Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714117.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_ERR9714117 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:09:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	638,310
Mapped reads	488,668 / 76.56%
Unmapped reads	149,642 / 23.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,746 / 2.31%
Read min/max/mean length	30 / 151 / 126.03
Duplicated reads (estimated)	421,668 / 66.06%
Duplication rate	44%
Clipped reads	452,726 / 70.93%

2.2. ACGT Content

Number/percentage of A's	16,826,797 / 27.31%
Number/percentage of C's	12,712,150 / 20.63%
Number/percentage of T's	15,958,794 / 25.9%
Number/percentage of G's	16,111,870 / 26.15%
Number/percentage of N's	434 / 0%
GC Percentage	46.78%

2.3. Coverage

Mean	0.0204

Standard Deviation	5.448

2.4. Mapping Quality

Mean Mapping Quality	51.68

2.5. Mismatches and indels

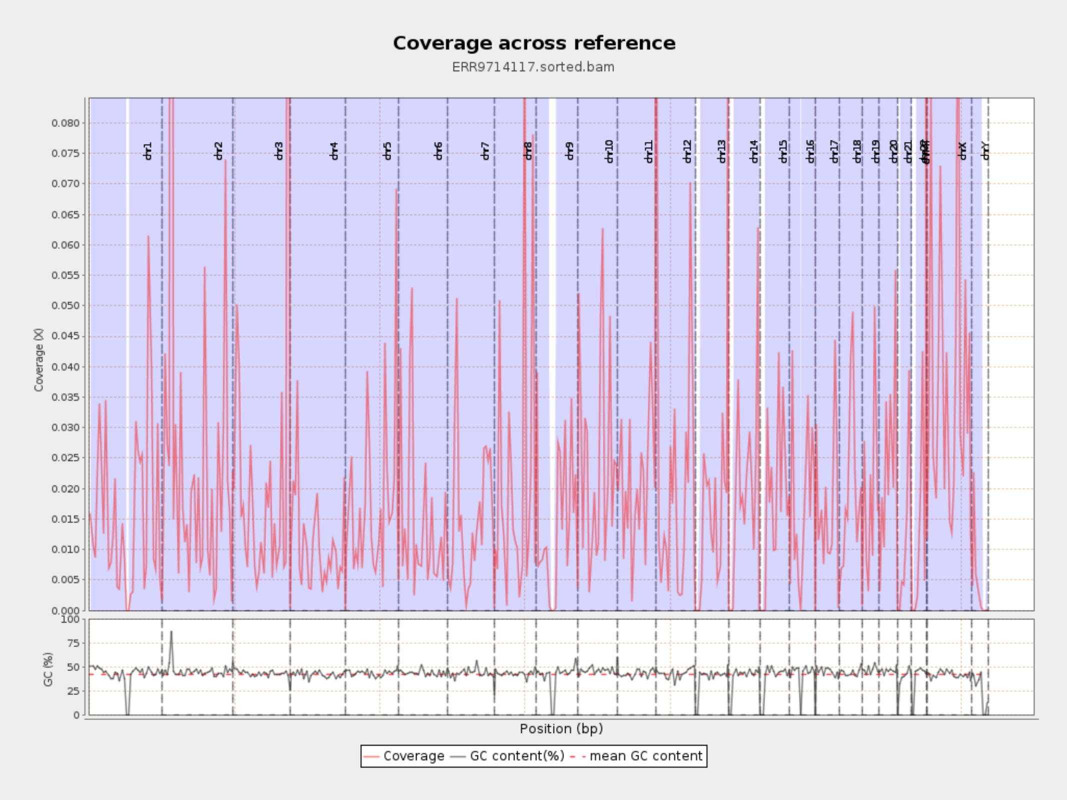
General error rate	4.73%
Mismatches	2,726,735
Insertions	68,004
Mapped reads with at least one insertion	13.31%
Deletions	242,015
Mapped reads with at least one deletion	46%
Homopolymer indels	30.62%

2.6. Chromosome stats

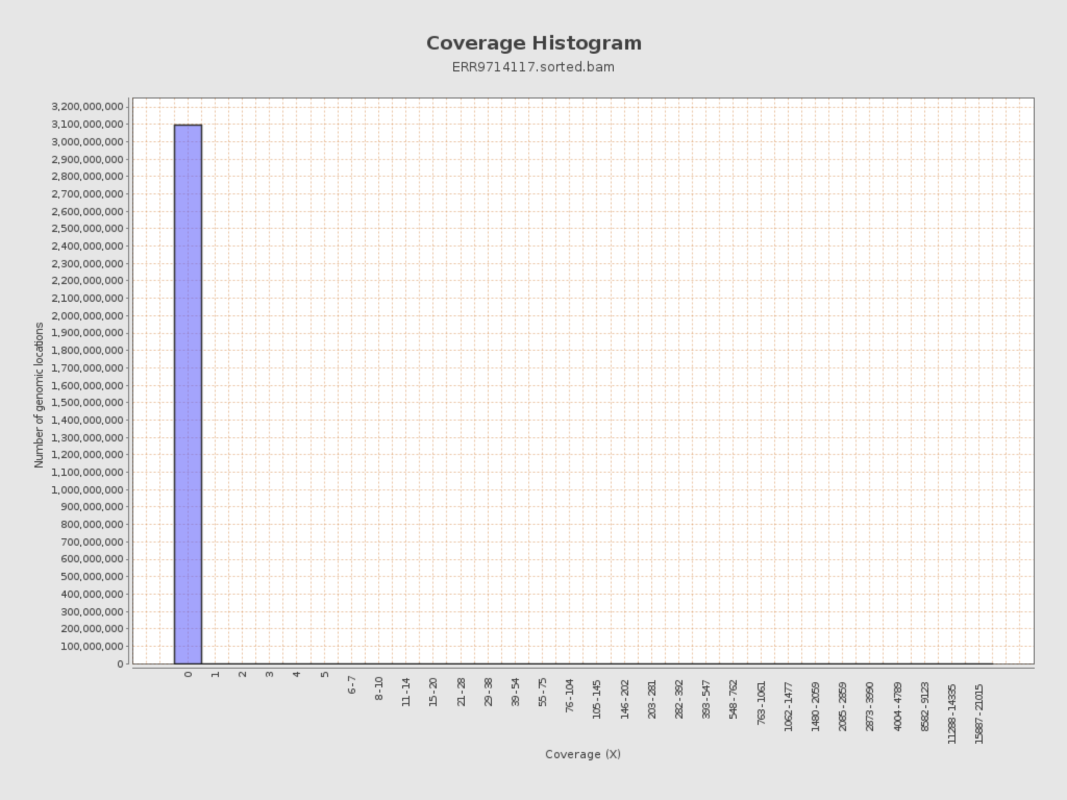
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4017070	0.0161	2.3057
chr2	243199373	8565707	0.0352	13.6512
chr3	198022430	5002035	0.0253	11.0915
chr4	191154276	2122882	0.0111	1.3413
chr5	180915260	3390867	0.0187	3.0506
chr6	171115067	2547138	0.0149	2.1104
chr7	159138663	2471660	0.0155	2.3441

chr8	146364022	3329075	0.0227	4.5545
chr9	141213431	1888842	0.0134	1.9363
chr10	135534747	3461901	0.0255	3.8941
chr11	135006516	2893454	0.0214	2.4753
chr12	133851895	2830642	0.0211	3.5811
chr13	115169878	1737830	0.0151	2.3872
chr14	107349540	2180436	0.0203	2.8774
chr15	102531392	1847308	0.018	2.3429
chr16	90354753	1599875	0.0177	2.1417
chr17	81195210	1419162	0.0175	2.6892
chr18	78077248	1560347	0.02	2.428
chr19	59128983	1099354	0.0186	2.3248
chr20	63025520	1580194	0.0251	2.926
chr21	48129895	561507	0.0117	2.5336
chr22	51304566	628097	0.0122	2.0763
chrMT	16571	65303	3.9408	25.2321
chrX	155270560	6087198	0.0392	5.0613
chrY	59373566	269709	0.0045	1.2953

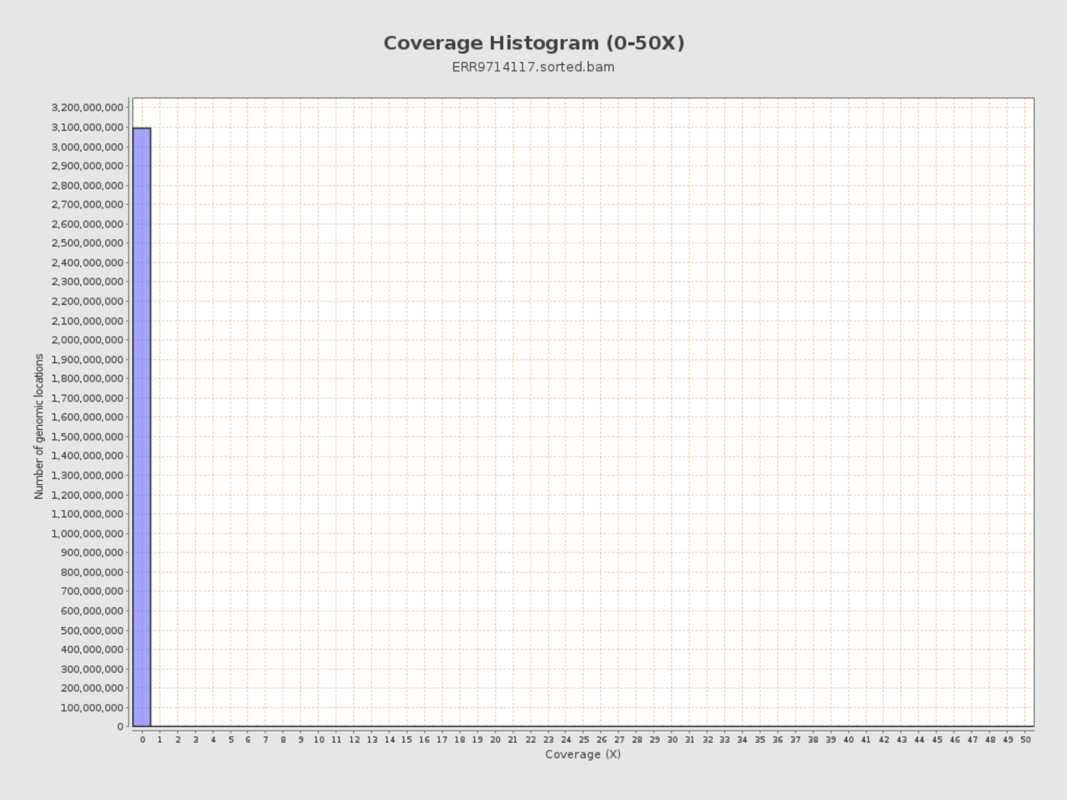
3. Results : Coverage across reference



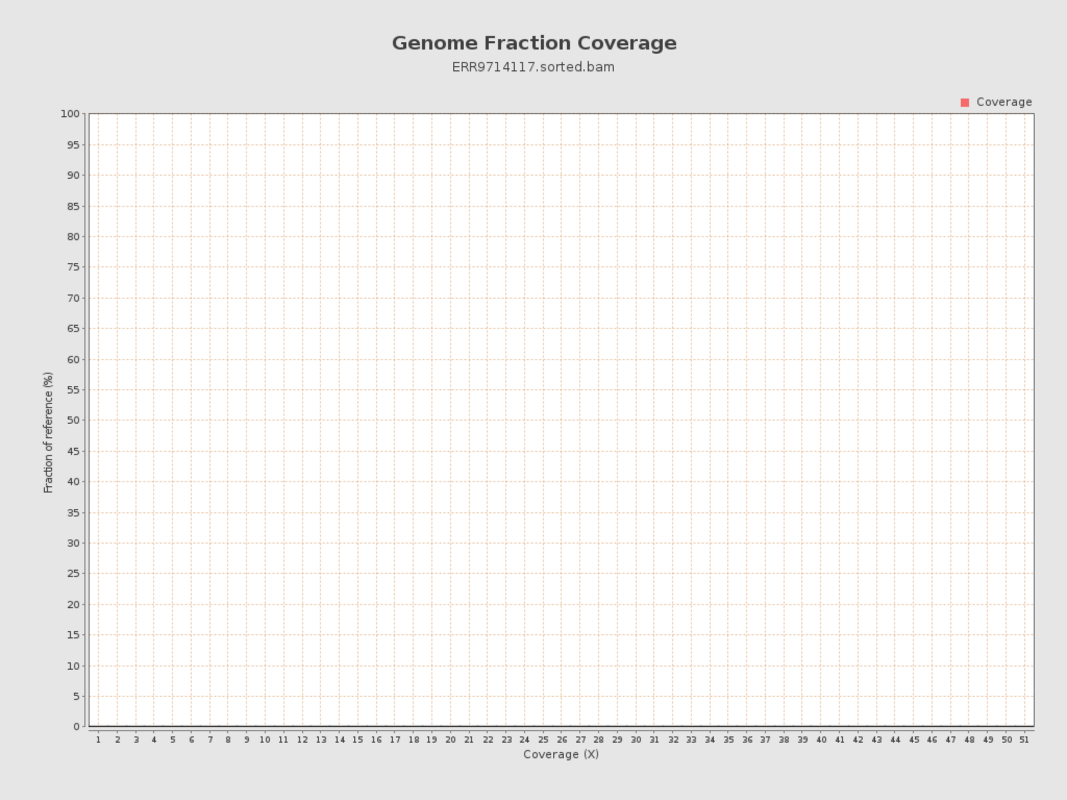
4. Results : Coverage Histogram



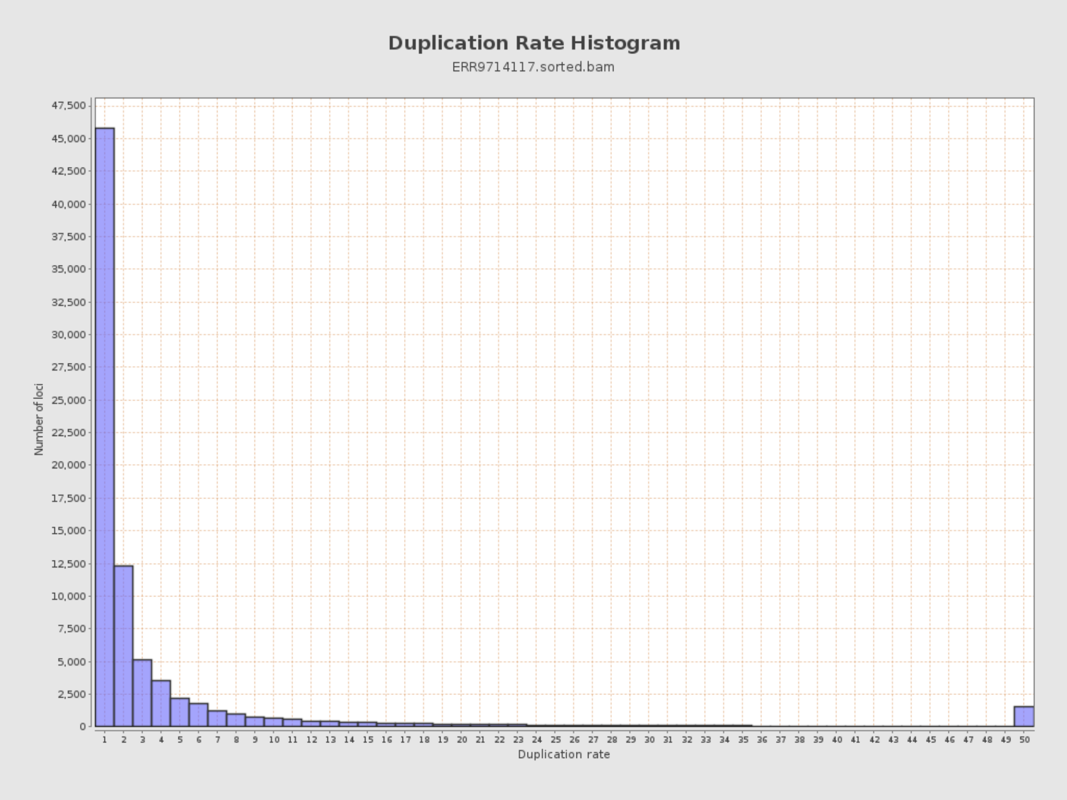
5. Results : Coverage Histogram (0-50X)



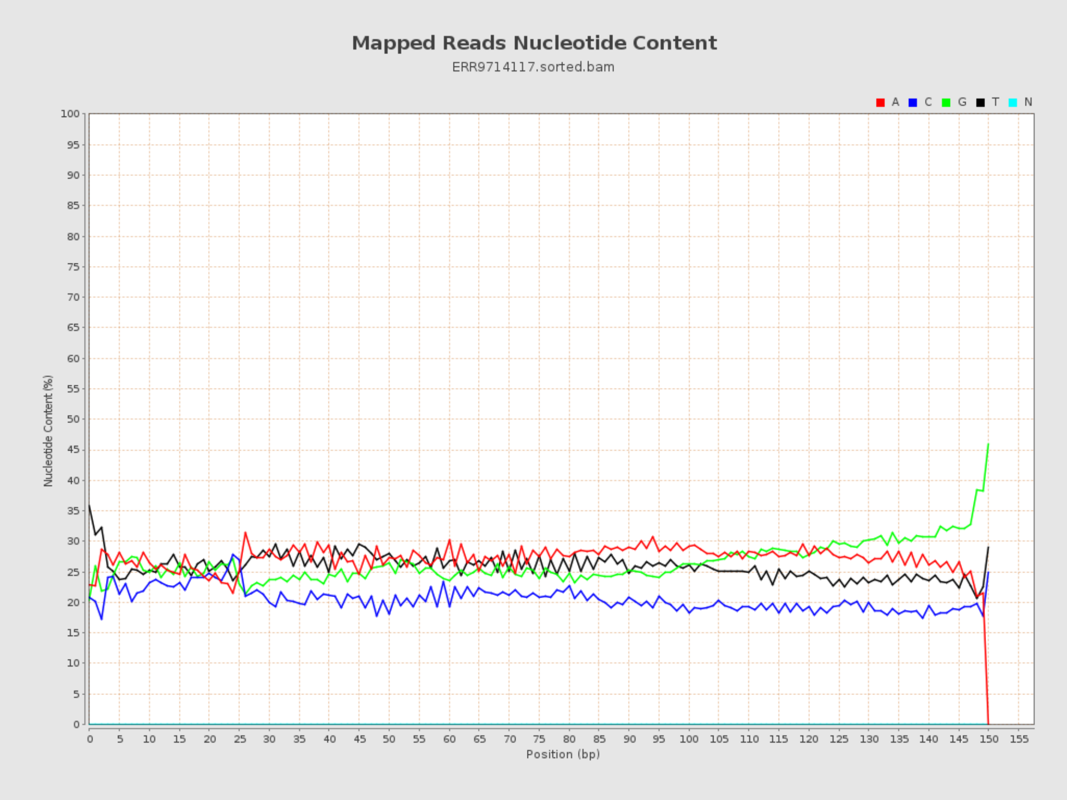
6. Results : Genome Fraction Coverage



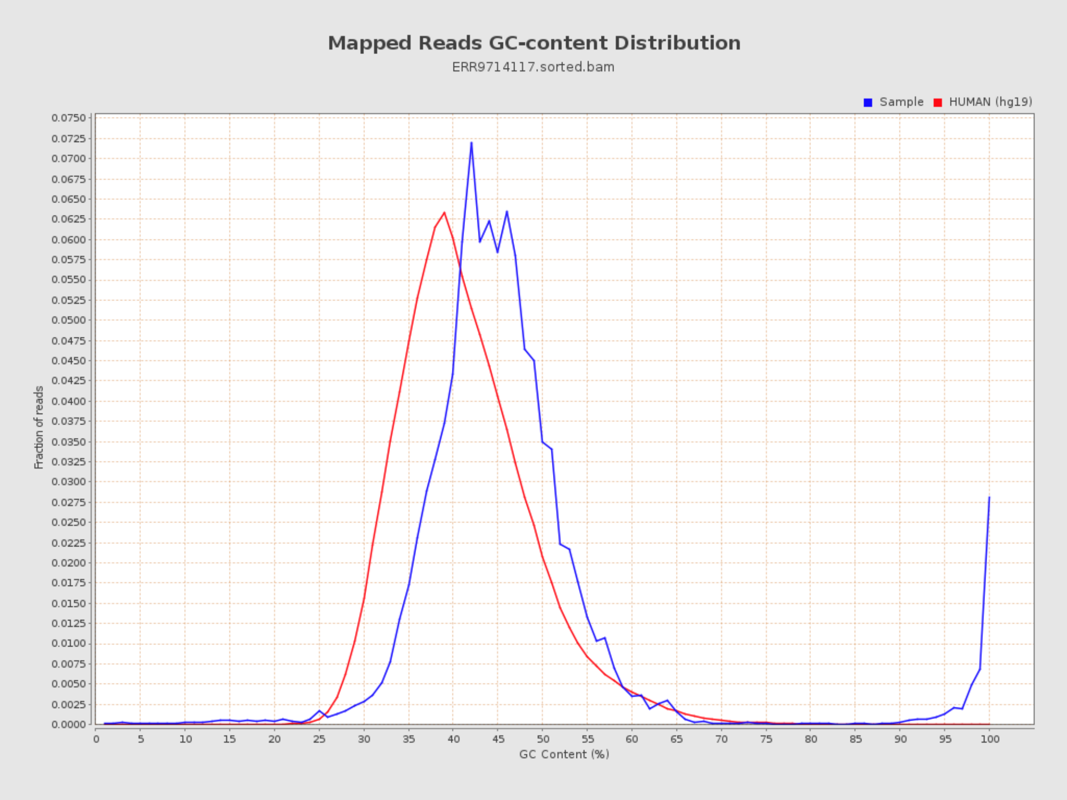
7. Results : Duplication Rate Histogram



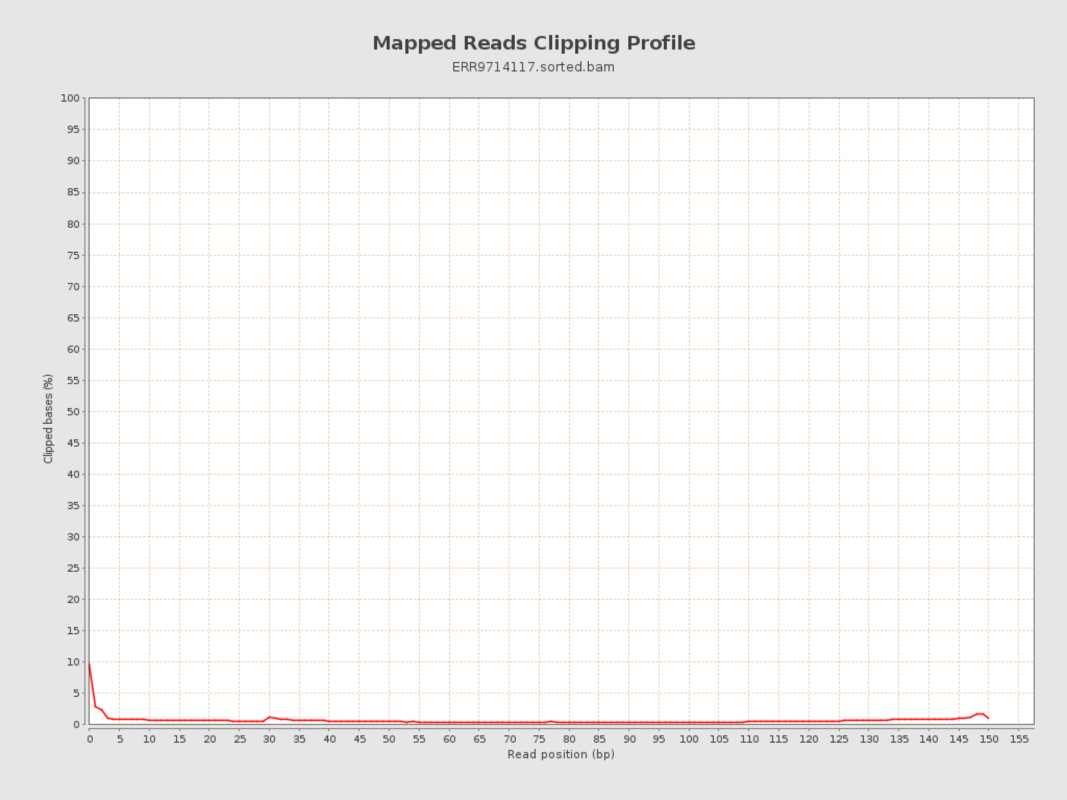
8. Results : Mapped Reads Nucleotide Content



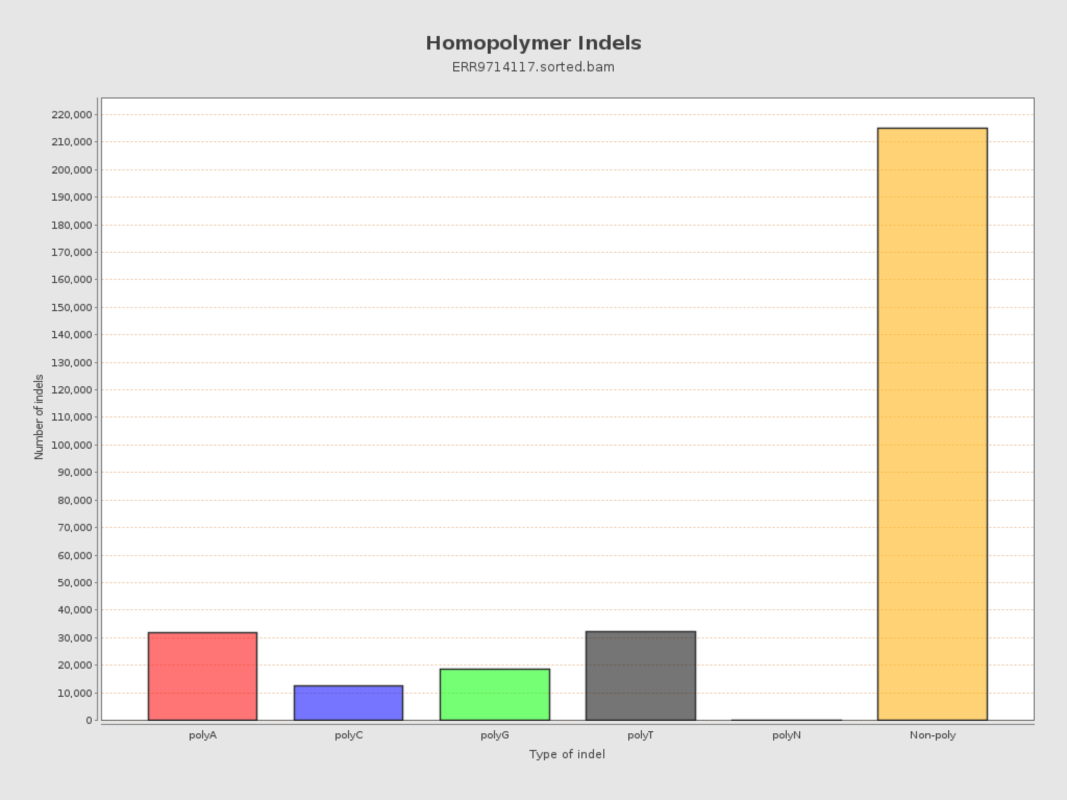
9. Results : Mapped Reads GC-content Distribution



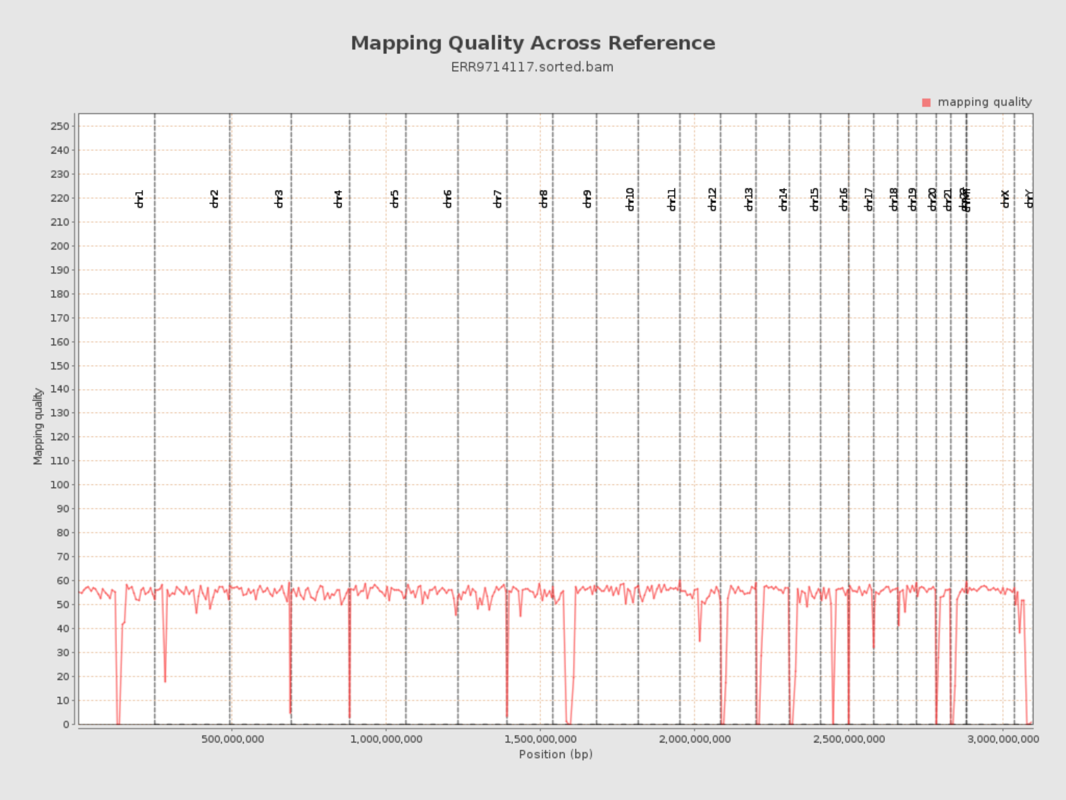
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram