Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:13:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714072.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_ERR9714072 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:13:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	543,670
Mapped reads	101,184 / 18.61%
Unmapped reads	442,486 / 81.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,178 / 0.58%
Read min/max/mean length	30 / 151 / 75.74
Duplicated reads (estimated)	89,969 / 16.55%
Duplication rate	39.21%
Clipped reads	83,509 / 15.36%

2.2. ACGT Content

Number/percentage of A's	2,193,990 / 19.77%
Number/percentage of C's	1,505,362 / 13.57%
Number/percentage of T's	2,049,238 / 18.47%
Number/percentage of G's	5,347,970 / 48.19%
Number/percentage of N's	253 / 0%
GC Percentage	61.76%

2.3. Coverage

Mean	0.0036

Standard Deviation	4.6734

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

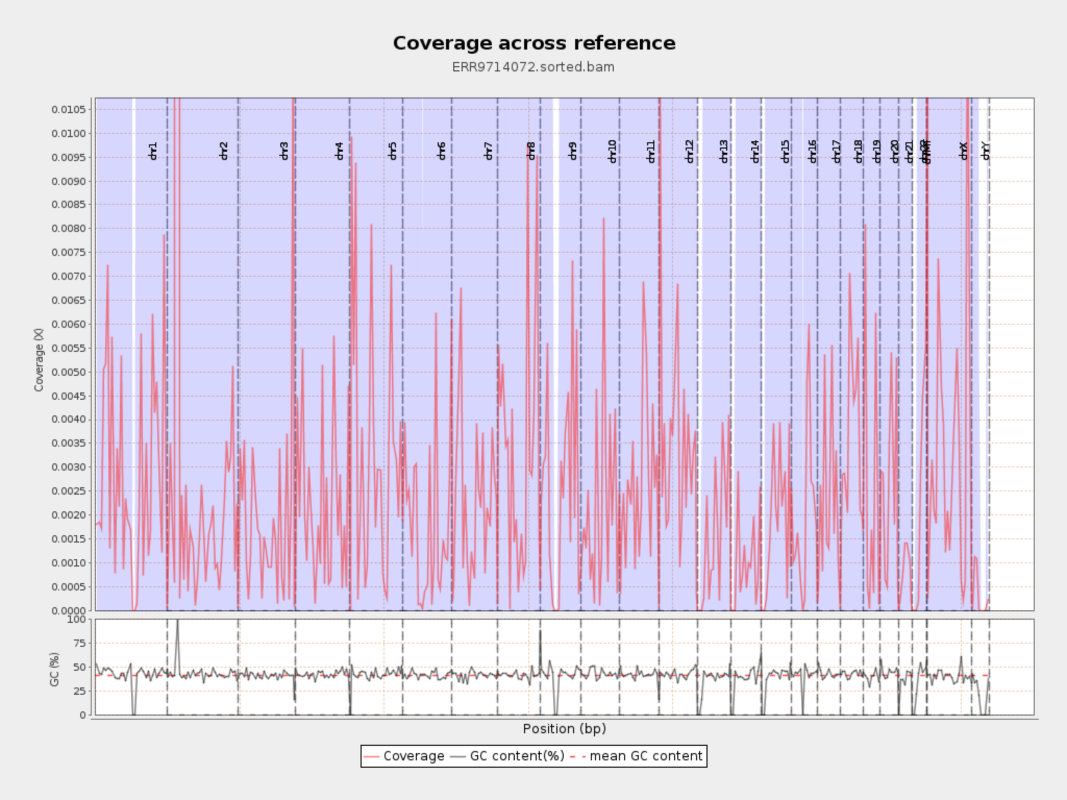
General error rate	4.15%
Mismatches	411,855
Insertions	12,943
Mapped reads with at least one insertion	11.25%
Deletions	30,350
Mapped reads with at least one deletion	27.42%
Homopolymer indels	32.8%

2.6. Chromosome stats

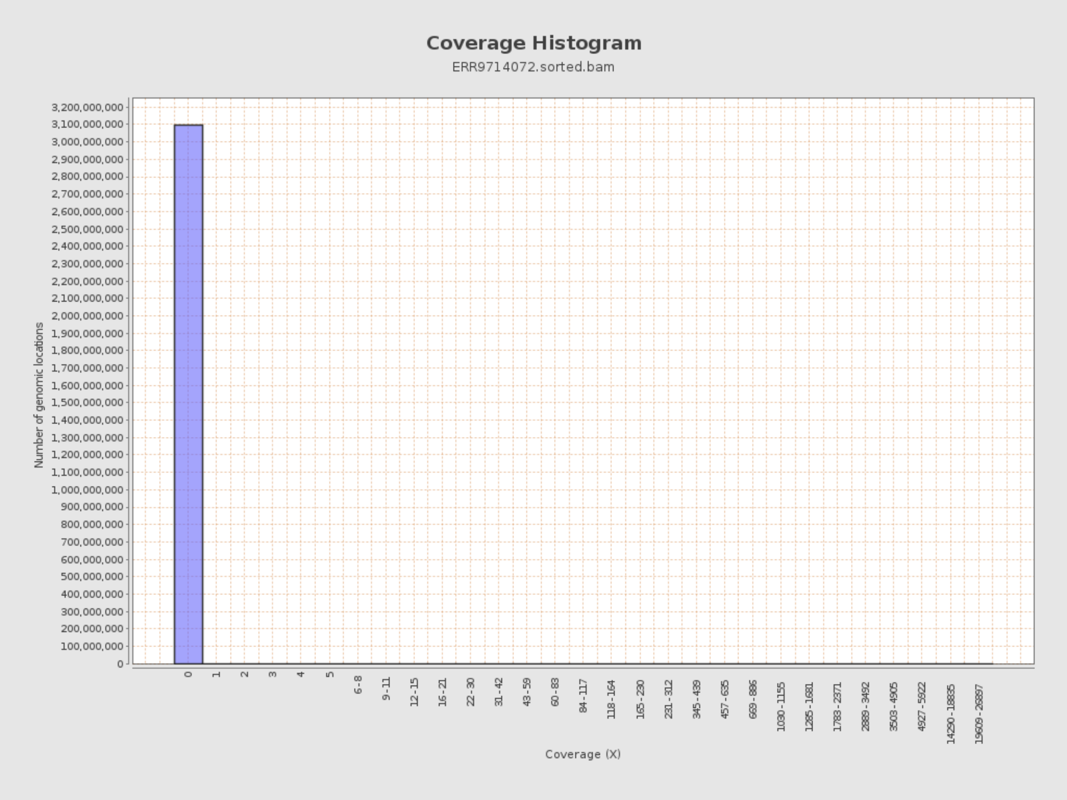
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	721743	0.0029	0.4342
chr2	243199373	4233945	0.0174	16.61
chr3	198022430	406179	0.0021	0.5212
chr4	191154276	423995	0.0022	0.4053
chr5	180915260	628983	0.0035	0.5441
chr6	171115067	305138	0.0018	0.3219
chr7	159138663	369248	0.0023	0.3966

chr8	146364022	495723	0.0034	0.5268
chr9	141213431	359677	0.0025	0.4465
chr10	135534747	297557	0.0022	0.373
chr11	135006516	363466	0.0027	0.3706
chr12	133851895	490853	0.0037	0.5056
chr13	115169878	182730	0.0016	0.3249
chr14	107349540	101503	0.0009	0.2329
chr15	102531392	195751	0.0019	0.3159
chr16	90354753	186413	0.0021	0.3826
chr17	81195210	182671	0.0022	0.3947
chr18	78077248	304124	0.0039	0.4894
chr19	59128983	138190	0.0023	0.4977
chr20	63025520	173171	0.0027	0.4139
chr21	48129895	39072	0.0008	0.1465
chr22	51304566	119152	0.0023	0.3593
chrMT	16571	34340	2.0723	16.4366
chrX	155270560	513709	0.0033	0.4716
chrY	59373566	19512	0.0003	0.0854

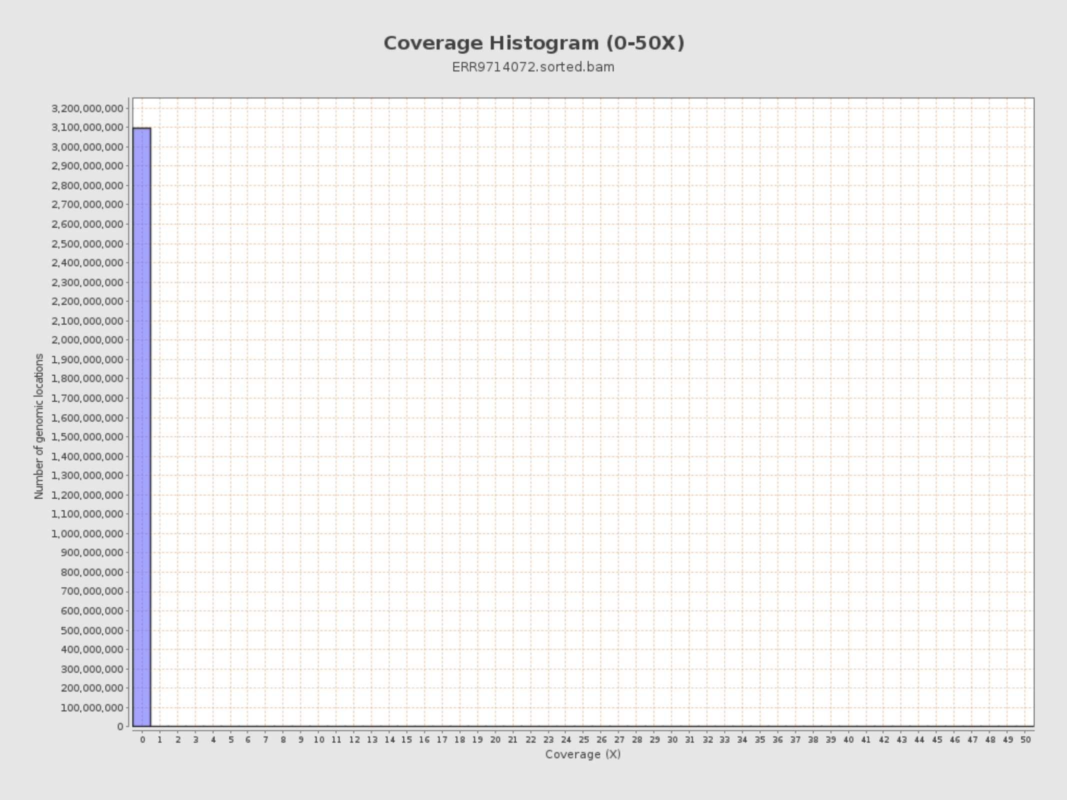
3. Results : Coverage across reference



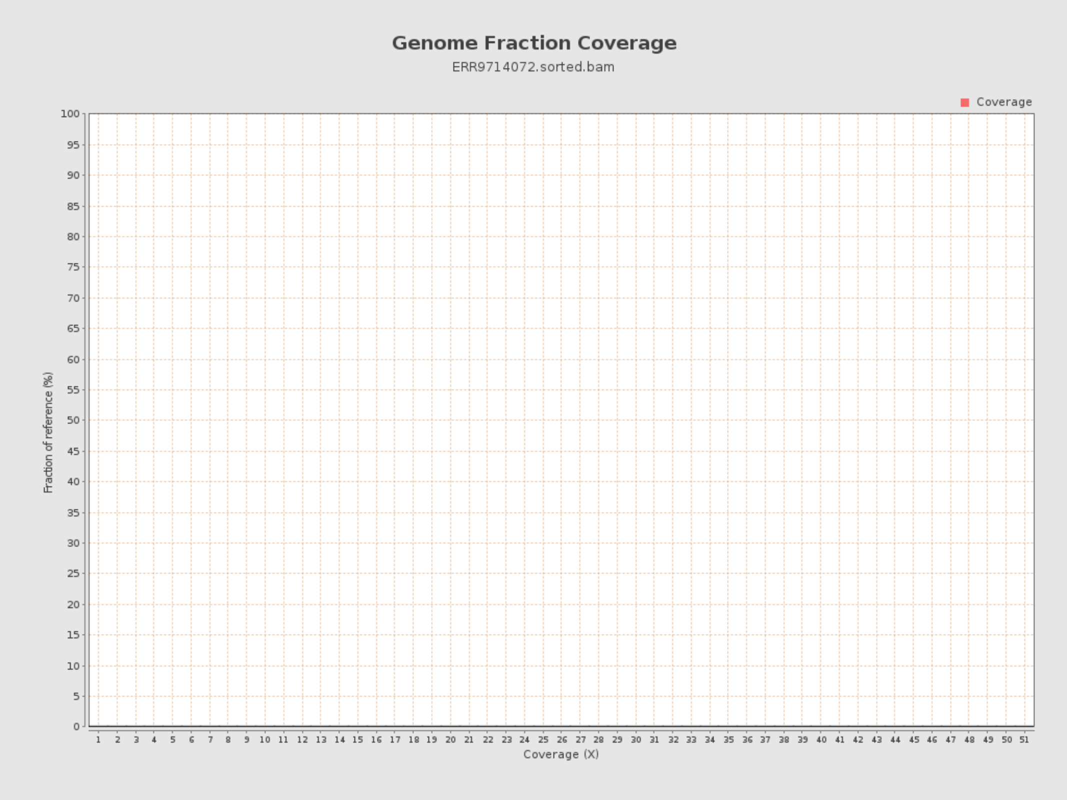
4. Results : Coverage Histogram



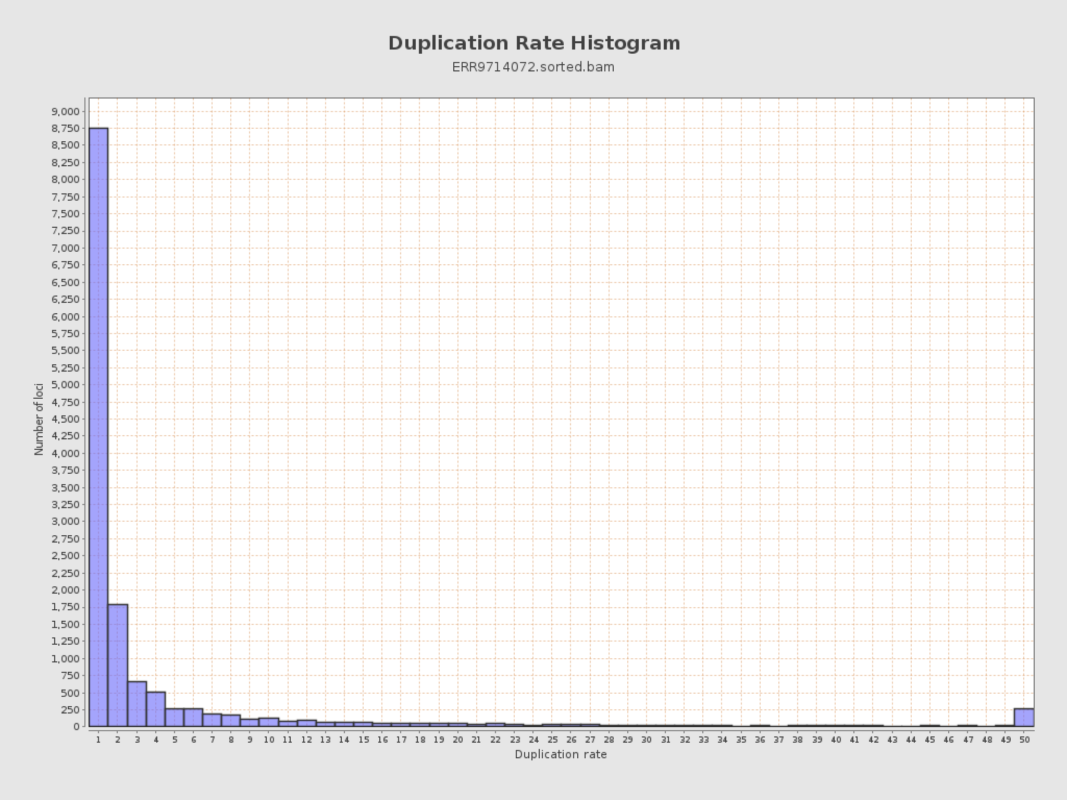
5. Results : Coverage Histogram (0-50X)



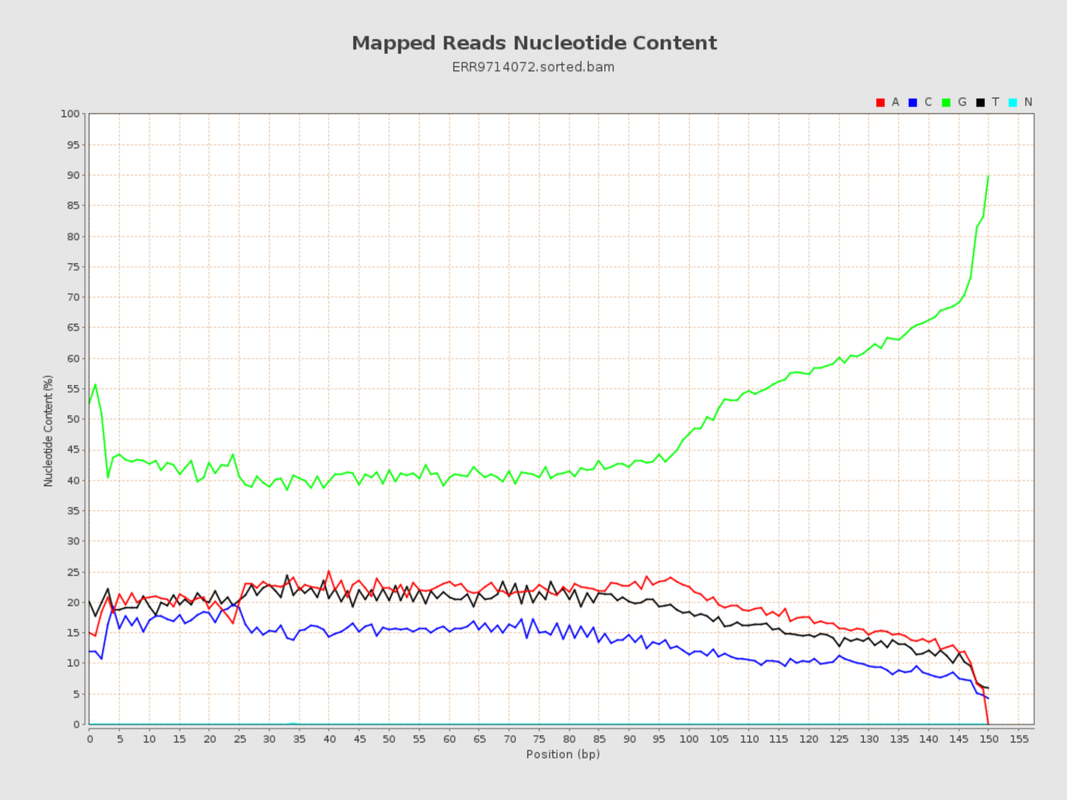
6. Results : Genome Fraction Coverage



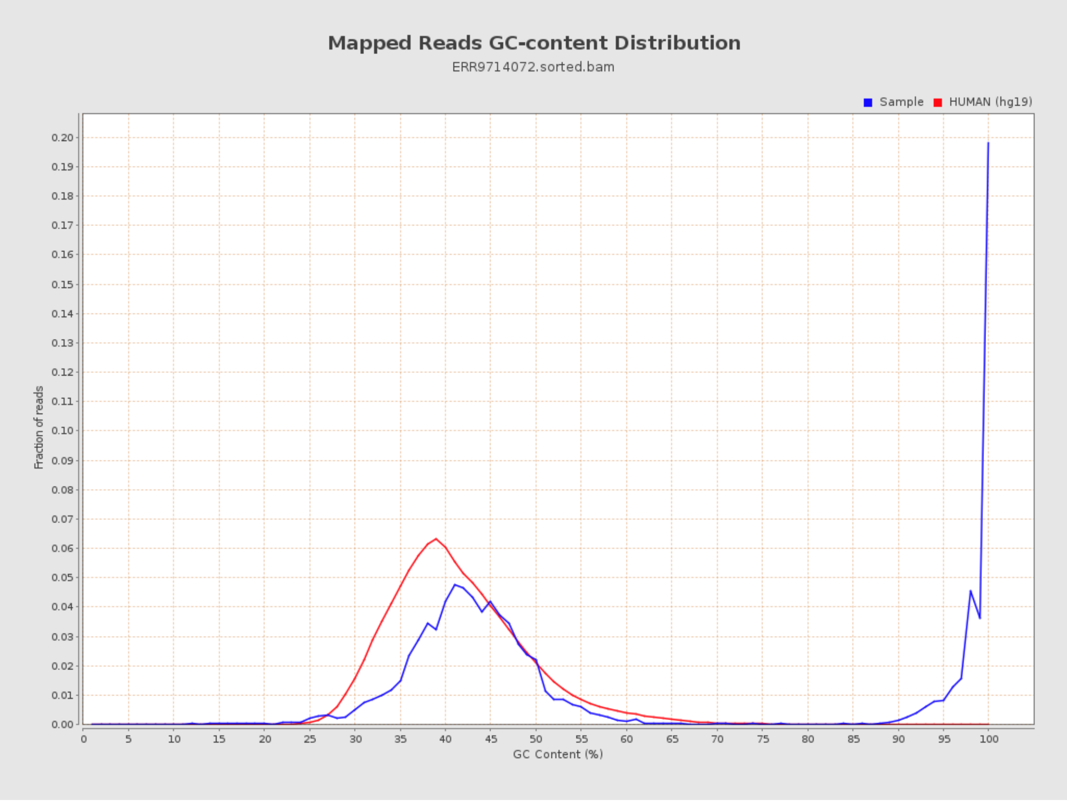
7. Results : Duplication Rate Histogram



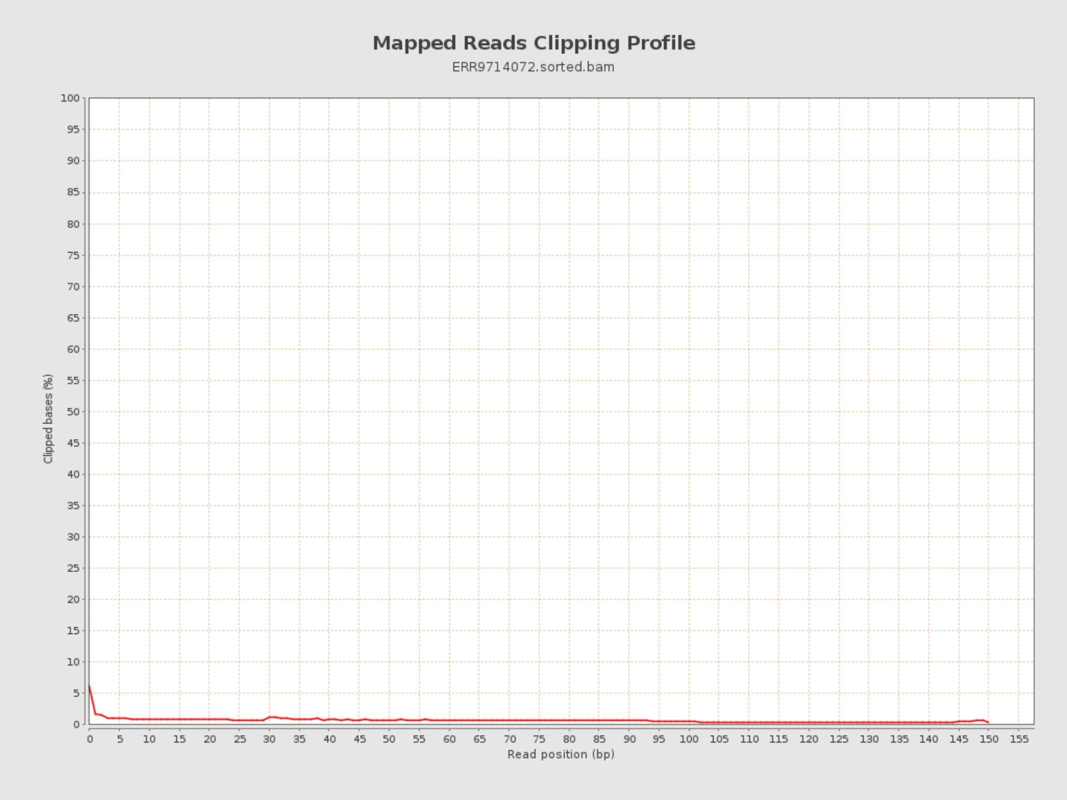
8. Results : Mapped Reads Nucleotide Content



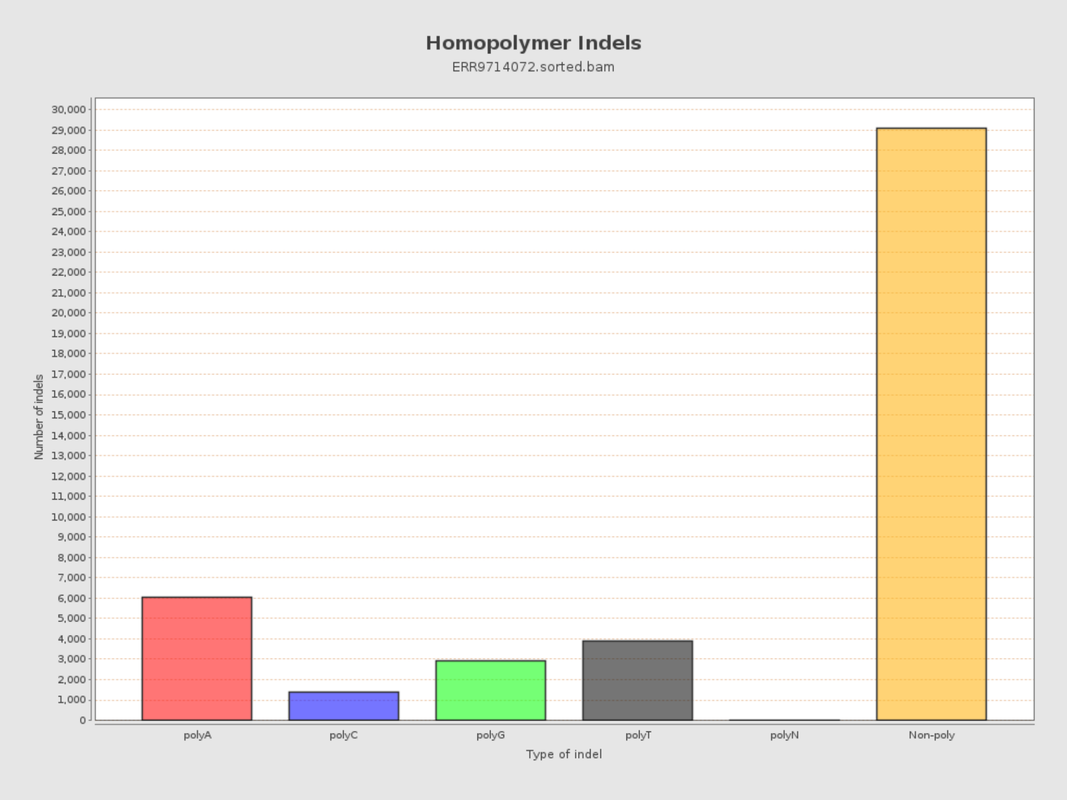
9. Results : Mapped Reads GC-content Distribution



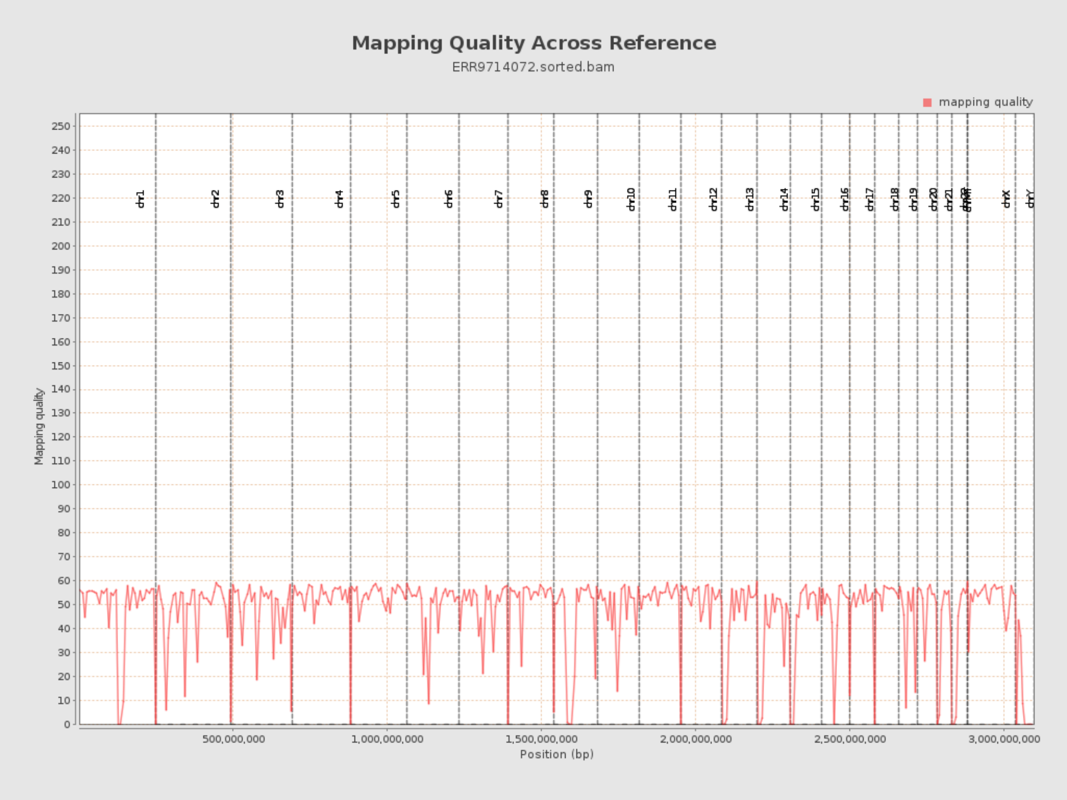
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram