

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:13:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094048.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_ERR2094048 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094048_1.fastq.gz ERR2094048_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:13:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	384,602
Mapped reads	363,502 / 94.51%
Unmapped reads	21,100 / 5.49%
Mapped paired reads	363,502 / 94.51%
Mapped reads, first in pair	182,550 / 47.46%
Mapped reads, second in pair	180,952 / 47.05%
Mapped reads, both in pair	360,926 / 93.84%
Mapped reads, singletons	2,576 / 0.67%
Secondary alignments	0
Supplementary alignments	13,375 / 3.48%
Read min/max/mean length	30 / 151 / 139.38
Duplicated reads (estimated)	342,699 / 89.1%
Duplication rate	50.77%
Clipped reads	150,316 / 39.08%

2.2. ACGT Content

Number/percentage of A's	12,898,256 / 27.55%
Number/percentage of C's	10,411,009 / 22.24%
Number/percentage of T's	12,509,037 / 26.72%
Number/percentage of G's	11,002,606 / 23.5%
Number/percentage of N's	621 / 0%

GC Percentage	45.73%
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2.3. Coverage

Mean	0.0155
Standard Deviation	3.8135

2.4. Mapping Quality

Mean Mapping Quality	45.34
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2.5. Insert size

Mean	498,980.95
Standard Deviation	6,213,542.76
P25/Median/P75	134 / 169 / 198

2.6. Mismatches and indels

General error rate	4.54%
Mismatches	2,075,982
Insertions	31,371
Mapped reads with at least one insertion	8.49%
Deletions	166,653
Mapped reads with at least one deletion	42.2%
Homopolymer indels	29.58%

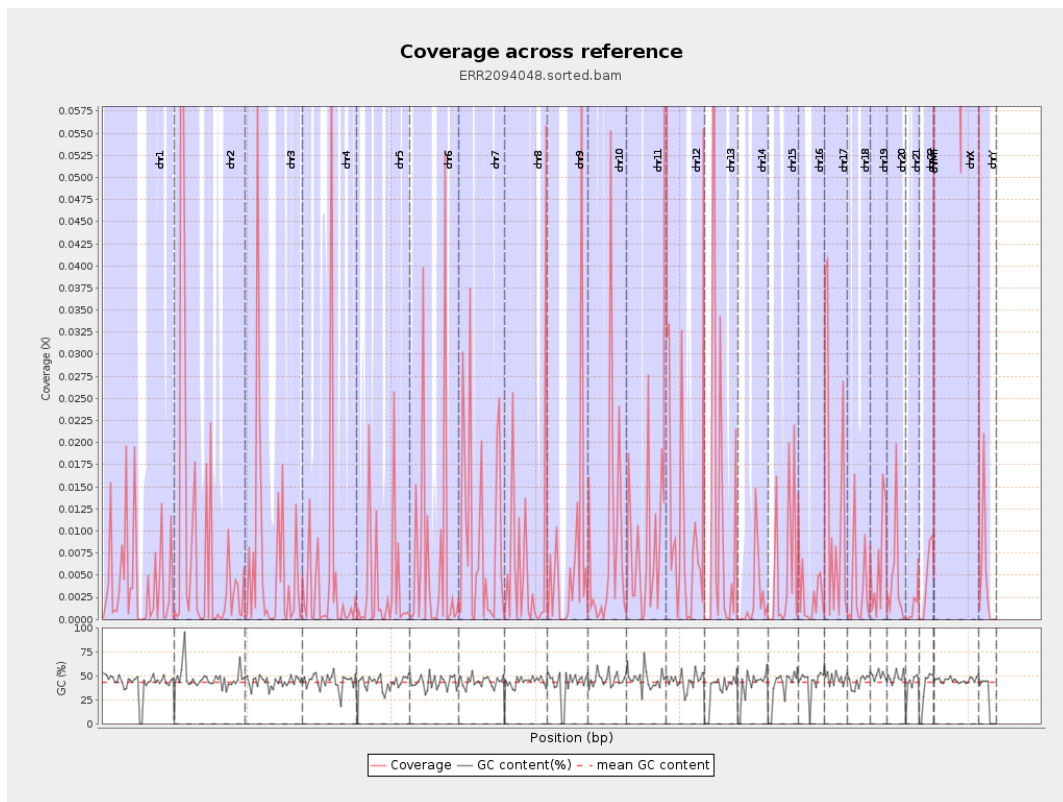
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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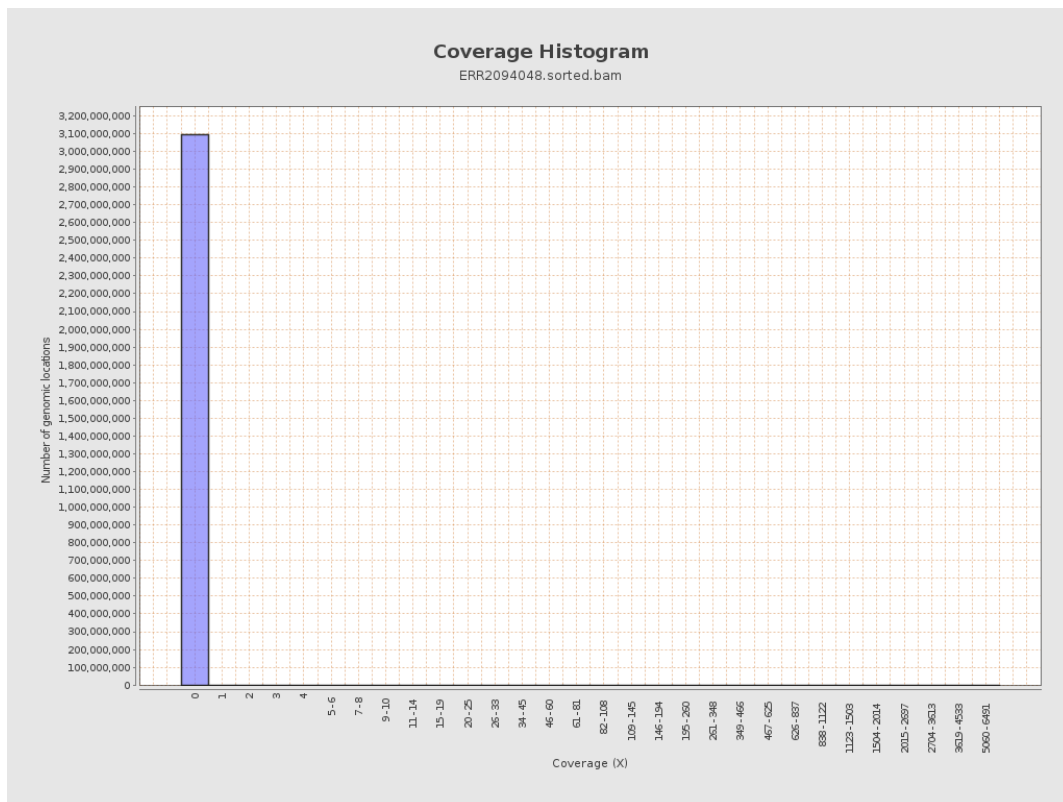
		bases	coverage	deviation
chr1	249250621	1040586	0.0042	1.3944
chr2	243199373	1932801	0.0079	2.3556
chr3	198022430	1269260	0.0064	2.3602
chr4	191154276	931228	0.0049	2.0142
chr5	180915260	645721	0.0036	1.4459
chr6	171115067	1172451	0.0069	3.3401
chr7	159138663	1375067	0.0086	2.5845
chr8	146364022	961505	0.0066	2.6053
chr9	141213431	977828	0.0069	2.8266
chr10	135534747	1113536	0.0082	2.4273
chr11	135006516	1318595	0.0098	2.4347
chr12	133851895	1414051	0.0106	2.7494
chr13	115169878	1204647	0.0105	2.7483
chr14	107349540	254687	0.0024	1.0141
chr15	102531392	514386	0.005	1.7164
chr16	90354753	255211	0.0028	0.9151
chr17	81195210	1090535	0.0134	3.315
chr18	78077248	264473	0.0034	1.1083
chr19	59128983	363677	0.0062	1.3215
chr20	63025520	296851	0.0047	0.9831
chr21	48129895	73163	0.0015	0.3205
chr22	51304566	219466	0.0043	0.8681
chrMT	16571	3202069	193.2333	804.7894
chrX	155270560	25924203	0.167	11.133

chrY	59373566	275579	0.0046	1.1054
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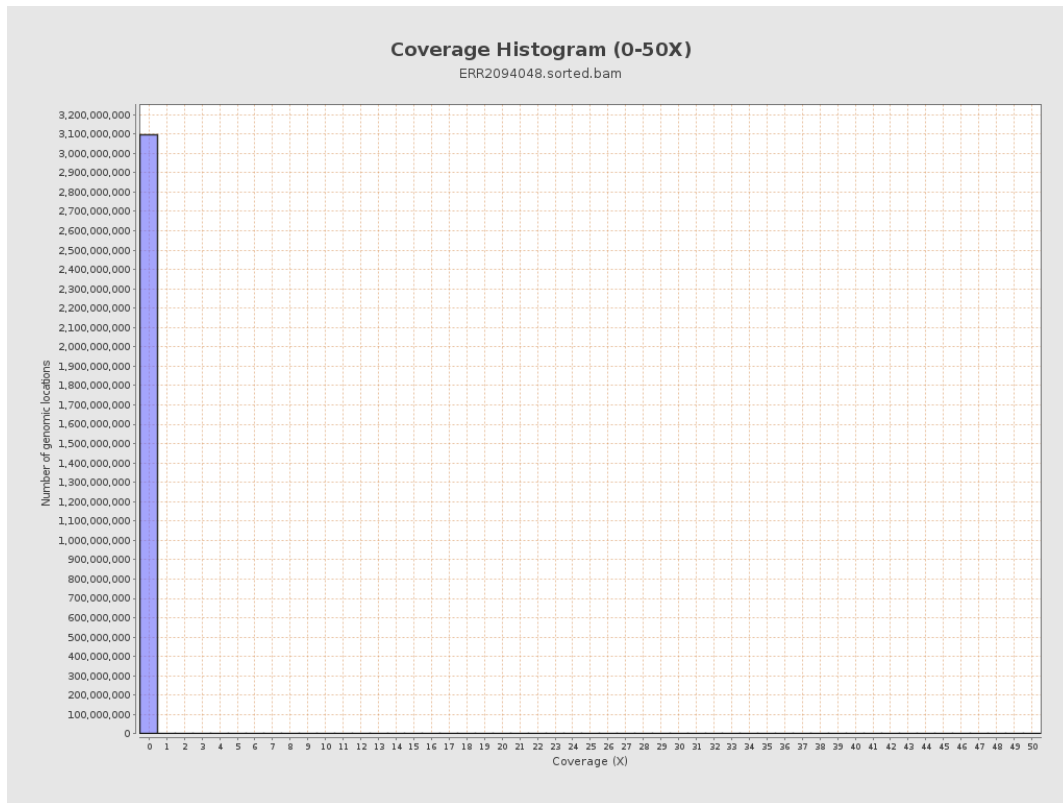
3. Results : Coverage across reference



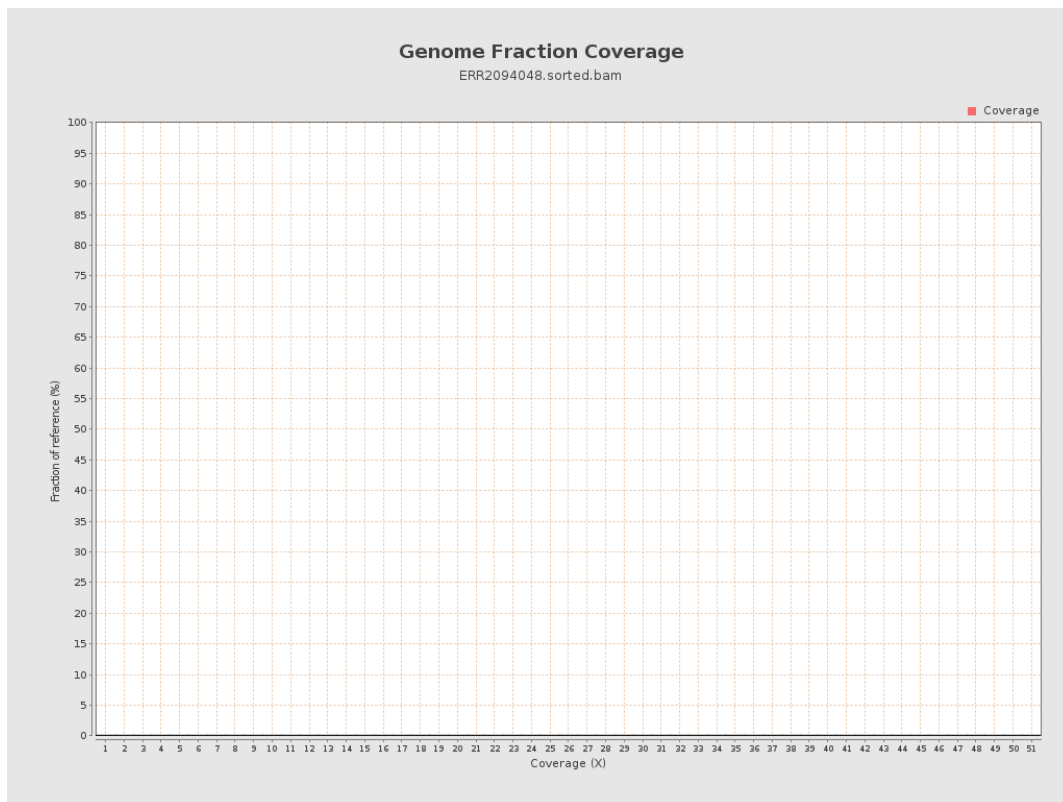
4. Results : Coverage Histogram



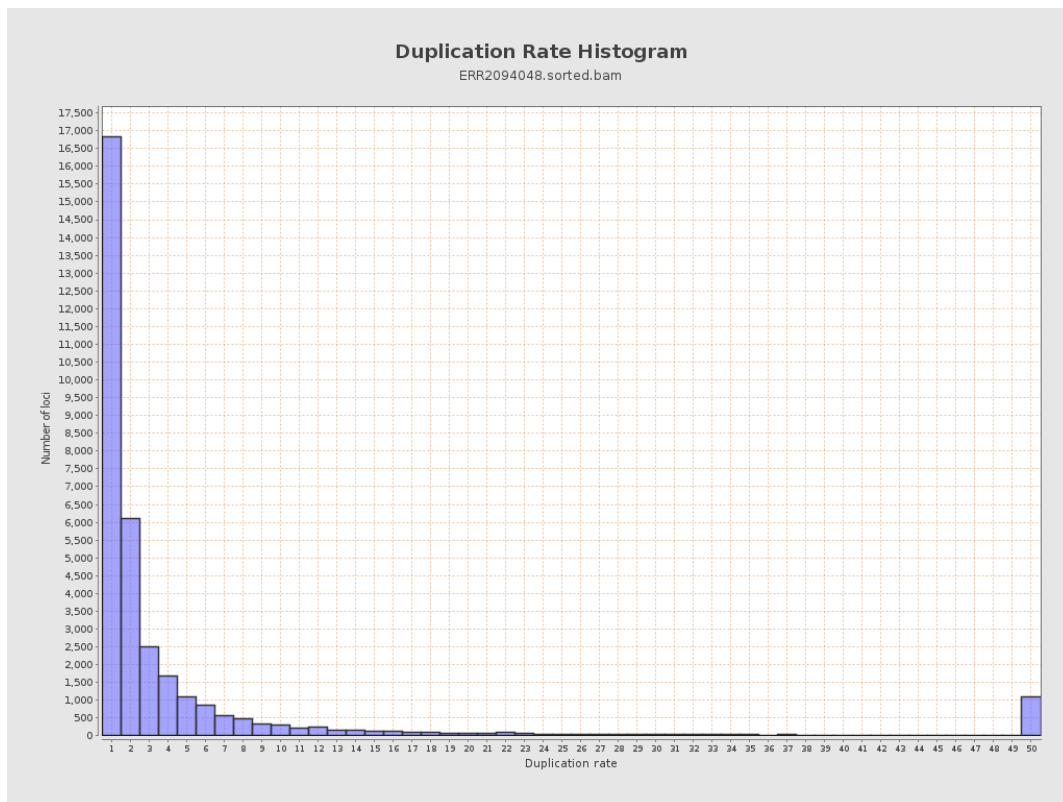
5. Results : Coverage Histogram (0-50X)



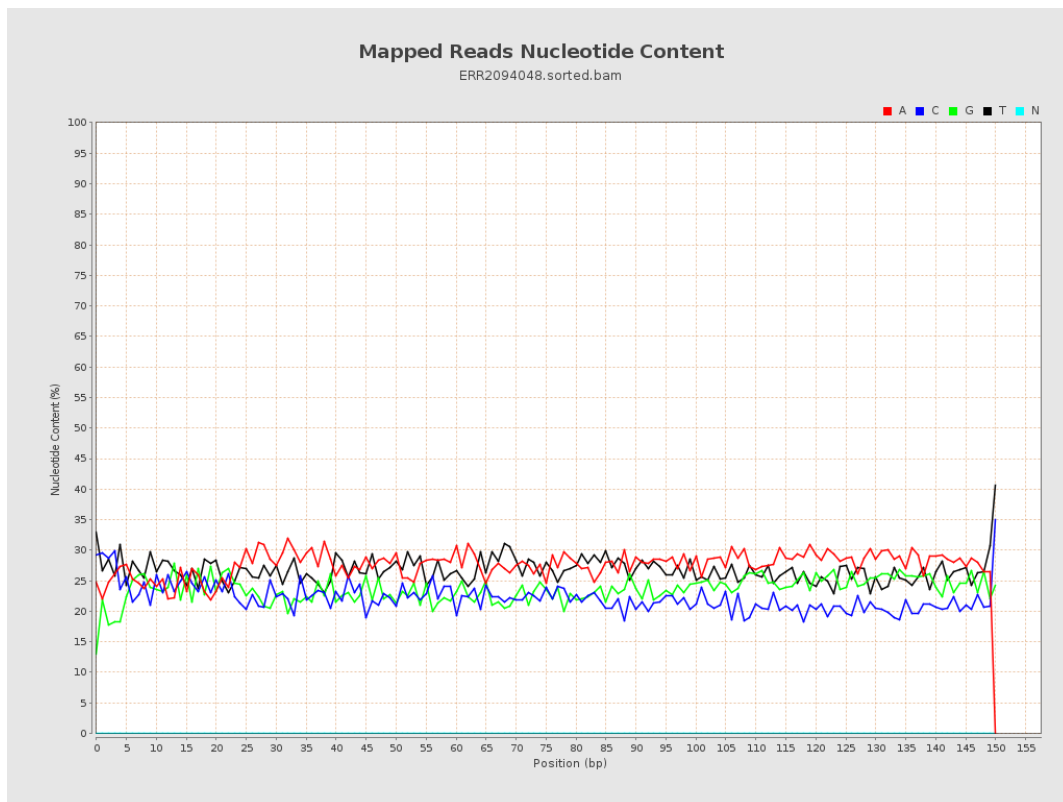
6. Results : Genome Fraction Coverage



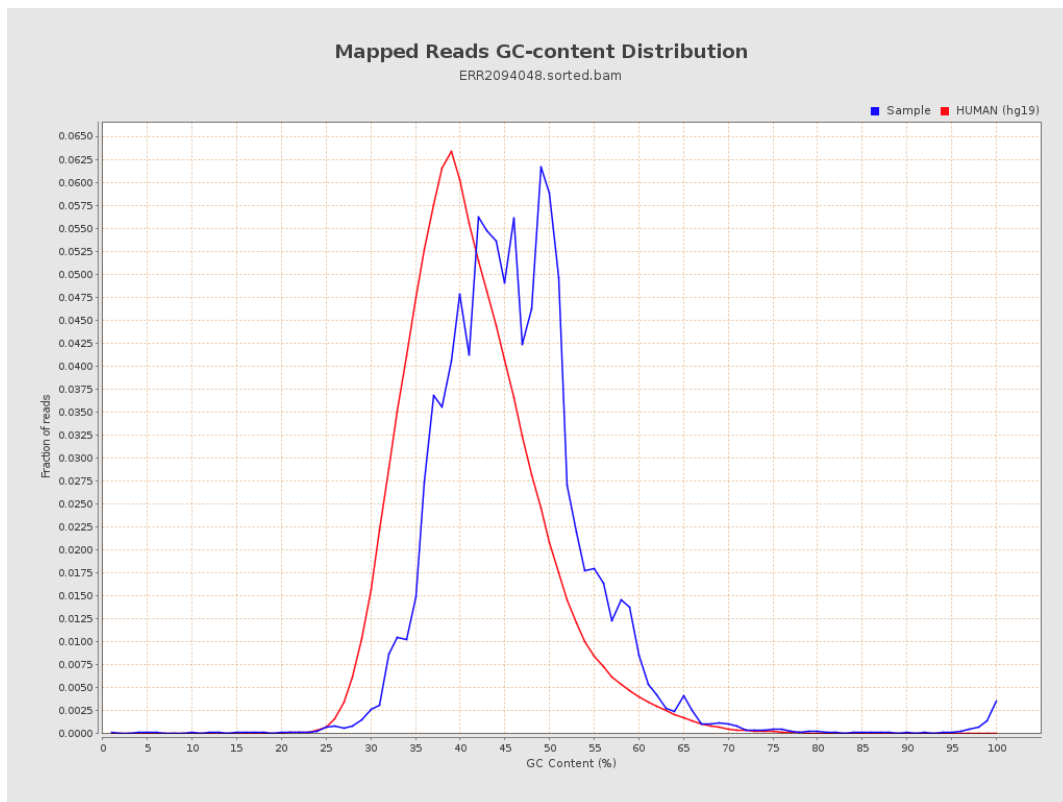
7. Results : Duplication Rate Histogram



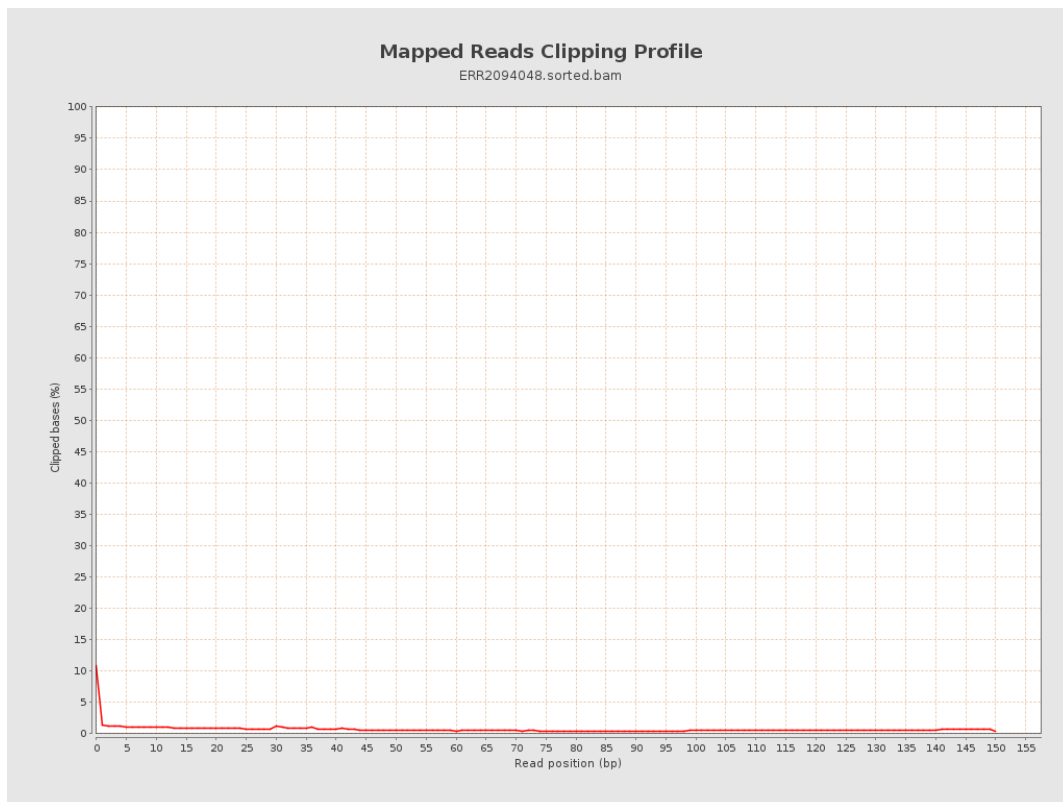
8. Results : Mapped Reads Nucleotide Content



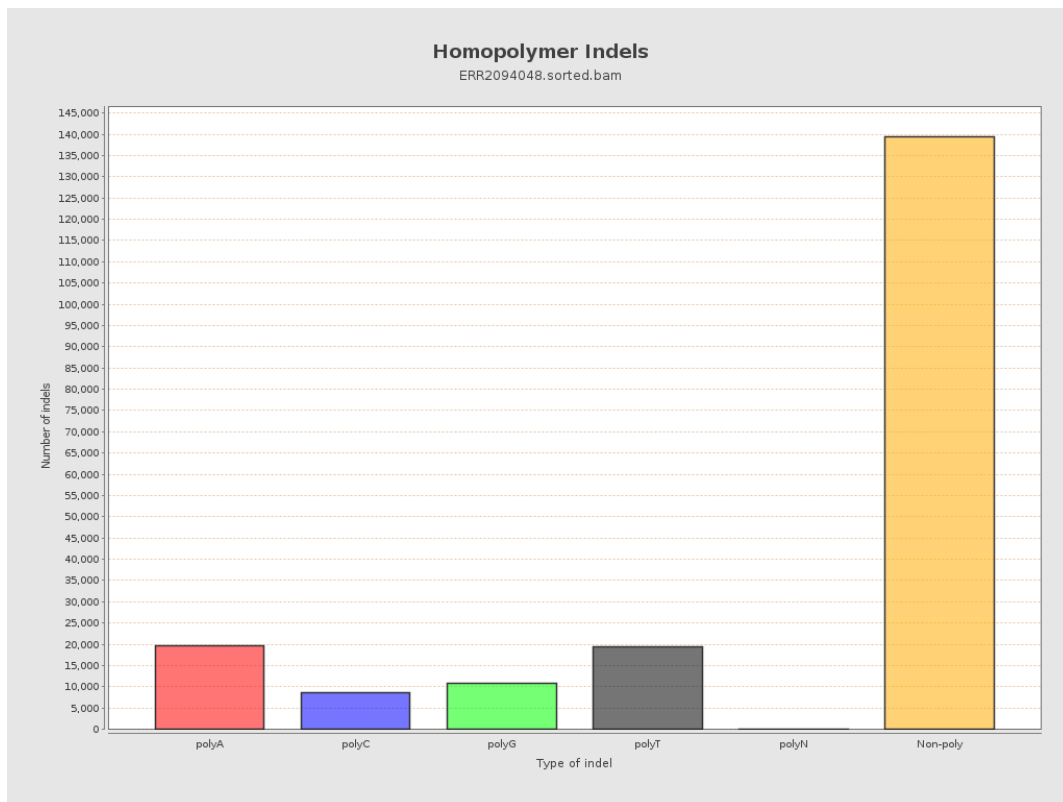
9. Results : Mapped Reads GC-content Distribution



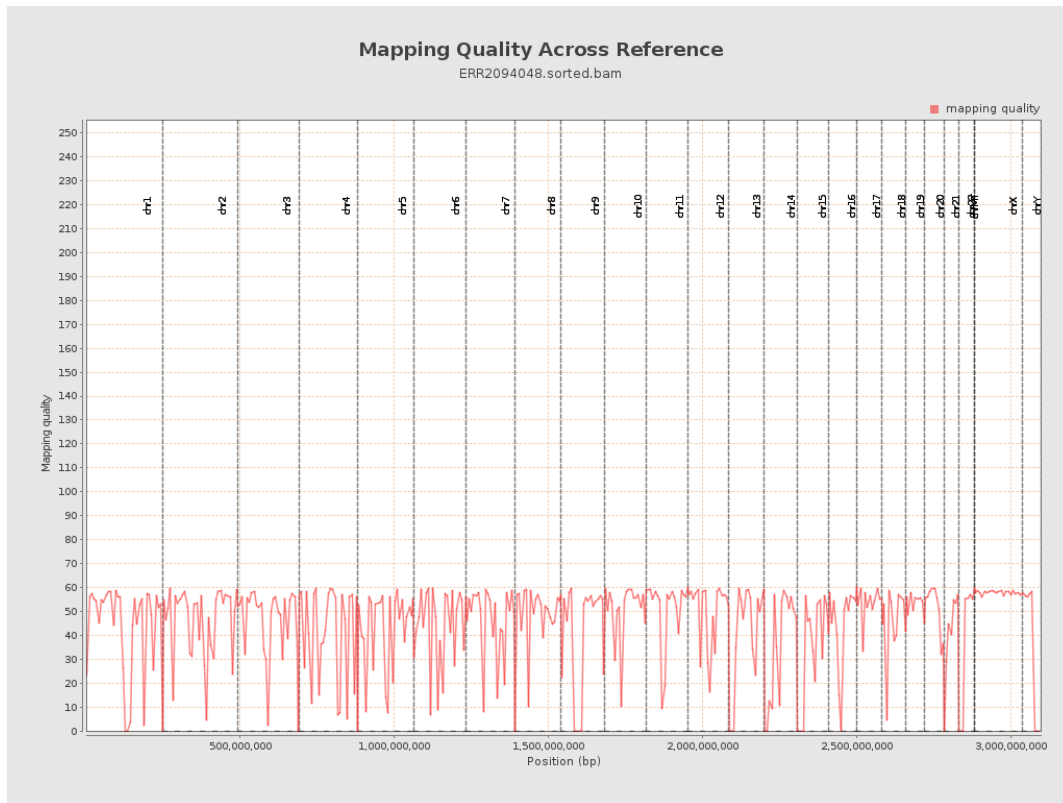
10. Results : Mapped Reads Clipping Profile



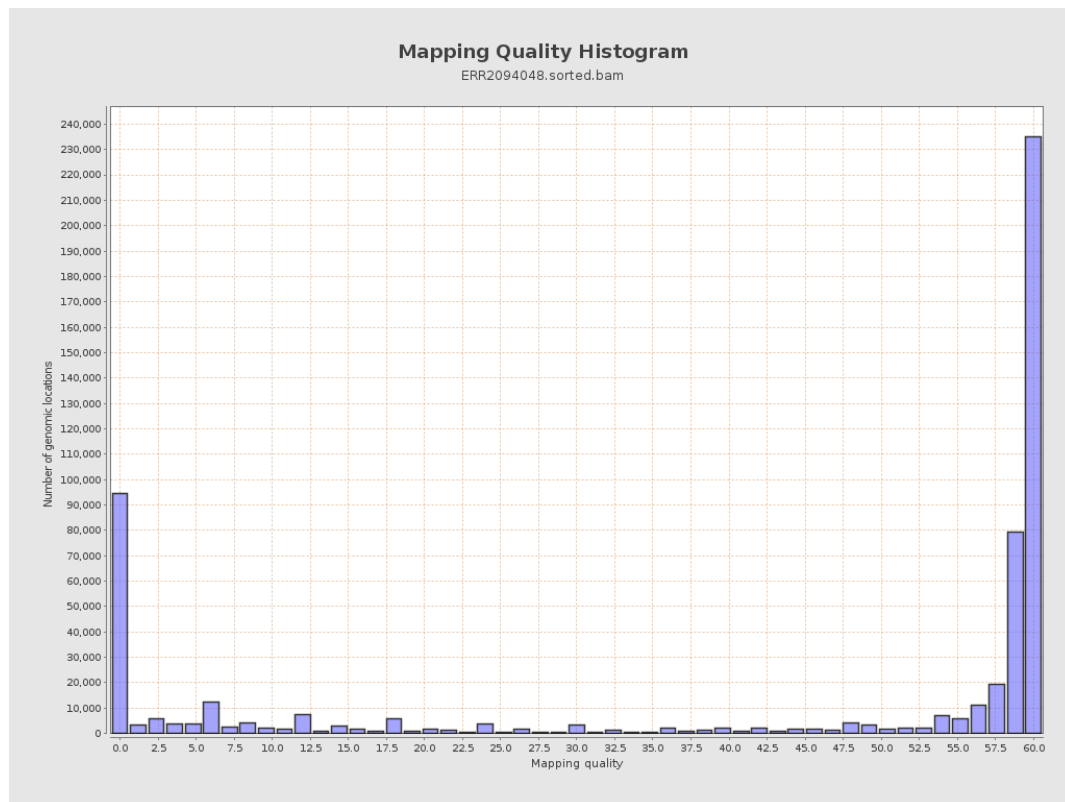
11. Results : Homopolymer Indels



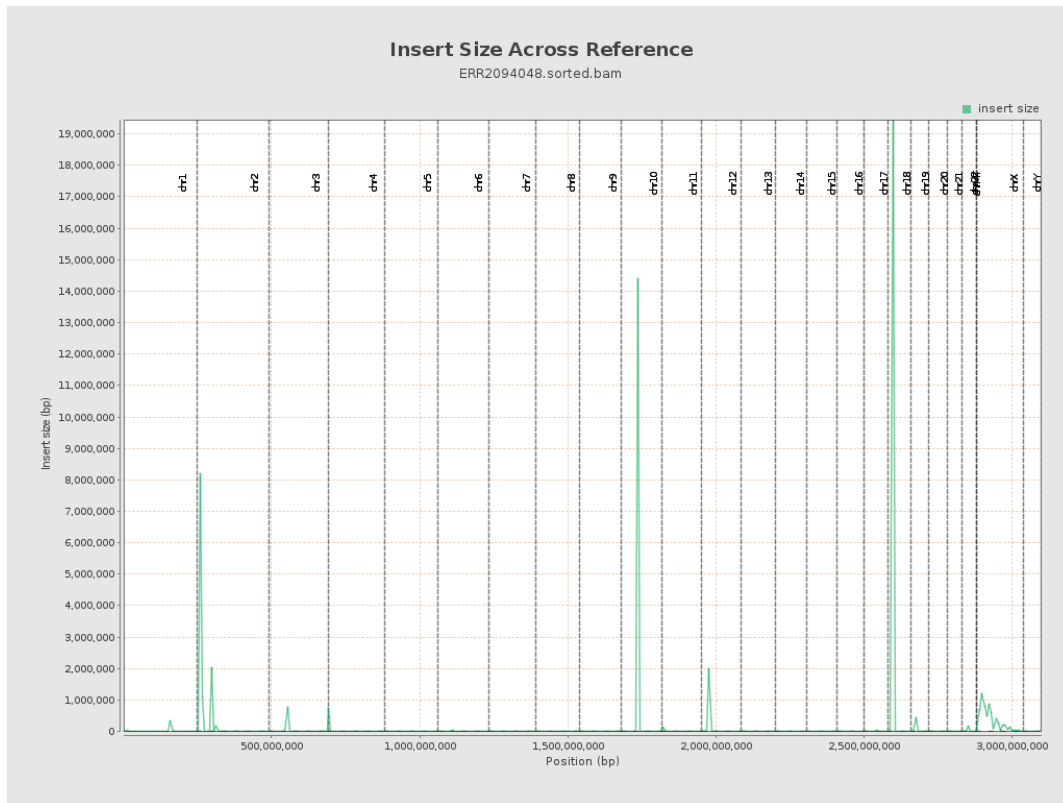
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

