Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975206.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_SRR975206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975206_1.fastq.gz SRR975206_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:35:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,867,864
Mapped reads	40,814,105 / 99.87%
Unmapped reads	53,759 / 0.13%
Mapped paired reads	40,814,105 / 99.87%
Mapped reads, first in pair	20,412,265 / 49.95%
Mapped reads, second in pair	20,401,840 / 49.92%
Mapped reads, both in pair	40,776,816 / 99.78%
Mapped reads, singletons	37,289 / 0.09%
Secondary alignments	0
Supplementary alignments	250,370 / 0.61%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	16,045,503 / 39.26%
Duplication rate	37.75%
Clipped reads	21,167,584 / 51.8%

2.2. ACGT Content

Number/percentage of A's	1,075,376,207 / 26.95%
Number/percentage of C's	930,129,767 / 23.31%
Number/percentage of T's	1,068,459,375 / 26.78%
Number/percentage of G's	915,527,766 / 22.95%
Number/percentage of N's	223,170 / 0.01%

GC Percentage	46.26%

2.3. Coverage

Mean	1.289
Standard Deviation	9.8254

2.4. Mapping Quality

Mean Mapping Quality	55.91

2.5. Insert size

Mean	240,246.63
Standard Deviation	4,829,748.4
P25/Median/P75	189 / 230 / 276

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	17,086,981
Insertions	274,810
Mapped reads with at least one insertion	0.67%
Deletions	225,773
Mapped reads with at least one deletion	0.54%
Homopolymer indels	36.84%

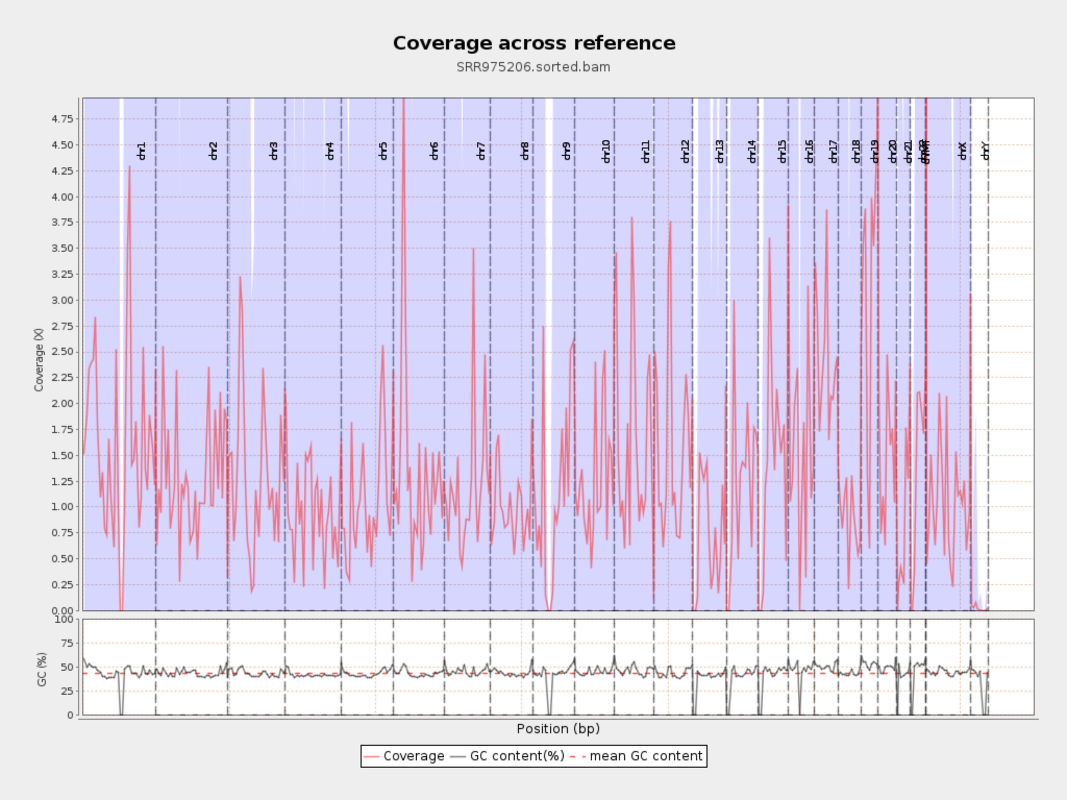
2.7. Chromosome stats

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

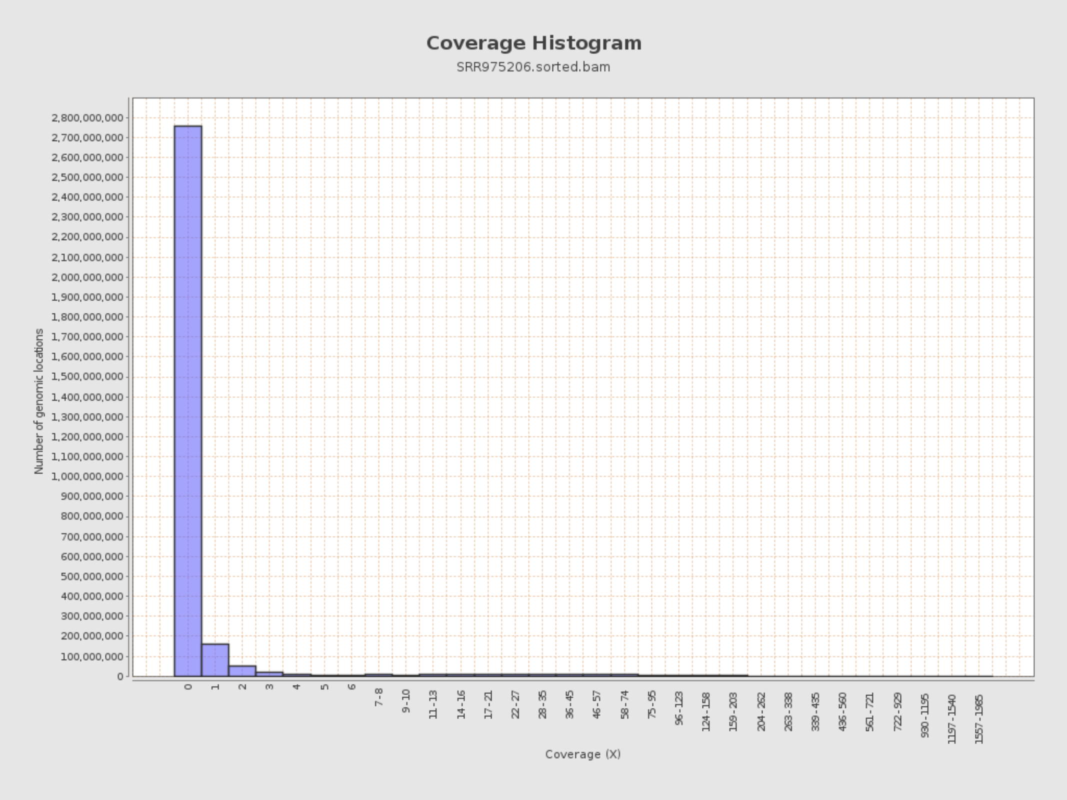
		bases	coverage	deviation
chr1	249250621	399646825	1.6034	11.3399
chr2	243199373	311225764	1.2797	9.6365
chr3	198022430	250973646	1.2674	9.5949
chr4	191154276	180949780	0.9466	8.3461
chr5	180915260	197708743	1.0928	8.8944
chr6	171115067	226454306	1.3234	10.2817
chr7	159138663	190985194	1.2001	9.615
chr8	146364022	145550617	0.9944	8.3277
chr9	141213431	155984513	1.1046	8.8263
chr10	135534747	169765101	1.2526	9.6328
chr11	135006516	225874682	1.6731	11.4335
chr12	133851895	218493932	1.6324	11.0853
chr13	115169878	84439883	0.7332	7.3749
chr14	107349540	132784498	1.2369	9.7081
chr15	102531392	139678133	1.3623	10.0387
chr16	90354753	138962101	1.538	10.3826
chr17	81195210	199563545	2.4578	13.6237
chr18	78077248	69180465	0.8861	7.9108
chr19	59128983	183345211	3.1008	14.7917
chr20	63025520	91557930	1.4527	10.1687
chr21	48129895	42427823	0.8815	8.1
chr22	51304566	68289759	1.3311	9.0585
chrMT	16571	320103	19.3171	26.8823
chrX	155270560	164841177	1.0616	9.4498

chrY	59373566	1201728	0.0202	0.8017

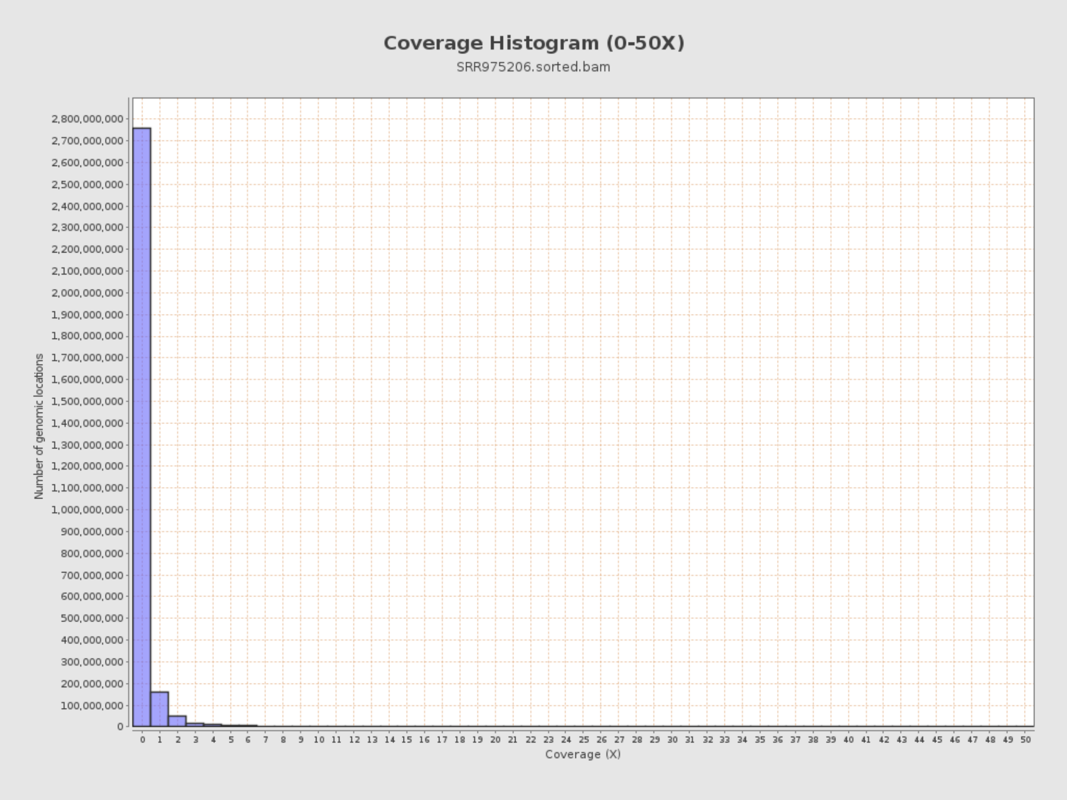
3. Results : Coverage across reference



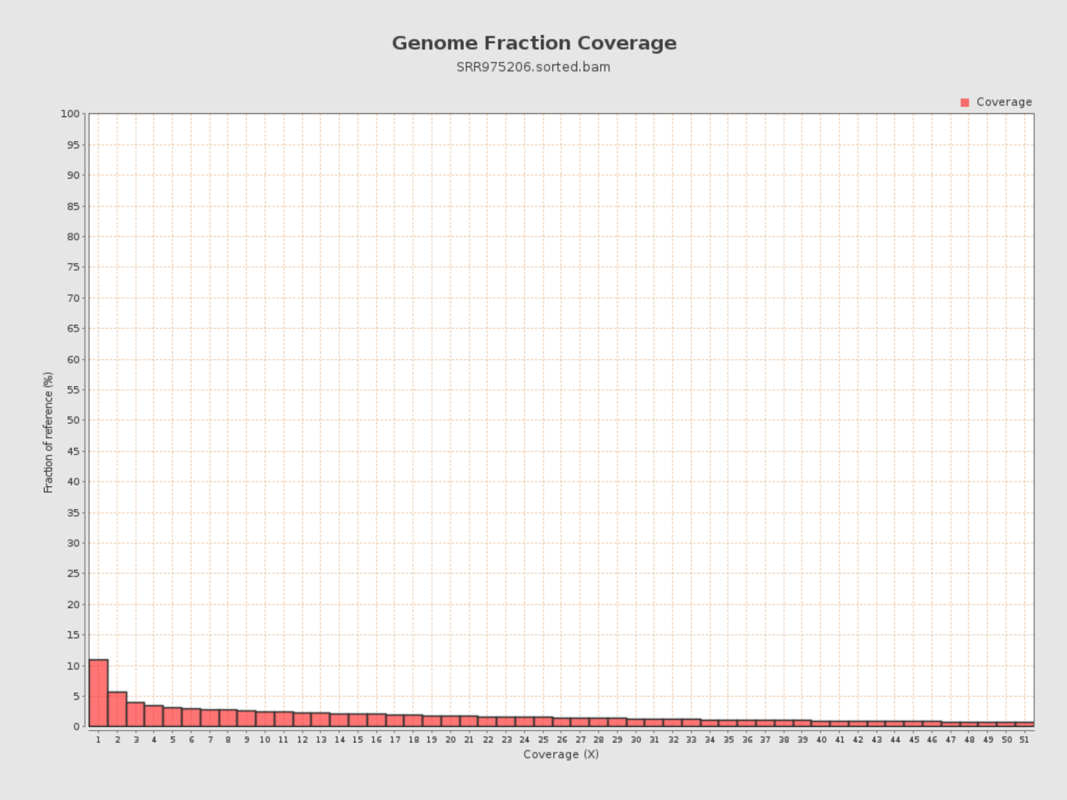
4. Results : Coverage Histogram



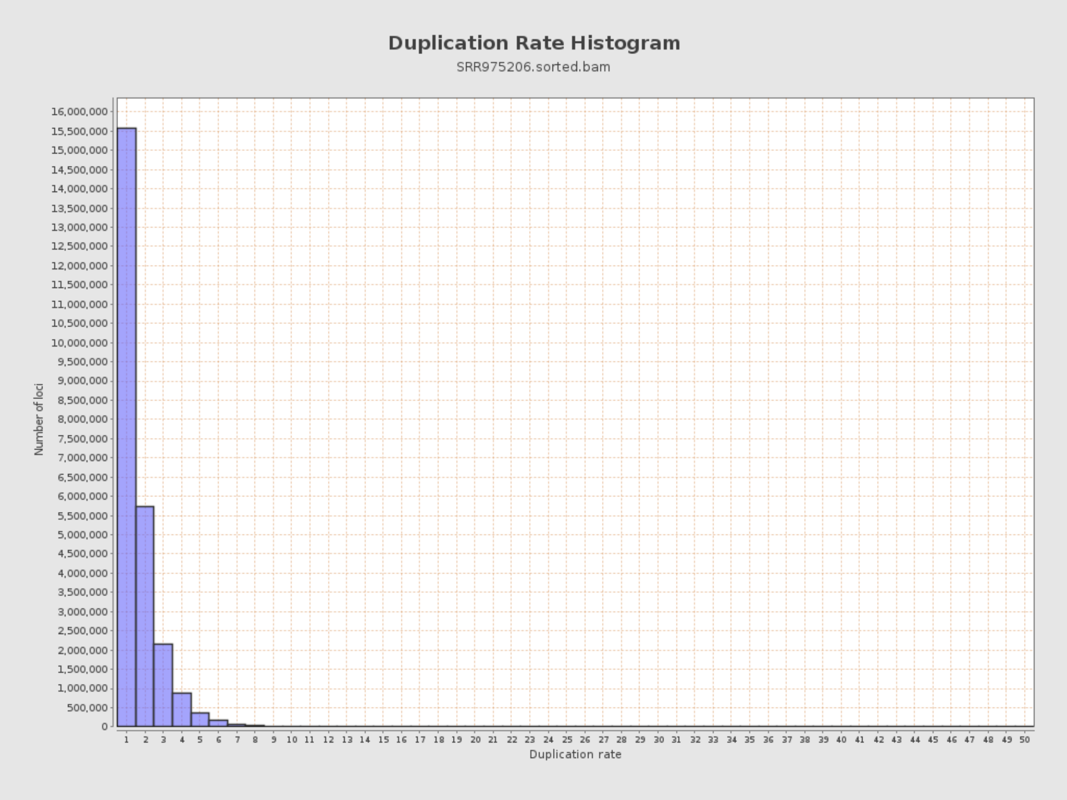
5. Results : Coverage Histogram (0-50X)



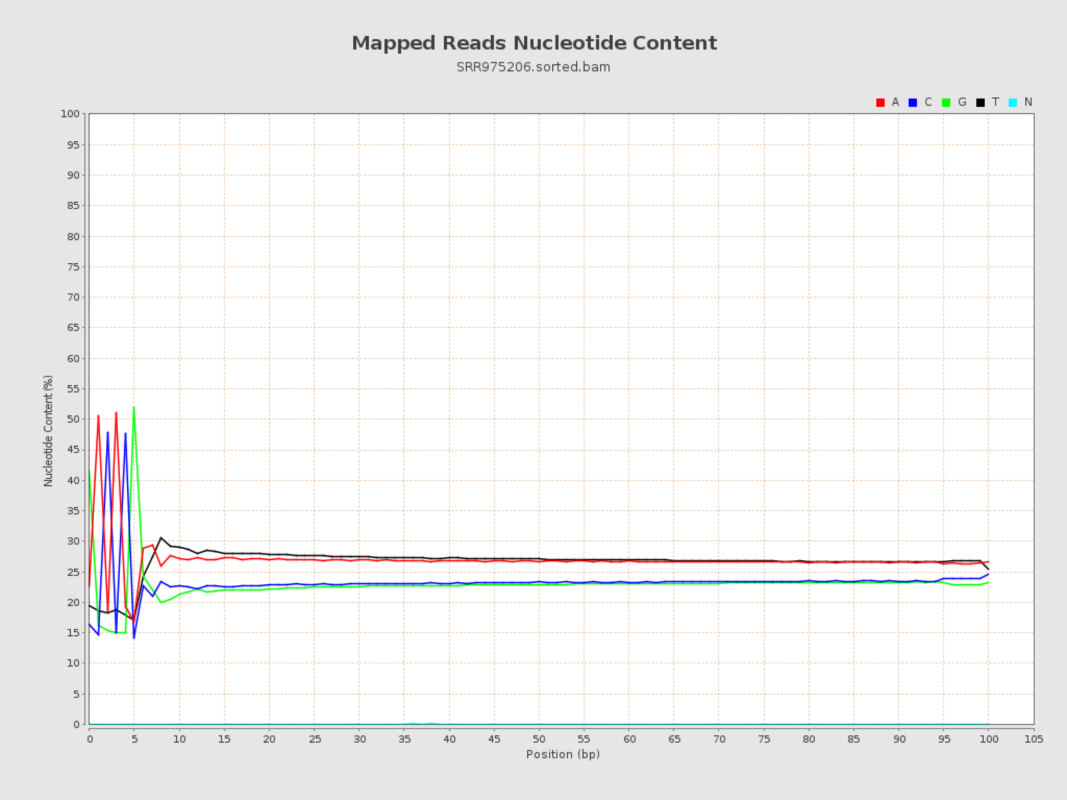
6. Results : Genome Fraction Coverage



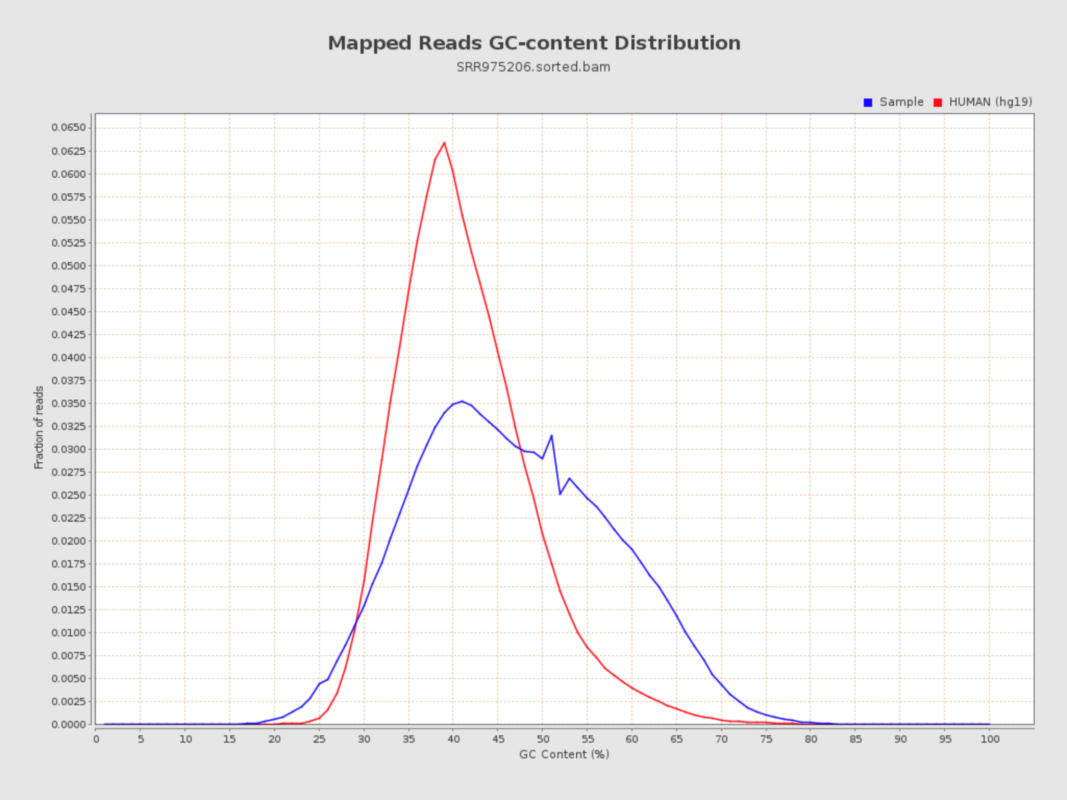
7. Results : Duplication Rate Histogram



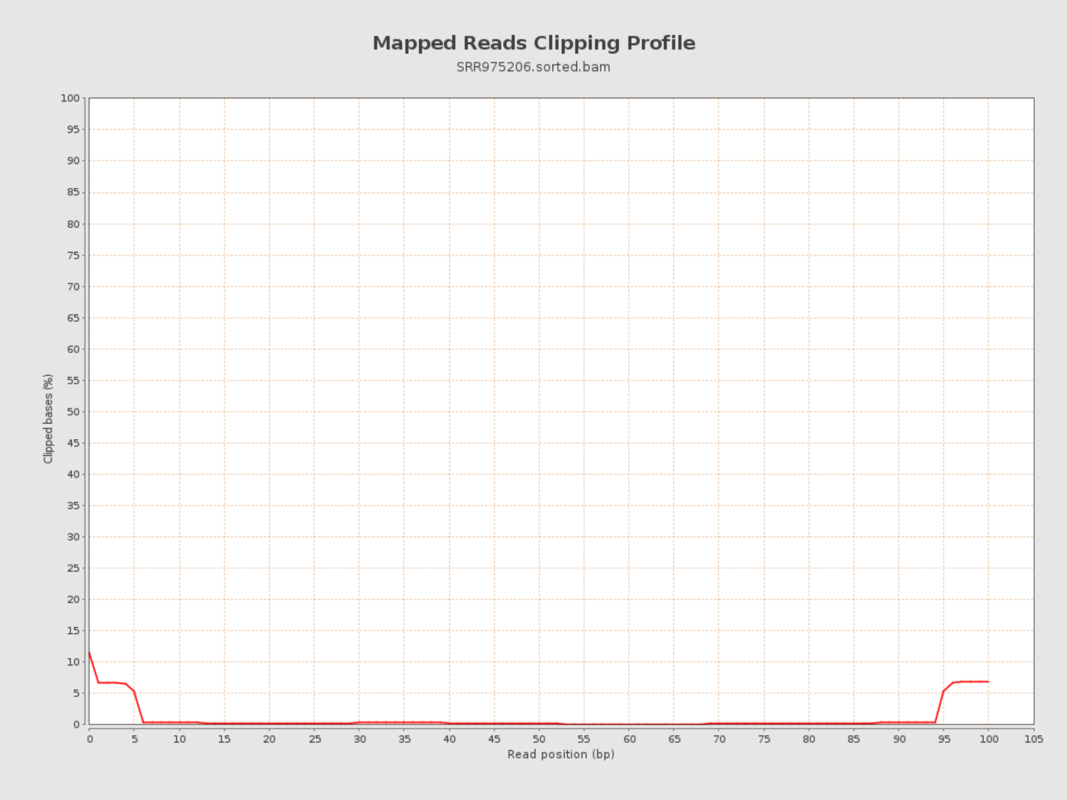
8. Results : Mapped Reads Nucleotide Content



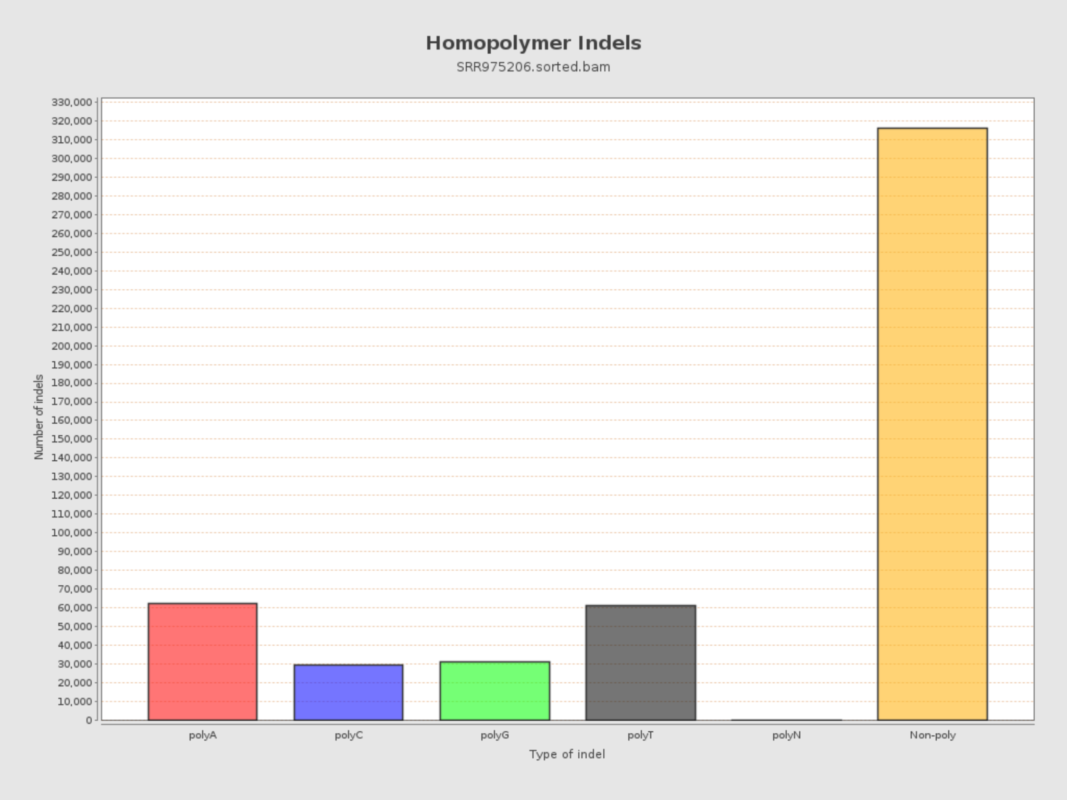
9. Results : Mapped Reads GC-content Distribution



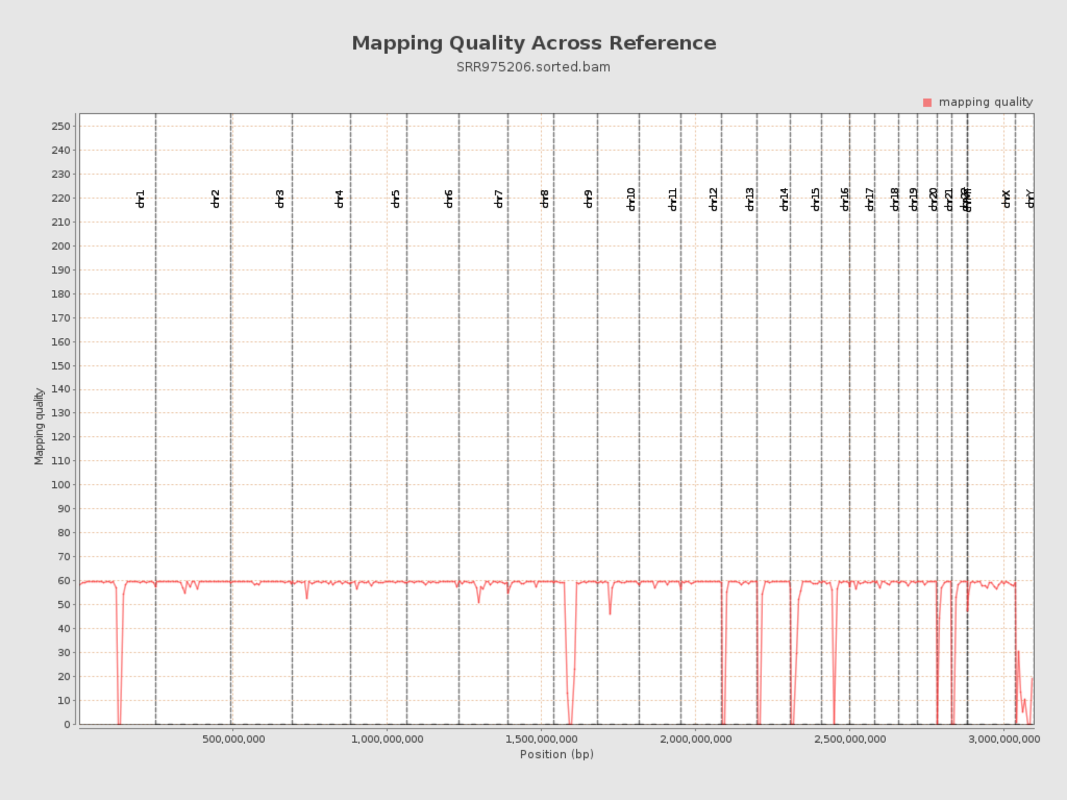
10. Results : Mapped Reads Clipping Profile



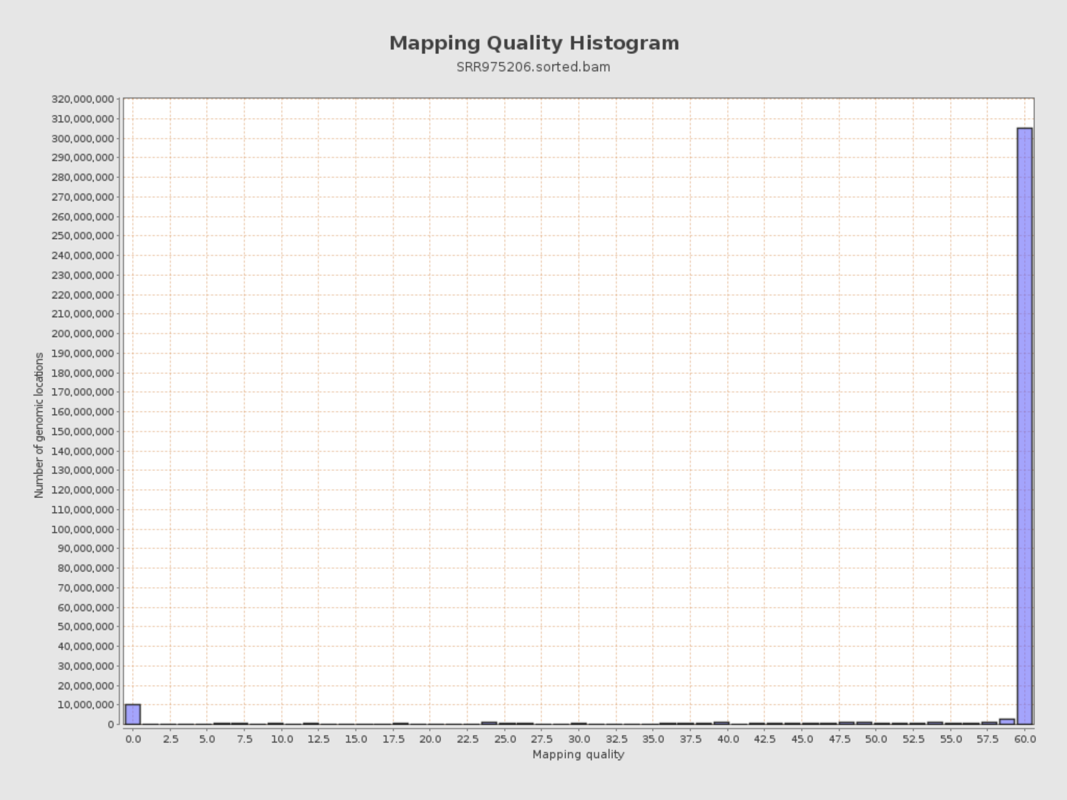
11. Results : Homopolymer Indels



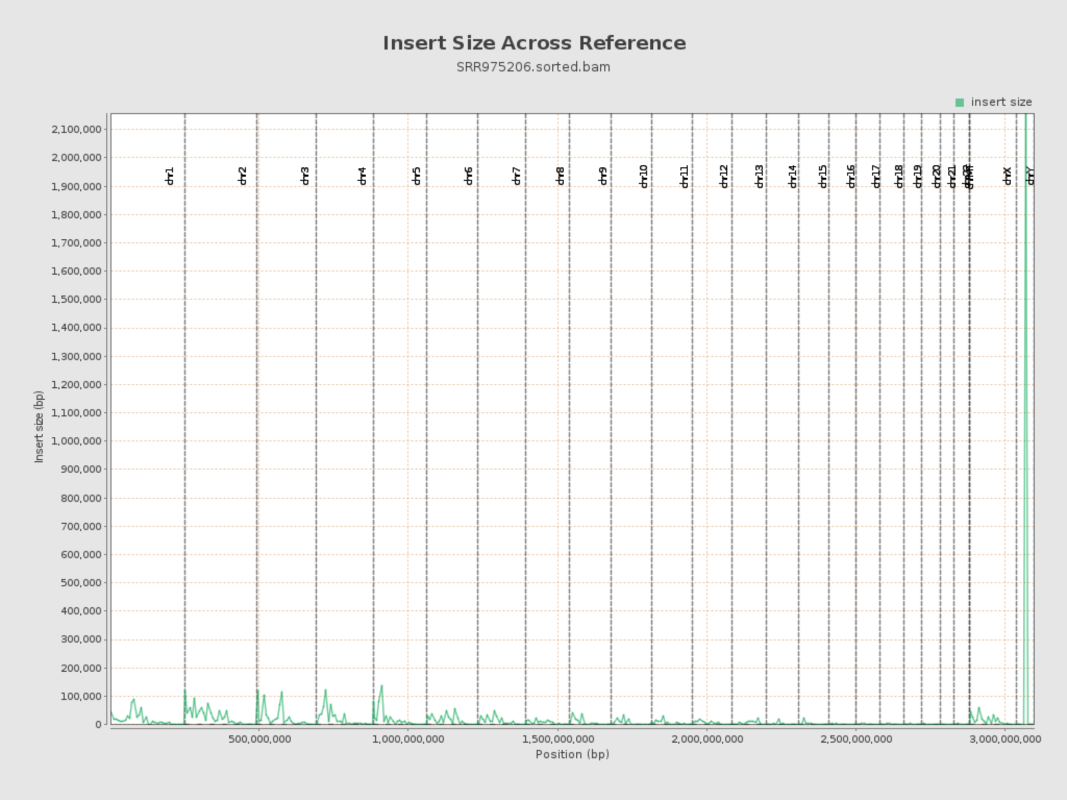
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram