Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:24:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094062.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_ERR2094062 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094062_1.fastq.gz ERR2094062_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:24:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	434,364
Mapped reads	401,472 / 92.43%
Unmapped reads	32,892 / 7.57%
Mapped paired reads	401,472 / 92.43%
Mapped reads, first in pair	201,819 / 46.46%
Mapped reads, second in pair	199,653 / 45.96%
Mapped reads, both in pair	397,634 / 91.54%
Mapped reads, singletons	3,838 / 0.88%
Secondary alignments	0
Supplementary alignments	22,606 / 5.2%
Read min/max/mean length	30 / 151 / 139.1
Duplicated reads (estimated)	367,884 / 84.69%
Duplication rate	47.65%
Clipped reads	188,706 / 43.44%

2.2. ACGT Content

Number/percentage of A's	14,261,560 / 27.72%
Number/percentage of C's	11,556,745 / 22.46%
Number/percentage of T's	13,563,544 / 26.36%
Number/percentage of G's	12,074,986 / 23.47%
Number/percentage of N's	435 / 0%

GC Percentage	45.92%

2.3. Coverage

Mean	0.0169
Standard Deviation	3.3029

2.4. Mapping Quality

Mean Mapping Quality	47.91

2.5. Insert size

Mean	1,235,497.91
Standard Deviation	10,082,297.07
P25/Median/P75	131 / 165 / 198

2.6. Mismatches and indels

General error rate	3.54%
Mismatches	1,770,206
Insertions	27,757
Mapped reads with at least one insertion	6.82%
Deletions	138,817
Mapped reads with at least one deletion	33.36%
Homopolymer indels	29.75%

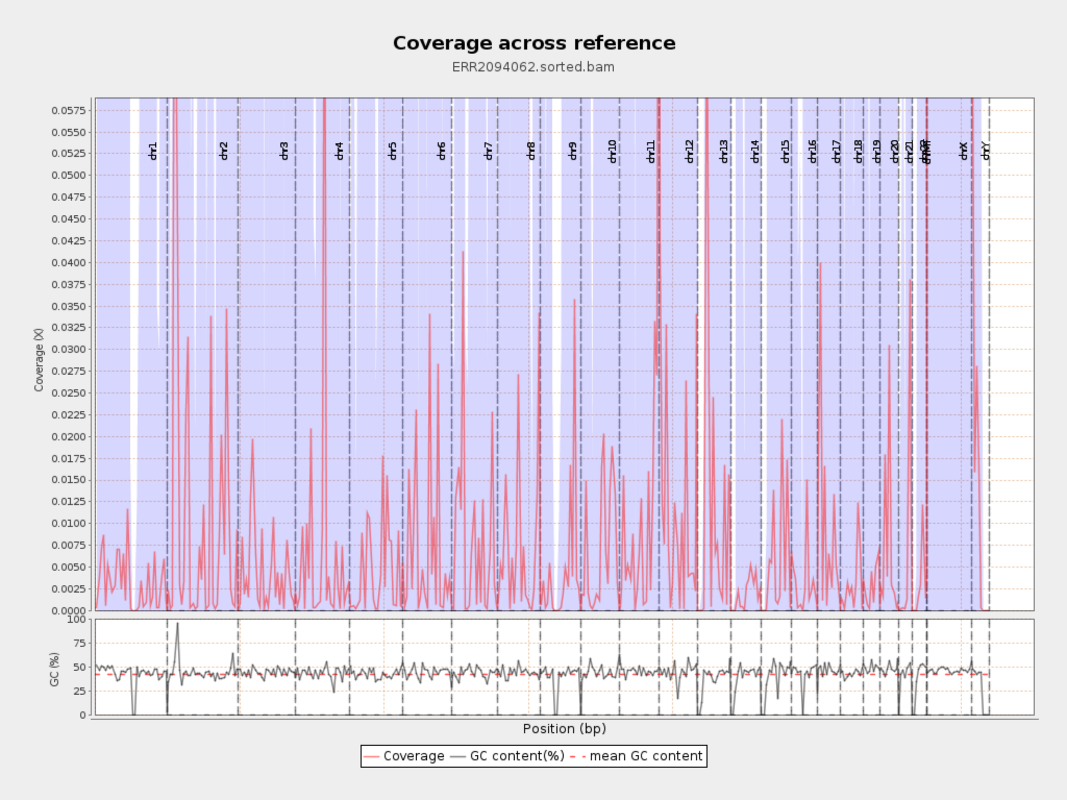
2.7. Chromosome stats

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

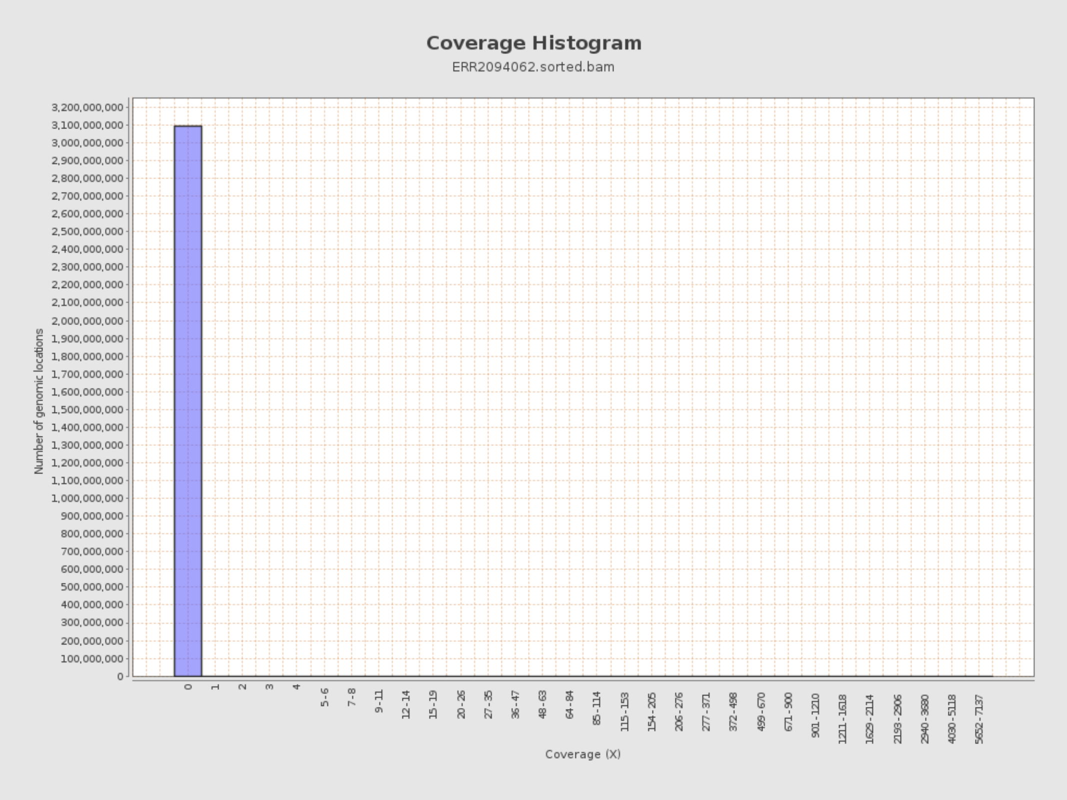
		bases	coverage	deviation
chr1	249250621	789547	0.0032	0.8131
chr2	243199373	2734876	0.0112	2.7612
chr3	198022430	860734	0.0043	0.9935
chr4	191154276	1378218	0.0072	1.7058
chr5	180915260	845703	0.0047	1.4104
chr6	171115067	1219822	0.0071	2.0398
chr7	159138663	1240228	0.0078	1.8523
chr8	146364022	1035475	0.0071	1.9878
chr9	141213431	648860	0.0046	1.3327
chr10	135534747	935841	0.0069	1.5058
chr11	135006516	1269145	0.0094	1.9056
chr12	133851895	1458445	0.0109	2.2674
chr13	115169878	1381674	0.012	2.7046
chr14	107349540	203793	0.0019	0.4758
chr15	102531392	590439	0.0058	1.2972
chr16	90354753	302333	0.0033	0.9371
chr17	81195210	819788	0.0101	1.8697
chr18	78077248	257115	0.0033	0.7985
chr19	59128983	168403	0.0028	0.5161
chr20	63025520	477308	0.0076	2.2224
chr21	48129895	366880	0.0076	2.4168
chr22	51304566	148347	0.0029	0.6864
chrMT	16571	3901804	235.4598	939.708
chrX	155270560	28609608	0.1843	7.6244

chrY	59373566	800269	0.0135	2.6018

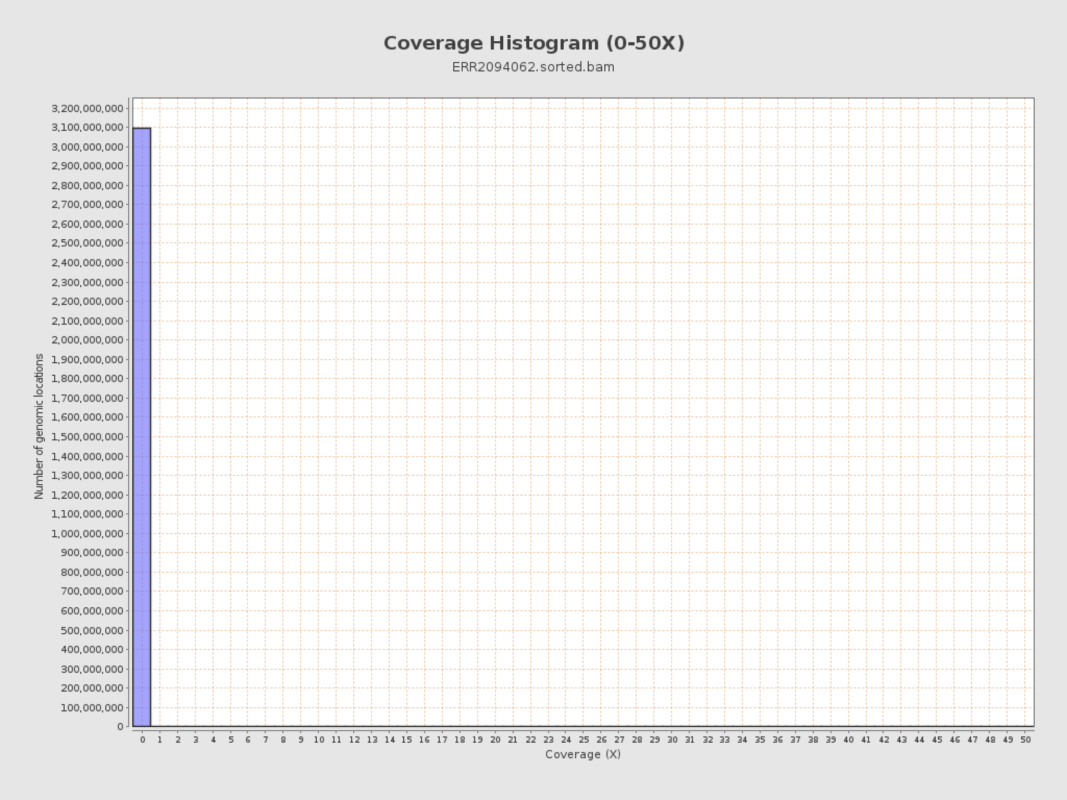
3. Results : Coverage across reference



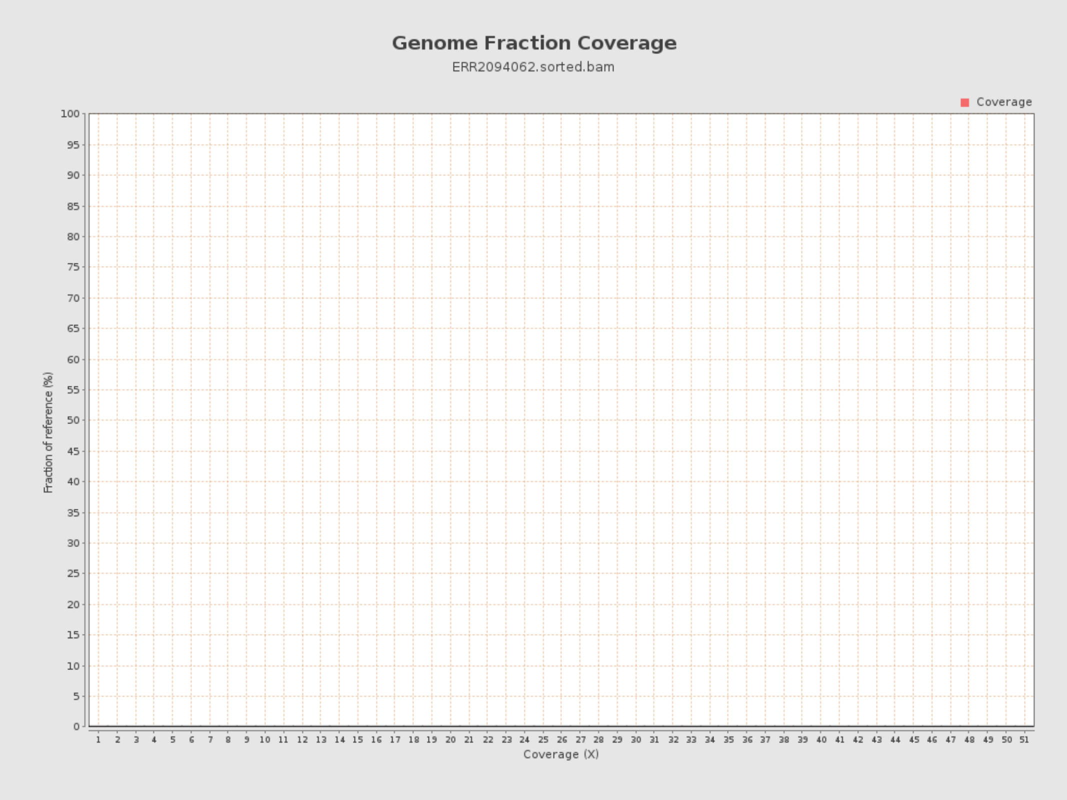
4. Results : Coverage Histogram



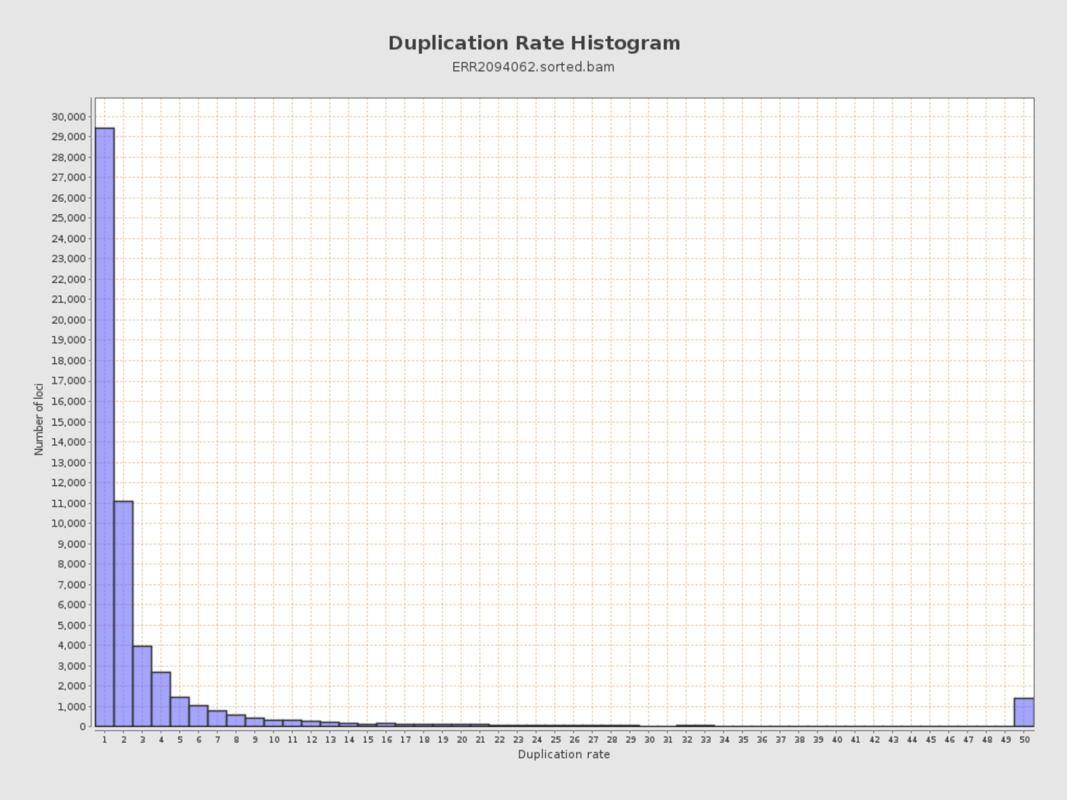
5. Results : Coverage Histogram (0-50X)



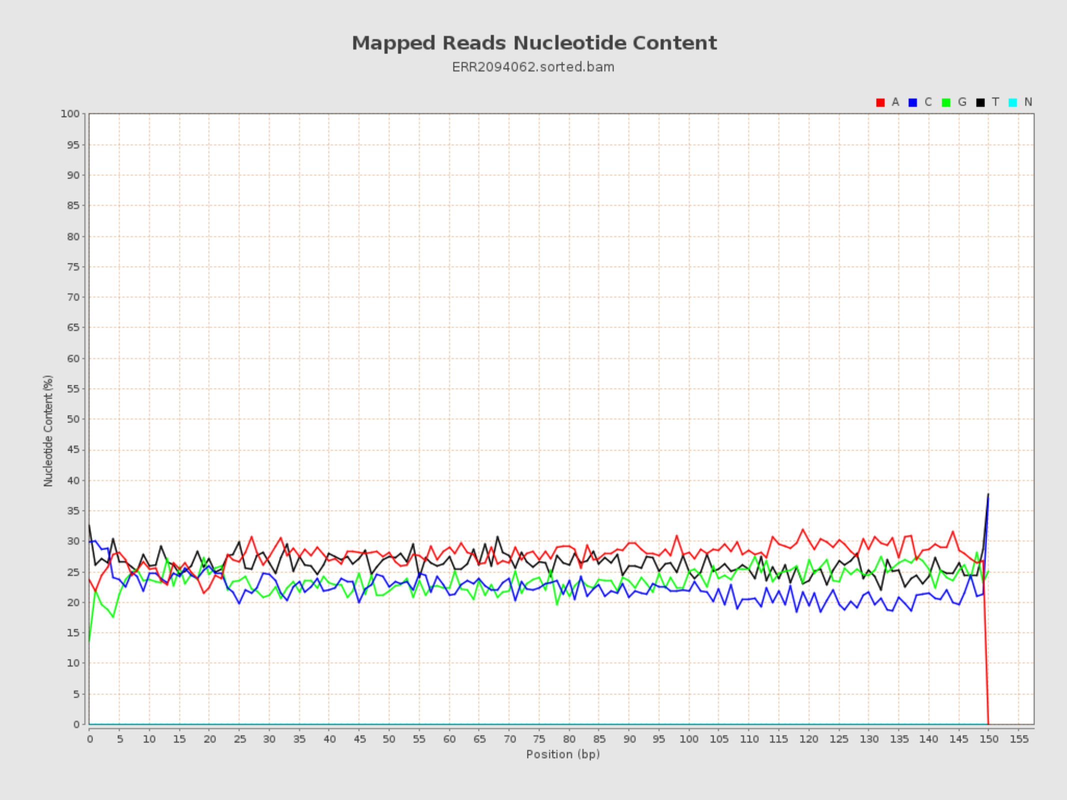
6. Results : Genome Fraction Coverage



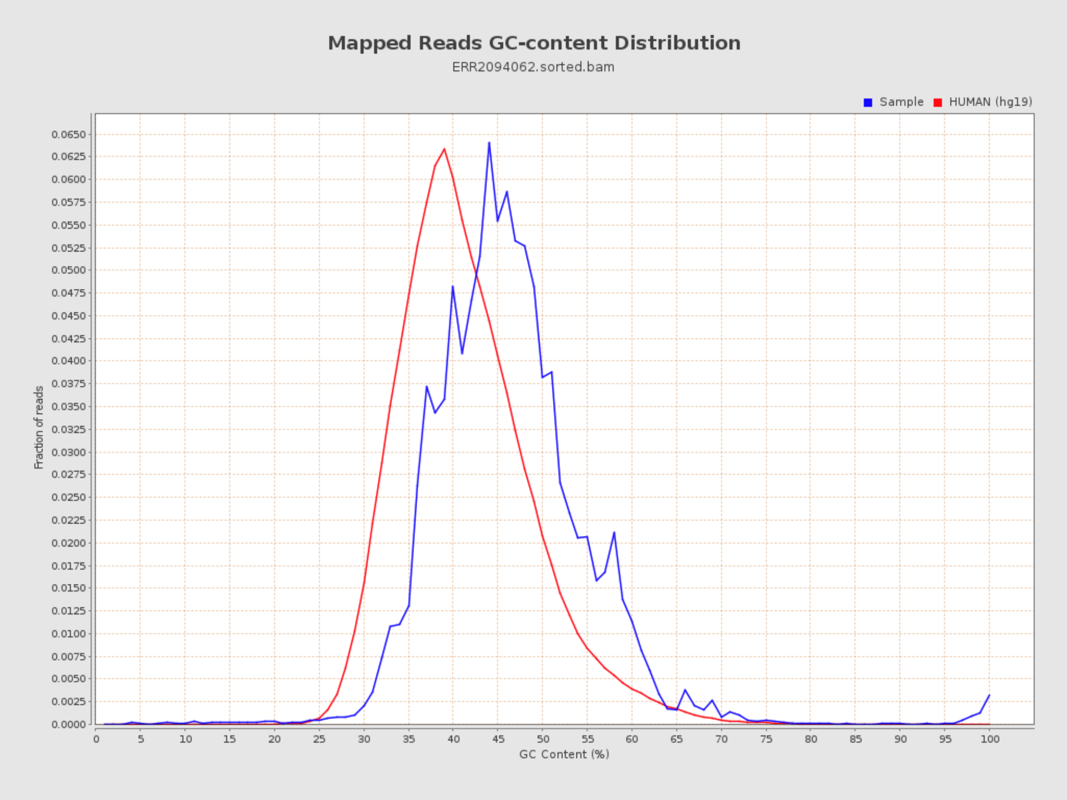
7. Results : Duplication Rate Histogram



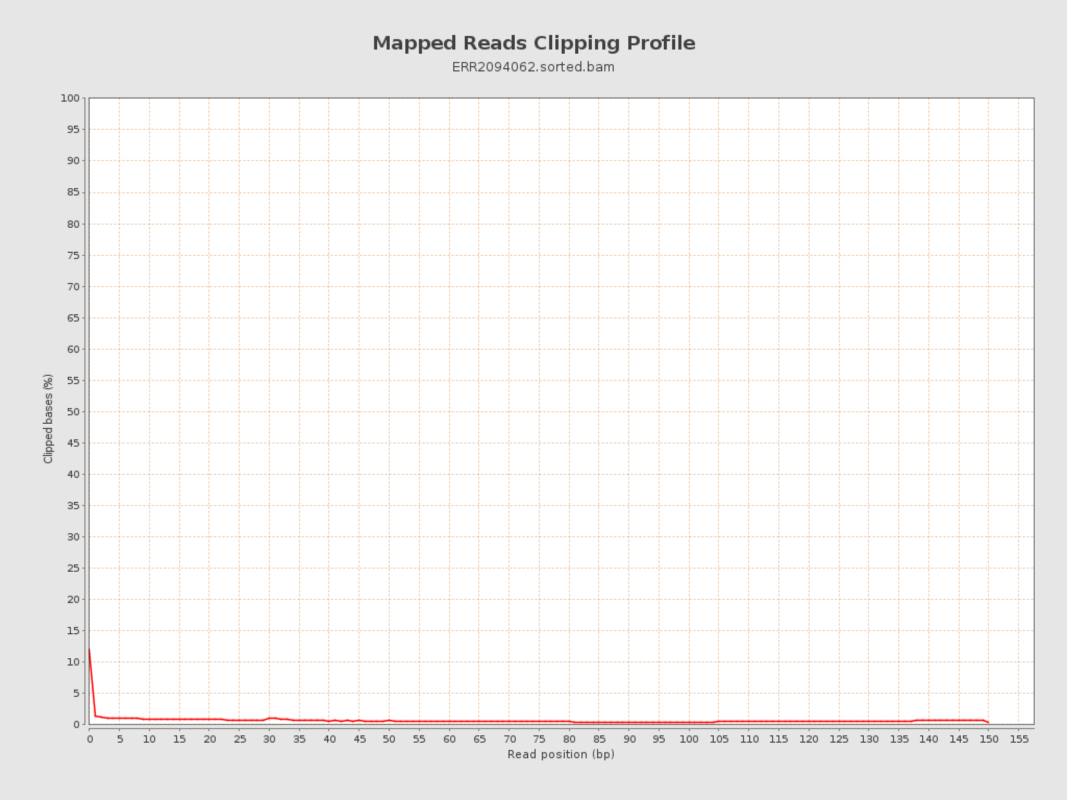
8. Results : Mapped Reads Nucleotide Content



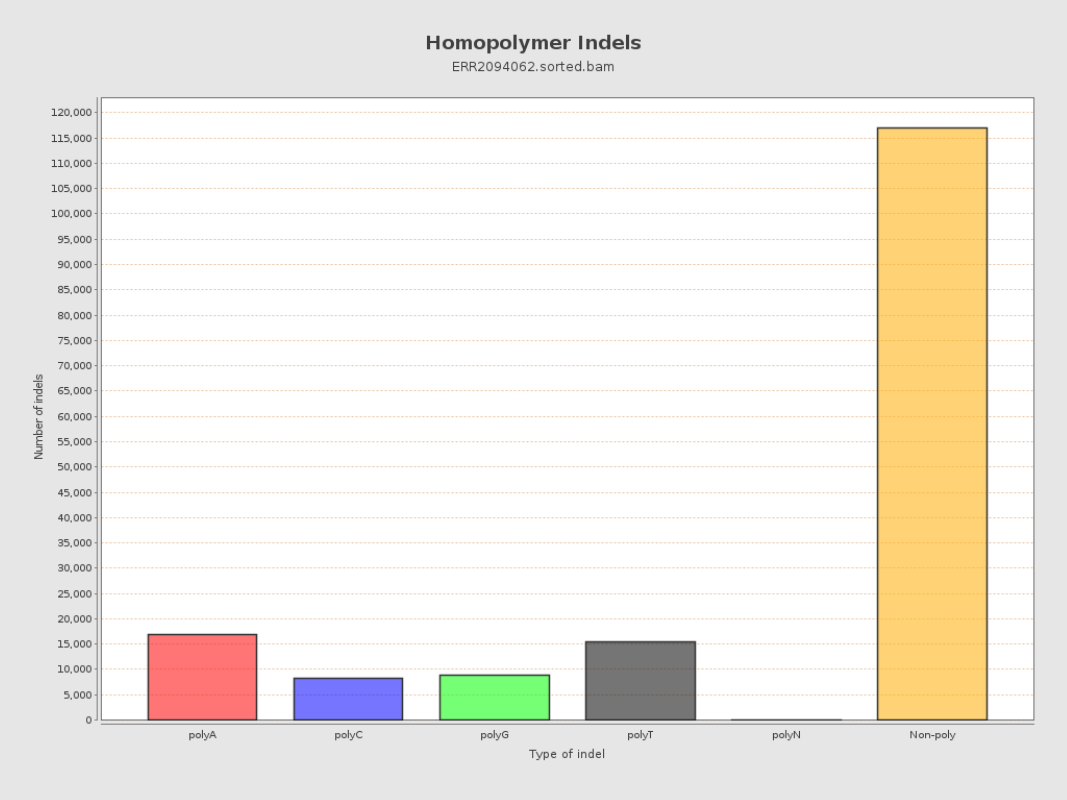
9. Results : Mapped Reads GC-content Distribution



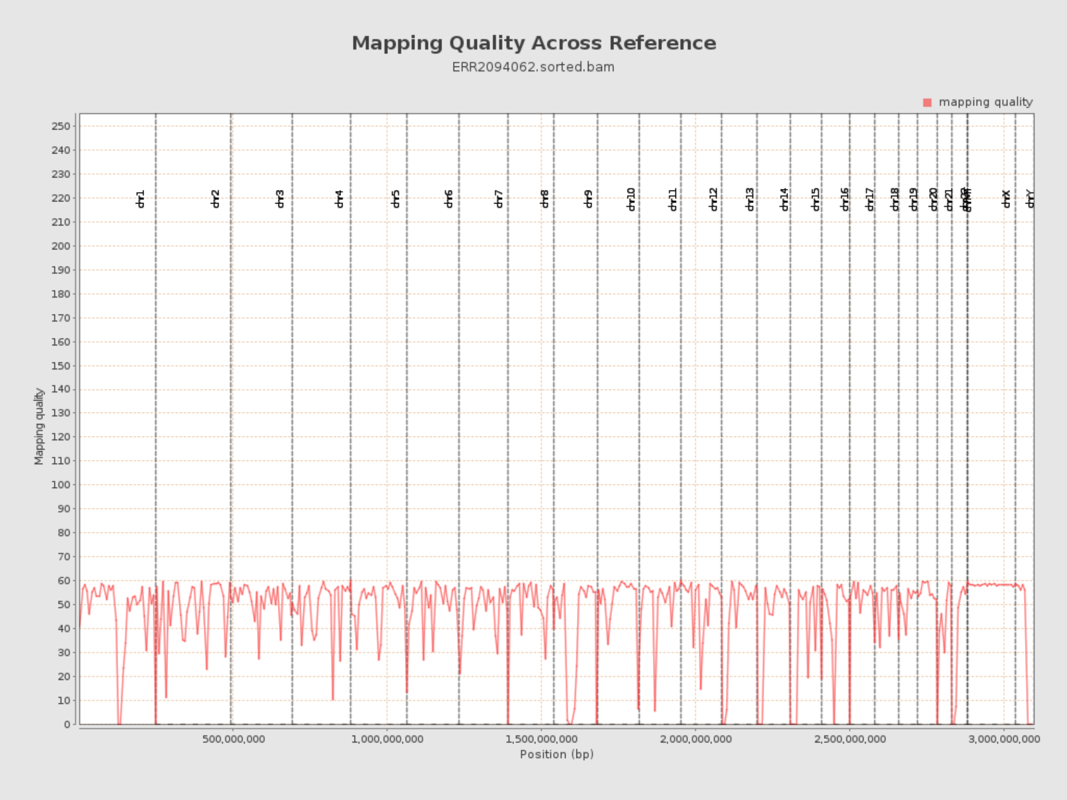
10. Results : Mapped Reads Clipping Profile



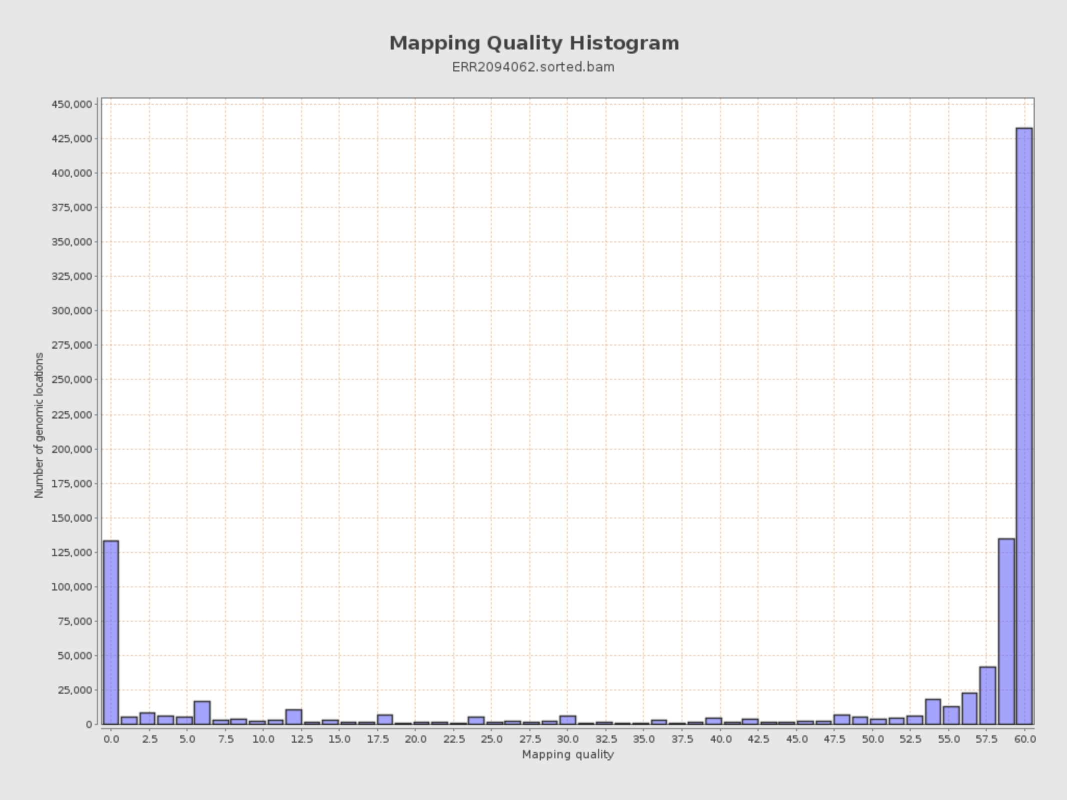
11. Results : Homopolymer Indels



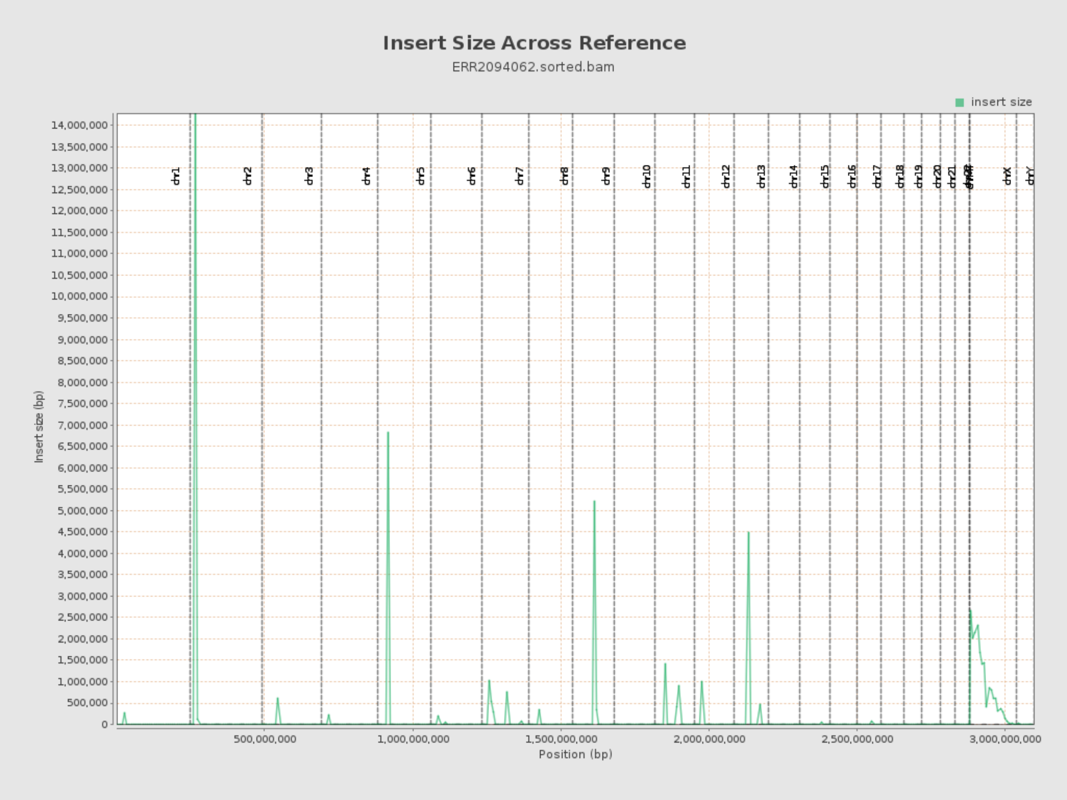
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram