Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 05:30:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038479.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_SRR5038479 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038479_1.fastq.gz SRR5038479_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 05:30:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038479.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,953,774
Mapped reads	20,862,607 / 95.03%
Unmapped reads	1,091,167 / 4.97%
Mapped paired reads	20,862,607 / 95.03%
Mapped reads, first in pair	10,570,040 / 48.15%
Mapped reads, second in pair	10,292,567 / 46.88%
Mapped reads, both in pair	20,490,786 / 93.34%
Mapped reads, singletons	371,821 / 1.69%
Secondary alignments	0
Supplementary alignments	317,205 / 1.44%
Read min/max/mean length	30 / 150 / 150.73
Duplicated reads (estimated)	5,083,930 / 23.16%
Duplication rate	17.1%
Clipped reads	10,299,206 / 46.91%

2.2. ACGT Content

Number/percentage of A's	785,012,620 / 28.06%
Number/percentage of C's	569,401,222 / 20.35%
Number/percentage of T's	798,465,515 / 28.54%
Number/percentage of G's	644,317,728 / 23.03%
Number/percentage of N's	223,064 / 0.01%

GC Percentage	43.39%

2.3. Coverage

Mean	0.9043
Standard Deviation	11.7031

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	74,366.6
Standard Deviation	2,657,563.23
P25/Median/P75	187 / 235 / 296

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	35,673,476
Insertions	479,783
Mapped reads with at least one insertion	2.19%
Deletions	971,989
Mapped reads with at least one deletion	4.5%
Homopolymer indels	47.28%

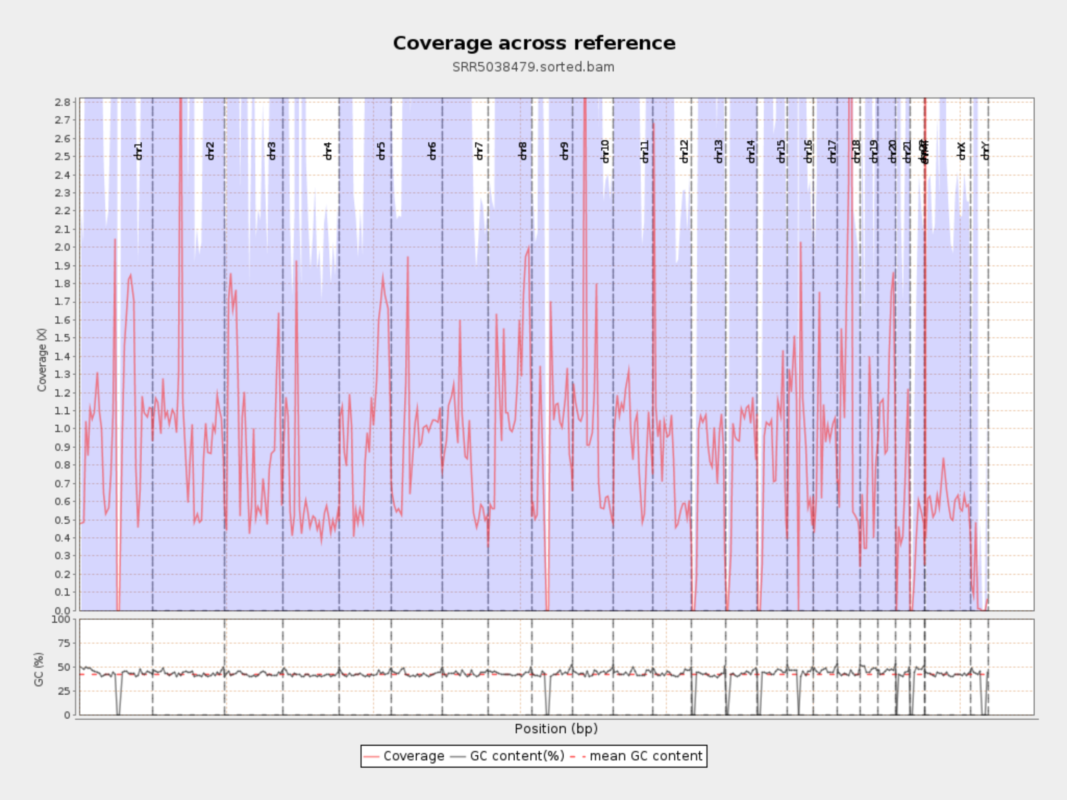
2.7. Chromosome stats

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

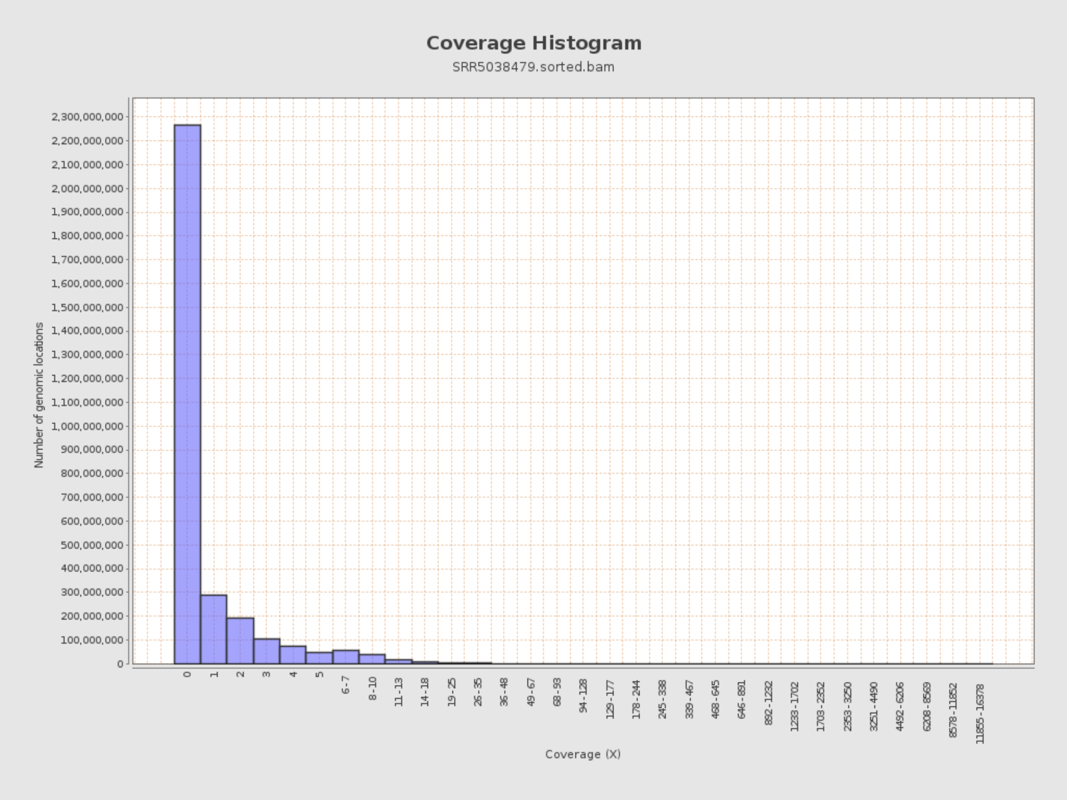
		bases	coverage	deviation
chr1	249250621	249743289	1.002	16.9152
chr2	243199373	250672260	1.0307	14.6411
chr3	198022430	189876324	0.9589	2.3336
chr4	191154276	118889000	0.622	11.4755
chr5	180915260	190483575	1.0529	2.4041
chr6	171115067	161804422	0.9456	10.7299
chr7	159138663	136301893	0.8565	13.4767
chr8	146364022	180264832	1.2316	5.3418
chr9	141213431	121705828	0.8619	20.7915
chr10	135534747	147428077	1.0878	22.6757
chr11	135006516	130294244	0.9651	9.0815
chr12	133851895	116829716	0.8728	2.3456
chr13	115169878	89829650	0.78	1.9855
chr14	107349540	90990655	0.8476	2.2691
chr15	102531392	79353910	0.7739	2.0437
chr16	90354753	86951283	0.9623	8.4466
chr17	81195210	76495189	0.9421	19.8971
chr18	78077248	113985533	1.4599	15.9217
chr19	59128983	41078706	0.6947	7.6313
chr20	63025520	78727191	1.2491	4.391
chr21	48129895	28052979	0.5829	5.6497
chr22	51304566	17608403	0.3432	1.3344
chrMT	16571	4381114	264.3844	171.8402
chrX	155270560	91835475	0.5915	2.8402

chrY	59373566	5707632	0.0961	12.1066

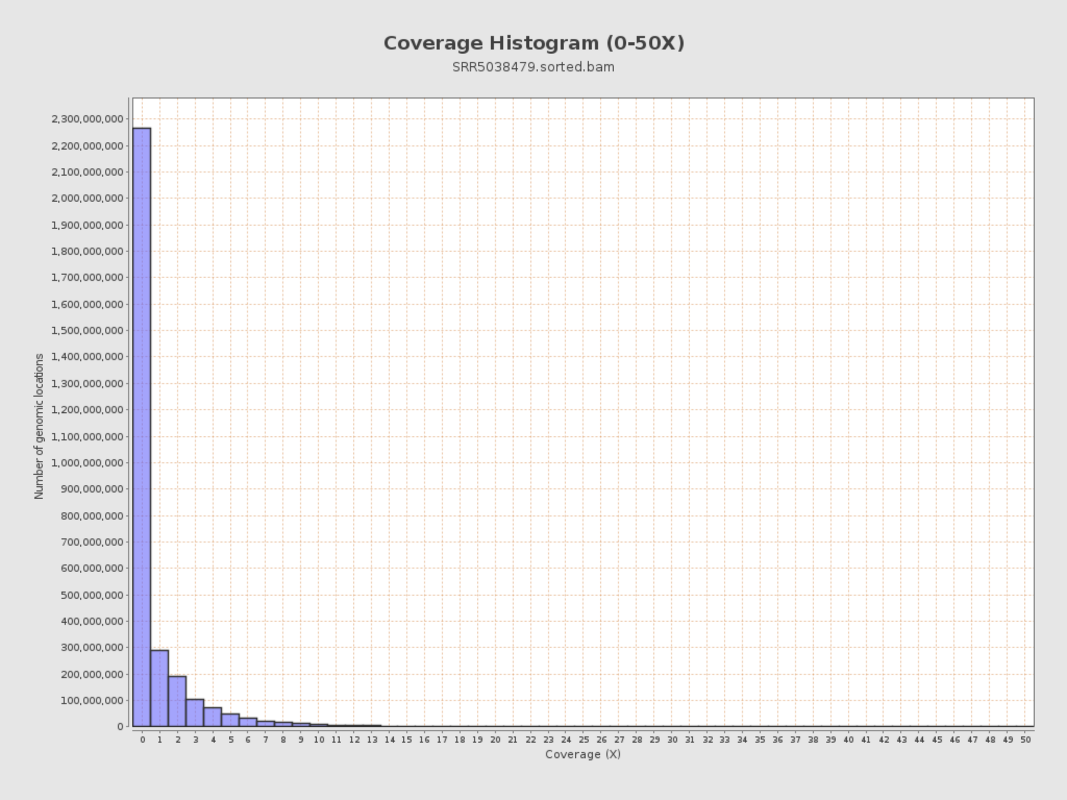
3. Results : Coverage across reference



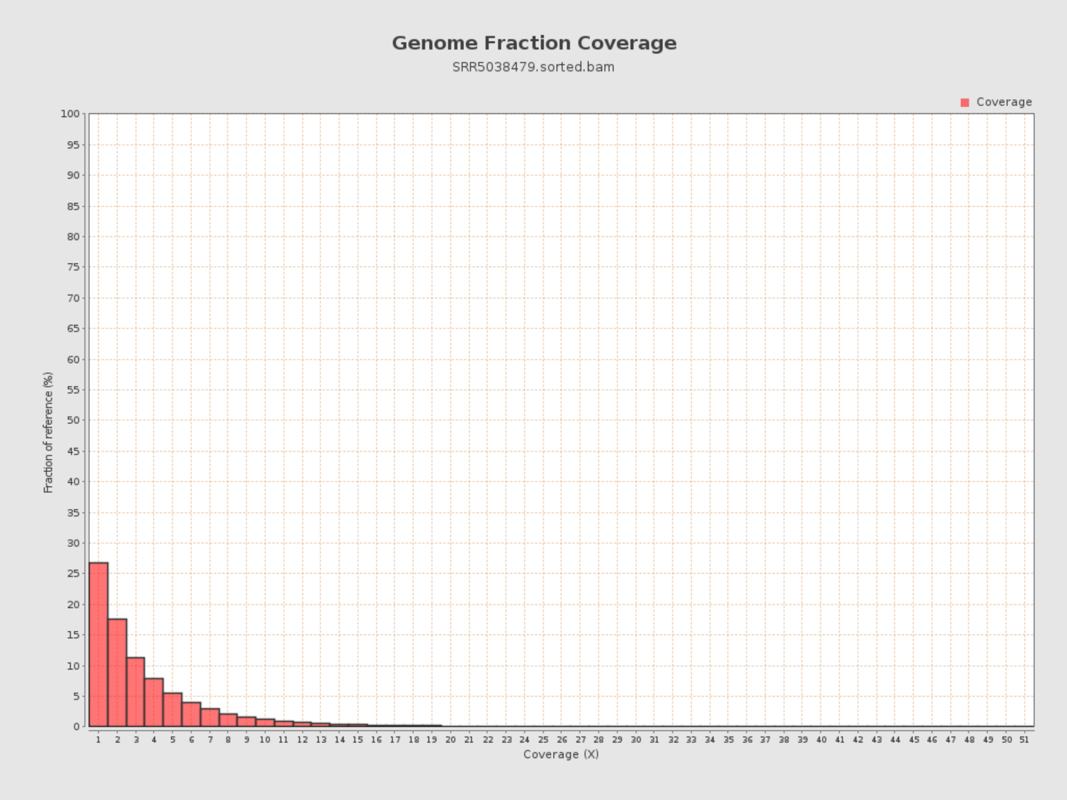
4. Results : Coverage Histogram



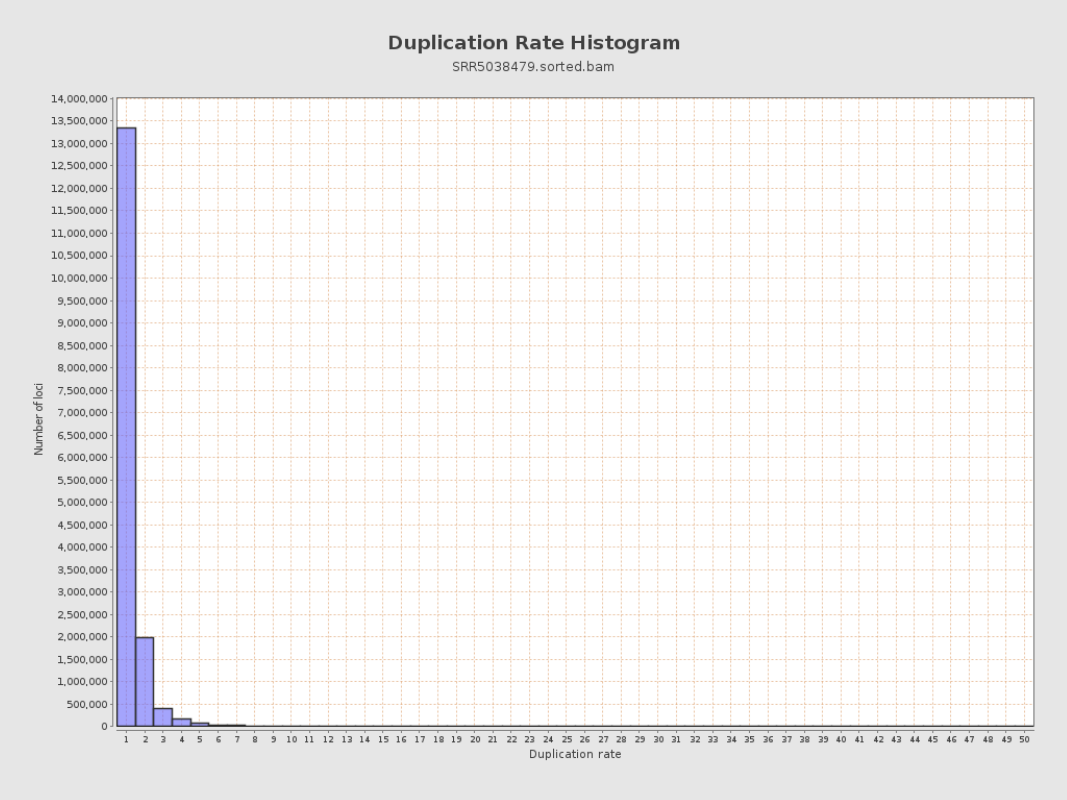
5. Results : Coverage Histogram (0-50X)



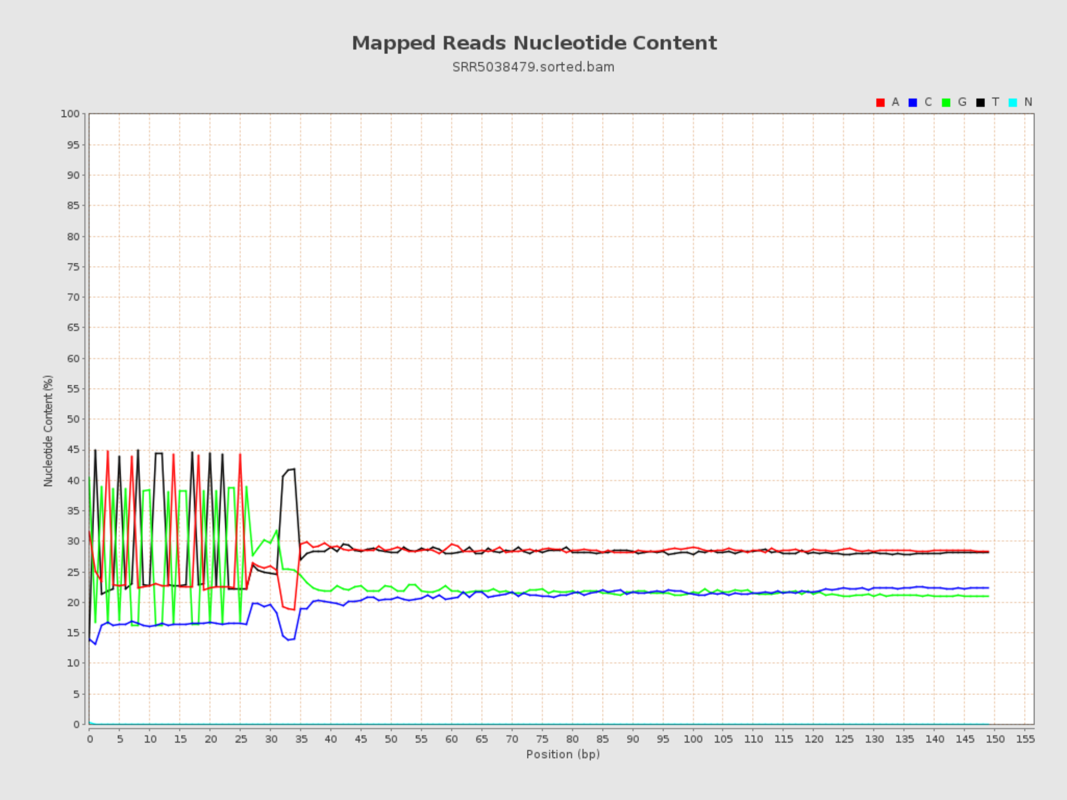
6. Results : Genome Fraction Coverage



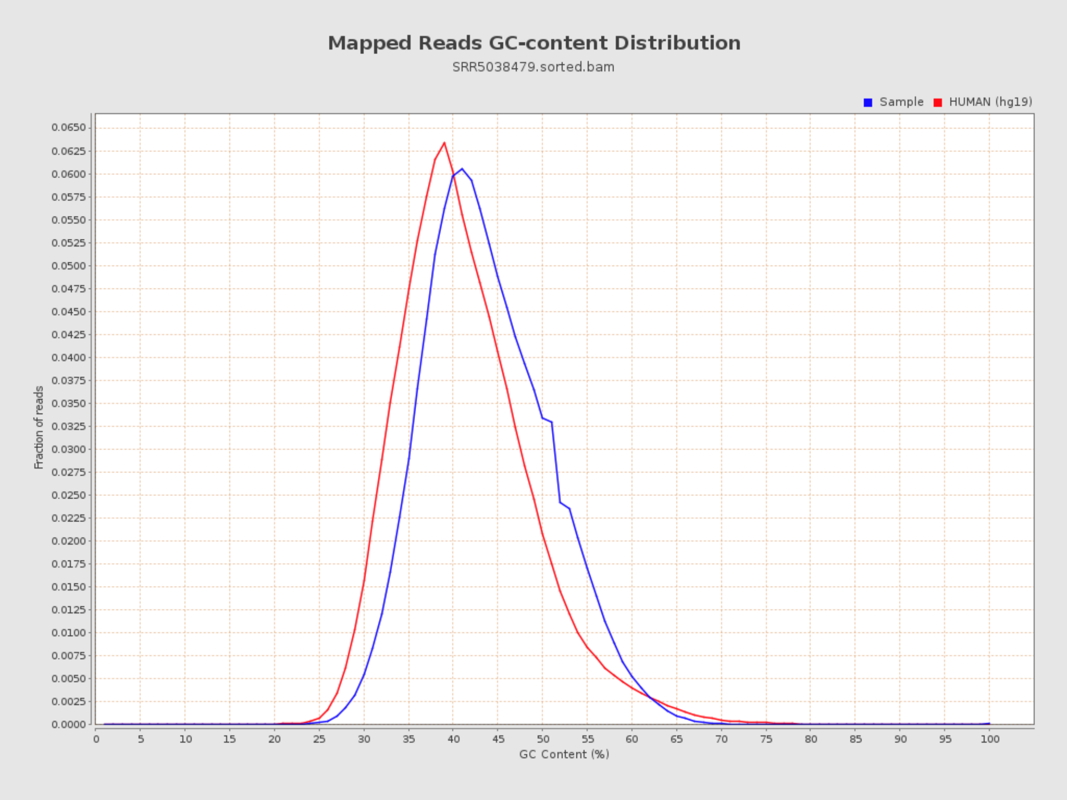
7. Results : Duplication Rate Histogram



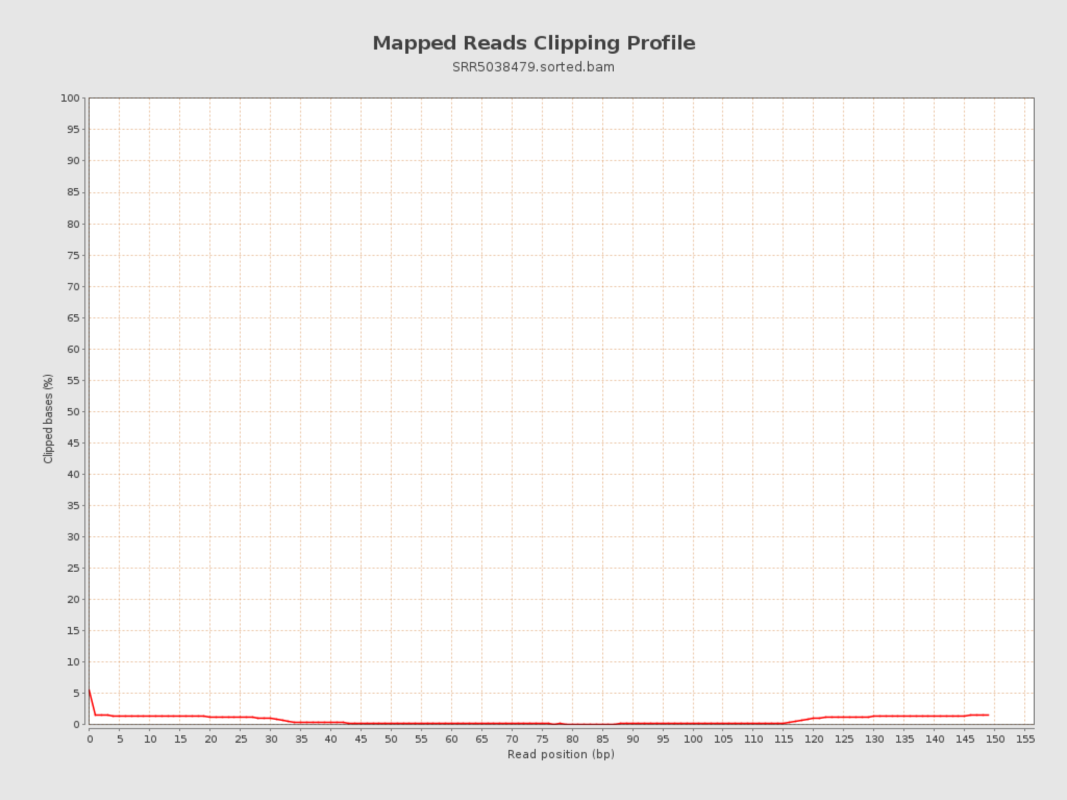
8. Results : Mapped Reads Nucleotide Content



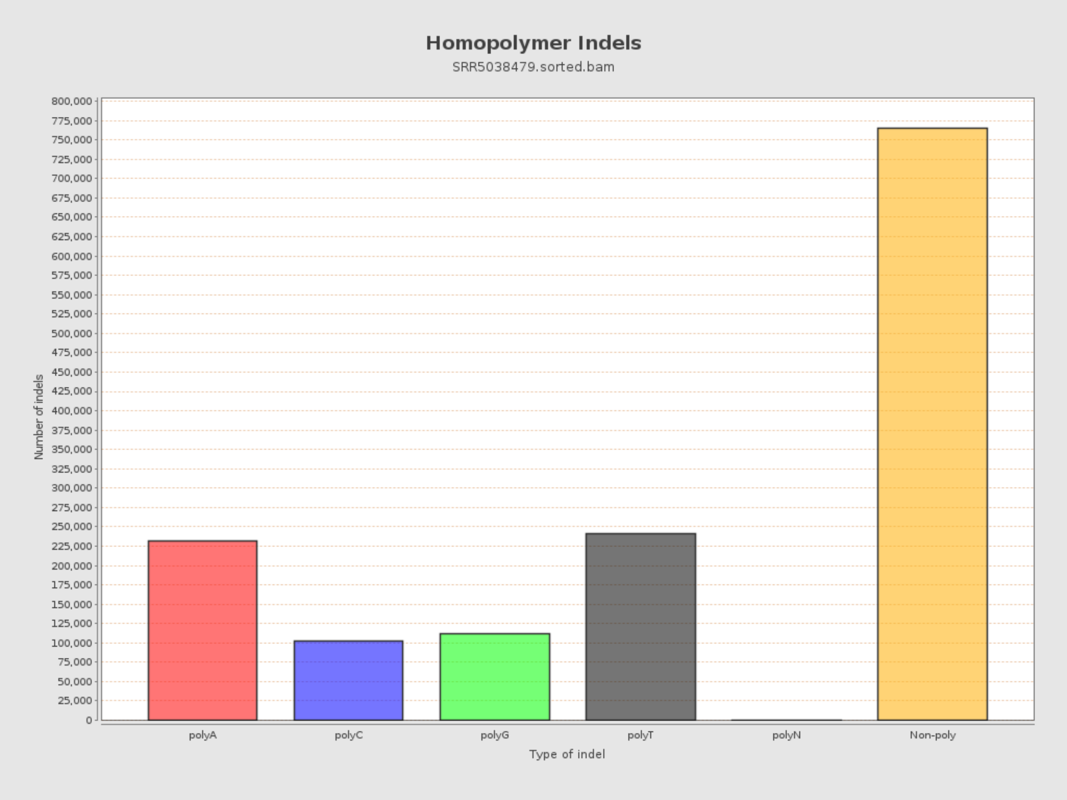
9. Results : Mapped Reads GC-content Distribution



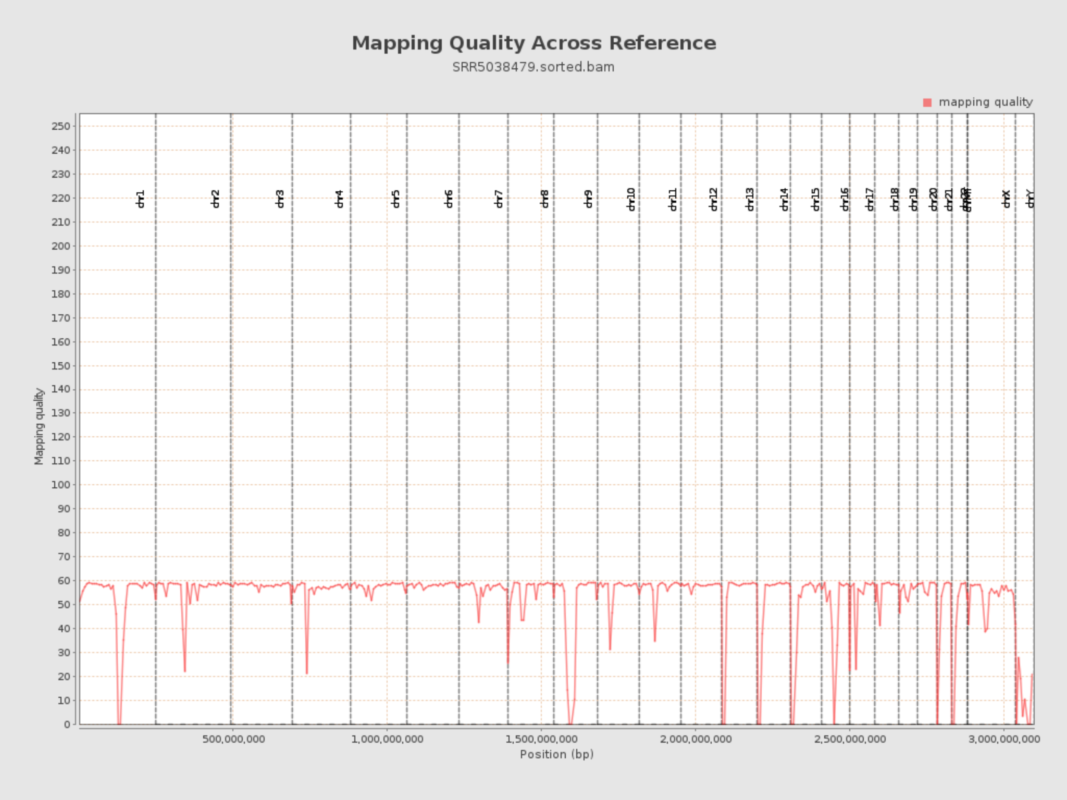
10. Results : Mapped Reads Clipping Profile



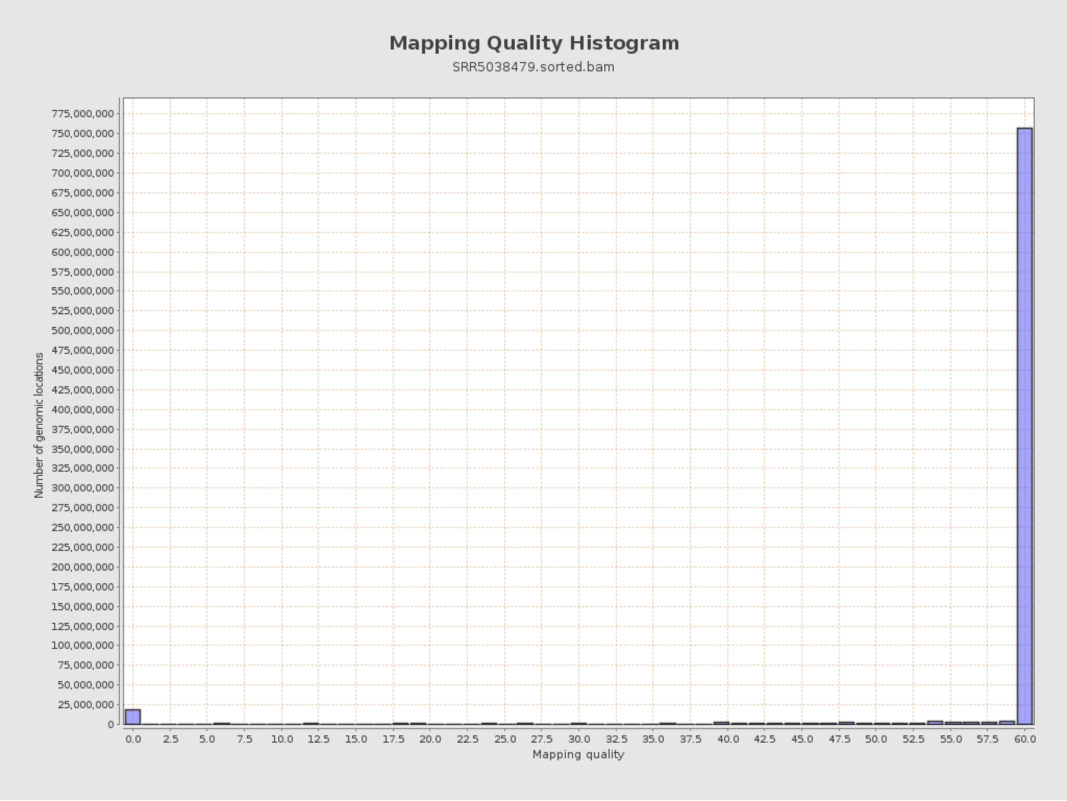
11. Results : Homopolymer Indels



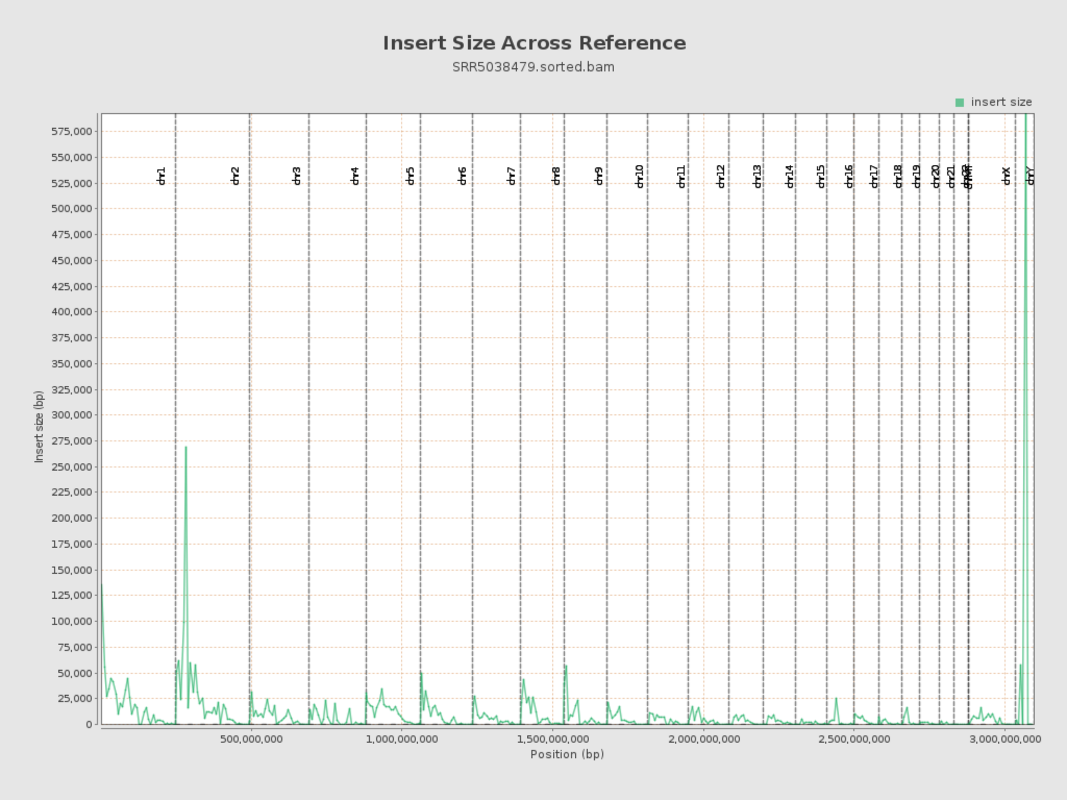
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram