Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:37:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714167.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_ERR9714167 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:37:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	841,976
Mapped reads	765,122 / 90.87%
Unmapped reads	76,854 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,820 / 1.29%
Read min/max/mean length	30 / 151 / 143.09
Duplicated reads (estimated)	752,687 / 89.4%
Duplication rate	36.57%
Clipped reads	698,377 / 82.95%

2.2. ACGT Content

Number/percentage of A's	23,970,245 / 22.81%
Number/percentage of C's	27,107,998 / 25.8%
Number/percentage of T's	22,759,105 / 21.66%
Number/percentage of G's	31,239,383 / 29.73%
Number/percentage of N's	788 / 0%
GC Percentage	55.53%

2.3. Coverage

Mean	0.0348

Standard Deviation	103.5395

2.4. Mapping Quality

Mean Mapping Quality	24.41

2.5. Mismatches and indels

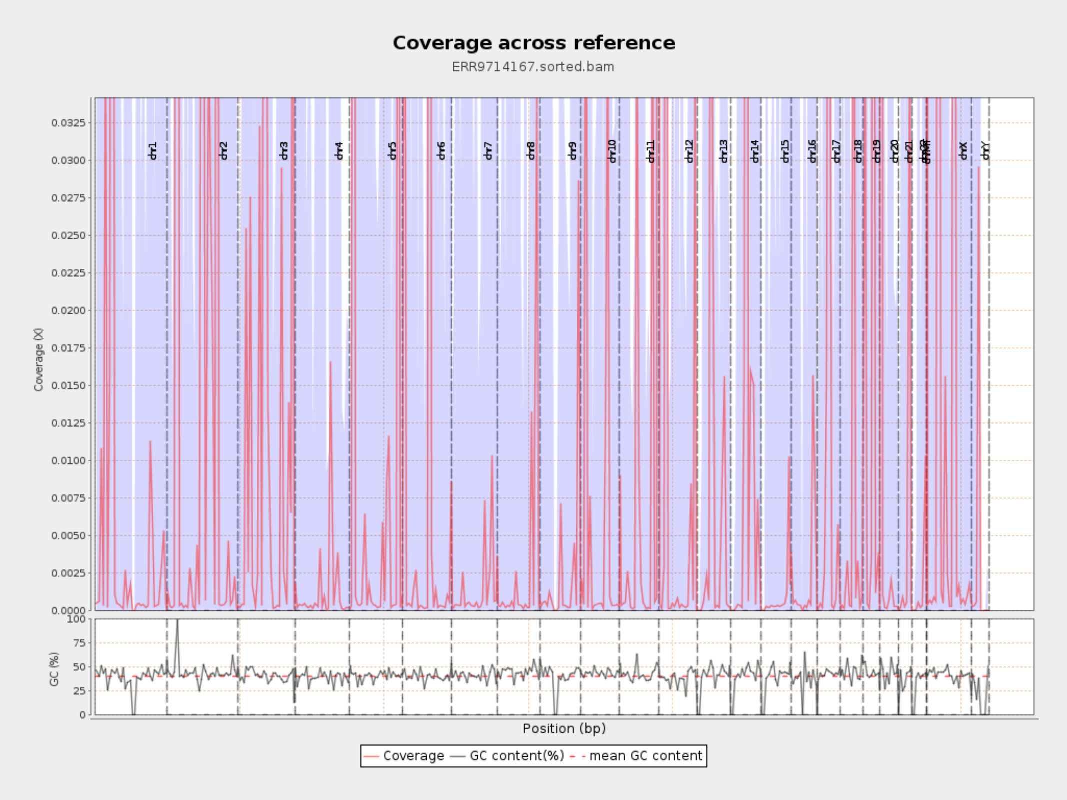
General error rate	3.97%
Mismatches	4,130,852
Insertions	39,367
Mapped reads with at least one insertion	5%
Deletions	554,114
Mapped reads with at least one deletion	71.09%
Homopolymer indels	7.62%

2.6. Chromosome stats

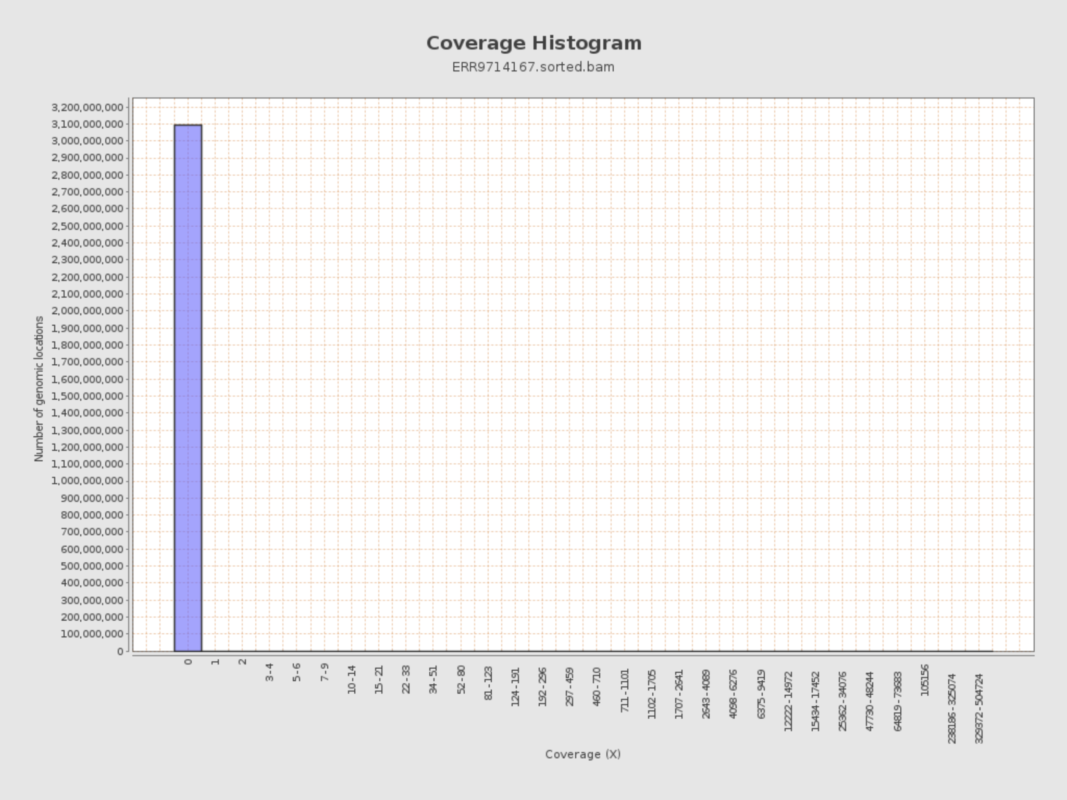
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1738808	0.007	3.0998
chr2	243199373	4068594	0.0167	8.0414
chr3	198022430	2772975	0.014	4.2548
chr4	191154276	261643	0.0014	0.5629
chr5	180915260	2036614	0.0113	7.2016
chr6	171115067	1685328	0.0098	3.7427
chr7	159138663	227476	0.0014	0.5598

chr8	146364022	425871	0.0029	1.1506
chr9	141213431	368301	0.0026	1.1245
chr10	135534747	938053	0.0069	3.1224
chr11	135006516	4679923	0.0347	27.0811
chr12	133851895	1174180	0.0088	4.5149
chr13	115169878	935508	0.0081	4.1766
chr14	107349540	1976520	0.0184	5.5689
chr15	102531392	114013	0.0011	0.5148
chr16	90354753	198222	0.0022	0.7718
chr17	81195210	790479	0.0097	5.1299
chr18	78077248	550887	0.0071	4.1112
chr19	59128983	1169388	0.0198	8.9449
chr20	63025520	78780046	1.25	723.945
chr21	48129895	323667	0.0067	2.3422
chr22	51304566	88955	0.0017	0.8147
chrMT	16571	329075	19.8585	168.0936
chrX	155270560	1834232	0.0118	5.1735
chrY	59373566	237406	0.004	1.2609

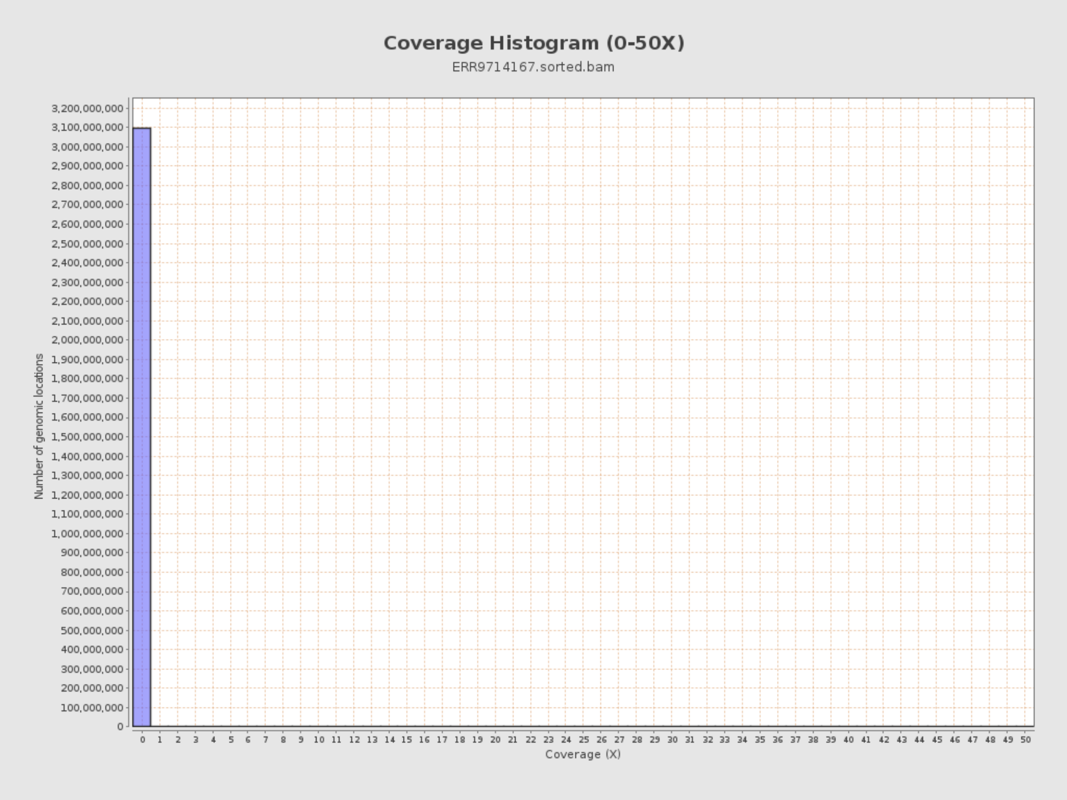
3. Results : Coverage across reference



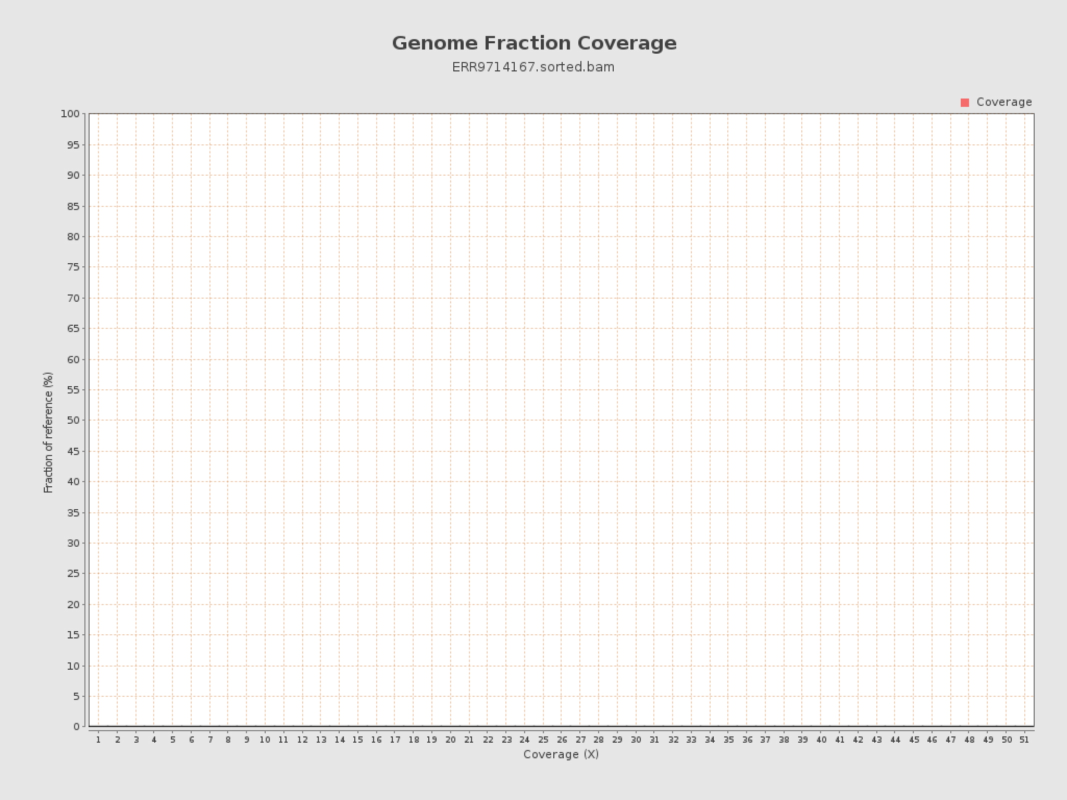
4. Results : Coverage Histogram



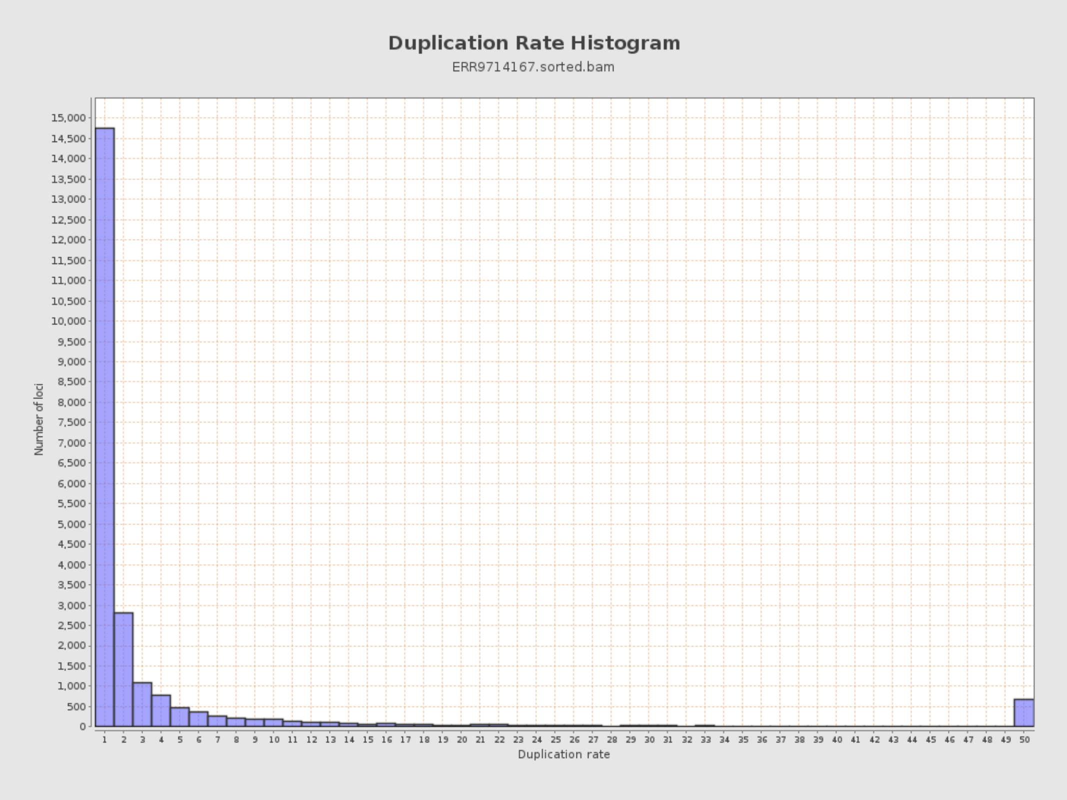
5. Results : Coverage Histogram (0-50X)



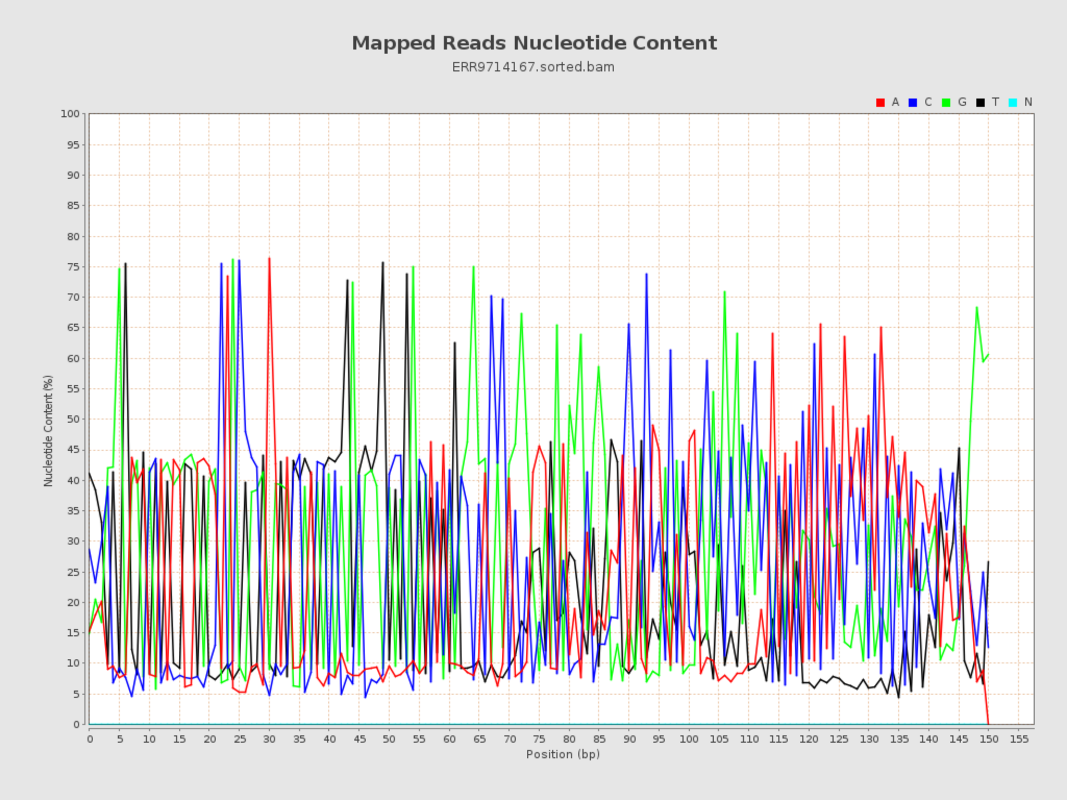
6. Results : Genome Fraction Coverage



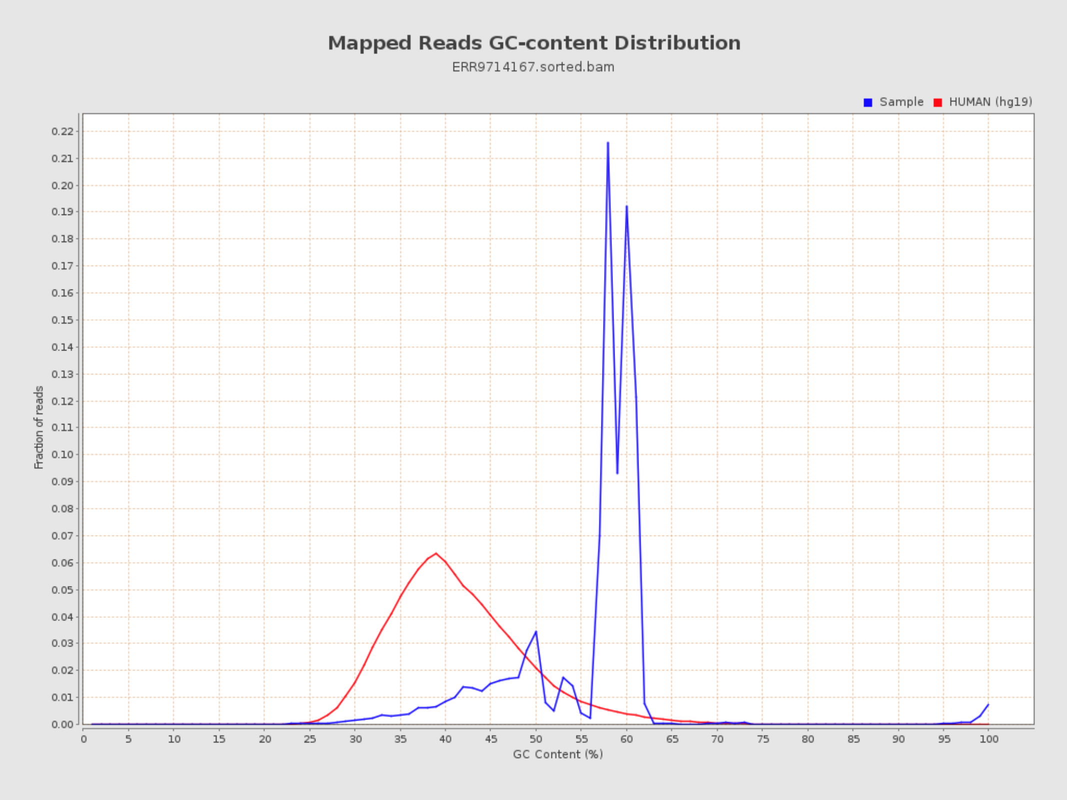
7. Results : Duplication Rate Histogram



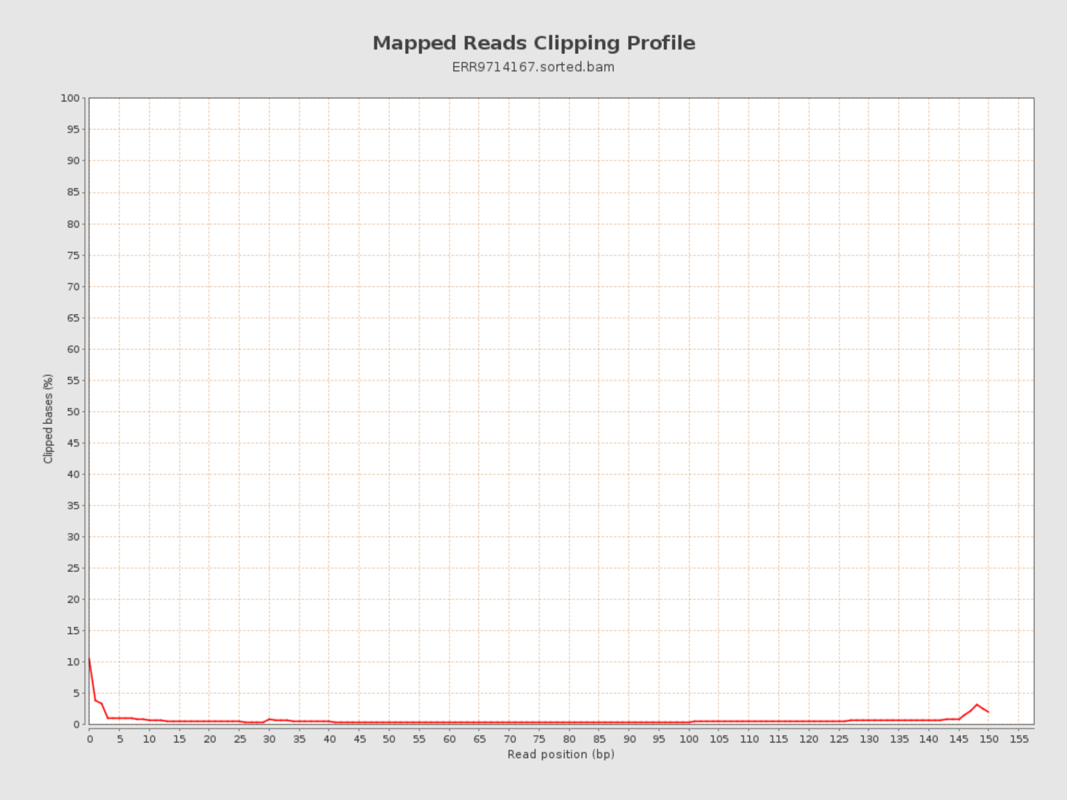
8. Results : Mapped Reads Nucleotide Content



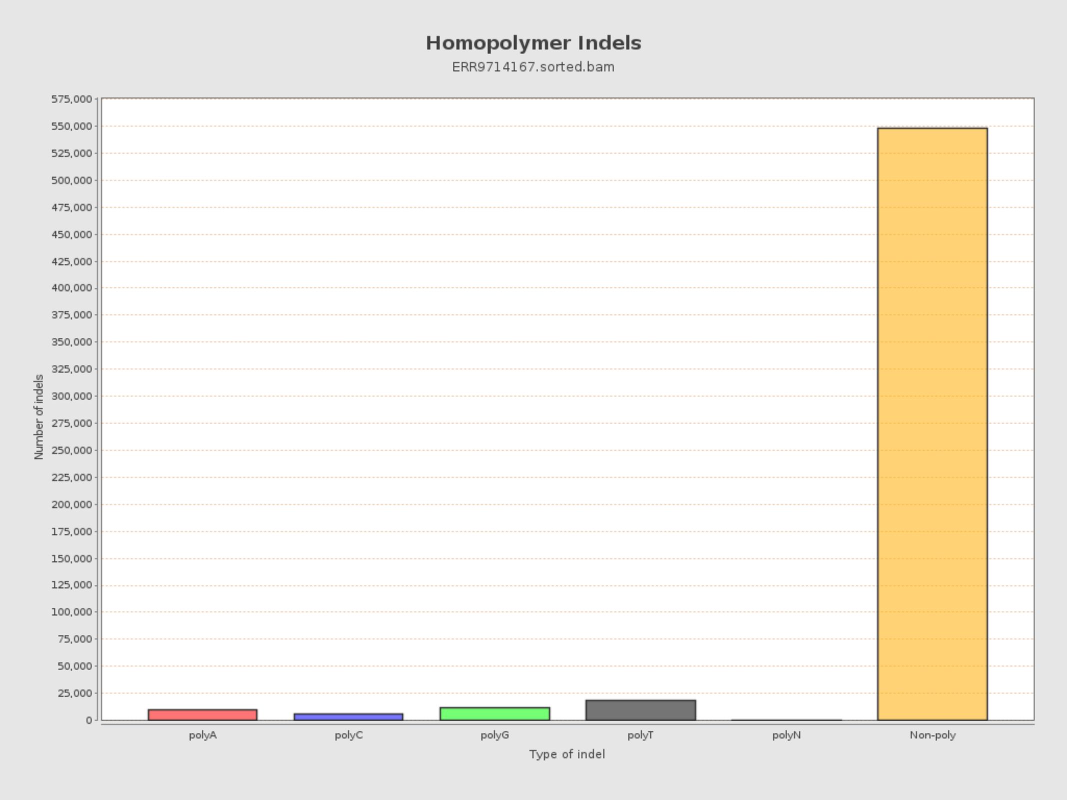
9. Results : Mapped Reads GC-content Distribution



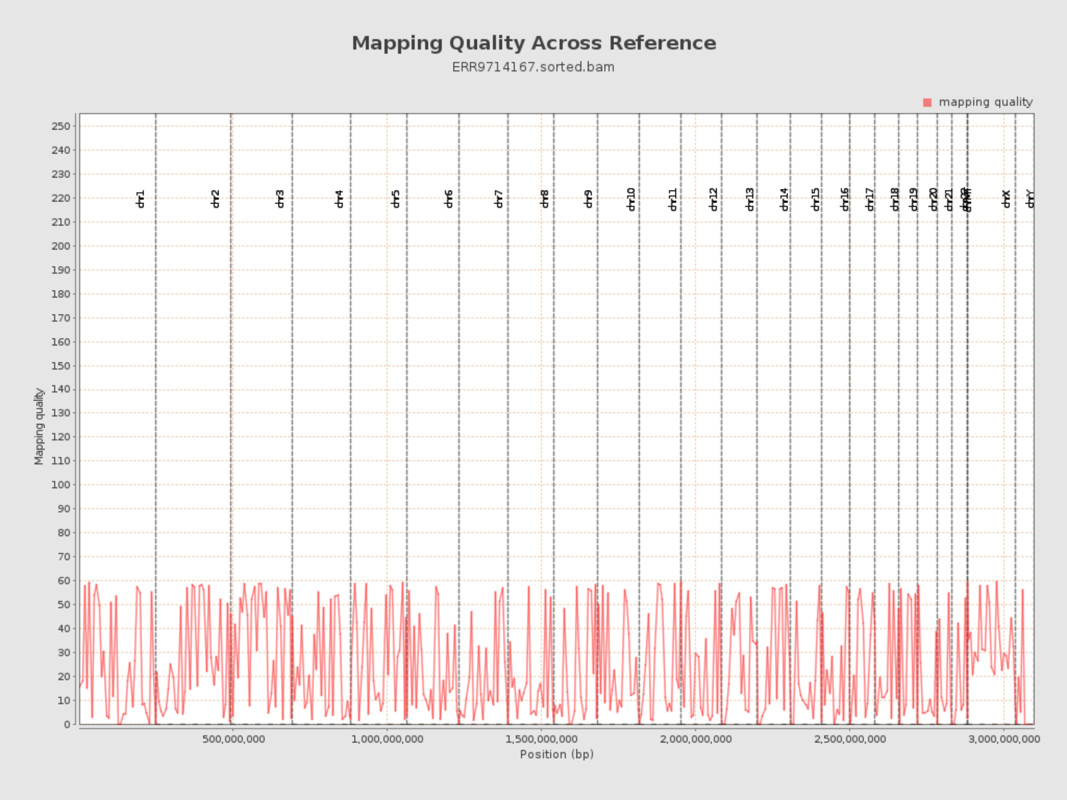
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram