Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 14:43:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038400.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_SRR5038400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038400_1.fastq.gz SRR5038400_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 14:43:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,201,984
Mapped reads	15,508,628 / 95.72%
Unmapped reads	693,356 / 4.28%
Mapped paired reads	15,508,628 / 95.72%
Mapped reads, first in pair	7,824,852 / 48.3%
Mapped reads, second in pair	7,683,776 / 47.42%
Mapped reads, both in pair	15,345,466 / 94.71%
Mapped reads, singletons	163,162 / 1.01%
Secondary alignments	0
Supplementary alignments	249,817 / 1.54%
Read min/max/mean length	30 / 150 / 150.8
Duplicated reads (estimated)	2,397,184 / 14.8%
Duplication rate	10.21%
Clipped reads	3,122,719 / 19.27%

2.2. ACGT Content

Number/percentage of A's	657,462,764 / 29.39%
Number/percentage of C's	456,246,594 / 20.39%
Number/percentage of T's	656,167,316 / 29.33%
Number/percentage of G's	467,462,012 / 20.89%
Number/percentage of N's	48,816 / 0%

GC Percentage	41.29%

2.3. Coverage

Mean	0.7232
Standard Deviation	10.2367

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	80,778.14
Standard Deviation	2,706,179.68
P25/Median/P75	206 / 250 / 304

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	30,407,361
Insertions	397,594
Mapped reads with at least one insertion	2.42%
Deletions	814,029
Mapped reads with at least one deletion	5.04%
Homopolymer indels	47.68%

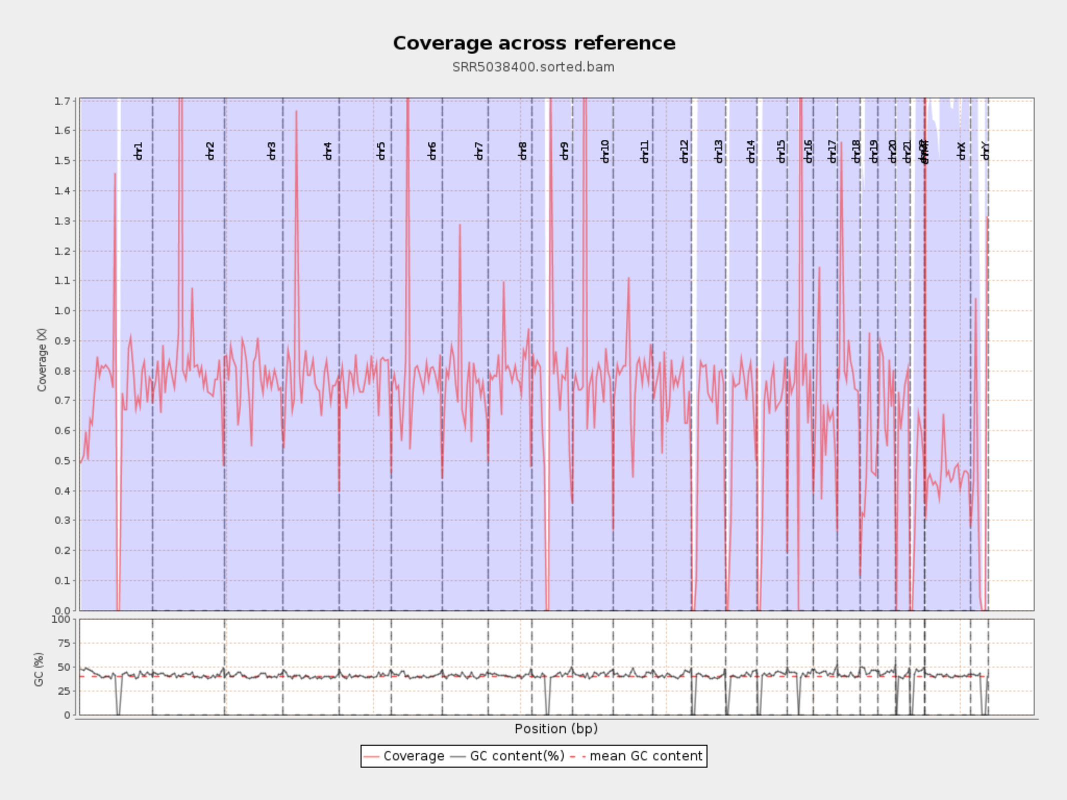
2.7. Chromosome stats

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

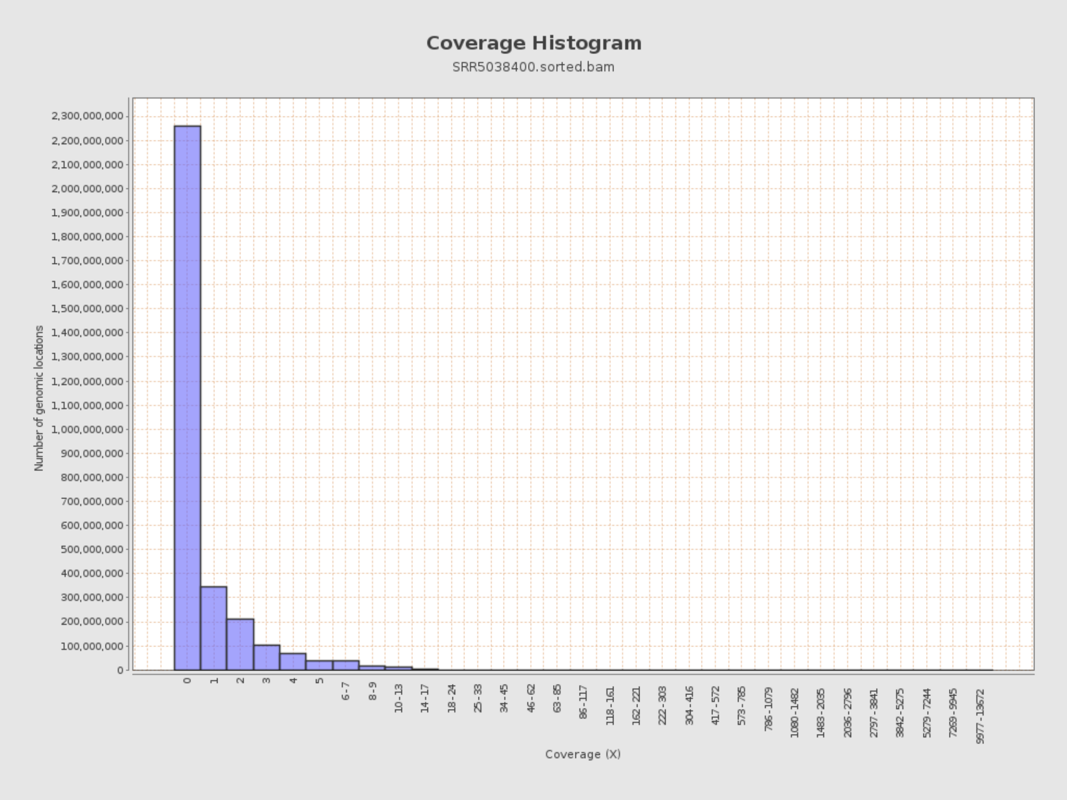
		bases	coverage	deviation
chr1	249250621	175388772	0.7037	12.2121
chr2	243199373	210714011	0.8664	14.1128
chr3	198022430	154764990	0.7816	1.7187
chr4	191154276	152048214	0.7954	6.7178
chr5	180915260	139103180	0.7689	1.843
chr6	171115067	139391243	0.8146	14.3402
chr7	159138663	120179811	0.7552	10.2632
chr8	146364022	116648708	0.797	3.3943
chr9	141213431	98586844	0.6981	22.1839
chr10	135534747	118648775	0.8754	17.1044
chr11	135006516	104631439	0.775	6.992
chr12	133851895	97446775	0.728	1.7005
chr13	115169878	72123348	0.6262	1.5059
chr14	107349540	66427937	0.6188	1.686
chr15	102531392	60955223	0.5945	1.4808
chr16	90354753	73186542	0.81	12.56
chr17	81195210	50773520	0.6253	8.2298
chr18	78077248	67137444	0.8599	18.4022
chr19	59128983	27698813	0.4684	6.659
chr20	63025520	45032206	0.7145	2.4813
chr21	48129895	29458787	0.6121	3.4634
chr22	51304566	19489660	0.3799	1.2718
chrMT	16571	2893005	174.5824	110.342
chrX	155270560	69290864	0.4463	2.2737

chrY	59373566	26915243	0.4533	10.8454

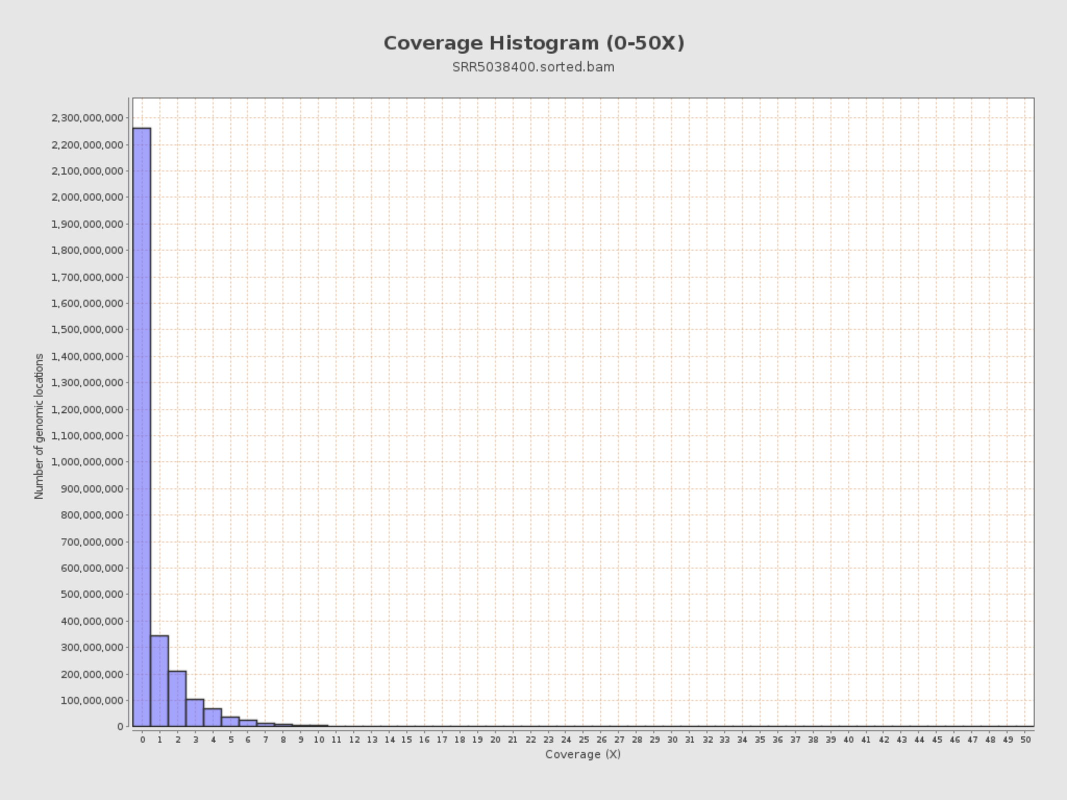
3. Results : Coverage across reference



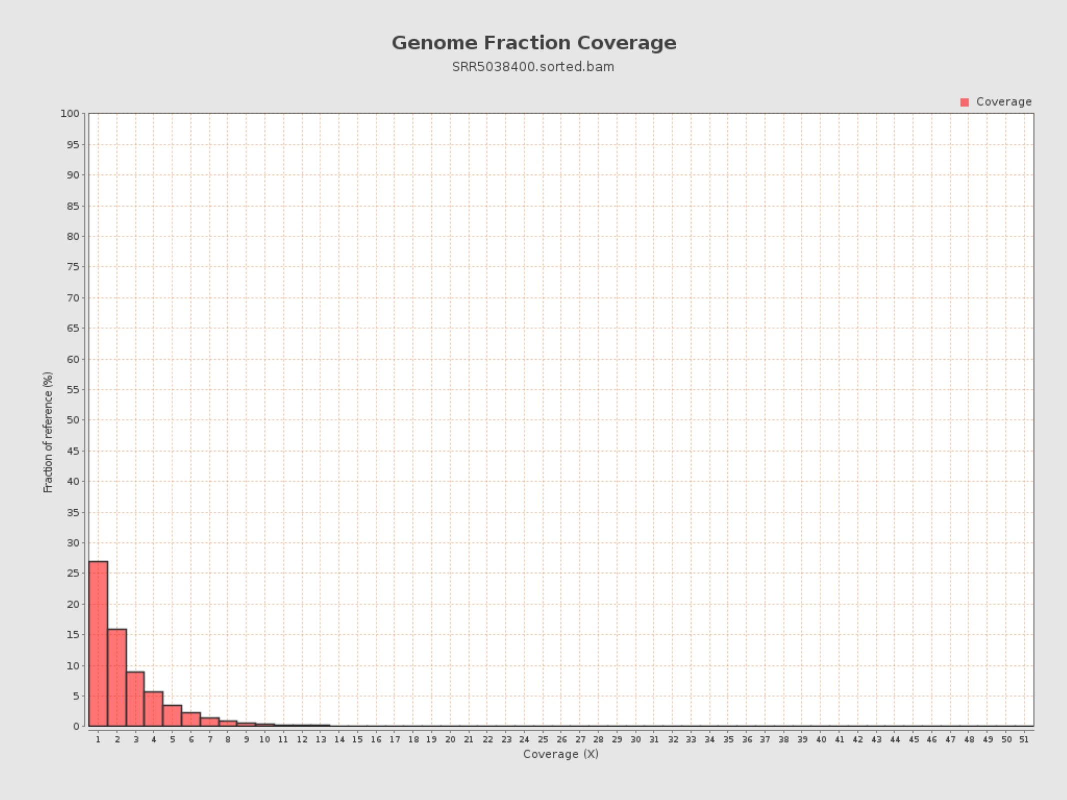
4. Results : Coverage Histogram



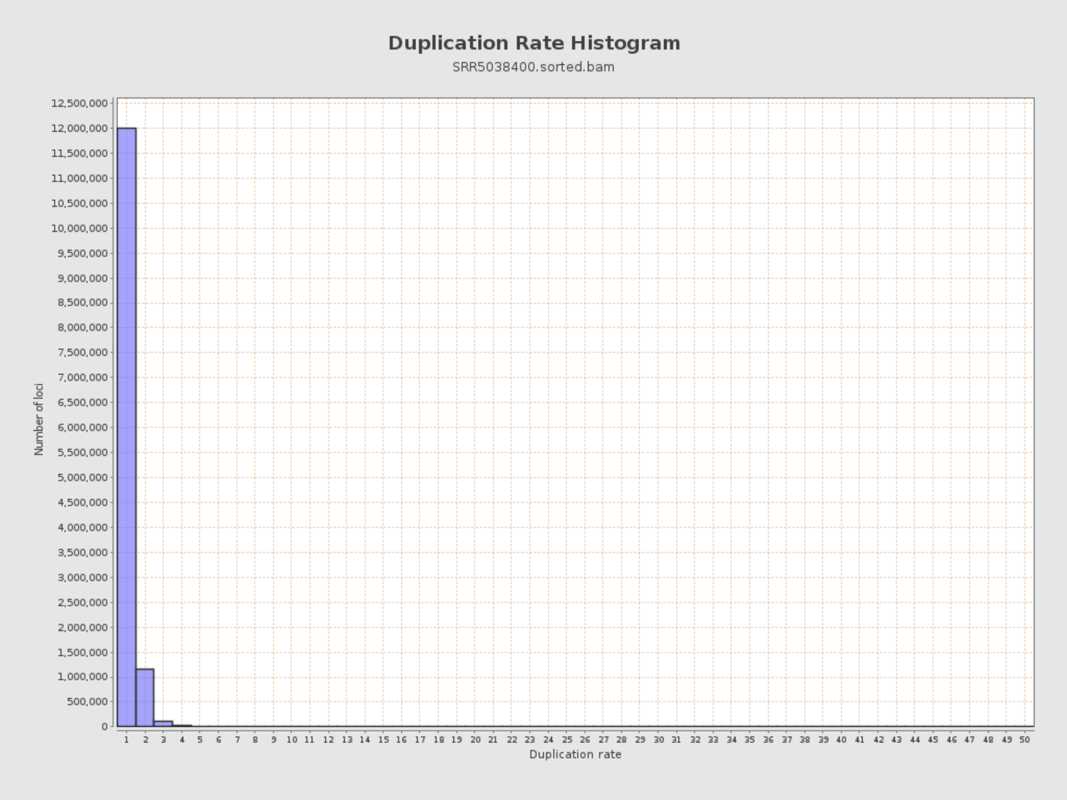
5. Results : Coverage Histogram (0-50X)



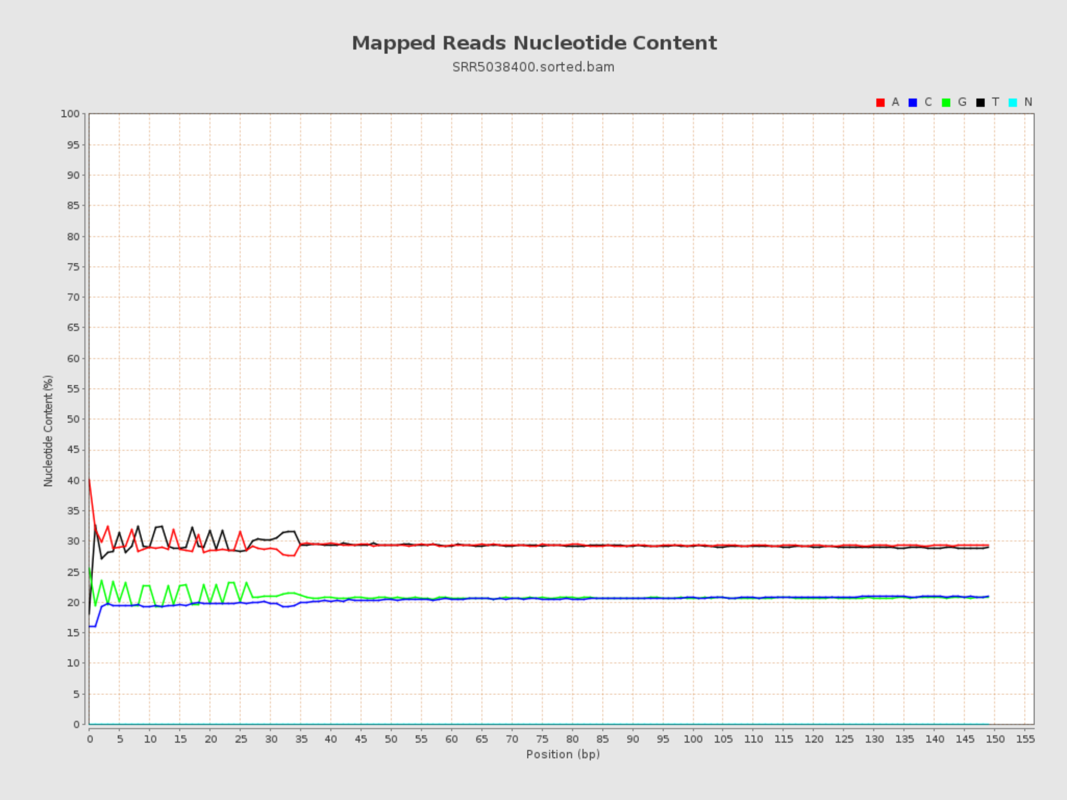
6. Results : Genome Fraction Coverage



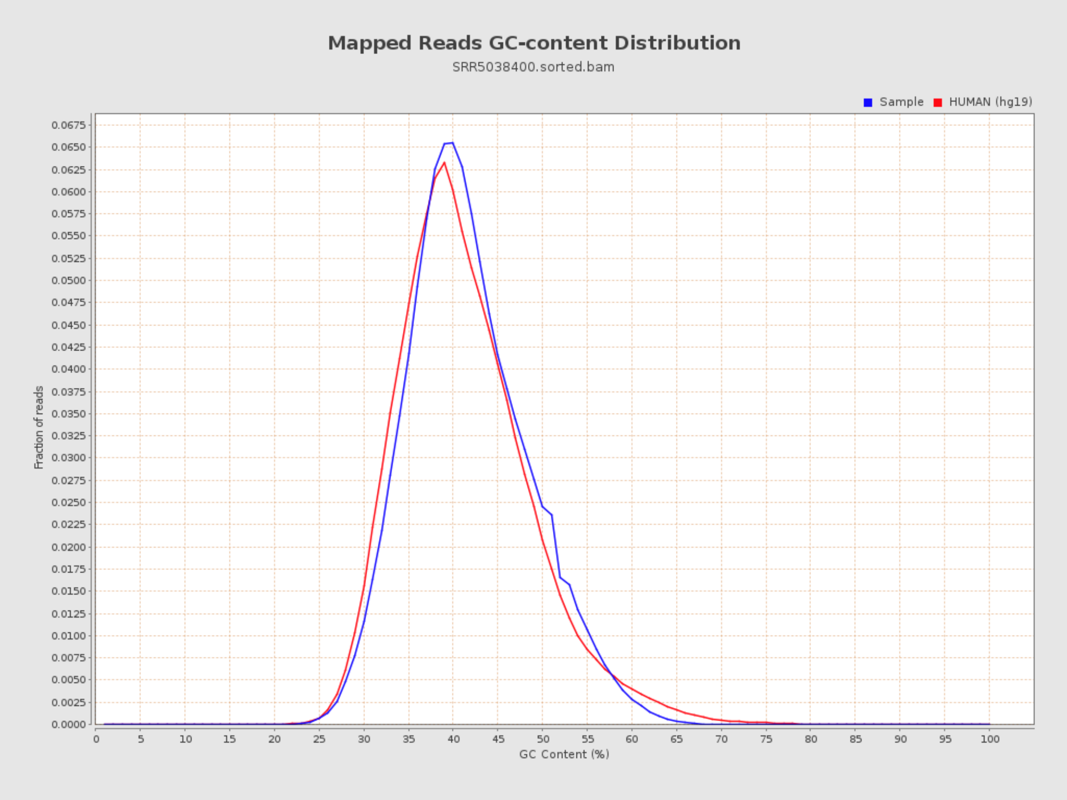
7. Results : Duplication Rate Histogram



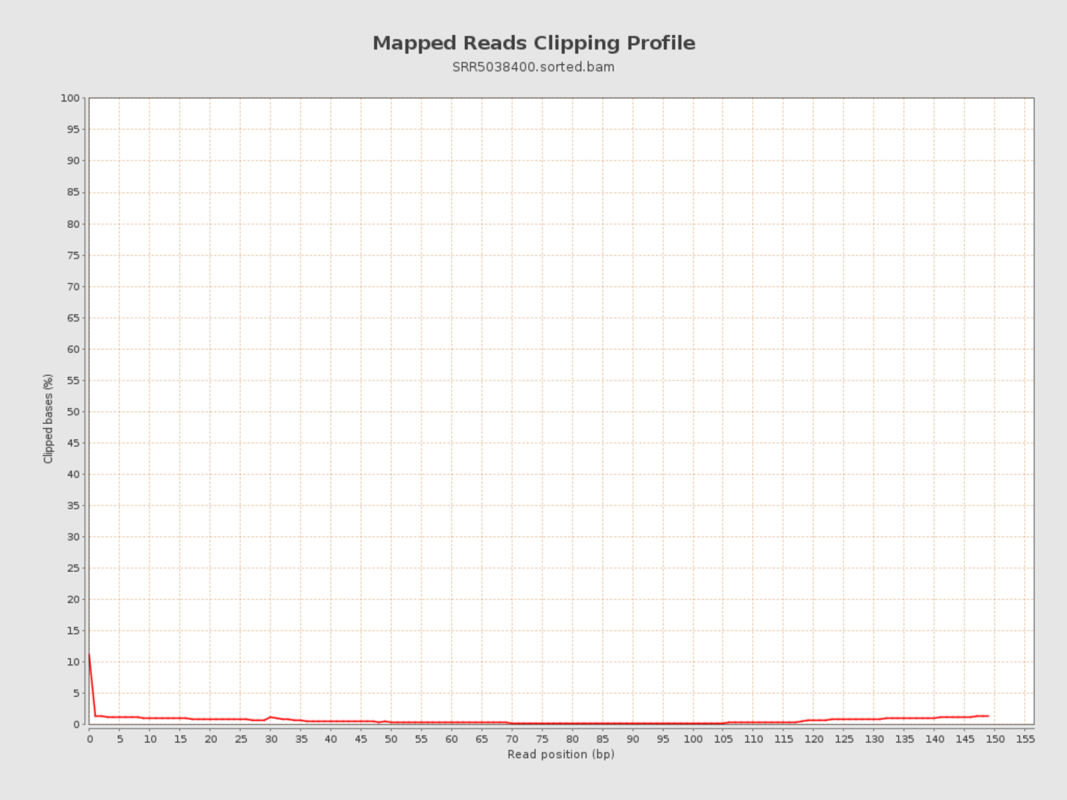
8. Results : Mapped Reads Nucleotide Content



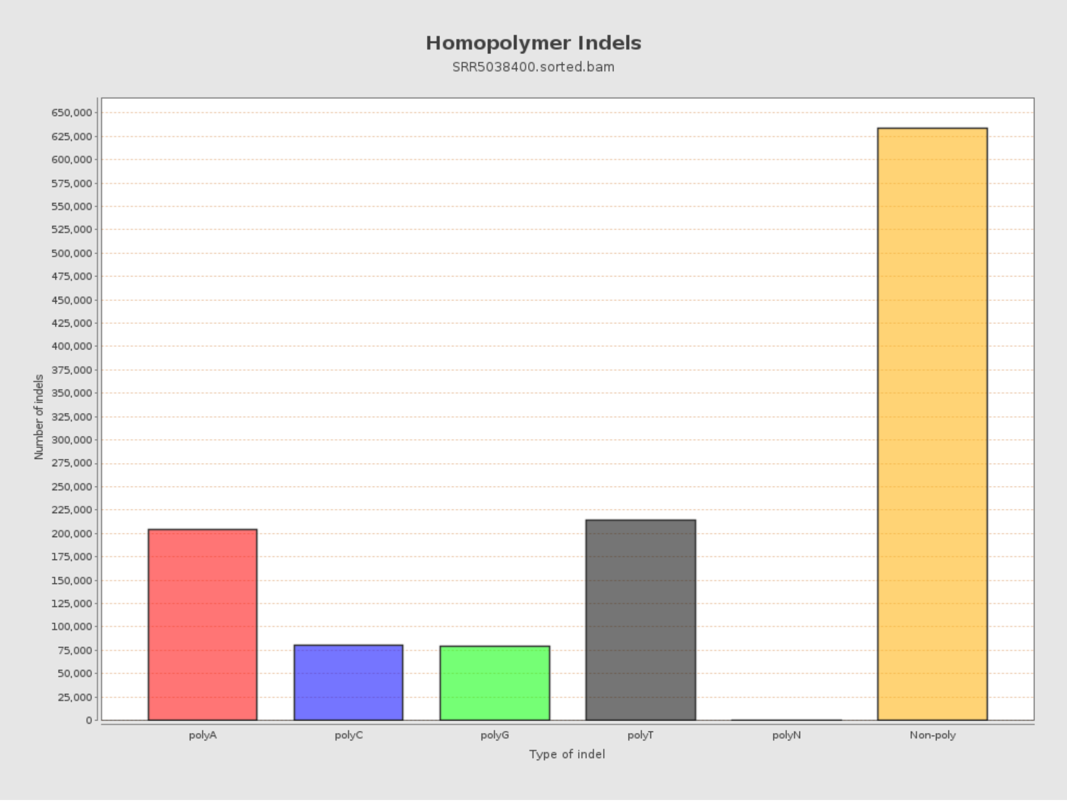
9. Results : Mapped Reads GC-content Distribution



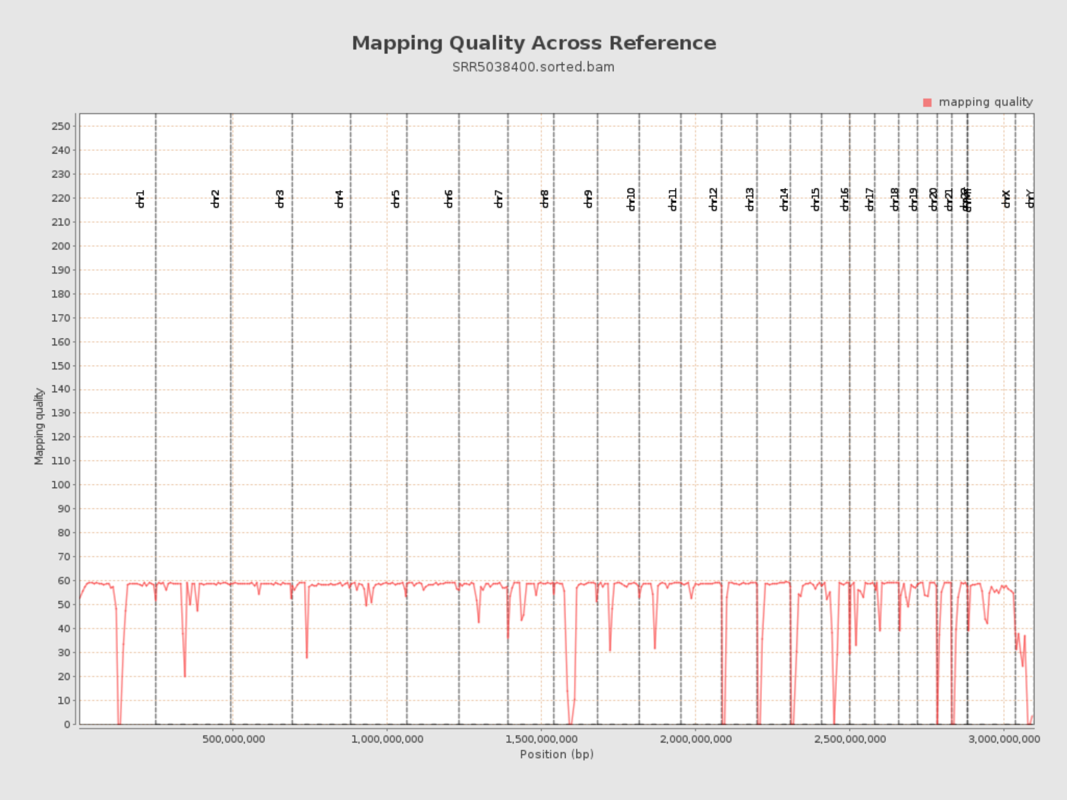
10. Results : Mapped Reads Clipping Profile



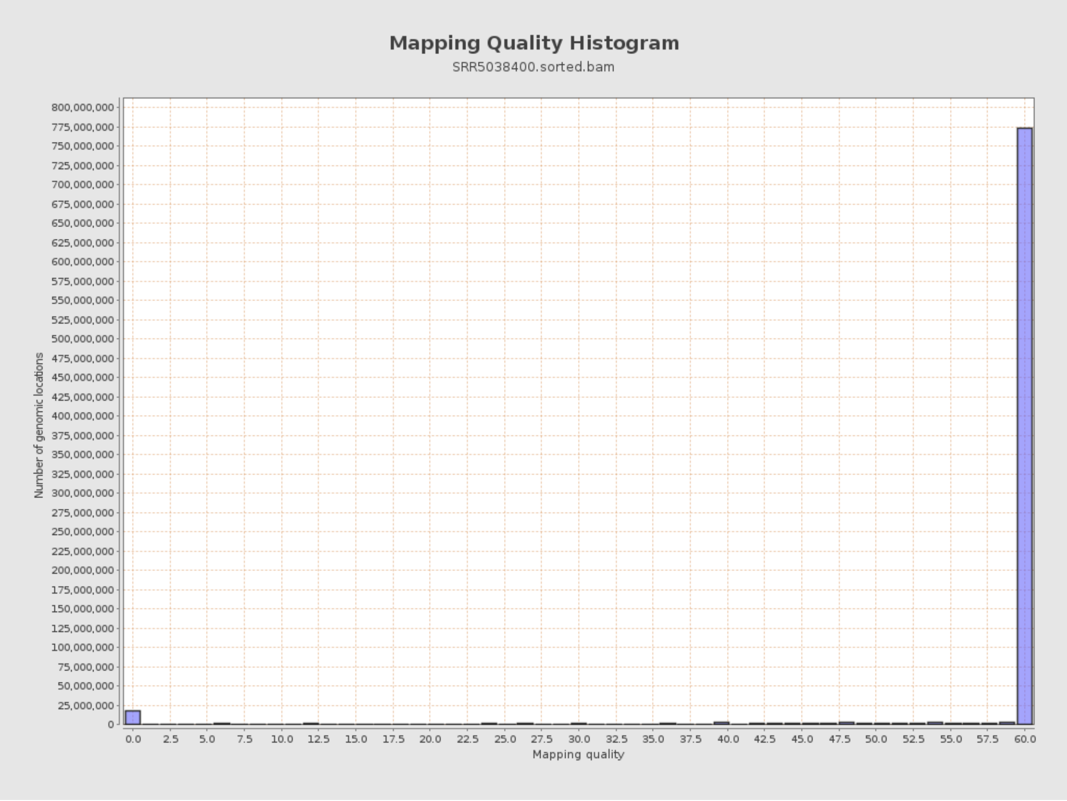
11. Results : Homopolymer Indels



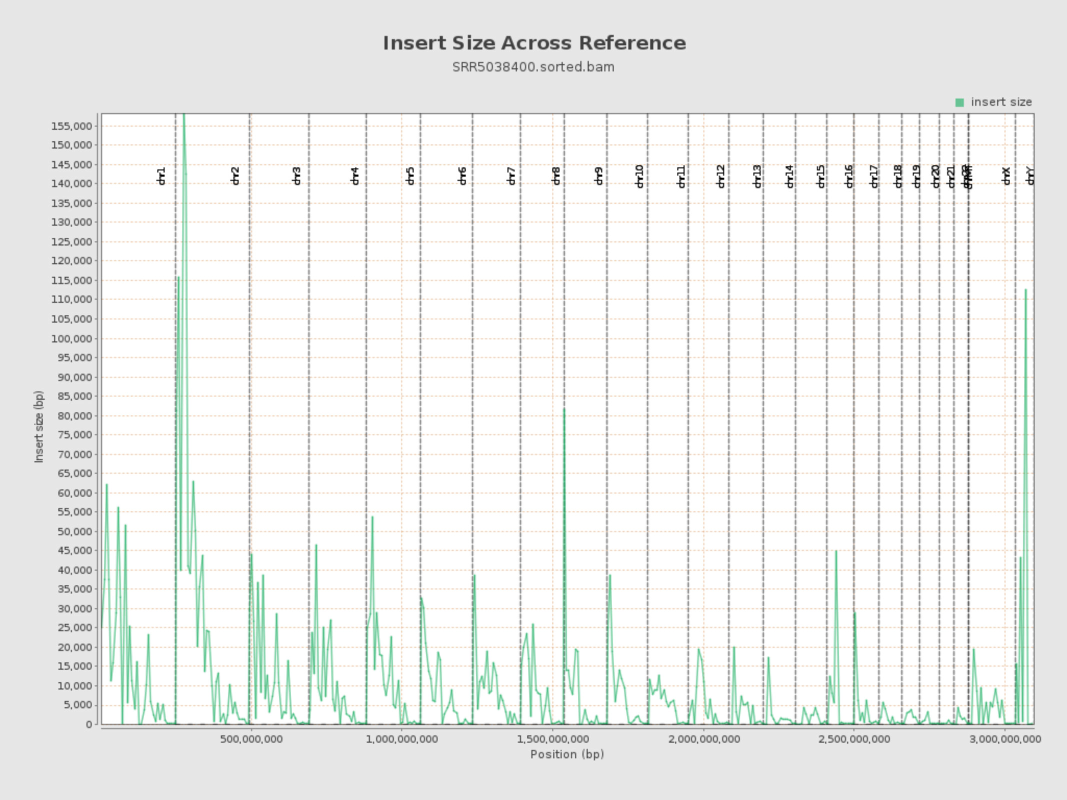
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram