Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 22:41:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926936.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_SRR926936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926936_1.fastq.gz SRR926936_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 22:41:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,615,168
Mapped reads	12,273,290 / 97.29%
Unmapped reads	341,878 / 2.71%
Mapped paired reads	12,273,290 / 97.29%
Mapped reads, first in pair	6,142,684 / 48.69%
Mapped reads, second in pair	6,130,606 / 48.6%
Mapped reads, both in pair	12,085,490 / 95.8%
Mapped reads, singletons	187,800 / 1.49%
Secondary alignments	0
Supplementary alignments	437,175 / 3.47%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	746,274 / 5.92%
Duplication rate	4.89%
Clipped reads	5,129,149 / 40.66%

2.2. ACGT Content

Number/percentage of A's	318,967,045 / 28.38%
Number/percentage of C's	223,224,829 / 19.86%
Number/percentage of T's	323,046,854 / 28.74%
Number/percentage of G's	258,632,181 / 23.01%
Number/percentage of N's	55,079 / 0%

GC Percentage	42.87%

2.3. Coverage

Mean	0.3633
Standard Deviation	1.4833

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	360,542.71
Standard Deviation	5,907,463.07
P25/Median/P75	139 / 182 / 246

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	10,005,002
Insertions	193,731
Mapped reads with at least one insertion	1.55%
Deletions	567,804
Mapped reads with at least one deletion	4.51%
Homopolymer indels	51.98%

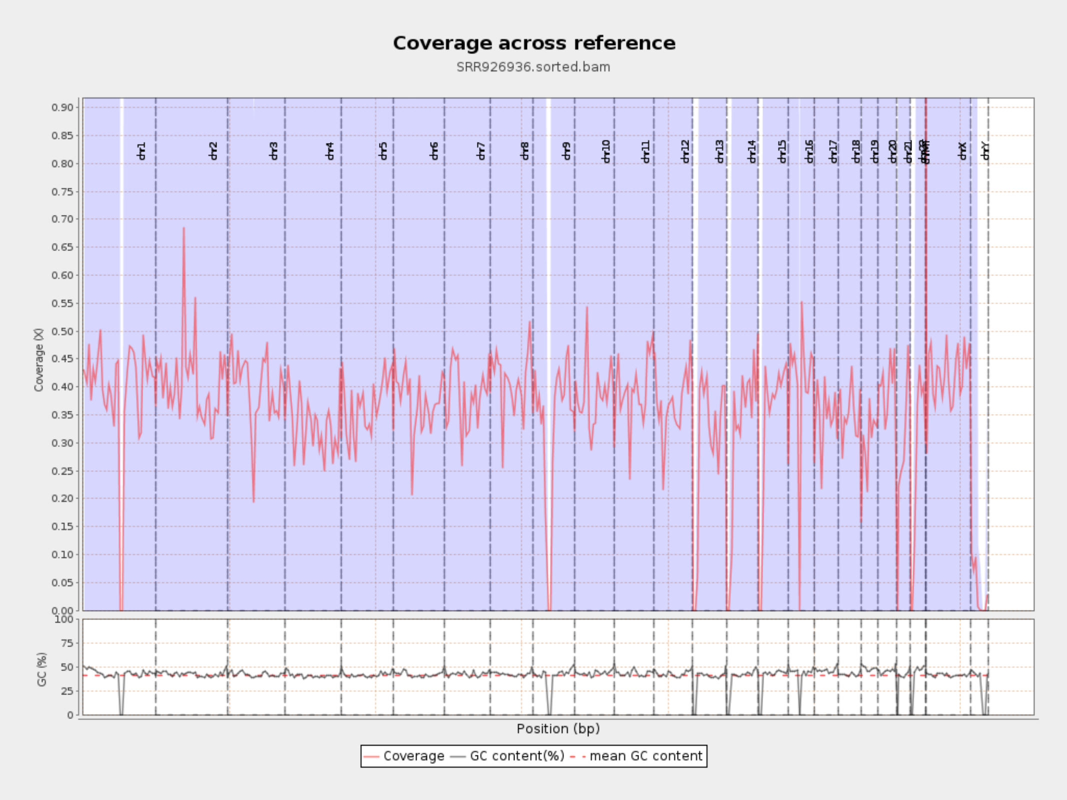
2.7. Chromosome stats

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

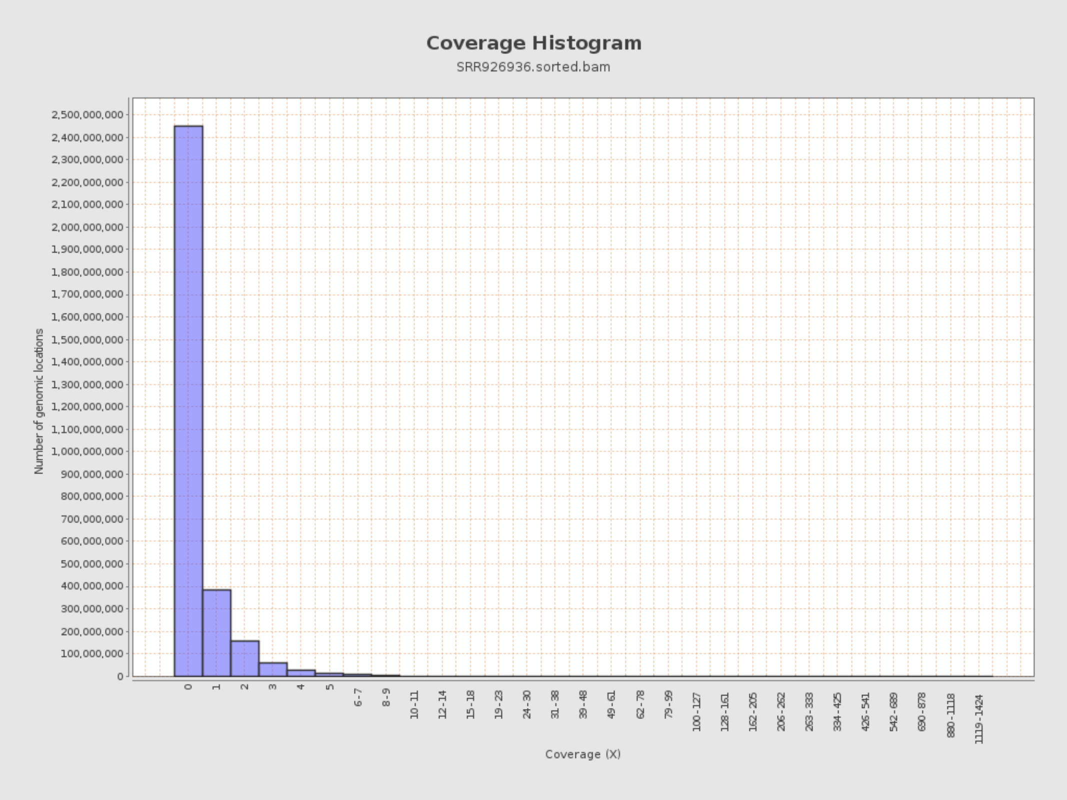
		bases	coverage	deviation
chr1	249250621	97394620	0.3907	1.7175
chr2	243199373	99334055	0.4084	2.8174
chr3	198022430	78479571	0.3963	0.9475
chr4	191154276	63978428	0.3347	1.2396
chr5	180915260	66525075	0.3677	0.8929
chr6	171115067	63942949	0.3737	1.0323
chr7	159138663	61195046	0.3845	1.0471
chr8	146364022	60103059	0.4106	1.0302
chr9	141213431	46666345	0.3305	1.5088
chr10	135534747	52010026	0.3837	2.4521
chr11	135006516	53069648	0.3931	1.2477
chr12	133851895	50044511	0.3739	0.9535
chr13	115169878	34263807	0.2975	0.8057
chr14	107349540	33447369	0.3116	0.8646
chr15	102531392	33964742	0.3313	0.8901
chr16	90354753	36044243	0.3989	2.3519
chr17	81195210	28445749	0.3503	1.0321
chr18	78077248	27420985	0.3512	1.5226
chr19	59128983	17944704	0.3035	1.2316
chr20	63025520	25382650	0.4027	1.0088
chr21	48129895	14027595	0.2915	1.1923
chr22	51304566	13767825	0.2684	0.8728
chrMT	16571	18244	1.101	1.441
chrX	155270560	65187872	0.4198	1.0476

chrY	59373566	2119113	0.0357	1.3188

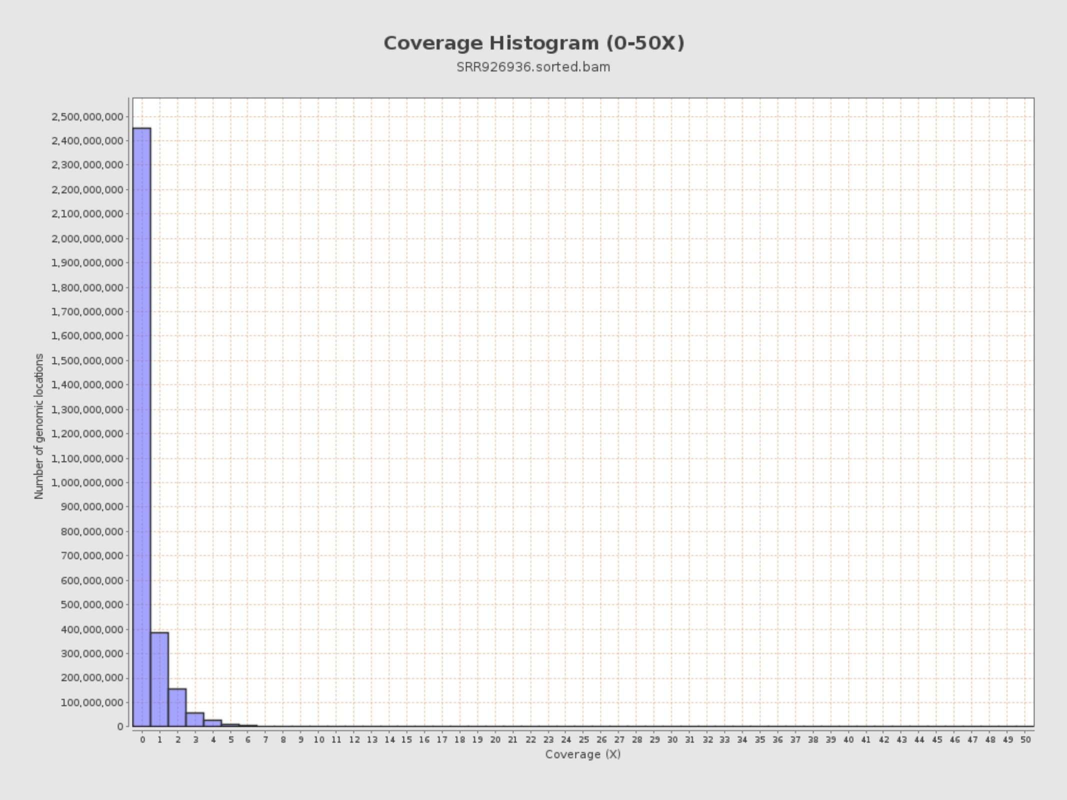
3. Results : Coverage across reference



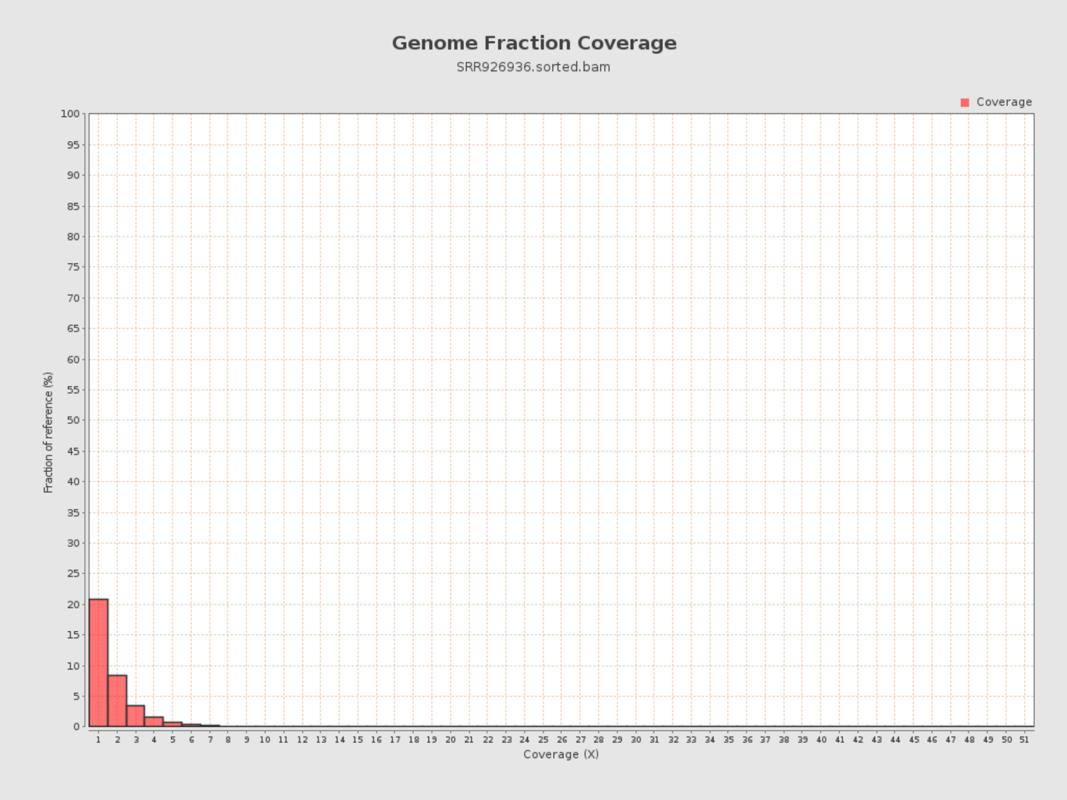
4. Results : Coverage Histogram



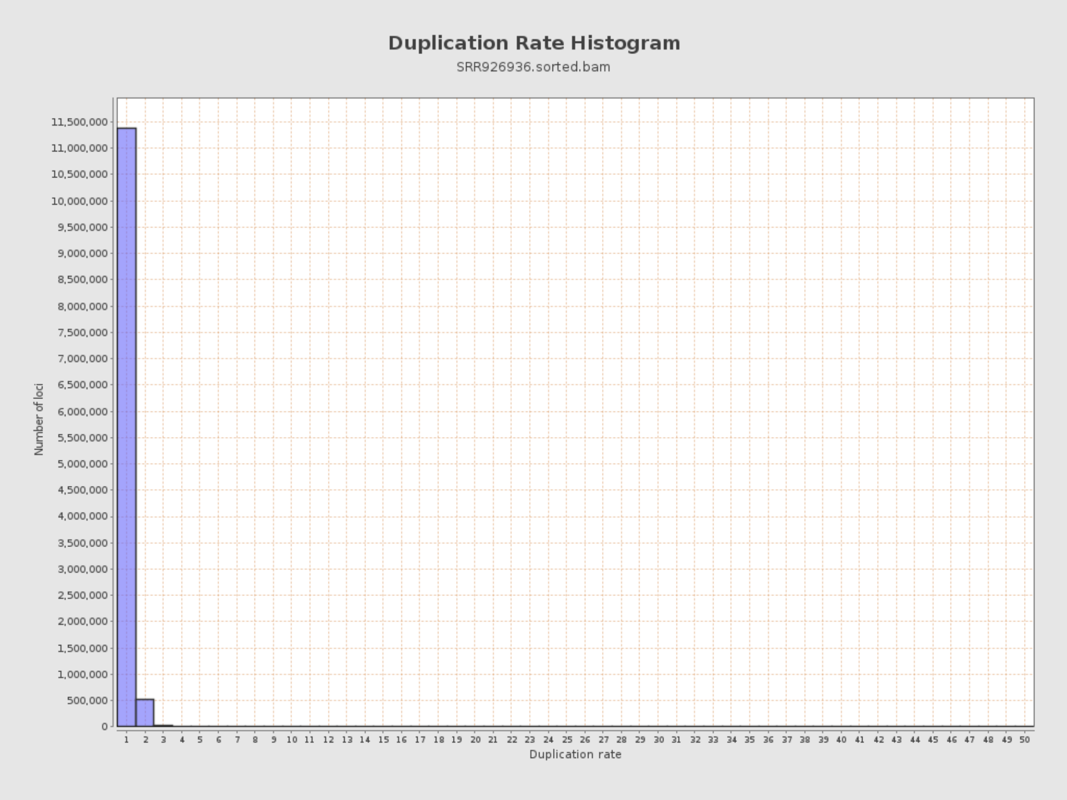
5. Results : Coverage Histogram (0-50X)



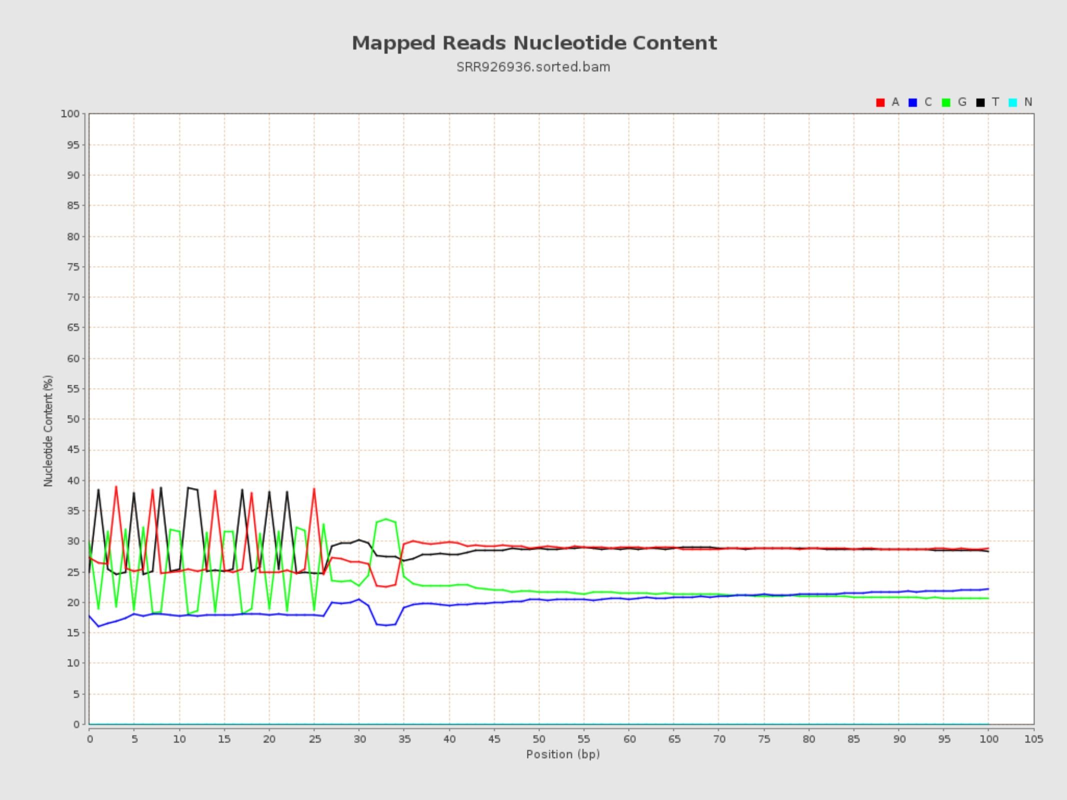
6. Results : Genome Fraction Coverage



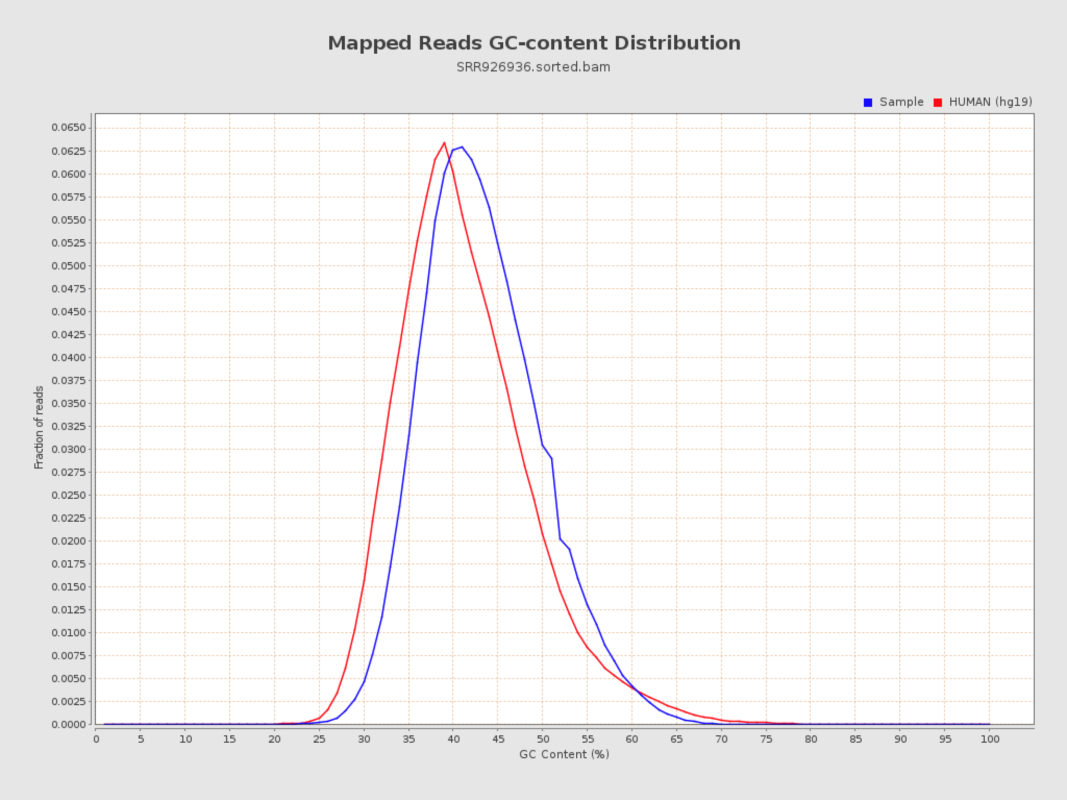
7. Results : Duplication Rate Histogram



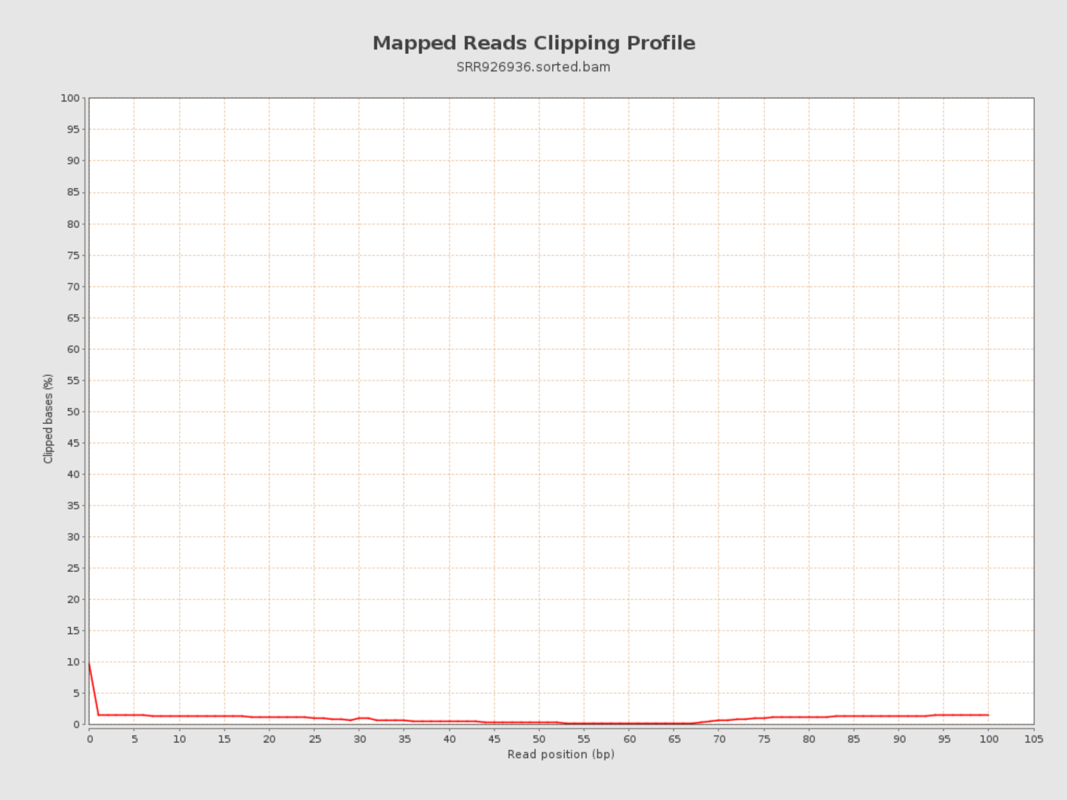
8. Results : Mapped Reads Nucleotide Content



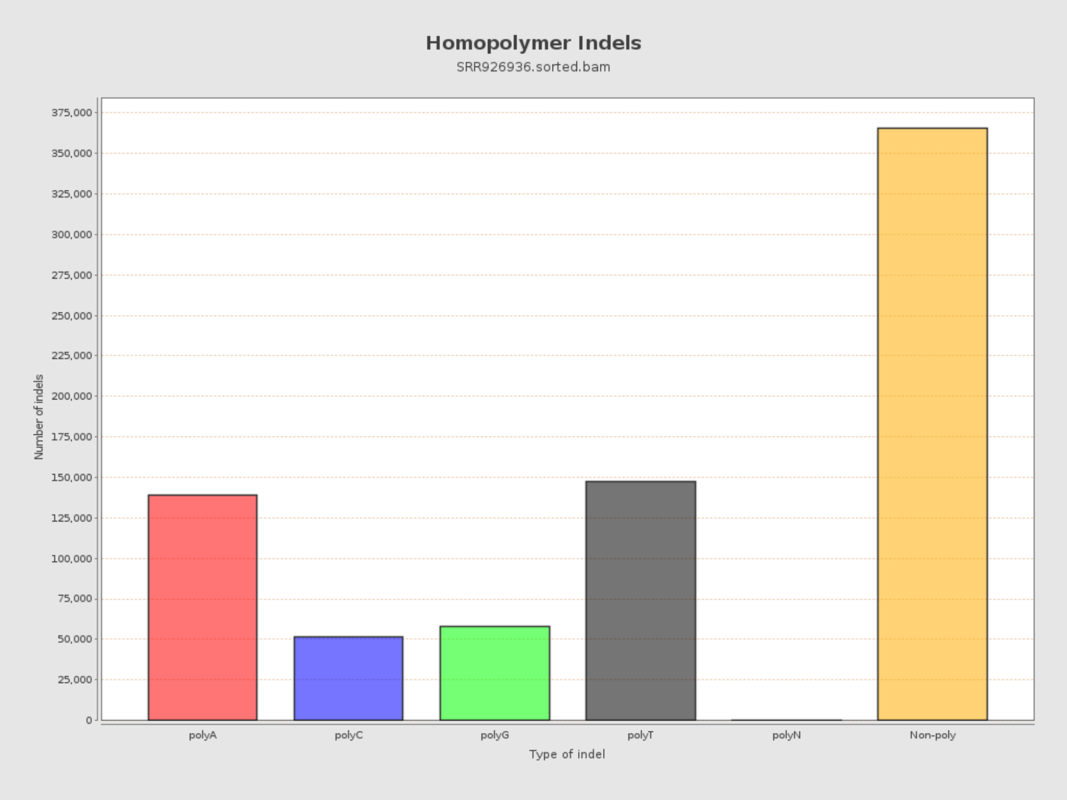
9. Results : Mapped Reads GC-content Distribution



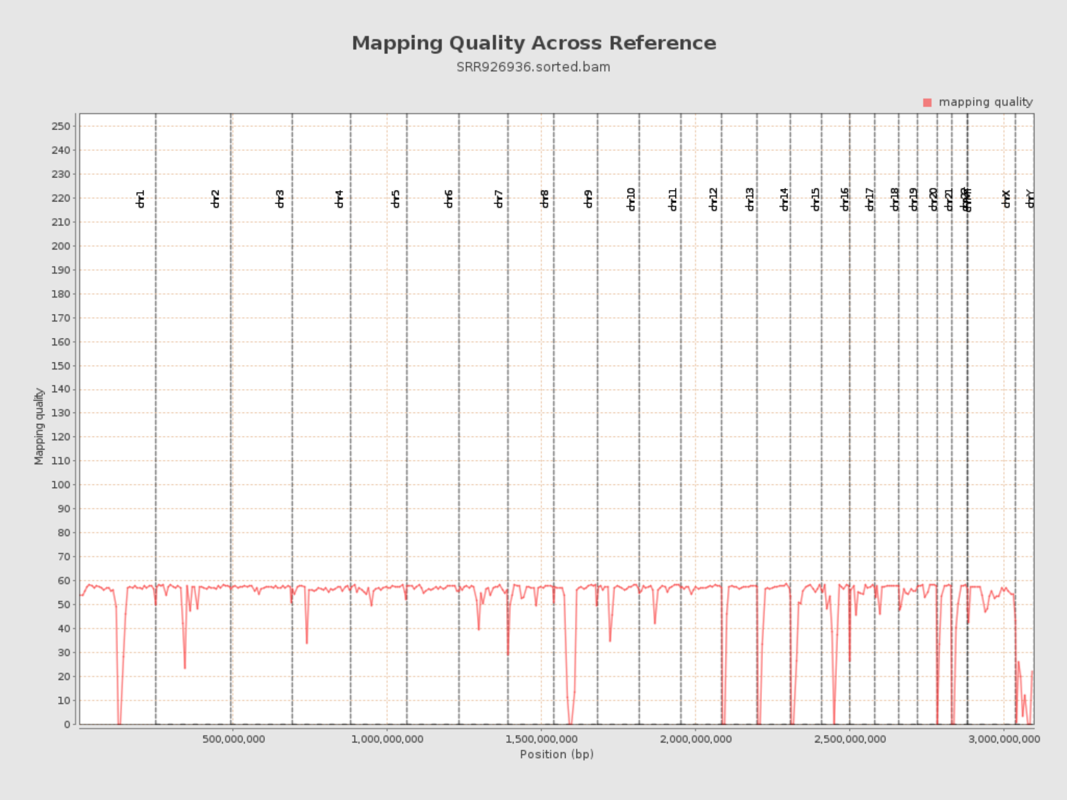
10. Results : Mapped Reads Clipping Profile



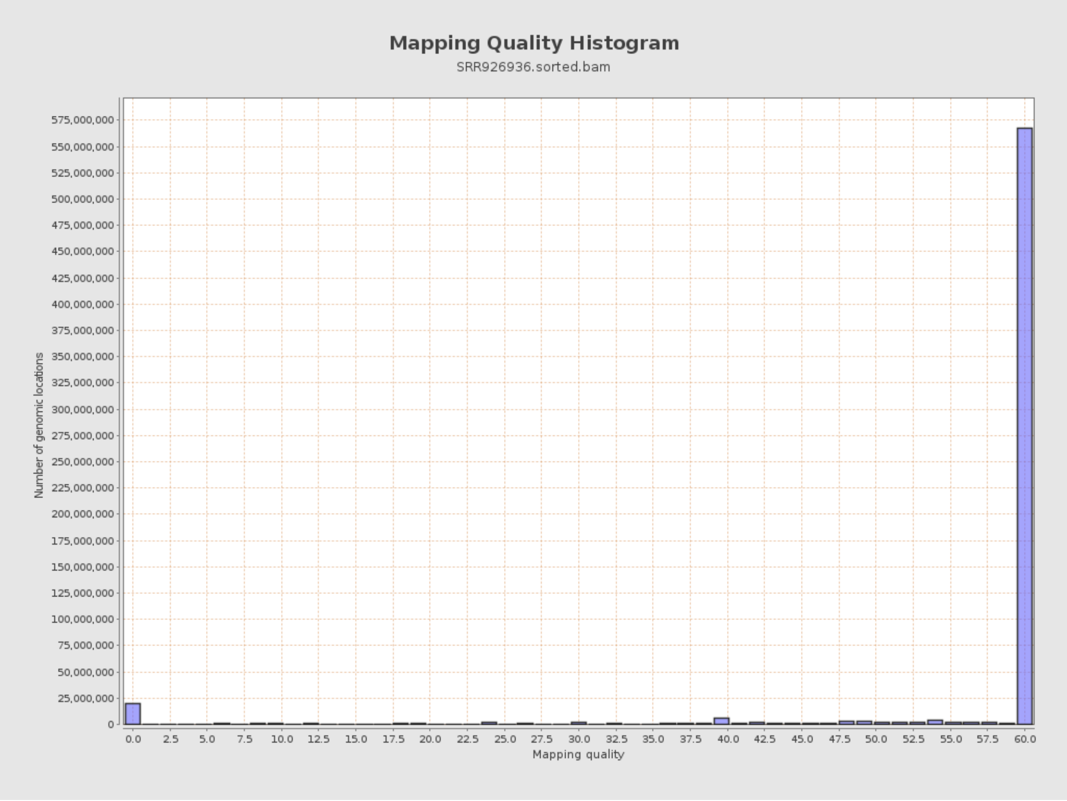
11. Results : Homopolymer Indels



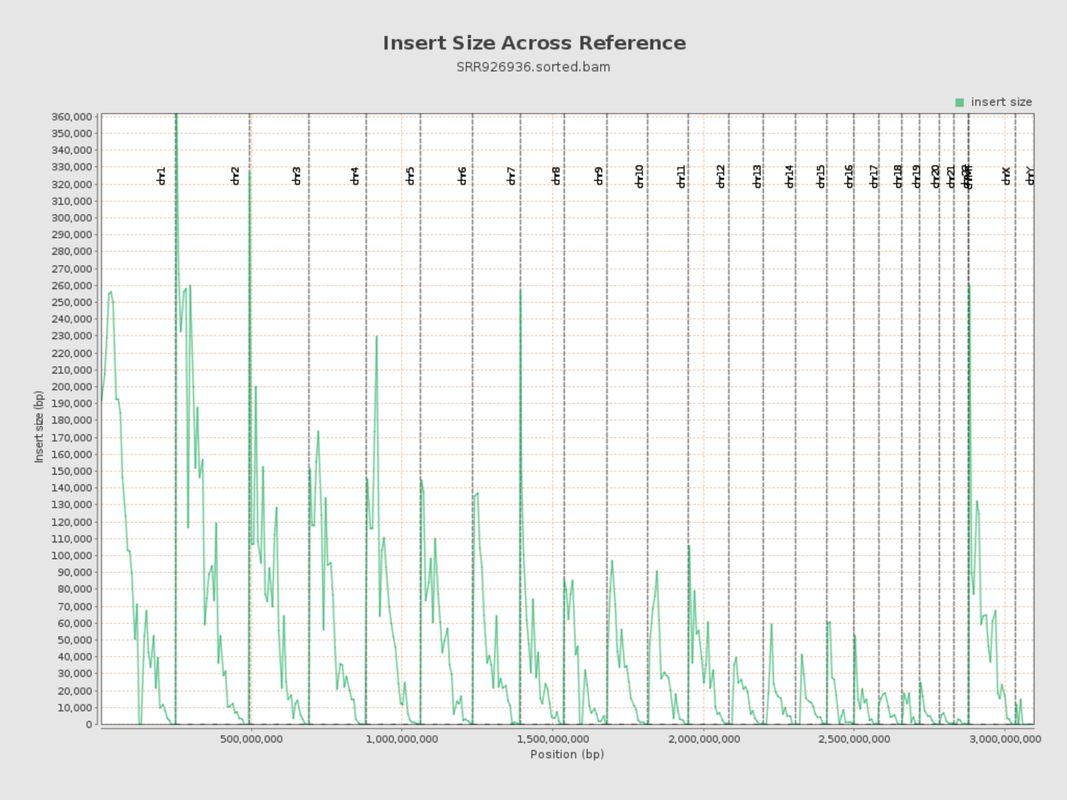
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram