Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:05:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093992.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_ERR2093992 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093992_1.fastq.gz ERR2093992_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:05:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	356,172
Mapped reads	338,892 / 95.15%
Unmapped reads	17,280 / 4.85%
Mapped paired reads	338,892 / 95.15%
Mapped reads, first in pair	170,397 / 47.84%
Mapped reads, second in pair	168,495 / 47.31%
Mapped reads, both in pair	335,652 / 94.24%
Mapped reads, singletons	3,240 / 0.91%
Secondary alignments	0
Supplementary alignments	24,539 / 6.89%
Read min/max/mean length	30 / 151 / 140.5
Duplicated reads (estimated)	319,015 / 89.57%
Duplication rate	51.76%
Clipped reads	177,759 / 49.91%

2.2. ACGT Content

Number/percentage of A's	11,078,718 / 26.3%
Number/percentage of C's	9,895,261 / 23.49%
Number/percentage of T's	10,452,966 / 24.81%
Number/percentage of G's	10,699,199 / 25.4%
Number/percentage of N's	450 / 0%

GC Percentage	48.89%

2.3. Coverage

Mean	0.0139
Standard Deviation	2.4754

2.4. Mapping Quality

Mean Mapping Quality	41.81

2.5. Insert size

Mean	1,362,494.95
Standard Deviation	10,568,017.64
P25/Median/P75	122 / 160 / 197

2.6. Mismatches and indels

General error rate	3.48%
Mismatches	1,419,336
Insertions	22,820
Mapped reads with at least one insertion	6.6%
Deletions	113,690
Mapped reads with at least one deletion	32.23%
Homopolymer indels	30.19%

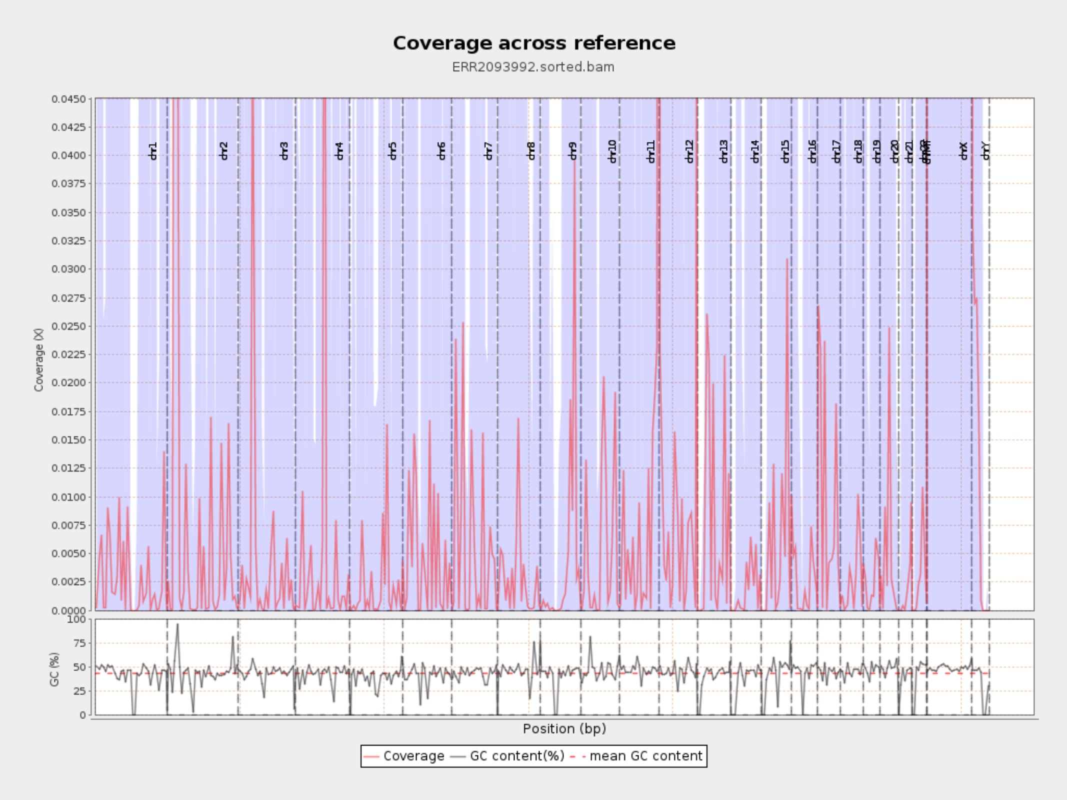
2.7. Chromosome stats

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

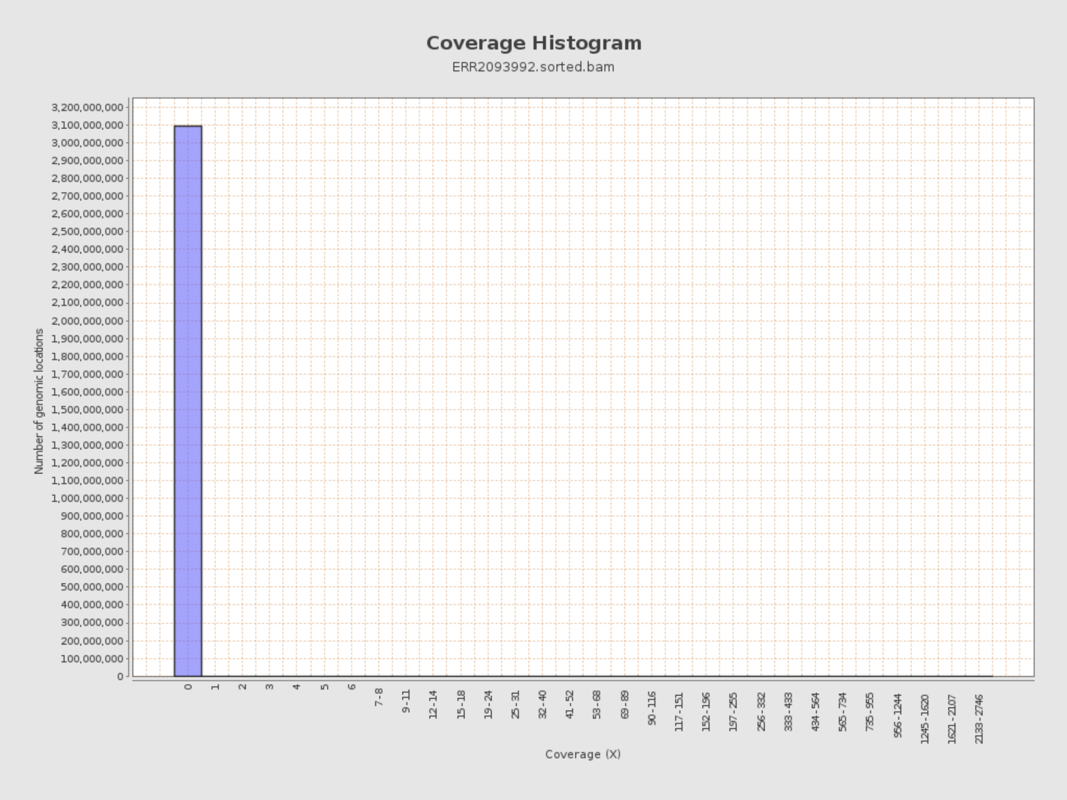
		bases	coverage	deviation
chr1	249250621	714463	0.0029	0.9075
chr2	243199373	2064858	0.0085	2.6101
chr3	198022430	795898	0.004	1.3488
chr4	191154276	985155	0.0052	1.5769
chr5	180915260	384120	0.0021	0.9579
chr6	171115067	834703	0.0049	1.3229
chr7	159138663	887990	0.0056	1.558
chr8	146364022	421719	0.0029	0.7842
chr9	141213431	646684	0.0046	1.4235
chr10	135534747	739023	0.0055	1.5078
chr11	135006516	1016381	0.0075	1.7886
chr12	133851895	966963	0.0072	1.6542
chr13	115169878	883665	0.0077	1.9943
chr14	107349540	195931	0.0018	0.5633
chr15	102531392	607704	0.0059	1.4884
chr16	90354753	256040	0.0028	0.7096
chr17	81195210	845551	0.0104	2.4877
chr18	78077248	225638	0.0029	0.8205
chr19	59128983	142900	0.0024	0.5572
chr20	63025520	330458	0.0052	1.6918
chr21	48129895	95383	0.002	0.3716
chr22	51304566	148350	0.0029	0.7114
chrMT	16571	817261	49.3187	213.2045
chrX	155270560	27146057	0.1748	8.5583

chrY	59373566	732965	0.0123	1.909

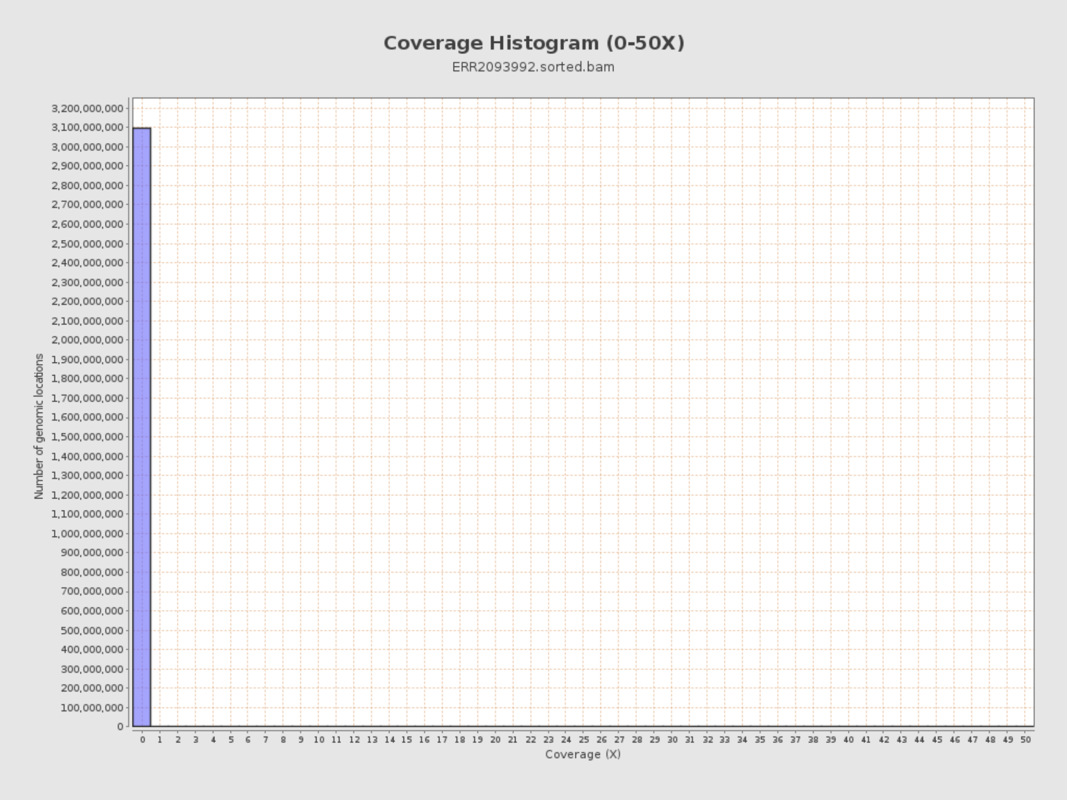
3. Results : Coverage across reference



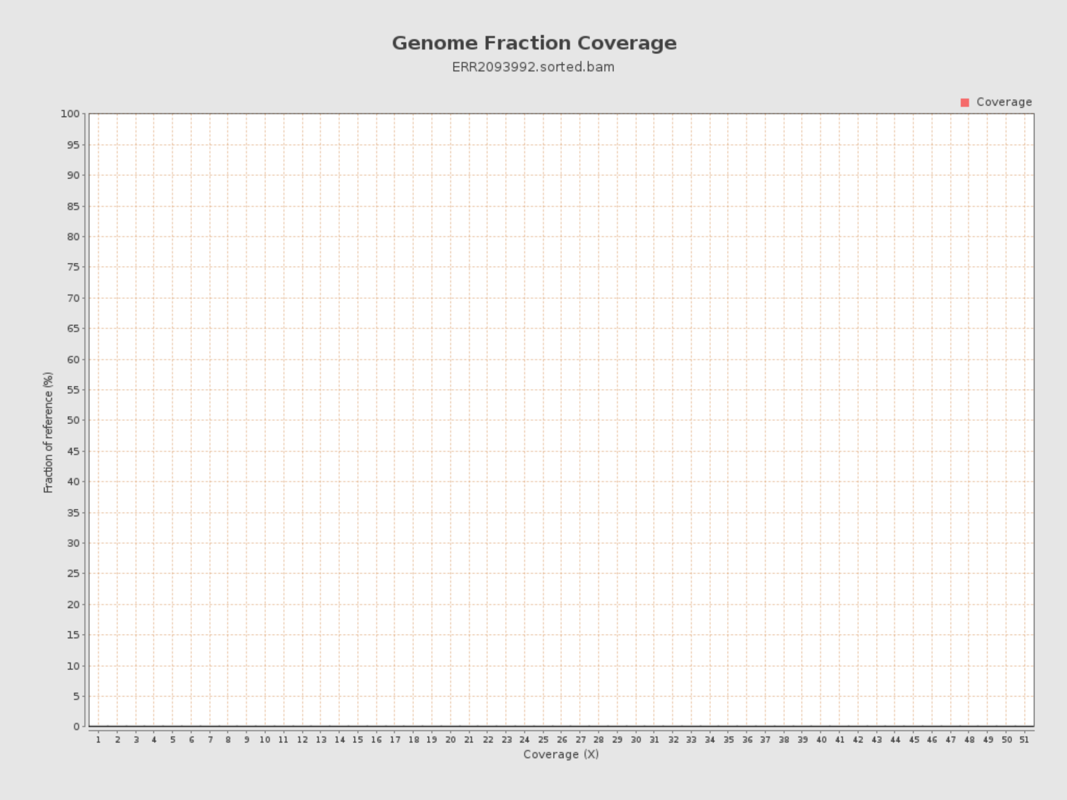
4. Results : Coverage Histogram



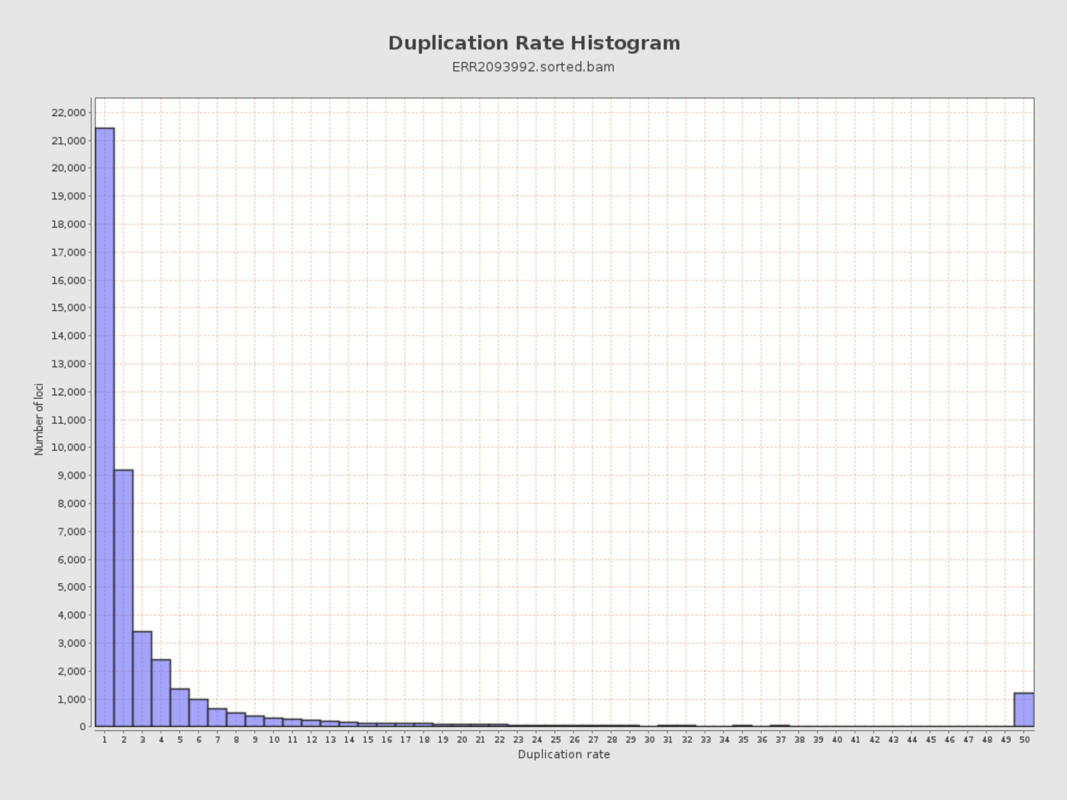
5. Results : Coverage Histogram (0-50X)



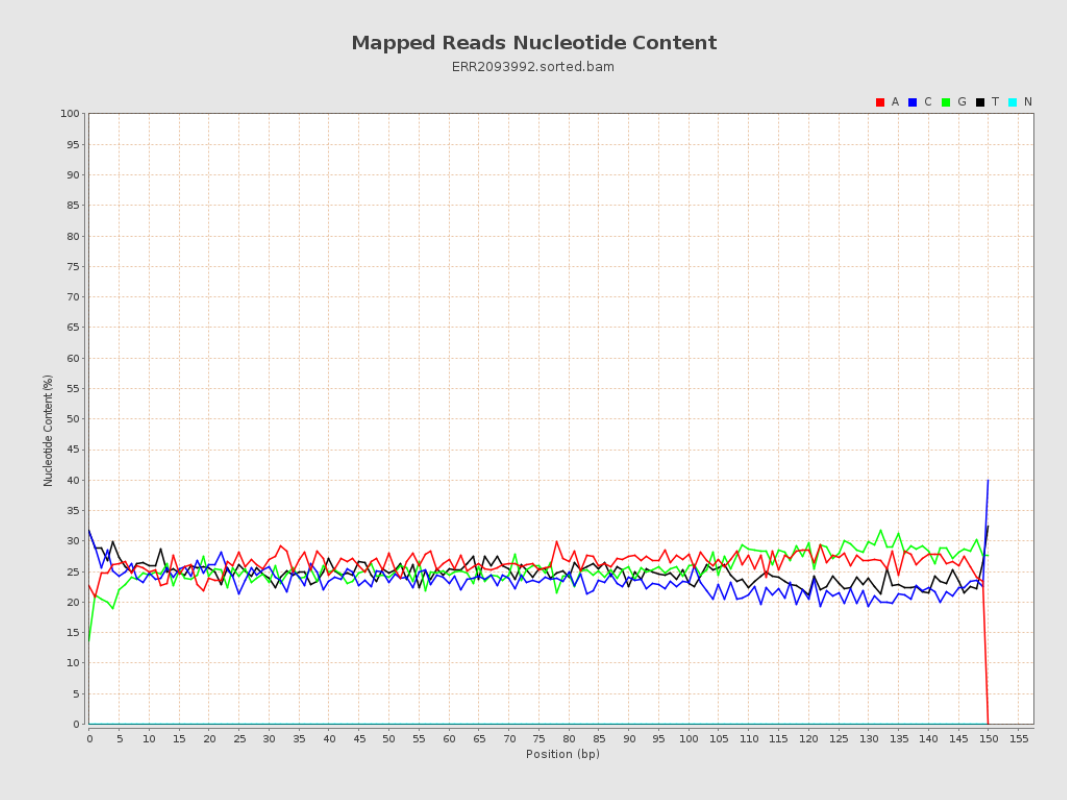
6. Results : Genome Fraction Coverage



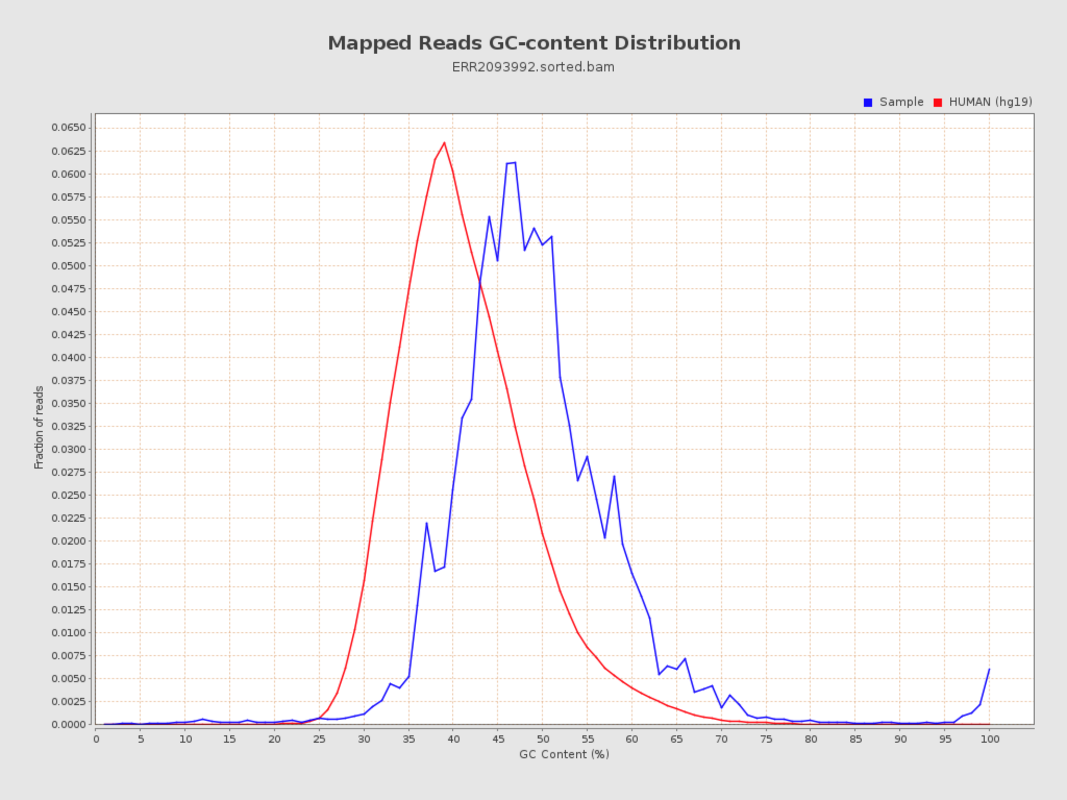
7. Results : Duplication Rate Histogram



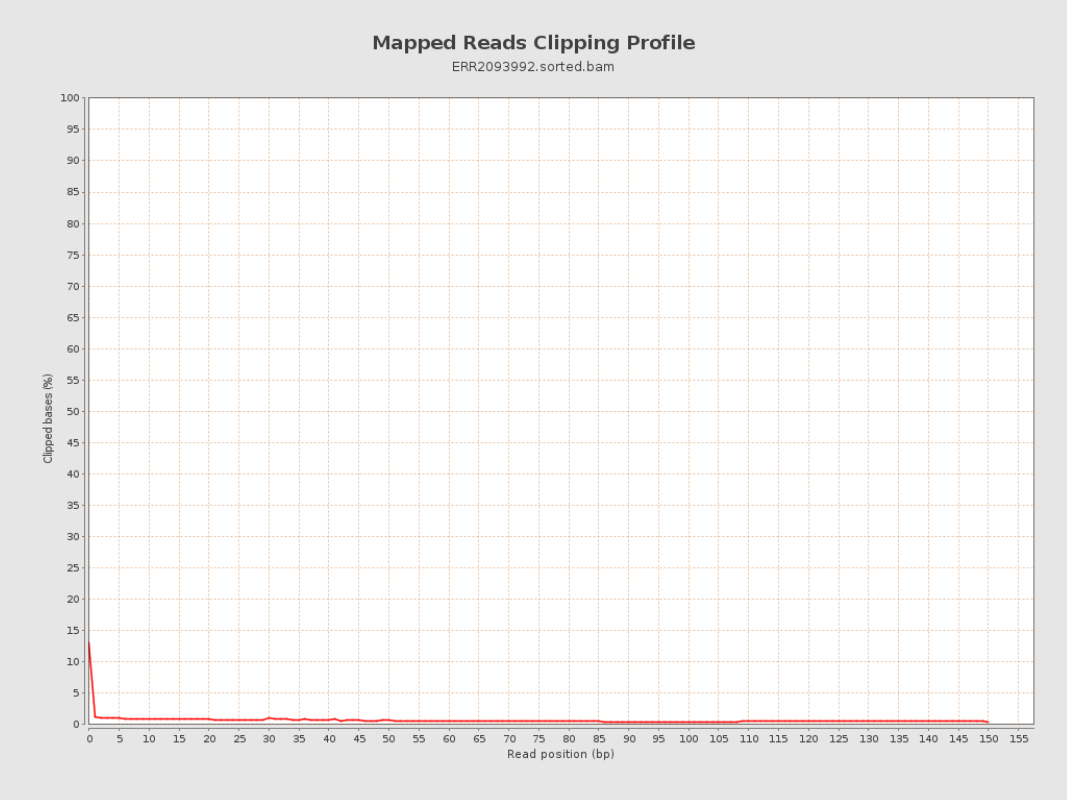
8. Results : Mapped Reads Nucleotide Content



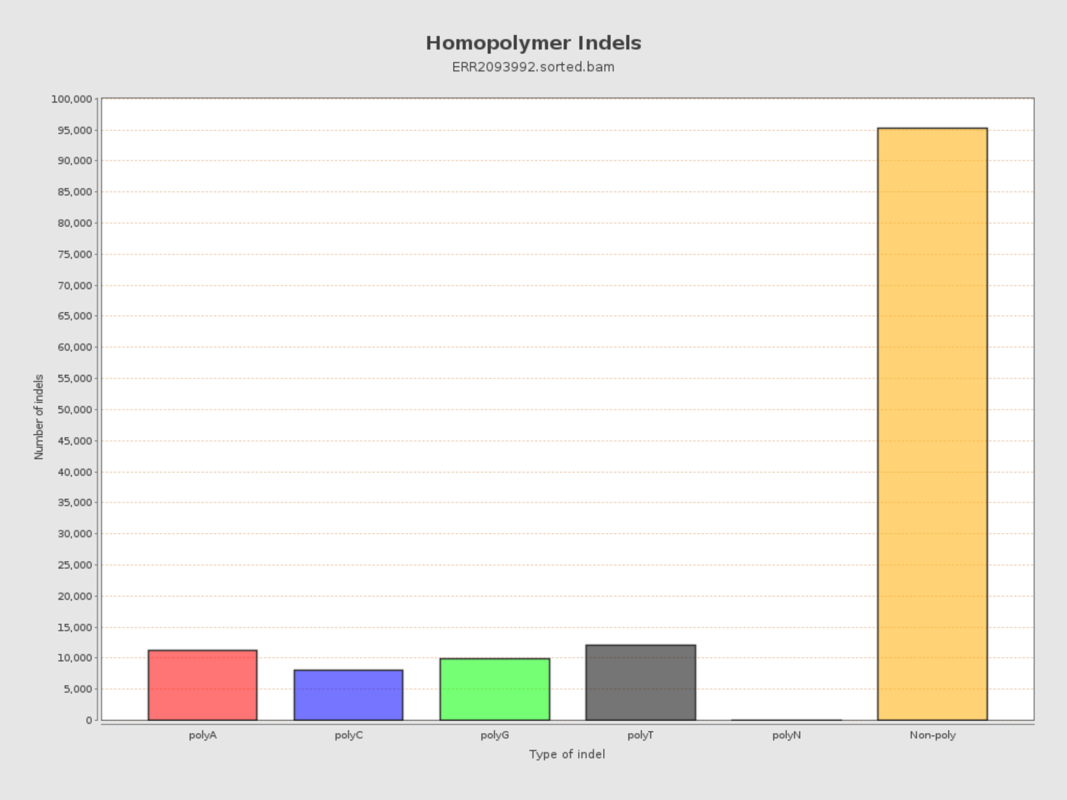
9. Results : Mapped Reads GC-content Distribution



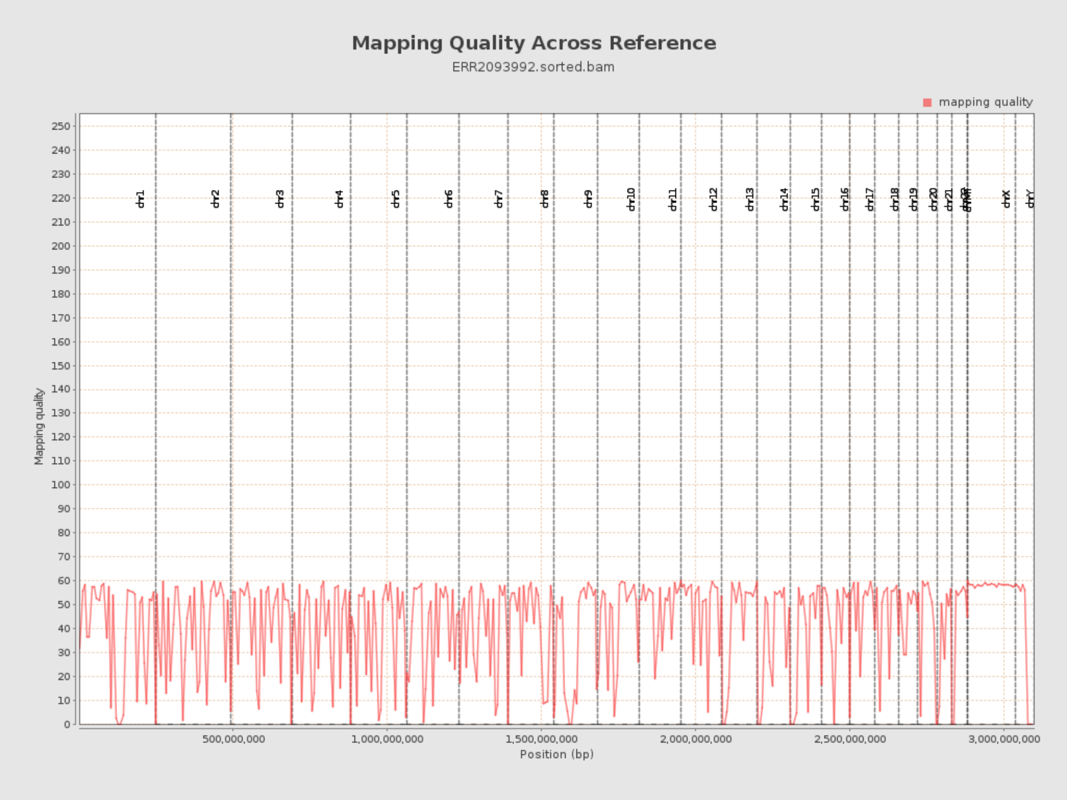
10. Results : Mapped Reads Clipping Profile



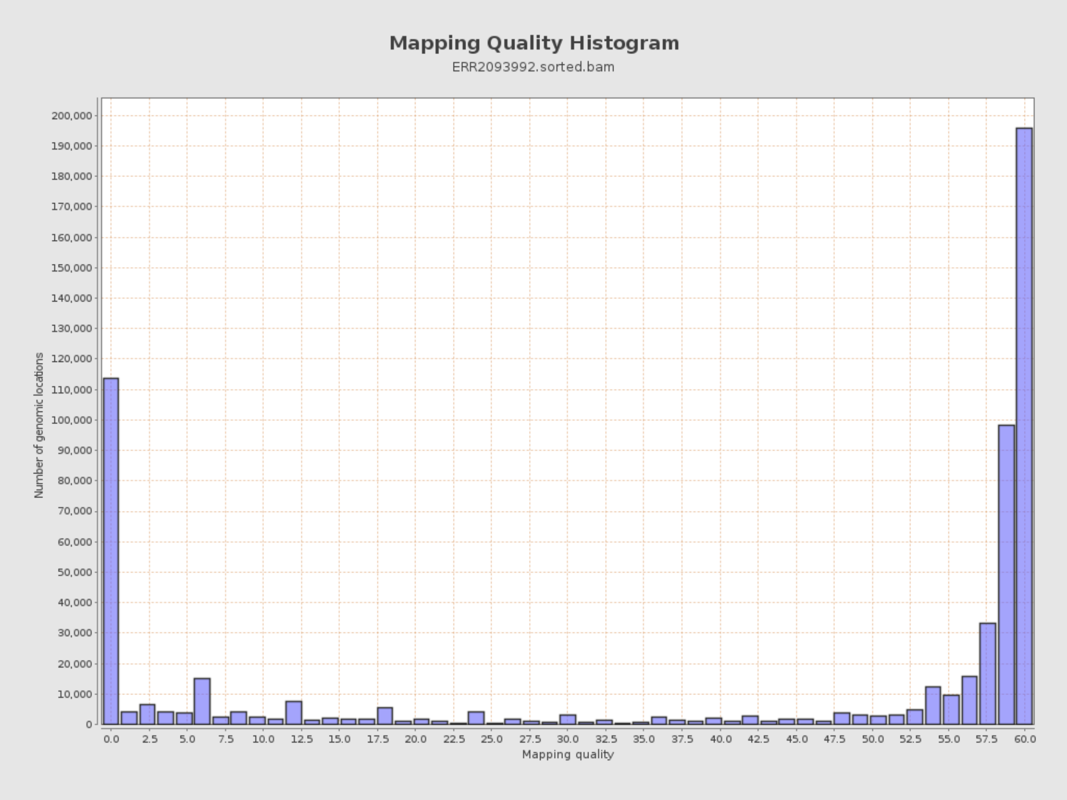
11. Results : Homopolymer Indels



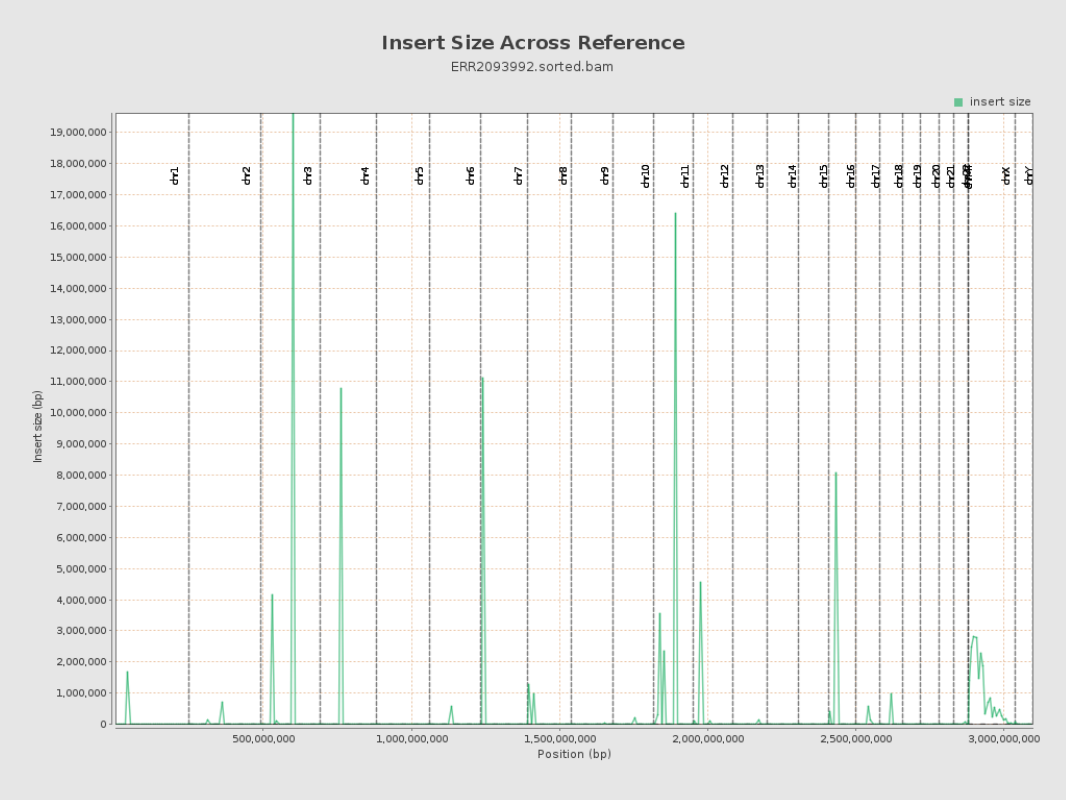
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram