Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:59:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714154.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_ERR9714154 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:59:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,056,508
Mapped reads	411,139 / 38.91%
Unmapped reads	645,369 / 61.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,787 / 1.78%
Read min/max/mean length	30 / 151 / 88.38
Duplicated reads (estimated)	356,156 / 33.71%
Duplication rate	43.12%
Clipped reads	363,663 / 34.42%

2.2. ACGT Content

Number/percentage of A's	12,710,939 / 25.33%
Number/percentage of C's	8,691,137 / 17.32%
Number/percentage of T's	11,905,137 / 23.72%
Number/percentage of G's	16,876,833 / 33.63%
Number/percentage of N's	725 / 0%
GC Percentage	50.95%

2.3. Coverage

Mean	0.0165

Standard Deviation	10.1111

2.4. Mapping Quality

Mean Mapping Quality	51.2

2.5. Mismatches and indels

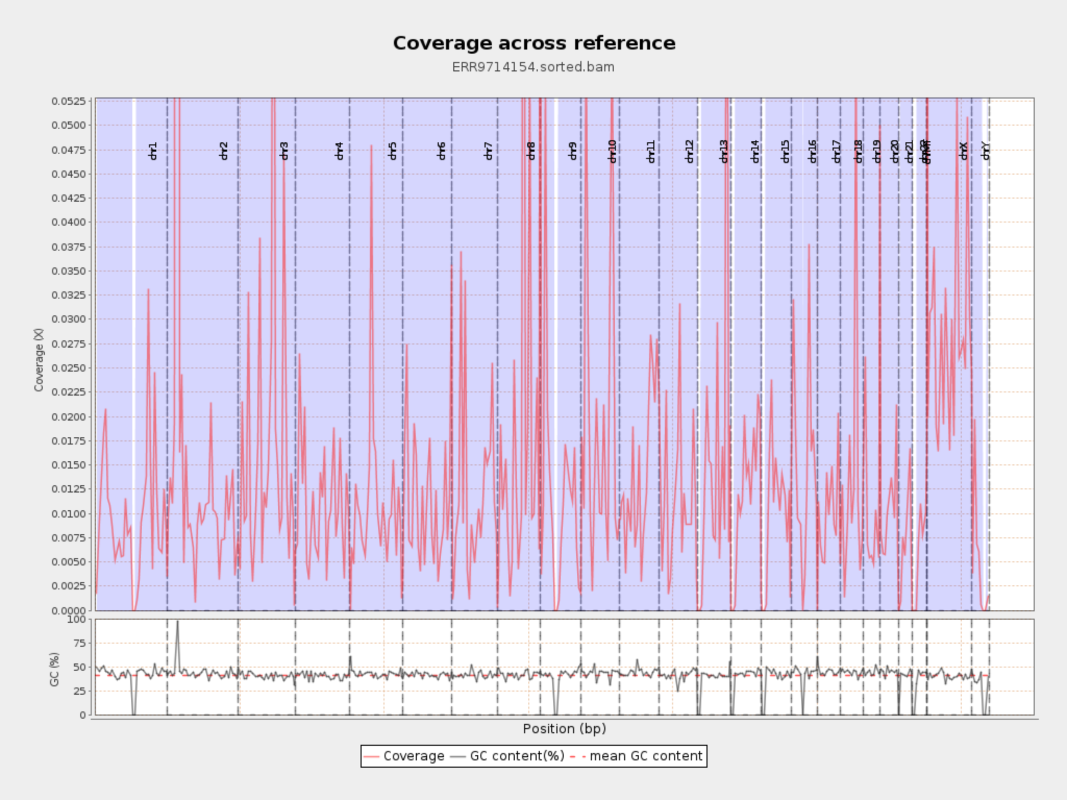
General error rate	3.98%
Mismatches	1,775,737
Insertions	56,965
Mapped reads with at least one insertion	12.52%
Deletions	137,388
Mapped reads with at least one deletion	31.79%
Homopolymer indels	31.65%

2.6. Chromosome stats

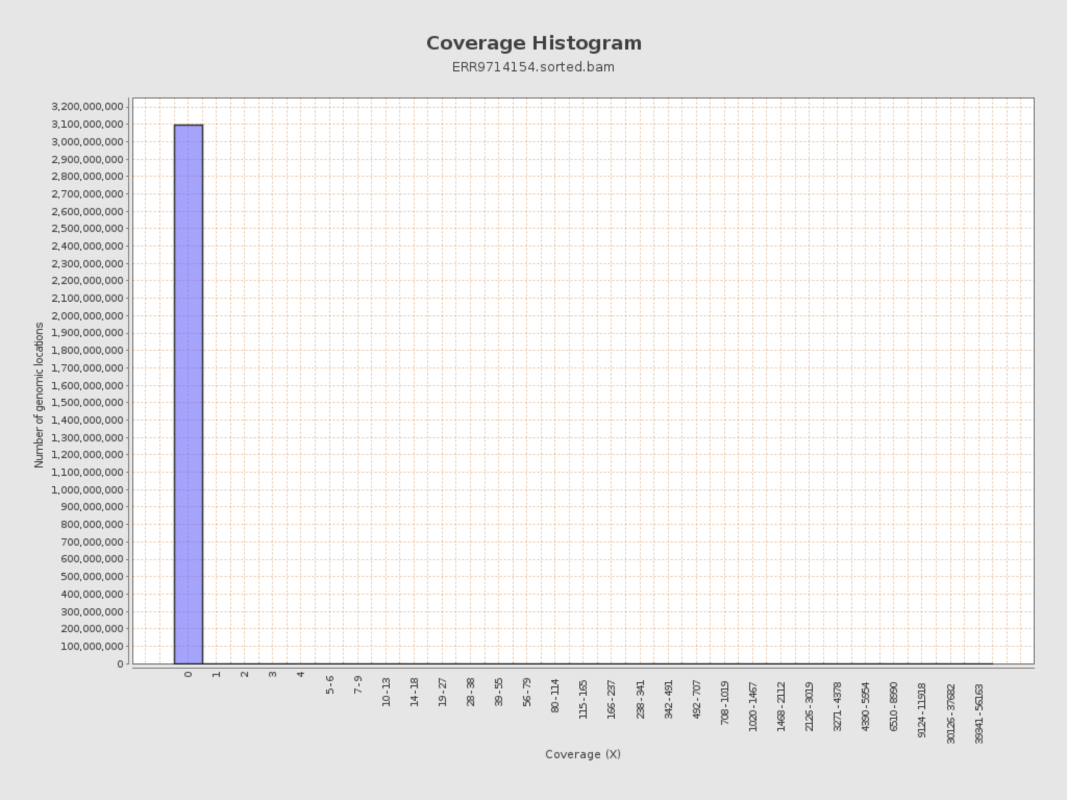
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2432183	0.0098	1.2786
chr2	243199373	10610230	0.0436	34.7403
chr3	198022430	3654902	0.0185	4.5261
chr4	191154276	2075487	0.0109	1.1169
chr5	180915260	2075939	0.0115	1.8861
chr6	171115067	1925732	0.0113	1.3971
chr7	159138663	1935068	0.0122	1.8555

chr8	146364022	2764563	0.0189	4.4332
chr9	141213431	1766008	0.0125	2.2577
chr10	135534747	2600246	0.0192	3.5388
chr11	135006516	1936100	0.0143	1.6812
chr12	133851895	1574145	0.0118	2.0071
chr13	115169878	1904164	0.0165	2.4862
chr14	107349540	1313011	0.0122	1.4655
chr15	102531392	1058721	0.0103	1.1668
chr16	90354753	1382565	0.0153	1.8945
chr17	81195210	820530	0.0101	0.9649
chr18	78077248	1137884	0.0146	2.7207
chr19	59128983	646382	0.0109	1.4039
chr20	63025520	666462	0.0106	0.907
chr21	48129895	345844	0.0072	0.8073
chr22	51304566	311579	0.0061	0.6764
chrMT	16571	1368138	82.5622	665.4598
chrX	155270560	4414327	0.0284	2.2104
chrY	59373566	288499	0.0049	0.7853

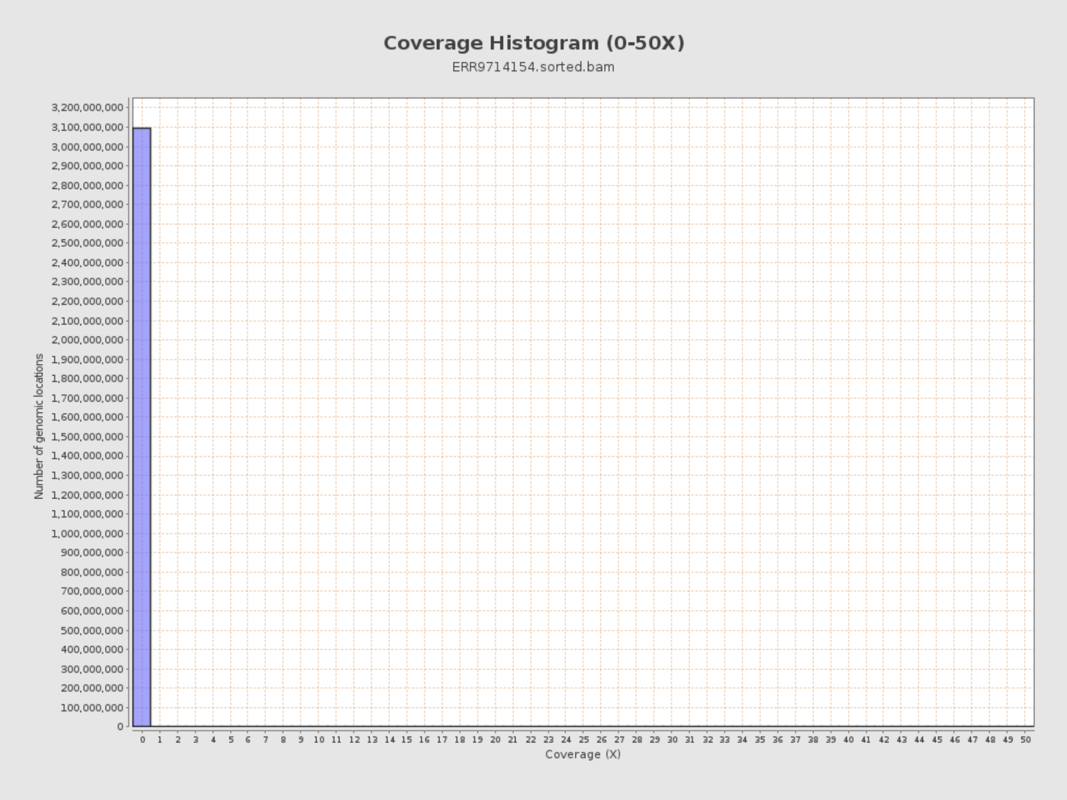
3. Results : Coverage across reference



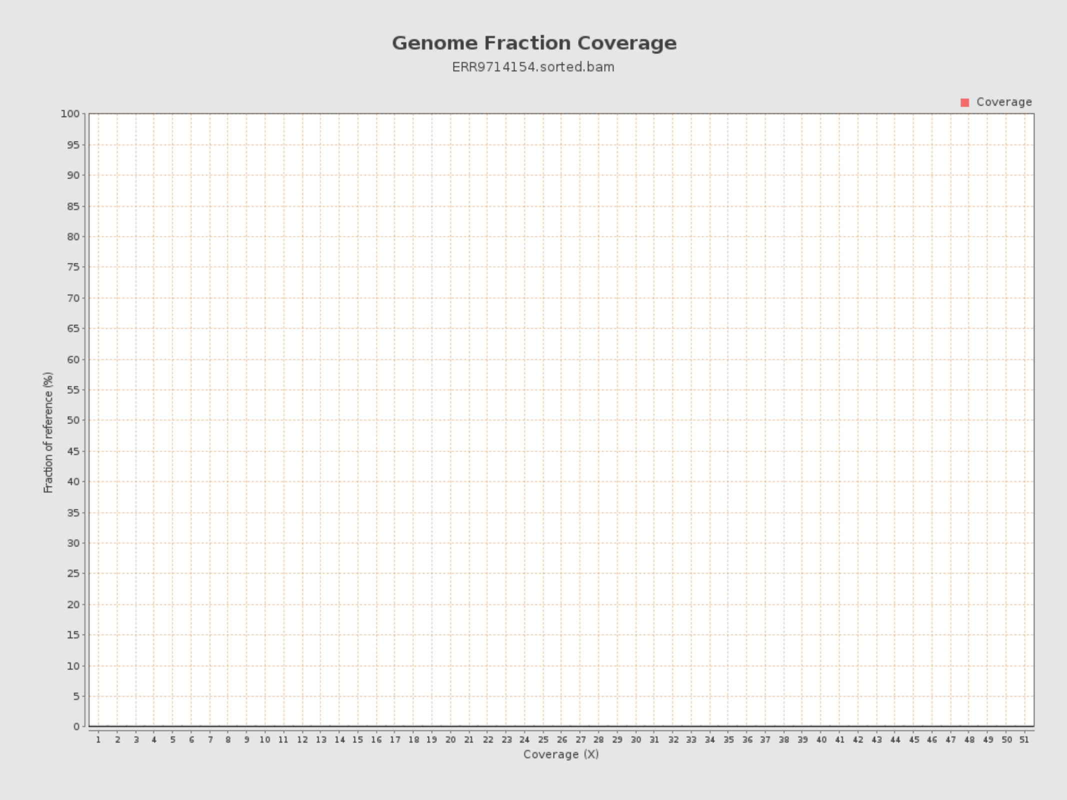
4. Results : Coverage Histogram



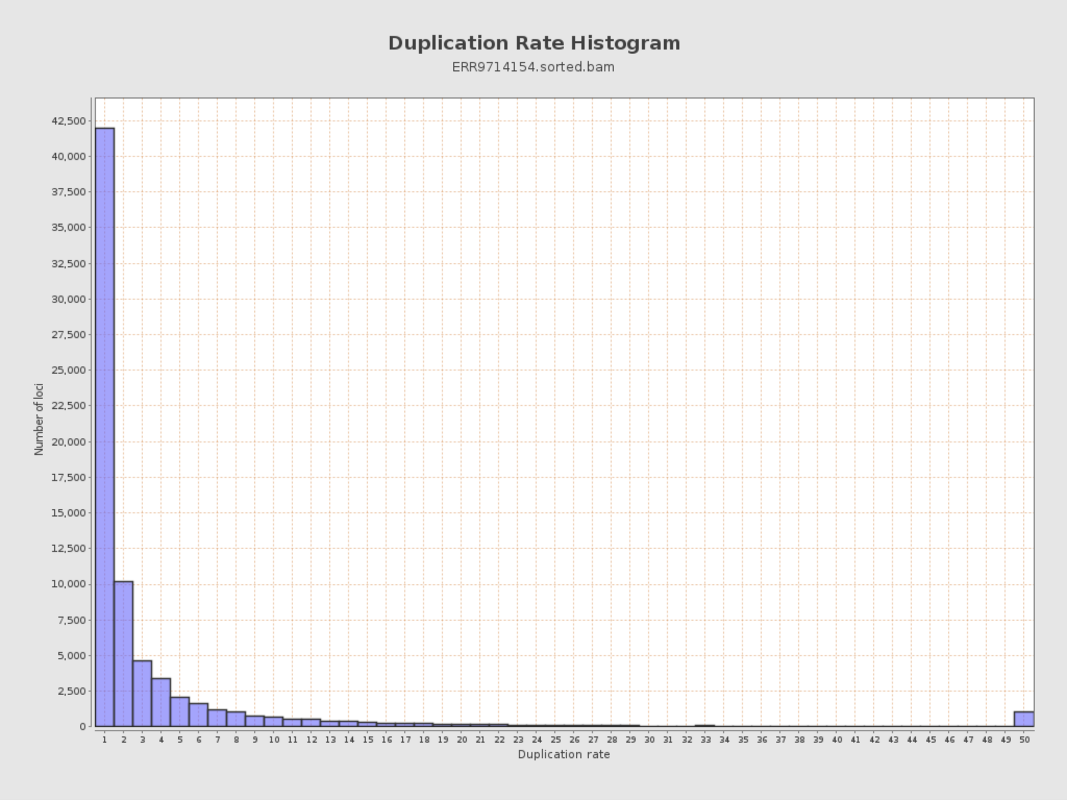
5. Results : Coverage Histogram (0-50X)



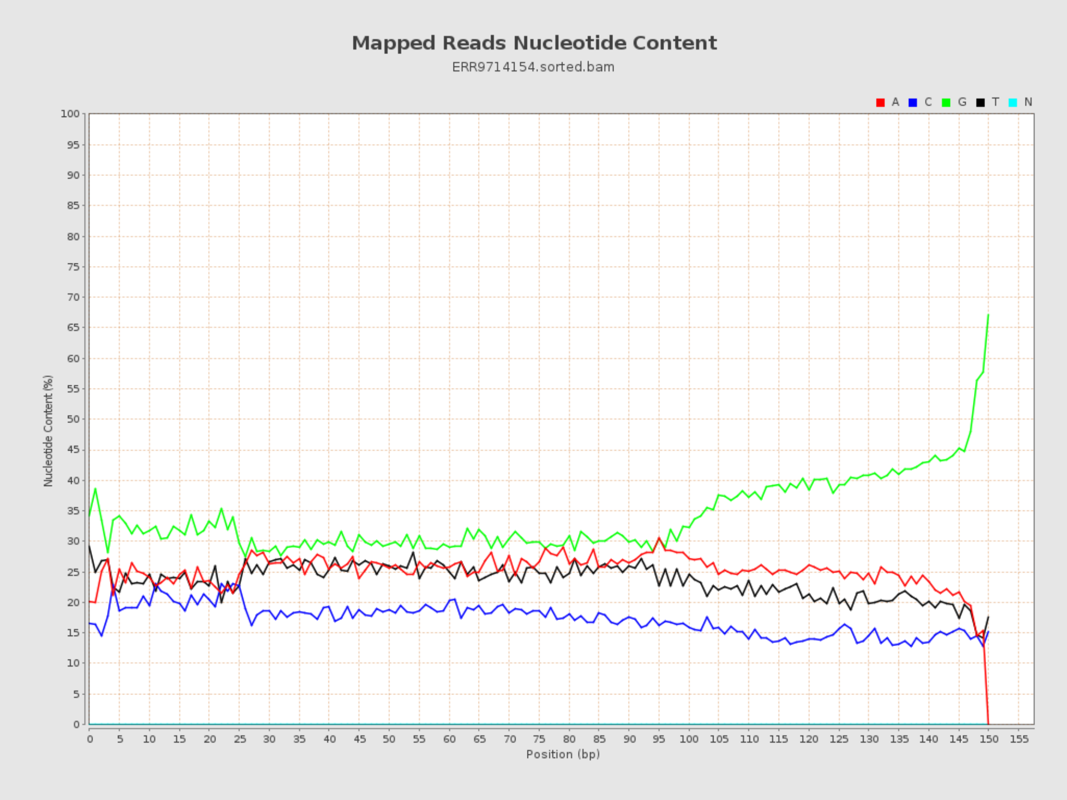
6. Results : Genome Fraction Coverage



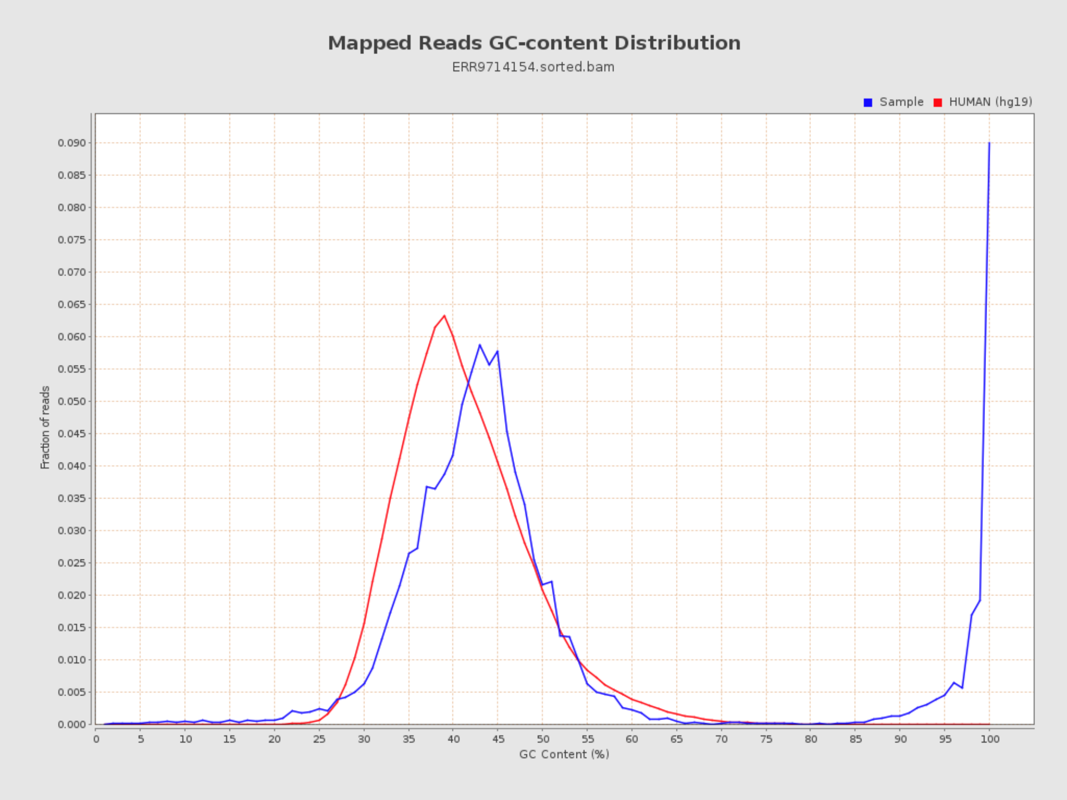
7. Results : Duplication Rate Histogram



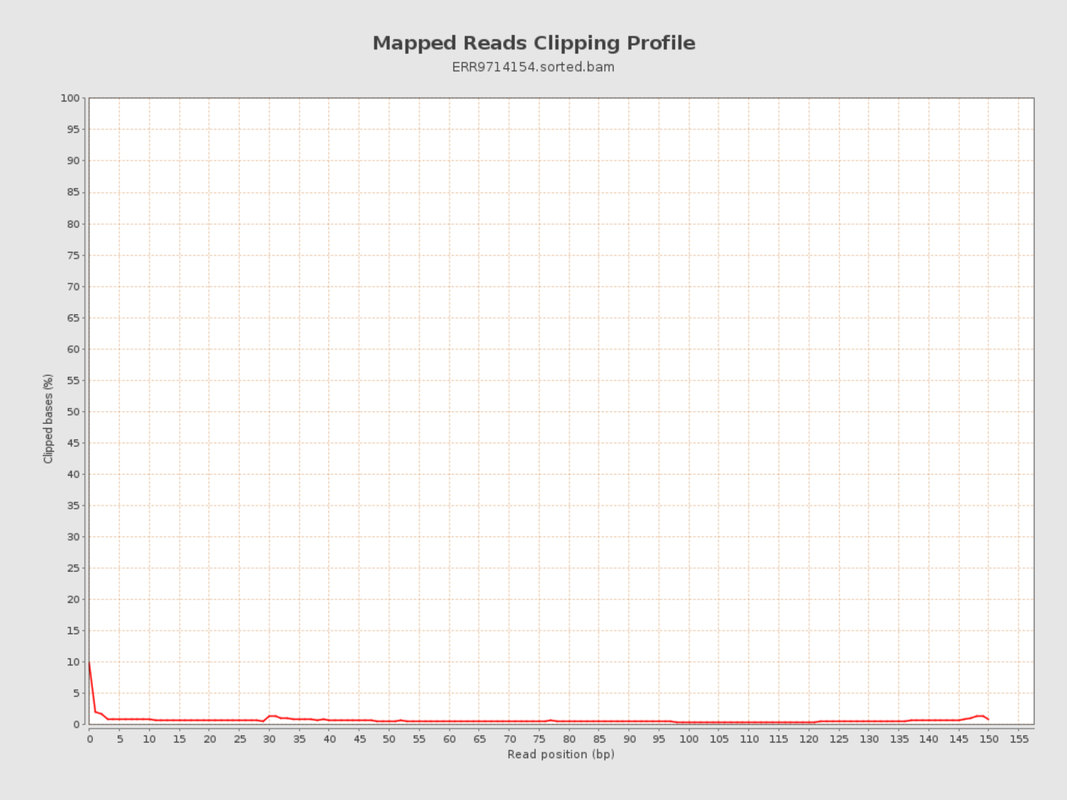
8. Results : Mapped Reads Nucleotide Content



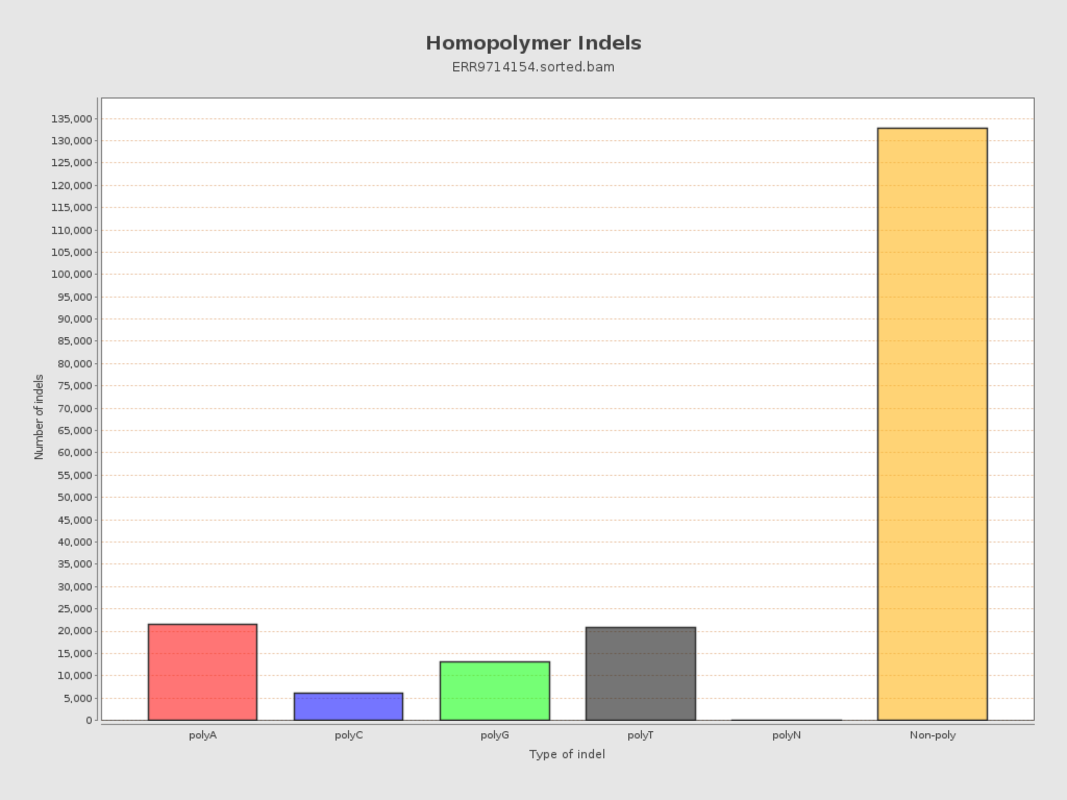
9. Results : Mapped Reads GC-content Distribution



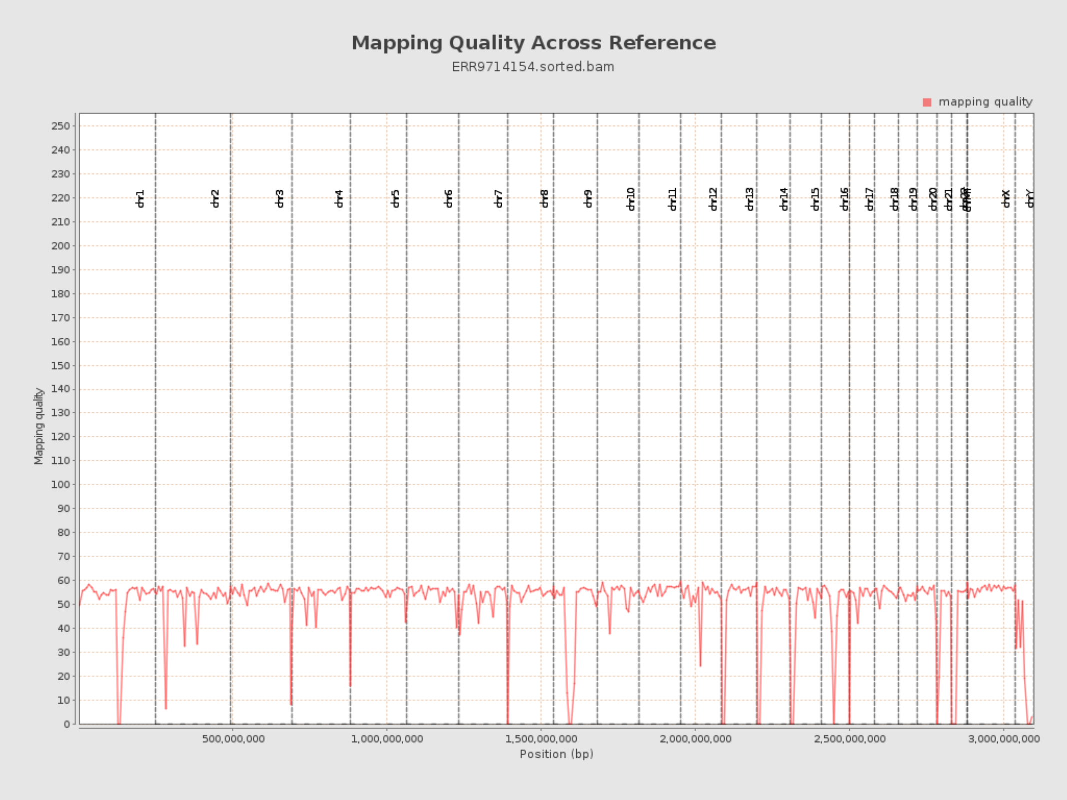
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram