Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:16:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093997.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_ERR2093997 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093997_1.fastq.gz ERR2093997_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:16:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	316,352
Mapped reads	303,724 / 96.01%
Unmapped reads	12,628 / 3.99%
Mapped paired reads	303,724 / 96.01%
Mapped reads, first in pair	152,700 / 48.27%
Mapped reads, second in pair	151,024 / 47.74%
Mapped reads, both in pair	301,068 / 95.17%
Mapped reads, singletons	2,656 / 0.84%
Secondary alignments	0
Supplementary alignments	19,191 / 6.07%
Read min/max/mean length	30 / 151 / 142.49
Duplicated reads (estimated)	284,974 / 90.08%
Duplication rate	50.44%
Clipped reads	152,513 / 48.21%

2.2. ACGT Content

Number/percentage of A's	10,106,793 / 26.32%
Number/percentage of C's	9,037,522 / 23.54%
Number/percentage of T's	9,603,905 / 25.01%
Number/percentage of G's	9,650,413 / 25.13%
Number/percentage of N's	368 / 0%

GC Percentage	48.67%

2.3. Coverage

Mean	0.0126
Standard Deviation	2.5485

2.4. Mapping Quality

Mean Mapping Quality	39.91

2.5. Insert size

Mean	1,122,795.04
Standard Deviation	9,552,936.97
P25/Median/P75	128 / 165 / 203

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,294,316
Insertions	20,878
Mapped reads with at least one insertion	6.78%
Deletions	101,569
Mapped reads with at least one deletion	32.08%
Homopolymer indels	29.35%

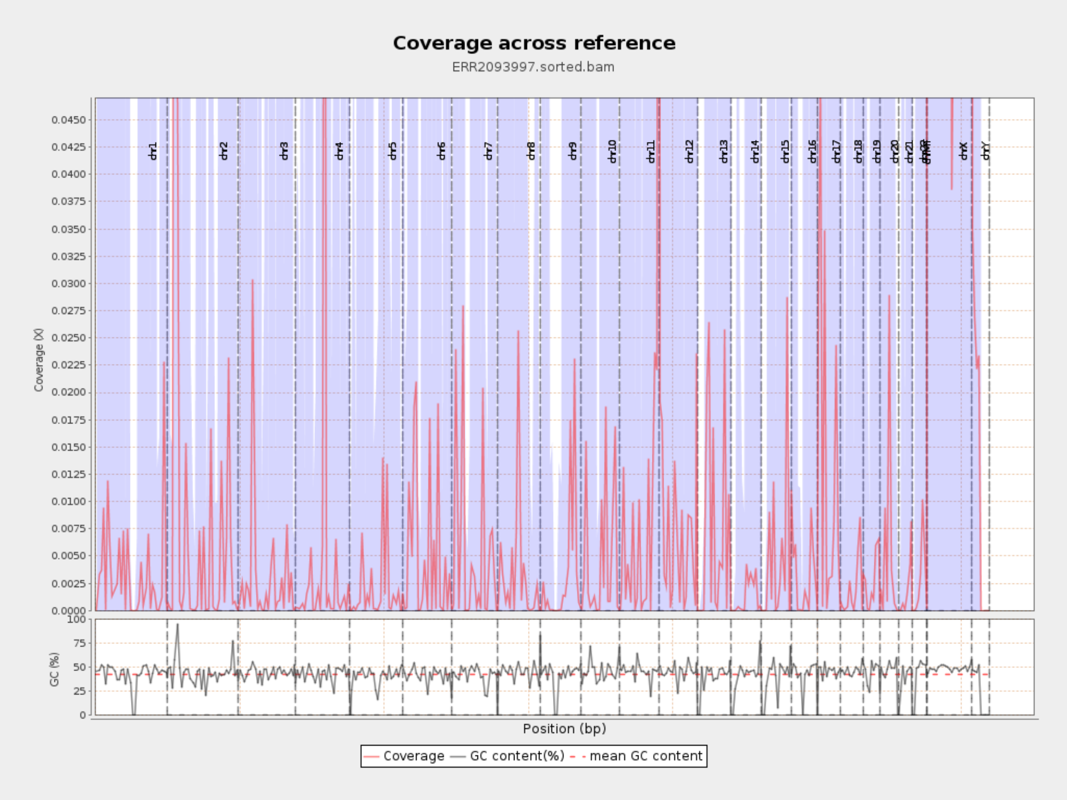
2.7. Chromosome stats

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

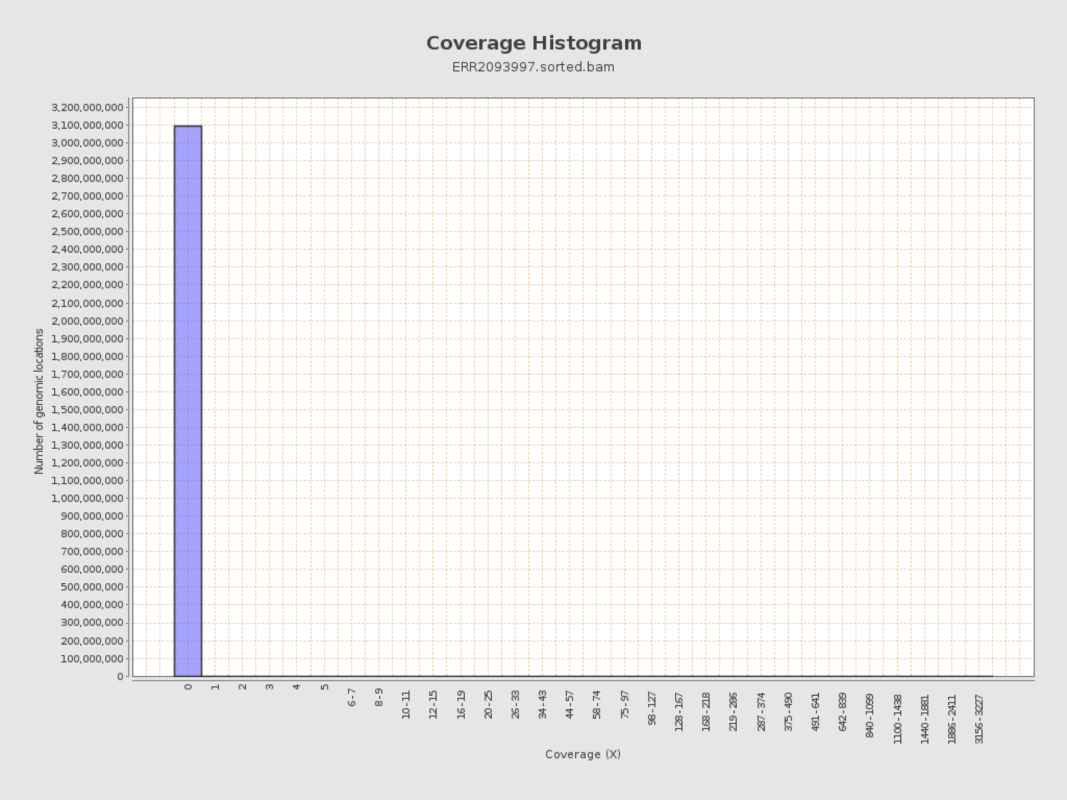
		bases	coverage	deviation
chr1	249250621	833685	0.0033	1.1169
chr2	243199373	2200285	0.009	2.8835
chr3	198022430	569958	0.0029	0.7948
chr4	191154276	1020085	0.0053	1.9158
chr5	180915260	381993	0.0021	0.9936
chr6	171115067	899877	0.0053	1.6809
chr7	159138663	842799	0.0053	1.5776
chr8	146364022	485887	0.0033	1.1303
chr9	141213431	473627	0.0034	0.9805
chr10	135534747	617908	0.0046	1.4572
chr11	135006516	1020723	0.0076	1.9269
chr12	133851895	885780	0.0066	1.559
chr13	115169878	869533	0.0076	2.0726
chr14	107349540	137131	0.0013	0.3984
chr15	102531392	481741	0.0047	1.4457
chr16	90354753	289812	0.0032	0.854
chr17	81195210	1217148	0.015	3.3687
chr18	78077248	159209	0.002	0.5685
chr19	59128983	150661	0.0025	0.6854
chr20	63025520	350424	0.0056	2.0353
chr21	48129895	89854	0.0019	0.3755
chr22	51304566	139284	0.0027	0.7052
chrMT	16571	1094403	66.0433	294.1261
chrX	155270560	23142954	0.149	8.2966

chrY	59373566	741102	0.0125	1.8106

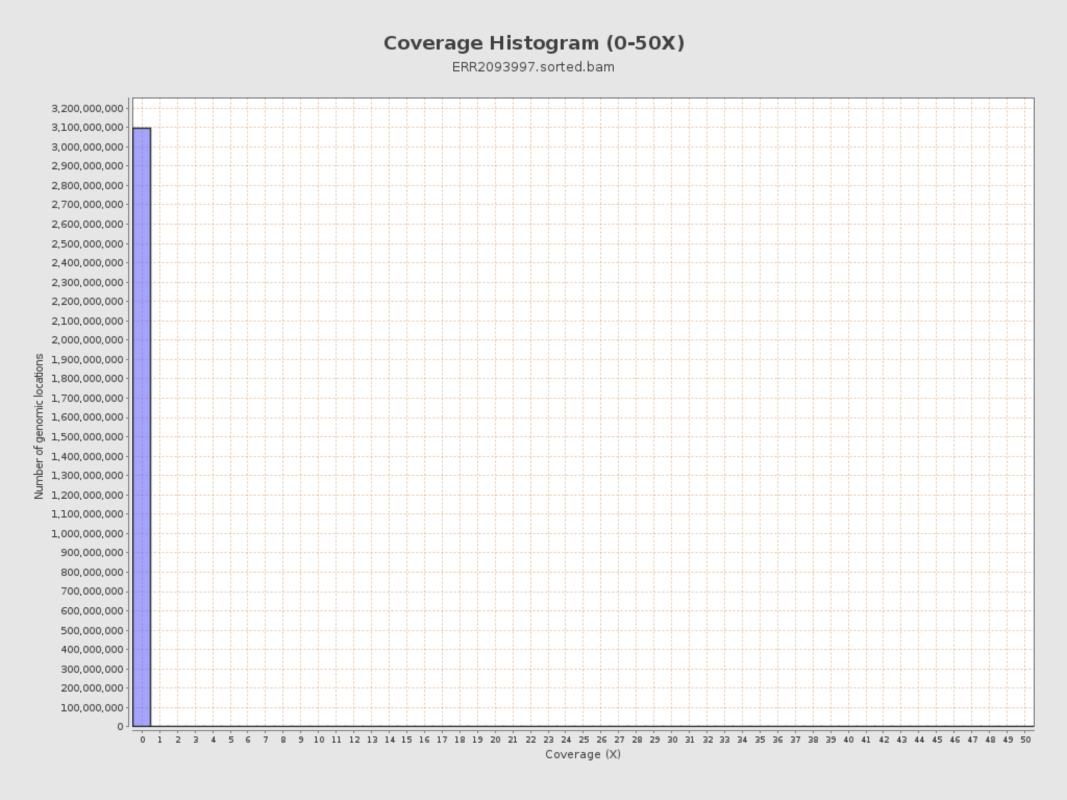
3. Results : Coverage across reference



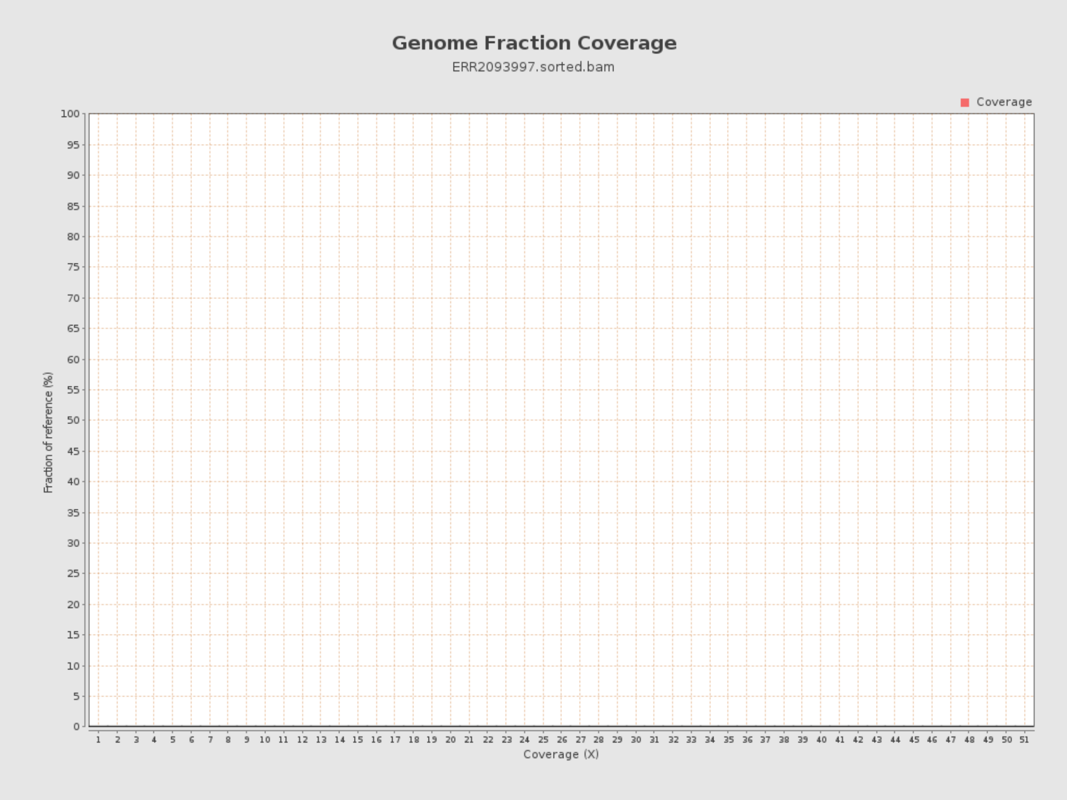
4. Results : Coverage Histogram



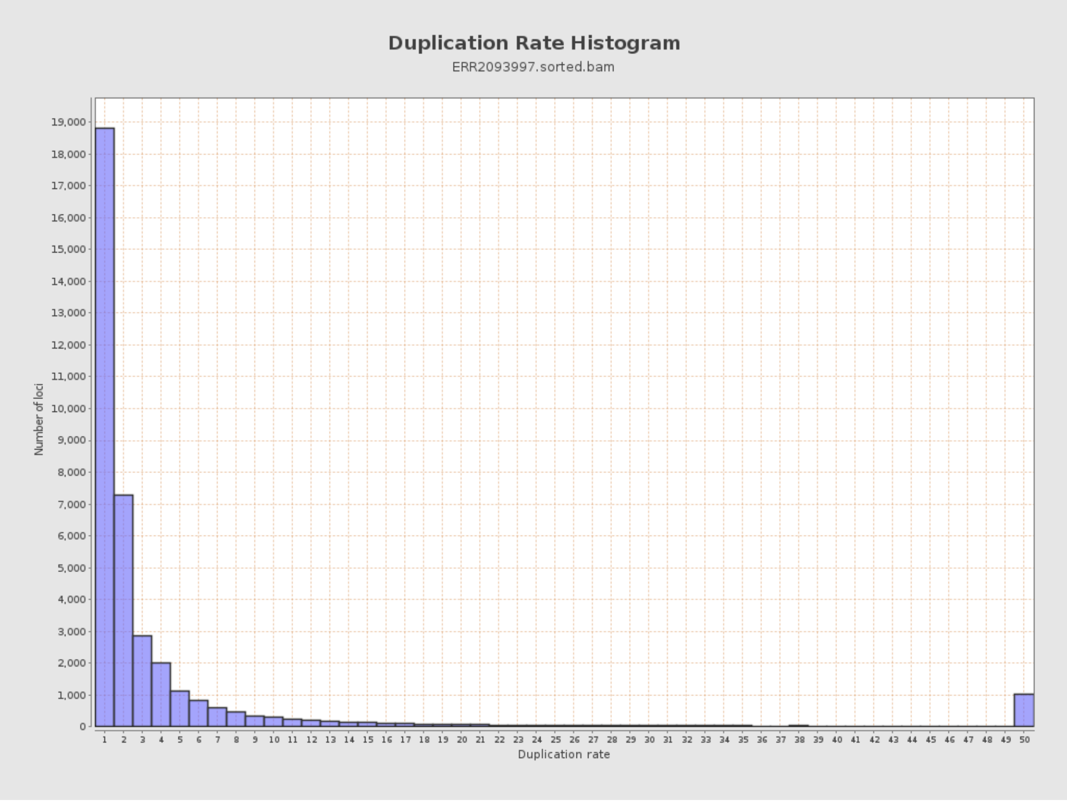
5. Results : Coverage Histogram (0-50X)



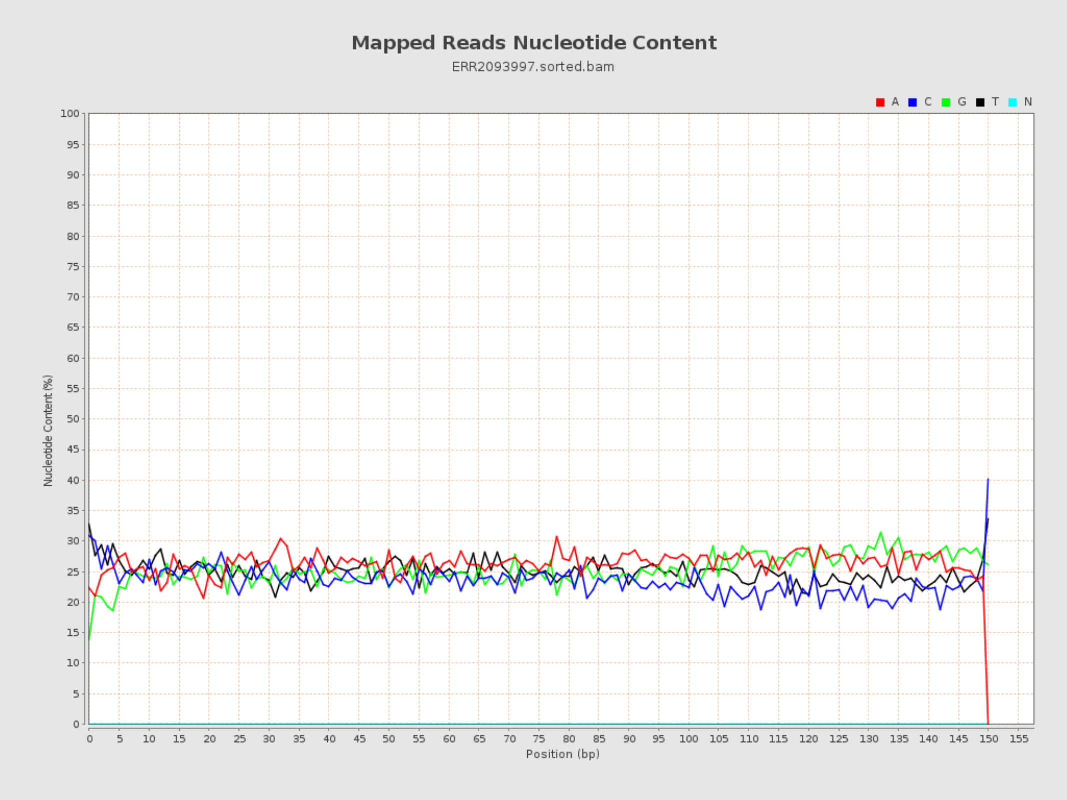
6. Results : Genome Fraction Coverage



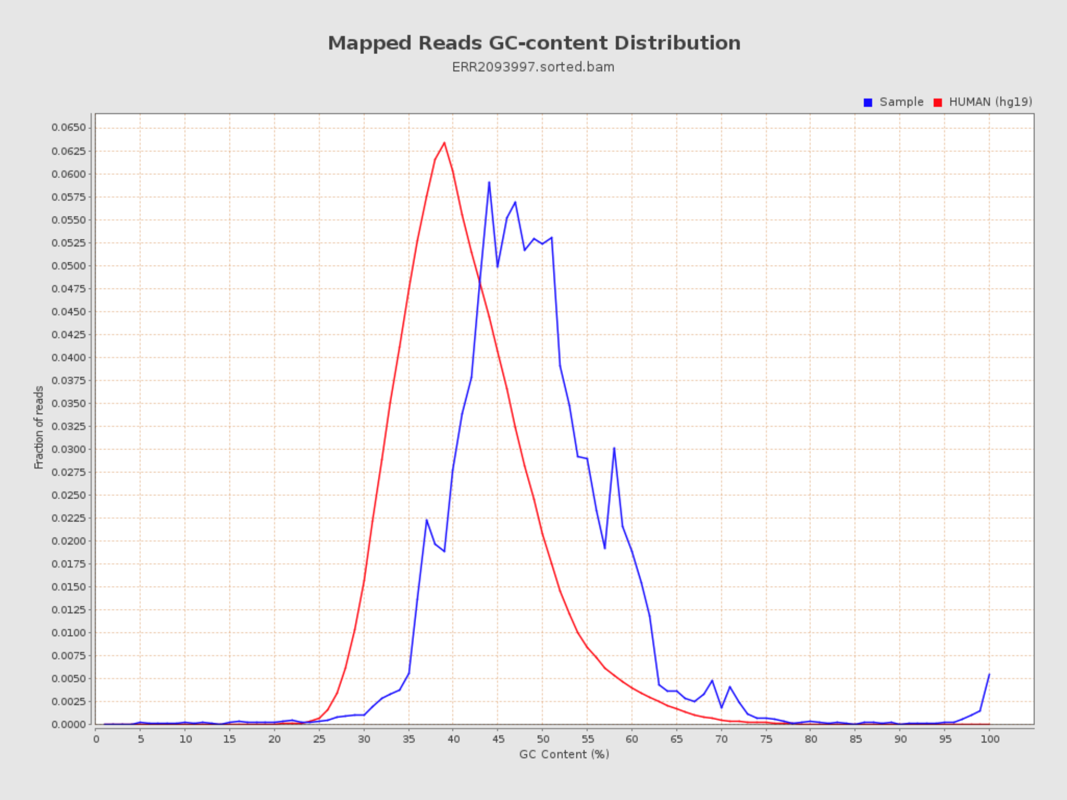
7. Results : Duplication Rate Histogram



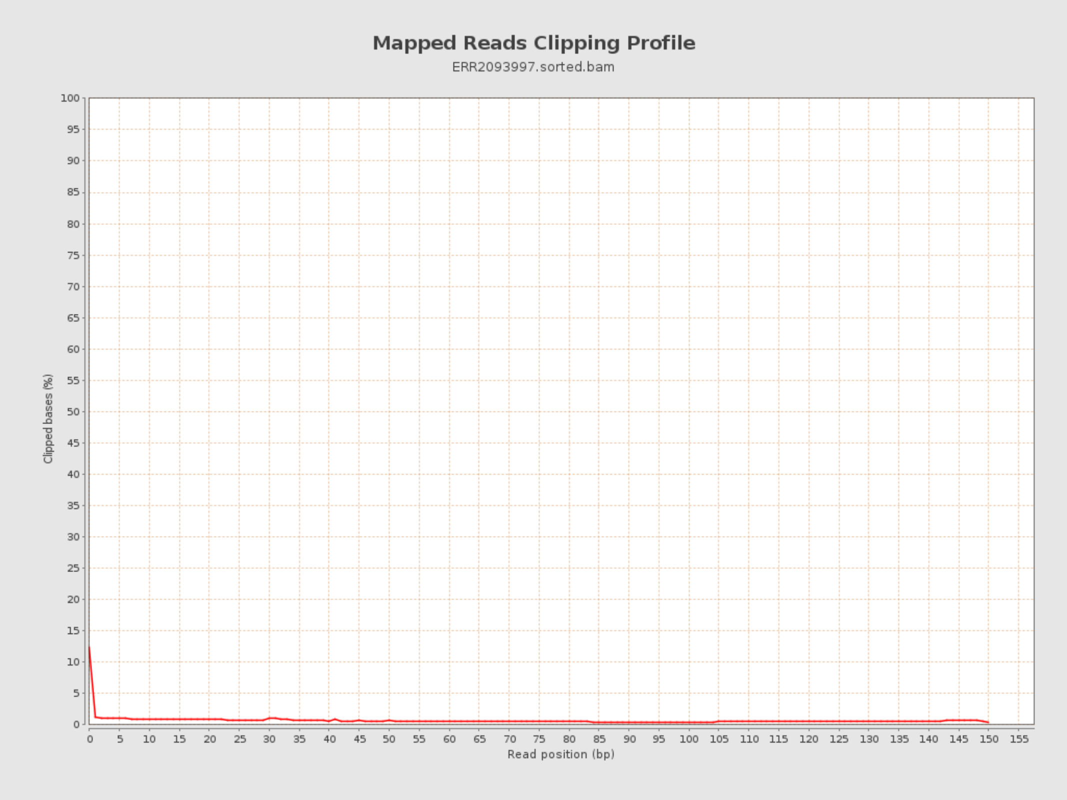
8. Results : Mapped Reads Nucleotide Content



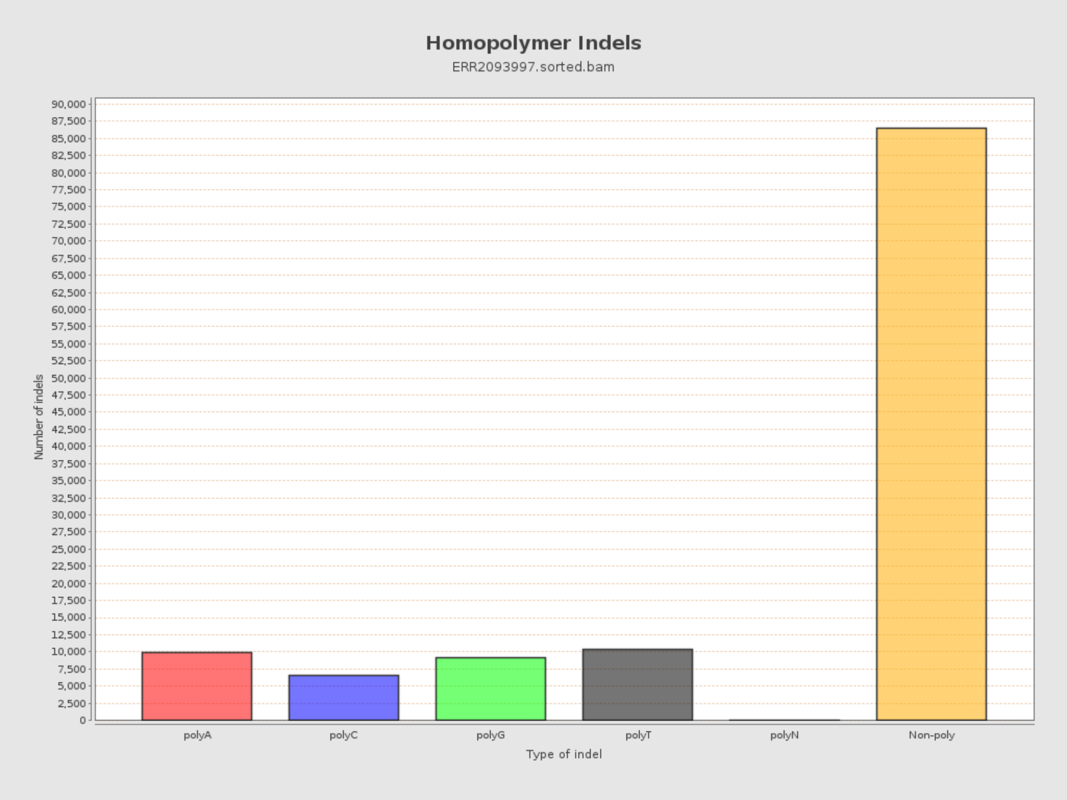
9. Results : Mapped Reads GC-content Distribution



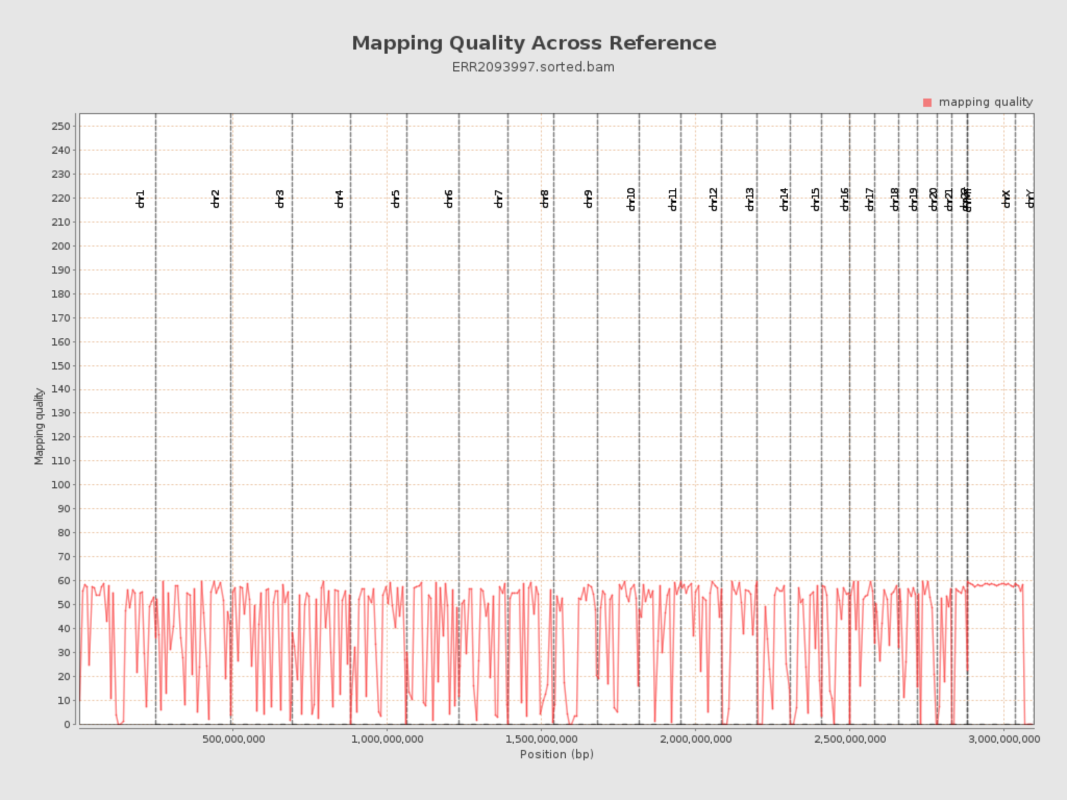
10. Results : Mapped Reads Clipping Profile



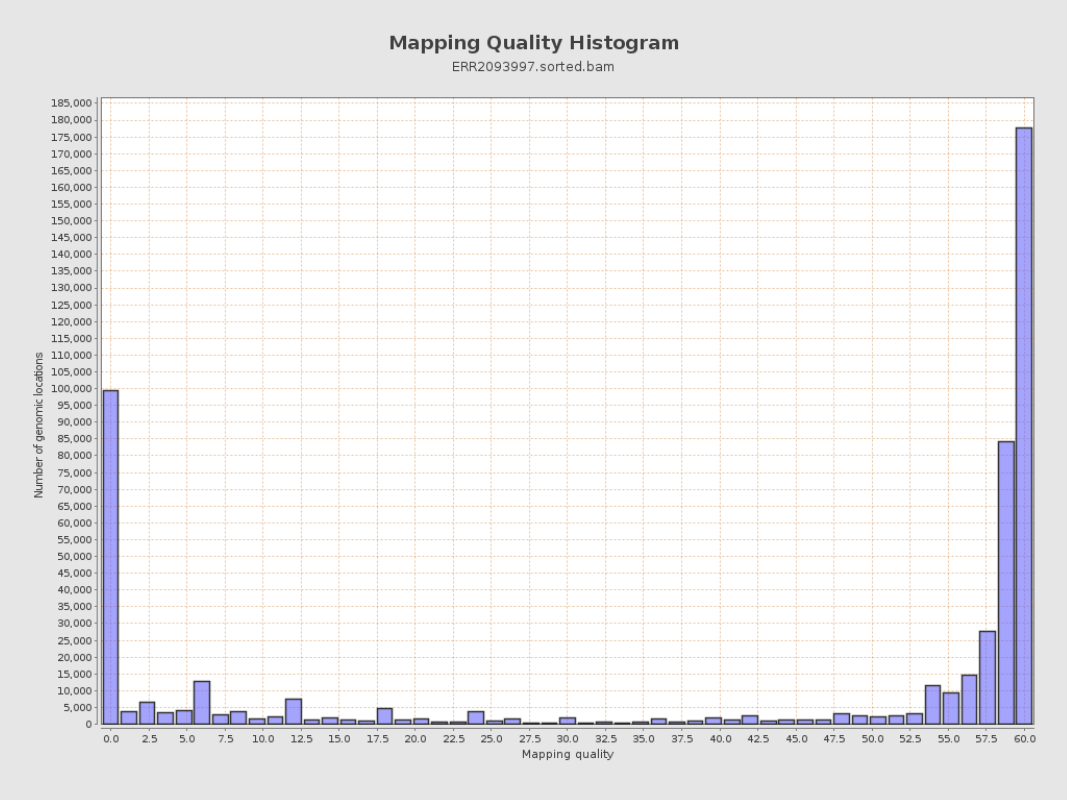
11. Results : Homopolymer Indels



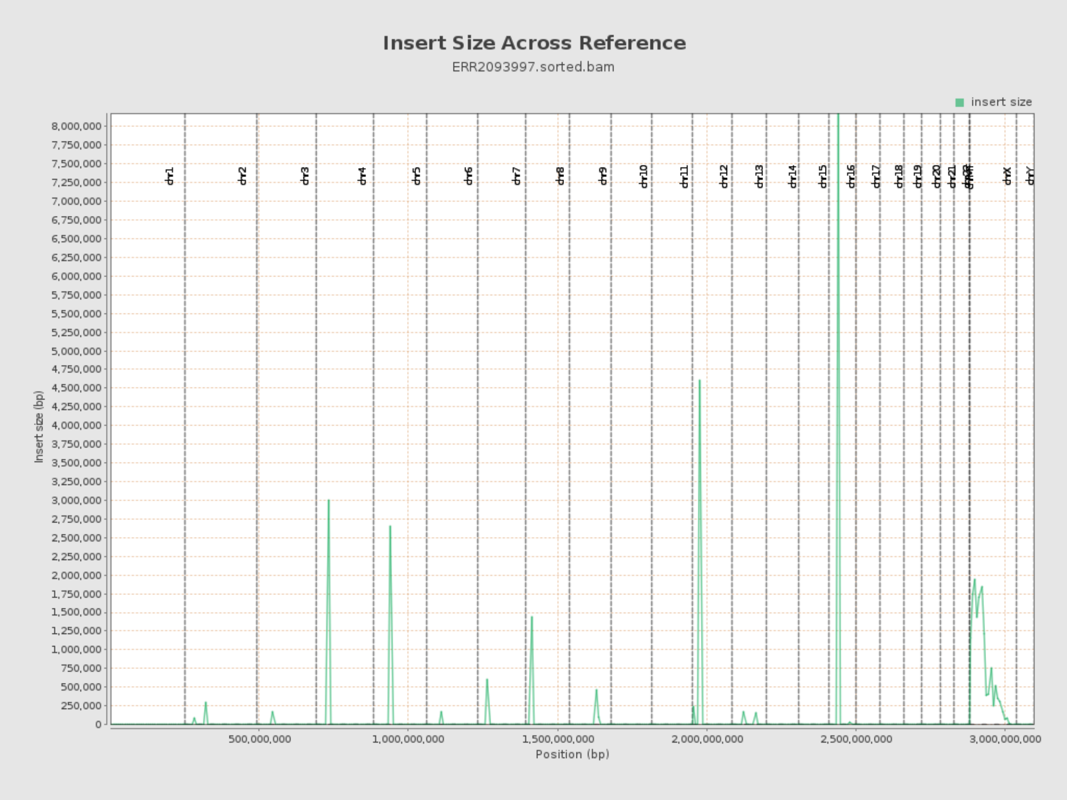
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram