

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:14:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173987.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_SRR10173987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173987_1.fastq.gz SRR10173987_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:14:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,114,578
Mapped reads	7,956,914 / 98.06%
Unmapped reads	157,664 / 1.94%
Mapped paired reads	7,956,914 / 98.06%
Mapped reads, first in pair	3,978,366 / 49.03%
Mapped reads, second in pair	3,978,548 / 49.03%
Mapped reads, both in pair	7,853,518 / 96.78%
Mapped reads, singletons	103,396 / 1.27%
Secondary alignments	0
Supplementary alignments	1,066,222 / 13.14%
Read min/max/mean length	30 / 133 / 124.72
Duplicated reads (estimated)	6,519,940 / 80.35%
Duplication rate	65.59%
Clipped reads	4,026,627 / 49.62%

2.2. ACGT Content

Number/percentage of A's	266,718,948 / 29.71%
Number/percentage of C's	179,936,060 / 20.04%
Number/percentage of T's	264,658,537 / 29.48%
Number/percentage of G's	186,495,338 / 20.77%
Number/percentage of N's	7,039 / 0%

GC Percentage	40.81%
---------------	--------

2.3. Coverage

Mean	0.2902
Standard Deviation	4.6958

2.4. Mapping Quality

Mean Mapping Quality	52.72
----------------------	-------

2.5. Insert size

Mean	1,018,596.97
Standard Deviation	9,763,511.07
P25/Median/P75	102 / 148 / 225

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	7,081,121
Insertions	89,952
Mapped reads with at least one insertion	1.09%
Deletions	260,338
Mapped reads with at least one deletion	3.2%
Homopolymer indels	41.31%

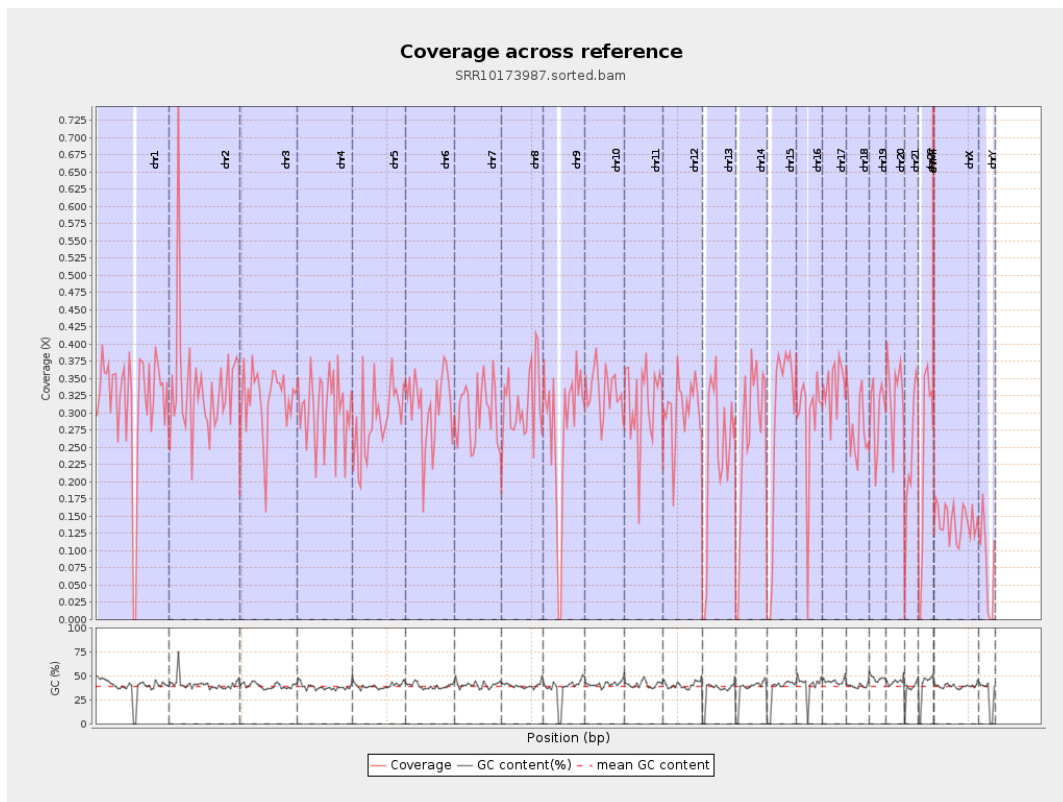
2.7. Chromosome stats

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

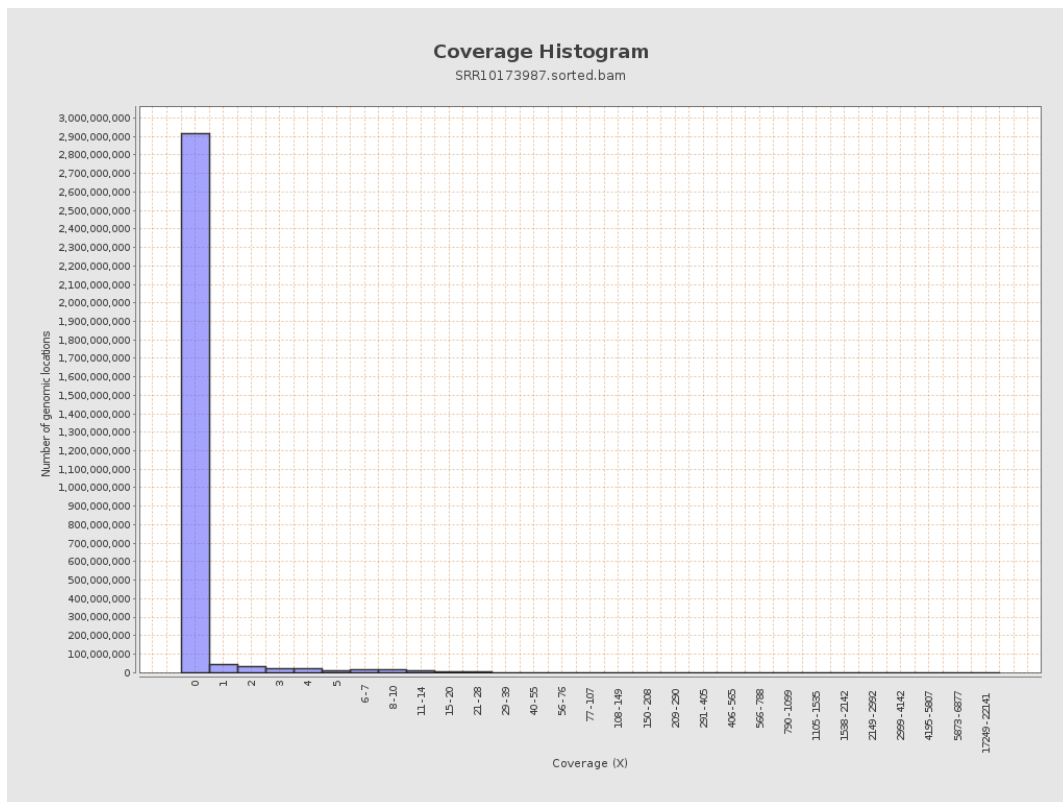
		bases	coverage	deviation
chr1	249250621	78442258	0.3147	2.1235
chr2	243199373	82189563	0.338	15.4591
chr3	198022430	63009257	0.3182	1.7788
chr4	191154276	58208740	0.3045	1.9833
chr5	180915260	52852822	0.2921	1.6897
chr6	171115067	52903498	0.3092	1.8617
chr7	159138663	48151561	0.3026	1.9065
chr8	146364022	45766506	0.3127	2.3625
chr9	141213431	38485445	0.2725	1.8496
chr10	135534747	44879675	0.3311	2.3445
chr11	135006516	42554883	0.3152	1.8047
chr12	133851895	40978055	0.3061	1.7989
chr13	115169878	27045768	0.2348	1.5324
chr14	107349540	28471432	0.2652	1.6402
chr15	102531392	28943490	0.2823	1.7152
chr16	90354753	26264392	0.2907	1.8752
chr17	81195210	27532628	0.3391	1.8856
chr18	78077248	21930179	0.2809	2.2779
chr19	59128983	17541511	0.2967	1.75
chr20	63025520	20828619	0.3305	1.8365
chr21	48129895	11533361	0.2396	1.7324
chr22	51304566	11987824	0.2337	1.6207
chrMT	16571	1304866	78.744	67.9777
chrX	155270560	22039877	0.1419	1.1794

chrY	59373566	4586368	0.0772	1.1939
------	----------	---------	--------	--------

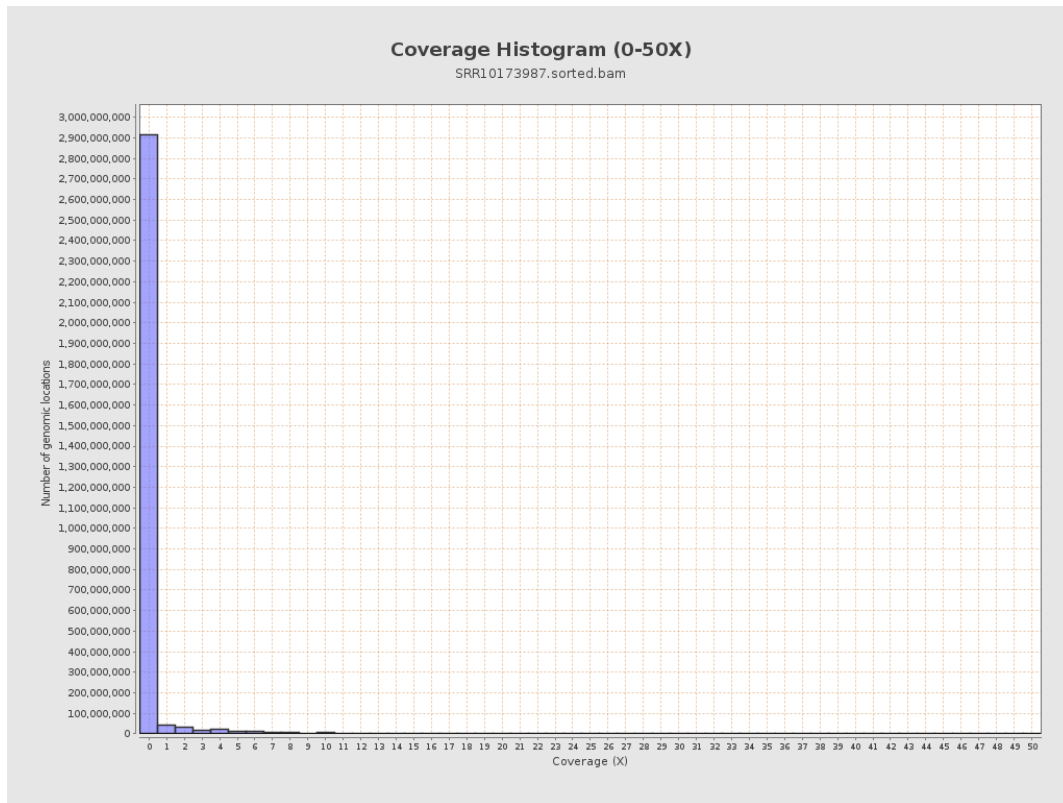
3. Results : Coverage across reference



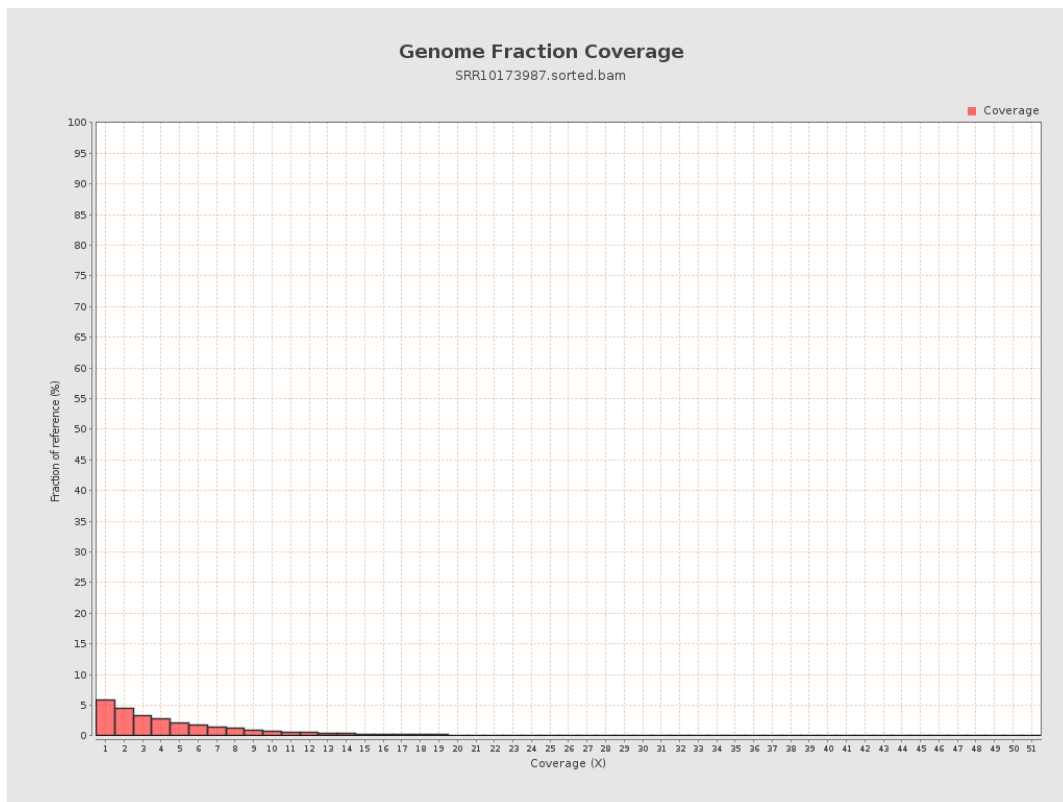
4. Results : Coverage Histogram



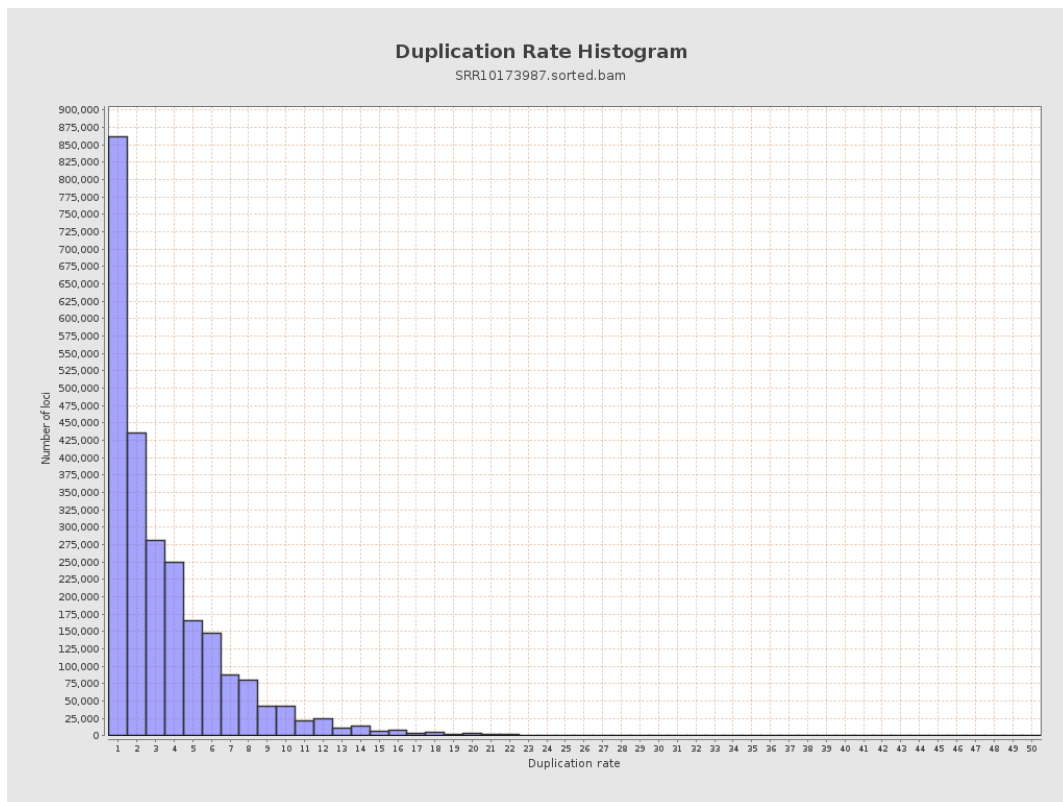
5. Results : Coverage Histogram (0-50X)



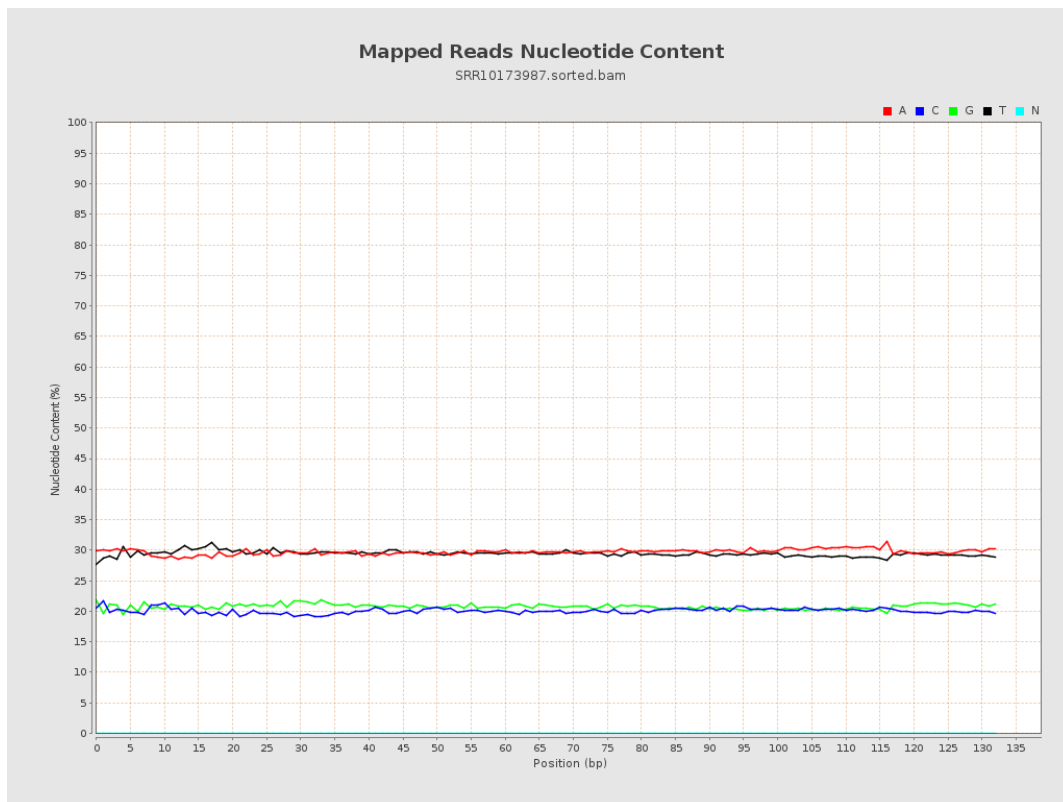
6. Results : Genome Fraction Coverage



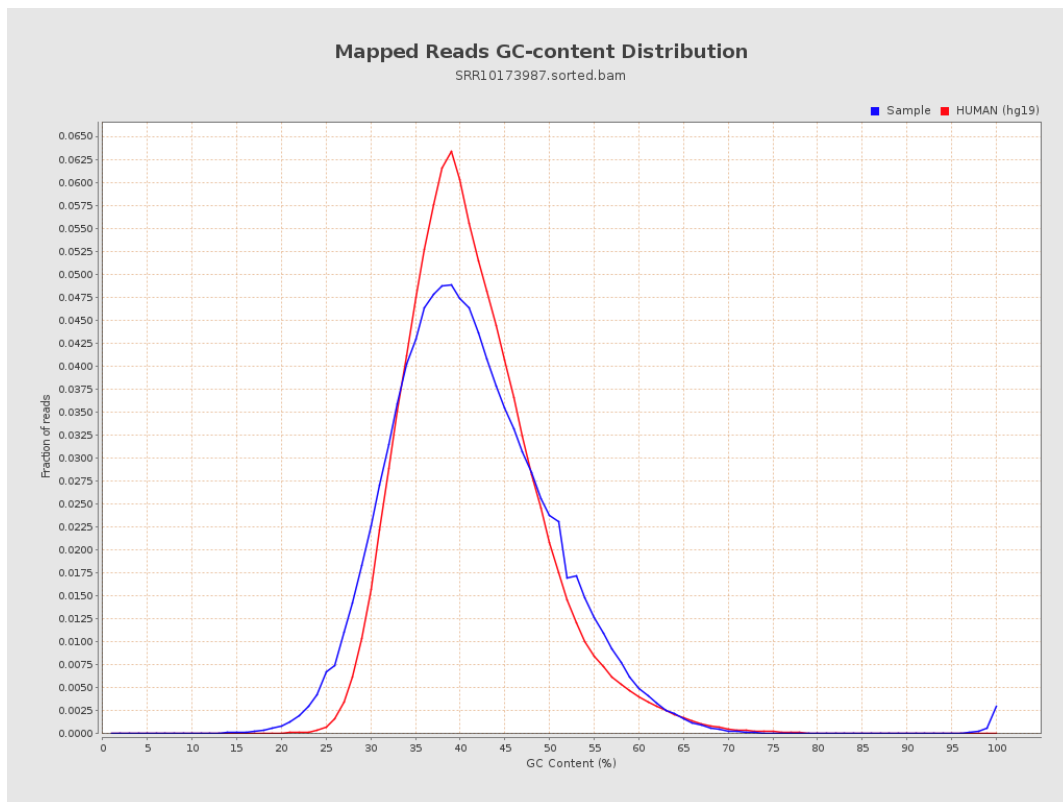
7. Results : Duplication Rate Histogram



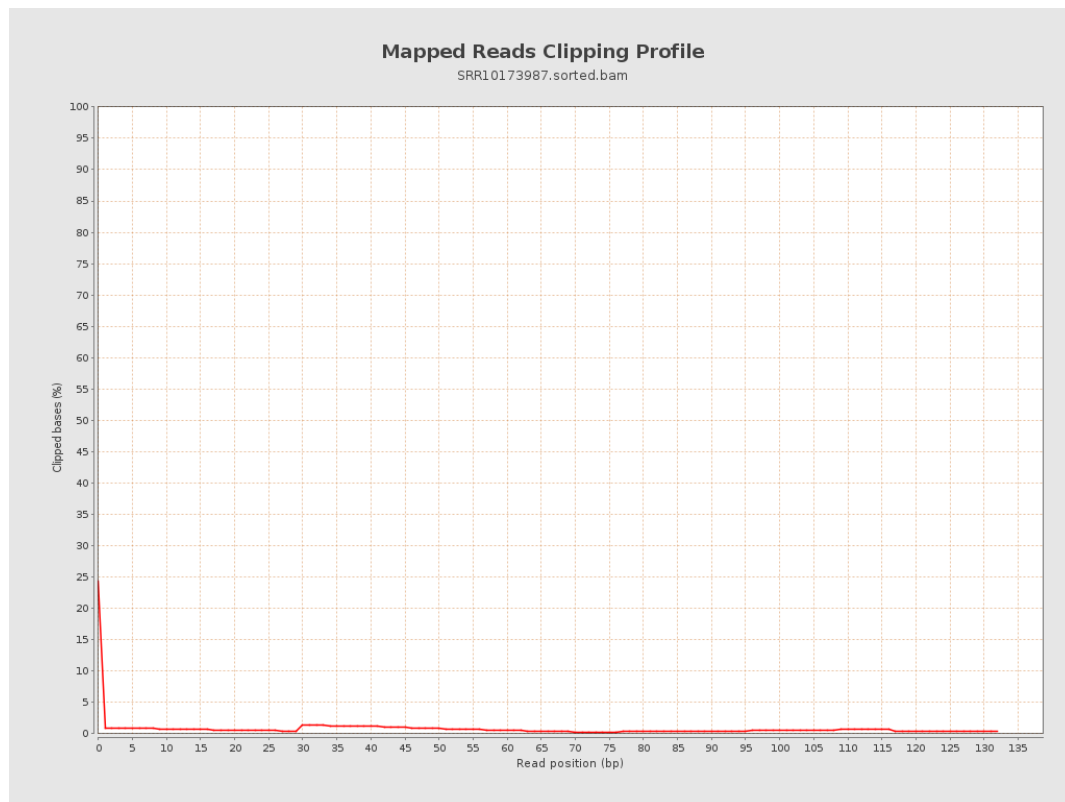
8. Results : Mapped Reads Nucleotide Content



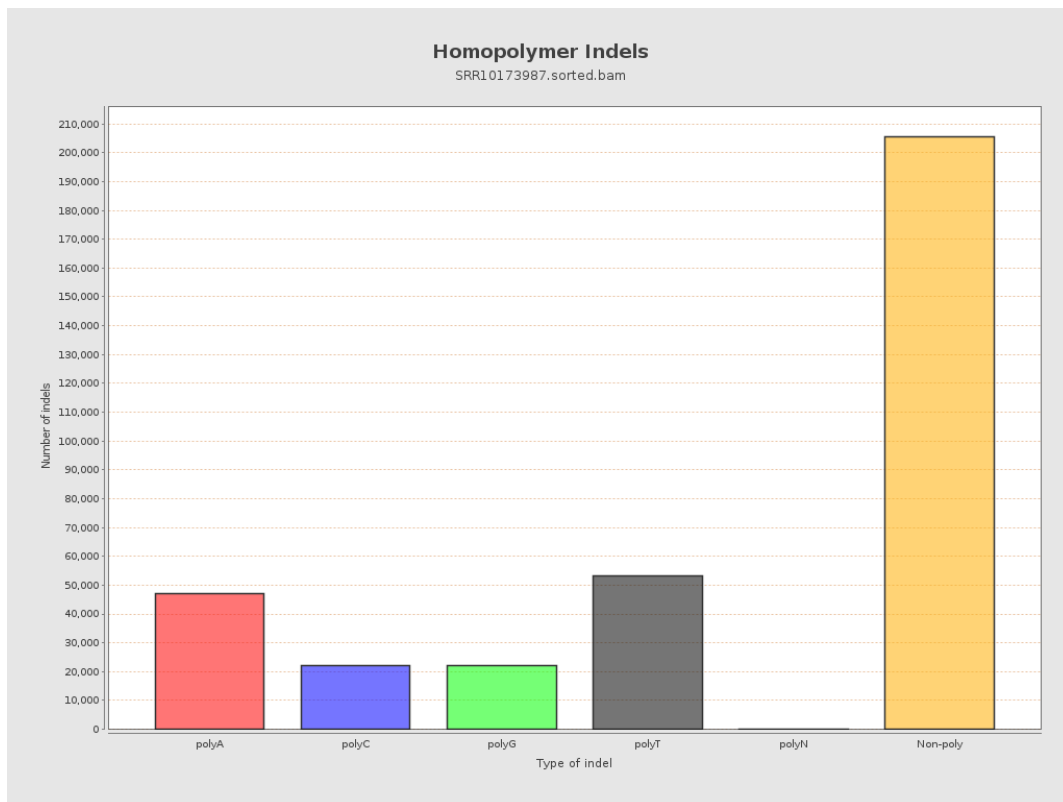
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



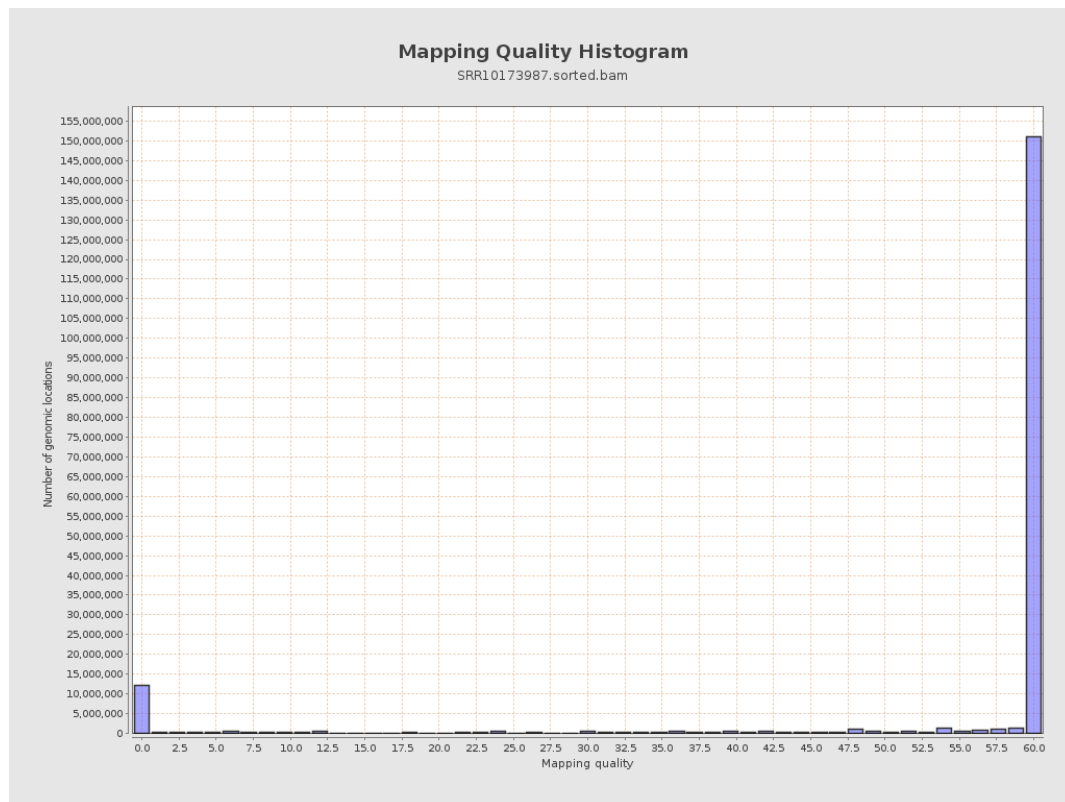
11. Results : Homopolymer Indels



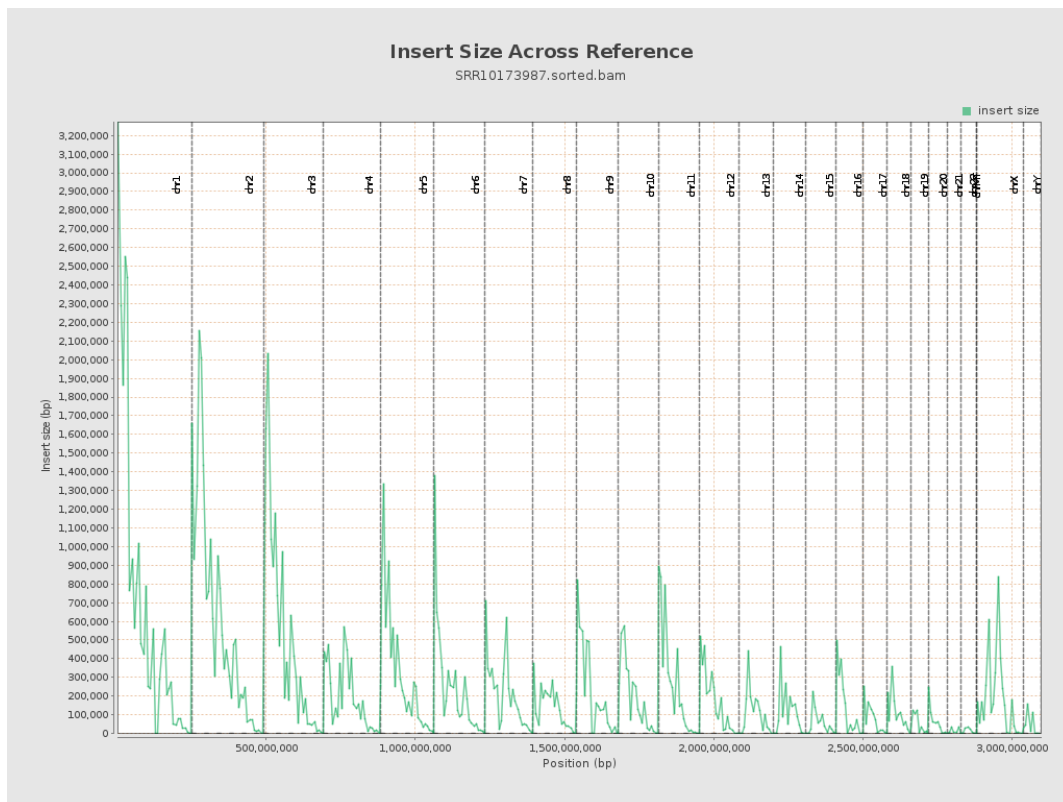
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

