Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 15:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926914.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_SRR926914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926914_1.fastq.gz SRR926914_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 15:06:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,674,908
Mapped reads	28,289,177 / 92.22%
Unmapped reads	2,385,731 / 7.78%
Mapped paired reads	28,289,177 / 92.22%
Mapped reads, first in pair	14,214,940 / 46.34%
Mapped reads, second in pair	14,074,237 / 45.88%
Mapped reads, both in pair	27,967,830 / 91.17%
Mapped reads, singletons	321,347 / 1.05%
Secondary alignments	0
Supplementary alignments	274,305 / 0.89%
Read min/max/mean length	30 / 101 / 101.36
Duplicated reads (estimated)	1,916,776 / 6.25%
Duplication rate	5.41%
Clipped reads	7,290,227 / 23.77%

2.2. ACGT Content

Number/percentage of A's	758,176,638 / 28.41%
Number/percentage of C's	540,389,199 / 20.25%
Number/percentage of T's	763,505,131 / 28.61%
Number/percentage of G's	605,966,631 / 22.71%
Number/percentage of N's	261,081 / 0.01%

GC Percentage	42.96%

2.3. Coverage

Mean	0.8626
Standard Deviation	3.3821

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	112,973.82
Standard Deviation	3,275,517.75
P25/Median/P75	152 / 194 / 257

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	27,201,879
Insertions	425,424
Mapped reads with at least one insertion	1.48%
Deletions	1,454,200
Mapped reads with at least one deletion	5%
Homopolymer indels	52.92%

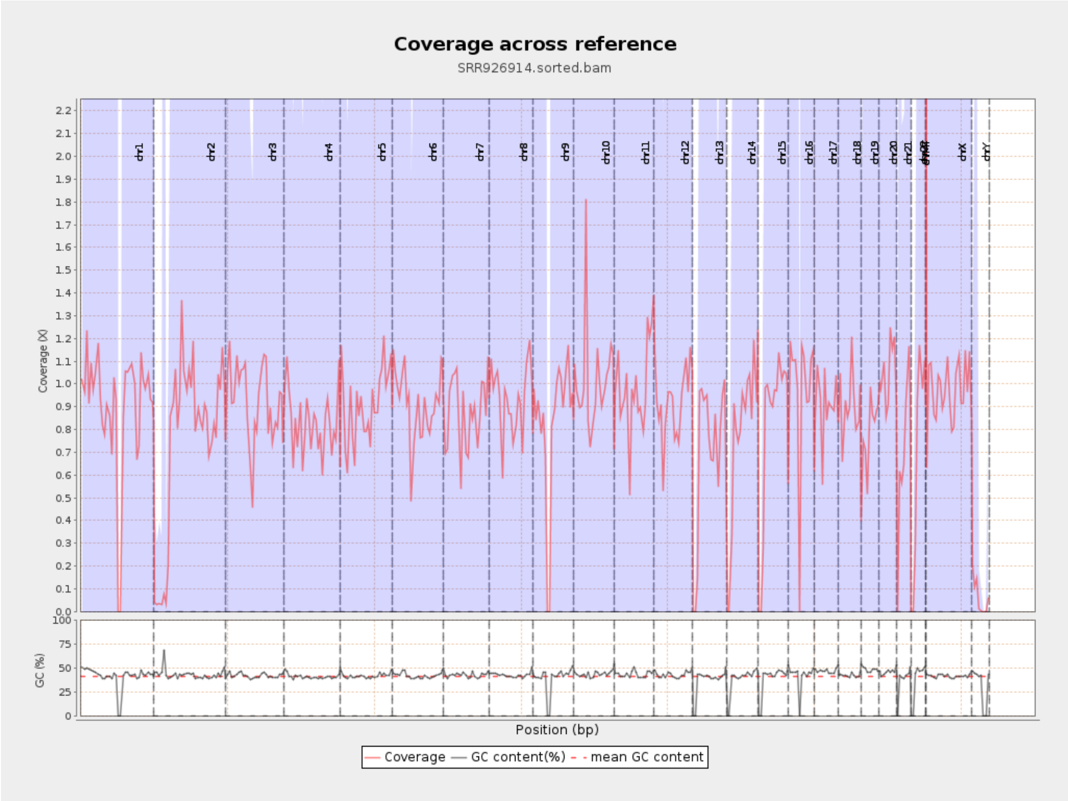
2.7. Chromosome stats

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

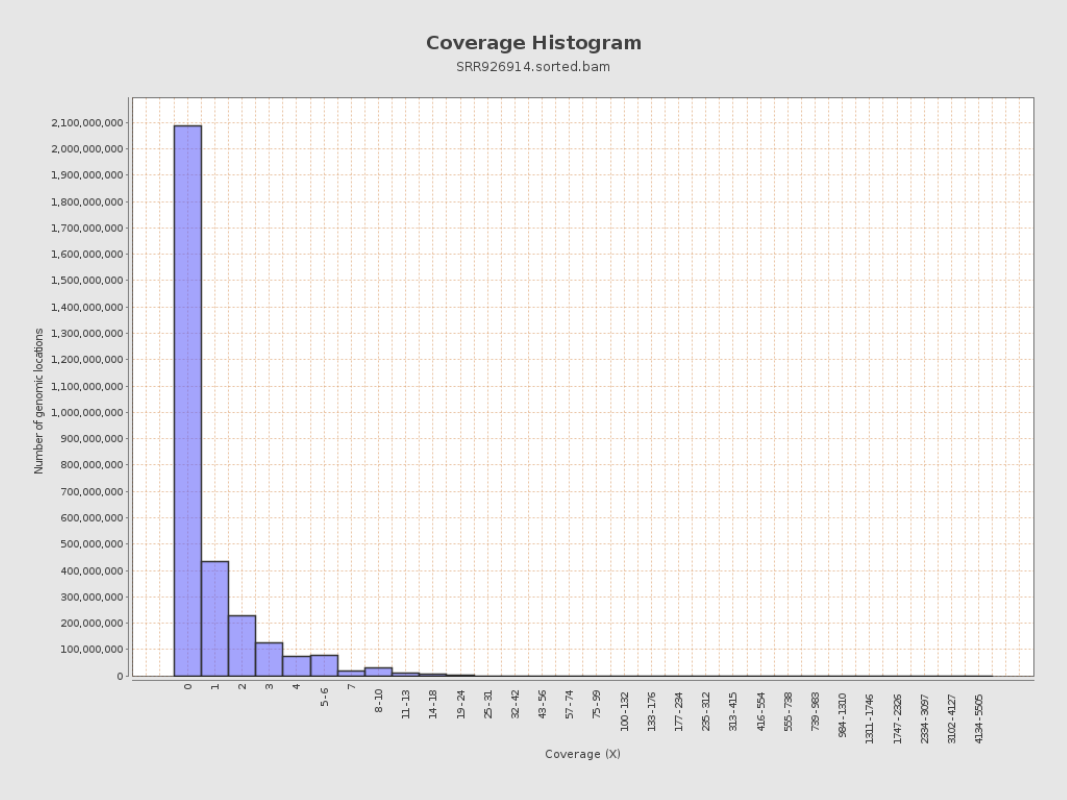
		bases	coverage	deviation
chr1	249250621	225302118	0.9039	3.0038
chr2	243199373	182672368	0.7511	4.1791
chr3	198022430	183528805	0.9268	1.9565
chr4	191154276	158292337	0.8281	2.044
chr5	180915260	164887627	0.9114	1.8893
chr6	171115067	155605275	0.9094	2.315
chr7	159138663	139157812	0.8744	2.1836
chr8	146364022	136809120	0.9347	2.1047
chr9	141213431	116968884	0.8283	3.2737
chr10	135534747	138434230	1.0214	10.8624
chr11	135006516	131010206	0.9704	2.3779
chr12	133851895	122880495	0.918	1.9714
chr13	115169878	80928958	0.7027	1.6512
chr14	107349540	82113455	0.7649	1.797
chr15	102531392	82521701	0.8048	1.9007
chr16	90354753	86399132	0.9562	3.8446
chr17	81195210	73523616	0.9055	2.1815
chr18	78077248	71605618	0.9171	3.3864
chr19	59128983	46008120	0.7781	2.1948
chr20	63025520	66178401	1.05	2.2781
chr21	48129895	34998535	0.7272	2.7099
chr22	51304566	36439975	0.7103	1.8754
chrMT	16571	160746	9.7004	6.6397
chrX	155270560	150353894	0.9683	2.0465

chrY	59373566	3572812	0.0602	1.2273

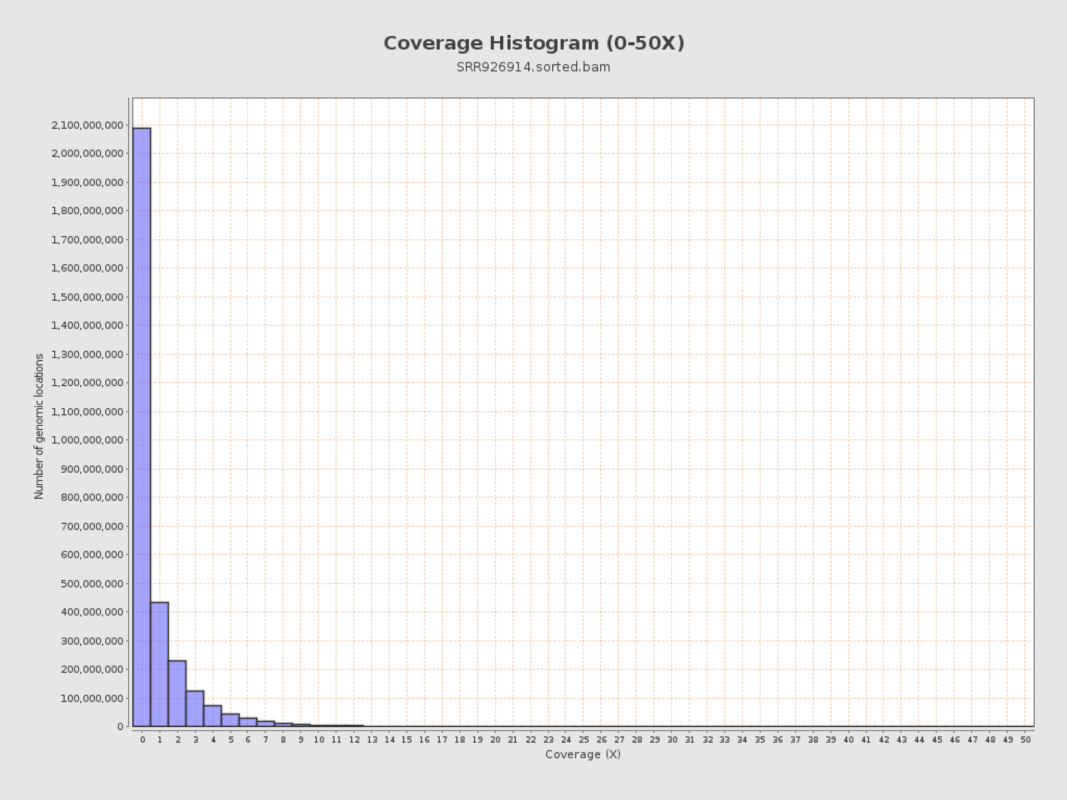
3. Results : Coverage across reference



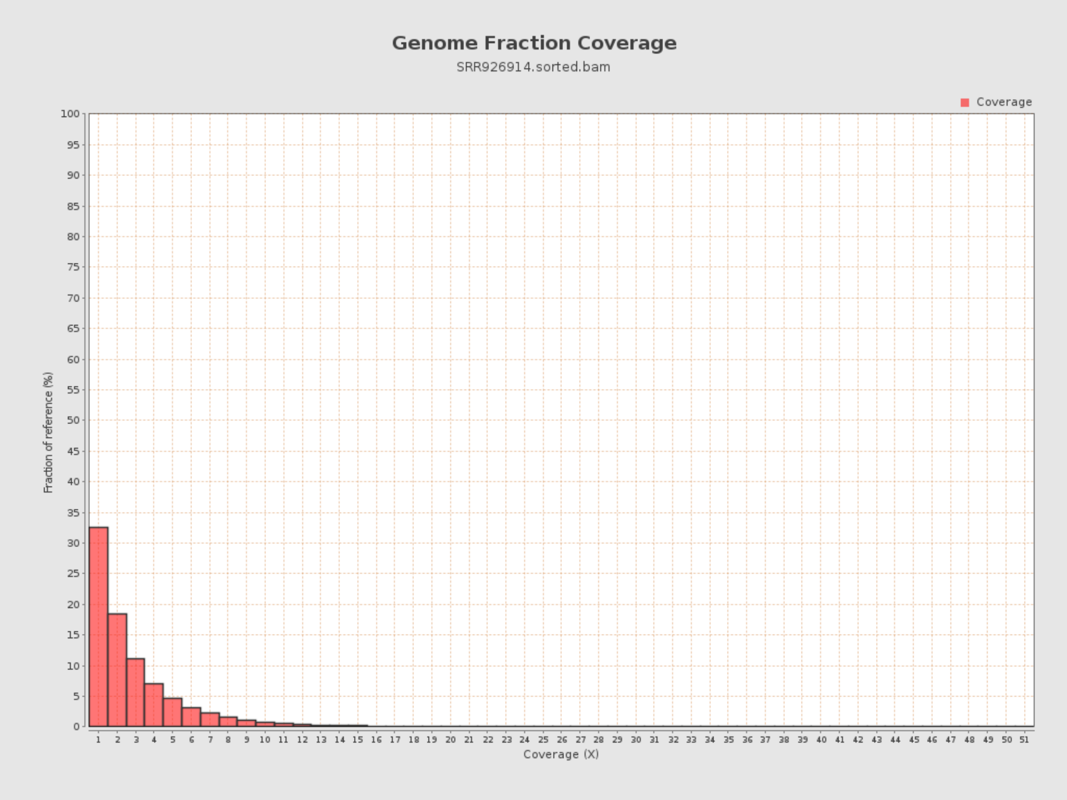
4. Results : Coverage Histogram



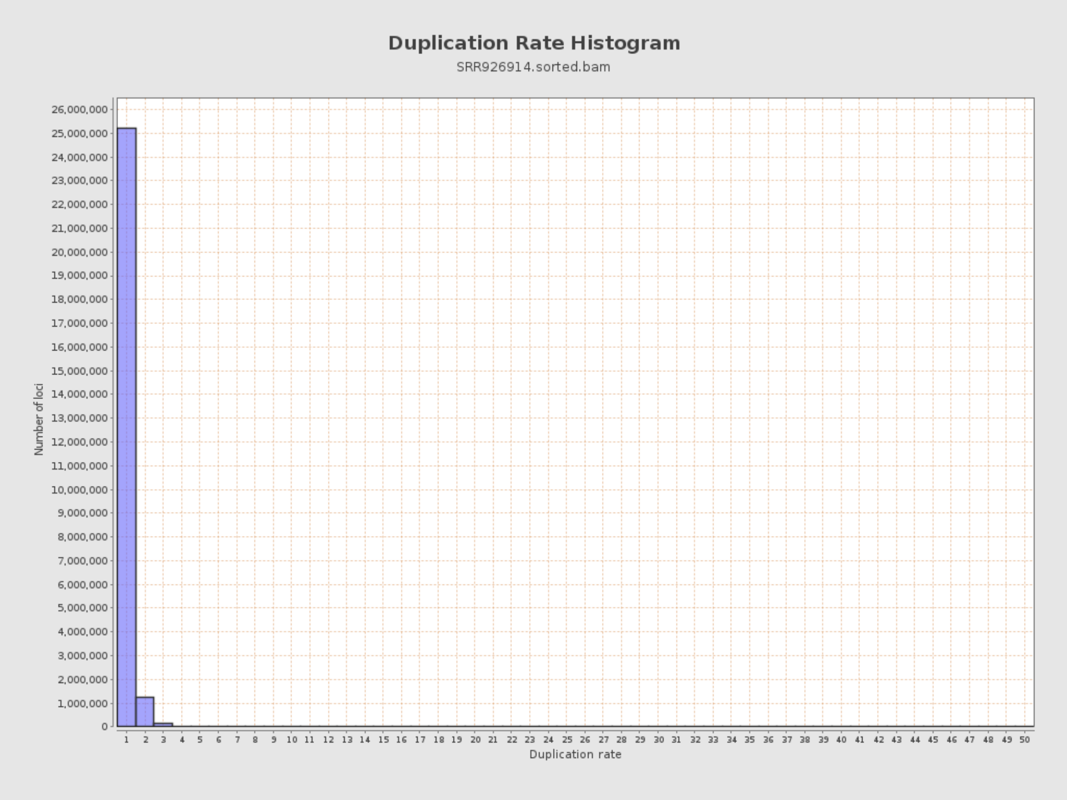
5. Results : Coverage Histogram (0-50X)



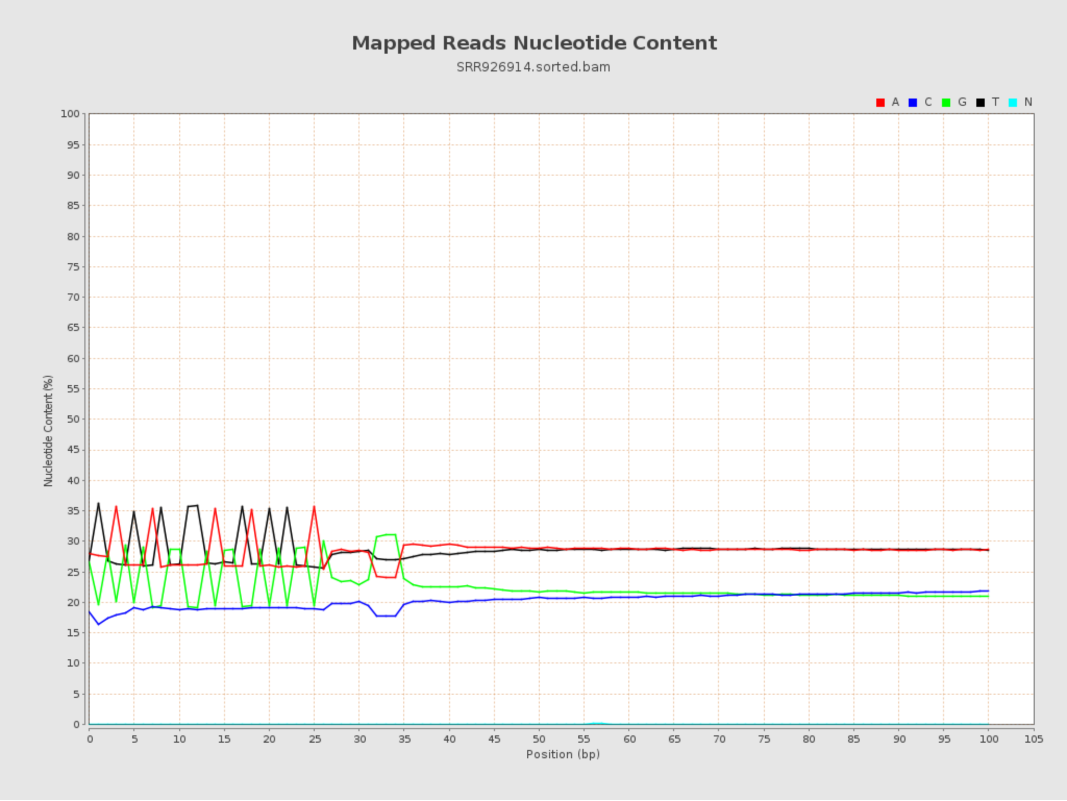
6. Results : Genome Fraction Coverage



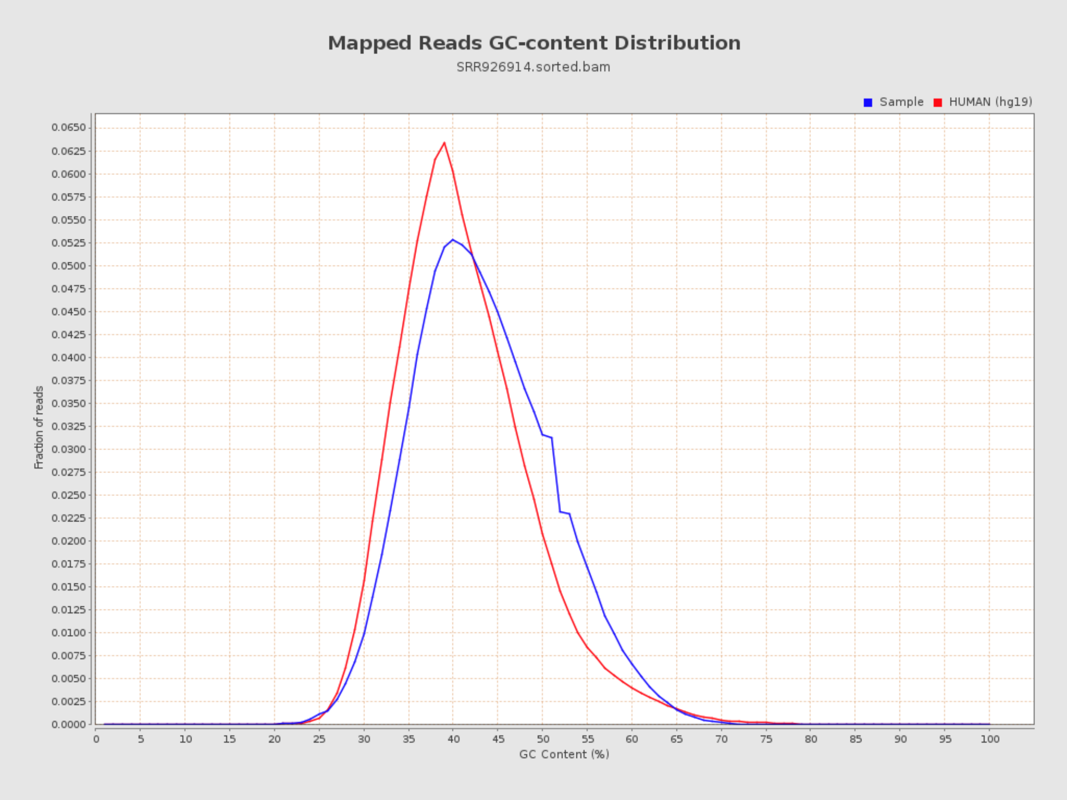
7. Results : Duplication Rate Histogram



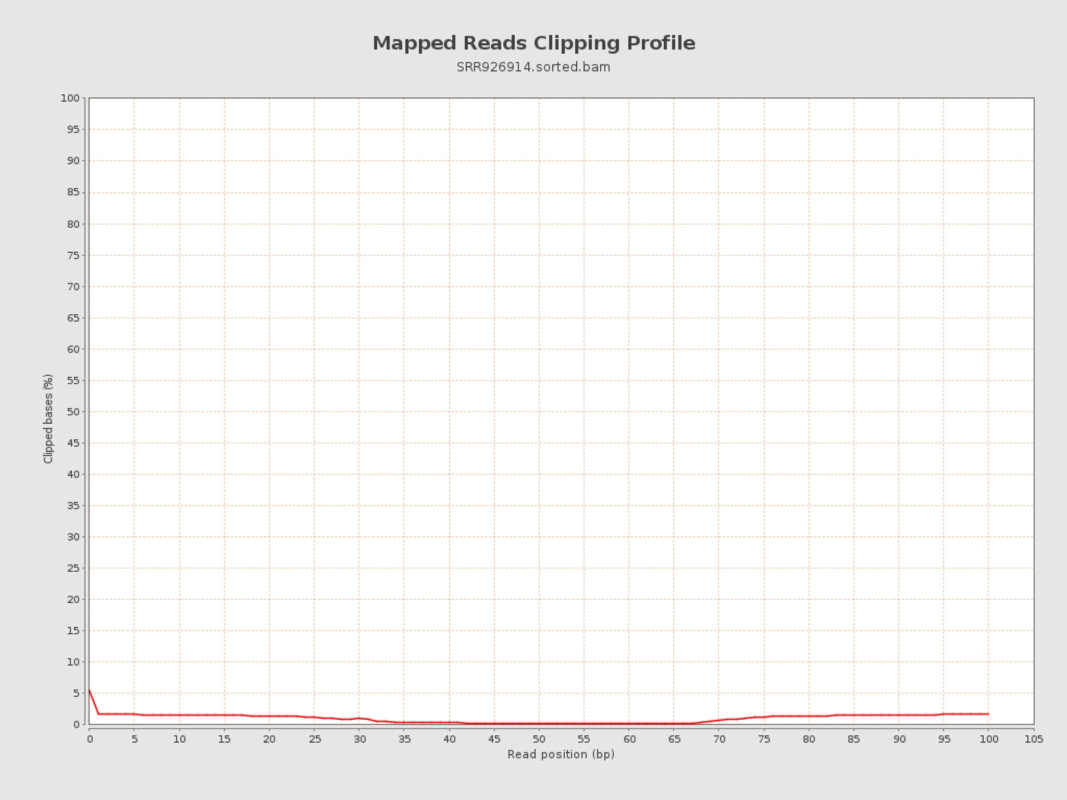
8. Results : Mapped Reads Nucleotide Content



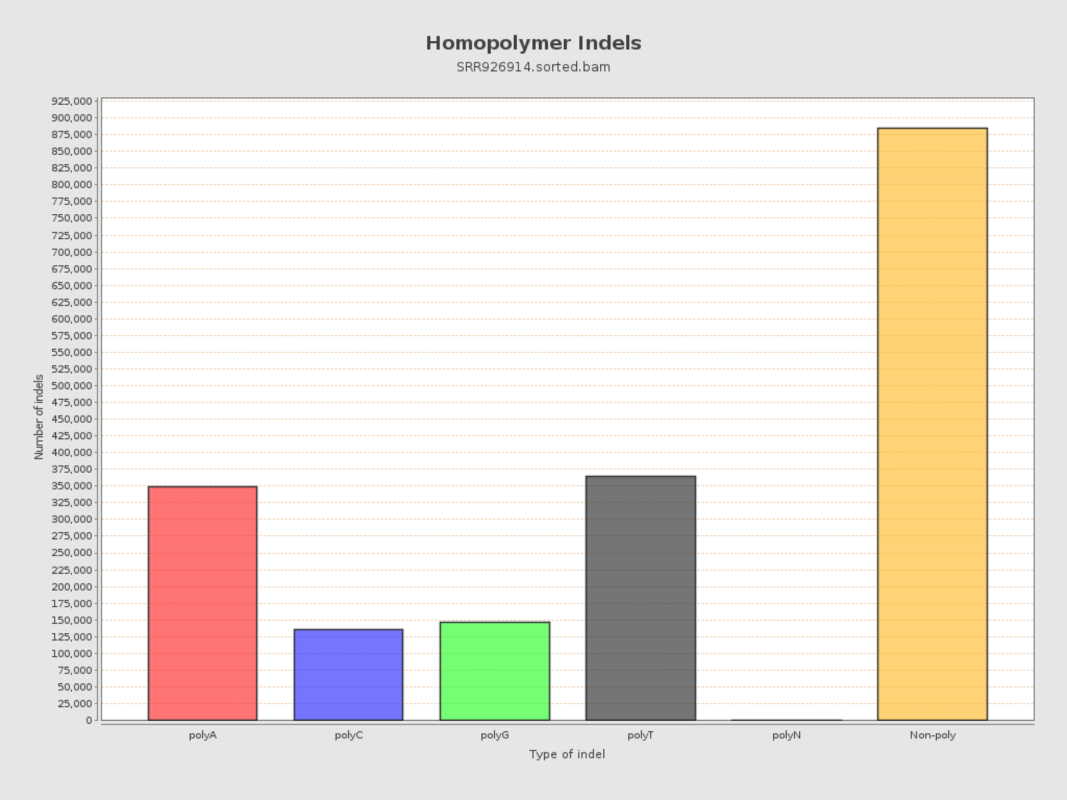
9. Results : Mapped Reads GC-content Distribution



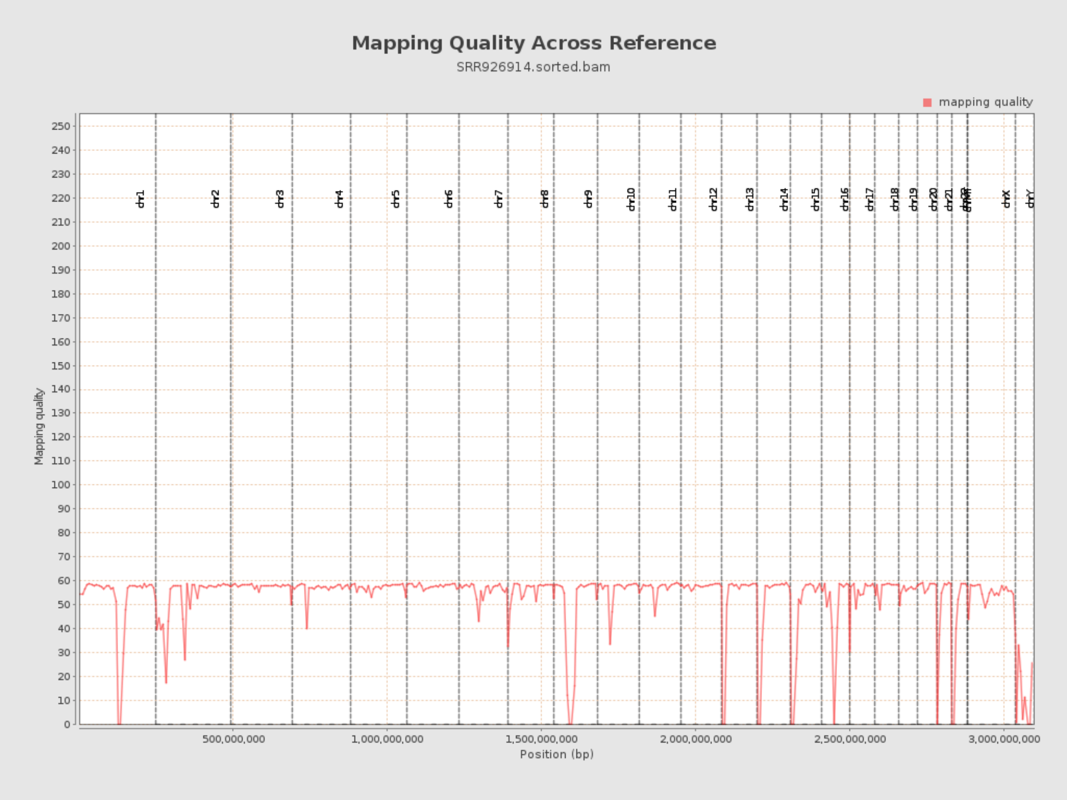
10. Results : Mapped Reads Clipping Profile



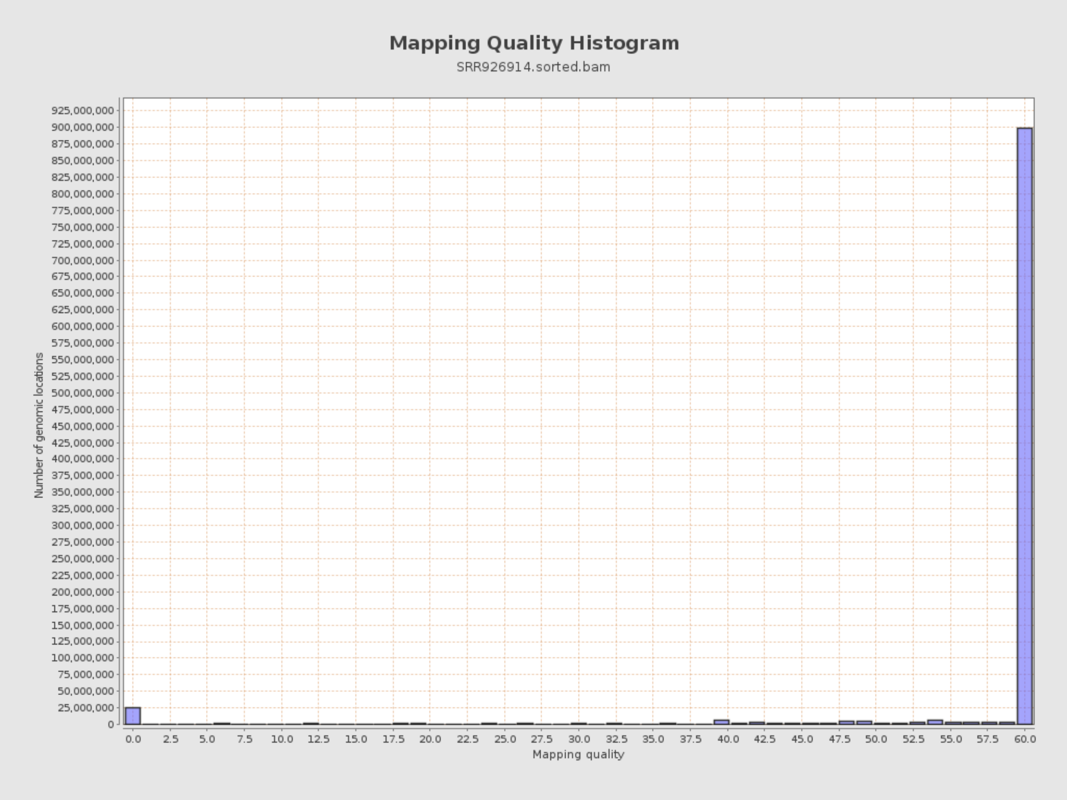
11. Results : Homopolymer Indels



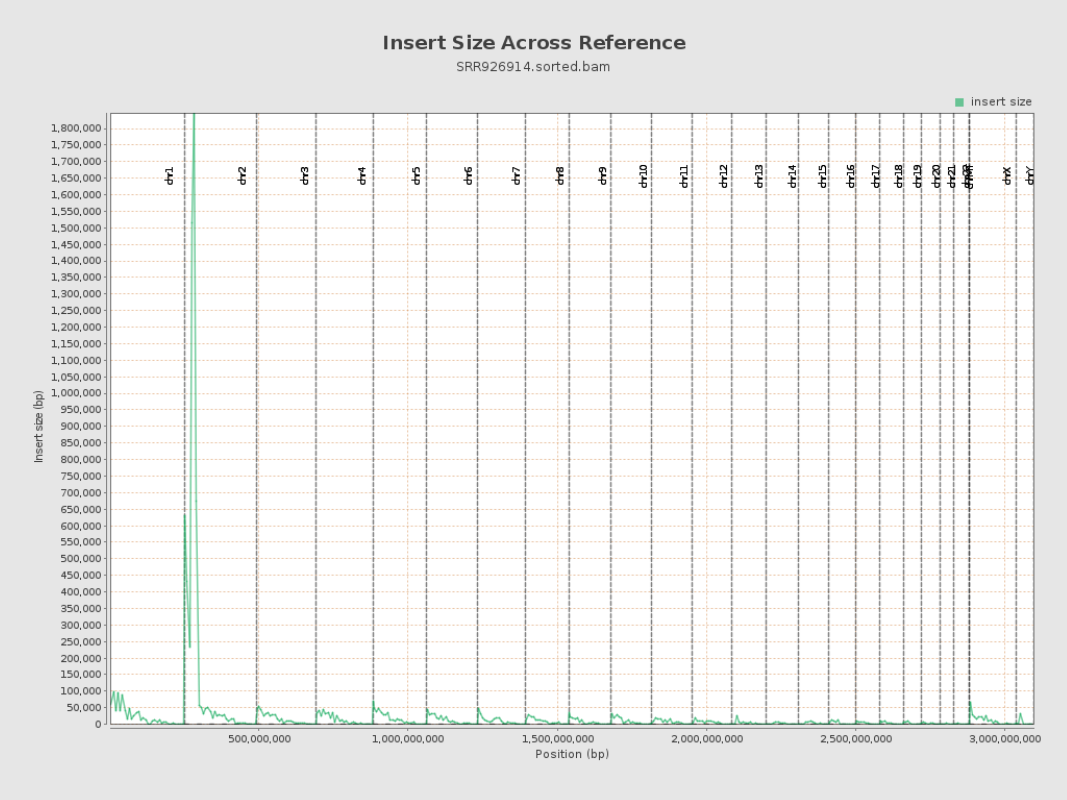
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram