Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 17:06:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038406.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_SRR5038406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038406_1.fastq.gz SRR5038406_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 17:06:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,142,256
Mapped reads	17,275,611 / 95.22%
Unmapped reads	866,645 / 4.78%
Mapped paired reads	17,275,611 / 95.22%
Mapped reads, first in pair	8,755,140 / 48.26%
Mapped reads, second in pair	8,520,471 / 46.96%
Mapped reads, both in pair	16,999,430 / 93.7%
Mapped reads, singletons	276,181 / 1.52%
Secondary alignments	0
Supplementary alignments	253,010 / 1.39%
Read min/max/mean length	30 / 150 / 150.7
Duplicated reads (estimated)	3,268,340 / 18.02%
Duplication rate	13.22%
Clipped reads	7,798,958 / 42.99%

2.2. ACGT Content

Number/percentage of A's	670,279,701 / 28.62%
Number/percentage of C's	464,083,650 / 19.81%
Number/percentage of T's	681,734,226 / 29.11%
Number/percentage of G's	525,950,599 / 22.46%
Number/percentage of N's	184,270 / 0.01%

GC Percentage	42.27%

2.3. Coverage

Mean	0.7571
Standard Deviation	9.1896

2.4. Mapping Quality

Mean Mapping Quality	53.4

2.5. Insert size

Mean	89,128.72
Standard Deviation	2,909,877.17
P25/Median/P75	212 / 263 / 329

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	29,456,887
Insertions	404,349
Mapped reads with at least one insertion	2.23%
Deletions	844,578
Mapped reads with at least one deletion	4.72%
Homopolymer indels	48.56%

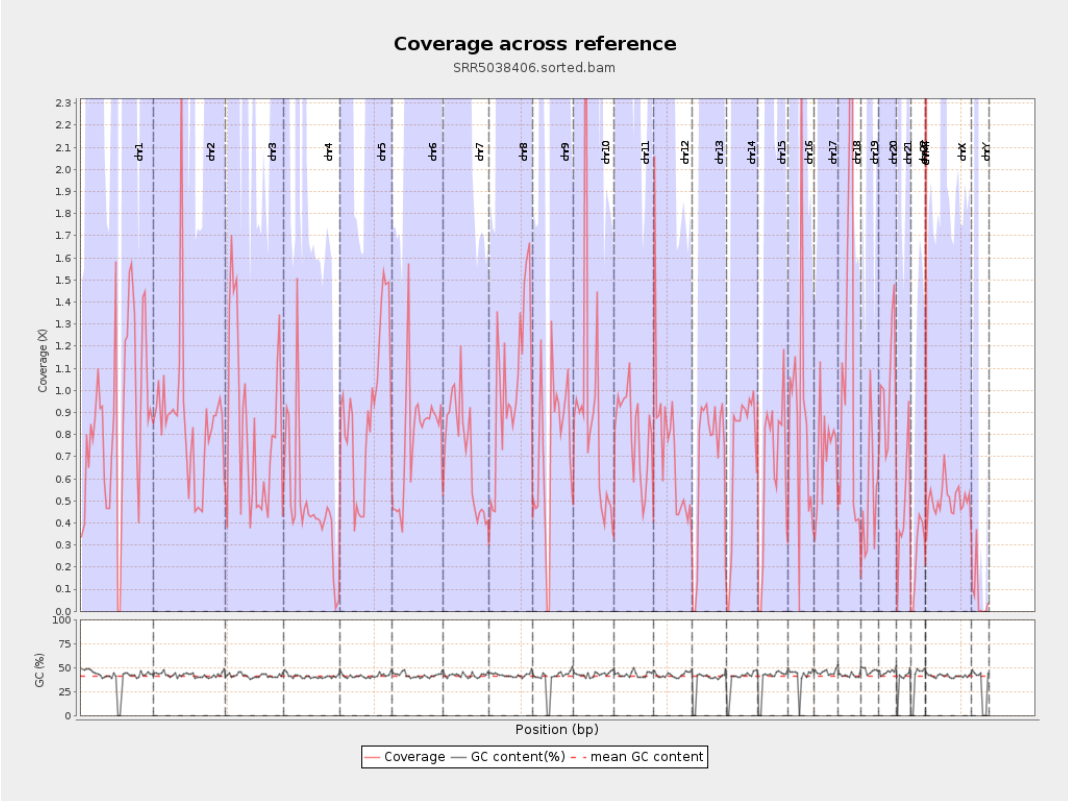
2.7. Chromosome stats

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

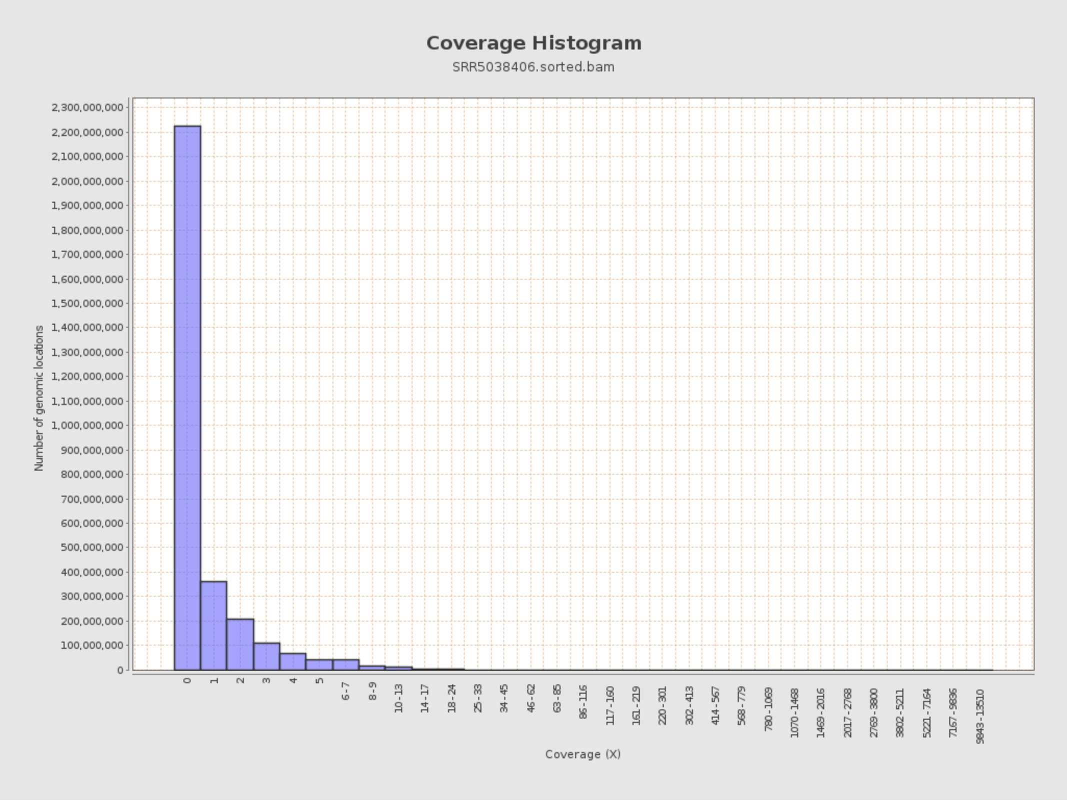
		bases	coverage	deviation
chr1	249250621	215636188	0.8651	13.501
chr2	243199373	210315846	0.8648	10.4104
chr3	198022430	163826970	0.8273	1.8373
chr4	191154276	91854782	0.4805	9.1193
chr5	180915260	163980537	0.9064	1.8557
chr6	171115067	136865993	0.7998	7.5162
chr7	159138663	113429369	0.7128	9.1858
chr8	146364022	151088011	1.0323	3.7036
chr9	141213431	100828395	0.714	15.9812
chr10	135534747	122543680	0.9041	21.074
chr11	135006516	108283414	0.8021	7.2087
chr12	133851895	98717951	0.7375	1.8304
chr13	115169878	80523160	0.6992	1.5843
chr14	107349540	78280612	0.7292	1.7094
chr15	102531392	65090911	0.6348	1.5429
chr16	90354753	77504489	0.8578	12.0243
chr17	81195210	57279605	0.7055	11.4283
chr18	78077248	94751804	1.2136	10.9817
chr19	59128983	30277167	0.5121	5.7087
chr20	63025520	63199432	1.0028	3.5581
chr21	48129895	22618557	0.4699	4.3255
chr22	51304566	13180900	0.2569	0.9381
chrMT	16571	1573961	94.9829	56.3013
chrX	155270560	77862718	0.5015	2.0854

chrY	59373566	4306186	0.0725	9.2031

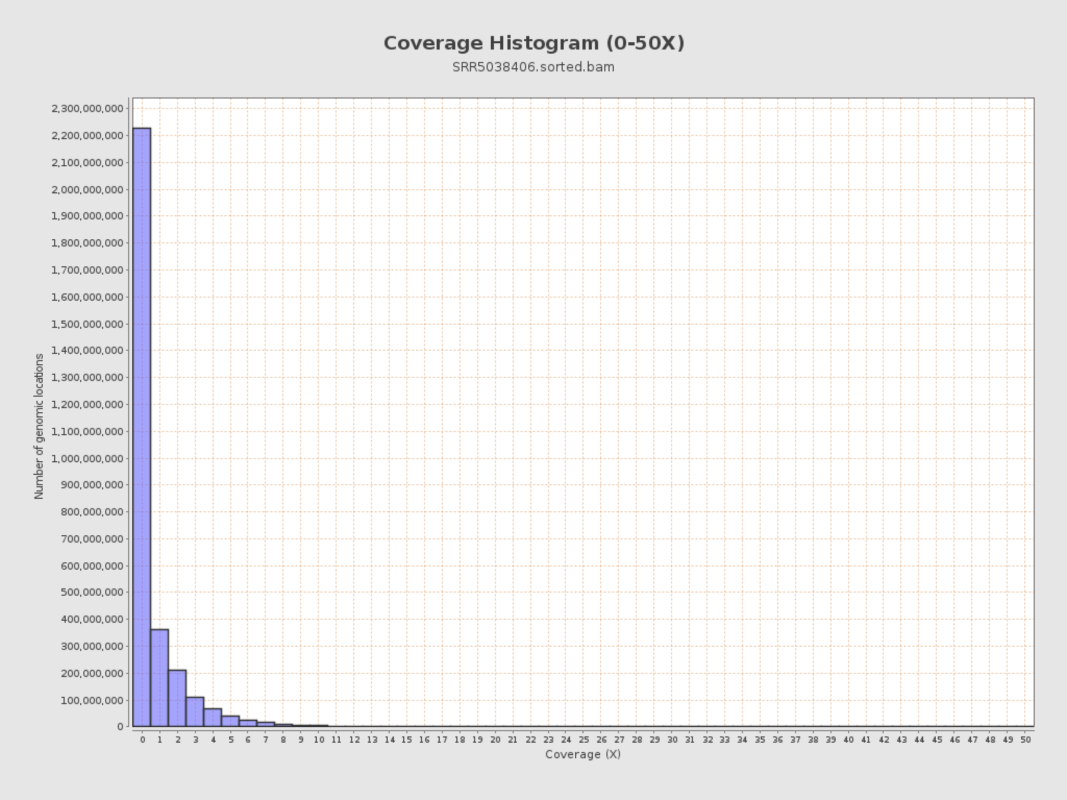
3. Results : Coverage across reference



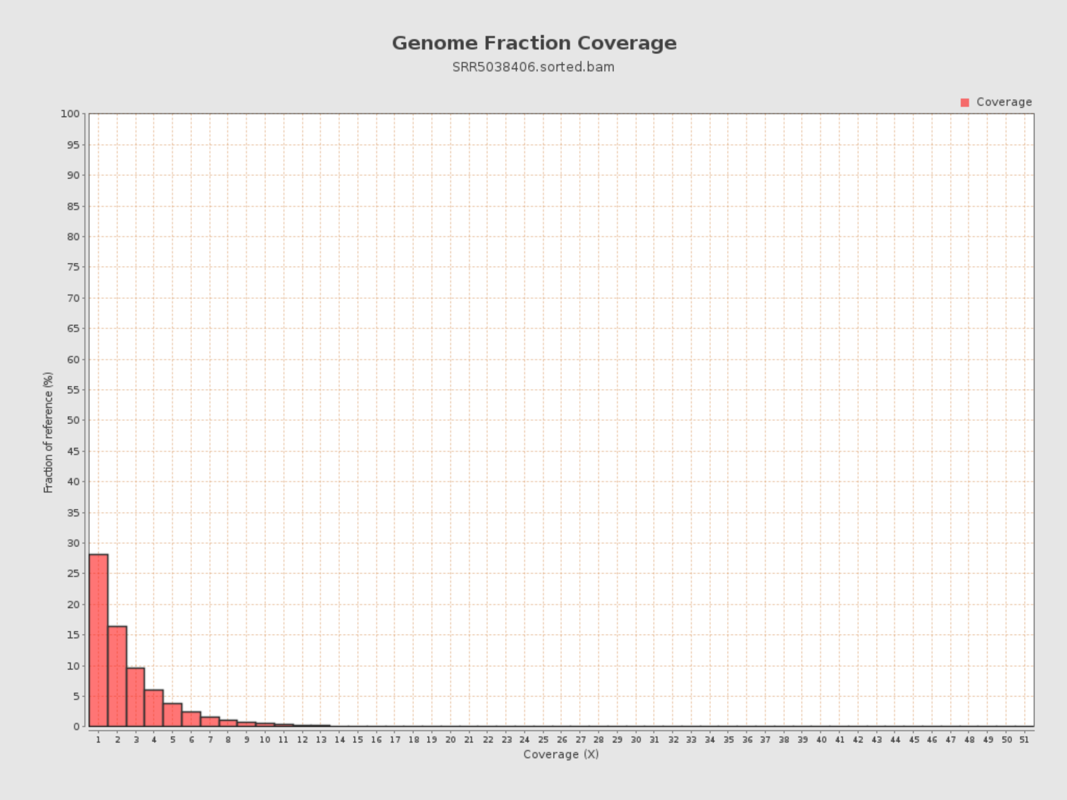
4. Results : Coverage Histogram



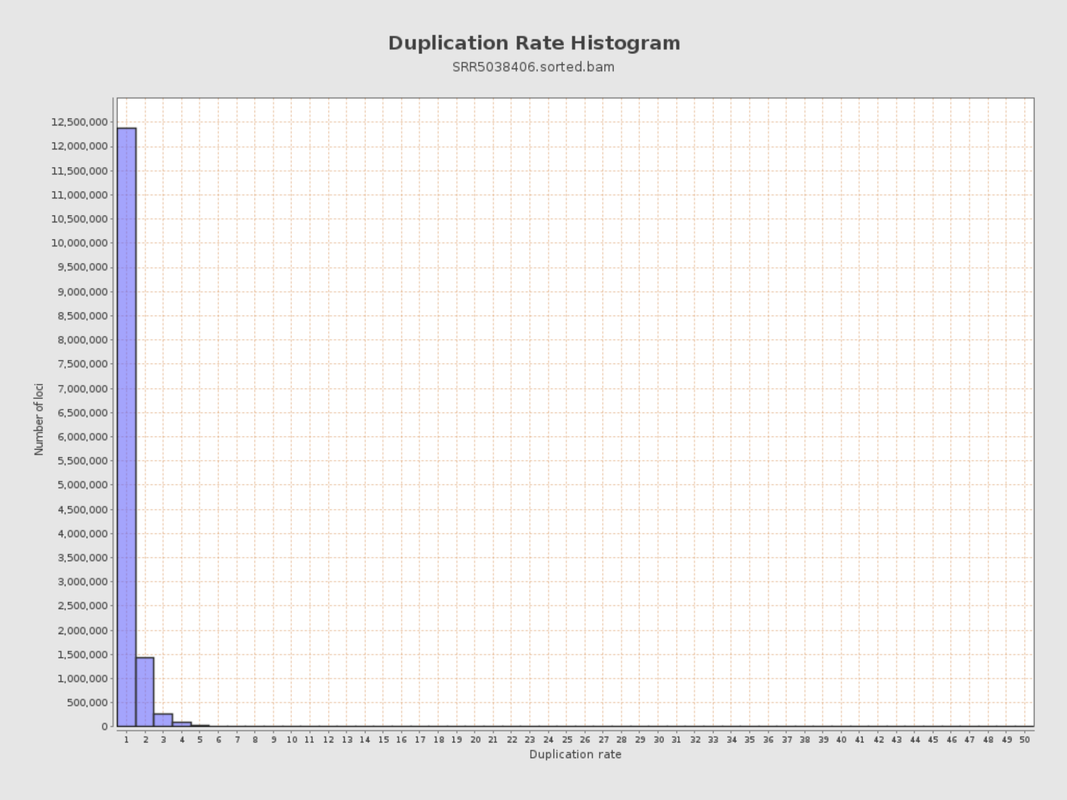
5. Results : Coverage Histogram (0-50X)



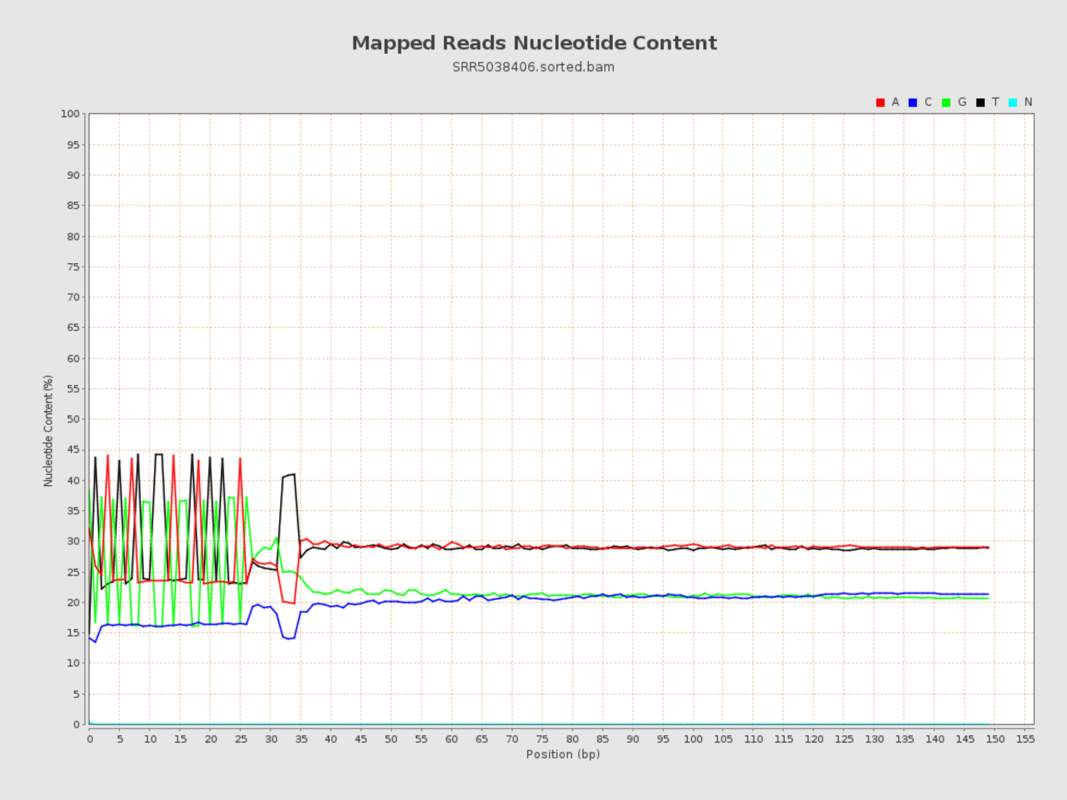
6. Results : Genome Fraction Coverage



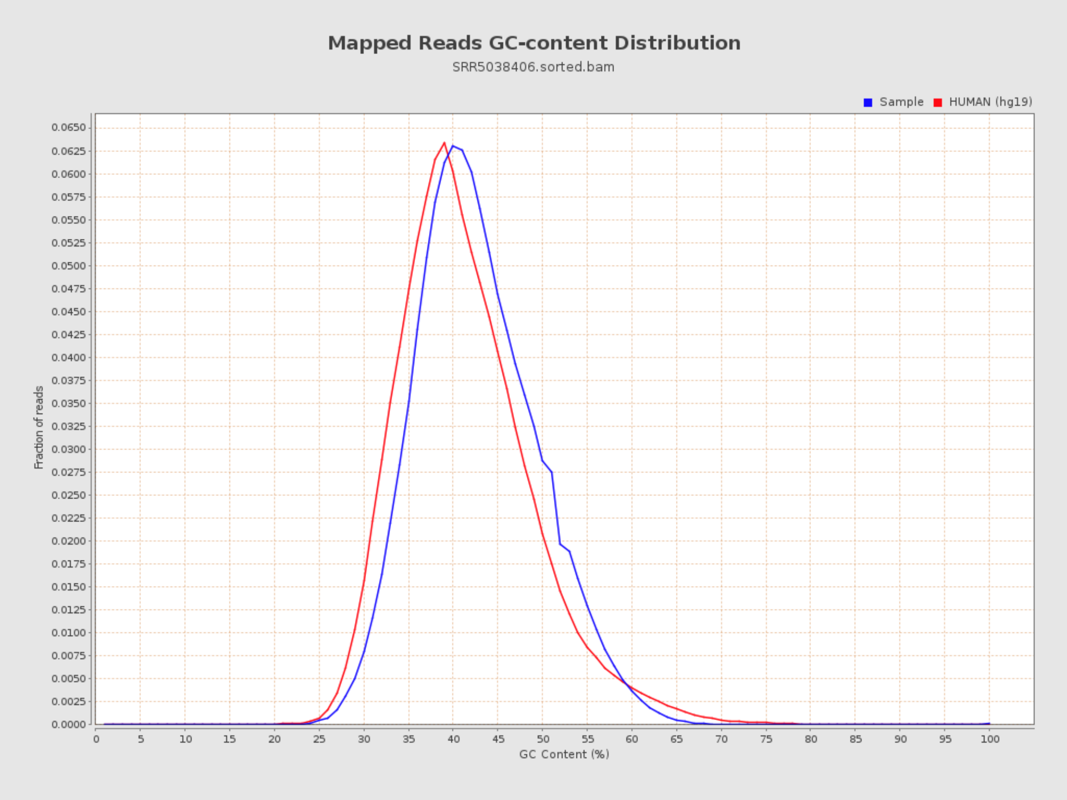
7. Results : Duplication Rate Histogram



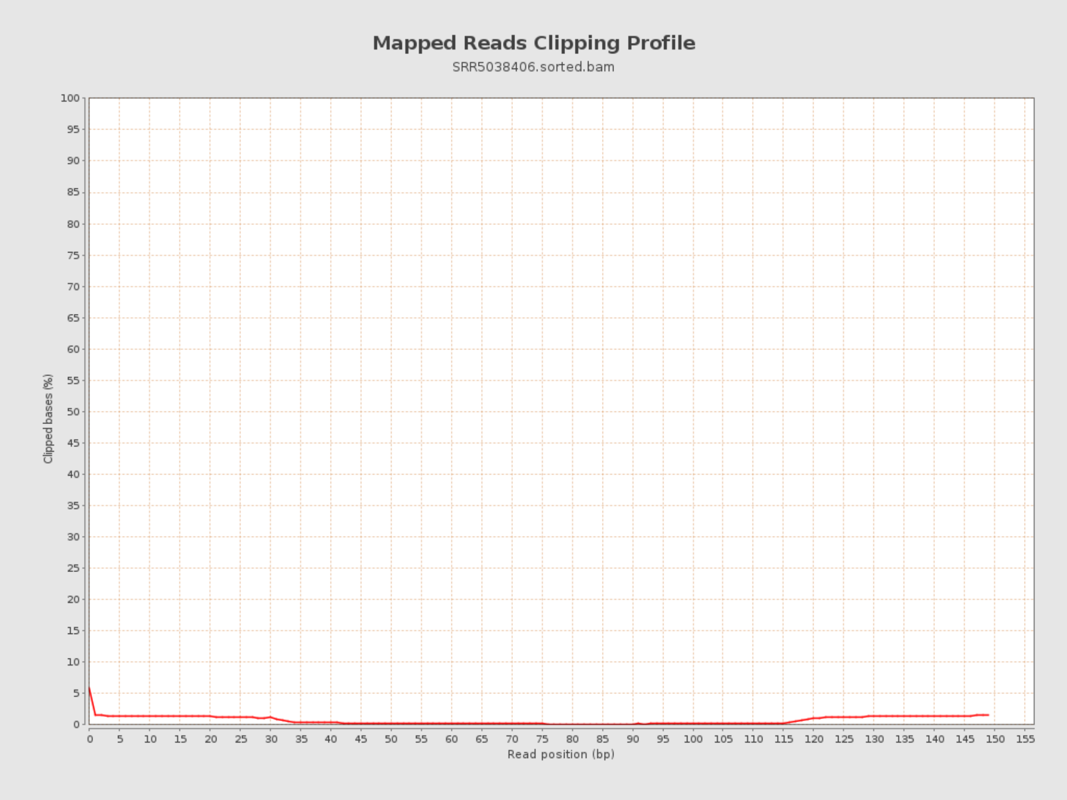
8. Results : Mapped Reads Nucleotide Content



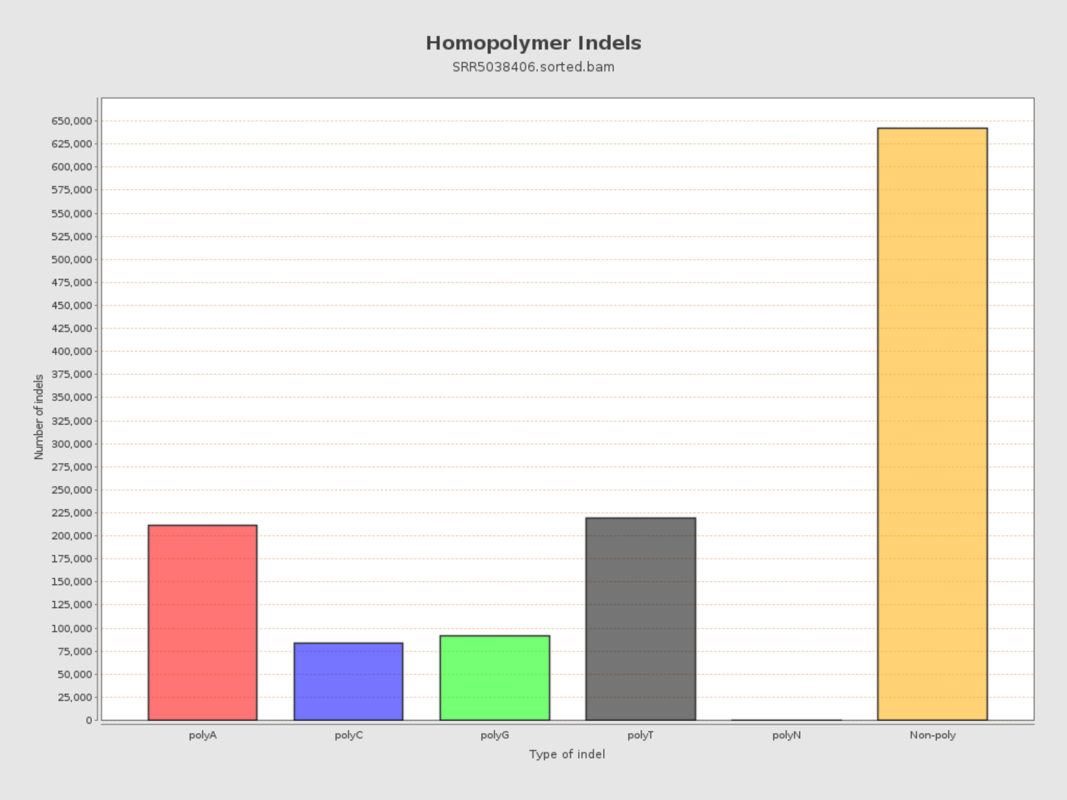
9. Results : Mapped Reads GC-content Distribution



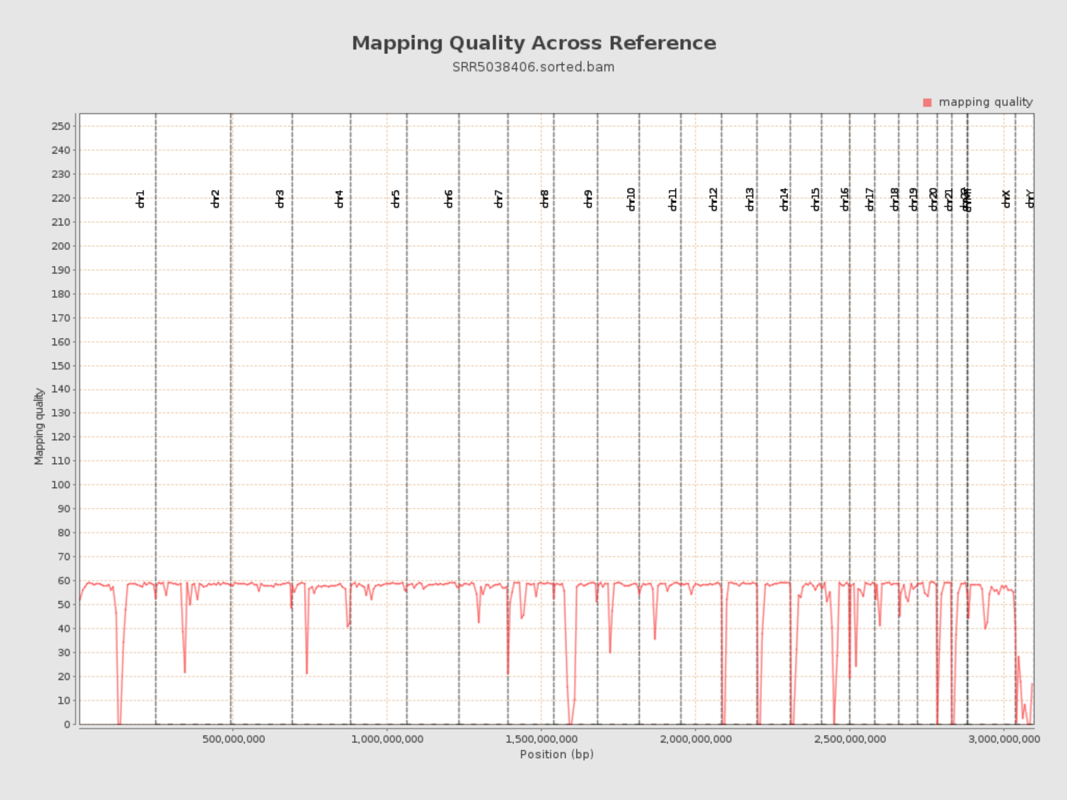
10. Results : Mapped Reads Clipping Profile



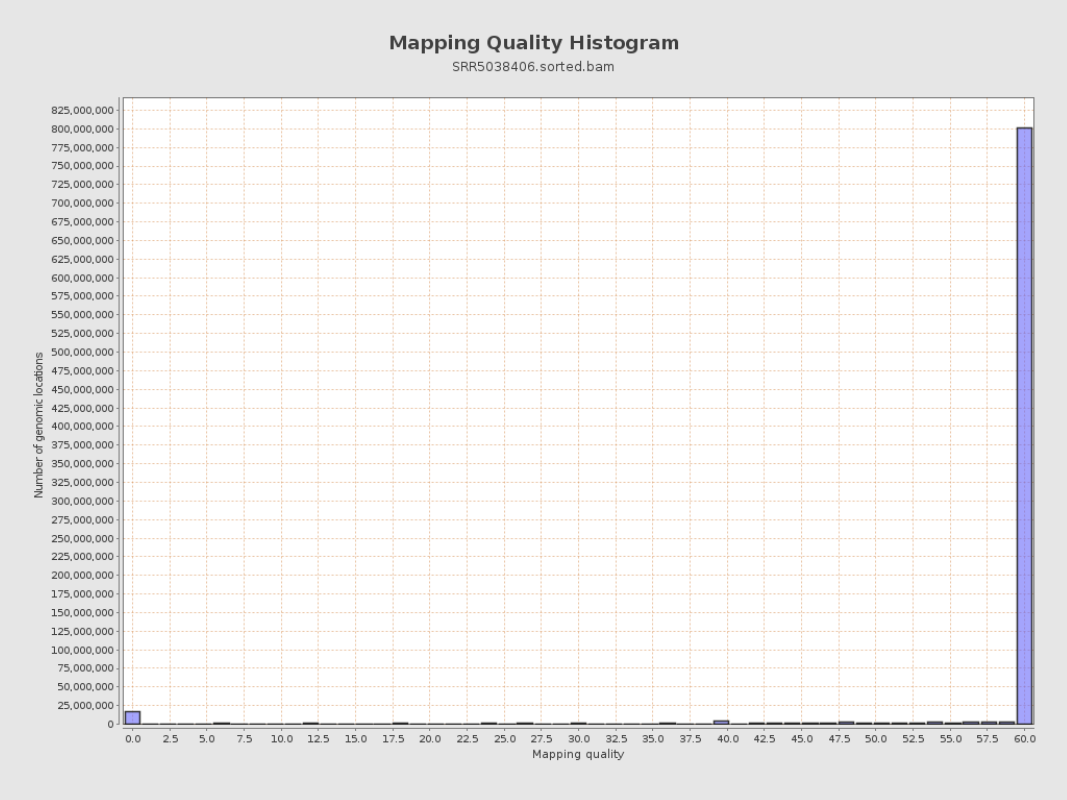
11. Results : Homopolymer Indels



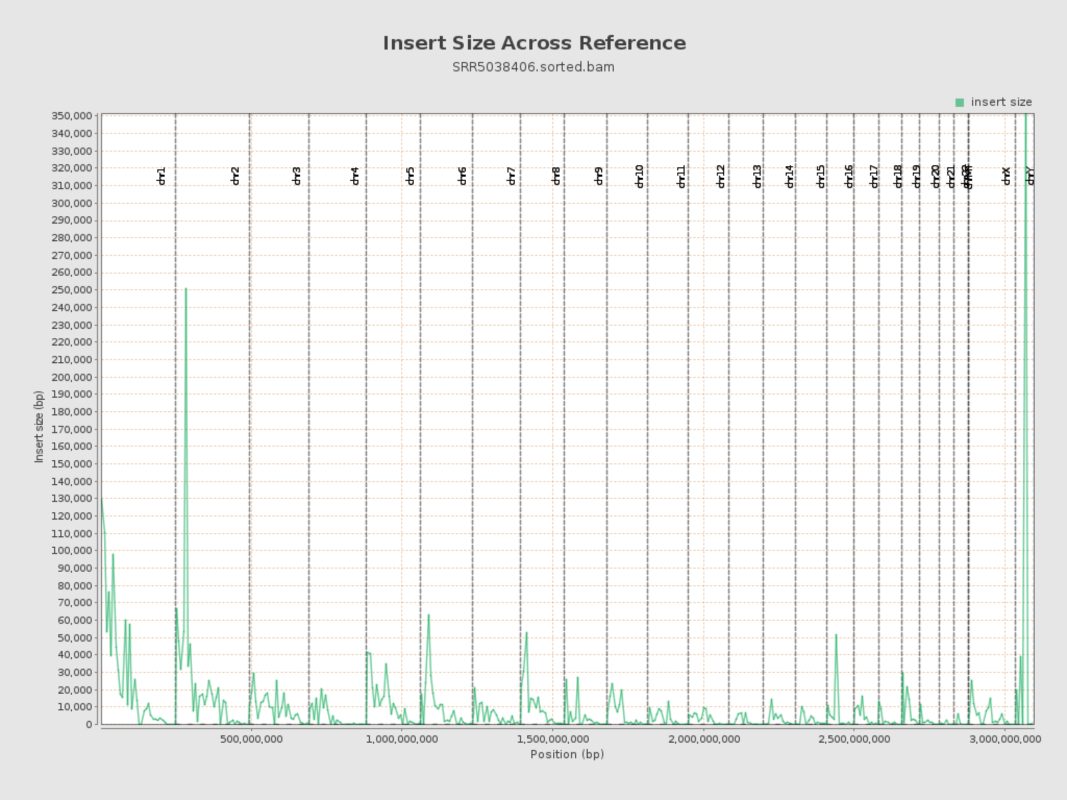
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram