Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:24:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714123.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_ERR9714123 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:24:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,288
Mapped reads	8,095 / 30.79%
Unmapped reads	18,193 / 69.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	291 / 1.11%
Read min/max/mean length	30 / 151 / 92.01
Duplicated reads (estimated)	5,392 / 20.51%
Duplication rate	37.27%
Clipped reads	7,443 / 28.31%

2.2. ACGT Content

Number/percentage of A's	254,490 / 26.35%
Number/percentage of C's	178,586 / 18.49%
Number/percentage of T's	241,071 / 24.96%
Number/percentage of G's	291,506 / 30.19%
Number/percentage of N's	12 / 0%
GC Percentage	48.68%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.1473

2.4. Mapping Quality

Mean Mapping Quality	39.87

2.5. Mismatches and indels

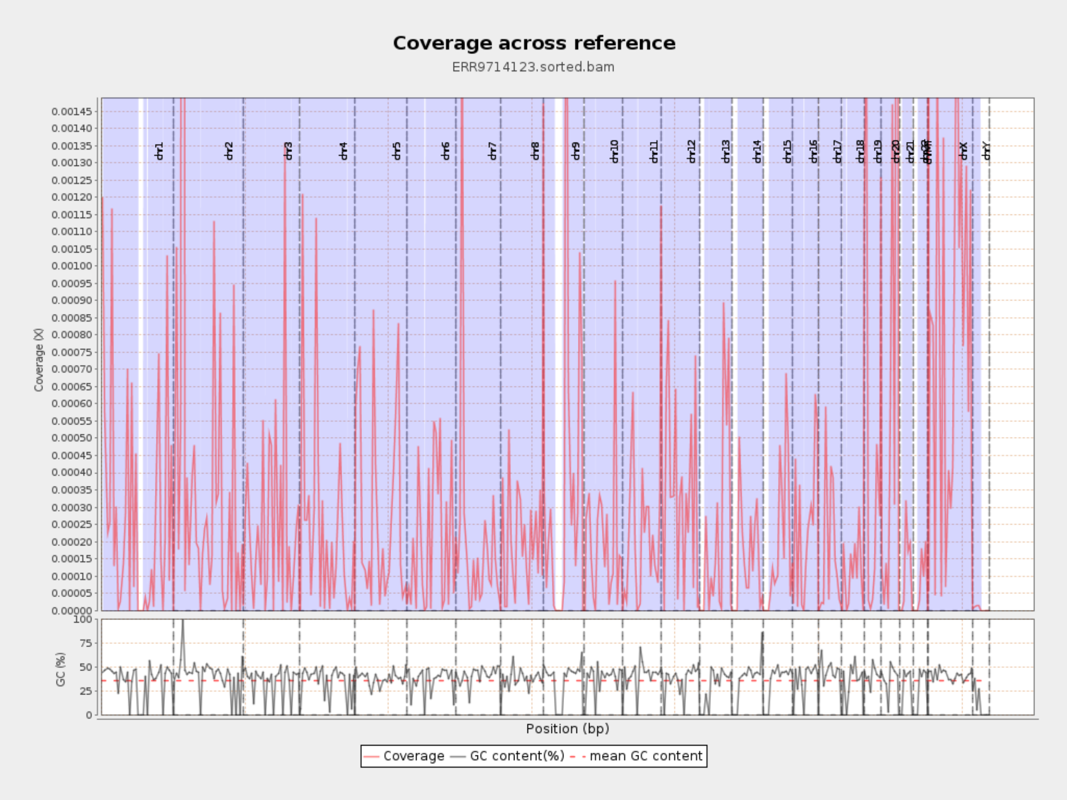
General error rate	4.31%
Mismatches	38,260
Insertions	979
Mapped reads with at least one insertion	11.28%
Deletions	3,162
Mapped reads with at least one deletion	37.13%
Homopolymer indels	31.66%

2.6. Chromosome stats

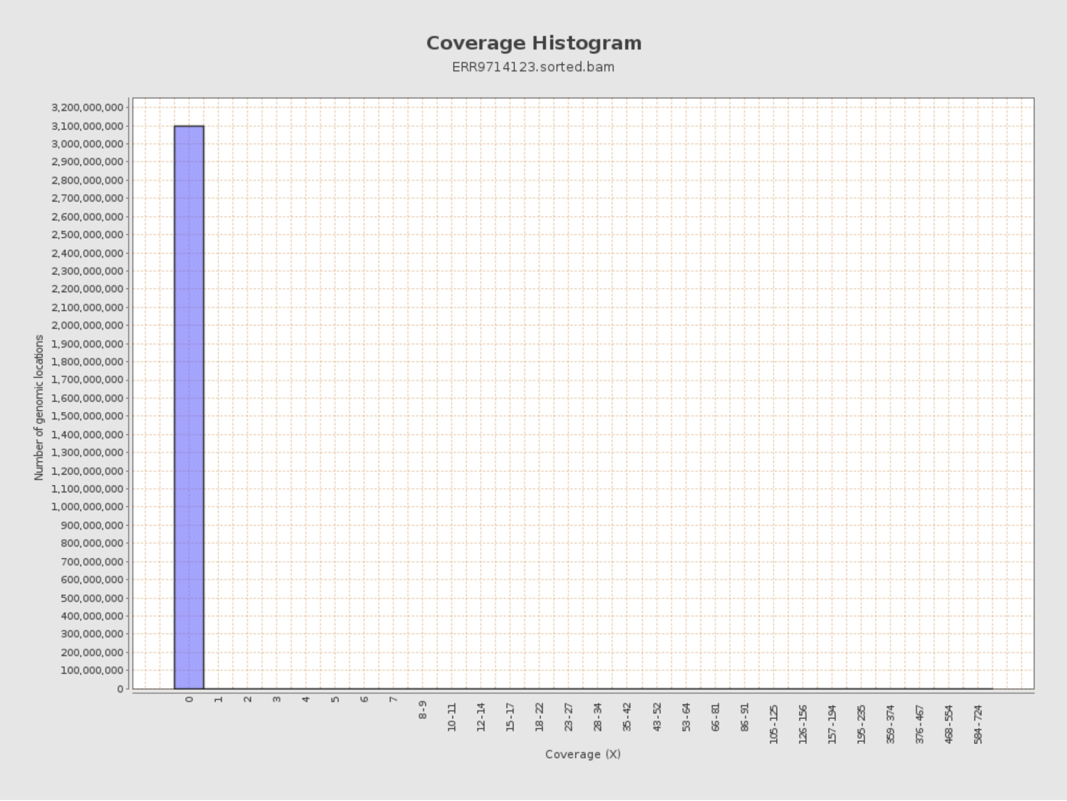
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	72581	0.0003	0.0653
chr2	243199373	176759	0.0007	0.4512
chr3	198022430	50276	0.0003	0.0584
chr4	191154276	48491	0.0003	0.0787
chr5	180915260	52471	0.0003	0.0672
chr6	171115067	34678	0.0002	0.0488
chr7	159138663	33514	0.0002	0.0637

chr8	146364022	29132	0.0002	0.0488
chr9	141213431	55458	0.0004	0.127
chr10	135534747	27424	0.0002	0.0476
chr11	135006516	29410	0.0002	0.0496
chr12	133851895	45396	0.0003	0.0706
chr13	115169878	24253	0.0002	0.0546
chr14	107349540	15555	0.0001	0.0332
chr15	102531392	20182	0.0002	0.0414
chr16	90354753	22831	0.0003	0.0549
chr17	81195210	13602	0.0002	0.0419
chr18	78077248	9081	0.0001	0.0248
chr19	59128983	26856	0.0005	0.1131
chr20	63025520	46891	0.0007	0.265
chr21	48129895	5520	0.0001	0.0324
chr22	51304566	3942	0.0001	0.024
chrMT	16571	12521	0.7556	6.1971
chrX	155270560	128099	0.0008	0.1128
chrY	59373566	321	0	0.0023

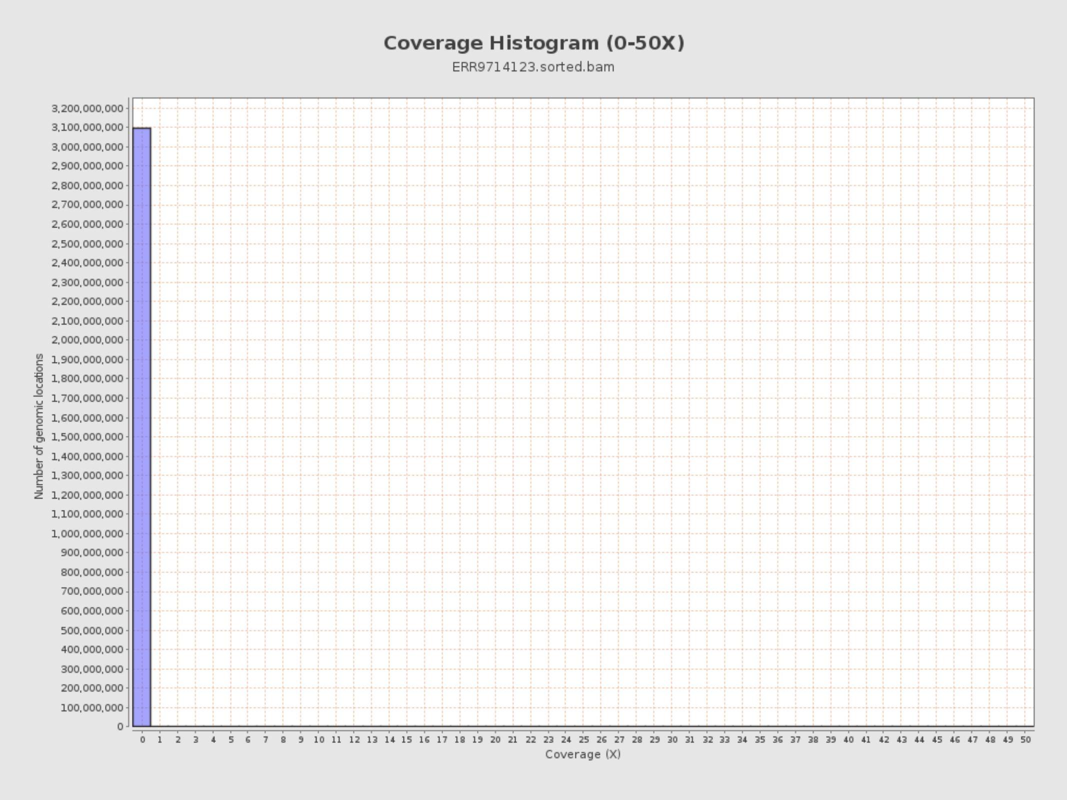
3. Results : Coverage across reference



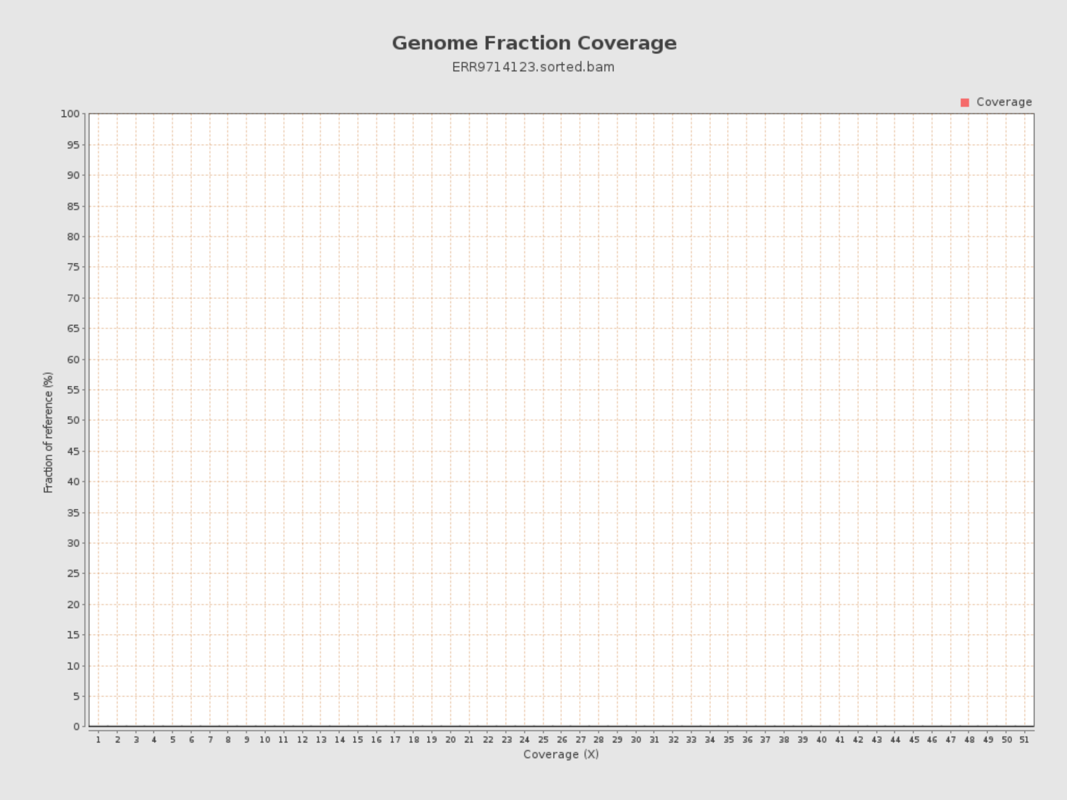
4. Results : Coverage Histogram



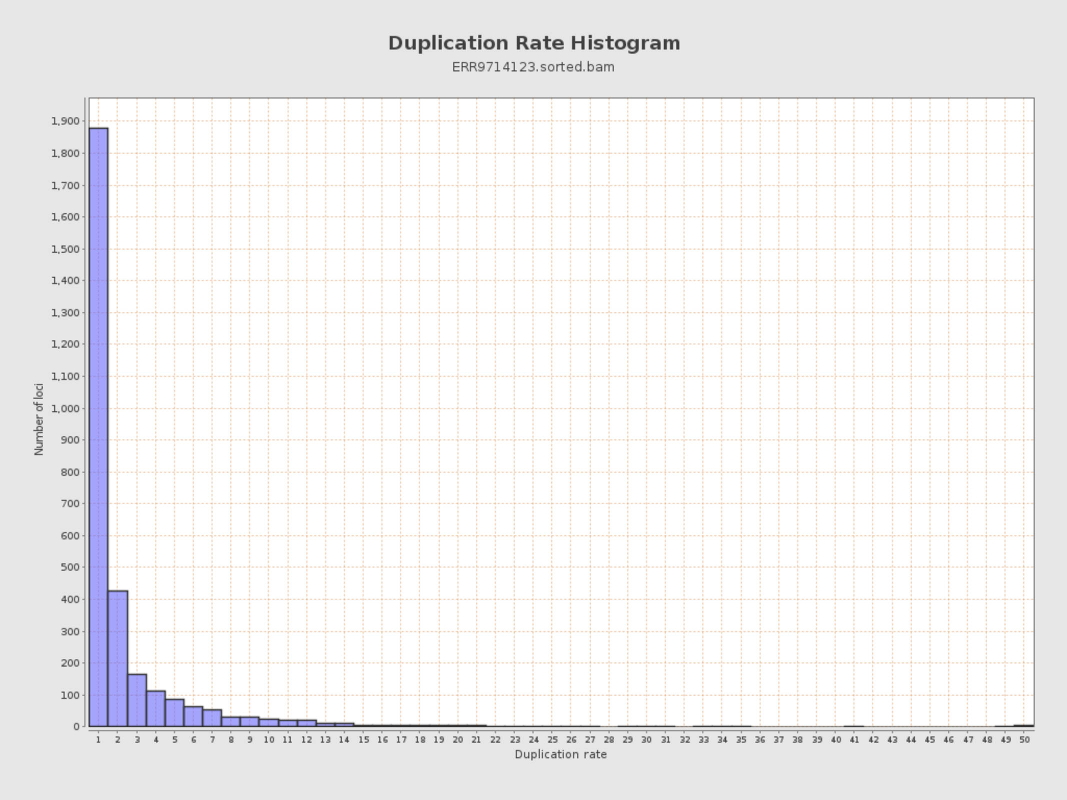
5. Results : Coverage Histogram (0-50X)



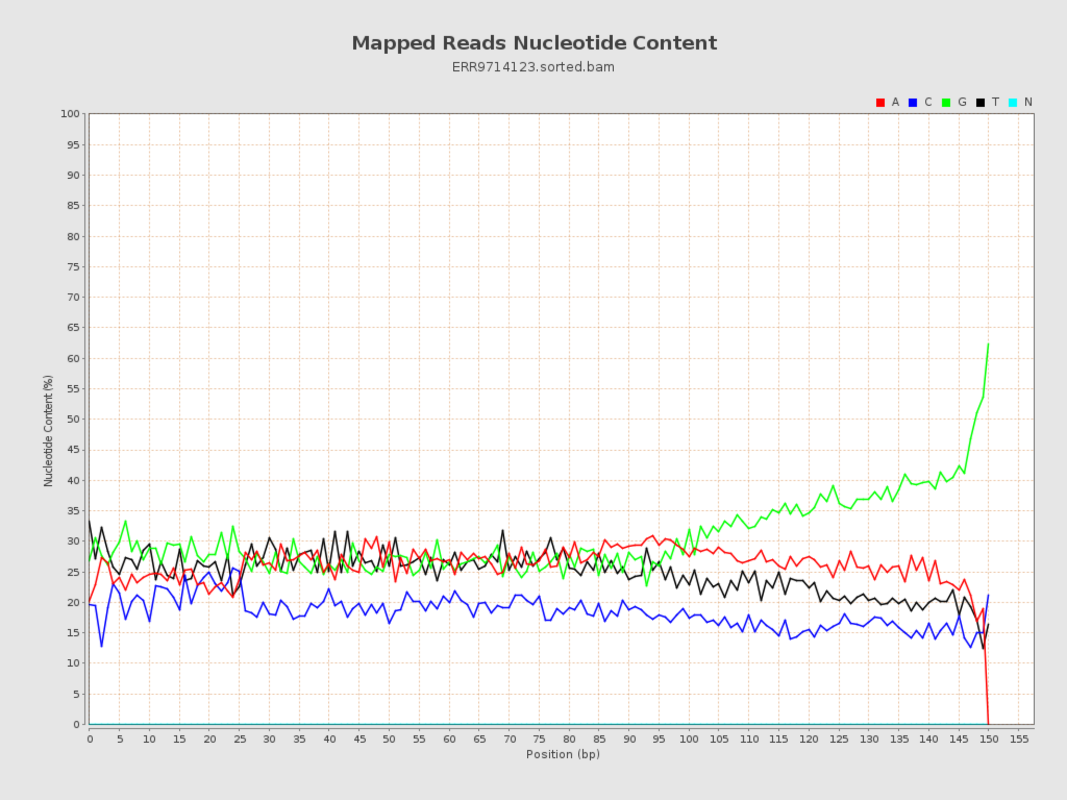
6. Results : Genome Fraction Coverage



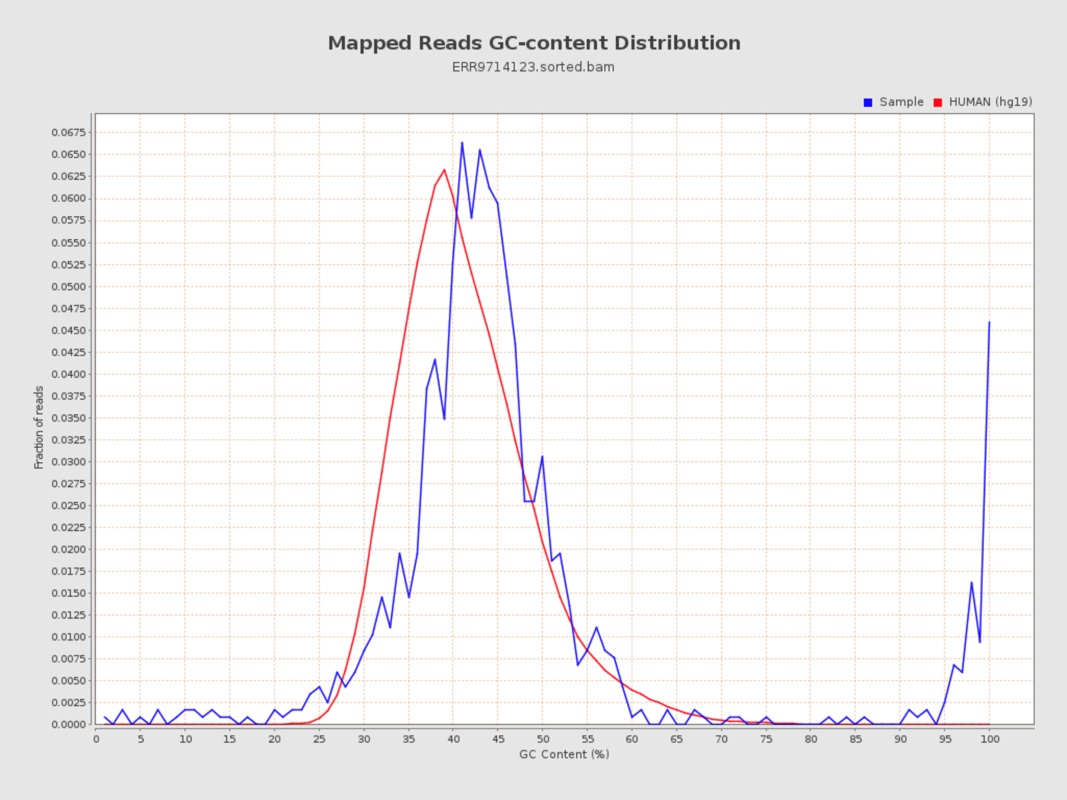
7. Results : Duplication Rate Histogram



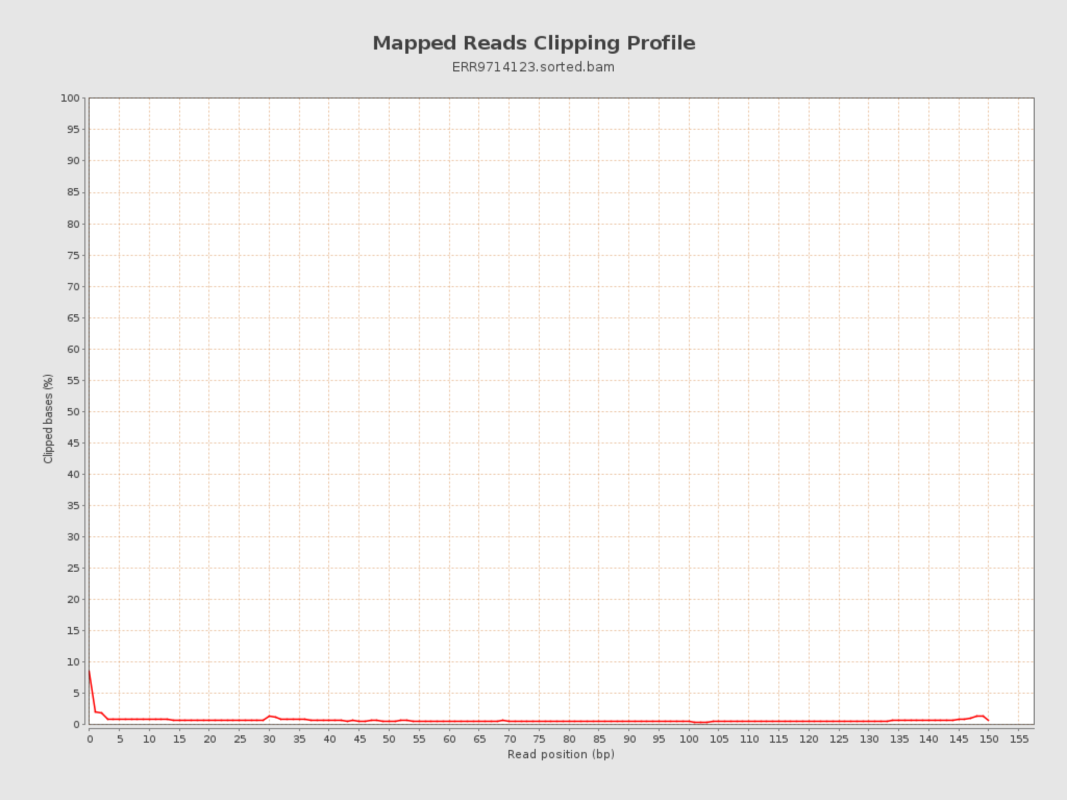
8. Results : Mapped Reads Nucleotide Content



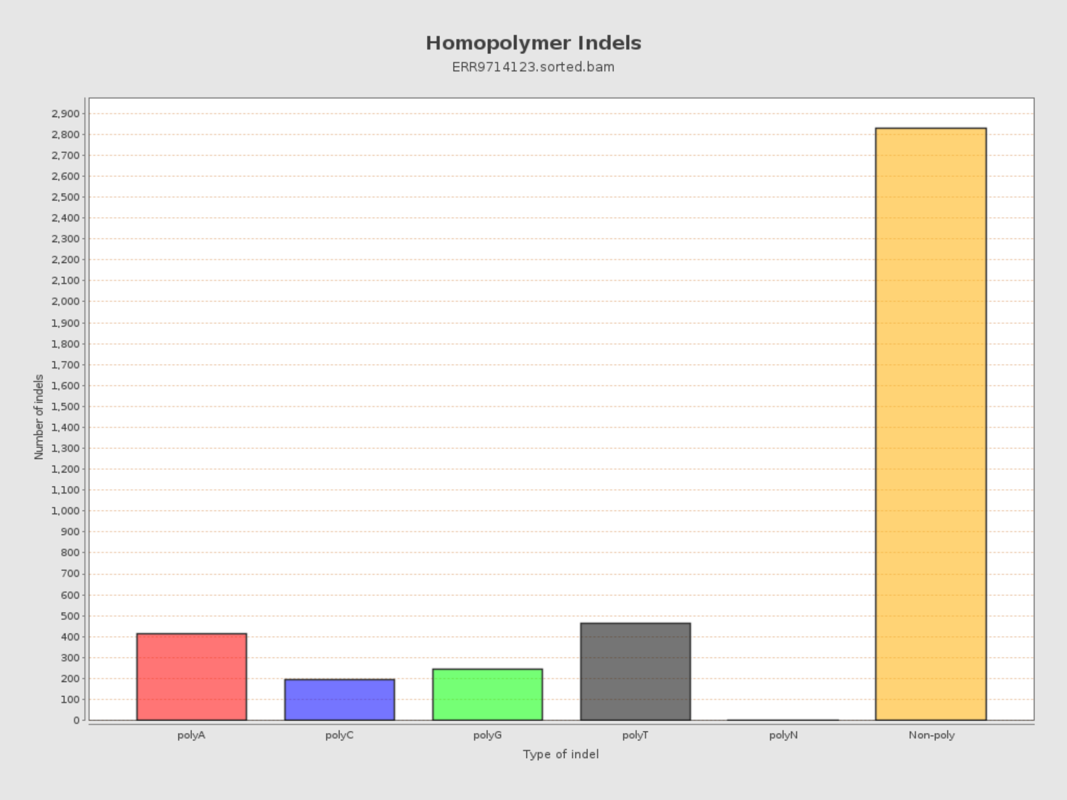
9. Results : Mapped Reads GC-content Distribution



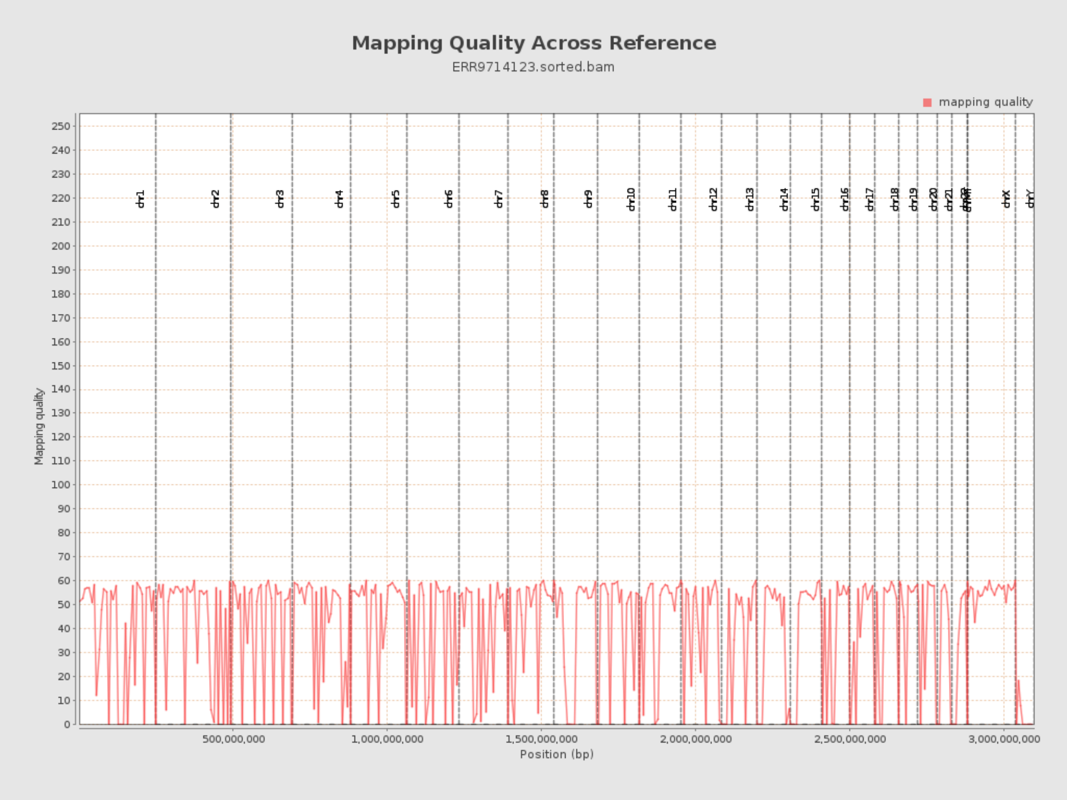
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram