Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:21:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093977.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_ERR2093977 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093977_1.fastq.gz ERR2093977_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:21:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	658,936
Mapped reads	532,544 / 80.82%
Unmapped reads	126,392 / 19.18%
Mapped paired reads	532,544 / 80.82%
Mapped reads, first in pair	266,972 / 40.52%
Mapped reads, second in pair	265,572 / 40.3%
Mapped reads, both in pair	527,484 / 80.05%
Mapped reads, singletons	5,060 / 0.77%
Secondary alignments	0
Supplementary alignments	6,272 / 0.95%
Read min/max/mean length	30 / 151 / 132.54
Duplicated reads (estimated)	521,317 / 79.11%
Duplication rate	32.36%
Clipped reads	287,266 / 43.6%

2.2. ACGT Content

Number/percentage of A's	19,058,472 / 26.63%
Number/percentage of C's	16,603,287 / 23.2%
Number/percentage of T's	19,768,684 / 27.62%
Number/percentage of G's	16,140,236 / 22.55%
Number/percentage of N's	843 / 0%

GC Percentage	45.75%

2.3. Coverage

Mean	0.0234
Standard Deviation	26.9724

2.4. Mapping Quality

Mean Mapping Quality	31.13

2.5. Insert size

Mean	107,840.72
Standard Deviation	3,463,594.72
P25/Median/P75	179 / 216 / 232

2.6. Mismatches and indels

General error rate	3.9%
Mismatches	1,921,013
Insertions	87,930
Mapped reads with at least one insertion	16.26%
Deletions	203,657
Mapped reads with at least one deletion	36.89%
Homopolymer indels	30.09%

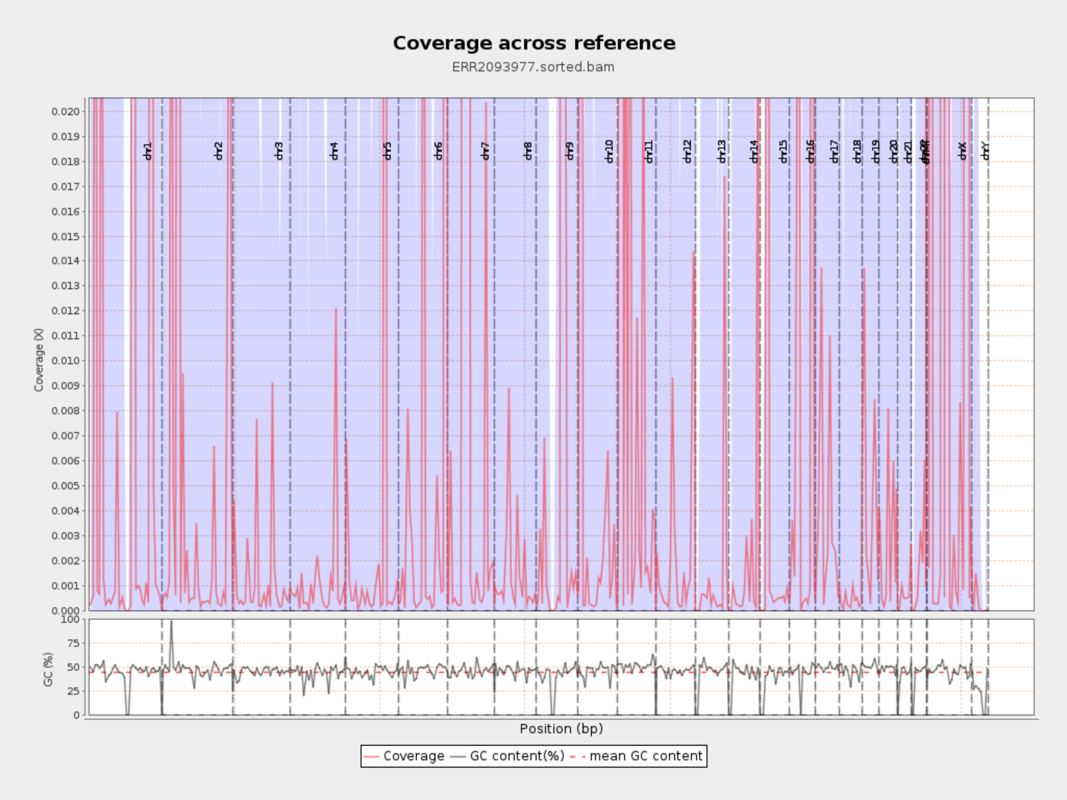
2.7. Chromosome stats

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

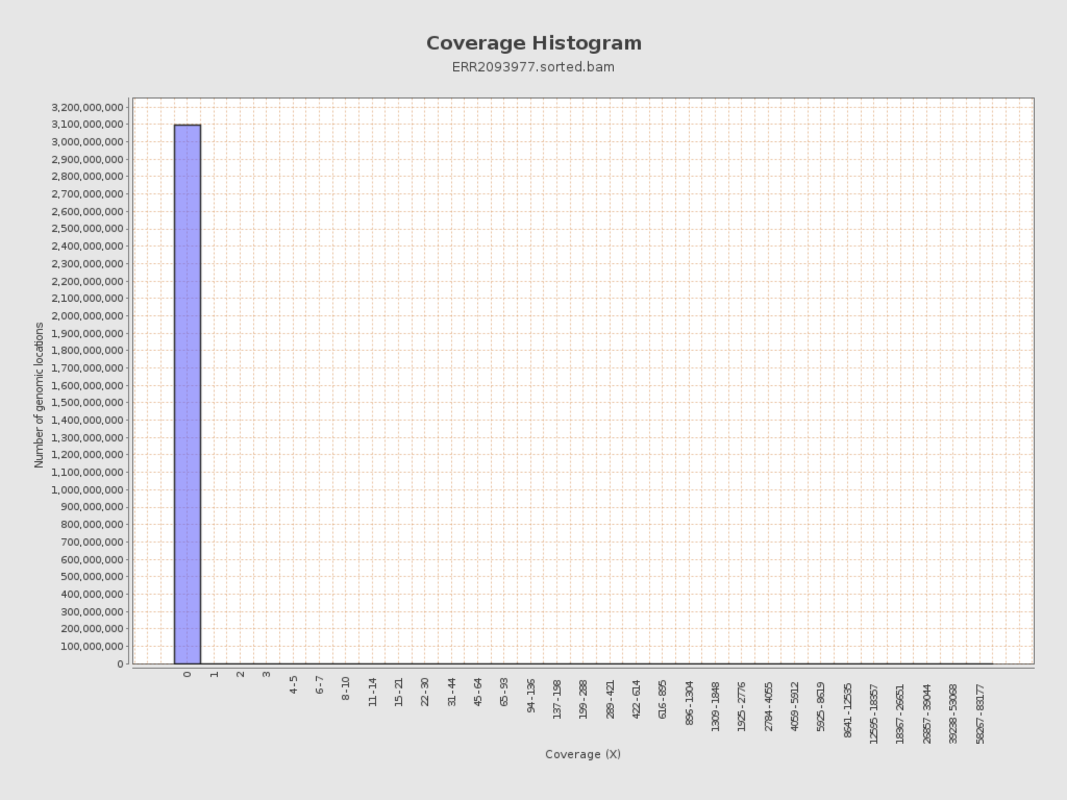
		bases	coverage	deviation
chr1	249250621	2279215	0.0091	4.8534
chr2	243199373	1732571	0.0071	4.416
chr3	198022430	267325	0.0013	0.5107
chr4	191154276	222663	0.0012	0.3577
chr5	180915260	807286	0.0045	2.6846
chr6	171115067	4324650	0.0253	17.5472
chr7	159138663	11787433	0.0741	42.6359
chr8	146364022	229094	0.0016	0.4601
chr9	141213431	2907106	0.0206	16.9379
chr10	135534747	2064419	0.0152	13.5891
chr11	135006516	12883155	0.0954	68.9286
chr12	133851895	336404	0.0025	0.8169
chr13	115169878	186374	0.0016	0.9833
chr14	107349540	299664	0.0028	1.3596
chr15	102531392	834228	0.0081	5.7841
chr16	90354753	1212549	0.0134	5.624
chr17	81195210	314614	0.0039	0.8789
chr18	78077248	31794	0.0004	0.0558
chr19	59128983	271542	0.0046	1.0561
chr20	63025520	165708	0.0026	0.6318
chr21	48129895	33909	0.0007	0.1529
chr22	51304566	93658	0.0018	0.4265
chrMT	16571	8646	0.5218	4.1065
chrX	155270560	29195274	0.188	87.3351

chrY	59373566	15031	0.0003	0.1043

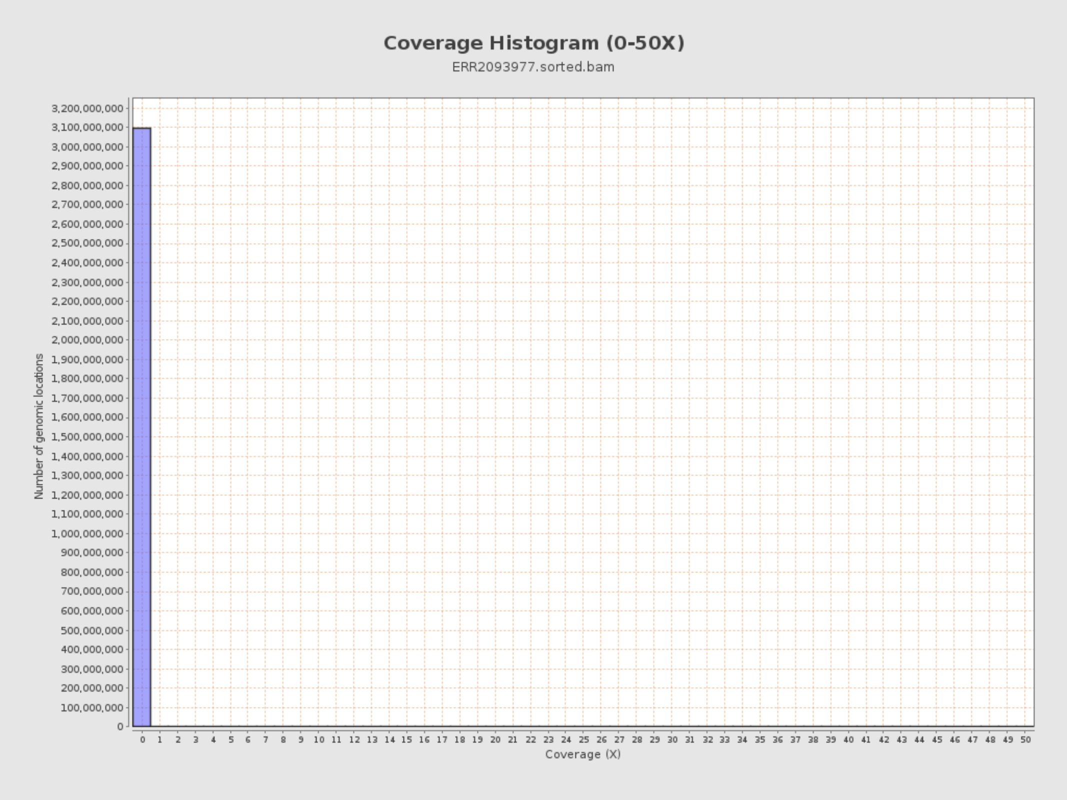
3. Results : Coverage across reference



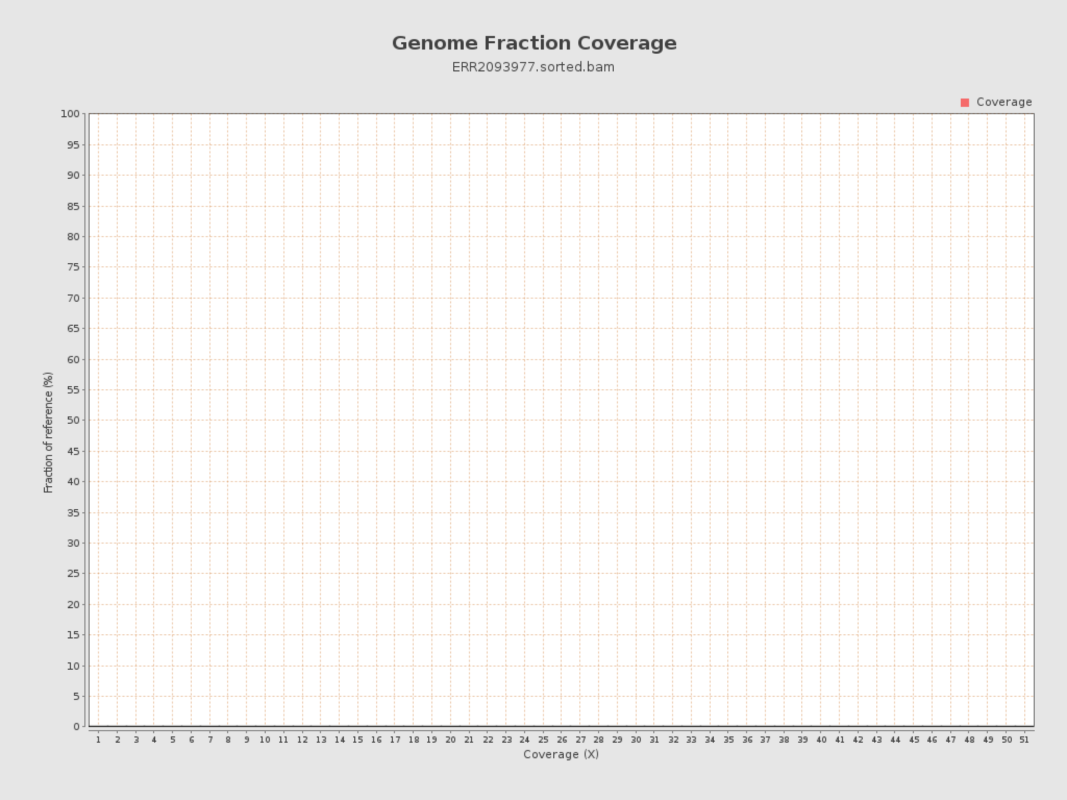
4. Results : Coverage Histogram



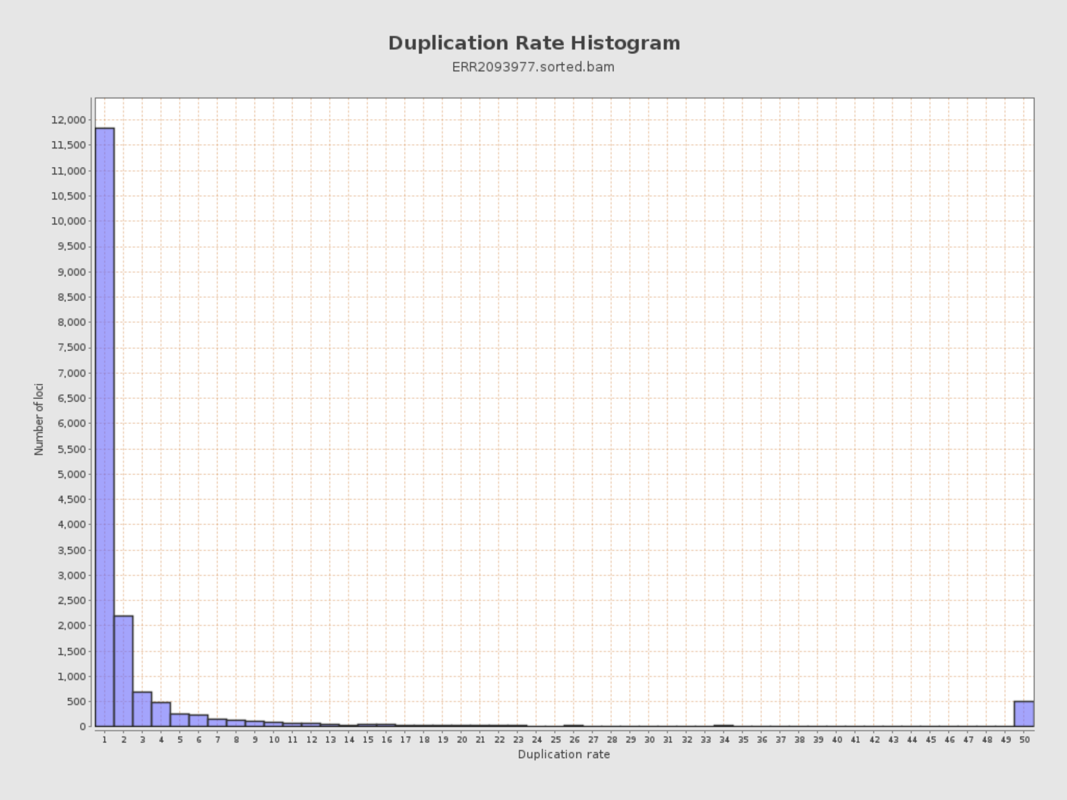
5. Results : Coverage Histogram (0-50X)



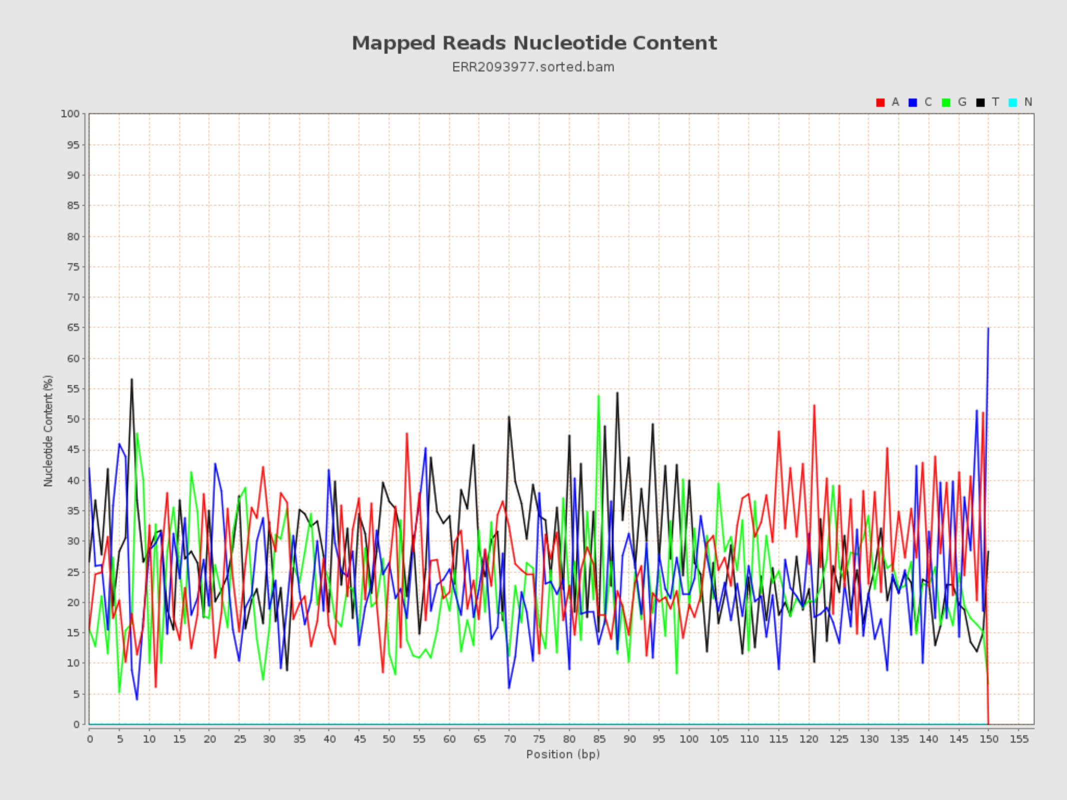
6. Results : Genome Fraction Coverage



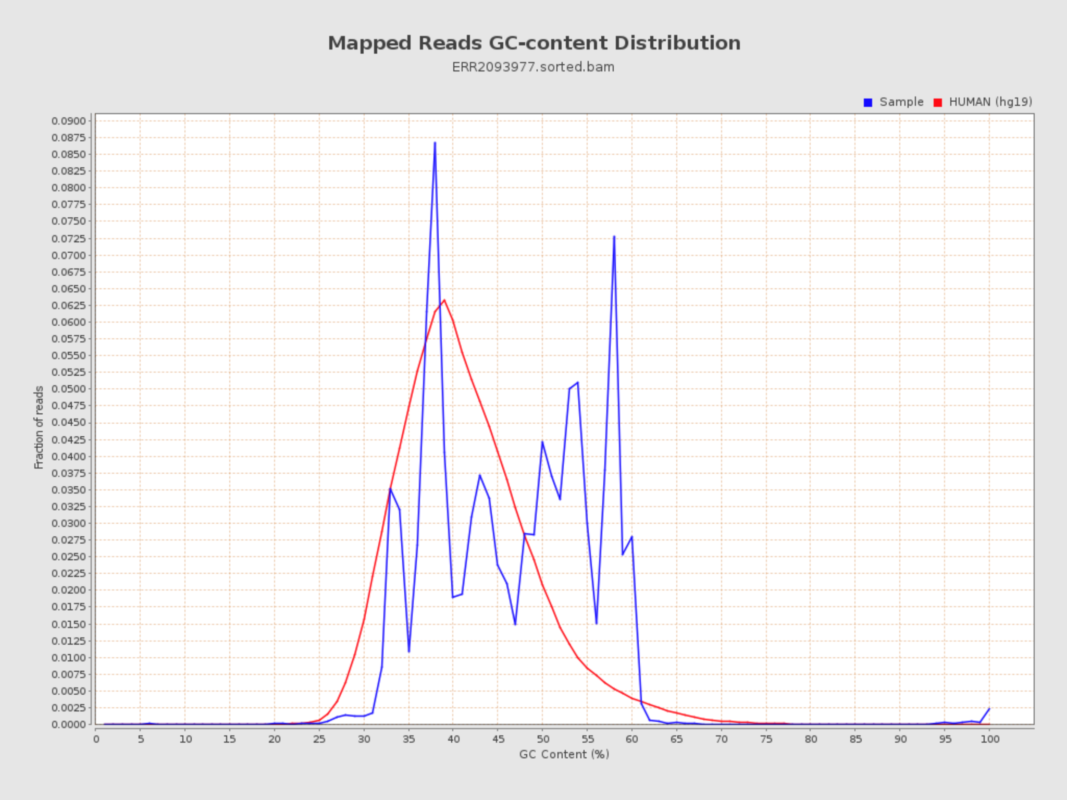
7. Results : Duplication Rate Histogram



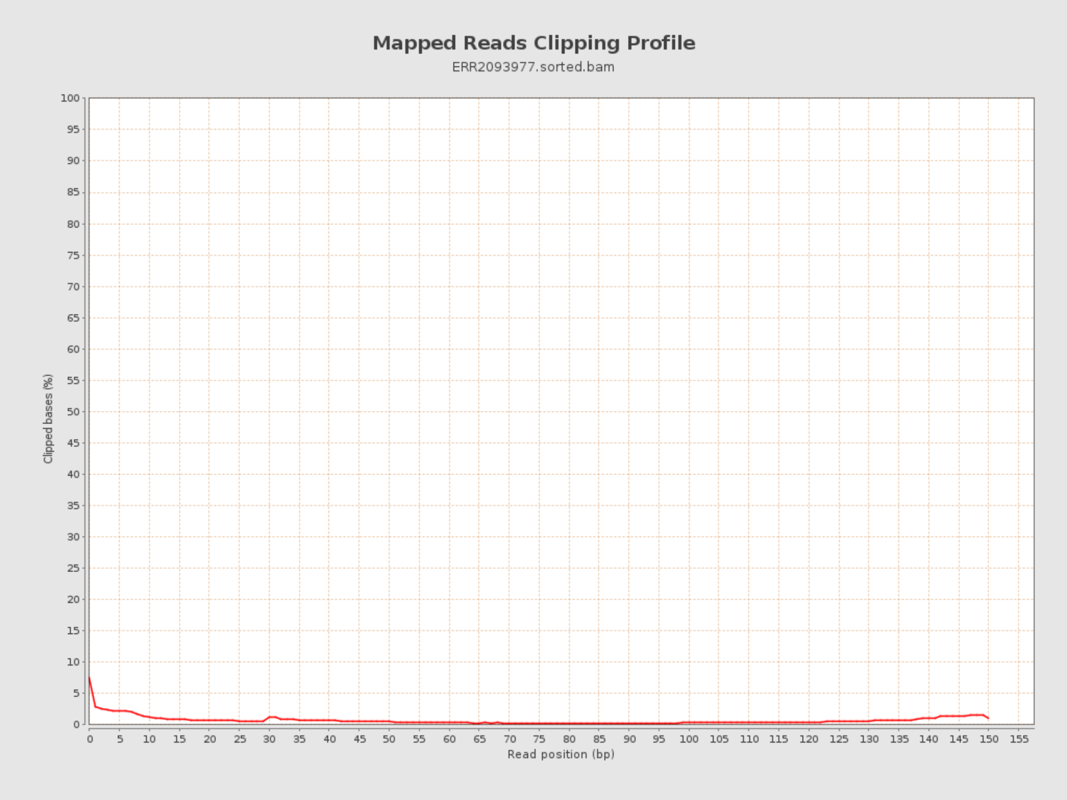
8. Results : Mapped Reads Nucleotide Content



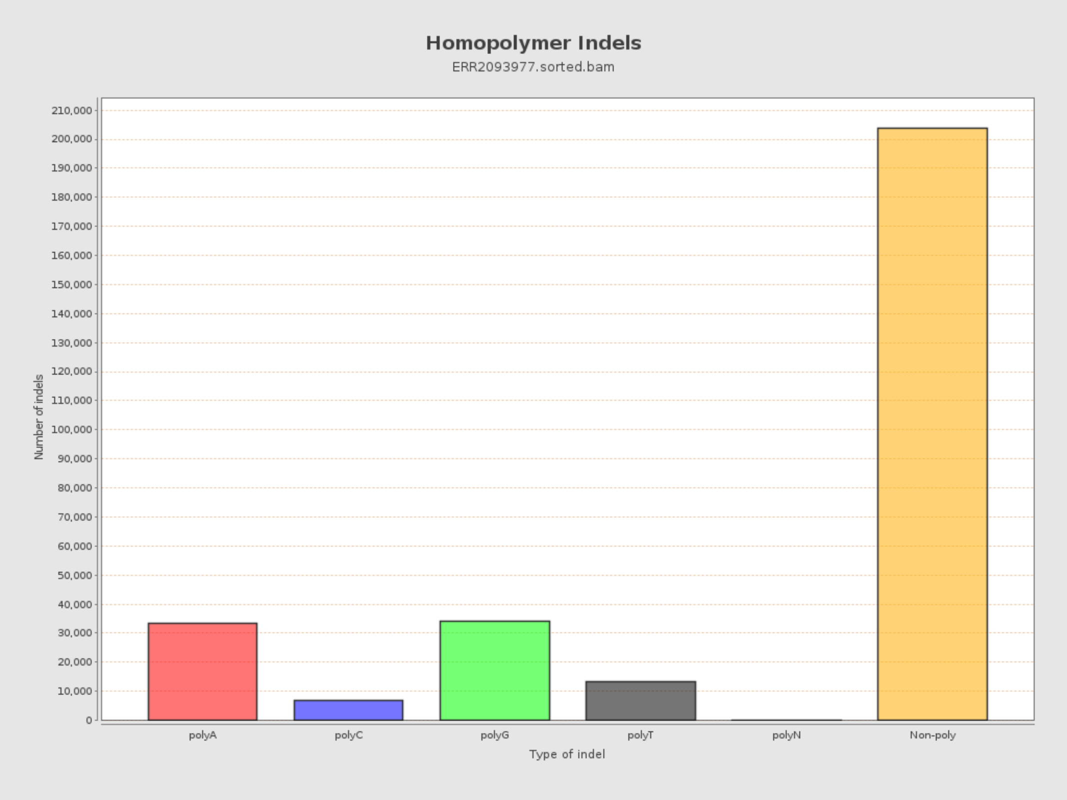
9. Results : Mapped Reads GC-content Distribution



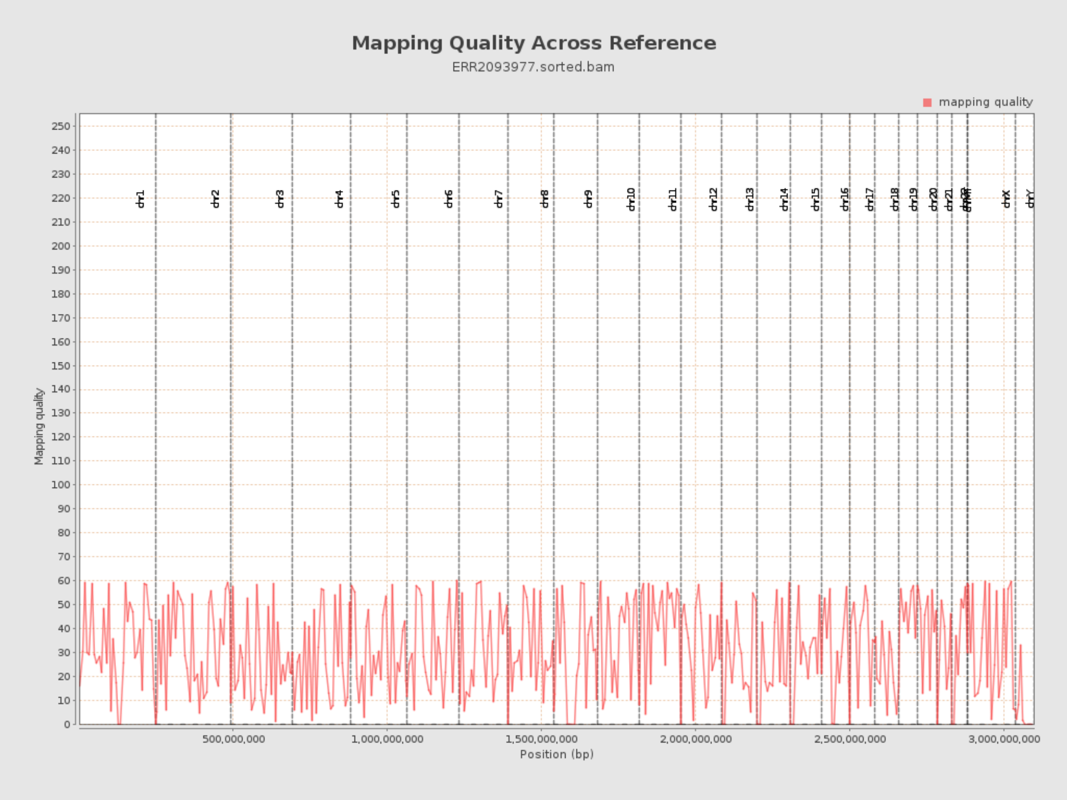
10. Results : Mapped Reads Clipping Profile



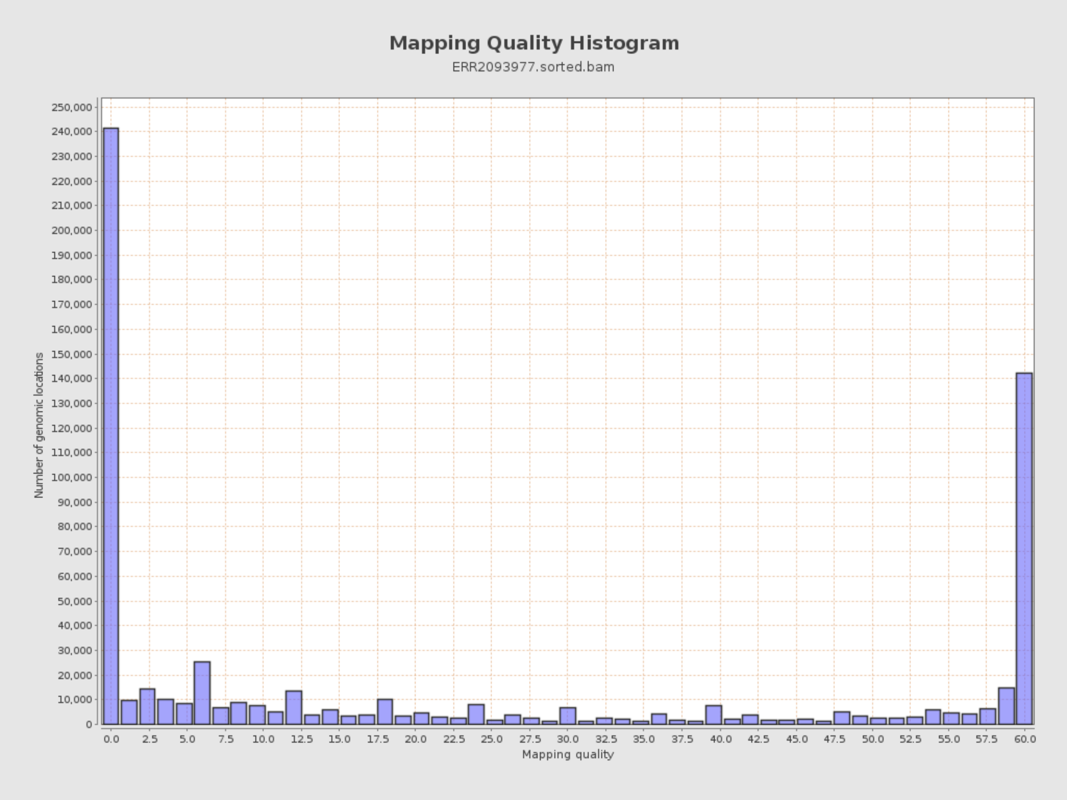
11. Results : Homopolymer Indels



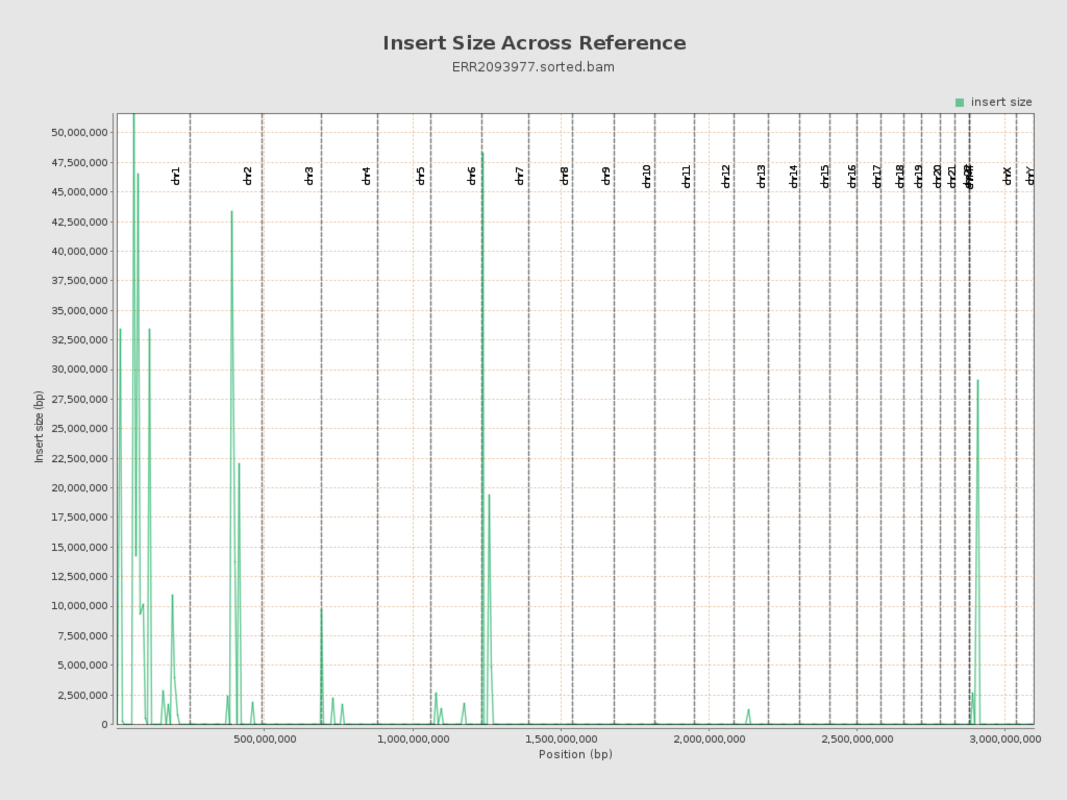
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram