Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 04:57:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038430.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_SRR5038430 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038430_1.fastq.gz SRR5038430_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 04:57:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038430.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,570,774
Mapped reads	15,774,342 / 95.19%
Unmapped reads	796,432 / 4.81%
Mapped paired reads	15,774,342 / 95.19%
Mapped reads, first in pair	7,961,404 / 48.04%
Mapped reads, second in pair	7,812,938 / 47.15%
Mapped reads, both in pair	15,601,332 / 94.15%
Mapped reads, singletons	173,010 / 1.04%
Secondary alignments	0
Supplementary alignments	275,420 / 1.66%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	2,657,860 / 16.04%
Duplication rate	10.97%
Clipped reads	3,570,460 / 21.55%

2.2. ACGT Content

Number/percentage of A's	666,964,976 / 29.45%
Number/percentage of C's	460,915,157 / 20.35%
Number/percentage of T's	664,837,771 / 29.36%
Number/percentage of G's	471,708,969 / 20.83%
Number/percentage of N's	49,692 / 0%

GC Percentage	41.18%

2.3. Coverage

Mean	0.732
Standard Deviation	11.1099

2.4. Mapping Quality

Mean Mapping Quality	53.79

2.5. Insert size

Mean	78,488.06
Standard Deviation	2,678,980.08
P25/Median/P75	192 / 237 / 292

2.6. Mismatches and indels

General error rate	1.43%
Mismatches	31,182,857
Insertions	425,210
Mapped reads with at least one insertion	2.52%
Deletions	816,329
Mapped reads with at least one deletion	4.96%
Homopolymer indels	46.57%

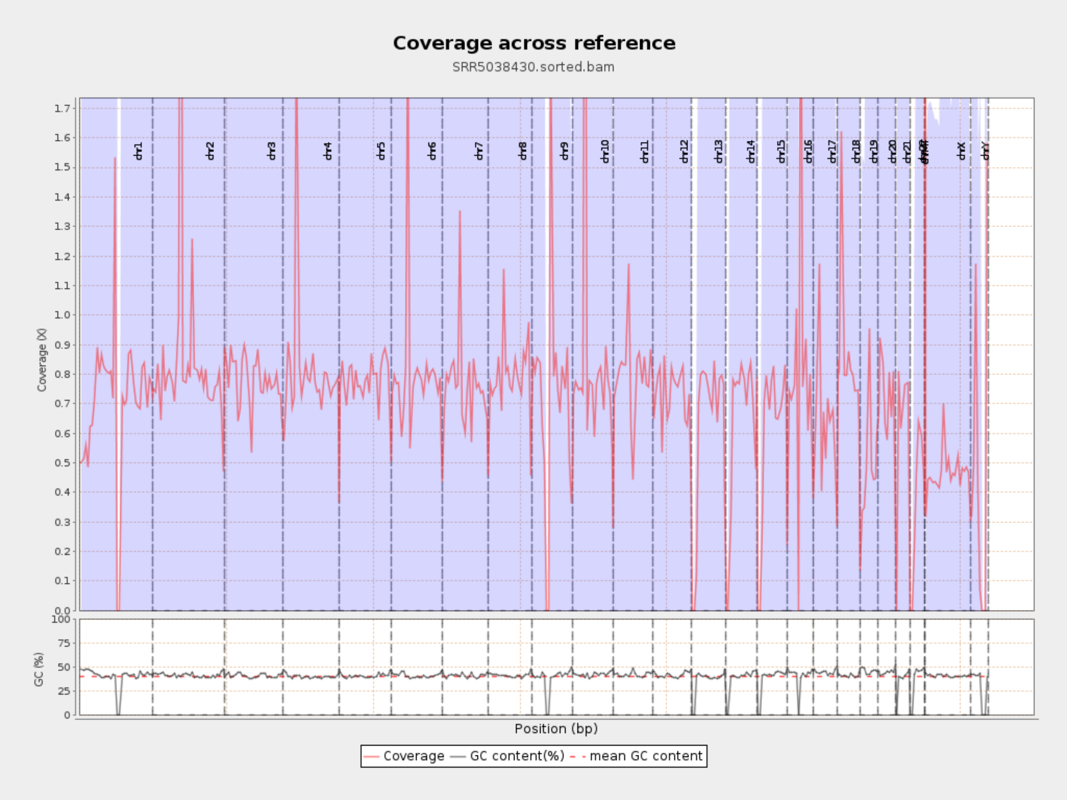
2.7. Chromosome stats

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

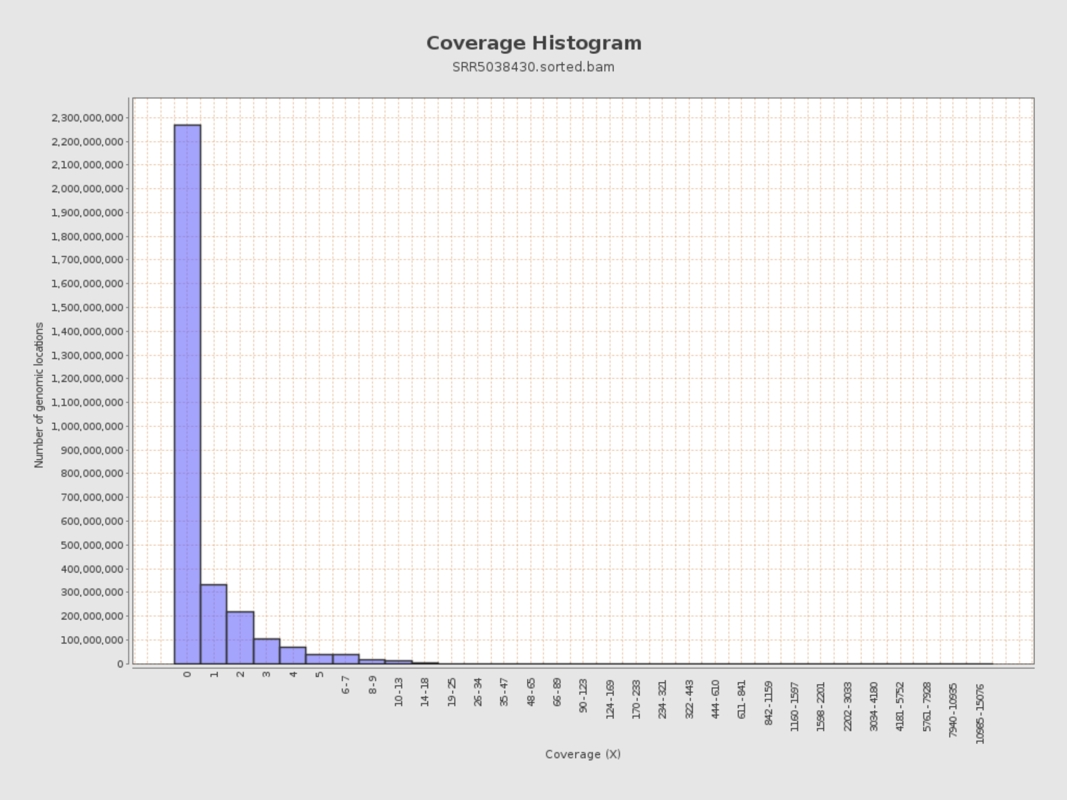
		bases	**coverage**	**deviation**
chr1	249250621	176977656	0.71	13.633
chr2	243199373	213930894	0.8797	16.1721
chr3	198022430	154664076	0.781	1.7465
chr4	191154276	156067196	0.8164	8.1421
chr5	180915260	140309604	0.7756	1.8935
chr6	171115067	139689917	0.8164	13.7705
chr7	159138663	121207323	0.7616	10.9215
chr8	146364022	116735274	0.7976	3.758
chr9	141213431	100443435	0.7113	24.3583
chr10	135534747	119728643	0.8834	18.3794
chr11	135006516	105727254	0.7831	7.1272
chr12	133851895	97490522	0.7283	1.7355
chr13	115169878	72091128	0.626	1.5138
chr14	107349540	66971344	0.6239	1.7834
chr15	102531392	61193357	0.5968	1.5014
chr16	90354753	73555224	0.8141	12.5347
chr17	81195210	51296088	0.6318	8.4882
chr18	78077248	68020699	0.8712	19.3716
chr19	59128983	28612689	0.4839	7.4739
chr20	63025520	45253663	0.718	2.852
chr21	48129895	30254943	0.6286	4.1883
chr22	51304566	19089159	0.3721	1.3795
chrMT	16571	4159288	250.998	143.6162
chrX	155270560	72087073	0.4643	2.3933

chrY	59373566	30562346	0.5147	13.4041

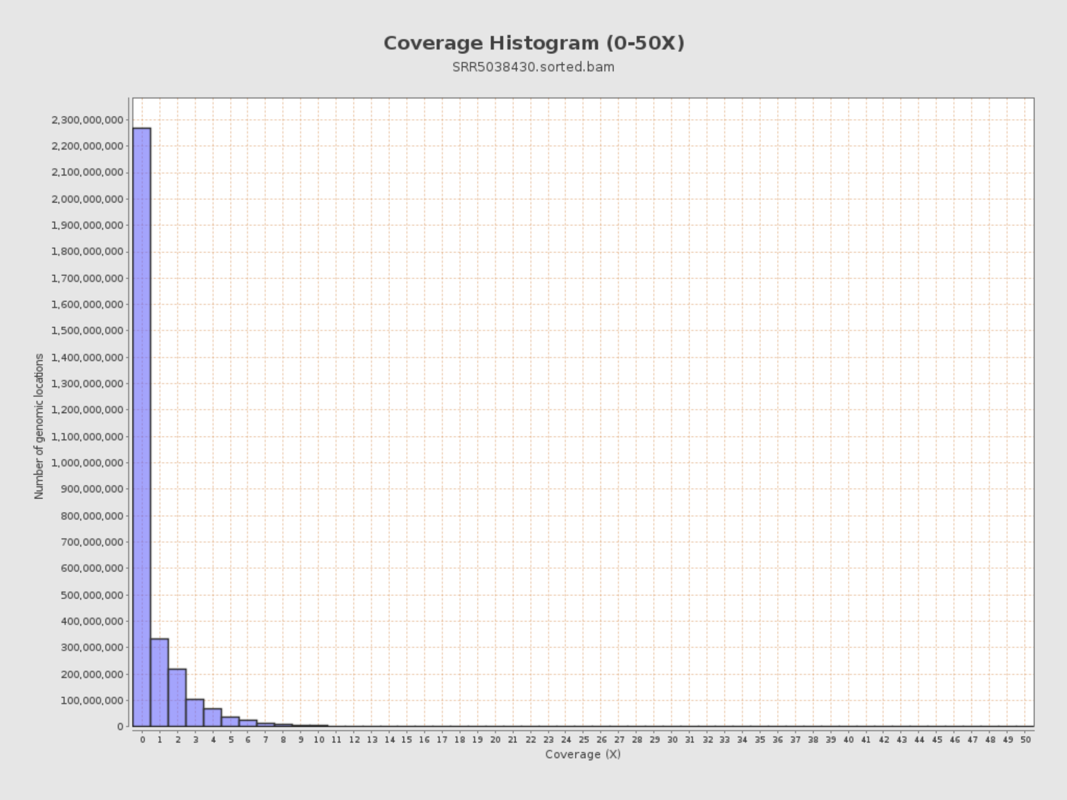
3. Results : Coverage across reference



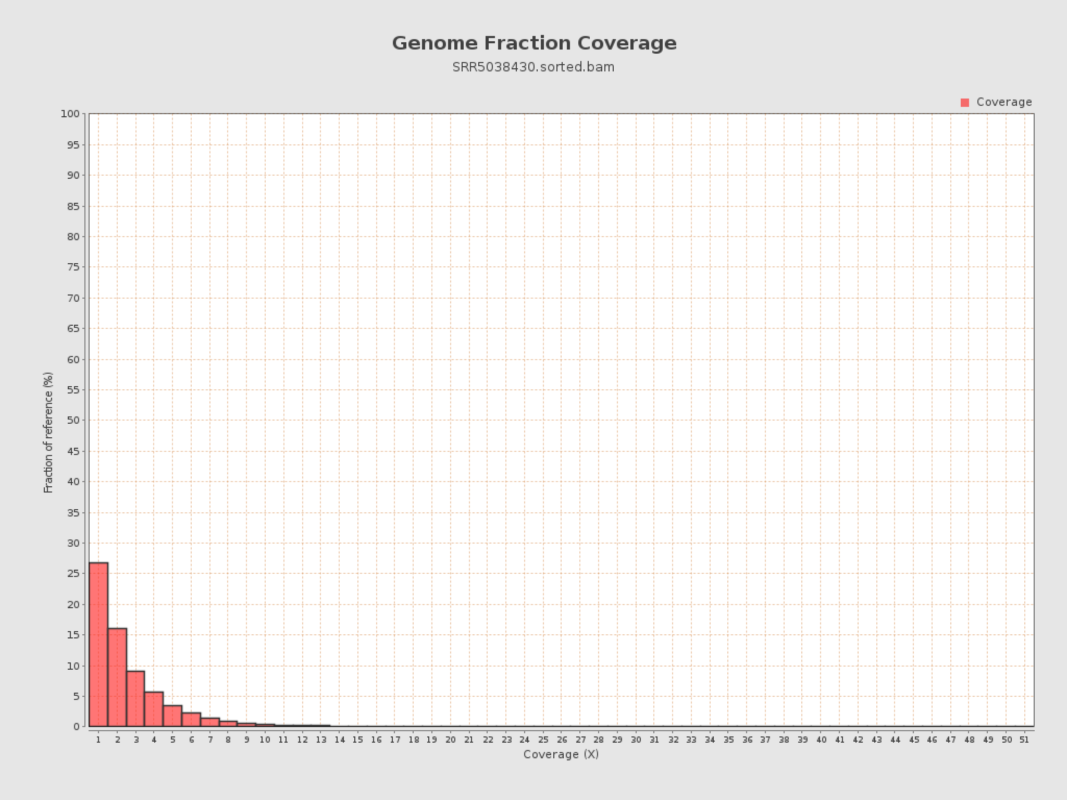
4. Results : Coverage Histogram



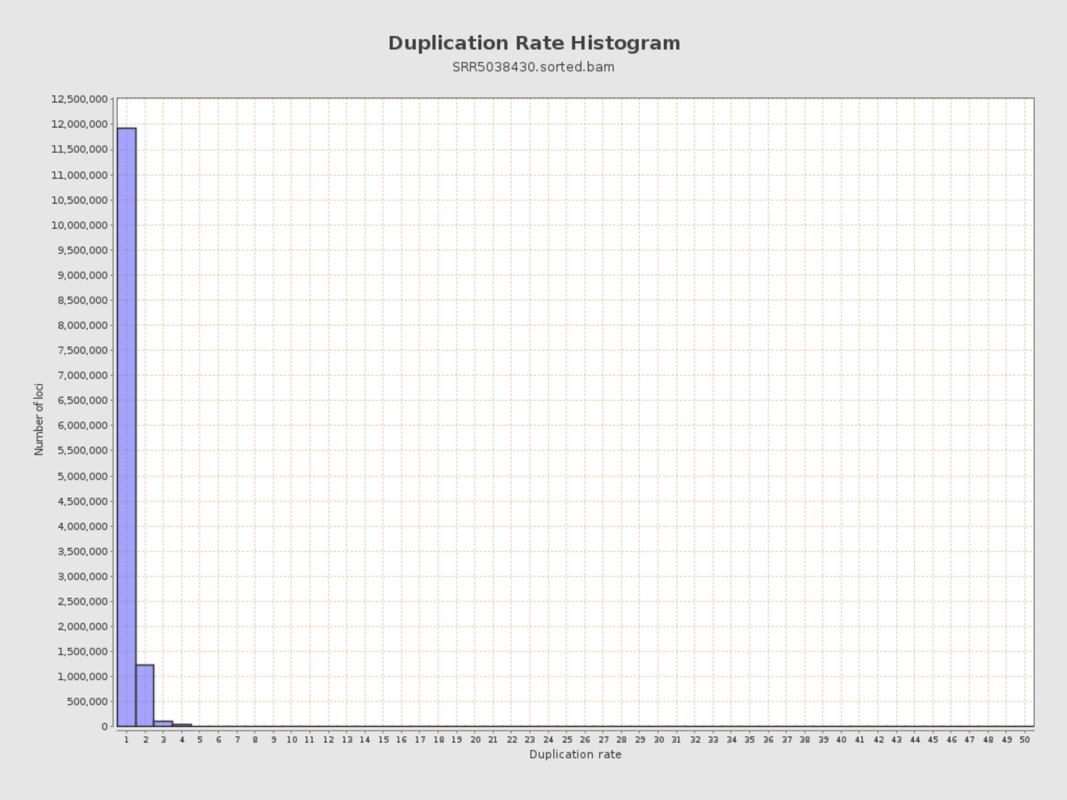
5. Results : Coverage Histogram (0-50X)



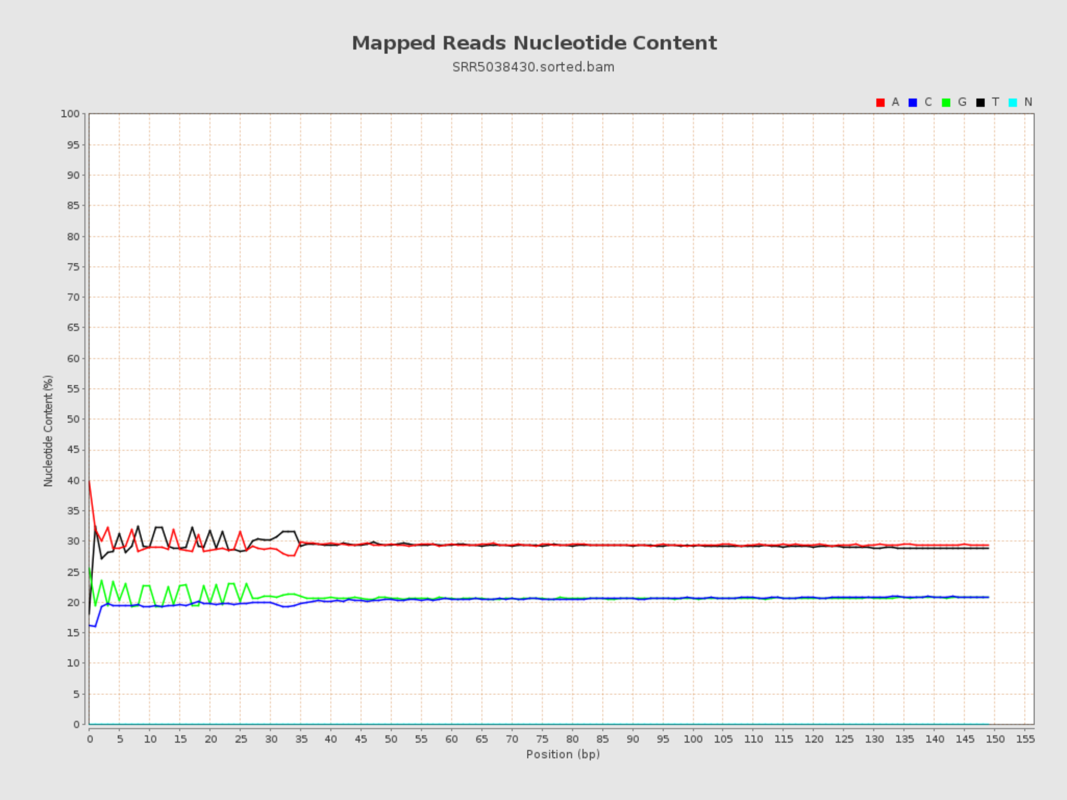
6. Results : Genome Fraction Coverage



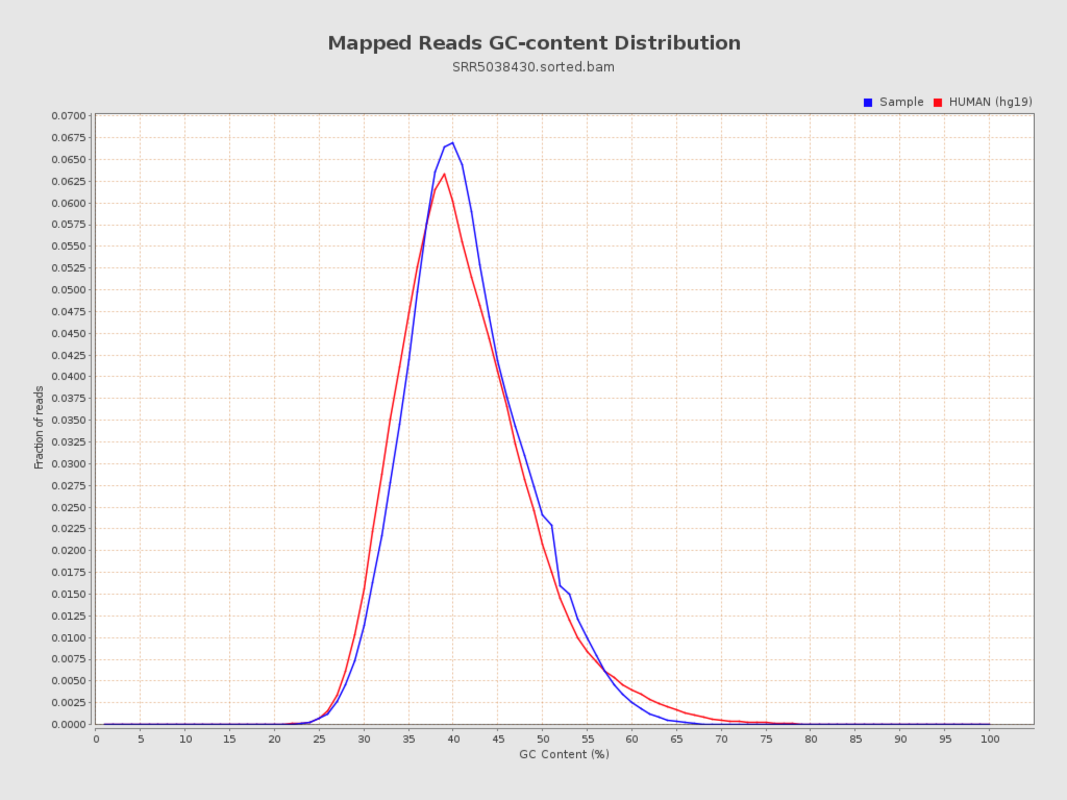
7. Results : Duplication Rate Histogram



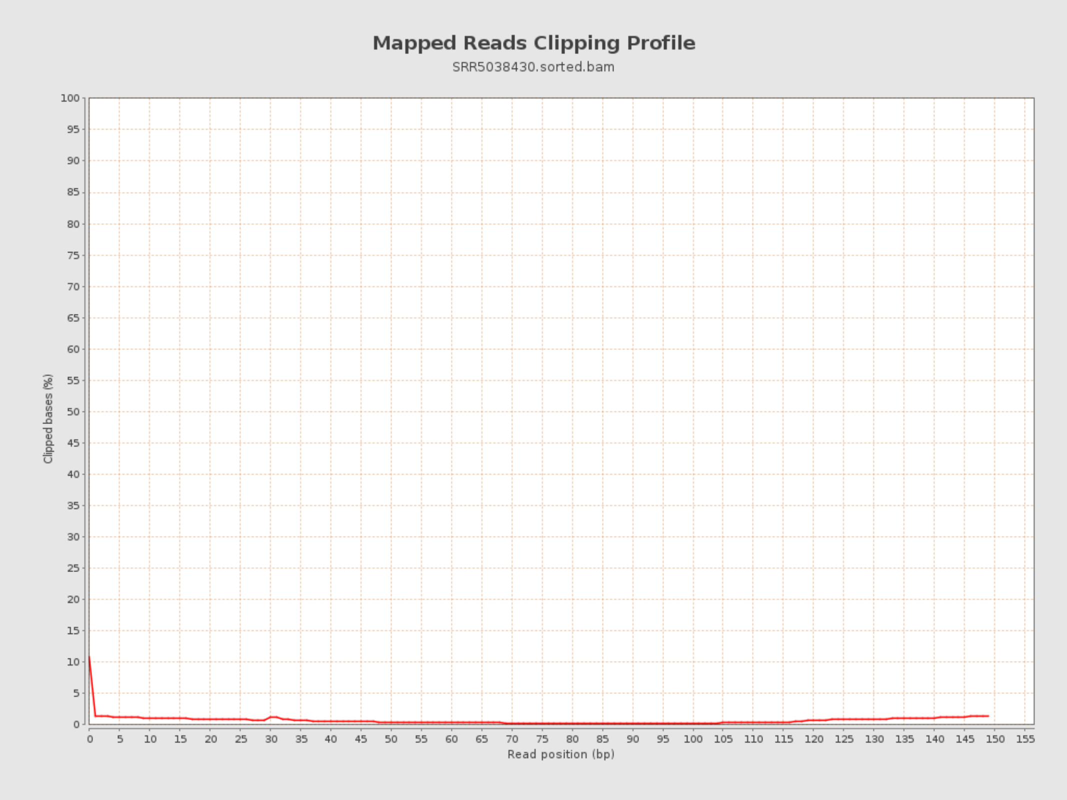
8. Results : Mapped Reads Nucleotide Content



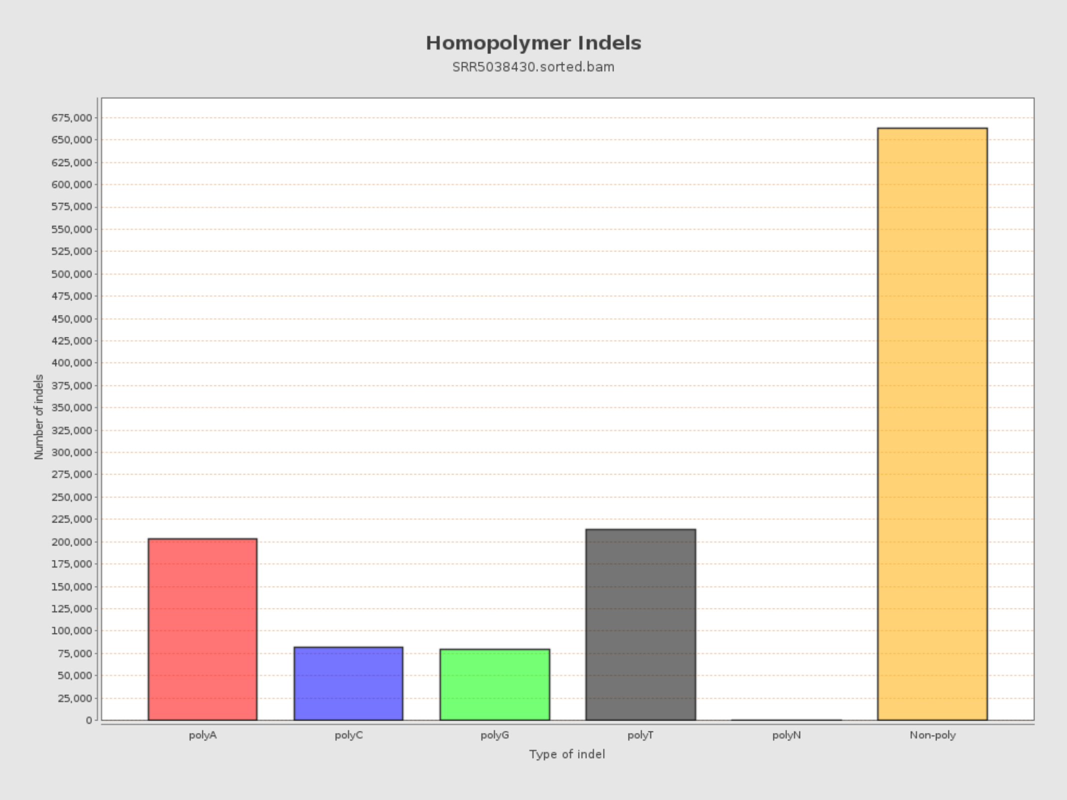
9. Results : Mapped Reads GC-content Distribution



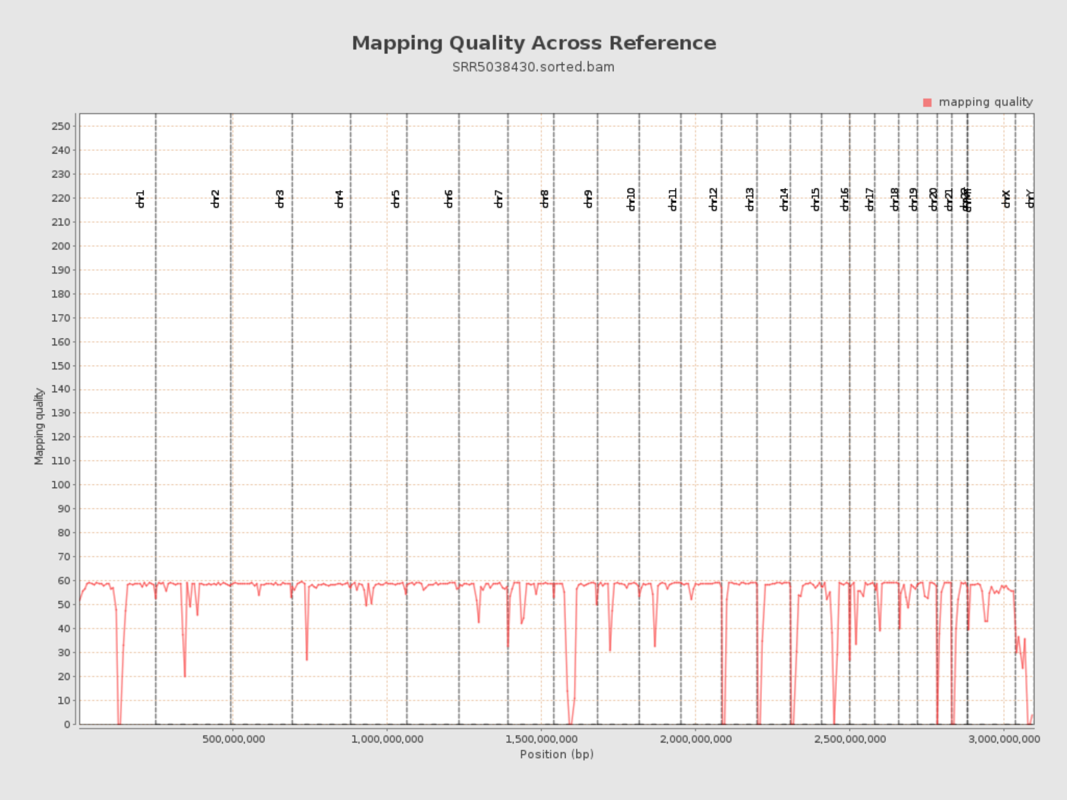
10. Results : Mapped Reads Clipping Profile



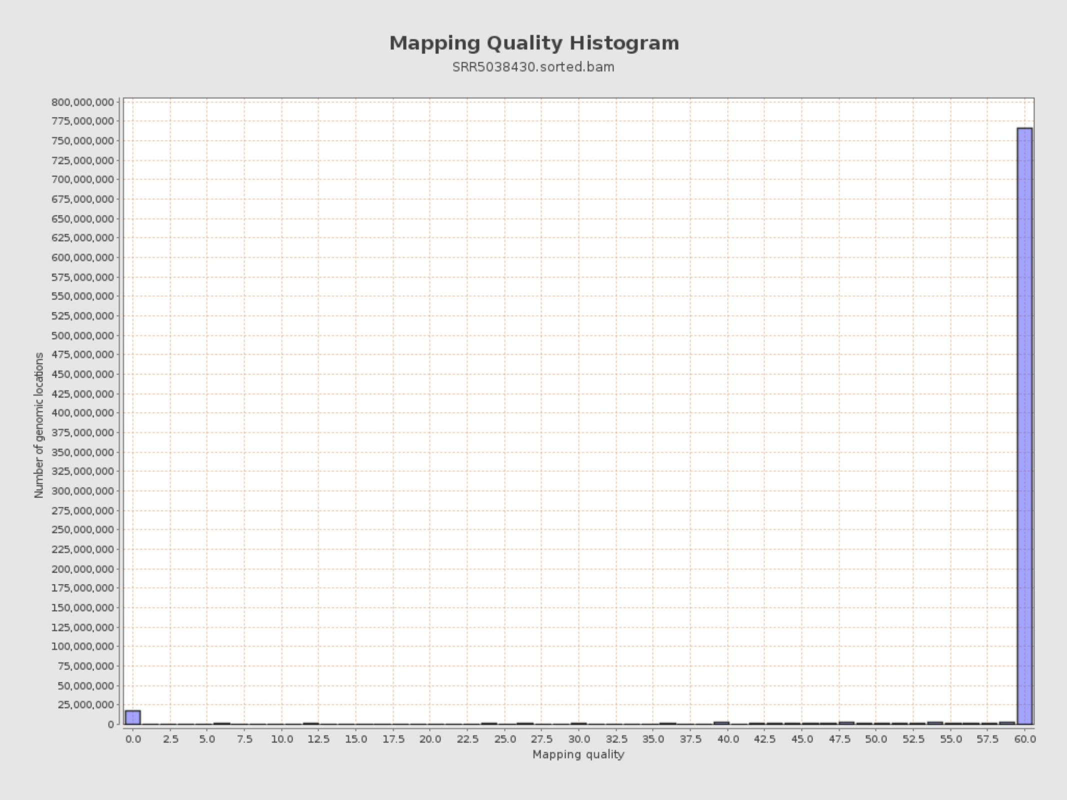
11. Results : Homopolymer Indels



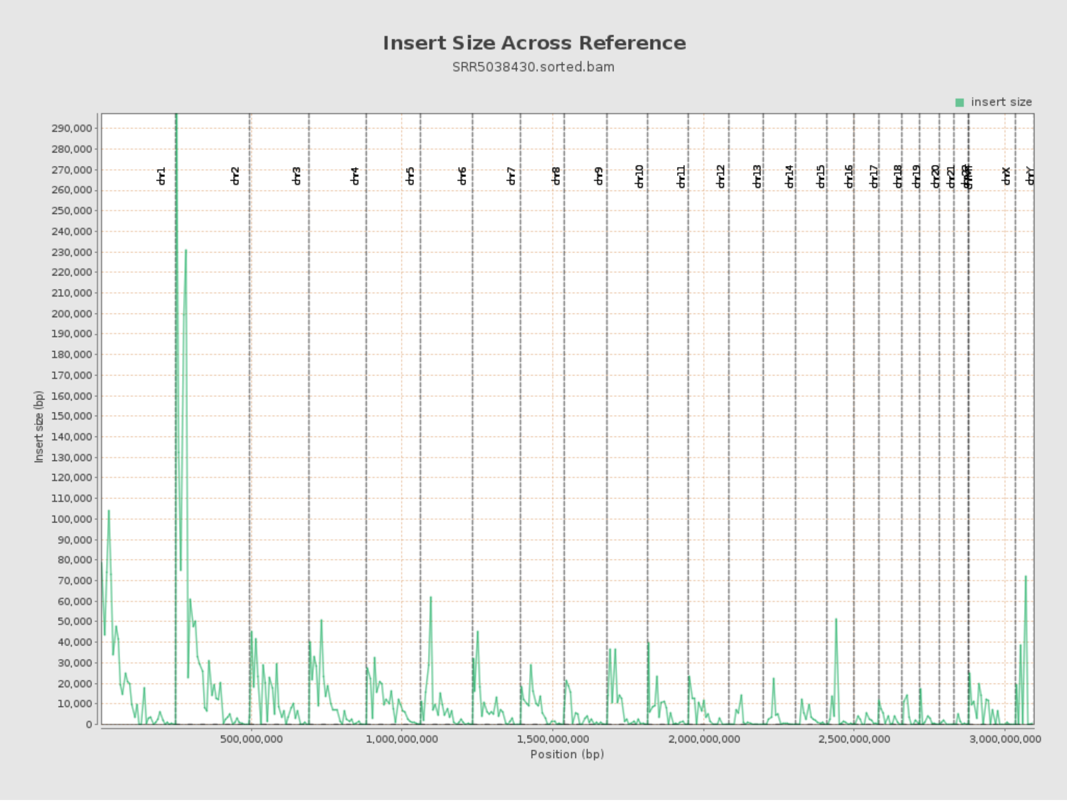
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram