Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 05:15:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094148.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_ERR2094148 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094148_1.fastq.gz ERR2094148_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 05:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	313,628
Mapped reads	292,214 / 93.17%
Unmapped reads	21,414 / 6.83%
Mapped paired reads	292,214 / 93.17%
Mapped reads, first in pair	146,878 / 46.83%
Mapped reads, second in pair	145,336 / 46.34%
Mapped reads, both in pair	289,462 / 92.29%
Mapped reads, singletons	2,752 / 0.88%
Secondary alignments	0
Supplementary alignments	20,839 / 6.64%
Read min/max/mean length	30 / 151 / 138.01
Duplicated reads (estimated)	265,859 / 84.77%
Duplication rate	48.38%
Clipped reads	148,678 / 47.41%

2.2. ACGT Content

Number/percentage of A's	10,028,674 / 27.52%
Number/percentage of C's	8,208,312 / 22.52%
Number/percentage of T's	9,507,239 / 26.09%
Number/percentage of G's	8,699,849 / 23.87%
Number/percentage of N's	393 / 0%

GC Percentage	46.39%

2.3. Coverage

Mean	0.012
Standard Deviation	2.2588

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Insert size

Mean	1,594,094.47
Standard Deviation	11,331,283.08
P25/Median/P75	122 / 156 / 193

2.6. Mismatches and indels

General error rate	3.85%
Mismatches	1,361,305
Insertions	22,027
Mapped reads with at least one insertion	7.4%
Deletions	106,587
Mapped reads with at least one deletion	35.33%
Homopolymer indels	29.43%

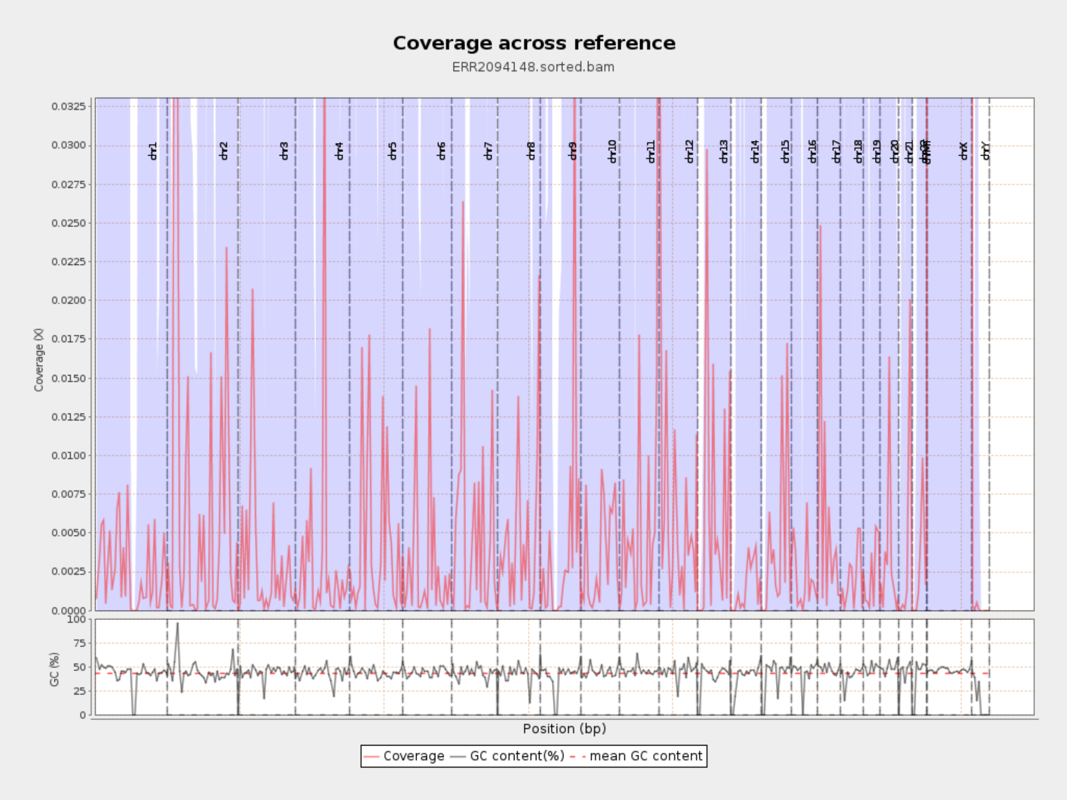
2.7. Chromosome stats

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

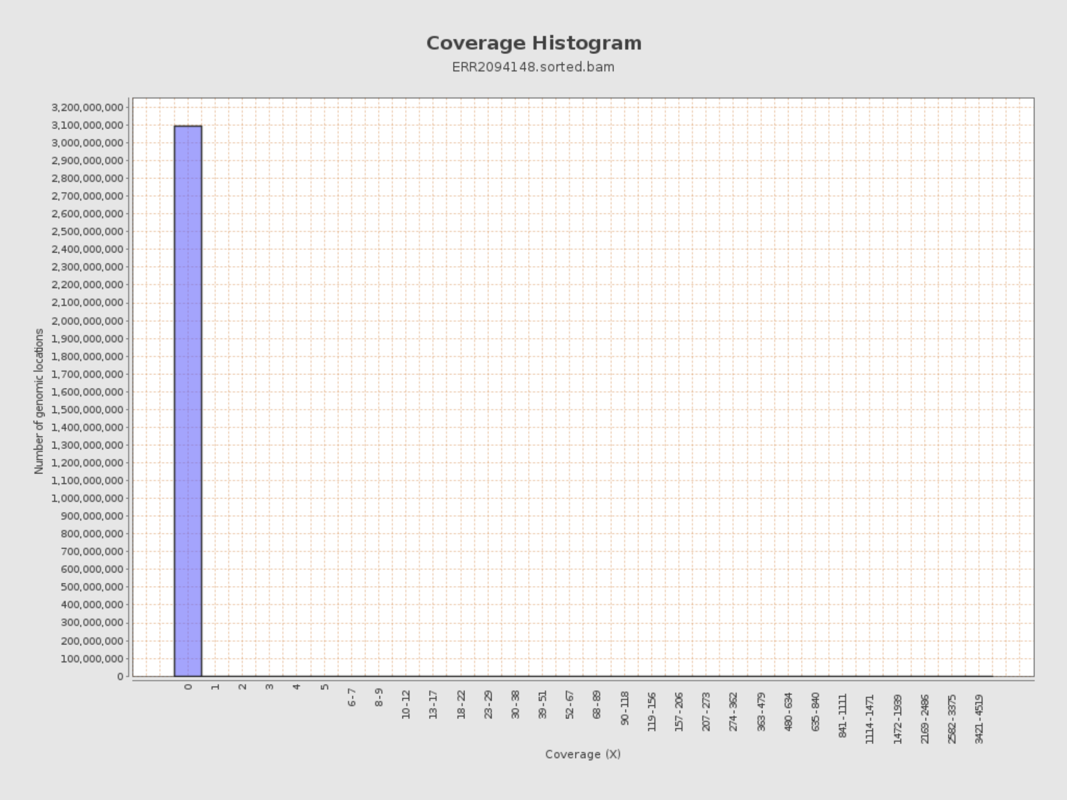
		bases	**coverage**	**deviation**
chr1	249250621	642661	0.0026	0.6727
chr2	243199373	1716332	0.0071	1.8169
chr3	198022430	613114	0.0031	0.7837
chr4	191154276	661110	0.0035	0.7988
chr5	180915260	798894	0.0044	1.2858
chr6	171115067	529175	0.0031	0.9523
chr7	159138663	817178	0.0051	1.1997
chr8	146364022	668361	0.0046	1.2164
chr9	141213431	602425	0.0043	1.4099
chr10	135534747	473599	0.0035	0.7384
chr11	135006516	687548	0.0051	1.1905
chr12	133851895	844934	0.0063	1.2825
chr13	115169878	714488	0.0062	1.3163
chr14	107349540	165898	0.0015	0.417
chr15	102531392	439331	0.0043	0.9355
chr16	90354753	199411	0.0022	0.5028
chr17	81195210	461959	0.0057	1.0843
chr18	78077248	169079	0.0022	0.4885
chr19	59128983	130790	0.0022	0.4947
chr20	63025520	222101	0.0035	1.1084
chr21	48129895	212418	0.0044	1.3467
chr22	51304566	143512	0.0028	0.615
chrMT	16571	2578000	155.573	619.7302
chrX	155270560	22760285	0.1466	5.9831

chrY	59373566	6600	0.0001	0.0355

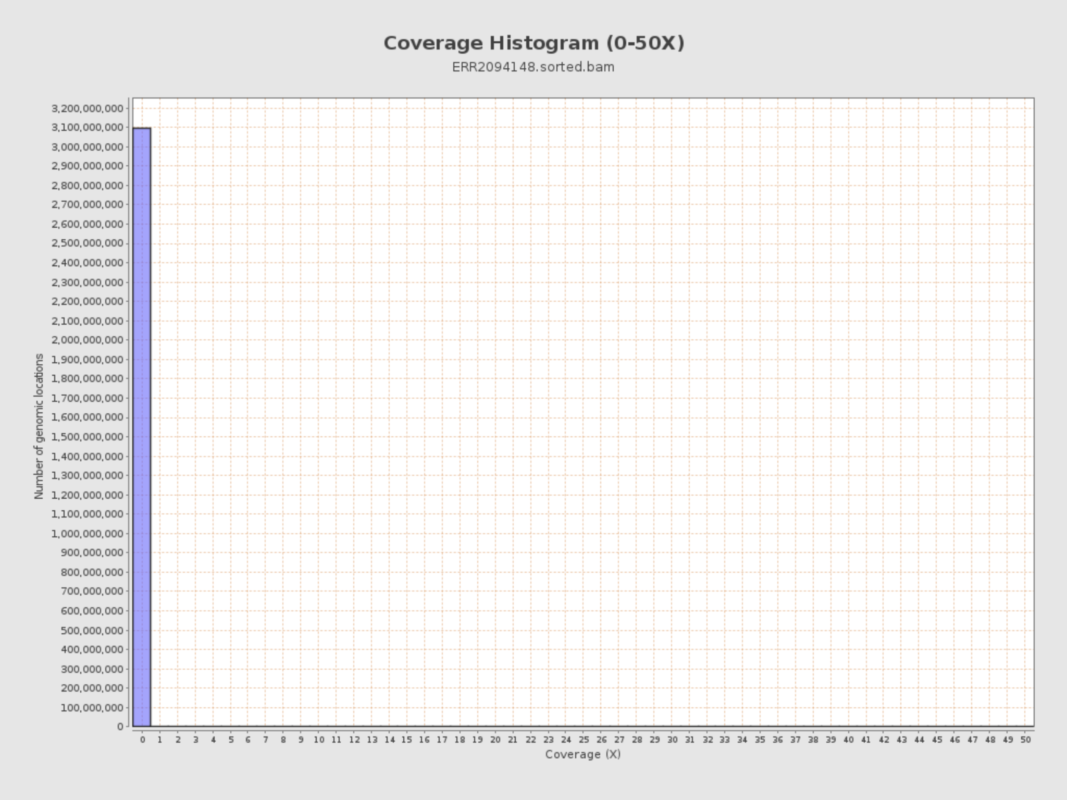
3. Results : Coverage across reference



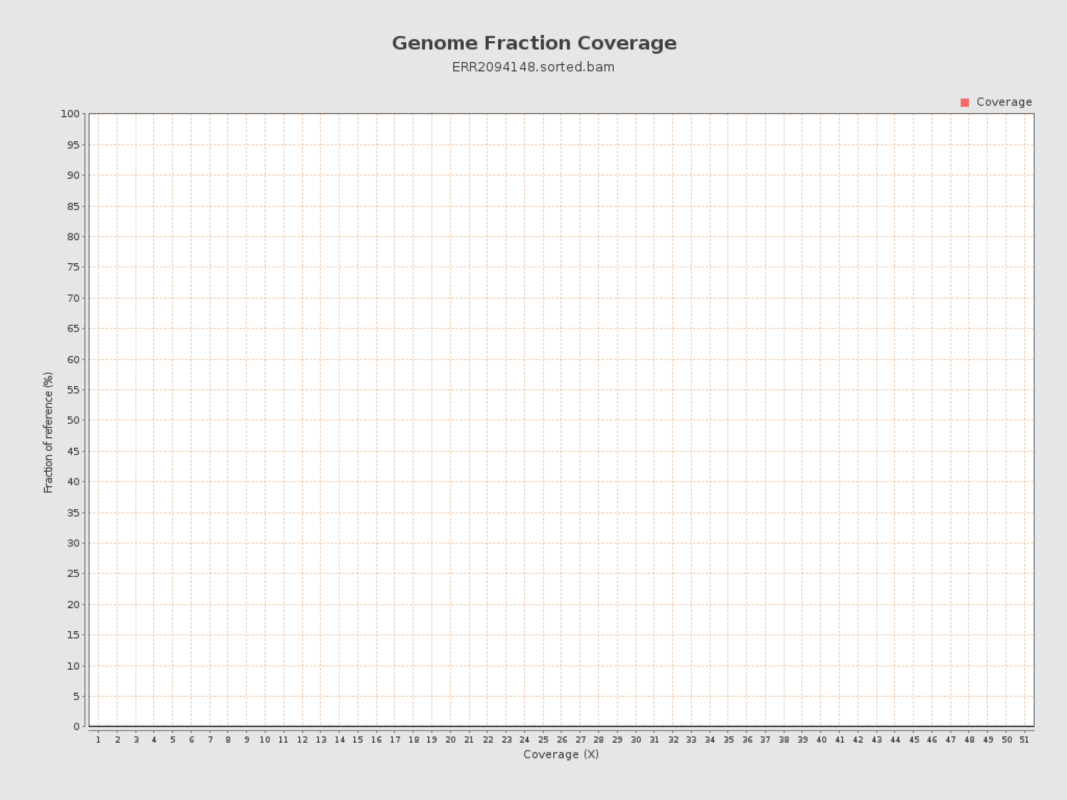
4. Results : Coverage Histogram



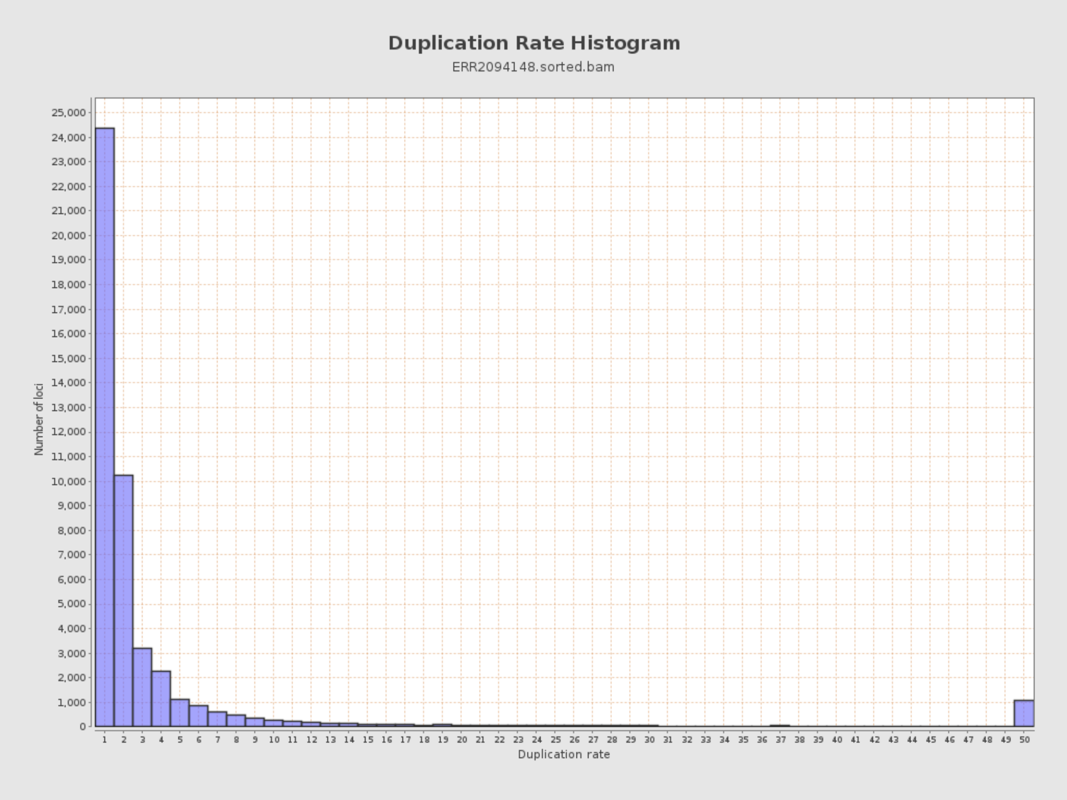
5. Results : Coverage Histogram (0-50X)



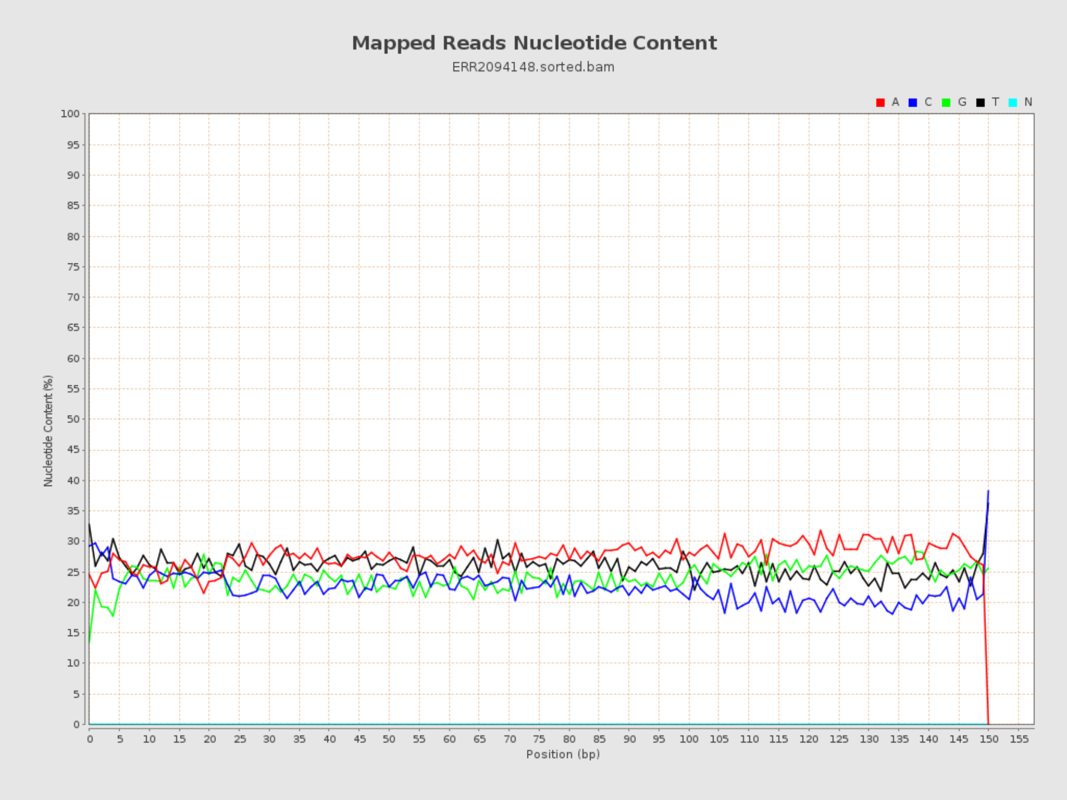
6. Results : Genome Fraction Coverage



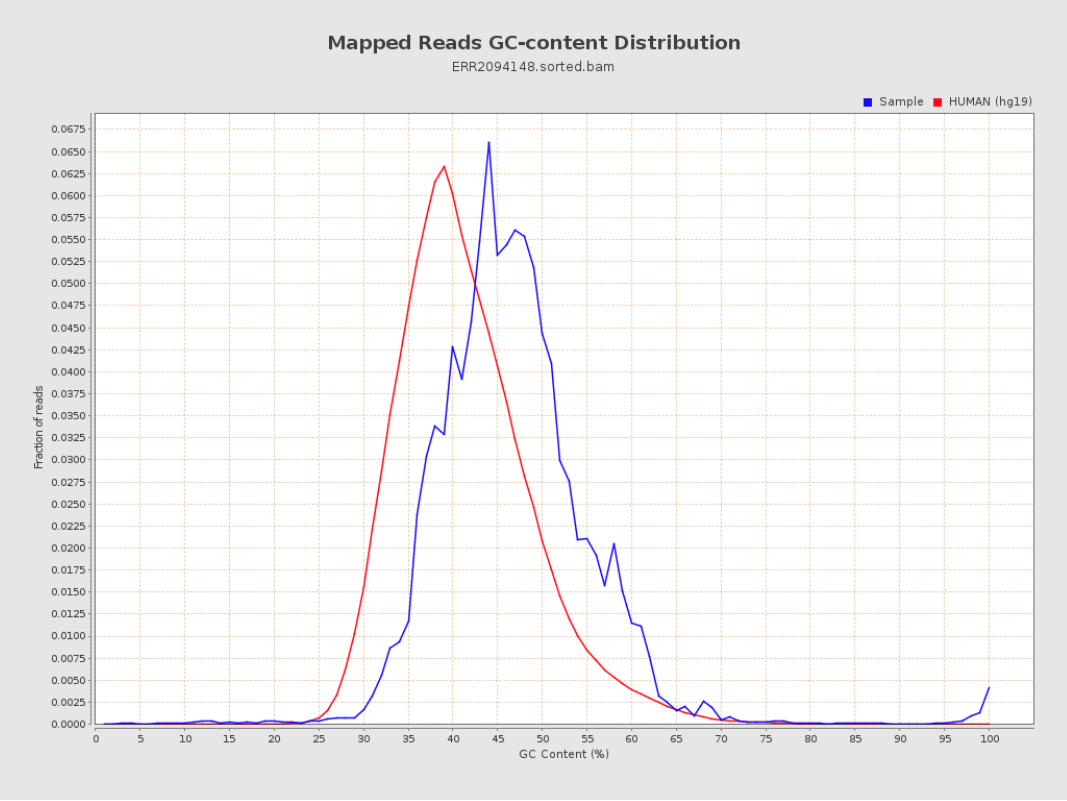
7. Results : Duplication Rate Histogram



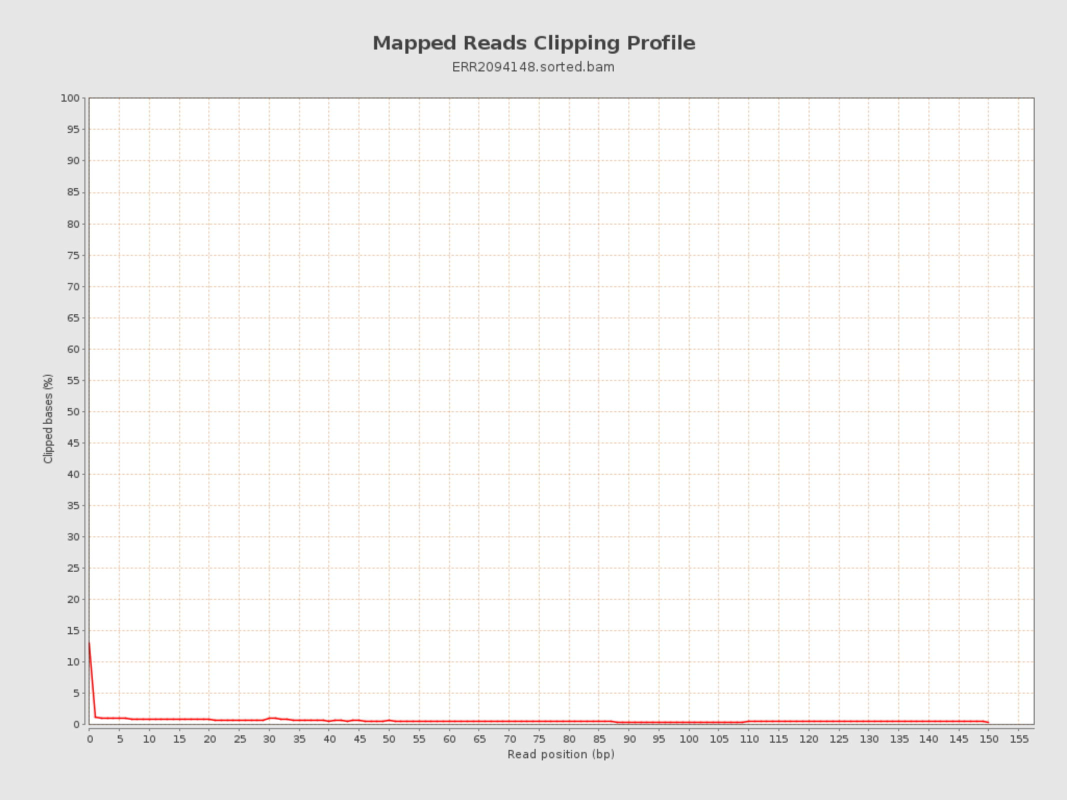
8. Results : Mapped Reads Nucleotide Content



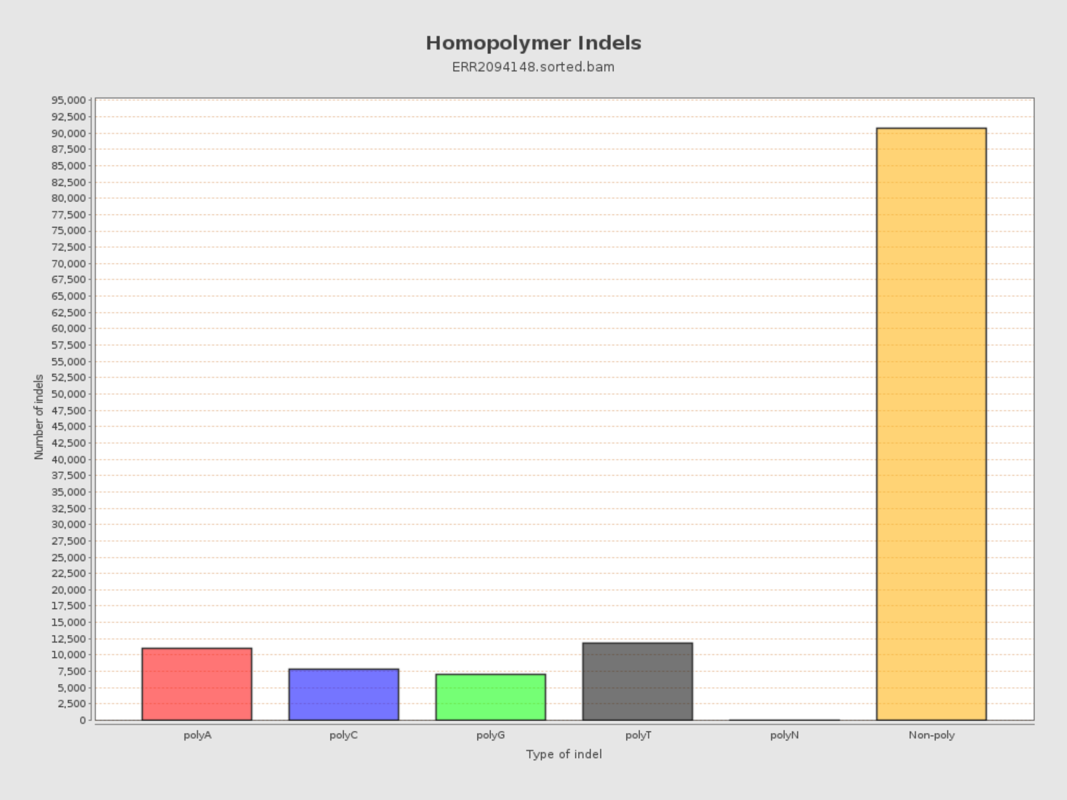
9. Results : Mapped Reads GC-content Distribution



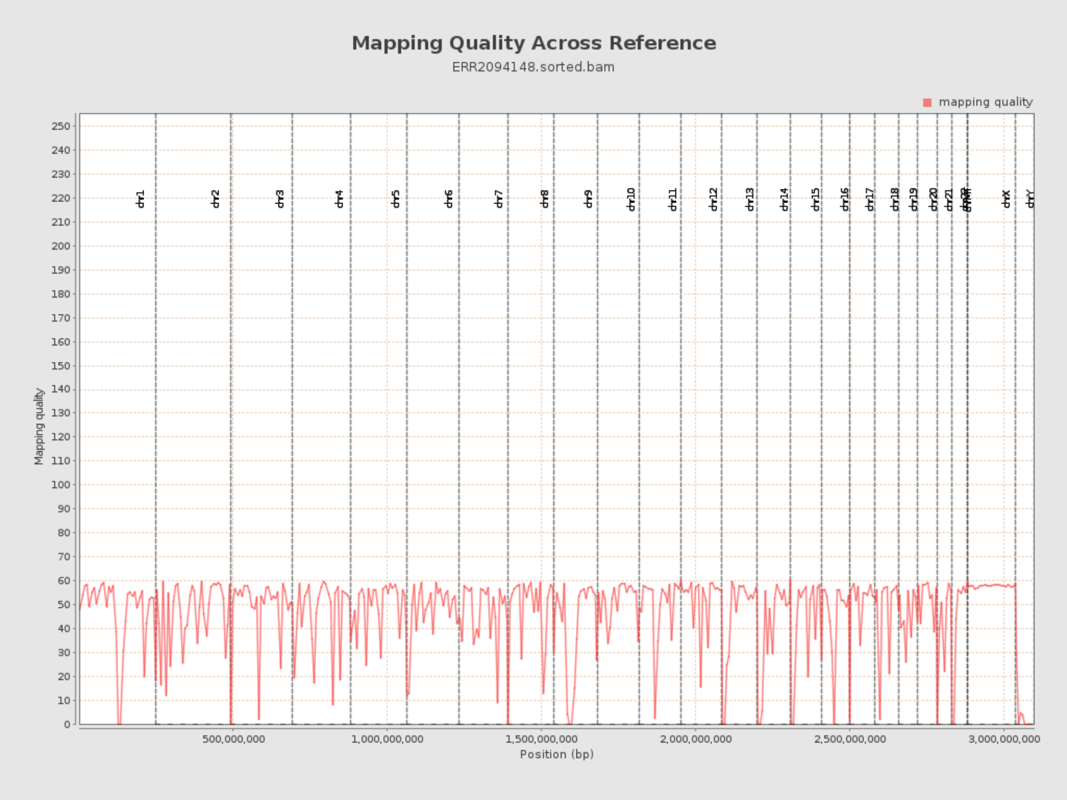
10. Results : Mapped Reads Clipping Profile



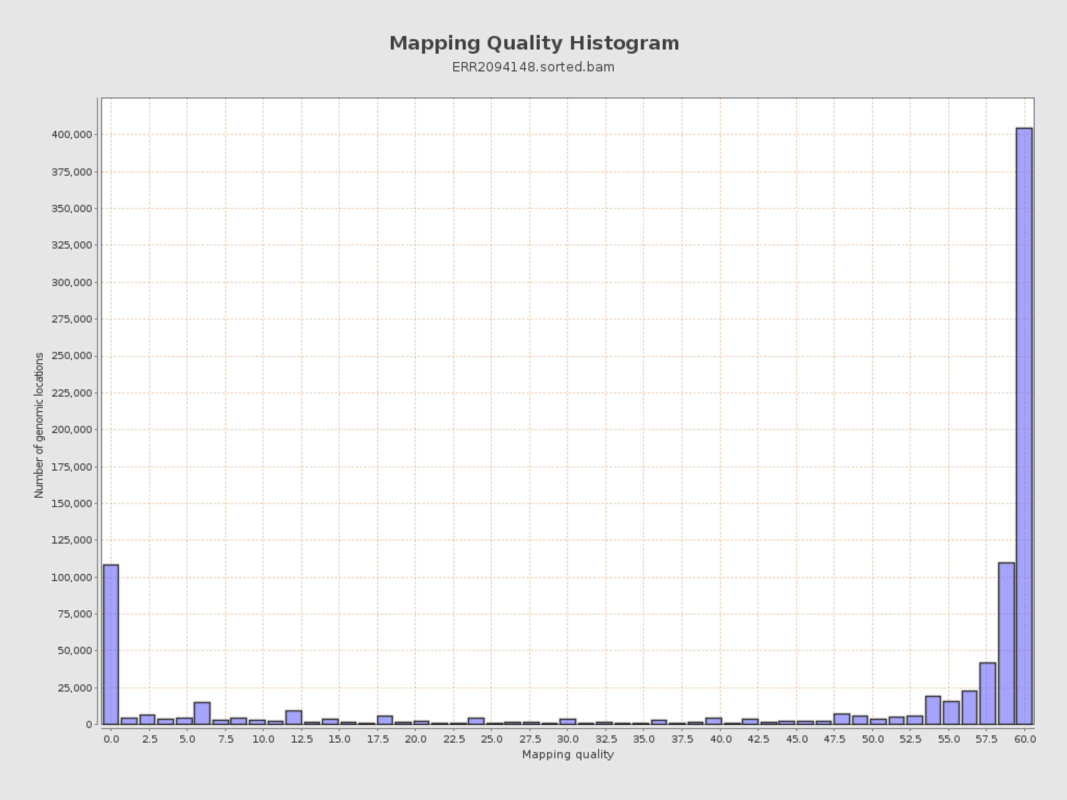
11. Results : Homopolymer Indels



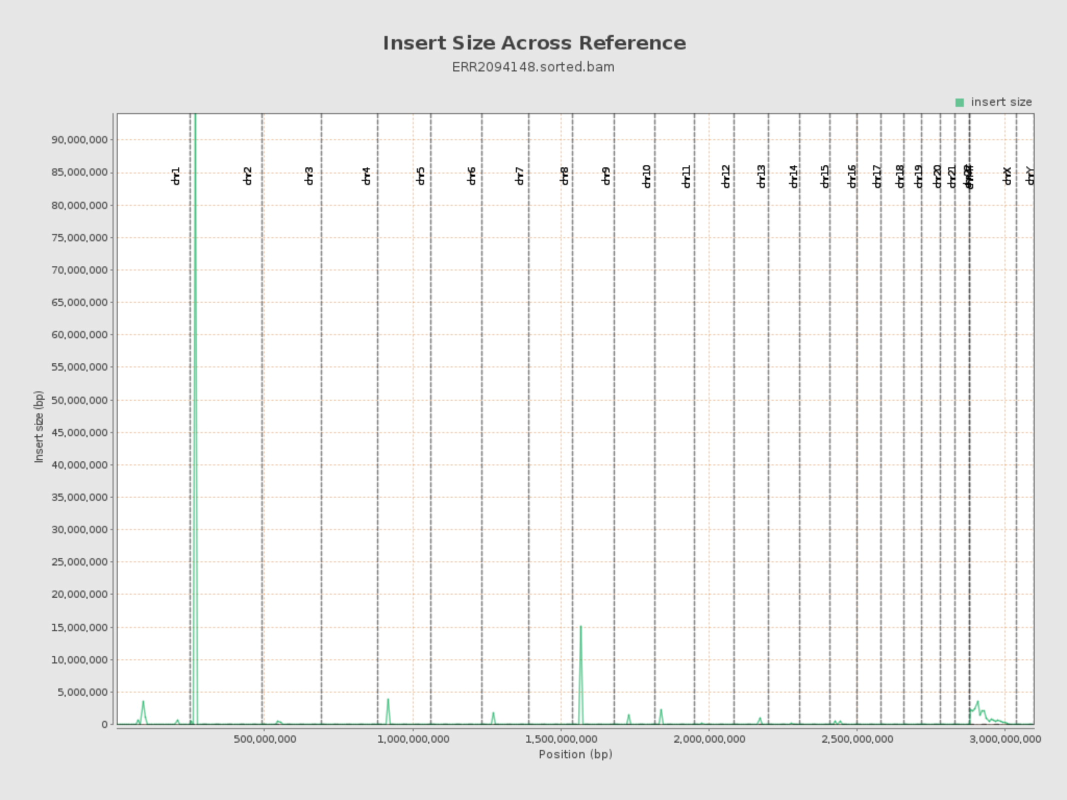
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram