Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:45:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714188.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_ERR9714188 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	72,632
Mapped reads	3,951 / 5.44%
Unmapped reads	68,681 / 94.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	165 / 0.23%
Read min/max/mean length	30 / 151 / 53.4
Duplicated reads (estimated)	3,095 / 4.26%
Duplication rate	32.52%
Clipped reads	3,321 / 4.57%

2.2. ACGT Content

Number/percentage of A's	37,207 / 11.88%
Number/percentage of C's	22,162 / 7.08%
Number/percentage of T's	27,795 / 8.87%
Number/percentage of G's	226,015 / 72.17%
Number/percentage of N's	7 / 0%
GC Percentage	79.24%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.233

2.4. Mapping Quality

Mean Mapping Quality	13.96

2.5. Mismatches and indels

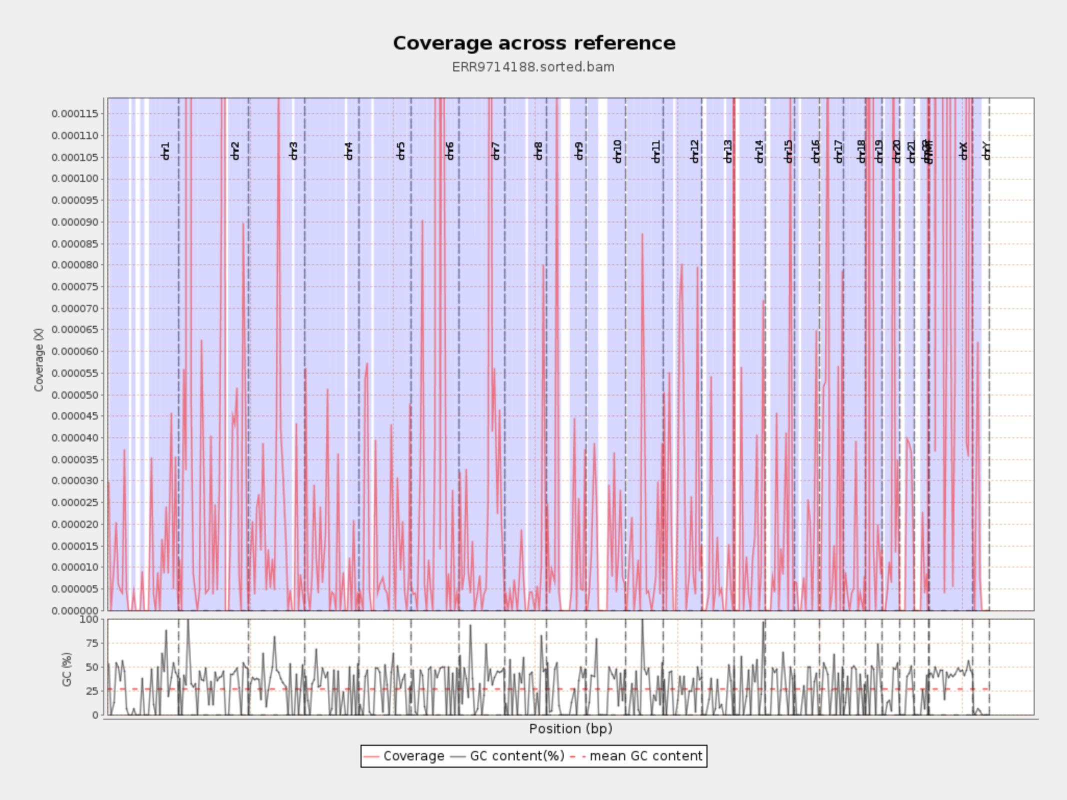
General error rate	3.25%
Mismatches	8,359
Insertions	353
Mapped reads with at least one insertion	6.38%
Deletions	376
Mapped reads with at least one deletion	9.24%
Homopolymer indels	43.76%

2.6. Chromosome stats

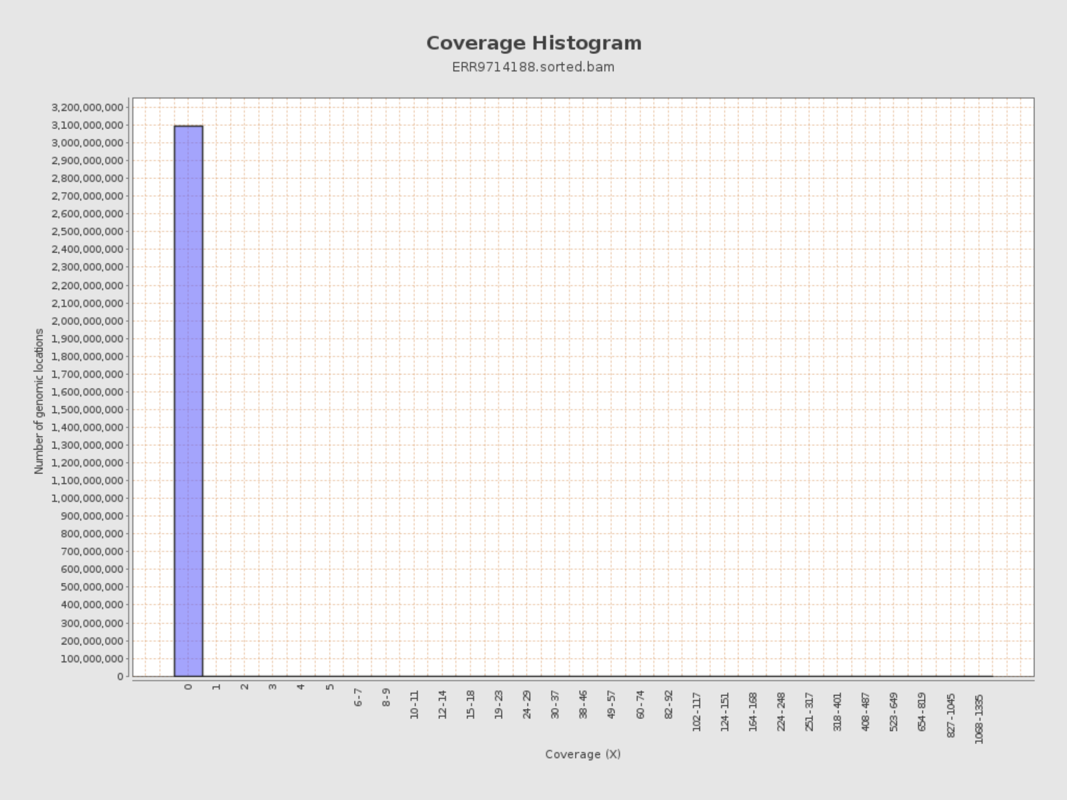
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2535	0	0.0047
chr2	243199373	212927	0.0009	0.8268
chr3	198022430	3896	0	0.0079
chr4	191154276	2256	0	0.0043
chr5	180915260	2584	0	0.0047
chr6	171115067	14062	0.0001	0.0585
chr7	159138663	4554	0	0.0272

chr8	146364022	1340	0	0.0061
chr9	141213431	2289	0	0.0074
chr10	135534747	1642	0	0.0052
chr11	135006516	2152	0	0.0105
chr12	133851895	3714	0	0.009
chr13	115169878	1613	0	0.0069
chr14	107349540	1735	0	0.0103
chr15	102531392	2037	0	0.0061
chr16	90354753	1161	0	0.0047
chr17	81195210	2810	0	0.018
chr18	78077248	544	0	0.0029
chr19	59128983	9583	0.0002	0.0824
chr20	63025520	1688	0	0.0121
chr21	48129895	975	0	0.0053
chr22	51304566	275	0	0.0031
chrMT	16571	592	0.0357	0.2447
chrX	155270560	38405	0.0002	0.0598
chrY	59373566	569	0	0.0072

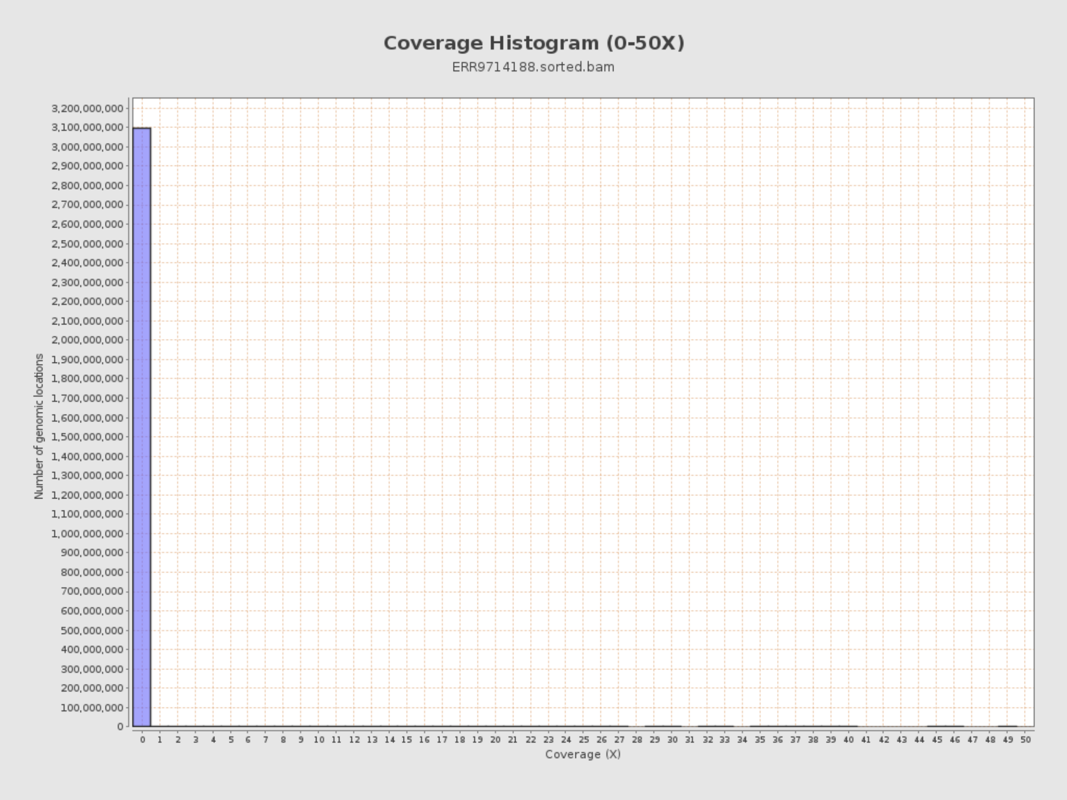
3. Results : Coverage across reference



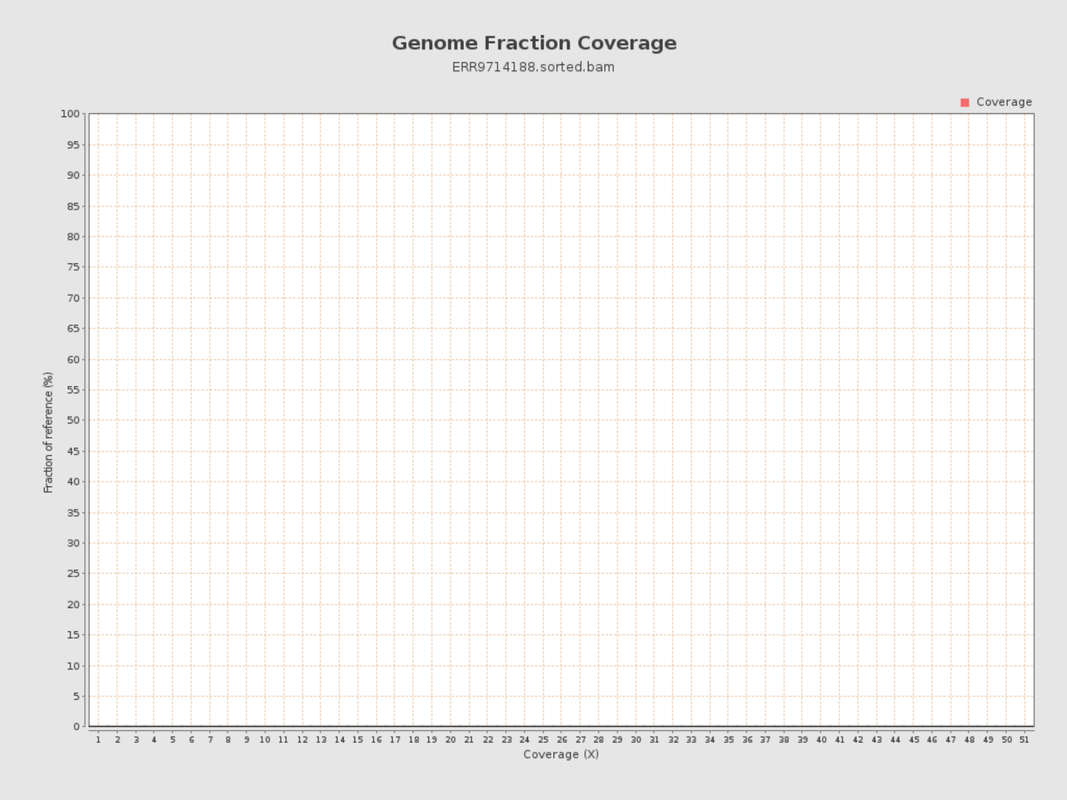
4. Results : Coverage Histogram



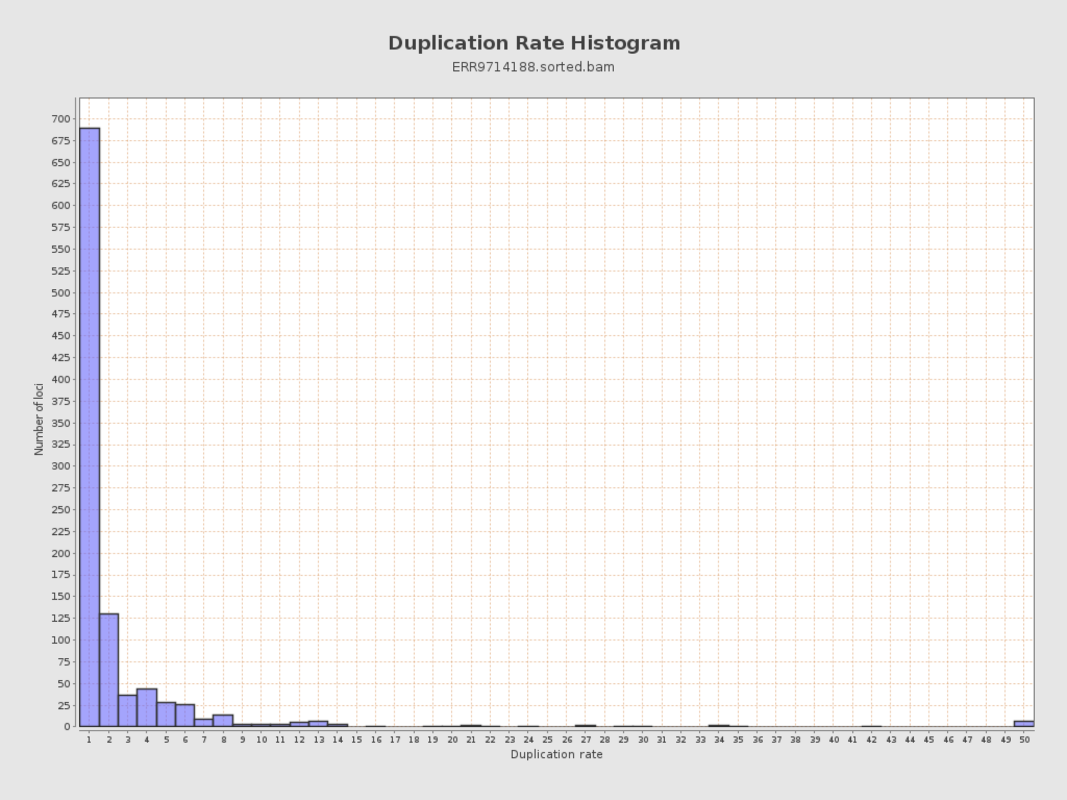
5. Results : Coverage Histogram (0-50X)



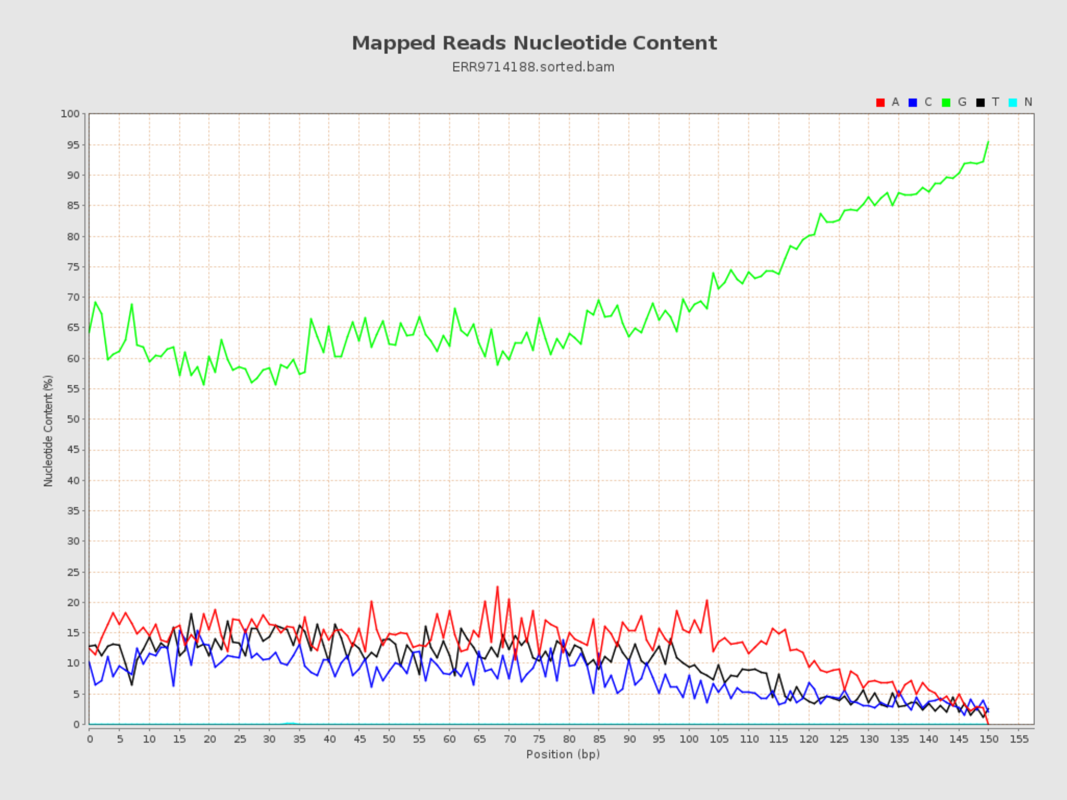
6. Results : Genome Fraction Coverage



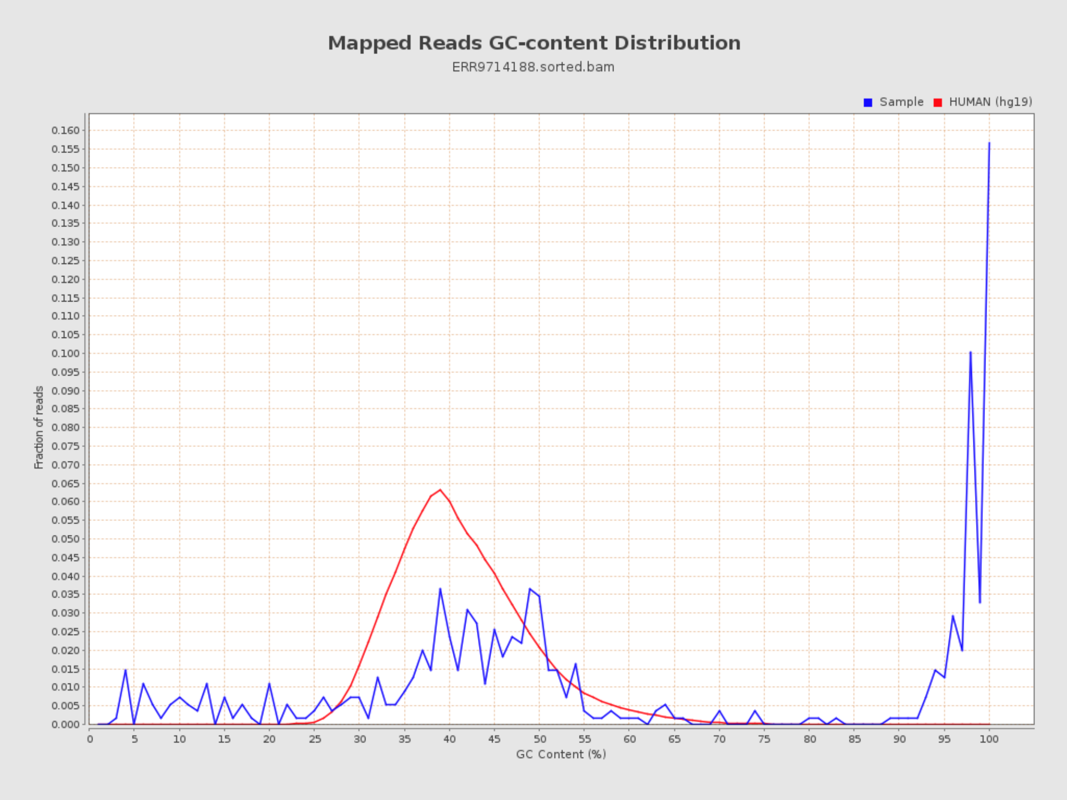
7. Results : Duplication Rate Histogram



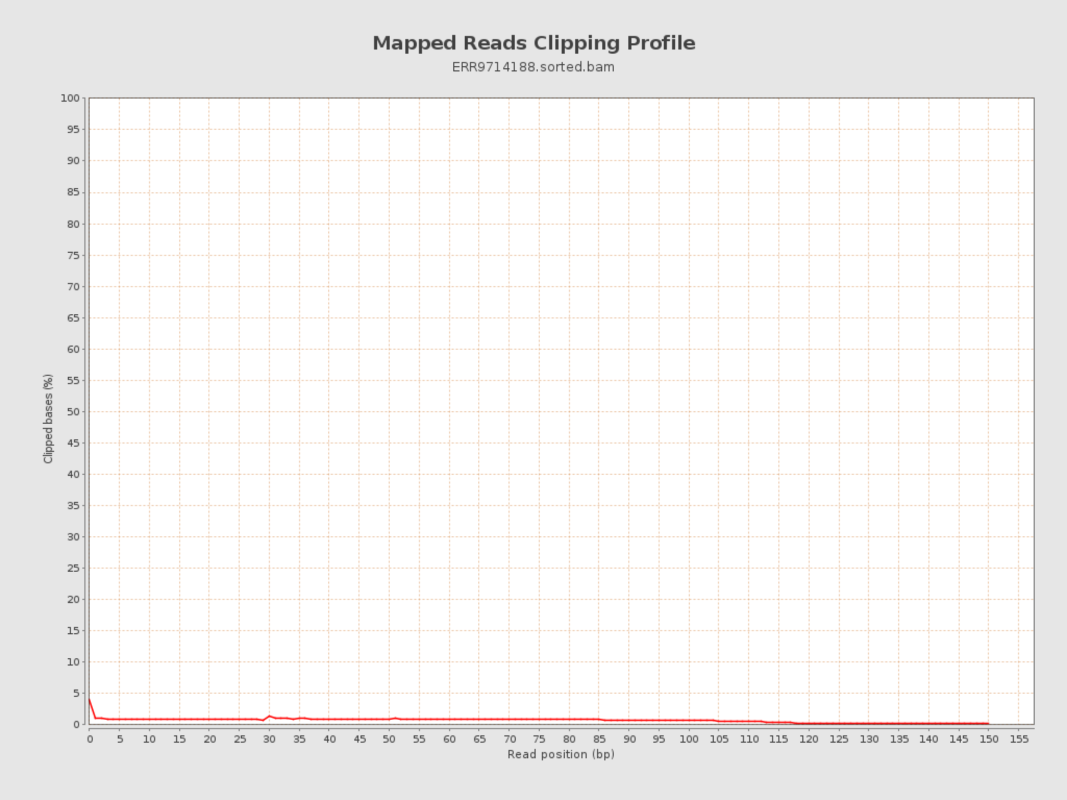
8. Results : Mapped Reads Nucleotide Content



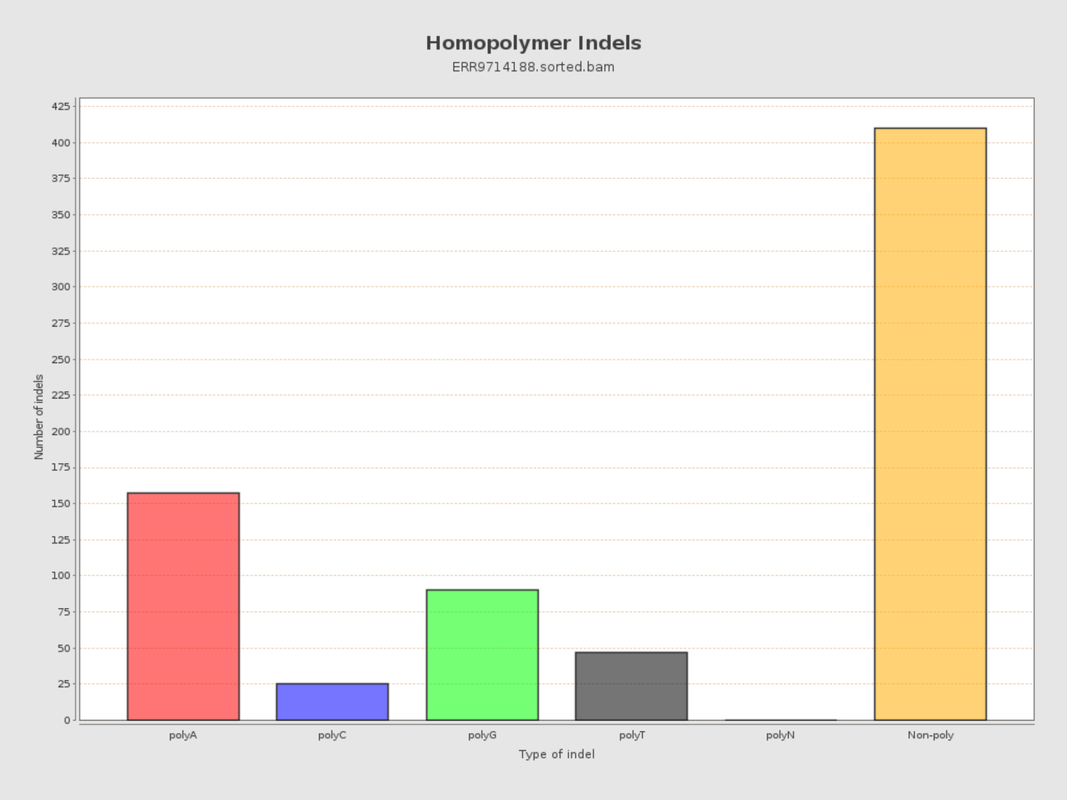
9. Results : Mapped Reads GC-content Distribution



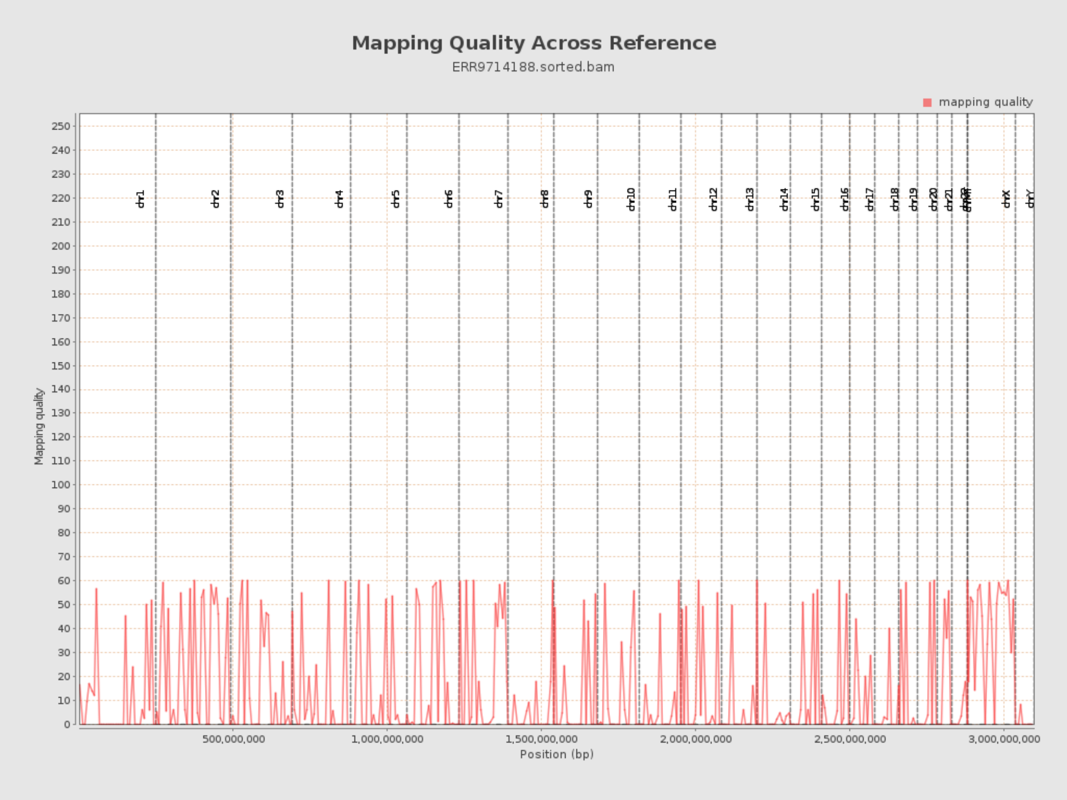
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram