Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:51:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714232.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_ERR9714232 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:51:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	269,374
Mapped reads	34,274 / 12.72%
Unmapped reads	235,100 / 87.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,384 / 0.51%
Read min/max/mean length	30 / 151 / 60.38
Duplicated reads (estimated)	33,330 / 12.37%
Duplication rate	27.19%
Clipped reads	18,213 / 6.76%

2.2. ACGT Content

Number/percentage of A's	127,535 / 3.48%
Number/percentage of C's	43,458 / 1.19%
Number/percentage of T's	55,356 / 1.51%
Number/percentage of G's	3,435,398 / 93.82%
Number/percentage of N's	48 / 0%
GC Percentage	95%

2.3. Coverage

Mean	0.0012

Standard Deviation	4.2517

2.4. Mapping Quality

Mean Mapping Quality	9.77

2.5. Mismatches and indels

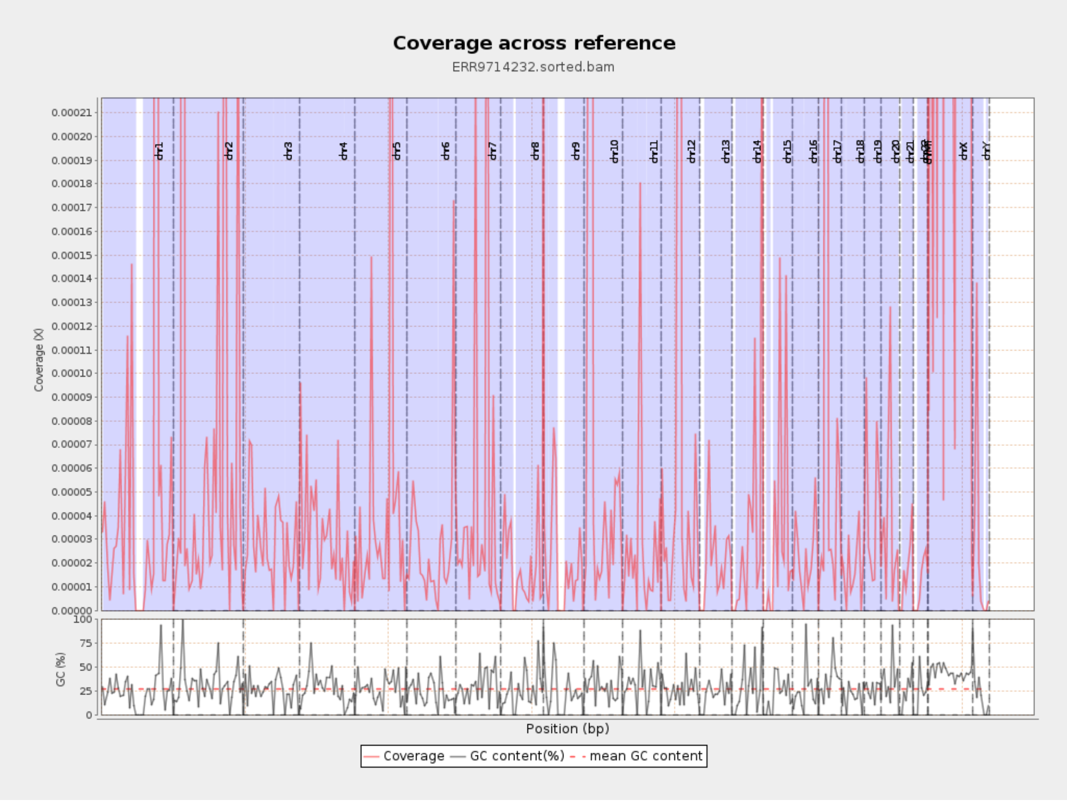
General error rate	3.63%
Mismatches	94,629
Insertions	5,035
Mapped reads with at least one insertion	9.6%
Deletions	2,176
Mapped reads with at least one deletion	6.07%
Homopolymer indels	68.63%

2.6. Chromosome stats

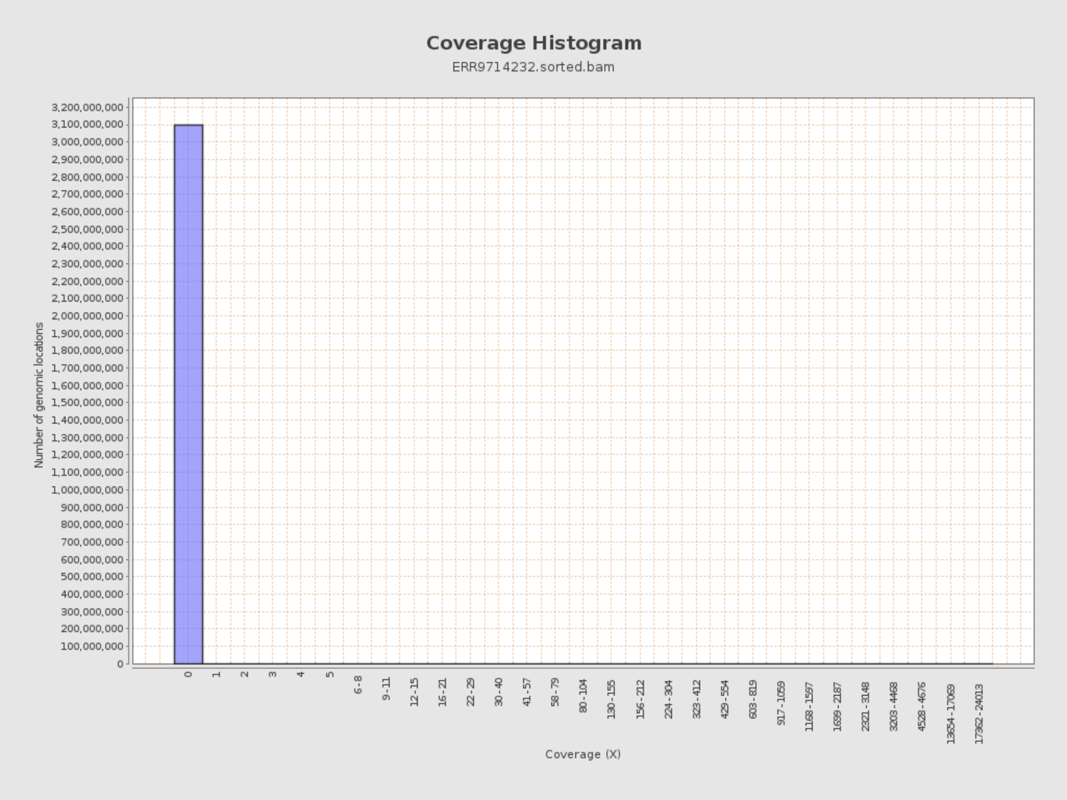
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16615	0.0001	0.1032
chr2	243199373	3439950	0.0141	15.1676
chr3	198022430	5649	0	0.0092
chr4	191154276	5782	0	0.0101
chr5	180915260	9012	0	0.024
chr6	171115067	4834	0	0.0112
chr7	159138663	8715	0.0001	0.045

chr8	146364022	2633	0	0.0059
chr9	141213431	2948	0	0.0091
chr10	135534747	14323	0.0001	0.1162
chr11	135006516	3648	0	0.0176
chr12	133851895	12956	0.0001	0.0707
chr13	115169878	2321	0	0.0049
chr14	107349540	4902	0	0.0389
chr15	102531392	3396	0	0.0158
chr16	90354753	2109	0	0.0065
chr17	81195210	8397	0.0001	0.1028
chr18	78077248	1366	0	0.0044
chr19	59128983	2429	0	0.0145
chr20	63025520	2424	0	0.0148
chr21	48129895	779	0	0.0048
chr22	51304566	575	0	0.0033
chrMT	16571	1180	0.0712	0.4301
chrX	155270560	113685	0.0007	0.1557
chrY	59373566	1623	0	0.0114

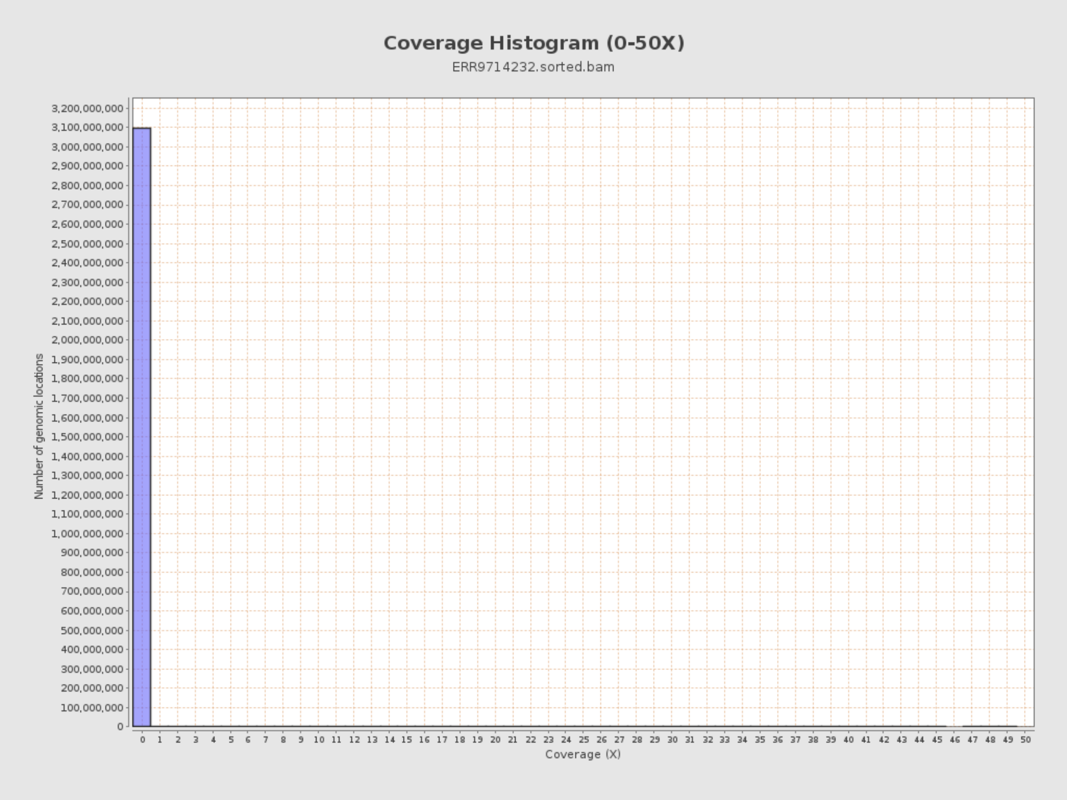
3. Results : Coverage across reference



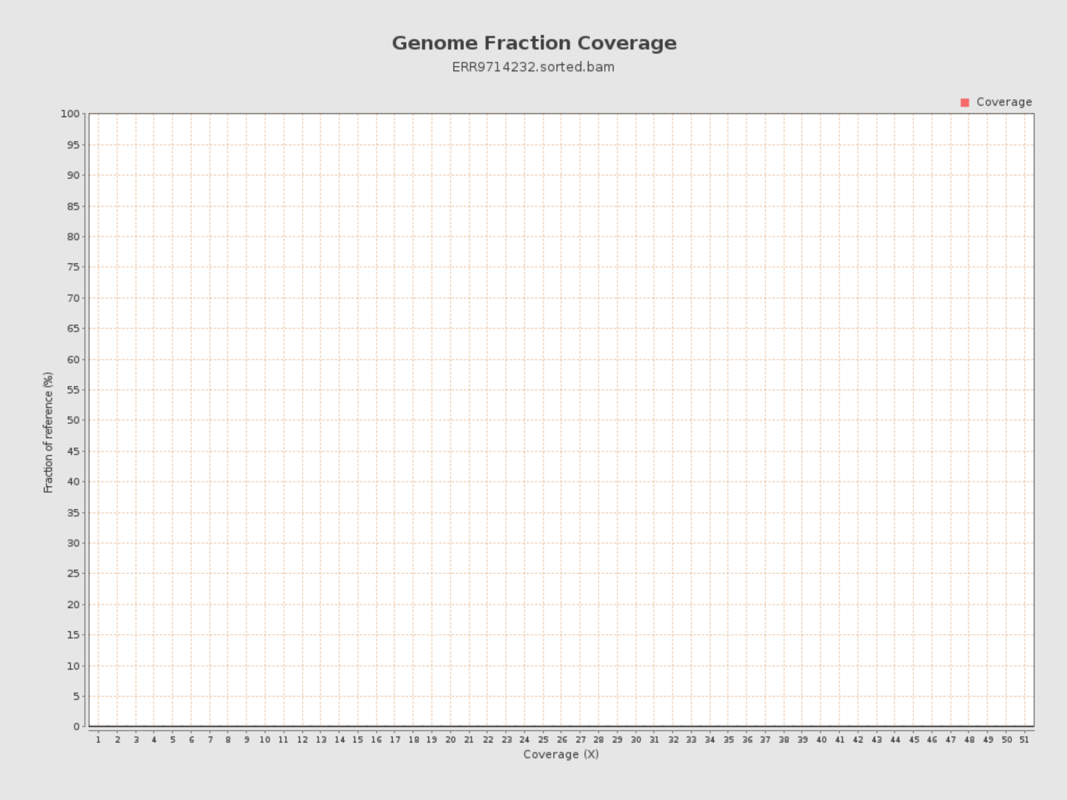
4. Results : Coverage Histogram



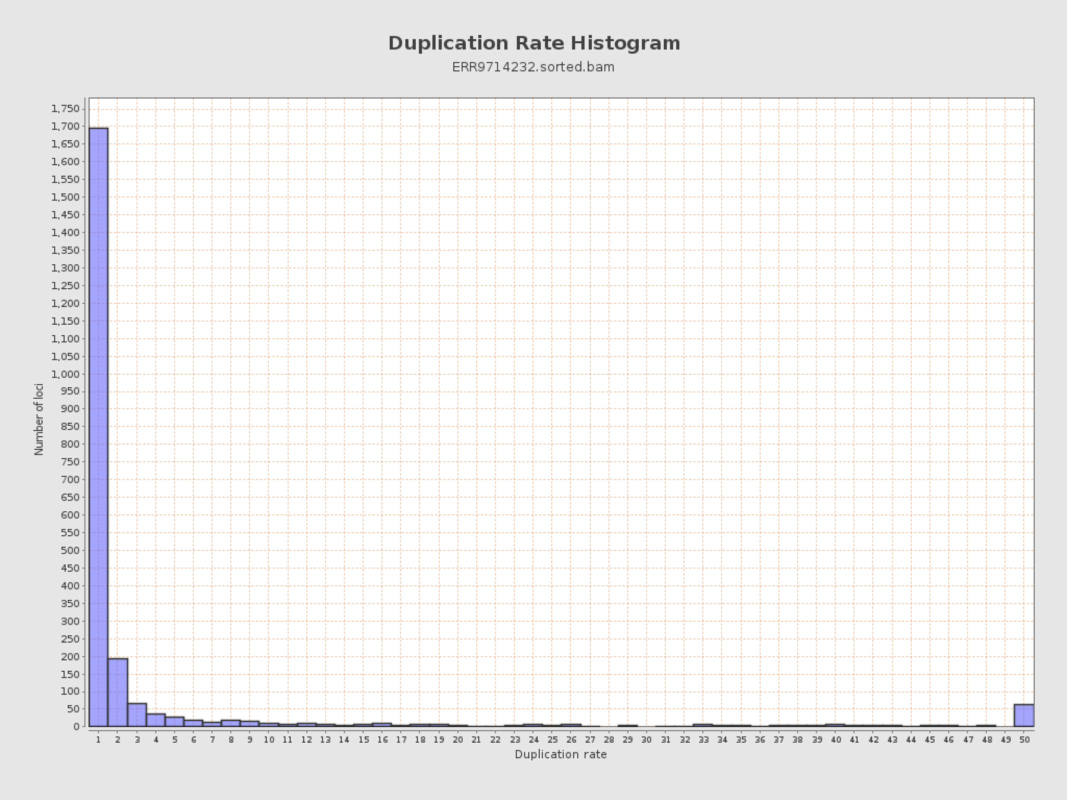
5. Results : Coverage Histogram (0-50X)



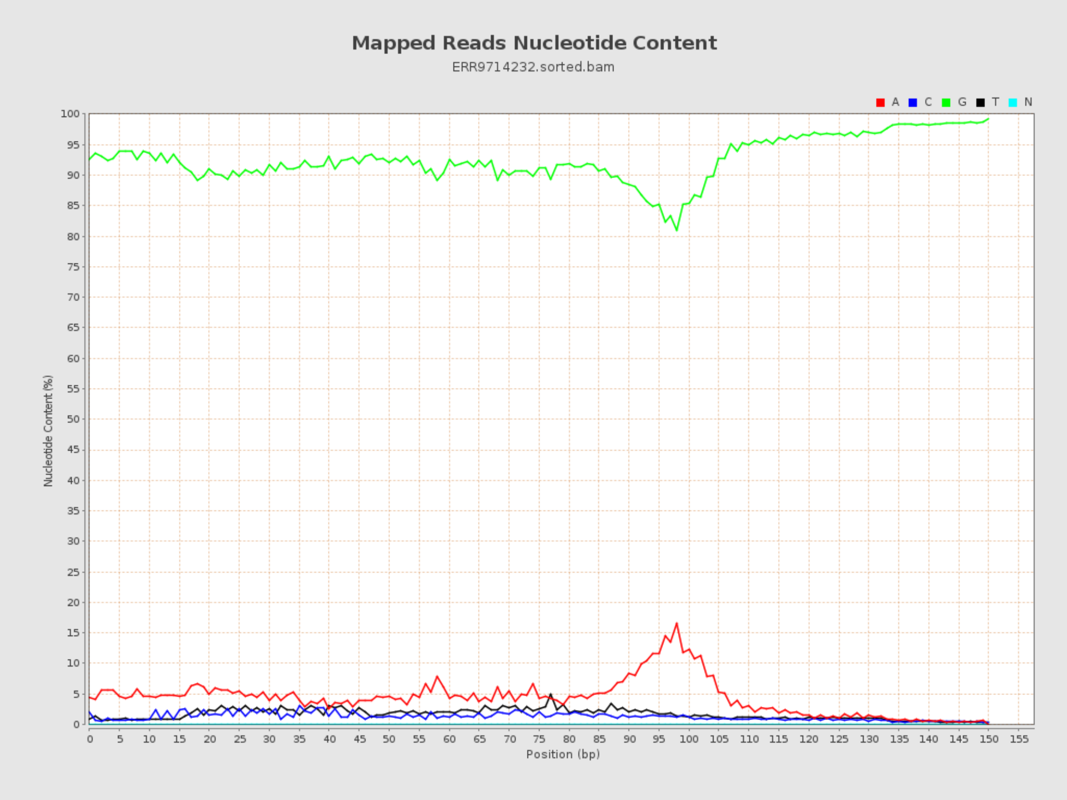
6. Results : Genome Fraction Coverage



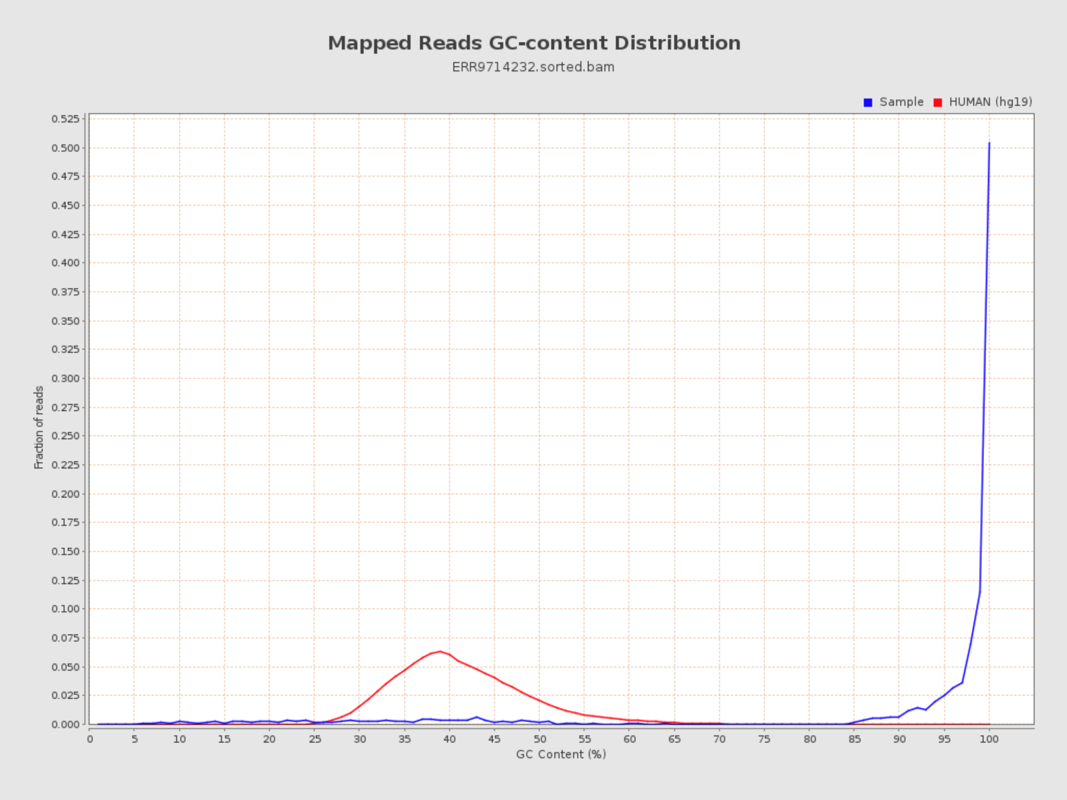
7. Results : Duplication Rate Histogram



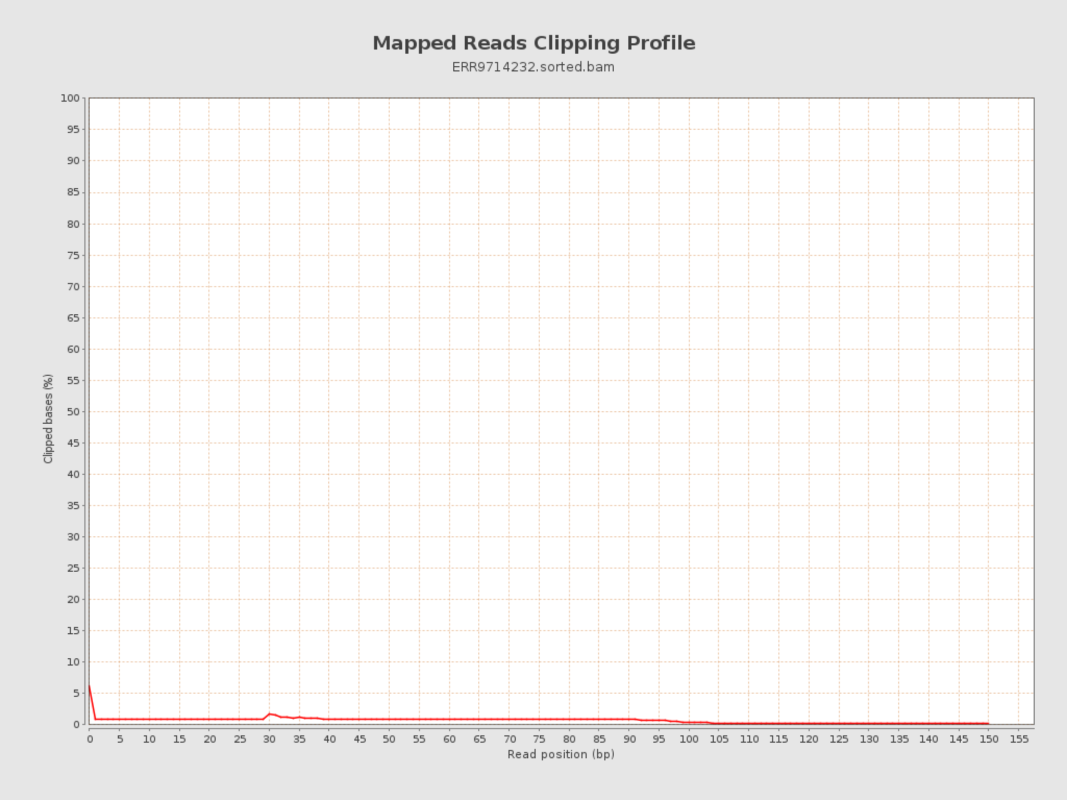
8. Results : Mapped Reads Nucleotide Content



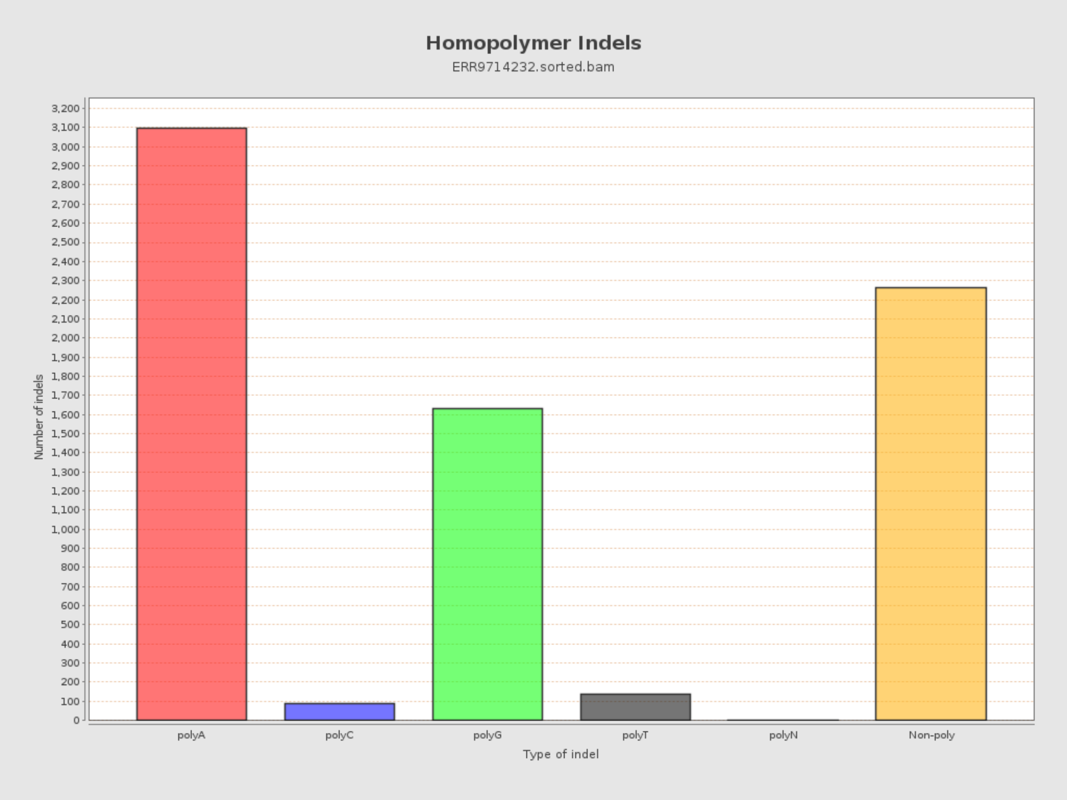
9. Results : Mapped Reads GC-content Distribution



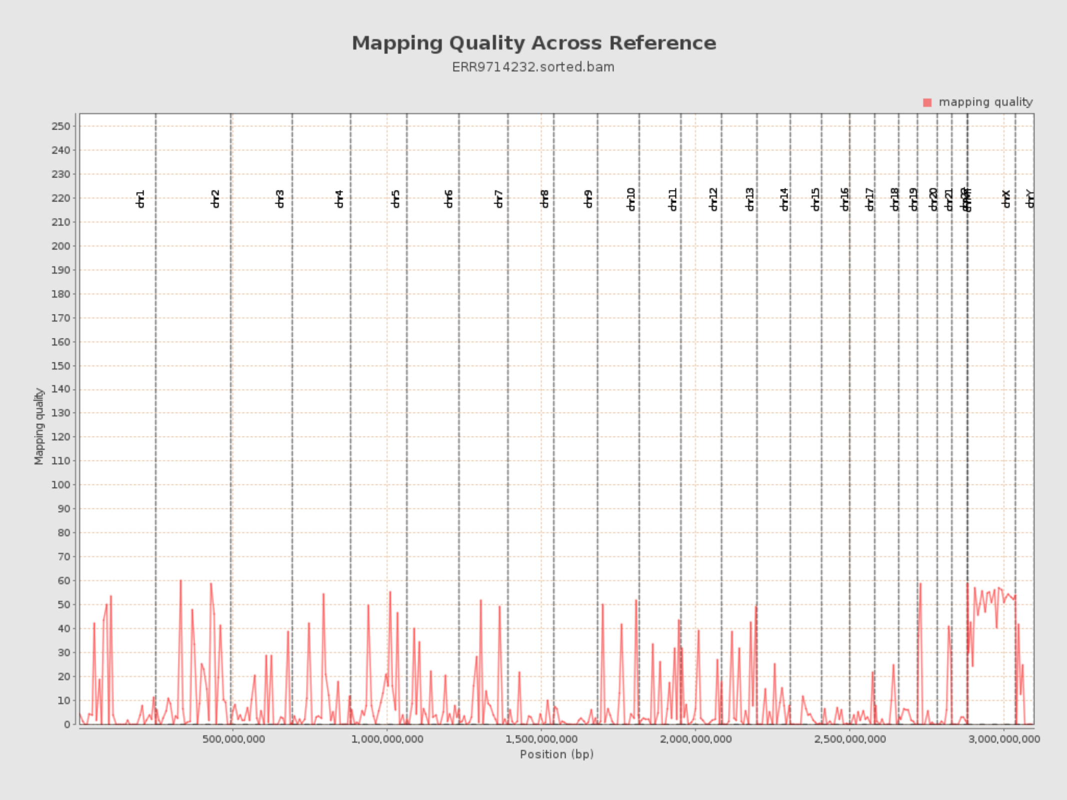
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram