Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714262.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_ERR9714262 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	227,728
Mapped reads	218,506 / 95.95%
Unmapped reads	9,222 / 4.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,741 / 2.96%
Read min/max/mean length	30 / 151 / 146.63
Duplicated reads (estimated)	174,312 / 76.54%
Duplication rate	40.96%
Clipped reads	207,122 / 90.95%

2.2. ACGT Content

Number/percentage of A's	8,123,674 / 29.34%
Number/percentage of C's	5,678,640 / 20.51%
Number/percentage of T's	7,735,306 / 27.93%
Number/percentage of G's	6,154,055 / 22.22%
Number/percentage of N's	234 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0091

Standard Deviation	1.5608

2.4. Mapping Quality

Mean Mapping Quality	50.99

2.5. Mismatches and indels

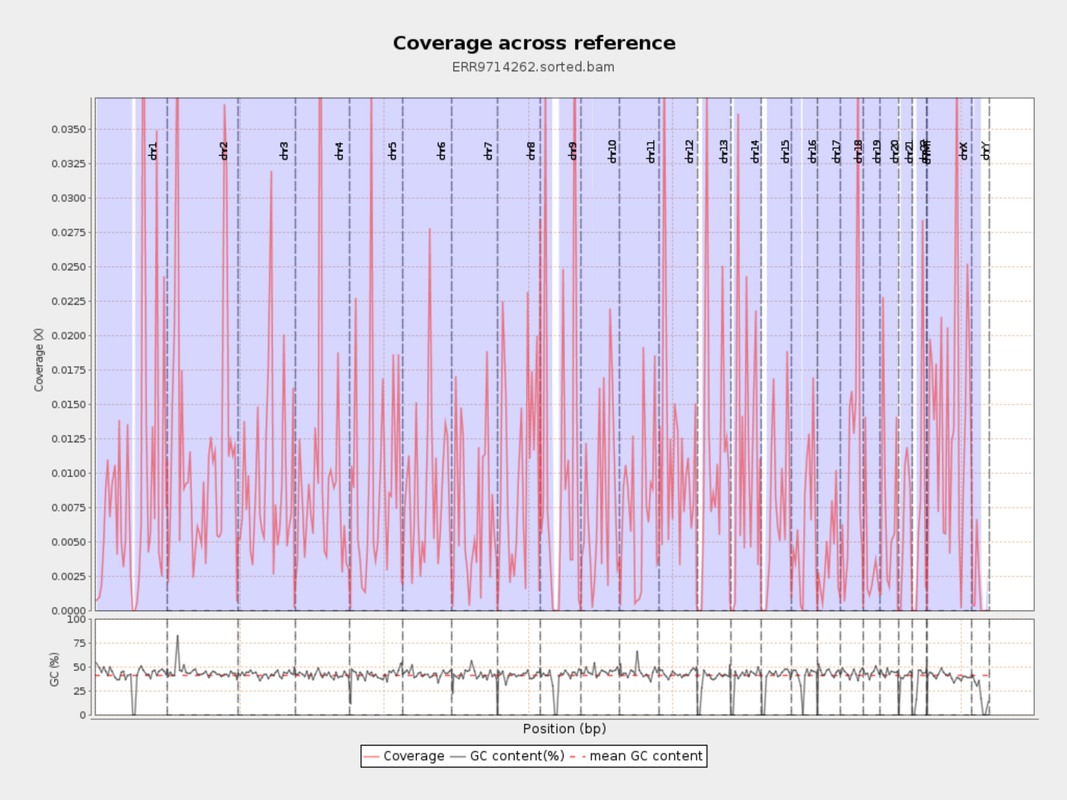
General error rate	4.12%
Mismatches	1,046,968
Insertions	30,725
Mapped reads with at least one insertion	13.71%
Deletions	89,720
Mapped reads with at least one deletion	39.2%
Homopolymer indels	27.54%

2.6. Chromosome stats

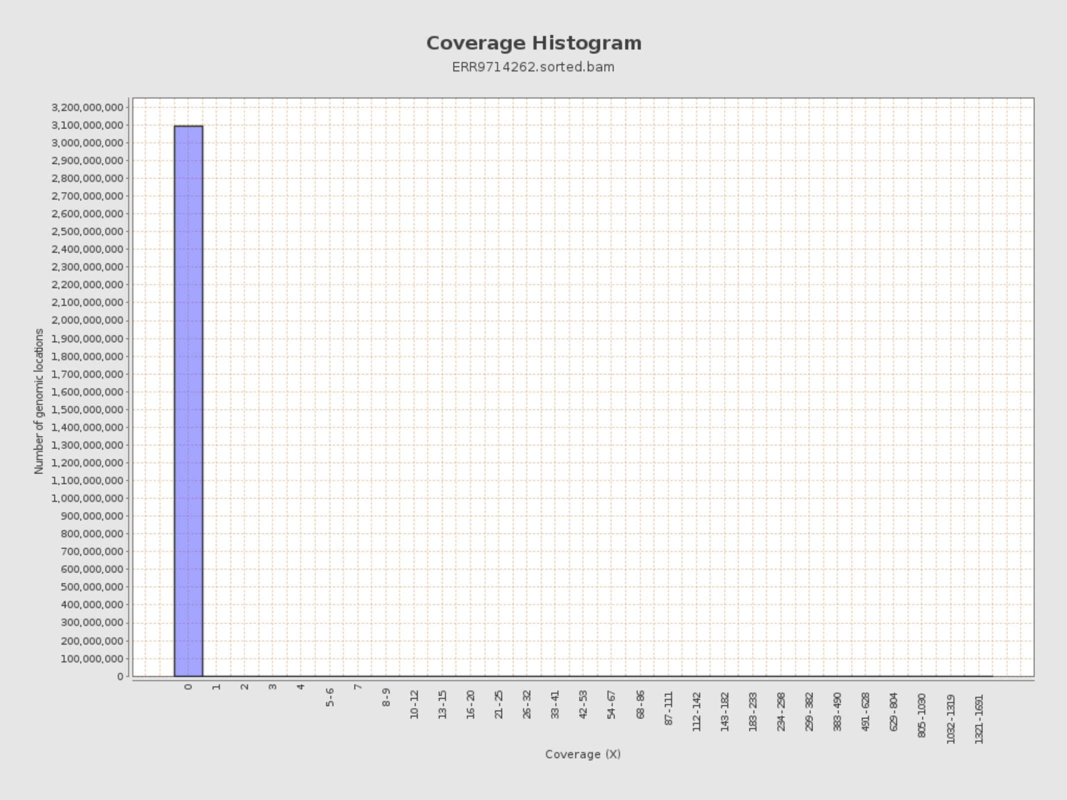
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2175481	0.0087	1.5751
chr2	243199373	2826987	0.0116	2.0826
chr3	198022430	1859967	0.0094	1.1752
chr4	191154276	1825066	0.0095	1.7673
chr5	180915260	1788276	0.0099	1.8046
chr6	171115067	1504514	0.0088	1.322
chr7	159138663	1126826	0.0071	1.0189

chr8	146364022	1425204	0.0097	1.4211
chr9	141213431	1489497	0.0105	1.9715
chr10	135534747	1069069	0.0079	1.1634
chr11	135006516	993330	0.0074	1.2258
chr12	133851895	1573121	0.0118	1.8478
chr13	115169878	1222973	0.0106	1.8231
chr14	107349540	1188198	0.0111	2.2503
chr15	102531392	768921	0.0075	1.0261
chr16	90354753	563136	0.0062	0.9406
chr17	81195210	308365	0.0038	0.669
chr18	78077248	952123	0.0122	2.5377
chr19	59128983	206794	0.0035	0.6164
chr20	63025520	473523	0.0075	1.2762
chr21	48129895	296195	0.0062	0.9685
chr22	51304566	344832	0.0067	1.6207
chrMT	16571	0	0	0
chrX	155270560	2164730	0.0139	1.3698
chrY	59373566	77032	0.0013	0.3436

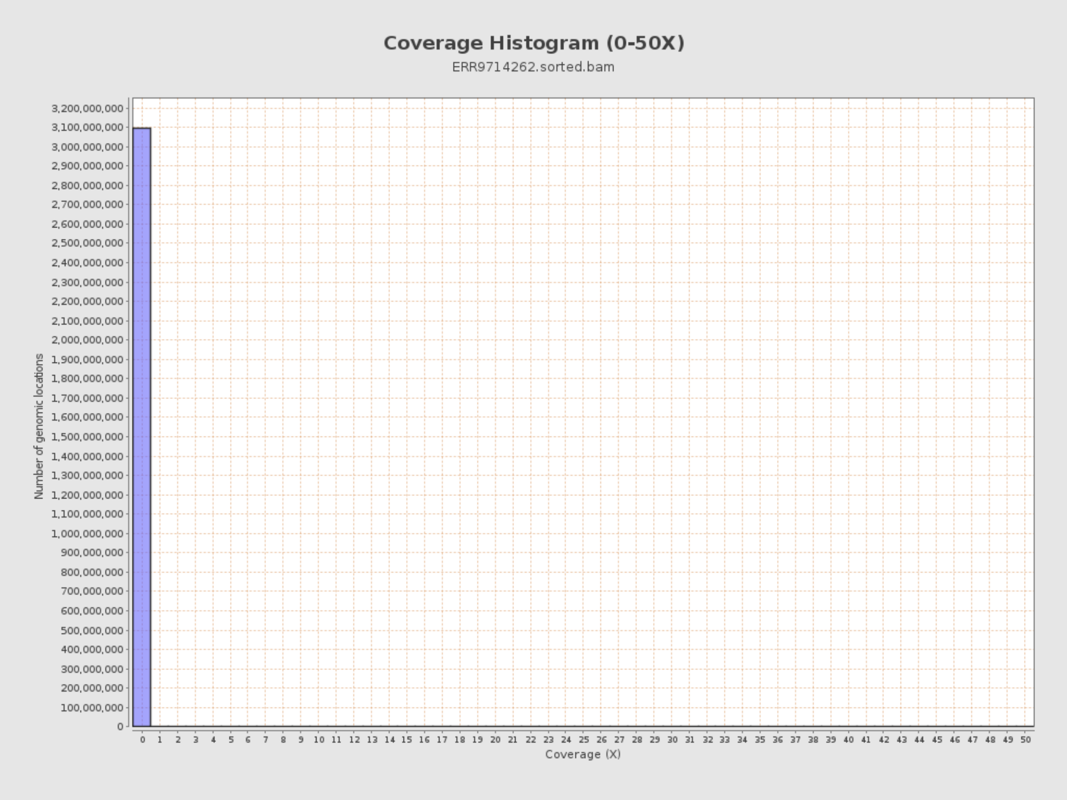
3. Results : Coverage across reference



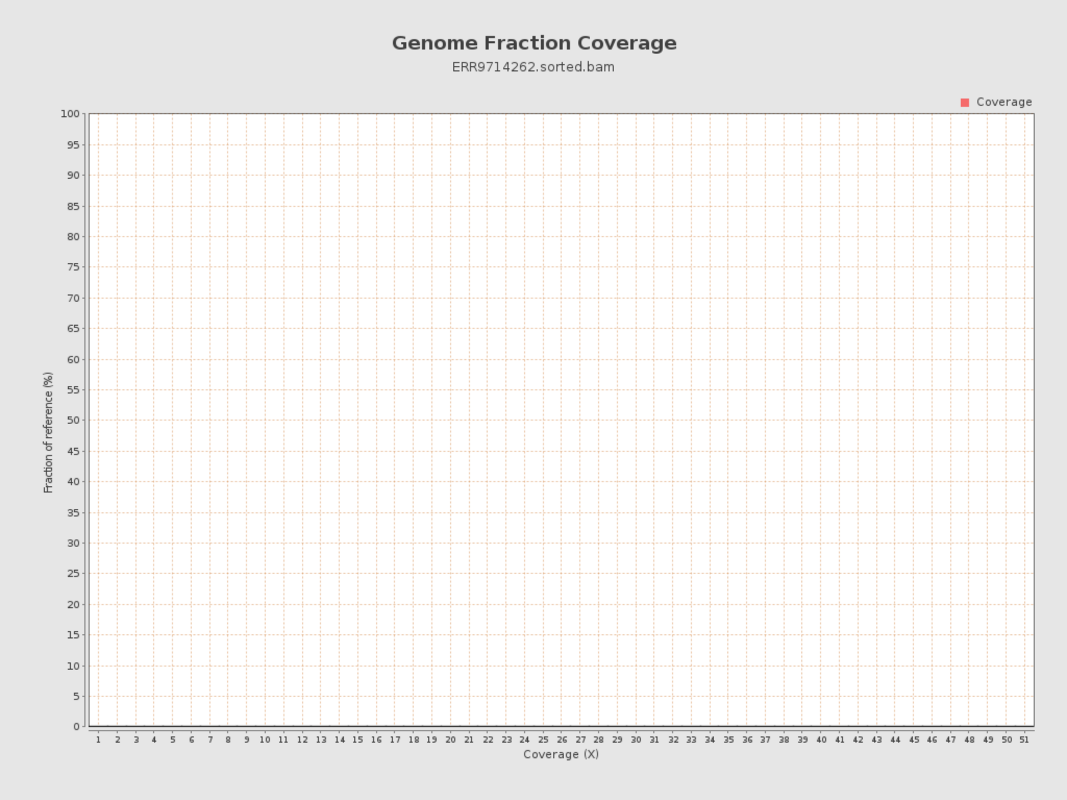
4. Results : Coverage Histogram



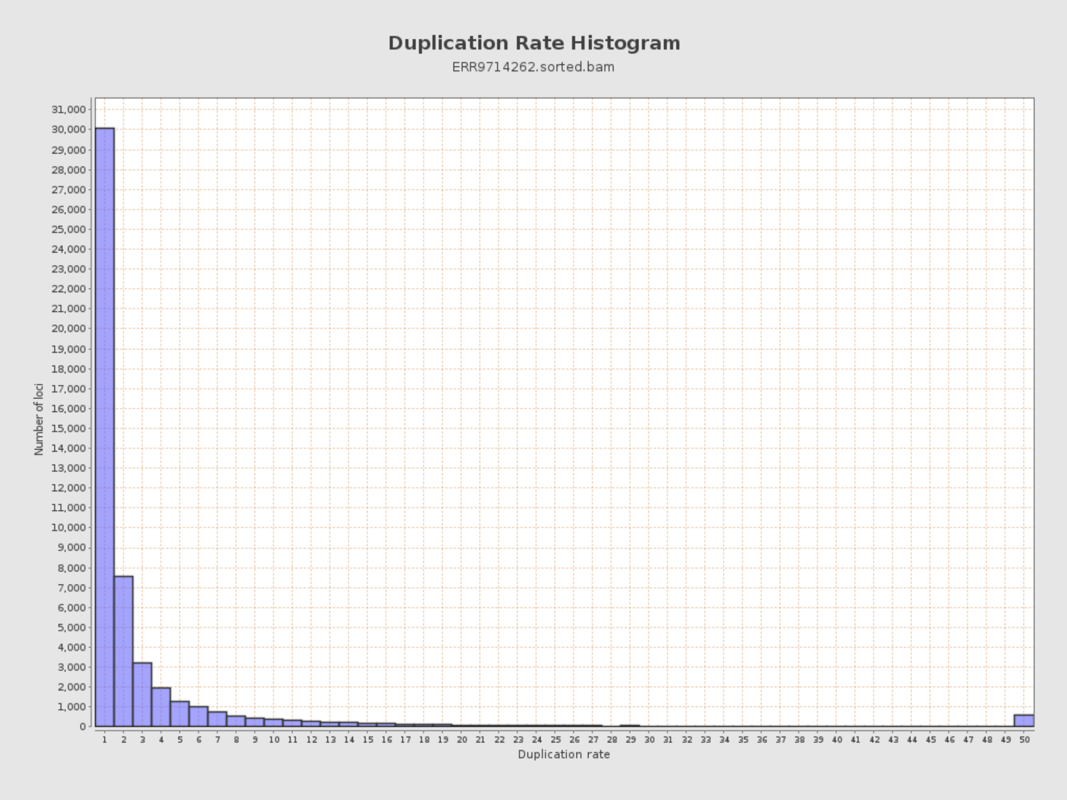
5. Results : Coverage Histogram (0-50X)



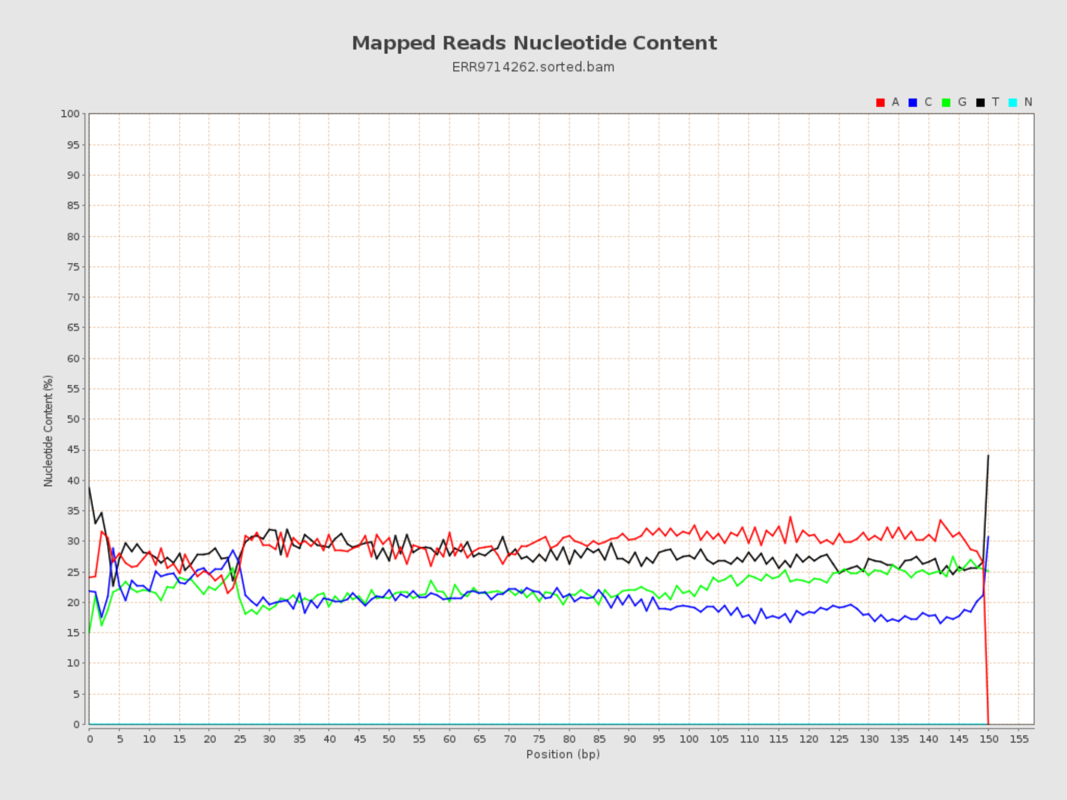
6. Results : Genome Fraction Coverage



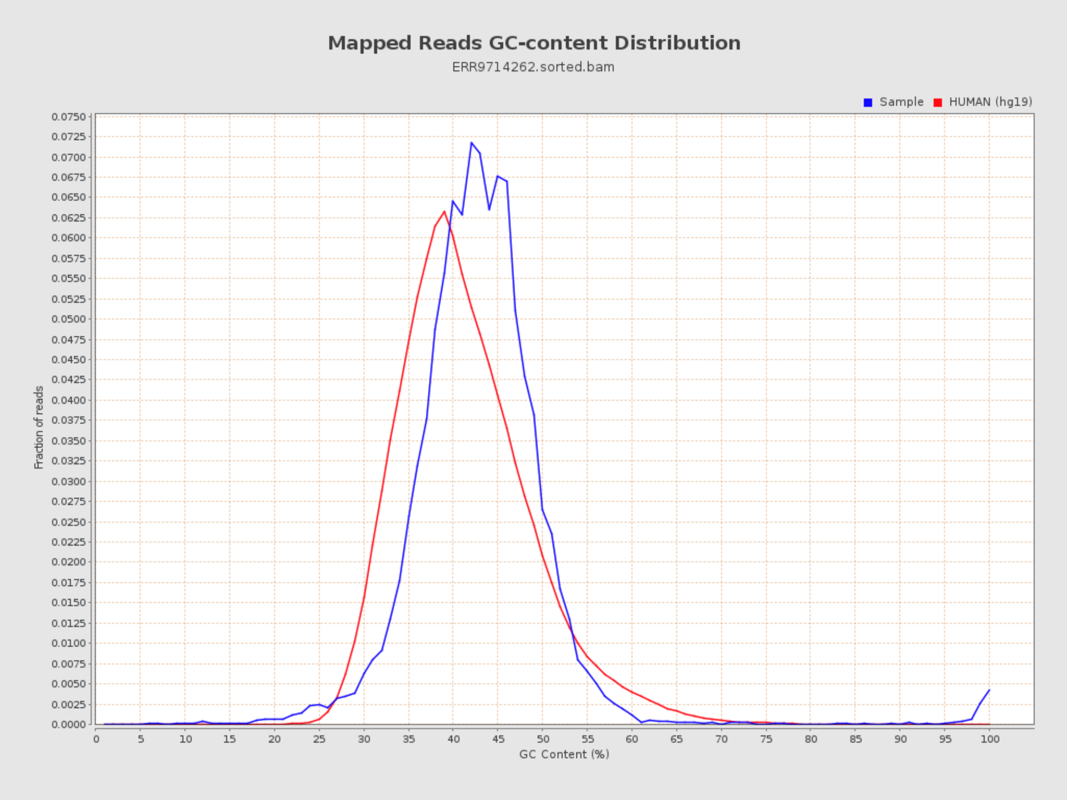
7. Results : Duplication Rate Histogram



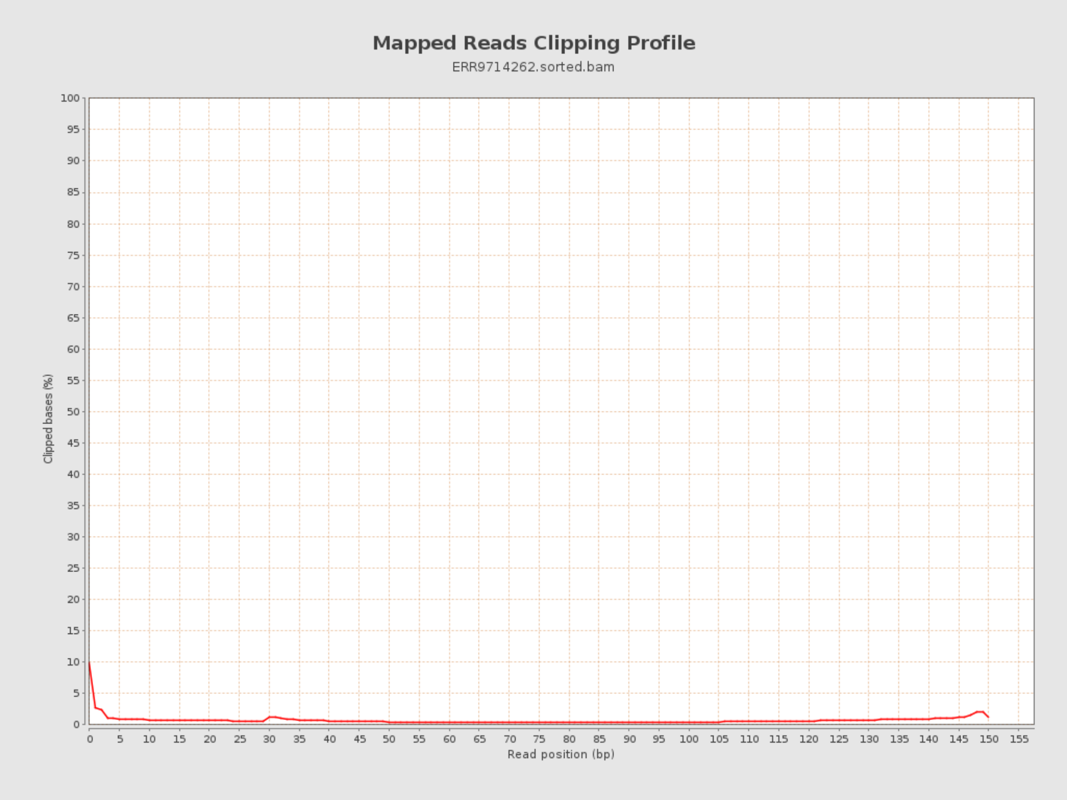
8. Results : Mapped Reads Nucleotide Content



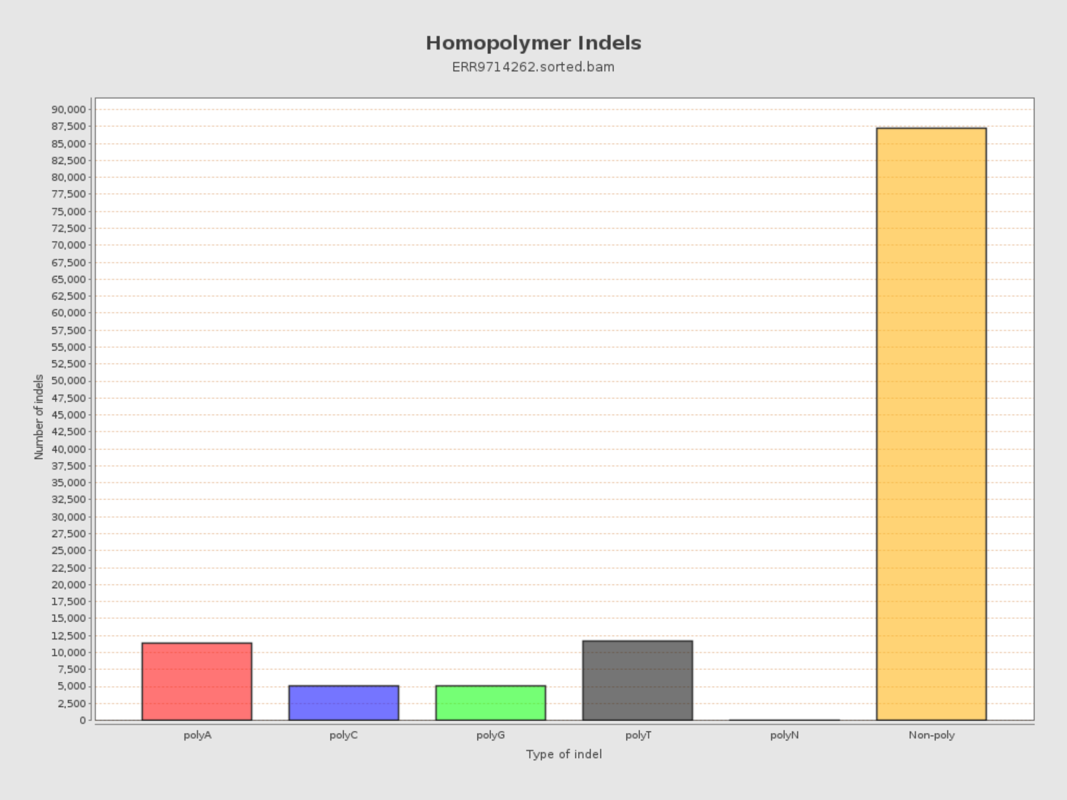
9. Results : Mapped Reads GC-content Distribution



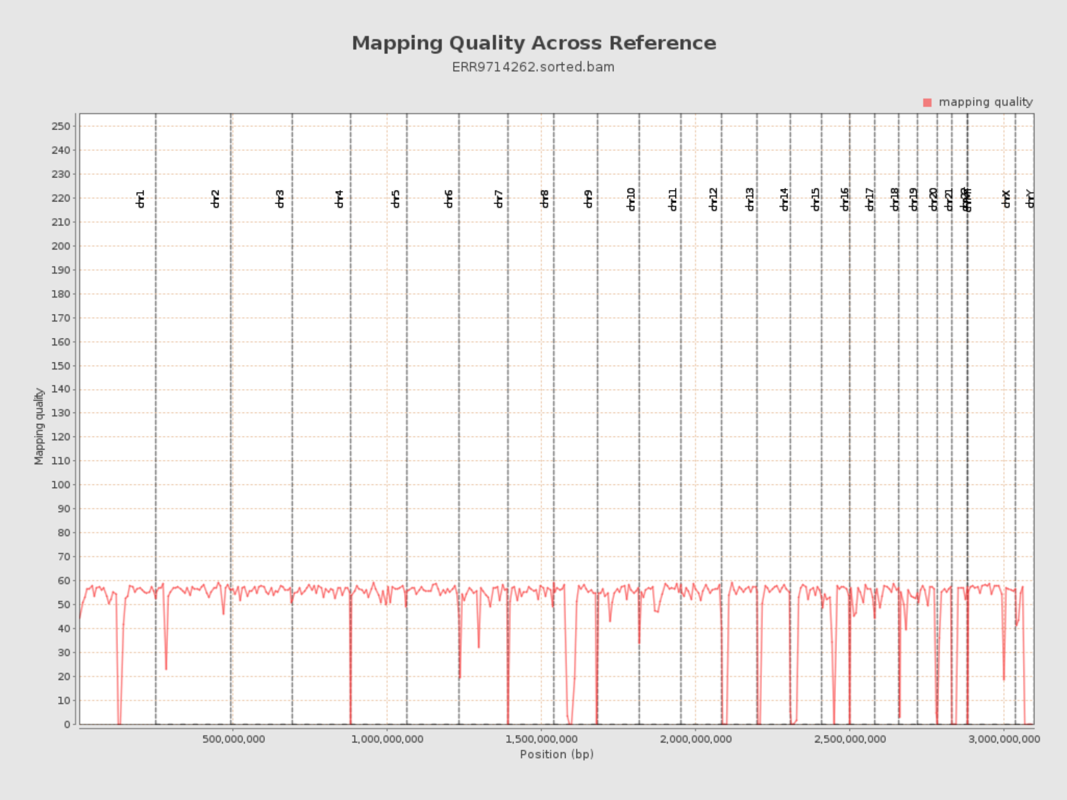
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram