Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:29:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714219.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_ERR9714219 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:29:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	215,582
Mapped reads	17,118 / 7.94%
Unmapped reads	198,464 / 92.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	544 / 0.25%
Read min/max/mean length	30 / 151 / 55.88
Duplicated reads (estimated)	14,083 / 6.53%
Duplication rate	39.65%
Clipped reads	13,852 / 6.43%

2.2. ACGT Content

Number/percentage of A's	319,454 / 18.34%
Number/percentage of C's	227,344 / 13.06%
Number/percentage of T's	286,585 / 16.46%
Number/percentage of G's	907,919 / 52.14%
Number/percentage of N's	72 / 0%
GC Percentage	65.19%

2.3. Coverage

Mean	0.0006

Standard Deviation	0.7916

2.4. Mapping Quality

Mean Mapping Quality	34.57

2.5. Mismatches and indels

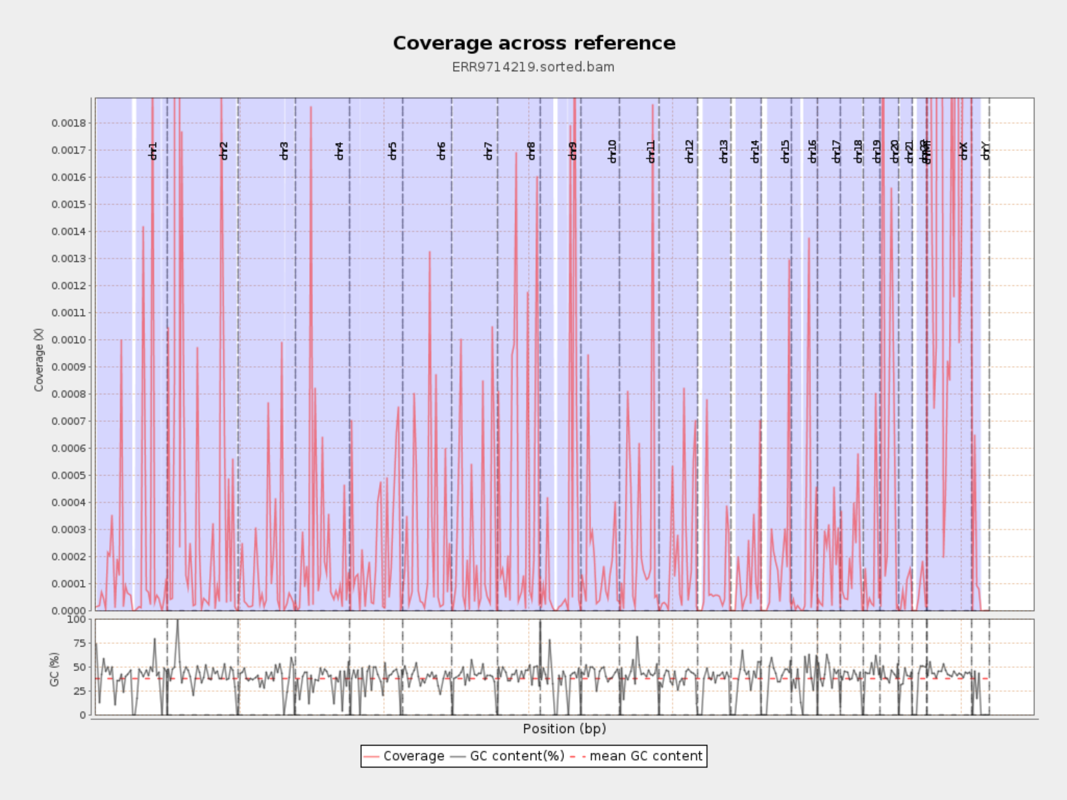
General error rate	3.79%
Mismatches	57,509
Insertions	1,763
Mapped reads with at least one insertion	8.39%
Deletions	4,096
Mapped reads with at least one deletion	22.68%
Homopolymer indels	36.97%

2.6. Chromosome stats

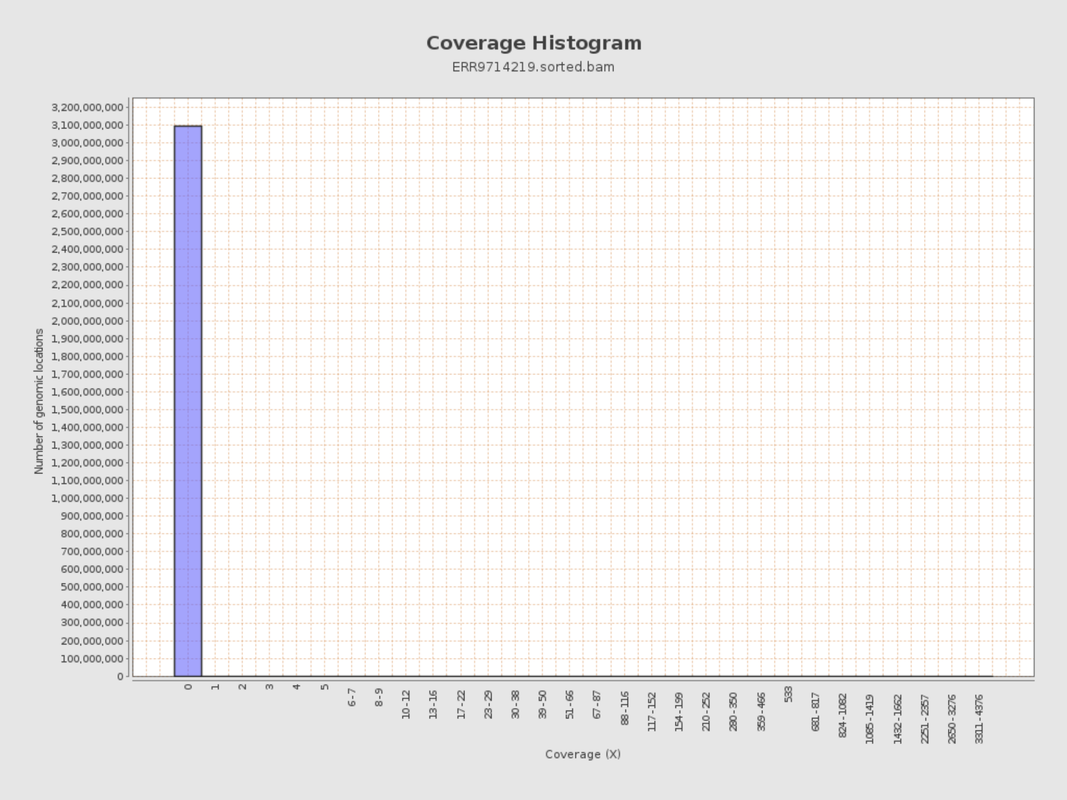
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	50389	0.0002	0.0842
chr2	243199373	765683	0.0031	2.7969
chr3	198022430	29091	0.0001	0.0564
chr4	191154276	44787	0.0002	0.0874
chr5	180915260	40059	0.0002	0.0646
chr6	171115067	45239	0.0003	0.0781
chr7	159138663	41936	0.0003	0.0838

chr8	146364022	64480	0.0004	0.1332
chr9	141213431	43892	0.0003	0.1344
chr10	135534747	24282	0.0002	0.0493
chr11	135006516	40866	0.0003	0.0897
chr12	133851895	30129	0.0002	0.0737
chr13	115169878	14525	0.0001	0.0507
chr14	107349540	14659	0.0001	0.0455
chr15	102531392	21967	0.0002	0.0725
chr16	90354753	21063	0.0002	0.0787
chr17	81195210	14638	0.0002	0.0509
chr18	78077248	15532	0.0002	0.0433
chr19	59128983	8811	0.0001	0.0581
chr20	63025520	47262	0.0007	0.2477
chr21	48129895	3262	0.0001	0.0173
chr22	51304566	2843	0.0001	0.0154
chrMT	16571	3412	0.2059	1.6589
chrX	155270560	372780	0.0024	0.3288
chrY	59373566	6358	0.0001	0.0503

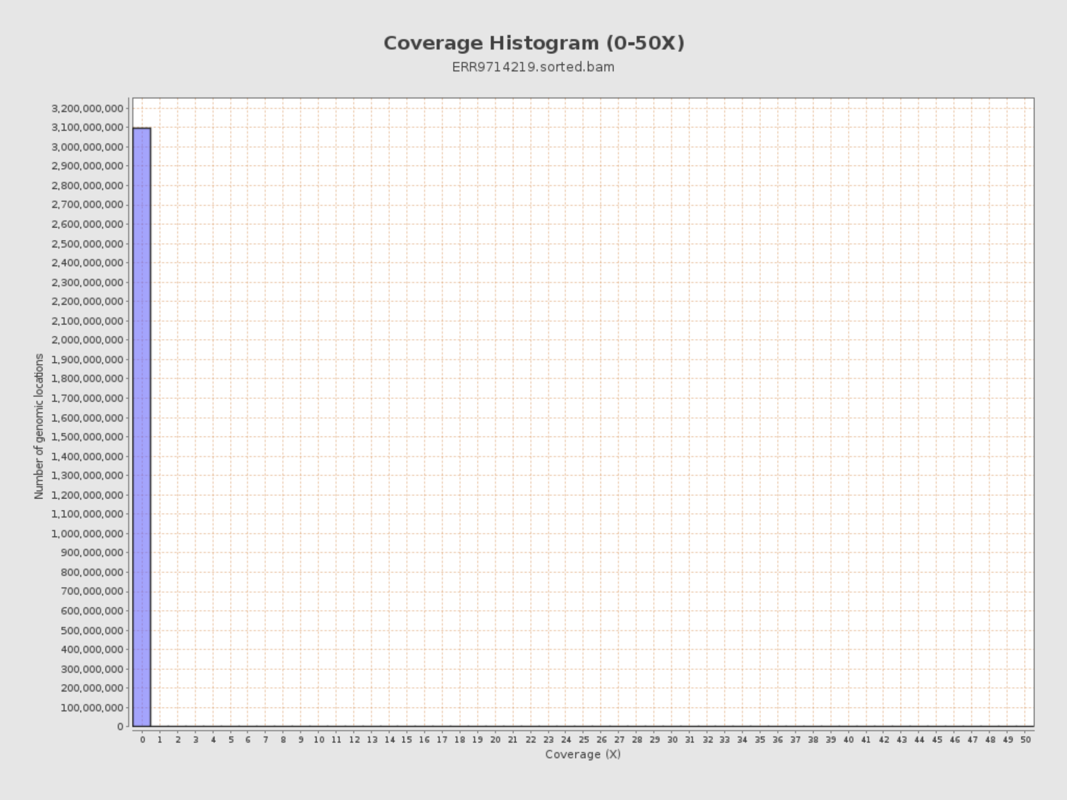
3. Results : Coverage across reference



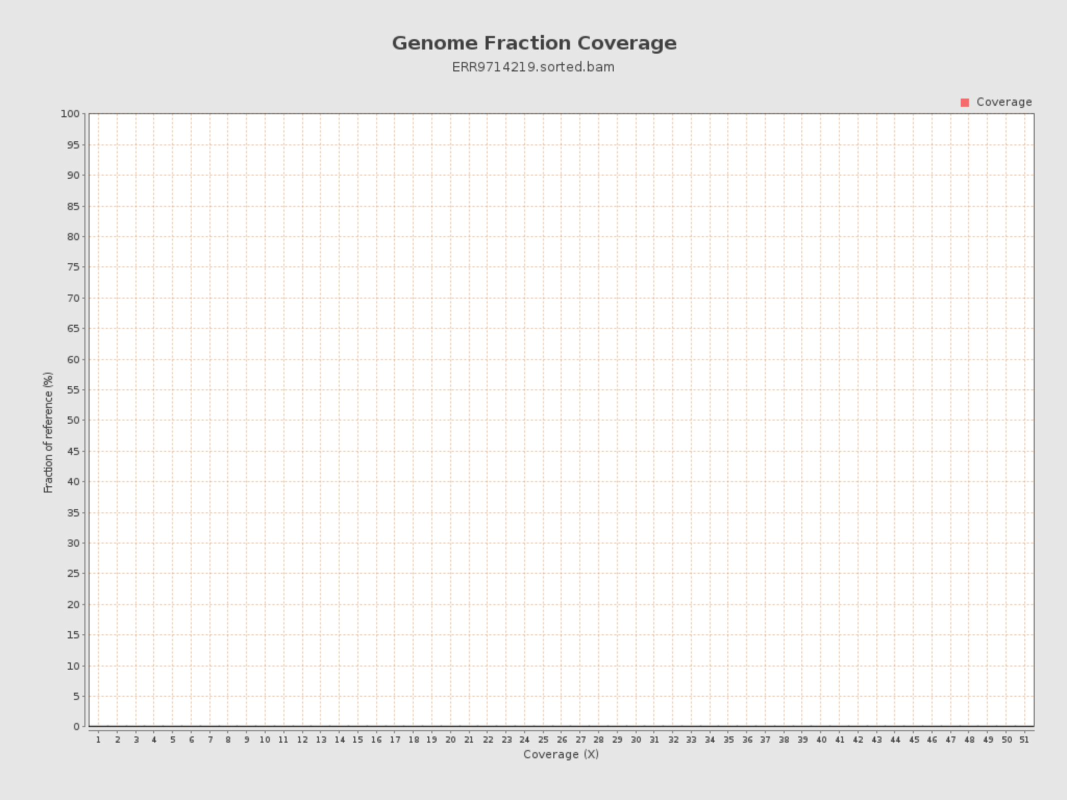
4. Results : Coverage Histogram



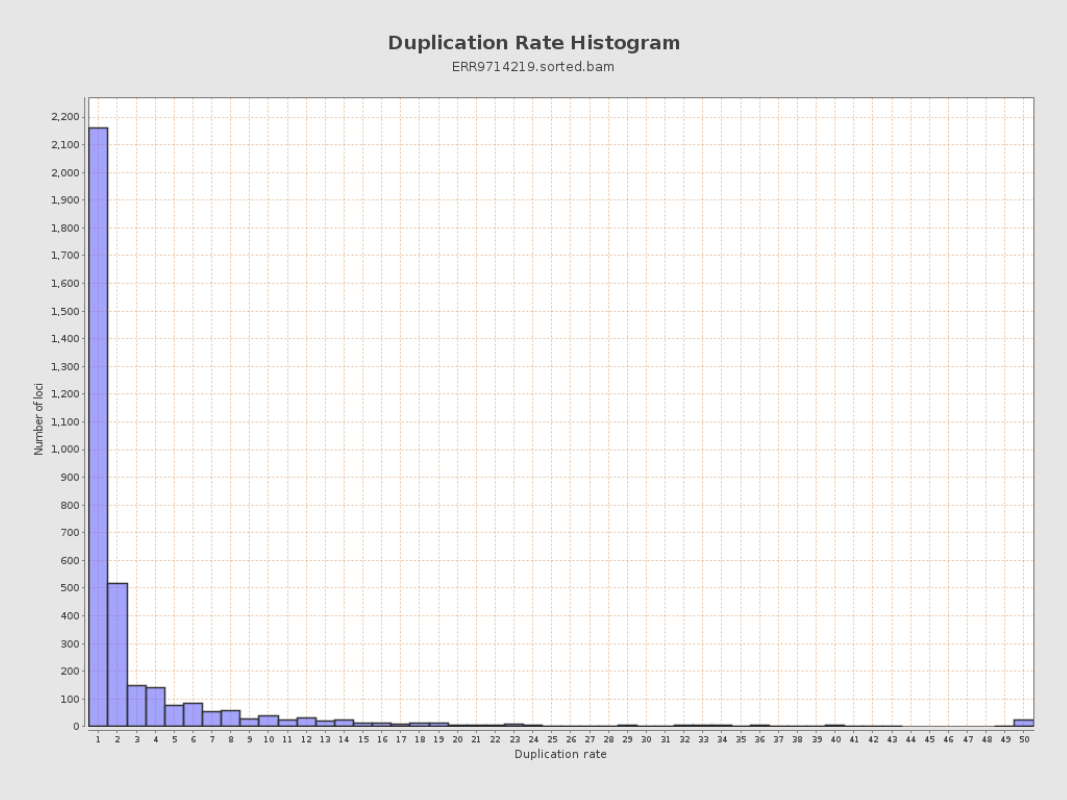
5. Results : Coverage Histogram (0-50X)



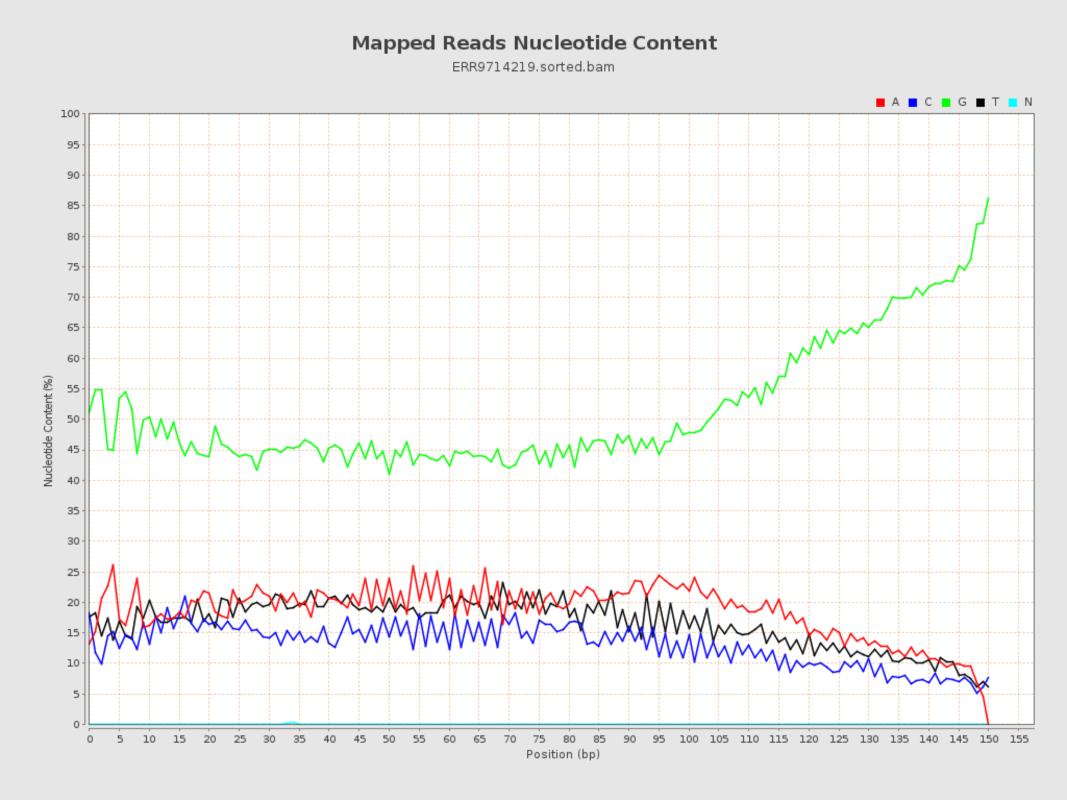
6. Results : Genome Fraction Coverage



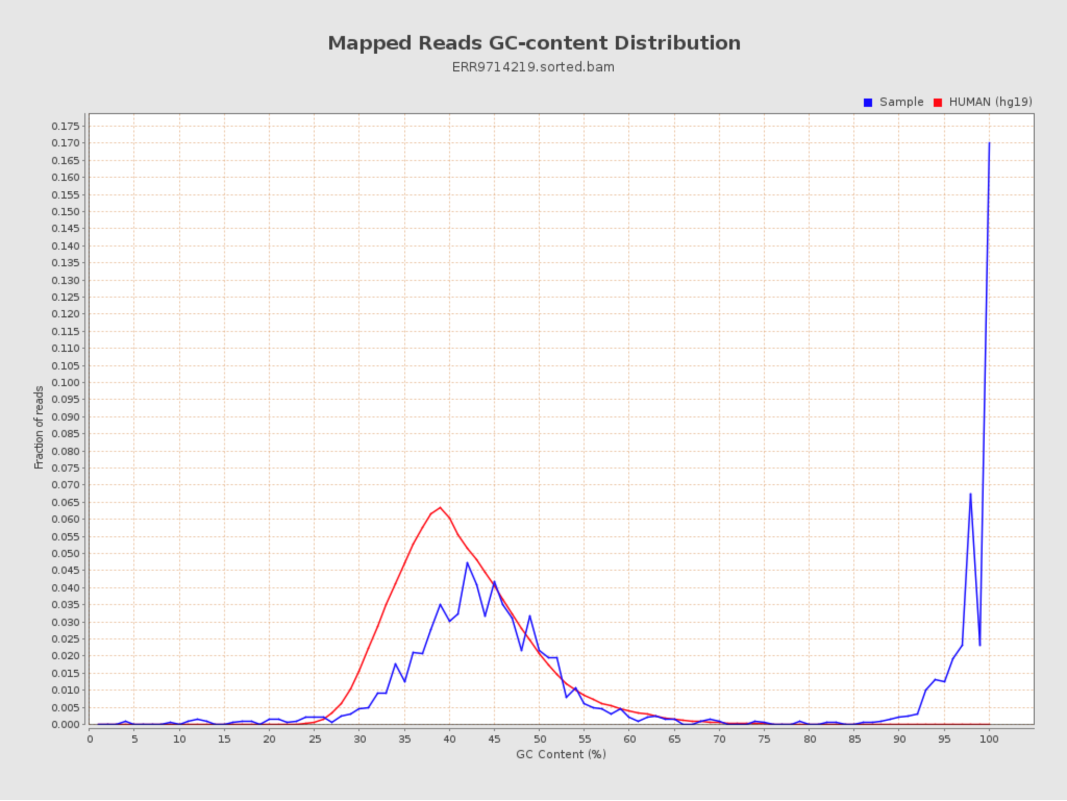
7. Results : Duplication Rate Histogram



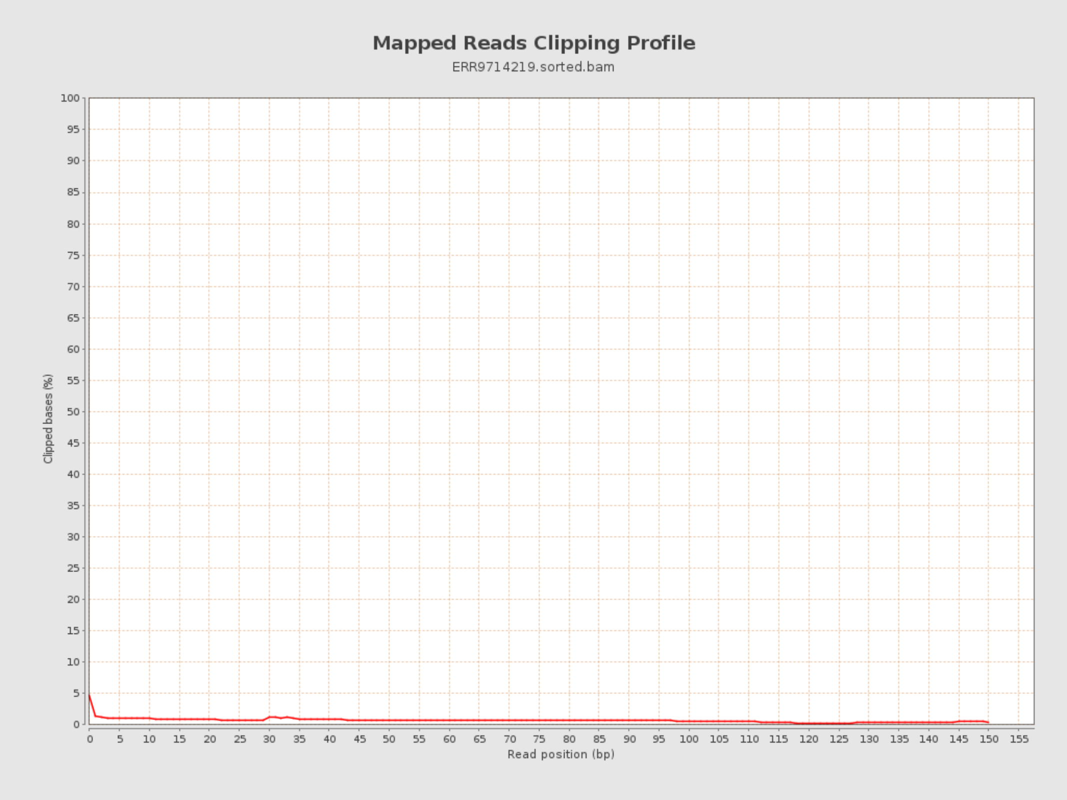
8. Results : Mapped Reads Nucleotide Content



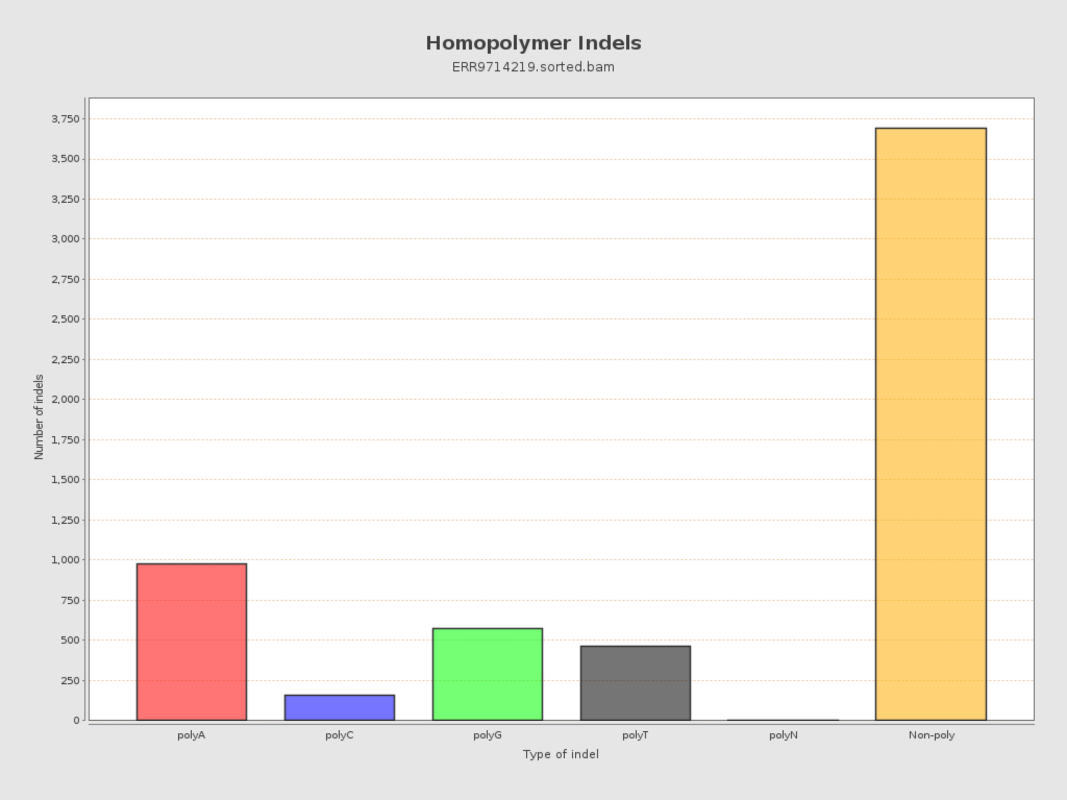
9. Results : Mapped Reads GC-content Distribution



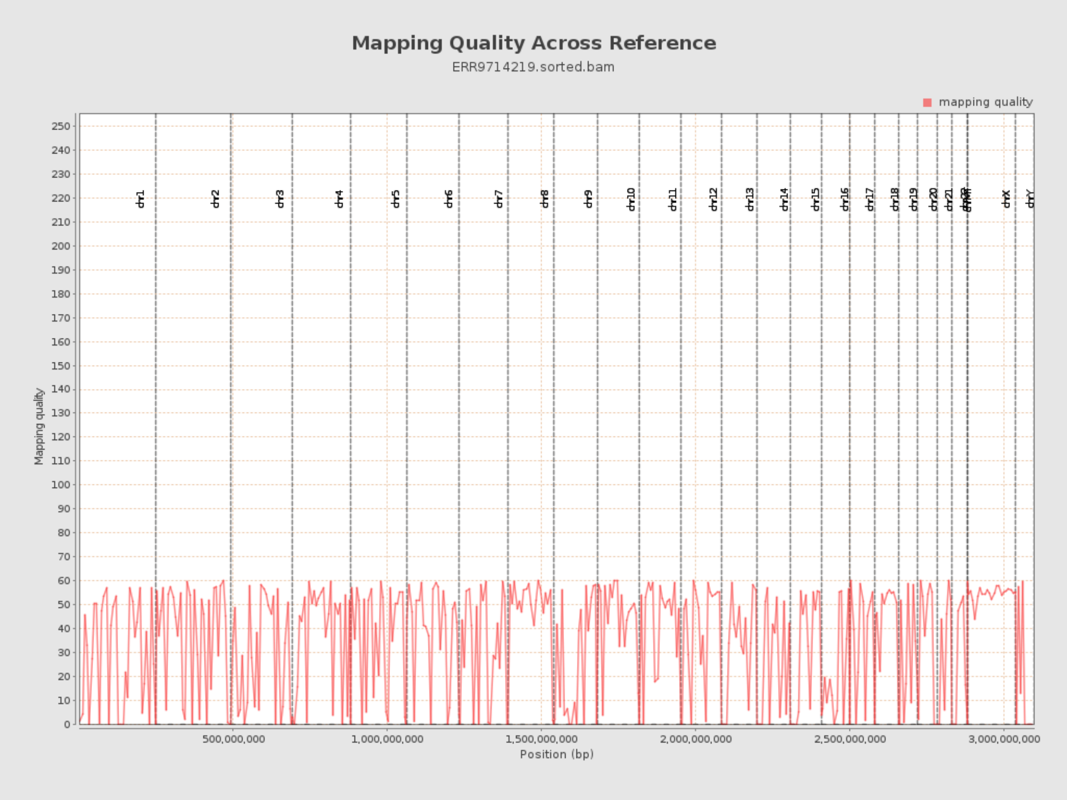
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram