Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:05:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094121.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_ERR2094121 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094121_1.fastq.gz ERR2094121_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:05:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	565,676
Mapped reads	493,191 / 87.19%
Unmapped reads	72,485 / 12.81%
Mapped paired reads	493,191 / 87.19%
Mapped reads, first in pair	247,170 / 43.69%
Mapped reads, second in pair	246,021 / 43.49%
Mapped reads, both in pair	489,772 / 86.58%
Mapped reads, singletons	3,419 / 0.6%
Secondary alignments	0
Supplementary alignments	34,699 / 6.13%
Read min/max/mean length	30 / 151 / 140.55
Duplicated reads (estimated)	514,753 / 91%
Duplication rate	46.32%
Clipped reads	244,545 / 43.23%

2.2. ACGT Content

Number/percentage of A's	20,457,631 / 30.28%
Number/percentage of C's	13,901,684 / 20.58%
Number/percentage of T's	18,819,542 / 27.86%
Number/percentage of G's	14,382,296 / 21.29%
Number/percentage of N's	676 / 0%

GC Percentage	41.86%

2.3. Coverage

Mean	0.0219
Standard Deviation	25.976

2.4. Mapping Quality

Mean Mapping Quality	15.1

2.5. Insert size

Mean	31,097.6
Standard Deviation	1,789,626.56
P25/Median/P75	167 / 217 / 237

2.6. Mismatches and indels

General error rate	1.87%
Mismatches	1,206,113
Insertions	28,282
Mapped reads with at least one insertion	5.66%
Deletions	57,198
Mapped reads with at least one deletion	11.3%
Homopolymer indels	47.79%

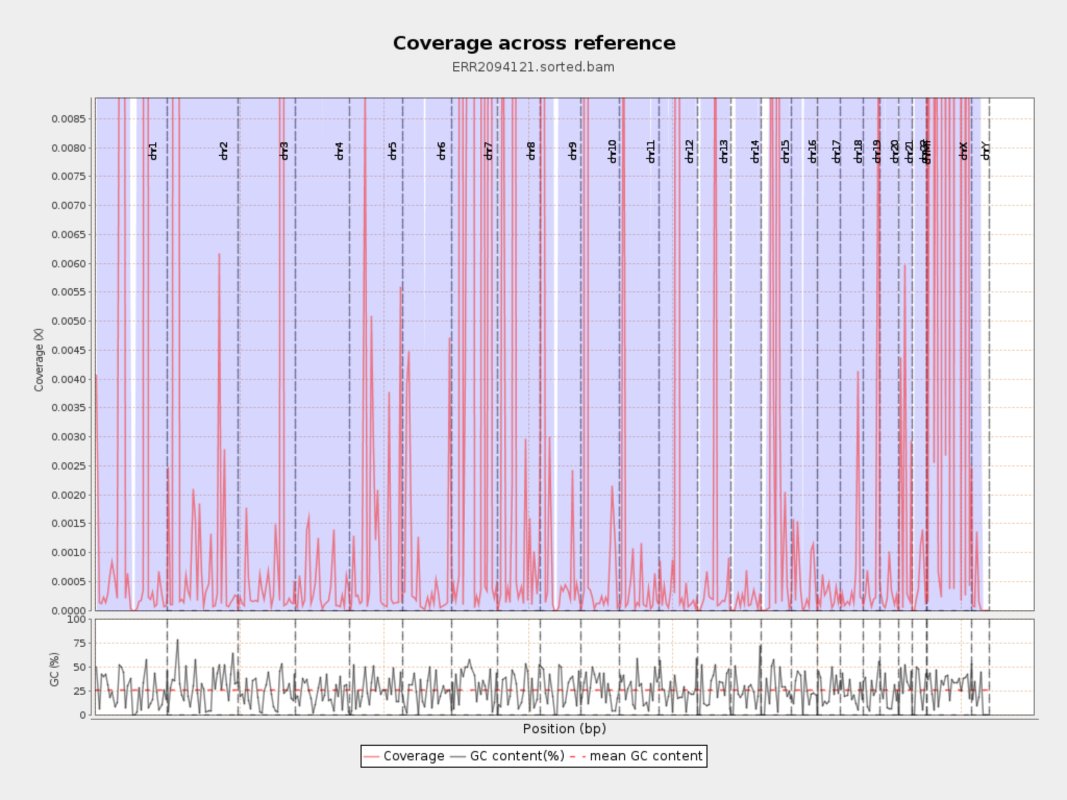
2.7. Chromosome stats

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

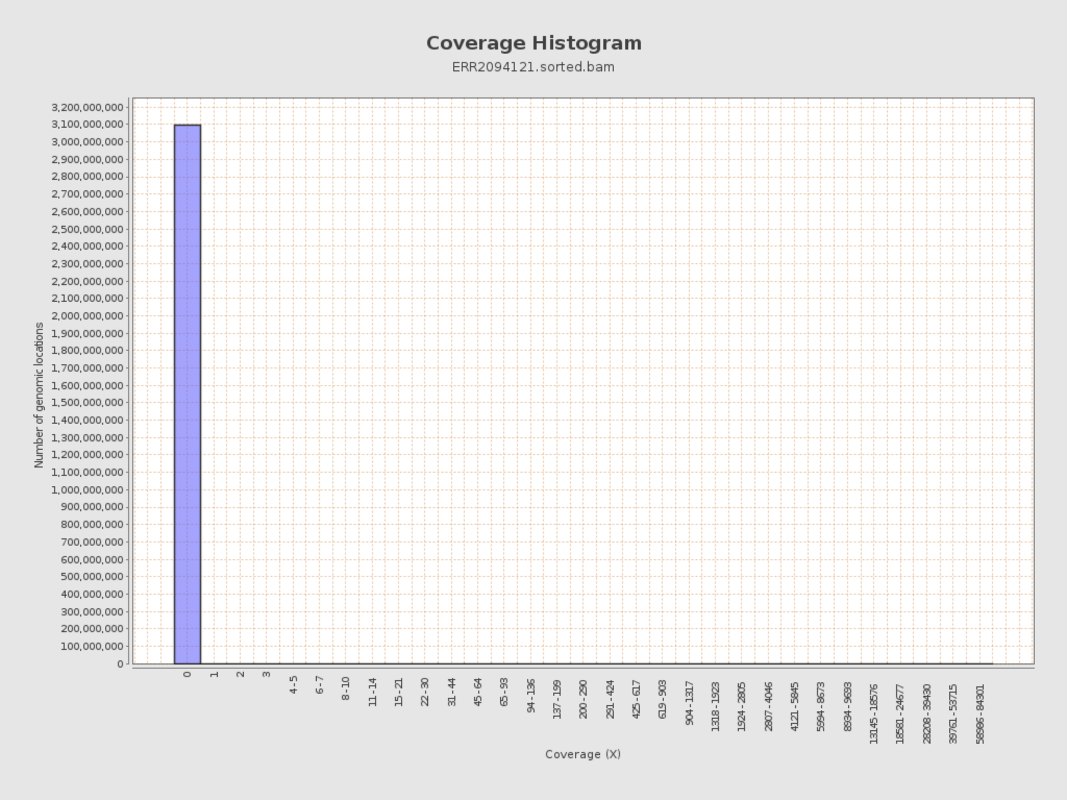
		bases	coverage	deviation
chr1	249250621	1436534	0.0058	4.7617
chr2	243199373	964722	0.004	2.6063
chr3	198022430	2051555	0.0104	10.6705
chr4	191154276	78094	0.0004	0.1438
chr5	180915260	258656	0.0014	0.5186
chr6	171115067	138771	0.0008	0.456
chr7	159138663	2821534	0.0177	6.643
chr8	146364022	481998	0.0033	1.9459
chr9	141213431	357745	0.0025	1.3669
chr10	135534747	1213220	0.009	4.5112
chr11	135006516	133094	0.001	0.6482
chr12	133851895	534108	0.004	4.4893
chr13	115169878	125881	0.0011	0.7247
chr14	107349540	19745	0.0002	0.0549
chr15	102531392	356501	0.0035	2.4842
chr16	90354753	50127	0.0006	0.1624
chr17	81195210	22080	0.0003	0.0799
chr18	78077248	49029	0.0006	0.3892
chr19	59128983	102380	0.0017	0.8077
chr20	63025520	18111	0.0003	0.1042
chr21	48129895	98325	0.002	0.6192
chr22	51304566	25638	0.0005	0.2129
chrMT	16571	46631918	2,814.0678	10,321.3722
chrX	155270560	9838484	0.0634	30.9152

chrY	59373566	12905	0.0002	0.1127

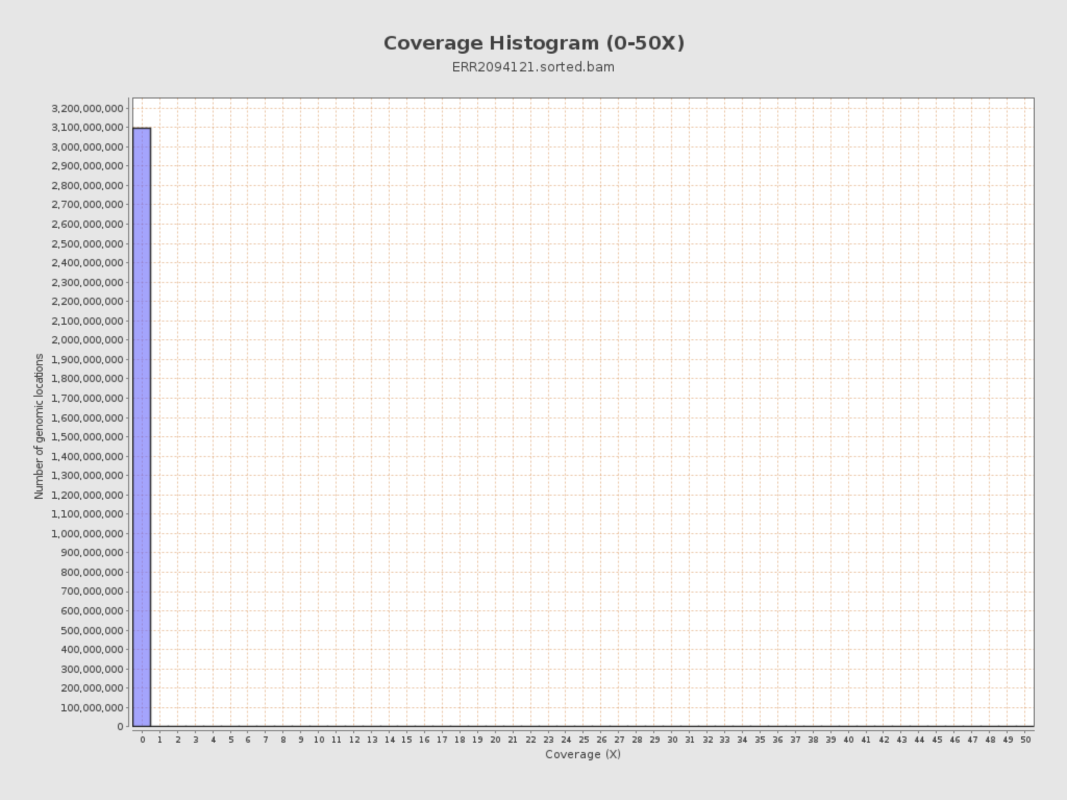
3. Results : Coverage across reference



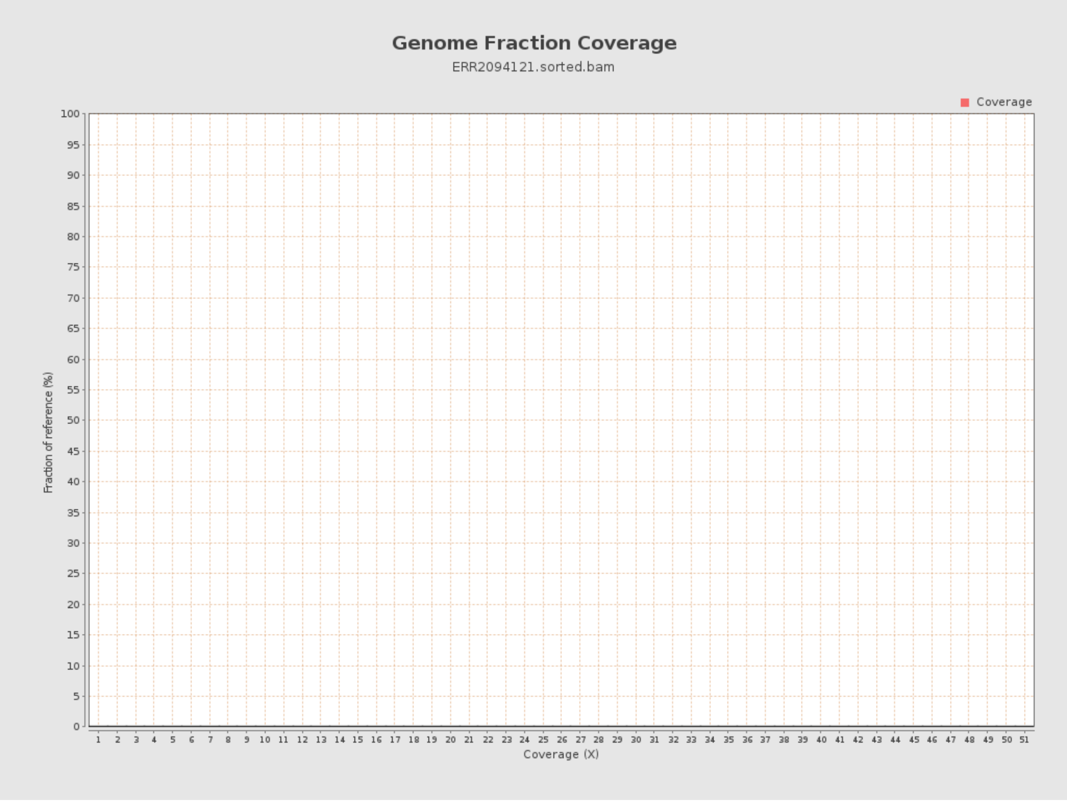
4. Results : Coverage Histogram



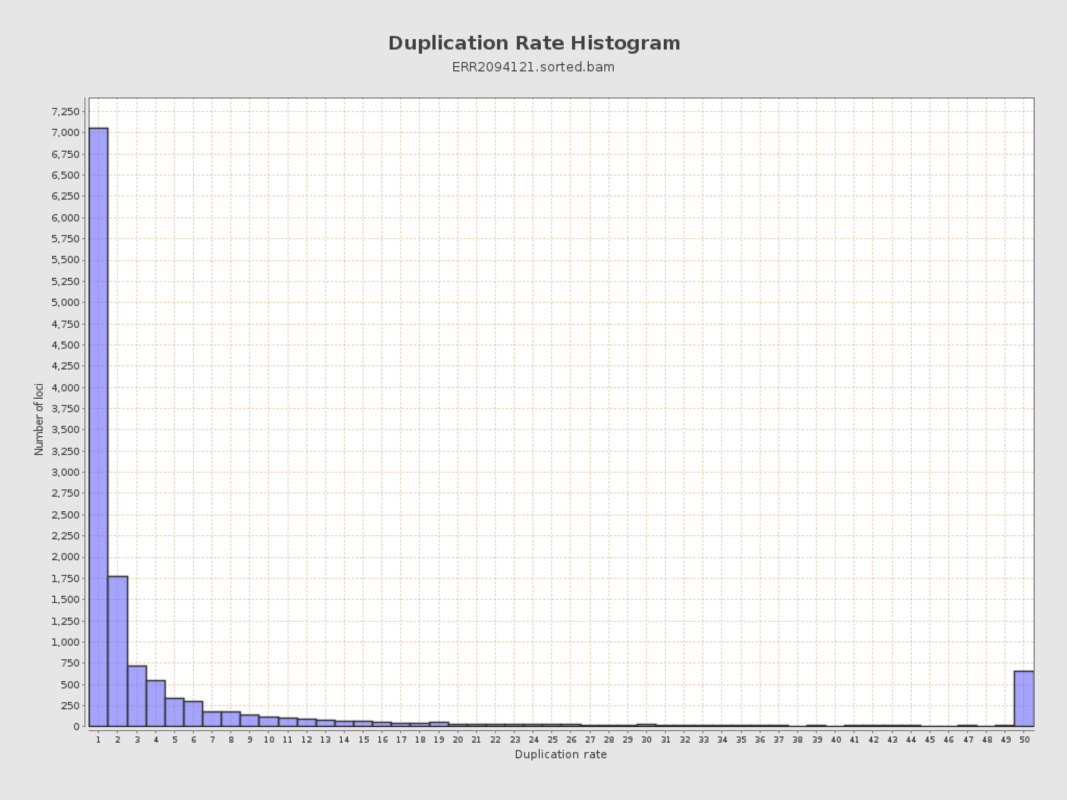
5. Results : Coverage Histogram (0-50X)



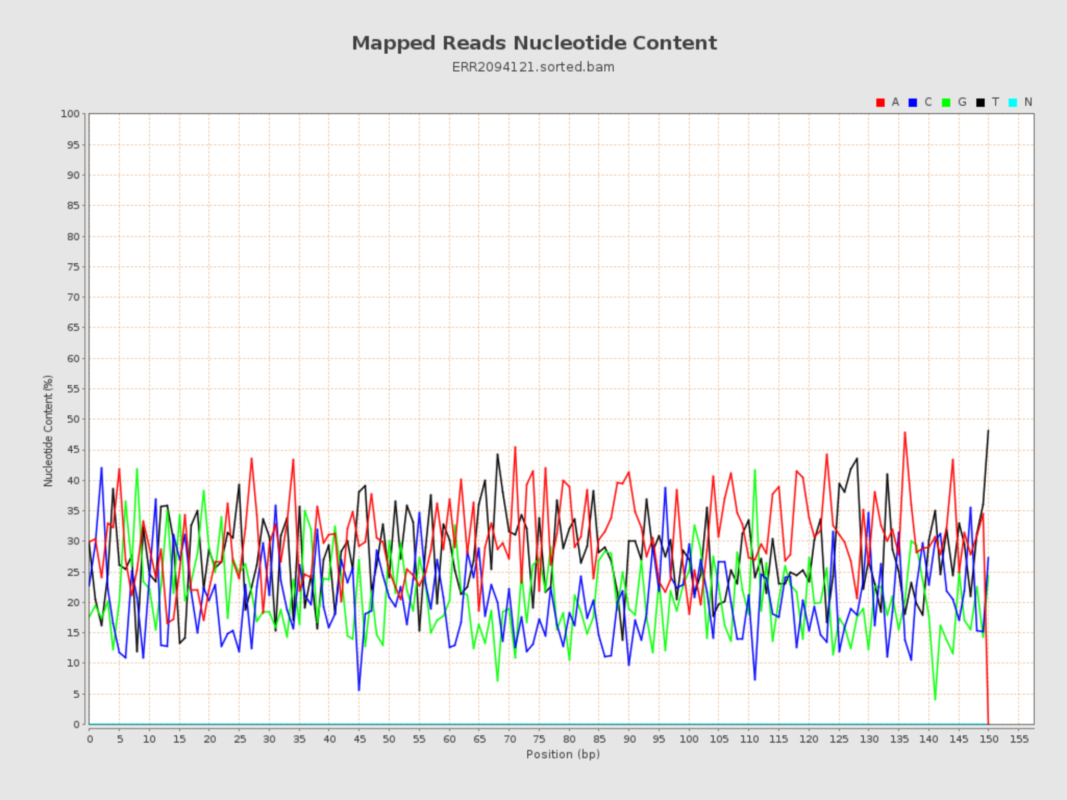
6. Results : Genome Fraction Coverage



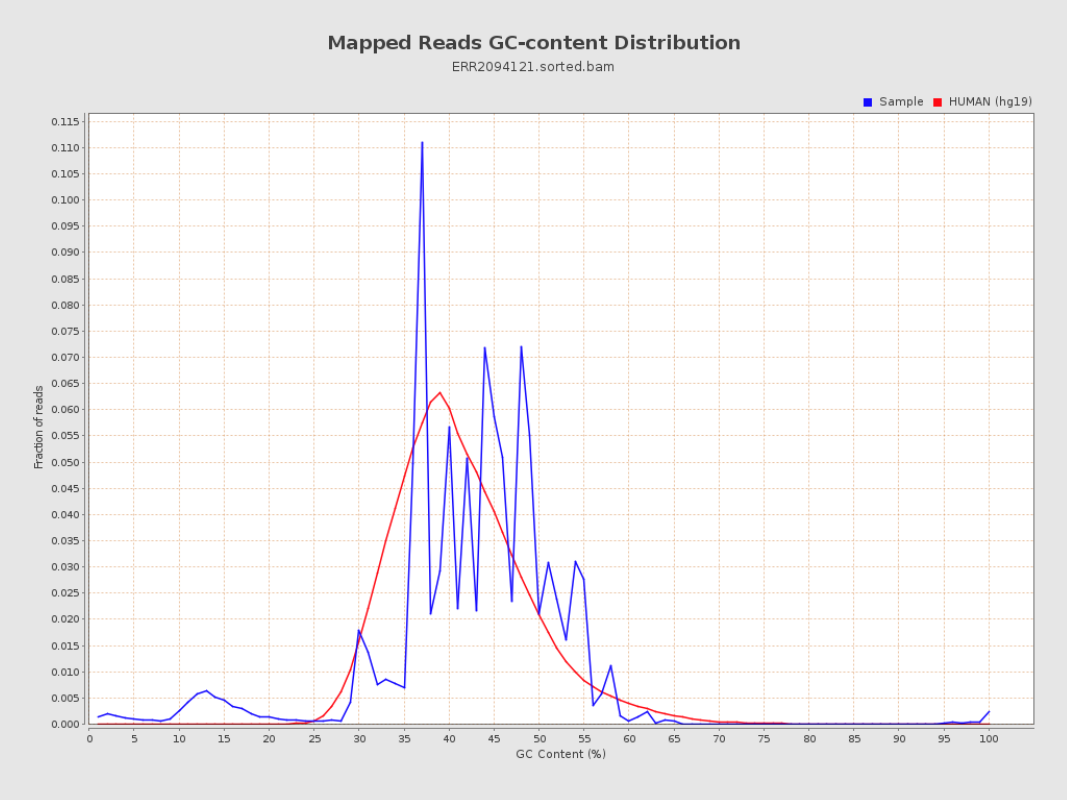
7. Results : Duplication Rate Histogram



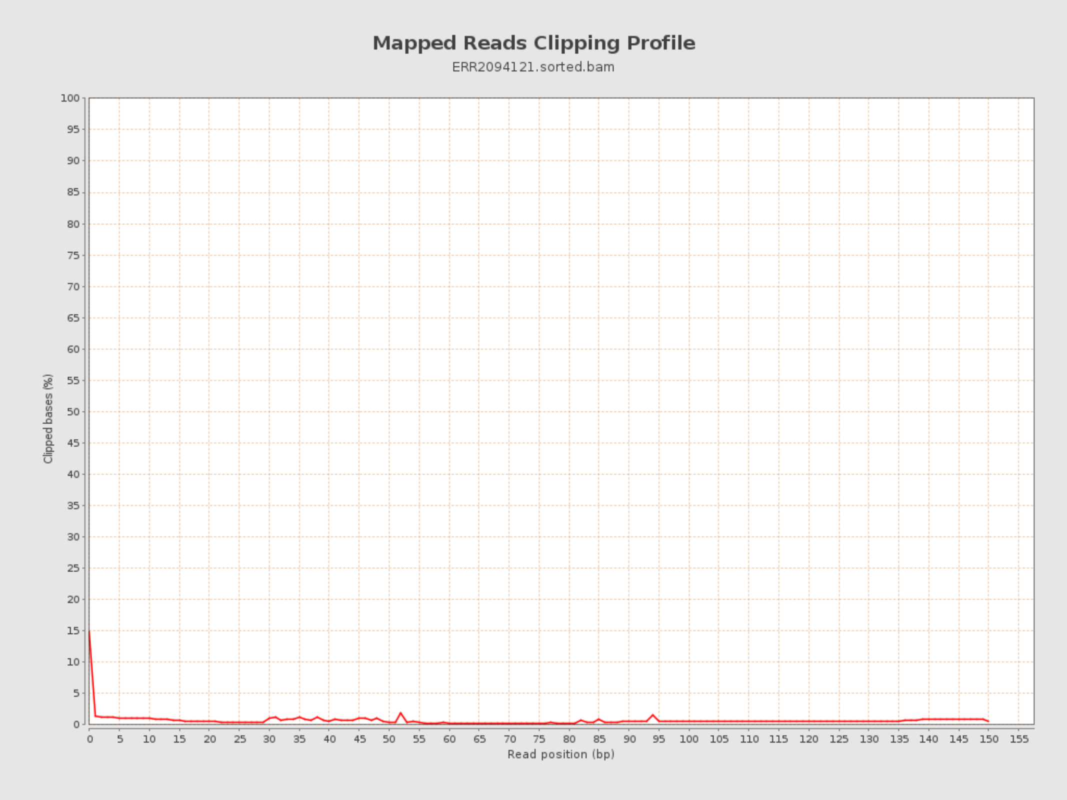
8. Results : Mapped Reads Nucleotide Content



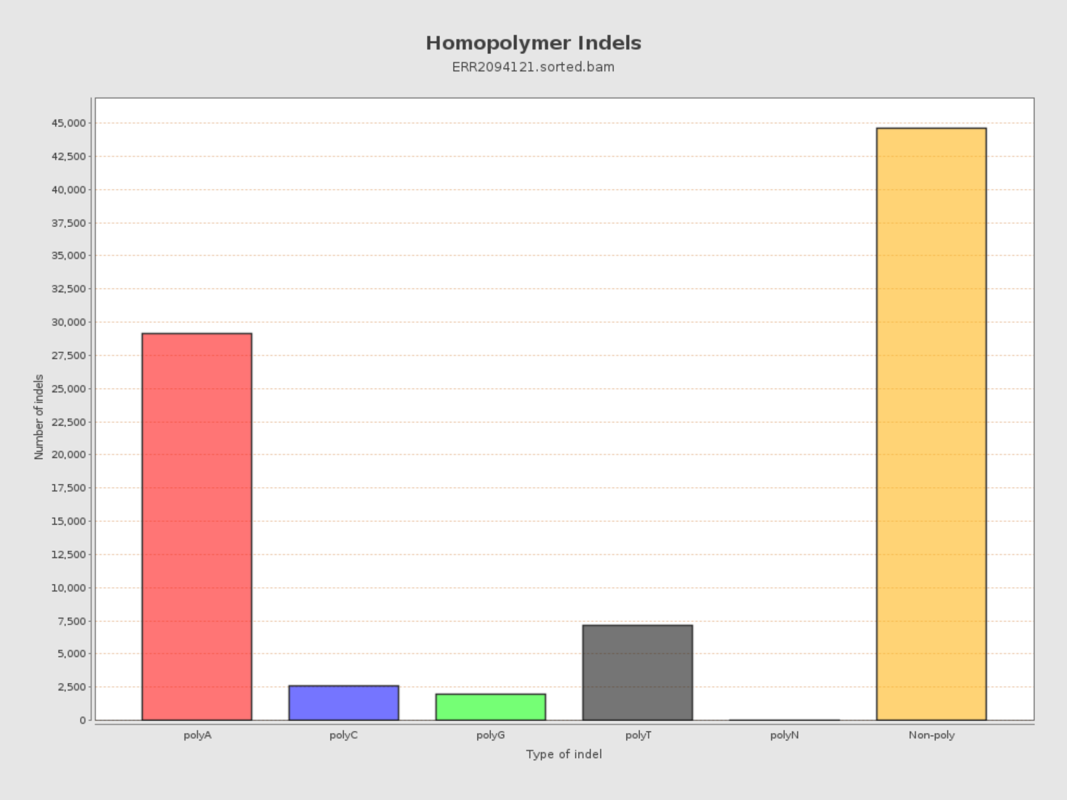
9. Results : Mapped Reads GC-content Distribution



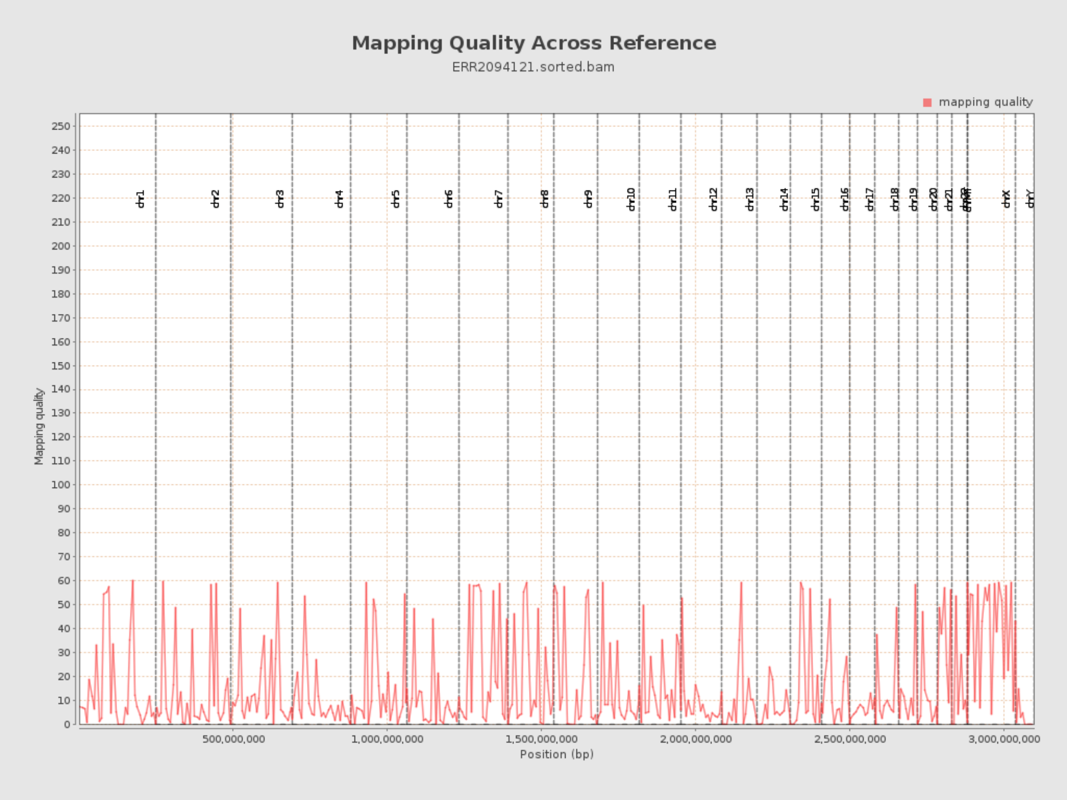
10. Results : Mapped Reads Clipping Profile



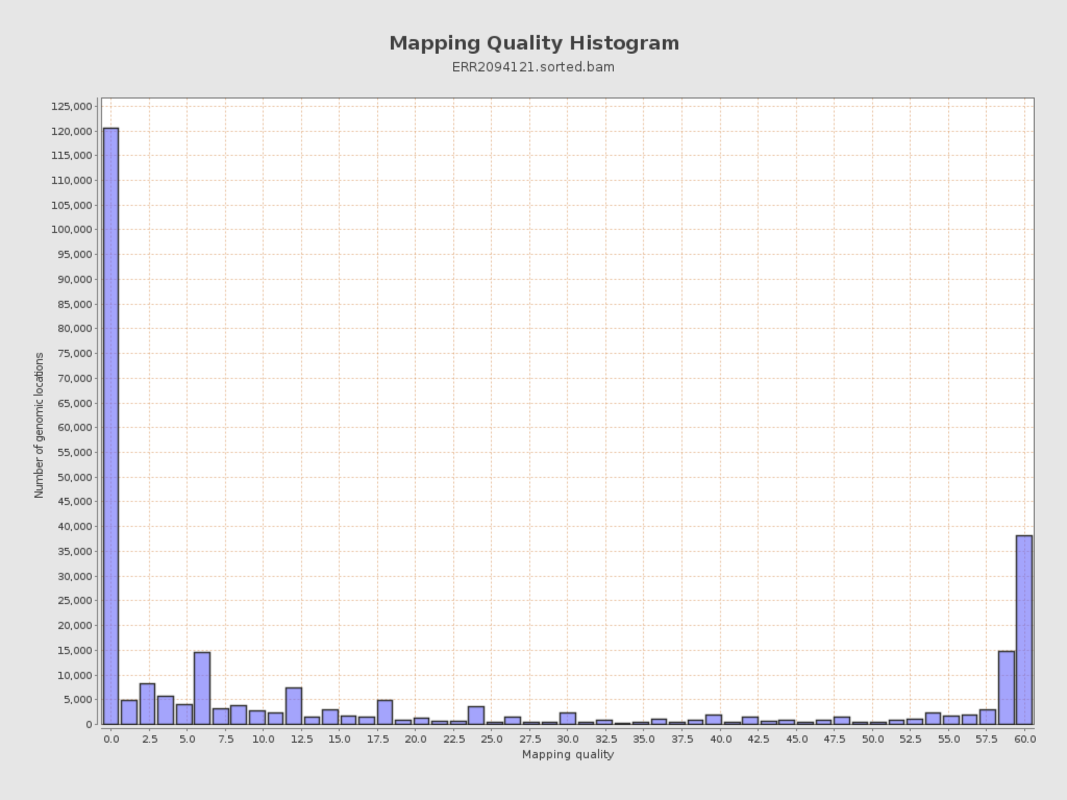
11. Results : Homopolymer Indels



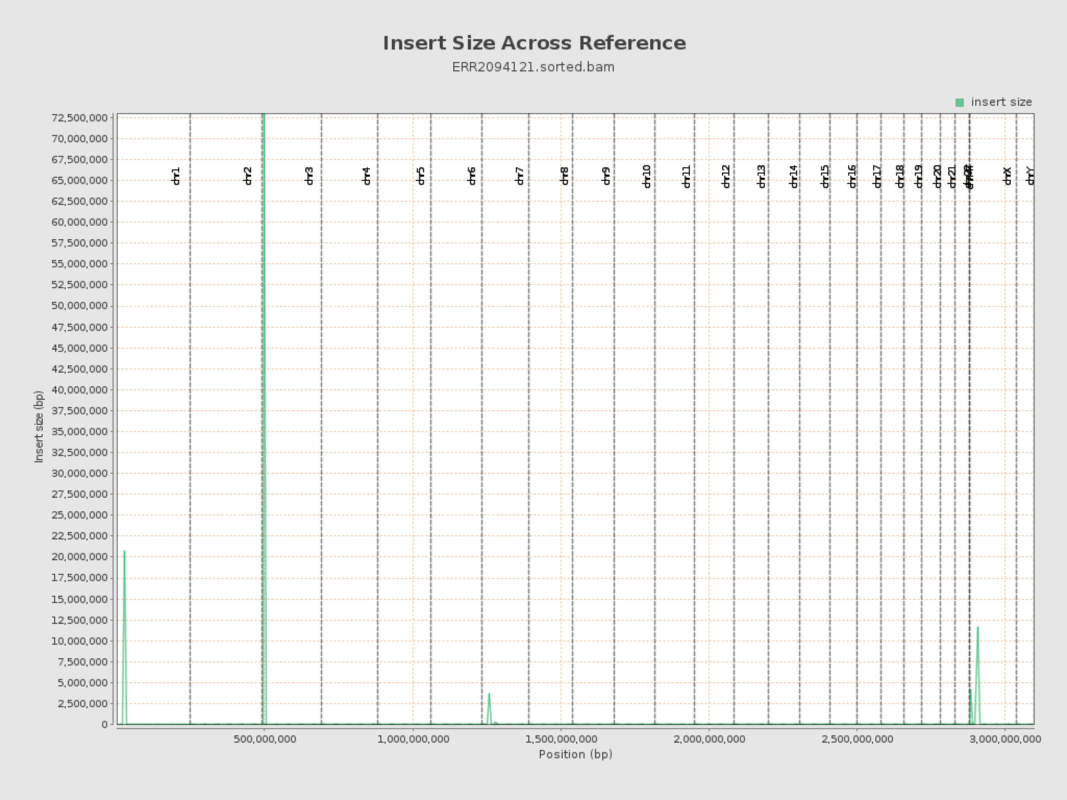
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram