

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:55:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714195.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_ERR9714195 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:55:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	67,174
Mapped reads	40,962 / 60.98%
Unmapped reads	26,212 / 39.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,434 / 2.13%
Read min/max/mean length	30 / 151 / 114.74
Duplicated reads (estimated)	29,008 / 43.18%
Duplication rate	39.3%
Clipped reads	38,560 / 57.4%

2.2. ACGT Content

Number/percentage of A's	1,401,151 / 27.3%
Number/percentage of C's	1,054,374 / 20.55%
Number/percentage of T's	1,326,056 / 25.84%
Number/percentage of G's	1,350,286 / 26.31%
Number/percentage of N's	15 / 0%
GC Percentage	46.86%

2.3. Coverage

Mean	0.0017

Standard Deviation	0.38
--------------------	------

2.4. Mapping Quality

Mean Mapping Quality	50.69
----------------------	-------

2.5. Mismatches and indels

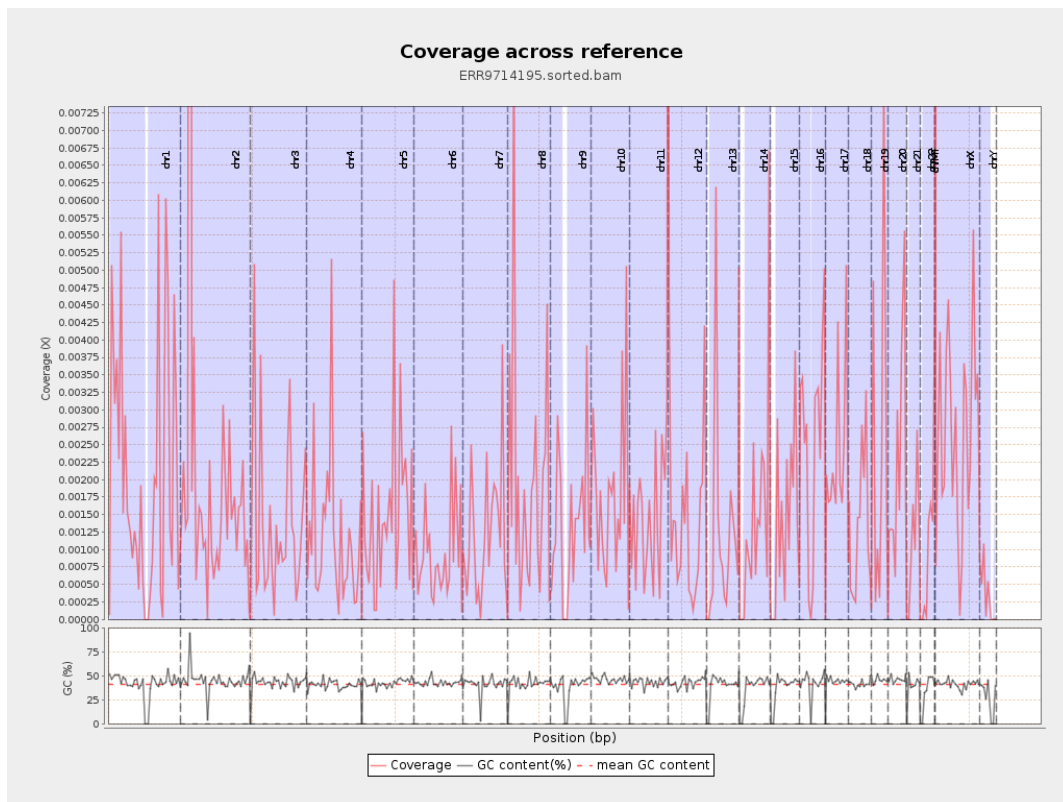
General error rate	4.12%
Mismatches	188,911
Insertions	6,499
Mapped reads with at least one insertion	15.27%
Deletions	15,873
Mapped reads with at least one deletion	36.28%
Homopolymer indels	27.52%

2.6. Chromosome stats

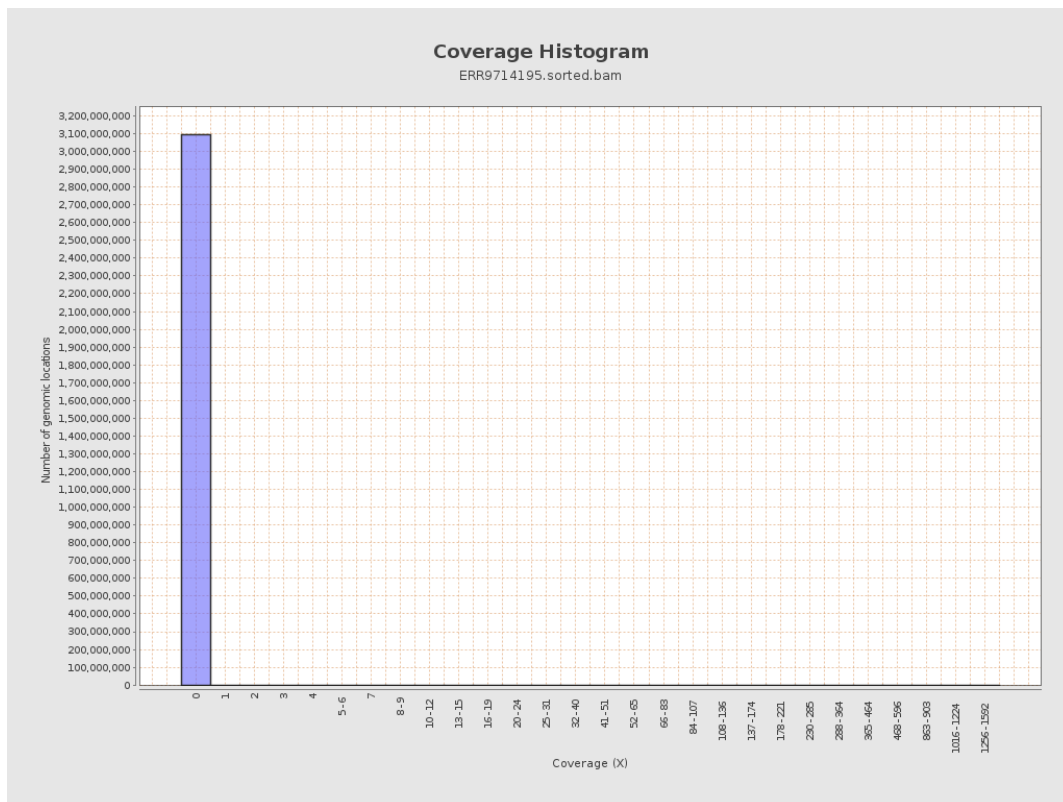
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	510102	0.002	0.299
chr2	243199373	632455	0.0026	1.0622
chr3	198022430	284901	0.0014	0.2504
chr4	191154276	230134	0.0012	0.2011
chr5	180915260	277859	0.0015	0.2168
chr6	171115067	167092	0.001	0.1431
chr7	159138663	192042	0.0012	0.1732

chr8	146364022	293428	0.002	0.359
chr9	141213431	181781	0.0013	0.189
chr10	135534747	241665	0.0018	0.2292
chr11	135006516	205429	0.0015	0.1941
chr12	133851895	198553	0.0015	0.2116
chr13	115169878	135784	0.0012	0.2514
chr14	107349540	158814	0.0015	0.2346
chr15	102531392	143558	0.0014	0.2236
chr16	90354753	227480	0.0025	0.3504
chr17	81195210	194515	0.0024	0.2767
chr18	78077248	109301	0.0014	0.1834
chr19	59128983	136483	0.0023	0.3921
chr20	63025520	145458	0.0023	0.3155
chr21	48129895	53817	0.0011	0.2057
chr22	51304566	45709	0.0009	0.1349
chrMT	16571	23810	1.4368	13.0513
chrX	155270560	407165	0.0026	0.2735
chrY	59373566	21281	0.0004	0.0796

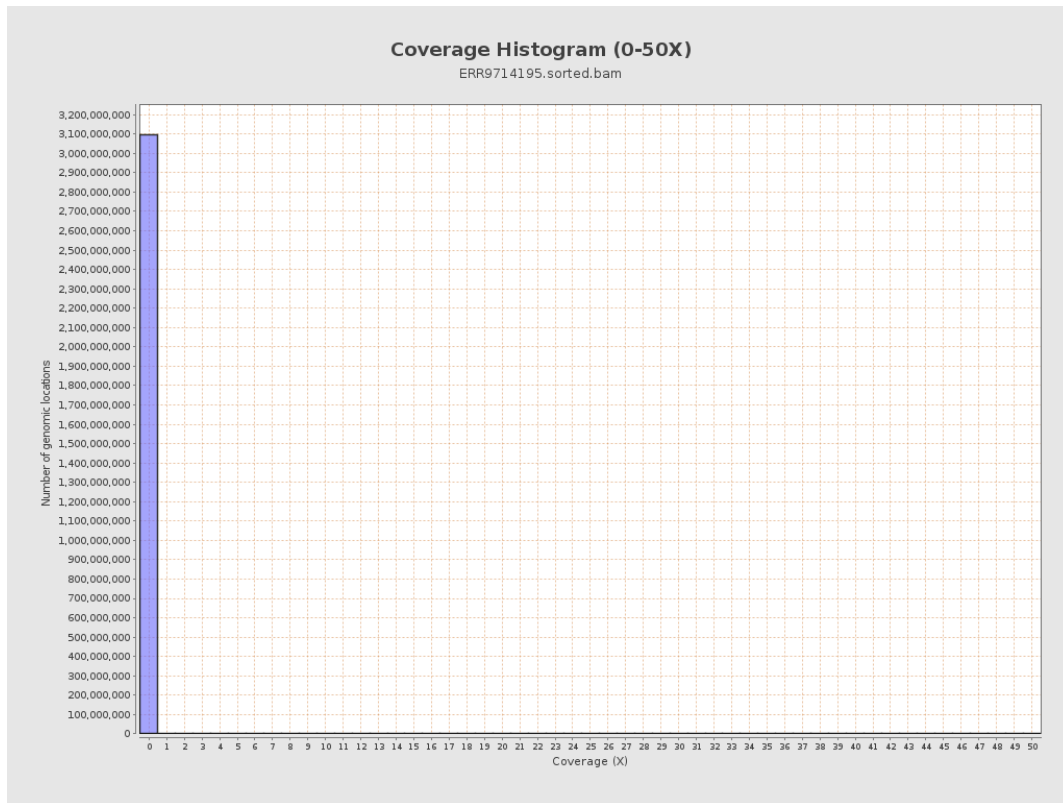
3. Results : Coverage across reference



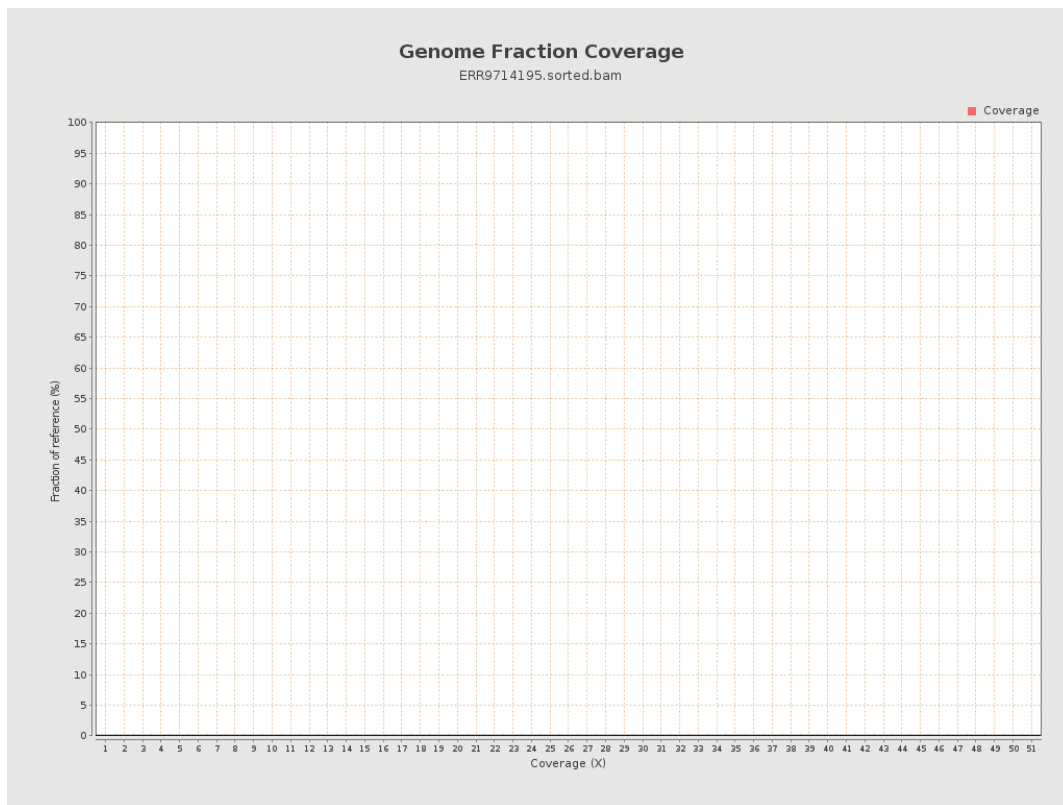
4. Results : Coverage Histogram



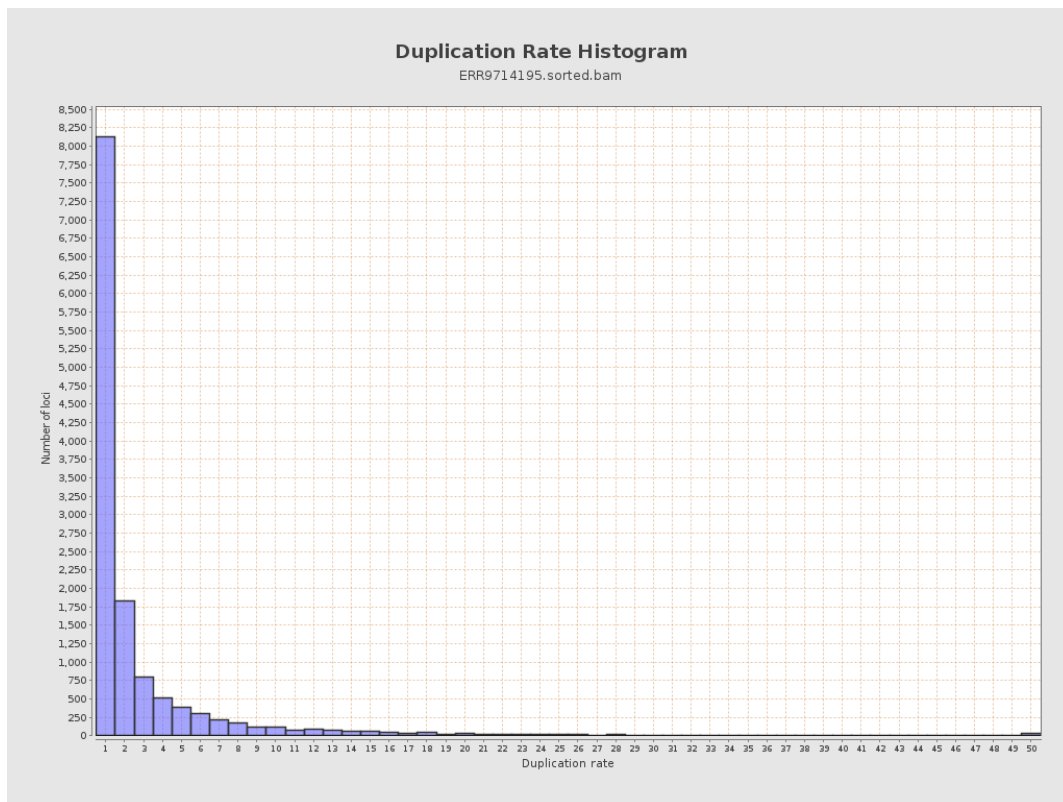
5. Results : Coverage Histogram (0-50X)



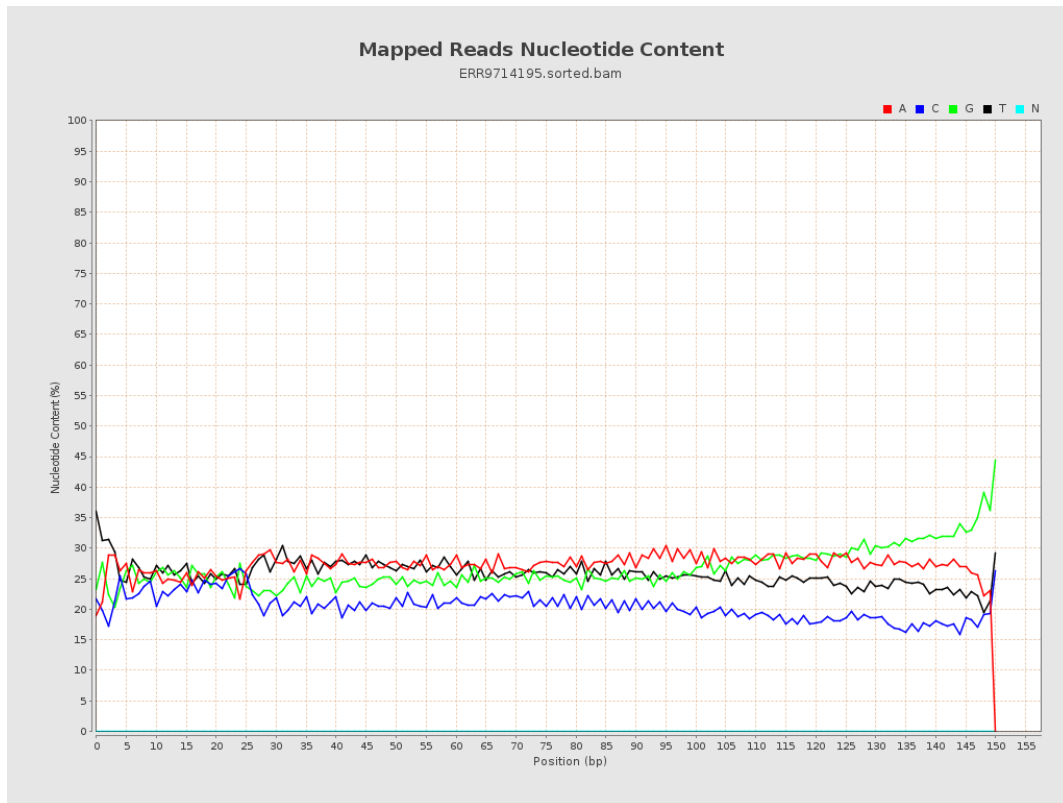
6. Results : Genome Fraction Coverage



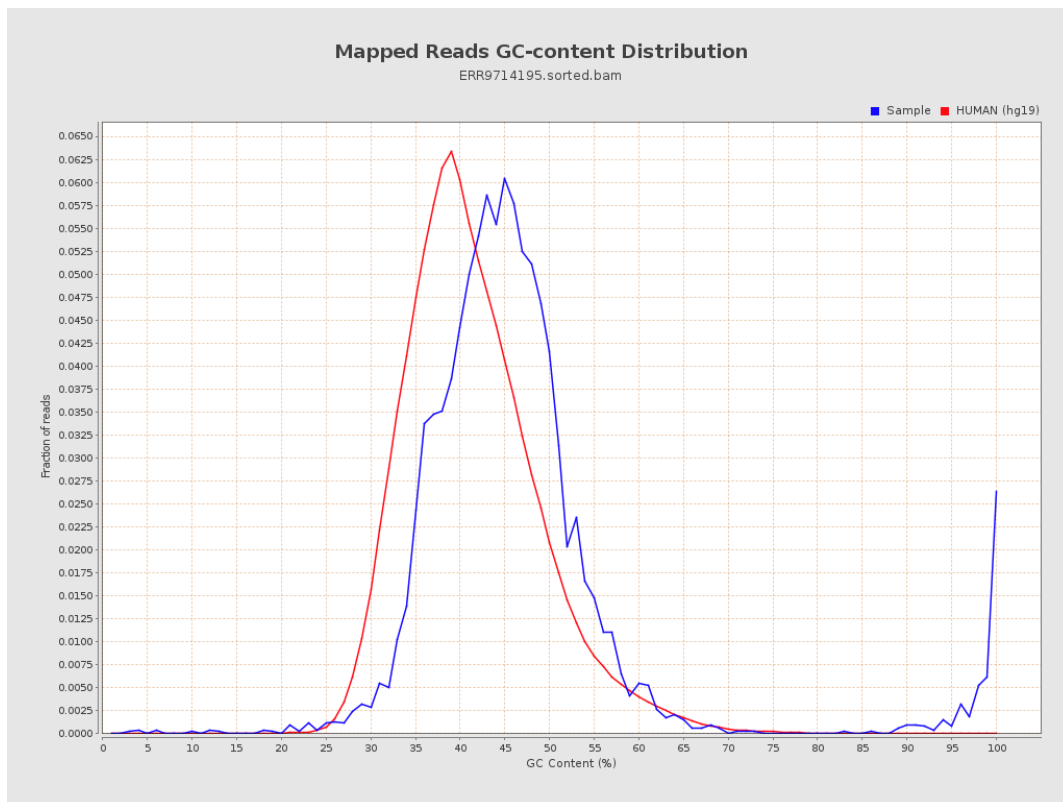
7. Results : Duplication Rate Histogram



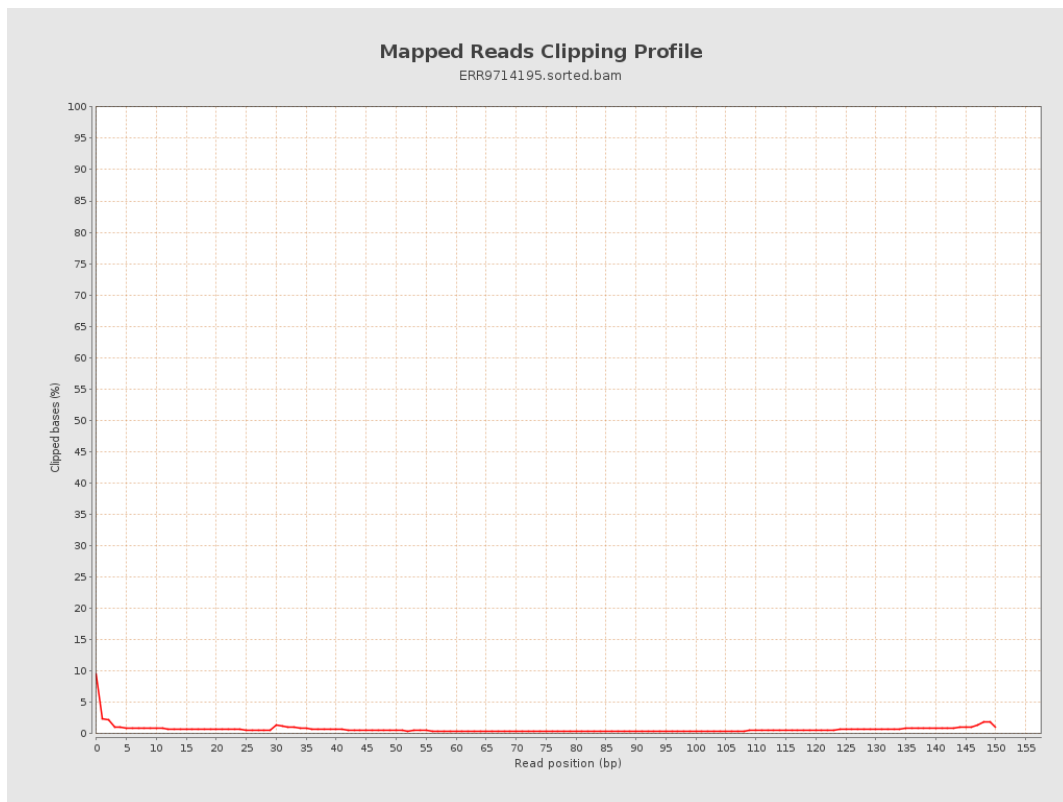
8. Results : Mapped Reads Nucleotide Content



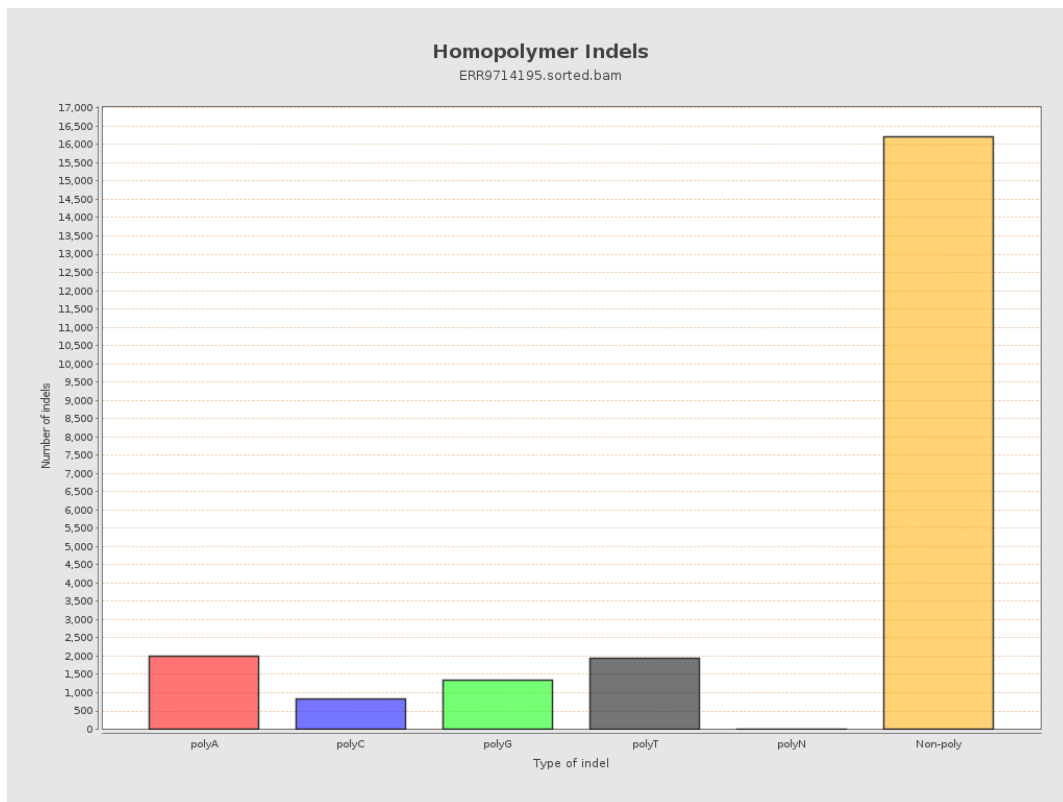
9. Results : Mapped Reads GC-content Distribution



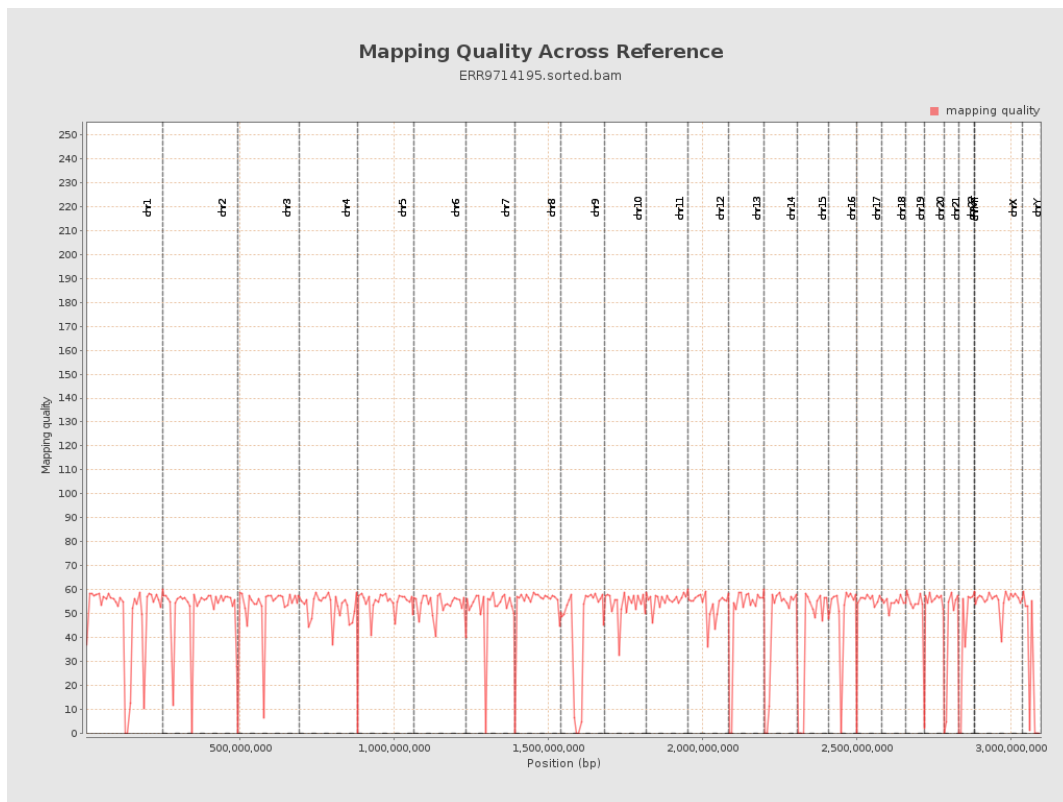
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

