Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:12:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975216.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_SRR975216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975216_1.fastq.gz SRR975216_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:12:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,199,150
Mapped reads	56,028,873 / 99.7%
Unmapped reads	170,277 / 0.3%
Mapped paired reads	56,028,873 / 99.7%
Mapped reads, first in pair	28,047,466 / 49.91%
Mapped reads, second in pair	27,981,407 / 49.79%
Mapped reads, both in pair	55,920,366 / 99.5%
Mapped reads, singletons	108,507 / 0.19%
Secondary alignments	0
Supplementary alignments	145,323 / 0.26%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	33,271,340 / 59.2%
Duplication rate	37.37%
Clipped reads	8,676,433 / 15.44%

2.2. ACGT Content

Number/percentage of A's	1,458,174,496 / 26.53%
Number/percentage of C's	1,257,727,489 / 22.89%
Number/percentage of T's	1,473,633,544 / 26.81%
Number/percentage of G's	1,305,623,256 / 23.76%
Number/percentage of N's	413,308 / 0.01%

GC Percentage	46.64%

2.3. Coverage

Mean	1.7759
Standard Deviation	26.092

2.4. Mapping Quality

Mean Mapping Quality	55.63

2.5. Insert size

Mean	170,916.49
Standard Deviation	4,239,833.54
P25/Median/P75	169 / 207 / 255

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	33,618,976
Insertions	460,648
Mapped reads with at least one insertion	0.81%
Deletions	1,356,713
Mapped reads with at least one deletion	2.38%
Homopolymer indels	49.13%

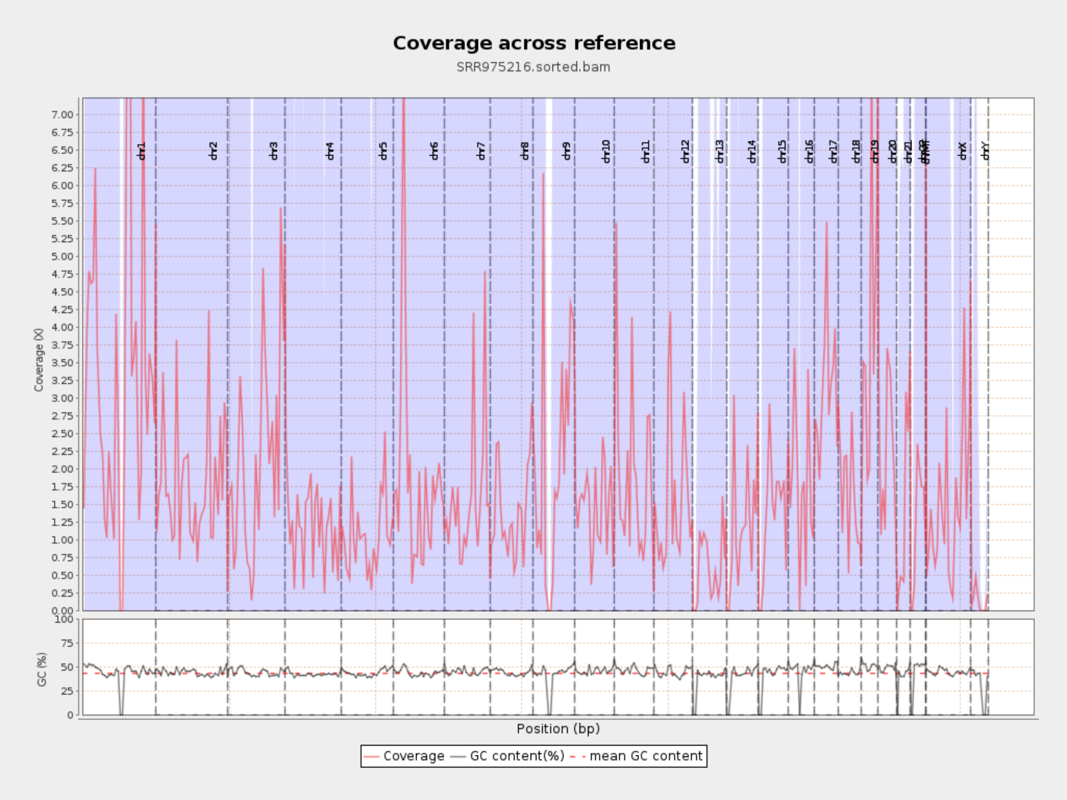
2.7. Chromosome stats

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

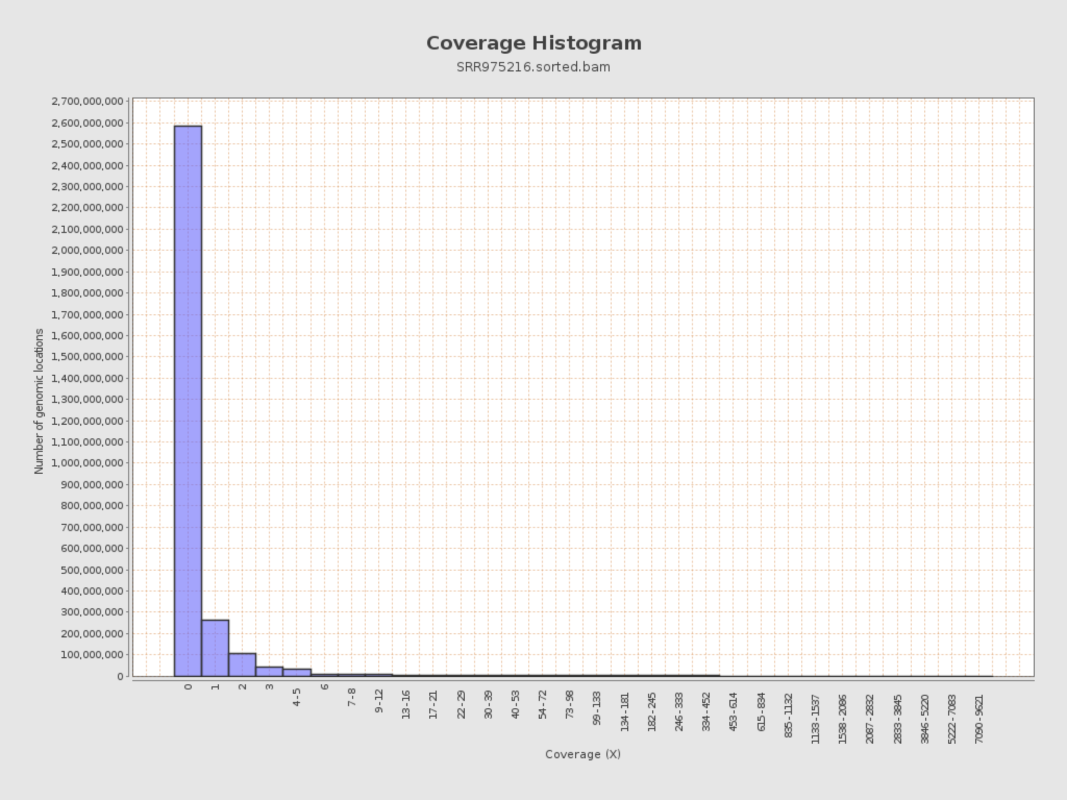
		bases	coverage	deviation
chr1	249250621	848876106	3.4057	41.4353
chr2	243199373	436428895	1.7945	24.3845
chr3	198022430	421401710	2.1281	30.1748
chr4	191154276	230415947	1.2054	19.5505
chr5	180915260	193533986	1.0697	17.1705
chr6	171115067	319518517	1.8673	27.612
chr7	159138663	256096355	1.6093	24.7514
chr8	146364022	205368039	1.4031	21.5569
chr9	141213431	288939524	2.0461	29.0298
chr10	135534747	199052803	1.4686	22.0307
chr11	135006516	256422617	1.8993	25.6847
chr12	133851895	218060351	1.6291	22.2123
chr13	115169878	69826986	0.6063	12.8717
chr14	107349540	124329751	1.1582	19.2401
chr15	102531392	132925625	1.2964	18.3425
chr16	90354753	156834483	1.7358	23.0663
chr17	81195210	259867076	3.2005	36.1827
chr18	78077248	130636047	1.6732	23.4956
chr19	59128983	233312523	3.9458	44.3657
chr20	63025520	139464438	2.2128	27.4844
chr21	48129895	70367103	1.462	22.5336
chr22	51304566	65157499	1.27	18.4113
chrMT	16571	110186	6.6493	10.5919
chrX	155270560	231914426	1.4936	24.4839

chrY	59373566	8837812	0.1489	4.0273

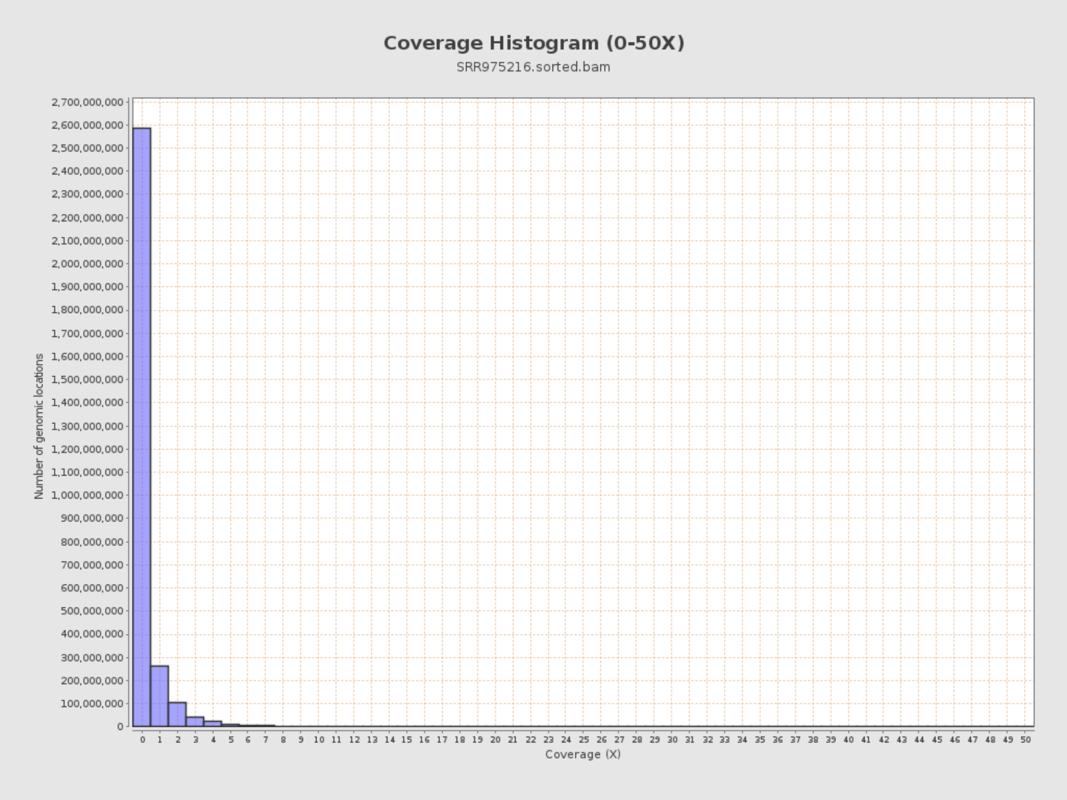
3. Results : Coverage across reference



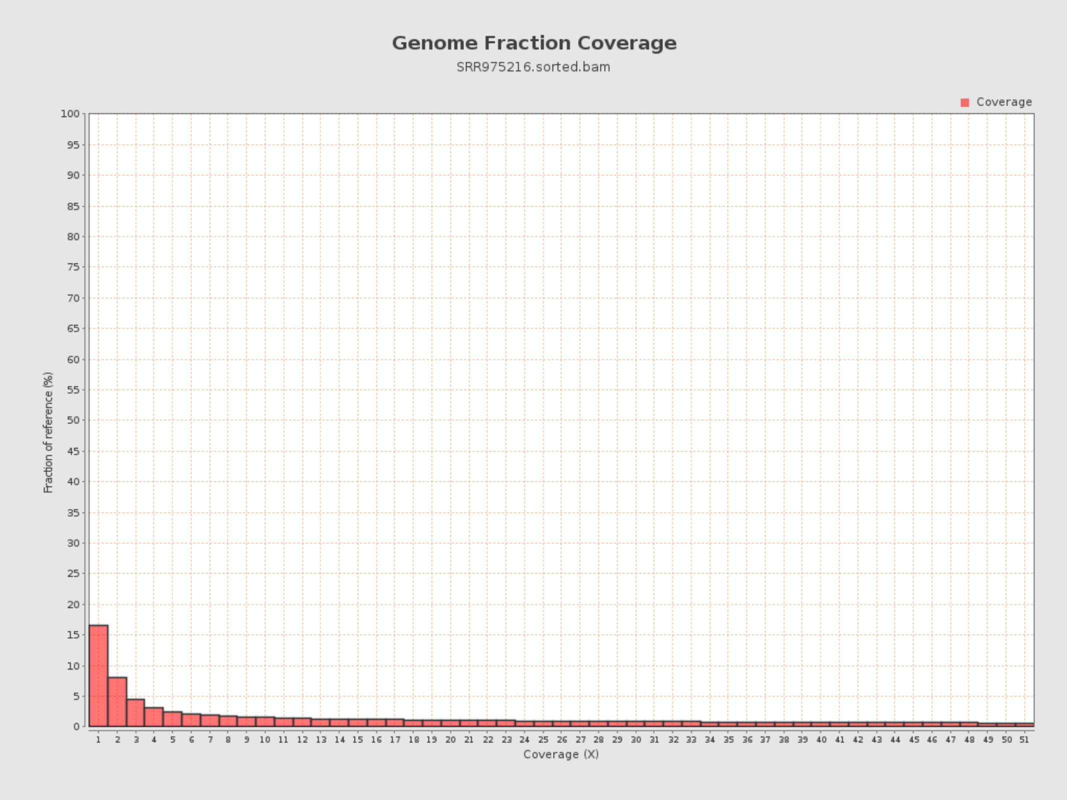
4. Results : Coverage Histogram



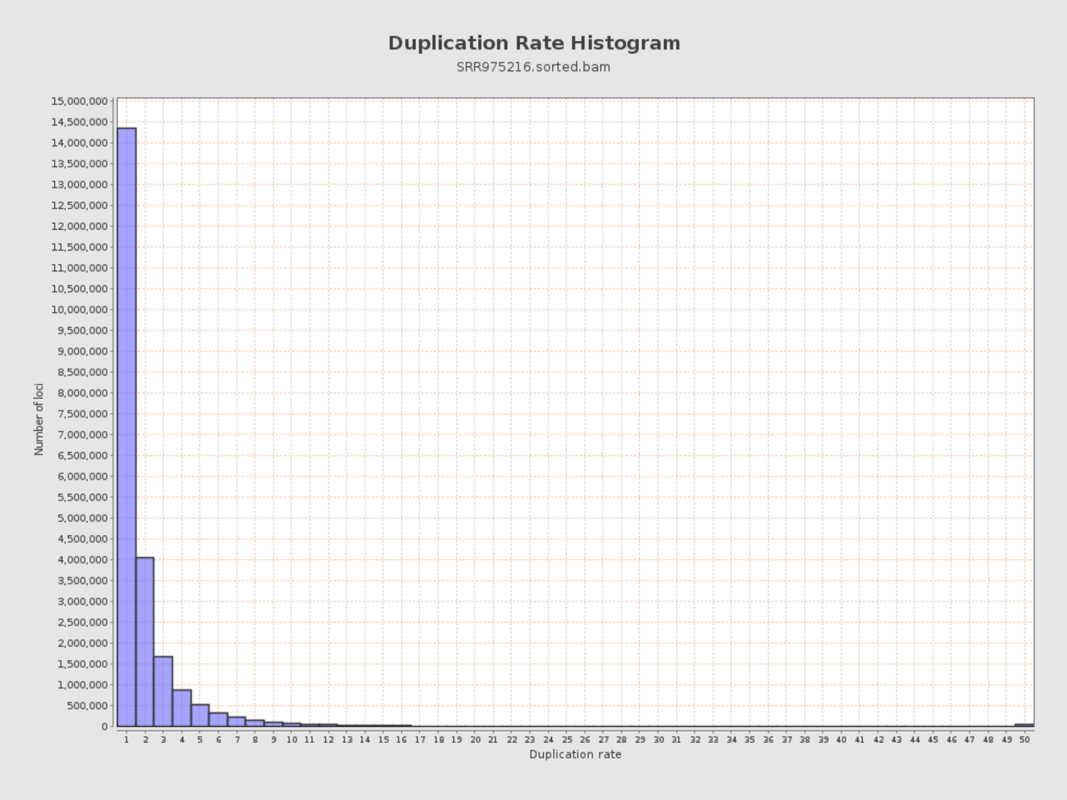
5. Results : Coverage Histogram (0-50X)



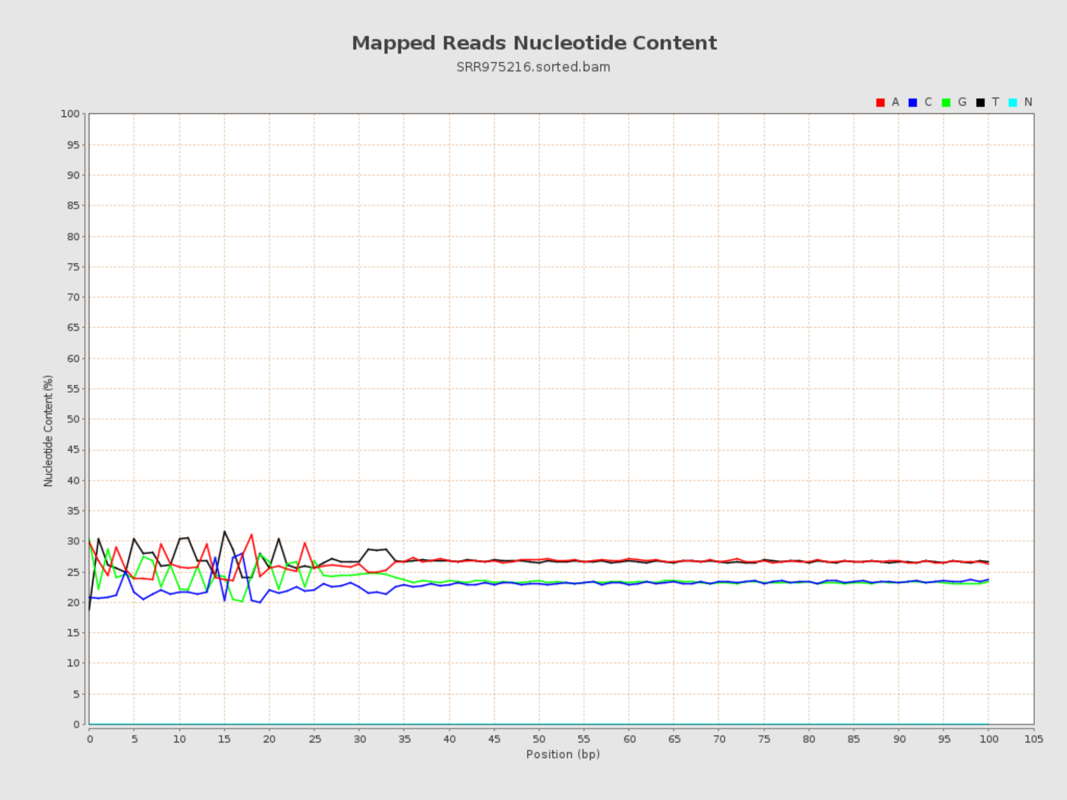
6. Results : Genome Fraction Coverage



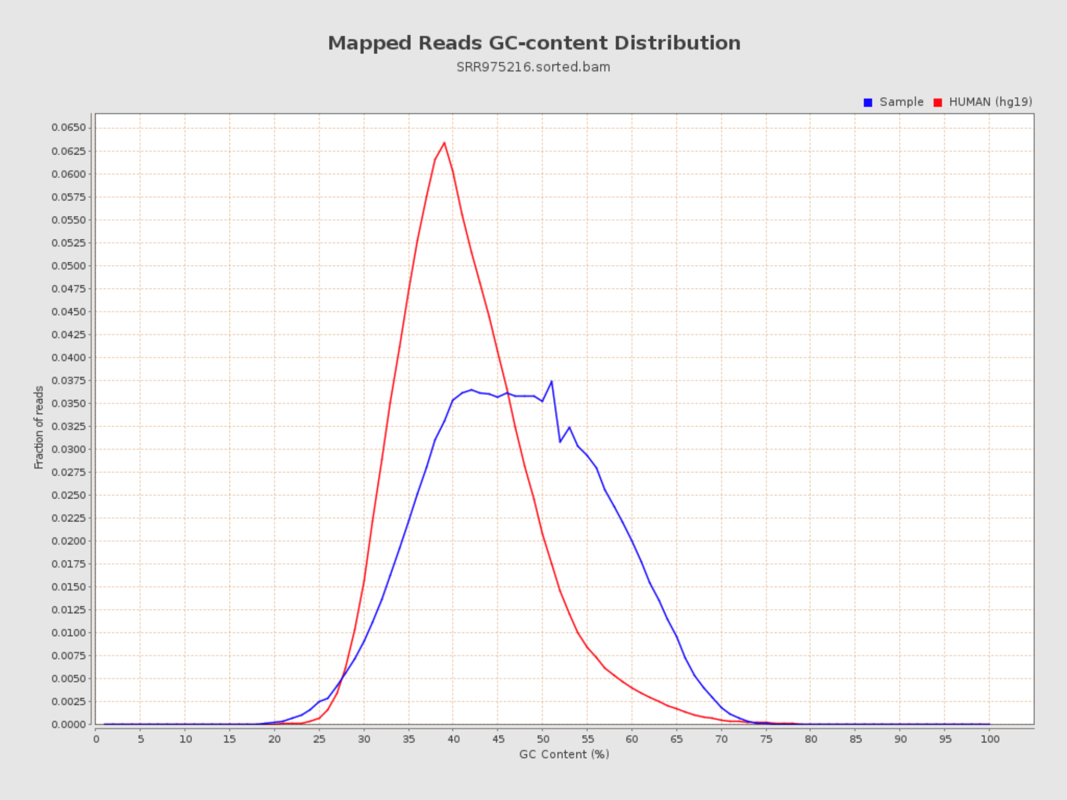
7. Results : Duplication Rate Histogram



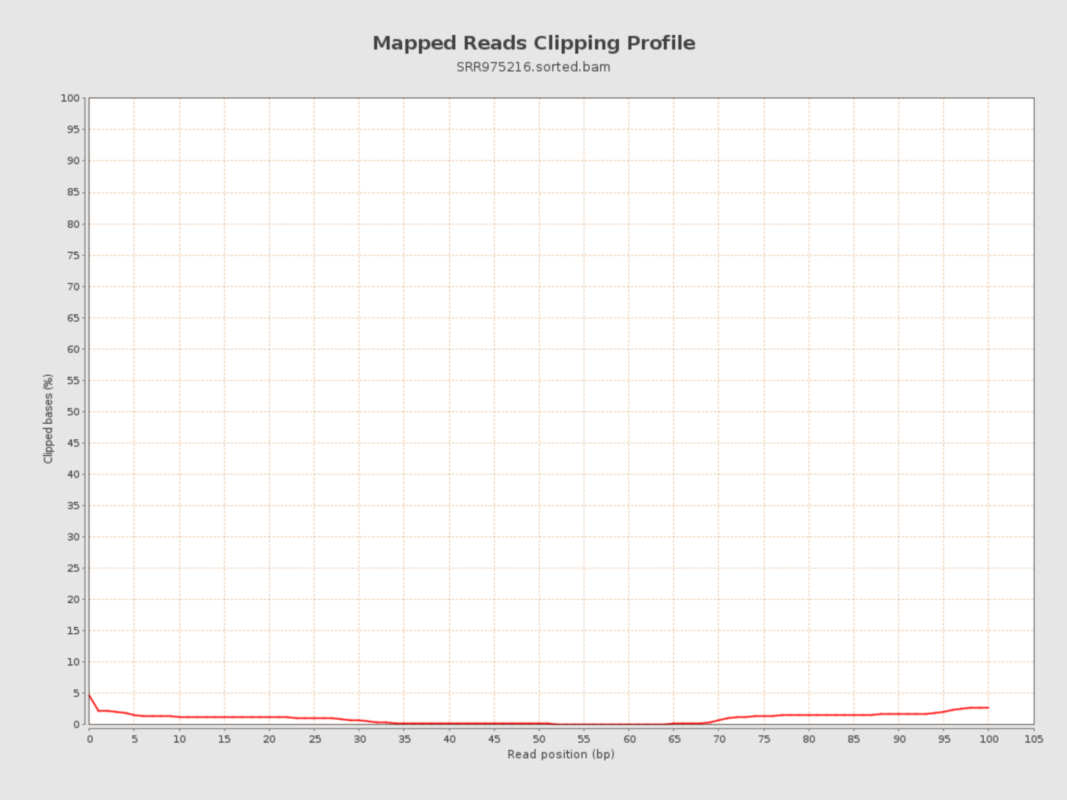
8. Results : Mapped Reads Nucleotide Content



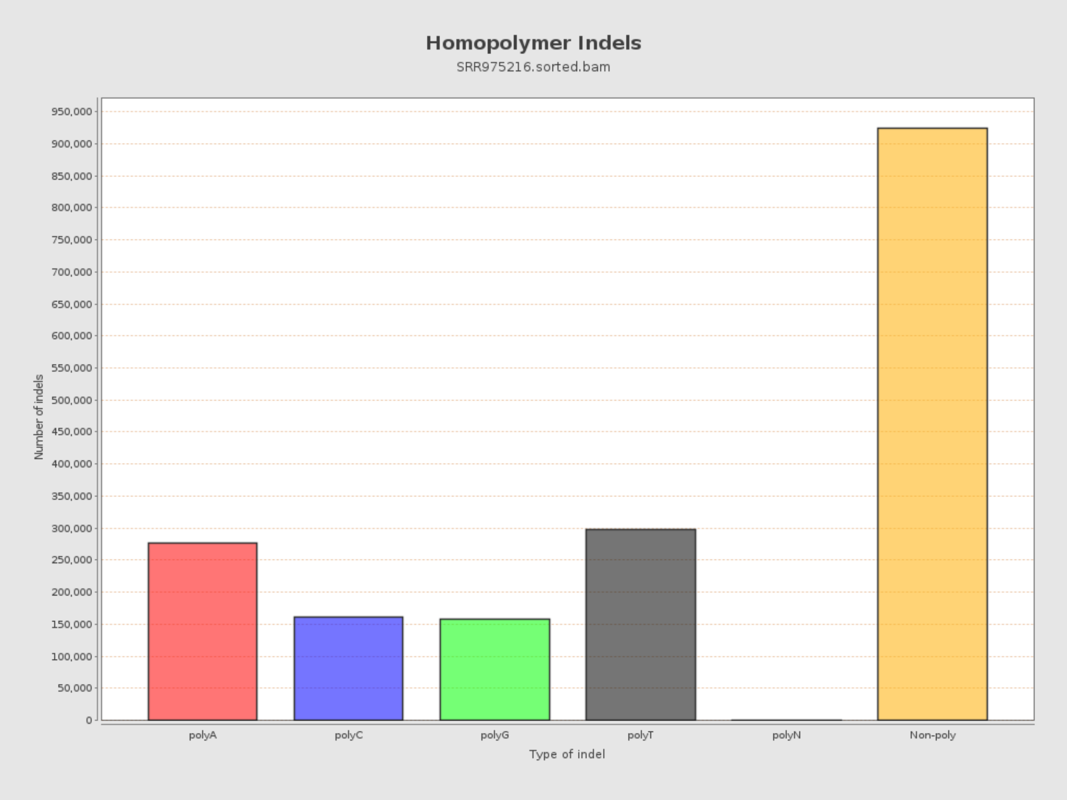
9. Results : Mapped Reads GC-content Distribution



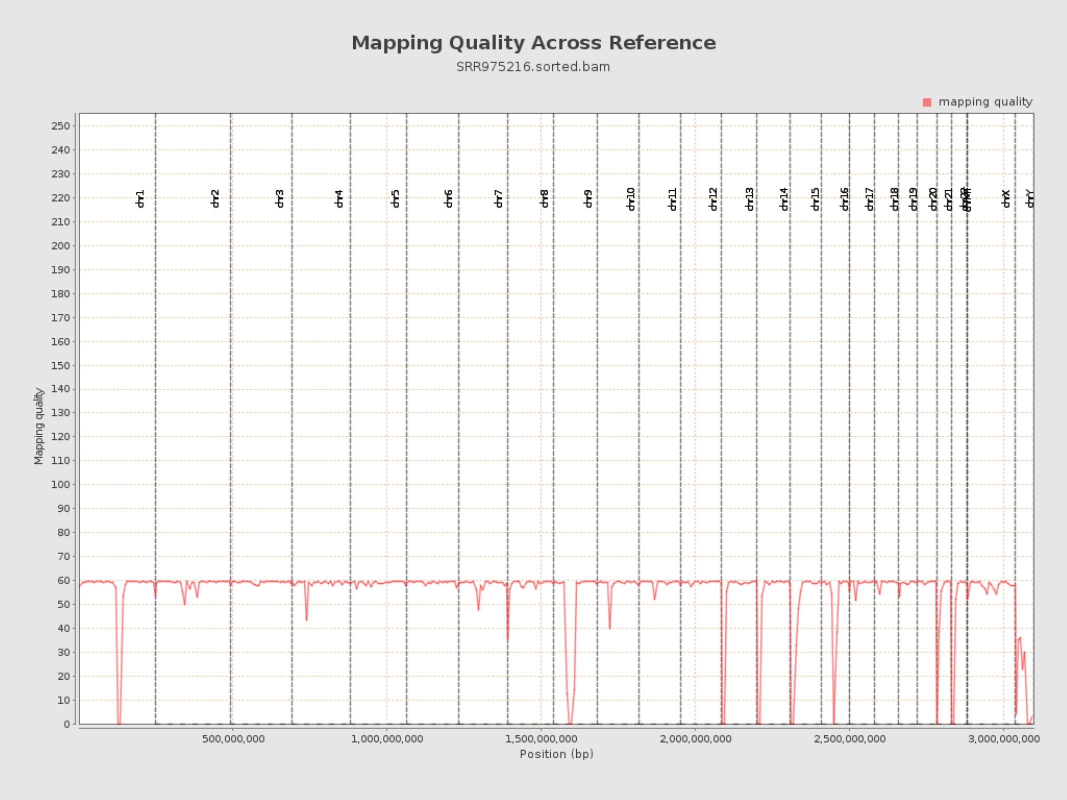
10. Results : Mapped Reads Clipping Profile



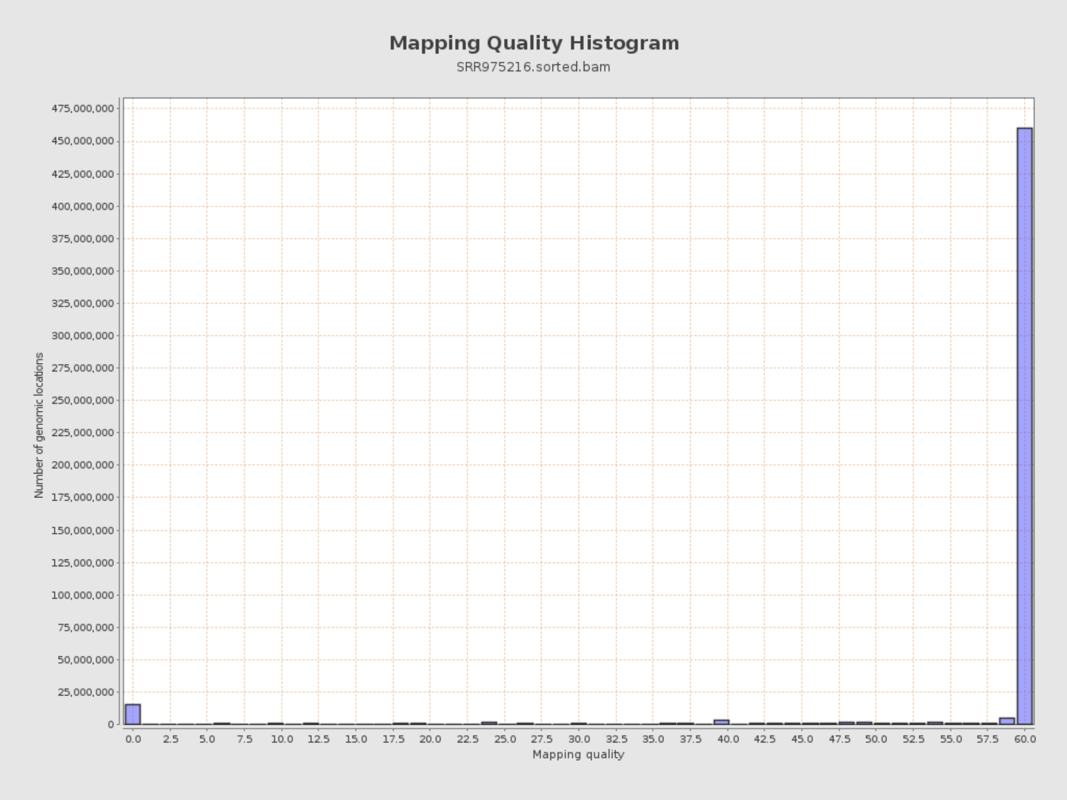
11. Results : Homopolymer Indels



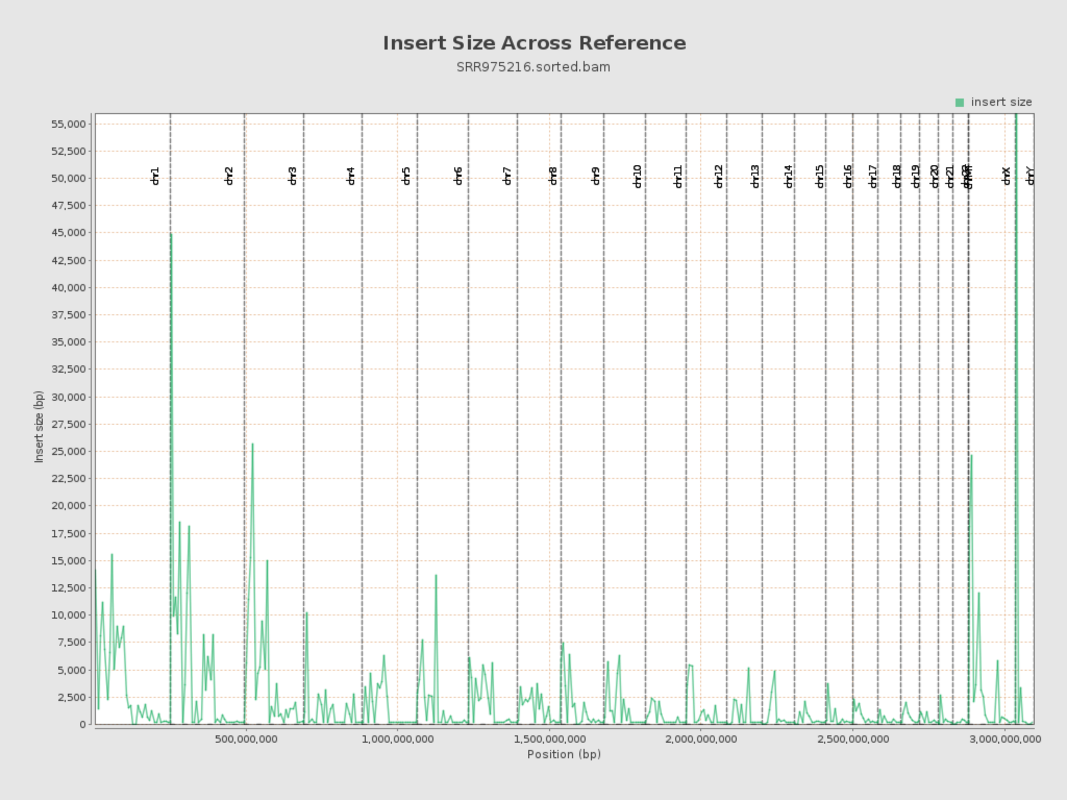
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram