

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:47:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714087.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_ERR9714087 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:47:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	550,642
Mapped reads	281,496 / 51.12%
Unmapped reads	269,146 / 48.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,505 / 0.82%
Read min/max/mean length	30 / 151 / 100.62
Duplicated reads (estimated)	269,219 / 48.89%
Duplication rate	35.91%
Clipped reads	254,880 / 46.29%

2.2. ACGT Content

Number/percentage of A's	9,367,719 / 26.68%
Number/percentage of C's	7,007,573 / 19.96%
Number/percentage of T's	8,984,075 / 25.59%
Number/percentage of G's	9,748,952 / 27.77%
Number/percentage of N's	337 / 0%
GC Percentage	47.73%

2.3. Coverage

Mean	0.0115

Standard Deviation	11.5469
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2.4. Mapping Quality

Mean Mapping Quality	32.98
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2.5. Mismatches and indels

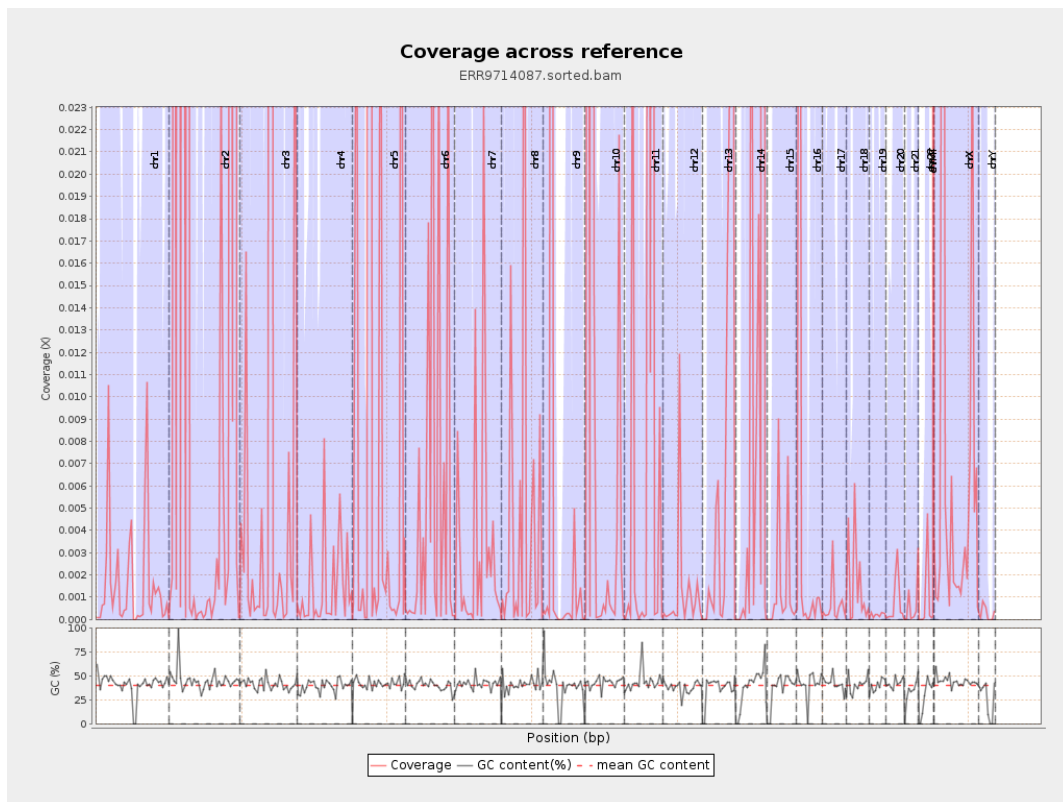
General error rate	3.18%
Mismatches	988,852
Insertions	34,610
Mapped reads with at least one insertion	11.79%
Deletions	90,965
Mapped reads with at least one deletion	31.19%
Homopolymer indels	28.43%

2.6. Chromosome stats

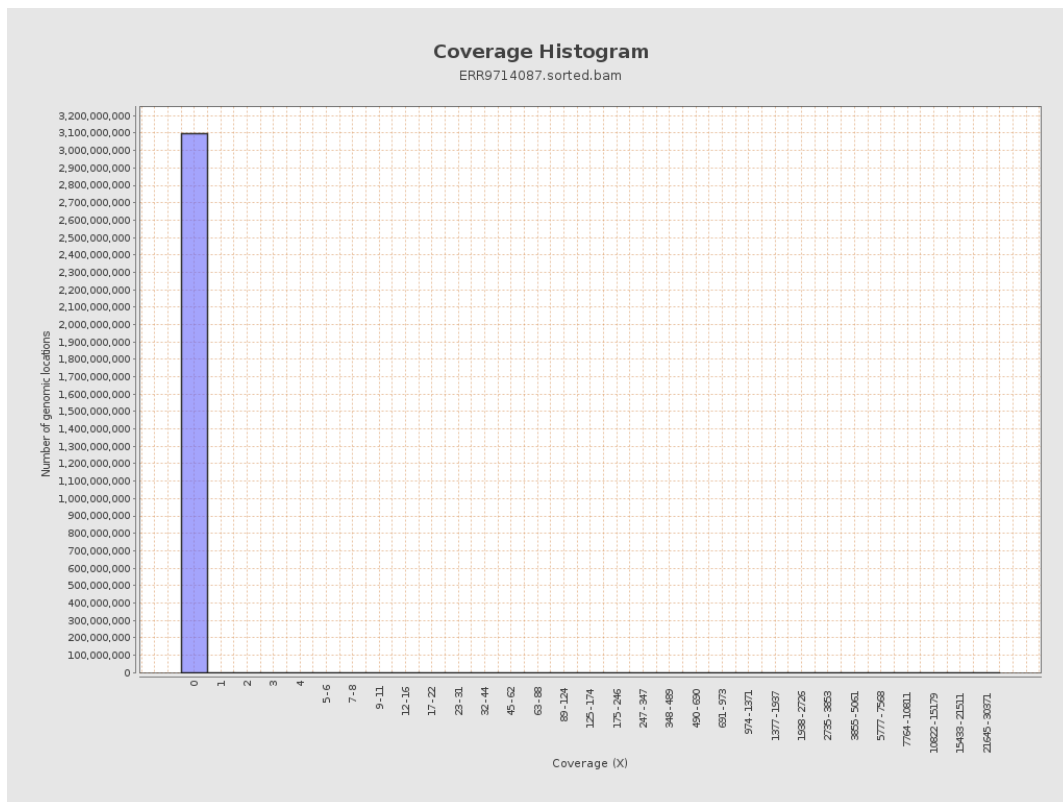
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	432148	0.0017	0.5138
chr2	243199373	10342201	0.0425	20.5812
chr3	198022430	2198487	0.0111	8.9431
chr4	191154276	278716	0.0015	0.4909
chr5	180915260	4123077	0.0228	21.2967
chr6	171115067	1108751	0.0065	2.3485
chr7	159138663	533220	0.0034	1.4131

chr8	146364022	722732	0.0049	2.3861
chr9	141213431	793232	0.0056	2.5169
chr10	135534747	4615083	0.0341	23.5244
chr11	135006516	1807323	0.0134	6.2474
chr12	133851895	166213	0.0012	0.6121
chr13	115169878	1090631	0.0095	4.0609
chr14	107349540	4782984	0.0446	33.9001
chr15	102531392	163460	0.0016	0.5461
chr16	90354753	554353	0.0061	4.262
chr17	81195210	52787	0.0007	0.1571
chr18	78077248	123817	0.0016	0.4134
chr19	59128983	12120	0.0002	0.0271
chr20	63025520	47257	0.0007	0.2577
chr21	48129895	30656	0.0006	0.2003
chr22	51304566	39406	0.0008	0.3659
chrMT	16571	312561	18.8619	151.6632
chrX	155270560	1156251	0.0074	2.6143
chrY	59373566	15147	0.0003	0.0659

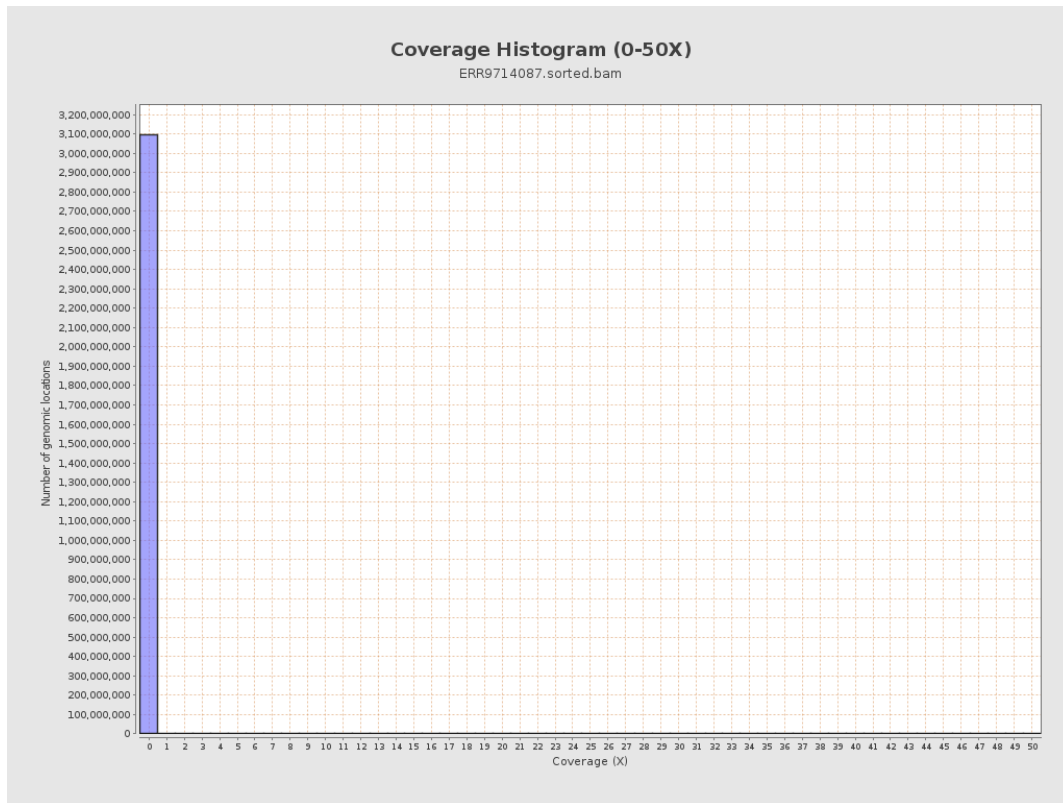
3. Results : Coverage across reference



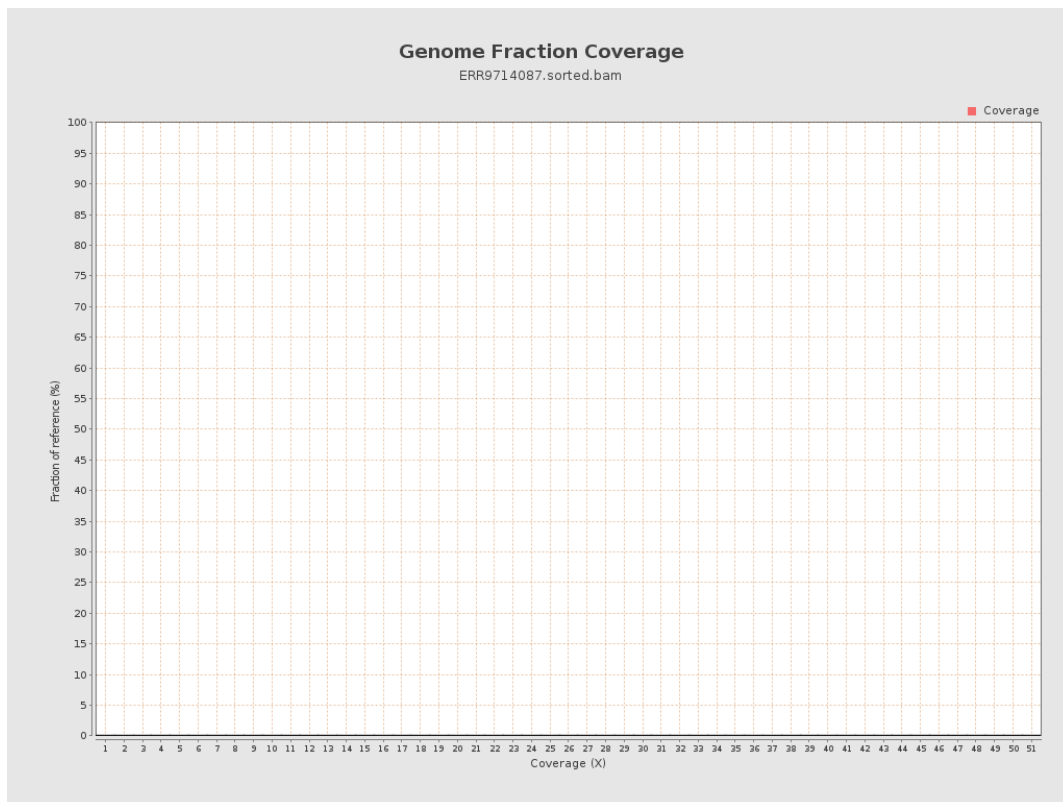
4. Results : Coverage Histogram



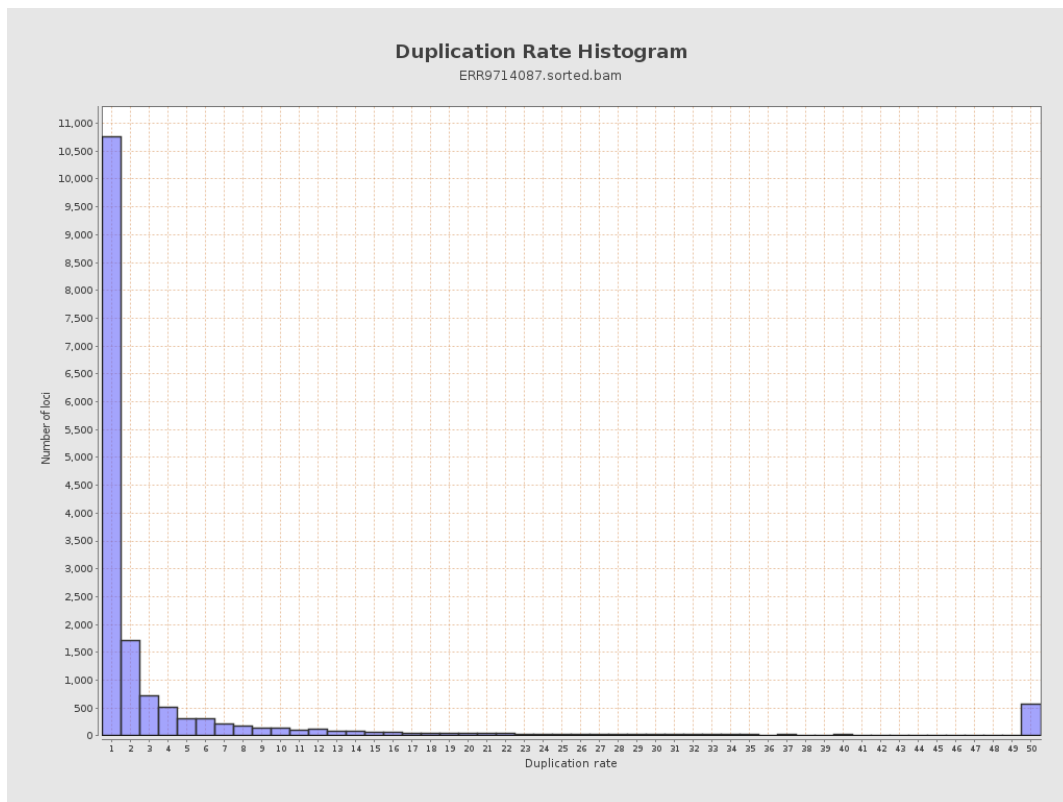
5. Results : Coverage Histogram (0-50X)



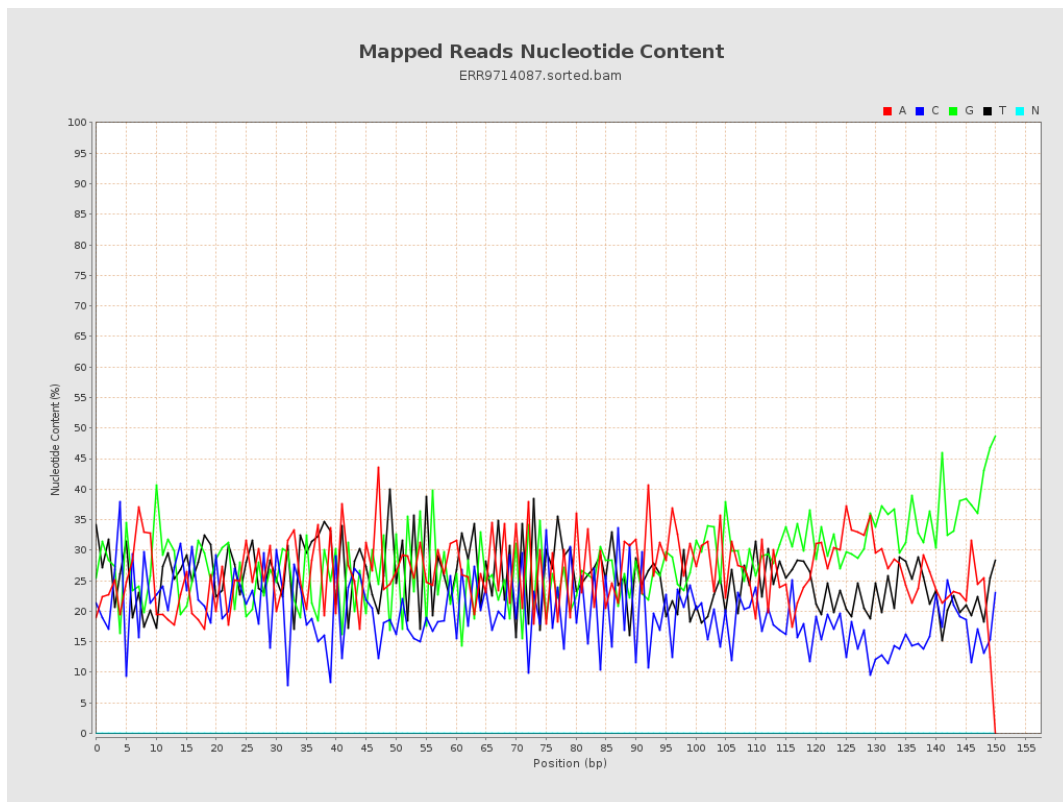
6. Results : Genome Fraction Coverage



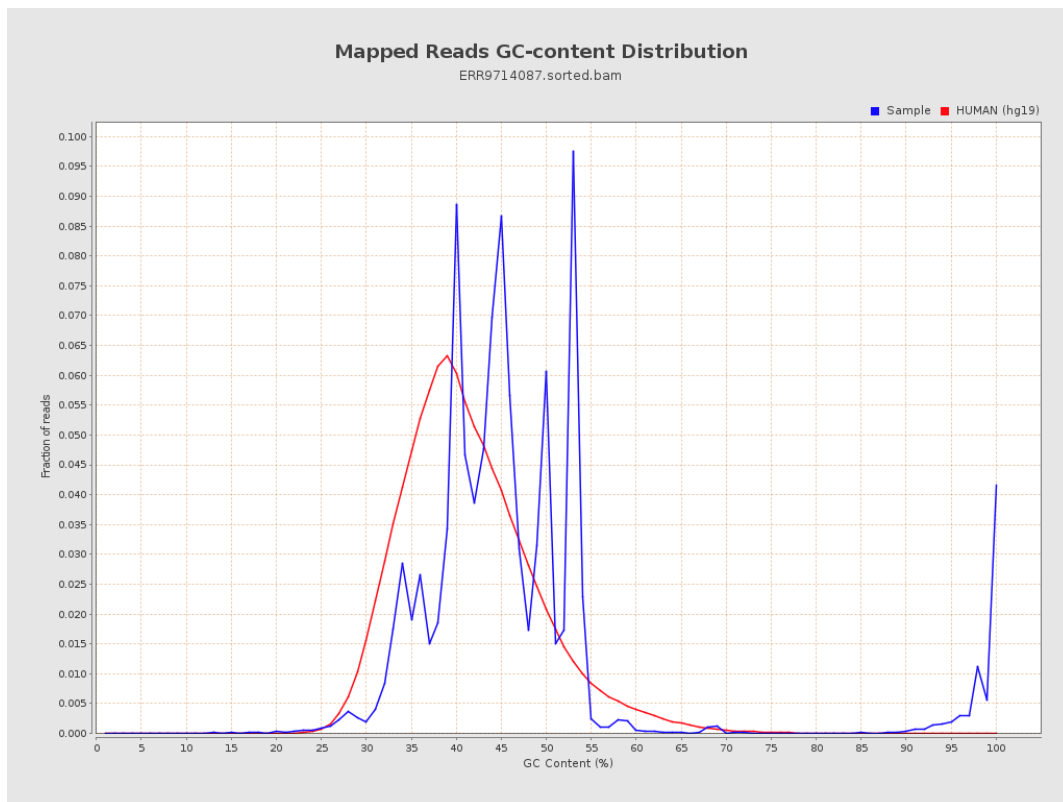
7. Results : Duplication Rate Histogram



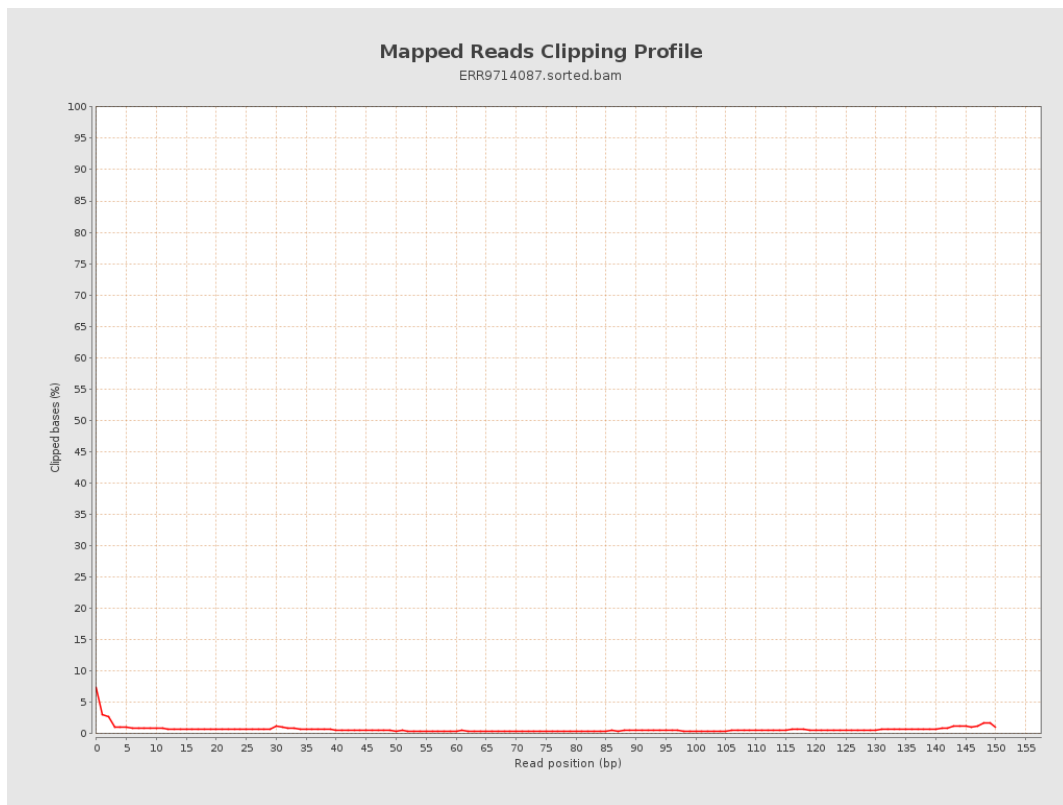
8. Results : Mapped Reads Nucleotide Content



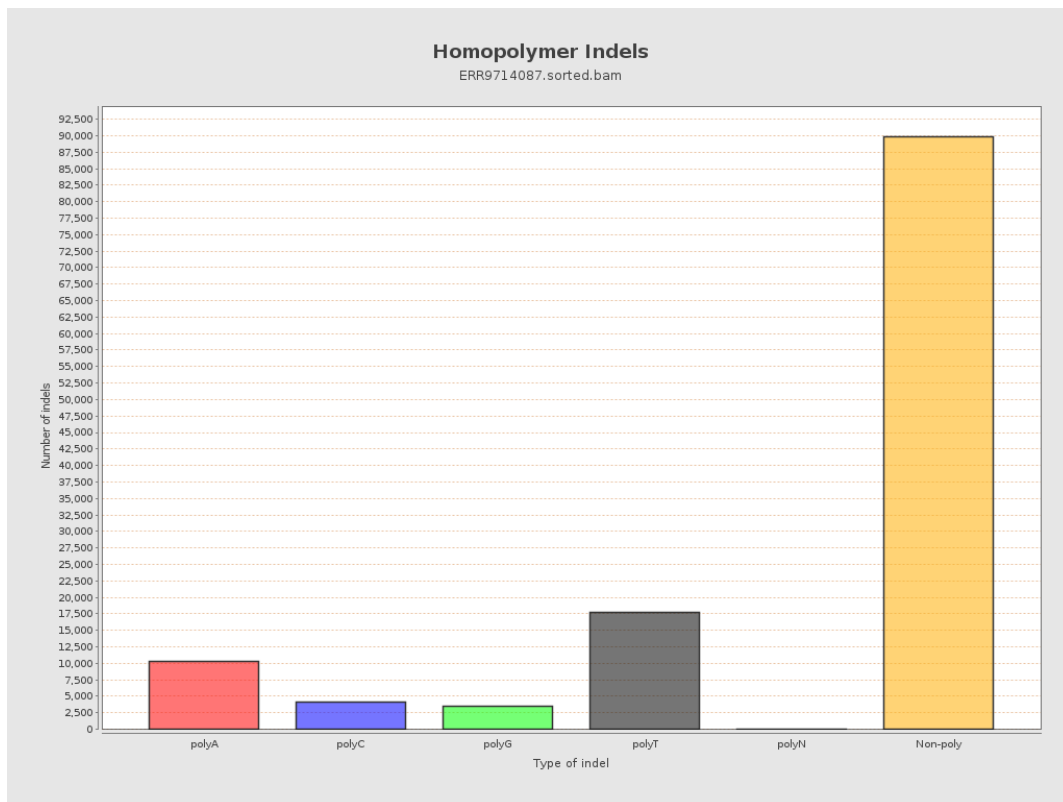
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

