

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:36:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714256.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_ERR9714256 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:36:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	279,386
Mapped reads	164,466 / 58.87%
Unmapped reads	114,920 / 41.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,487 / 0.53%
Read min/max/mean length	30 / 151 / 109
Duplicated reads (estimated)	159,038 / 56.92%
Duplication rate	30.44%
Clipped reads	158,246 / 56.64%

2.2. ACGT Content

Number/percentage of A's	5,981,068 / 31.09%
Number/percentage of C's	3,397,286 / 17.66%
Number/percentage of T's	5,232,381 / 27.2%
Number/percentage of G's	4,624,132 / 24.04%
Number/percentage of N's	120 / 0%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0062

Standard Deviation	24.11
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2.4. Mapping Quality

Mean Mapping Quality	19.16
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2.5. Mismatches and indels

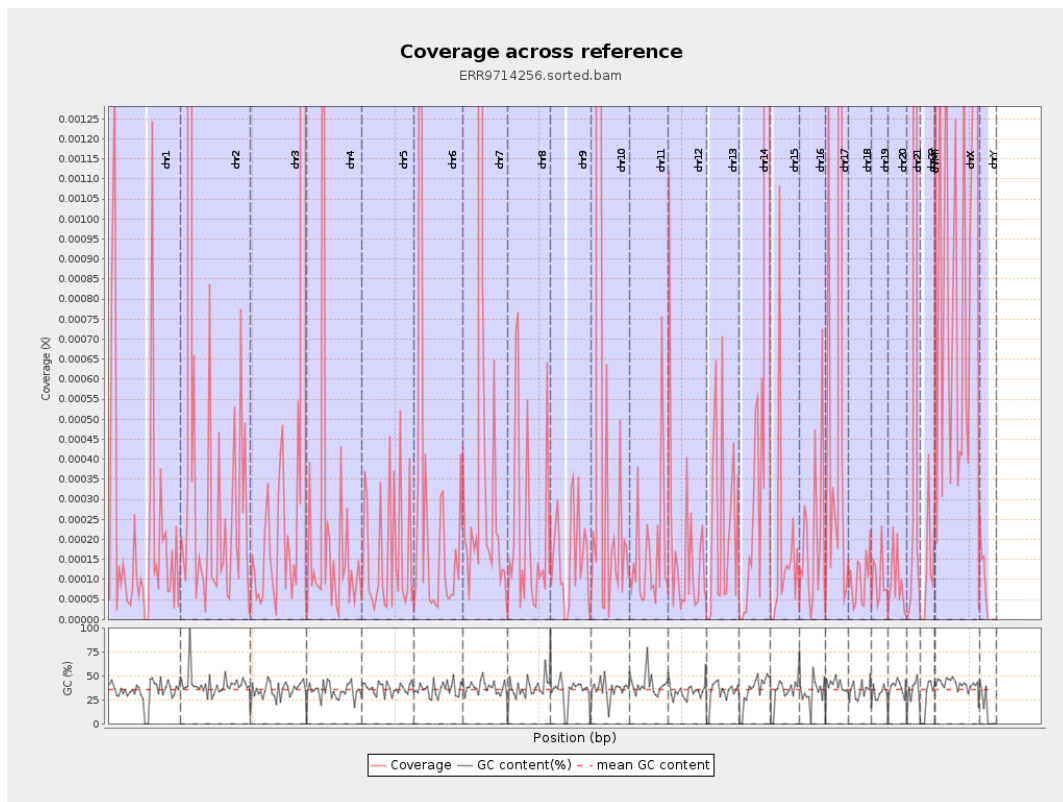
General error rate	3.86%
Mismatches	607,023
Insertions	58,407
Mapped reads with at least one insertion	34.82%
Deletions	24,892
Mapped reads with at least one deletion	14.36%
Homopolymer indels	64.65%

2.6. Chromosome stats

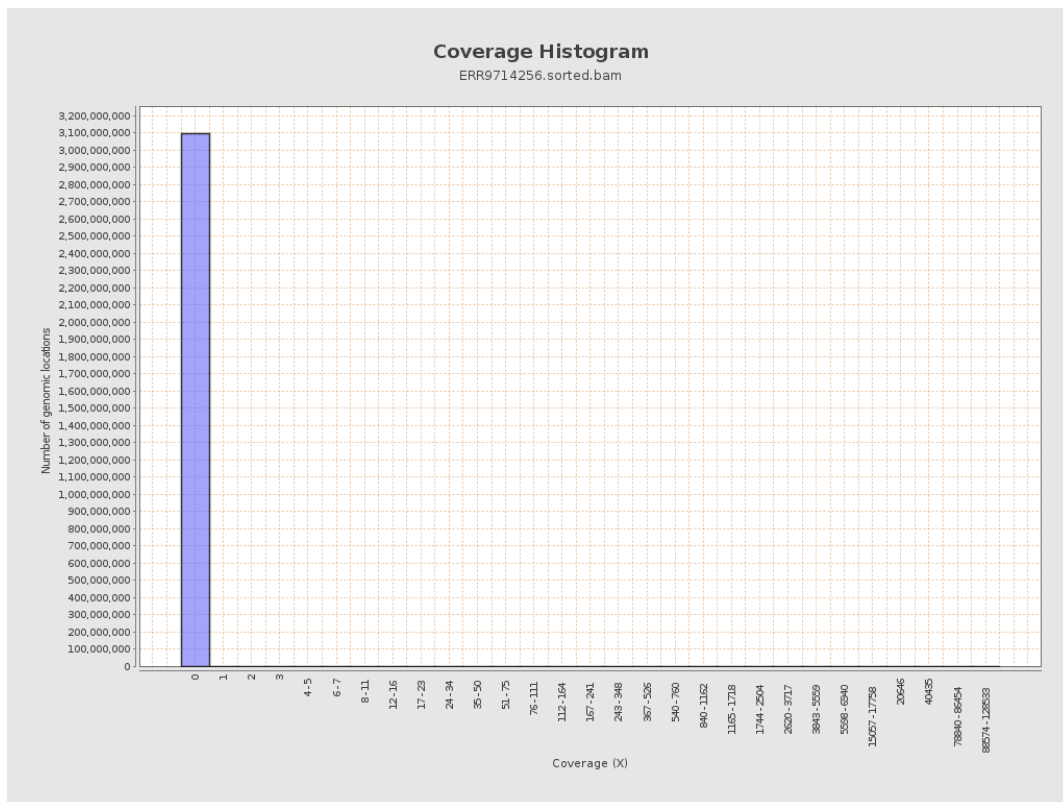
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	52595	0.0002	0.0593
chr2	243199373	1082185	0.0044	4.4143
chr3	198022430	576724	0.0029	3.0098
chr4	191154276	45476	0.0002	0.0486
chr5	180915260	29522	0.0002	0.0347
chr6	171115067	44690	0.0003	0.0558
chr7	159138663	884744	0.0056	5.3554

chr8	146364022	32685	0.0002	0.0464
chr9	141213431	22171	0.0002	0.0291
chr10	135534747	15835767	0.1168	114.8614
chr11	135006516	21661	0.0002	0.0396
chr12	133851895	24554	0.0002	0.0487
chr13	115169878	25974	0.0002	0.061
chr14	107349540	226013	0.0021	1.4262
chr15	102531392	17432	0.0002	0.0619
chr16	90354753	18580	0.0002	0.0832
chr17	81195210	86285	0.0011	0.646
chr18	78077248	7736	0.0001	0.0191
chr19	59128983	5905	0.0001	0.0181
chr20	63025520	6186	0.0001	0.0231
chr21	48129895	64454	0.0013	0.1992
chr22	51304566	6259	0.0001	0.0292
chrMT	16571	41639	2.5128	20.4857
chrX	155270560	136778	0.0009	0.1168
chrY	59373566	4258	0.0001	0.0208

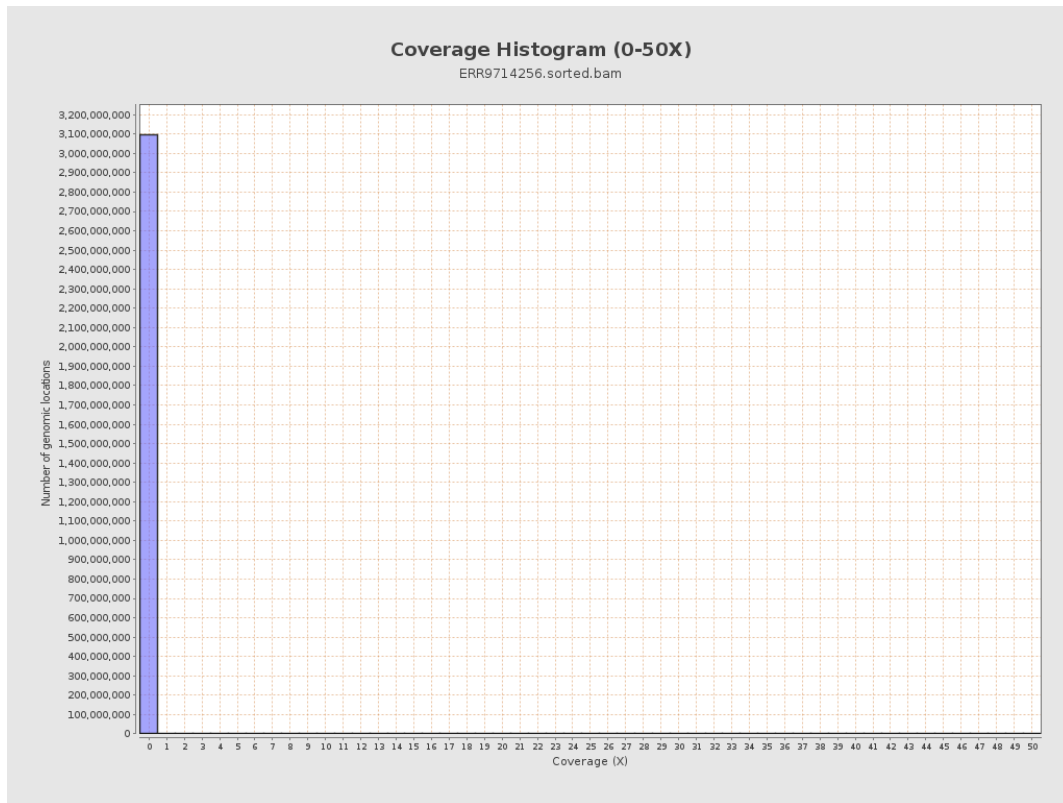
3. Results : Coverage across reference



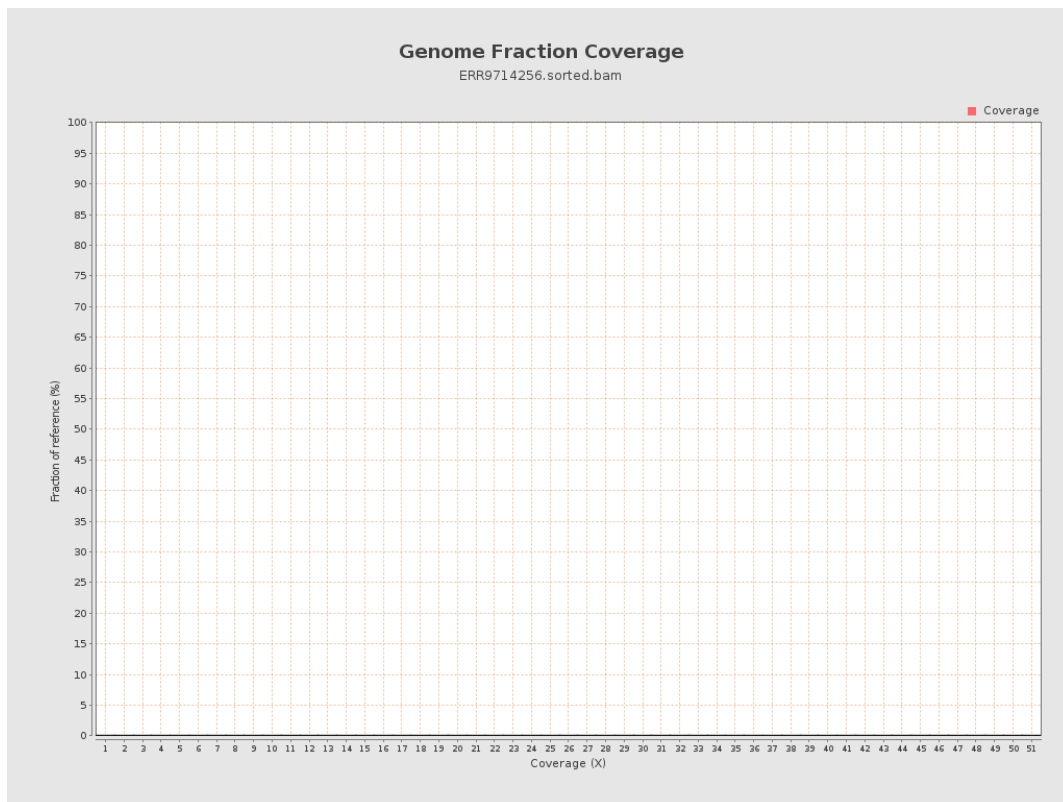
4. Results : Coverage Histogram



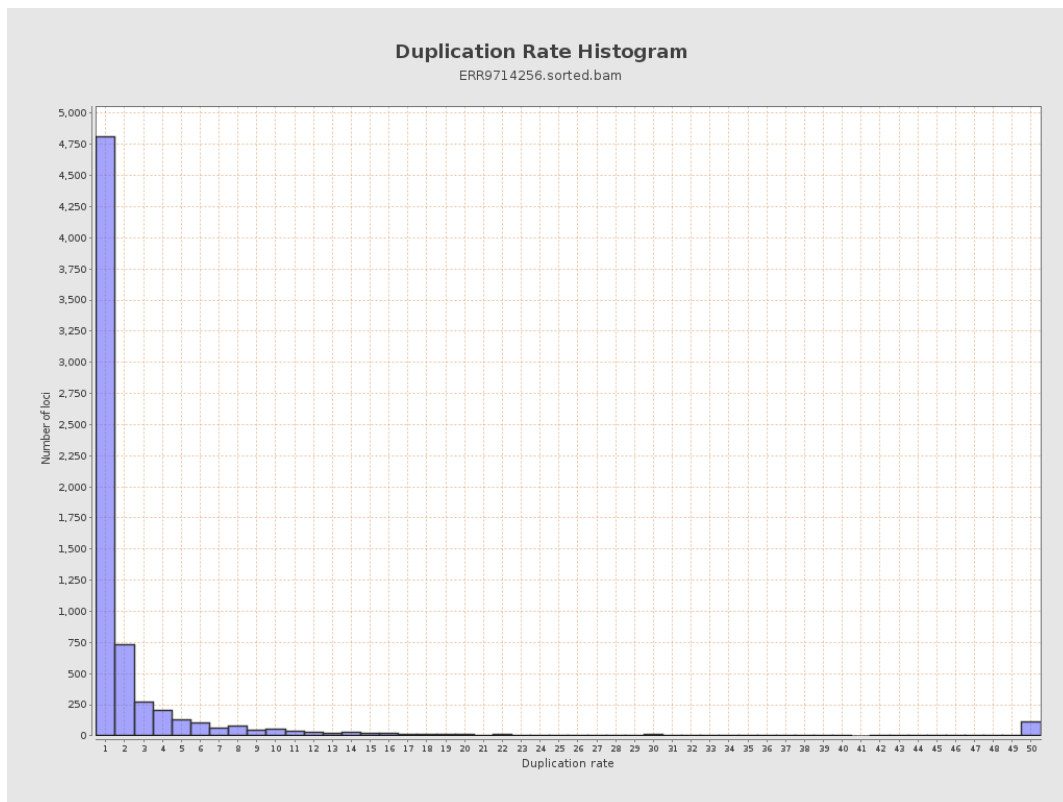
5. Results : Coverage Histogram (0-50X)



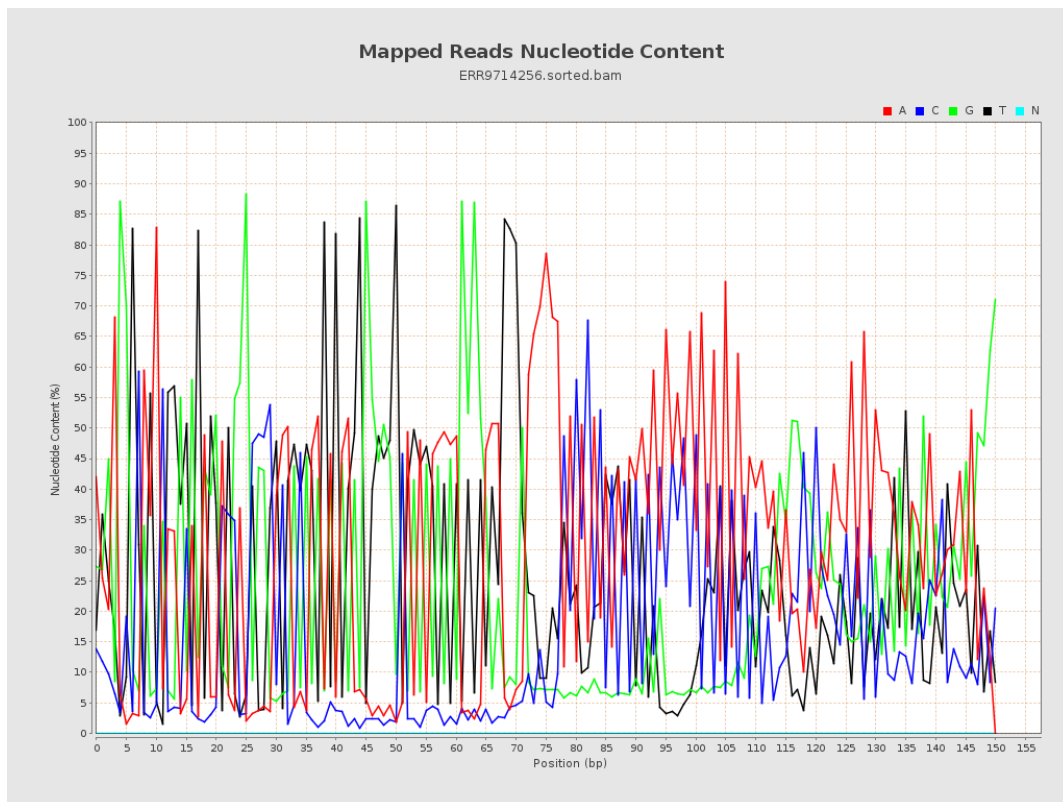
6. Results : Genome Fraction Coverage



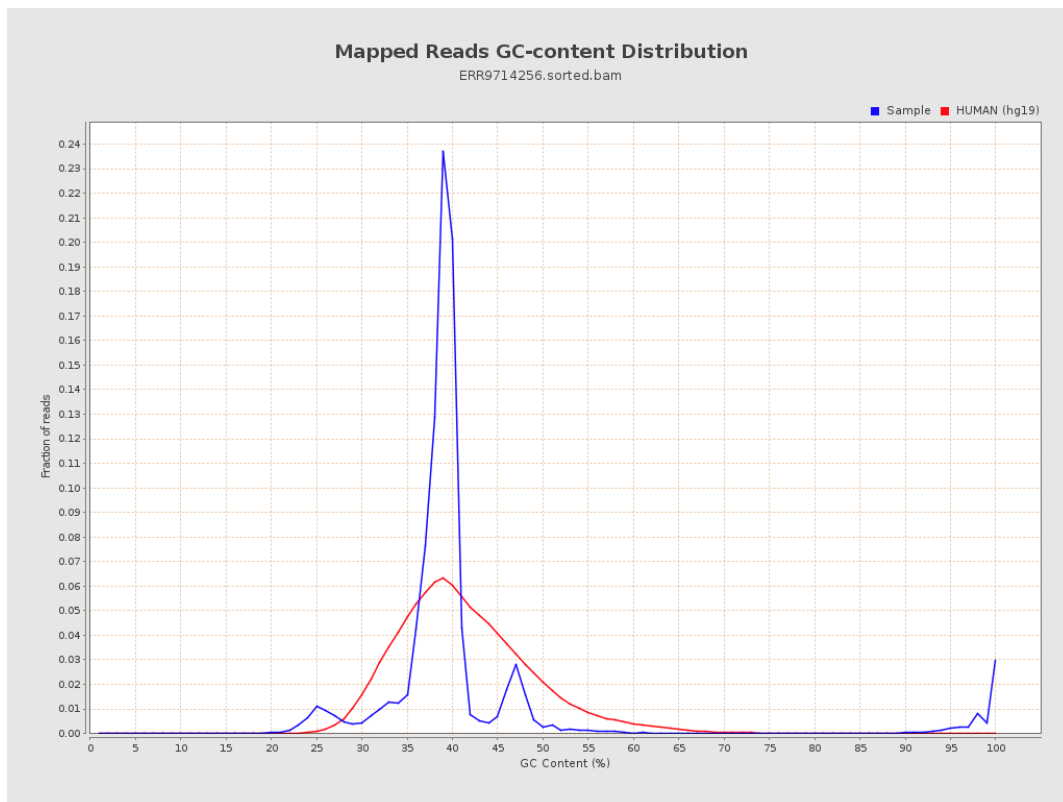
7. Results : Duplication Rate Histogram



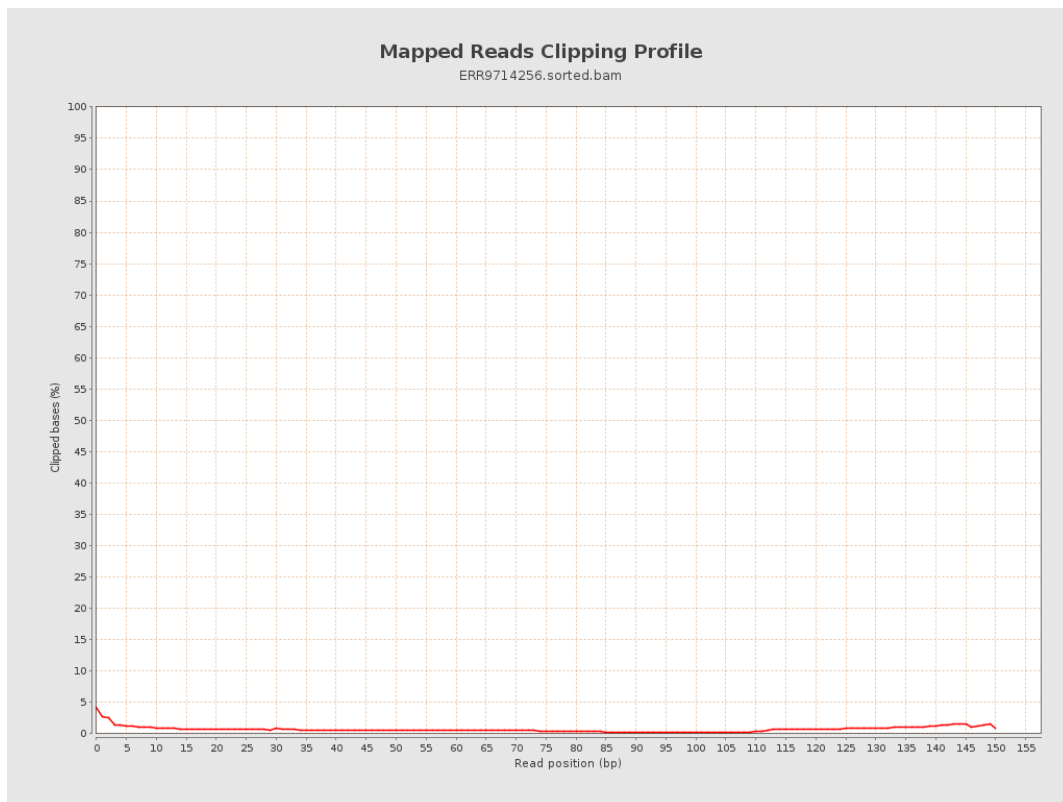
8. Results : Mapped Reads Nucleotide Content



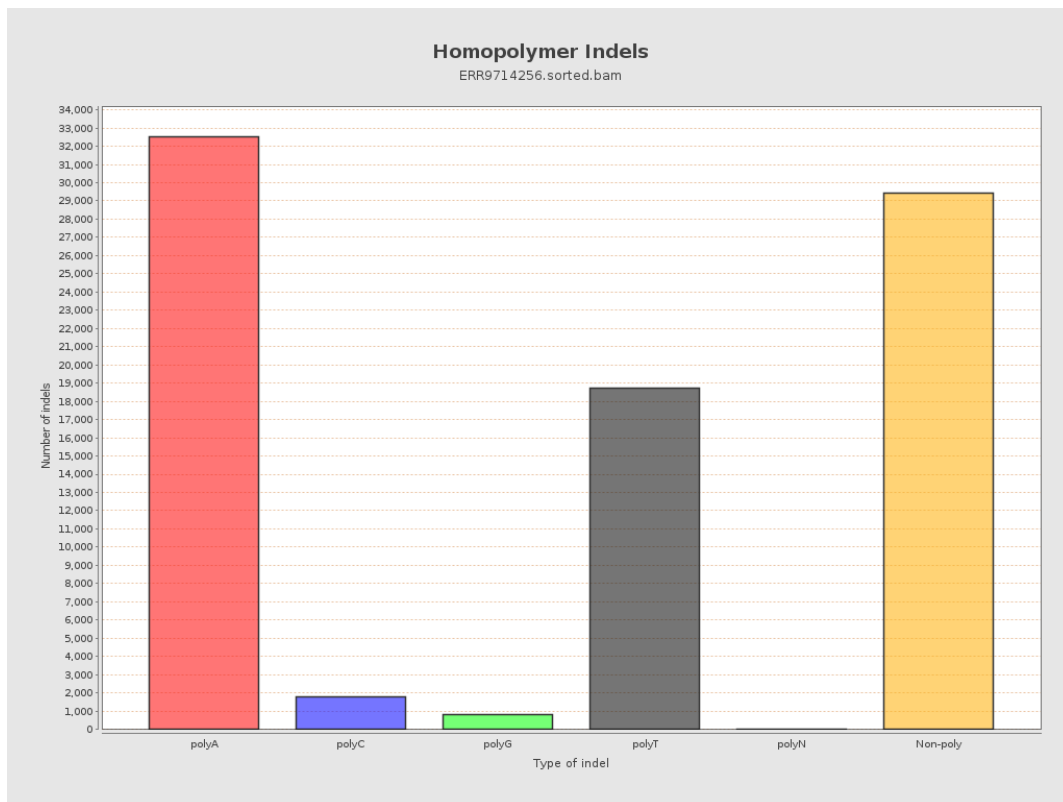
9. Results : Mapped Reads GC-content Distribution



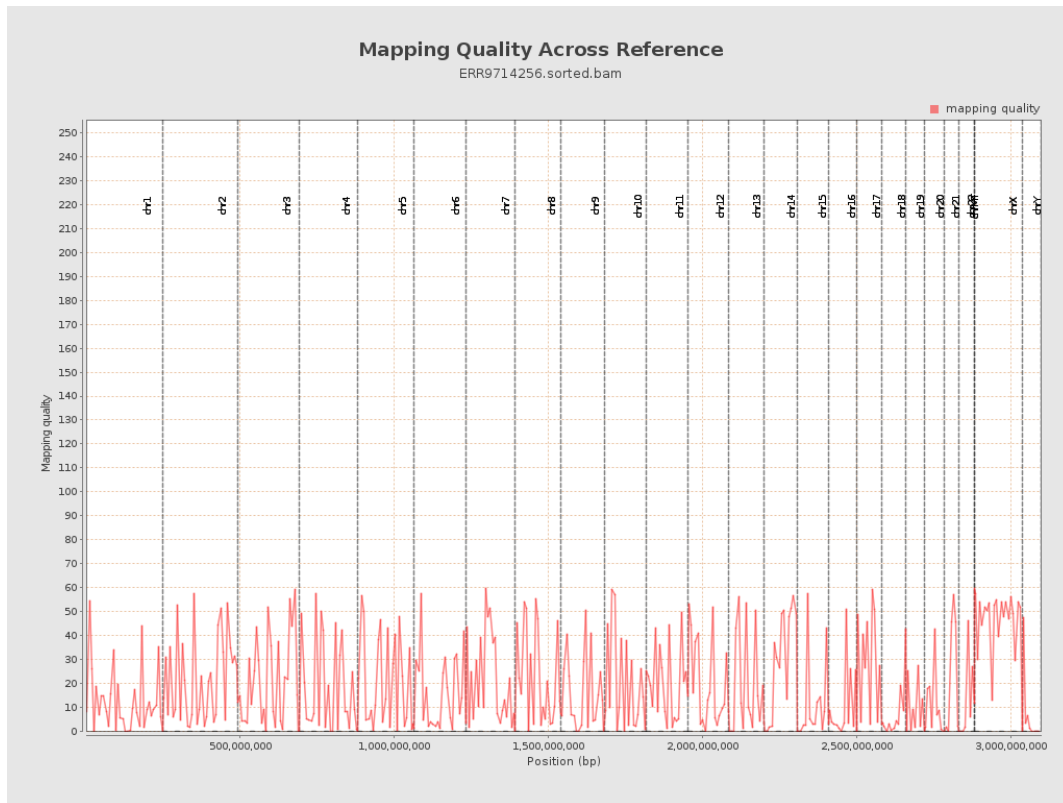
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

