Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:51:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714264.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_ERR9714264 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:51:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	442,060
Mapped reads	45,012 / 10.18%
Unmapped reads	397,048 / 89.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,137 / 0.26%
Read min/max/mean length	30 / 151 / 59.8
Duplicated reads (estimated)	39,272 / 8.88%
Duplication rate	37.76%
Clipped reads	34,051 / 7.7%

2.2. ACGT Content

Number/percentage of A's	643,045 / 14.42%
Number/percentage of C's	416,592 / 9.34%
Number/percentage of T's	559,637 / 12.55%
Number/percentage of G's	2,839,173 / 63.68%
Number/percentage of N's	98 / 0%
GC Percentage	73.02%

2.3. Coverage

Mean	0.0015

Standard Deviation	2.9532

2.4. Mapping Quality

Mean Mapping Quality	39.73

2.5. Mismatches and indels

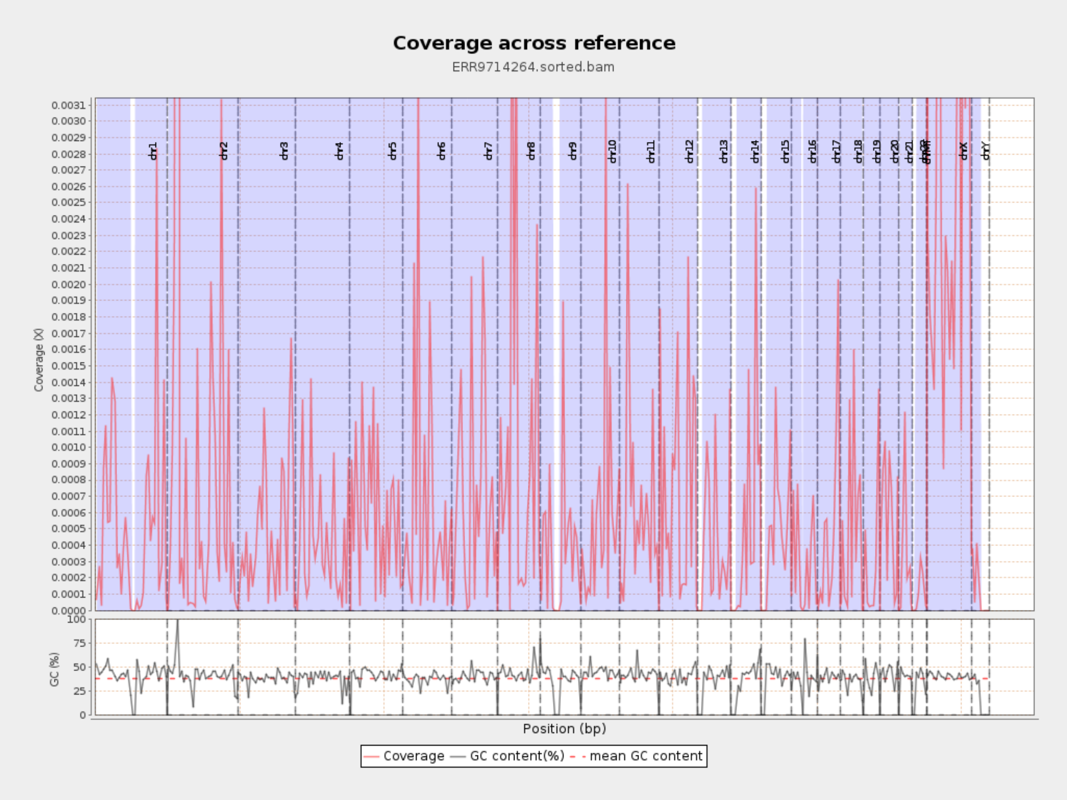
General error rate	3.55%
Mismatches	136,164
Insertions	4,421
Mapped reads with at least one insertion	7.68%
Deletions	8,011
Mapped reads with at least one deletion	17.12%
Homopolymer indels	37.69%

2.6. Chromosome stats

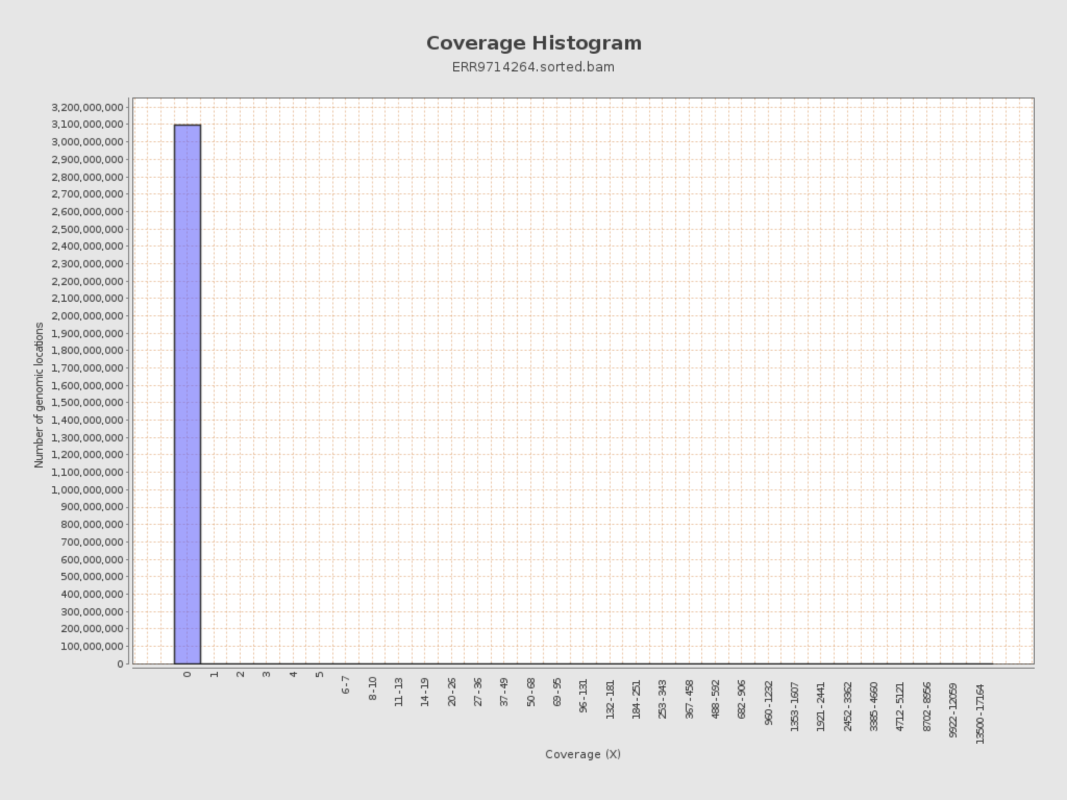
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	127719	0.0005	0.1309
chr2	243199373	2589647	0.0106	10.5215
chr3	198022430	100887	0.0005	0.1016
chr4	191154276	77513	0.0004	0.0852
chr5	180915260	109497	0.0006	0.1253
chr6	171115067	111404	0.0007	0.179
chr7	159138663	110351	0.0007	0.2372

chr8	146364022	158088	0.0011	0.3042
chr9	141213431	54032	0.0004	0.0772
chr10	135534747	82299	0.0006	0.1873
chr11	135006516	84199	0.0006	0.1471
chr12	133851895	101491	0.0008	0.1559
chr13	115169878	44272	0.0004	0.0829
chr14	107349540	60377	0.0006	0.1454
chr15	102531392	50930	0.0005	0.109
chr16	90354753	25808	0.0003	0.0517
chr17	81195210	40083	0.0005	0.1489
chr18	78077248	42618	0.0005	0.1118
chr19	59128983	17221	0.0003	0.104
chr20	63025520	36184	0.0006	0.1019
chr21	48129895	17316	0.0004	0.0892
chr22	51304566	5509	0.0001	0.0265
chrMT	16571	14556	0.8784	7.612
chrX	155270560	440066	0.0028	0.3123
chrY	59373566	7071	0.0001	0.0288

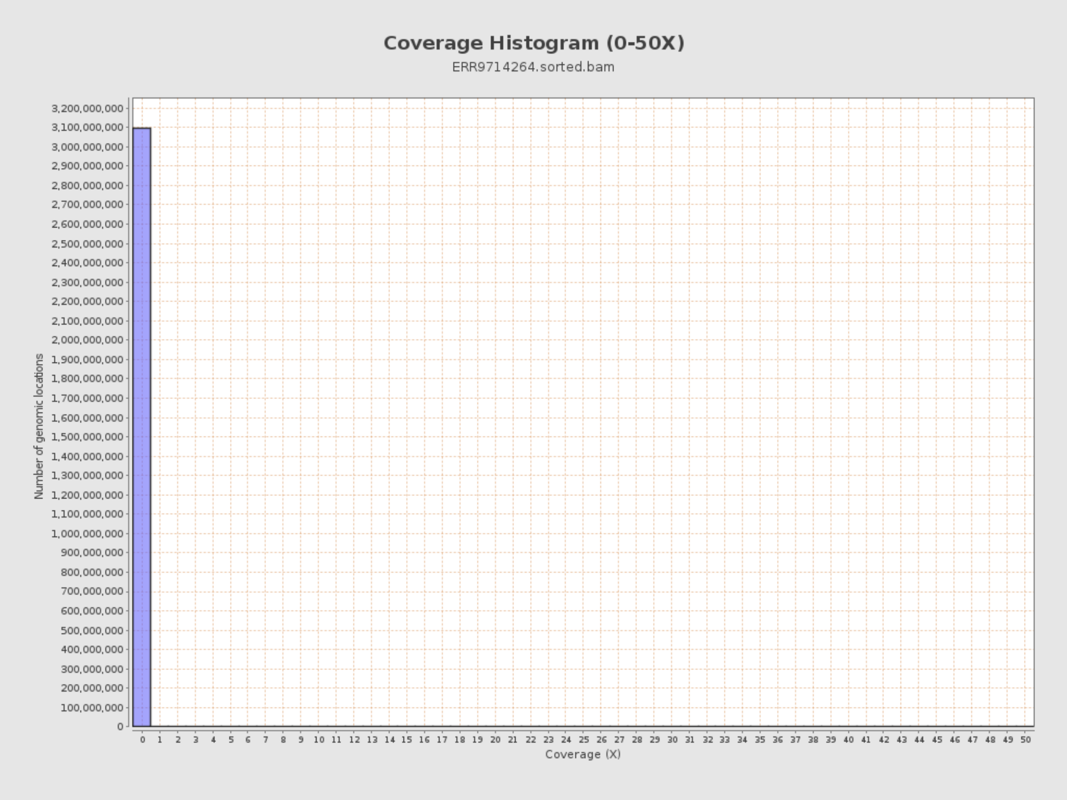
3. Results : Coverage across reference



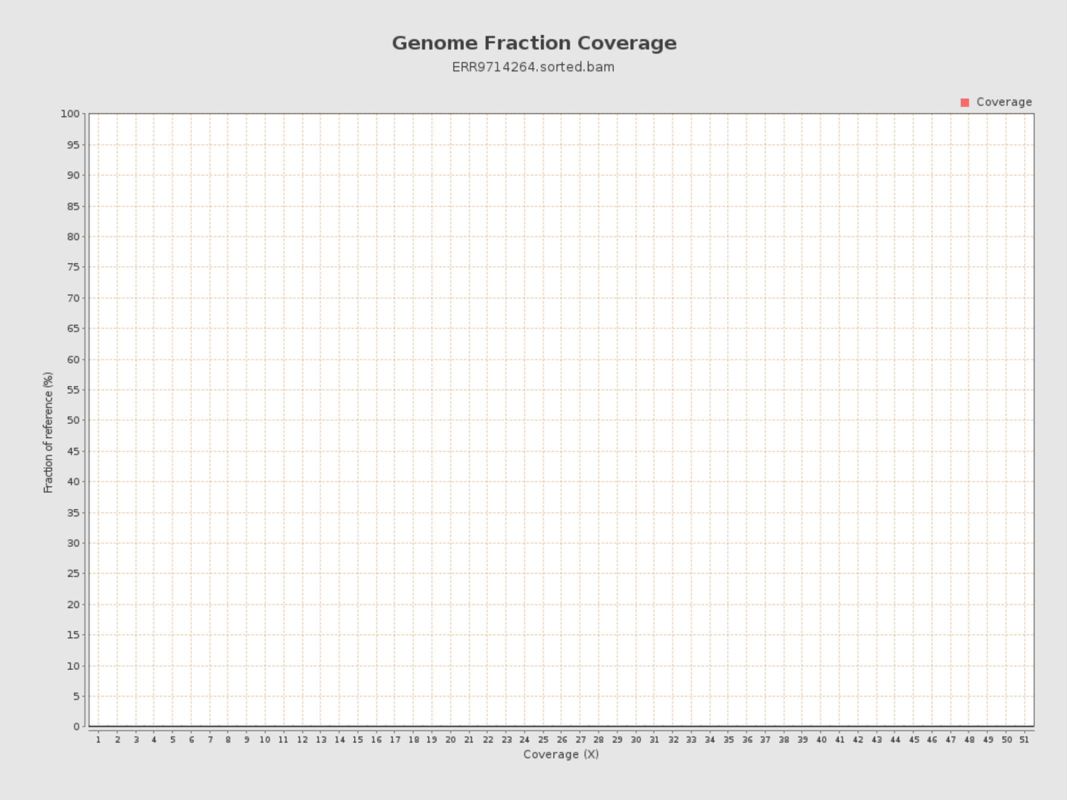
4. Results : Coverage Histogram



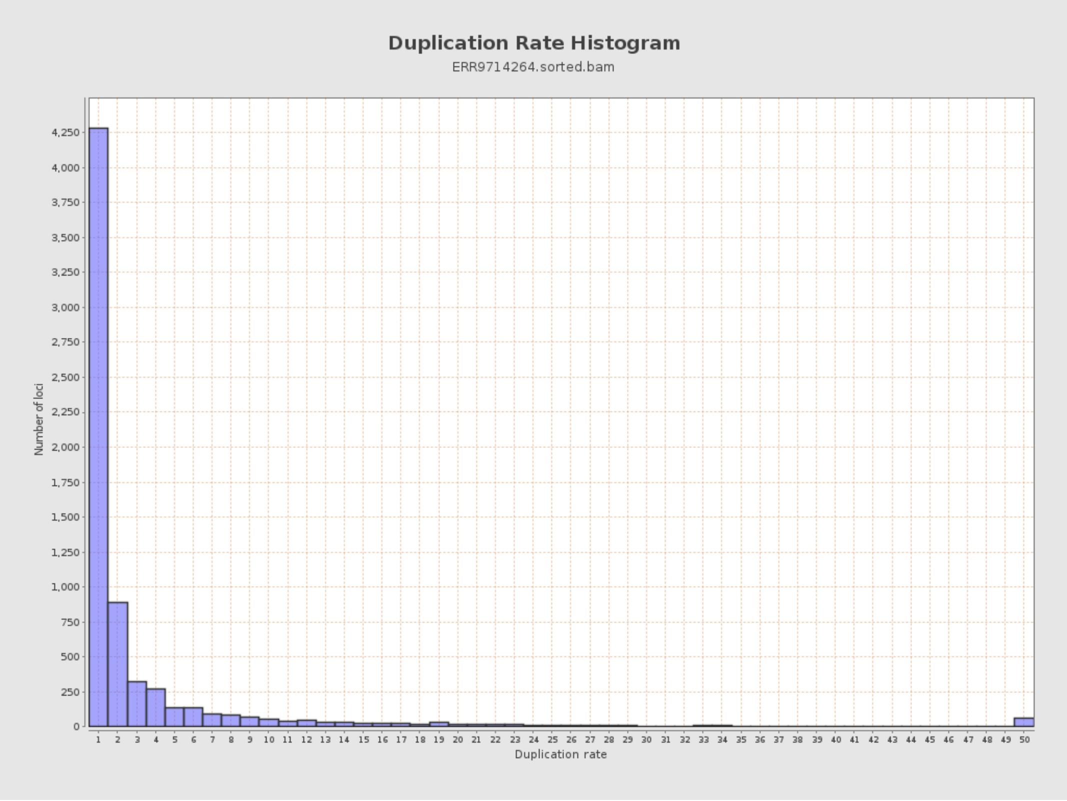
5. Results : Coverage Histogram (0-50X)



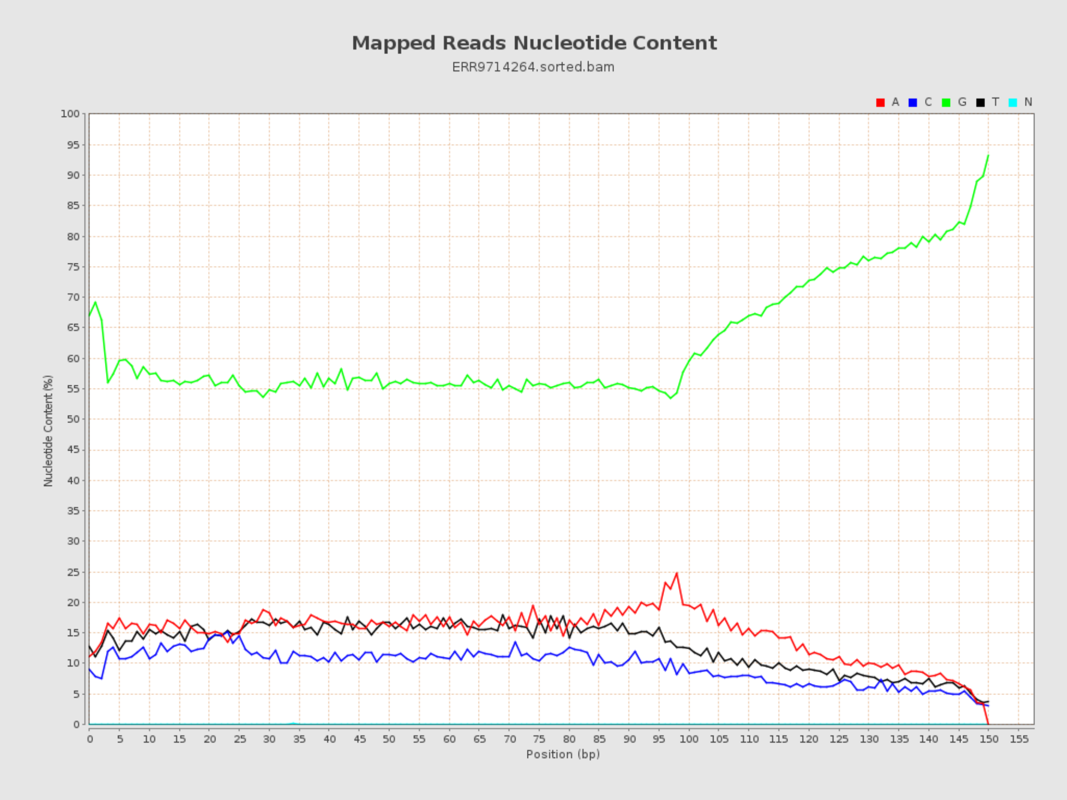
6. Results : Genome Fraction Coverage



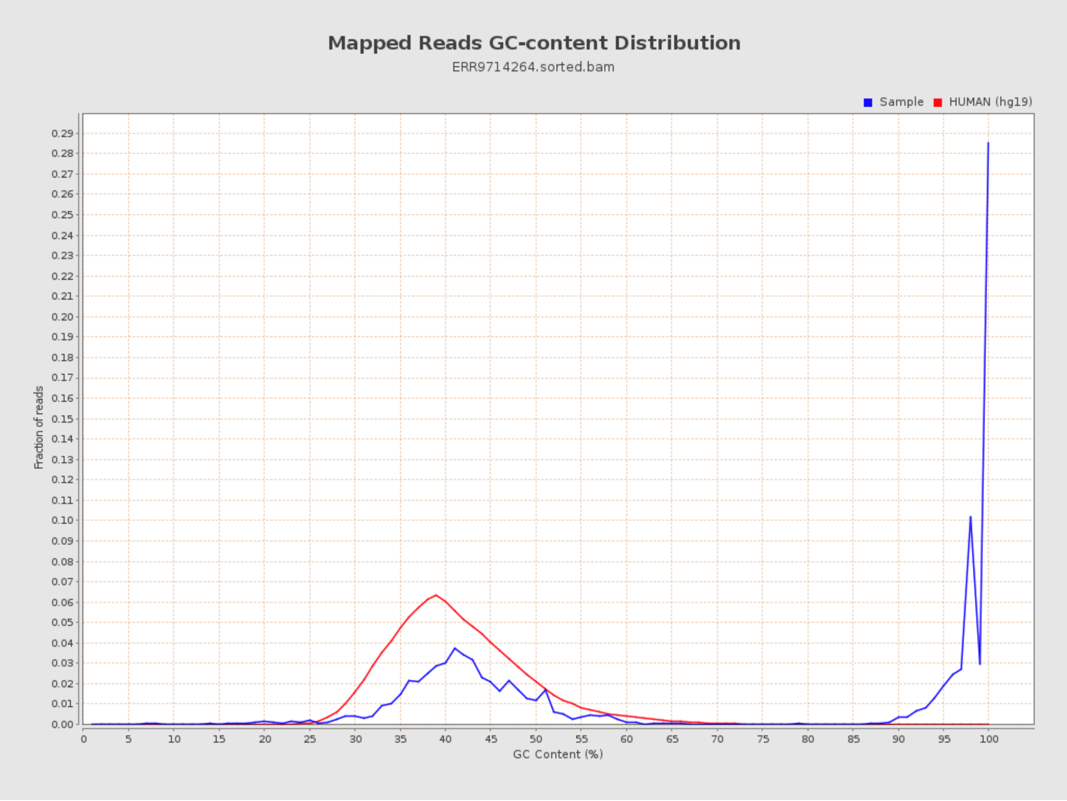
7. Results : Duplication Rate Histogram



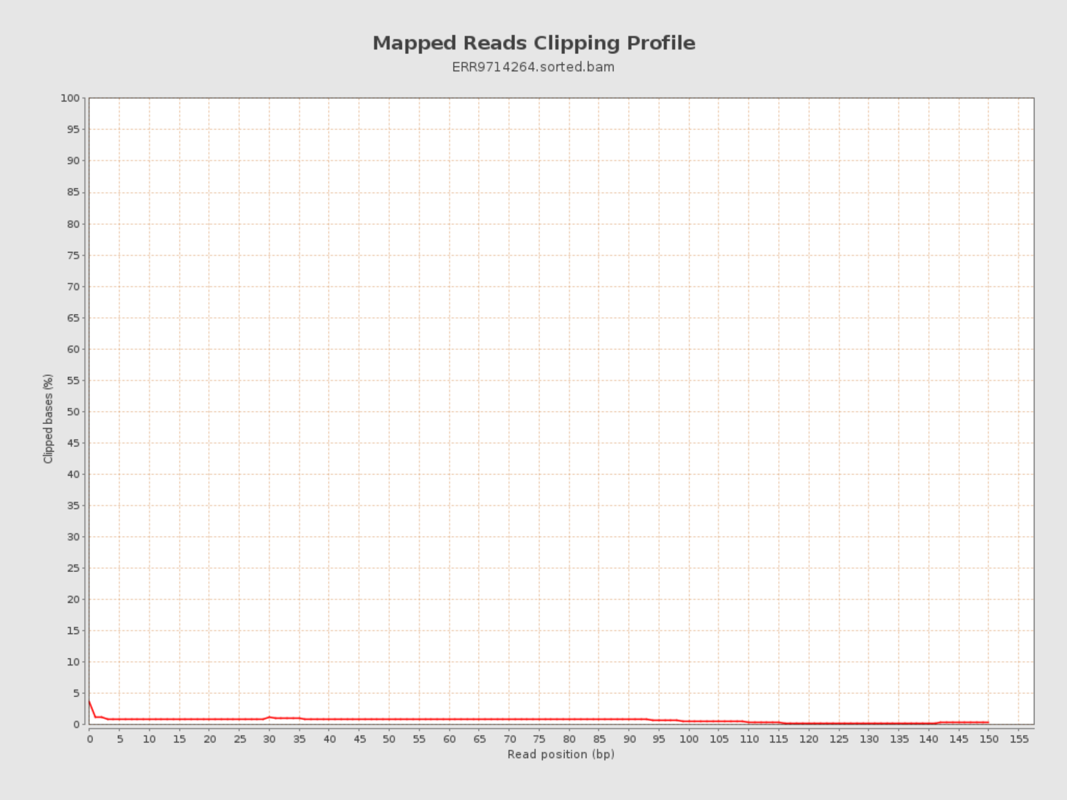
8. Results : Mapped Reads Nucleotide Content



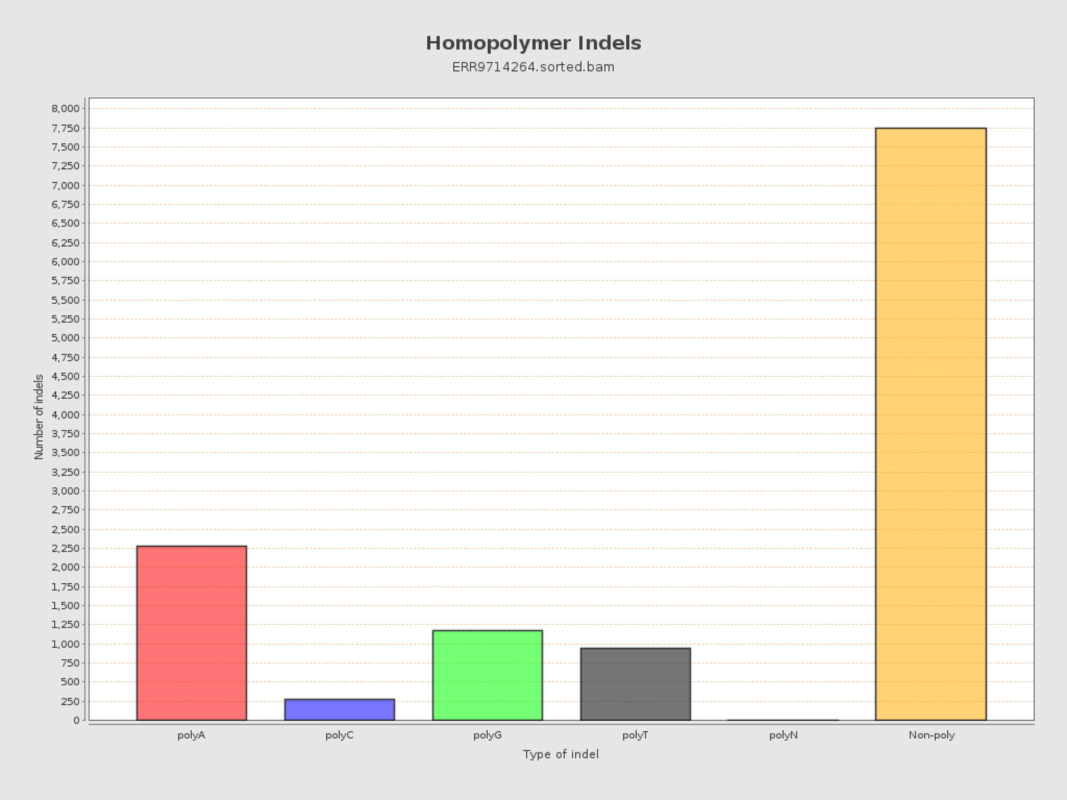
9. Results : Mapped Reads GC-content Distribution



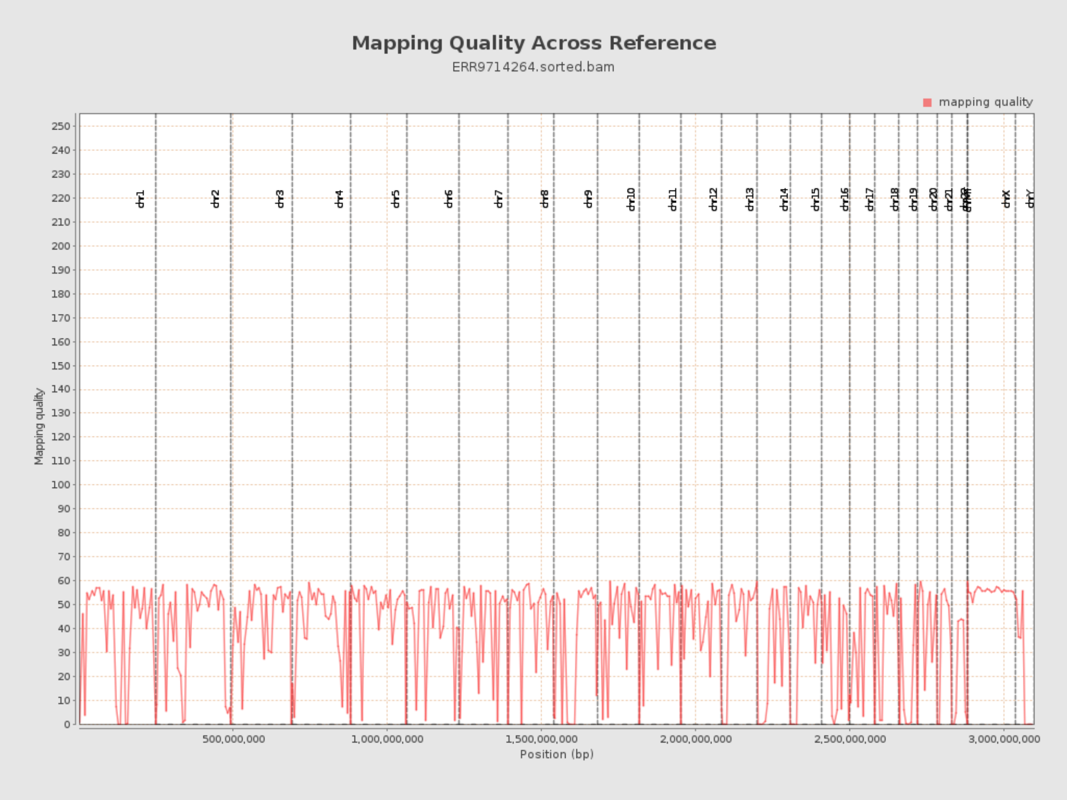
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram