

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:57:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714267.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_ERR9714267 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:57:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	441,346
Mapped reads	69,058 / 15.65%
Unmapped reads	372,288 / 84.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,144 / 0.26%
Read min/max/mean length	30 / 151 / 62.04
Duplicated reads (estimated)	67,636 / 15.32%
Duplication rate	32.23%
Clipped reads	36,299 / 8.22%

2.2. ACGT Content

Number/percentage of A's	189,757 / 2.66%
Number/percentage of C's	84,592 / 1.19%
Number/percentage of T's	103,859 / 1.46%
Number/percentage of G's	6,755,080 / 94.7%
Number/percentage of N's	153 / 0%
GC Percentage	95.88%

2.3. Coverage

Mean	0.0023

Standard Deviation	8.627
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2.4. Mapping Quality

Mean Mapping Quality	10.22
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2.5. Mismatches and indels

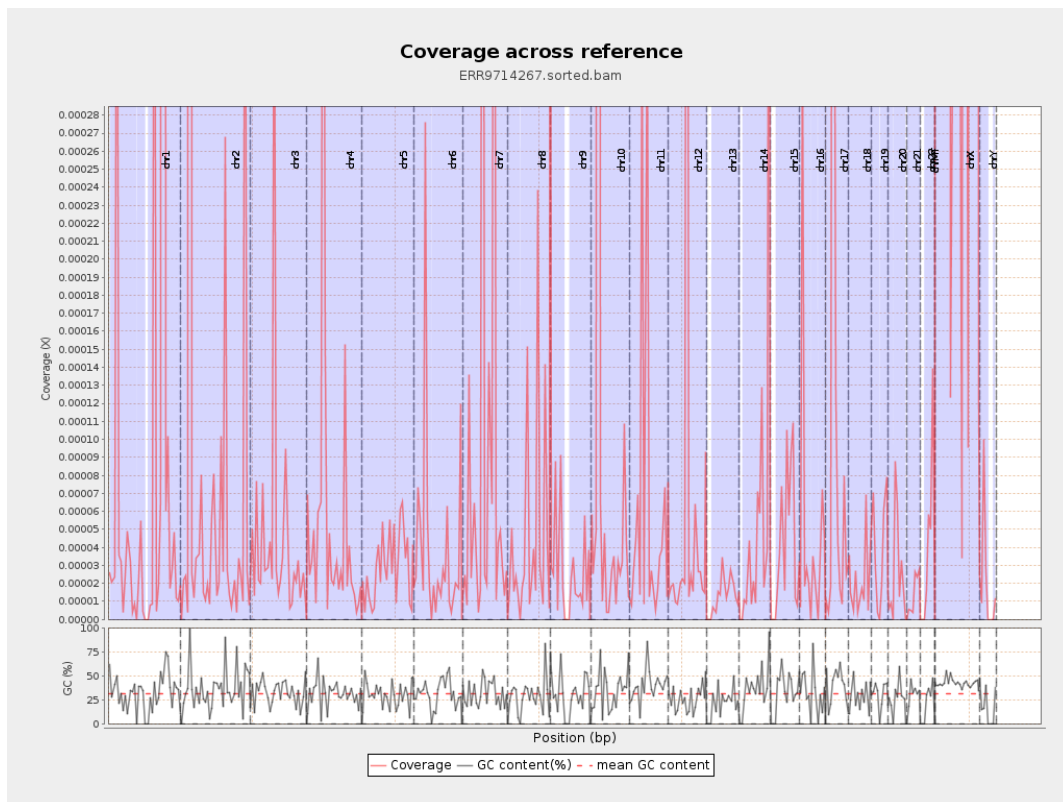
General error rate	3.28%
Mismatches	180,391
Insertions	7,624
Mapped reads with at least one insertion	7.84%
Deletions	3,689
Mapped reads with at least one deletion	5.17%
Homopolymer indels	62.58%

2.6. Chromosome stats

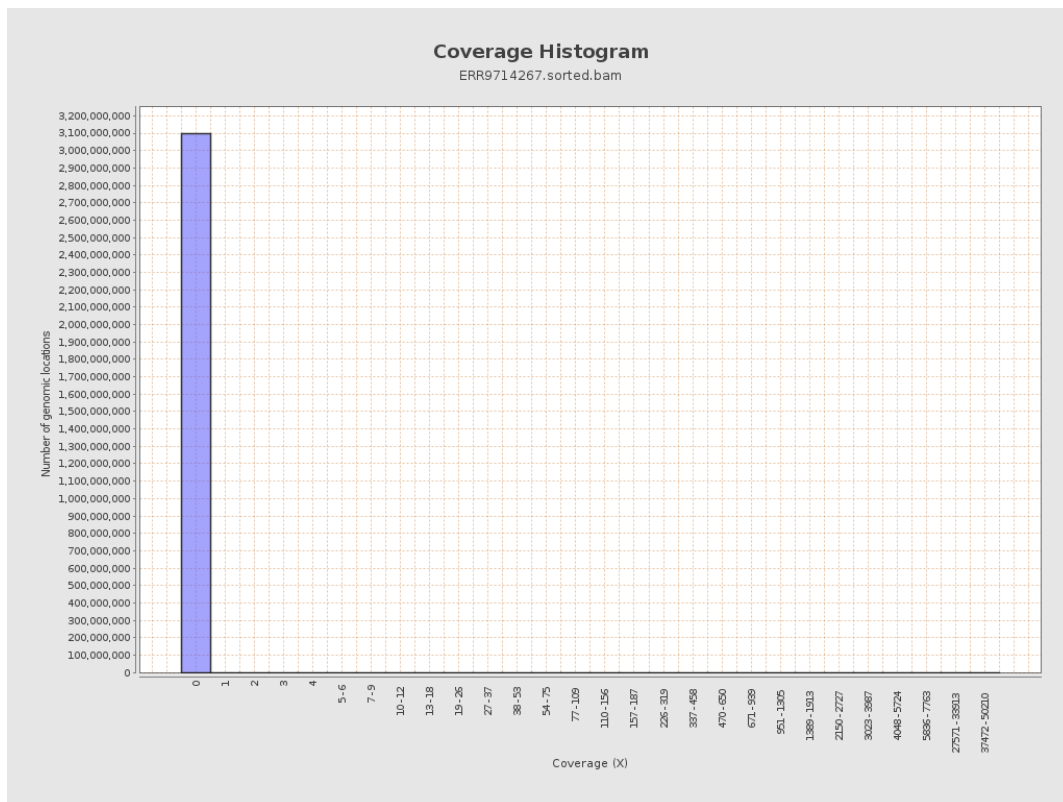
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	52574	0.0002	0.4544
chr2	243199373	6750455	0.0278	30.772
chr3	198022430	9129	0	0.0236
chr4	191154276	11633	0.0001	0.0288
chr5	180915260	5264	0	0.0074
chr6	171115067	6837	0	0.0186
chr7	159138663	17569	0.0001	0.0826

chr8	146364022	6702	0	0.0183
chr9	141213431	4180	0	0.0108
chr10	135534747	40944	0.0003	0.5689
chr11	135006516	8480	0.0001	0.0363
chr12	133851895	8938	0.0001	0.0546
chr13	115169878	1527	0	0.0036
chr14	107349540	7660	0.0001	0.0732
chr15	102531392	4188	0	0.0155
chr16	90354753	4696	0.0001	0.0211
chr17	81195210	8274	0.0001	0.0982
chr18	78077248	1592	0	0.0074
chr19	59128983	2201	0	0.0123
chr20	63025520	1700	0	0.0159
chr21	48129895	639	0	0.0038
chr22	51304566	2041	0	0.0117
chrMT	16571	2027	0.1223	1.2144
chrX	155270560	190950	0.0012	0.2226
chrY	59373566	1275	0	0.0089

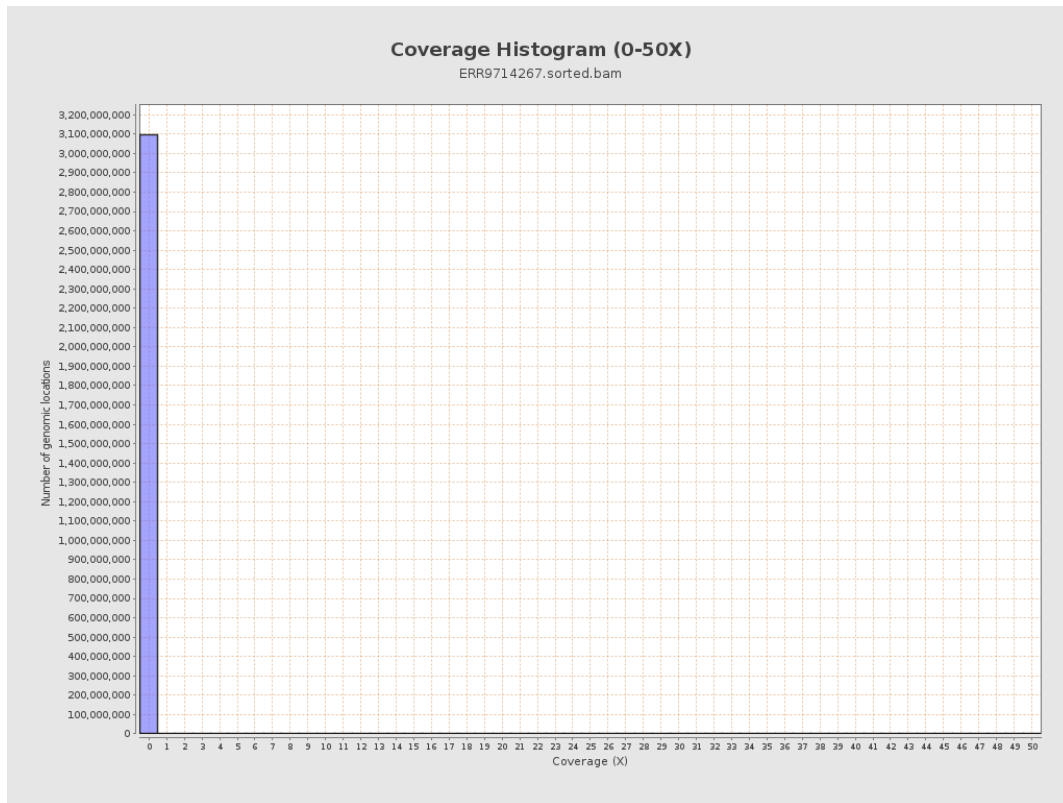
3. Results : Coverage across reference



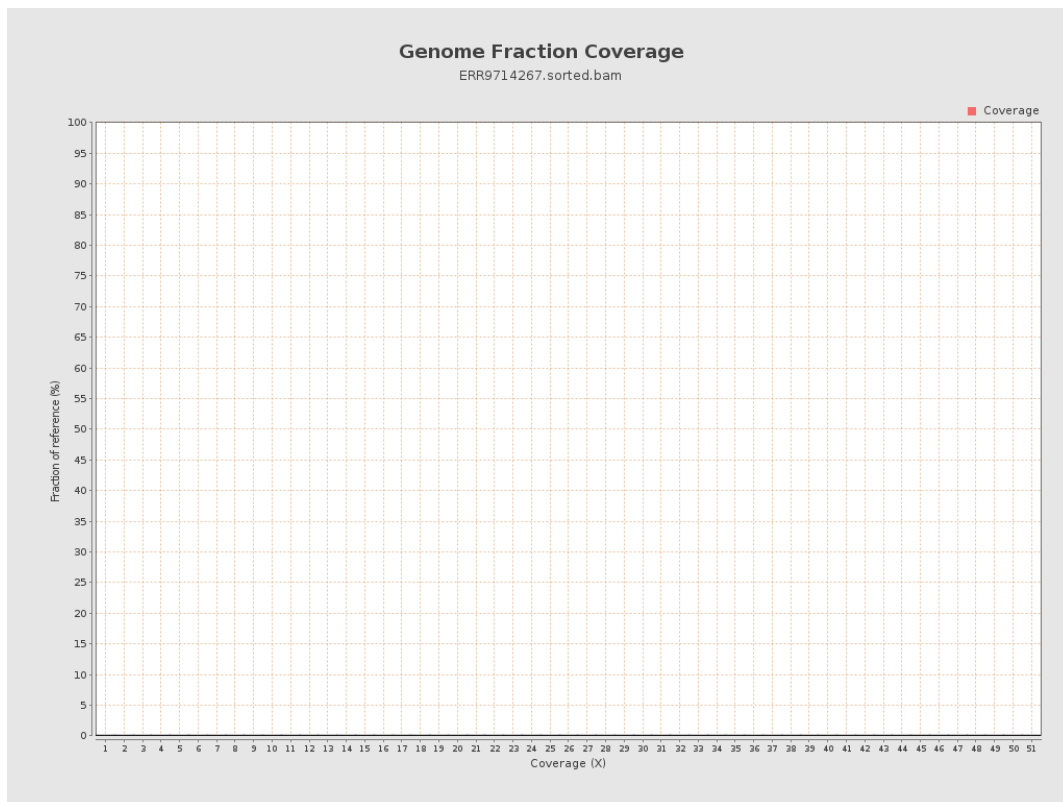
4. Results : Coverage Histogram



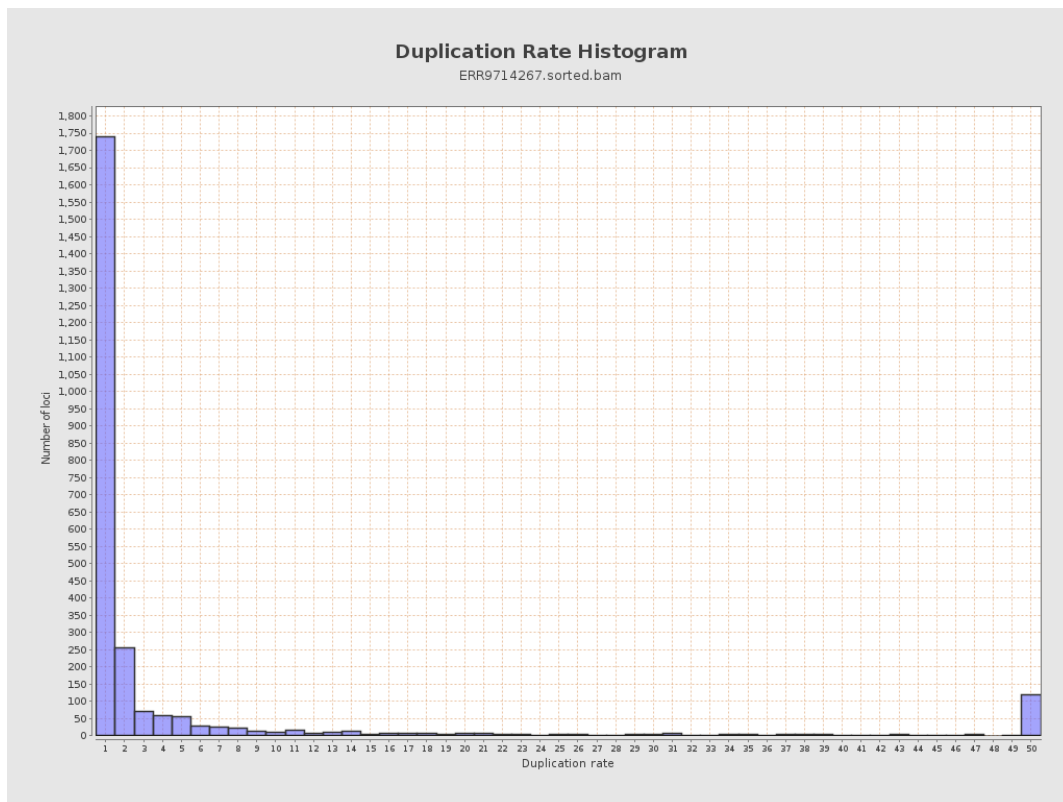
5. Results : Coverage Histogram (0-50X)



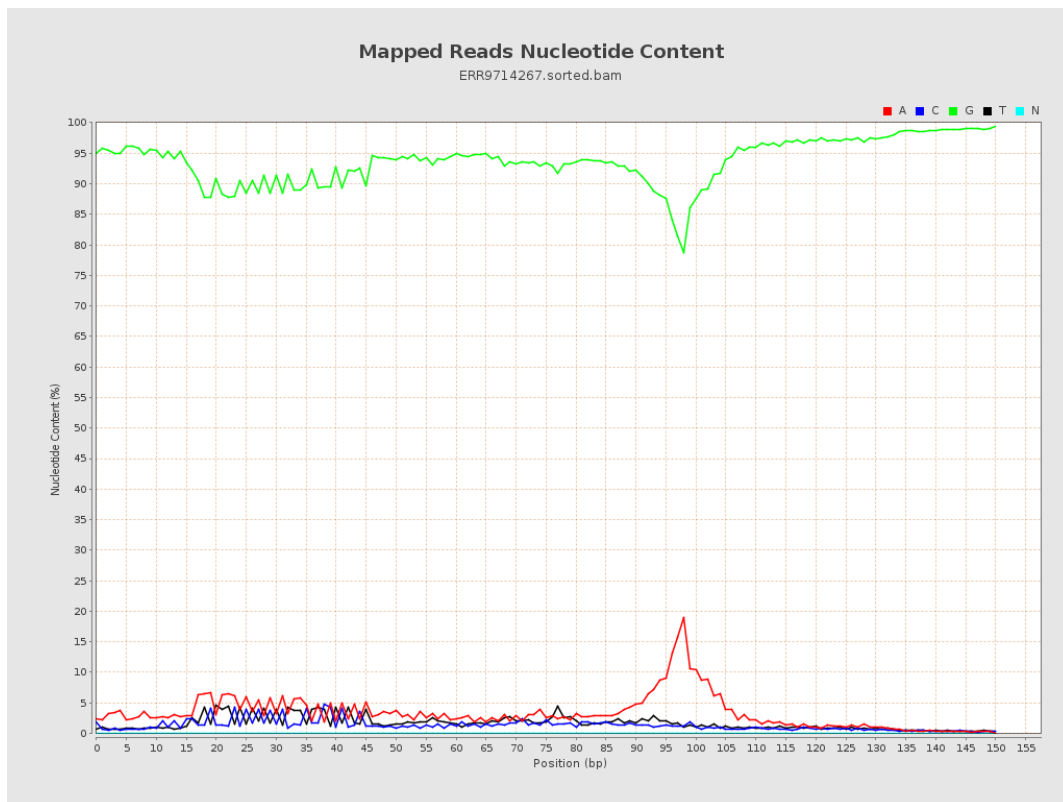
6. Results : Genome Fraction Coverage



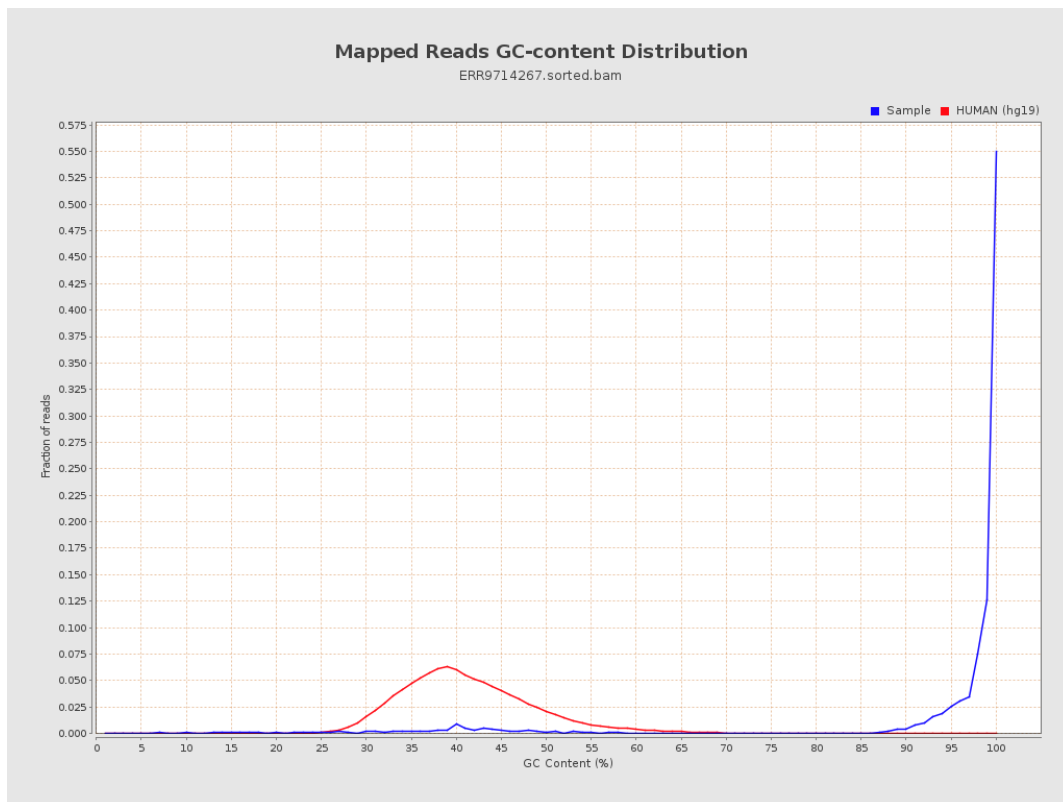
7. Results : Duplication Rate Histogram



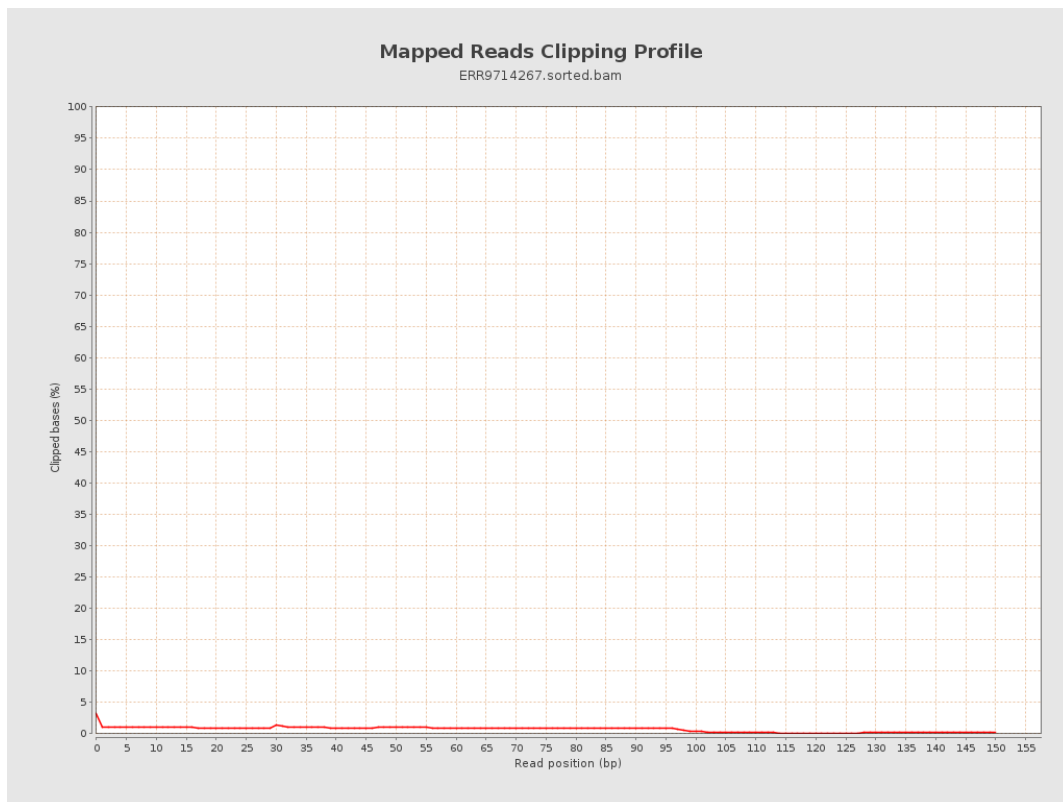
8. Results : Mapped Reads Nucleotide Content



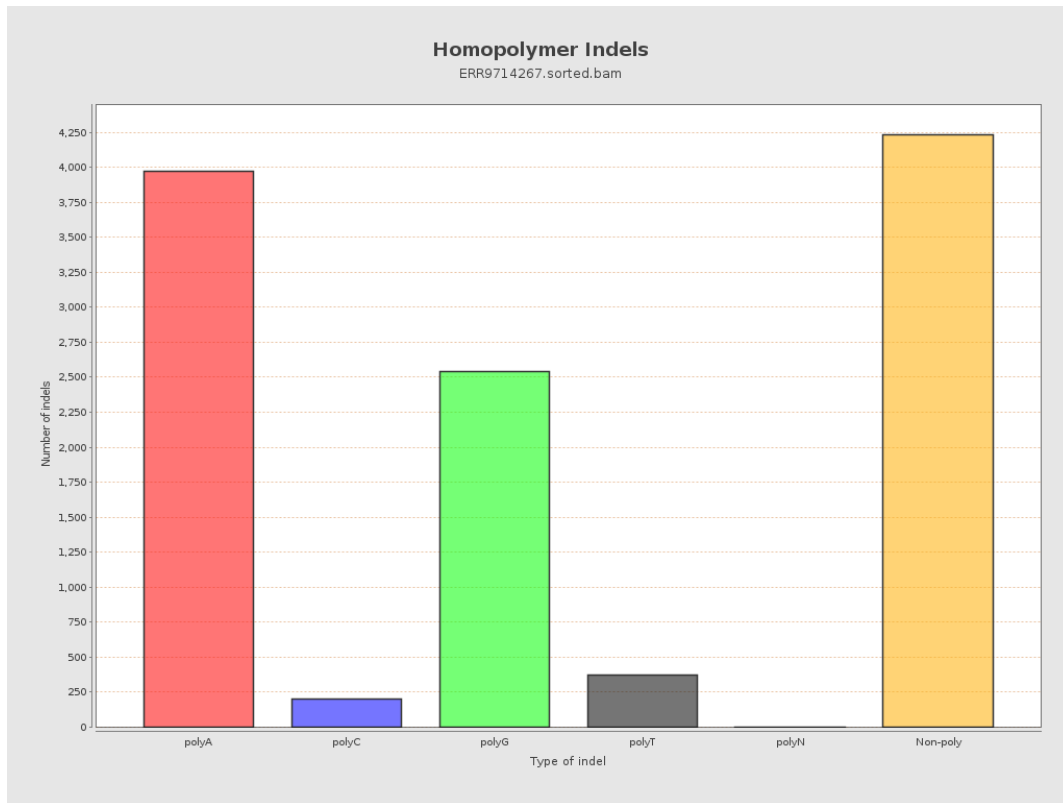
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

