

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:59:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094042.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_ERR2094042 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094042_1.fastq.gz ERR2094042_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:59:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	418,392
Mapped reads	397,797 / 95.08%
Unmapped reads	20,595 / 4.92%
Mapped paired reads	397,797 / 95.08%
Mapped reads, first in pair	199,790 / 47.75%
Mapped reads, second in pair	198,007 / 47.33%
Mapped reads, both in pair	394,972 / 94.4%
Mapped reads, singletons	2,825 / 0.68%
Secondary alignments	0
Supplementary alignments	11,963 / 2.86%
Read min/max/mean length	30 / 151 / 140.91
Duplicated reads (estimated)	373,976 / 89.38%
Duplication rate	50.11%
Clipped reads	157,213 / 37.58%

2.2. ACGT Content

Number/percentage of A's	14,333,163 / 27.52%
Number/percentage of C's	11,645,965 / 22.36%
Number/percentage of T's	13,923,406 / 26.73%
Number/percentage of G's	12,182,049 / 23.39%
Number/percentage of N's	455 / 0%

GC Percentage	45.75%
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2.3. Coverage

Mean	0.0172
Standard Deviation	4.4178

2.4. Mapping Quality

Mean Mapping Quality	43.84
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2.5. Insert size

Mean	472,059.52
Standard Deviation	6,250,129.32
P25/Median/P75	143 / 172 / 206

2.6. Mismatches and indels

General error rate	4.38%
Mismatches	2,210,648
Insertions	38,716
Mapped reads with at least one insertion	9.58%
Deletions	173,891
Mapped reads with at least one deletion	40.62%
Homopolymer indels	29.57%

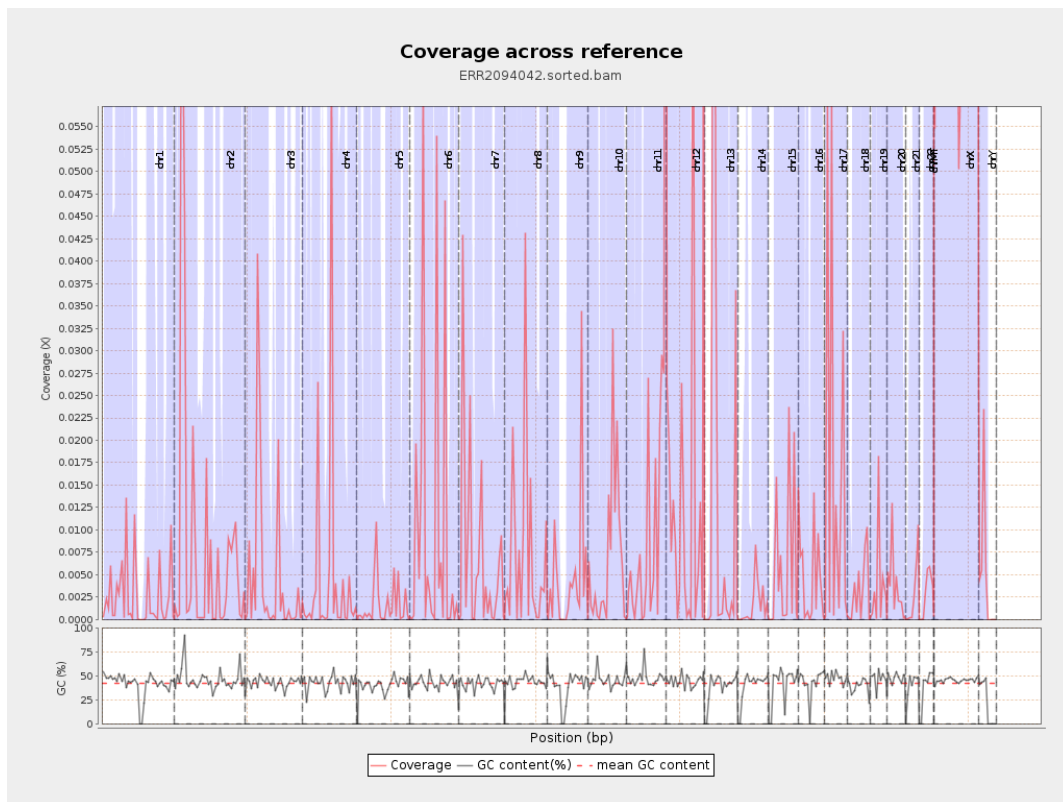
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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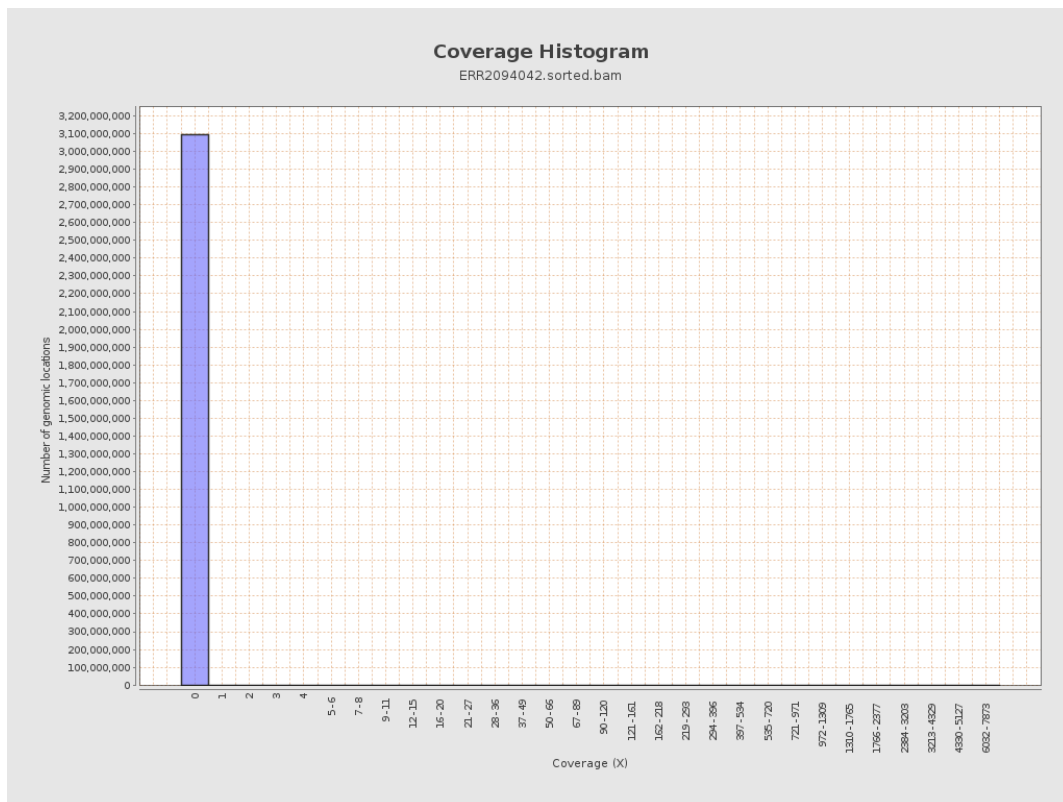
		bases	coverage	deviation
chr1	249250621	638864	0.0026	0.8716
chr2	243199373	1929739	0.0079	2.2969
chr3	198022430	922701	0.0047	1.742
chr4	191154276	954220	0.005	2.2581
chr5	180915260	325917	0.0018	0.5899
chr6	171115067	1758336	0.0103	4.1553
chr7	159138663	1043495	0.0066	2.2897
chr8	146364022	1057235	0.0072	2.1058
chr9	141213431	652658	0.0046	1.7434
chr10	135534747	937813	0.0069	2.1661
chr11	135006516	1325544	0.0098	2.3242
chr12	133851895	1866191	0.0139	5.0165
chr13	115169878	1540301	0.0134	4.2766
chr14	107349540	179201	0.0017	0.5928
chr15	102531392	569909	0.0056	1.7805
chr16	90354753	431218	0.0048	1.2966
chr17	81195210	1408450	0.0173	4.3335
chr18	78077248	256763	0.0033	0.9037
chr19	59128983	230093	0.0039	1.2909
chr20	63025520	239274	0.0038	1.0836
chr21	48129895	134120	0.0028	0.5412
chr22	51304566	145114	0.0028	0.5914
chrMT	16571	3928787	237.0881	976.9503
chrX	155270560	30598936	0.1971	13.033

chrY	59373566	288535	0.0049	1.684
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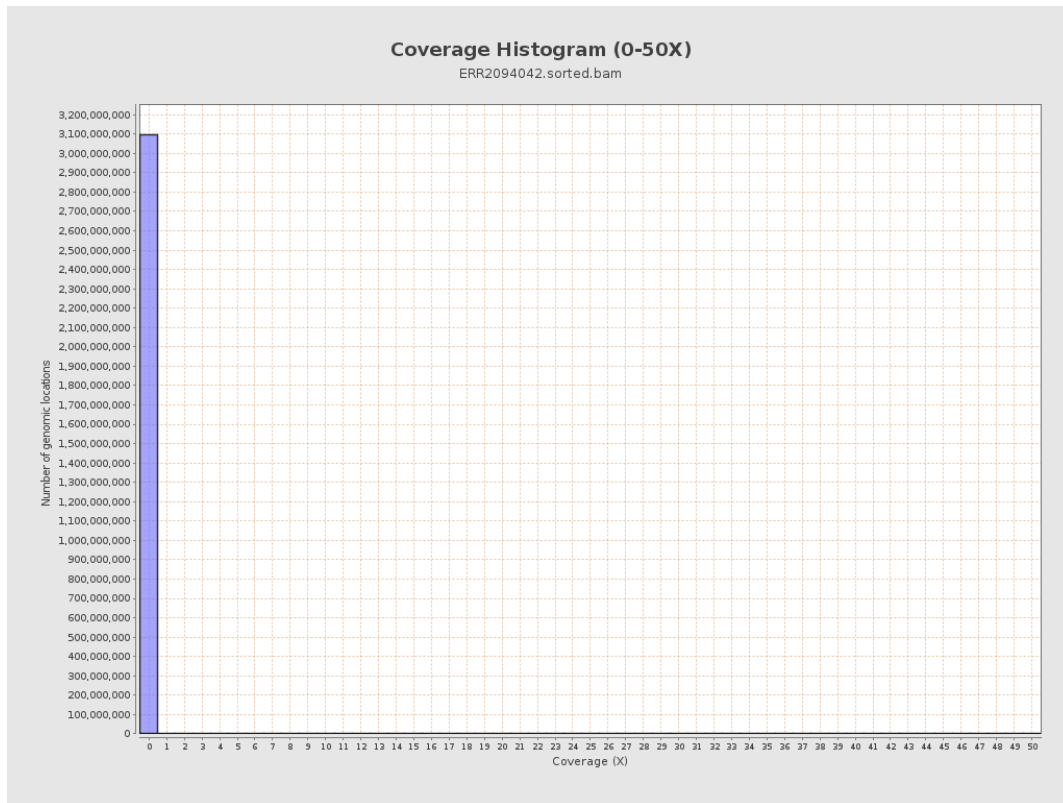
3. Results : Coverage across reference



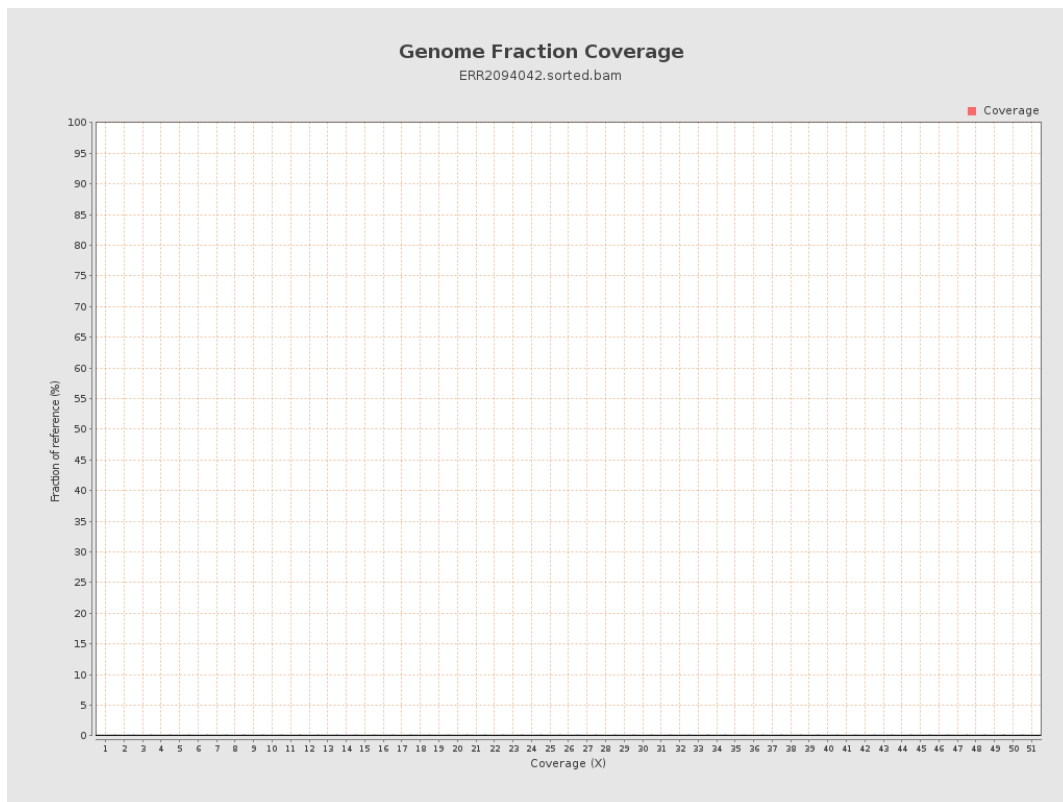
4. Results : Coverage Histogram



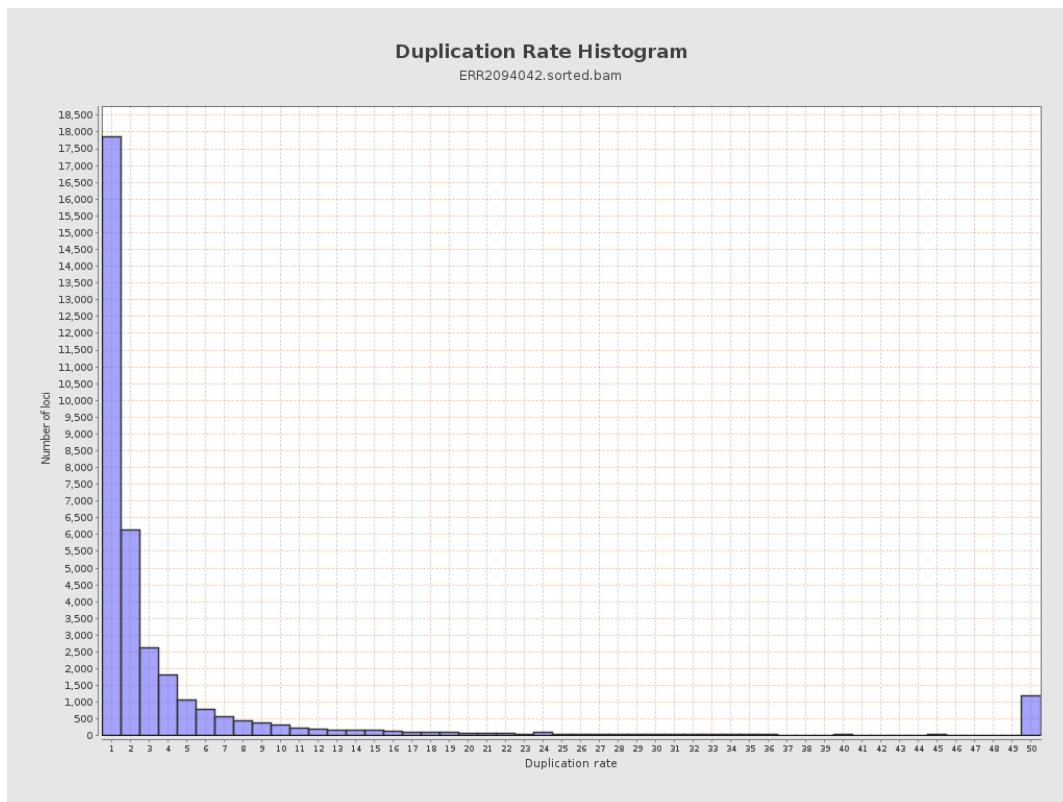
5. Results : Coverage Histogram (0-50X)



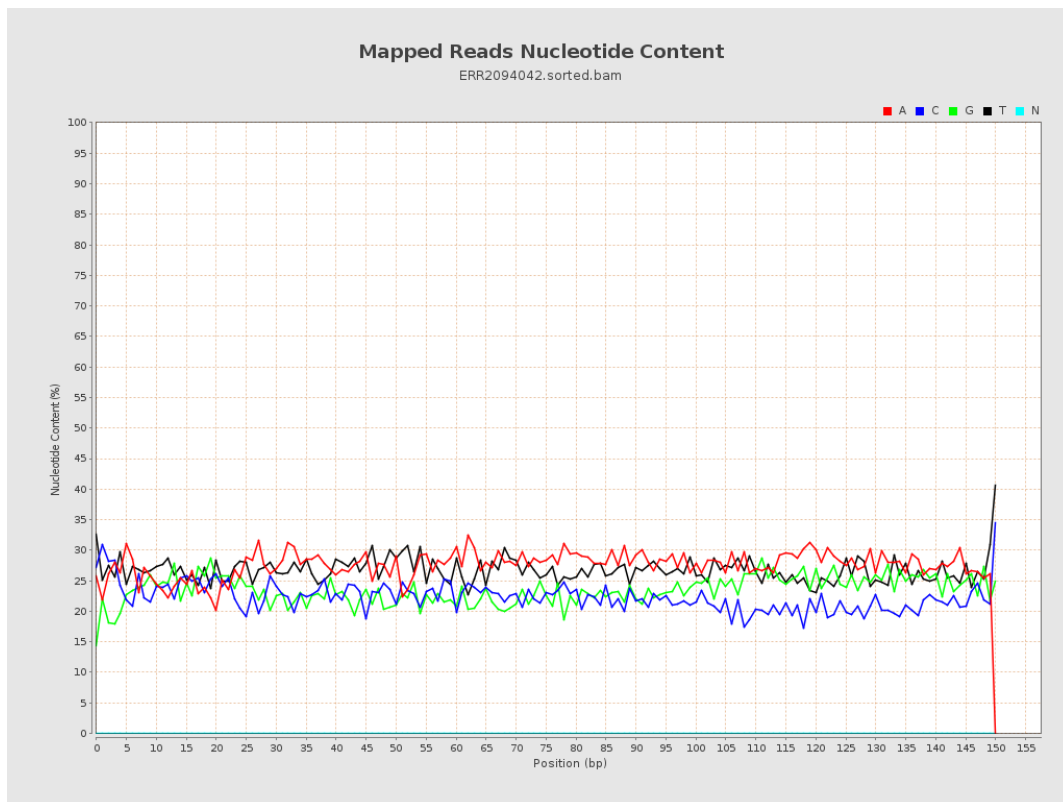
6. Results : Genome Fraction Coverage



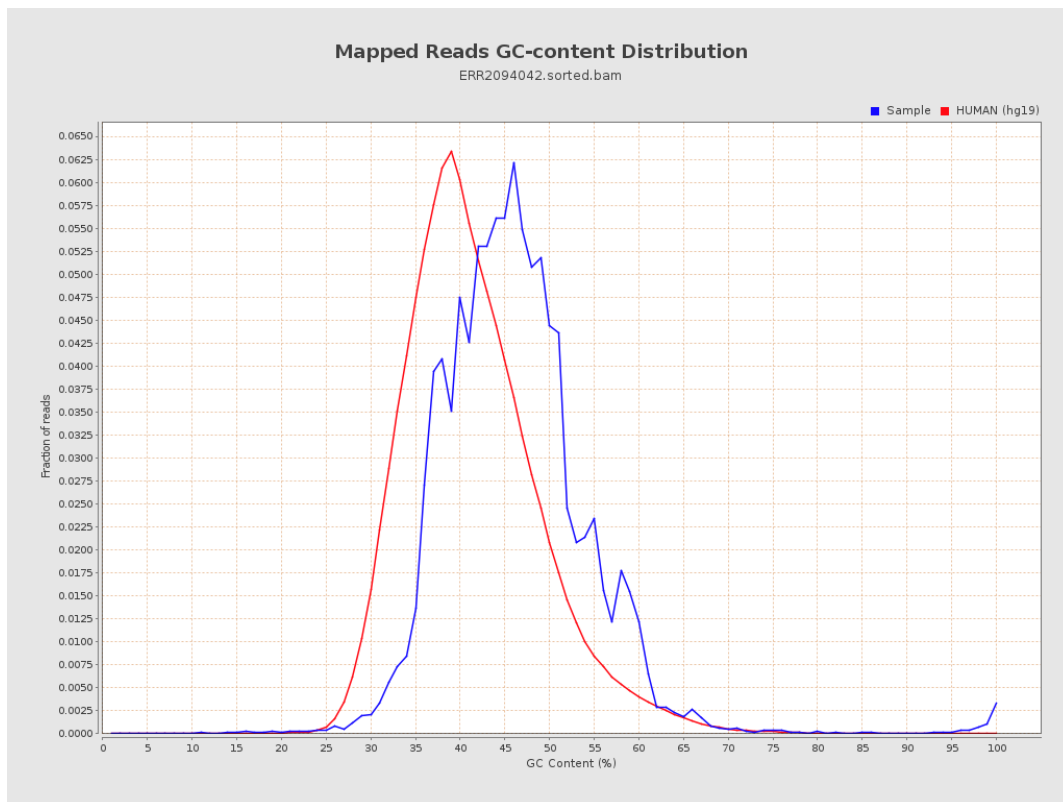
7. Results : Duplication Rate Histogram



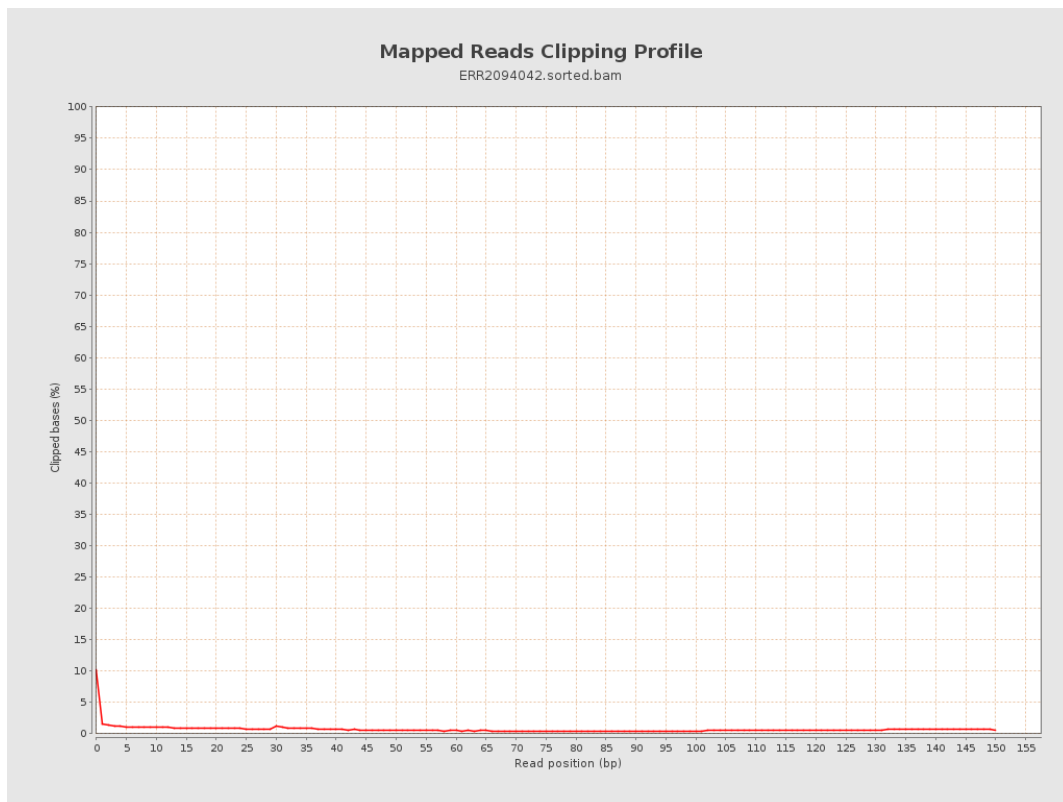
8. Results : Mapped Reads Nucleotide Content



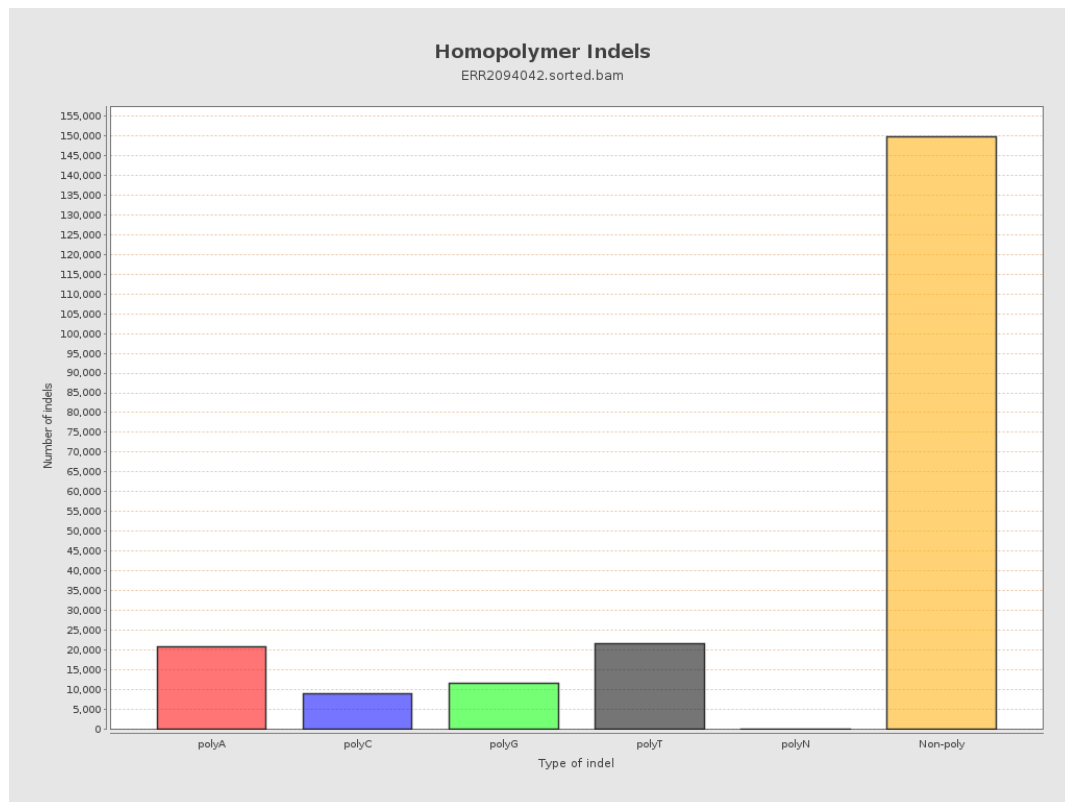
9. Results : Mapped Reads GC-content Distribution



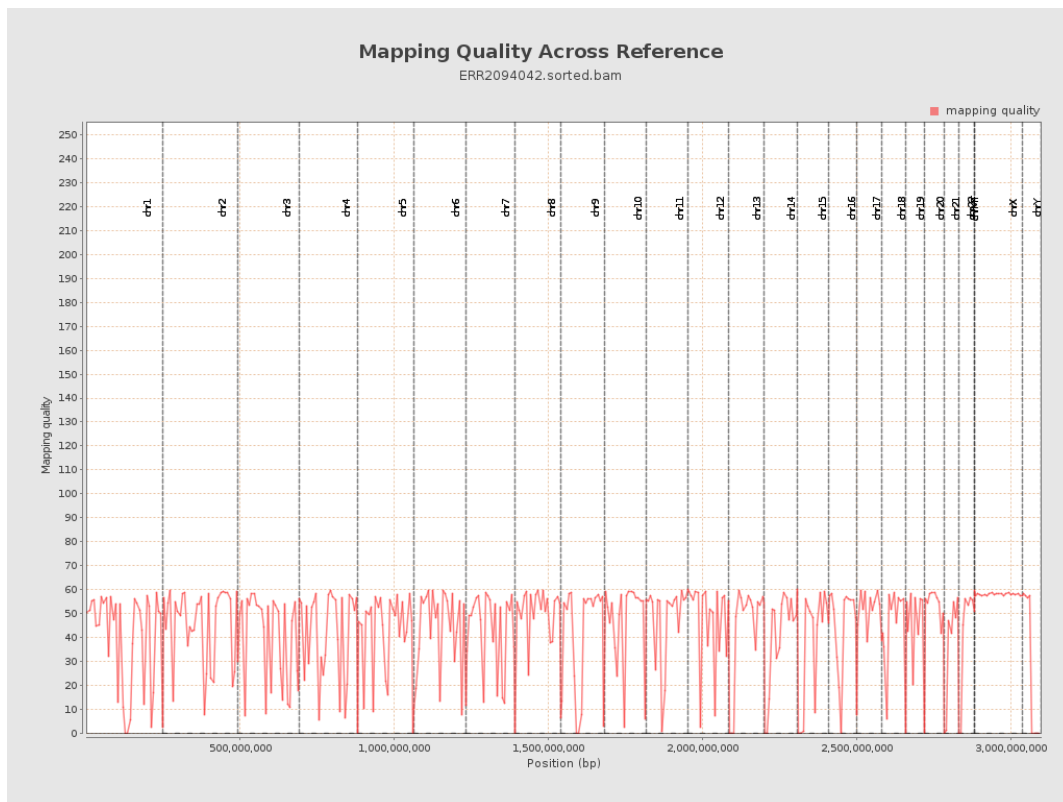
10. Results : Mapped Reads Clipping Profile



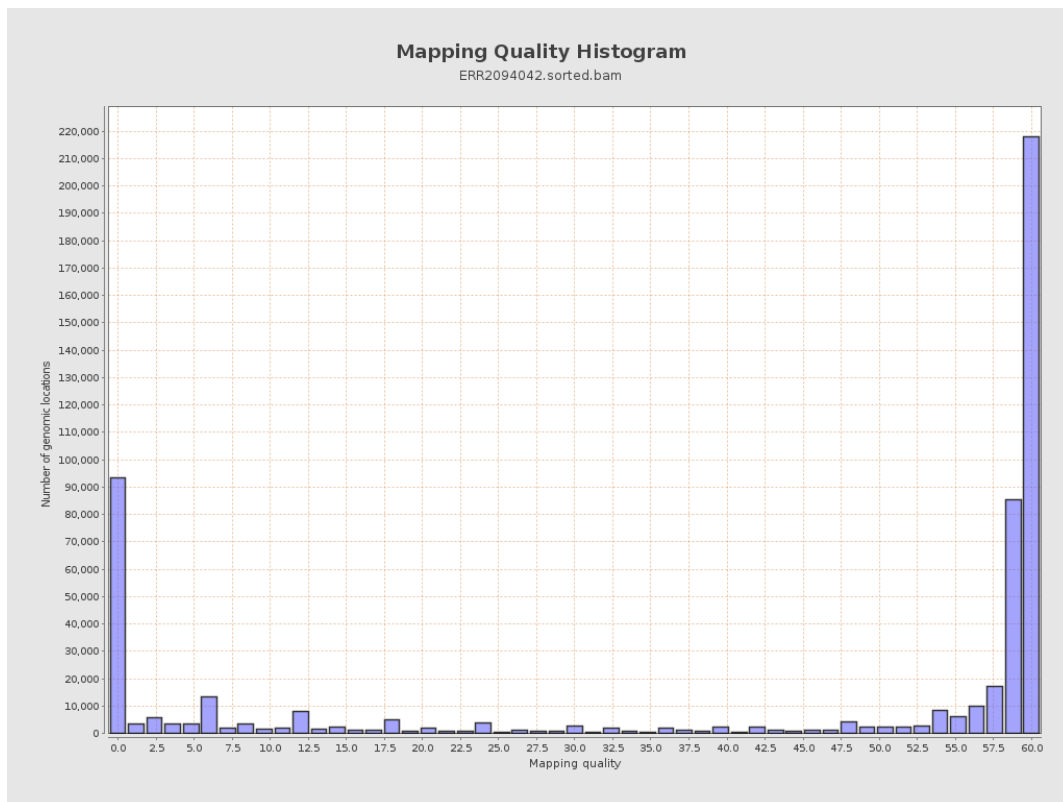
11. Results : Homopolymer Indels



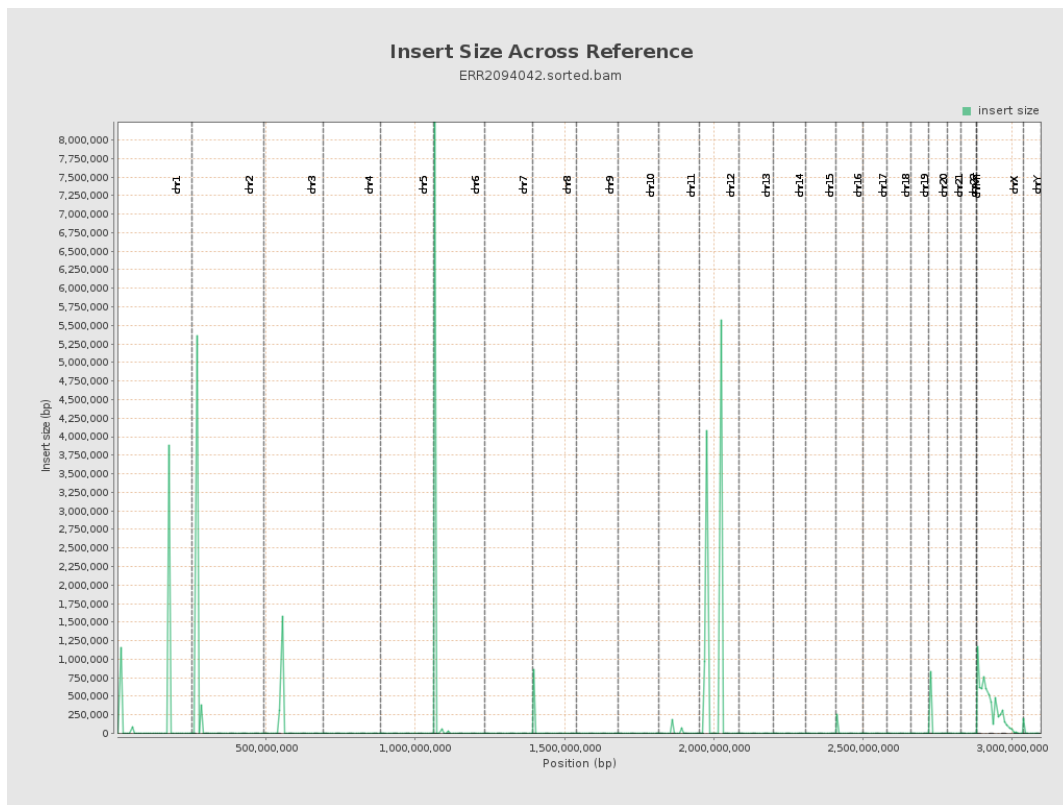
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

