Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 12:57:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038443.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_SRR5038443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038443_1.fastq.gz SRR5038443_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 12:57:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,629,564
Mapped reads	16,619,629 / 94.27%
Unmapped reads	1,009,935 / 5.73%
Mapped paired reads	16,619,629 / 94.27%
Mapped reads, first in pair	8,437,394 / 47.86%
Mapped reads, second in pair	8,182,235 / 46.41%
Mapped reads, both in pair	16,317,002 / 92.55%
Mapped reads, singletons	302,627 / 1.72%
Secondary alignments	0
Supplementary alignments	250,314 / 1.42%
Read min/max/mean length	30 / 150 / 150.71
Duplicated reads (estimated)	3,233,159 / 18.34%
Duplication rate	13.38%
Clipped reads	7,454,800 / 42.29%

2.2. ACGT Content

Number/percentage of A's	650,943,360 / 28.89%
Number/percentage of C's	442,299,426 / 19.63%
Number/percentage of T's	664,795,799 / 29.5%
Number/percentage of G's	495,039,129 / 21.97%
Number/percentage of N's	177,246 / 0.01%

GC Percentage	41.6%

2.3. Coverage

Mean	0.7284
Standard Deviation	10.795

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	85,997.5
Standard Deviation	2,861,066.48
P25/Median/P75	207 / 259 / 327

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	29,744,830
Insertions	385,224
Mapped reads with at least one insertion	2.21%
Deletions	793,602
Mapped reads with at least one deletion	4.61%
Homopolymer indels	47.8%

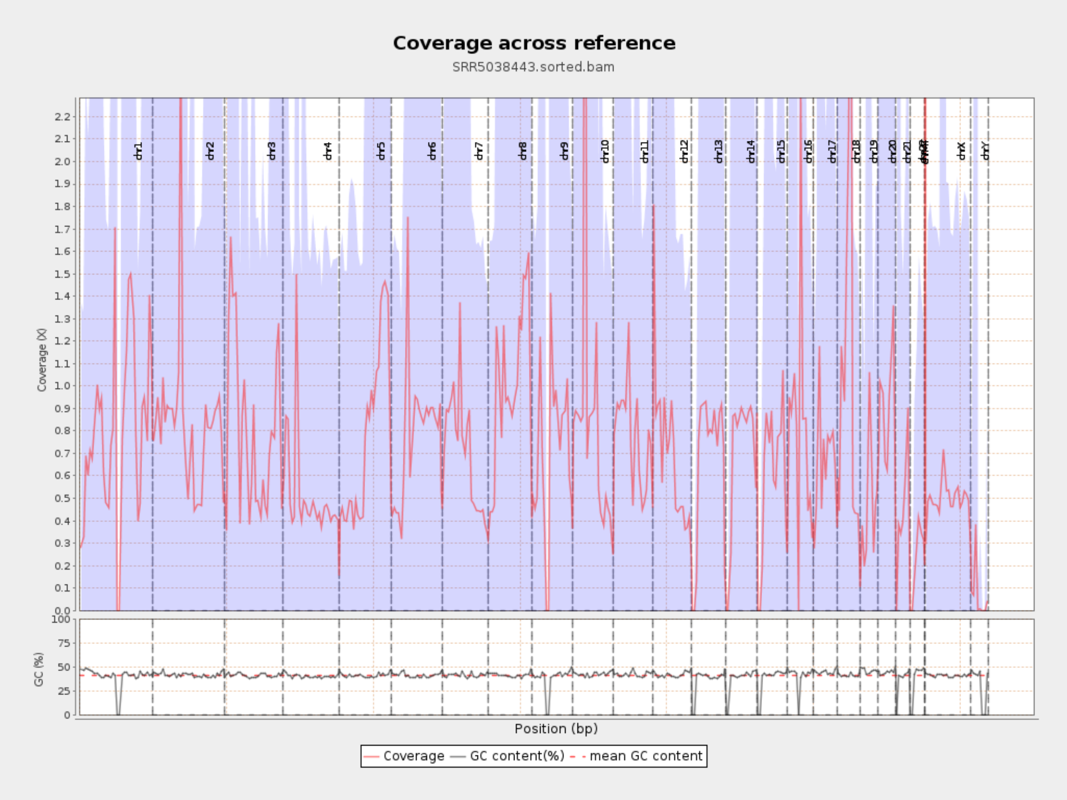
2.7. Chromosome stats

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

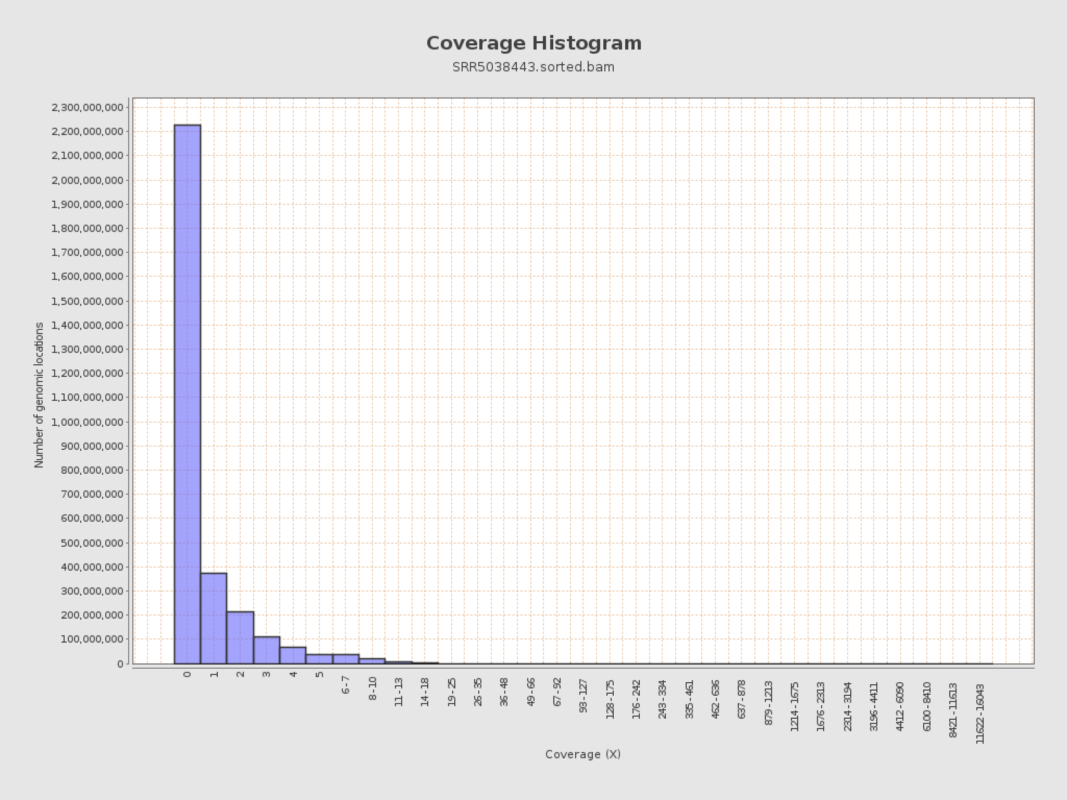
		bases	coverage	deviation
chr1	249250621	200640641	0.805	15.7473
chr2	243199373	205028399	0.843	11.0237
chr3	198022430	159817419	0.8071	1.8091
chr4	191154276	98945953	0.5176	8.699
chr5	180915260	139094430	0.7688	1.6459
chr6	171115067	136336857	0.7968	9.6288
chr7	159138663	110956227	0.6972	11.7775
chr8	146364022	148799079	1.0166	4.1195
chr9	141213431	97613985	0.6913	17.6617
chr10	135534747	123983576	0.9148	28.6567
chr11	135006516	103618277	0.7675	9.2745
chr12	133851895	93906333	0.7016	1.6994
chr13	115169878	79171723	0.6874	1.5075
chr14	107349540	74227138	0.6915	1.6381
chr15	102531392	60637967	0.5914	1.4235
chr16	90354753	71468022	0.791	10.9338
chr17	81195210	53245929	0.6558	12.0854
chr18	78077248	91513532	1.1721	12.1698
chr19	59128983	27296928	0.4617	6.3926
chr20	63025520	57438344	0.9114	3.0952
chr21	48129895	22026872	0.4577	3.9284
chr22	51304566	11794637	0.2299	0.8496
chrMT	16571	5520955	333.1697	171.8871
chrX	155270560	77337179	0.4981	2.4042

chrY	59373566	4360608	0.0734	8.1052

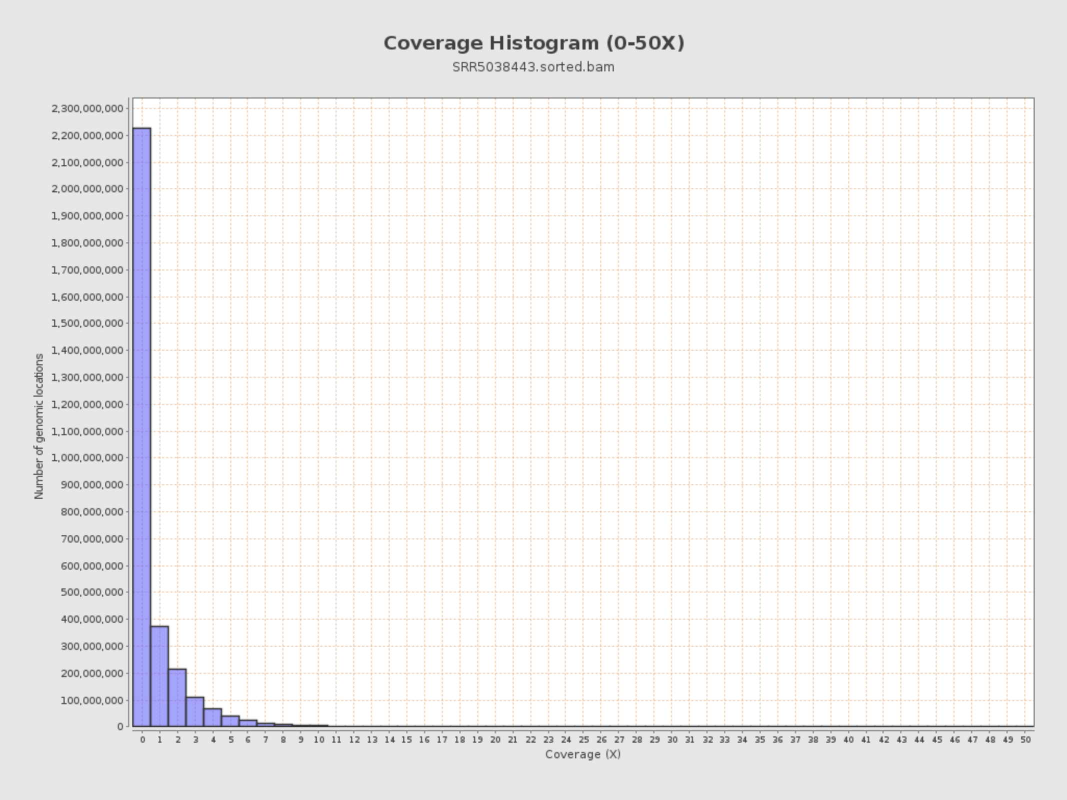
3. Results : Coverage across reference



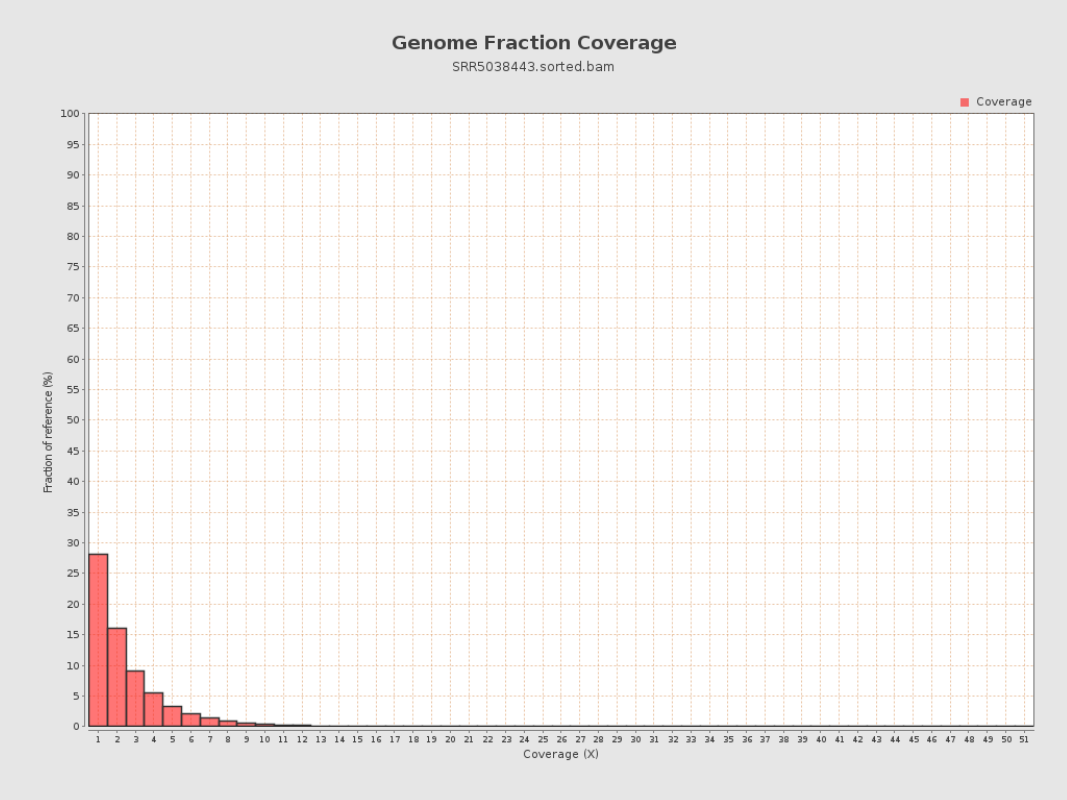
4. Results : Coverage Histogram



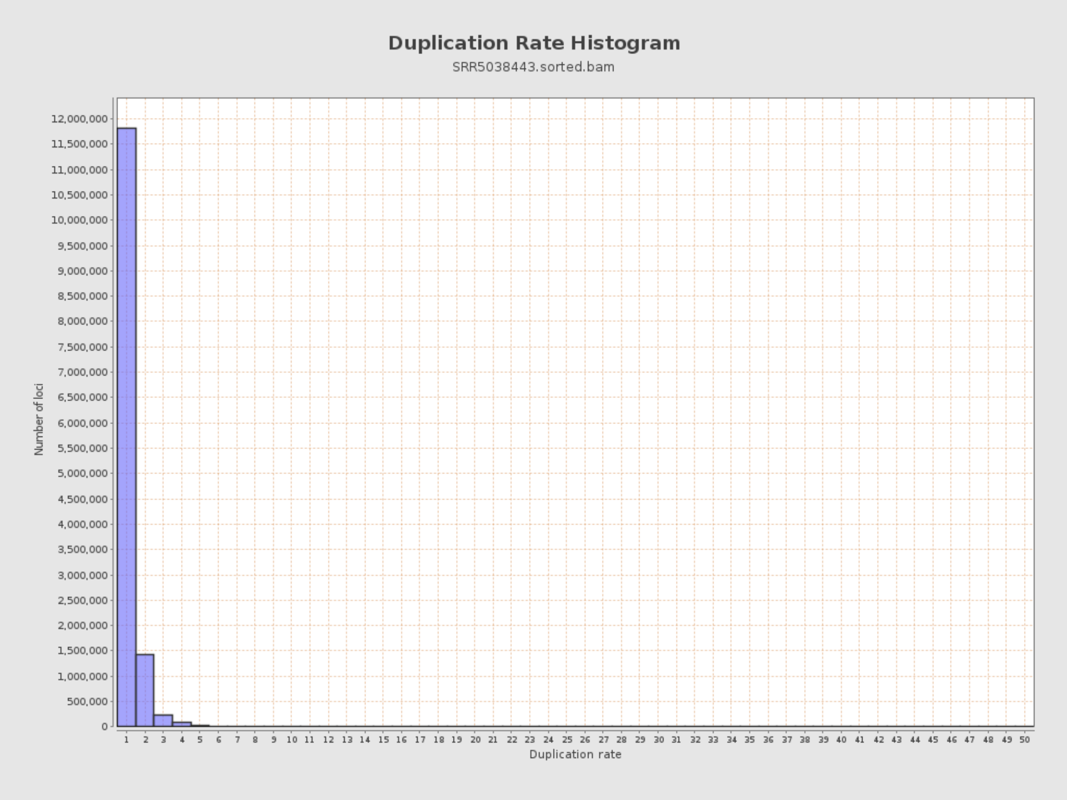
5. Results : Coverage Histogram (0-50X)



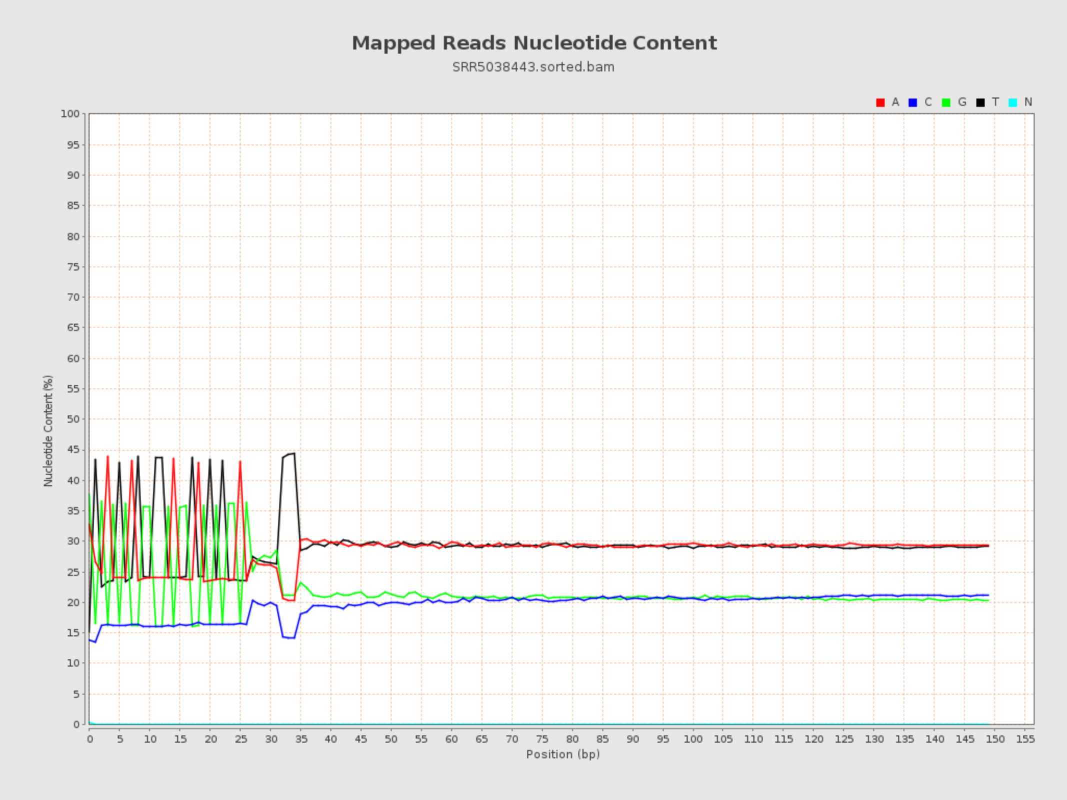
6. Results : Genome Fraction Coverage



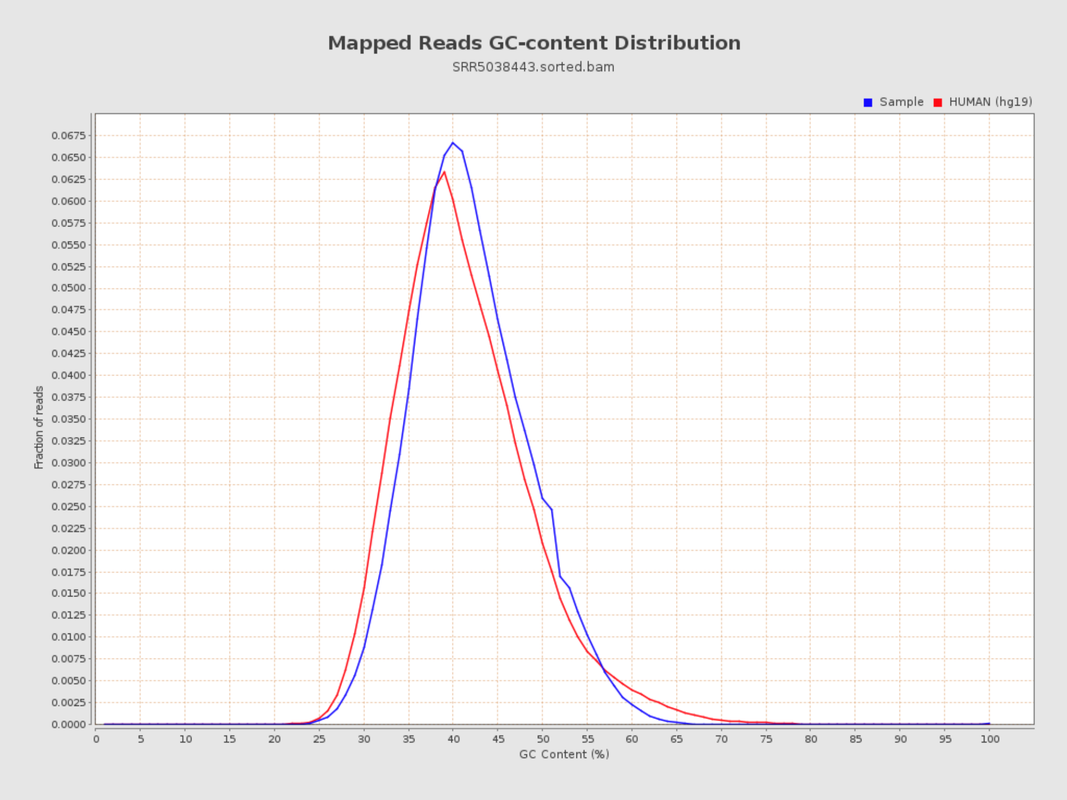
7. Results : Duplication Rate Histogram



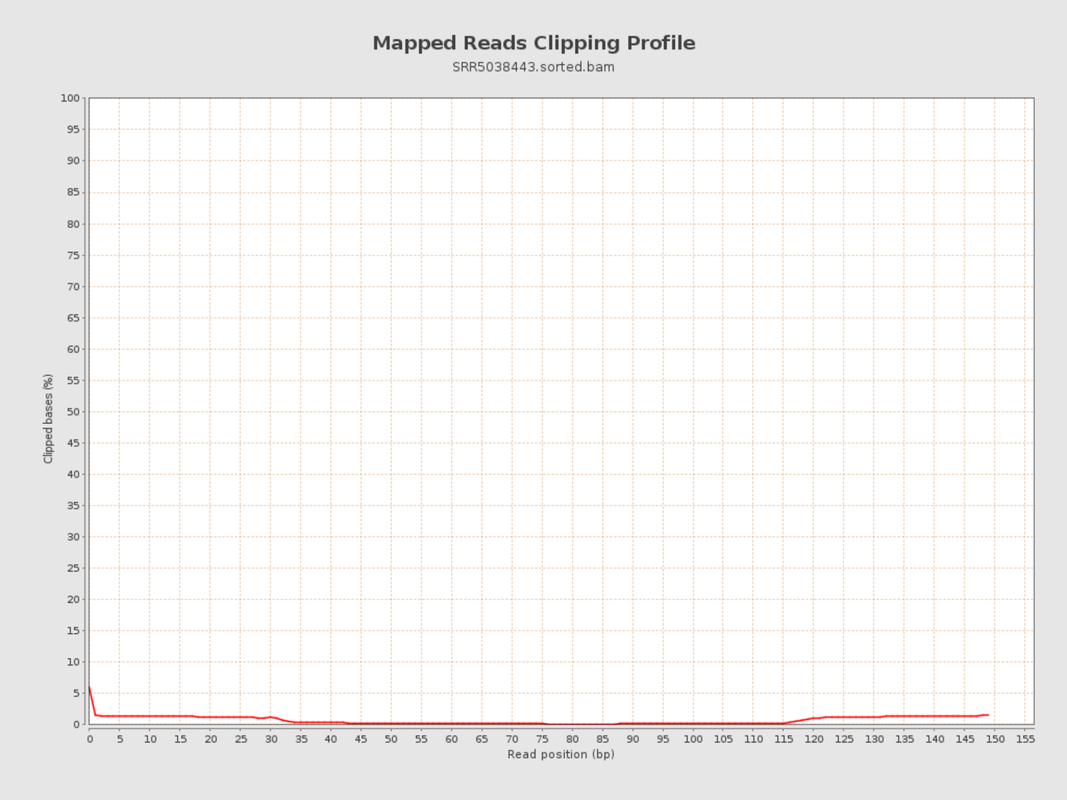
8. Results : Mapped Reads Nucleotide Content



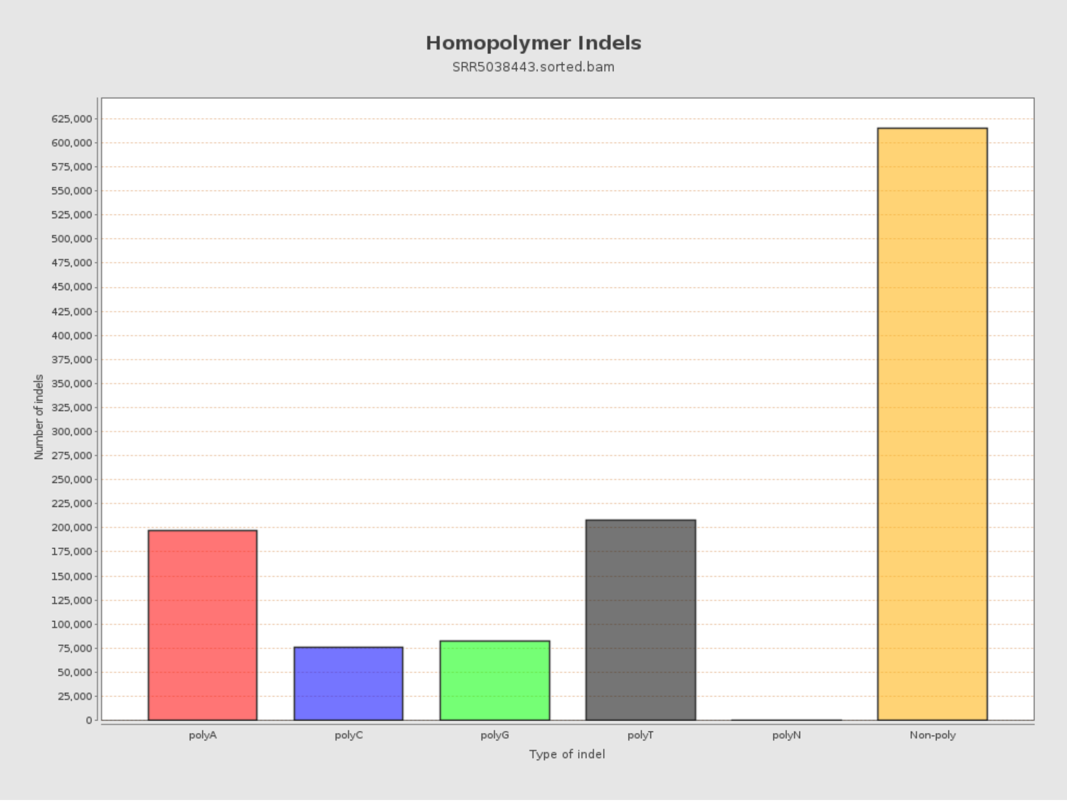
9. Results : Mapped Reads GC-content Distribution



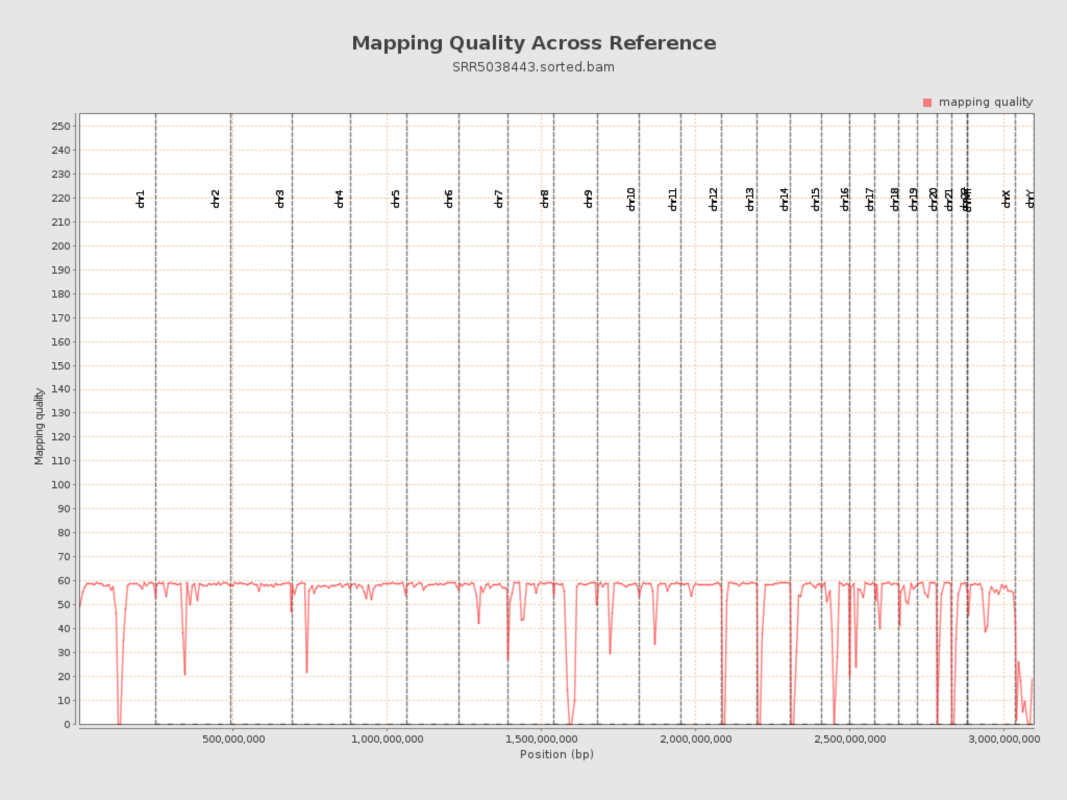
10. Results : Mapped Reads Clipping Profile



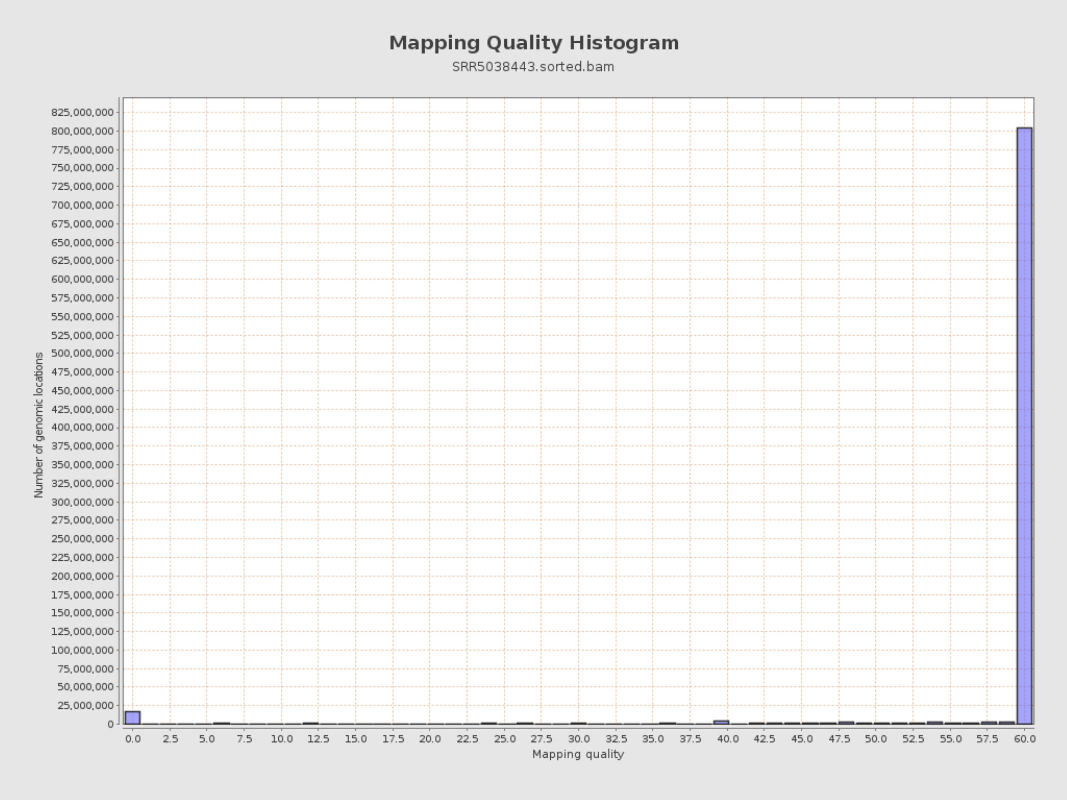
11. Results : Homopolymer Indels



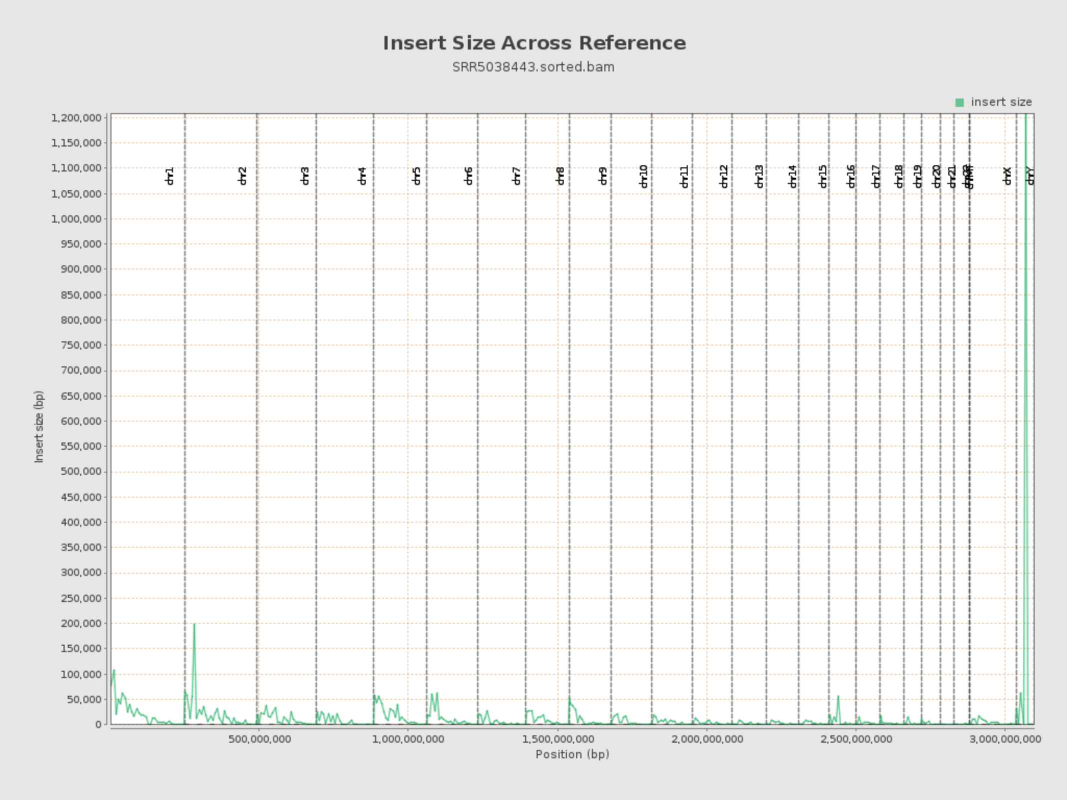
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram