Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 07:00:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617388.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_SRR617388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617388_1.fastq.gz SRR617388_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 07:00:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,661,226 / 95.82%
Unmapped reads	1,338,774 / 4.18%
Mapped paired reads	30,661,226 / 95.82%
Mapped reads, first in pair	15,408,403 / 48.15%
Mapped reads, second in pair	15,252,823 / 47.67%
Mapped reads, both in pair	30,155,416 / 94.24%
Mapped reads, singletons	505,810 / 1.58%
Secondary alignments	0
Supplementary alignments	98,531 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,634,887 / 5.11%
Duplication rate	1.52%
Clipped reads	2,342,693 / 7.32%

2.2. ACGT Content

Number/percentage of A's	910,004,433 / 30.25%
Number/percentage of C's	597,822,345 / 19.87%
Number/percentage of T's	899,389,300 / 29.9%
Number/percentage of G's	599,994,626 / 19.95%
Number/percentage of N's	985,912 / 0.03%

GC Percentage	39.82%

2.3. Coverage

Mean	0.972
Standard Deviation	9.9346

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	70,455.36
Standard Deviation	2,542,984.45
P25/Median/P75	173 / 216 / 282

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	26,379,205
Insertions	308,203
Mapped reads with at least one insertion	0.97%
Deletions	370,541
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.33%

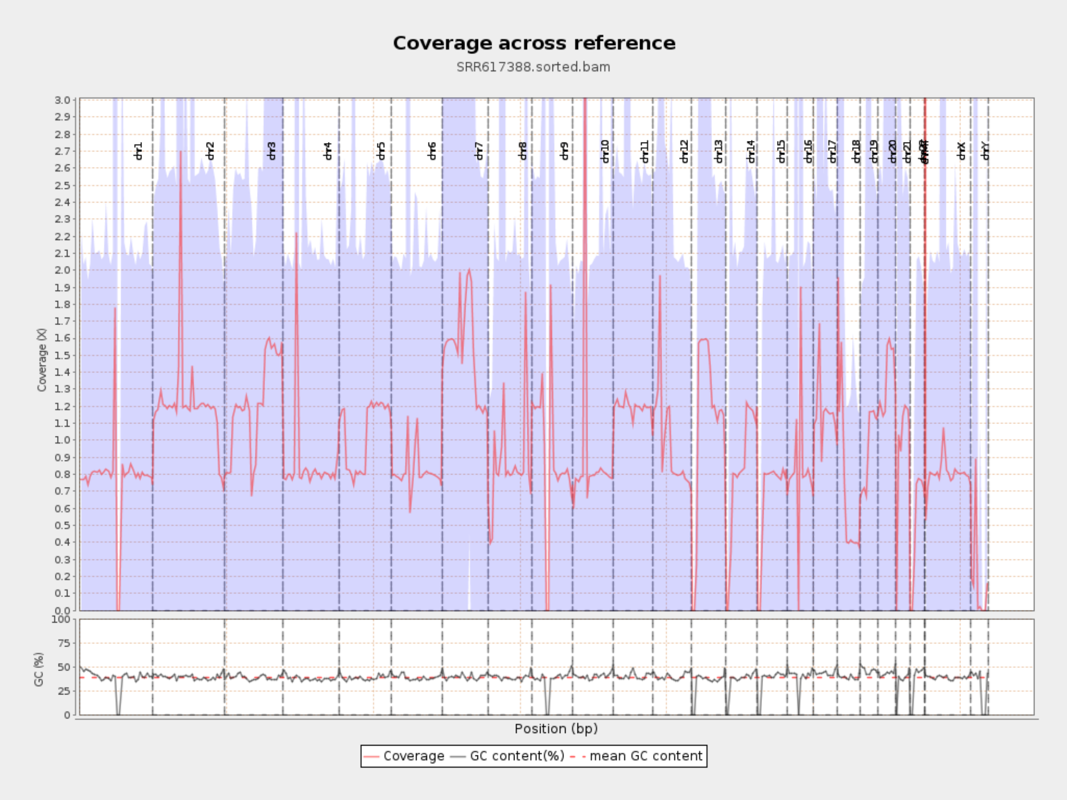
2.7. Chromosome stats

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

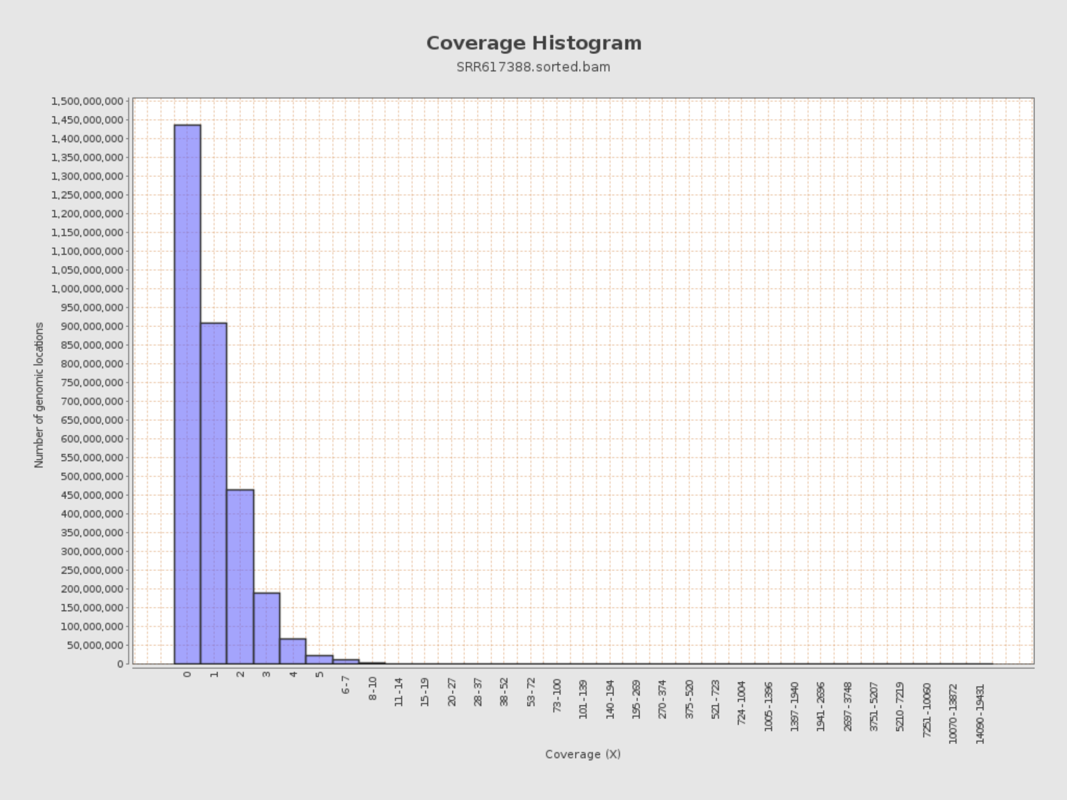
		bases	coverage	deviation
chr1	249250621	195207210	0.7832	20.0699
chr2	243199373	297010814	1.2213	9.0847
chr3	198022430	239318119	1.2085	1.4851
chr4	191154276	164468209	0.8604	9.8234
chr5	180915260	188813908	1.0437	1.4677
chr6	171115067	140667718	0.8221	3.7
chr7	159138663	244260520	1.5349	10.9016
chr8	146364022	126560967	0.8647	7.836
chr9	141213431	126964149	0.8991	15.3091
chr10	135534747	126897945	0.9363	20.2393
chr11	135006516	161381031	1.1954	5.6034
chr12	133851895	132703960	0.9914	1.4387
chr13	115169878	130774873	1.1355	1.342
chr14	107349540	87017312	0.8106	1.3828
chr15	102531392	67884499	0.6621	1.1347
chr16	90354753	75605312	0.8368	7.8489
chr17	81195210	94218610	1.1604	7.4482
chr18	78077248	54380620	0.6965	15.6525
chr19	59128983	56394212	0.9537	9.5774
chr20	63025520	86454894	1.3717	2.4327
chr21	48129895	47913270	0.9955	3.3
chr22	51304566	26828442	0.5229	0.9364
chrMT	16571	2062829	124.4843	20.9541
chrX	155270560	124879636	0.8043	3.0255

chrY	59373566	10427473	0.1756	8.6451

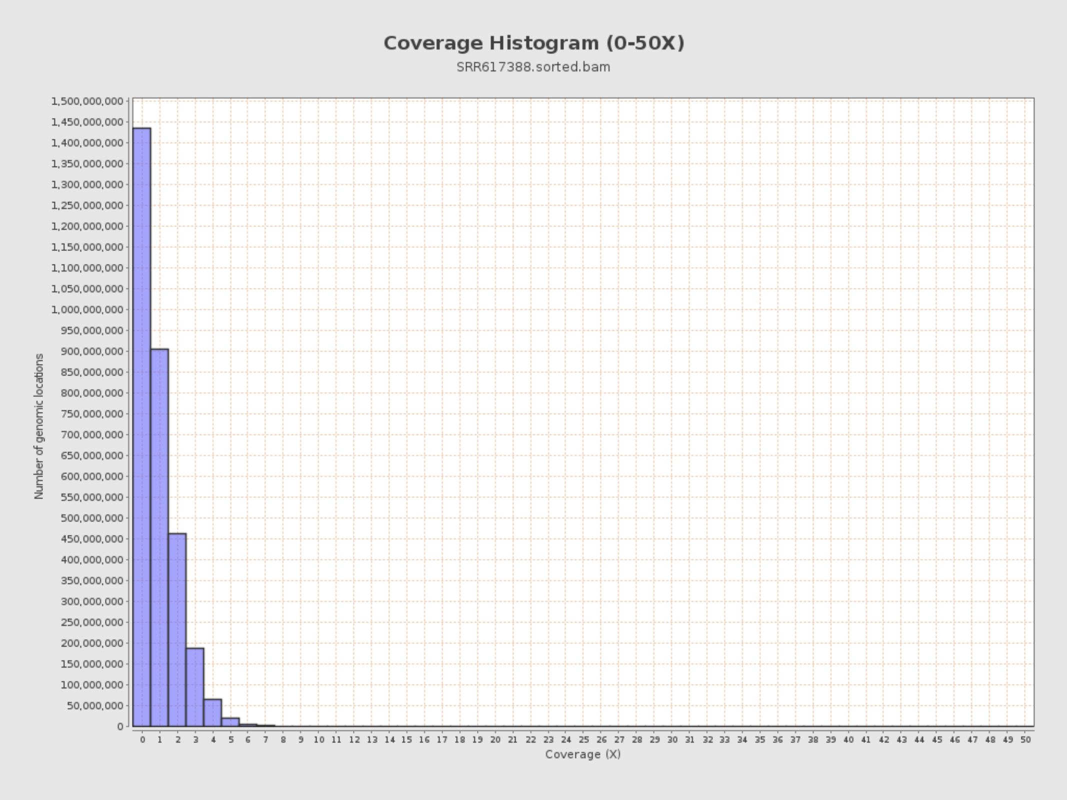
3. Results : Coverage across reference



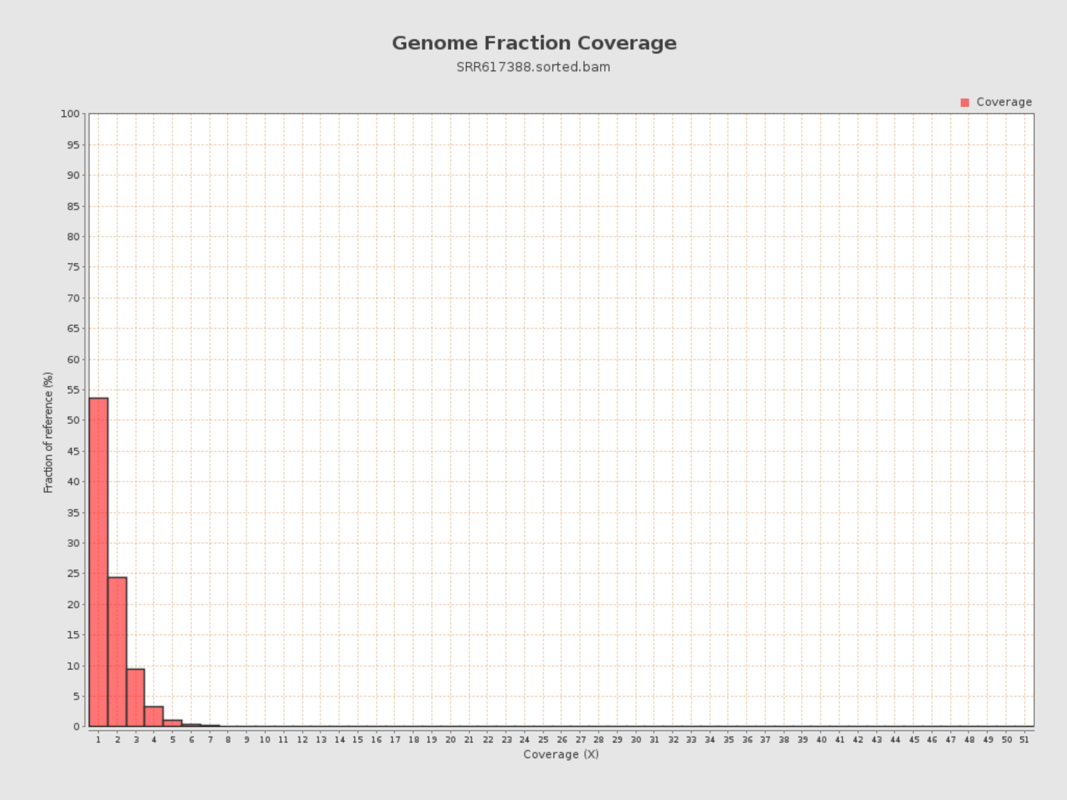
4. Results : Coverage Histogram



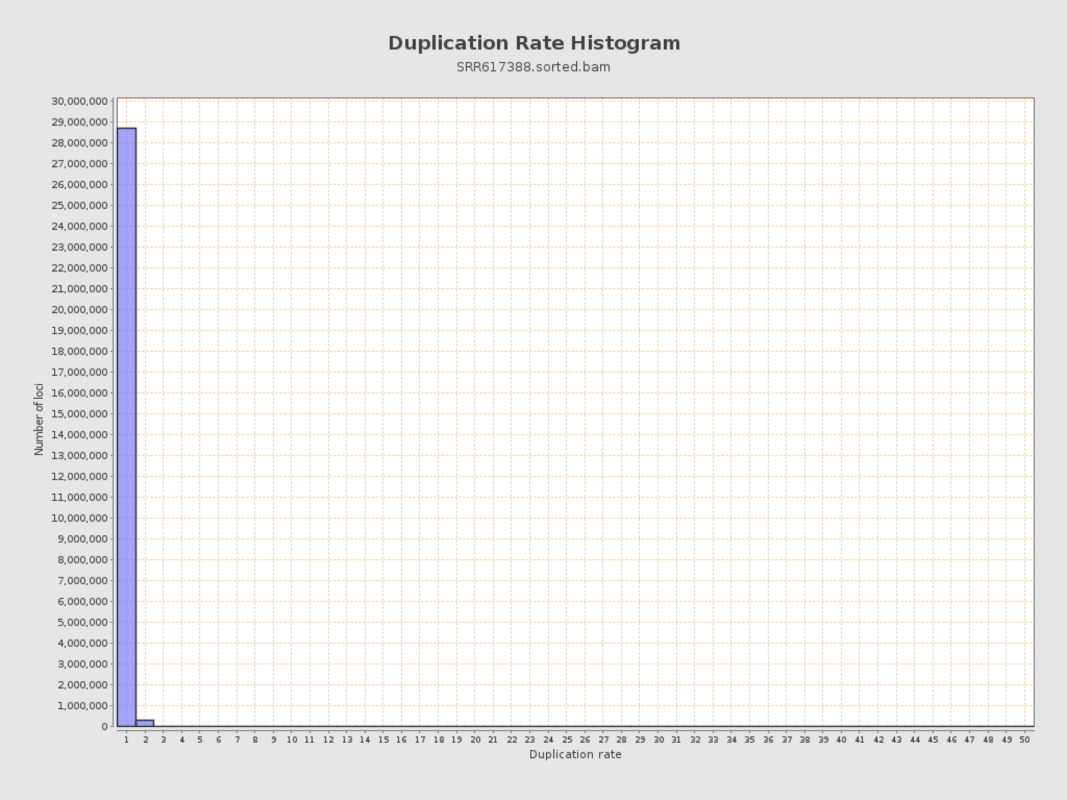
5. Results : Coverage Histogram (0-50X)



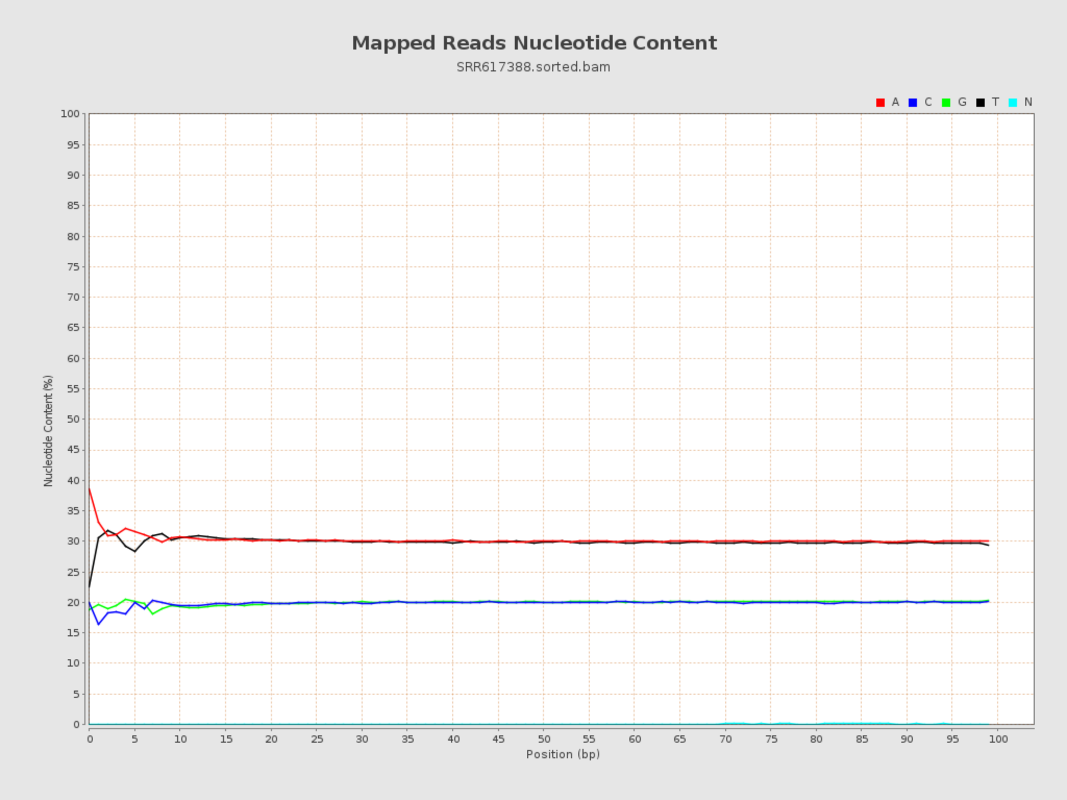
6. Results : Genome Fraction Coverage



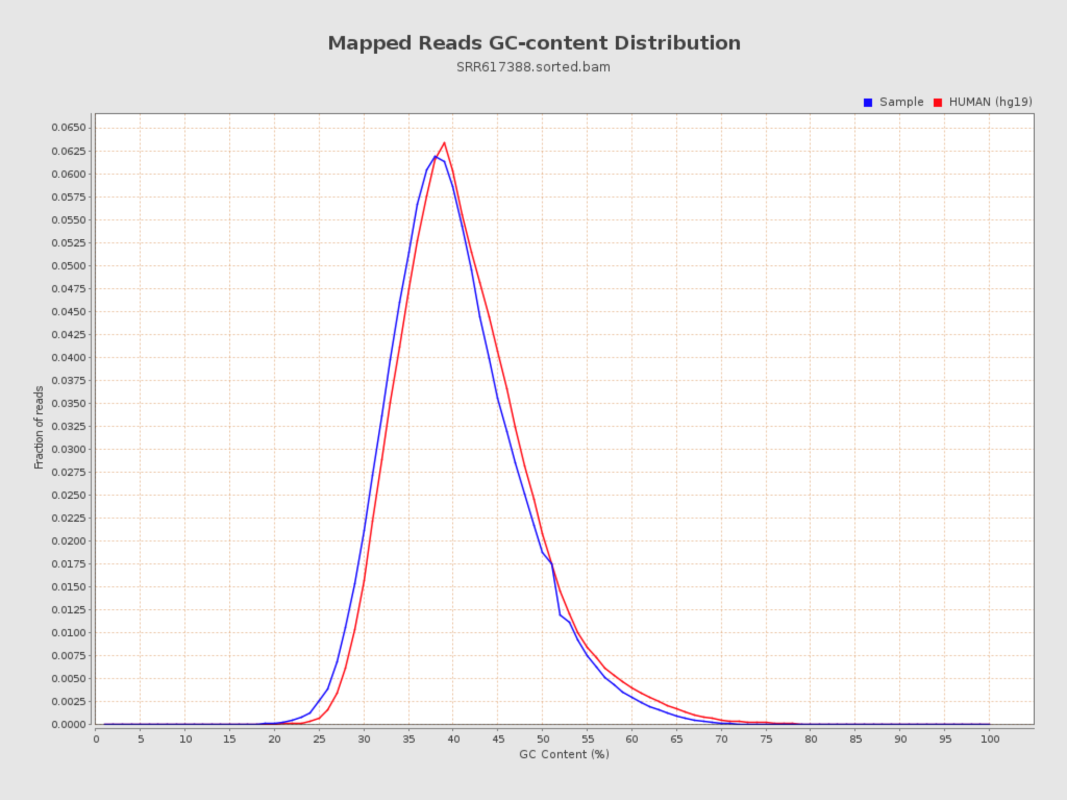
7. Results : Duplication Rate Histogram



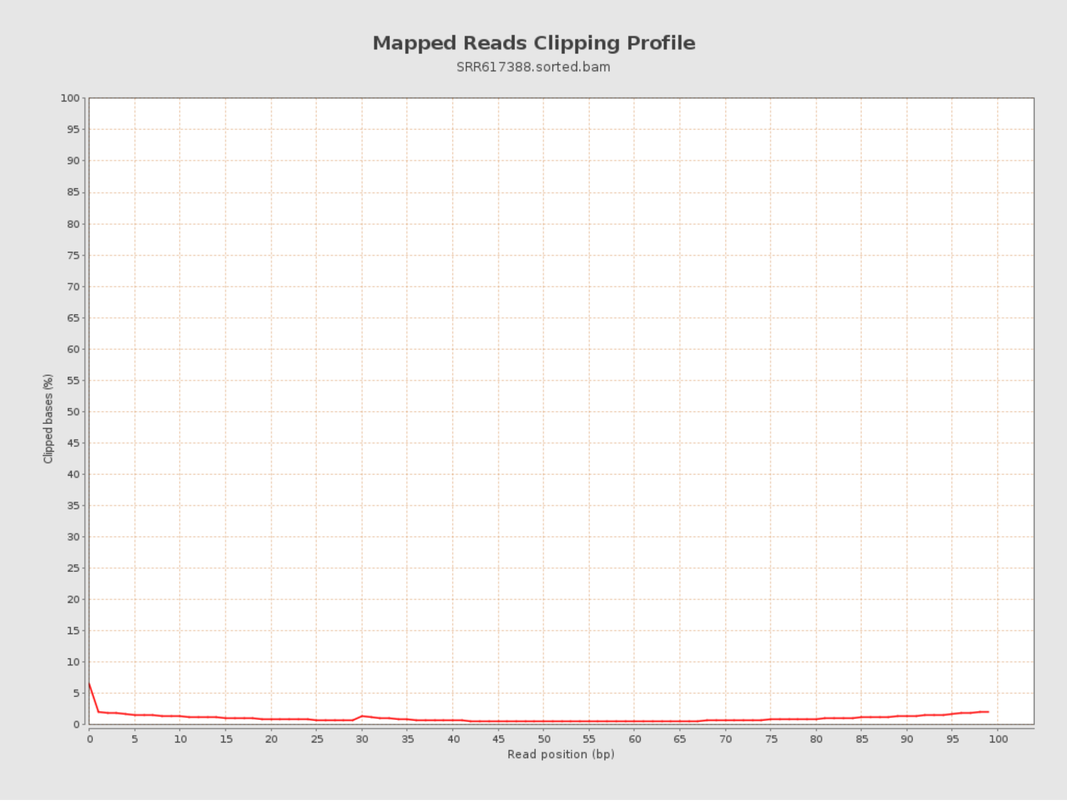
8. Results : Mapped Reads Nucleotide Content



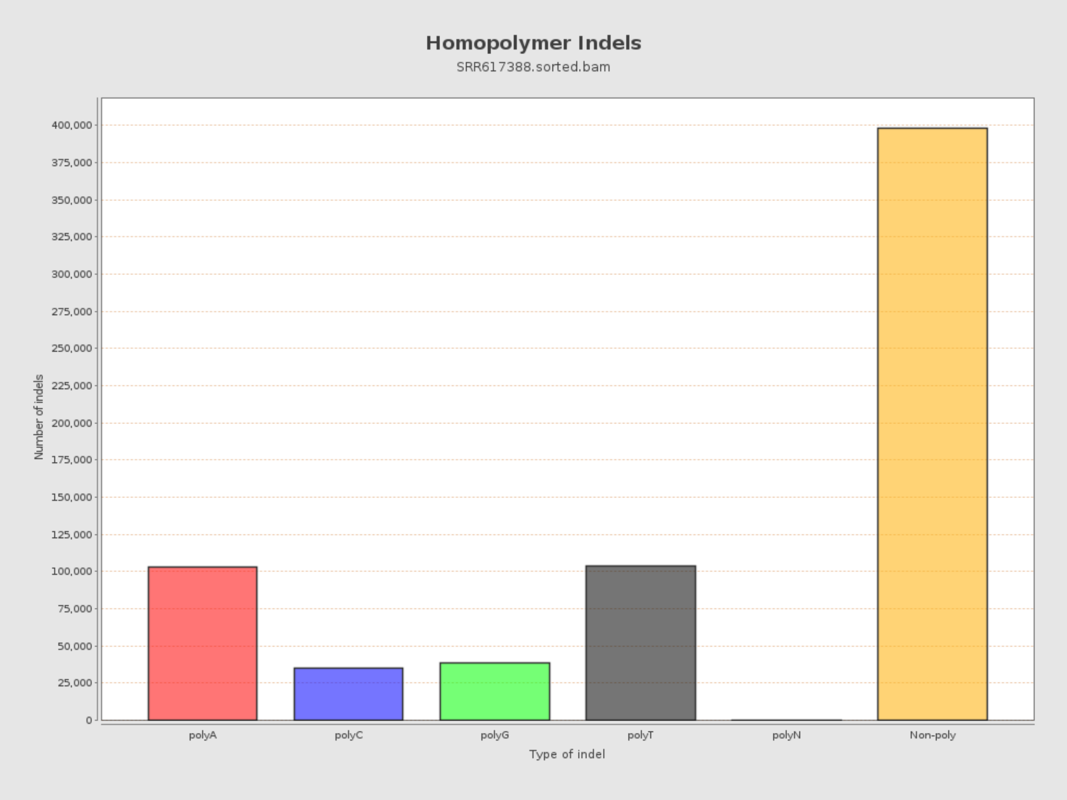
9. Results : Mapped Reads GC-content Distribution



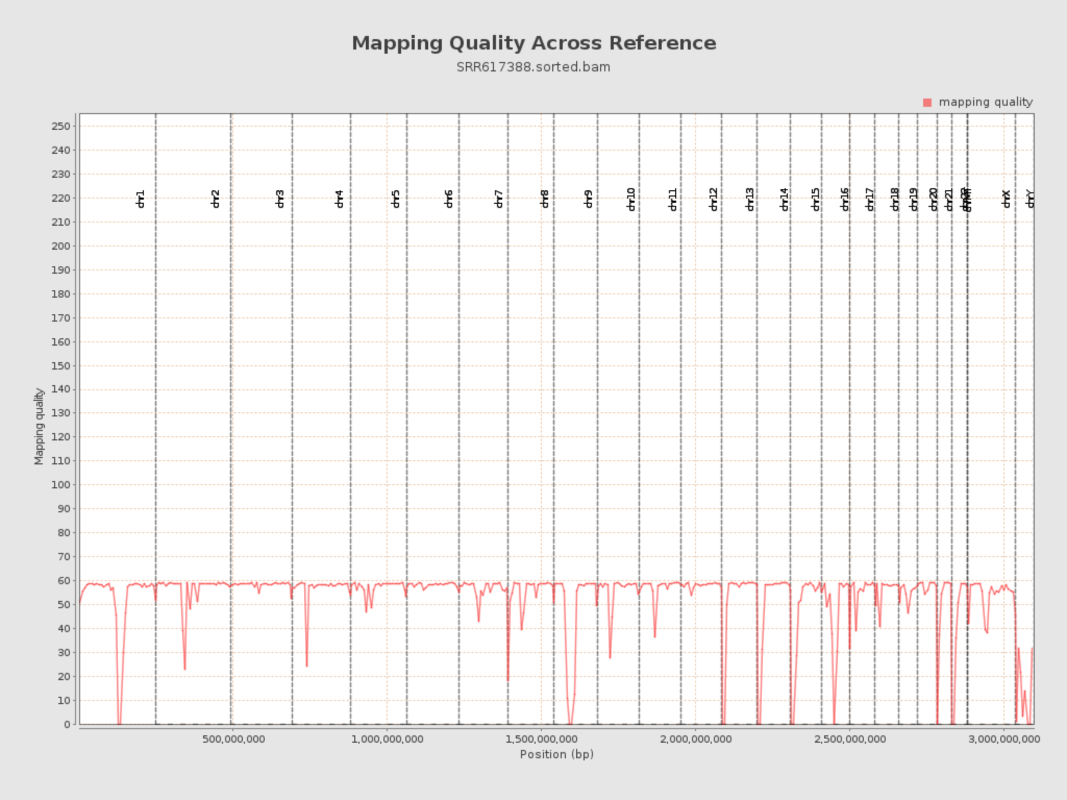
10. Results : Mapped Reads Clipping Profile



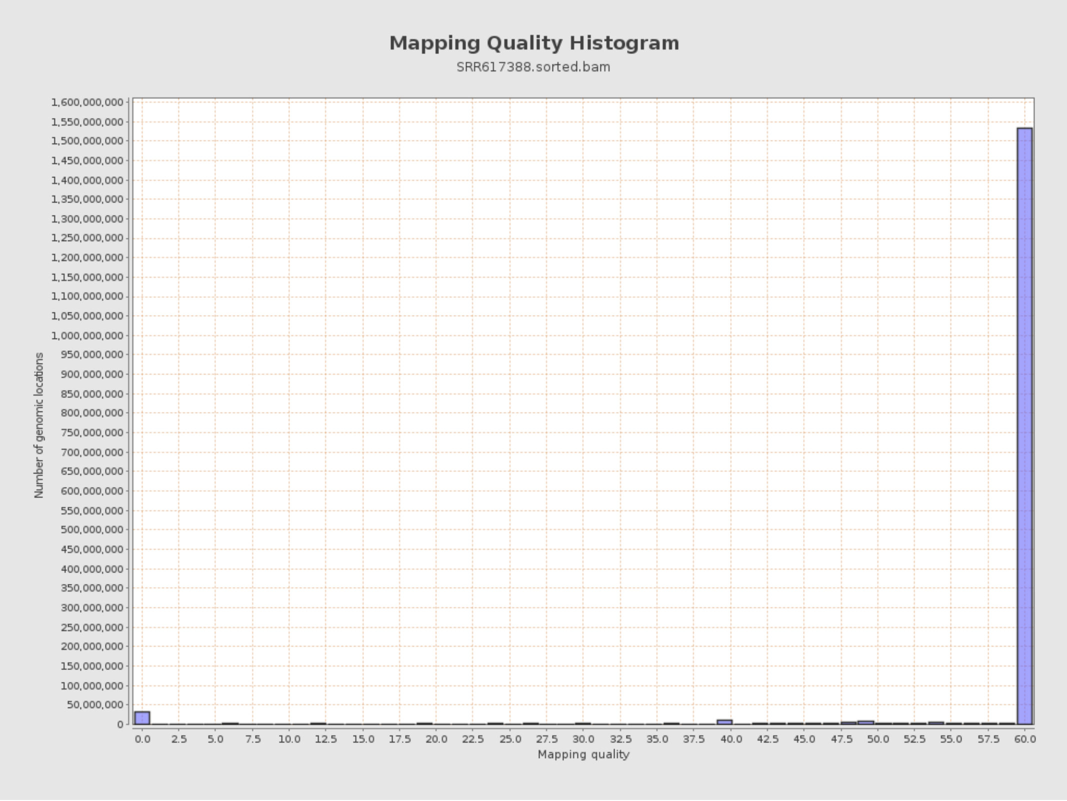
11. Results : Homopolymer Indels



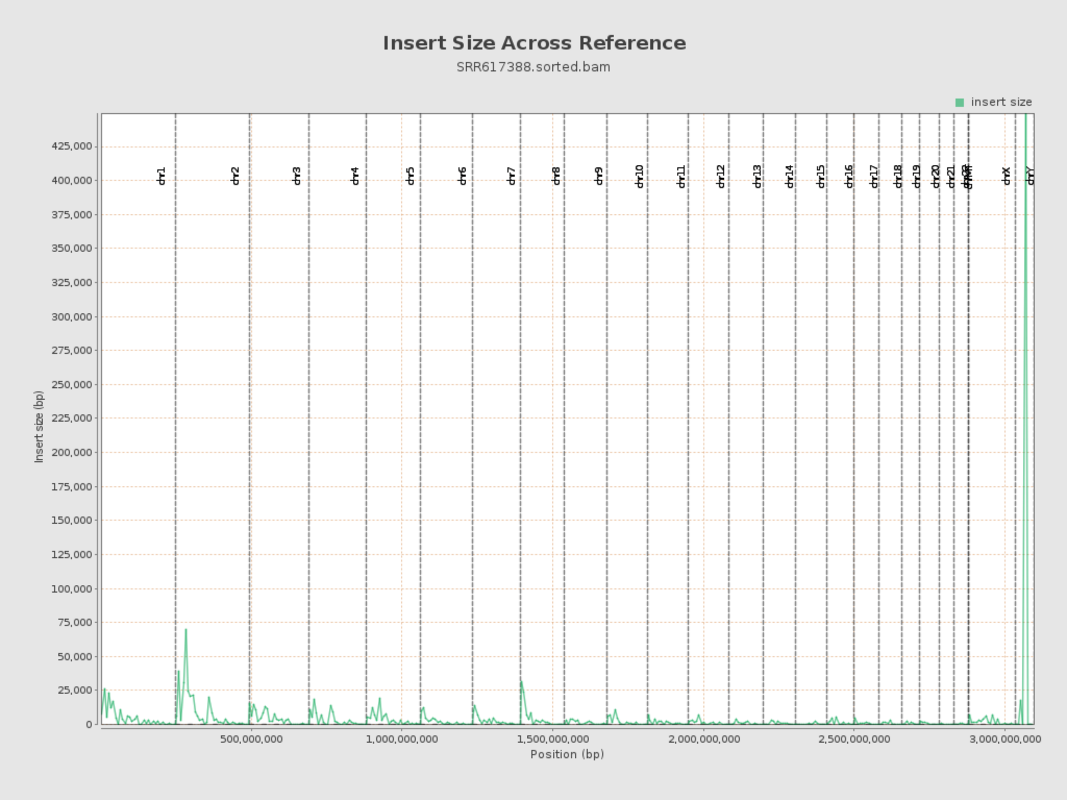
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram