Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 18:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038457.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_SRR5038457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038457_1.fastq.gz SRR5038457_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 18:28:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,144,228
Mapped reads	12,097,465 / 92.04%
Unmapped reads	1,046,763 / 7.96%
Mapped paired reads	12,097,465 / 92.04%
Mapped reads, first in pair	6,115,255 / 46.52%
Mapped reads, second in pair	5,982,210 / 45.51%
Mapped reads, both in pair	11,942,772 / 90.86%
Mapped reads, singletons	154,693 / 1.18%
Secondary alignments	0
Supplementary alignments	204,982 / 1.56%
Read min/max/mean length	30 / 150 / 150.81
Duplicated reads (estimated)	1,812,206 / 13.79%
Duplication rate	9.08%
Clipped reads	3,164,961 / 24.08%

2.2. ACGT Content

Number/percentage of A's	492,907,695 / 28.69%
Number/percentage of C's	357,942,572 / 20.83%
Number/percentage of T's	492,903,395 / 28.69%
Number/percentage of G's	374,448,270 / 21.79%
Number/percentage of N's	35,532 / 0%

GC Percentage	42.62%

2.3. Coverage

Mean	0.5554
Standard Deviation	9.1962

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	74,145.45
Standard Deviation	2,535,562.71
P25/Median/P75	218 / 258 / 307

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	23,524,572
Insertions	288,108
Mapped reads with at least one insertion	2.25%
Deletions	578,186
Mapped reads with at least one deletion	4.6%
Homopolymer indels	46.77%

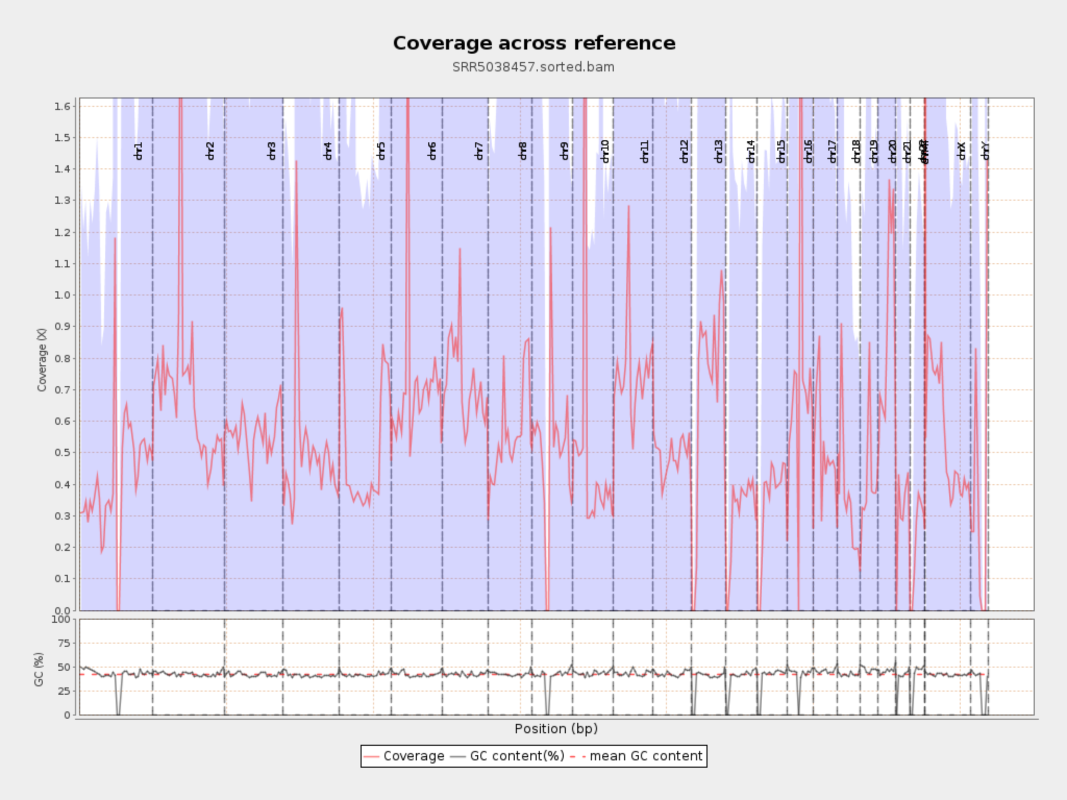
2.7. Chromosome stats

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

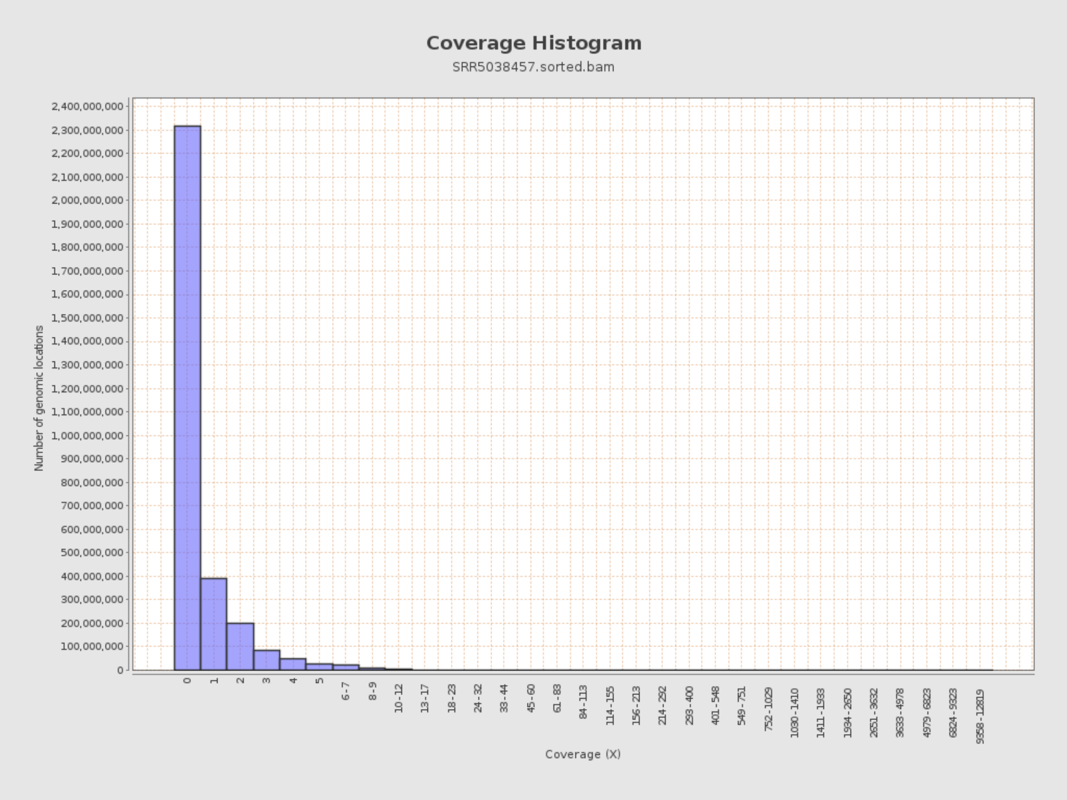
		bases	coverage	deviation
chr1	249250621	104409353	0.4189	13.0542
chr2	243199373	171287448	0.7043	10.0402
chr3	198022430	111844404	0.5648	1.2765
chr4	191154276	94260048	0.4931	7.0034
chr5	180915260	93412209	0.5163	1.2844
chr6	171115067	124864944	0.7297	16.0405
chr7	159138663	115737419	0.7273	8.6513
chr8	146364022	83253626	0.5688	2.3743
chr9	141213431	70397905	0.4985	14.0104
chr10	135534747	71544680	0.5279	17.7081
chr11	135006516	100112441	0.7415	9.5938
chr12	133851895	65838922	0.4919	1.1716
chr13	115169878	82185413	0.7136	1.485
chr14	107349540	32770460	0.3053	1.004
chr15	102531392	35239324	0.3437	0.9355
chr16	90354753	69008698	0.7638	12.6509
chr17	81195210	41425595	0.5102	8.3139
chr18	78077248	27811096	0.3562	11.2425
chr19	59128983	24135465	0.4082	7.4324
chr20	63025520	57071195	0.9055	2.6688
chr21	48129895	15477948	0.3216	3.025
chr22	51304566	11468235	0.2235	0.7856
chrMT	16571	5604380	338.2041	245.552
chrX	155270560	85866717	0.553	2.4332

chrY	59373566	24388654	0.4108	10.6787

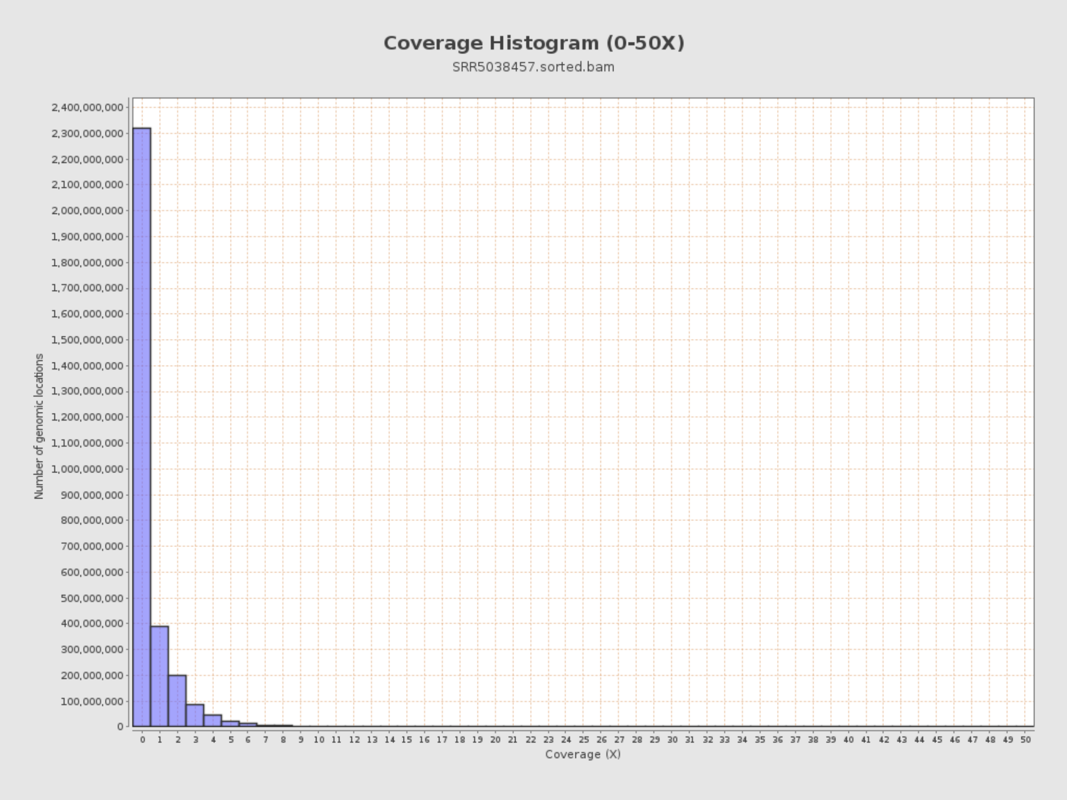
3. Results : Coverage across reference



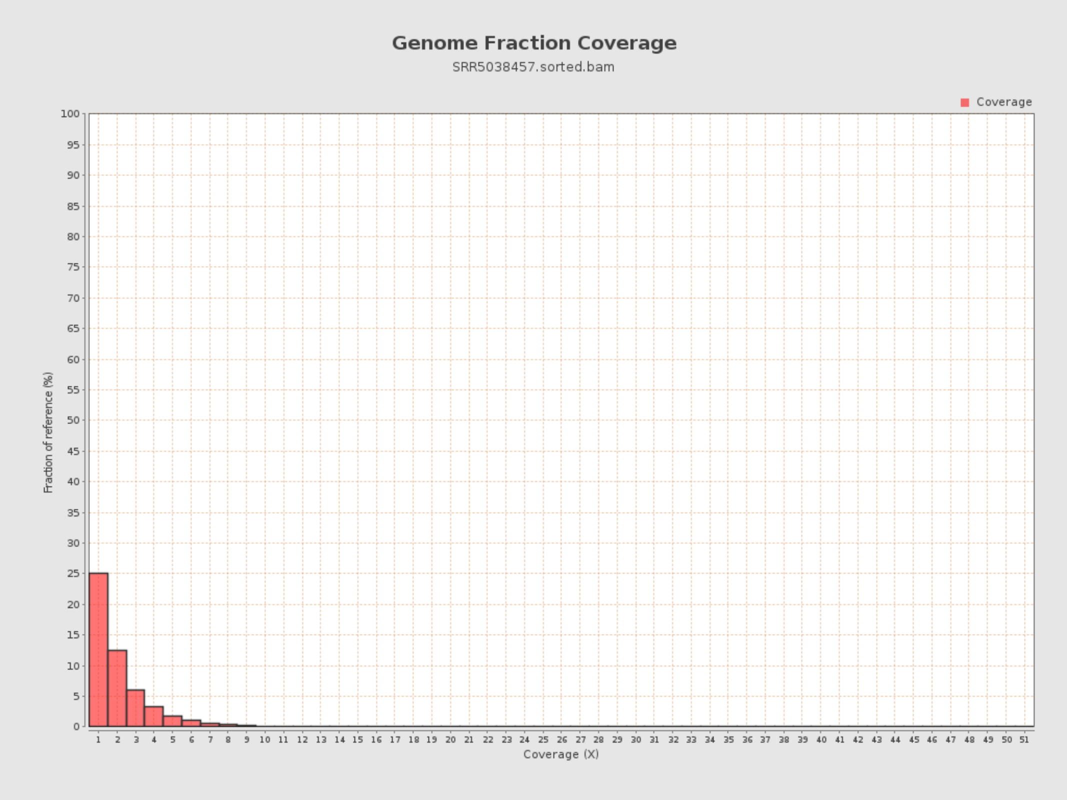
4. Results : Coverage Histogram



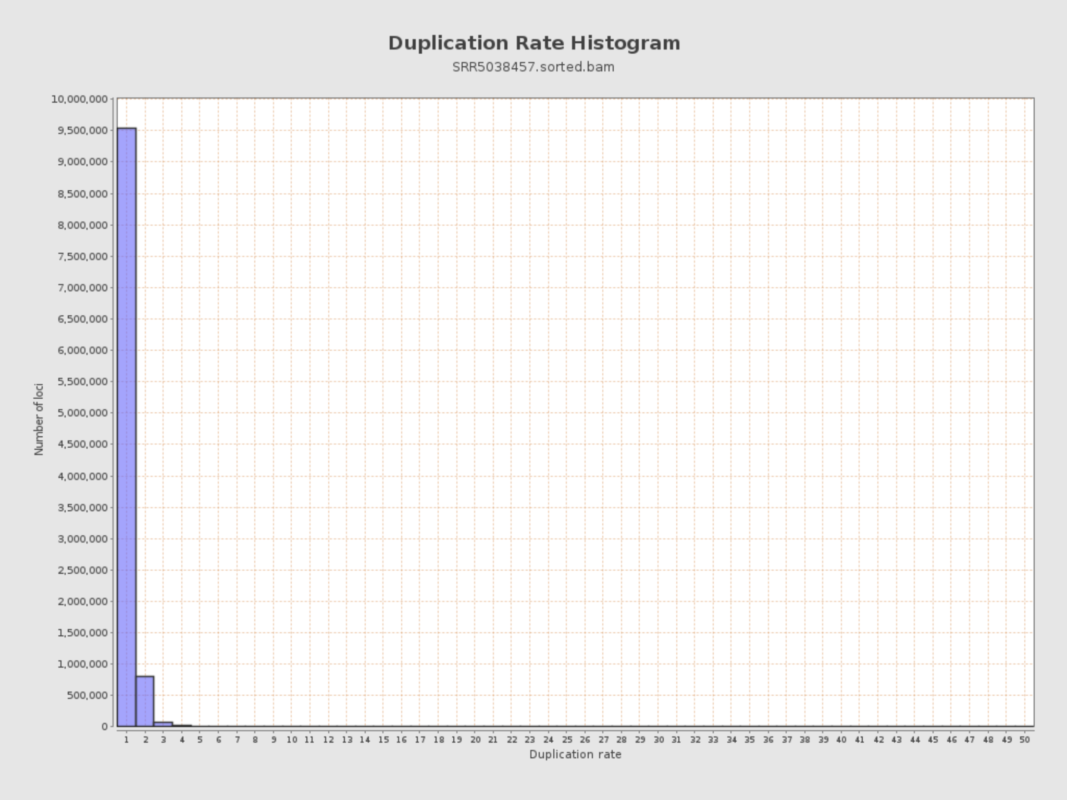
5. Results : Coverage Histogram (0-50X)



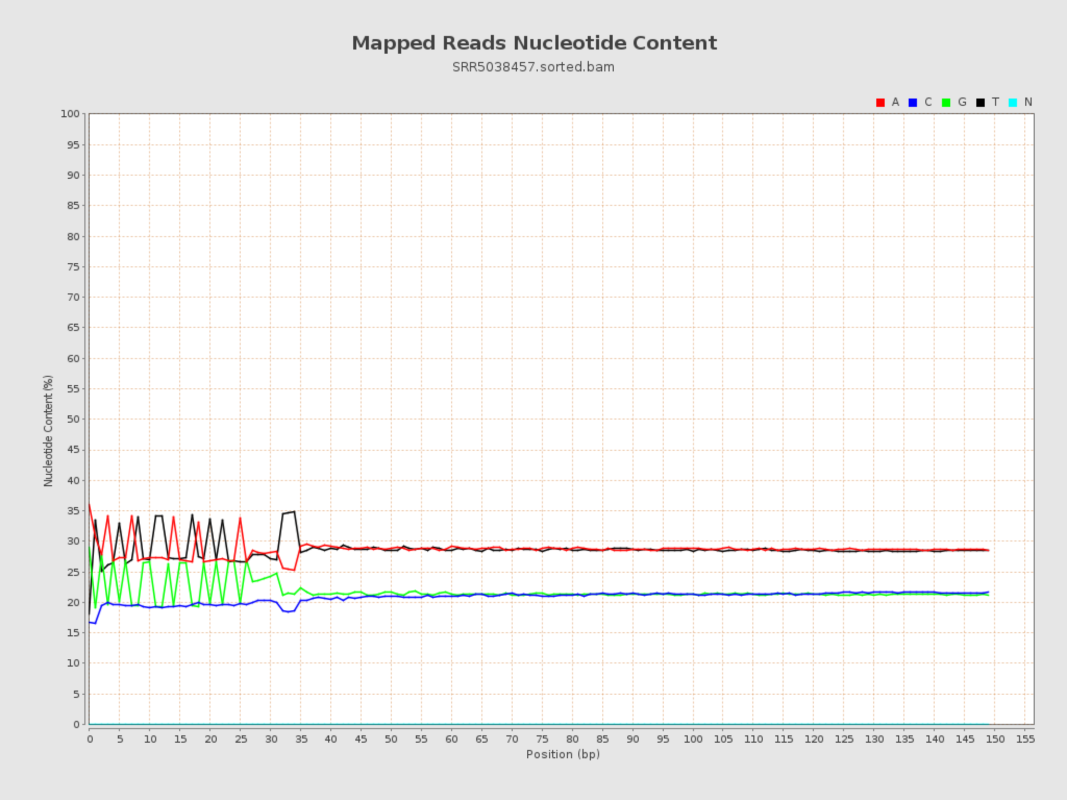
6. Results : Genome Fraction Coverage



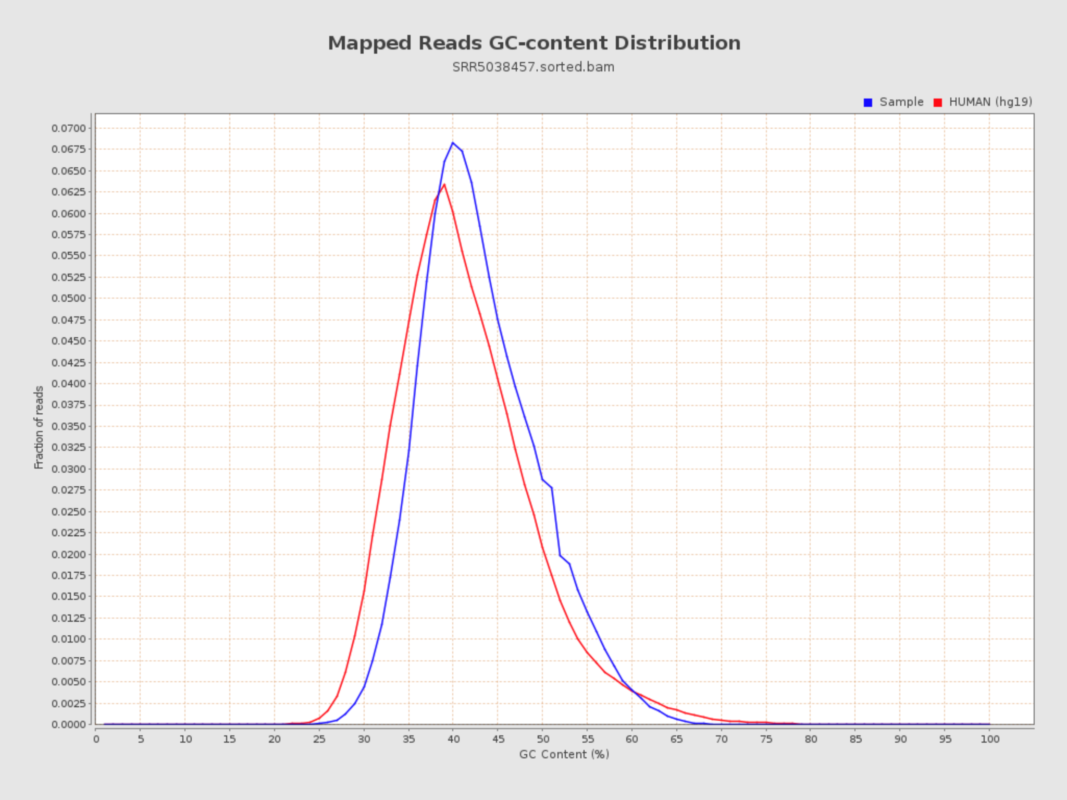
7. Results : Duplication Rate Histogram



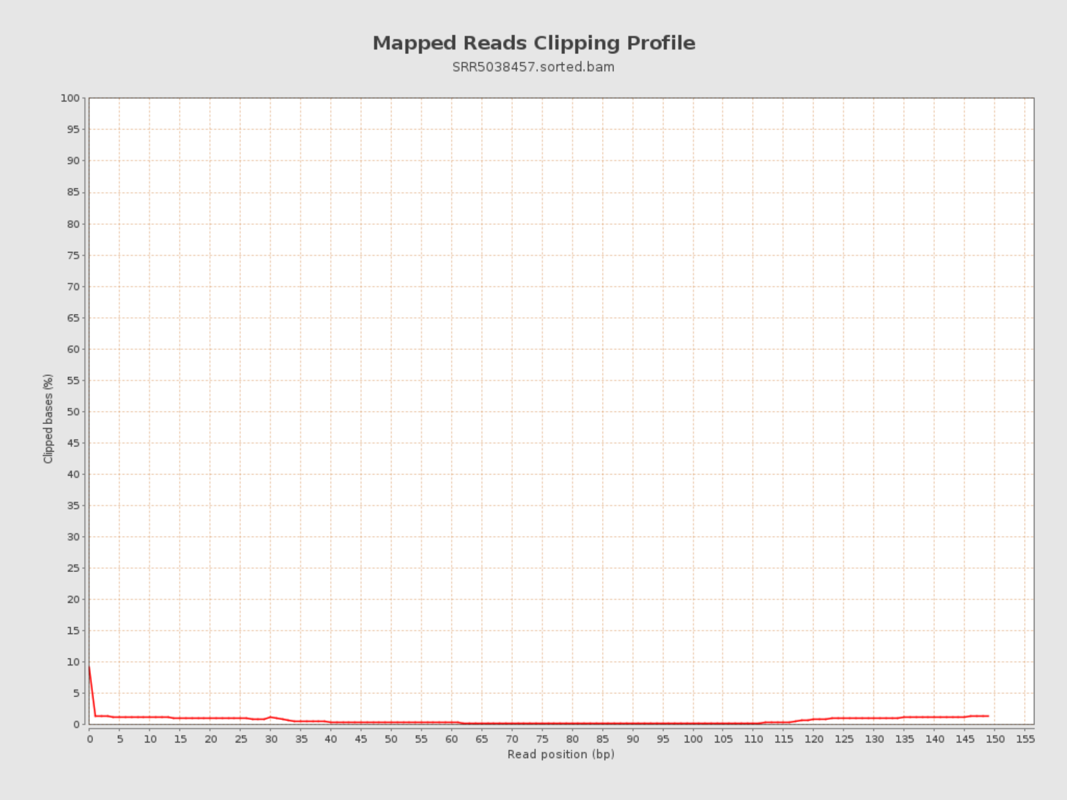
8. Results : Mapped Reads Nucleotide Content



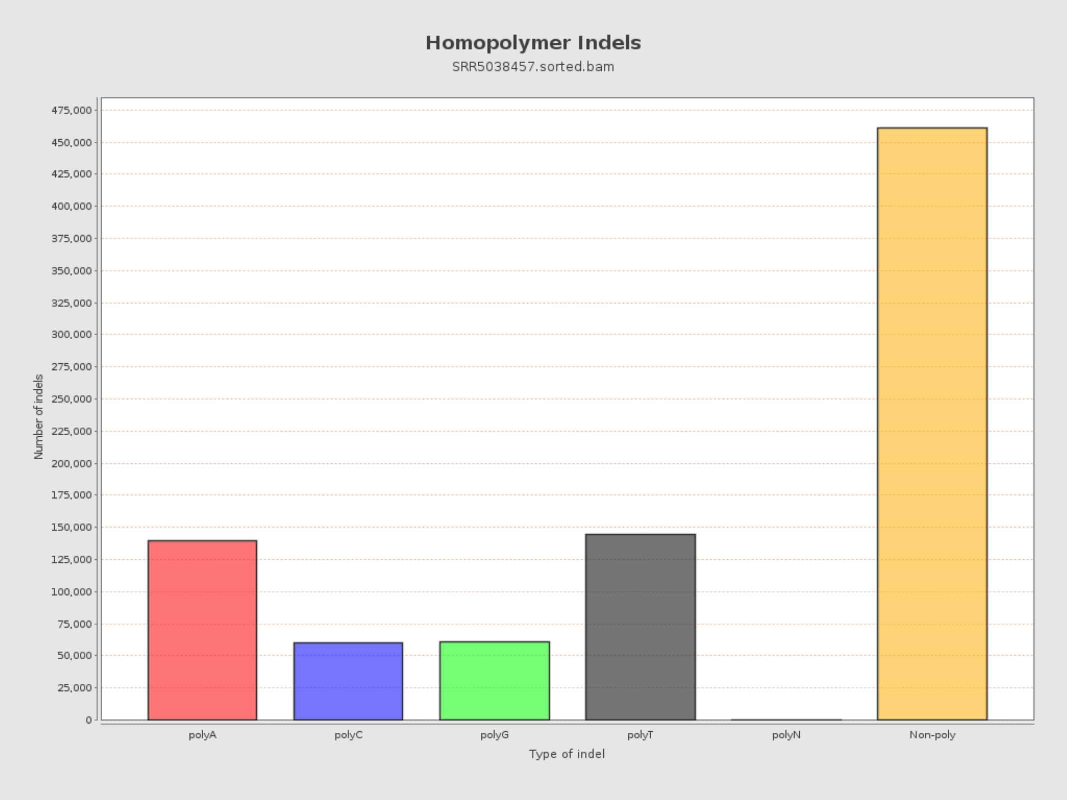
9. Results : Mapped Reads GC-content Distribution



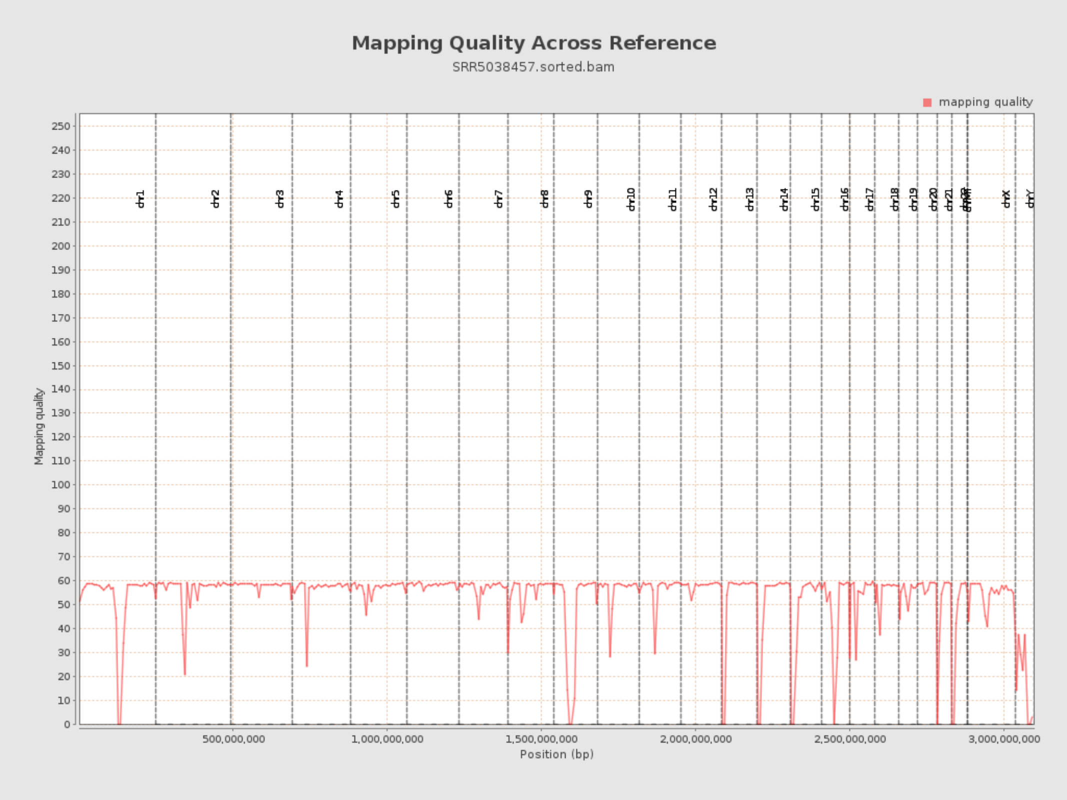
10. Results : Mapped Reads Clipping Profile



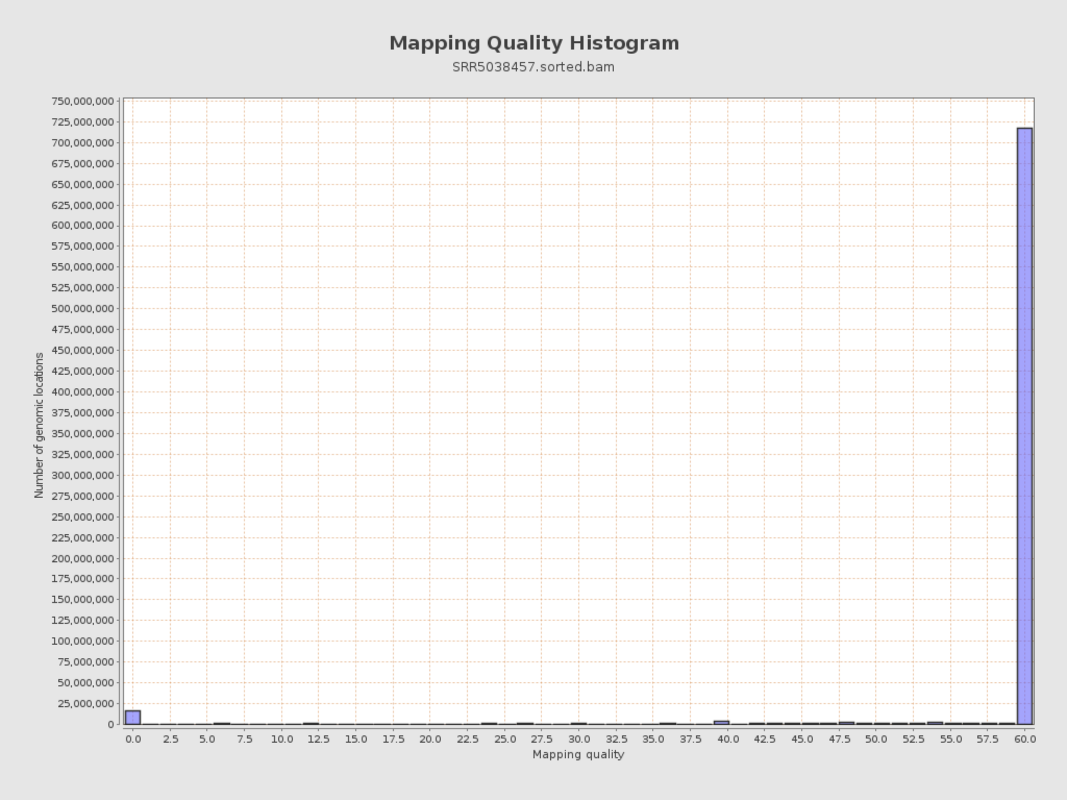
11. Results : Homopolymer Indels



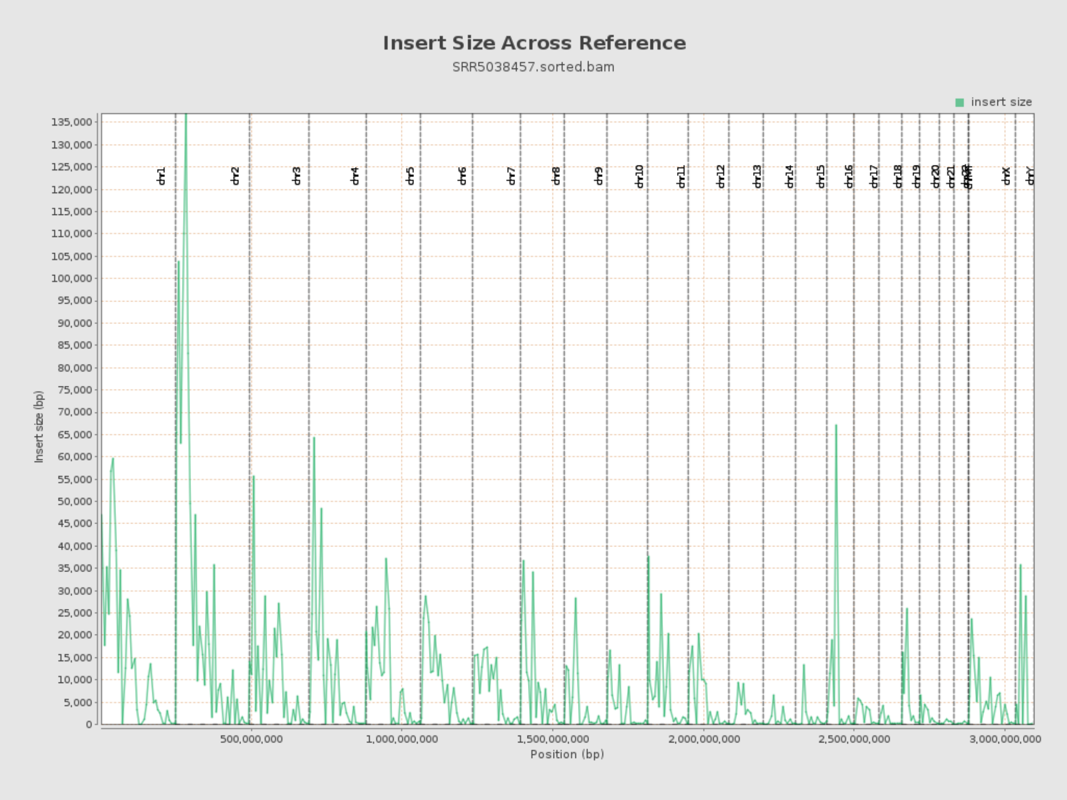
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram