

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:52:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093987.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_ERR2093987 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093987_1.fastq.gz ERR2093987_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:52:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	447,882
Mapped reads	438,132 / 97.82%
Unmapped reads	9,750 / 2.18%
Mapped paired reads	438,132 / 97.82%
Mapped reads, first in pair	219,858 / 49.09%
Mapped reads, second in pair	218,274 / 48.73%
Mapped reads, both in pair	434,688 / 97.05%
Mapped reads, singletons	3,444 / 0.77%
Secondary alignments	0
Supplementary alignments	20,217 / 4.51%
Read min/max/mean length	30 / 151 / 147.77
Duplicated reads (estimated)	439,899 / 98.22%
Duplication rate	45.01%
Clipped reads	176,395 / 39.38%

2.2. ACGT Content

Number/percentage of A's	16,371,653 / 27.84%
Number/percentage of C's	12,612,940 / 21.45%
Number/percentage of T's	15,721,591 / 26.73%
Number/percentage of G's	14,100,945 / 23.98%
Number/percentage of N's	632 / 0%

GC Percentage	45.43%
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2.3. Coverage

Mean	0.0192
Standard Deviation	10.1435

2.4. Mapping Quality

Mean Mapping Quality	33.92
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2.5. Insert size

Mean	694,111.97
Standard Deviation	7,332,838.99
P25/Median/P75	152 / 187 / 222

2.6. Mismatches and indels

General error rate	2.59%
Mismatches	1,476,635
Insertions	21,209
Mapped reads with at least one insertion	4.77%
Deletions	118,760
Mapped reads with at least one deletion	26.4%
Homopolymer indels	34.45%

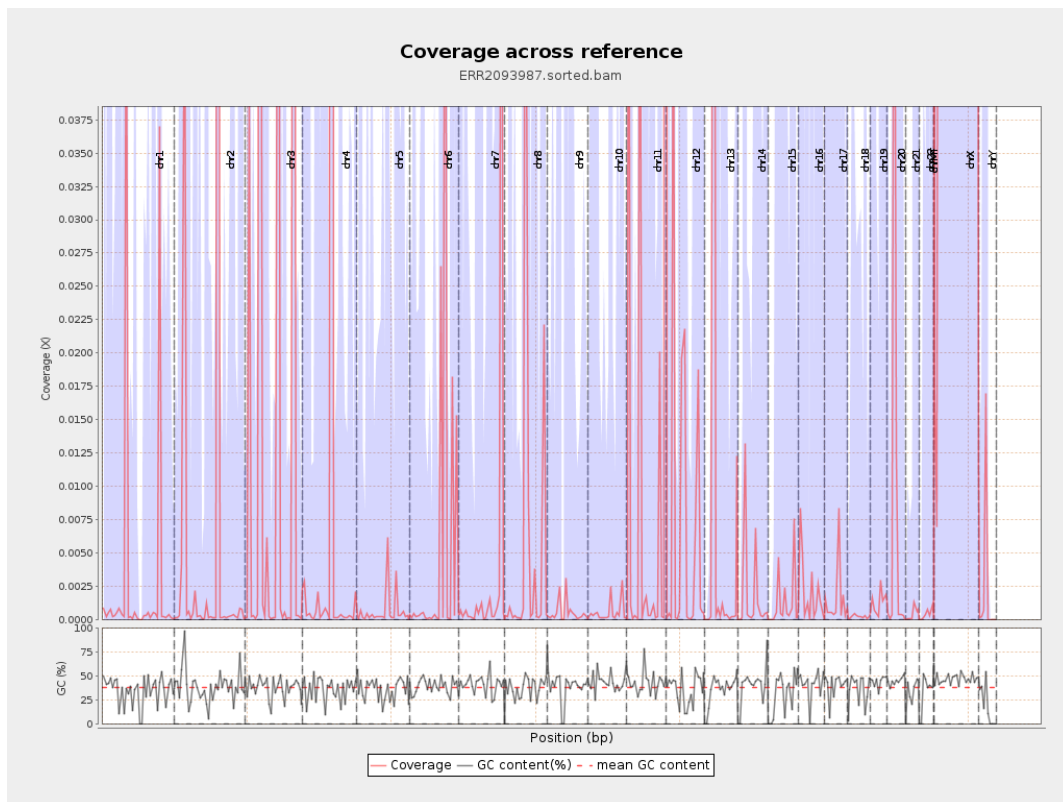
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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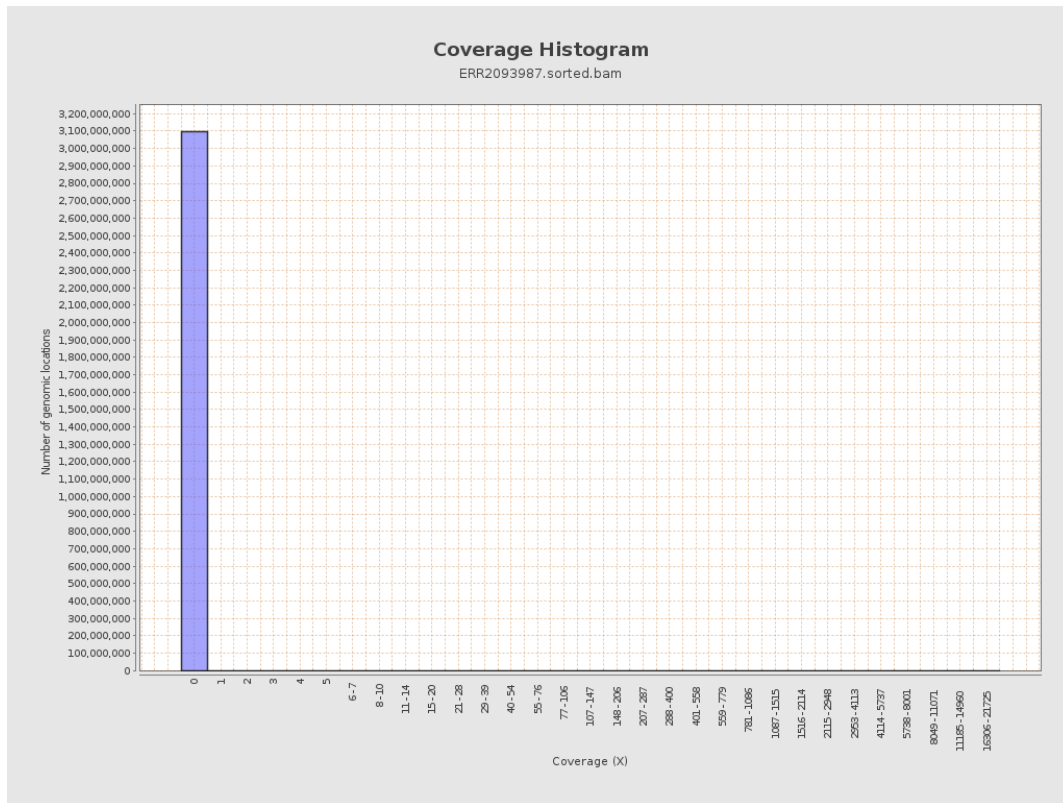
		bases	coverage	deviation
chr1	249250621	765764	0.0031	2.7896
chr2	243199373	1711334	0.007	6.4928
chr3	198022430	2618710	0.0132	6.9364
chr4	191154276	7051465	0.0369	19.5962
chr5	180915260	116624	0.0006	0.3085
chr6	171115067	1059887	0.0062	4.3227
chr7	159138663	702104	0.0044	2.6555
chr8	146364022	784865	0.0054	2.5591
chr9	141213431	76107	0.0005	0.1569
chr10	135534747	72095	0.0005	0.2327
chr11	135006516	2365630	0.0175	9.2719
chr12	133851895	941801	0.007	3.2294
chr13	115169878	784335	0.0068	5.8414
chr14	107349540	184993	0.0017	0.9801
chr15	102531392	137625	0.0013	0.5027
chr16	90354753	186947	0.0021	0.5875
chr17	81195210	117303	0.0014	0.6686
chr18	78077248	15995	0.0002	0.0356
chr19	59128983	74890	0.0013	0.2846
chr20	63025520	661597	0.0105	3.9979
chr21	48129895	19980	0.0004	0.1008
chr22	51304566	21620	0.0004	0.0825
chrMT	16571	5763772	347.8228	1,856.0719
chrX	155270560	32960904	0.2123	30.1057

chrY	59373566	139143	0.0023	1.4551
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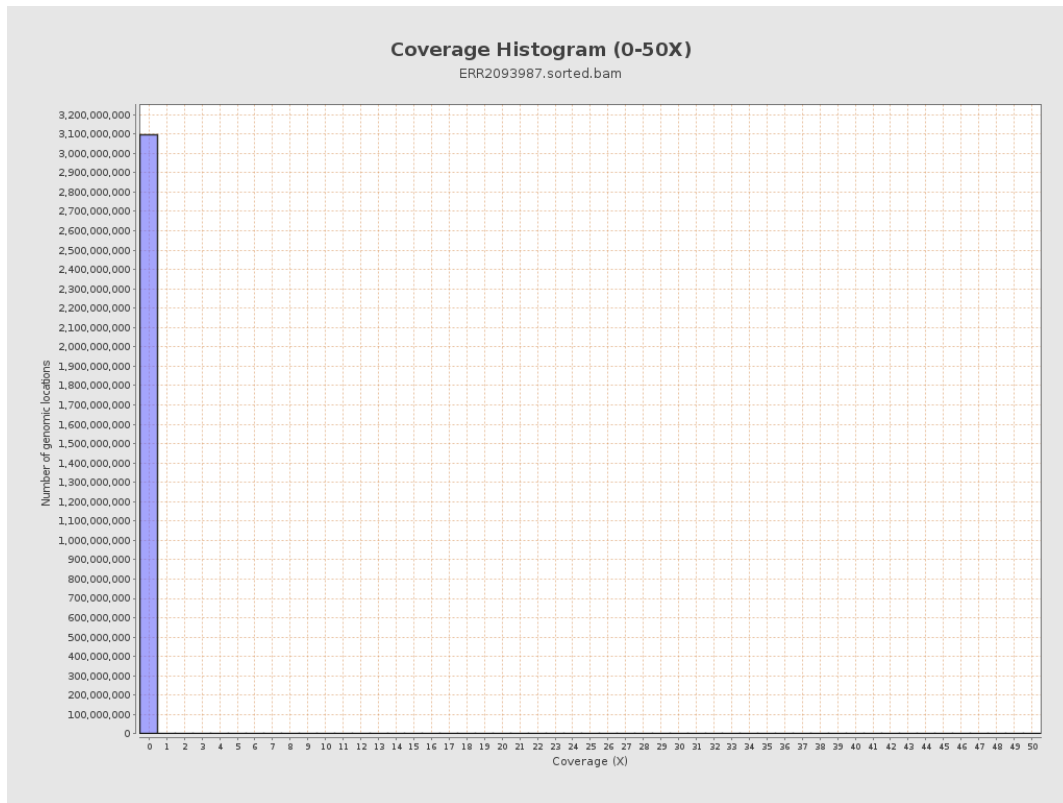
3. Results : Coverage across reference



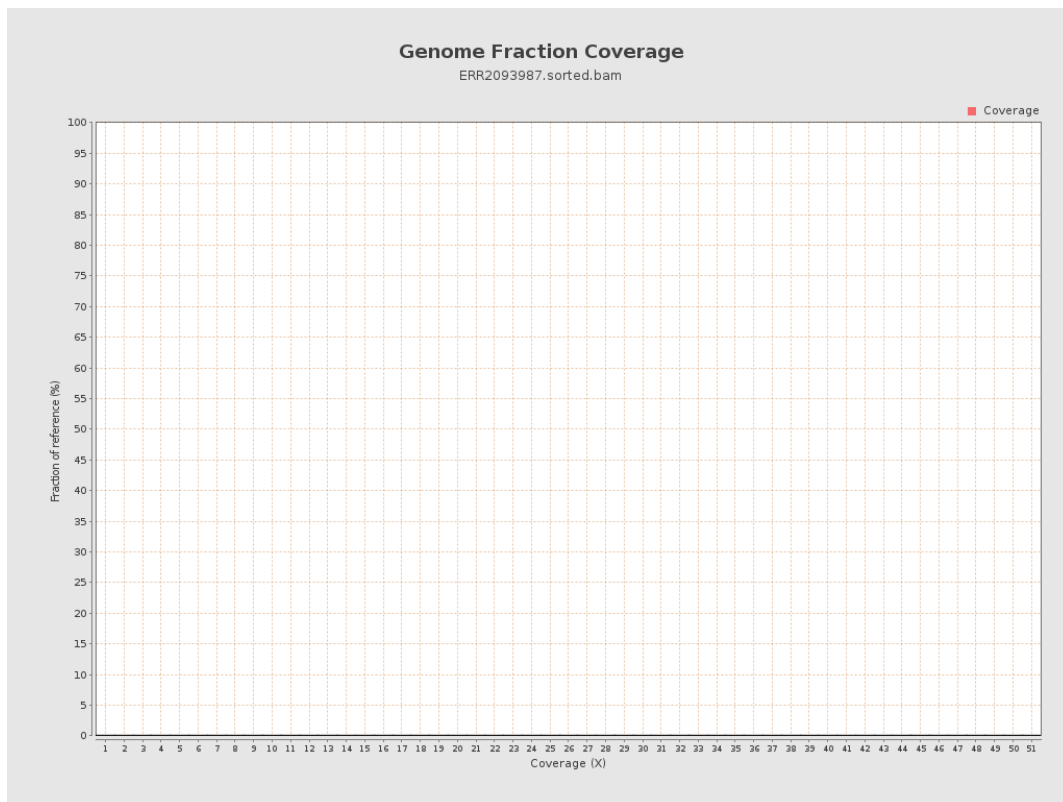
4. Results : Coverage Histogram



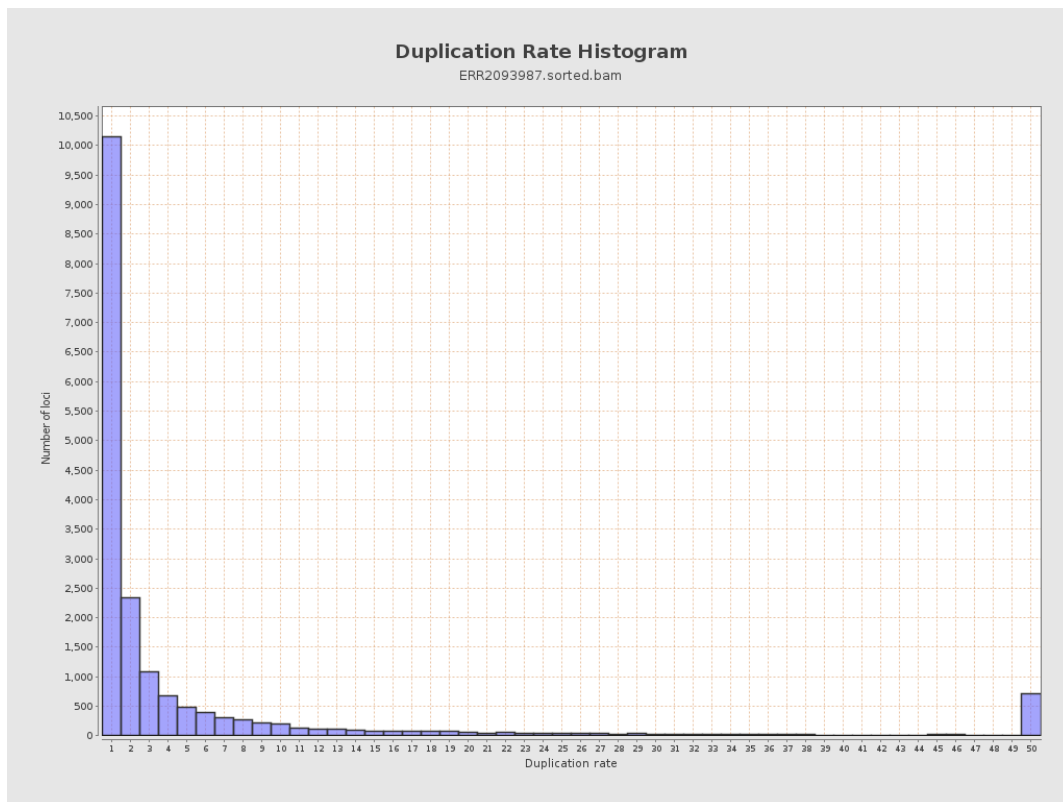
5. Results : Coverage Histogram (0-50X)



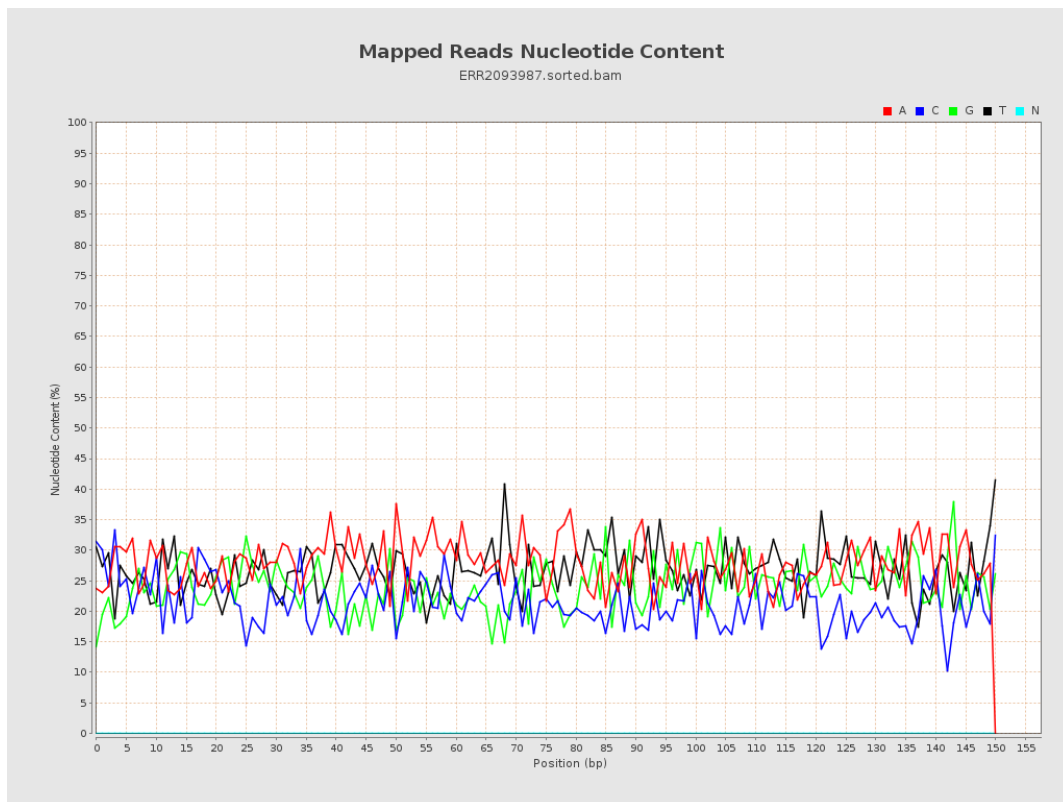
6. Results : Genome Fraction Coverage



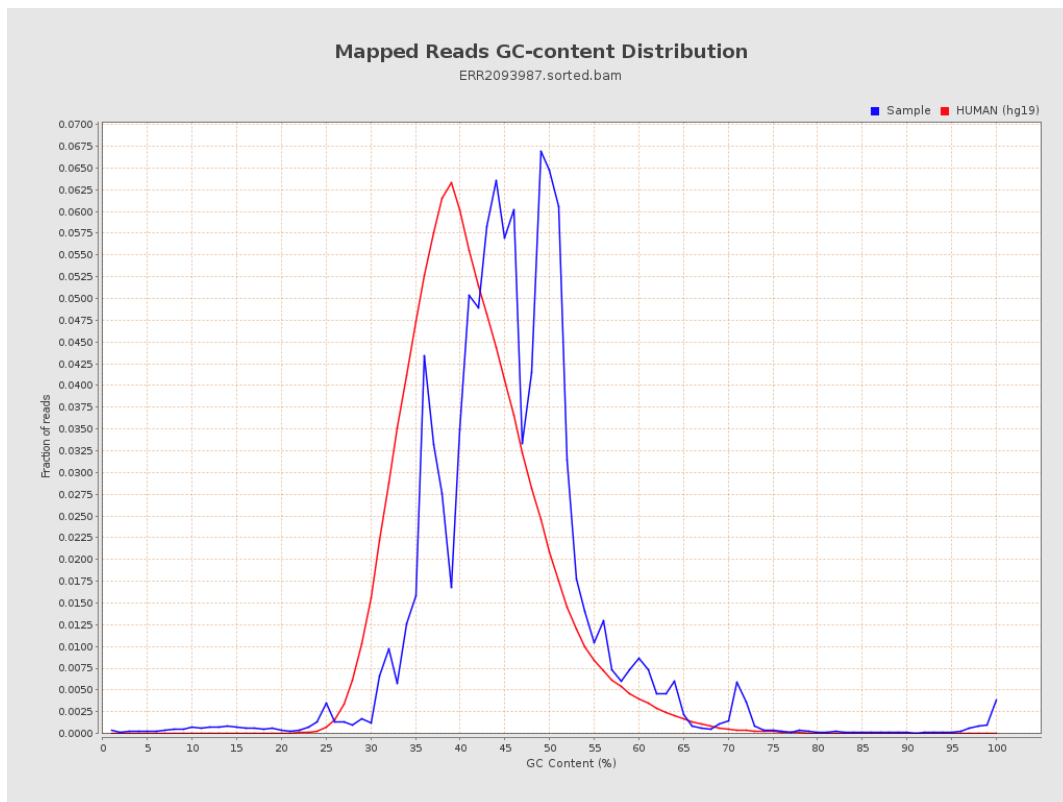
7. Results : Duplication Rate Histogram



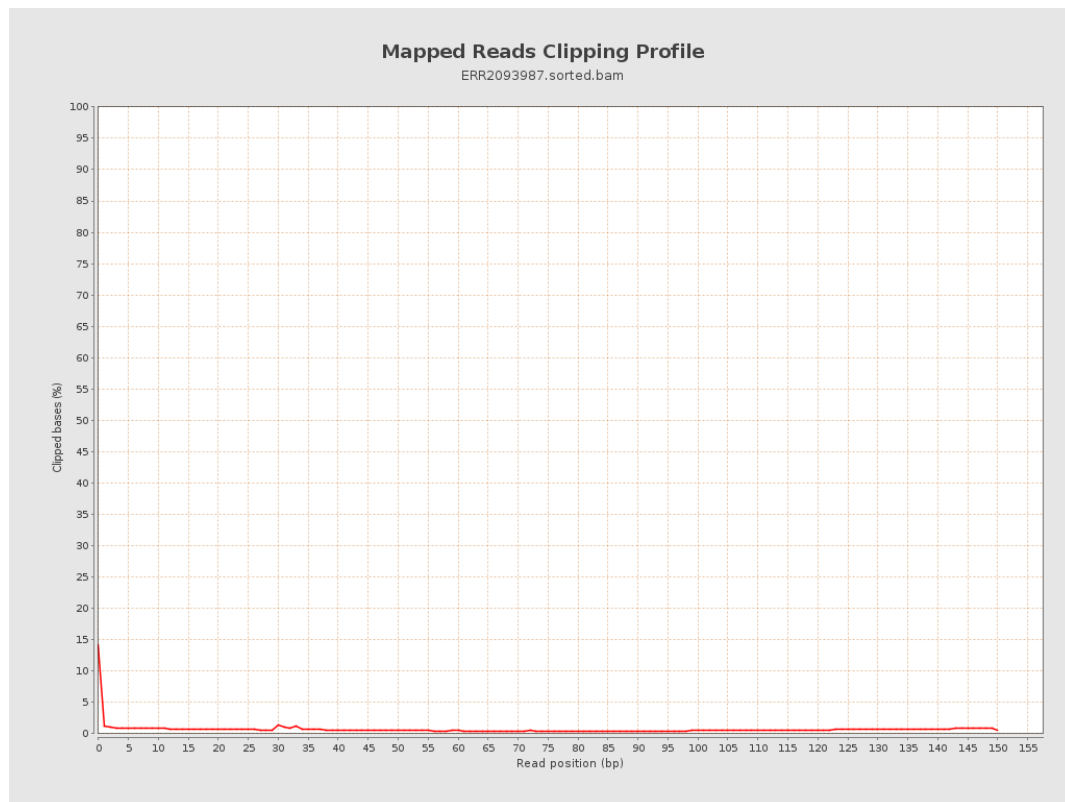
8. Results : Mapped Reads Nucleotide Content



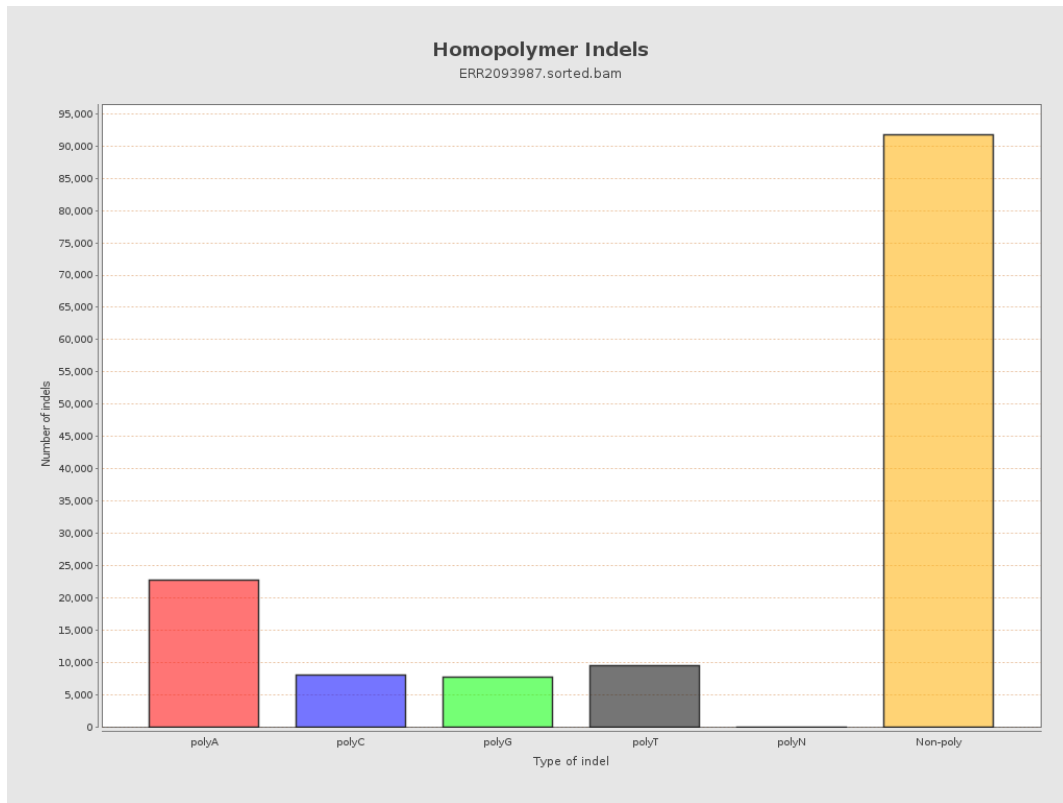
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



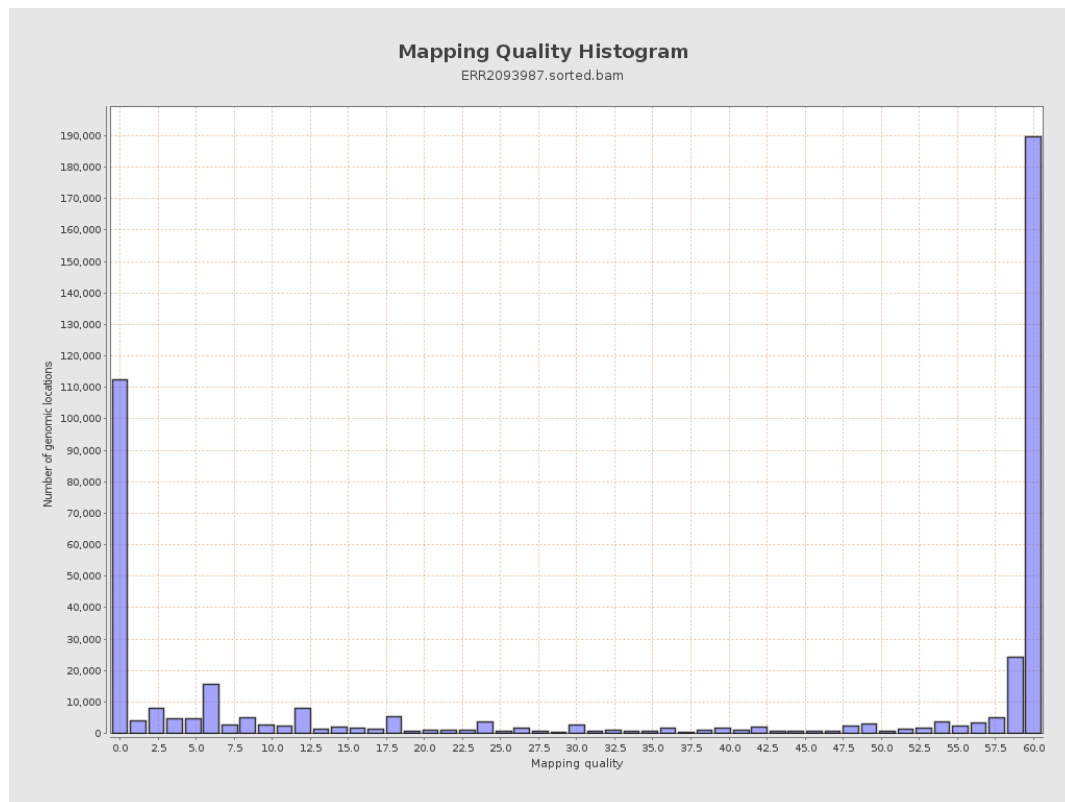
11. Results : Homopolymer Indels



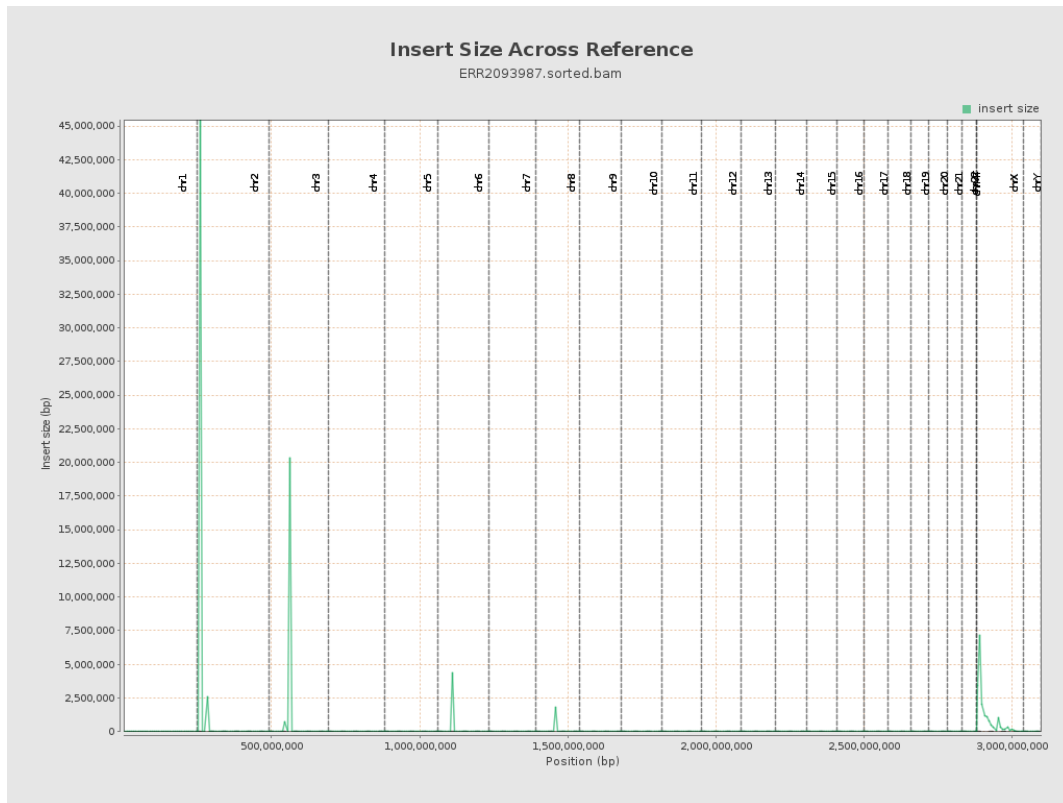
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

