Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 10:44:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038440.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_SRR5038440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038440_1.fastq.gz SRR5038440_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 10:44:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,060,414
Mapped reads	17,227,941 / 95.39%
Unmapped reads	832,473 / 4.61%
Mapped paired reads	17,227,941 / 95.39%
Mapped reads, first in pair	8,741,664 / 48.4%
Mapped reads, second in pair	8,486,277 / 46.99%
Mapped reads, both in pair	16,925,480 / 93.72%
Mapped reads, singletons	302,461 / 1.67%
Secondary alignments	0
Supplementary alignments	283,315 / 1.57%
Read min/max/mean length	30 / 150 / 150.78
Duplicated reads (estimated)	3,508,868 / 19.43%
Duplication rate	14.44%
Clipped reads	7,870,456 / 43.58%

2.2. ACGT Content

Number/percentage of A's	673,831,349 / 28.9%
Number/percentage of C's	455,254,934 / 19.53%
Number/percentage of T's	690,031,886 / 29.59%
Number/percentage of G's	512,277,921 / 21.97%
Number/percentage of N's	187,100 / 0.01%

GC Percentage	41.5%

2.3. Coverage

Mean	0.7537
Standard Deviation	9.8785

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	89,228.73
Standard Deviation	2,893,393.33
P25/Median/P75	218 / 273 / 340

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	30,078,894
Insertions	422,641
Mapped reads with at least one insertion	2.32%
Deletions	836,864
Mapped reads with at least one deletion	4.68%
Homopolymer indels	47.62%

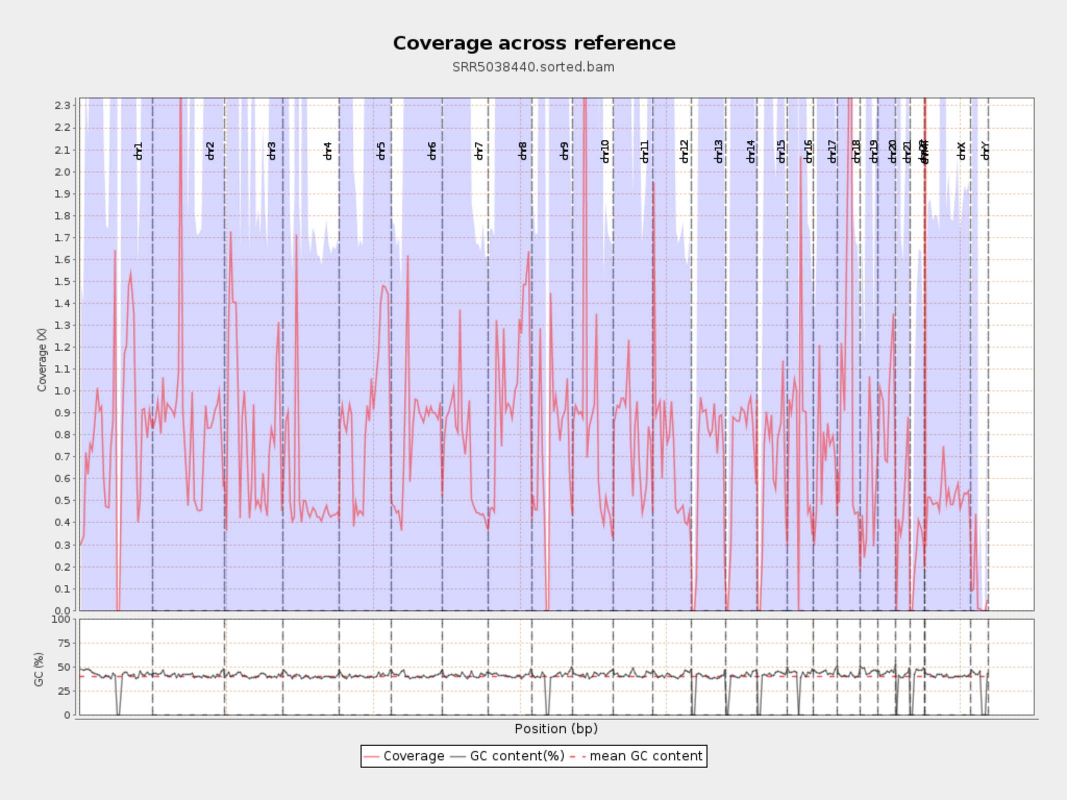
2.7. Chromosome stats

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

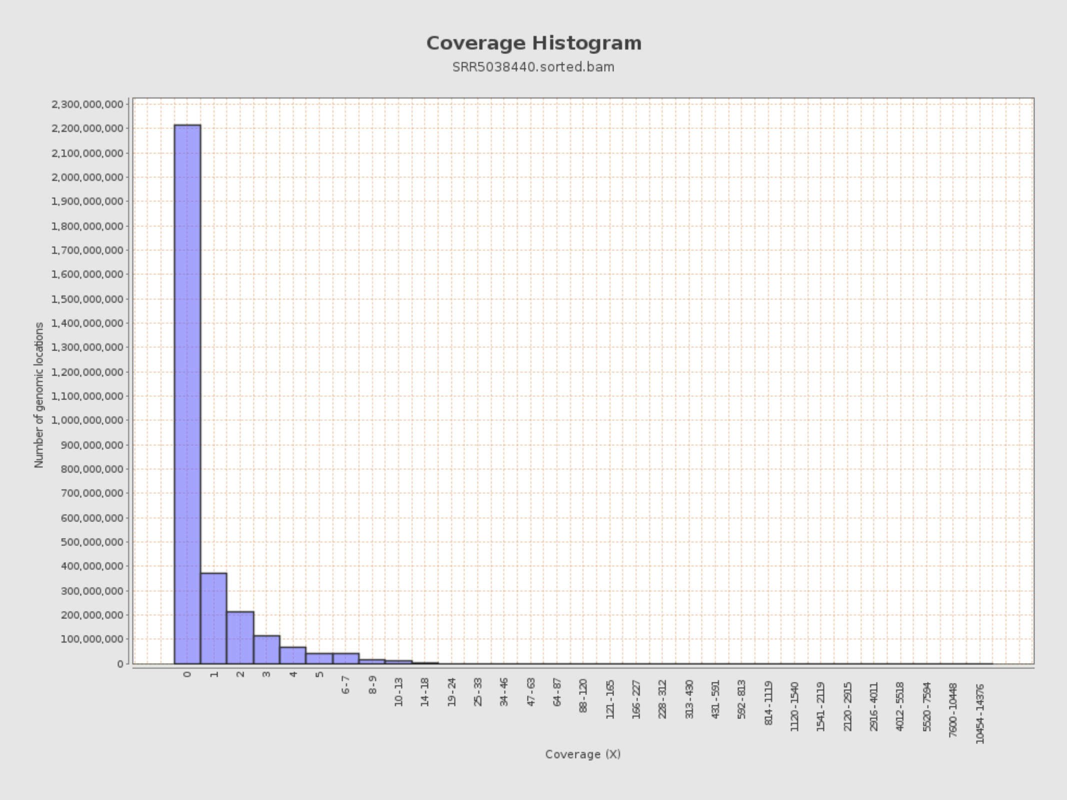
		bases	coverage	deviation
chr1	249250621	199832194	0.8017	14.2522
chr2	243199373	211479398	0.8696	10.8487
chr3	198022430	163013788	0.8232	1.807
chr4	191154276	103212979	0.5399	10.0594
chr5	180915260	163739860	0.9051	1.826
chr6	171115067	139997803	0.8182	7.9484
chr7	159138663	114044969	0.7166	10.8141
chr8	146364022	151304956	1.0338	3.9217
chr9	141213431	100194475	0.7095	17.3456
chr10	135534747	123832255	0.9137	23.6201
chr11	135006516	107268153	0.7945	8.0807
chr12	133851895	97465096	0.7282	1.7767
chr13	115169878	80501261	0.699	1.5576
chr14	107349540	76720316	0.7147	1.6642
chr15	102531392	63358653	0.6179	1.4838
chr16	90354753	71815331	0.7948	9.1993
chr17	81195210	56141467	0.6914	11.805
chr18	78077248	93967711	1.2035	11.8356
chr19	59128983	30341723	0.5131	5.9765
chr20	63025520	59691893	0.9471	3.4353
chr21	48129895	22756465	0.4728	4.4052
chr22	51304566	12080549	0.2355	0.9498
chrMT	16571	5731358	345.8668	174.582
chrX	155270560	79646107	0.513	2.376

chrY	59373566	5100236	0.0859	9.3853

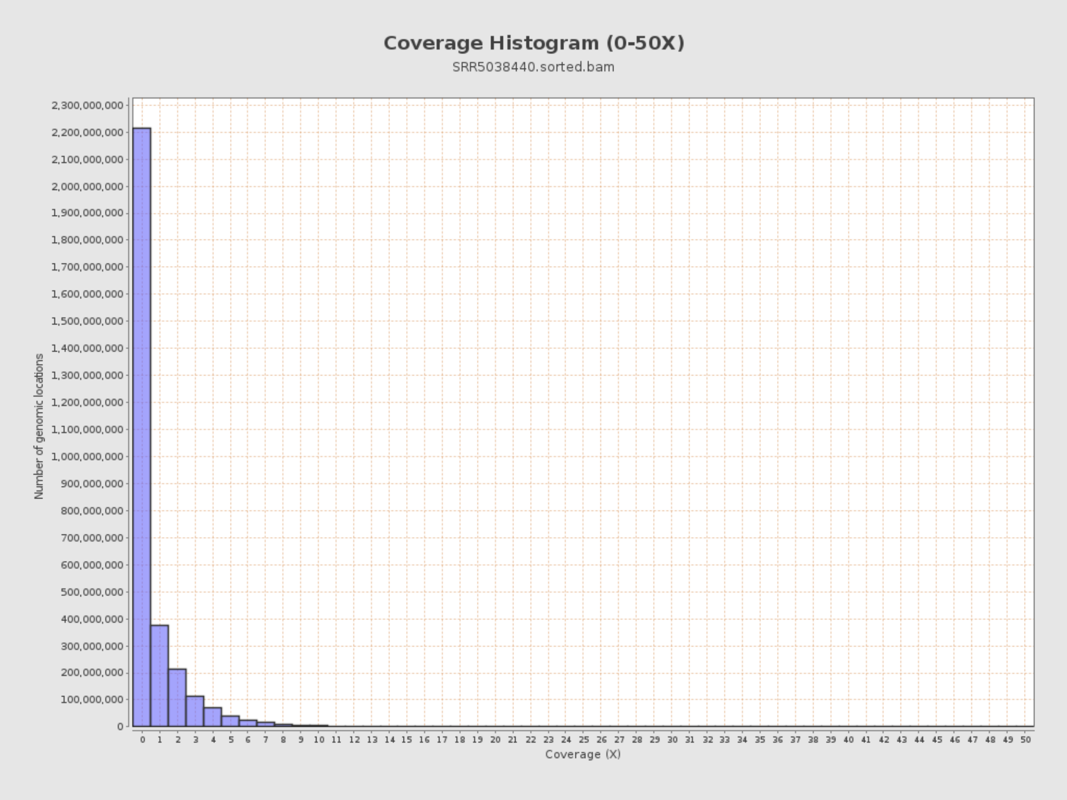
3. Results : Coverage across reference



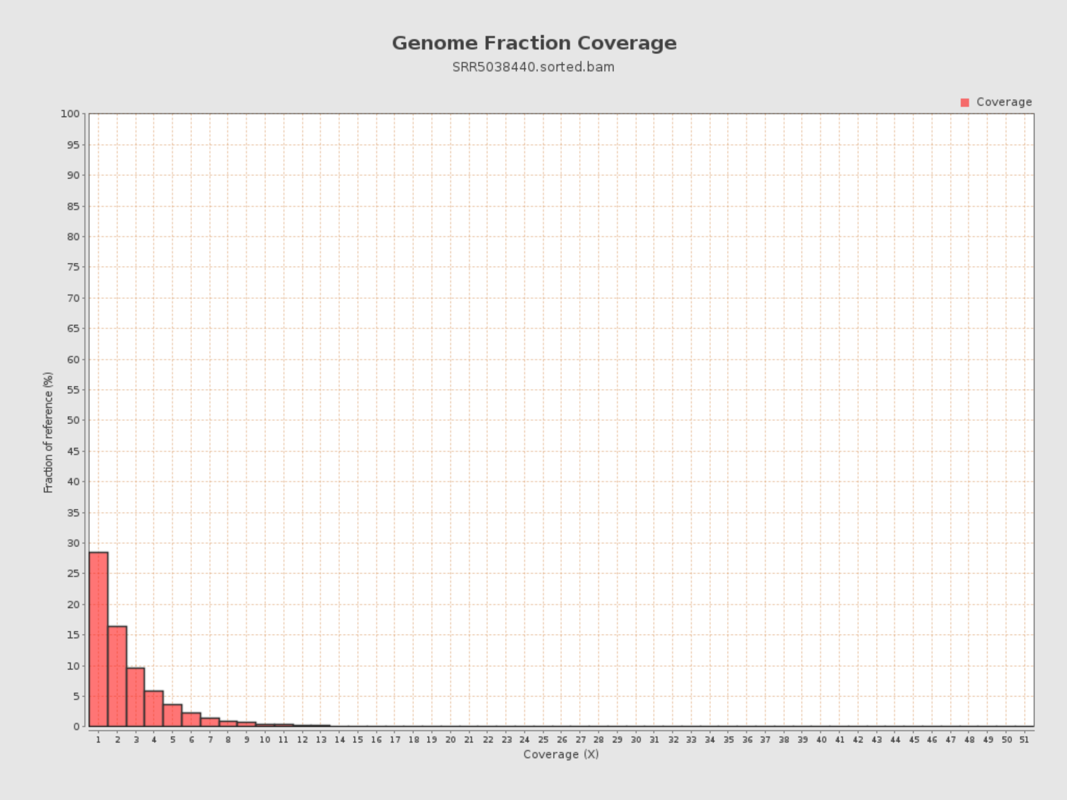
4. Results : Coverage Histogram



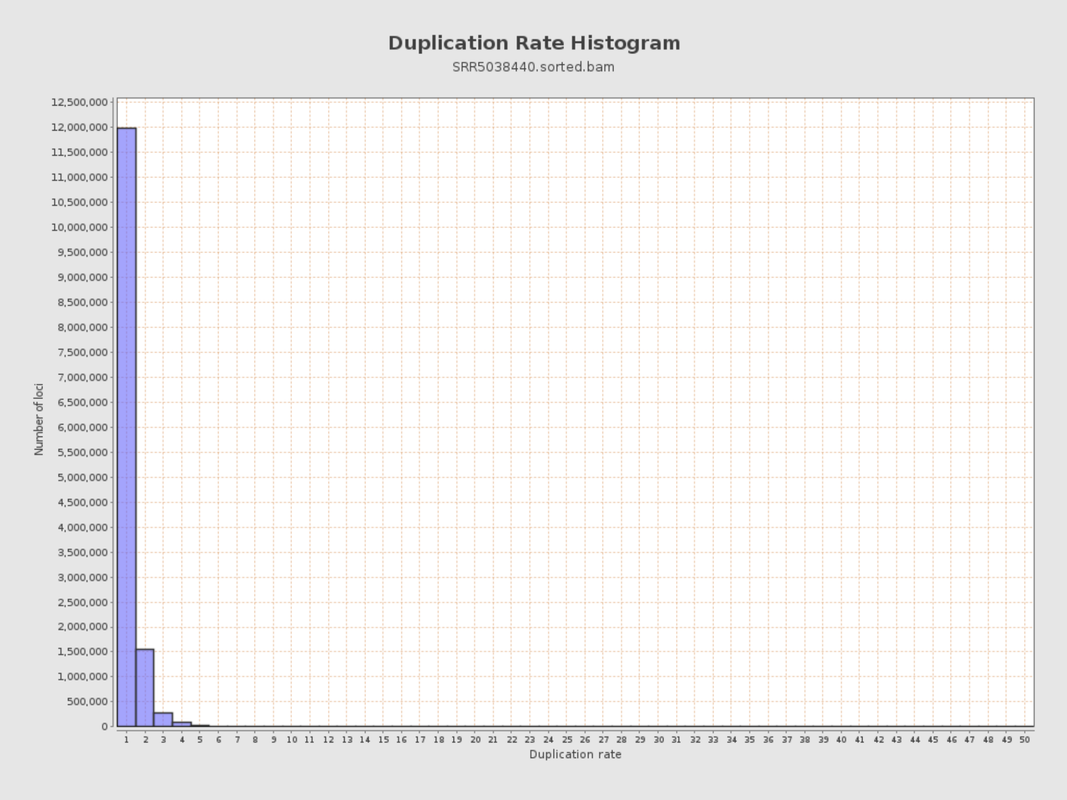
5. Results : Coverage Histogram (0-50X)



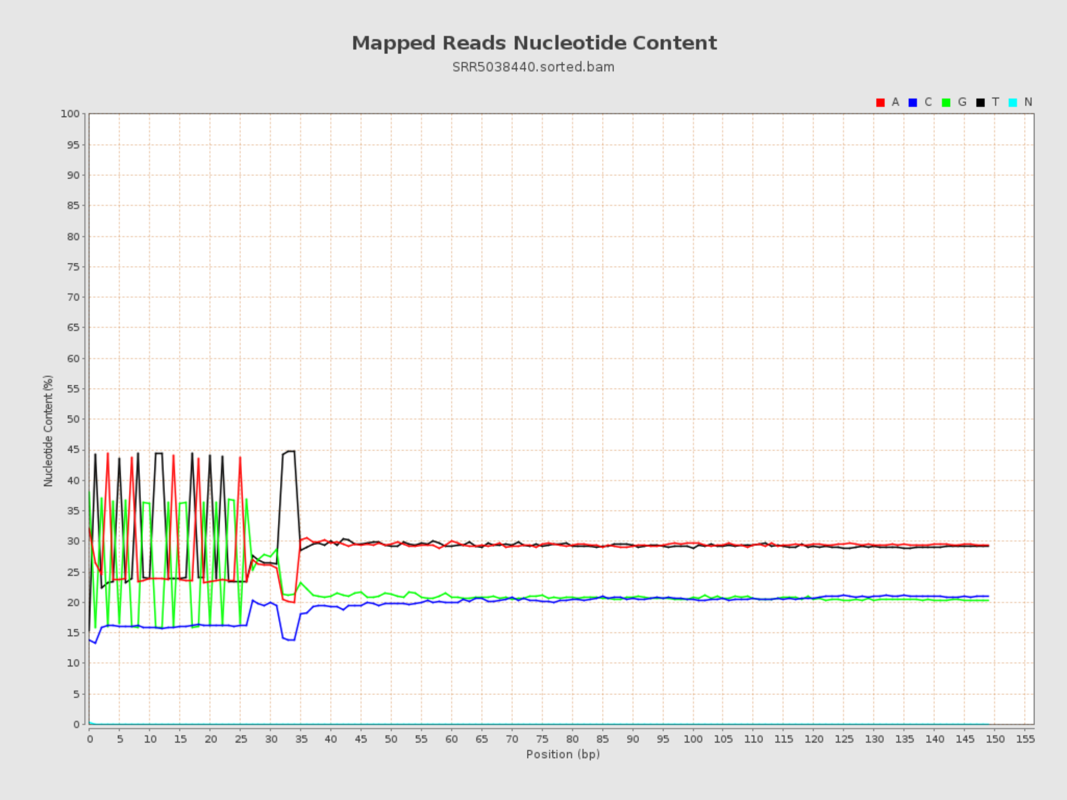
6. Results : Genome Fraction Coverage



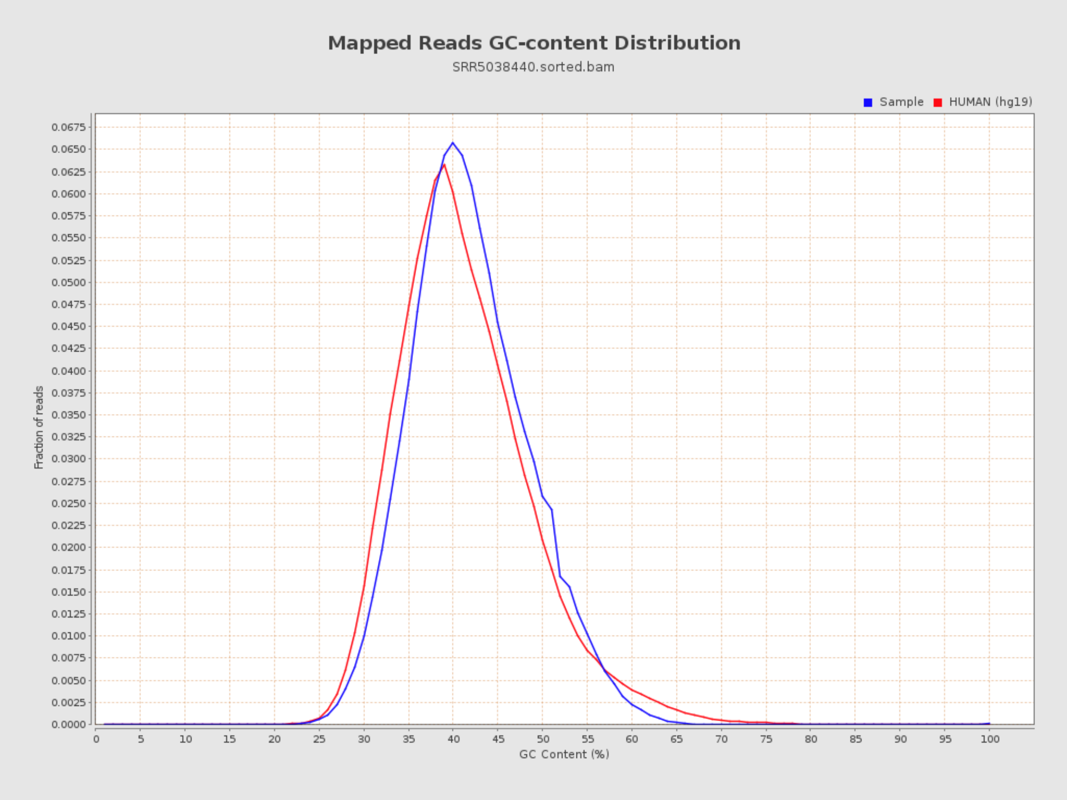
7. Results : Duplication Rate Histogram



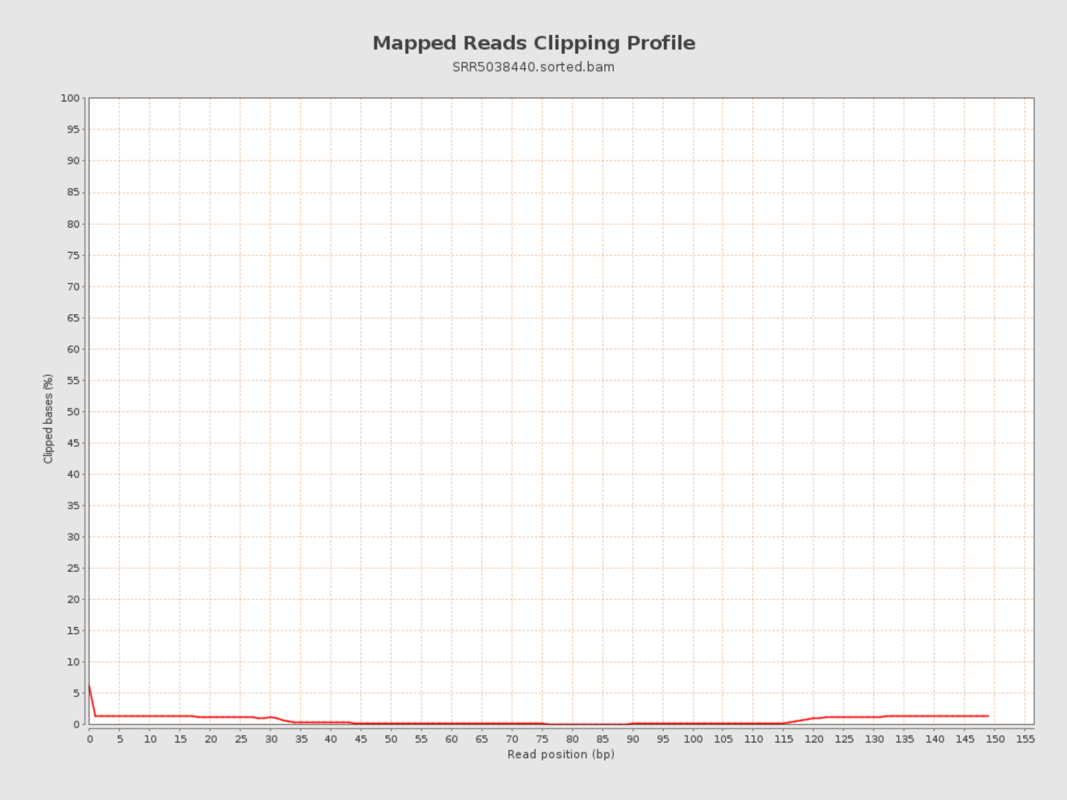
8. Results : Mapped Reads Nucleotide Content



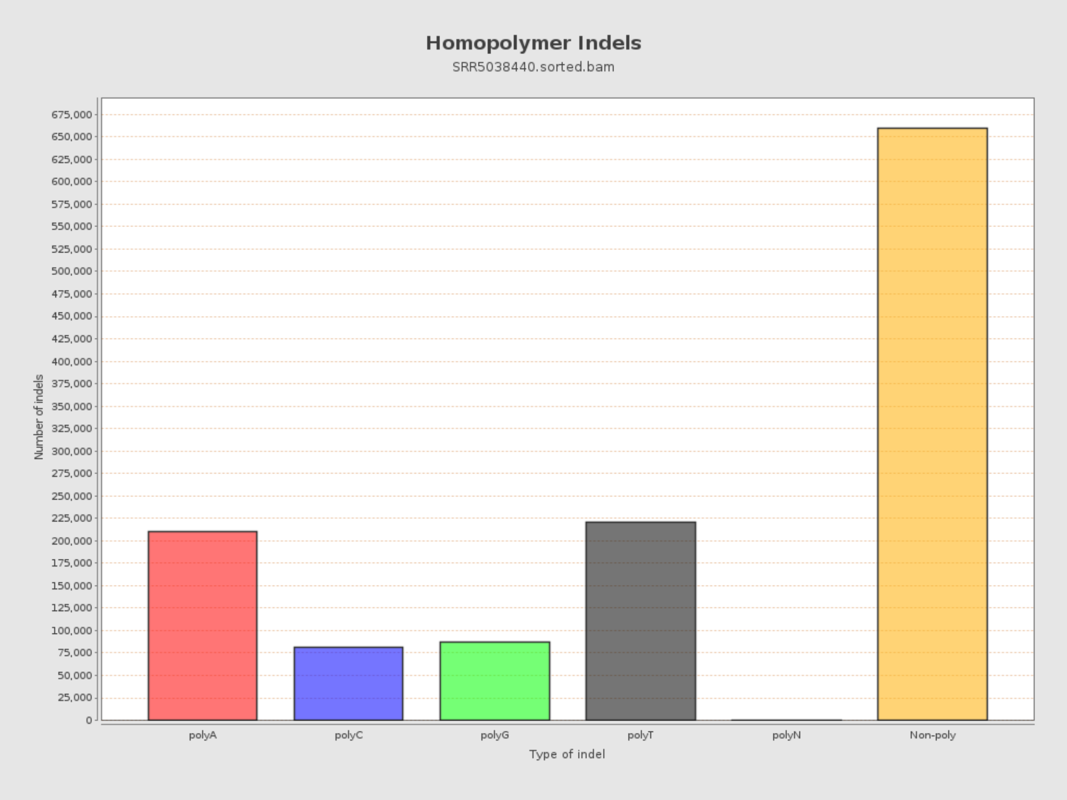
9. Results : Mapped Reads GC-content Distribution



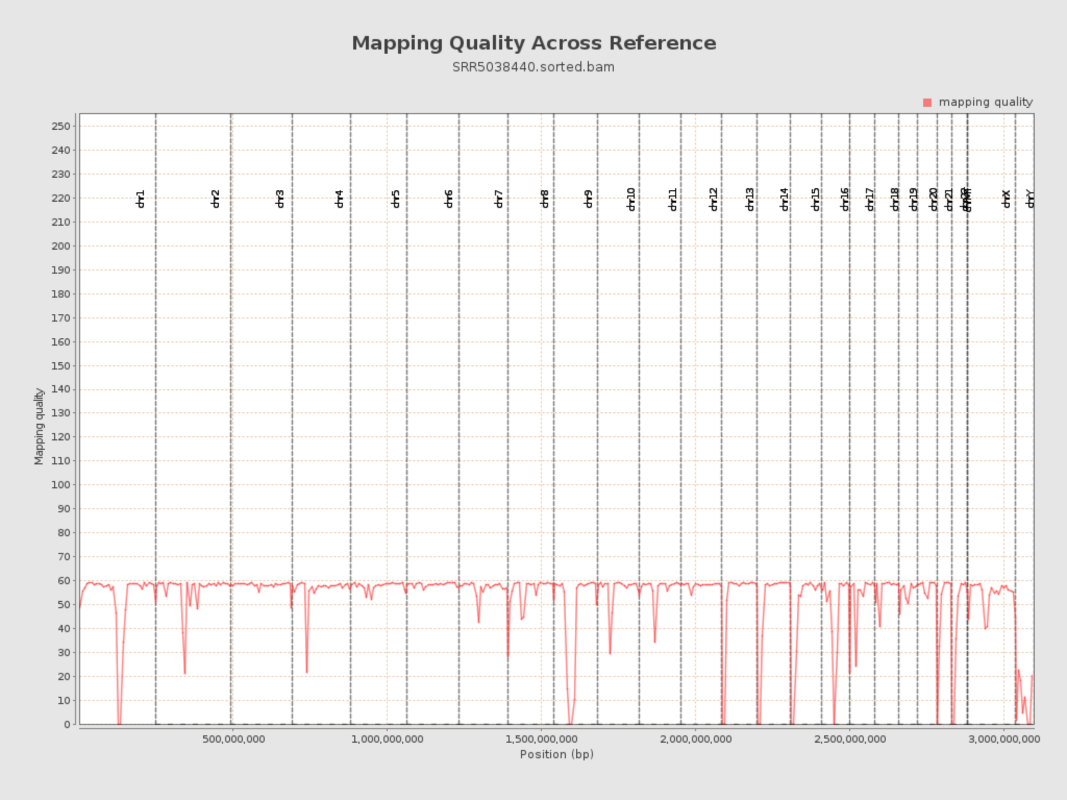
10. Results : Mapped Reads Clipping Profile



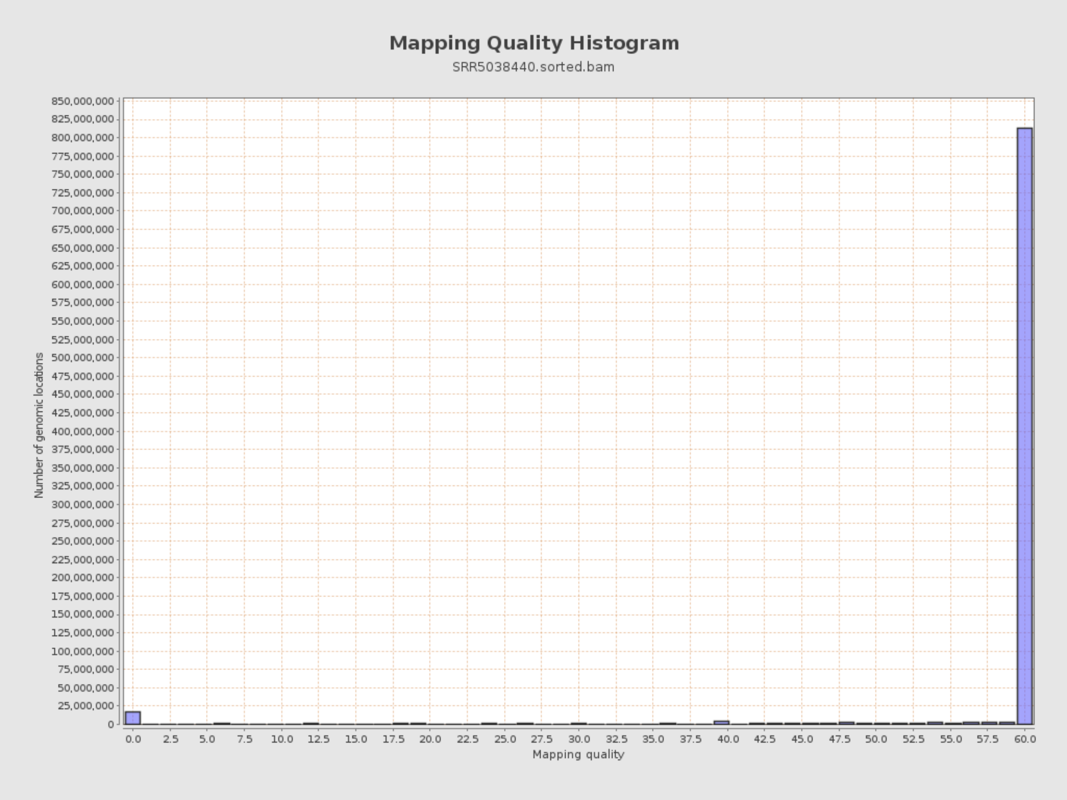
11. Results : Homopolymer Indels



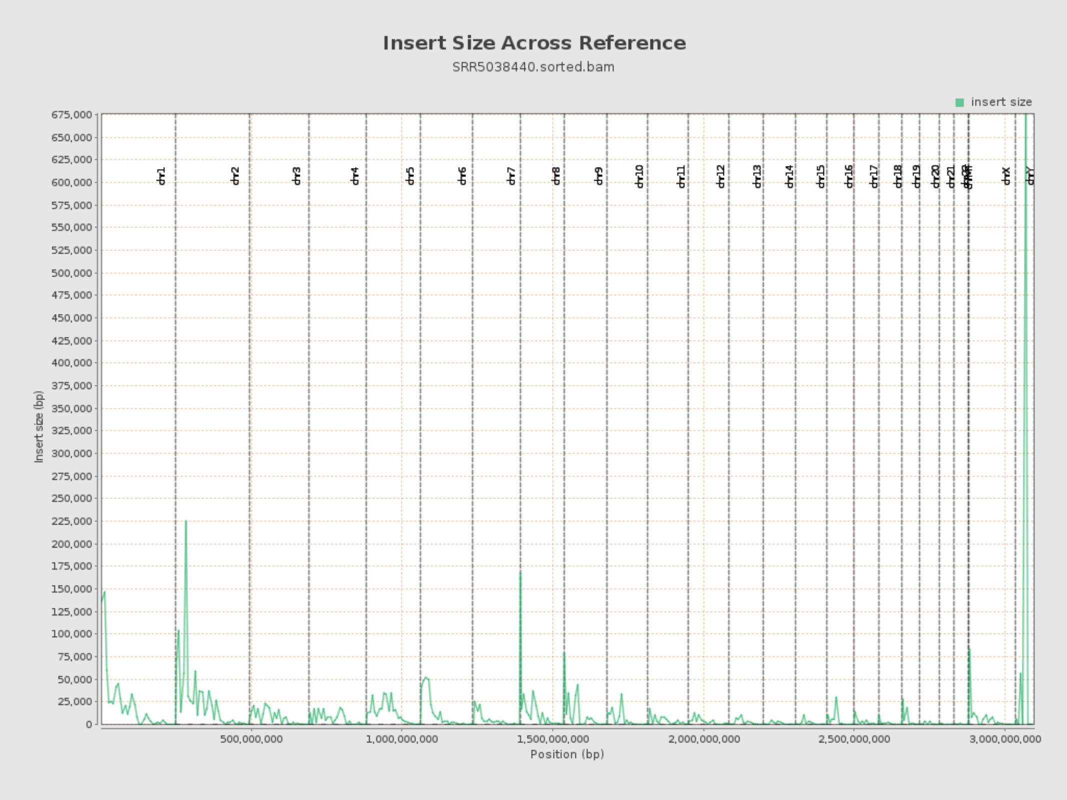
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram