Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 08:20:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038436.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_SRR5038436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038436_1.fastq.gz SRR5038436_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 08:20:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,049,544
Mapped reads	16,127,441 / 94.59%
Unmapped reads	922,103 / 5.41%
Mapped paired reads	16,127,441 / 94.59%
Mapped reads, first in pair	8,146,586 / 47.78%
Mapped reads, second in pair	7,980,855 / 46.81%
Mapped reads, both in pair	15,937,822 / 93.48%
Mapped reads, singletons	189,619 / 1.11%
Secondary alignments	0
Supplementary alignments	229,414 / 1.35%
Read min/max/mean length	30 / 150 / 150.7
Duplicated reads (estimated)	2,606,274 / 15.29%
Duplication rate	11%
Clipped reads	3,201,494 / 18.78%

2.2. ACGT Content

Number/percentage of A's	681,252,923 / 29.27%
Number/percentage of C's	478,421,512 / 20.55%
Number/percentage of T's	679,293,542 / 29.18%
Number/percentage of G's	488,682,809 / 20.99%
Number/percentage of N's	49,759 / 0%

GC Percentage	41.55%

2.3. Coverage

Mean	0.7524
Standard Deviation	10.8008

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	71,697.53
Standard Deviation	2,564,808.82
P25/Median/P75	202 / 245 / 300

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	32,022,316
Insertions	391,356
Mapped reads with at least one insertion	2.3%
Deletions	815,442
Mapped reads with at least one deletion	4.87%
Homopolymer indels	47.62%

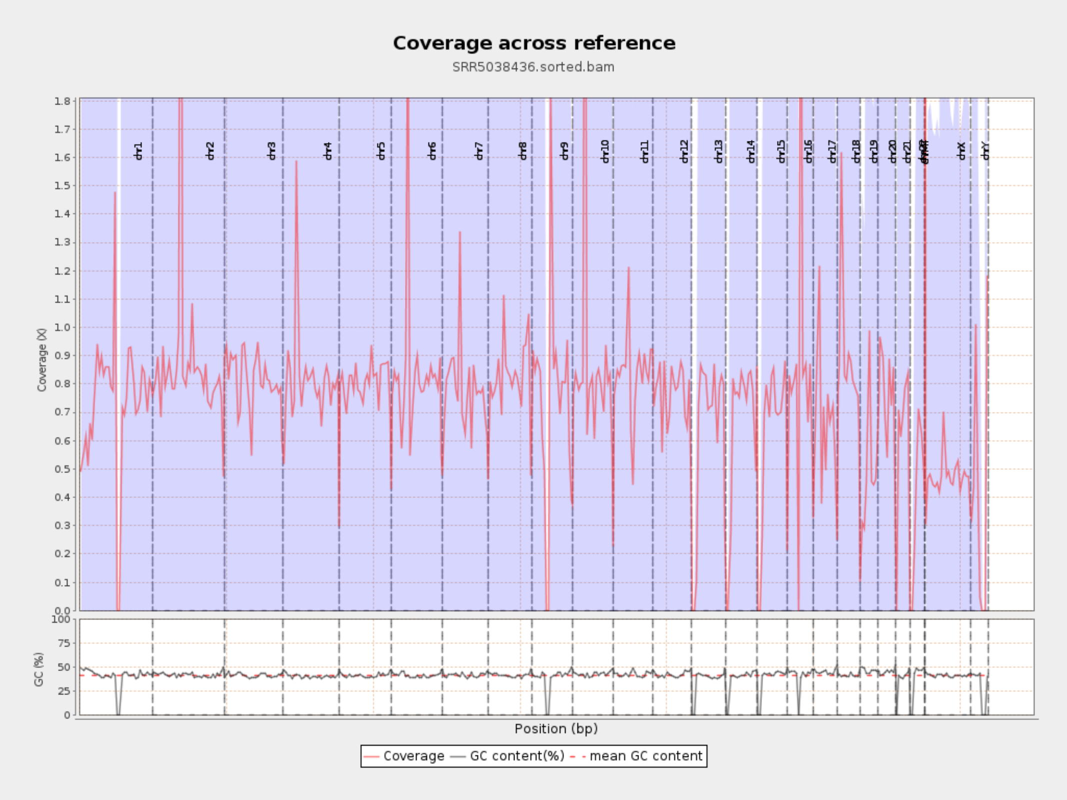
2.7. Chromosome stats

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

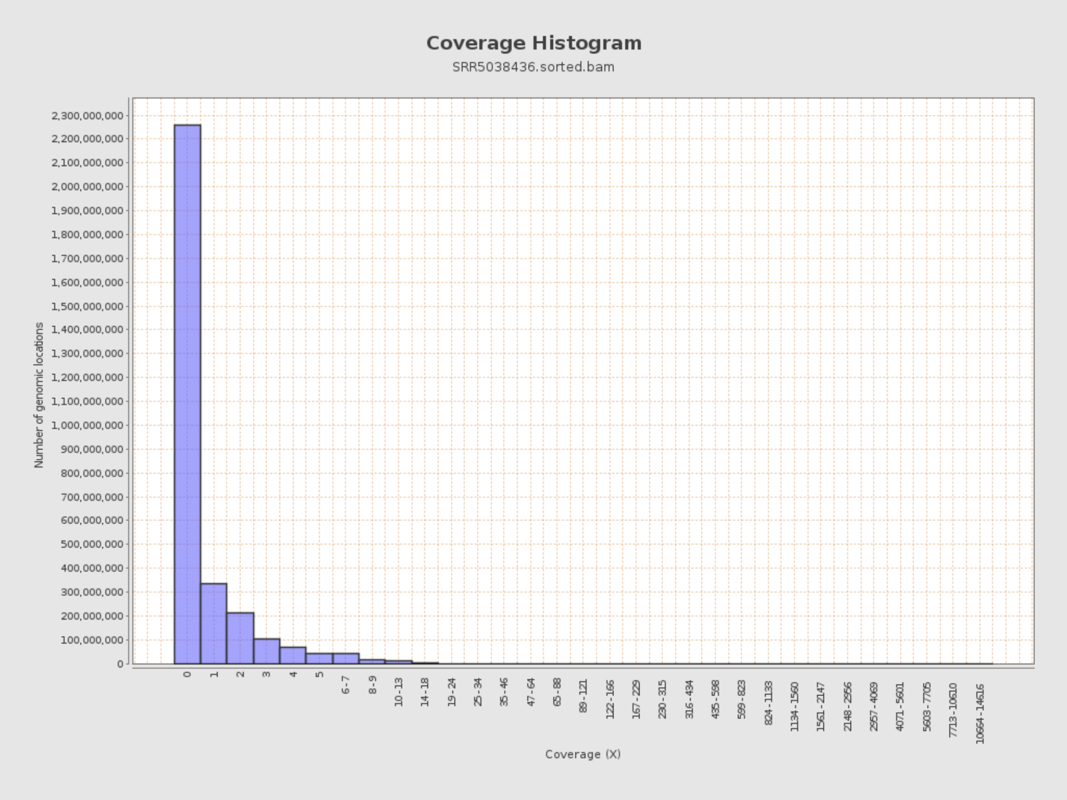
		bases	coverage	deviation
chr1	249250621	182576141	0.7325	12.4834
chr2	243199373	219812858	0.9038	14.7515
chr3	198022430	161895439	0.8176	1.7987
chr4	191154276	156386729	0.8181	6.0433
chr5	180915260	145231132	0.8028	1.9172
chr6	171115067	145944659	0.8529	15.6006
chr7	159138663	123869993	0.7784	11.2293
chr8	146364022	121299014	0.8287	3.5472
chr9	141213431	103650780	0.734	23.6562
chr10	135534747	123335120	0.91	17.9543
chr11	135006516	110454353	0.8181	7.7887
chr12	133851895	101894925	0.7613	1.7787
chr13	115169878	73402902	0.6373	1.5436
chr14	107349540	68302905	0.6363	1.7283
chr15	102531392	63260207	0.617	1.5562
chr16	90354753	77594214	0.8588	14.1049
chr17	81195210	53498112	0.6589	8.8712
chr18	78077248	69882786	0.895	19.5675
chr19	59128983	27744525	0.4692	7.0732
chr20	63025520	47901932	0.76	2.4231
chr21	48129895	29947588	0.6222	3.324
chr22	51304566	20284333	0.3954	1.3113
chrMT	16571	2270236	137.0005	79.9093
chrX	155270560	72950301	0.4698	2.4134

chrY	59373566	25847490	0.4353	9.8652

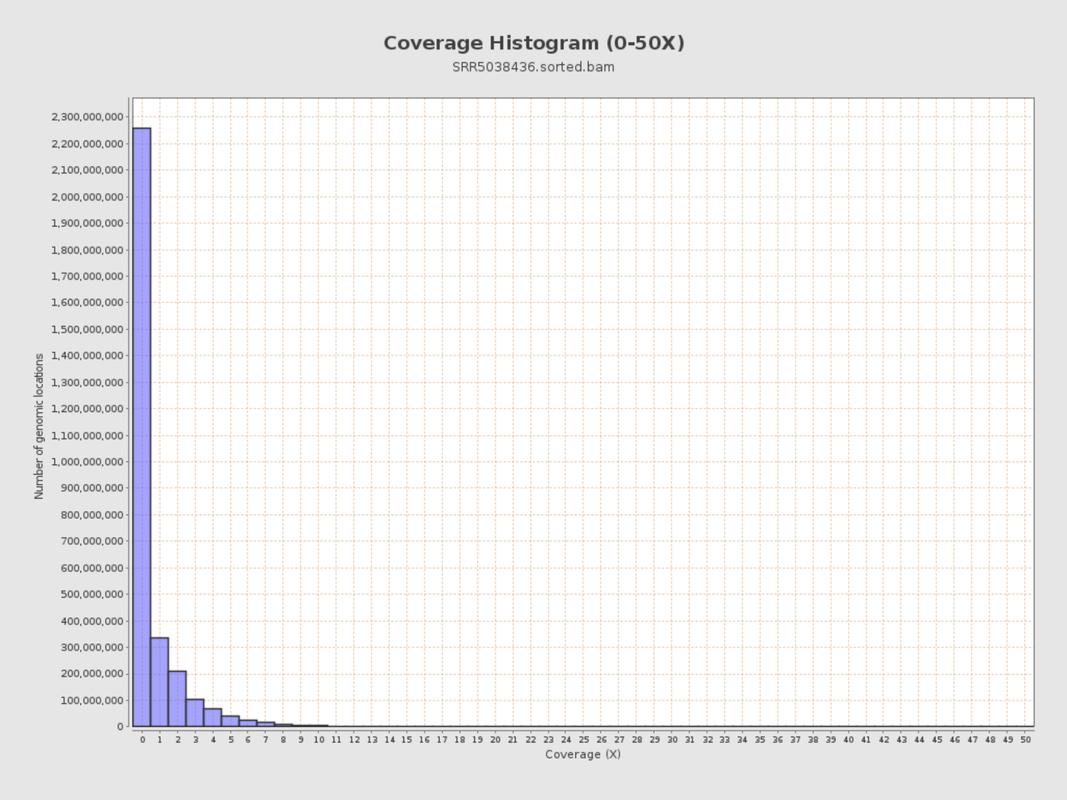
3. Results : Coverage across reference



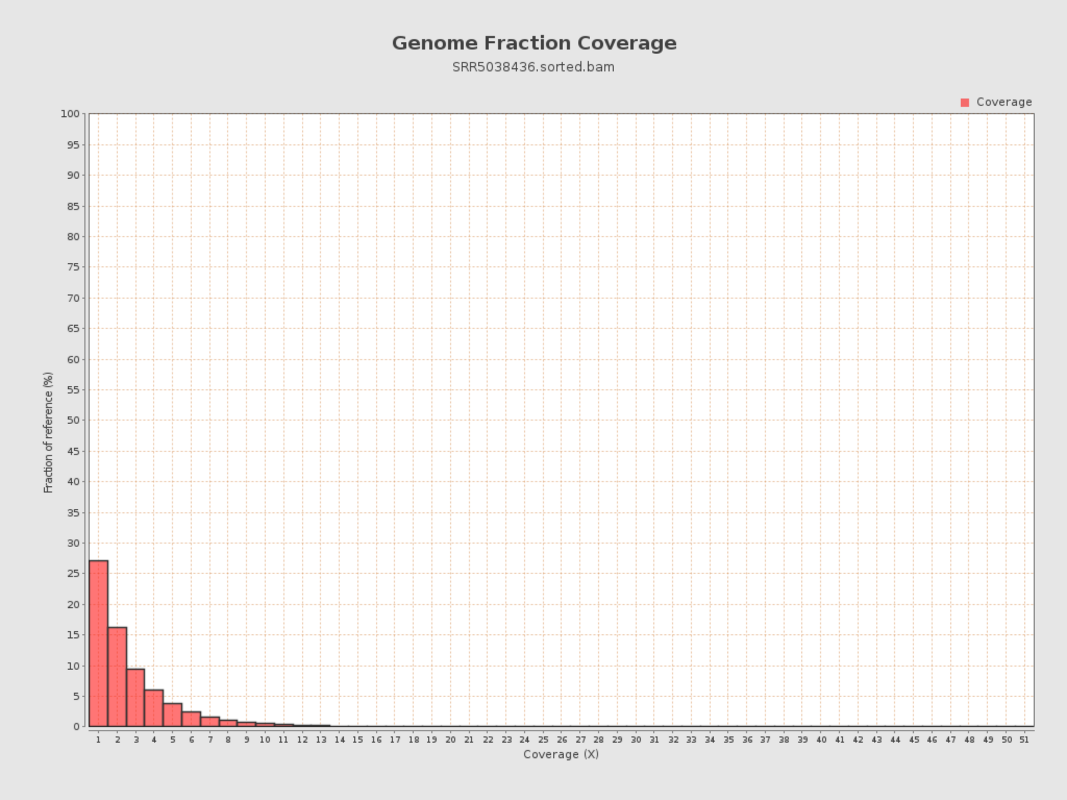
4. Results : Coverage Histogram



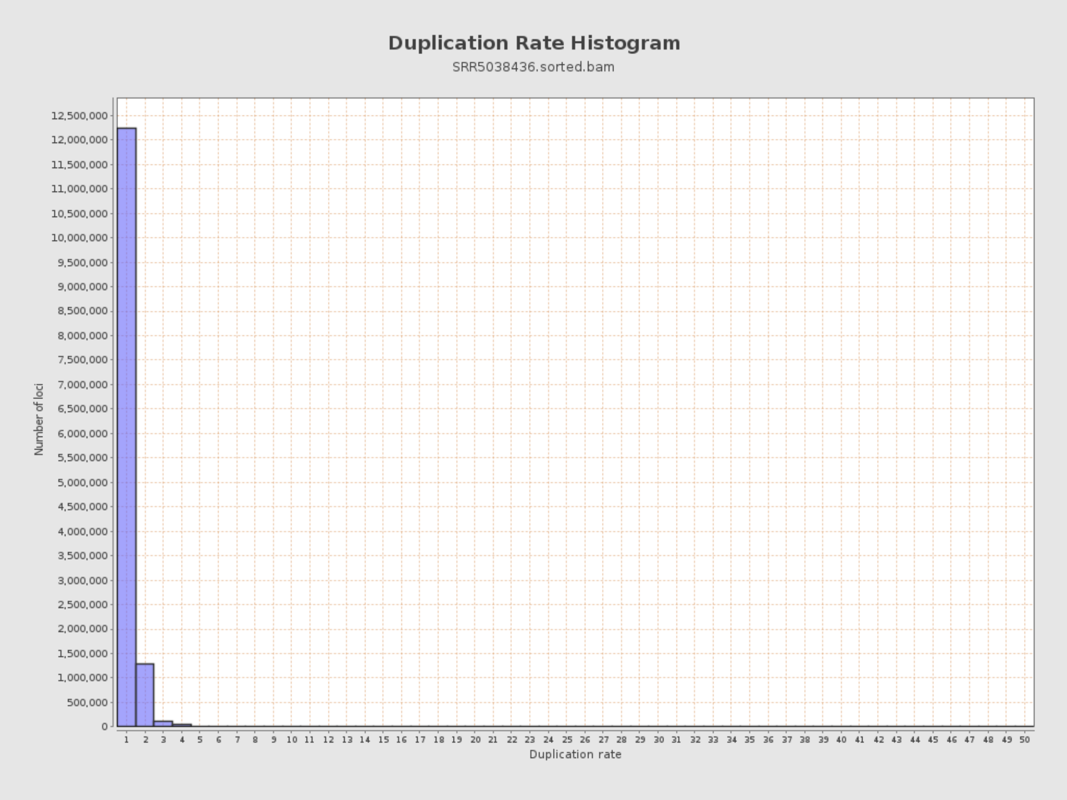
5. Results : Coverage Histogram (0-50X)



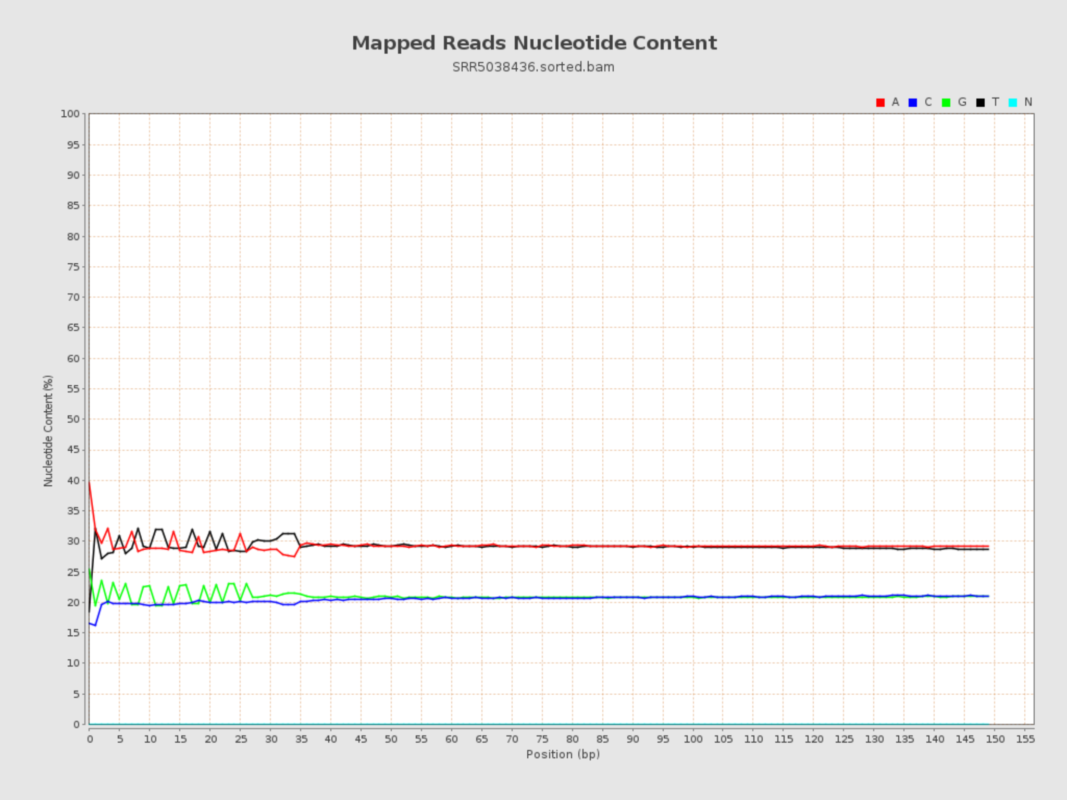
6. Results : Genome Fraction Coverage



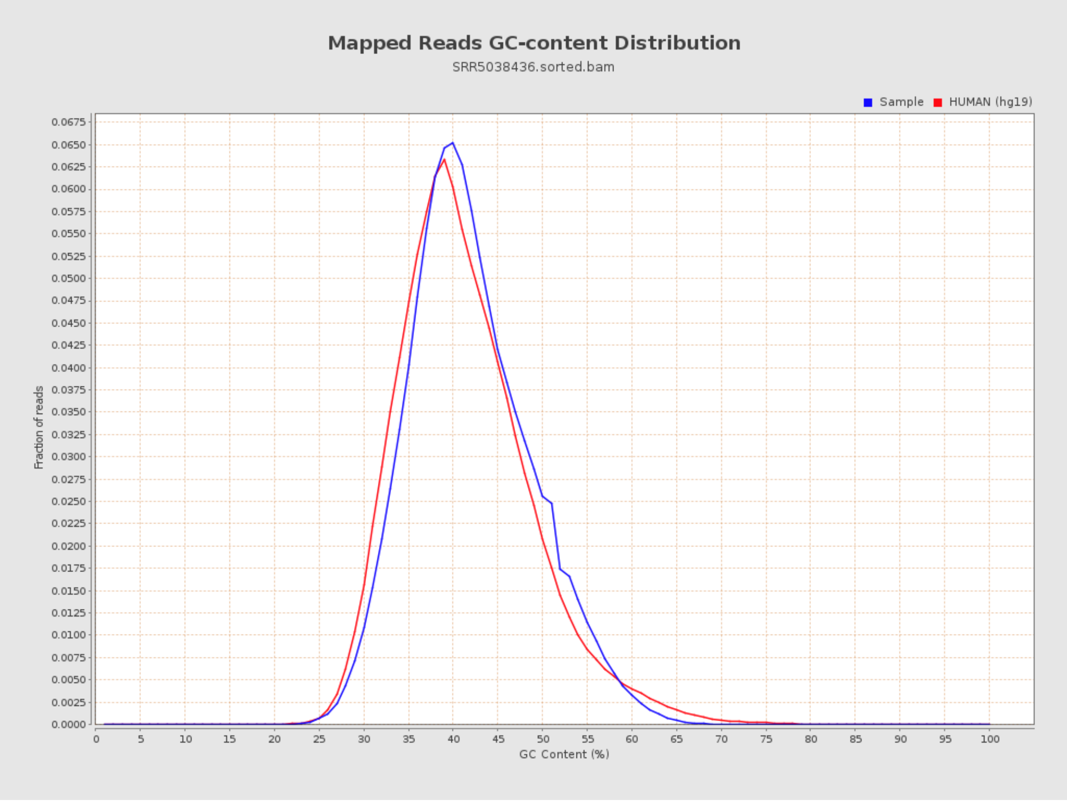
7. Results : Duplication Rate Histogram



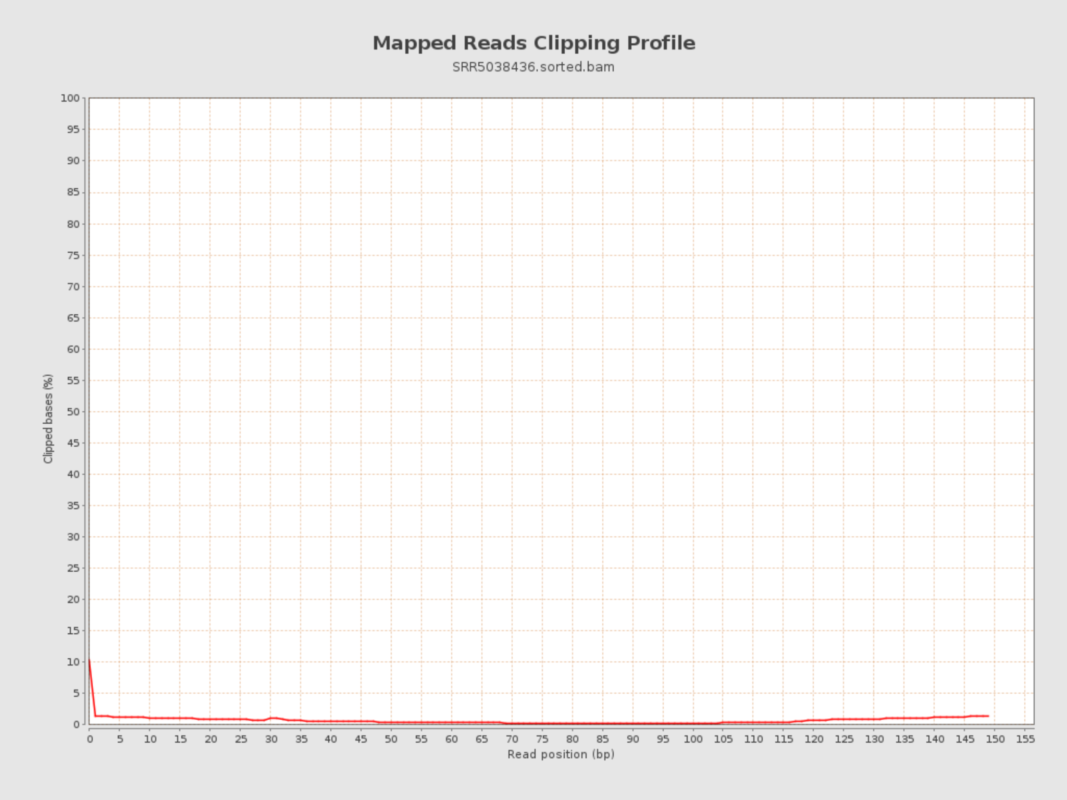
8. Results : Mapped Reads Nucleotide Content



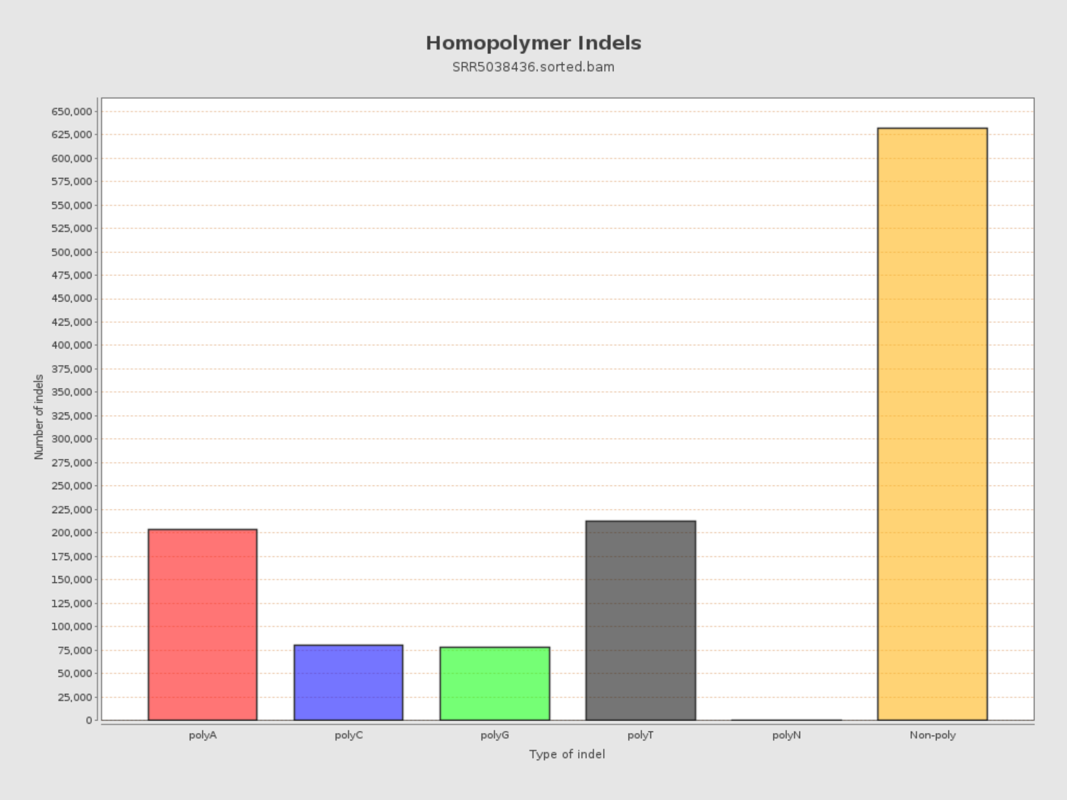
9. Results : Mapped Reads GC-content Distribution



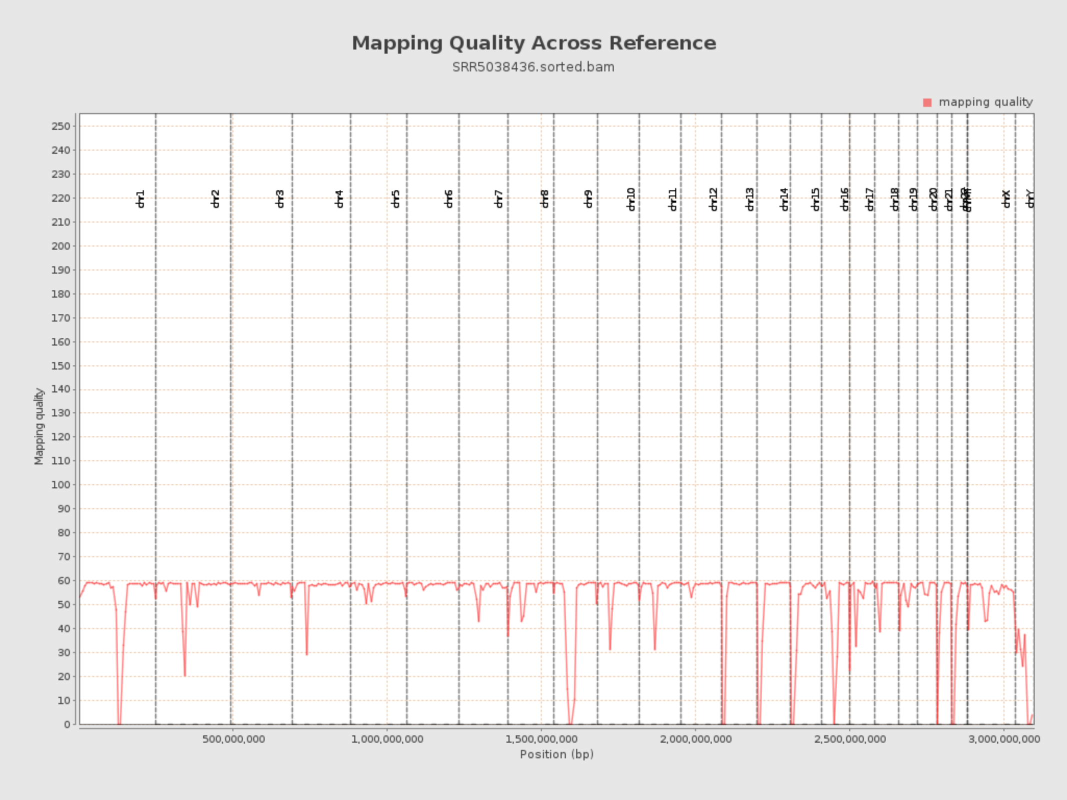
10. Results : Mapped Reads Clipping Profile



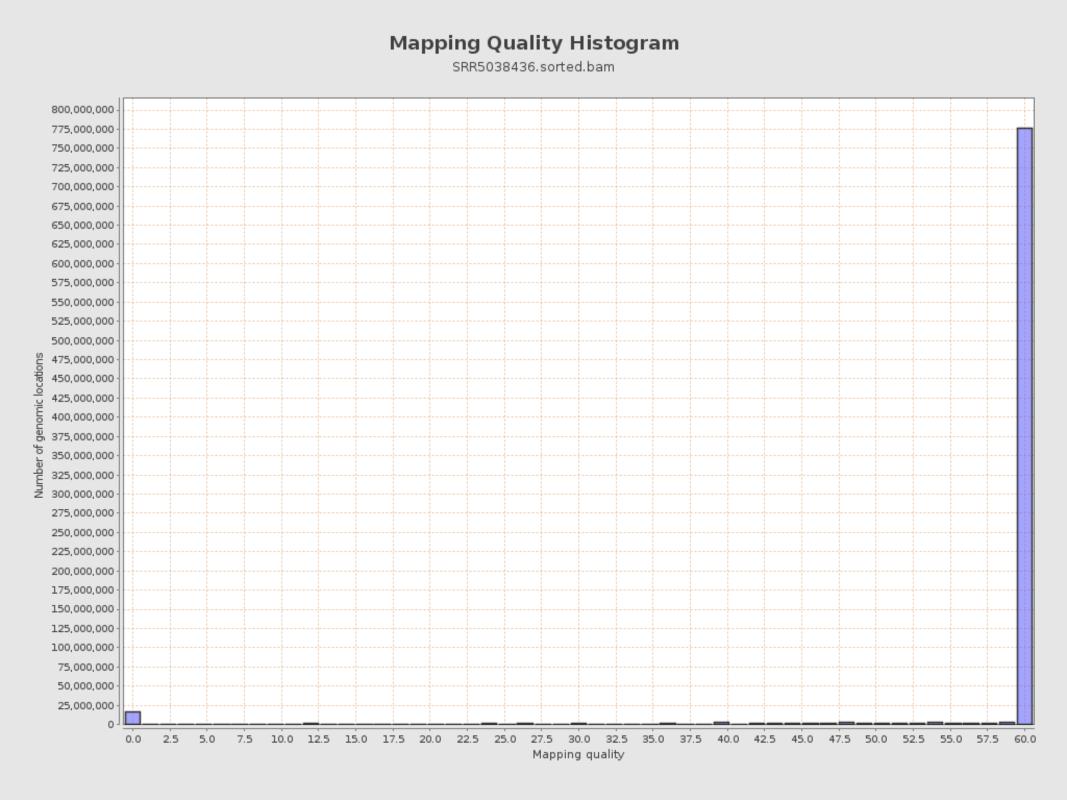
11. Results : Homopolymer Indels



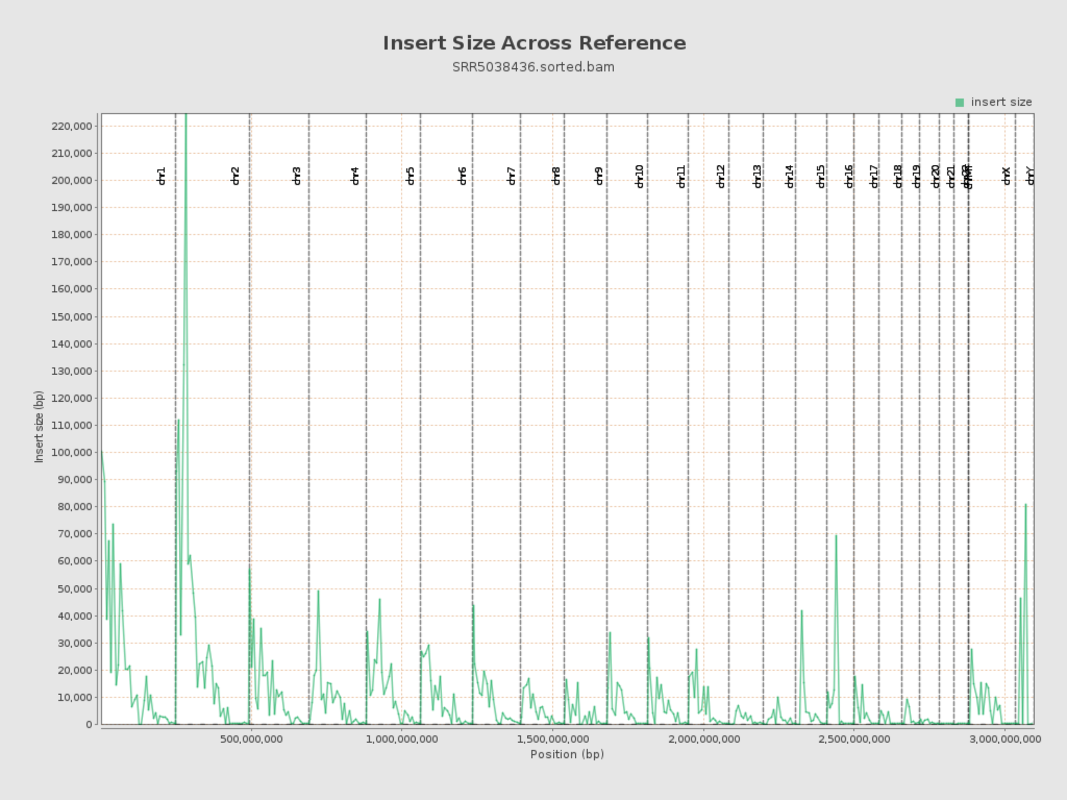
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram