Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 06:01:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617387.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_SRR617387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617387_1.fastq.gz SRR617387_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 06:01:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617387.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,297,022 / 91.55%
Unmapped reads	2,702,978 / 8.45%
Mapped paired reads	29,297,022 / 91.55%
Mapped reads, first in pair	14,795,178 / 46.23%
Mapped reads, second in pair	14,501,844 / 45.32%
Mapped reads, both in pair	28,573,800 / 89.29%
Mapped reads, singletons	723,222 / 2.26%
Secondary alignments	0
Supplementary alignments	86,551 / 0.27%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	1,535,661 / 4.8%
Duplication rate	1.51%
Clipped reads	2,911,861 / 9.1%

2.2. ACGT Content

Number/percentage of A's	870,432,146 / 30.43%
Number/percentage of C's	564,859,047 / 19.75%
Number/percentage of T's	856,978,555 / 29.96%
Number/percentage of G's	567,734,173 / 19.85%
Number/percentage of N's	716,136 / 0.03%

GC Percentage	39.59%

2.3. Coverage

Mean	0.9244
Standard Deviation	9.5189

2.4. Mapping Quality

Mean Mapping Quality	53.31

2.5. Insert size

Mean	58,038.7
Standard Deviation	2,293,761.98
P25/Median/P75	169 / 207 / 265

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	37,567,270
Insertions	290,820
Mapped reads with at least one insertion	0.96%
Deletions	347,395
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.06%

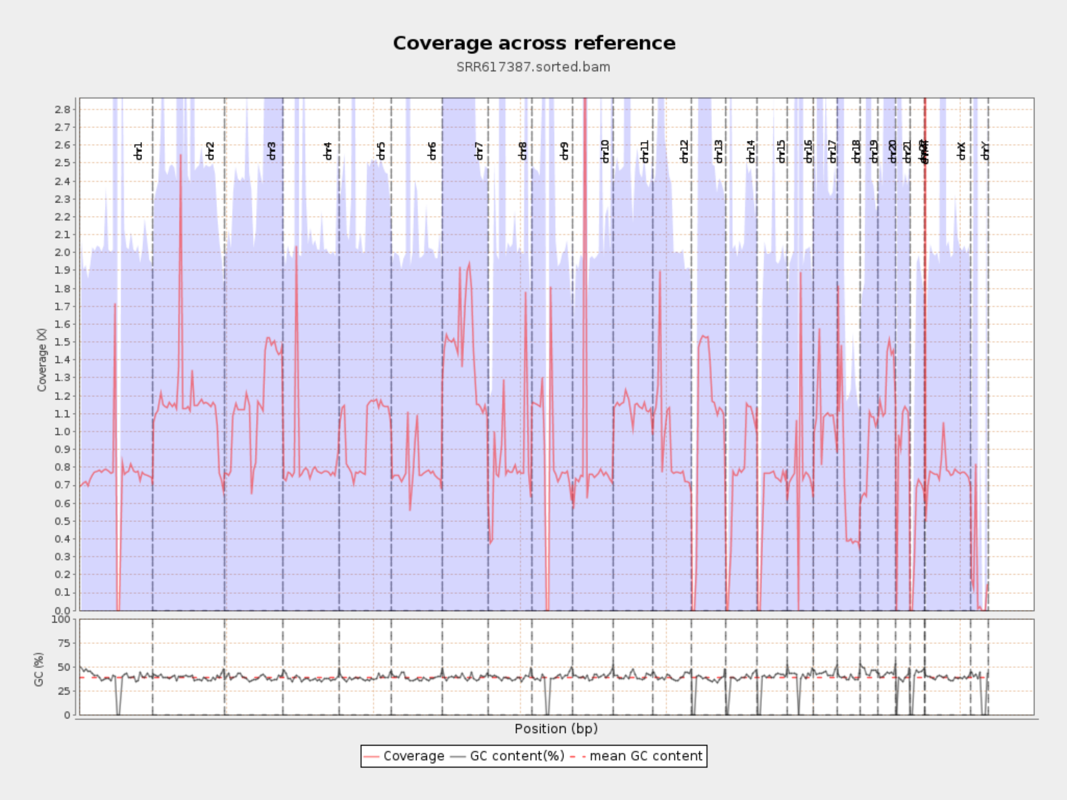
2.7. Chromosome stats

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

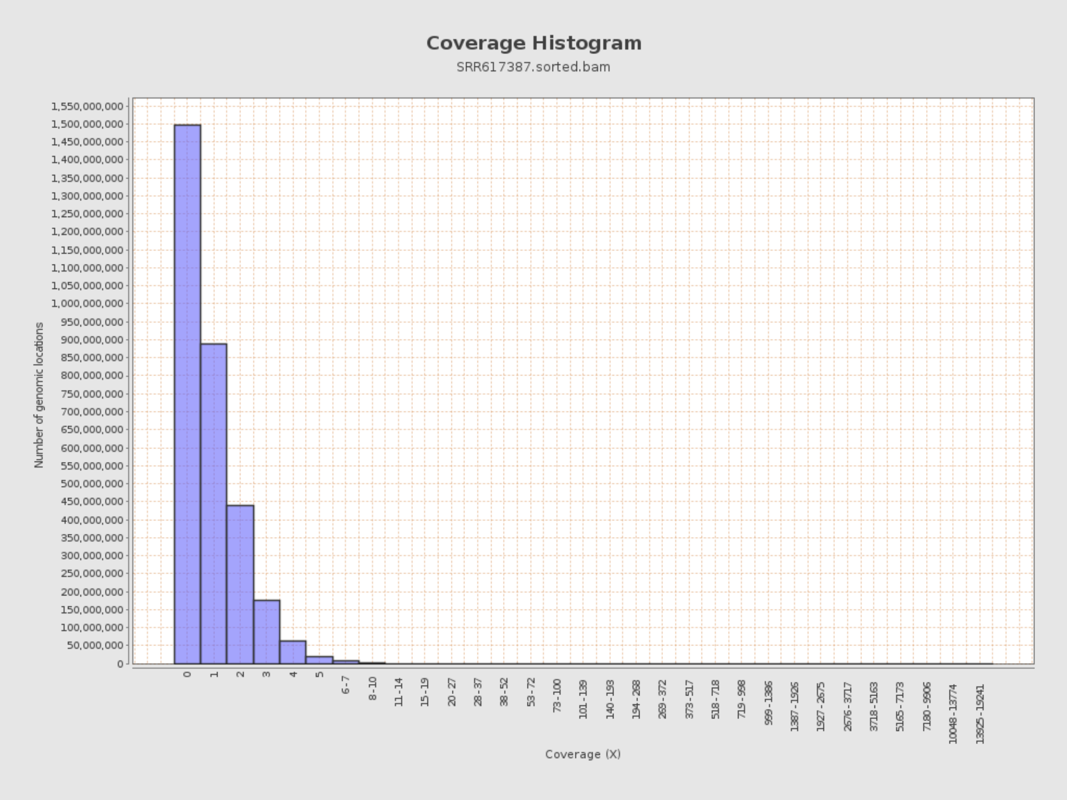
		bases	coverage	deviation
chr1	249250621	185599554	0.7446	19.5433
chr2	243199373	282978120	1.1636	8.4844
chr3	198022430	228397220	1.1534	1.4654
chr4	191154276	157544699	0.8242	8.6169
chr5	180915260	180281935	0.9965	1.45
chr6	171115067	134657418	0.7869	3.6168
chr7	159138663	232576283	1.4615	10.7712
chr8	146364022	120749886	0.825	7.4152
chr9	141213431	120211392	0.8513	14.2813
chr10	135534747	120752646	0.8909	19.8217
chr11	135006516	153273524	1.1353	5.2943
chr12	133851895	126283656	0.9435	1.3552
chr13	115169878	125464464	1.0894	1.3037
chr14	107349540	82617145	0.7696	1.3601
chr15	102531392	64063237	0.6248	1.0698
chr16	90354753	71856152	0.7953	7.9226
chr17	81195210	87824082	1.0816	6.9309
chr18	78077248	51672308	0.6618	14.5666
chr19	59128983	52173336	0.8824	9.3629
chr20	63025520	81163739	1.2878	2.3501
chr21	48129895	45457480	0.9445	3.0508
chr22	51304566	24884844	0.485	0.9038
chrMT	16571	1905516	114.991	20.2442
chrX	155270560	119556479	0.77	2.9331

chrY	59373566	9602085	0.1617	7.7457

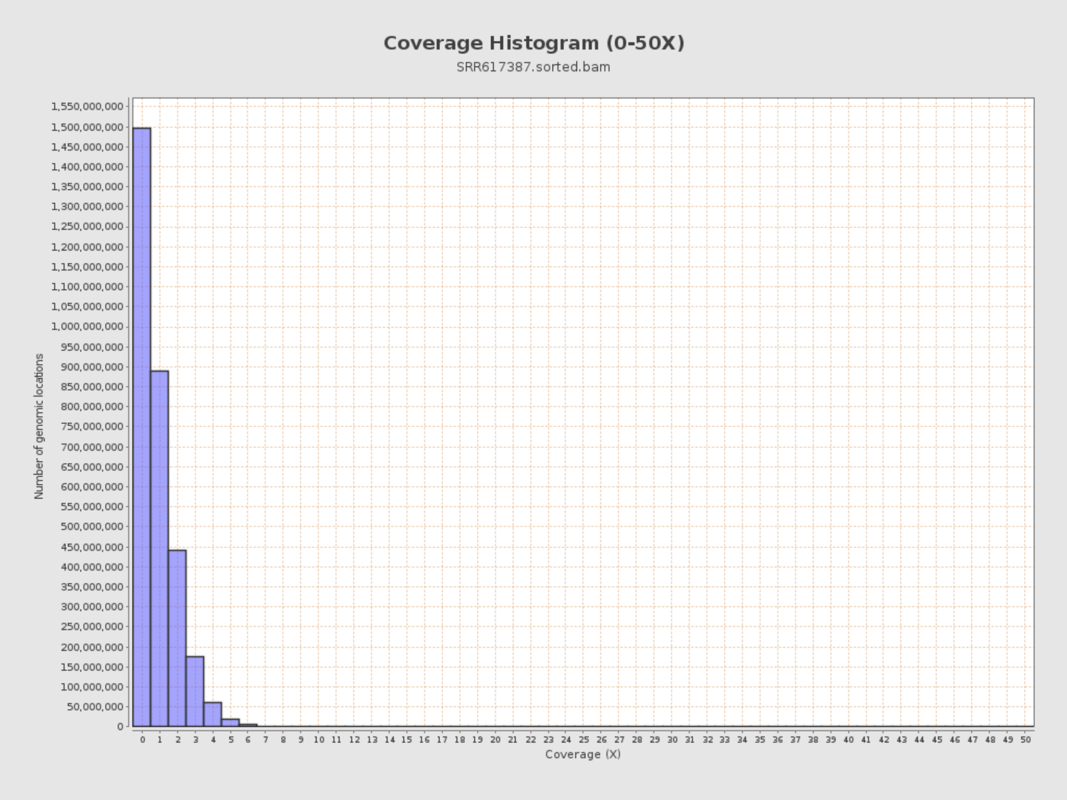
3. Results : Coverage across reference



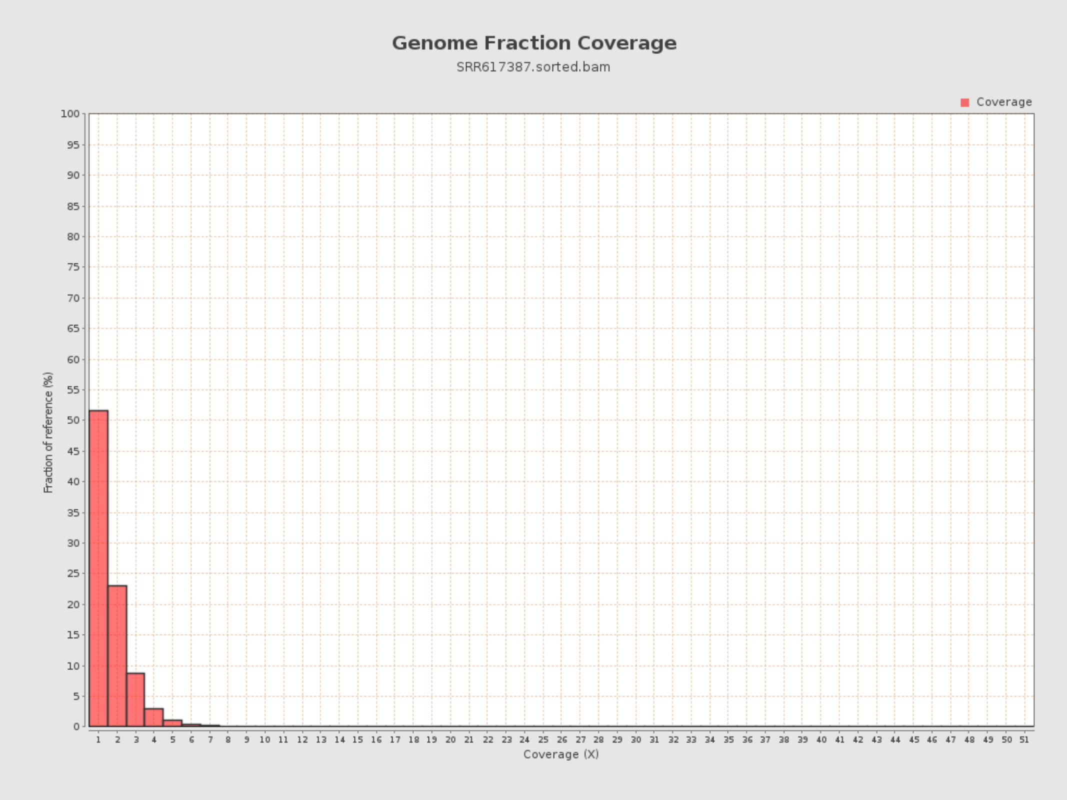
4. Results : Coverage Histogram



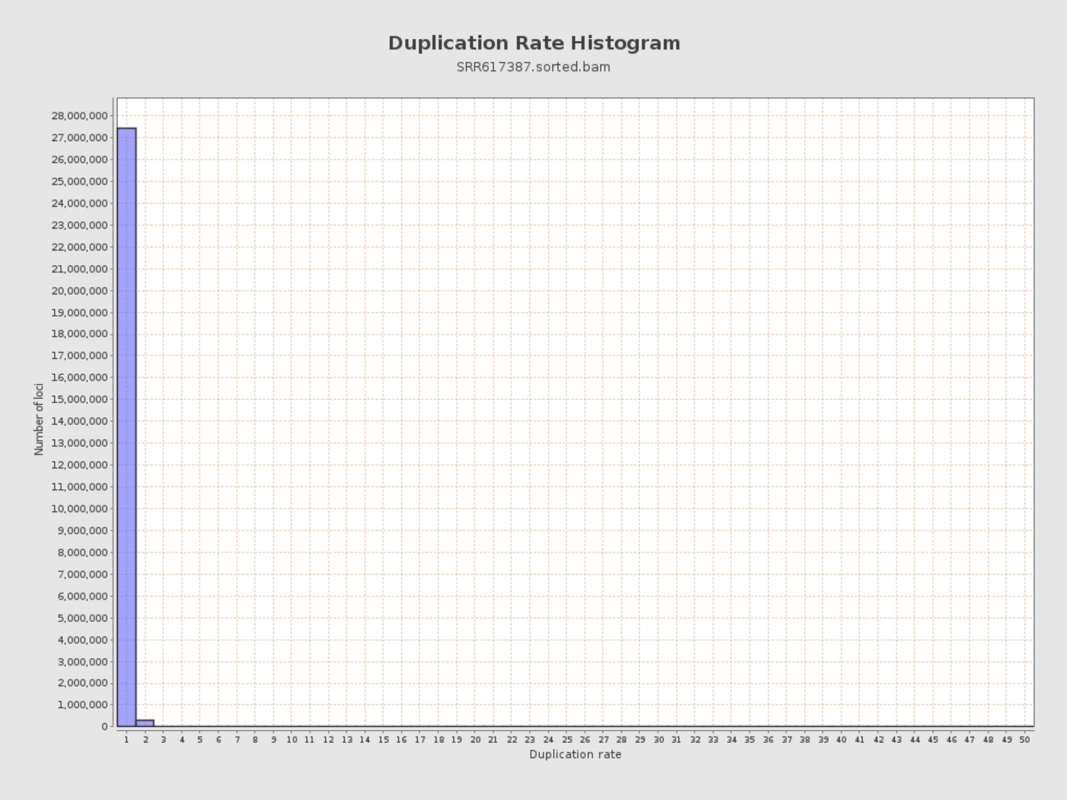
5. Results : Coverage Histogram (0-50X)



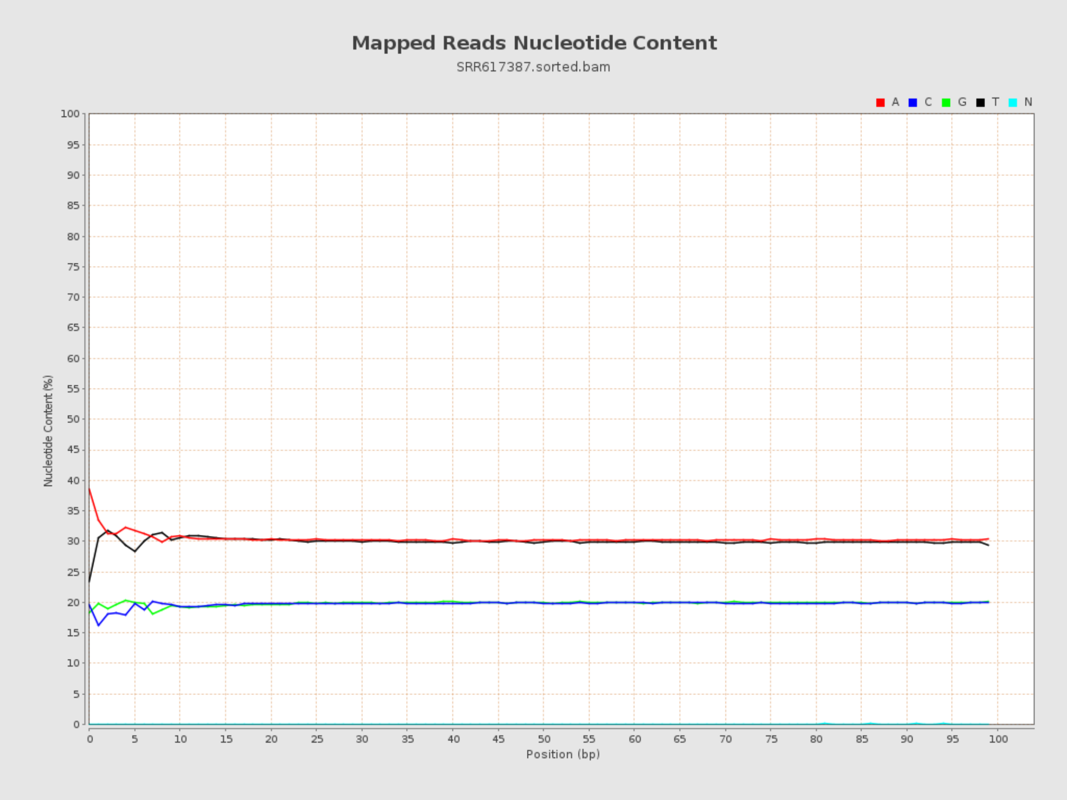
6. Results : Genome Fraction Coverage



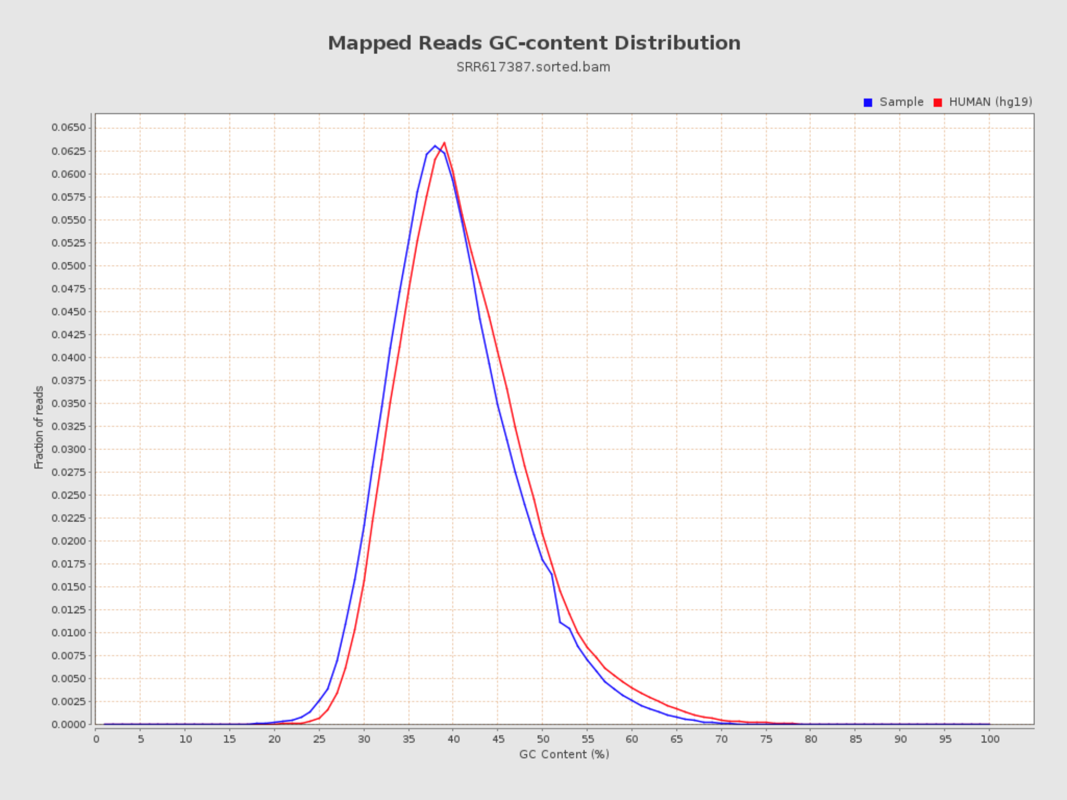
7. Results : Duplication Rate Histogram



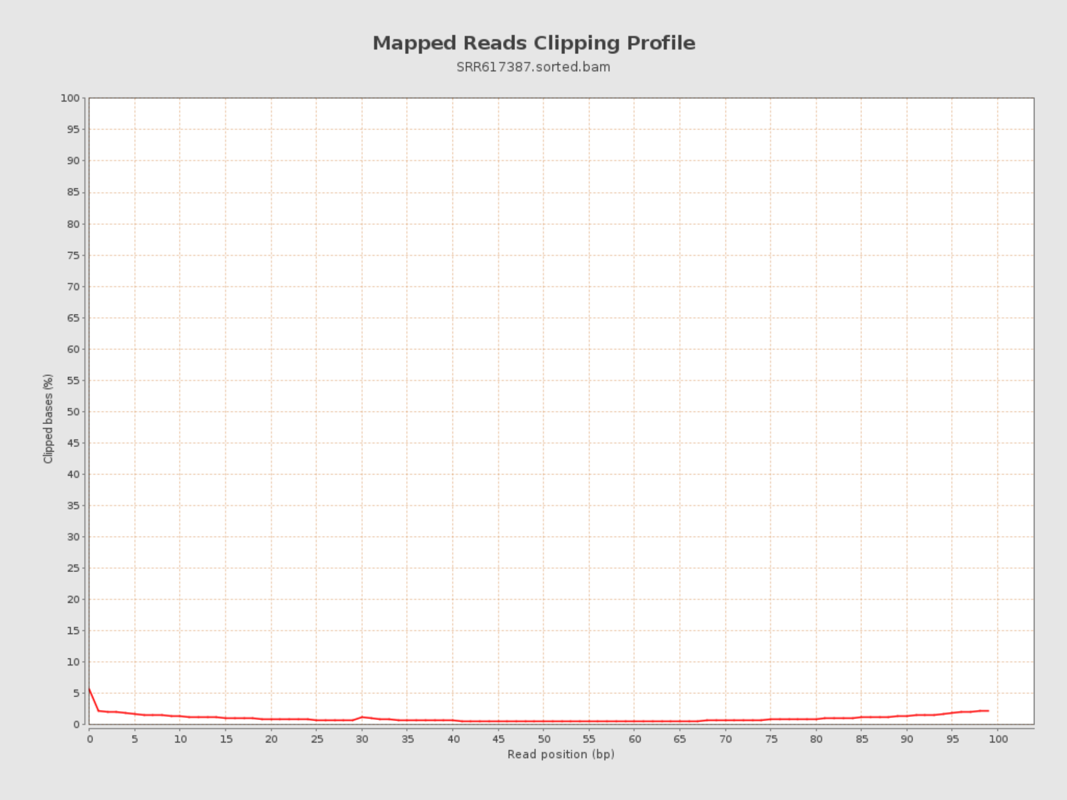
8. Results : Mapped Reads Nucleotide Content



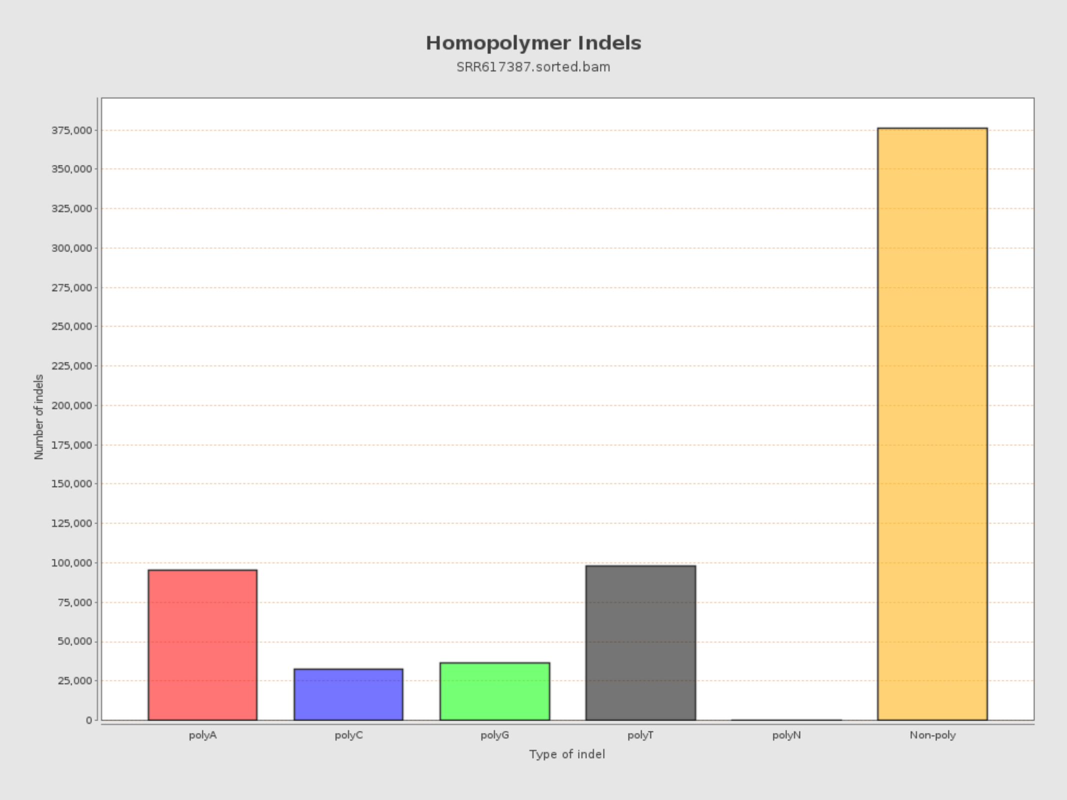
9. Results : Mapped Reads GC-content Distribution



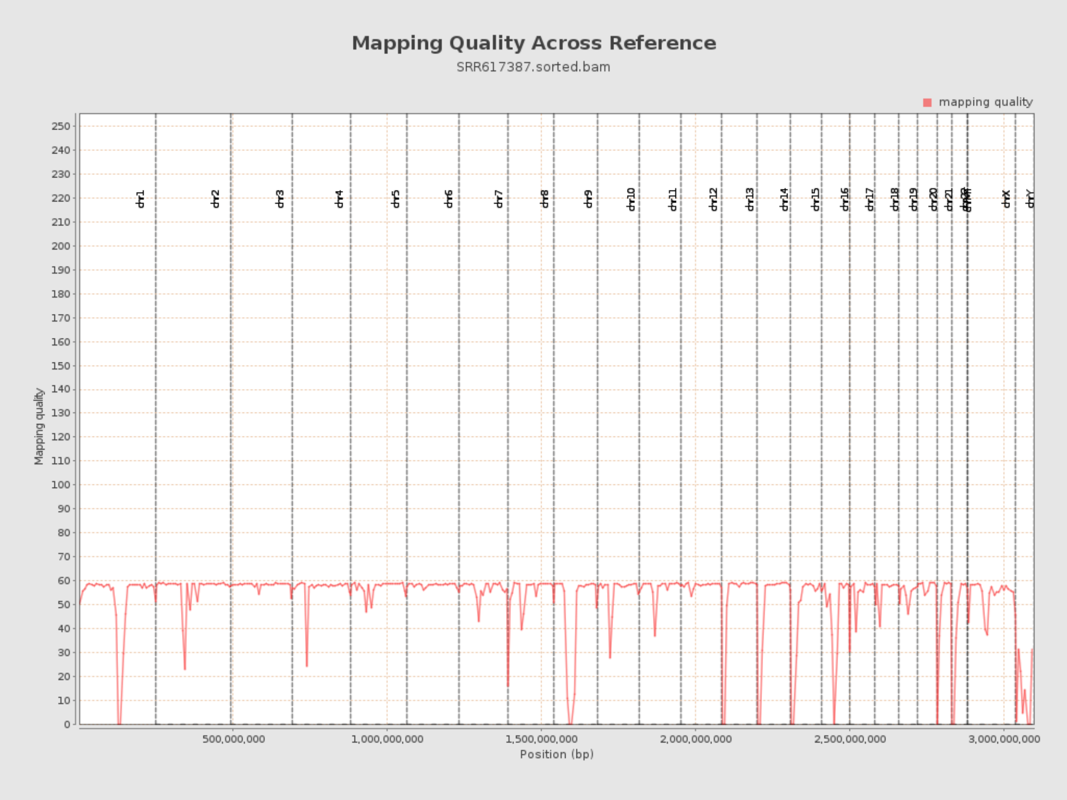
10. Results : Mapped Reads Clipping Profile



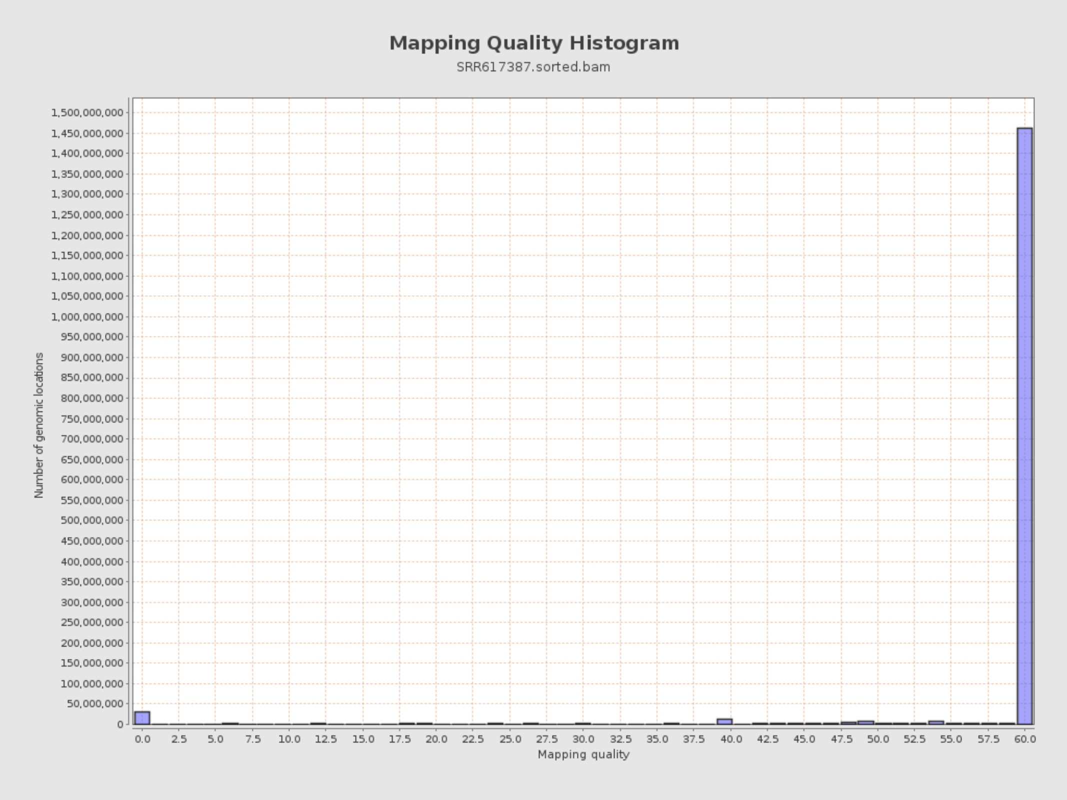
11. Results : Homopolymer Indels



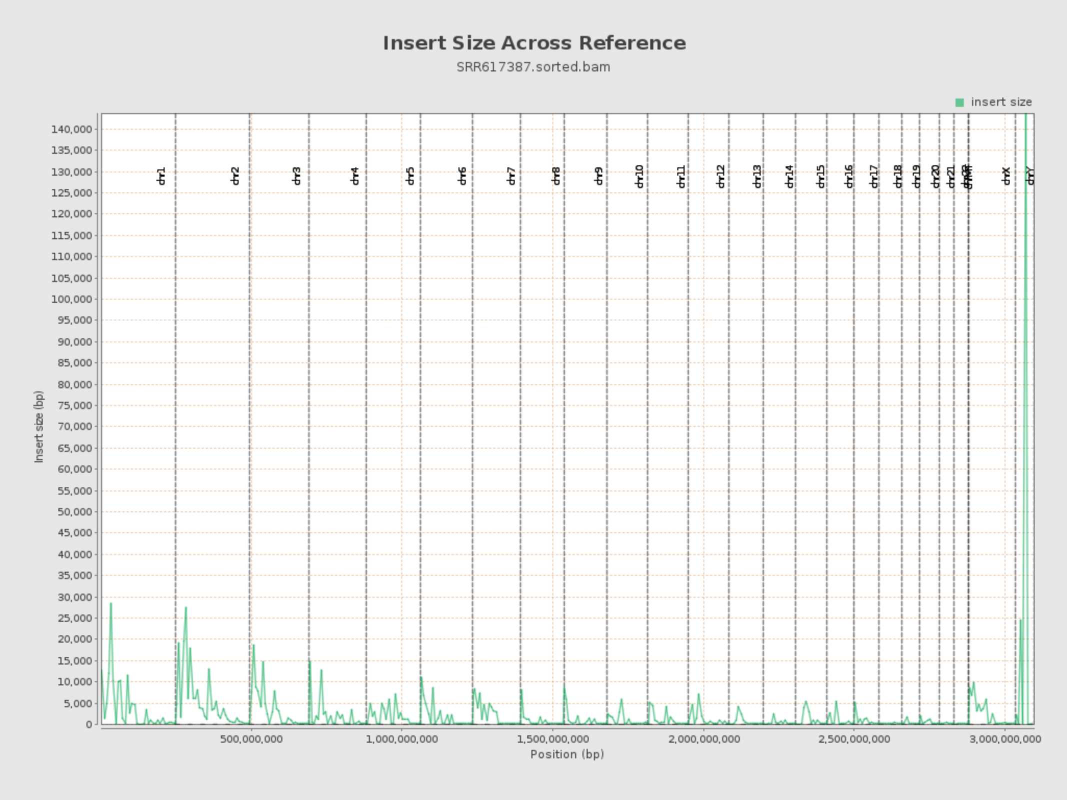
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram