Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:26:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714102.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_ERR9714102 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:26:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	665,886
Mapped reads	320,737 / 48.17%
Unmapped reads	345,149 / 51.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,842 / 1.78%
Read min/max/mean length	30 / 151 / 102.37
Duplicated reads (estimated)	285,982 / 42.95%
Duplication rate	41.43%
Clipped reads	287,362 / 43.15%

2.2. ACGT Content

Number/percentage of A's	10,225,790 / 25.63%
Number/percentage of C's	7,687,199 / 19.27%
Number/percentage of T's	9,656,256 / 24.21%
Number/percentage of G's	12,320,368 / 30.89%
Number/percentage of N's	484 / 0%
GC Percentage	50.16%

2.3. Coverage

Mean	0.0132

Standard Deviation	6.1512

2.4. Mapping Quality

Mean Mapping Quality	49.01

2.5. Mismatches and indels

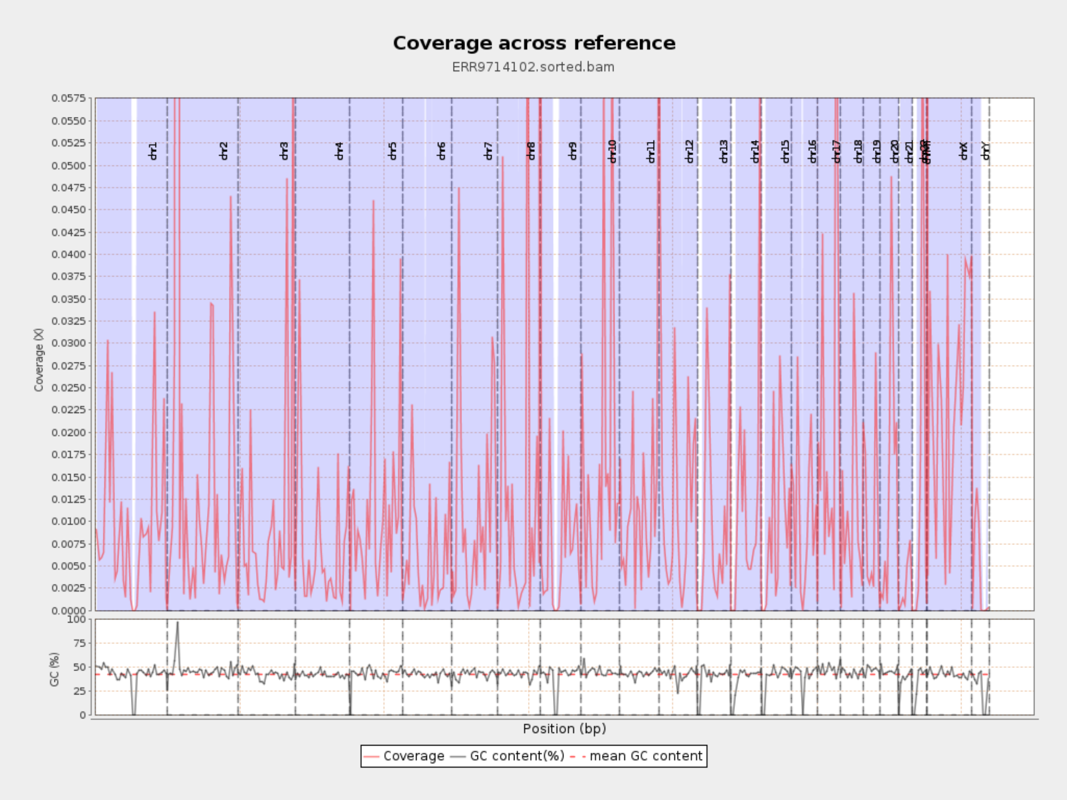
General error rate	4.56%
Mismatches	1,650,542
Insertions	48,315
Mapped reads with at least one insertion	14.24%
Deletions	136,324
Mapped reads with at least one deletion	39.15%
Homopolymer indels	32.2%

2.6. Chromosome stats

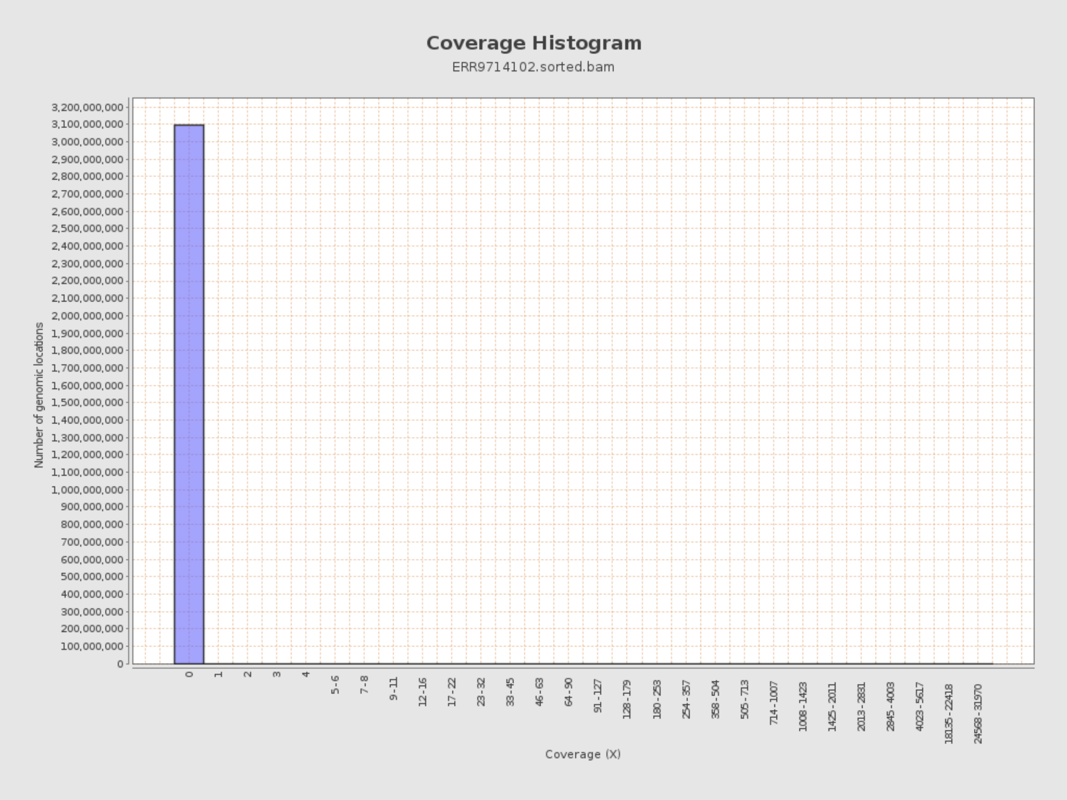
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2432590	0.0098	1.6851
chr2	243199373	7386638	0.0304	20.0547
chr3	198022430	2092037	0.0106	3.4117
chr4	191154276	1372057	0.0072	1.5851
chr5	180915260	2159655	0.0119	2.3116
chr6	171115067	1054295	0.0062	1.1123
chr7	159138663	1783773	0.0112	2.4303

chr8	146364022	1857984	0.0127	3.0644
chr9	141213431	1312415	0.0093	2.6606
chr10	135534747	2231618	0.0165	3.3165
chr11	135006516	1409176	0.0104	1.356
chr12	133851895	1654071	0.0124	2.0809
chr13	115169878	1128577	0.0098	1.9006
chr14	107349540	1371336	0.0128	2.766
chr15	102531392	999977	0.0098	1.7121
chr16	90354753	958208	0.0106	1.5739
chr17	81195210	1903993	0.0234	6.1859
chr18	78077248	875529	0.0112	1.9087
chr19	59128983	553090	0.0094	1.2862
chr20	63025520	904394	0.0143	2.5052
chr21	48129895	142120	0.003	0.4721
chr22	51304566	741917	0.0145	4.056
chrMT	16571	569096	34.3429	275.7632
chrX	155270560	3599410	0.0232	2.7356
chrY	59373566	264506	0.0045	1.095

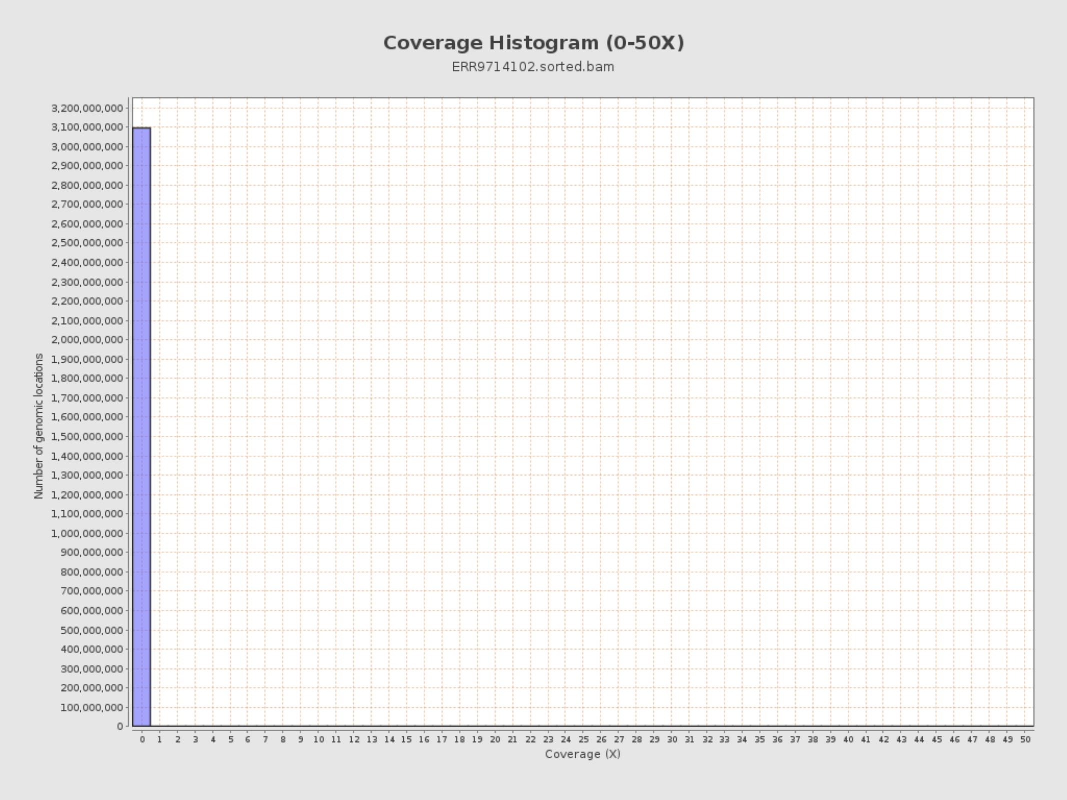
3. Results : Coverage across reference



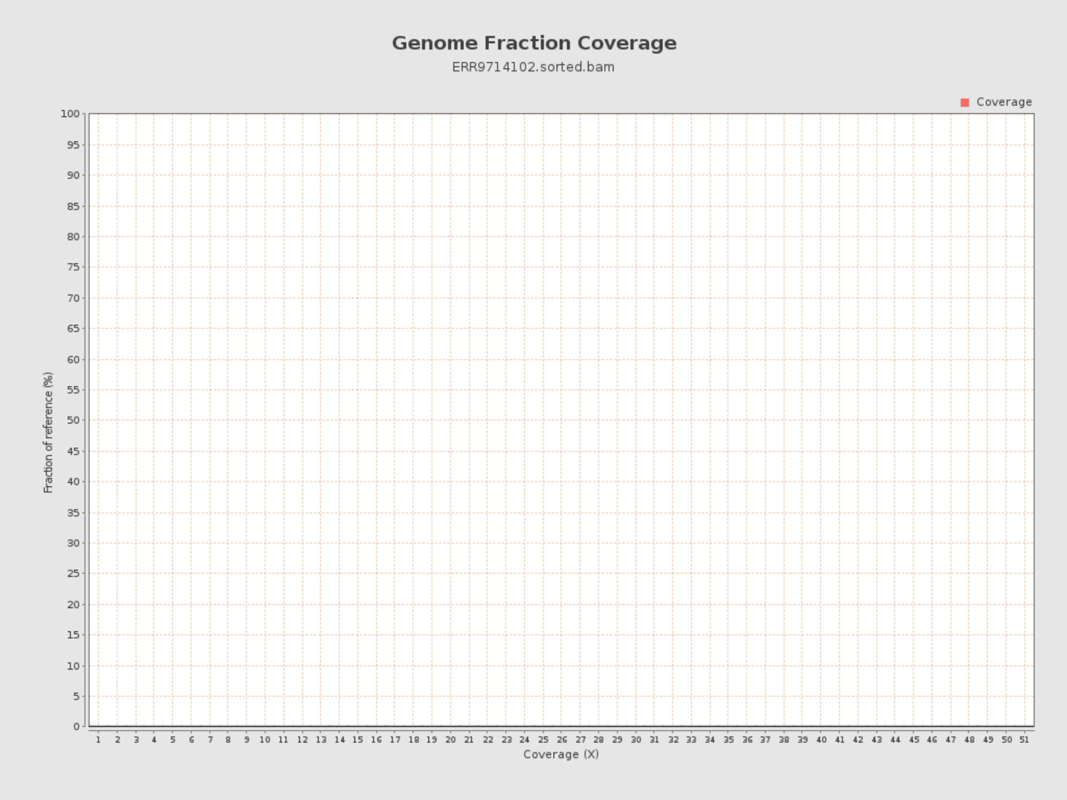
4. Results : Coverage Histogram



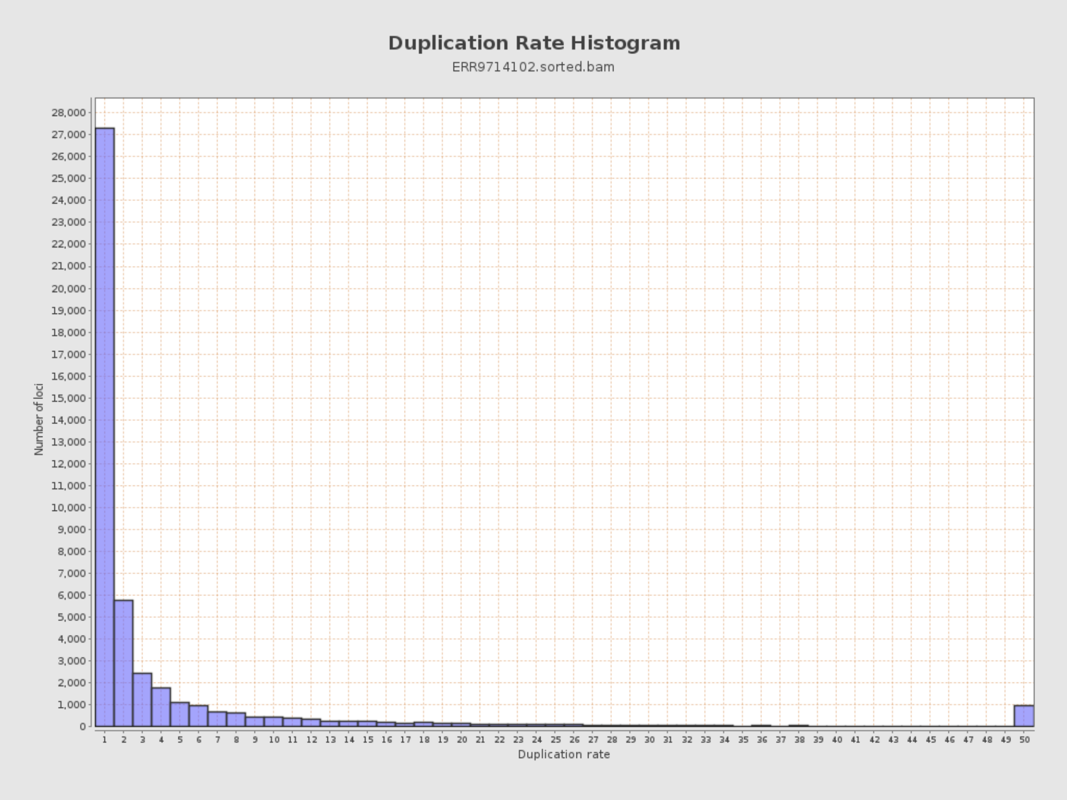
5. Results : Coverage Histogram (0-50X)



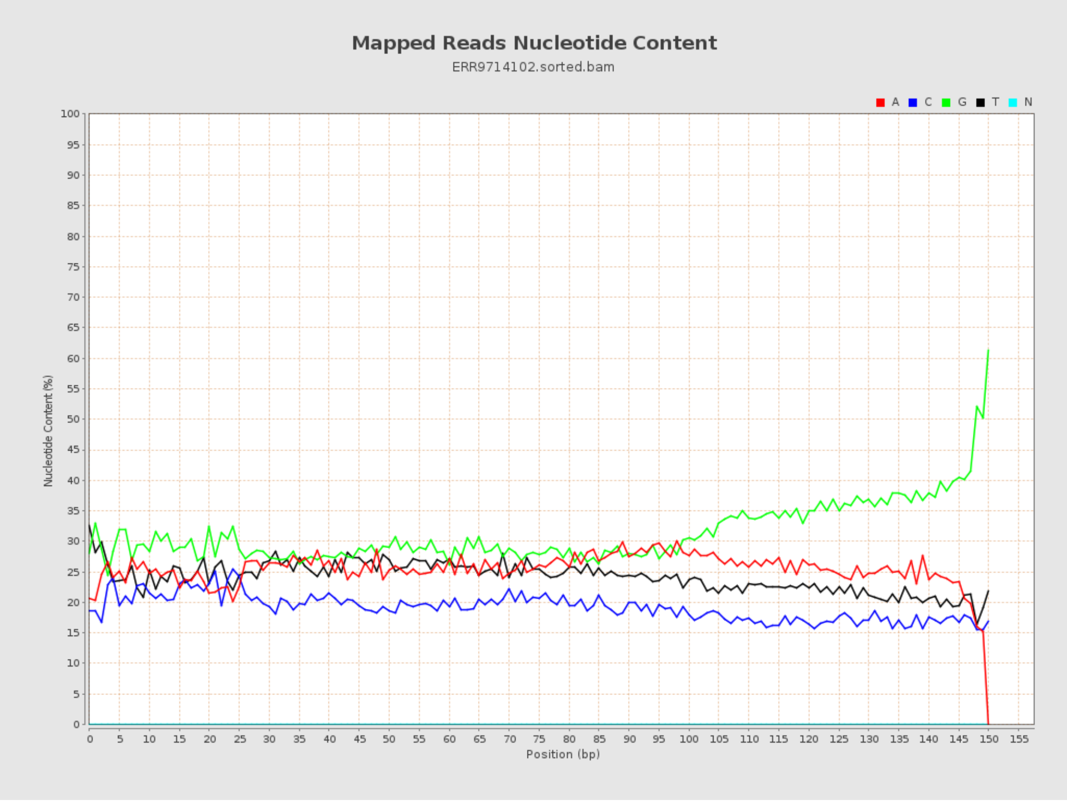
6. Results : Genome Fraction Coverage



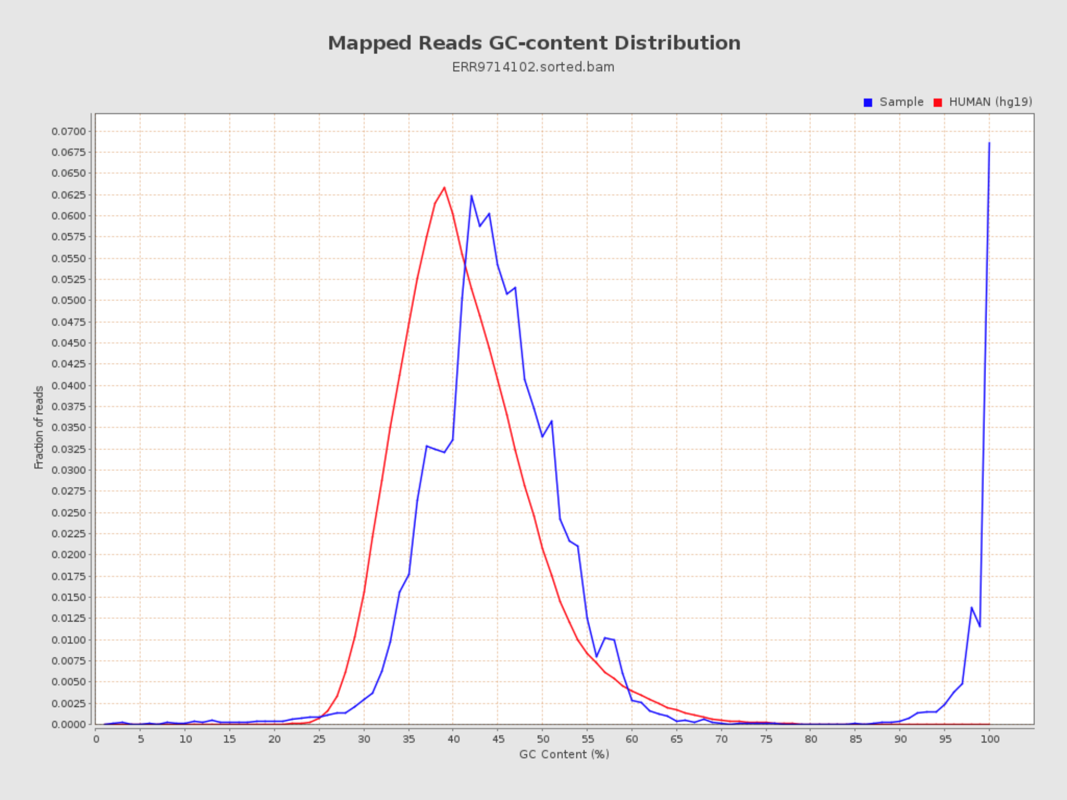
7. Results : Duplication Rate Histogram



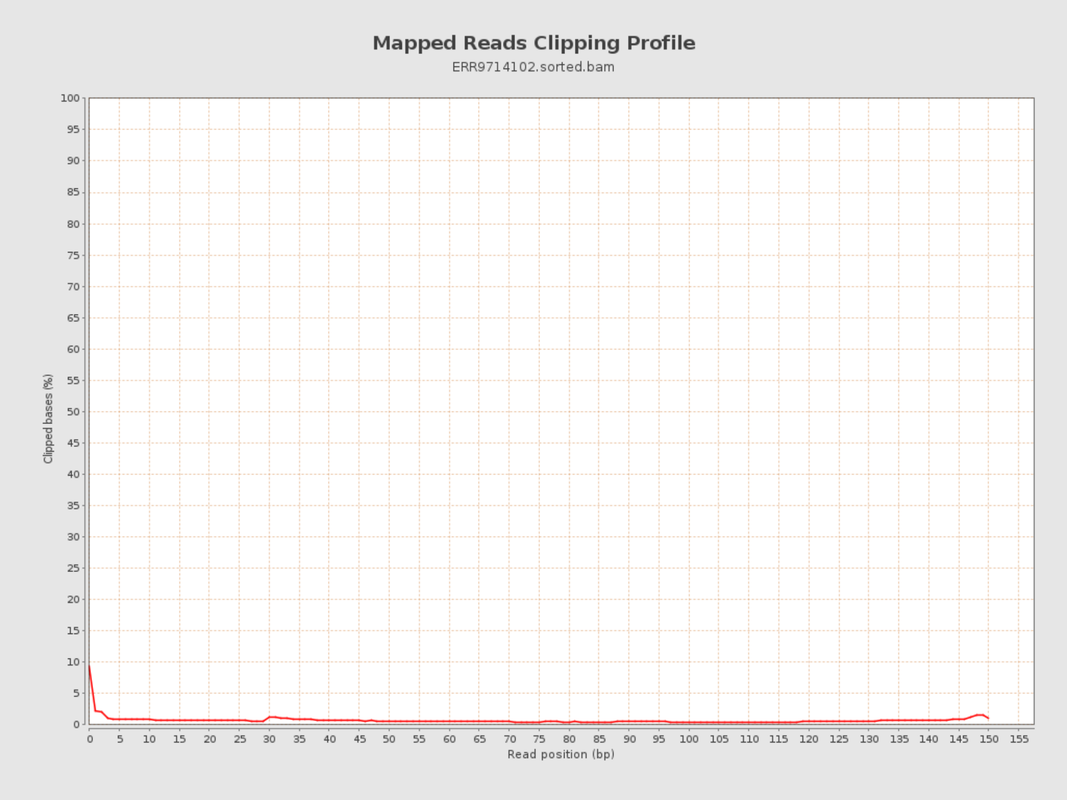
8. Results : Mapped Reads Nucleotide Content



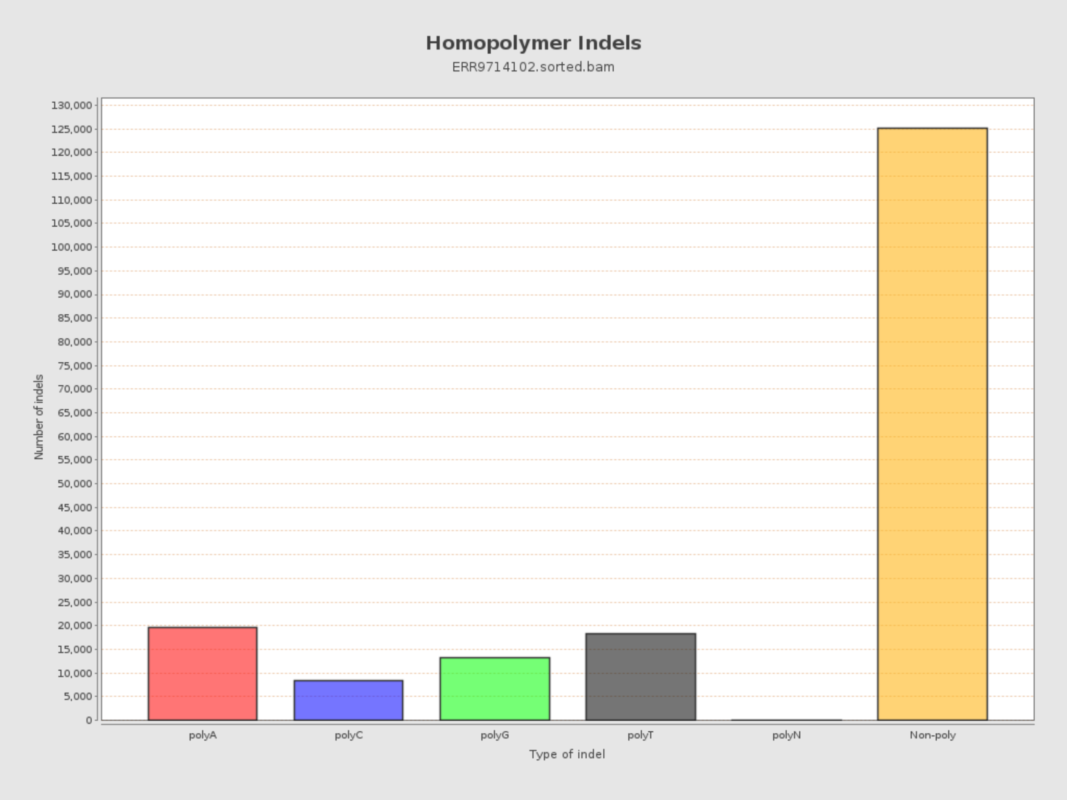
9. Results : Mapped Reads GC-content Distribution



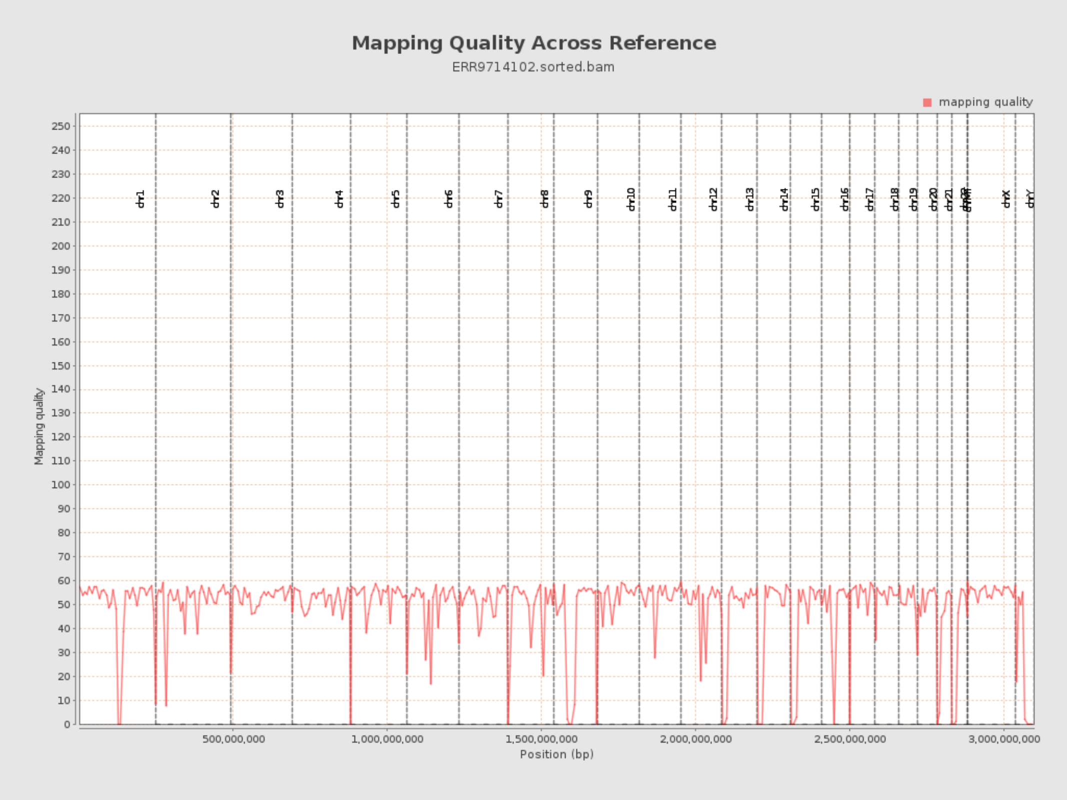
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram