Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 12:21:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038394.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_SRR5038394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038394_1.fastq.gz SRR5038394_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 12:21:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,506,684
Mapped reads	14,158,927 / 97.6%
Unmapped reads	347,757 / 2.4%
Mapped paired reads	14,158,927 / 97.6%
Mapped reads, first in pair	7,148,094 / 49.27%
Mapped reads, second in pair	7,010,833 / 48.33%
Mapped reads, both in pair	14,003,888 / 96.53%
Mapped reads, singletons	155,039 / 1.07%
Secondary alignments	0
Supplementary alignments	220,451 / 1.52%
Read min/max/mean length	30 / 150 / 150.77
Duplicated reads (estimated)	2,234,452 / 15.4%
Duplication rate	10.13%
Clipped reads	3,075,848 / 21.2%

2.2. ACGT Content

Number/percentage of A's	607,631,368 / 29.87%
Number/percentage of C's	403,251,485 / 19.82%
Number/percentage of T's	607,482,594 / 29.86%
Number/percentage of G's	415,734,509 / 20.44%
Number/percentage of N's	41,381 / 0%

GC Percentage	40.26%

2.3. Coverage

Mean	0.6576
Standard Deviation	9.3433

2.4. Mapping Quality

Mean Mapping Quality	53.81

2.5. Insert size

Mean	78,035.14
Standard Deviation	2,661,136.18
P25/Median/P75	207 / 253 / 312

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	28,342,001
Insertions	395,925
Mapped reads with at least one insertion	2.61%
Deletions	766,532
Mapped reads with at least one deletion	5.18%
Homopolymer indels	47.13%

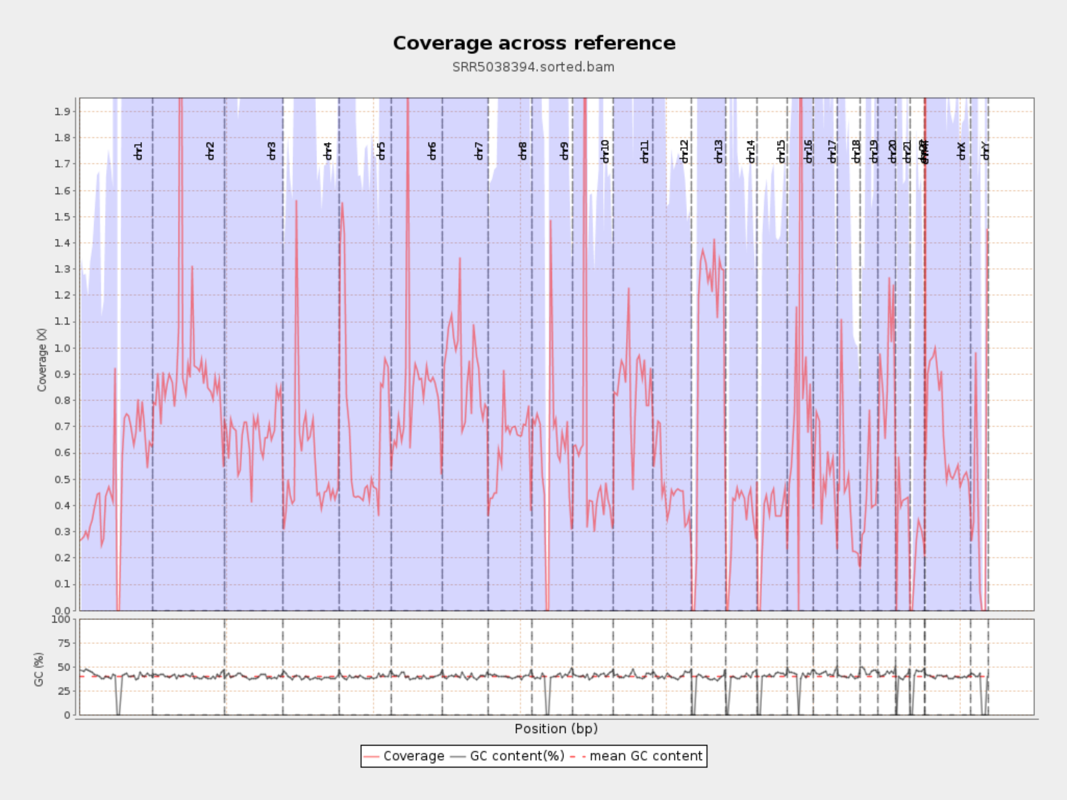
2.7. Chromosome stats

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

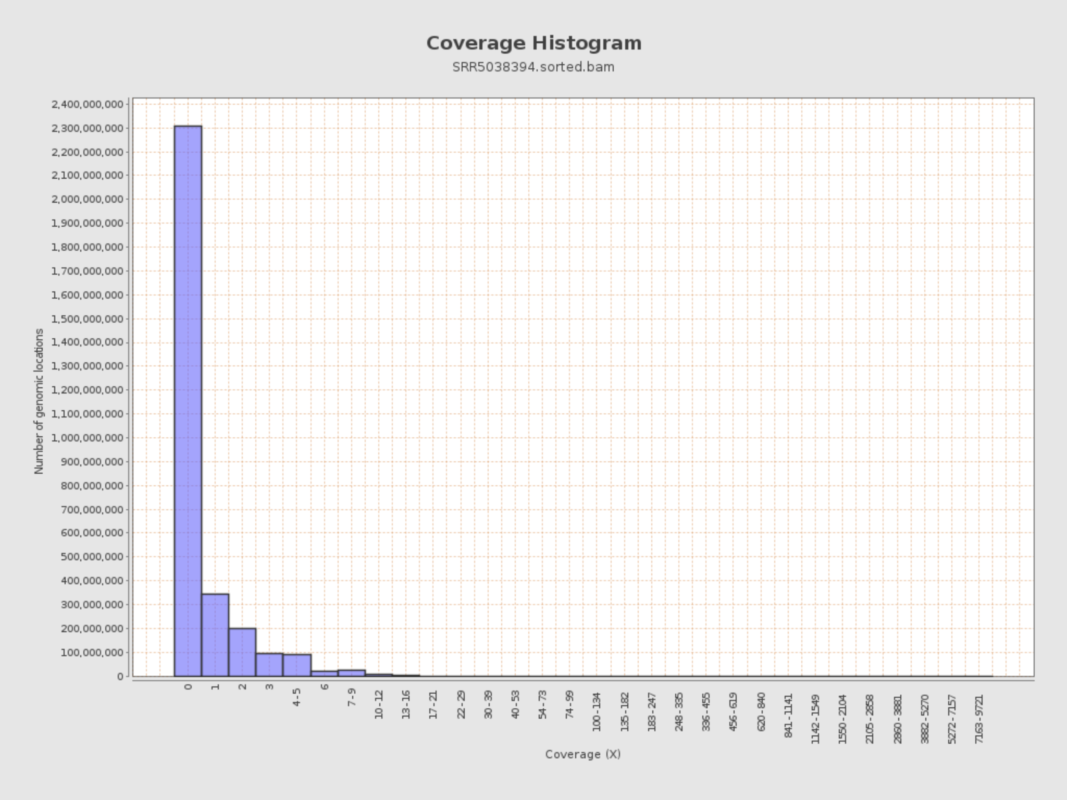
		bases	coverage	deviation
chr1	249250621	124145464	0.4981	8.12
chr2	243199373	230957663	0.9497	14.2121
chr3	198022430	133125760	0.6723	1.5609
chr4	191154276	106034484	0.5547	7.2327
chr5	180915260	125186236	0.692	1.745
chr6	171115067	146043567	0.8535	13.7512
chr7	159138663	146071337	0.9179	10.0336
chr8	146364022	91583792	0.6257	2.8655
chr9	141213431	83494043	0.5913	16.1979
chr10	135534747	81245087	0.5994	18.7122
chr11	135006516	115036813	0.8521	7.2253
chr12	133851895	62304873	0.4655	1.3496
chr13	115169878	122257303	1.0615	2.1186
chr14	107349540	36871188	0.3435	1.3018
chr15	102531392	34404469	0.3356	1.0217
chr16	90354753	77447613	0.8572	15.4657
chr17	81195210	42525121	0.5237	5.5249
chr18	78077248	33773606	0.4326	13.2339
chr19	59128983	24485699	0.4141	5.1696
chr20	63025520	58532974	0.9287	2.8847
chr21	48129895	18738699	0.3893	3.7051
chr22	51304566	10493261	0.2045	1.0464
chrMT	16571	849506	51.2646	35.5411
chrX	155270560	103184387	0.6645	2.3031

chrY	59373566	26864481	0.4525	12.8925

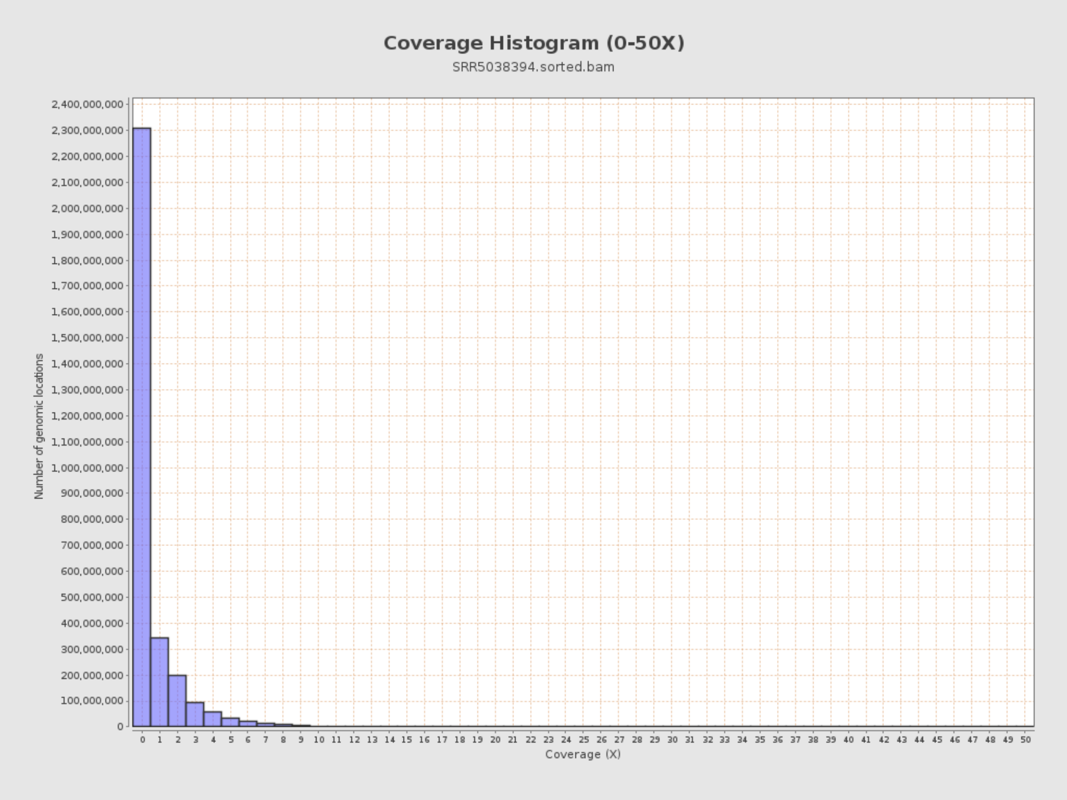
3. Results : Coverage across reference



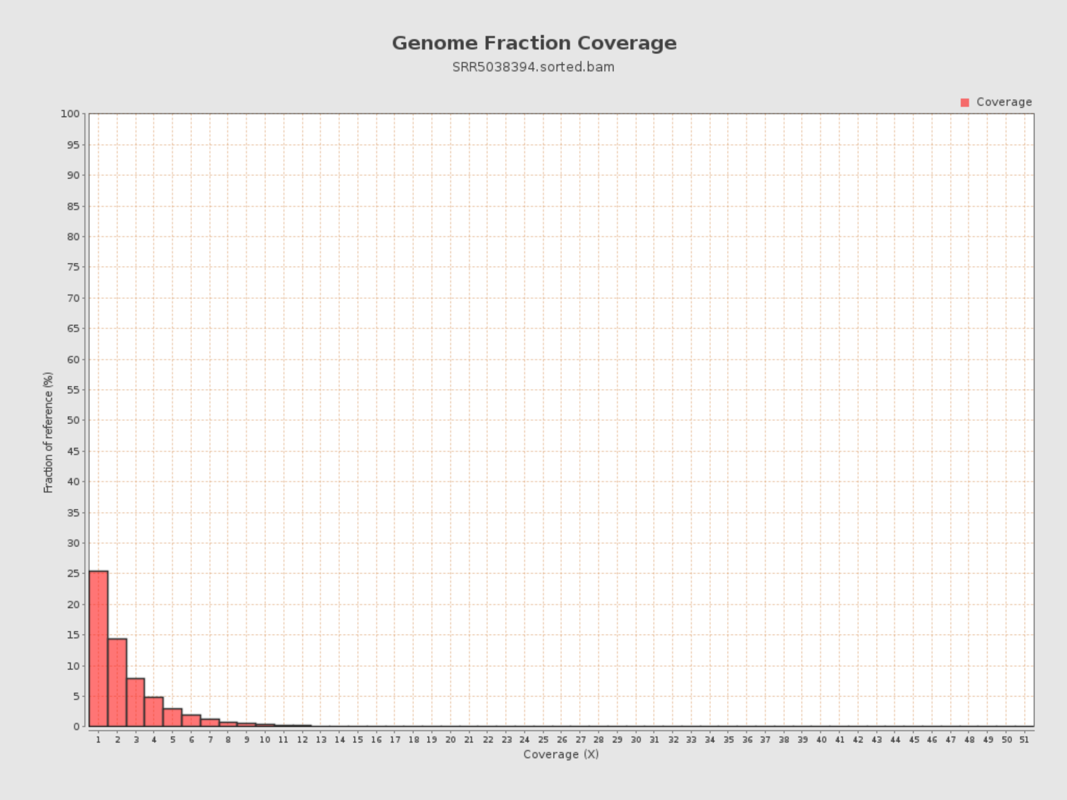
4. Results : Coverage Histogram



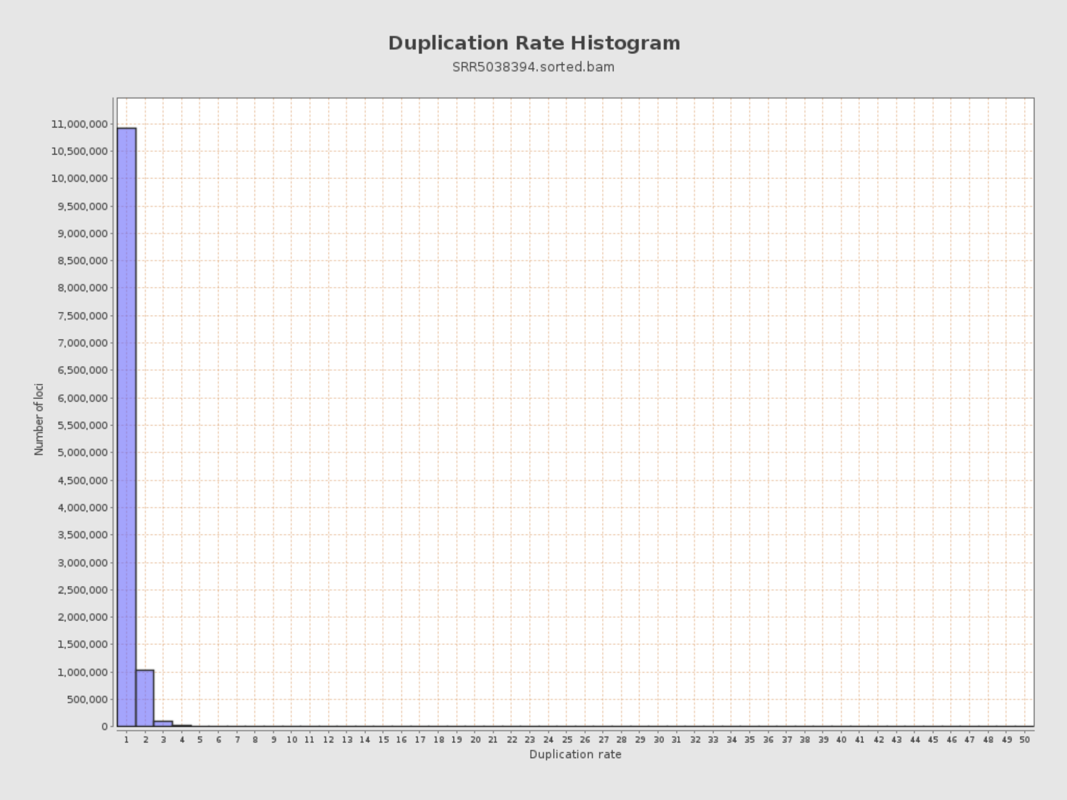
5. Results : Coverage Histogram (0-50X)



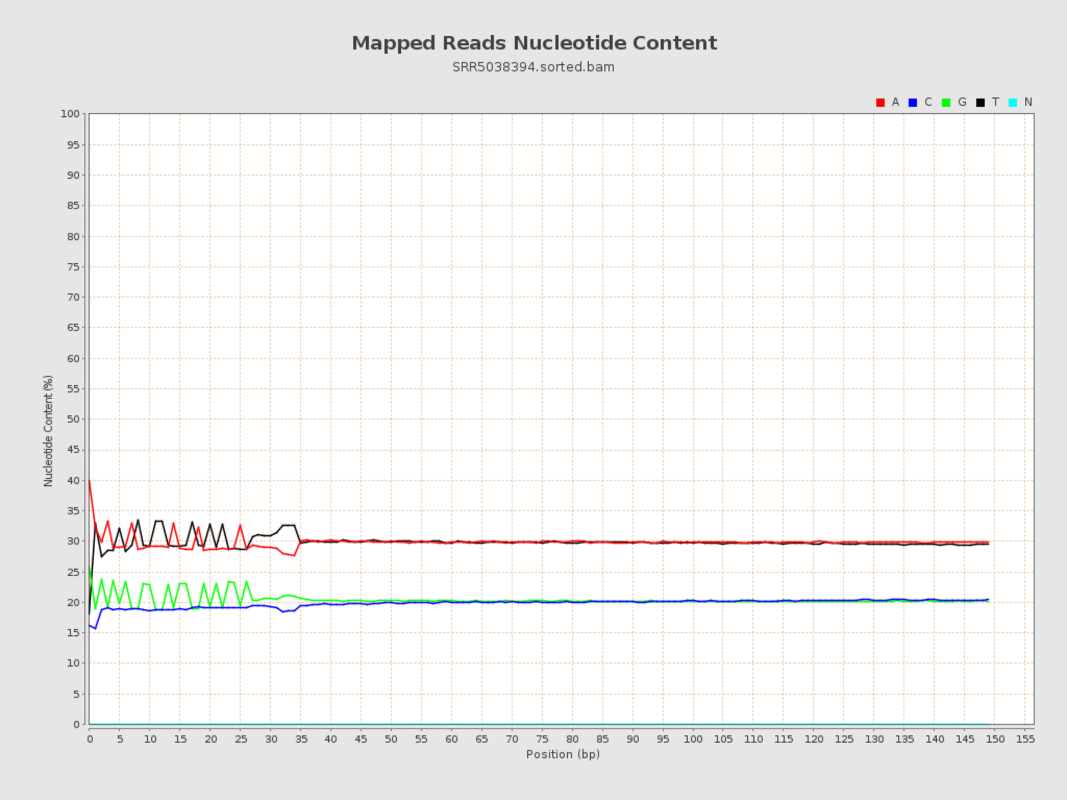
6. Results : Genome Fraction Coverage



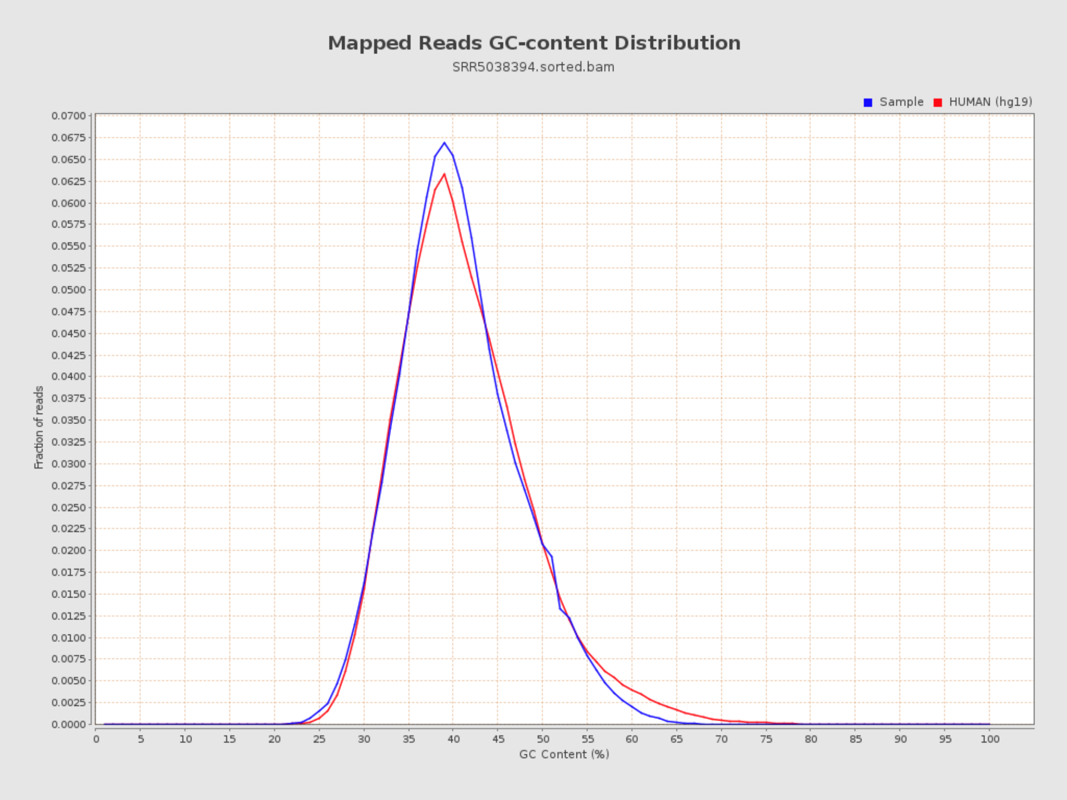
7. Results : Duplication Rate Histogram



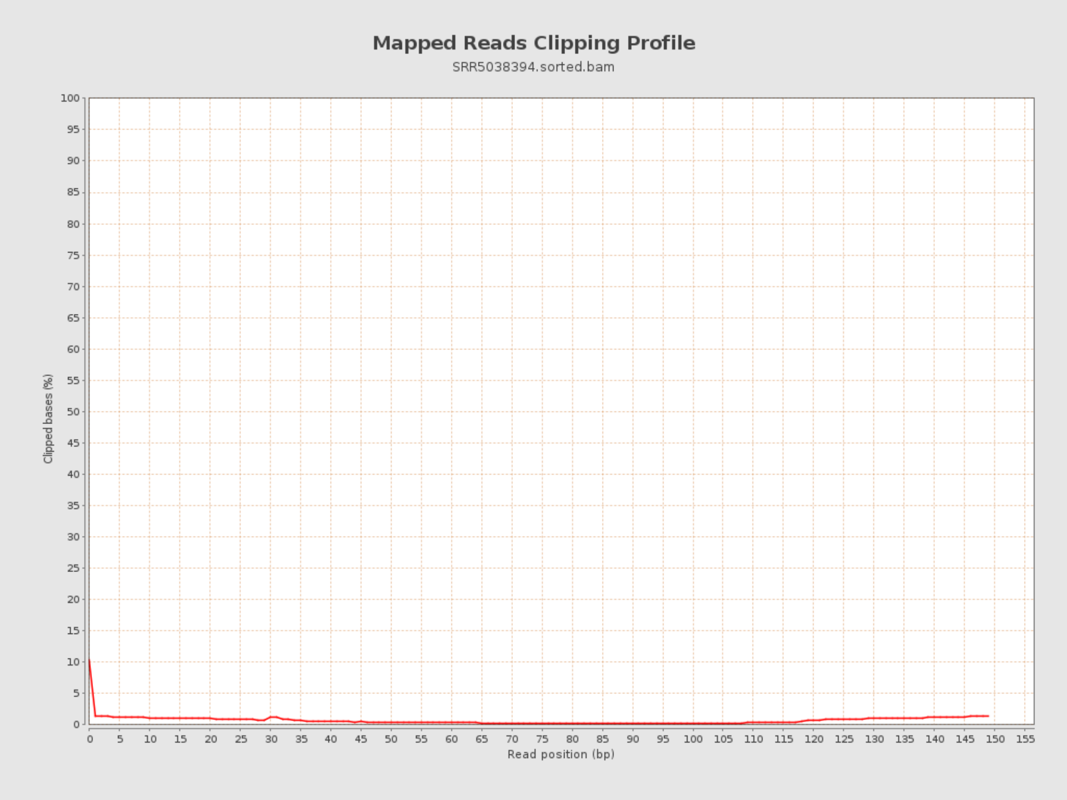
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



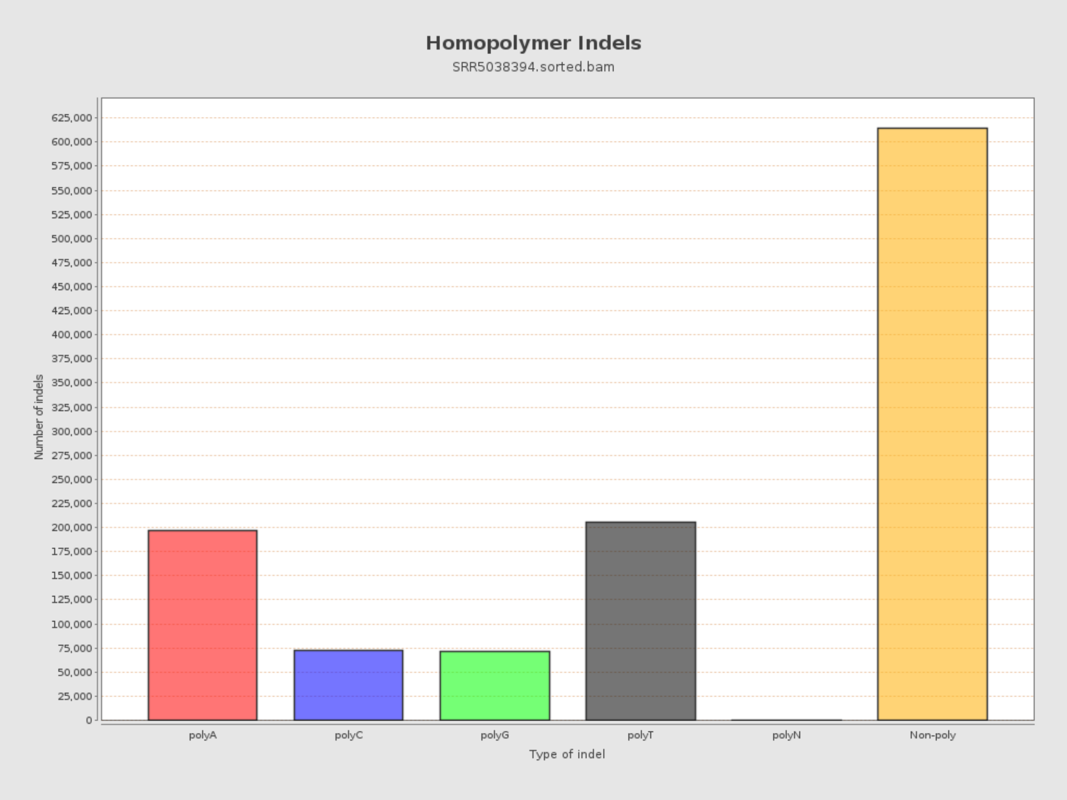
10. Results : Mapped Reads Clipping Profile



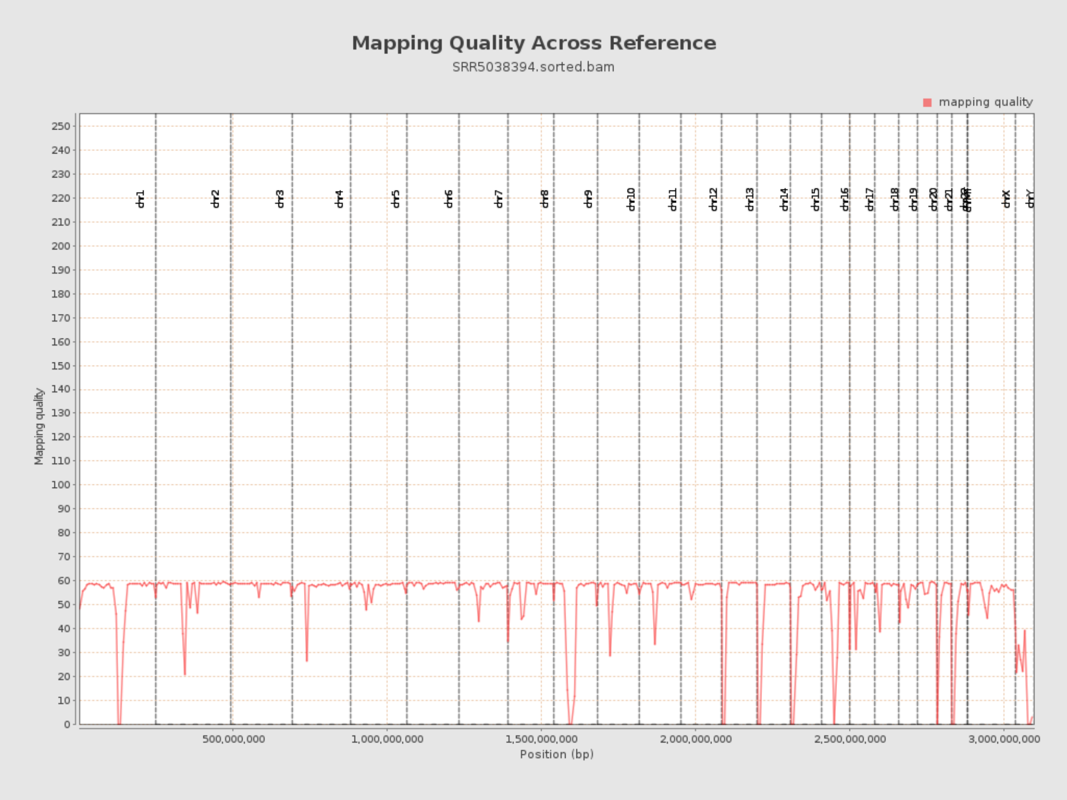
Mapped Reads Clipping Profile

SRR5038394.sorted.bam

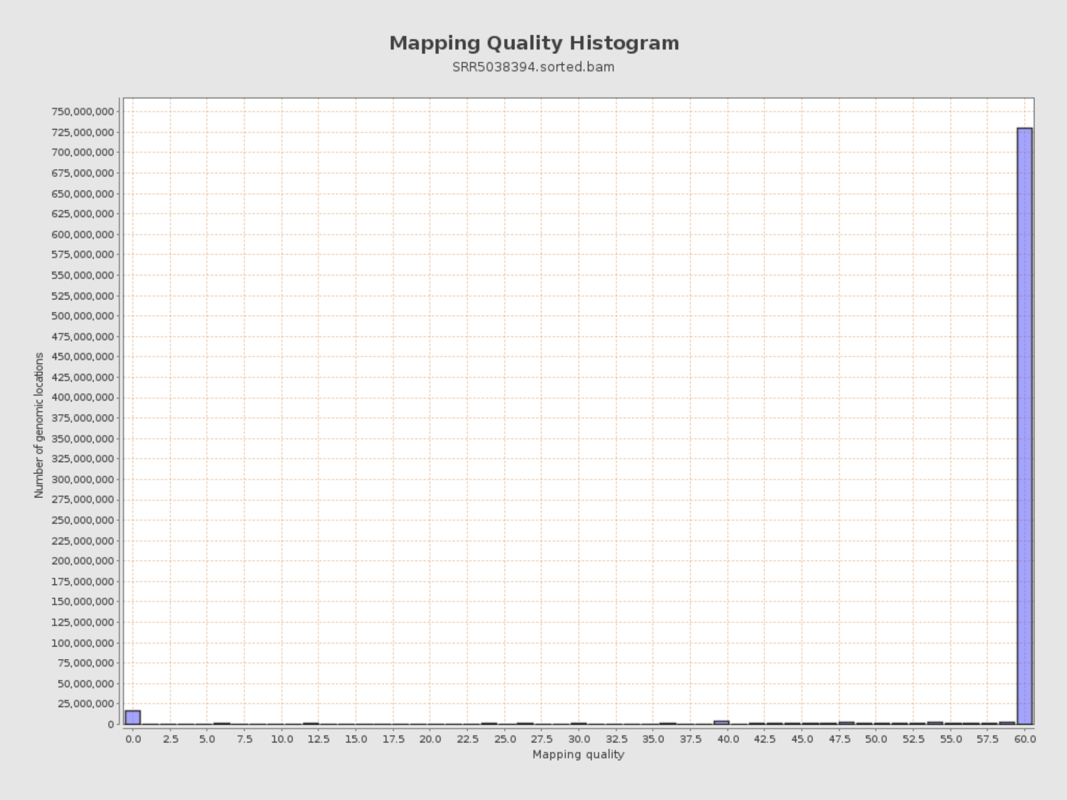
11. Results : Homopolymer Indels



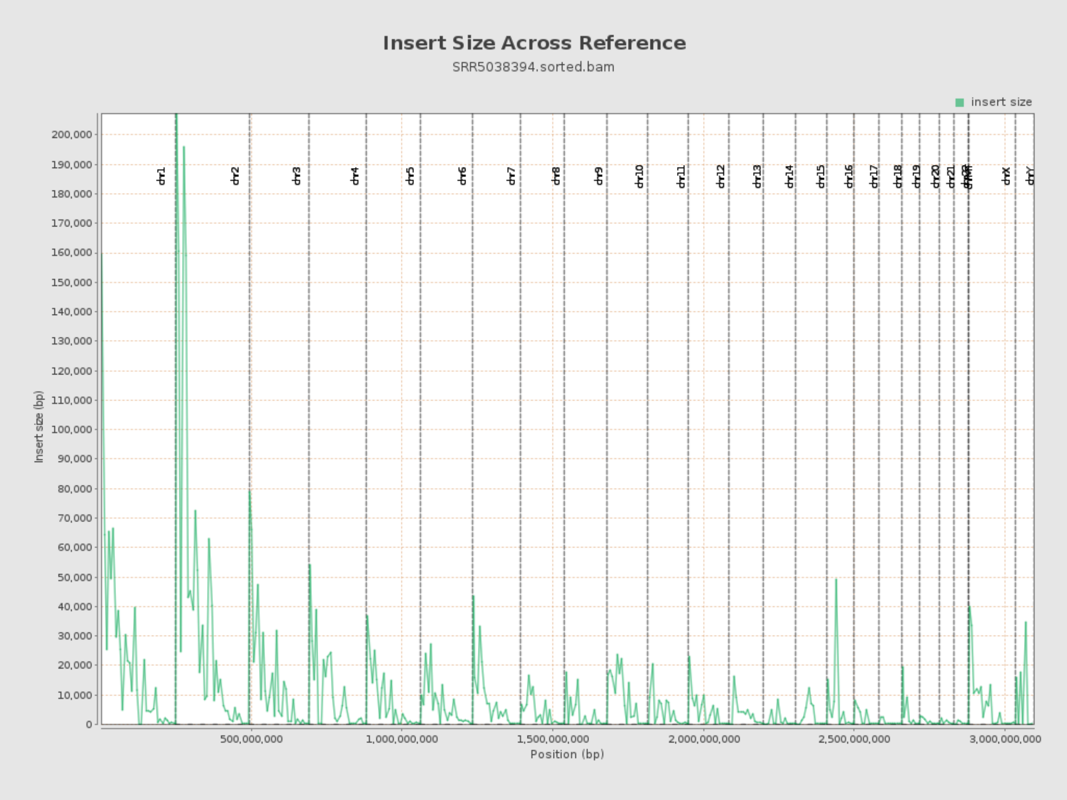
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram