Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 14:51:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038498.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_SRR5038498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038498_1.fastq.gz SRR5038498_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 14:51:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,413,106
Mapped reads	15,488,491 / 88.95%
Unmapped reads	1,924,615 / 11.05%
Mapped paired reads	15,488,491 / 88.95%
Mapped reads, first in pair	7,869,137 / 45.19%
Mapped reads, second in pair	7,619,354 / 43.76%
Mapped reads, both in pair	15,181,028 / 87.18%
Mapped reads, singletons	307,463 / 1.77%
Secondary alignments	0
Supplementary alignments	271,424 / 1.56%
Read min/max/mean length	30 / 150 / 150.78
Duplicated reads (estimated)	3,642,187 / 20.92%
Duplication rate	16.06%
Clipped reads	7,976,735 / 45.81%

2.2. ACGT Content

Number/percentage of A's	584,590,129 / 28.35%
Number/percentage of C's	413,288,101 / 20.04%
Number/percentage of T's	594,359,582 / 28.82%
Number/percentage of G's	469,660,432 / 22.78%
Number/percentage of N's	163,241 / 0.01%

GC Percentage	42.82%

2.3. Coverage

Mean	0.6666
Standard Deviation	10.905

2.4. Mapping Quality

Mean Mapping Quality	53.19

2.5. Insert size

Mean	87,684.6
Standard Deviation	2,891,219.08
P25/Median/P75	191 / 243 / 309

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	26,372,184
Insertions	374,793
Mapped reads with at least one insertion	2.29%
Deletions	720,478
Mapped reads with at least one deletion	4.48%
Homopolymer indels	47.33%

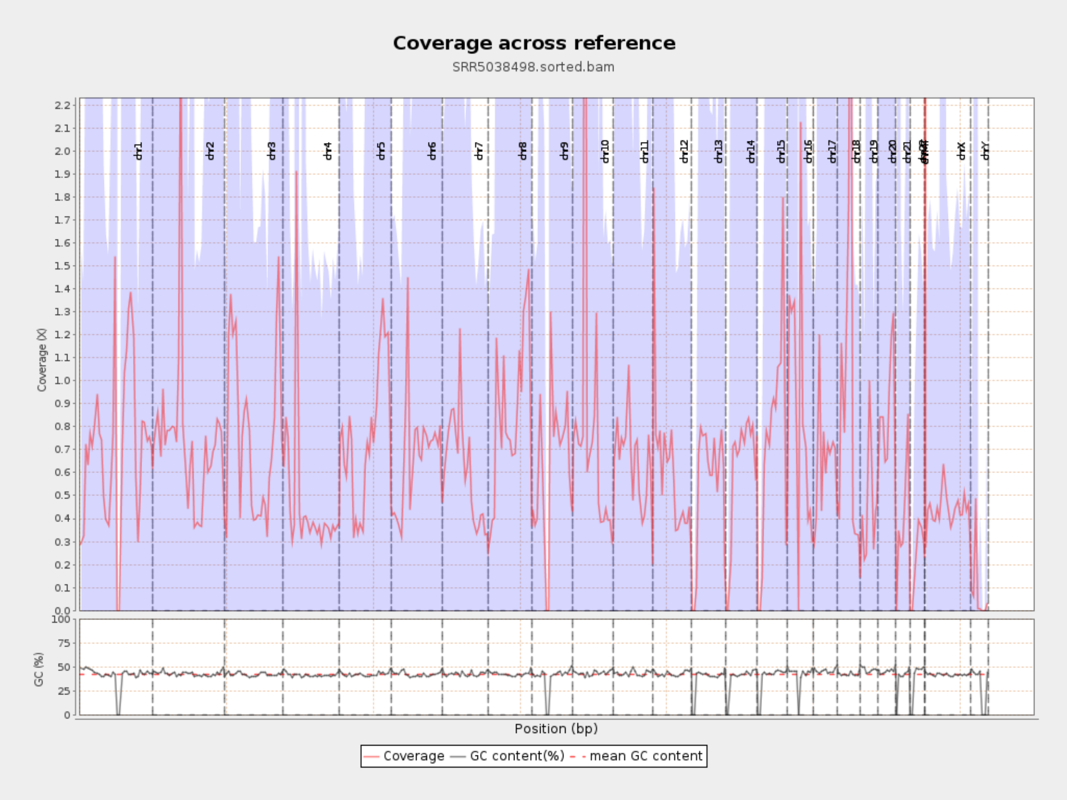
2.7. Chromosome stats

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

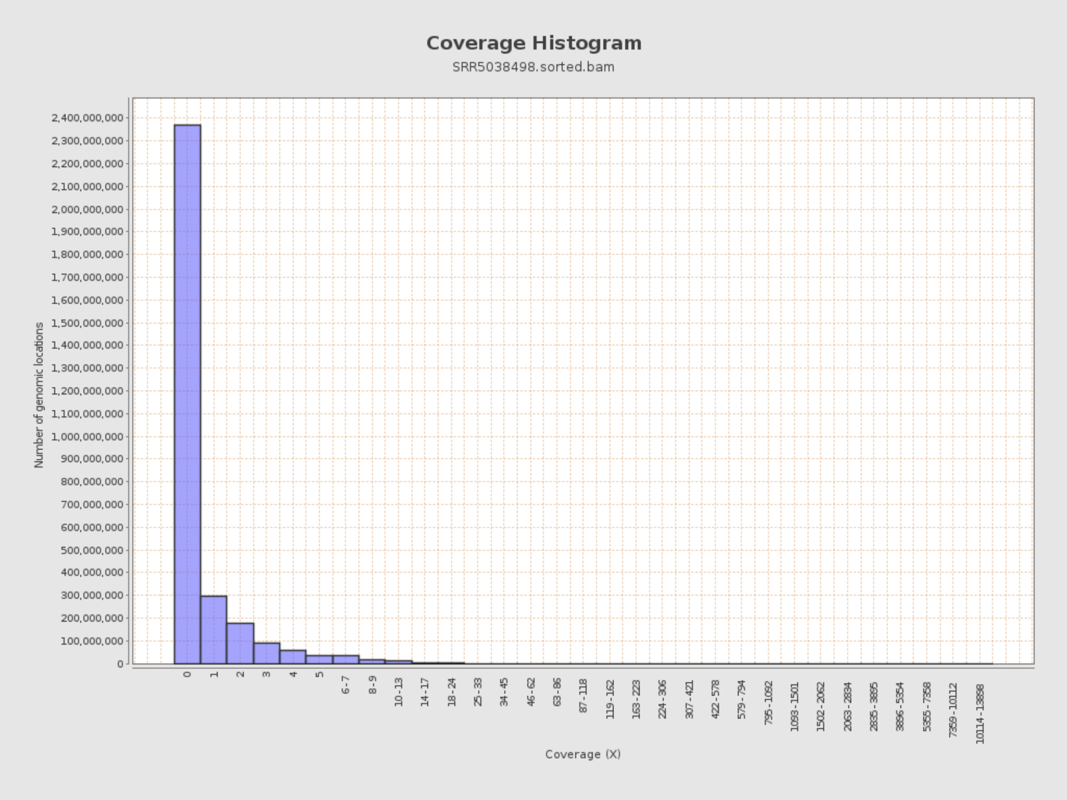
		bases	coverage	deviation
chr1	249250621	177597494	0.7125	13.2657
chr2	243199373	183071890	0.7528	11.7771
chr3	198022430	151554602	0.7653	1.9547
chr4	191154276	89729217	0.4694	12.3504
chr5	180915260	136950777	0.757	1.7878
chr6	171115067	116476510	0.6807	8.0835
chr7	159138663	97457367	0.6124	10.3214
chr8	146364022	127676359	0.8723	3.9627
chr9	141213431	86635194	0.6135	16.6233
chr10	135534747	115507502	0.8522	30.7829
chr11	135006516	88262272	0.6538	7.6042
chr12	133851895	83348917	0.6227	1.7332
chr13	115169878	64616152	0.5611	1.4805
chr14	107349540	65320009	0.6085	1.6537
chr15	102531392	76153028	0.7427	1.8748
chr16	90354753	76046863	0.8416	9.8007
chr17	81195210	52477311	0.6463	13.2316
chr18	78077248	81747035	1.047	12.4463
chr19	59128983	26620077	0.4502	5.6696
chr20	63025520	55341110	0.8781	4.3859
chr21	48129895	19743484	0.4102	5.4784
chr22	51304566	11709144	0.2282	0.9763
chrMT	16571	6278755	378.9002	228.7041
chrX	155270560	68129044	0.4388	2.137

chrY	59373566	5063089	0.0853	12.5981

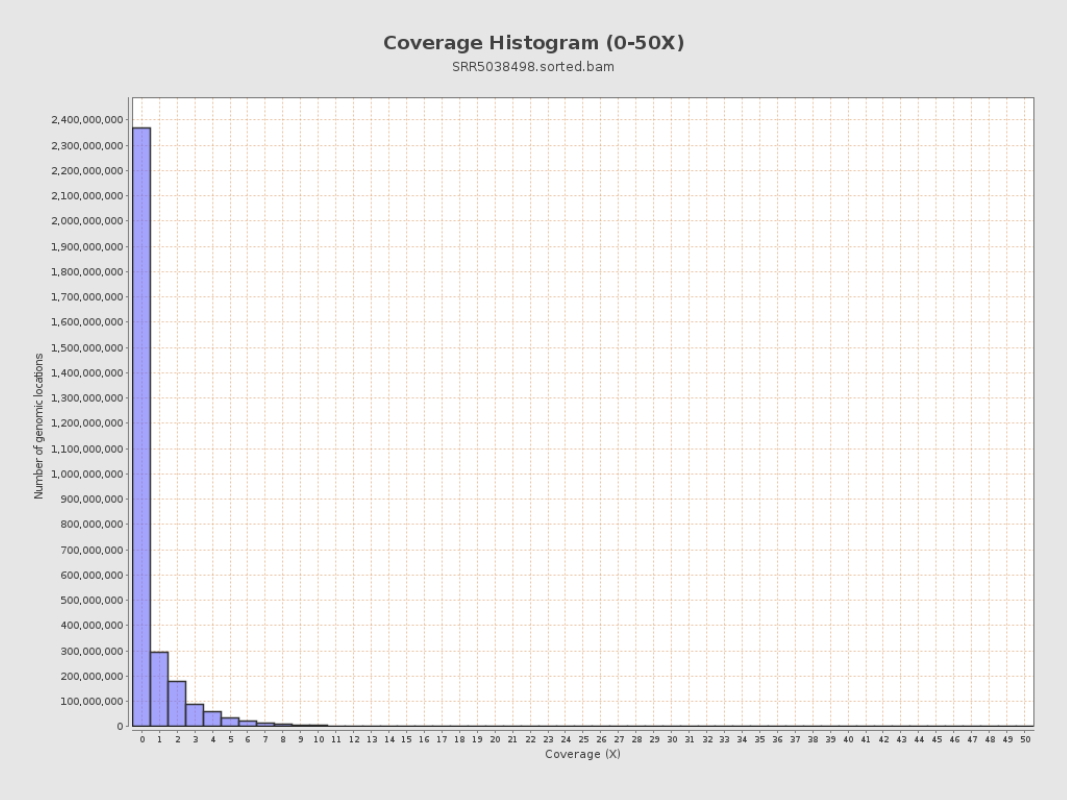
3. Results : Coverage across reference



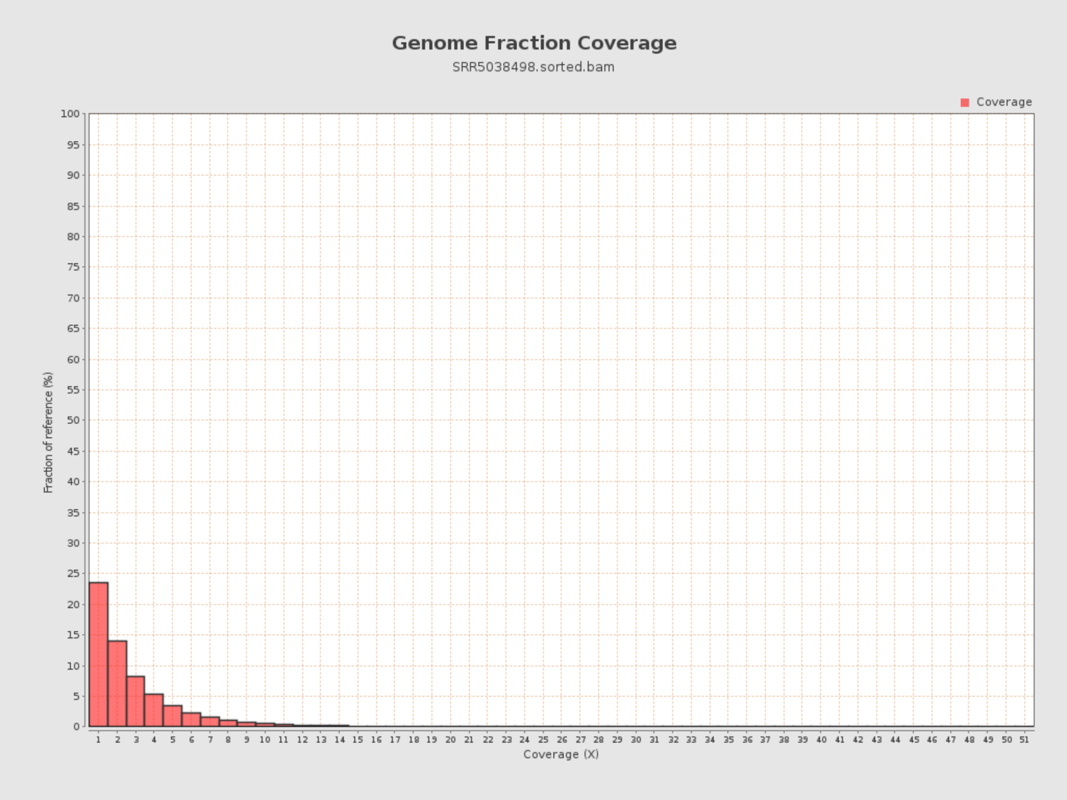
4. Results : Coverage Histogram



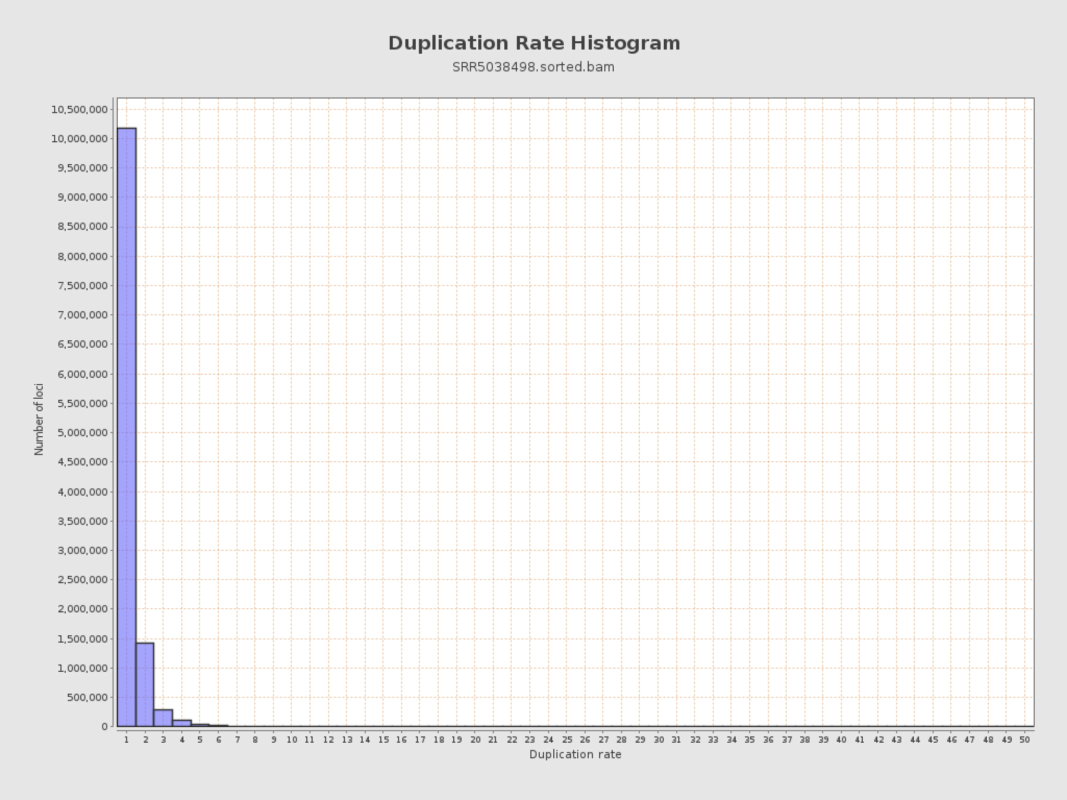
5. Results : Coverage Histogram (0-50X)



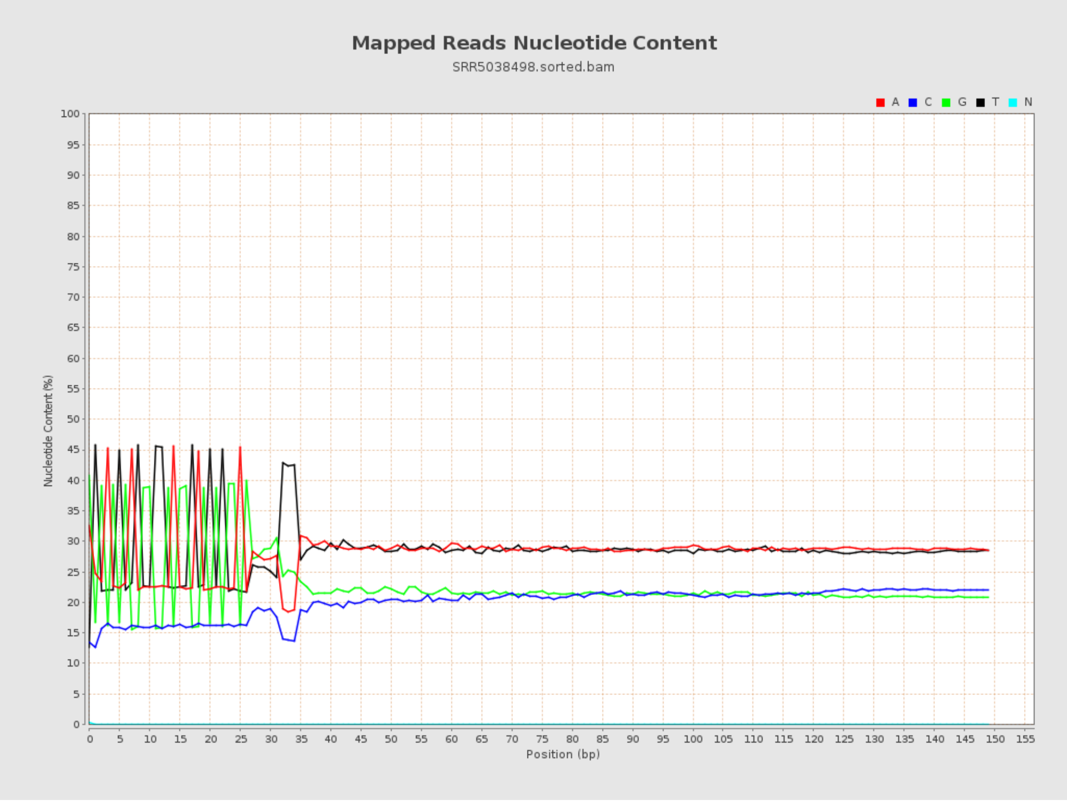
6. Results : Genome Fraction Coverage



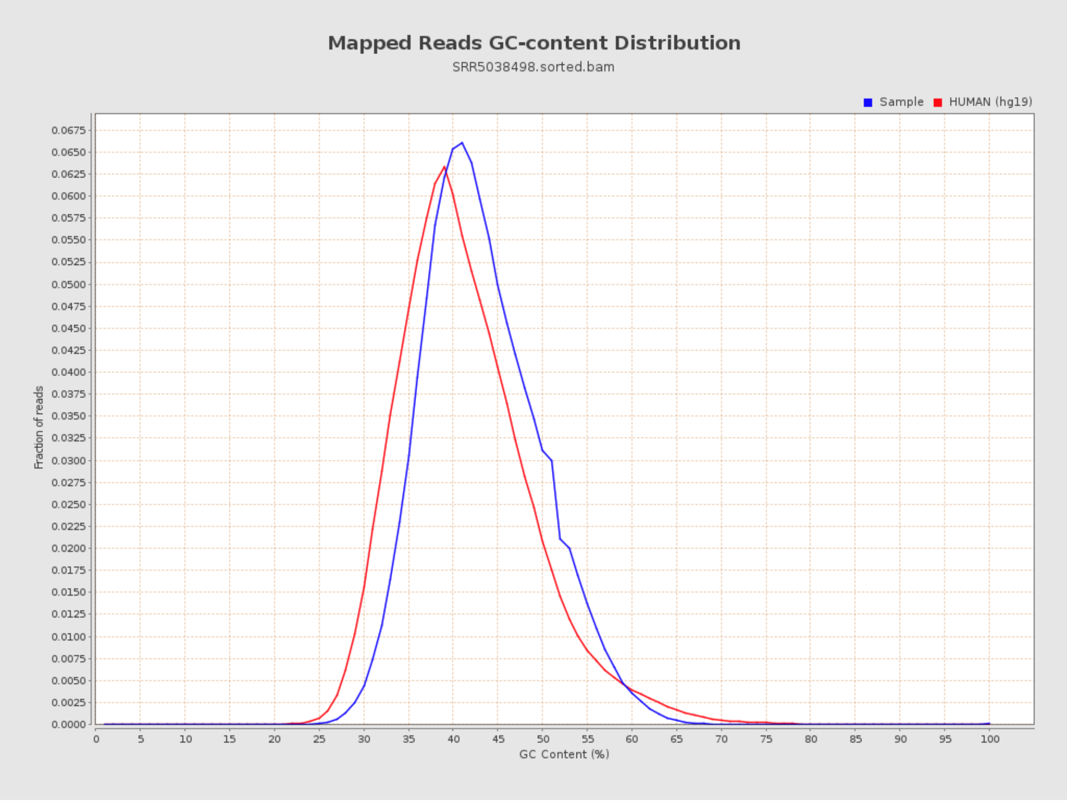
7. Results : Duplication Rate Histogram



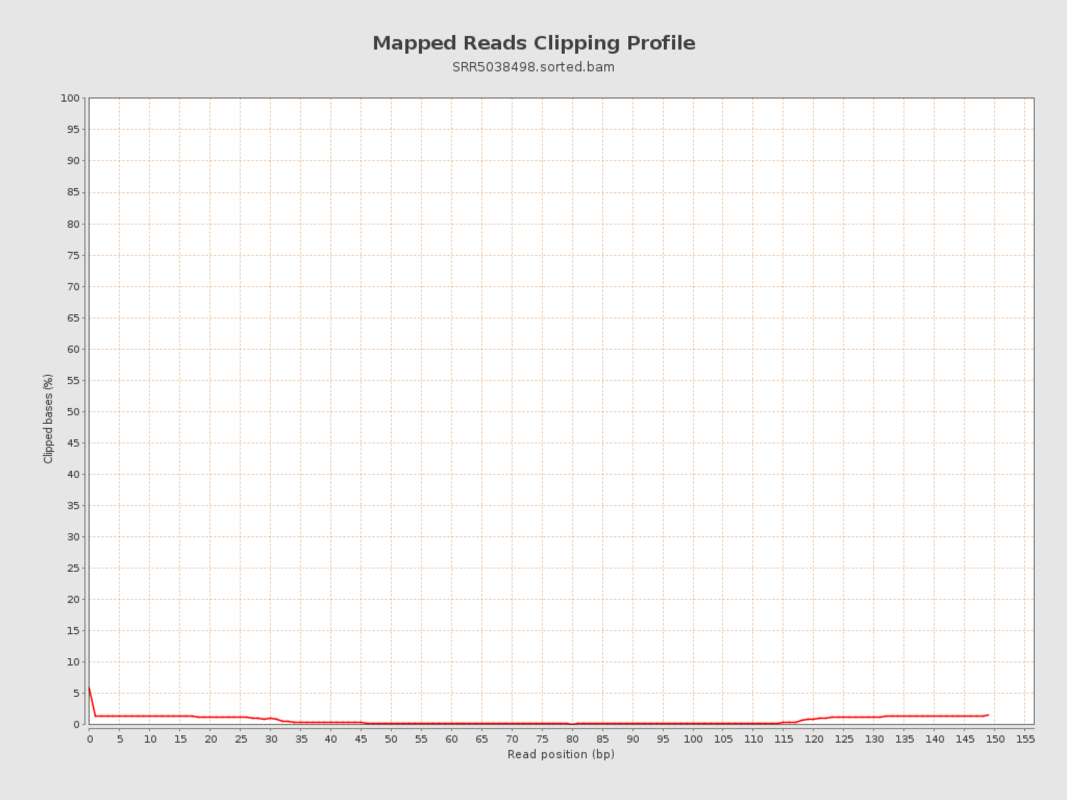
8. Results : Mapped Reads Nucleotide Content



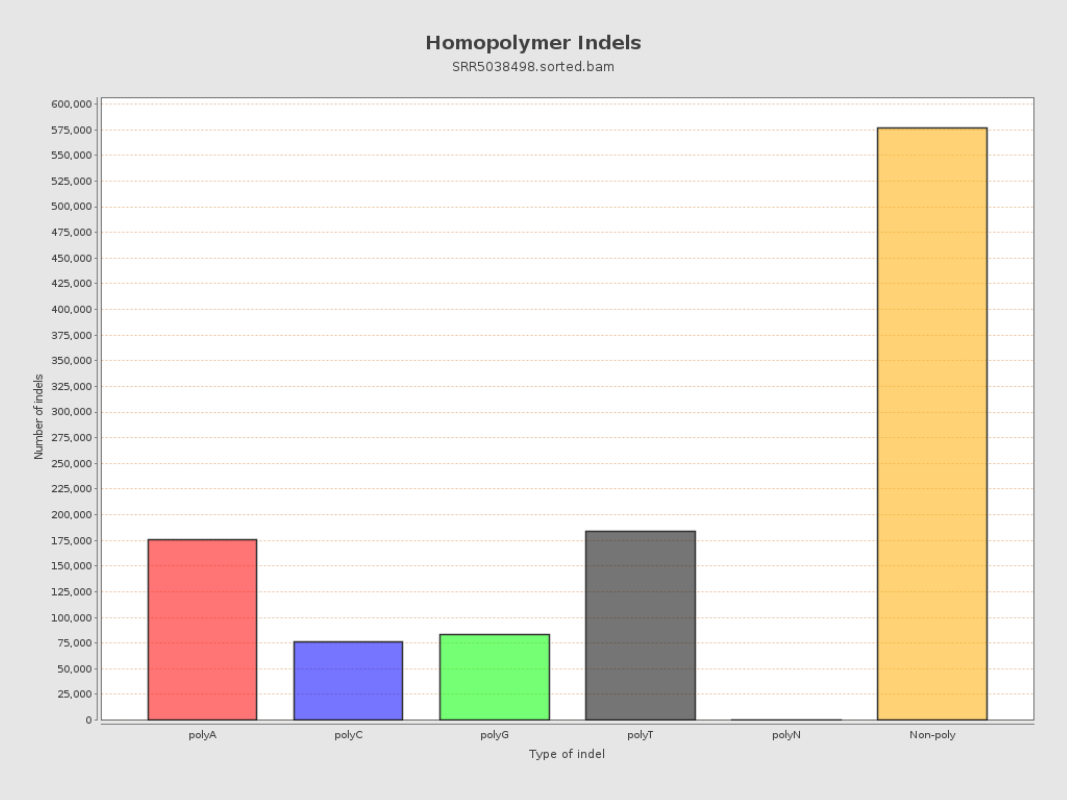
9. Results : Mapped Reads GC-content Distribution



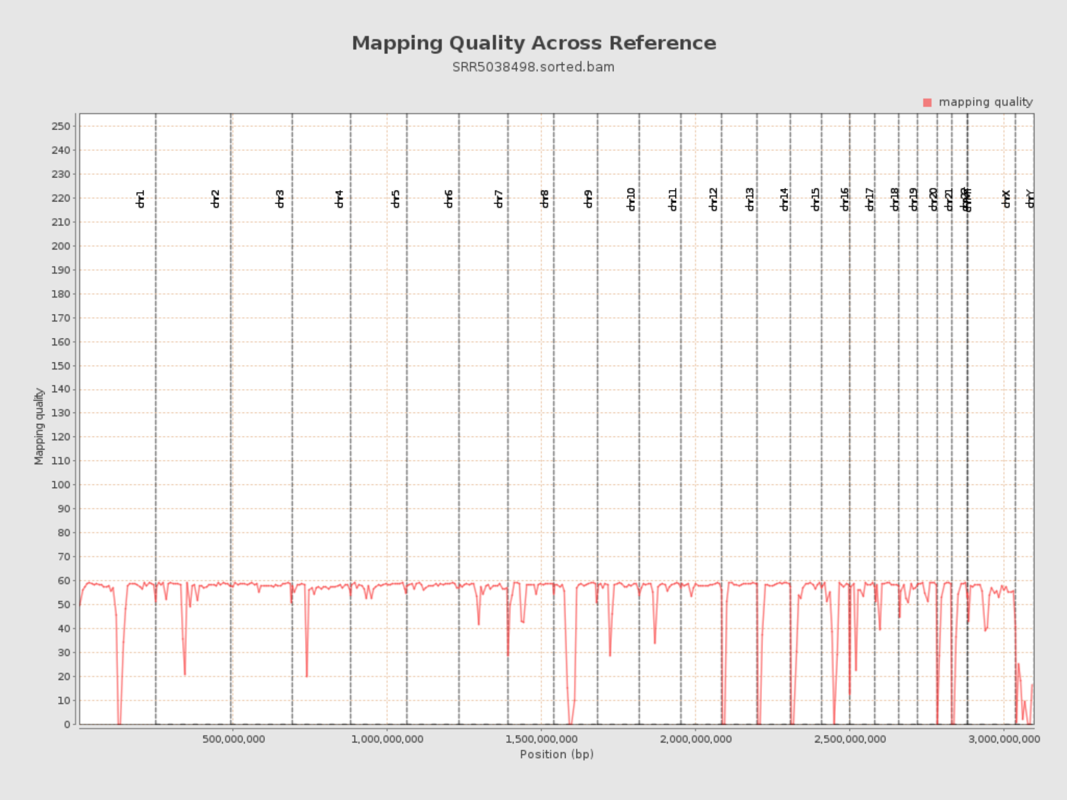
10. Results : Mapped Reads Clipping Profile



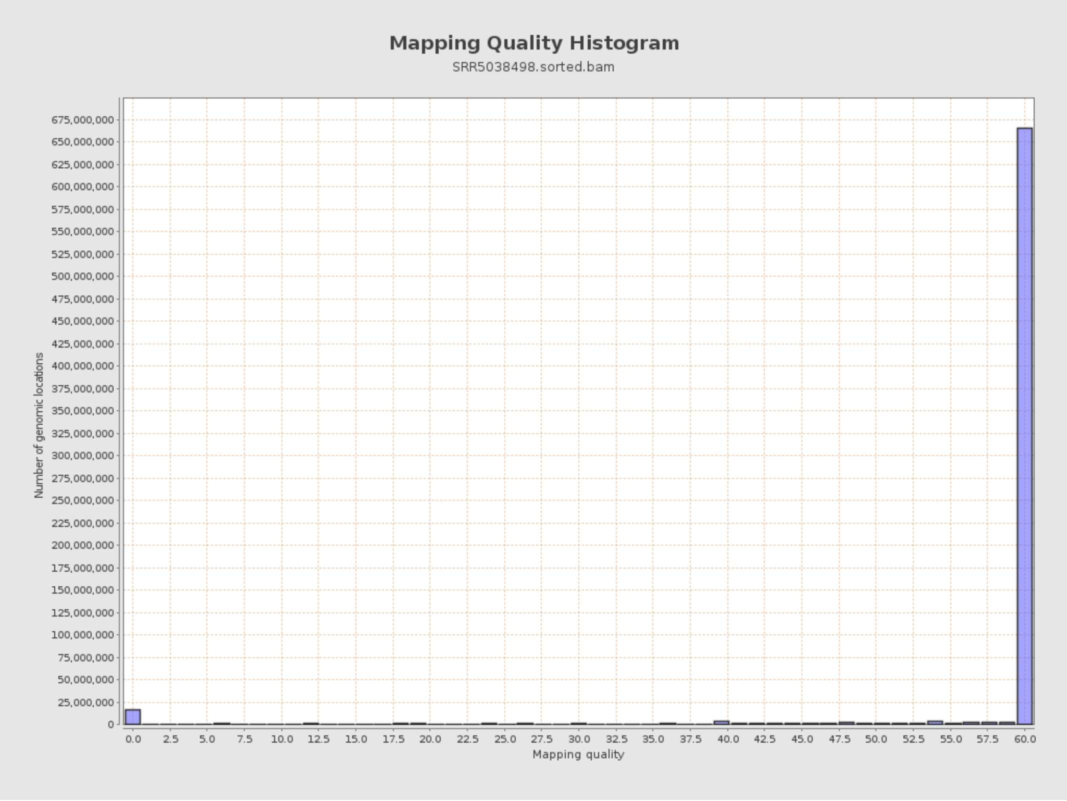
11. Results : Homopolymer Indels



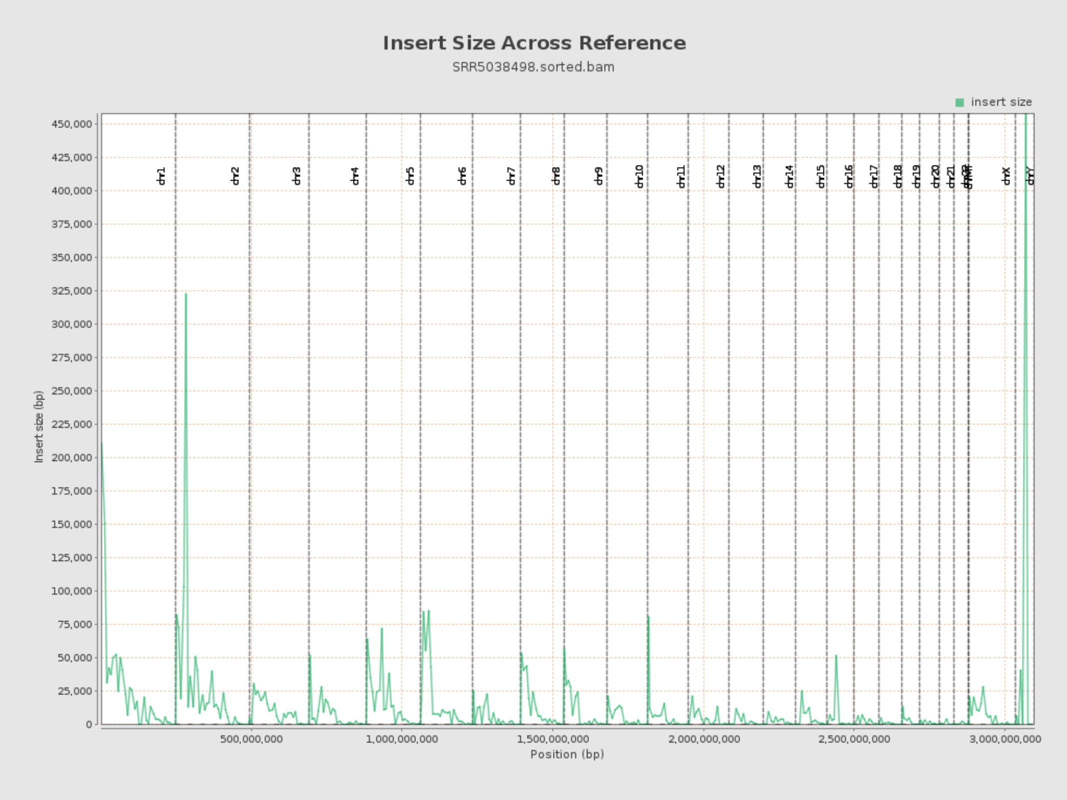
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram