Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:03:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714115.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_ERR9714115 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:03:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	585,478
Mapped reads	520,072 / 88.83%
Unmapped reads	65,406 / 11.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,011 / 2.22%
Read min/max/mean length	30 / 151 / 138.36
Duplicated reads (estimated)	466,435 / 79.67%
Duplication rate	44.52%
Clipped reads	490,924 / 83.85%

2.2. ACGT Content

Number/percentage of A's	17,595,070 / 26.41%
Number/percentage of C's	15,200,931 / 22.81%
Number/percentage of T's	16,761,644 / 25.16%
Number/percentage of G's	17,072,485 / 25.62%
Number/percentage of N's	519 / 0%
GC Percentage	48.44%

2.3. Coverage

Mean	0.0221

Standard Deviation	7.233

2.4. Mapping Quality

Mean Mapping Quality	51.6

2.5. Mismatches and indels

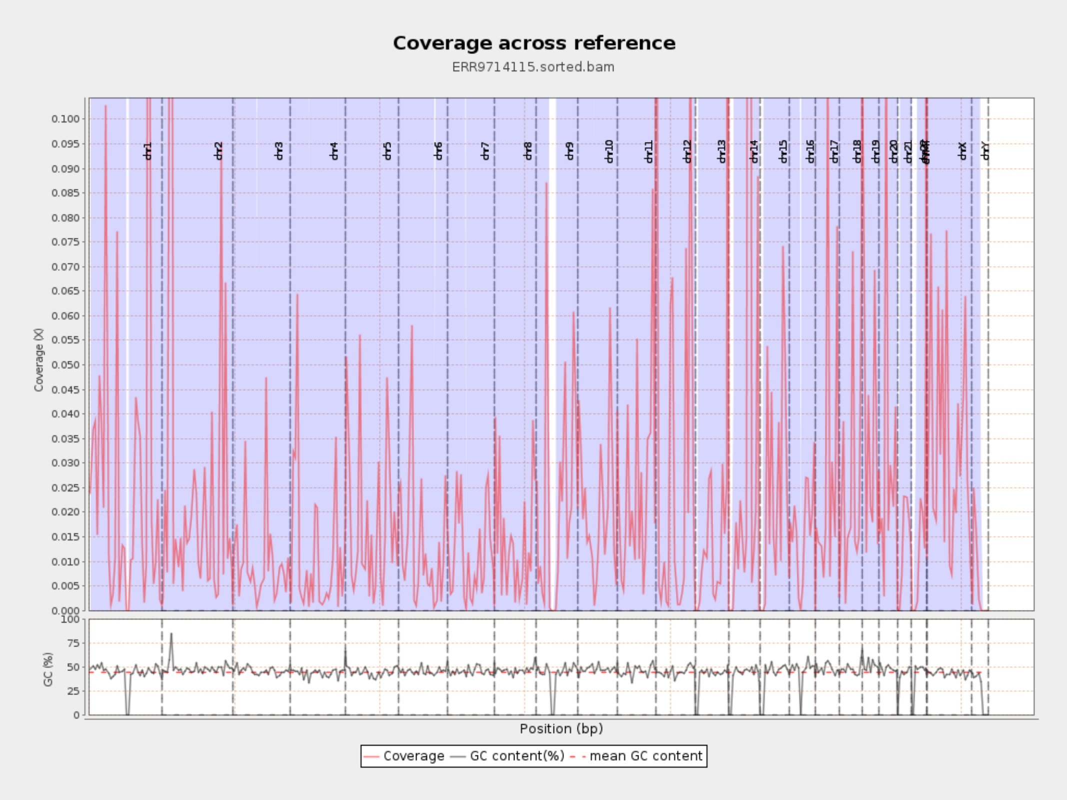
General error rate	4.58%
Mismatches	2,898,138
Insertions	65,417
Mapped reads with at least one insertion	12.14%
Deletions	270,740
Mapped reads with at least one deletion	49.44%
Homopolymer indels	28.43%

2.6. Chromosome stats

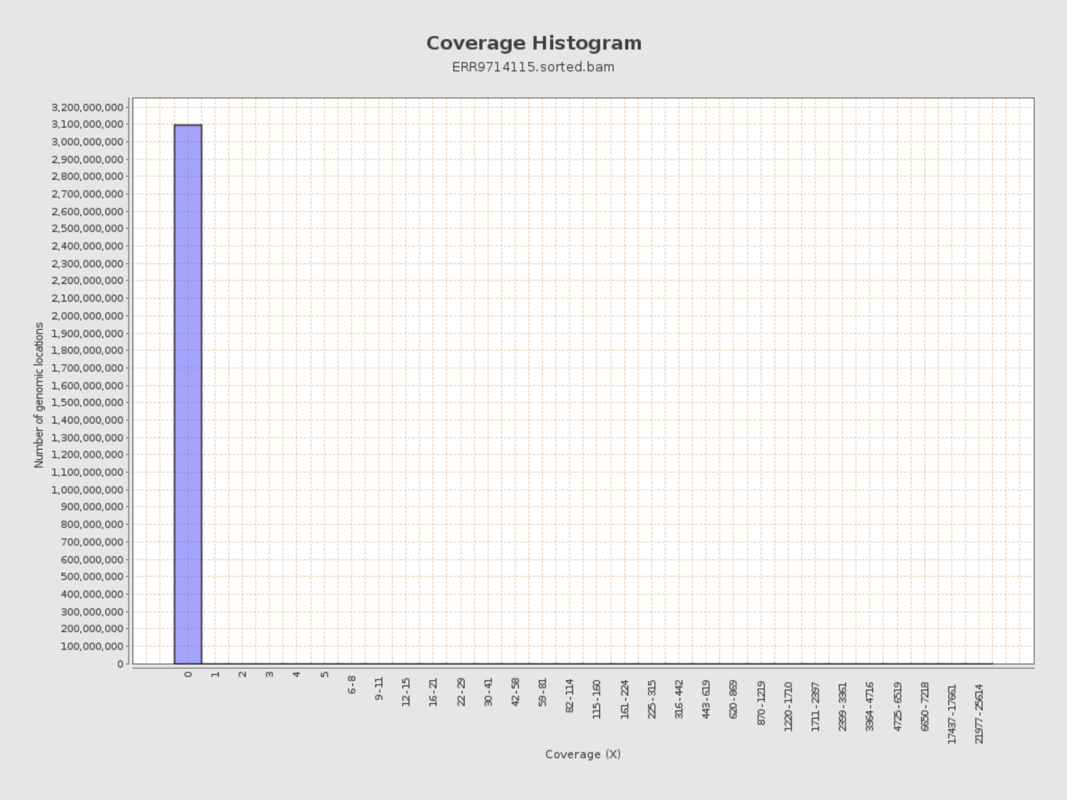
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6851019	0.0275	7.2339
chr2	243199373	6672323	0.0274	7.9442
chr3	198022430	1992302	0.0101	1.6678
chr4	191154276	2215468	0.0116	2.7147
chr5	180915260	3203958	0.0177	3.7336
chr6	171115067	2356047	0.0138	2.4311
chr7	159138663	1812390	0.0114	1.9738

chr8	146364022	2155609	0.0147	2.5849
chr9	141213431	2930417	0.0208	5.445
chr10	135534747	2912022	0.0215	3.4089
chr11	135006516	3493224	0.0259	4.6134
chr12	133851895	4118798	0.0308	7.4138
chr13	115169878	2111647	0.0183	6.4507
chr14	107349540	5578512	0.052	29.0504
chr15	102531392	2594080	0.0253	4.5484
chr16	90354753	1498752	0.0166	2.3323
chr17	81195210	2573759	0.0317	6.3839
chr18	78077248	1901858	0.0244	5.81
chr19	59128983	2282715	0.0386	4.5114
chr20	63025520	2133534	0.0339	6.9153
chr21	48129895	621051	0.0129	2.3627
chr22	51304566	554707	0.0108	1.1774
chrMT	16571	47131	2.8442	20.4005
chrX	155270560	5381011	0.0347	3.4986
chrY	59373566	357540	0.006	1.0946

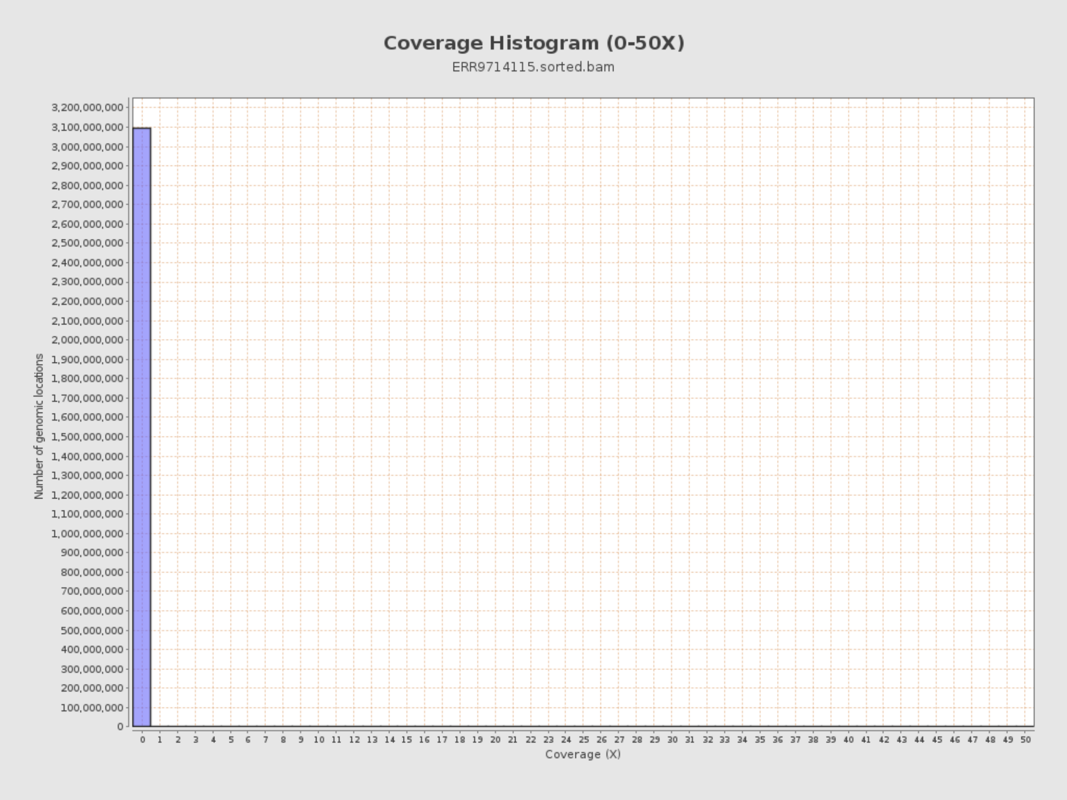
3. Results : Coverage across reference



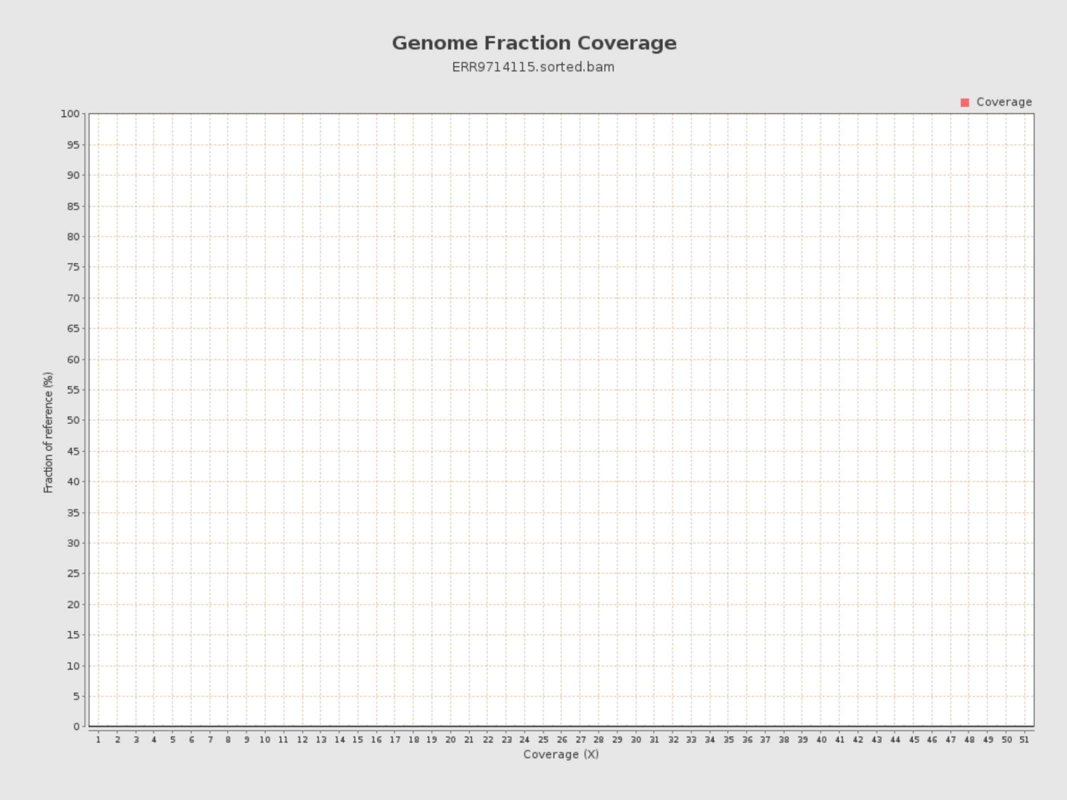
4. Results : Coverage Histogram



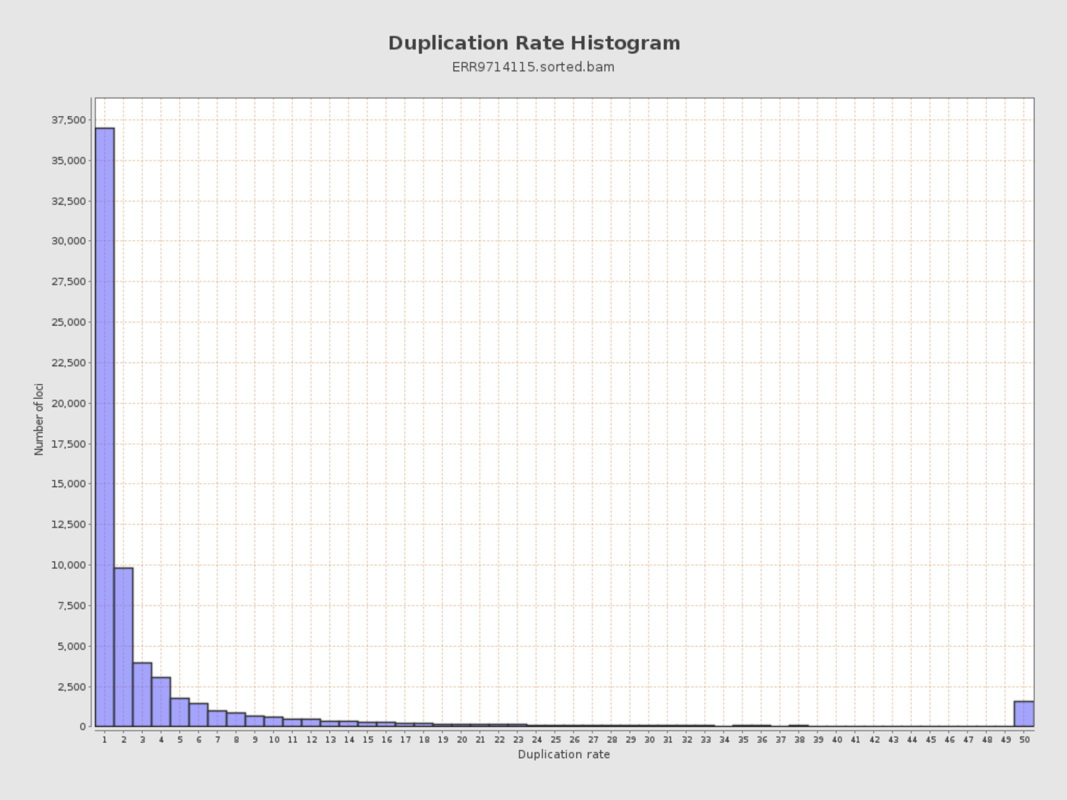
5. Results : Coverage Histogram (0-50X)



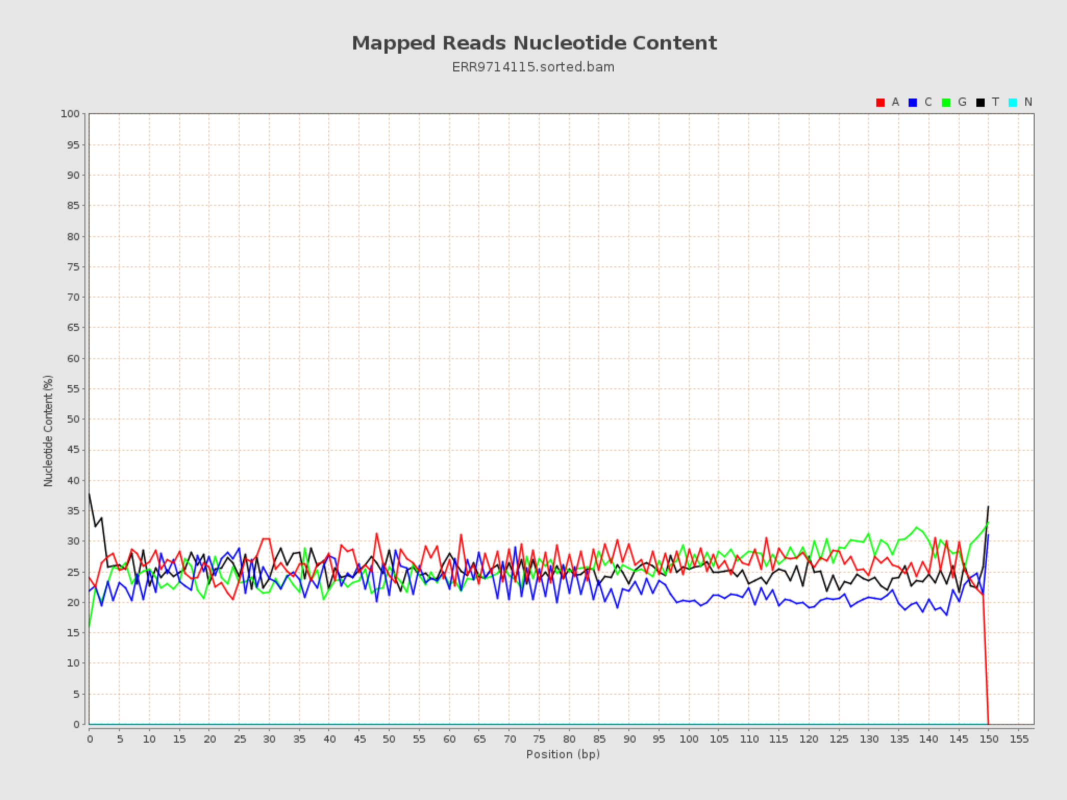
6. Results : Genome Fraction Coverage



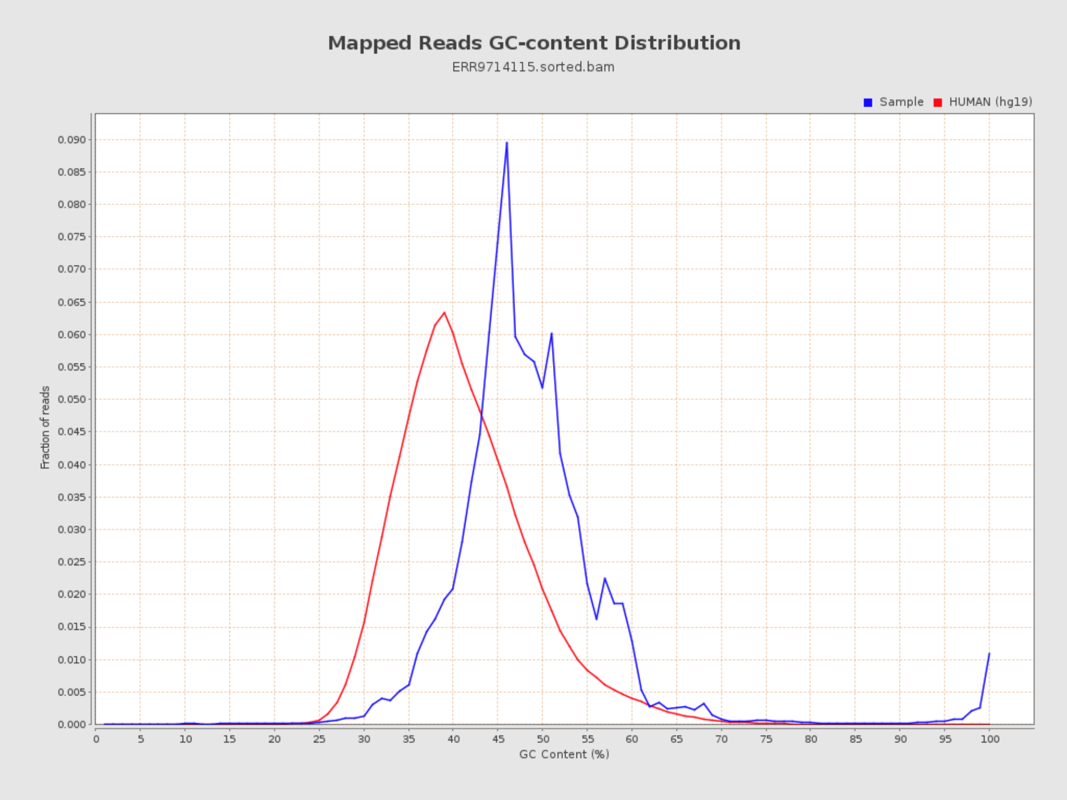
7. Results : Duplication Rate Histogram



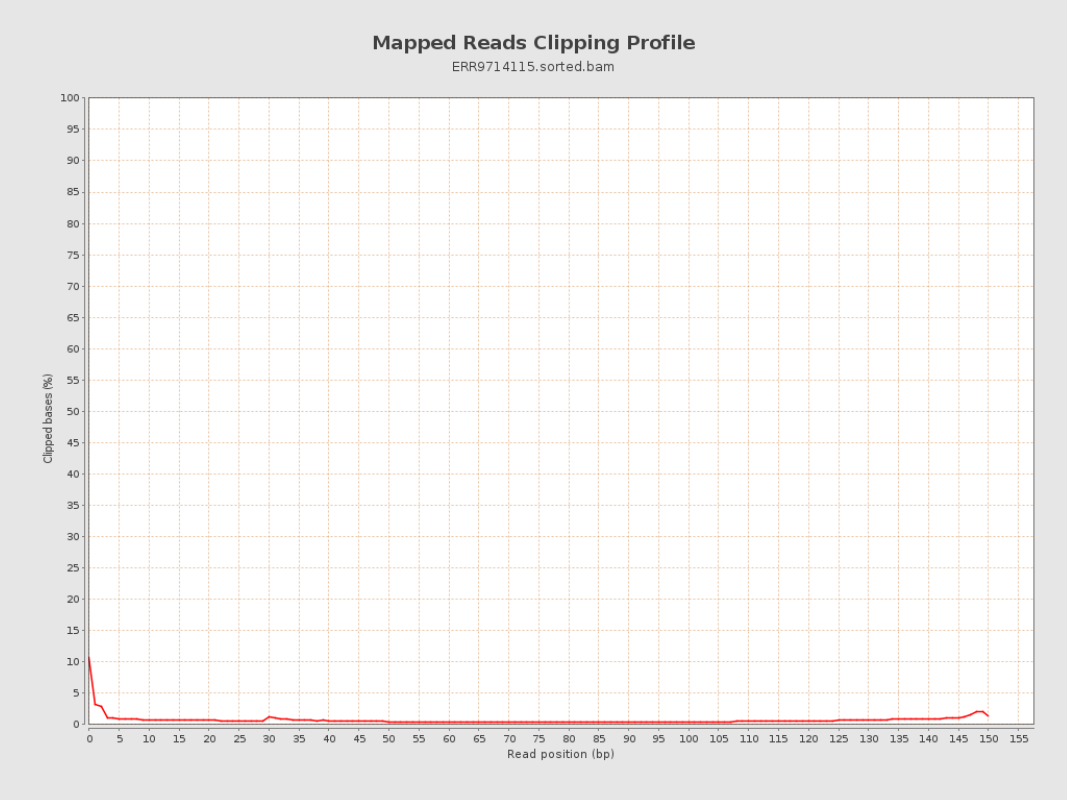
8. Results : Mapped Reads Nucleotide Content



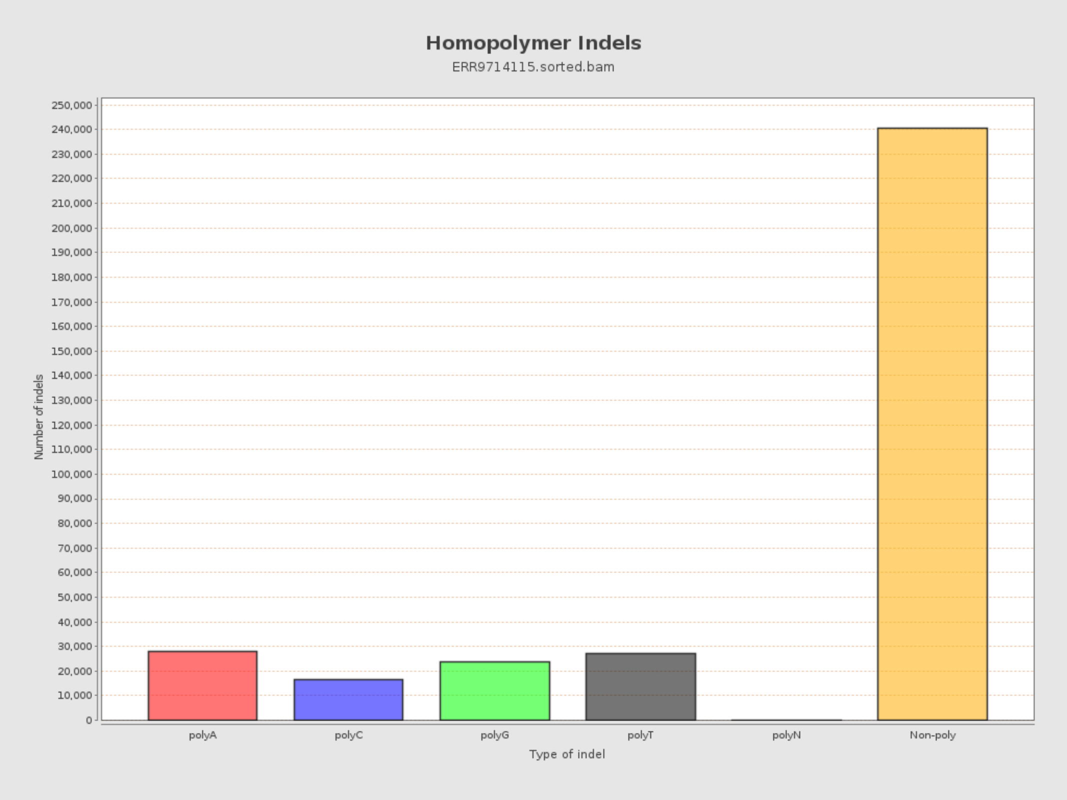
9. Results : Mapped Reads GC-content Distribution



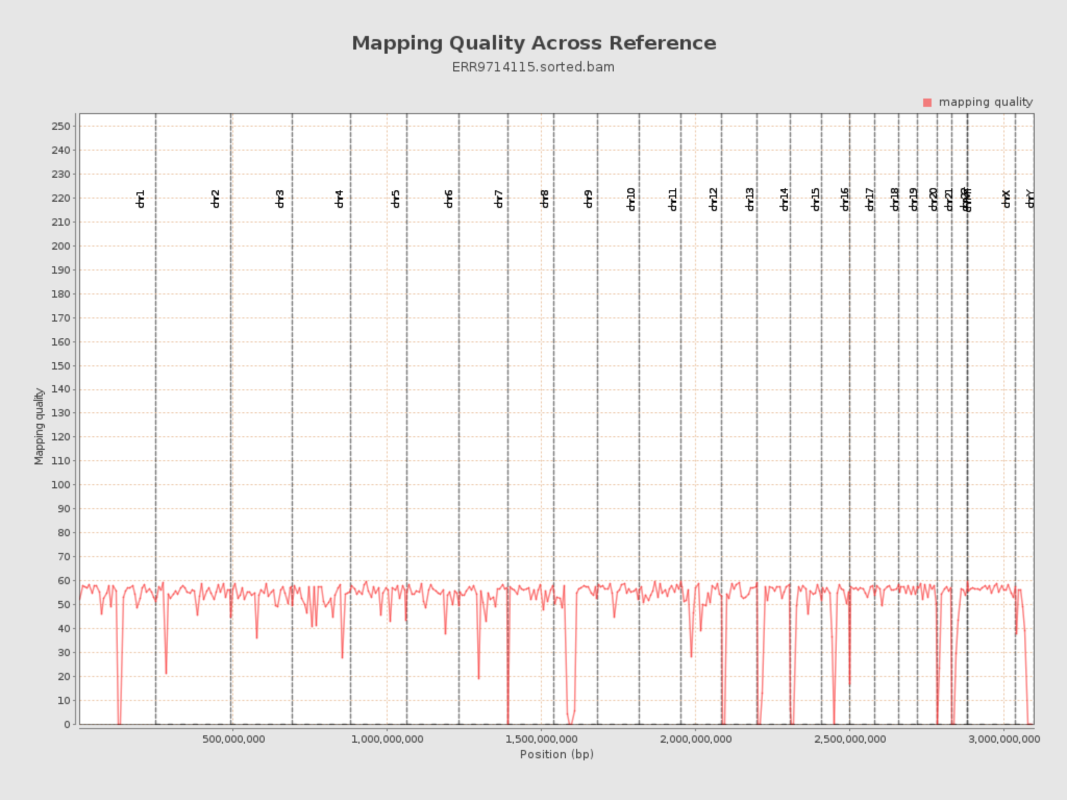
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram