Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714215.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_ERR9714215 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:24:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	159,704
Mapped reads	16,650 / 10.43%
Unmapped reads	143,054 / 89.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	513 / 0.32%
Read min/max/mean length	30 / 151 / 59.76
Duplicated reads (estimated)	13,833 / 8.66%
Duplication rate	37.15%
Clipped reads	14,649 / 9.17%

2.2. ACGT Content

Number/percentage of A's	346,796 / 20.97%
Number/percentage of C's	234,869 / 14.21%
Number/percentage of T's	309,990 / 18.75%
Number/percentage of G's	761,710 / 46.07%
Number/percentage of N's	18 / 0%
GC Percentage	60.28%

2.3. Coverage

Mean	0.0005

Standard Deviation	0.6207

2.4. Mapping Quality

Mean Mapping Quality	33.87

2.5. Mismatches and indels

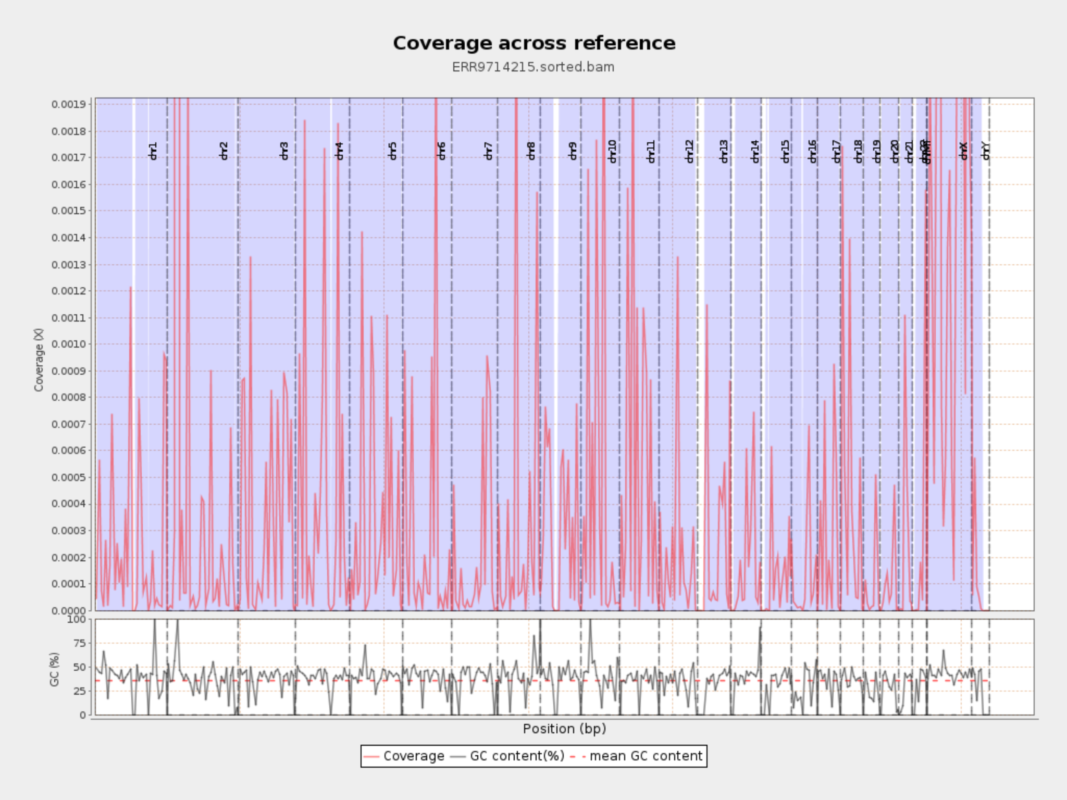
General error rate	3.81%
Mismatches	56,460
Insertions	1,745
Mapped reads with at least one insertion	9.23%
Deletions	4,087
Mapped reads with at least one deletion	23.08%
Homopolymer indels	32.54%

2.6. Chromosome stats

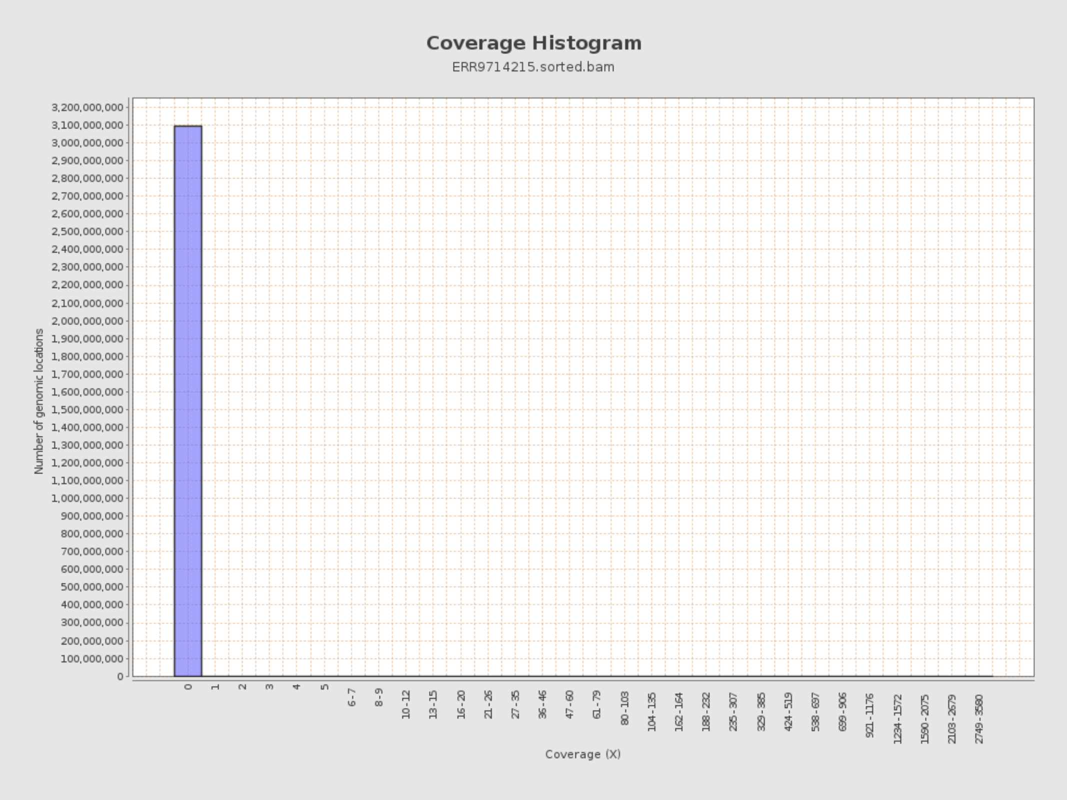
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61708	0.0002	0.076
chr2	243199373	574892	0.0024	2.173
chr3	198022430	73343	0.0004	0.1003
chr4	191154276	81204	0.0004	0.1256
chr5	180915260	62495	0.0003	0.0979
chr6	171115067	51147	0.0003	0.1029
chr7	159138663	30297	0.0002	0.0935

chr8	146364022	50854	0.0003	0.1349
chr9	141213431	43728	0.0003	0.0779
chr10	135534747	63822	0.0005	0.166
chr11	135006516	75622	0.0006	0.1748
chr12	133851895	26872	0.0002	0.0754
chr13	115169878	23998	0.0002	0.0673
chr14	107349540	18638	0.0002	0.0535
chr15	102531392	13686	0.0001	0.0437
chr16	90354753	12946	0.0001	0.0477
chr17	81195210	23396	0.0003	0.0839
chr18	78077248	39199	0.0005	0.1598
chr19	59128983	5503	0.0001	0.0274
chr20	63025520	6505	0.0001	0.0303
chr21	48129895	12815	0.0003	0.0832
chr22	51304566	13986	0.0003	0.1359
chrMT	16571	0	0	0
chrX	155270560	308502	0.002	0.3149
chrY	59373566	5876	0.0001	0.0473

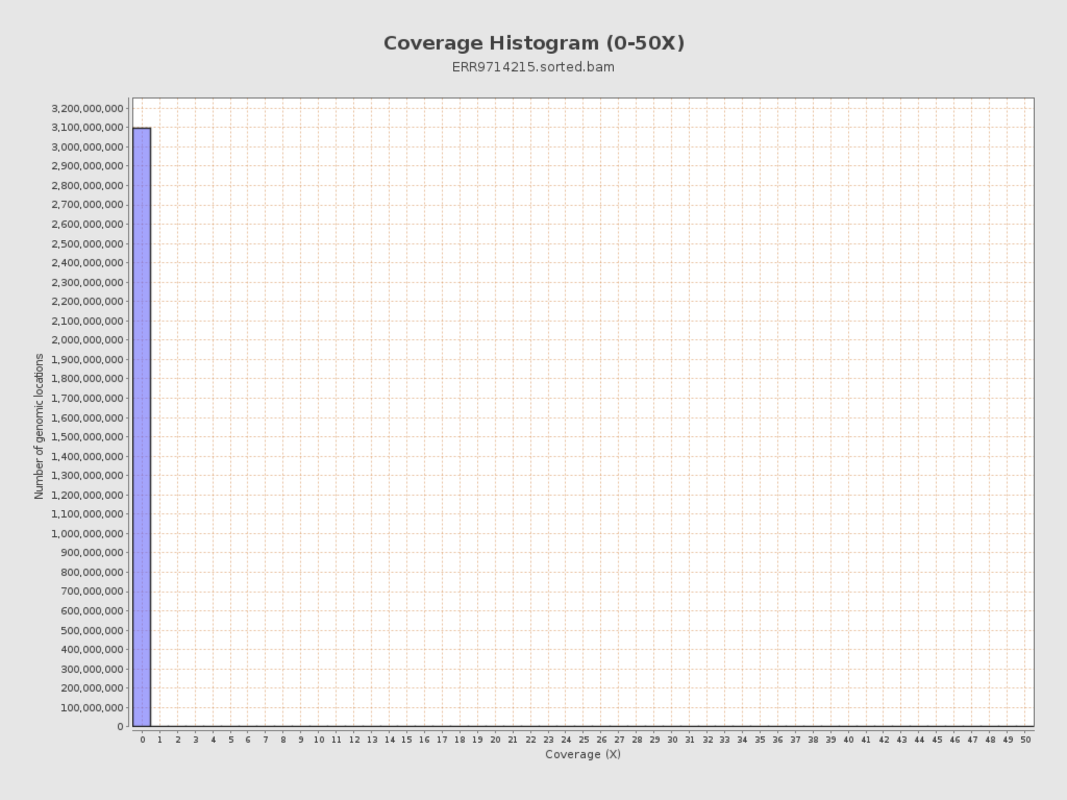
3. Results : Coverage across reference



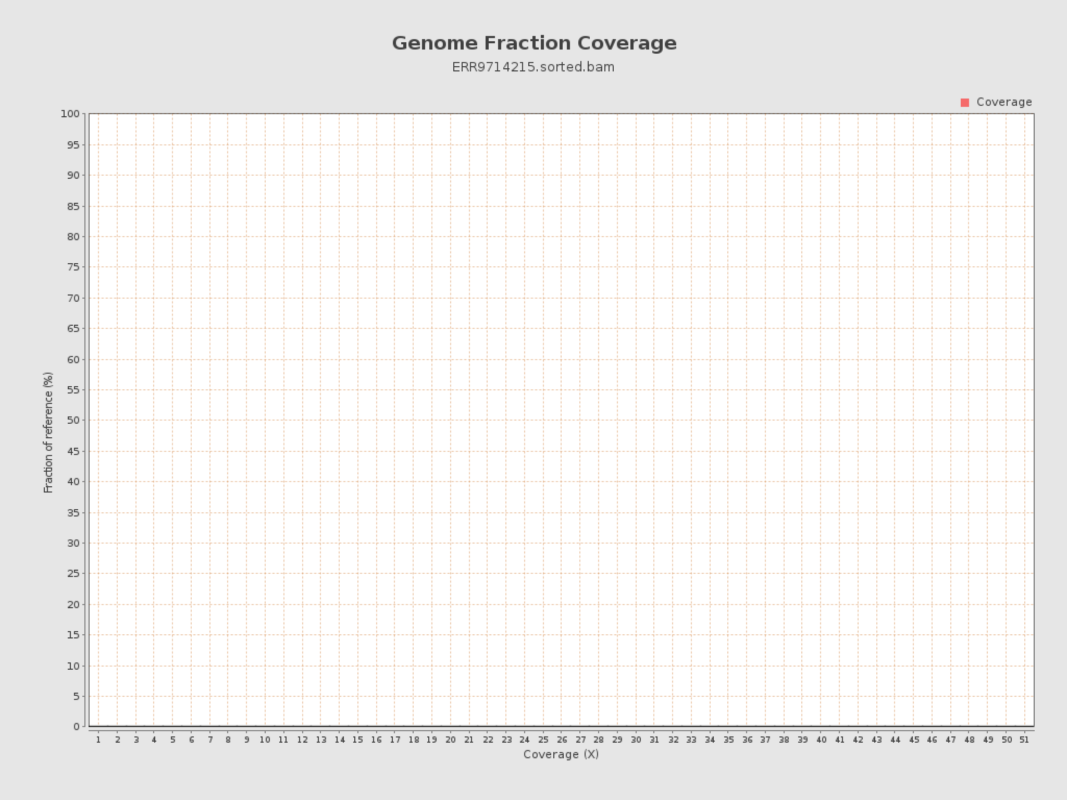
4. Results : Coverage Histogram



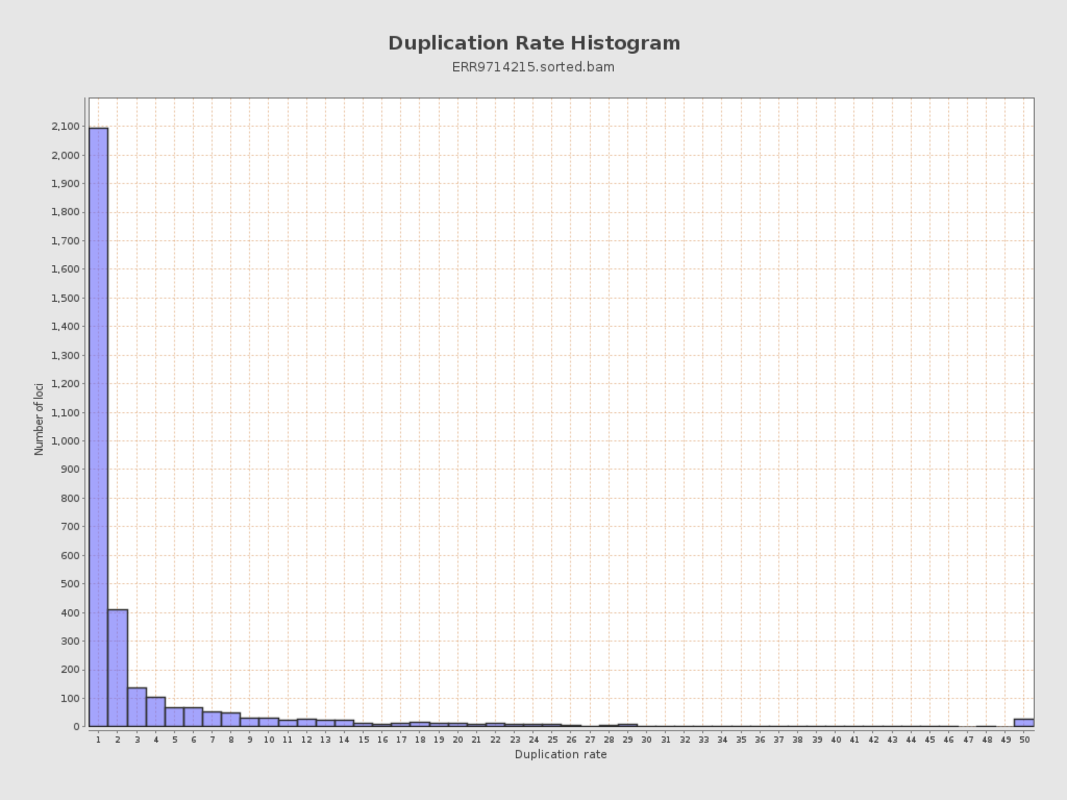
5. Results : Coverage Histogram (0-50X)



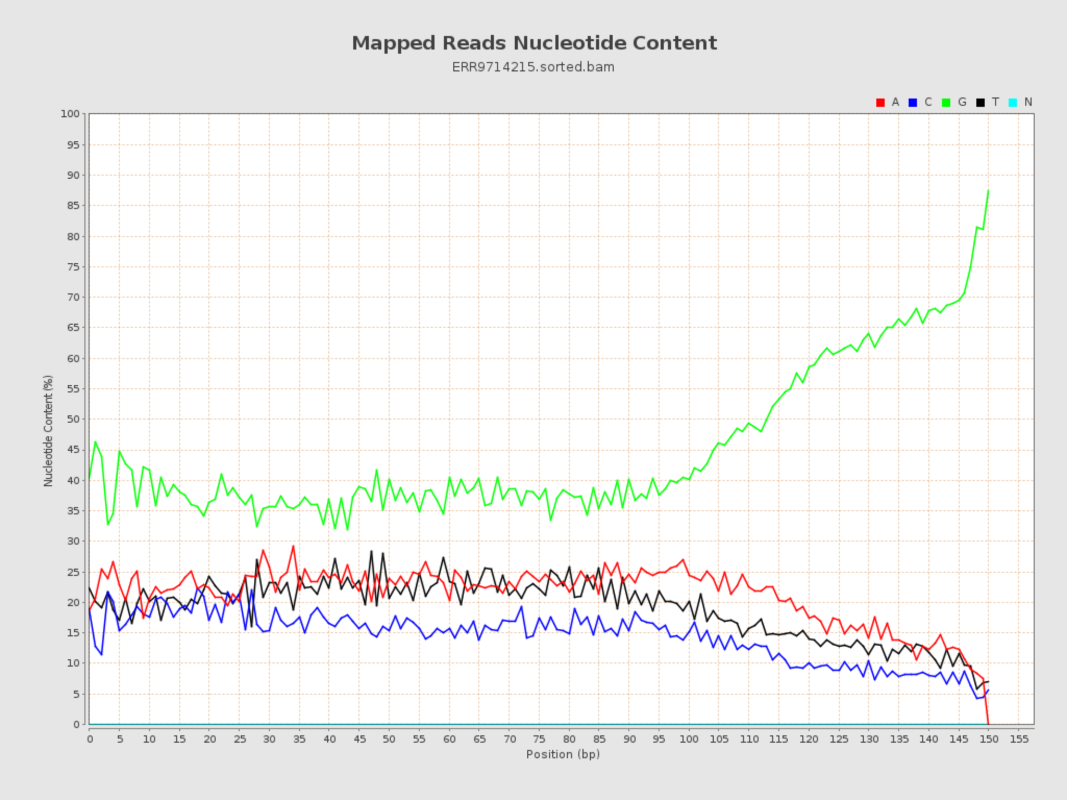
6. Results : Genome Fraction Coverage



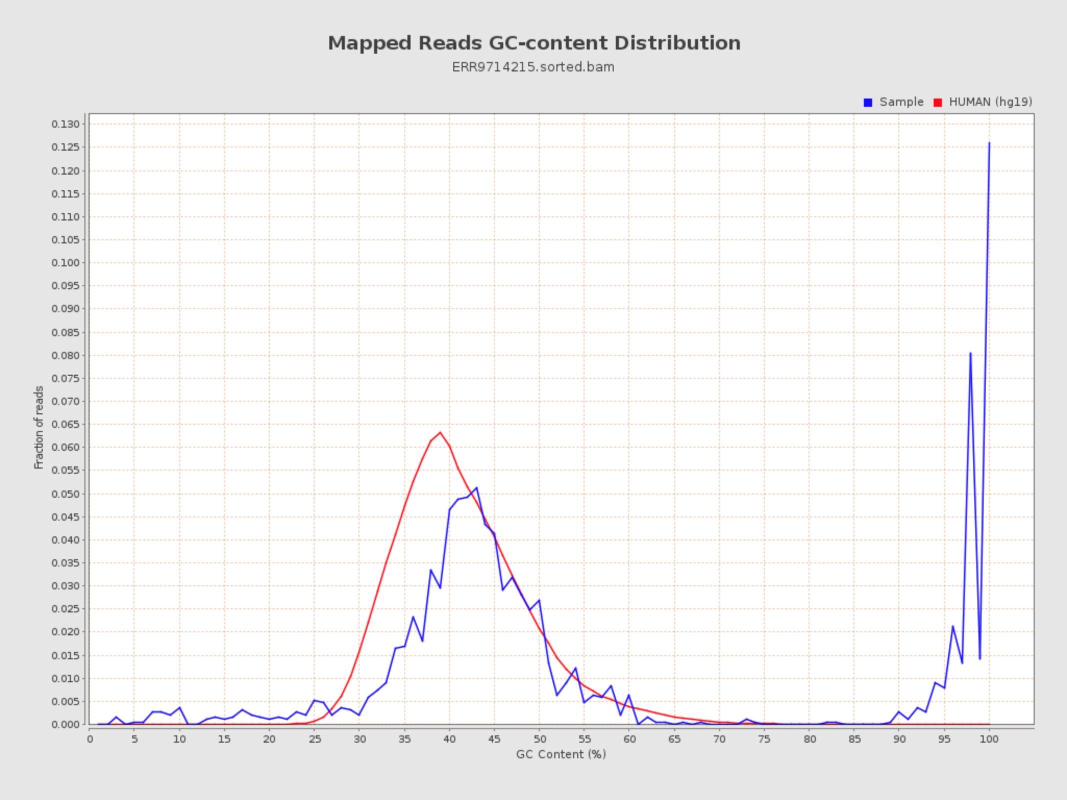
7. Results : Duplication Rate Histogram



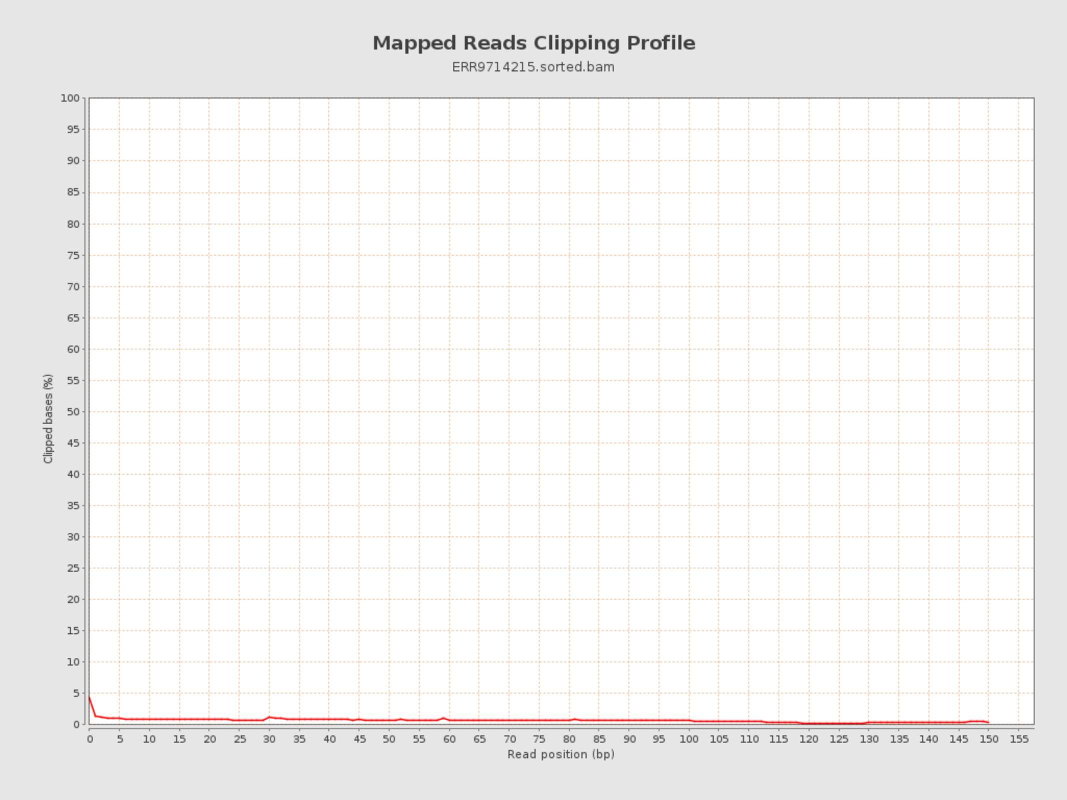
8. Results : Mapped Reads Nucleotide Content



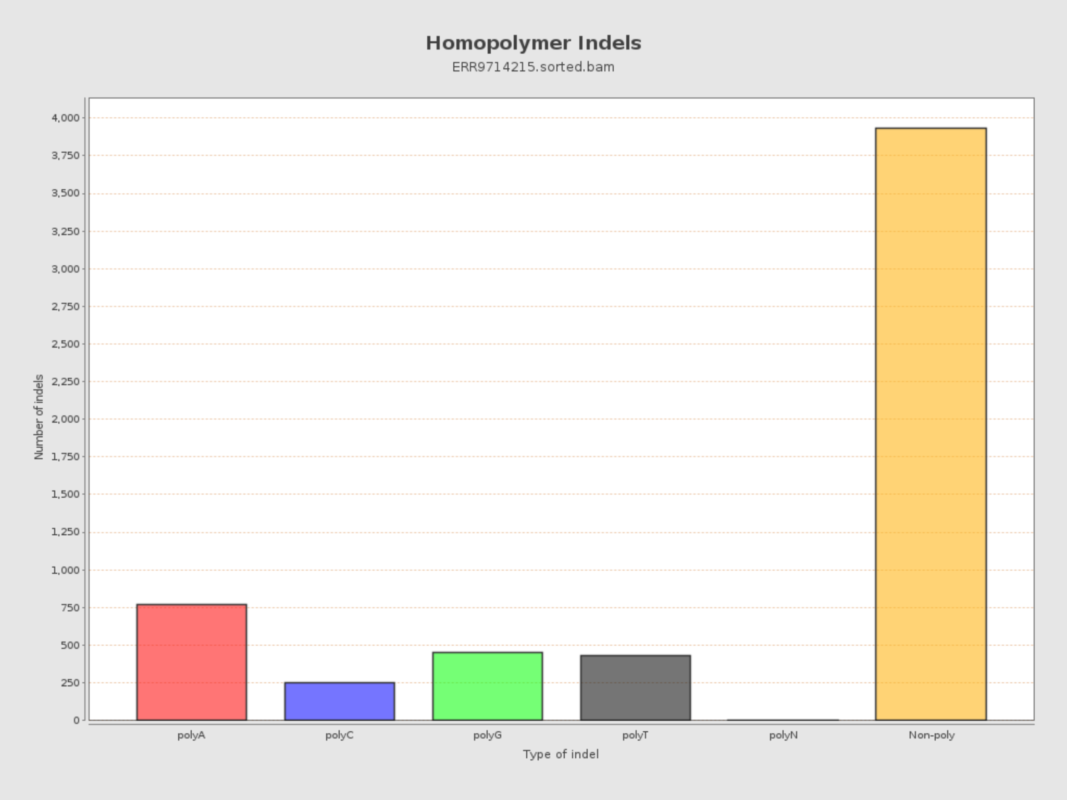
9. Results : Mapped Reads GC-content Distribution



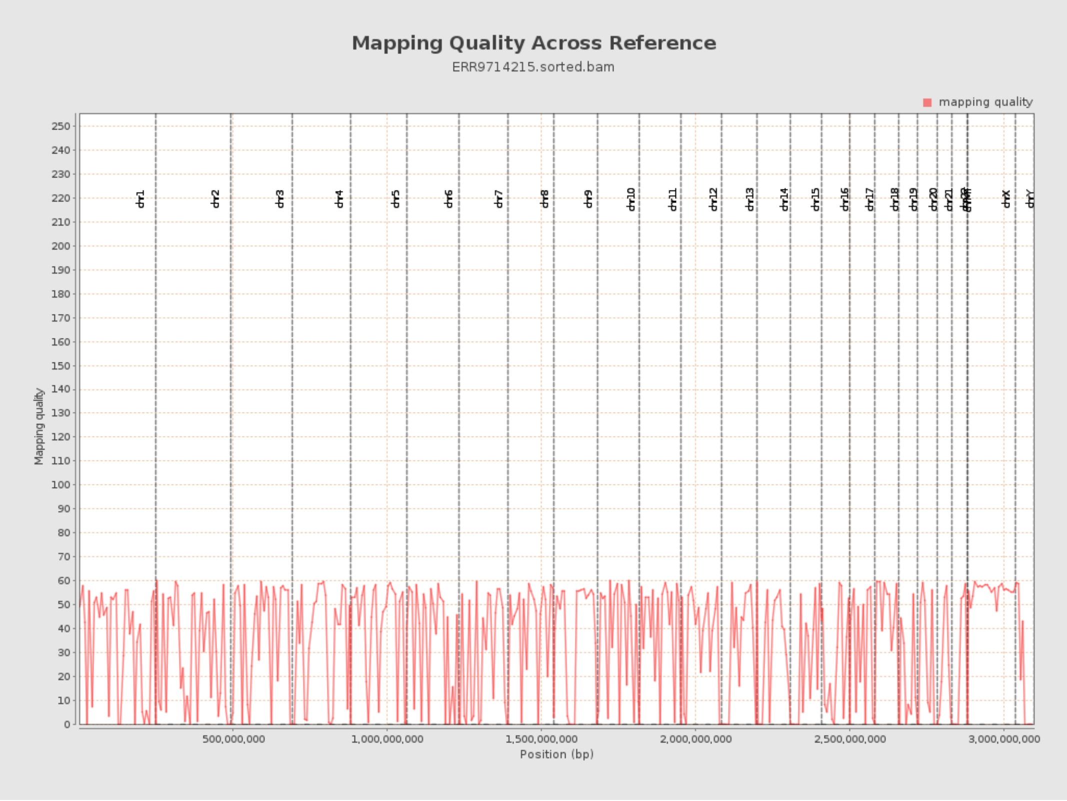
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram