

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:47:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714189.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_ERR9714189 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:47:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,884
Mapped reads	15,665 / 27.06%
Unmapped reads	42,219 / 72.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	530 / 0.92%
Read min/max/mean length	30 / 151 / 80.3
Duplicated reads (estimated)	13,074 / 22.59%
Duplication rate	49.86%
Clipped reads	12,639 / 21.84%

2.2. ACGT Content

Number/percentage of A's	371,466 / 21%
Number/percentage of C's	324,169 / 18.33%
Number/percentage of T's	345,416 / 19.53%
Number/percentage of G's	727,873 / 41.15%
Number/percentage of N's	21 / 0%
GC Percentage	59.47%

2.3. Coverage

Mean	0.0006

Standard Deviation	0.5315
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2.4. Mapping Quality

Mean Mapping Quality	27.11
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2.5. Mismatches and indels

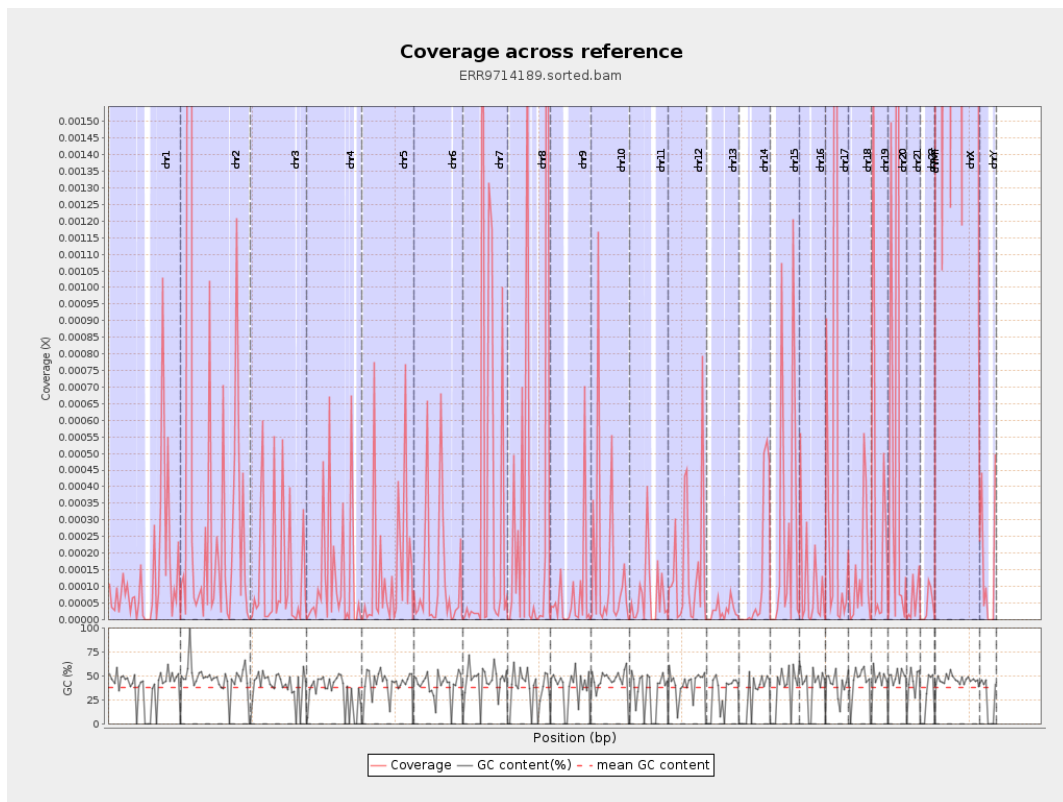
General error rate	3.92%
Mismatches	64,259
Insertions	1,122
Mapped reads with at least one insertion	5.72%
Deletions	4,588
Mapped reads with at least one deletion	27.88%
Homopolymer indels	32.22%

2.6. Chromosome stats

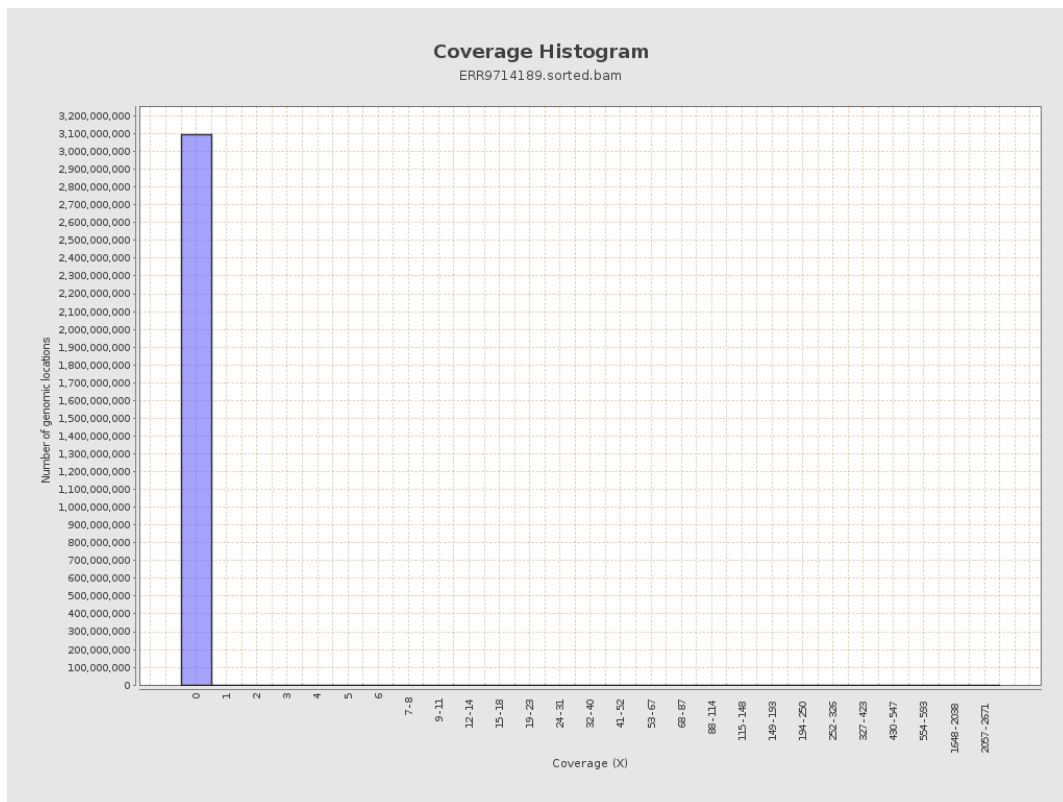
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31570	0.0001	0.0972
chr2	243199373	476121	0.002	1.7732
chr3	198022430	25724	0.0001	0.0462
chr4	191154276	23571	0.0001	0.0503
chr5	180915260	26740	0.0001	0.0558
chr6	171115067	21284	0.0001	0.0448
chr7	159138663	50751	0.0003	0.1593

chr8	146364022	54954	0.0004	0.2018
chr9	141213431	10198	0.0001	0.04
chr10	135534747	20978	0.0002	0.1417
chr11	135006516	9374	0.0001	0.0208
chr12	133851895	21594	0.0002	0.0461
chr13	115169878	2651	0	0.0076
chr14	107349540	13067	0.0001	0.0438
chr15	102531392	26583	0.0003	0.0856
chr16	90354753	8686	0.0001	0.0315
chr17	81195210	42366	0.0005	0.1347
chr18	78077248	11397	0.0001	0.0487
chr19	59128983	20566	0.0003	0.1562
chr20	63025520	46559	0.0007	0.2648
chr21	48129895	2740	0.0001	0.0164
chr22	51304566	2196	0	0.0121
chrMT	16571	0	0	0
chrX	155270560	845855	0.0054	0.7344
chrY	59373566	9526	0.0002	0.0312

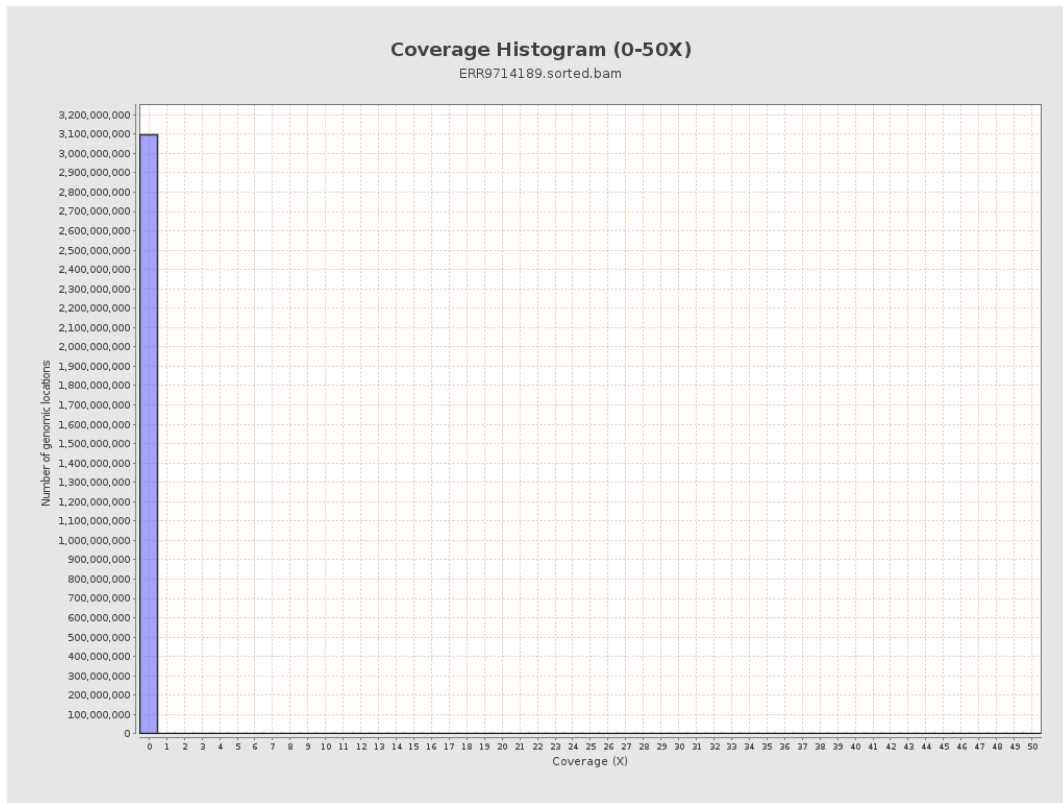
3. Results : Coverage across reference



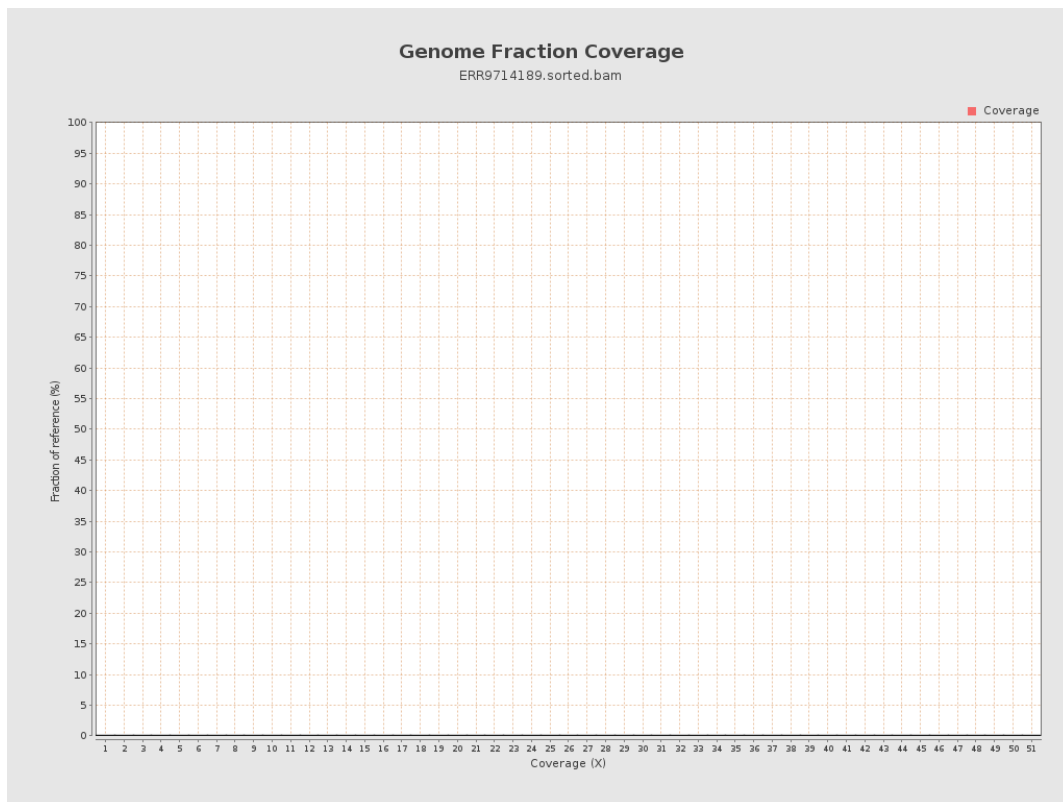
4. Results : Coverage Histogram



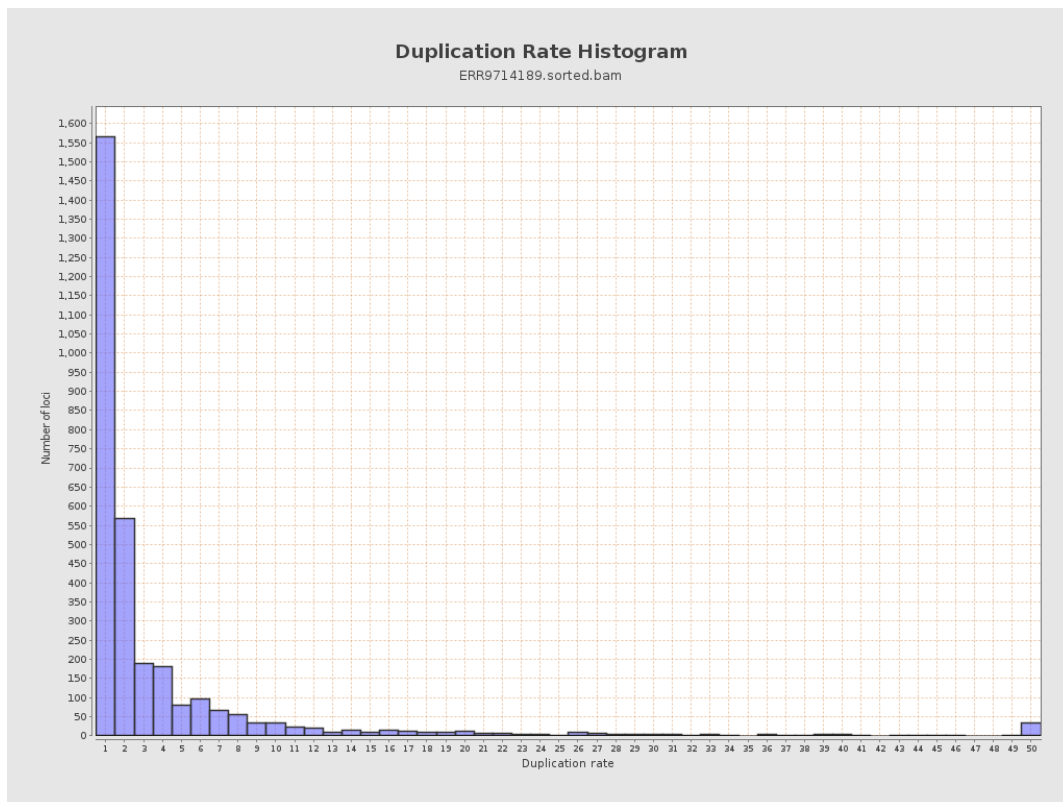
5. Results : Coverage Histogram (0-50X)



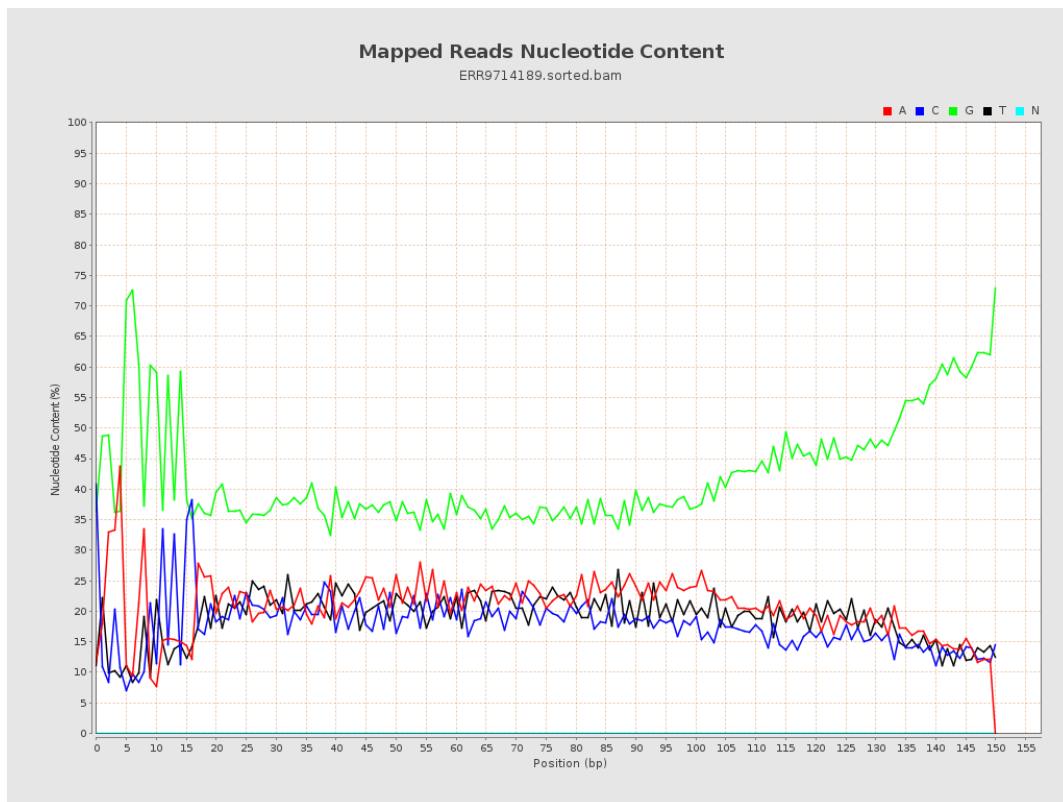
6. Results : Genome Fraction Coverage



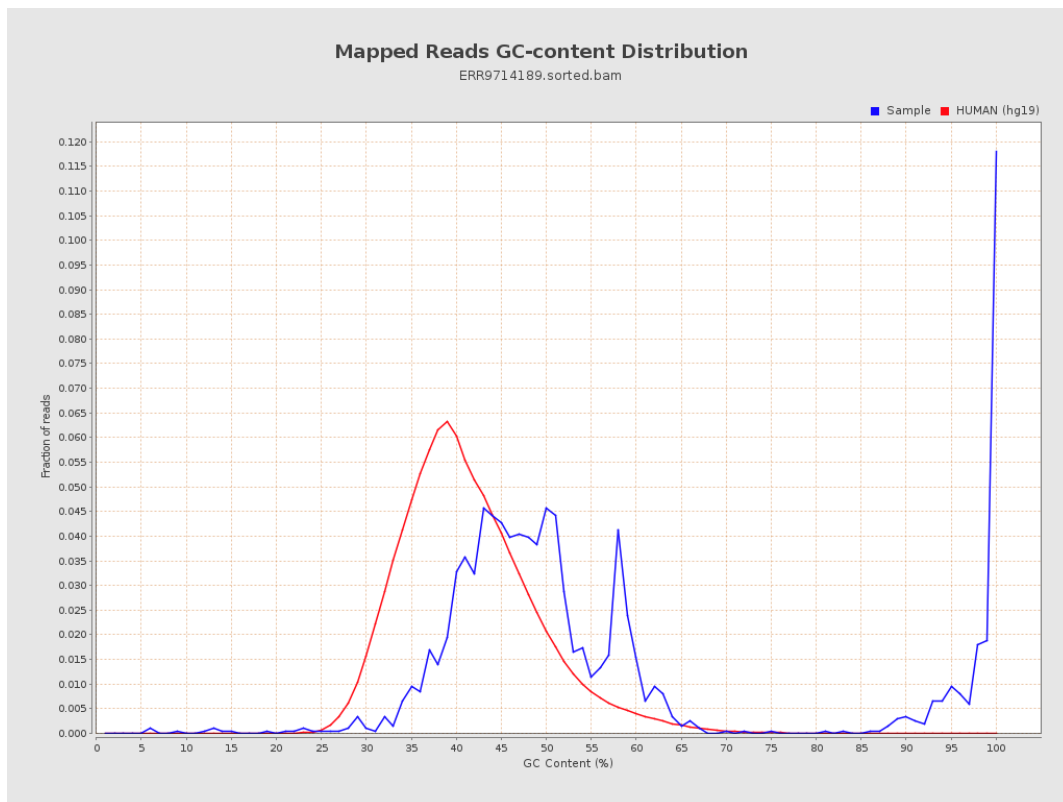
7. Results : Duplication Rate Histogram



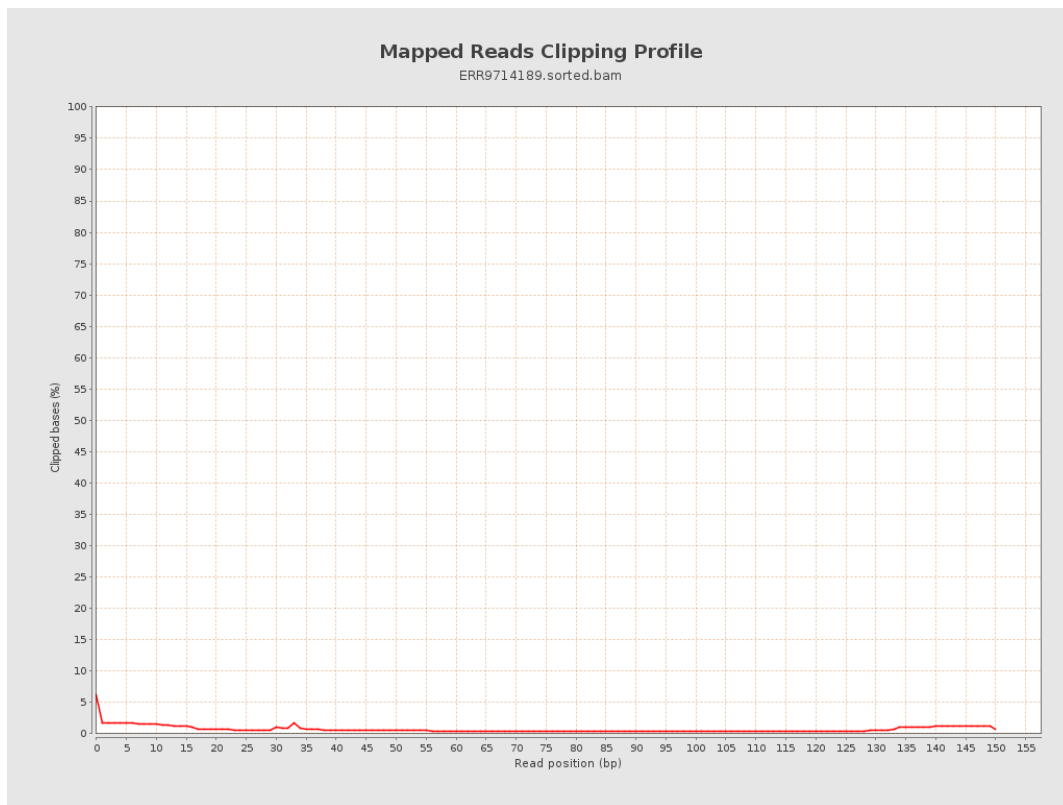
8. Results : Mapped Reads Nucleotide Content



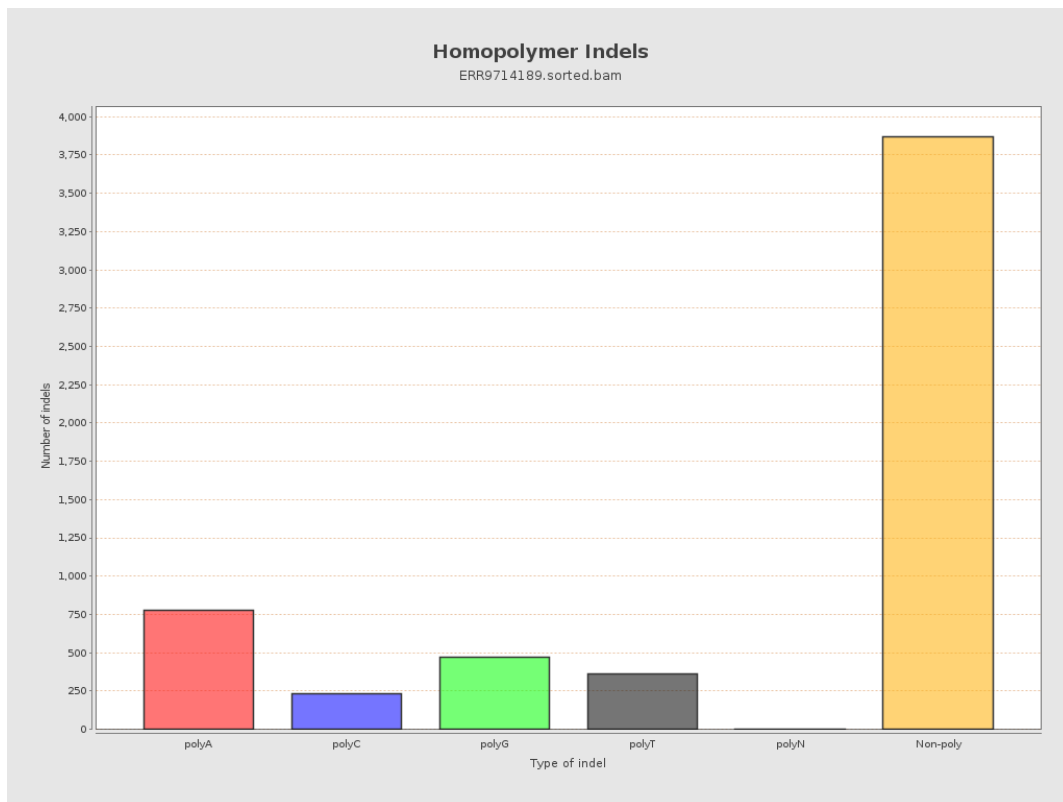
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

