Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:14:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093996.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_ERR2093996 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093996_1.fastq.gz ERR2093996_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:14:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	353,836
Mapped reads	340,329 / 96.18%
Unmapped reads	13,507 / 3.82%
Mapped paired reads	340,329 / 96.18%
Mapped reads, first in pair	171,085 / 48.35%
Mapped reads, second in pair	169,244 / 47.83%
Mapped reads, both in pair	337,314 / 95.33%
Mapped reads, singletons	3,015 / 0.85%
Secondary alignments	0
Supplementary alignments	22,675 / 6.41%
Read min/max/mean length	30 / 151 / 142.6
Duplicated reads (estimated)	320,203 / 90.49%
Duplication rate	50.63%
Clipped reads	173,151 / 48.94%

2.2. ACGT Content

Number/percentage of A's	11,297,092 / 26.33%
Number/percentage of C's	10,097,774 / 23.53%
Number/percentage of T's	10,669,356 / 24.86%
Number/percentage of G's	10,848,770 / 25.28%
Number/percentage of N's	417 / 0%

GC Percentage	48.81%

2.3. Coverage

Mean	0.0141
Standard Deviation	2.6145

2.4. Mapping Quality

Mean Mapping Quality	40.71

2.5. Insert size

Mean	1,229,102.95
Standard Deviation	10,041,005.03
P25/Median/P75	127 / 164 / 200

2.6. Mismatches and indels

General error rate	3.56%
Mismatches	1,481,692
Insertions	23,067
Mapped reads with at least one insertion	6.66%
Deletions	116,708
Mapped reads with at least one deletion	32.88%
Homopolymer indels	28.09%

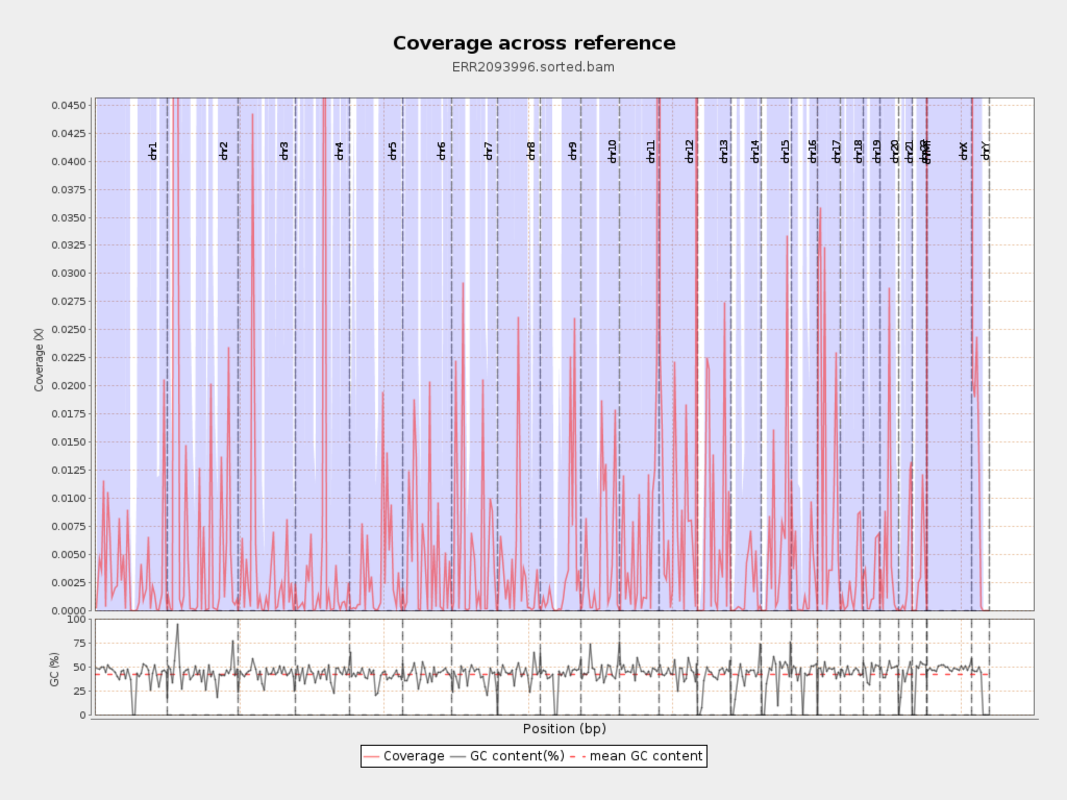
2.7. Chromosome stats

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

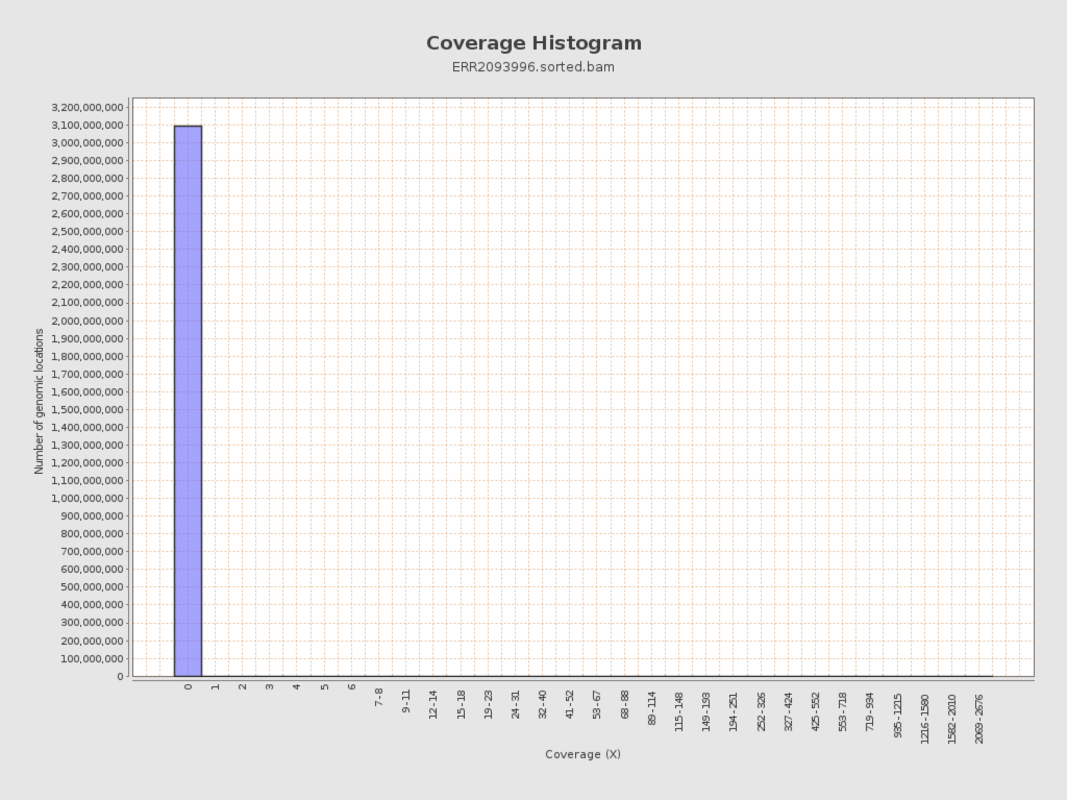
		bases	coverage	deviation
chr1	249250621	849366	0.0034	1.0969
chr2	243199373	2231842	0.0092	2.8003
chr3	198022430	739881	0.0037	1.1836
chr4	191154276	945258	0.0049	1.7234
chr5	180915260	609919	0.0034	1.3619
chr6	171115067	864330	0.0051	1.3487
chr7	159138663	903863	0.0057	1.6452
chr8	146364022	509980	0.0035	1.0734
chr9	141213431	570759	0.004	1.1149
chr10	135534747	631758	0.0047	1.4362
chr11	135006516	938039	0.0069	1.7498
chr12	133851895	1211721	0.0091	2.2355
chr13	115169878	835147	0.0073	1.9349
chr14	107349540	194552	0.0018	0.6172
chr15	102531392	608560	0.0059	1.5133
chr16	90354753	278325	0.0031	0.8155
chr17	81195210	1113983	0.0137	3.1397
chr18	78077248	195480	0.0025	0.7134
chr19	59128983	158528	0.0027	0.7157
chr20	63025520	357499	0.0057	1.9064
chr21	48129895	178482	0.0037	0.8582
chr22	51304566	154661	0.003	0.7187
chrMT	16571	1024525	61.8264	264.8387
chrX	155270560	27061635	0.1743	8.8186

chrY	59373566	553681	0.0093	1.2467

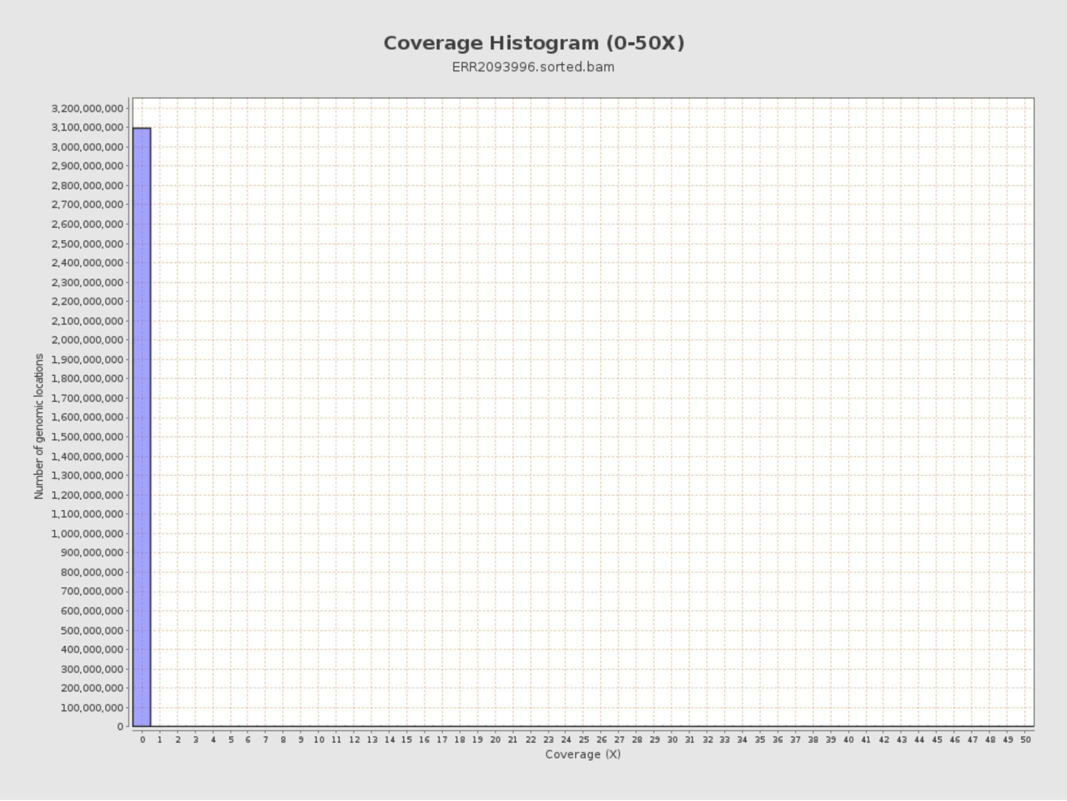
3. Results : Coverage across reference



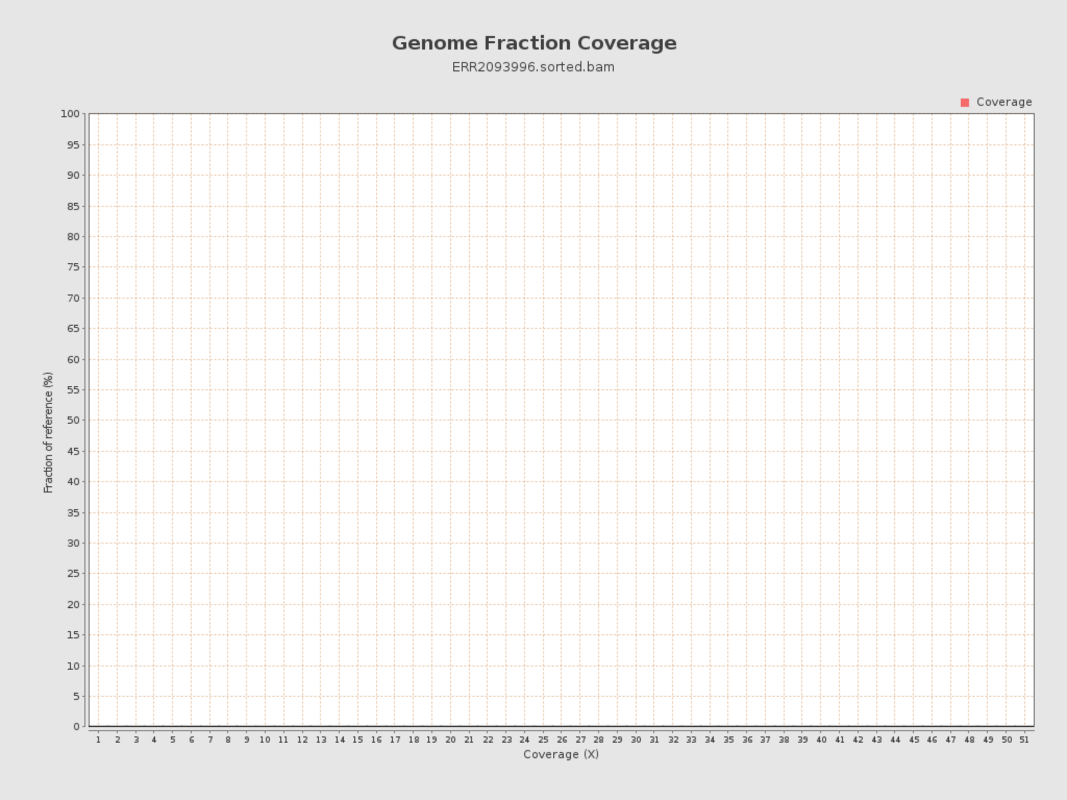
4. Results : Coverage Histogram



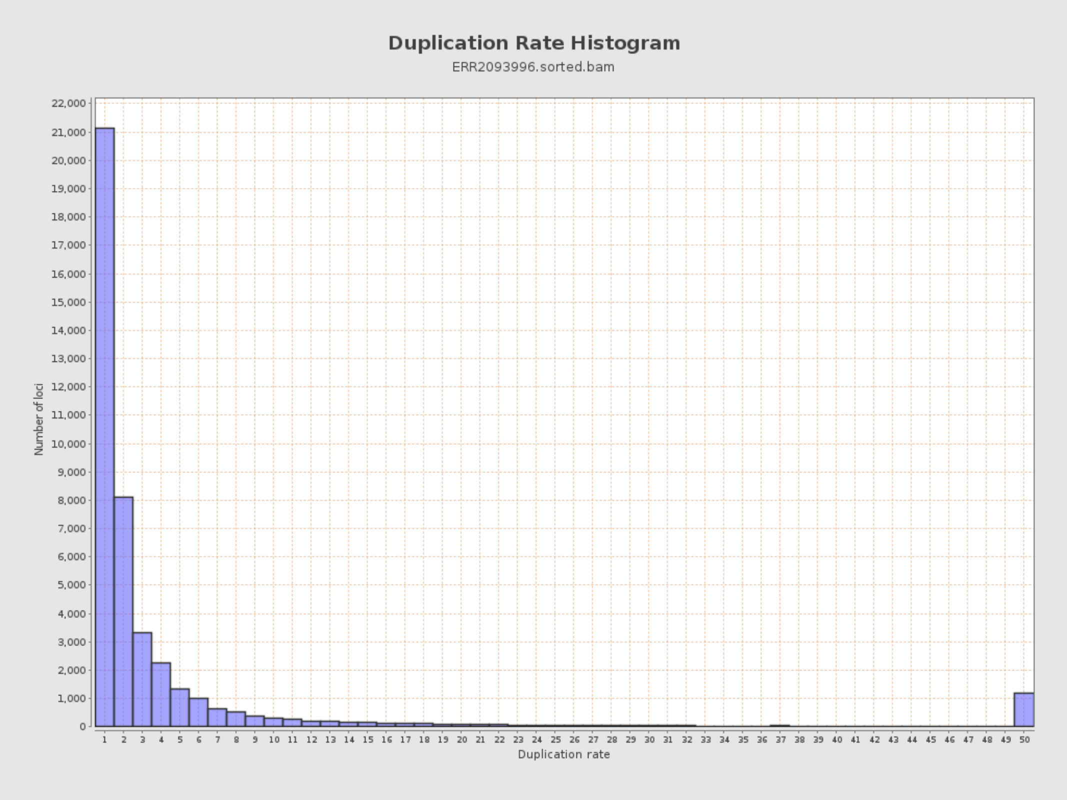
5. Results : Coverage Histogram (0-50X)



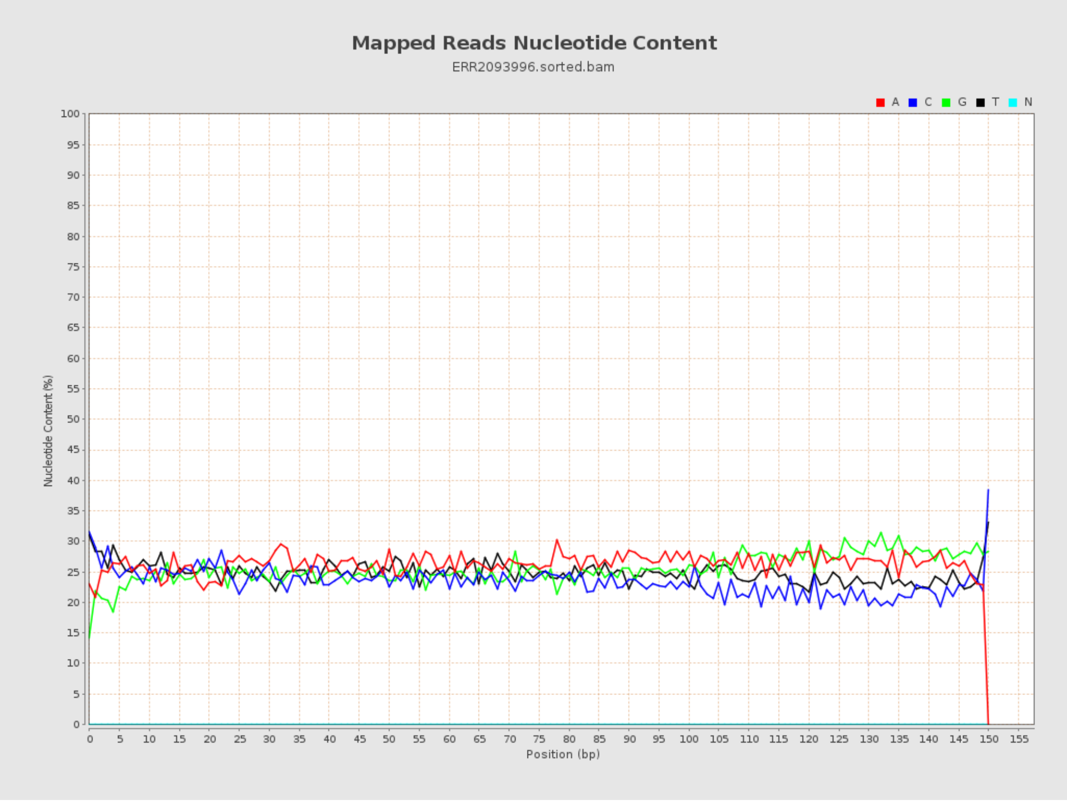
6. Results : Genome Fraction Coverage



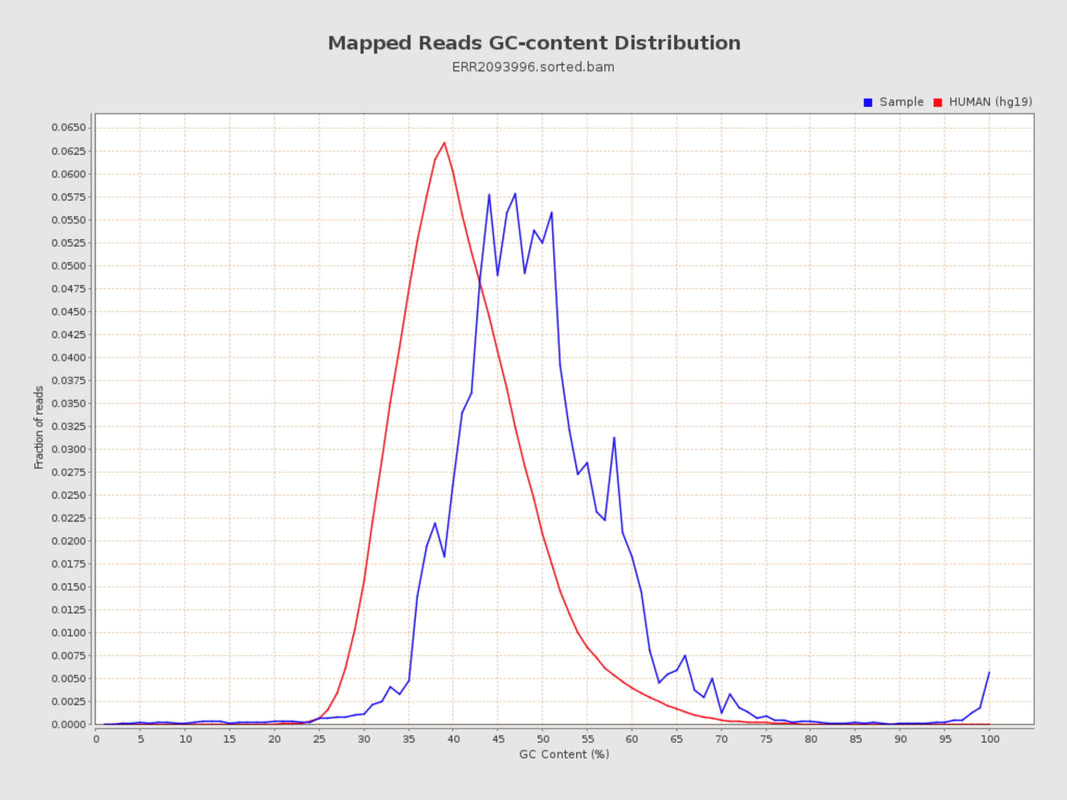
7. Results : Duplication Rate Histogram



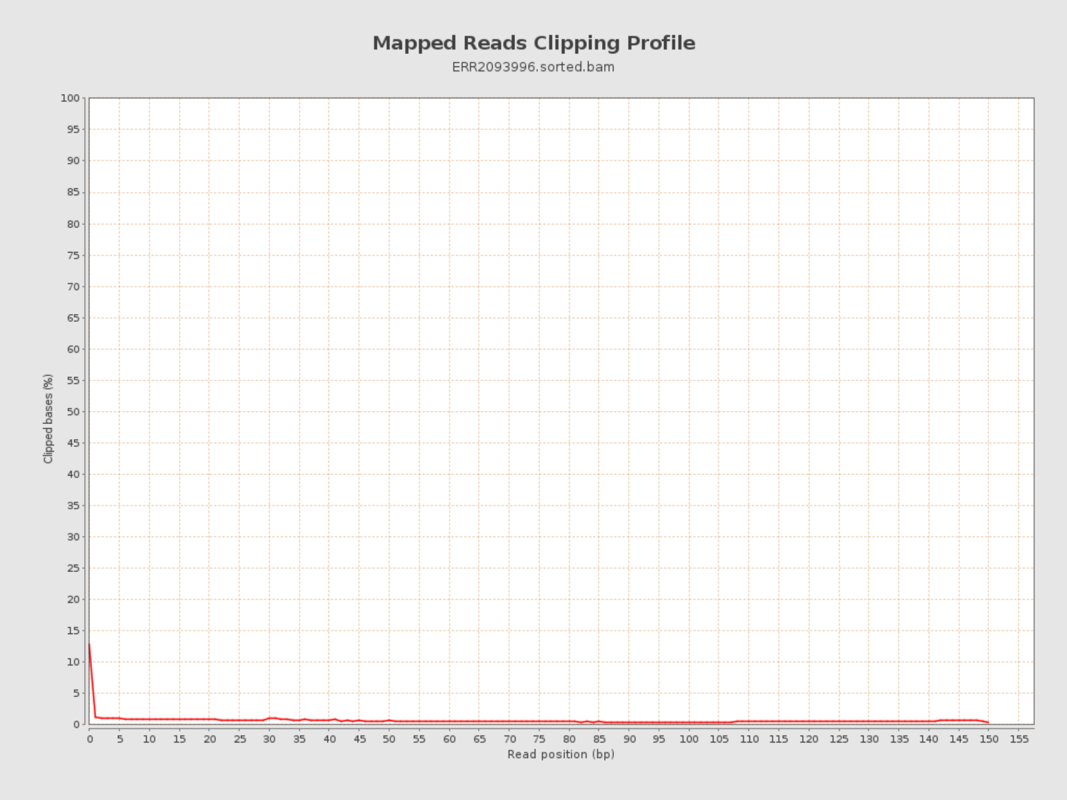
8. Results : Mapped Reads Nucleotide Content



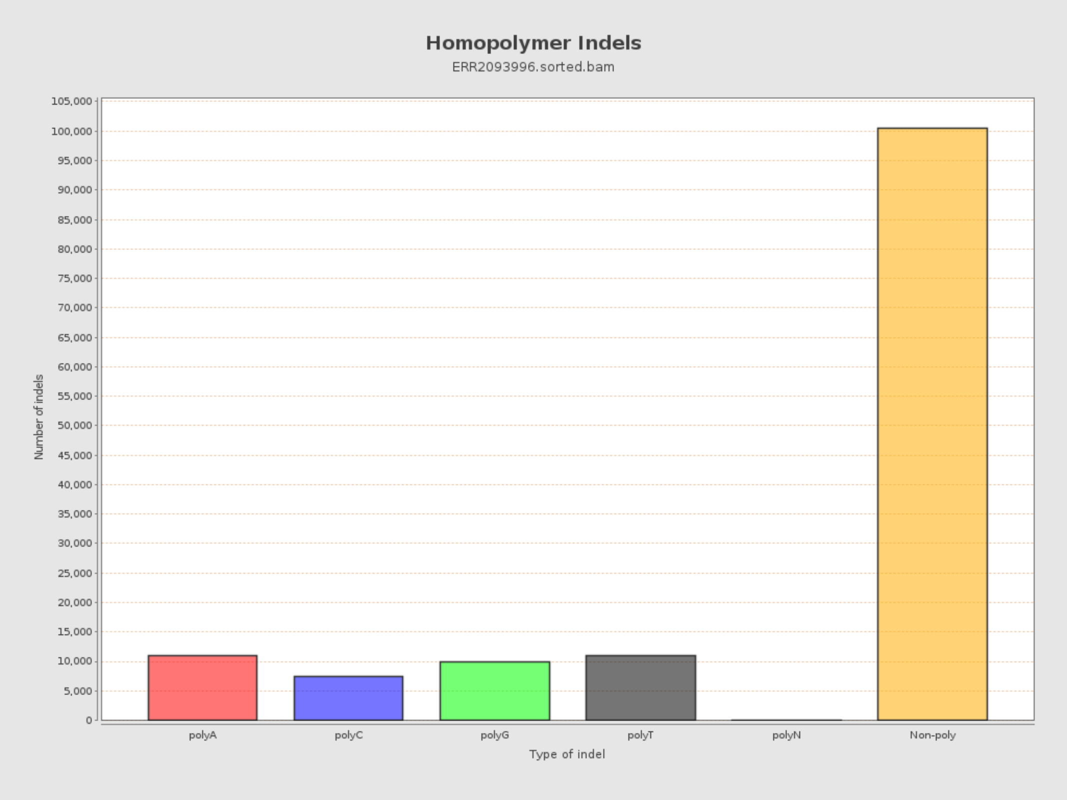
9. Results : Mapped Reads GC-content Distribution



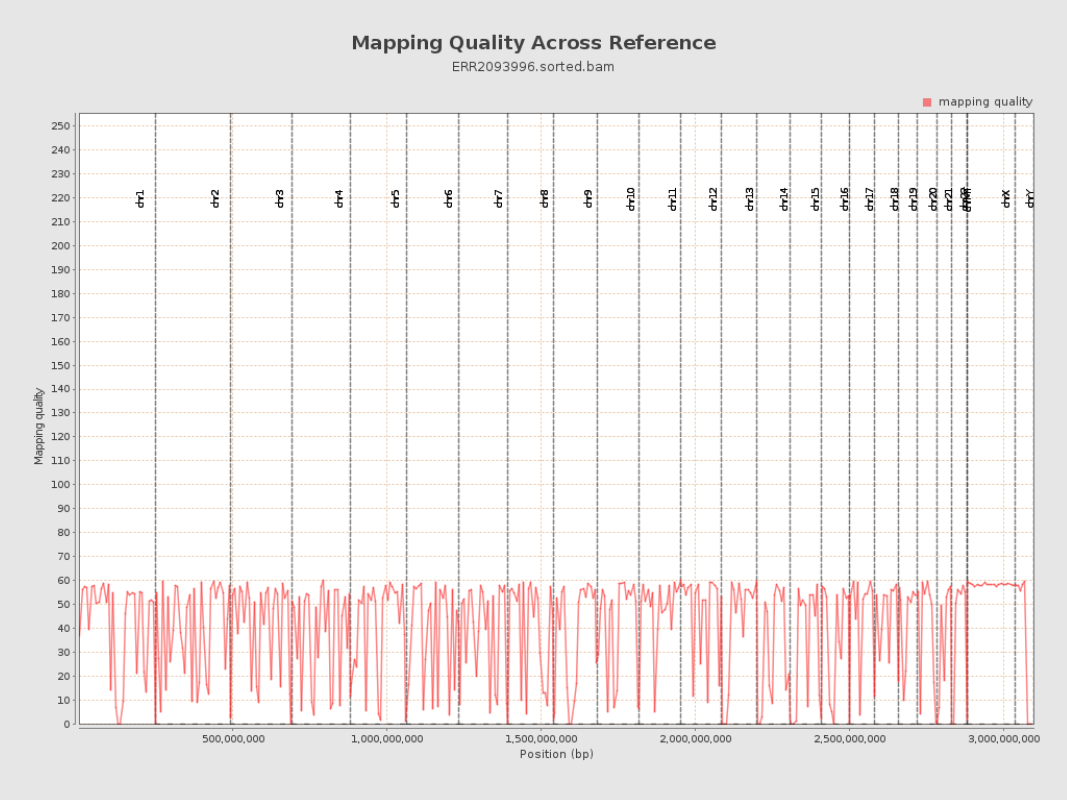
10. Results : Mapped Reads Clipping Profile



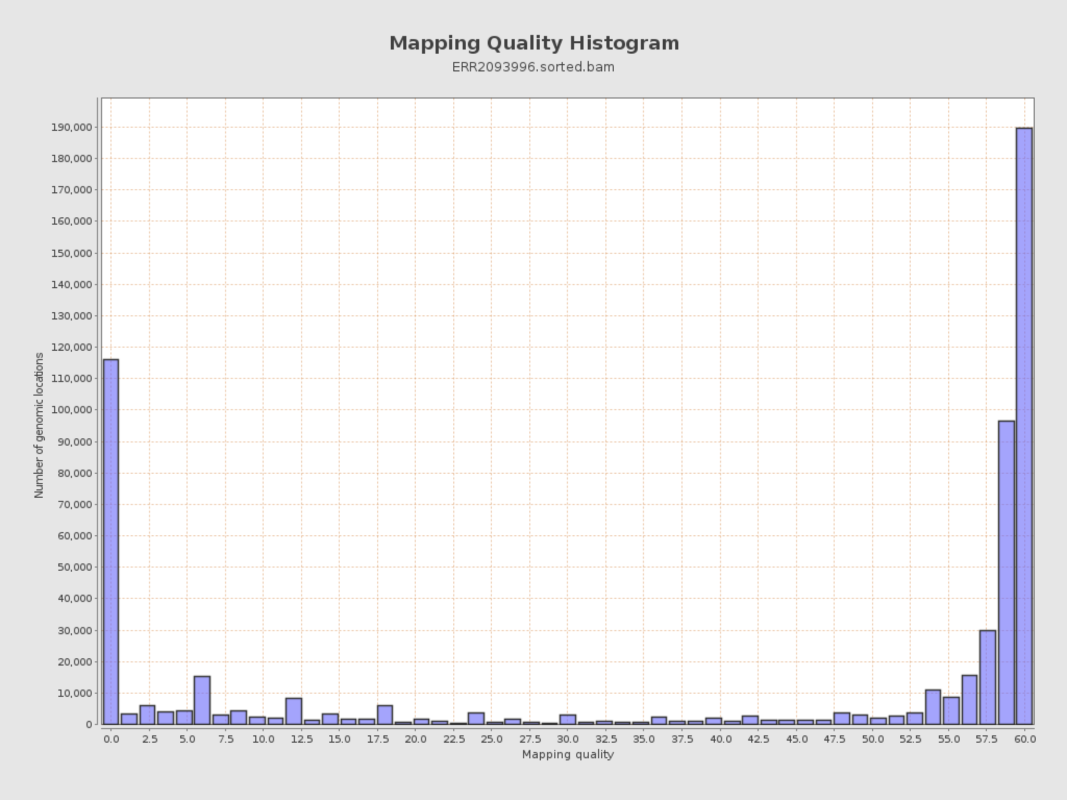
11. Results : Homopolymer Indels



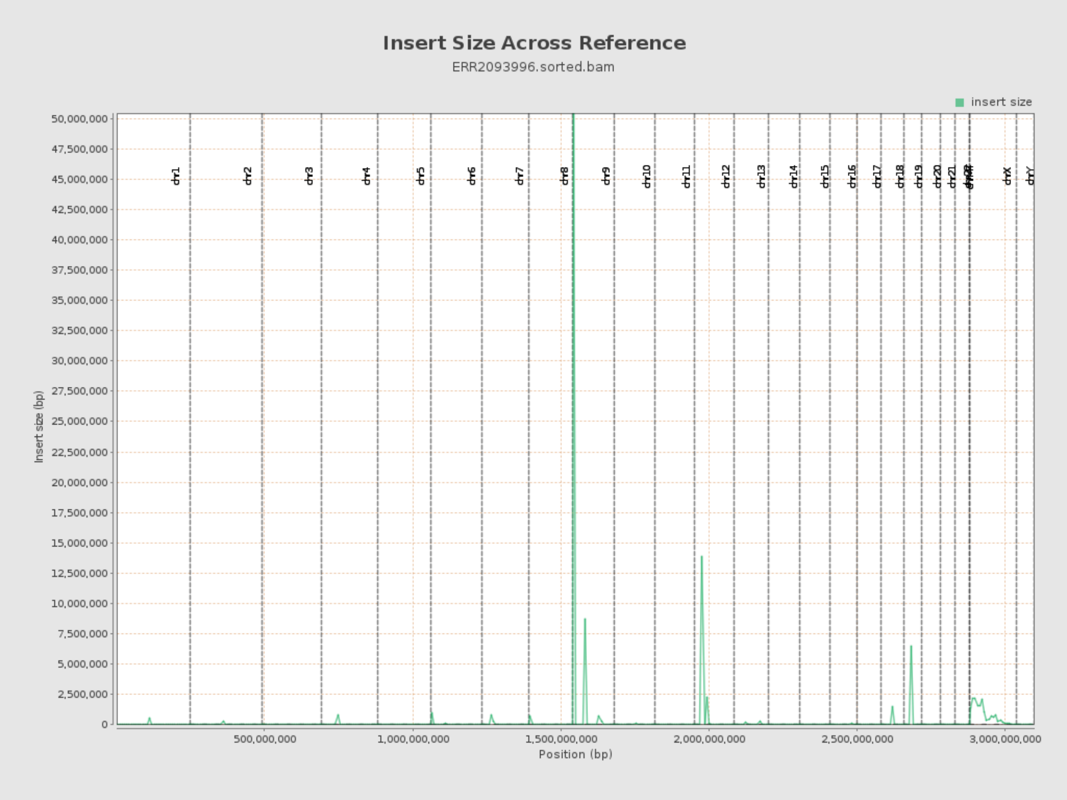
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram