Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 20:44:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926995.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_SRR926995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926995_1.fastq.gz SRR926995_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 20:44:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,681,332
Mapped reads	11,400,807 / 97.6%
Unmapped reads	280,525 / 2.4%
Mapped paired reads	11,400,807 / 97.6%
Mapped reads, first in pair	5,709,868 / 48.88%
Mapped reads, second in pair	5,690,939 / 48.72%
Mapped reads, both in pair	11,230,392 / 96.14%
Mapped reads, singletons	170,415 / 1.46%
Secondary alignments	0
Supplementary alignments	269,104 / 2.3%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	739,581 / 6.33%
Duplication rate	5.36%
Clipped reads	4,890,739 / 41.87%

2.2. ACGT Content

Number/percentage of A's	294,850,980 / 28.58%
Number/percentage of C's	199,675,727 / 19.35%
Number/percentage of T's	300,468,743 / 29.12%
Number/percentage of G's	236,506,783 / 22.92%
Number/percentage of N's	189,237 / 0.02%

GC Percentage	42.28%

2.3. Coverage

Mean	0.3335
Standard Deviation	1.3805

2.4. Mapping Quality

Mean Mapping Quality	52.88

2.5. Insert size

Mean	227,637.14
Standard Deviation	4,668,342.75
P25/Median/P75	136 / 180 / 247

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	9,828,783
Insertions	174,419
Mapped reads with at least one insertion	1.5%
Deletions	534,379
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.87%

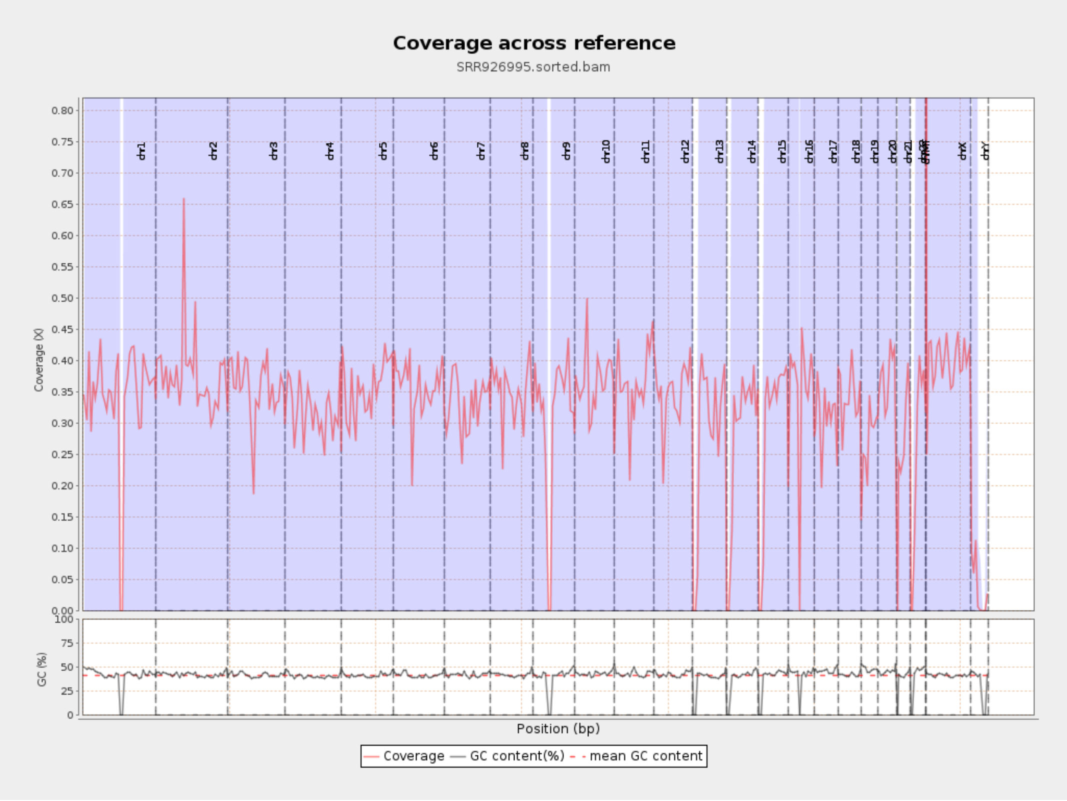
2.7. Chromosome stats

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

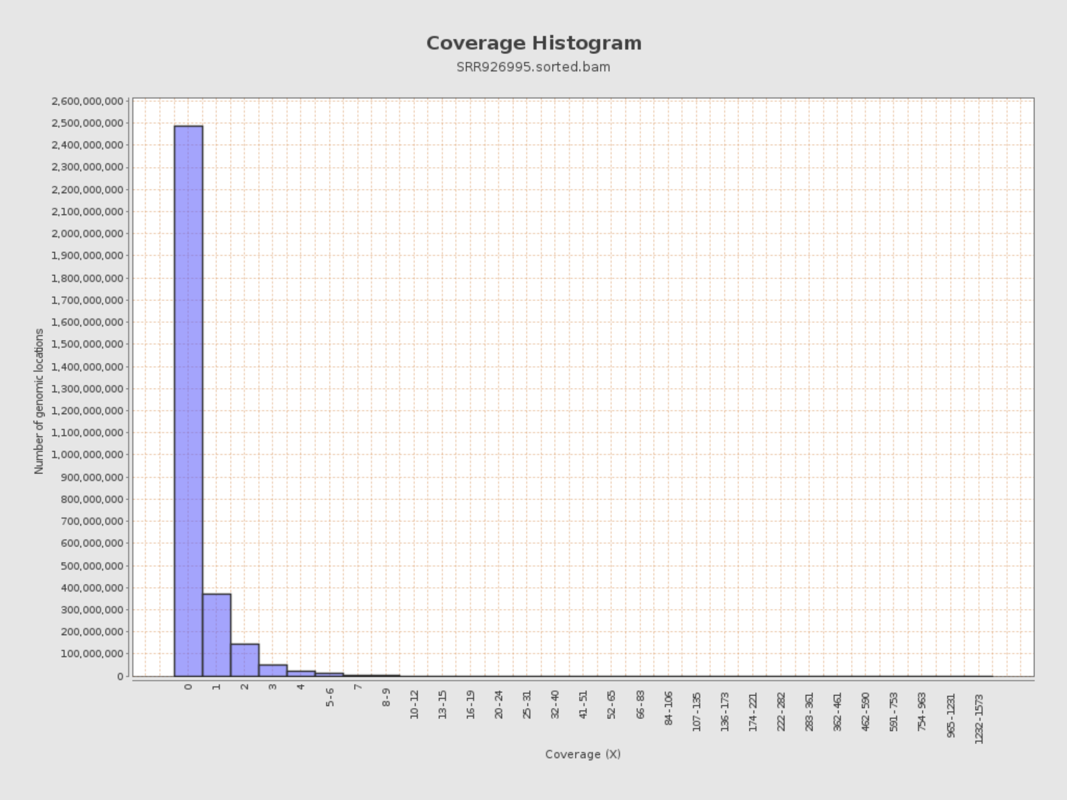
		bases	coverage	deviation
chr1	249250621	84730630	0.3399	1.8424
chr2	243199373	91886748	0.3778	2.4151
chr3	198022430	70259819	0.3548	0.864
chr4	191154276	61460422	0.3215	1.108
chr5	180915260	64655987	0.3574	0.8729
chr6	171115067	61330143	0.3584	1.1658
chr7	159138663	52599150	0.3305	1.0484
chr8	146364022	51252479	0.3502	0.9809
chr9	141213431	44176468	0.3128	1.5536
chr10	135534747	49598344	0.3659	2.2102
chr11	135006516	48892847	0.3622	1.0915
chr12	133851895	47076621	0.3517	0.8842
chr13	115169878	32558199	0.2827	0.7736
chr14	107349540	30099019	0.2804	0.786
chr15	102531392	29616280	0.2889	0.7916
chr16	90354753	31225240	0.3456	1.7908
chr17	81195210	25247845	0.311	1.0061
chr18	78077248	26684794	0.3418	1.5477
chr19	59128983	16051618	0.2715	1.2341
chr20	63025520	23543520	0.3736	0.948
chr21	48129895	12700947	0.2639	1.2619
chr22	51304566	12916945	0.2518	0.7983
chrMT	16571	156074	9.4185	9.0361
chrX	155270560	61681820	0.3973	0.9943

chrY	59373566	2075206	0.035	1.4118

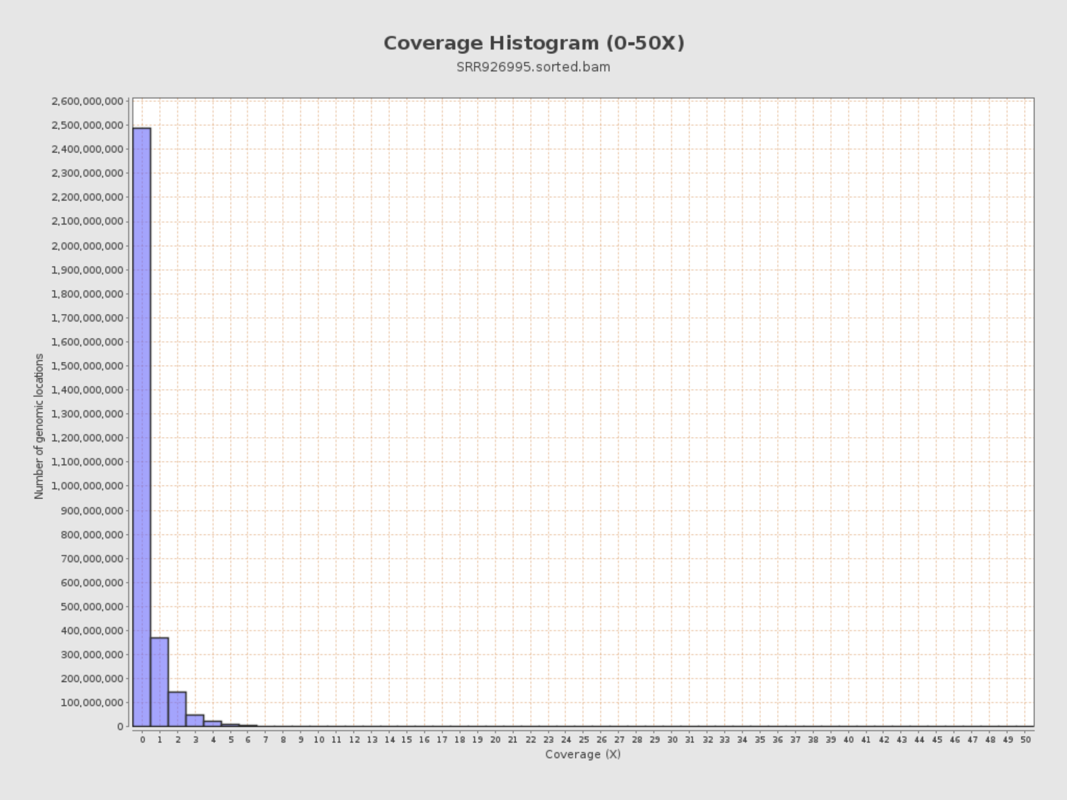
3. Results : Coverage across reference



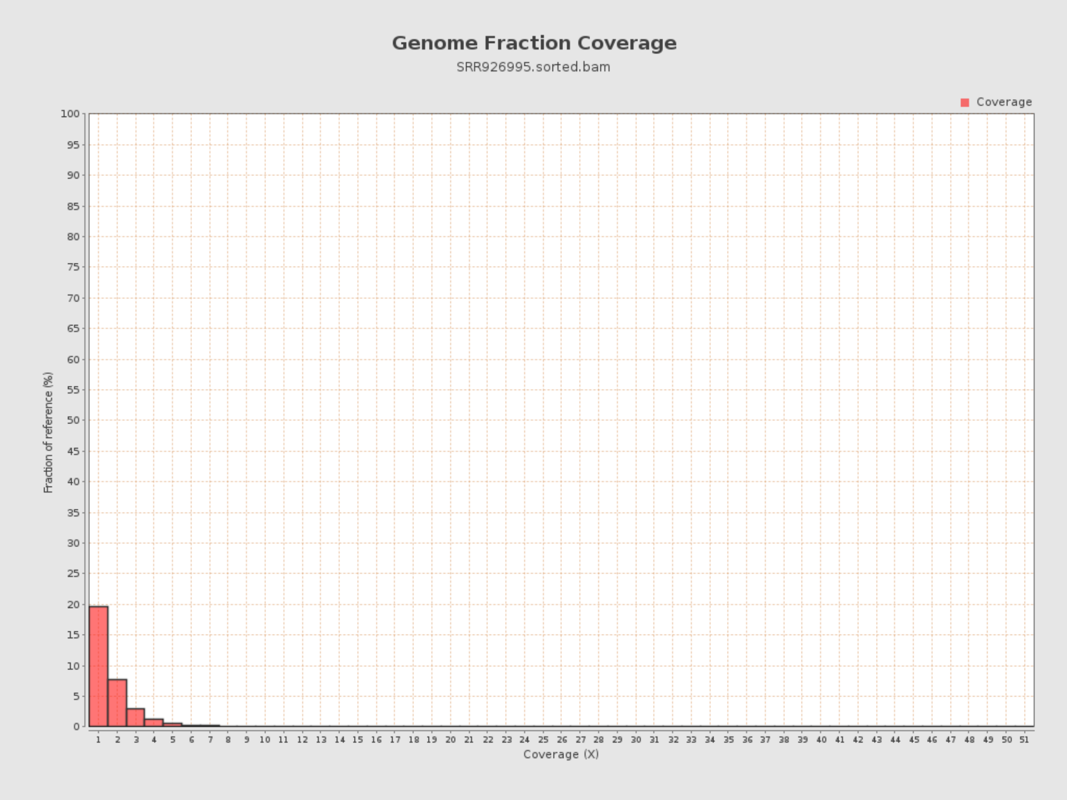
4. Results : Coverage Histogram



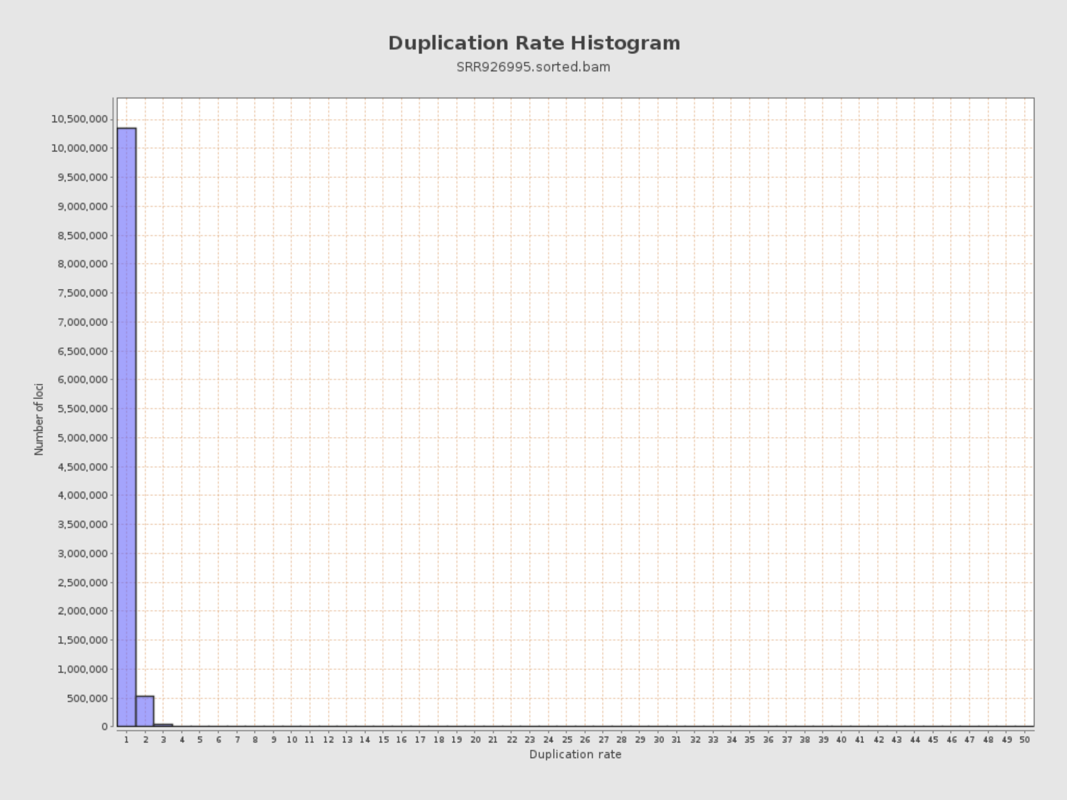
5. Results : Coverage Histogram (0-50X)



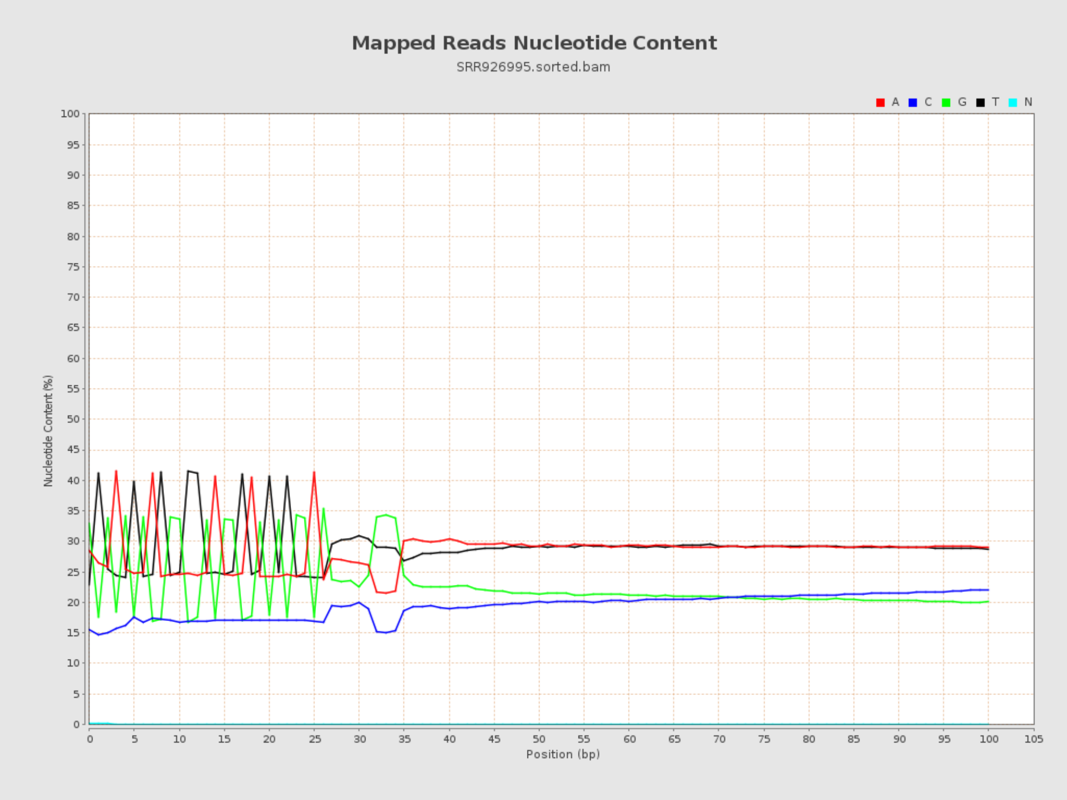
6. Results : Genome Fraction Coverage



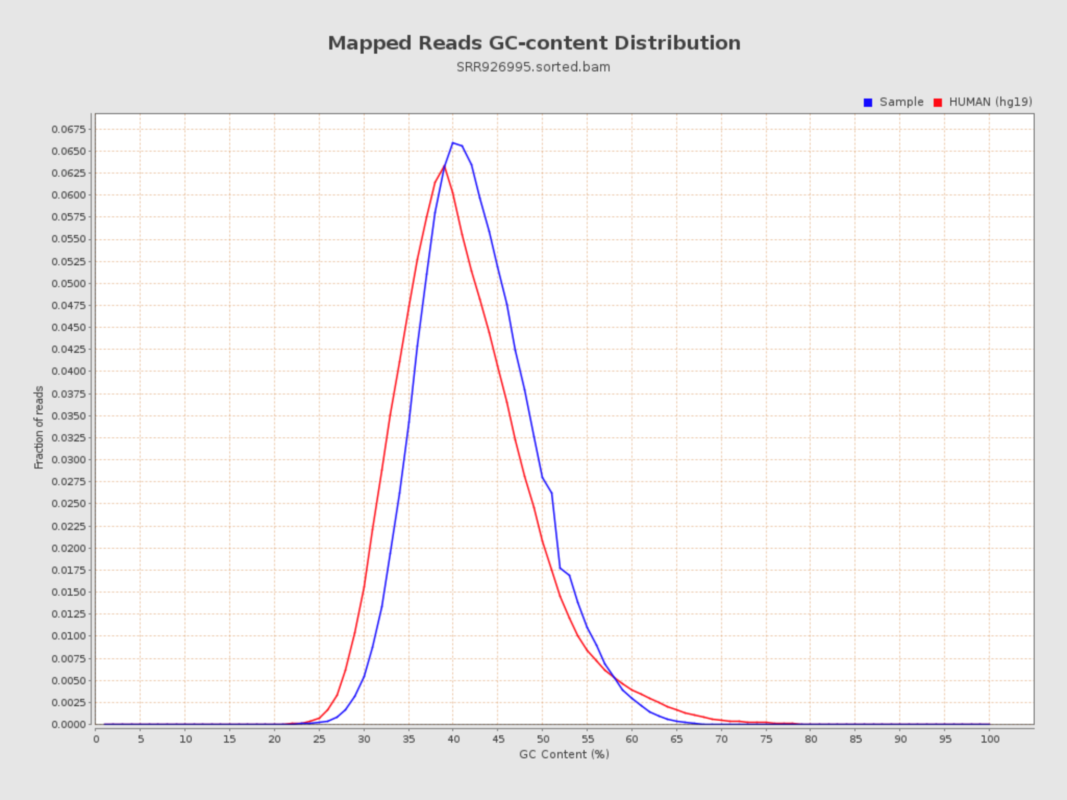
7. Results : Duplication Rate Histogram



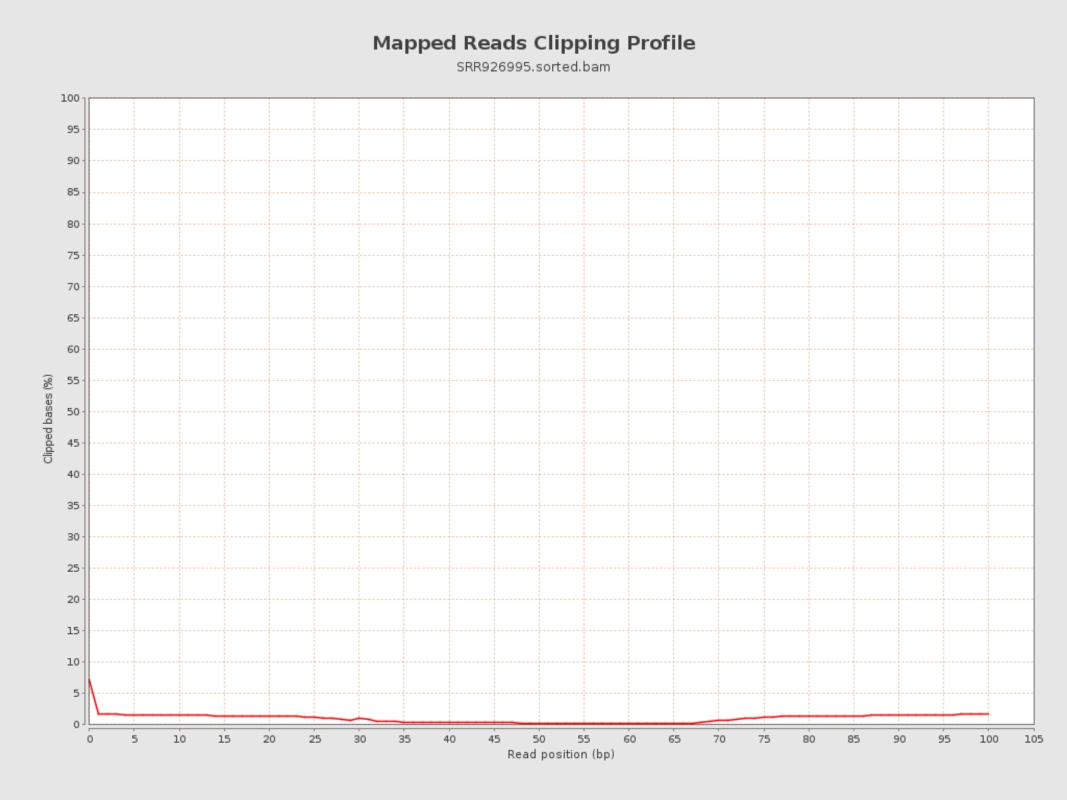
8. Results : Mapped Reads Nucleotide Content



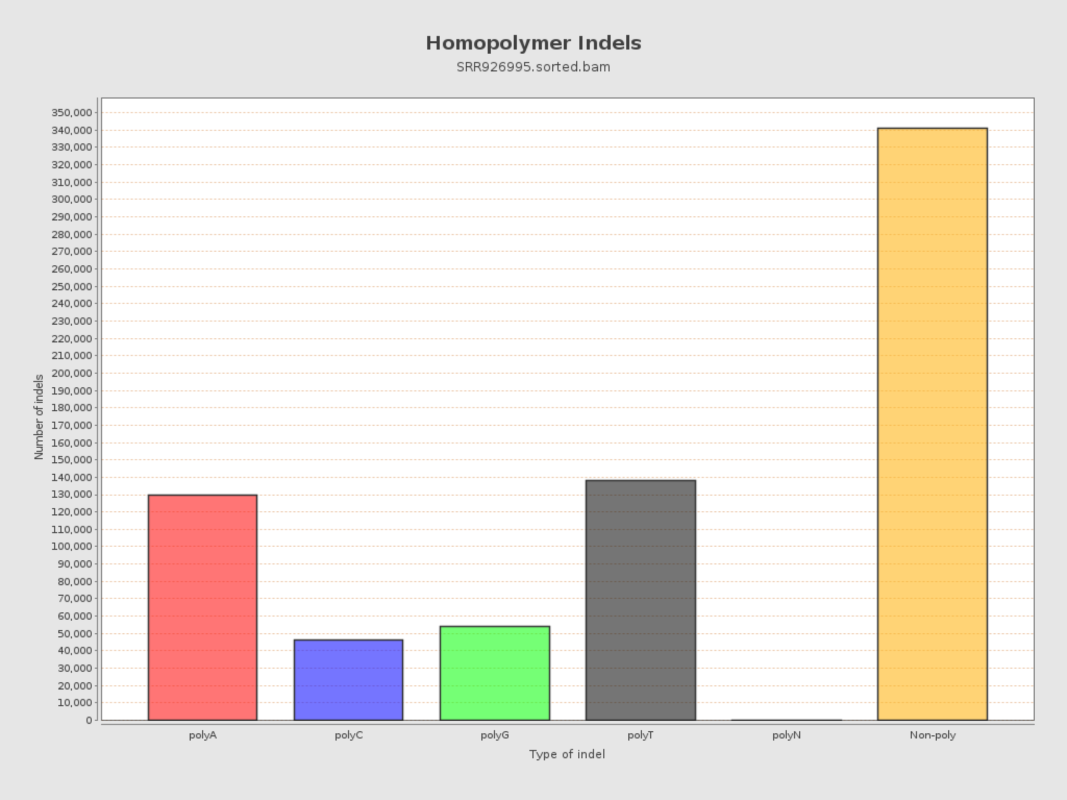
9. Results : Mapped Reads GC-content Distribution



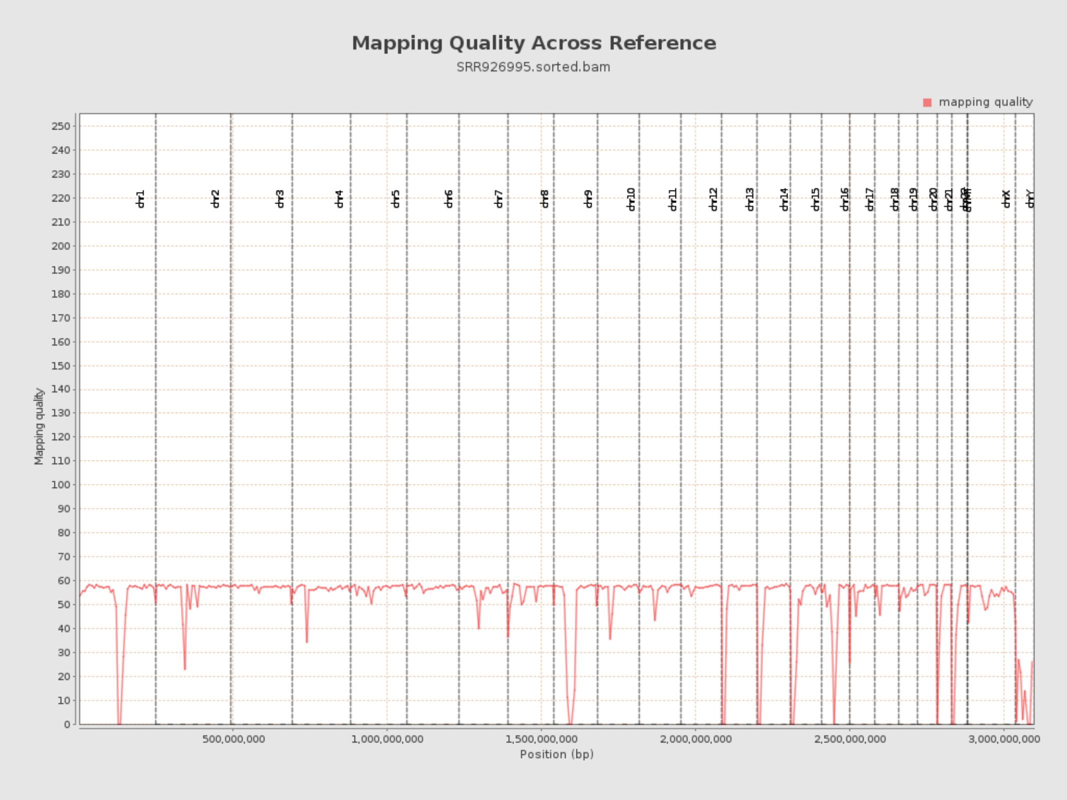
10. Results : Mapped Reads Clipping Profile



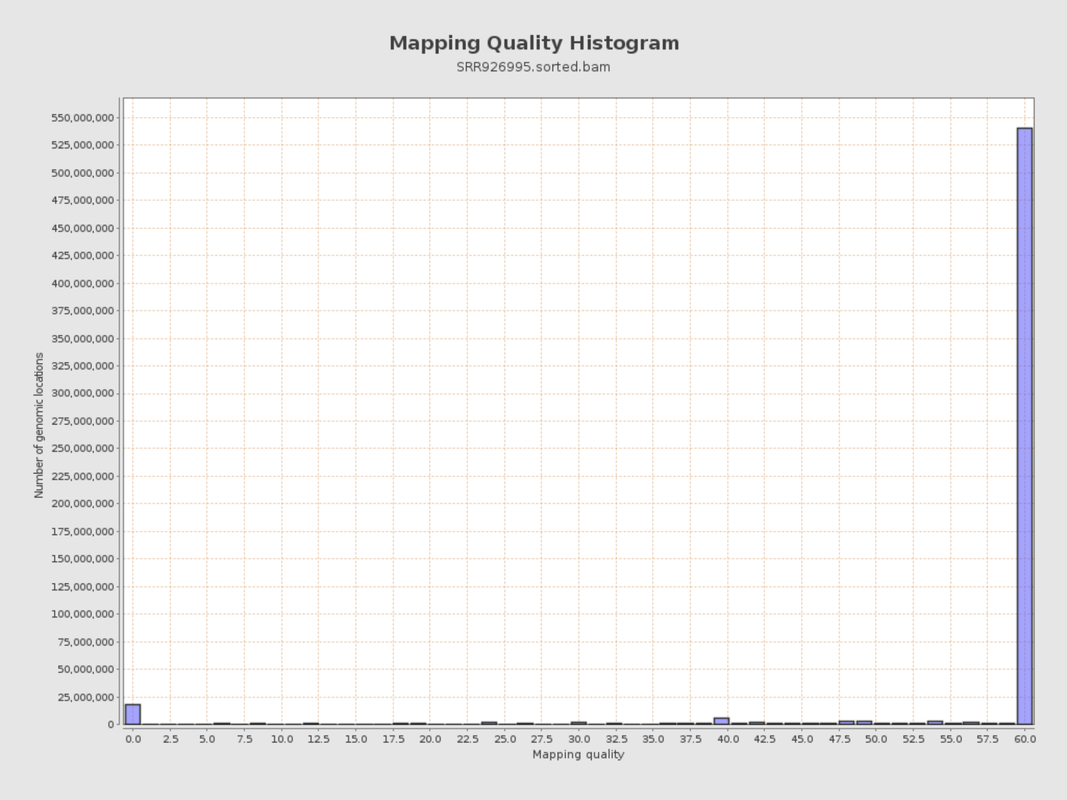
11. Results : Homopolymer Indels



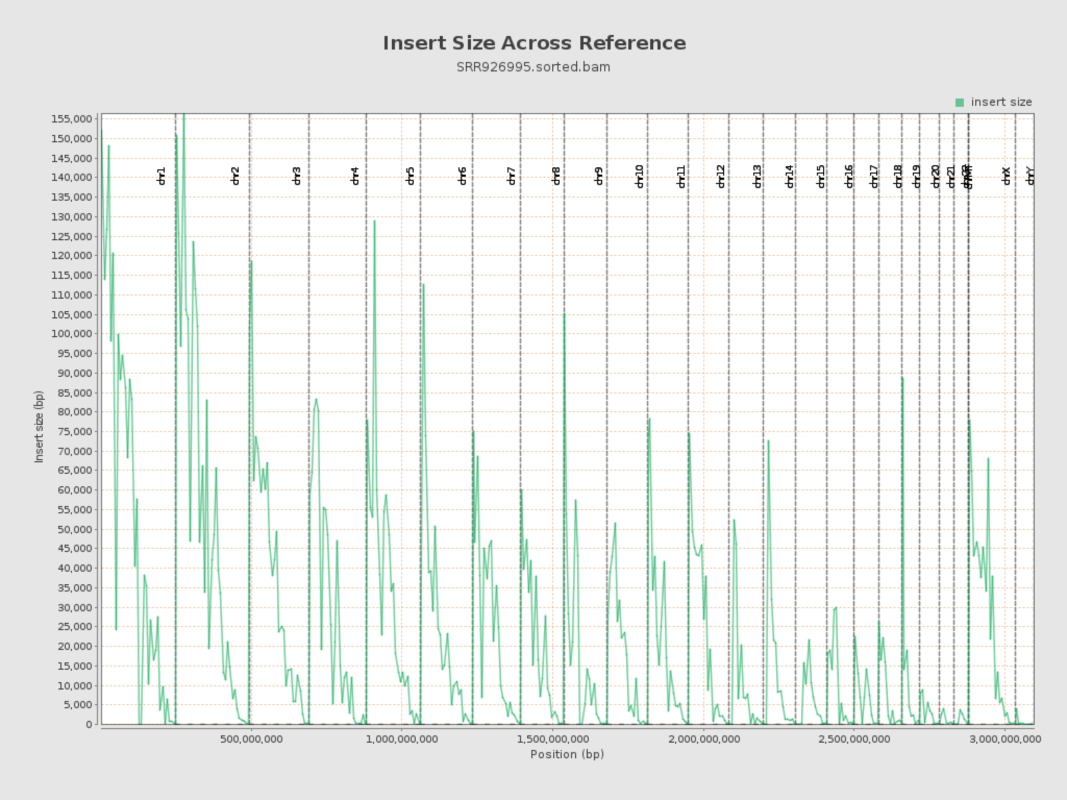
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram