Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 22:33:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038465.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_SRR5038465 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038465_1.fastq.gz SRR5038465_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 22:33:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038465.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,834,032
Mapped reads	12,486,526 / 97.29%
Unmapped reads	347,506 / 2.71%
Mapped paired reads	12,486,526 / 97.29%
Mapped reads, first in pair	6,306,858 / 49.14%
Mapped reads, second in pair	6,179,668 / 48.15%
Mapped reads, both in pair	12,344,994 / 96.19%
Mapped reads, singletons	141,532 / 1.1%
Secondary alignments	0
Supplementary alignments	117,053 / 0.91%
Read min/max/mean length	30 / 150 / 150.47
Duplicated reads (estimated)	1,183,062 / 9.22%
Duplication rate	6.99%
Clipped reads	1,397,874 / 10.89%

2.2. ACGT Content

Number/percentage of A's	532,069,617 / 29%
Number/percentage of C's	388,856,486 / 21.19%
Number/percentage of T's	526,860,234 / 28.71%
Number/percentage of G's	386,970,707 / 21.09%
Number/percentage of N's	41,528 / 0%

GC Percentage	42.28%

2.3. Coverage

Mean	0.5929
Standard Deviation	5.8153

2.4. Mapping Quality

Mean Mapping Quality	54.45

2.5. Insert size

Mean	83,624.15
Standard Deviation	2,881,893.68
P25/Median/P75	217 / 264 / 328

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	19,769,162
Insertions	223,543
Mapped reads with at least one insertion	1.69%
Deletions	237,899
Mapped reads with at least one deletion	1.82%
Homopolymer indels	44.29%

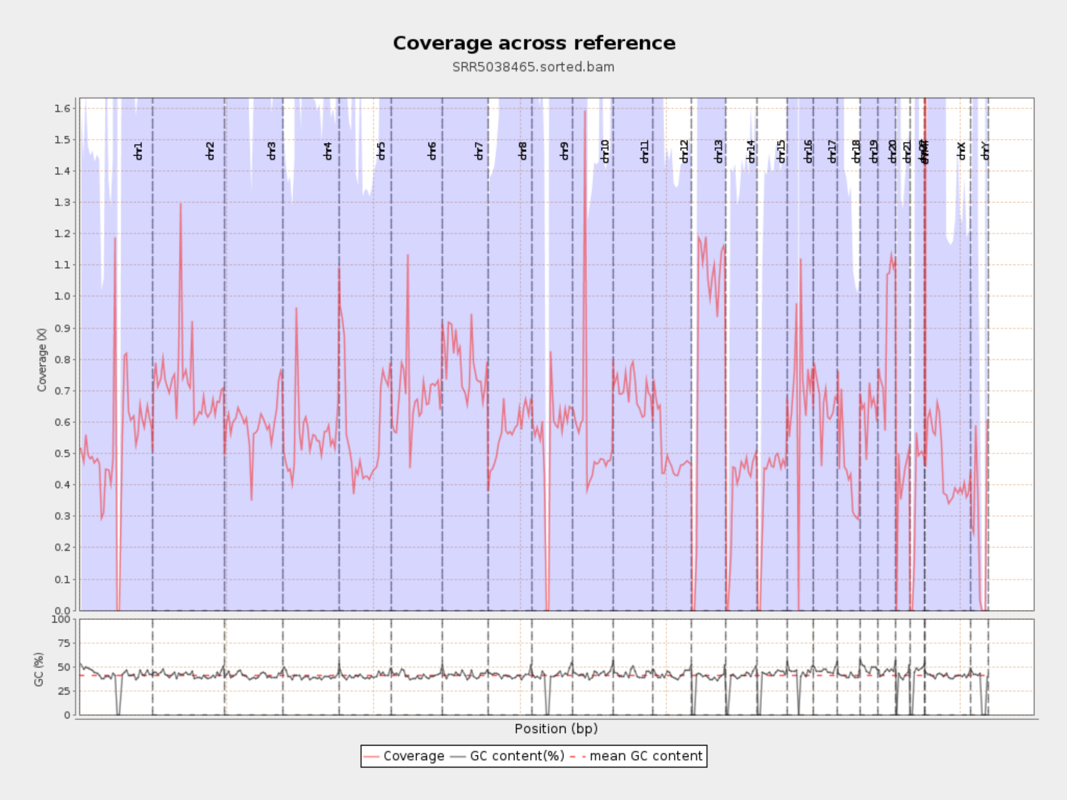
2.7. Chromosome stats

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

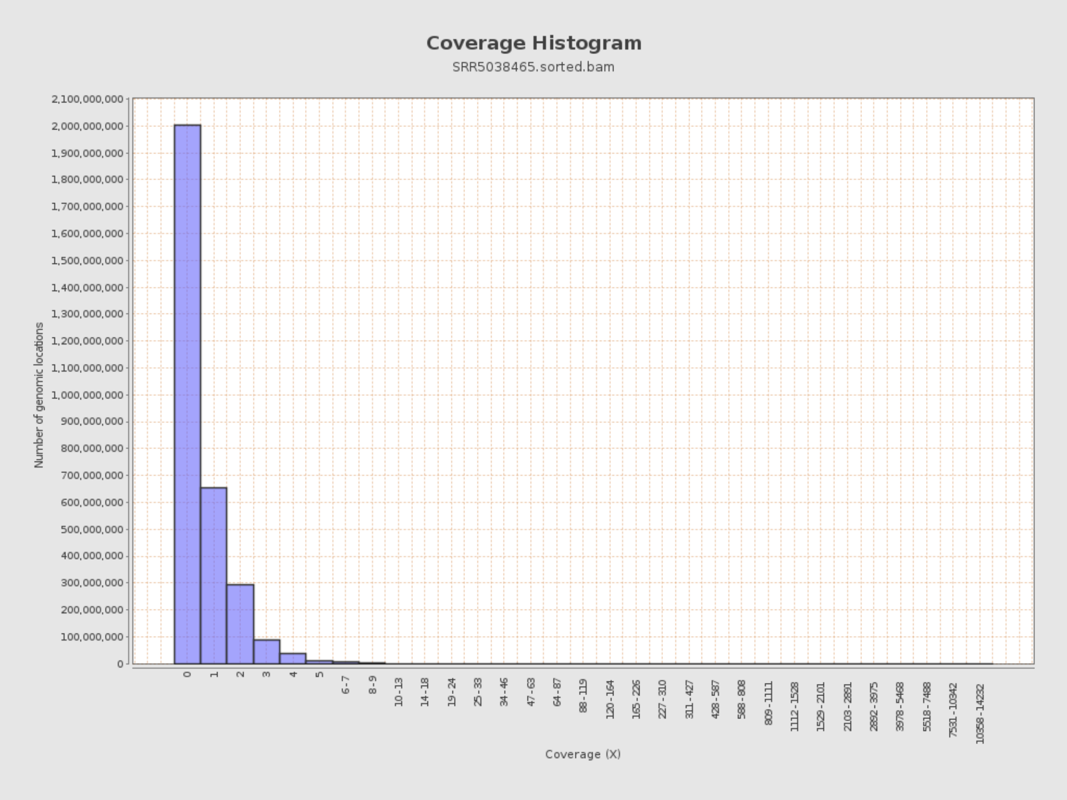
		bases	**coverage**	**deviation**
chr1	249250621	131190095	0.5263	14.5269
chr2	243199373	175140524	0.7202	4.8518
chr3	198022430	118374822	0.5978	0.9833
chr4	191154276	105266325	0.5507	4.1146
chr5	180915260	105338903	0.5823	1.0339
chr6	171115067	117101854	0.6843	5.1499
chr7	159138663	125285403	0.7873	4.6873
chr8	146364022	83827206	0.5727	4.0839
chr9	141213431	76003688	0.5382	6.7545
chr10	135534747	76268217	0.5627	9.2813
chr11	135006516	94818719	0.7023	3.5751
chr12	133851895	67901897	0.5073	0.9309
chr13	115169878	105642654	0.9173	1.2663
chr14	107349540	40506013	0.3773	0.8601
chr15	102531392	39558639	0.3858	0.7931
chr16	90354753	62639999	0.6933	3.9302
chr17	81195210	53519426	0.6591	3.0147
chr18	78077248	33786128	0.4327	7.011
chr19	59128983	37872194	0.6405	6.6459
chr20	63025520	57415003	0.911	1.8313
chr21	48129895	19574663	0.4067	2.5472
chr22	51304566	18062385	0.3521	2.0513
chrMT	16571	3735405	225.4182	28.3584
chrX	155270560	70895674	0.4566	1.2249

chrY	59373566	15729497	0.2649	5.0481

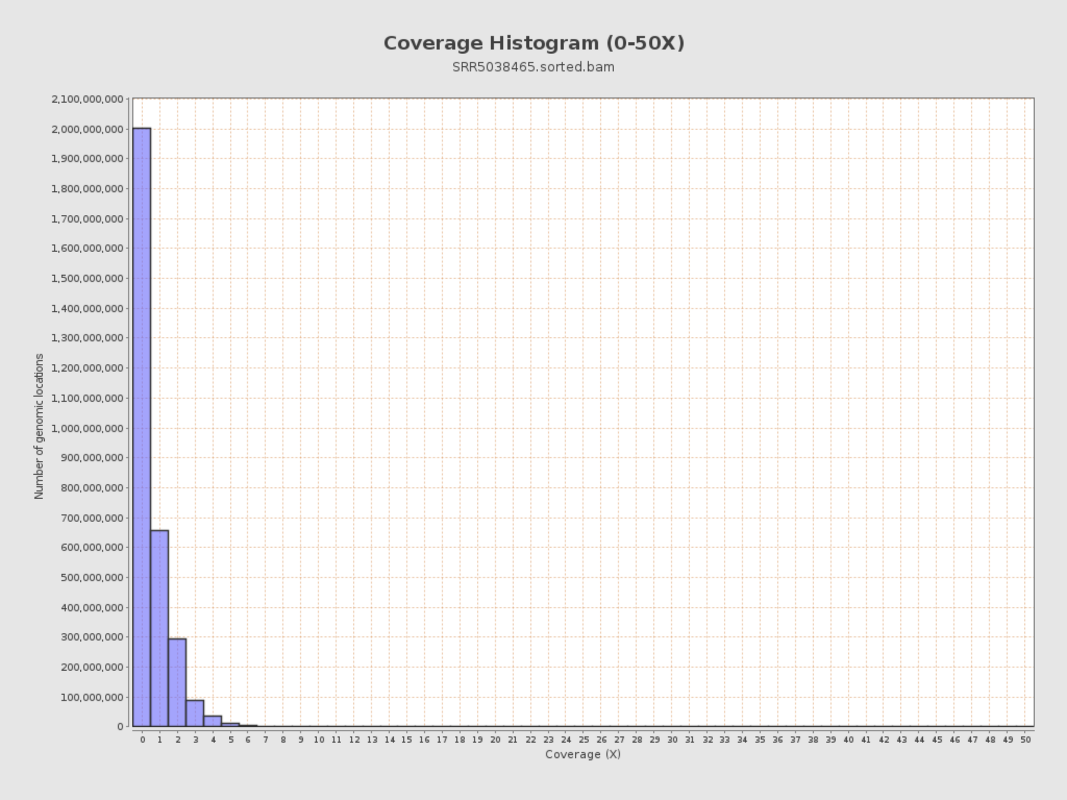
3. Results : Coverage across reference



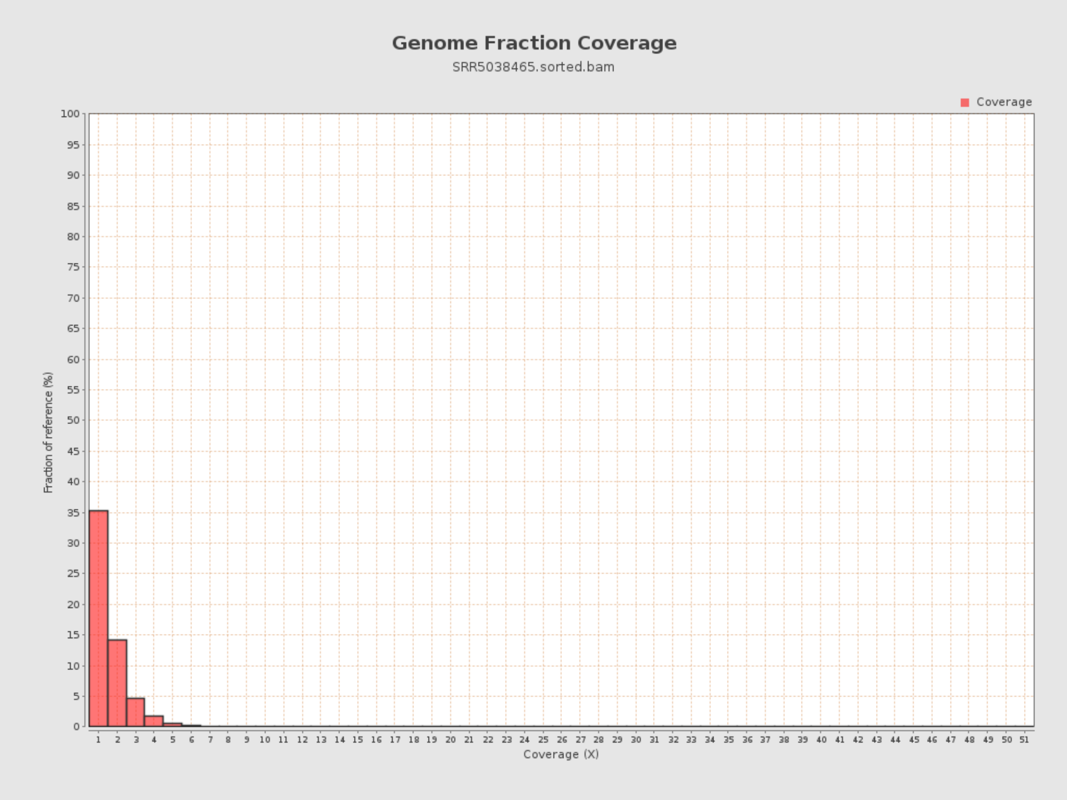
4. Results : Coverage Histogram



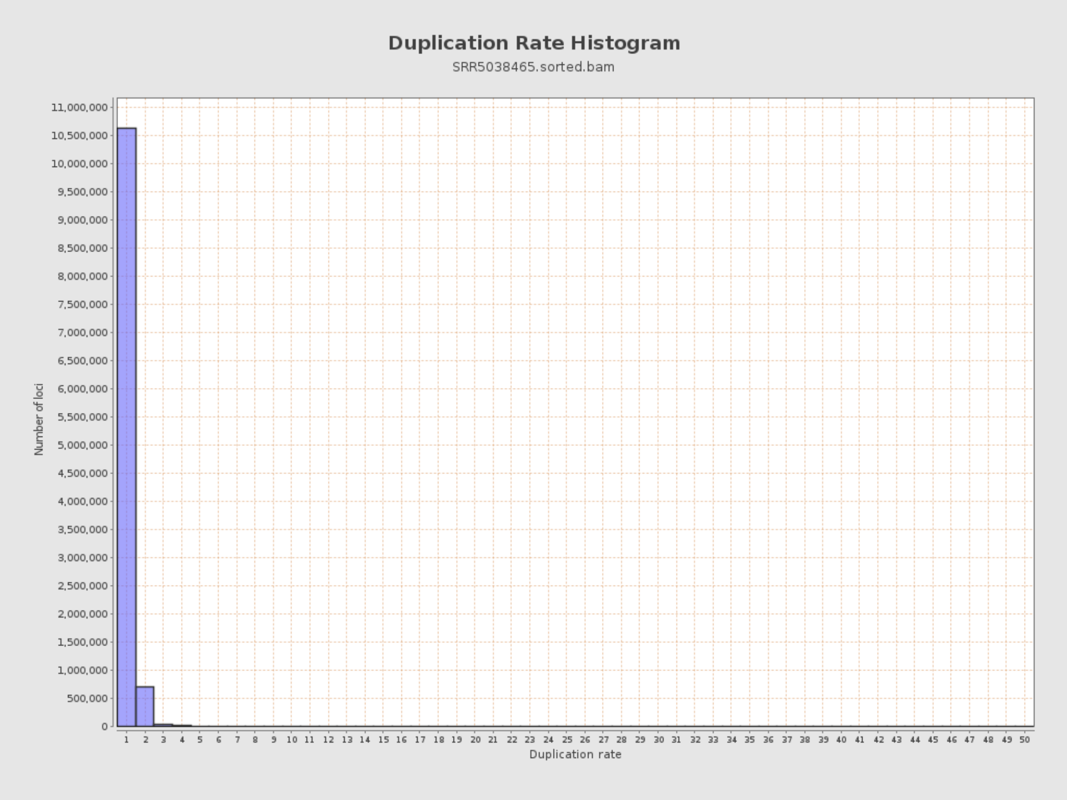
5. Results : Coverage Histogram (0-50X)



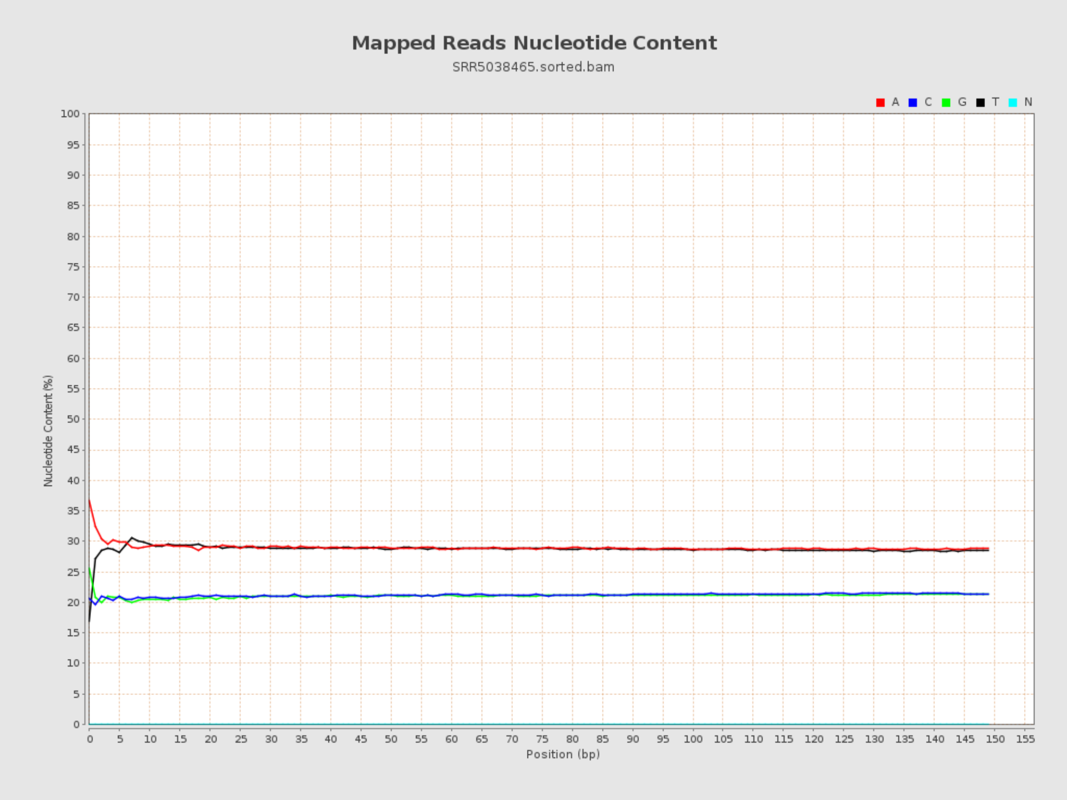
6. Results : Genome Fraction Coverage



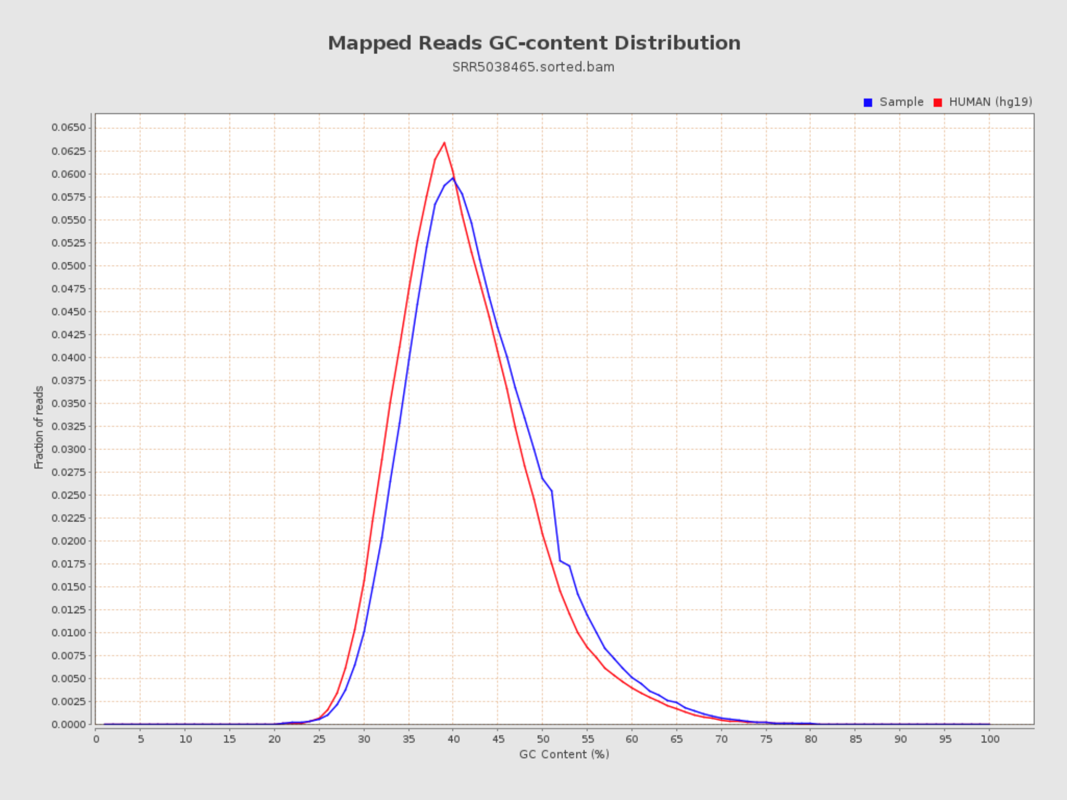
7. Results : Duplication Rate Histogram



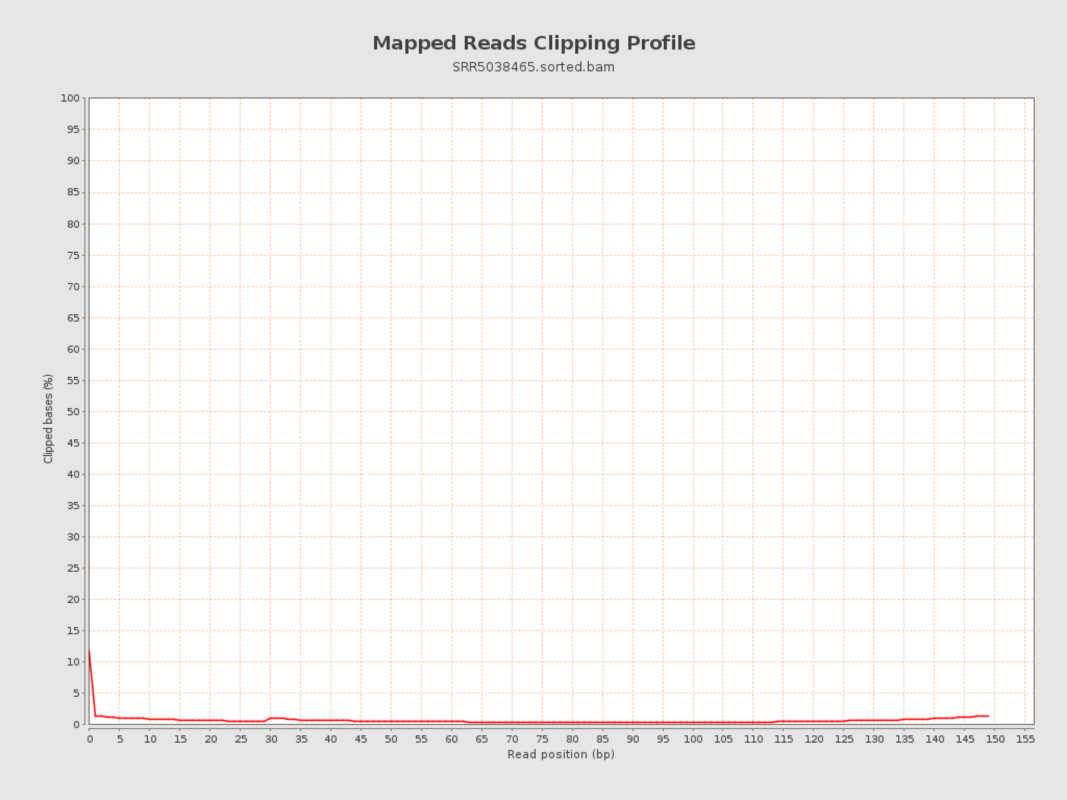
8. Results : Mapped Reads Nucleotide Content



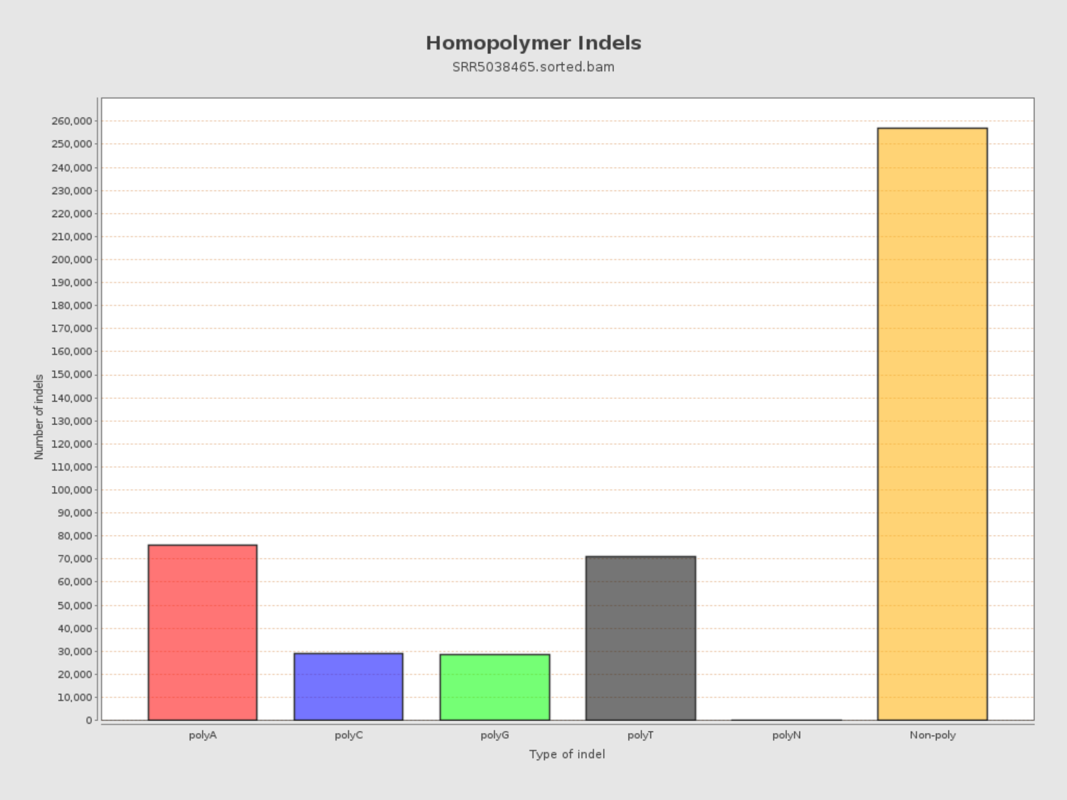
9. Results : Mapped Reads GC-content Distribution



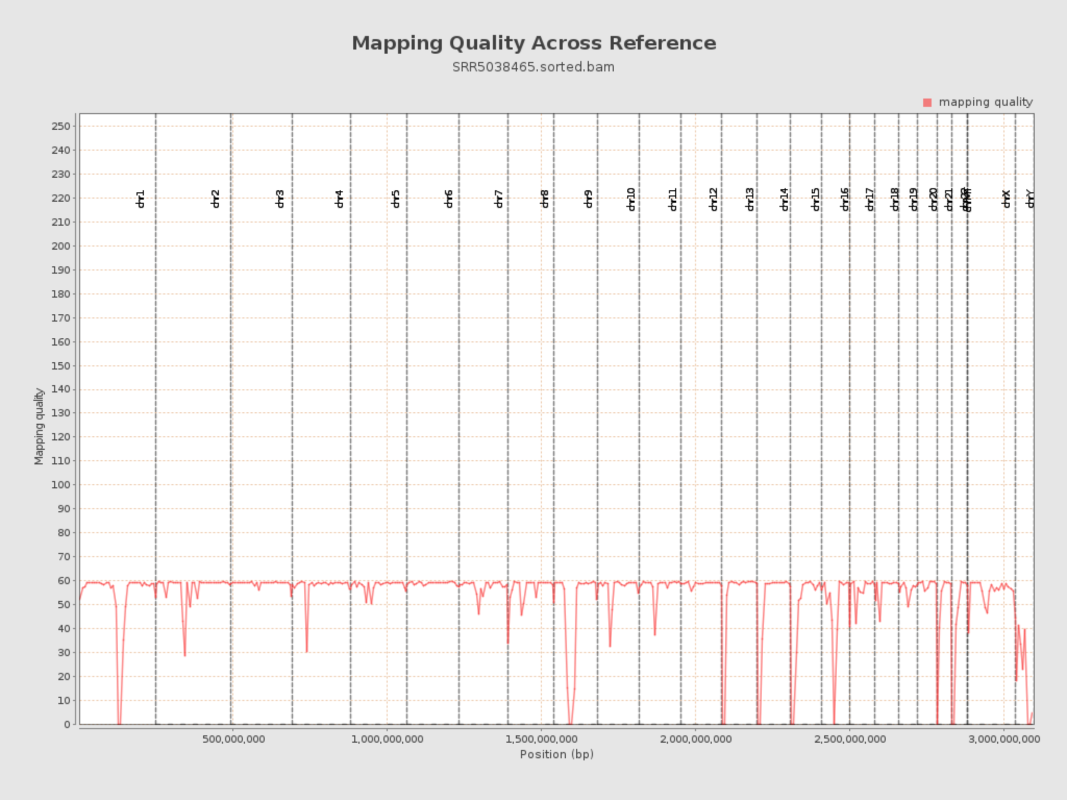
10. Results : Mapped Reads Clipping Profile



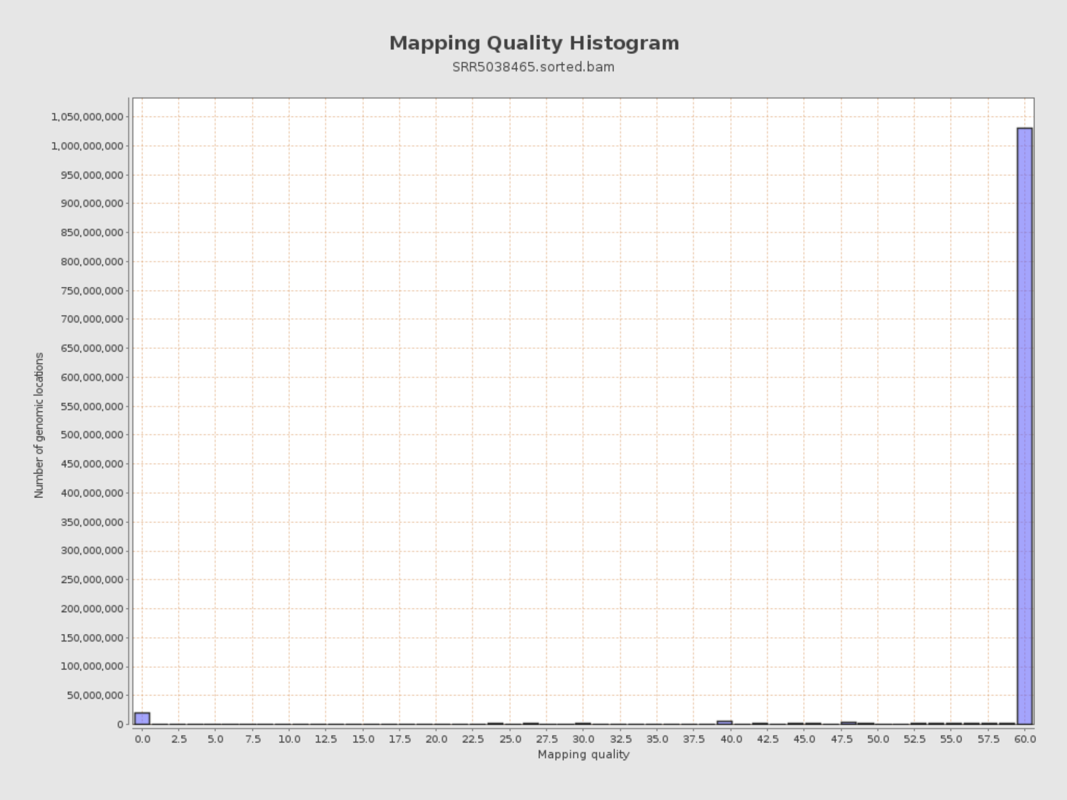
11. Results : Homopolymer Indels



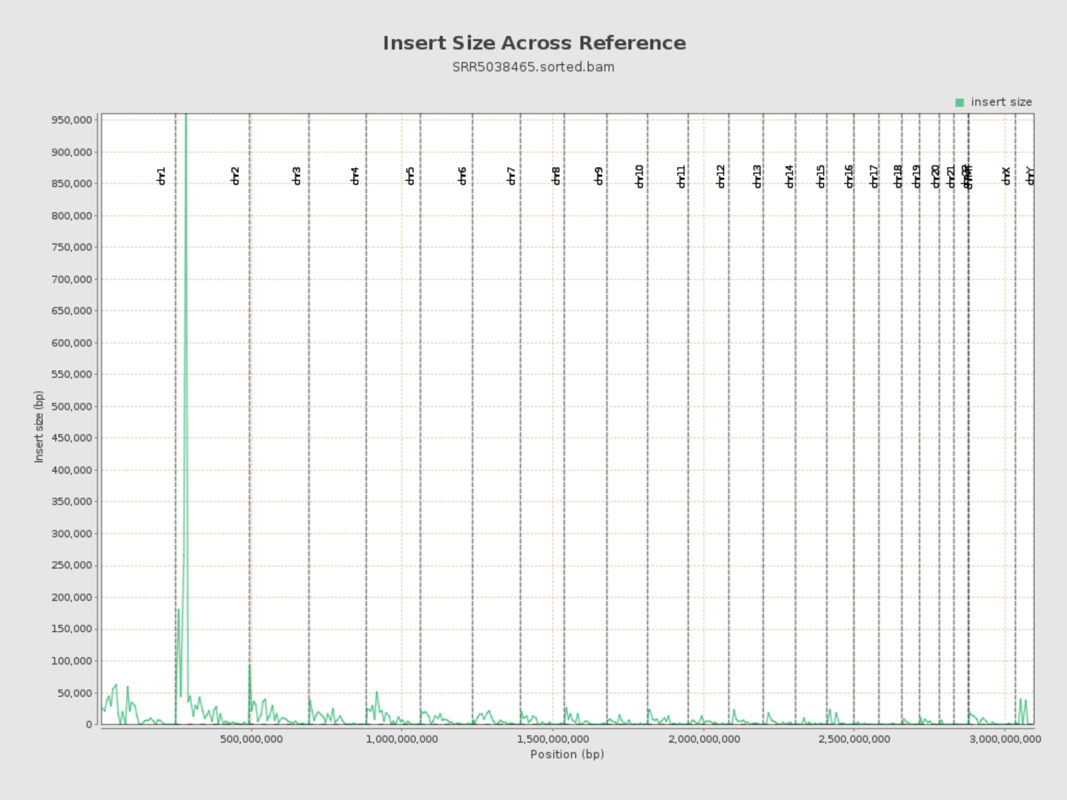
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram