

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:42:59

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam ERR2094114.sorted.bam -c -nw 400 -hm 3
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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_ERR2094114 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094114_1.fastq.gz ERR2094114_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:42:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	389,032
Mapped reads	371,947 / 95.61%
Unmapped reads	17,085 / 4.39%
Mapped paired reads	371,947 / 95.61%
Mapped reads, first in pair	186,751 / 48%
Mapped reads, second in pair	185,196 / 47.6%
Mapped reads, both in pair	369,138 / 94.89%
Mapped reads, singletons	2,809 / 0.72%
Secondary alignments	0
Supplementary alignments	28,204 / 7.25%
Read min/max/mean length	30 / 151 / 135.71
Duplicated reads (estimated)	360,786 / 92.74%
Duplication rate	55.35%
Clipped reads	197,789 / 50.84%

2.2. ACGT Content

Number/percentage of A's	12,485,518 / 28.3%
Number/percentage of C's	9,566,433 / 21.68%
Number/percentage of T's	11,861,505 / 26.88%
Number/percentage of G's	10,206,638 / 23.13%
Number/percentage of N's	414 / 0%

GC Percentage	44.82%
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2.3. Coverage

Mean	0.0145
Standard Deviation	3.1801

2.4. Mapping Quality

Mean Mapping Quality	40.67
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2.5. Insert size

Mean	1,803,953.83
Standard Deviation	11,833,862.1
P25/Median/P75	109 / 137 / 166

2.6. Mismatches and indels

General error rate	3.62%
Mismatches	1,534,766
Insertions	30,233
Mapped reads with at least one insertion	8.01%
Deletions	122,630
Mapped reads with at least one deletion	32.01%
Homopolymer indels	27.78%

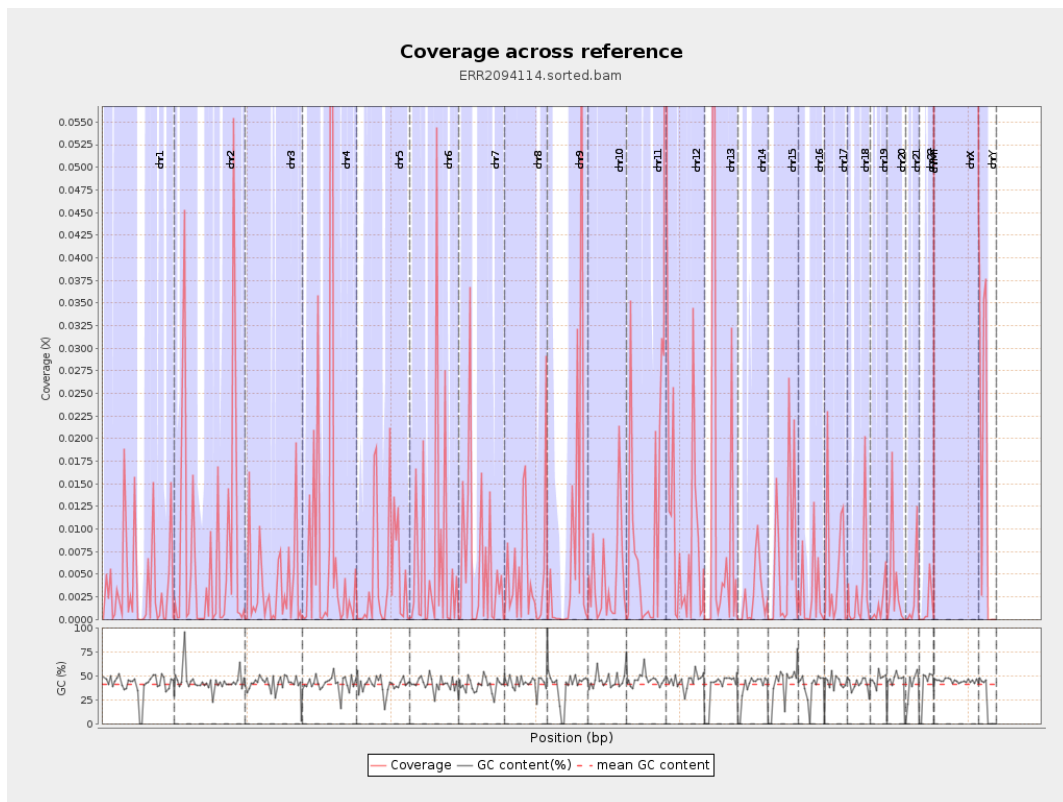
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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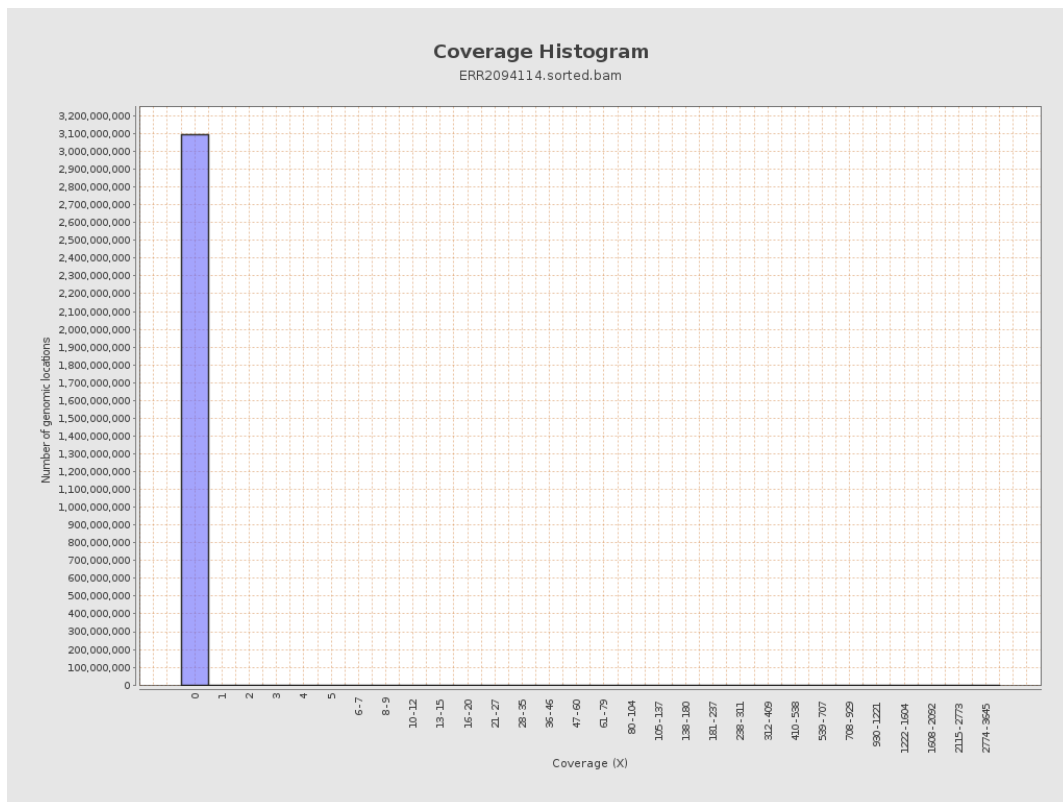
		bases	coverage	deviation
chr1	249250621	904591	0.0036	1.3626
chr2	243199373	1804239	0.0074	2.8373
chr3	198022430	718731	0.0036	1.1964
chr4	191154276	1953475	0.0102	2.8574
chr5	180915260	876271	0.0048	1.8057
chr6	171115067	1168221	0.0068	2.3568
chr7	159138663	960167	0.006	1.9041
chr8	146364022	788598	0.0054	1.607
chr9	141213431	1071936	0.0076	3.4267
chr10	135534747	569464	0.0042	1.2441
chr11	135006516	1447212	0.0107	2.9223
chr12	133851895	1333740	0.01	2.4823
chr13	115169878	1201048	0.0104	2.9254
chr14	107349540	264125	0.0025	0.9096
chr15	102531392	639305	0.0062	1.7863
chr16	90354753	265371	0.0029	0.9705
chr17	81195210	460823	0.0057	1.6189
chr18	78077248	260472	0.0033	1.2986
chr19	59128983	86968	0.0015	0.5763
chr20	63025520	236104	0.0037	1.4279
chr21	48129895	118926	0.0025	0.9448
chr22	51304566	62339	0.0012	0.406
chrMT	16571	13868	0.8369	5.293
chrX	155270560	27017385	0.174	10.8145

chrY	59373566	786354	0.0132	2.9223
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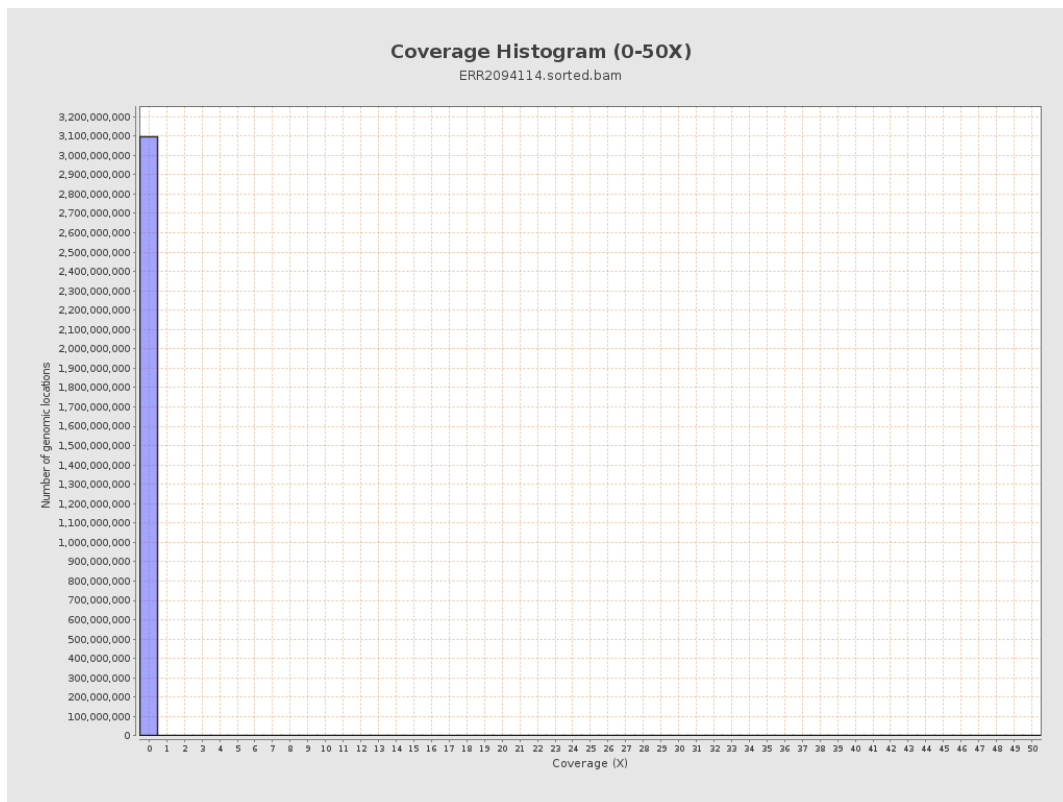
3. Results : Coverage across reference



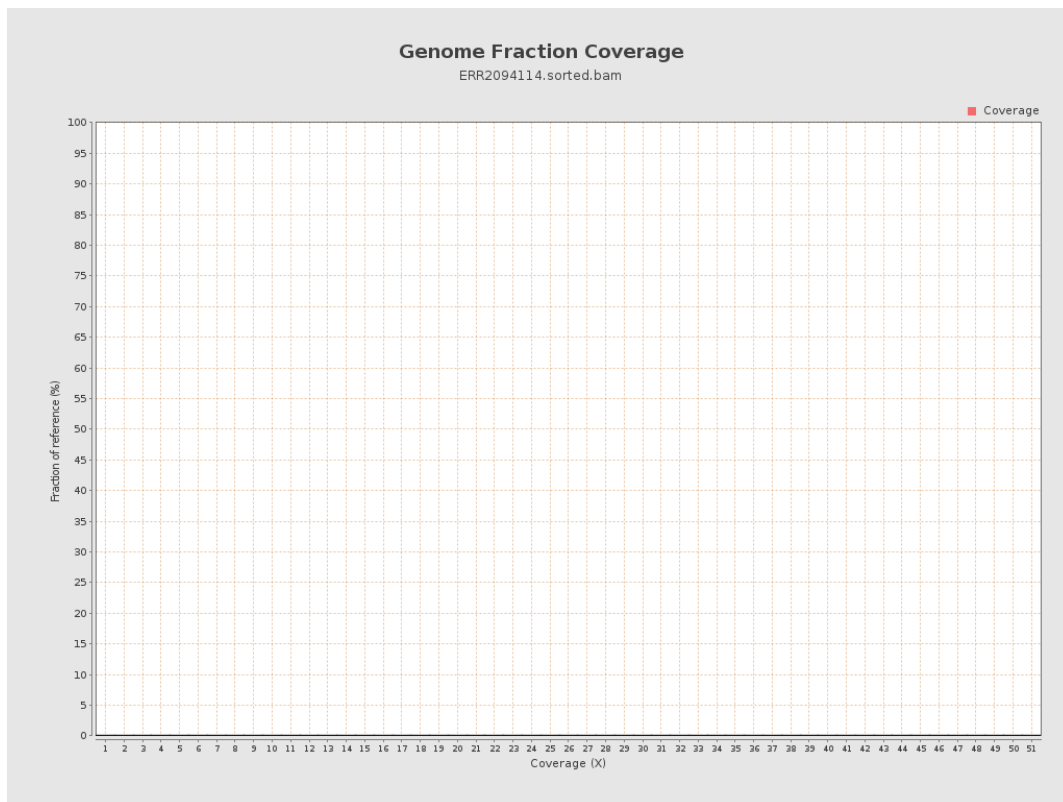
4. Results : Coverage Histogram



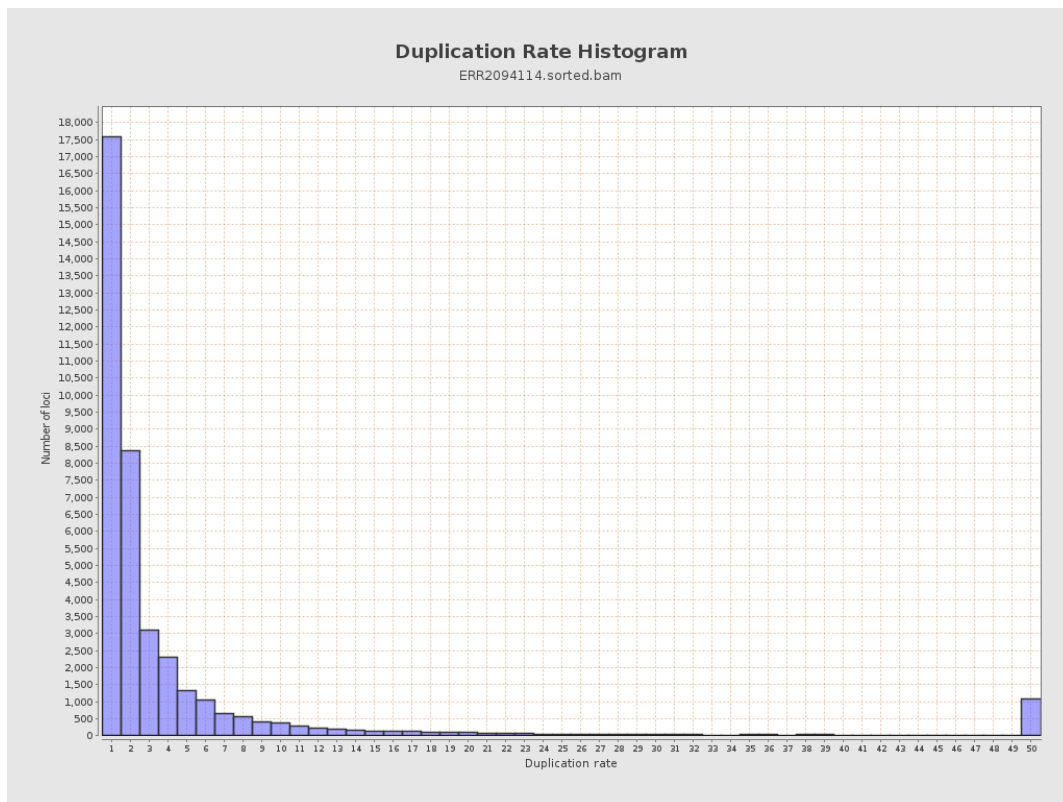
5. Results : Coverage Histogram (0-50X)



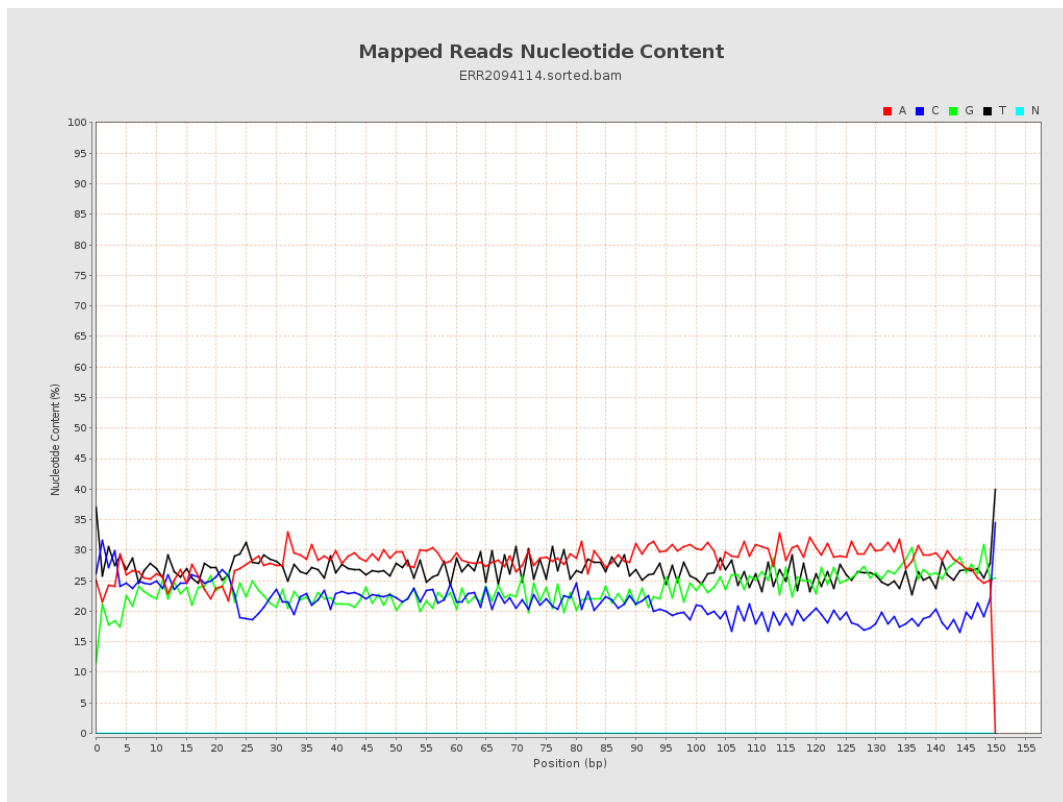
6. Results : Genome Fraction Coverage



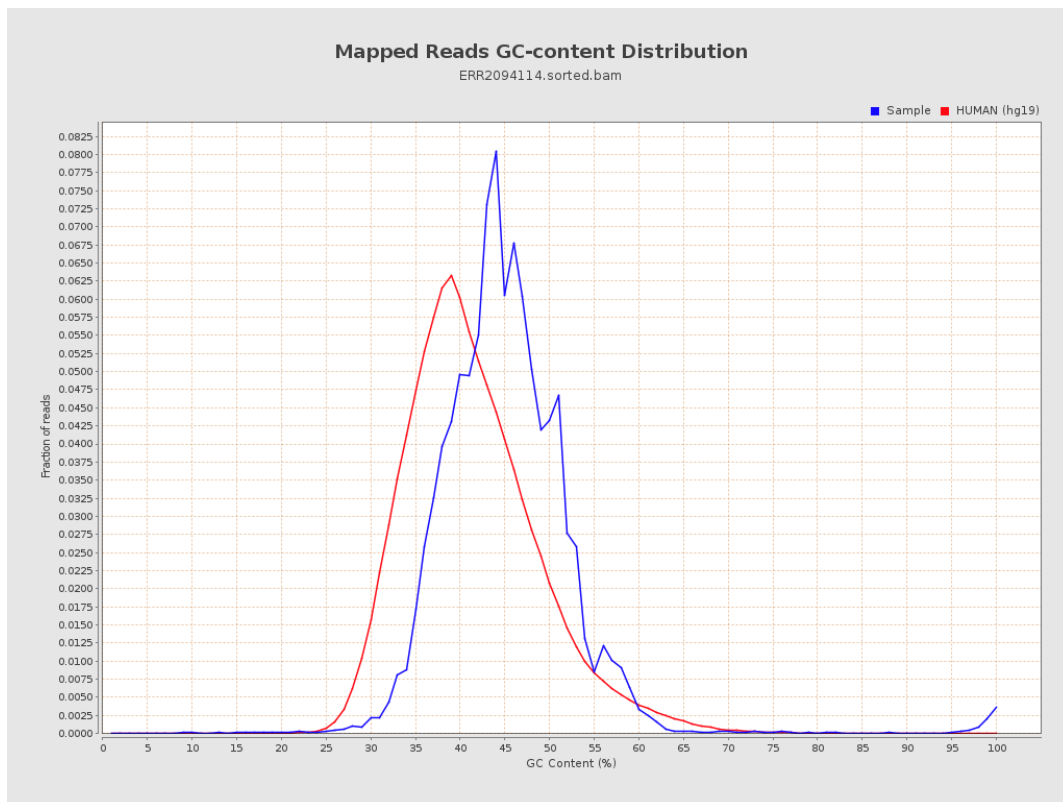
7. Results : Duplication Rate Histogram



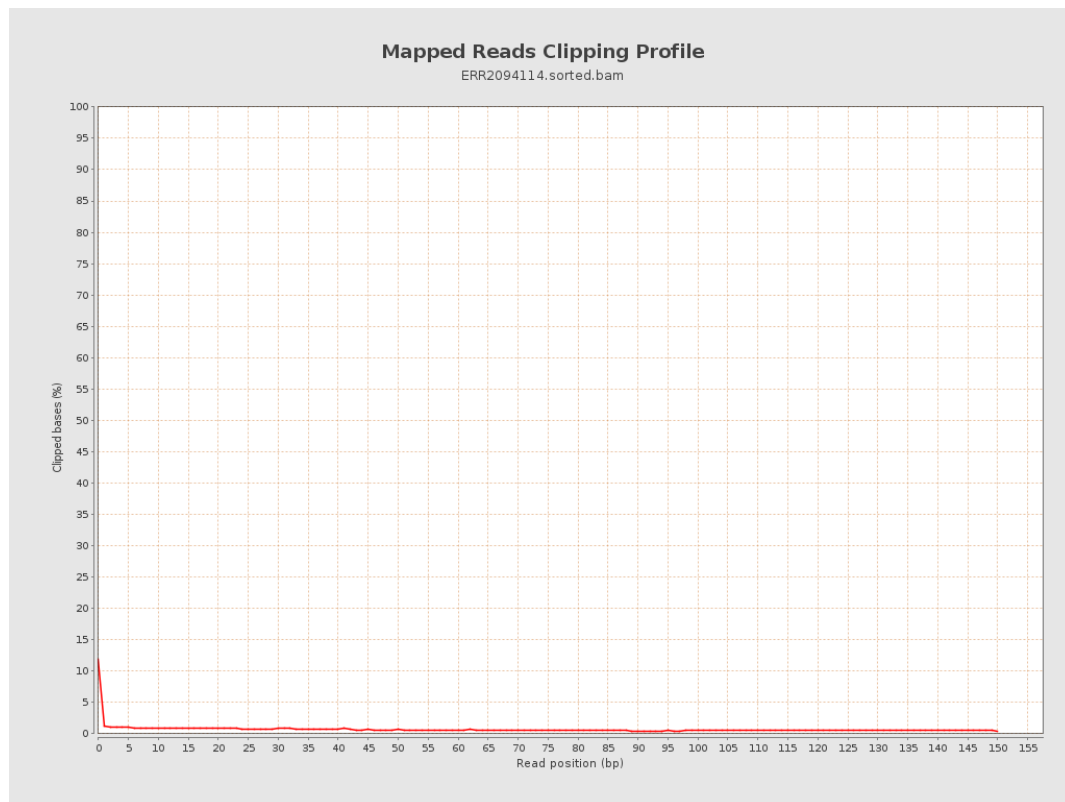
8. Results : Mapped Reads Nucleotide Content



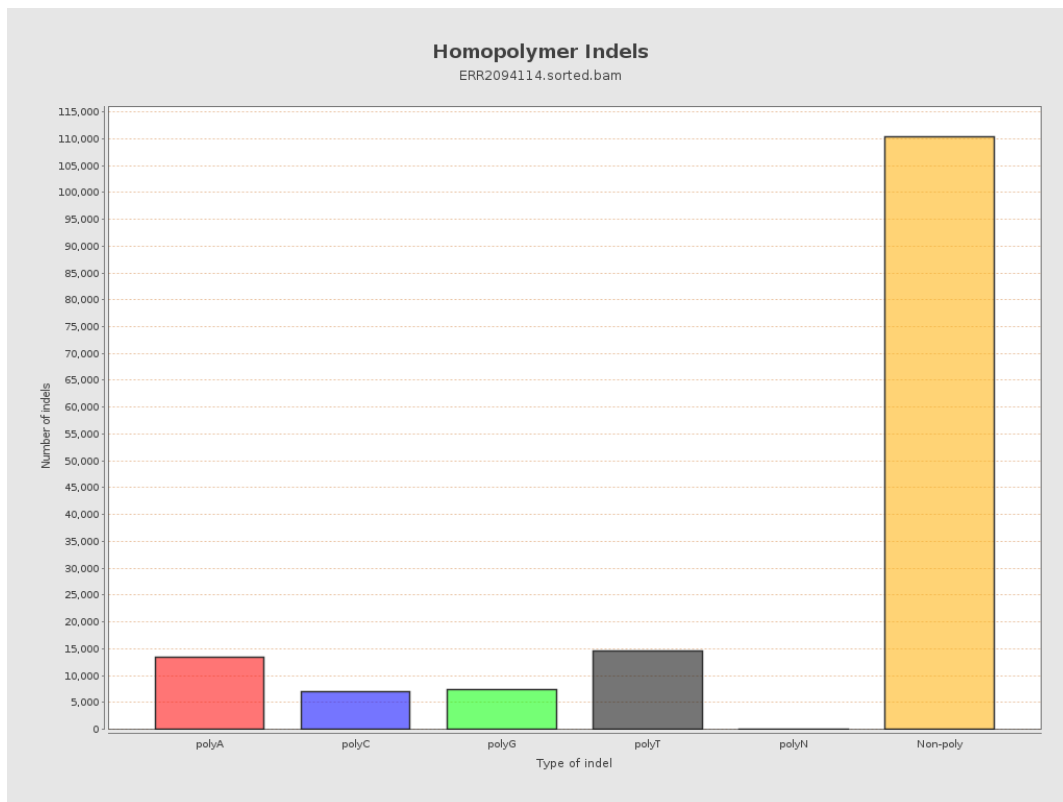
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



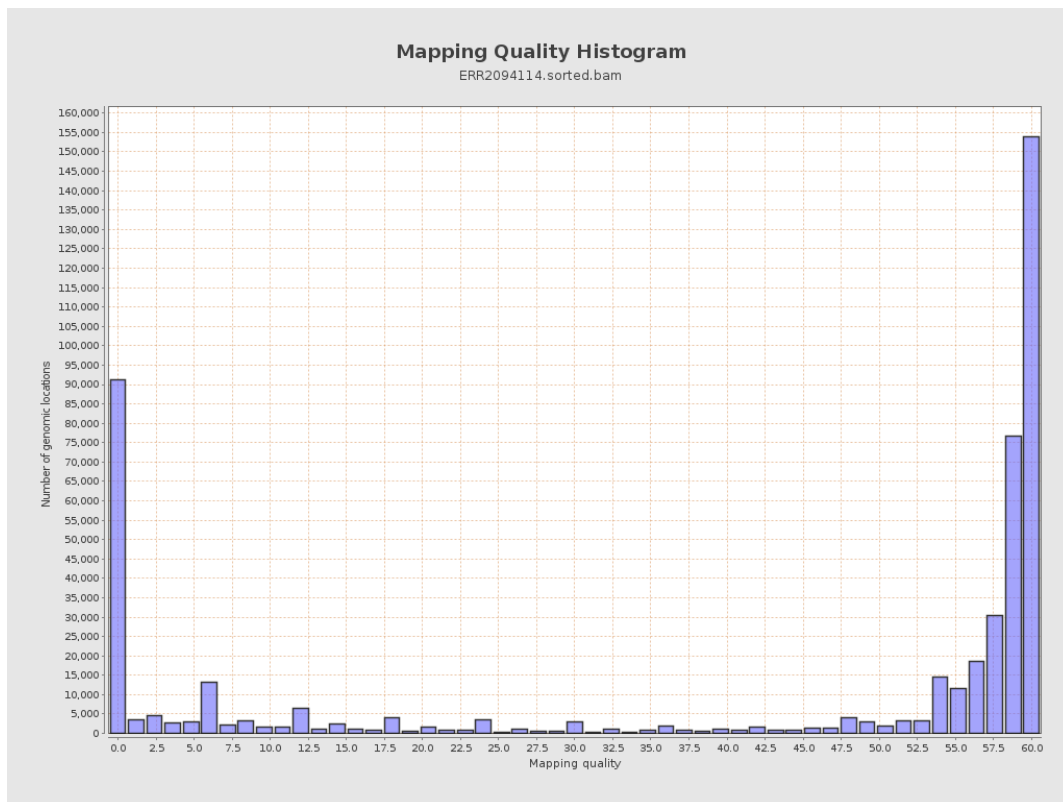
11. Results : Homopolymer Indels



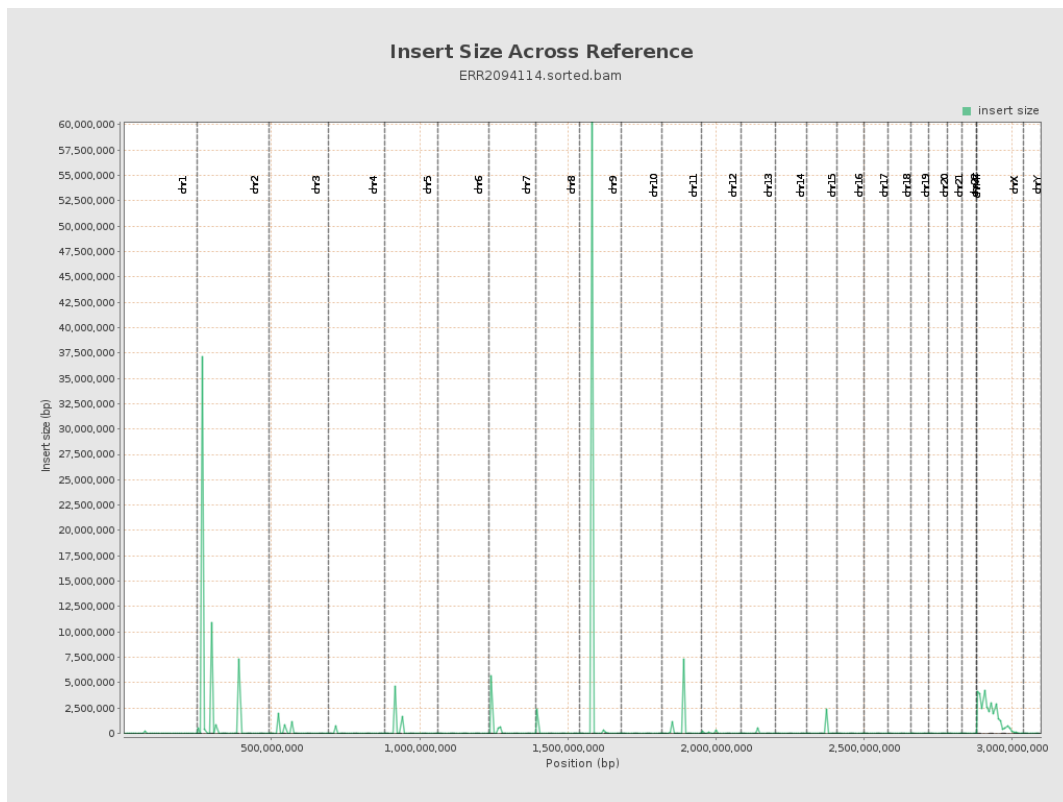
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

