

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:39:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094034.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_ERR2094034 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094034_1.fastq.gz ERR2094034_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:39:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	400,716
Mapped reads	370,289 / 92.41%
Unmapped reads	30,427 / 7.59%
Mapped paired reads	370,289 / 92.41%
Mapped reads, first in pair	186,195 / 46.47%
Mapped reads, second in pair	184,094 / 45.94%
Mapped reads, both in pair	365,614 / 91.24%
Mapped reads, singletons	4,675 / 1.17%
Secondary alignments	0
Supplementary alignments	19,810 / 4.94%
Read min/max/mean length	30 / 151 / 141.11
Duplicated reads (estimated)	342,395 / 85.45%
Duplication rate	45.57%
Clipped reads	177,941 / 44.41%

2.2. ACGT Content

Number/percentage of A's	13,214,656 / 28.11%
Number/percentage of C's	10,285,930 / 21.88%
Number/percentage of T's	12,618,214 / 26.84%
Number/percentage of G's	10,884,863 / 23.16%
Number/percentage of N's	556 / 0%

GC Percentage	45.04%
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2.3. Coverage

Mean	0.0154
Standard Deviation	5.0637

2.4. Mapping Quality

Mean Mapping Quality	45.57
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2.5. Insert size

Mean	576,385.15
Standard Deviation	6,902,296.82
P25/Median/P75	133 / 166 / 210

2.6. Mismatches and indels

General error rate	3.41%
Mismatches	1,557,436
Insertions	25,882
Mapped reads with at least one insertion	6.85%
Deletions	123,336
Mapped reads with at least one deletion	32.13%
Homopolymer indels	29.56%

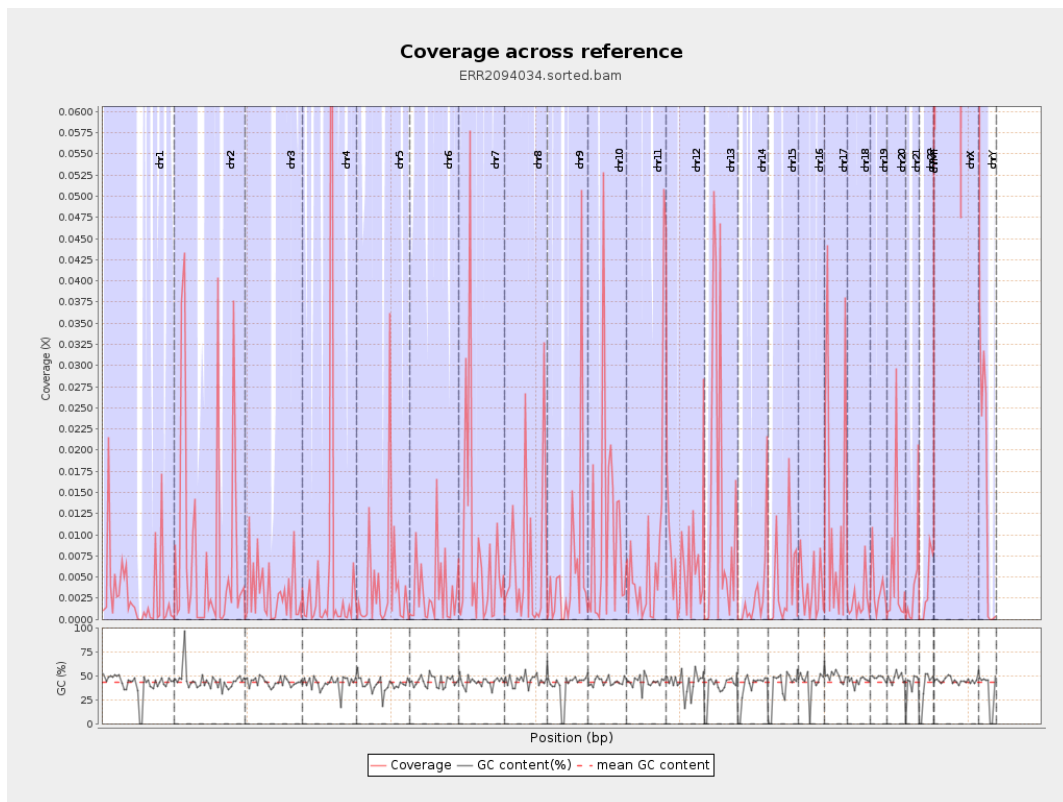
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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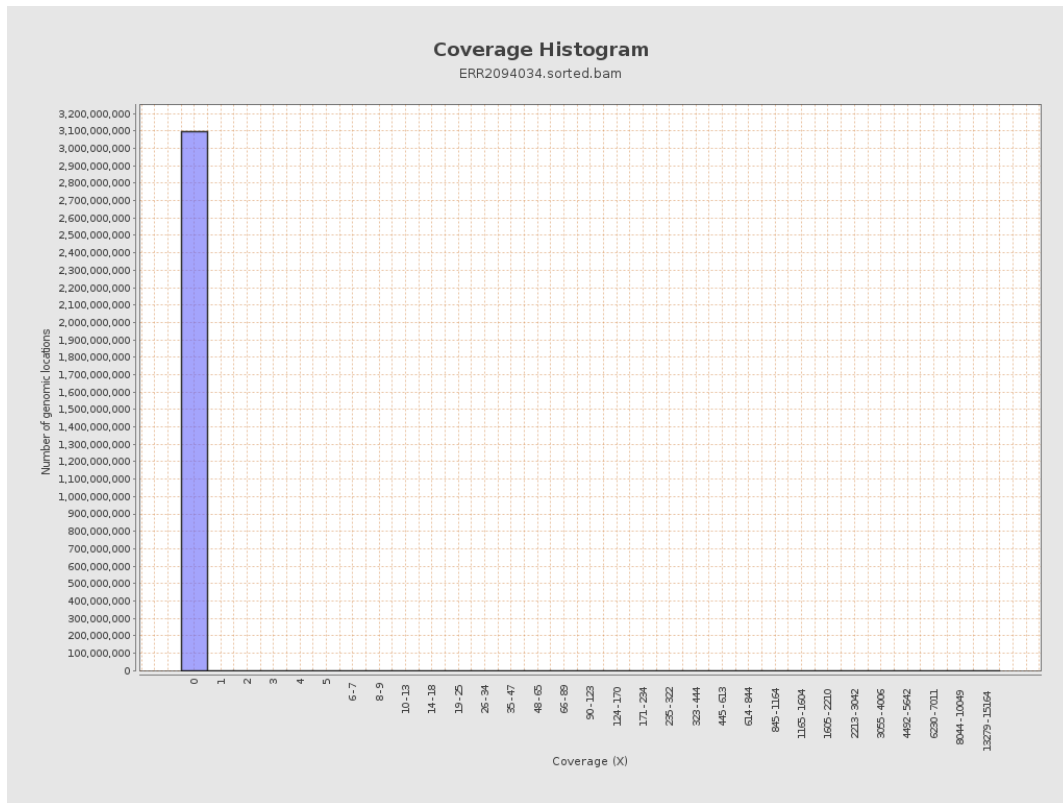
		bases	coverage	deviation
chr1	249250621	763881	0.0031	0.8867
chr2	243199373	1957014	0.008	2.3503
chr3	198022430	616567	0.0031	0.7849
chr4	191154276	1168371	0.0061	2.0057
chr5	180915260	738700	0.0041	1.9137
chr6	171115067	565460	0.0033	0.8585
chr7	159138663	1274437	0.008	2.4794
chr8	146364022	941518	0.0064	1.7919
chr9	141213431	831813	0.0059	2.018
chr10	135534747	1352471	0.01	3.0501
chr11	135006516	1008802	0.0075	2.1345
chr12	133851895	886871	0.0066	1.4142
chr13	115169878	1524733	0.0132	3.5533
chr14	107349540	331227	0.0031	0.7935
chr15	102531392	425463	0.0041	0.9726
chr16	90354753	334405	0.0037	0.8936
chr17	81195210	1070151	0.0132	2.3738
chr18	78077248	169242	0.0022	0.4653
chr19	59128983	207247	0.0035	0.6305
chr20	63025520	375507	0.006	1.9641
chr21	48129895	191654	0.004	0.5146
chr22	51304566	183195	0.0036	0.362
chrMT	16571	6856278	413.7516	1,724.3384
chrX	155270560	23209119	0.1495	10.4663

chrY	59373566	840601	0.0142	2.6725
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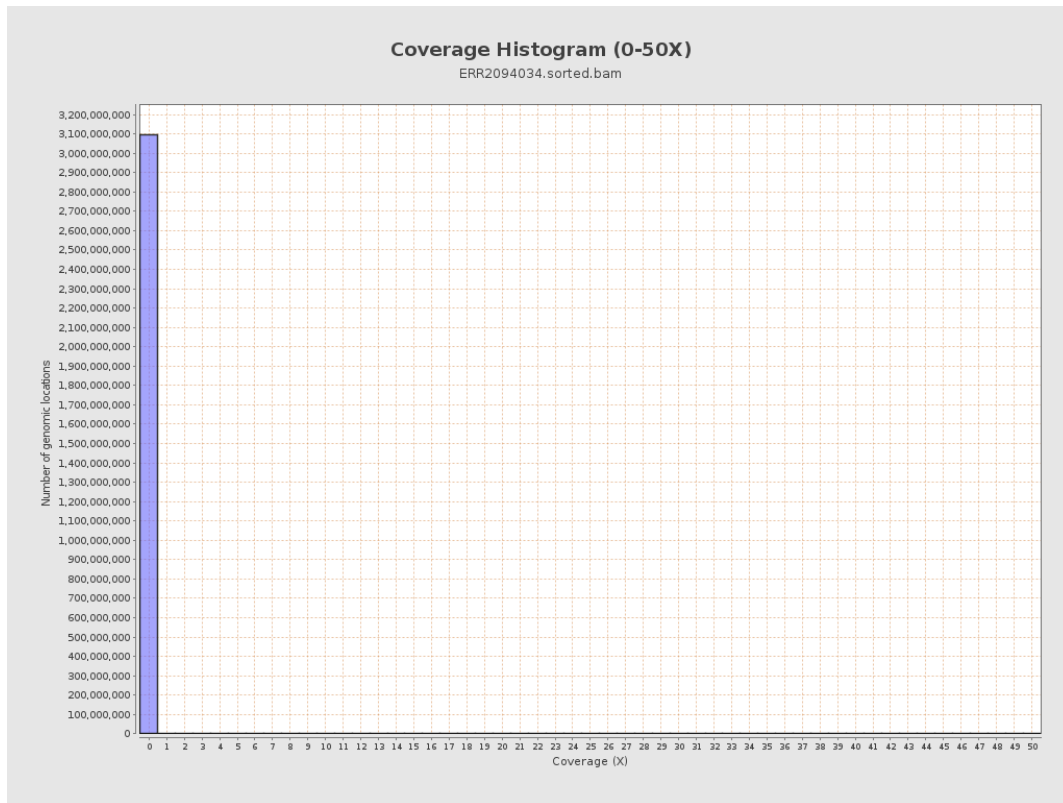
3. Results : Coverage across reference



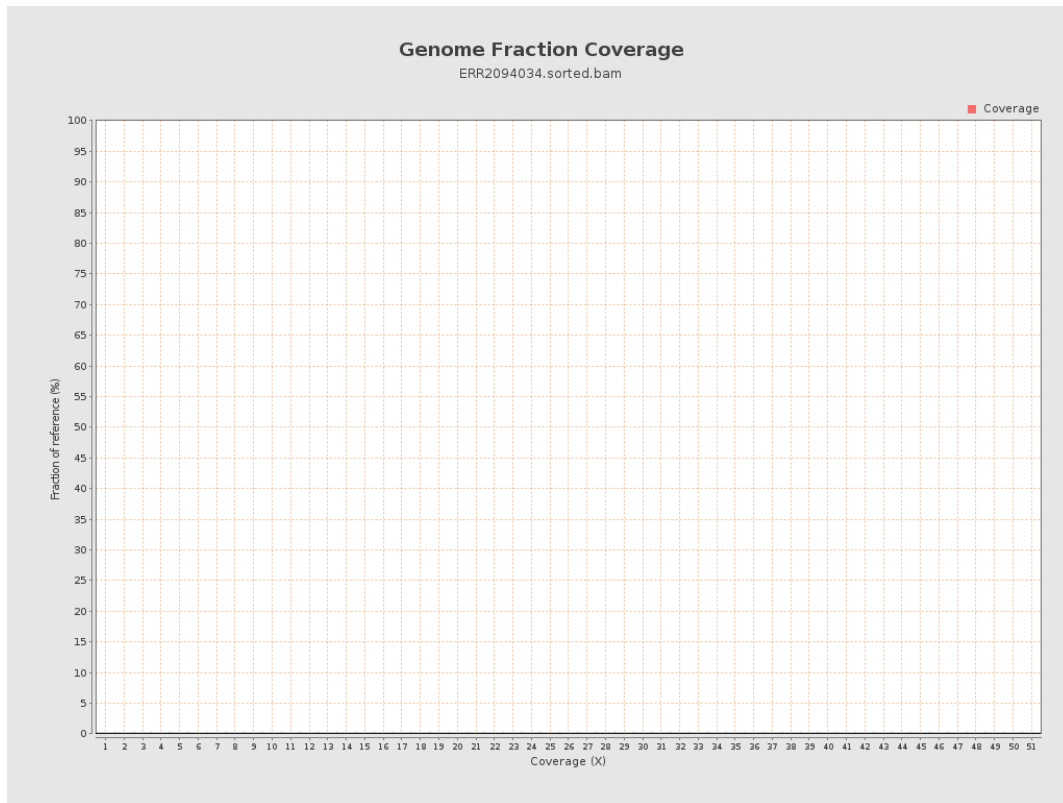
4. Results : Coverage Histogram



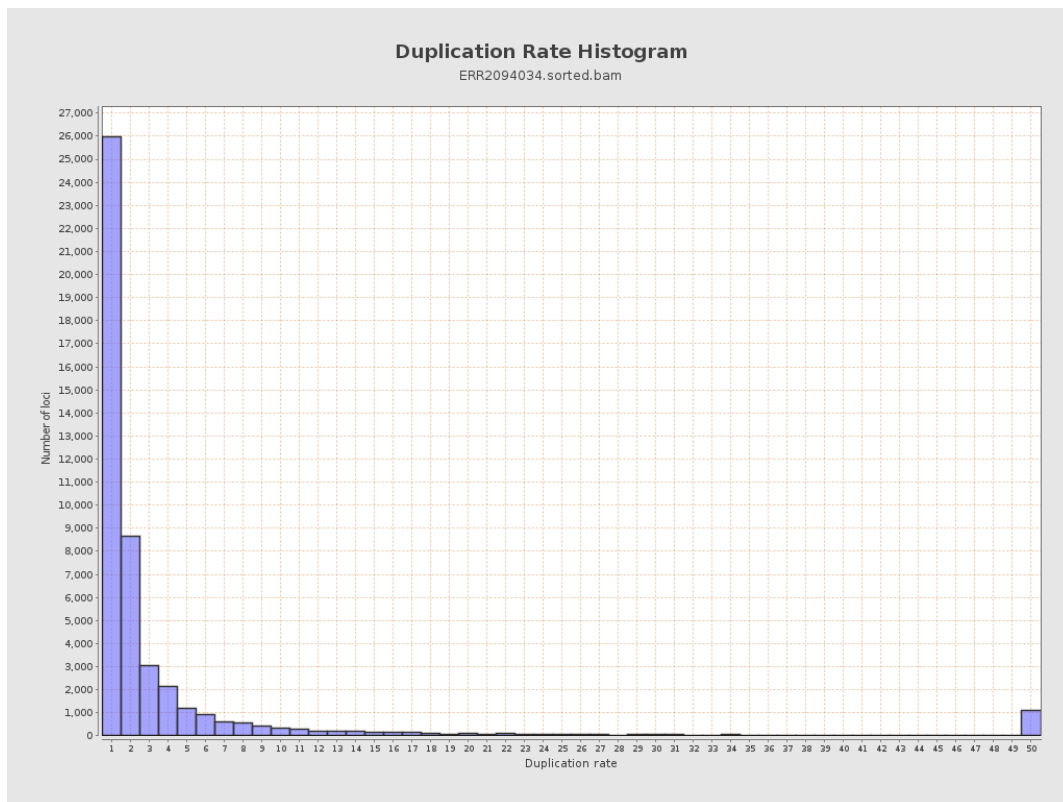
5. Results : Coverage Histogram (0-50X)



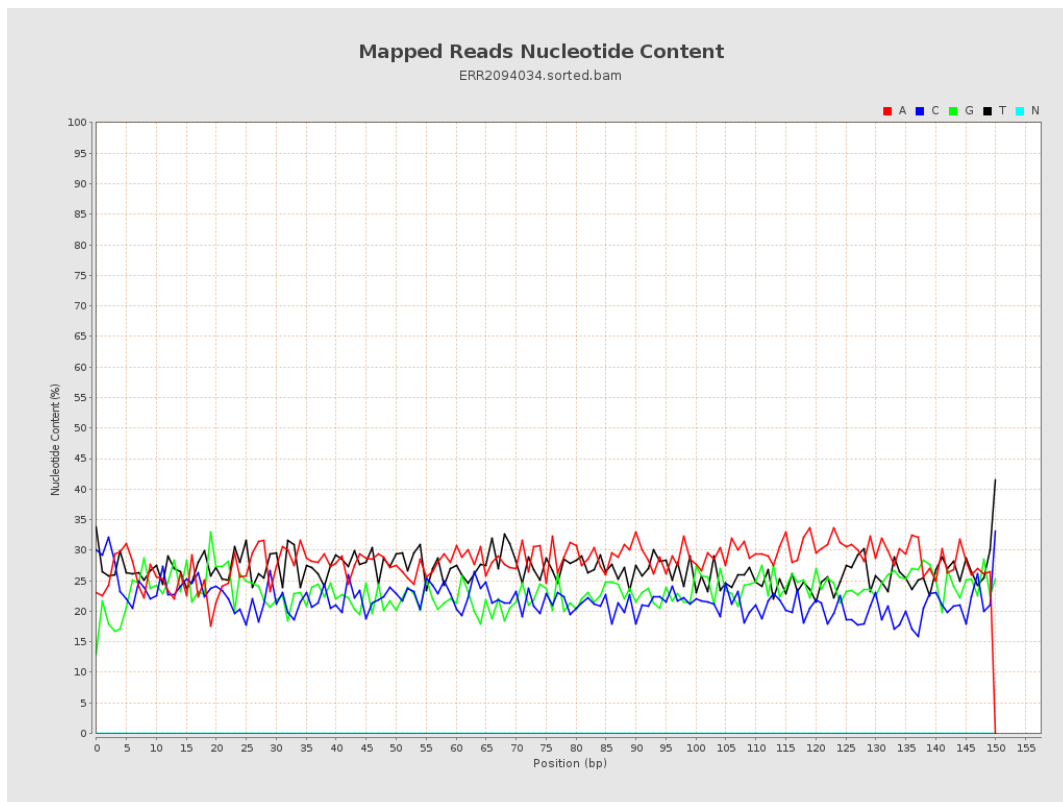
6. Results : Genome Fraction Coverage



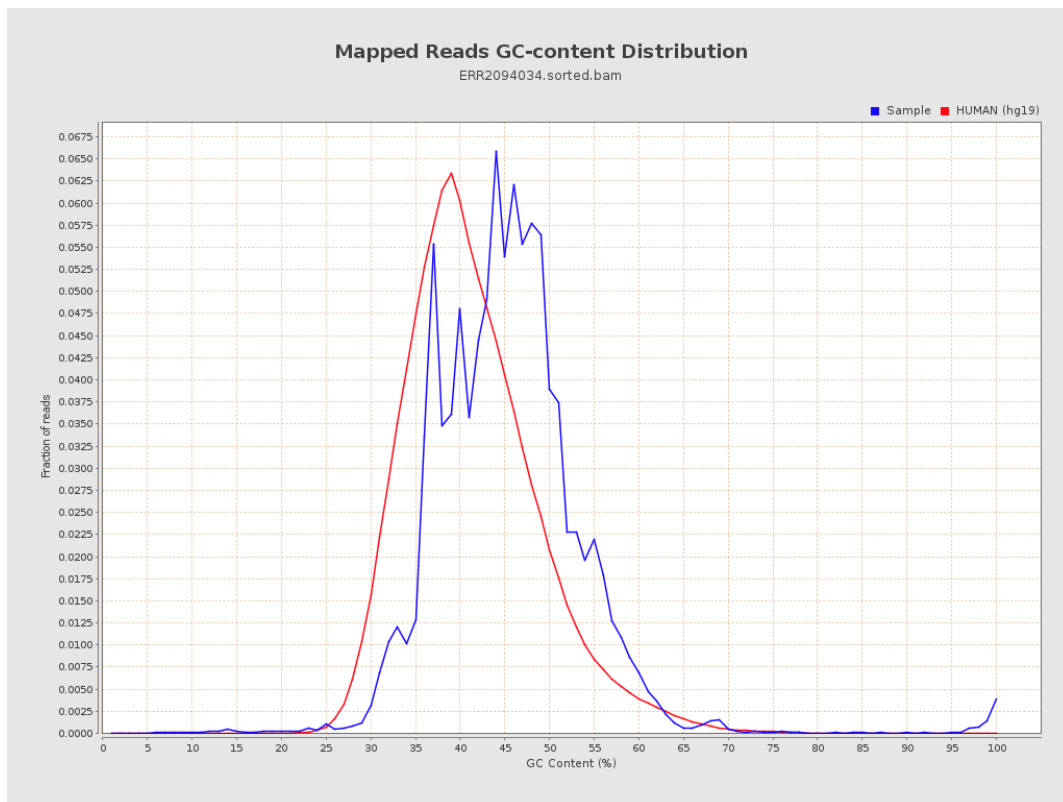
7. Results : Duplication Rate Histogram



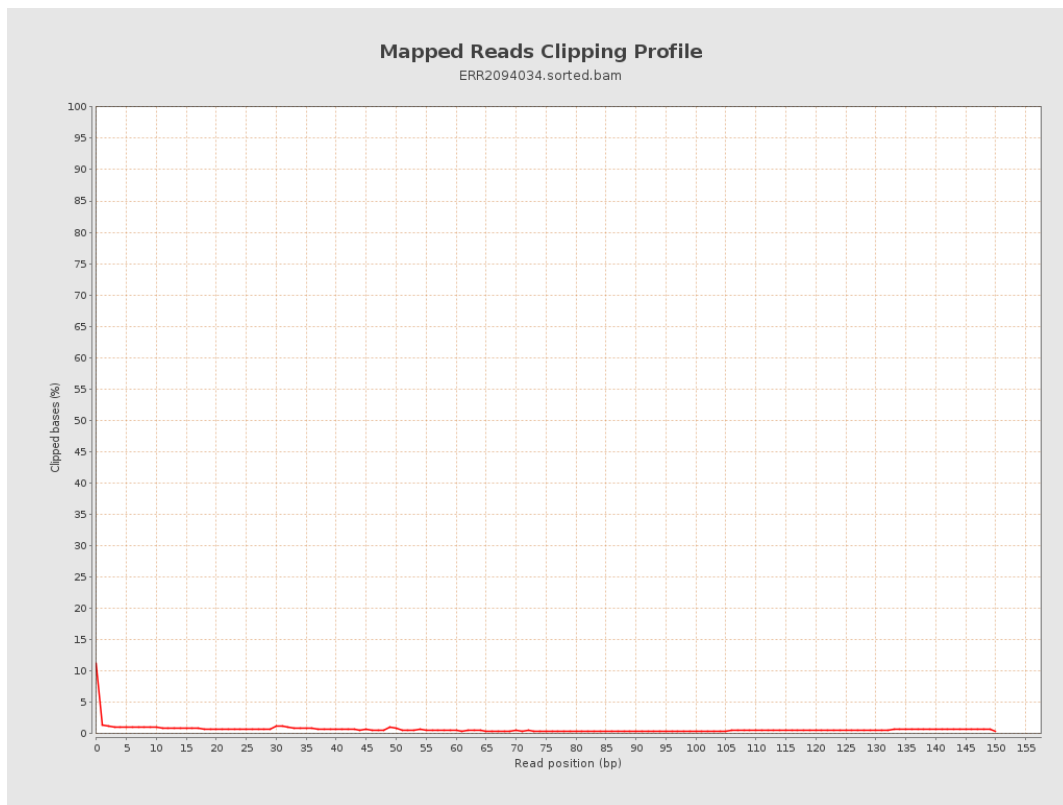
8. Results : Mapped Reads Nucleotide Content



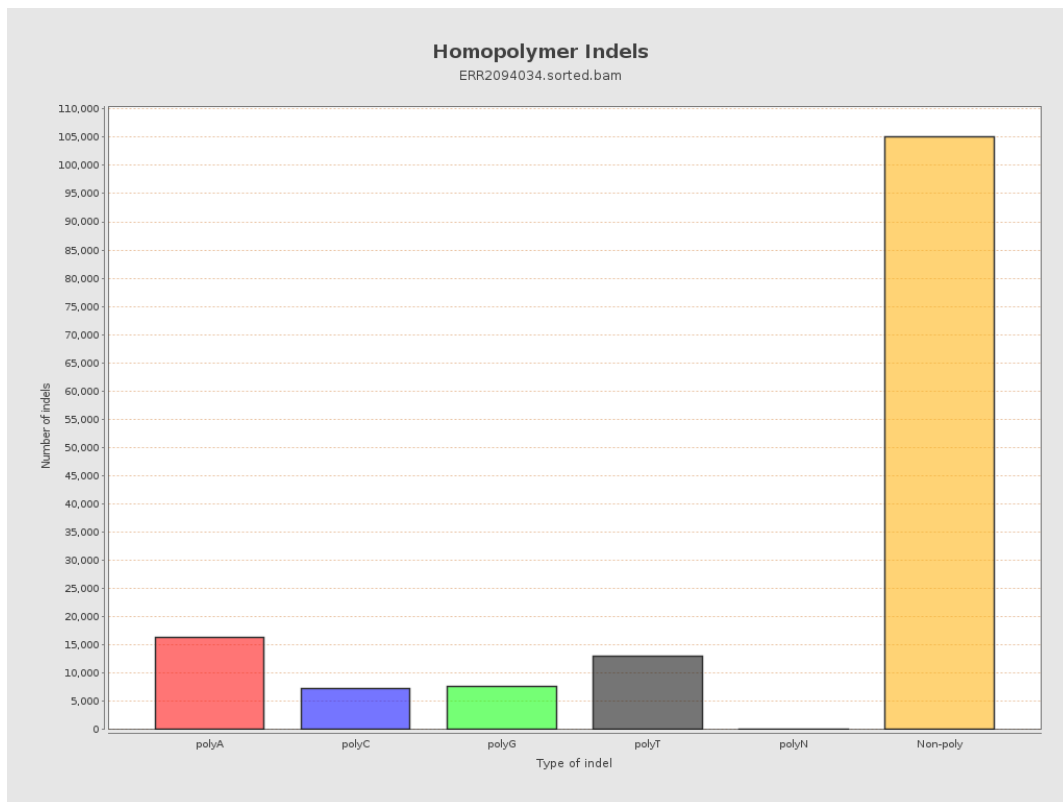
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



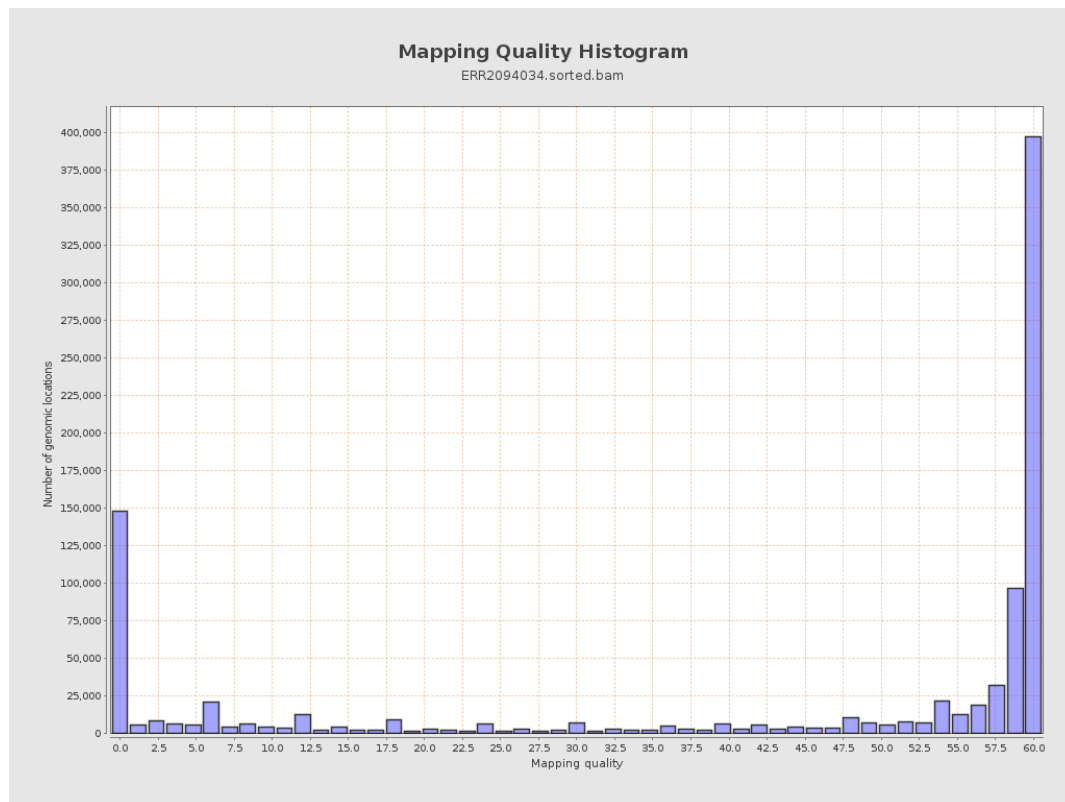
11. Results : Homopolymer Indels



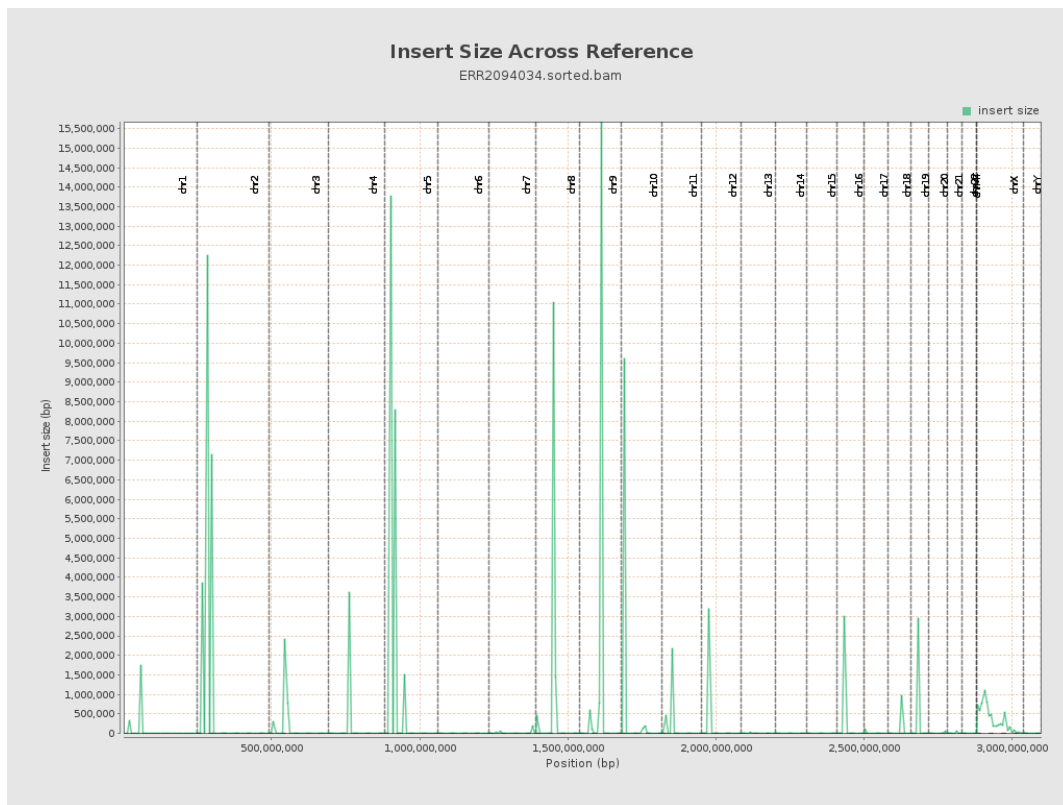
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

