

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:18:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093976.sorted.bam -c -nw 400 -hm 3
```

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_ERR2093976 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093976_1.fastq.gz ERR2093976_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:18:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	479,620
Mapped reads	225,380 / 46.99%
Unmapped reads	254,240 / 53.01%
Mapped paired reads	225,380 / 46.99%
Mapped reads, first in pair	111,118 / 23.17%
Mapped reads, second in pair	114,262 / 23.82%
Mapped reads, both in pair	214,252 / 44.67%
Mapped reads, singletons	11,128 / 2.32%
Secondary alignments	0
Supplementary alignments	9,274 / 1.93%
Read min/max/mean length	30 / 151 / 115.57
Duplicated reads (estimated)	203,963 / 42.53%
Duplication rate	29.85%
Clipped reads	127,114 / 26.5%

2.2. ACGT Content

Number/percentage of A's	7,363,634 / 25.85%
Number/percentage of C's	6,076,912 / 21.33%
Number/percentage of T's	7,935,383 / 27.85%
Number/percentage of G's	7,112,517 / 24.97%
Number/percentage of N's	302 / 0%

GC Percentage	46.3%
---------------	-------

2.3. Coverage

Mean	0.0092
Standard Deviation	20.1716

2.4. Mapping Quality

Mean Mapping Quality	27
----------------------	----

2.5. Insert size

Mean	390,089.79
Standard Deviation	6,394,608.68
P25/Median/P75	173 / 237 / 237

2.6. Mismatches and indels

General error rate	2.63%
Mismatches	730,727
Insertions	9,130
Mapped reads with at least one insertion	3.82%
Deletions	18,556
Mapped reads with at least one deletion	8.01%
Homopolymer indels	49.18%

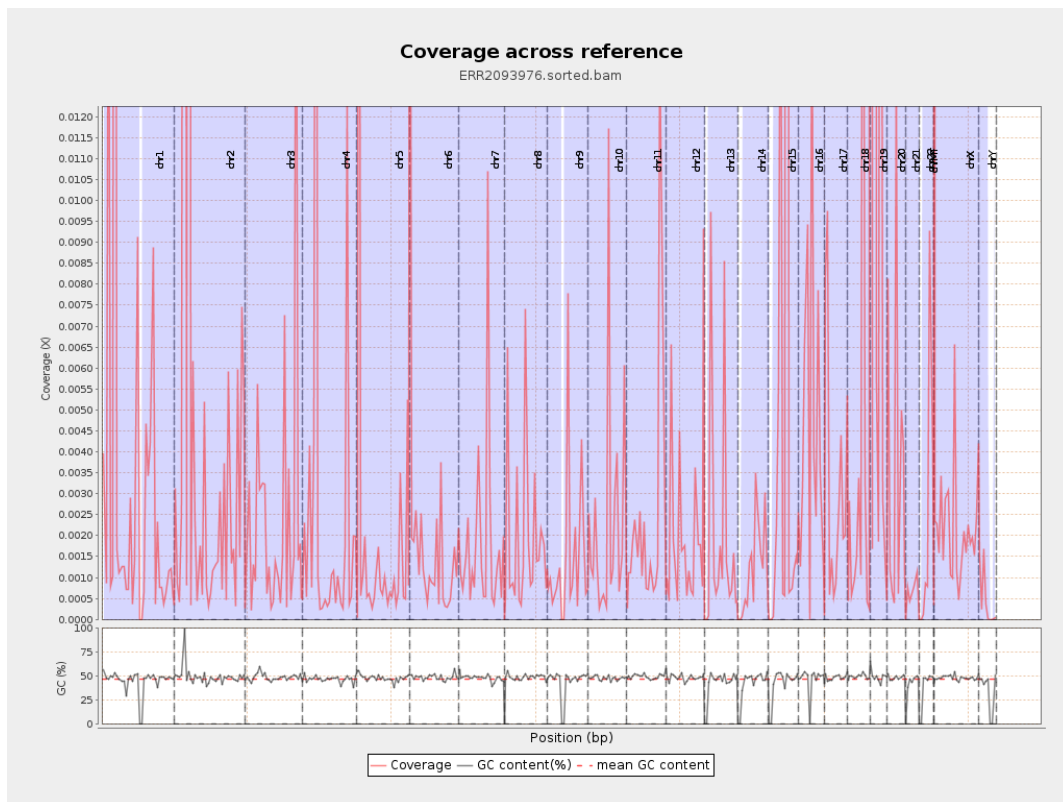
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

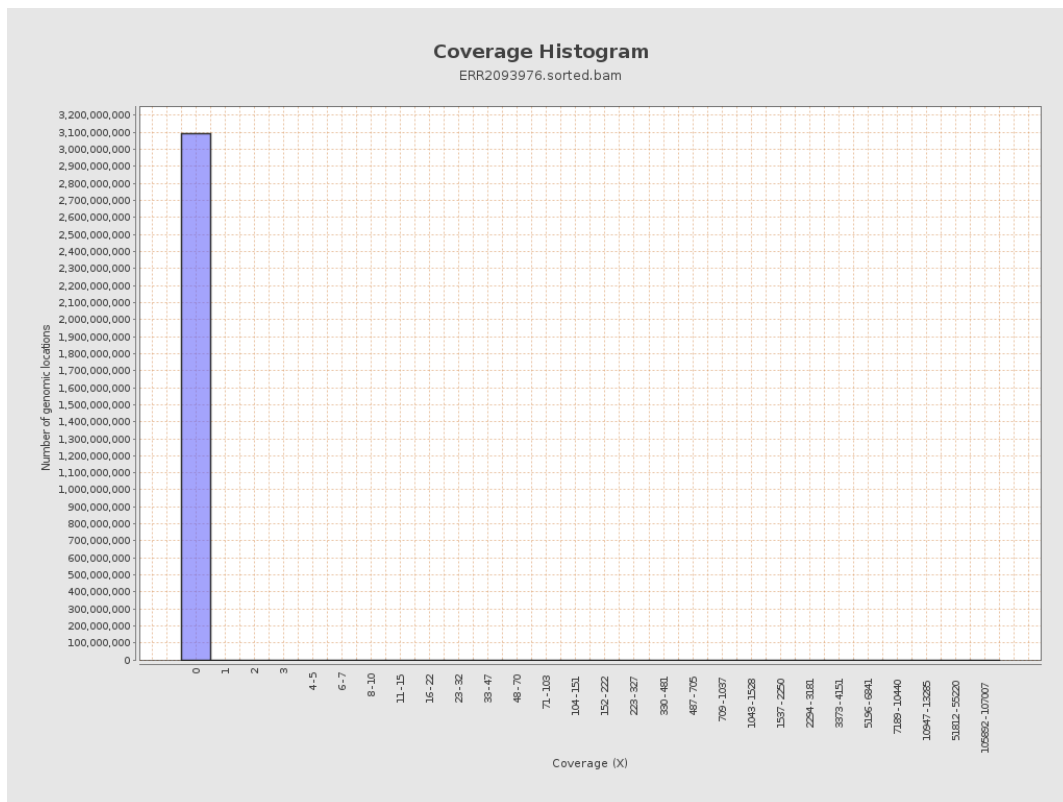
		bases	coverage	deviation
chr1	249250621	983475	0.0039	1.9036
chr2	243199373	1796328	0.0074	4.651
chr3	198022430	507876	0.0026	0.9821
chr4	191154276	514451	0.0027	1.1842
chr5	180915260	470764	0.0026	1.393
chr6	171115067	362792	0.0021	1.3224
chr7	159138663	291768	0.0018	0.3263
chr8	146364022	284096	0.0019	0.4321
chr9	141213431	210294	0.0015	0.2616
chr10	135534747	309731	0.0023	0.7403
chr11	135006516	365775	0.0027	0.6445
chr12	133851895	261676	0.002	0.4051
chr13	115169878	218992	0.0019	0.5529
chr14	107349540	133922	0.0012	0.1956
chr15	102531392	1067042	0.0104	6.1083
chr16	90354753	439692	0.0049	0.9377
chr17	81195210	270326	0.0033	0.7031
chr18	78077248	305094	0.0039	1.3332
chr19	59128983	2778040	0.047	19.4983
chr20	63025520	243169	0.0039	0.8835
chr21	48129895	31832	0.0007	0.1149
chr22	51304566	117845	0.0023	0.5845
chrMT	16571	16205126	977.9208	8,543.7116
chrX	155270560	331627	0.0021	0.3523

chrY	59373566	26399	0.0004	0.1257
------	----------	-------	--------	--------

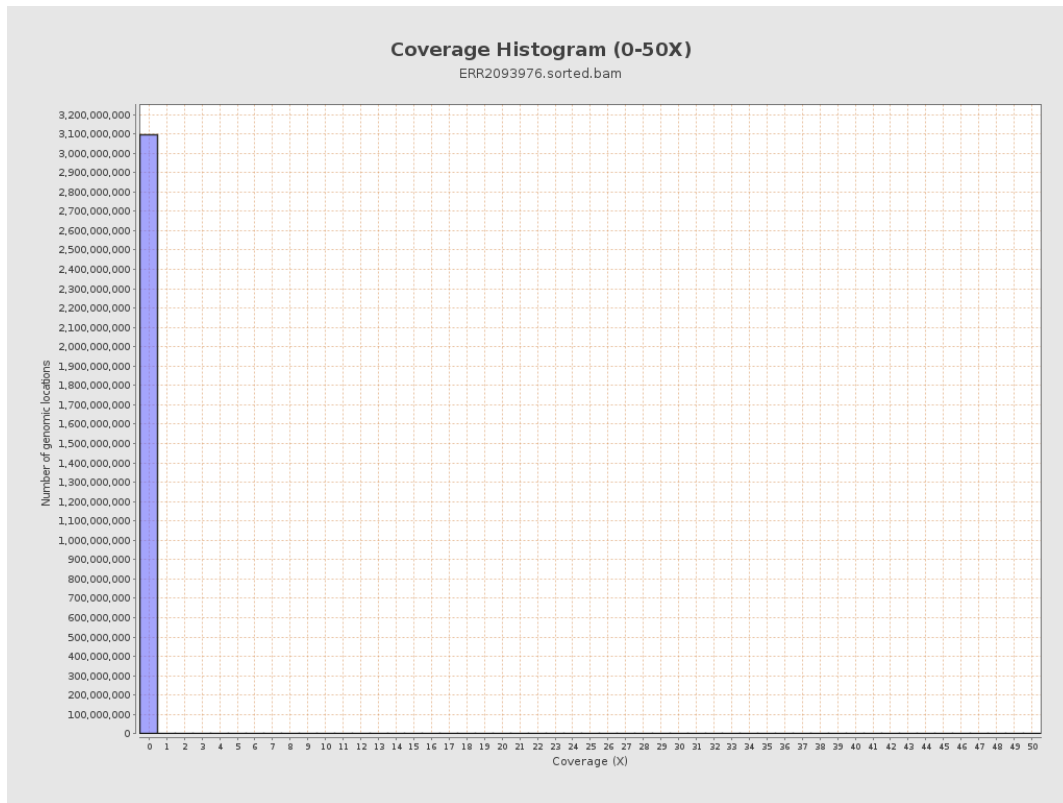
3. Results : Coverage across reference



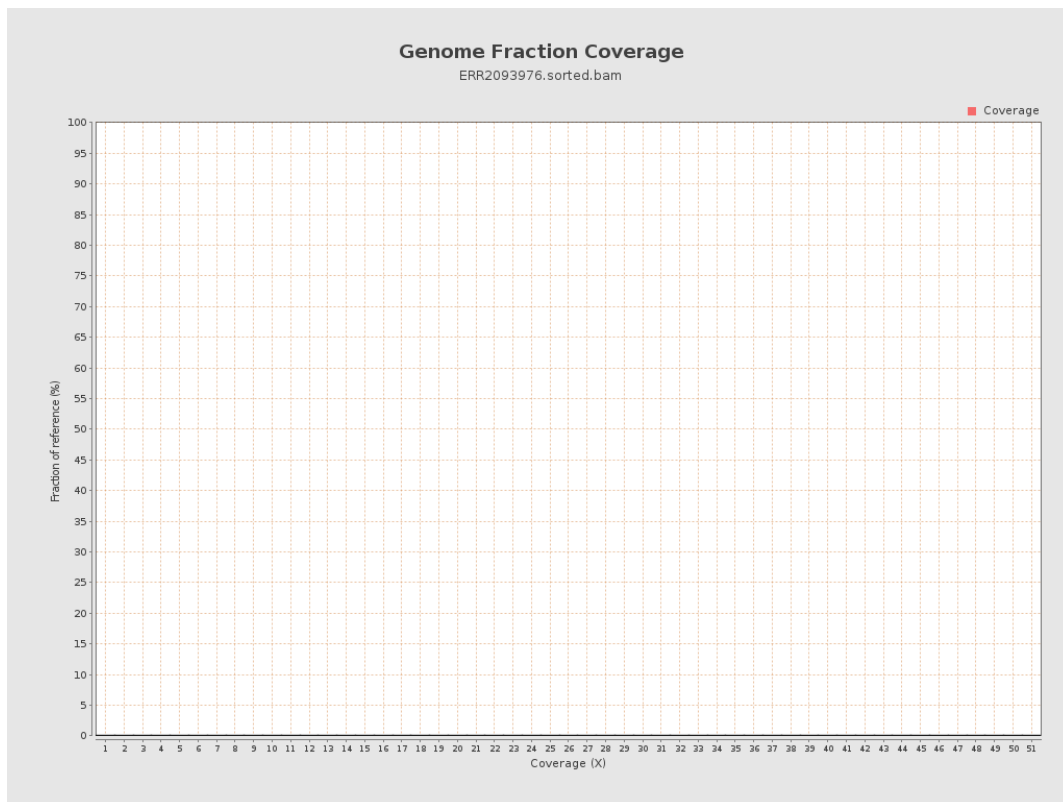
4. Results : Coverage Histogram



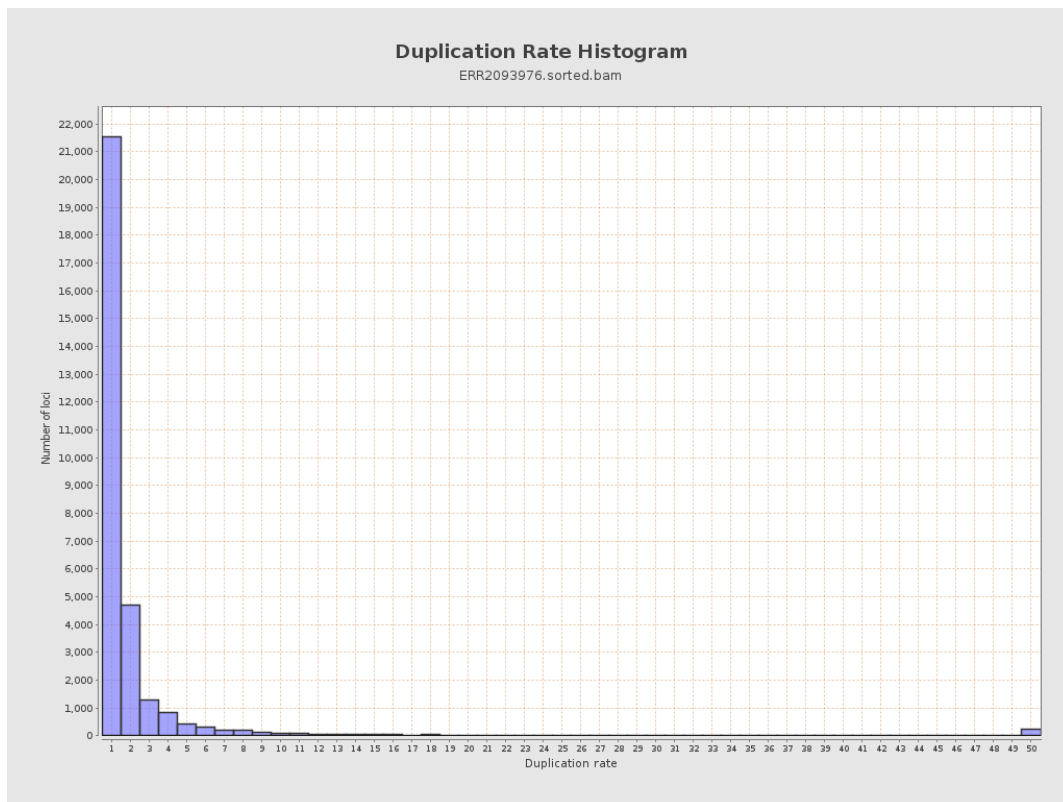
5. Results : Coverage Histogram (0-50X)



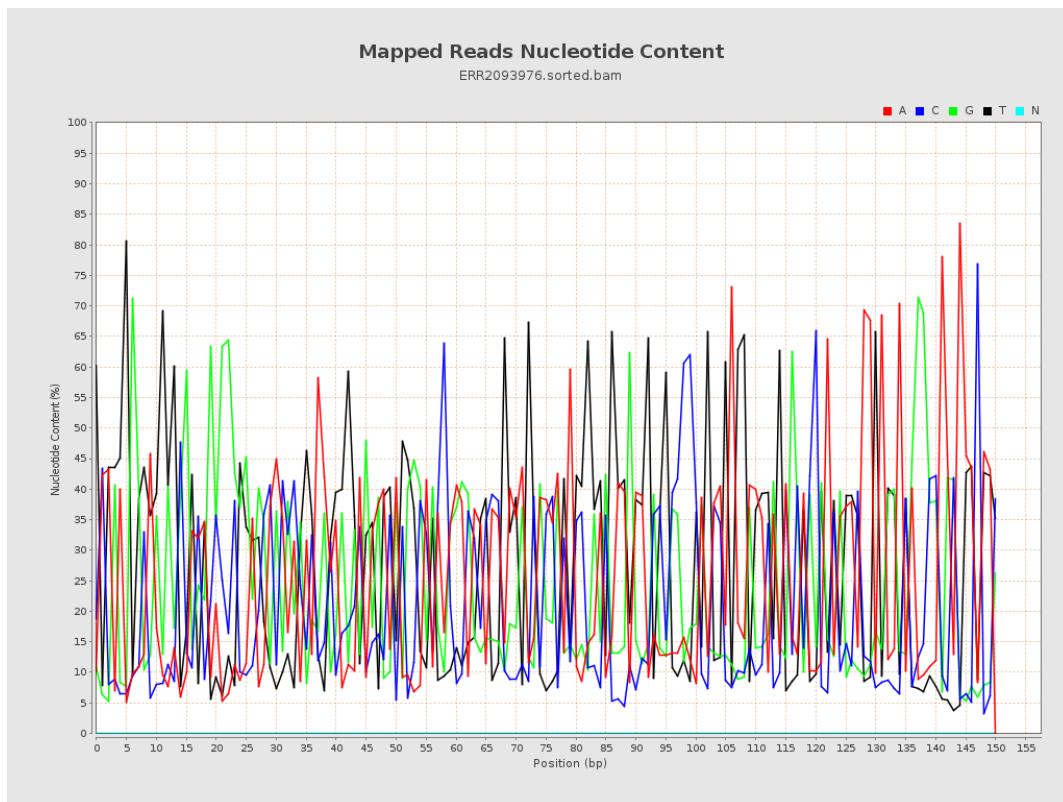
6. Results : Genome Fraction Coverage



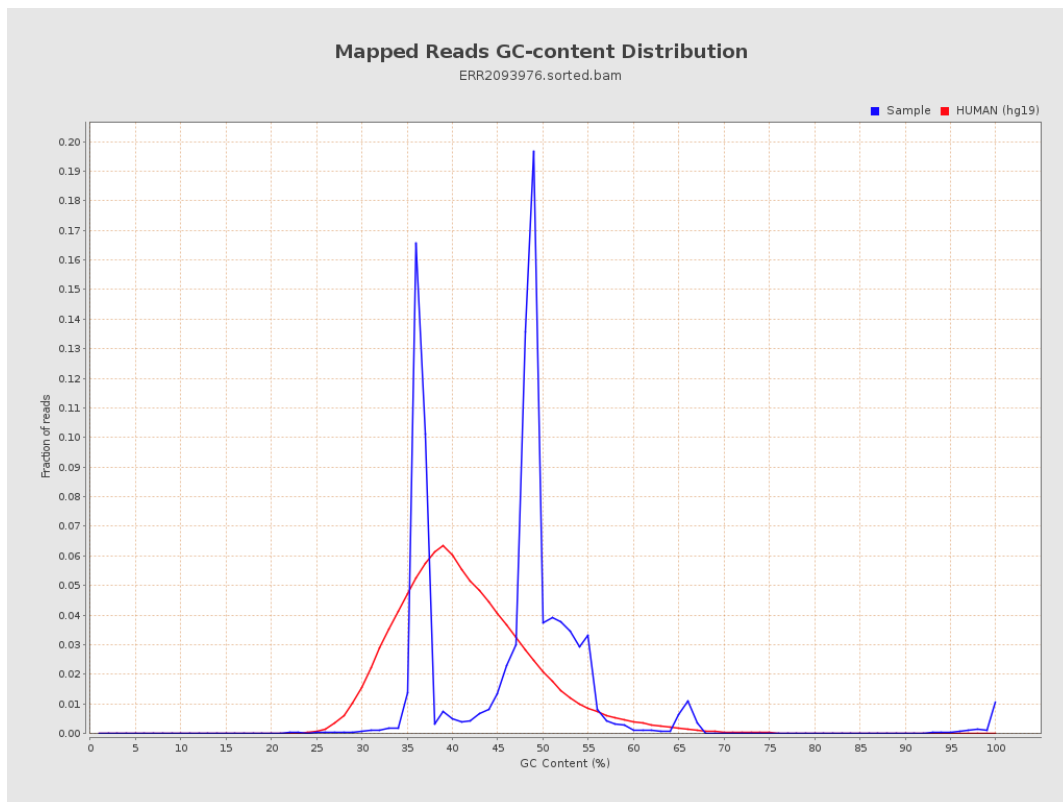
7. Results : Duplication Rate Histogram



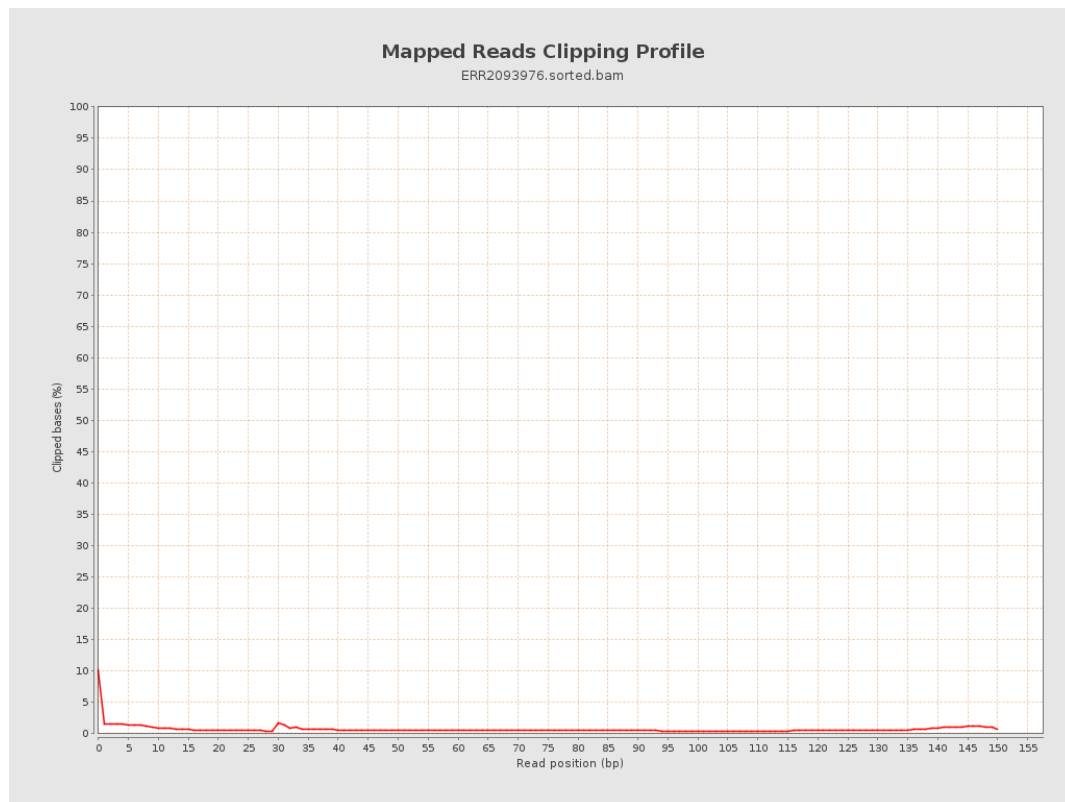
8. Results : Mapped Reads Nucleotide Content



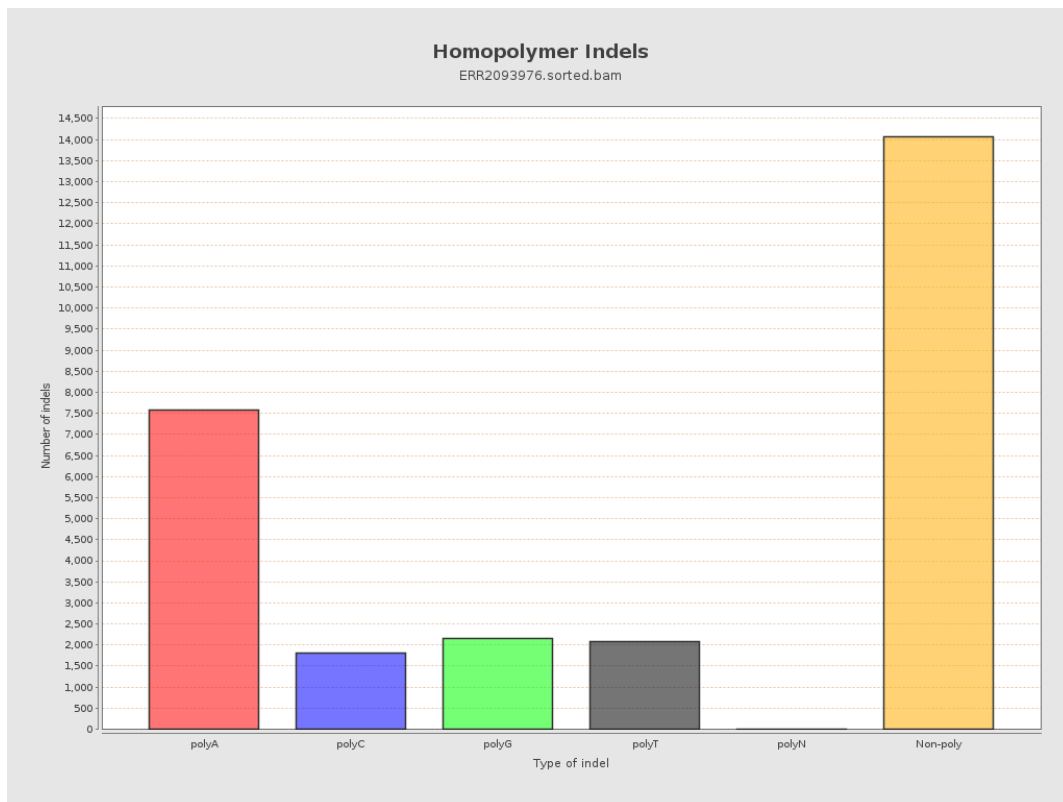
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



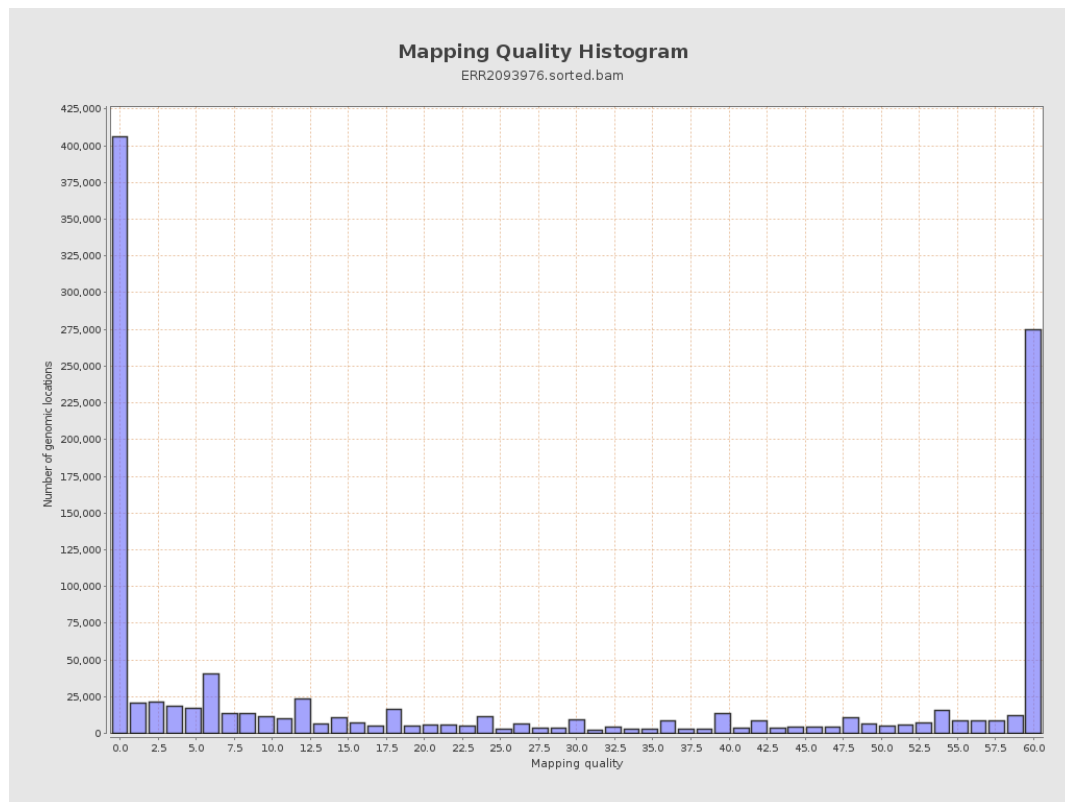
11. Results : Homopolymer Indels



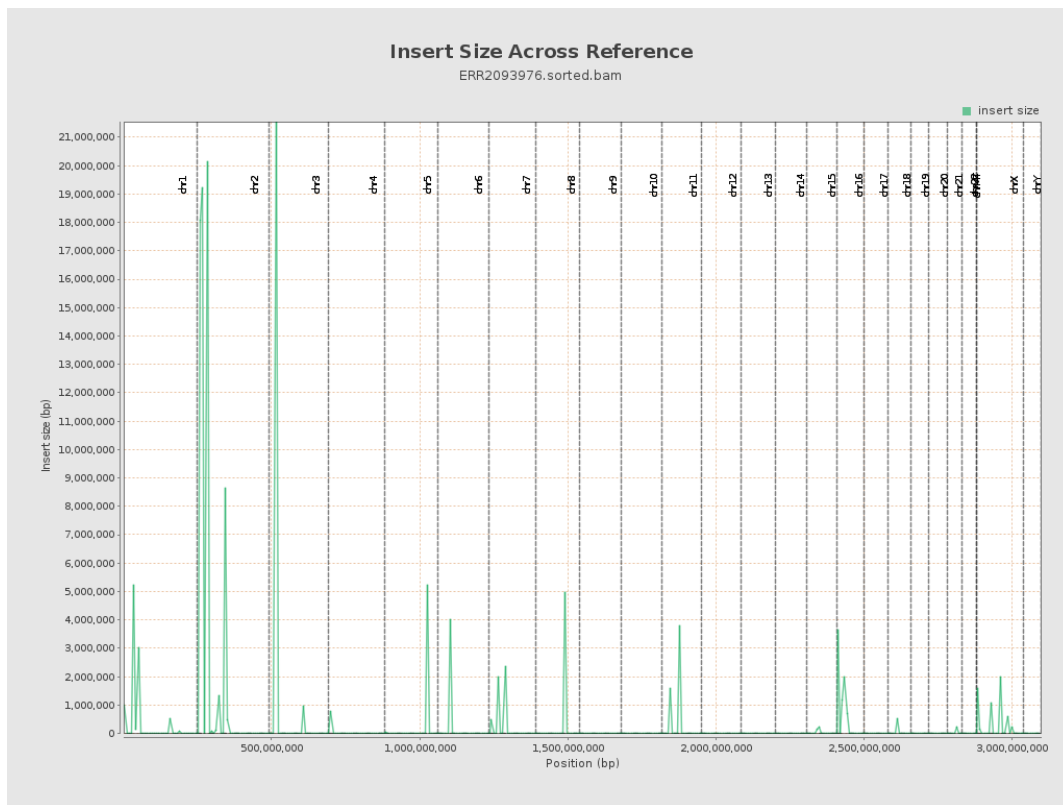
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

