Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 03:00:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038474.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_SRR5038474 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038474_1.fastq.gz SRR5038474_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 03:00:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038474.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,410,056
Mapped reads	74,930,260 / 99.36%
Unmapped reads	479,796 / 0.64%
Mapped paired reads	74,930,260 / 99.36%
Mapped reads, first in pair	37,663,701 / 49.95%
Mapped reads, second in pair	37,266,559 / 49.42%
Mapped reads, both in pair	74,508,080 / 98.8%
Mapped reads, singletons	422,180 / 0.56%
Secondary alignments	0
Supplementary alignments	105,450 / 0.14%
Read min/max/mean length	30 / 150 / 150.06
Duplicated reads (estimated)	28,578,793 / 37.9%
Duplication rate	36.12%
Clipped reads	5,492,044 / 7.28%

2.2. ACGT Content

Number/percentage of A's	2,784,330,023 / 25.05%
Number/percentage of C's	2,772,728,877 / 24.95%
Number/percentage of T's	2,803,903,383 / 25.23%
Number/percentage of G's	2,752,592,185 / 24.77%
Number/percentage of N's	859,875 / 0.01%

GC Percentage	49.71%

2.3. Coverage

Mean	3.5909
Standard Deviation	22.7396

2.4. Mapping Quality

Mean Mapping Quality	55.73

2.5. Insert size

Mean	18,938.17
Standard Deviation	1,440,363.26
P25/Median/P75	200 / 233 / 274

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	65,768,312
Insertions	531,359
Mapped reads with at least one insertion	0.68%
Deletions	644,209
Mapped reads with at least one deletion	0.84%
Homopolymer indels	46.39%

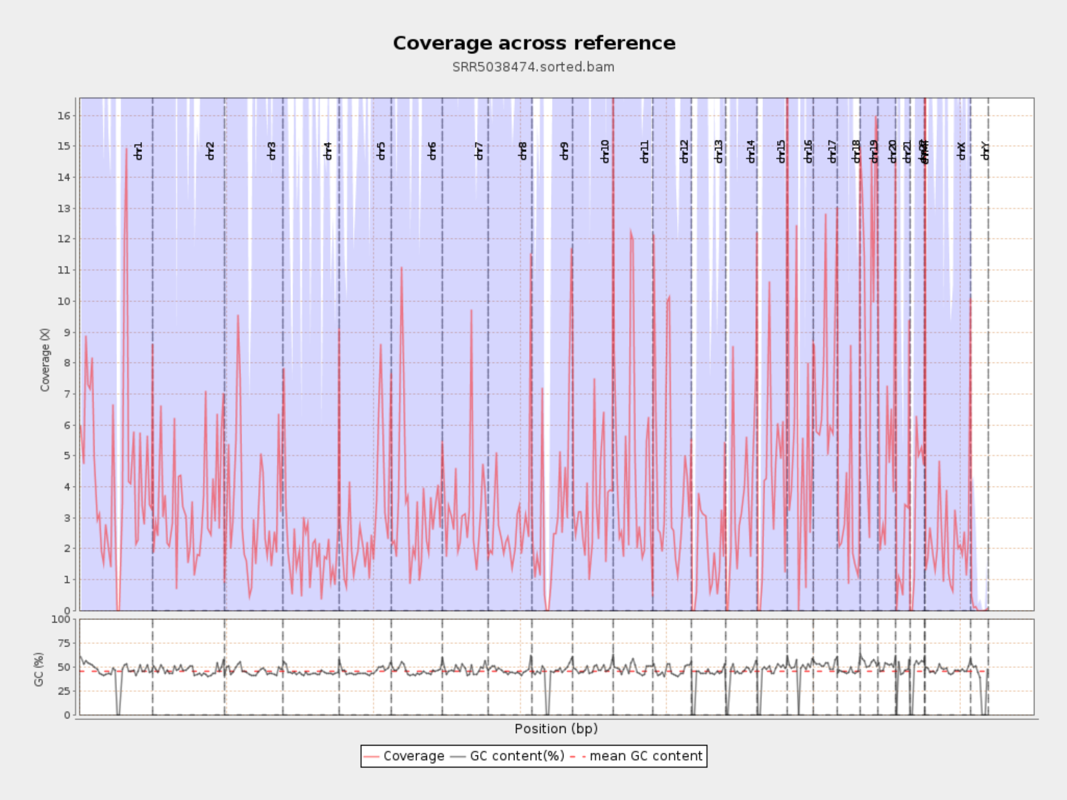
2.7. Chromosome stats

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

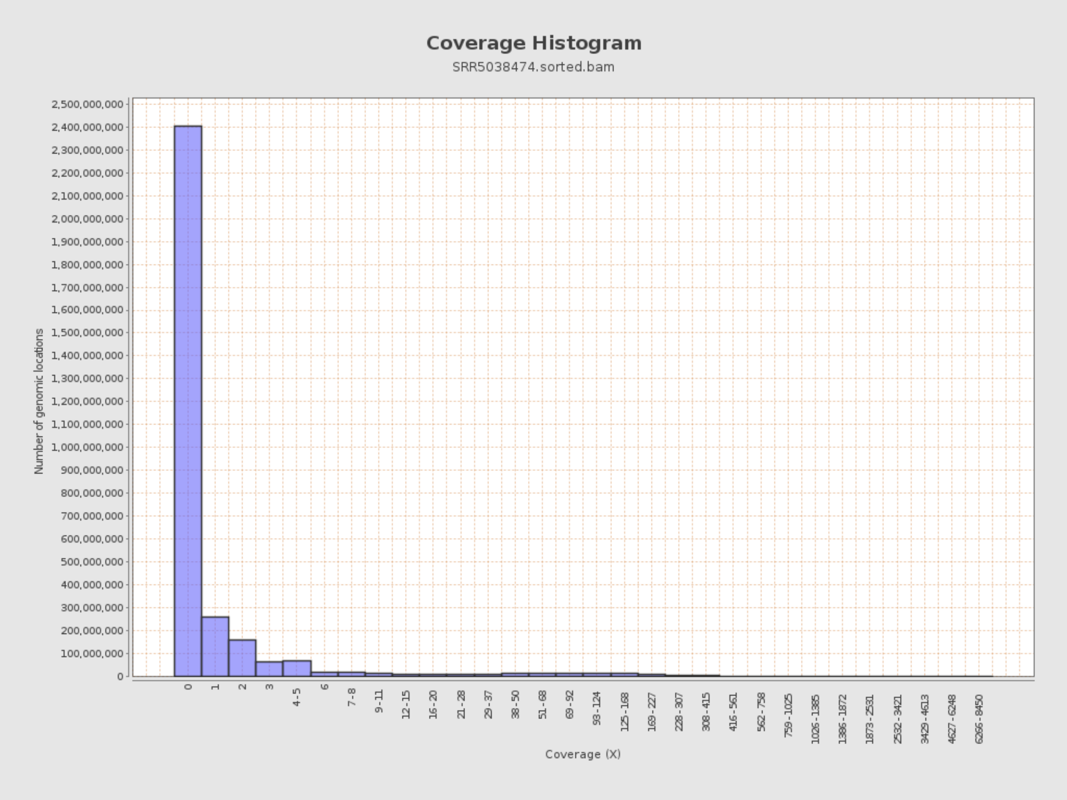
		bases	coverage	deviation
chr1	249250621	1139428958	4.5714	26.5379
chr2	243199373	819613070	3.3701	22.3274
chr3	198022430	643585462	3.2501	21.1066
chr4	191154276	374690177	1.9601	14.8457
chr5	180915260	544888320	3.0118	21.155
chr6	171115067	556141984	3.2501	21.121
chr7	159138663	528779212	3.3228	21.3379
chr8	146364022	430907625	2.9441	20.8679
chr9	141213431	457578789	3.2403	21.3829
chr10	135534747	459576710	3.3908	21.1087
chr11	135006516	656229267	4.8607	27.7718
chr12	133851895	586586762	4.3824	24.8087
chr13	115169878	209888077	1.8224	15.0938
chr14	107349540	380914193	3.5484	22.5194
chr15	102531392	400698360	3.9081	22.8763
chr16	90354753	485481359	5.3731	28.8849
chr17	81195210	618463304	7.617	32.6827
chr18	78077248	214935341	2.7529	23.5135
chr19	59128983	641796013	10.8542	39.1518
chr20	63025520	309871203	4.9166	27.8852
chr21	48129895	117858626	2.4488	21.9542
chr22	51304566	191885580	3.7401	19.7282
chrMT	16571	1086684	65.5775	25.6715
chrX	155270560	340770245	2.1947	15.6974

chrY	59373566	4542172	0.0765	2.2042

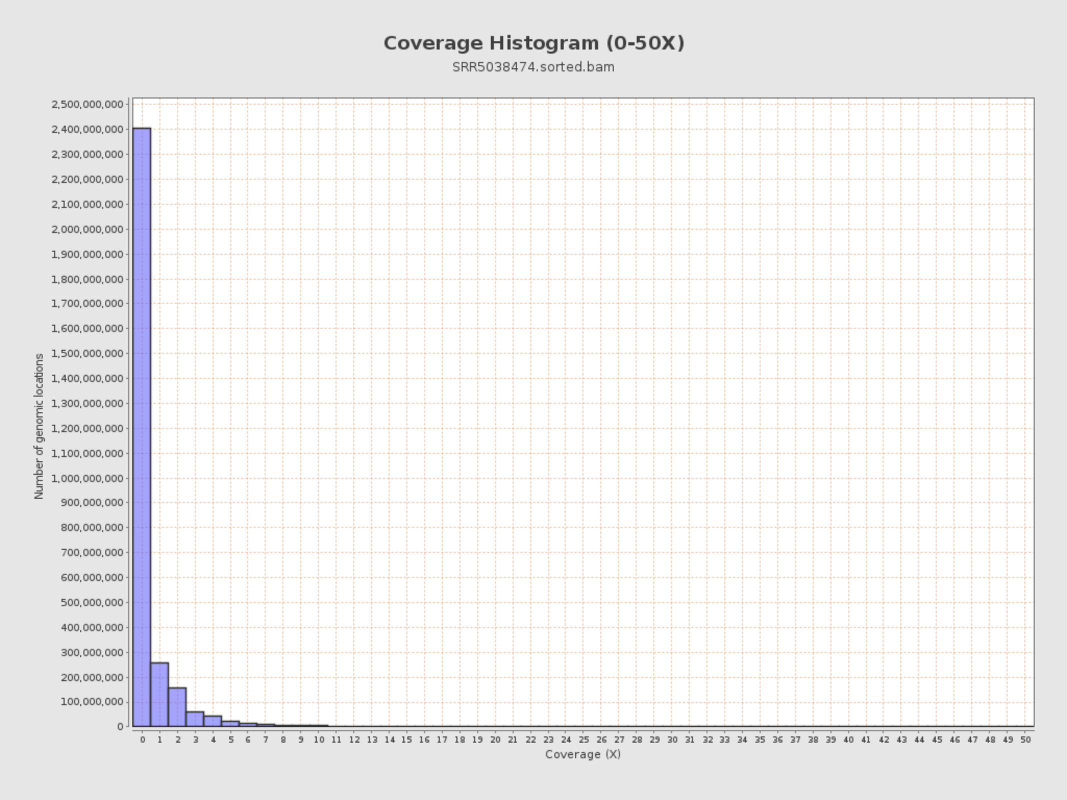
3. Results : Coverage across reference



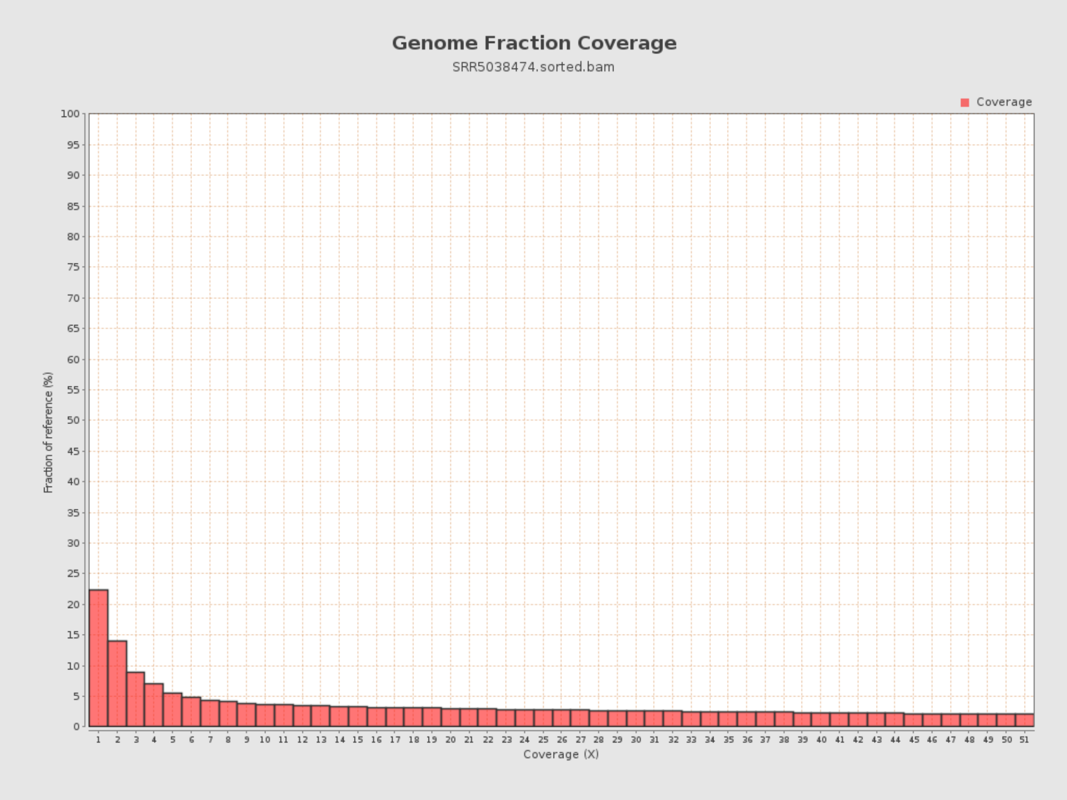
4. Results : Coverage Histogram



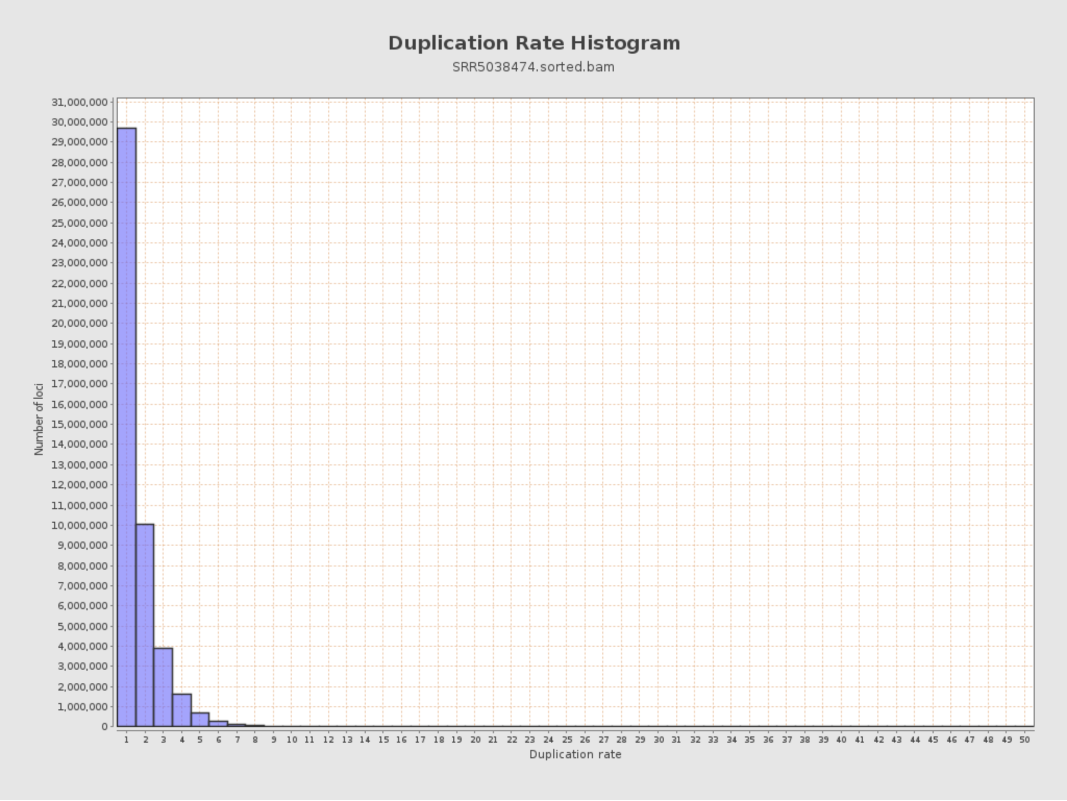
5. Results : Coverage Histogram (0-50X)



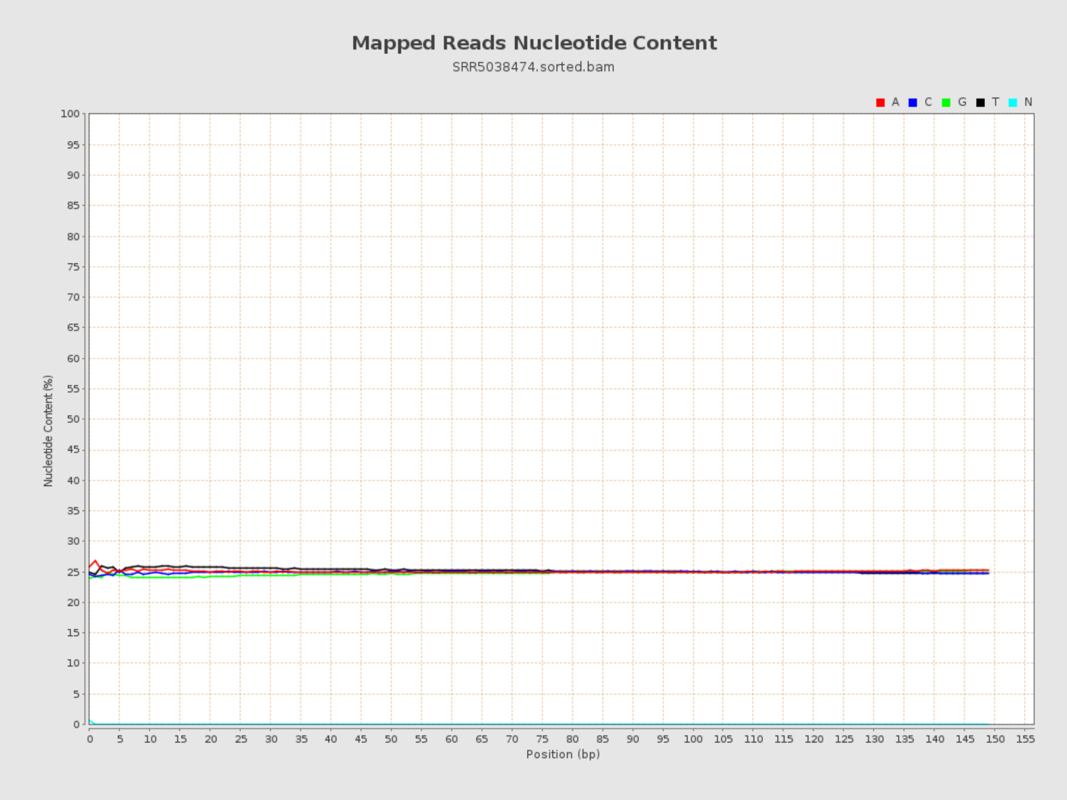
6. Results : Genome Fraction Coverage



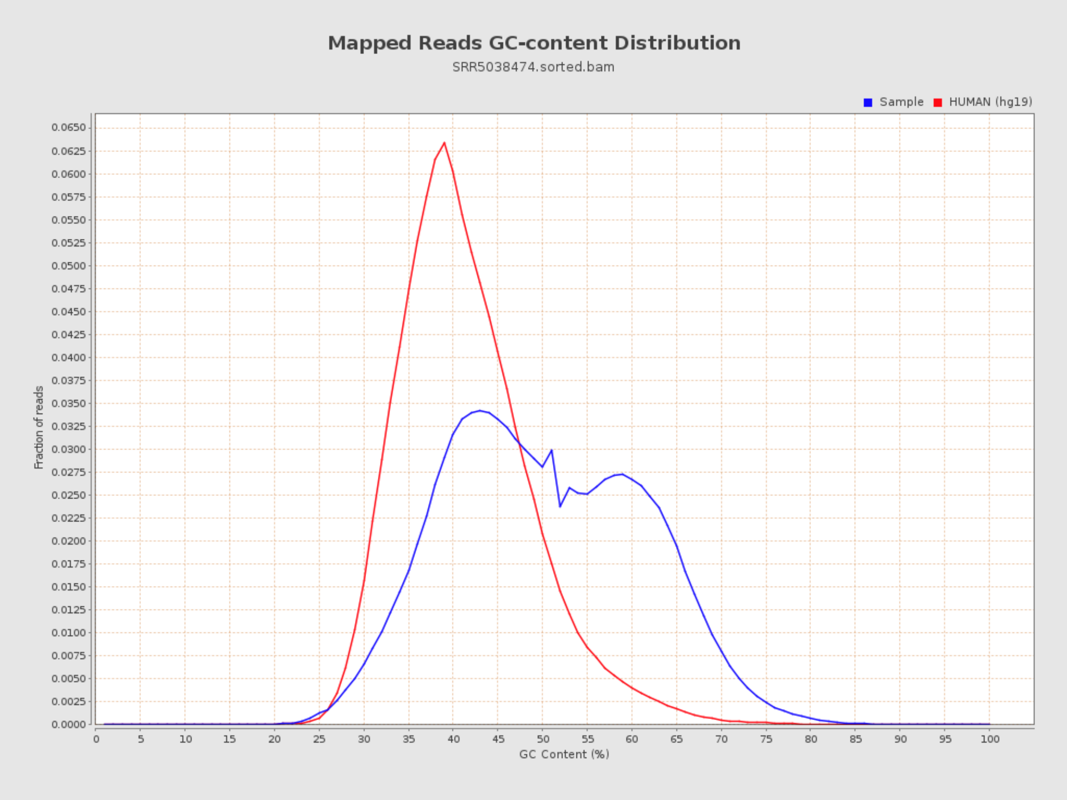
7. Results : Duplication Rate Histogram



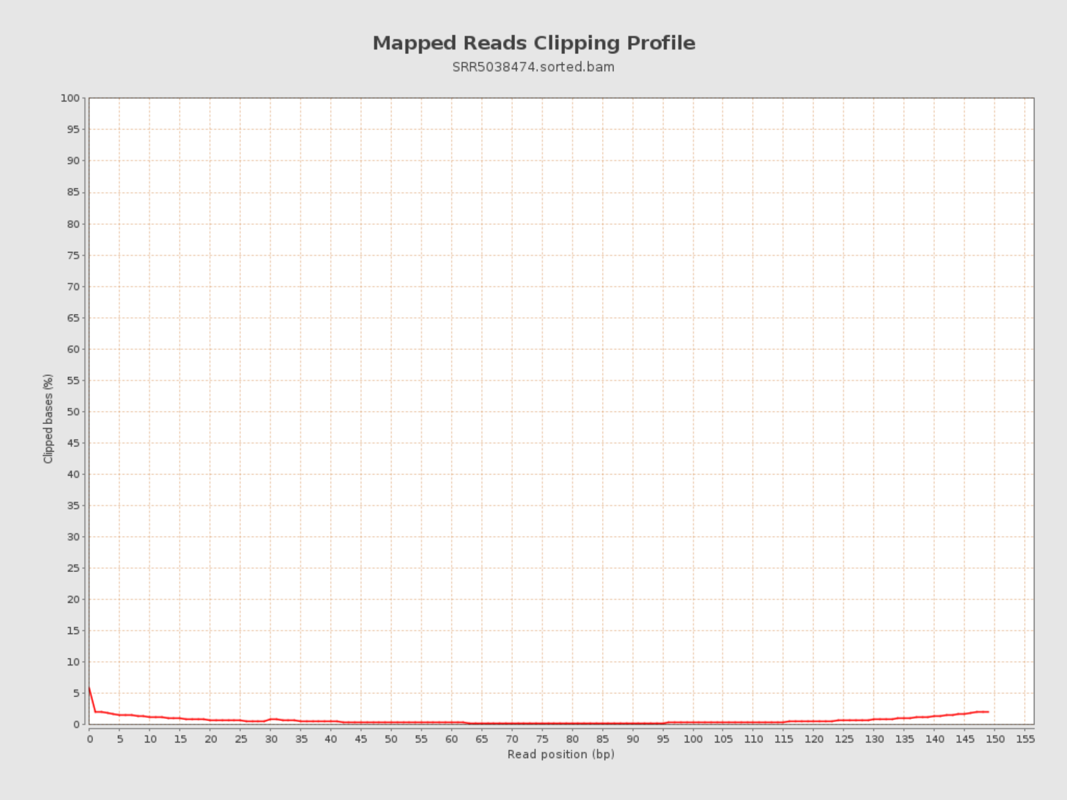
8. Results : Mapped Reads Nucleotide Content



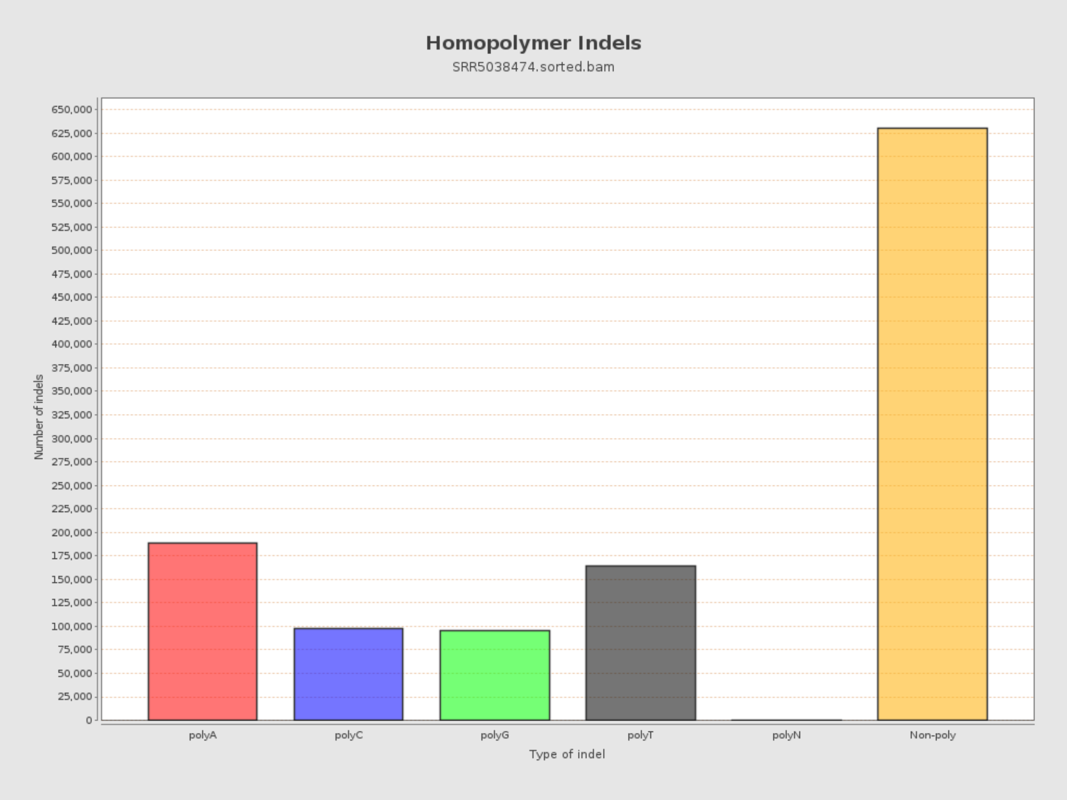
9. Results : Mapped Reads GC-content Distribution



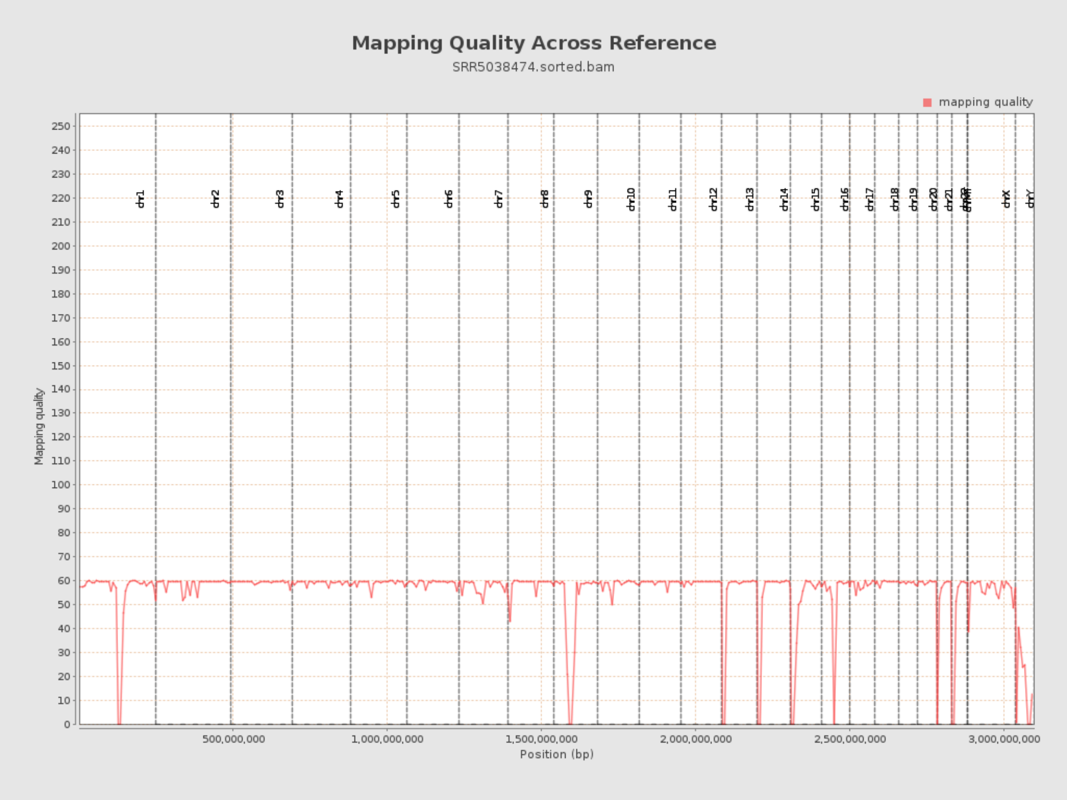
10. Results : Mapped Reads Clipping Profile



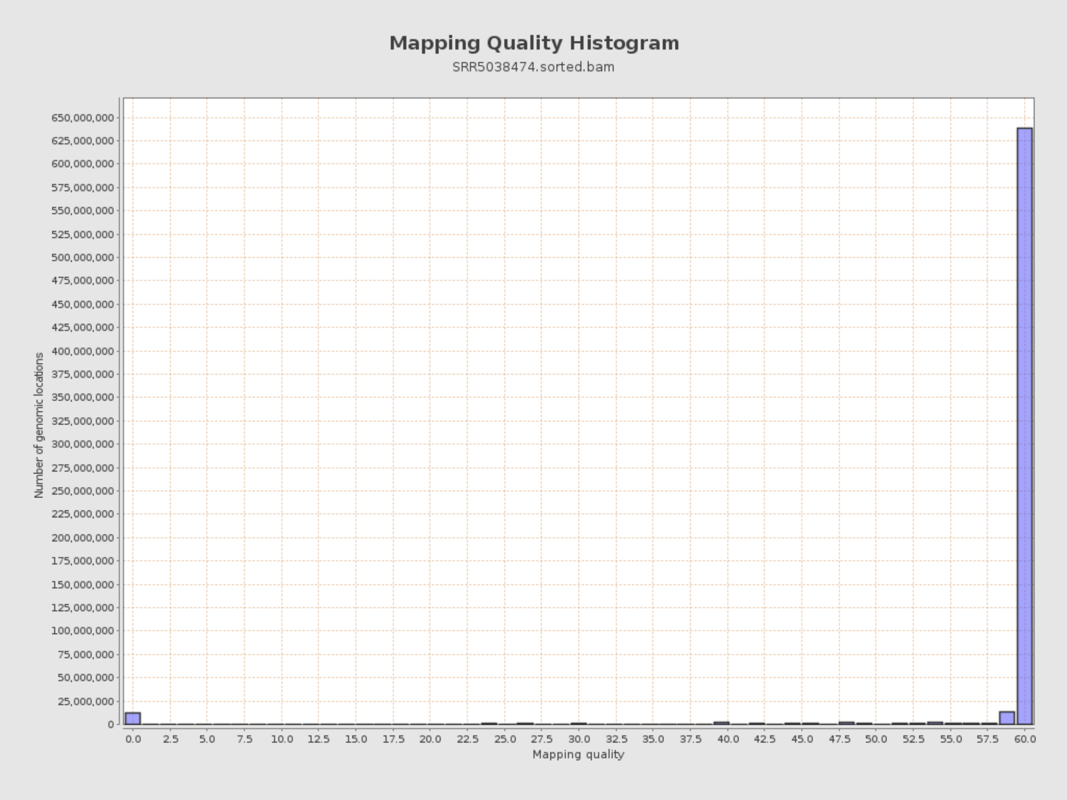
11. Results : Homopolymer Indels



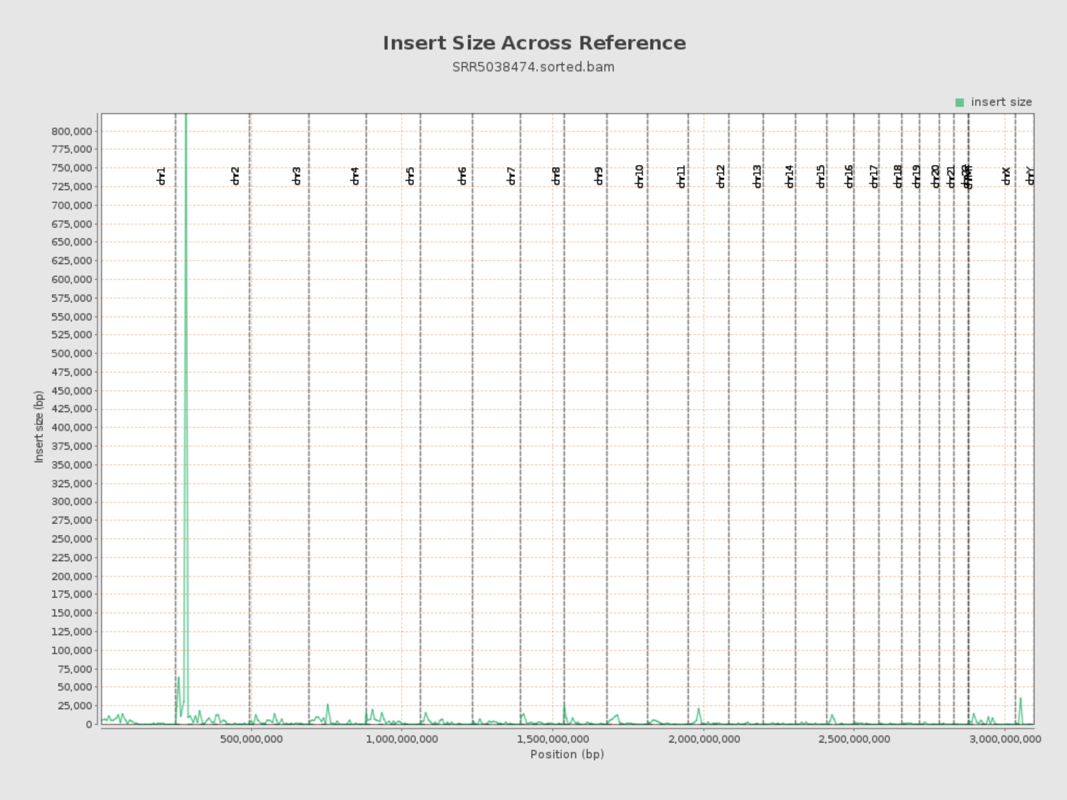
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram