Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 20:39:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927046.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_SRR927046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927046_1.fastq.gz SRR927046_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 20:39:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,288,372
Mapped reads	32,587,138 / 97.89%
Unmapped reads	701,234 / 2.11%
Mapped paired reads	32,587,138 / 97.89%
Mapped reads, first in pair	16,375,777 / 49.19%
Mapped reads, second in pair	16,211,361 / 48.7%
Mapped reads, both in pair	32,179,422 / 96.67%
Mapped reads, singletons	407,716 / 1.22%
Secondary alignments	0
Supplementary alignments	301,780 / 0.91%
Read min/max/mean length	30 / 101 / 101.38
Duplicated reads (estimated)	2,612,302 / 7.85%
Duplication rate	6.28%
Clipped reads	9,314,723 / 27.98%

2.2. ACGT Content

Number/percentage of A's	877,563,078 / 28.78%
Number/percentage of C's	601,368,321 / 19.72%
Number/percentage of T's	890,397,556 / 29.2%
Number/percentage of G's	679,215,141 / 22.28%
Number/percentage of N's	461,566 / 0.02%

GC Percentage	42%

2.3. Coverage

Mean	0.9856
Standard Deviation	3.7119

2.4. Mapping Quality

Mean Mapping Quality	53.48

2.5. Insert size

Mean	105,524.66
Standard Deviation	3,182,361.96
P25/Median/P75	150 / 194 / 261

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	32,749,316
Insertions	492,927
Mapped reads with at least one insertion	1.49%
Deletions	1,602,956
Mapped reads with at least one deletion	4.79%
Homopolymer indels	52.81%

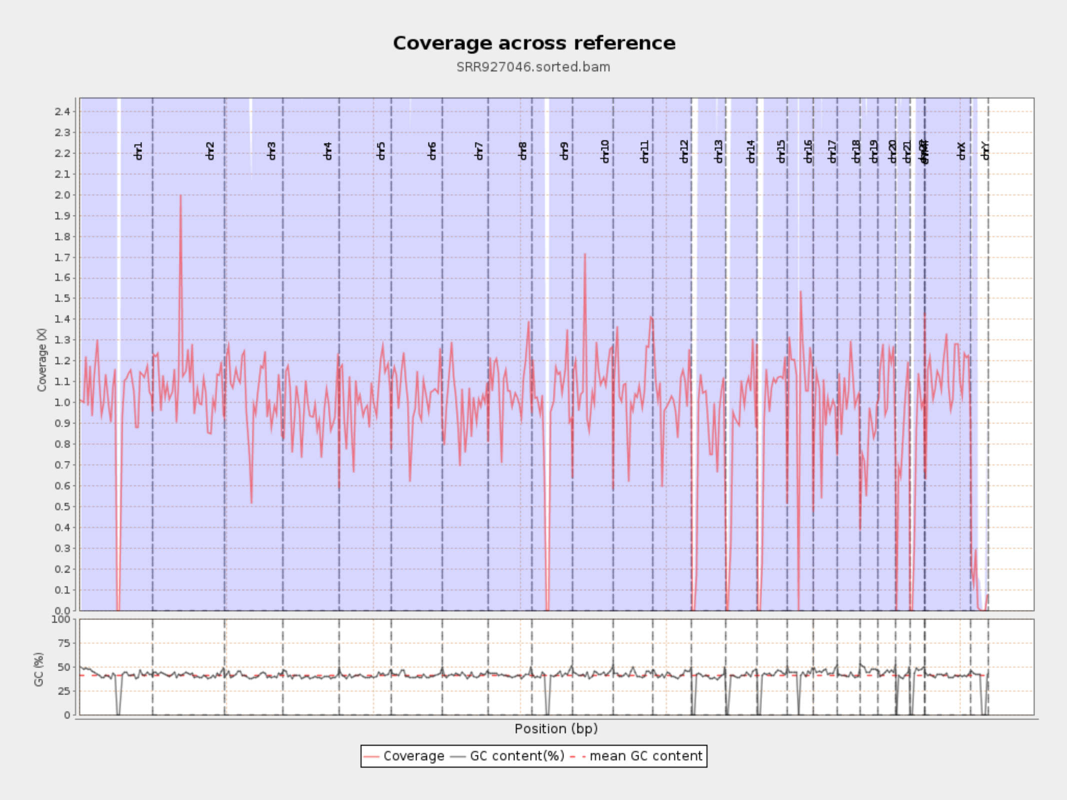
2.7. Chromosome stats

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

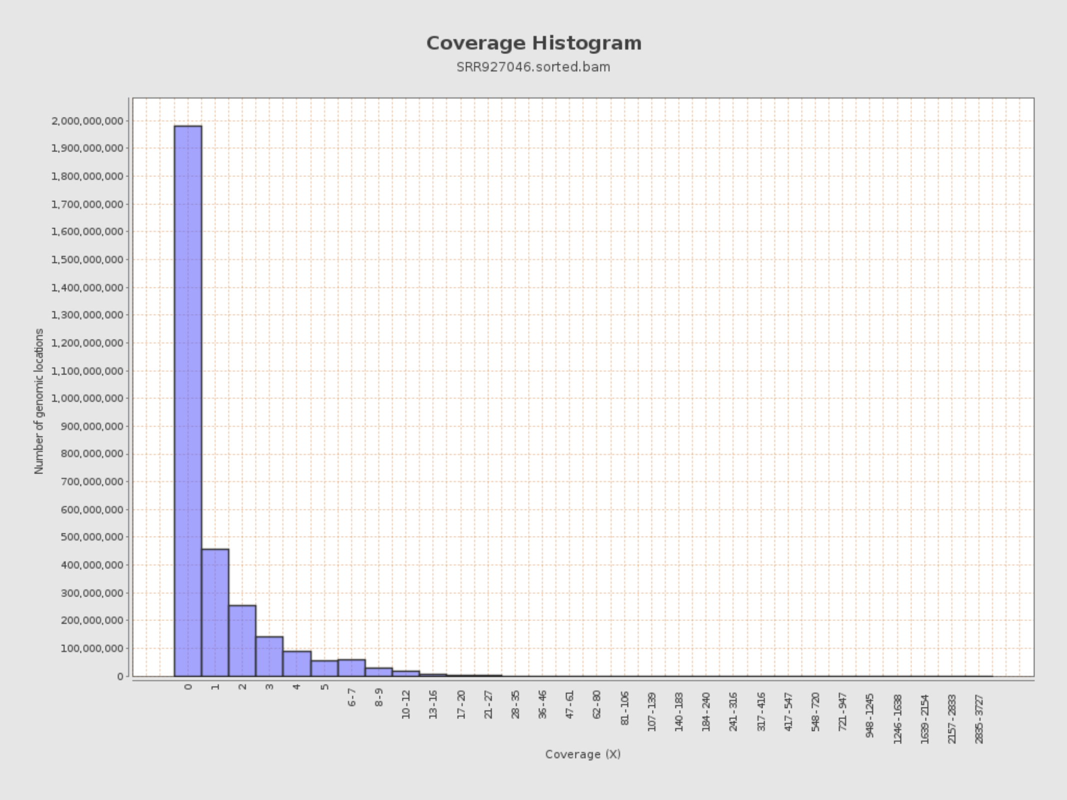
		bases	coverage	deviation
chr1	249250621	249318046	1.0003	4.4385
chr2	243199373	268770297	1.1051	6.7264
chr3	198022430	206946648	1.0451	2.0262
chr4	191154276	184019035	0.9627	2.8894
chr5	180915260	184762465	1.0213	1.974
chr6	171115067	178948439	1.0458	2.0874
chr7	159138663	155412208	0.9766	2.4985
chr8	146364022	158812702	1.0851	2.4701
chr9	141213431	130643022	0.9251	4.5444
chr10	135534747	153241207	1.1306	7.4726
chr11	135006516	144843152	1.0729	2.8839
chr12	133851895	137555942	1.0277	2.0241
chr13	115169878	91588657	0.7952	1.7507
chr14	107349540	90671231	0.8446	1.8825
chr15	102531392	89174921	0.8697	1.9008
chr16	90354753	97435038	1.0784	4.9135
chr17	81195210	76901316	0.9471	3.0418
chr18	78077248	82678273	1.0589	4.5674
chr19	59128983	46581486	0.7878	2.7949
chr20	63025520	70466539	1.1181	2.2957
chr21	48129895	38480868	0.7995	2.5437
chr22	51304566	34652256	0.6754	1.7506
chrMT	16571	23697	1.43	1.8051
chrX	155270560	174346405	1.1229	2.4977

chrY	59373566	4996186	0.0841	3.8046

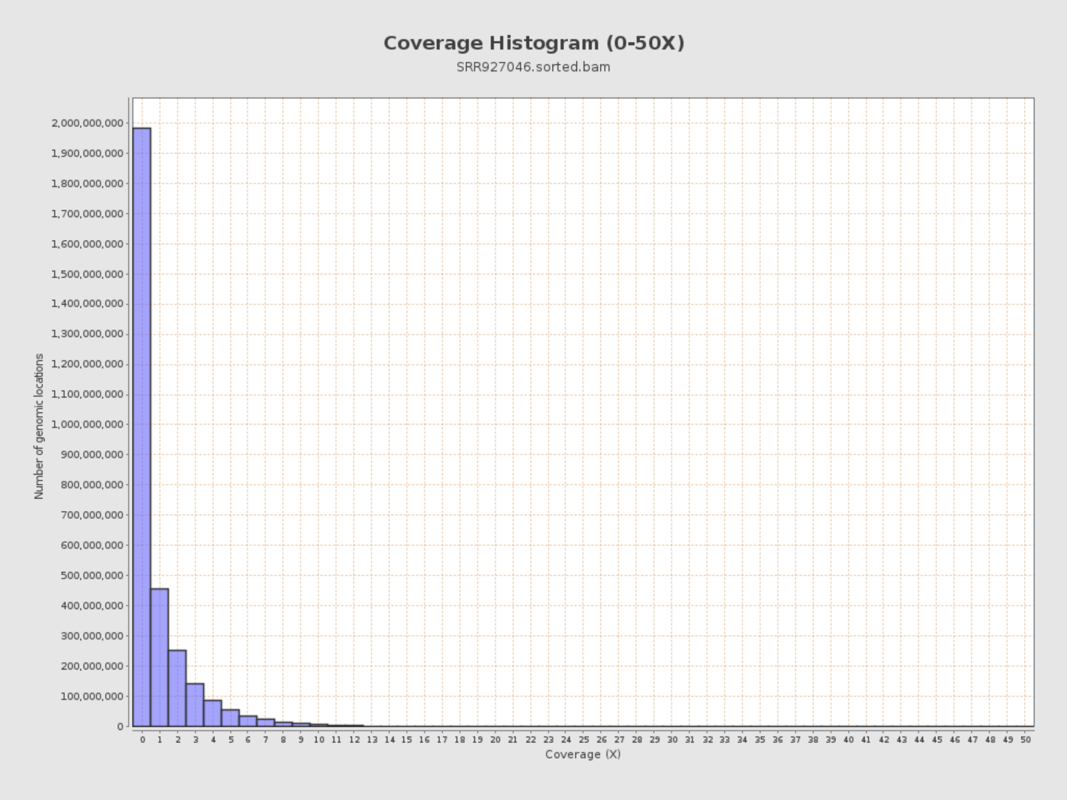
3. Results : Coverage across reference



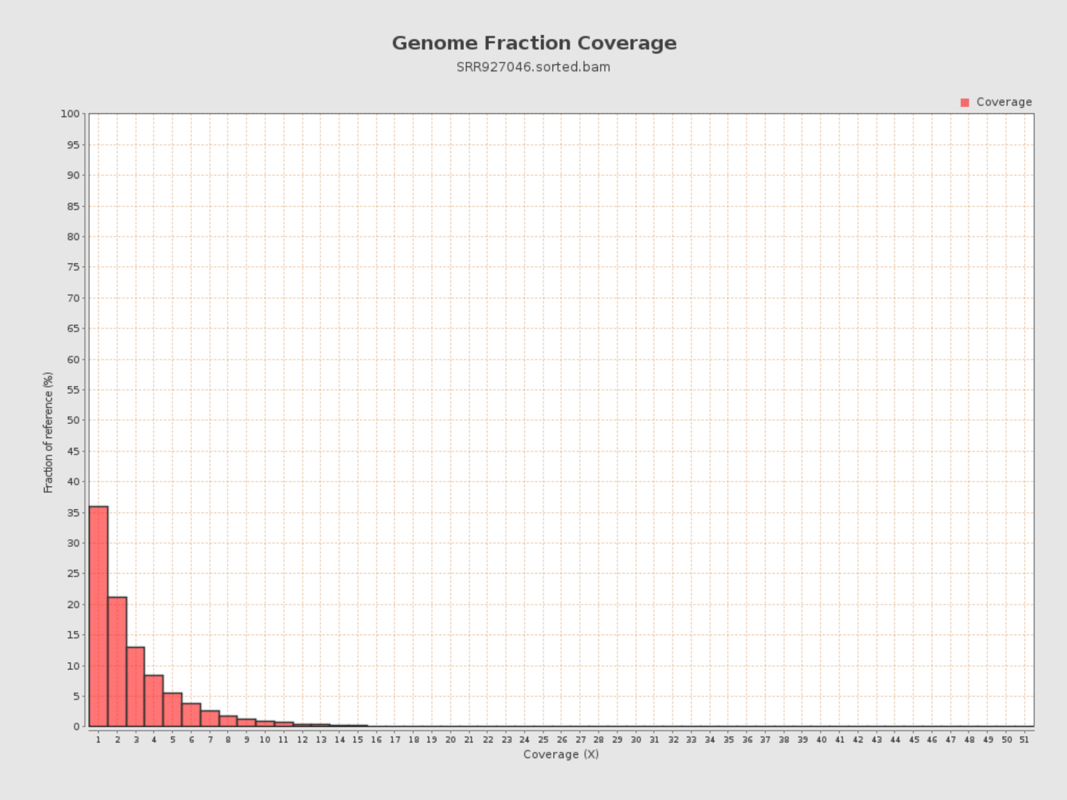
4. Results : Coverage Histogram



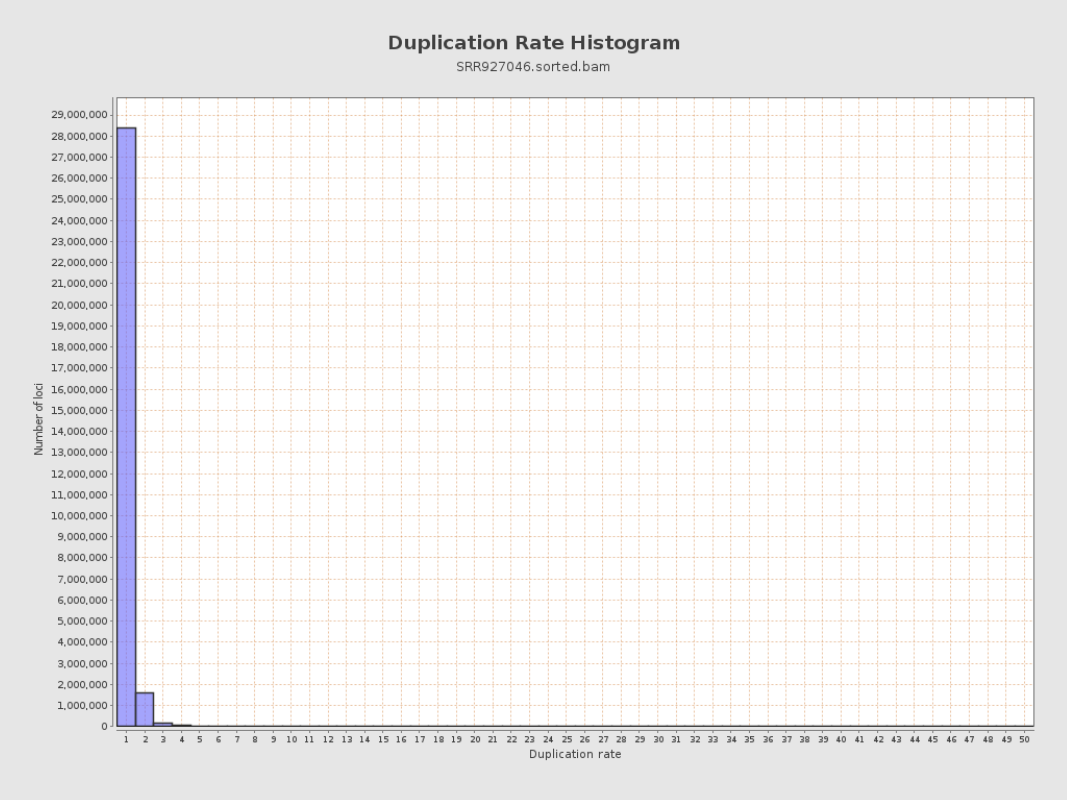
5. Results : Coverage Histogram (0-50X)



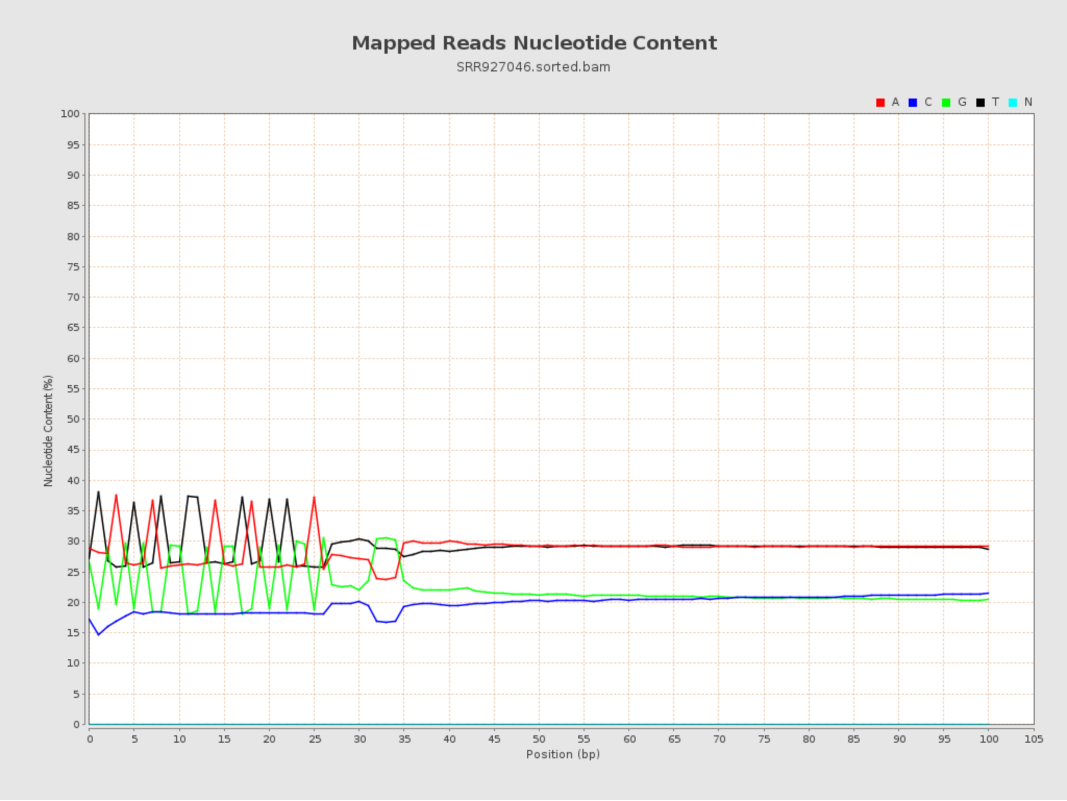
6. Results : Genome Fraction Coverage



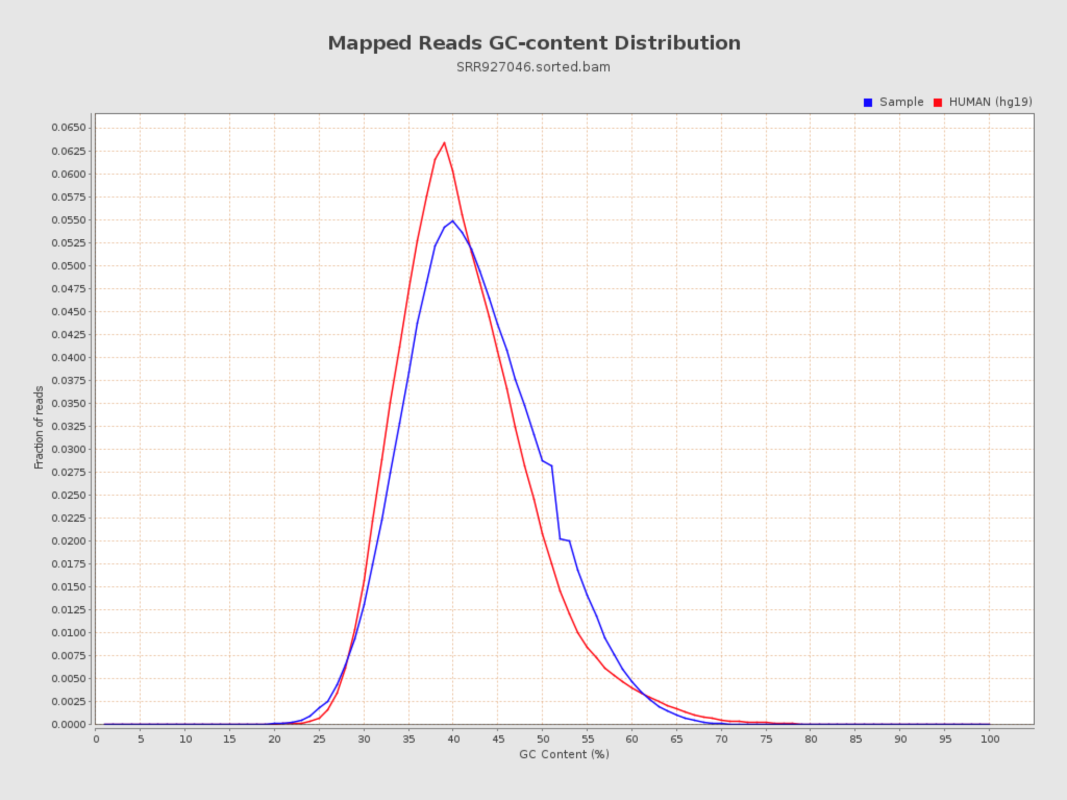
7. Results : Duplication Rate Histogram



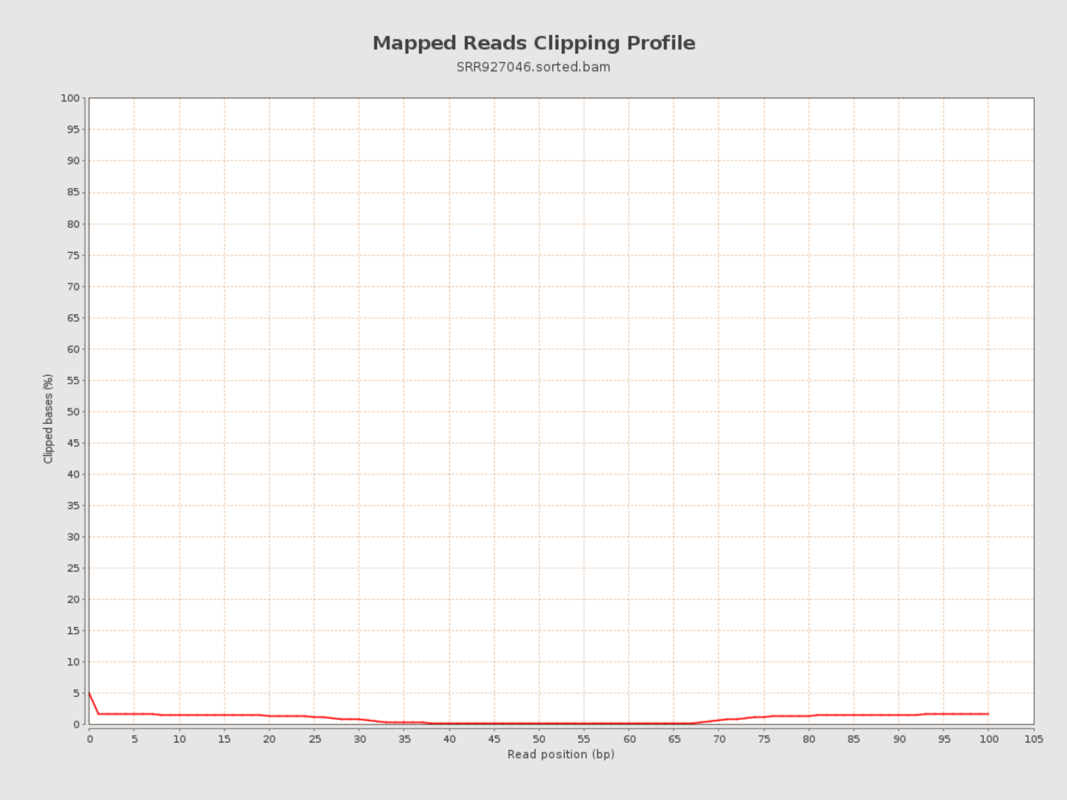
8. Results : Mapped Reads Nucleotide Content



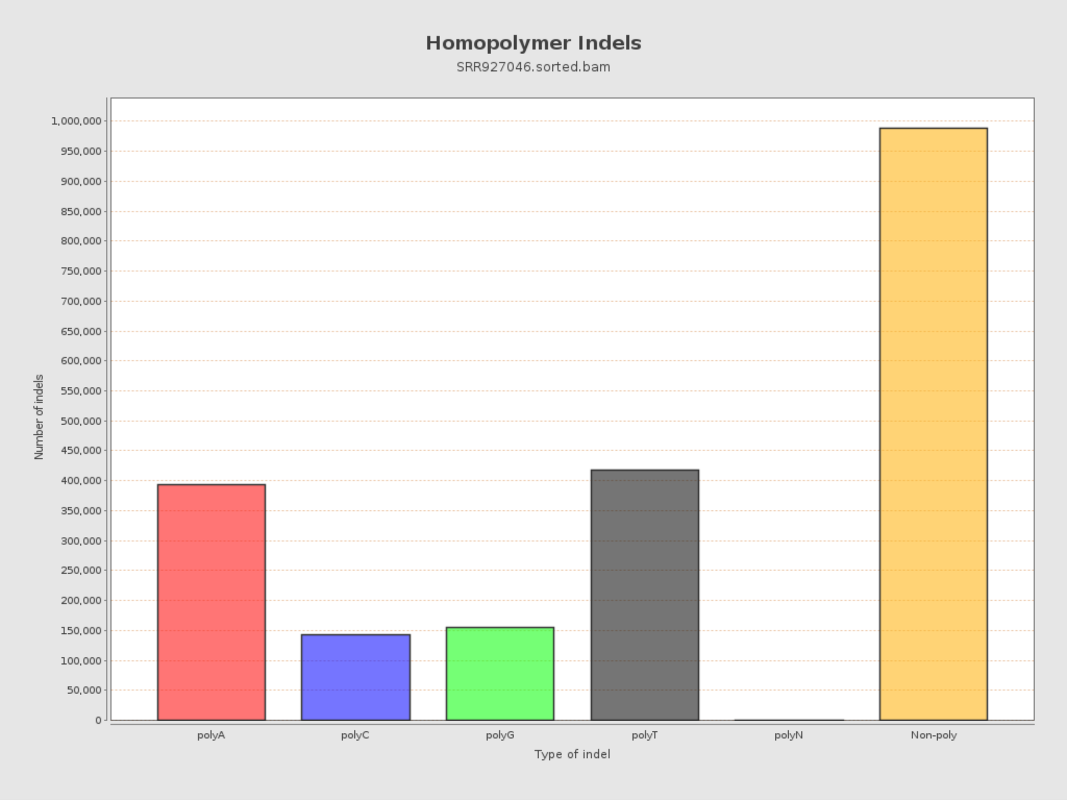
9. Results : Mapped Reads GC-content Distribution



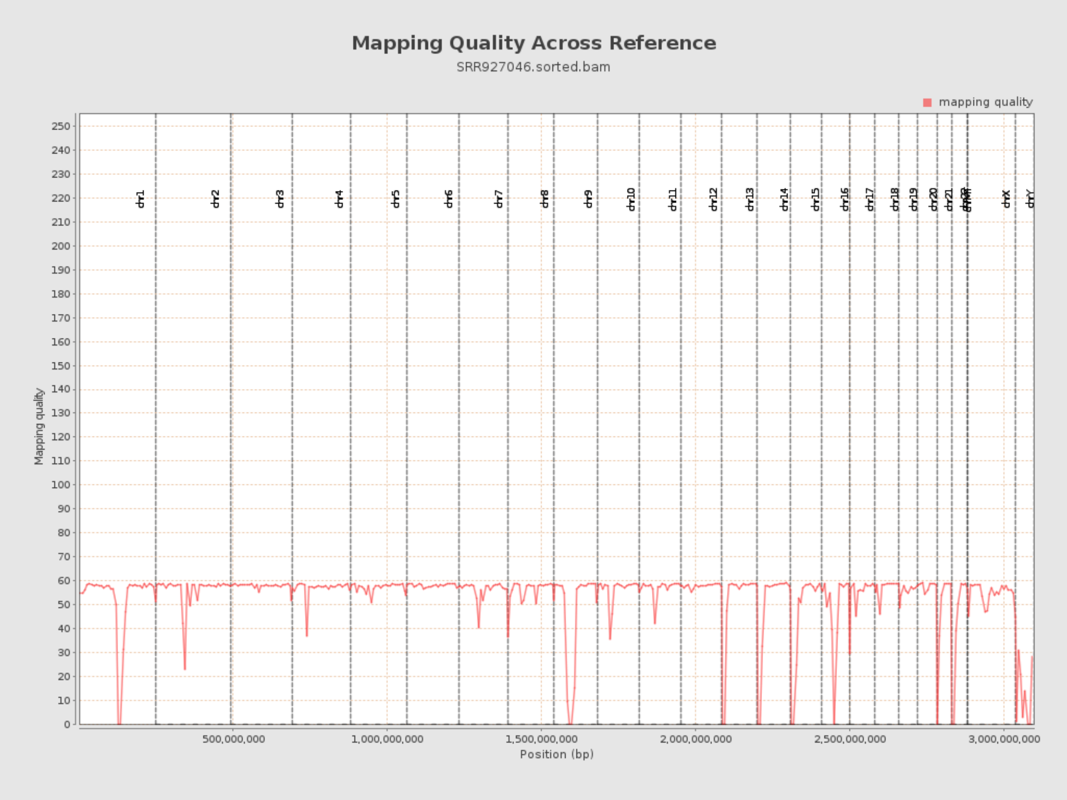
10. Results : Mapped Reads Clipping Profile



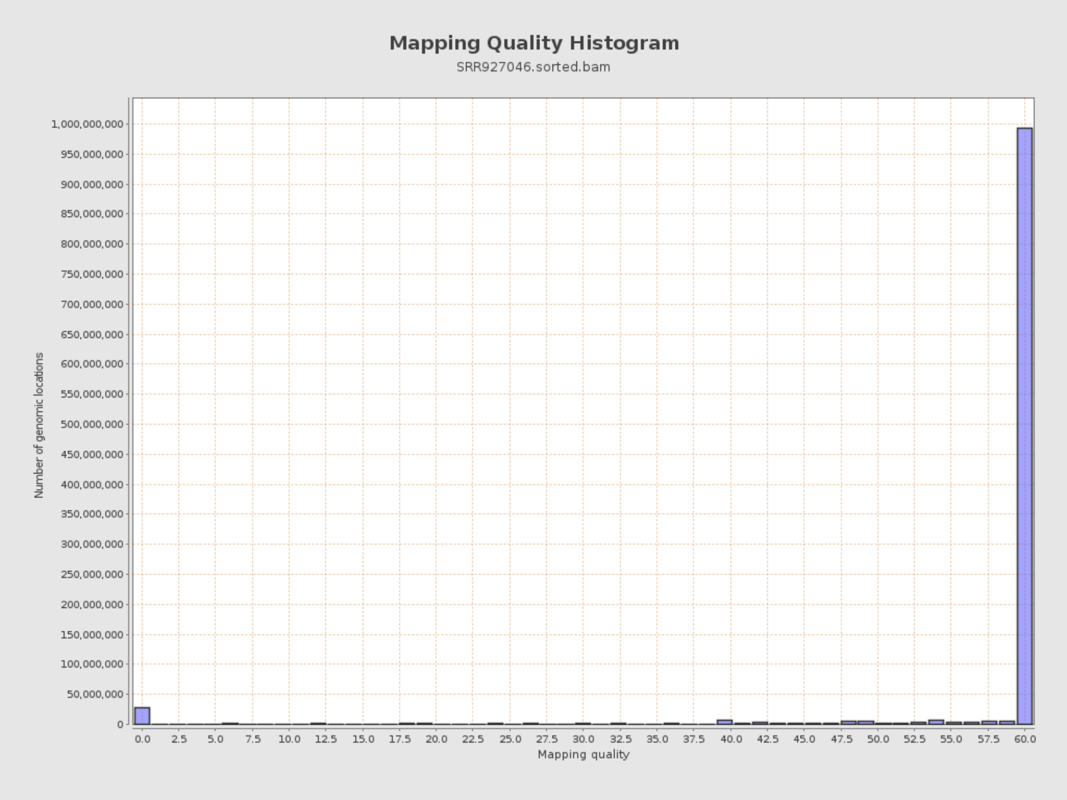
11. Results : Homopolymer Indels



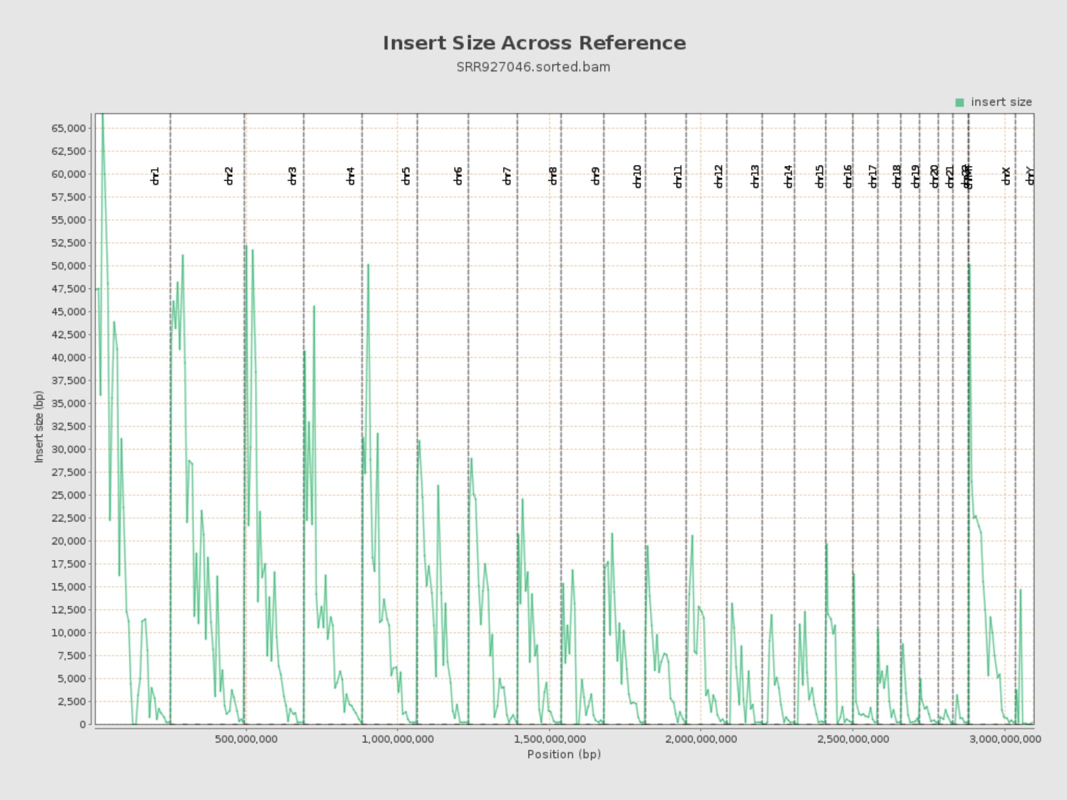
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram