Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/15 16:25:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630877.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 SRR630877_1.fastq.gz SRR630877_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 15 16:25:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,204,428
Mapped reads	53,943,794 / 99.52%
Unmapped reads	260,634 / 0.48%
Mapped paired reads	53,943,794 / 99.52%
Mapped reads, first in pair	27,026,962 / 49.86%
Mapped reads, second in pair	26,916,832 / 49.66%
Mapped reads, both in pair	53,818,358 / 99.29%
Mapped reads, singletons	125,436 / 0.23%
Secondary alignments	0
Supplementary alignments	311,660 / 0.57%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	11,021,934 / 20.33%
Duplication rate	18.9%
Clipped reads	5,534,357 / 10.21%

2.2. ACGT Content

Number/percentage of A's	1,632,364,648 / 31.03%
Number/percentage of C's	999,545,730 / 19%
Number/percentage of T's	1,600,091,500 / 30.42%
Number/percentage of G's	1,026,282,546 / 19.51%
Number/percentage of N's	2,234,518 / 0.04%

GC Percentage	38.51%

2.3. Coverage

Mean	1.6997
Standard Deviation	6.6149

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	173,023.54
Standard Deviation	3,869,795.46
P25/Median/P75	148 / 193 / 266

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	35,546,260
Insertions	12,232,921
Mapped reads with at least one insertion	22.5%
Deletions	747,408
Mapped reads with at least one deletion	1.36%
Homopolymer indels	23.39%

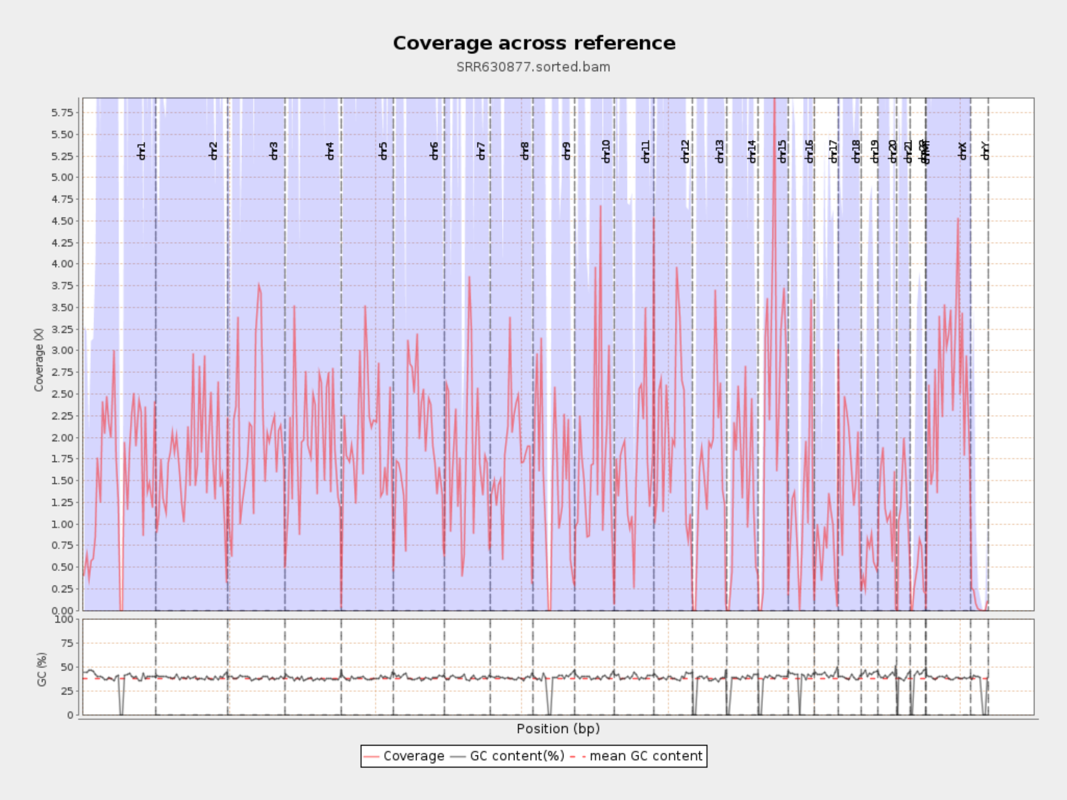
2.7. Chromosome stats

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

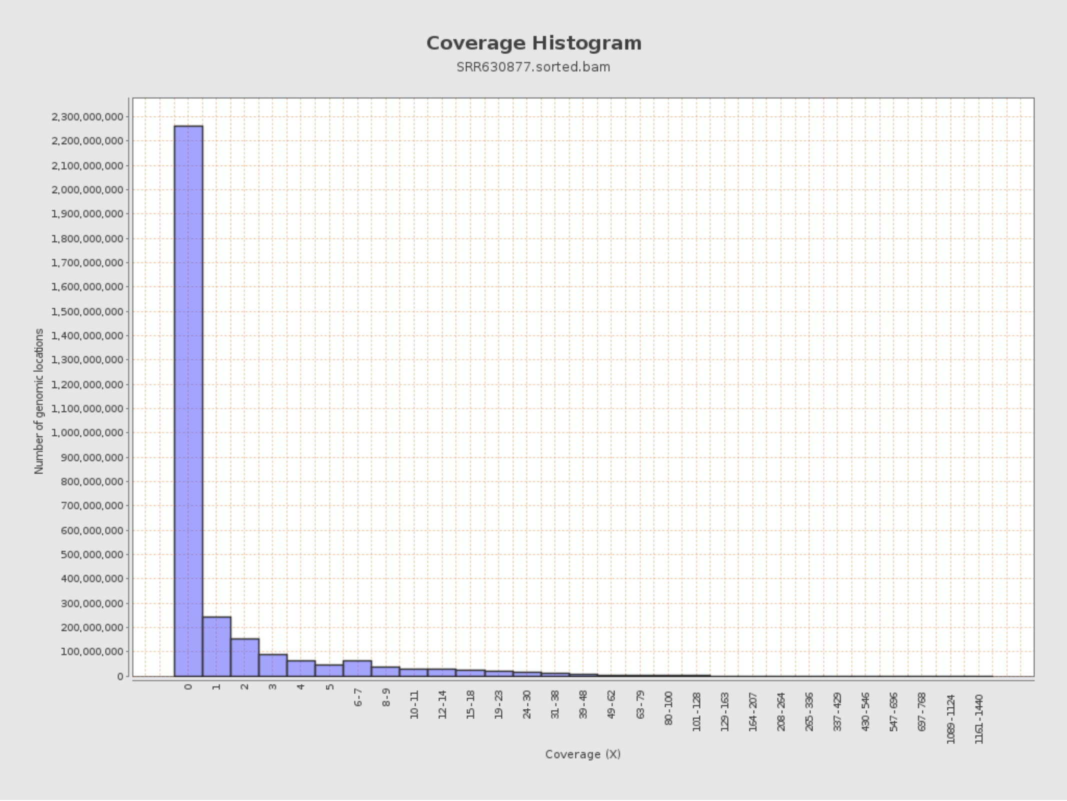
		bases	coverage	deviation
chr1	249250621	387094876	1.553	5.8949
chr2	243199373	416162644	1.7112	6.5787
chr3	198022430	399804130	2.019	7.1226
chr4	191154276	376198764	1.968	6.3217
chr5	180915260	354133245	1.9575	6.4452
chr6	171115067	339826535	1.986	6.649
chr7	159138663	278441128	1.7497	7.1468
chr8	146364022	258921165	1.769	5.9986
chr9	141213431	215593495	1.5267	6.3079
chr10	135534747	245817844	1.8137	8.9819
chr11	135006516	228963986	1.6959	6.6323
chr12	133851895	264133616	1.9733	6.8522
chr13	115169878	187159076	1.6251	6.4298
chr14	107349540	153861189	1.4333	6.2457
chr15	102531392	261475576	2.5502	9.2854
chr16	90354753	103822375	1.1491	5.1843
chr17	81195210	62720131	0.7725	2.9982
chr18	78077248	131507003	1.6843	5.7464
chr19	59128983	33703777	0.57	2.8779
chr20	63025520	77397750	1.228	5.234
chr21	48129895	54469518	1.1317	4.2177
chr22	51304566	20404213	0.3977	2.1199
chrMT	16571	260	0.0157	0.1648
chrX	155270560	405444506	2.6112	9.3741

chrY	59373566	4829782	0.0813	1.4312

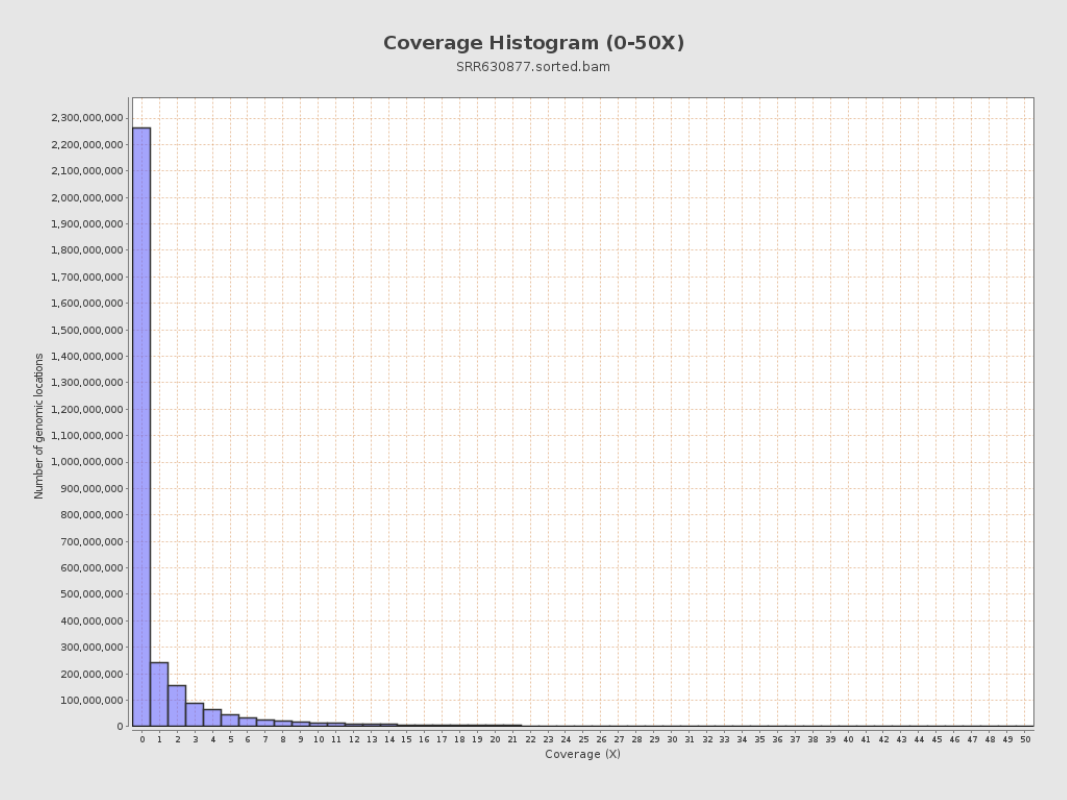
3. Results : Coverage across reference



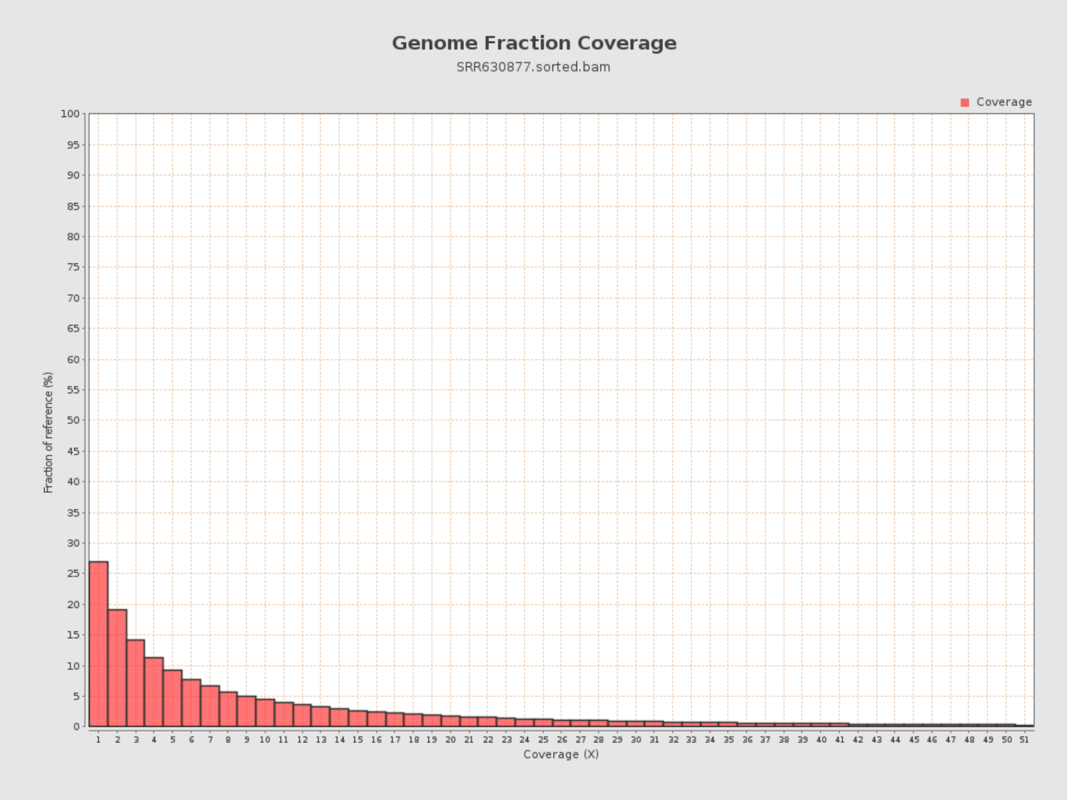
4. Results : Coverage Histogram



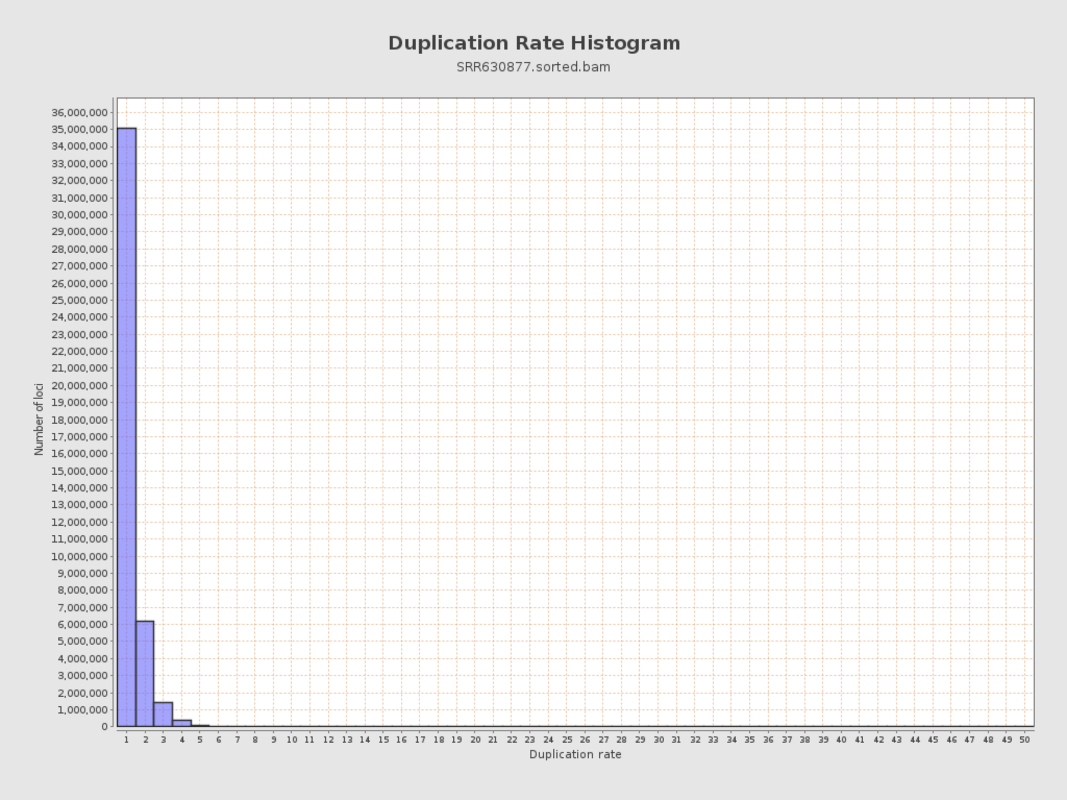
5. Results : Coverage Histogram (0-50X)



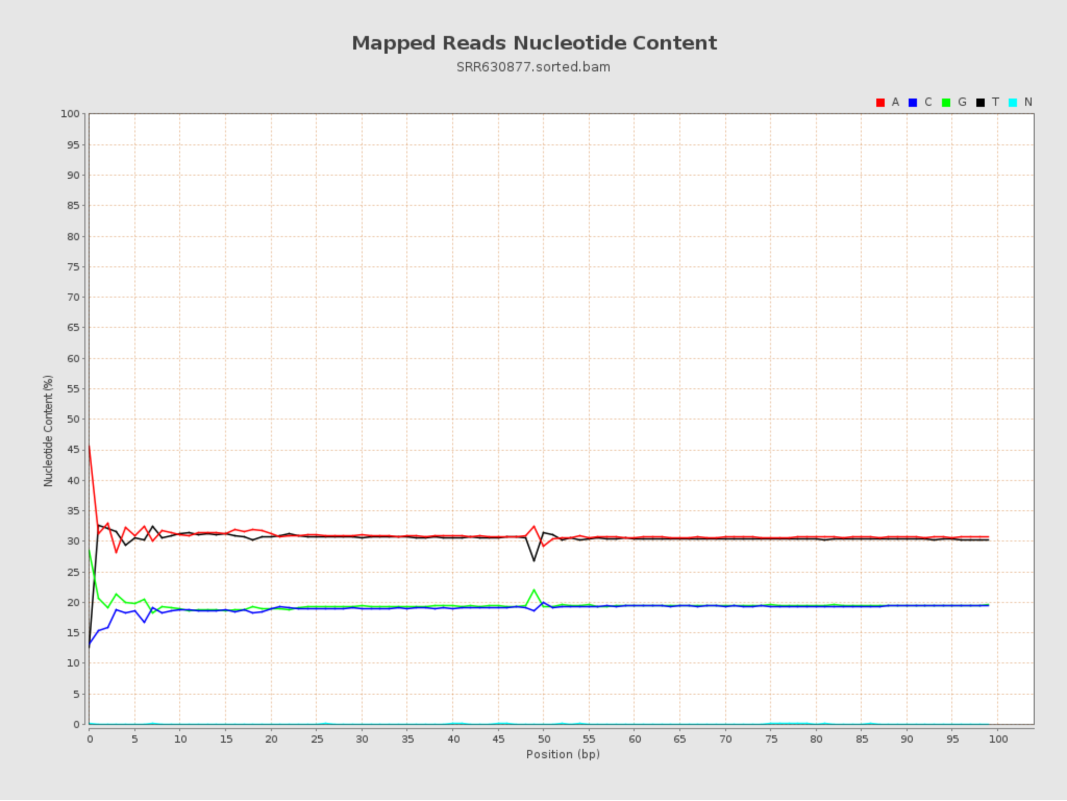
6. Results : Genome Fraction Coverage



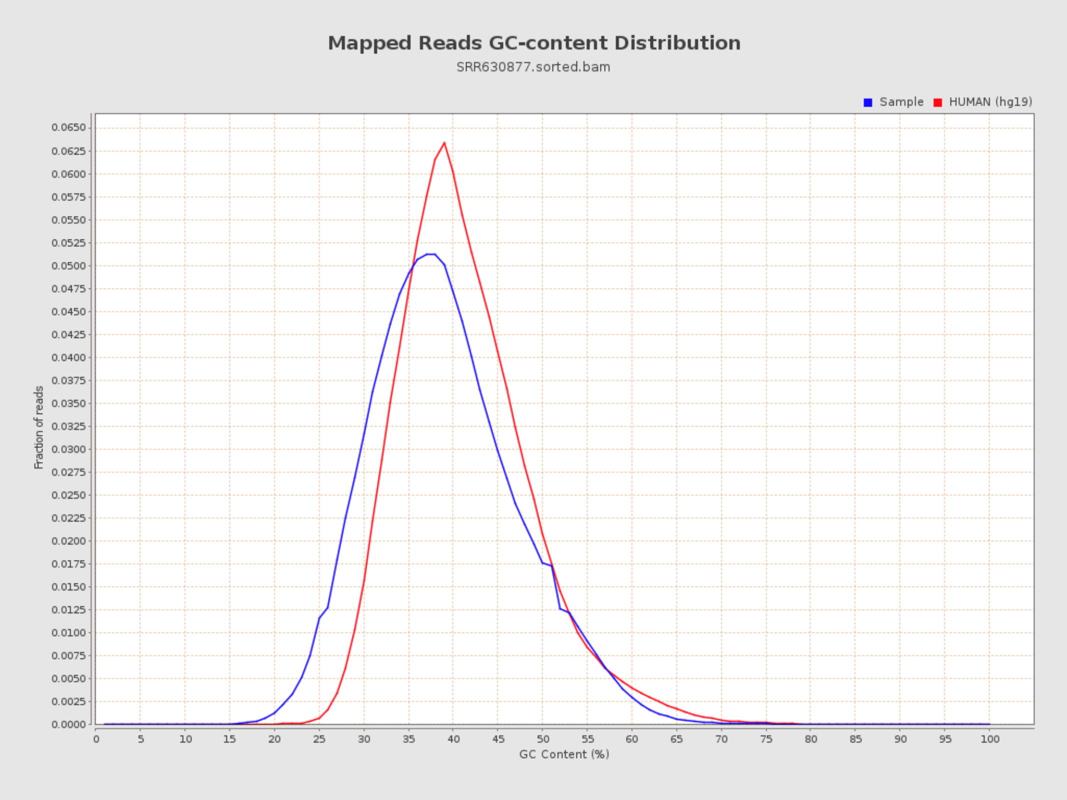
7. Results : Duplication Rate Histogram



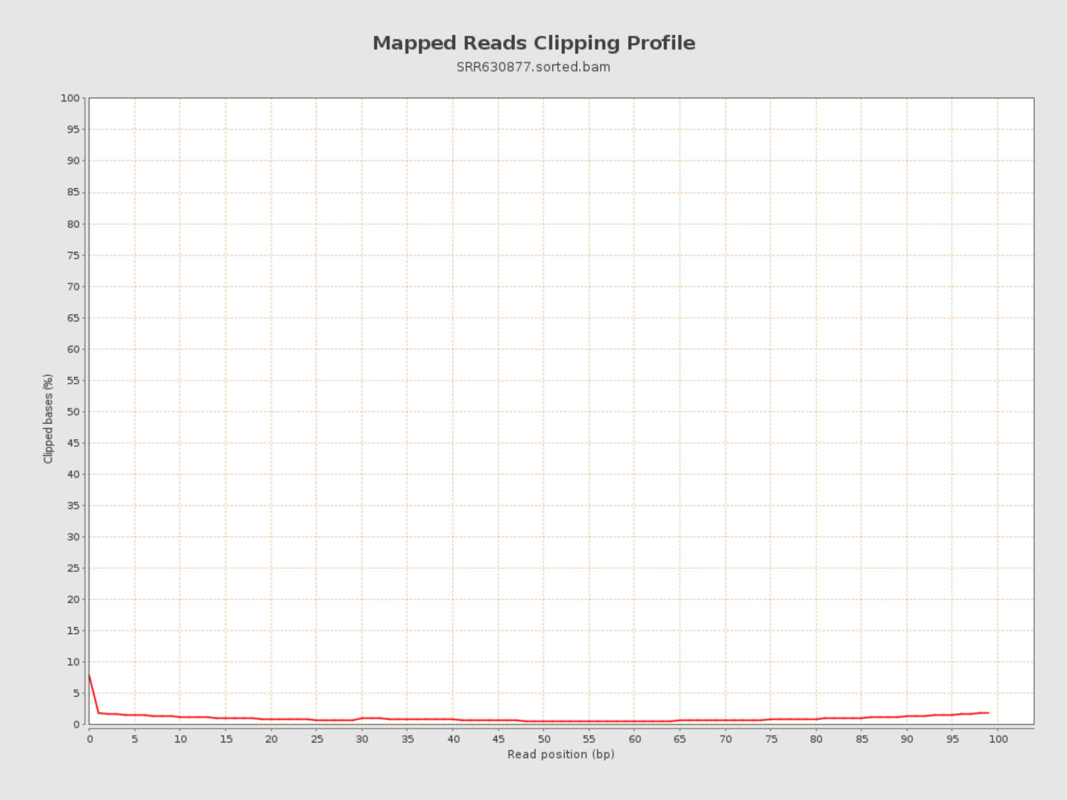
8. Results : Mapped Reads Nucleotide Content



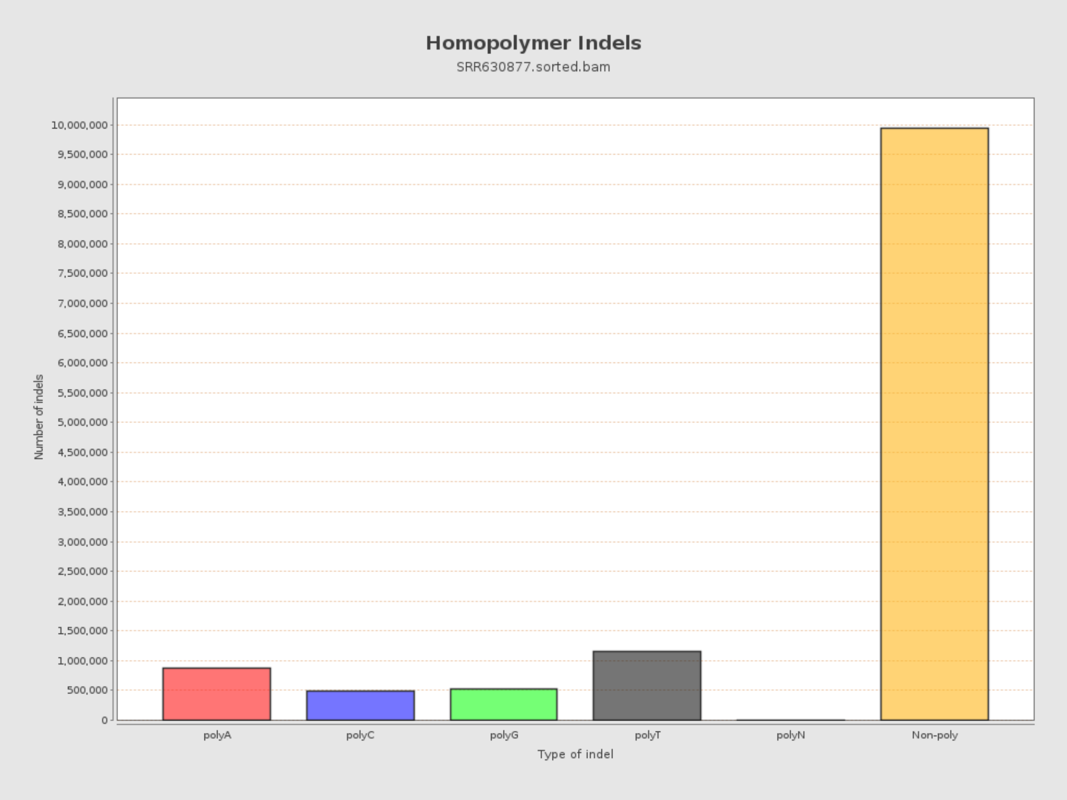
9. Results : Mapped Reads GC-content Distribution



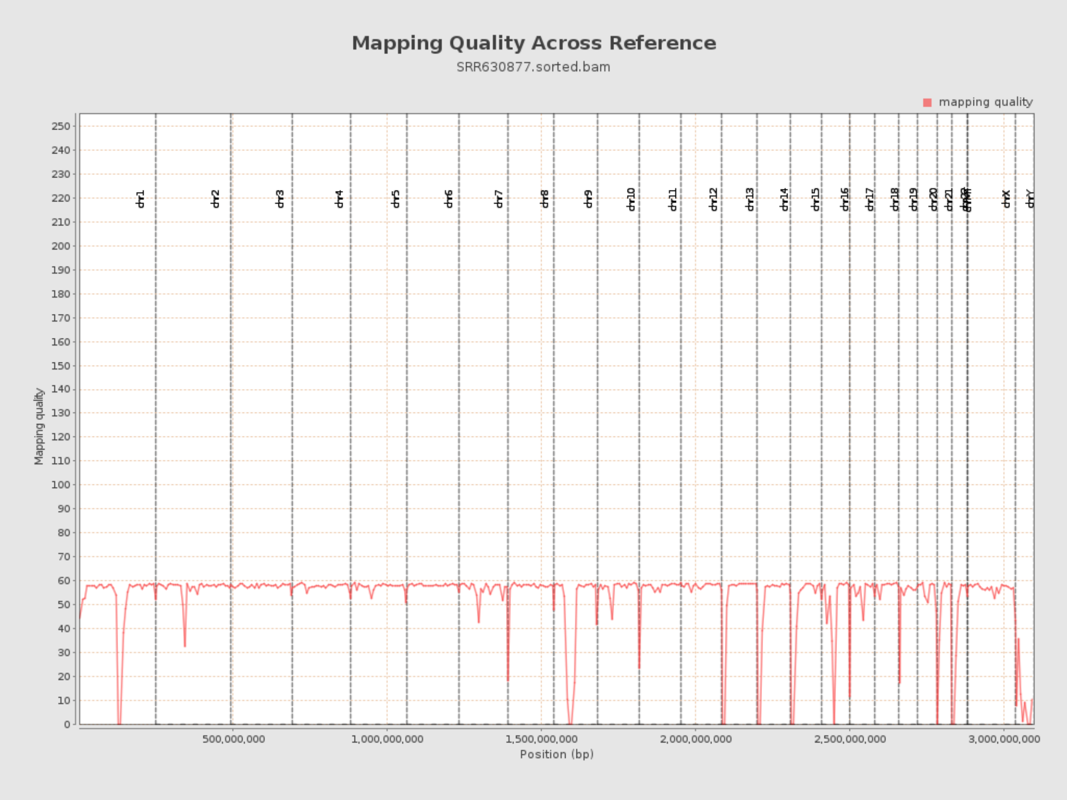
10. Results : Mapped Reads Clipping Profile



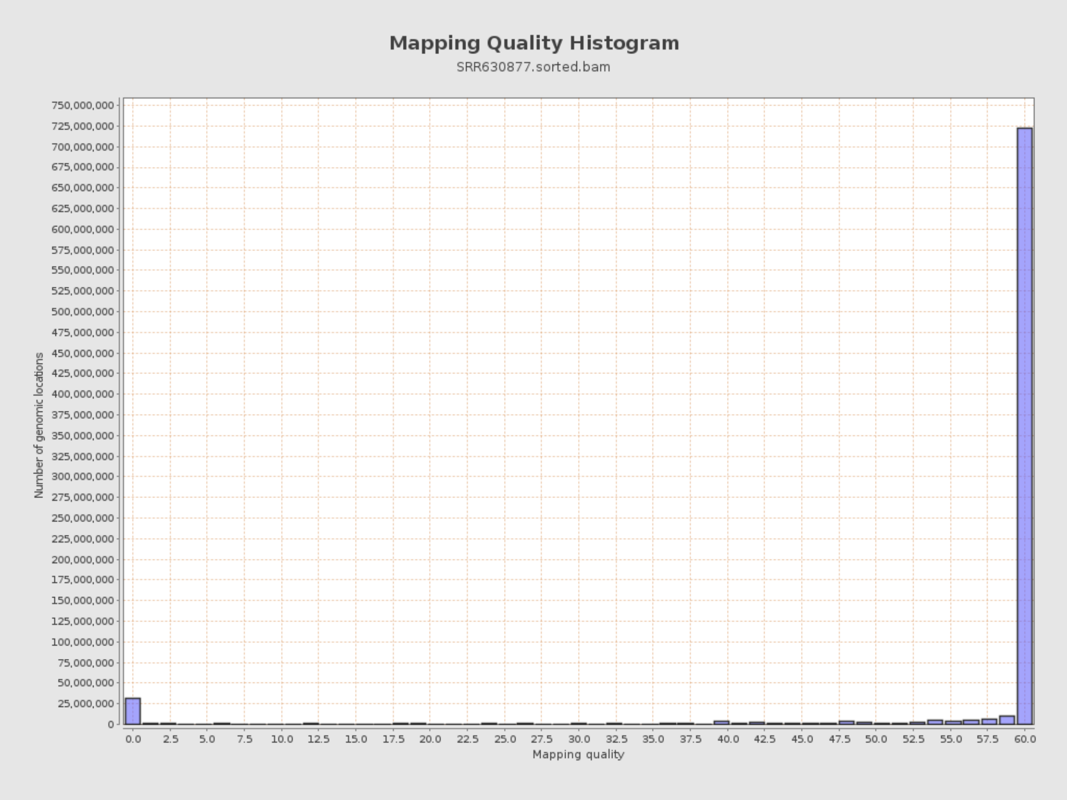
11. Results : Homopolymer Indels



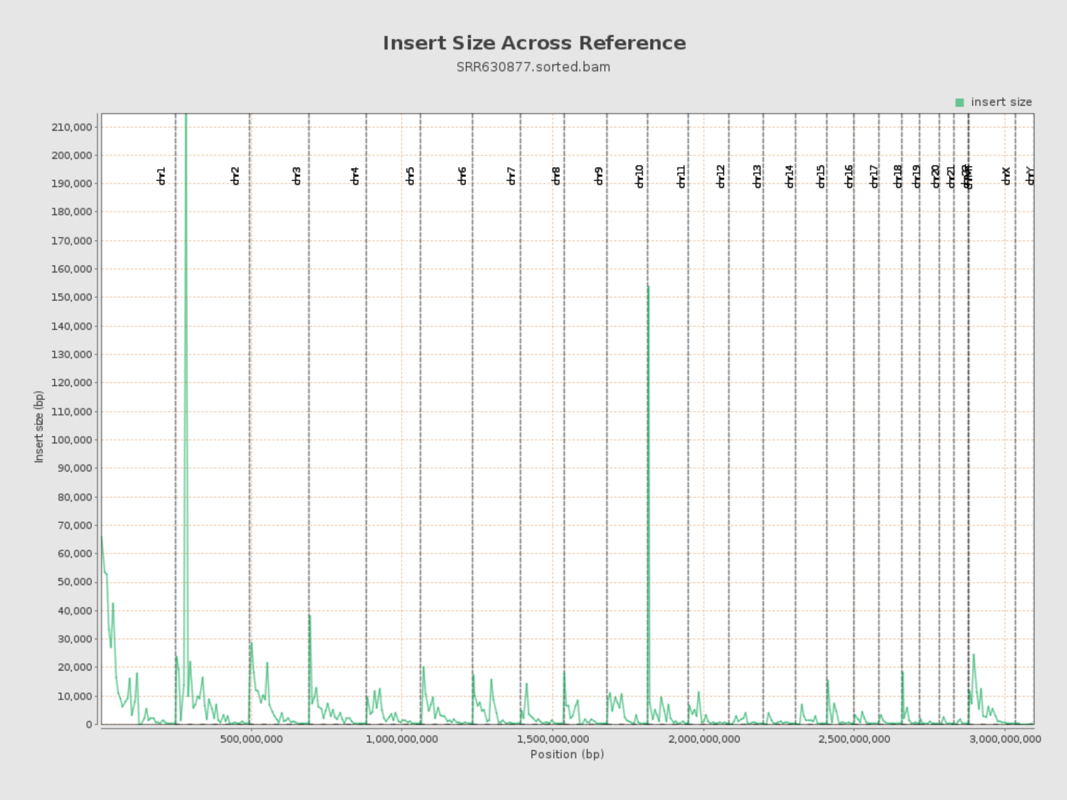
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram