Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 01:26:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038421.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_SRR5038421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038421_1.fastq.gz SRR5038421_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 01:26:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,728,918
Mapped reads	16,089,564 / 96.18%
Unmapped reads	639,354 / 3.82%
Mapped paired reads	16,089,564 / 96.18%
Mapped reads, first in pair	8,150,556 / 48.72%
Mapped reads, second in pair	7,939,008 / 47.46%
Mapped reads, both in pair	15,822,028 / 94.58%
Mapped reads, singletons	267,536 / 1.6%
Secondary alignments	0
Supplementary alignments	250,154 / 1.5%
Read min/max/mean length	30 / 150 / 150.75
Duplicated reads (estimated)	3,188,393 / 19.06%
Duplication rate	13.42%
Clipped reads	7,252,337 / 43.35%

2.2. ACGT Content

Number/percentage of A's	626,991,611 / 28.75%
Number/percentage of C's	431,848,818 / 19.8%
Number/percentage of T's	639,452,075 / 29.32%
Number/percentage of G's	482,199,691 / 22.11%
Number/percentage of N's	177,694 / 0.01%

GC Percentage	41.92%

2.3. Coverage

Mean	0.7049
Standard Deviation	10.8922

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	72,281.29
Standard Deviation	2,553,489.94
P25/Median/P75	199 / 249 / 313

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	29,169,547
Insertions	386,790
Mapped reads with at least one insertion	2.29%
Deletions	782,859
Mapped reads with at least one deletion	4.68%
Homopolymer indels	47.14%

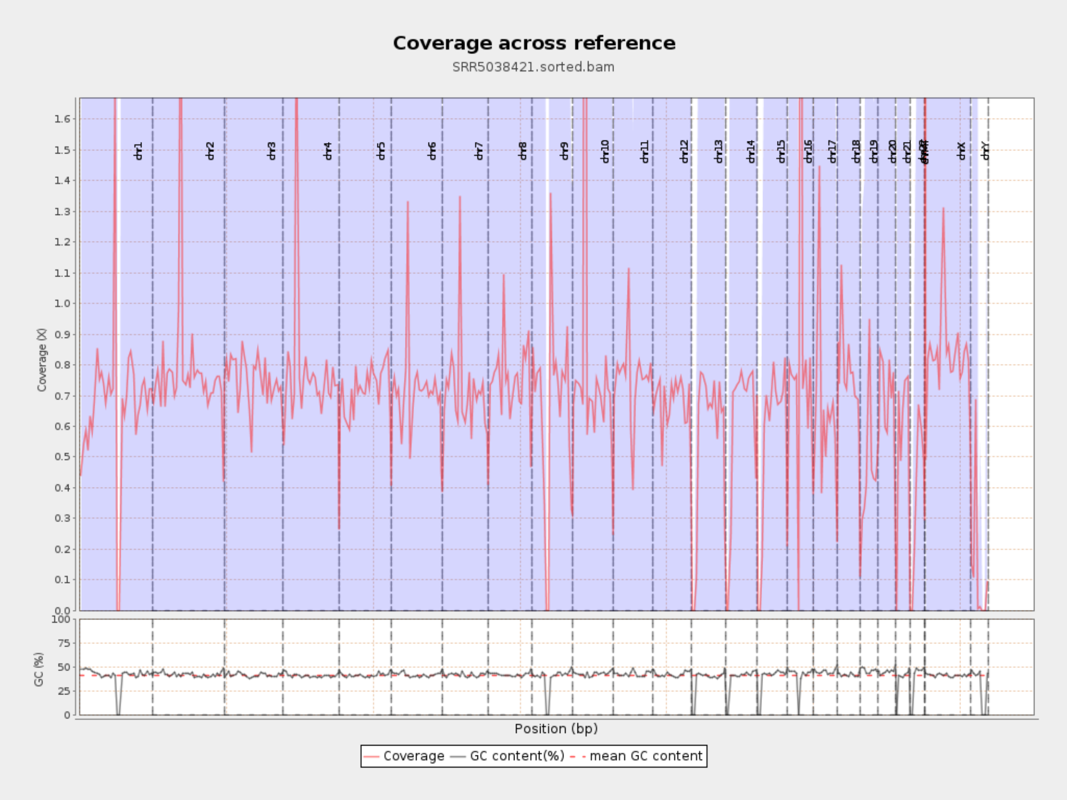
2.7. Chromosome stats

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

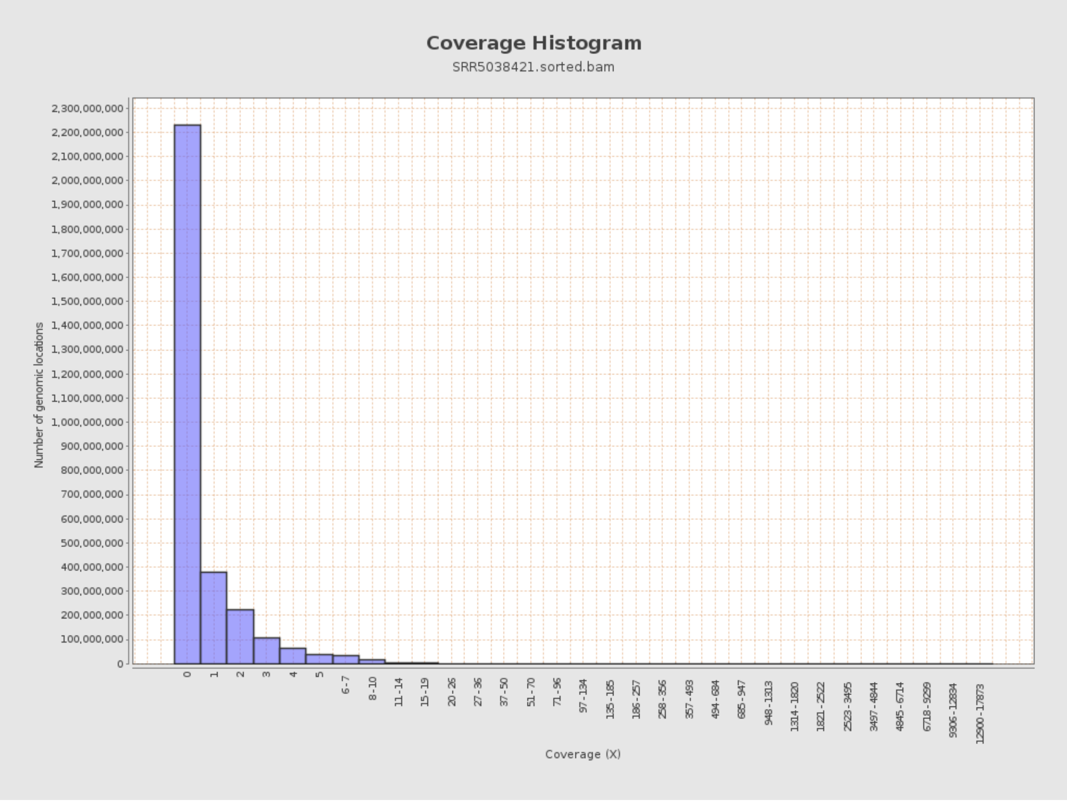
		bases	coverage	deviation
chr1	249250621	168518608	0.6761	17.5486
chr2	243199373	193665498	0.7963	9.6708
chr3	198022430	149088050	0.7529	1.6793
chr4	191154276	149522040	0.7822	8.4011
chr5	180915260	129772020	0.7173	1.5469
chr6	171115067	124296251	0.7264	6.7478
chr7	159138663	113375770	0.7124	11.2458
chr8	146364022	111106896	0.7591	3.5446
chr9	141213431	91350454	0.6469	16.423
chr10	135534747	120529250	0.8893	28.1459
chr11	135006516	100452418	0.7441	8.0798
chr12	133851895	90525333	0.6763	1.6094
chr13	115169878	65690288	0.5704	1.363
chr14	107349540	63488801	0.5914	1.5548
chr15	102531392	57742769	0.5632	1.3598
chr16	90354753	77699472	0.8599	17.1132
chr17	81195210	52696207	0.649	13.0538
chr18	78077248	61064386	0.7821	12.229
chr19	59128983	26808464	0.4534	8.0395
chr20	63025520	43599224	0.6918	2.6998
chr21	48129895	27865430	0.579	3.9667
chr22	51304566	18927998	0.3689	1.1515
chrMT	16571	6304292	380.4413	199.8761
chrX	155270560	130296827	0.8392	4.0448

chrY	59373566	7839474	0.132	9.6501

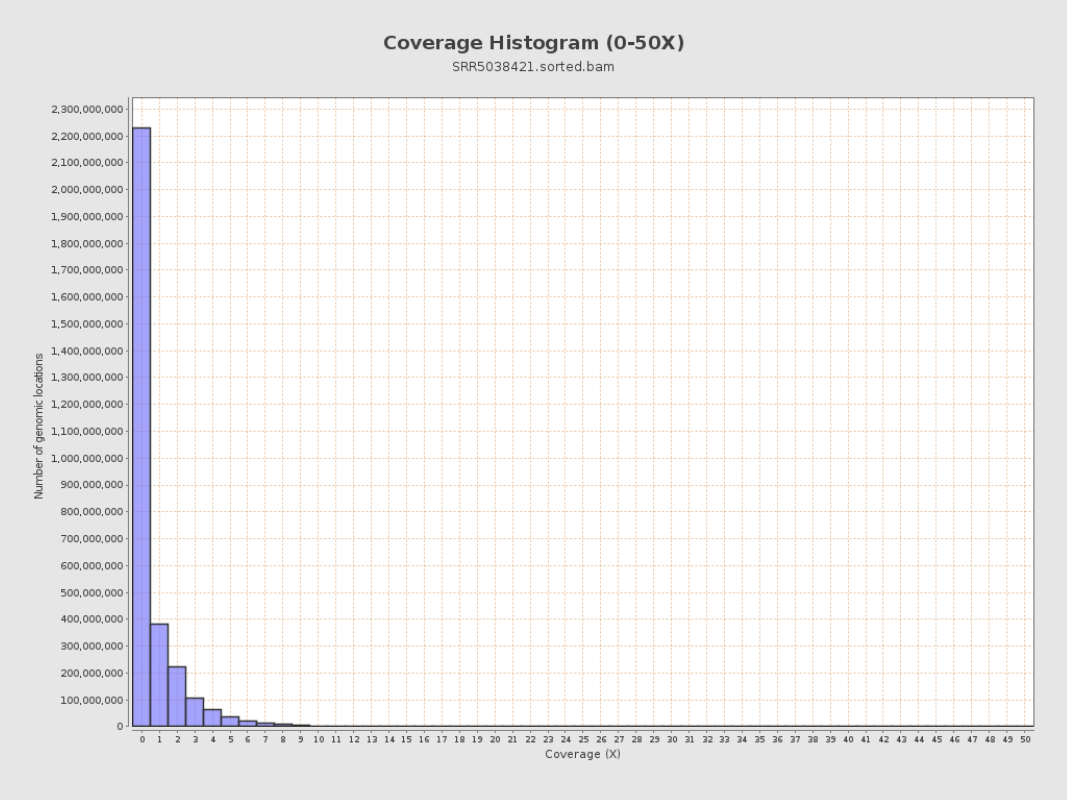
3. Results : Coverage across reference



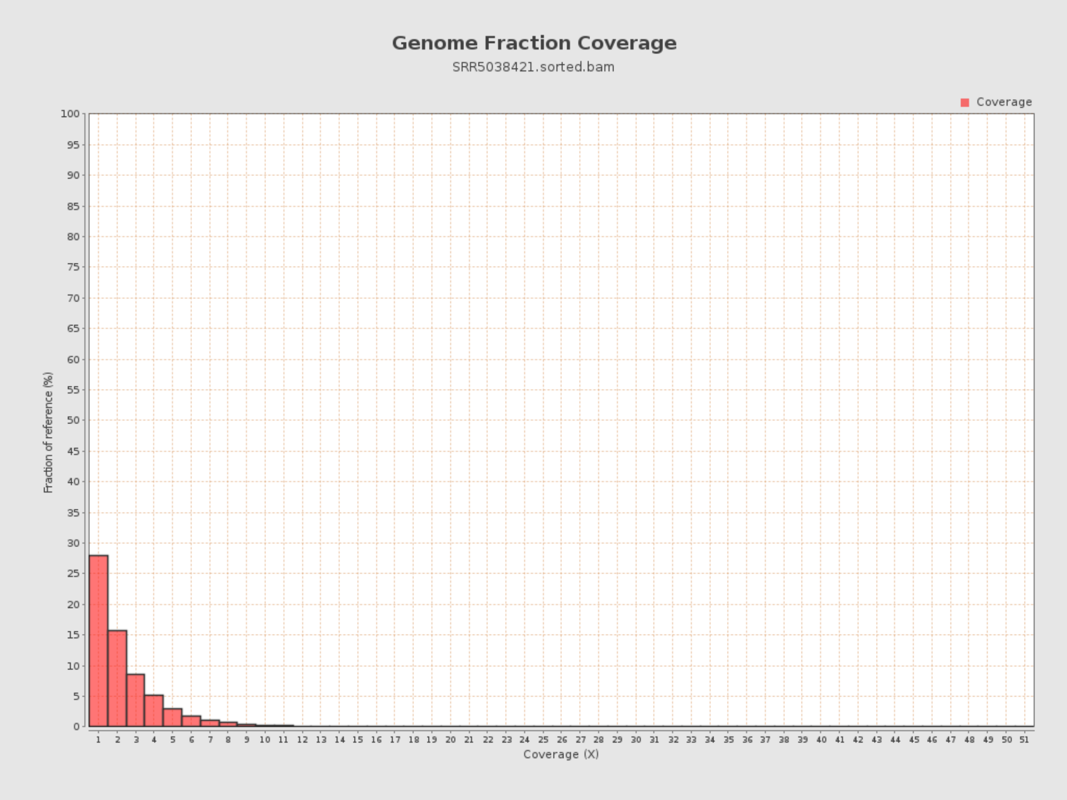
4. Results : Coverage Histogram



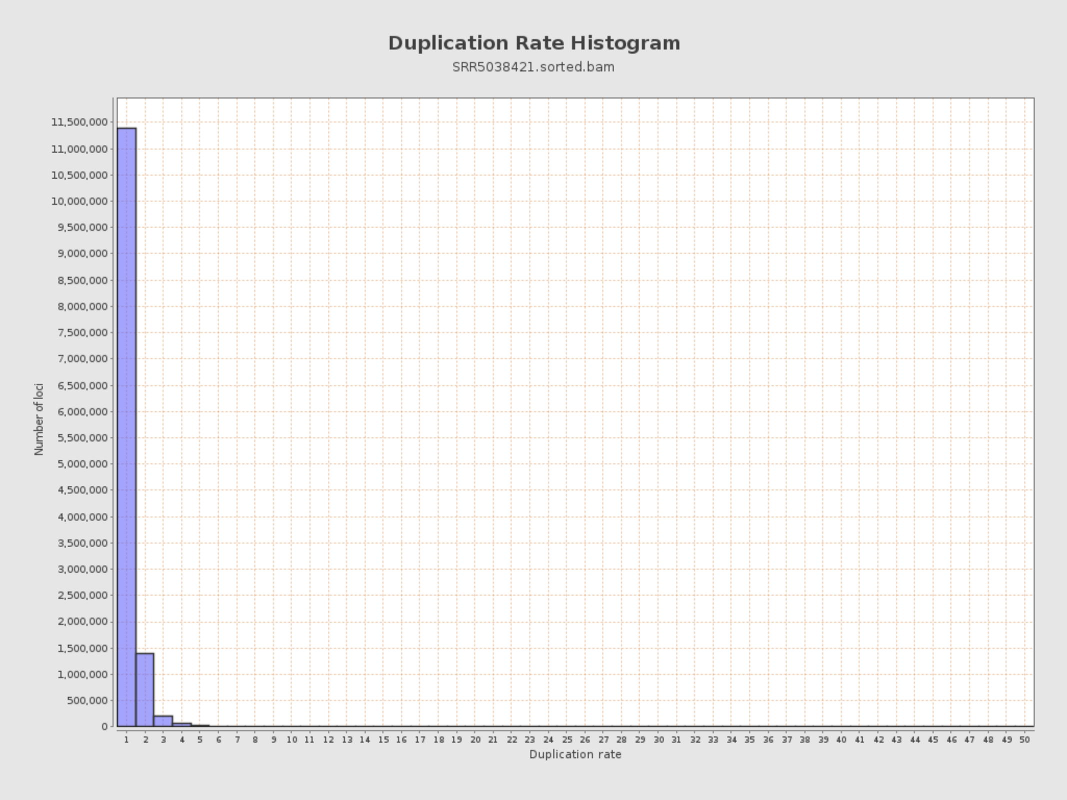
5. Results : Coverage Histogram (0-50X)



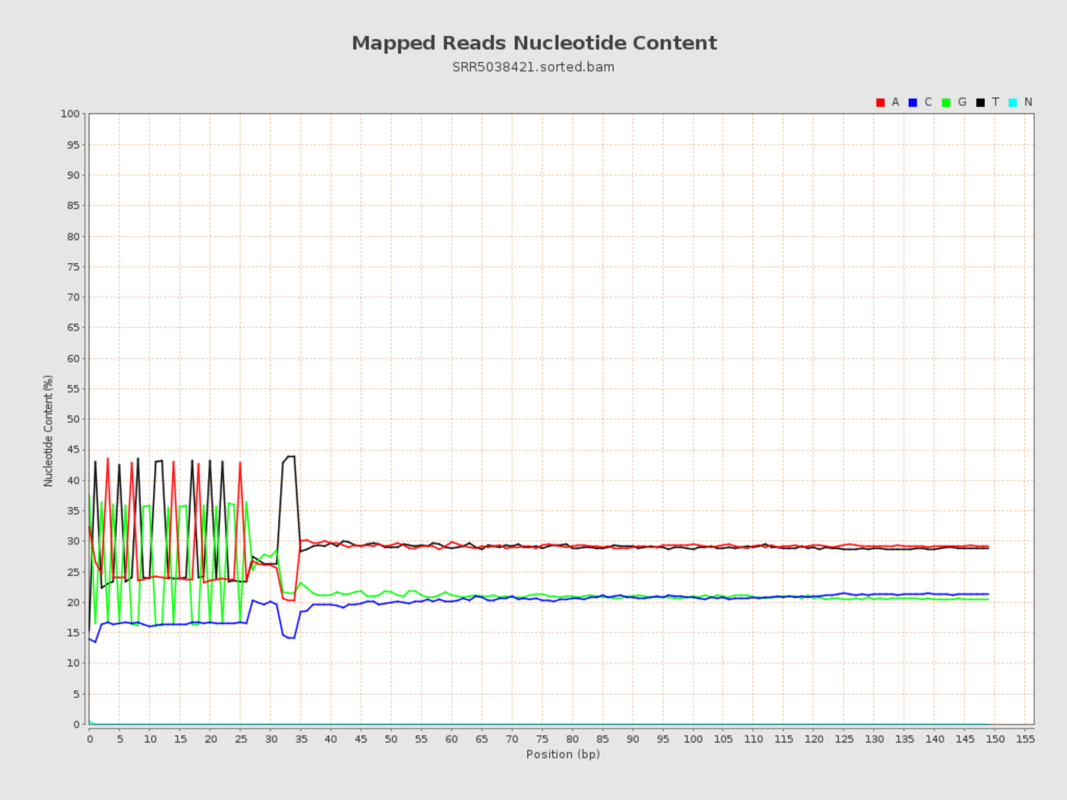
6. Results : Genome Fraction Coverage



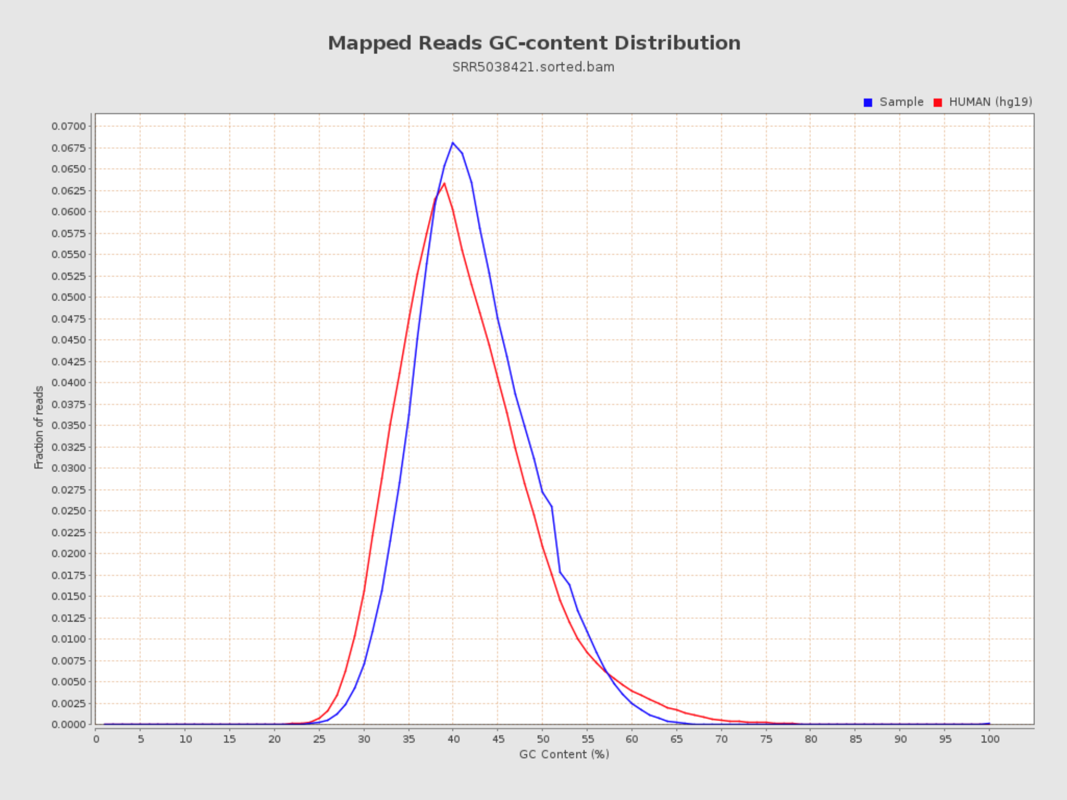
7. Results : Duplication Rate Histogram



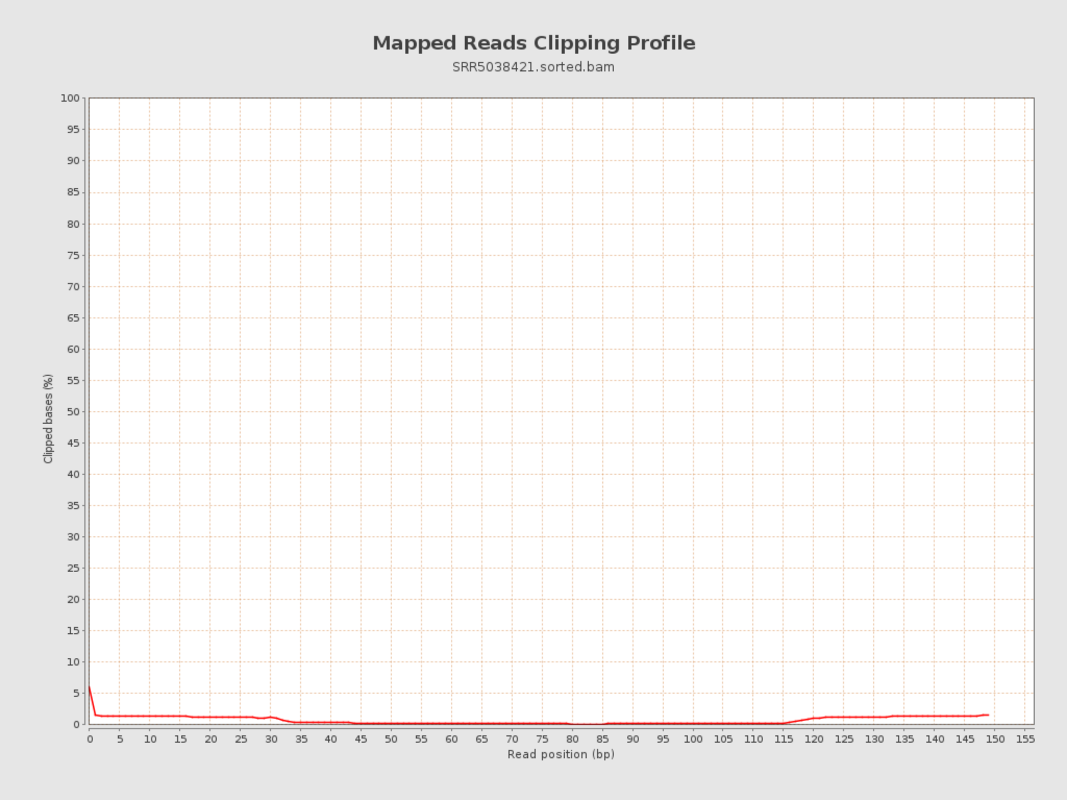
8. Results : Mapped Reads Nucleotide Content



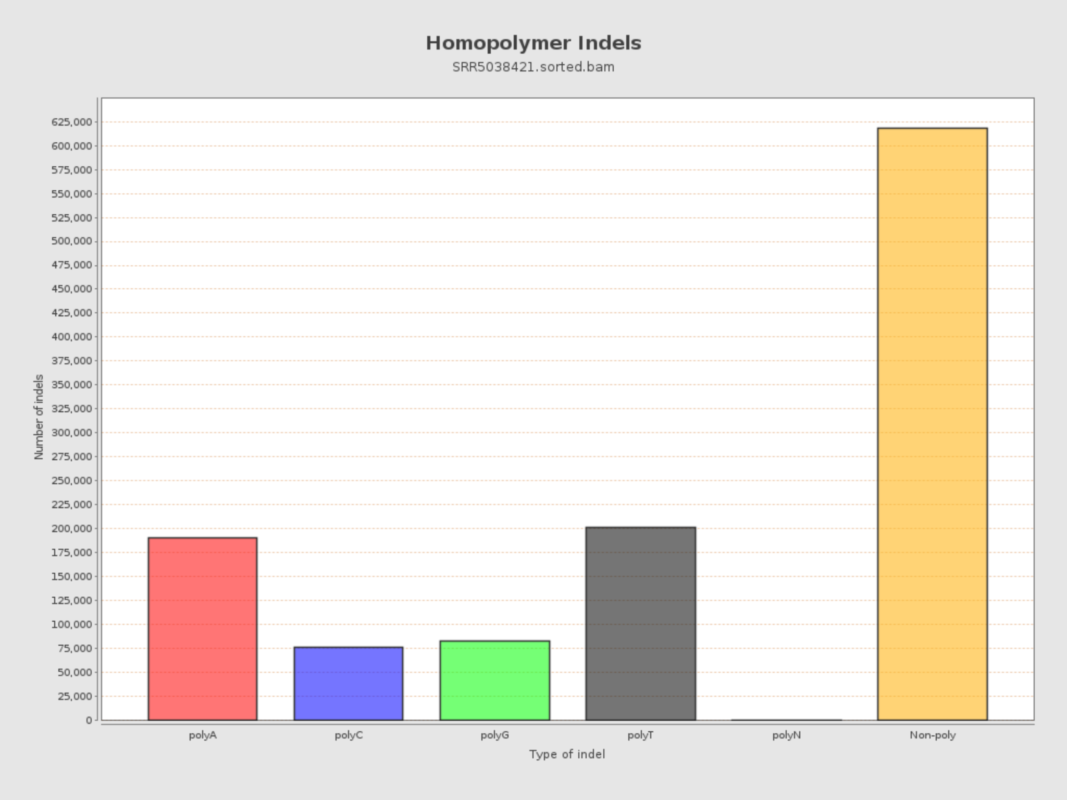
9. Results : Mapped Reads GC-content Distribution



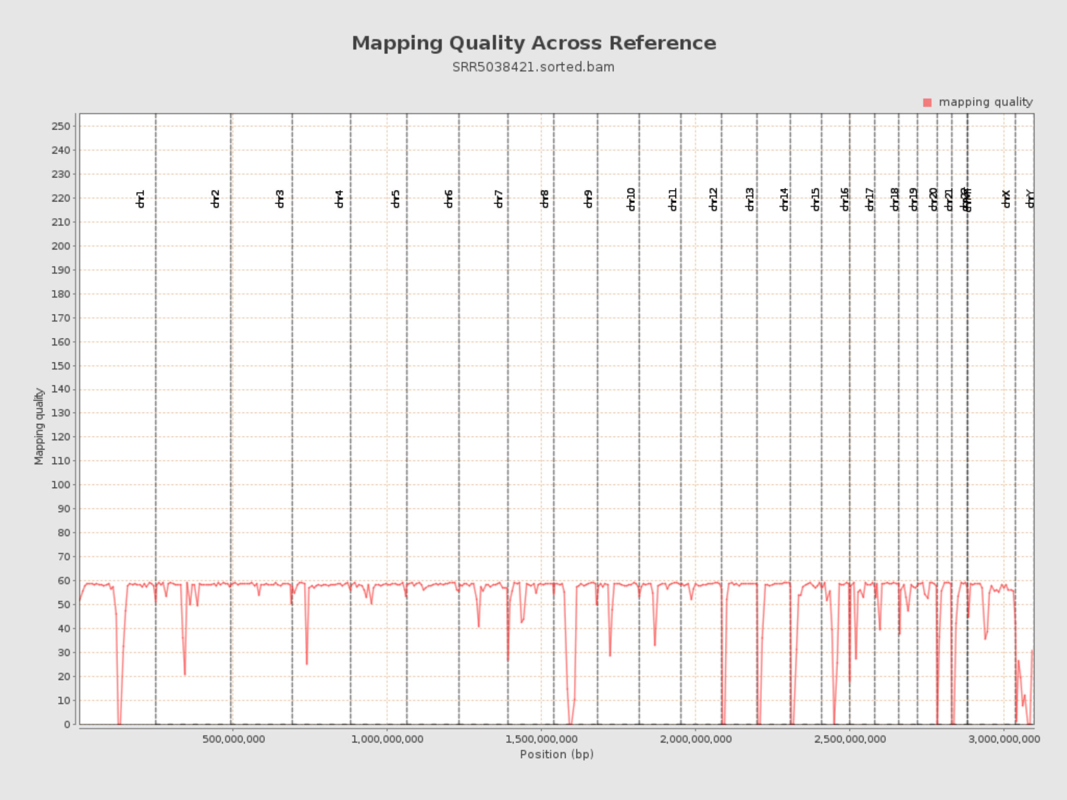
10. Results : Mapped Reads Clipping Profile



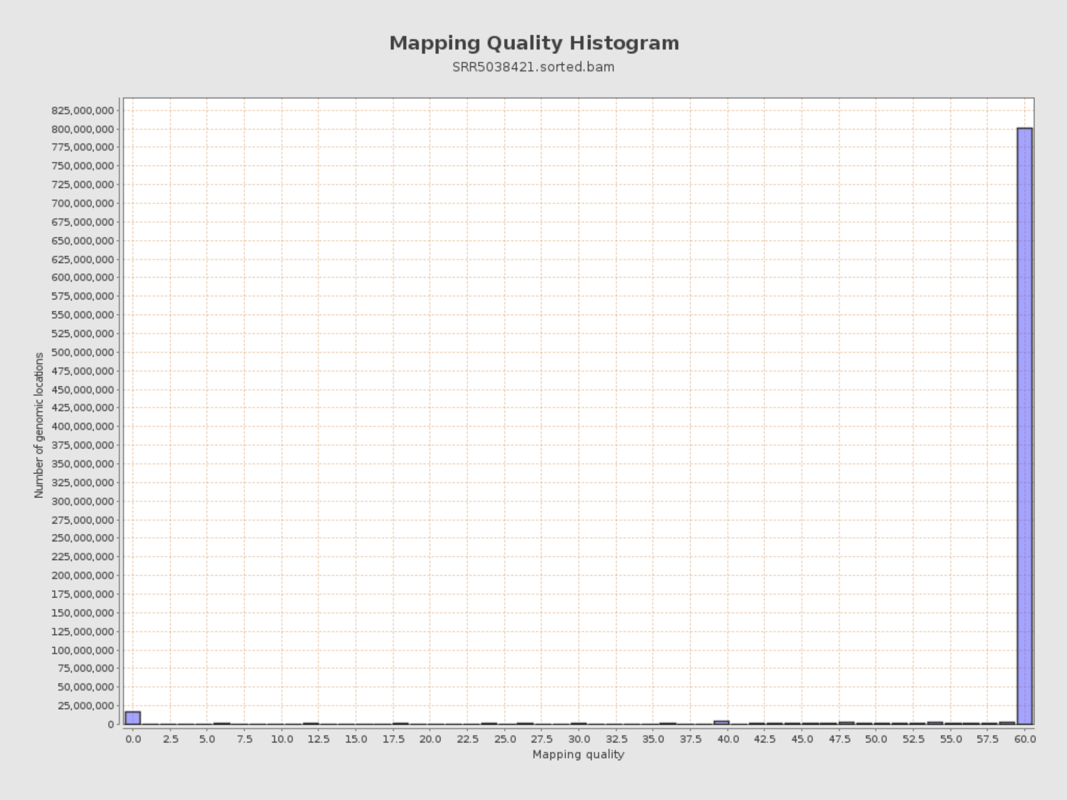
11. Results : Homopolymer Indels



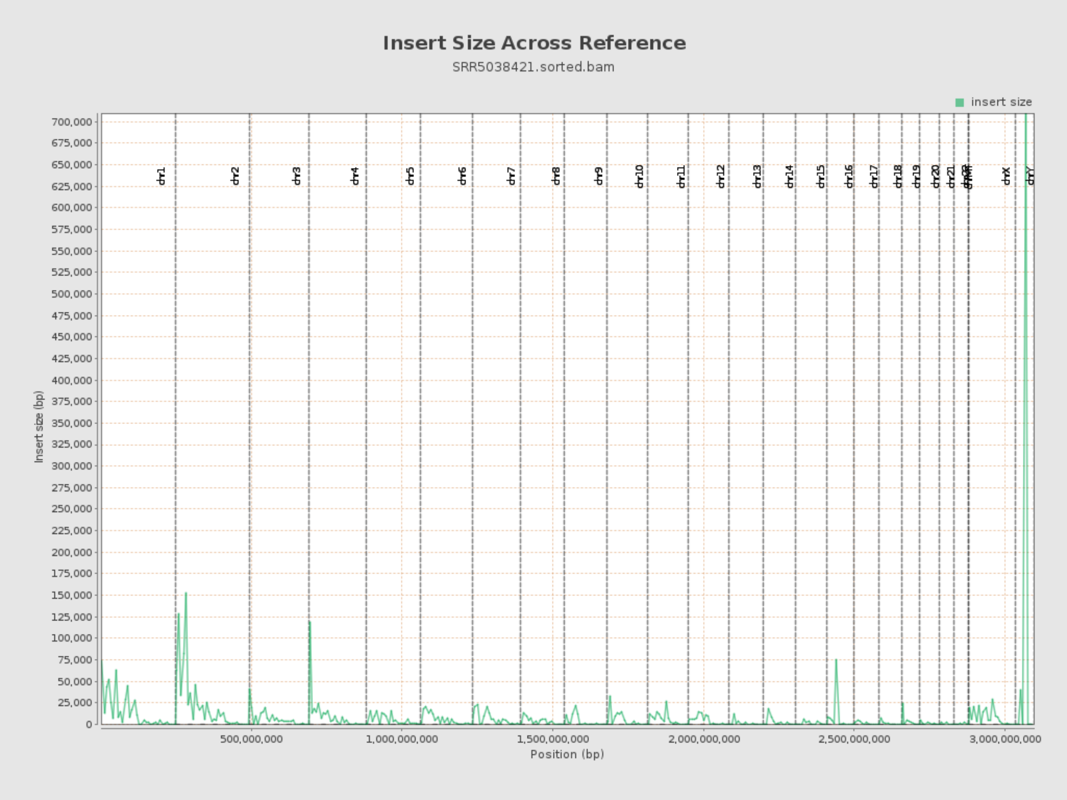
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram