Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:28:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975190.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_SRR975190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975190_1.fastq.gz SRR975190_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:27:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,216,288
Mapped reads	43,107,837 / 99.75%
Unmapped reads	108,451 / 0.25%
Mapped paired reads	43,107,837 / 99.75%
Mapped reads, first in pair	21,580,675 / 49.94%
Mapped reads, second in pair	21,527,162 / 49.81%
Mapped reads, both in pair	43,029,068 / 99.57%
Mapped reads, singletons	78,769 / 0.18%
Secondary alignments	0
Supplementary alignments	114,820 / 0.27%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	22,009,794 / 50.93%
Duplication rate	37.26%
Clipped reads	6,547,215 / 15.15%

2.2. ACGT Content

Number/percentage of A's	1,121,217,064 / 26.71%
Number/percentage of C's	947,793,851 / 22.58%
Number/percentage of T's	1,133,856,746 / 27.02%
Number/percentage of G's	993,897,803 / 23.68%
Number/percentage of N's	317,114 / 0.01%

GC Percentage	46.26%

2.3. Coverage

Mean	1.3563
Standard Deviation	17.45

2.4. Mapping Quality

Mean Mapping Quality	55.82

2.5. Insert size

Mean	190,191.85
Standard Deviation	4,376,077.52
P25/Median/P75	171 / 210 / 258

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	26,836,317
Insertions	323,382
Mapped reads with at least one insertion	0.74%
Deletions	1,028,031
Mapped reads with at least one deletion	2.35%
Homopolymer indels	50.09%

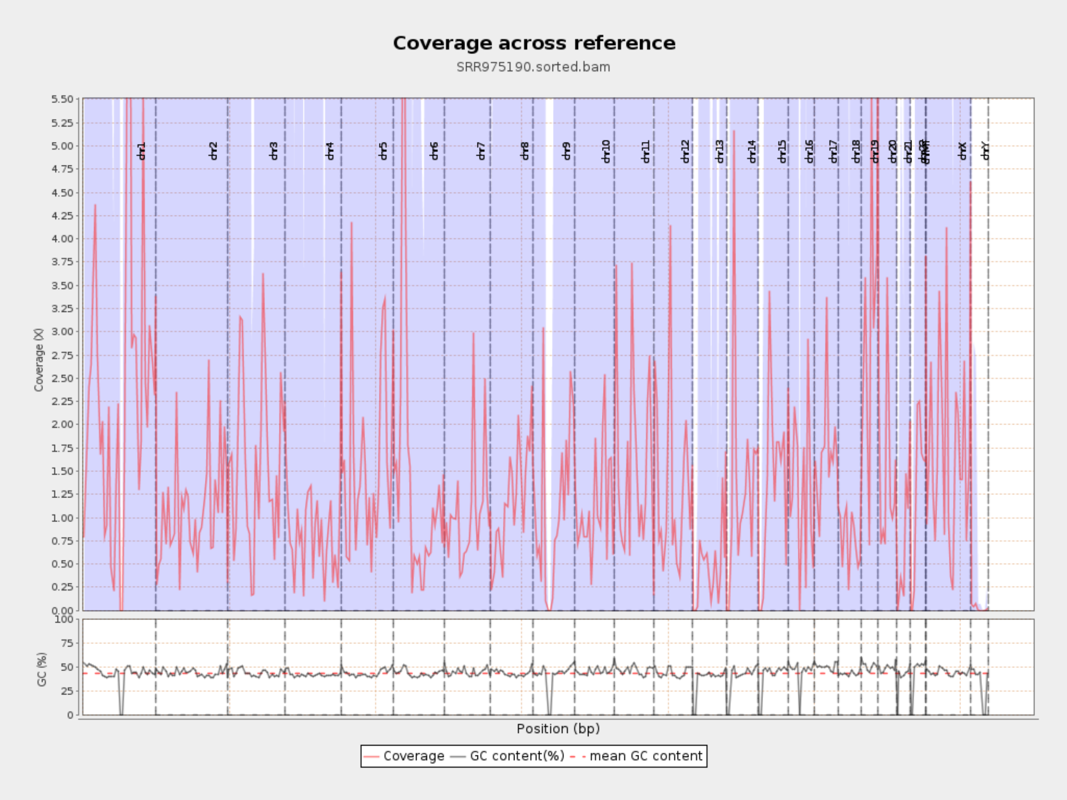
2.7. Chromosome stats

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

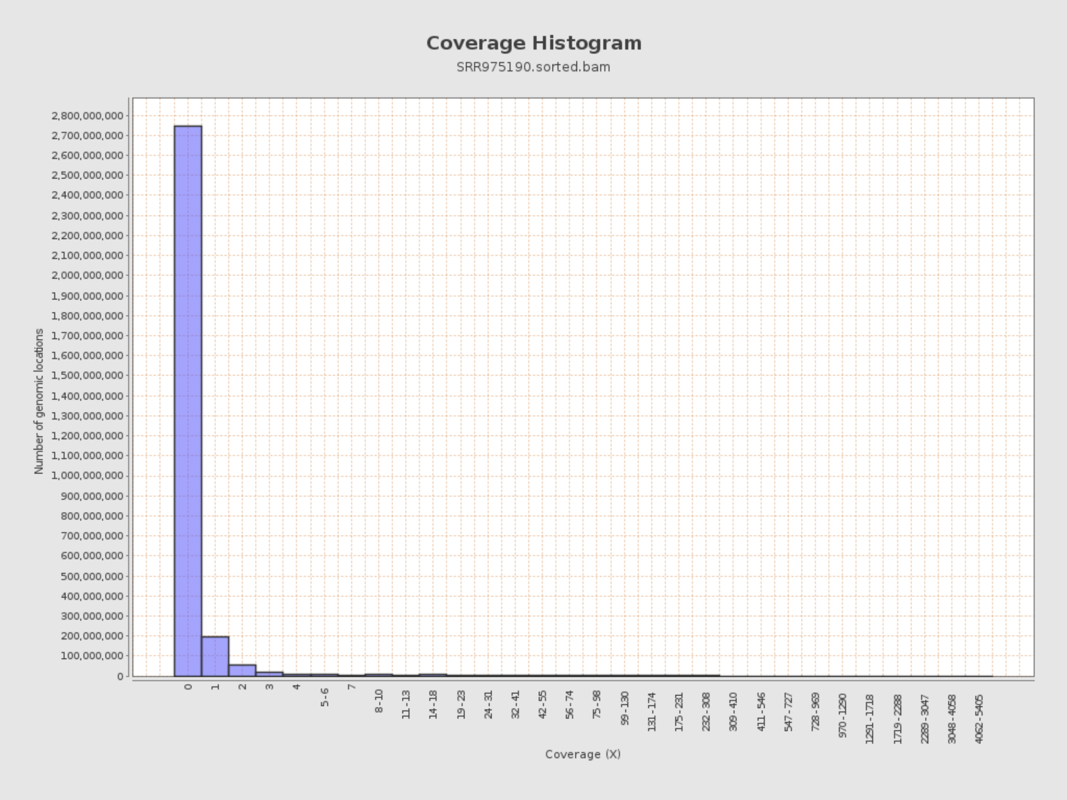
		bases	coverage	deviation
chr1	249250621	603203632	2.4201	26.5887
chr2	243199373	265156222	1.0903	13.3817
chr3	198022430	308132795	1.556	18.492
chr4	191154276	153254159	0.8017	11.2932
chr5	180915260	293256026	1.621	19.9116
chr6	171115067	241644422	1.4122	19.2123
chr7	159138663	169085968	1.0625	13.7547
chr8	146364022	174615841	1.193	16.4541
chr9	141213431	150213515	1.0637	14.6663
chr10	135534747	154566413	1.1404	14.4622
chr11	135006516	215178641	1.5938	17.3732
chr12	133851895	187788896	1.403	16.0294
chr13	115169878	53337704	0.4631	9.0731
chr14	107349540	146221379	1.3621	17.651
chr15	102531392	132608179	1.2933	15.4864
chr16	90354753	115873413	1.2824	14.8519
chr17	81195210	138865342	1.7103	16.5672
chr18	78077248	60254079	0.7717	10.9368
chr19	59128983	179718334	3.0394	28.3068
chr20	63025520	88657015	1.4067	17.3936
chr21	48129895	34610727	0.7191	10.2116
chr22	51304566	65332632	1.2734	15.2039
chrMT	16571	63300	3.8199	9.5898
chrX	155270560	265549310	1.7102	23.931

chrY	59373566	1433021	0.0241	1.4158

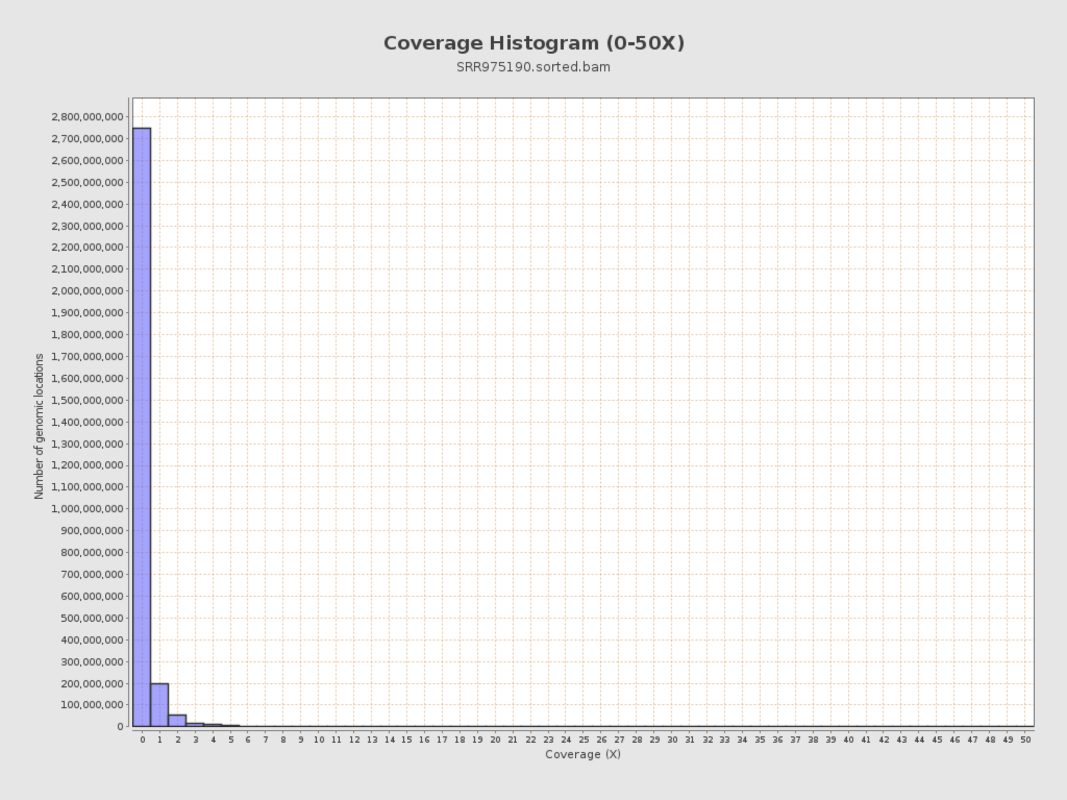
3. Results : Coverage across reference



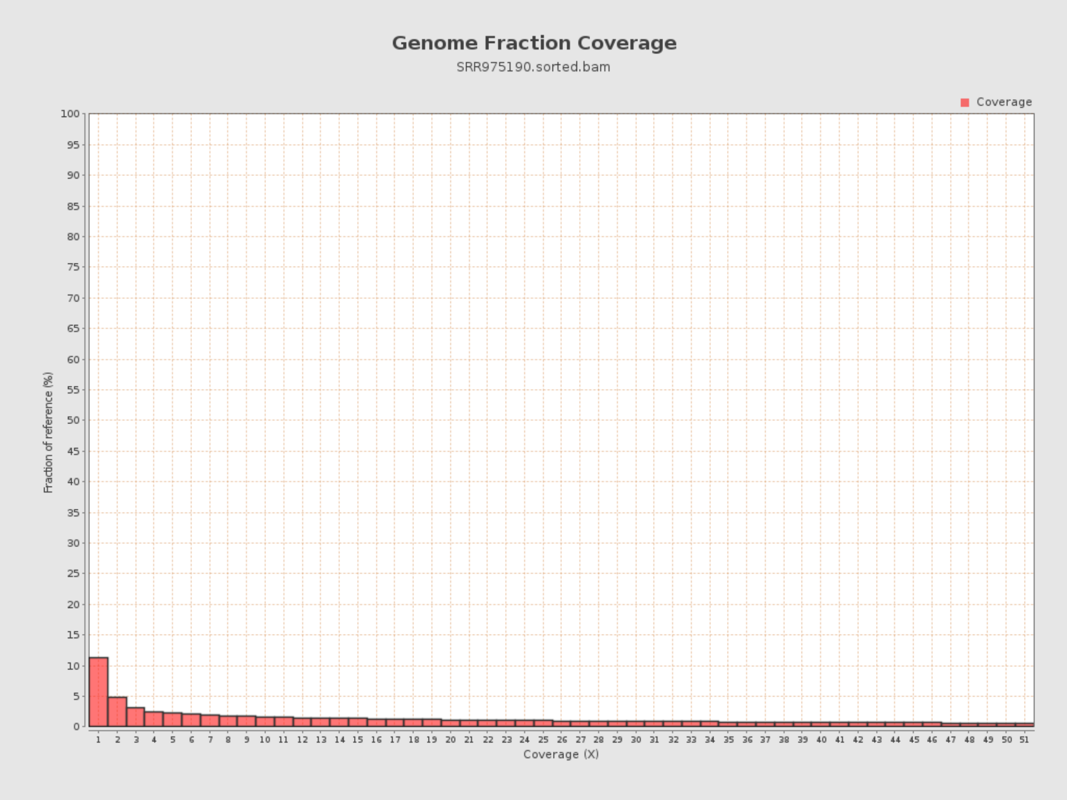
4. Results : Coverage Histogram



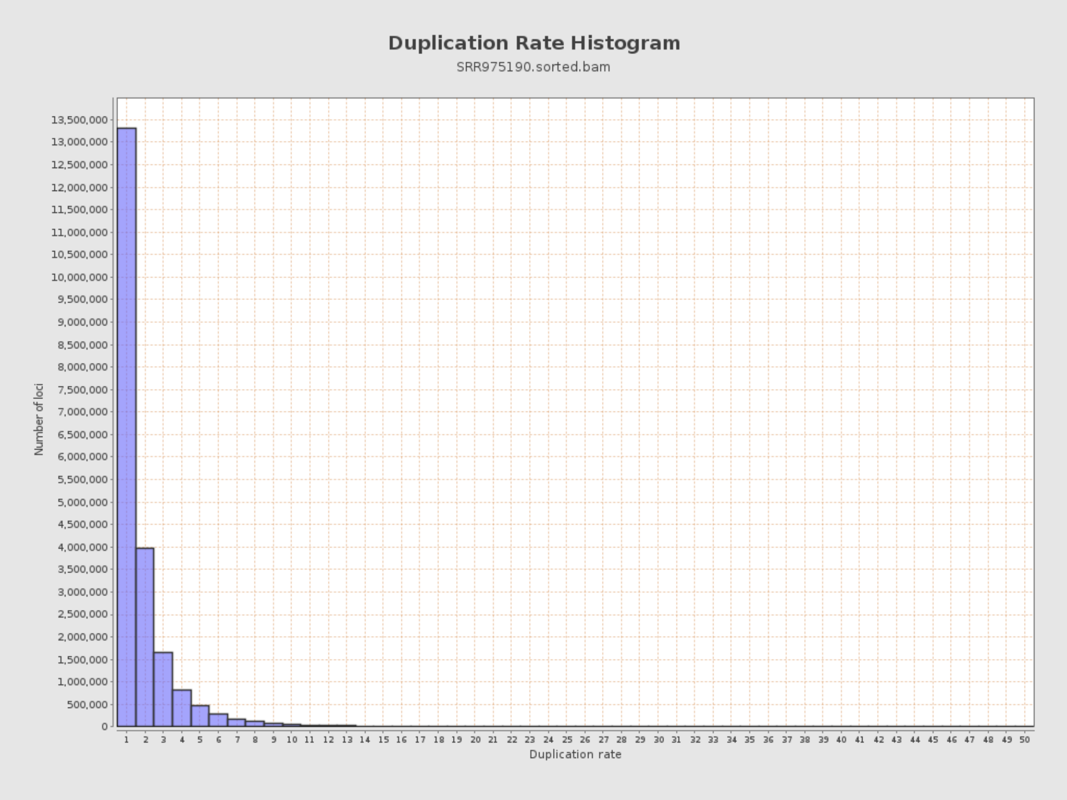
5. Results : Coverage Histogram (0-50X)



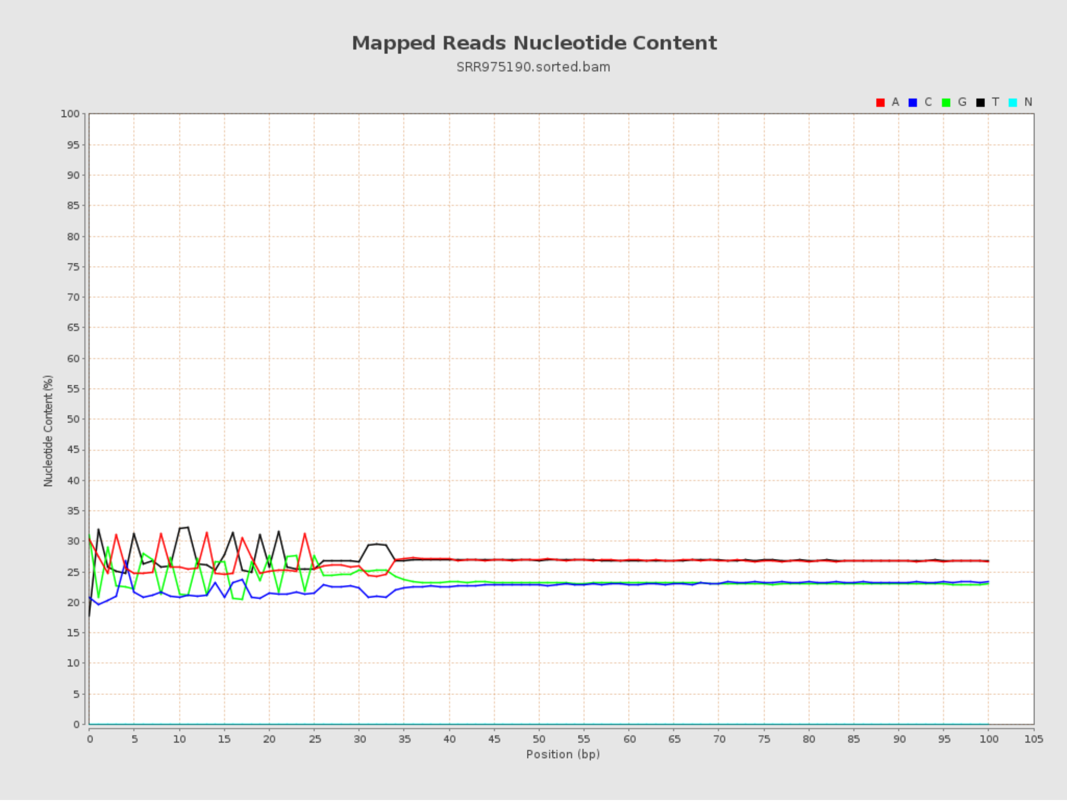
6. Results : Genome Fraction Coverage



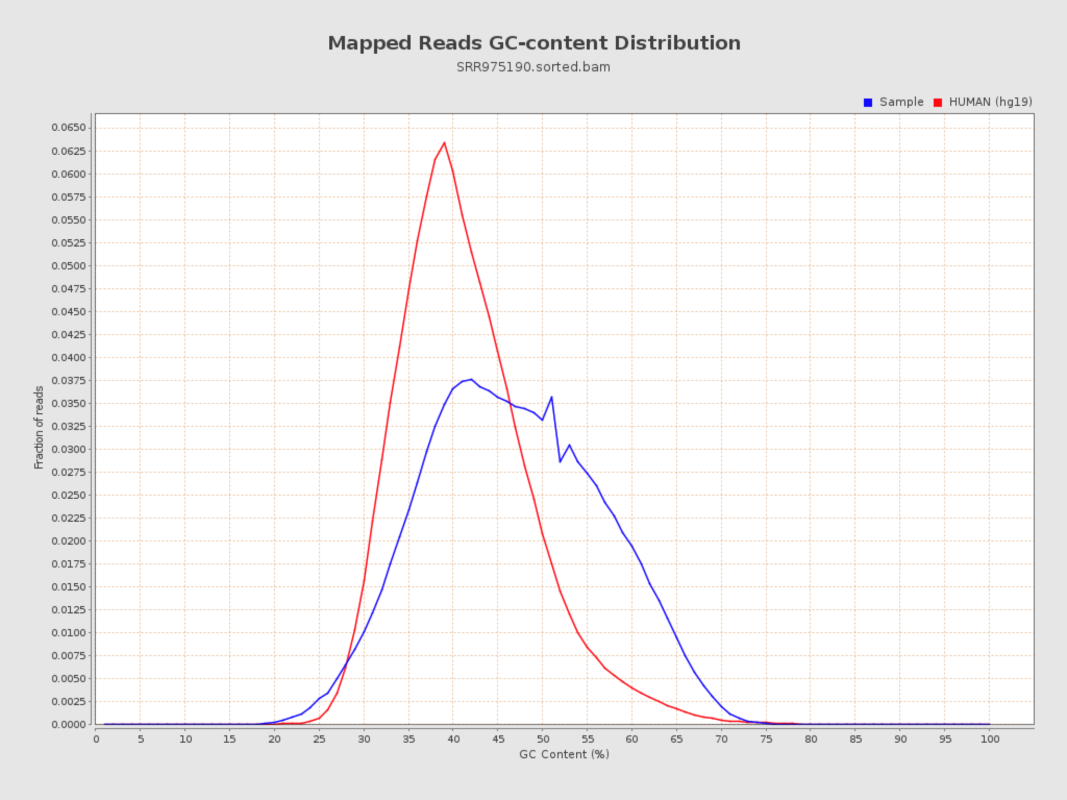
7. Results : Duplication Rate Histogram



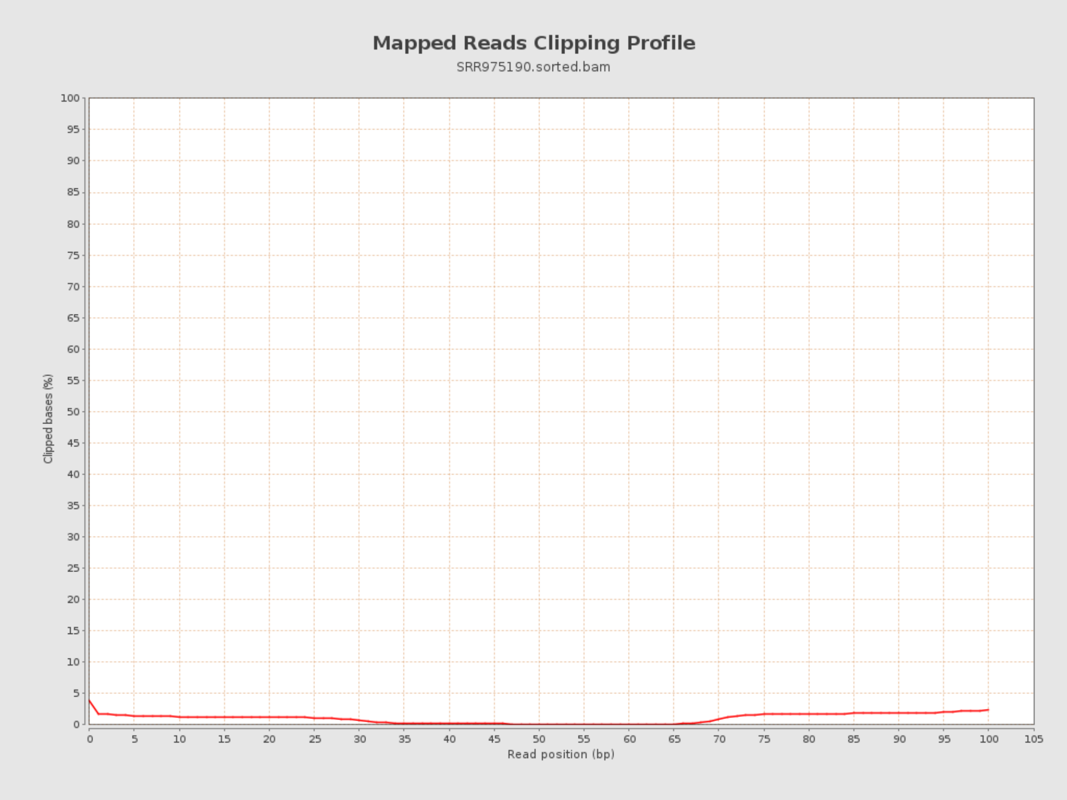
8. Results : Mapped Reads Nucleotide Content



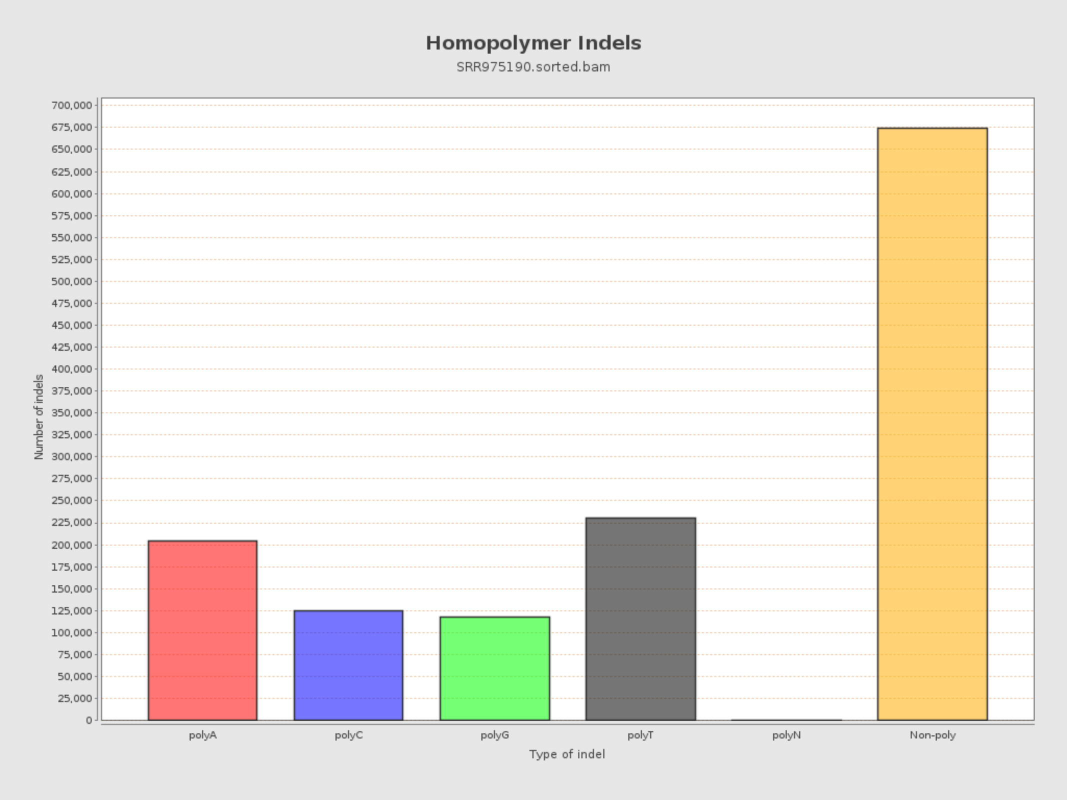
9. Results : Mapped Reads GC-content Distribution



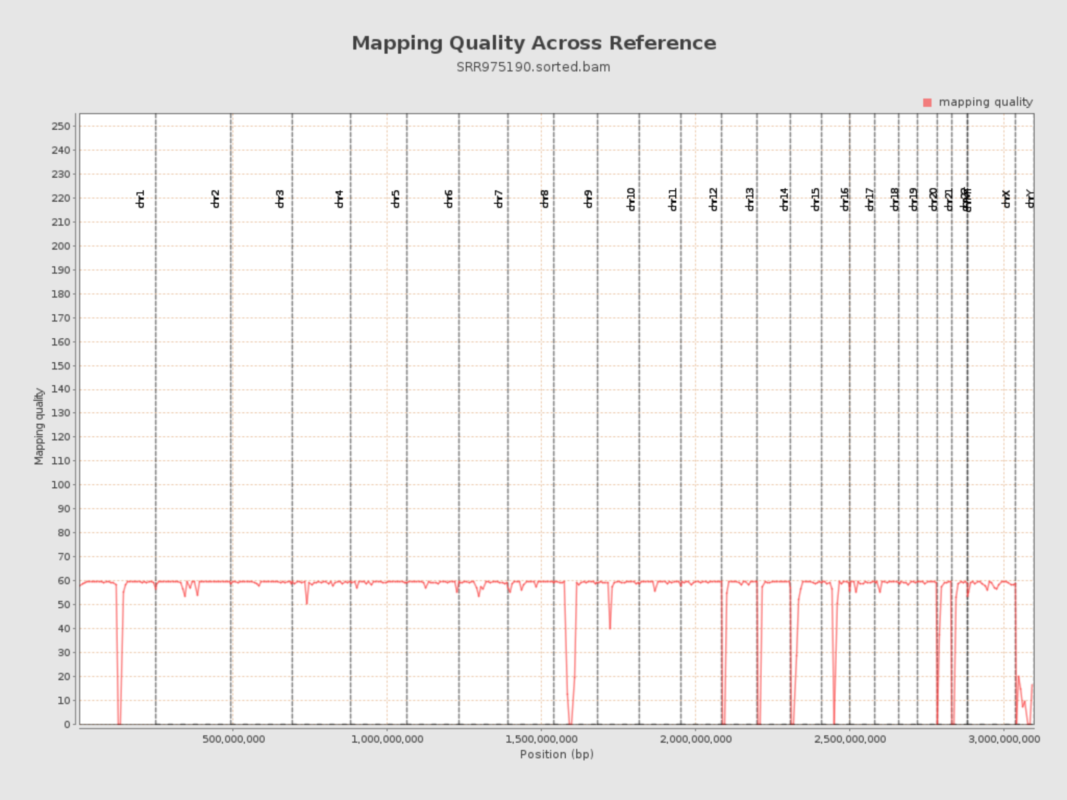
10. Results : Mapped Reads Clipping Profile



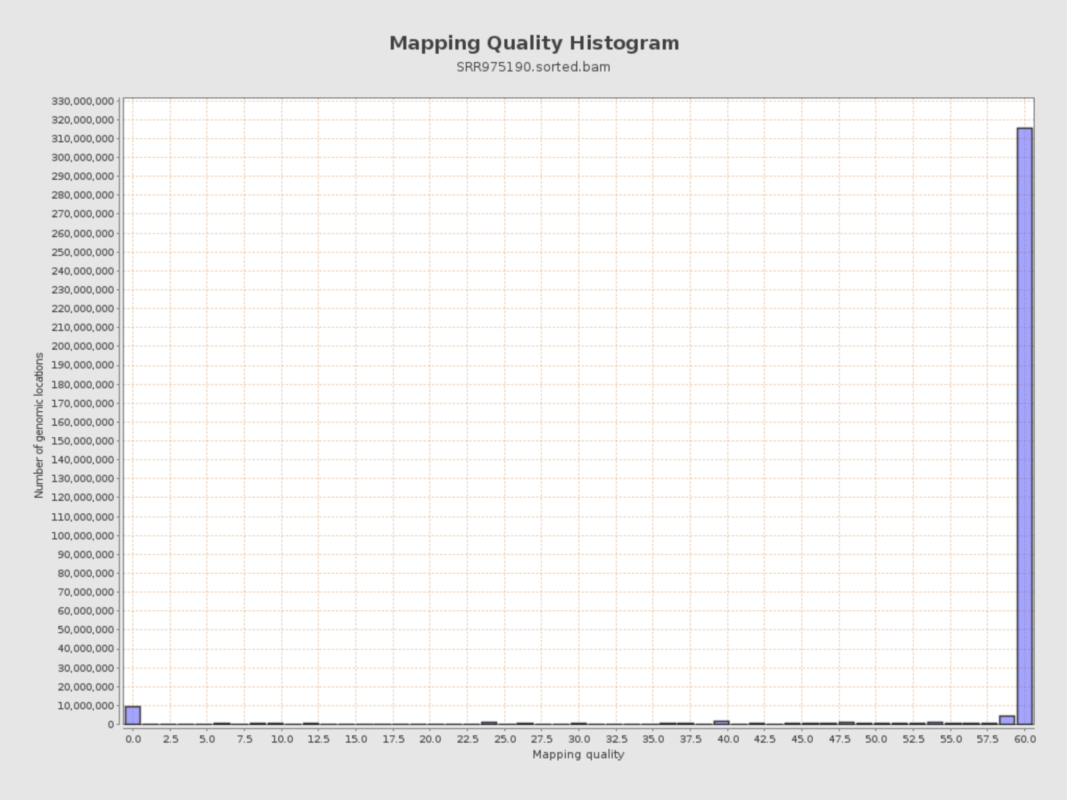
11. Results : Homopolymer Indels



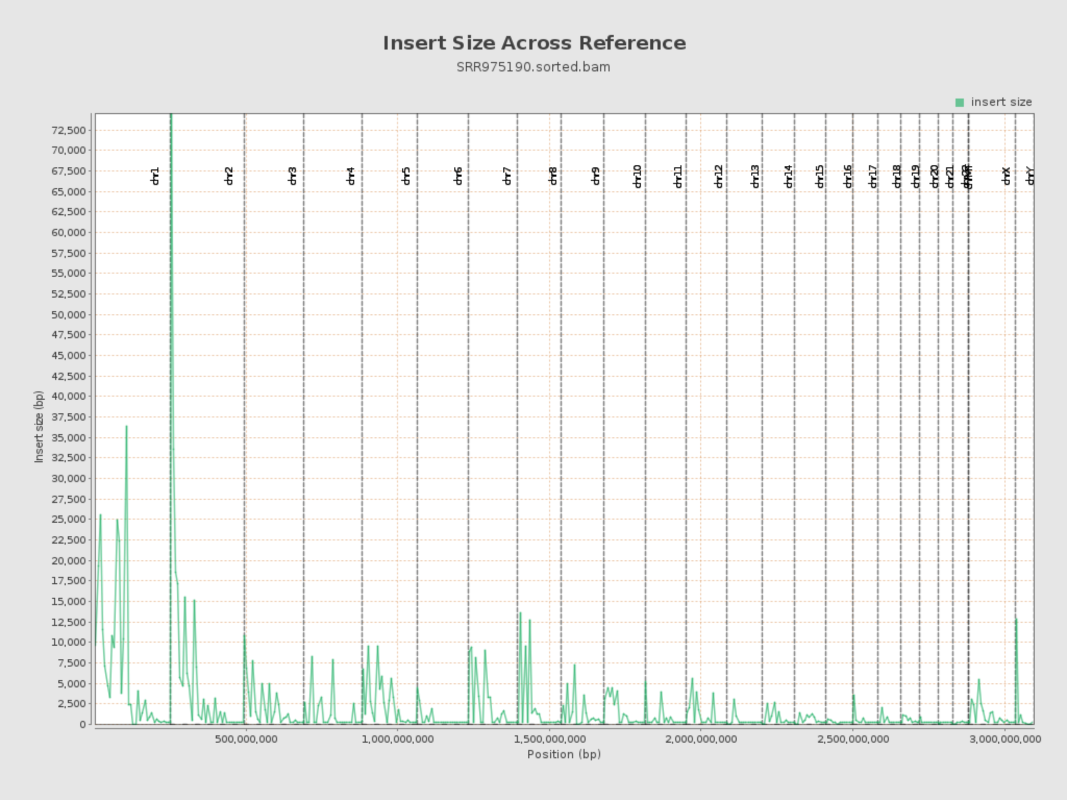
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram