Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:03:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093991.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_ERR2093991 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093991_1.fastq.gz ERR2093991_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:02:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	383,566
Mapped reads	364,053 / 94.91%
Unmapped reads	19,513 / 5.09%
Mapped paired reads	364,053 / 94.91%
Mapped reads, first in pair	183,015 / 47.71%
Mapped reads, second in pair	181,038 / 47.2%
Mapped reads, both in pair	360,716 / 94.04%
Mapped reads, singletons	3,337 / 0.87%
Secondary alignments	0
Supplementary alignments	21,359 / 5.57%
Read min/max/mean length	30 / 151 / 140.53
Duplicated reads (estimated)	344,175 / 89.73%
Duplication rate	50.59%
Clipped reads	172,339 / 44.93%

2.2. ACGT Content

Number/percentage of A's	12,035,124 / 26.17%
Number/percentage of C's	10,894,699 / 23.69%
Number/percentage of T's	11,399,995 / 24.79%
Number/percentage of G's	11,662,343 / 25.36%
Number/percentage of N's	397 / 0%

GC Percentage	49.04%

2.3. Coverage

Mean	0.0151
Standard Deviation	3.139

2.4. Mapping Quality

Mean Mapping Quality	41.37

2.5. Insert size

Mean	975,688.68
Standard Deviation	8,926,681.55
P25/Median/P75	127 / 164 / 204

2.6. Mismatches and indels

General error rate	3.42%
Mismatches	1,520,740
Insertions	24,267
Mapped reads with at least one insertion	6.54%
Deletions	122,841
Mapped reads with at least one deletion	32.41%
Homopolymer indels	30.75%

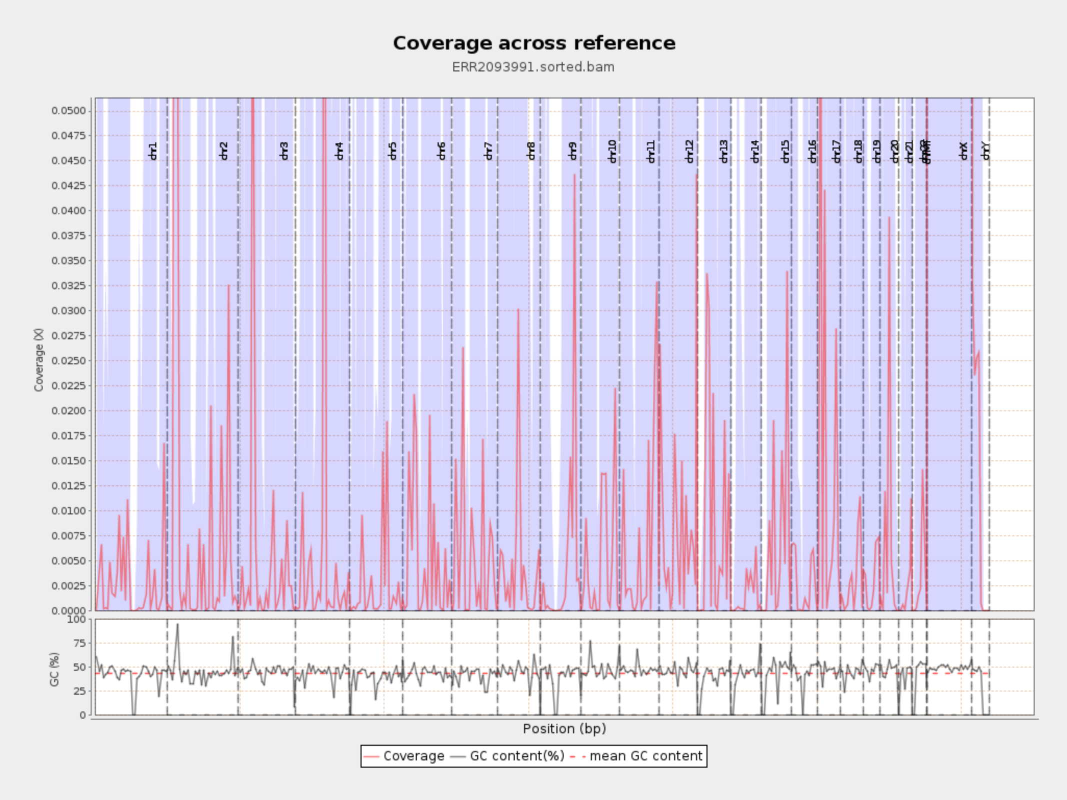
2.7. Chromosome stats

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

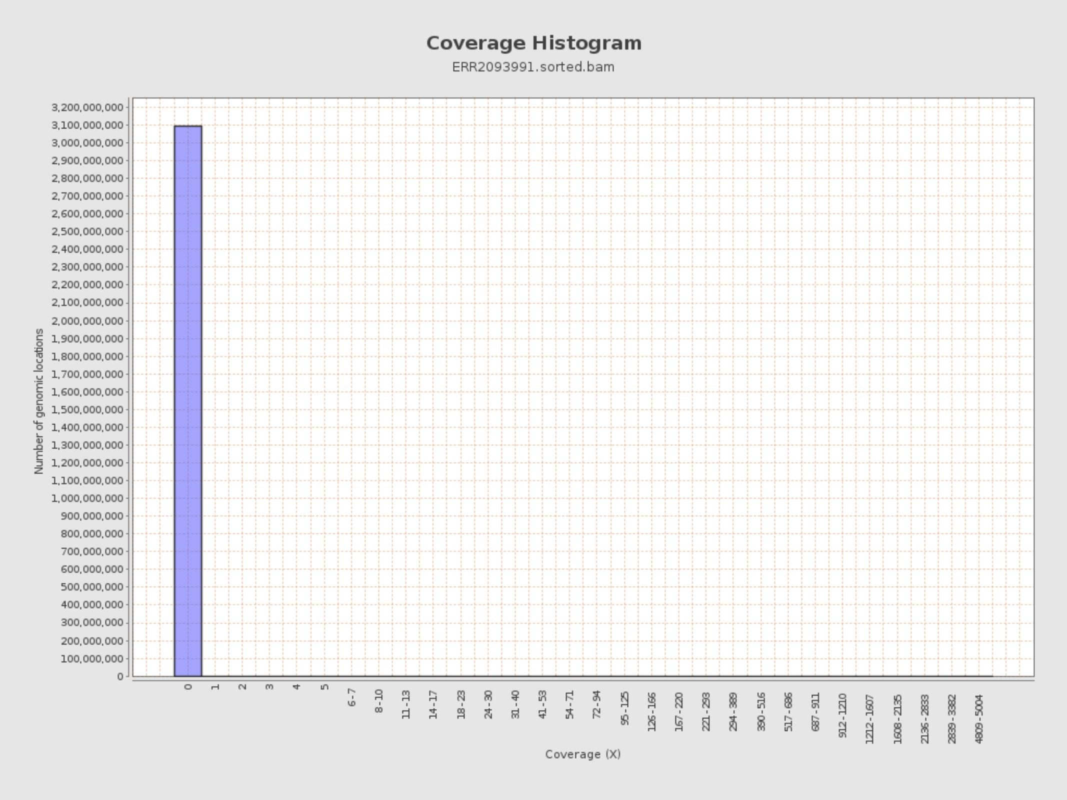
		bases	coverage	deviation
chr1	249250621	687163	0.0028	0.9105
chr2	243199373	2246264	0.0092	2.9092
chr3	198022430	978889	0.0049	1.7972
chr4	191154276	1222101	0.0064	2.1114
chr5	180915260	475297	0.0026	1.2623
chr6	171115067	900640	0.0053	1.6069
chr7	159138663	819230	0.0051	1.3977
chr8	146364022	619373	0.0042	1.3844
chr9	141213431	672826	0.0048	1.5541
chr10	135534747	678709	0.005	1.4241
chr11	135006516	947908	0.007	1.9556
chr12	133851895	1067200	0.008	1.7984
chr13	115169878	1013658	0.0088	2.5247
chr14	107349540	156377	0.0015	0.4605
chr15	102531392	719822	0.007	1.9076
chr16	90354753	246733	0.0027	0.6882
chr17	81195210	1251660	0.0154	3.8788
chr18	78077248	248812	0.0032	0.853
chr19	59128983	171314	0.0029	0.7933
chr20	63025520	461226	0.0073	2.6788
chr21	48129895	107484	0.0022	0.3955
chr22	51304566	165961	0.0032	0.9793
chrMT	16571	2110706	127.3735	536.0494
chrX	155270560	28079555	0.1808	10.0182

chrY	59373566	753828	0.0127	2.0266

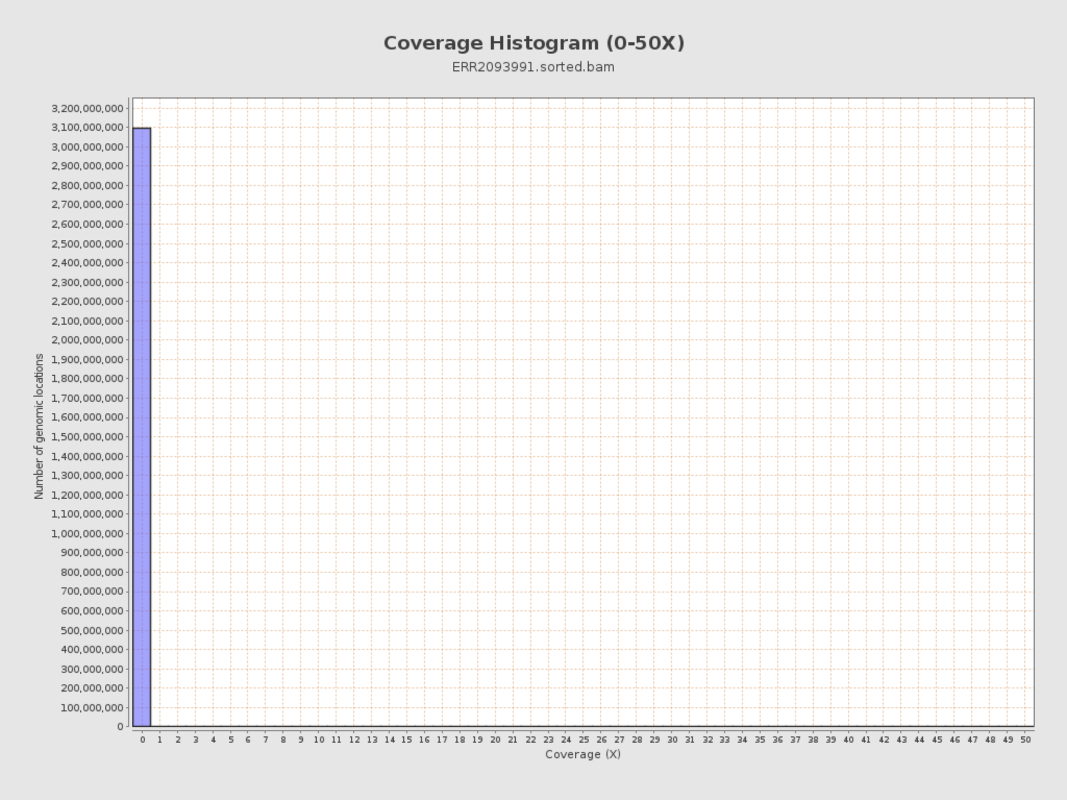
3. Results : Coverage across reference



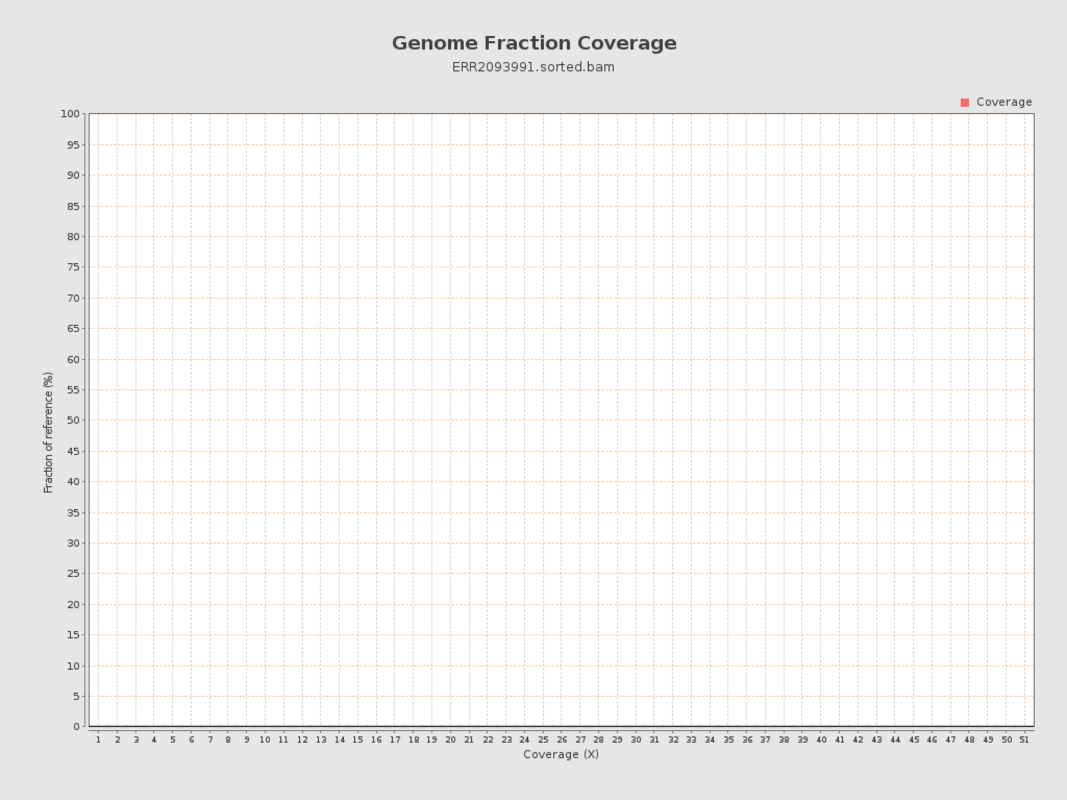
4. Results : Coverage Histogram



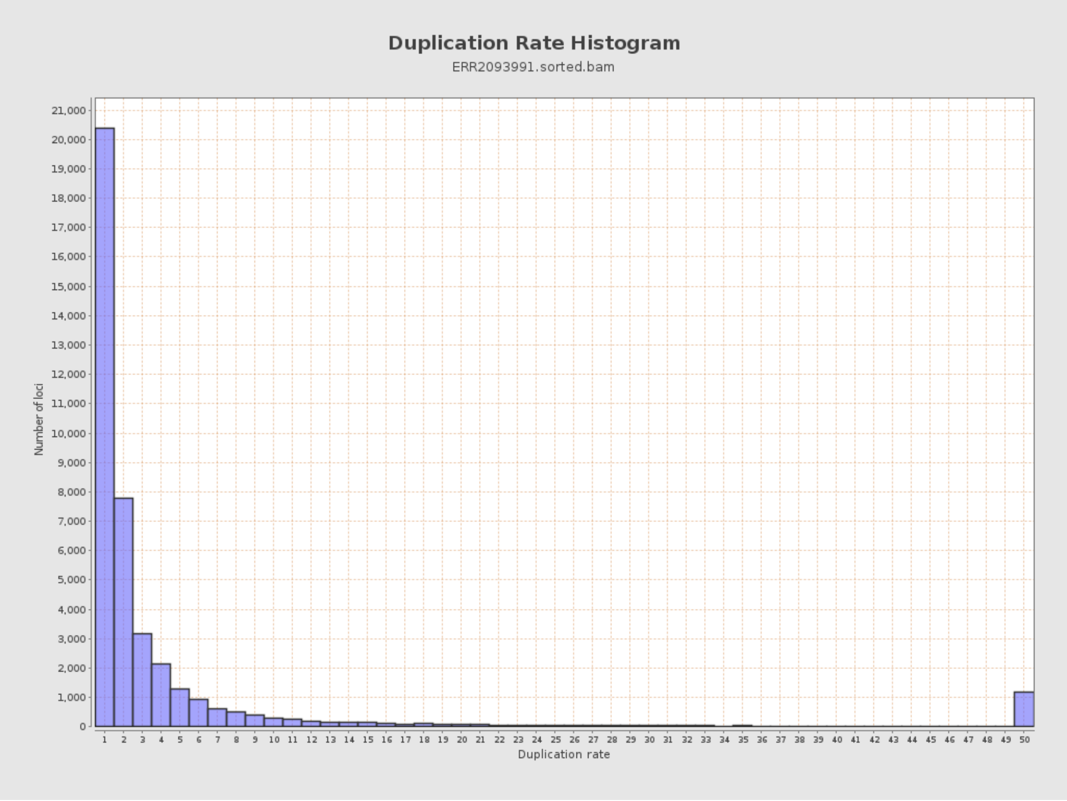
5. Results : Coverage Histogram (0-50X)



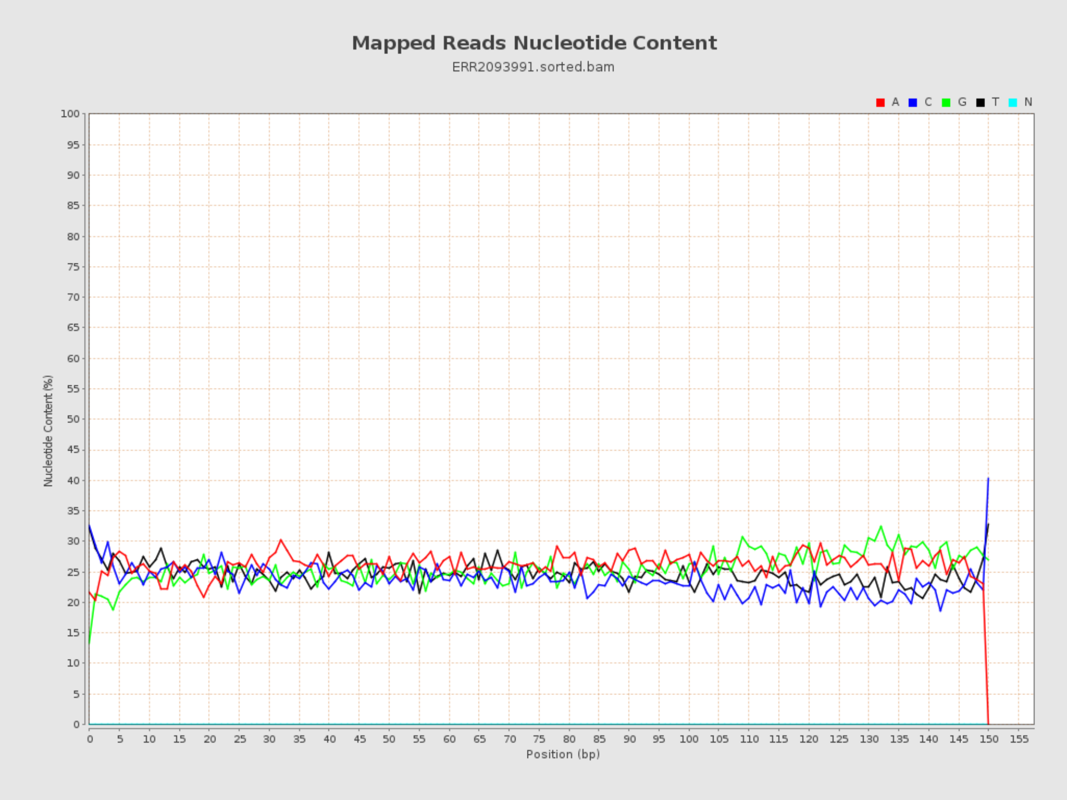
6. Results : Genome Fraction Coverage



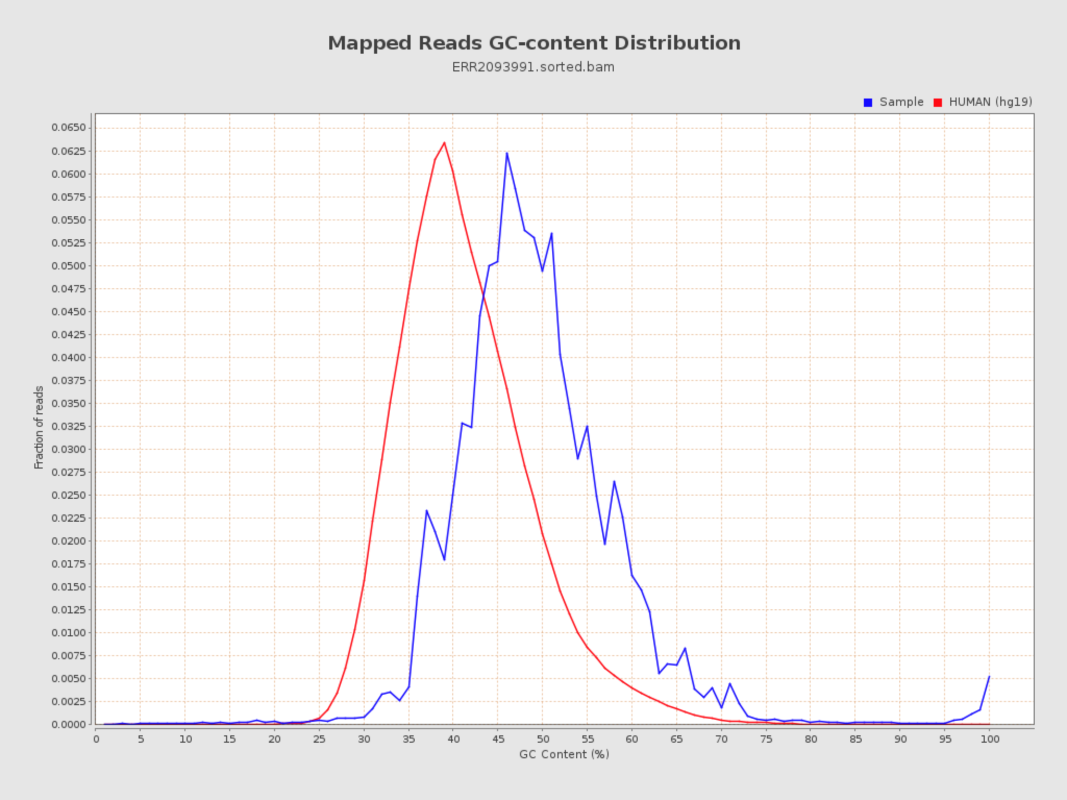
7. Results : Duplication Rate Histogram



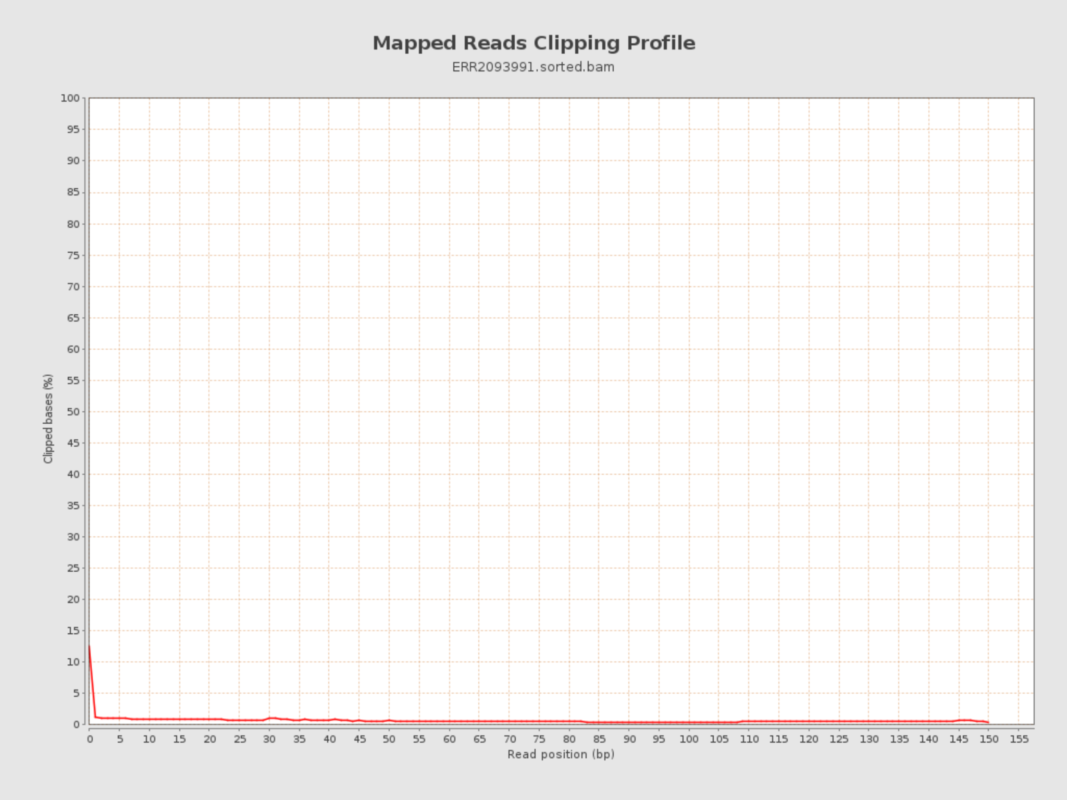
8. Results : Mapped Reads Nucleotide Content



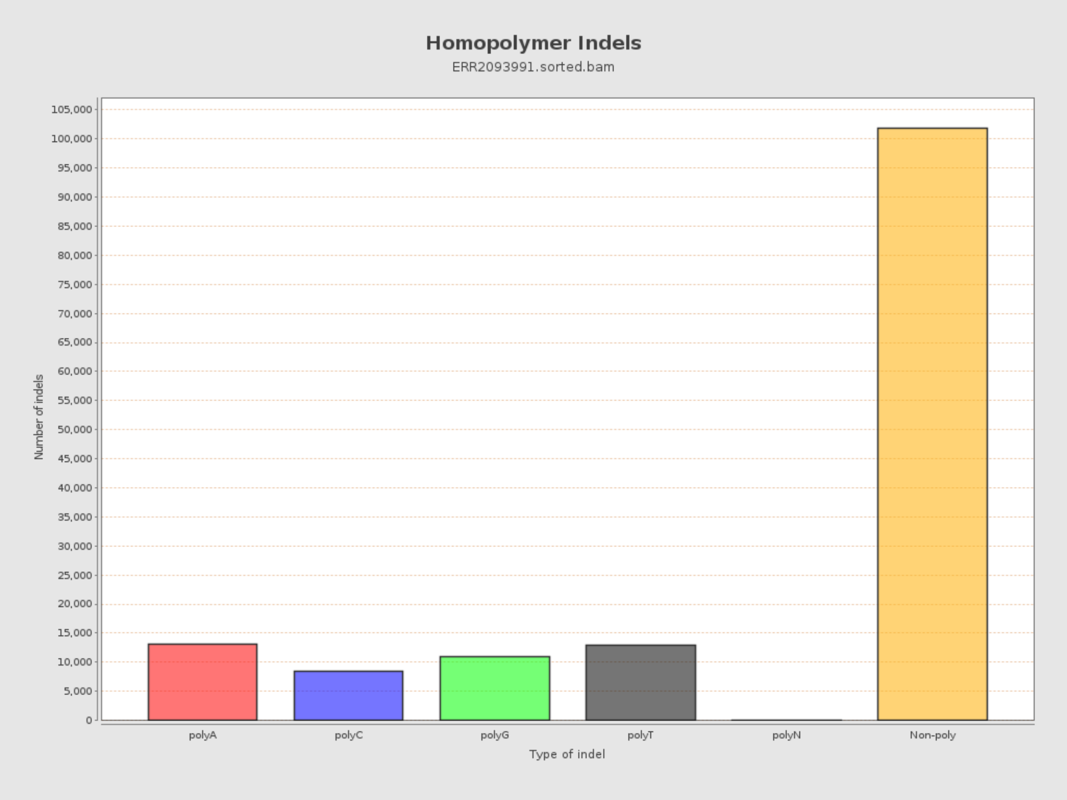
9. Results : Mapped Reads GC-content Distribution



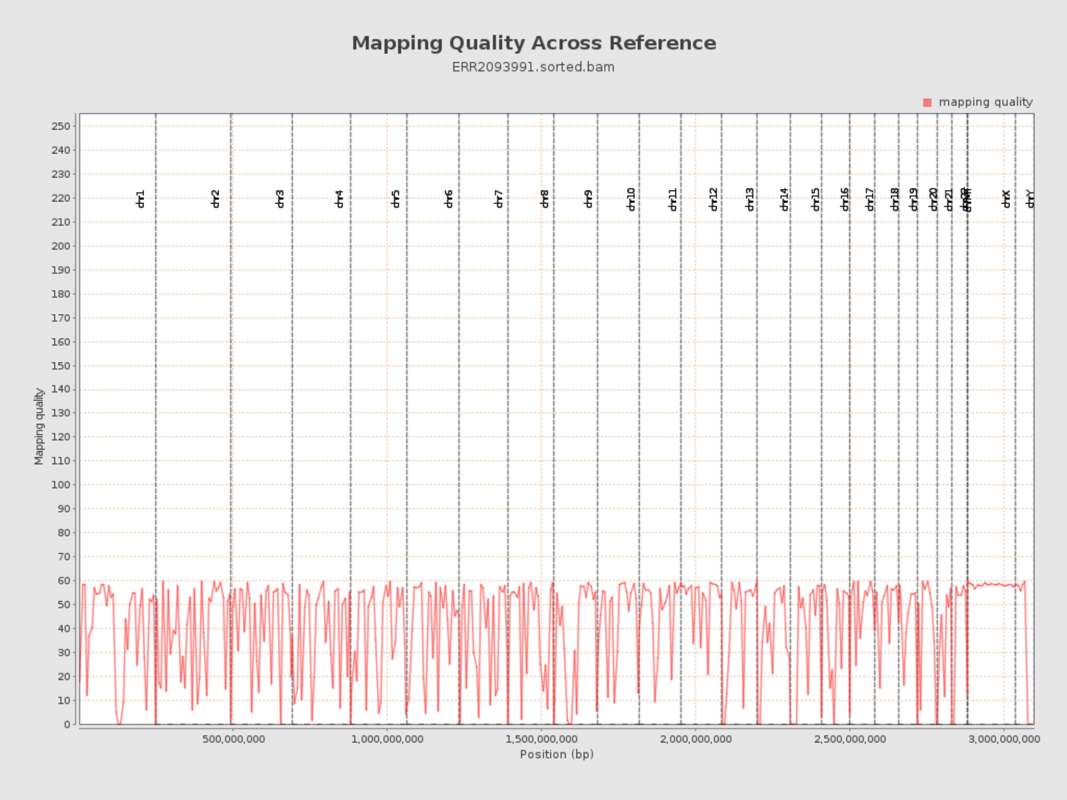
10. Results : Mapped Reads Clipping Profile



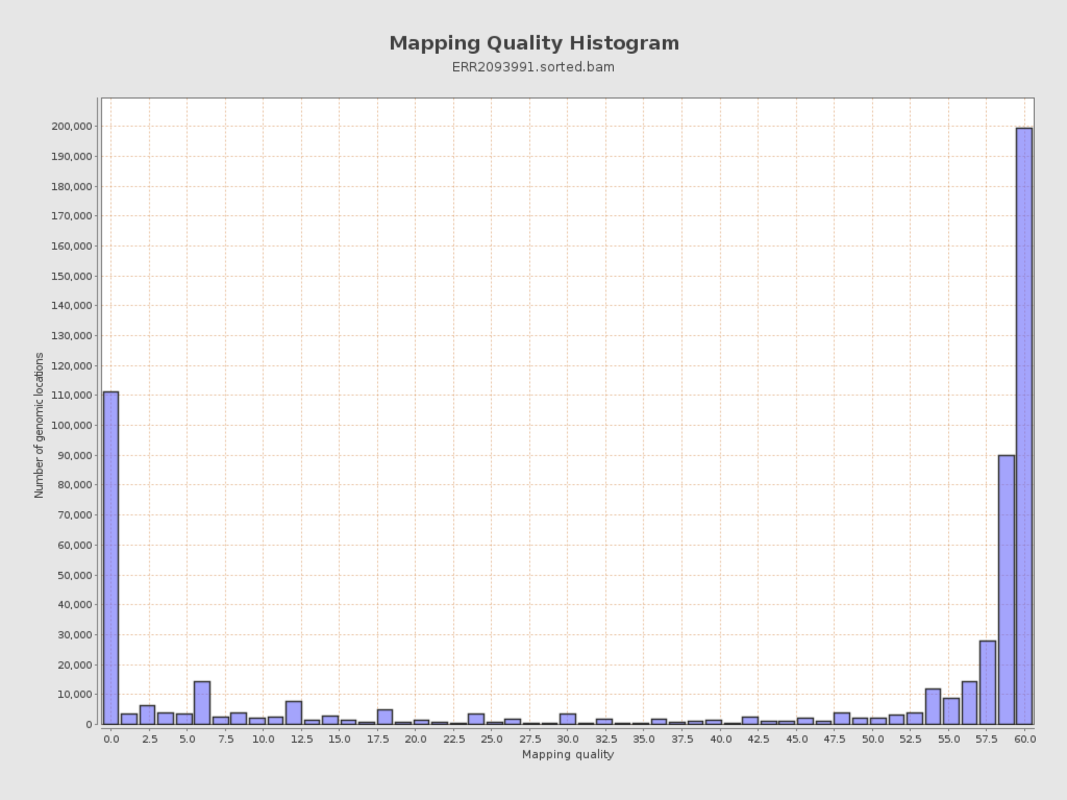
11. Results : Homopolymer Indels



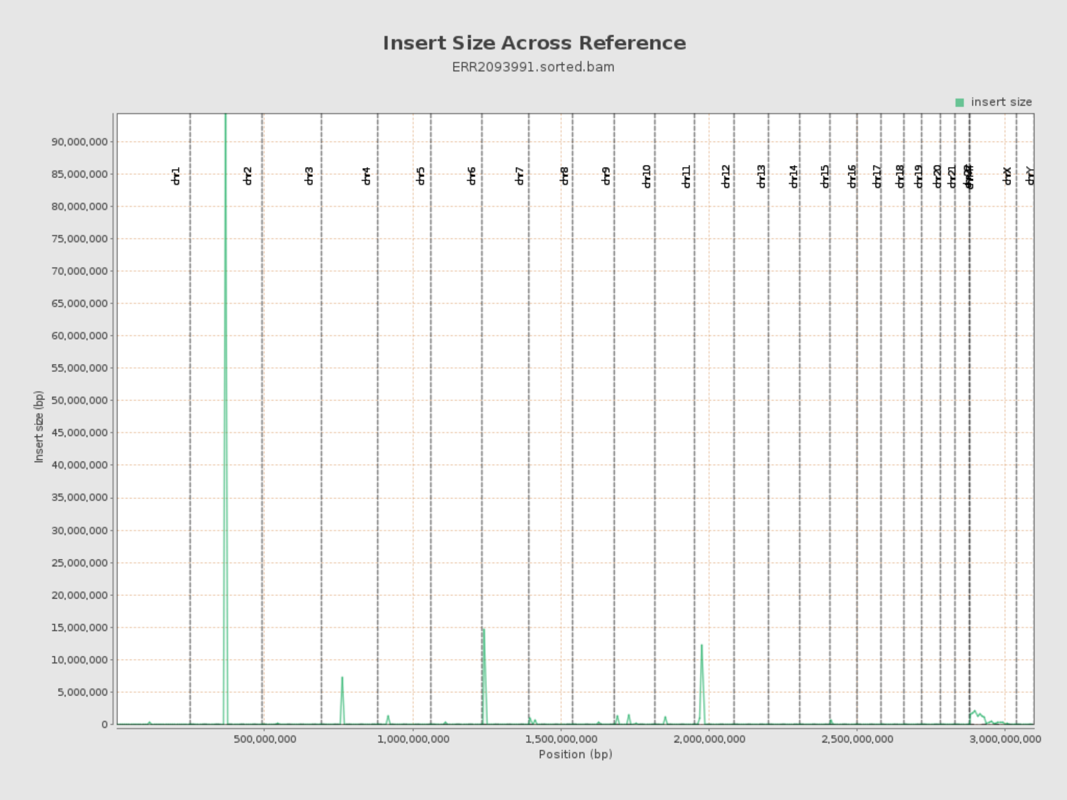
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram