

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:26:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094129.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_ERR2094129 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094129_1.fastq.gz ERR2094129_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:26:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	481,778
Mapped reads	457,082 / 94.87%
Unmapped reads	24,696 / 5.13%
Mapped paired reads	457,082 / 94.87%
Mapped reads, first in pair	229,479 / 47.63%
Mapped reads, second in pair	227,603 / 47.24%
Mapped reads, both in pair	454,278 / 94.29%
Mapped reads, singletons	2,804 / 0.58%
Secondary alignments	0
Supplementary alignments	6,150 / 1.28%
Read min/max/mean length	30 / 151 / 144.16
Duplicated reads (estimated)	452,559 / 93.94%
Duplication rate	43.63%
Clipped reads	136,465 / 28.33%

2.2. ACGT Content

Number/percentage of A's	17,351,098 / 27.5%
Number/percentage of C's	14,039,873 / 22.25%
Number/percentage of T's	17,076,265 / 27.07%
Number/percentage of G's	14,620,540 / 23.17%
Number/percentage of N's	725 / 0%

GC Percentage	45.43%
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2.3. Coverage

Mean	0.0205
Standard Deviation	21.0765

2.4. Mapping Quality

Mean Mapping Quality	31.69
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2.5. Insert size

Mean	135,413.8
Standard Deviation	3,878,402.8
P25/Median/P75	162 / 207 / 237

2.6. Mismatches and indels

General error rate	2.57%
Mismatches	1,403,648
Insertions	57,743
Mapped reads with at least one insertion	12.54%
Deletions	96,208
Mapped reads with at least one deletion	19.64%
Homopolymer indels	34.52%

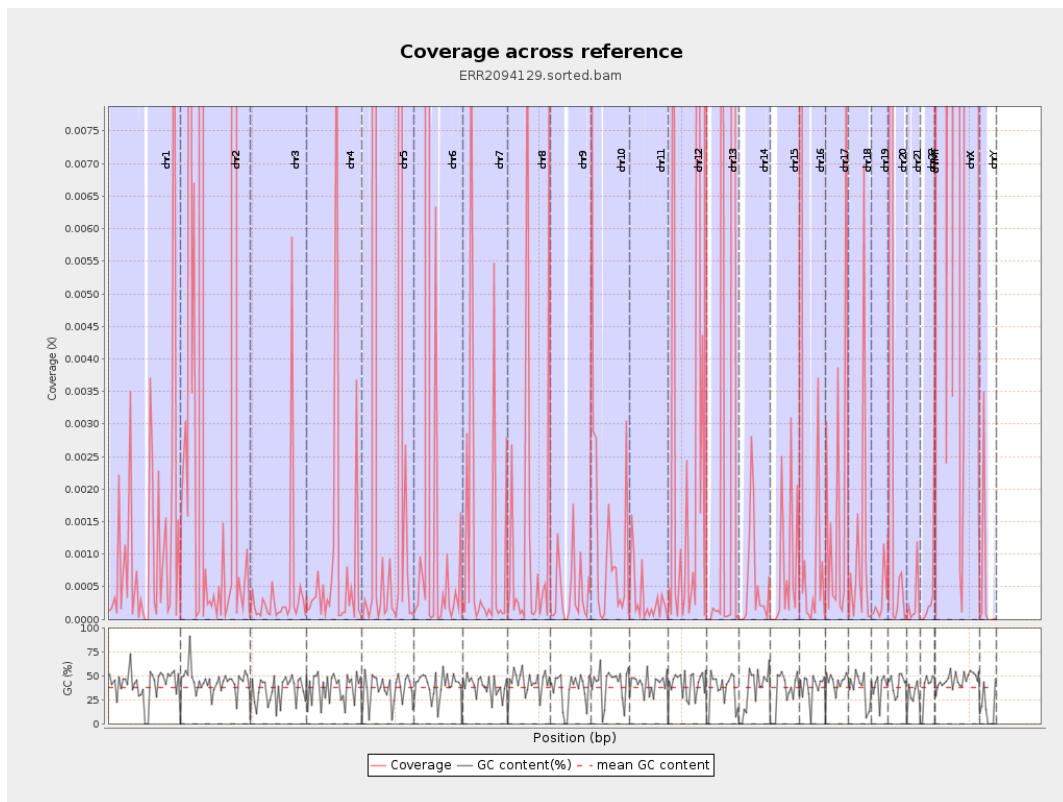
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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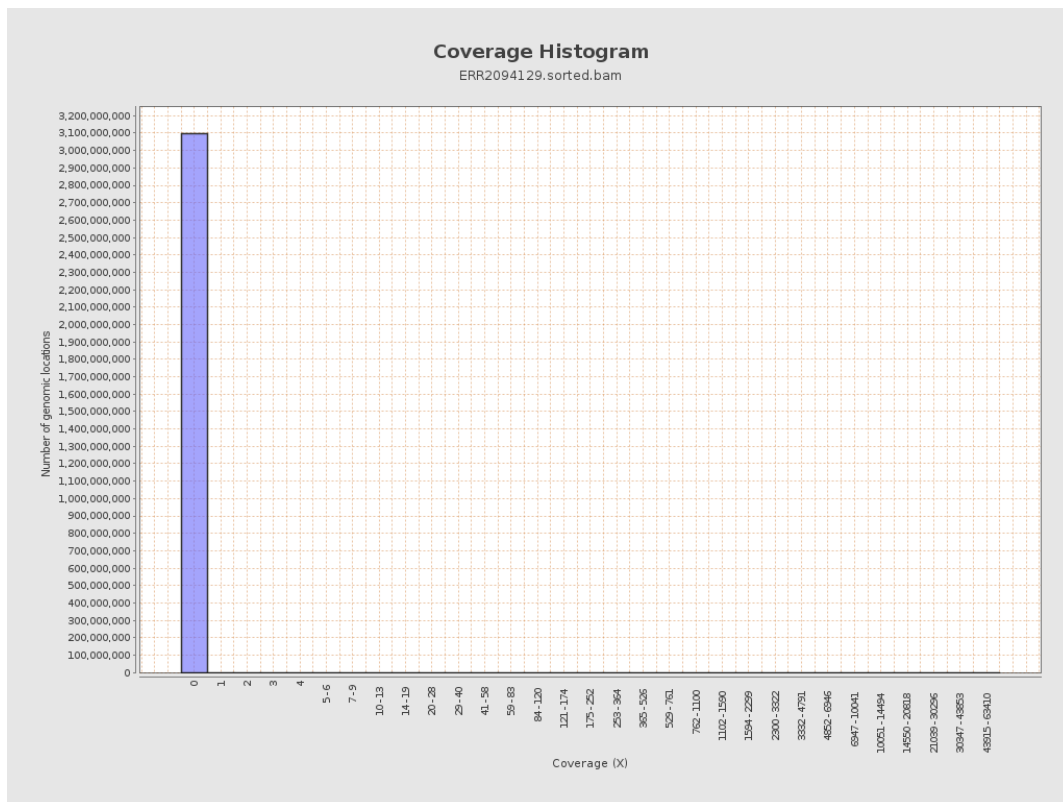
		bases	coverage	deviation
chr1	249250621	308377	0.0012	0.626
chr2	243199373	3433284	0.0141	10.7768
chr3	198022430	83258	0.0004	0.2938
chr4	191154276	160278	0.0008	0.4804
chr5	180915260	1330334	0.0074	5.0733
chr6	171115067	2984466	0.0174	17.3264
chr7	159138663	181913	0.0011	0.5476
chr8	146364022	193177	0.0013	0.5895
chr9	141213431	56701	0.0004	0.1186
chr10	135534747	177880	0.0013	0.4814
chr11	135006516	44376	0.0003	0.0841
chr12	133851895	895691	0.0067	3.4995
chr13	115169878	496300	0.0043	2.6652
chr14	107349540	63248	0.0006	0.2158
chr15	102531392	73091	0.0007	0.2685
chr16	90354753	261058	0.0029	1.9447
chr17	81195210	145985	0.0018	0.6743
chr18	78077248	87857	0.0011	0.4361
chr19	59128983	19228	0.0003	0.0562
chr20	63025520	257559	0.0041	1.8421
chr21	48129895	12587	0.0003	0.0611
chr22	51304566	15008	0.0003	0.0952
chrMT	16571	31629277	1,908.7126	7,866.9747
chrX	155270560	20535682	0.1323	36.0401

chrY	59373566	28525	0.0005	0.2547
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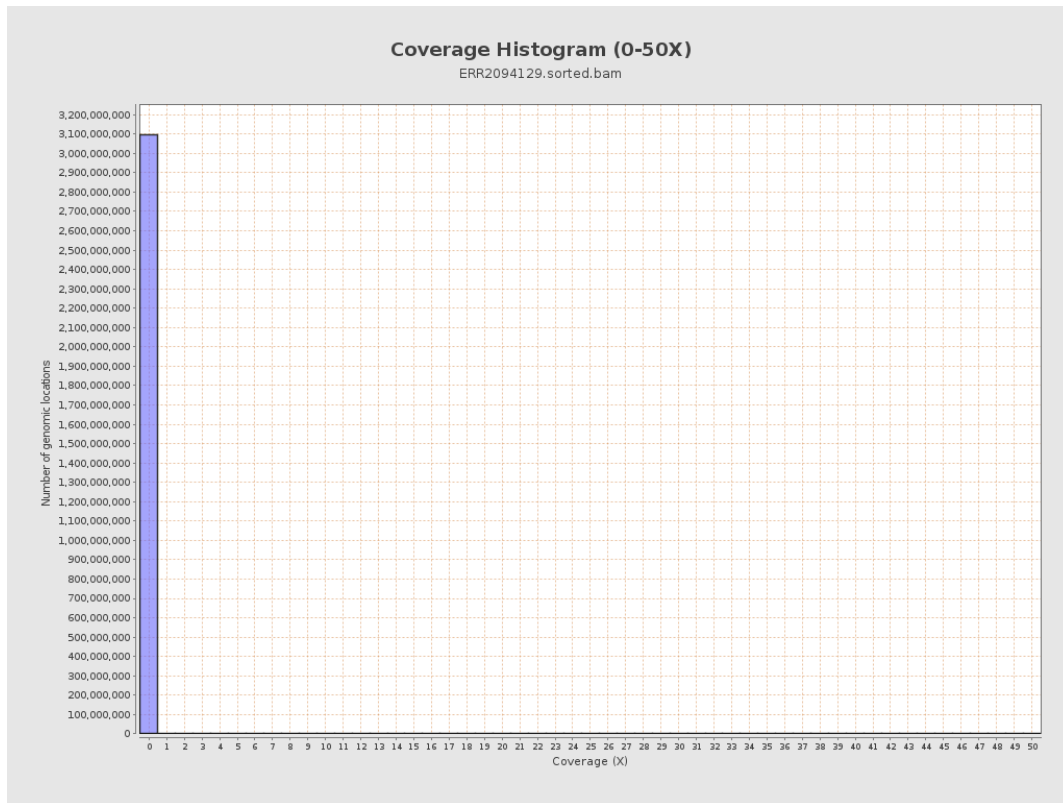
3. Results : Coverage across reference



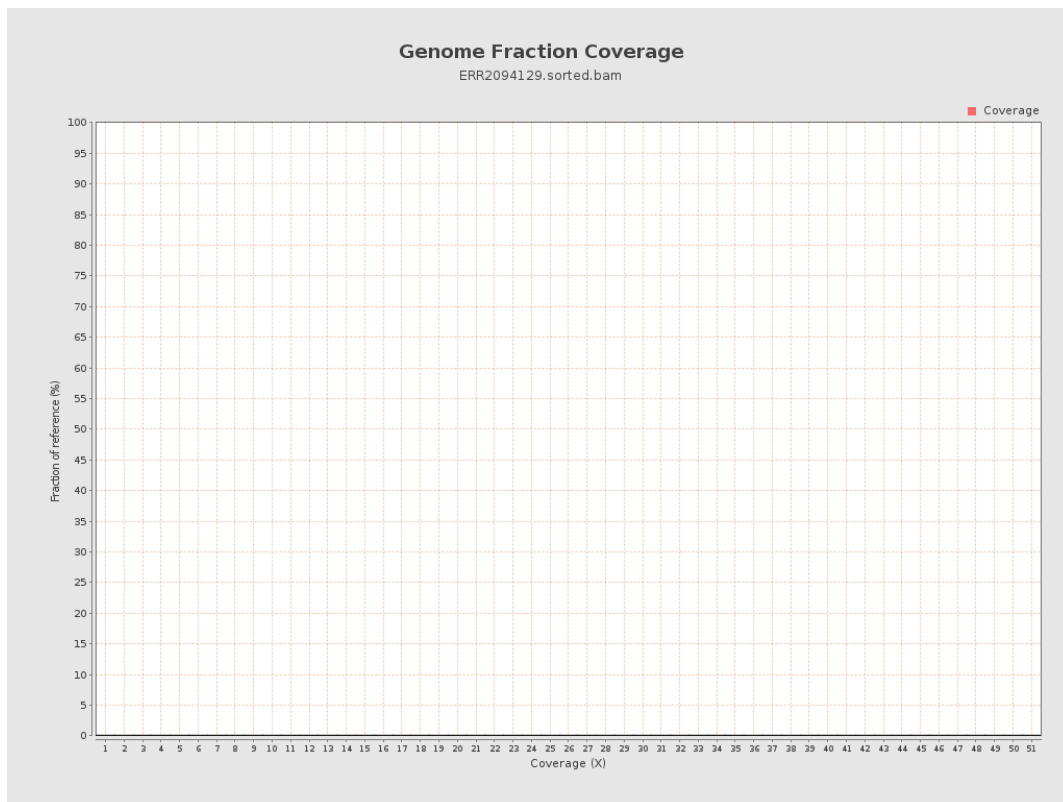
4. Results : Coverage Histogram



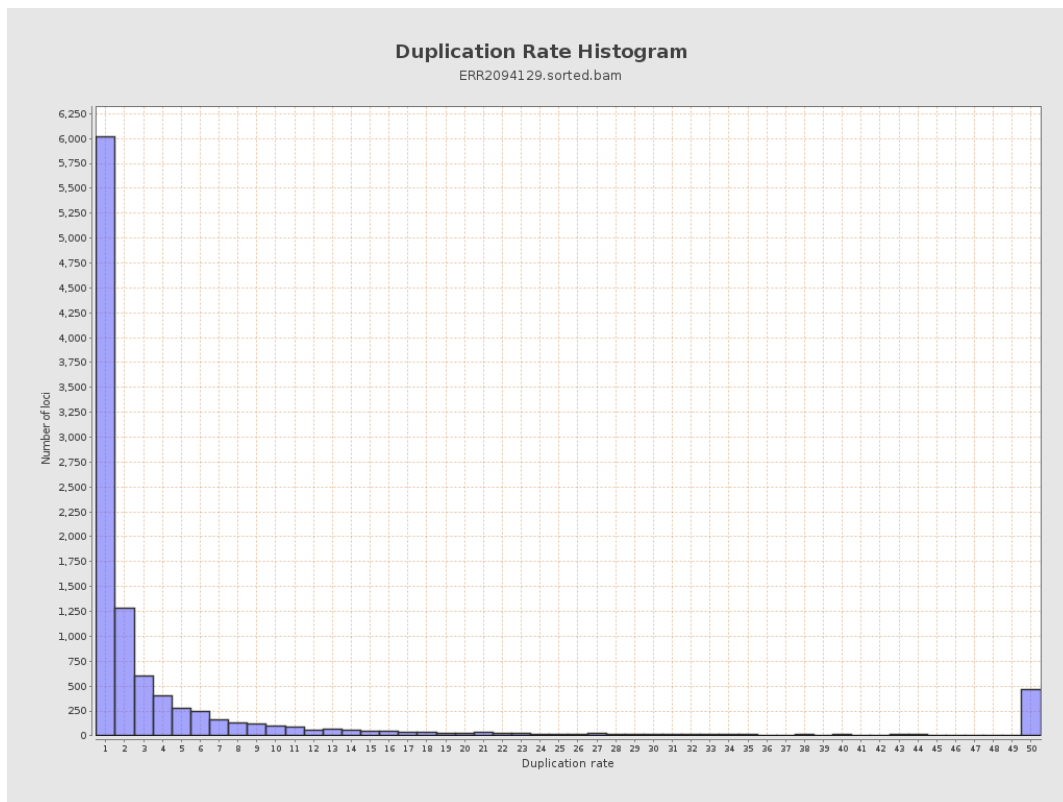
5. Results : Coverage Histogram (0-50X)



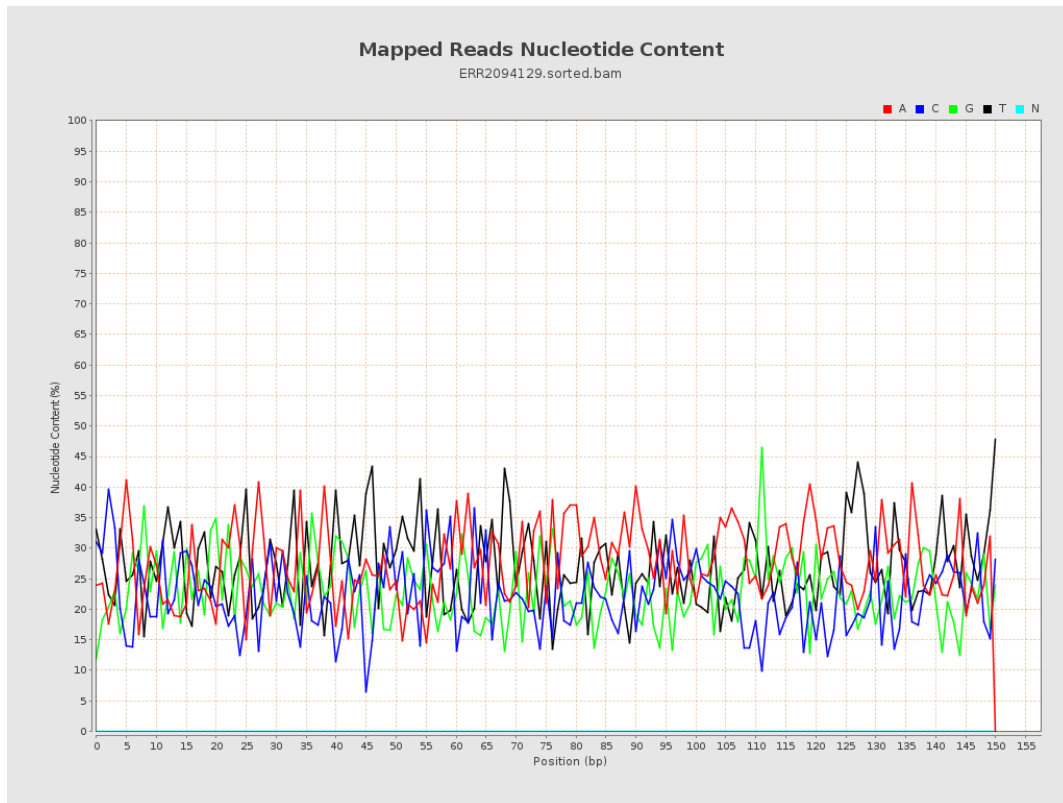
6. Results : Genome Fraction Coverage



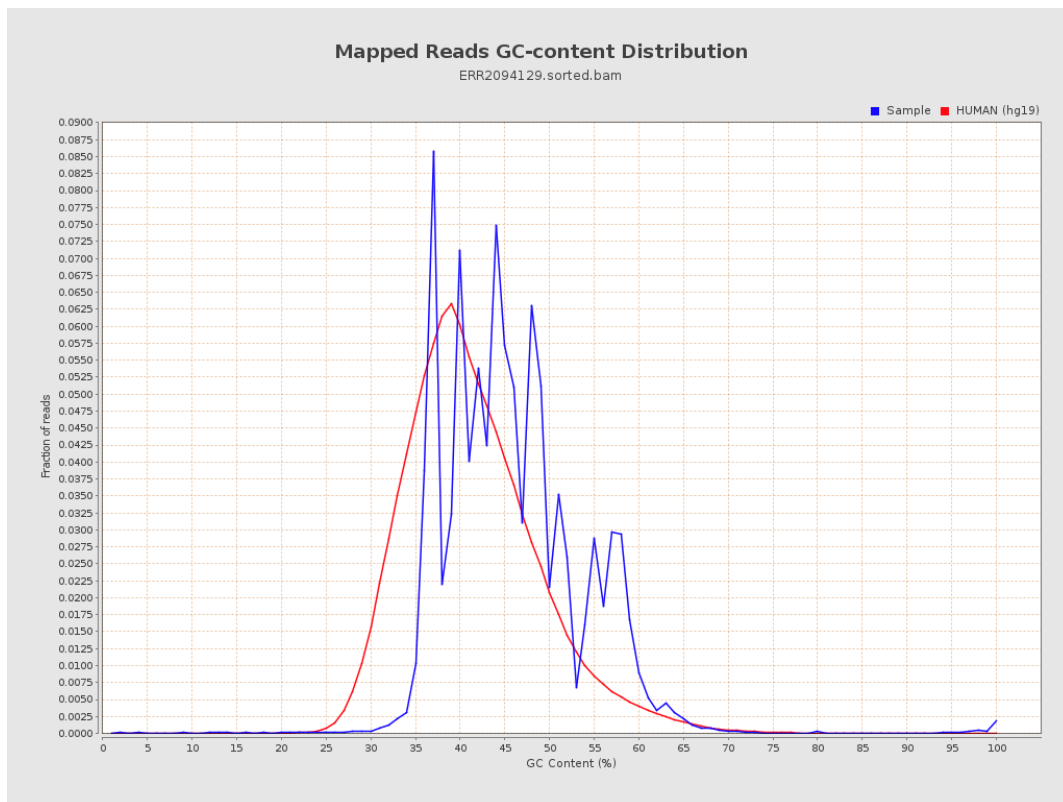
7. Results : Duplication Rate Histogram



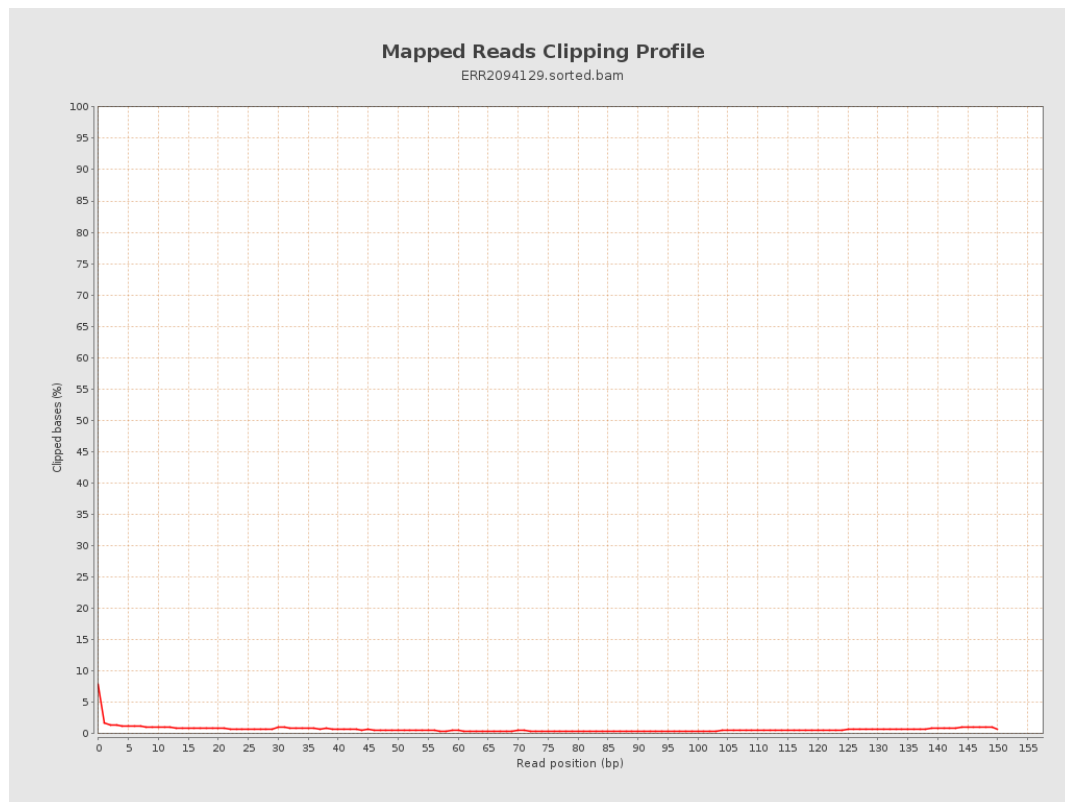
8. Results : Mapped Reads Nucleotide Content



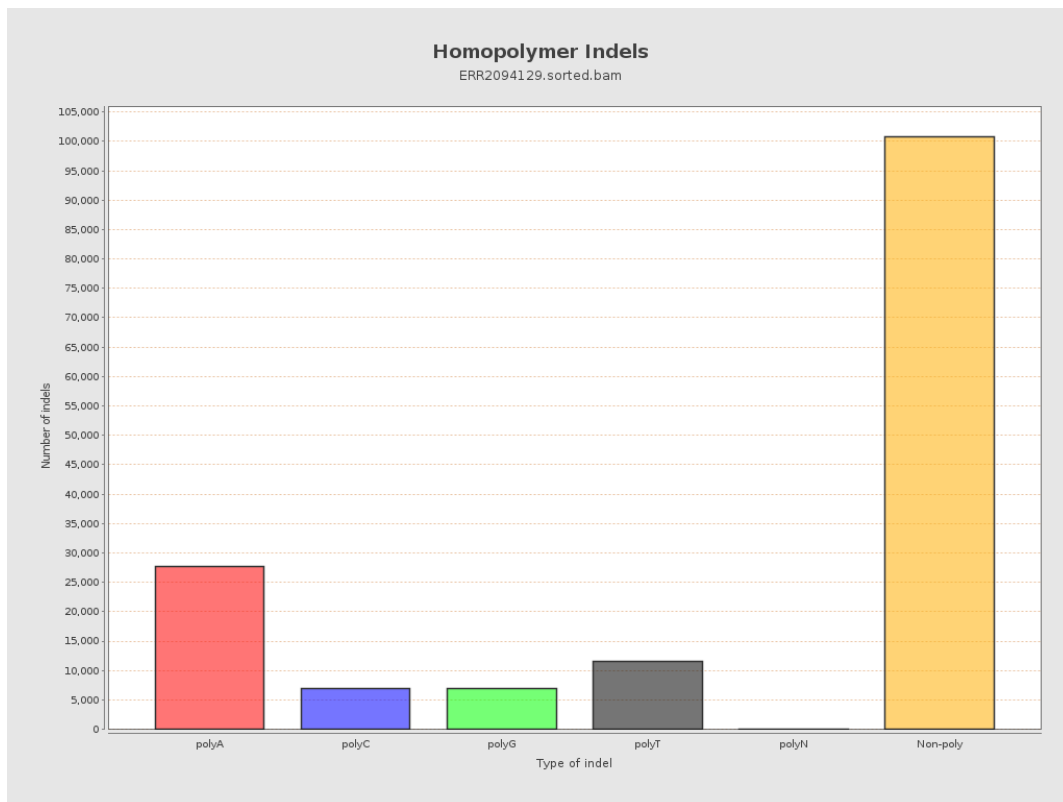
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



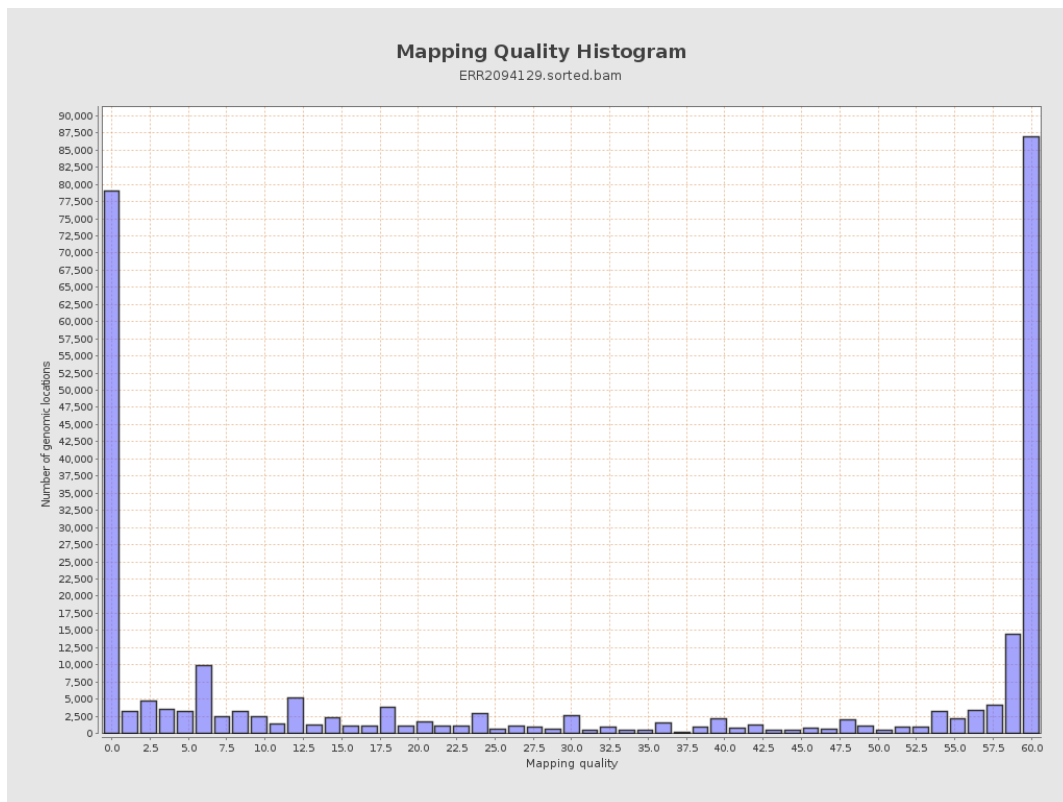
11. Results : Homopolymer Indels



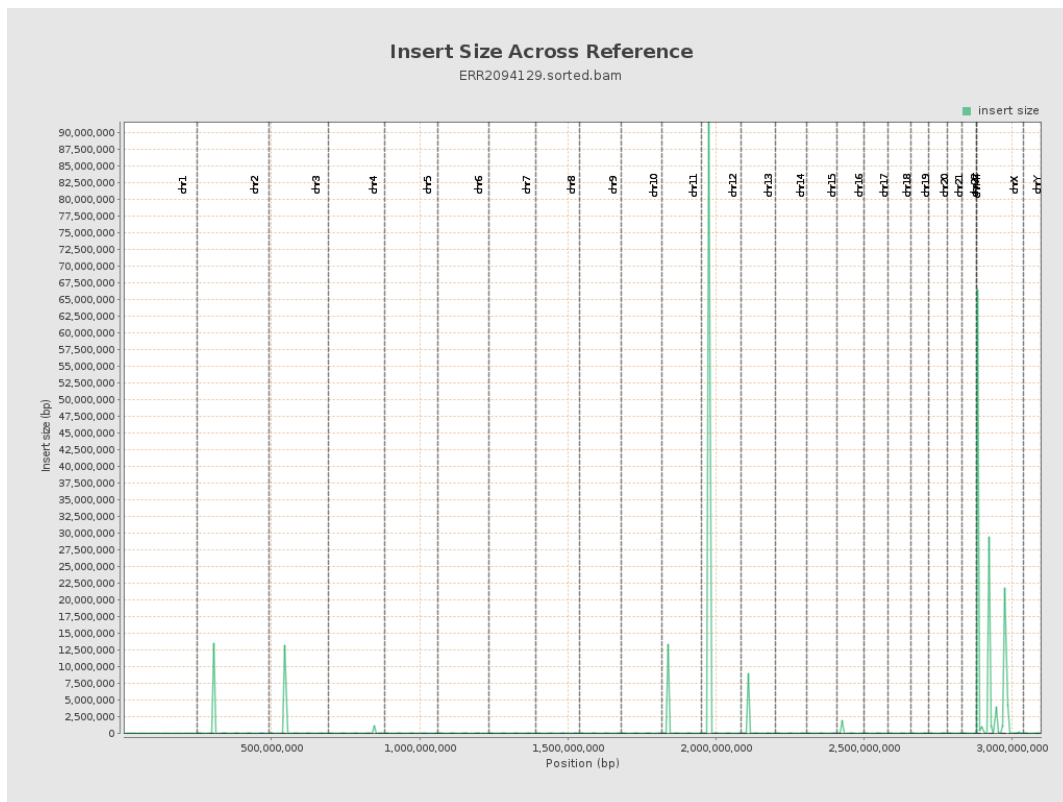
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

