Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 12:21:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630501.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630501_1.fastq.gz SRR630501_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 12:21:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	108,566,022
Mapped reads	108,212,483 / 99.67%
Unmapped reads	353,539 / 0.33%
Mapped paired reads	108,212,483 / 99.67%
Mapped reads, first in pair	54,230,706 / 49.95%
Mapped reads, second in pair	53,981,777 / 49.72%
Mapped reads, both in pair	107,928,992 / 99.41%
Mapped reads, singletons	283,491 / 0.26%
Secondary alignments	0
Supplementary alignments	628,382 / 0.58%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	18,014,680 / 16.59%
Duplication rate	14.69%
Clipped reads	10,111,351 / 9.31%

2.2. ACGT Content

Number/percentage of A's	3,344,106,390 / 31.12%
Number/percentage of C's	2,011,671,790 / 18.72%
Number/percentage of T's	3,325,718,107 / 30.95%
Number/percentage of G's	2,031,524,645 / 18.9%
Number/percentage of N's	34,157,541 / 0.32%

GC Percentage	37.62%

2.3. Coverage

Mean	3.4724
Standard Deviation	11.6276

2.4. Mapping Quality

Mean Mapping Quality	53.93

2.5. Insert size

Mean	45,885.61
Standard Deviation	2,032,090.6
P25/Median/P75	253 / 317 / 387

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	131,168,582
Insertions	950,051
Mapped reads with at least one insertion	0.86%
Deletions	1,009,672
Mapped reads with at least one deletion	0.91%
Homopolymer indels	43.94%

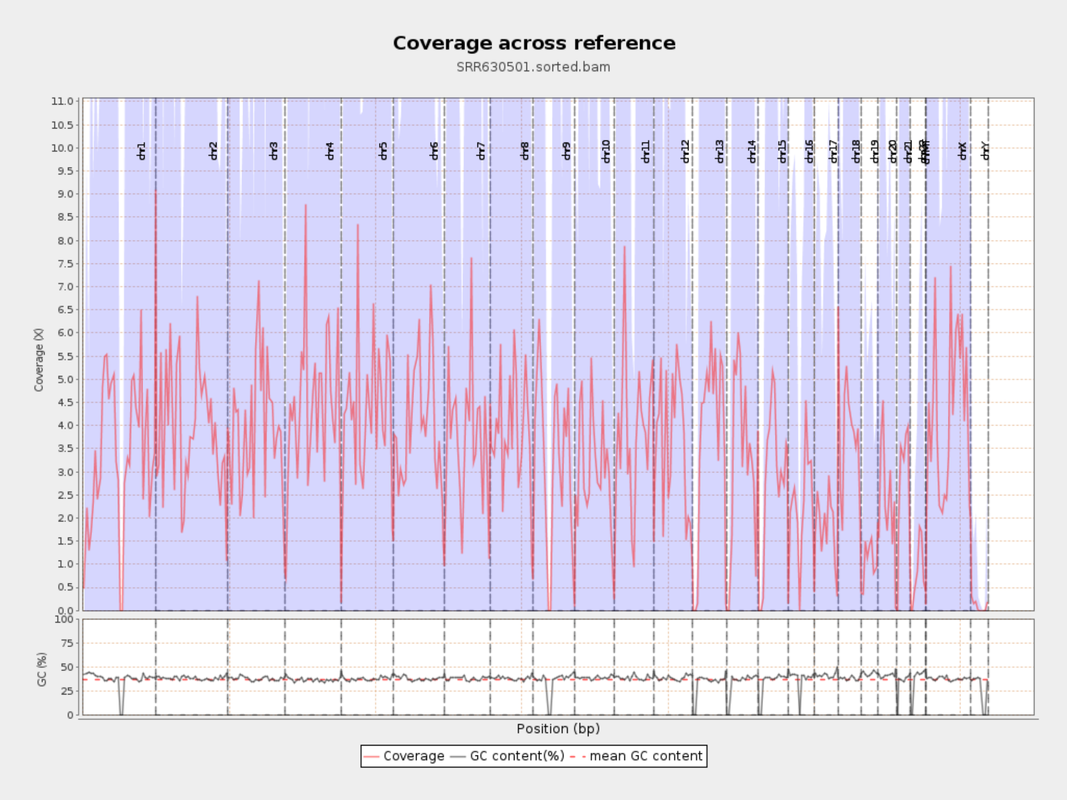
2.7. Chromosome stats

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

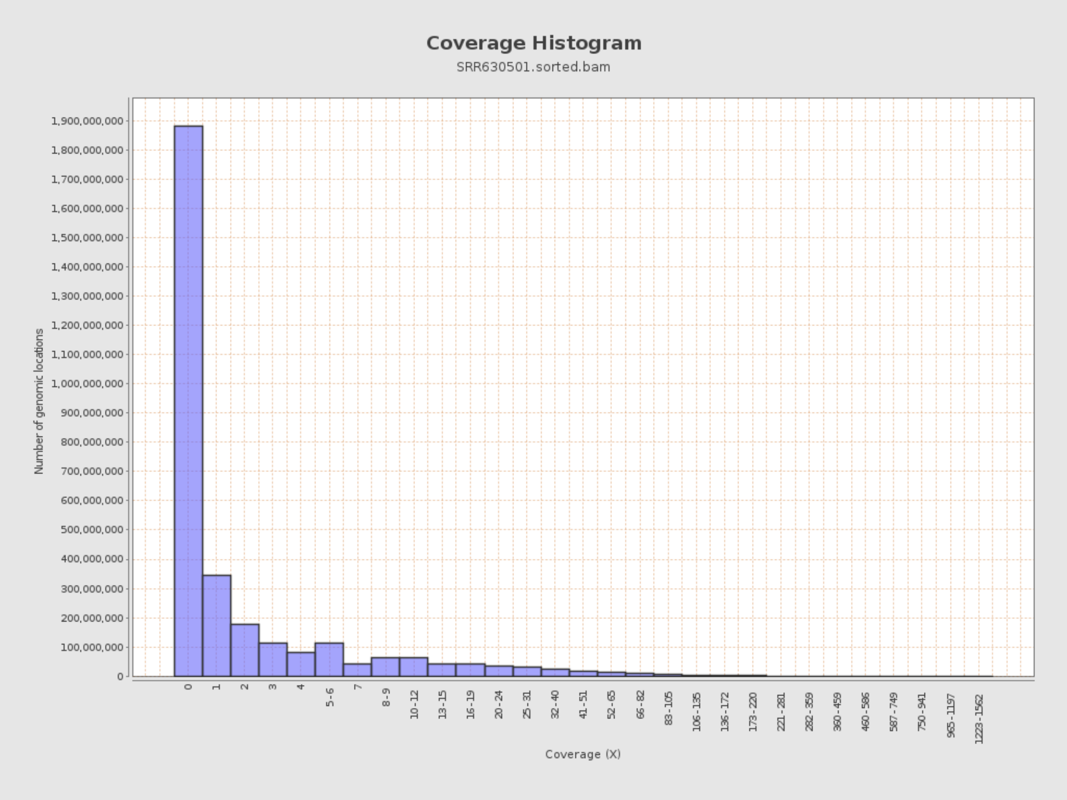
		bases	coverage	deviation
chr1	249250621	842784325	3.3813	11.2067
chr2	243199373	955859073	3.9304	12.0446
chr3	198022430	776085788	3.9192	11.4275
chr4	191154276	854817764	4.4719	14.4314
chr5	180915260	774140390	4.279	13.5899
chr6	171115067	695972263	4.0673	12.3726
chr7	159138663	581737525	3.6555	11.4601
chr8	146364022	574867728	3.9277	12.5462
chr9	141213431	473084729	3.3501	11.2518
chr10	135534747	427648298	3.1553	10.5625
chr11	135006516	514829857	3.8134	12.9832
chr12	133851895	486460368	3.6343	10.5174
chr13	115169878	435571341	3.782	13.0814
chr14	107349540	351977892	3.2788	12.2764
chr15	102531392	286430623	2.7936	9.672
chr16	90354753	200081215	2.2144	8.054
chr17	81195210	151406199	1.8647	6.0324
chr18	78077248	297295311	3.8077	11.2516
chr19	59128983	64904360	1.0977	4.2411
chr20	63025520	156303983	2.48	8.4615
chr21	48129895	132022459	2.743	11.3923
chr22	51304566	42619984	0.8307	3.9358
chrMT	16571	2221	0.134	0.7075
chrX	155270560	666650928	4.2935	14.5215

chrY	59373566	5873415	0.0989	1.4369

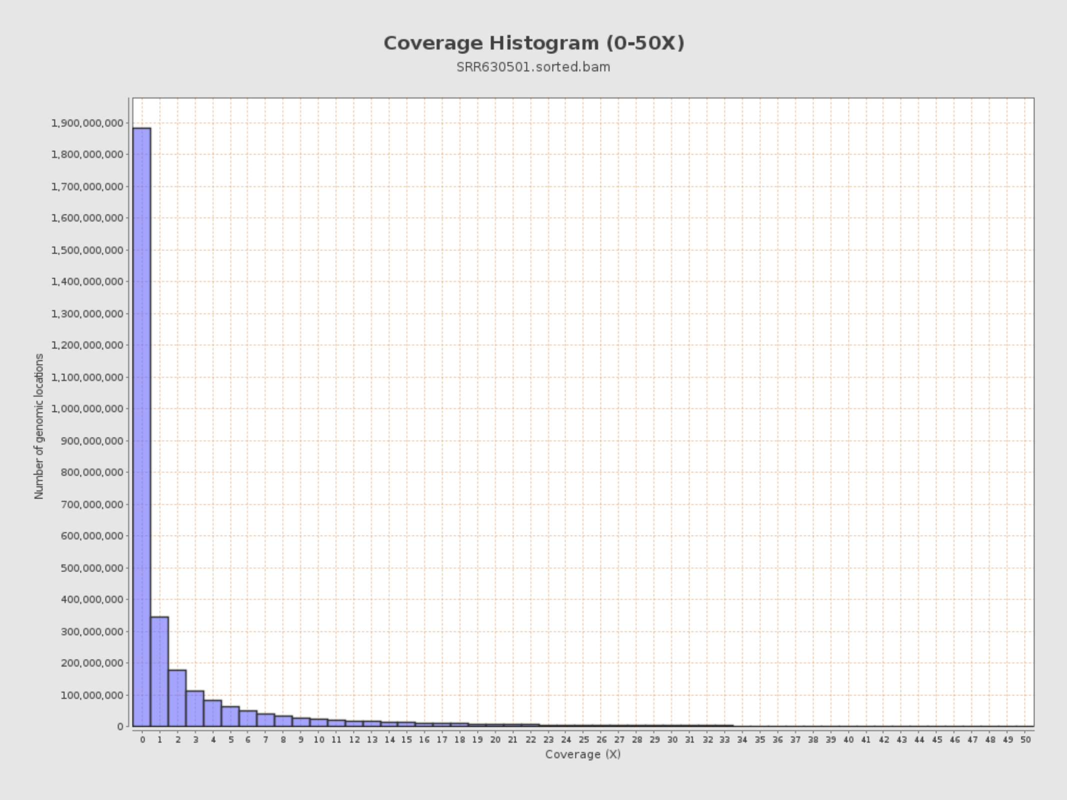
3. Results : Coverage across reference



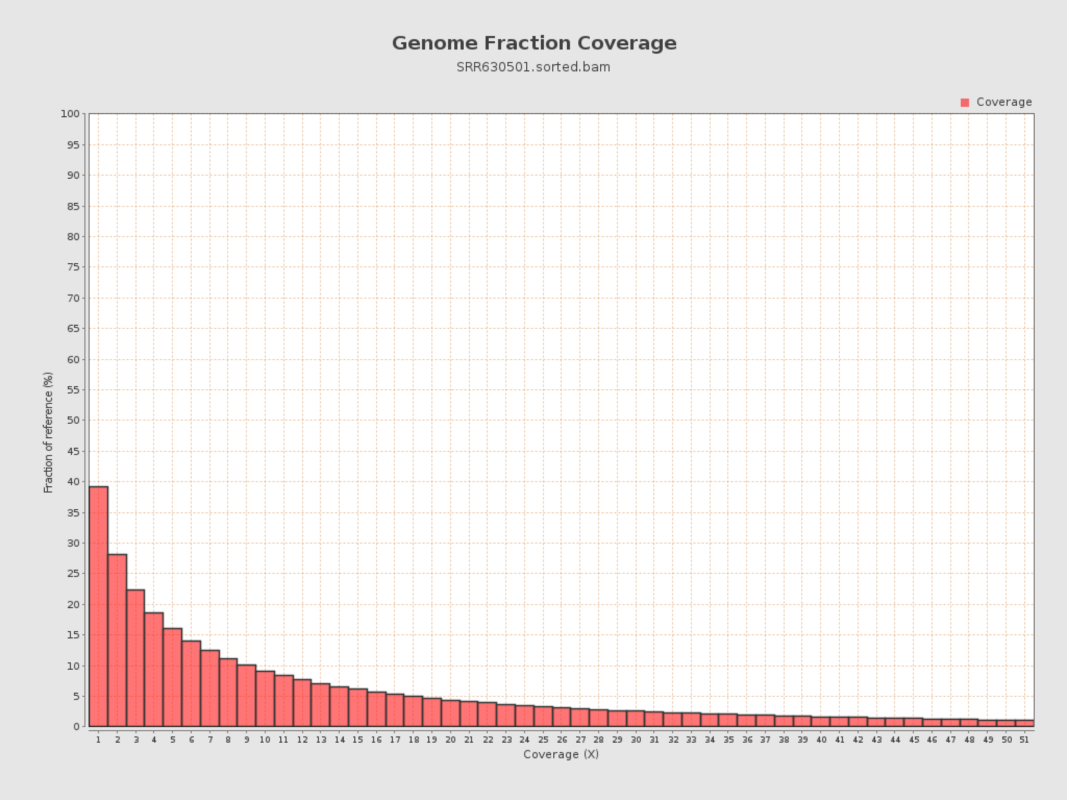
4. Results : Coverage Histogram



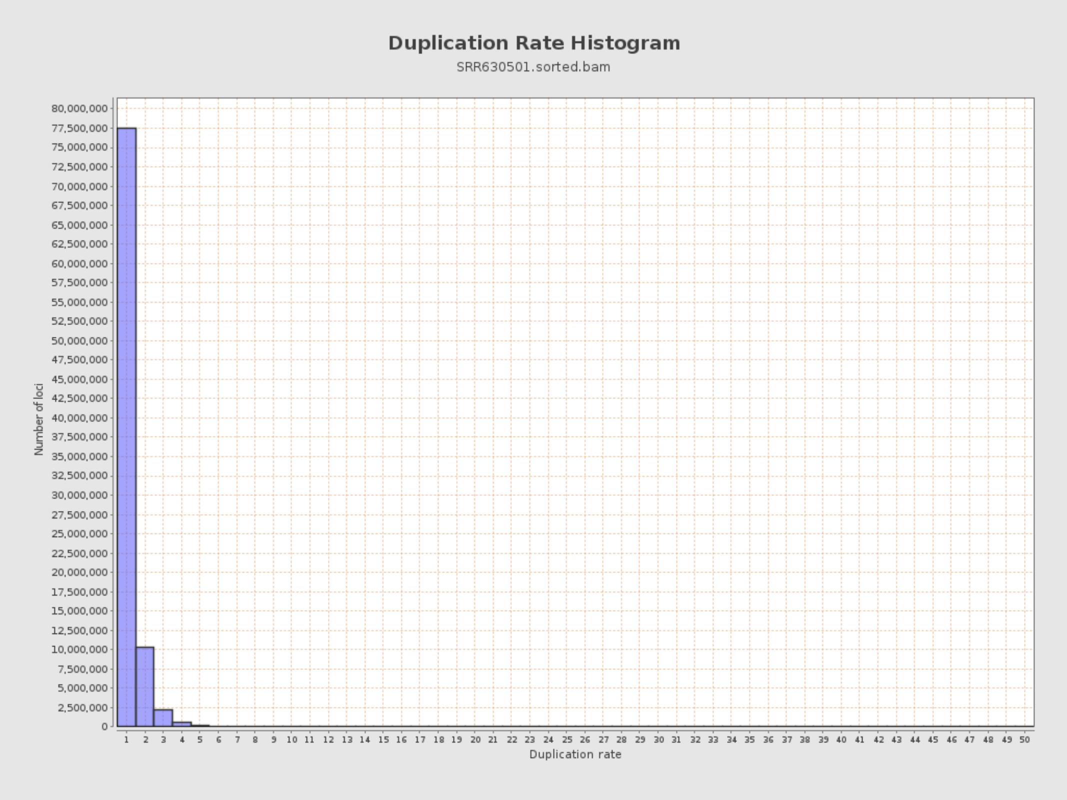
5. Results : Coverage Histogram (0-50X)



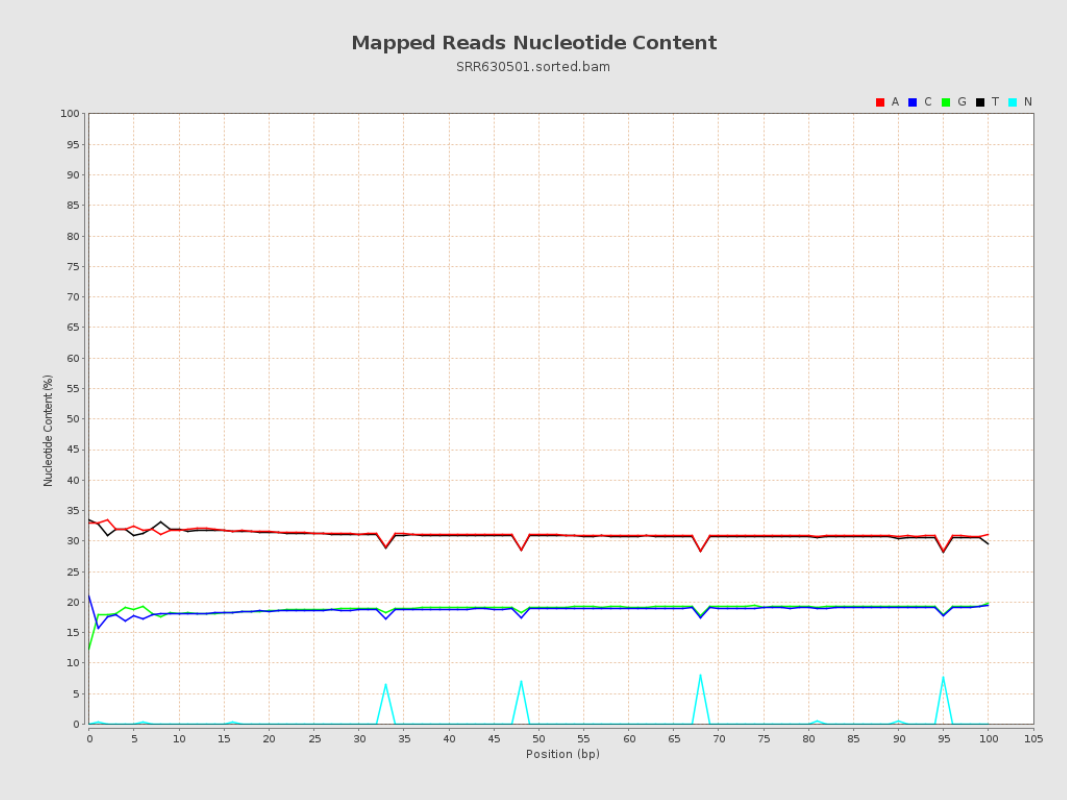
6. Results : Genome Fraction Coverage



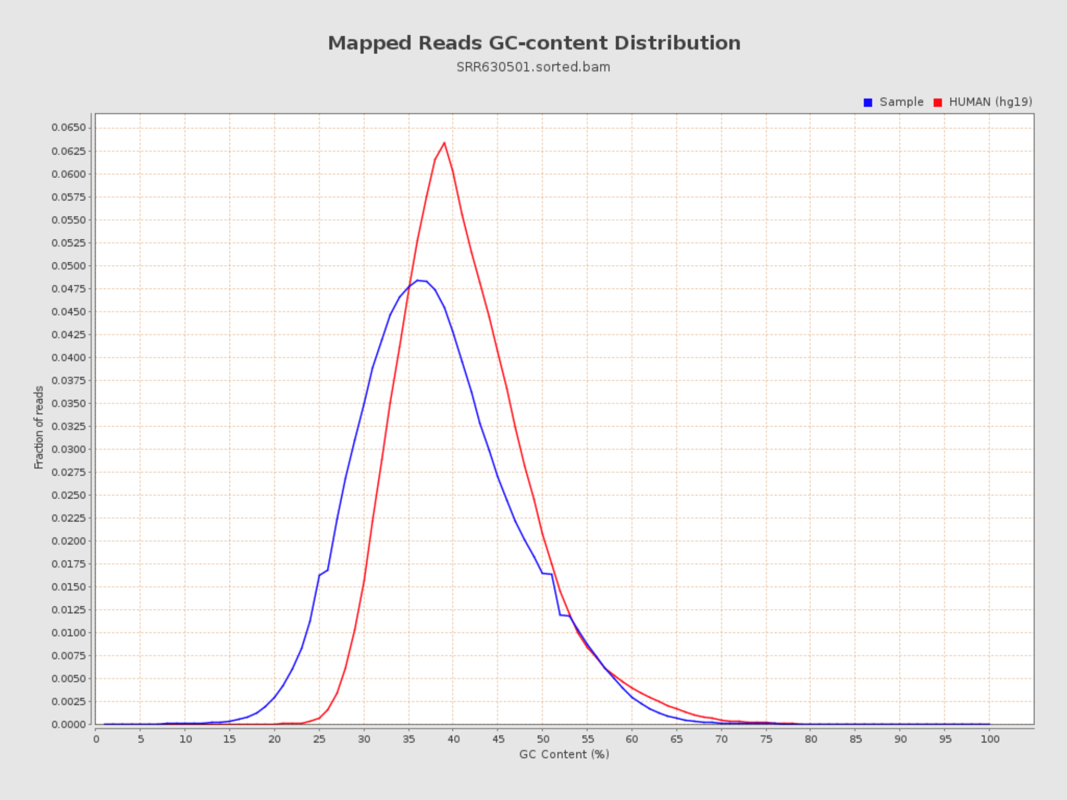
7. Results : Duplication Rate Histogram



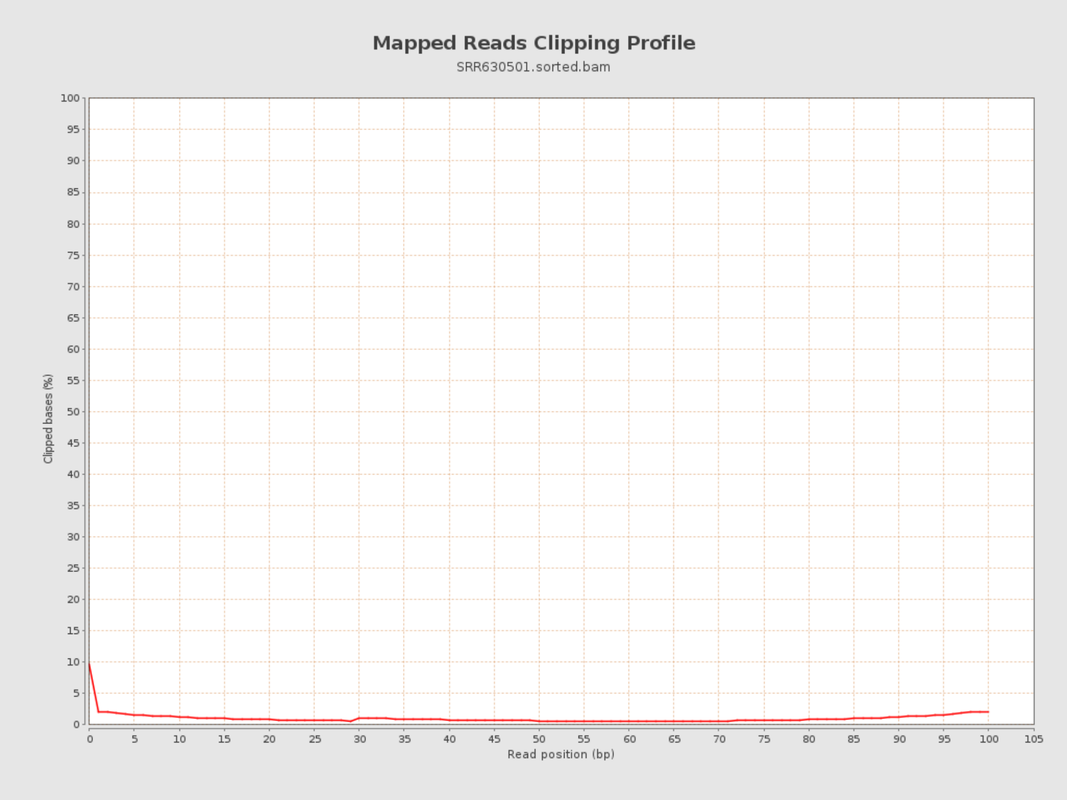
8. Results : Mapped Reads Nucleotide Content



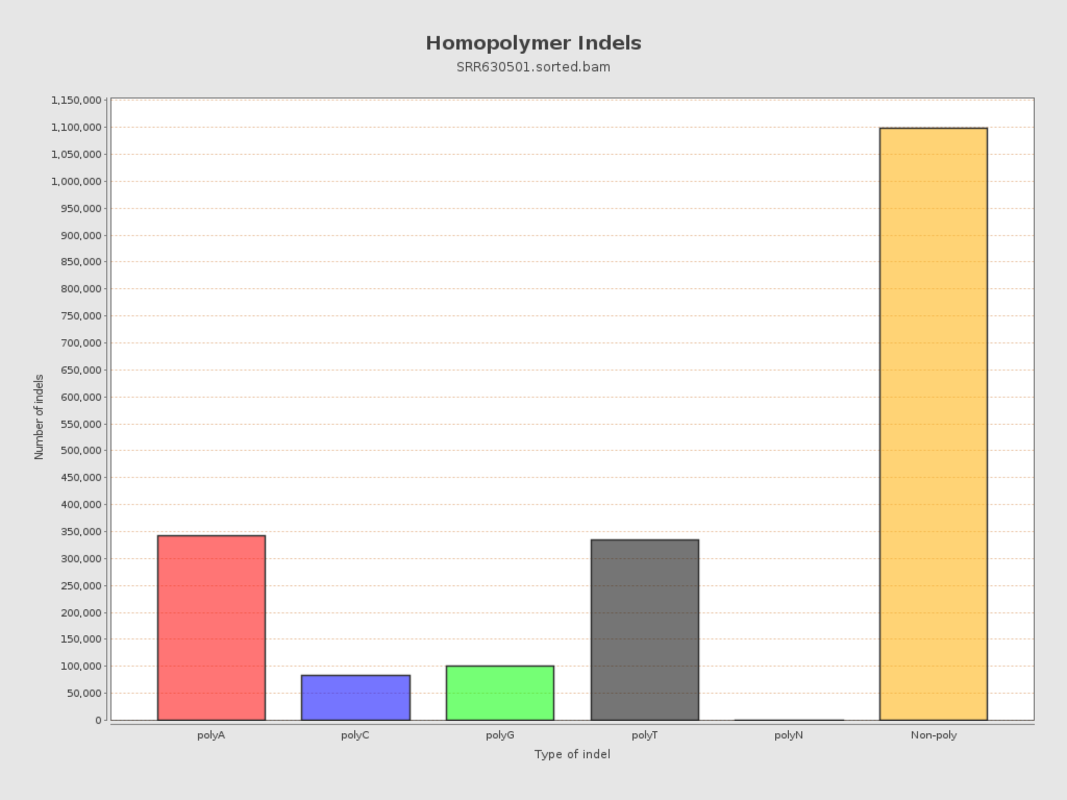
9. Results : Mapped Reads GC-content Distribution



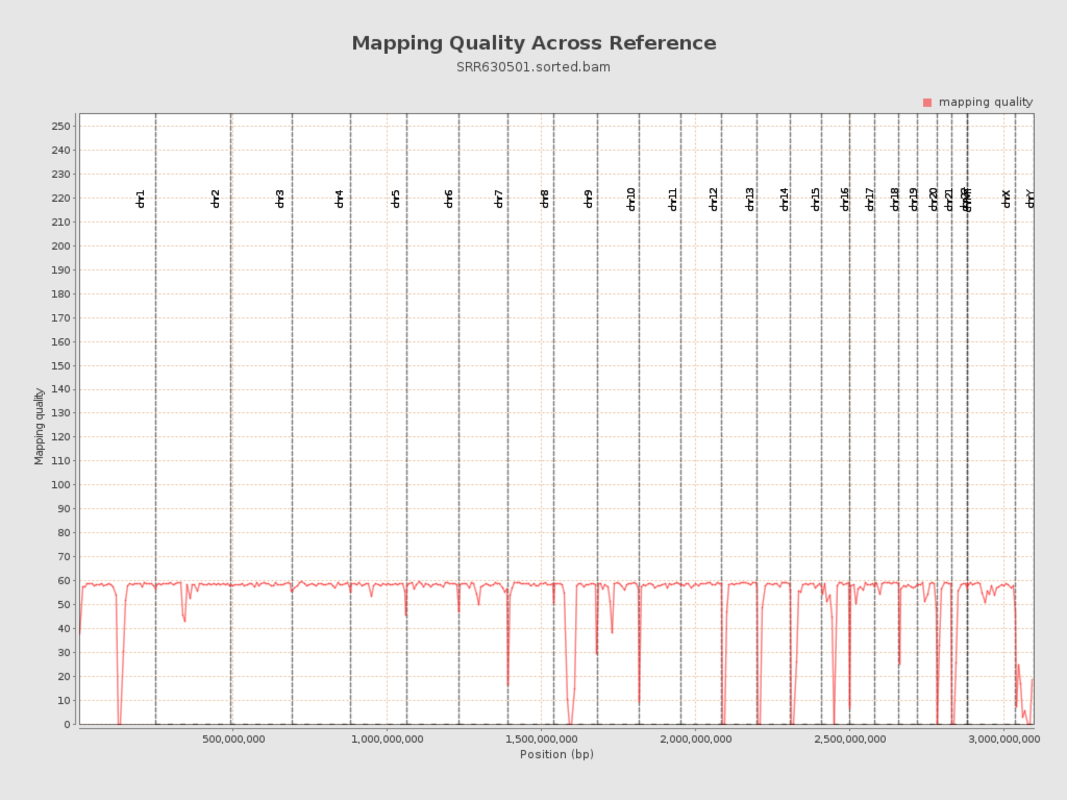
10. Results : Mapped Reads Clipping Profile



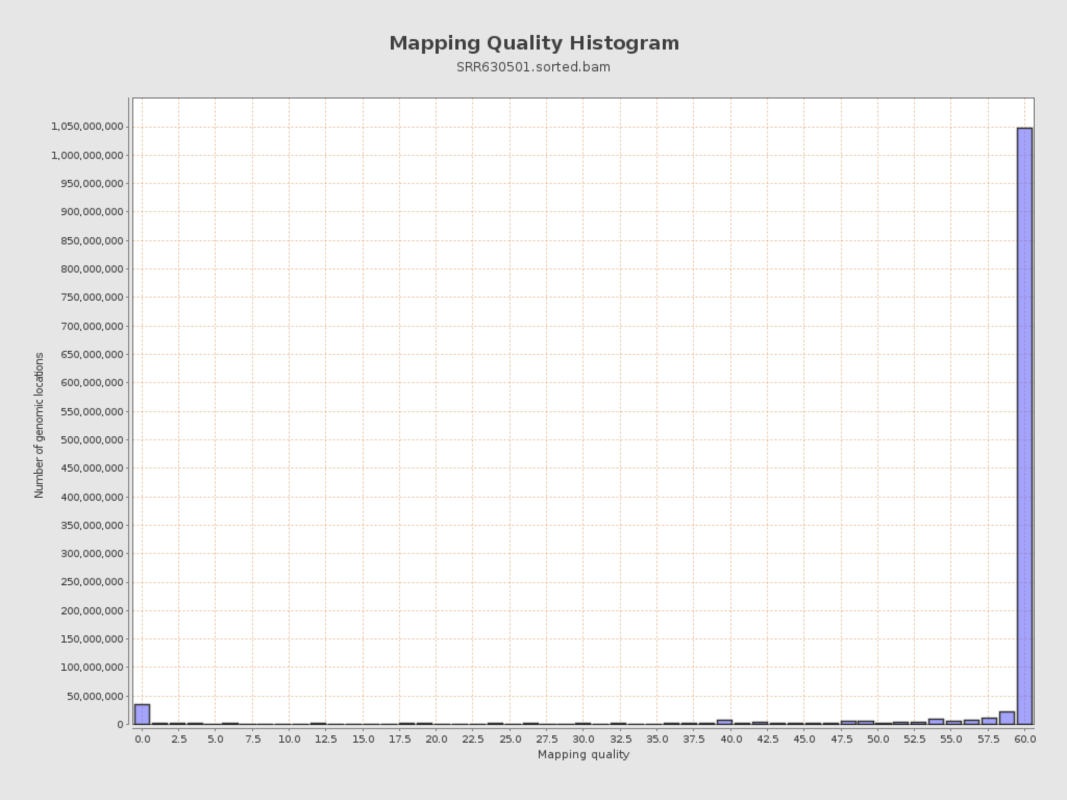
11. Results : Homopolymer Indels



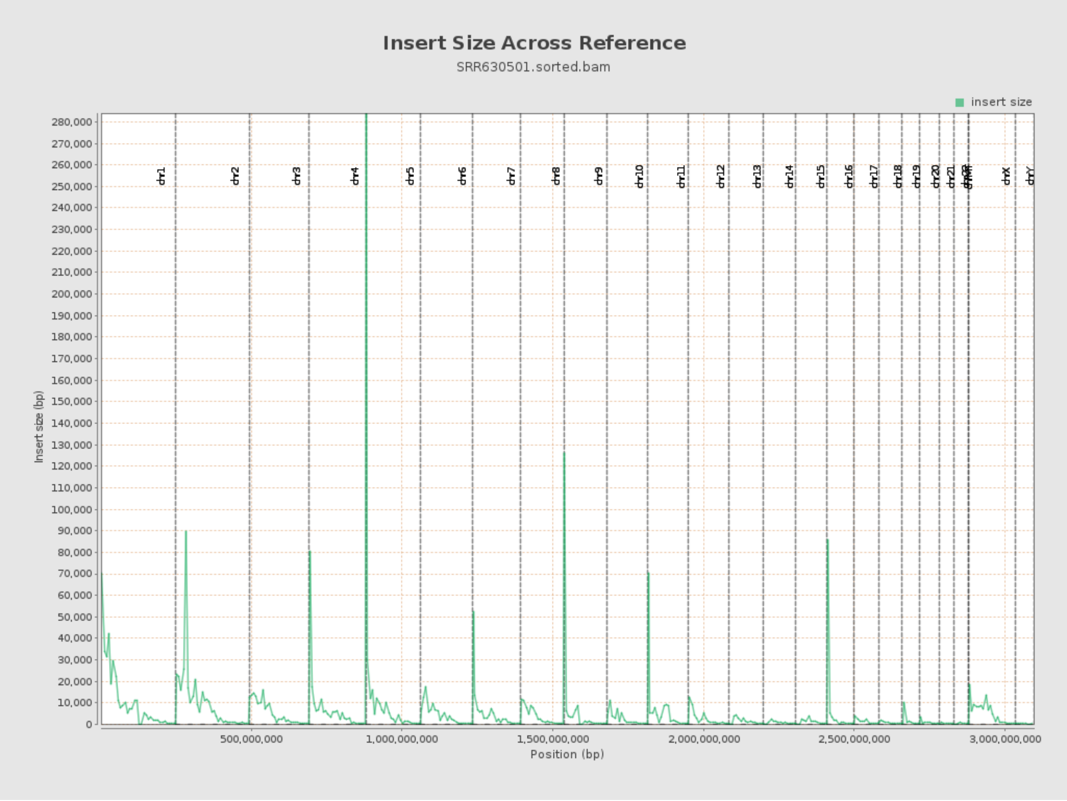
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram