Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 22:36:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038416.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_SRR5038416 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038416_1.fastq.gz SRR5038416_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 22:36:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038416.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,850,194
Mapped reads	13,538,528 / 97.75%
Unmapped reads	311,666 / 2.25%
Mapped paired reads	13,538,528 / 97.75%
Mapped reads, first in pair	6,833,217 / 49.34%
Mapped reads, second in pair	6,705,311 / 48.41%
Mapped reads, both in pair	13,397,220 / 96.73%
Mapped reads, singletons	141,308 / 1.02%
Secondary alignments	0
Supplementary alignments	223,561 / 1.61%
Read min/max/mean length	30 / 150 / 150.84
Duplicated reads (estimated)	1,761,577 / 12.72%
Duplication rate	8.49%
Clipped reads	3,379,371 / 24.4%

2.2. ACGT Content

Number/percentage of A's	555,580,742 / 28.75%
Number/percentage of C's	401,045,951 / 20.76%
Number/percentage of T's	555,875,684 / 28.77%
Number/percentage of G's	419,698,228 / 21.72%
Number/percentage of N's	40,611 / 0%

GC Percentage	42.48%

2.3. Coverage

Mean	0.6246
Standard Deviation	8.5431

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	89,451.12
Standard Deviation	2,880,299.65
P25/Median/P75	217 / 258 / 309

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	25,318,945
Insertions	305,861
Mapped reads with at least one insertion	2.15%
Deletions	632,736
Mapped reads with at least one deletion	4.51%
Homopolymer indels	47.75%

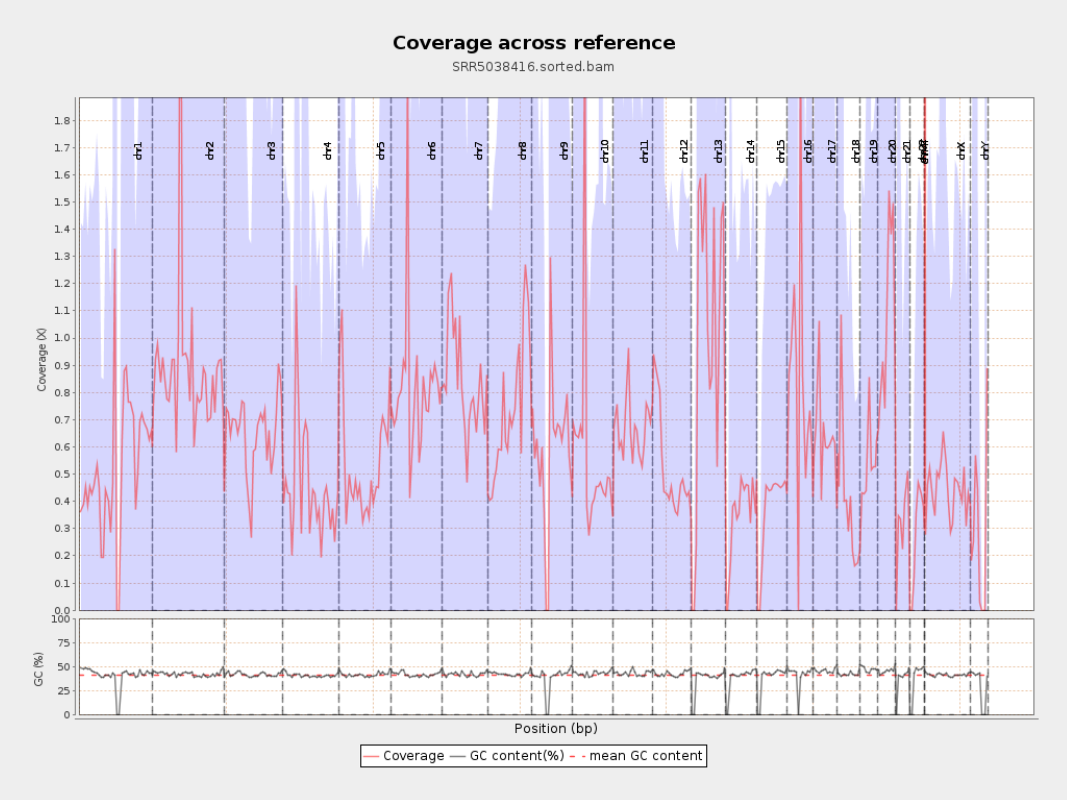
2.7. Chromosome stats

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

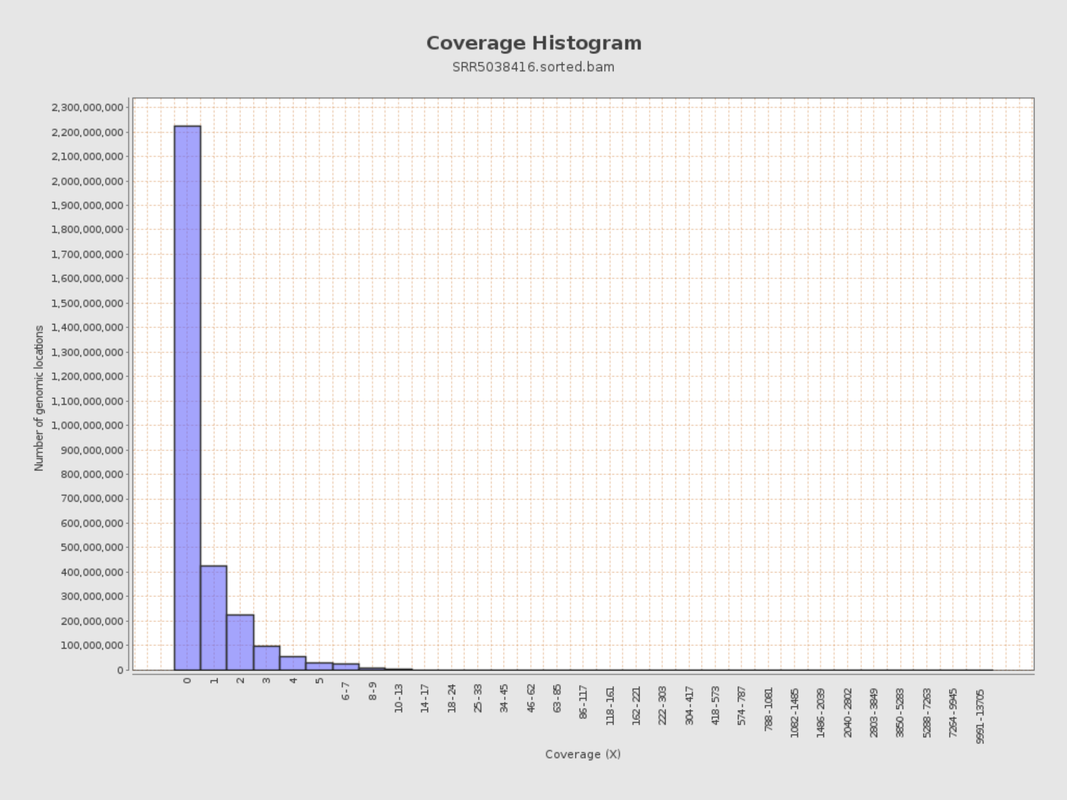
		bases	coverage	deviation
chr1	249250621	131024304	0.5257	14.0828
chr2	243199373	220087150	0.905	10.9837
chr3	198022430	128825748	0.6506	1.3153
chr4	191154276	85035380	0.4449	5.343
chr5	180915260	98670763	0.5454	1.2777
chr6	171115067	140400645	0.8205	13.2024
chr7	159138663	133524616	0.839	7.6869
chr8	146364022	108101951	0.7386	2.7678
chr9	141213431	82217921	0.5822	14.9953
chr10	135534747	79912281	0.5896	13.3264
chr11	135006516	89043304	0.6595	7.6392
chr12	133851895	71157397	0.5316	1.2242
chr13	115169878	117847892	1.0233	1.9176
chr14	107349540	36595253	0.3409	1.101
chr15	102531392	36789051	0.3588	0.9172
chr16	90354753	75008122	0.8302	8.842
chr17	81195210	51350069	0.6324	9.4552
chr18	78077248	30936887	0.3962	13.0327
chr19	59128983	30717305	0.5195	8.1901
chr20	63025520	67737951	1.0748	2.4126
chr21	48129895	15754429	0.3273	2.3272
chr22	51304566	14230881	0.2774	0.8363
chrMT	16571	2014267	121.5537	84.1133
chrX	155270560	68650802	0.4421	2.0379

chrY	59373566	17856175	0.3007	6.9131

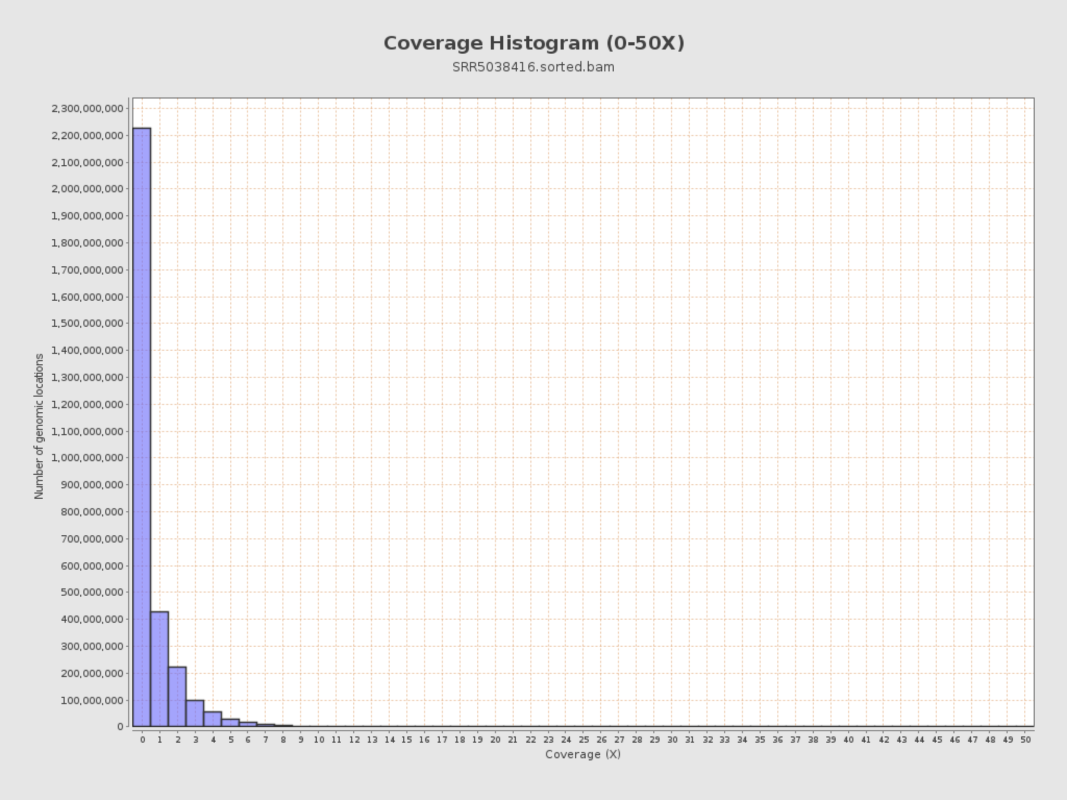
3. Results : Coverage across reference



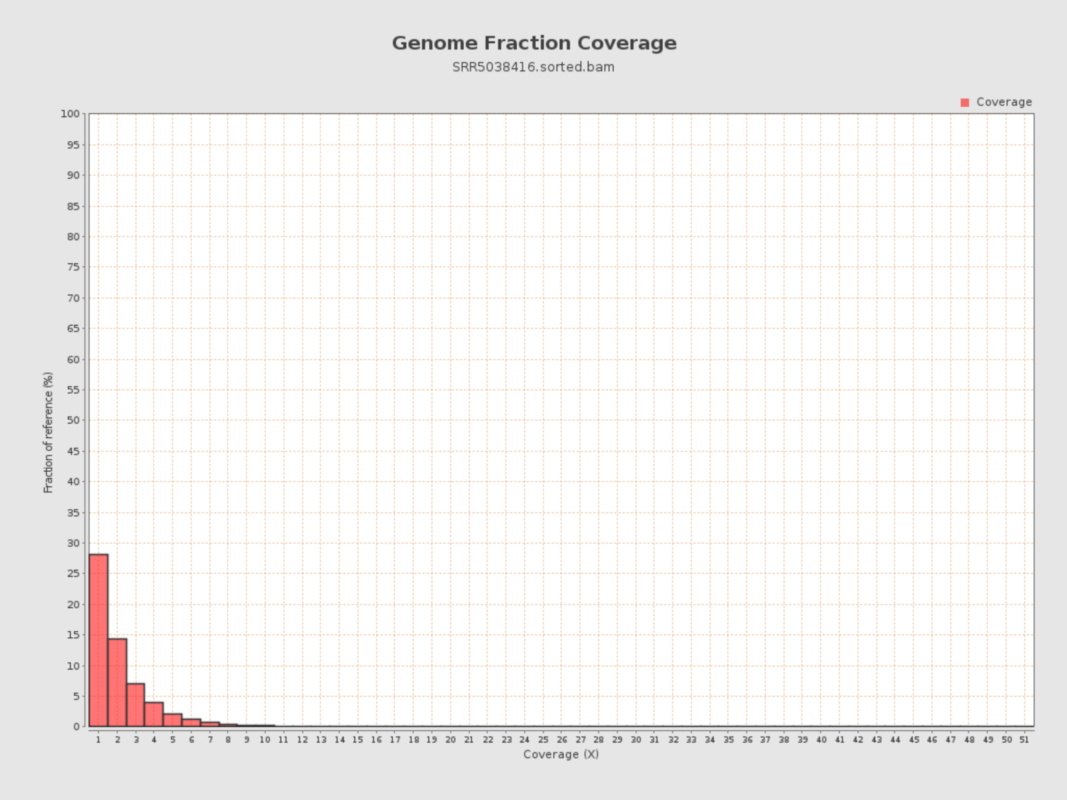
4. Results : Coverage Histogram



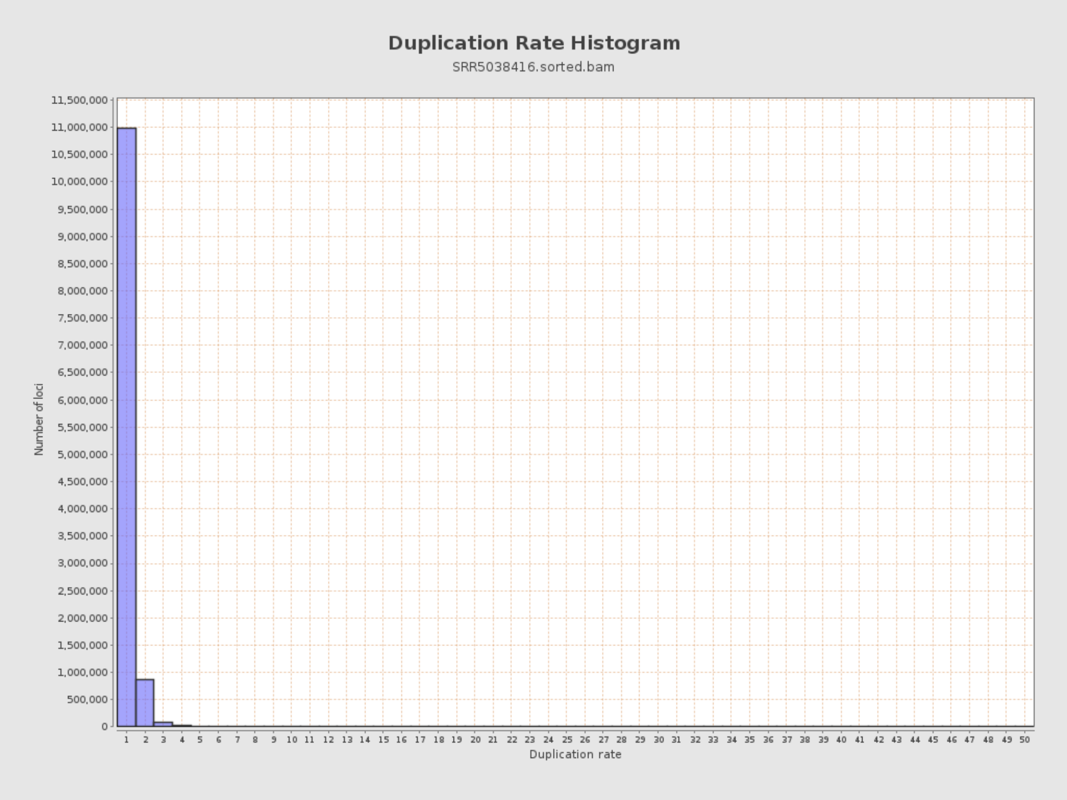
5. Results : Coverage Histogram (0-50X)



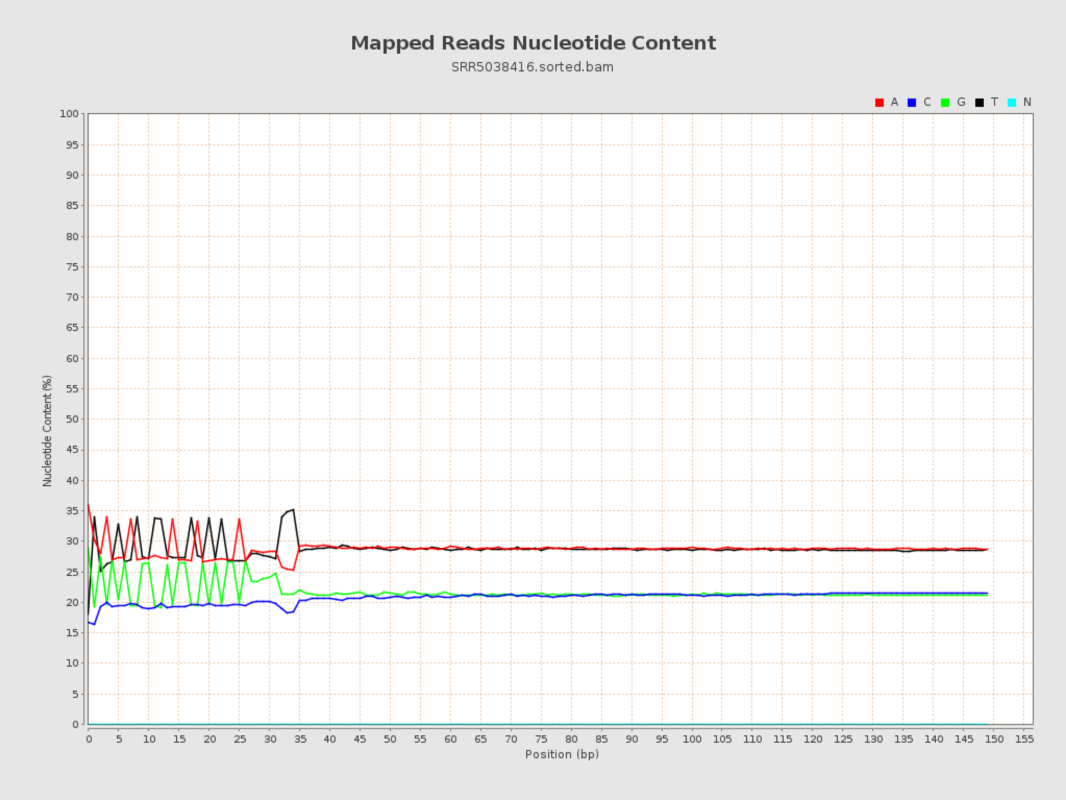
6. Results : Genome Fraction Coverage



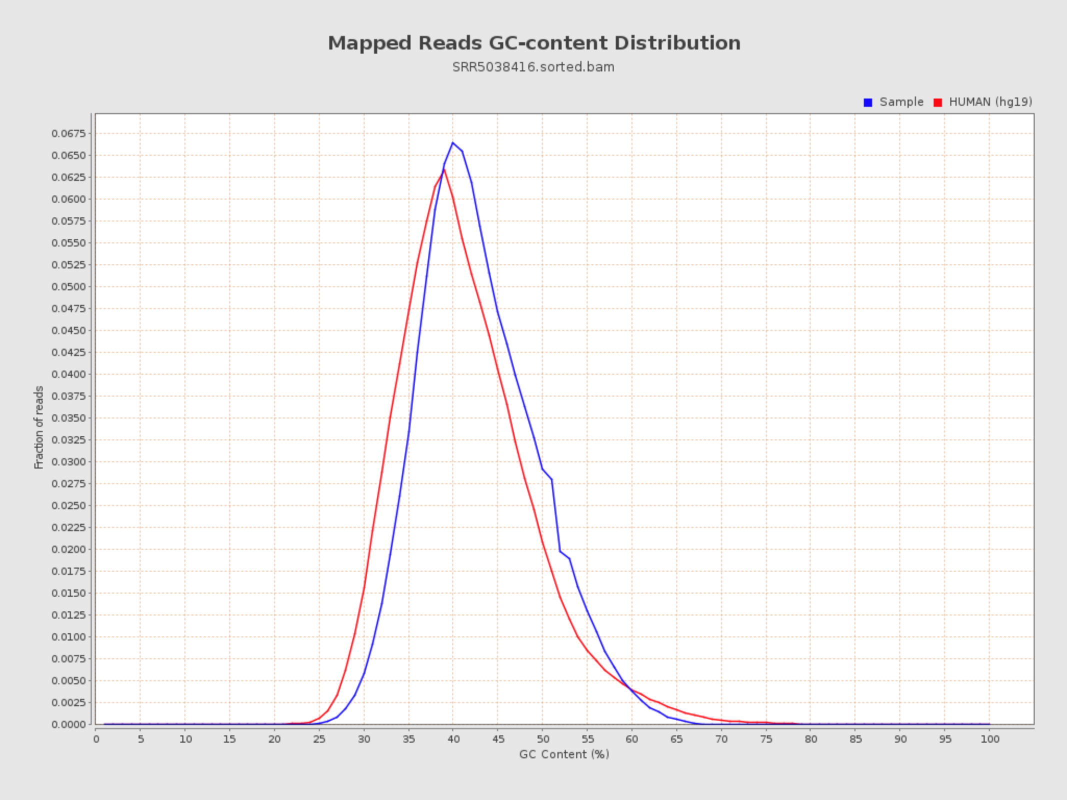
7. Results : Duplication Rate Histogram



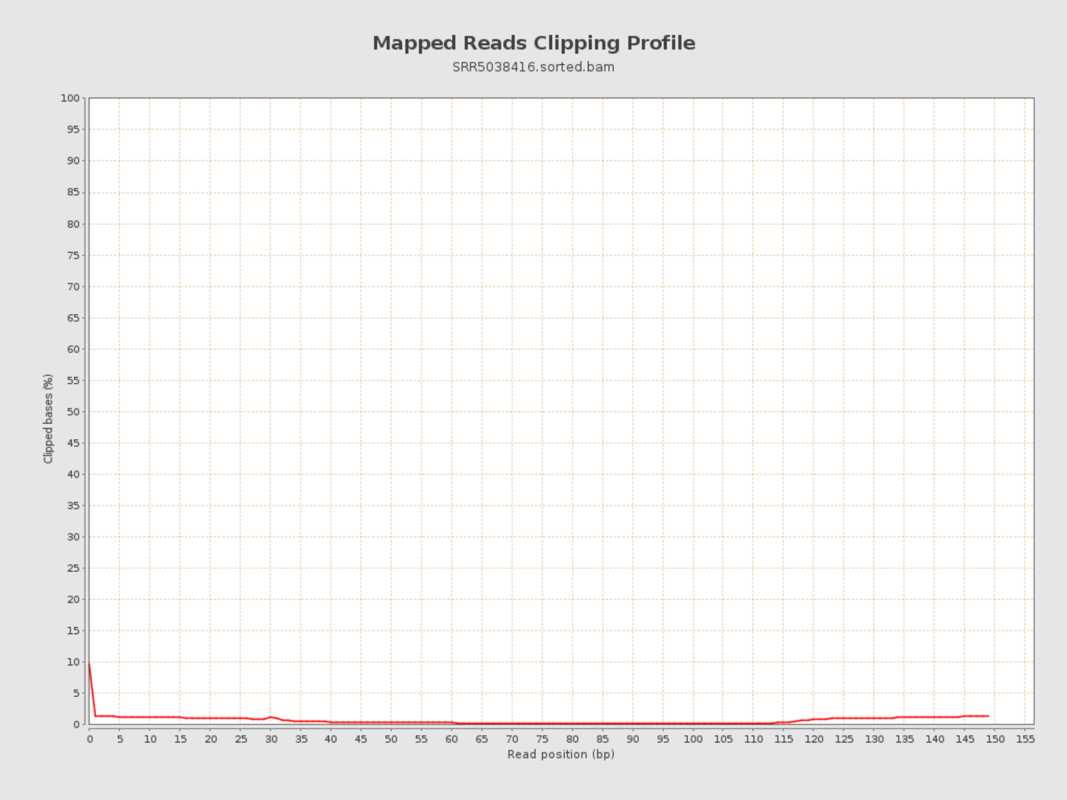
8. Results : Mapped Reads Nucleotide Content



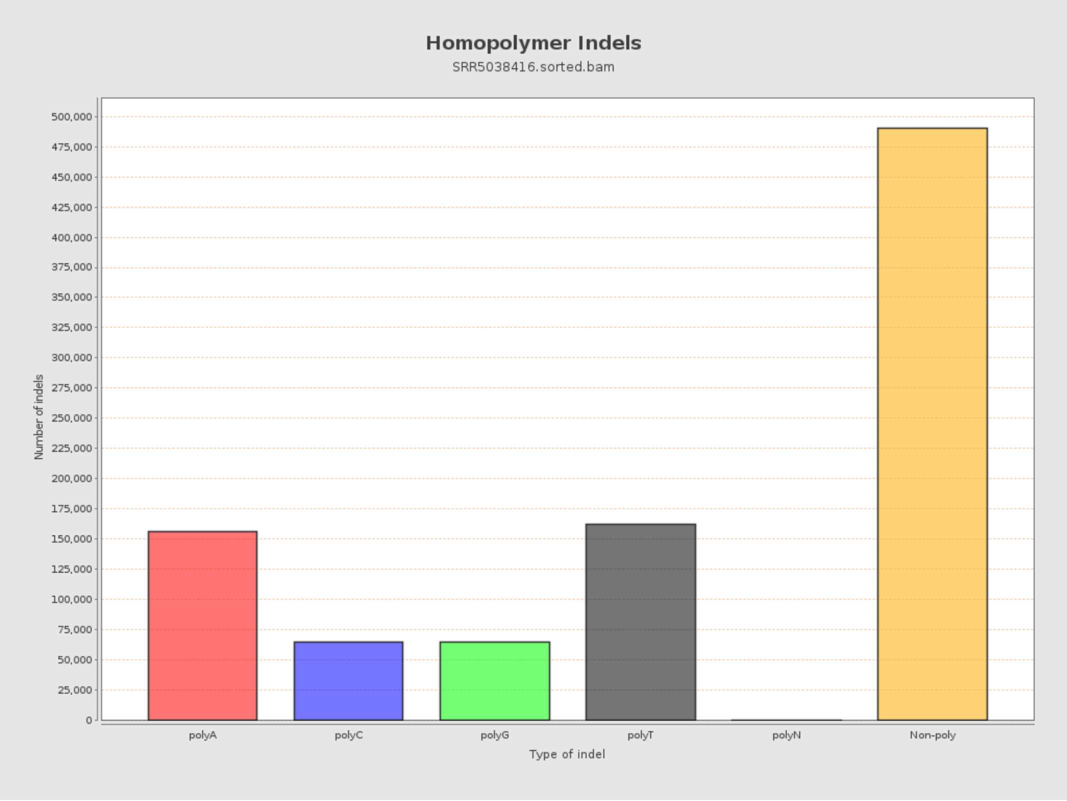
9. Results : Mapped Reads GC-content Distribution



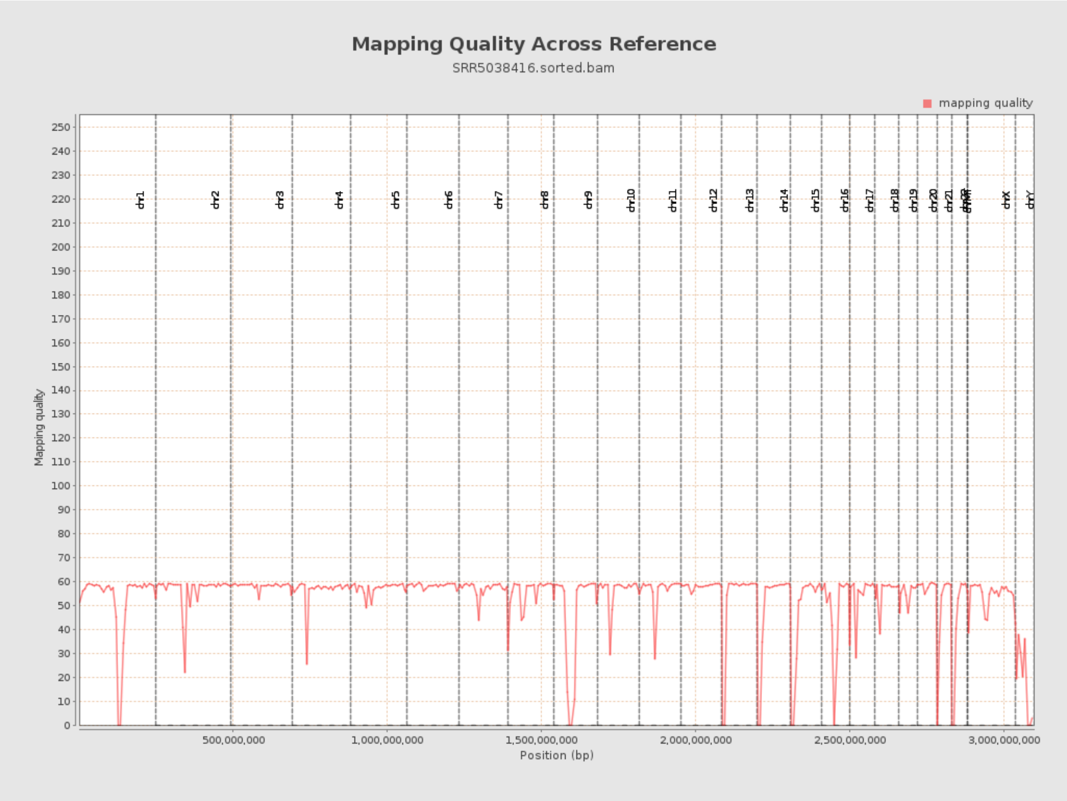
10. Results : Mapped Reads Clipping Profile



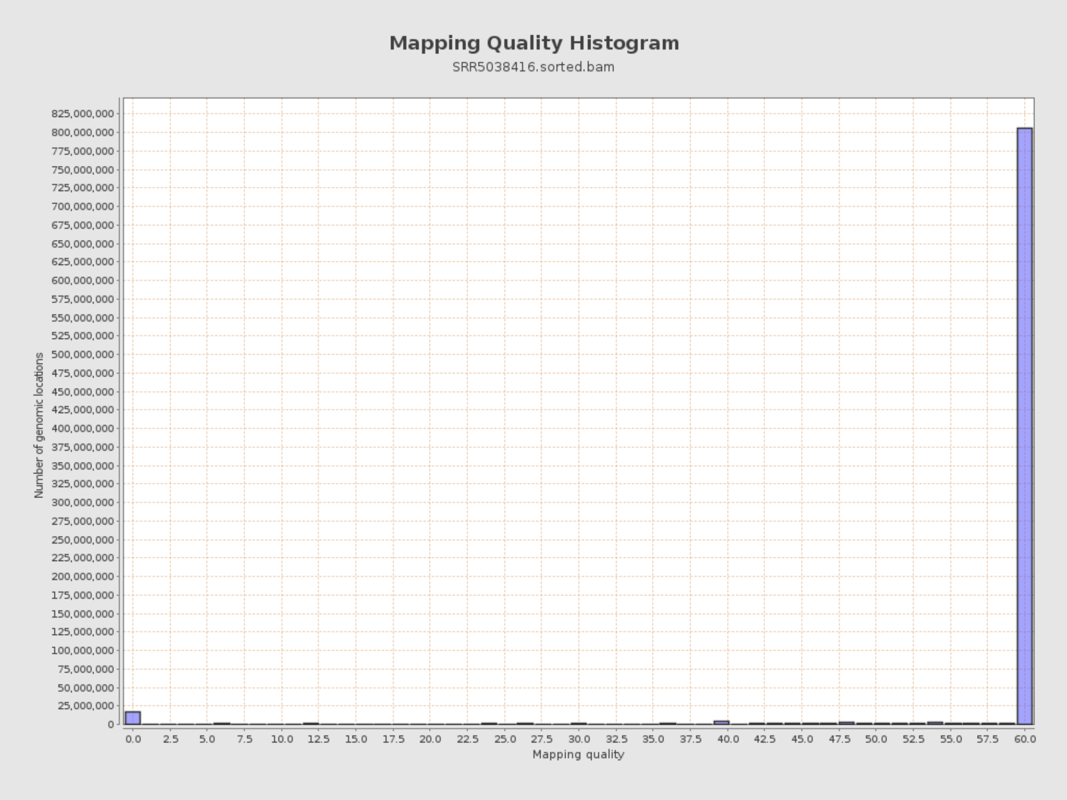
11. Results : Homopolymer Indels



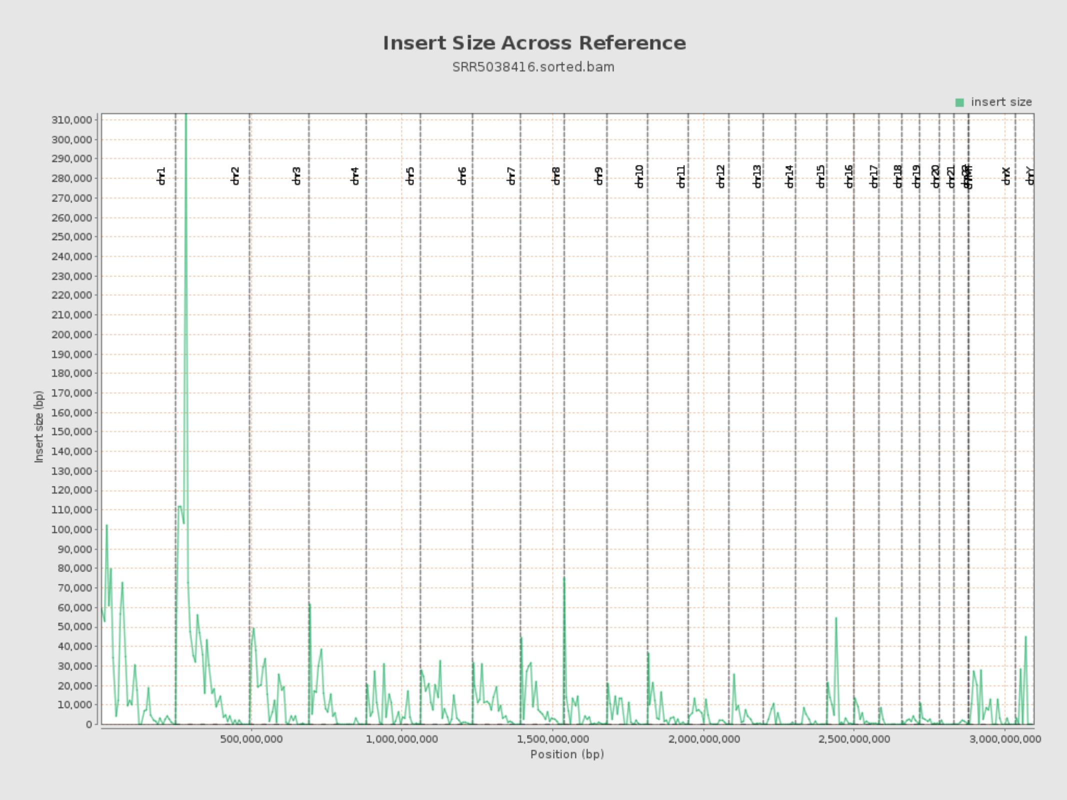
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram