Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:23:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094138.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_ERR2094138 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094138_1.fastq.gz ERR2094138_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:23:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,596
Mapped reads	587,891 / 97.4%
Unmapped reads	15,705 / 2.6%
Mapped paired reads	587,891 / 97.4%
Mapped reads, first in pair	294,869 / 48.85%
Mapped reads, second in pair	293,022 / 48.55%
Mapped reads, both in pair	585,476 / 97%
Mapped reads, singletons	2,415 / 0.4%
Secondary alignments	0
Supplementary alignments	28,804 / 4.77%
Read min/max/mean length	30 / 151 / 150.9
Duplicated reads (estimated)	608,087 / 100.74%
Duplication rate	41.26%
Clipped reads	158,398 / 26.24%

2.2. ACGT Content

Number/percentage of A's	25,478,255 / 29.97%
Number/percentage of C's	17,676,375 / 20.79%
Number/percentage of T's	23,842,465 / 28.05%
Number/percentage of G's	18,016,391 / 21.19%
Number/percentage of N's	984 / 0%

GC Percentage	41.98%

2.3. Coverage

Mean	0.0275
Standard Deviation	43.3572

2.4. Mapping Quality

Mean Mapping Quality	14.54

2.5. Insert size

Mean	18,736.8
Standard Deviation	1,461,331.74
P25/Median/P75	212 / 231 / 256

2.6. Mismatches and indels

General error rate	1.65%
Mismatches	1,345,710
Insertions	31,675
Mapped reads with at least one insertion	5.33%
Deletions	60,149
Mapped reads with at least one deletion	10.04%
Homopolymer indels	55.94%

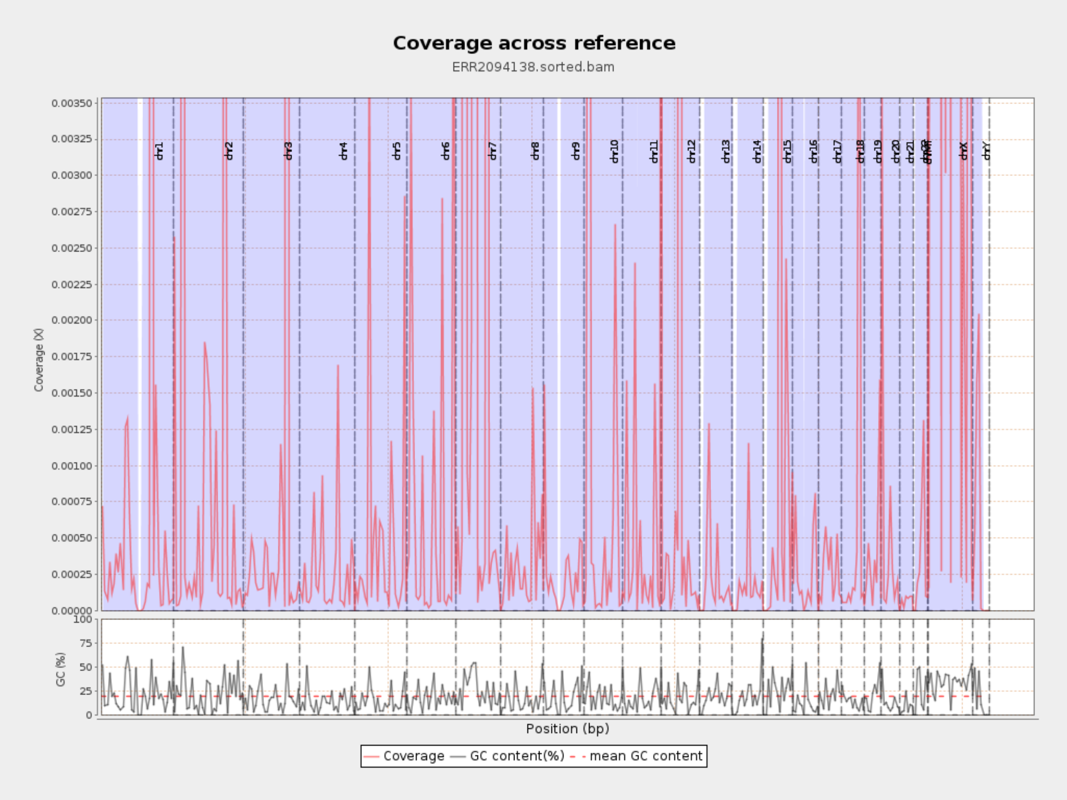
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

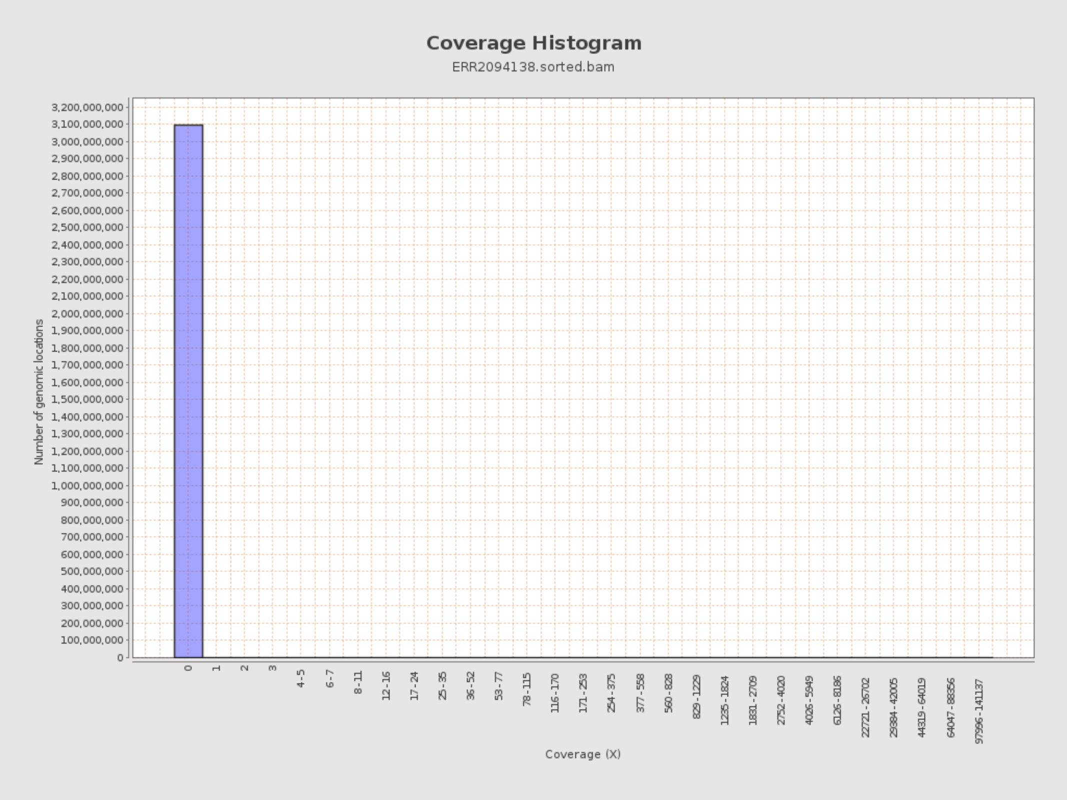
		bases	coverage	deviation
chr1	249250621	600528	0.0024	2.6657
chr2	243199373	430425	0.0018	1.03
chr3	198022430	803792	0.0041	4.17
chr4	191154276	54040	0.0003	0.1528
chr5	180915260	99721	0.0006	0.2437
chr6	171115067	144839	0.0008	0.5071
chr7	159138663	1132370	0.0071	3.4258
chr8	146364022	48787	0.0003	0.1547
chr9	141213431	36843	0.0003	0.0898
chr10	135534747	143137	0.0011	0.4071
chr11	135006516	70123	0.0005	0.1879
chr12	133851895	755323	0.0056	6.5055
chr13	115169878	23952	0.0002	0.0675
chr14	107349540	20102	0.0002	0.0499
chr15	102531392	201839	0.002	2.1918
chr16	90354753	23881	0.0003	0.103
chr17	81195210	21998	0.0003	0.0806
chr18	78077248	60439	0.0008	0.6306
chr19	59128983	24049	0.0004	0.1321
chr20	63025520	34142	0.0005	0.122
chr21	48129895	3384	0.0001	0.0218
chr22	51304566	20297	0.0004	0.1933
chrMT	16571	72819629	4,394.4016	17,931.3469
chrX	155270560	7560754	0.0487	31.9151

chrY	59373566	32613	0.0005	0.1709

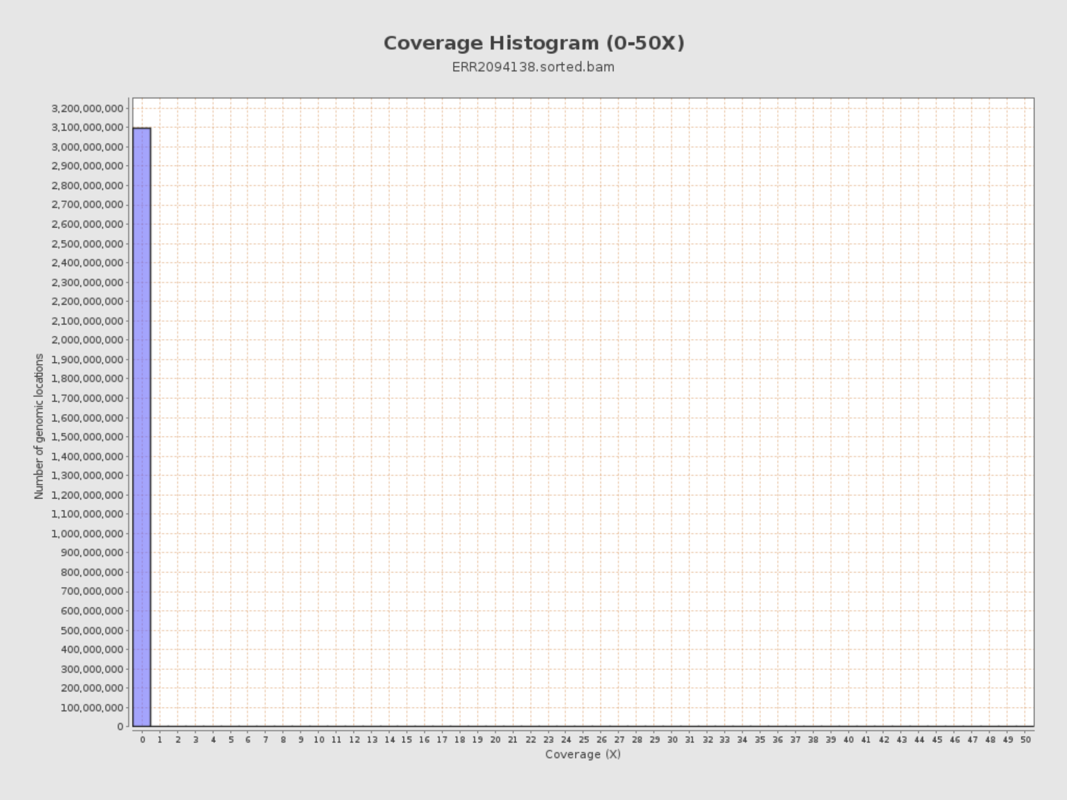
3. Results : Coverage across reference



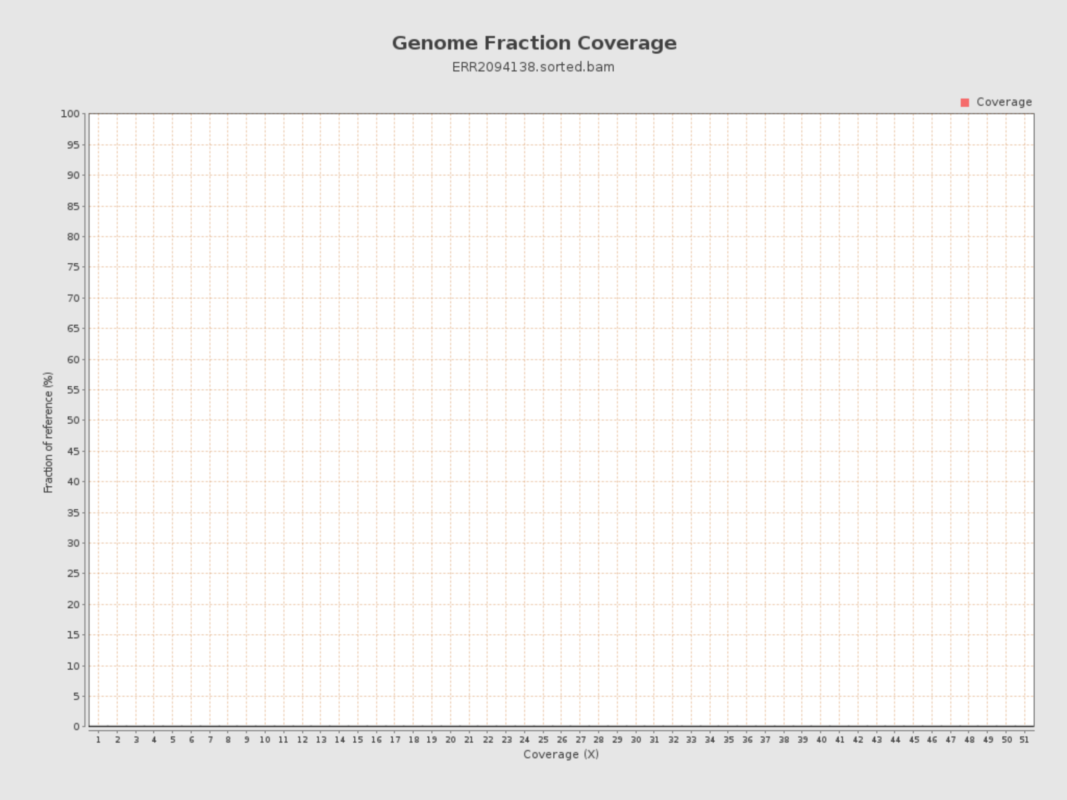
4. Results : Coverage Histogram



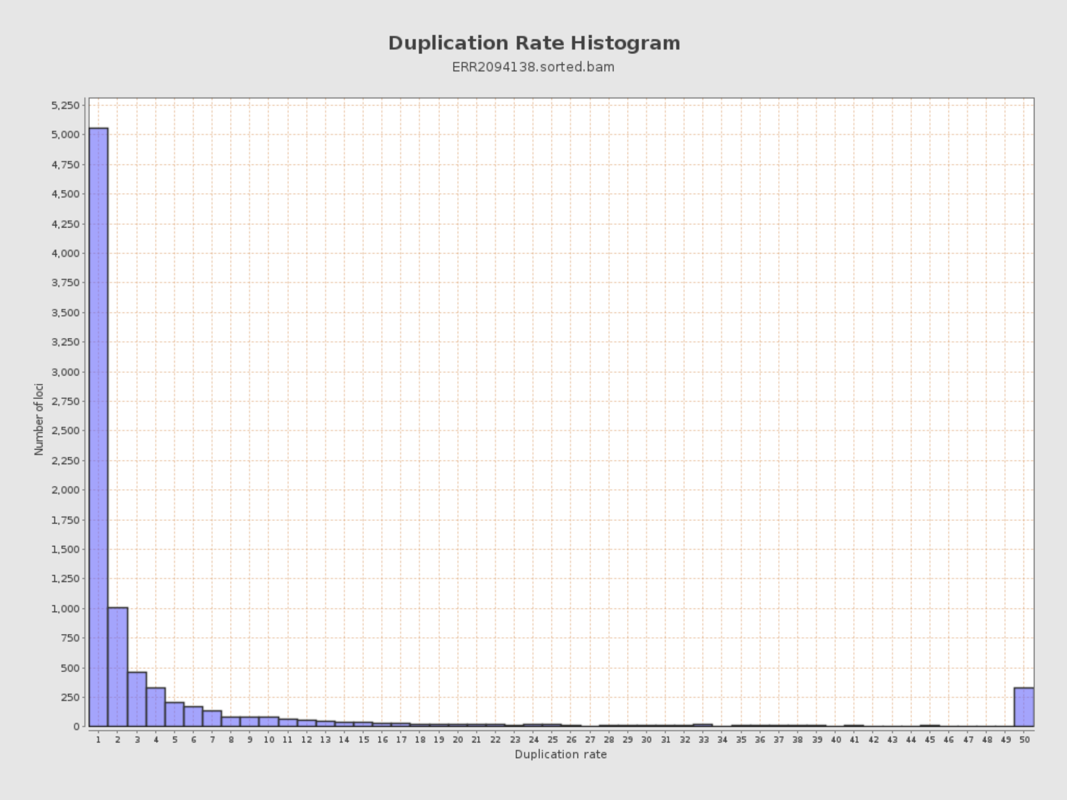
5. Results : Coverage Histogram (0-50X)



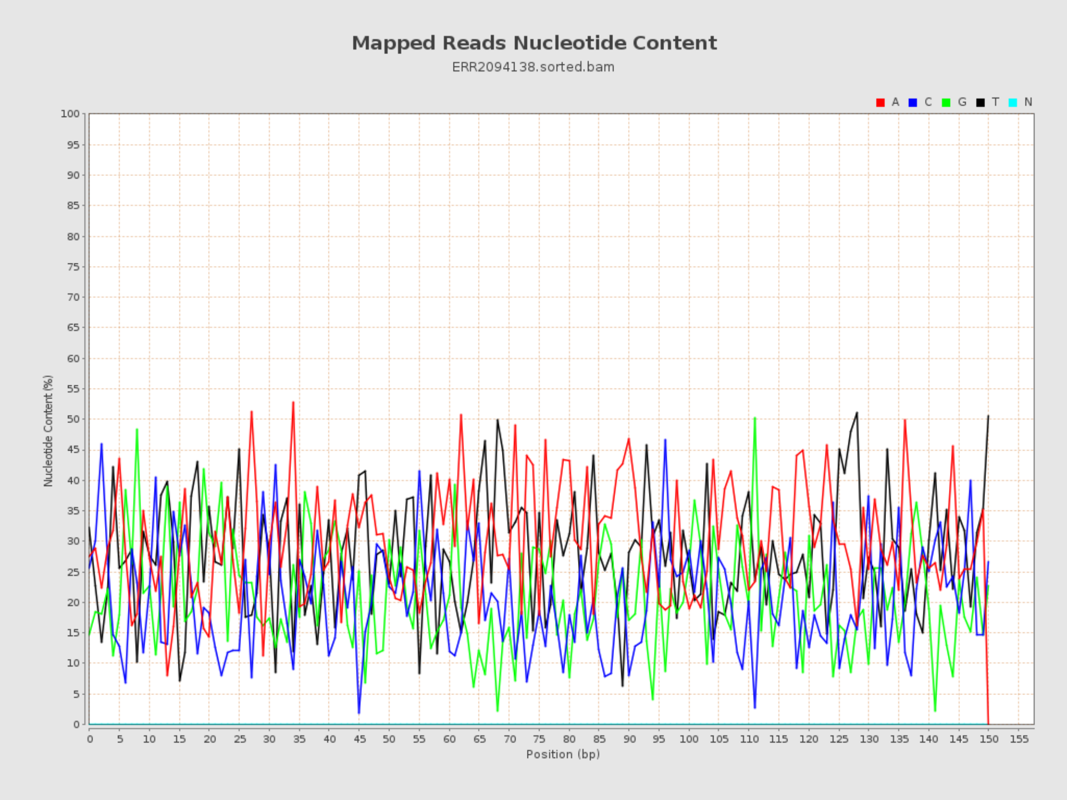
6. Results : Genome Fraction Coverage



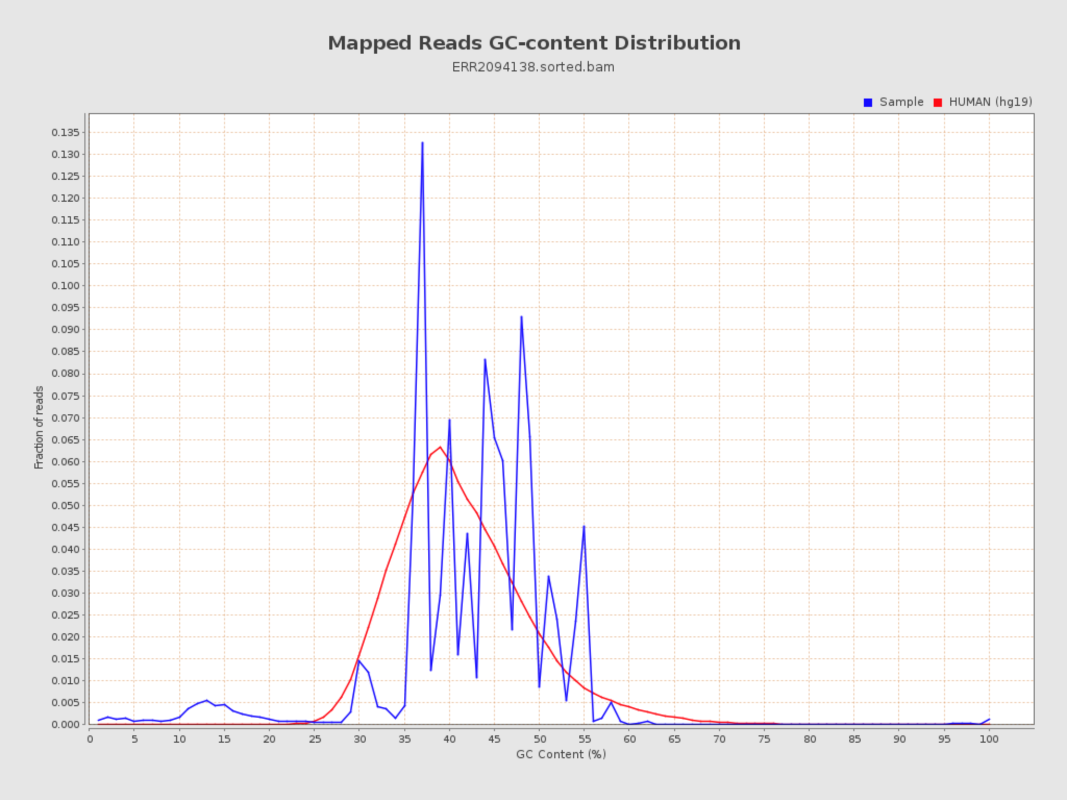
7. Results : Duplication Rate Histogram



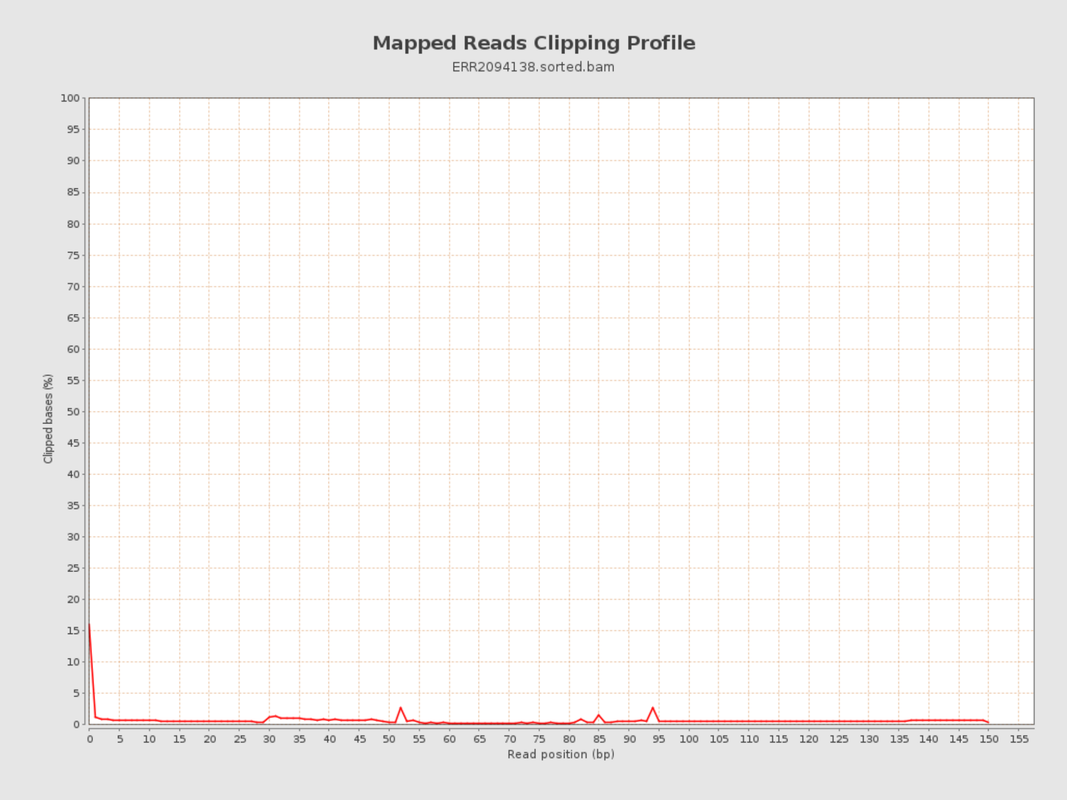
8. Results : Mapped Reads Nucleotide Content



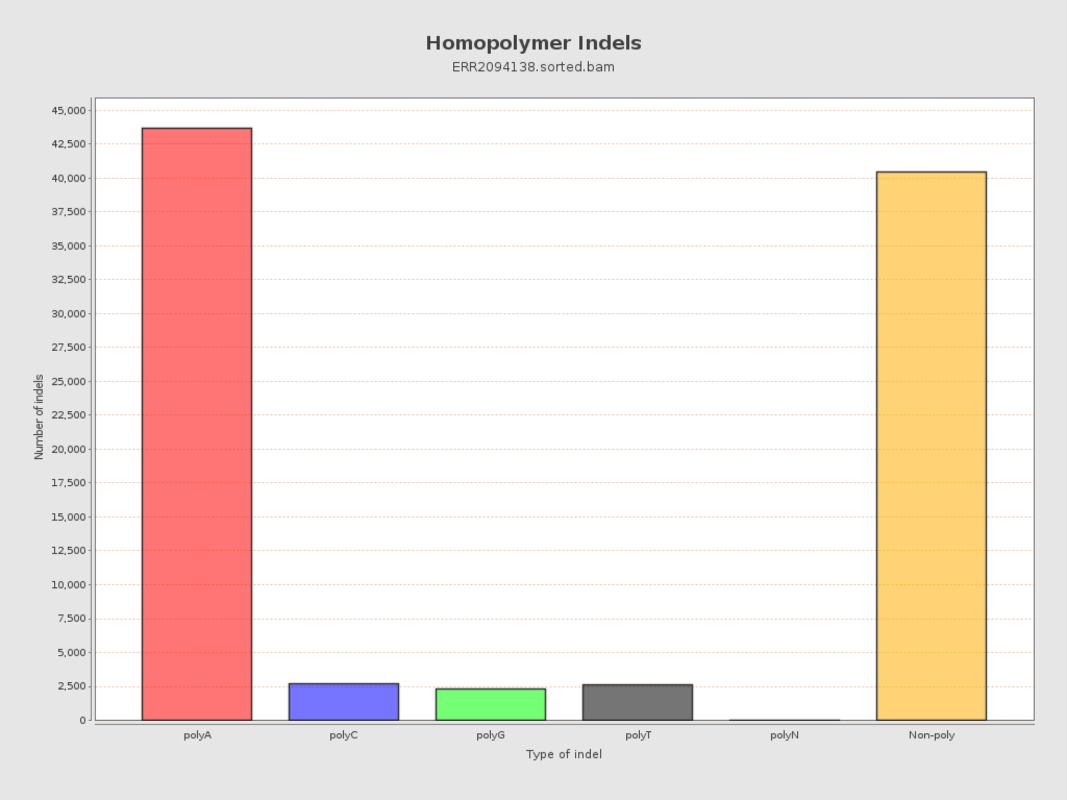
9. Results : Mapped Reads GC-content Distribution



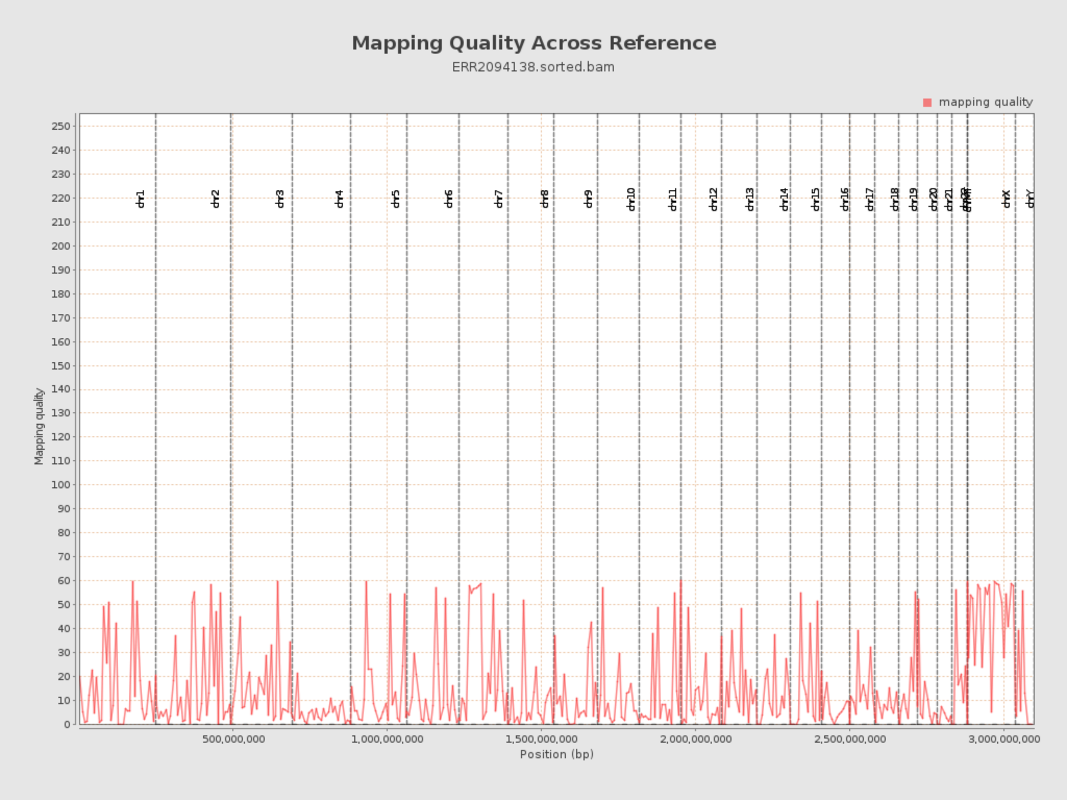
10. Results : Mapped Reads Clipping Profile



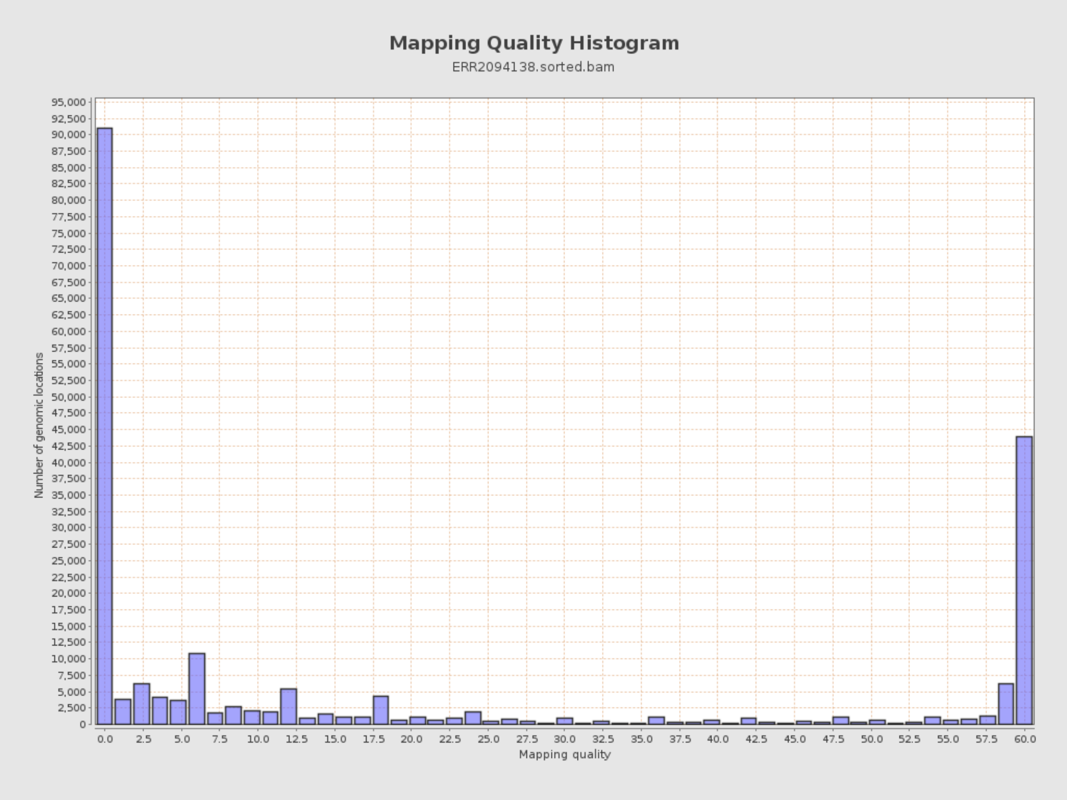
11. Results : Homopolymer Indels



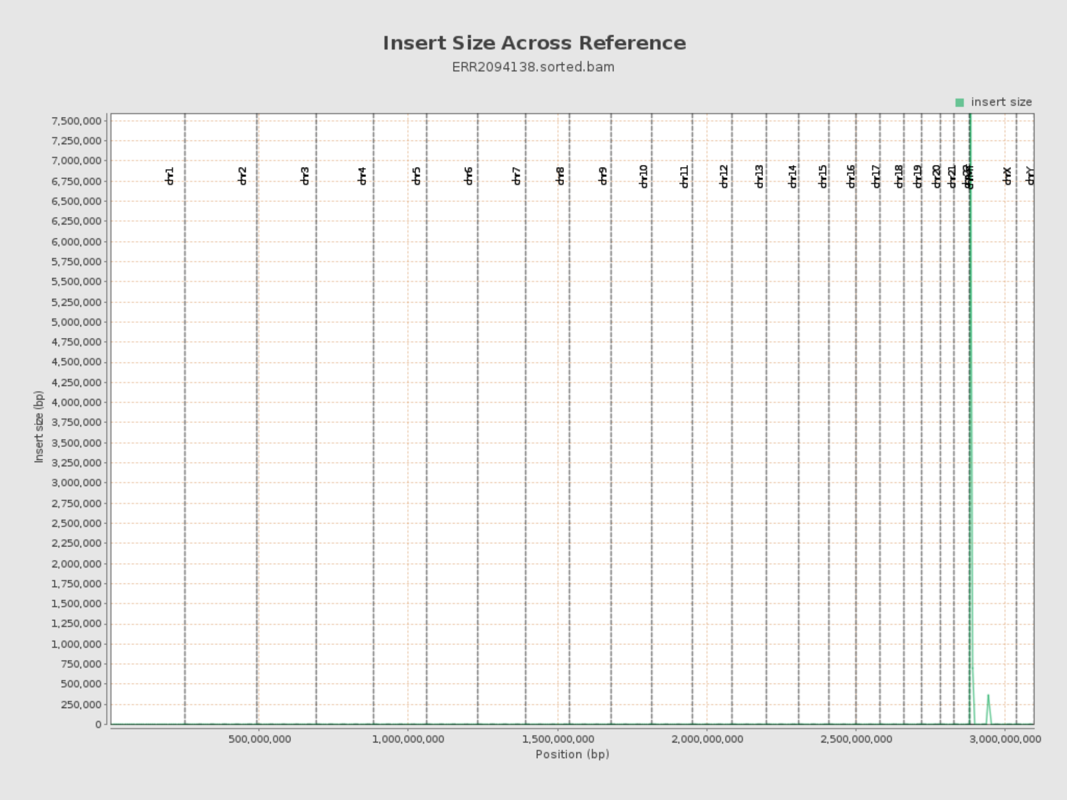
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram