Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:59:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714092.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_ERR9714092 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:59:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	561,278
Mapped reads	307,186 / 54.73%
Unmapped reads	254,092 / 45.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,551 / 1.52%
Read min/max/mean length	30 / 151 / 113.38
Duplicated reads (estimated)	261,196 / 46.54%
Duplication rate	43.69%
Clipped reads	279,402 / 49.78%

2.2. ACGT Content

Number/percentage of A's	10,050,172 / 26.23%
Number/percentage of C's	7,807,466 / 20.37%
Number/percentage of T's	9,553,100 / 24.93%
Number/percentage of G's	10,908,978 / 28.47%
Number/percentage of N's	321 / 0%
GC Percentage	48.84%

2.3. Coverage

Mean	0.0127

Standard Deviation	4.2291

2.4. Mapping Quality

Mean Mapping Quality	50.83

2.5. Mismatches and indels

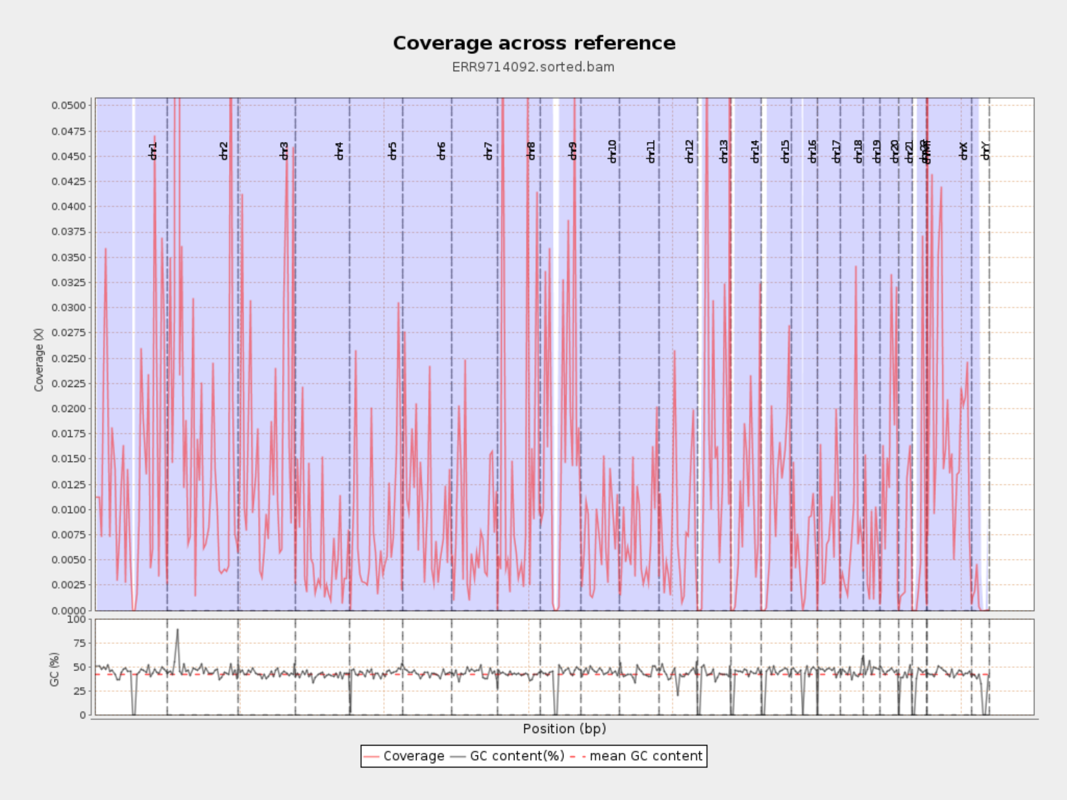
General error rate	4.68%
Mismatches	1,683,384
Insertions	41,264
Mapped reads with at least one insertion	12.68%
Deletions	144,551
Mapped reads with at least one deletion	43.52%
Homopolymer indels	29.54%

2.6. Chromosome stats

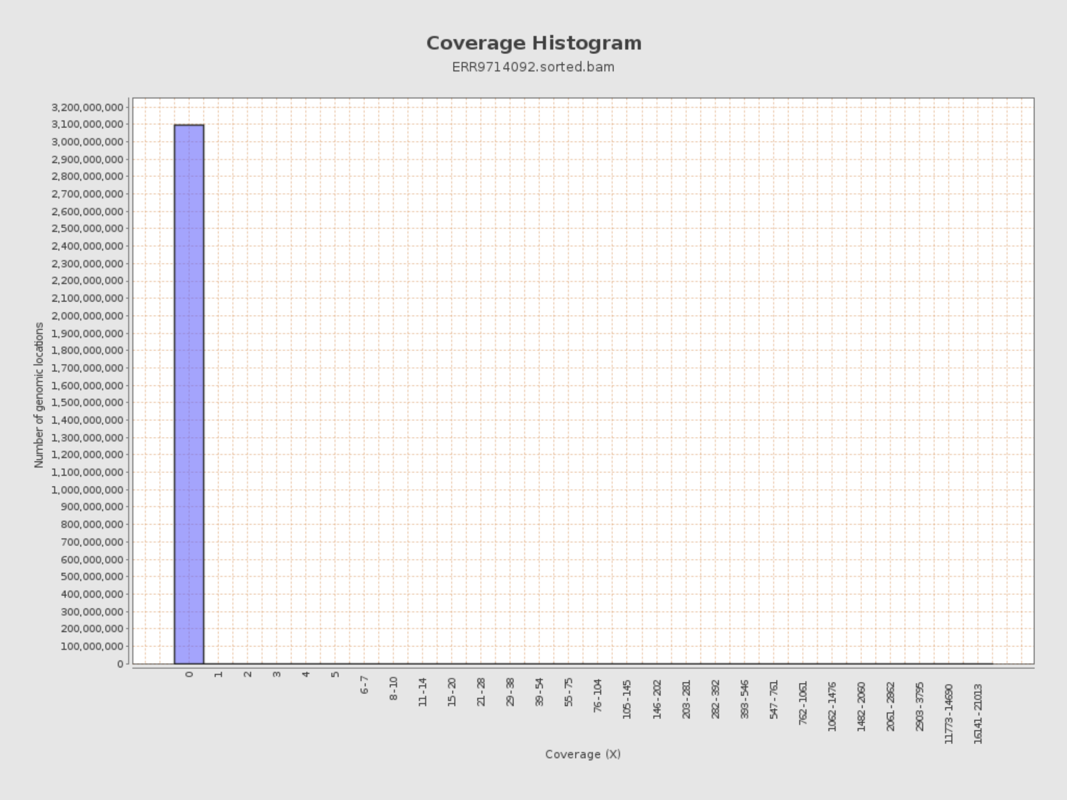
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3557946	0.0143	2.1363
chr2	243199373	7340721	0.0302	13.5122
chr3	198022430	3286908	0.0166	2.7307
chr4	191154276	1138330	0.006	1.2182
chr5	180915260	1596118	0.0088	1.9372
chr6	171115067	1811168	0.0106	1.5206
chr7	159138663	1298113	0.0082	1.4643

chr8	146364022	1977806	0.0135	3.3523
chr9	141213431	2523207	0.0179	2.5547
chr10	135534747	948939	0.007	0.9533
chr11	135006516	1074502	0.008	1.1275
chr12	133851895	1050641	0.0078	1.0983
chr13	115169878	2025484	0.0176	2.9297
chr14	107349540	1122667	0.0105	2.2446
chr15	102531392	1209214	0.0118	1.3442
chr16	90354753	547784	0.0061	0.8519
chr17	81195210	687944	0.0085	1.5384
chr18	78077248	658705	0.0084	1.3736
chr19	59128983	363972	0.0062	0.9263
chr20	63025520	1048998	0.0166	2.2275
chr21	48129895	312842	0.0065	1.4005
chr22	51304566	357457	0.007	2.2074
chrMT	16571	273110	16.4812	119.4155
chrX	155270560	2972448	0.0191	1.892
chrY	59373566	61465	0.001	0.199

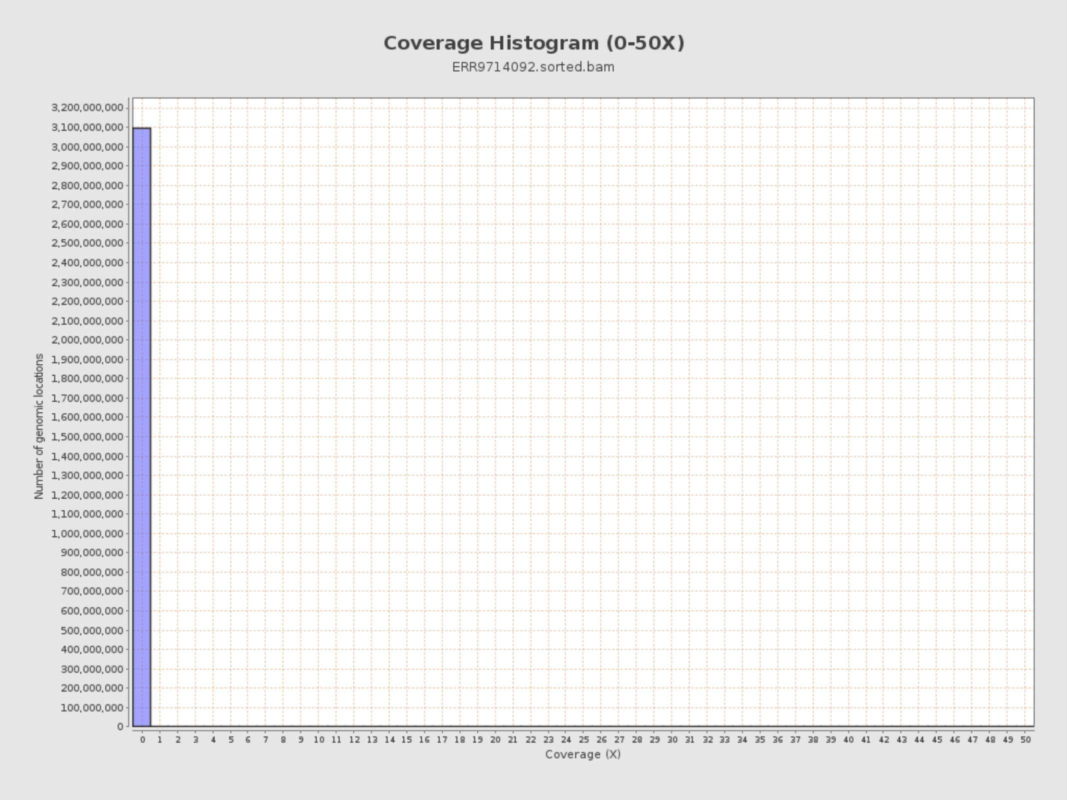
3. Results : Coverage across reference



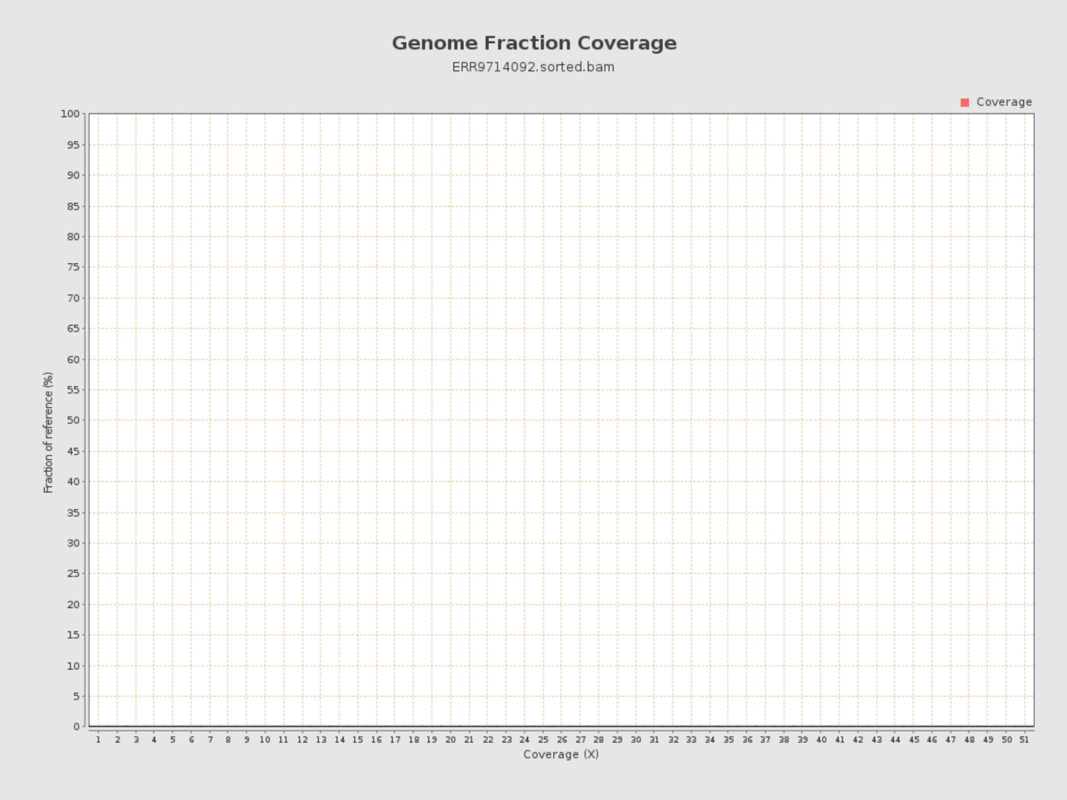
4. Results : Coverage Histogram



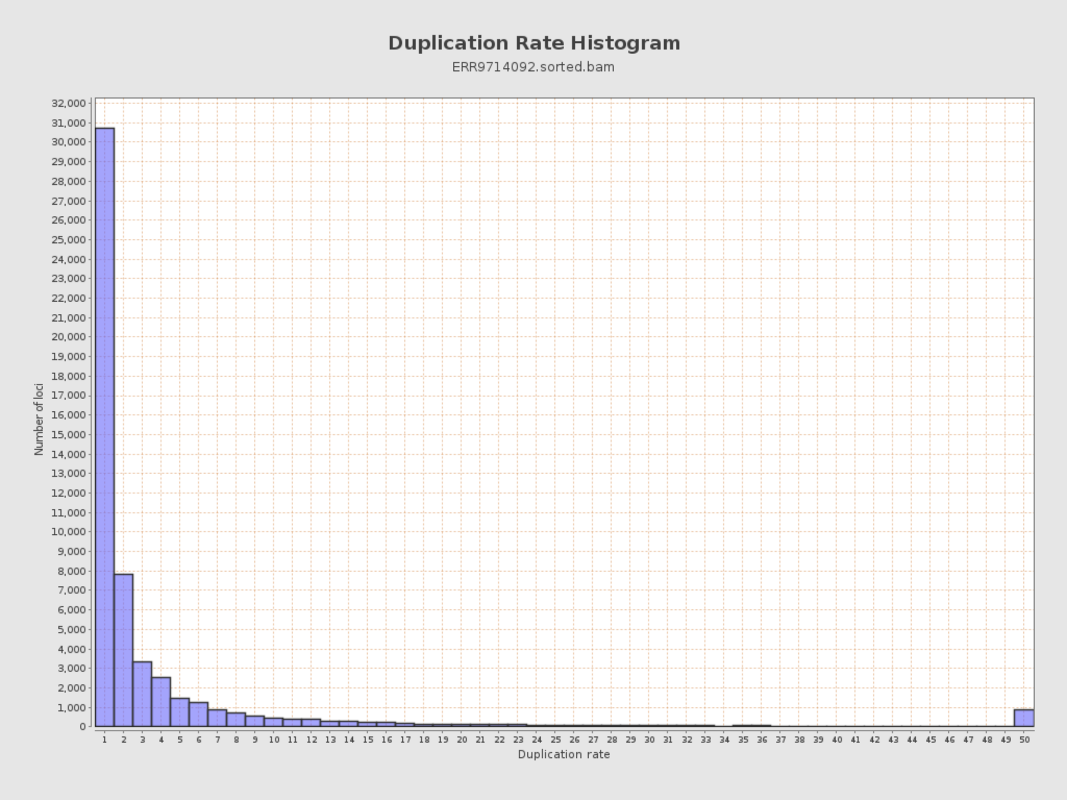
5. Results : Coverage Histogram (0-50X)



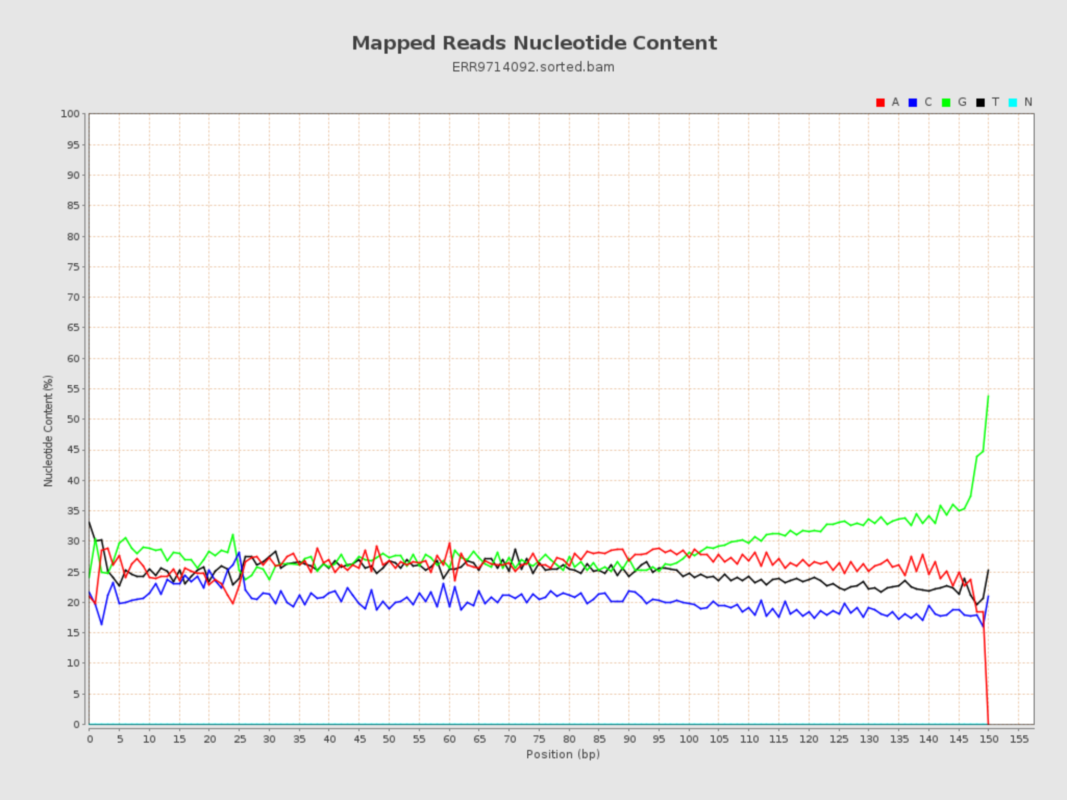
6. Results : Genome Fraction Coverage



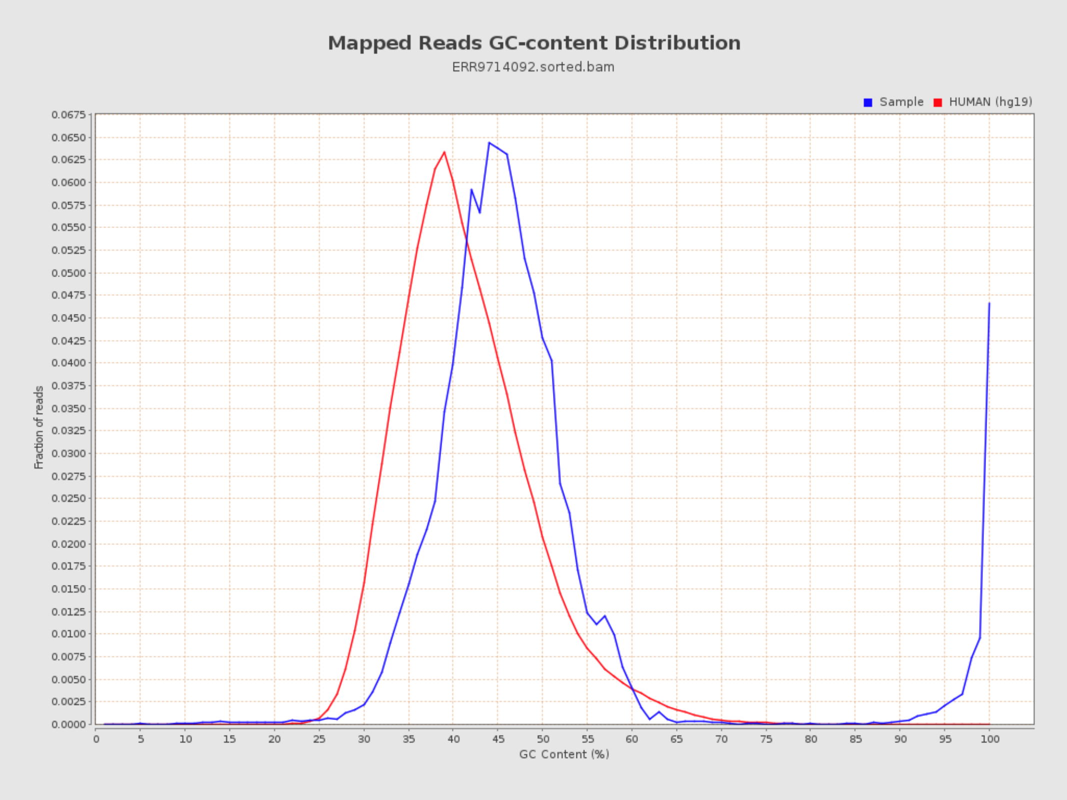
7. Results : Duplication Rate Histogram



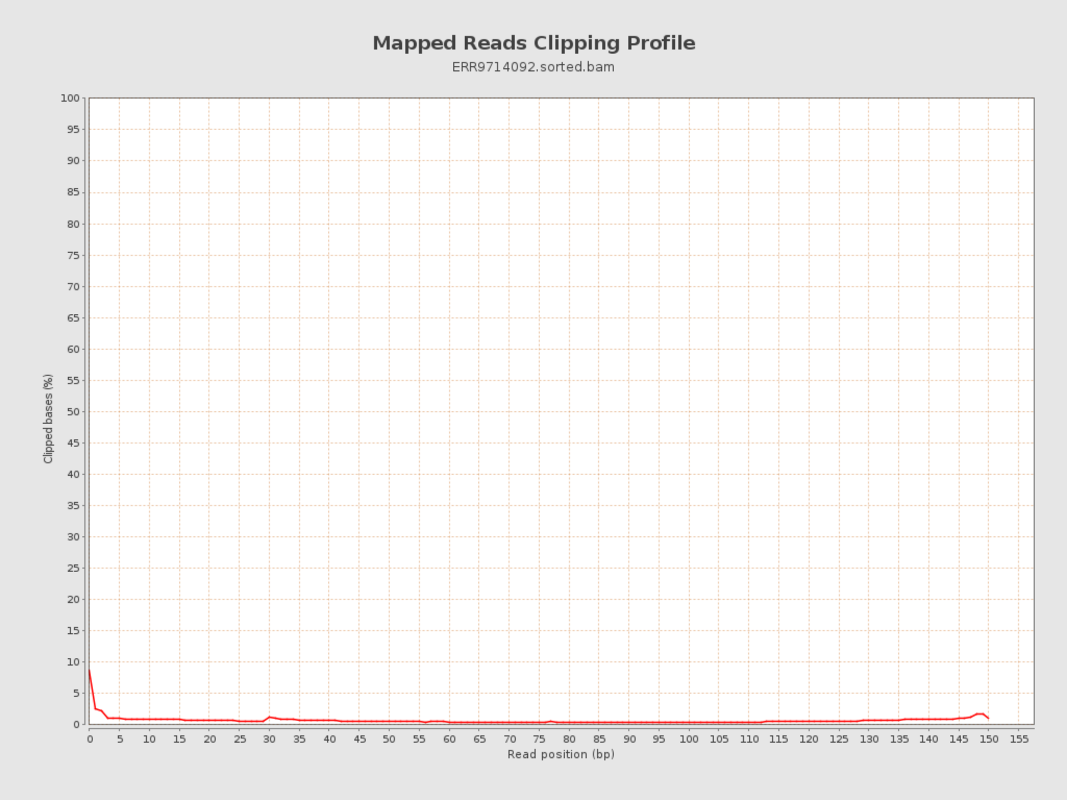
8. Results : Mapped Reads Nucleotide Content



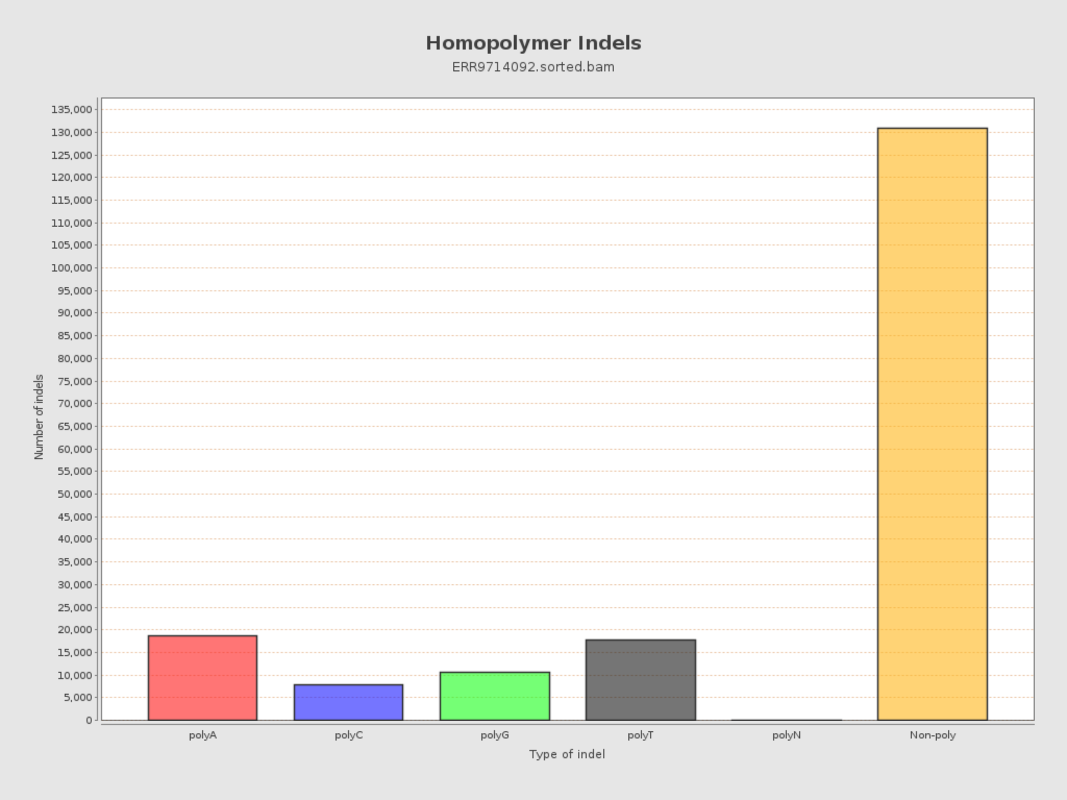
9. Results : Mapped Reads GC-content Distribution



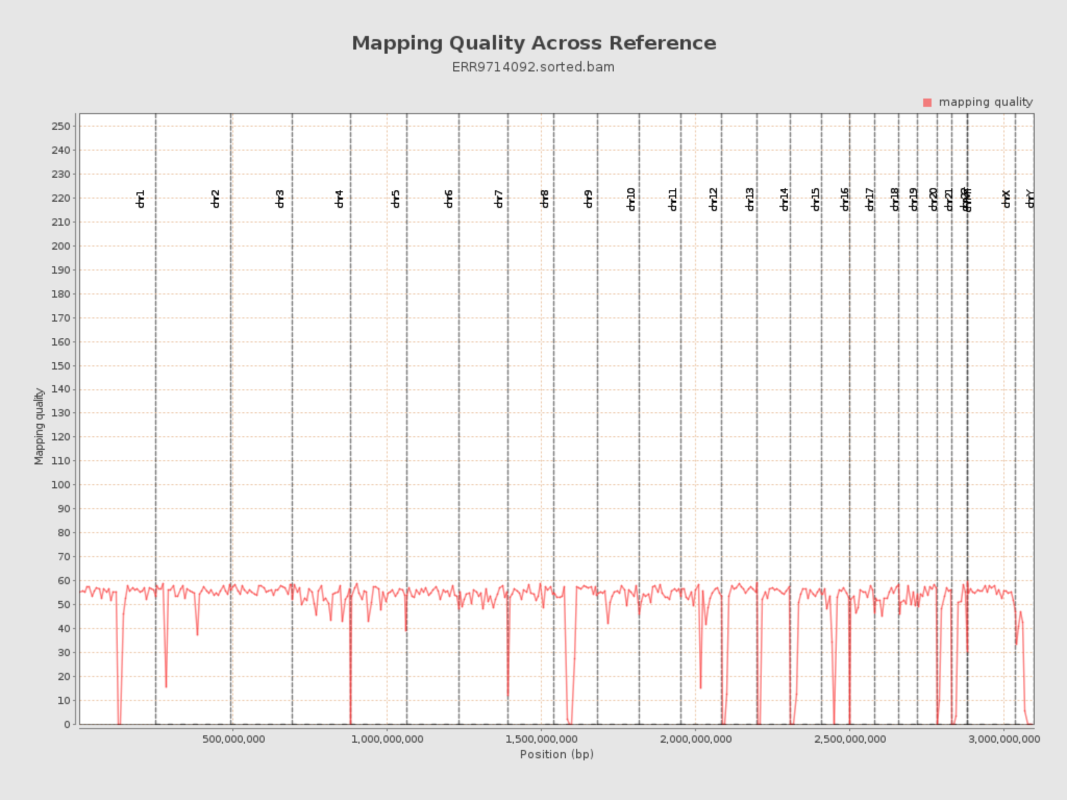
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram