Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:45:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094115.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_ERR2094115 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094115_1.fastq.gz ERR2094115_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:45:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	407,974
Mapped reads	390,325 / 95.67%
Unmapped reads	17,649 / 4.33%
Mapped paired reads	390,325 / 95.67%
Mapped reads, first in pair	196,277 / 48.11%
Mapped reads, second in pair	194,048 / 47.56%
Mapped reads, both in pair	386,984 / 94.86%
Mapped reads, singletons	3,341 / 0.82%
Secondary alignments	0
Supplementary alignments	31,533 / 7.73%
Read min/max/mean length	30 / 151 / 138.13
Duplicated reads (estimated)	376,943 / 92.39%
Duplication rate	53.48%
Clipped reads	213,984 / 52.45%

2.2. ACGT Content

Number/percentage of A's	13,561,419 / 28.86%
Number/percentage of C's	10,159,499 / 21.62%
Number/percentage of T's	12,634,451 / 26.88%
Number/percentage of G's	10,641,419 / 22.64%
Number/percentage of N's	505 / 0%

GC Percentage	44.26%

2.3. Coverage

Mean	0.0155
Standard Deviation	3.382

2.4. Mapping Quality

Mean Mapping Quality	39.64

2.5. Insert size

Mean	1,992,791.06
Standard Deviation	12,371,070.43
P25/Median/P75	112 / 141 / 170

2.6. Mismatches and indels

General error rate	3.45%
Mismatches	1,554,050
Insertions	30,262
Mapped reads with at least one insertion	7.63%
Deletions	123,297
Mapped reads with at least one deletion	30.66%
Homopolymer indels	28.84%

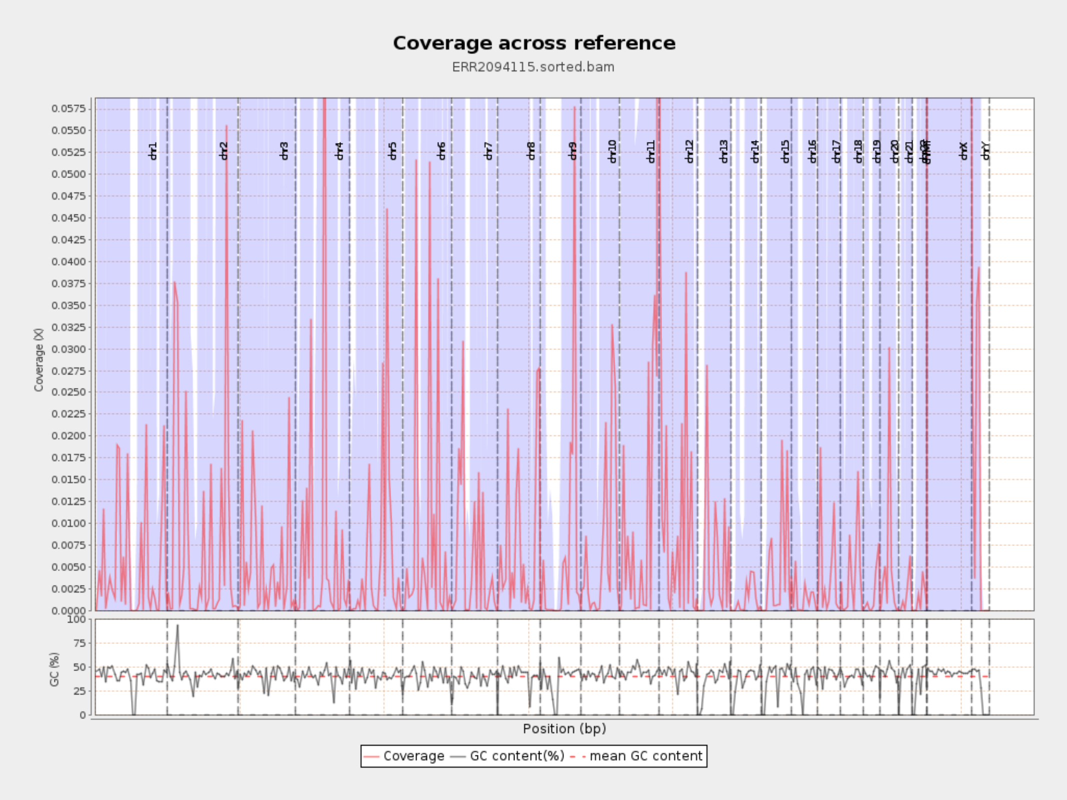
2.7. Chromosome stats

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

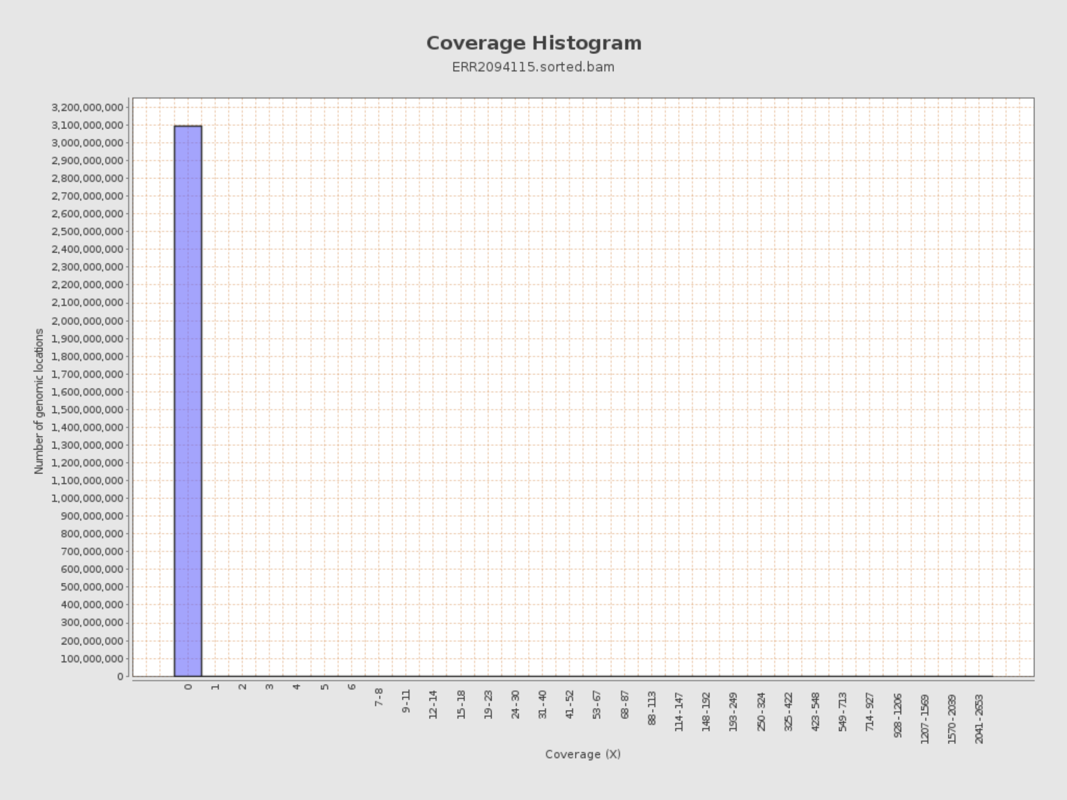
		bases	coverage	deviation
chr1	249250621	1275587	0.0051	1.8407
chr2	243199373	1928354	0.0079	2.6808
chr3	198022430	1050001	0.0053	1.7037
chr4	191154276	1531634	0.008	2.6039
chr5	180915260	1154651	0.0064	2.8796
chr6	171115067	1442381	0.0084	3.1204
chr7	159138663	923449	0.0058	2.0032
chr8	146364022	1080500	0.0074	2.1045
chr9	141213431	912430	0.0065	2.5273
chr10	135534747	950148	0.007	2.0971
chr11	135006516	1713129	0.0127	3.9987
chr12	133851895	1407556	0.0105	2.924
chr13	115169878	609070	0.0053	1.6582
chr14	107349540	131549	0.0012	0.4679
chr15	102531392	462862	0.0045	1.2959
chr16	90354753	142215	0.0016	0.4392
chr17	81195210	345026	0.0042	1.144
chr18	78077248	323936	0.0041	1.2745
chr19	59128983	111608	0.0019	0.5499
chr20	63025520	352089	0.0056	2.0632
chr21	48129895	84569	0.0018	0.3819
chr22	51304566	64994	0.0013	0.3016
chrMT	16571	76476	4.6151	29.7278
chrX	155270560	29044120	0.1871	11.4019

chrY	59373566	739311	0.0125	2.6739

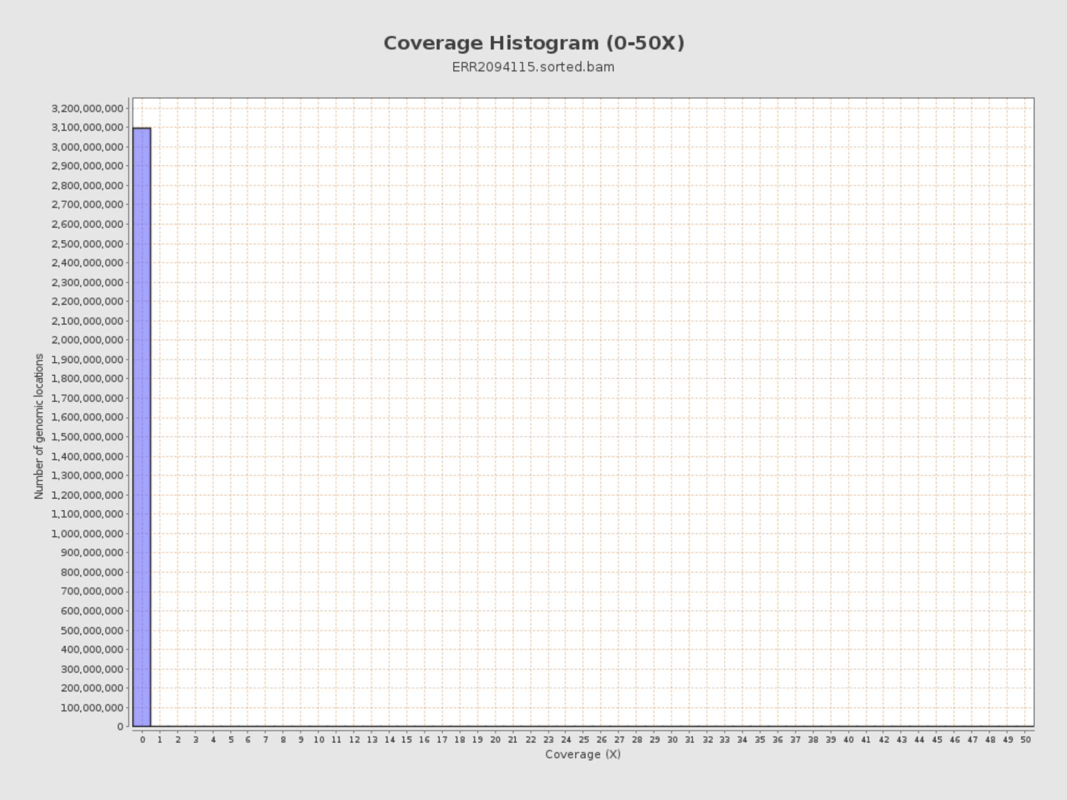
3. Results : Coverage across reference



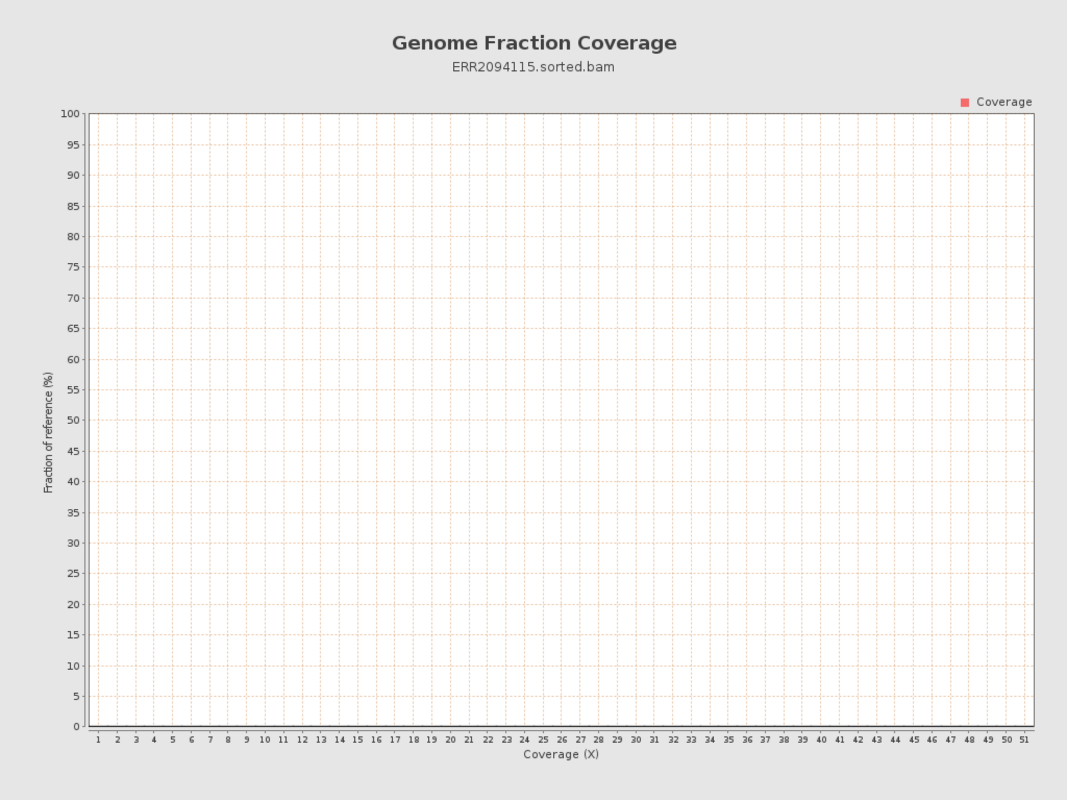
4. Results : Coverage Histogram



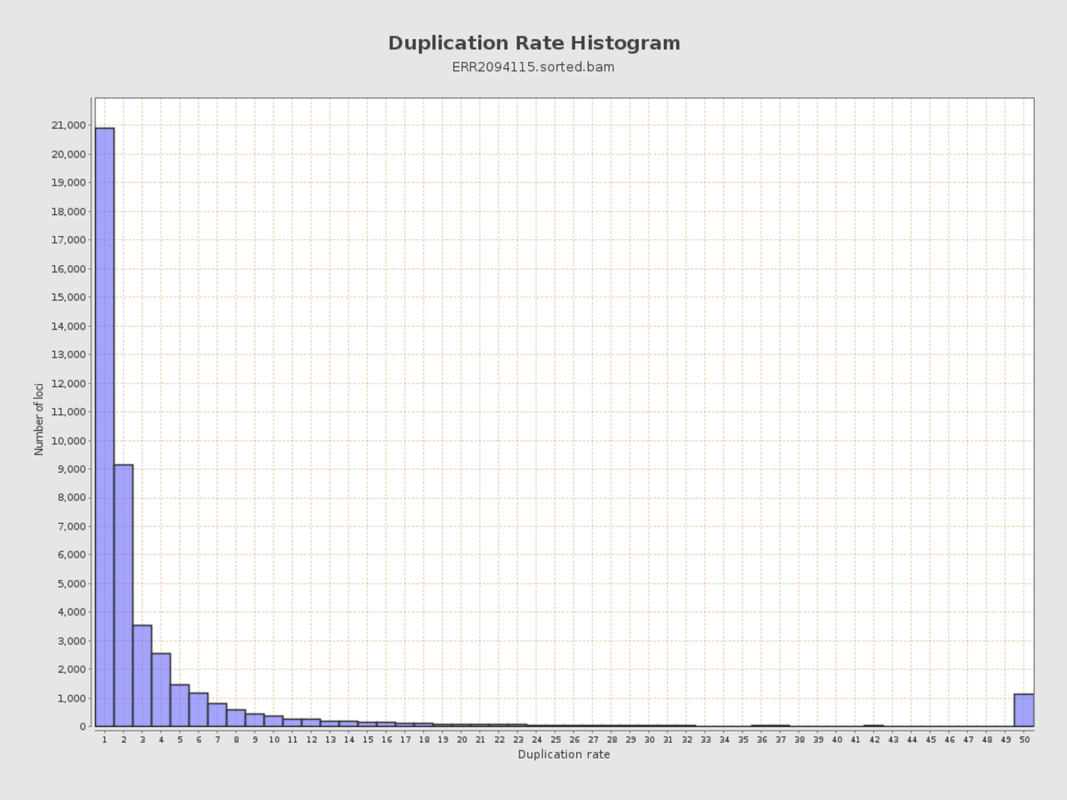
5. Results : Coverage Histogram (0-50X)



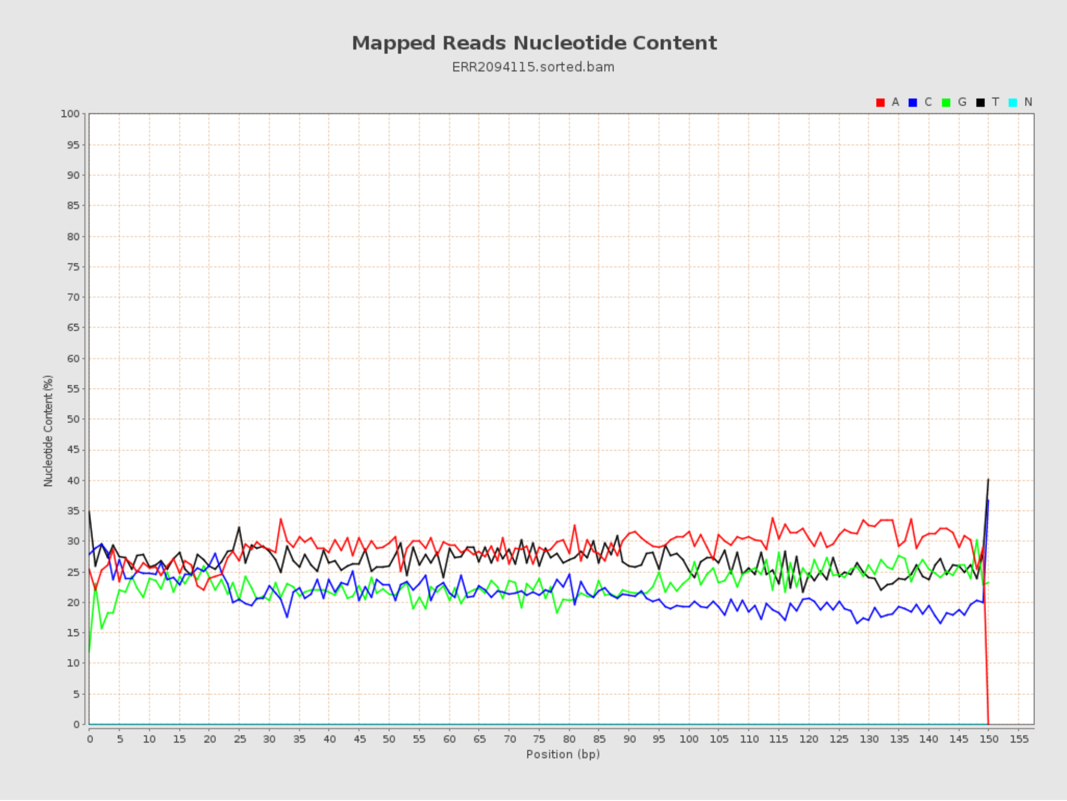
6. Results : Genome Fraction Coverage



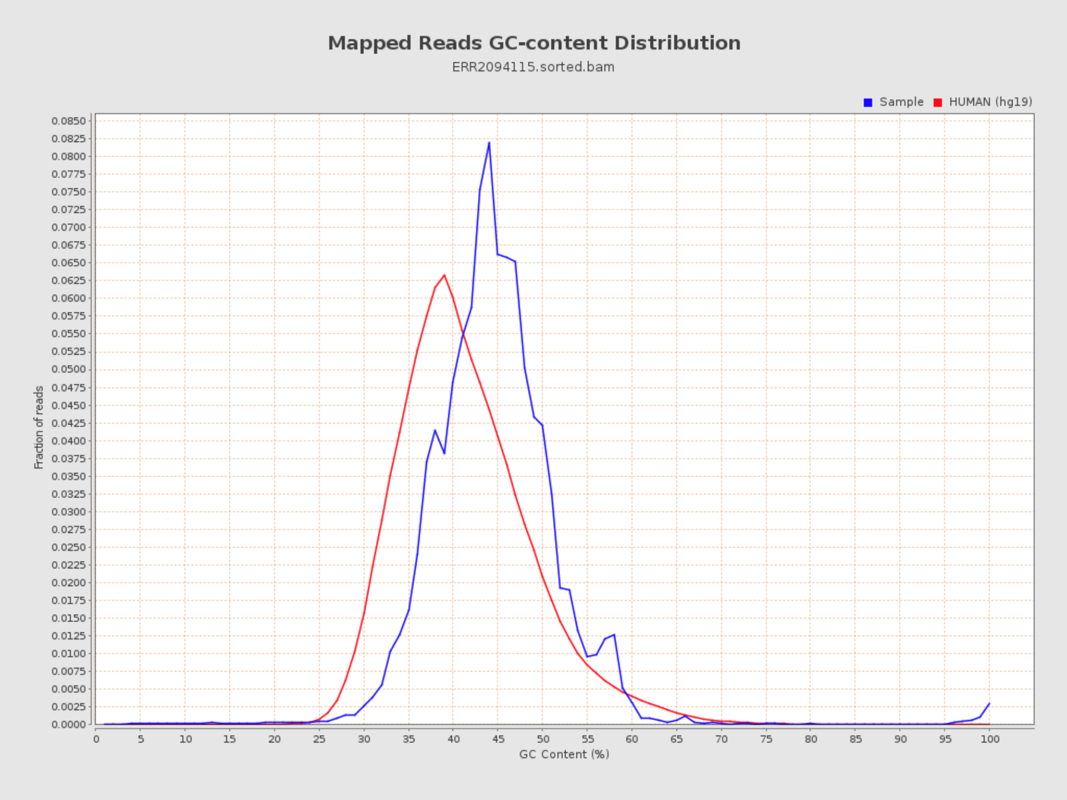
7. Results : Duplication Rate Histogram



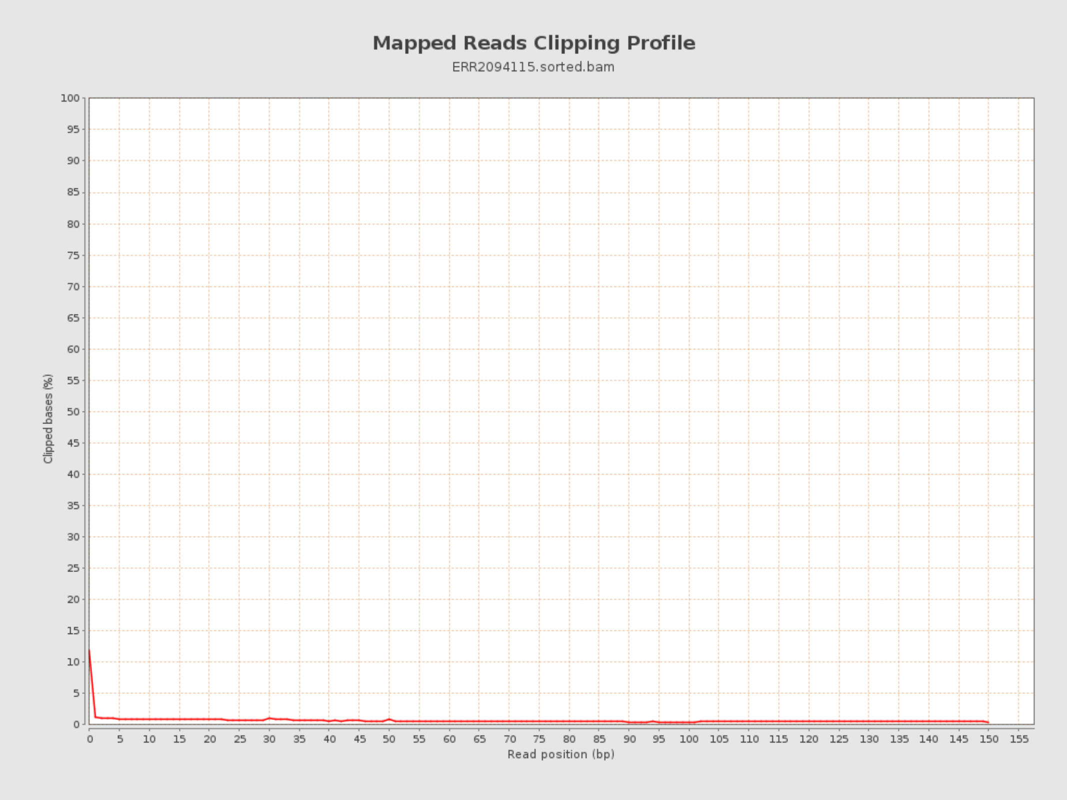
8. Results : Mapped Reads Nucleotide Content



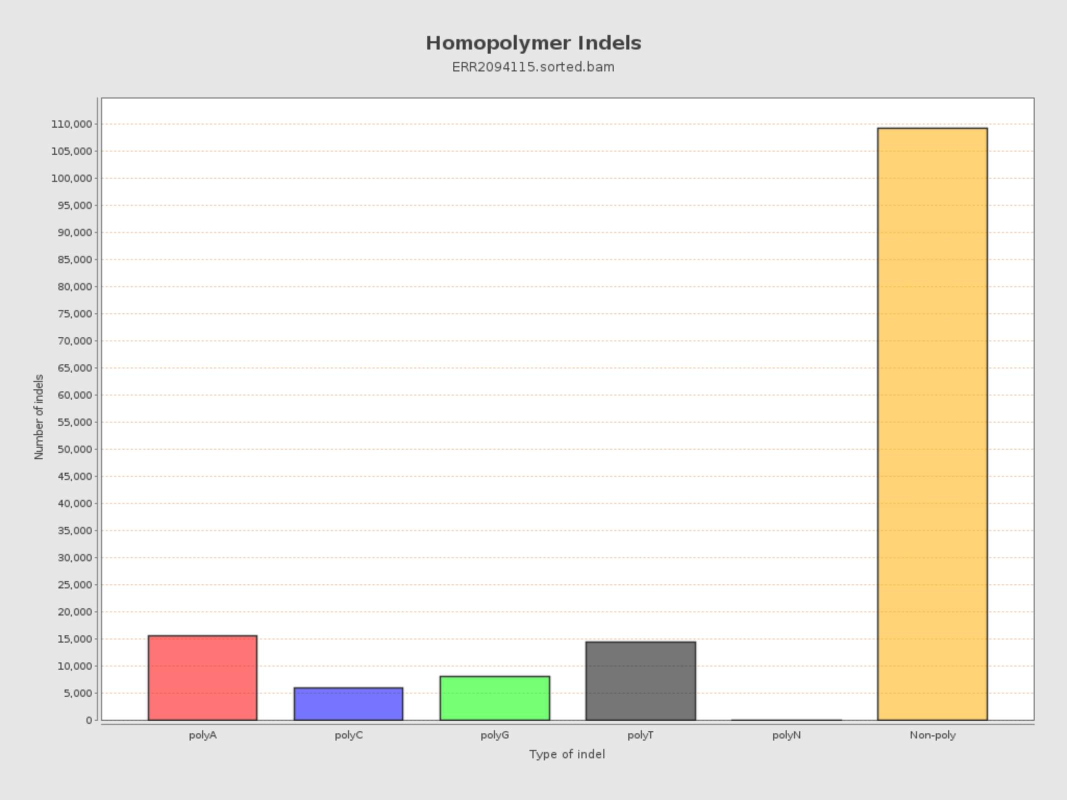
9. Results : Mapped Reads GC-content Distribution



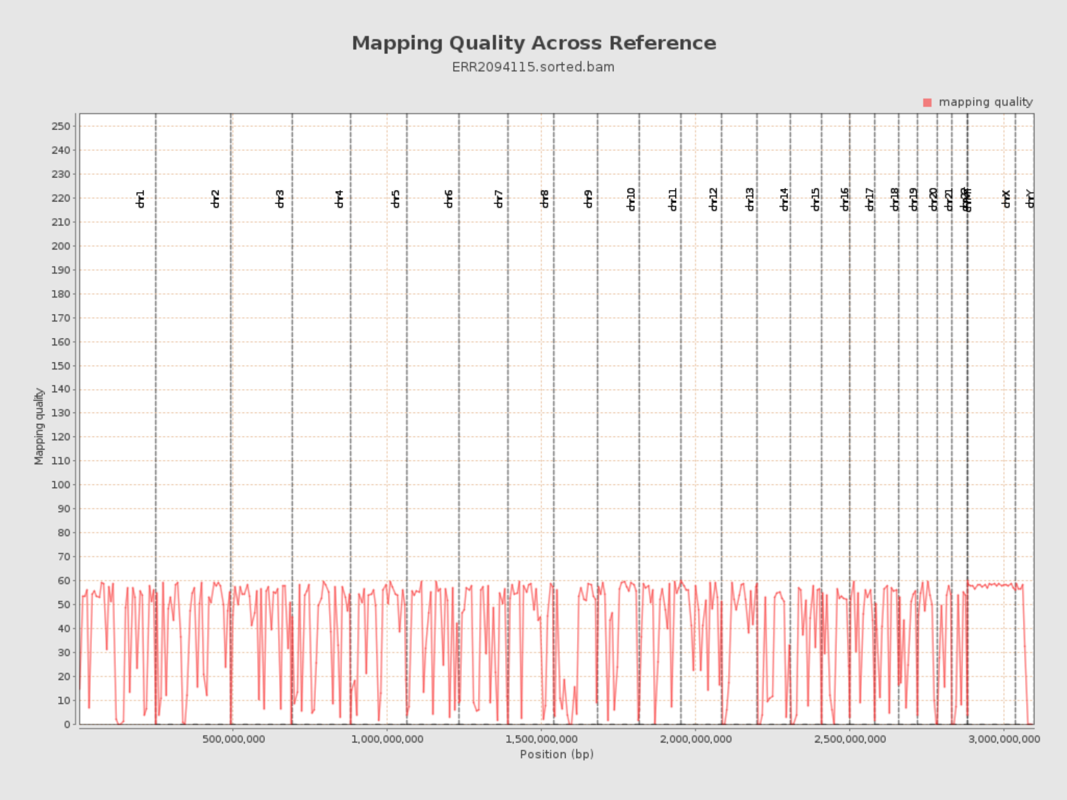
10. Results : Mapped Reads Clipping Profile



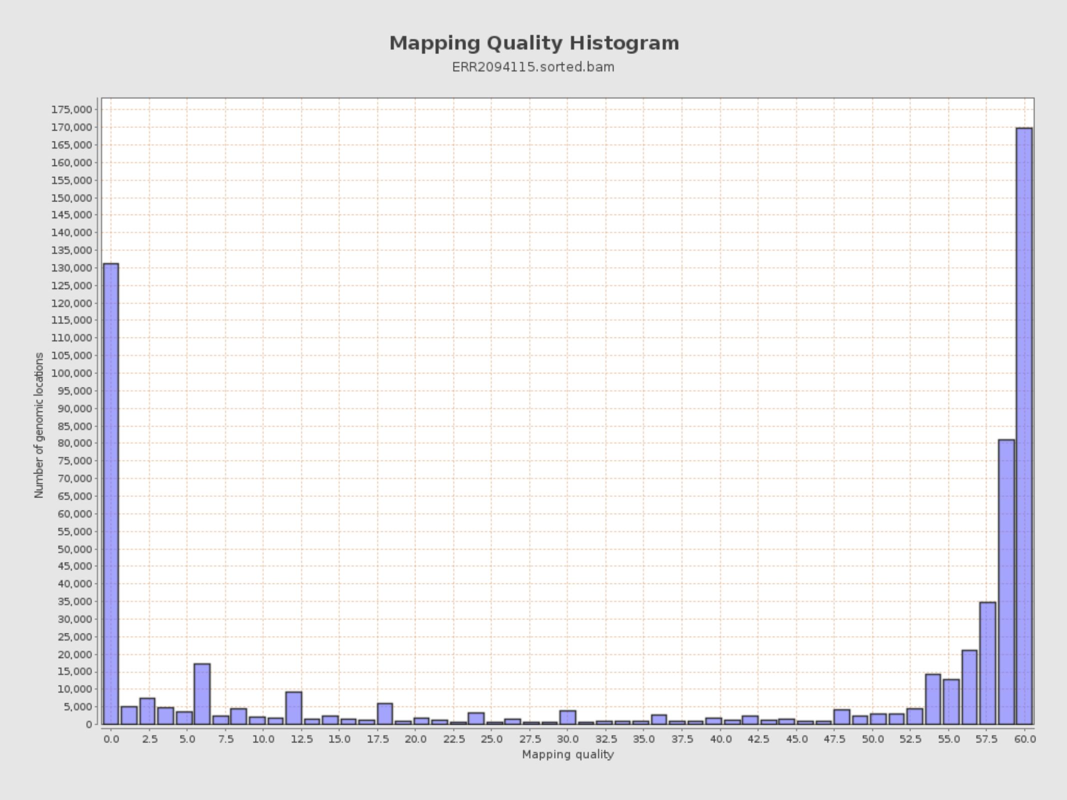
11. Results : Homopolymer Indels



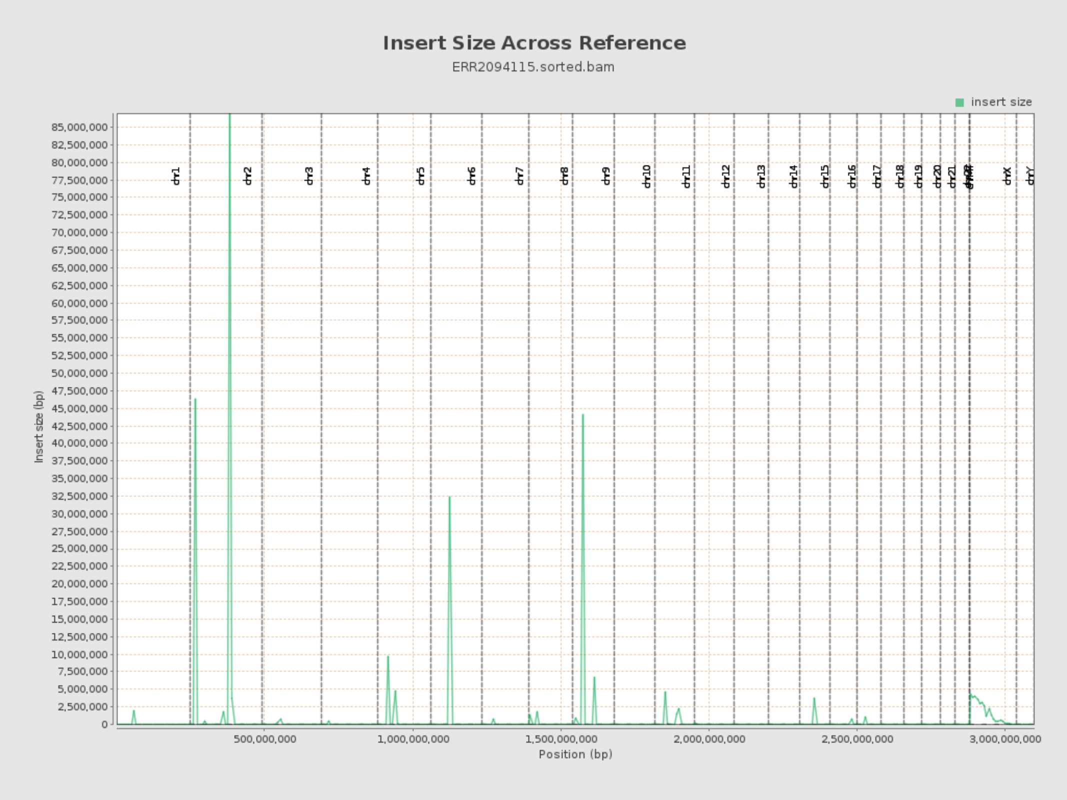
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram