Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:22:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093999.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_ERR2093999 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093999_1.fastq.gz ERR2093999_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:22:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	408,108
Mapped reads	385,027 / 94.34%
Unmapped reads	23,081 / 5.66%
Mapped paired reads	385,027 / 94.34%
Mapped reads, first in pair	193,450 / 47.4%
Mapped reads, second in pair	191,577 / 46.94%
Mapped reads, both in pair	381,624 / 93.51%
Mapped reads, singletons	3,403 / 0.83%
Secondary alignments	0
Supplementary alignments	21,032 / 5.15%
Read min/max/mean length	30 / 151 / 140.42
Duplicated reads (estimated)	363,650 / 89.11%
Duplication rate	50.84%
Clipped reads	179,597 / 44.01%

2.2. ACGT Content

Number/percentage of A's	12,989,867 / 26.55%
Number/percentage of C's	11,423,941 / 23.35%
Number/percentage of T's	12,337,926 / 25.22%
Number/percentage of G's	12,170,990 / 24.88%
Number/percentage of N's	555 / 0%

GC Percentage	48.23%

2.3. Coverage

Mean	0.0161
Standard Deviation	2.9698

2.4. Mapping Quality

Mean Mapping Quality	40.38

2.5. Insert size

Mean	903,067.47
Standard Deviation	8,608,052.84
P25/Median/P75	130 / 164 / 201

2.6. Mismatches and indels

General error rate	3.66%
Mismatches	1,722,253
Insertions	29,323
Mapped reads with at least one insertion	7.51%
Deletions	138,328
Mapped reads with at least one deletion	34.52%
Homopolymer indels	28.52%

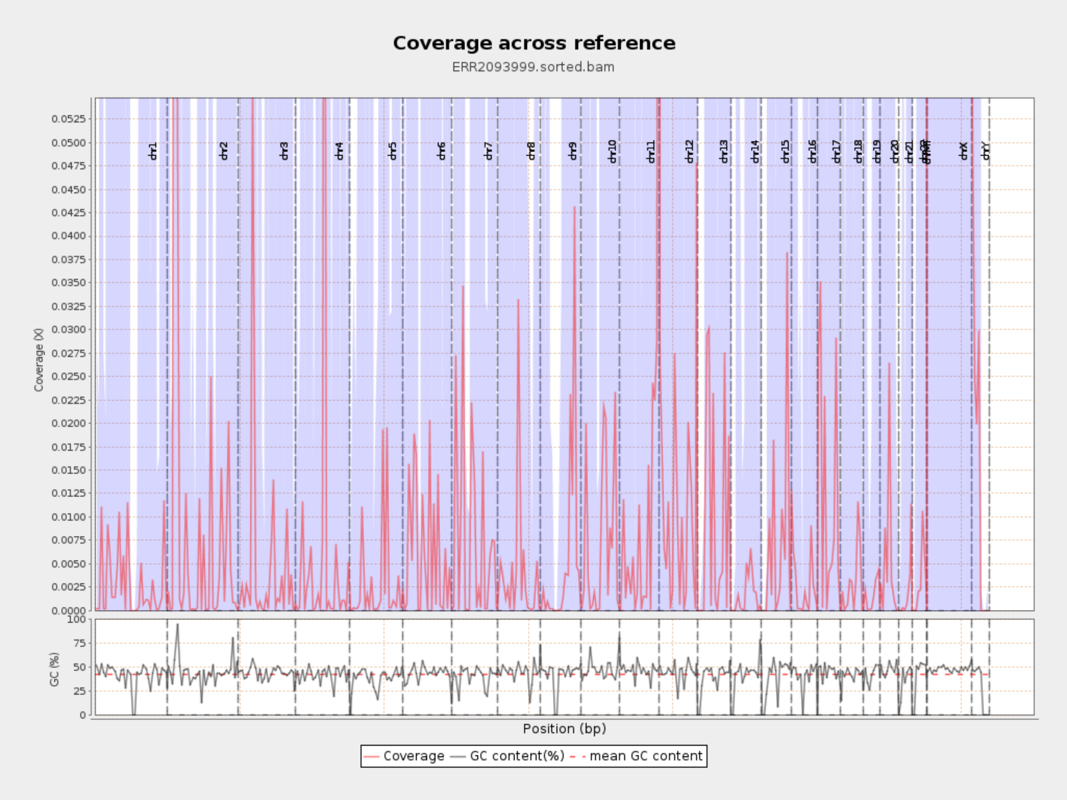
2.7. Chromosome stats

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

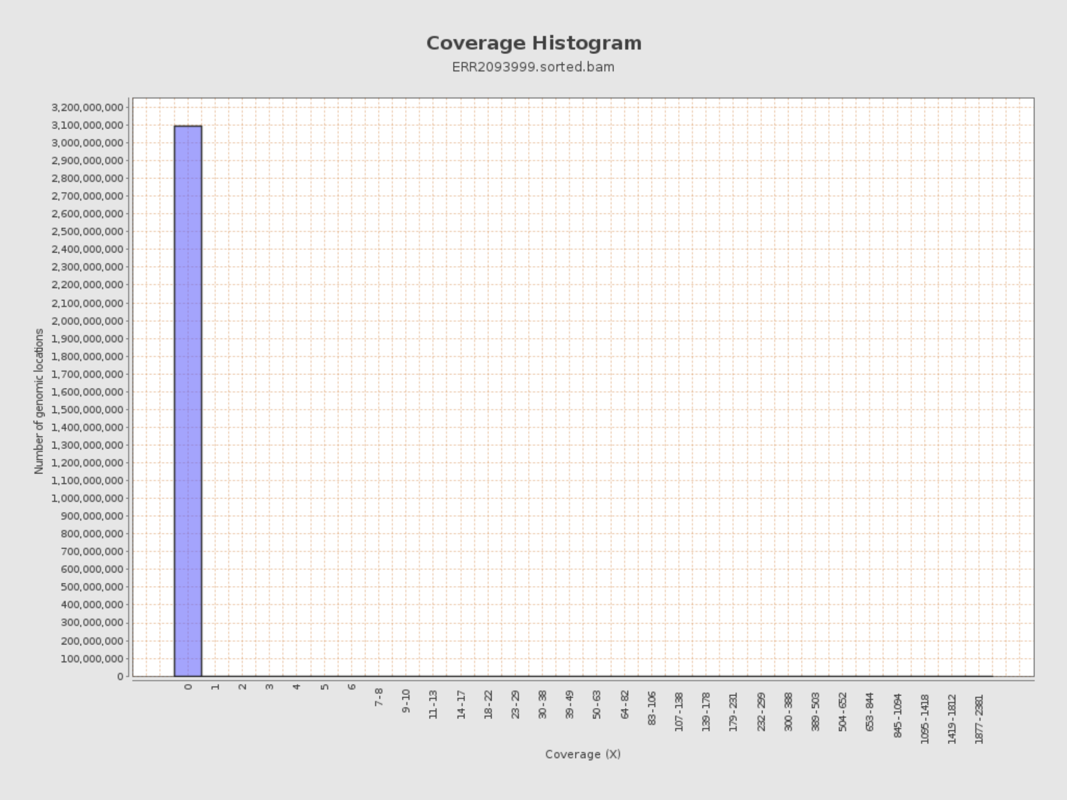
		bases	**coverage**	**deviation**
chr1	249250621	710799	0.0029	0.9444
chr2	243199373	2525062	0.0104	3.1013
chr3	198022430	876128	0.0044	1.5256
chr4	191154276	1304246	0.0068	2.2952
chr5	180915260	517073	0.0029	1.3969
chr6	171115067	1058295	0.0062	1.7129
chr7	159138663	1174622	0.0074	2.0194
chr8	146364022	568087	0.0039	1.3208
chr9	141213431	778033	0.0055	1.6611
chr10	135534747	971576	0.0072	2.1082
chr11	135006516	1220115	0.009	2.2173
chr12	133851895	1315801	0.0098	2.3368
chr13	115169878	1090793	0.0095	2.5359
chr14	107349540	172120	0.0016	0.5382
chr15	102531392	713190	0.007	1.6682
chr16	90354753	268743	0.003	0.789
chr17	81195210	1042534	0.0128	3.0696
chr18	78077248	248472	0.0032	0.9253
chr19	59128983	92223	0.0016	0.4157
chr20	63025520	347501	0.0055	1.7771
chr21	48129895	96949	0.002	0.3531
chr22	51304566	144030	0.0028	0.7876
chrMT	16571	1105853	66.7342	280.6155
chrX	155270560	30700586	0.1977	9.9145

chrY	59373566	839882	0.0141	2.2075

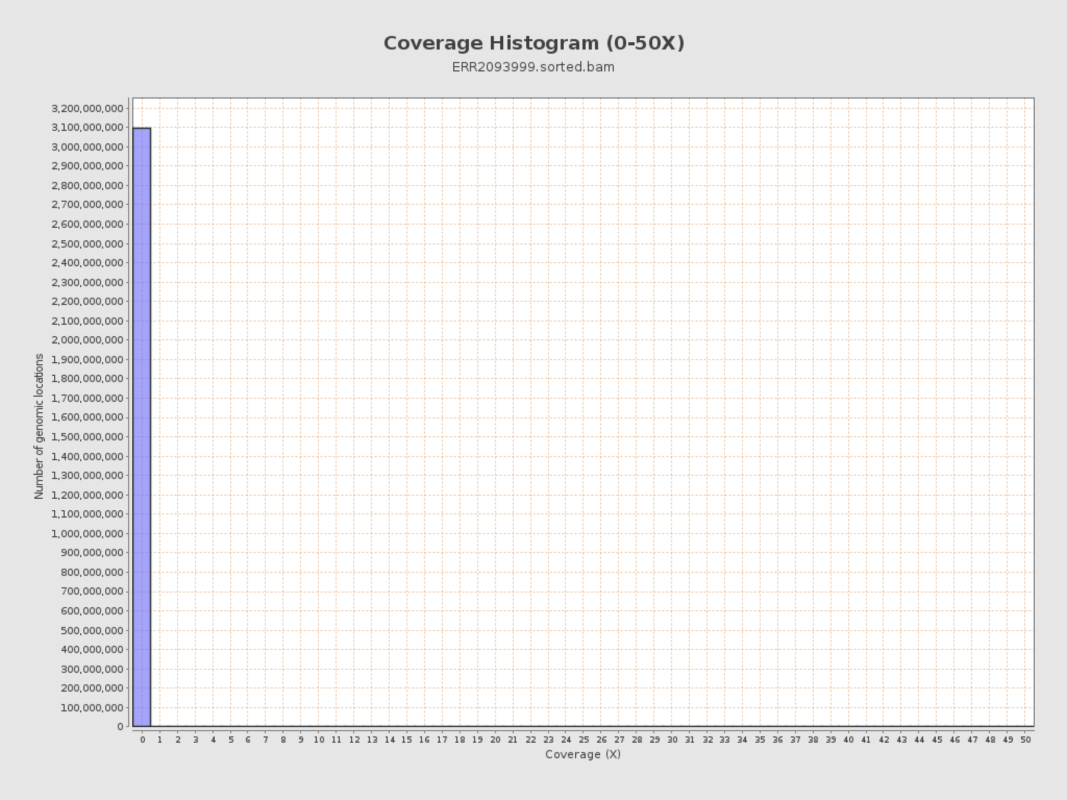
3. Results : Coverage across reference



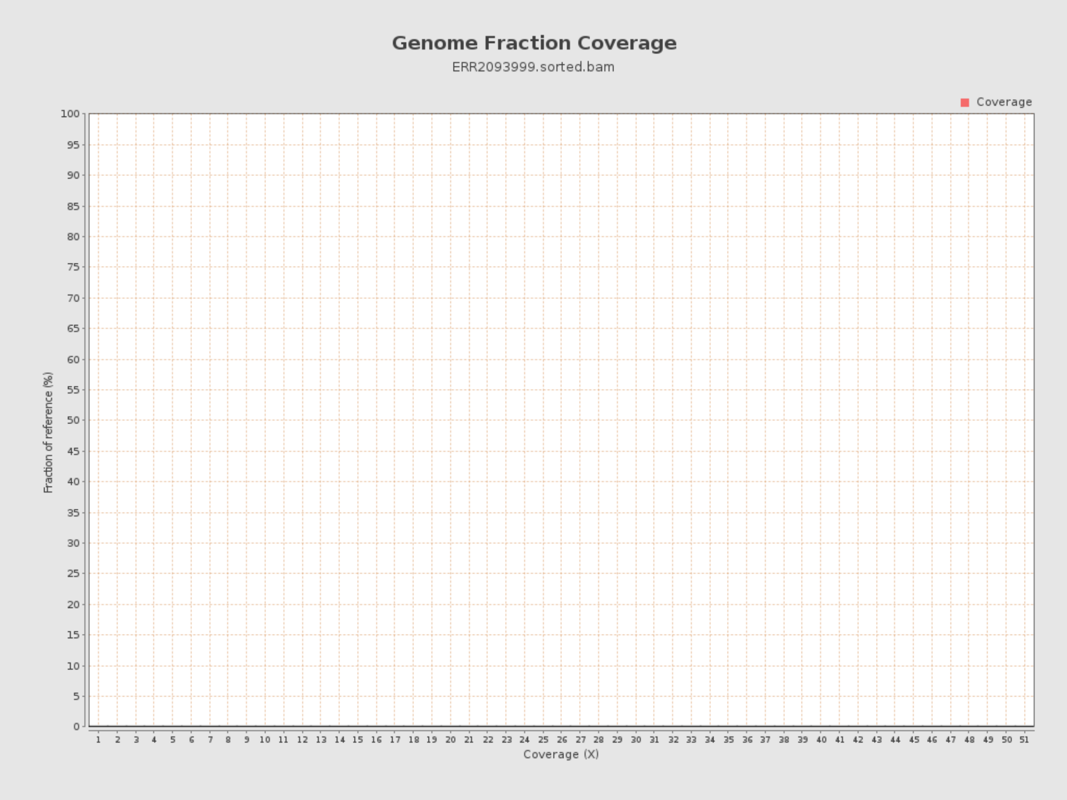
4. Results : Coverage Histogram



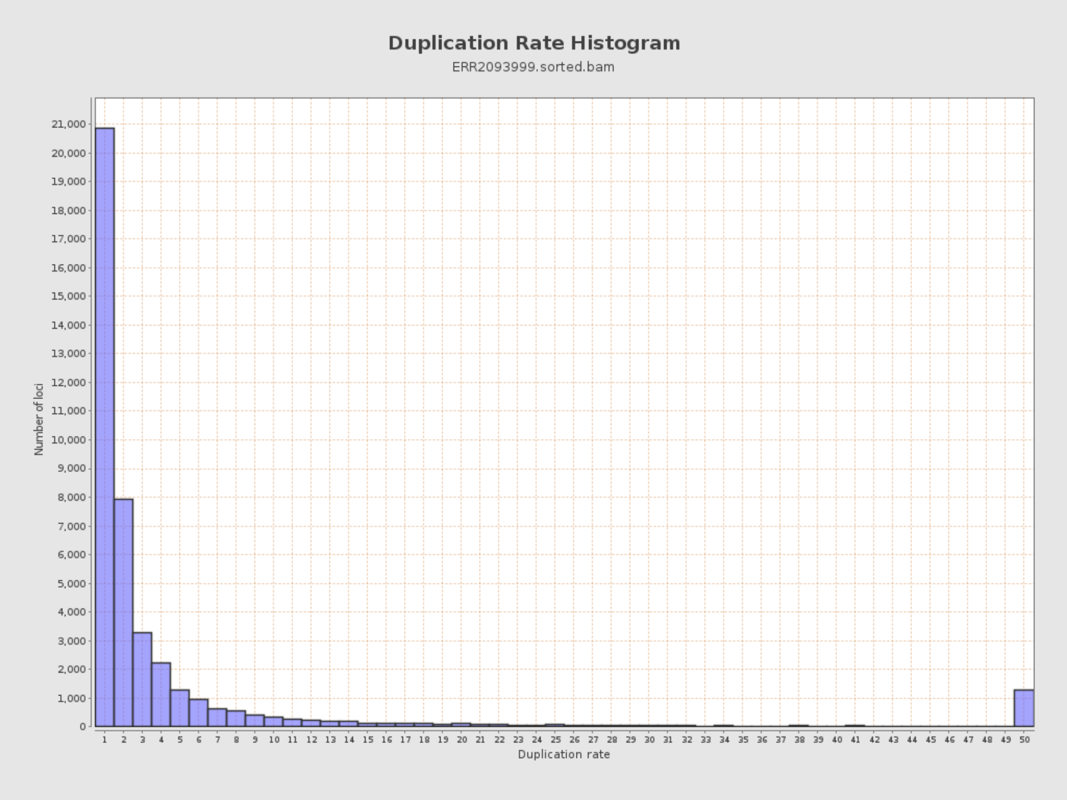
5. Results : Coverage Histogram (0-50X)



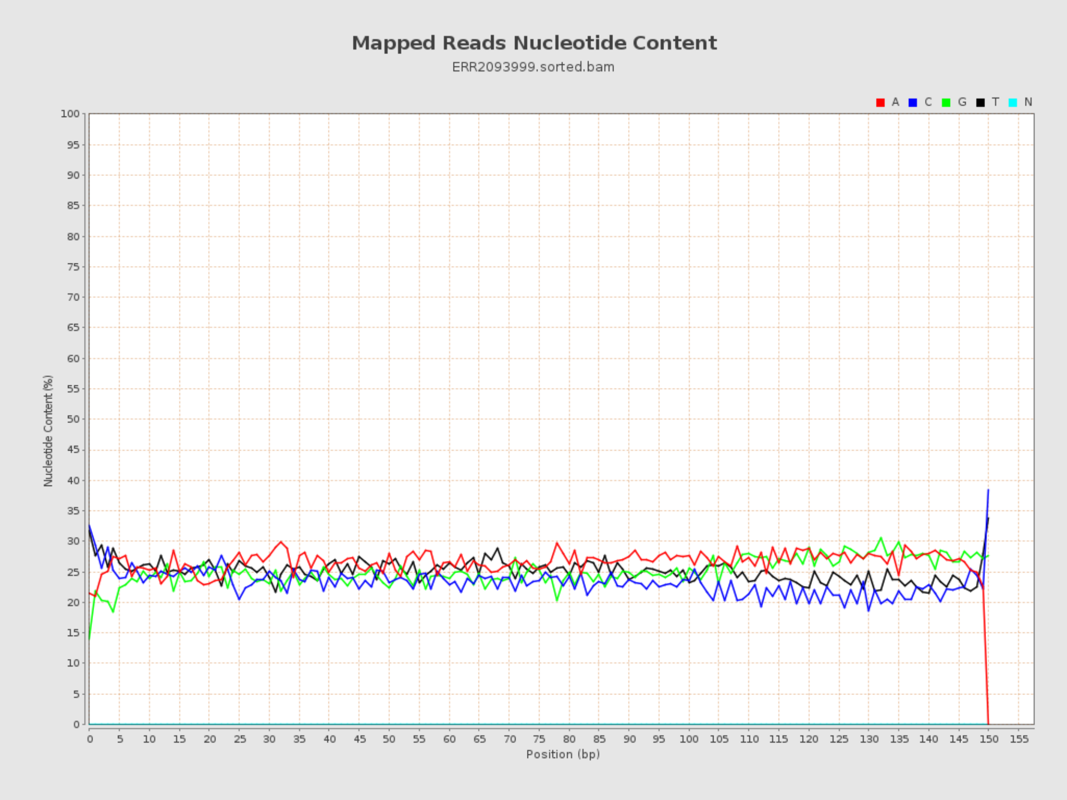
6. Results : Genome Fraction Coverage



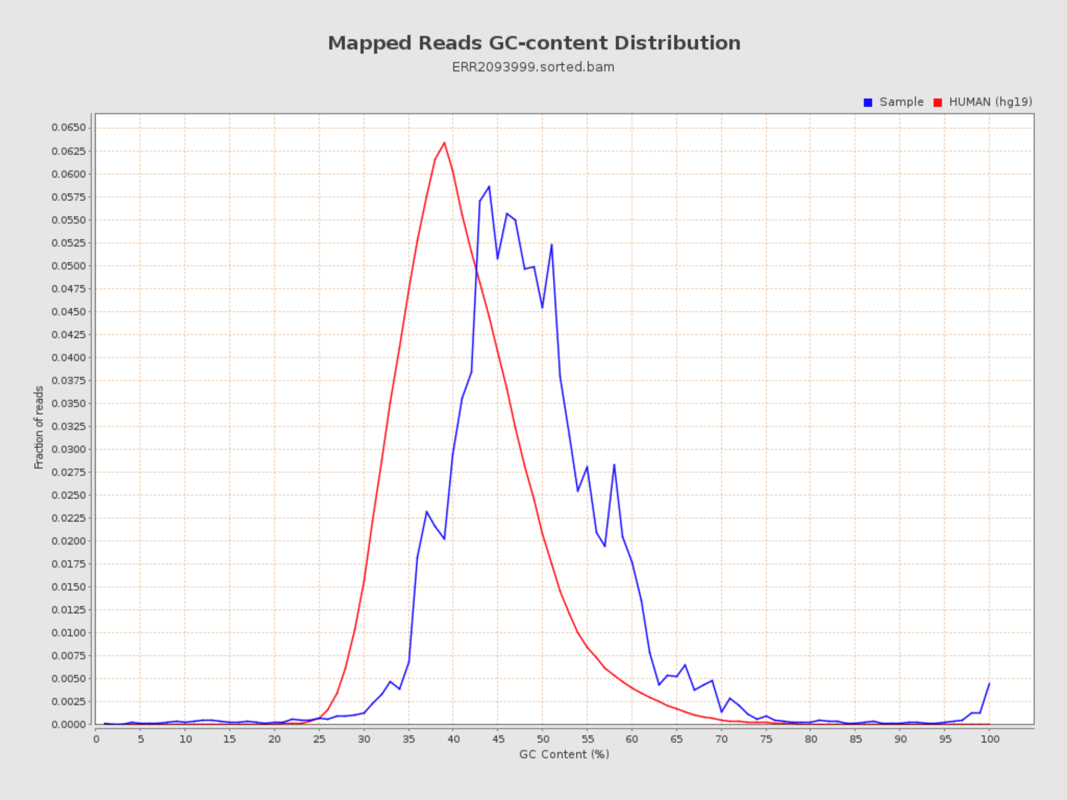
7. Results : Duplication Rate Histogram



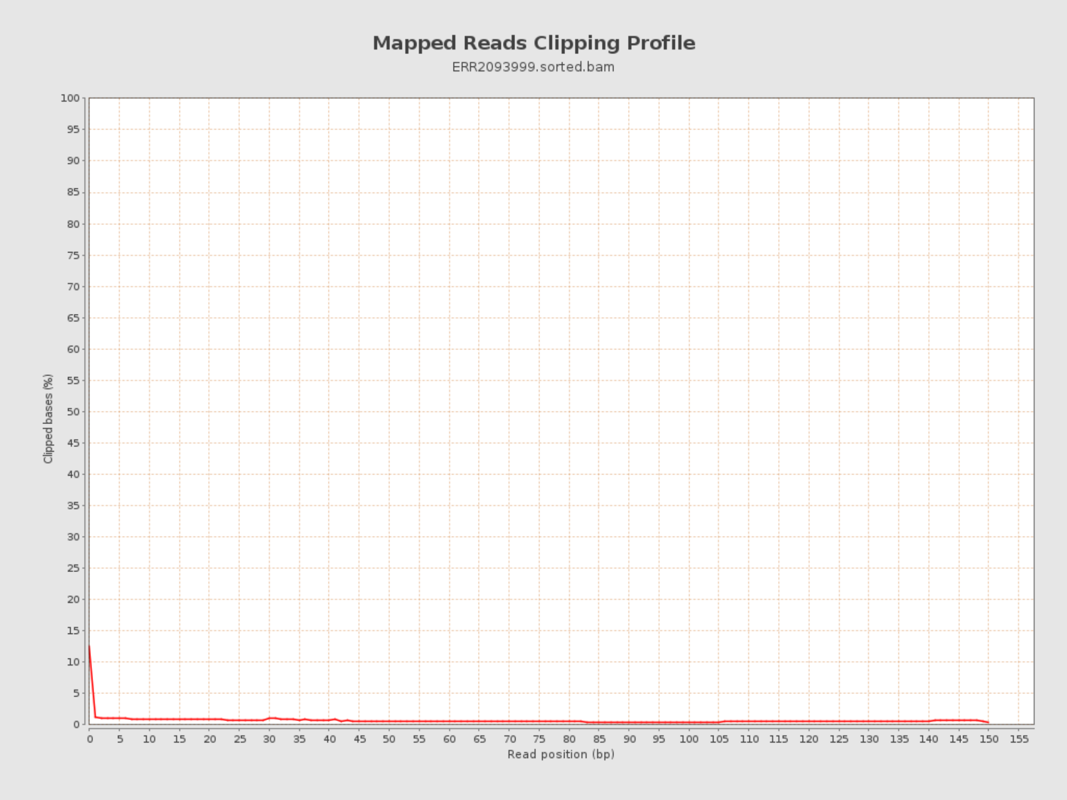
8. Results : Mapped Reads Nucleotide Content



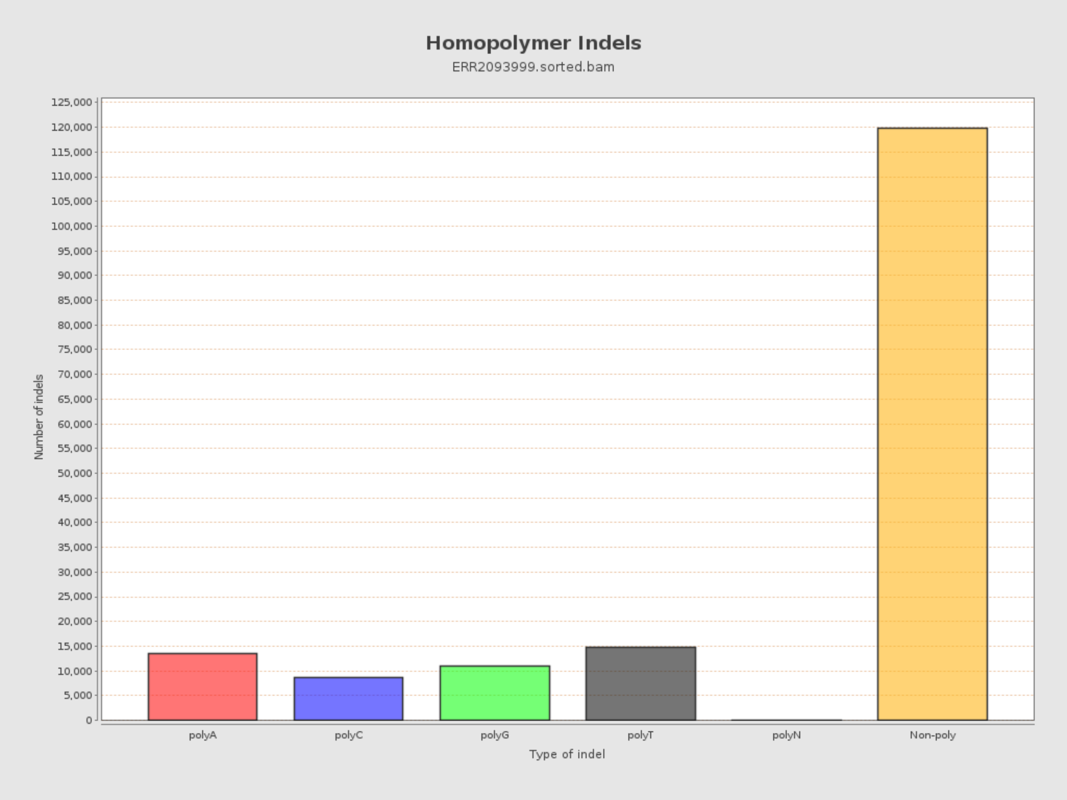
9. Results : Mapped Reads GC-content Distribution



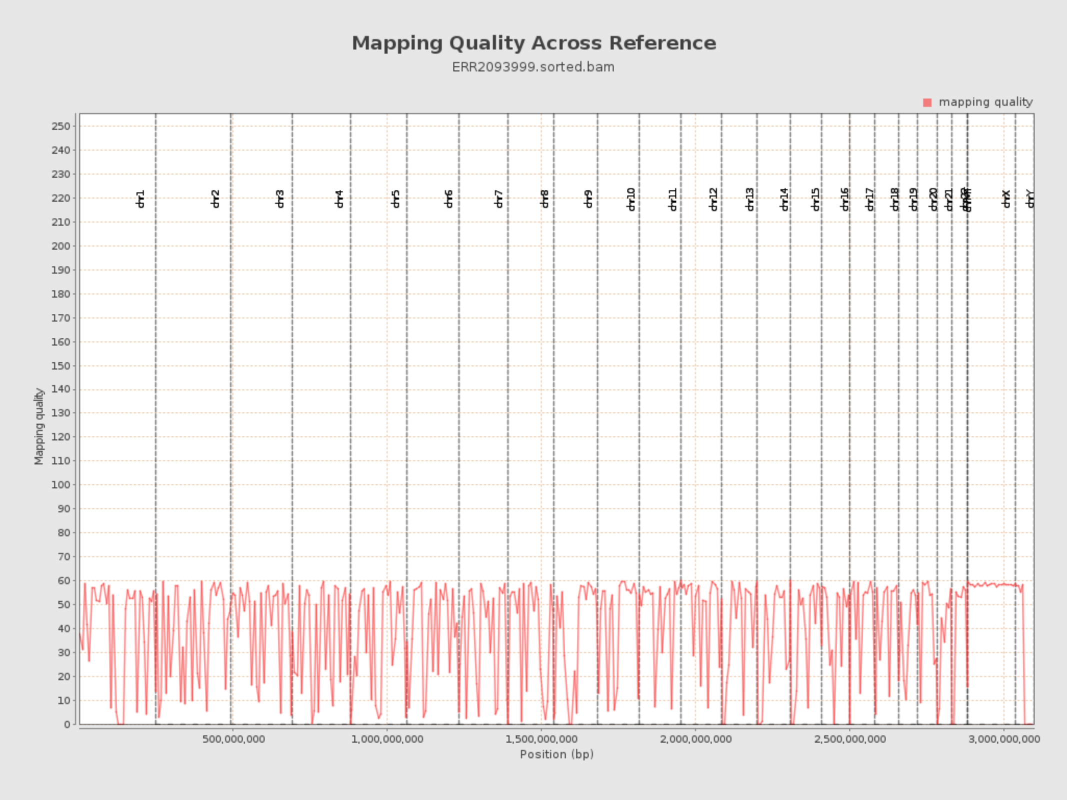
10. Results : Mapped Reads Clipping Profile



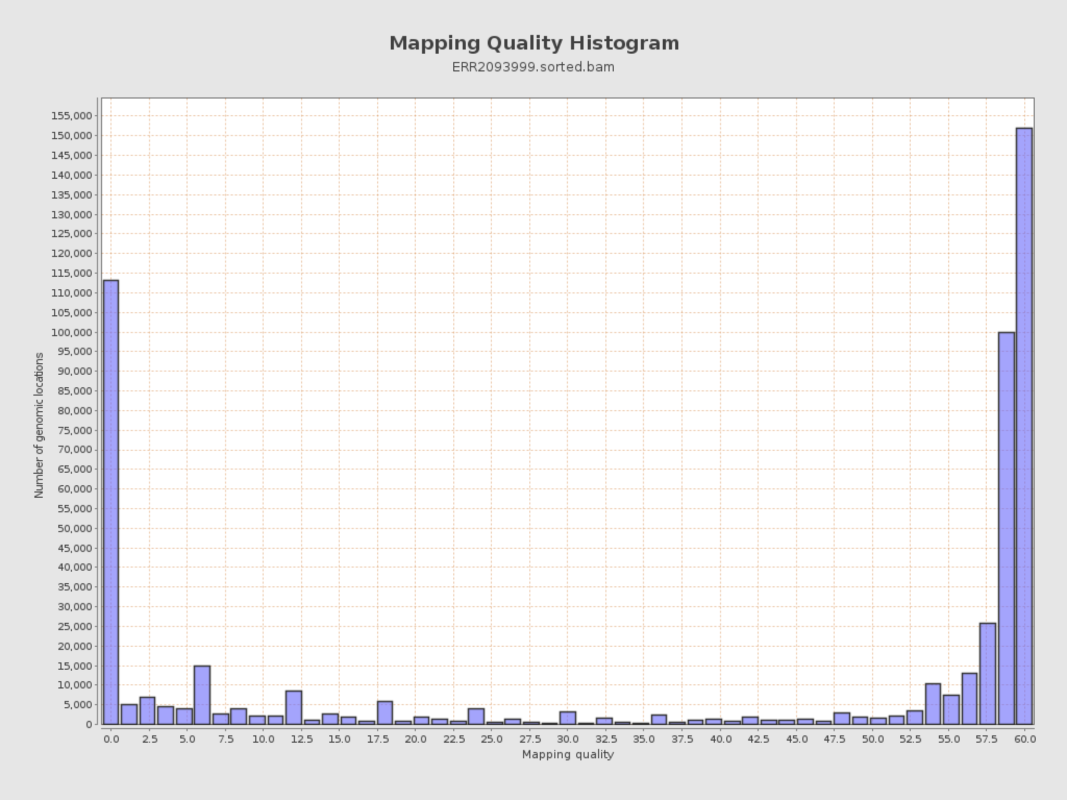
11. Results : Homopolymer Indels



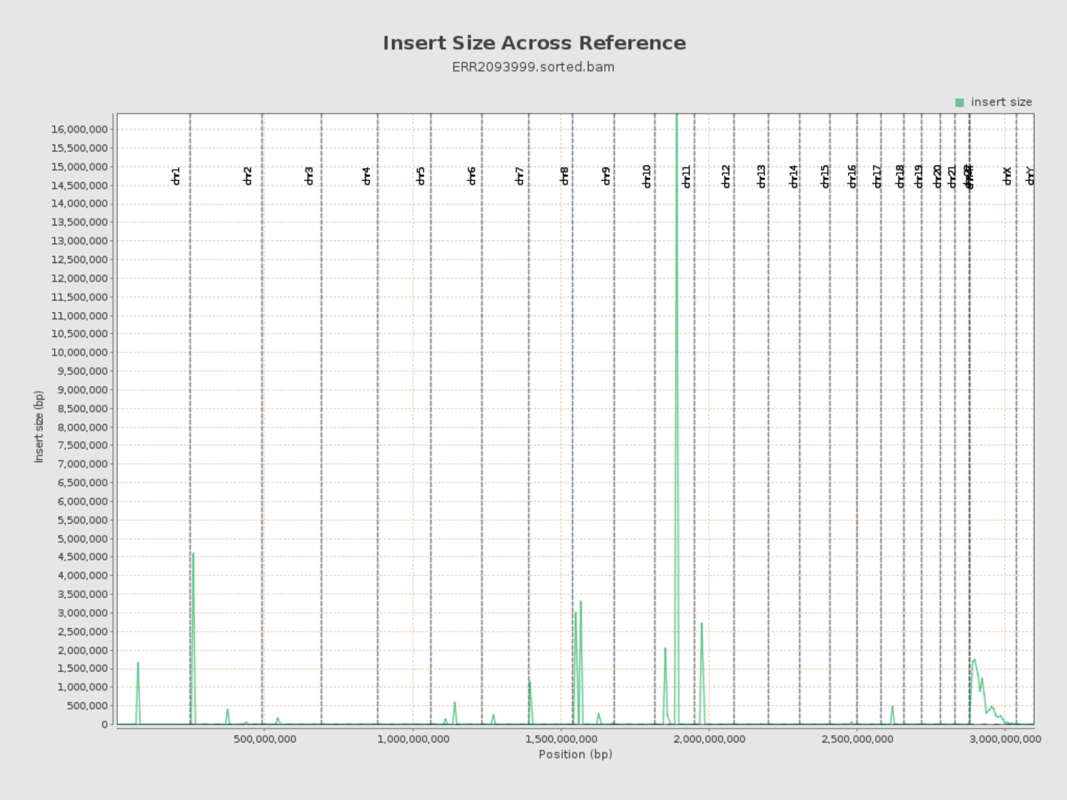
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram