Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:00:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714114.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_ERR9714114 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	638,140
Mapped reads	459,829 / 72.06%
Unmapped reads	178,311 / 27.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,163 / 2.38%
Read min/max/mean length	30 / 151 / 122.65
Duplicated reads (estimated)	447,008 / 70.05%
Duplication rate	35.38%
Clipped reads	425,903 / 66.74%

2.2. ACGT Content

Number/percentage of A's	16,859,783 / 28.91%
Number/percentage of C's	11,524,223 / 19.76%
Number/percentage of T's	15,914,500 / 27.29%
Number/percentage of G's	14,022,426 / 24.04%
Number/percentage of N's	500 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0193

Standard Deviation	13.0333

2.4. Mapping Quality

Mean Mapping Quality	26.73

2.5. Mismatches and indels

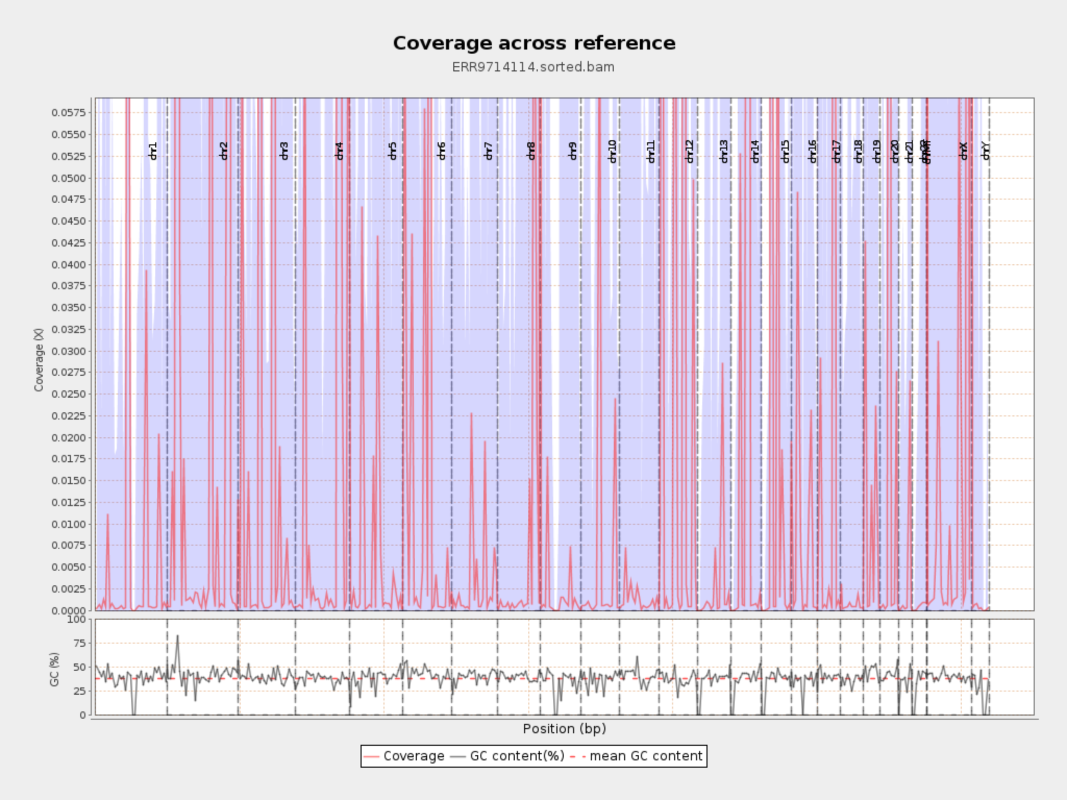
General error rate	4.22%
Mismatches	2,365,844
Insertions	40,532
Mapped reads with at least one insertion	8.52%
Deletions	206,139
Mapped reads with at least one deletion	43.41%
Homopolymer indels	30.95%

2.6. Chromosome stats

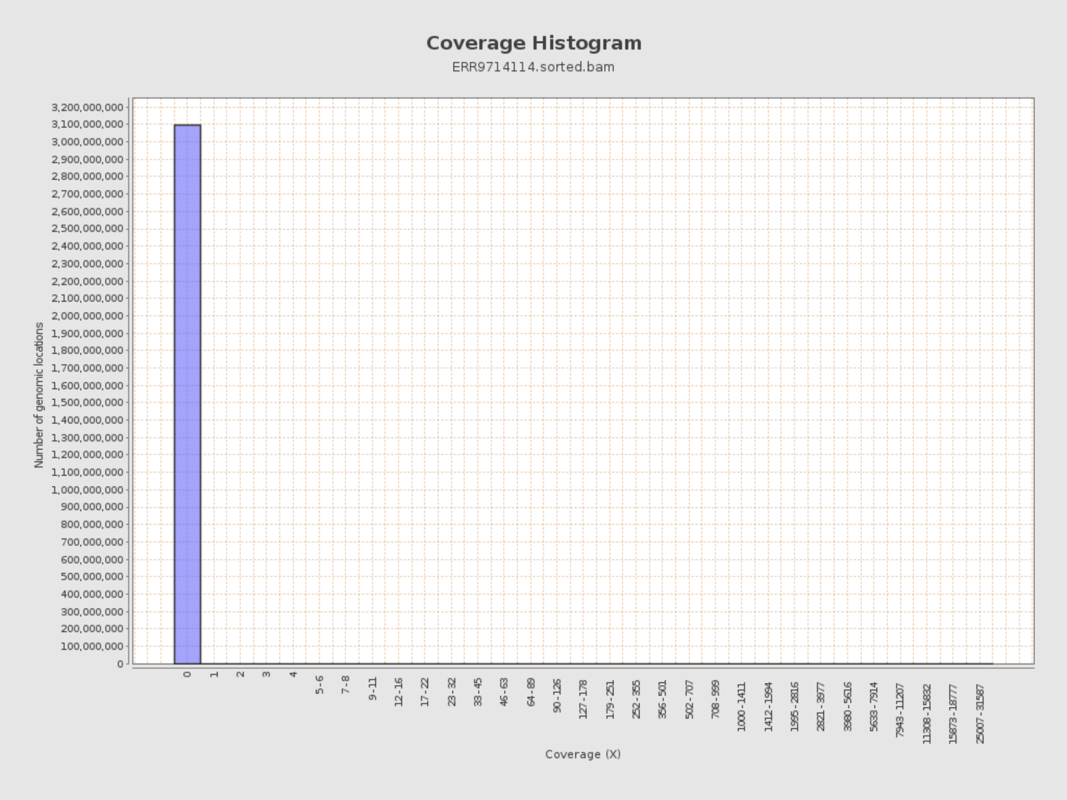
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1772691	0.0071	5.0006
chr2	243199373	13754944	0.0566	29.5341
chr3	198022430	7459884	0.0377	23.5254
chr4	191154276	5487646	0.0287	15.0161
chr5	180915260	1023394	0.0057	2.2197
chr6	171115067	3832010	0.0224	11.6078
chr7	159138663	559779	0.0035	1.5485

chr8	146364022	1103412	0.0075	4.2578
chr9	141213431	1147923	0.0081	5.8058
chr10	135534747	820171	0.0061	3.8304
chr11	135006516	195883	0.0015	0.4523
chr12	133851895	5083219	0.038	18.0104
chr13	115169878	334728	0.0029	1.2234
chr14	107349540	3483690	0.0325	9.6814
chr15	102531392	2602400	0.0254	8.8633
chr16	90354753	827554	0.0092	3.0176
chr17	81195210	2622953	0.0323	19.9626
chr18	78077248	55764	0.0007	0.1512
chr19	59128983	644718	0.0109	3.4066
chr20	63025520	2145201	0.034	15.6243
chr21	48129895	216519	0.0045	2.236
chr22	51304566	24810	0.0005	0.0992
chrMT	16571	820500	49.5142	413.4899
chrX	155270560	3595525	0.0232	6.6925
chrY	59373566	19838	0.0003	0.0558

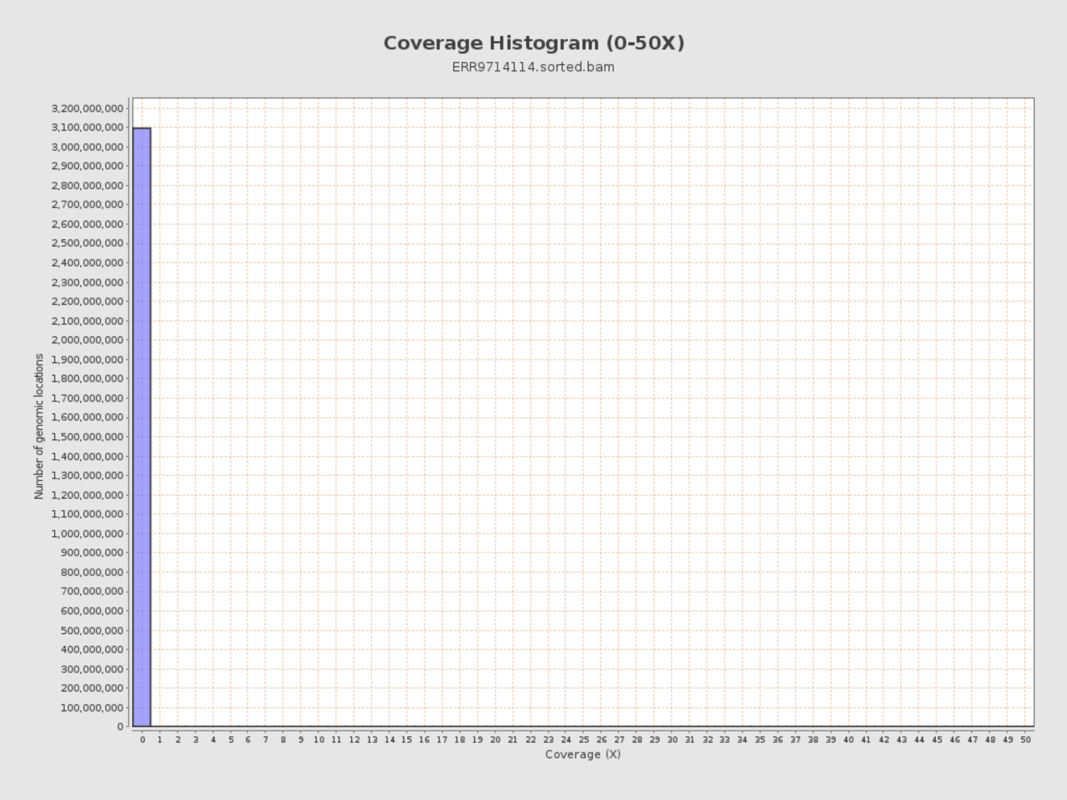
3. Results : Coverage across reference



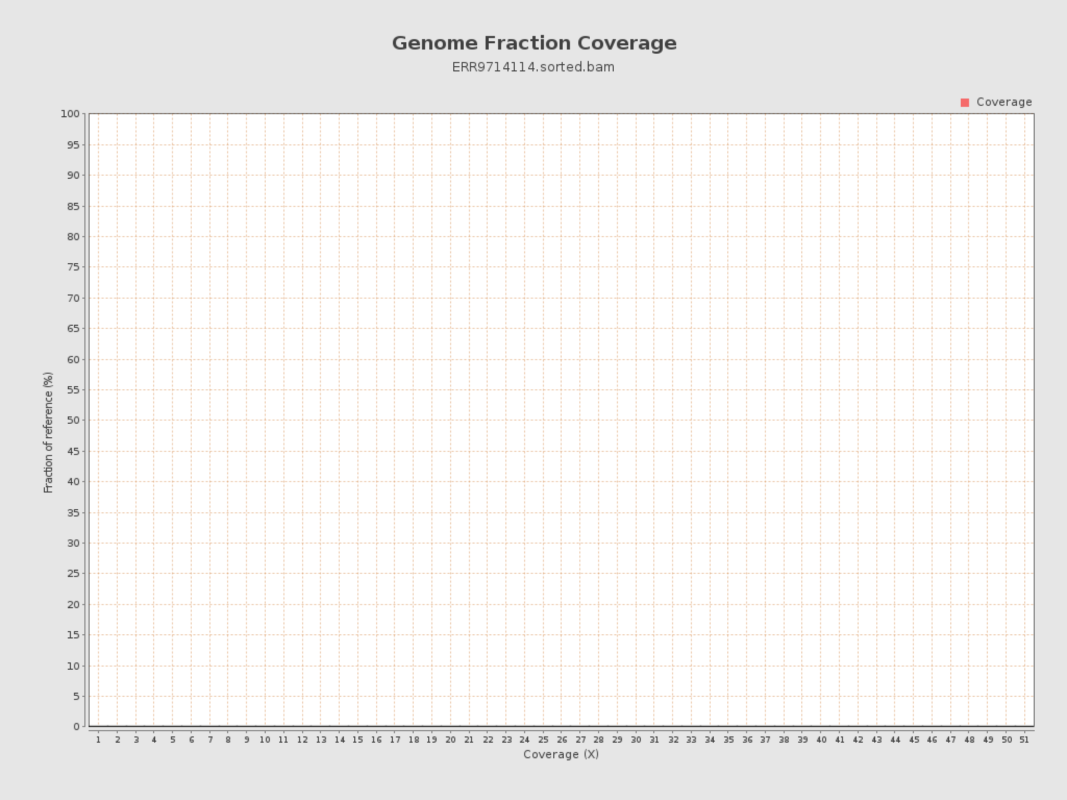
4. Results : Coverage Histogram



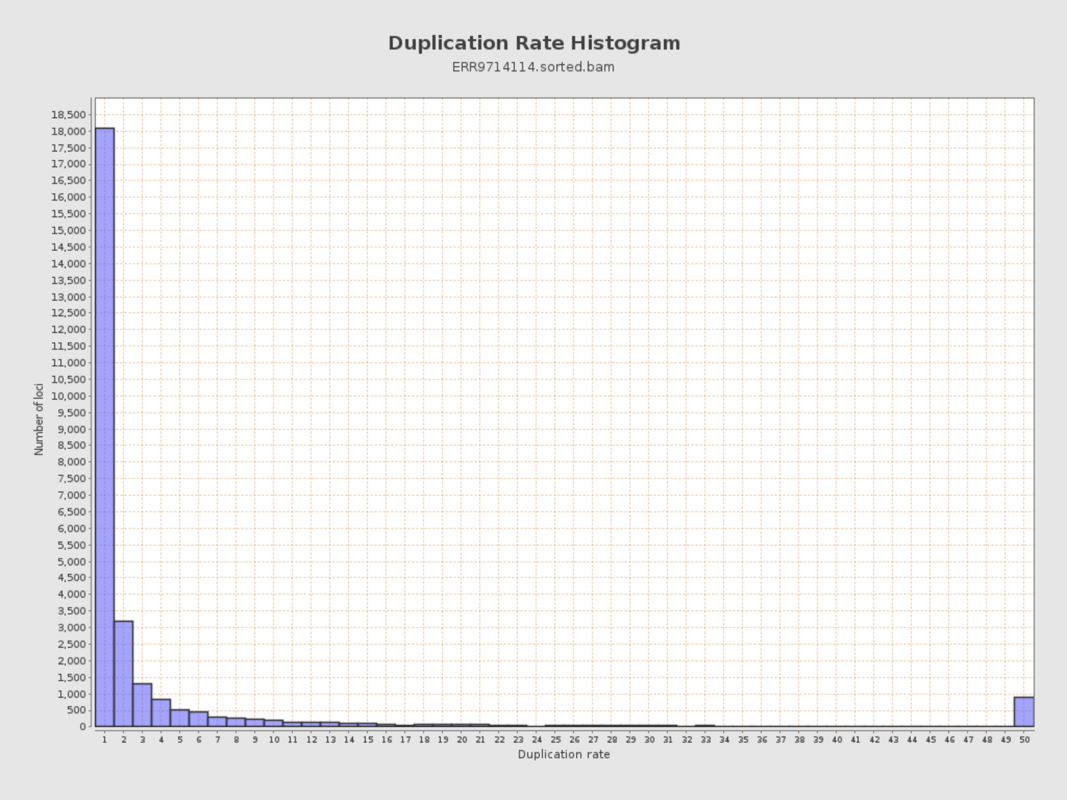
5. Results : Coverage Histogram (0-50X)



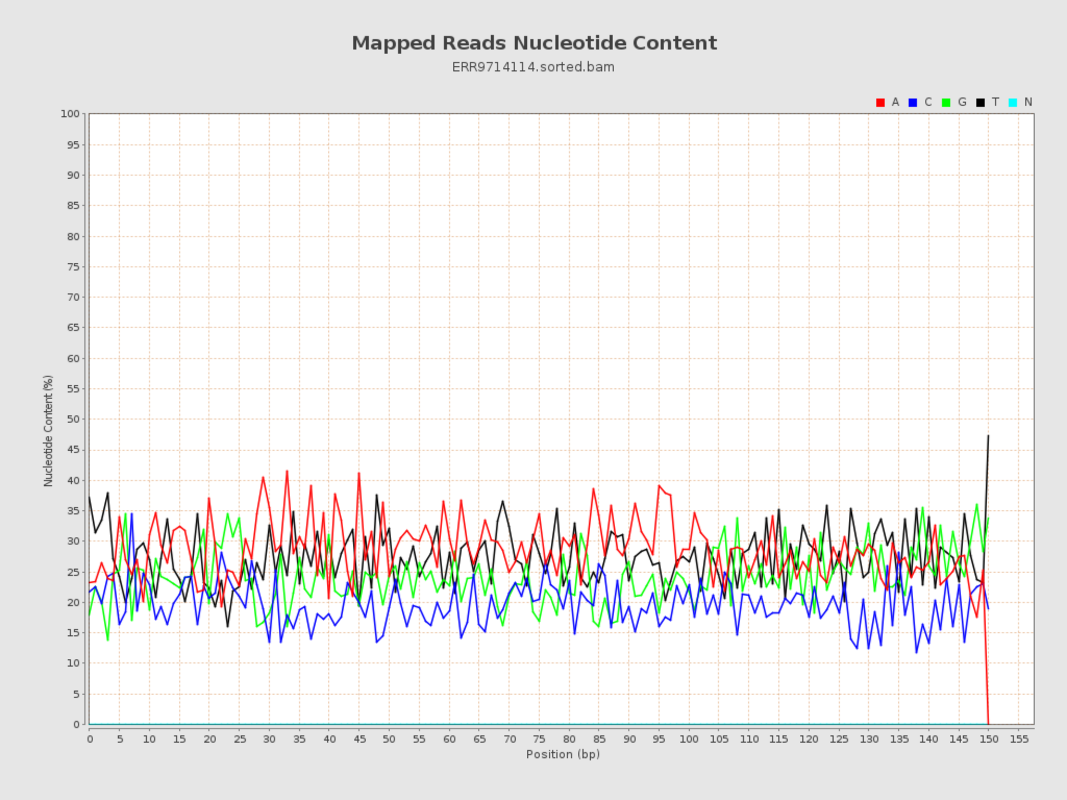
6. Results : Genome Fraction Coverage



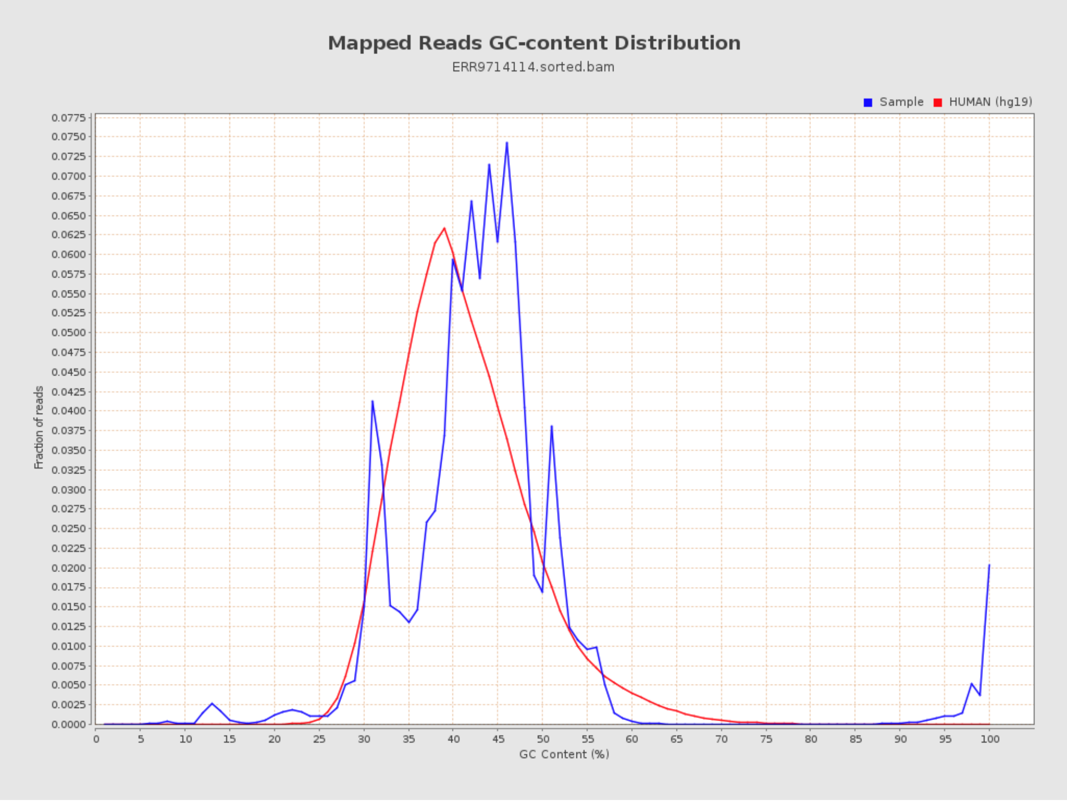
7. Results : Duplication Rate Histogram



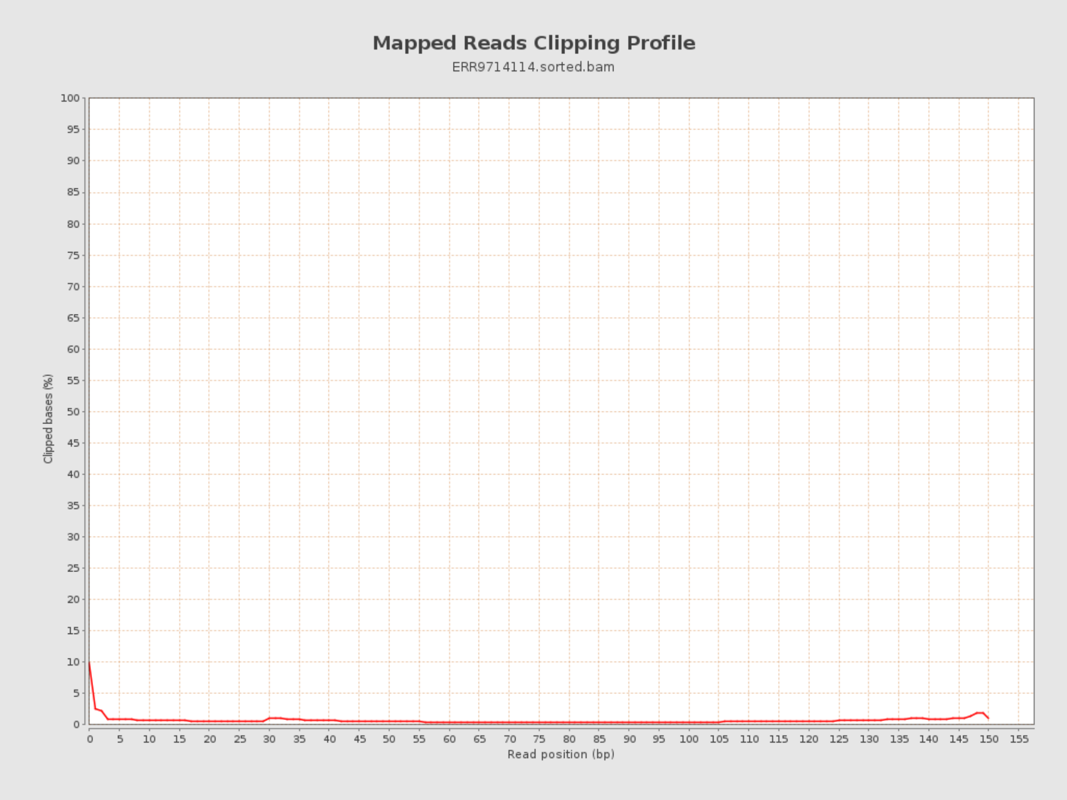
8. Results : Mapped Reads Nucleotide Content



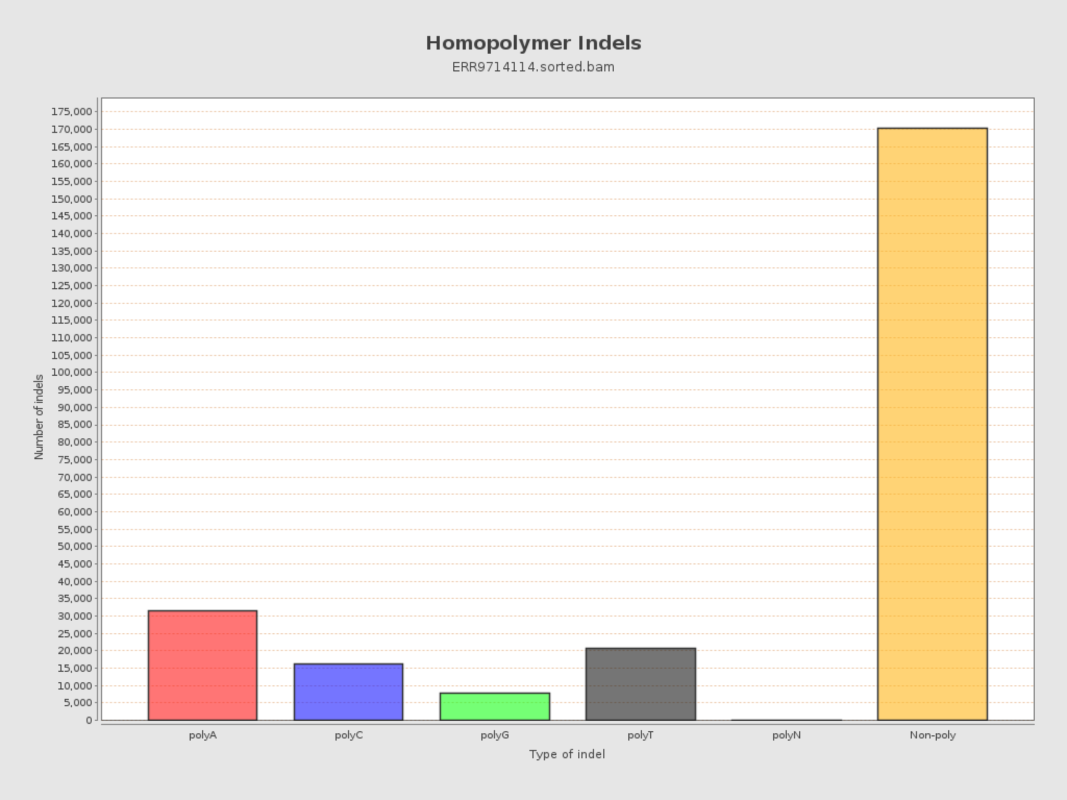
9. Results : Mapped Reads GC-content Distribution



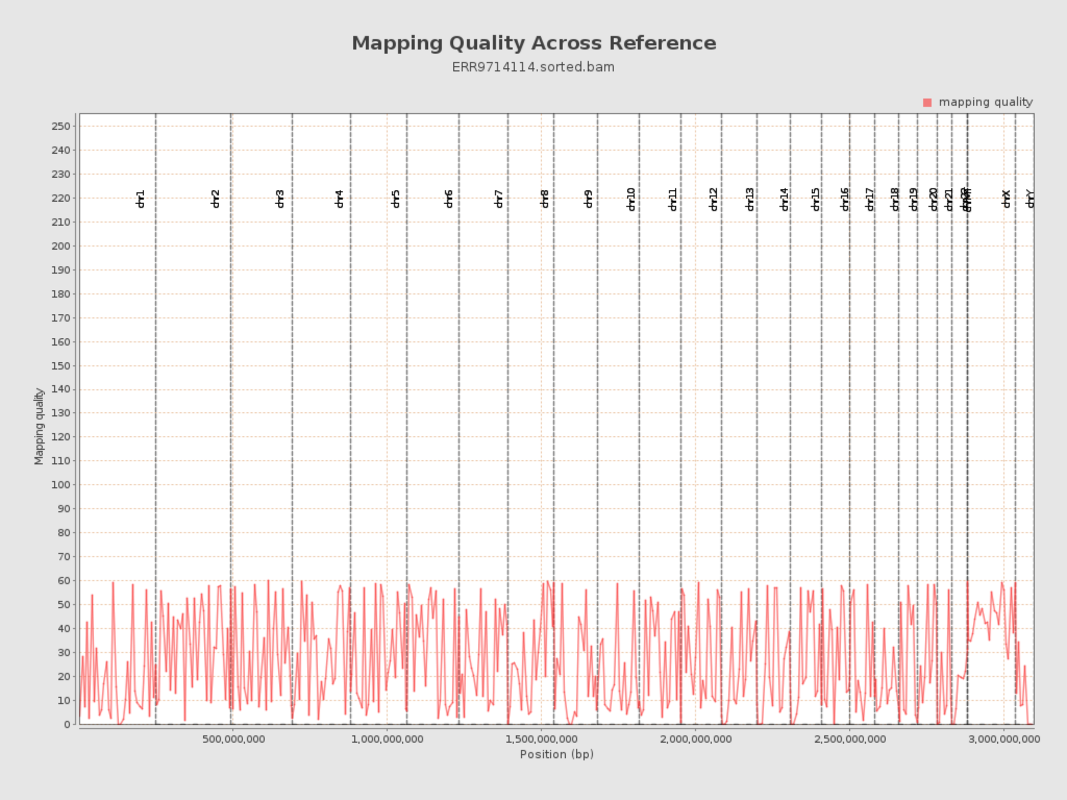
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram