Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:54:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093988.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_ERR2093988 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093988_1.fastq.gz ERR2093988_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:54:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2093988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	336,586
Mapped reads	322,671 / 95.87%
Unmapped reads	13,915 / 4.13%
Mapped paired reads	322,671 / 95.87%
Mapped reads, first in pair	162,357 / 48.24%
Mapped reads, second in pair	160,314 / 47.63%
Mapped reads, both in pair	319,498 / 94.92%
Mapped reads, singletons	3,173 / 0.94%
Secondary alignments	0
Supplementary alignments	19,597 / 5.82%
Read min/max/mean length	30 / 151 / 143.32
Duplicated reads (estimated)	302,765 / 89.95%
Duplication rate	48.88%
Clipped reads	159,507 / 47.39%

2.2. ACGT Content

Number/percentage of A's	10,816,941 / 26.3%
Number/percentage of C's	9,669,960 / 23.51%
Number/percentage of T's	10,241,980 / 24.9%
Number/percentage of G's	10,401,500 / 25.29%
Number/percentage of N's	383 / 0%

GC Percentage	48.8%

2.3. Coverage

Mean	0.0135
Standard Deviation	2.6946

2.4. Mapping Quality

Mean Mapping Quality	39.7

2.5. Insert size

Mean	986,813.54
Standard Deviation	9,035,008.42
P25/Median/P75	133 / 167 / 203

2.6. Mismatches and indels

General error rate	3.49%
Mismatches	1,393,039
Insertions	20,874
Mapped reads with at least one insertion	6.34%
Deletions	109,746
Mapped reads with at least one deletion	32.62%
Homopolymer indels	31.01%

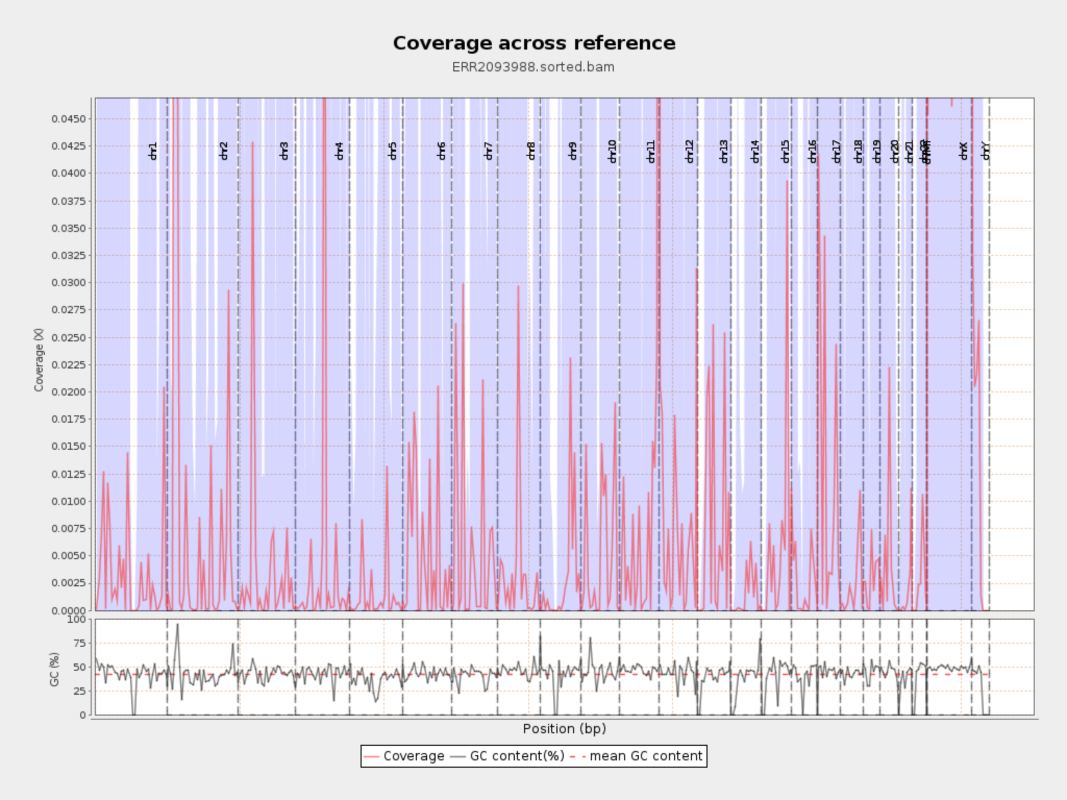
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

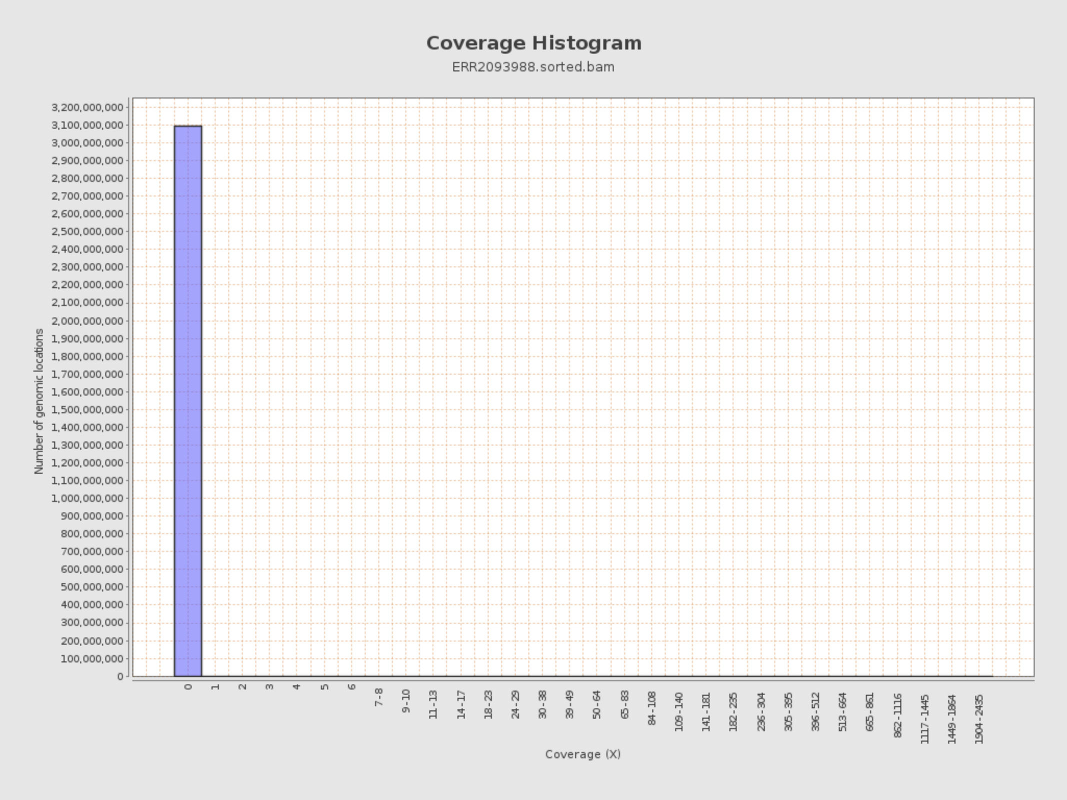
		bases	**coverage**	**deviation**
chr1	249250621	872668	0.0035	1.1335
chr2	243199373	2057897	0.0085	2.7745
chr3	198022430	687862	0.0035	1.1721
chr4	191154276	896278	0.0047	2.0382
chr5	180915260	264518	0.0015	0.7392
chr6	171115067	908745	0.0053	1.6333
chr7	159138663	861469	0.0054	1.7193
chr8	146364022	487158	0.0033	1.1415
chr9	141213431	450201	0.0032	0.9185
chr10	135534747	671471	0.005	1.5365
chr11	135006516	972970	0.0072	1.8462
chr12	133851895	897914	0.0067	1.6221
chr13	115169878	911544	0.0079	2.1019
chr14	107349540	150375	0.0014	0.5002
chr15	102531392	563069	0.0055	1.5571
chr16	90354753	260220	0.0029	0.7487
chr17	81195210	1138984	0.014	3.4314
chr18	78077248	201552	0.0026	0.6856
chr19	59128983	174084	0.0029	0.7061
chr20	63025520	284771	0.0045	1.5773
chr21	48129895	92578	0.0019	0.3627
chr22	51304566	131283	0.0026	0.6963
chrMT	16571	1277369	77.0846	327.1412
chrX	155270560	25943367	0.1671	9.0177

chrY	59373566	713452	0.012	1.8515

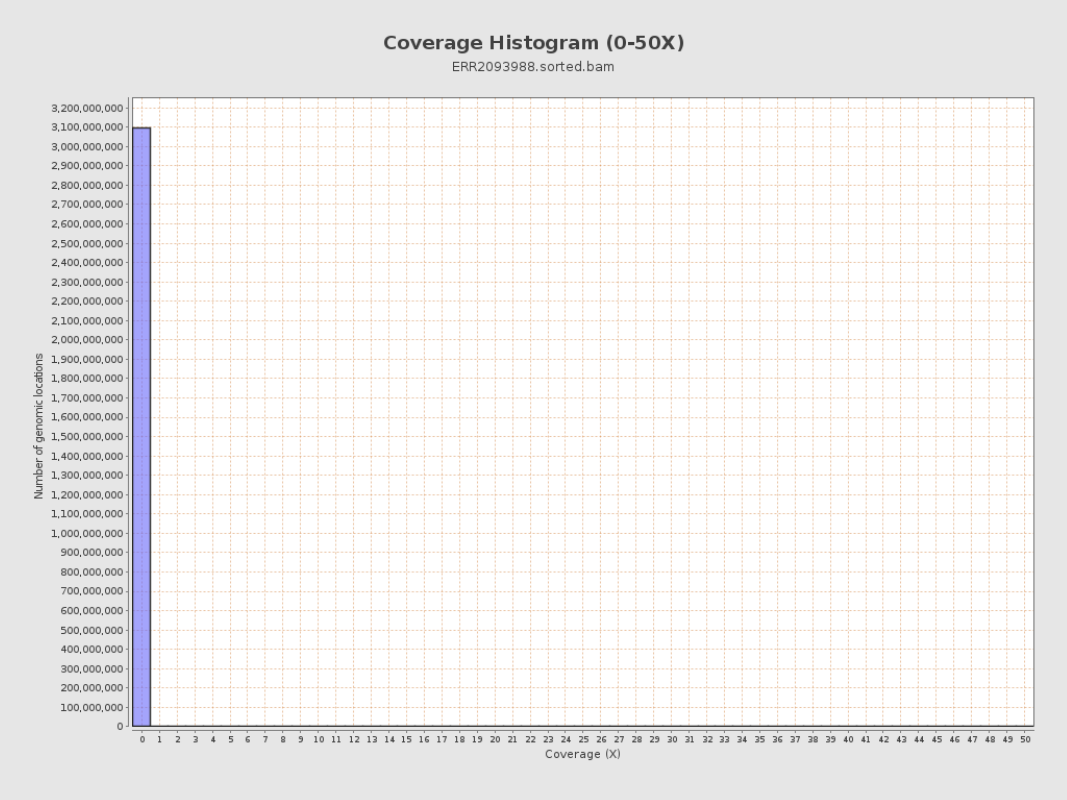
3. Results : Coverage across reference



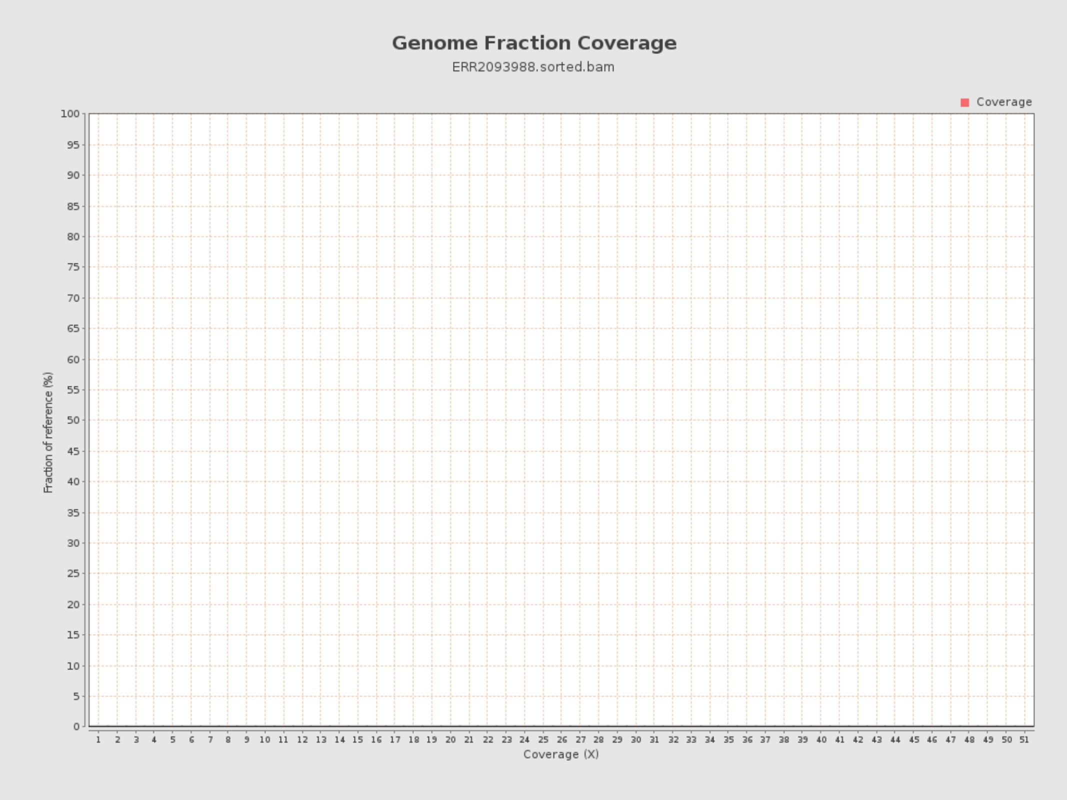
4. Results : Coverage Histogram



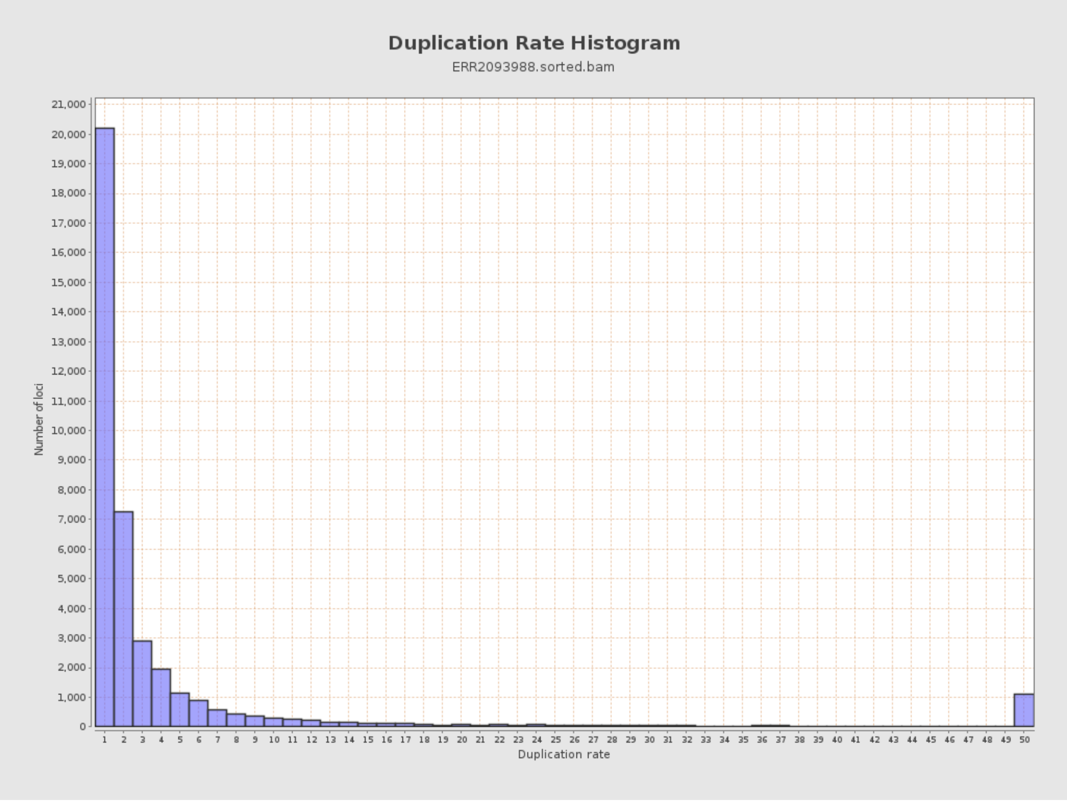
5. Results : Coverage Histogram (0-50X)



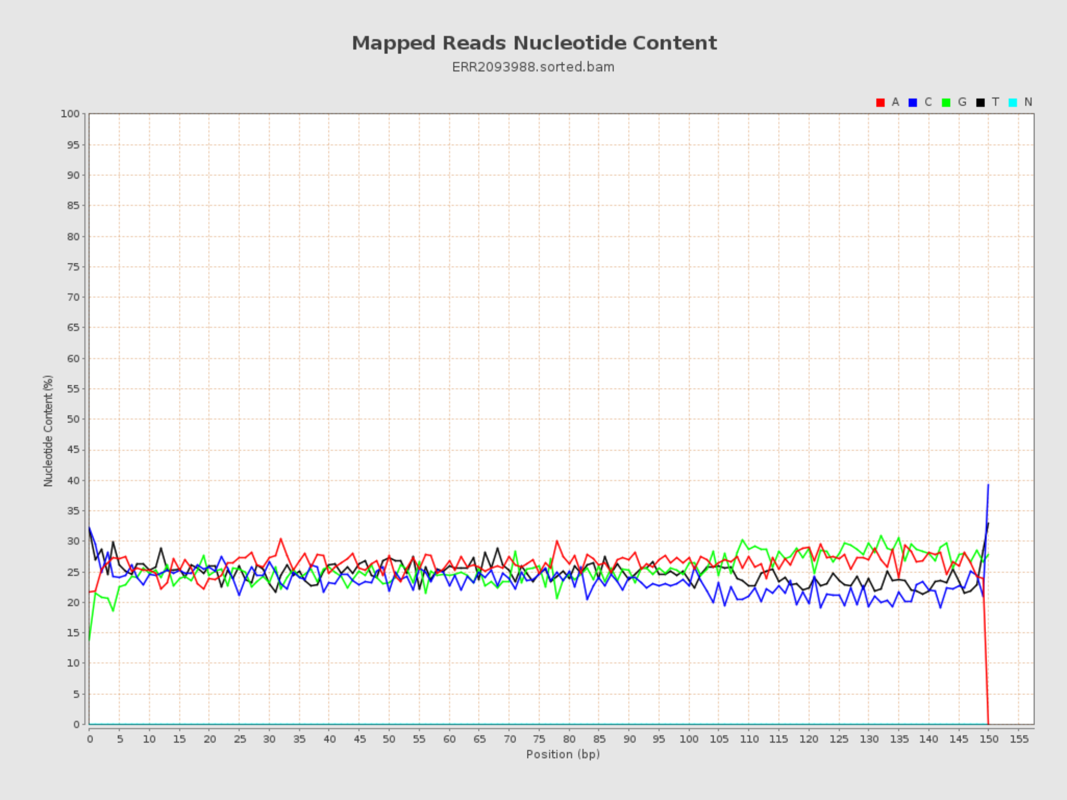
6. Results : Genome Fraction Coverage



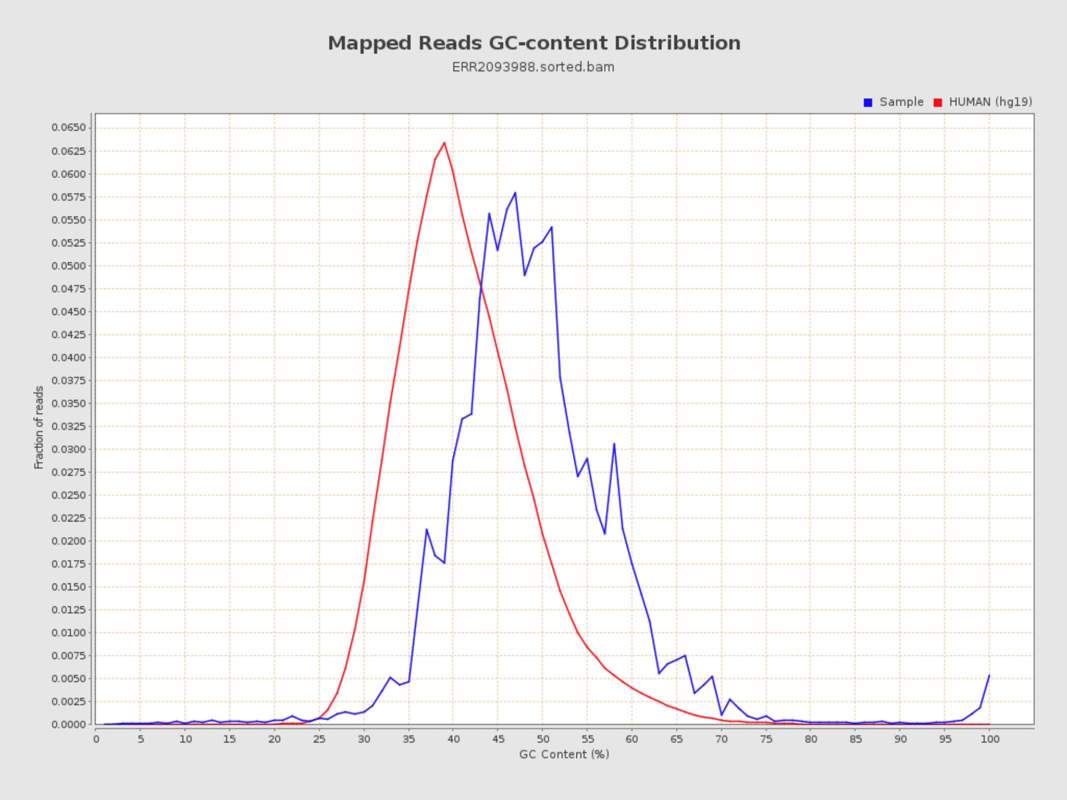
7. Results : Duplication Rate Histogram



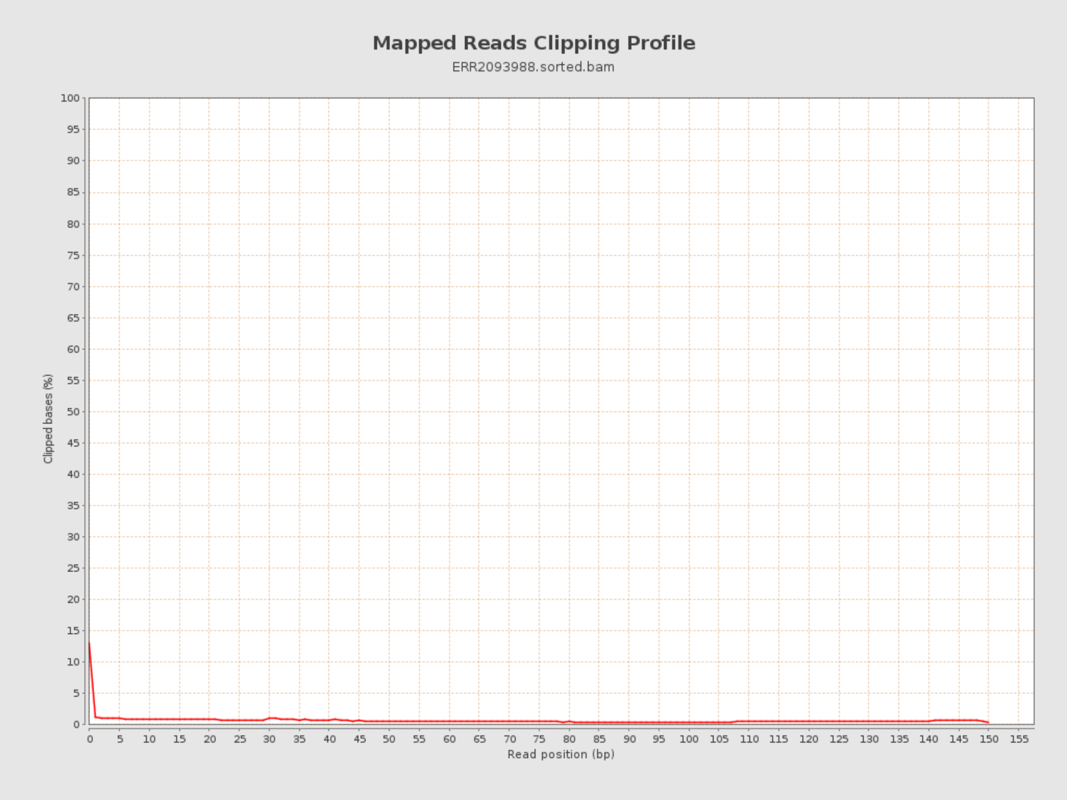
8. Results : Mapped Reads Nucleotide Content



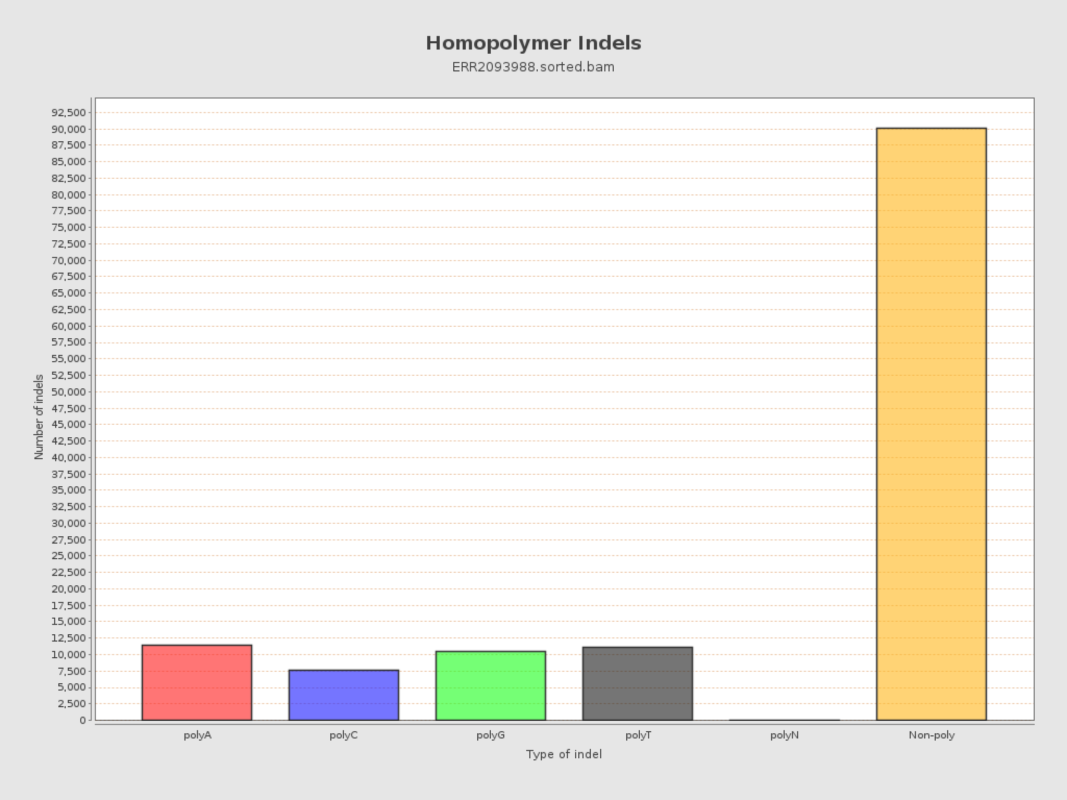
9. Results : Mapped Reads GC-content Distribution



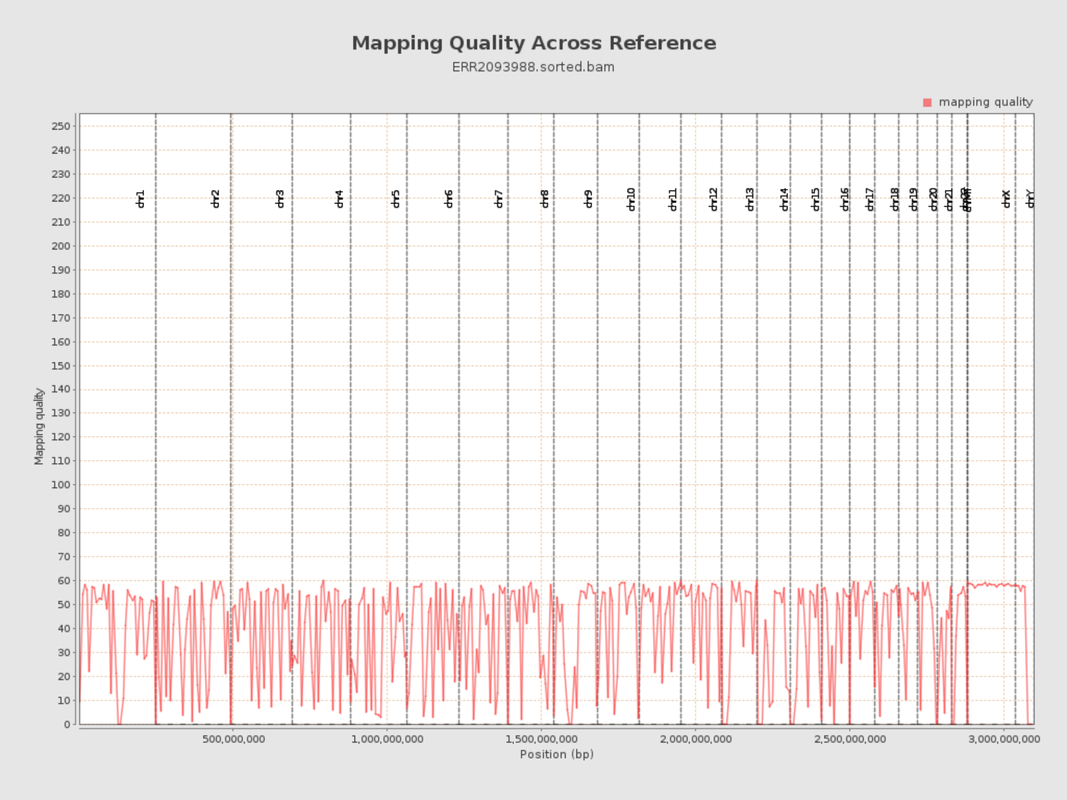
10. Results : Mapped Reads Clipping Profile



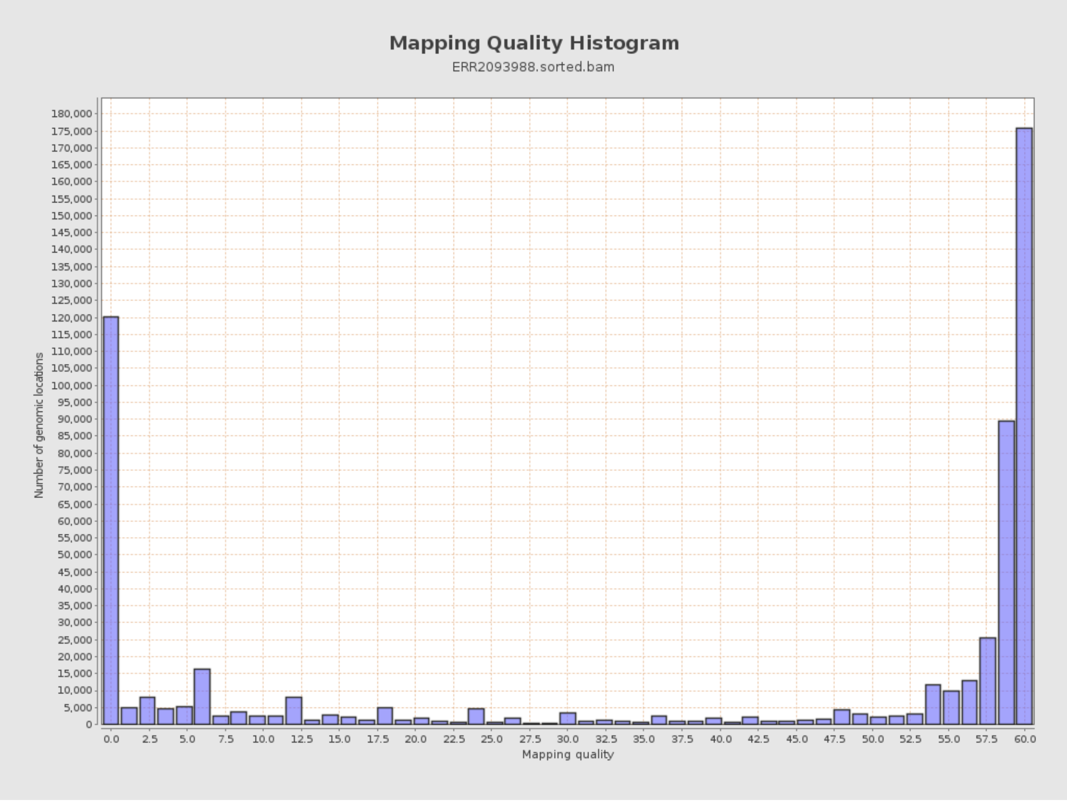
11. Results : Homopolymer Indels



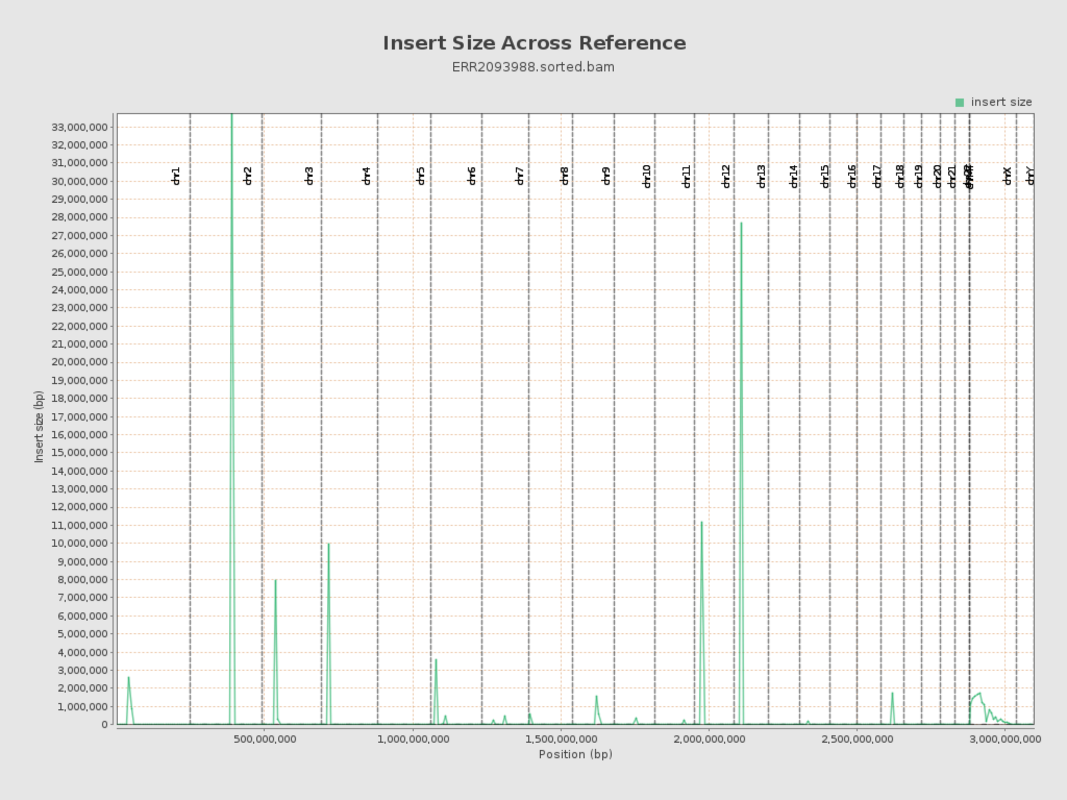
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram