Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:21:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975201.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_SRR975201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975201_1.fastq.gz SRR975201_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:21:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,382,046
Mapped reads	5,309,028 / 98.64%
Unmapped reads	73,018 / 1.36%
Mapped paired reads	5,309,028 / 98.64%
Mapped reads, first in pair	2,657,115 / 49.37%
Mapped reads, second in pair	2,651,913 / 49.27%
Mapped reads, both in pair	5,285,074 / 98.2%
Mapped reads, singletons	23,954 / 0.45%
Secondary alignments	0
Supplementary alignments	90,052 / 1.67%
Read min/max/mean length	30 / 151 / 151.82
Duplicated reads (estimated)	1,186,854 / 22.05%
Duplication rate	18.06%
Clipped reads	3,868,087 / 71.87%

2.2. ACGT Content

Number/percentage of A's	213,943,577 / 29.68%
Number/percentage of C's	142,146,653 / 19.72%
Number/percentage of T's	216,862,724 / 30.09%
Number/percentage of G's	147,745,532 / 20.5%
Number/percentage of N's	70,393 / 0.01%

GC Percentage	40.22%

2.3. Coverage

Mean	0.233
Standard Deviation	4.5264

2.4. Mapping Quality

Mean Mapping Quality	53

2.5. Insert size

Mean	79,523.22
Standard Deviation	2,635,561.53
P25/Median/P75	142 / 177 / 225

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	9,407,503
Insertions	164,406
Mapped reads with at least one insertion	2.88%
Deletions	262,494
Mapped reads with at least one deletion	4.71%
Homopolymer indels	43.46%

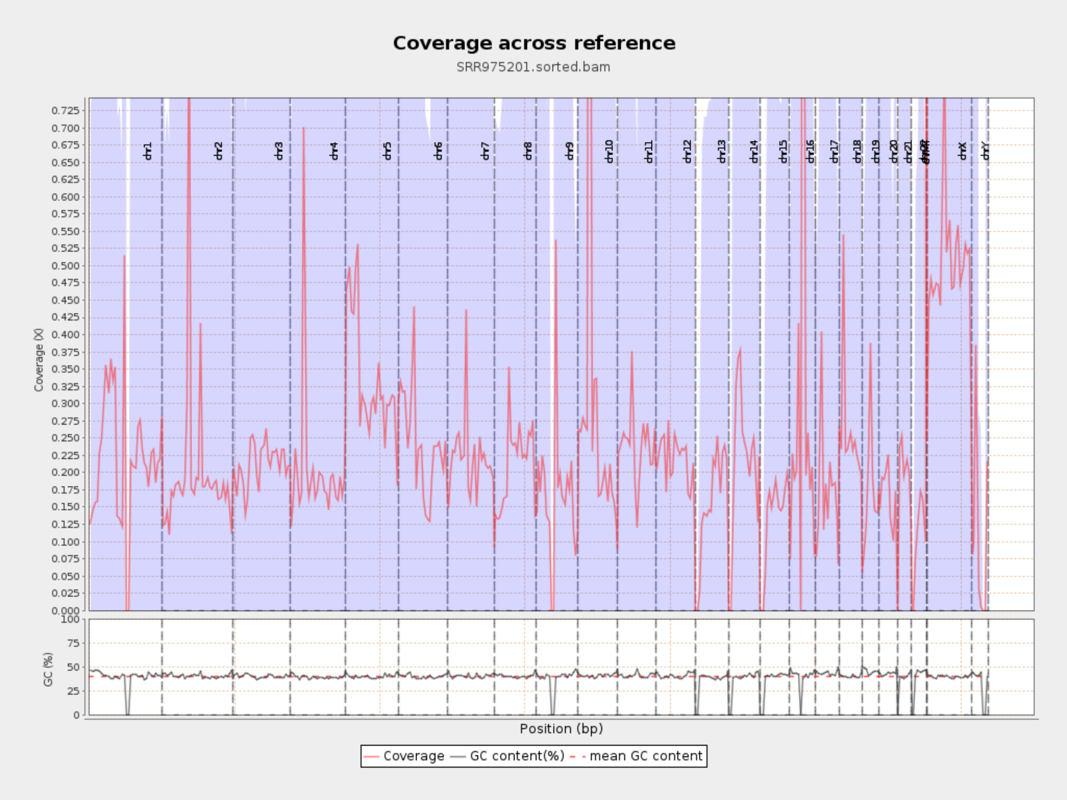
2.7. Chromosome stats

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

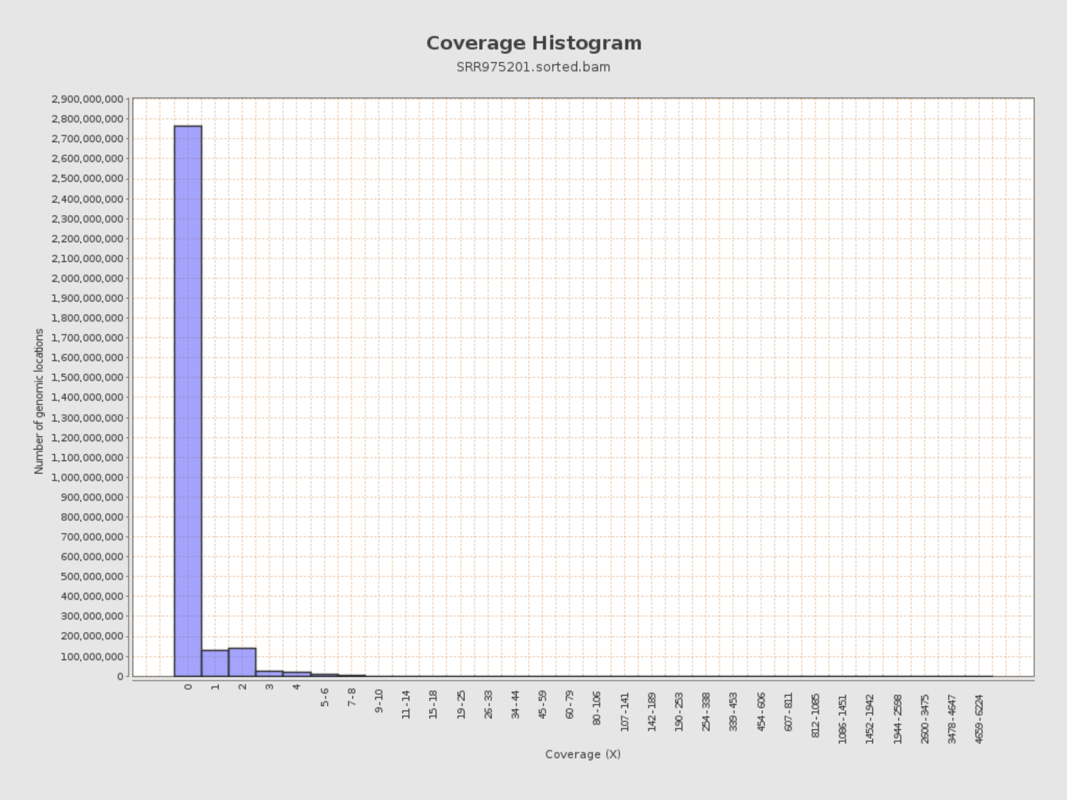
		bases	coverage	deviation
chr1	249250621	55322988	0.222	5.3595
chr2	243199373	49855947	0.205	4.9978
chr3	198022430	42039128	0.2123	0.8639
chr4	191154276	38299563	0.2004	3.1359
chr5	180915260	61084711	0.3376	1.0152
chr6	171115067	41339654	0.2416	2.2346
chr7	159138663	35502634	0.2231	3.2204
chr8	146364022	31293486	0.2138	1.383
chr9	141213431	24208841	0.1714	6.4193
chr10	135534747	42668312	0.3148	12.5213
chr11	135006516	31738246	0.2351	2.6801
chr12	133851895	29262618	0.2186	0.7673
chr13	115169878	17791202	0.1545	0.6112
chr14	107349540	23017067	0.2144	0.8885
chr15	102531392	13697794	0.1336	0.57
chr16	90354753	29332568	0.3246	9.7215
chr17	81195210	13856384	0.1707	4.0111
chr18	78077248	20595238	0.2638	6.6041
chr19	59128983	10599063	0.1793	2.8987
chr20	63025520	10592791	0.1681	1.2722
chr21	48129895	9162203	0.1904	1.7674
chr22	51304566	5244014	0.1022	0.5697
chrMT	16571	204970	12.3692	7.9561
chrX	155270560	78534362	0.5058	2.2921

chrY	59373566	6099848	0.1027	5.8886

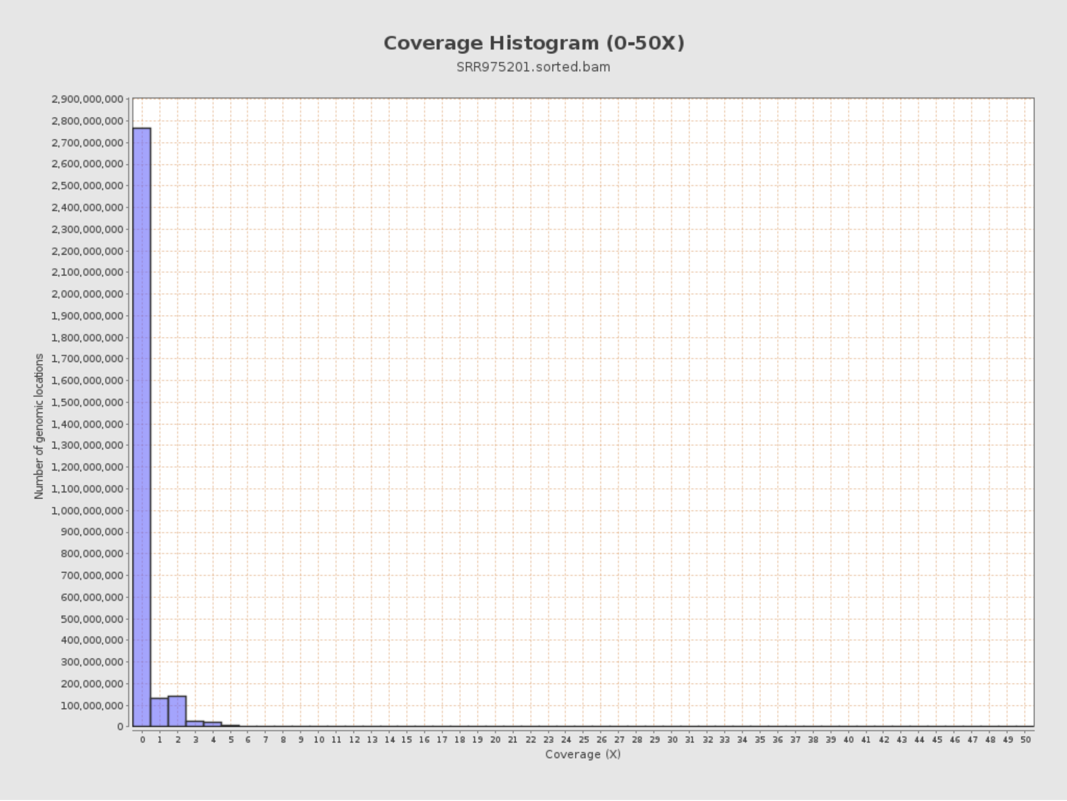
3. Results : Coverage across reference



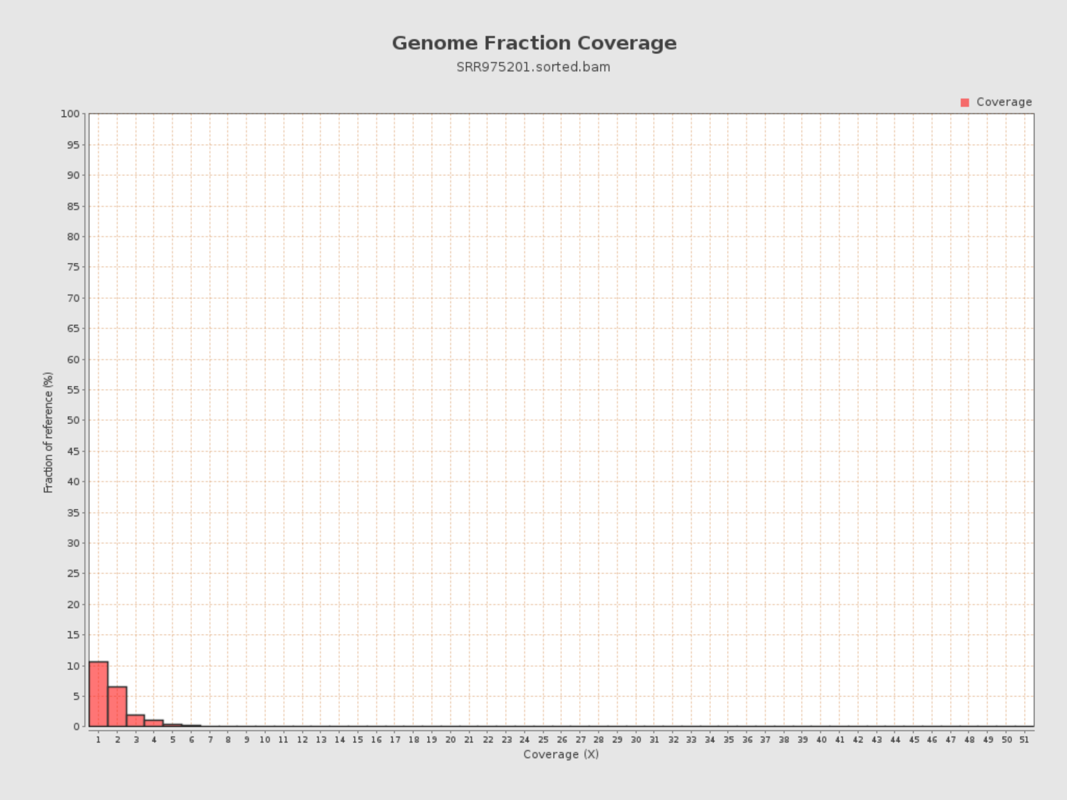
4. Results : Coverage Histogram



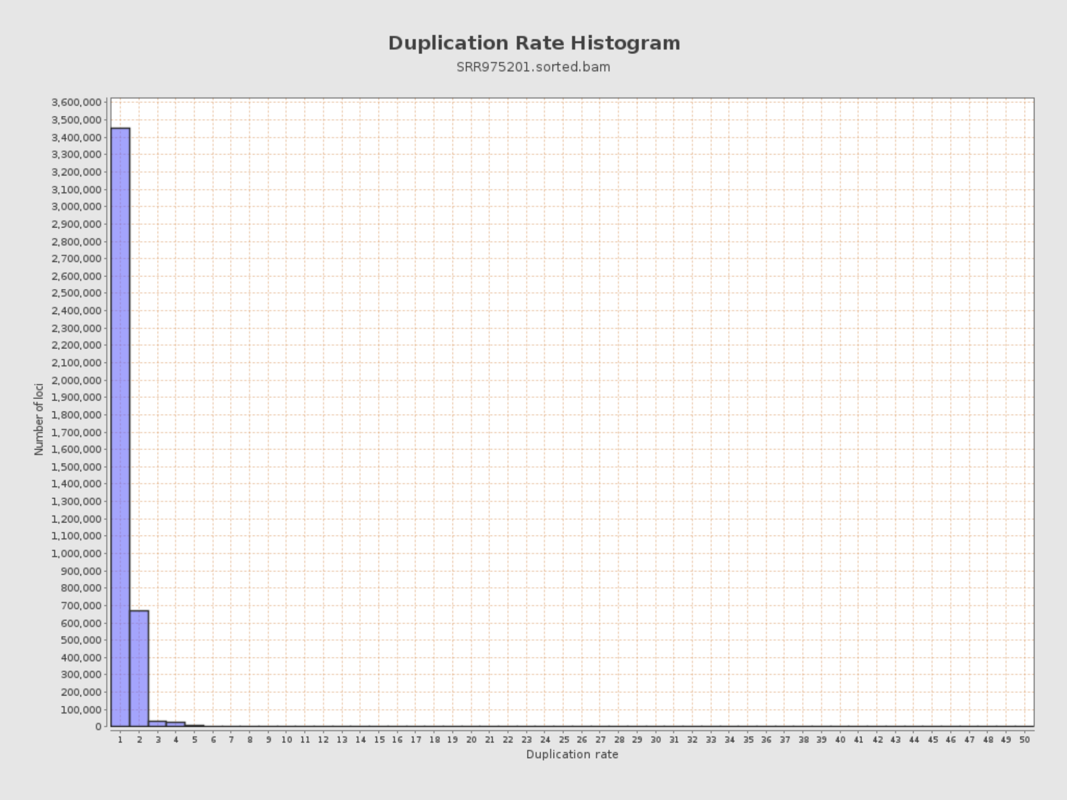
5. Results : Coverage Histogram (0-50X)



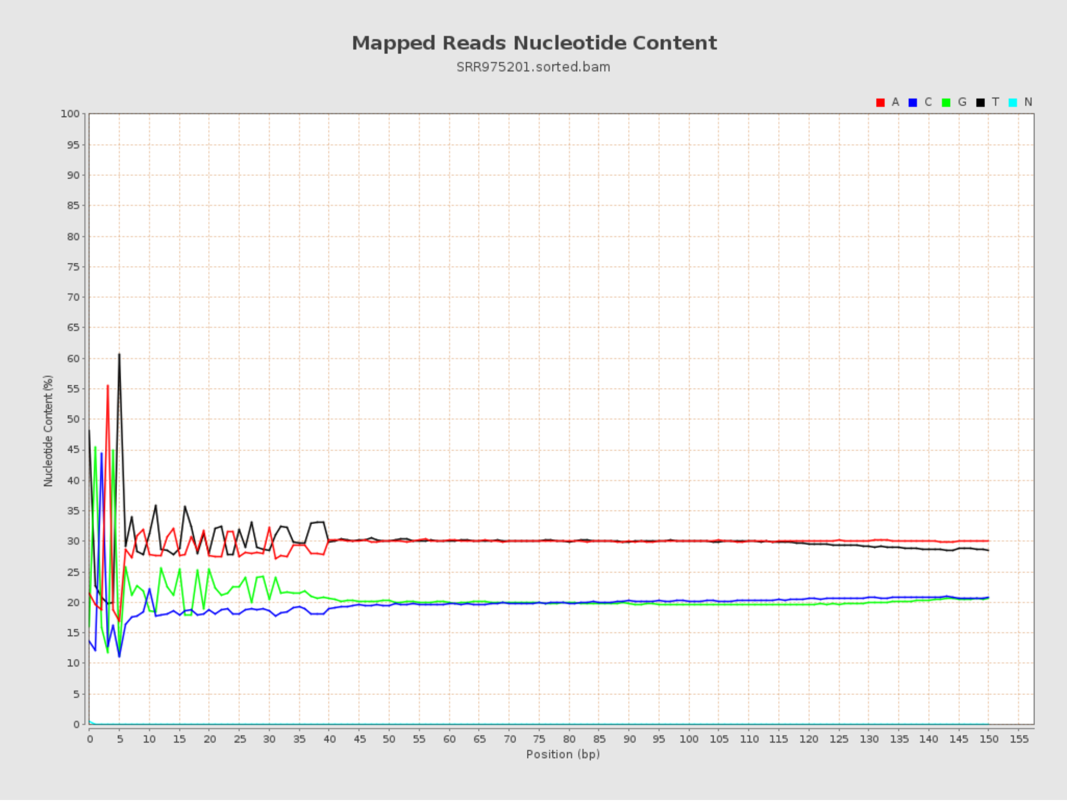
6. Results : Genome Fraction Coverage



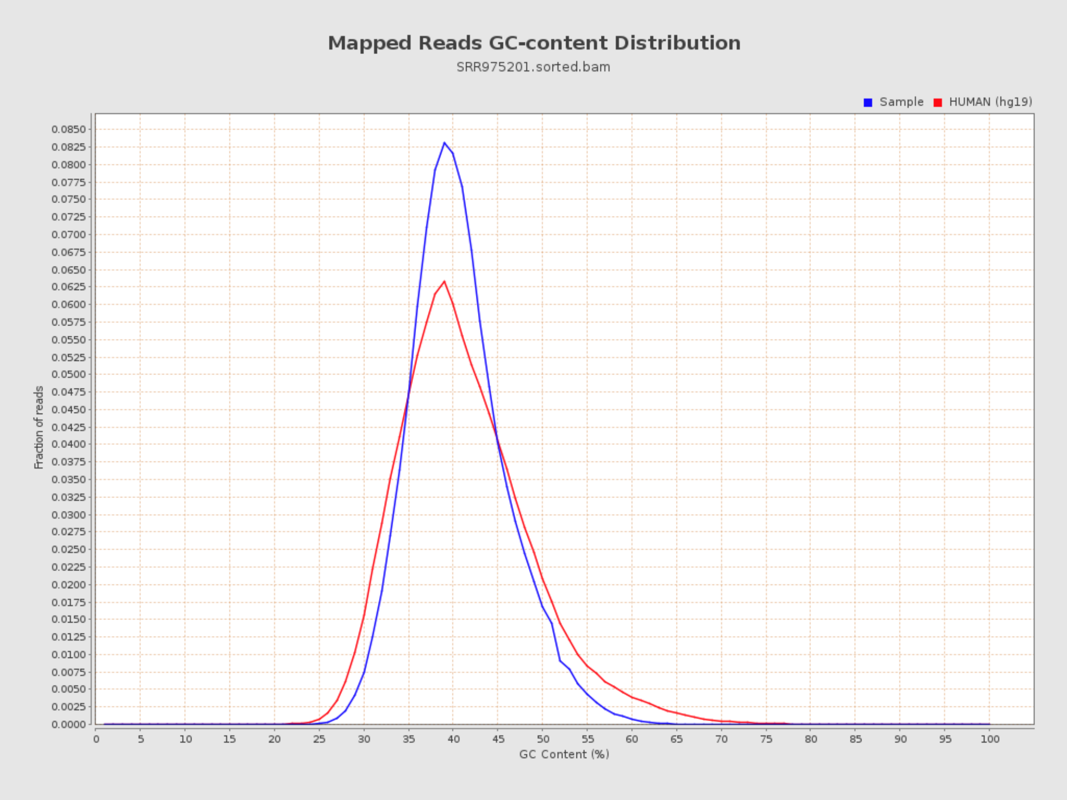
7. Results : Duplication Rate Histogram



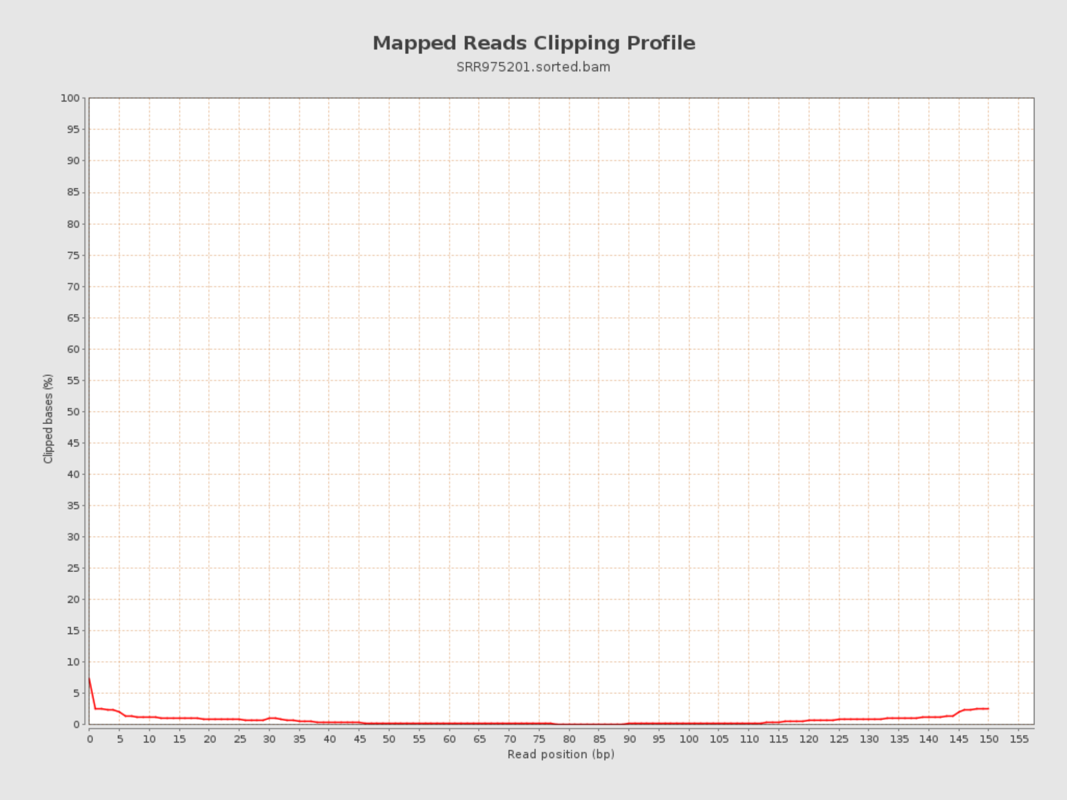
8. Results : Mapped Reads Nucleotide Content



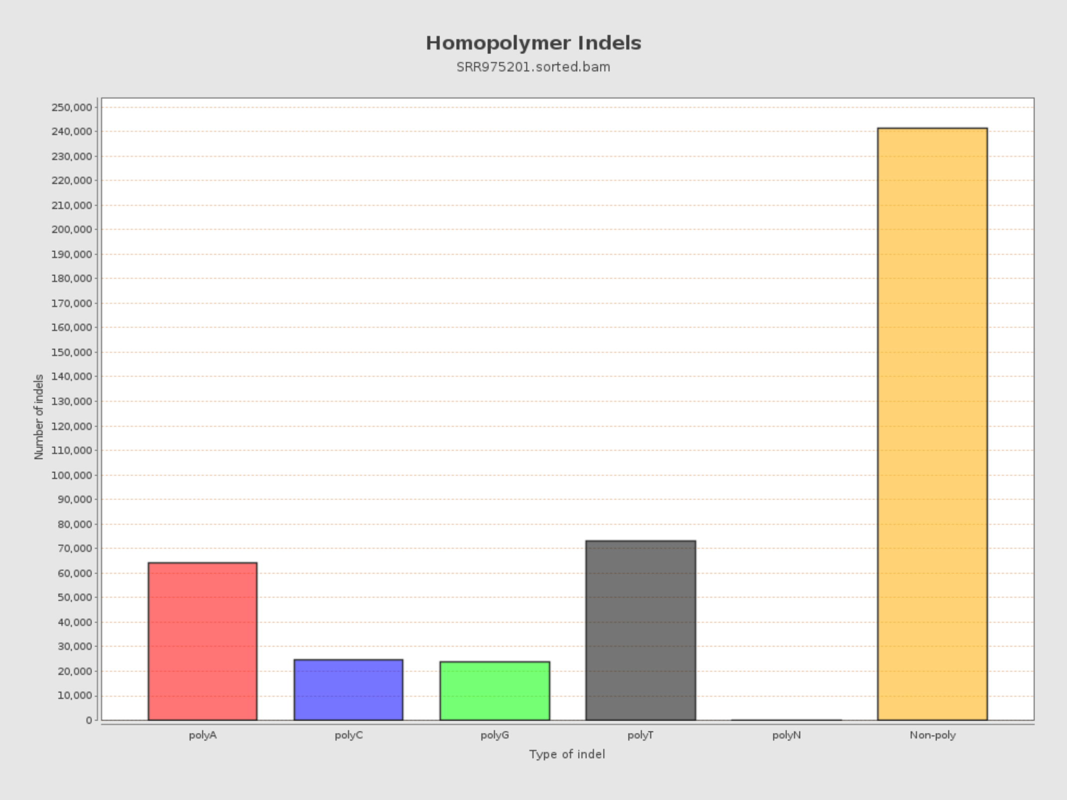
9. Results : Mapped Reads GC-content Distribution



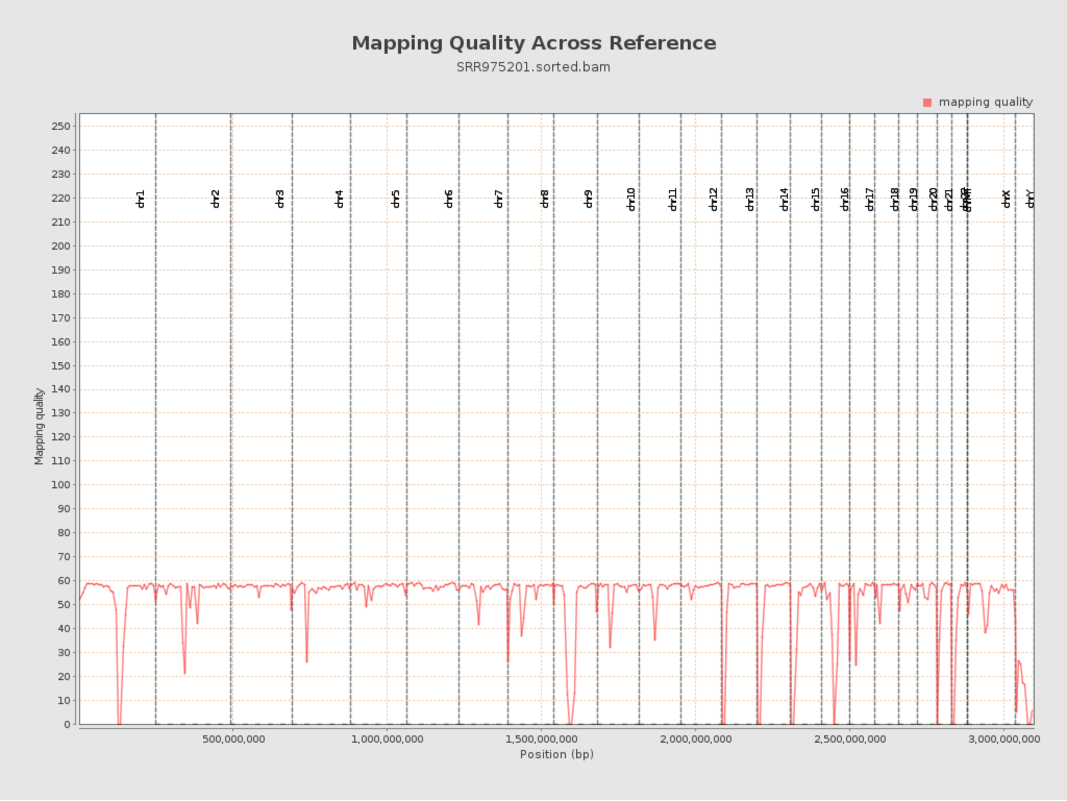
10. Results : Mapped Reads Clipping Profile



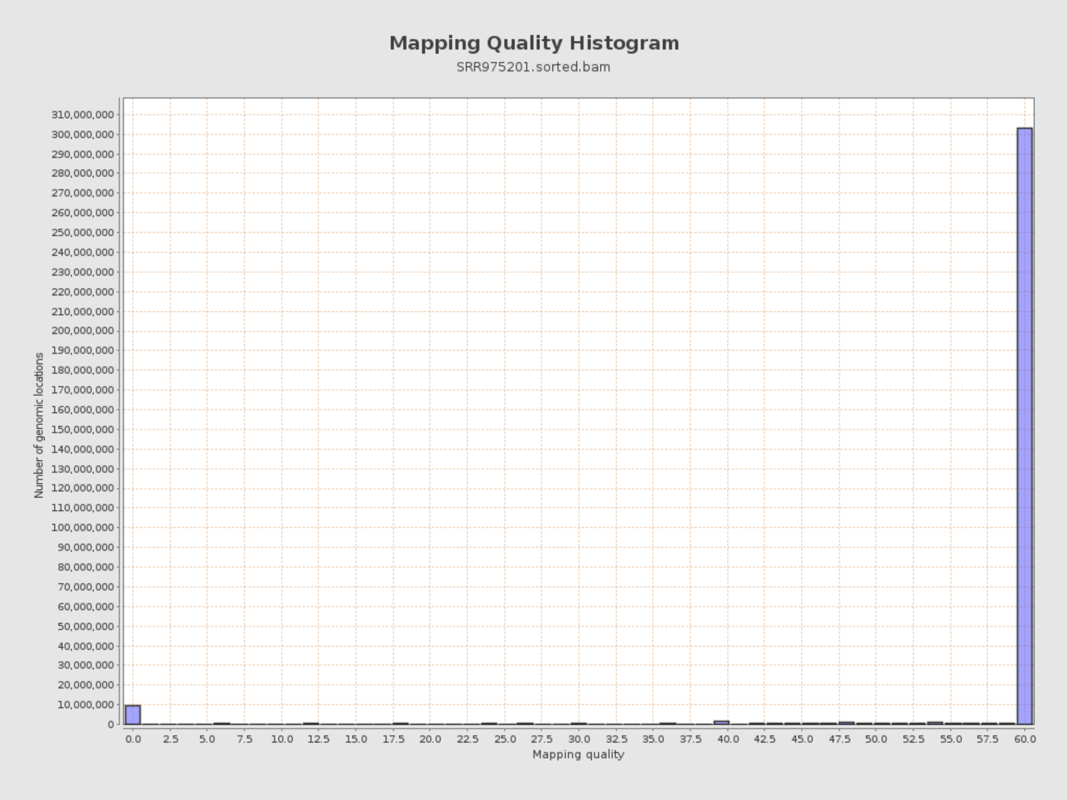
11. Results : Homopolymer Indels



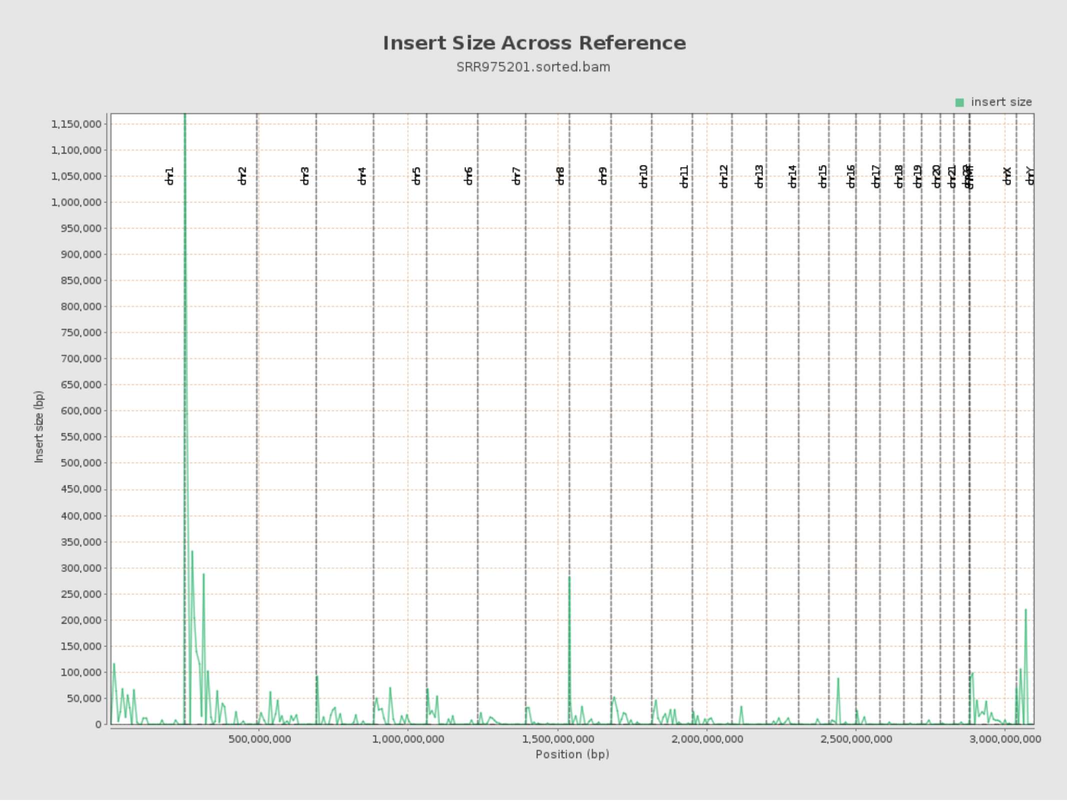
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram