

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 04:43:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094142.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_ERR2094142 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094142_1.fastq.gz ERR2094142_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 04:43:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	394,592
Mapped reads	368,491 / 93.39%
Unmapped reads	26,101 / 6.61%
Mapped paired reads	368,491 / 93.39%
Mapped reads, first in pair	185,479 / 47.01%
Mapped reads, second in pair	183,012 / 46.38%
Mapped reads, both in pair	363,492 / 92.12%
Mapped reads, singletons	4,999 / 1.27%
Secondary alignments	0
Supplementary alignments	20,130 / 5.1%
Read min/max/mean length	30 / 151 / 140.84
Duplicated reads (estimated)	345,107 / 87.46%
Duplication rate	46.89%
Clipped reads	181,319 / 45.95%

2.2. ACGT Content

Number/percentage of A's	13,053,012 / 28.45%
Number/percentage of C's	9,850,709 / 21.47%
Number/percentage of T's	12,540,535 / 27.34%
Number/percentage of G's	10,431,832 / 22.74%
Number/percentage of N's	533 / 0%

GC Percentage	44.21%
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2.3. Coverage

Mean	0.0152
Standard Deviation	4.691

2.4. Mapping Quality

Mean Mapping Quality	45.15
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2.5. Insert size

Mean	460,789.21
Standard Deviation	6,329,030.66
P25/Median/P75	127 / 166 / 203

2.6. Mismatches and indels

General error rate	3.8%
Mismatches	1,714,637
Insertions	22,906
Mapped reads with at least one insertion	6.06%
Deletions	139,481
Mapped reads with at least one deletion	36.45%
Homopolymer indels	28.62%

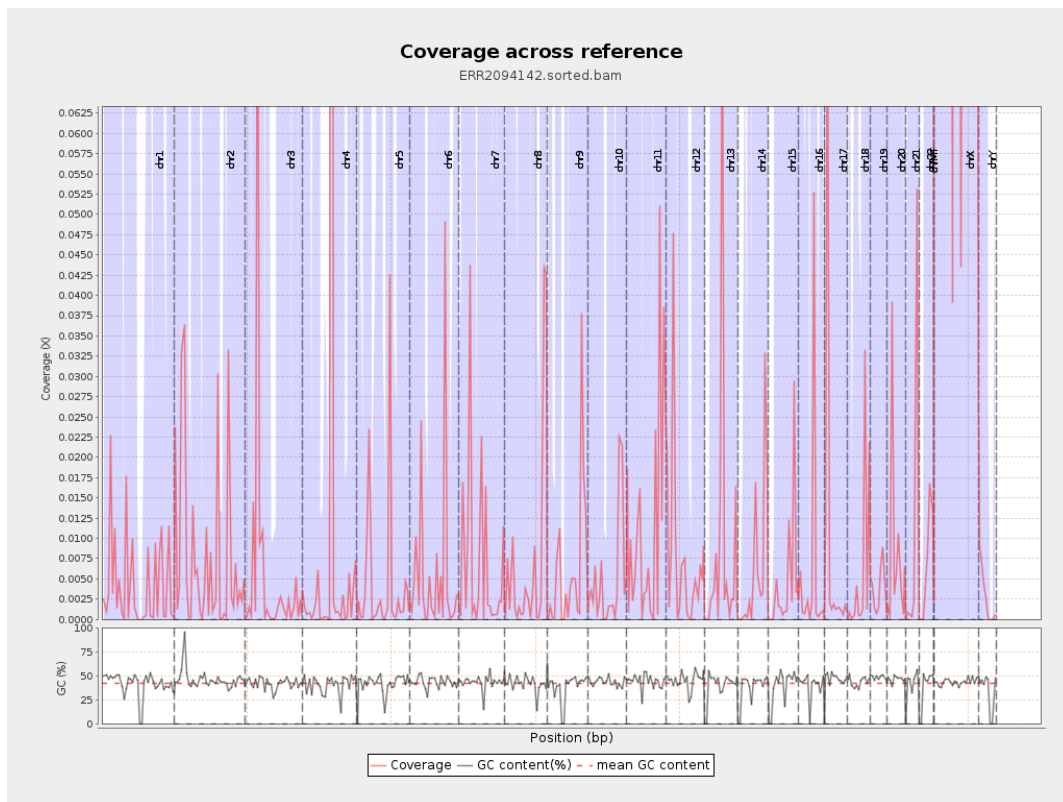
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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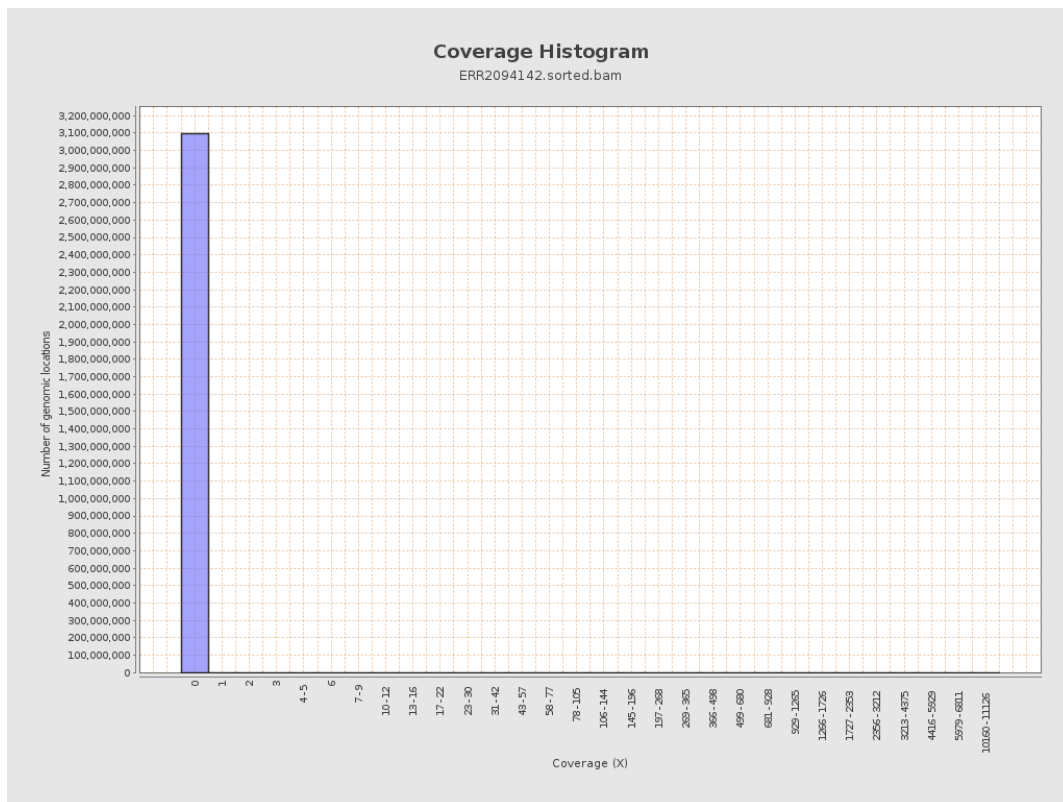
		bases	coverage	deviation
chr1	249250621	1075410	0.0043	1.4362
chr2	243199373	1847208	0.0076	2.2064
chr3	198022430	1186592	0.006	3.7594
chr4	191154276	2250351	0.0118	4.7115
chr5	180915260	802812	0.0044	2.2509
chr6	171115067	969012	0.0057	1.9232
chr7	159138663	1077574	0.0068	2.166
chr8	146364022	978662	0.0067	2.3275
chr9	141213431	843992	0.006	1.5039
chr10	135534747	644233	0.0048	1.2721
chr11	135006516	1509136	0.0112	3.5165
chr12	133851895	1015367	0.0076	2.0301
chr13	115169878	1086579	0.0094	4.6418
chr14	107349540	685842	0.0064	1.2921
chr15	102531392	460703	0.0045	1.6849
chr16	90354753	534322	0.0059	3.2214
chr17	81195210	791708	0.0098	2.9238
chr18	78077248	438949	0.0056	2.4701
chr19	59128983	216521	0.0037	0.5074
chr20	63025520	513750	0.0082	3.1703
chr21	48129895	516058	0.0107	3.7986
chr22	51304566	333474	0.0065	1.1092
chrMT	16571	4364158	263.3612	1,154.025
chrX	155270560	22616691	0.1457	12.388

chrY	59373566	162946	0.0027	0.5586
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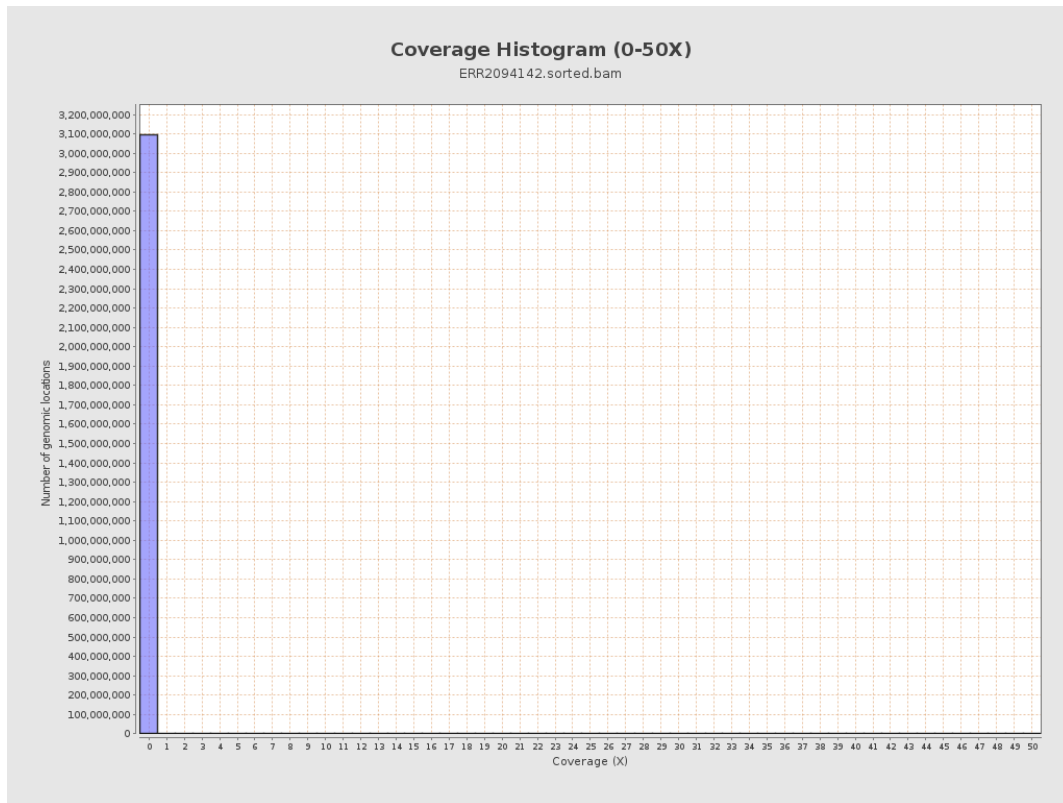
3. Results : Coverage across reference



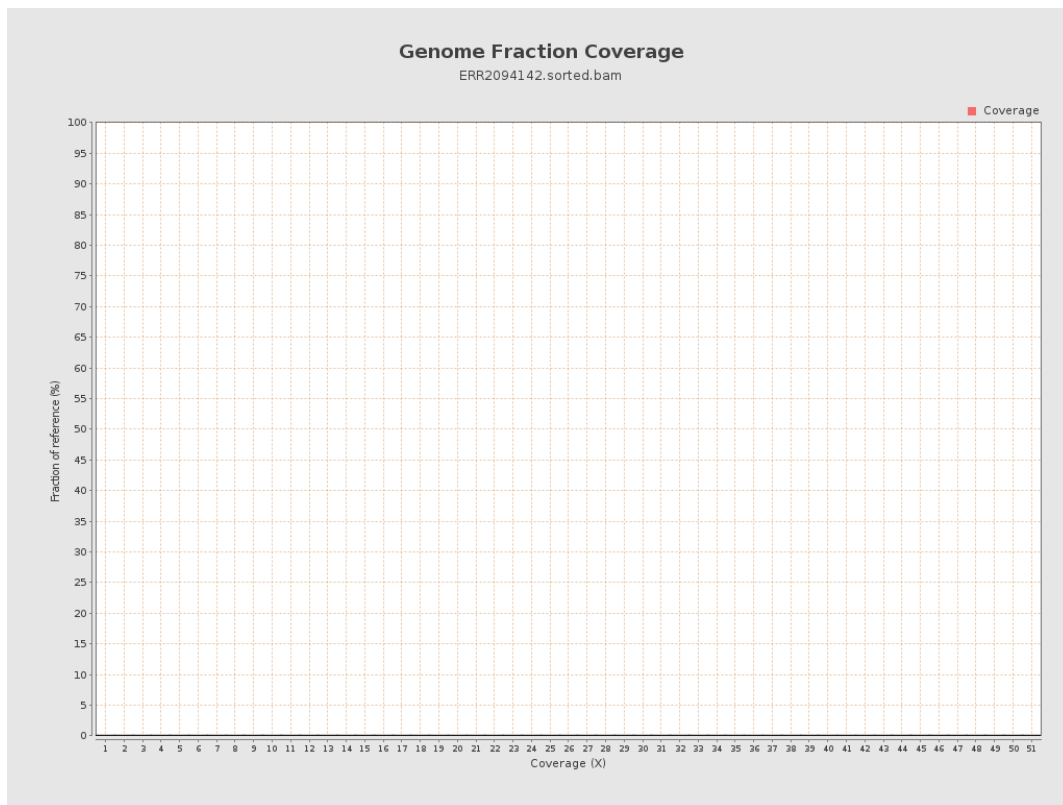
4. Results : Coverage Histogram



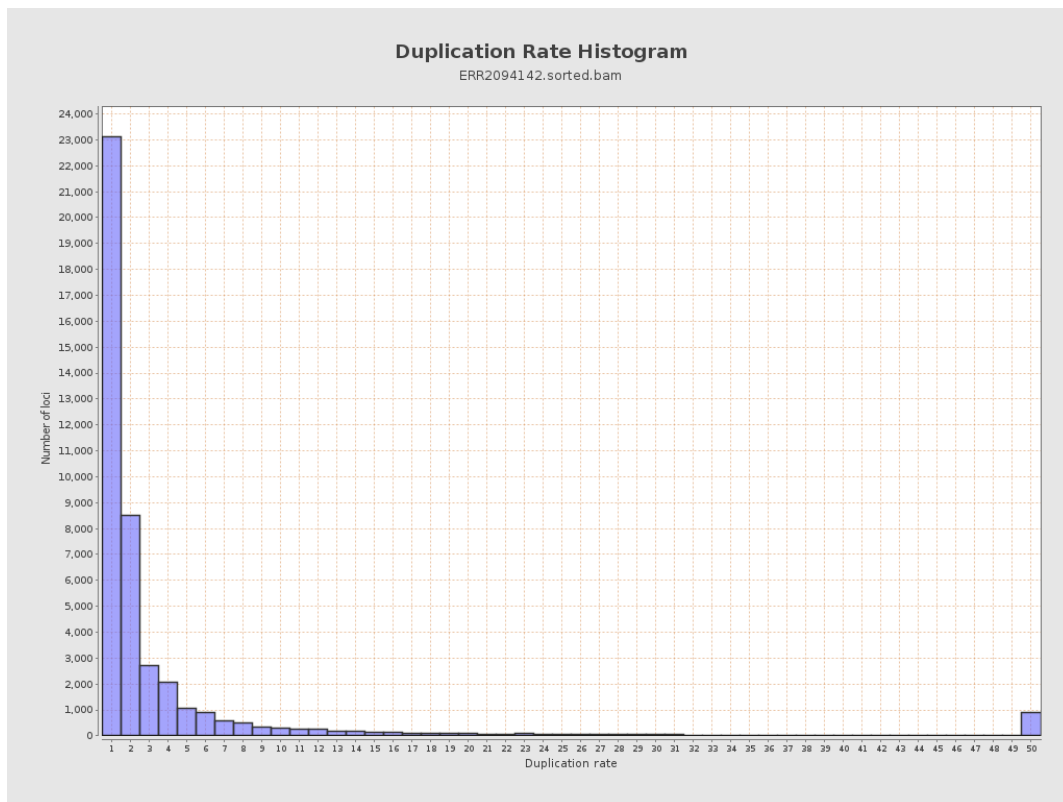
5. Results : Coverage Histogram (0-50X)



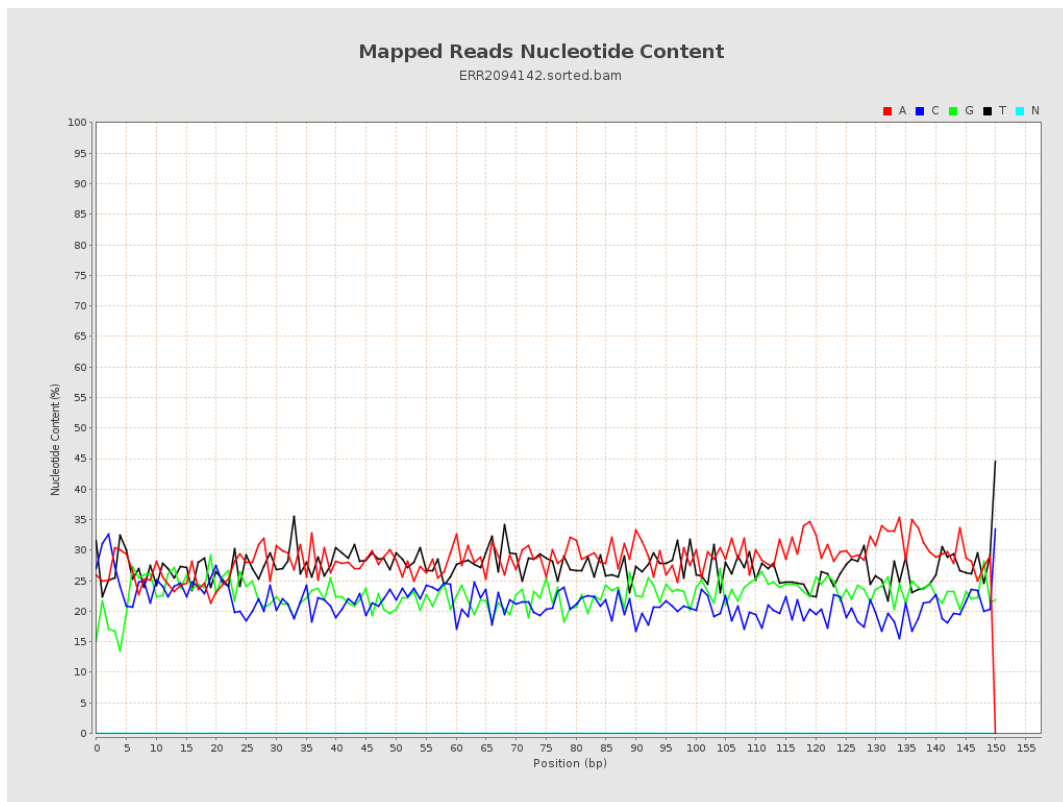
6. Results : Genome Fraction Coverage



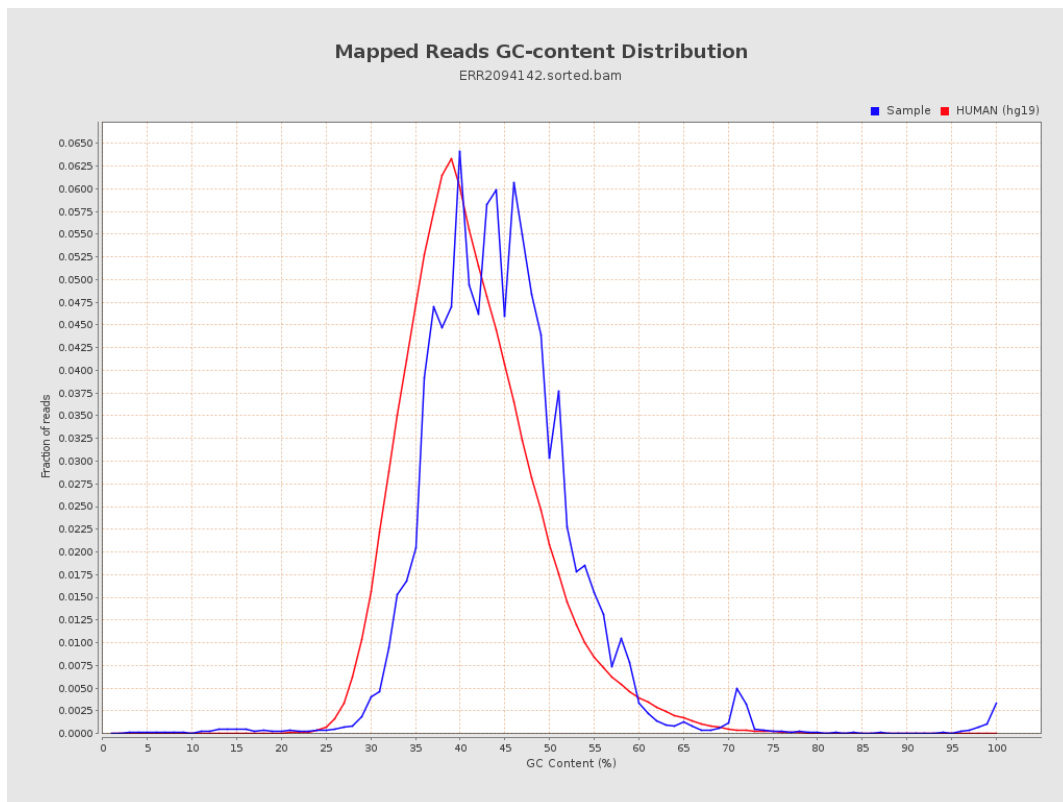
7. Results : Duplication Rate Histogram



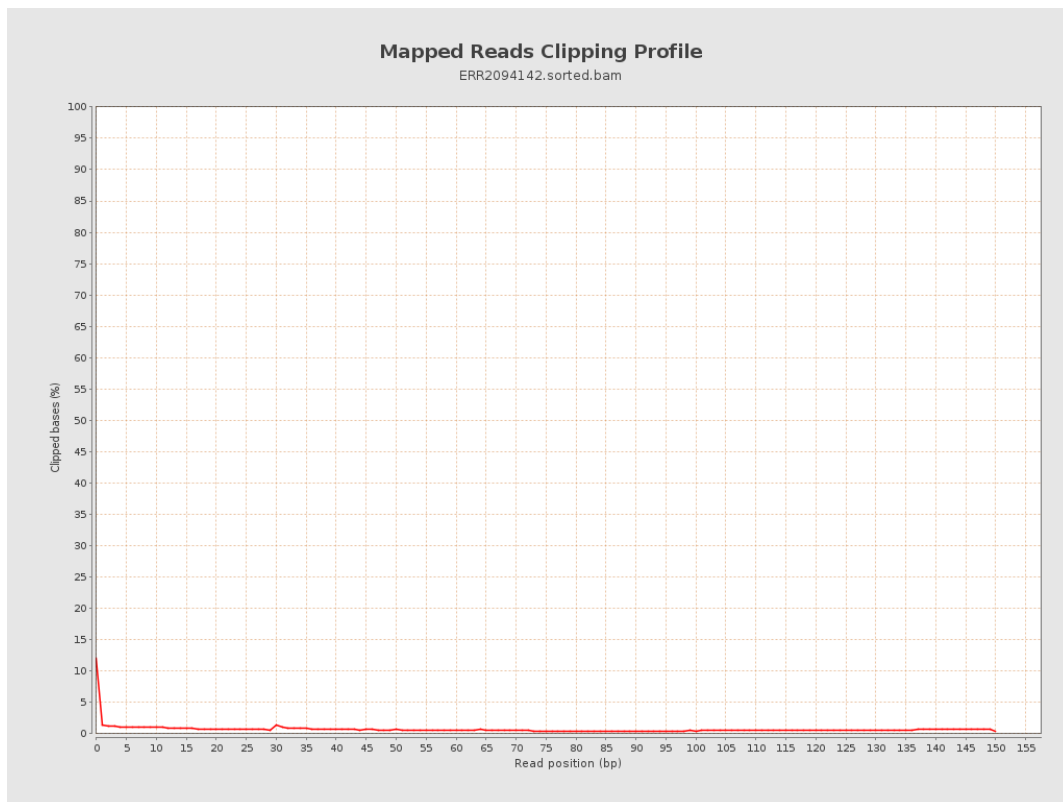
8. Results : Mapped Reads Nucleotide Content



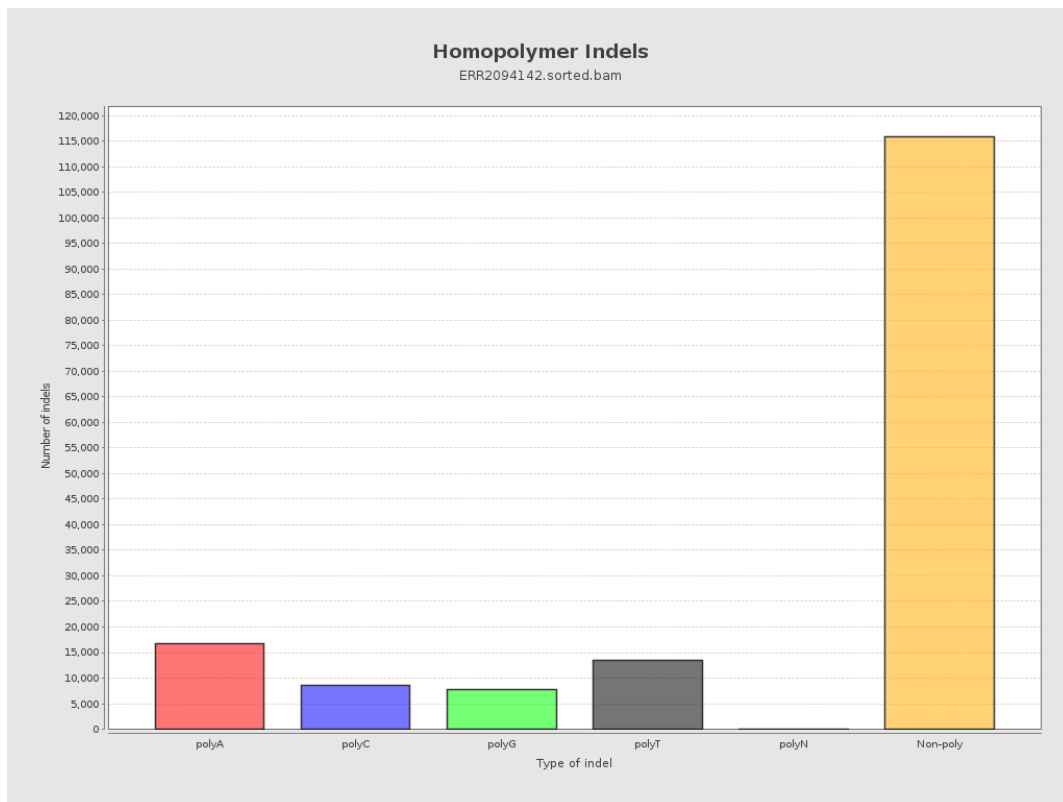
9. Results : Mapped Reads GC-content Distribution



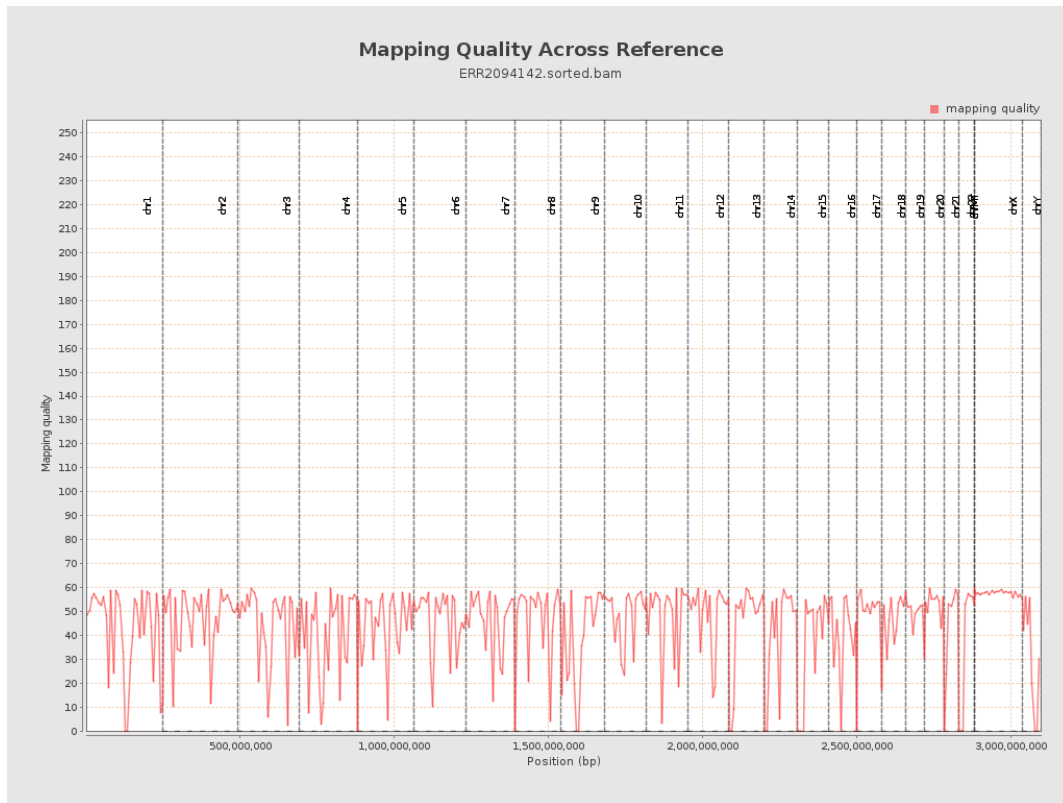
10. Results : Mapped Reads Clipping Profile



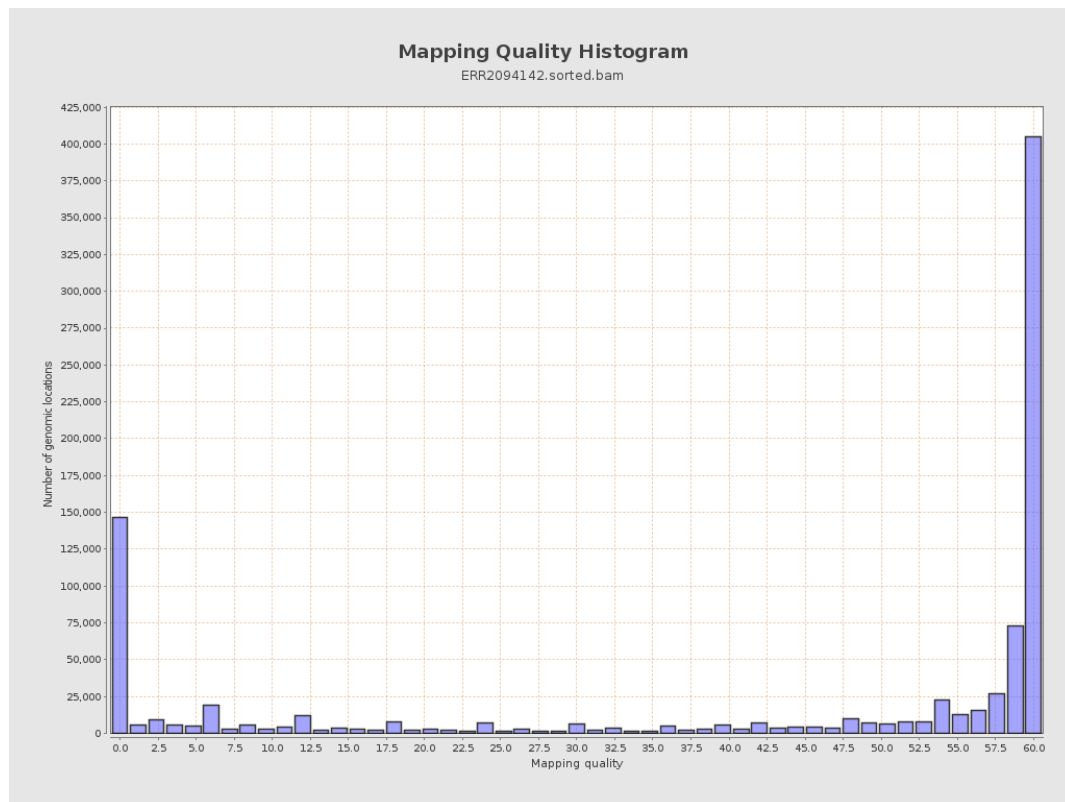
11. Results : Homopolymer Indels



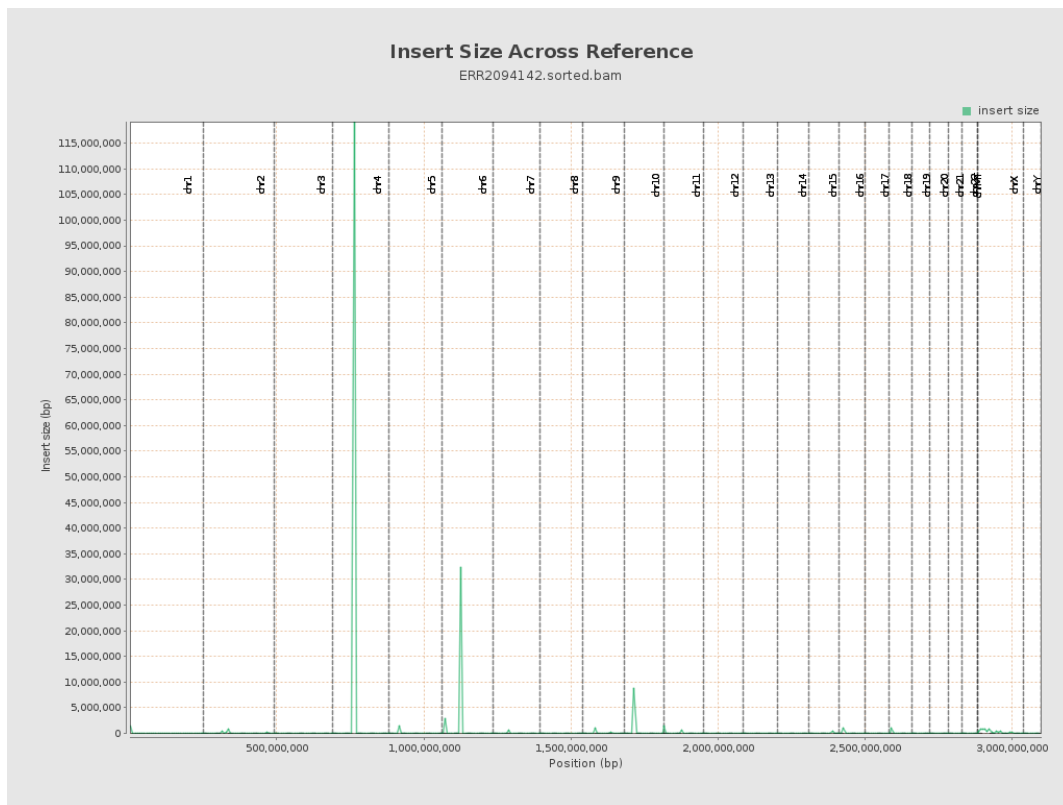
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

