Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 00:50:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617382.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_SRR617382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617382_1.fastq.gz SRR617382_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 00:50:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,303,628 / 91.57%
Unmapped reads	2,696,372 / 8.43%
Mapped paired reads	29,303,628 / 91.57%
Mapped reads, first in pair	14,916,864 / 46.62%
Mapped reads, second in pair	14,386,764 / 44.96%
Mapped reads, both in pair	28,430,410 / 88.85%
Mapped reads, singletons	873,218 / 2.73%
Secondary alignments	0
Supplementary alignments	88,455 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,490,165 / 4.66%
Duplication rate	1.5%
Clipped reads	2,876,900 / 8.99%

2.2. ACGT Content

Number/percentage of A's	865,874,388 / 30.34%
Number/percentage of C's	564,990,267 / 19.79%
Number/percentage of T's	857,782,299 / 30.05%
Number/percentage of G's	564,905,211 / 19.79%
Number/percentage of N's	770,019 / 0.03%

GC Percentage	39.59%

2.3. Coverage

Mean	0.9223
Standard Deviation	9.0513

2.4. Mapping Quality

Mean Mapping Quality	53.2

2.5. Insert size

Mean	66,998.92
Standard Deviation	2,497,488.46
P25/Median/P75	171 / 212 / 275

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	43,125,039
Insertions	320,801
Mapped reads with at least one insertion	1.06%
Deletions	375,130
Mapped reads with at least one deletion	1.24%
Homopolymer indels	40.53%

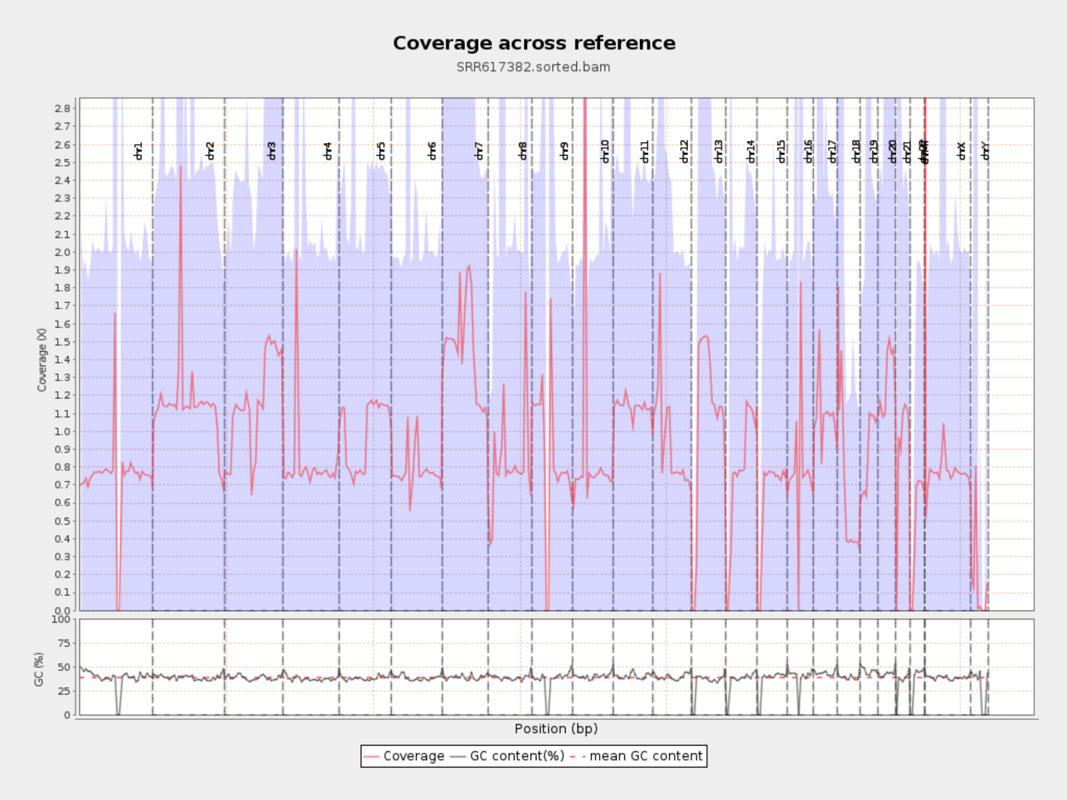
2.7. Chromosome stats

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

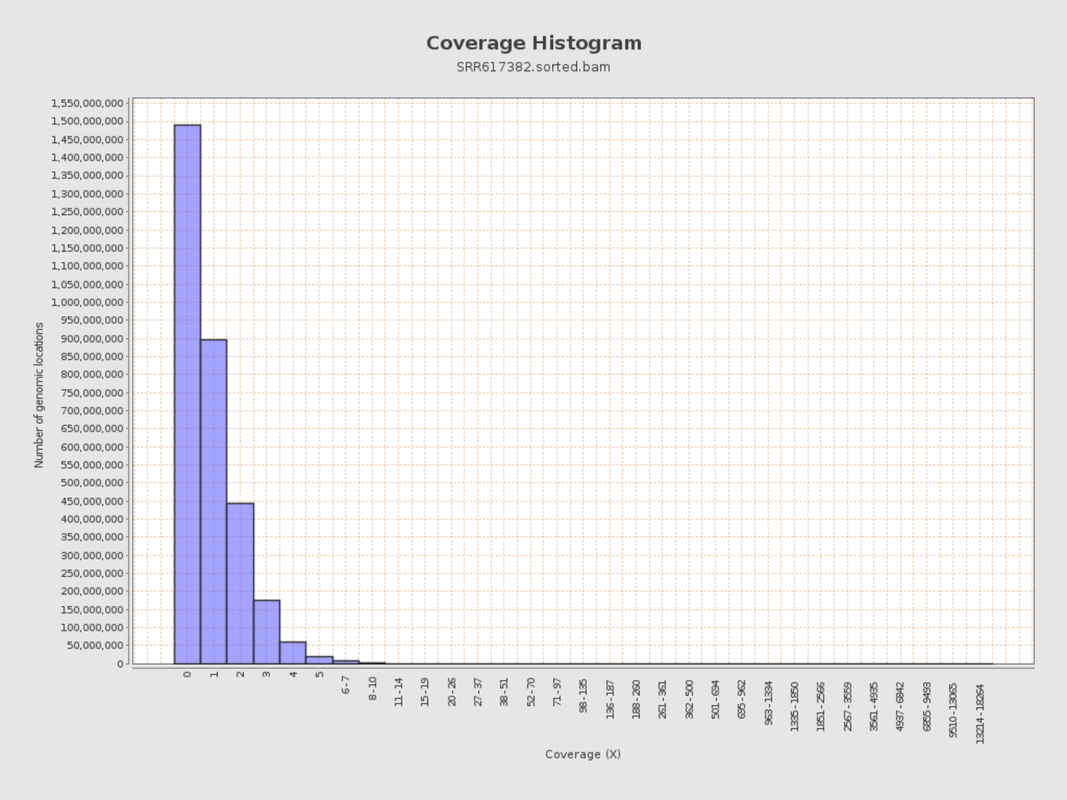
		bases	coverage	deviation
chr1	249250621	185132888	0.7428	18.5396
chr2	243199373	281730091	1.1584	8.0576
chr3	198022430	228057560	1.1517	1.4425
chr4	191154276	156357638	0.818	8.4521
chr5	180915260	179725358	0.9934	1.4146
chr6	171115067	134324981	0.785	3.4873
chr7	159138663	232374215	1.4602	10.4404
chr8	146364022	120320416	0.8221	6.9416
chr9	141213431	120054661	0.8502	13.2904
chr10	135534747	119447726	0.8813	18.619
chr11	135006516	152972148	1.1331	5.1299
chr12	133851895	126173265	0.9426	1.3345
chr13	115169878	125154863	1.0867	1.3009
chr14	107349540	82562278	0.7691	1.3504
chr15	102531392	64183388	0.626	1.0396
chr16	90354753	71704521	0.7936	7.6376
chr17	81195210	88383779	1.0885	6.6067
chr18	78077248	51346364	0.6576	14.0618
chr19	59128983	52519776	0.8882	9.0894
chr20	63025520	81181174	1.2881	2.3046
chr21	48129895	45460189	0.9445	3.0199
chr22	51304566	25181138	0.4908	0.8913
chrMT	16571	1977507	119.3354	22.291
chrX	155270560	119337459	0.7686	2.8454

chrY	59373566	9555618	0.1609	7.5672

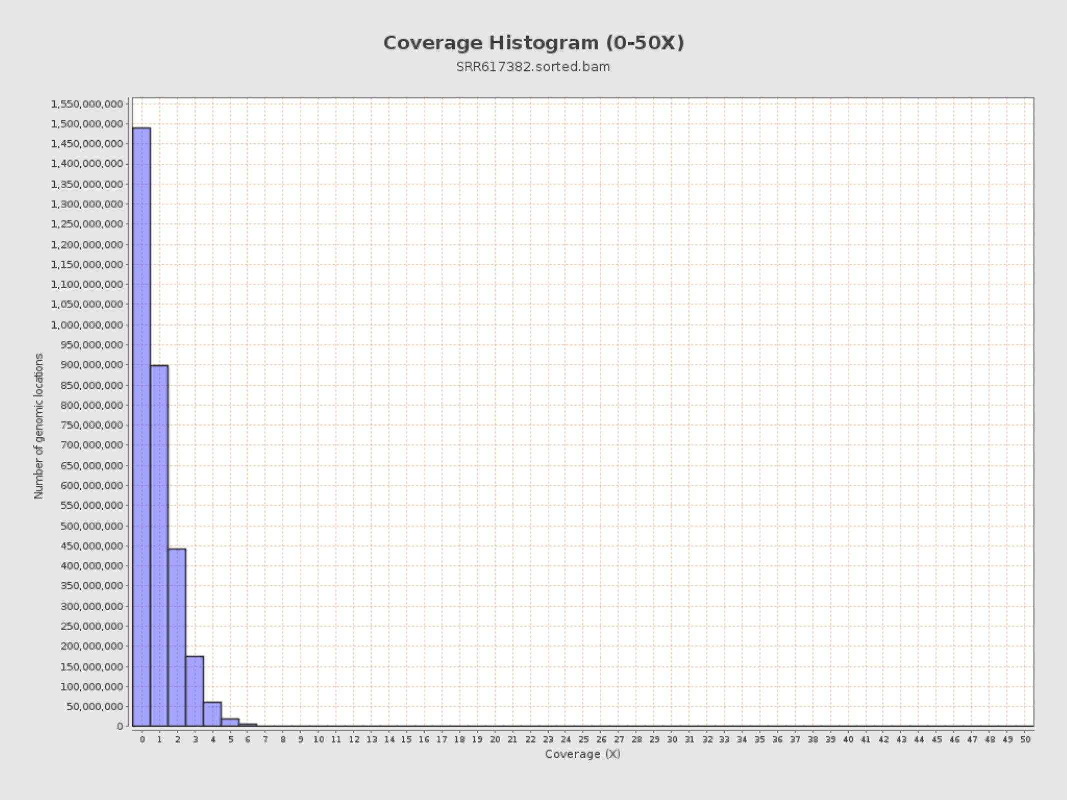
3. Results : Coverage across reference



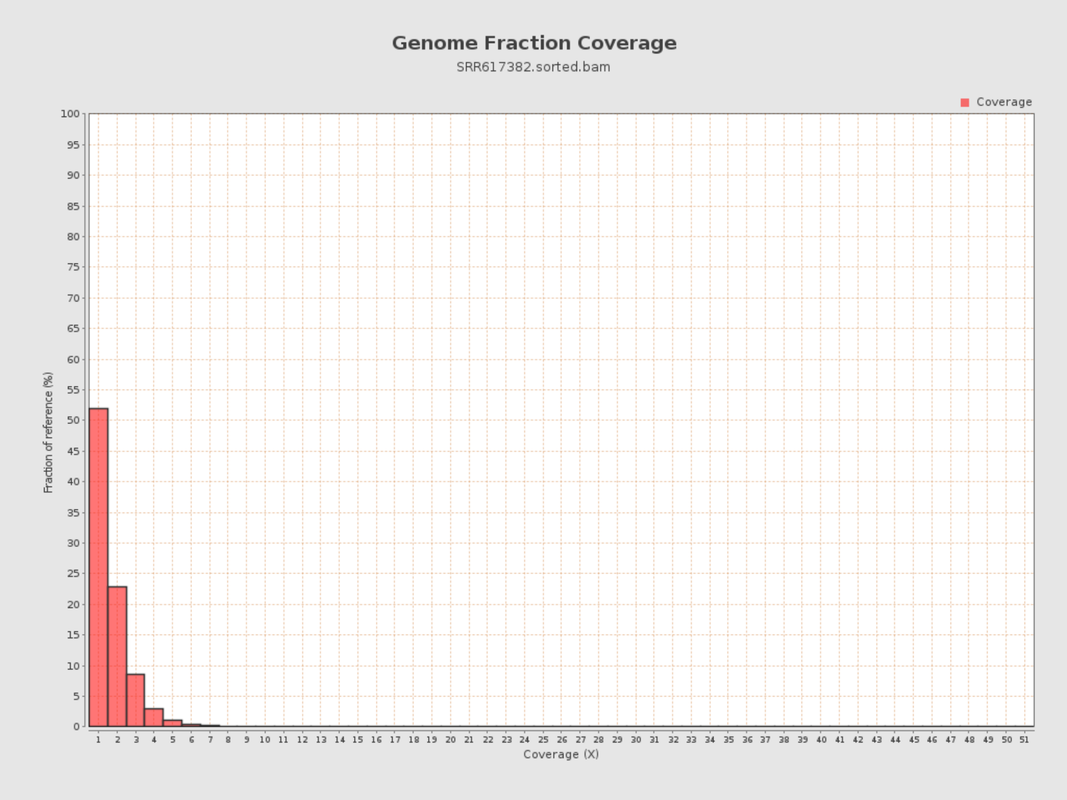
4. Results : Coverage Histogram



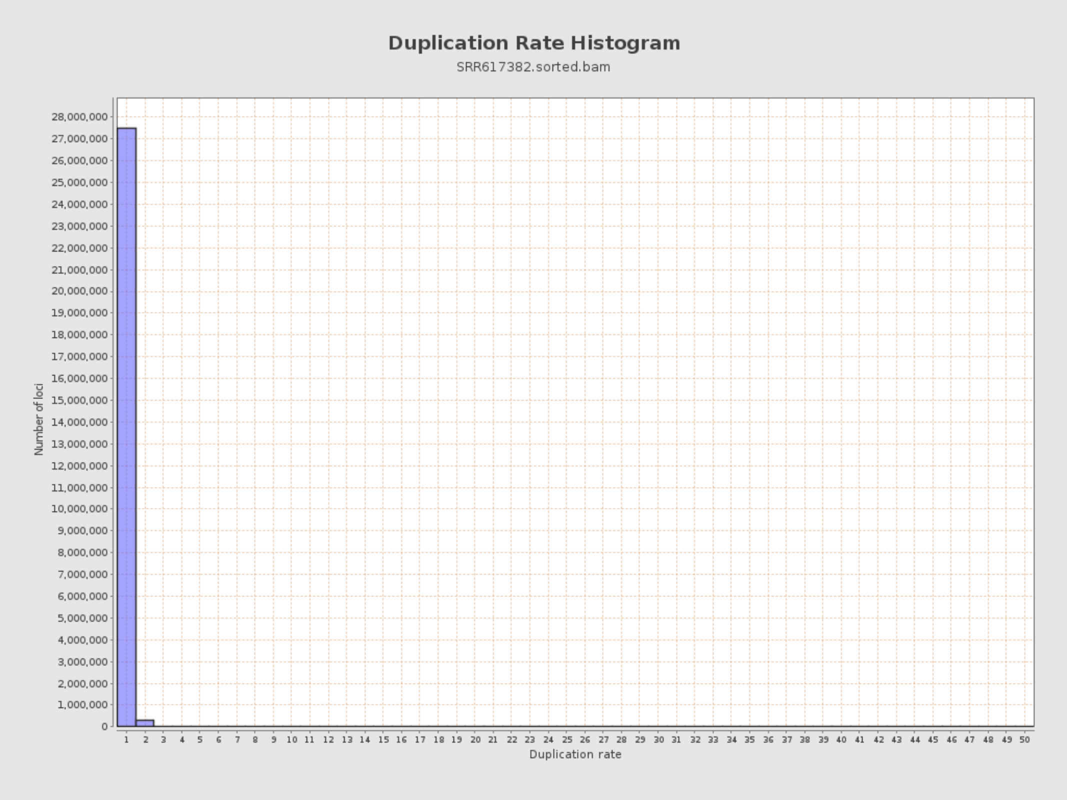
5. Results : Coverage Histogram (0-50X)



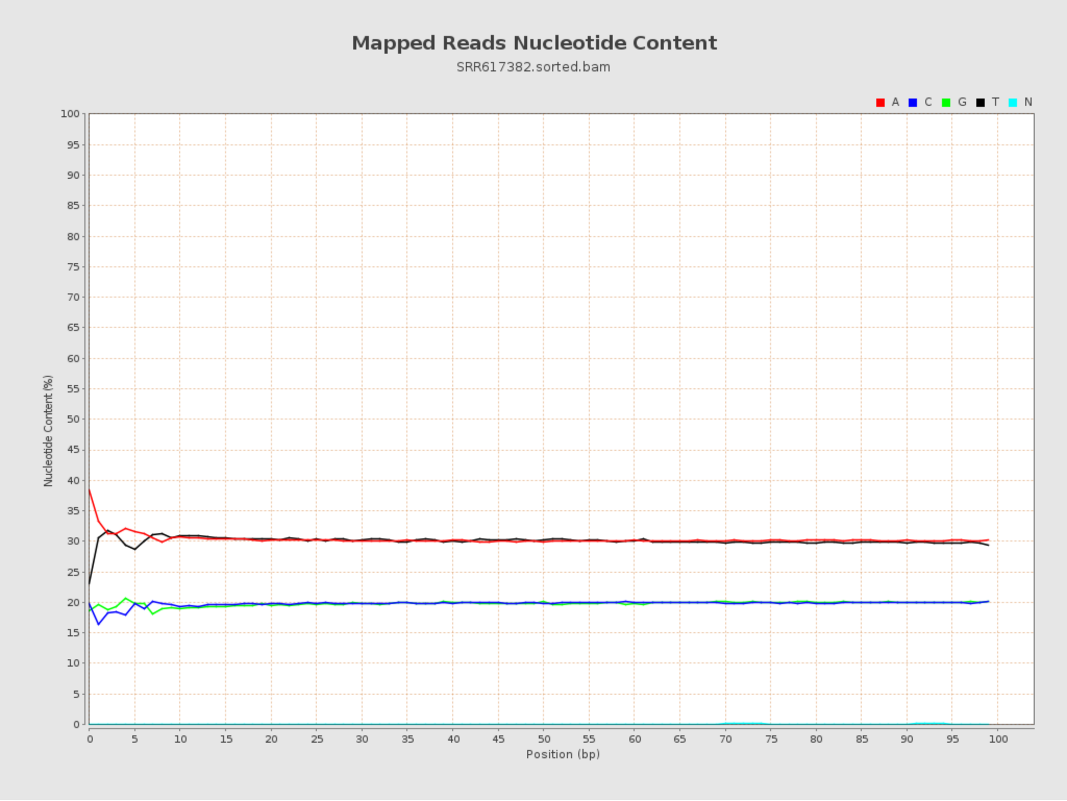
6. Results : Genome Fraction Coverage



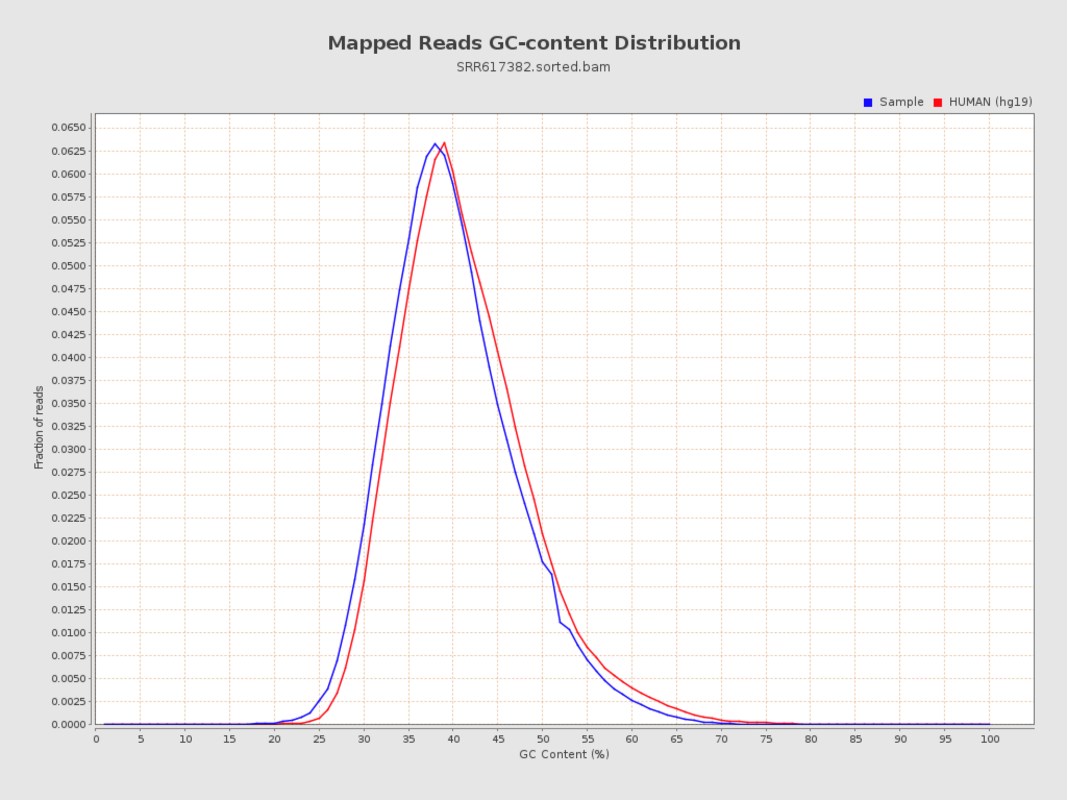
7. Results : Duplication Rate Histogram



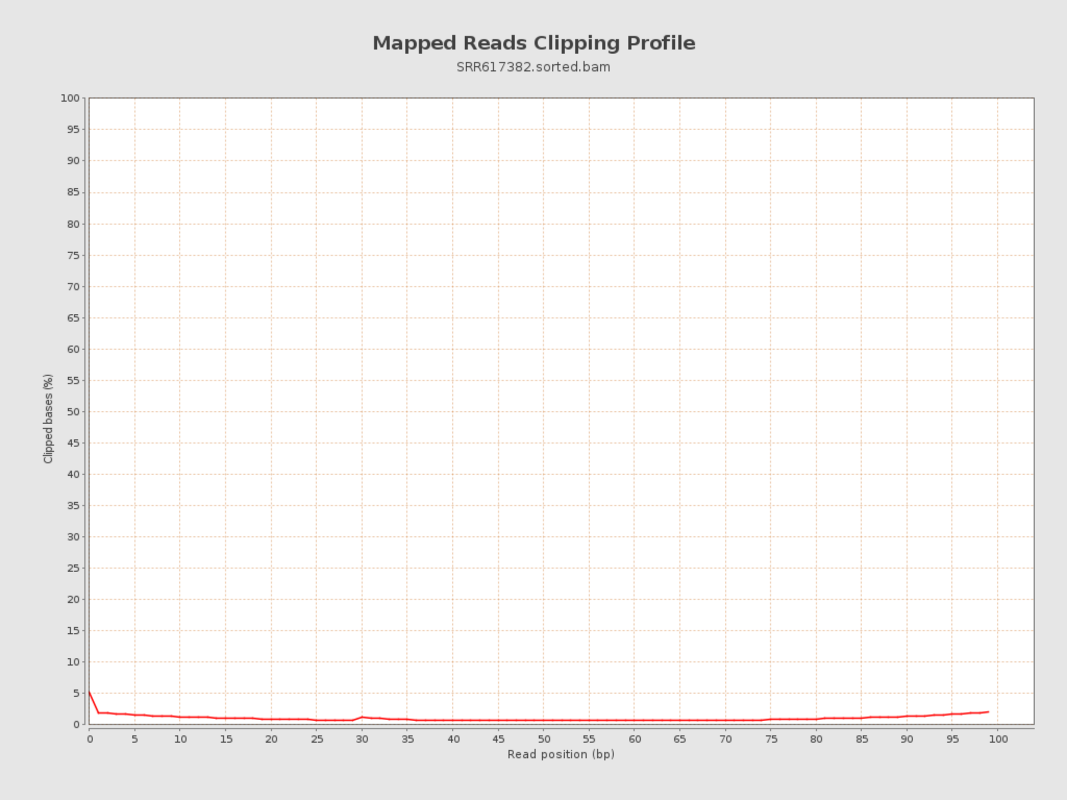
8. Results : Mapped Reads Nucleotide Content



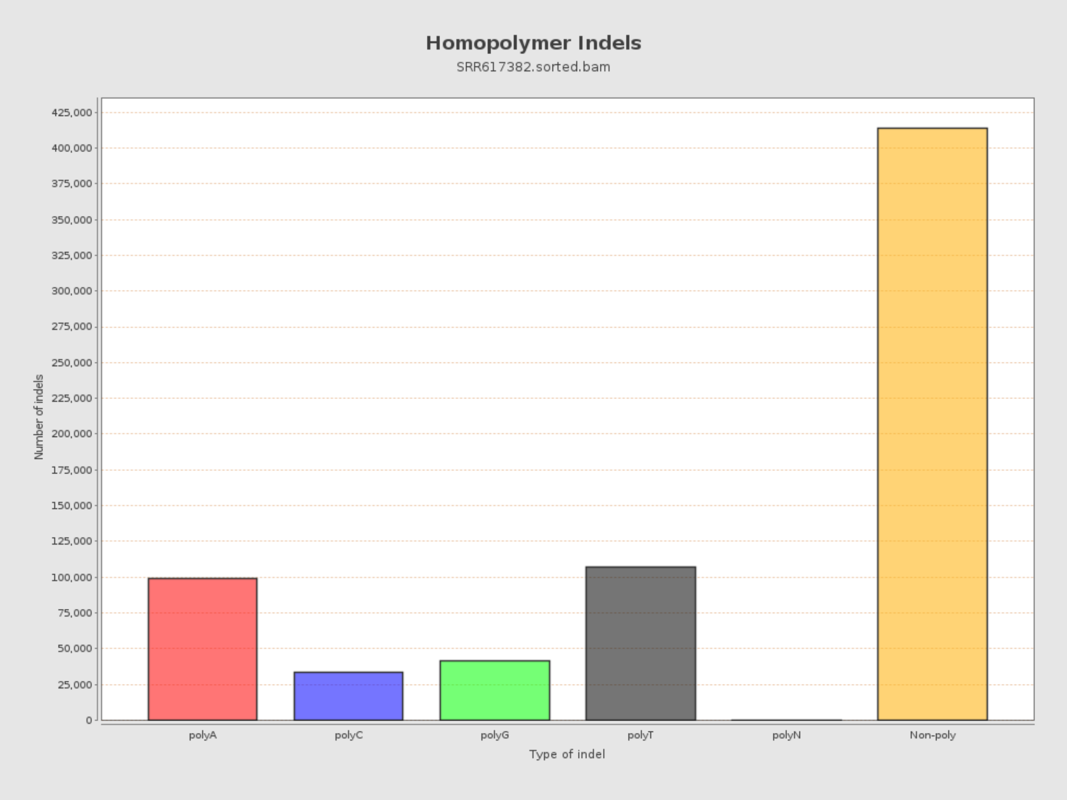
9. Results : Mapped Reads GC-content Distribution



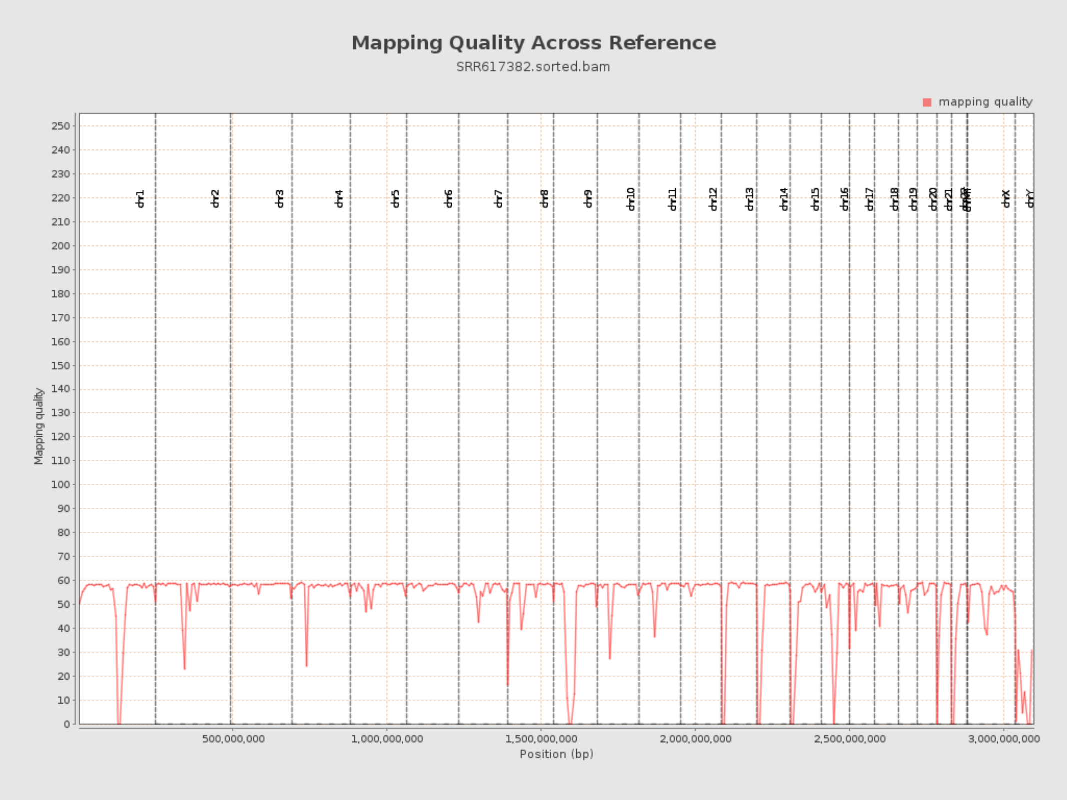
10. Results : Mapped Reads Clipping Profile



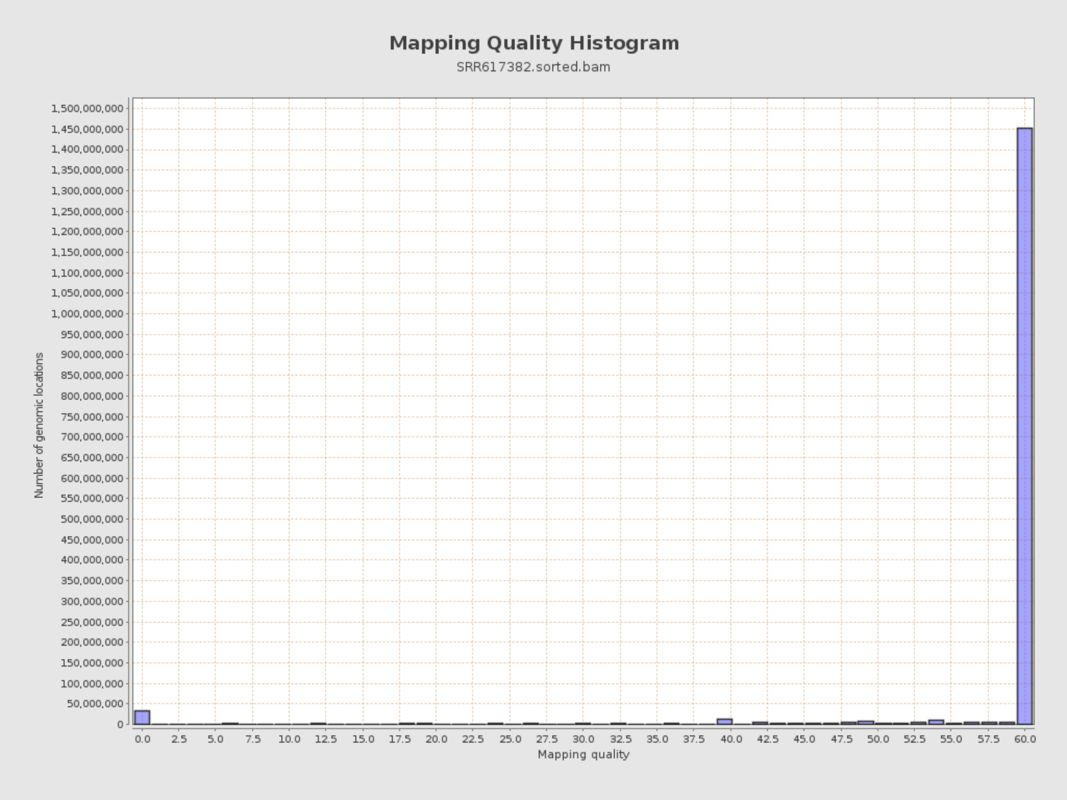
11. Results : Homopolymer Indels



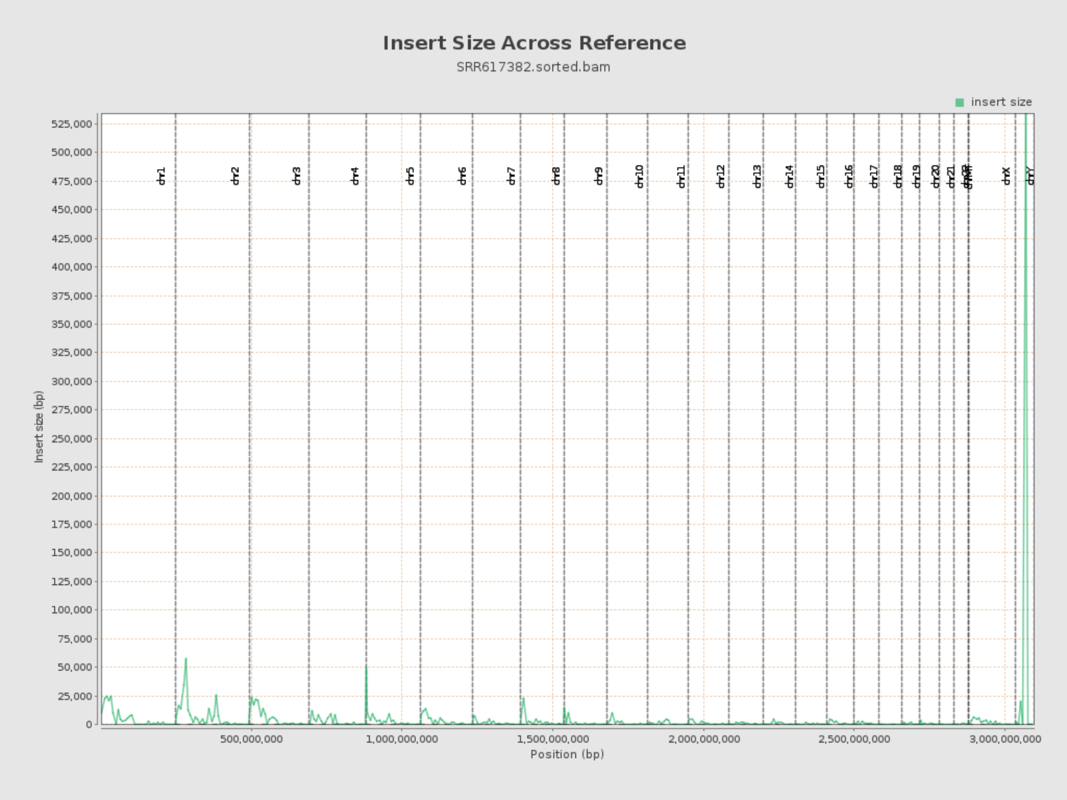
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram