

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:19:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714248.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_ERR9714248 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:19:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	357,840
Mapped reads	56,261 / 15.72%
Unmapped reads	301,579 / 84.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,882 / 0.53%
Read min/max/mean length	30 / 151 / 61.15
Duplicated reads (estimated)	55,528 / 15.52%
Duplication rate	32.01%
Clipped reads	32,409 / 9.06%

2.2. ACGT Content

Number/percentage of A's	163,780 / 2.92%
Number/percentage of C's	60,991 / 1.09%
Number/percentage of T's	82,140 / 1.47%
Number/percentage of G's	5,297,050 / 94.52%
Number/percentage of N's	157 / 0%
GC Percentage	95.61%

2.3. Coverage

Mean	0.0018

Standard Deviation	6.7848
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2.4. Mapping Quality

Mean Mapping Quality	11.73
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2.5. Mismatches and indels

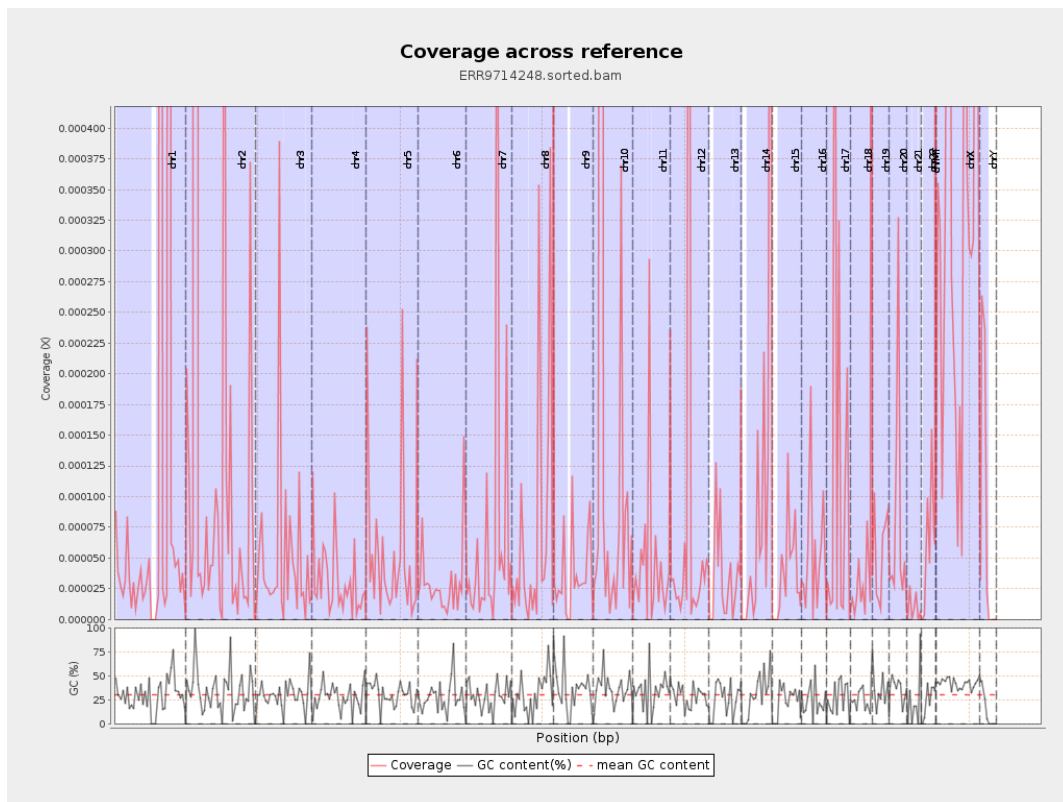
General error rate	3.19%
Mismatches	133,183
Insertions	6,399
Mapped reads with at least one insertion	7.28%
Deletions	2,573
Mapped reads with at least one deletion	4.34%
Homopolymer indels	66.04%

2.6. Chromosome stats

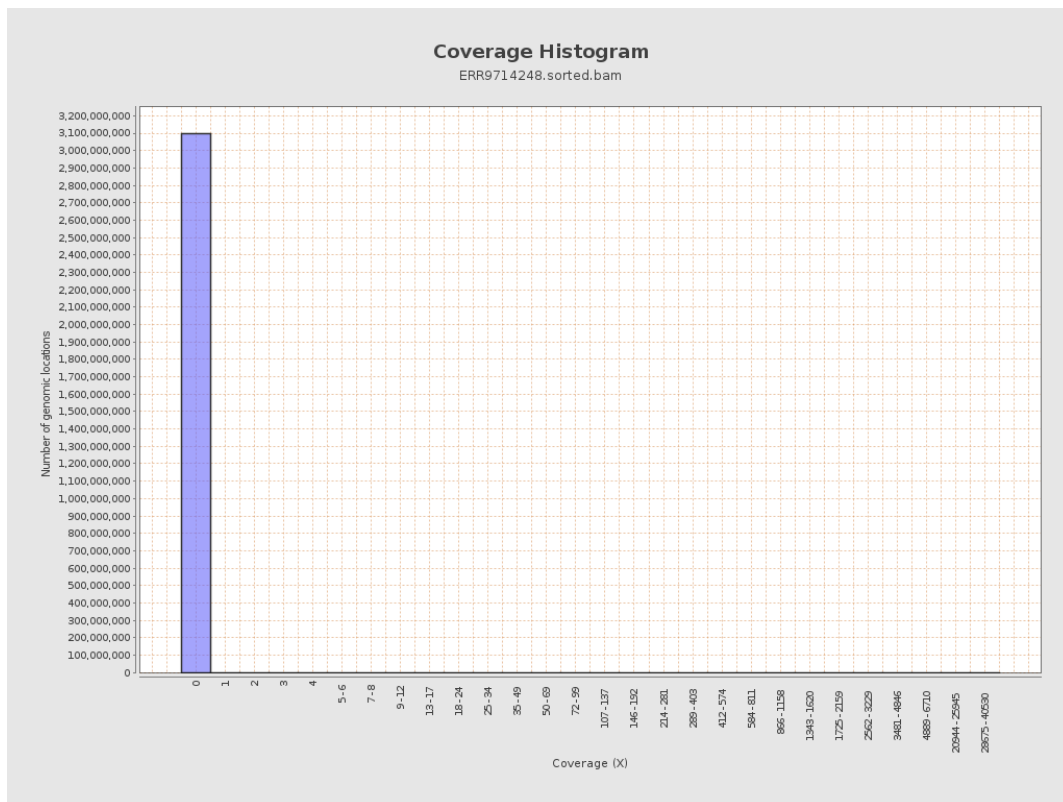
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	53513	0.0002	0.3372
chr2	243199373	5303717	0.0218	24.2024
chr3	198022430	10002	0.0001	0.0174
chr4	191154276	6099	0	0.0108
chr5	180915260	9519	0.0001	0.0162
chr6	171115067	5298	0	0.0118
chr7	159138663	12180	0.0001	0.0737

chr8	146364022	10195	0.0001	0.0245
chr9	141213431	5679	0	0.0143
chr10	135534747	29963	0.0002	0.3377
chr11	135006516	6202	0	0.0271
chr12	133851895	10968	0.0001	0.0686
chr13	115169878	4135	0	0.0125
chr14	107349540	12337	0.0001	0.0749
chr15	102531392	3881	0	0.0156
chr16	90354753	4754	0.0001	0.012
chr17	81195210	11653	0.0001	0.108
chr18	78077248	7539	0.0001	0.1116
chr19	59128983	3159	0.0001	0.0156
chr20	63025520	5170	0.0001	0.0285
chr21	48129895	483	0	0.0037
chr22	51304566	3043	0.0001	0.0136
chrMT	16571	35271	2.1285	9.0191
chrX	155270560	55514	0.0004	0.0567
chrY	59373566	4207	0.0001	0.0201

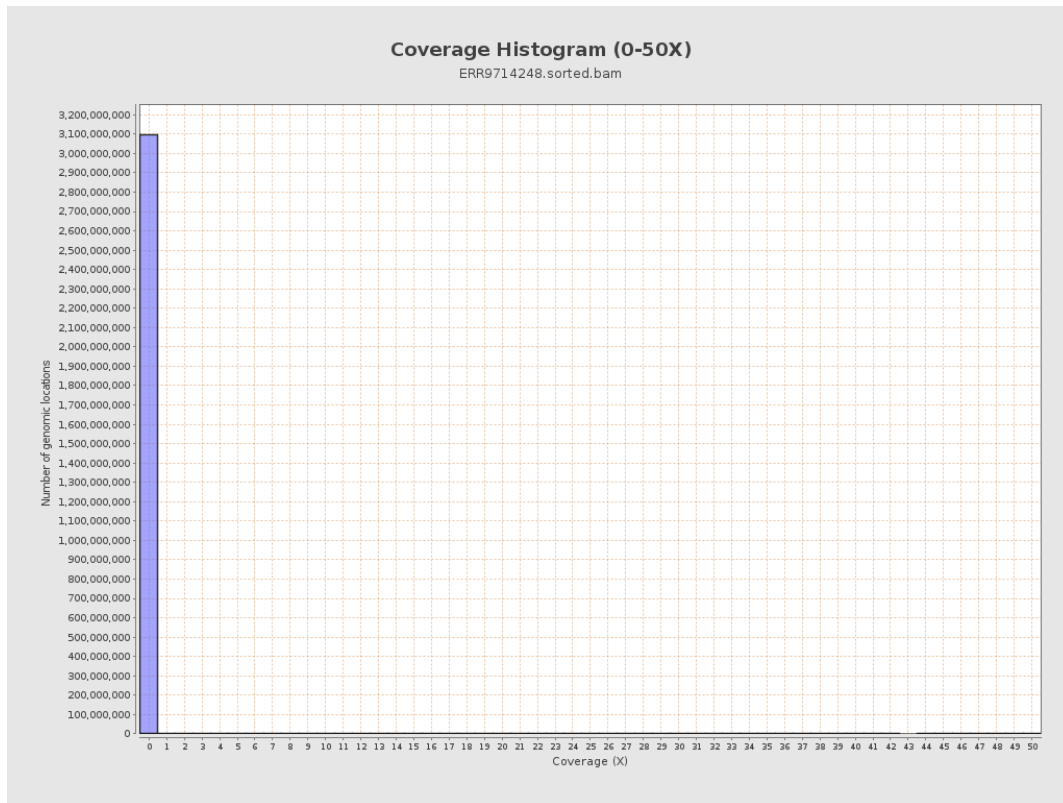
3. Results : Coverage across reference



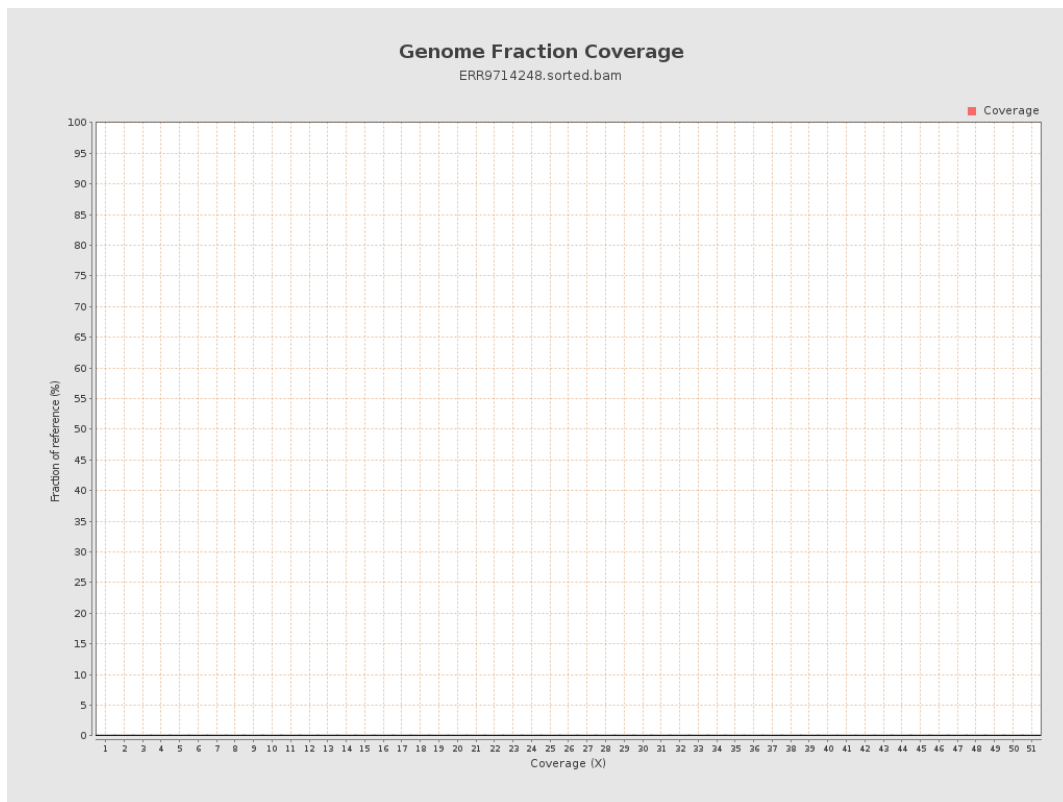
4. Results : Coverage Histogram



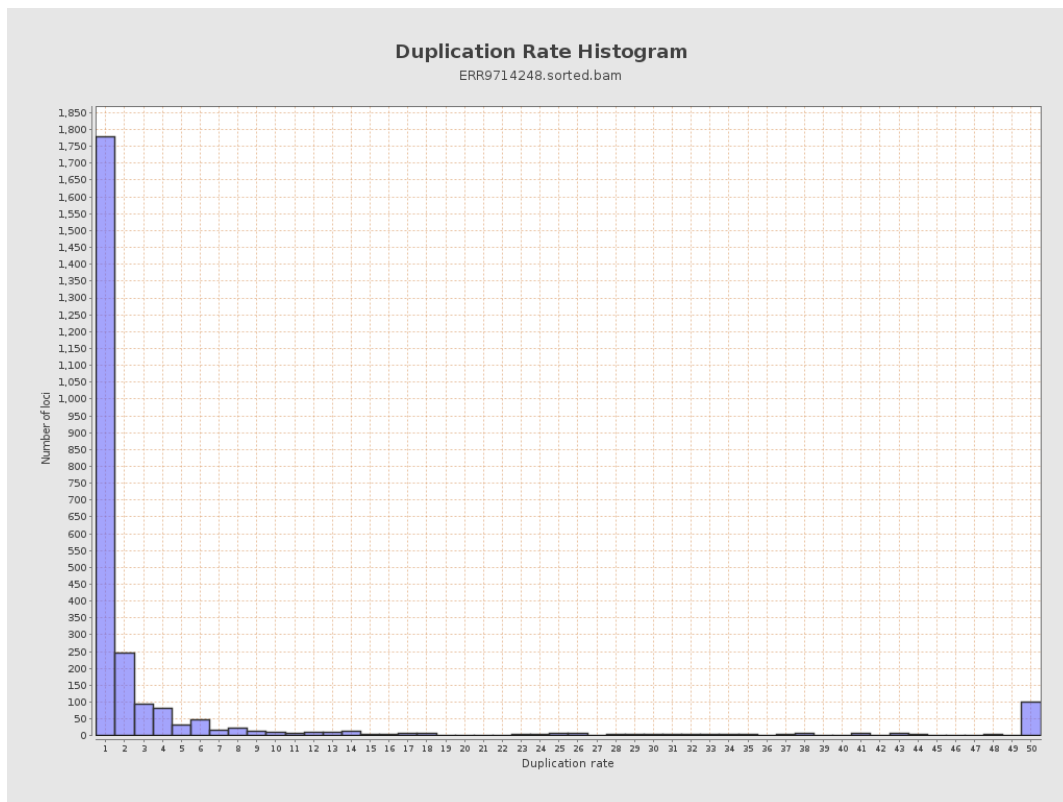
5. Results : Coverage Histogram (0-50X)



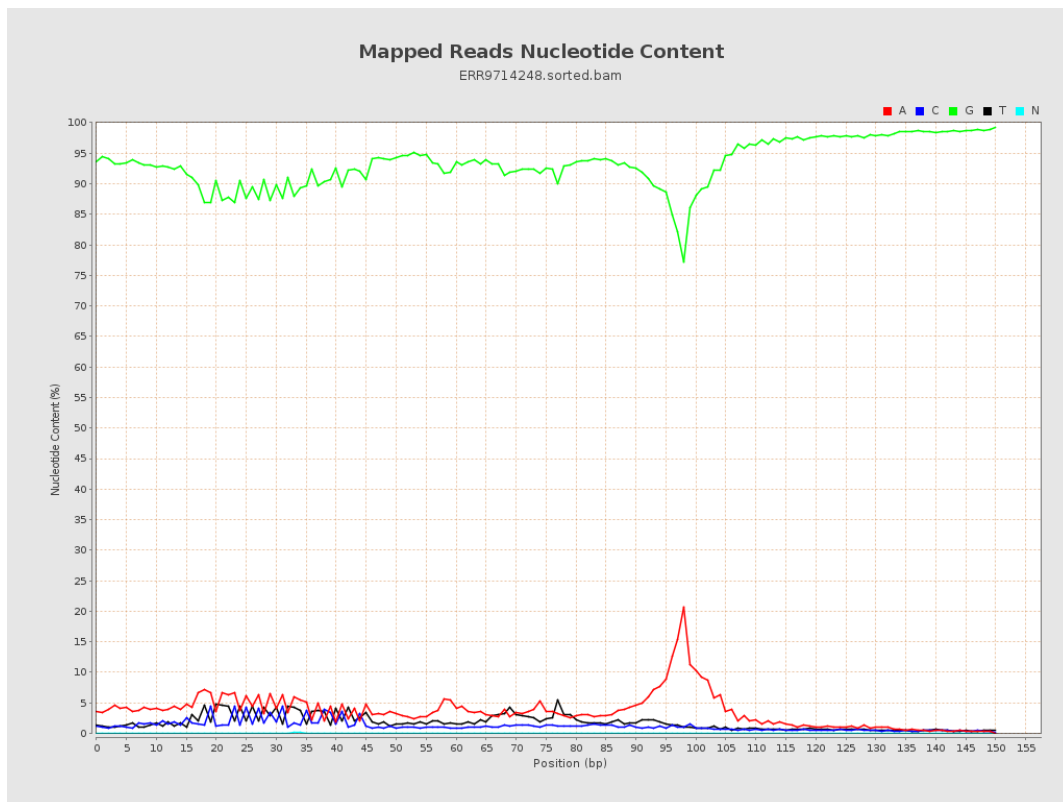
6. Results : Genome Fraction Coverage



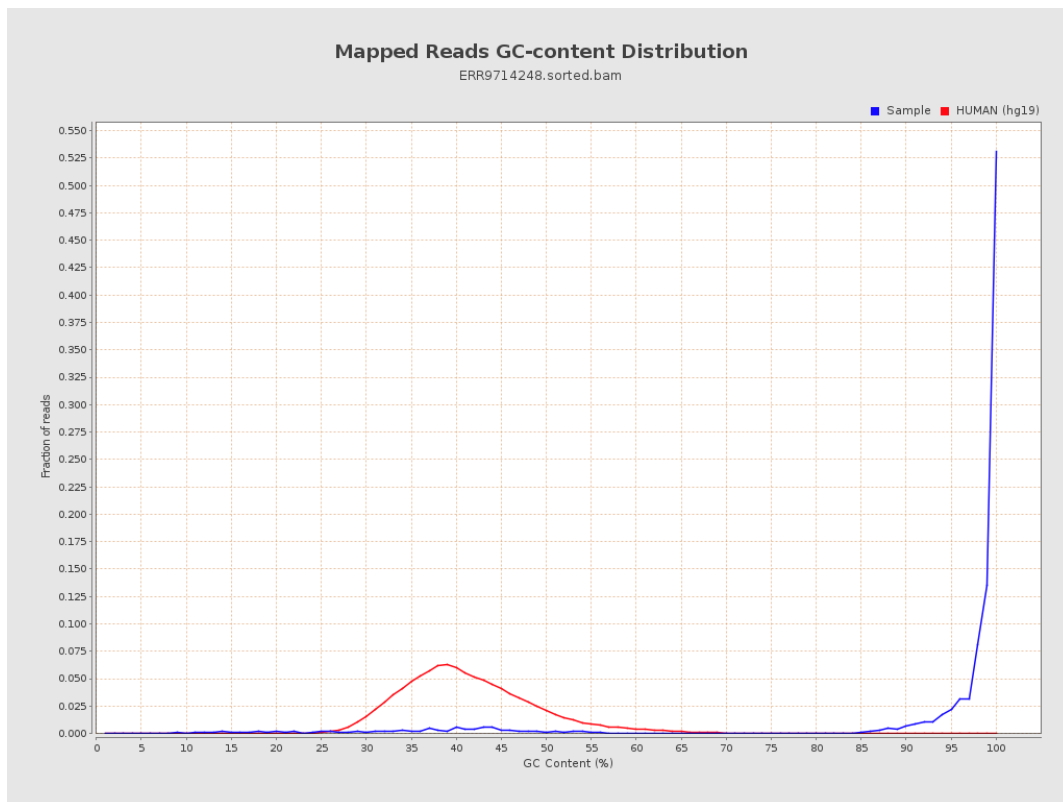
7. Results : Duplication Rate Histogram



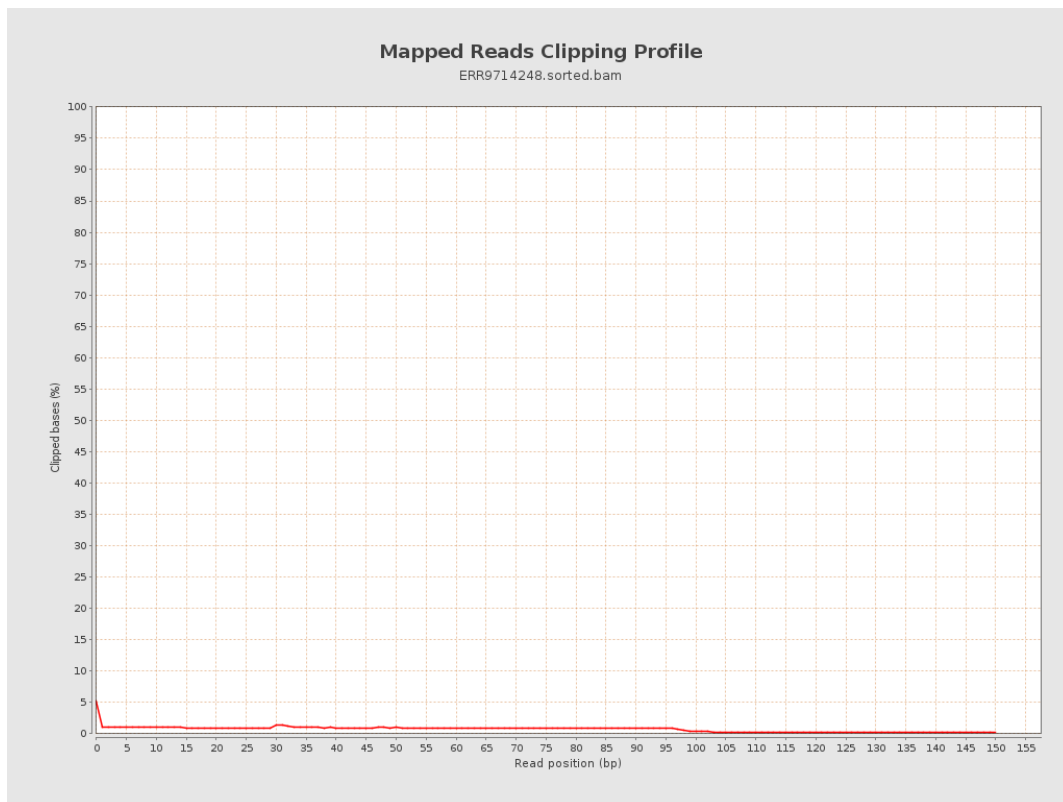
8. Results : Mapped Reads Nucleotide Content



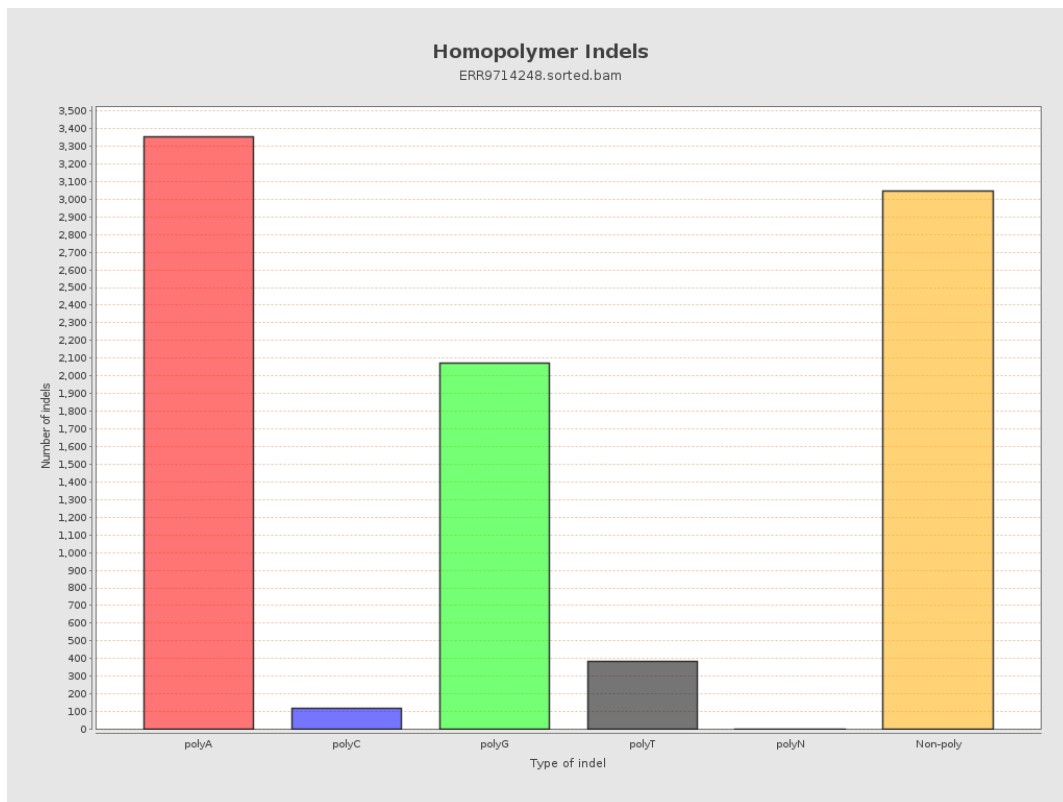
9. Results : Mapped Reads GC-content Distribution



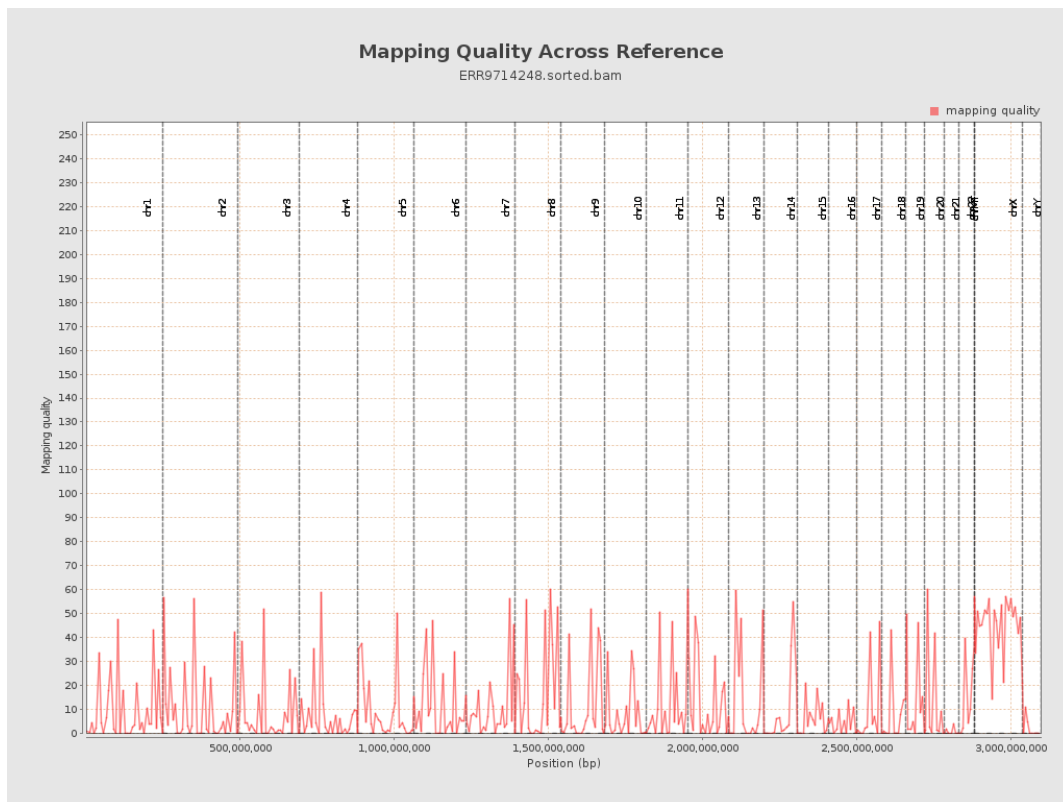
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

