Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 15:42:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926915.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_SRR926915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926915_1.fastq.gz SRR926915_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 15:42:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,750,560
Mapped reads	31,584,414 / 96.44%
Unmapped reads	1,166,146 / 3.56%
Mapped paired reads	31,584,414 / 96.44%
Mapped reads, first in pair	15,855,034 / 48.41%
Mapped reads, second in pair	15,729,380 / 48.03%
Mapped reads, both in pair	31,049,476 / 94.81%
Mapped reads, singletons	534,938 / 1.63%
Secondary alignments	0
Supplementary alignments	1,135,536 / 3.47%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	3,067,585 / 9.37%
Duplication rate	7.73%
Clipped reads	13,421,896 / 40.98%

2.2. ACGT Content

Number/percentage of A's	824,898,252 / 28.57%
Number/percentage of C's	564,514,700 / 19.55%
Number/percentage of T's	830,592,261 / 28.77%
Number/percentage of G's	666,683,393 / 23.09%
Number/percentage of N's	215,913 / 0.01%

GC Percentage	42.65%

2.3. Coverage

Mean	0.9333
Standard Deviation	3.2396

2.4. Mapping Quality

Mean Mapping Quality	51.48

2.5. Insert size

Mean	415,145.83
Standard Deviation	6,325,561.07
P25/Median/P75	144 / 191 / 261

2.6. Mismatches and indels

General error rate	1%
Mismatches	27,968,319
Insertions	487,351
Mapped reads with at least one insertion	1.52%
Deletions	1,562,620
Mapped reads with at least one deletion	4.82%
Homopolymer indels	52.26%

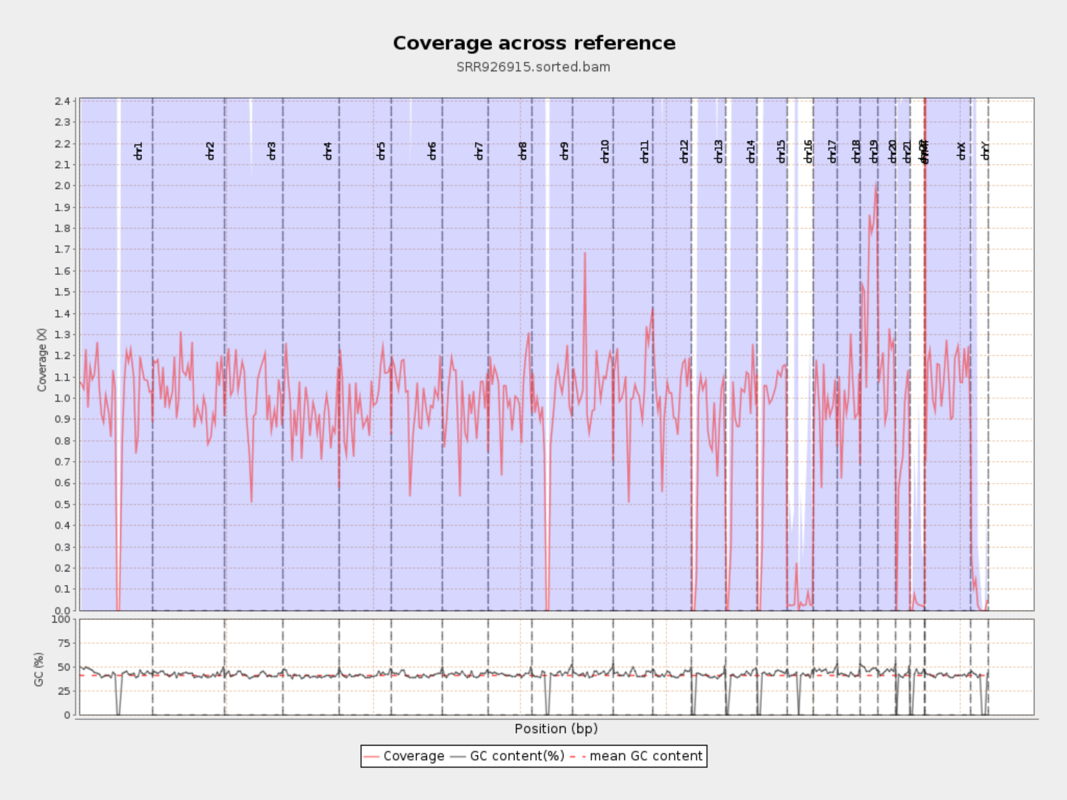
2.7. Chromosome stats

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

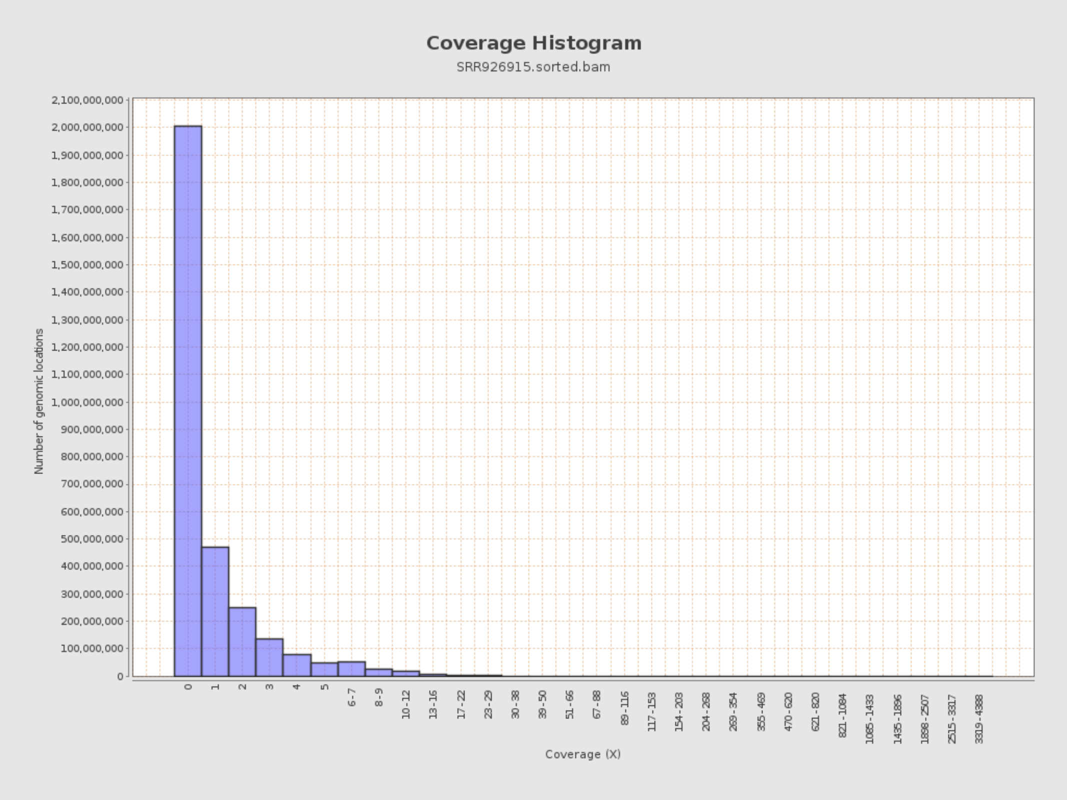
		bases	coverage	deviation
chr1	249250621	244846929	0.9823	3.3381
chr2	243199373	253266171	1.0414	4.1549
chr3	198022430	200624690	1.0131	2.066
chr4	191154276	177684166	0.9295	2.1934
chr5	180915260	179215308	0.9906	1.9754
chr6	171115067	171094205	0.9999	2.3062
chr7	159138663	153430439	0.9641	2.3272
chr8	146364022	150348142	1.0272	2.1929
chr9	141213431	125482080	0.8886	2.7129
chr10	135534747	147722793	1.0899	9.3863
chr11	135006516	142088049	1.0525	2.2801
chr12	133851895	134996141	1.0085	2.4874
chr13	115169878	89932514	0.7809	1.8623
chr14	107349540	89835791	0.8369	1.8868
chr15	102531392	88383025	0.862	2.0063
chr16	90354753	4363635	0.0483	1.8467
chr17	81195210	77786384	0.958	2.2273
chr18	78077248	78035810	0.9995	2.4882
chr19	59128983	95467356	1.6146	3.475
chr20	63025520	70439528	1.1176	2.2836
chr21	48129895	35985543	0.7477	2.4915
chr22	51304566	1515961	0.0295	0.5812
chrMT	16571	3891753	234.8532	148.7698
chrX	155270560	168929470	1.088	2.1413

chrY	59373566	3816335	0.0643	1.3943

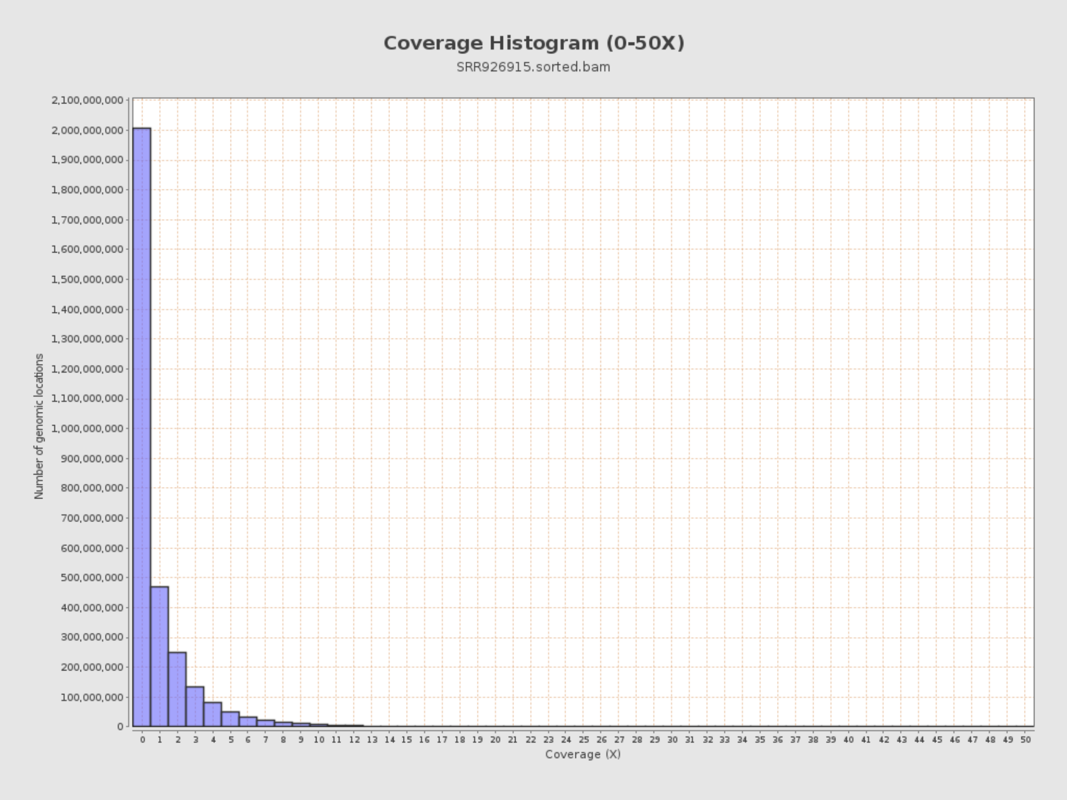
3. Results : Coverage across reference



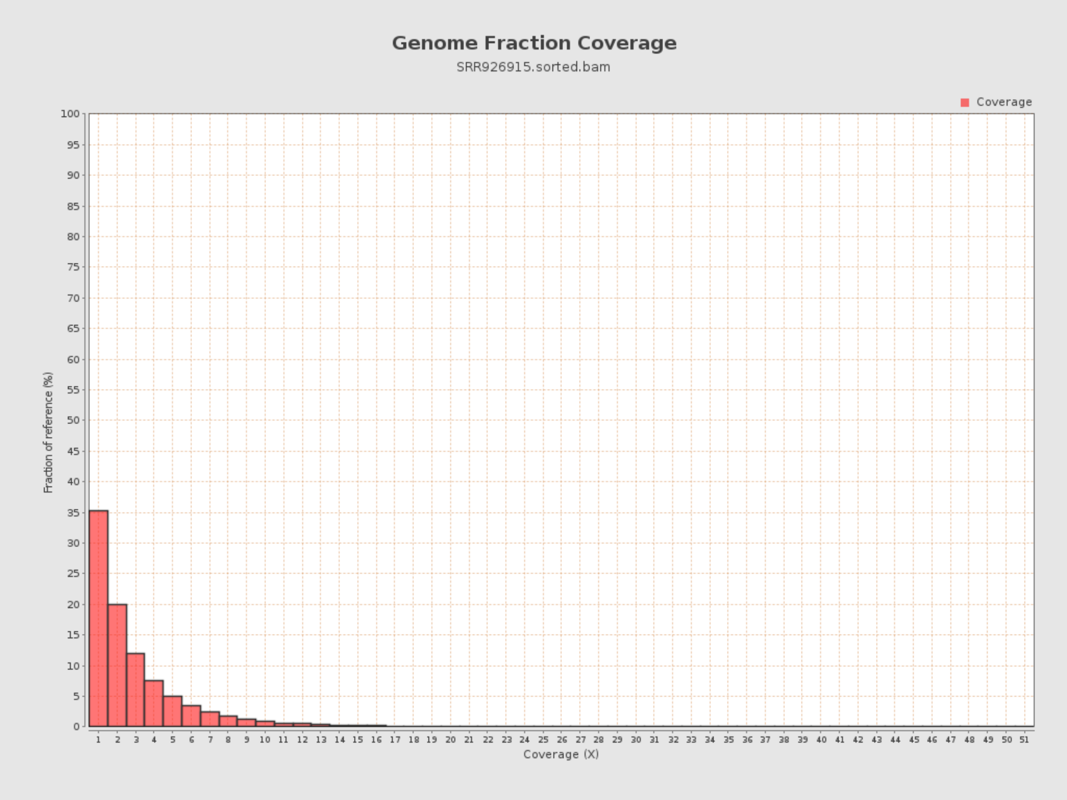
4. Results : Coverage Histogram



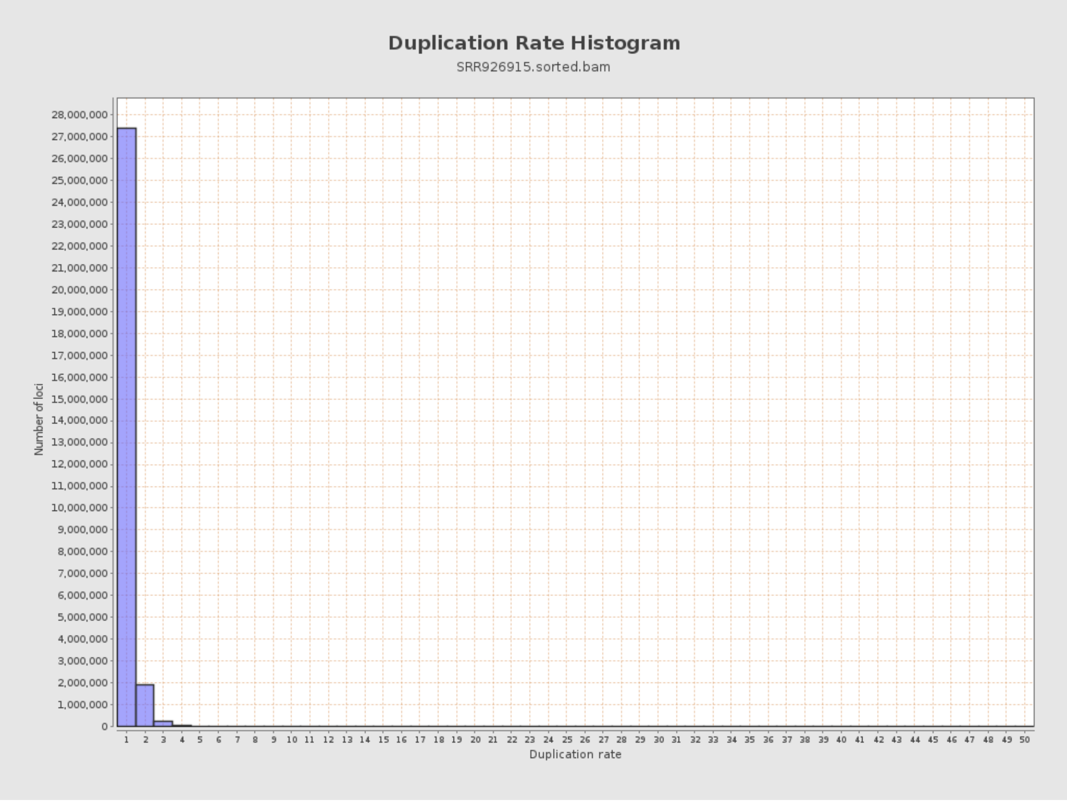
5. Results : Coverage Histogram (0-50X)



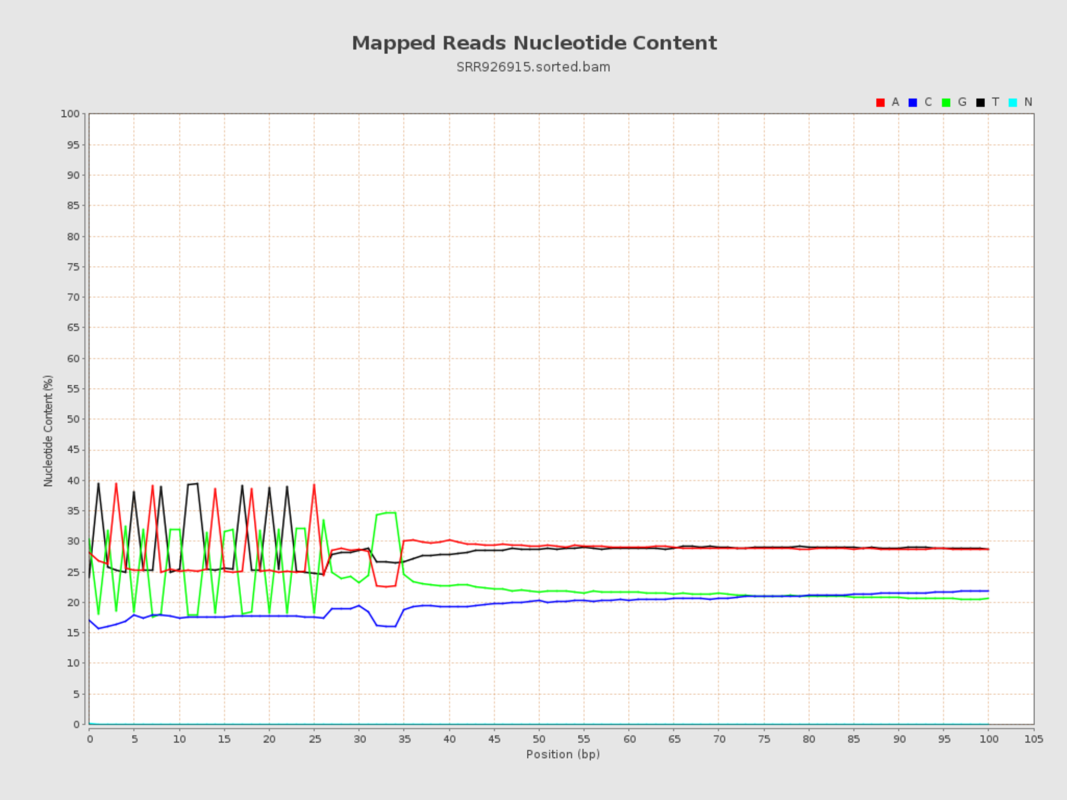
6. Results : Genome Fraction Coverage



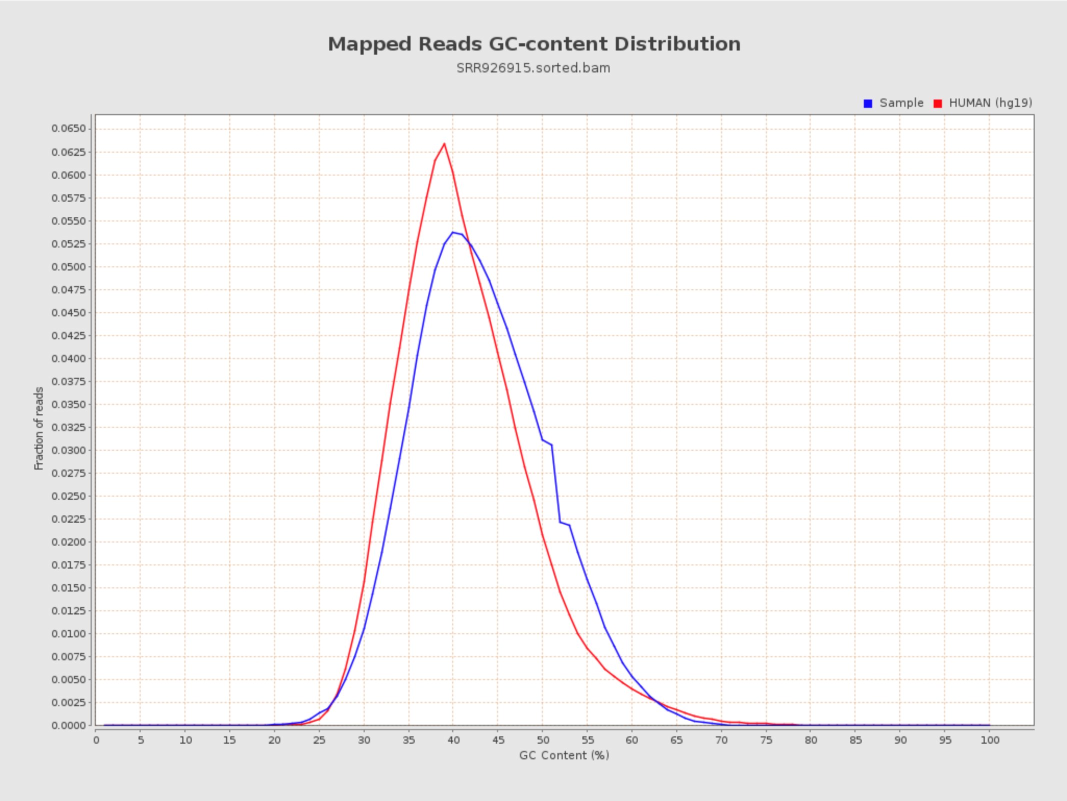
7. Results : Duplication Rate Histogram



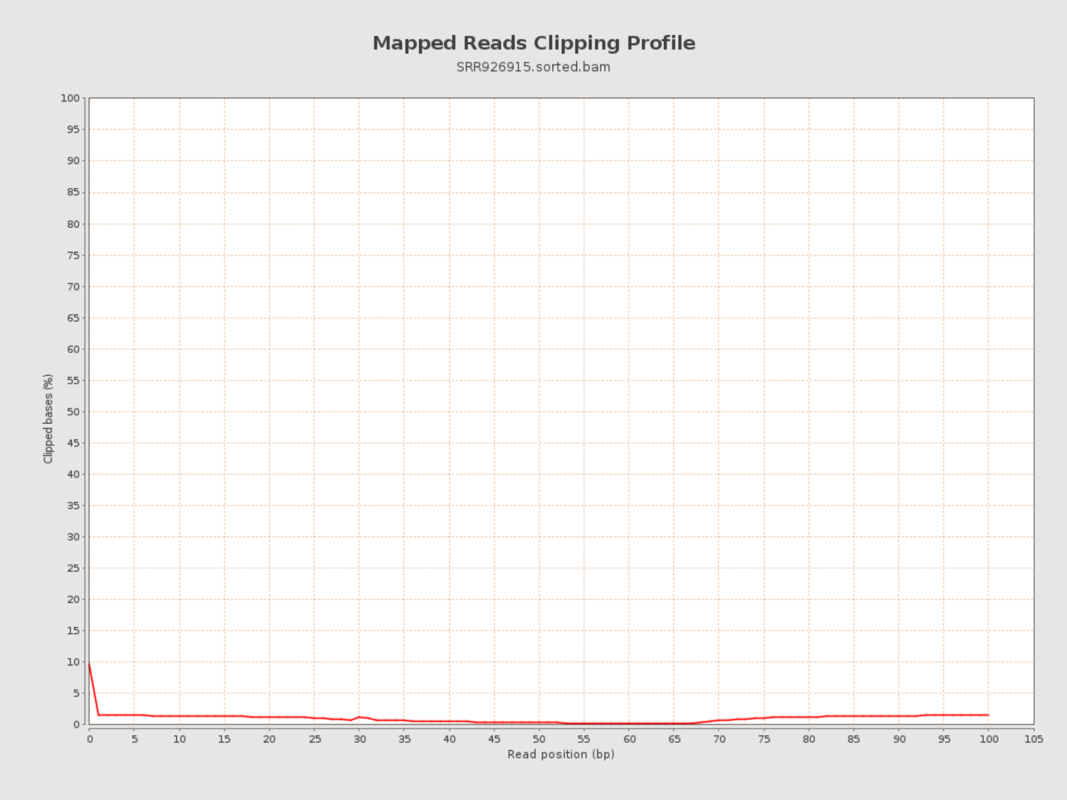
8. Results : Mapped Reads Nucleotide Content



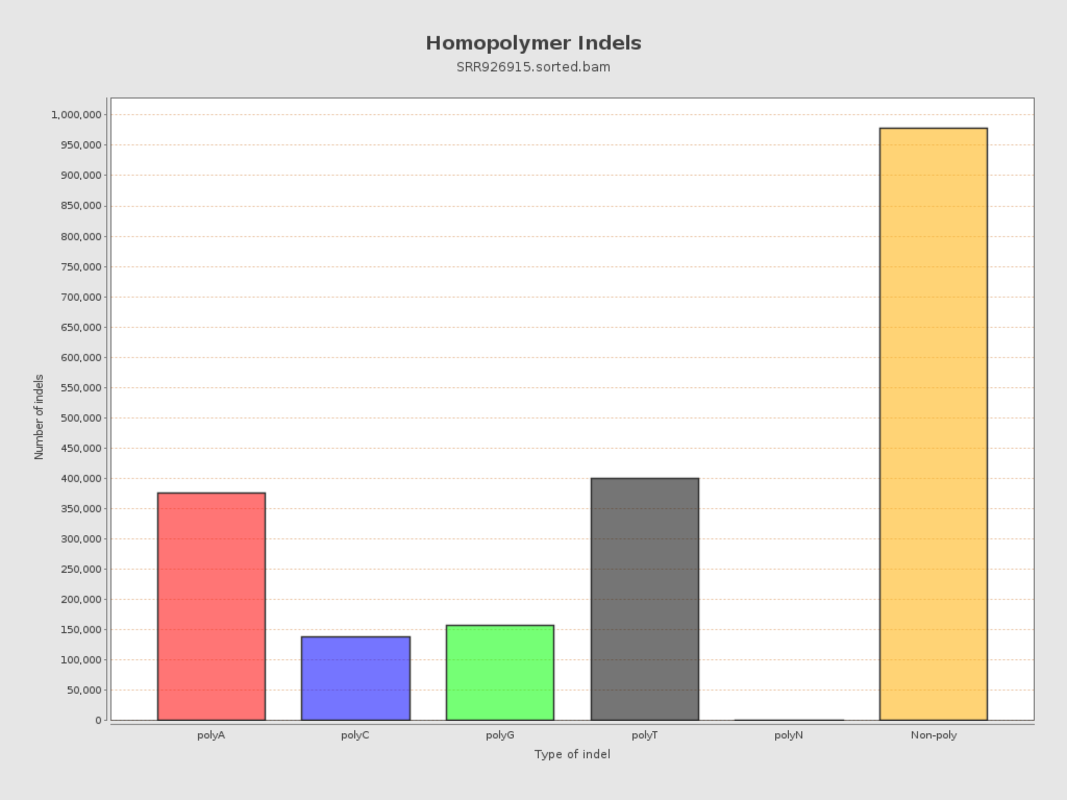
9. Results : Mapped Reads GC-content Distribution



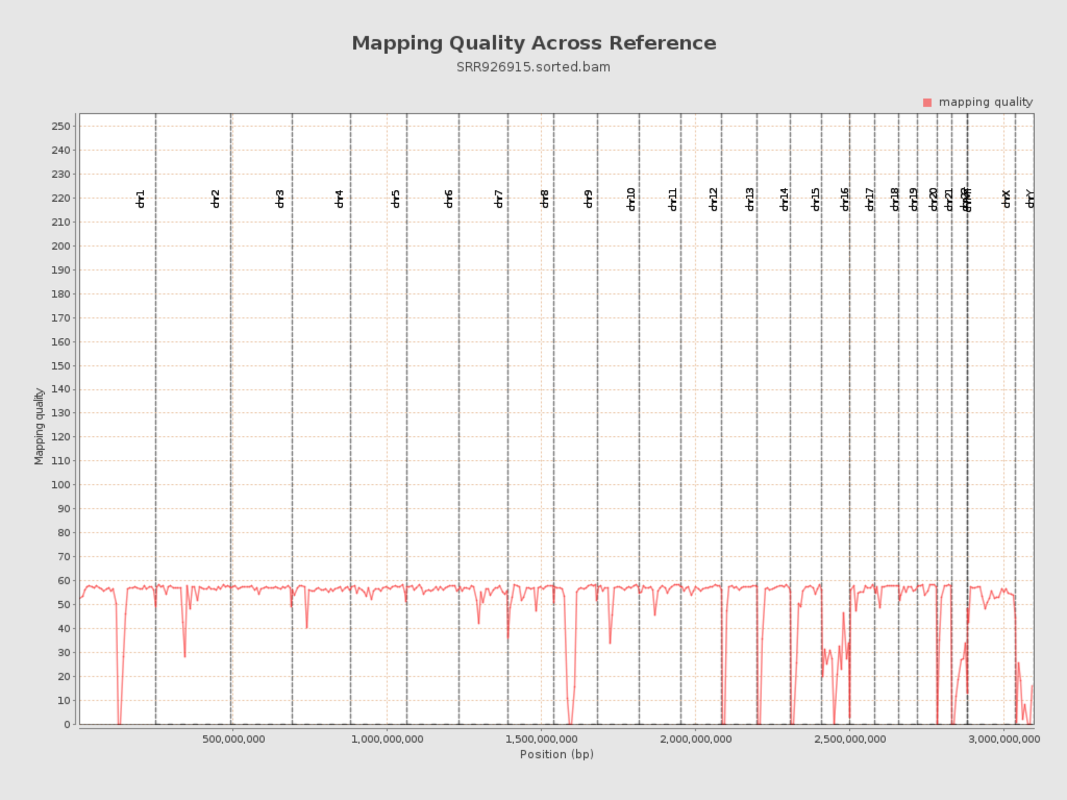
10. Results : Mapped Reads Clipping Profile



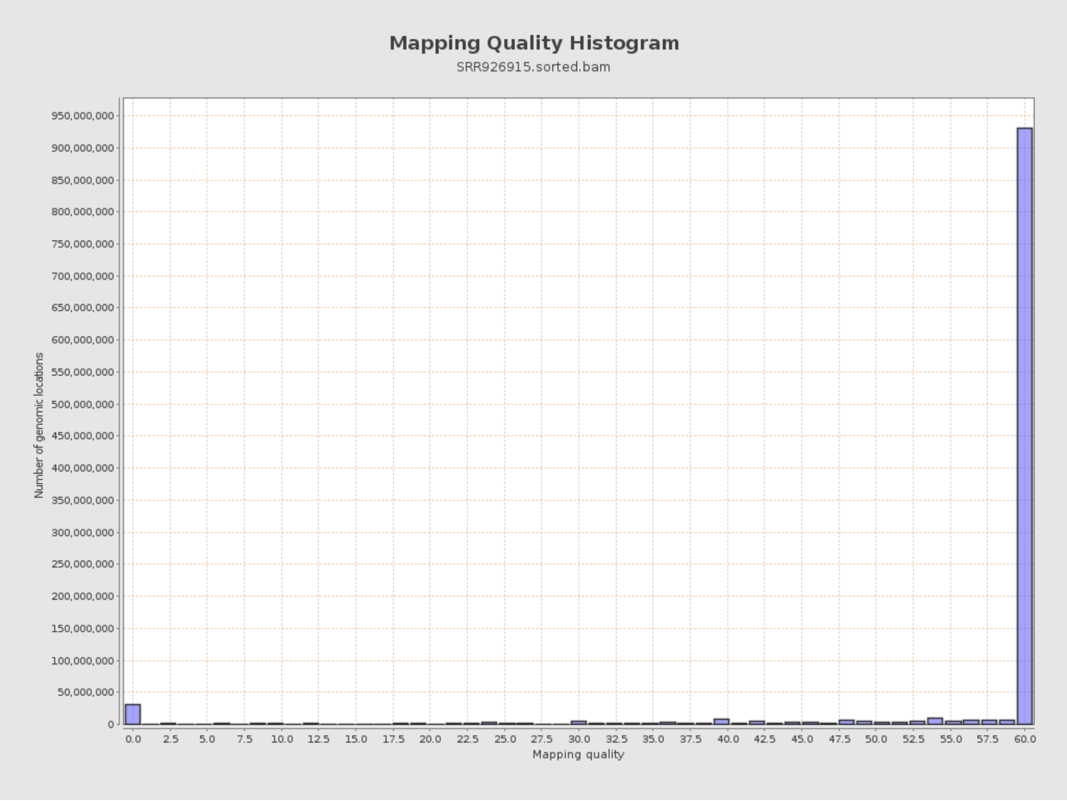
11. Results : Homopolymer Indels



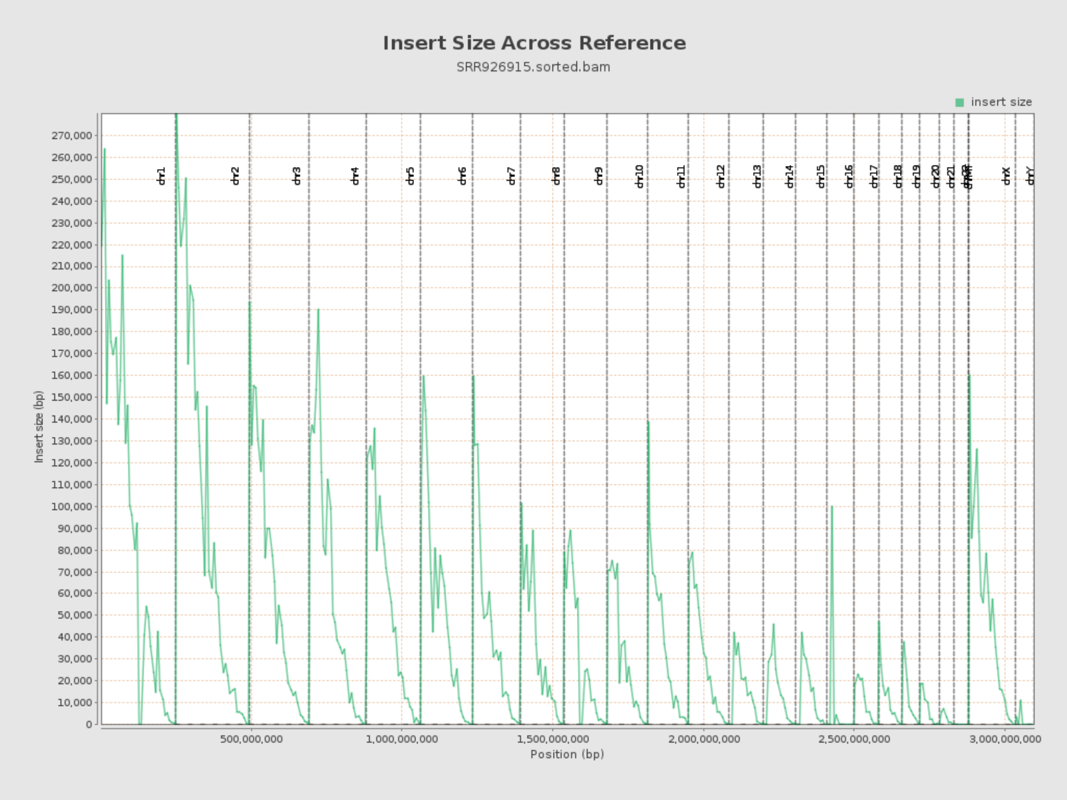
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram