Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 18:51:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038409.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_SRR5038409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038409_1.fastq.gz SRR5038409_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 18:51:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	83,224,894
Mapped reads	82,939,211 / 99.66%
Unmapped reads	285,683 / 0.34%
Mapped paired reads	82,939,211 / 99.66%
Mapped reads, first in pair	41,528,586 / 49.9%
Mapped reads, second in pair	41,410,625 / 49.76%
Mapped reads, both in pair	82,795,752 / 99.48%
Mapped reads, singletons	143,459 / 0.17%
Secondary alignments	0
Supplementary alignments	204,461 / 0.25%
Read min/max/mean length	30 / 150 / 150.12
Duplicated reads (estimated)	32,276,548 / 38.78%
Duplication rate	35.97%
Clipped reads	3,853,451 / 4.63%

2.2. ACGT Content

Number/percentage of A's	3,069,678,246 / 24.84%
Number/percentage of C's	3,113,613,856 / 25.2%
Number/percentage of T's	3,092,407,969 / 25.03%
Number/percentage of G's	3,078,859,631 / 24.92%
Number/percentage of N's	1,193,542 / 0.01%

GC Percentage	50.12%

2.3. Coverage

Mean	3.992
Standard Deviation	25.3855

2.4. Mapping Quality

Mean Mapping Quality	55.83

2.5. Insert size

Mean	26,500.29
Standard Deviation	1,719,283.03
P25/Median/P75	206 / 241 / 285

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	56,092,589
Insertions	708,702
Mapped reads with at least one insertion	0.81%
Deletions	847,339
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.61%

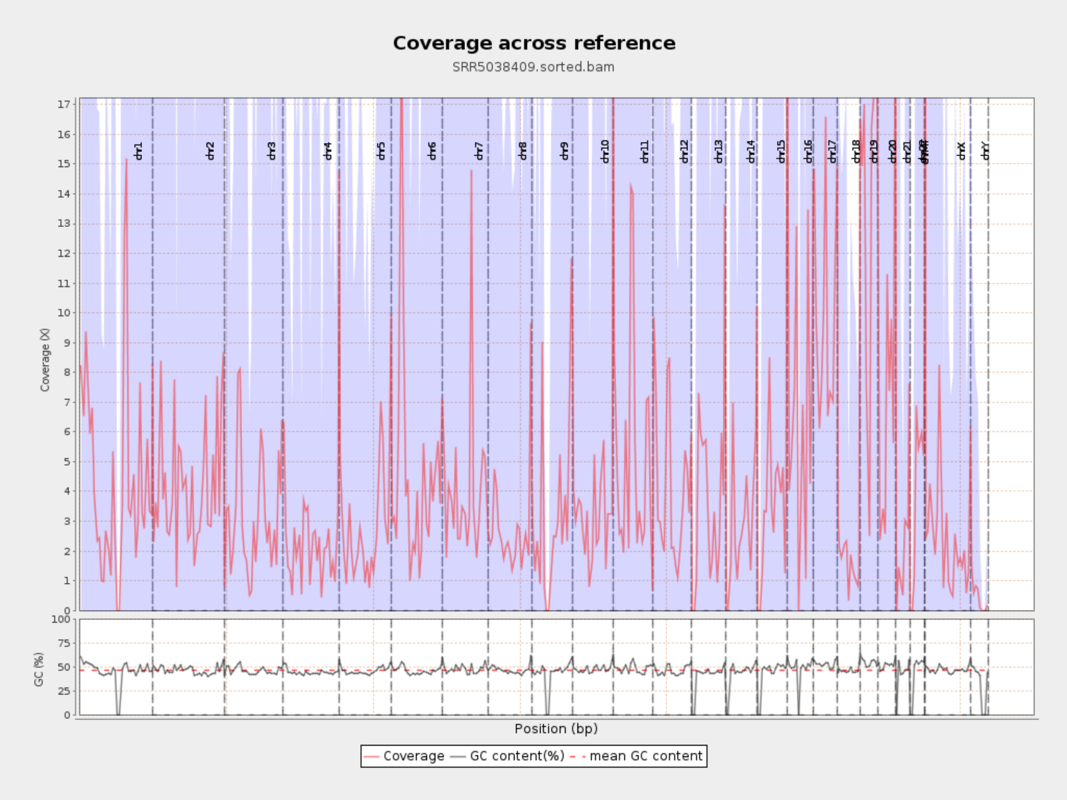
2.7. Chromosome stats

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

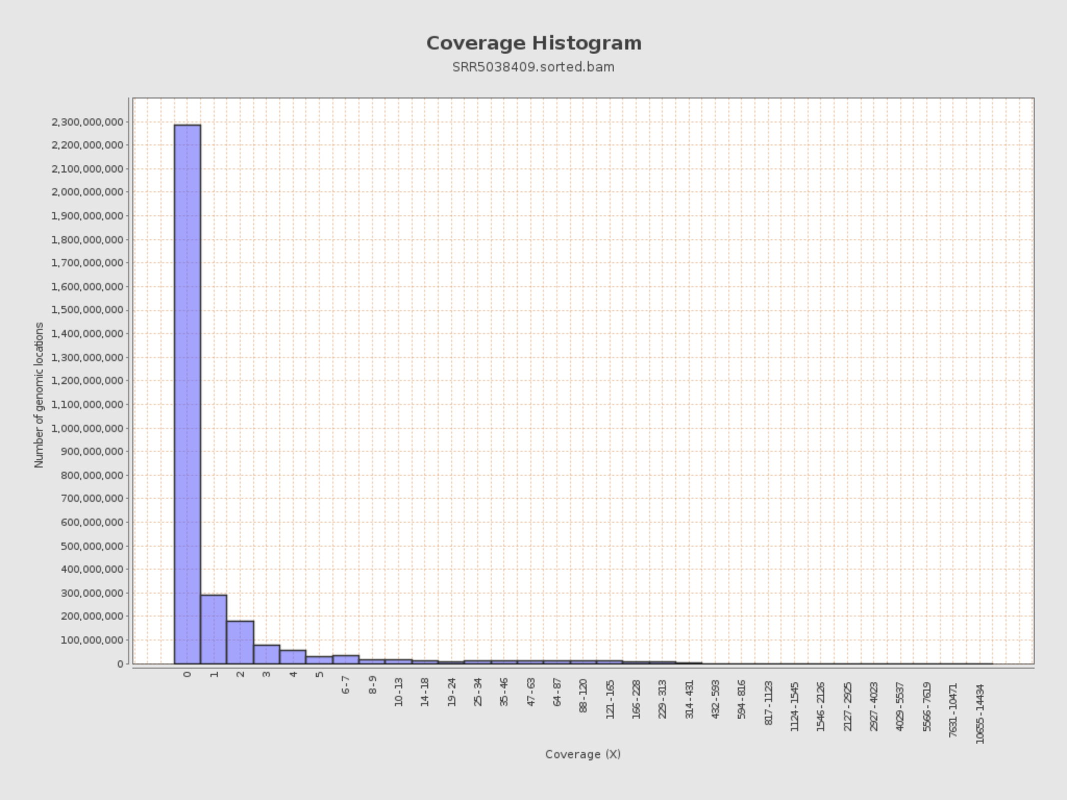
		bases	coverage	deviation
chr1	249250621	1112193055	4.4621	25.6113
chr2	243199373	1022402002	4.204	28.3527
chr3	198022430	629806891	3.1805	19.9614
chr4	191154276	414498321	2.1684	15.7214
chr5	180915260	530898271	2.9345	20.9936
chr6	171115067	774185379	4.5244	29.3001
chr7	159138663	659461724	4.1439	28.3041
chr8	146364022	402910331	2.7528	18.5787
chr9	141213431	464913587	3.2923	21.522
chr10	135534747	418277347	3.0861	18.6479
chr11	135006516	758565764	5.6187	32.0664
chr12	133851895	559190173	4.1777	22.7724
chr13	115169878	398995680	3.4644	27.636
chr14	107349540	305107774	2.8422	17.6735
chr15	102531392	337069192	3.2875	18.8202
chr16	90354753	627623828	6.9462	35.2413
chr17	81195210	811041545	9.9888	41.9336
chr18	78077248	125194707	1.6035	11.5346
chr19	59128983	839027636	14.1898	49.6388
chr20	63025520	447220333	7.0959	39.1886
chr21	48129895	105191117	2.1856	24.9825
chr22	51304566	211050879	4.1137	21.1132
chrMT	16571	1754367	105.8697	36.4597
chrX	155270560	374996227	2.4151	17.7965

chrY	59373566	26579436	0.4477	6.0004

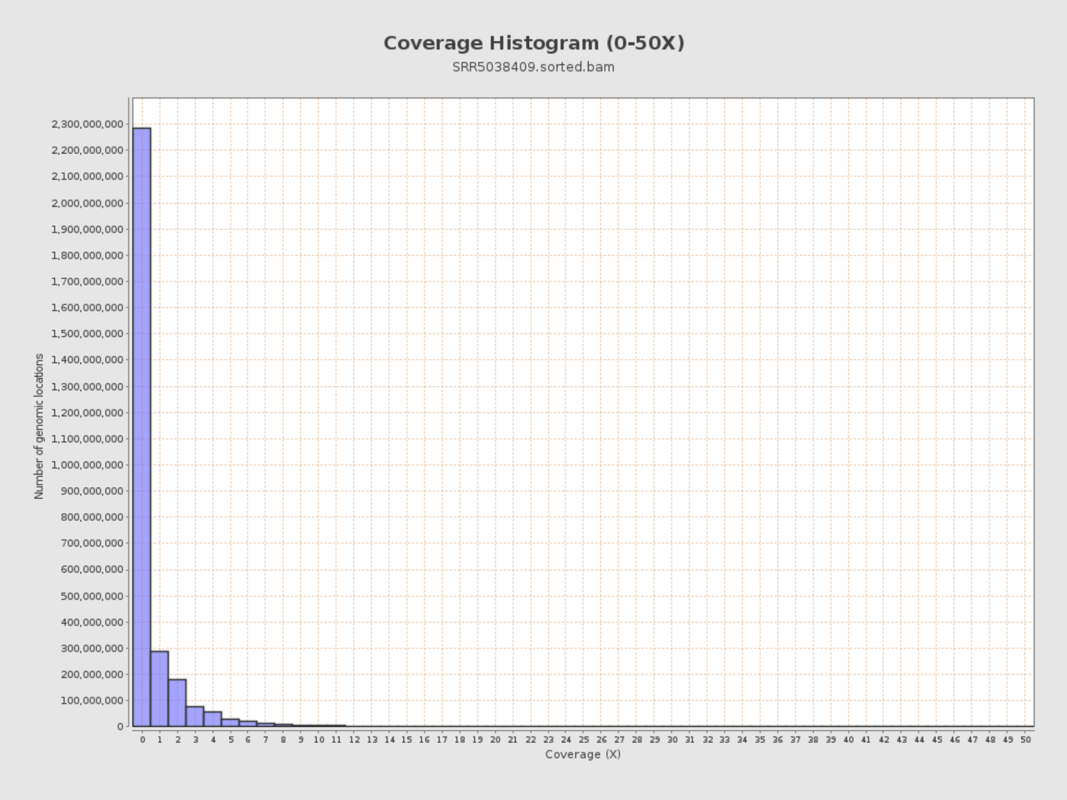
3. Results : Coverage across reference



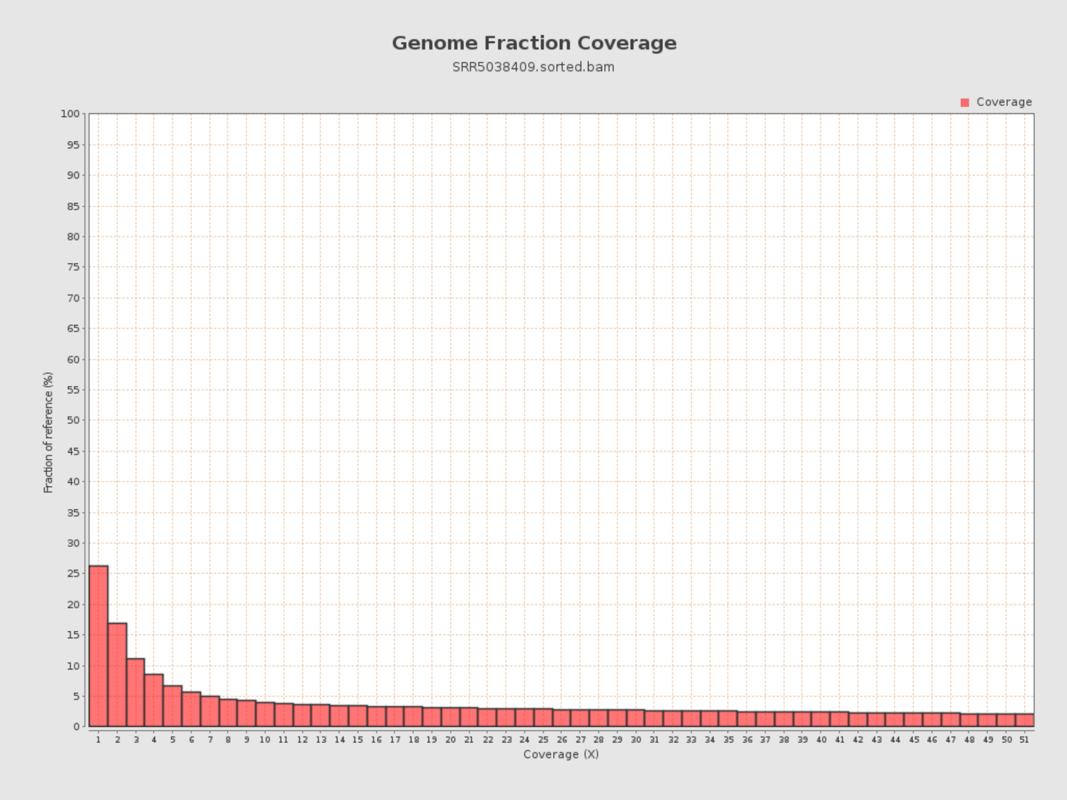
4. Results : Coverage Histogram



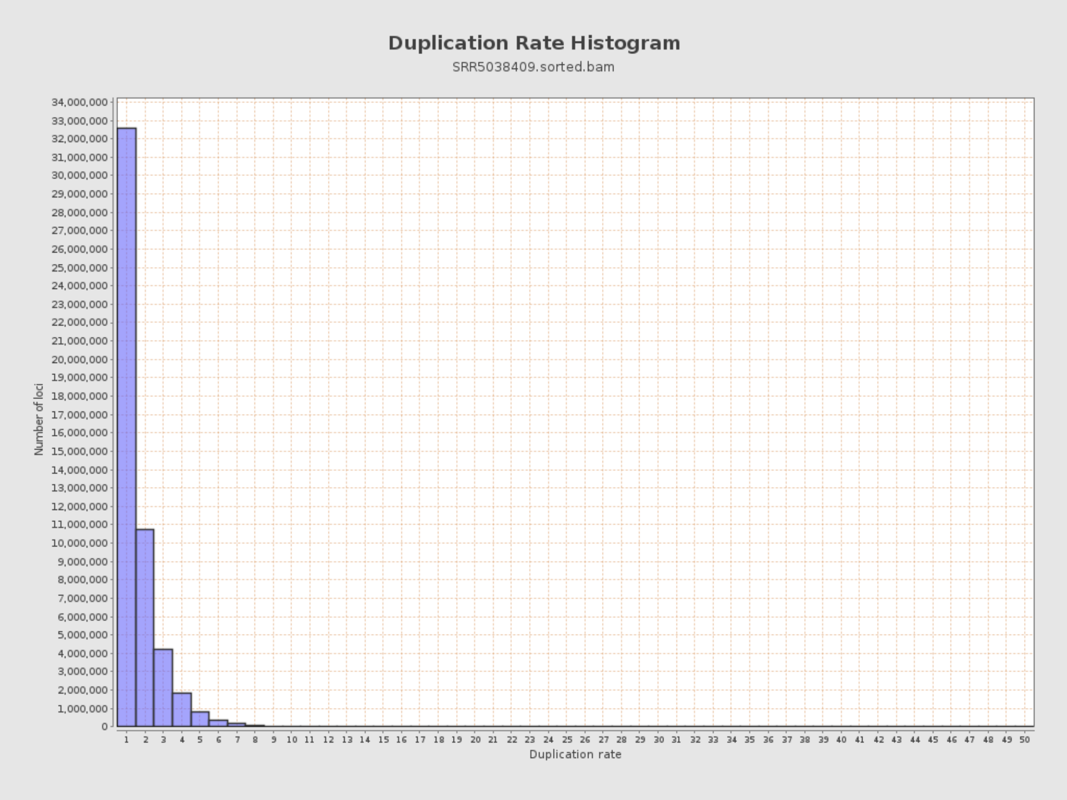
5. Results : Coverage Histogram (0-50X)



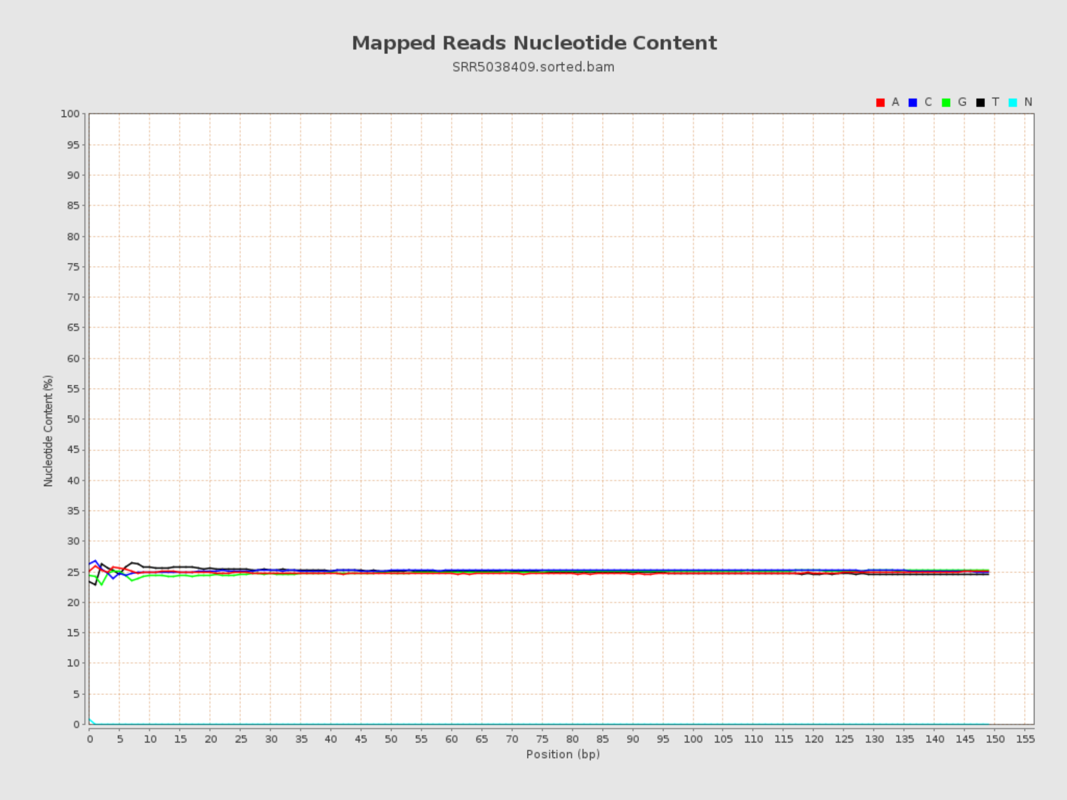
6. Results : Genome Fraction Coverage



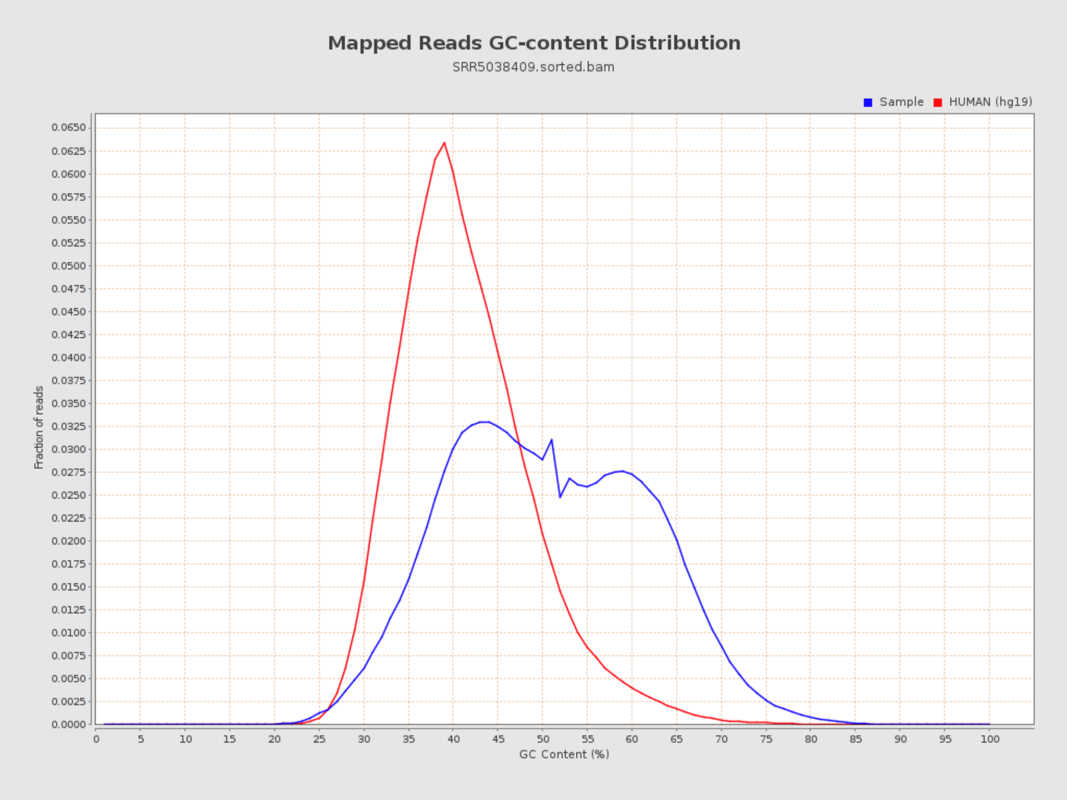
7. Results : Duplication Rate Histogram



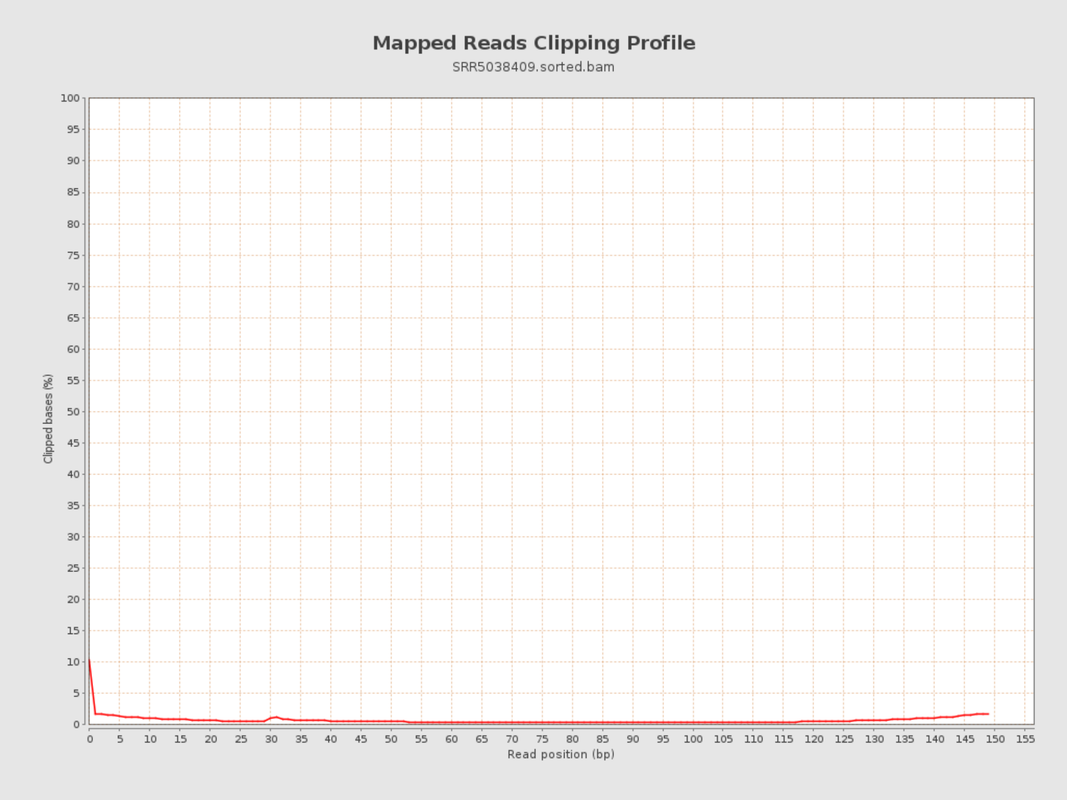
8. Results : Mapped Reads Nucleotide Content



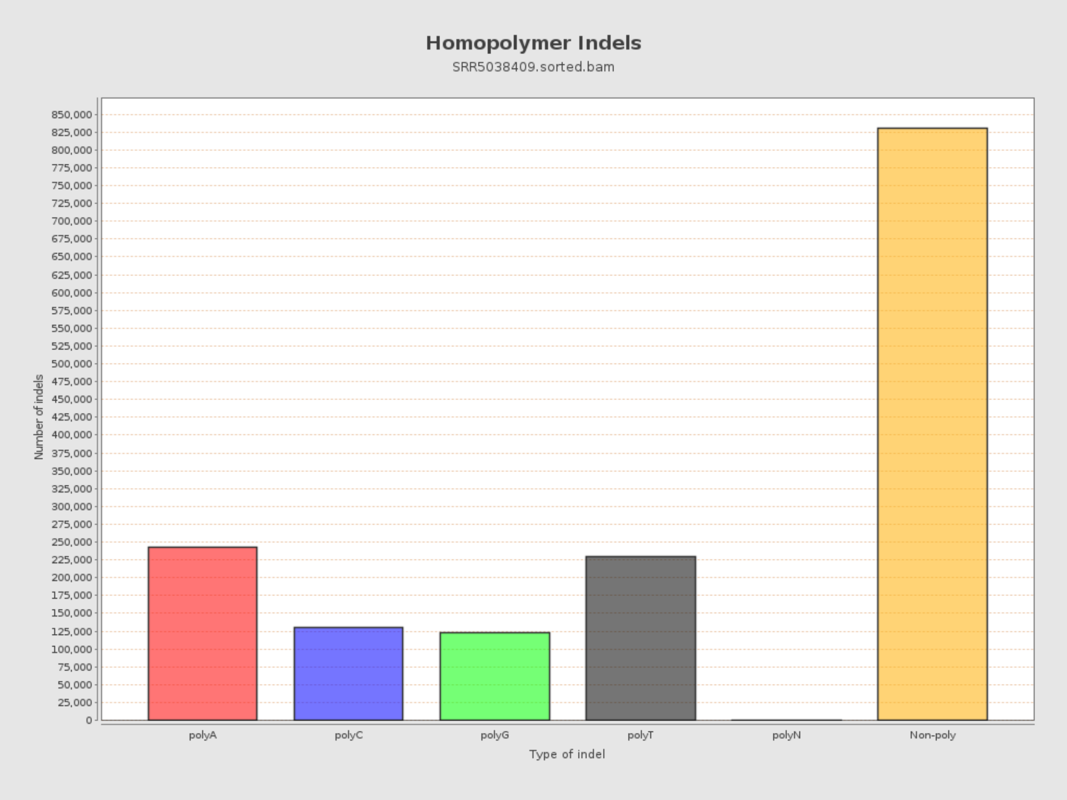
9. Results : Mapped Reads GC-content Distribution



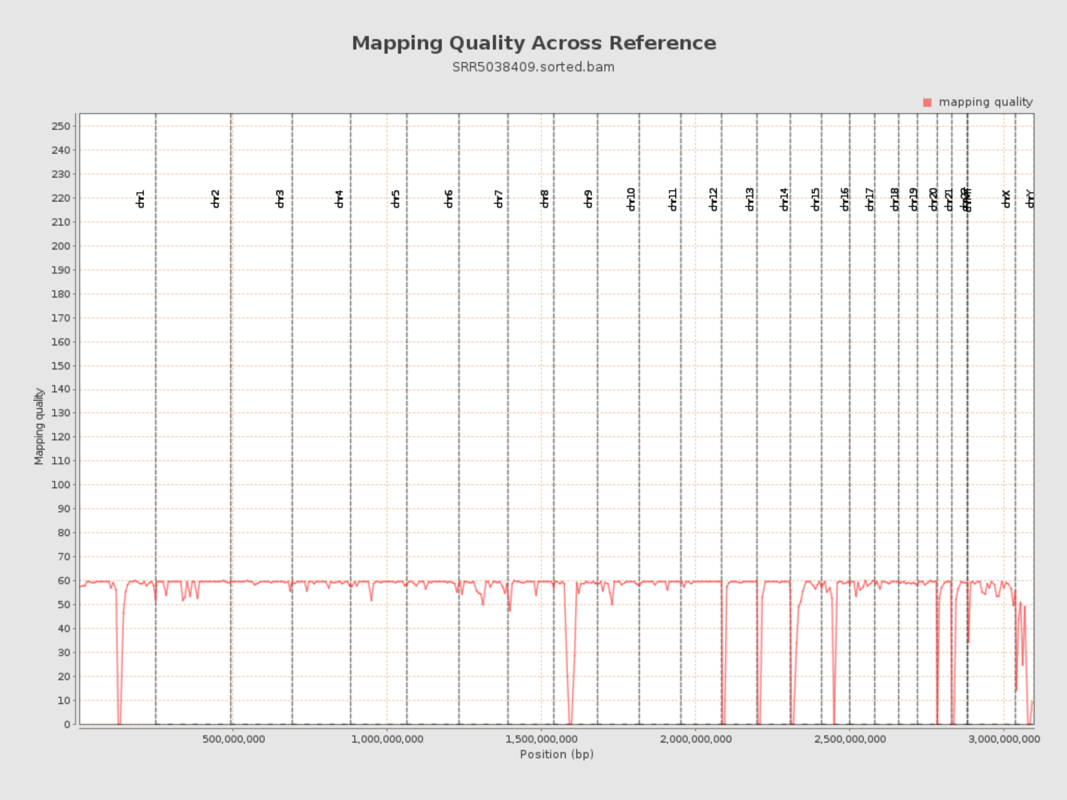
10. Results : Mapped Reads Clipping Profile



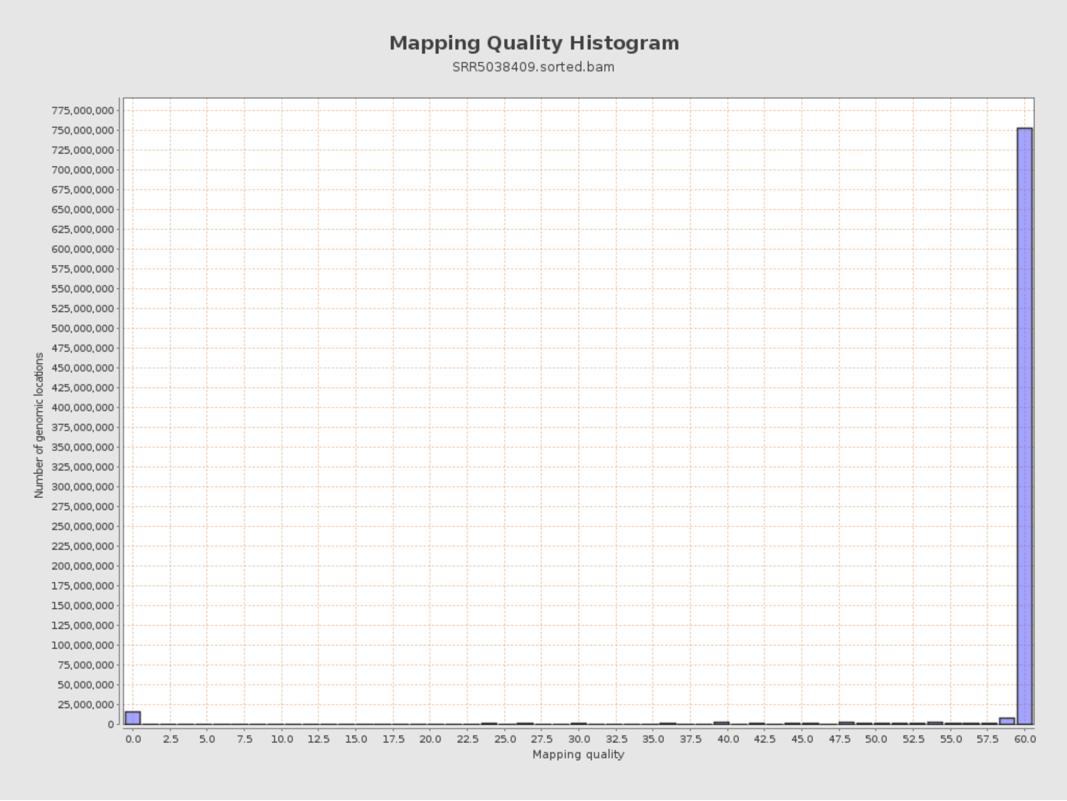
11. Results : Homopolymer Indels



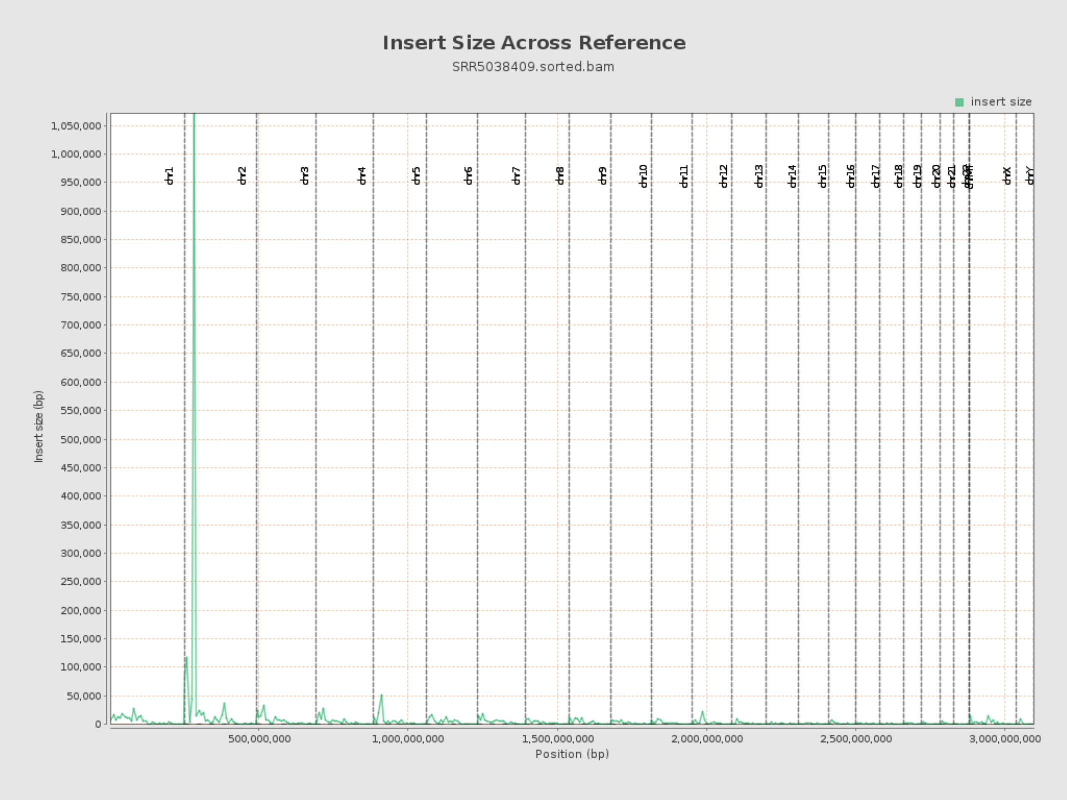
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram