Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:40:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094113.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_ERR2094113 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094113_1.fastq.gz ERR2094113_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:40:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,540
Mapped reads	407,198 / 96.14%
Unmapped reads	16,342 / 3.86%
Mapped paired reads	407,198 / 96.14%
Mapped reads, first in pair	204,450 / 48.27%
Mapped reads, second in pair	202,748 / 47.87%
Mapped reads, both in pair	404,412 / 95.48%
Mapped reads, singletons	2,786 / 0.66%
Secondary alignments	0
Supplementary alignments	32,438 / 7.66%
Read min/max/mean length	30 / 151 / 140.47
Duplicated reads (estimated)	390,225 / 92.13%
Duplication rate	51.18%
Clipped reads	221,043 / 52.19%

2.2. ACGT Content

Number/percentage of A's	14,245,801 / 28.55%
Number/percentage of C's	10,888,939 / 21.82%
Number/percentage of T's	13,319,614 / 26.7%
Number/percentage of G's	11,438,988 / 22.93%
Number/percentage of N's	440 / 0%

GC Percentage	44.75%

2.3. Coverage

Mean	0.0164
Standard Deviation	3.3973

2.4. Mapping Quality

Mean Mapping Quality	40.38

2.5. Insert size

Mean	1,815,746.83
Standard Deviation	11,688,662.51
P25/Median/P75	116 / 149 / 180

2.6. Mismatches and indels

General error rate	3.43%
Mismatches	1,633,599
Insertions	34,816
Mapped reads with at least one insertion	8.44%
Deletions	132,184
Mapped reads with at least one deletion	31.46%
Homopolymer indels	28.31%

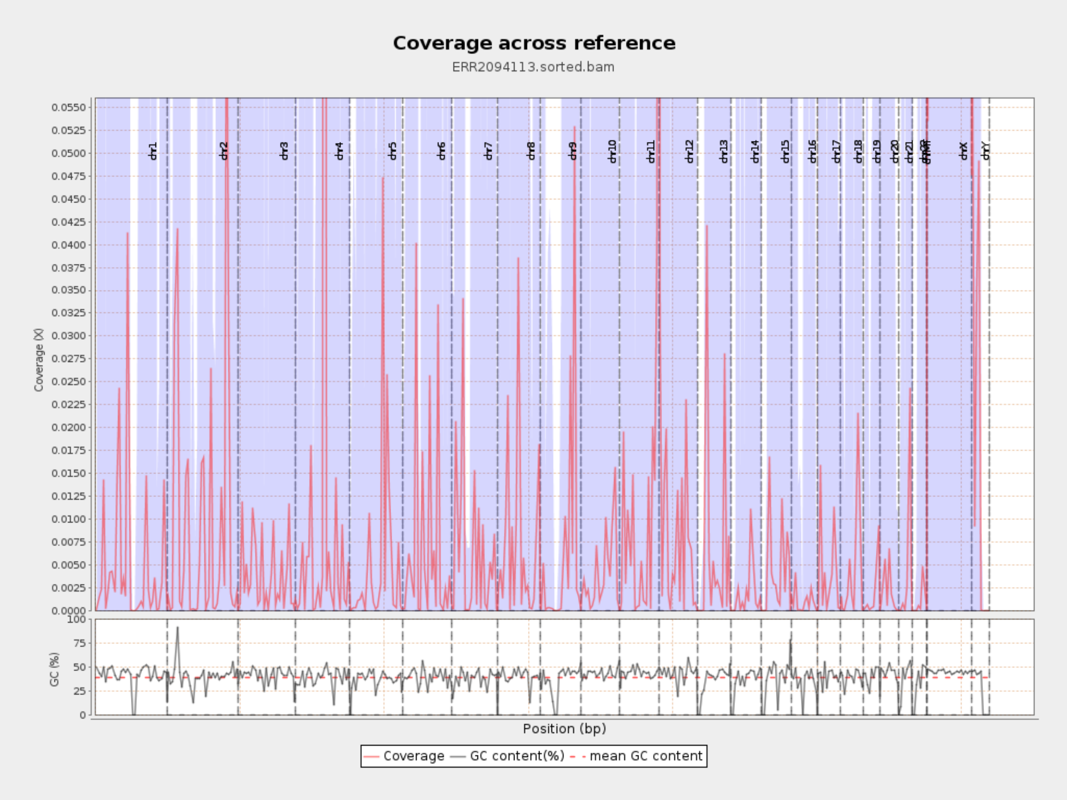
2.7. Chromosome stats

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

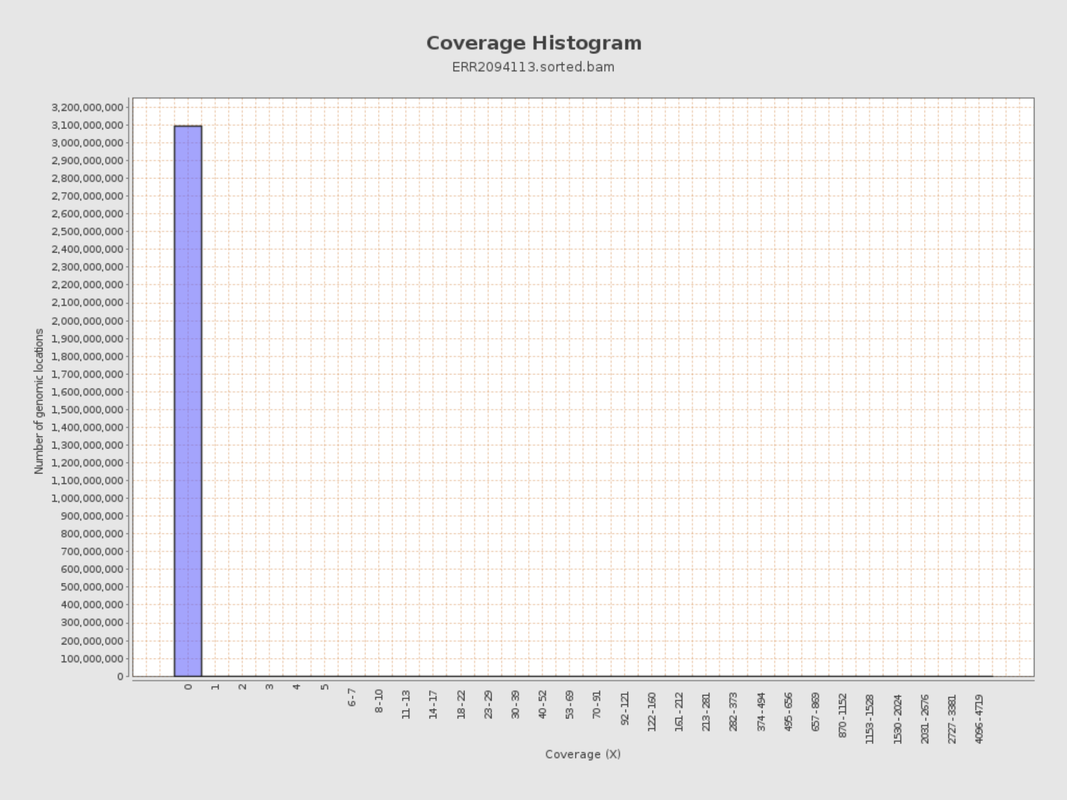
		bases	coverage	deviation
chr1	249250621	1258456	0.005	1.9925
chr2	243199373	2410001	0.0099	3.3198
chr3	198022430	759376	0.0038	0.9761
chr4	191154276	3114592	0.0163	5.1754
chr5	180915260	1026768	0.0057	2.7222
chr6	171115067	1193696	0.007	2.3477
chr7	159138663	995427	0.0063	1.7106
chr8	146364022	1087478	0.0074	1.9583
chr9	141213431	891767	0.0063	2.2727
chr10	135534747	540734	0.004	0.9445
chr11	135006516	1353287	0.01	2.6098
chr12	133851895	1099937	0.0082	1.8355
chr13	115169878	772049	0.0067	1.5591
chr14	107349540	193421	0.0018	0.7981
chr15	102531392	442443	0.0043	1.0926
chr16	90354753	95532	0.0011	0.3039
chr17	81195210	339063	0.0042	1.0928
chr18	78077248	394797	0.0051	1.6338
chr19	59128983	113454	0.0019	0.7599
chr20	63025520	146243	0.0023	0.6022
chr21	48129895	236652	0.0049	1.8547
chr22	51304566	54905	0.0011	0.376
chrMT	16571	162259	9.7917	54.1516
chrX	155270560	31098213	0.2003	11.2287

chrY	59373566	1021816	0.0172	3.1042

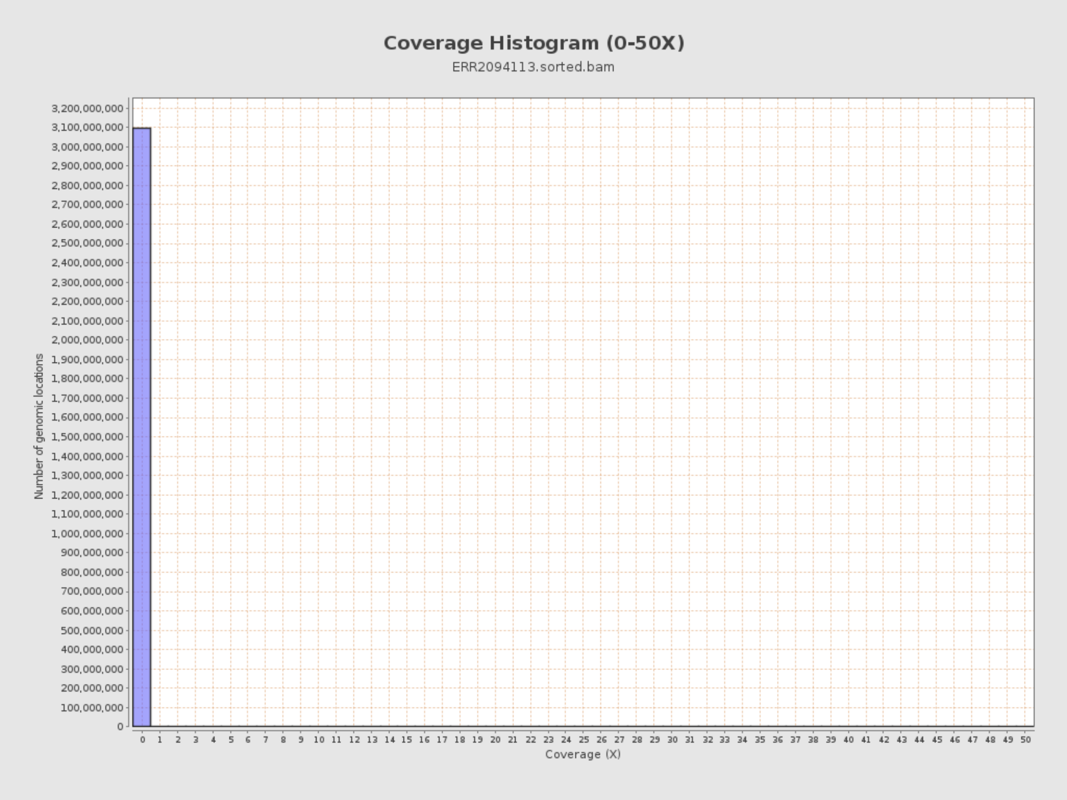
3. Results : Coverage across reference



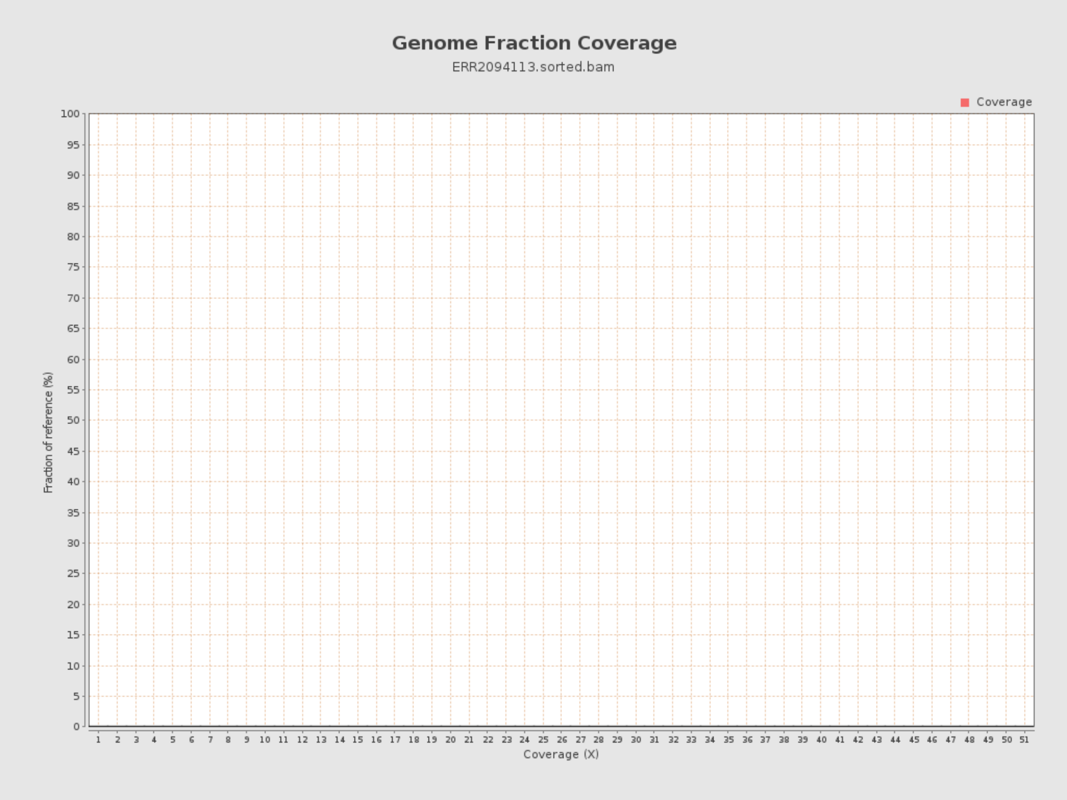
4. Results : Coverage Histogram



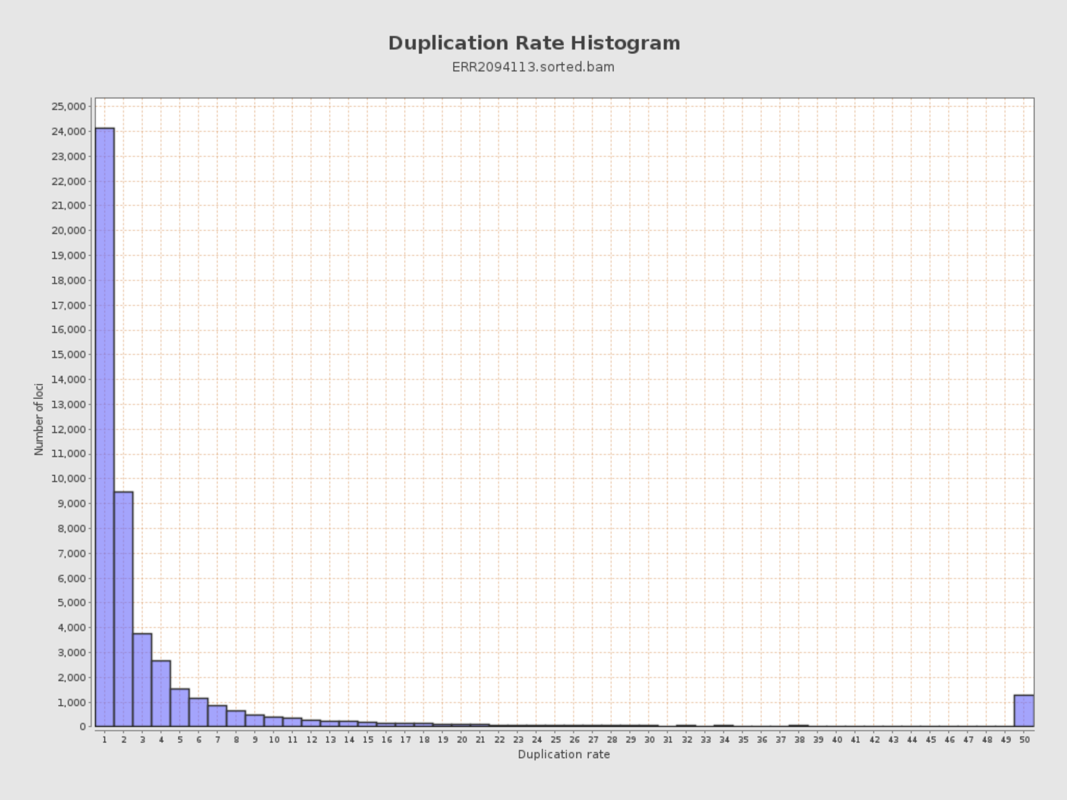
5. Results : Coverage Histogram (0-50X)



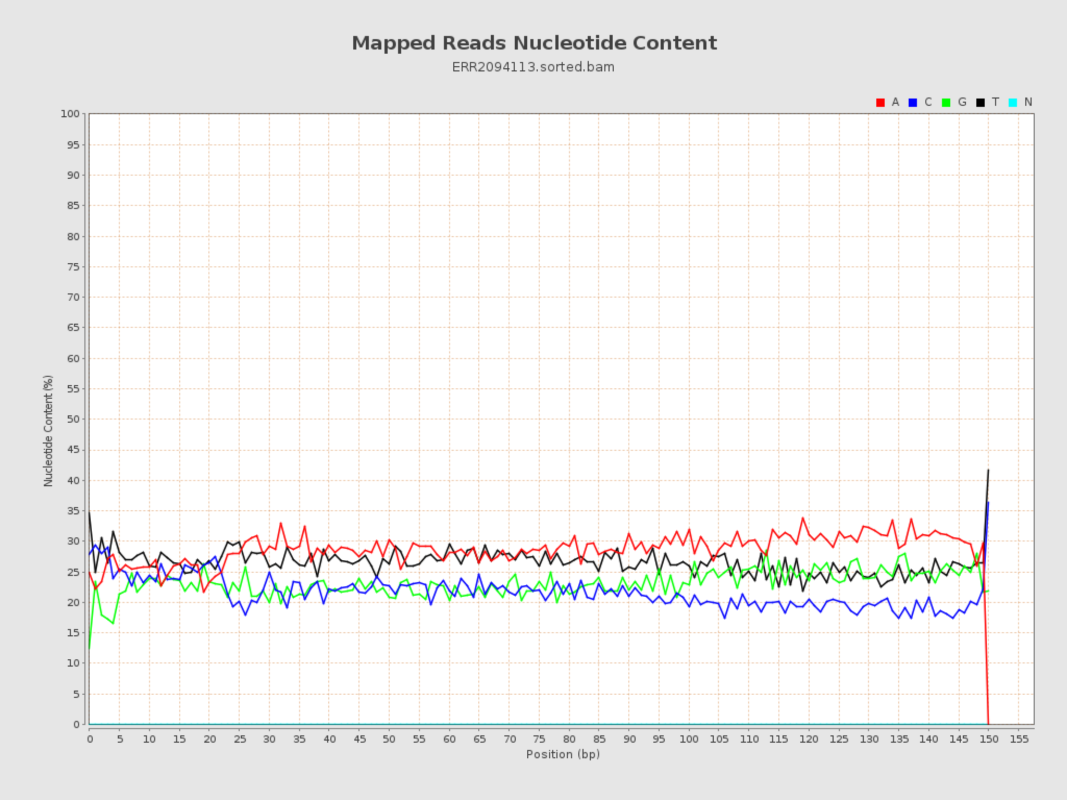
6. Results : Genome Fraction Coverage



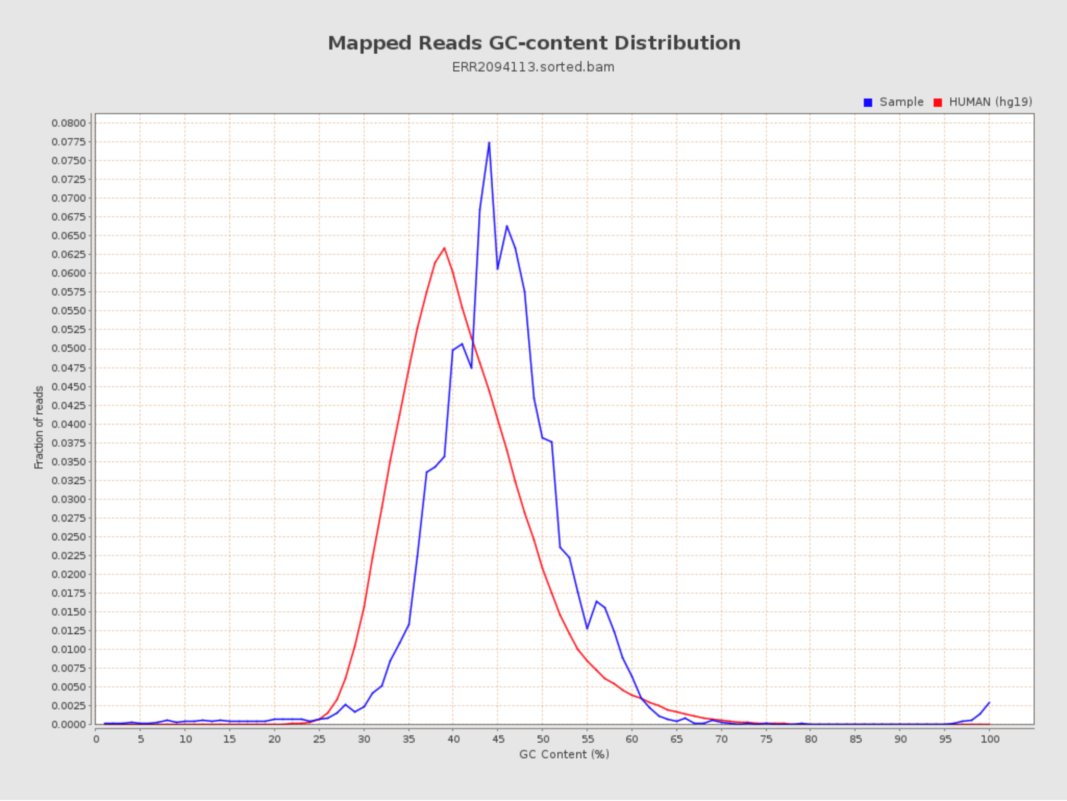
7. Results : Duplication Rate Histogram



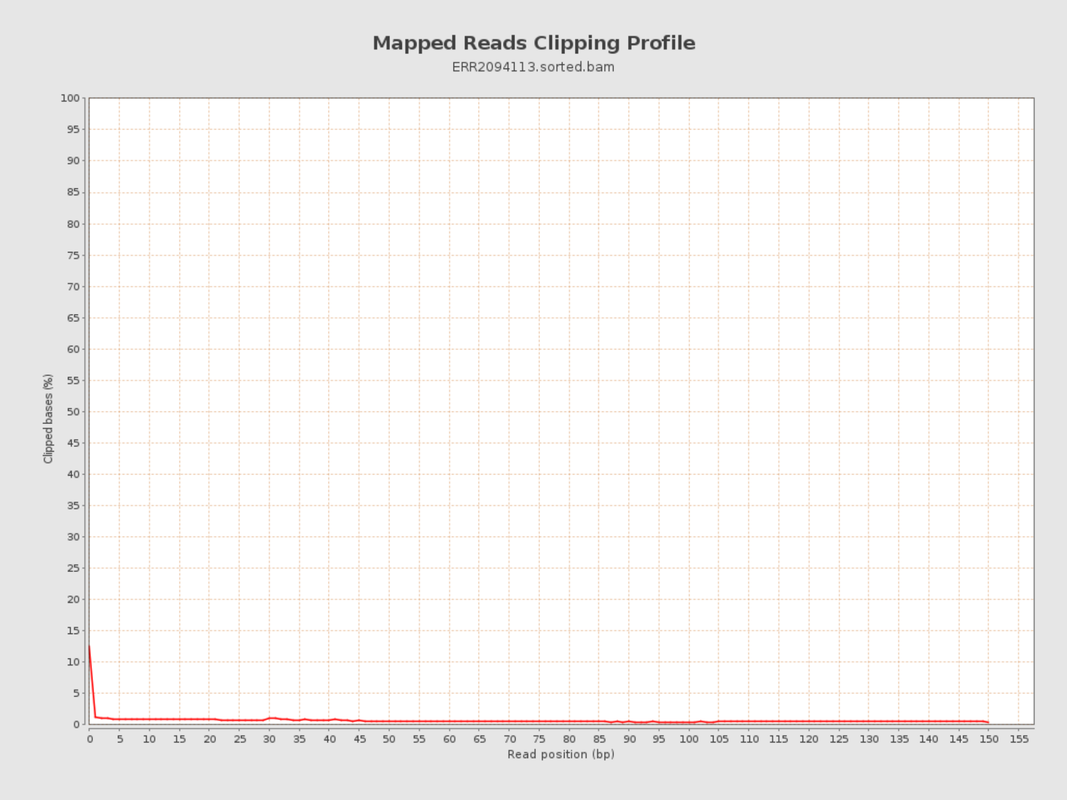
8. Results : Mapped Reads Nucleotide Content



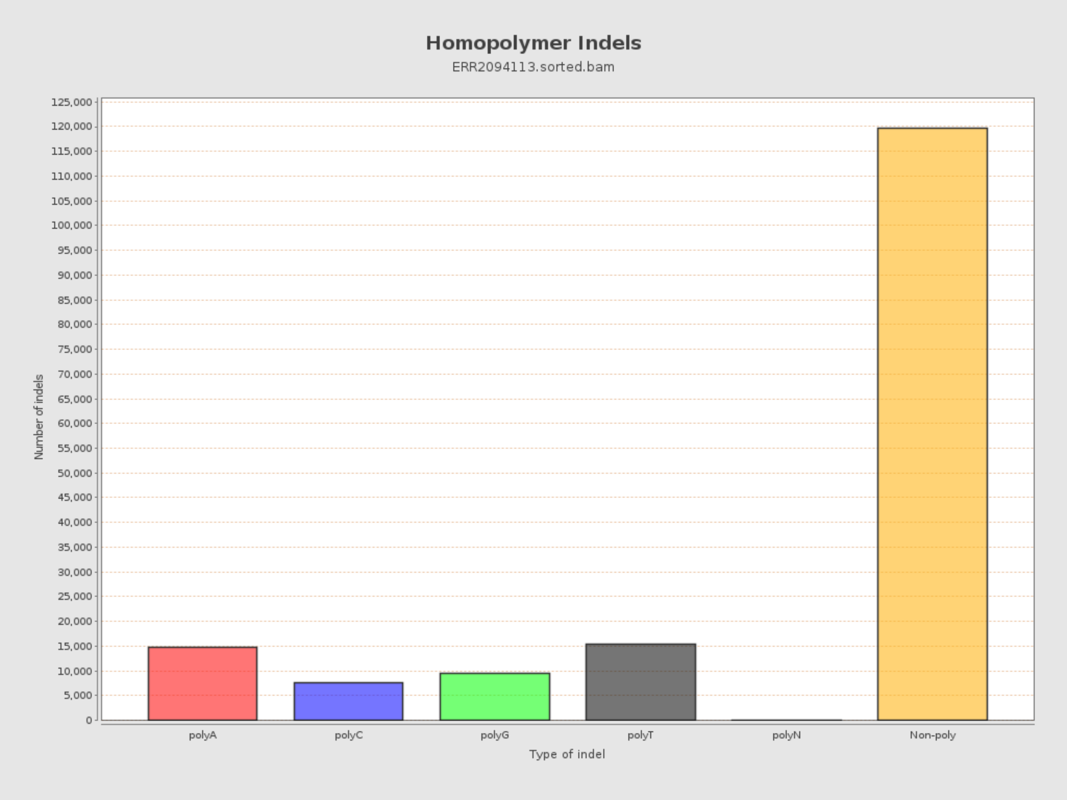
9. Results : Mapped Reads GC-content Distribution



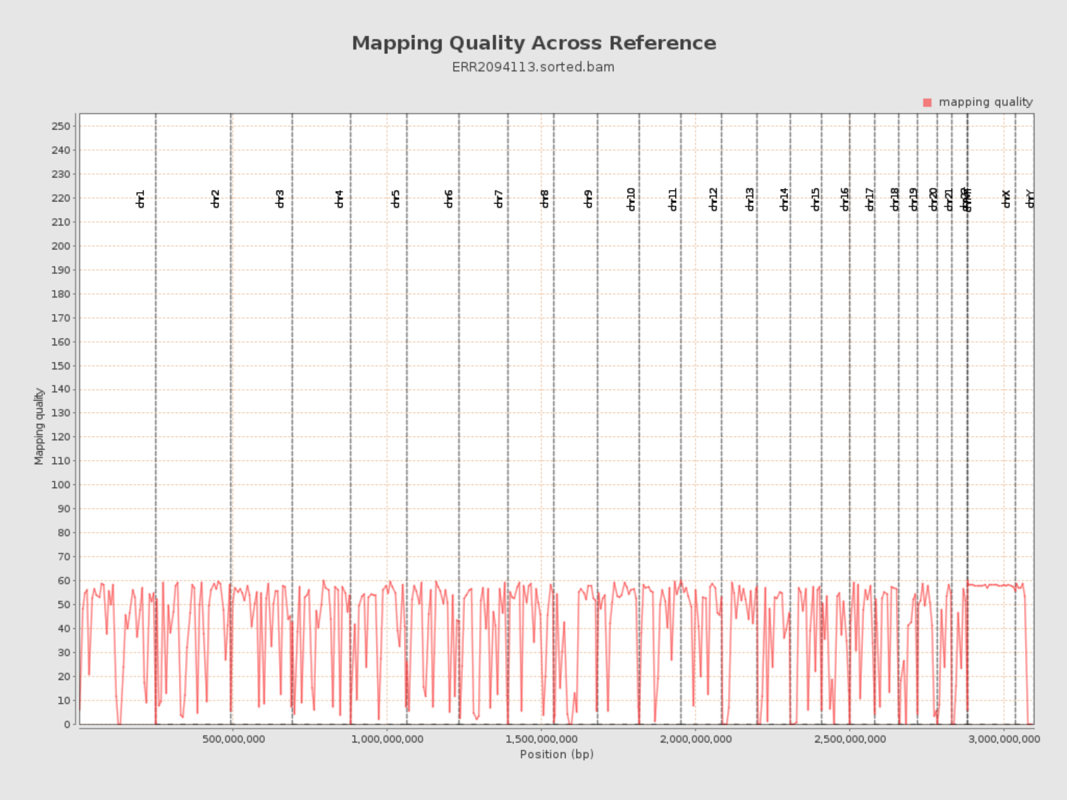
10. Results : Mapped Reads Clipping Profile



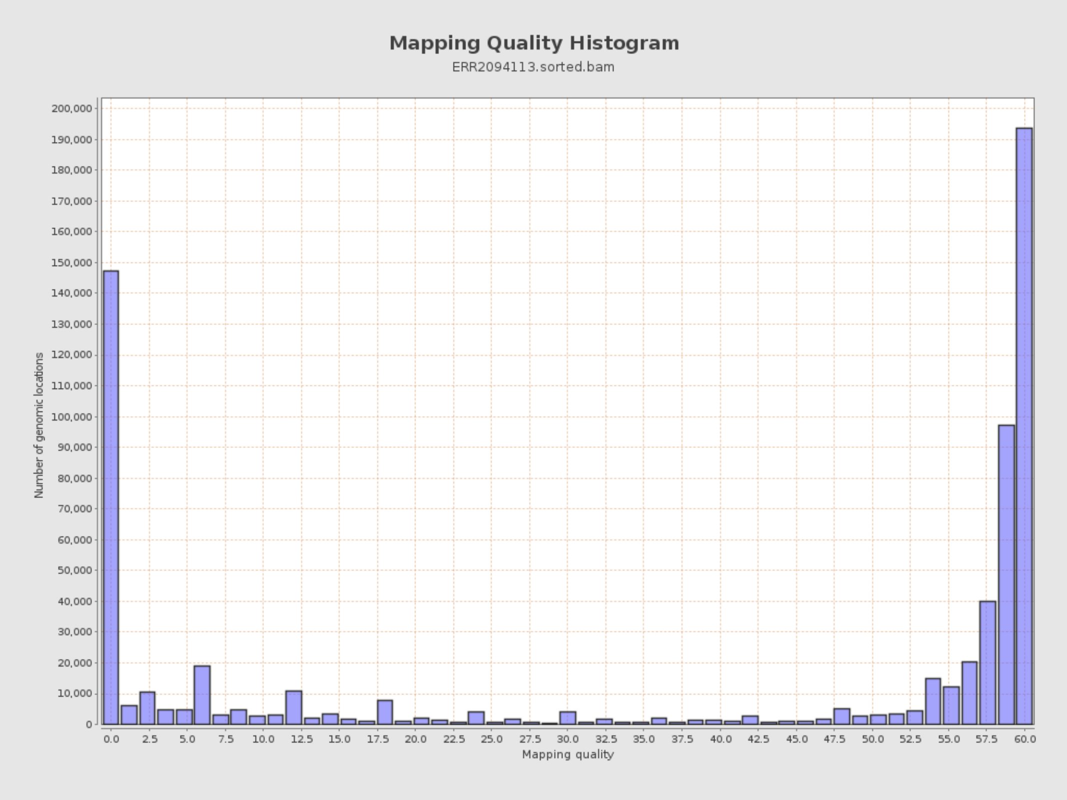
11. Results : Homopolymer Indels



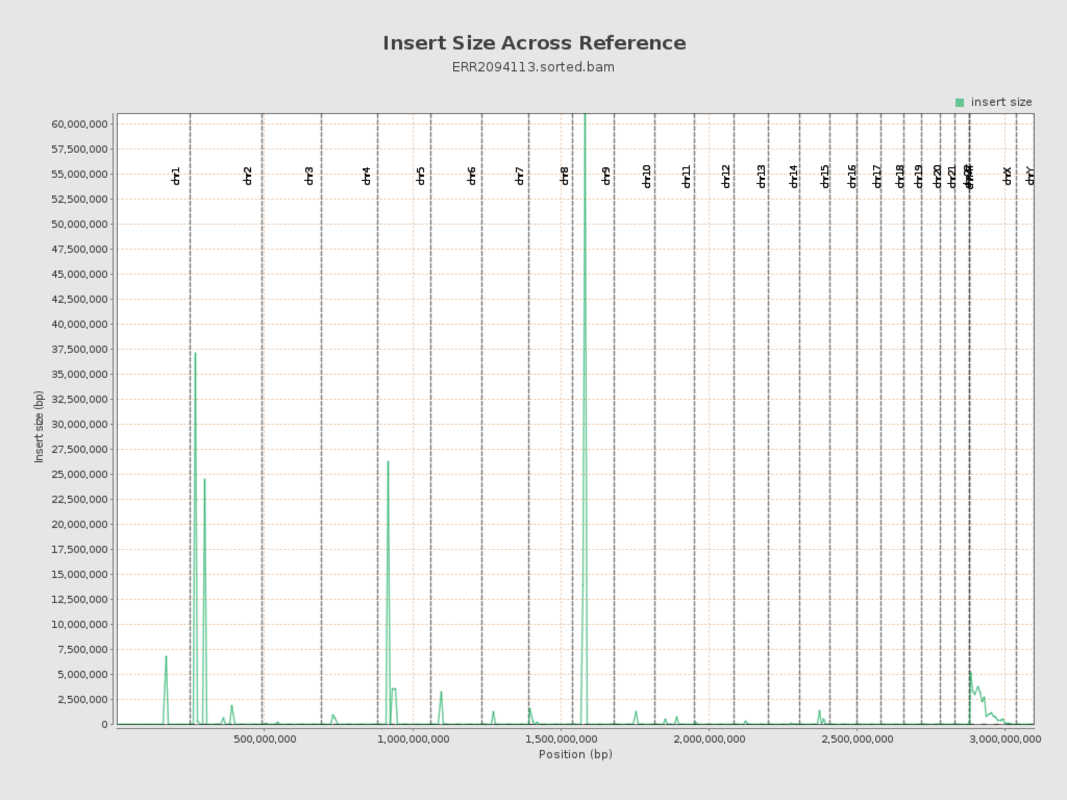
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram