

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:37:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093981.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_ERR2093981 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093981_1.fastq.gz ERR2093981_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:37:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	332,610
Mapped reads	303,532 / 91.26%
Unmapped reads	29,078 / 8.74%
Mapped paired reads	303,532 / 91.26%
Mapped reads, first in pair	152,652 / 45.9%
Mapped reads, second in pair	150,880 / 45.36%
Mapped reads, both in pair	300,550 / 90.36%
Mapped reads, singletons	2,982 / 0.9%
Secondary alignments	0
Supplementary alignments	17,317 / 5.21%
Read min/max/mean length	30 / 151 / 136.84
Duplicated reads (estimated)	283,213 / 85.15%
Duplication rate	49.09%
Clipped reads	147,841 / 44.45%

2.2. ACGT Content

Number/percentage of A's	10,030,437 / 26.27%
Number/percentage of C's	8,936,167 / 23.4%
Number/percentage of T's	9,518,324 / 24.93%
Number/percentage of G's	9,699,658 / 25.4%
Number/percentage of N's	416 / 0%

GC Percentage	48.8%
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2.3. Coverage

Mean	0.0126
Standard Deviation	2.4443

2.4. Mapping Quality

Mean Mapping Quality	41.95
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2.5. Insert size

Mean	906,309.87
Standard Deviation	8,742,962.16
P25/Median/P75	129 / 165 / 199

2.6. Mismatches and indels

General error rate	3.59%
Mismatches	1,327,742
Insertions	21,861
Mapped reads with at least one insertion	7.07%
Deletions	104,690
Mapped reads with at least one deletion	33.15%
Homopolymer indels	29.54%

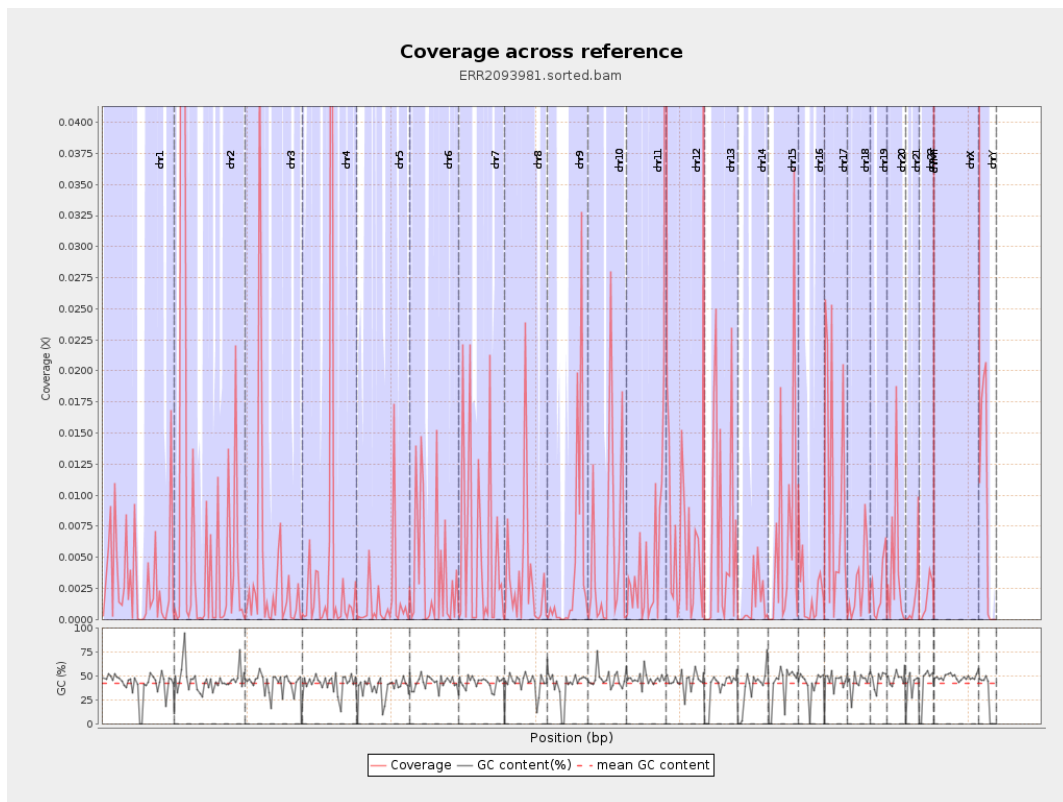
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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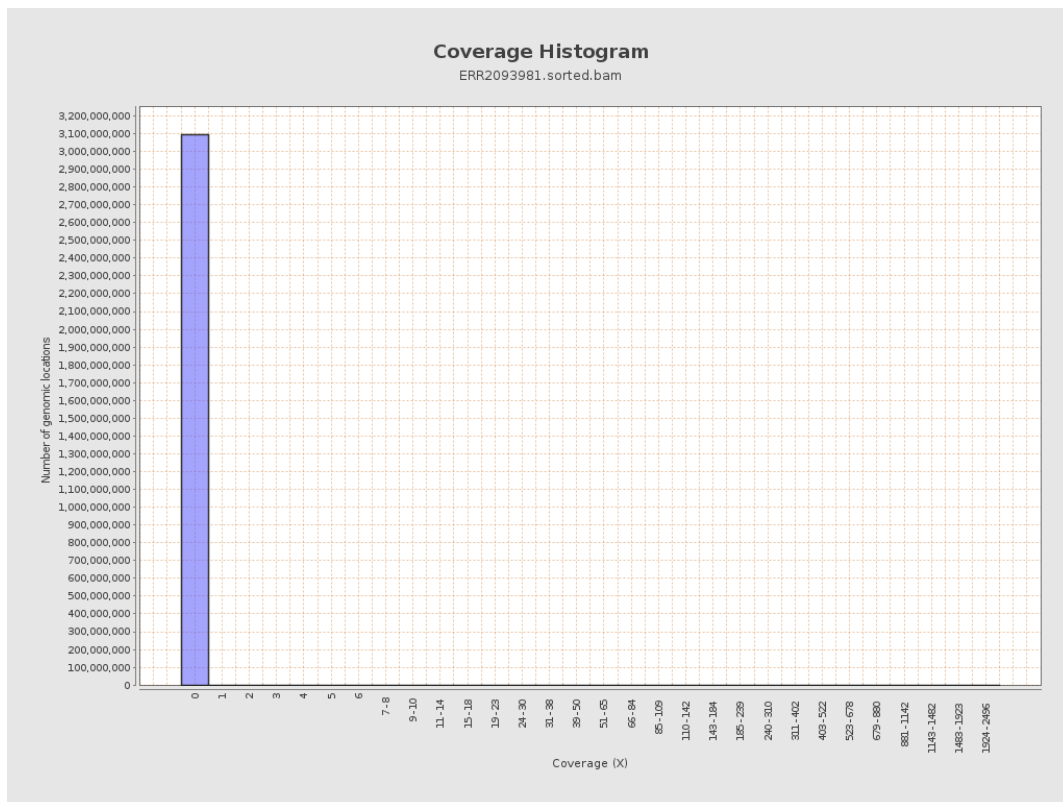
		bases	coverage	deviation
chr1	249250621	781760	0.0031	0.978
chr2	243199373	1863289	0.0077	2.4681
chr3	198022430	678434	0.0034	1.1605
chr4	191154276	940450	0.0049	1.6204
chr5	180915260	263195	0.0015	0.8812
chr6	171115067	653226	0.0038	1.1634
chr7	159138663	844499	0.0053	1.5642
chr8	146364022	484419	0.0033	1.067
chr9	141213431	578140	0.0041	1.2709
chr10	135534747	749667	0.0055	1.6061
chr11	135006516	683447	0.0051	1.3141
chr12	133851895	909014	0.0068	1.6745
chr13	115169878	777547	0.0068	1.9076
chr14	107349540	137911	0.0013	0.4422
chr15	102531392	662497	0.0065	1.8025
chr16	90354753	206874	0.0023	0.654
chr17	81195210	888221	0.0109	2.5229
chr18	78077248	224166	0.0029	0.7772
chr19	59128983	139973	0.0024	0.6692
chr20	63025520	272765	0.0043	1.36
chr21	48129895	85213	0.0018	0.3047
chr22	51304566	81313	0.0016	0.3769
chrMT	16571	913961	55.1542	225.2636
chrX	155270560	24578733	0.1583	8.563

chrY	59373566	509337	0.0086	1.1762
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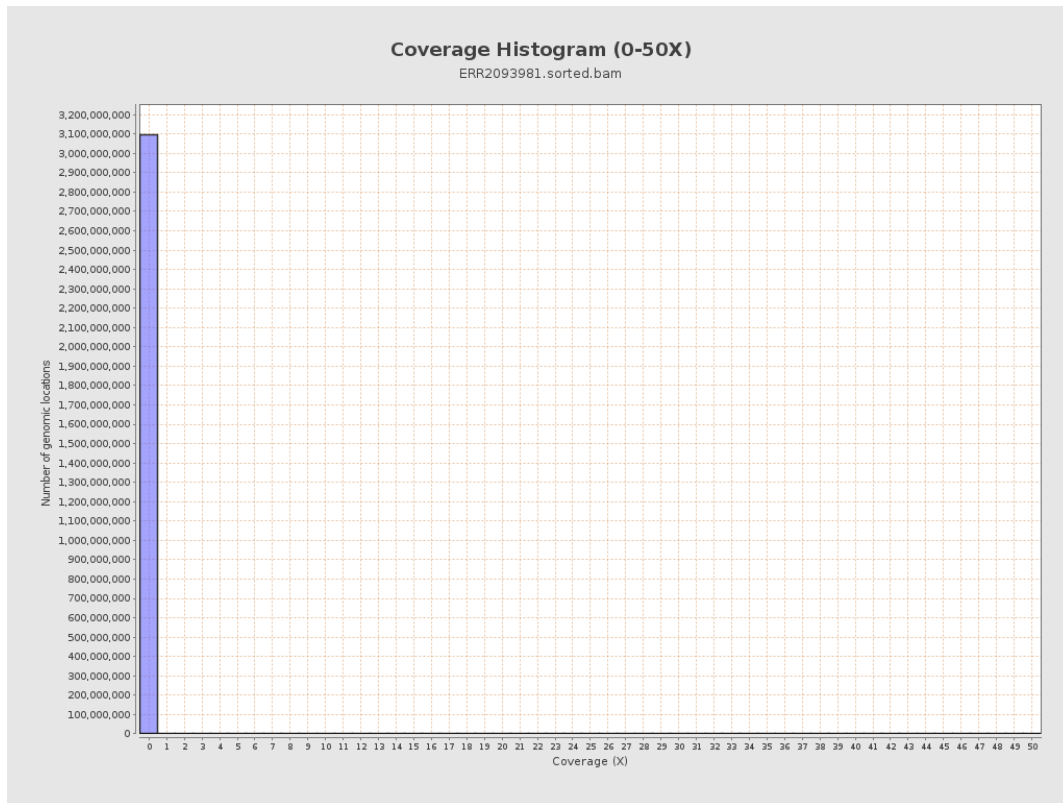
3. Results : Coverage across reference



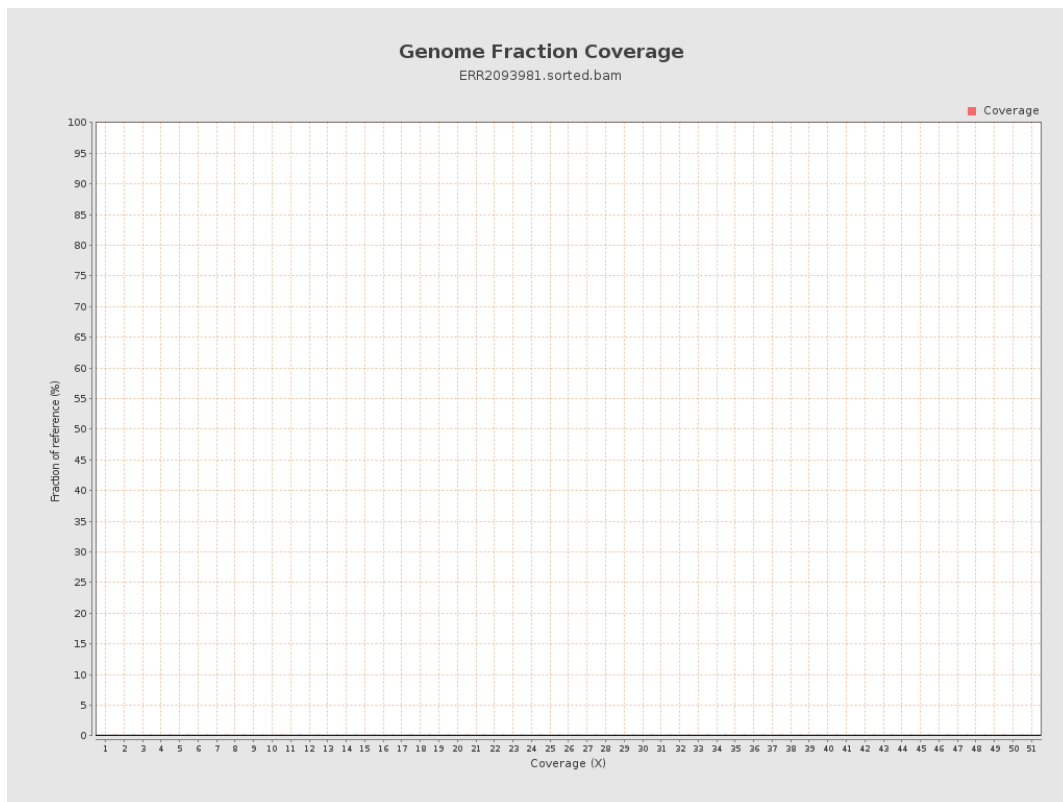
4. Results : Coverage Histogram



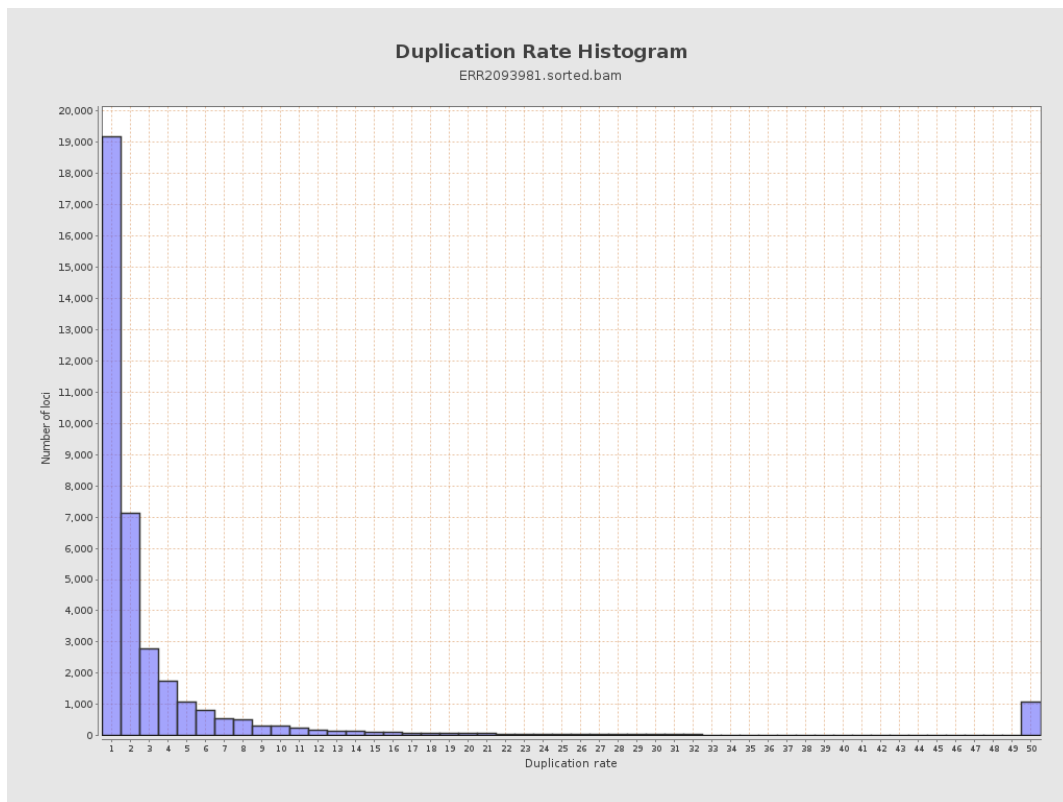
5. Results : Coverage Histogram (0-50X)



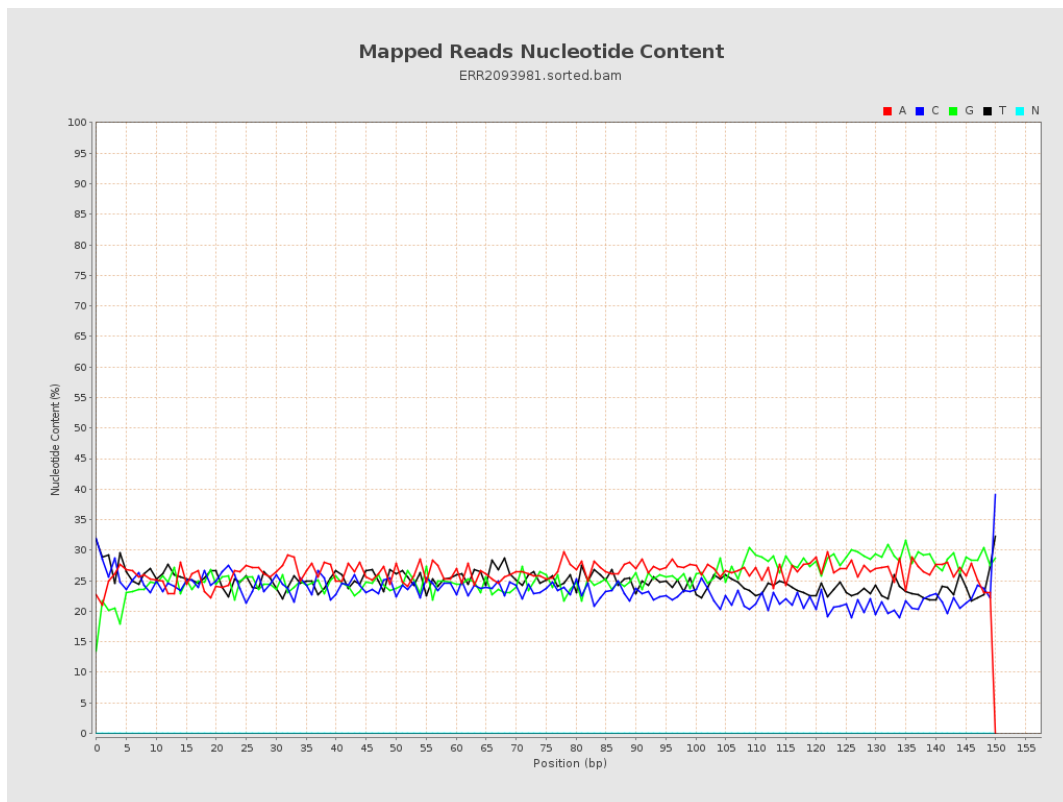
6. Results : Genome Fraction Coverage



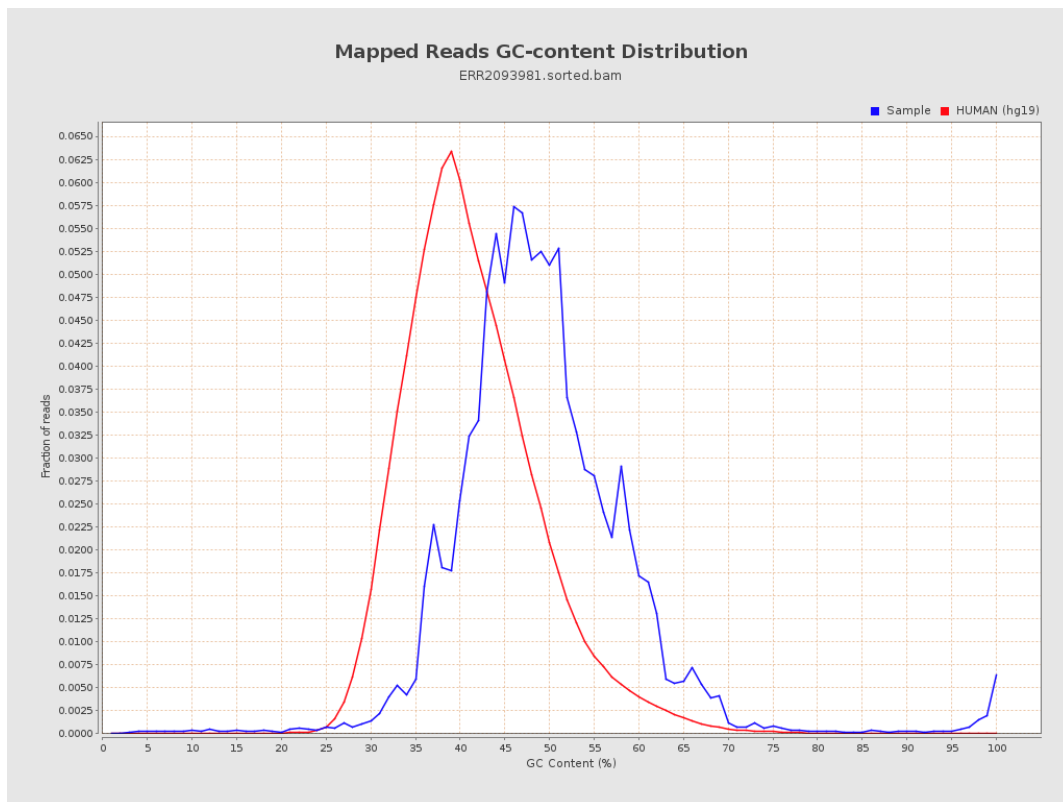
7. Results : Duplication Rate Histogram



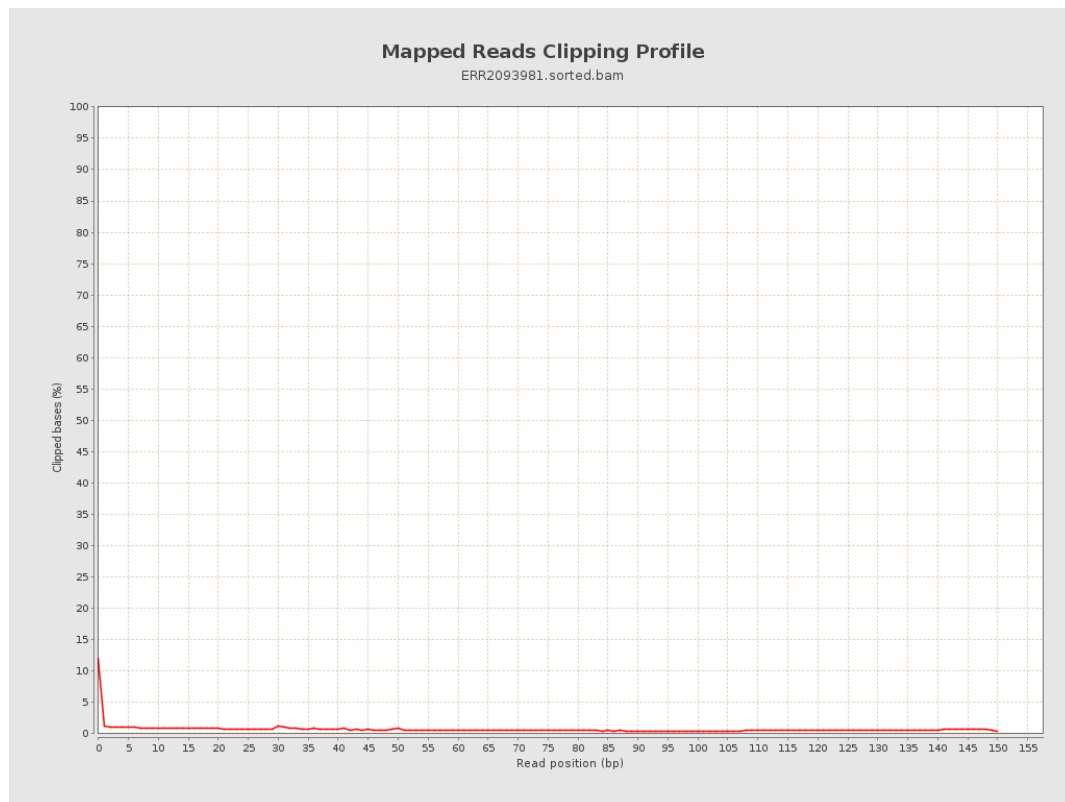
8. Results : Mapped Reads Nucleotide Content



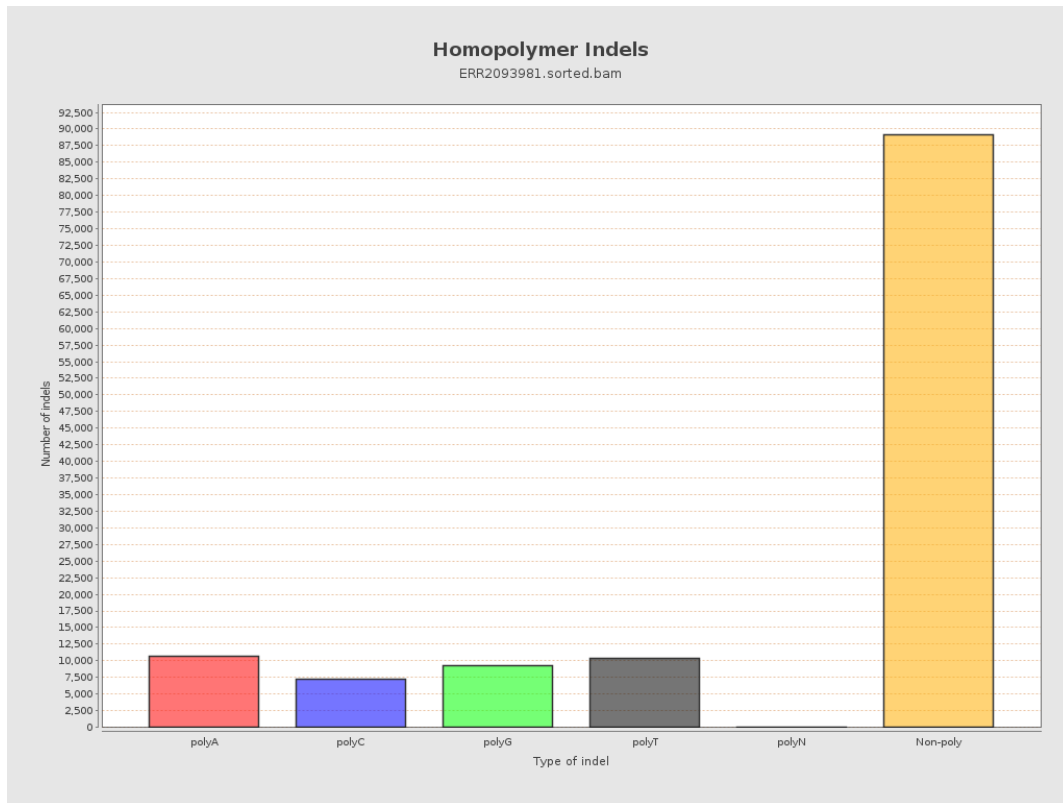
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



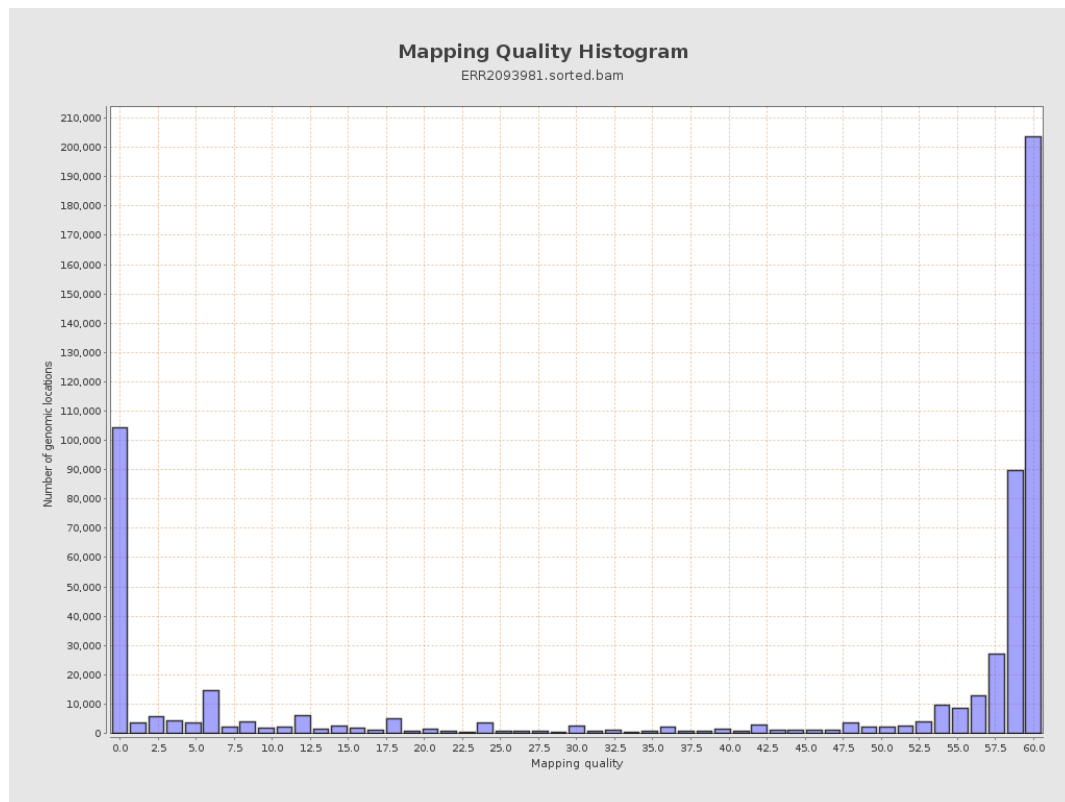
11. Results : Homopolymer Indels



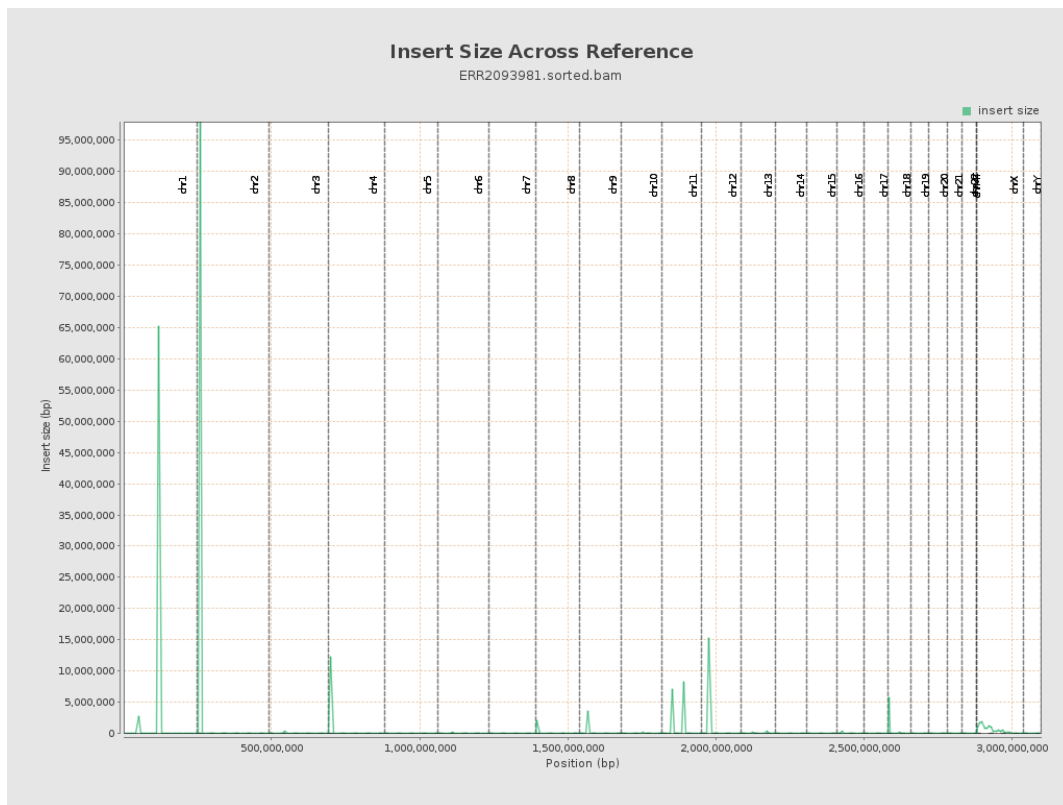
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

