Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 13:46:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038445.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_SRR5038445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038445_1.fastq.gz SRR5038445_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 13:46:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,695,706
Mapped reads	11,941,488 / 94.06%
Unmapped reads	754,218 / 5.94%
Mapped paired reads	11,941,488 / 94.06%
Mapped reads, first in pair	6,042,763 / 47.6%
Mapped reads, second in pair	5,898,725 / 46.46%
Mapped reads, both in pair	11,777,730 / 92.77%
Mapped reads, singletons	163,758 / 1.29%
Secondary alignments	0
Supplementary alignments	182,467 / 1.44%
Read min/max/mean length	30 / 150 / 150.73
Duplicated reads (estimated)	1,663,057 / 13.1%
Duplication rate	9.31%
Clipped reads	3,095,618 / 24.38%

2.2. ACGT Content

Number/percentage of A's	493,295,396 / 29.09%
Number/percentage of C's	344,500,258 / 20.32%
Number/percentage of T's	495,261,981 / 29.21%
Number/percentage of G's	362,396,274 / 21.37%
Number/percentage of N's	36,022 / 0%

GC Percentage	41.69%

2.3. Coverage

Mean	0.5481
Standard Deviation	6.6161

2.4. Mapping Quality

Mean Mapping Quality	53.77

2.5. Insert size

Mean	72,580.41
Standard Deviation	2,528,106.71
P25/Median/P75	216 / 259 / 312

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	22,407,985
Insertions	293,053
Mapped reads with at least one insertion	2.31%
Deletions	595,627
Mapped reads with at least one deletion	4.79%
Homopolymer indels	47.4%

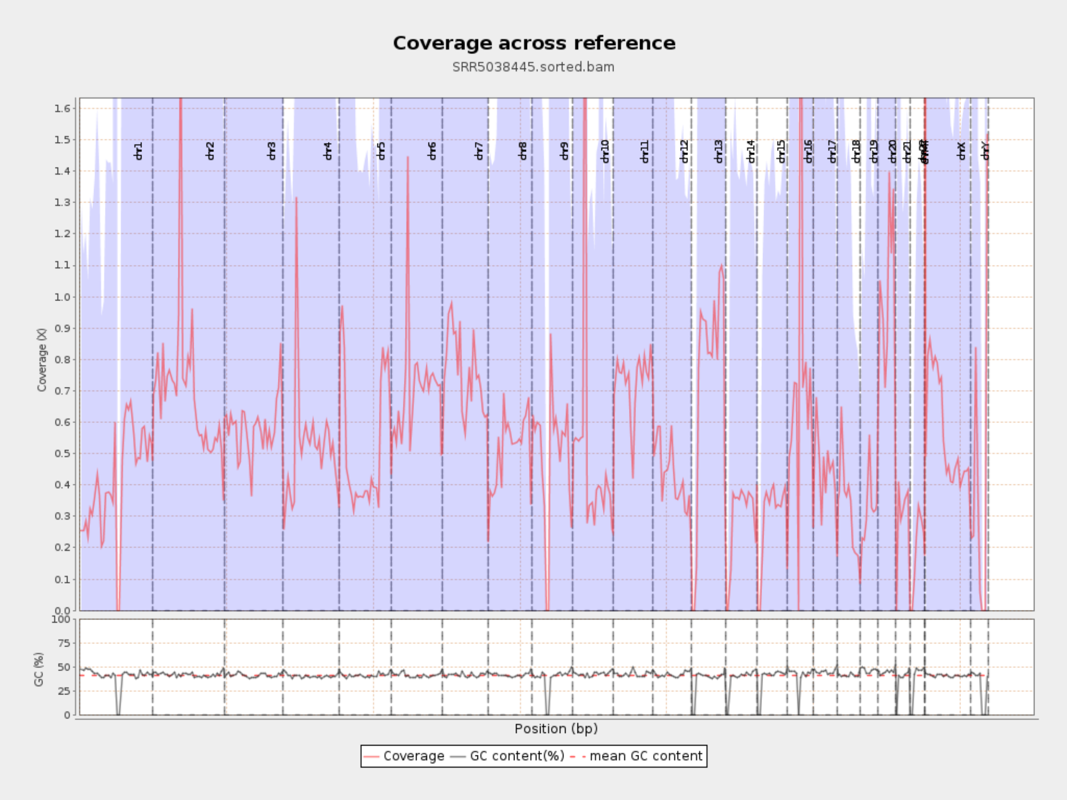
2.7. Chromosome stats

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

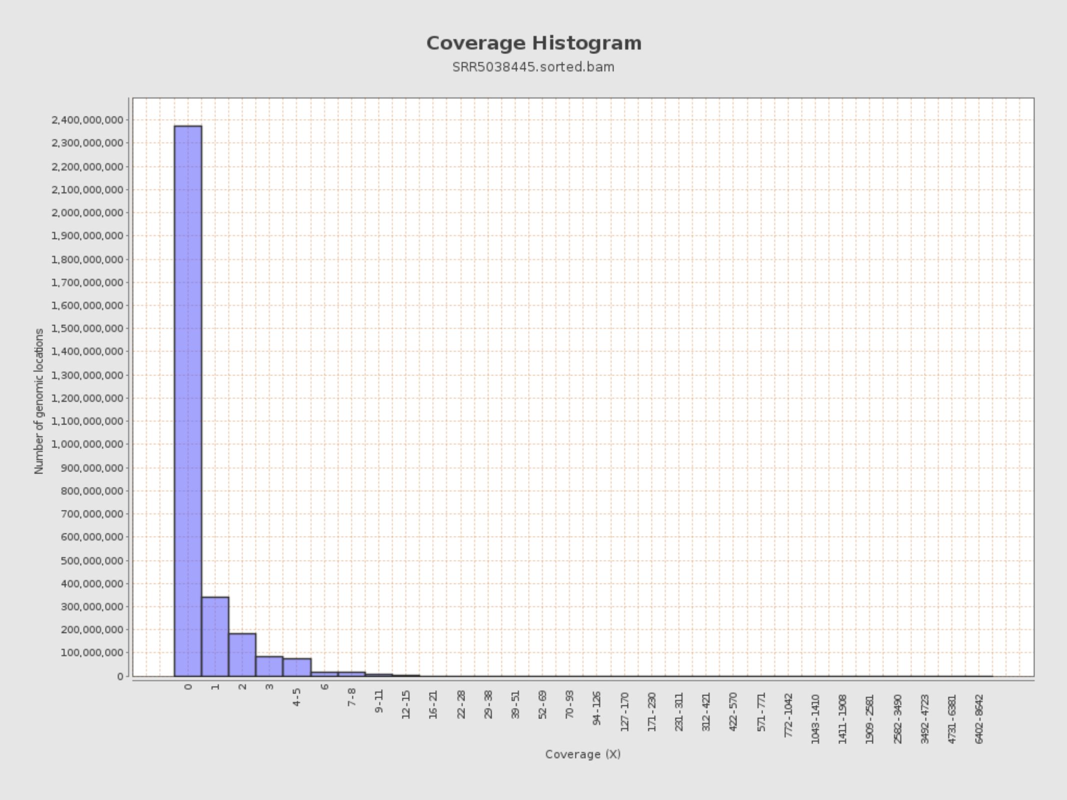
		bases	coverage	deviation
chr1	249250621	102159174	0.4099	4.0309
chr2	243199373	171575681	0.7055	7.9971
chr3	198022430	115500997	0.5833	1.3784
chr4	191154276	99061647	0.5182	6.2333
chr5	180915260	95127617	0.5258	1.3474
chr6	171115067	122053070	0.7133	7.7966
chr7	159138663	119816352	0.7529	6.5076
chr8	146364022	75765570	0.5177	1.8641
chr9	141213431	68132559	0.4825	8.9673
chr10	135534747	72097403	0.5319	17.5219
chr11	135006516	97149273	0.7196	3.7415
chr12	133851895	57955678	0.433	1.1587
chr13	115169878	87427846	0.7591	1.6687
chr14	107349540	31182514	0.2905	0.9769
chr15	102531392	30157448	0.2941	0.9058
chr16	90354753	67592550	0.7481	14.0992
chr17	81195210	35940339	0.4426	3.4921
chr18	78077248	25780798	0.3302	7.1116
chr19	59128983	18511682	0.3131	2.5262
chr20	63025520	63321149	1.0047	2.7144
chr21	48129895	14383158	0.2988	3.1122
chr22	51304566	9698772	0.189	0.8401
chrMT	16571	3984845	240.471	112.2165
chrX	155270560	87514715	0.5636	1.6326

chrY	59373566	24792843	0.4176	12.088

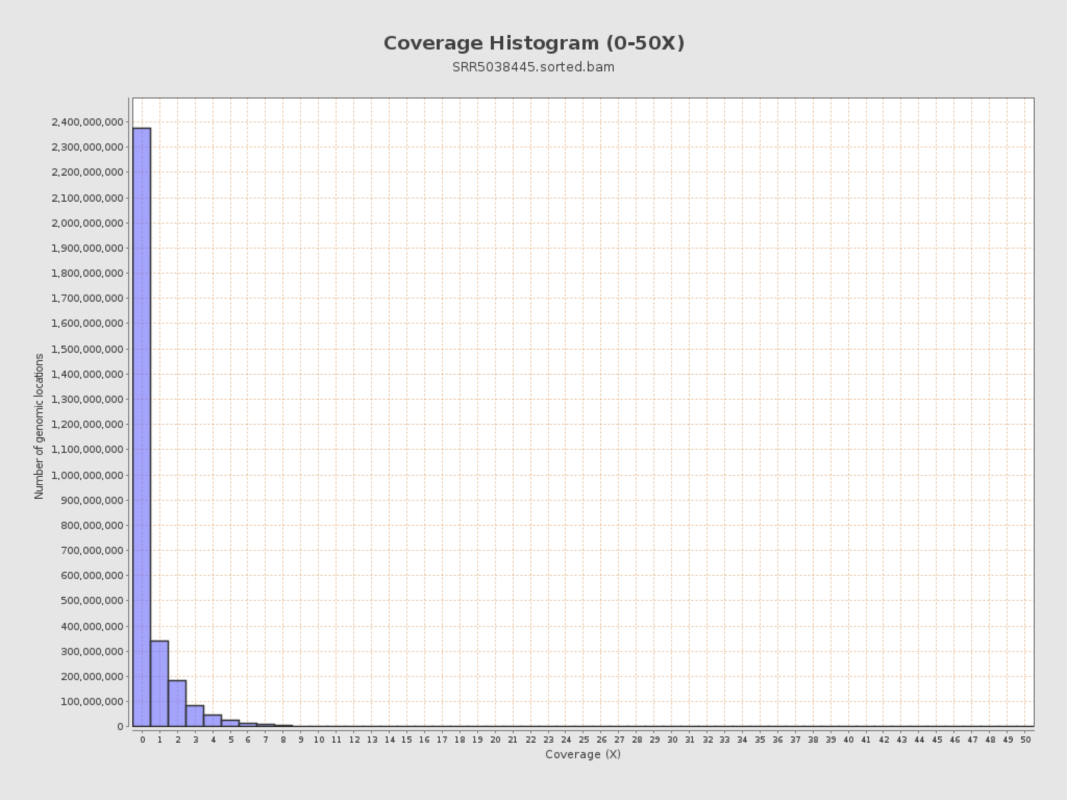
3. Results : Coverage across reference



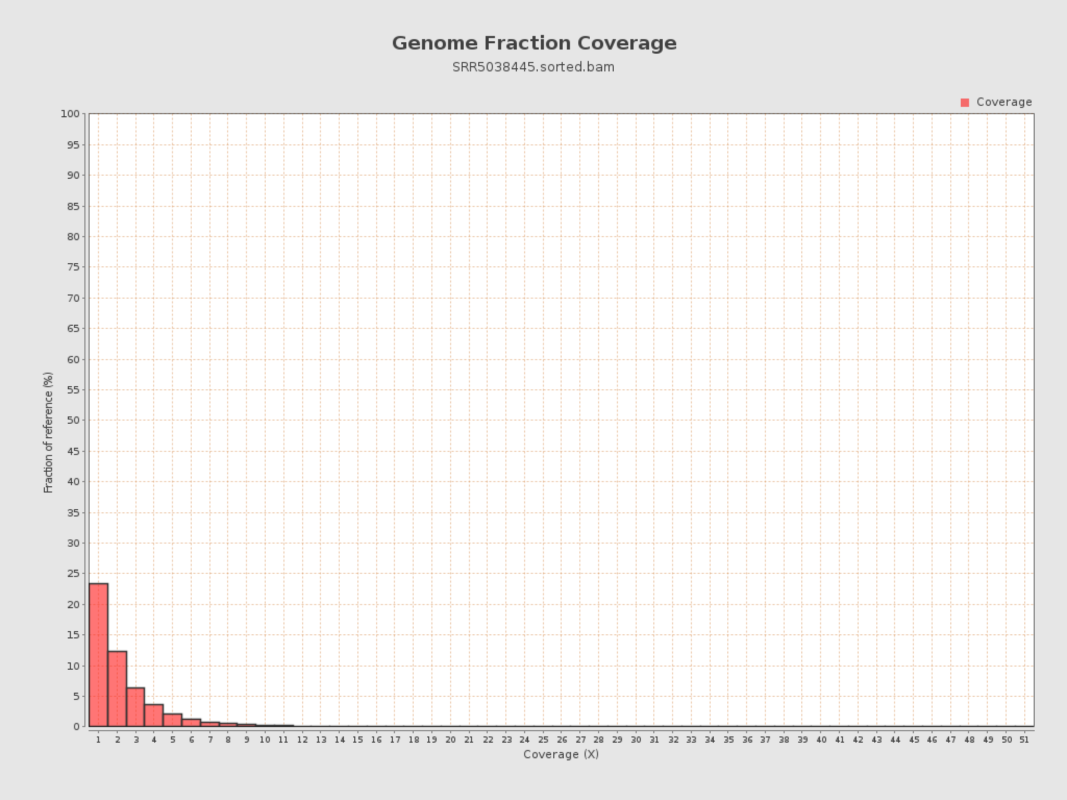
4. Results : Coverage Histogram



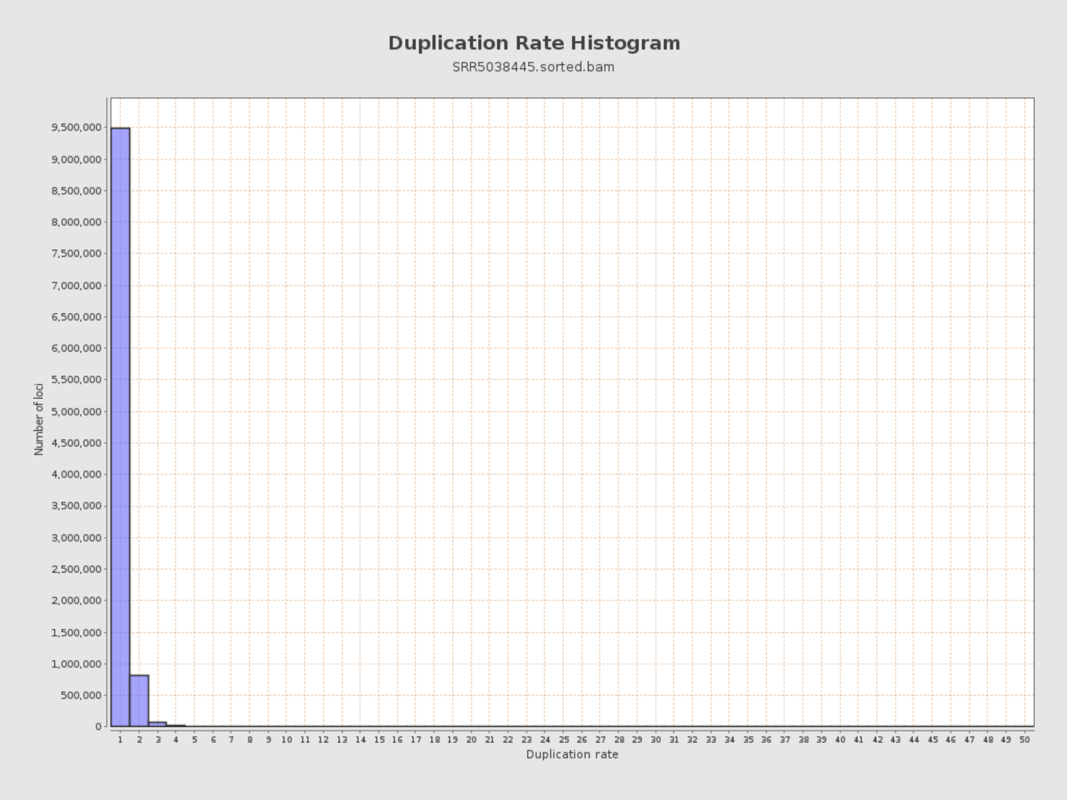
5. Results : Coverage Histogram (0-50X)



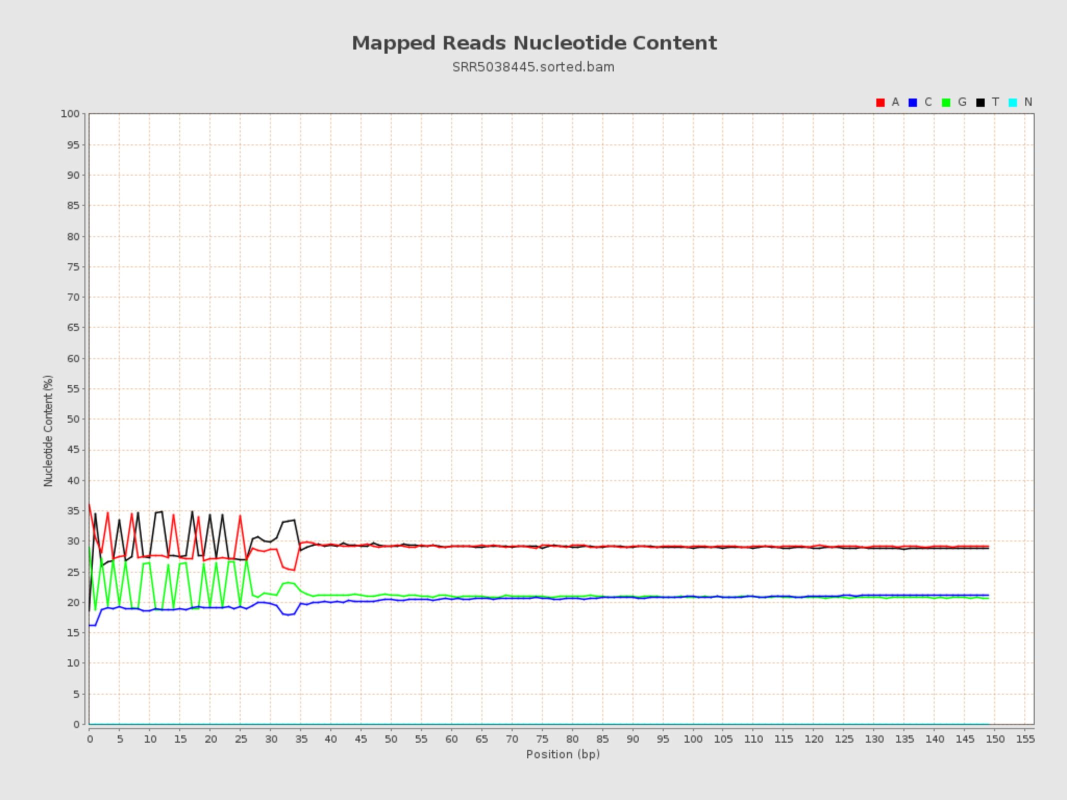
6. Results : Genome Fraction Coverage



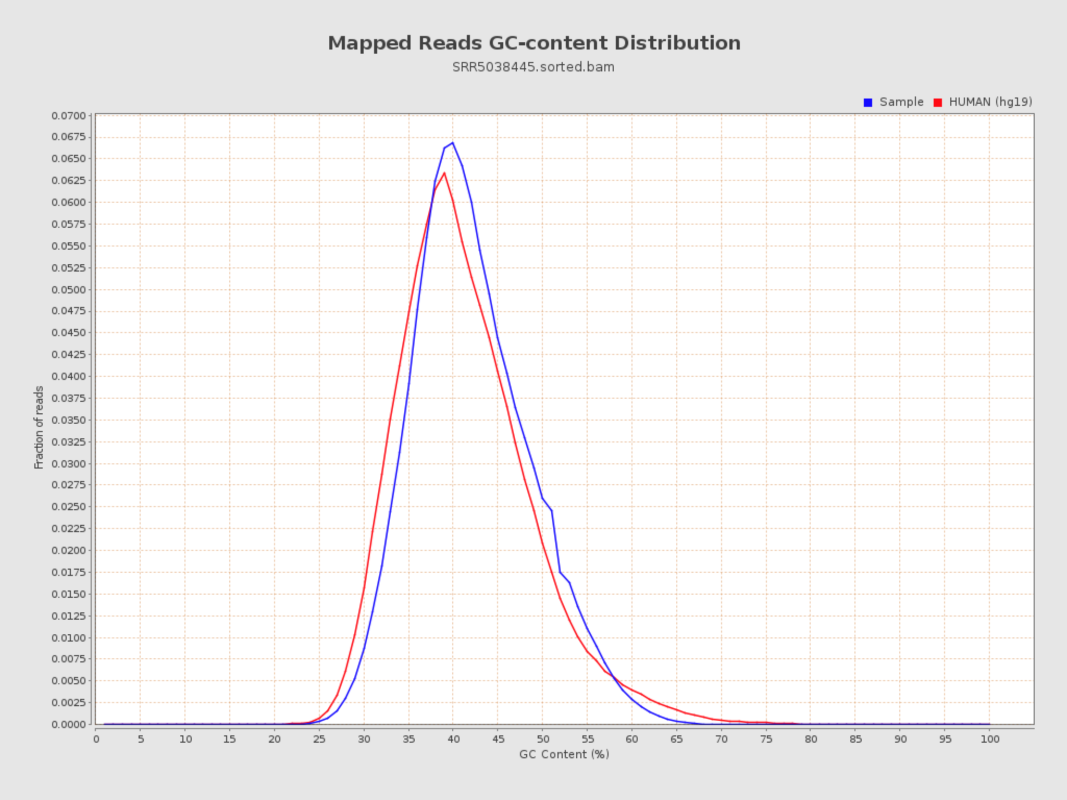
7. Results : Duplication Rate Histogram



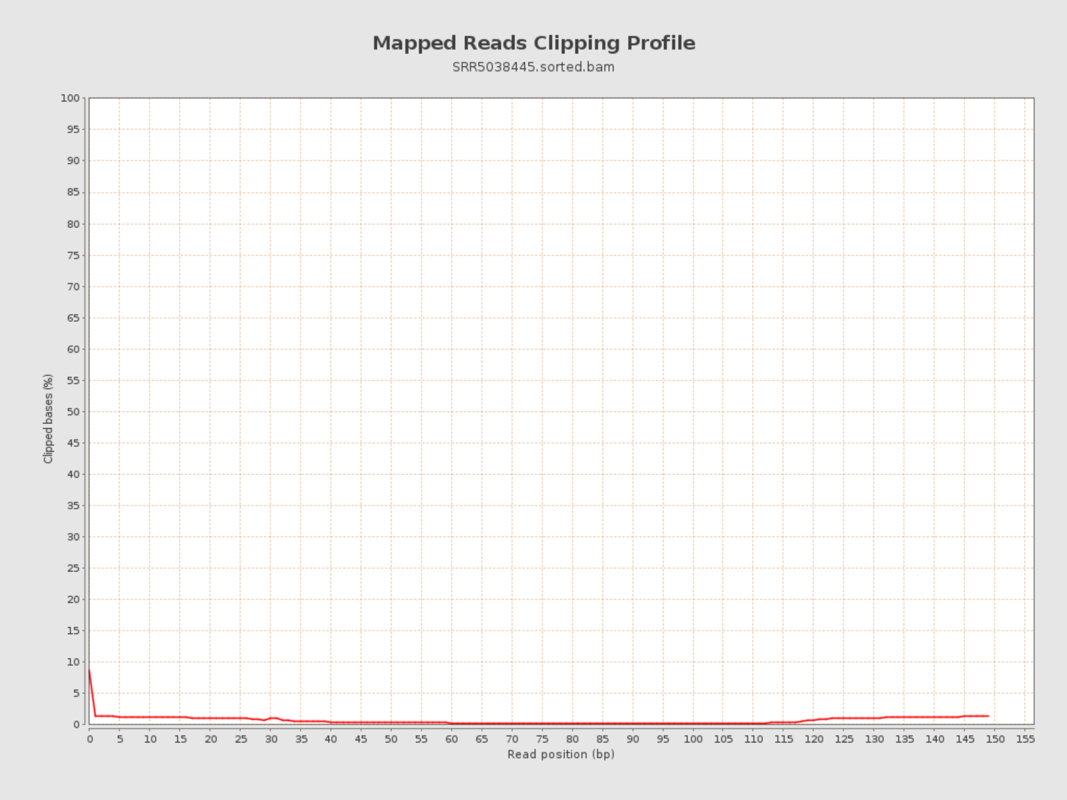
8. Results : Mapped Reads Nucleotide Content



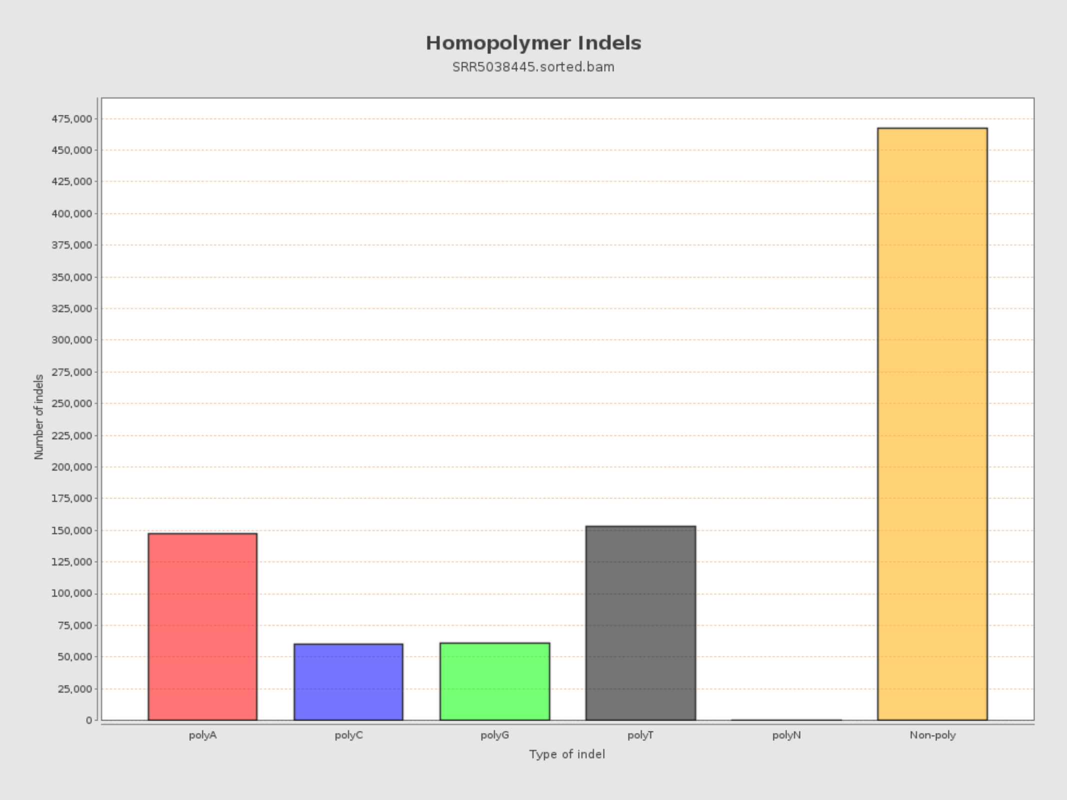
9. Results : Mapped Reads GC-content Distribution



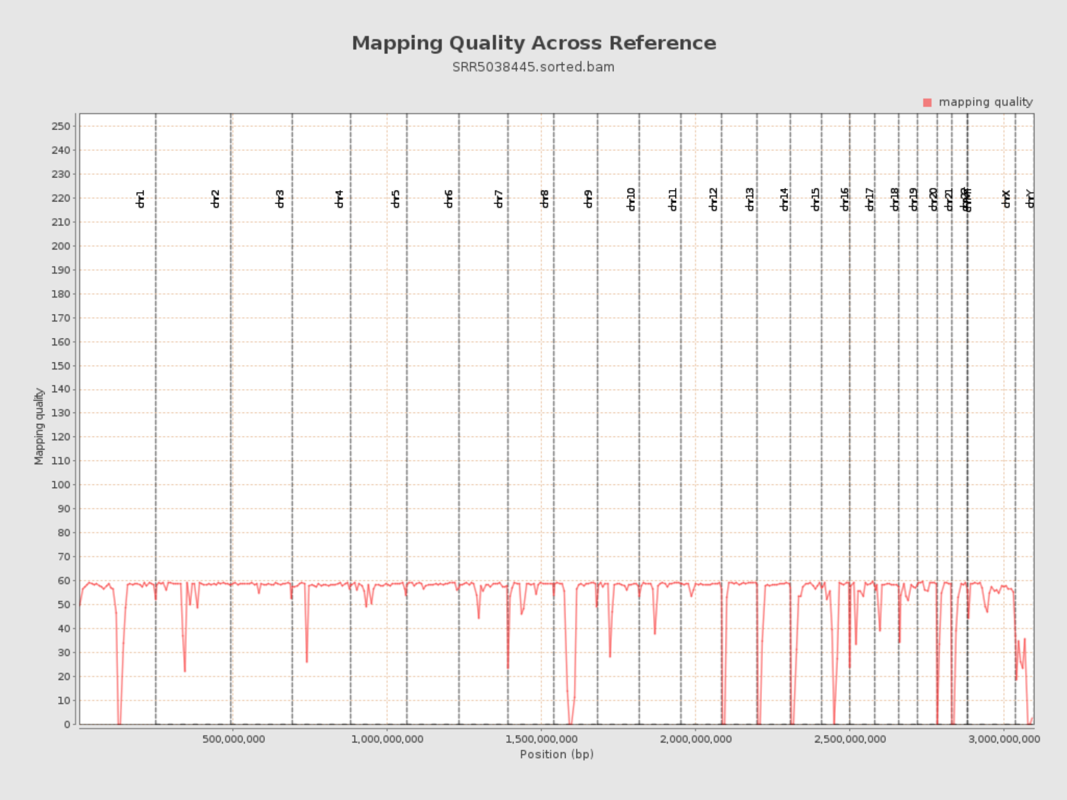
10. Results : Mapped Reads Clipping Profile



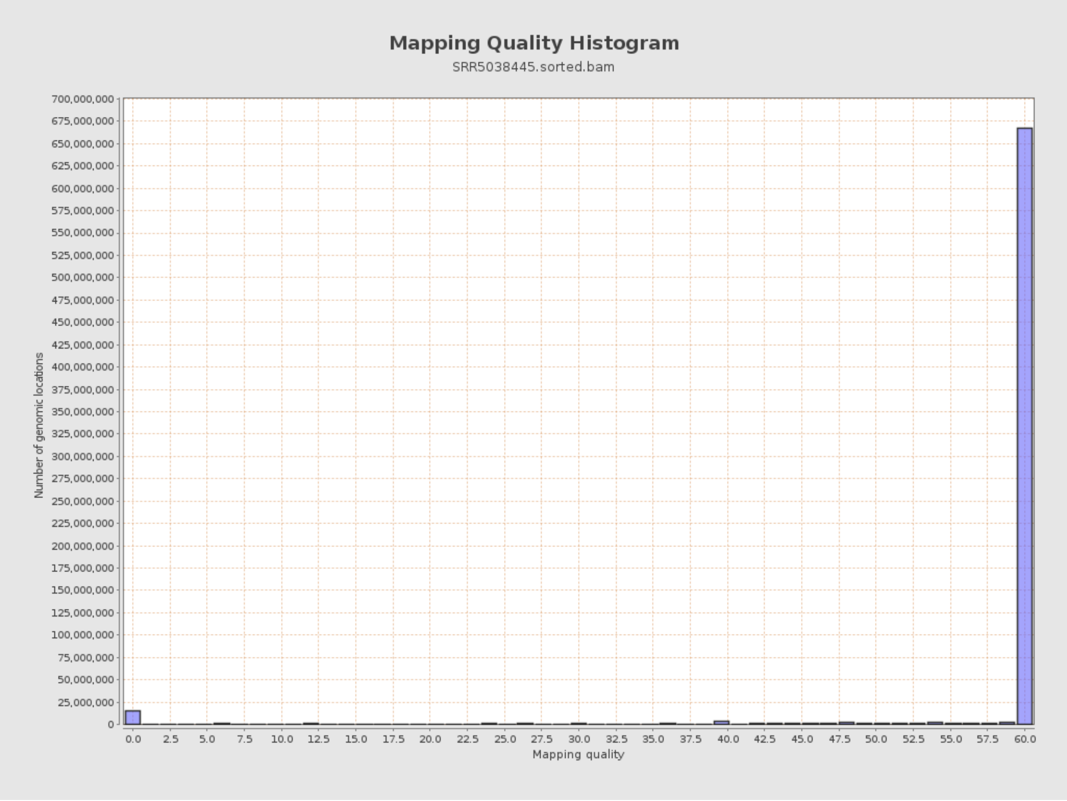
11. Results : Homopolymer Indels



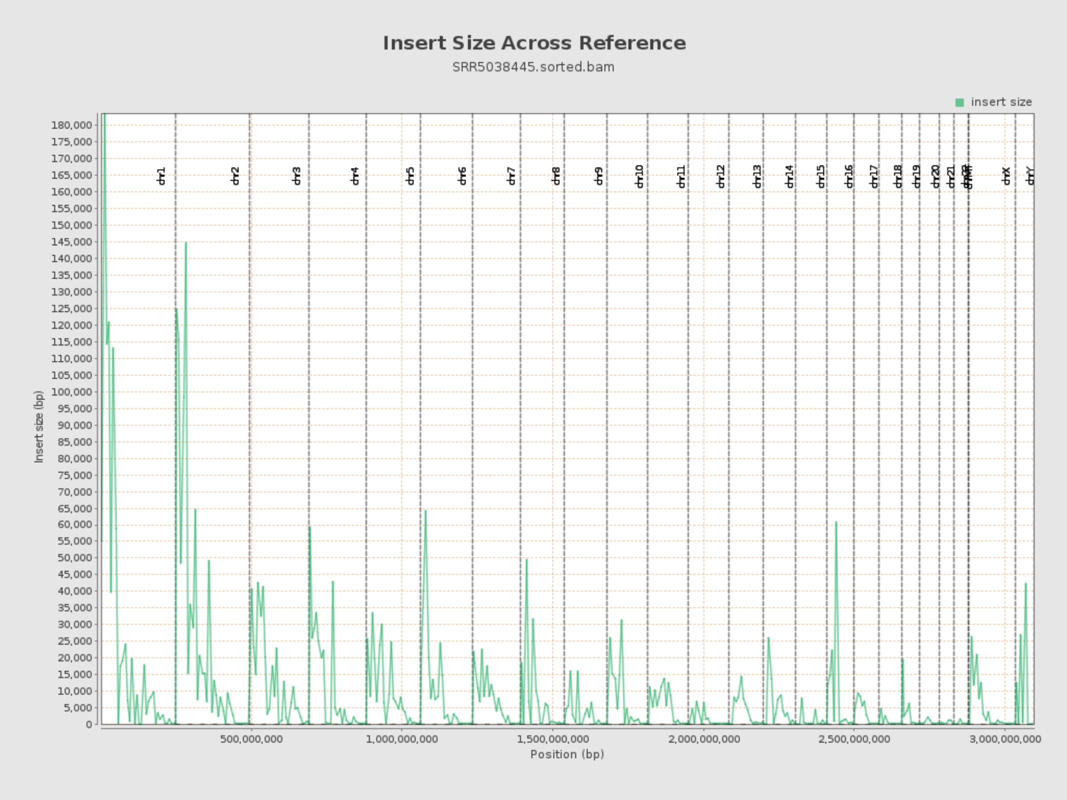
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram