Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 00:55:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094094.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_ERR2094094 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094094_1.fastq.gz ERR2094094_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 00:55:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	808,670
Mapped reads	766,276 / 94.76%
Unmapped reads	42,394 / 5.24%
Mapped paired reads	766,276 / 94.76%
Mapped reads, first in pair	384,913 / 47.6%
Mapped reads, second in pair	381,363 / 47.16%
Mapped reads, both in pair	760,418 / 94.03%
Mapped reads, singletons	5,858 / 0.72%
Secondary alignments	0
Supplementary alignments	54,540 / 6.74%
Read min/max/mean length	30 / 151 / 134.32
Duplicated reads (estimated)	766,082 / 94.73%
Duplication rate	57.26%
Clipped reads	402,204 / 49.74%

2.2. ACGT Content

Number/percentage of A's	25,271,984 / 28%
Number/percentage of C's	19,855,509 / 22%
Number/percentage of T's	23,937,307 / 26.52%
Number/percentage of G's	21,180,765 / 23.47%
Number/percentage of N's	1,103 / 0%

GC Percentage	45.47%

2.3. Coverage

Mean	0.0297
Standard Deviation	7.1517

2.4. Mapping Quality

Mean Mapping Quality	40.11

2.5. Insert size

Mean	1,650,182.02
Standard Deviation	11,518,092.61
P25/Median/P75	109 / 135 / 166

2.6. Mismatches and indels

General error rate	3.54%
Mismatches	3,078,137
Insertions	63,160
Mapped reads with at least one insertion	8.14%
Deletions	242,256
Mapped reads with at least one deletion	30.66%
Homopolymer indels	26.14%

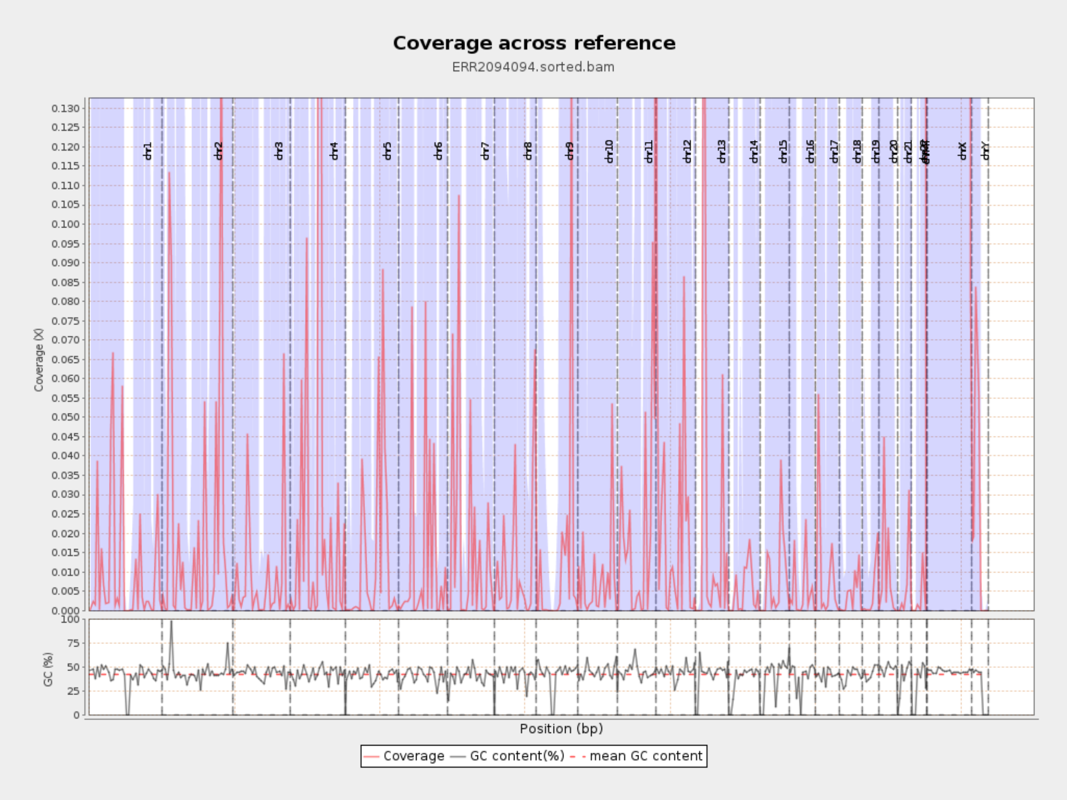
2.7. Chromosome stats

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

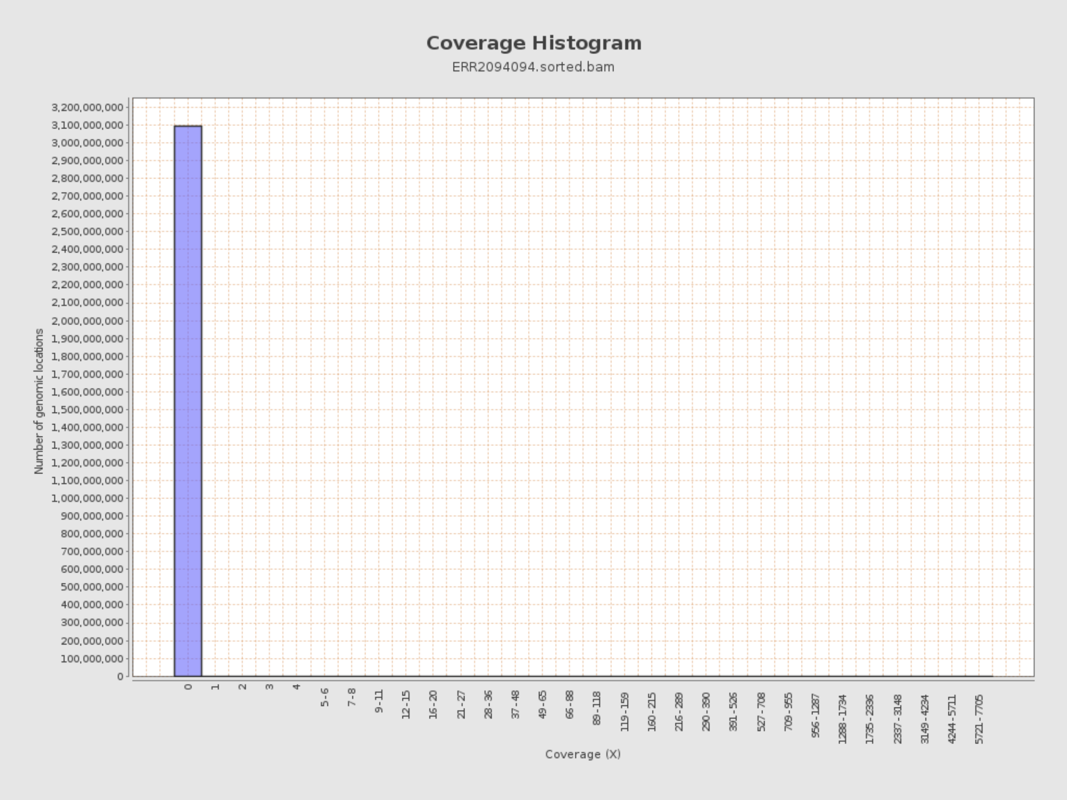
		bases	coverage	deviation
chr1	249250621	2661576	0.0107	4.7716
chr2	243199373	4715727	0.0194	7.4617
chr3	198022430	1566355	0.0079	3.3894
chr4	191154276	5729758	0.03	9.215
chr5	180915260	2413729	0.0133	6.1998
chr6	171115067	2194541	0.0128	4.956
chr7	159138663	2795018	0.0176	5.512
chr8	146364022	1802307	0.0123	3.8157
chr9	141213431	1792765	0.0127	6.1784
chr10	135534747	1159322	0.0086	2.8007
chr11	135006516	3068455	0.0227	6.9233
chr12	133851895	2902527	0.0217	5.4176
chr13	115169878	2505083	0.0218	6.6564
chr14	107349540	533161	0.005	1.7821
chr15	102531392	904791	0.0088	2.0724
chr16	90354753	457106	0.0051	1.9299
chr17	81195210	711846	0.0088	3.7656
chr18	78077248	323768	0.0041	1.1342
chr19	59128983	260215	0.0044	1.6056
chr20	63025520	631531	0.01	3.6305
chr21	48129895	321132	0.0067	2.2217
chr22	51304566	164791	0.0032	1.2608
chrMT	16571	29031	1.7519	10.1759
chrX	155270560	51089616	0.329	22.0309

chrY	59373566	1320614	0.0222	4.9961

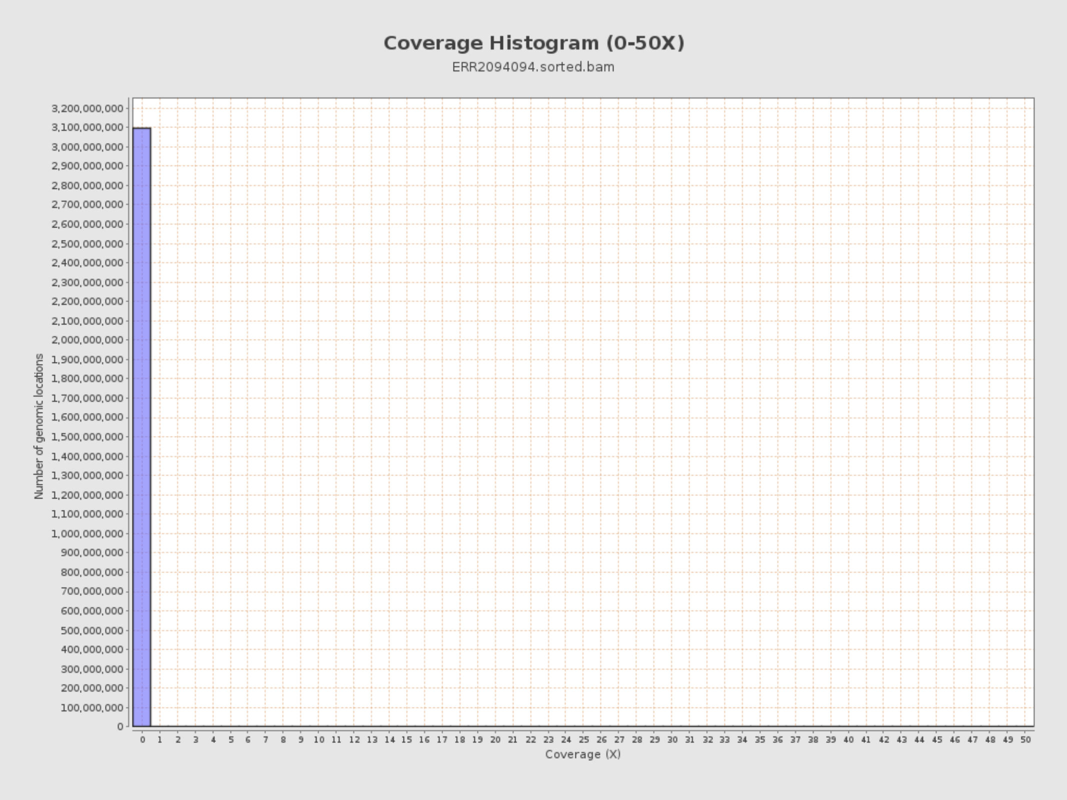
3. Results : Coverage across reference



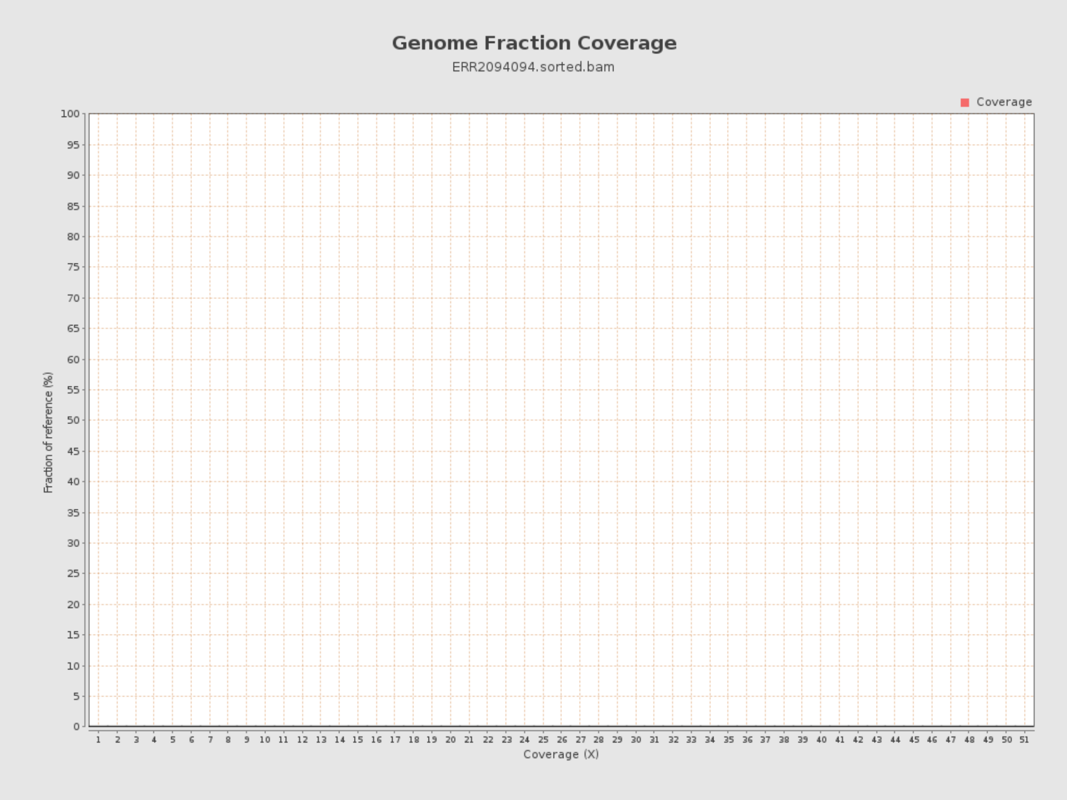
4. Results : Coverage Histogram



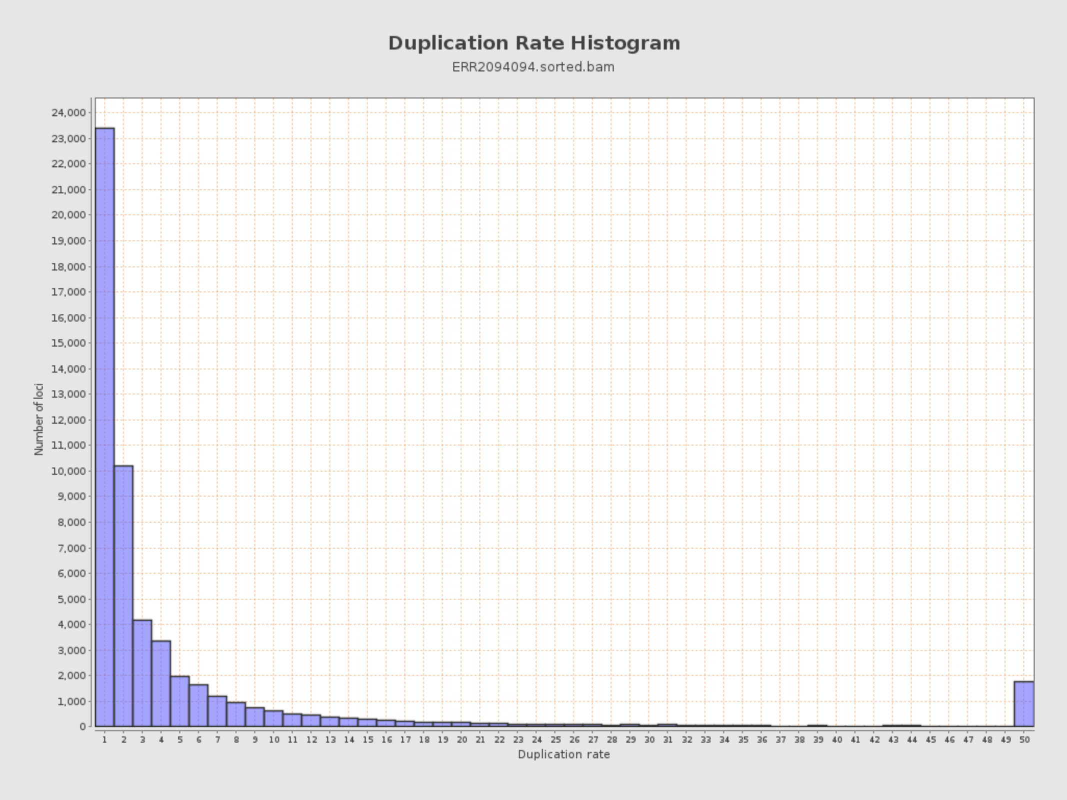
5. Results : Coverage Histogram (0-50X)



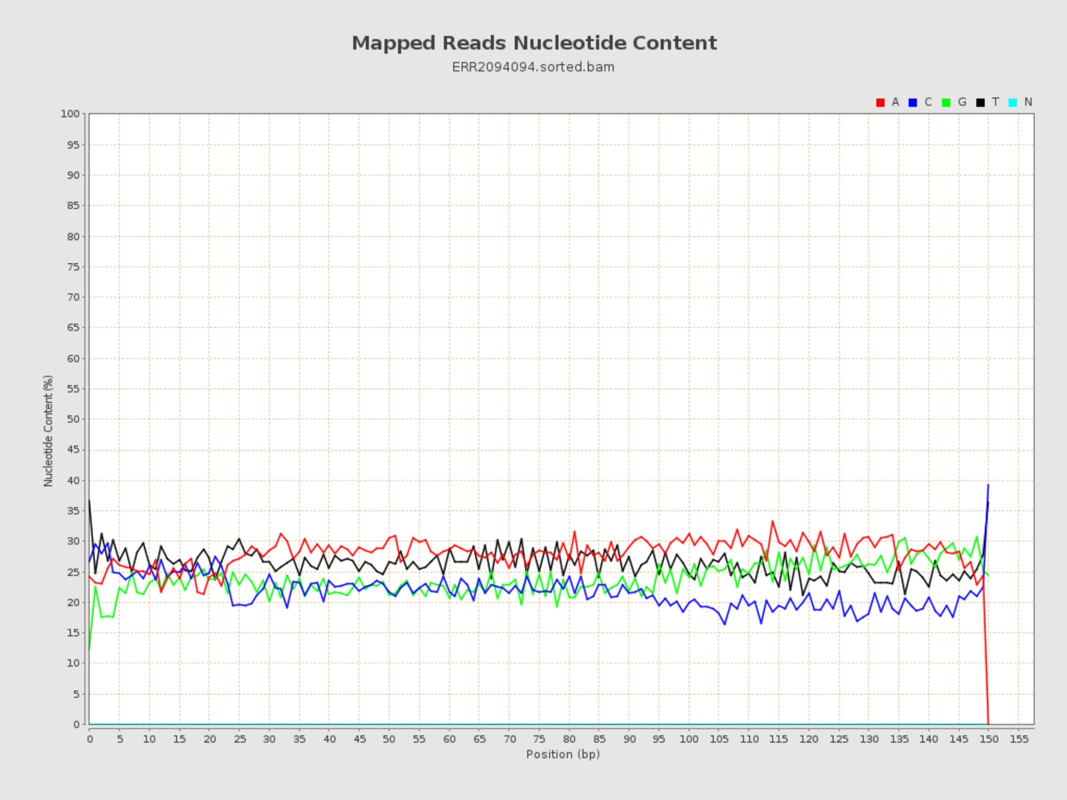
6. Results : Genome Fraction Coverage



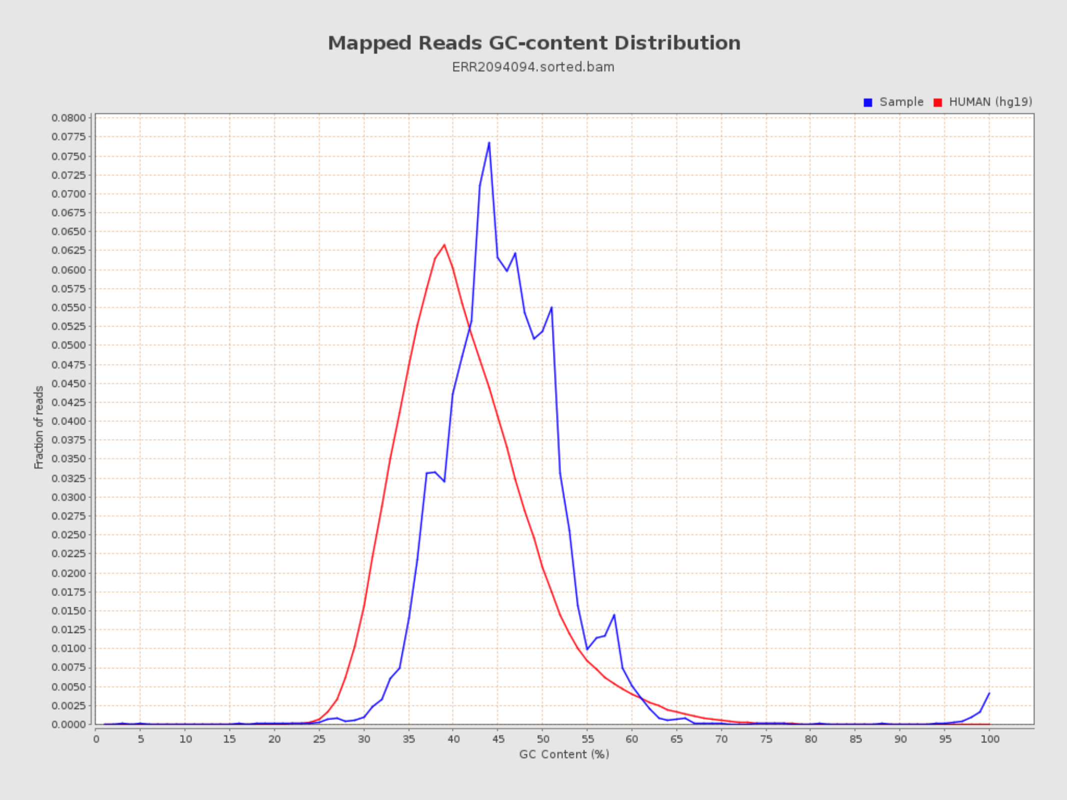
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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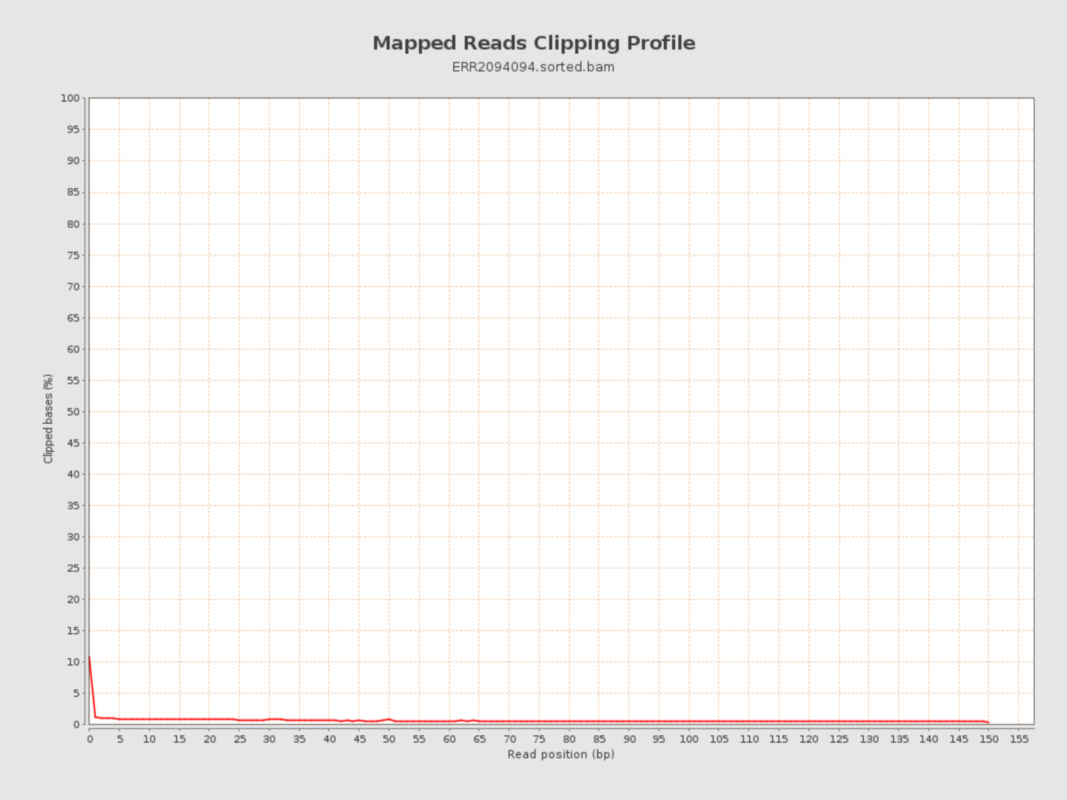
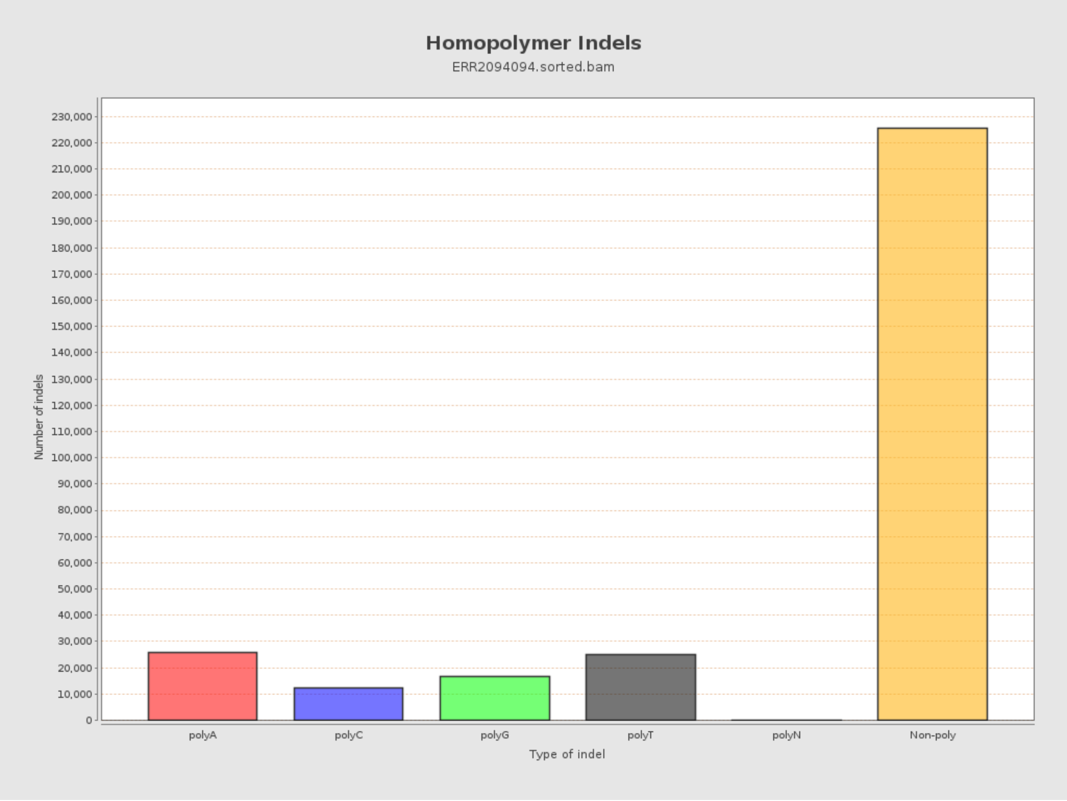
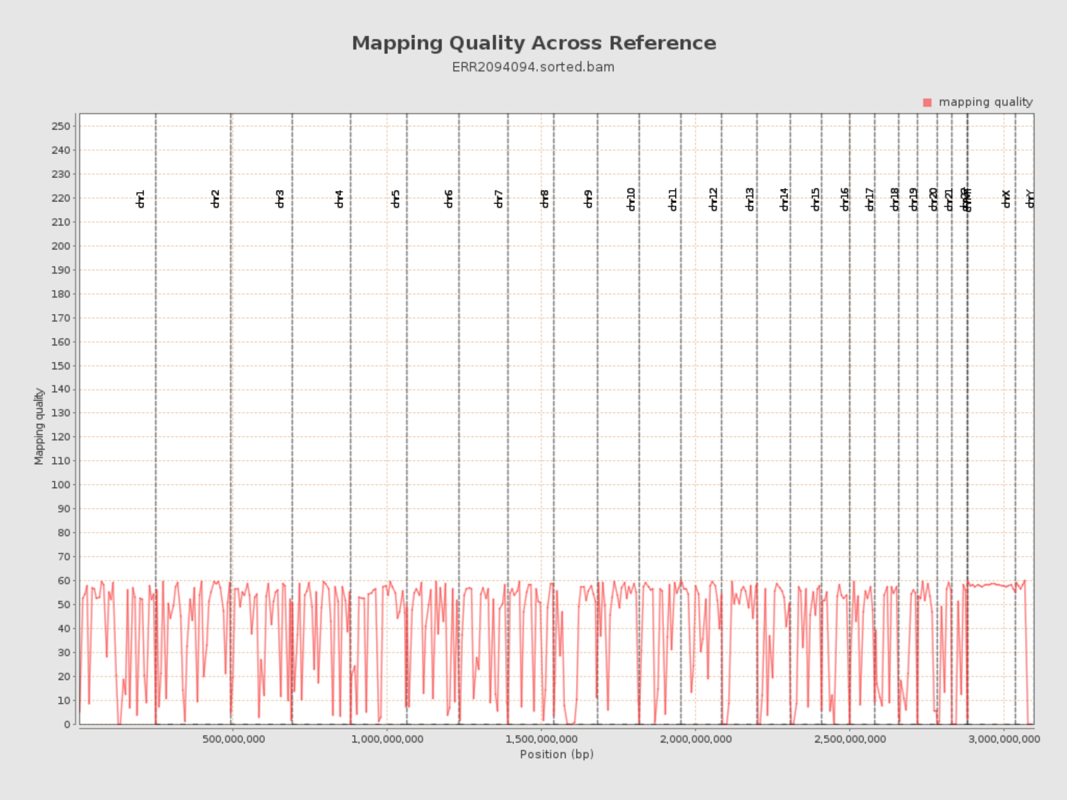
10. Results : Mapped Reads Clipping Profile



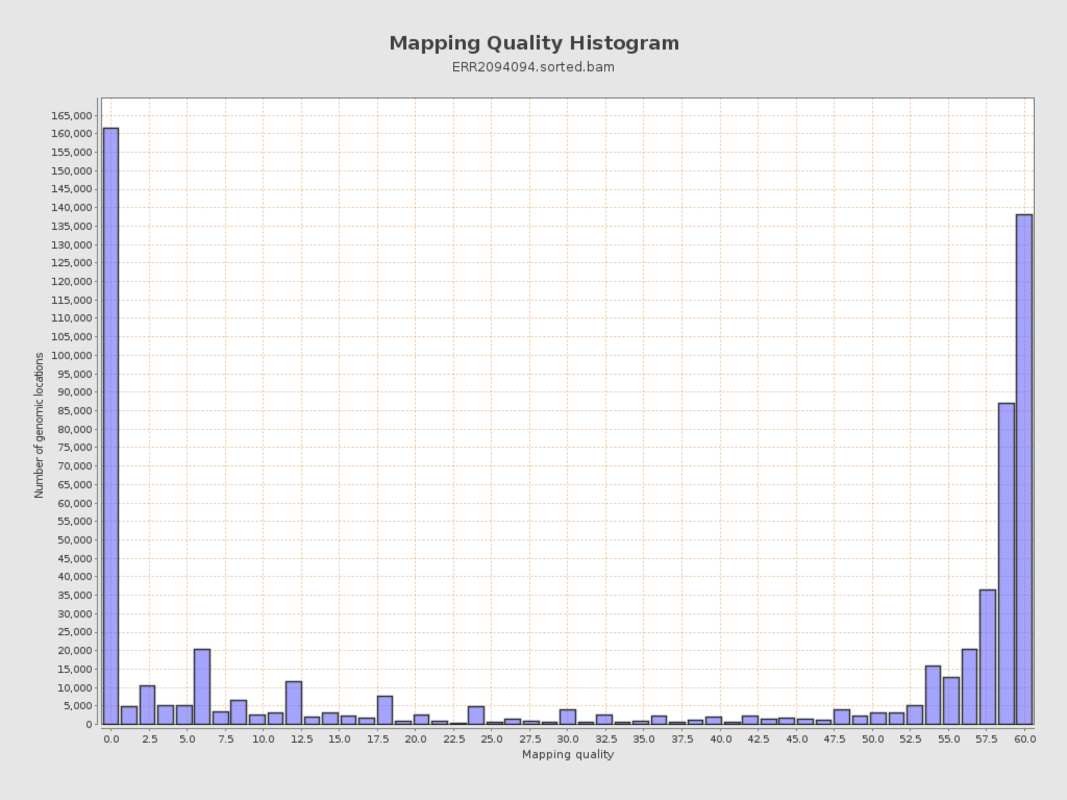
11. Results : Homopolymer Indels



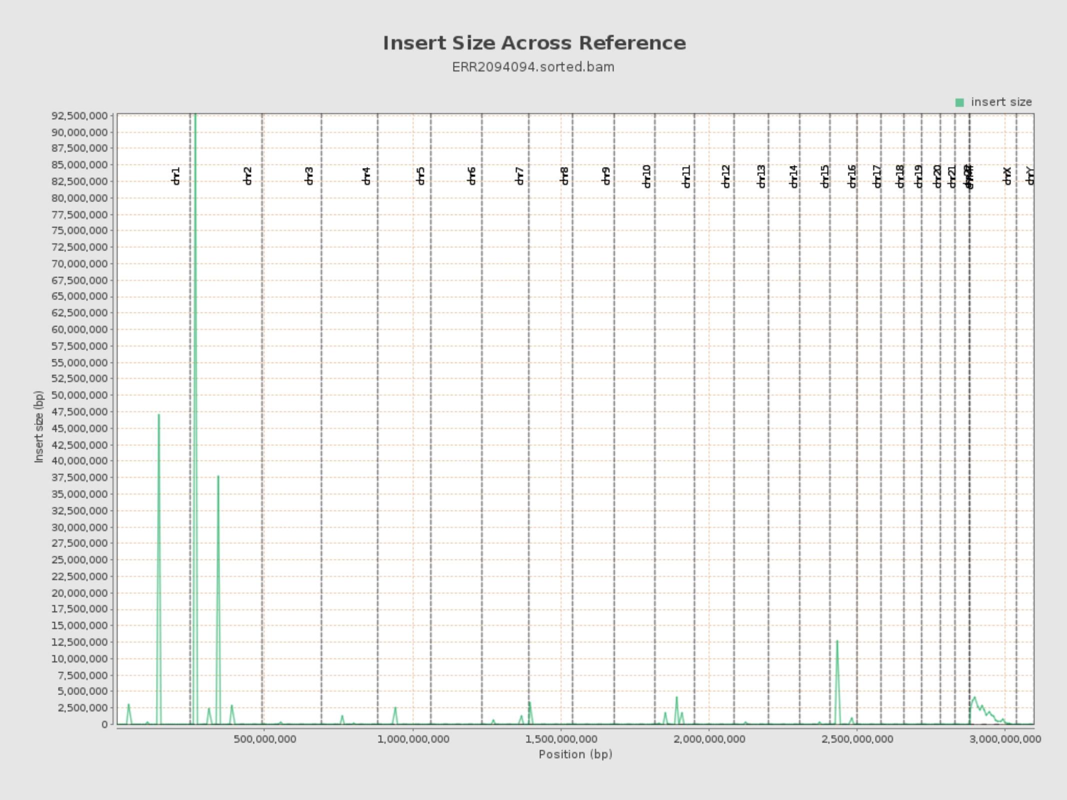
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram