Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:22:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094027.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_ERR2094027 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094027_1.fastq.gz ERR2094027_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:22:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	370,950
Mapped reads	335,617 / 90.47%
Unmapped reads	35,333 / 9.53%
Mapped paired reads	335,617 / 90.47%
Mapped reads, first in pair	168,711 / 45.48%
Mapped reads, second in pair	166,906 / 44.99%
Mapped reads, both in pair	331,210 / 89.29%
Mapped reads, singletons	4,407 / 1.19%
Secondary alignments	0
Supplementary alignments	18,756 / 5.06%
Read min/max/mean length	30 / 151 / 137.61
Duplicated reads (estimated)	311,838 / 84.06%
Duplication rate	45.89%
Clipped reads	162,245 / 43.74%

2.2. ACGT Content

Number/percentage of A's	11,696,728 / 27.85%
Number/percentage of C's	9,359,727 / 22.29%
Number/percentage of T's	11,169,373 / 26.59%
Number/percentage of G's	9,773,268 / 23.27%
Number/percentage of N's	409 / 0%

GC Percentage	45.56%

2.3. Coverage

Mean	0.0138
Standard Deviation	4.621

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Insert size

Mean	555,868.59
Standard Deviation	6,929,361.84
P25/Median/P75	128 / 164 / 206

2.6. Mismatches and indels

General error rate	3.33%
Mismatches	1,355,511
Insertions	24,009
Mapped reads with at least one insertion	7.04%
Deletions	106,027
Mapped reads with at least one deletion	30.5%
Homopolymer indels	29.06%

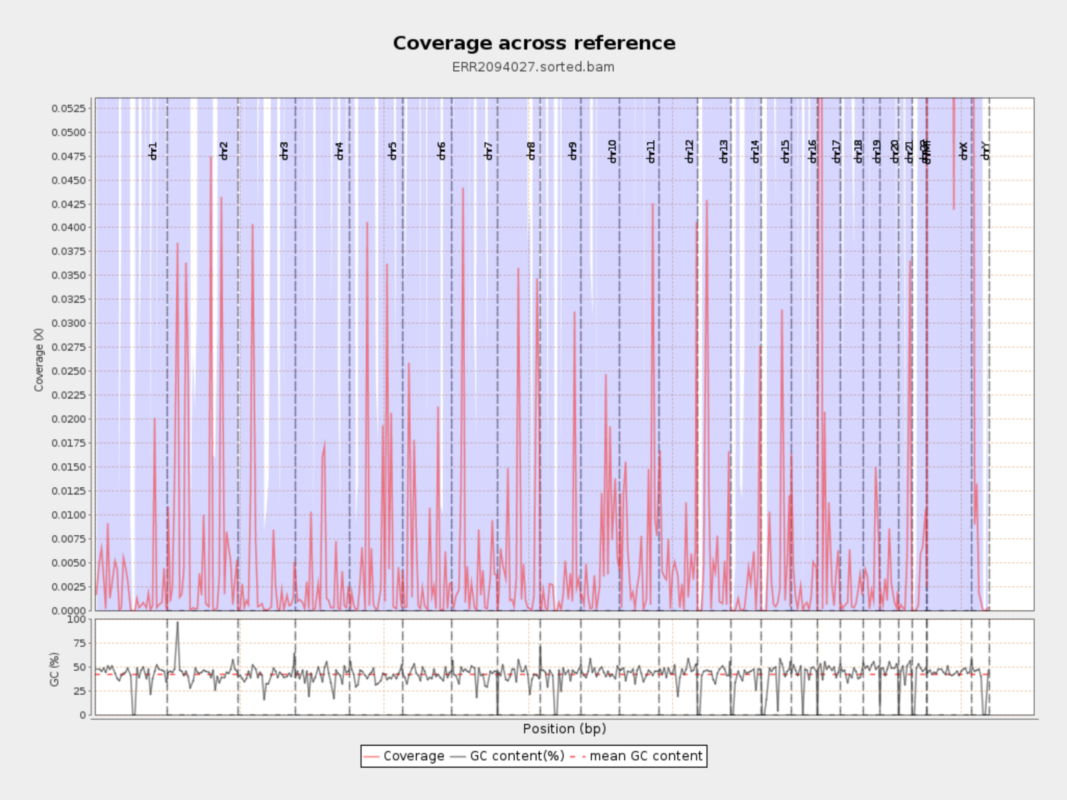
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

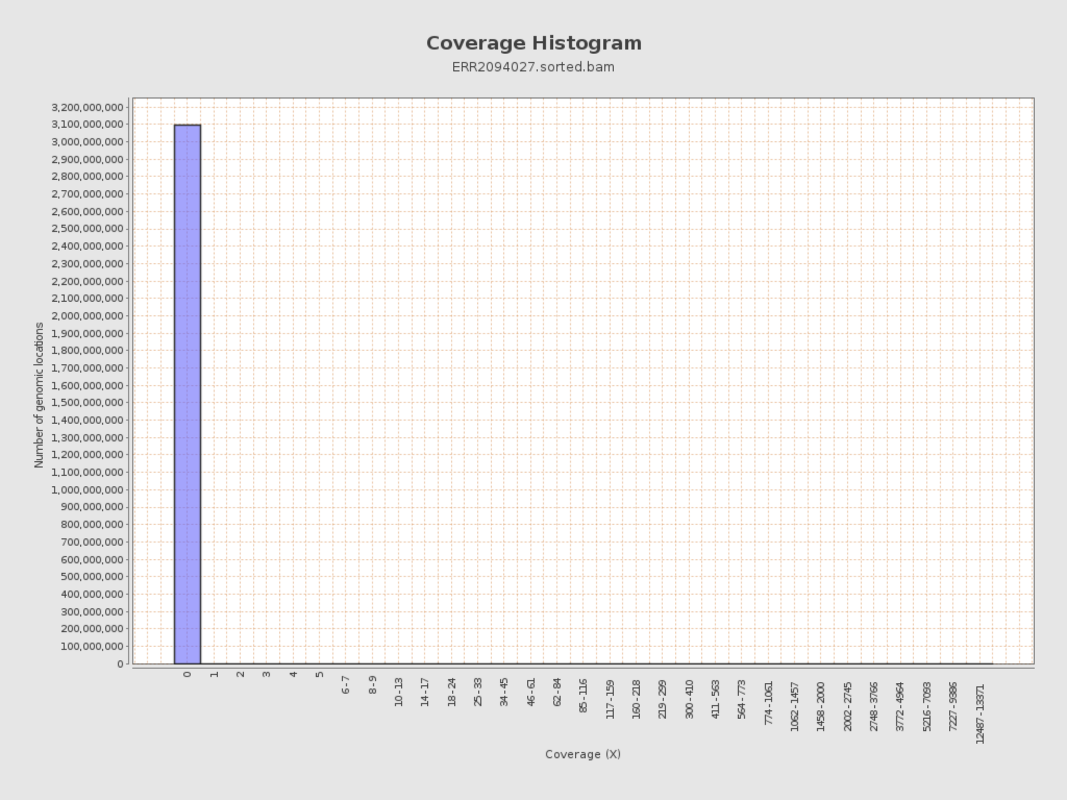
		bases	coverage	deviation
chr1	249250621	664912	0.0027	0.8589
chr2	243199373	2115274	0.0087	2.6635
chr3	198022430	662824	0.0033	1.2399
chr4	191154276	572869	0.003	0.795
chr5	180915260	1167972	0.0065	2.8864
chr6	171115067	830726	0.0049	1.6542
chr7	159138663	811644	0.0051	1.7872
chr8	146364022	1035561	0.0071	2.3147
chr9	141213431	456483	0.0032	1.4837
chr10	135534747	837354	0.0062	1.6558
chr11	135006516	1038182	0.0077	2.1016
chr12	133851895	725433	0.0054	1.2226
chr13	115169878	783978	0.0068	1.6289
chr14	107349540	384133	0.0036	0.6923
chr15	102531392	517995	0.0051	1.5963
chr16	90354753	243109	0.0027	0.8459
chr17	81195210	1809225	0.0223	5.3771
chr18	78077248	128301	0.0016	0.4939
chr19	59128983	265657	0.0045	0.956
chr20	63025520	153128	0.0024	0.5369
chr21	48129895	380840	0.0079	2.8504
chr22	51304566	190699	0.0037	0.3787
chrMT	16571	5908737	356.5709	1,510.3914
chrX	155270560	20332459	0.1309	9.6183

chrY	59373566	705733	0.0119	4.55

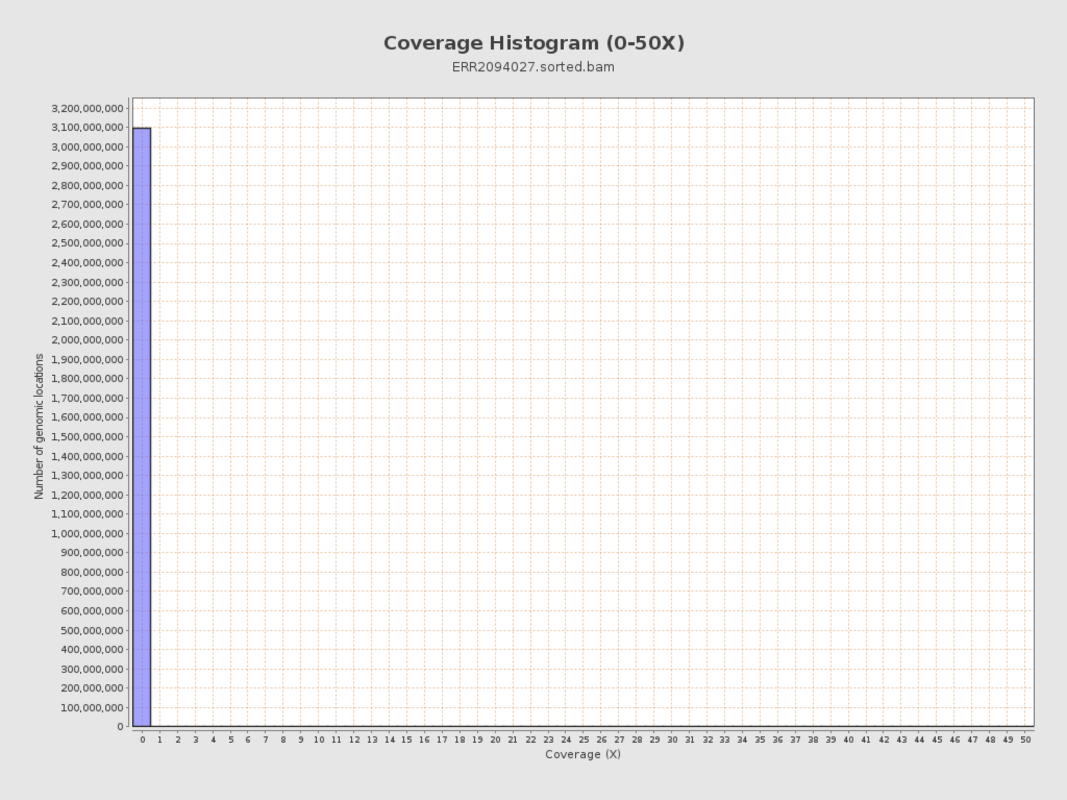
3. Results : Coverage across reference



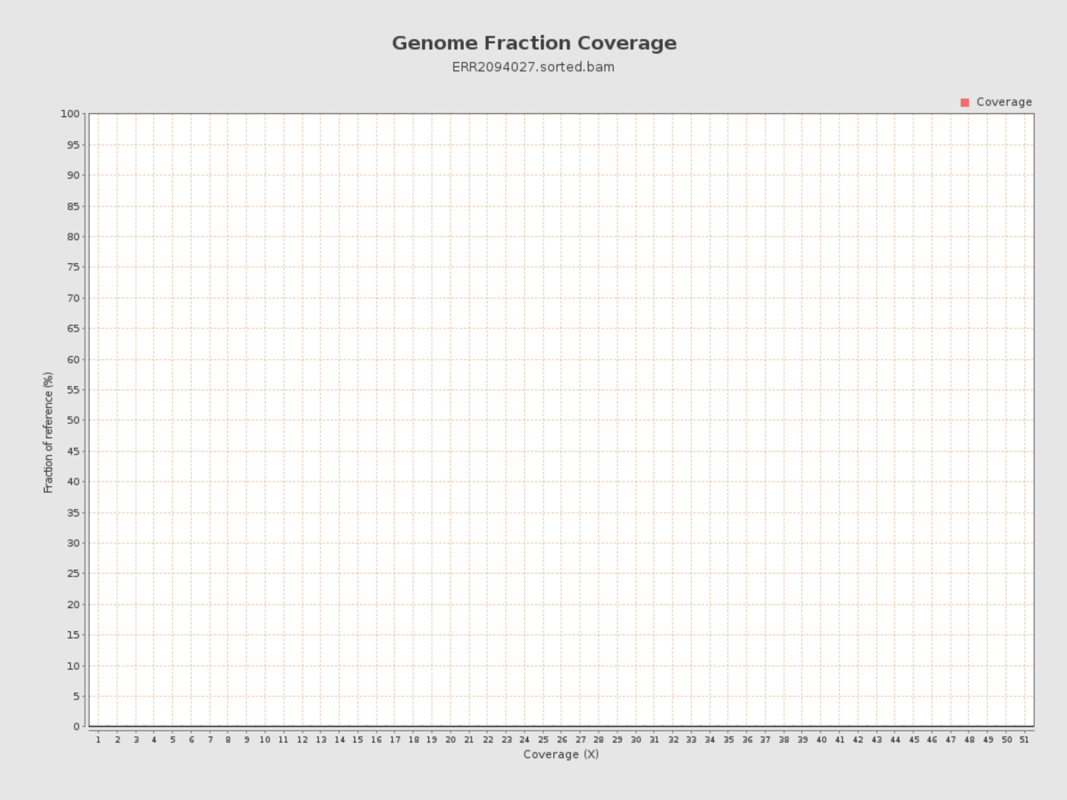
4. Results : Coverage Histogram



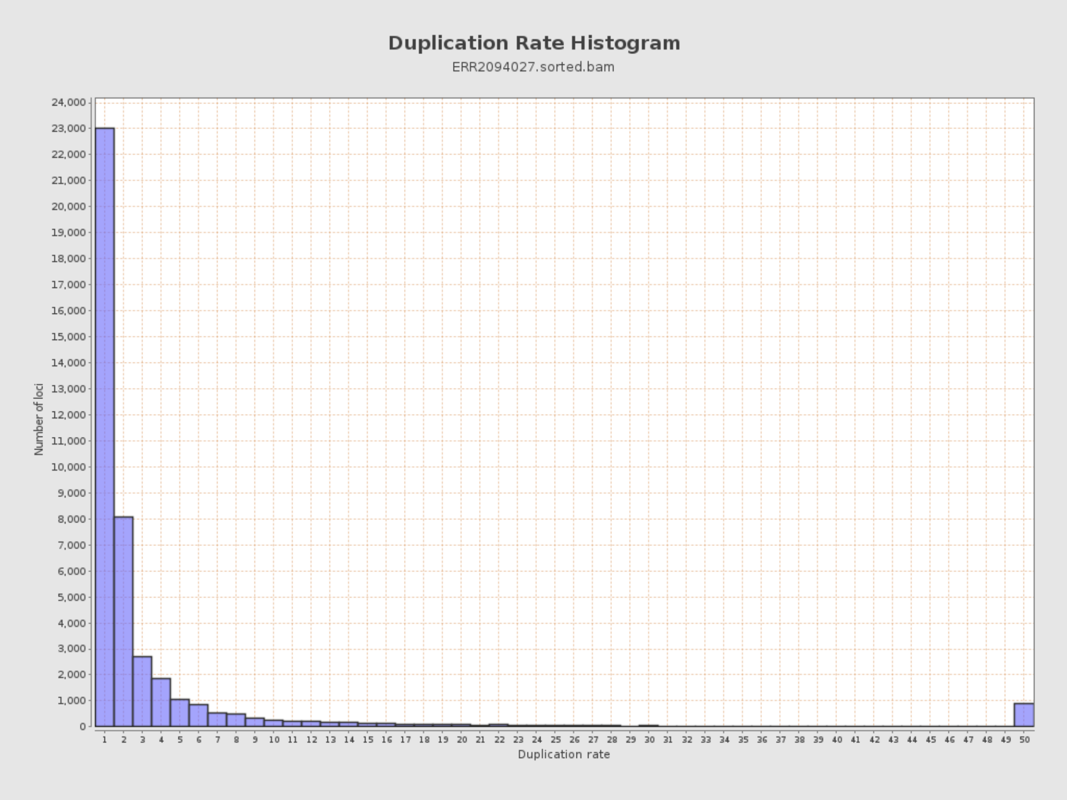
5. Results : Coverage Histogram (0-50X)



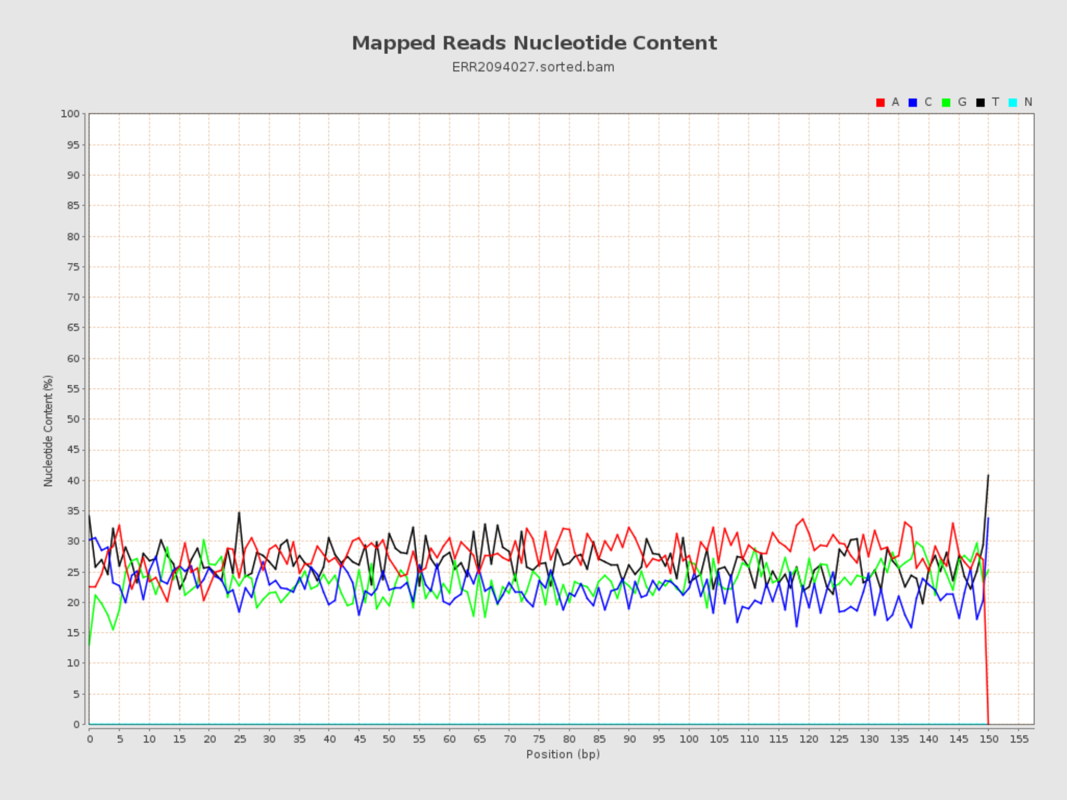
6. Results : Genome Fraction Coverage



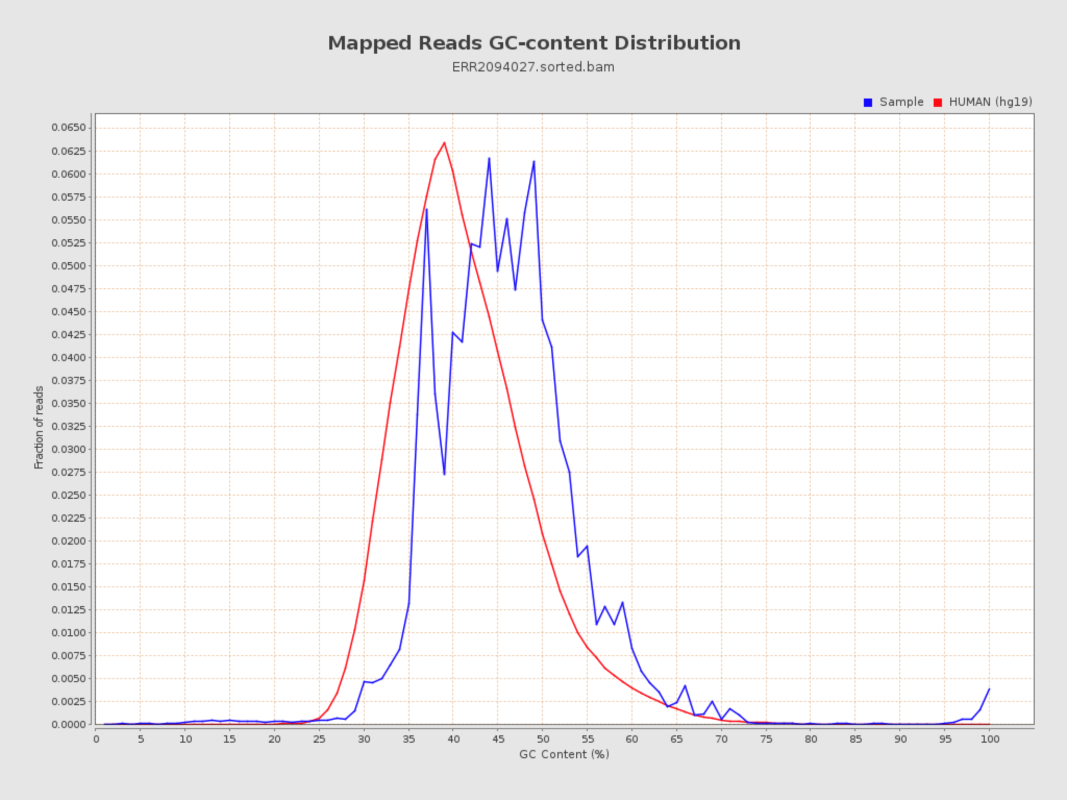
7. Results : Duplication Rate Histogram



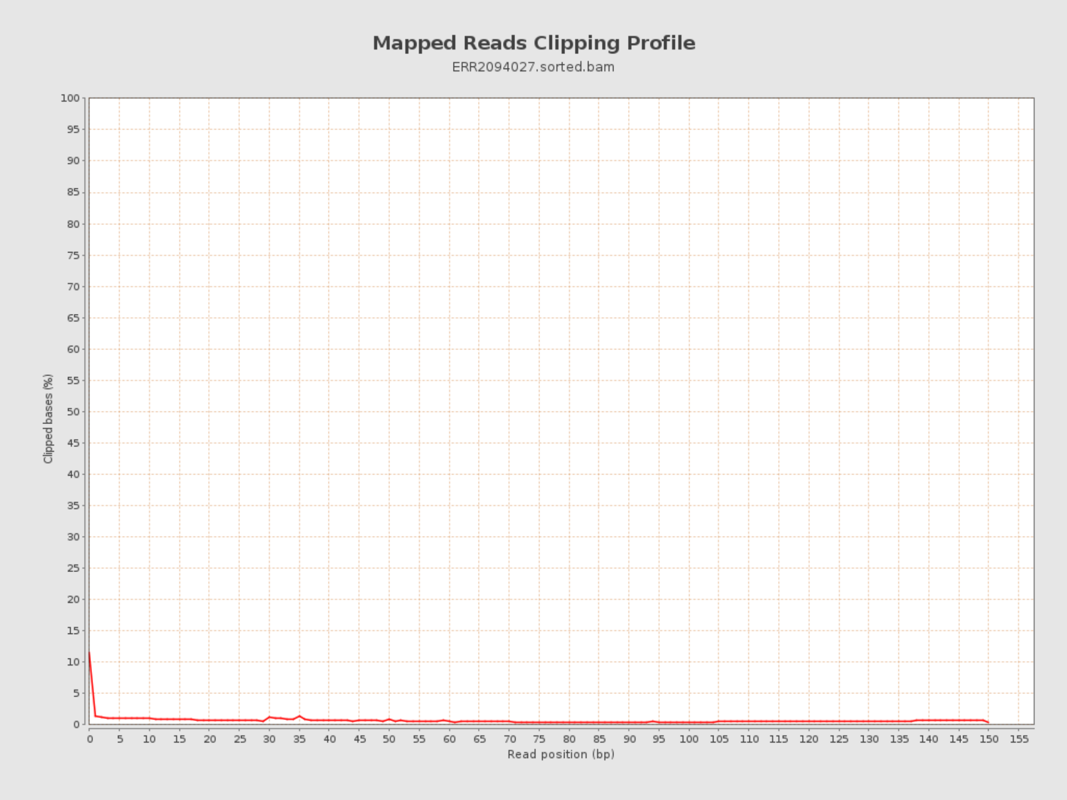
8. Results : Mapped Reads Nucleotide Content



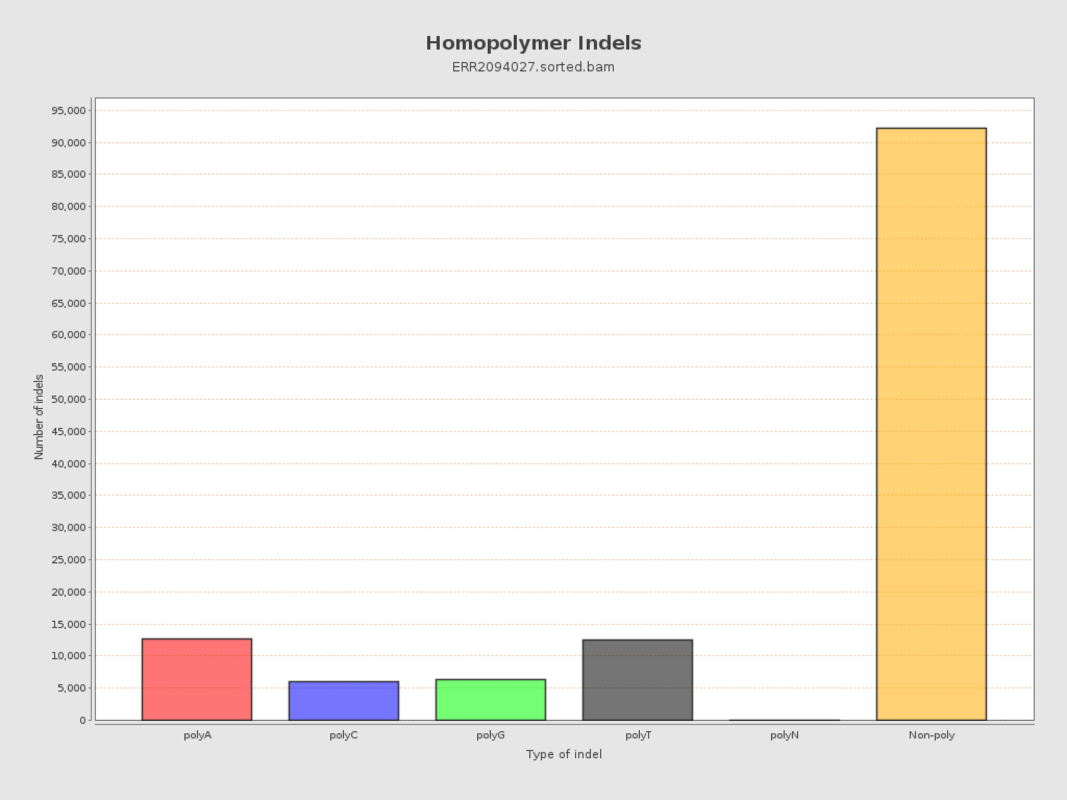
9. Results : Mapped Reads GC-content Distribution



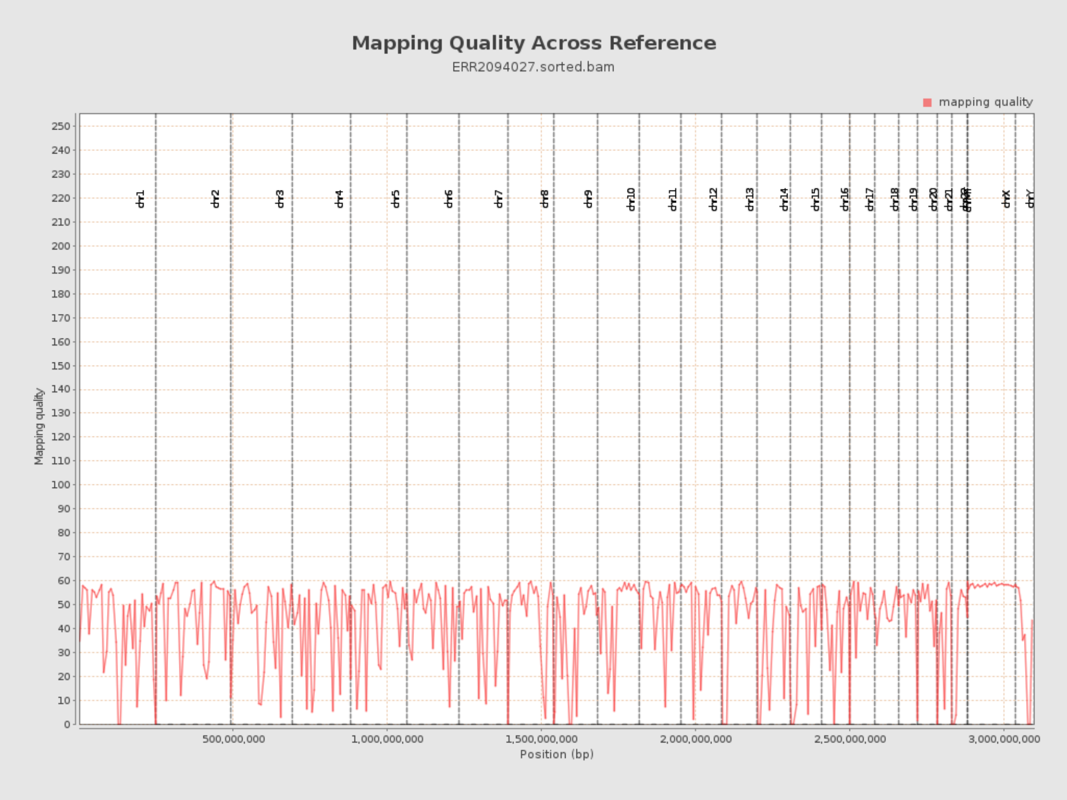
10. Results : Mapped Reads Clipping Profile



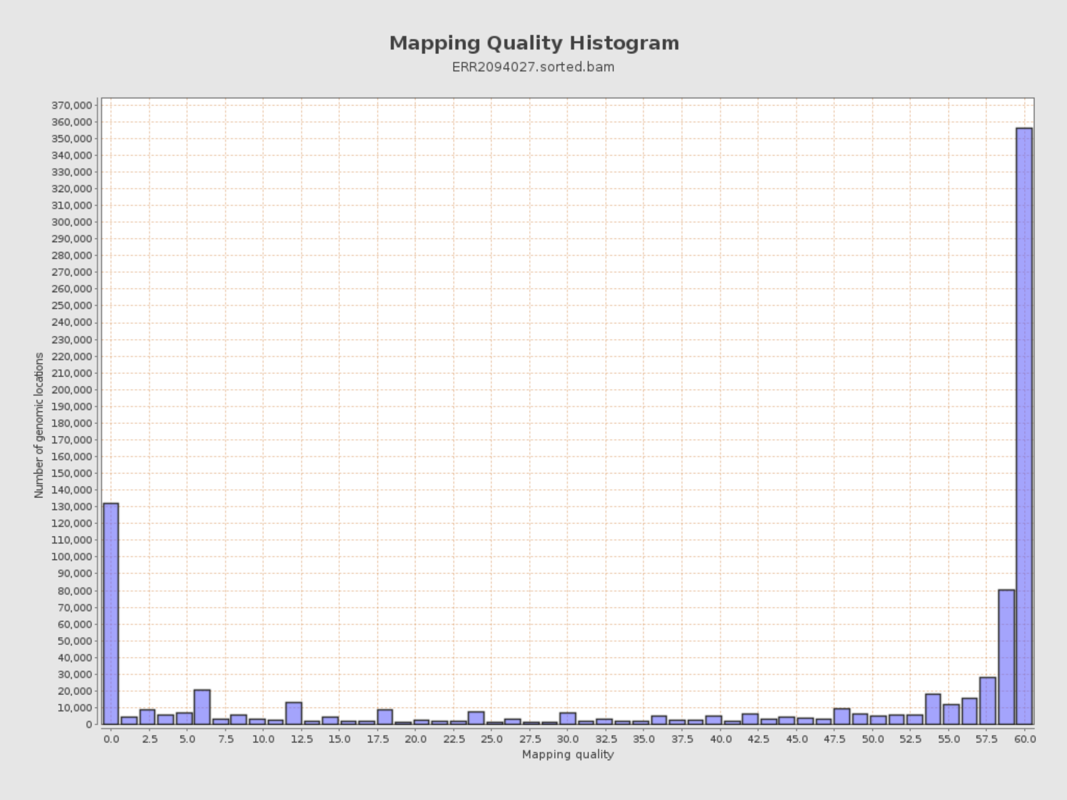
11. Results : Homopolymer Indels



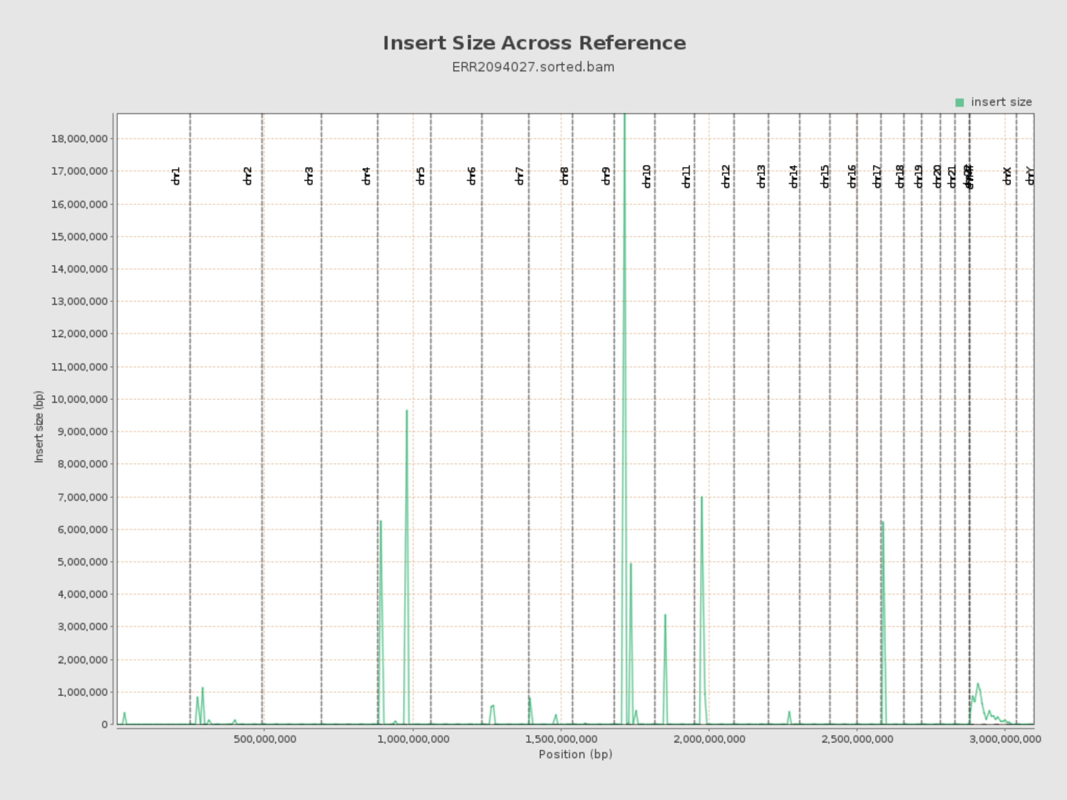
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram