Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 01:58:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617413.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_SRR617413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617413_1.fastq.gz SRR617413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 01:58:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	28,615,241 / 89.42%
Unmapped reads	3,384,759 / 10.58%
Mapped paired reads	28,615,241 / 89.42%
Mapped reads, first in pair	14,636,623 / 45.74%
Mapped reads, second in pair	13,978,618 / 43.68%
Mapped reads, both in pair	27,699,582 / 86.56%
Mapped reads, singletons	915,659 / 2.86%
Secondary alignments	0
Supplementary alignments	402,186 / 1.26%
Read min/max/mean length	30 / 100 / 100.52
Duplicated reads (estimated)	1,239,171 / 3.87%
Duplication rate	3.97%
Clipped reads	4,138,606 / 12.93%

2.2. ACGT Content

Number/percentage of A's	836,113,737 / 29.88%
Number/percentage of C's	561,208,393 / 20.06%
Number/percentage of T's	826,619,035 / 29.54%
Number/percentage of G's	572,790,695 / 20.47%
Number/percentage of N's	1,138,746 / 0.04%

GC Percentage	40.53%

2.3. Coverage

Mean	0.904
Standard Deviation	2.7624

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	47,530.47
Standard Deviation	2,071,440.58
P25/Median/P75	169 / 208 / 269

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	42,419,853
Insertions	231,013
Mapped reads with at least one insertion	0.79%
Deletions	270,930
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.95%

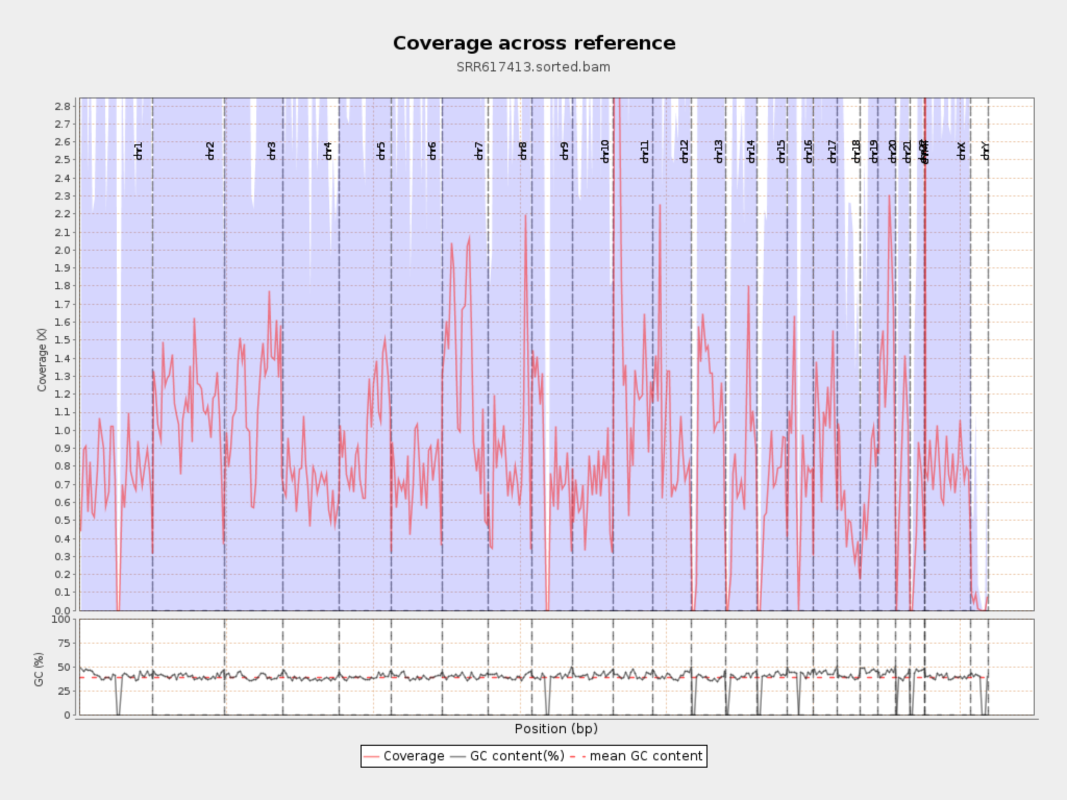
2.7. Chromosome stats

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

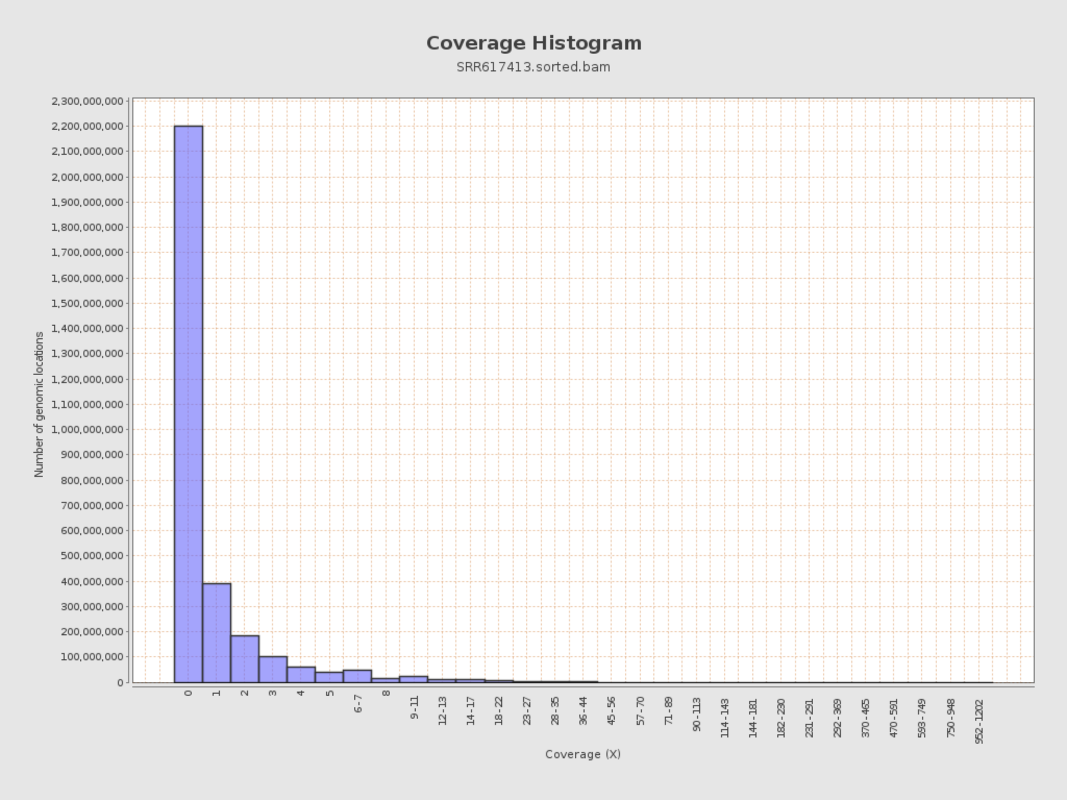
		bases	coverage	deviation
chr1	249250621	180079149	0.7225	2.586
chr2	243199373	279608515	1.1497	2.9108
chr3	198022430	236701457	1.1953	3.2312
chr4	191154276	135263093	0.7076	2.1721
chr5	180915260	179442525	0.9919	2.7244
chr6	171115067	128566955	0.7513	2.4699
chr7	159138663	209339498	1.3155	3.0667
chr8	146364022	123806830	0.8459	3.0613
chr9	141213431	112096307	0.7938	2.4625
chr10	135534747	89647671	0.6614	2.2845
chr11	135006516	207637112	1.538	3.6258
chr12	133851895	133399371	0.9966	2.6299
chr13	115169878	122061654	1.0598	2.6418
chr14	107349540	80896284	0.7536	2.7284
chr15	102531392	63906040	0.6233	2.2109
chr16	90354753	69982393	0.7745	3.1169
chr17	81195210	85348783	1.0512	3.4415
chr18	78077248	40241539	0.5154	1.8823
chr19	59128983	39474903	0.6676	2.1862
chr20	63025520	94722640	1.5029	4.4451
chr21	48129895	38241878	0.7946	2.3832
chr22	51304566	22392793	0.4365	1.9505
chrMT	16571	171897	10.3734	5.6121
chrX	155270560	123240232	0.7937	2.4282

chrY	59373566	2203248	0.0371	0.5133

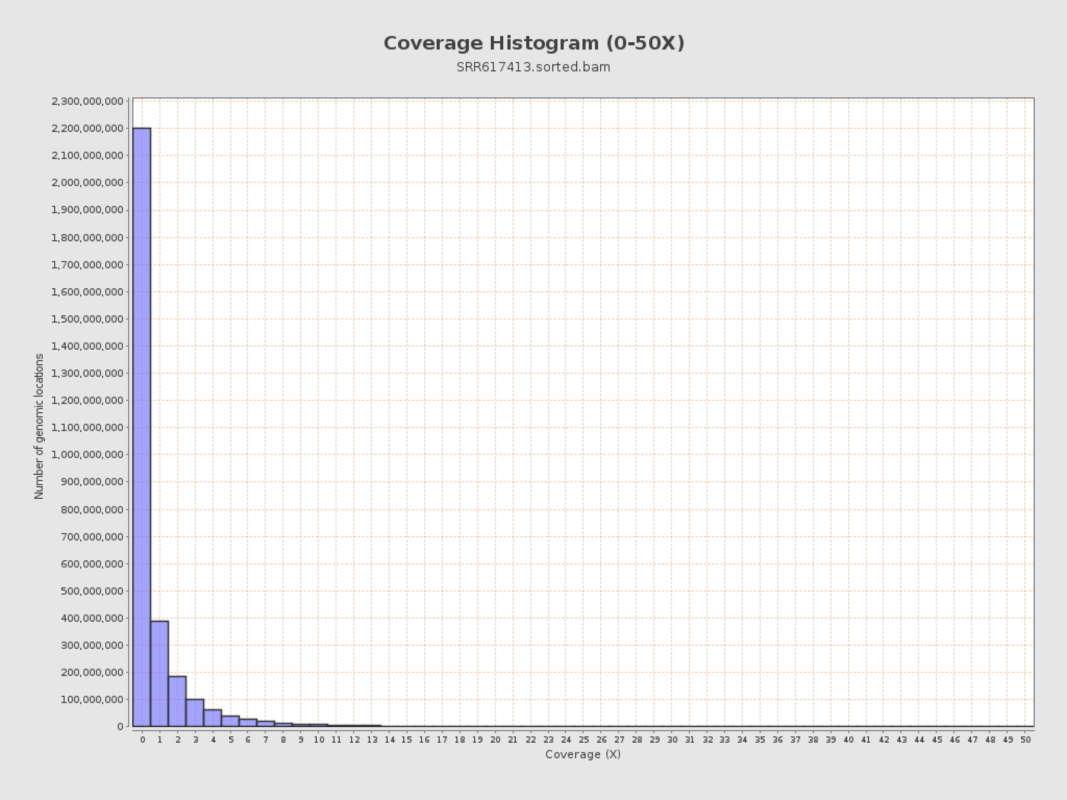
3. Results : Coverage across reference



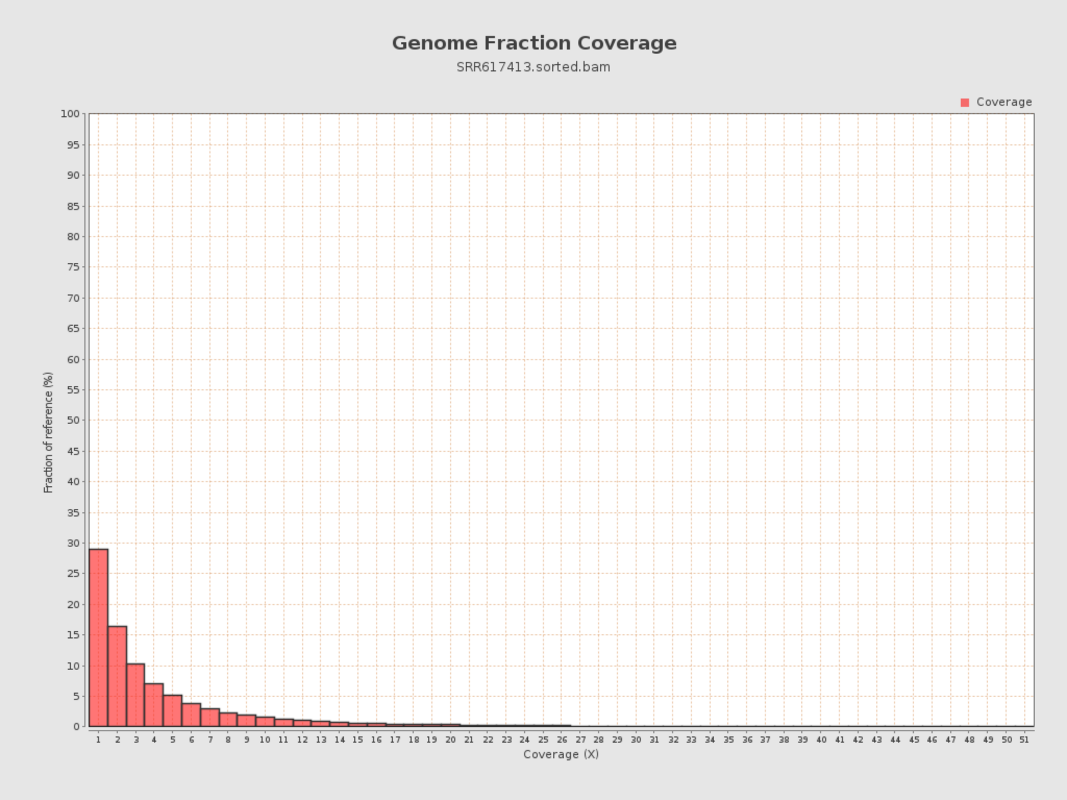
4. Results : Coverage Histogram



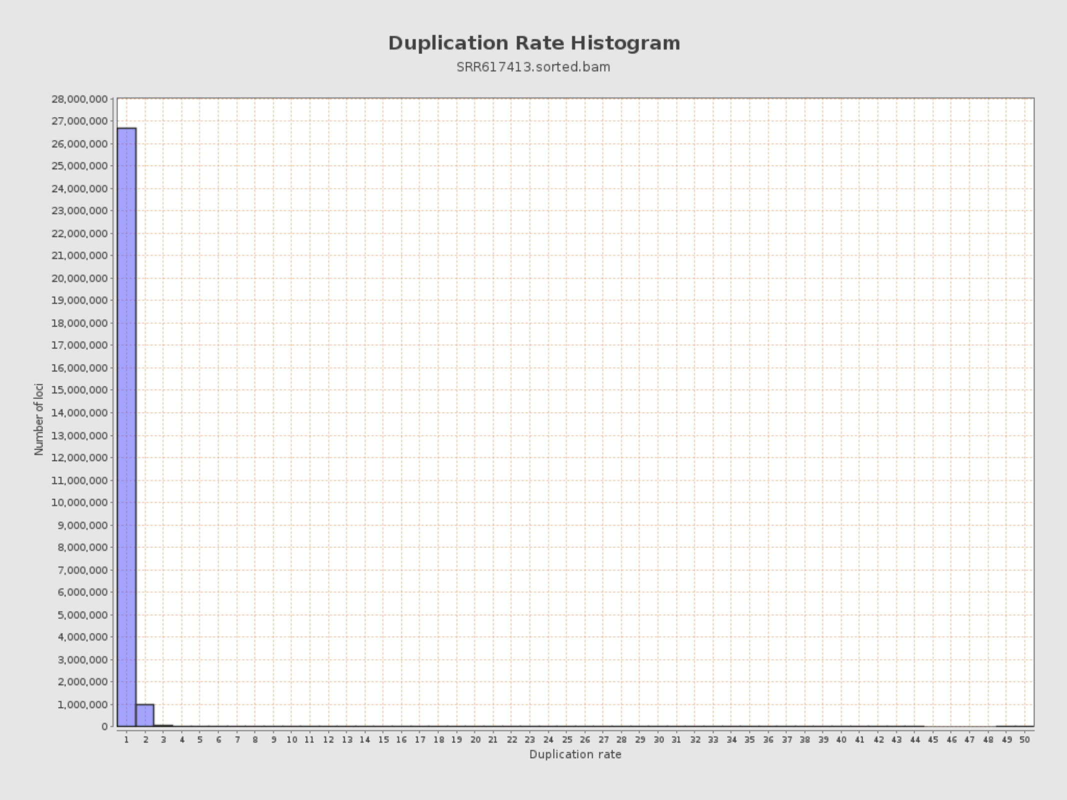
5. Results : Coverage Histogram (0-50X)



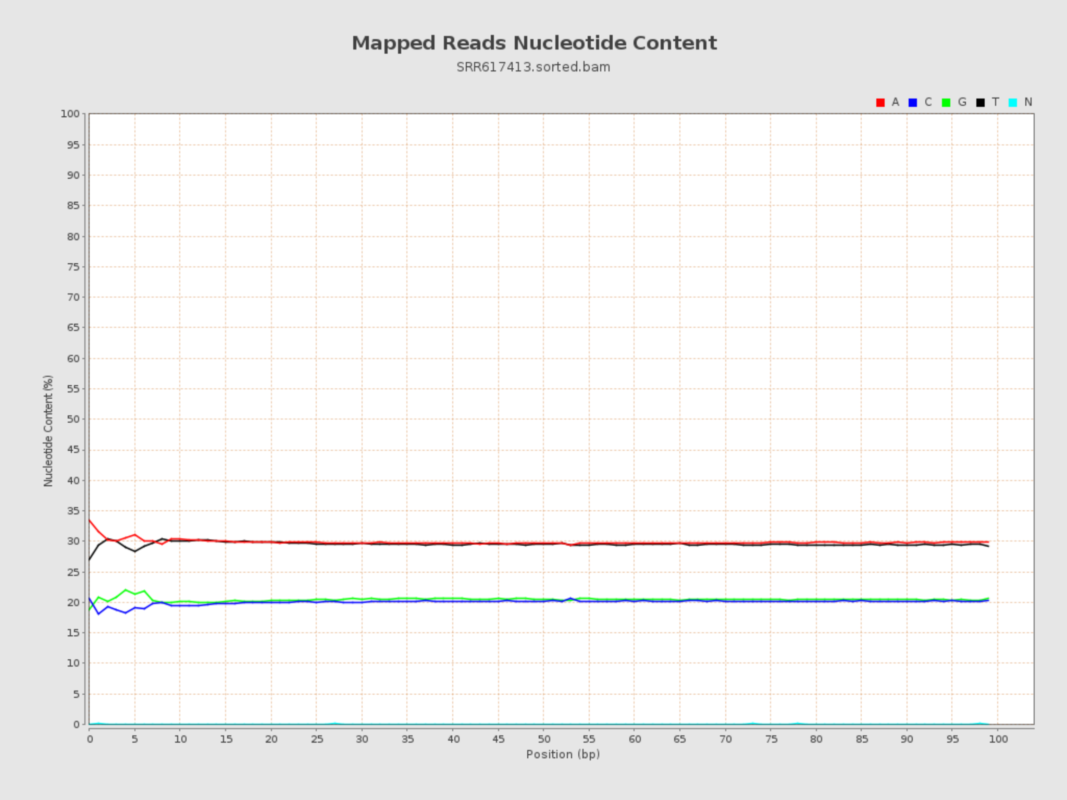
6. Results : Genome Fraction Coverage



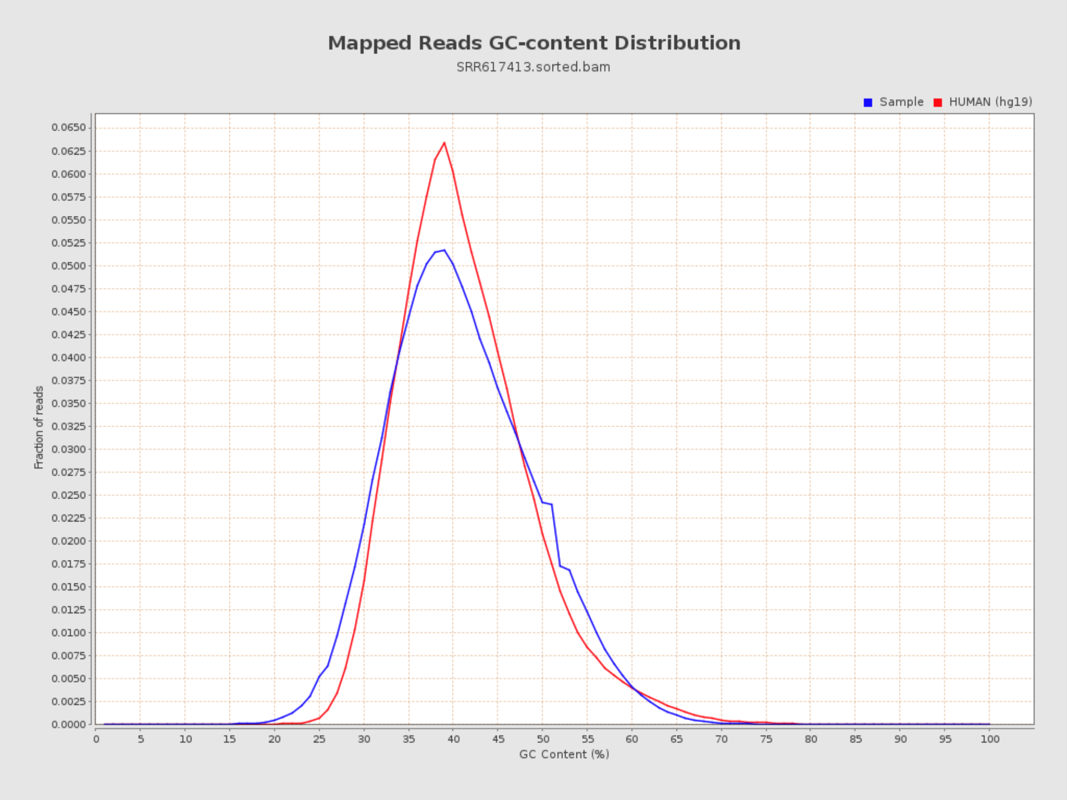
7. Results : Duplication Rate Histogram



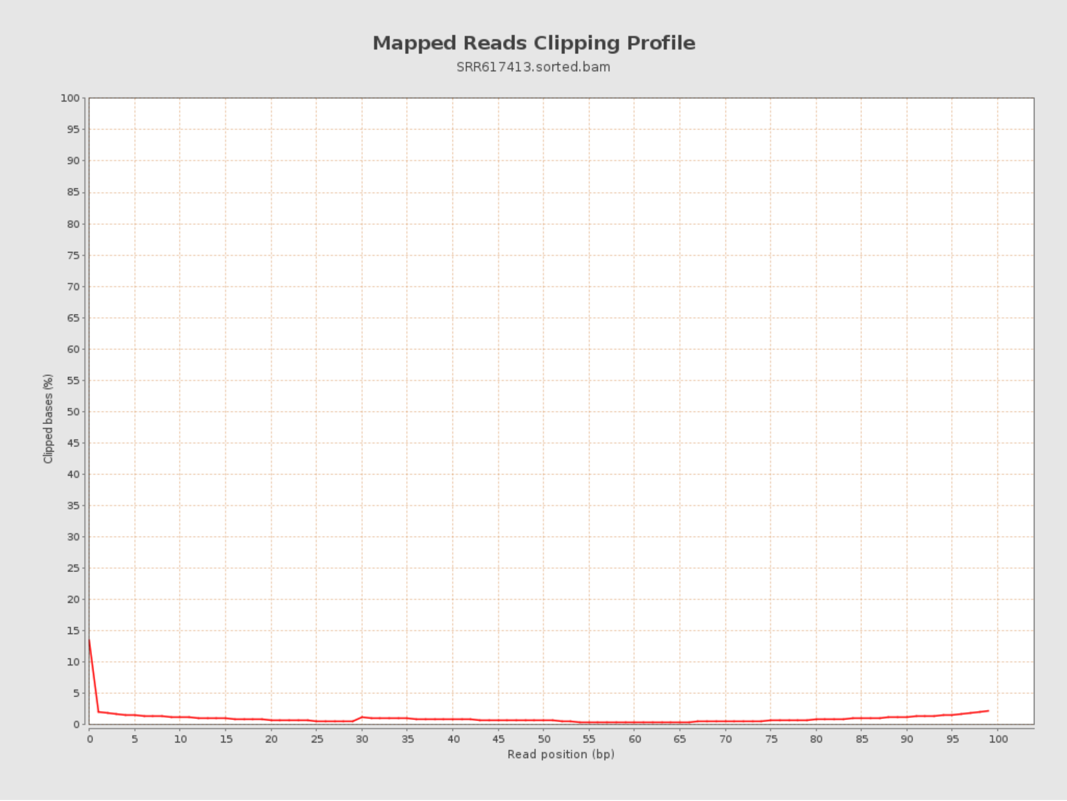
8. Results : Mapped Reads Nucleotide Content



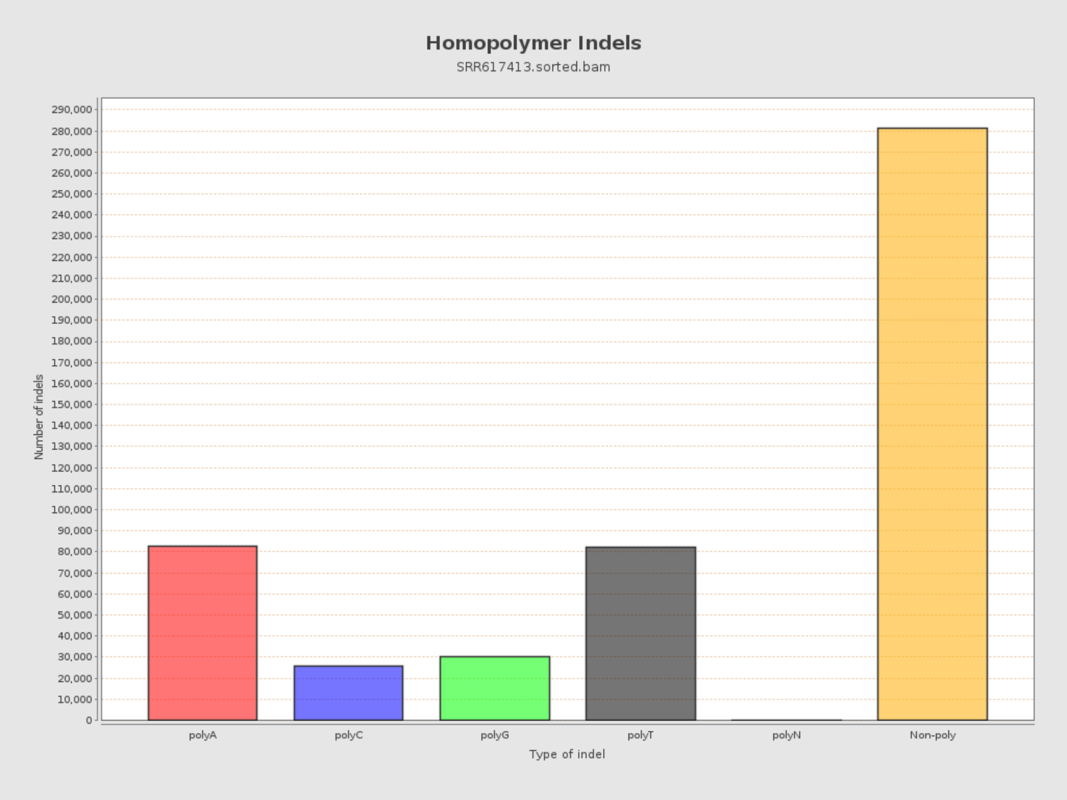
9. Results : Mapped Reads GC-content Distribution



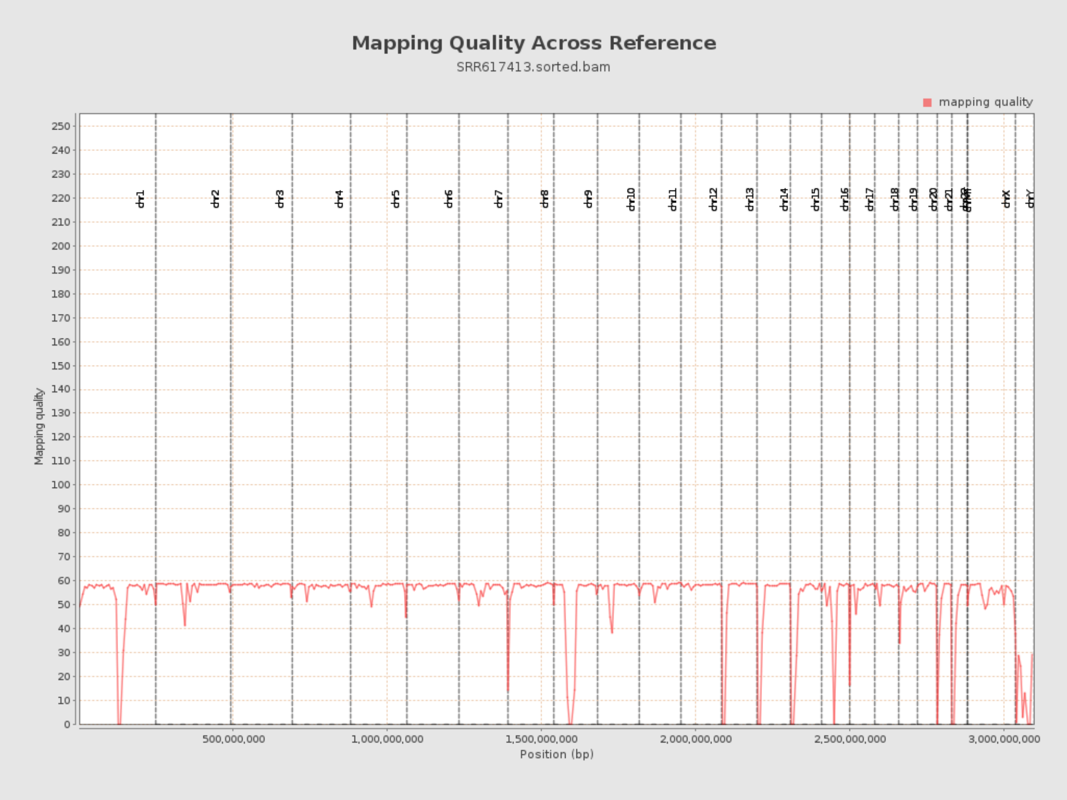
10. Results : Mapped Reads Clipping Profile



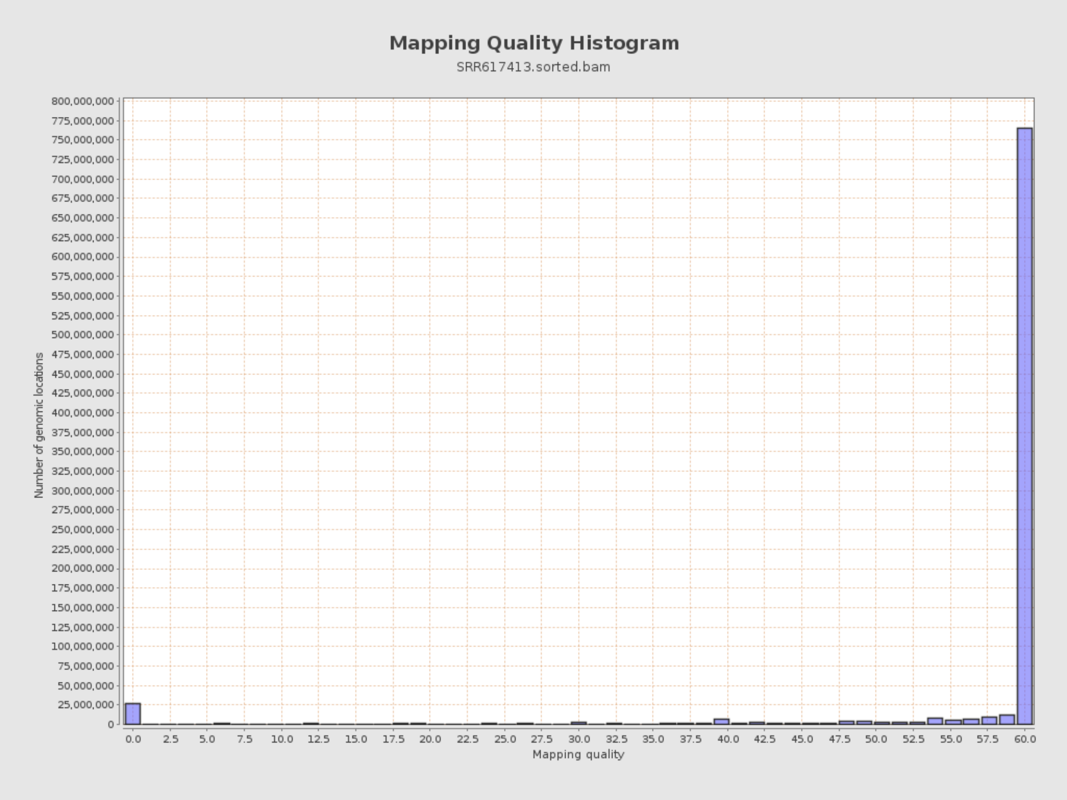
11. Results : Homopolymer Indels



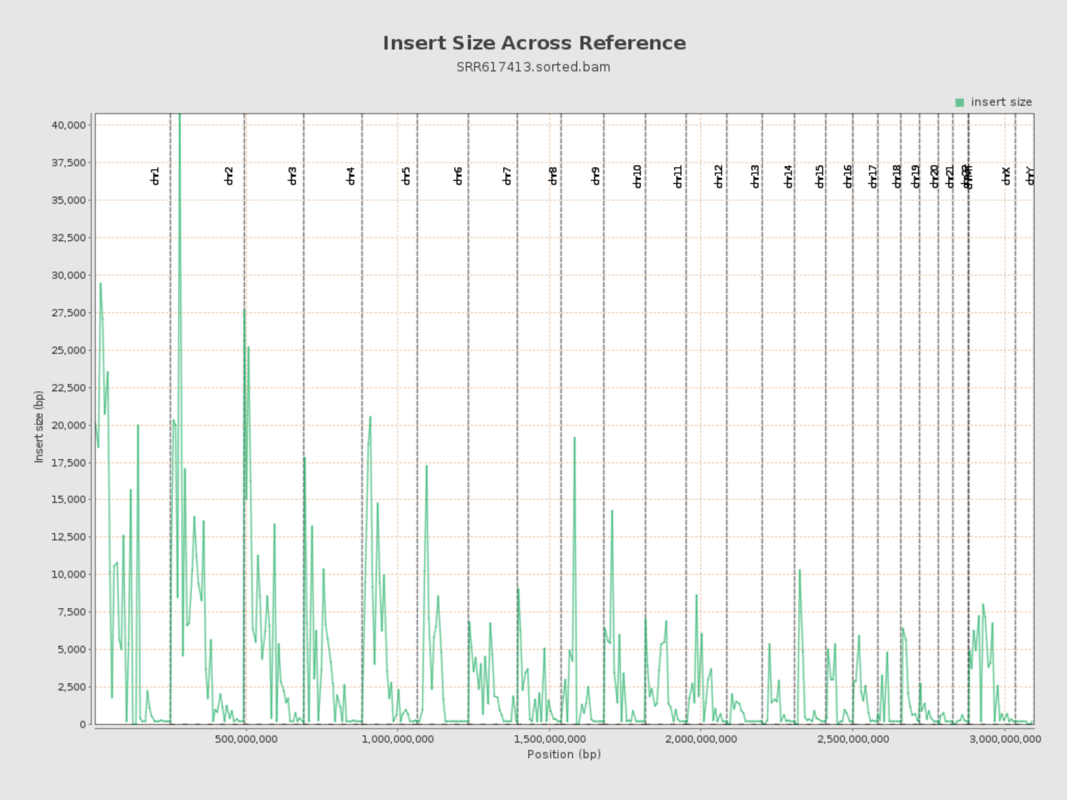
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram