Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:17:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714120.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_ERR9714120 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:17:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	850,600
Mapped reads	325,332 / 38.25%
Unmapped reads	525,268 / 61.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,833 / 1.86%
Read min/max/mean length	30 / 151 / 86.97
Duplicated reads (estimated)	277,694 / 32.65%
Duplication rate	42.26%
Clipped reads	294,339 / 34.6%

2.2. ACGT Content

Number/percentage of A's	10,287,535 / 25.86%
Number/percentage of C's	7,126,929 / 17.91%
Number/percentage of T's	9,732,853 / 24.46%
Number/percentage of G's	12,641,135 / 31.77%
Number/percentage of N's	505 / 0%
GC Percentage	49.68%

2.3. Coverage

Mean	0.0131

Standard Deviation	6.7764

2.4. Mapping Quality

Mean Mapping Quality	50.62

2.5. Mismatches and indels

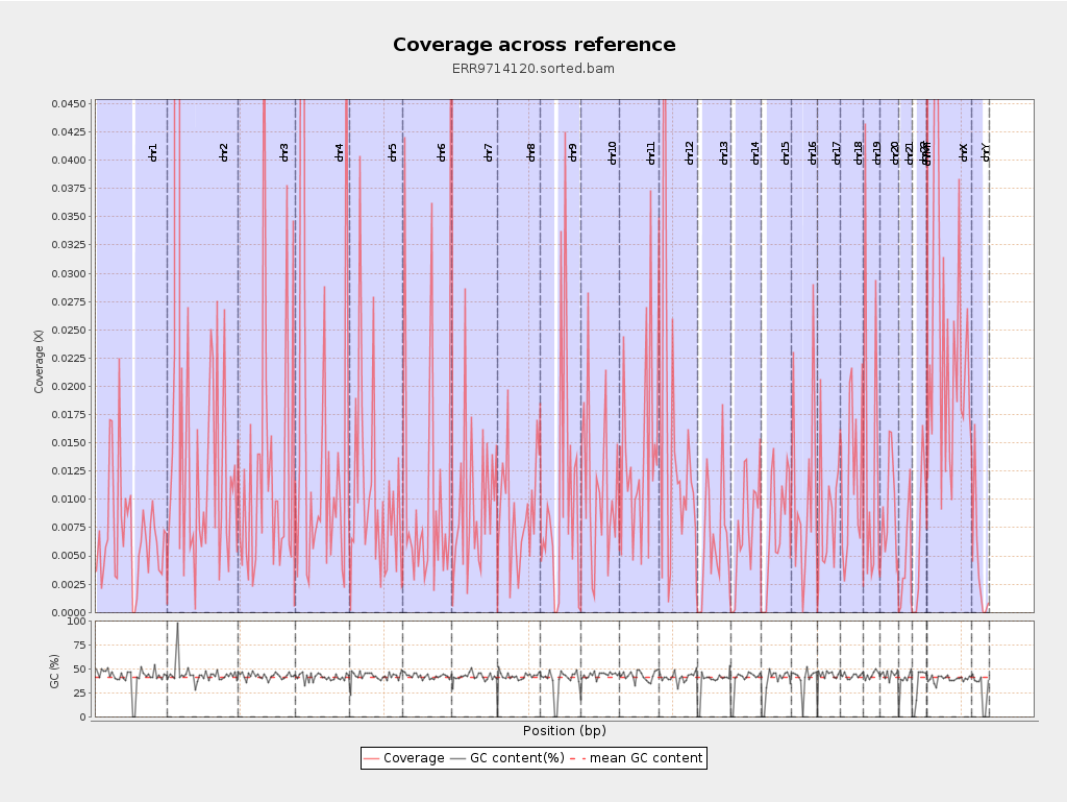
General error rate	4%
Mismatches	1,415,053
Insertions	47,934
Mapped reads with at least one insertion	13.69%
Deletions	110,237
Mapped reads with at least one deletion	32.47%
Homopolymer indels	28.58%

2.6. Chromosome stats

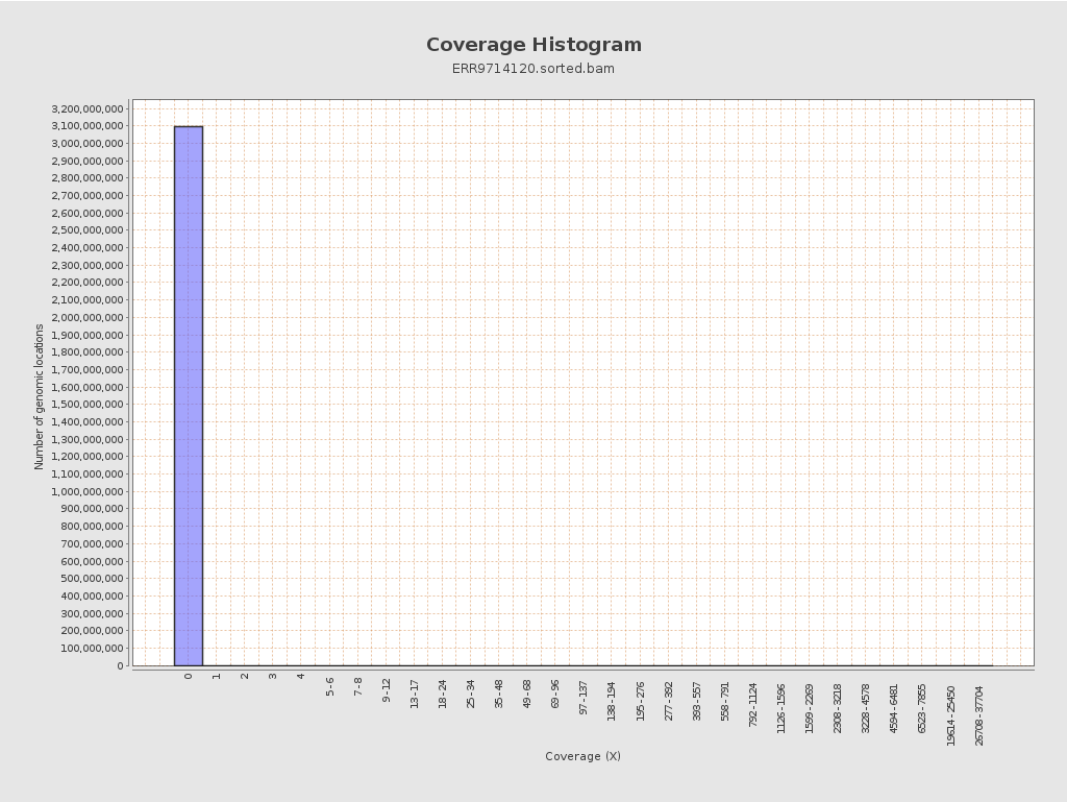
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1700144	0.0068	0.8692
chr2	243199373	8197378	0.0337	23.1055
chr3	198022430	2540554	0.0128	2.8855
chr4	191154276	3271487	0.0171	3.6593
chr5	180915260	1927153	0.0107	1.9929
chr6	171115067	1895419	0.0111	2.0902
chr7	159138663	1504608	0.0095	1.4023

chr8	146364022	1295029	0.0088	0.8989
chr9	141213431	1402130	0.0099	1.5788
chr10	135534747	1482431	0.0109	1.3345
chr11	135006516	1841119	0.0136	1.6872
chr12	133851895	2062550	0.0154	3.4841
chr13	115169878	697782	0.0061	0.6394
chr14	107349540	802172	0.0075	0.8294
chr15	102531392	759790	0.0074	0.8708
chr16	90354753	909020	0.0101	1.3516
chr17	81195210	724741	0.0089	1.0904
chr18	78077248	919978	0.0118	1.3082
chr19	59128983	759412	0.0128	2.1535
chr20	63025520	570955	0.0091	1.0427
chr21	48129895	210237	0.0044	0.6704
chr22	51304566	324001	0.0063	0.6503
chrMT	16571	605806	36.5582	295.3356
chrX	155270560	3801130	0.0245	2.4808
chrY	59373566	245080	0.0041	0.5523

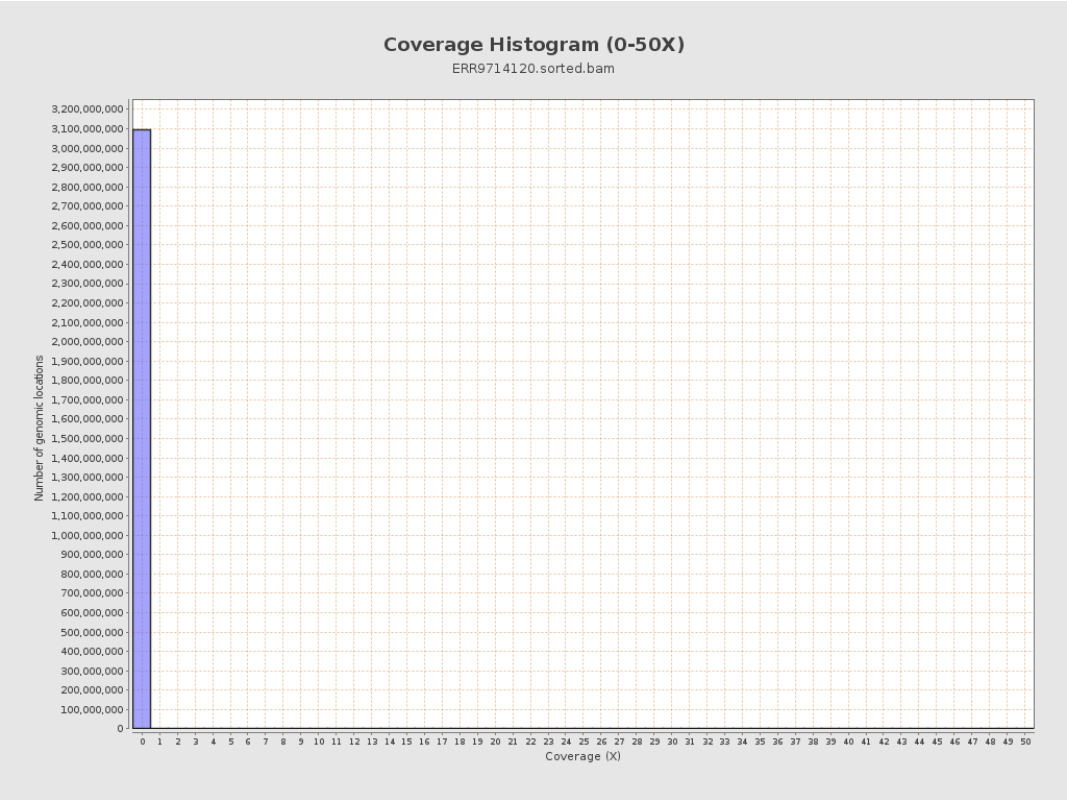
3. Results : Coverage across reference



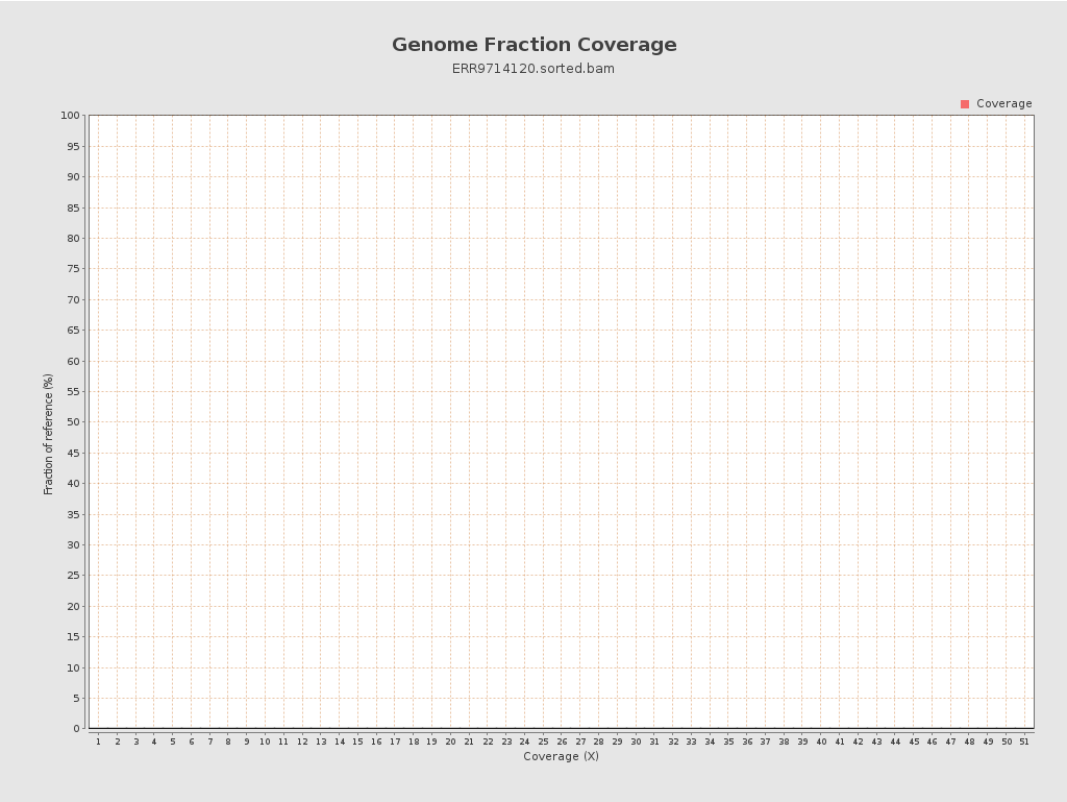
4. Results : Coverage Histogram



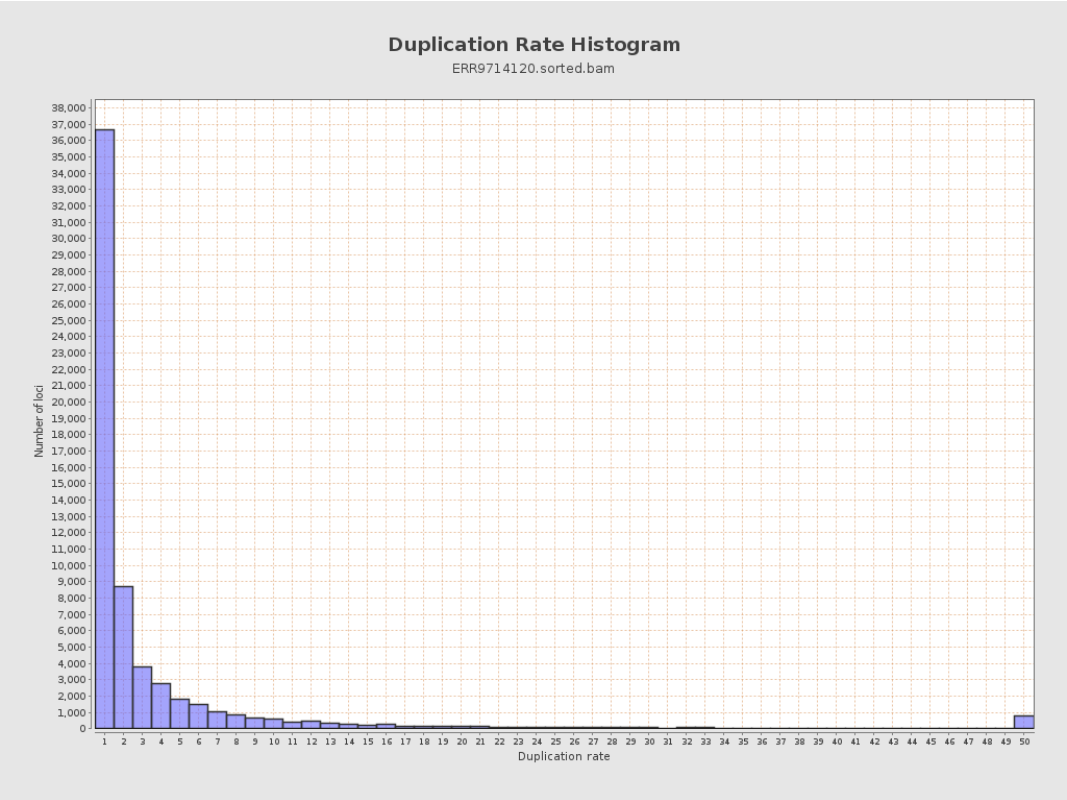
5. Results : Coverage Histogram (0-50X)



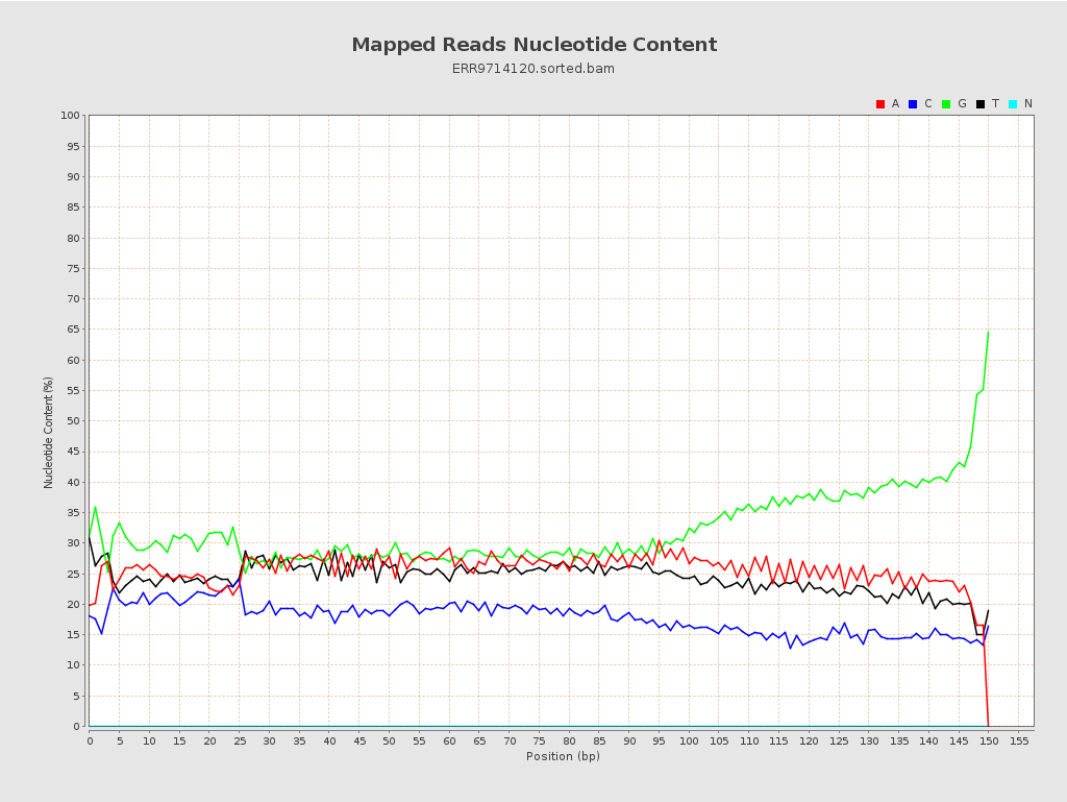
6. Results : Genome Fraction Coverage



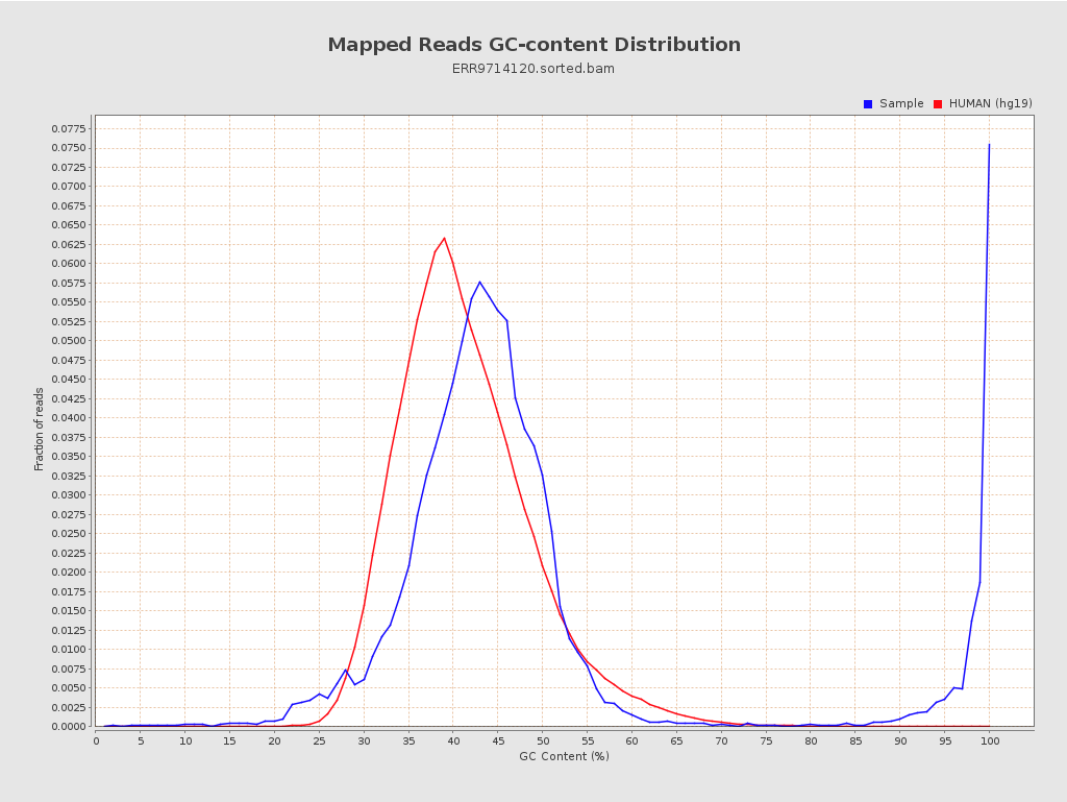
7. Results : Duplication Rate Histogram



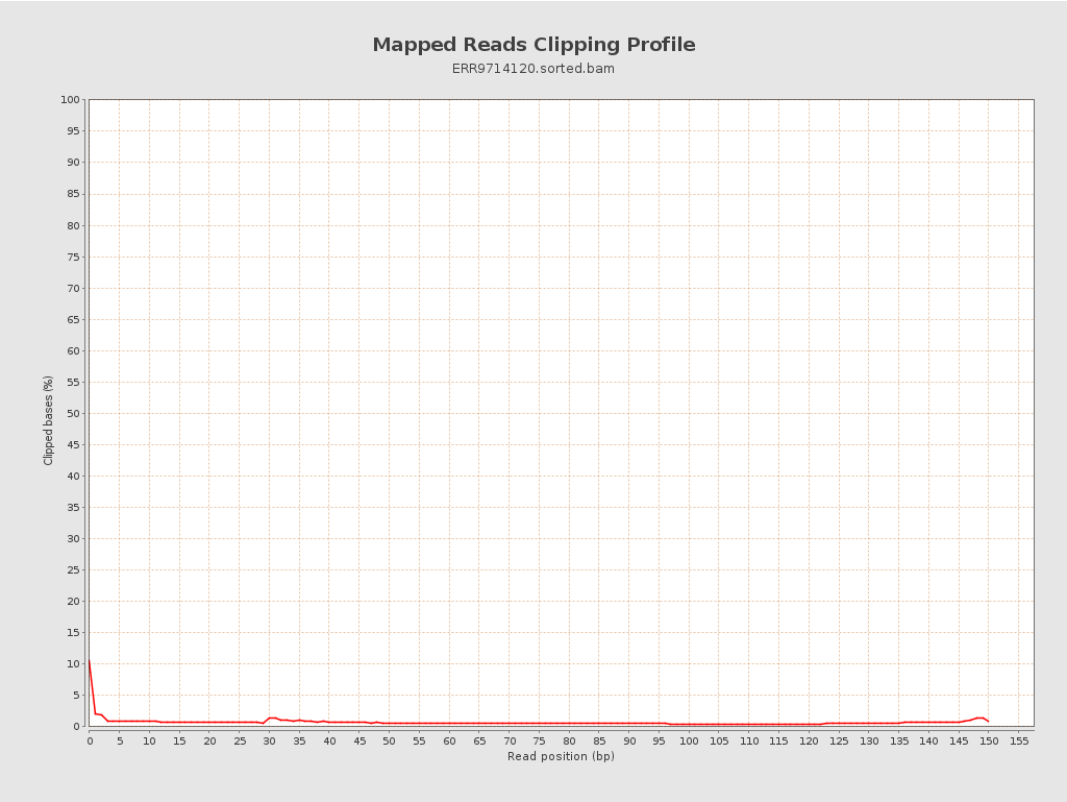
8. Results : Mapped Reads Nucleotide Content



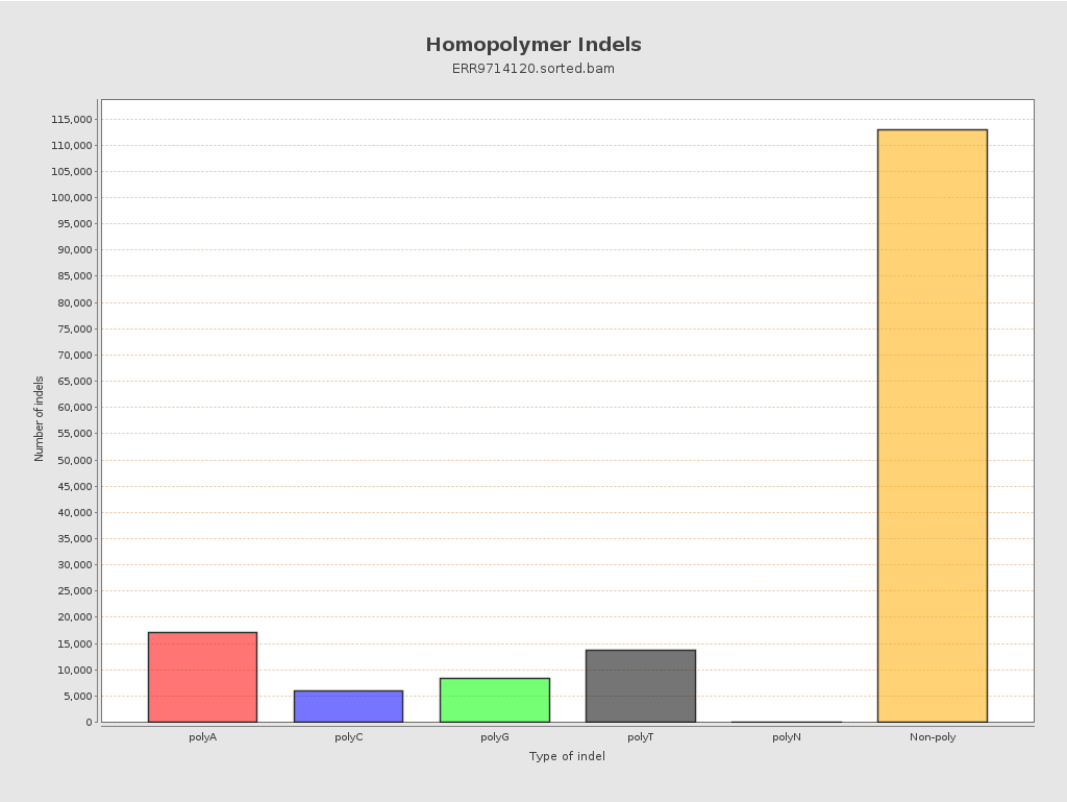
9. Results : Mapped Reads GC-content Distribution



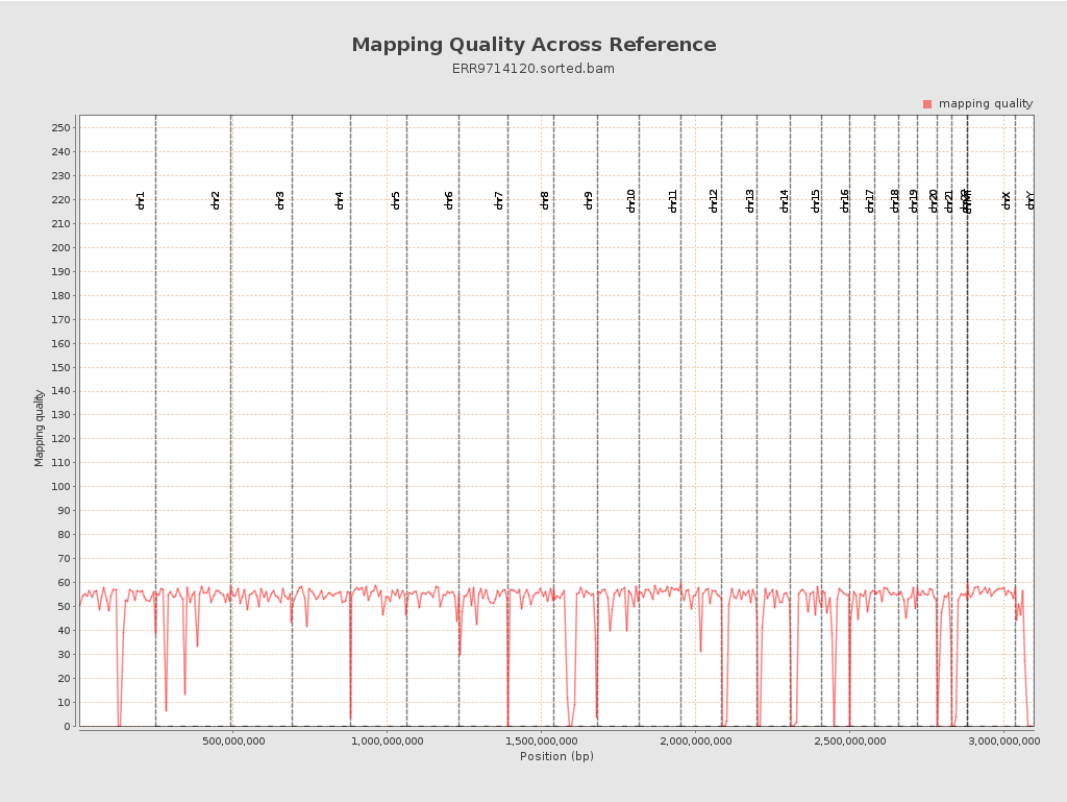
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram