

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 06:51:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174085.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_SRR10174085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174085_1.fastq.gz SRR10174085_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 06:51:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,265,614
Mapped reads	3,206,396 / 98.19%
Unmapped reads	59,218 / 1.81%
Mapped paired reads	3,206,396 / 98.19%
Mapped reads, first in pair	1,600,758 / 49.02%
Mapped reads, second in pair	1,605,638 / 49.17%
Mapped reads, both in pair	3,169,252 / 97.05%
Mapped reads, singletons	37,144 / 1.14%
Secondary alignments	0
Supplementary alignments	378,031 / 11.58%
Read min/max/mean length	30 / 133 / 124.94
Duplicated reads (estimated)	2,567,291 / 78.62%
Duplication rate	65.86%
Clipped reads	1,430,430 / 43.8%

2.2. ACGT Content

Number/percentage of A's	109,721,816 / 29.87%
Number/percentage of C's	73,177,140 / 19.92%
Number/percentage of T's	108,816,590 / 29.62%
Number/percentage of G's	75,642,191 / 20.59%
Number/percentage of N's	2,553 / 0%

GC Percentage	40.51%
---------------	--------

2.3. Coverage

Mean	0.1187
Standard Deviation	2.2356

2.4. Mapping Quality

Mean Mapping Quality	52.74
----------------------	-------

2.5. Insert size

Mean	920,884.9
Standard Deviation	8,934,750.6
P25/Median/P75	109 / 159 / 240

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	2,997,903
Insertions	38,358
Mapped reads with at least one insertion	1.15%
Deletions	88,556
Mapped reads with at least one deletion	2.7%
Homopolymer indels	42.27%

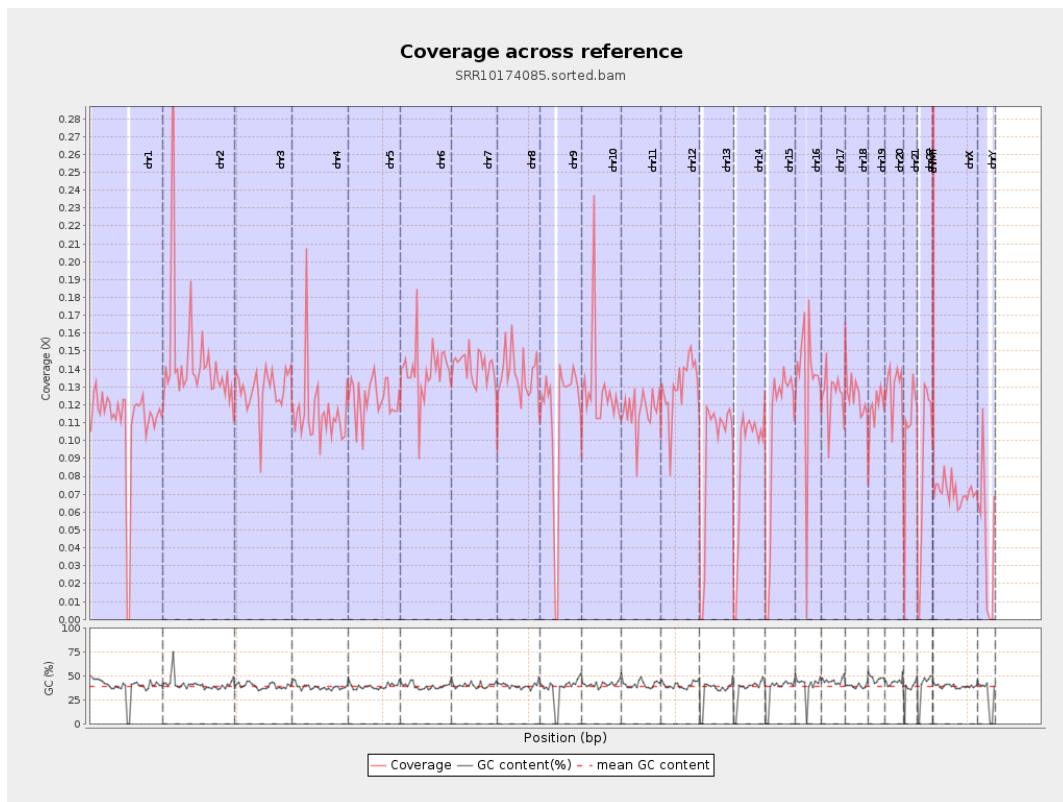
2.7. Chromosome stats

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

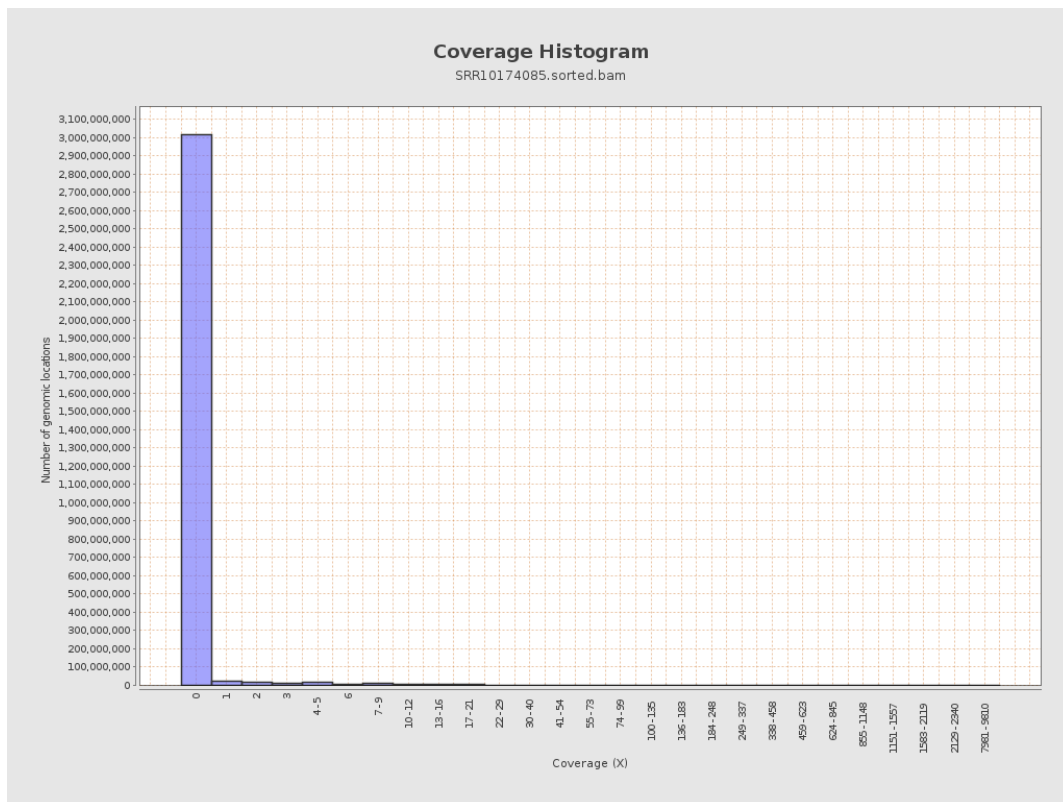
		bases	coverage	deviation
chr1	249250621	27362791	0.1098	1.1301
chr2	243199373	35037025	0.1441	6.9138
chr3	198022430	25419925	0.1284	1.0897
chr4	191154276	22151081	0.1159	1.1979
chr5	180915260	22353113	0.1236	1.0714
chr6	171115067	23843765	0.1393	1.2688
chr7	159138663	22499821	0.1414	1.3664
chr8	146364022	20065334	0.1371	1.4345
chr9	141213431	16165498	0.1145	1.2754
chr10	135534747	17406982	0.1284	1.5028
chr11	135006516	15769845	0.1168	1.0343
chr12	133851895	17509506	0.1308	1.1224
chr13	115169878	10789014	0.0937	0.934
chr14	107349540	9598724	0.0894	0.8964
chr15	102531392	10639470	0.1038	0.9816
chr16	90354753	11962335	0.1324	1.2072
chr17	81195210	10258219	0.1263	1.1096
chr18	78077248	9790329	0.1254	1.4723
chr19	59128983	7008488	0.1185	1.0867
chr20	63025520	8172702	0.1297	1.1051
chr21	48129895	5153977	0.1071	1.1149
chr22	51304566	4435854	0.0865	0.9558
chrMT	16571	289829	17.4901	21.0013
chrX	155270560	11107425	0.0715	0.8021

chrY	59373566	2787026	0.0469	0.7685
------	----------	---------	--------	--------

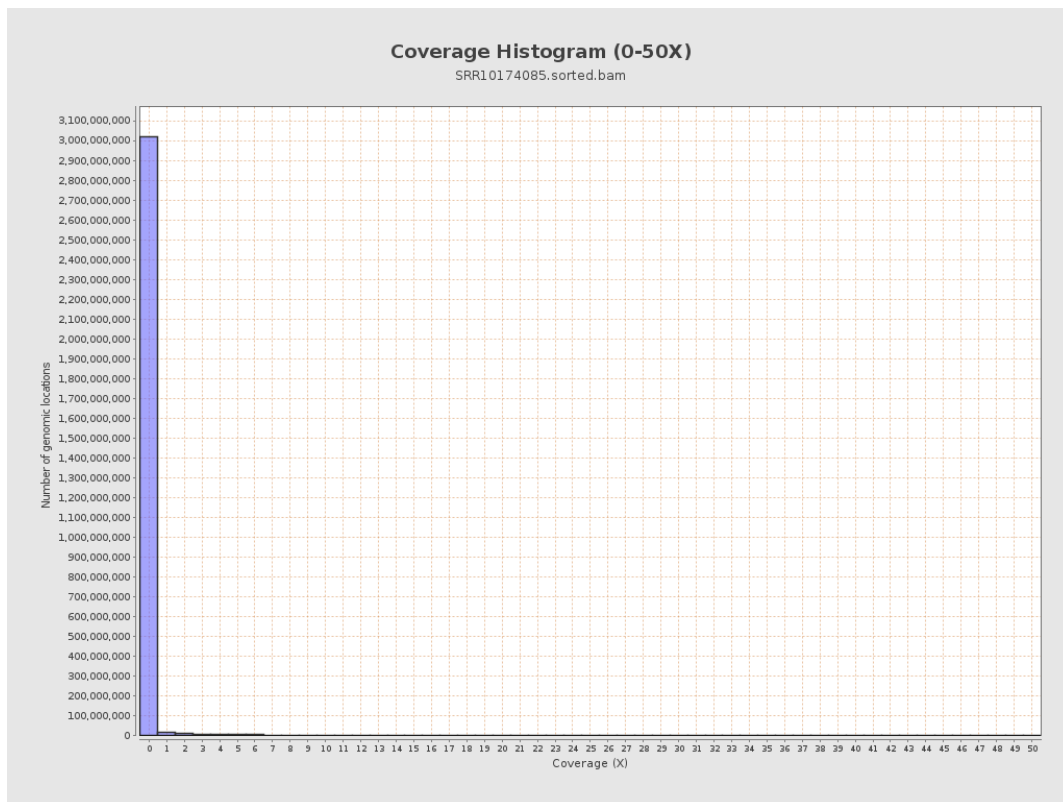
3. Results : Coverage across reference



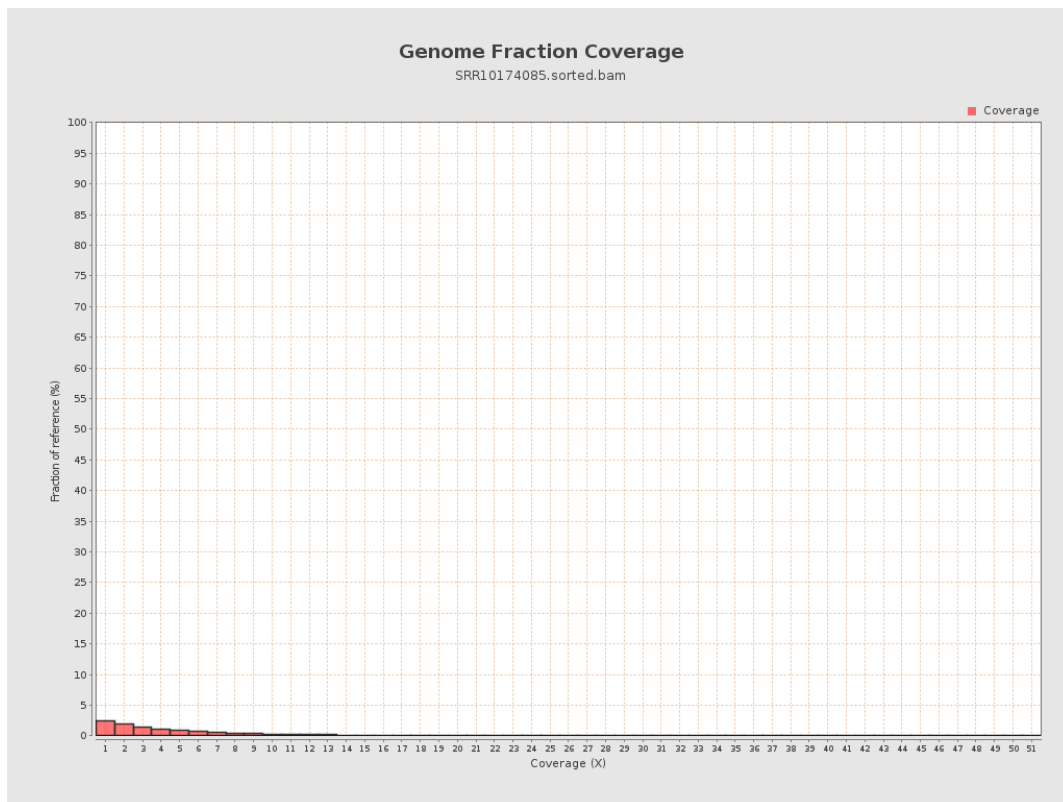
4. Results : Coverage Histogram



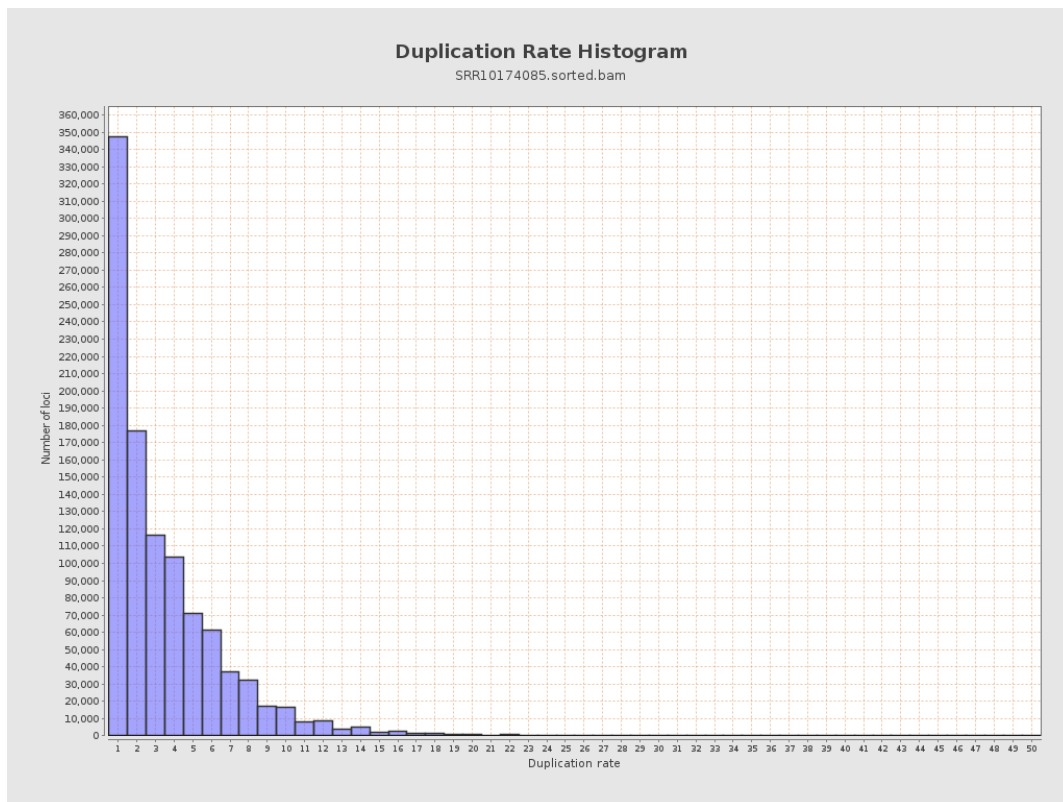
5. Results : Coverage Histogram (0-50X)



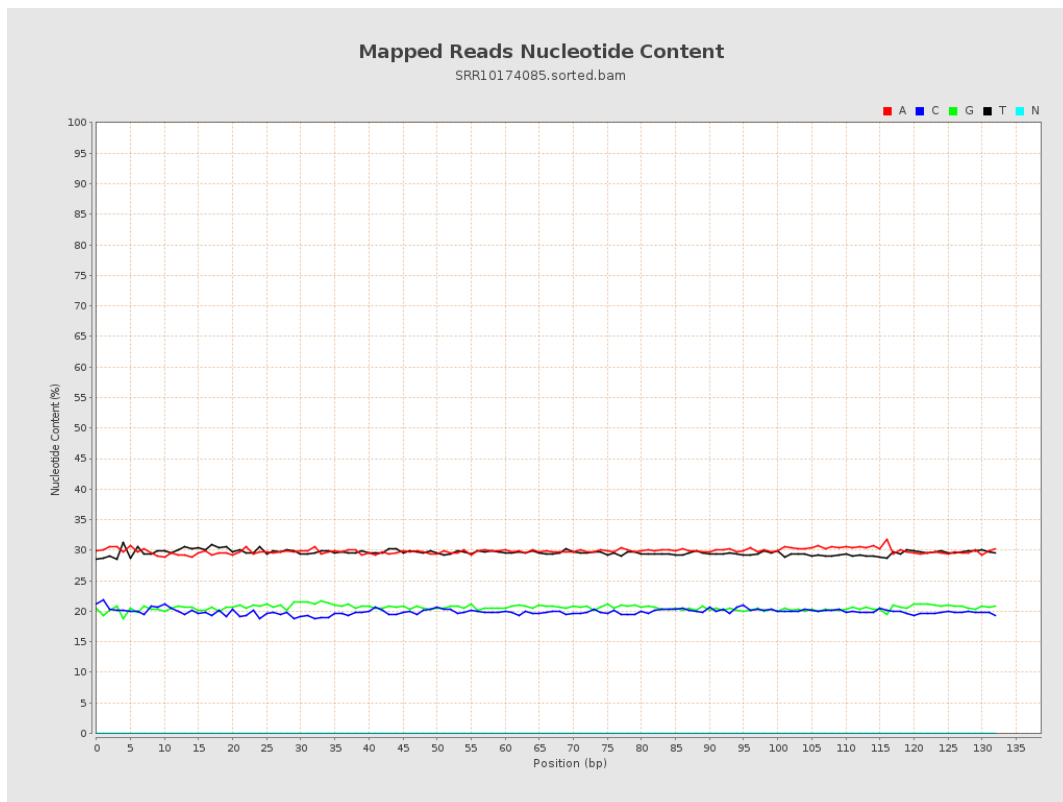
6. Results : Genome Fraction Coverage



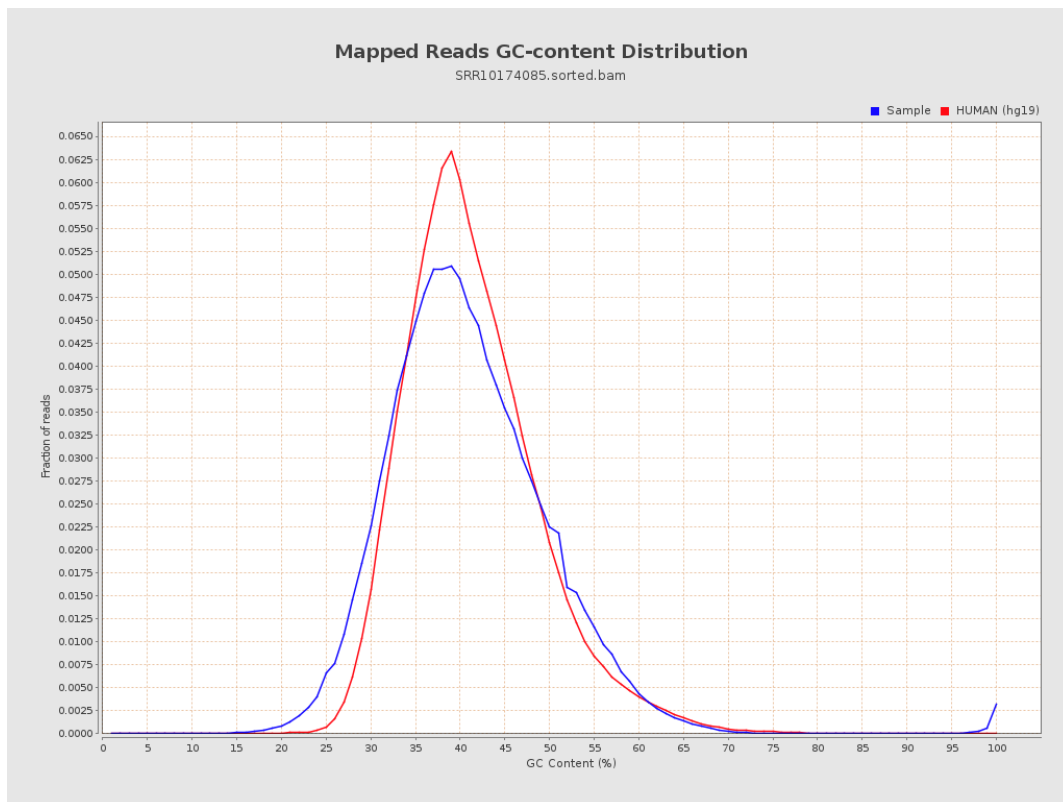
7. Results : Duplication Rate Histogram



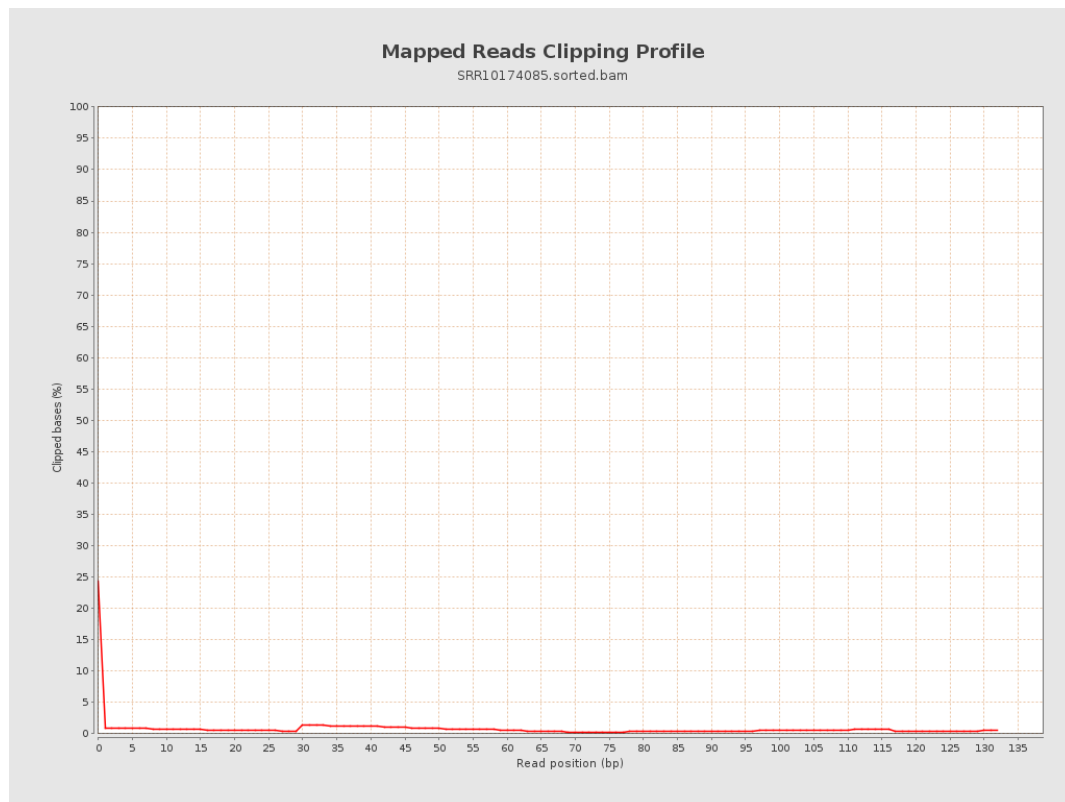
8. Results : Mapped Reads Nucleotide Content



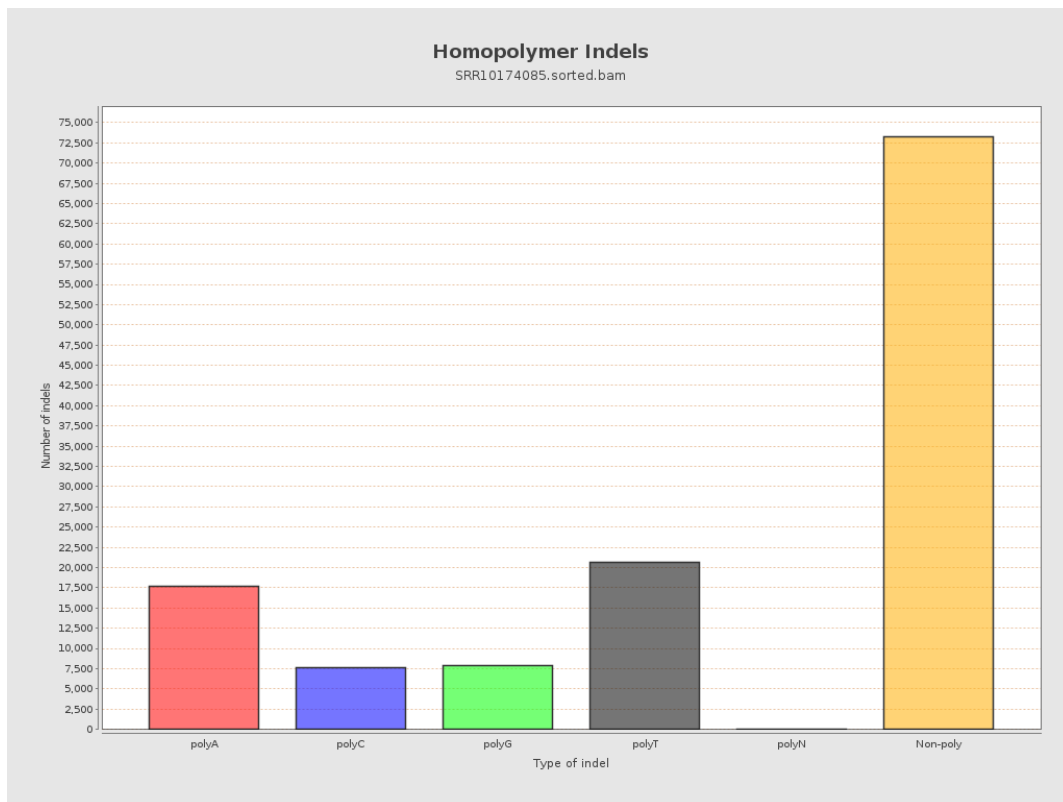
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



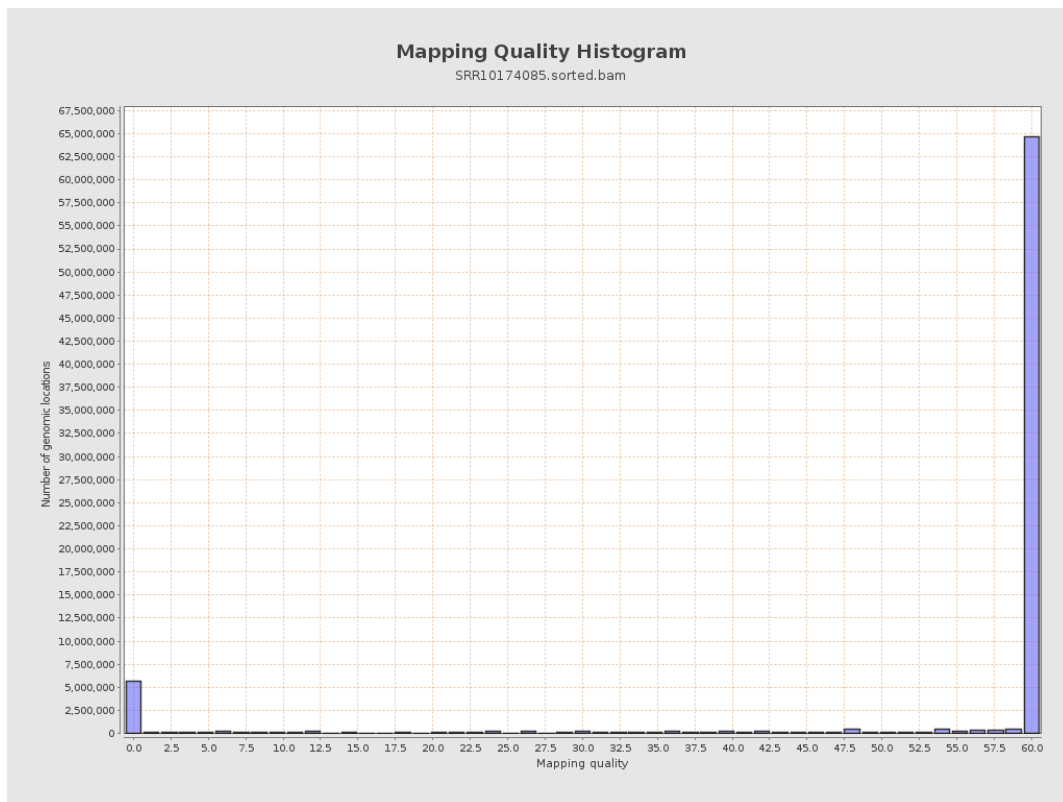
11. Results : Homopolymer Indels



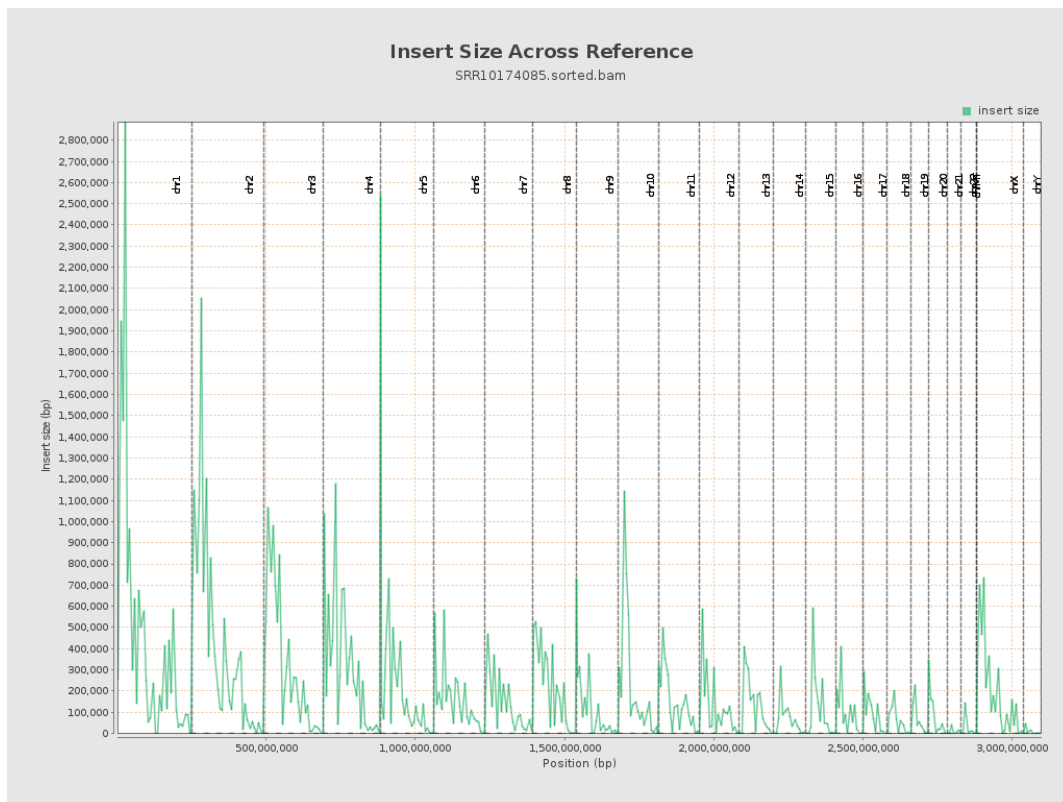
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

