

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:05:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714202.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_ERR9714202 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714202.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:05:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714202.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	112,102
Mapped reads	21,947 / 19.58%
Unmapped reads	90,155 / 80.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	758 / 0.68%
Read min/max/mean length	30 / 151 / 68.93
Duplicated reads (estimated)	16,707 / 14.9%
Duplication rate	39.46%
Clipped reads	19,924 / 17.77%

2.2. ACGT Content

Number/percentage of A's	678,831 / 26.7%
Number/percentage of C's	475,761 / 18.71%
Number/percentage of T's	636,539 / 25.04%
Number/percentage of G's	751,304 / 29.55%
Number/percentage of N's	25 / 0%
GC Percentage	48.26%

2.3. Coverage

Mean	0.0008

Standard Deviation	0.3262
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2.4. Mapping Quality

Mean Mapping Quality	44.45
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2.5. Mismatches and indels

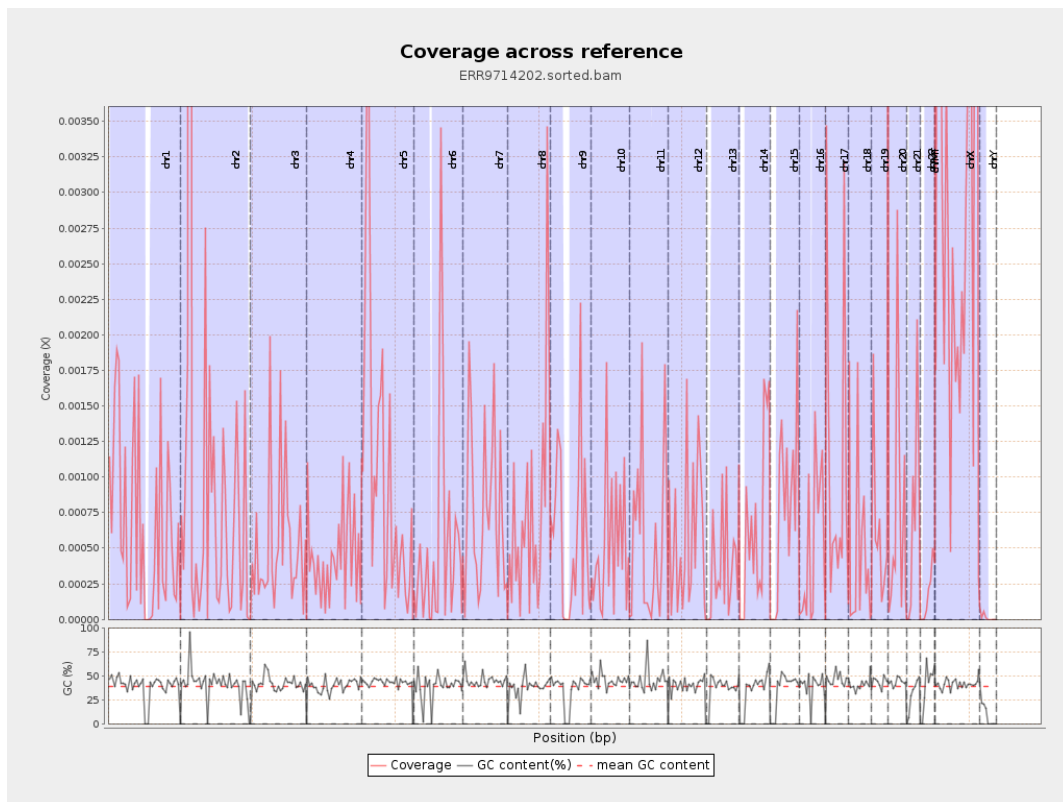
General error rate	4.22%
Mismatches	98,006
Insertions	2,734
Mapped reads with at least one insertion	11.54%
Deletions	8,105
Mapped reads with at least one deletion	35.14%
Homopolymer indels	30.33%

2.6. Chromosome stats

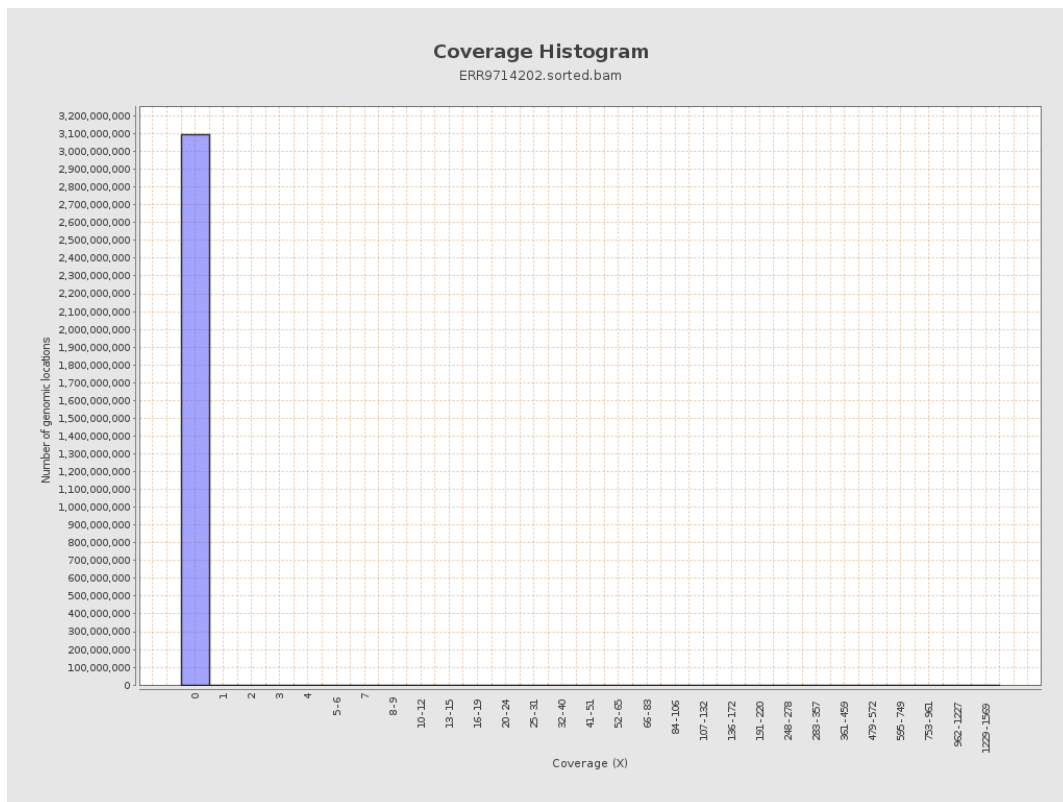
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	172396	0.0007	0.1383
chr2	243199373	427960	0.0018	1.0341
chr3	198022430	103309	0.0005	0.1116
chr4	191154276	84149	0.0004	0.0945
chr5	180915260	183082	0.001	0.1739
chr6	171115067	85677	0.0005	0.1441
chr7	159138663	118478	0.0007	0.1505

chr8	146364022	110684	0.0008	0.1484
chr9	141213431	81955	0.0006	0.1432
chr10	135534747	70456	0.0005	0.1324
chr11	135006516	74497	0.0006	0.1293
chr12	133851895	78090	0.0006	0.1283
chr13	115169878	41156	0.0004	0.09
chr14	107349540	67594	0.0006	0.1348
chr15	102531392	76385	0.0007	0.1514
chr16	90354753	46504	0.0005	0.1144
chr17	81195210	89293	0.0011	0.2359
chr18	78077248	37713	0.0005	0.1153
chr19	59128983	44499	0.0008	0.1573
chr20	63025520	48933	0.0008	0.1775
chr21	48129895	33872	0.0007	0.1378
chr22	51304566	8985	0.0002	0.0445
chrMT	16571	27822	1.679	13.0304
chrX	155270560	481947	0.0031	0.3169
chrY	59373566	1120	0	0.0056

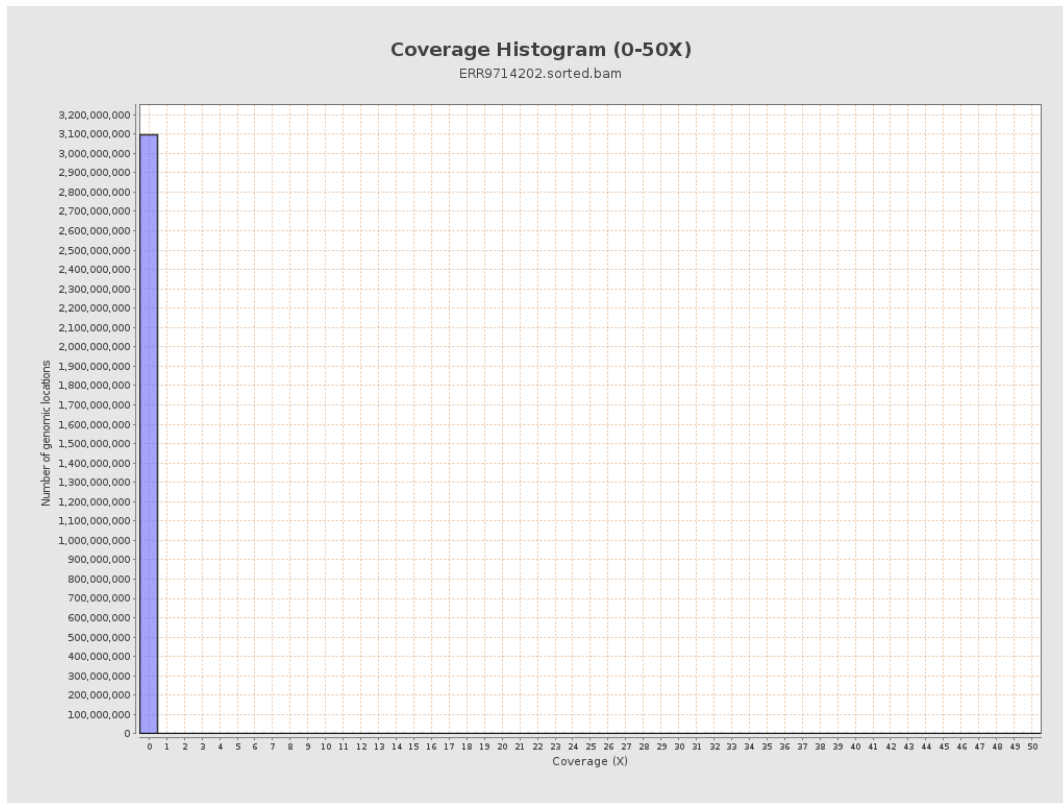
3. Results : Coverage across reference



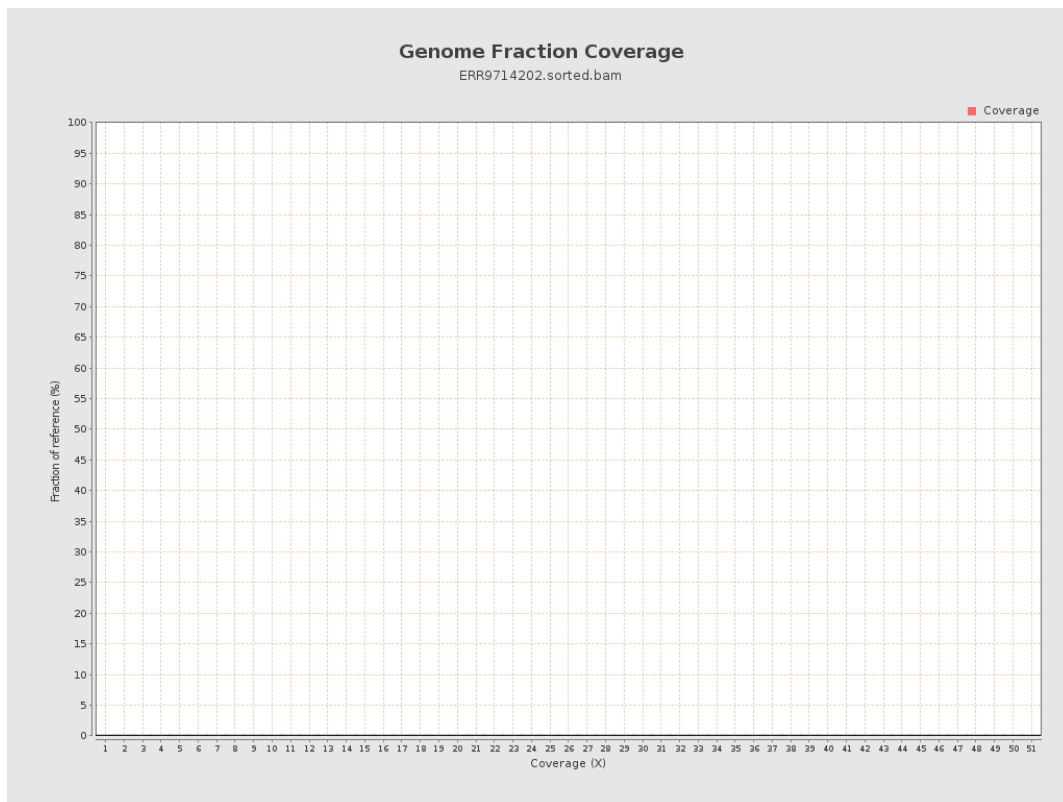
4. Results : Coverage Histogram



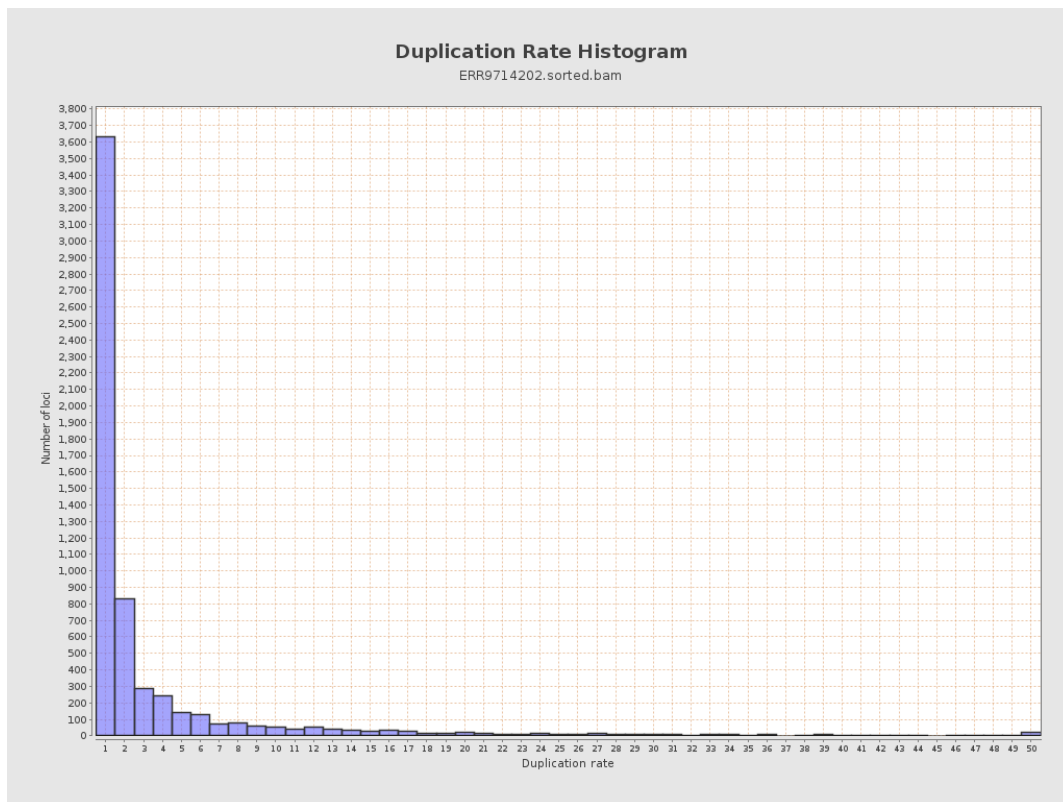
5. Results : Coverage Histogram (0-50X)



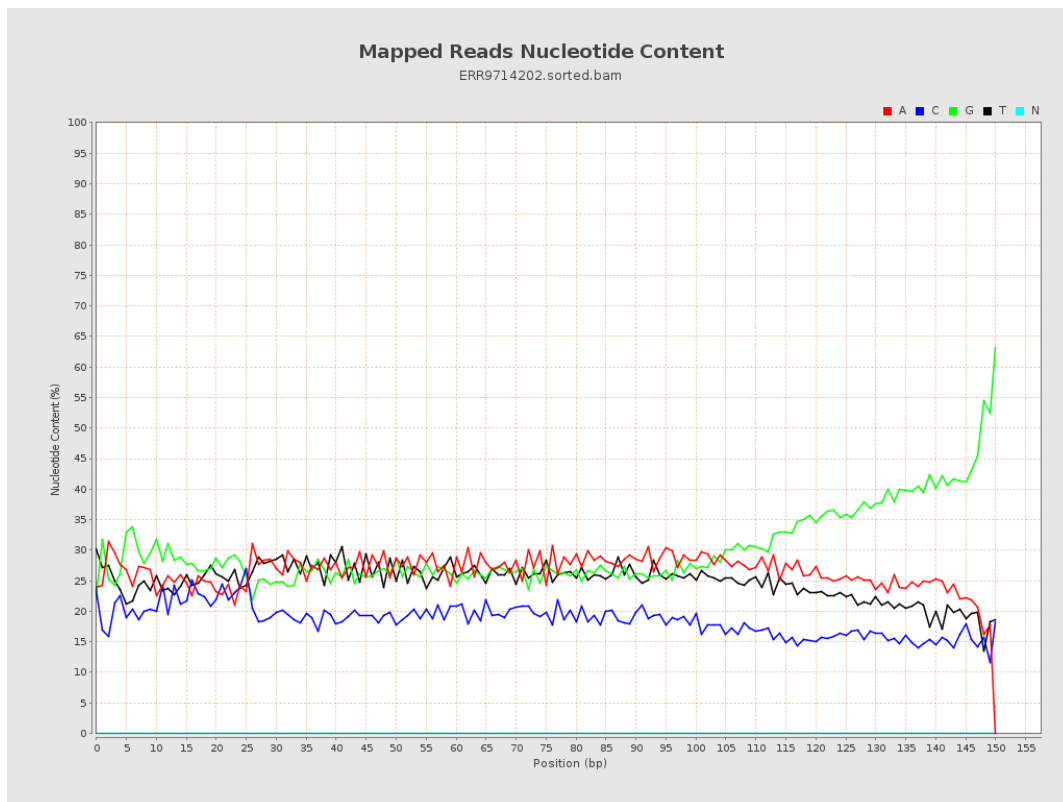
6. Results : Genome Fraction Coverage



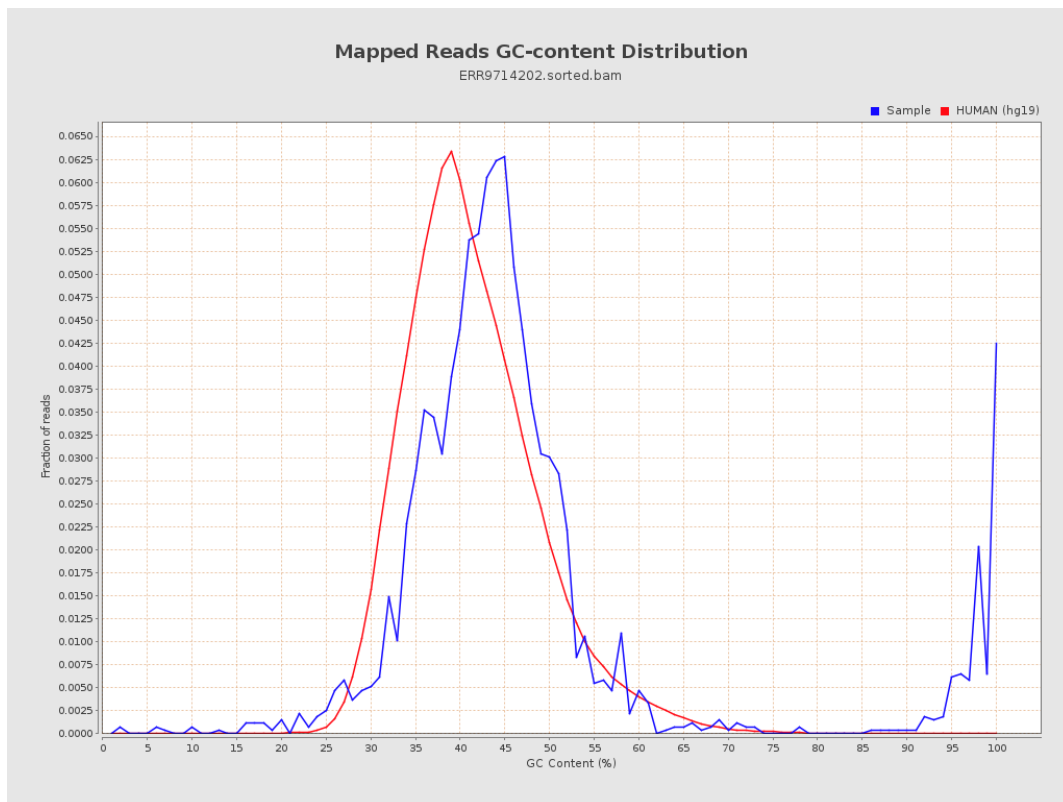
7. Results : Duplication Rate Histogram



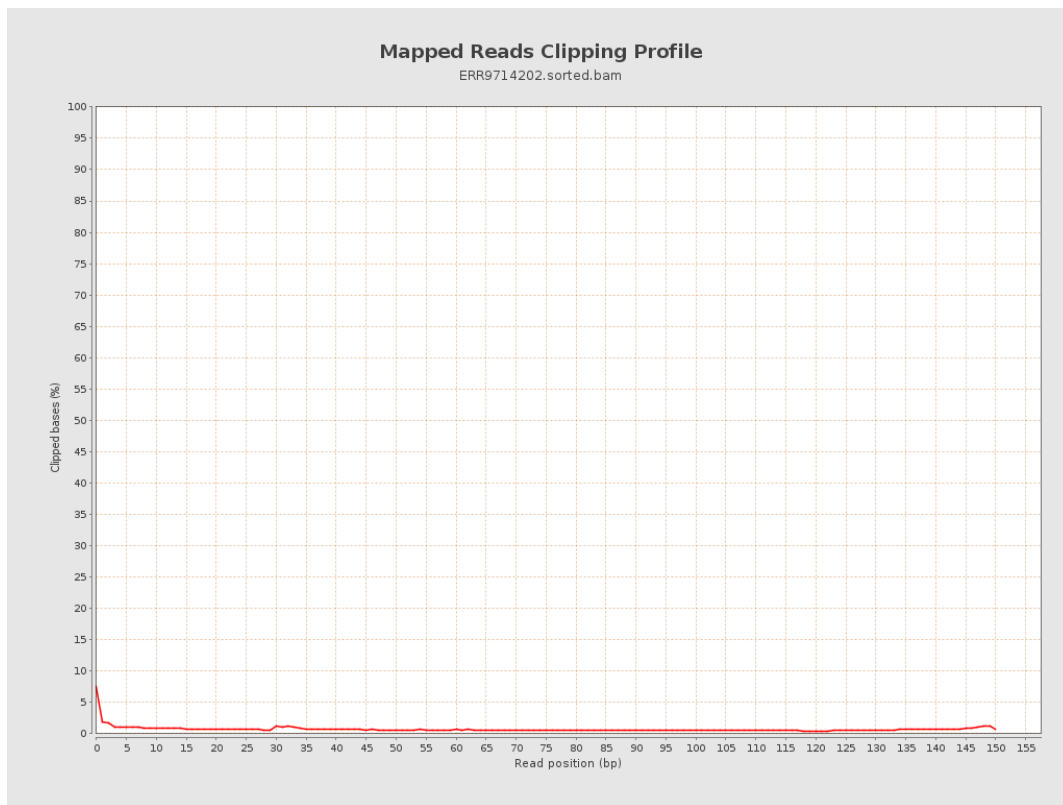
8. Results : Mapped Reads Nucleotide Content



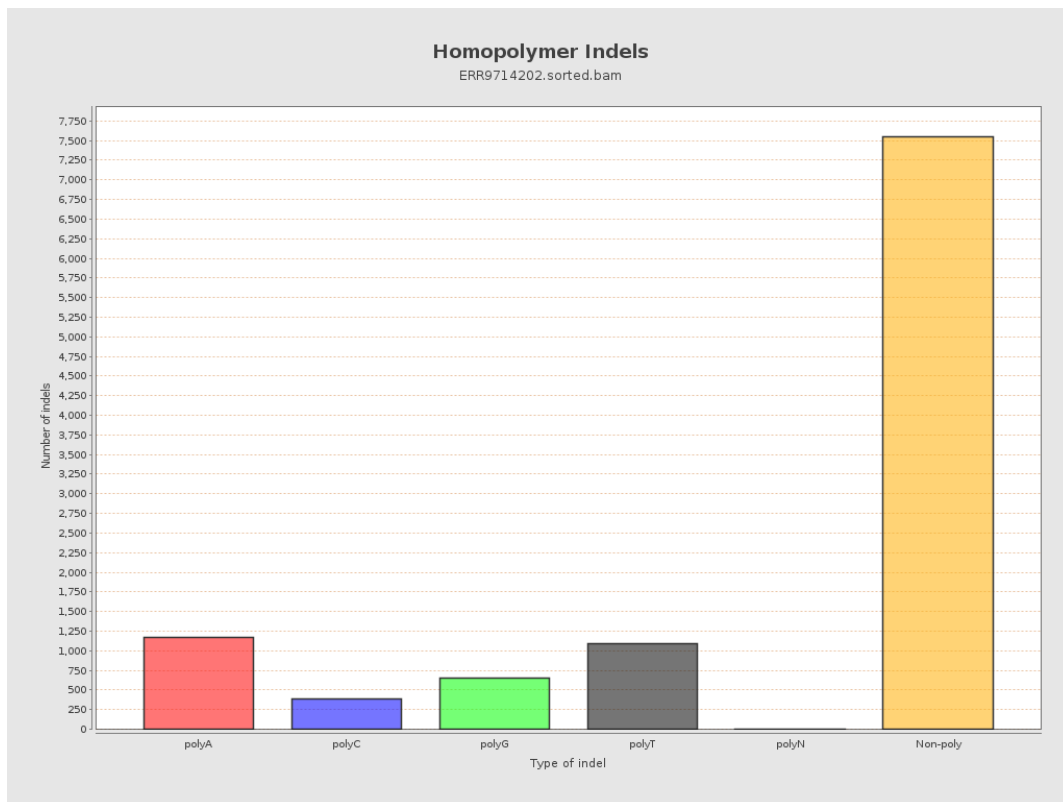
9. Results : Mapped Reads GC-content Distribution



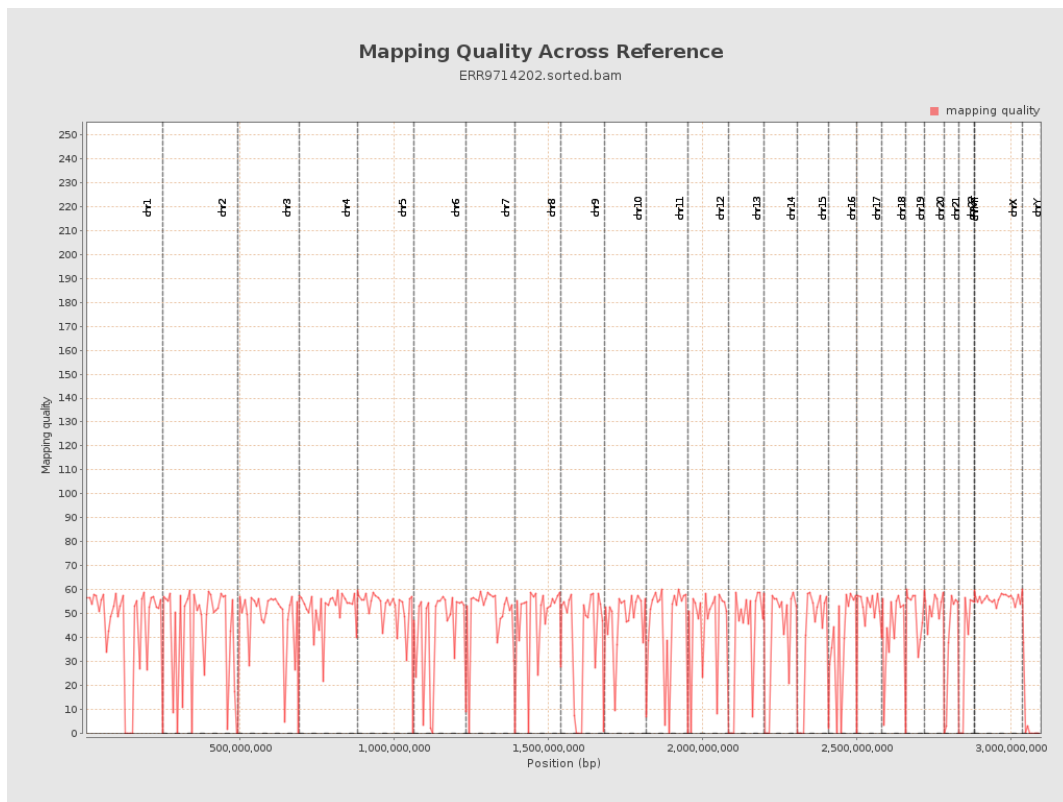
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

