Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 16:53:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926917.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_SRR926917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926917_1.fastq.gz SRR926917_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 16:53:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,092,888
Mapped reads	28,200,032 / 93.71%
Unmapped reads	1,892,856 / 6.29%
Mapped paired reads	28,200,032 / 93.71%
Mapped reads, first in pair	14,207,887 / 47.21%
Mapped reads, second in pair	13,992,145 / 46.5%
Mapped reads, both in pair	27,815,496 / 92.43%
Mapped reads, singletons	384,536 / 1.28%
Secondary alignments	0
Supplementary alignments	248,077 / 0.82%
Read min/max/mean length	30 / 101 / 101.34
Duplicated reads (estimated)	2,104,555 / 6.99%
Duplication rate	5.85%
Clipped reads	8,018,525 / 26.65%

2.2. ACGT Content

Number/percentage of A's	750,784,021 / 28.48%
Number/percentage of C's	527,627,182 / 20.01%
Number/percentage of T's	756,874,924 / 28.71%
Number/percentage of G's	601,060,562 / 22.8%
Number/percentage of N's	249,061 / 0.01%

GC Percentage	42.81%

2.3. Coverage

Mean	0.8524
Standard Deviation	3.5564

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	109,392.52
Standard Deviation	3,286,096.4
P25/Median/P75	149 / 192 / 257

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	27,257,099
Insertions	421,230
Mapped reads with at least one insertion	1.47%
Deletions	1,450,733
Mapped reads with at least one deletion	5.01%
Homopolymer indels	53.04%

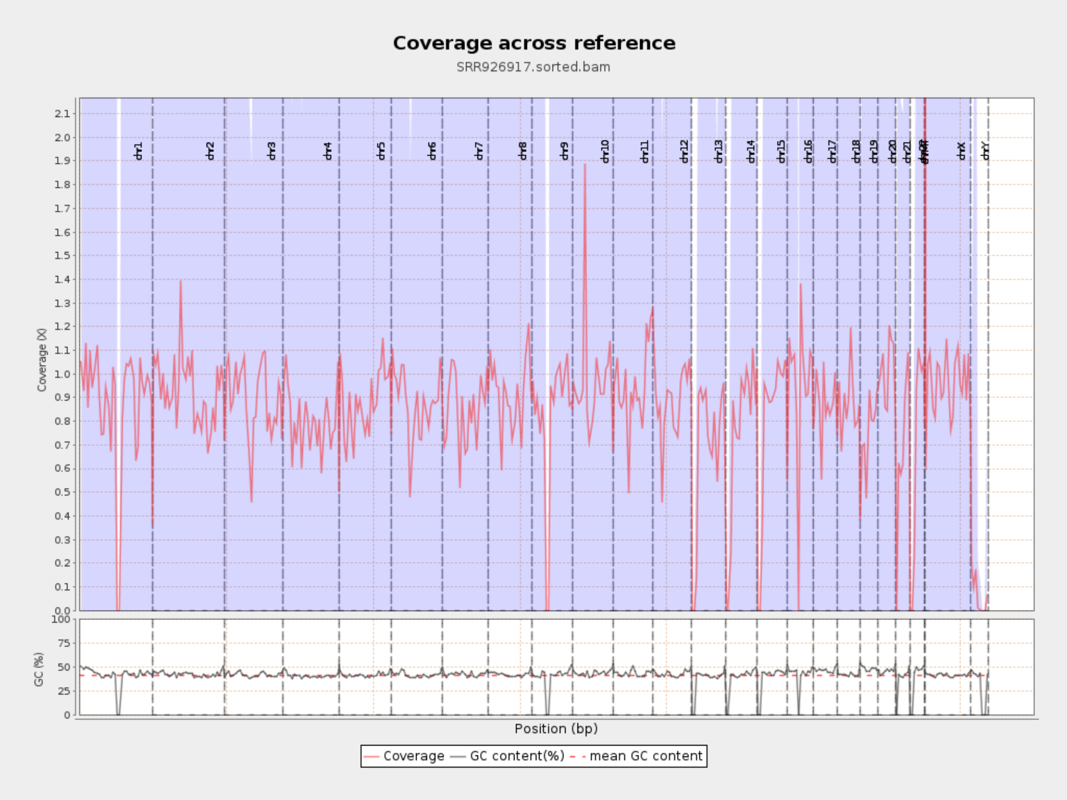
2.7. Chromosome stats

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

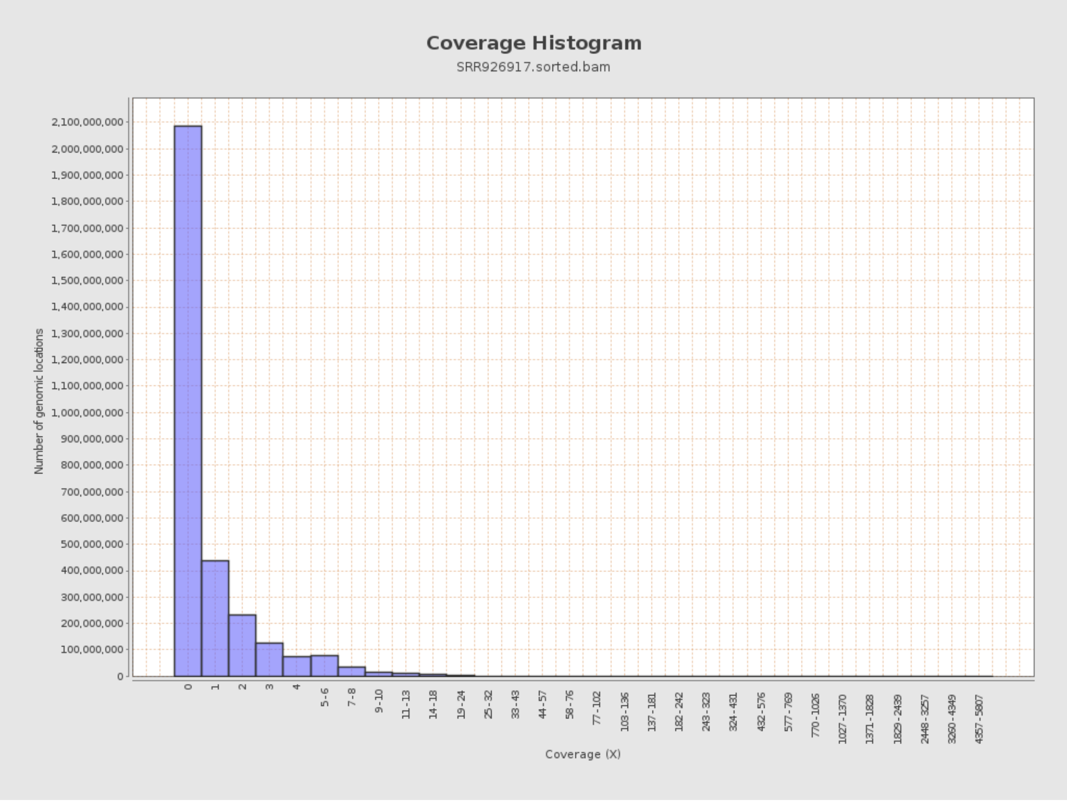
		bases	coverage	deviation
chr1	249250621	217499058	0.8726	3.1281
chr2	243199373	226736710	0.9323	4.6664
chr3	198022430	177277997	0.8952	1.9181
chr4	191154276	153288783	0.8019	1.9223
chr5	180915260	159656922	0.8825	1.8227
chr6	171115067	150167451	0.8776	1.8278
chr7	159138663	135210833	0.8496	2.1212
chr8	146364022	134093950	0.9162	2.1362
chr9	141213431	115269948	0.8163	3.6221
chr10	135534747	133265270	0.9833	11.5558
chr11	135006516	126515086	0.9371	2.3847
chr12	133851895	118994772	0.889	1.9109
chr13	115169878	78262455	0.6795	1.6108
chr14	107349540	78665292	0.7328	1.7585
chr15	102531392	79902600	0.7793	1.8578
chr16	90354753	84828168	0.9388	4.675
chr17	81195210	70339897	0.8663	2.0992
chr18	78077248	69371201	0.8885	3.5962
chr19	59128983	43702660	0.7391	2.1538
chr20	63025520	64222987	1.019	2.1714
chr21	48129895	34035395	0.7072	2.5472
chr22	51304566	35115901	0.6845	1.7853
chrMT	16571	174793	10.5481	7.3724
chrX	155270560	148279553	0.955	2.0424

chrY	59373566	3764112	0.0634	1.5267

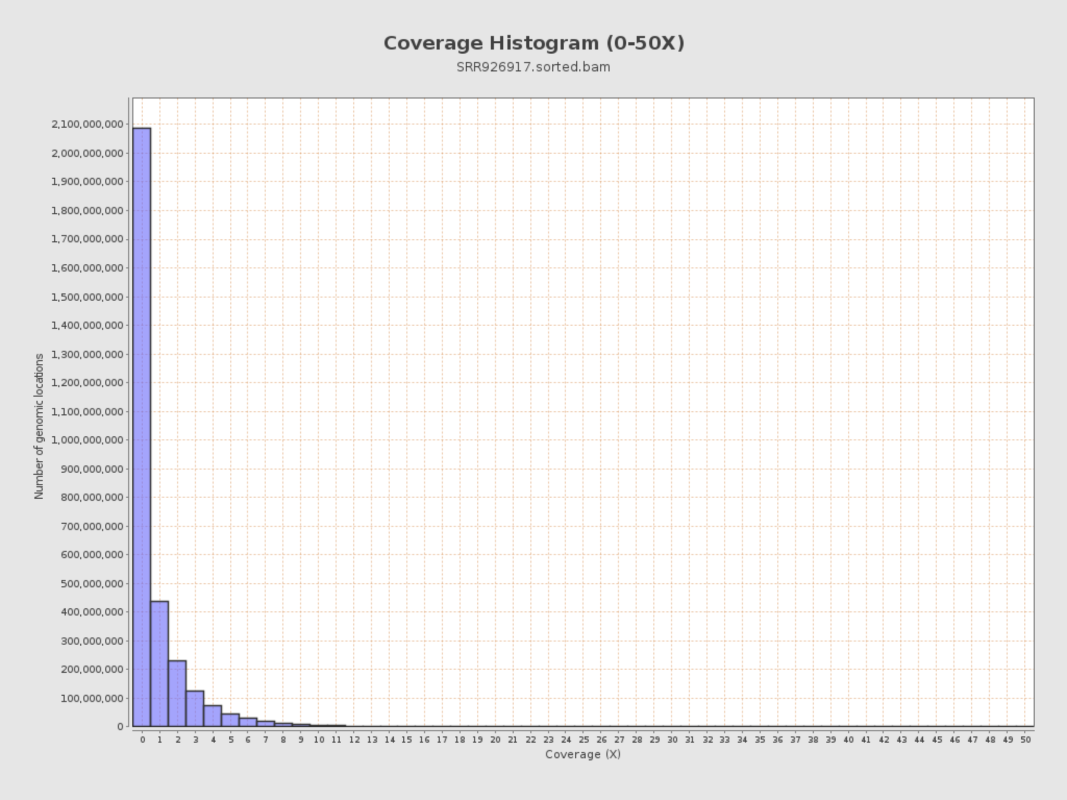
3. Results : Coverage across reference



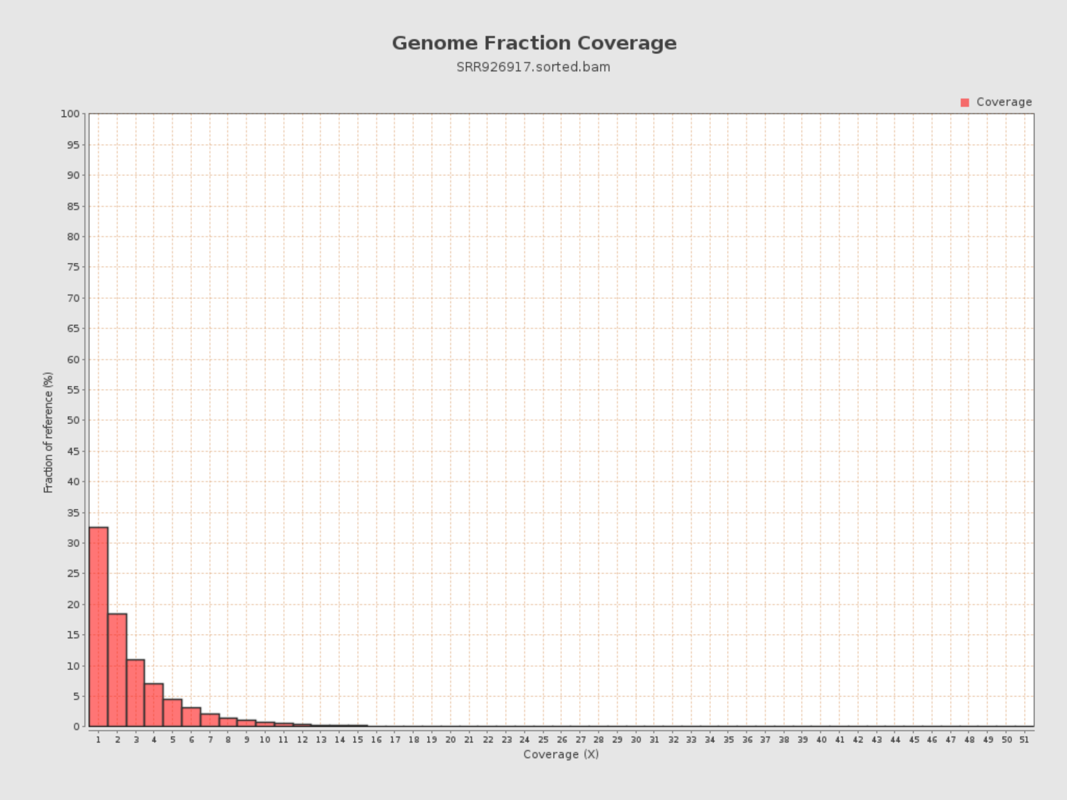
4. Results : Coverage Histogram



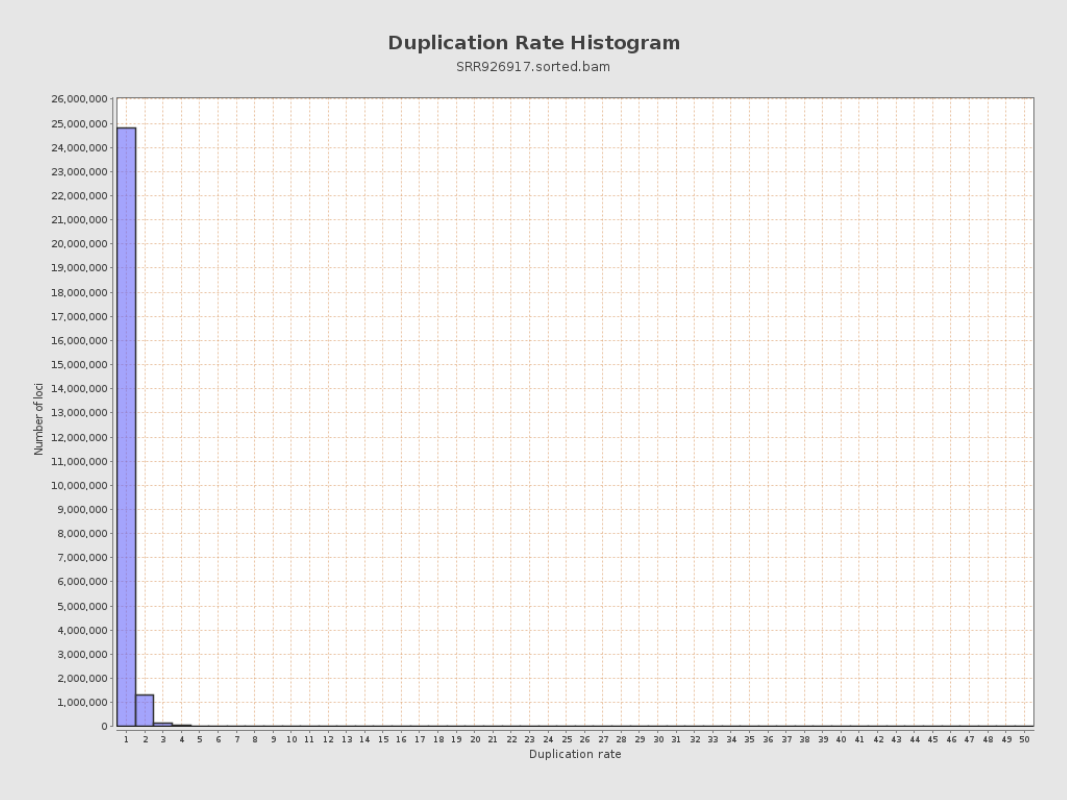
5. Results : Coverage Histogram (0-50X)



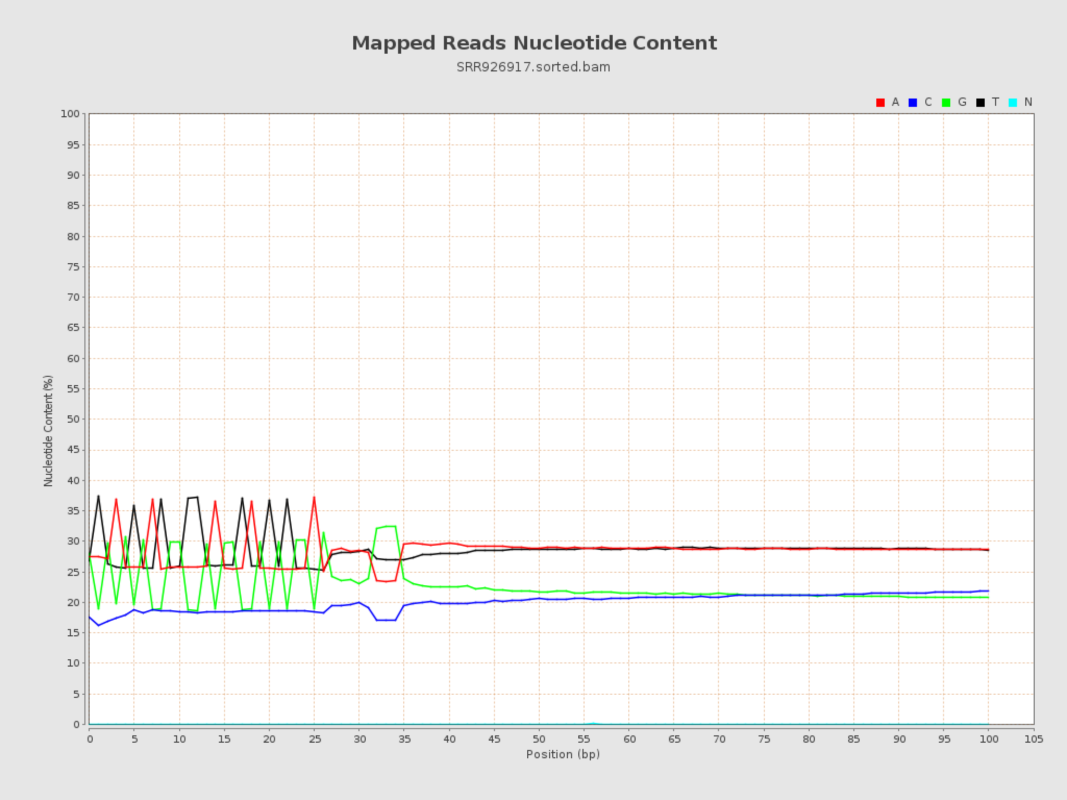
6. Results : Genome Fraction Coverage



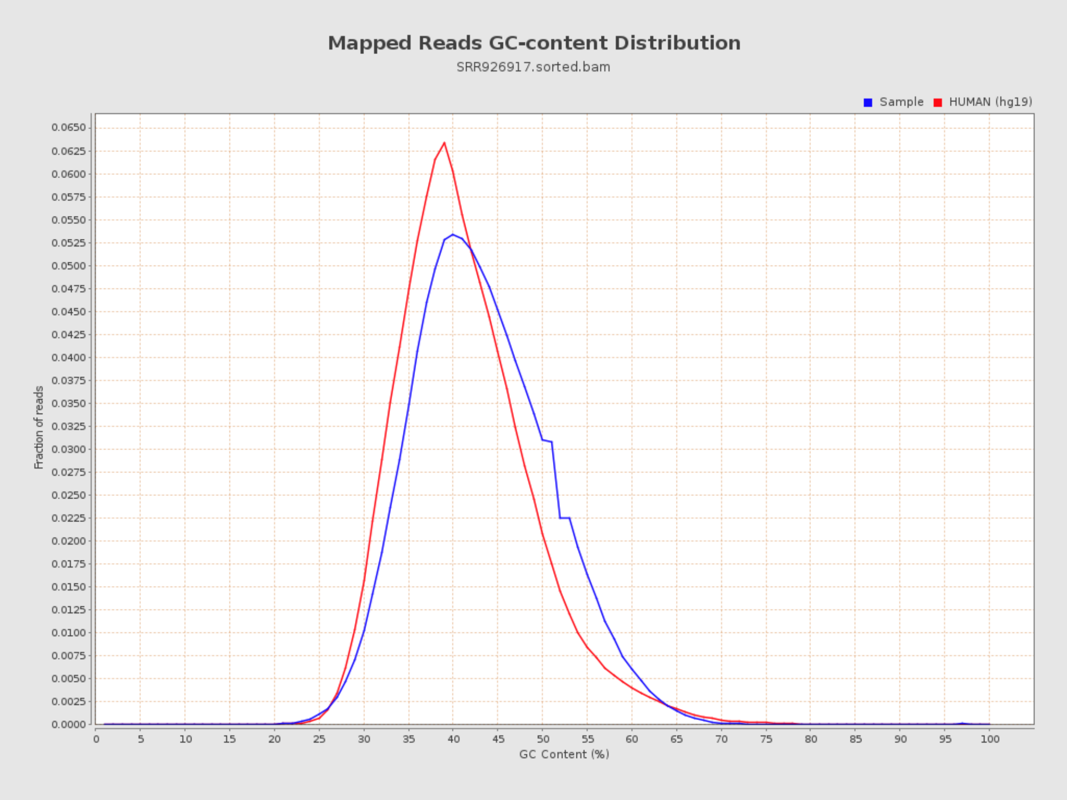
7. Results : Duplication Rate Histogram



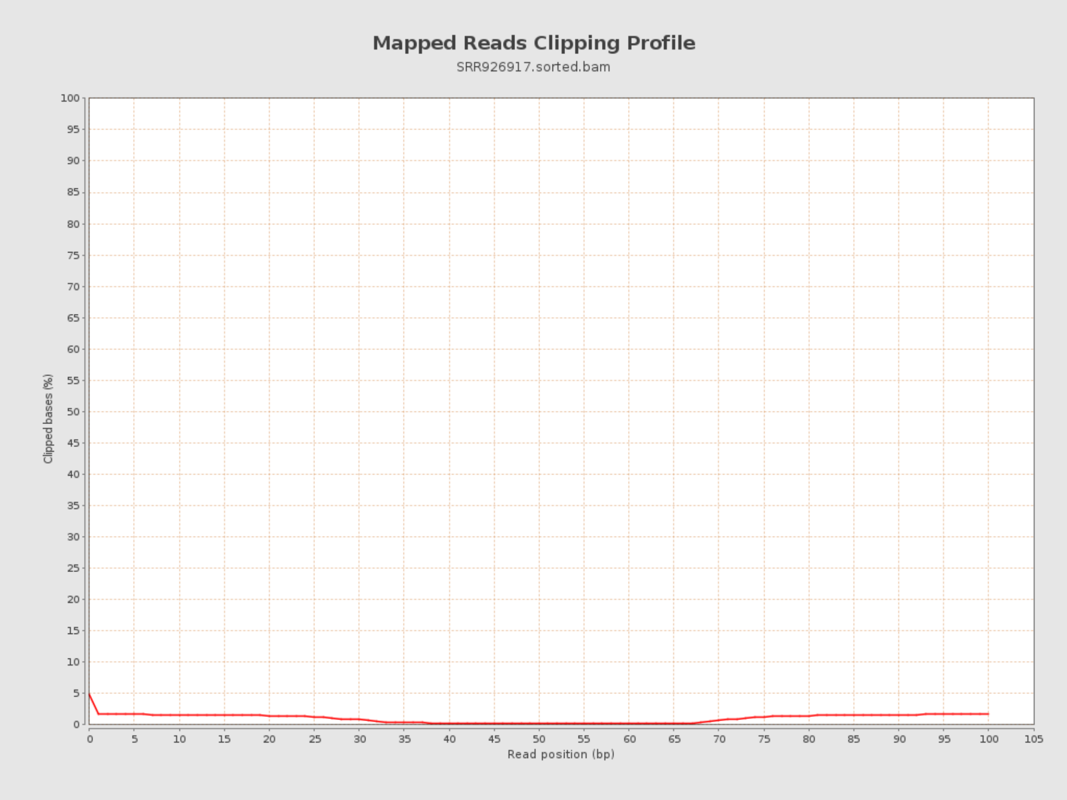
8. Results : Mapped Reads Nucleotide Content



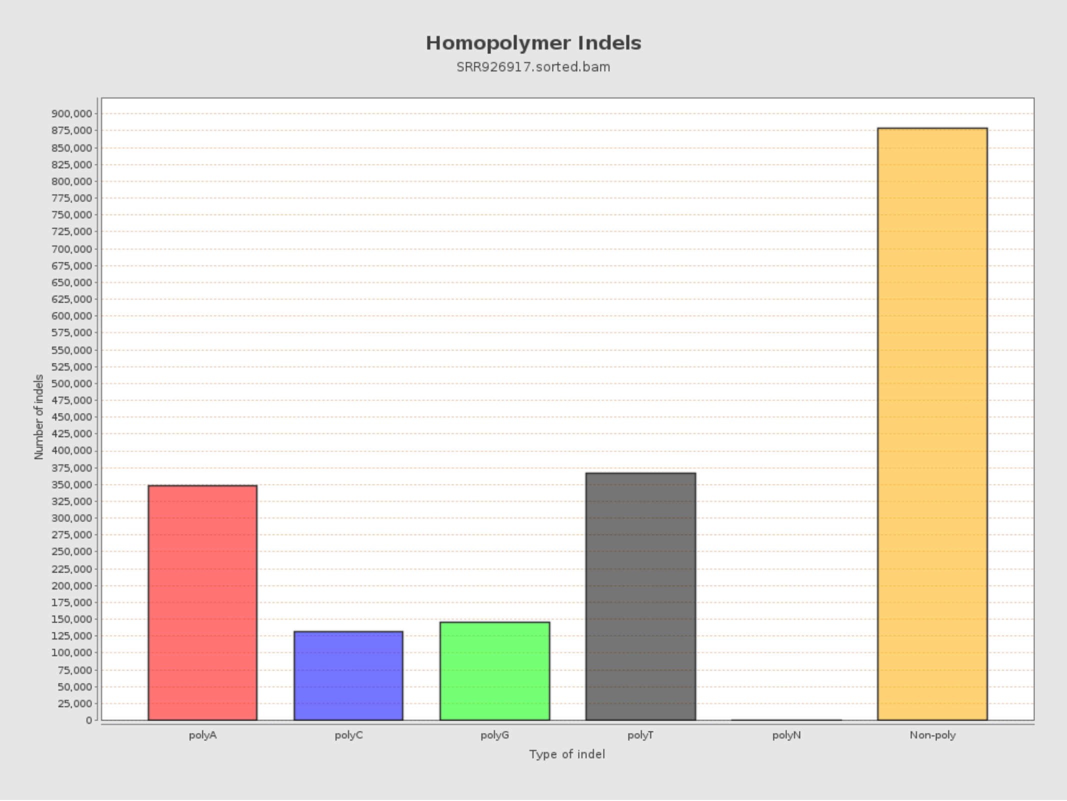
9. Results : Mapped Reads GC-content Distribution



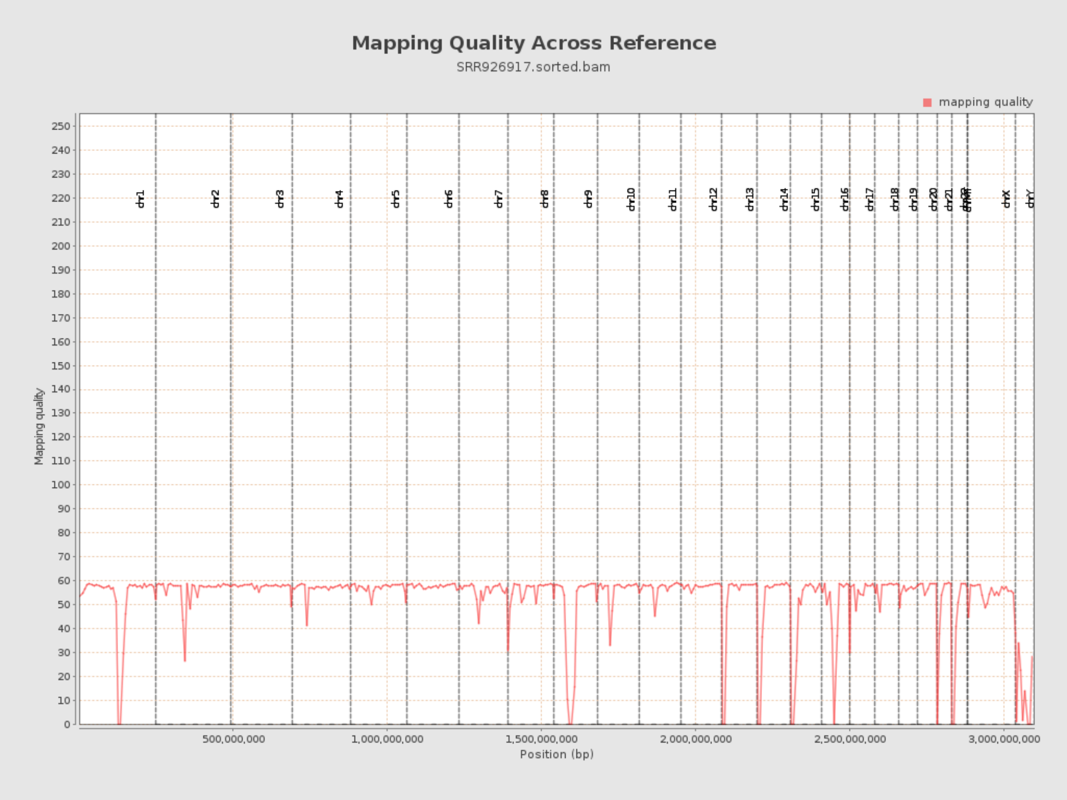
10. Results : Mapped Reads Clipping Profile



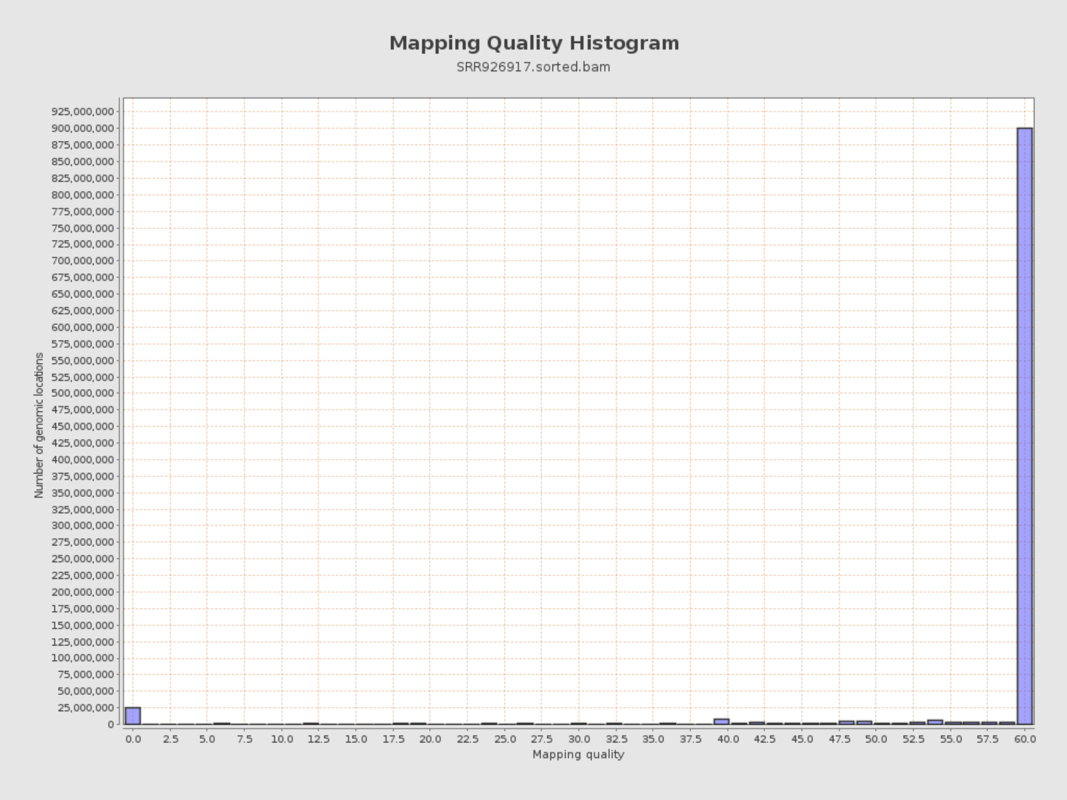
11. Results : Homopolymer Indels



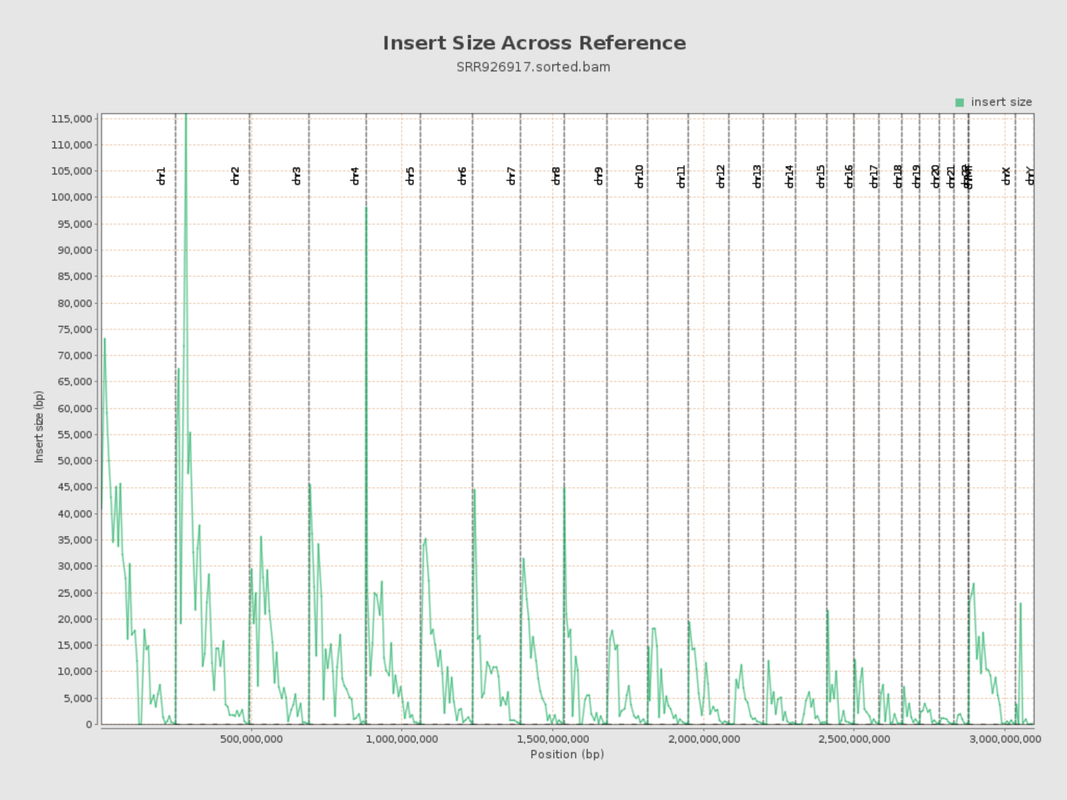
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram