Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 21:10:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038413.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_SRR5038413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038413_1.fastq.gz SRR5038413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 21:10:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,434,548
Mapped reads	77,983,729 / 99.43%
Unmapped reads	450,819 / 0.57%
Mapped paired reads	77,983,729 / 99.43%
Mapped reads, first in pair	39,134,592 / 49.89%
Mapped reads, second in pair	38,849,137 / 49.53%
Mapped reads, both in pair	77,656,418 / 99.01%
Mapped reads, singletons	327,311 / 0.42%
Secondary alignments	0
Supplementary alignments	187,407 / 0.24%
Read min/max/mean length	30 / 150 / 150.12
Duplicated reads (estimated)	31,963,442 / 40.75%
Duplication rate	38.28%
Clipped reads	6,105,782 / 7.78%

2.2. ACGT Content

Number/percentage of A's	2,845,889,718 / 24.61%
Number/percentage of C's	2,937,351,526 / 25.4%
Number/percentage of T's	2,862,829,572 / 24.75%
Number/percentage of G's	2,919,577,177 / 25.24%
Number/percentage of N's	439,468 / 0%

GC Percentage	50.64%

2.3. Coverage

Mean	3.7368
Standard Deviation	24.9346

2.4. Mapping Quality

Mean Mapping Quality	55.81

2.5. Insert size

Mean	22,738.28
Standard Deviation	1,571,271.58
P25/Median/P75	190 / 222 / 261

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	62,801,048
Insertions	598,549
Mapped reads with at least one insertion	0.73%
Deletions	699,630
Mapped reads with at least one deletion	0.87%
Homopolymer indels	45.76%

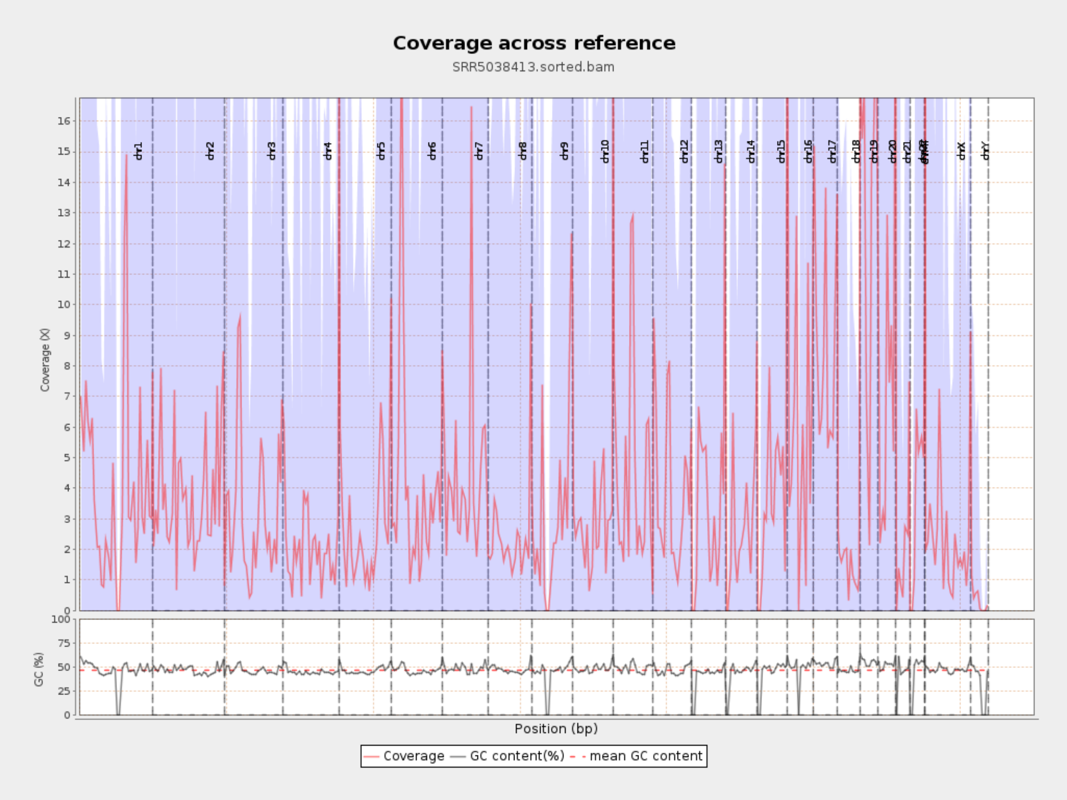
2.7. Chromosome stats

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

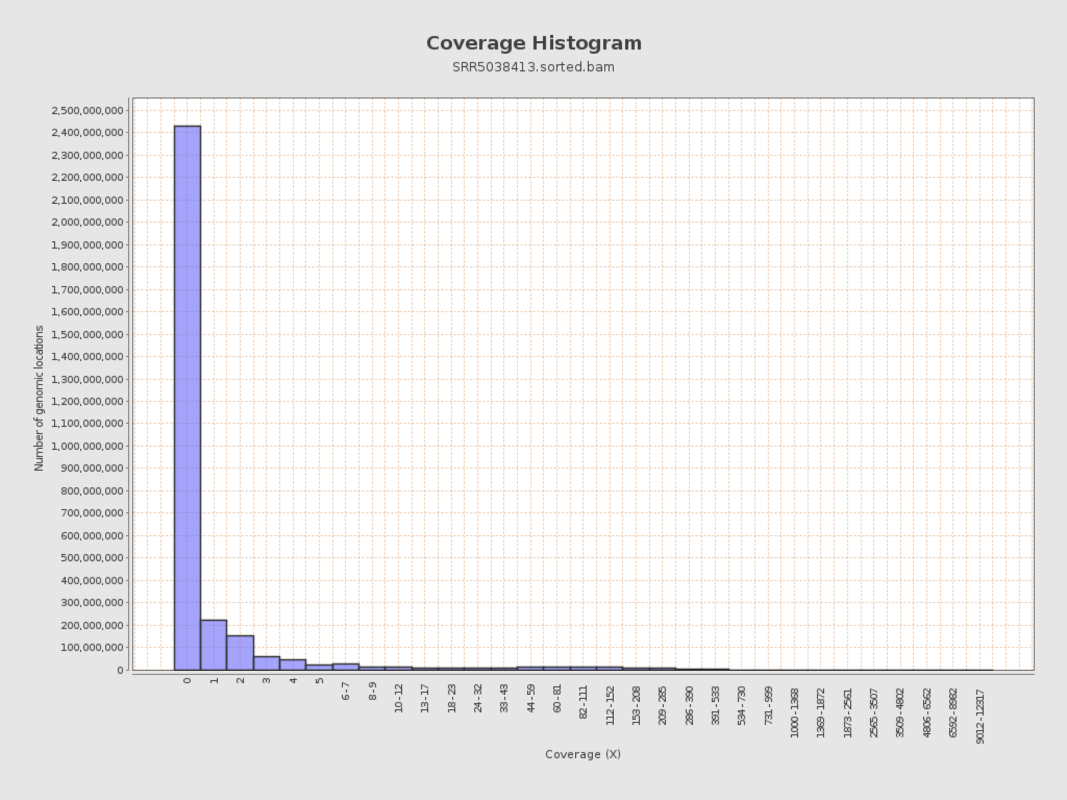
		bases	**coverage**	**deviation**
chr1	249250621	1006932913	4.0398	24.4672
chr2	243199373	919359828	3.7803	25.5164
chr3	198022430	636036504	3.2119	21.3266
chr4	191154276	389585920	2.0381	15.7257
chr5	180915260	518957736	2.8685	22.1461
chr6	171115067	684658318	4.0012	27.1482
chr7	159138663	725330271	4.5579	31.6278
chr8	146364022	358364939	2.4484	17.8682
chr9	141213431	455814344	3.2278	21.9479
chr10	135534747	364420744	2.6888	17.1023
chr11	135006516	668018734	4.948	29.4016
chr12	133851895	522607203	3.9044	22.4344
chr13	115169878	377168038	3.2749	27.8074
chr14	107349540	279522710	2.6039	16.9959
chr15	102531392	347382971	3.3881	20.3575
chr16	90354753	573649245	6.3489	34.1445
chr17	81195210	714753280	8.8029	38.759
chr18	78077248	112191319	1.4369	11.0101
chr19	59128983	790116722	13.3626	47.9165
chr20	63025520	450830662	7.1531	41.4993
chr21	48129895	97531500	2.0264	29.3021
chr22	51304566	202833082	3.9535	21.38
chrMT	16571	1126170	67.9603	25.4537
chrX	155270560	350295028	2.256	17.0277

chrY	59373566	20559012	0.3463	5.2112

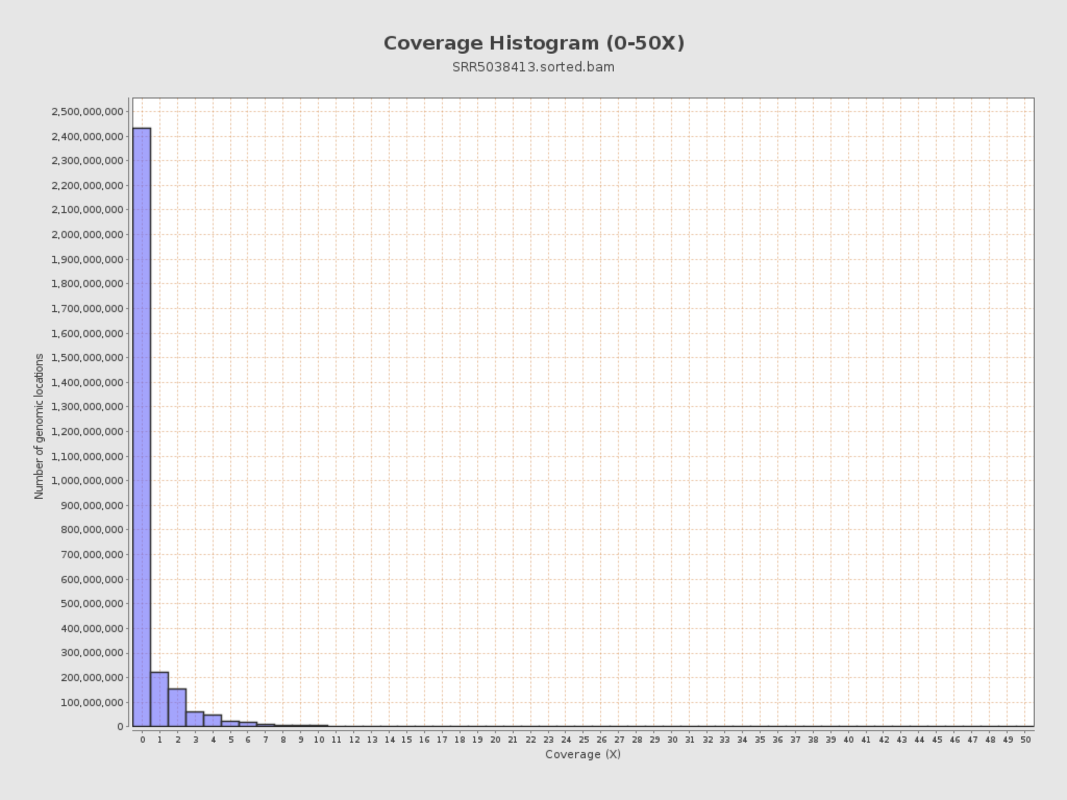
3. Results : Coverage across reference



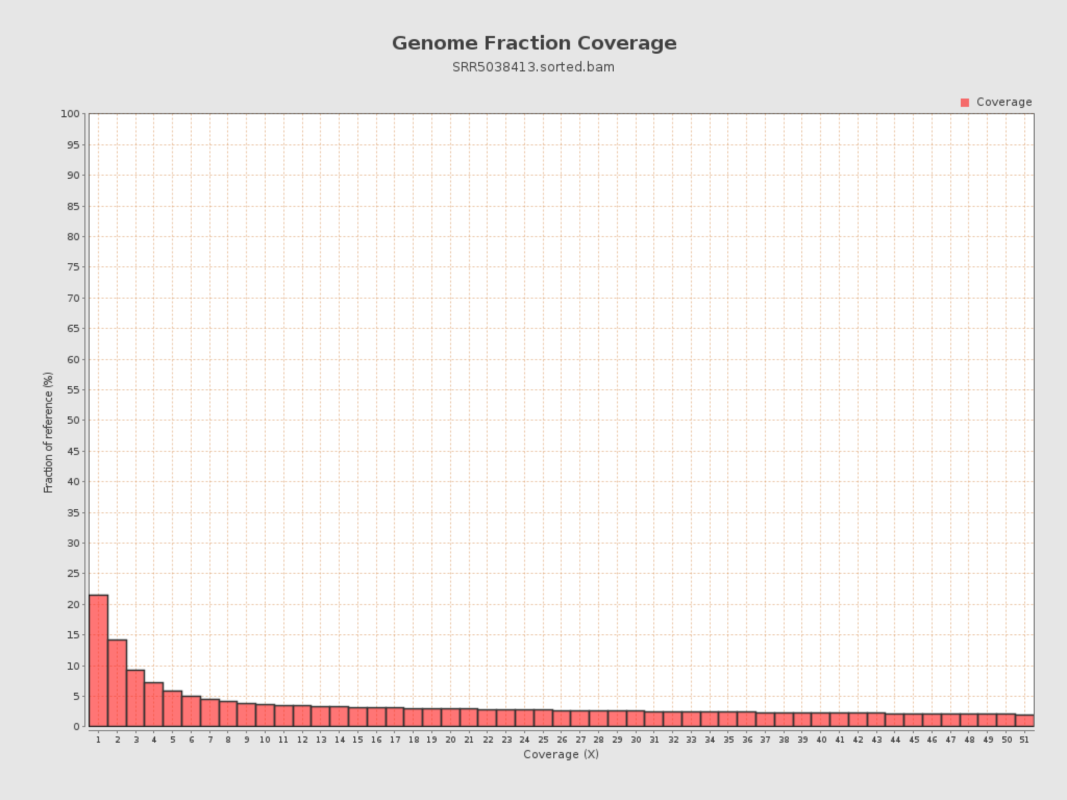
4. Results : Coverage Histogram



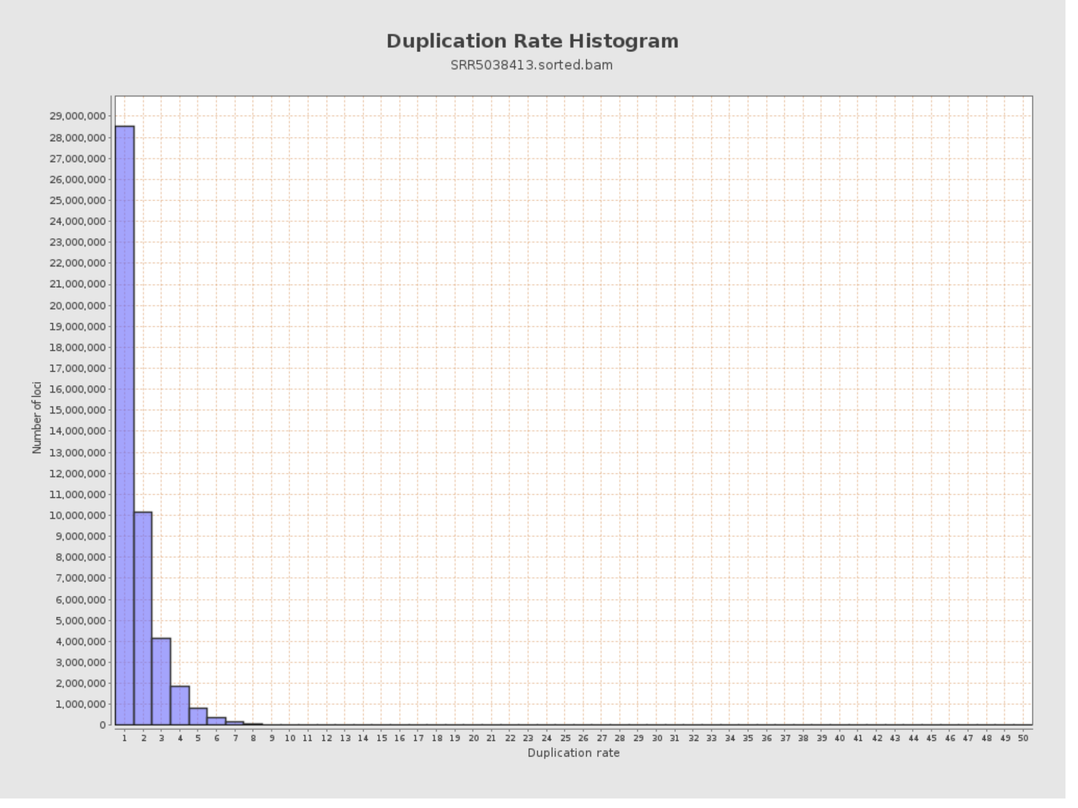
5. Results : Coverage Histogram (0-50X)



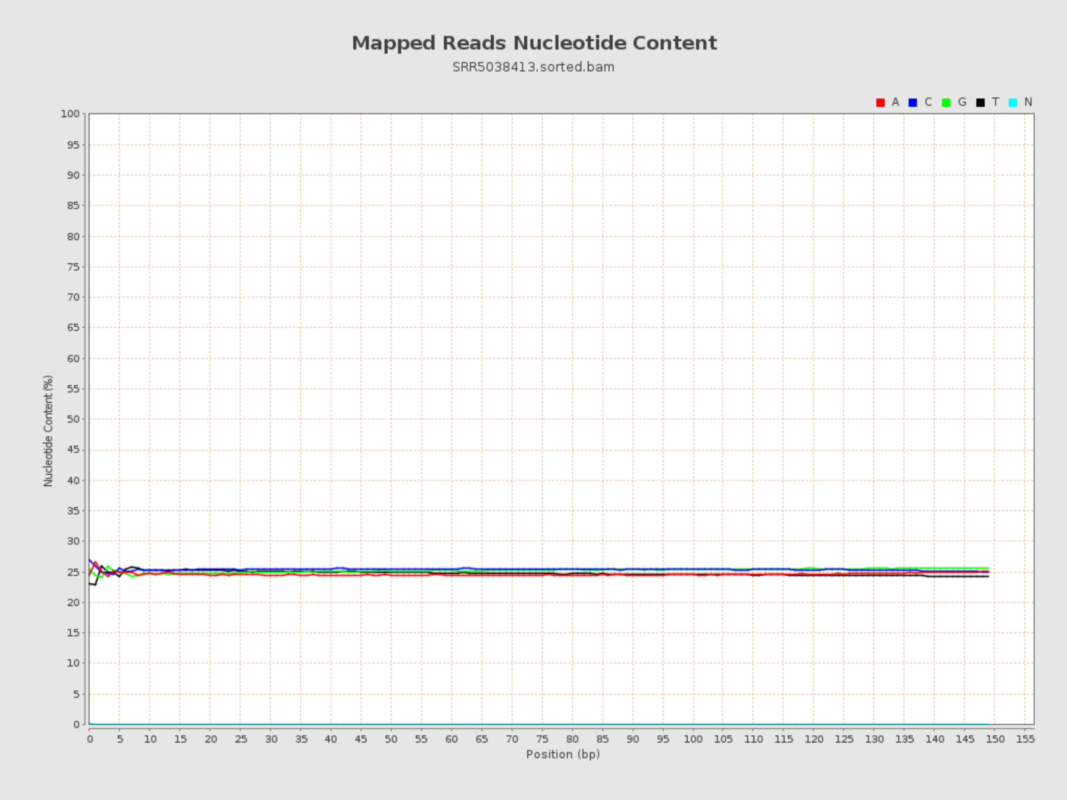
6. Results : Genome Fraction Coverage



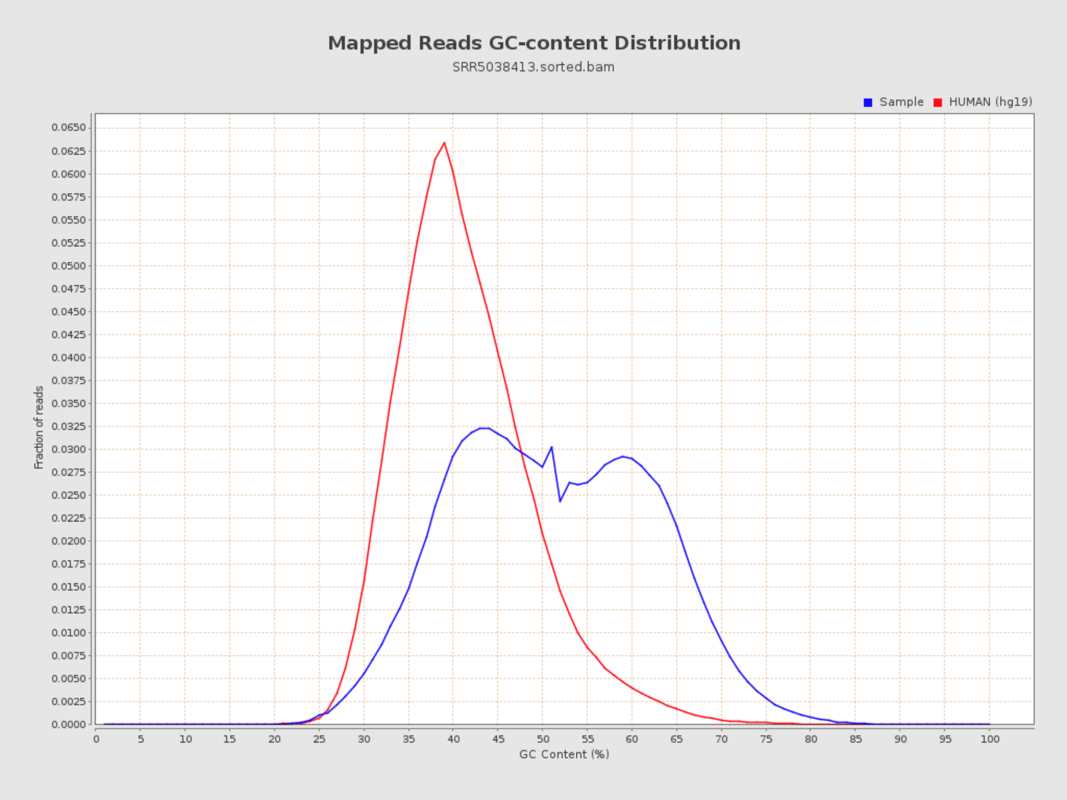
7. Results : Duplication Rate Histogram



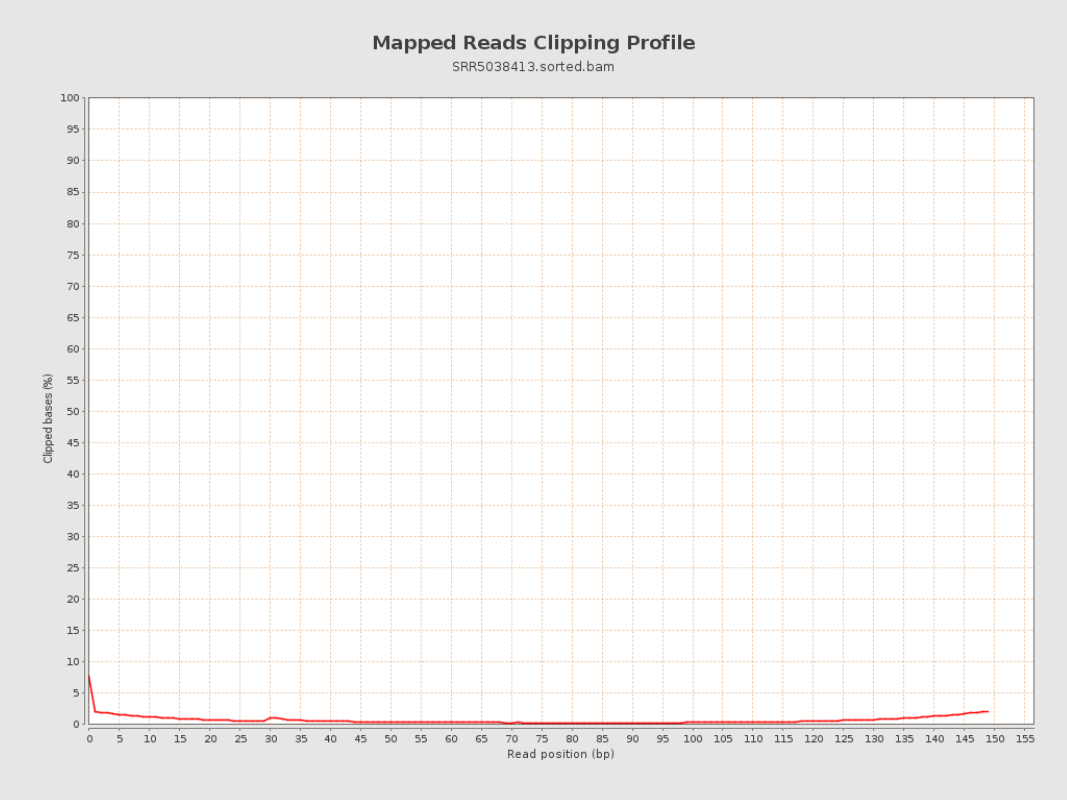
8. Results : Mapped Reads Nucleotide Content



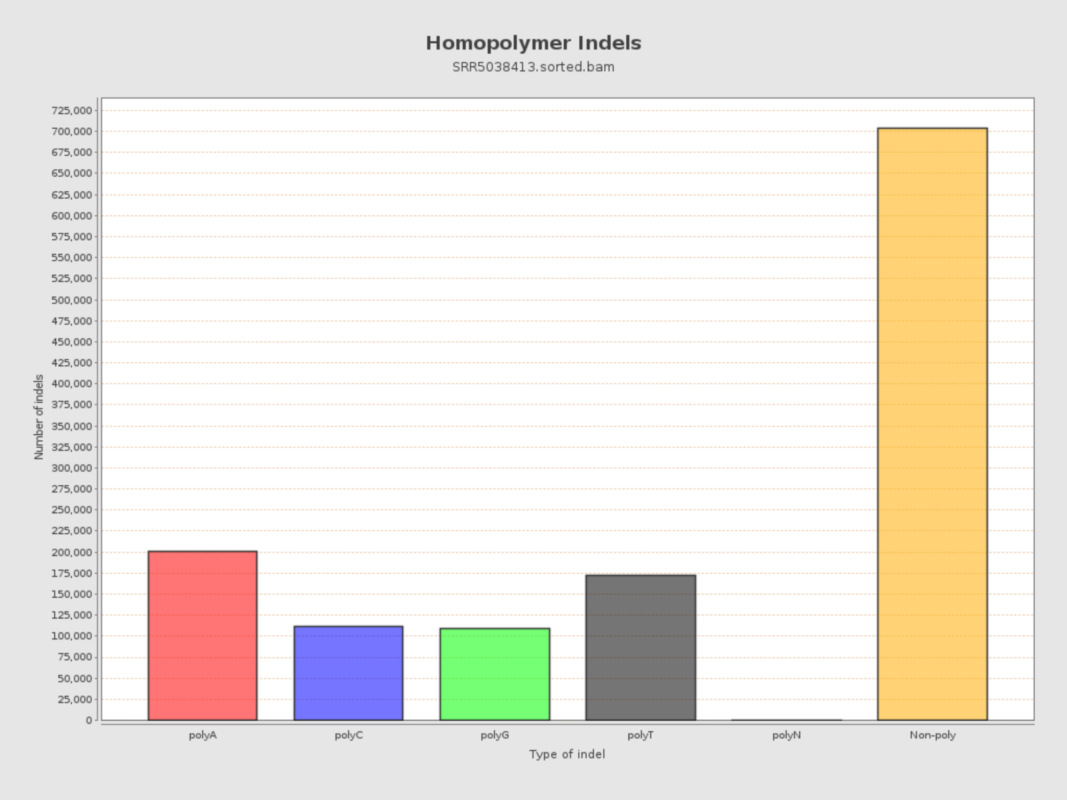
9. Results : Mapped Reads GC-content Distribution



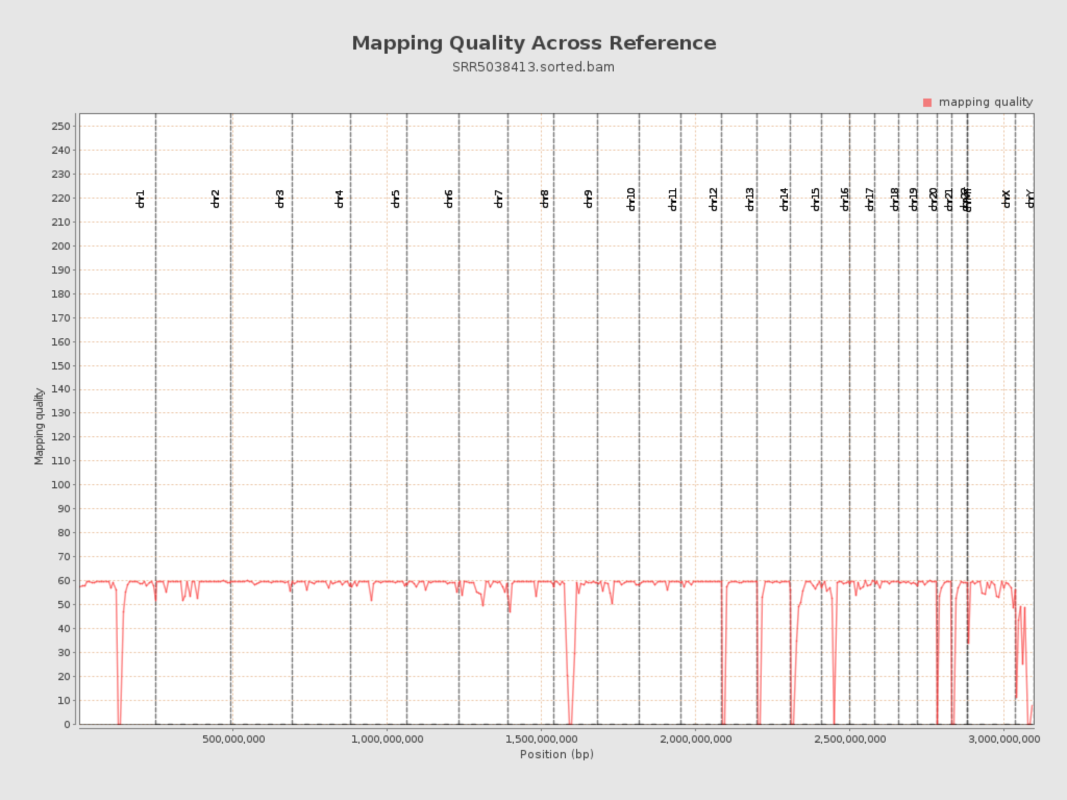
10. Results : Mapped Reads Clipping Profile



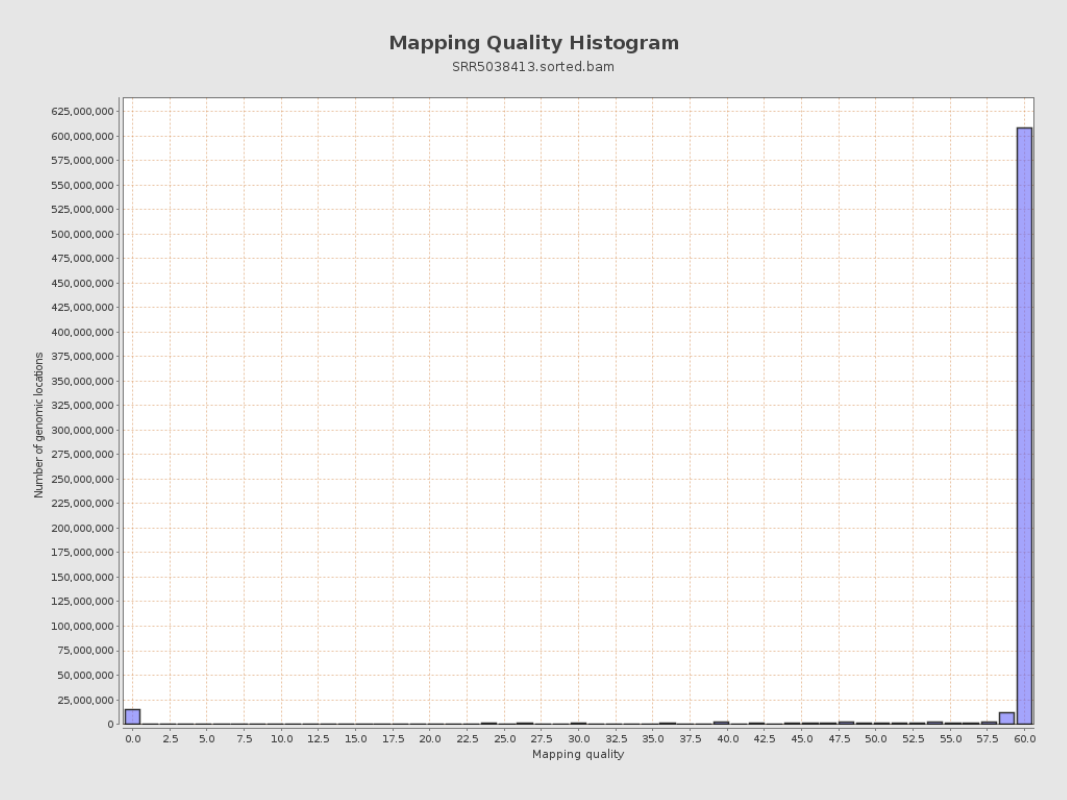
11. Results : Homopolymer Indels



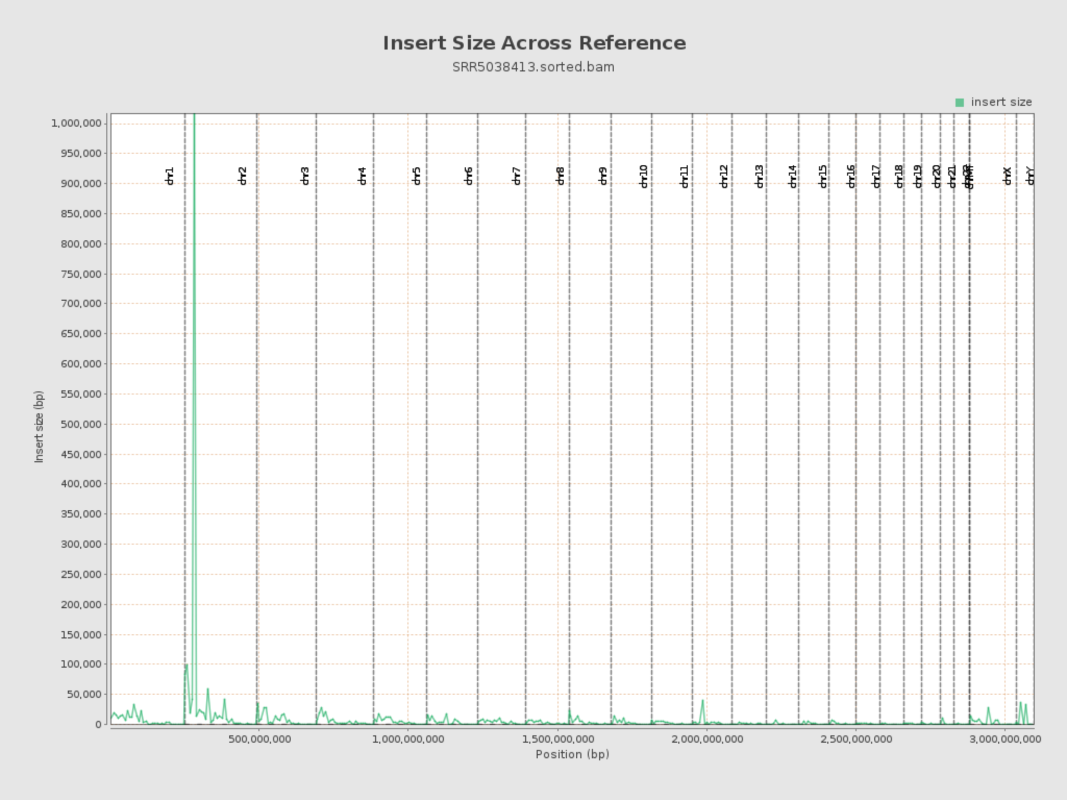
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram