

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:35:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094089.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_ERR2094089 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094089_1.fastq.gz ERR2094089_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:35:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,119,866
Mapped reads	1,963,310 / 92.61%
Unmapped reads	156,556 / 7.39%
Mapped paired reads	1,963,310 / 92.61%
Mapped reads, first in pair	985,907 / 46.51%
Mapped reads, second in pair	977,403 / 46.11%
Mapped reads, both in pair	1,947,876 / 91.89%
Mapped reads, singletons	15,434 / 0.73%
Secondary alignments	0
Supplementary alignments	137,380 / 6.48%
Read min/max/mean length	30 / 151 / 135.08
Duplicated reads (estimated)	1,989,285 / 93.84%
Duplication rate	55.11%
Clipped reads	1,052,856 / 49.67%

2.2. ACGT Content

Number/percentage of A's	69,077,853 / 29.05%
Number/percentage of C's	50,424,773 / 21.21%
Number/percentage of T's	64,758,869 / 27.24%
Number/percentage of G's	53,510,212 / 22.5%
Number/percentage of N's	2,716 / 0%

GC Percentage	43.71%
---------------	--------

2.3. Coverage

Mean	0.0783
Standard Deviation	14.7369

2.4. Mapping Quality

Mean Mapping Quality	41.21
----------------------	-------

2.5. Insert size

Mean	1,715,742.2
Standard Deviation	11,591,019.4
P25/Median/P75	114 / 147 / 177

2.6. Mismatches and indels

General error rate	3.6%
Mismatches	8,236,718
Insertions	168,888
Mapped reads with at least one insertion	8.43%
Deletions	676,112
Mapped reads with at least one deletion	33.34%
Homopolymer indels	28.29%

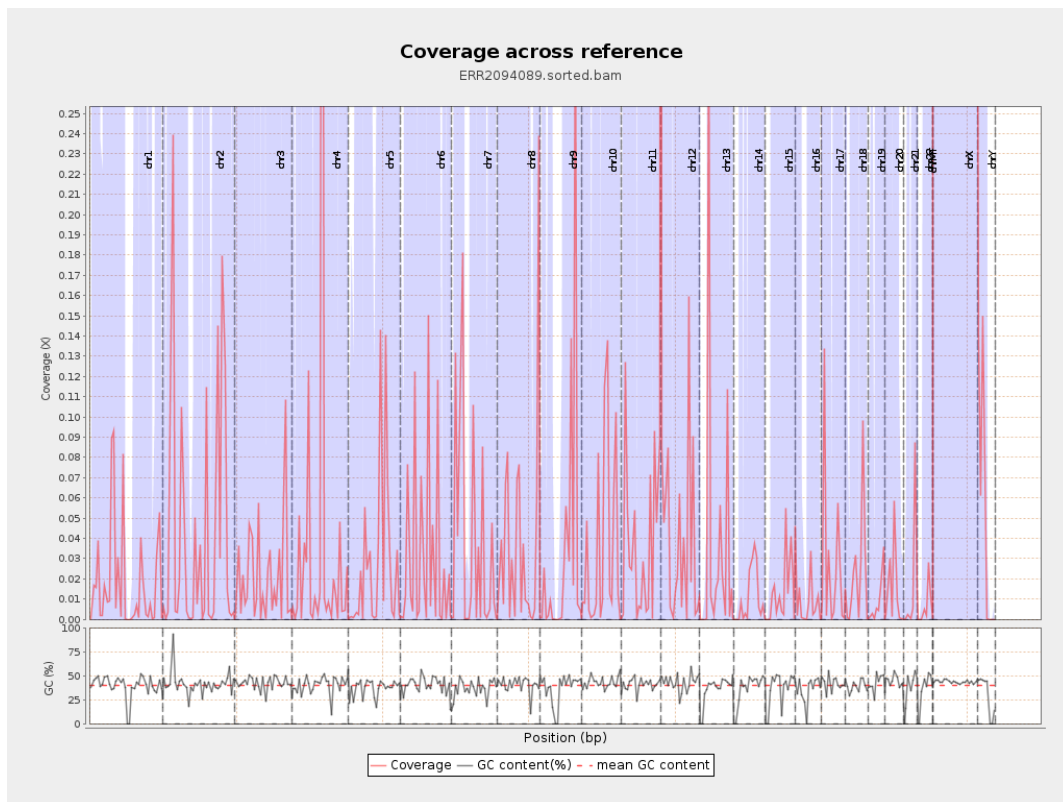
2.7. Chromosome stats

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

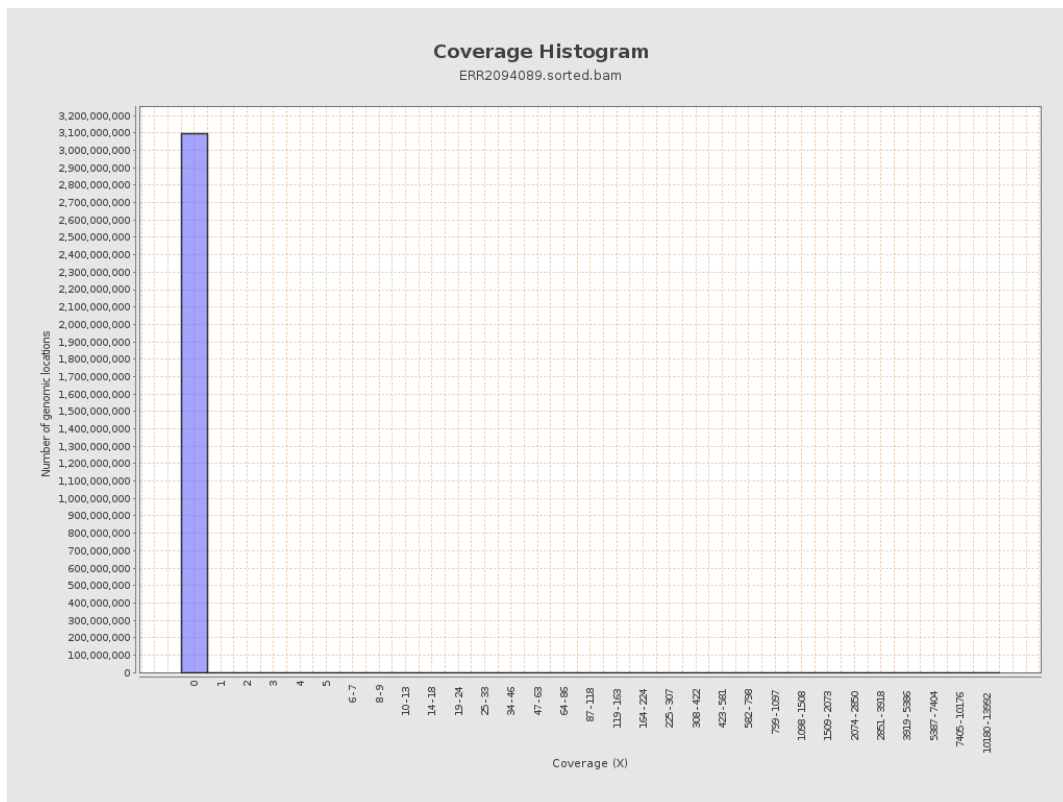
		bases	coverage	deviation
chr1	249250621	4497947	0.018	7.0214
chr2	243199373	10348054	0.0425	12.0335
chr3	198022430	4270274	0.0216	6.3875
chr4	191154276	8968921	0.0469	11.496
chr5	180915260	4826791	0.0267	10.8592
chr6	171115067	5392684	0.0315	9.9606
chr7	159138663	5873643	0.0369	11.0657
chr8	146364022	5576202	0.0381	11.9196
chr9	141213431	4871346	0.0345	13.4686
chr10	135534747	4859353	0.0359	10.6097
chr11	135006516	5467219	0.0405	9.7612
chr12	133851895	5451575	0.0407	9.5112
chr13	115169878	4341349	0.0377	10.5687
chr14	107349540	1181255	0.011	3.7307
chr15	102531392	1397539	0.0136	3.2922
chr16	90354753	842233	0.0093	2.963
chr17	81195210	2248309	0.0277	8.0827
chr18	78077248	1837657	0.0235	7.428
chr19	59128983	516279	0.0087	2.681
chr20	63025520	913820	0.0145	4.2466
chr21	48129895	817067	0.017	6.3612
chr22	51304566	362771	0.0071	2.4633
chrMT	16571	605283	36.5266	215.3579
chrX	155270560	153936740	0.9914	51.4501

chrY	59373566	2963800	0.0499	9.5313
------	----------	---------	--------	--------

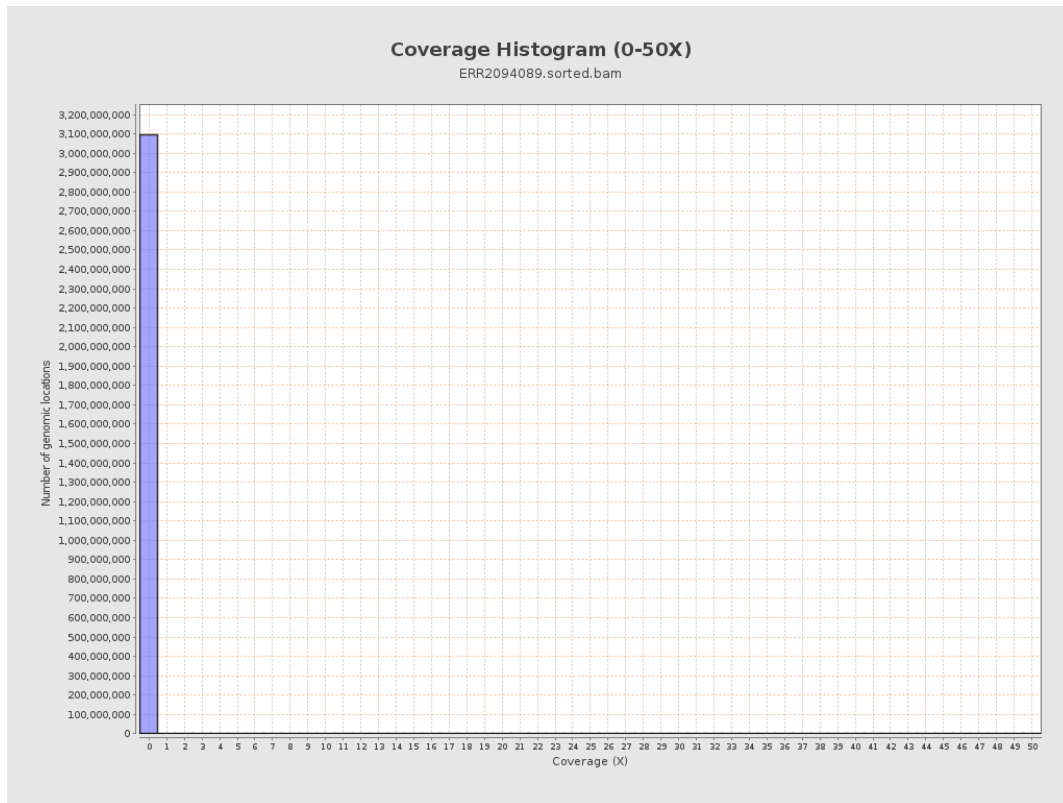
3. Results : Coverage across reference



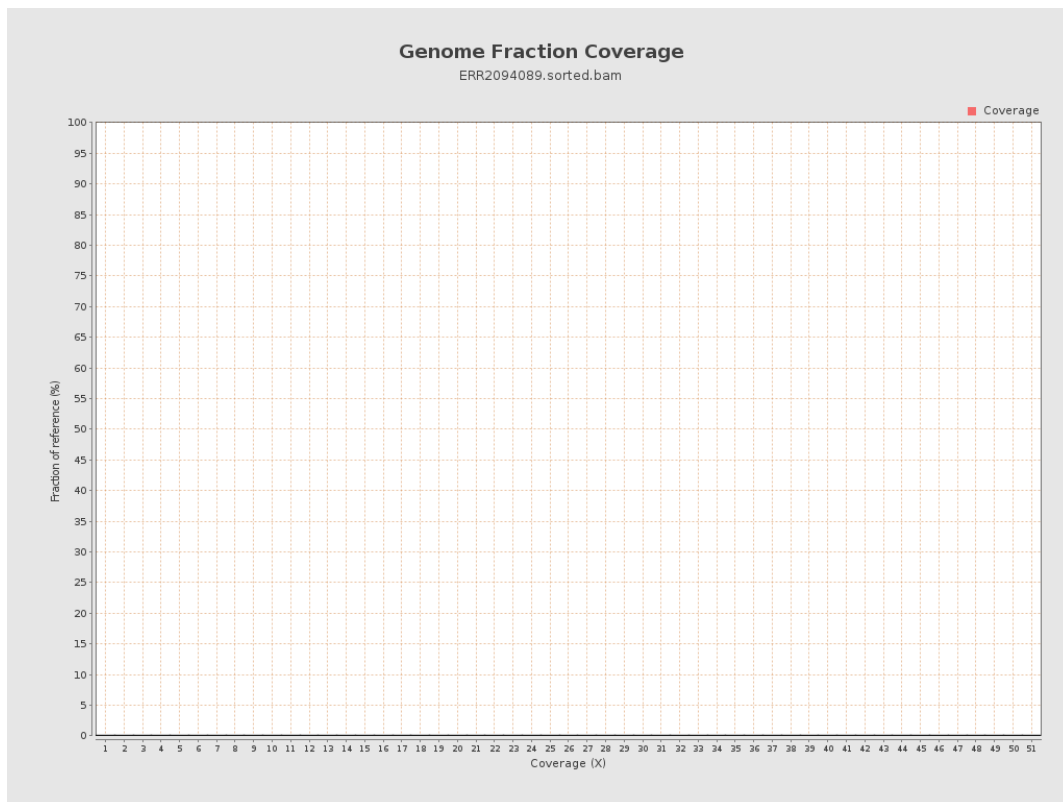
4. Results : Coverage Histogram



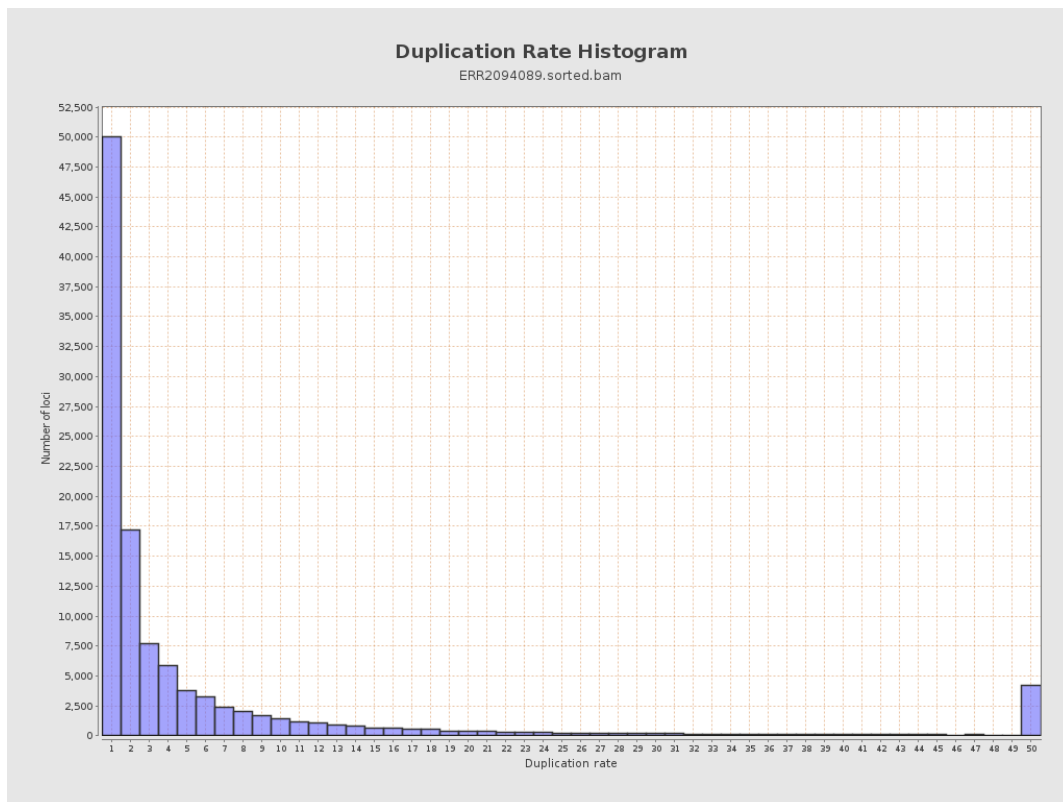
5. Results : Coverage Histogram (0-50X)



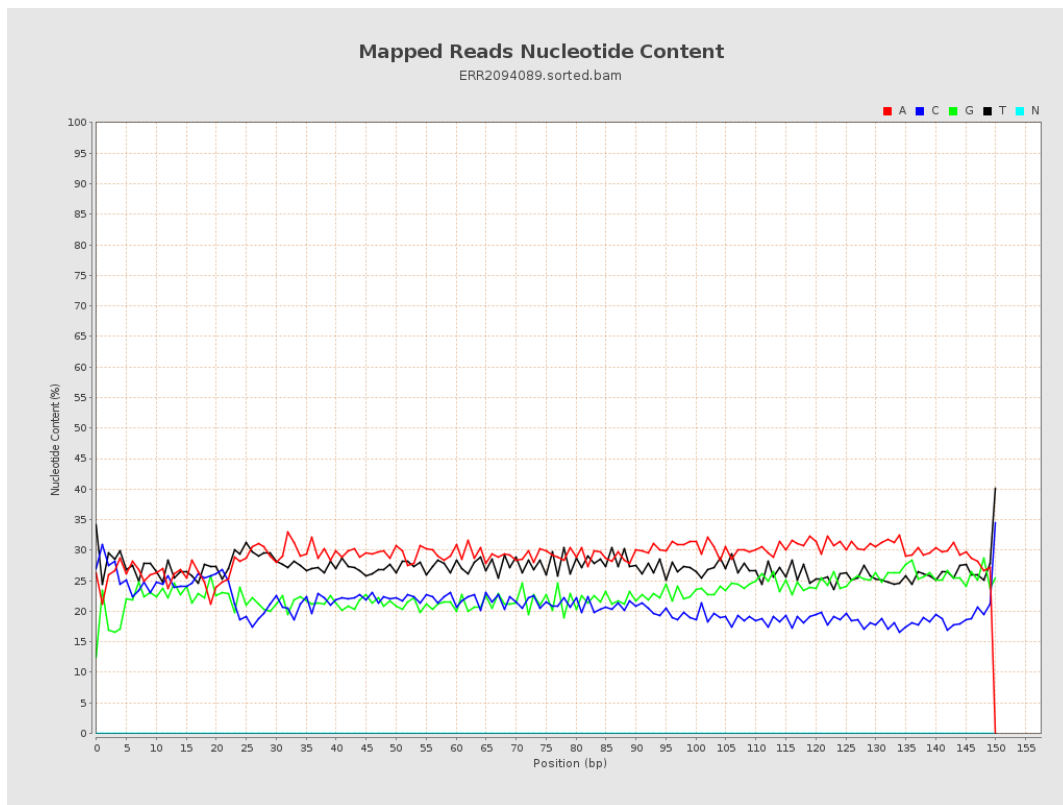
6. Results : Genome Fraction Coverage



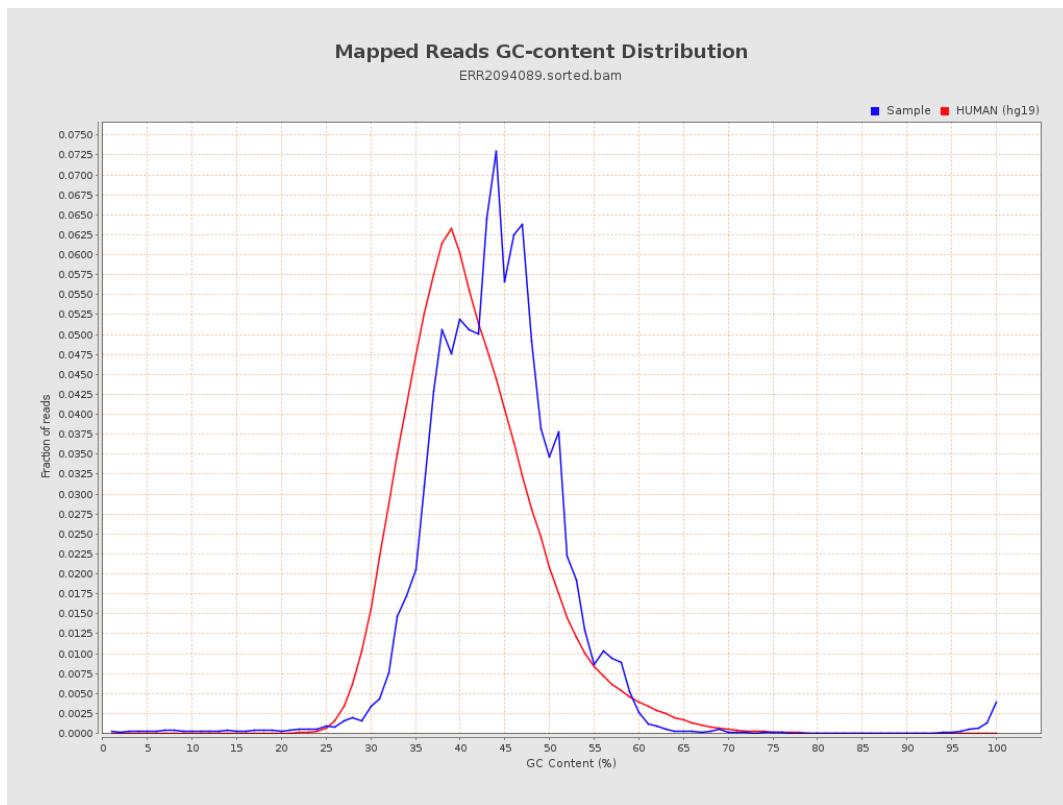
7. Results : Duplication Rate Histogram



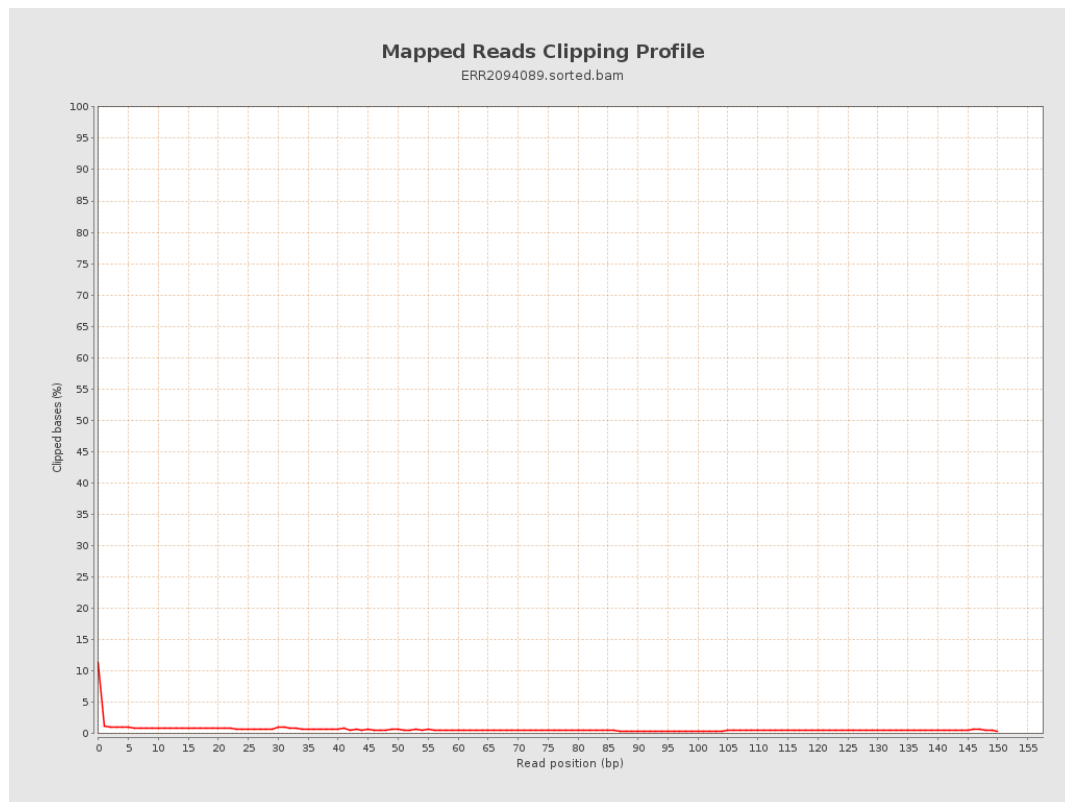
8. Results : Mapped Reads Nucleotide Content



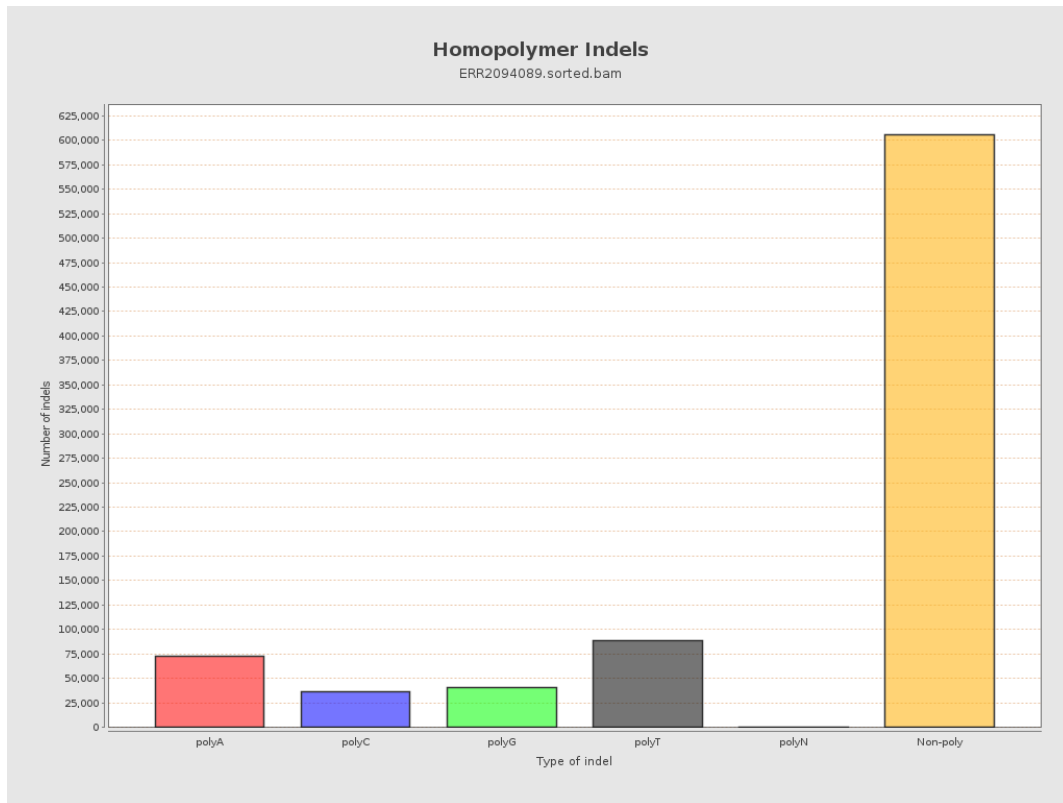
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



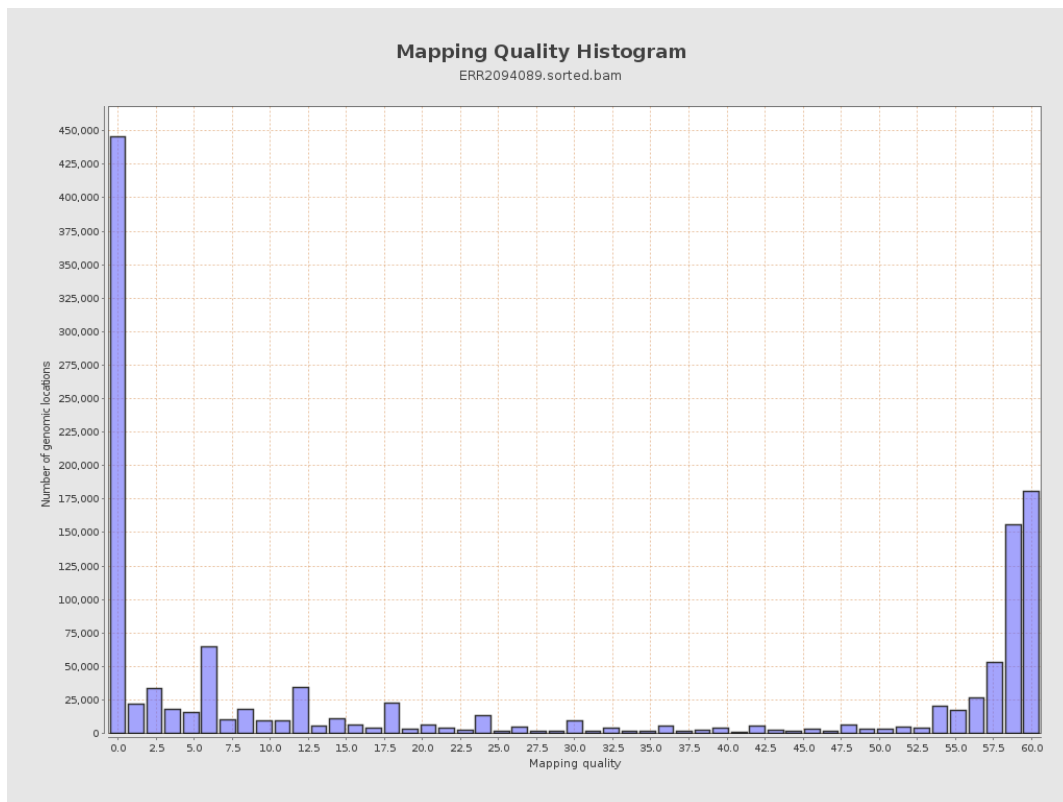
11. Results : Homopolymer Indels



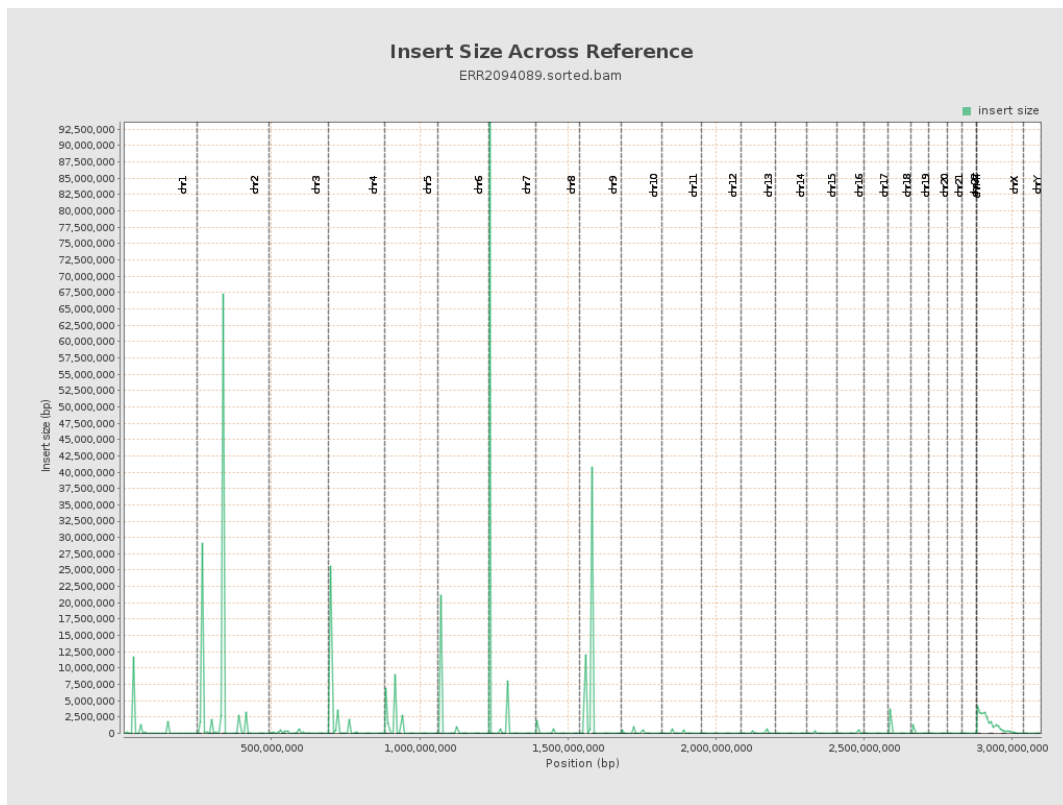
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

