Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:00:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093990.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_ERR2093990 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093990_1.fastq.gz ERR2093990_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:00:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	309,640
Mapped reads	294,635 / 95.15%
Unmapped reads	15,005 / 4.85%
Mapped paired reads	294,635 / 95.15%
Mapped reads, first in pair	148,181 / 47.86%
Mapped reads, second in pair	146,454 / 47.3%
Mapped reads, both in pair	291,690 / 94.2%
Mapped reads, singletons	2,945 / 0.95%
Secondary alignments	0
Supplementary alignments	19,010 / 6.14%
Read min/max/mean length	30 / 151 / 141.05
Duplicated reads (estimated)	275,129 / 88.85%
Duplication rate	48.87%
Clipped reads	151,066 / 48.79%

2.2. ACGT Content

Number/percentage of A's	9,720,519 / 26.41%
Number/percentage of C's	8,637,842 / 23.47%
Number/percentage of T's	9,164,122 / 24.9%
Number/percentage of G's	9,284,354 / 25.22%
Number/percentage of N's	438 / 0%

GC Percentage	48.69%

2.3. Coverage

Mean	0.0121
Standard Deviation	2.3174

2.4. Mapping Quality

Mean Mapping Quality	40.53

2.5. Insert size

Mean	1,004,056.53
Standard Deviation	9,115,276.25
P25/Median/P75	127 / 163 / 199

2.6. Mismatches and indels

General error rate	3.52%
Mismatches	1,250,313
Insertions	19,994
Mapped reads with at least one insertion	6.66%
Deletions	99,326
Mapped reads with at least one deletion	32.37%
Homopolymer indels	29.17%

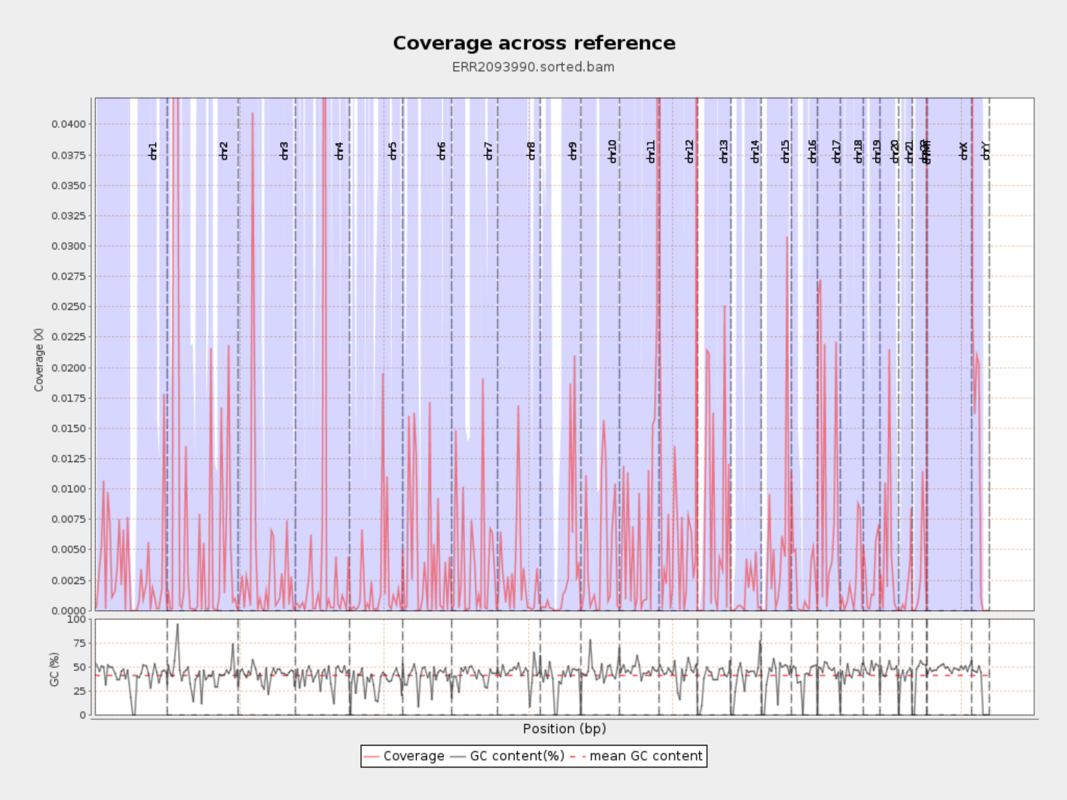
2.7. Chromosome stats

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

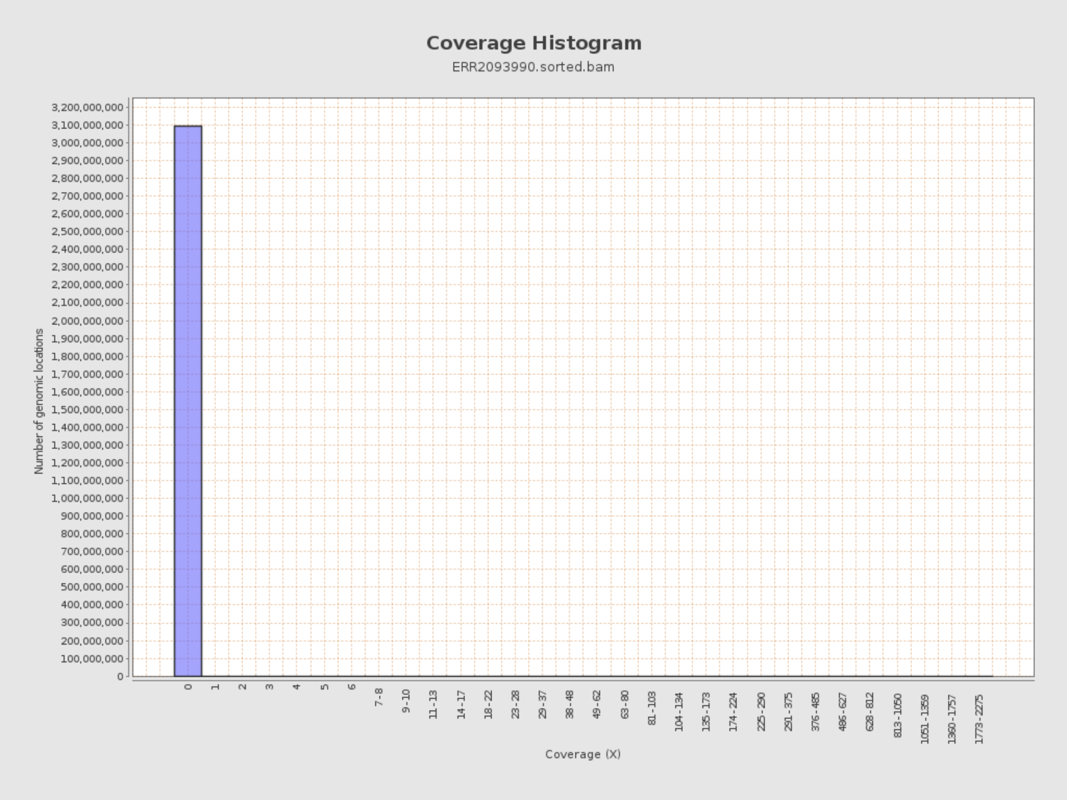
		bases	coverage	deviation
chr1	249250621	805638	0.0032	1.0022
chr2	243199373	2095271	0.0086	2.5727
chr3	198022430	681958	0.0034	1.0526
chr4	191154276	875511	0.0046	1.491
chr5	180915260	381013	0.0021	1.1036
chr6	171115067	758609	0.0044	1.2881
chr7	159138663	601959	0.0038	1.1473
chr8	146364022	403438	0.0028	0.8186
chr9	141213431	467271	0.0033	0.9161
chr10	135534747	597016	0.0044	1.2878
chr11	135006516	1002770	0.0074	1.8231
chr12	133851895	838640	0.0063	1.5033
chr13	115169878	828419	0.0072	1.8737
chr14	107349540	139172	0.0013	0.3989
chr15	102531392	476000	0.0046	1.2503
chr16	90354753	227638	0.0025	0.7034
chr17	81195210	898262	0.0111	2.6394
chr18	78077248	194119	0.0025	0.734
chr19	59128983	165540	0.0028	0.7406
chr20	63025520	321395	0.0051	1.611
chr21	48129895	89543	0.0019	0.3632
chr22	51304566	135005	0.0026	0.7009
chrMT	16571	670475	40.4607	204.1739
chrX	155270560	23235369	0.1496	7.997

chrY	59373566	578234	0.0097	1.3106

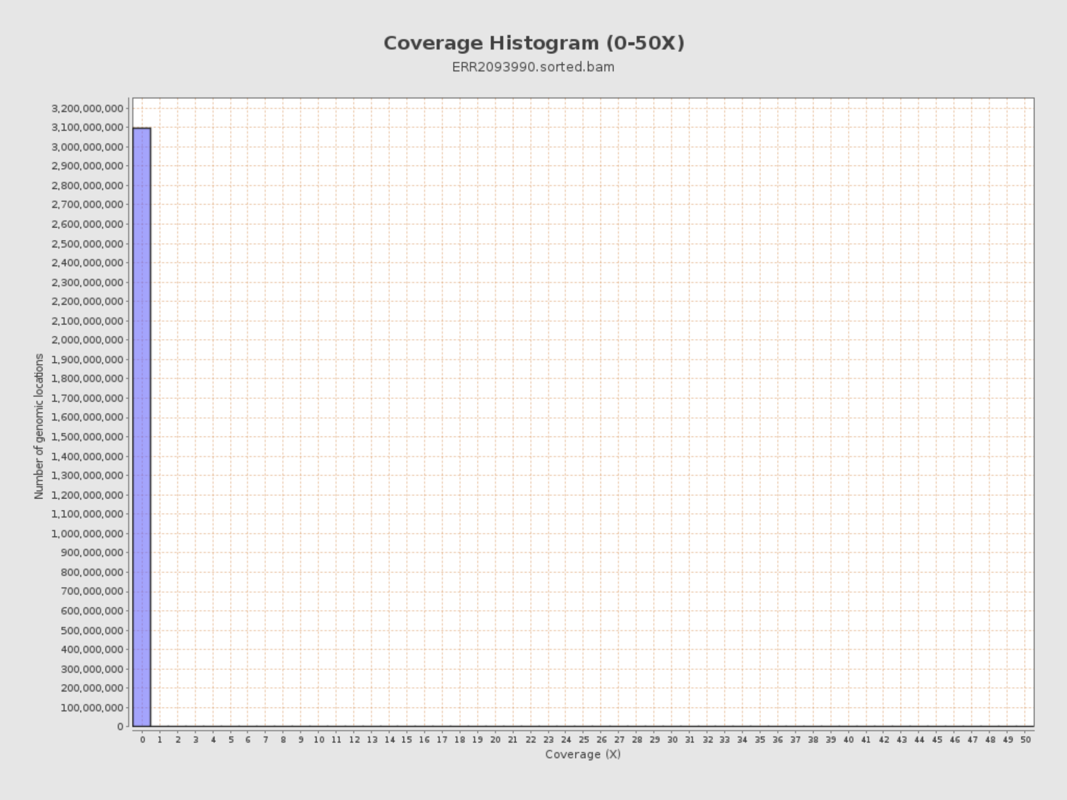
3. Results : Coverage across reference



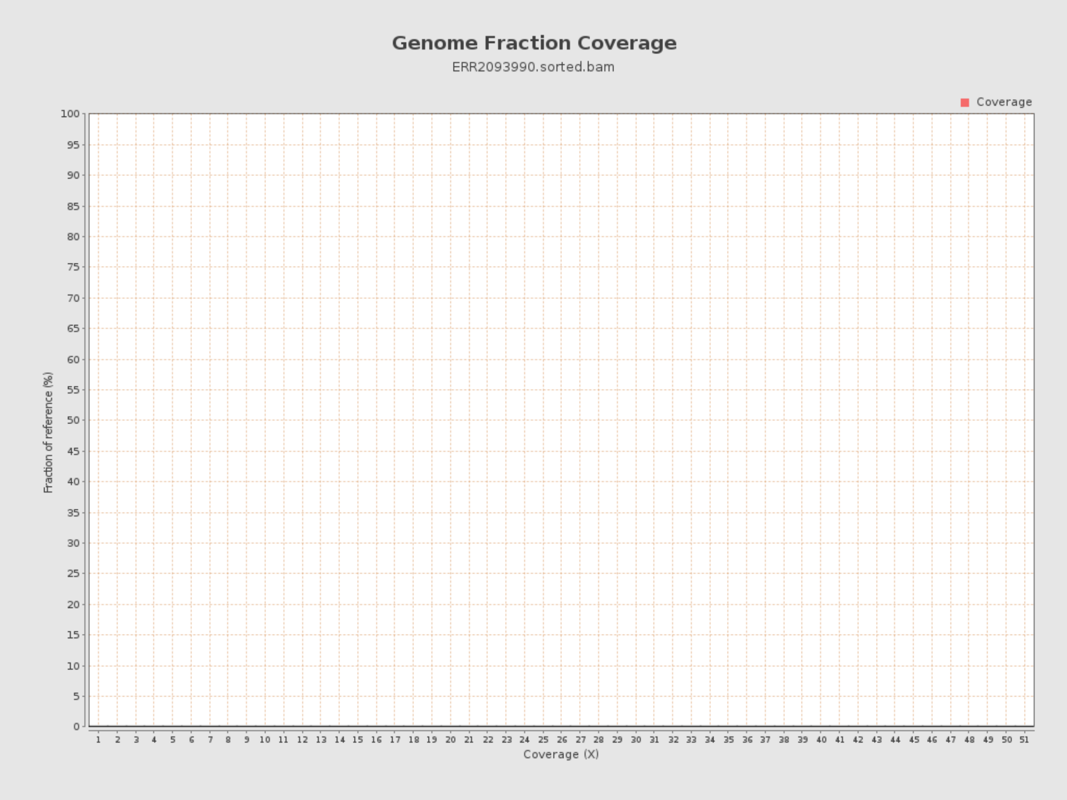
4. Results : Coverage Histogram



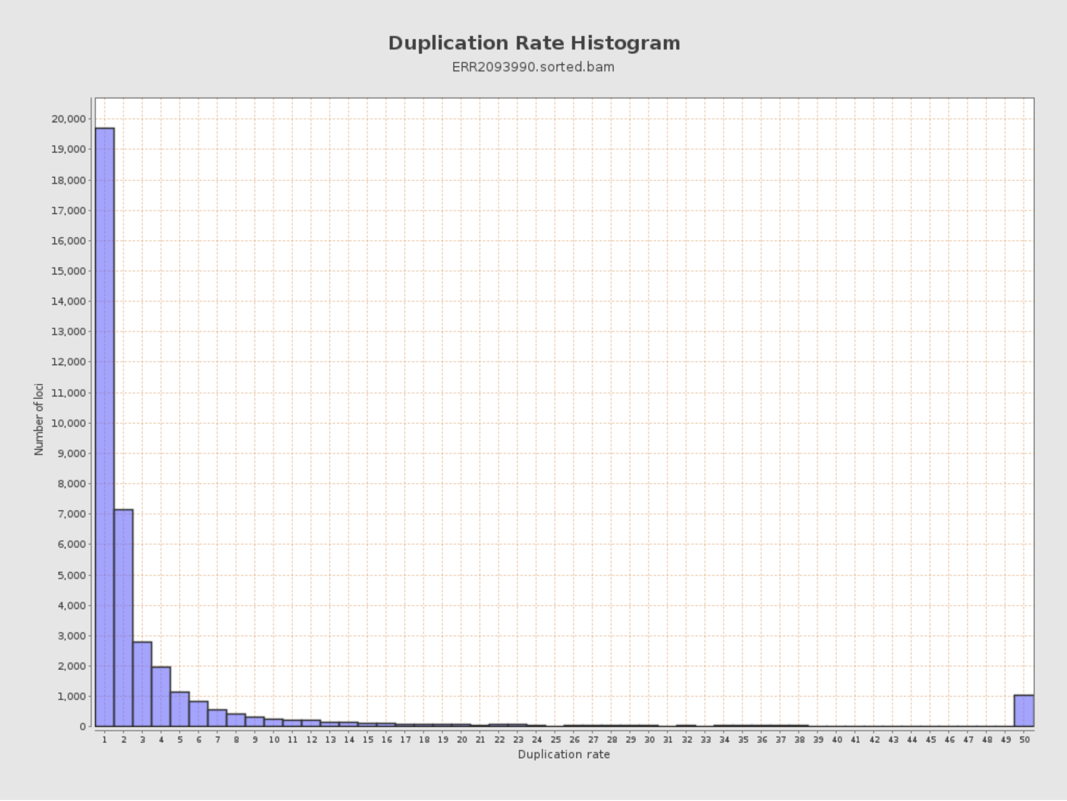
5. Results : Coverage Histogram (0-50X)



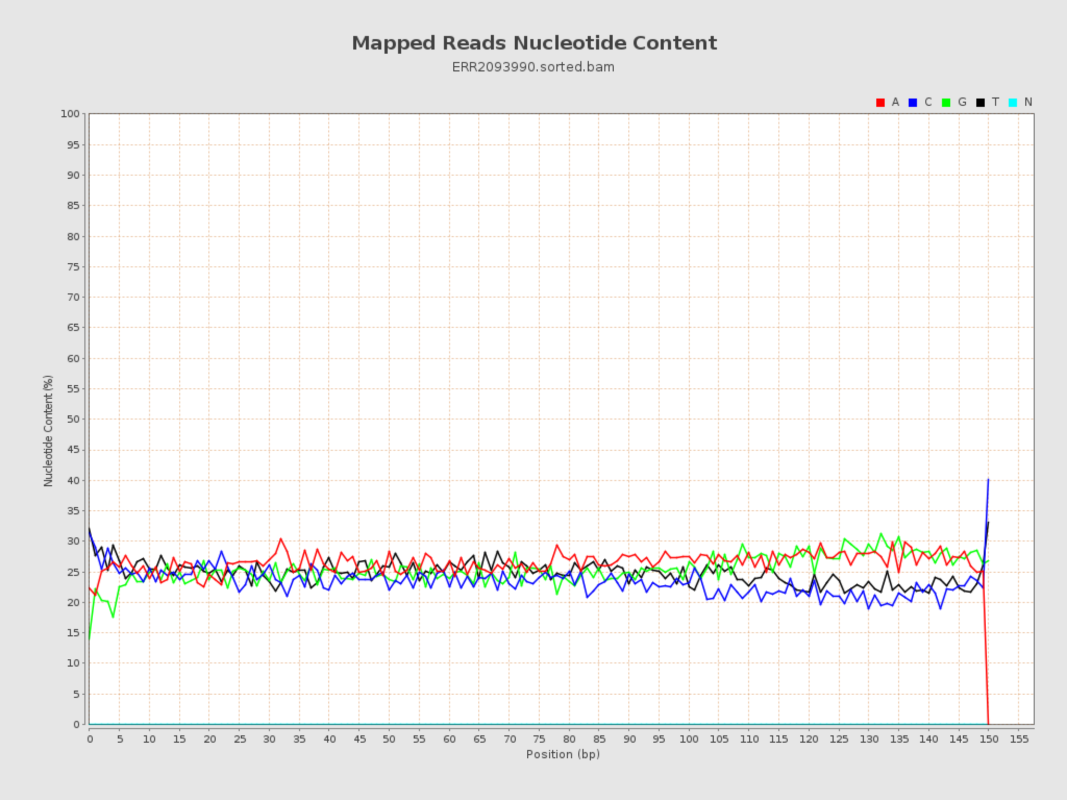
6. Results : Genome Fraction Coverage



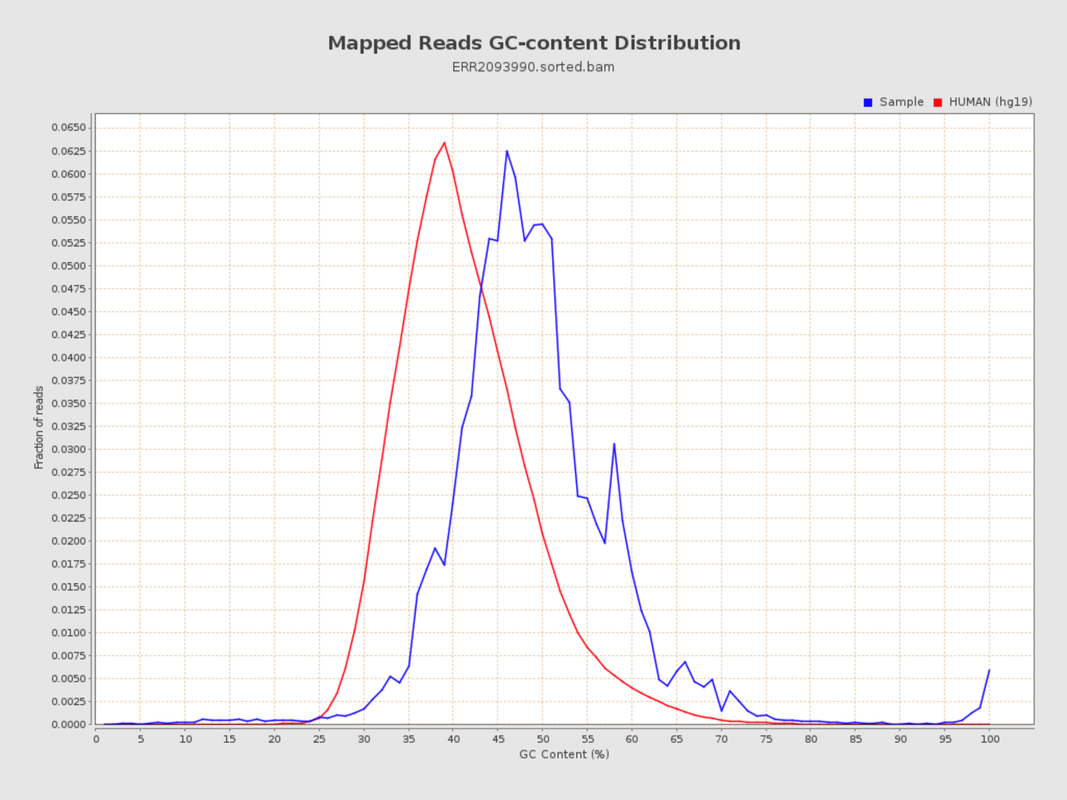
7. Results : Duplication Rate Histogram



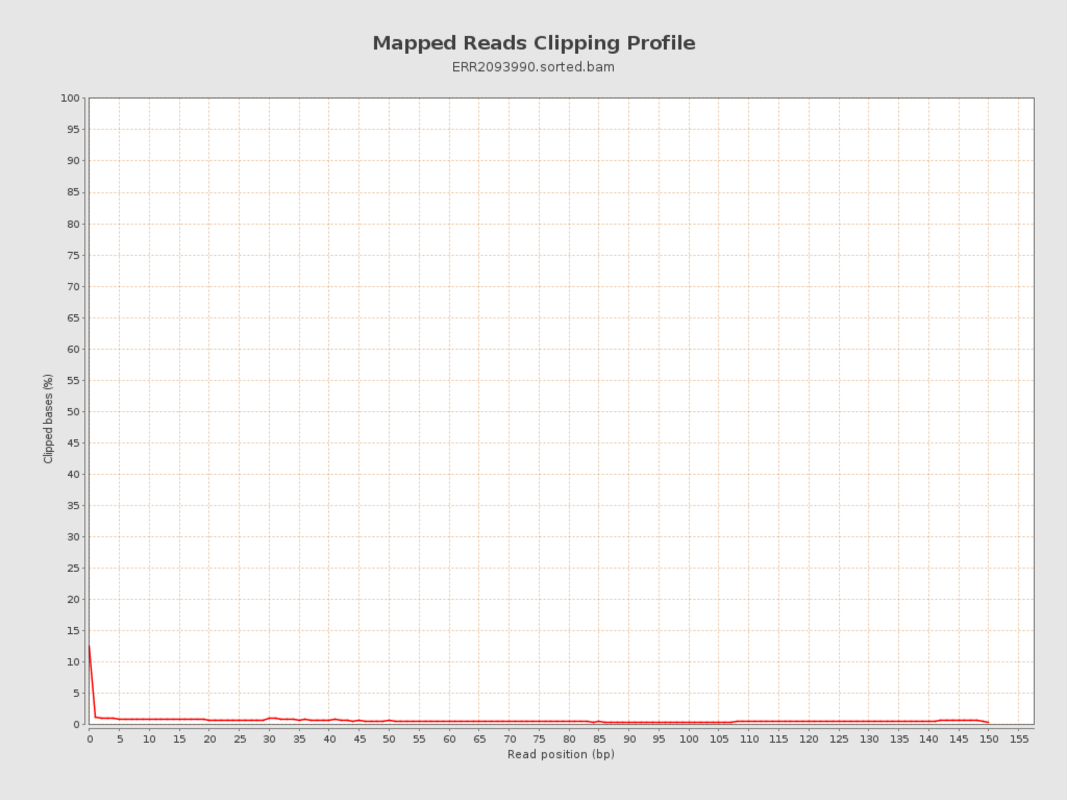
8. Results : Mapped Reads Nucleotide Content



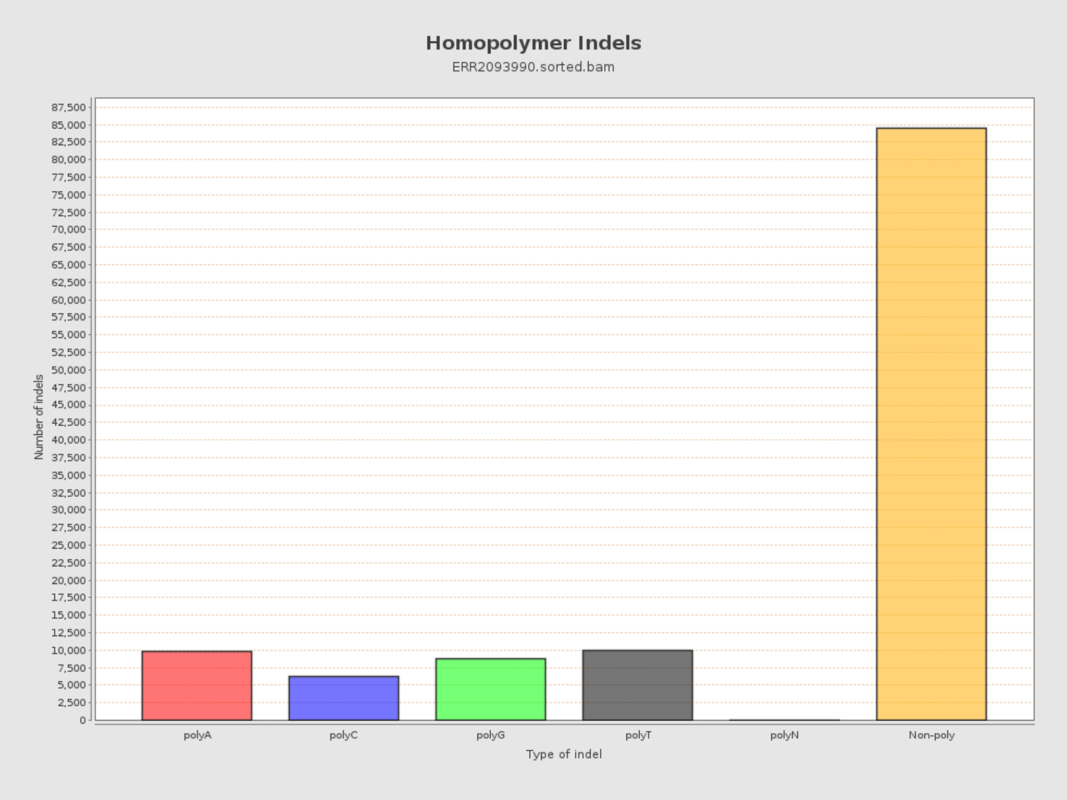
9. Results : Mapped Reads GC-content Distribution



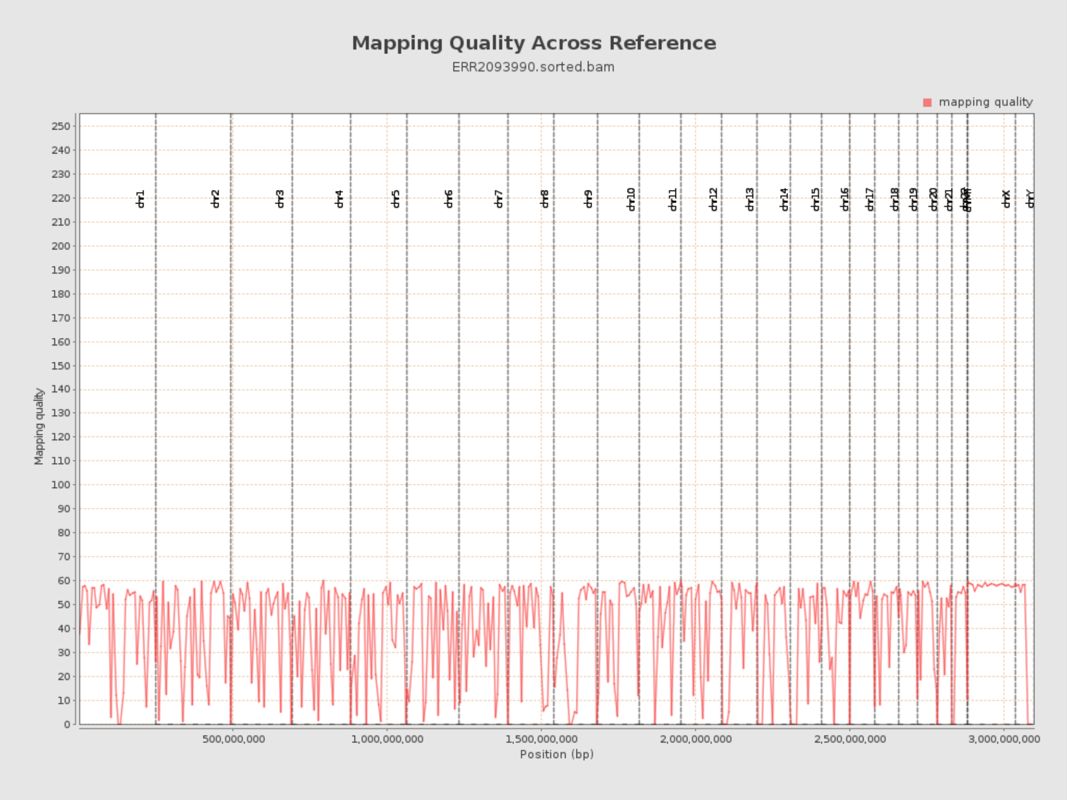
10. Results : Mapped Reads Clipping Profile



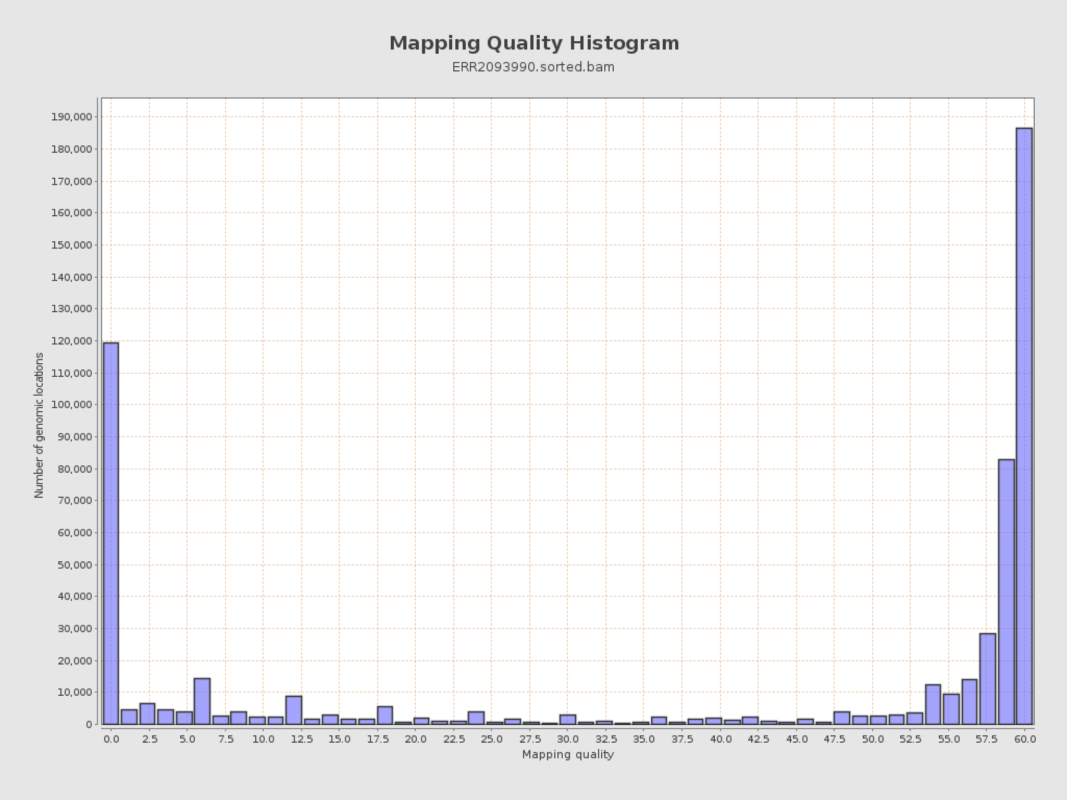
11. Results : Homopolymer Indels



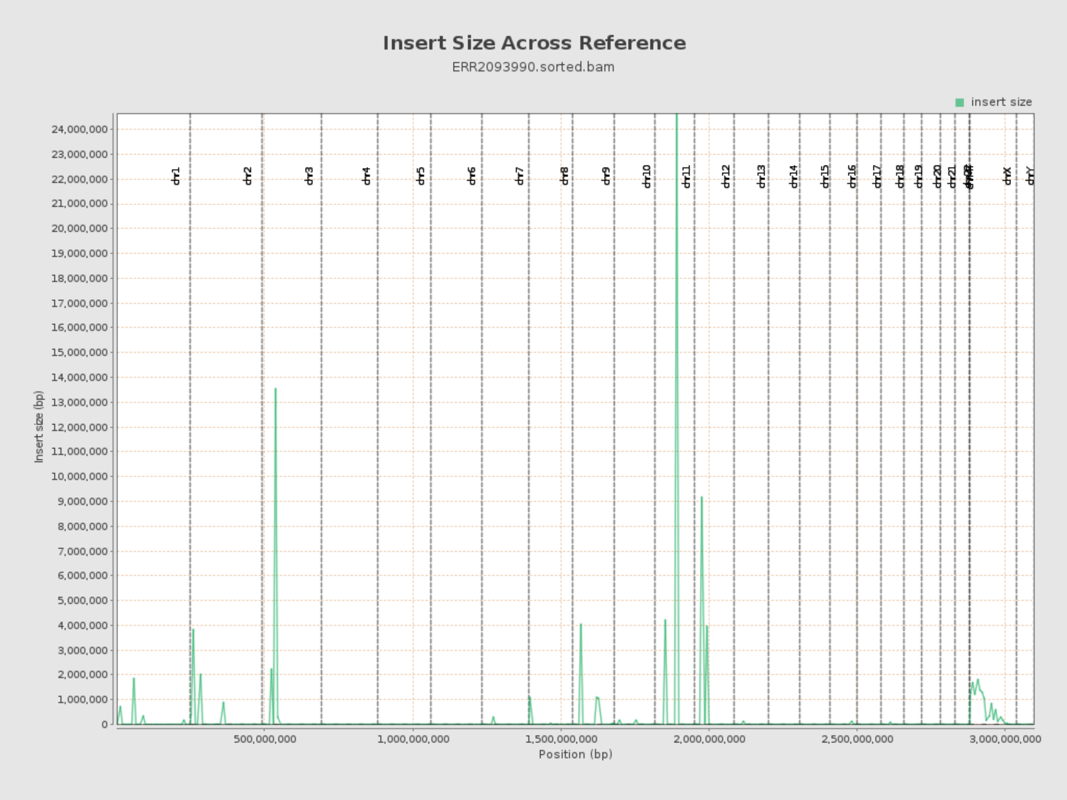
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram