Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 07:05:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038483.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_SRR5038483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038483_1.fastq.gz SRR5038483_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 07:05:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,194,056
Mapped reads	18,946,362 / 89.39%
Unmapped reads	2,247,694 / 10.61%
Mapped paired reads	18,946,362 / 89.39%
Mapped reads, first in pair	9,636,480 / 45.47%
Mapped reads, second in pair	9,309,882 / 43.93%
Mapped reads, both in pair	18,538,464 / 87.47%
Mapped reads, singletons	407,898 / 1.92%
Secondary alignments	0
Supplementary alignments	349,830 / 1.65%
Read min/max/mean length	30 / 150 / 150.82
Duplicated reads (estimated)	3,657,190 / 17.26%
Duplication rate	13.23%
Clipped reads	9,439,917 / 44.54%

2.2. ACGT Content

Number/percentage of A's	719,180,158 / 28.45%
Number/percentage of C's	508,389,415 / 20.11%
Number/percentage of T's	732,388,477 / 28.97%
Number/percentage of G's	568,130,663 / 22.47%
Number/percentage of N's	194,663 / 0.01%

GC Percentage	42.58%

2.3. Coverage

Mean	0.8173
Standard Deviation	12.0199

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	101,204.58
Standard Deviation	3,077,139.73
P25/Median/P75	184 / 235 / 301

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	34,386,950
Insertions	482,554
Mapped reads with at least one insertion	2.39%
Deletions	911,257
Mapped reads with at least one deletion	4.62%
Homopolymer indels	46.6%

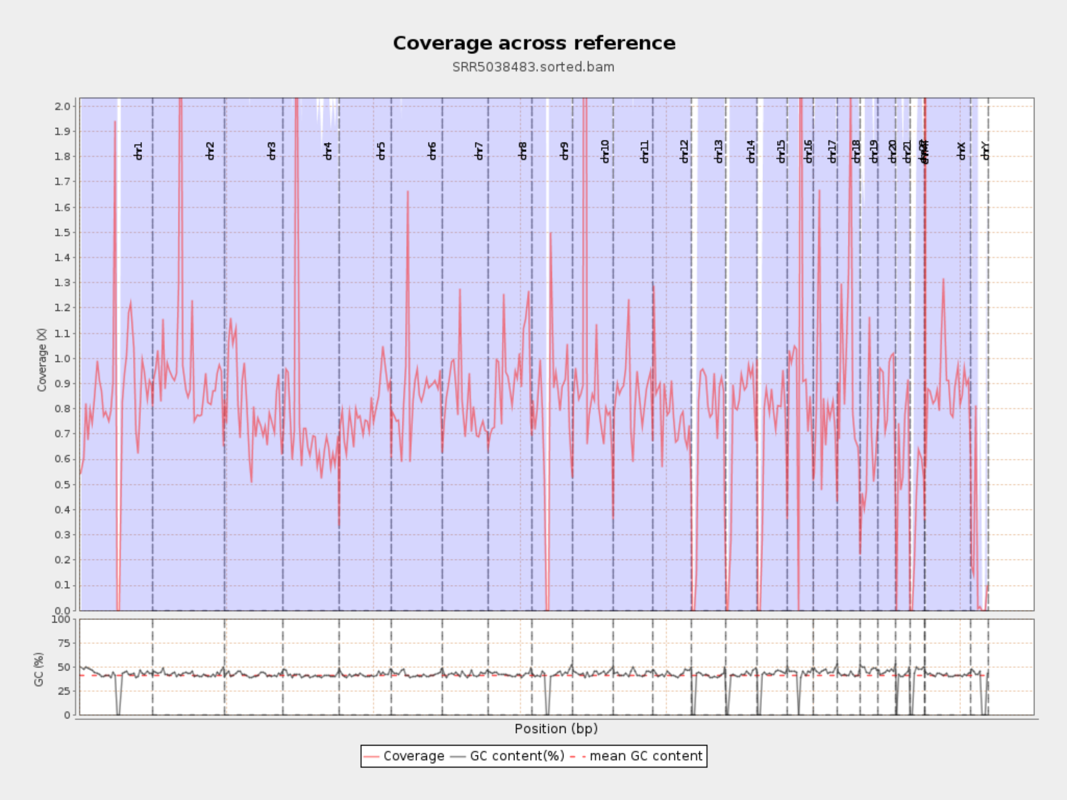
2.7. Chromosome stats

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

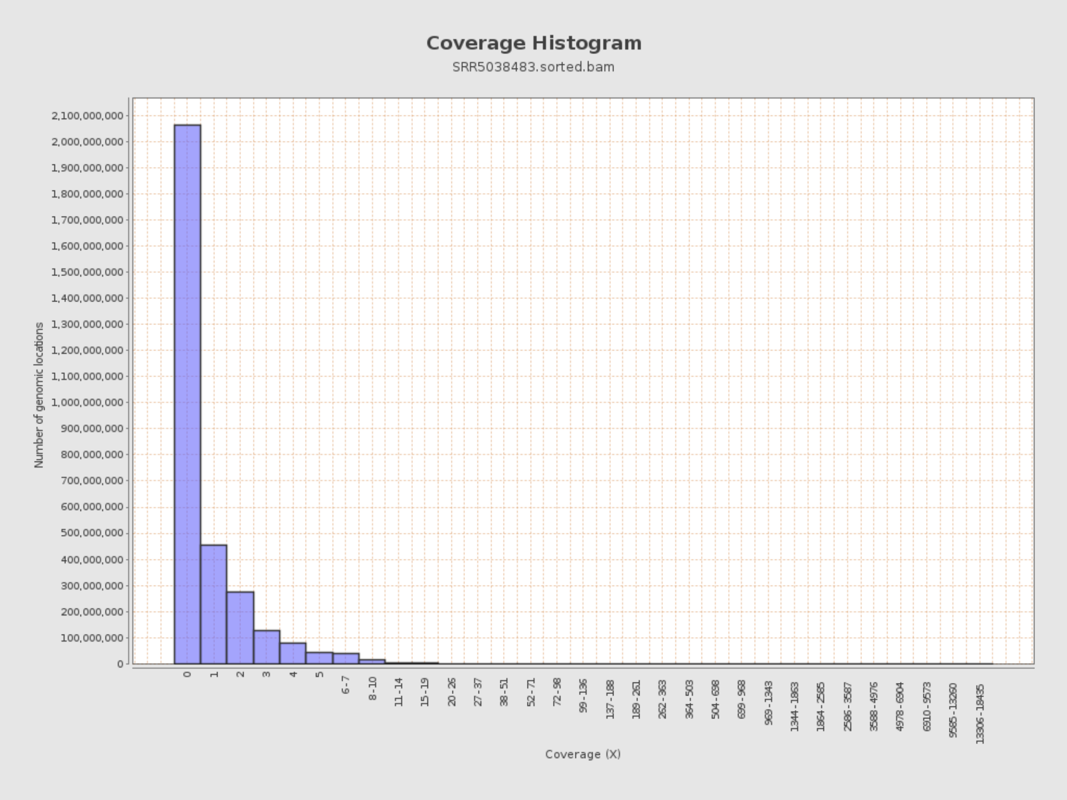
		bases	coverage	deviation
chr1	249250621	207732644	0.8334	18.2997
chr2	243199373	238010204	0.9787	12.6167
chr3	198022430	160663917	0.8113	1.7122
chr4	191154276	145070326	0.7589	13.5133
chr5	180915260	142702010	0.7888	1.591
chr6	171115067	149735101	0.8751	8.5398
chr7	159138663	130285195	0.8187	8.7885
chr8	146364022	136791599	0.9346	3.5687
chr9	141213431	108185069	0.7661	17.2961
chr10	135534747	142944484	1.0547	31.5458
chr11	135006516	115198200	0.8533	8.3118
chr12	133851895	105862800	0.7909	1.703
chr13	115169878	81861451	0.7108	1.4624
chr14	107349540	77209793	0.7192	1.6764
chr15	102531392	67722956	0.6605	1.4216
chr16	90354753	89477287	0.9903	15.2007
chr17	81195210	64313991	0.7921	14.986
chr18	78077248	78703285	1.008	13.6542
chr19	59128983	35528873	0.6009	8.7661
chr20	63025520	55264574	0.8769	4.2946
chr21	48129895	29003900	0.6026	6.3194
chr22	51304566	19399614	0.3781	1.1586
chrMT	16571	1630710	98.4075	50.231
chrX	155270560	137577861	0.8861	3.8648

chrY	59373566	9289445	0.1565	13.5806

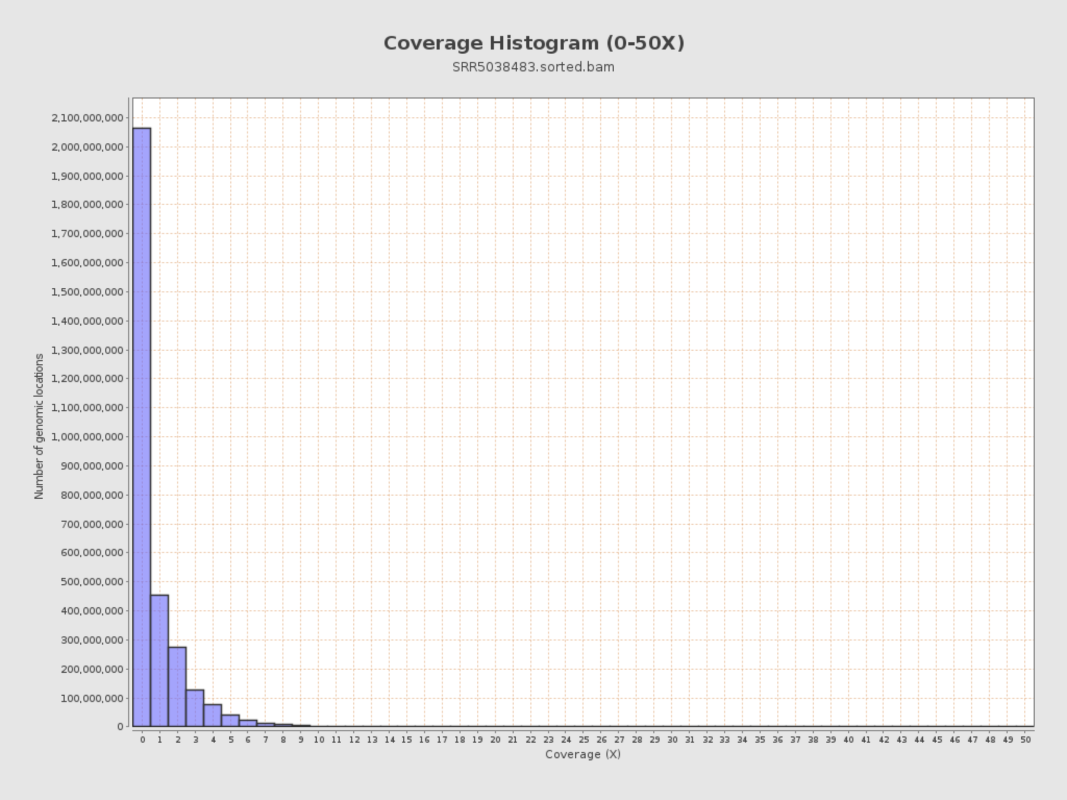
3. Results : Coverage across reference



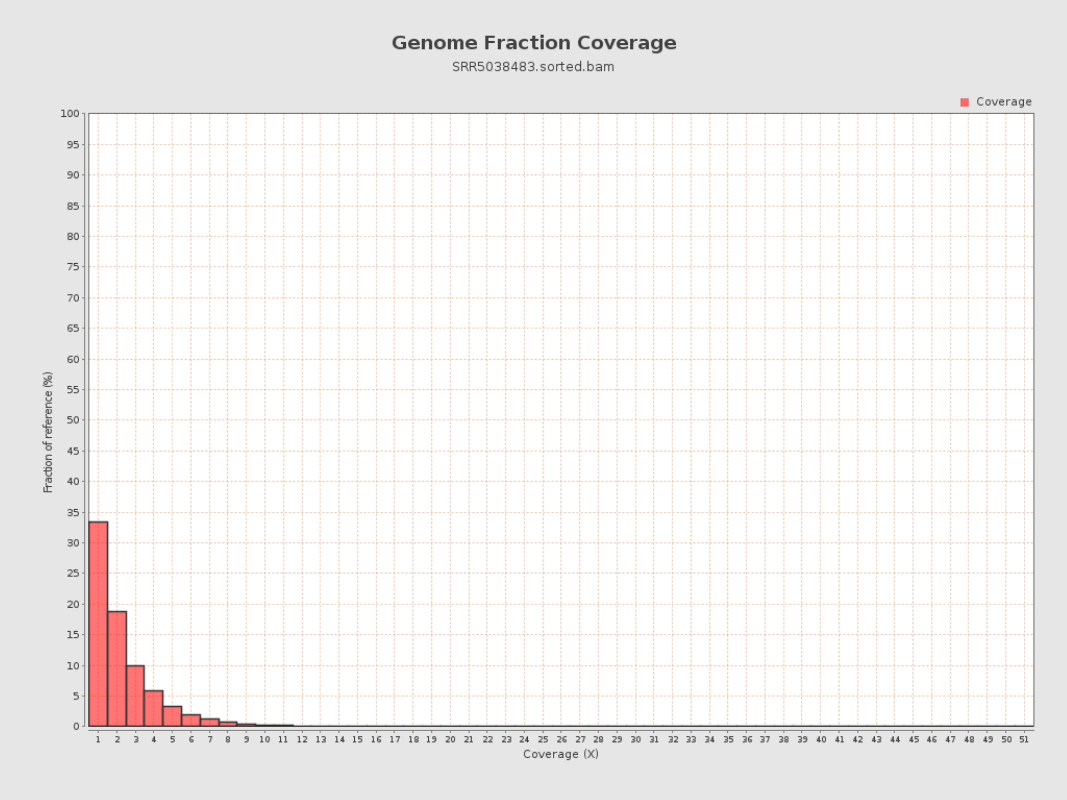
4. Results : Coverage Histogram



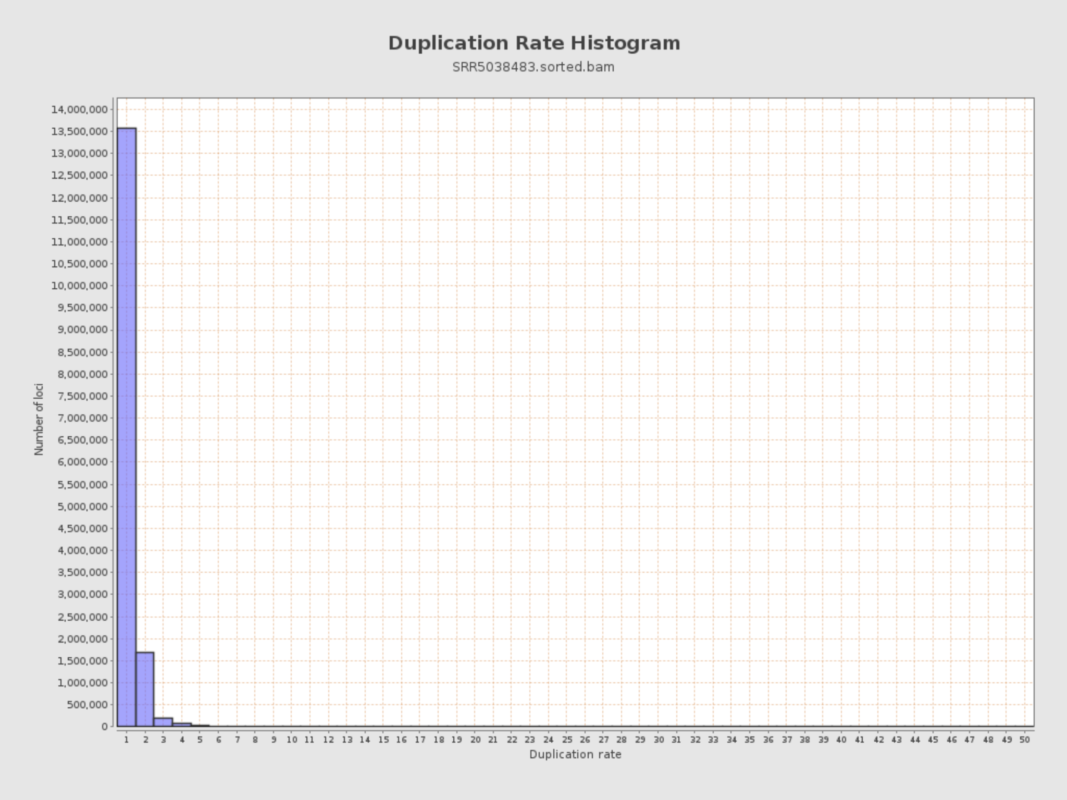
5. Results : Coverage Histogram (0-50X)



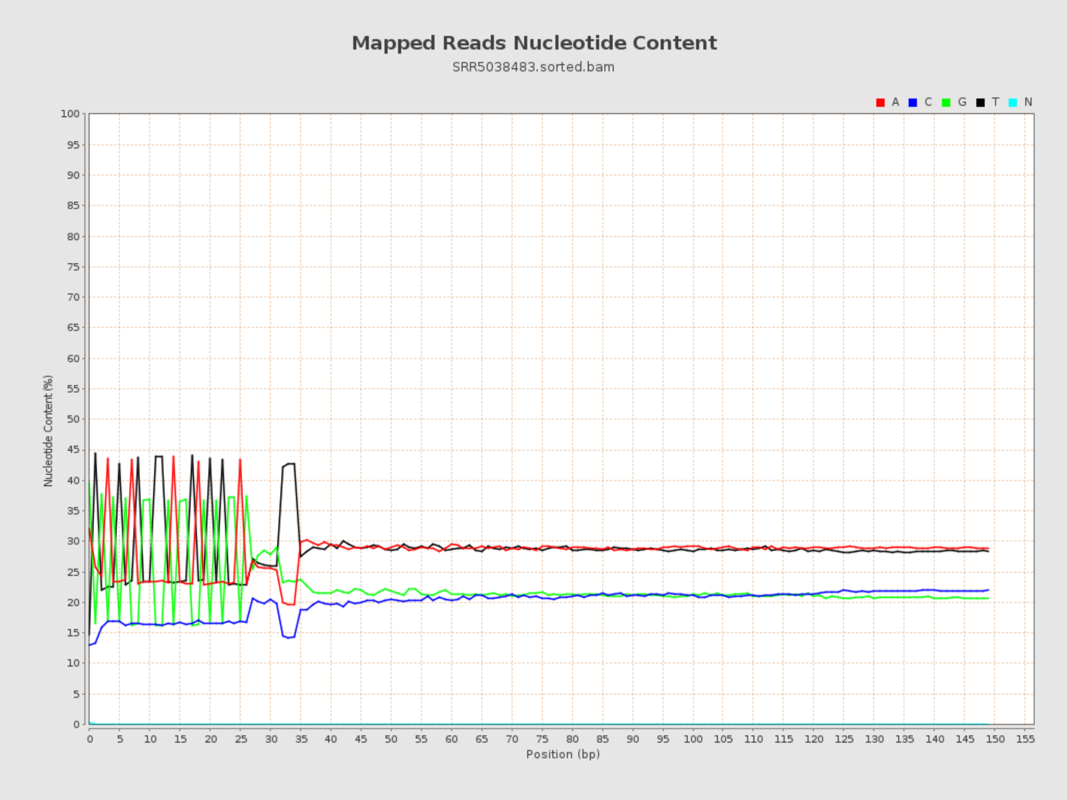
6. Results : Genome Fraction Coverage



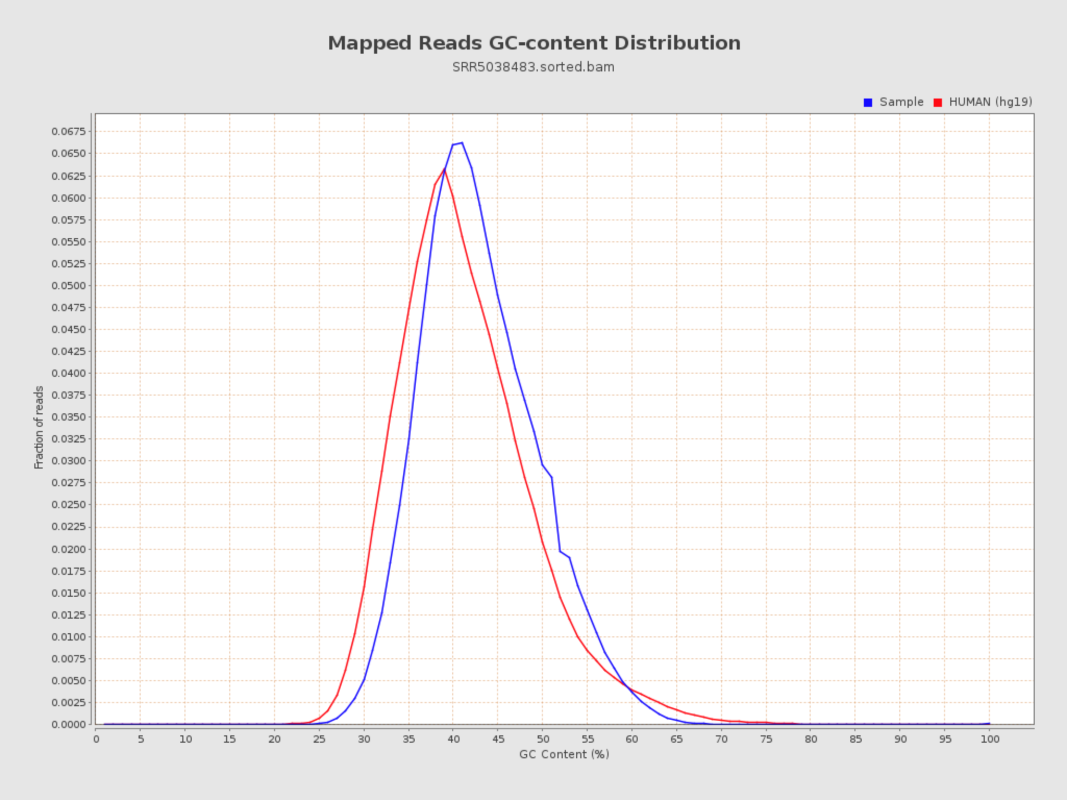
7. Results : Duplication Rate Histogram



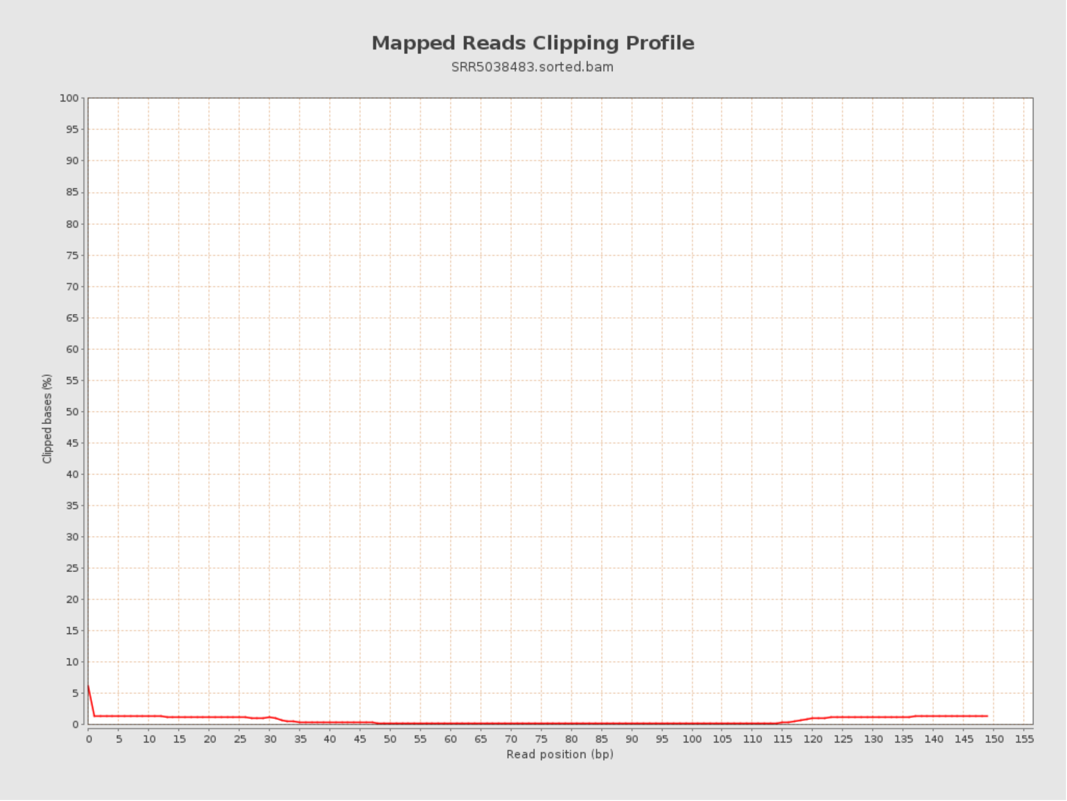
8. Results : Mapped Reads Nucleotide Content



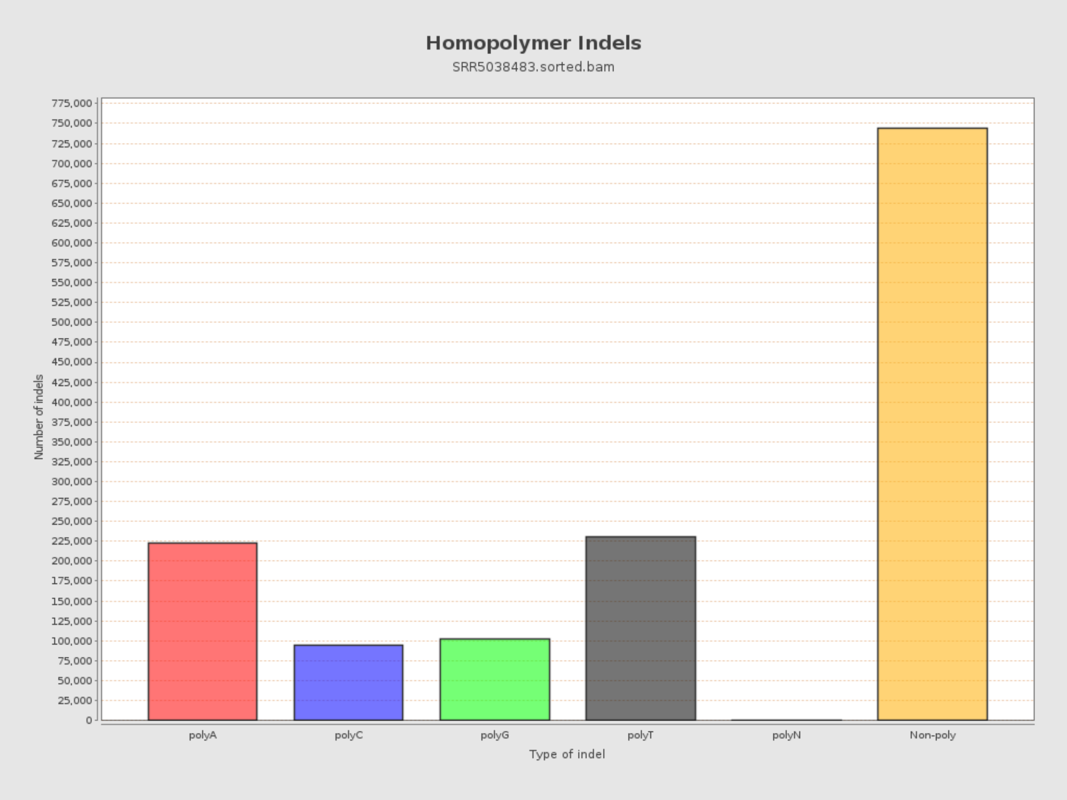
9. Results : Mapped Reads GC-content Distribution



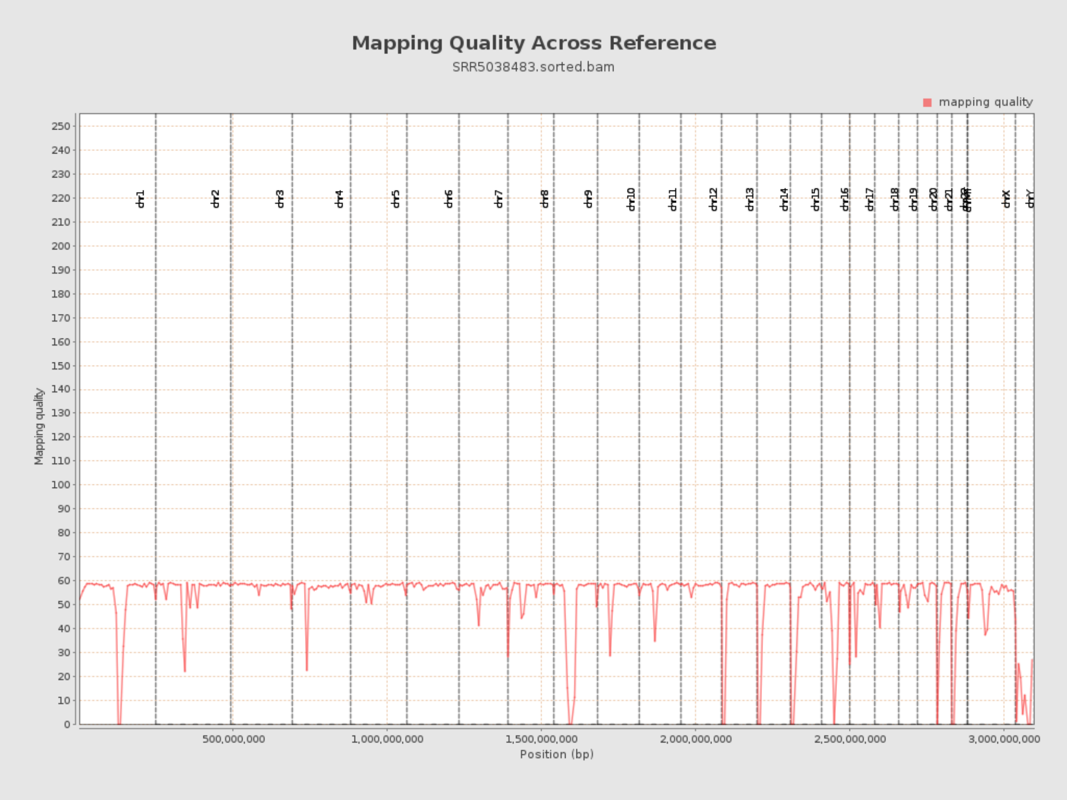
10. Results : Mapped Reads Clipping Profile



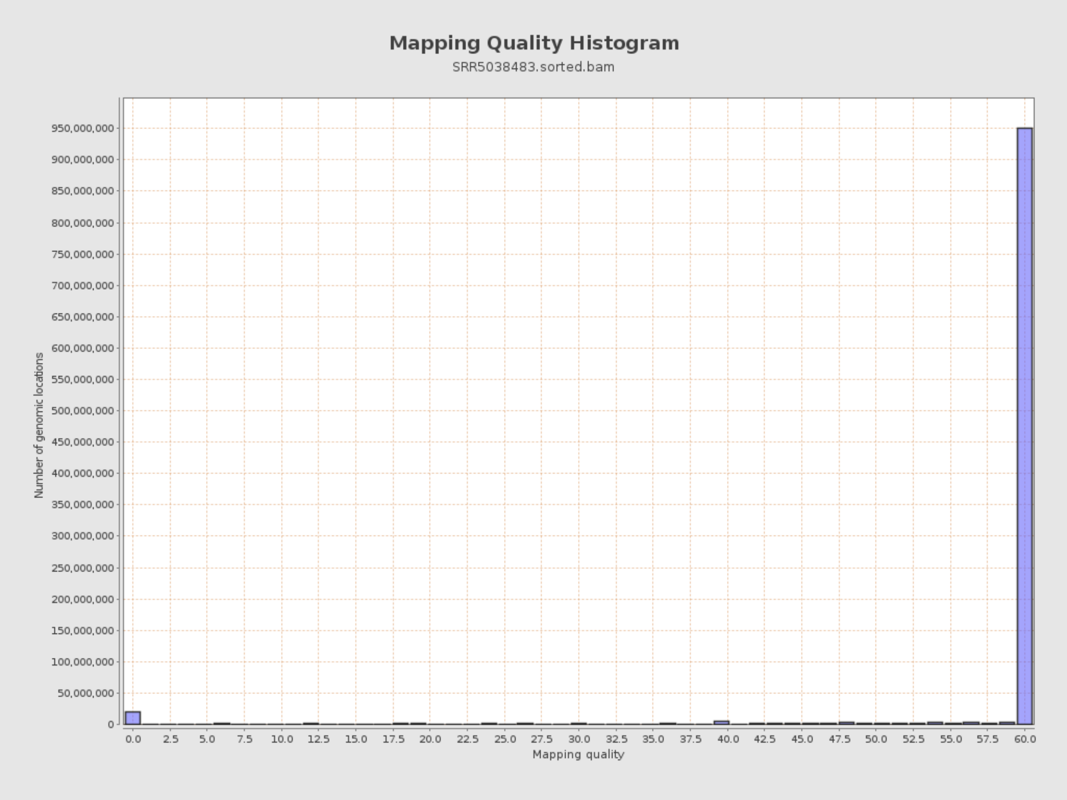
11. Results : Homopolymer Indels



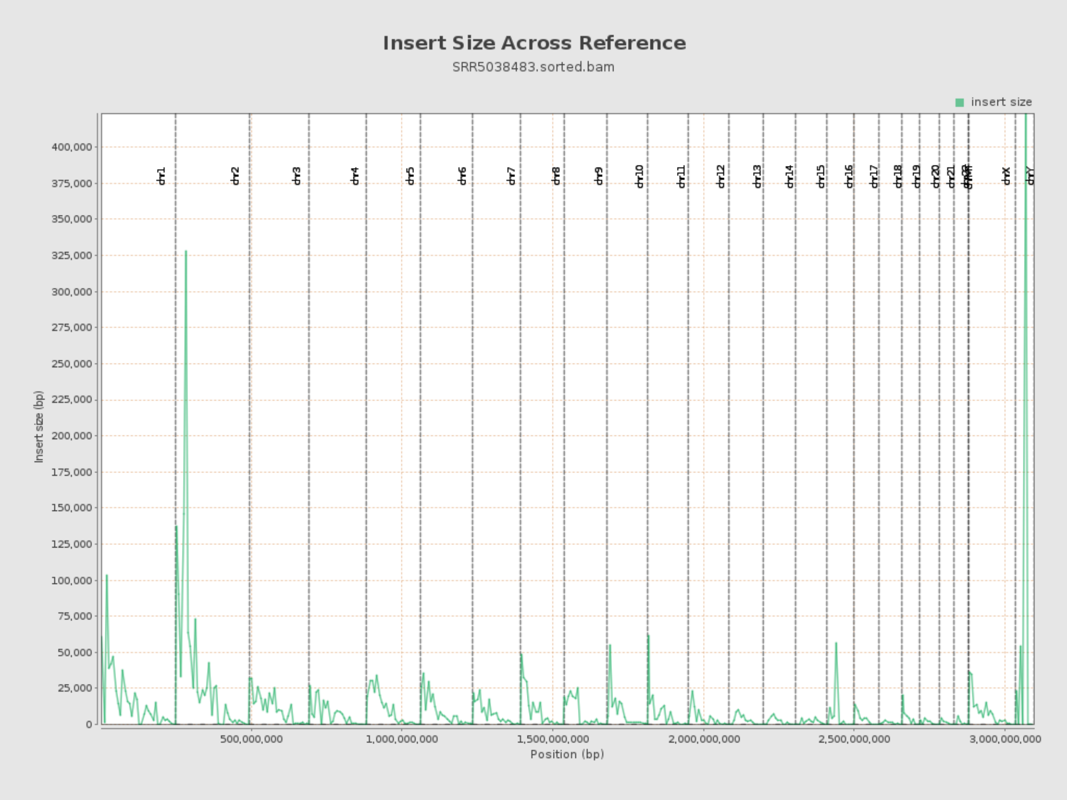
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram