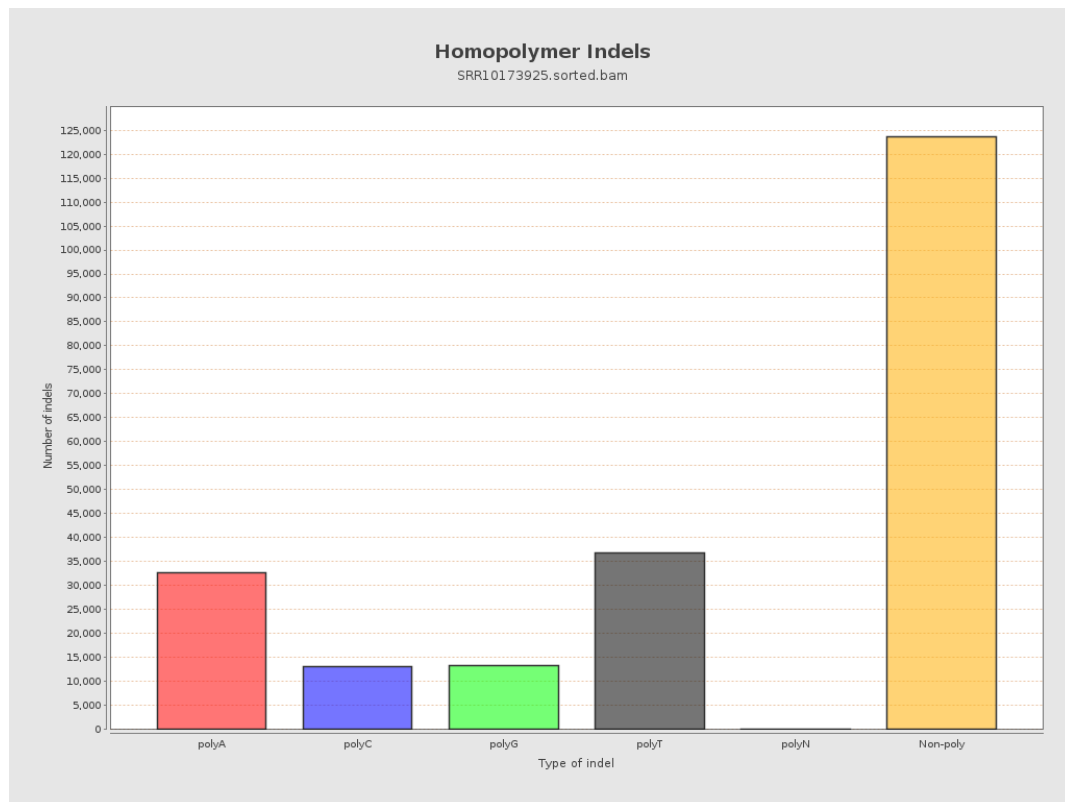
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



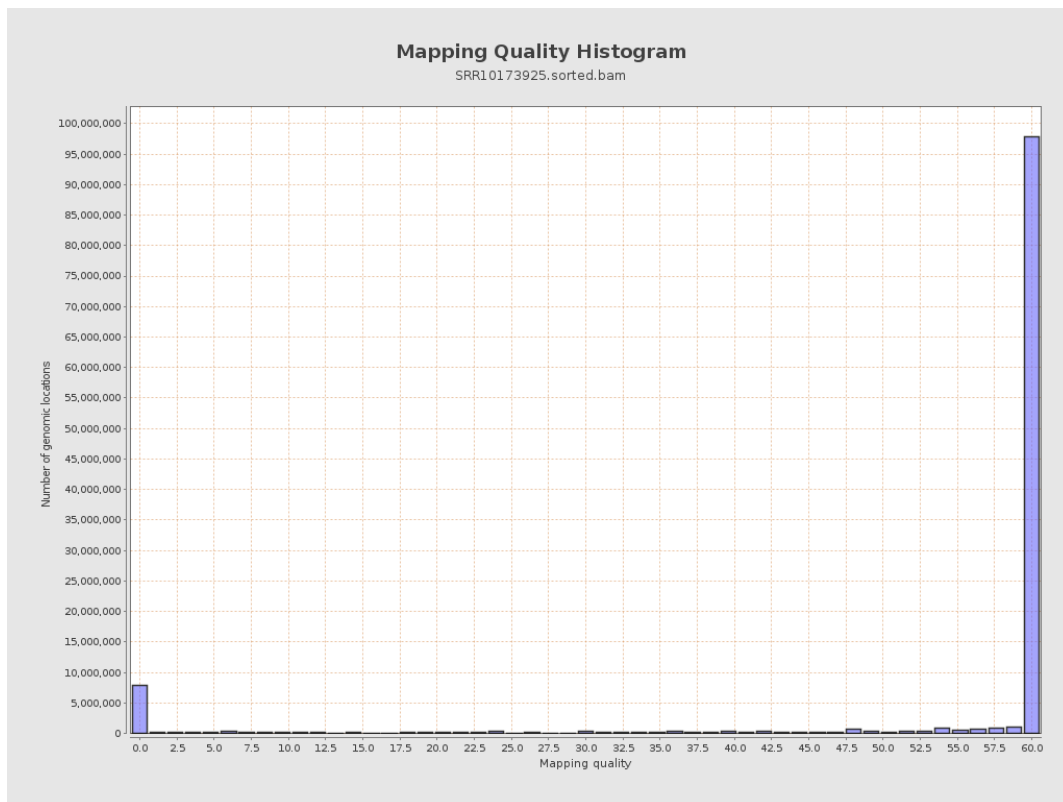
11. Results : Homopolymer Indels



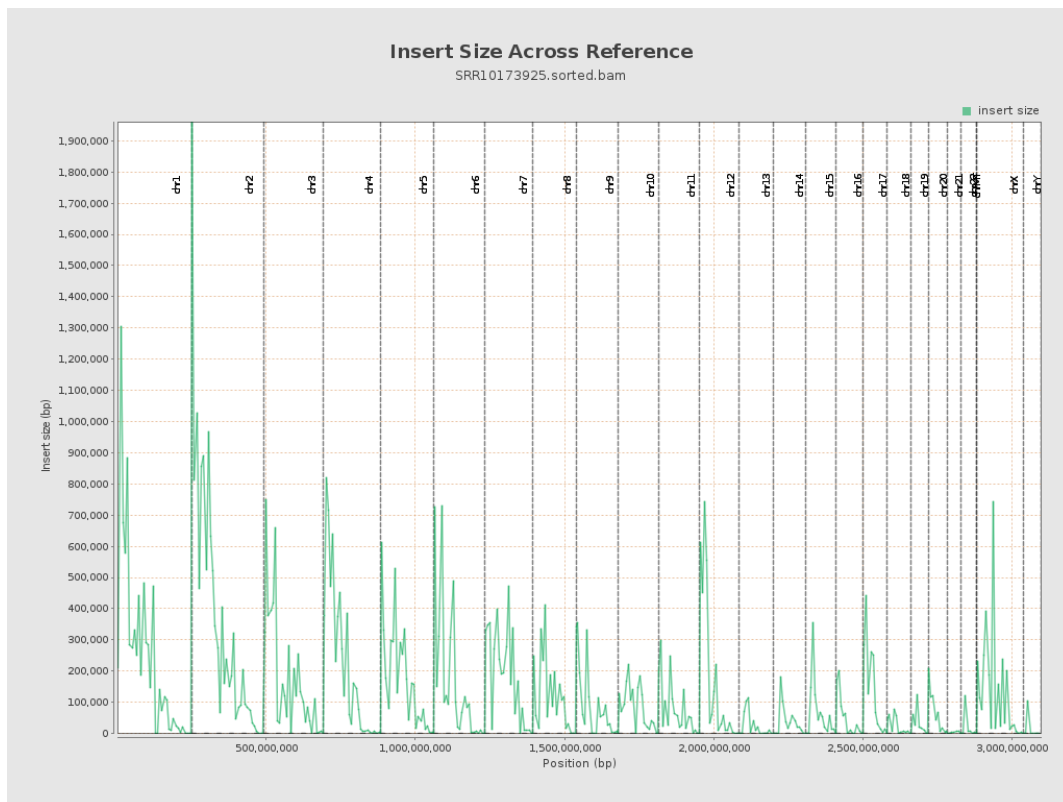
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

