Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714165.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_ERR9714165 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714165.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:32:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	798,096
Mapped reads	725,433 / 90.9%
Unmapped reads	72,663 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,716 / 3.22%
Read min/max/mean length	30 / 151 / 141.32
Duplicated reads (estimated)	649,505 / 81.38%
Duplication rate	42.4%
Clipped reads	688,658 / 86.29%

2.2. ACGT Content

Number/percentage of A's	26,920,932 / 29.33%
Number/percentage of C's	18,611,822 / 20.27%
Number/percentage of T's	25,433,897 / 27.71%
Number/percentage of G's	20,830,904 / 22.69%
Number/percentage of N's	576 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0302

Standard Deviation	6.3533

2.4. Mapping Quality

Mean Mapping Quality	50.93

2.5. Mismatches and indels

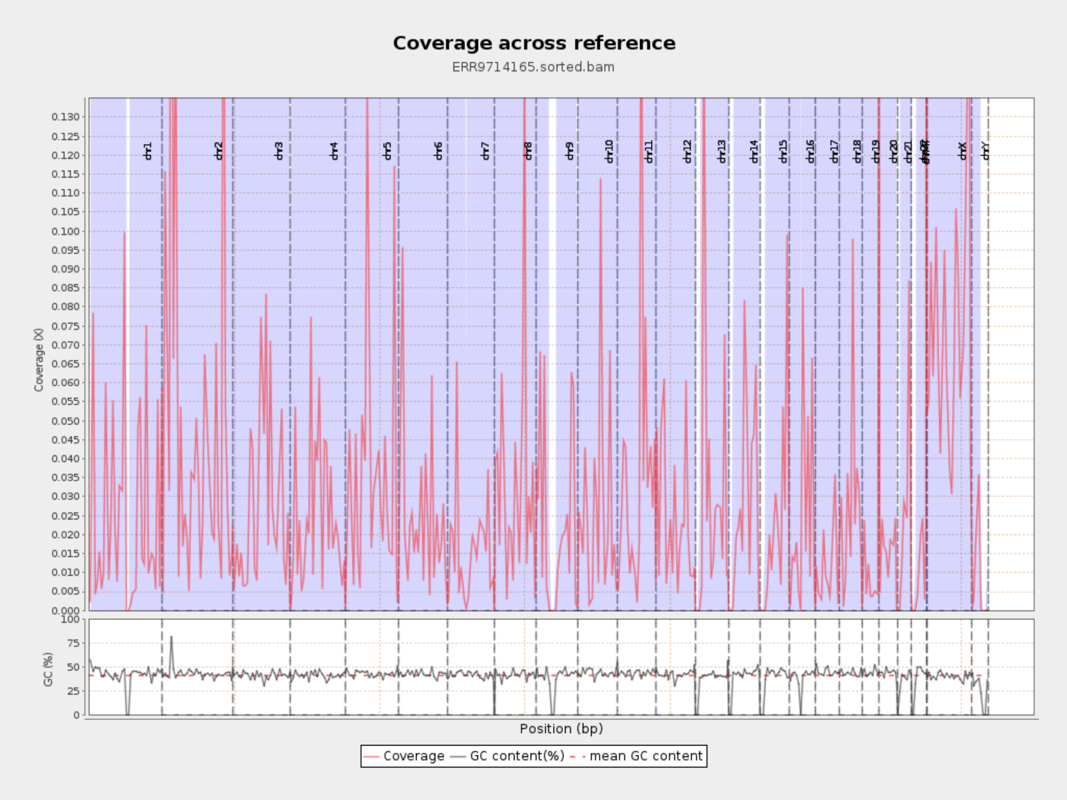
General error rate	3.99%
Mismatches	3,336,649
Insertions	110,869
Mapped reads with at least one insertion	14.87%
Deletions	293,379
Mapped reads with at least one deletion	38.72%
Homopolymer indels	27.28%

2.6. Chromosome stats

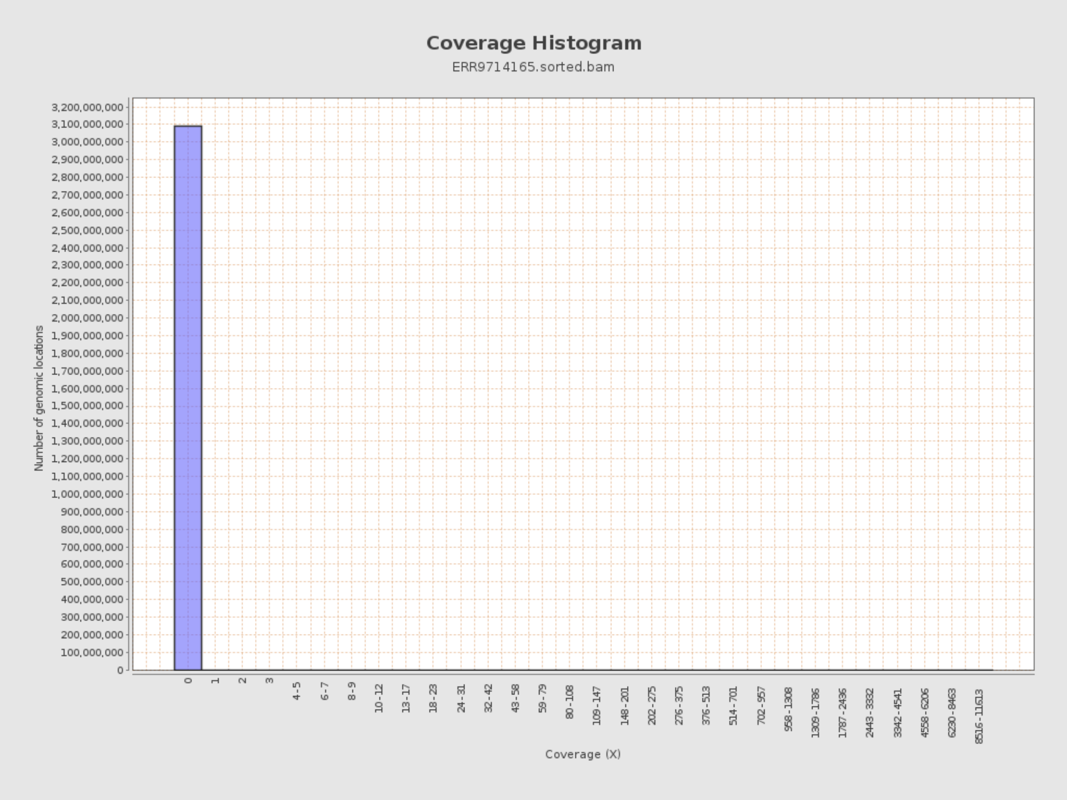
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6179950	0.0248	4.9331
chr2	243199373	12668513	0.0521	12.4254
chr3	198022430	5603072	0.0283	4.7001
chr4	191154276	4883581	0.0255	4.2676
chr5	180915260	6708144	0.0371	6.7978
chr6	171115067	4344025	0.0254	5.2205
chr7	159138663	2635088	0.0166	2.4449

chr8	146364022	5036315	0.0344	7.9281
chr9	141213431	3189420	0.0226	4.5625
chr10	135534747	3787549	0.0279	3.6343
chr11	135006516	5108094	0.0378	10.4227
chr12	133851895	3302731	0.0247	3.9143
chr13	115169878	3378985	0.0293	7.1612
chr14	107349540	3154088	0.0294	4.5724
chr15	102531392	2279009	0.0222	5.216
chr16	90354753	2206300	0.0244	5.3762
chr17	81195210	937917	0.0116	1.9496
chr18	78077248	2289599	0.0293	6.1799
chr19	59128983	836176	0.0141	4.2894
chr20	63025520	999372	0.0159	1.7248
chr21	48129895	1197012	0.0249	6.8264
chr22	51304566	437005	0.0085	1.3721
chrMT	16571	7371	0.4448	3.063
chrX	155270560	11808105	0.076	7.2469
chrY	59373566	446658	0.0075	2.0679

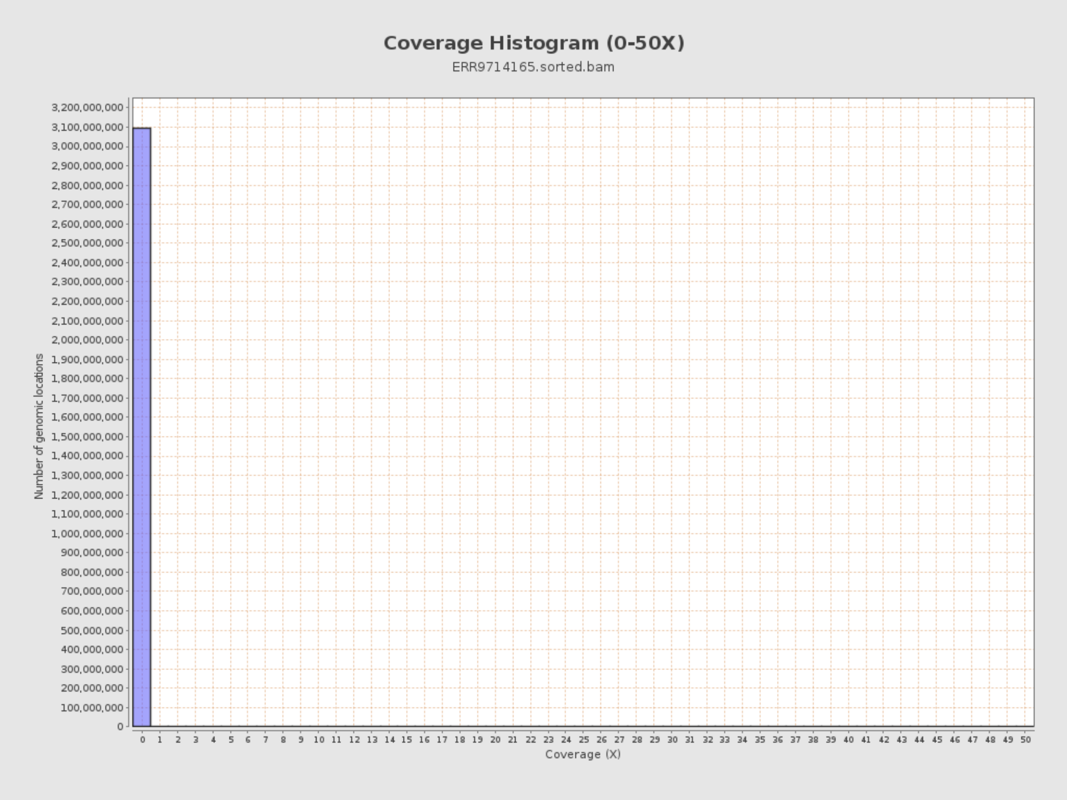
3. Results : Coverage across reference



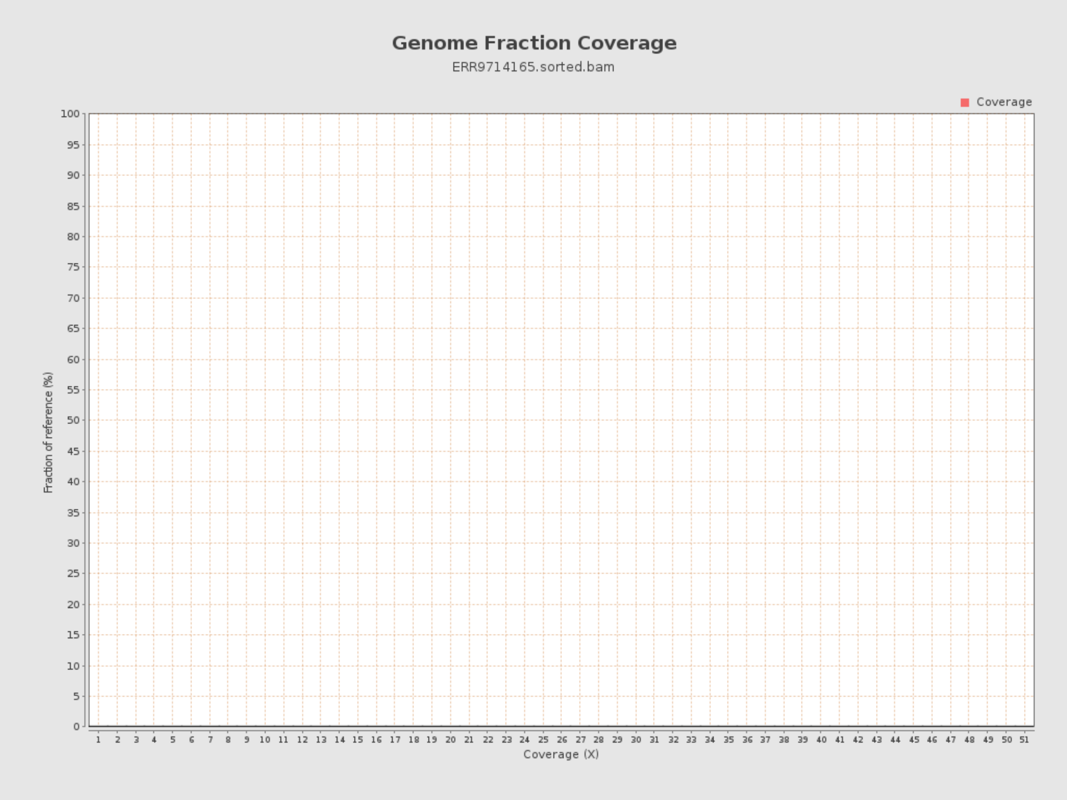
4. Results : Coverage Histogram



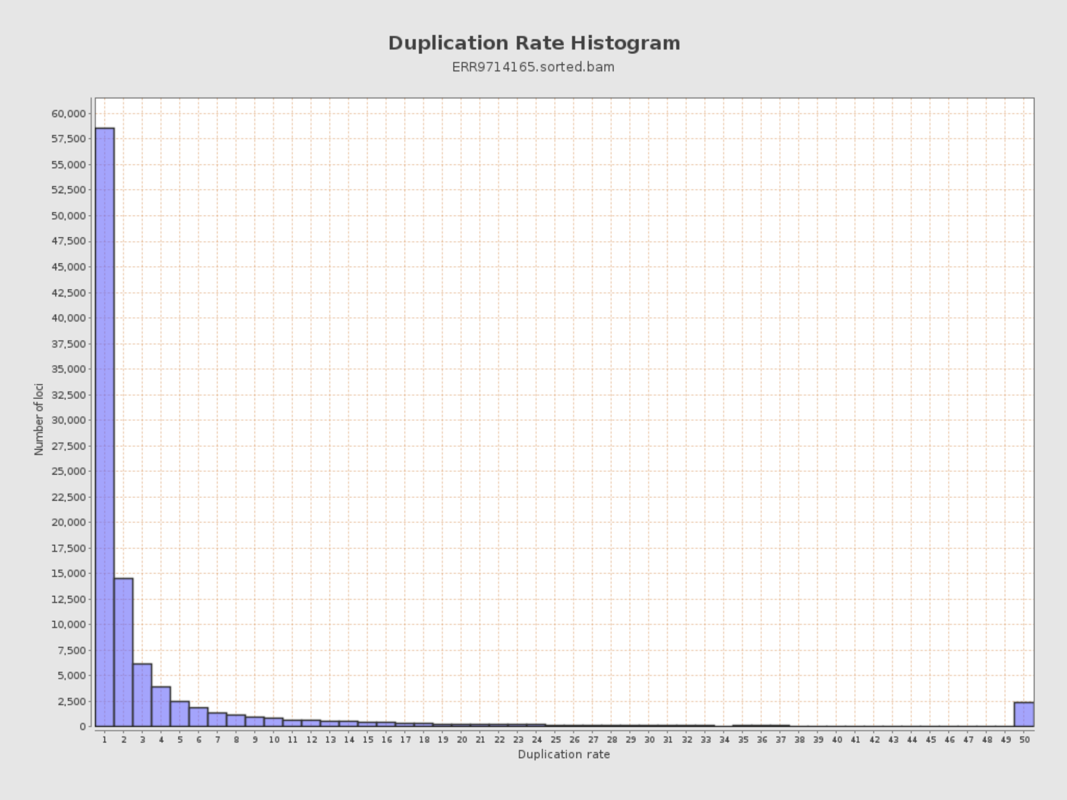
5. Results : Coverage Histogram (0-50X)



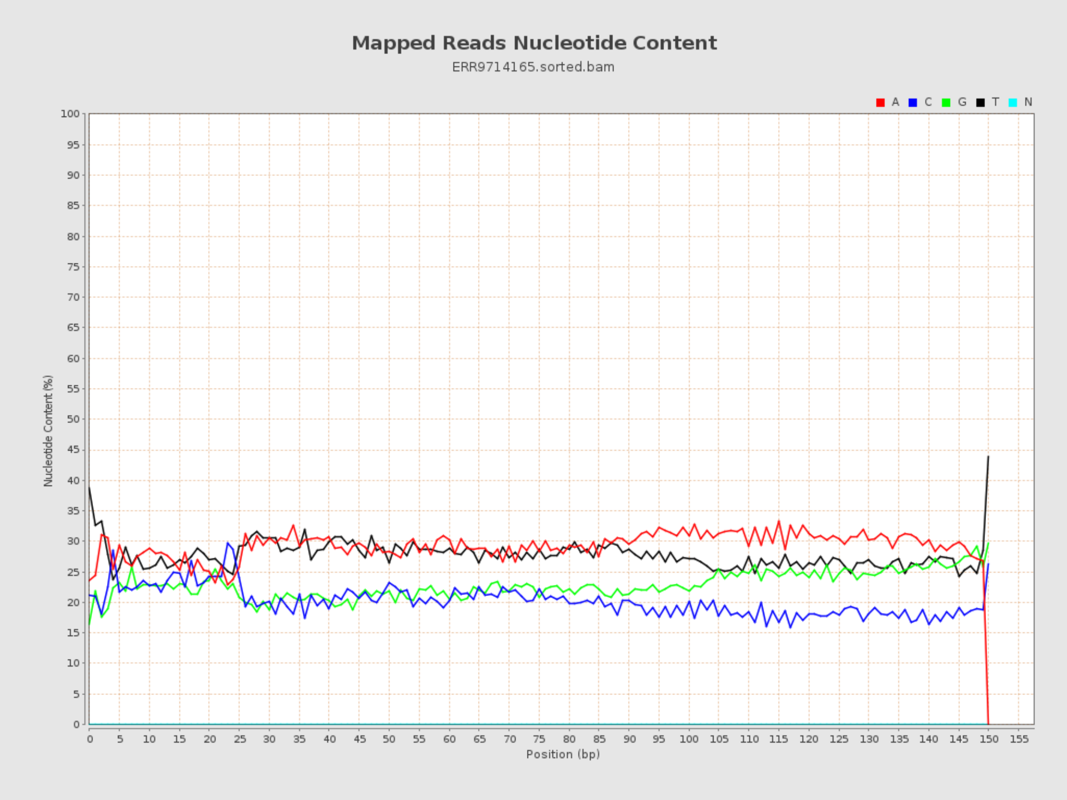
6. Results : Genome Fraction Coverage



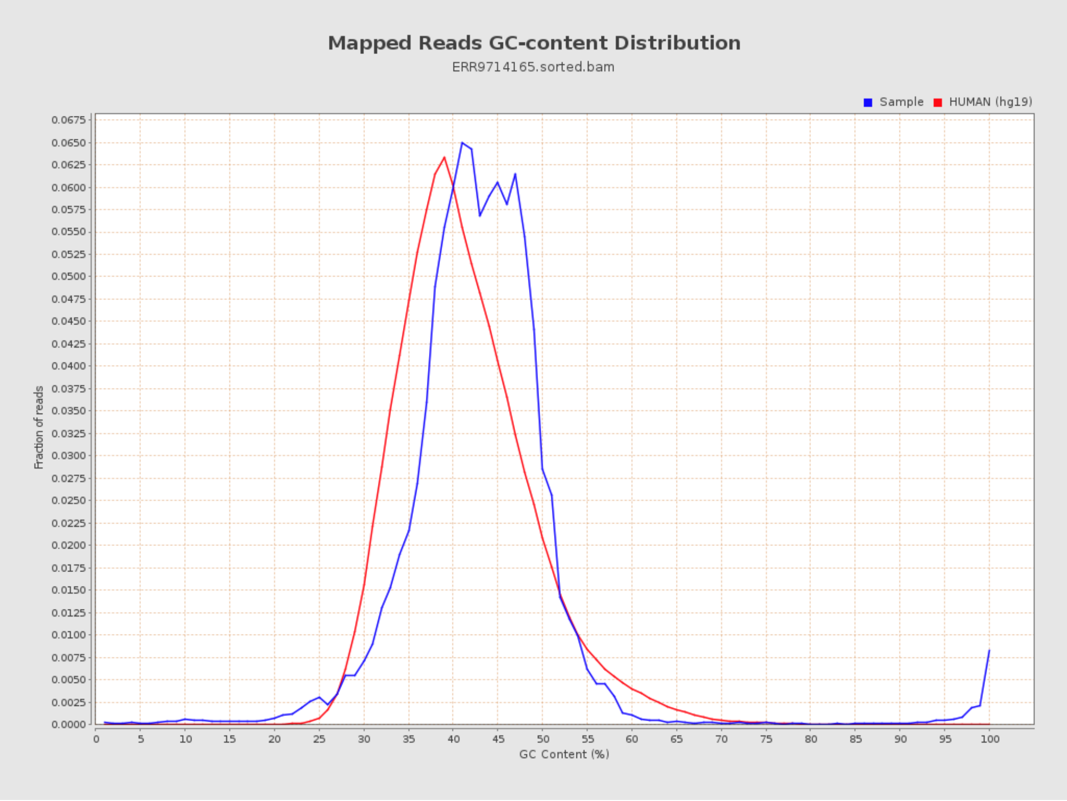
7. Results : Duplication Rate Histogram



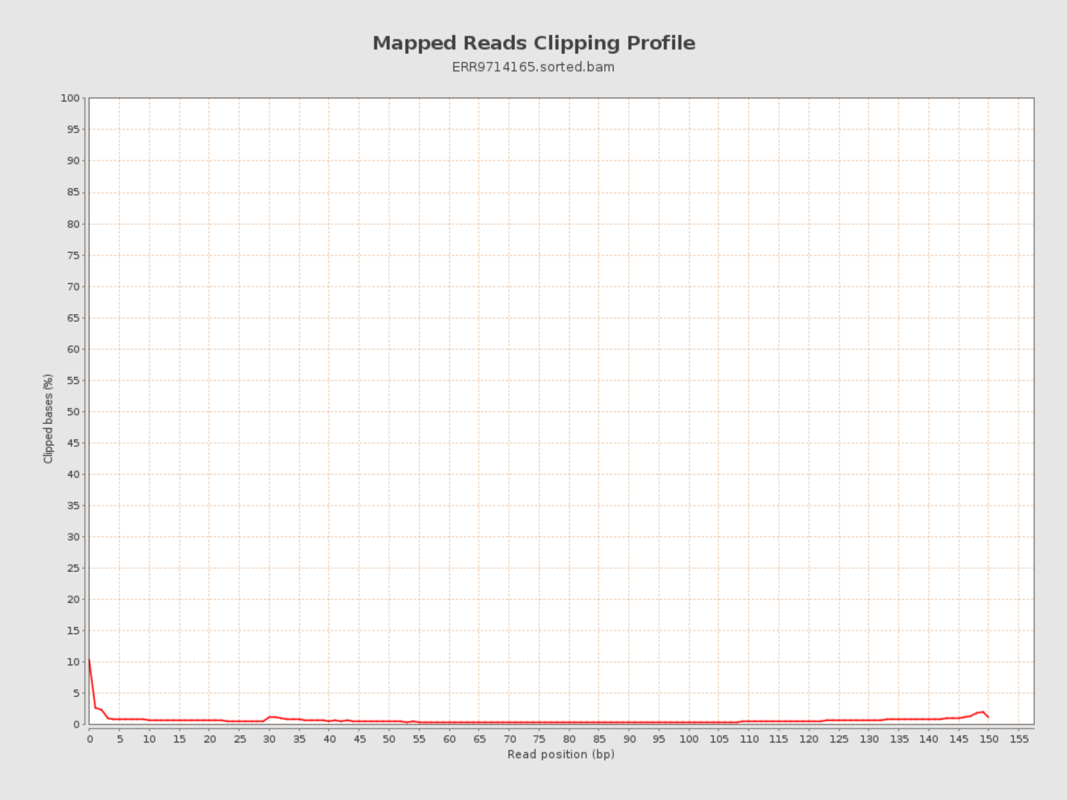
8. Results : Mapped Reads Nucleotide Content



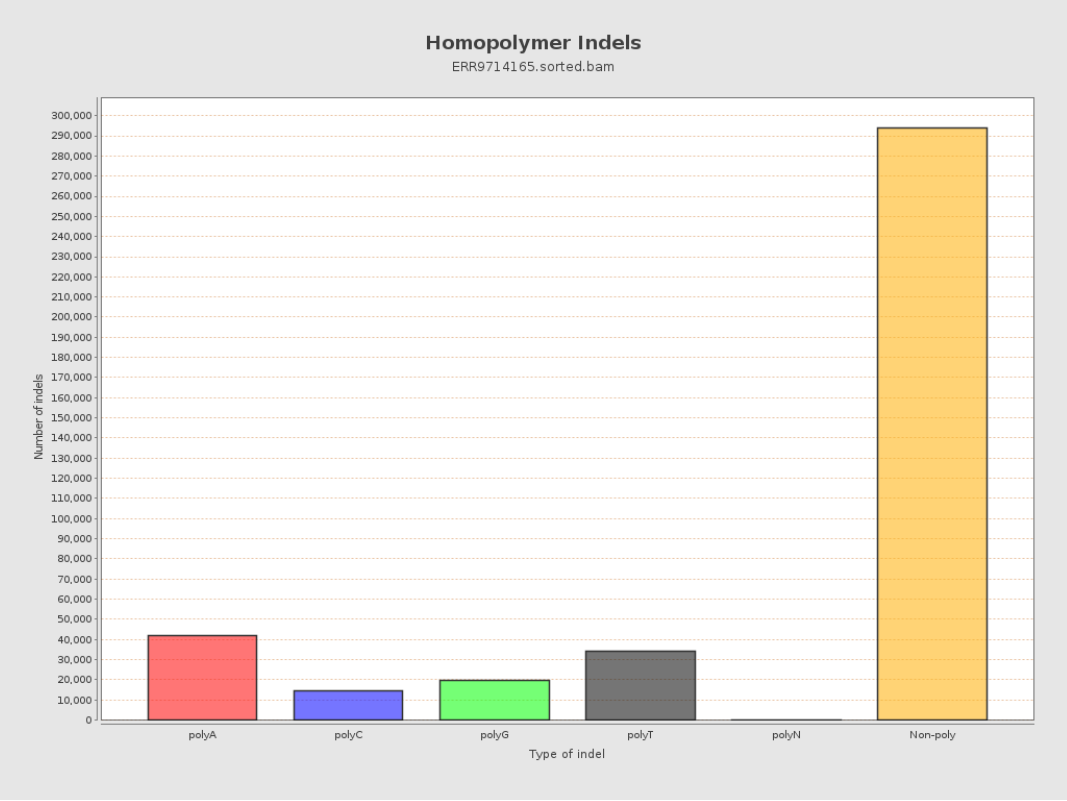
9. Results : Mapped Reads GC-content Distribution



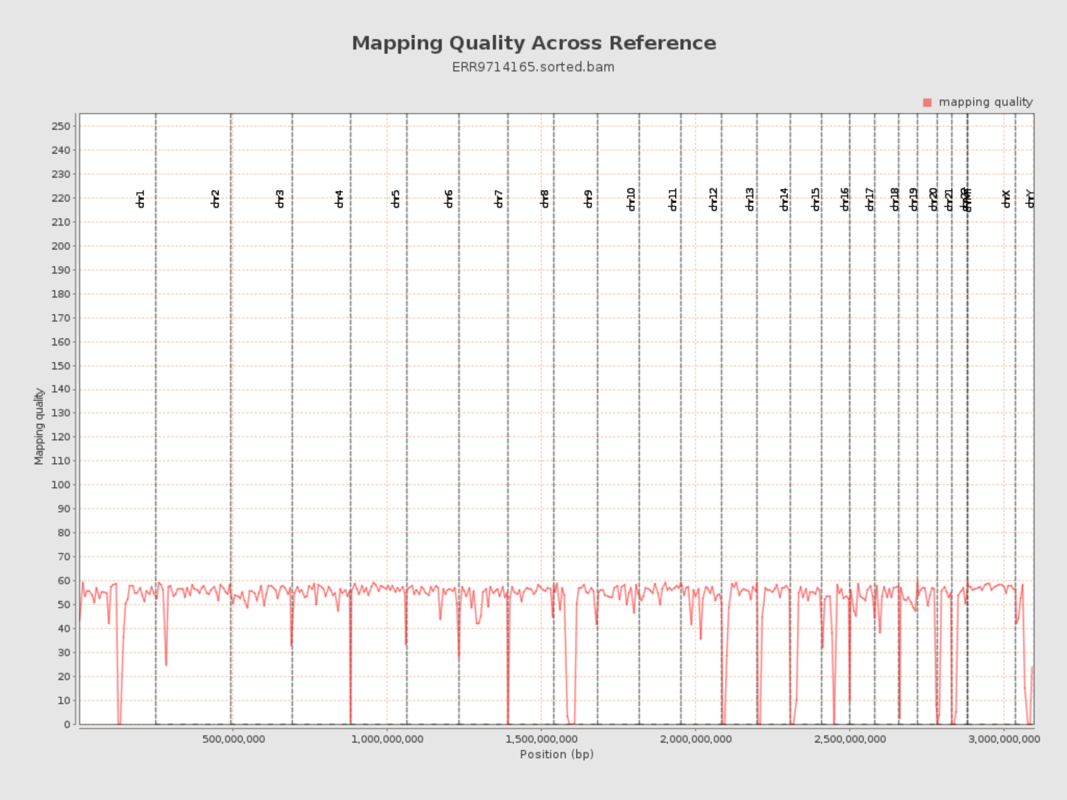
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram