Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 20:04:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038459.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_SRR5038459 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038459_1.fastq.gz SRR5038459_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 20:04:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038459.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,086,514
Mapped reads	12,339,653 / 94.29%
Unmapped reads	746,861 / 5.71%
Mapped paired reads	12,339,653 / 94.29%
Mapped reads, first in pair	6,281,449 / 48%
Mapped reads, second in pair	6,058,204 / 46.29%
Mapped reads, both in pair	12,077,766 / 92.29%
Mapped reads, singletons	261,887 / 2%
Secondary alignments	0
Supplementary alignments	190,152 / 1.45%
Read min/max/mean length	30 / 150 / 150.73
Duplicated reads (estimated)	1,896,083 / 14.49%
Duplication rate	10.51%
Clipped reads	5,809,447 / 44.39%

2.2. ACGT Content

Number/percentage of A's	476,543,325 / 28.65%
Number/percentage of C's	328,728,199 / 19.76%
Number/percentage of T's	487,057,209 / 29.28%
Number/percentage of G's	371,079,821 / 22.31%
Number/percentage of N's	126,681 / 0.01%

GC Percentage	42.07%

2.3. Coverage

Mean	0.5377
Standard Deviation	7.5053

2.4. Mapping Quality

Mean Mapping Quality	53.36

2.5. Insert size

Mean	95,311.87
Standard Deviation	3,028,414.72
P25/Median/P75	210 / 263 / 330

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	22,438,674
Insertions	287,628
Mapped reads with at least one insertion	2.22%
Deletions	583,947
Mapped reads with at least one deletion	4.56%
Homopolymer indels	47.64%

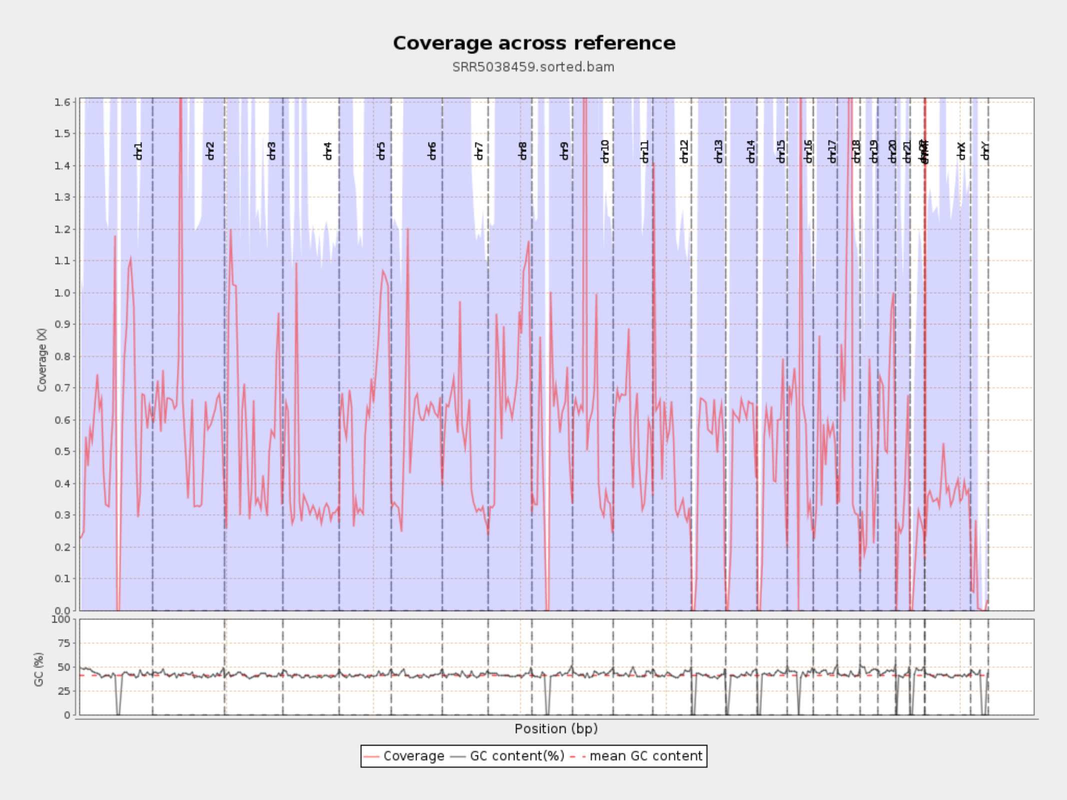
2.7. Chromosome stats

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

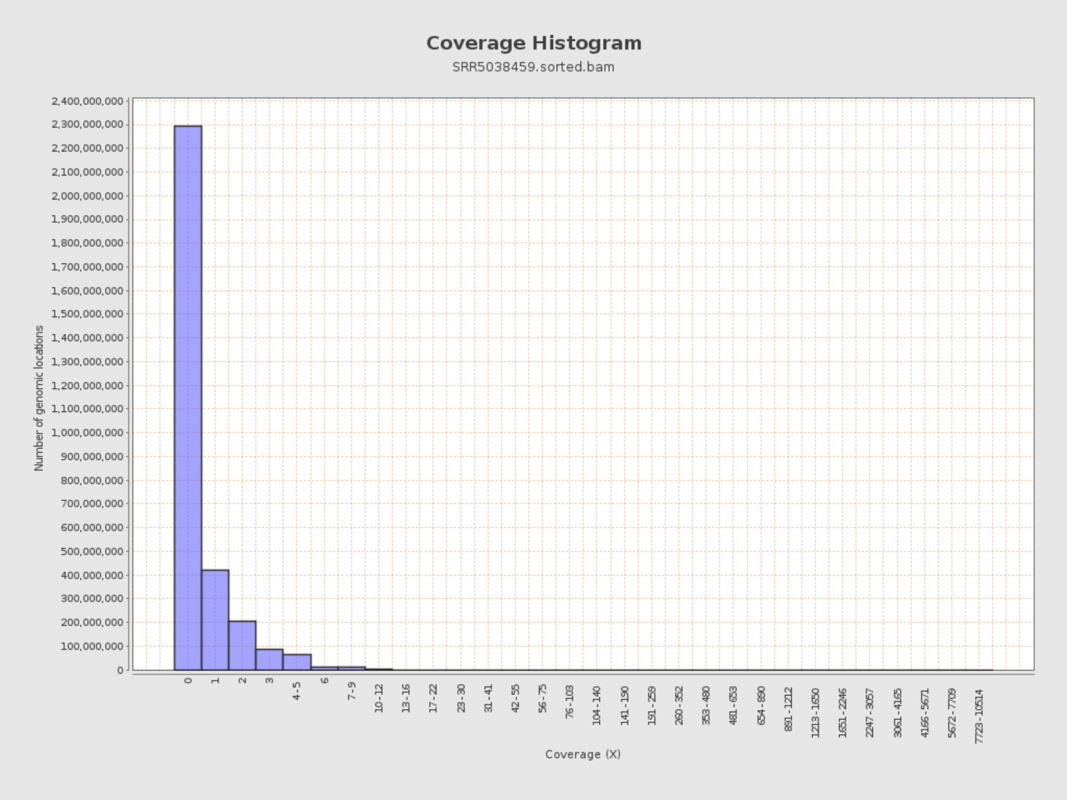
		bases	**coverage**	**deviation**
chr1	249250621	143787303	0.5769	10.5106
chr2	243199373	151371873	0.6224	8.0974
chr3	198022430	115301939	0.5823	1.3124
chr4	191154276	72135150	0.3774	6.5514
chr5	180915260	116285176	0.6428	1.2948
chr6	171115067	98690029	0.5767	6.2364
chr7	159138663	81634044	0.513	7.8993
chr8	146364022	106930030	0.7306	2.9239
chr9	141213431	71386497	0.5055	12.1558
chr10	135534747	91245263	0.6732	20.0984
chr11	135006516	76796194	0.5688	6.2158
chr12	133851895	68652226	0.5129	1.2731
chr13	115169878	56804955	0.4932	1.0999
chr14	107349540	54196873	0.5049	1.1743
chr15	102531392	45092674	0.4398	1.0555
chr16	90354753	52867688	0.5851	8.0611
chr17	81195210	40338171	0.4968	8.9631
chr18	78077248	67175160	0.8604	8.1798
chr19	59128983	21818900	0.369	4.3777
chr20	63025520	44316098	0.7031	2.3311
chr21	48129895	15988704	0.3322	2.959
chr22	51304566	9226779	0.1798	0.6704
chrMT	16571	2273854	137.2189	74.3368
chrX	155270560	57043510	0.3674	1.7075

chrY	59373566	3310863	0.0558	6.2418

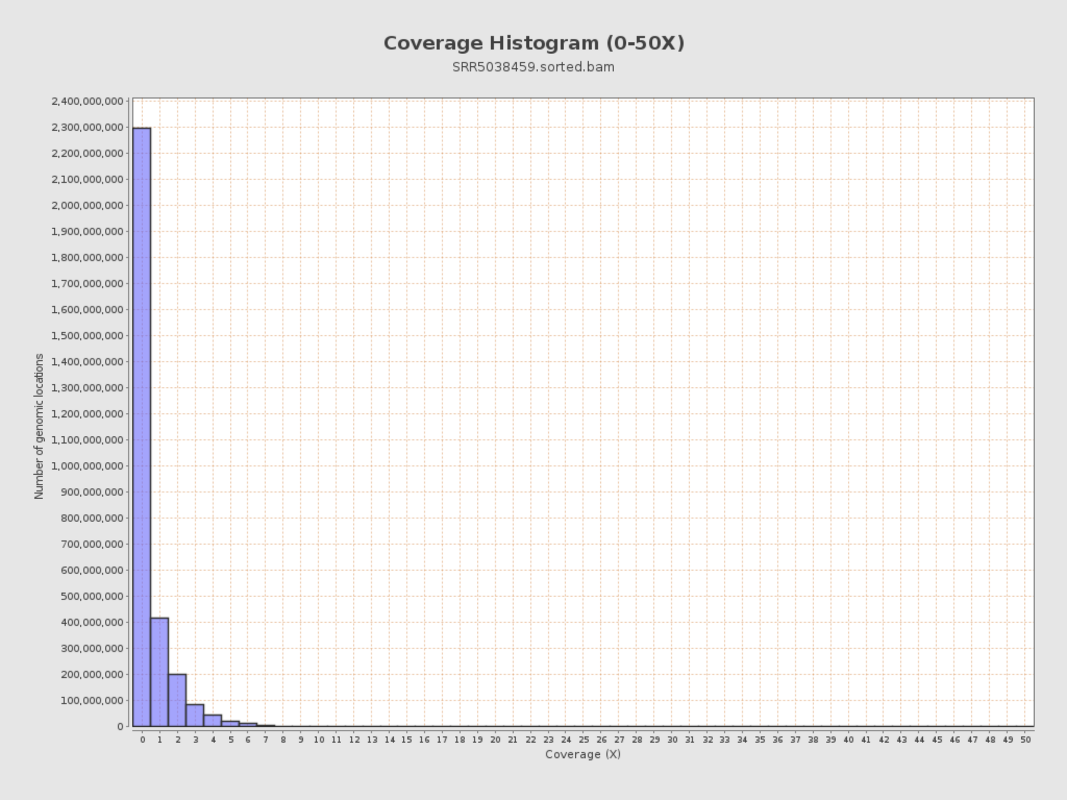
3. Results : Coverage across reference



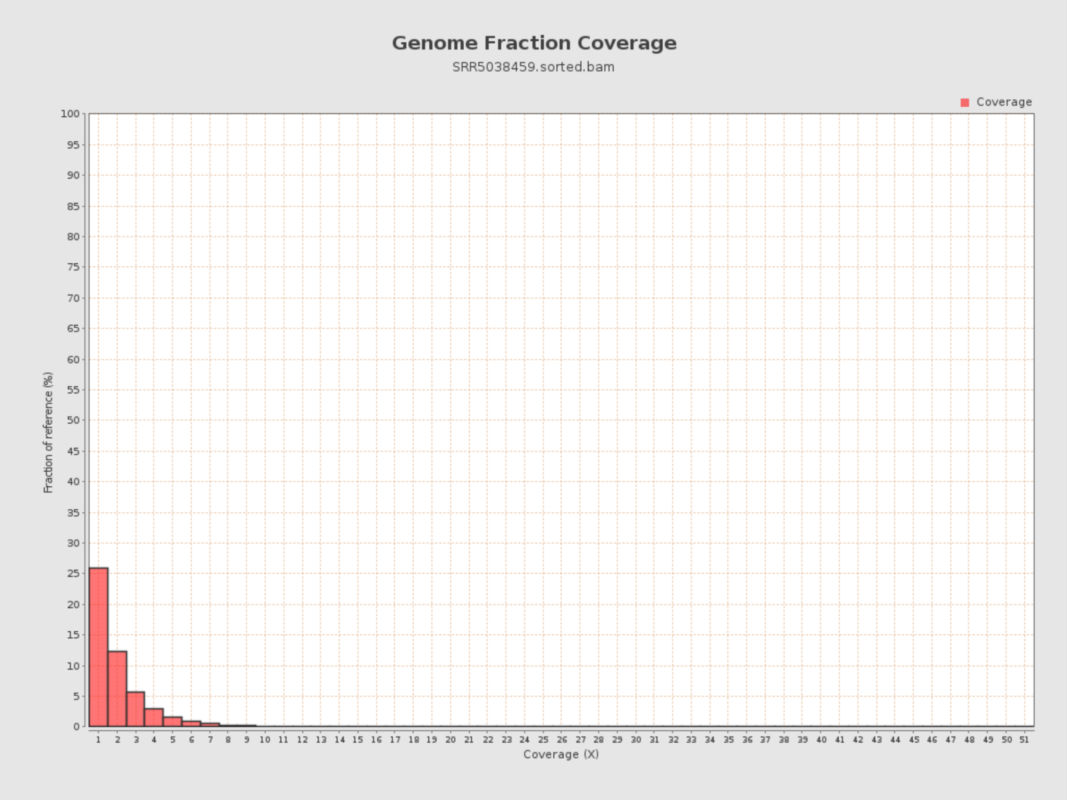
4. Results : Coverage Histogram



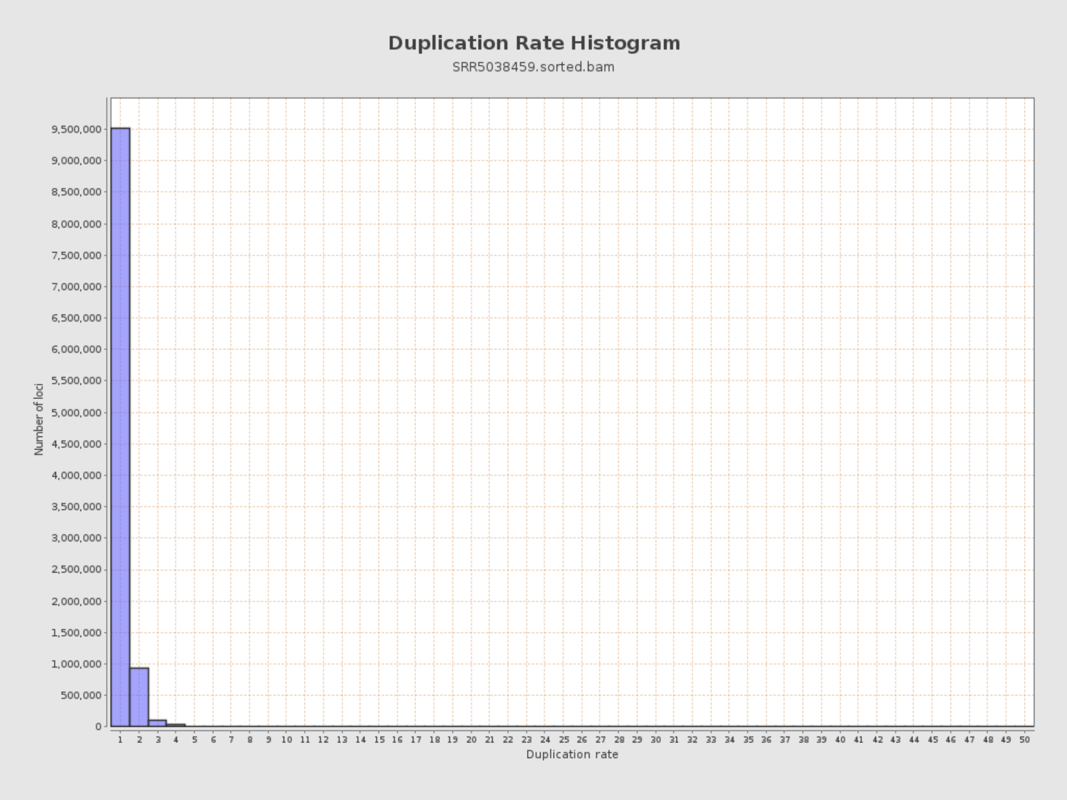
5. Results : Coverage Histogram (0-50X)



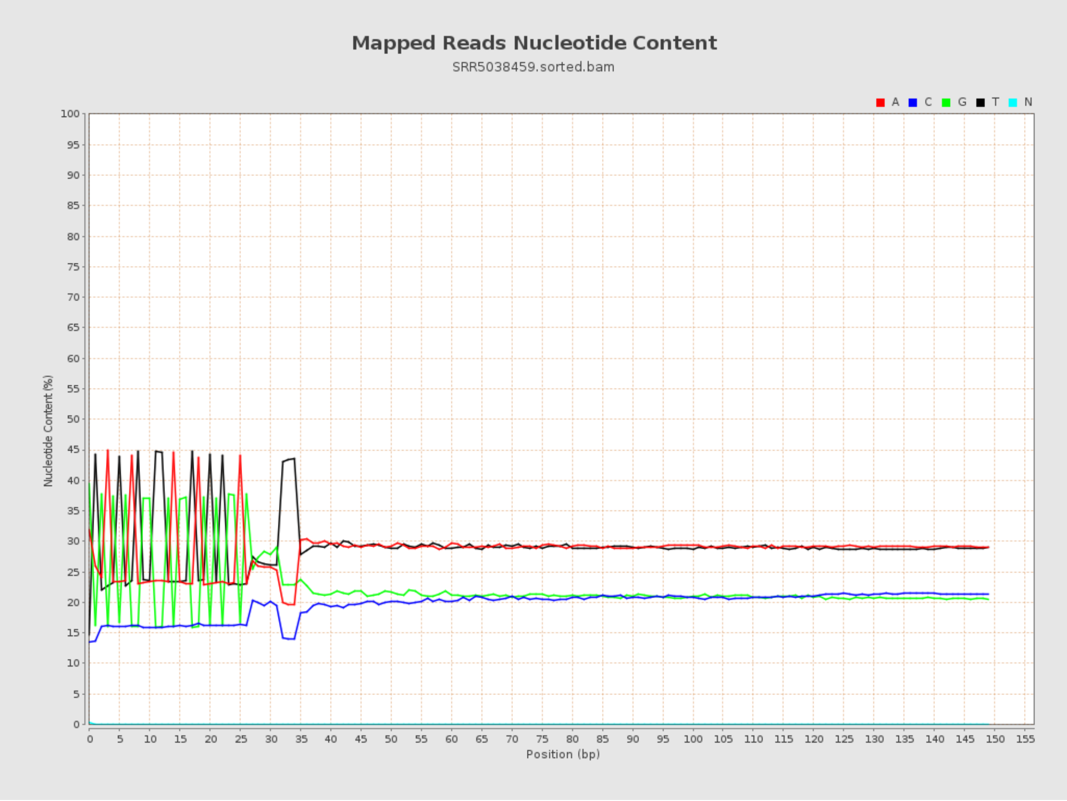
6. Results : Genome Fraction Coverage



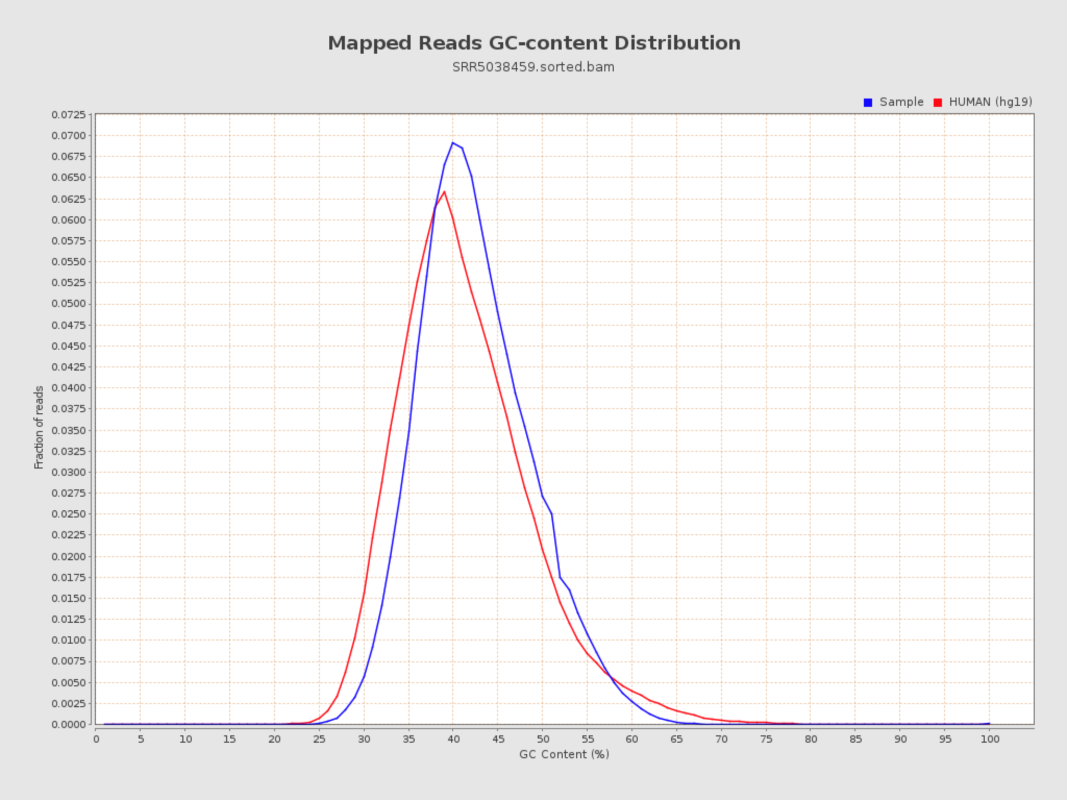
7. Results : Duplication Rate Histogram



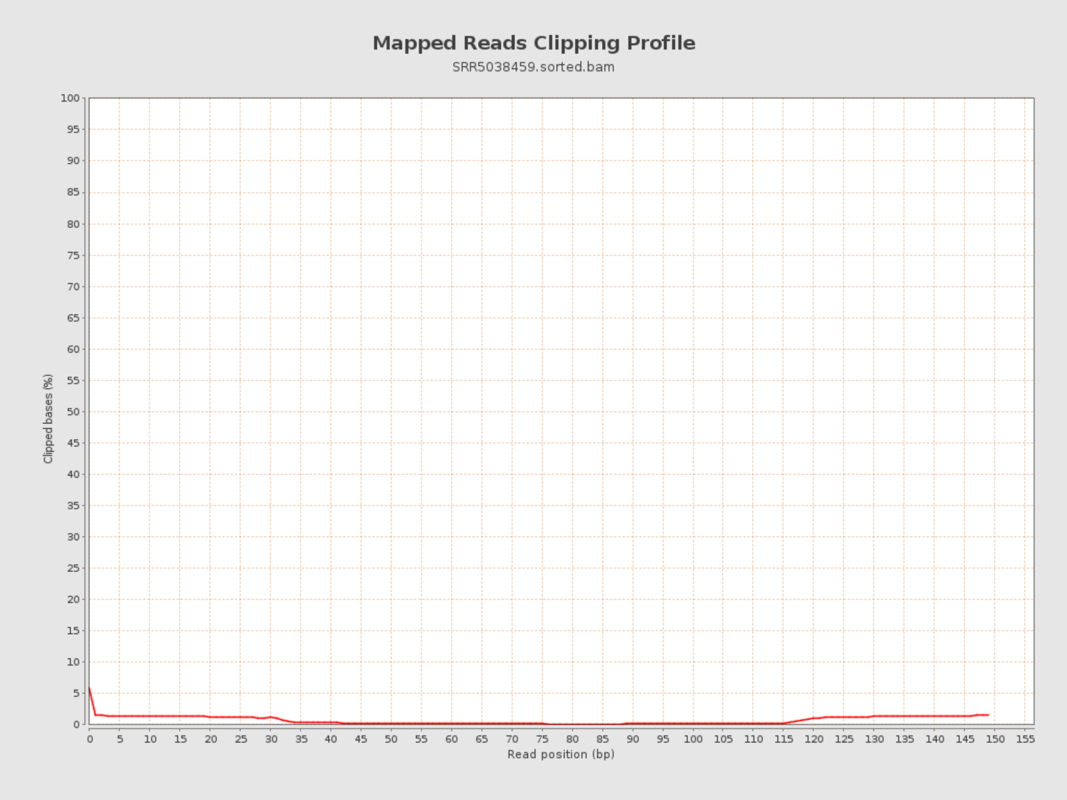
8. Results : Mapped Reads Nucleotide Content



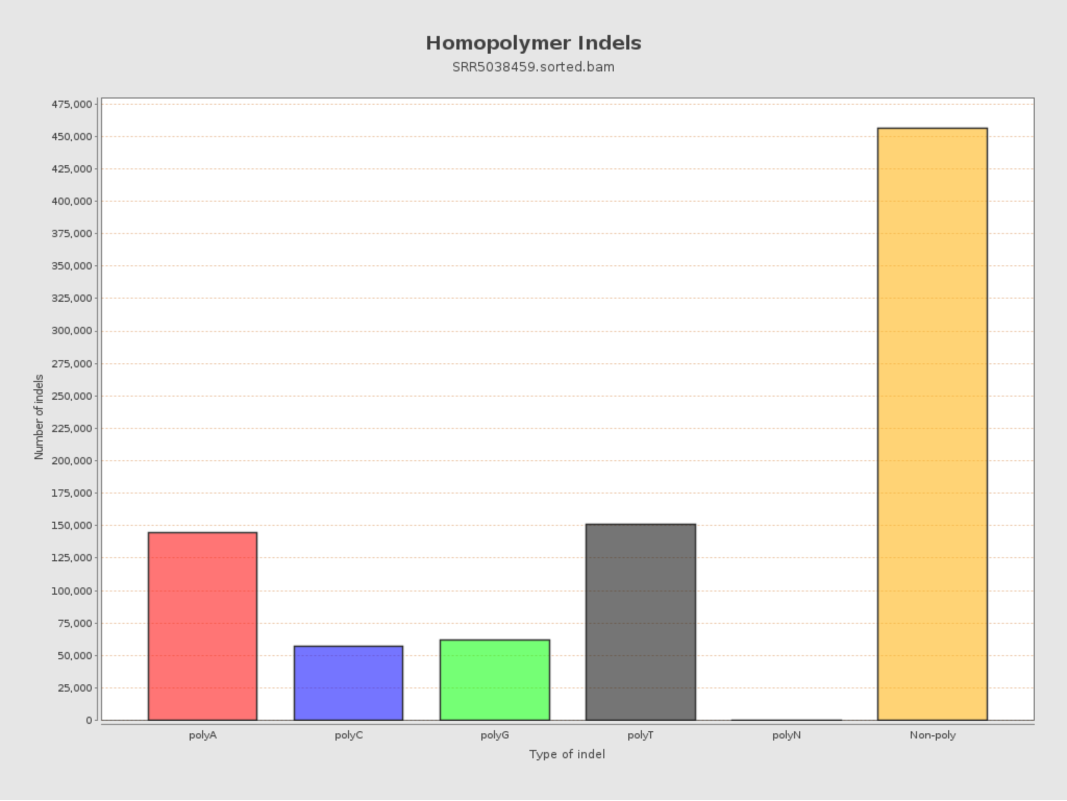
9. Results : Mapped Reads GC-content Distribution



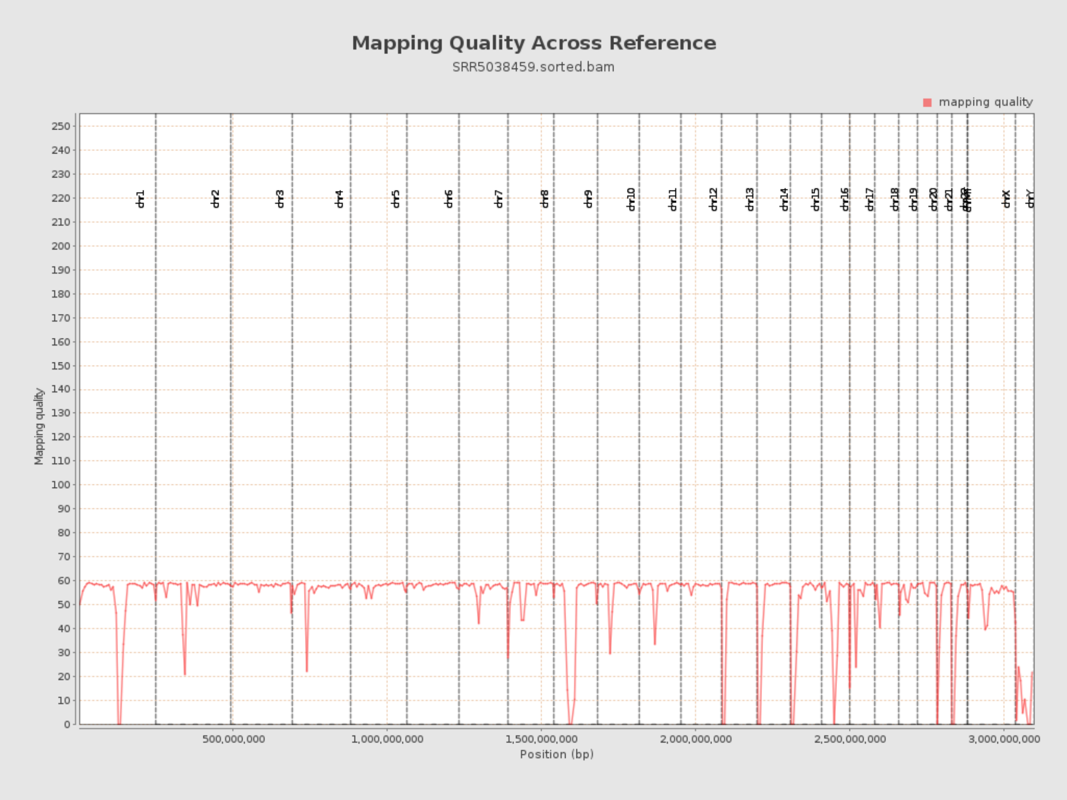
10. Results : Mapped Reads Clipping Profile



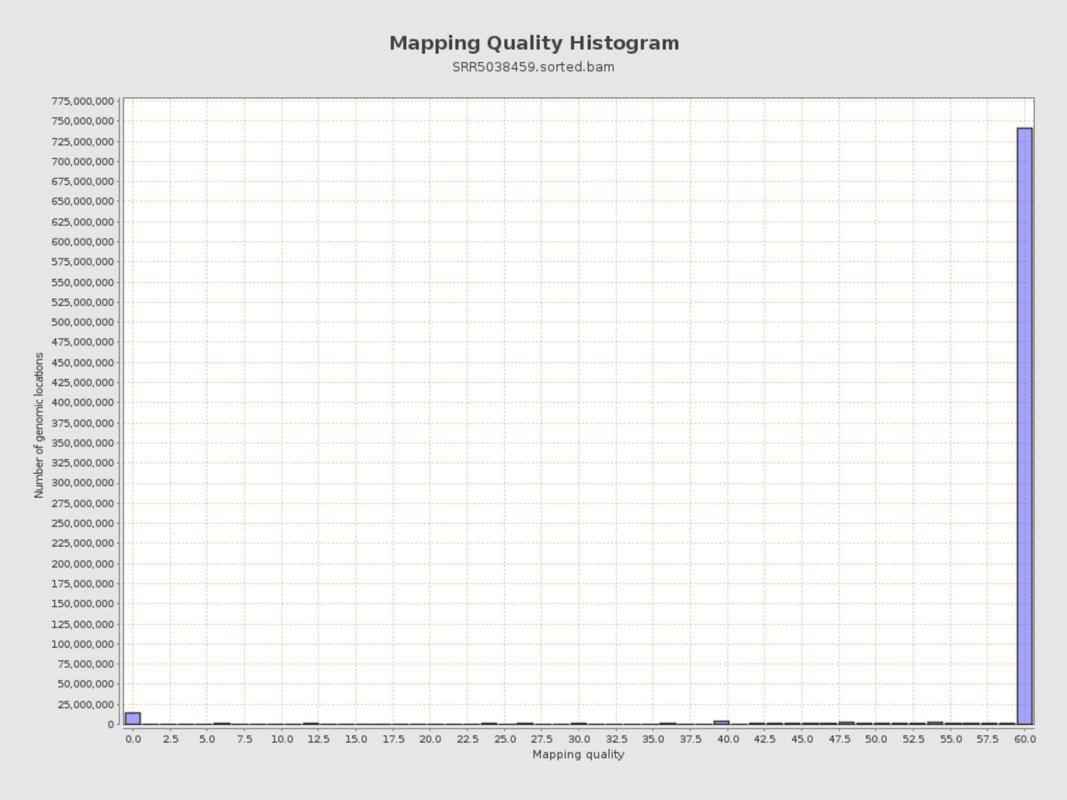
11. Results : Homopolymer Indels



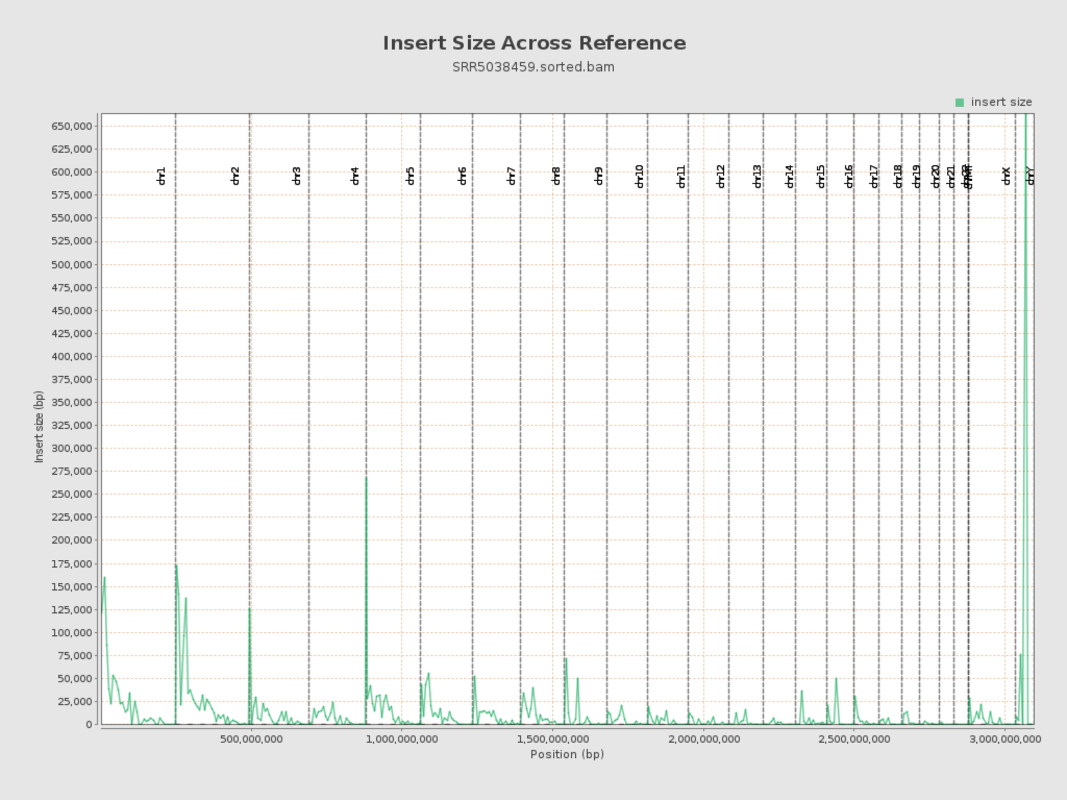
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram