Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 19:40:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038410.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_SRR5038410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038410_1.fastq.gz SRR5038410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 19:40:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,158,768
Mapped reads	10,878,410 / 97.49%
Unmapped reads	280,358 / 2.51%
Mapped paired reads	10,878,410 / 97.49%
Mapped reads, first in pair	5,504,174 / 49.33%
Mapped reads, second in pair	5,374,236 / 48.16%
Mapped reads, both in pair	10,733,662 / 96.19%
Mapped reads, singletons	144,748 / 1.3%
Secondary alignments	0
Supplementary alignments	230,561 / 2.07%
Read min/max/mean length	30 / 150 / 151.07
Duplicated reads (estimated)	1,645,048 / 14.74%
Duplication rate	8.32%
Clipped reads	2,990,595 / 26.8%

2.2. ACGT Content

Number/percentage of A's	456,681,099 / 29.6%
Number/percentage of C's	305,825,464 / 19.82%
Number/percentage of T's	458,743,407 / 29.74%
Number/percentage of G's	321,442,559 / 20.84%
Number/percentage of N's	32,046 / 0%

GC Percentage	40.66%

2.3. Coverage

Mean	0.4987
Standard Deviation	8.7713

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	99,543.24
Standard Deviation	2,920,132.74
P25/Median/P75	224 / 265 / 317

2.6. Mismatches and indels

General error rate	1.5%
Mismatches	22,253,020
Insertions	292,679
Mapped reads with at least one insertion	2.51%
Deletions	543,177
Mapped reads with at least one deletion	4.78%
Homopolymer indels	45.99%

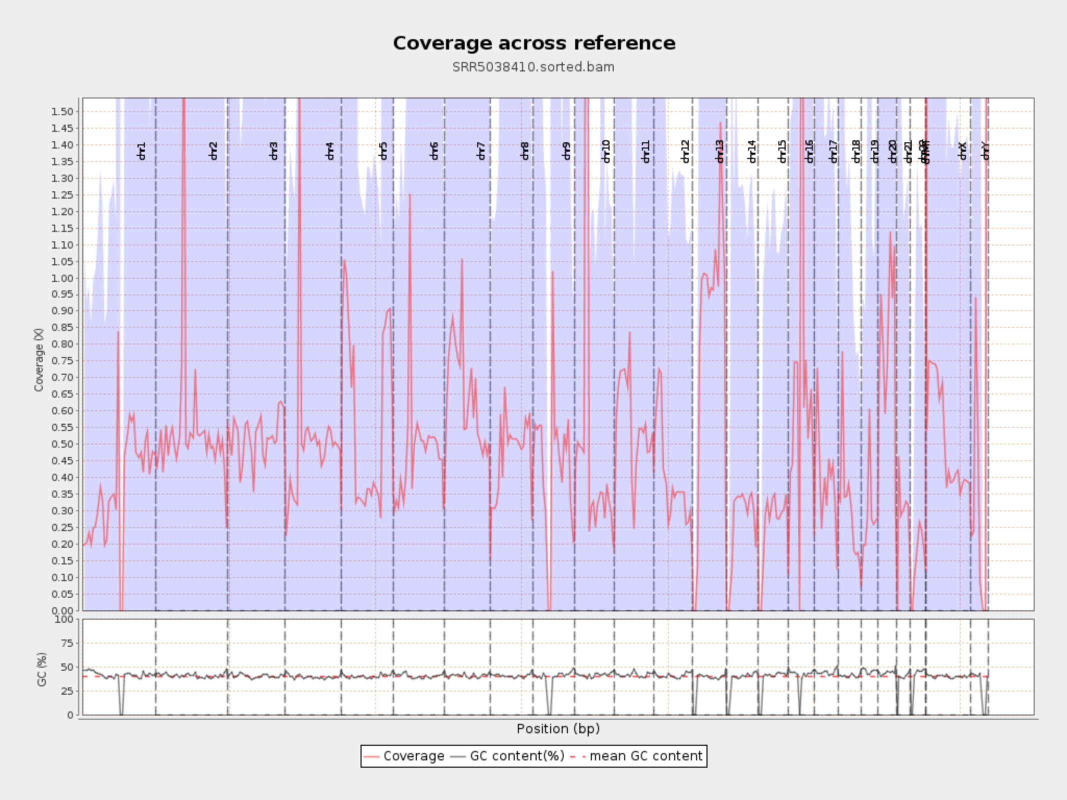
2.7. Chromosome stats

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

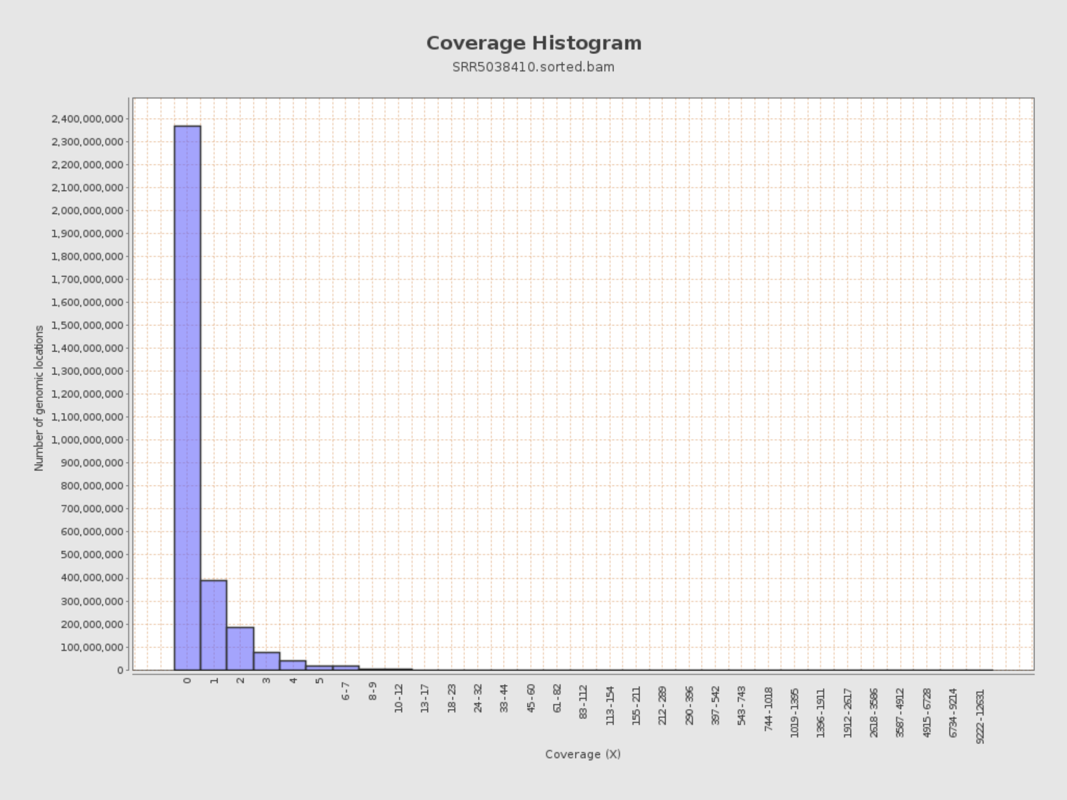
		bases	coverage	deviation
chr1	249250621	92575964	0.3714	8.5971
chr2	243199373	135989141	0.5592	8.9463
chr3	198022430	102999311	0.5201	1.2544
chr4	191154276	97429211	0.5097	8.4566
chr5	180915260	104991483	0.5803	1.3436
chr6	171115067	84055296	0.4912	7.9242
chr7	159138663	103163312	0.6483	8.1139
chr8	146364022	69682721	0.4761	2.0206
chr9	141213431	62281938	0.441	11.3814
chr10	135534747	72635553	0.5359	25.4153
chr11	135006516	75759826	0.5612	5.0544
chr12	133851895	53718294	0.4013	1.0401
chr13	115169878	98065019	0.8515	1.6316
chr14	107349540	28406398	0.2646	0.916
chr15	102531392	25739108	0.251	0.7577
chr16	90354753	67726431	0.7496	16.9604
chr17	81195210	33144745	0.4082	3.4572
chr18	78077248	25005584	0.3203	9.4887
chr19	59128983	16881464	0.2855	4.6482
chr20	63025520	53049090	0.8417	2.9694
chr21	48129895	13906855	0.2889	3.736
chr22	51304566	7937082	0.1547	0.7652
chrMT	16571	1122723	67.7523	34.9799
chrX	155270560	79868475	0.5144	1.6553

chrY	59373566	37785519	0.6364	16.9962

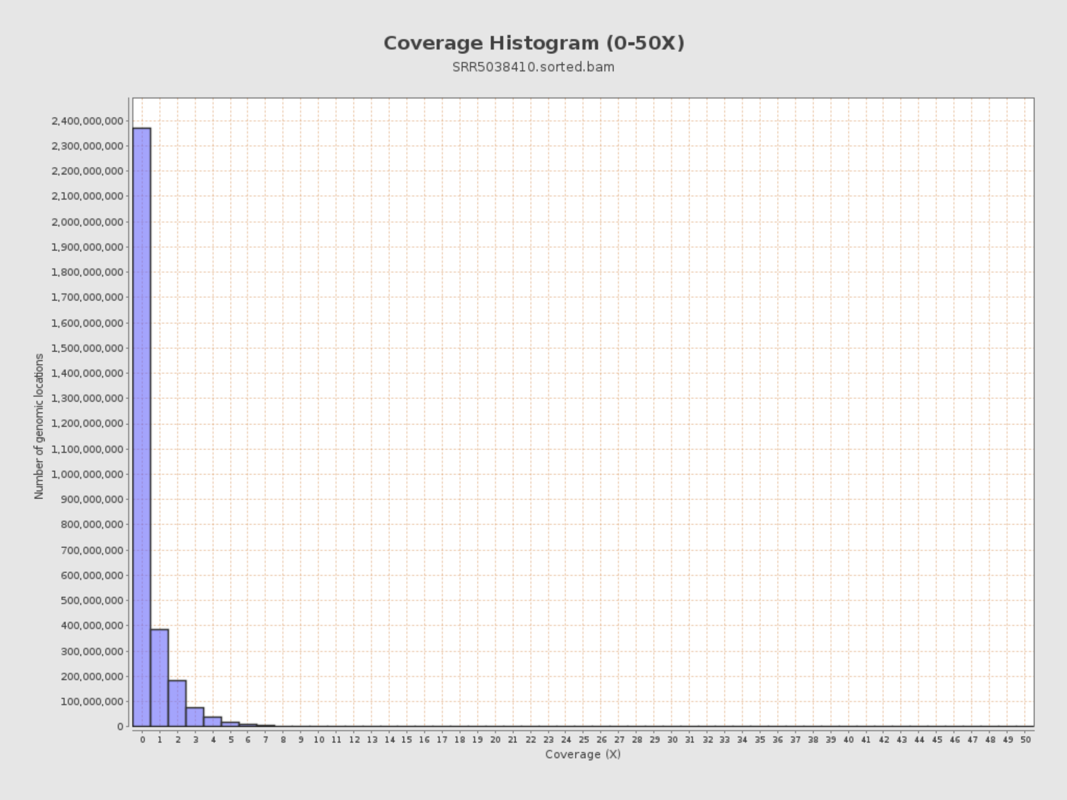
3. Results : Coverage across reference



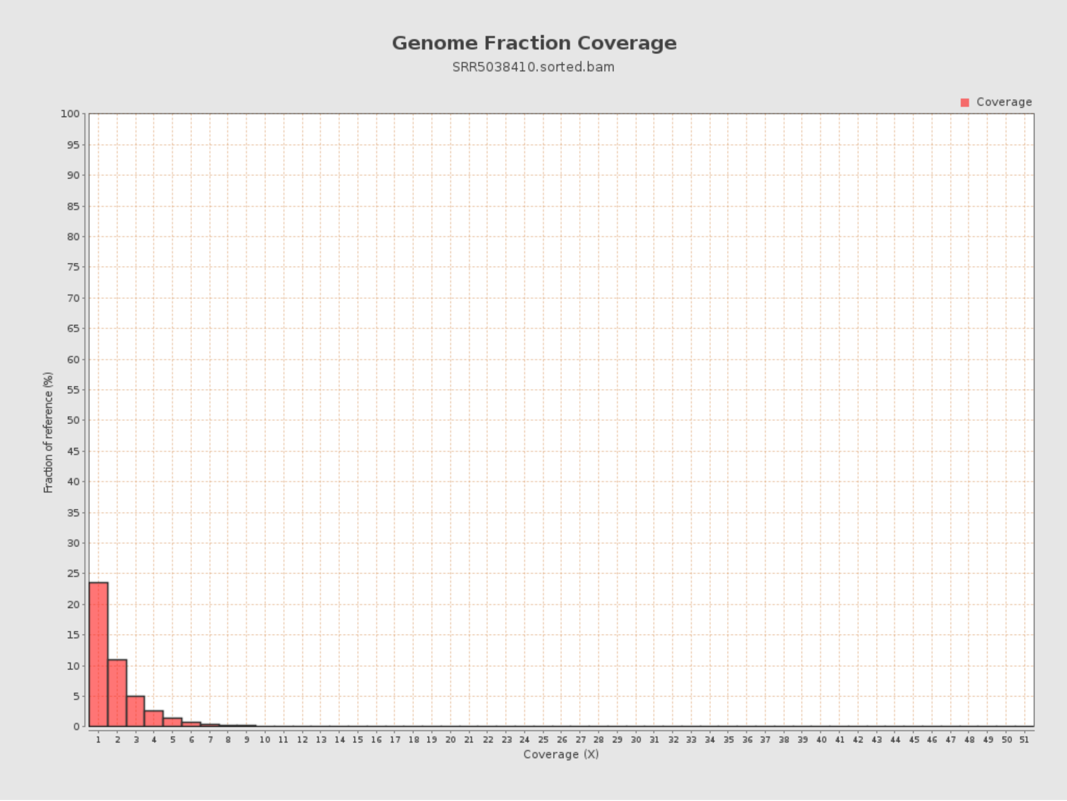
4. Results : Coverage Histogram



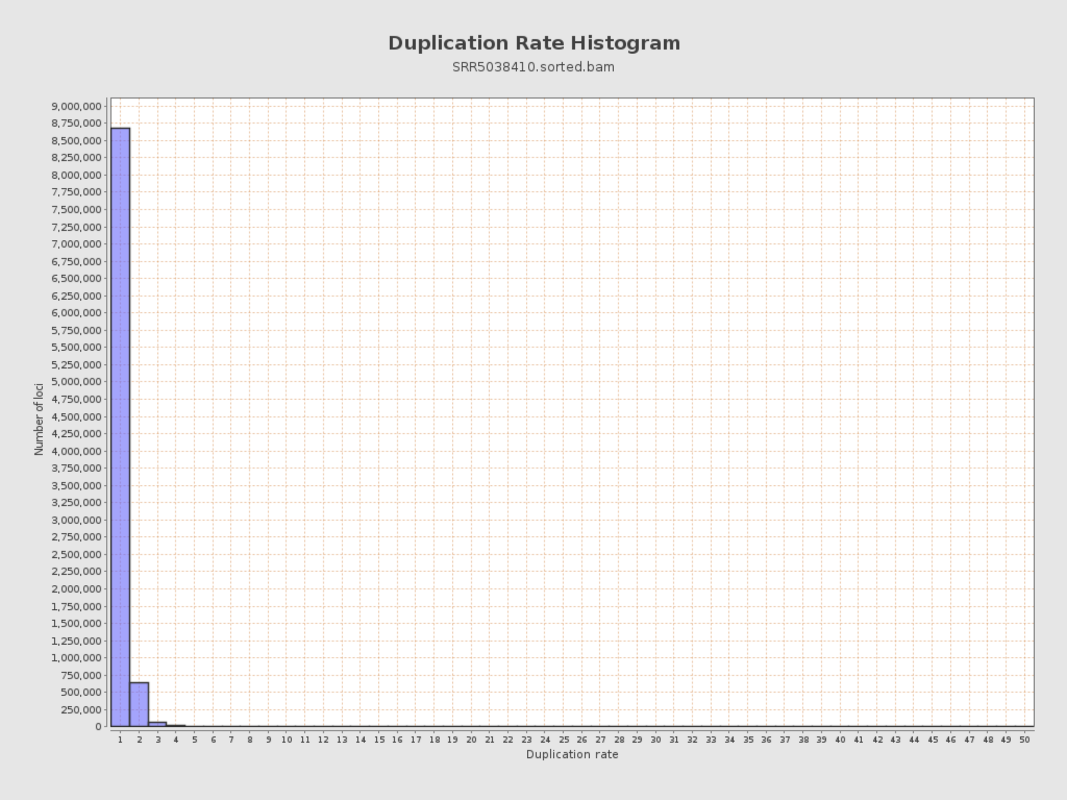
5. Results : Coverage Histogram (0-50X)



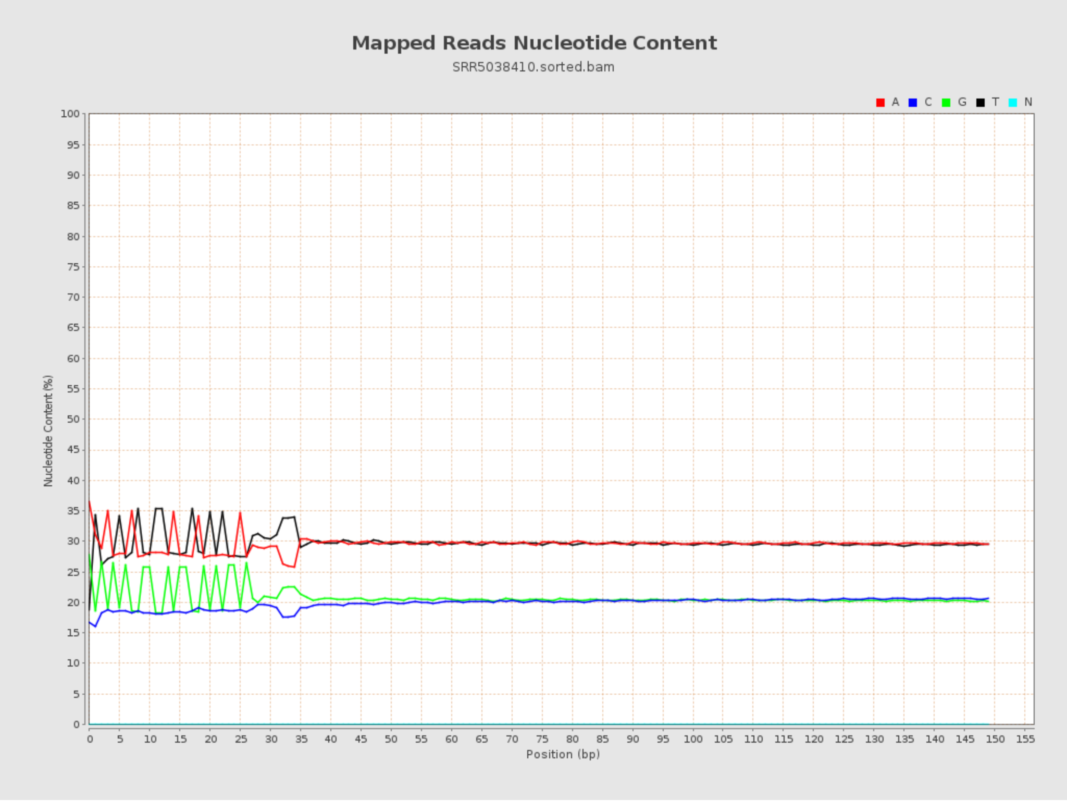
6. Results : Genome Fraction Coverage



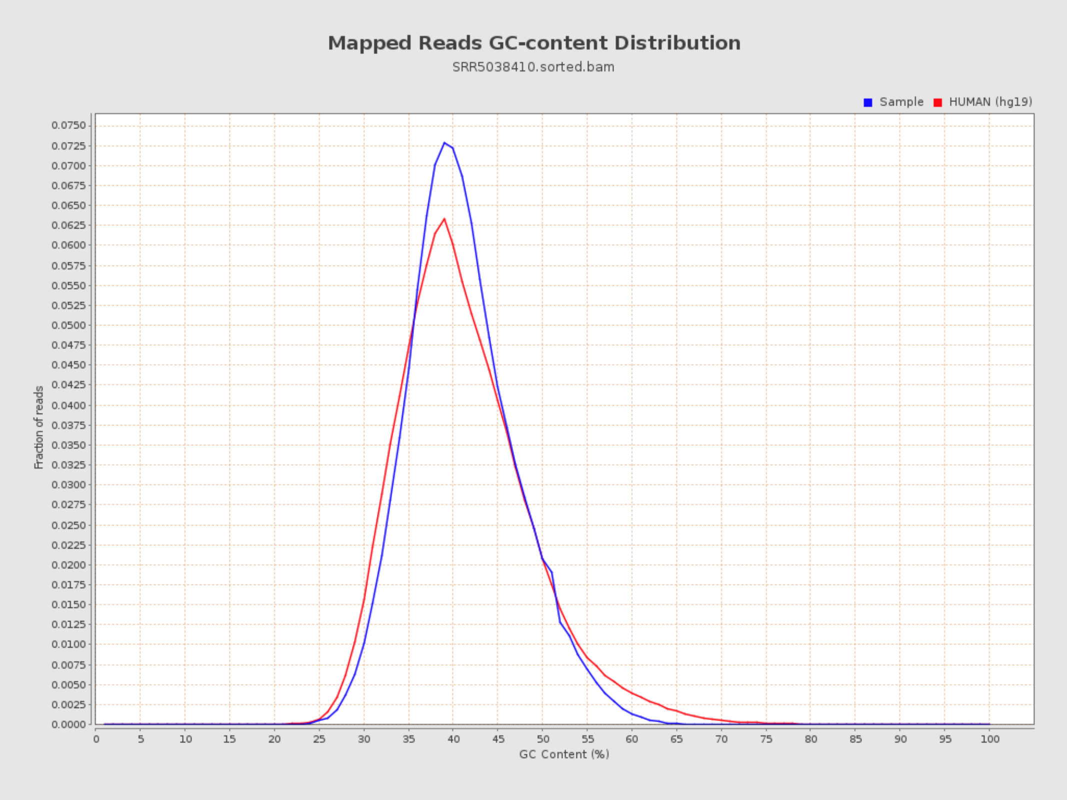
7. Results : Duplication Rate Histogram



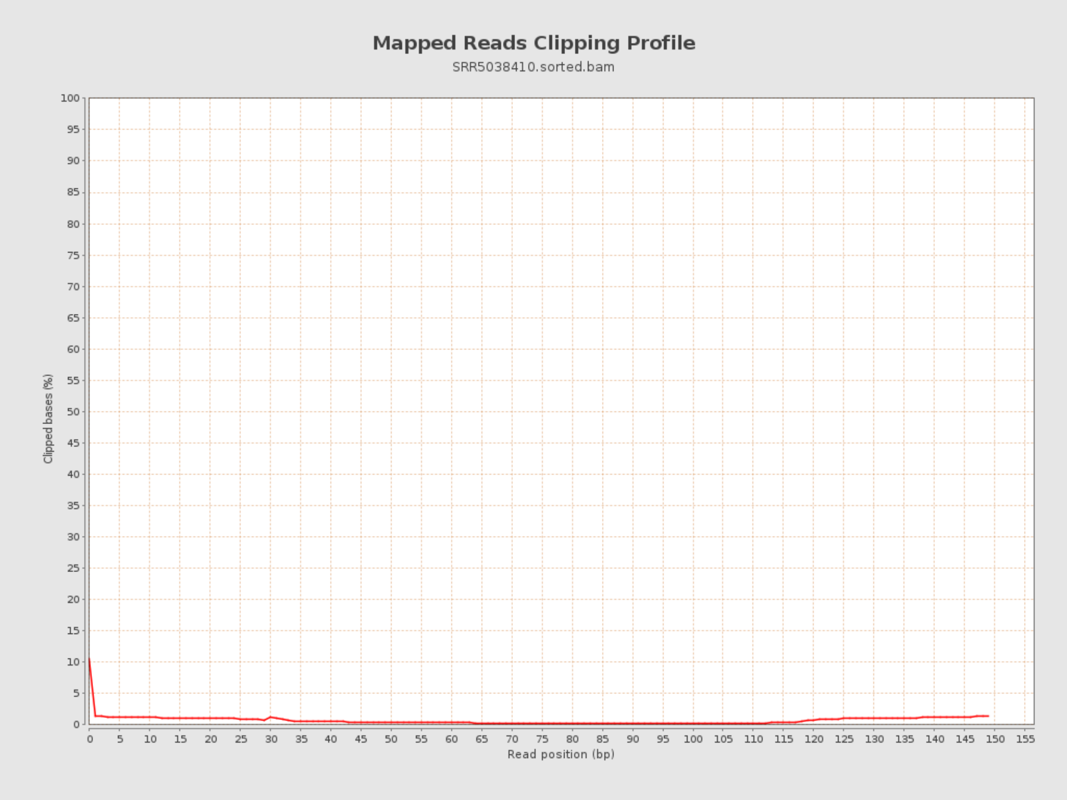
8. Results : Mapped Reads Nucleotide Content



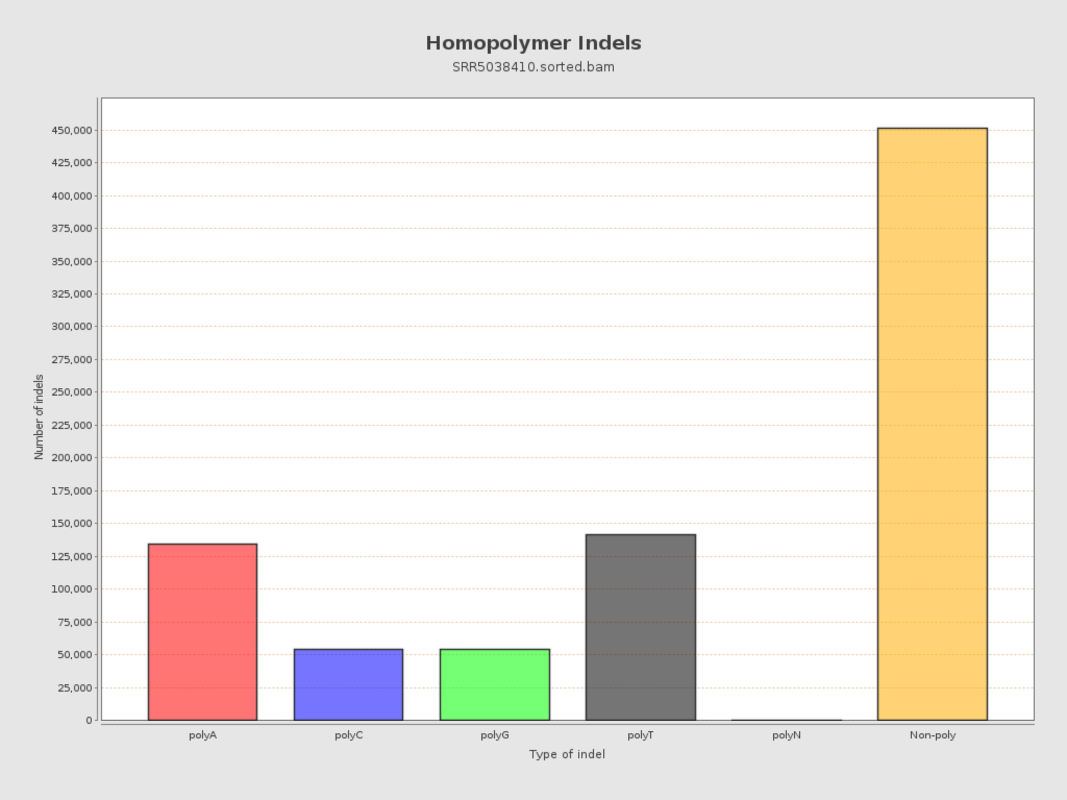
9. Results : Mapped Reads GC-content Distribution



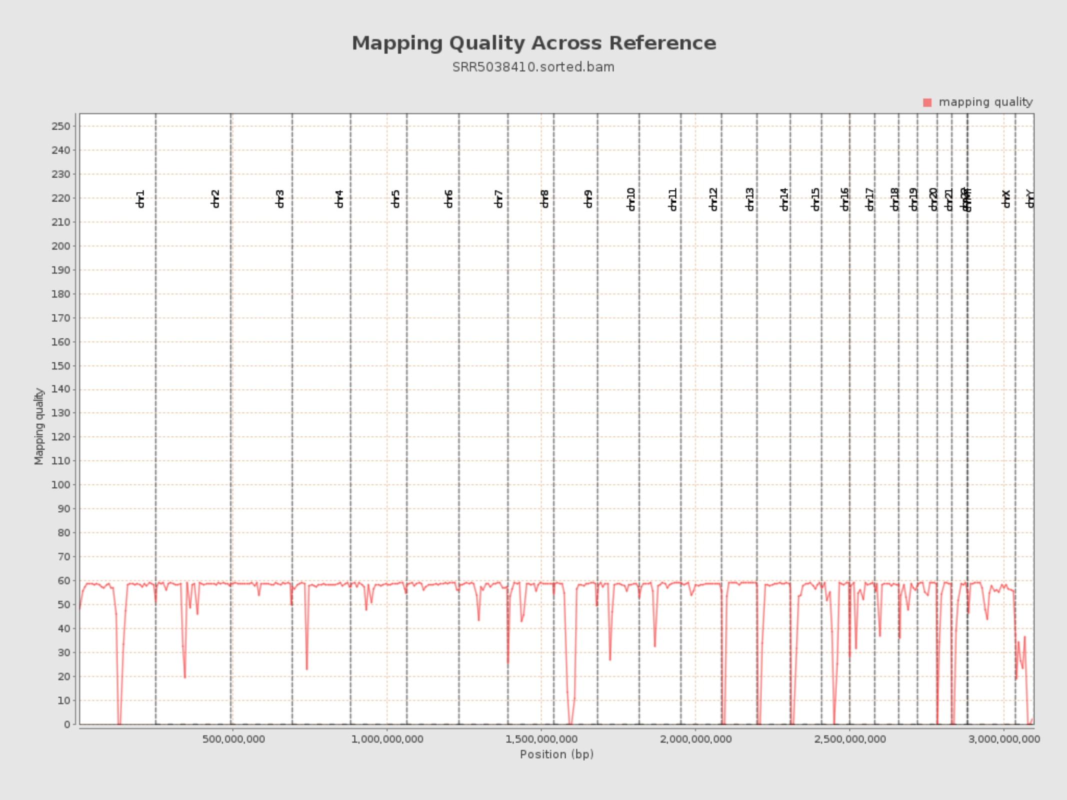
10. Results : Mapped Reads Clipping Profile



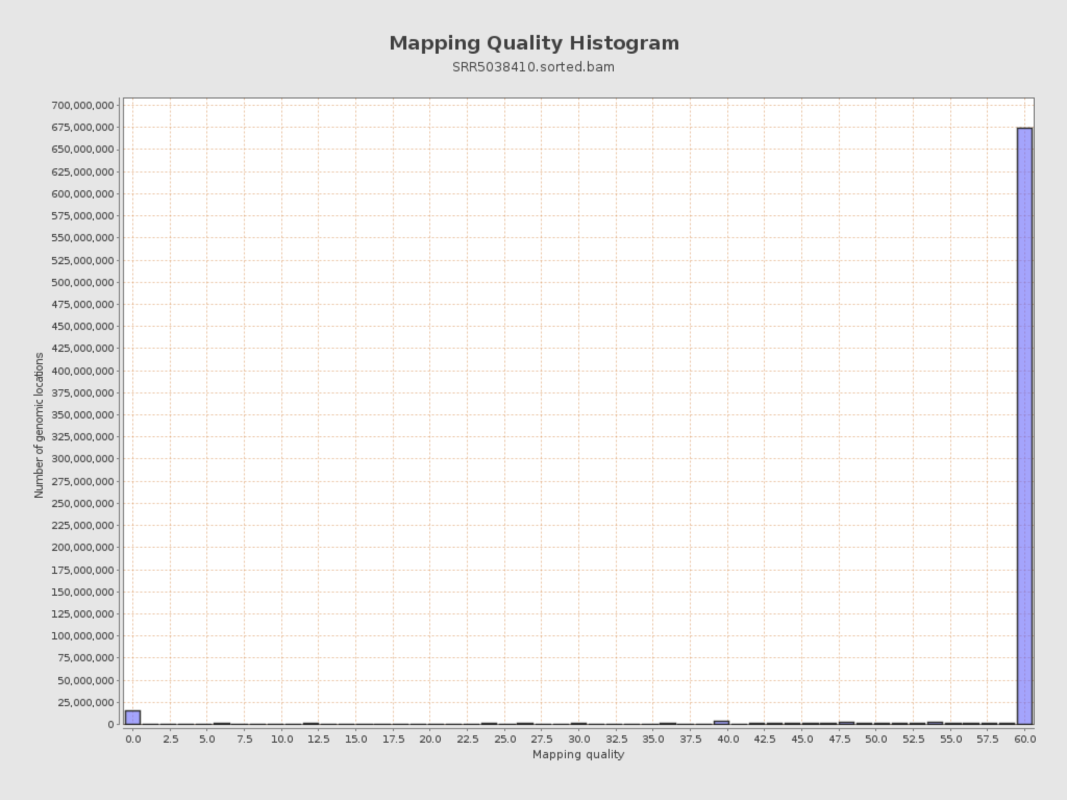
11. Results : Homopolymer Indels



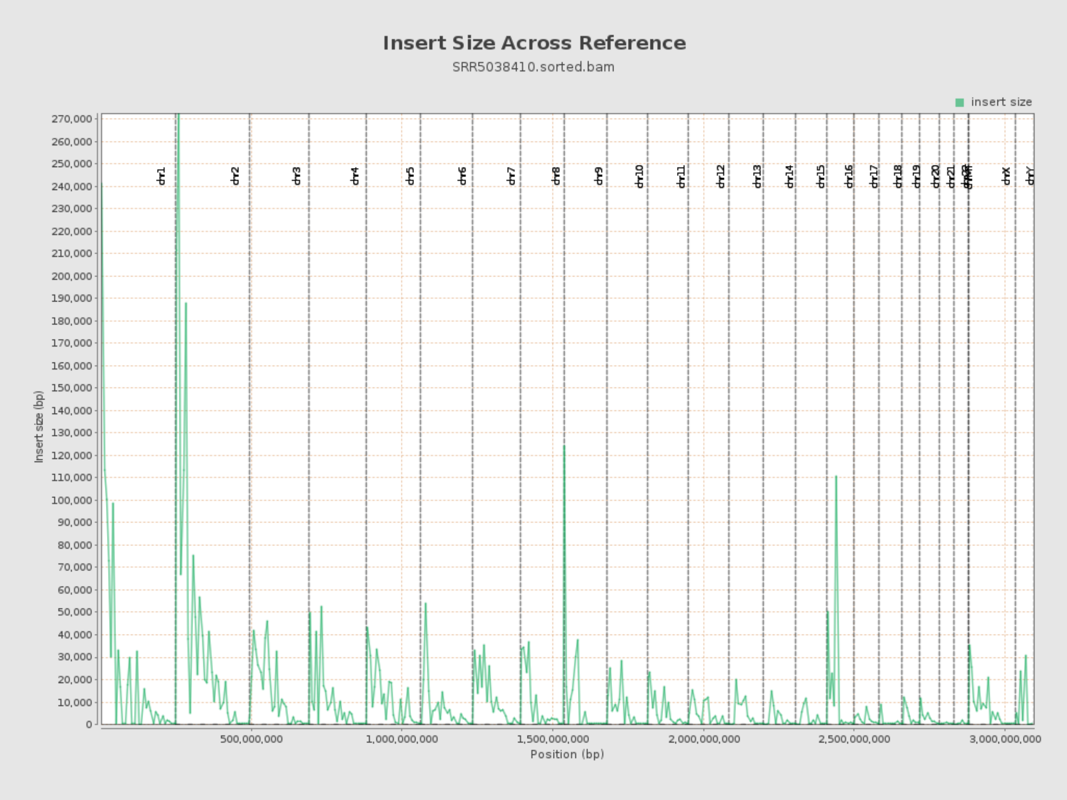
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram