Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:58:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714237.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_ERR9714237 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:58:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	305,844
Mapped reads	28,252 / 9.24%
Unmapped reads	277,592 / 90.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	815 / 0.27%
Read min/max/mean length	30 / 151 / 55.51
Duplicated reads (estimated)	24,507 / 8.01%
Duplication rate	35.64%
Clipped reads	22,321 / 7.3%

2.2. ACGT Content

Number/percentage of A's	444,092 / 15.54%
Number/percentage of C's	311,679 / 10.91%
Number/percentage of T's	415,941 / 14.56%
Number/percentage of G's	1,685,015 / 58.98%
Number/percentage of N's	142 / 0%
GC Percentage	69.89%

2.3. Coverage

Mean	0.0009

Standard Deviation	1.7633

2.4. Mapping Quality

Mean Mapping Quality	35.03

2.5. Mismatches and indels

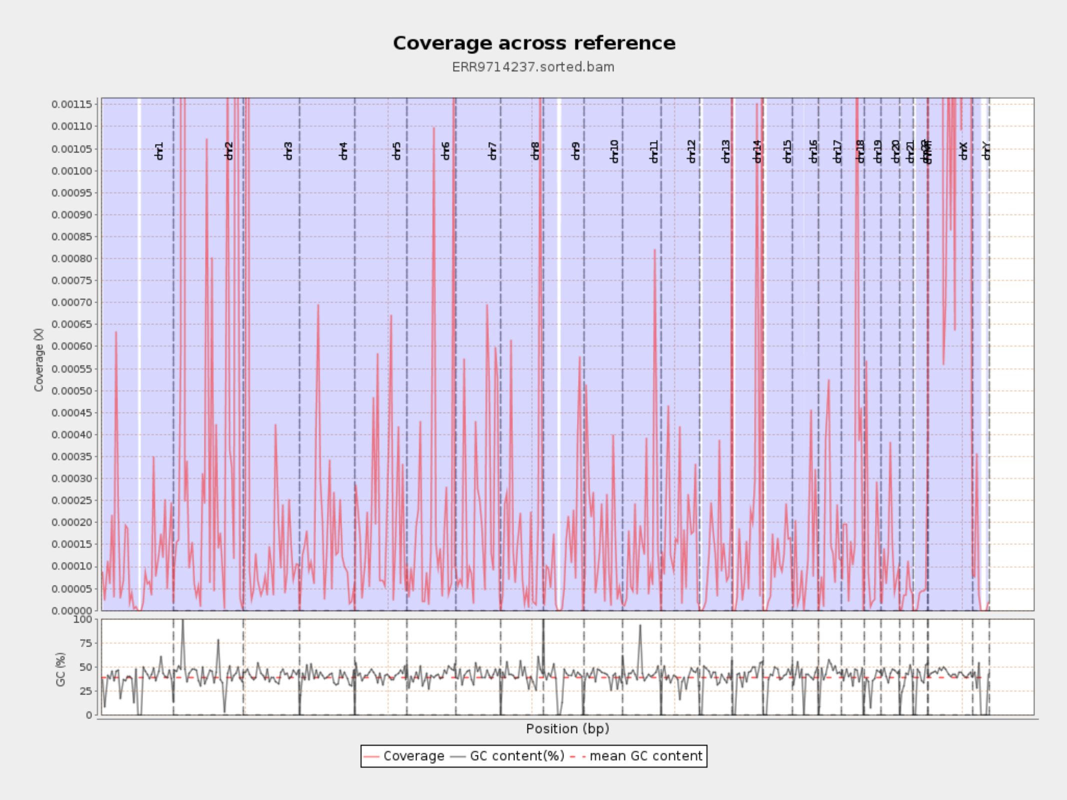
General error rate	3.17%
Mismatches	77,497
Insertions	2,369
Mapped reads with at least one insertion	6.54%
Deletions	4,888
Mapped reads with at least one deletion	16.78%
Homopolymer indels	52.98%

2.6. Chromosome stats

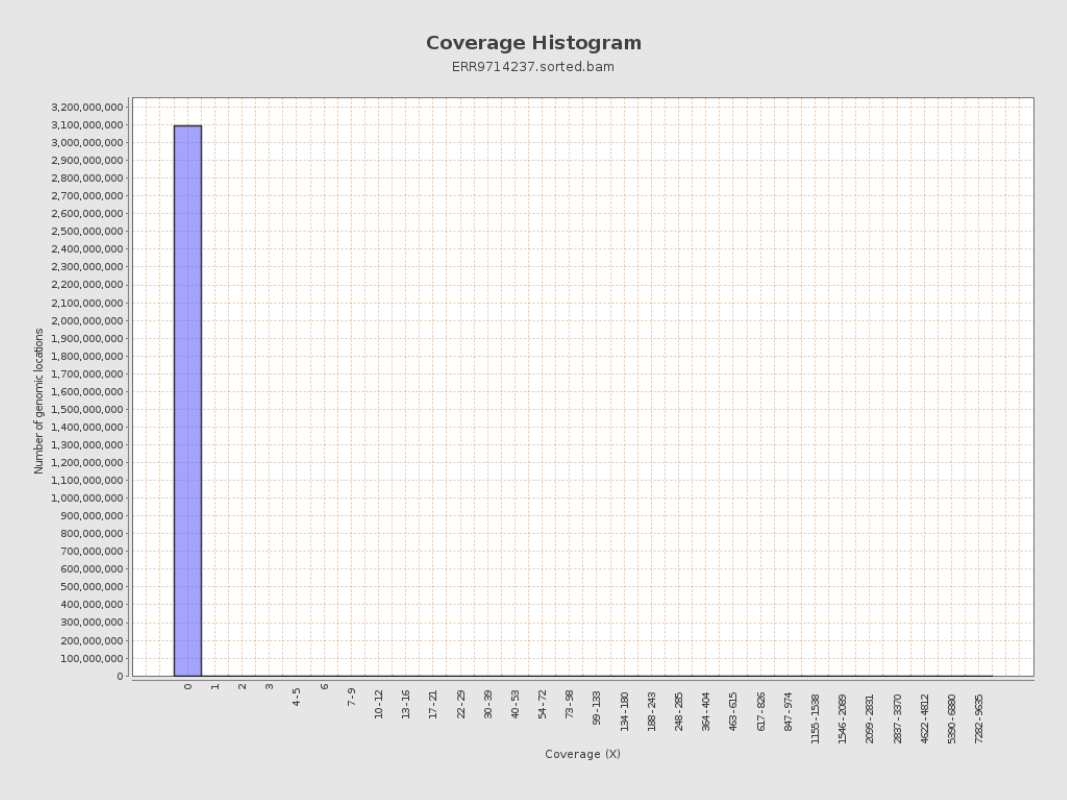
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29119	0.0001	0.0274
chr2	243199373	1455351	0.006	5.8149
chr3	198022430	46087	0.0002	0.1367
chr4	191154276	31765	0.0002	0.0362
chr5	180915260	39965	0.0002	0.0422
chr6	171115067	37185	0.0002	0.0767
chr7	159138663	37637	0.0002	0.0786

chr8	146364022	29169	0.0002	0.0483
chr9	141213431	18536	0.0001	0.0337
chr10	135534747	22351	0.0002	0.0388
chr11	135006516	20675	0.0002	0.047
chr12	133851895	24270	0.0002	0.0417
chr13	115169878	16132	0.0001	0.0348
chr14	107349540	30009	0.0003	0.0998
chr15	102531392	10626	0.0001	0.0165
chr16	90354753	11661	0.0001	0.0265
chr17	81195210	13740	0.0002	0.0546
chr18	78077248	25246	0.0003	0.1186
chr19	59128983	8710	0.0001	0.0336
chr20	63025520	8076	0.0001	0.029
chr21	48129895	2025	0	0.0096
chr22	51304566	2202	0	0.0095
chrMT	16571	560111	33.8007	279.2736
chrX	155270560	391680	0.0025	0.717
chrY	59373566	4206	0.0001	0.0221

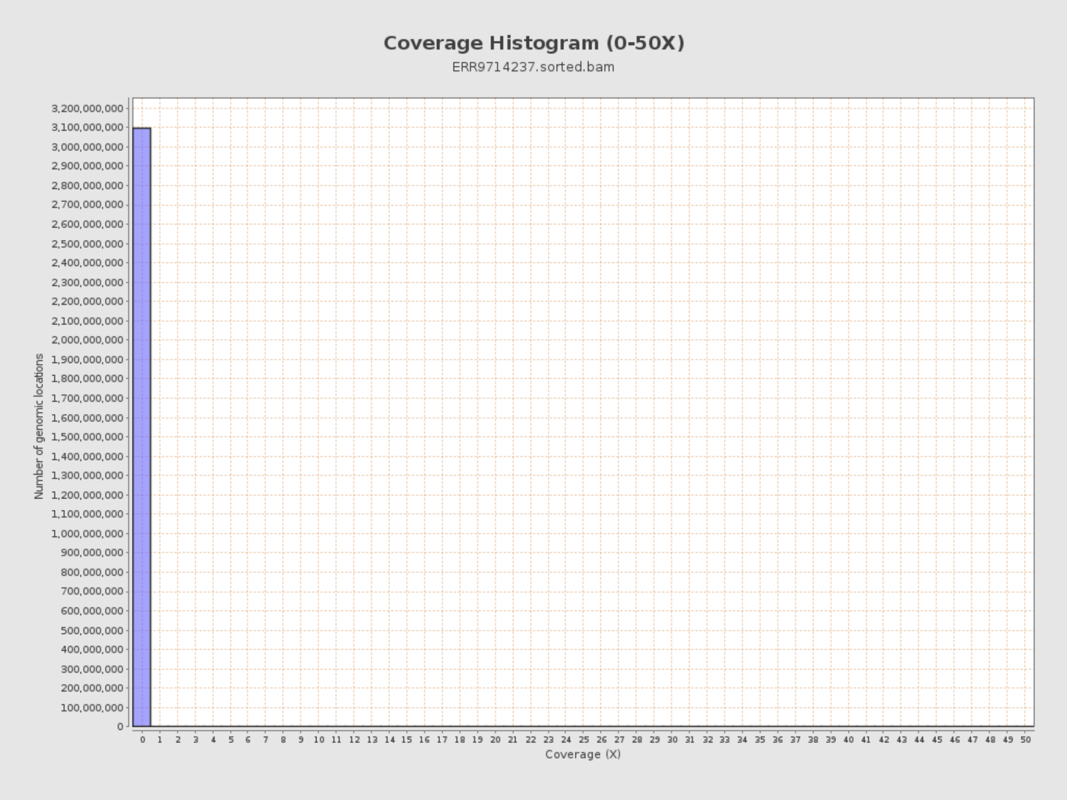
3. Results : Coverage across reference



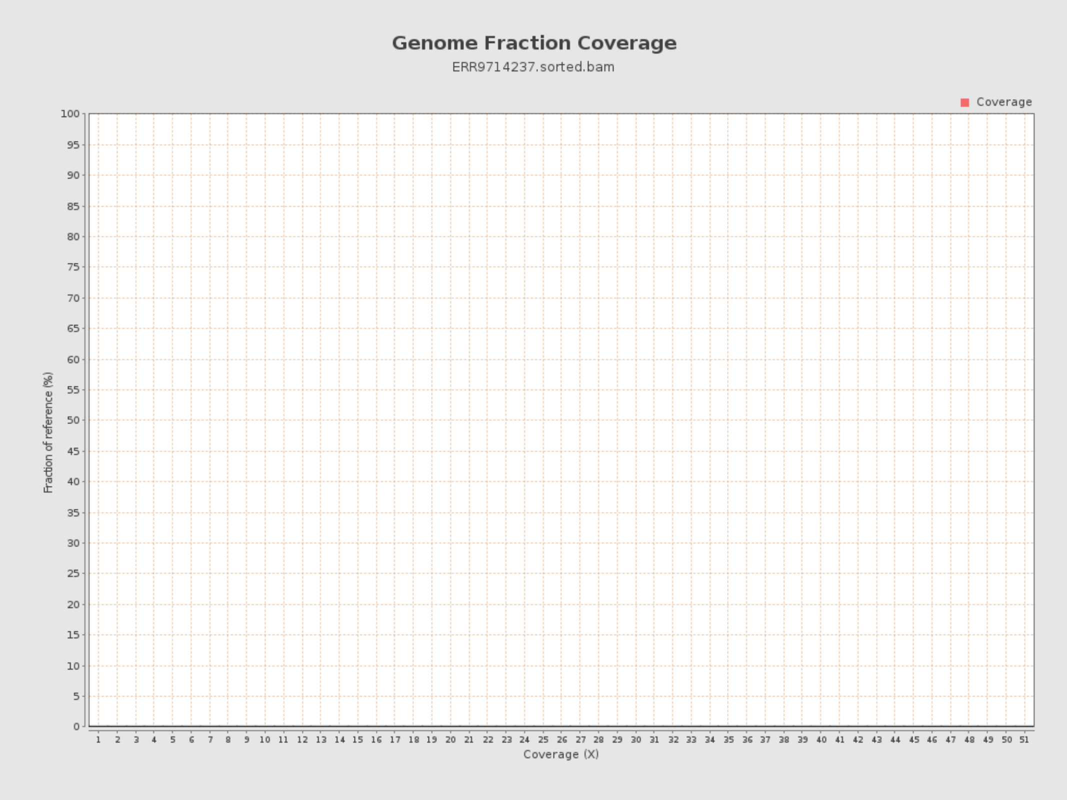
4. Results : Coverage Histogram



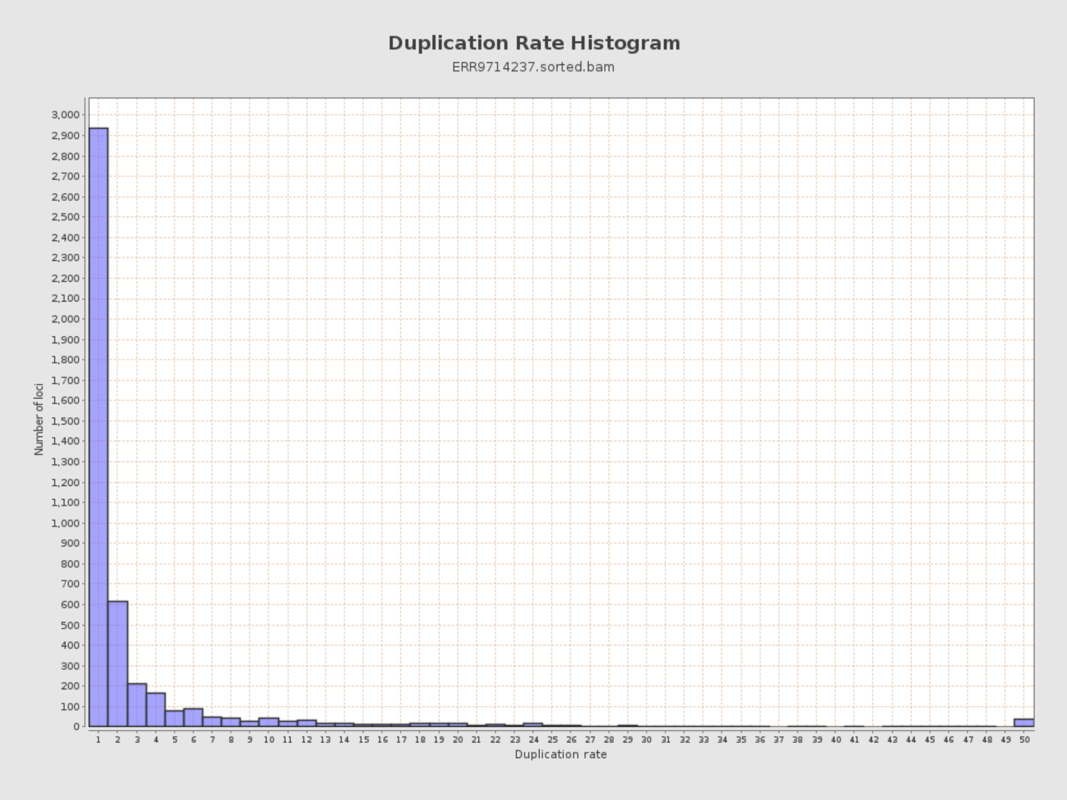
5. Results : Coverage Histogram (0-50X)



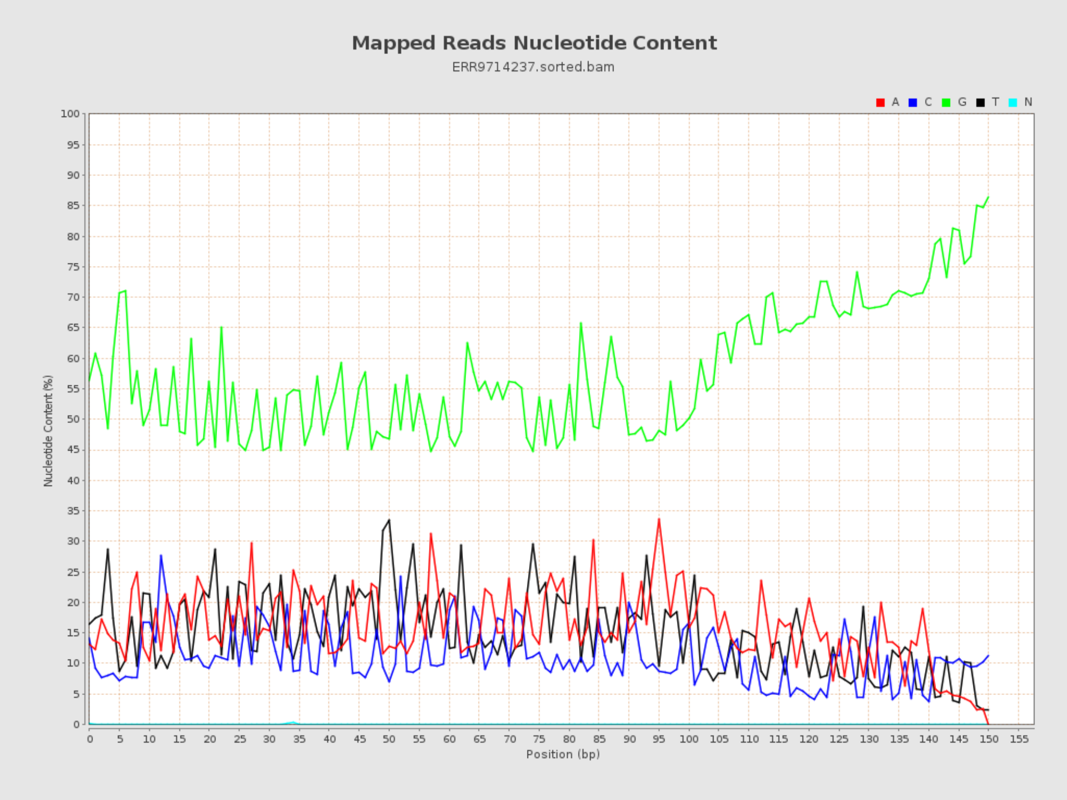
6. Results : Genome Fraction Coverage



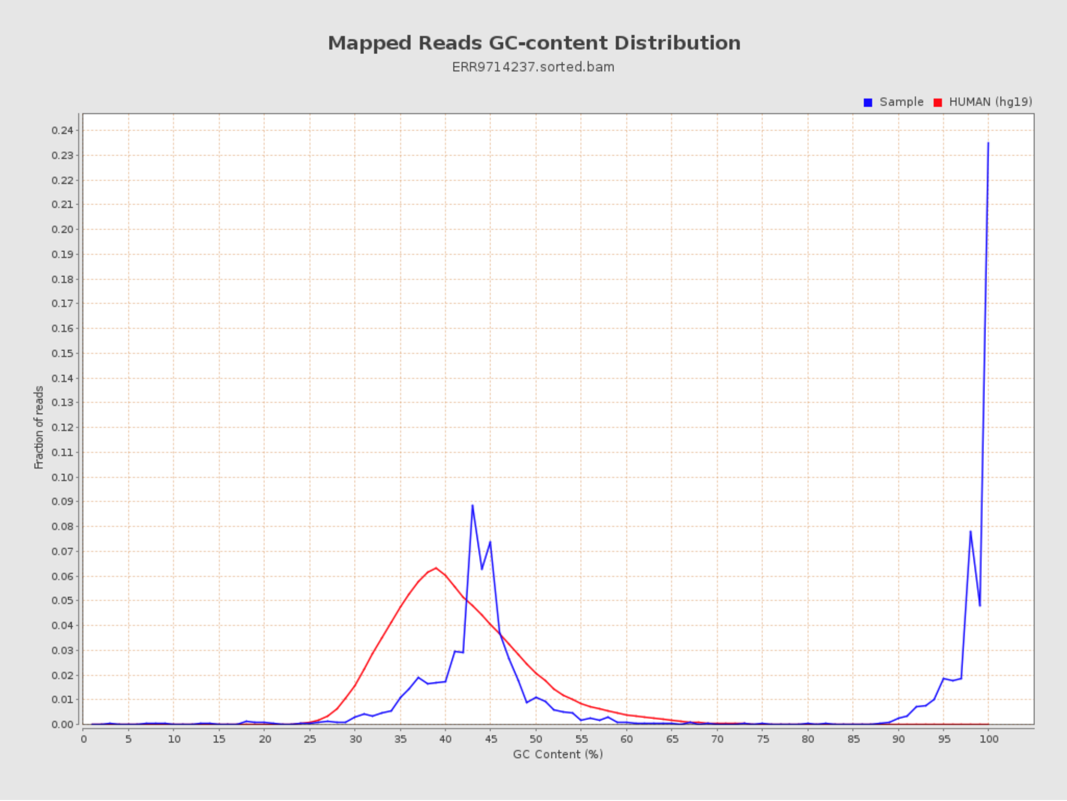
7. Results : Duplication Rate Histogram



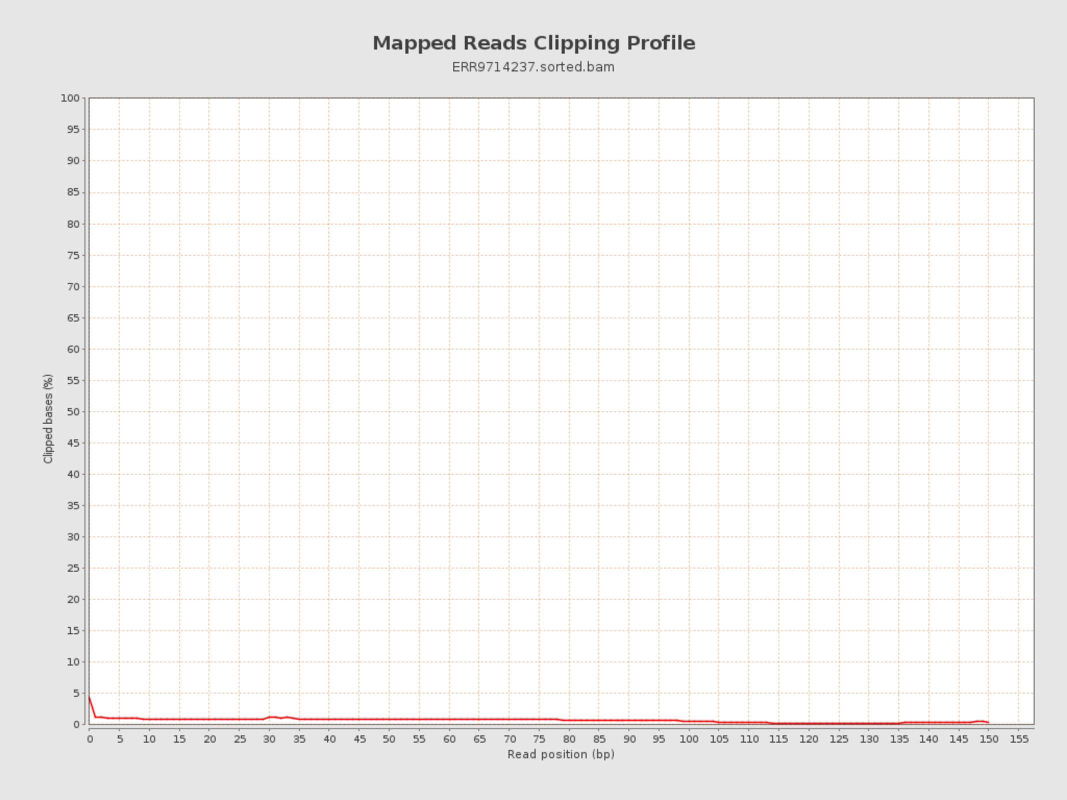
8. Results : Mapped Reads Nucleotide Content



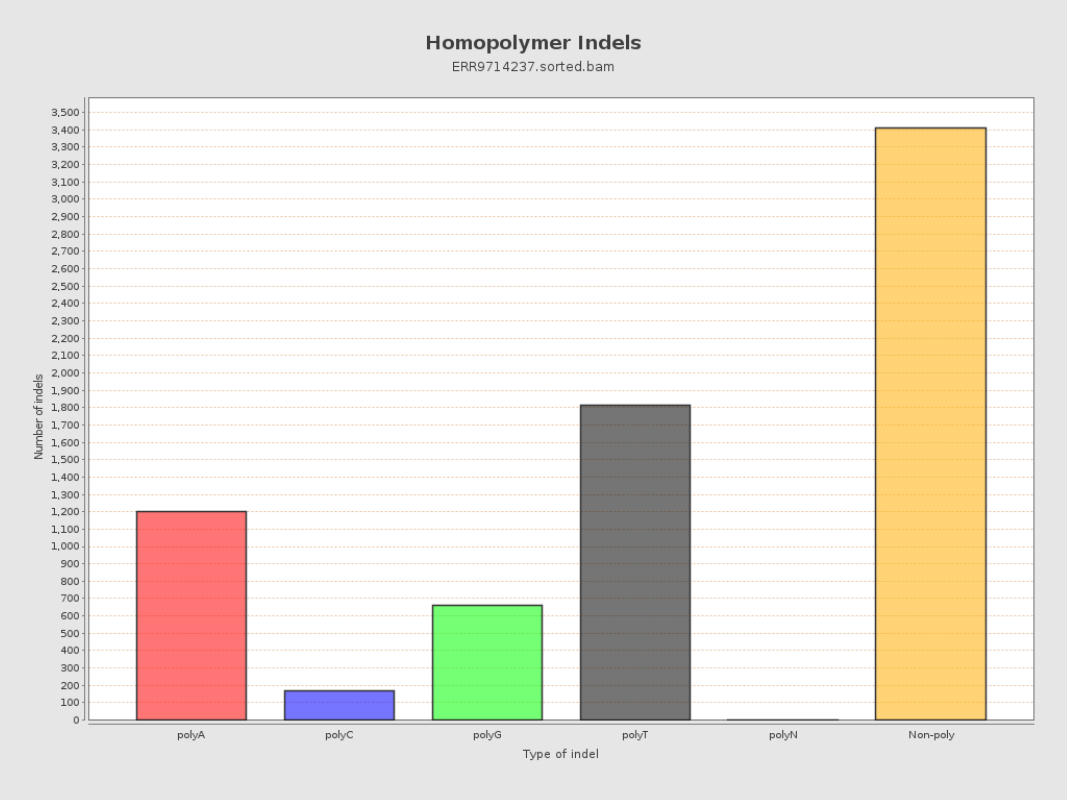
9. Results : Mapped Reads GC-content Distribution



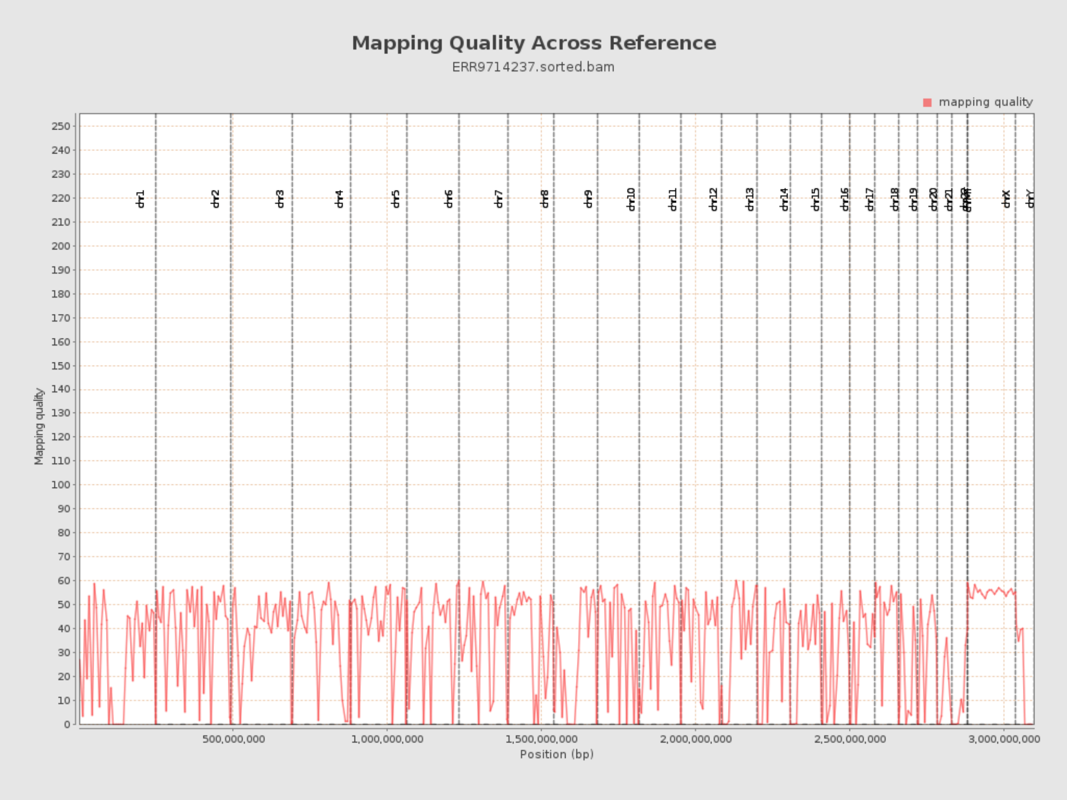
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram