

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:37:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094033.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_ERR2094033 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094033_1.fastq.gz ERR2094033_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:37:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	352,050
Mapped reads	319,644 / 90.8%
Unmapped reads	32,406 / 9.2%
Mapped paired reads	319,644 / 90.8%
Mapped reads, first in pair	160,834 / 45.68%
Mapped reads, second in pair	158,810 / 45.11%
Mapped reads, both in pair	314,560 / 89.35%
Mapped reads, singletons	5,084 / 1.44%
Secondary alignments	0
Supplementary alignments	19,997 / 5.68%
Read min/max/mean length	30 / 151 / 139.28
Duplicated reads (estimated)	288,024 / 81.81%
Duplication rate	44.5%
Clipped reads	172,825 / 49.09%

2.2. ACGT Content

Number/percentage of A's	11,147,962 / 28.32%
Number/percentage of C's	8,602,529 / 21.85%
Number/percentage of T's	10,560,035 / 26.83%
Number/percentage of G's	9,054,189 / 23%
Number/percentage of N's	563 / 0%

GC Percentage	44.85%
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2.3. Coverage

Mean	0.013
Standard Deviation	3.2971

2.4. Mapping Quality

Mean Mapping Quality	47.11
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2.5. Insert size

Mean	677,628.47
Standard Deviation	7,602,530.43
P25/Median/P75	127 / 162 / 201

2.6. Mismatches and indels

General error rate	3.52%
Mismatches	1,339,721
Insertions	23,487
Mapped reads with at least one insertion	7.2%
Deletions	105,136
Mapped reads with at least one deletion	31.72%
Homopolymer indels	30.8%

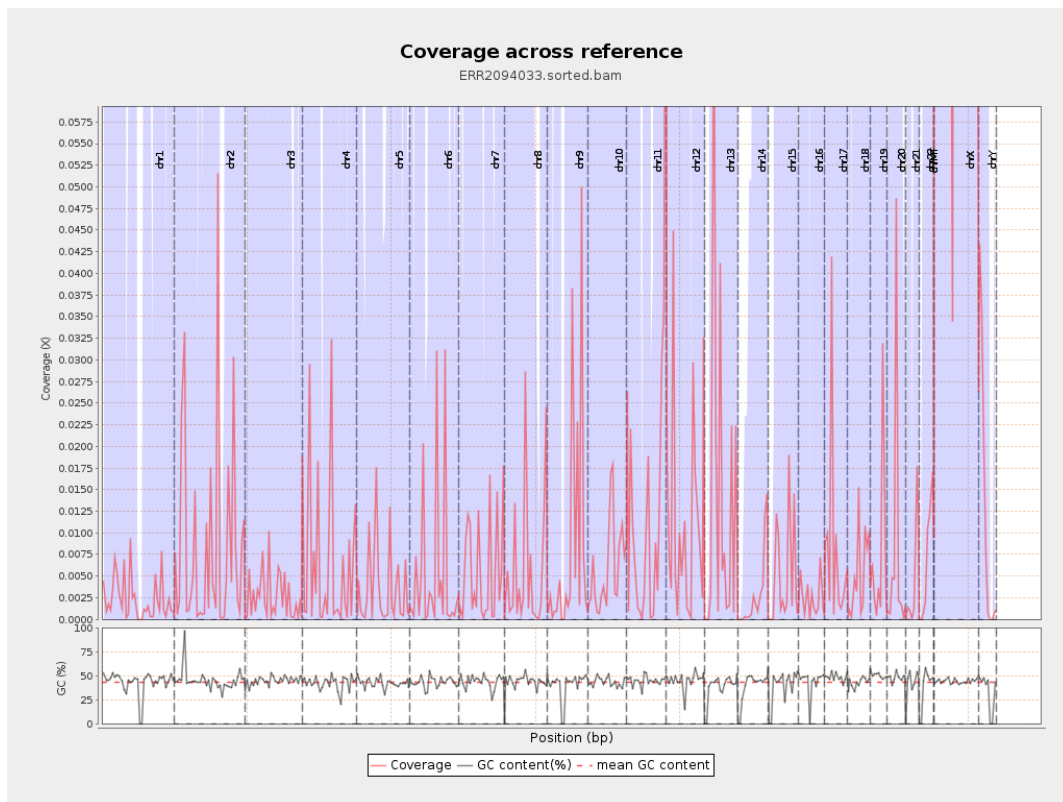
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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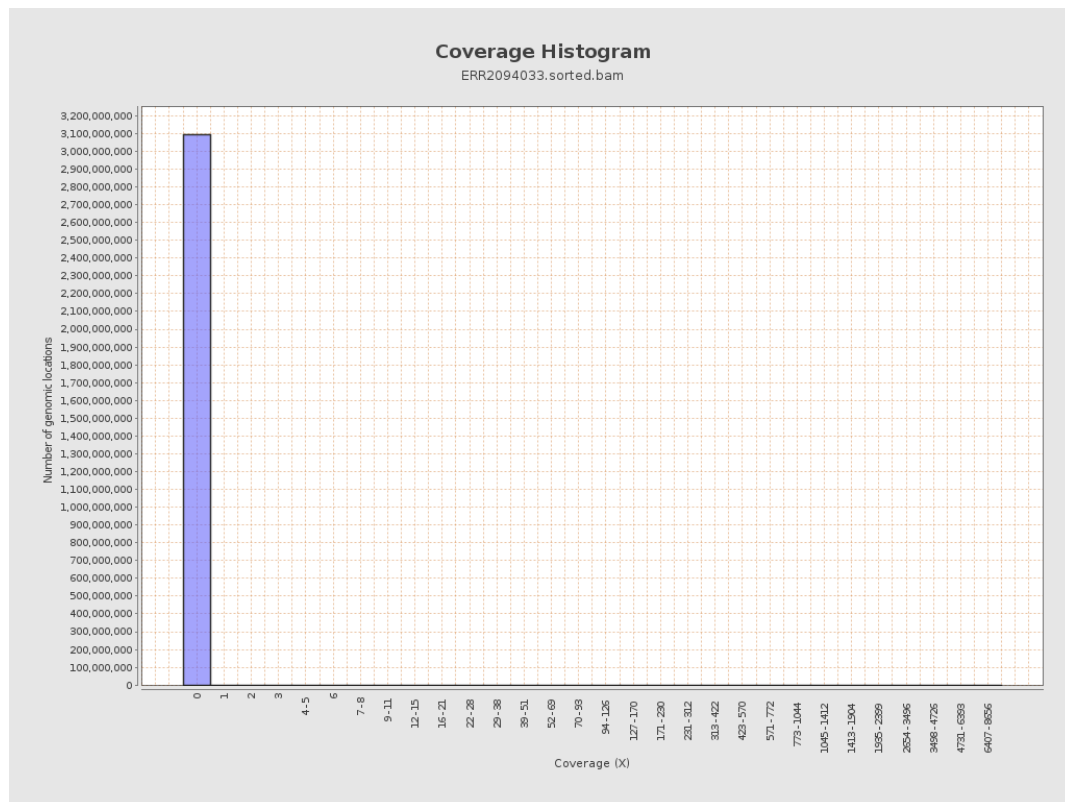
		bases	coverage	deviation
chr1	249250621	604047	0.0024	0.5304
chr2	243199373	2049964	0.0084	2.3979
chr3	198022430	529459	0.0027	0.6597
chr4	191154276	1296271	0.0068	1.8008
chr5	180915260	675442	0.0037	1.0541
chr6	171115067	907876	0.0053	2.0304
chr7	159138663	871140	0.0055	1.2429
chr8	146364022	824384	0.0056	1.5333
chr9	141213431	1112587	0.0079	2.1864
chr10	135534747	820567	0.0061	1.3284
chr11	135006516	1456165	0.0108	2.0615
chr12	133851895	1451045	0.0108	2.4267
chr13	115169878	1566997	0.0136	3.2077
chr14	107349540	315143	0.0029	0.4044
chr15	102531392	510927	0.005	1.0141
chr16	90354753	220960	0.0024	0.3185
chr17	81195210	662712	0.0082	1.9663
chr18	78077248	406864	0.0052	1.3695
chr19	59128983	396941	0.0067	2.1234
chr20	63025520	496340	0.0079	2.7792
chr21	48129895	228582	0.0047	1.0419
chr22	51304566	347772	0.0068	0.5817
chrMT	16571	3979257	240.1338	1,000.7974
chrX	155270560	17640947	0.1136	6.8287

chrY	59373566	728978	0.0123	2.2942
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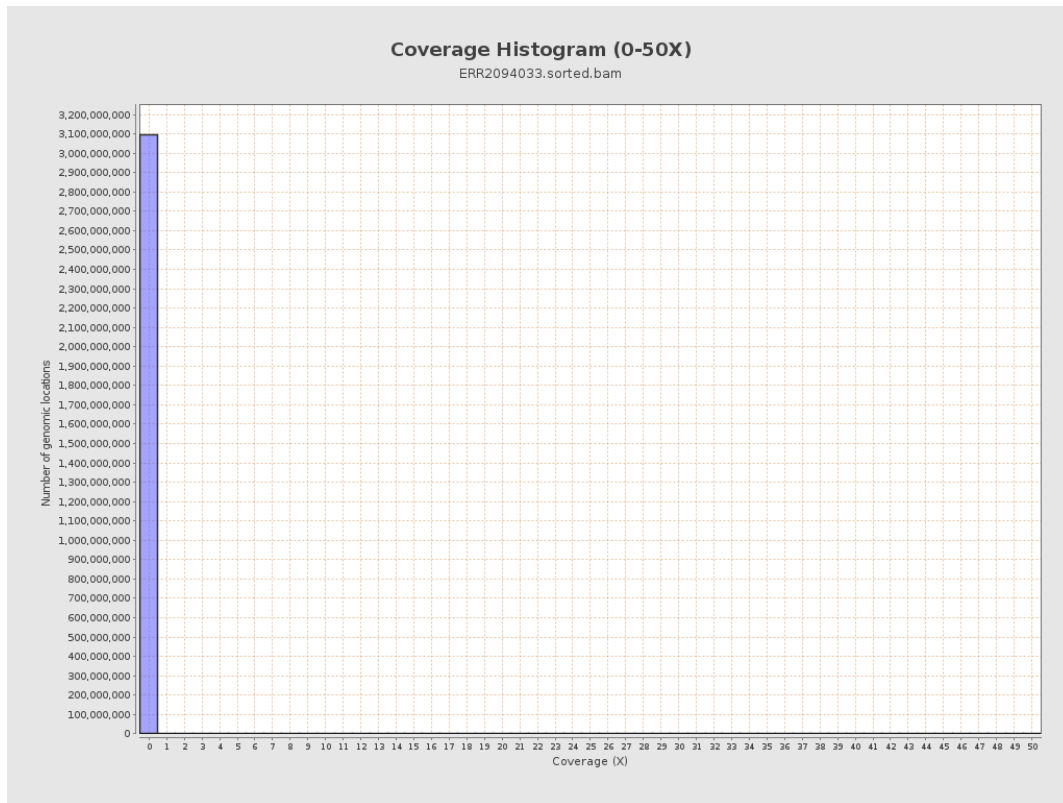
3. Results : Coverage across reference



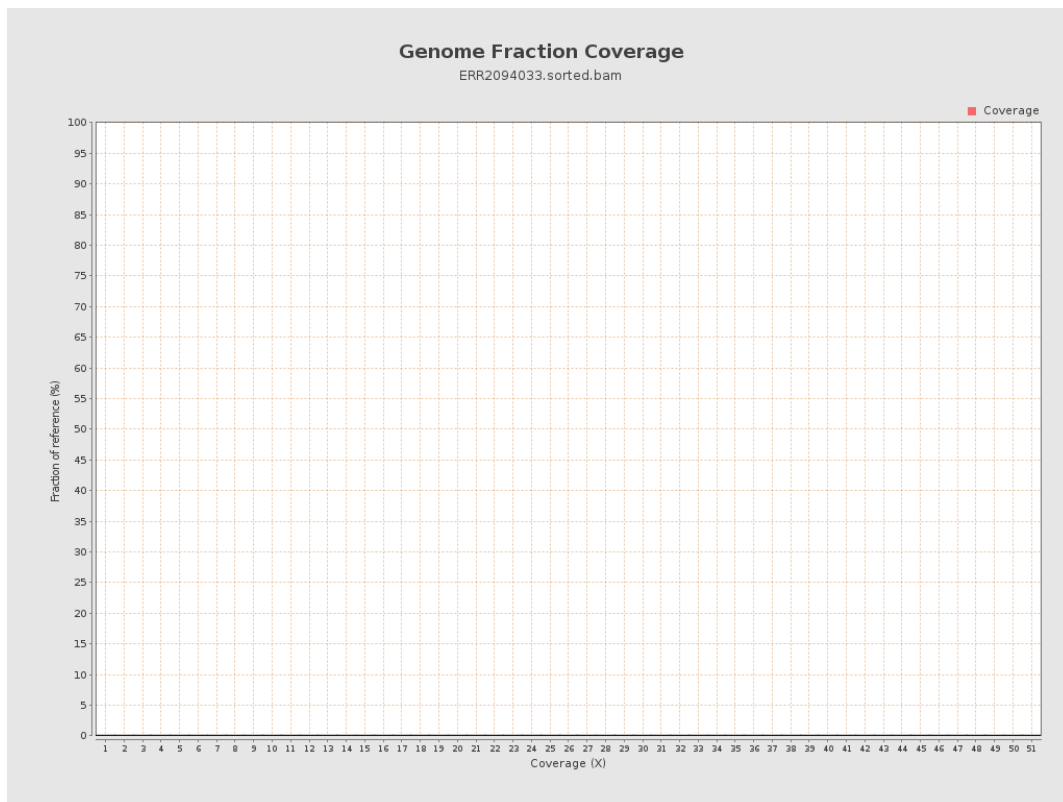
4. Results : Coverage Histogram



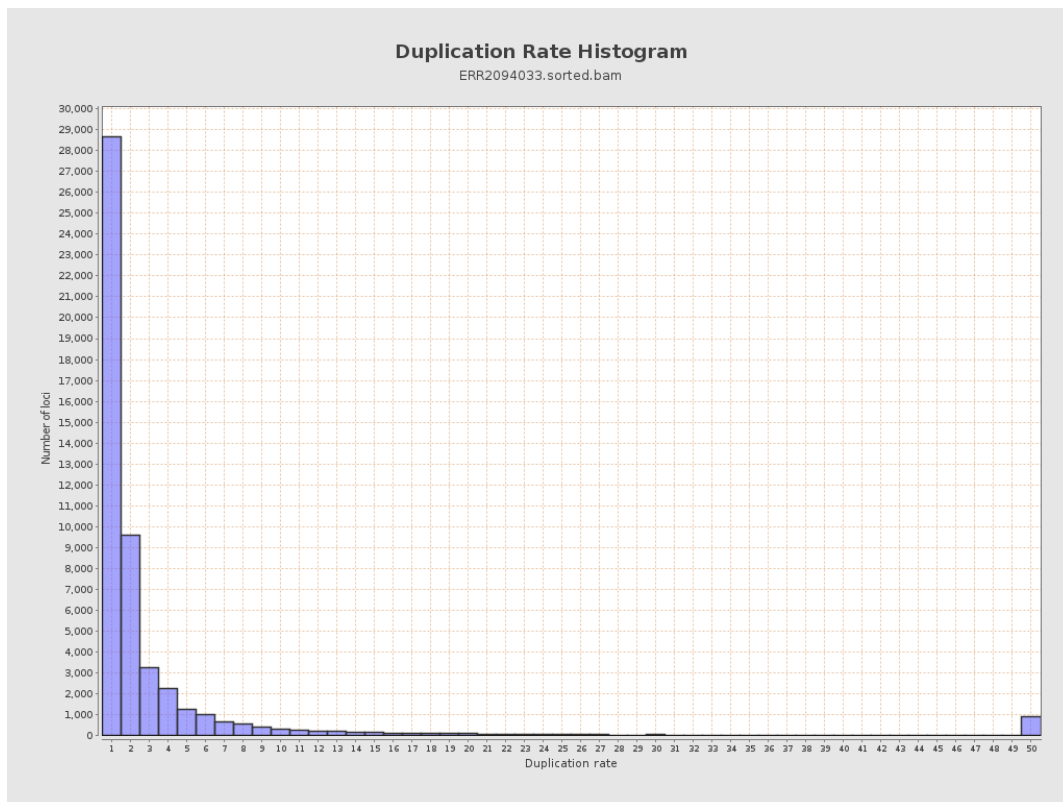
5. Results : Coverage Histogram (0-50X)



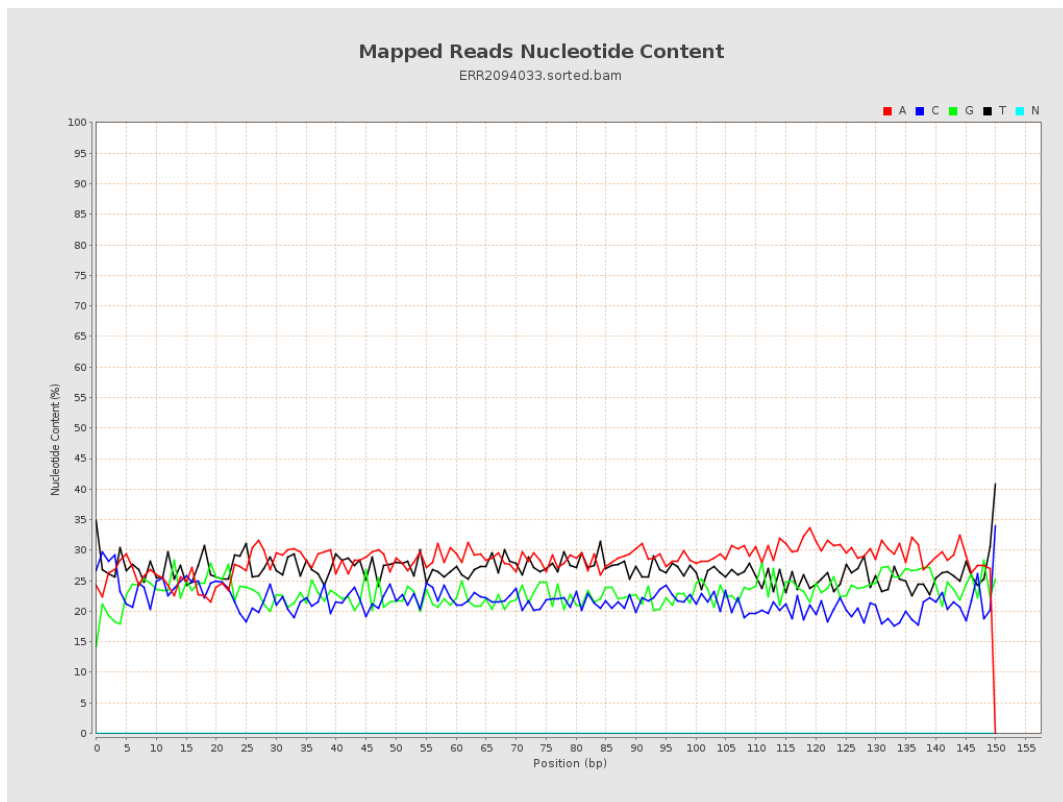
6. Results : Genome Fraction Coverage



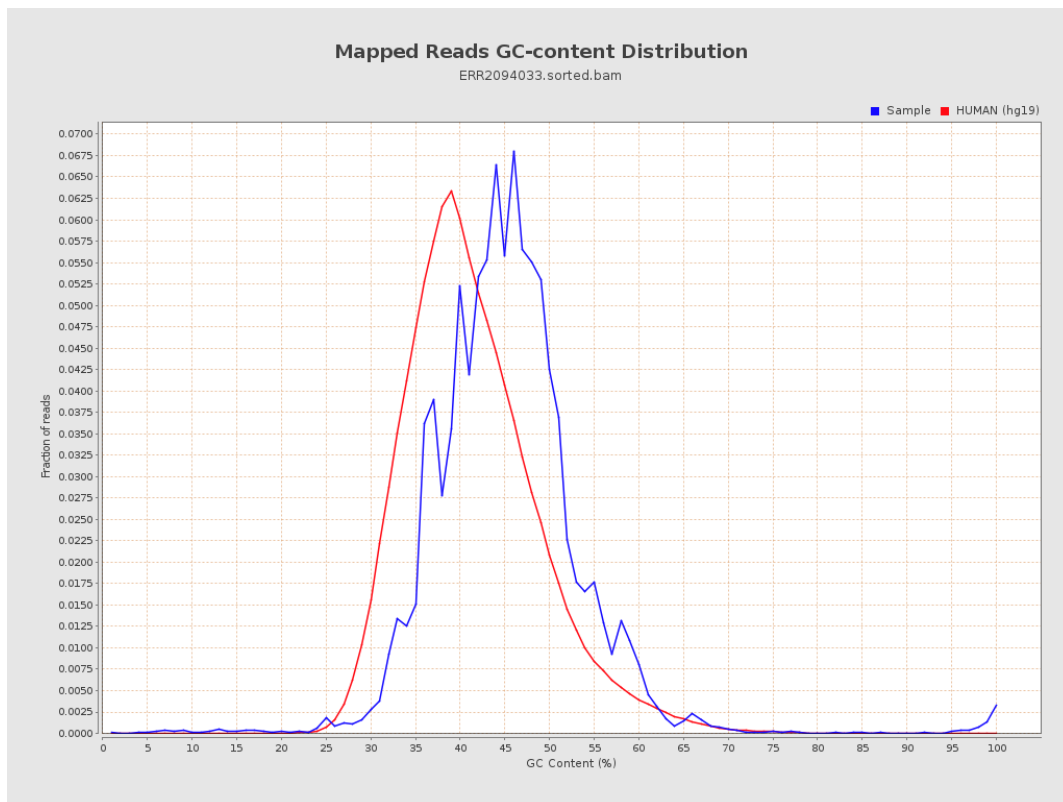
7. Results : Duplication Rate Histogram



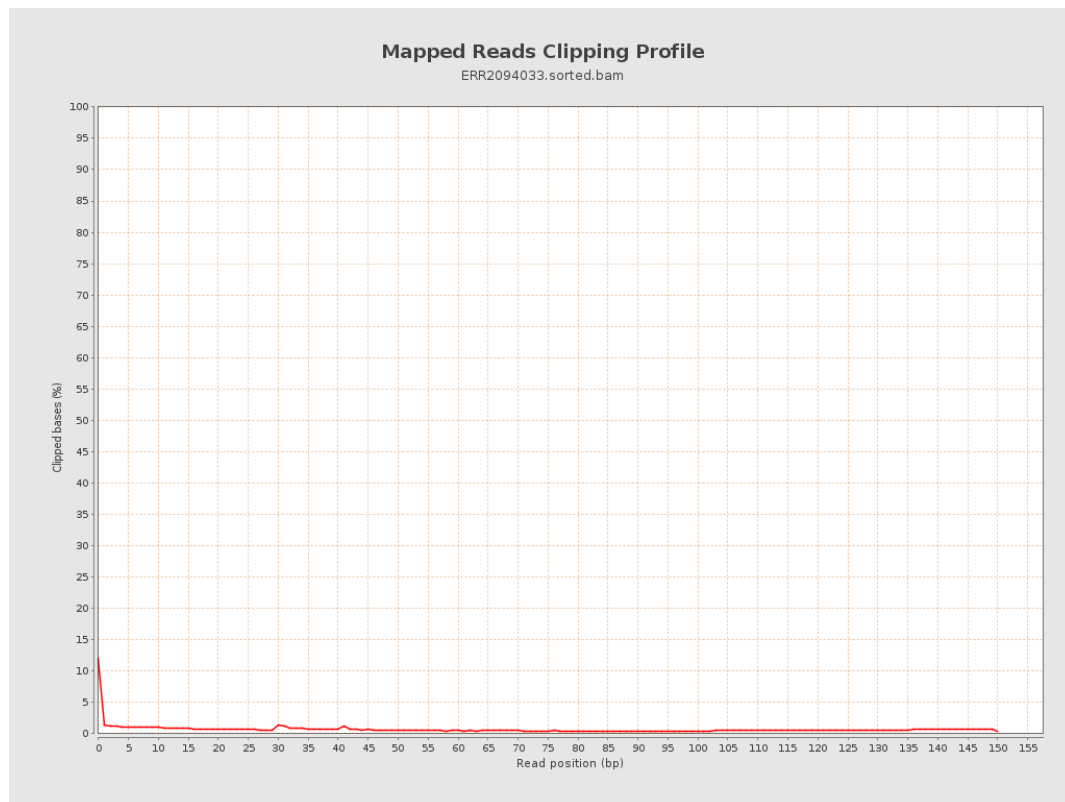
8. Results : Mapped Reads Nucleotide Content



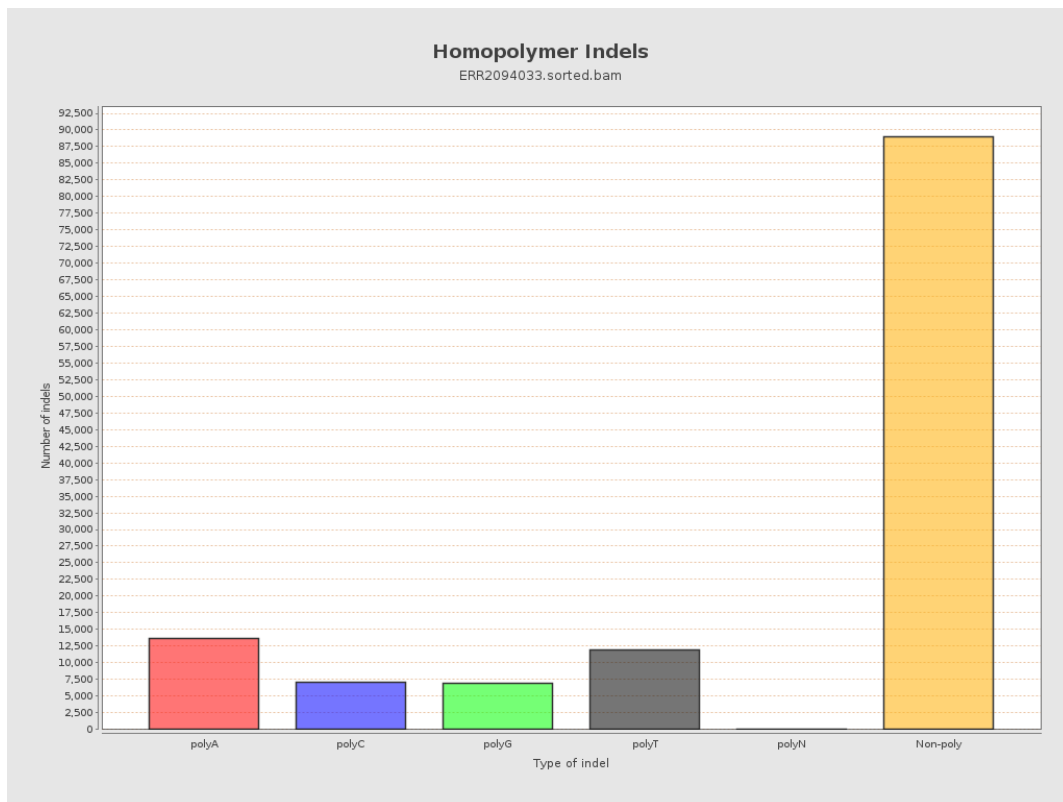
9. Results : Mapped Reads GC-content Distribution



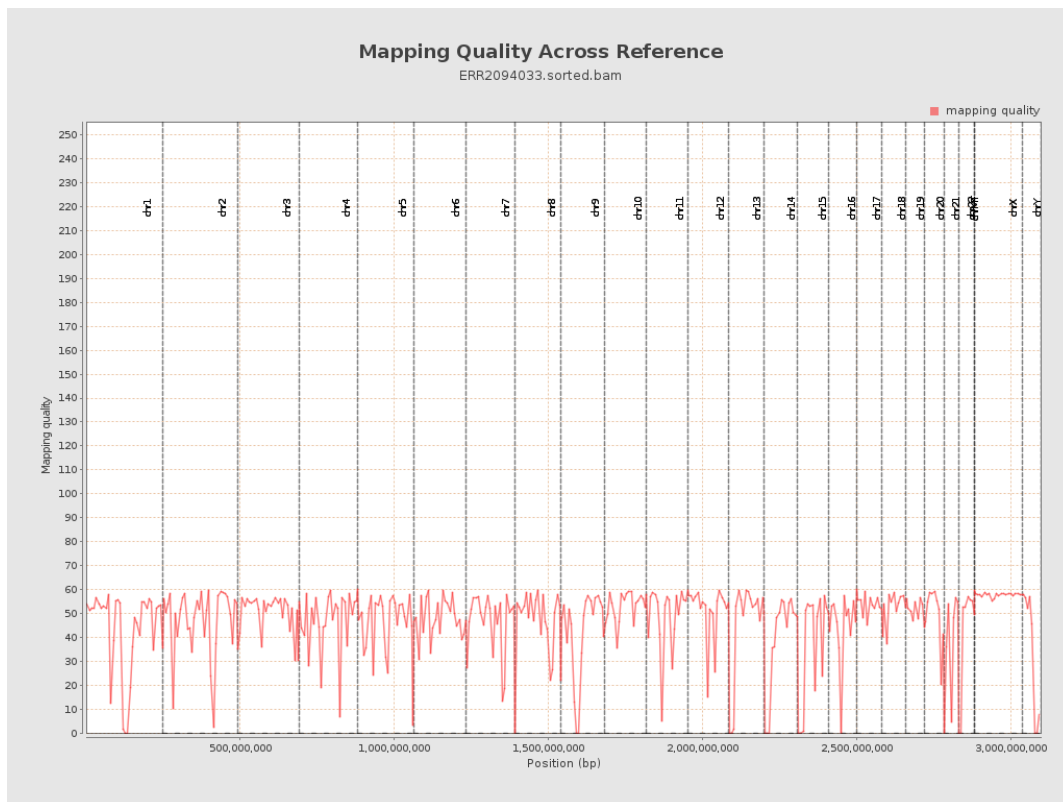
10. Results : Mapped Reads Clipping Profile



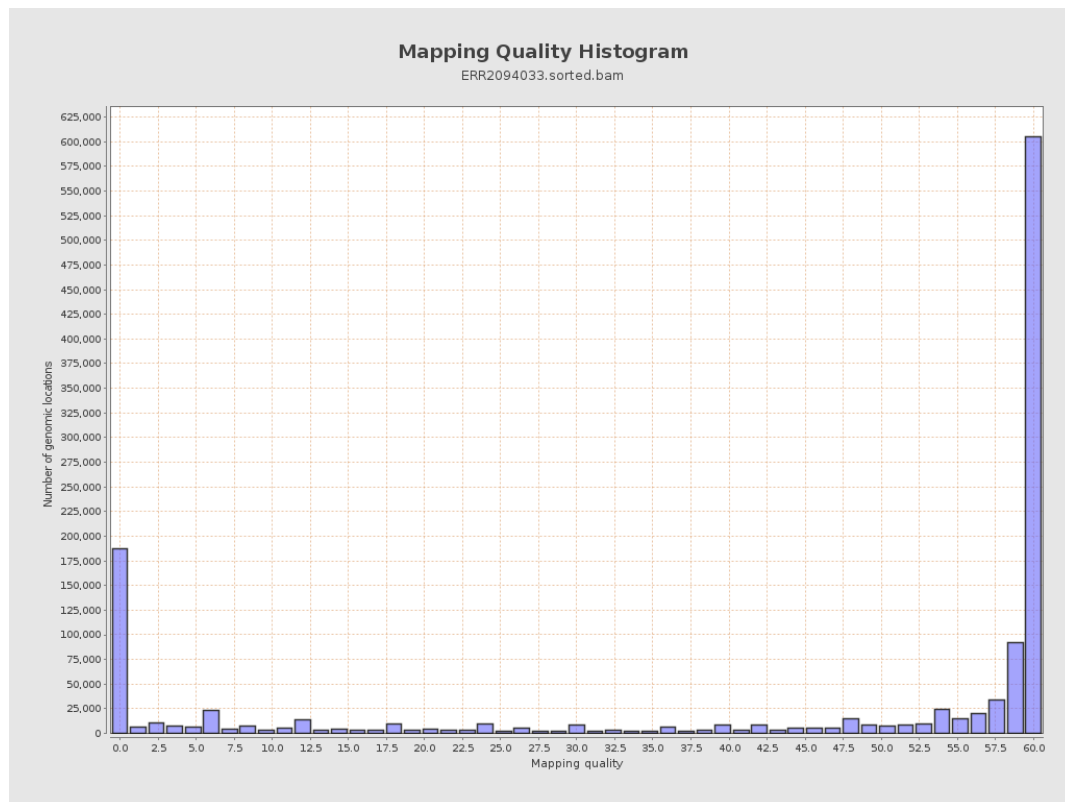
11. Results : Homopolymer Indels



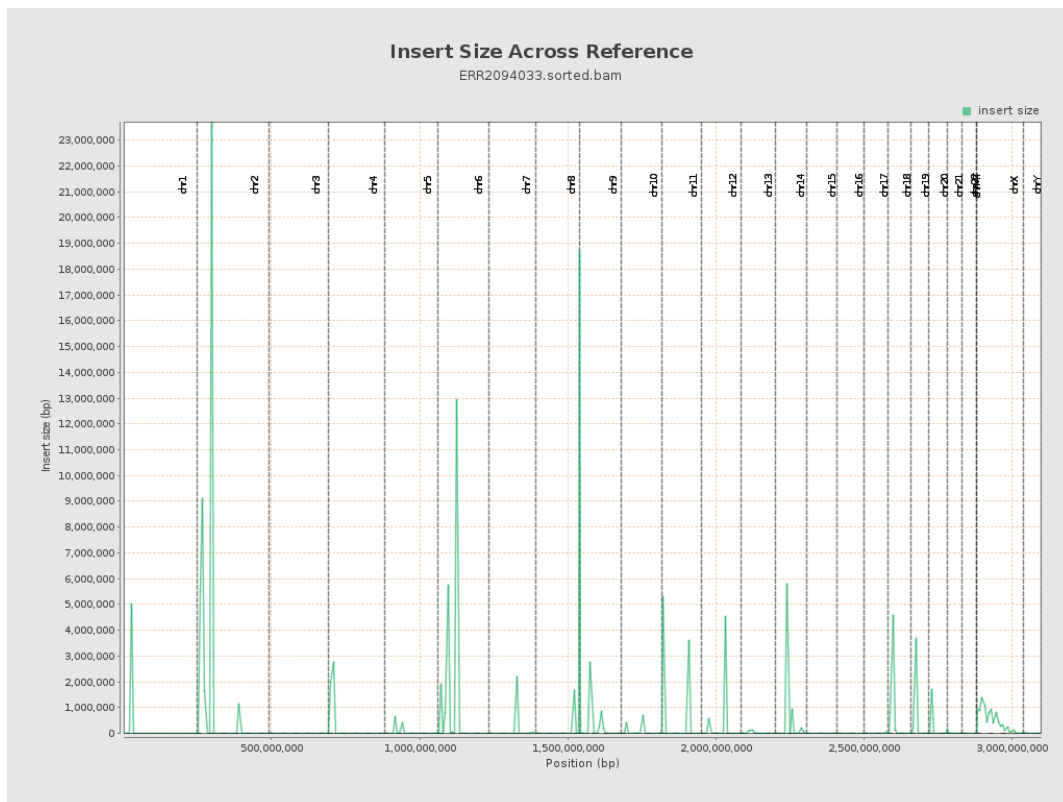
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

