Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093993.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_ERR2093993 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093993_1.fastq.gz ERR2093993_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:07:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	376,678
Mapped reads	362,099 / 96.13%
Unmapped reads	14,579 / 3.87%
Mapped paired reads	362,099 / 96.13%
Mapped reads, first in pair	182,156 / 48.36%
Mapped reads, second in pair	179,943 / 47.77%
Mapped reads, both in pair	358,424 / 95.15%
Mapped reads, singletons	3,675 / 0.98%
Secondary alignments	0
Supplementary alignments	23,590 / 6.26%
Read min/max/mean length	30 / 151 / 142.69
Duplicated reads (estimated)	341,280 / 90.6%
Duplication rate	50.2%
Clipped reads	183,804 / 48.8%

2.2. ACGT Content

Number/percentage of A's	12,010,000 / 26.36%
Number/percentage of C's	10,704,735 / 23.49%
Number/percentage of T's	11,317,215 / 24.84%
Number/percentage of G's	11,534,037 / 25.31%
Number/percentage of N's	478 / 0%

GC Percentage	48.81%

2.3. Coverage

Mean	0.015
Standard Deviation	2.8367

2.4. Mapping Quality

Mean Mapping Quality	40.03

2.5. Insert size

Mean	1,158,725.13
Standard Deviation	9,614,515.77
P25/Median/P75	128 / 164 / 201

2.6. Mismatches and indels

General error rate	3.53%
Mismatches	1,560,070
Insertions	23,947
Mapped reads with at least one insertion	6.49%
Deletions	123,070
Mapped reads with at least one deletion	32.71%
Homopolymer indels	29.23%

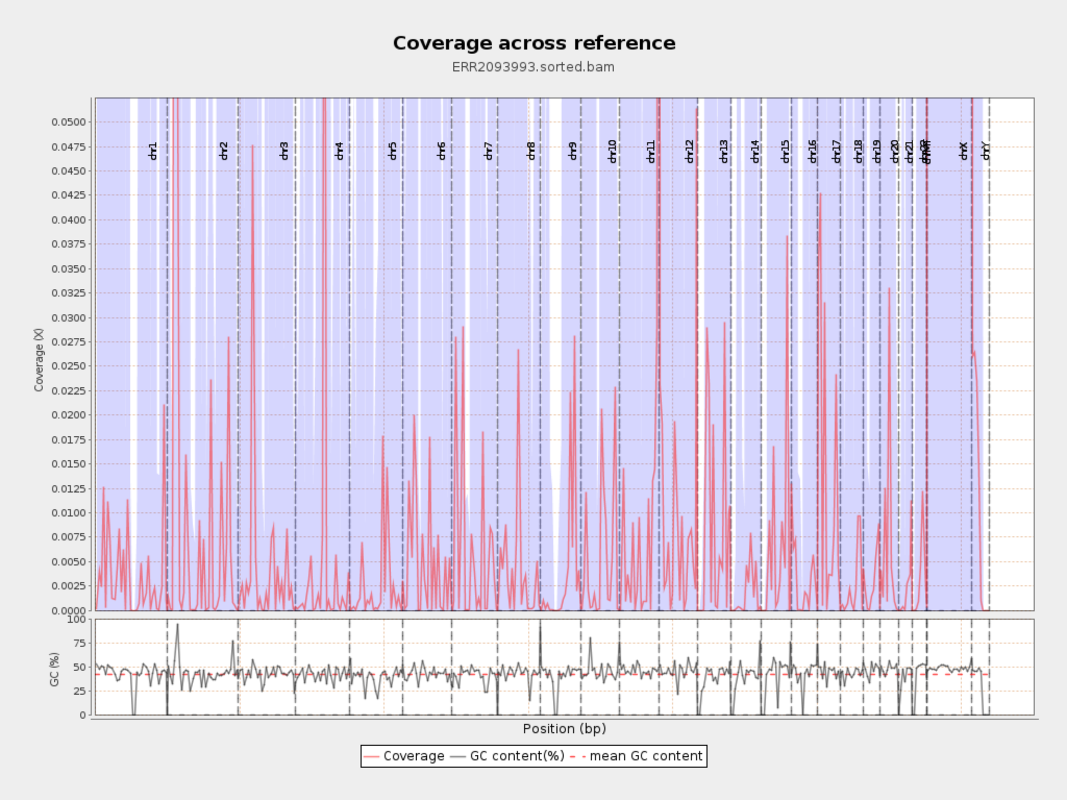
2.7. Chromosome stats

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

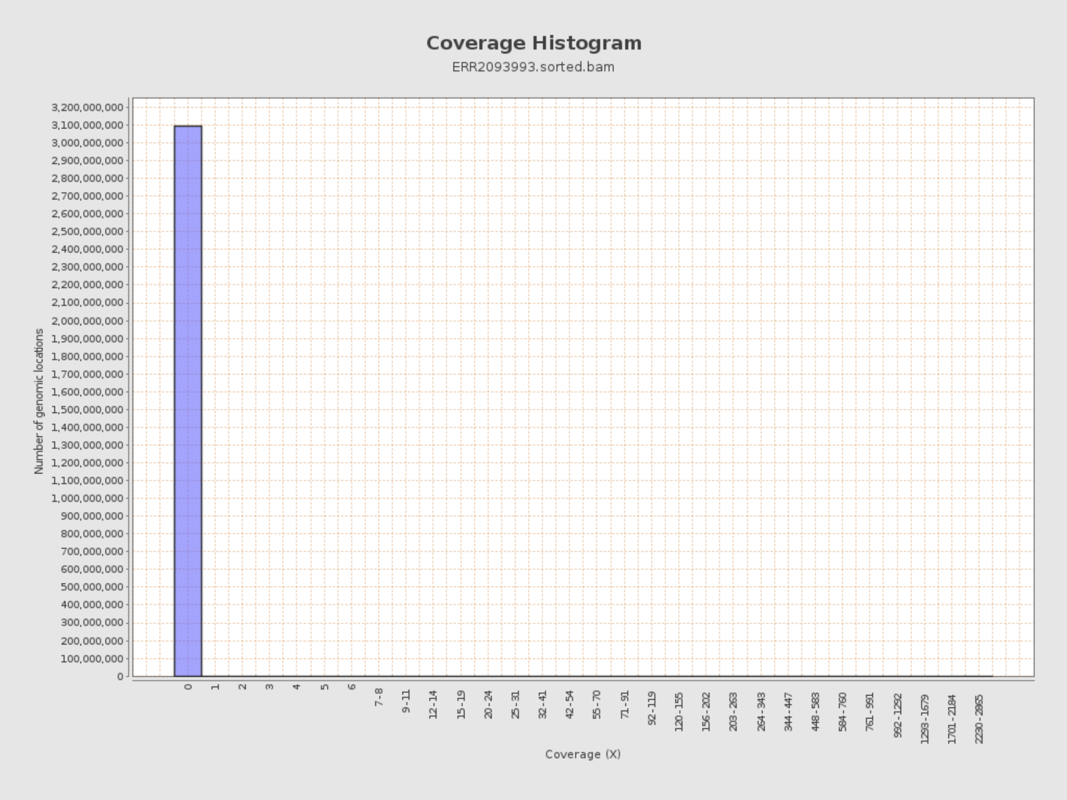
		bases	coverage	deviation
chr1	249250621	893672	0.0036	1.1602
chr2	243199373	2388781	0.0098	2.9978
chr3	198022430	816612	0.0041	1.2579
chr4	191154276	1065783	0.0056	1.963
chr5	180915260	472998	0.0026	1.193
chr6	171115067	853894	0.005	1.3555
chr7	159138663	933598	0.0059	1.7169
chr8	146364022	584430	0.004	1.1861
chr9	141213431	565274	0.004	1.192
chr10	135534747	719822	0.0053	1.6688
chr11	135006516	1031342	0.0076	1.9367
chr12	133851895	1059616	0.0079	1.9069
chr13	115169878	969686	0.0084	2.1839
chr14	107349540	180946	0.0017	0.6091
chr15	102531392	653101	0.0064	1.7289
chr16	90354753	285725	0.0032	0.8611
chr17	81195210	1179538	0.0145	3.3317
chr18	78077248	203229	0.0026	0.8199
chr19	59128983	168519	0.0029	0.6878
chr20	63025520	436235	0.0069	2.3311
chr21	48129895	109125	0.0023	0.4346
chr22	51304566	157531	0.0031	0.7817
chrMT	16571	1230581	74.2611	306.9407
chrX	155270560	28800199	0.1855	9.6307

chrY	59373566	641630	0.0108	1.5141

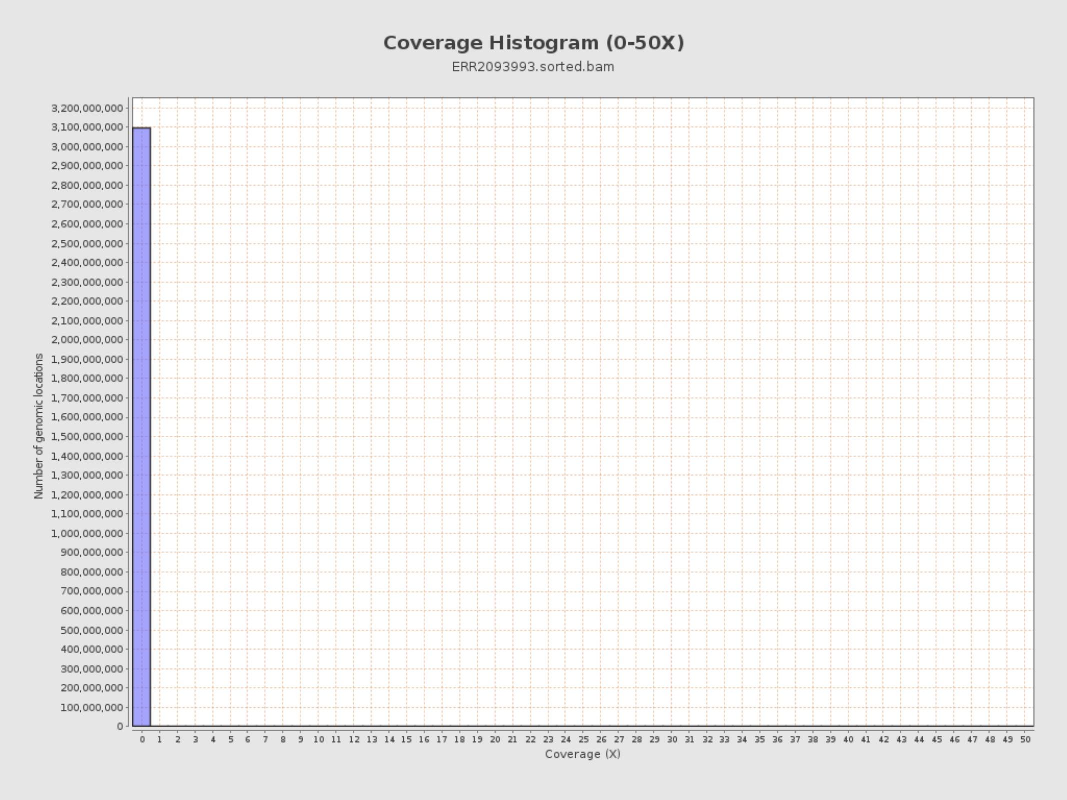
3. Results : Coverage across reference



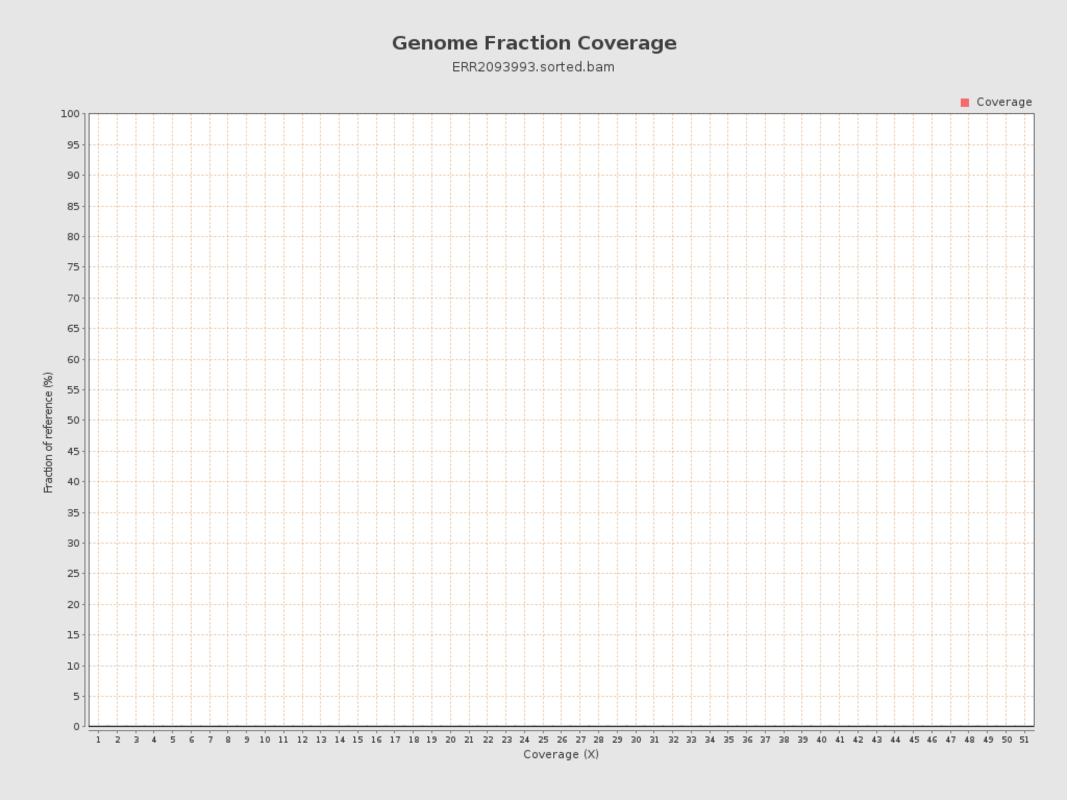
4. Results : Coverage Histogram



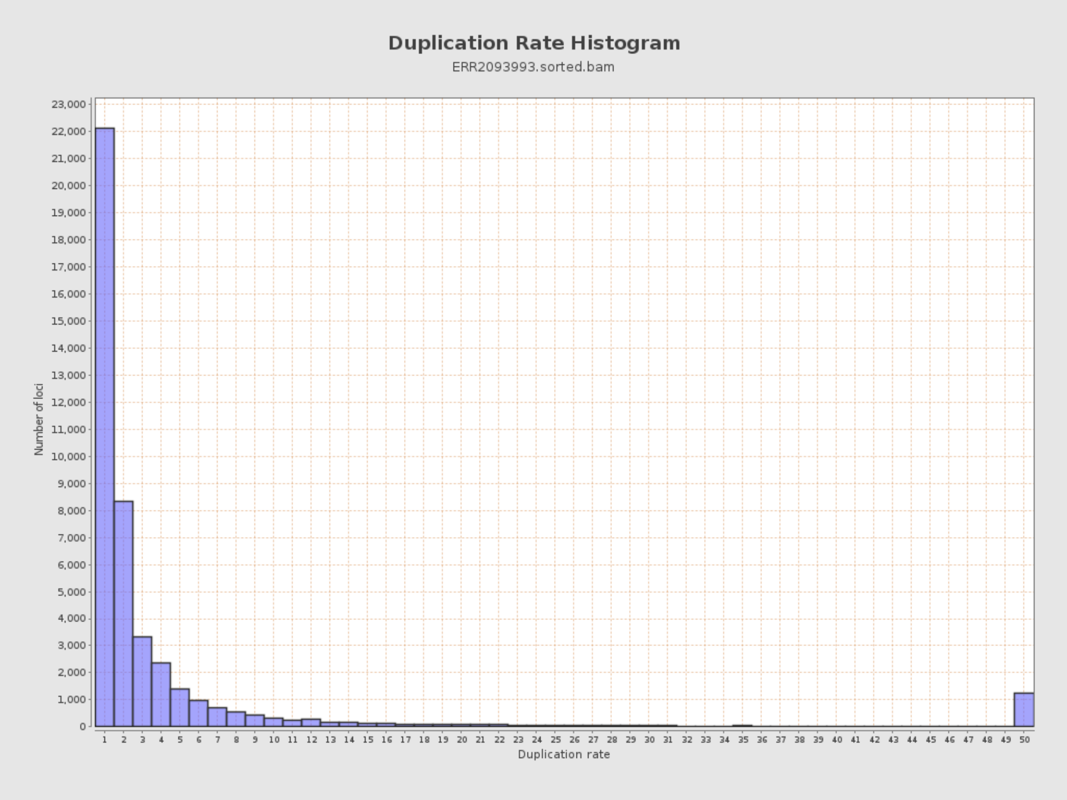
5. Results : Coverage Histogram (0-50X)



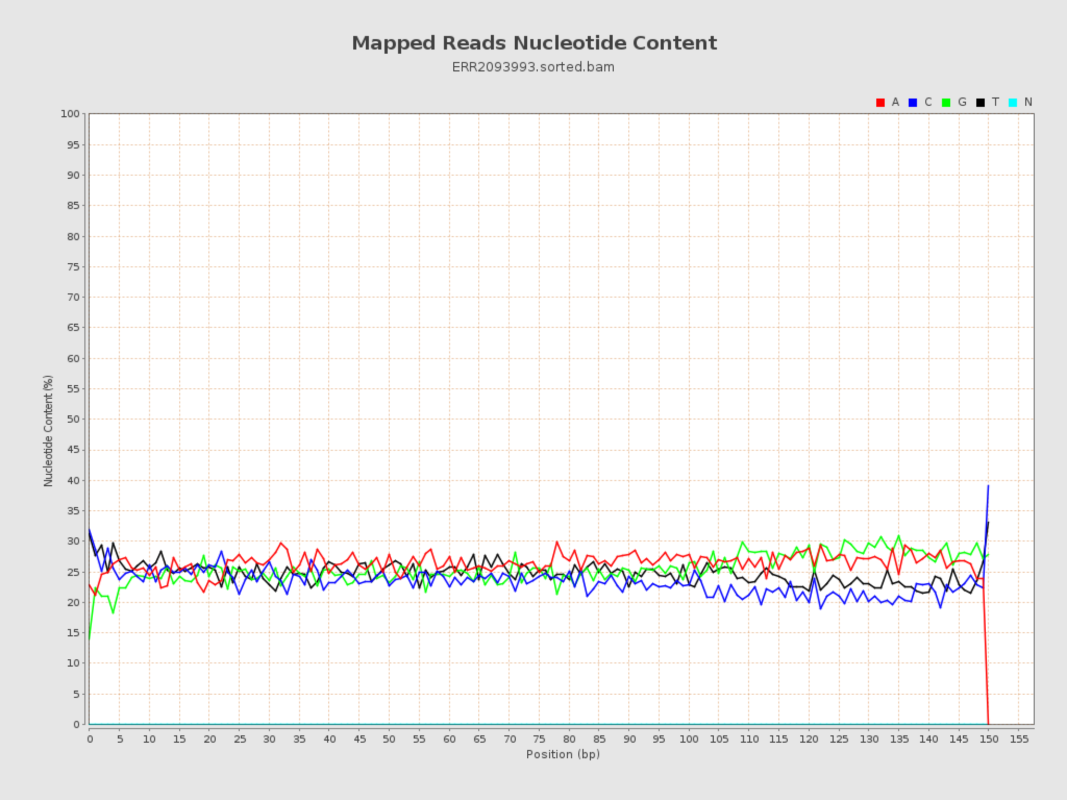
6. Results : Genome Fraction Coverage



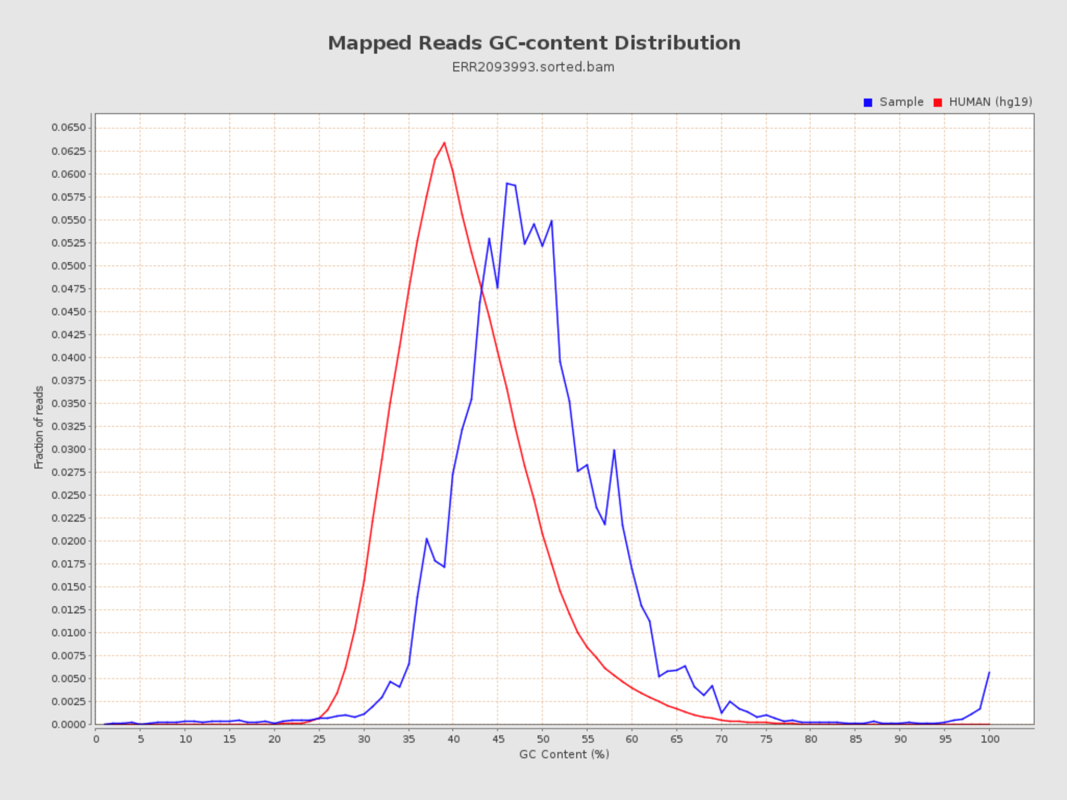
7. Results : Duplication Rate Histogram



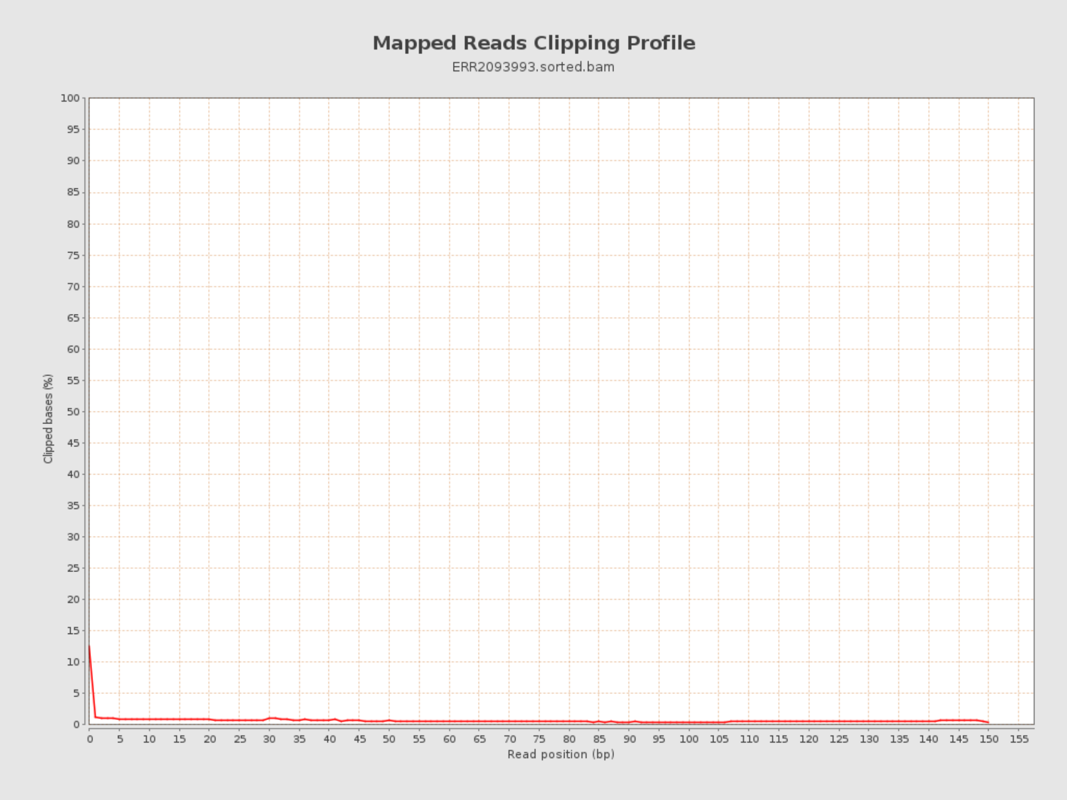
8. Results : Mapped Reads Nucleotide Content



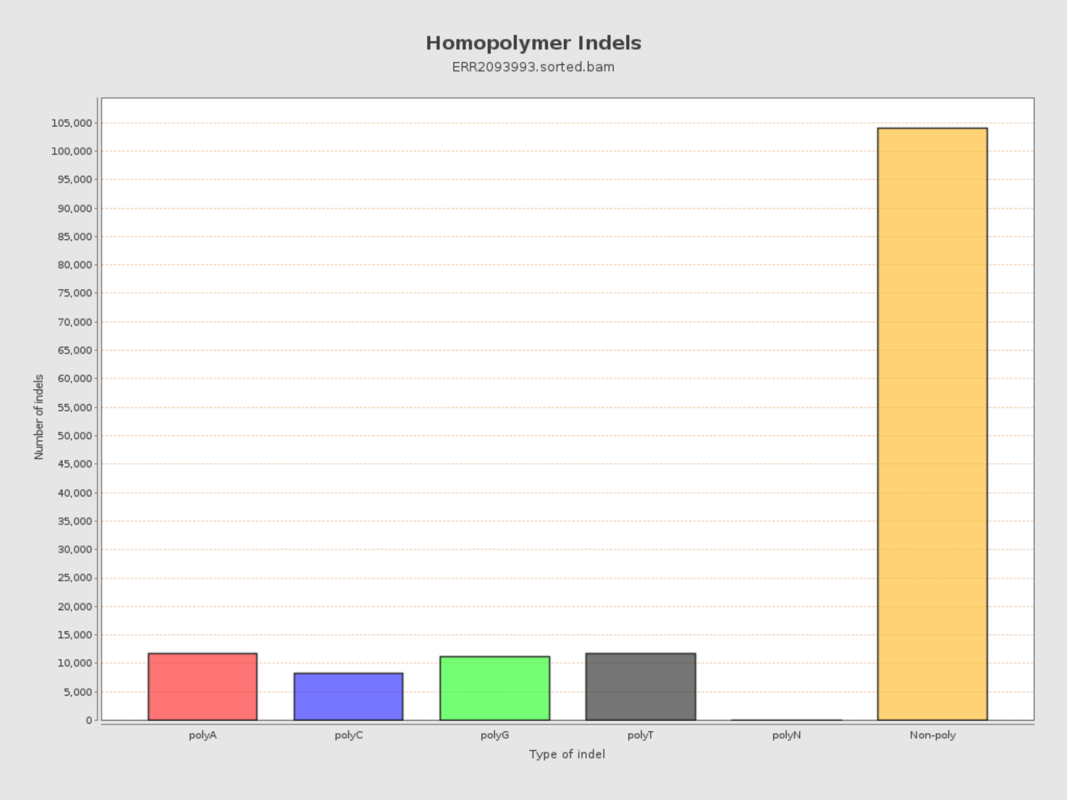
9. Results : Mapped Reads GC-content Distribution



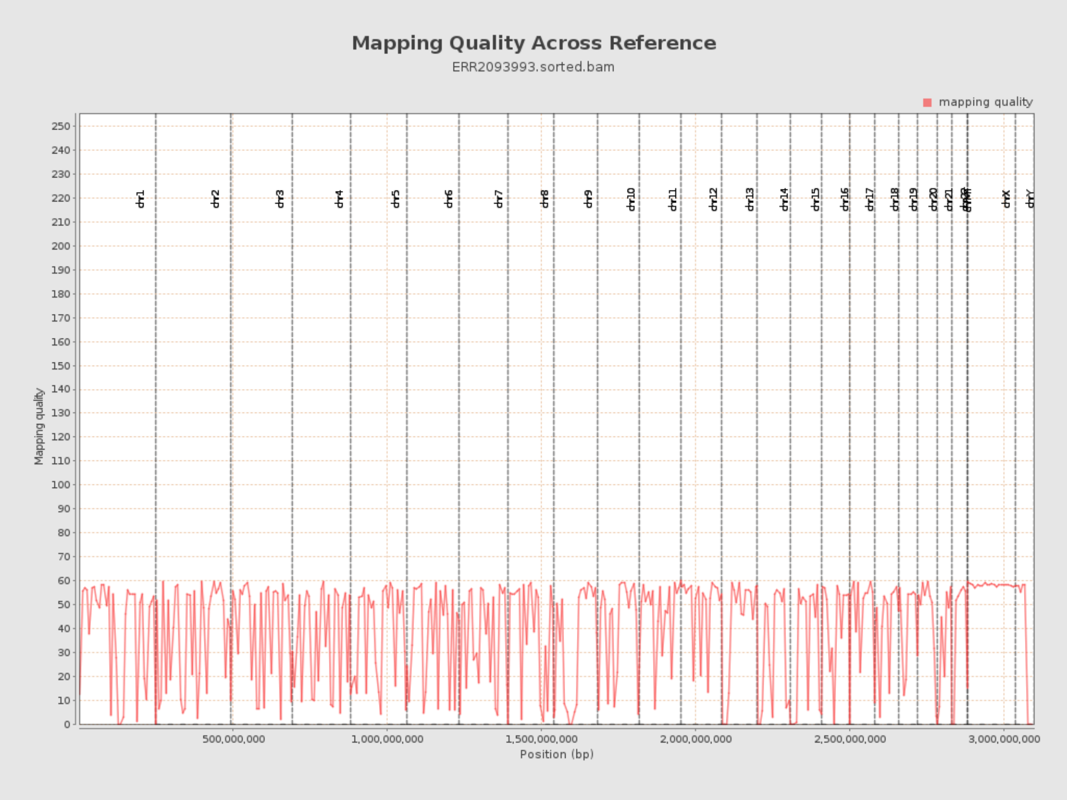
10. Results : Mapped Reads Clipping Profile



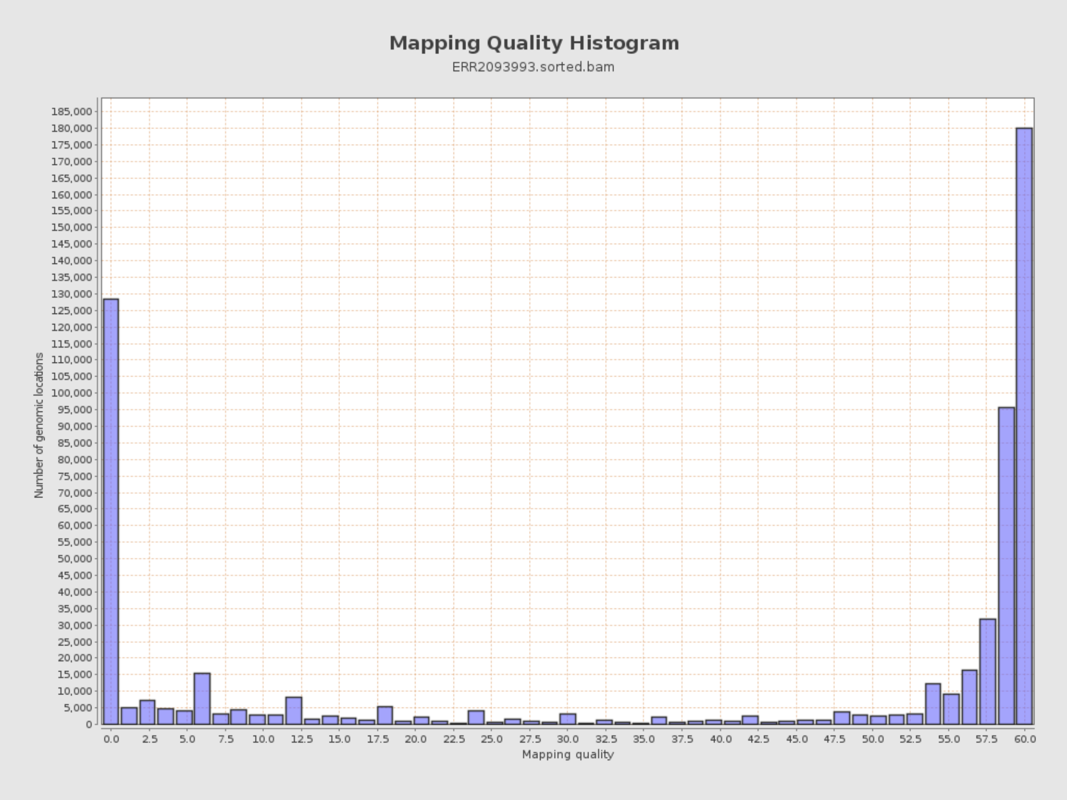
11. Results : Homopolymer Indels



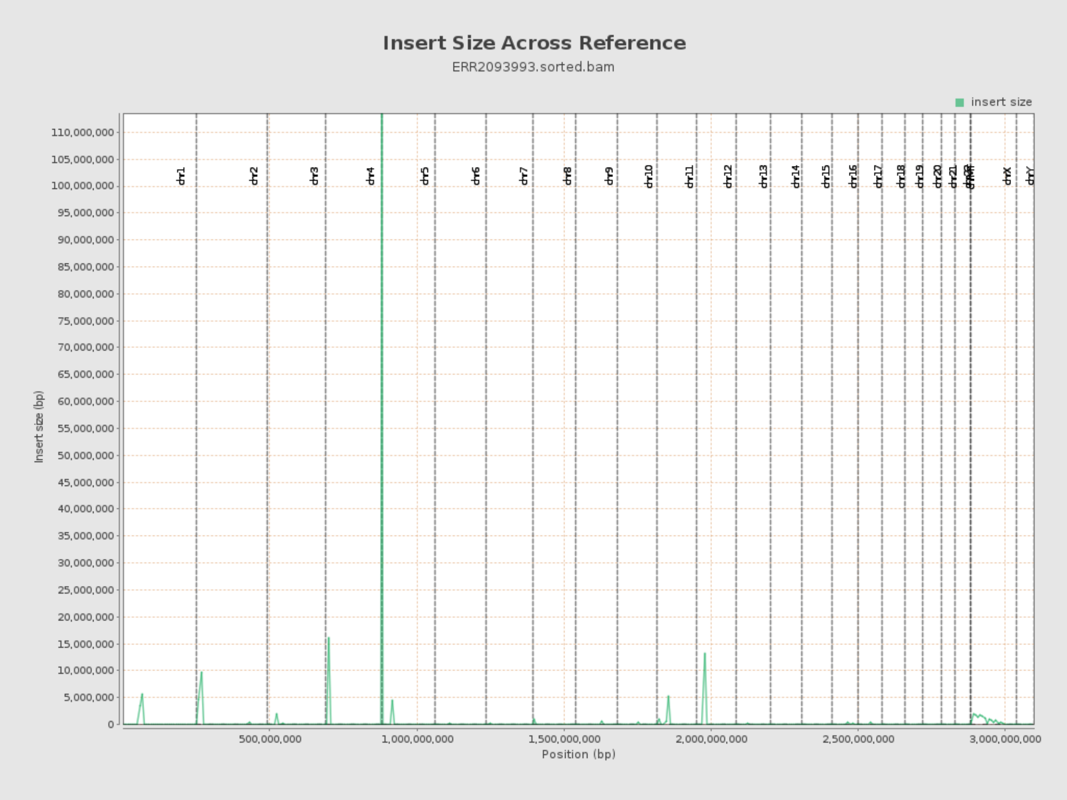
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram