

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:49:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094072.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_ERR2094072 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094072_1.fastq.gz ERR2094072_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:49:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	387,272
Mapped reads	374,102 / 96.6%
Unmapped reads	13,170 / 3.4%
Mapped paired reads	374,102 / 96.6%
Mapped reads, first in pair	187,979 / 48.54%
Mapped reads, second in pair	186,123 / 48.06%
Mapped reads, both in pair	371,574 / 95.95%
Mapped reads, singletons	2,528 / 0.65%
Secondary alignments	0
Supplementary alignments	13,017 / 3.36%
Read min/max/mean length	30 / 151 / 141.61
Duplicated reads (estimated)	355,325 / 91.75%
Duplication rate	50.95%
Clipped reads	147,623 / 38.12%

2.2. ACGT Content

Number/percentage of A's	12,825,062 / 26.55%
Number/percentage of C's	11,365,310 / 23.53%
Number/percentage of T's	12,280,490 / 25.42%
Number/percentage of G's	11,829,861 / 24.49%
Number/percentage of N's	528 / 0%

GC Percentage	48.02%
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2.3. Coverage

Mean	0.016
Standard Deviation	4.0511

2.4. Mapping Quality

Mean Mapping Quality	39.22
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2.5. Insert size

Mean	519,365.89
Standard Deviation	6,648,849.45
P25/Median/P75	133 / 166 / 195

2.6. Mismatches and indels

General error rate	4.12%
Mismatches	1,912,346
Insertions	31,871
Mapped reads with at least one insertion	8.3%
Deletions	150,323
Mapped reads with at least one deletion	38.22%
Homopolymer indels	28.05%

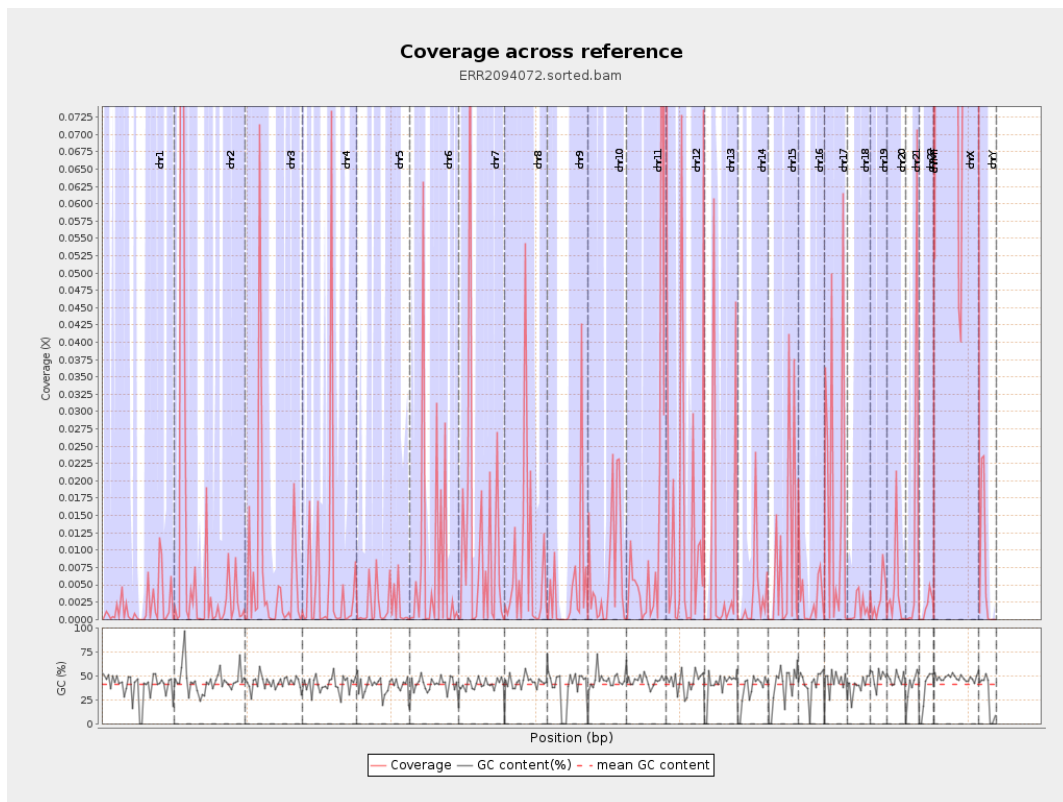
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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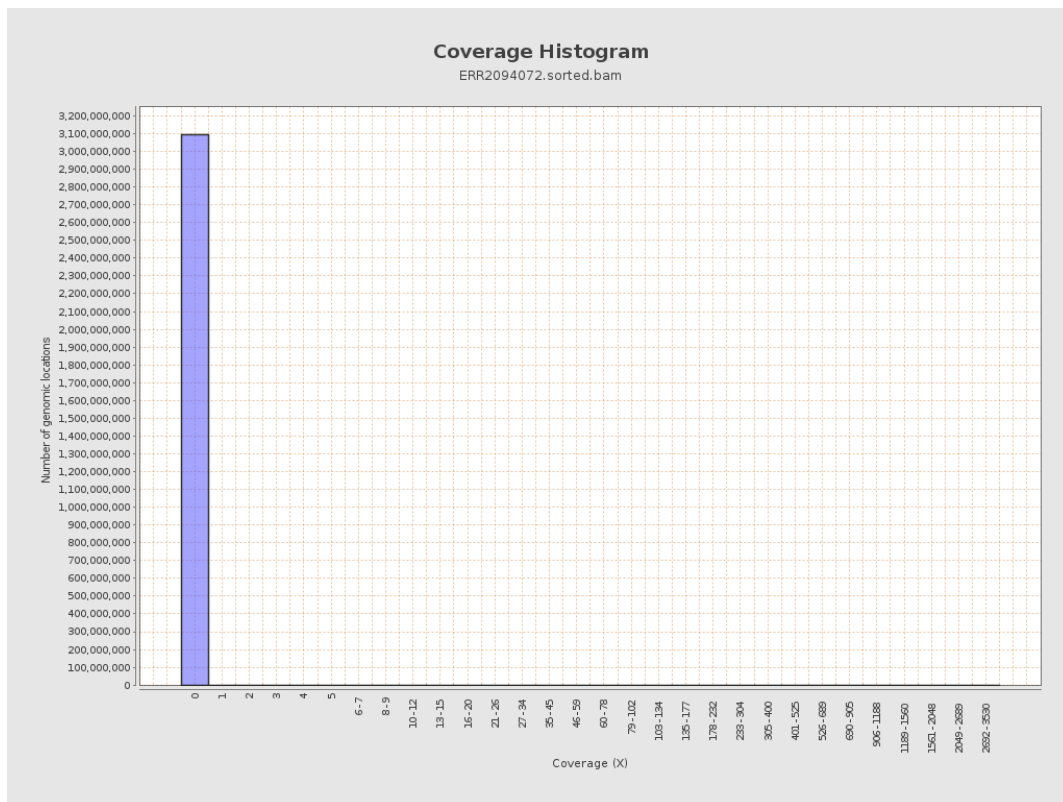
		bases	coverage	deviation
chr1	249250621	432211	0.0017	0.6951
chr2	243199373	2183937	0.009	3.5586
chr3	198022430	1171904	0.0059	2.2088
chr4	191154276	1098989	0.0057	1.8938
chr5	180915260	334278	0.0018	0.7156
chr6	171115067	1268762	0.0074	3.6121
chr7	159138663	1731458	0.0109	3.7768
chr8	146364022	1062519	0.0073	2.5978
chr9	141213431	650549	0.0046	1.9821
chr10	135534747	915264	0.0068	2.1702
chr11	135006516	1913226	0.0142	4.0127
chr12	133851895	1817065	0.0136	4.2272
chr13	115169878	900389	0.0078	2.5552
chr14	107349540	377408	0.0035	1.4872
chr15	102531392	850320	0.0083	2.5904
chr16	90354753	305947	0.0034	1.1357
chr17	81195210	1486262	0.0183	5.593
chr18	78077248	115792	0.0015	0.4846
chr19	59128983	172833	0.0029	0.7358
chr20	63025520	267382	0.0042	1.1041
chr21	48129895	605128	0.0126	5.3694
chr22	51304566	88259	0.0017	0.4385
chrMT	16571	1510574	91.1577	415.0863
chrX	155270560	27763520	0.1788	12.8358

chrY	59373566	393635	0.0066	1.711
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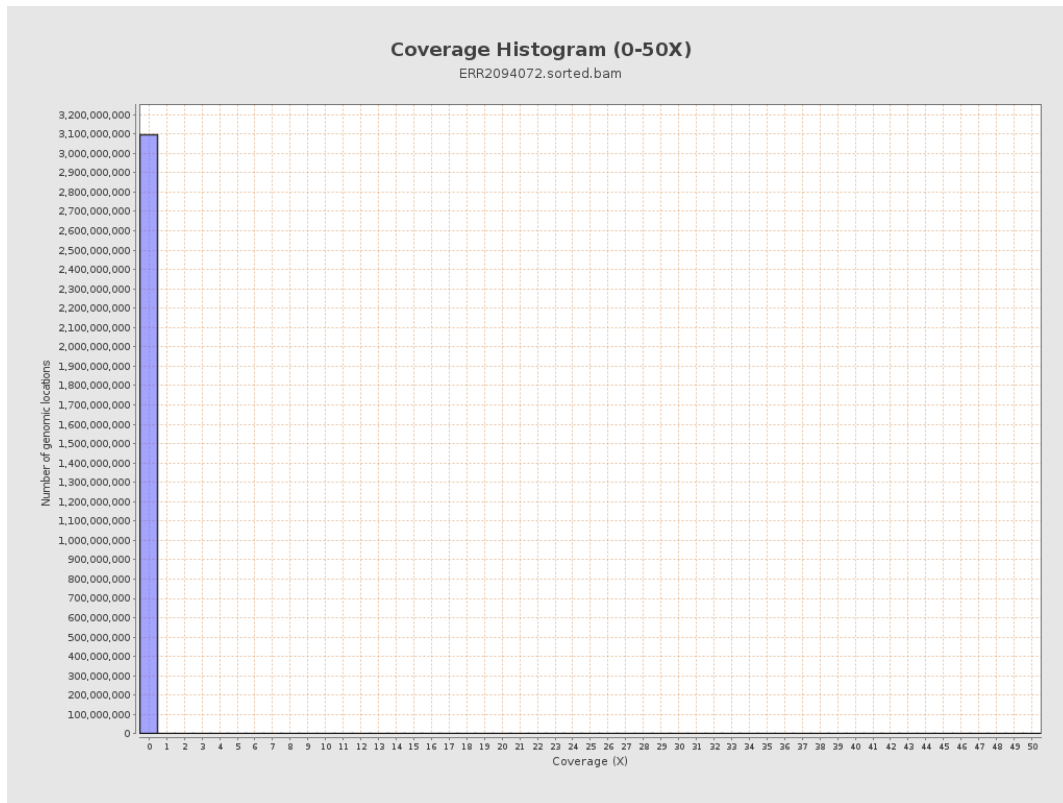
3. Results : Coverage across reference



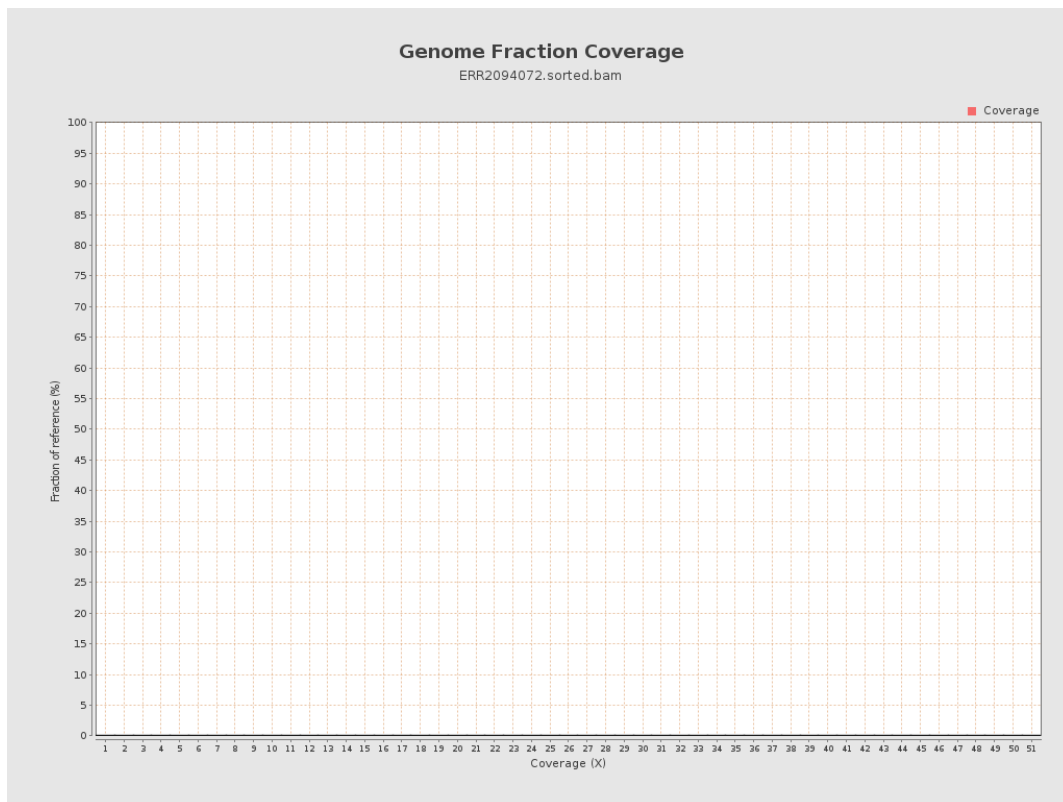
4. Results : Coverage Histogram



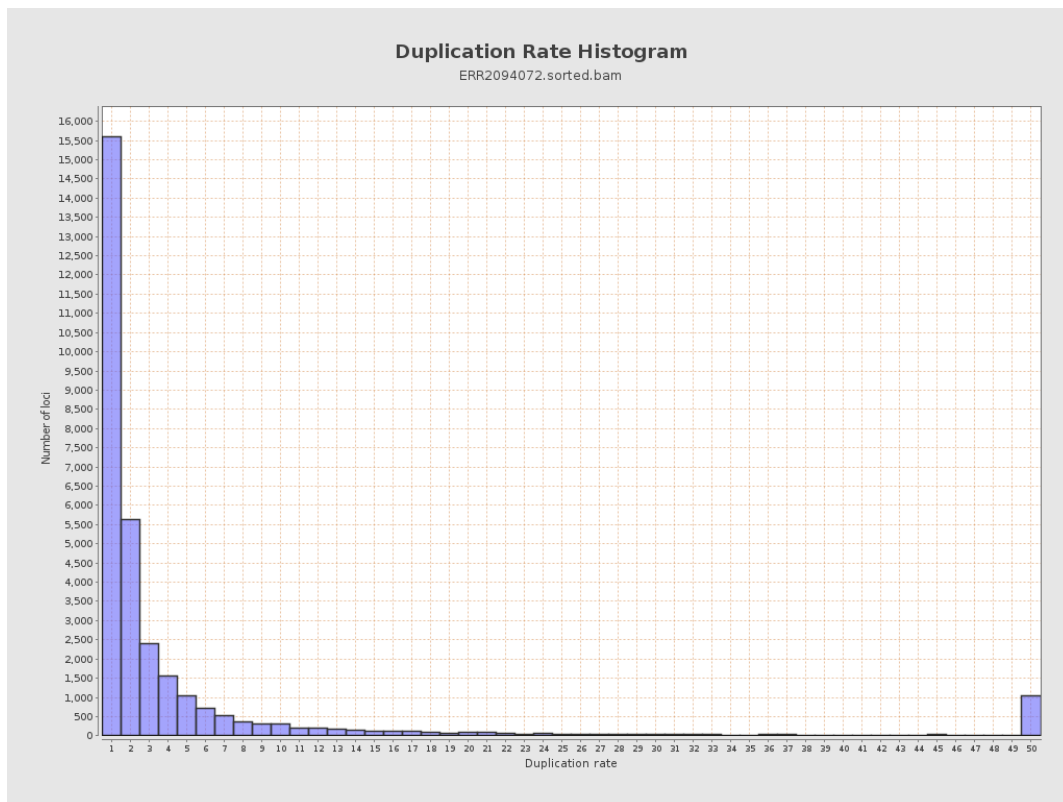
5. Results : Coverage Histogram (0-50X)



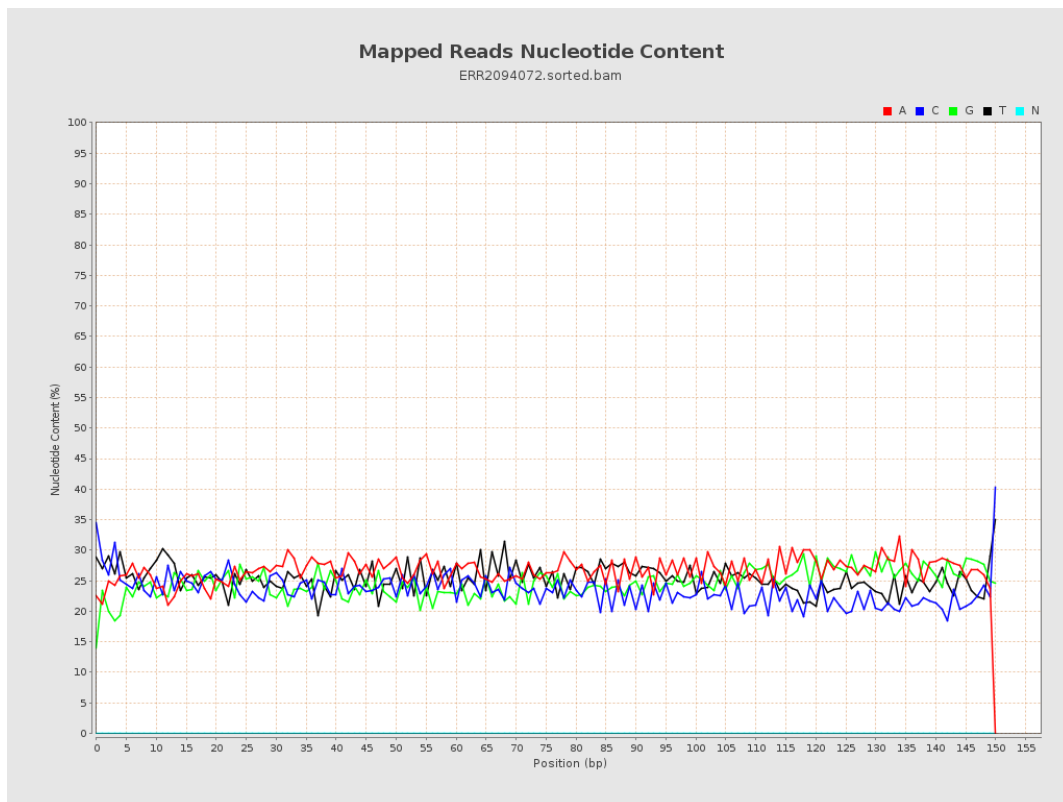
6. Results : Genome Fraction Coverage



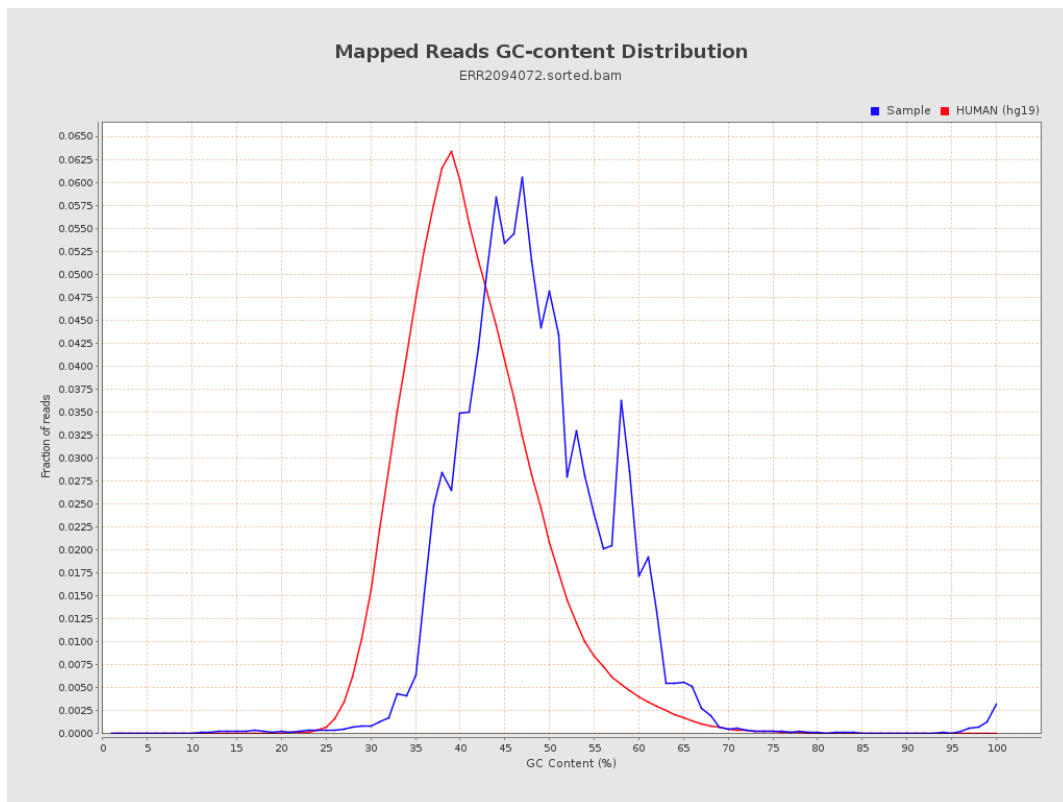
7. Results : Duplication Rate Histogram



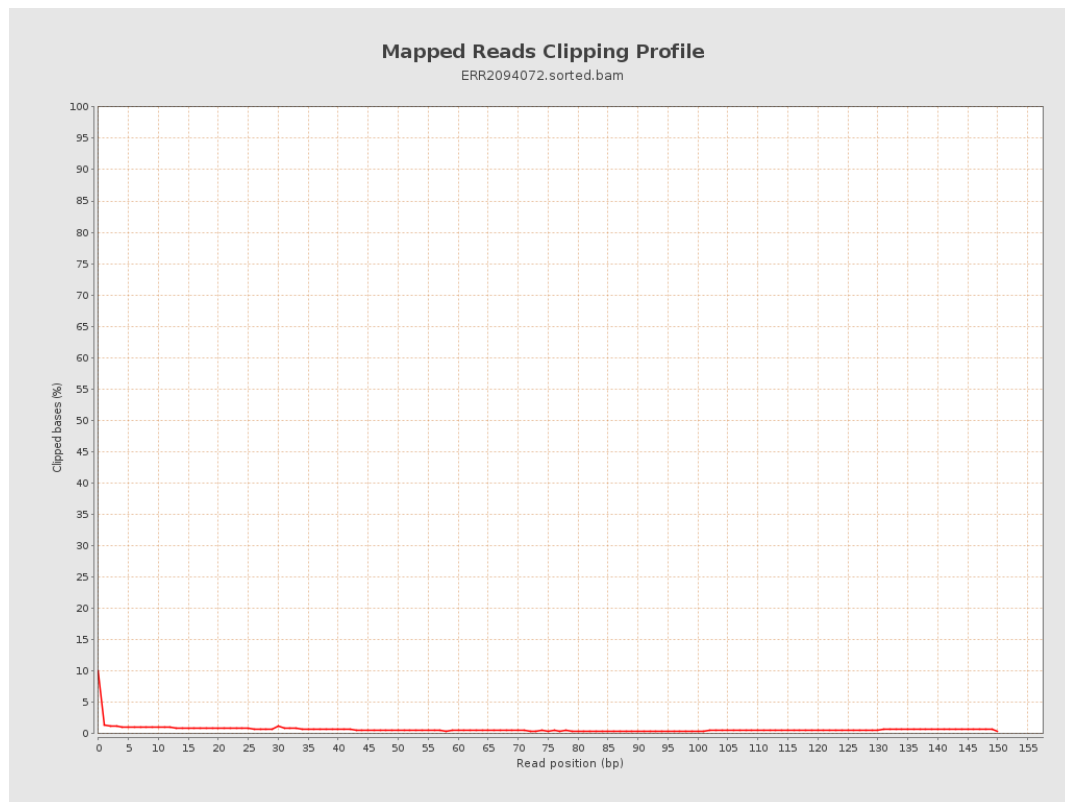
8. Results : Mapped Reads Nucleotide Content



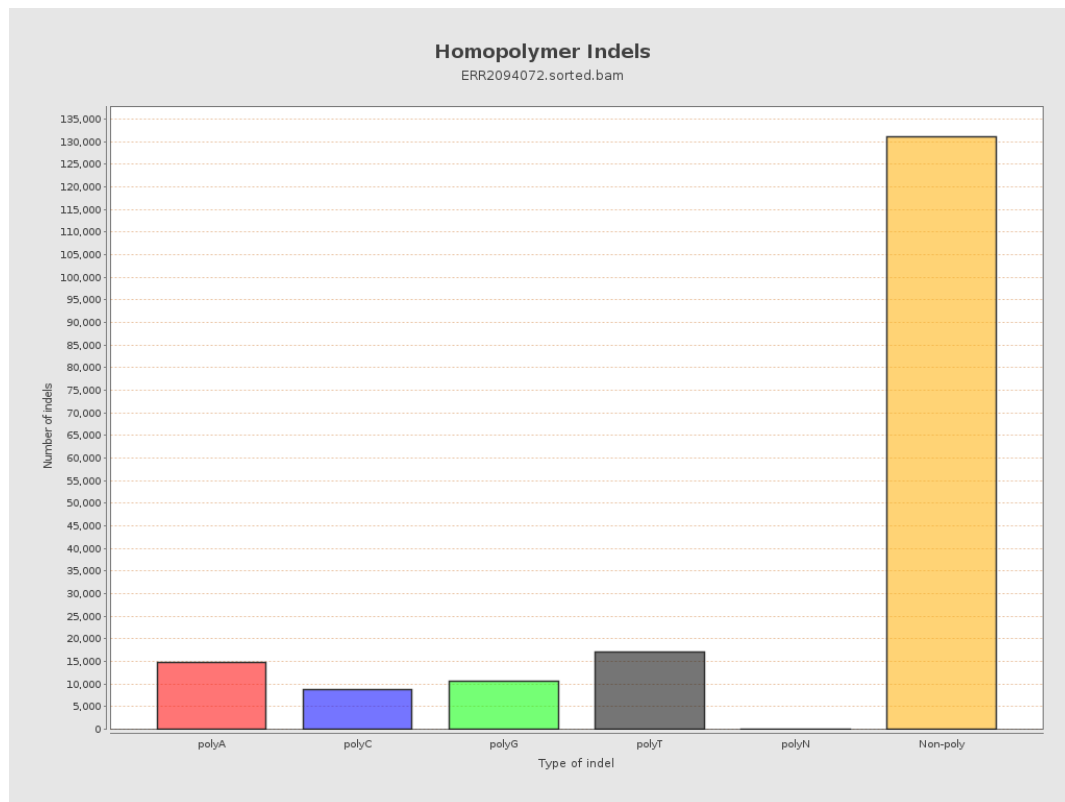
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



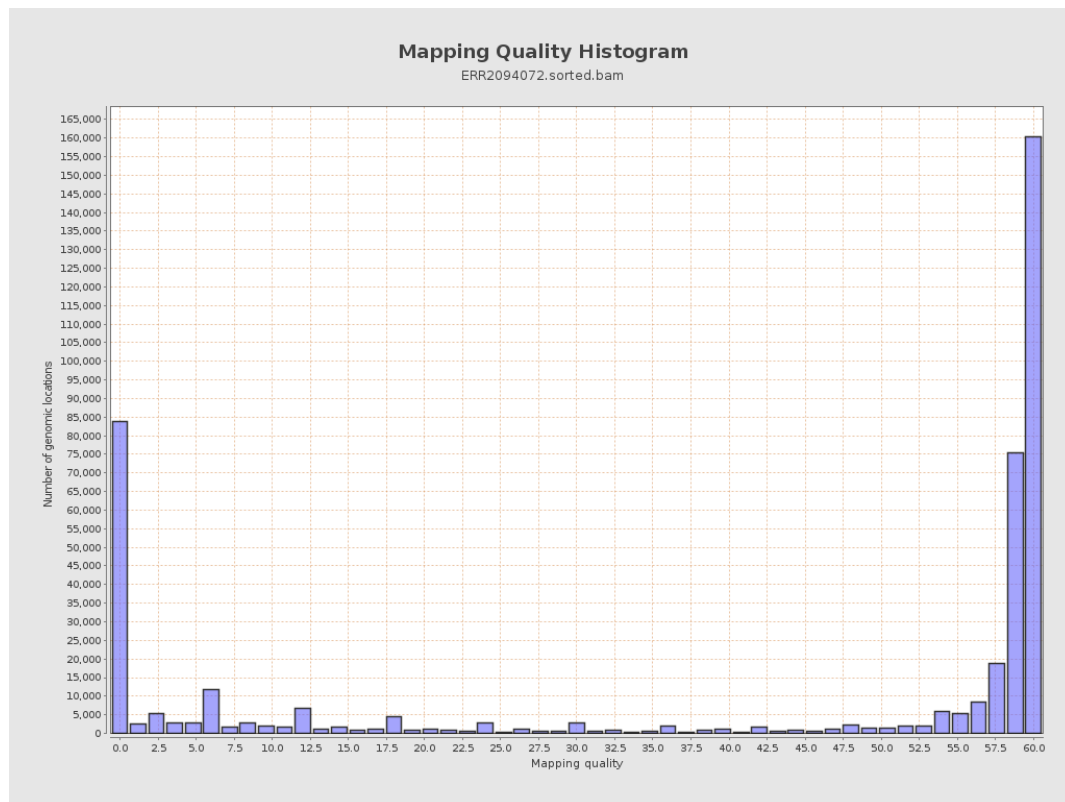
11. Results : Homopolymer Indels



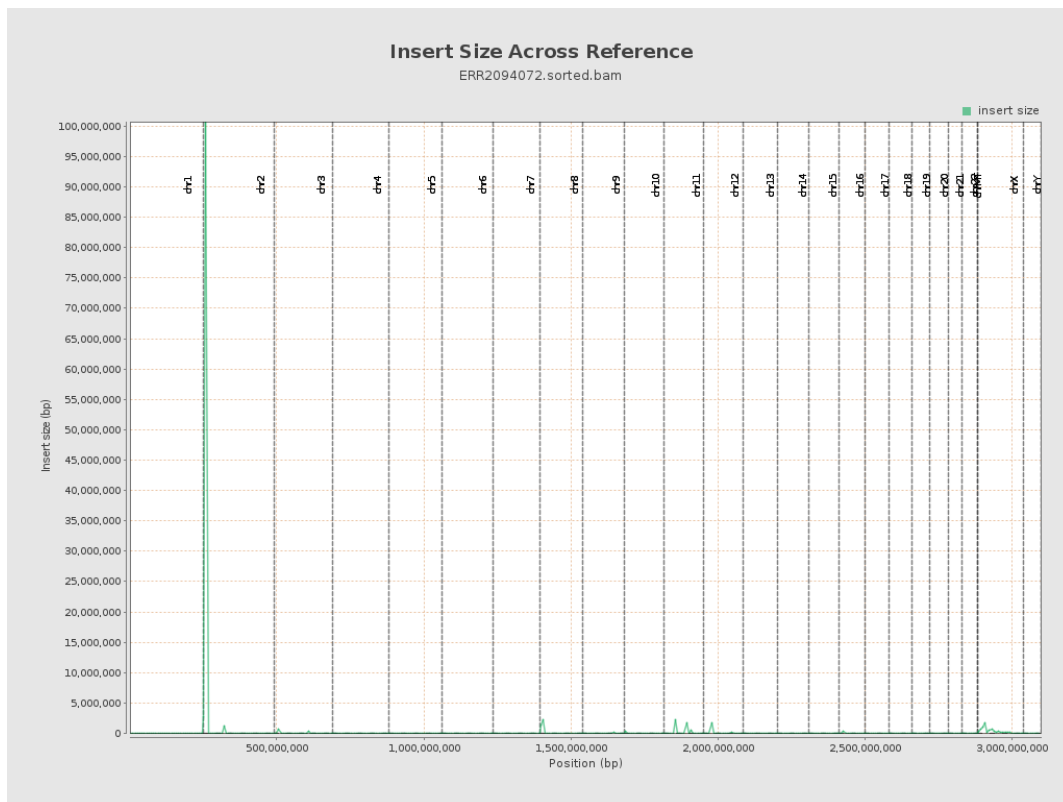
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

