

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:49:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093986.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_ERR2093986 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093986_1.fastq.gz ERR2093986_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:49:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	388,532
Mapped reads	371,589 / 95.64%
Unmapped reads	16,943 / 4.36%
Mapped paired reads	371,589 / 95.64%
Mapped reads, first in pair	186,867 / 48.1%
Mapped reads, second in pair	184,722 / 47.54%
Mapped reads, both in pair	368,074 / 94.73%
Mapped reads, singletons	3,515 / 0.9%
Secondary alignments	0
Supplementary alignments	22,750 / 5.86%
Read min/max/mean length	30 / 151 / 142.95
Duplicated reads (estimated)	349,944 / 90.07%
Duplication rate	50.08%
Clipped reads	182,577 / 46.99%

2.2. ACGT Content

Number/percentage of A's	12,472,871 / 26.28%
Number/percentage of C's	11,208,622 / 23.62%
Number/percentage of T's	11,807,309 / 24.88%
Number/percentage of G's	11,963,663 / 25.21%
Number/percentage of N's	456 / 0%

GC Percentage	48.83%
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2.3. Coverage

Mean	0.0156
Standard Deviation	3.0468

2.4. Mapping Quality

Mean Mapping Quality	41.48
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2.5. Insert size

Mean	1,106,485.55
Standard Deviation	9,490,894.58
P25/Median/P75	133 / 167 / 203

2.6. Mismatches and indels

General error rate	3.51%
Mismatches	1,612,105
Insertions	25,450
Mapped reads with at least one insertion	6.74%
Deletions	125,154
Mapped reads with at least one deletion	32.32%
Homopolymer indels	28.83%

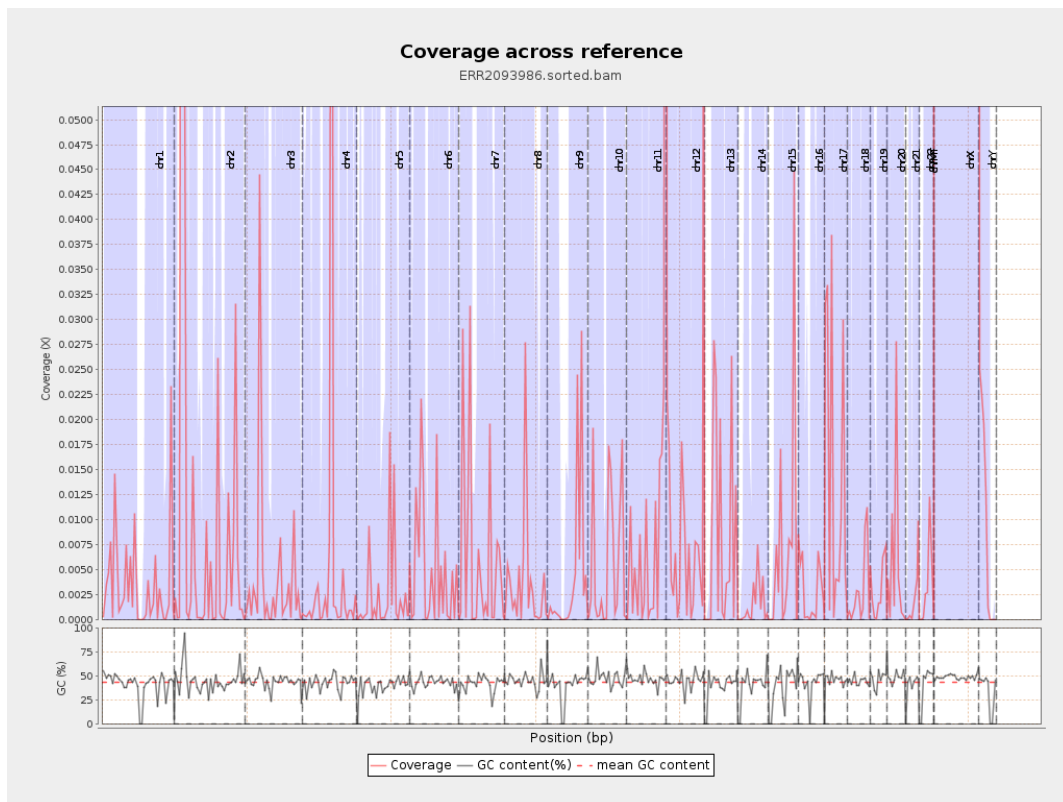
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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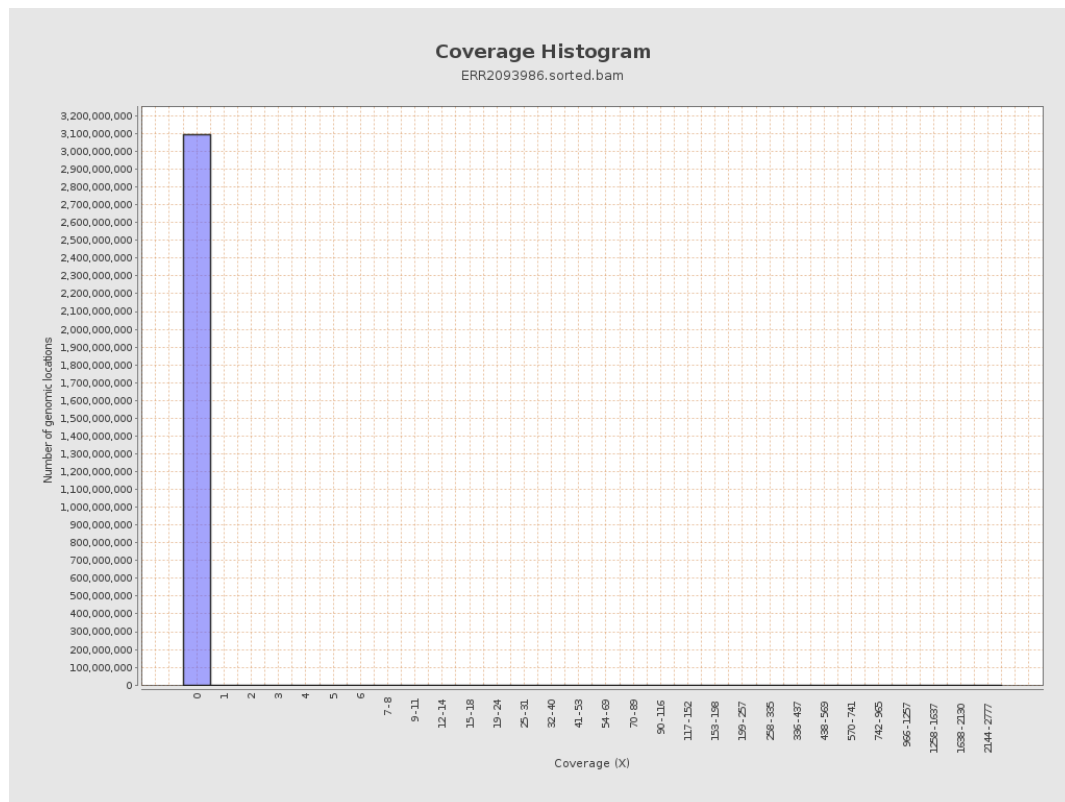
		bases	coverage	deviation
chr1	249250621	877911	0.0035	1.1583
chr2	243199373	2543934	0.0105	3.2304
chr3	198022430	762027	0.0038	1.2105
chr4	191154276	1197356	0.0063	2.3184
chr5	180915260	460647	0.0025	1.2176
chr6	171115067	853479	0.005	1.4182
chr7	159138663	966783	0.0061	1.8005
chr8	146364022	520431	0.0036	1.0926
chr9	141213431	598681	0.0042	1.2225
chr10	135534747	749975	0.0055	1.667
chr11	135006516	1065381	0.0079	2.0628
chr12	133851895	1064111	0.0079	2.0105
chr13	115169878	956356	0.0083	2.192
chr14	107349540	157986	0.0015	0.5457
chr15	102531392	707666	0.0069	1.9041
chr16	90354753	259138	0.0029	0.6866
chr17	81195210	1204120	0.0148	3.6085
chr18	78077248	231563	0.003	0.8382
chr19	59128983	162752	0.0028	0.7363
chr20	63025520	372345	0.0059	1.9797
chr21	48129895	96899	0.002	0.3891
chr22	51304566	159955	0.0031	0.798
chrMT	16571	1210306	73.0376	317.6684
chrX	155270560	30563326	0.1968	10.5401

chrY	59373566	566956	0.0095	1.2643
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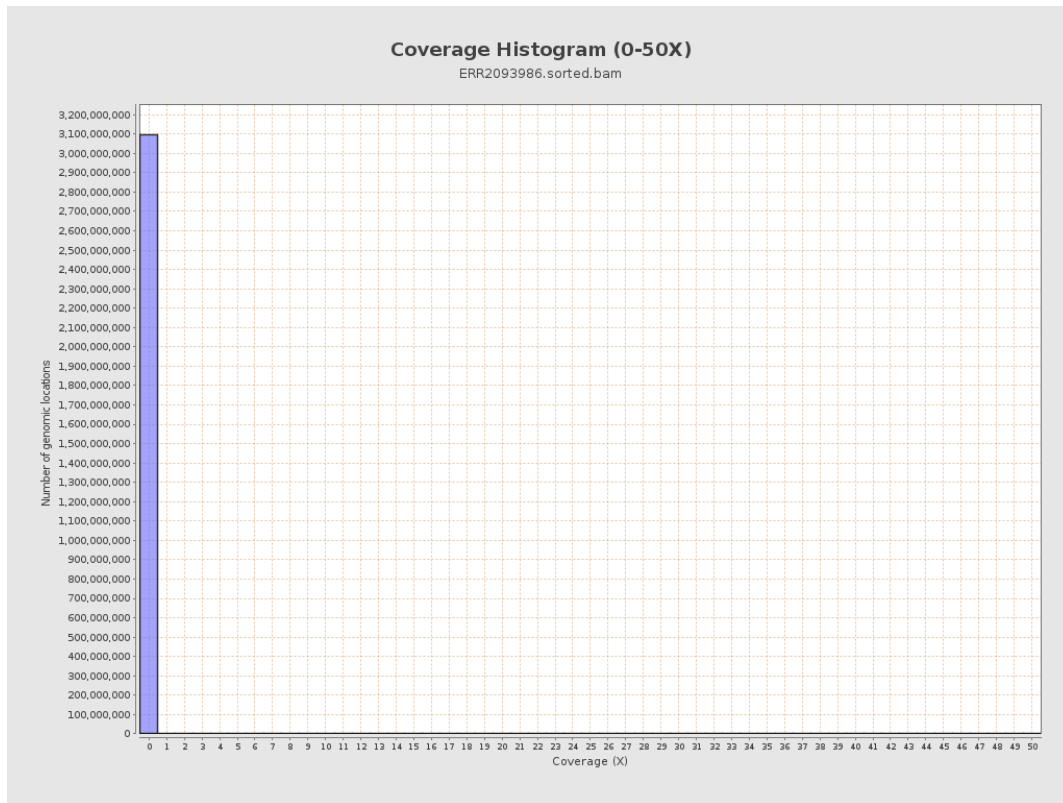
3. Results : Coverage across reference



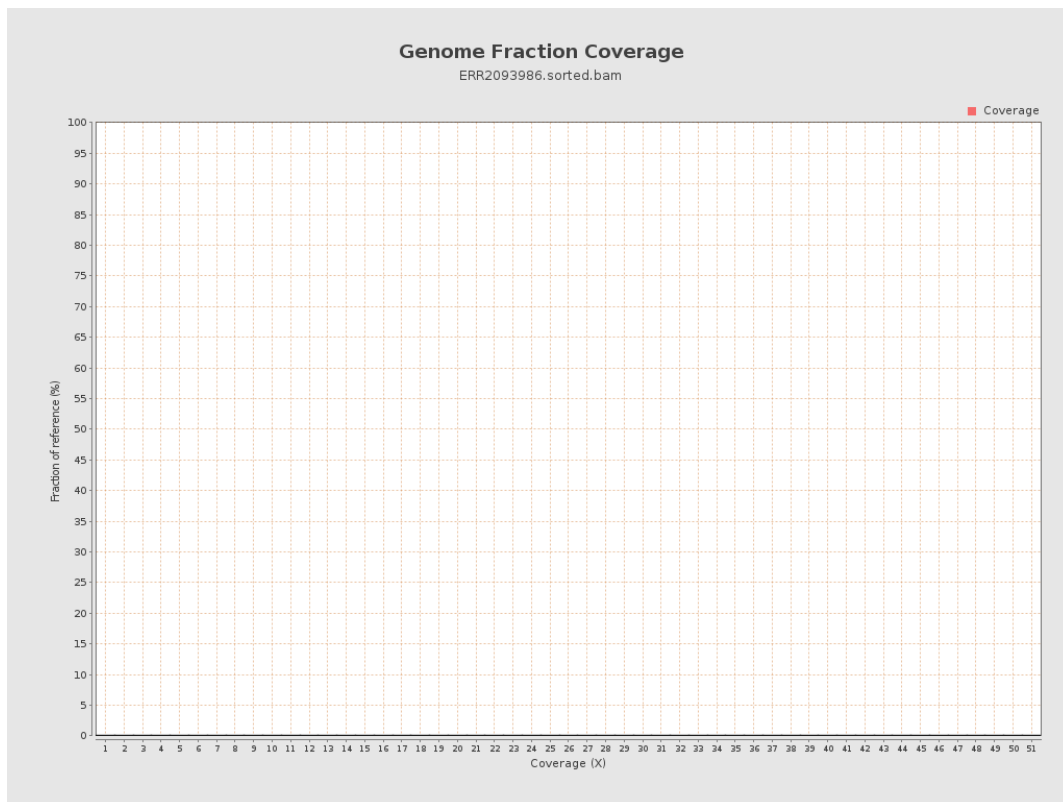
4. Results : Coverage Histogram



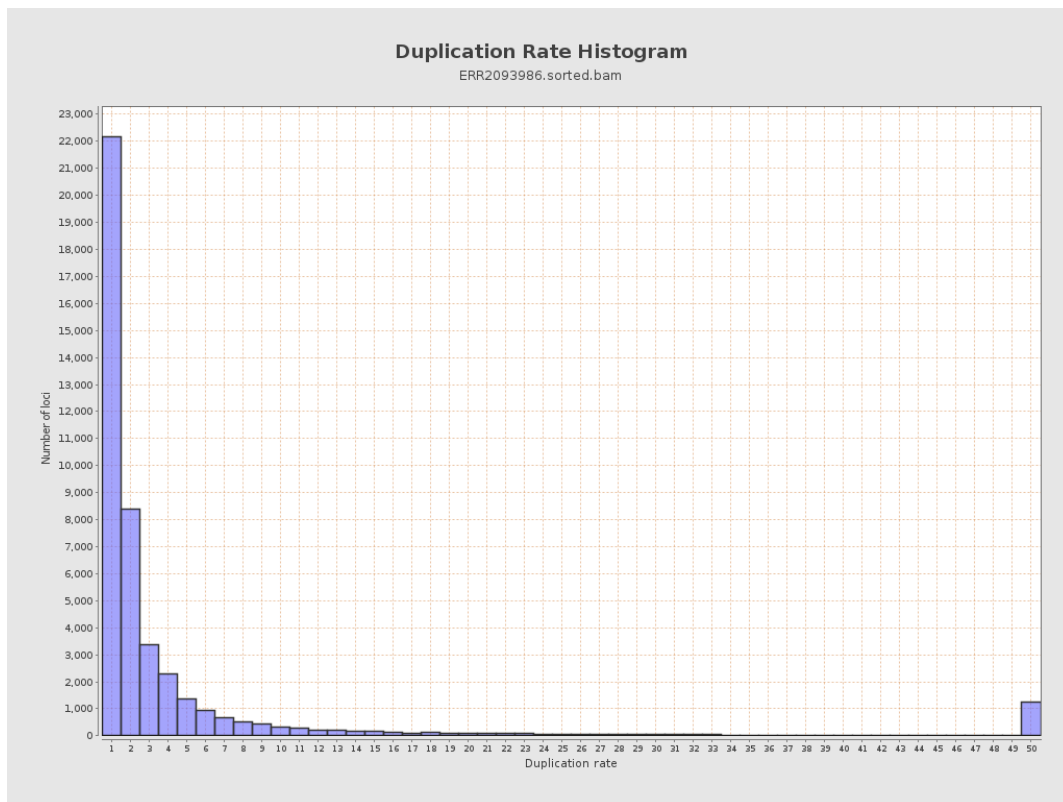
5. Results : Coverage Histogram (0-50X)



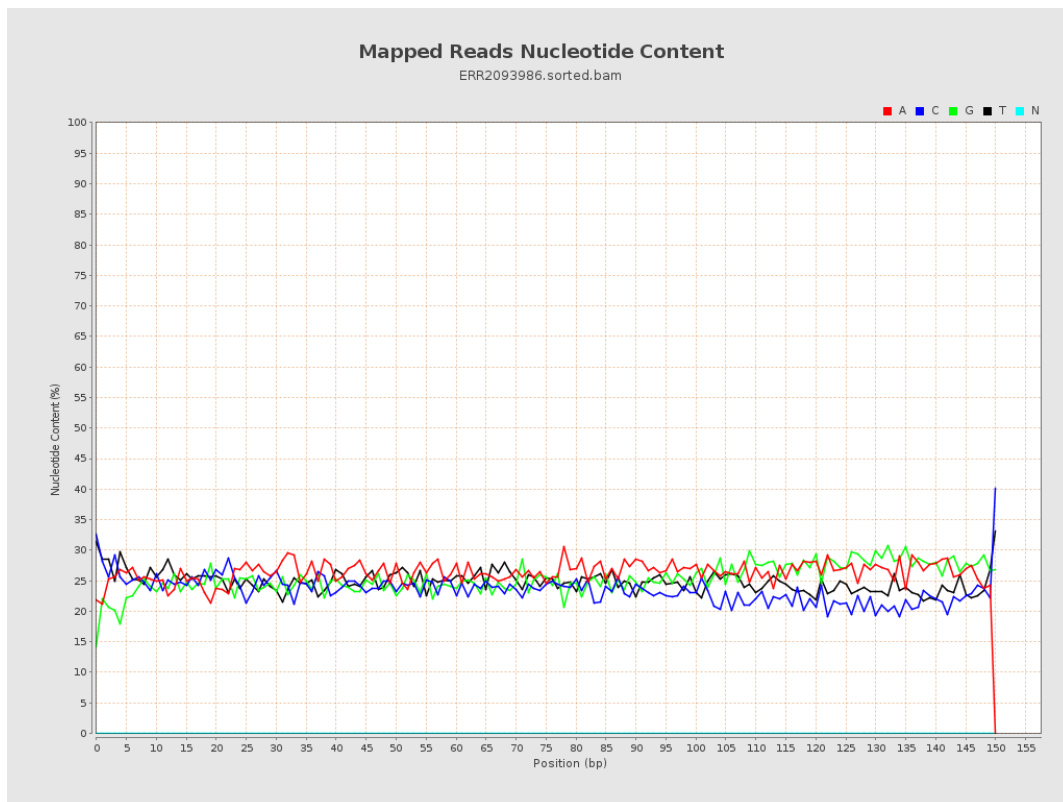
6. Results : Genome Fraction Coverage



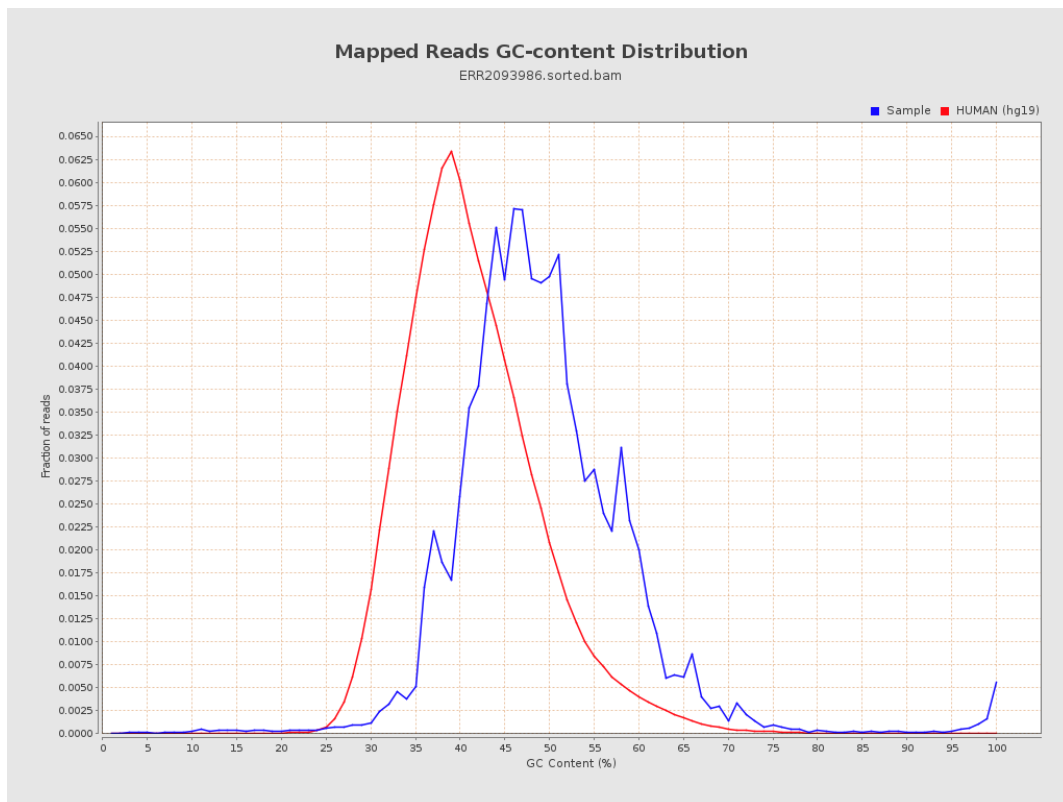
7. Results : Duplication Rate Histogram



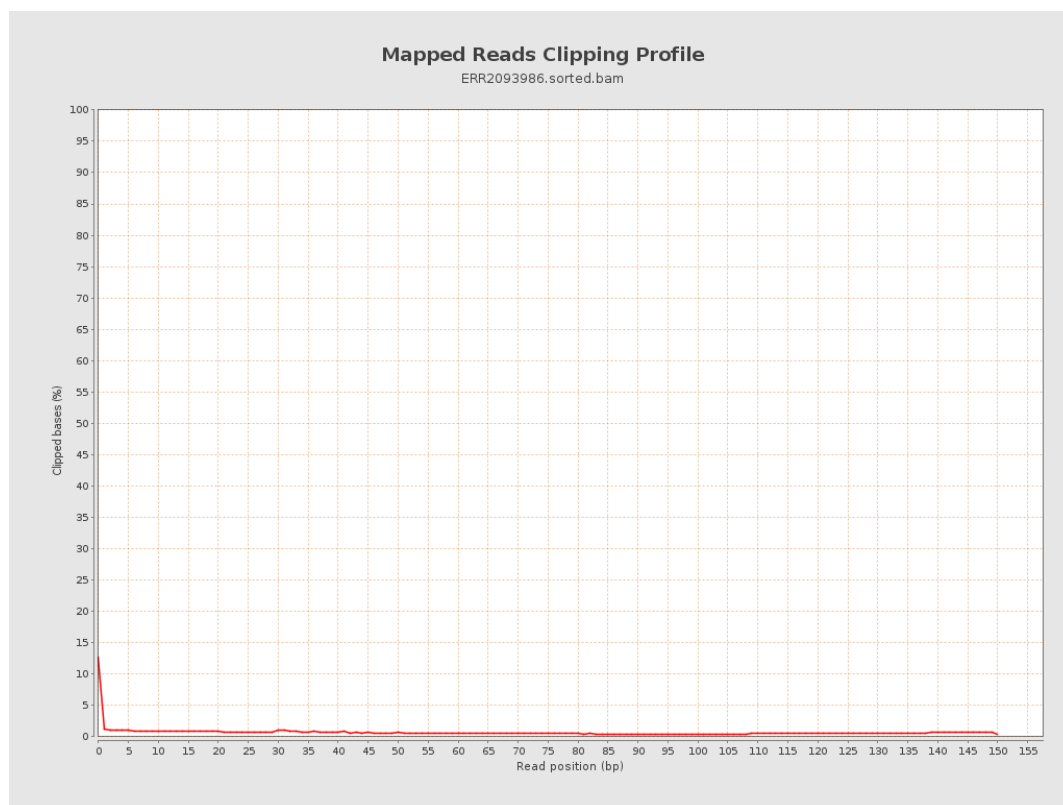
8. Results : Mapped Reads Nucleotide Content



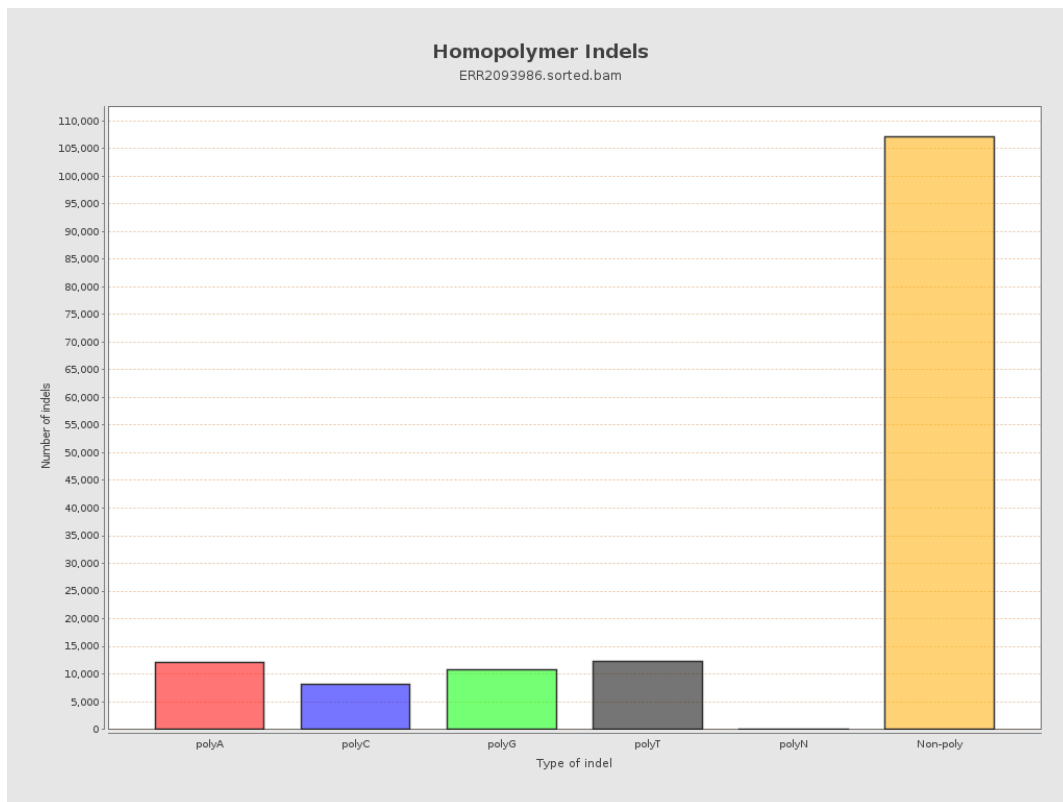
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



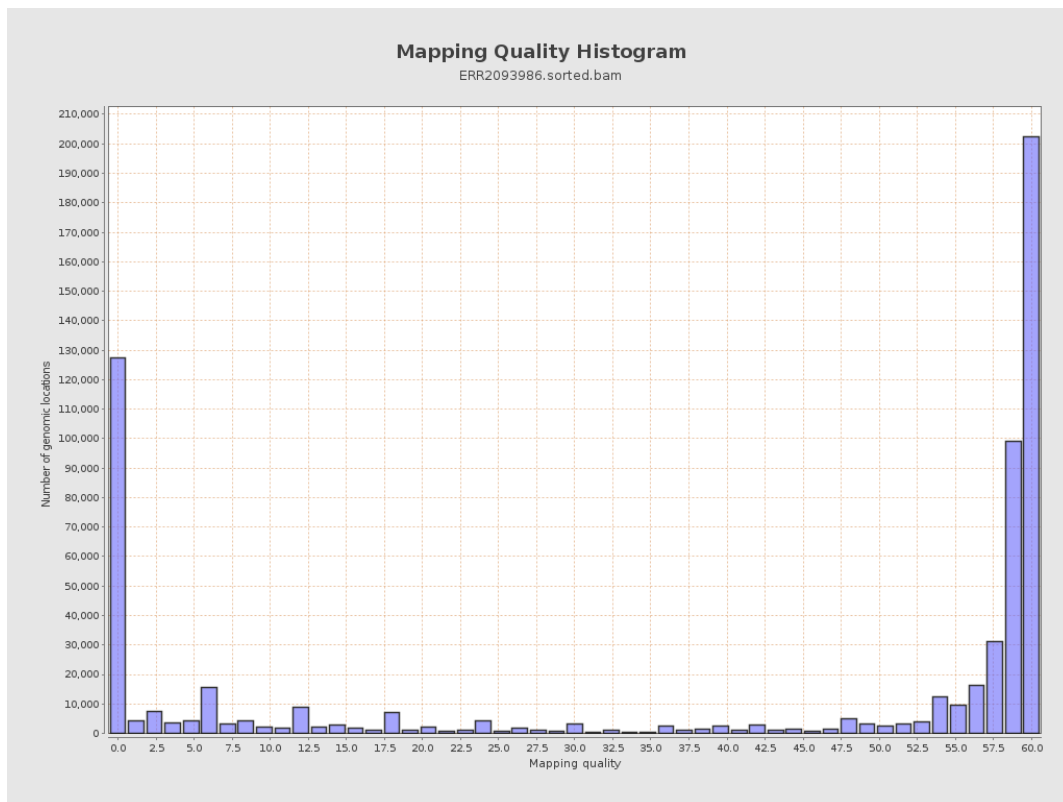
11. Results : Homopolymer Indels



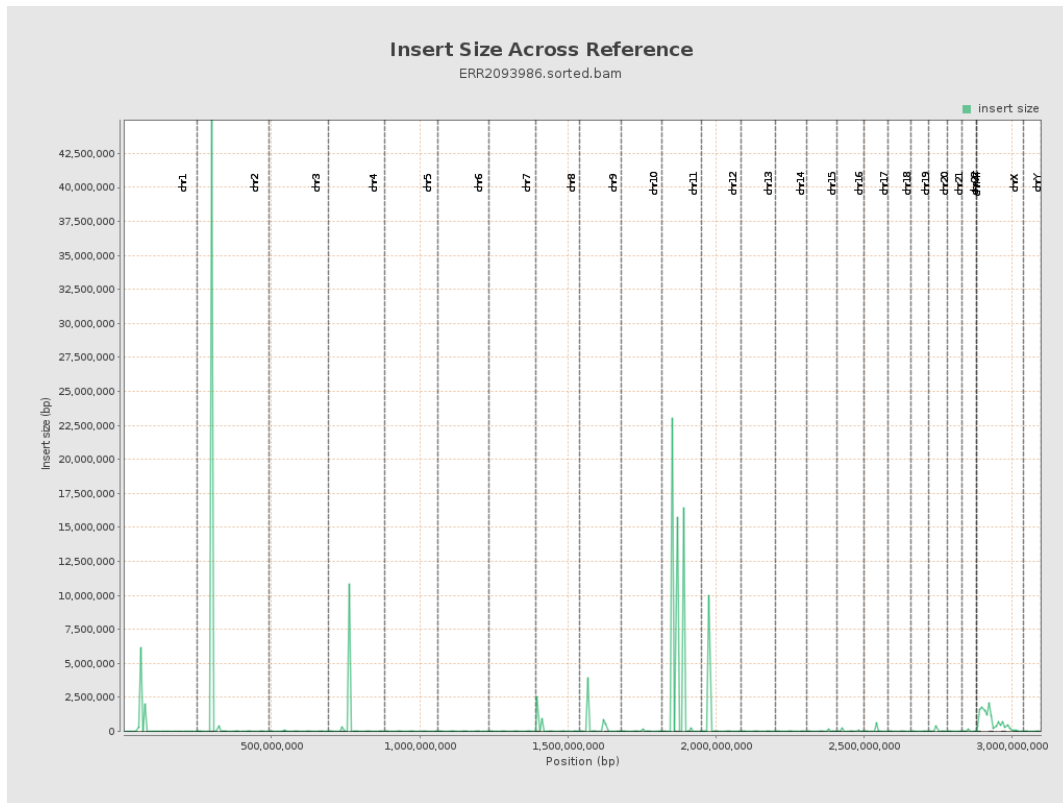
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

