

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 00:45:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174043.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_SRR10174043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174043_1.fastq.gz SRR10174043_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 00:45:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,418,428
Mapped reads	3,325,415 / 97.28%
Unmapped reads	93,013 / 2.72%
Mapped paired reads	3,325,415 / 97.28%
Mapped reads, first in pair	1,665,211 / 48.71%
Mapped reads, second in pair	1,660,204 / 48.57%
Mapped reads, both in pair	3,264,242 / 95.49%
Mapped reads, singletons	61,173 / 1.79%
Secondary alignments	0
Supplementary alignments	332,868 / 9.74%
Read min/max/mean length	30 / 133 / 127.89
Duplicated reads (estimated)	2,537,275 / 74.22%
Duplication rate	64.53%
Clipped reads	1,465,320 / 42.87%

2.2. ACGT Content

Number/percentage of A's	117,592,030 / 30.16%
Number/percentage of C's	76,157,498 / 19.53%
Number/percentage of T's	117,351,672 / 30.1%
Number/percentage of G's	78,770,680 / 20.2%
Number/percentage of N's	4,443 / 0%

GC Percentage	39.74%
---------------	--------

2.3. Coverage

Mean	0.126
Standard Deviation	1.9122

2.4. Mapping Quality

Mean Mapping Quality	52.64
----------------------	-------

2.5. Insert size

Mean	807,810.39
Standard Deviation	8,203,794.1
P25/Median/P75	140 / 197 / 286

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	3,934,103
Insertions	41,254
Mapped reads with at least one insertion	1.2%
Deletions	85,792
Mapped reads with at least one deletion	2.51%
Homopolymer indels	43.09%

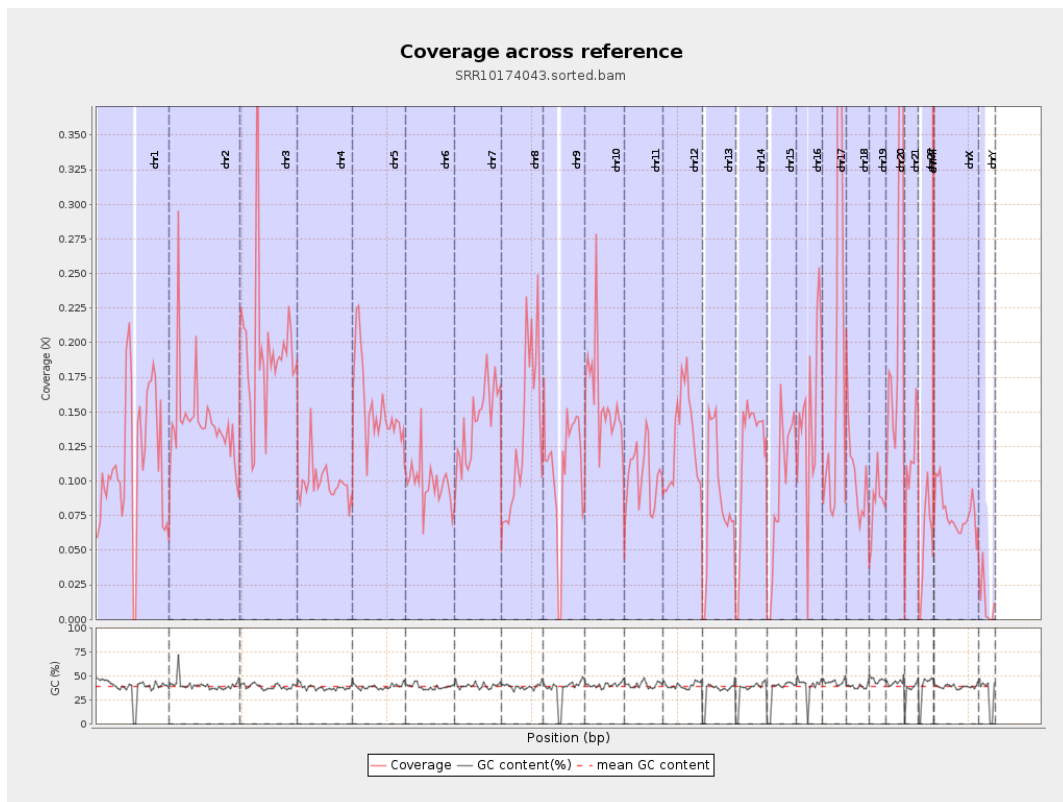
2.7. Chromosome stats

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

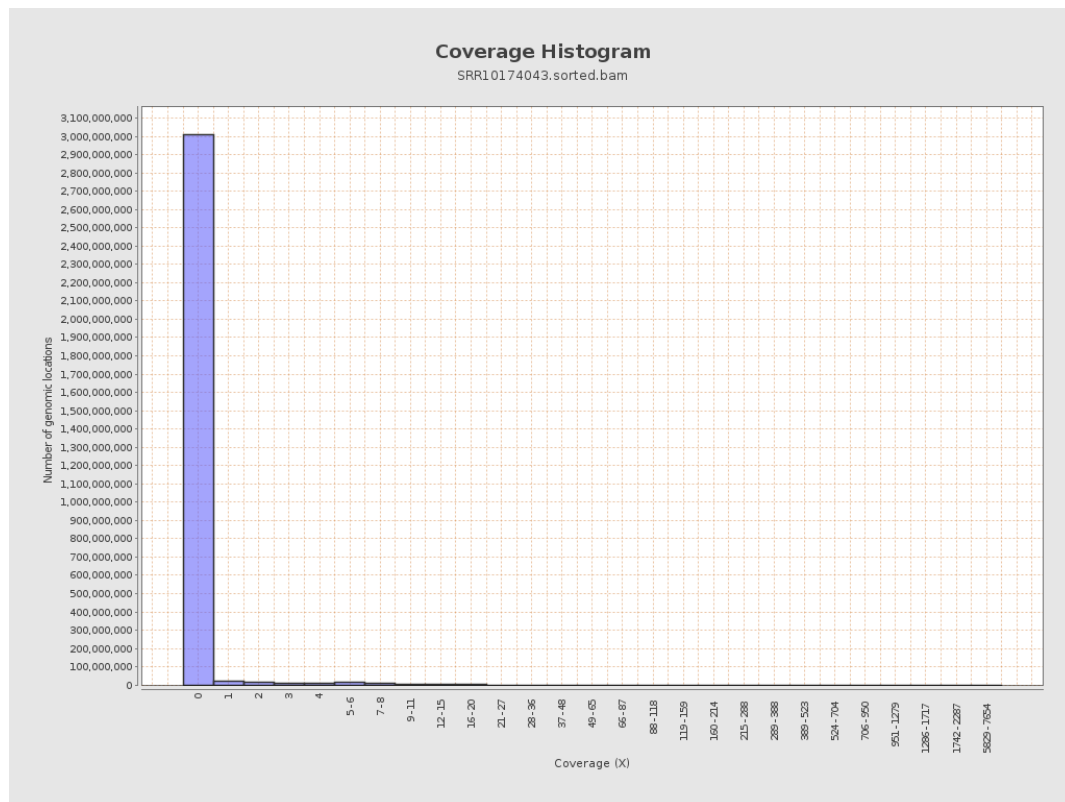
		bases	coverage	deviation
chr1	249250621	28353778	0.1138	1.4411
chr2	243199373	34636819	0.1424	5.4263
chr3	198022430	38348557	0.1937	1.256
chr4	191154276	18834938	0.0985	1.0221
chr5	180915260	27706375	0.1531	1.0999
chr6	171115067	16822709	0.0983	0.9684
chr7	159138663	22924307	0.1441	1.4209
chr8	146364022	19478241	0.1331	1.3976
chr9	141213431	15256881	0.108	1.0755
chr10	135534747	21563676	0.1591	1.8006
chr11	135006516	13973620	0.1035	0.9234
chr12	133851895	17429119	0.1302	1.0163
chr13	115169878	9775893	0.0849	0.8234
chr14	107349540	12765490	0.1189	0.9804
chr15	102531392	9712697	0.0947	0.8554
chr16	90354753	13634576	0.1509	1.3463
chr17	81195210	16598195	0.2044	1.3401
chr18	78077248	8133973	0.1042	1.4468
chr19	59128983	4998939	0.0845	1.0748
chr20	63025520	17016252	0.27	1.5492
chr21	48129895	5392982	0.1121	0.9729
chr22	51304566	2793030	0.0544	0.6235
chrMT	16571	1307771	78.9193	58.4798
chrX	155270560	11922194	0.0768	0.7727

chrY	59373566	710790	0.012	0.4854
------	----------	--------	-------	--------

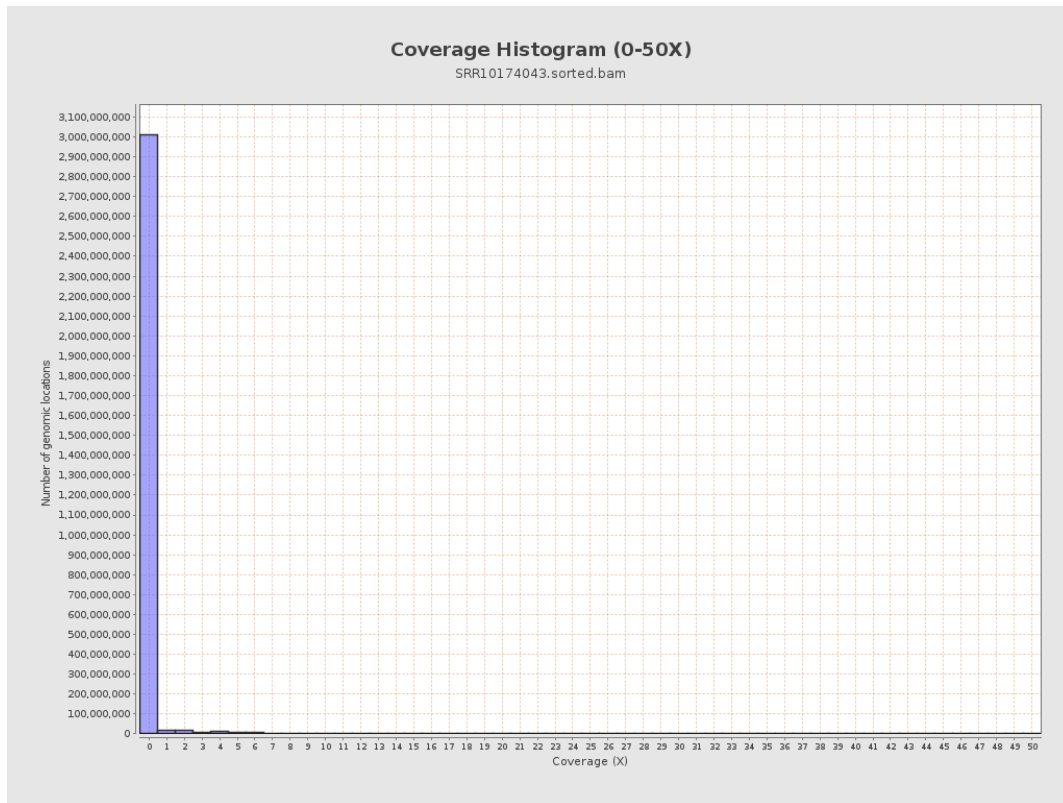
3. Results : Coverage across reference



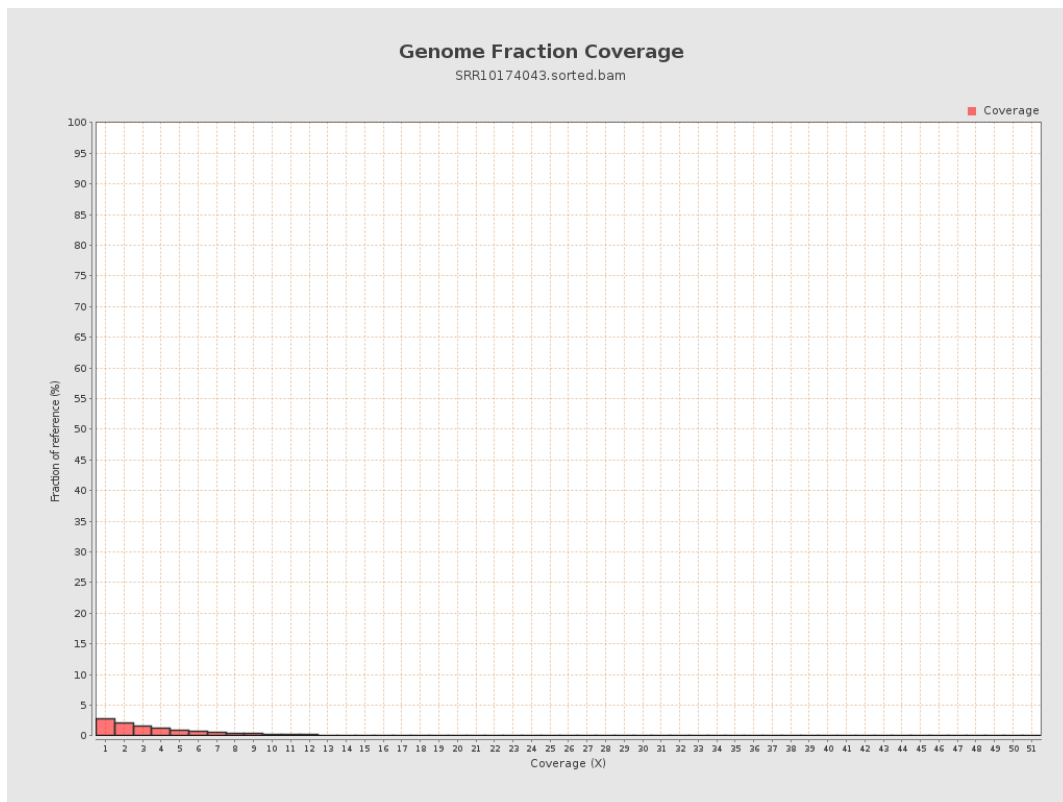
4. Results : Coverage Histogram



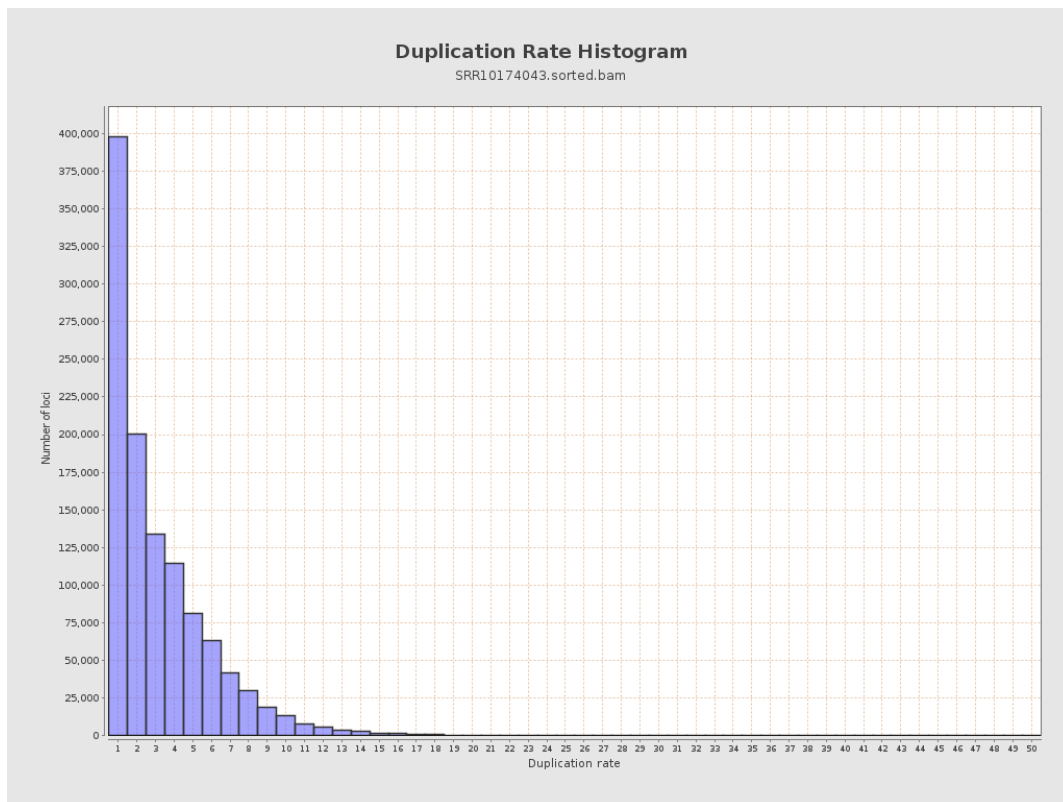
5. Results : Coverage Histogram (0-50X)



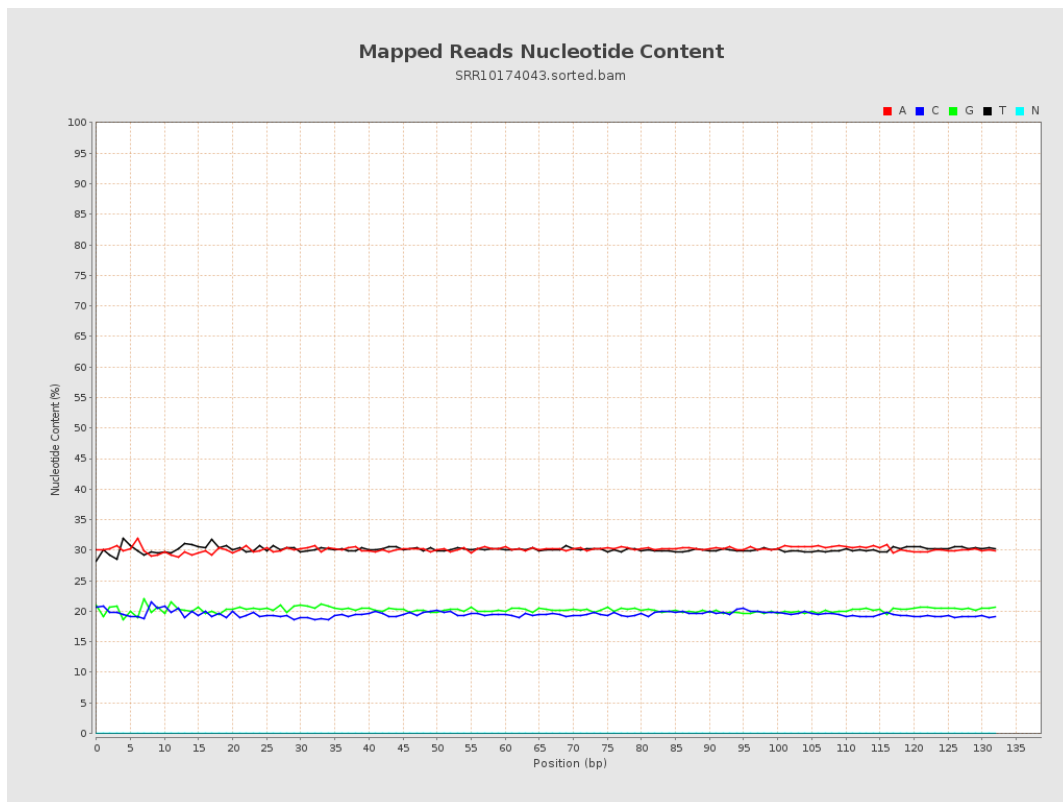
6. Results : Genome Fraction Coverage



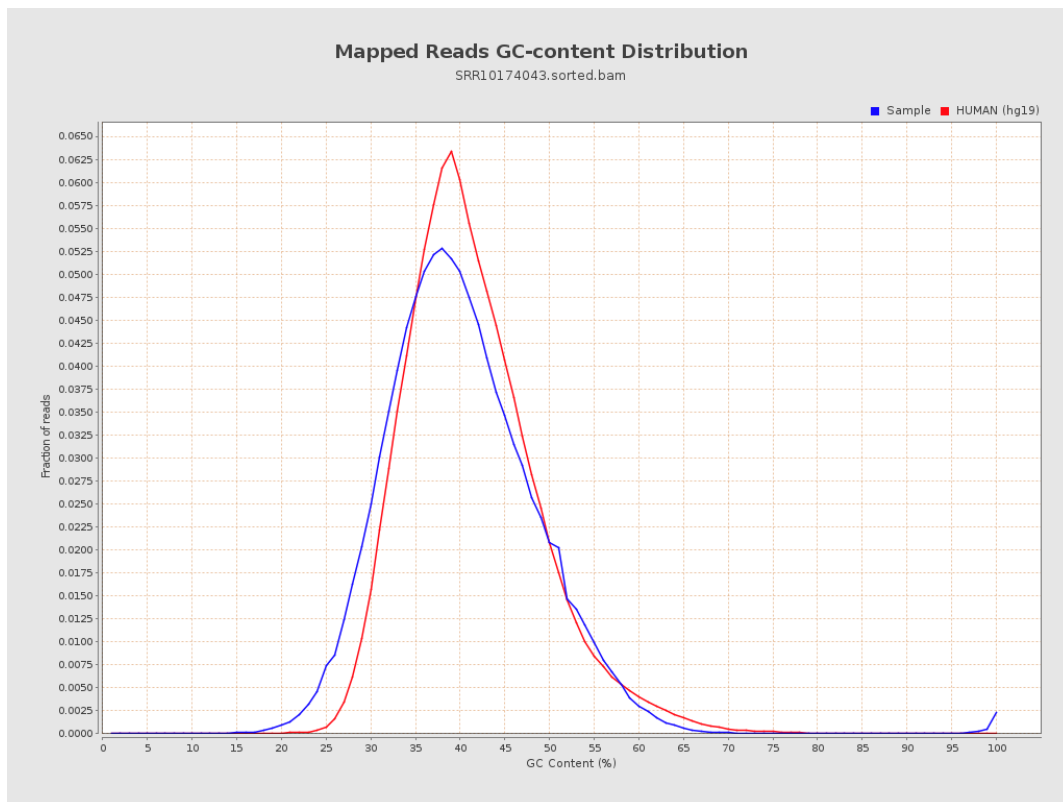
7. Results : Duplication Rate Histogram



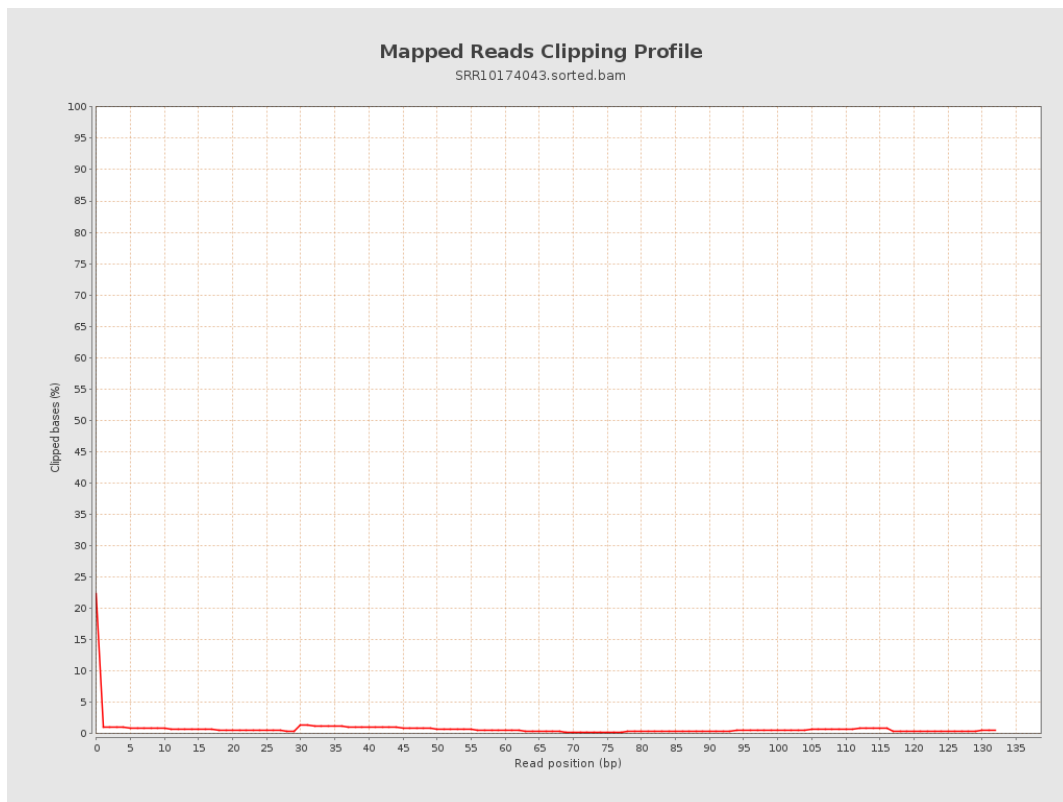
8. Results : Mapped Reads Nucleotide Content



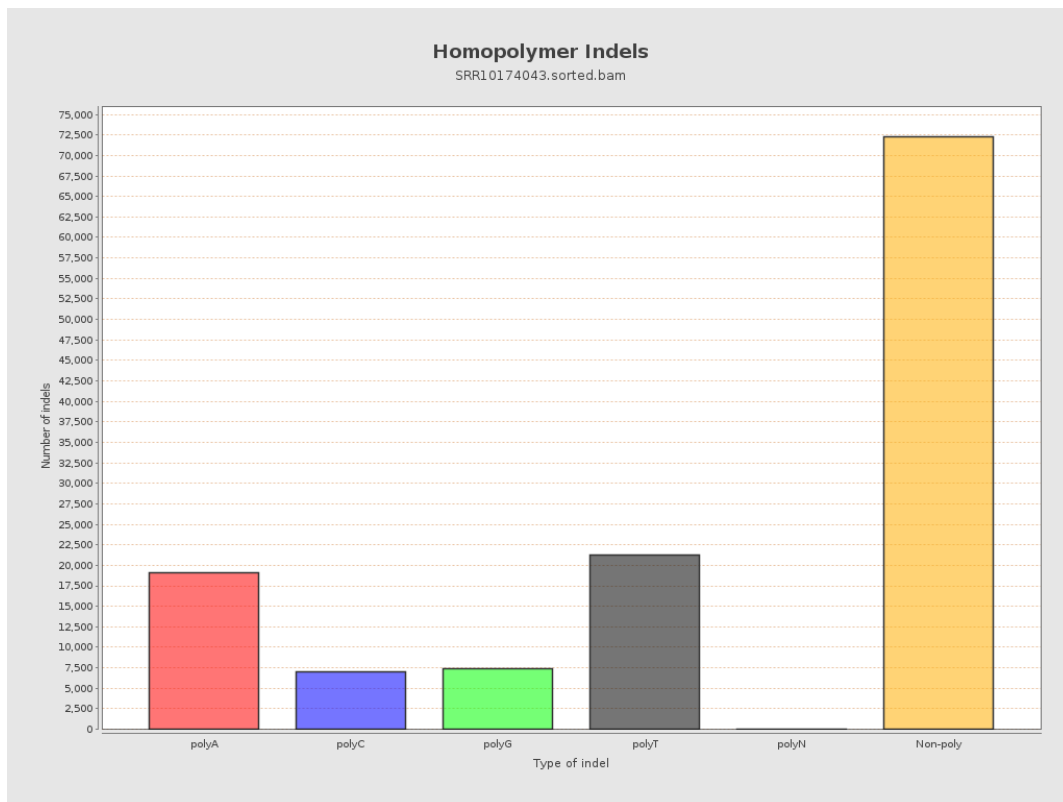
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



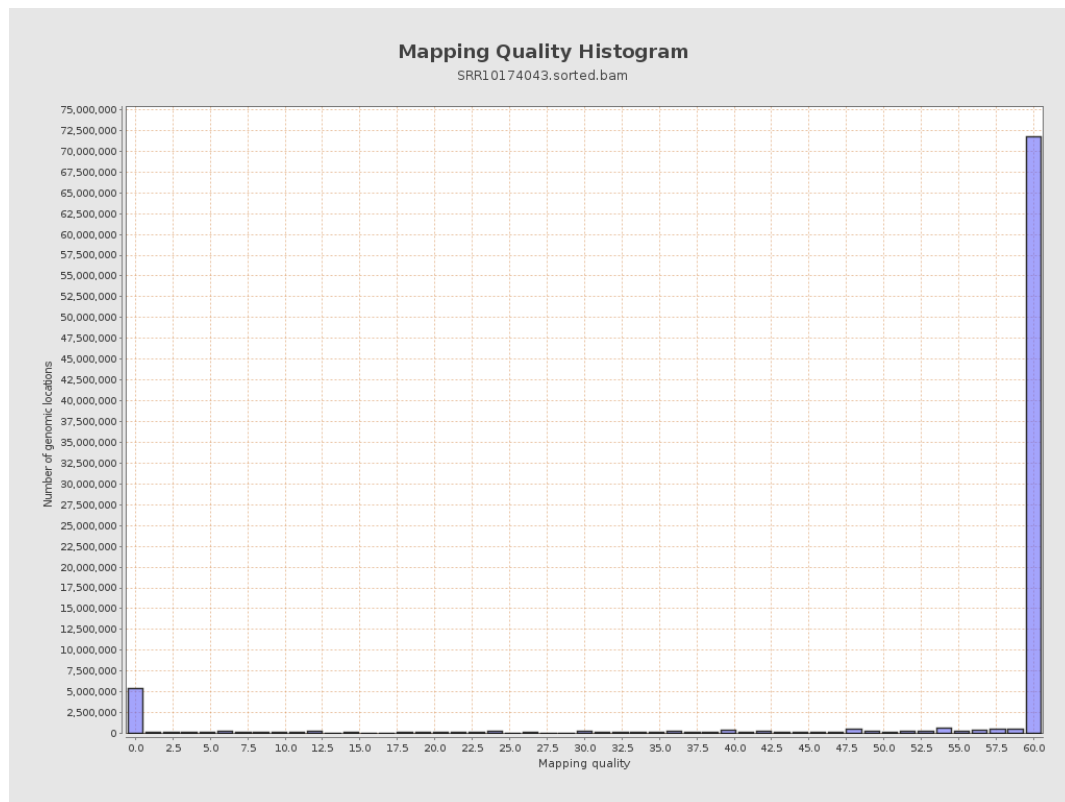
11. Results : Homopolymer Indels



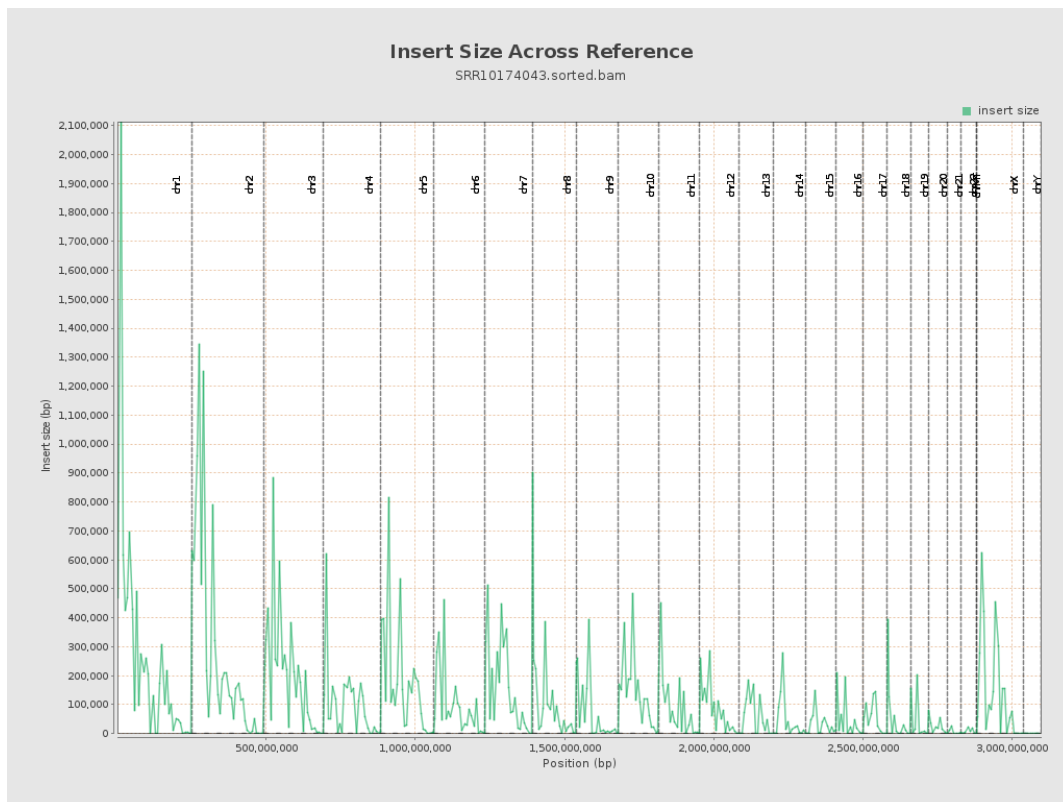
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

