

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 02:50:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094133.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_ERR2094133 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094133_1.fastq.gz ERR2094133_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 02:50:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	502,792
Mapped reads	470,693 / 93.62%
Unmapped reads	32,099 / 6.38%
Mapped paired reads	470,693 / 93.62%
Mapped reads, first in pair	235,954 / 46.93%
Mapped reads, second in pair	234,739 / 46.69%
Mapped reads, both in pair	468,038 / 93.09%
Mapped reads, singletons	2,655 / 0.53%
Secondary alignments	0
Supplementary alignments	4,328 / 0.86%
Read min/max/mean length	30 / 151 / 145.3
Duplicated reads (estimated)	469,559 / 93.39%
Duplication rate	38.78%
Clipped reads	107,710 / 21.42%

2.2. ACGT Content

Number/percentage of A's	19,001,758 / 27.85%
Number/percentage of C's	14,628,082 / 21.44%
Number/percentage of T's	19,325,631 / 28.32%
Number/percentage of G's	15,279,097 / 22.39%
Number/percentage of N's	1,021 / 0%

GC Percentage	43.83%
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2.3. Coverage

Mean	0.0221
Standard Deviation	36.4651

2.4. Mapping Quality

Mean Mapping Quality	23.95
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2.5. Insert size

Mean	17,424.08
Standard Deviation	1,110,101.33
P25/Median/P75	212 / 231 / 261

2.6. Mismatches and indels

General error rate	1.74%
Mismatches	1,147,745
Insertions	25,552
Mapped reads with at least one insertion	5.35%
Deletions	63,305
Mapped reads with at least one deletion	13.08%
Homopolymer indels	62.54%

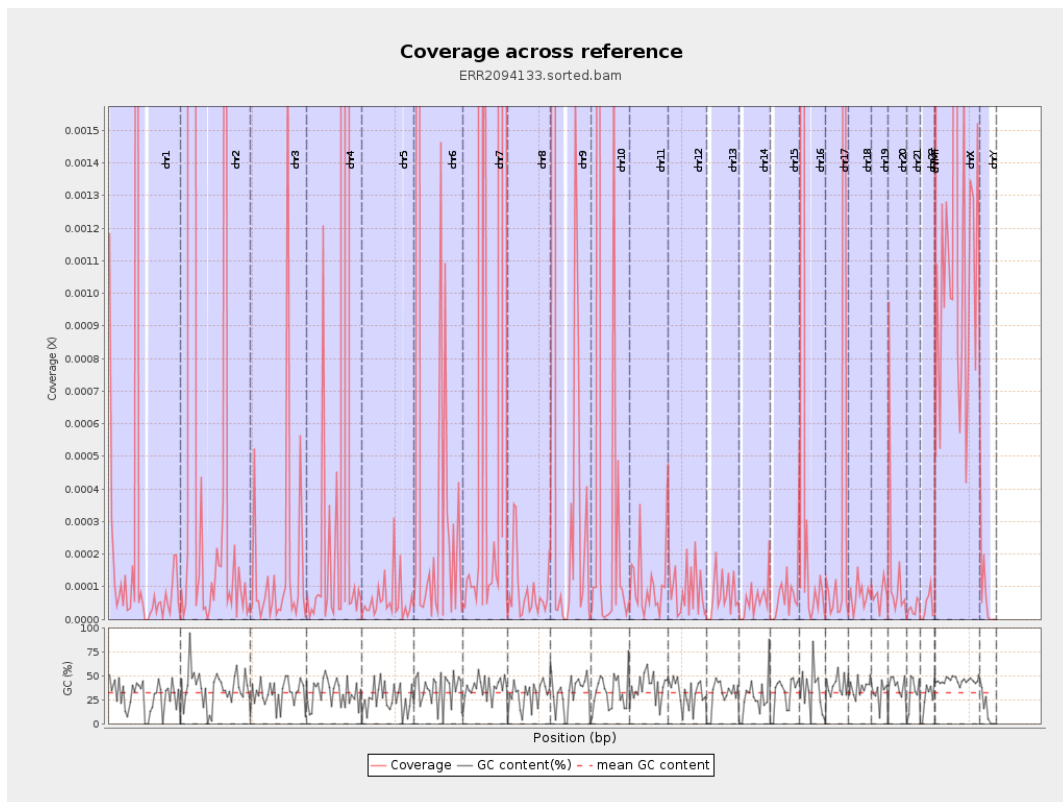
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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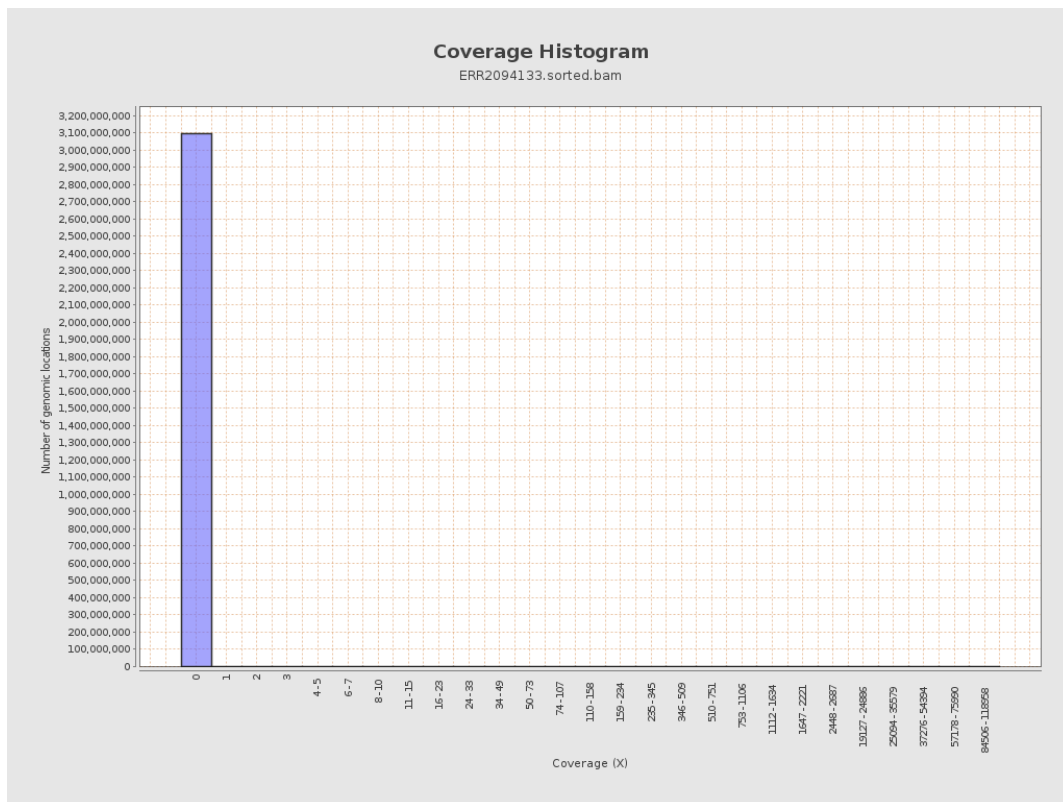
		bases	coverage	deviation
chr1	249250621	69724	0.0003	0.2388
chr2	243199373	1167278	0.0048	3.013
chr3	198022430	32288	0.0002	0.0921
chr4	191154276	443679	0.0023	1.7
chr5	180915260	11193	0.0001	0.0177
chr6	171115067	115523	0.0007	0.3234
chr7	159138663	5218033	0.0328	28.5569
chr8	146364022	13428	0.0001	0.0387
chr9	141213431	170634	0.0012	0.8042
chr10	135534747	78188	0.0006	0.2477
chr11	135006516	15266	0.0001	0.0287
chr12	133851895	12114	0.0001	0.0194
chr13	115169878	8169	0.0001	0.0155
chr14	107349540	6705	0.0001	0.0303
chr15	102531392	7411	0.0001	0.0184
chr16	90354753	124706	0.0014	0.9737
chr17	81195210	42959	0.0005	0.3095
chr18	78077248	5865	0.0001	0.0115
chr19	59128983	4347	0.0001	0.0105
chr20	63025520	9729	0.0002	0.0534
chr21	48129895	1583	0	0.0086
chr22	51304566	2117	0	0.0086
chrMT	16571	60592004	3,656.5086	15,068.0503
chrX	155270560	178883	0.0012	0.1708

chrY	59373566	6329	0.0001	0.0355
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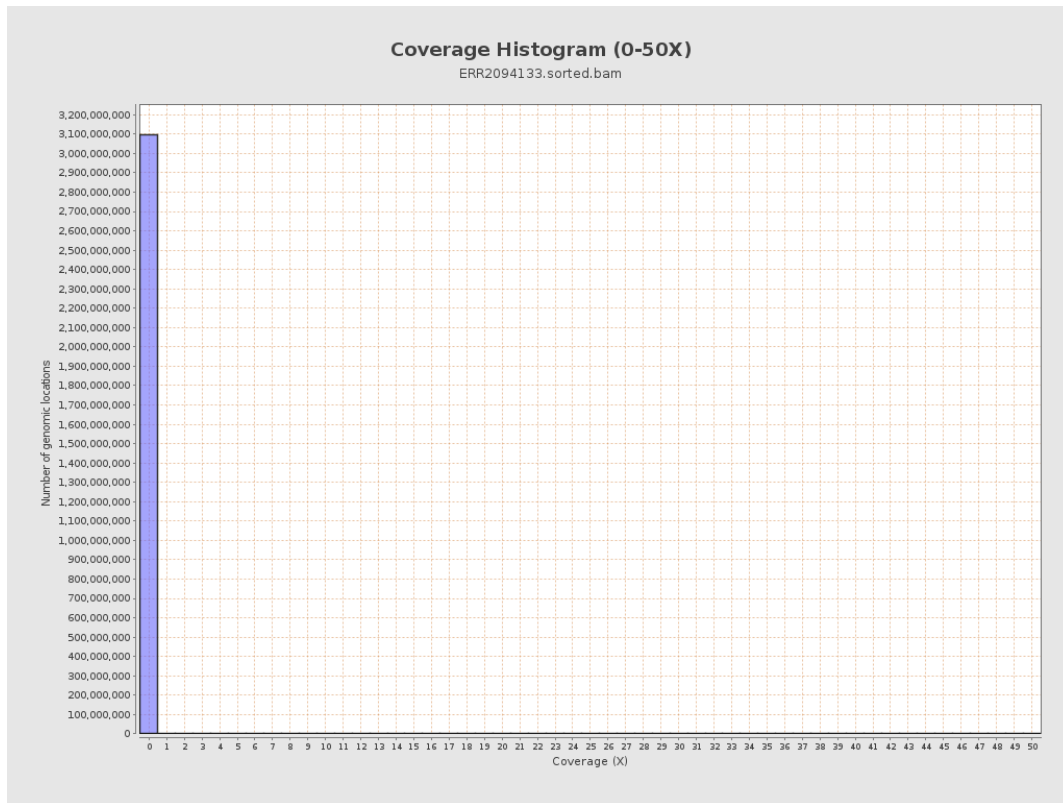
3. Results : Coverage across reference



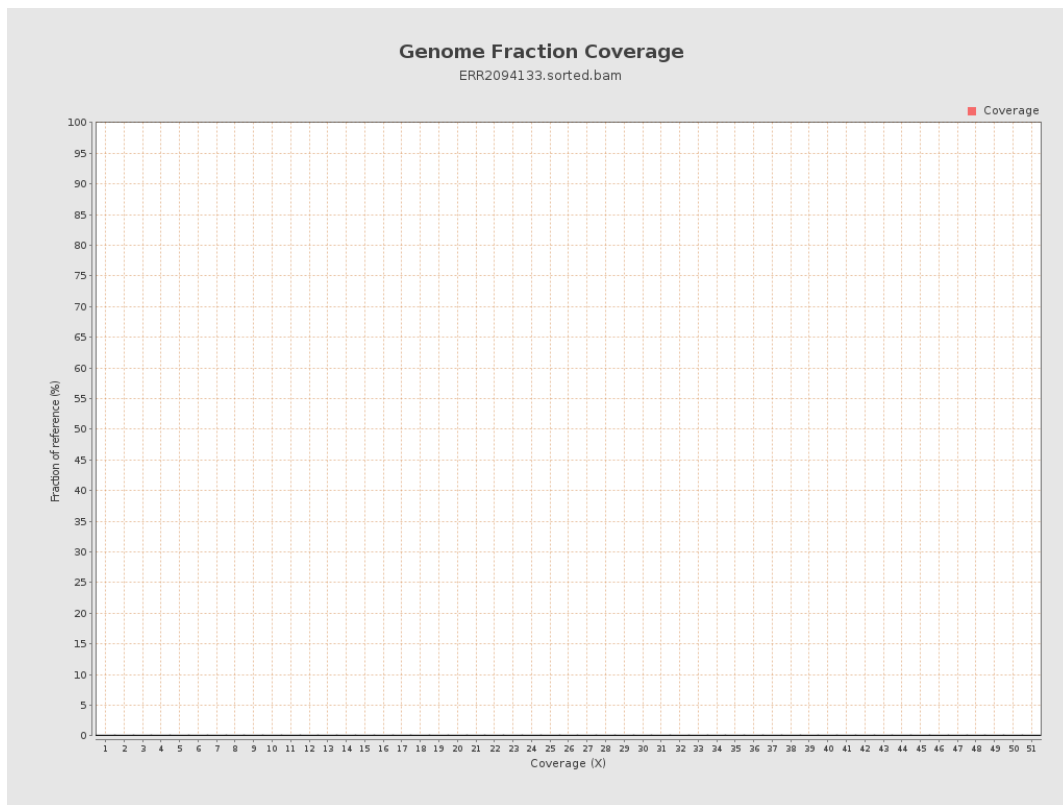
4. Results : Coverage Histogram



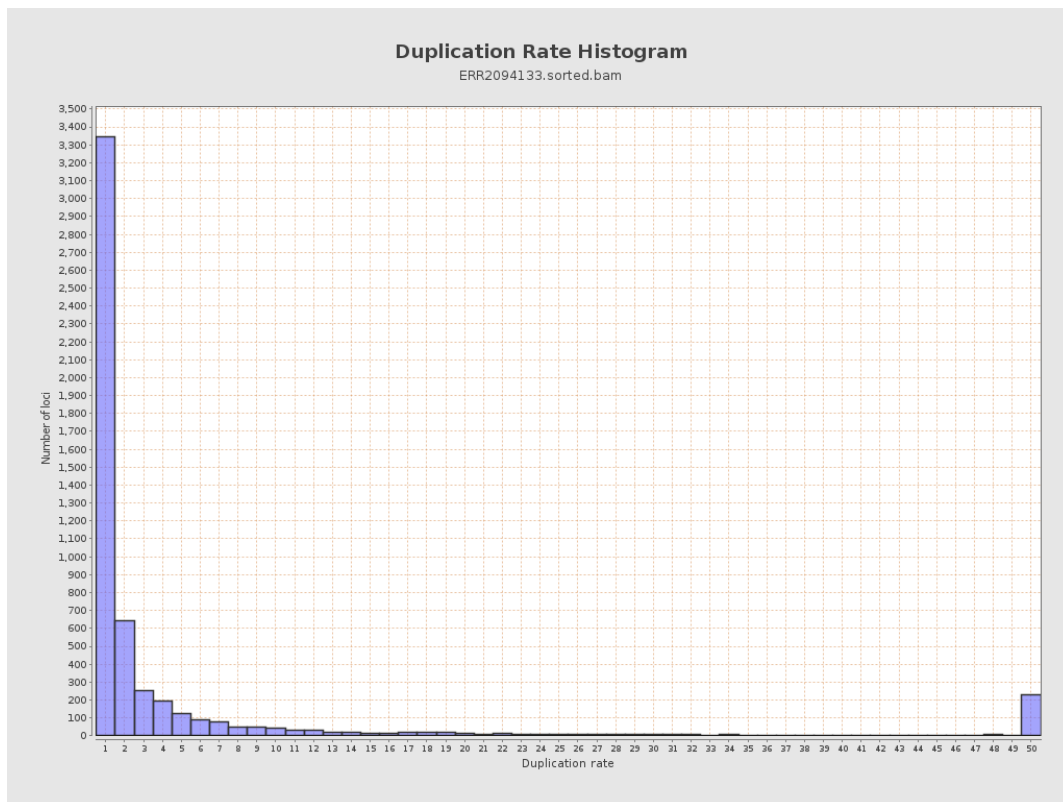
5. Results : Coverage Histogram (0-50X)



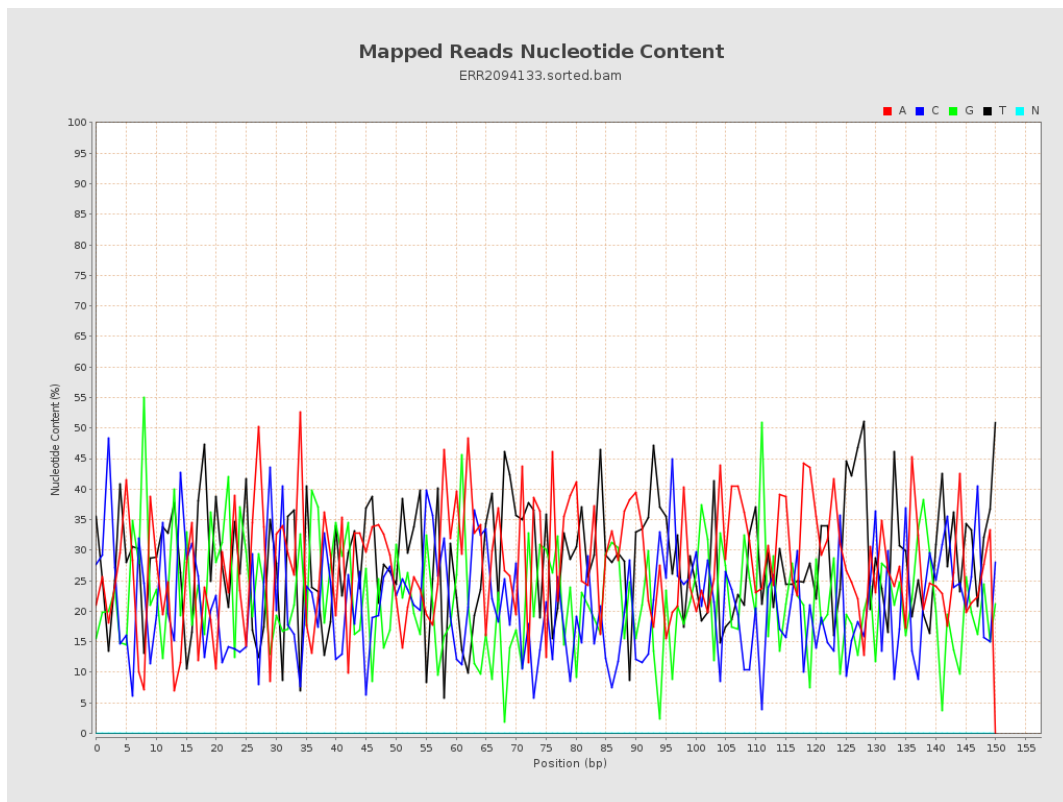
6. Results : Genome Fraction Coverage



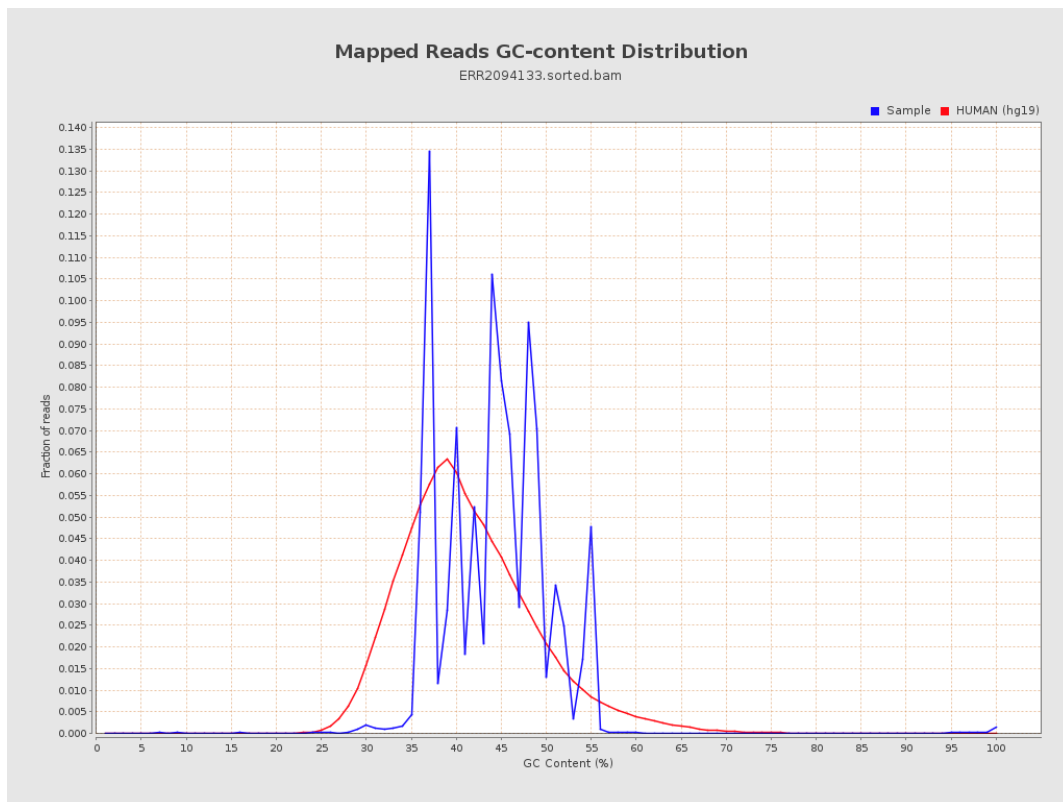
7. Results : Duplication Rate Histogram



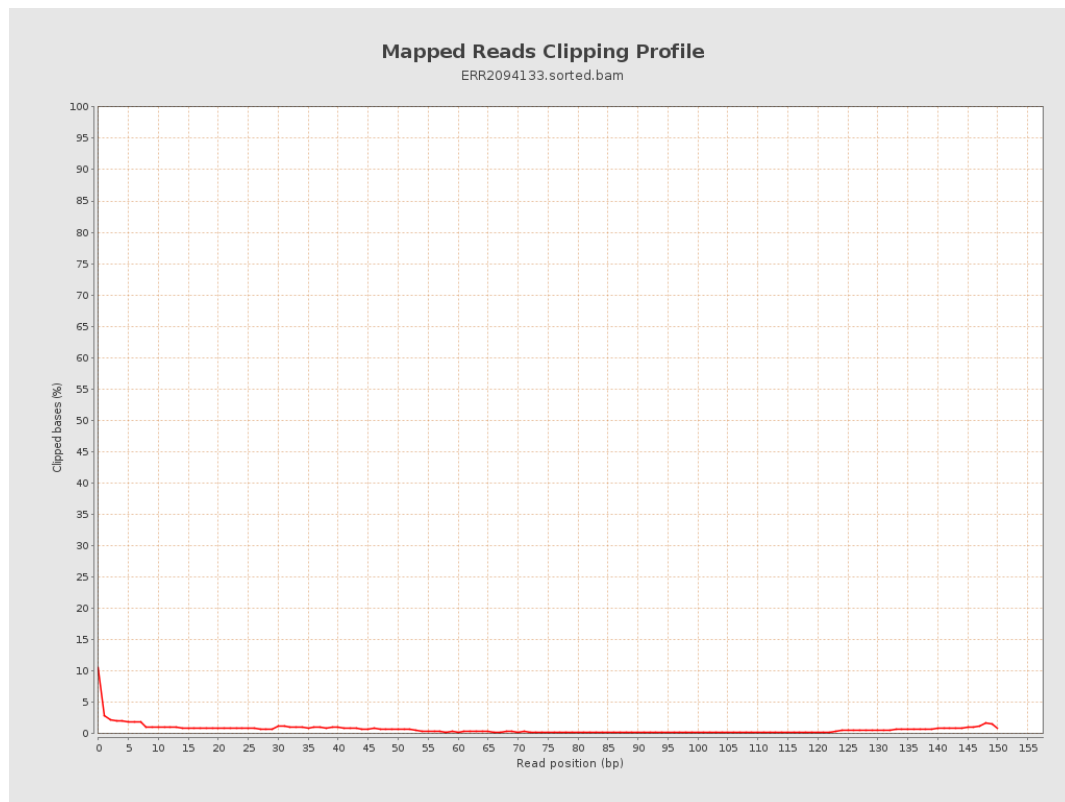
8. Results : Mapped Reads Nucleotide Content



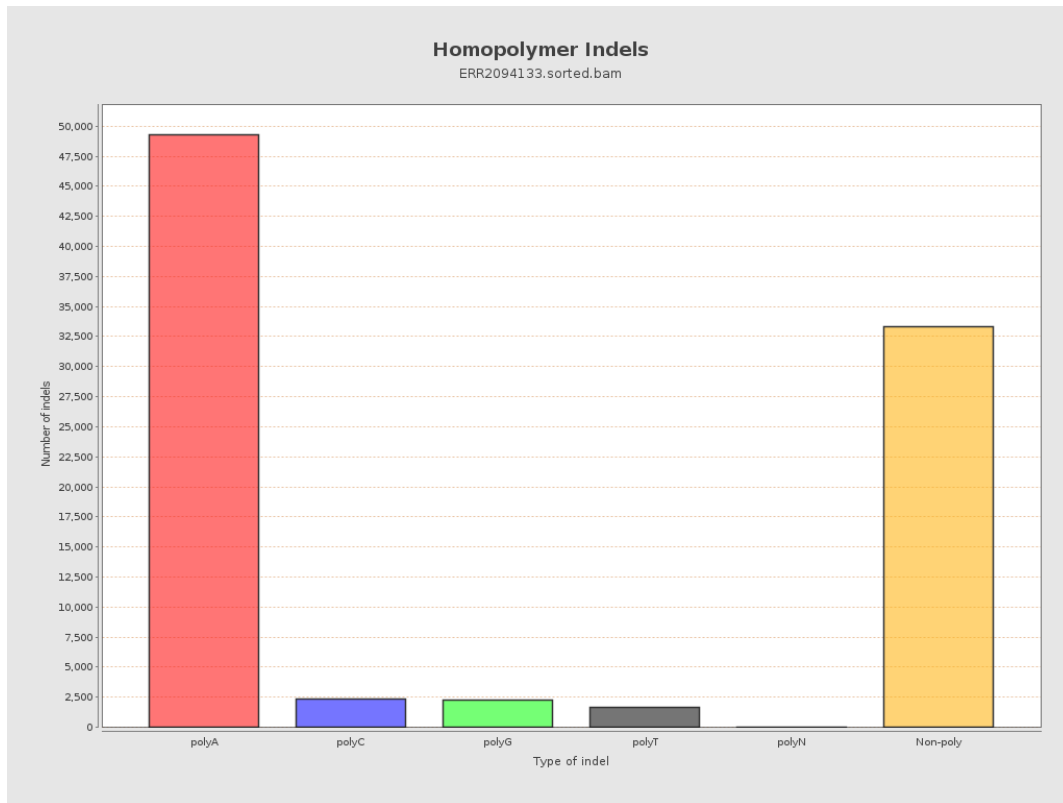
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



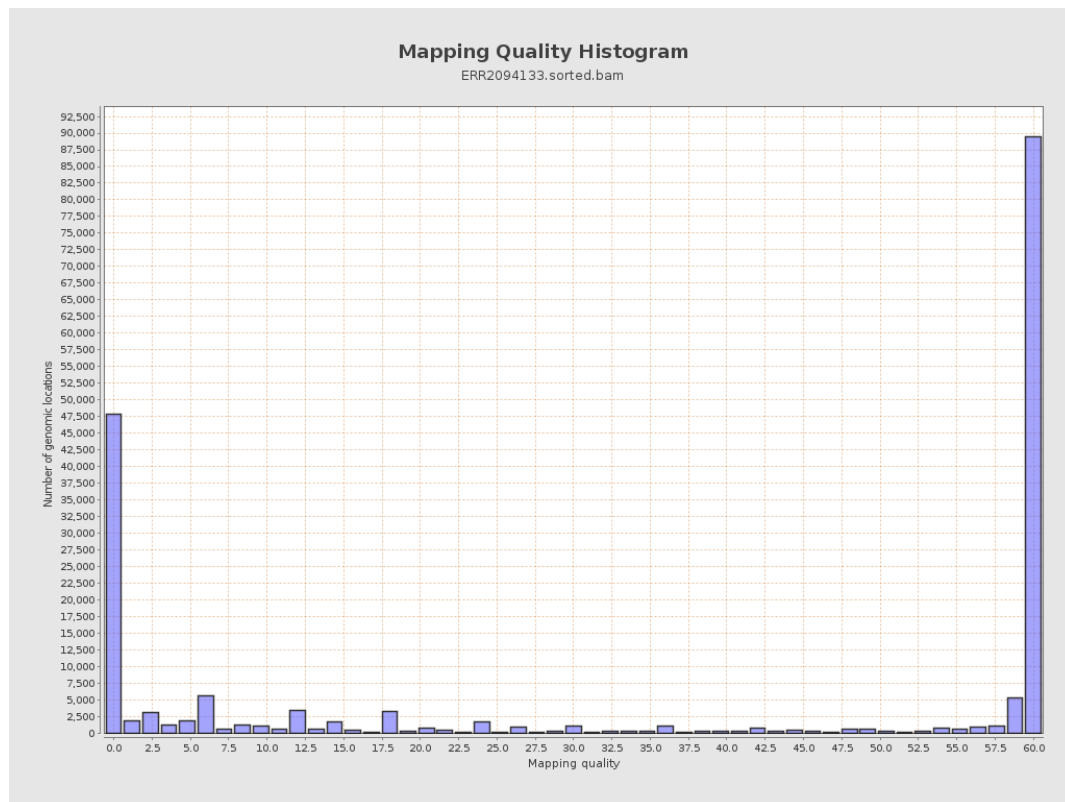
11. Results : Homopolymer Indels



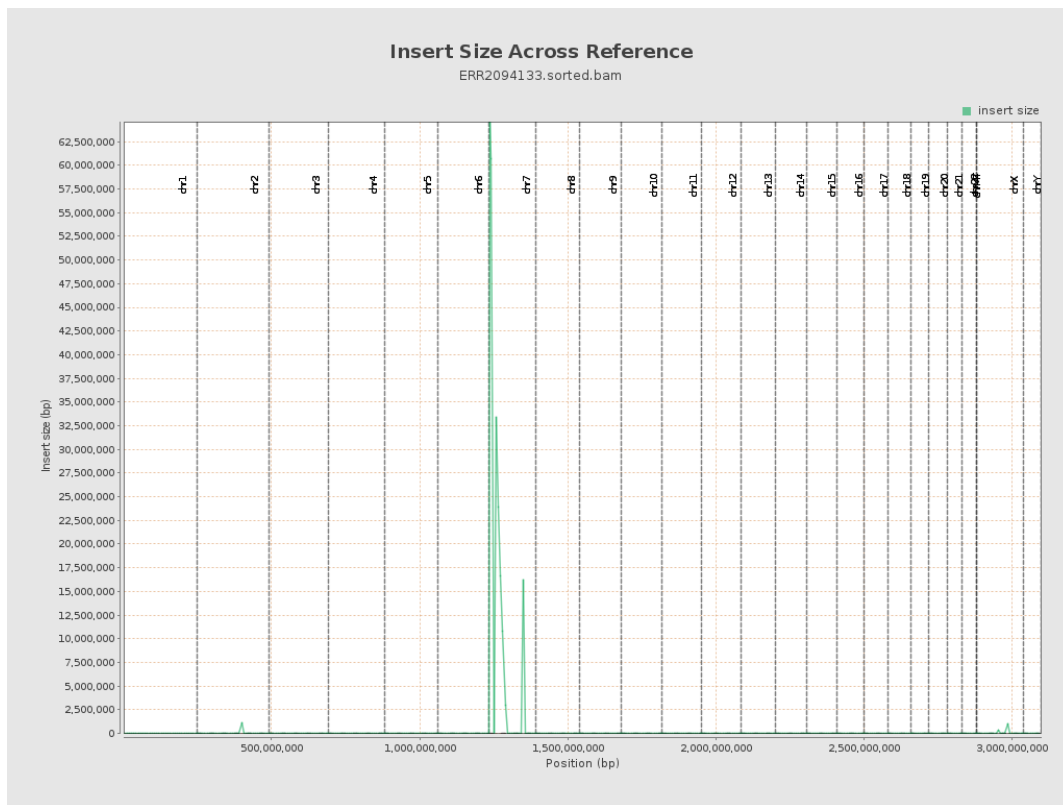
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

