

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:49:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714088.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_ERR9714088 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:49:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	496,190
Mapped reads	326,452 / 65.79%
Unmapped reads	169,738 / 34.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,627 / 2.34%
Read min/max/mean length	30 / 151 / 117.23
Duplicated reads (estimated)	258,491 / 52.1%
Duplication rate	42.65%
Clipped reads	308,635 / 62.2%

2.2. ACGT Content

Number/percentage of A's	11,121,773 / 27.22%
Number/percentage of C's	8,741,509 / 21.4%
Number/percentage of T's	10,555,110 / 25.84%
Number/percentage of G's	10,435,654 / 25.54%
Number/percentage of N's	249 / 0%
GC Percentage	46.94%

2.3. Coverage

Mean	0.0135

Standard Deviation	1.9835
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2.4. Mapping Quality

Mean Mapping Quality	52.57
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2.5. Mismatches and indels

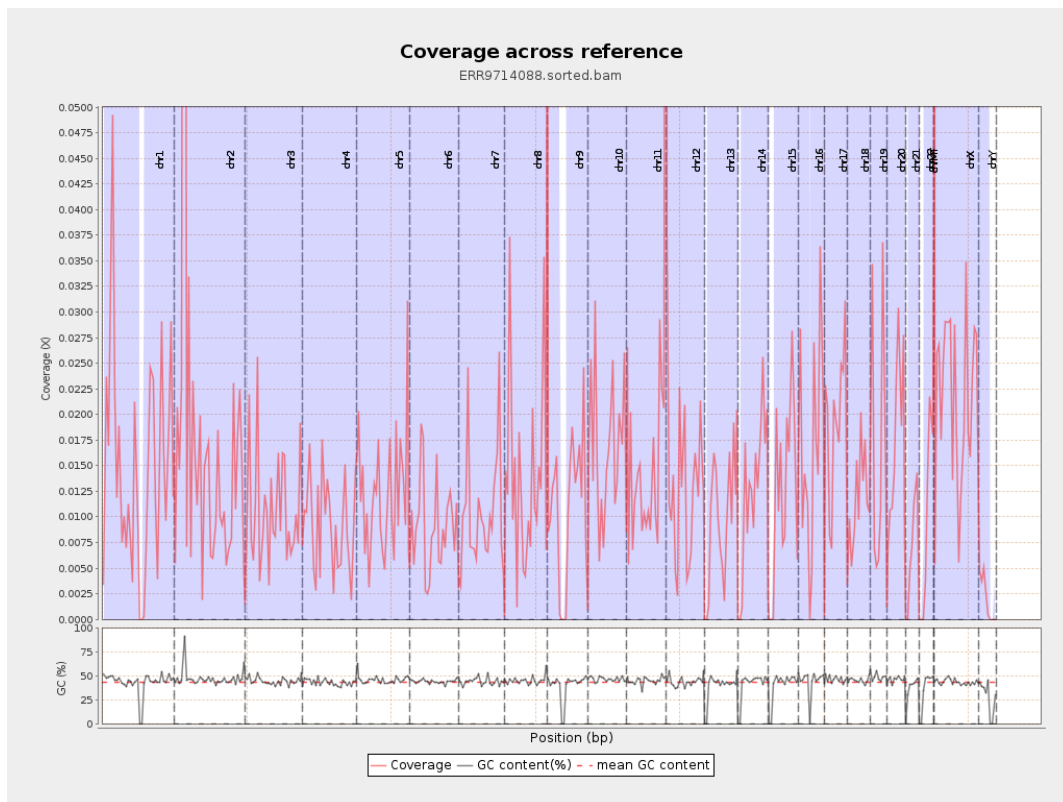
General error rate	4.24%
Mismatches	1,587,066
Insertions	45,842
Mapped reads with at least one insertion	13.56%
Deletions	137,386
Mapped reads with at least one deletion	40.15%
Homopolymer indels	29.25%

2.6. Chromosome stats

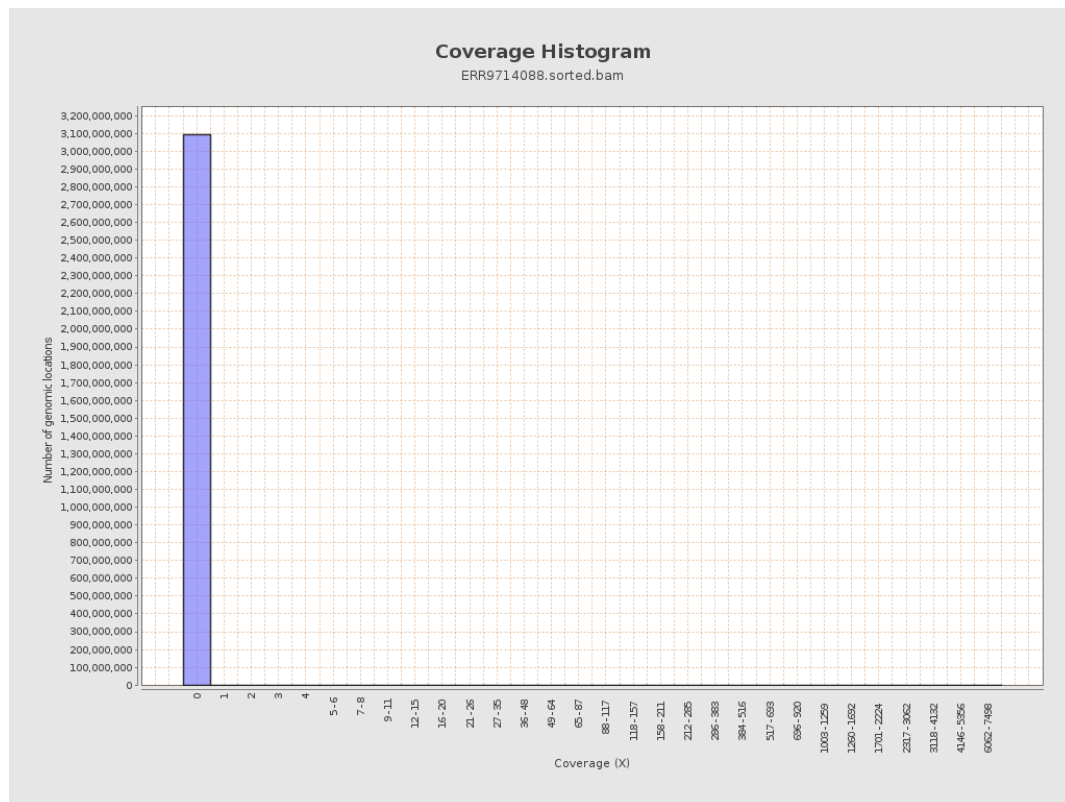
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3697837	0.0148	1.5438
chr2	243199373	4681799	0.0193	5.1679
chr3	198022430	2148332	0.0108	1.0158
chr4	191154276	1745189	0.0091	0.9745
chr5	180915260	2239851	0.0124	1.1563
chr6	171115067	1524866	0.0089	0.8157
chr7	159138663	1613922	0.0101	1.0057

chr8	146364022	1991903	0.0136	1.5554
chr9	141213431	1594010	0.0113	1.2317
chr10	135534747	2272289	0.0168	1.6414
chr11	135006516	1933882	0.0143	1.3939
chr12	133851895	1779441	0.0133	1.3676
chr13	115169878	1070263	0.0093	0.9383
chr14	107349540	1340258	0.0125	1.3014
chr15	102531392	1251324	0.0122	1.2188
chr16	90354753	1498671	0.0166	1.8806
chr17	81195210	1531301	0.0189	1.8728
chr18	78077248	941727	0.0121	0.993
chr19	59128983	923279	0.0156	1.6149
chr20	63025520	1119253	0.0178	1.4508
chr21	48129895	325360	0.0068	0.6575
chr22	51304566	521567	0.0102	1.1534
chrMT	16571	427837	25.8184	237.224
chrX	155270560	3366815	0.0217	1.3924
chrY	59373566	117100	0.002	0.2684

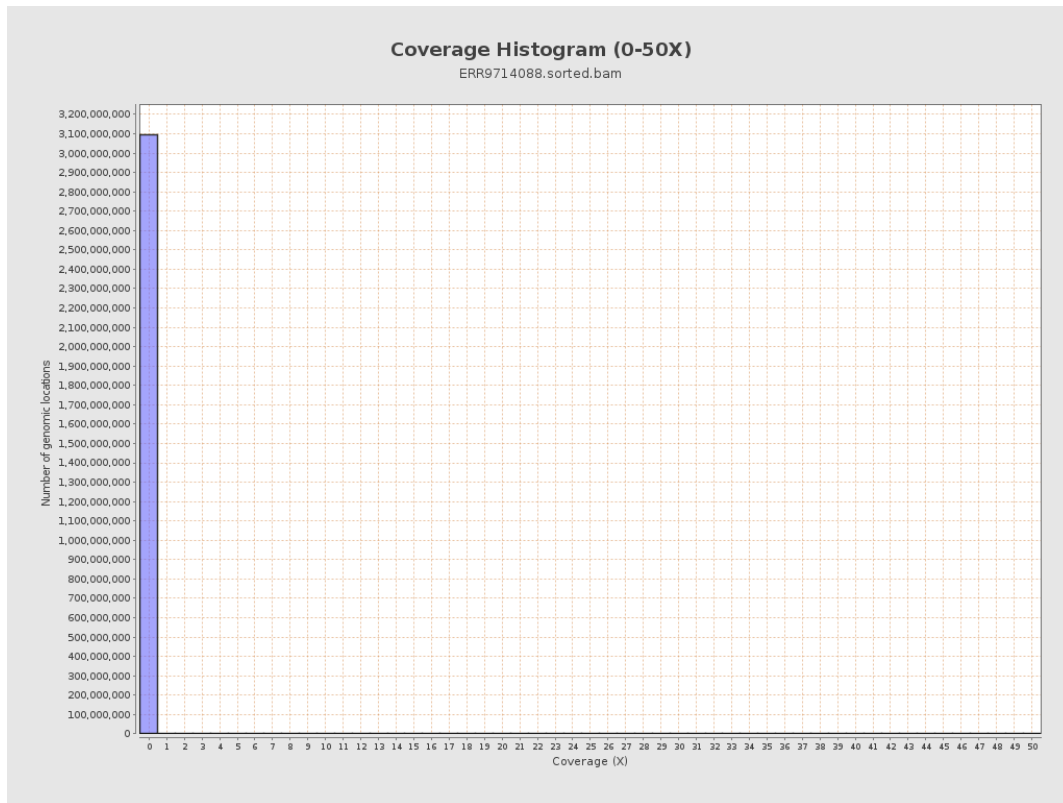
3. Results : Coverage across reference



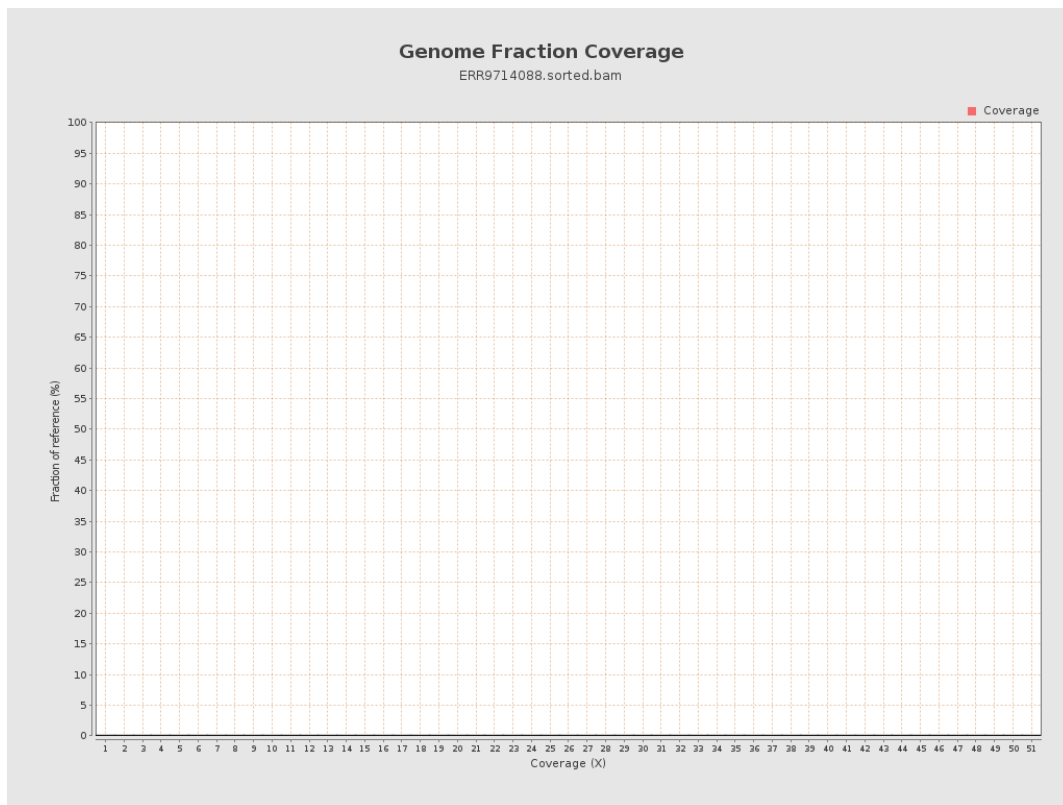
4. Results : Coverage Histogram



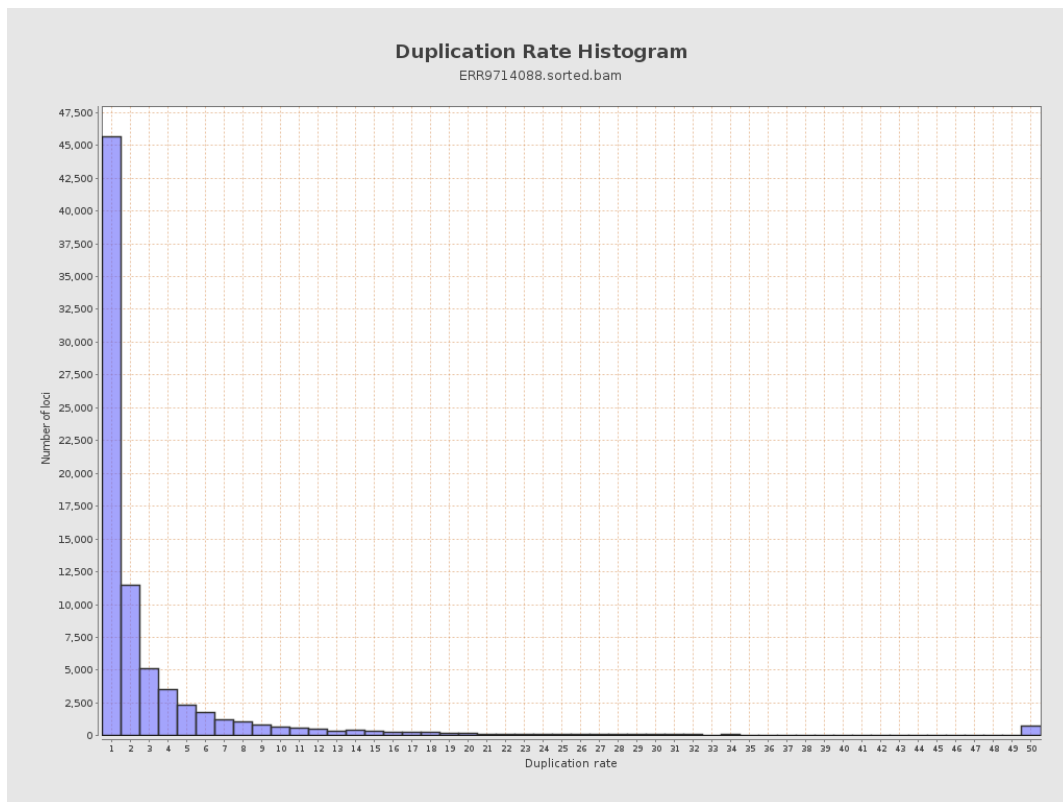
5. Results : Coverage Histogram (0-50X)



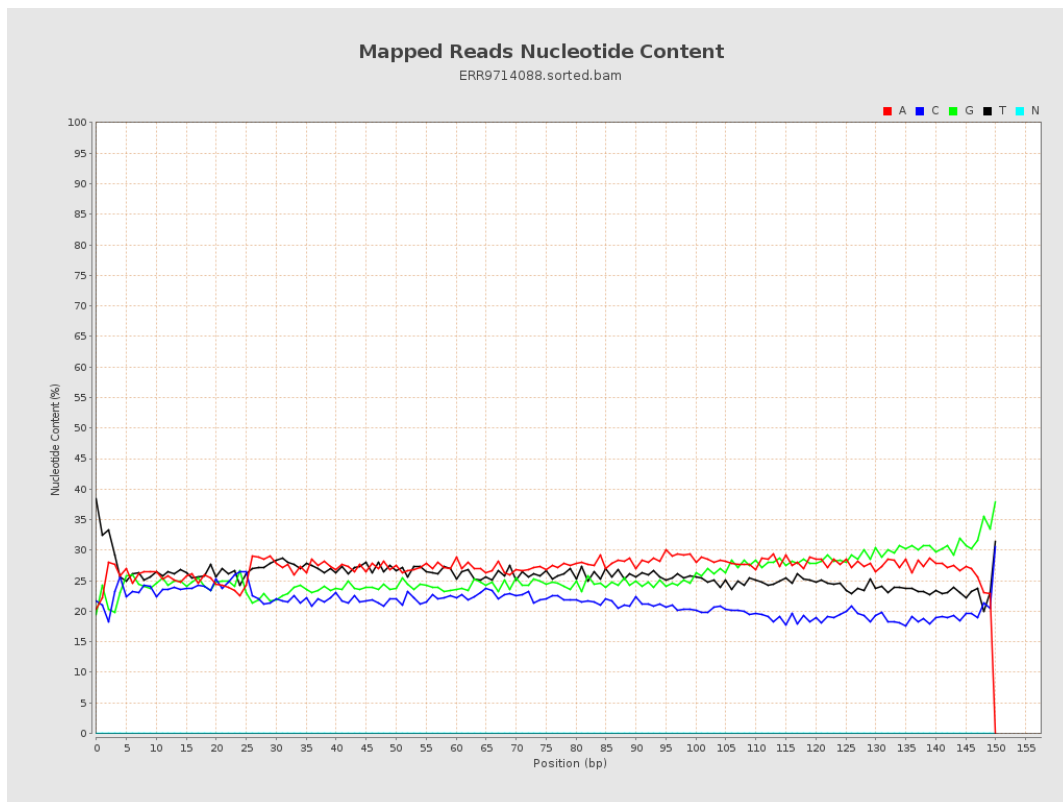
6. Results : Genome Fraction Coverage



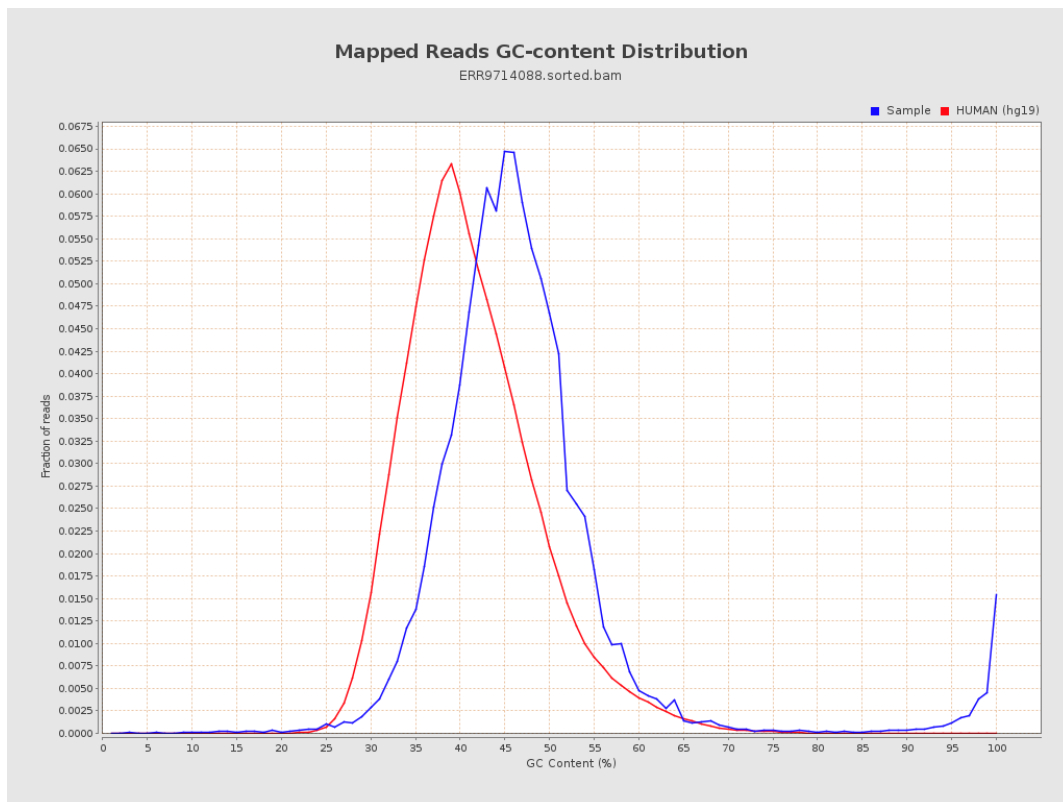
7. Results : Duplication Rate Histogram



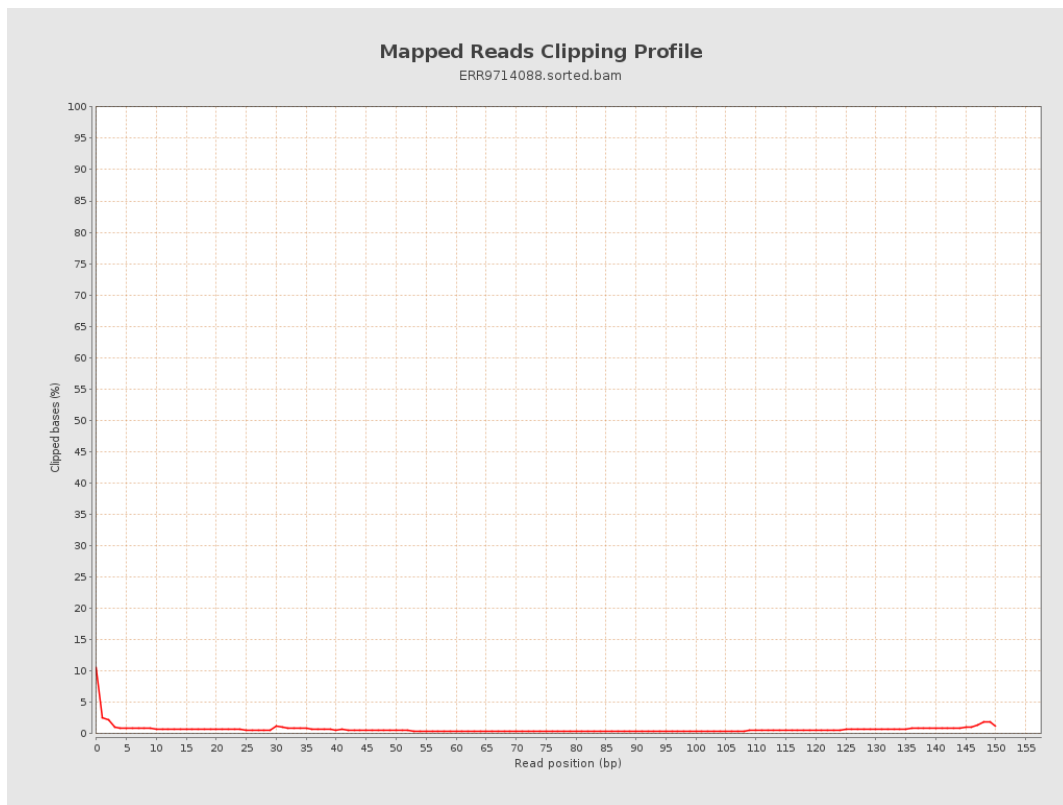
8. Results : Mapped Reads Nucleotide Content



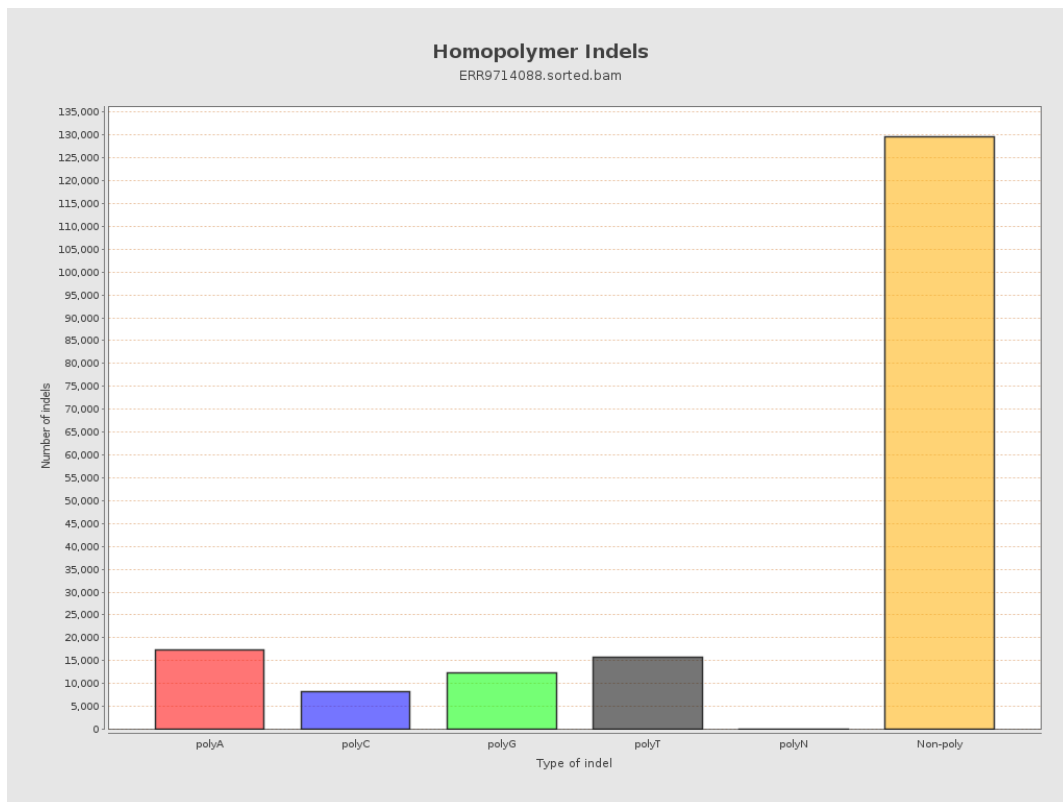
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

