Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 20:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926926.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_SRR926926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926926_1.fastq.gz SRR926926_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 20:22:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,515,182
Mapped reads	11,078,941 / 96.21%
Unmapped reads	436,241 / 3.79%
Mapped paired reads	11,078,941 / 96.21%
Mapped reads, first in pair	5,556,772 / 48.26%
Mapped reads, second in pair	5,522,169 / 47.96%
Mapped reads, both in pair	10,868,852 / 94.39%
Mapped reads, singletons	210,089 / 1.82%
Secondary alignments	0
Supplementary alignments	323,098 / 2.81%
Read min/max/mean length	30 / 101 / 102.16
Duplicated reads (estimated)	794,654 / 6.9%
Duplication rate	5.93%
Clipped reads	5,291,664 / 45.95%

2.2. ACGT Content

Number/percentage of A's	279,006,343 / 28.2%
Number/percentage of C's	191,655,072 / 19.37%
Number/percentage of T's	286,378,794 / 28.94%
Number/percentage of G's	232,322,088 / 23.48%
Number/percentage of N's	48,332 / 0%

GC Percentage	42.85%

2.3. Coverage

Mean	0.3199
Standard Deviation	1.3613

2.4. Mapping Quality

Mean Mapping Quality	52.64

2.5. Insert size

Mean	278,883.63
Standard Deviation	5,279,488.88
P25/Median/P75	137 / 182 / 247

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	9,681,550
Insertions	177,186
Mapped reads with at least one insertion	1.57%
Deletions	540,578
Mapped reads with at least one deletion	4.75%
Homopolymer indels	51.74%

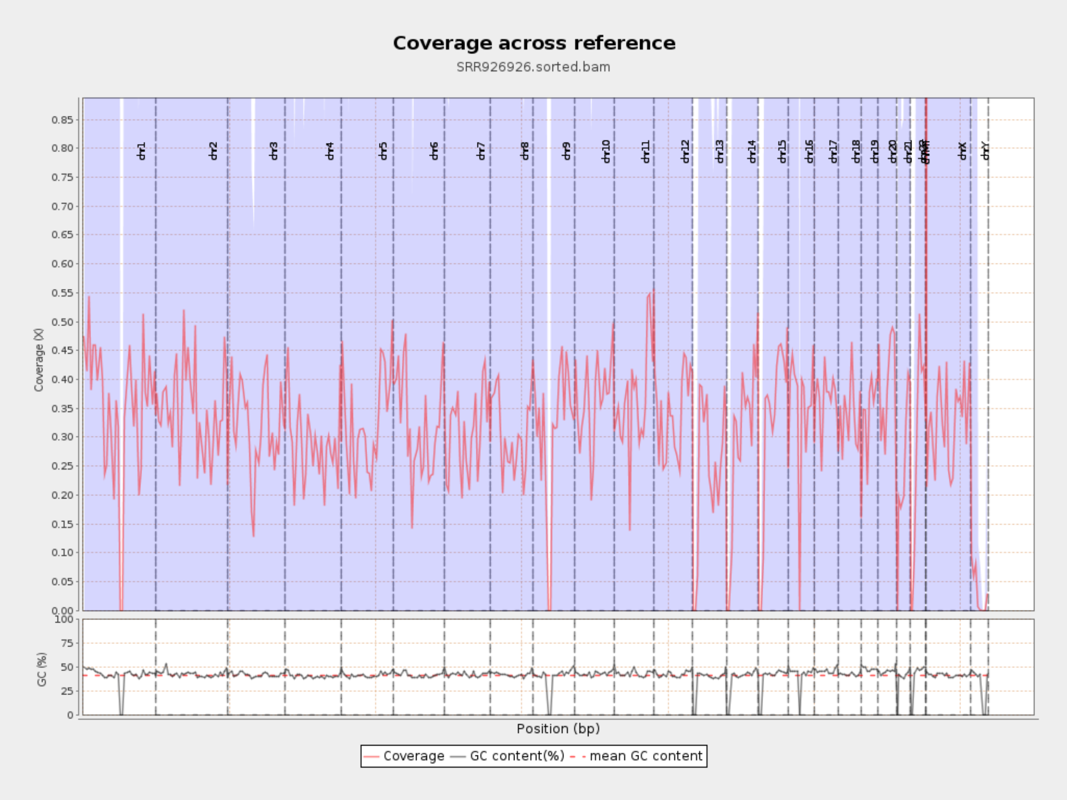
2.7. Chromosome stats

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

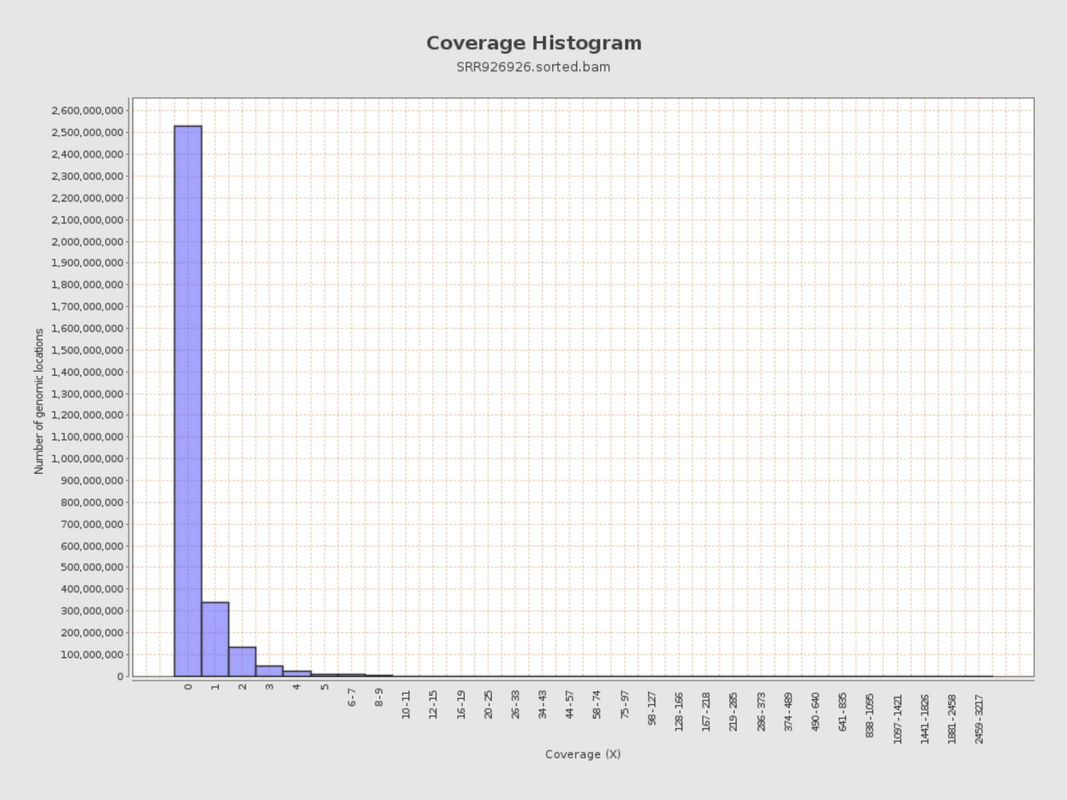
		bases	coverage	deviation
chr1	249250621	87549328	0.3513	1.2958
chr2	243199373	84607192	0.3479	2.9819
chr3	198022430	63187090	0.3191	0.8671
chr4	191154276	55592776	0.2908	1.1614
chr5	180915260	59596434	0.3294	0.8839
chr6	171115067	54564864	0.3189	1.0958
chr7	159138663	49182269	0.3091	0.9556
chr8	146364022	44523502	0.3042	0.8897
chr9	141213431	43842293	0.3105	1.2498
chr10	135534747	49234041	0.3633	1.8613
chr11	135006516	48914805	0.3623	1.0255
chr12	133851895	45947579	0.3433	0.9578
chr13	115169878	27886081	0.2421	0.7479
chr14	107349540	30970731	0.2885	0.8615
chr15	102531392	32426897	0.3163	0.8849
chr16	90354753	31293988	0.3463	1.7133
chr17	81195210	30033233	0.3699	1.0093
chr18	78077248	26140743	0.3348	1.2891
chr19	59128983	20320265	0.3437	1.1076
chr20	63025520	24802182	0.3935	1.0164
chr21	48129895	12090249	0.2512	1.1716
chr22	51304566	14575686	0.2841	0.8956
chrMT	16571	319704	19.293	14.9525
chrX	155270560	50747839	0.3268	0.9103

chrY	59373566	1865372	0.0314	1.2533

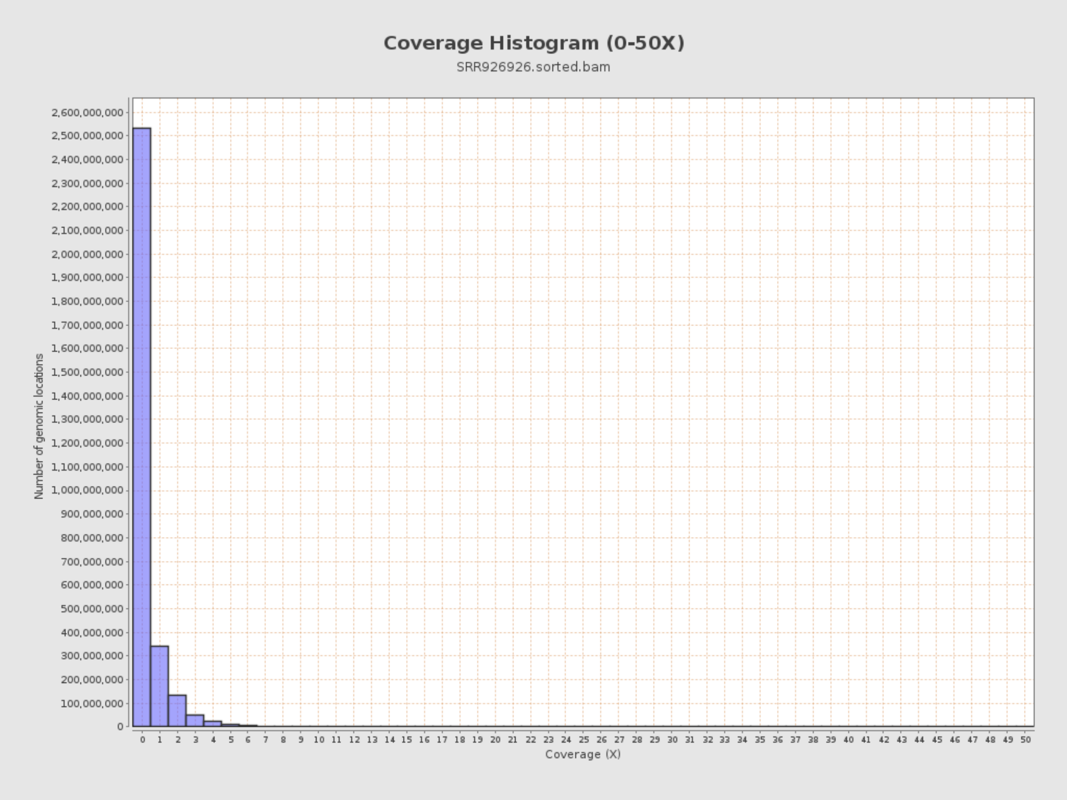
3. Results : Coverage across reference



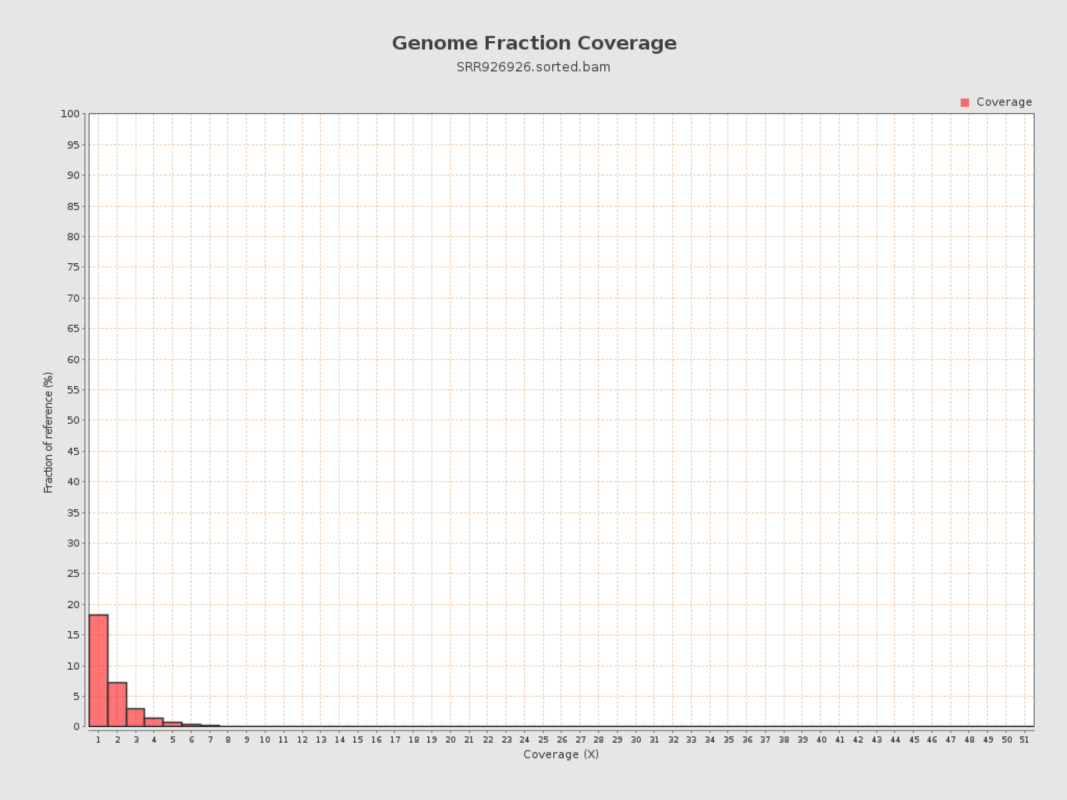
4. Results : Coverage Histogram



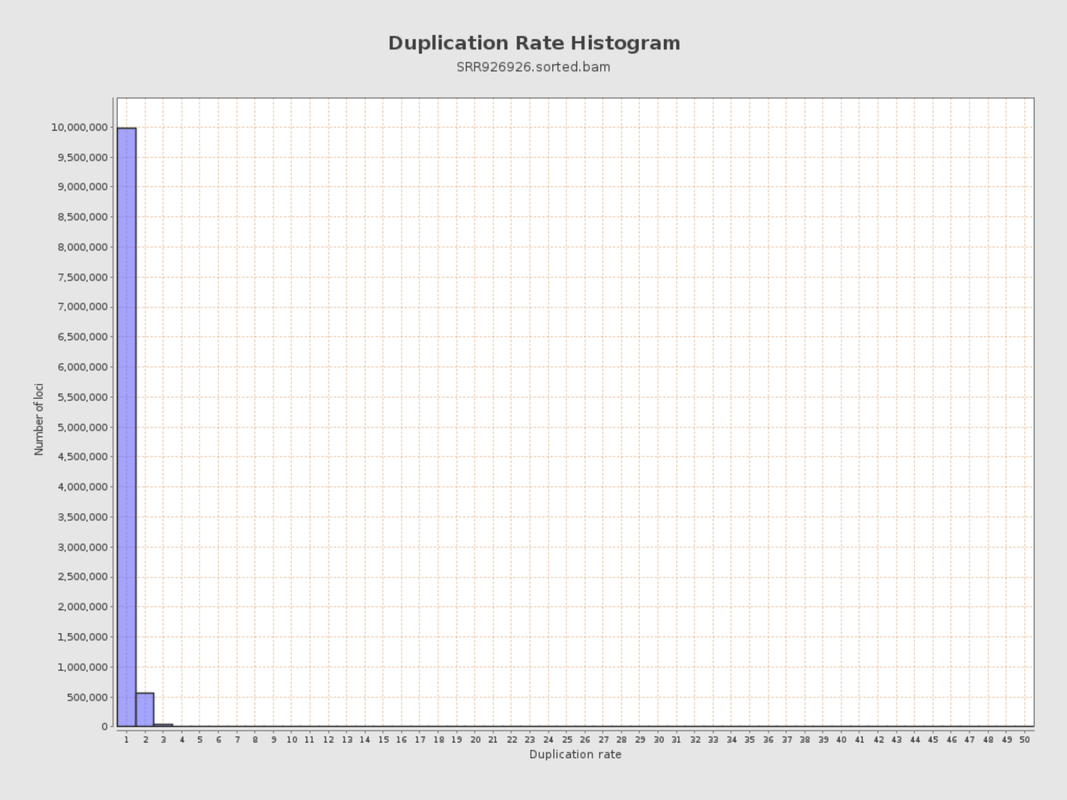
5. Results : Coverage Histogram (0-50X)



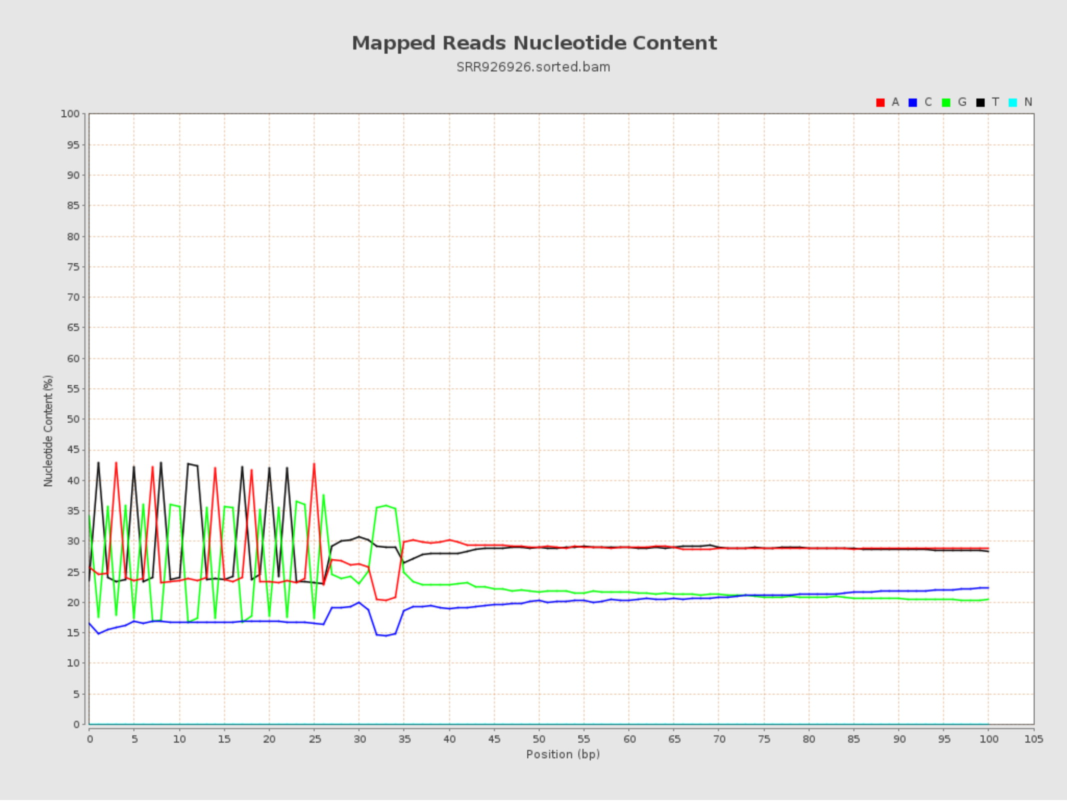
6. Results : Genome Fraction Coverage



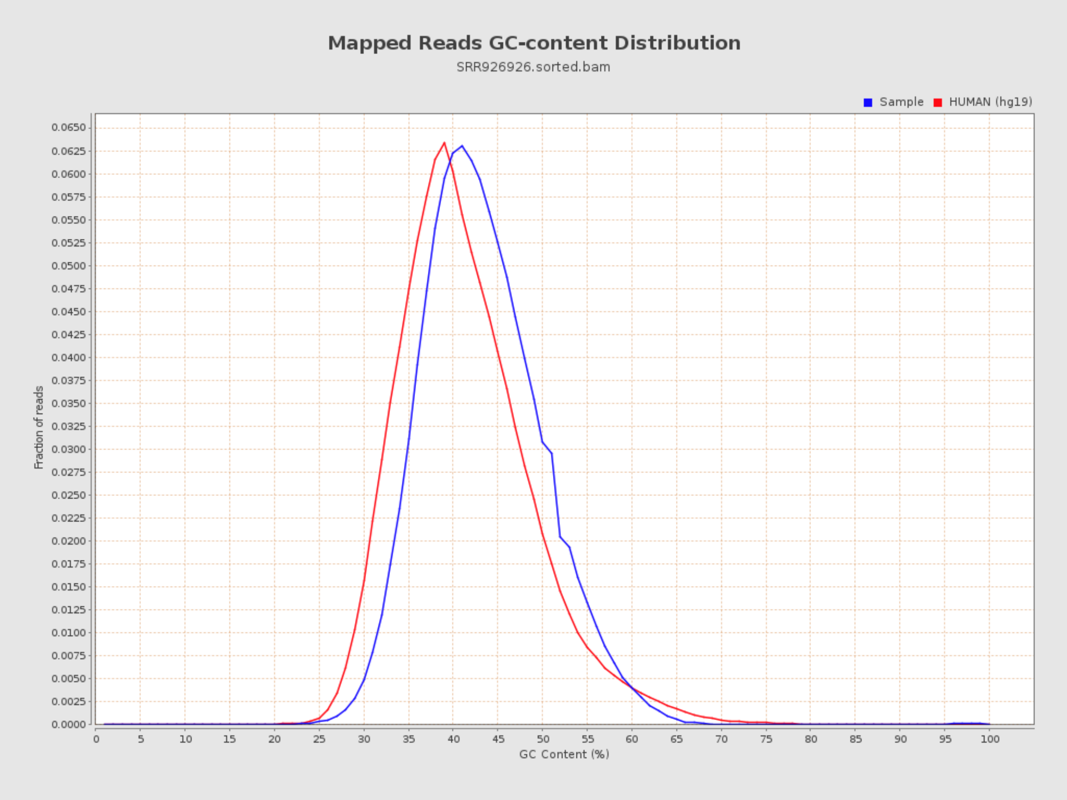
7. Results : Duplication Rate Histogram



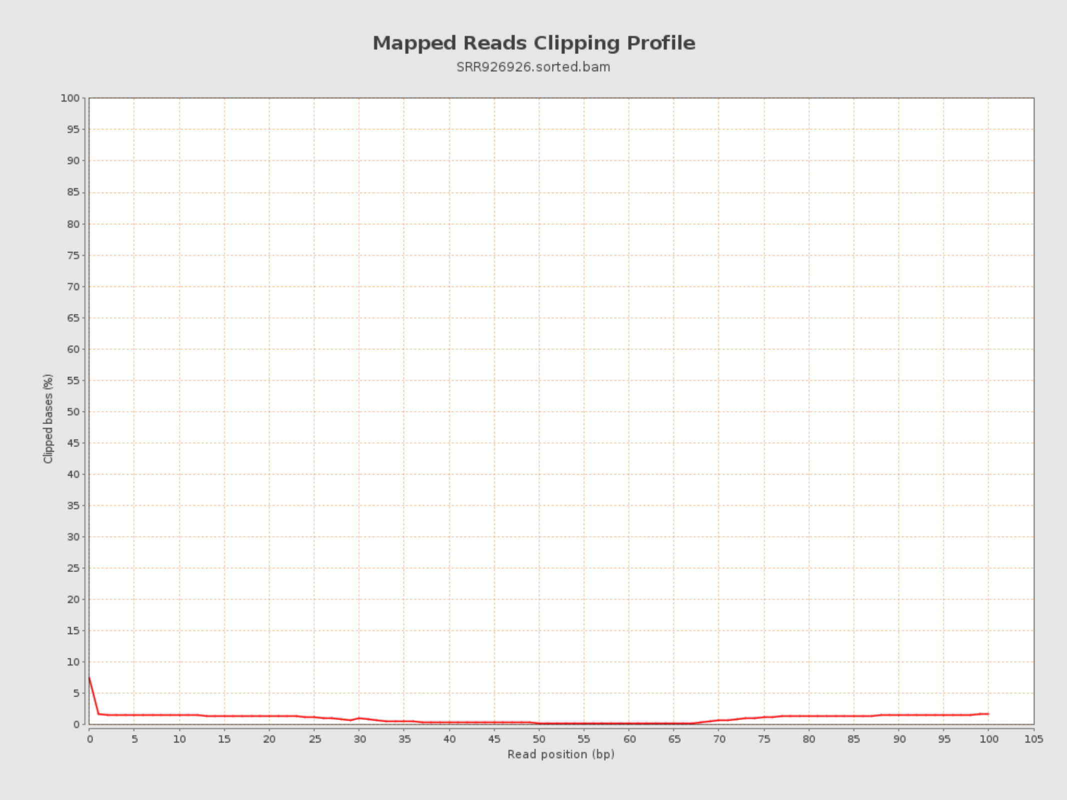
8. Results : Mapped Reads Nucleotide Content



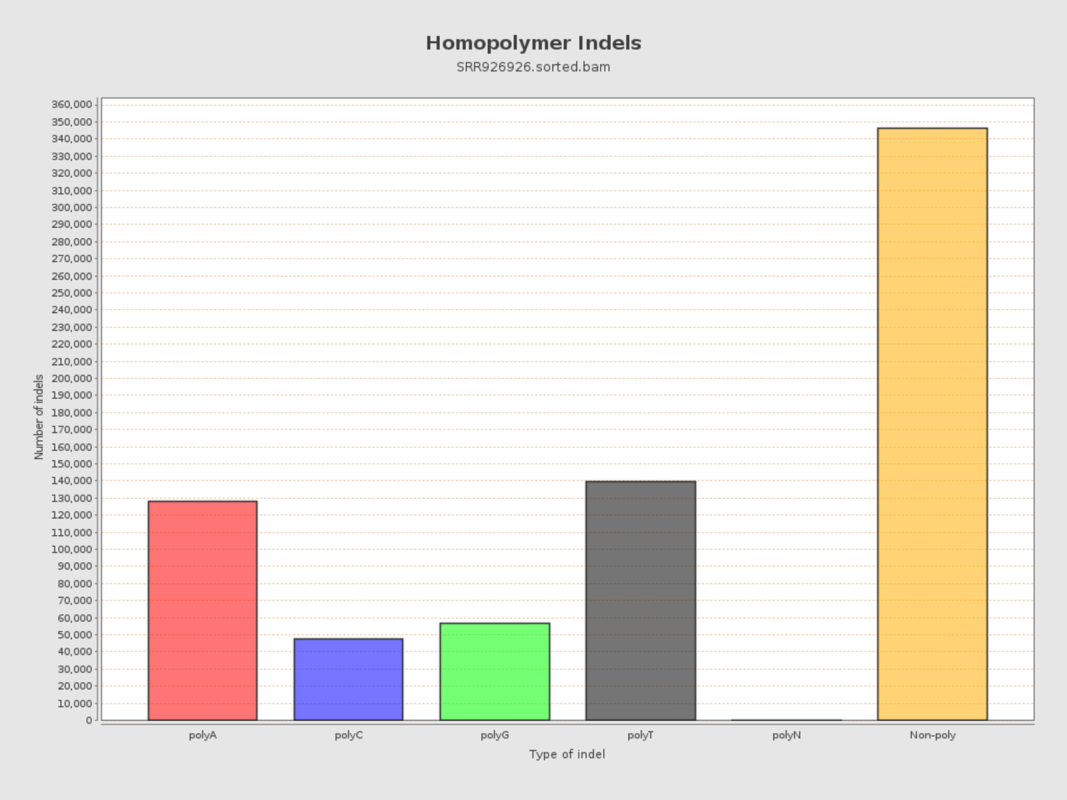
9. Results : Mapped Reads GC-content Distribution



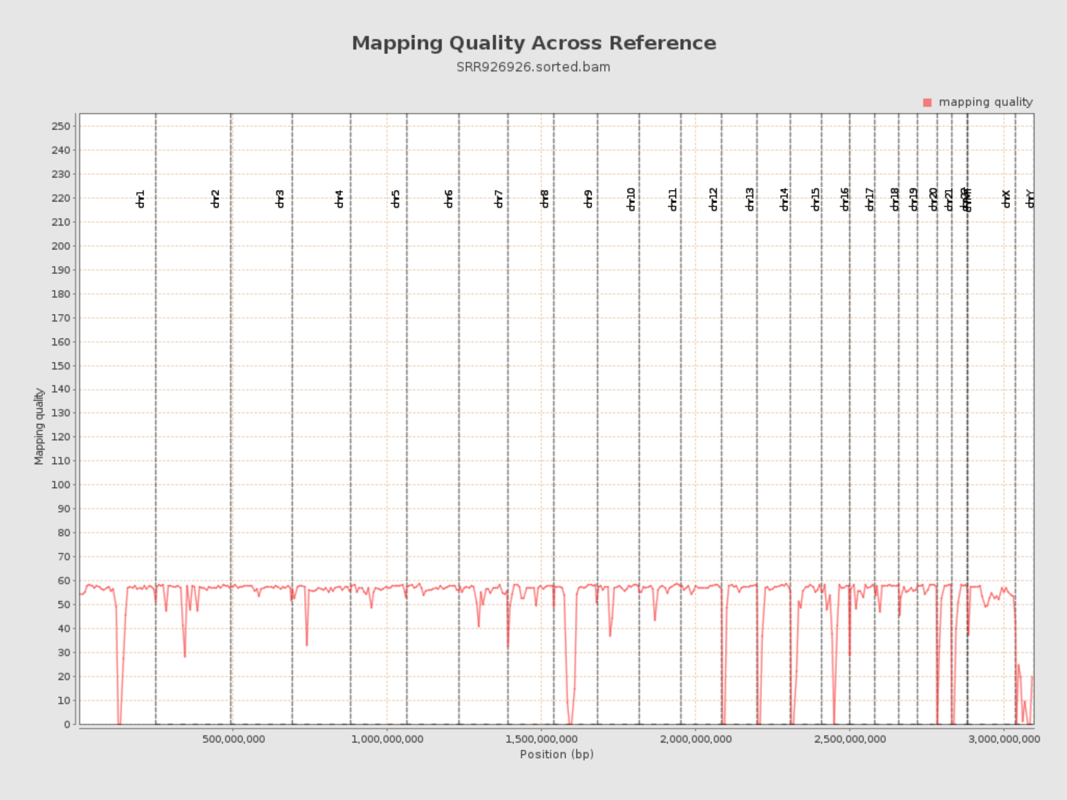
10. Results : Mapped Reads Clipping Profile



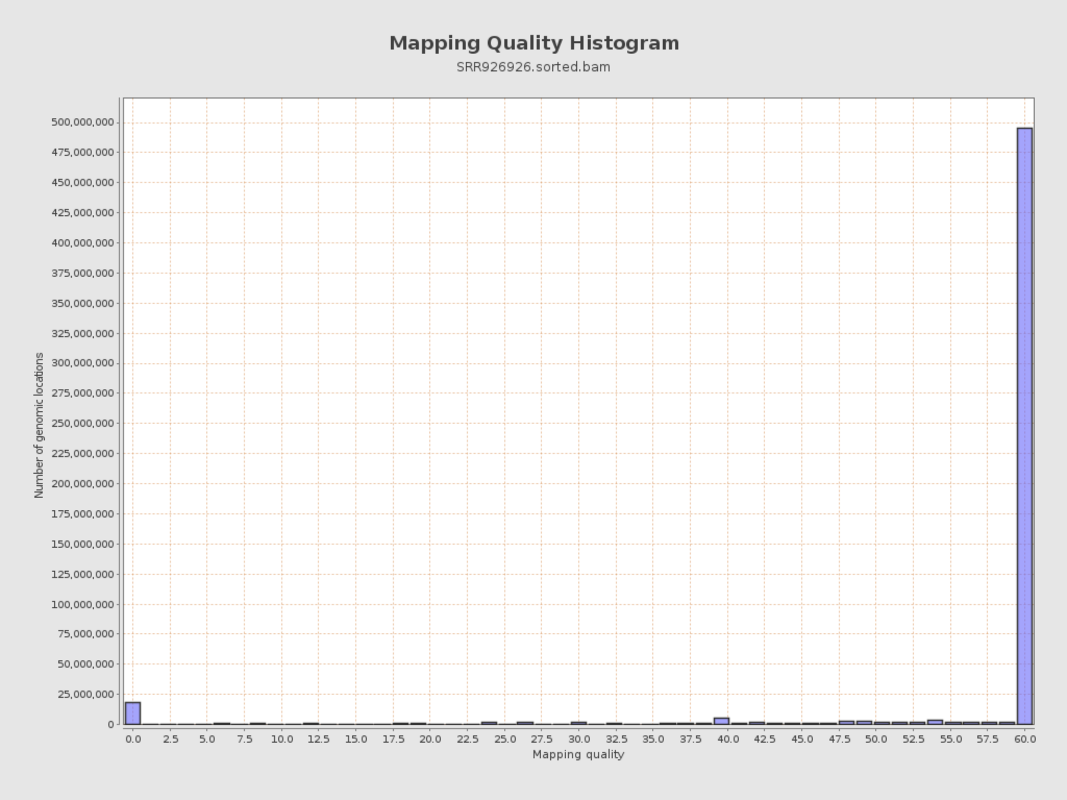
11. Results : Homopolymer Indels



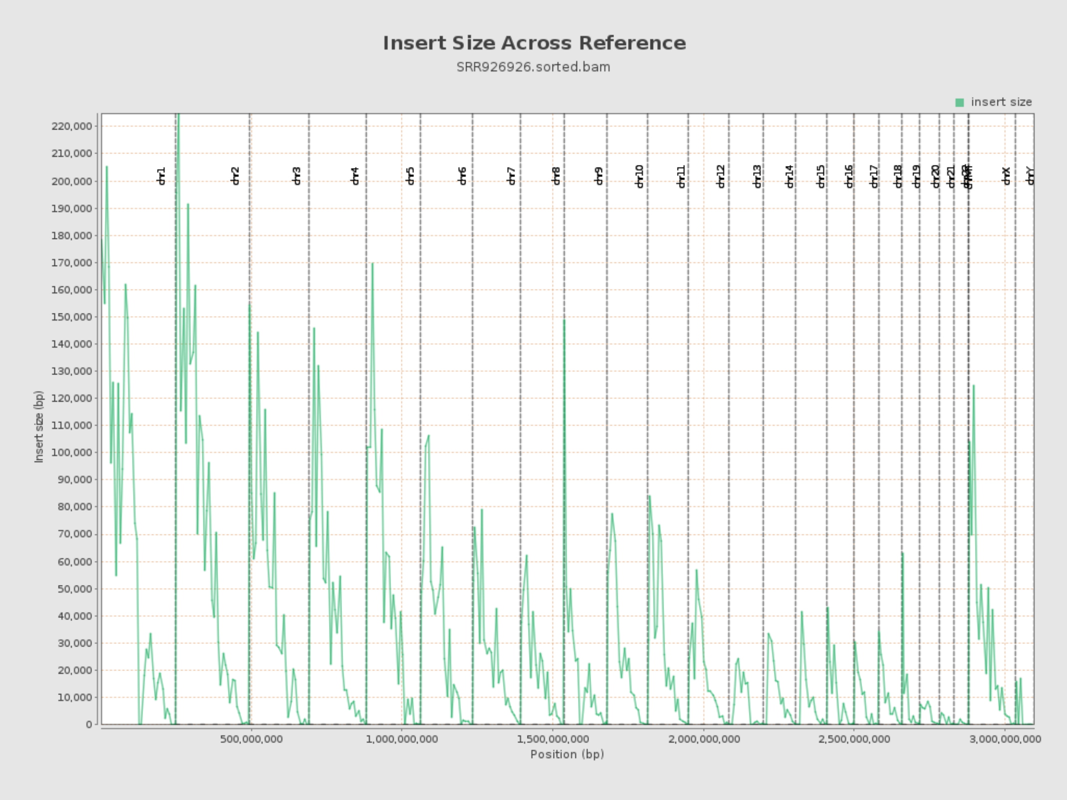
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram