Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:29:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714125.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_ERR9714125 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:29:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	691,982
Mapped reads	495,156 / 71.56%
Unmapped reads	196,826 / 28.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,481 / 2.67%
Read min/max/mean length	30 / 151 / 121.13
Duplicated reads (estimated)	408,850 / 59.08%
Duplication rate	43.85%
Clipped reads	464,511 / 67.13%

2.2. ACGT Content

Number/percentage of A's	18,194,104 / 28.93%
Number/percentage of C's	12,448,202 / 19.79%
Number/percentage of T's	17,262,631 / 27.45%
Number/percentage of G's	14,984,680 / 23.83%
Number/percentage of N's	648 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0207

Standard Deviation	3.4584

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Mismatches and indels

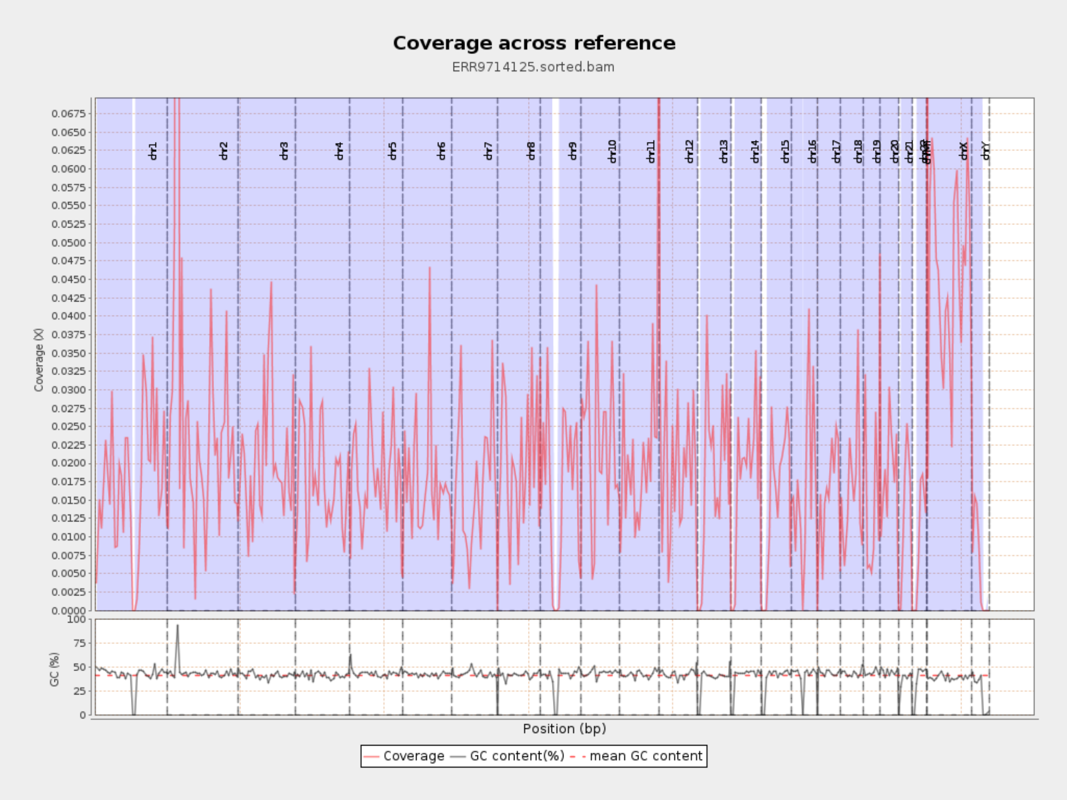
General error rate	3.95%
Mismatches	2,267,013
Insertions	67,853
Mapped reads with at least one insertion	13.21%
Deletions	190,022
Mapped reads with at least one deletion	36.66%
Homopolymer indels	29.99%

2.6. Chromosome stats

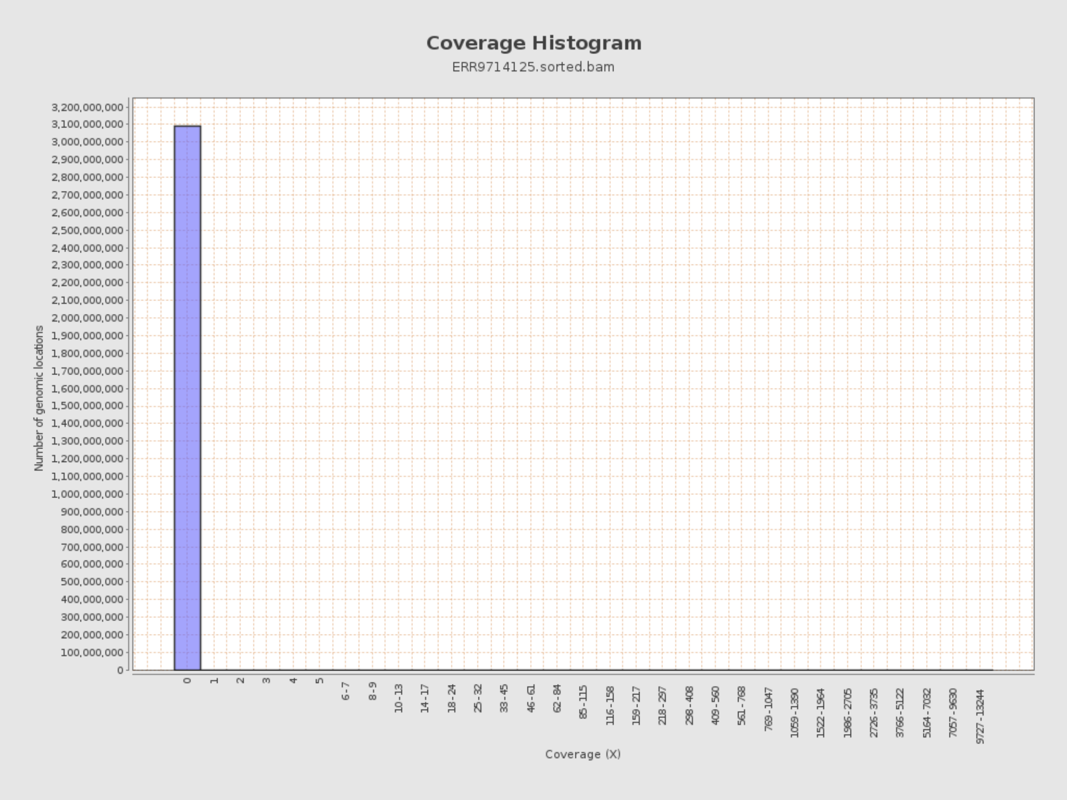
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4269180	0.0171	1.5032
chr2	243199373	7582713	0.0312	8.5388
chr3	198022430	4024843	0.0203	1.7175
chr4	191154276	3415881	0.0179	1.7134
chr5	180915260	3433223	0.019	1.5594
chr6	171115067	3001211	0.0175	1.4002
chr7	159138663	2632570	0.0165	1.3858

chr8	146364022	2854139	0.0195	1.7438
chr9	141213431	2304213	0.0163	1.5125
chr10	135534747	3064806	0.0226	1.9715
chr11	135006516	2665350	0.0197	1.5201
chr12	133851895	2586132	0.0193	1.7469
chr13	115169878	2076085	0.018	1.6653
chr14	107349540	1979065	0.0184	1.7773
chr15	102531392	1576003	0.0154	1.2719
chr16	90354753	1530640	0.0169	1.4512
chr17	81195210	1291078	0.0159	1.3979
chr18	78077248	1306374	0.0167	1.395
chr19	59128983	878671	0.0149	1.7461
chr20	63025520	1191982	0.0189	1.5557
chr21	48129895	599225	0.0125	1.1597
chr22	51304566	478909	0.0093	0.8903
chrMT	16571	1824350	110.0929	846.1235
chrX	155270560	7088713	0.0457	2.0174
chrY	59373566	352694	0.0059	0.7145

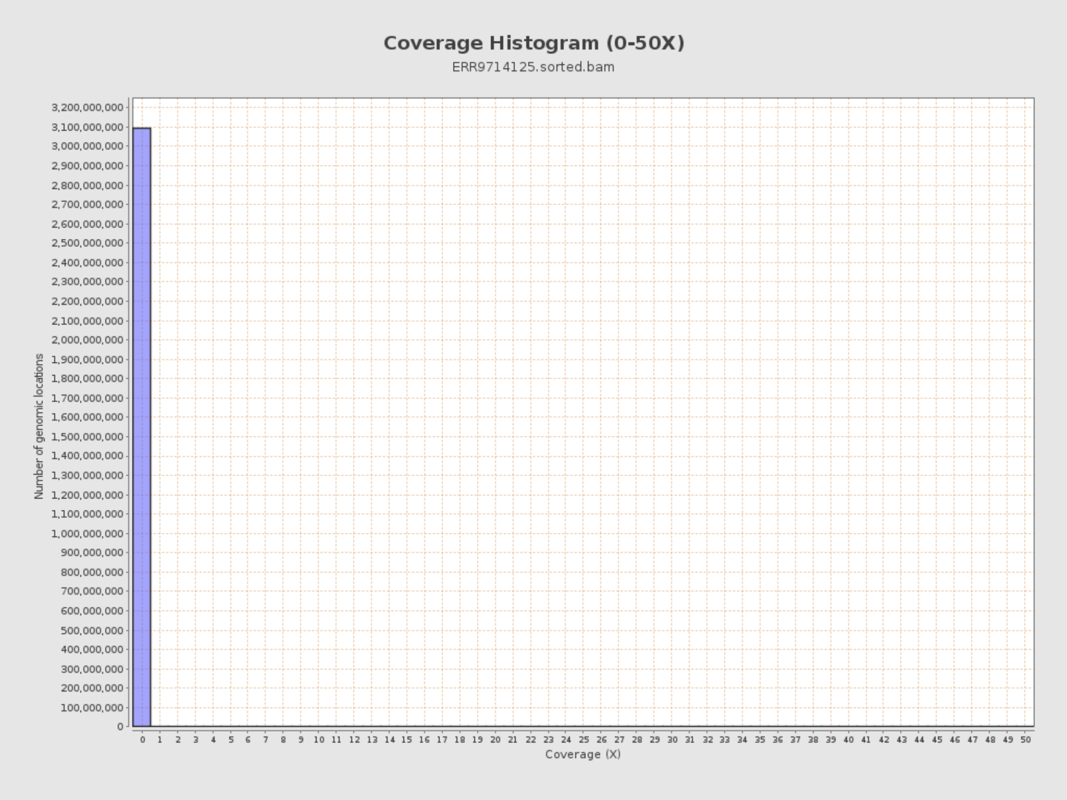
3. Results : Coverage across reference



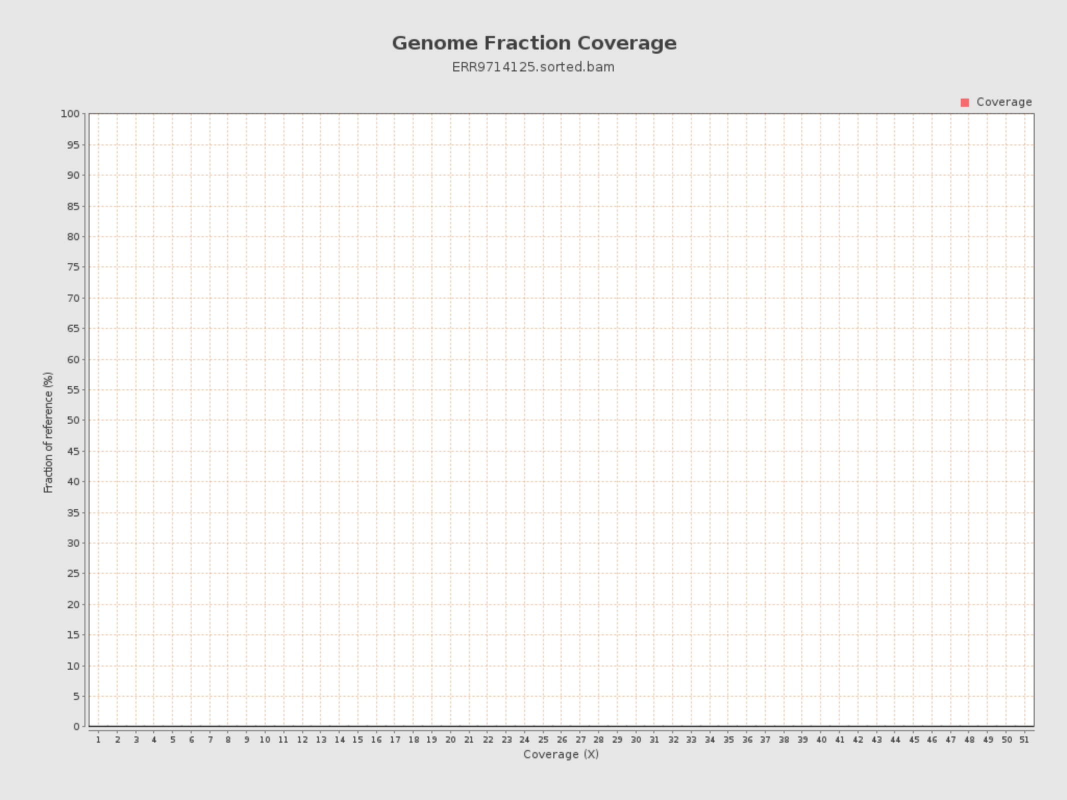
4. Results : Coverage Histogram



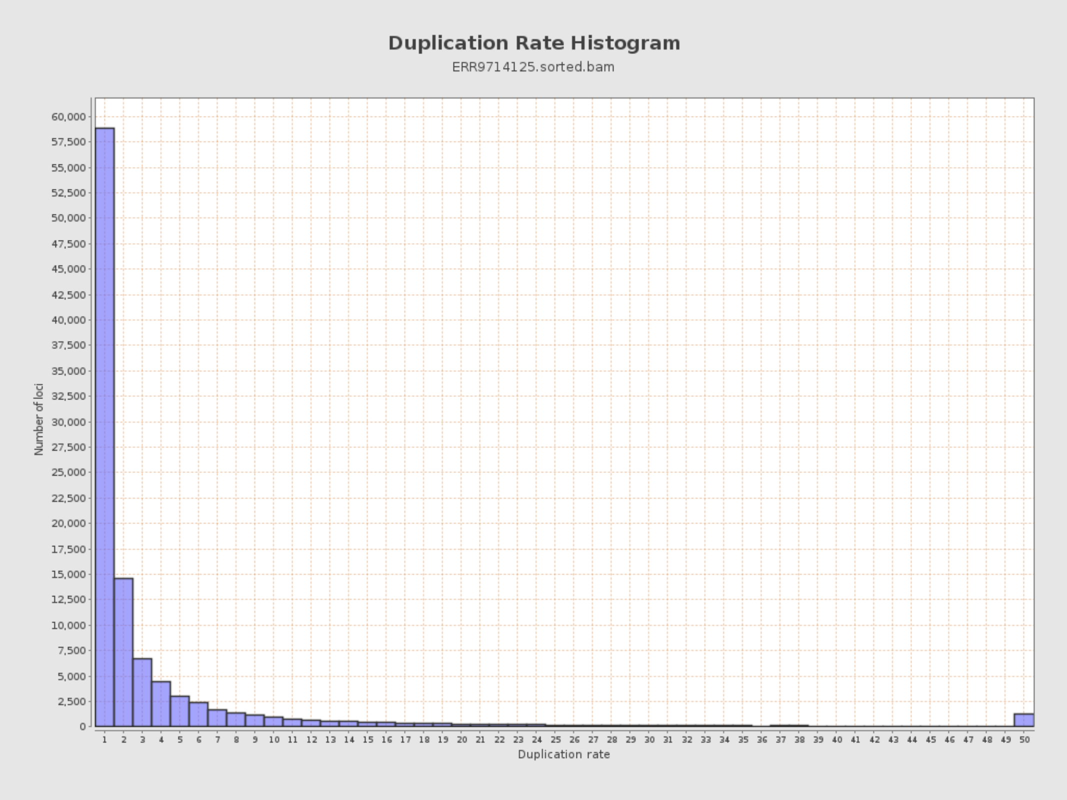
5. Results : Coverage Histogram (0-50X)



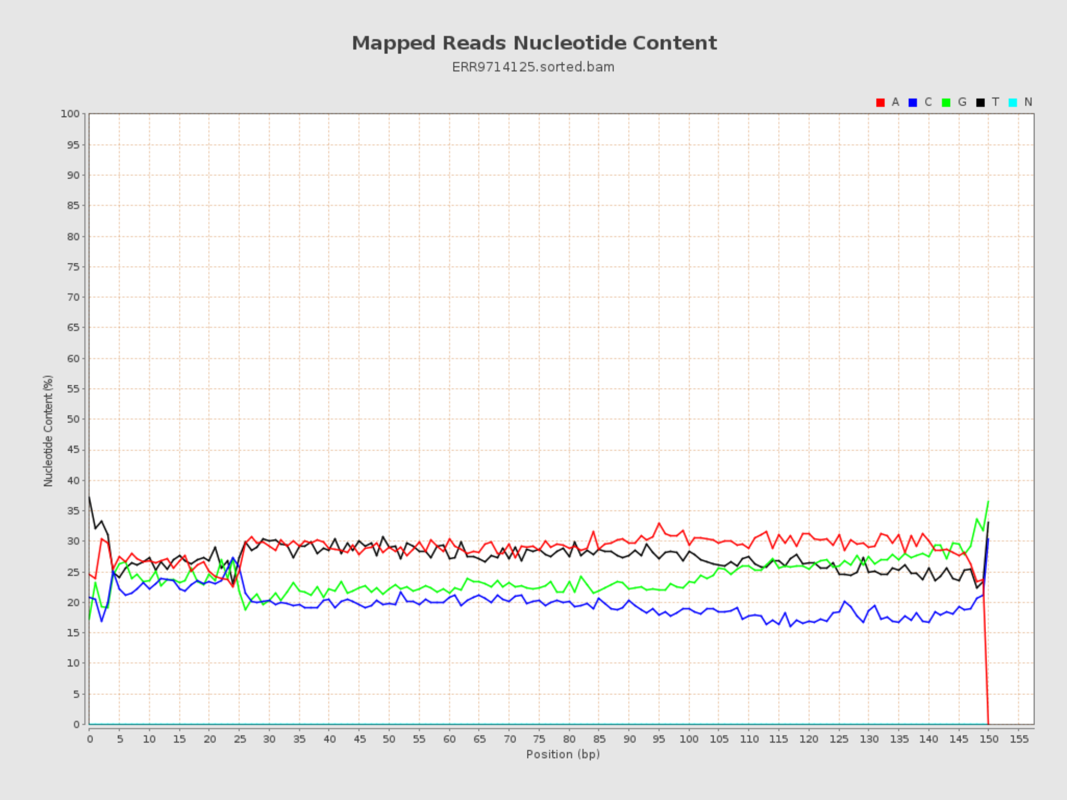
6. Results : Genome Fraction Coverage



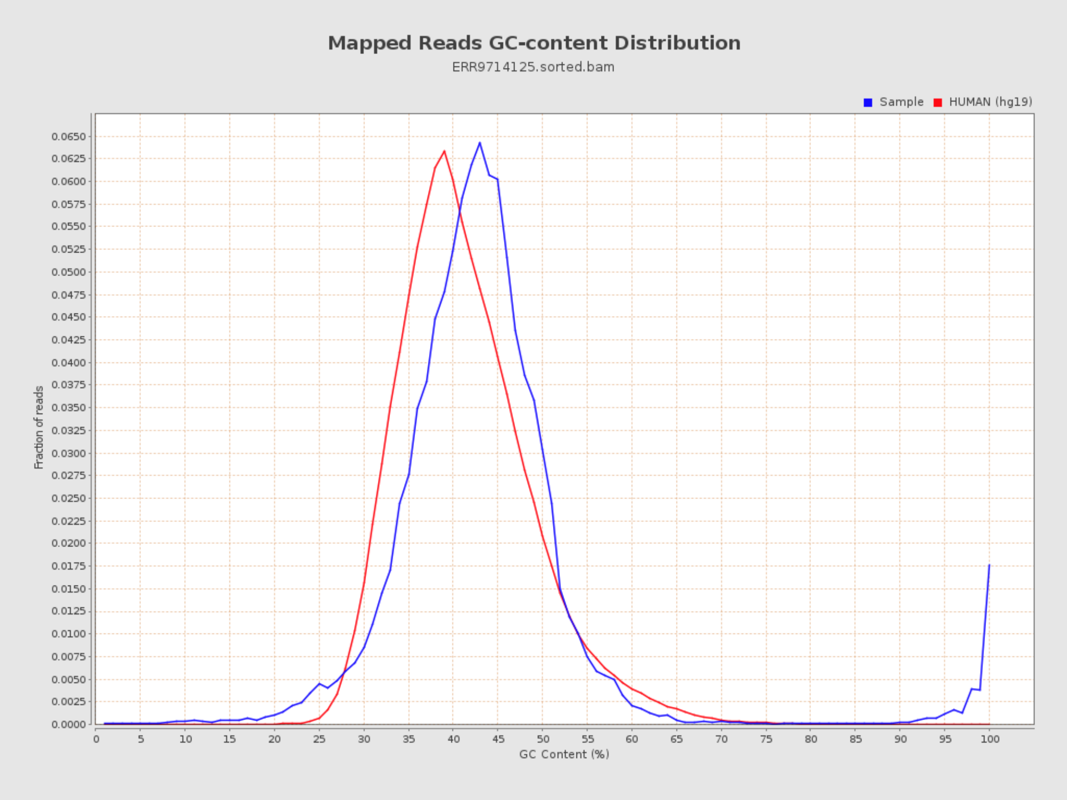
7. Results : Duplication Rate Histogram



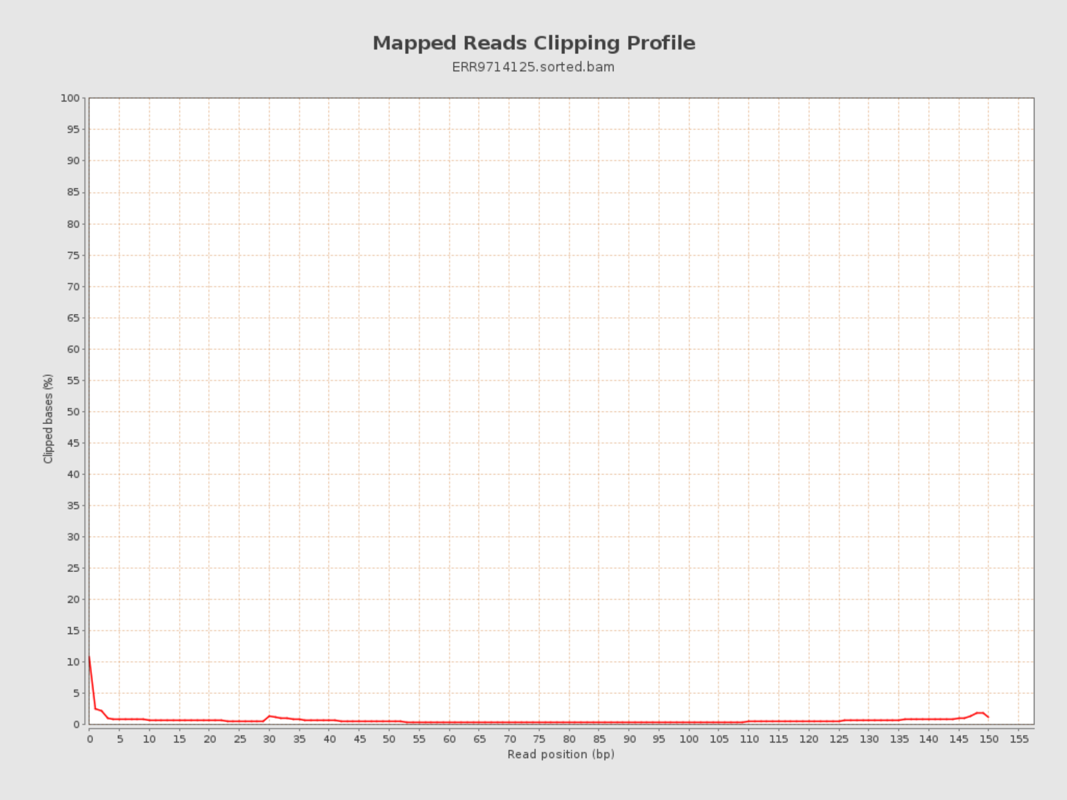
8. Results : Mapped Reads Nucleotide Content



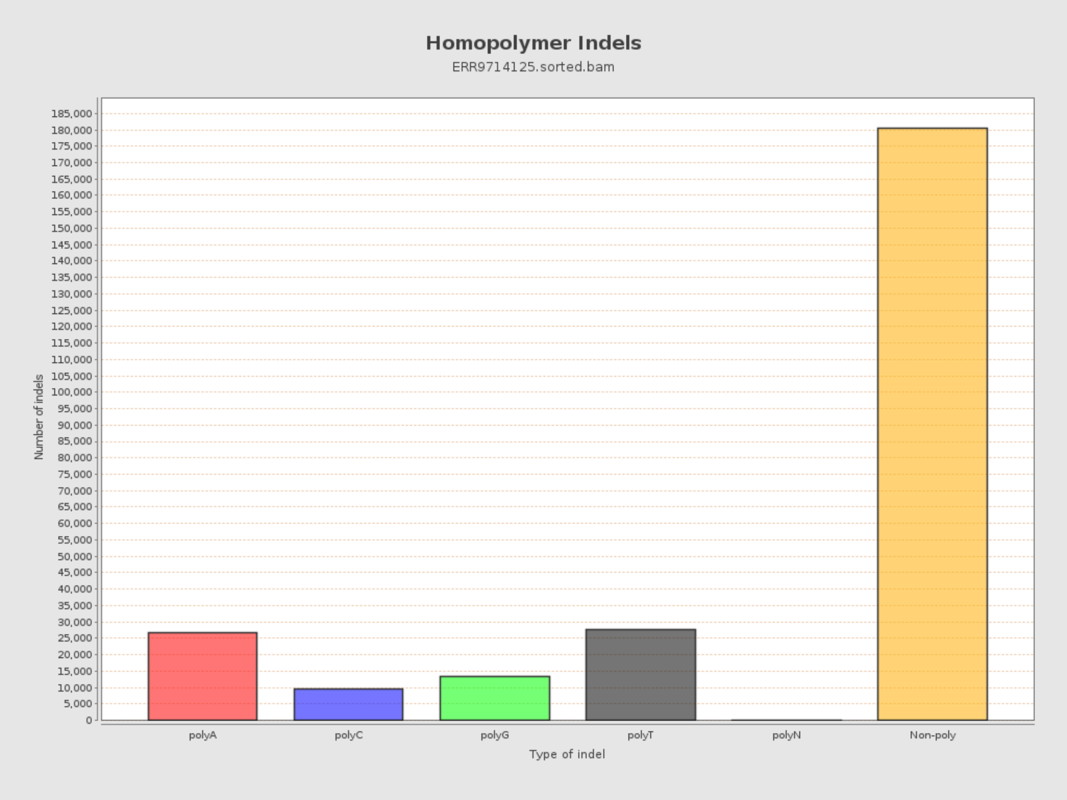
9. Results : Mapped Reads GC-content Distribution



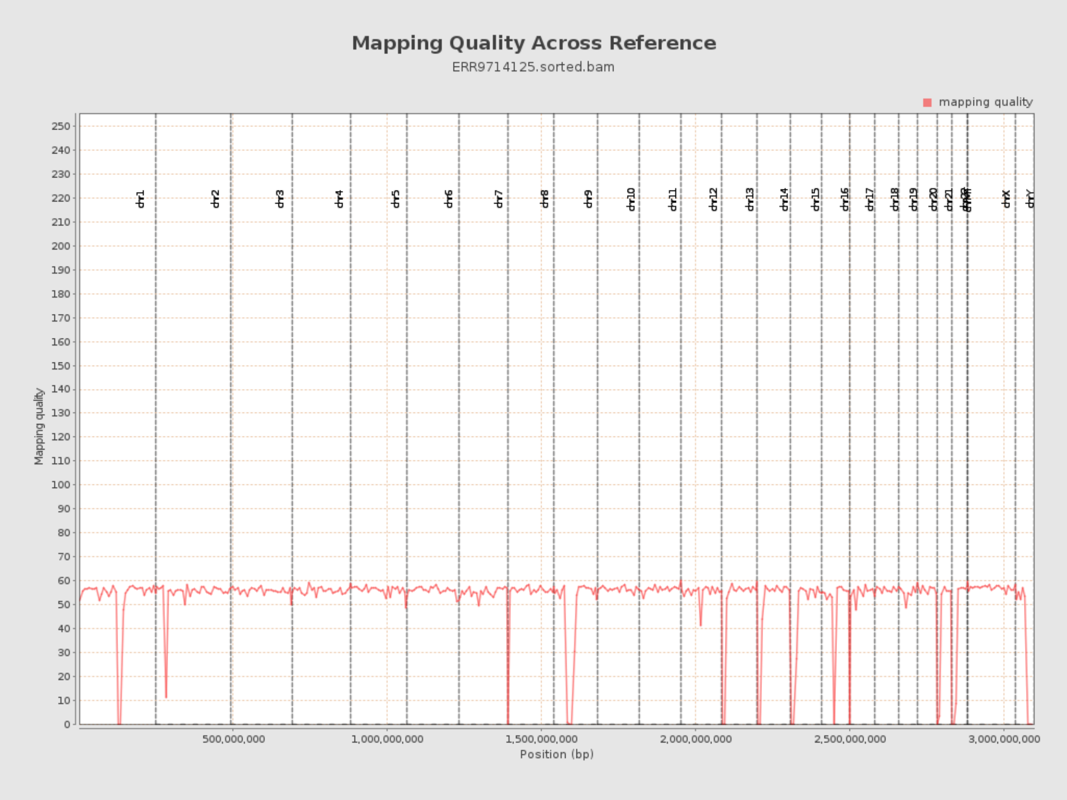
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram