Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975218.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_SRR975218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975218_1.fastq.gz SRR975218_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:19:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,424,054
Mapped reads	42,299,315 / 99.71%
Unmapped reads	124,739 / 0.29%
Mapped paired reads	42,299,315 / 99.71%
Mapped reads, first in pair	21,173,925 / 49.91%
Mapped reads, second in pair	21,125,390 / 49.8%
Mapped reads, both in pair	42,224,242 / 99.53%
Mapped reads, singletons	75,073 / 0.18%
Secondary alignments	0
Supplementary alignments	103,987 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	22,208,319 / 52.35%
Duplication rate	32.39%
Clipped reads	6,780,608 / 15.98%

2.2. ACGT Content

Number/percentage of A's	1,106,544,575 / 26.69%
Number/percentage of C's	939,911,187 / 22.67%
Number/percentage of T's	1,116,232,921 / 26.92%
Number/percentage of G's	983,025,709 / 23.71%
Number/percentage of N's	311,623 / 0.01%

GC Percentage	46.38%

2.3. Coverage

Mean	1.3398
Standard Deviation	18.5353

2.4. Mapping Quality

Mean Mapping Quality	55.79

2.5. Insert size

Mean	136,584.1
Standard Deviation	3,715,464.99
P25/Median/P75	170 / 210 / 261

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	29,072,357
Insertions	365,566
Mapped reads with at least one insertion	0.85%
Deletions	1,127,772
Mapped reads with at least one deletion	2.62%
Homopolymer indels	49.97%

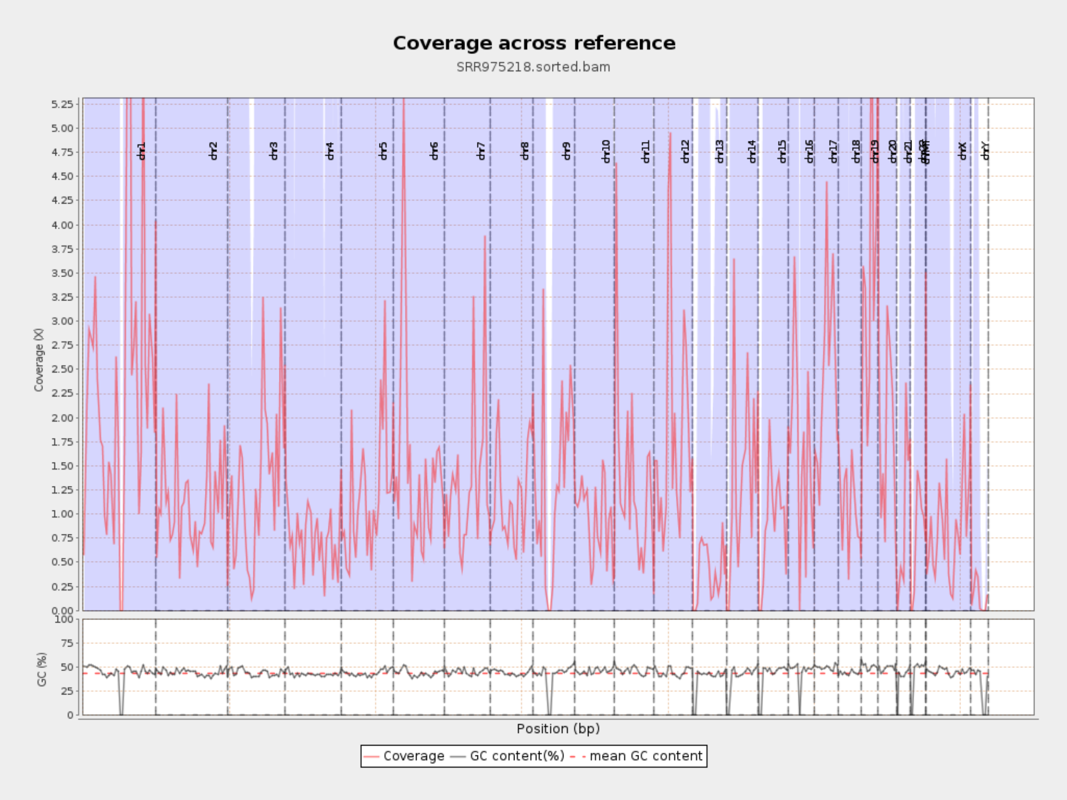
2.7. Chromosome stats

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

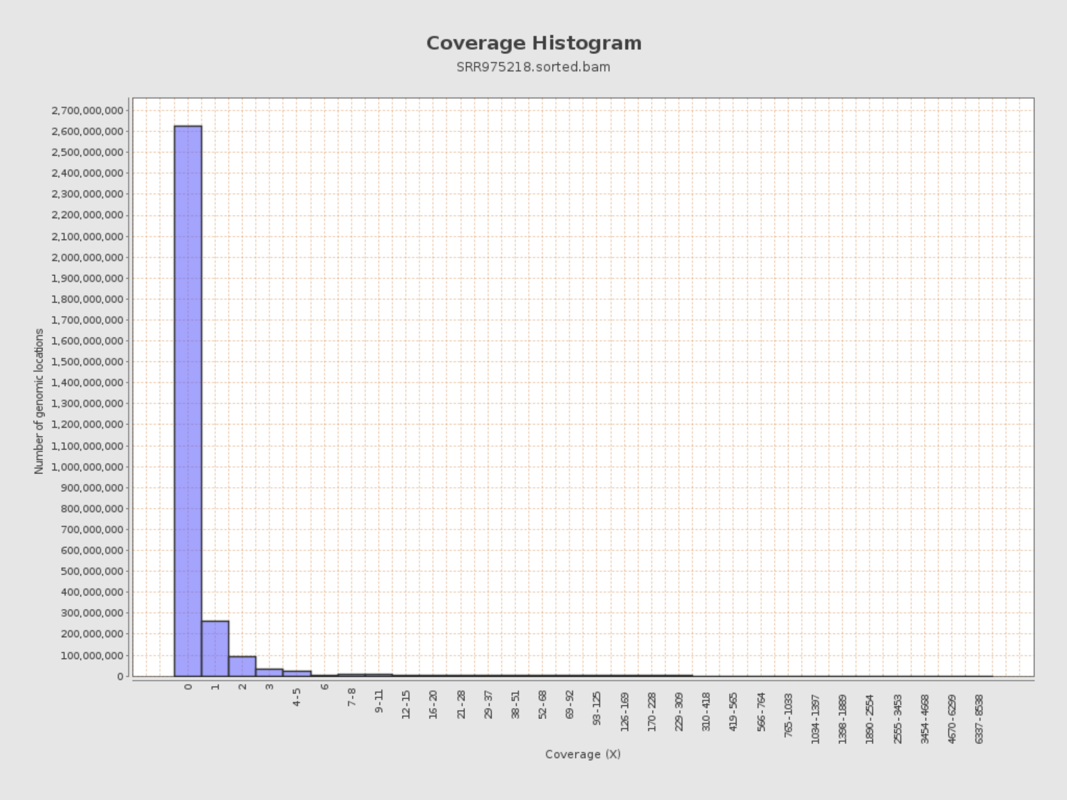
		bases	coverage	deviation
chr1	249250621	595530690	2.3893	28.4753
chr2	243199373	272209930	1.1193	14.4489
chr3	198022430	254577272	1.2856	16.581
chr4	191154276	140816161	0.7367	10.5208
chr5	180915260	218727003	1.209	15.686
chr6	171115067	256007653	1.4961	19.3087
chr7	159138663	213931053	1.3443	20.0193
chr8	146364022	174955618	1.1953	15.2815
chr9	141213431	180169952	1.2759	17.0644
chr10	135534747	130219051	0.9608	13.6273
chr11	135006516	180022823	1.3334	17.0104
chr12	133851895	254707508	1.9029	23.3776
chr13	115169878	46225205	0.4014	6.7432
chr14	107349540	147656504	1.3755	18.8219
chr15	102531392	89659435	0.8745	12.5856
chr16	90354753	146526064	1.6217	20.2223
chr17	81195210	204543981	2.5192	28.1892
chr18	78077248	86086854	1.1026	14.9089
chr19	59128983	212531870	3.5944	37.7901
chr20	63025520	114966381	1.8241	22.4315
chr21	48129895	46247574	0.9609	15.4539
chr22	51304566	40088403	0.7814	11.2075
chrMT	16571	58132	3.5081	5.091
chrX	155270560	132091649	0.8507	15.232

chrY	59373566	9133115	0.1538	3.4686

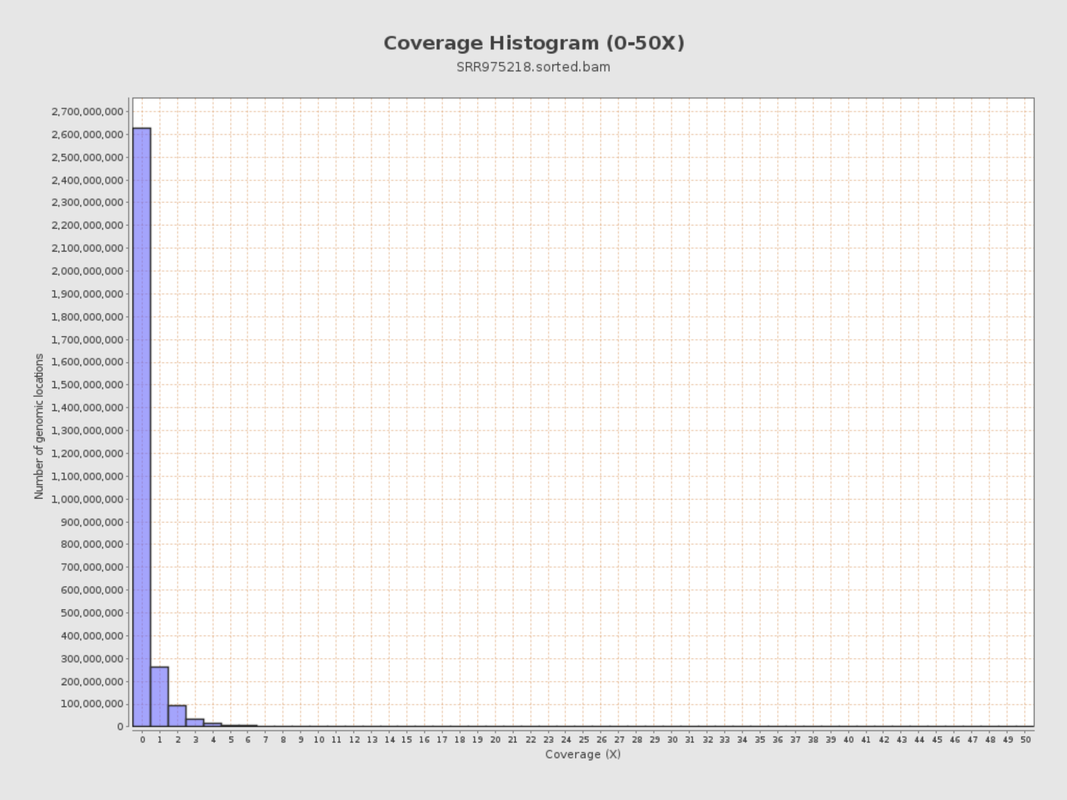
3. Results : Coverage across reference



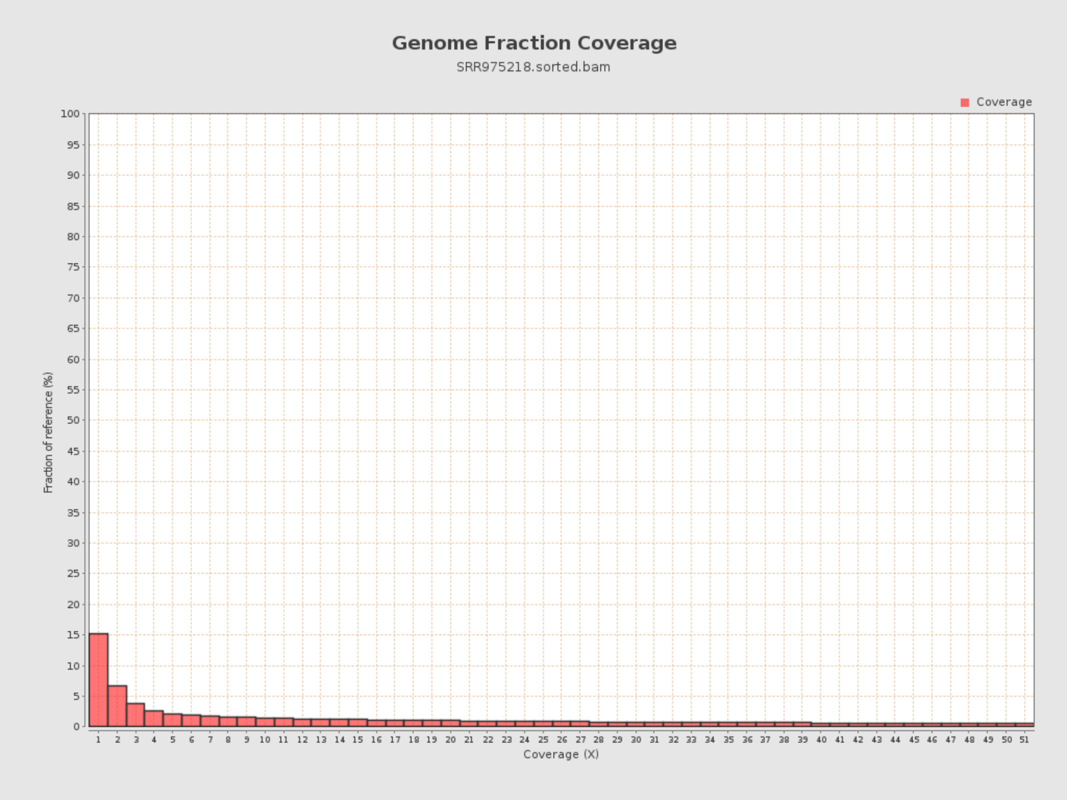
4. Results : Coverage Histogram



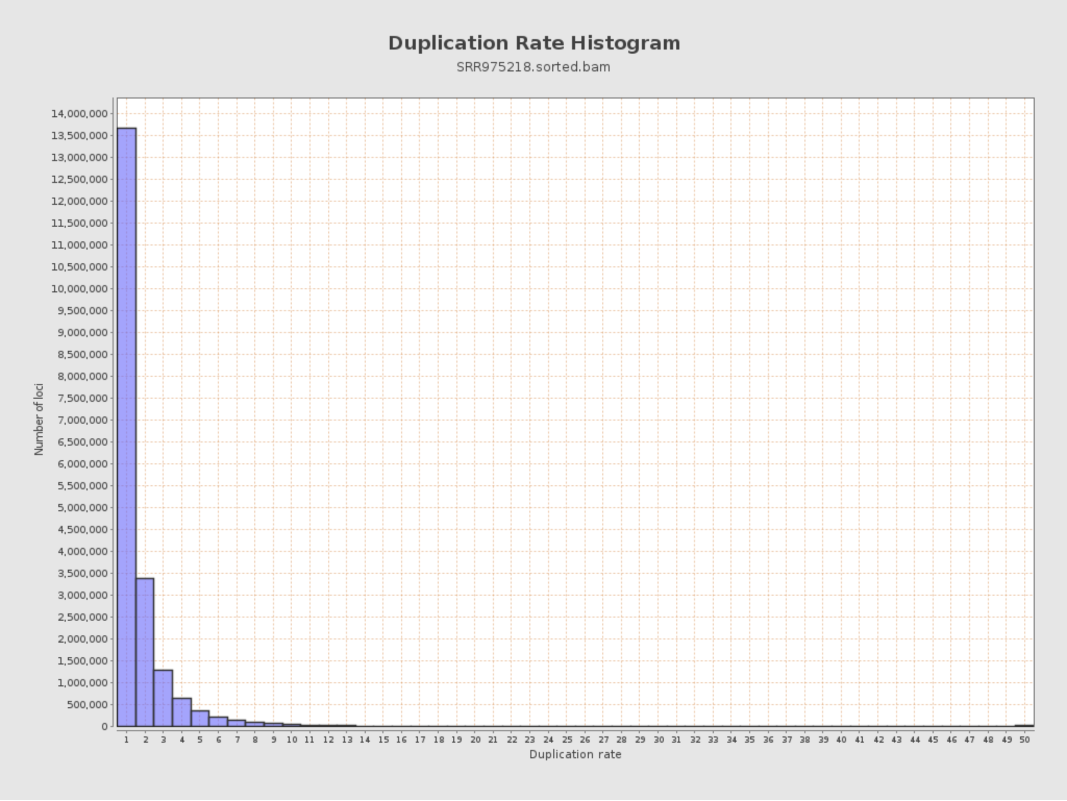
5. Results : Coverage Histogram (0-50X)



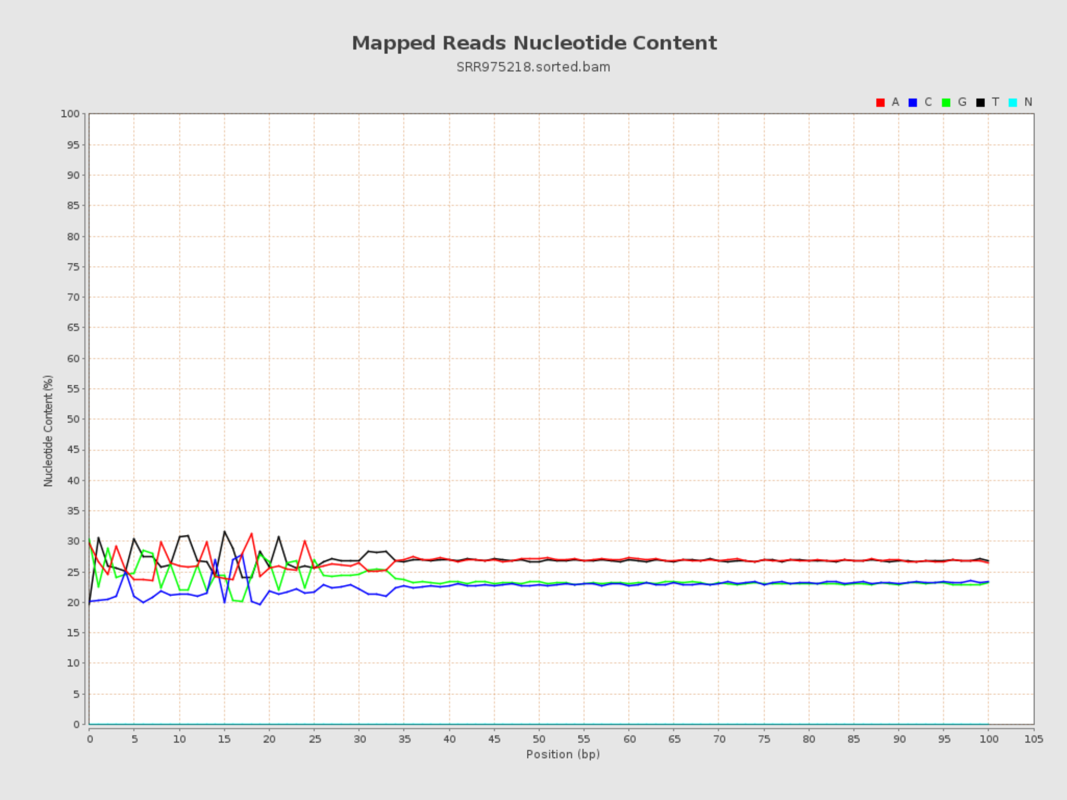
6. Results : Genome Fraction Coverage



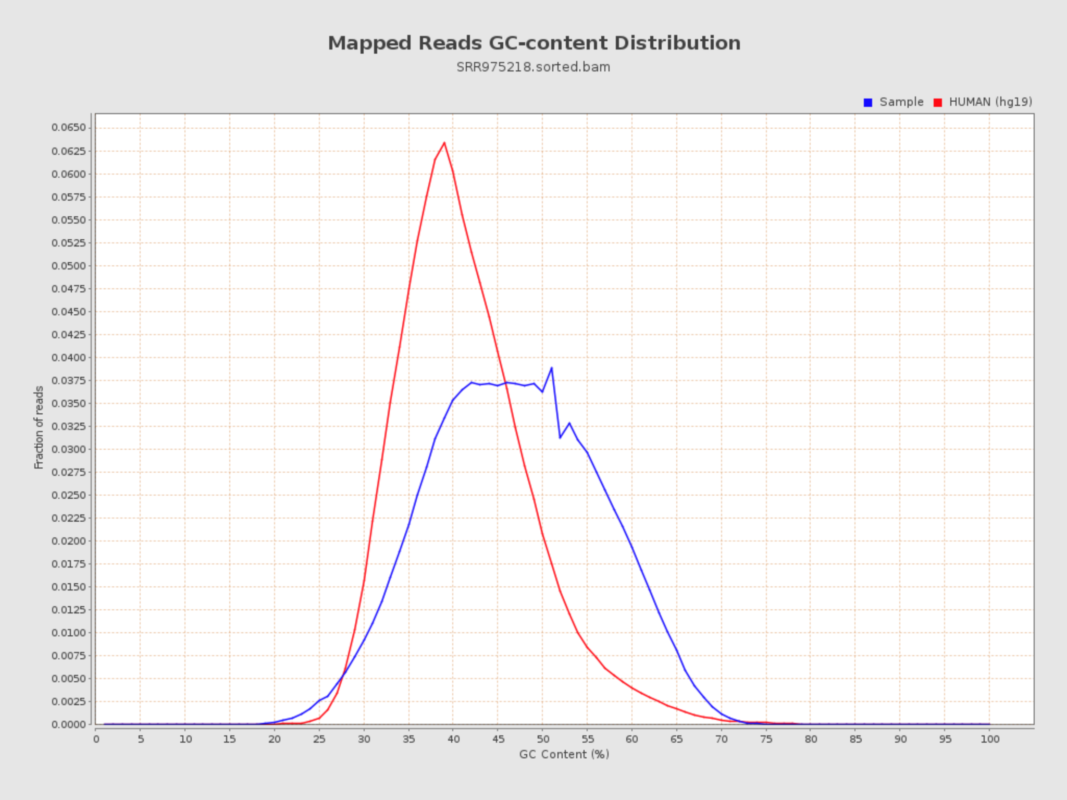
7. Results : Duplication Rate Histogram



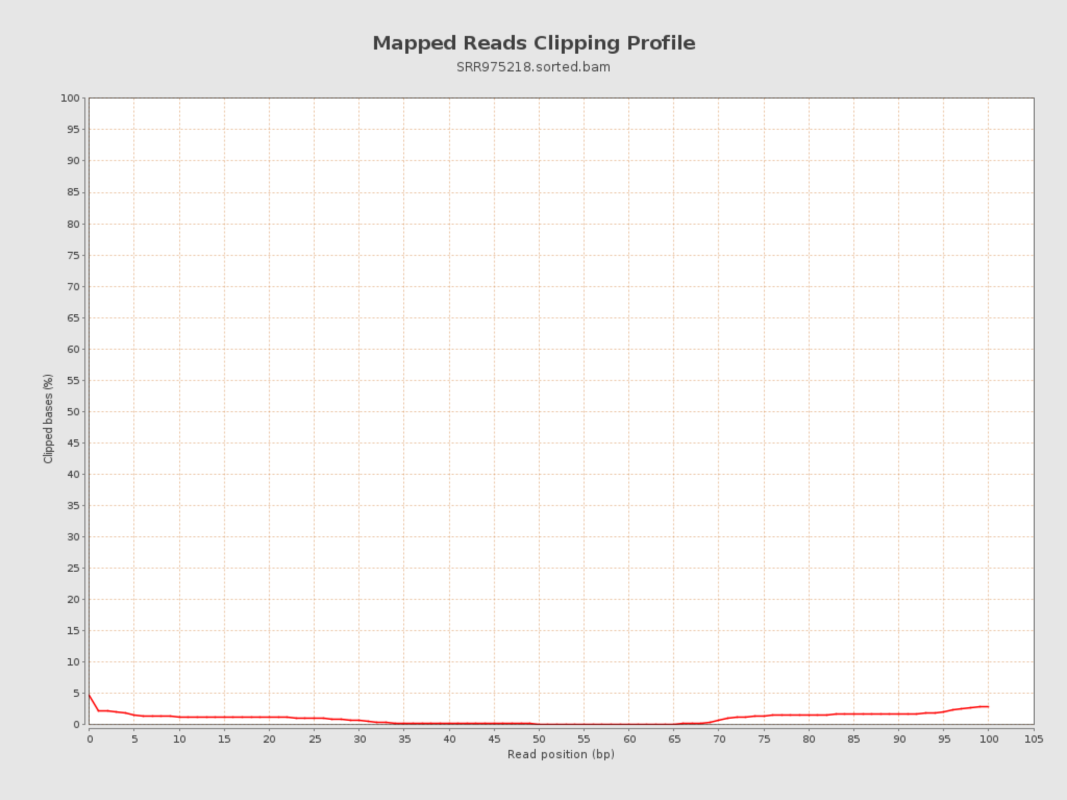
8. Results : Mapped Reads Nucleotide Content



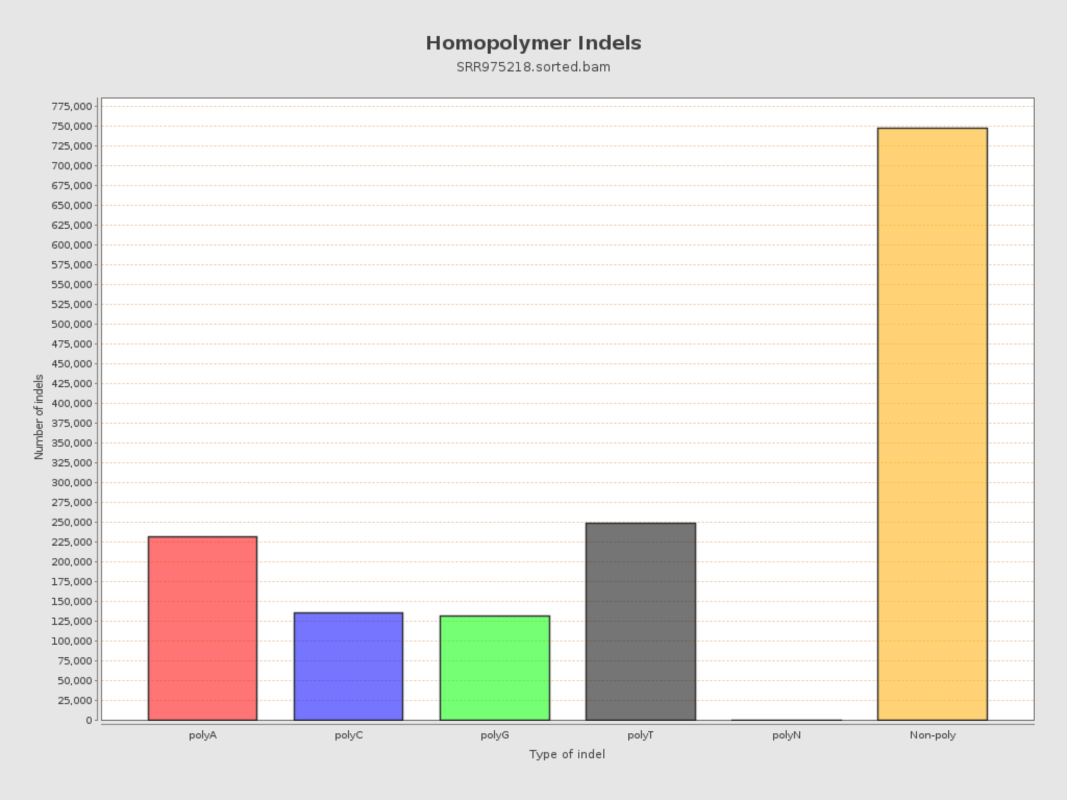
9. Results : Mapped Reads GC-content Distribution



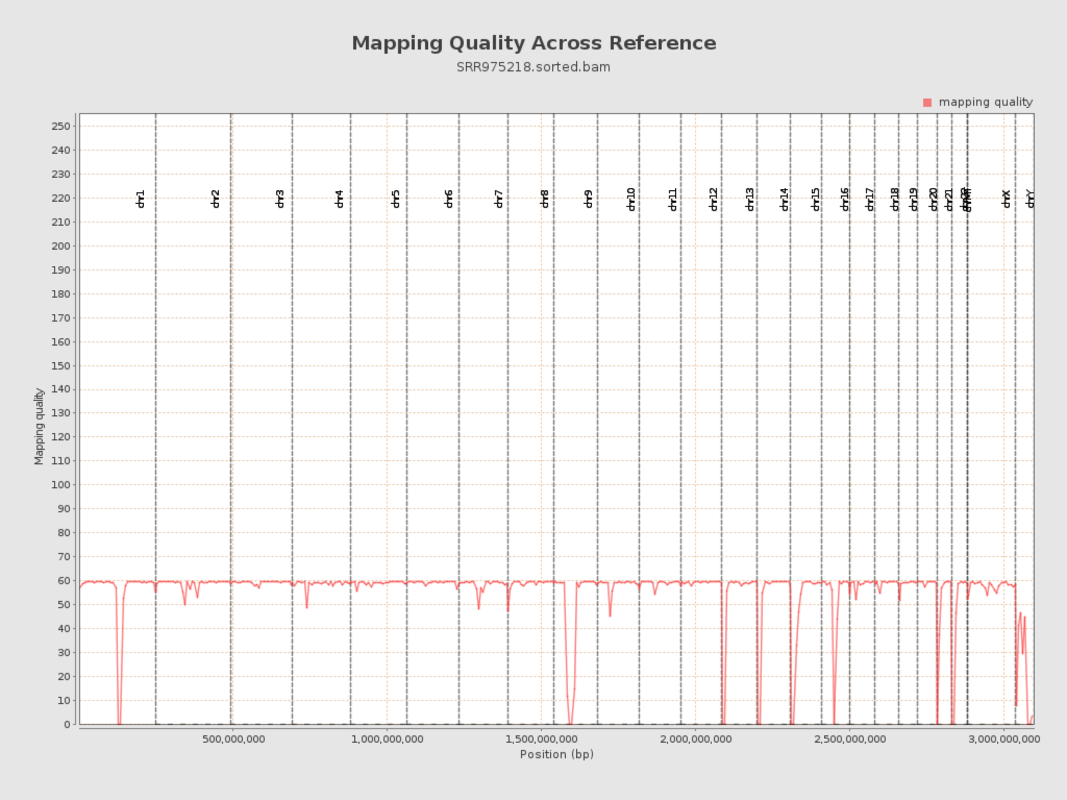
10. Results : Mapped Reads Clipping Profile



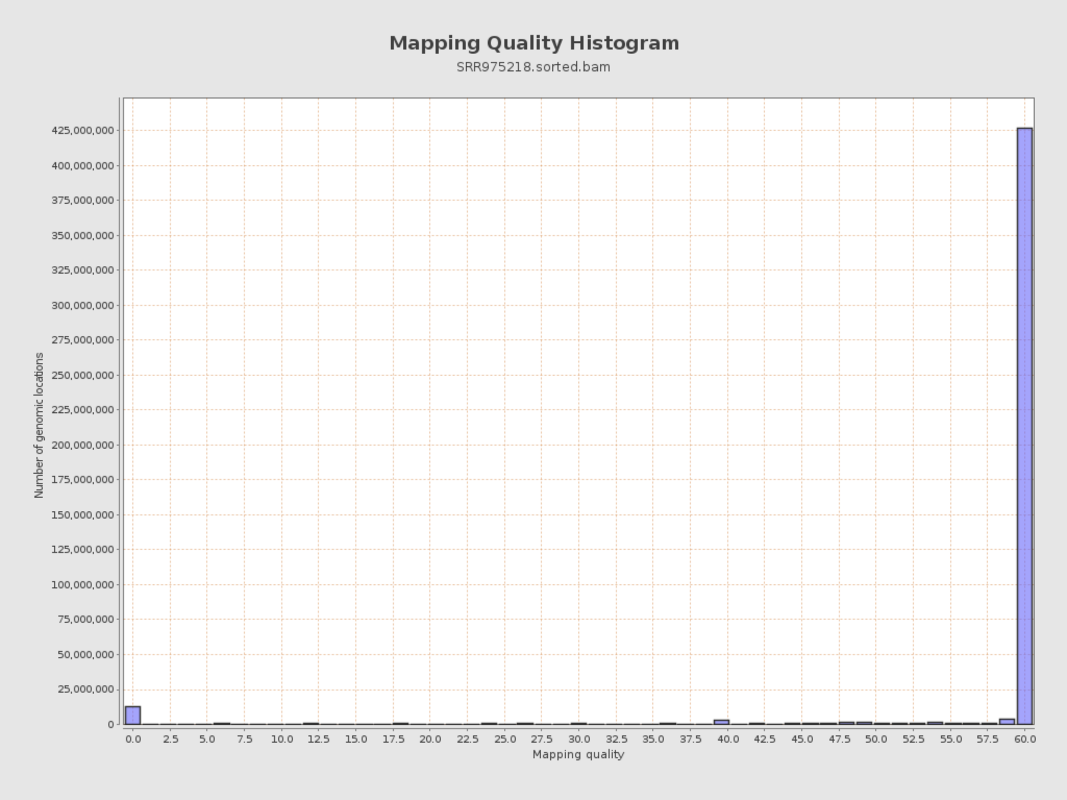
11. Results : Homopolymer Indels



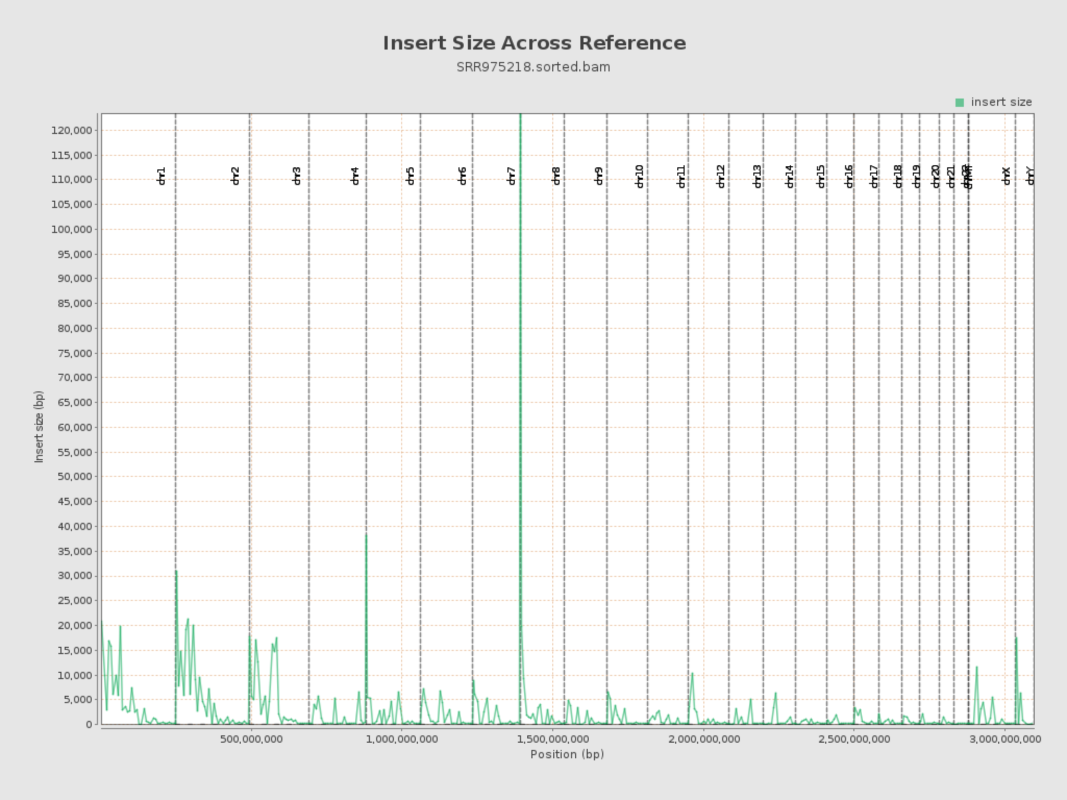
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram