Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 19:15:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617403.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_SRR617403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617403_1.fastq.gz SRR617403_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 19:15:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,271,929 / 94.6%
Unmapped reads	1,728,071 / 5.4%
Mapped paired reads	30,271,929 / 94.6%
Mapped reads, first in pair	15,251,542 / 47.66%
Mapped reads, second in pair	15,020,387 / 46.94%
Mapped reads, both in pair	29,752,770 / 92.98%
Mapped reads, singletons	519,159 / 1.62%
Secondary alignments	0
Supplementary alignments	494,936 / 1.55%
Read min/max/mean length	30 / 100 / 100.64
Duplicated reads (estimated)	1,430,179 / 4.47%
Duplication rate	4.25%
Clipped reads	3,173,981 / 9.92%

2.2. ACGT Content

Number/percentage of A's	889,403,570 / 29.83%
Number/percentage of C's	599,664,474 / 20.12%
Number/percentage of T's	881,287,355 / 29.56%
Number/percentage of G's	609,995,610 / 20.46%
Number/percentage of N's	741,318 / 0.02%

GC Percentage	40.58%

2.3. Coverage

Mean	0.9632
Standard Deviation	2.9583

2.4. Mapping Quality

Mean Mapping Quality	53.92

2.5. Insert size

Mean	55,819.57
Standard Deviation	2,259,558.1
P25/Median/P75	171 / 209 / 271

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	25,422,073
Insertions	244,705
Mapped reads with at least one insertion	0.8%
Deletions	292,508
Mapped reads with at least one deletion	0.95%
Homopolymer indels	45.07%

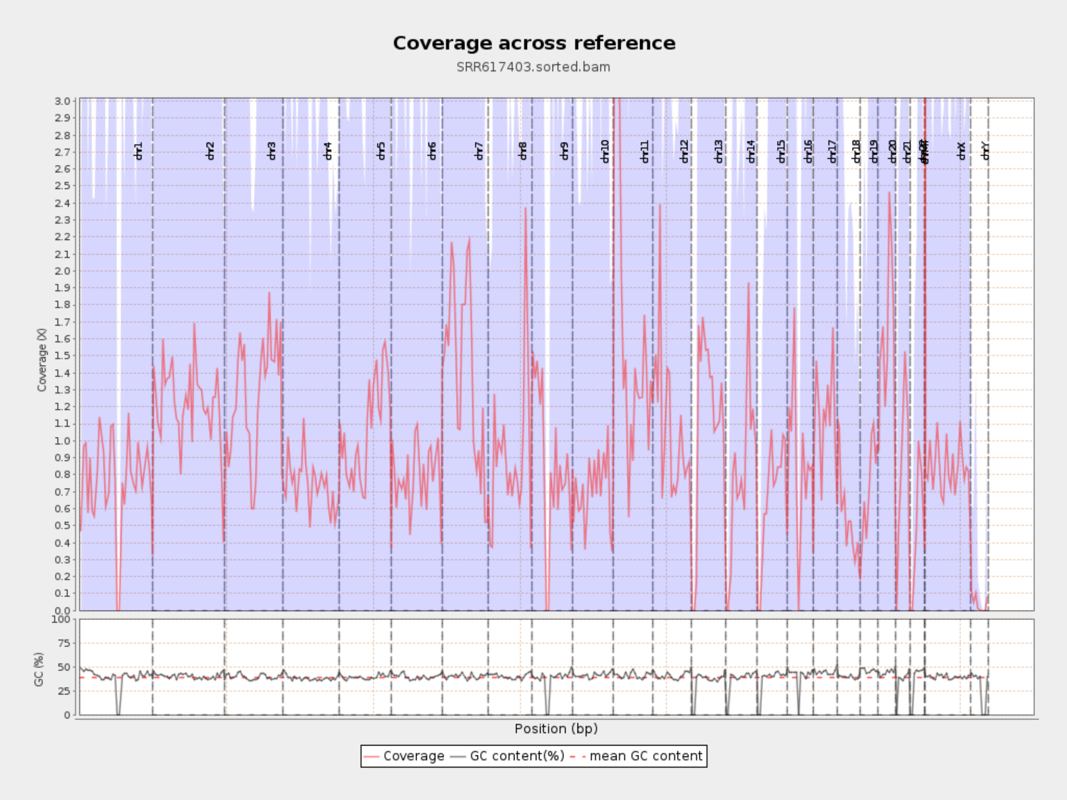
2.7. Chromosome stats

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

		bases	coverage	deviation
chr1	249250621	191948012	0.7701	2.7657
chr2	243199373	297433739	1.223	3.122
chr3	198022430	251807947	1.2716	3.4599
chr4	191154276	142759723	0.7468	2.2932
chr5	180915260	190880606	1.0551	2.8941
chr6	171115067	136308190	0.7966	2.6165
chr7	159138663	222811450	1.4001	3.2624
chr8	146364022	131874194	0.901	3.2944
chr9	141213431	119125215	0.8436	2.6436
chr10	135534747	95779850	0.7067	2.4339
chr11	135006516	221356584	1.6396	3.8732
chr12	133851895	142058960	1.0613	2.8138
chr13	115169878	128831329	1.1186	2.7849
chr14	107349540	86664520	0.8073	2.9281
chr15	102531392	68353105	0.6667	2.3911
chr16	90354753	75512433	0.8357	3.365
chr17	81195210	92146992	1.1349	3.7841
chr18	78077248	42704770	0.547	2.0258
chr19	59128983	42920986	0.7259	2.3817
chr20	63025520	102044890	1.6191	4.8004
chr21	48129895	40900359	0.8498	2.5774
chr22	51304566	24203666	0.4718	2.1098
chrMT	16571	181808	10.9715	5.026
chrX	155270560	130719471	0.8419	2.5832

chrY	59373566	2422034	0.0408	0.6153

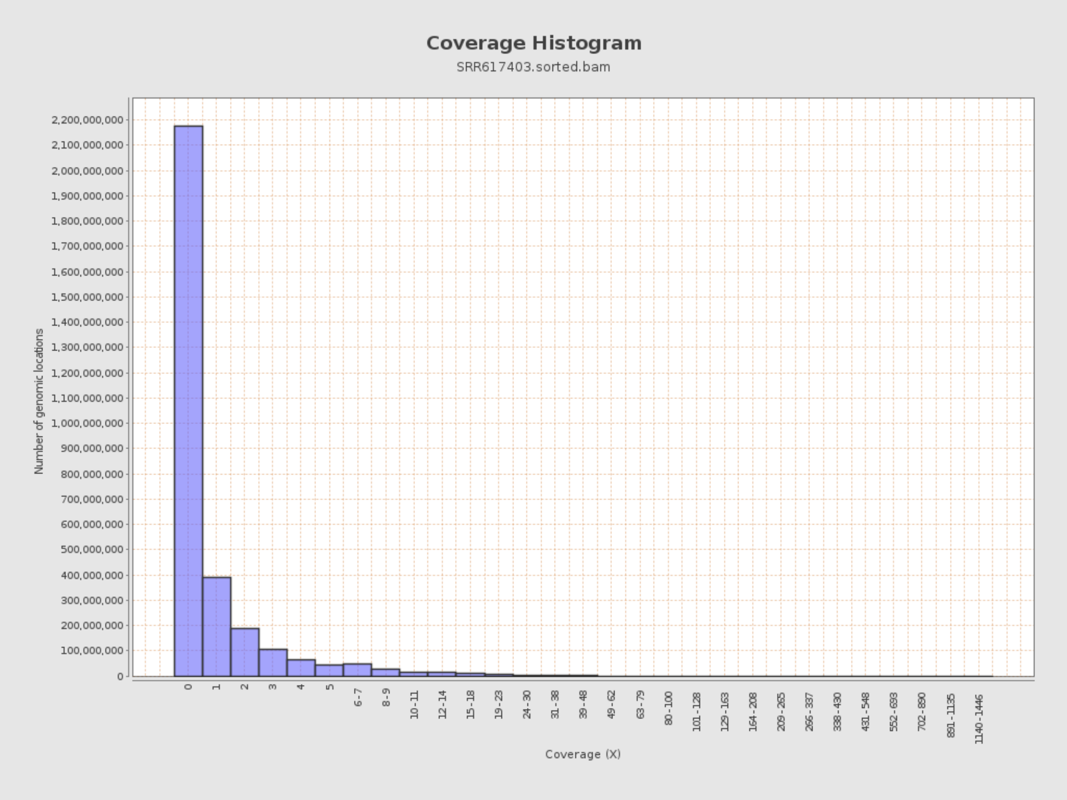
3. Results : Coverage across reference



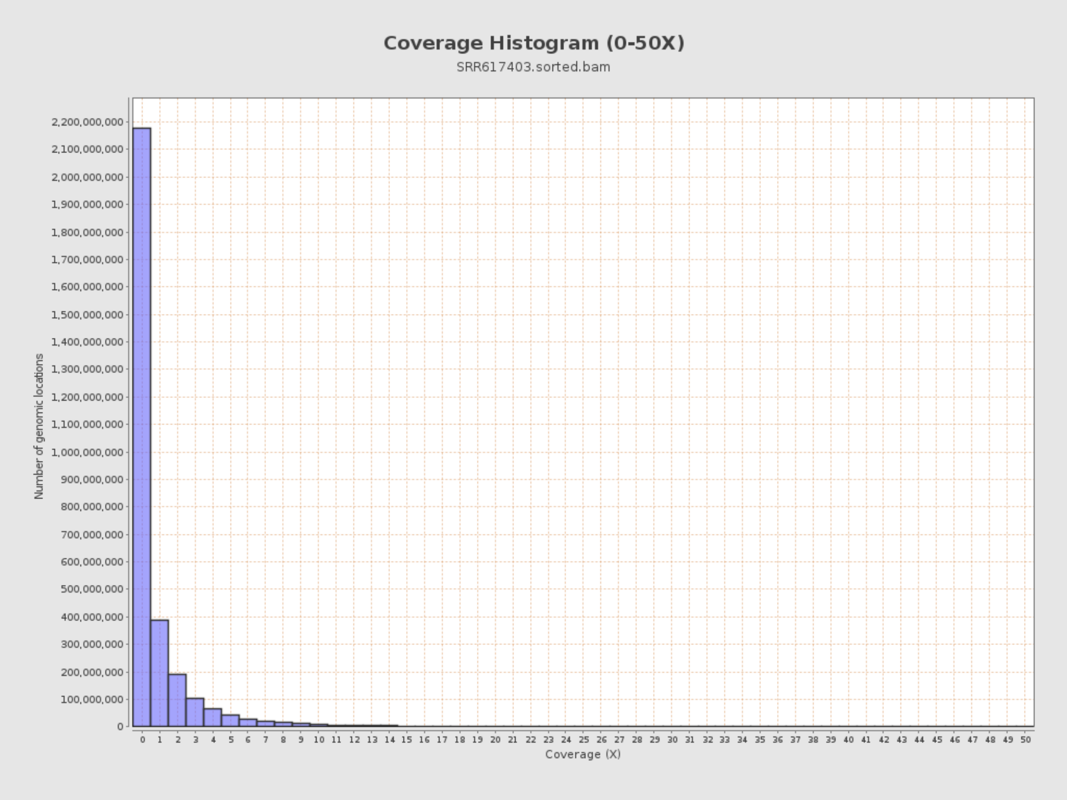
Coverage across reference

SRR617403.sorted.bam

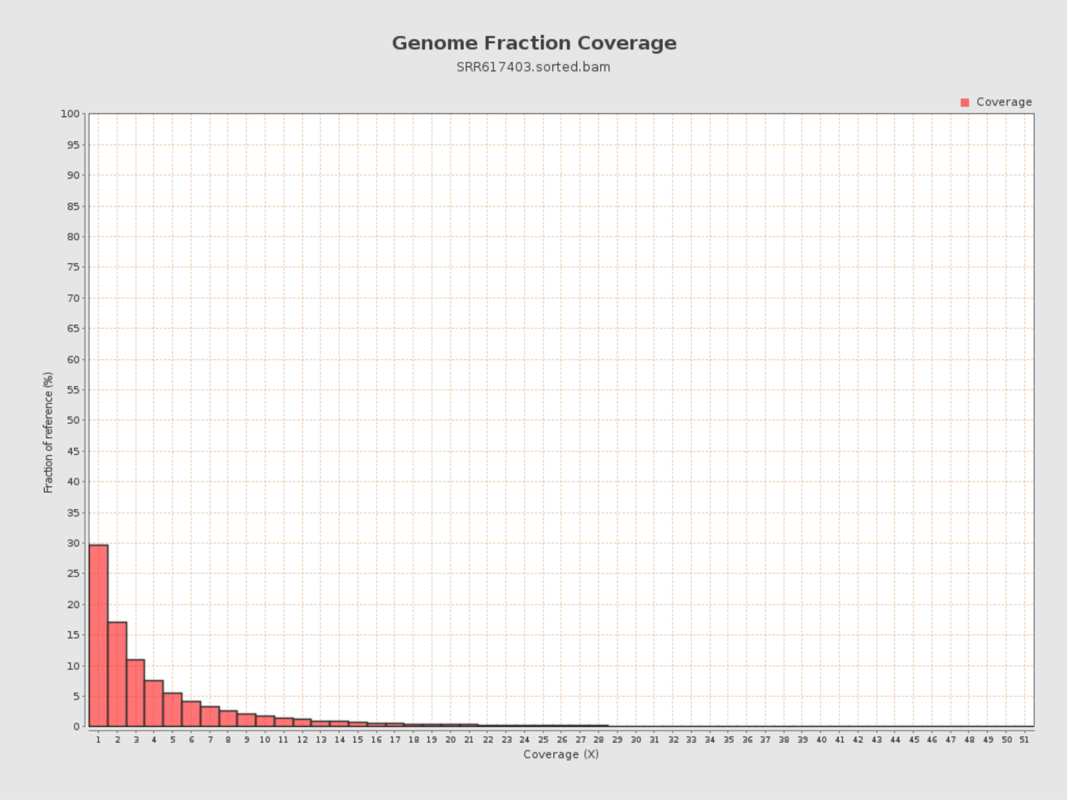
4. Results : Coverage Histogram



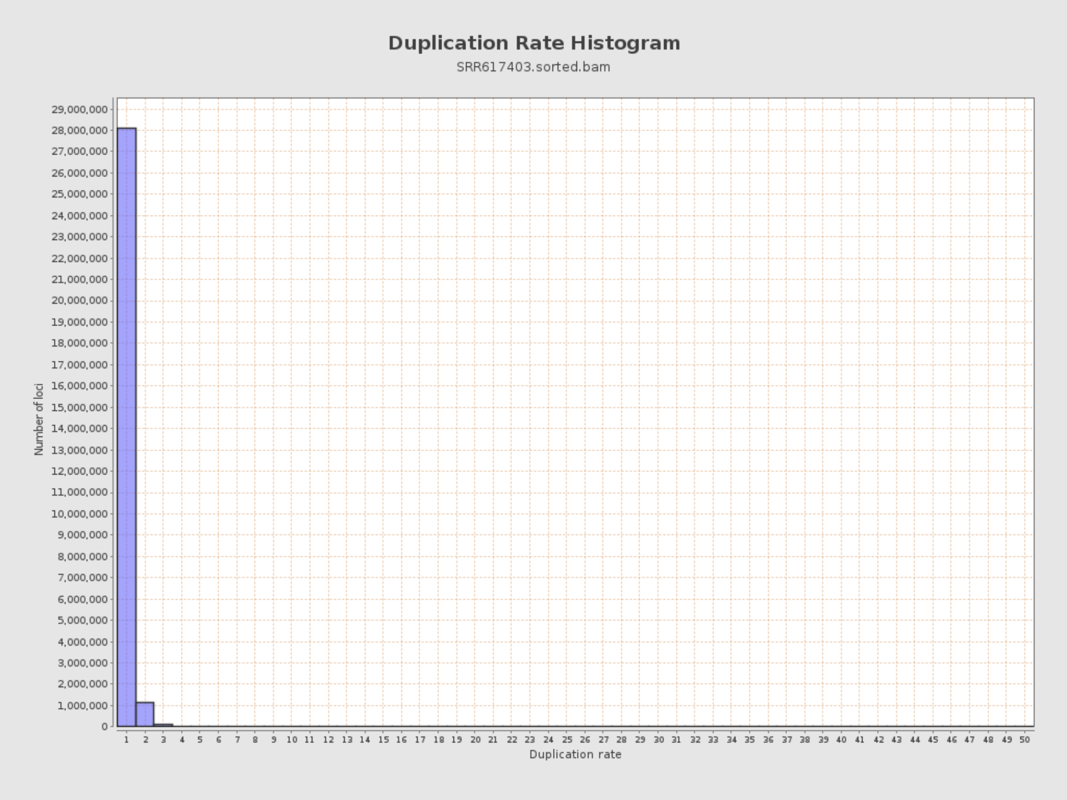
5. Results : Coverage Histogram (0-50X)



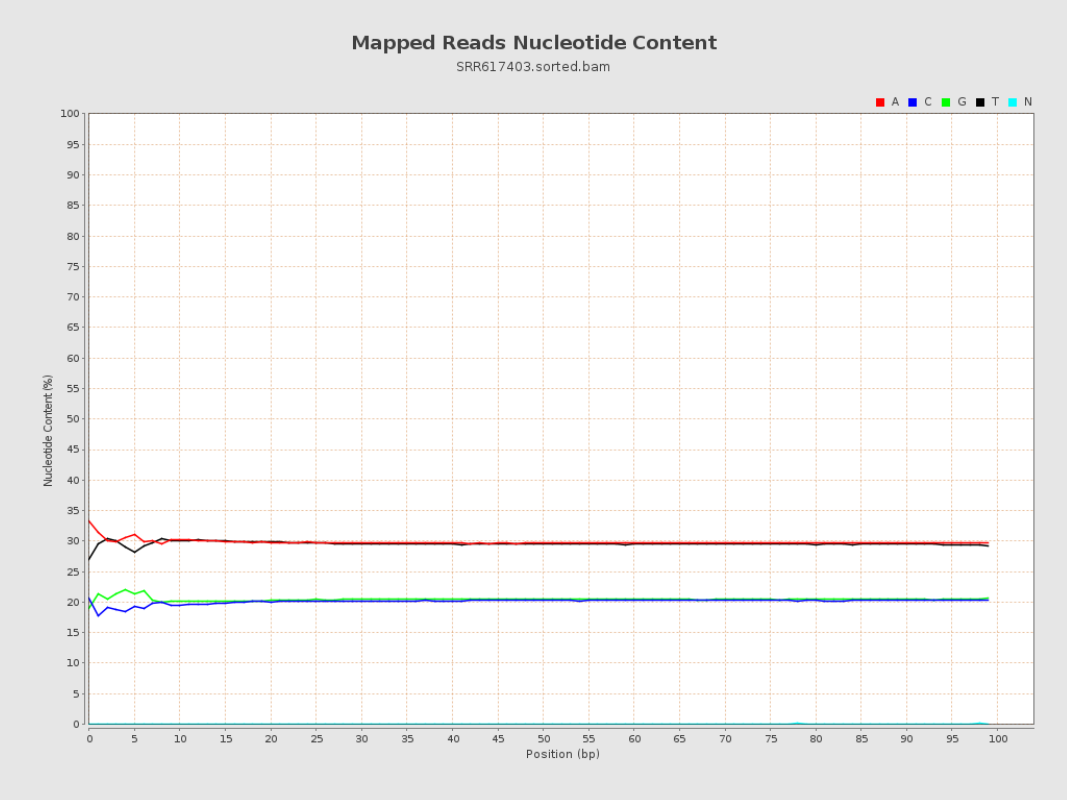
6. Results : Genome Fraction Coverage



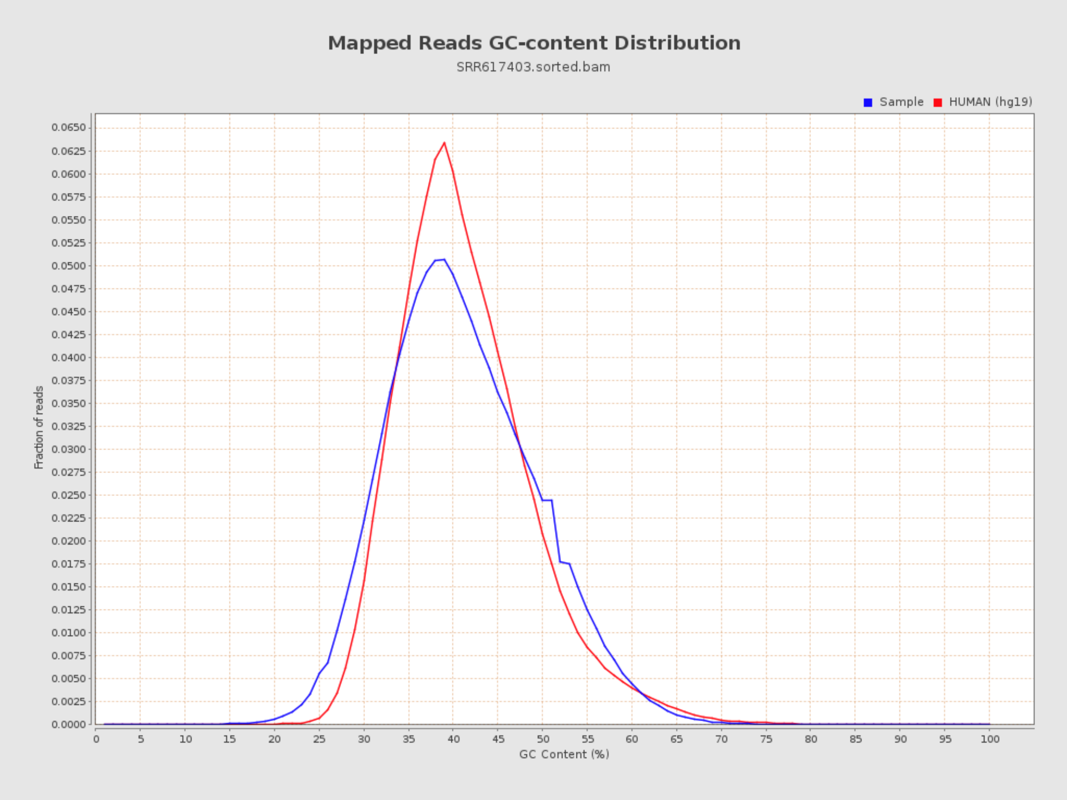
7. Results : Duplication Rate Histogram



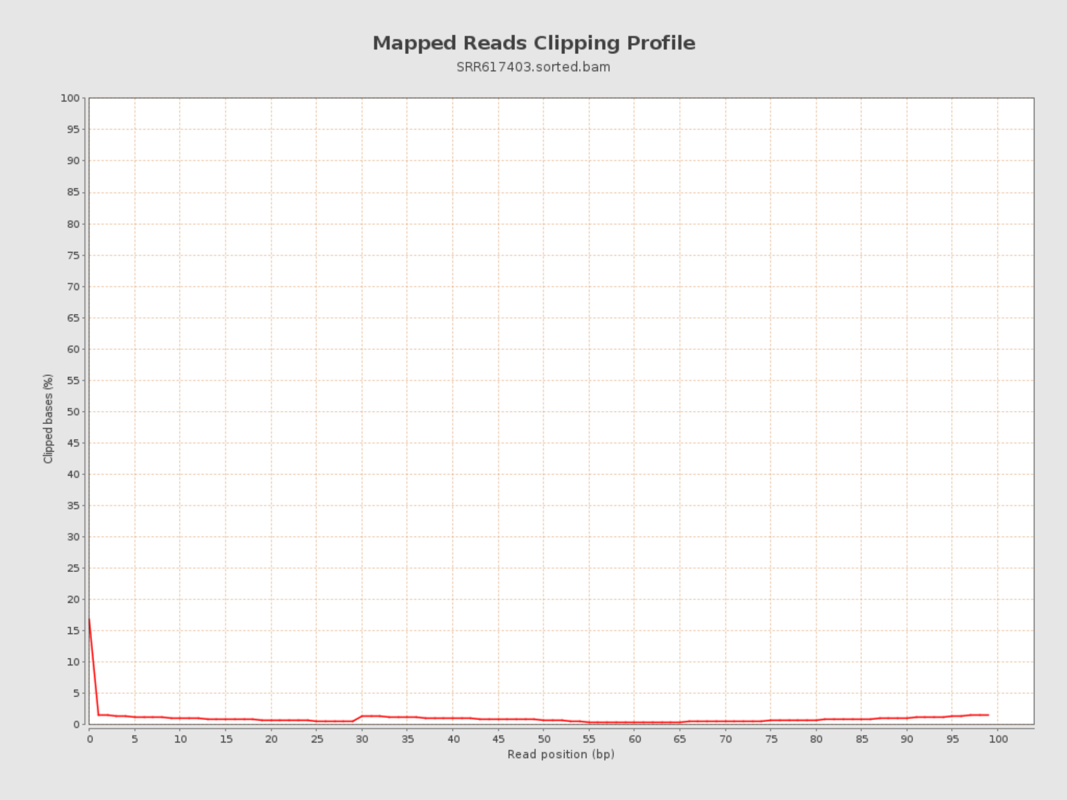
8. Results : Mapped Reads Nucleotide Content



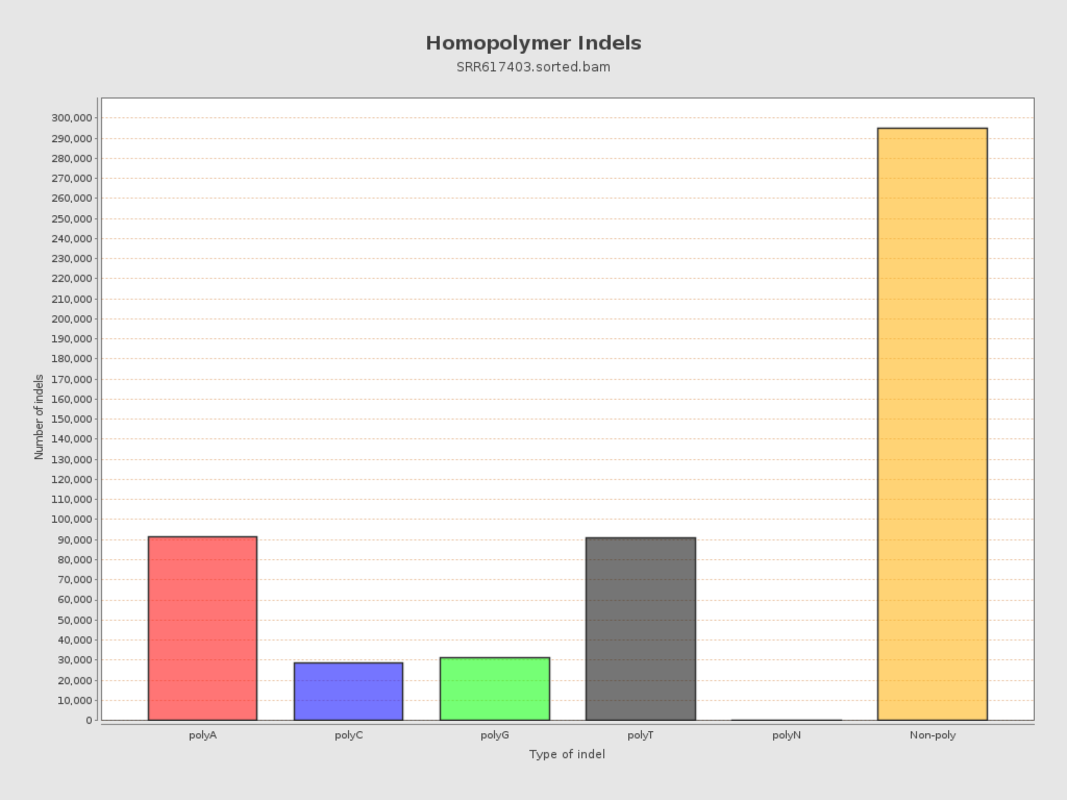
9. Results : Mapped Reads GC-content Distribution



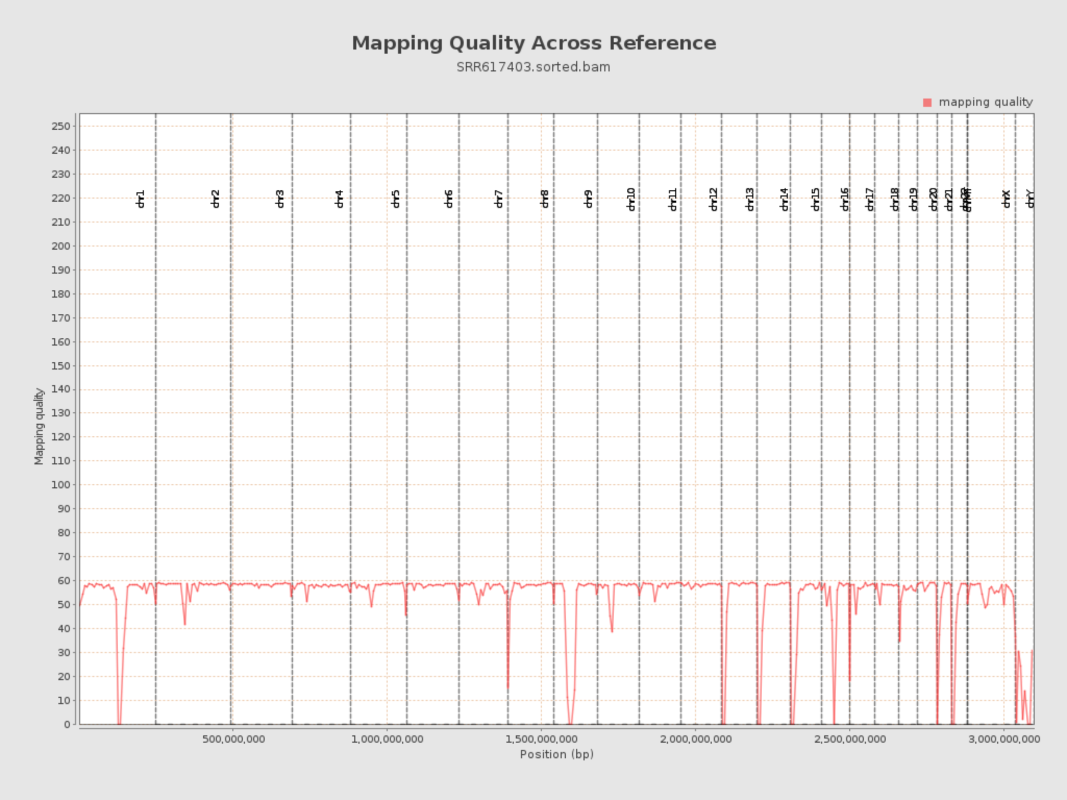
10. Results : Mapped Reads Clipping Profile



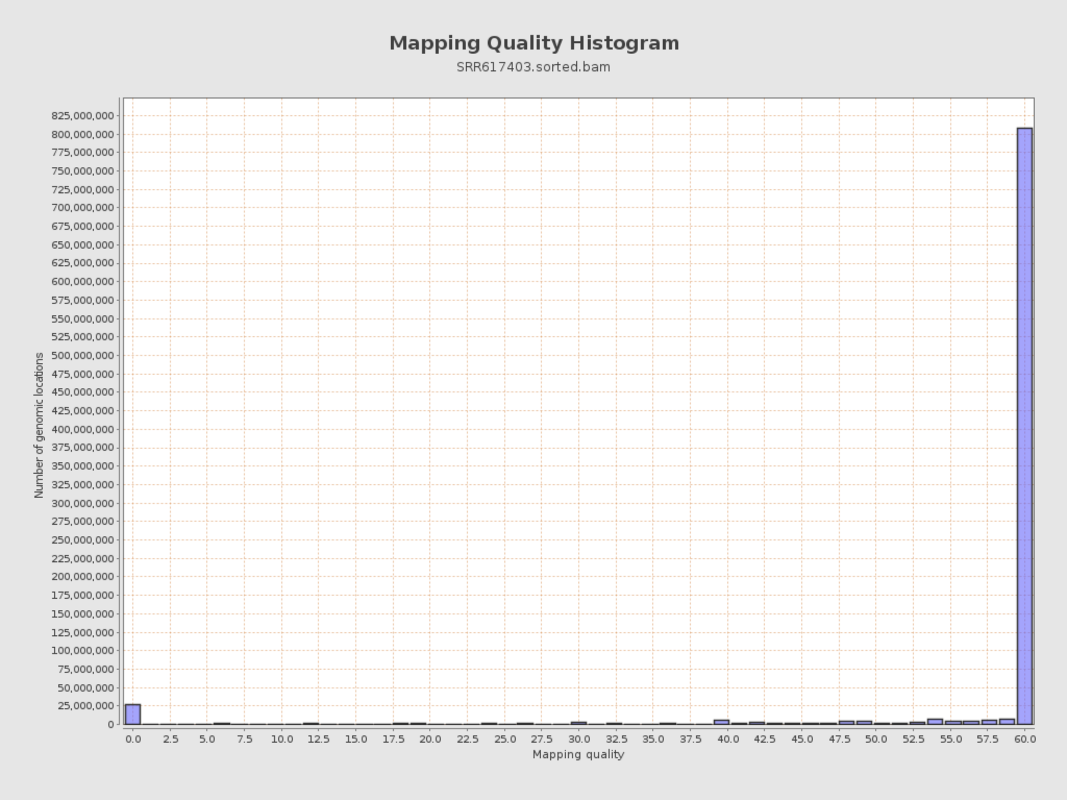
11. Results : Homopolymer Indels



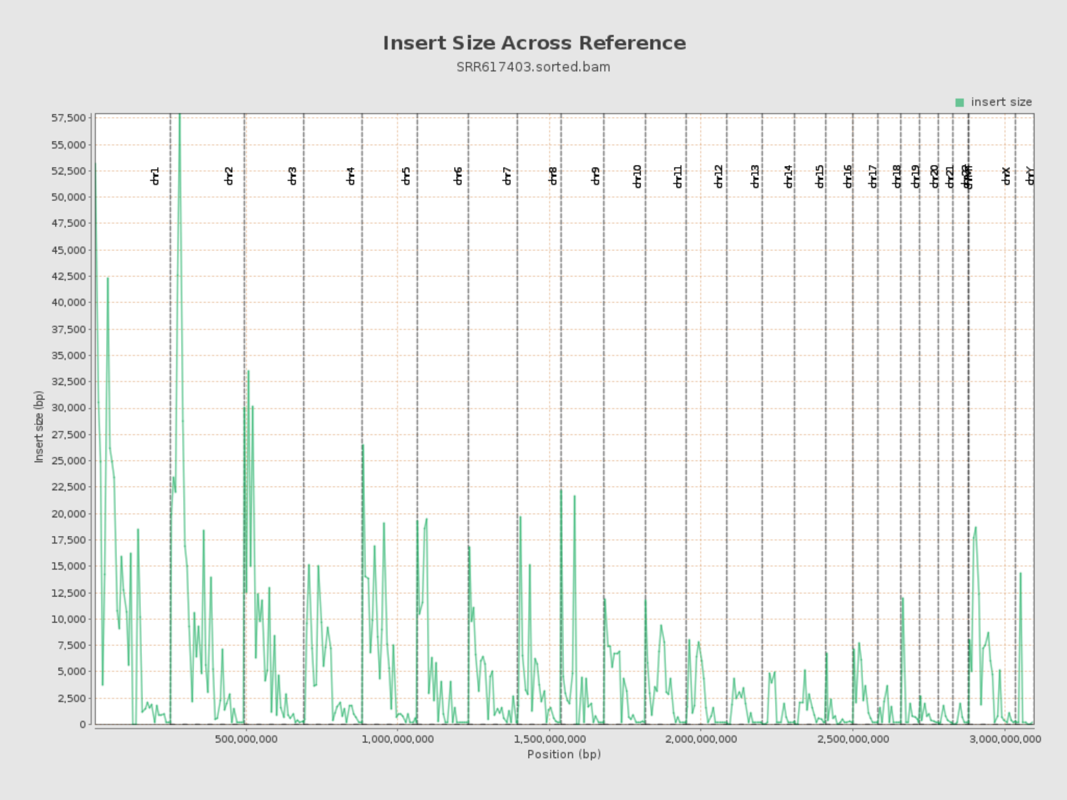
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram