Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/16 13:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630890.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 SRR630890_1.fastq.gz SRR630890_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 16 13:34:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,111,368
Mapped reads	52,502,411 / 98.85%
Unmapped reads	608,957 / 1.15%
Mapped paired reads	52,502,411 / 98.85%
Mapped reads, first in pair	26,455,918 / 49.81%
Mapped reads, second in pair	26,046,493 / 49.04%
Mapped reads, both in pair	52,056,134 / 98.01%
Mapped reads, singletons	446,277 / 0.84%
Secondary alignments	0
Supplementary alignments	304,762 / 0.57%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	9,980,674 / 18.79%
Duplication rate	17.3%
Clipped reads	5,878,708 / 11.07%

2.2. ACGT Content

Number/percentage of A's	1,577,367,709 / 30.74%
Number/percentage of C's	985,111,025 / 19.2%
Number/percentage of T's	1,549,166,593 / 30.19%
Number/percentage of G's	1,009,734,609 / 19.68%
Number/percentage of N's	10,134,244 / 0.2%

GC Percentage	38.87%

2.3. Coverage

Mean	1.658
Standard Deviation	6.5316

2.4. Mapping Quality

Mean Mapping Quality	50.98

2.5. Insert size

Mean	394,955.67
Standard Deviation	5,961,659.03
P25/Median/P75	151 / 196 / 267

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	57,817,702
Insertions	4,404,862
Mapped reads with at least one insertion	8.32%
Deletions	649,611
Mapped reads with at least one deletion	1.21%
Homopolymer indels	25.86%

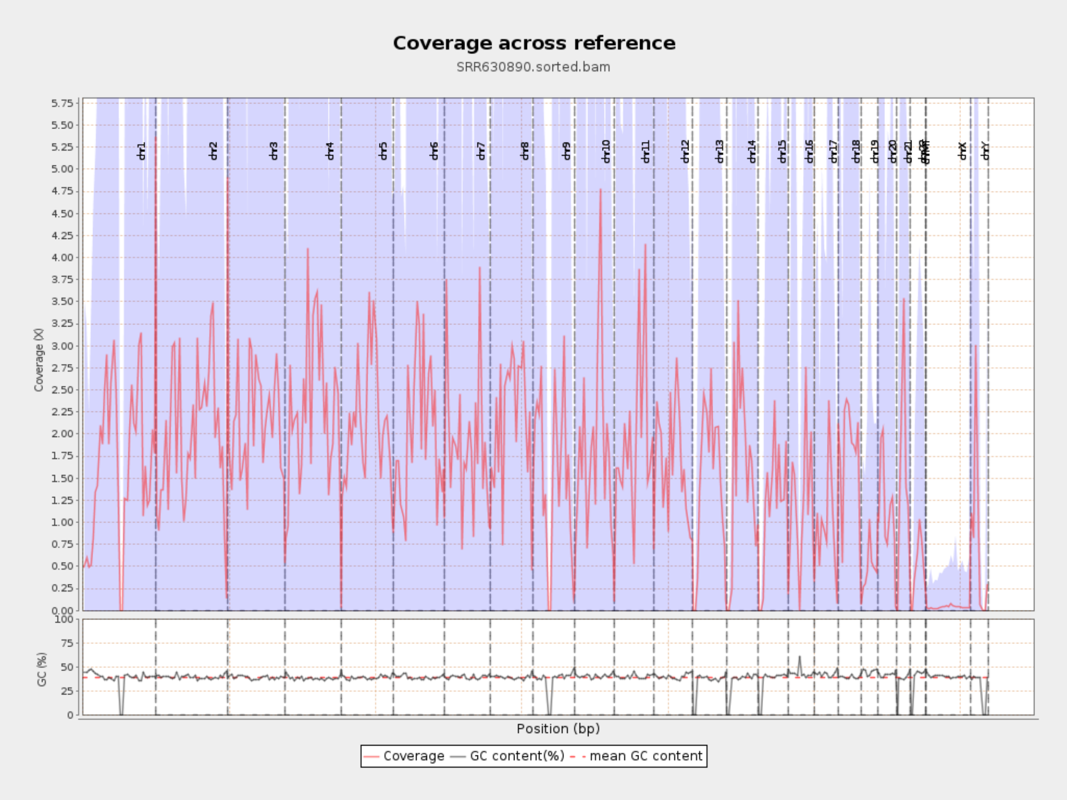
2.7. Chromosome stats

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

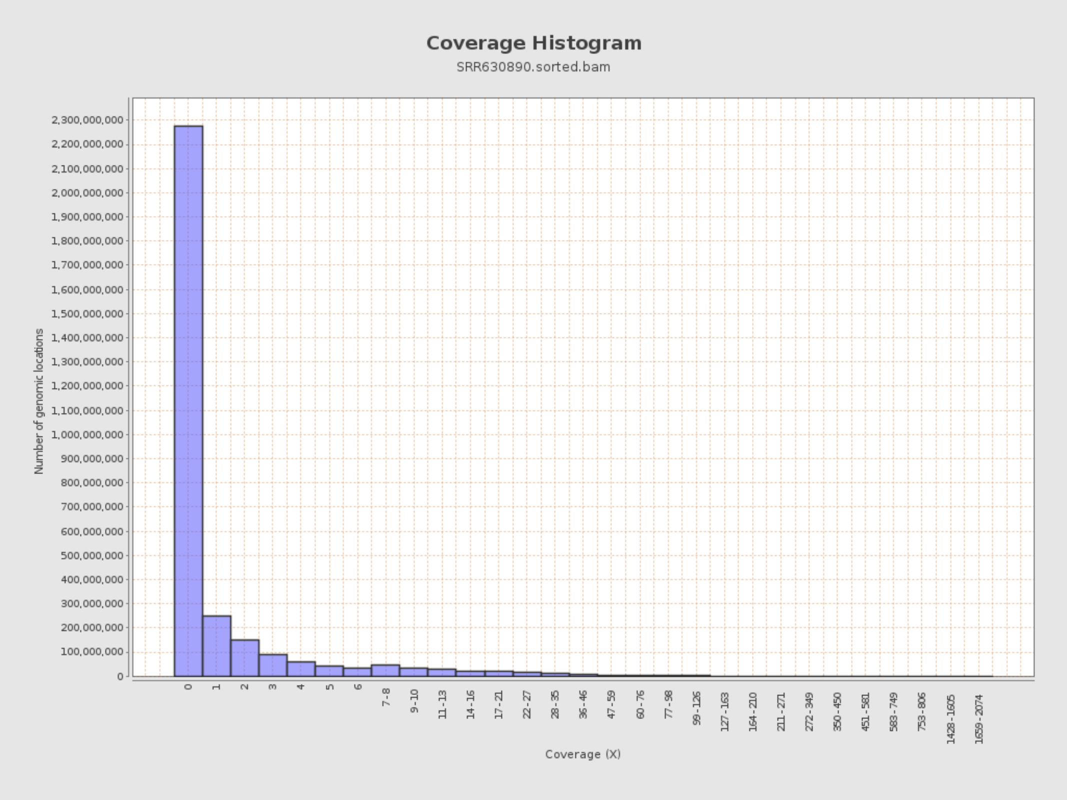
		bases	coverage	deviation
chr1	249250621	417581055	1.6753	6.7634
chr2	243199373	483342540	1.9874	7.1073
chr3	198022430	434639821	2.1949	7.4584
chr4	191154276	439674856	2.3001	8.3089
chr5	180915260	385498336	2.1308	7.3052
chr6	171115067	347879965	2.033	7.3985
chr7	159138663	296767220	1.8648	7.4135
chr8	146364022	319075974	2.18	8.1841
chr9	141213431	223573730	1.5832	6.4838
chr10	135534747	248201858	1.8313	7.6351
chr11	135006516	262993963	1.948	6.8544
chr12	133851895	224818742	1.6796	6.1911
chr13	115169878	169429279	1.4711	5.2131
chr14	107349540	169651873	1.5804	6.124
chr15	102531392	122753683	1.1972	4.4194
chr16	90354753	106073009	1.174	4.6431
chr17	81195210	82441253	1.0153	4.3695
chr18	78077248	141266103	1.8093	5.7184
chr19	59128983	29704599	0.5024	2.0886
chr20	63025520	74620879	1.184	5.0694
chr21	48129895	69280191	1.4394	6.0775
chr22	51304566	26263517	0.5119	2.2132
chrMT	16571	3036	0.1832	0.8939
chrX	155270560	8090533	0.0521	0.8576

chrY	59373566	49152221	0.8278	4.2637

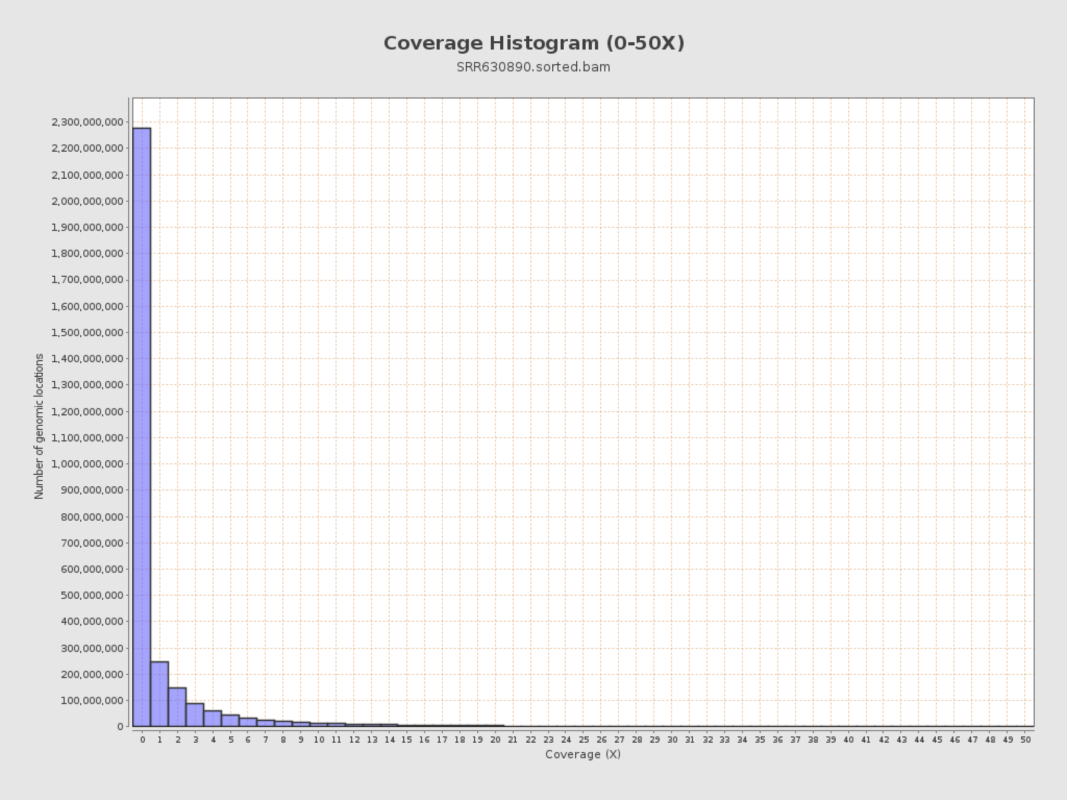
3. Results : Coverage across reference



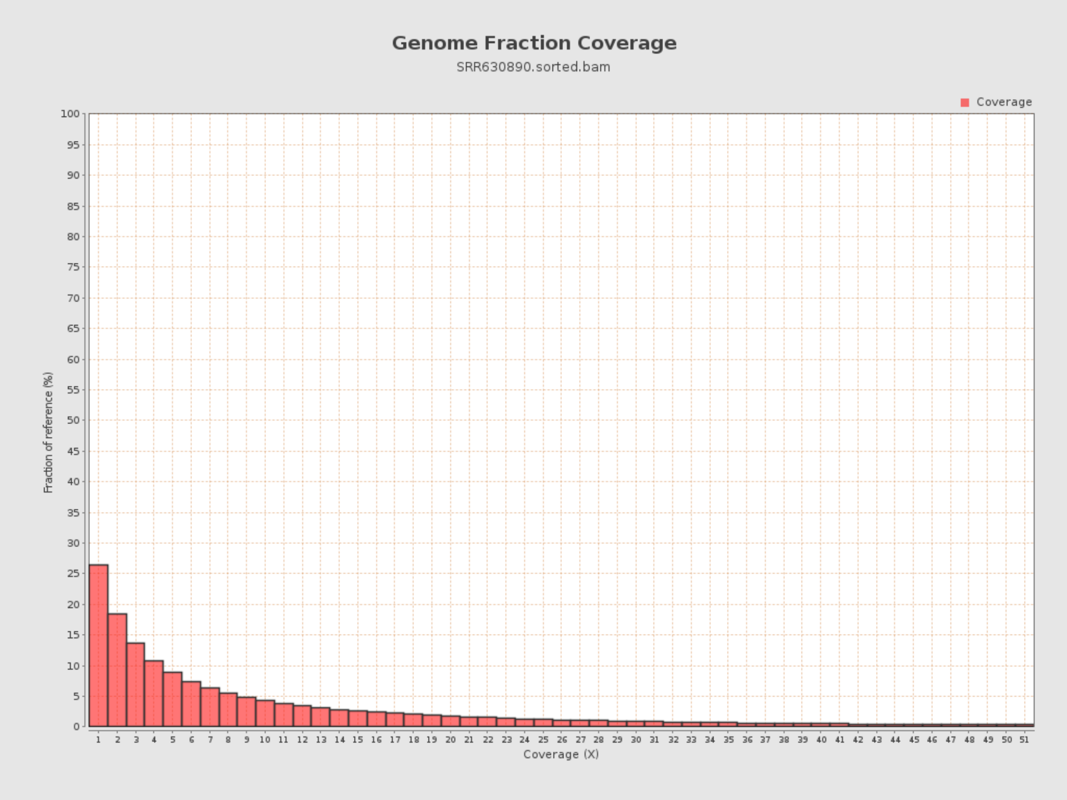
4. Results : Coverage Histogram



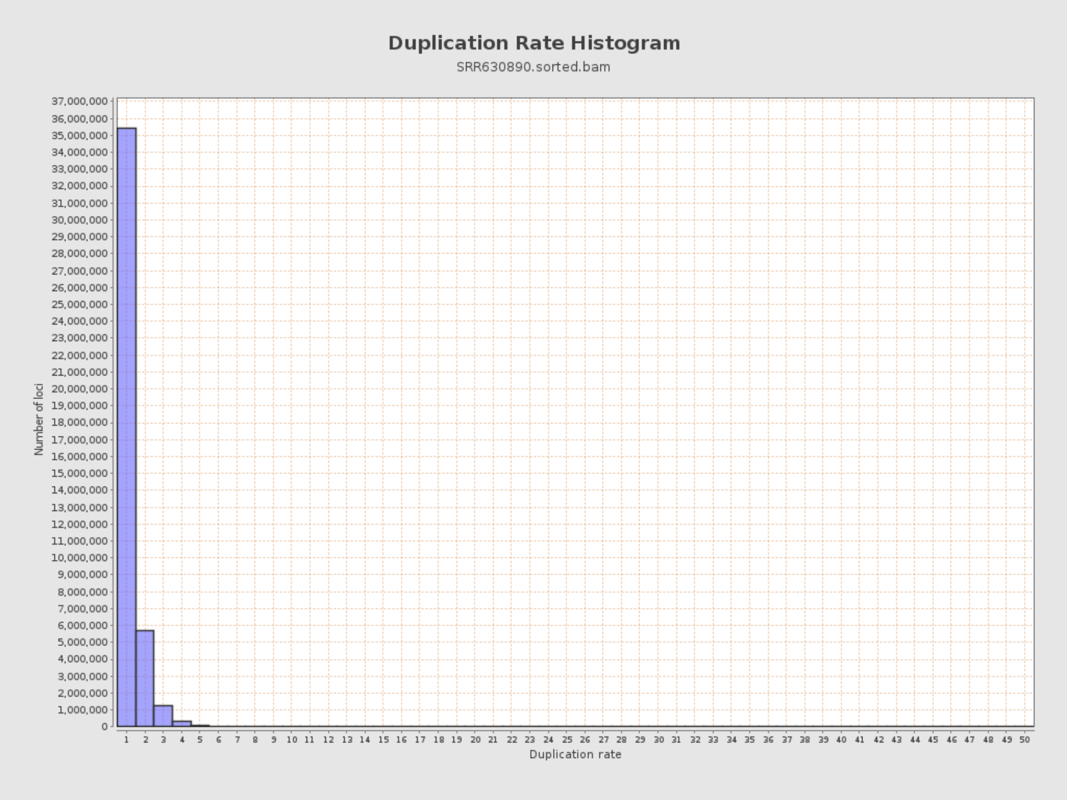
5. Results : Coverage Histogram (0-50X)



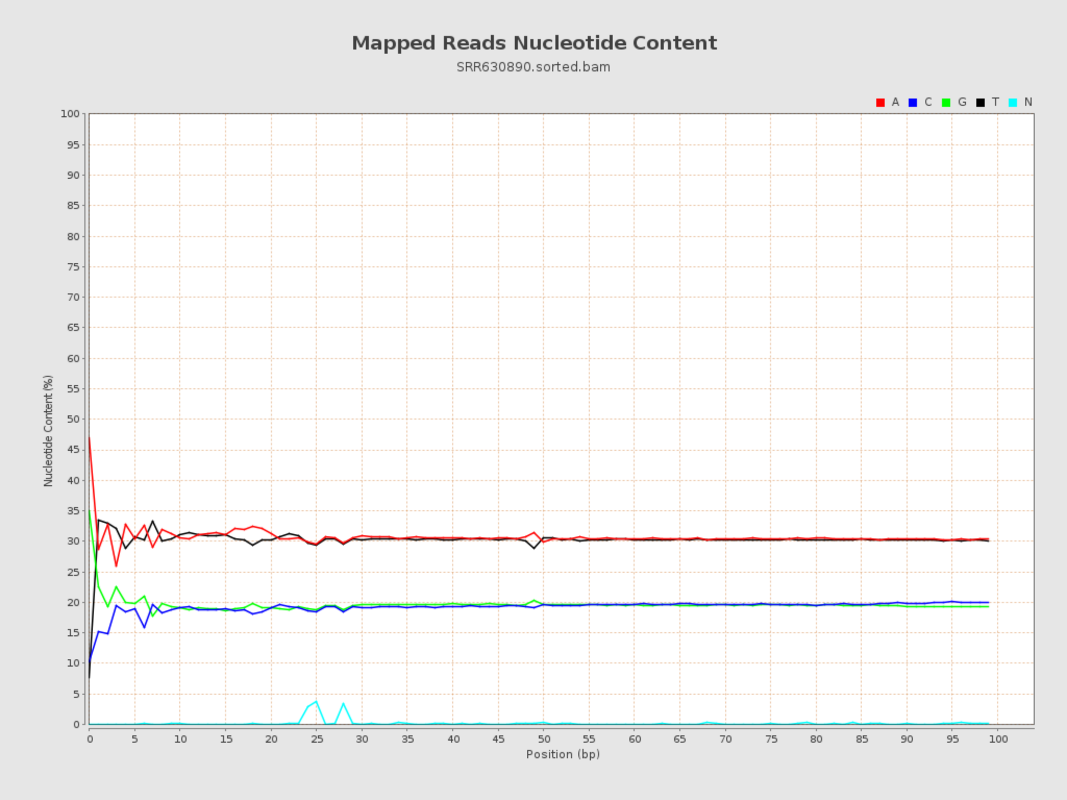
6. Results : Genome Fraction Coverage



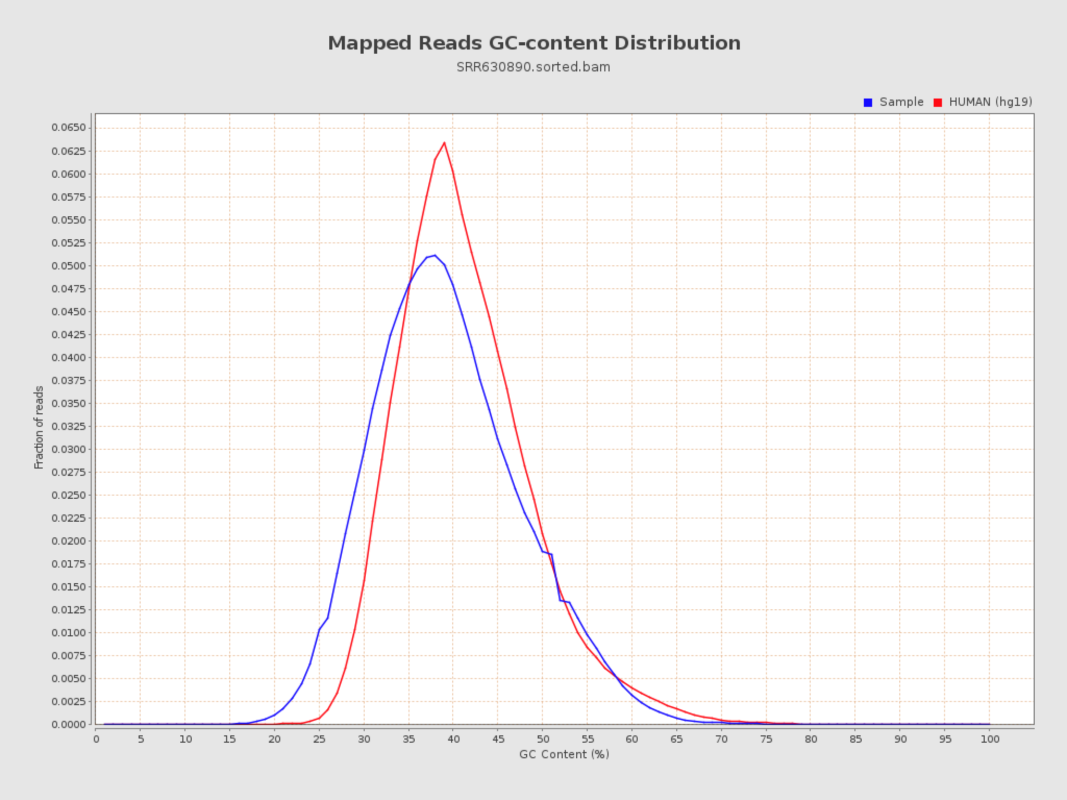
7. Results : Duplication Rate Histogram



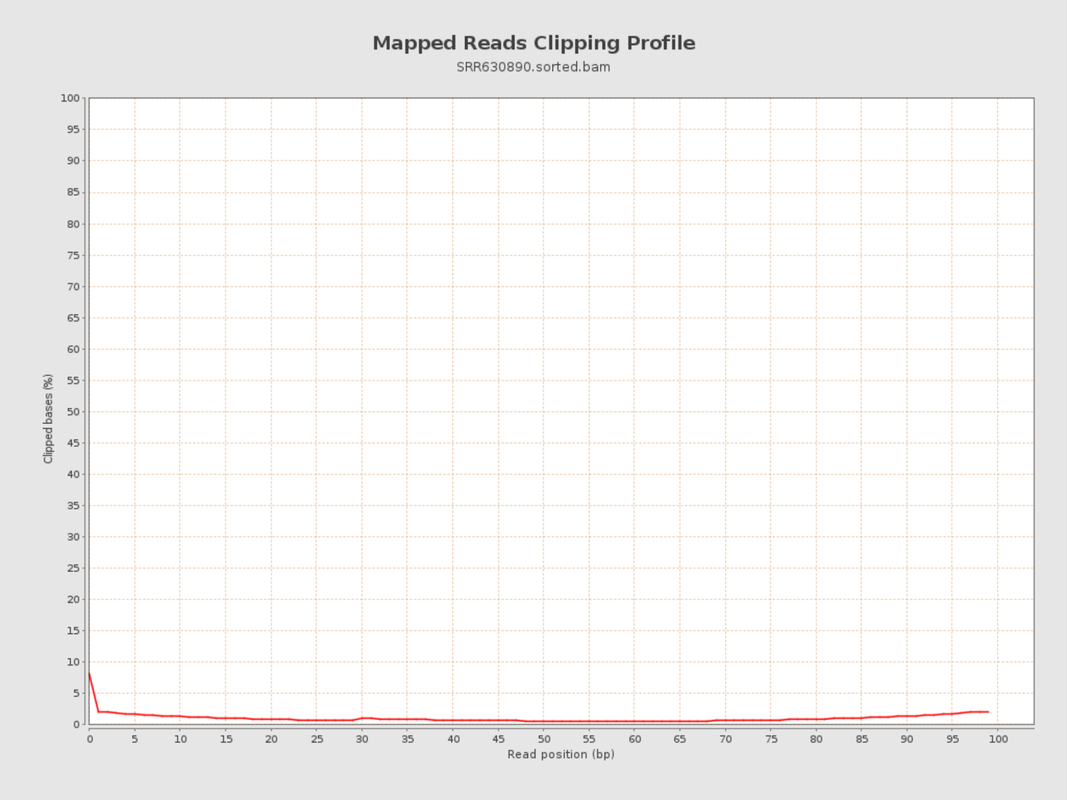
8. Results : Mapped Reads Nucleotide Content



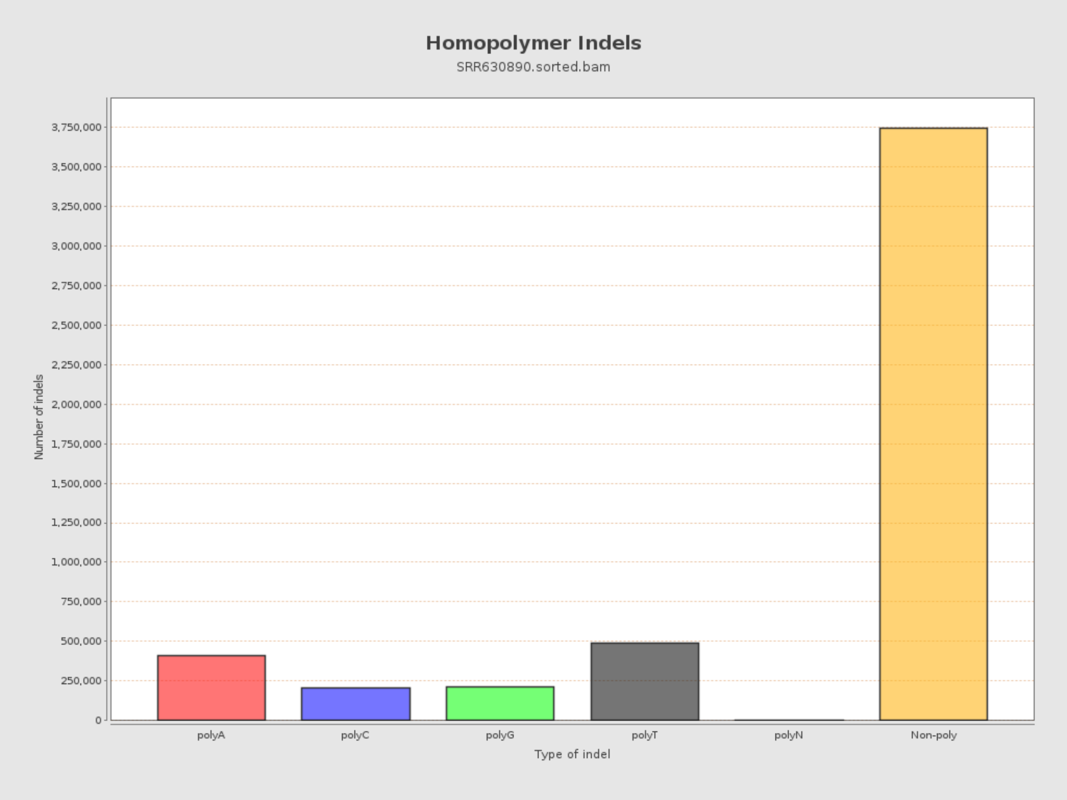
9. Results : Mapped Reads GC-content Distribution



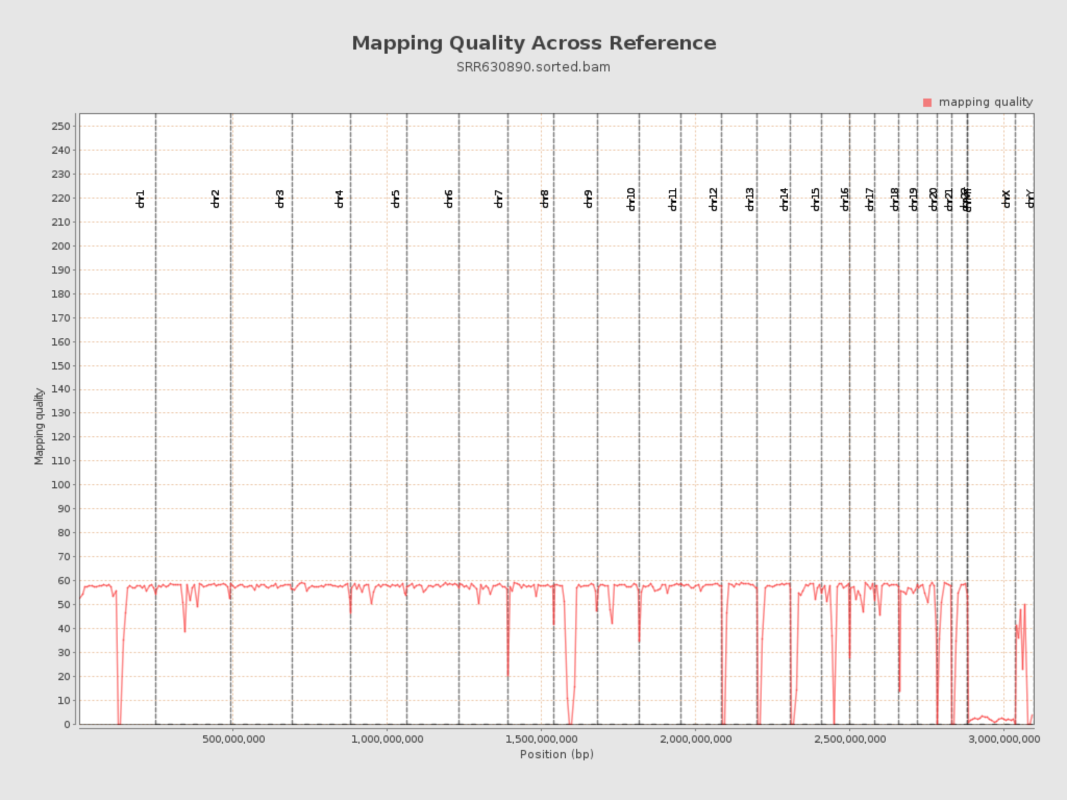
10. Results : Mapped Reads Clipping Profile



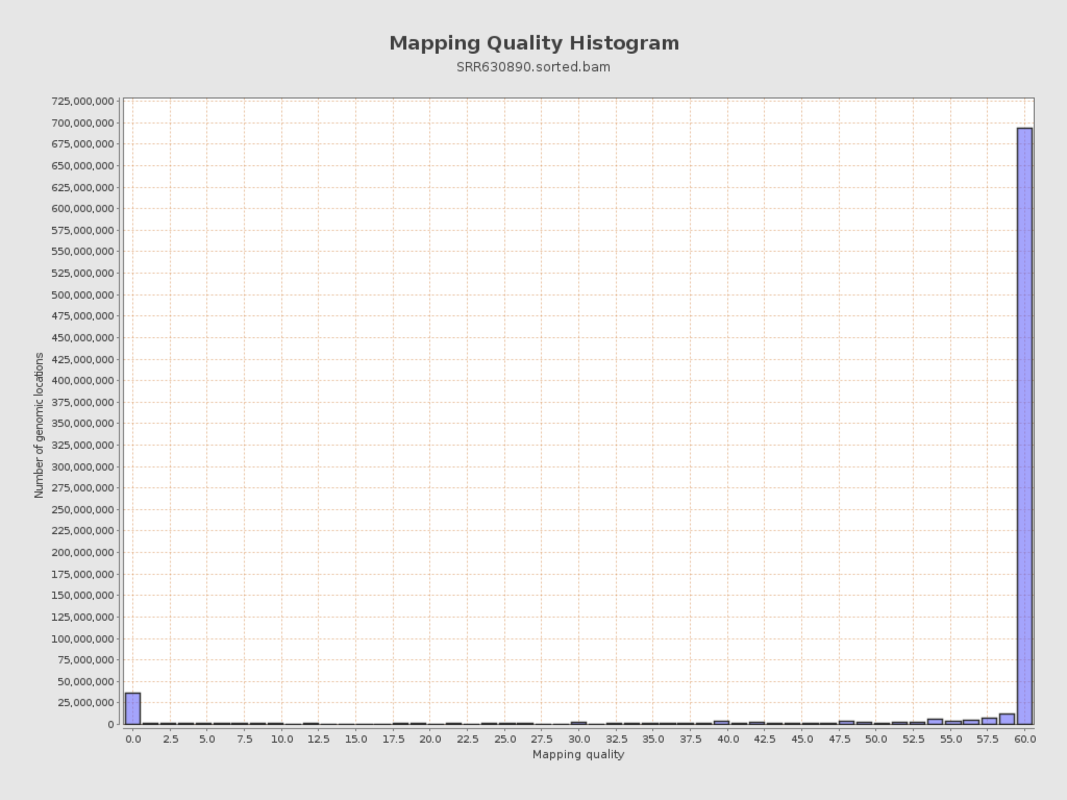
11. Results : Homopolymer Indels



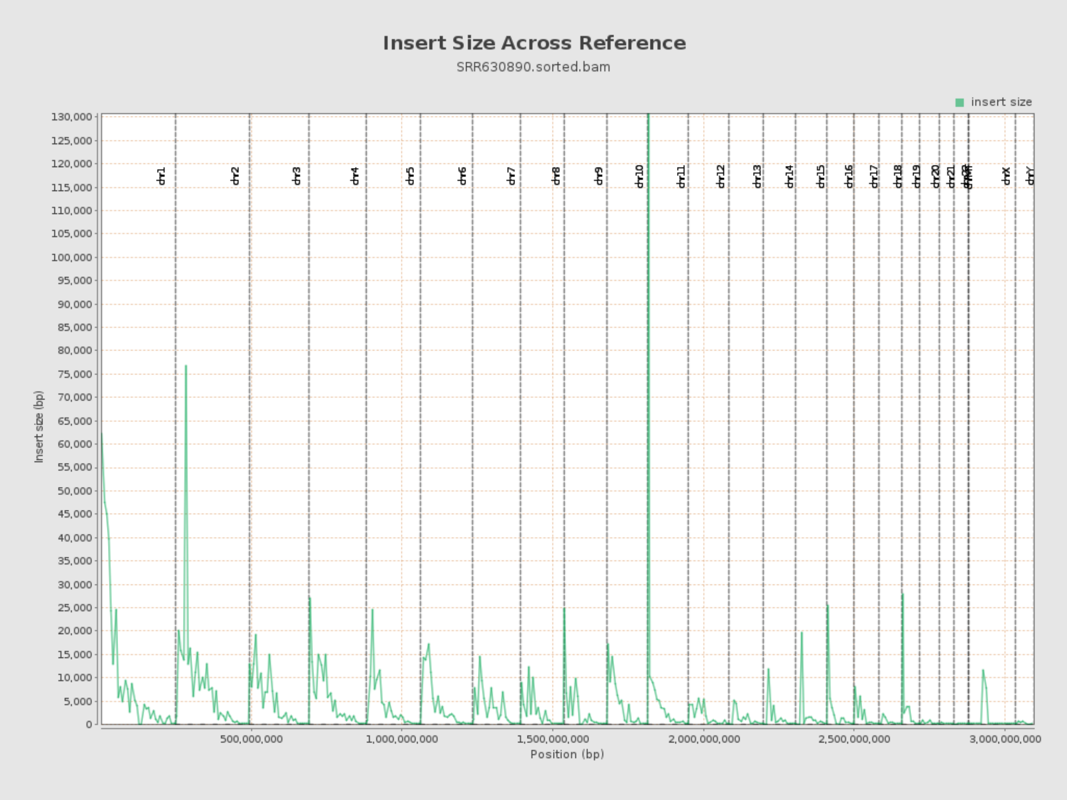
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram