

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:47:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094116.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_ERR2094116 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094116_1.fastq.gz ERR2094116_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:47:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	298,632
Mapped reads	285,283 / 95.53%
Unmapped reads	13,349 / 4.47%
Mapped paired reads	285,283 / 95.53%
Mapped reads, first in pair	143,364 / 48.01%
Mapped reads, second in pair	141,919 / 47.52%
Mapped reads, both in pair	282,922 / 94.74%
Mapped reads, singletons	2,361 / 0.79%
Secondary alignments	0
Supplementary alignments	23,378 / 7.83%
Read min/max/mean length	30 / 151 / 139.16
Duplicated reads (estimated)	271,812 / 91.02%
Duplication rate	52.92%
Clipped reads	157,114 / 52.61%

2.2. ACGT Content

Number/percentage of A's	9,998,396 / 28.67%
Number/percentage of C's	7,514,608 / 21.55%
Number/percentage of T's	9,464,326 / 27.14%
Number/percentage of G's	7,894,212 / 22.64%
Number/percentage of N's	342 / 0%

GC Percentage	44.19%
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2.3. Coverage

Mean	0.0115
Standard Deviation	2.4844

2.4. Mapping Quality

Mean Mapping Quality	40.94
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2.5. Insert size

Mean	2,000,078.05
Standard Deviation	12,623,430.81
P25/Median/P75	112 / 147 / 178

2.6. Mismatches and indels

General error rate	3.64%
Mismatches	1,222,124
Insertions	23,837
Mapped reads with at least one insertion	8.25%
Deletions	95,690
Mapped reads with at least one deletion	32.52%
Homopolymer indels	28.27%

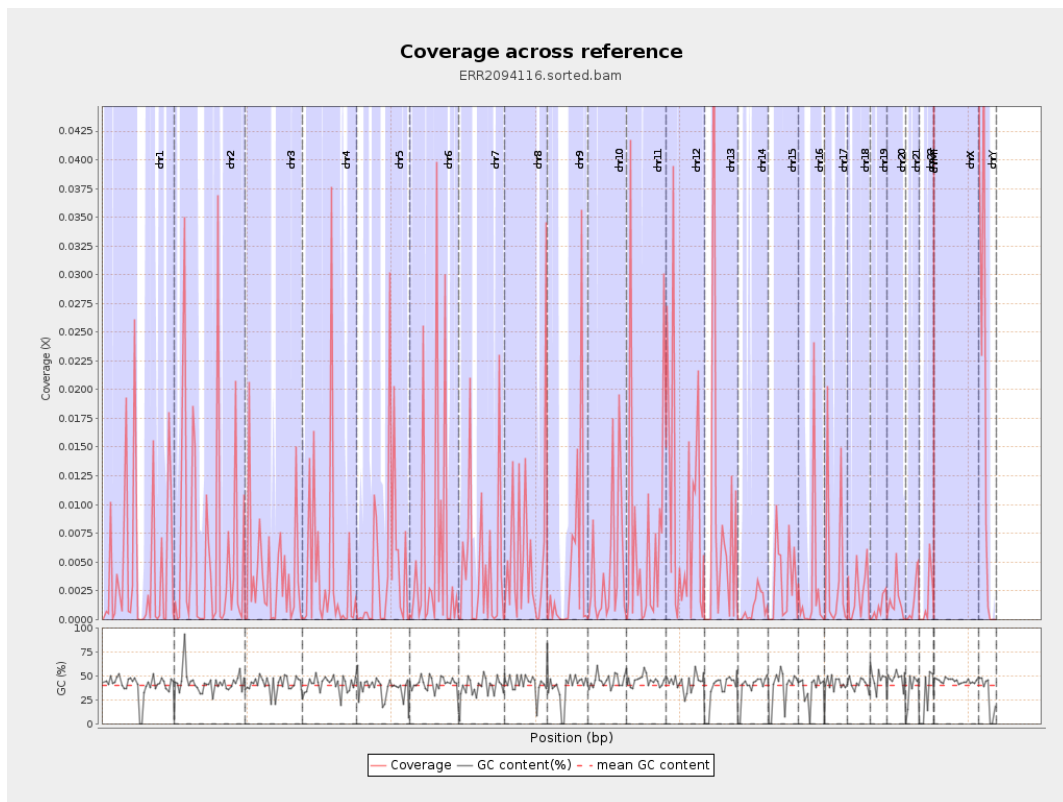
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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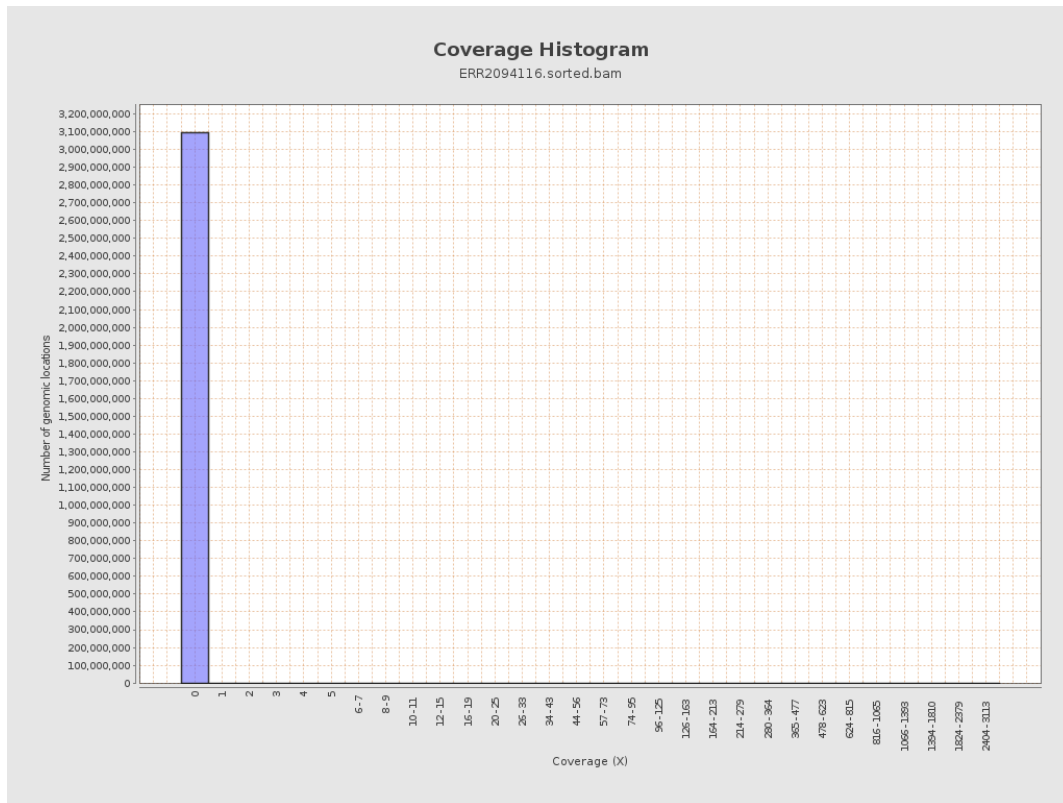
		bases	coverage	deviation
chr1	249250621	1037910	0.0042	1.6431
chr2	243199373	1502301	0.0062	1.8842
chr3	198022430	775203	0.0039	1.159
chr4	191154276	775998	0.0041	1.2132
chr5	180915260	810317	0.0045	1.8582
chr6	171115067	987972	0.0058	2.1936
chr7	159138663	713999	0.0045	1.3936
chr8	146364022	849210	0.0058	1.767
chr9	141213431	569614	0.004	1.3367
chr10	135534747	580516	0.0043	1.1488
chr11	135006516	1016087	0.0075	1.9801
chr12	133851895	1251328	0.0093	1.9776
chr13	115169878	882714	0.0077	2.3116
chr14	107349540	106583	0.001	0.3125
chr15	102531392	326610	0.0032	0.772
chr16	90354753	254411	0.0028	1.5314
chr17	81195210	324199	0.004	1.2742
chr18	78077248	181728	0.0023	0.5665
chr19	59128983	57629	0.001	0.2144
chr20	63025520	102868	0.0016	0.4716
chr21	48129895	78759	0.0016	0.3743
chr22	51304566	77807	0.0015	0.5914
chrMT	16571	190237	11.4801	60.2894
chrX	155270560	21259818	0.1369	8.549

chrY	59373566	853385	0.0144	3.7064
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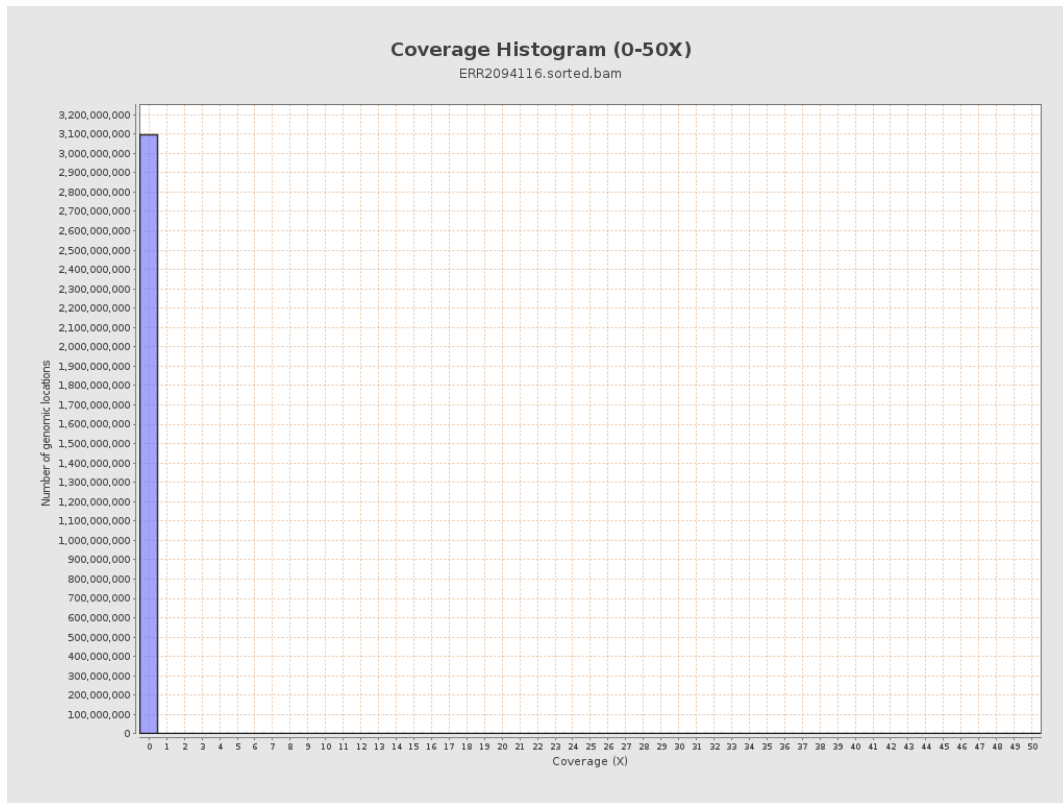
3. Results : Coverage across reference



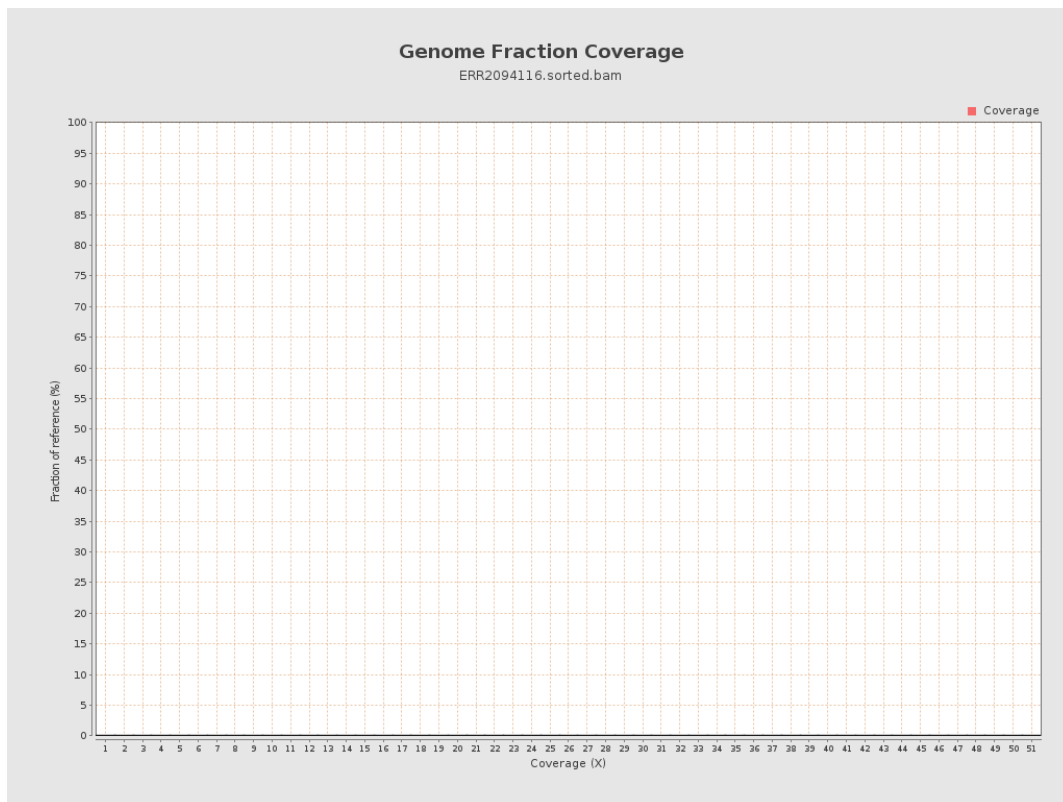
4. Results : Coverage Histogram



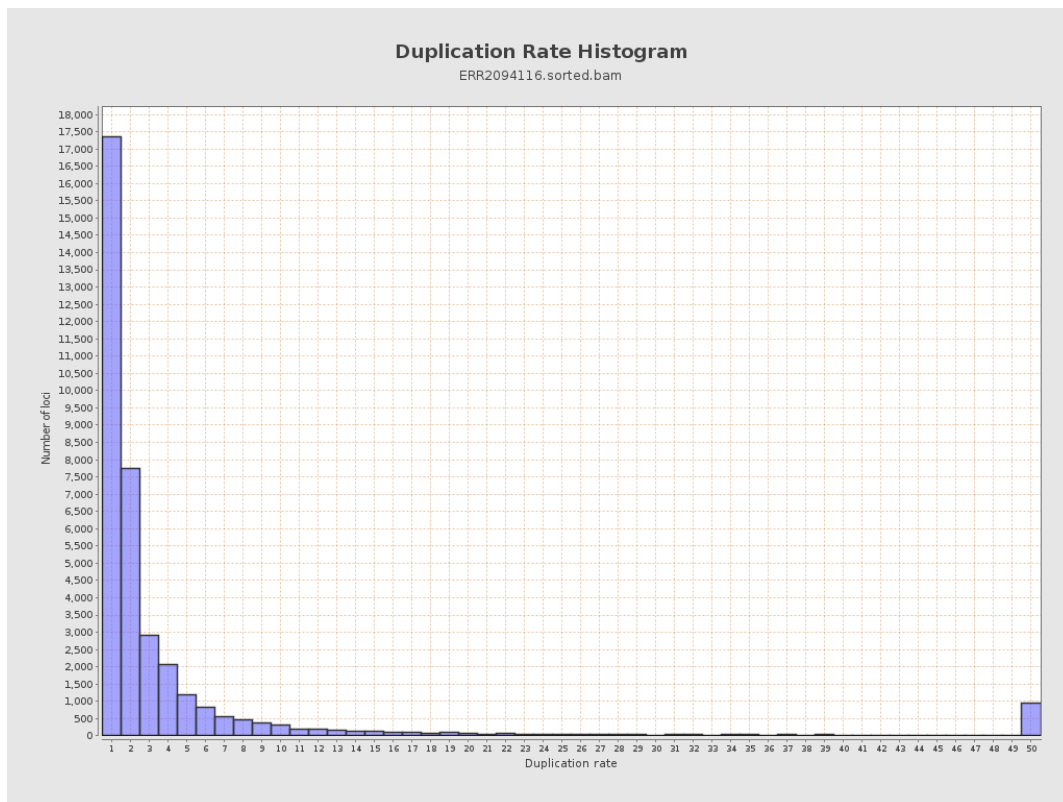
5. Results : Coverage Histogram (0-50X)



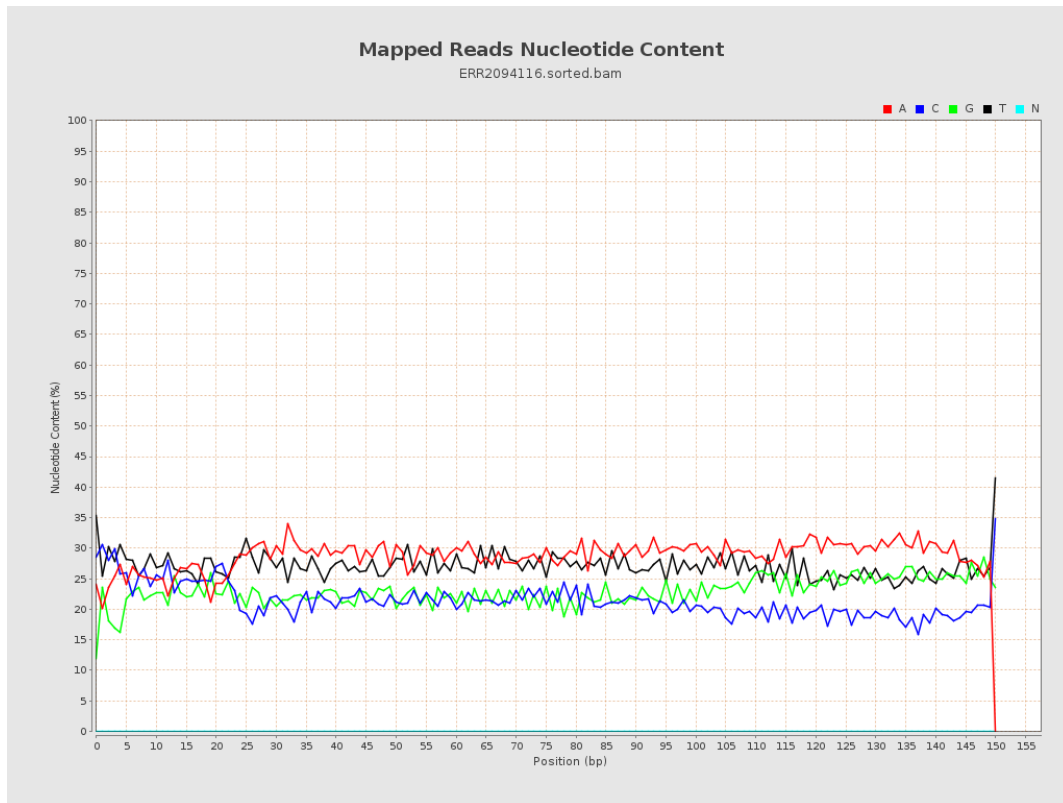
6. Results : Genome Fraction Coverage



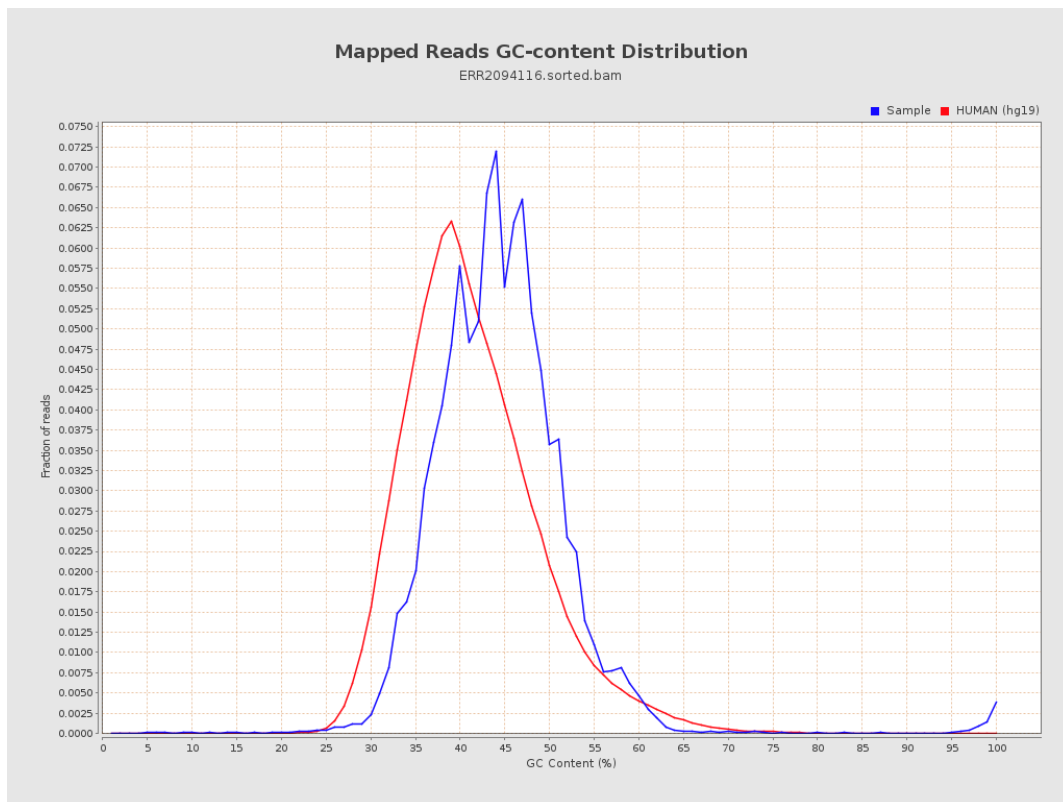
7. Results : Duplication Rate Histogram



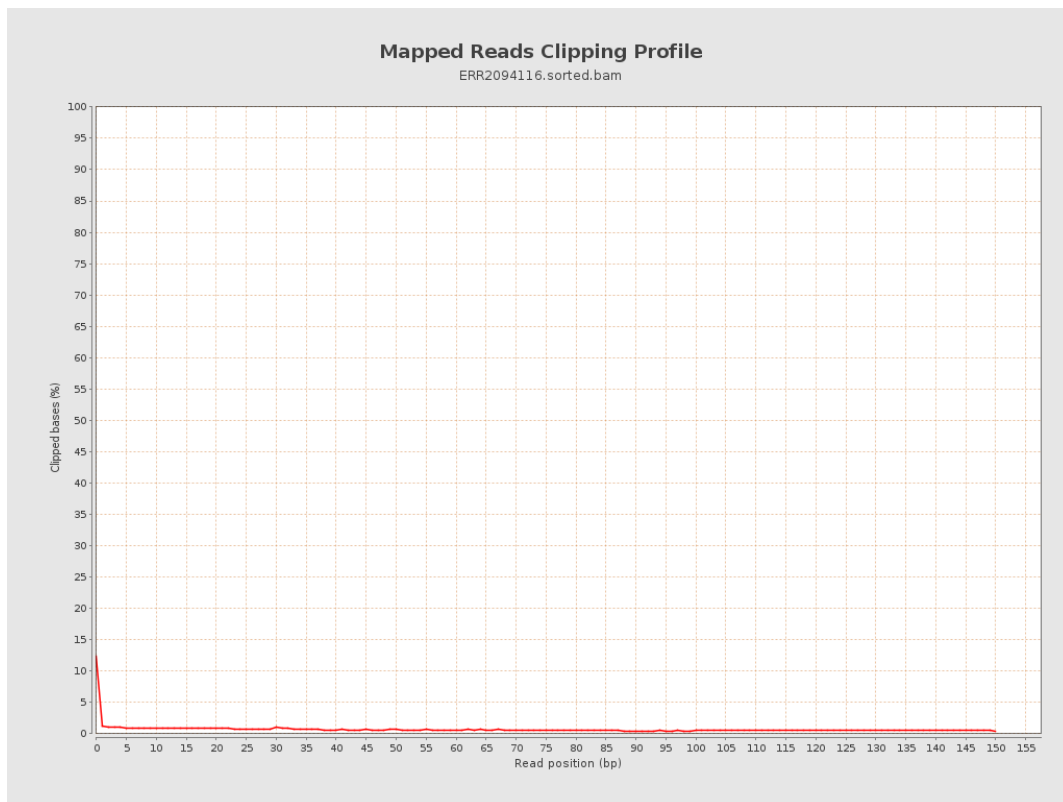
8. Results : Mapped Reads Nucleotide Content



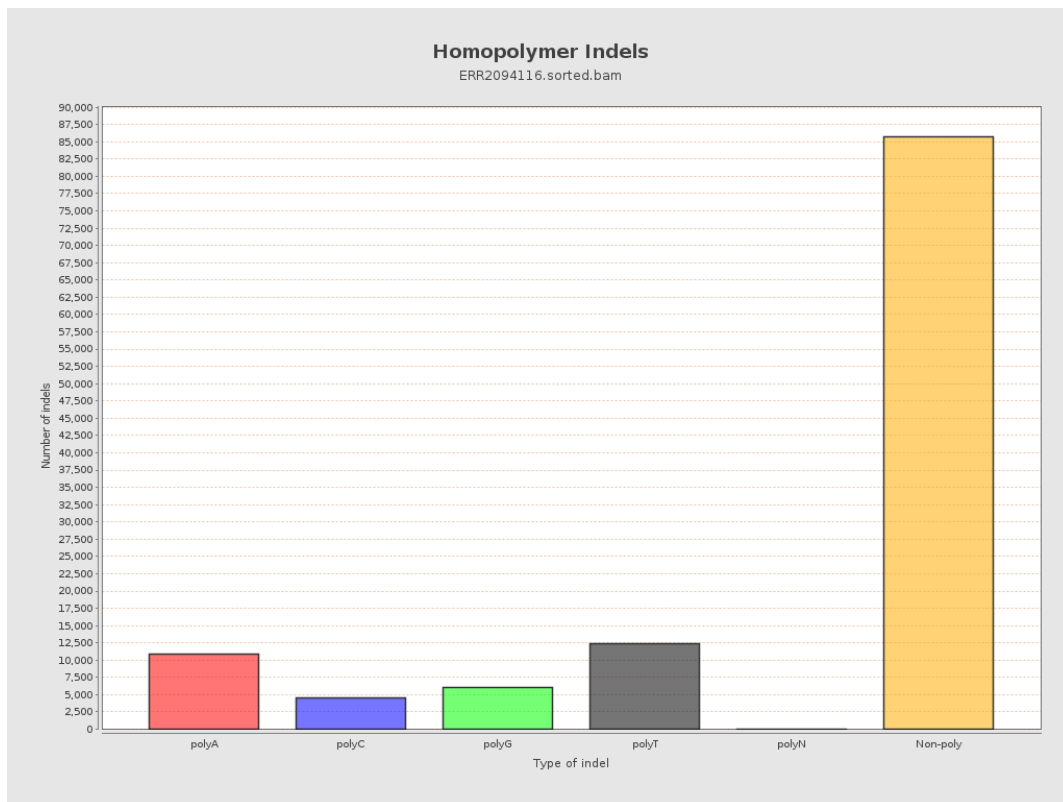
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



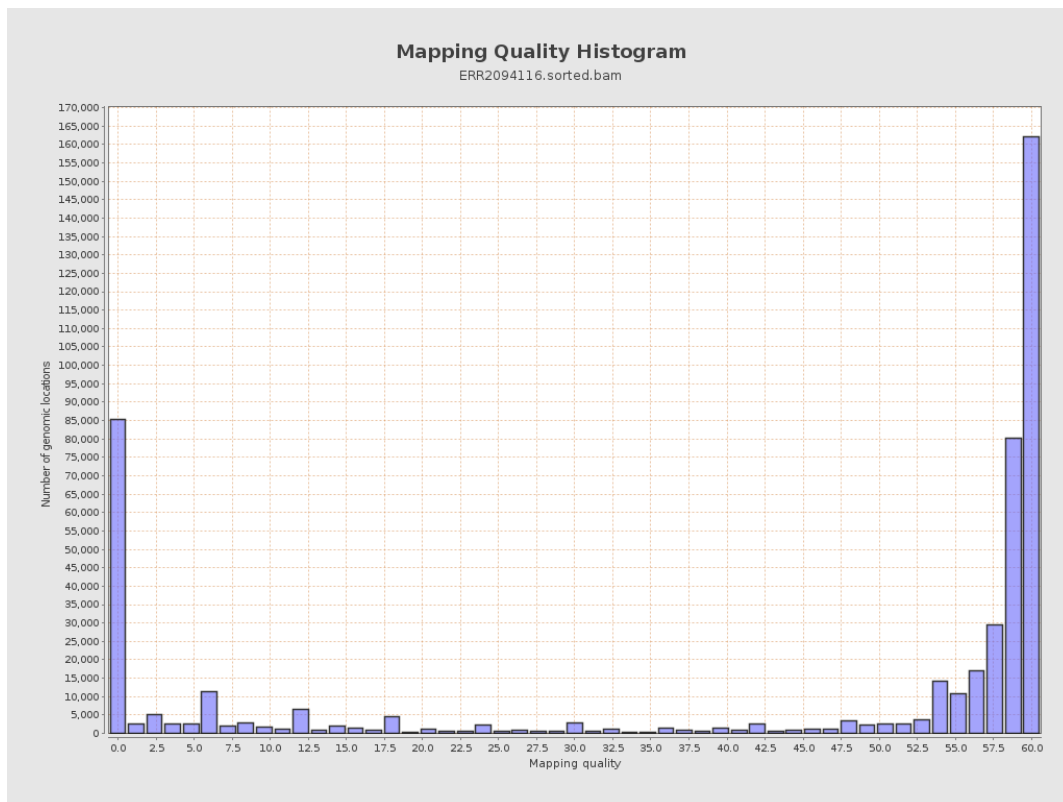
11. Results : Homopolymer Indels



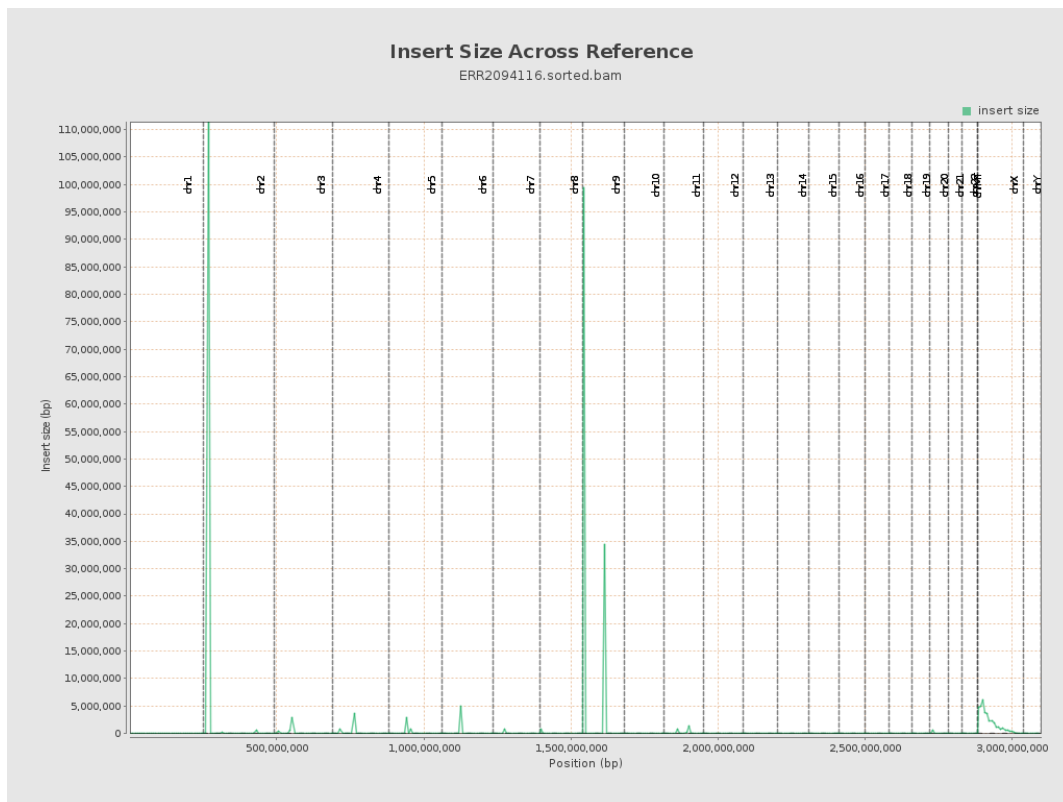
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

