Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 00:39:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926945.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_SRR926945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926945_1.fastq.gz SRR926945_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 00:39:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,681,706
Mapped reads	12,247,358 / 96.58%
Unmapped reads	434,348 / 3.42%
Mapped paired reads	12,247,358 / 96.58%
Mapped reads, first in pair	6,129,564 / 48.33%
Mapped reads, second in pair	6,117,794 / 48.24%
Mapped reads, both in pair	12,083,762 / 95.28%
Mapped reads, singletons	163,596 / 1.29%
Secondary alignments	0
Supplementary alignments	240,848 / 1.9%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	728,611 / 5.75%
Duplication rate	4.72%
Clipped reads	5,173,161 / 40.79%

2.2. ACGT Content

Number/percentage of A's	312,129,195 / 27.9%
Number/percentage of C's	224,974,586 / 20.11%
Number/percentage of T's	318,504,305 / 28.47%
Number/percentage of G's	262,894,931 / 23.5%
Number/percentage of N's	48,246 / 0%

GC Percentage	43.62%

2.3. Coverage

Mean	0.3616
Standard Deviation	1.5886

2.4. Mapping Quality

Mean Mapping Quality	53.11

2.5. Insert size

Mean	205,587.67
Standard Deviation	4,553,893.54
P25/Median/P75	145 / 187 / 250

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	10,125,664
Insertions	185,218
Mapped reads with at least one insertion	1.48%
Deletions	546,419
Mapped reads with at least one deletion	4.35%
Homopolymer indels	51.76%

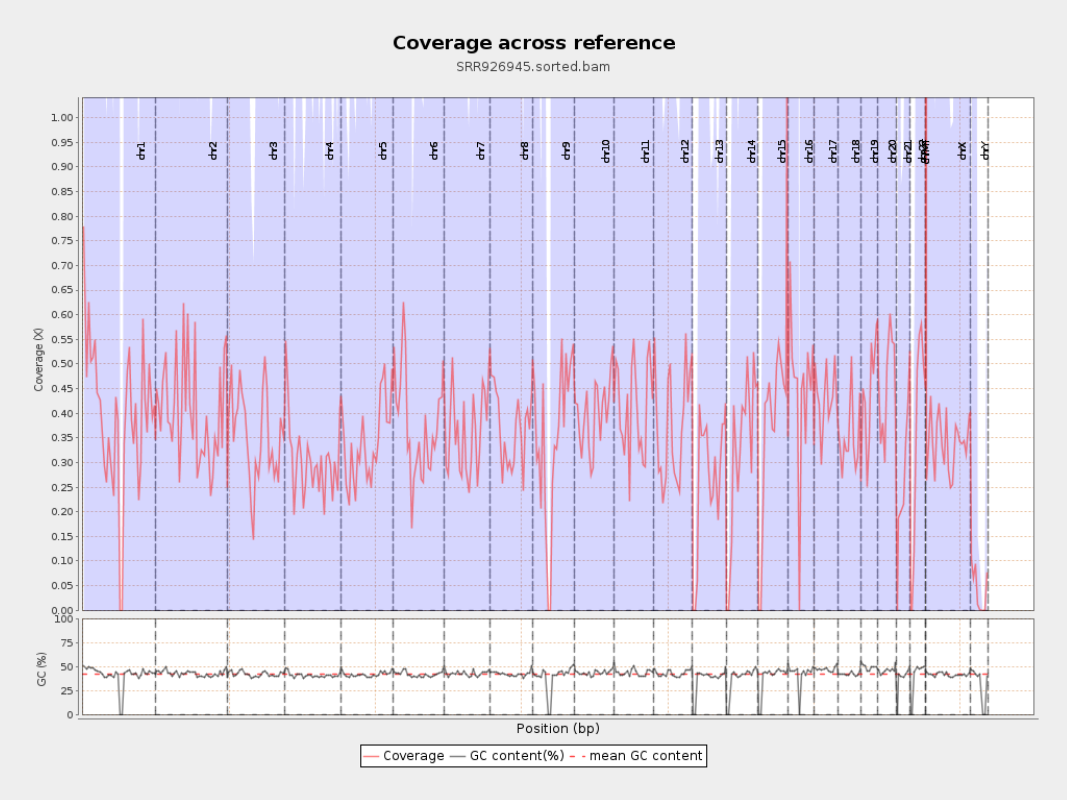
2.7. Chromosome stats

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

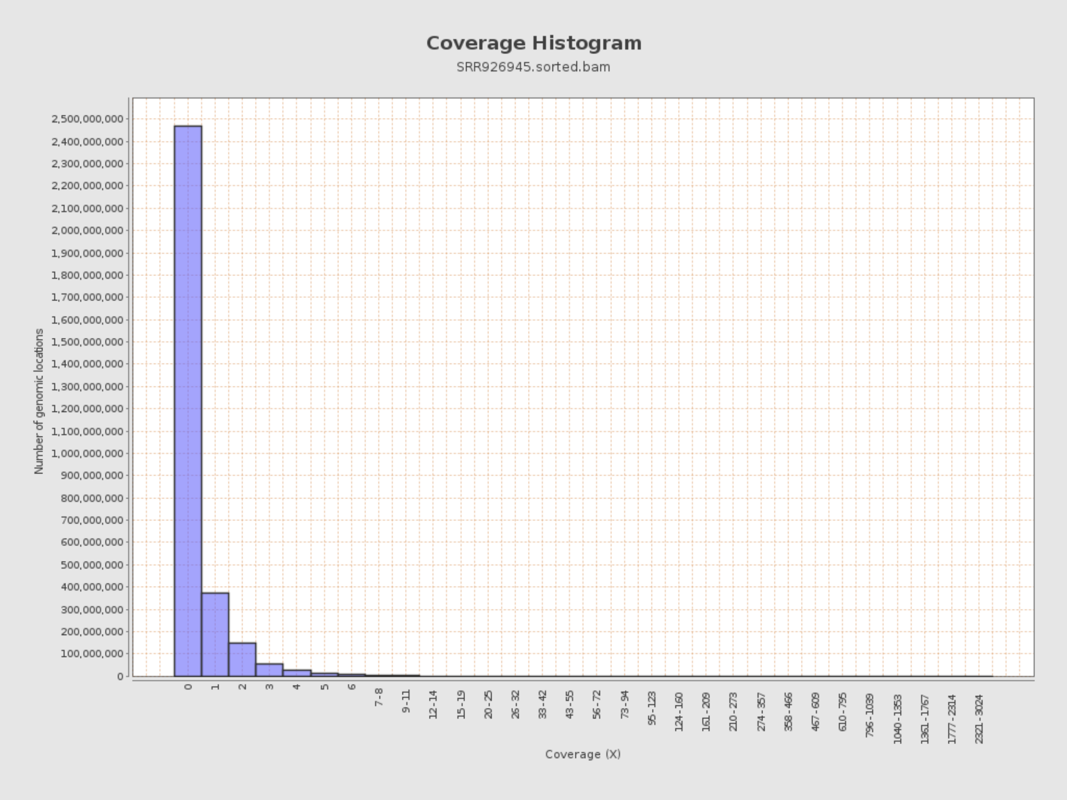
		bases	**coverage**	**deviation**
chr1	249250621	98463605	0.395	1.6835
chr2	243199373	97851847	0.4024	3.1846
chr3	198022430	69728141	0.3521	0.9098
chr4	191154276	57933662	0.3031	1.1752
chr5	180915260	62162765	0.3436	0.8969
chr6	171115067	63353332	0.3702	1.0509
chr7	159138663	57610182	0.362	1.1026
chr8	146364022	53566838	0.366	1.0114
chr9	141213431	48638909	0.3444	1.4736
chr10	135534747	53797778	0.3969	1.9936
chr11	135006516	55322572	0.4098	1.4989
chr12	133851895	50198637	0.375	1.0166
chr13	115169878	30587804	0.2656	0.7734
chr14	107349540	34792477	0.3241	0.9152
chr15	102531392	39292700	0.3832	1.0342
chr16	90354753	40096006	0.4438	2.0892
chr17	81195210	35306522	0.4348	1.2001
chr18	78077248	27002079	0.3458	1.4546
chr19	59128983	25758886	0.4356	1.3887
chr20	63025520	28807811	0.4571	1.1642
chr21	48129895	13087316	0.2719	1.0885
chr22	51304566	18305615	0.3568	1.0339
chrMT	16571	2580614	155.7307	143.3587
chrX	155270560	52644692	0.3391	0.9626

chrY	59373566	2476552	0.0417	1.269

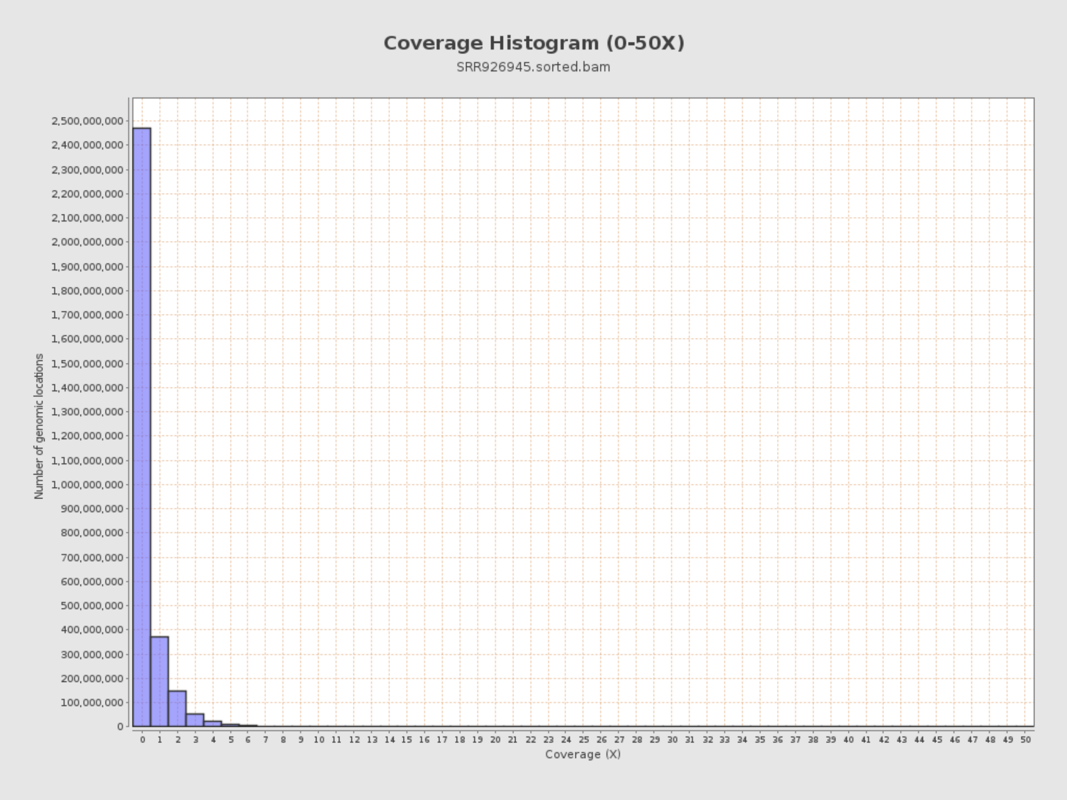
3. Results : Coverage across reference



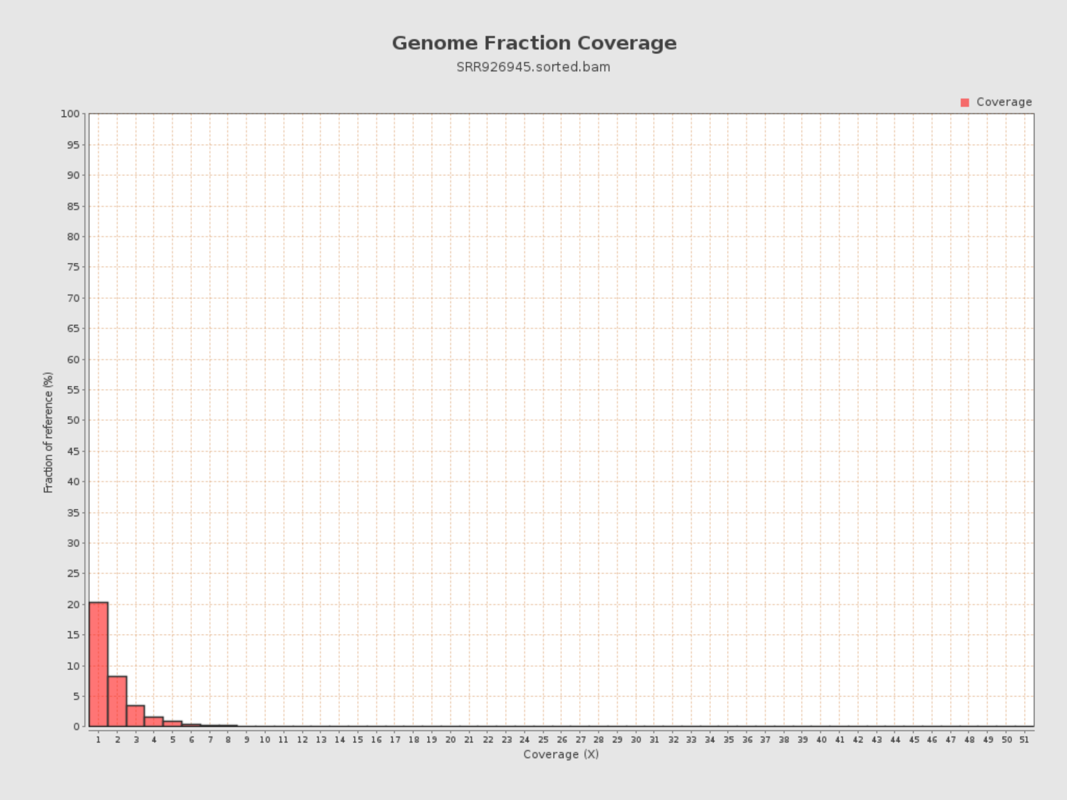
4. Results : Coverage Histogram



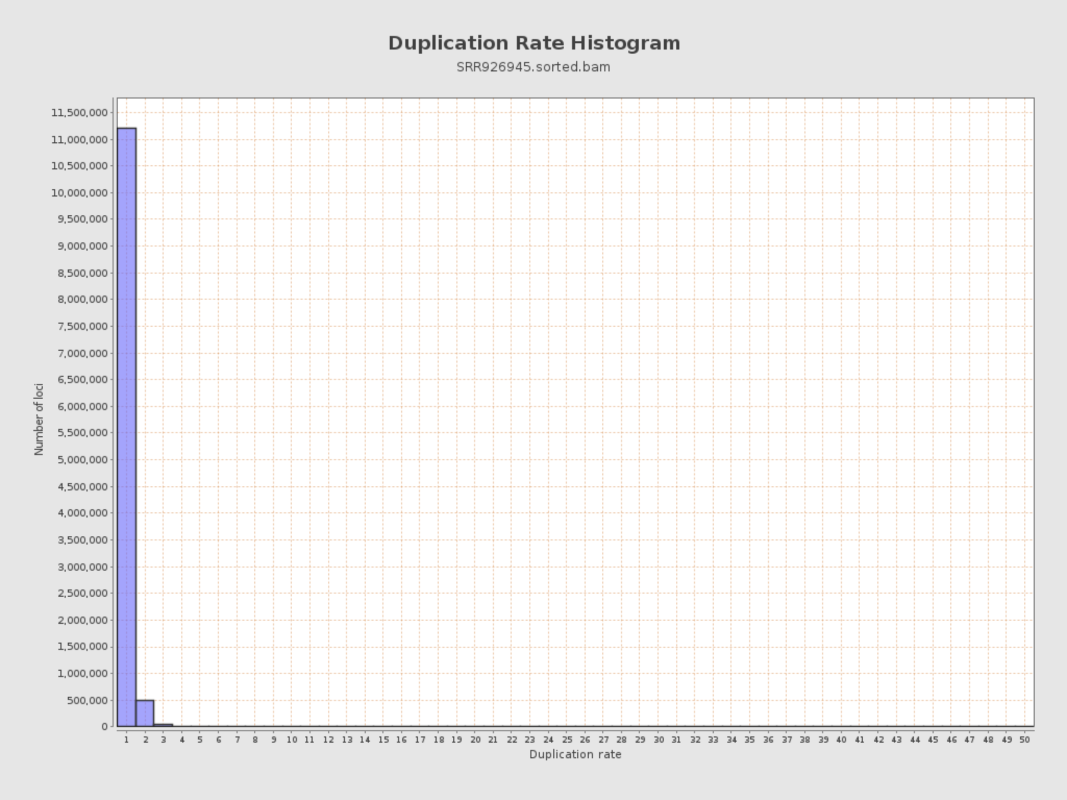
5. Results : Coverage Histogram (0-50X)



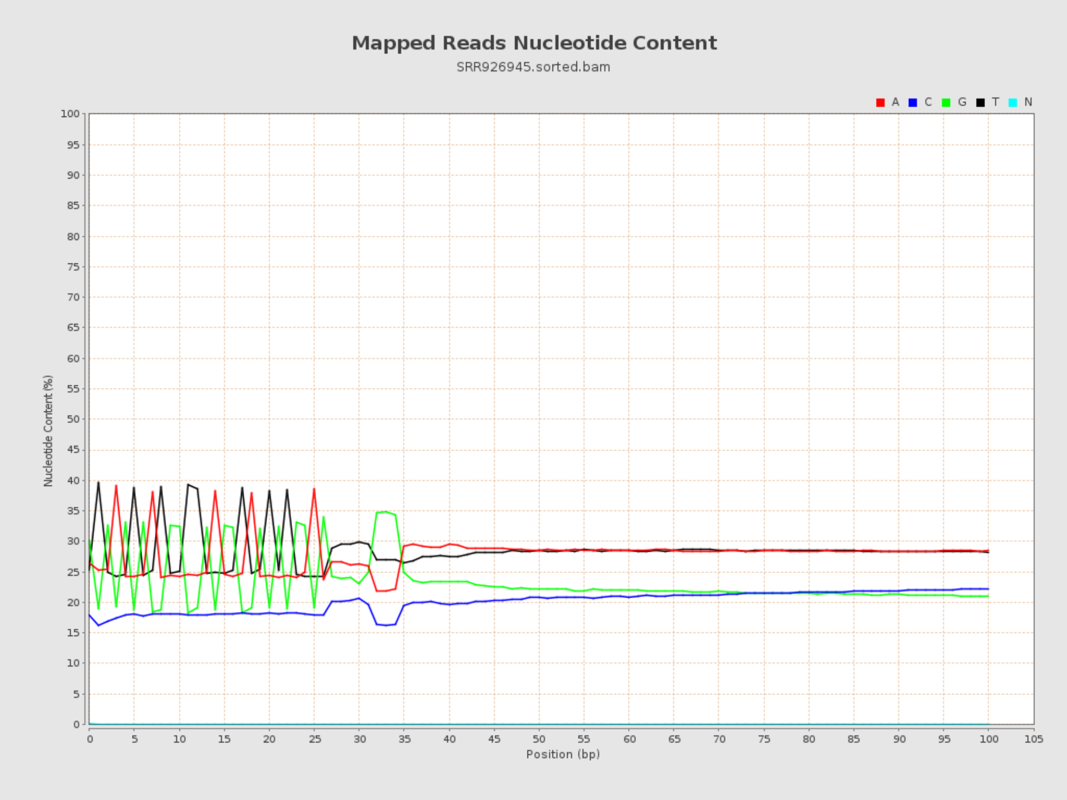
6. Results : Genome Fraction Coverage



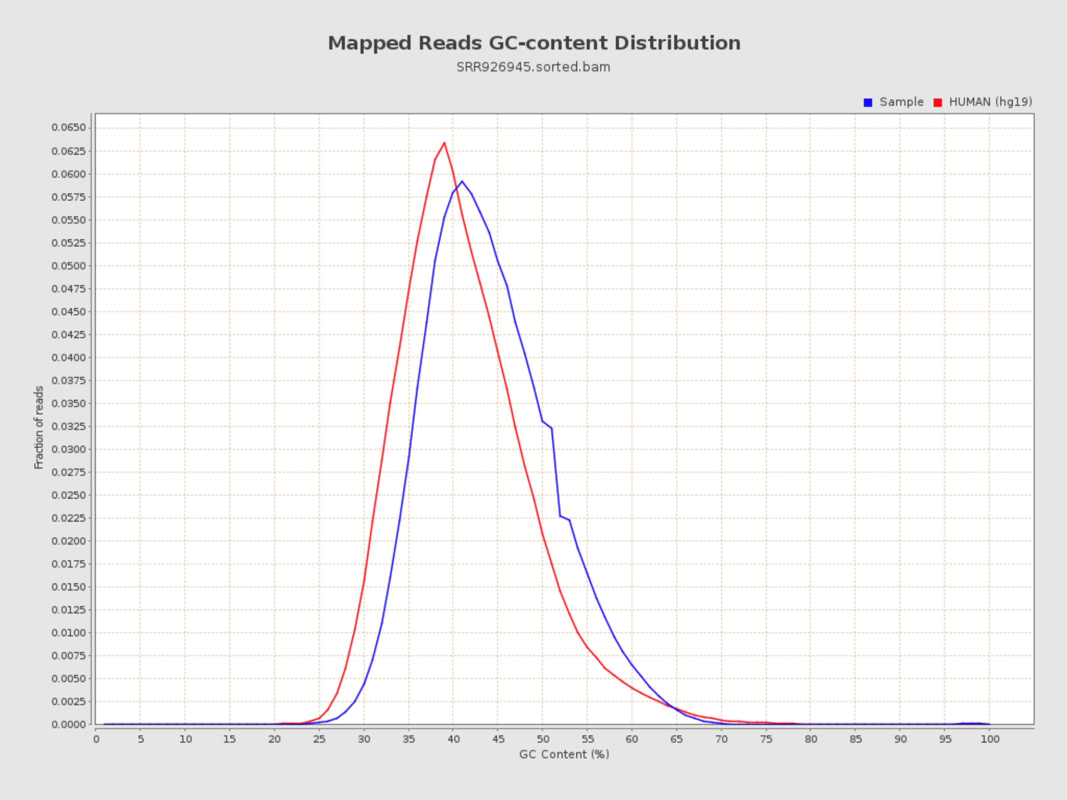
7. Results : Duplication Rate Histogram



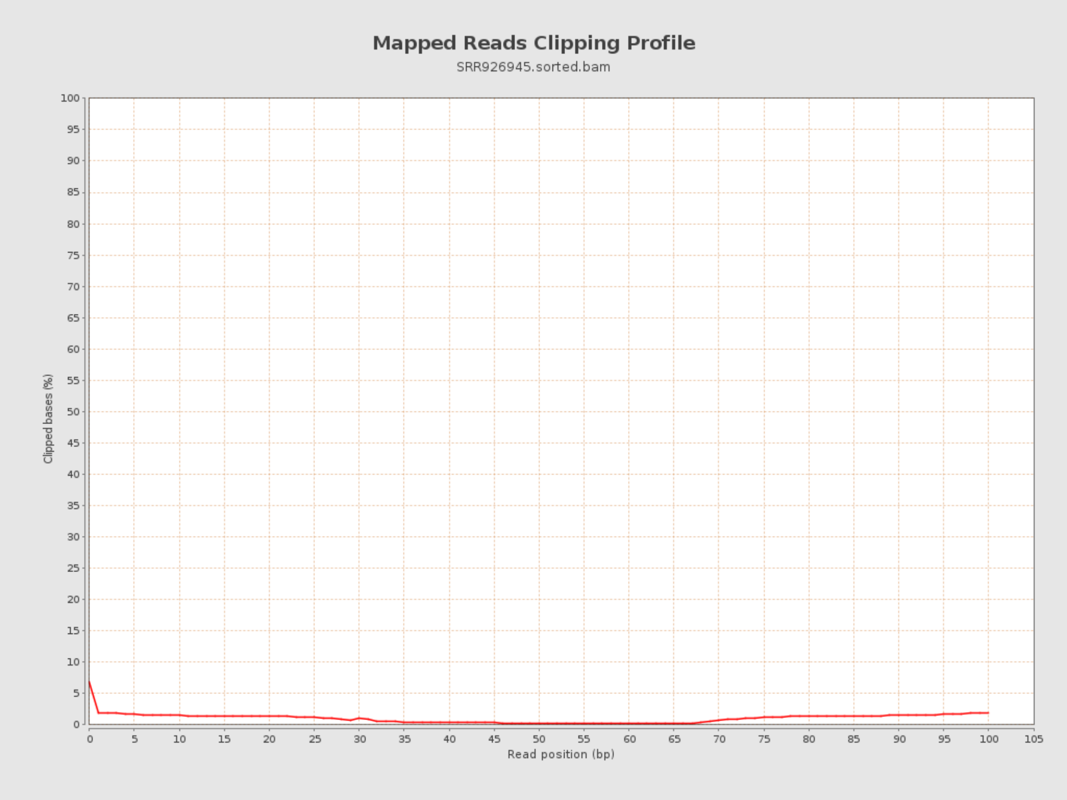
8. Results : Mapped Reads Nucleotide Content



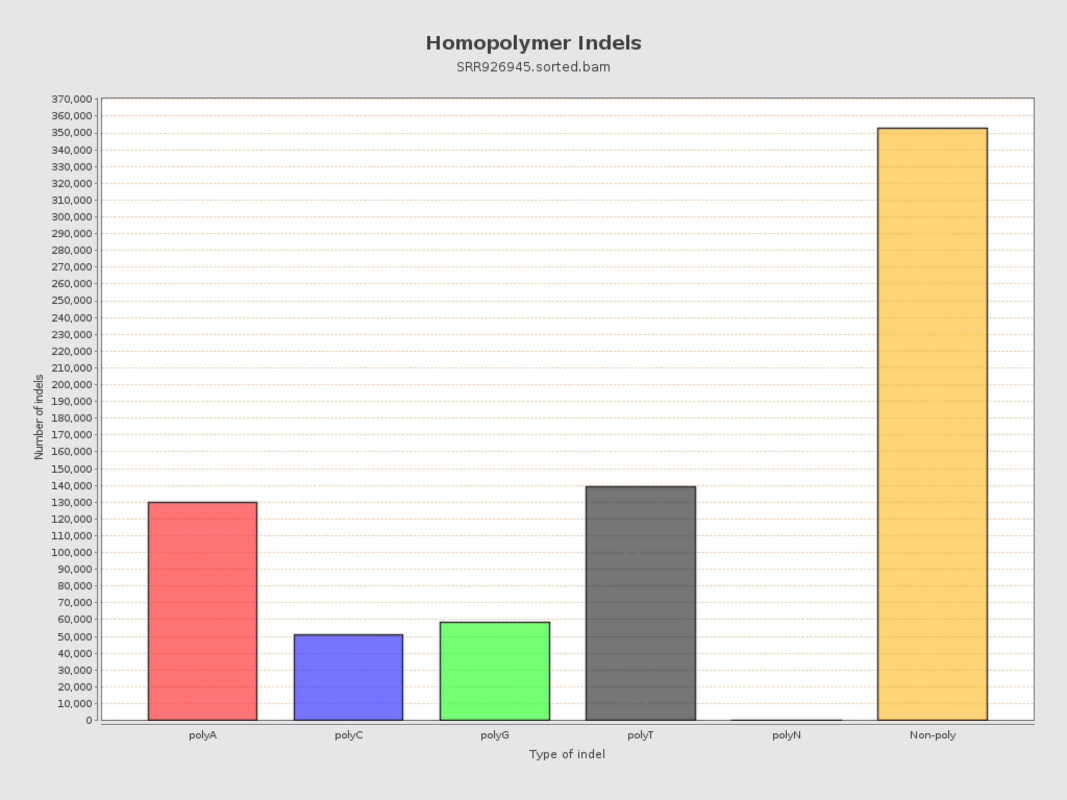
9. Results : Mapped Reads GC-content Distribution



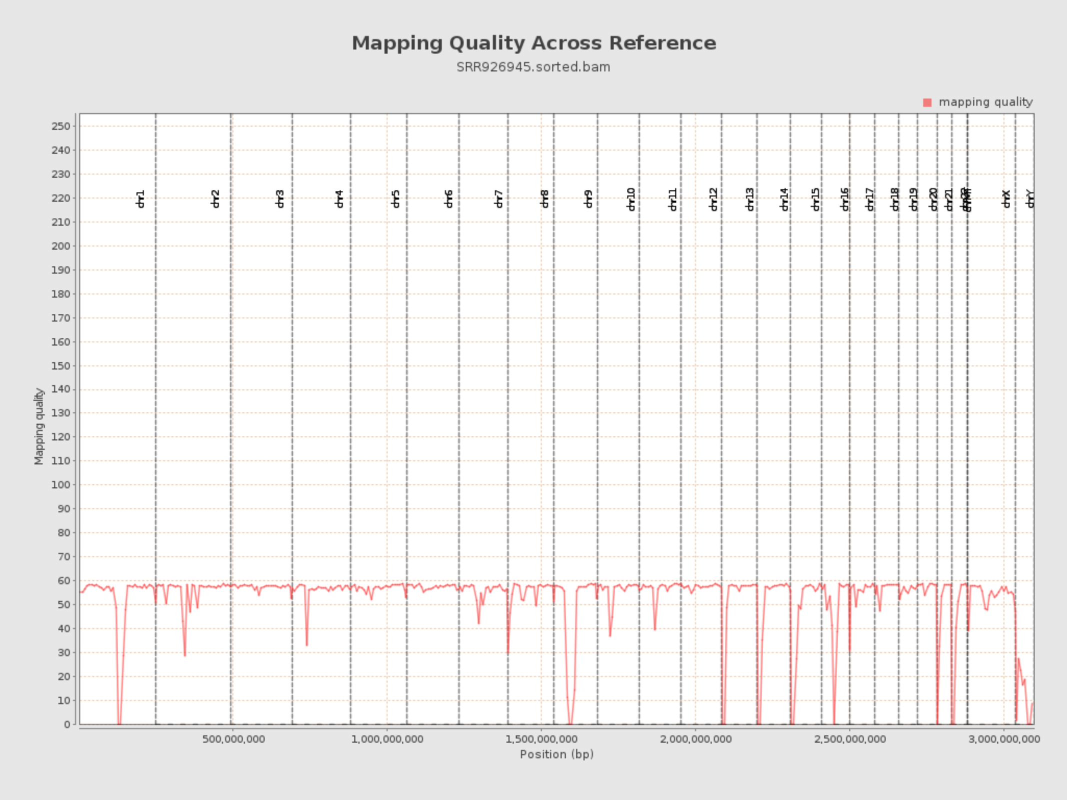
10. Results : Mapped Reads Clipping Profile



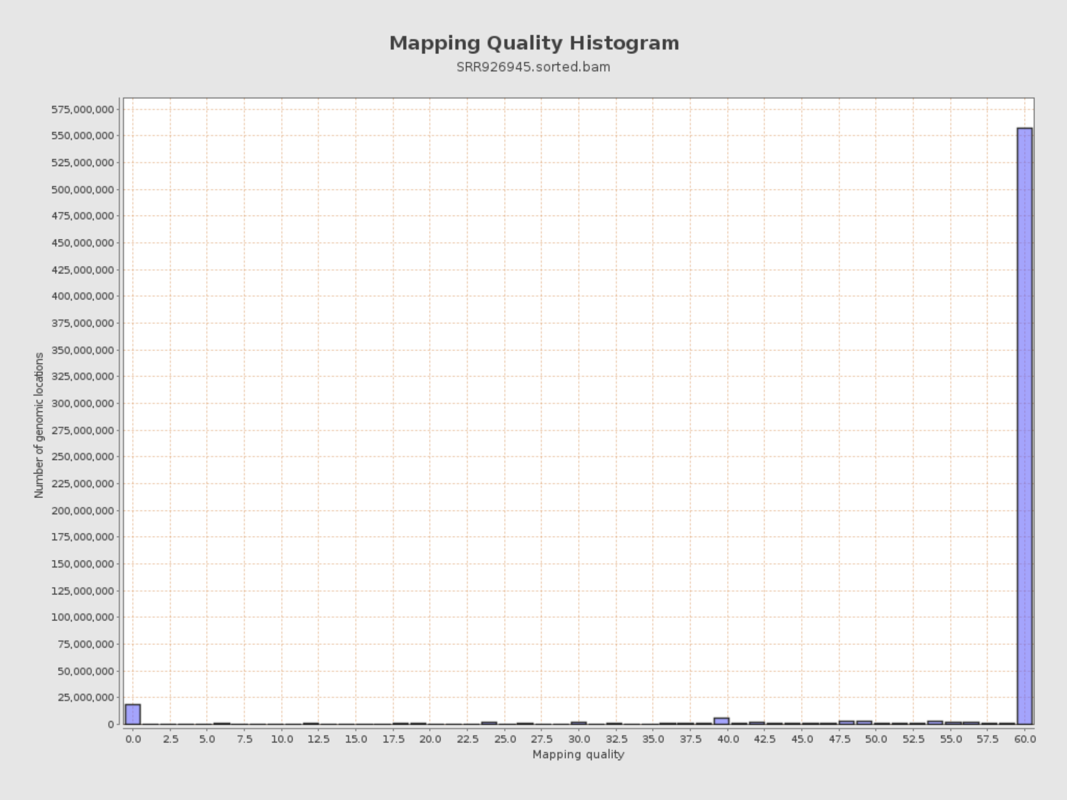
11. Results : Homopolymer Indels



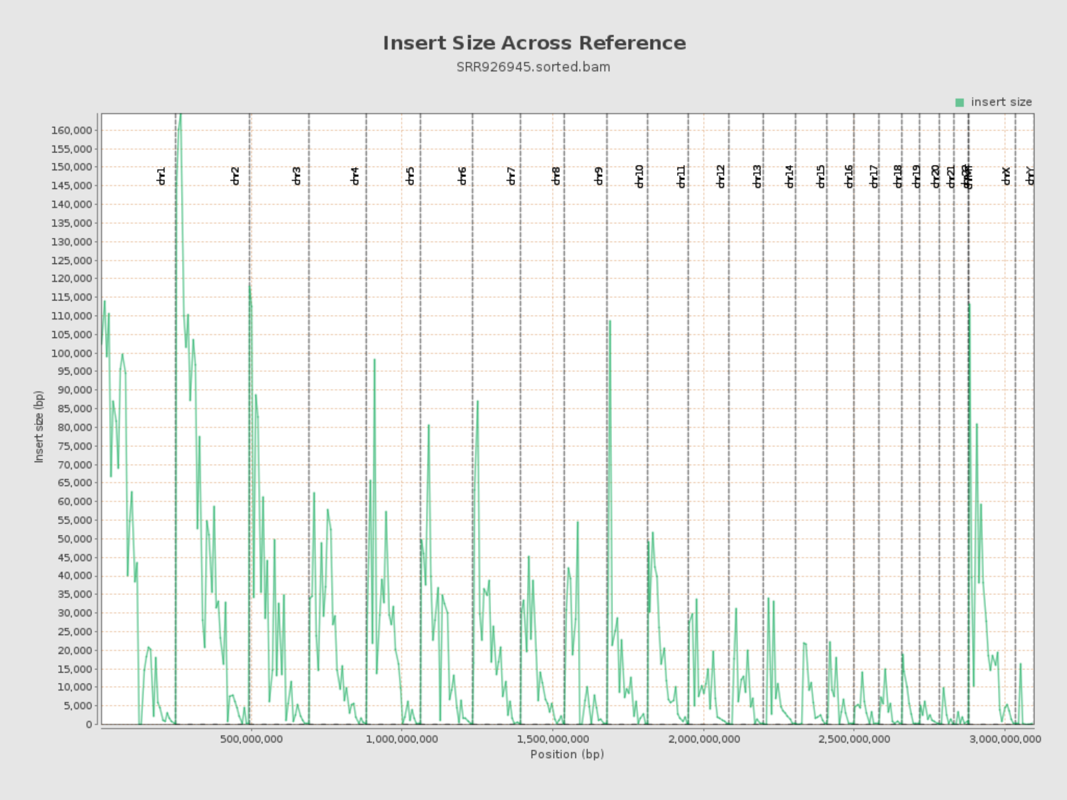
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram