Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:39:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975192.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_SRR975192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975192_1.fastq.gz SRR975192_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:39:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	39,605,836
Mapped reads	39,541,394 / 99.84%
Unmapped reads	64,442 / 0.16%
Mapped paired reads	39,541,394 / 99.84%
Mapped reads, first in pair	19,771,455 / 49.92%
Mapped reads, second in pair	19,769,939 / 49.92%
Mapped reads, both in pair	39,496,998 / 99.73%
Mapped reads, singletons	44,396 / 0.11%
Secondary alignments	0
Supplementary alignments	101,391 / 0.26%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	22,763,147 / 57.47%
Duplication rate	43.26%
Clipped reads	23,058,895 / 58.22%

2.2. ACGT Content

Number/percentage of A's	997,821,292 / 26.95%
Number/percentage of C's	804,012,298 / 21.71%
Number/percentage of T's	1,045,453,435 / 28.23%
Number/percentage of G's	855,406,057 / 23.1%
Number/percentage of N's	254,016 / 0.01%

GC Percentage	44.81%

2.3. Coverage

Mean	1.1966
Standard Deviation	17.8921

2.4. Mapping Quality

Mean Mapping Quality	55.7

2.5. Insert size

Mean	172,613.45
Standard Deviation	4,116,996.36
P25/Median/P75	188 / 232 / 283

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	21,940,241
Insertions	363,671
Mapped reads with at least one insertion	0.91%
Deletions	943,595
Mapped reads with at least one deletion	2.35%
Homopolymer indels	48.6%

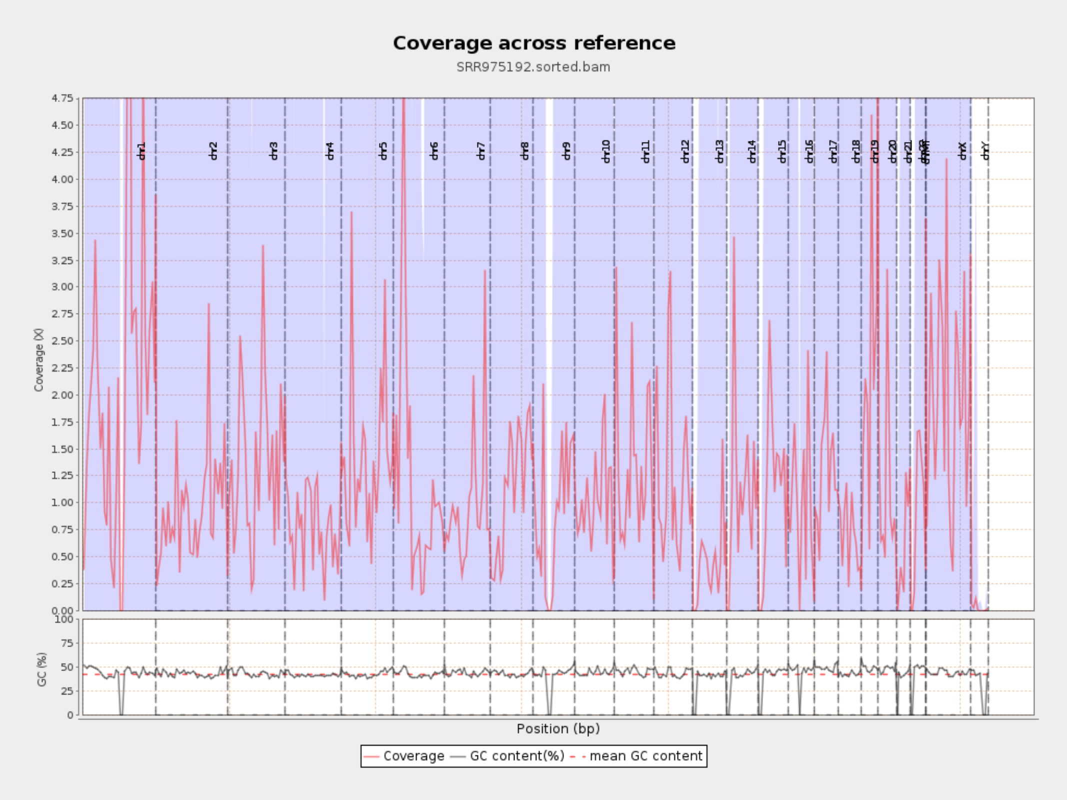
2.7. Chromosome stats

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

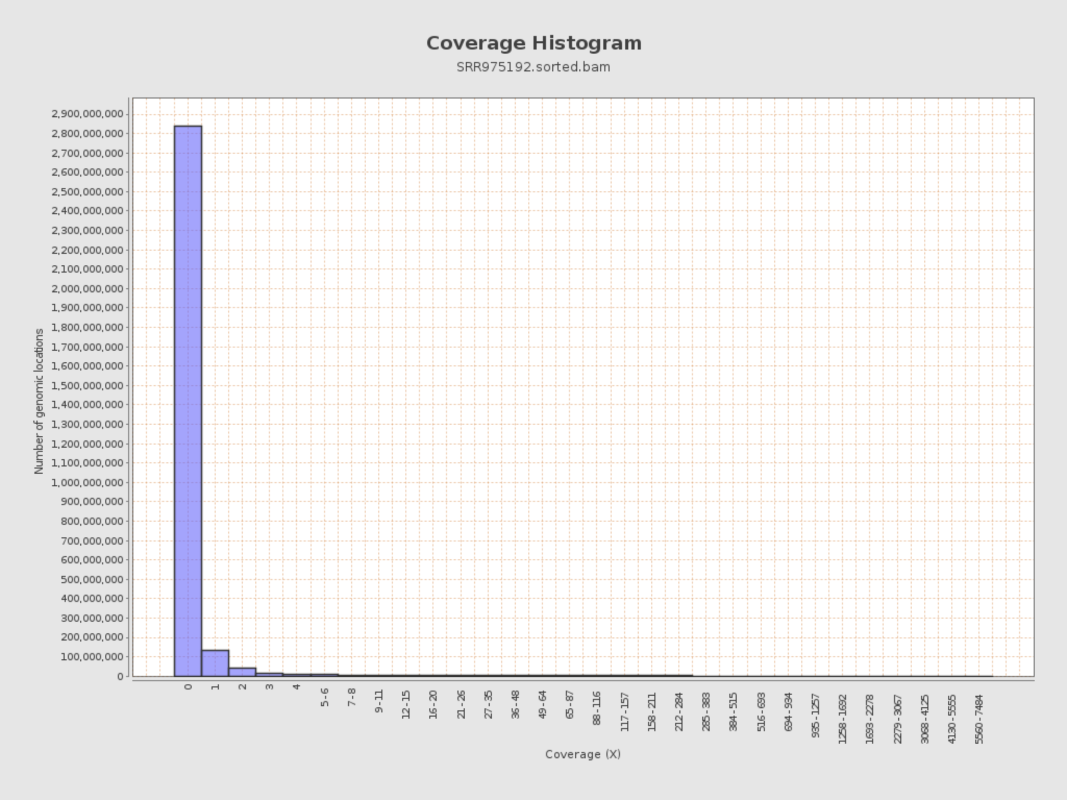
		bases	coverage	deviation
chr1	249250621	533145437	2.139	26.7388
chr2	243199373	232660615	0.9567	13.4467
chr3	198022430	269303279	1.36	18.0718
chr4	191154276	146785317	0.7679	12.2814
chr5	180915260	258720459	1.4301	19.782
chr6	171115067	205553093	1.2013	18.2063
chr7	159138663	155872102	0.9795	15.8237
chr8	146364022	164311284	1.1226	17.4961
chr9	141213431	125676013	0.89	13.1233
chr10	135534747	141472491	1.0438	15.42
chr11	135006516	179409067	1.3289	17.4488
chr12	133851895	173084552	1.2931	17.289
chr13	115169878	50133060	0.4353	9.3903
chr14	107349540	121785624	1.1345	16.4482
chr15	102531392	109699862	1.0699	14.4887
chr16	90354753	87566400	0.9691	13.6576
chr17	81195210	106127461	1.3071	16.4731
chr18	78077248	56306220	0.7212	12.0903
chr19	59128983	133582851	2.2592	33.6325
chr20	63025520	68447621	1.086	15.3969
chr21	48129895	29269339	0.6081	9.2523
chr22	51304566	47574004	0.9273	13.4046
chrMT	16571	60401	3.645	9.2893
chrX	155270560	306282219	1.9726	27.6267

chrY	59373566	1487592	0.0251	1.553

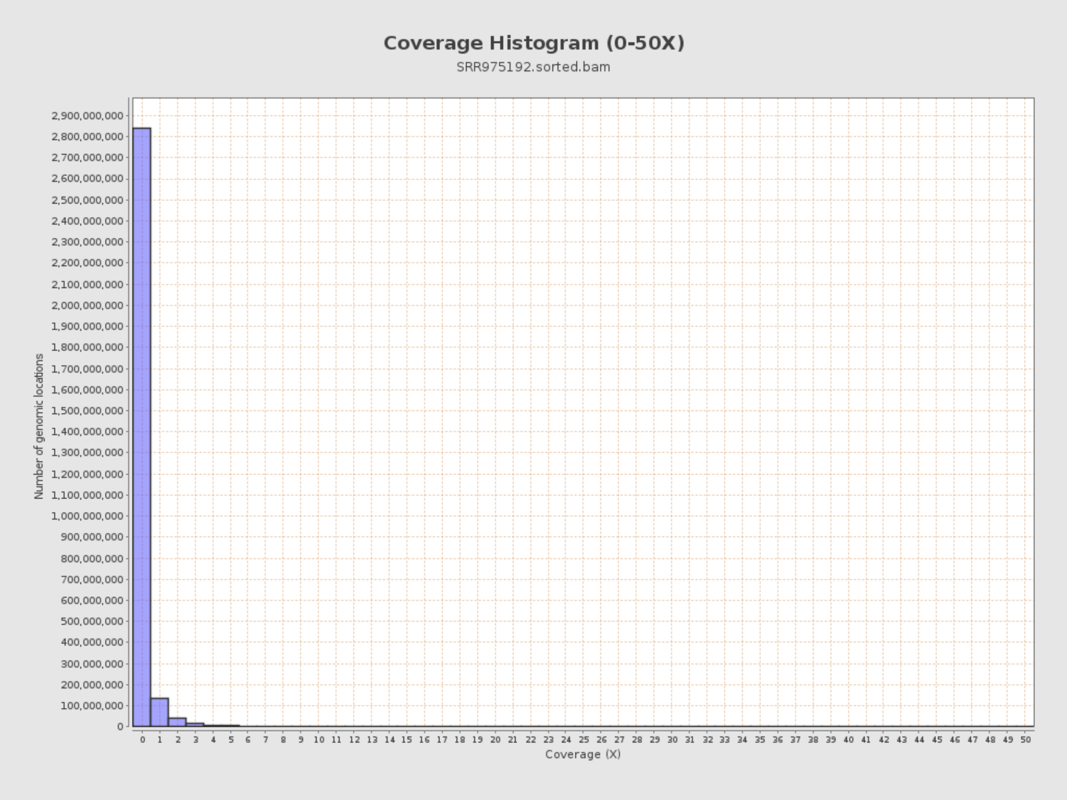
3. Results : Coverage across reference



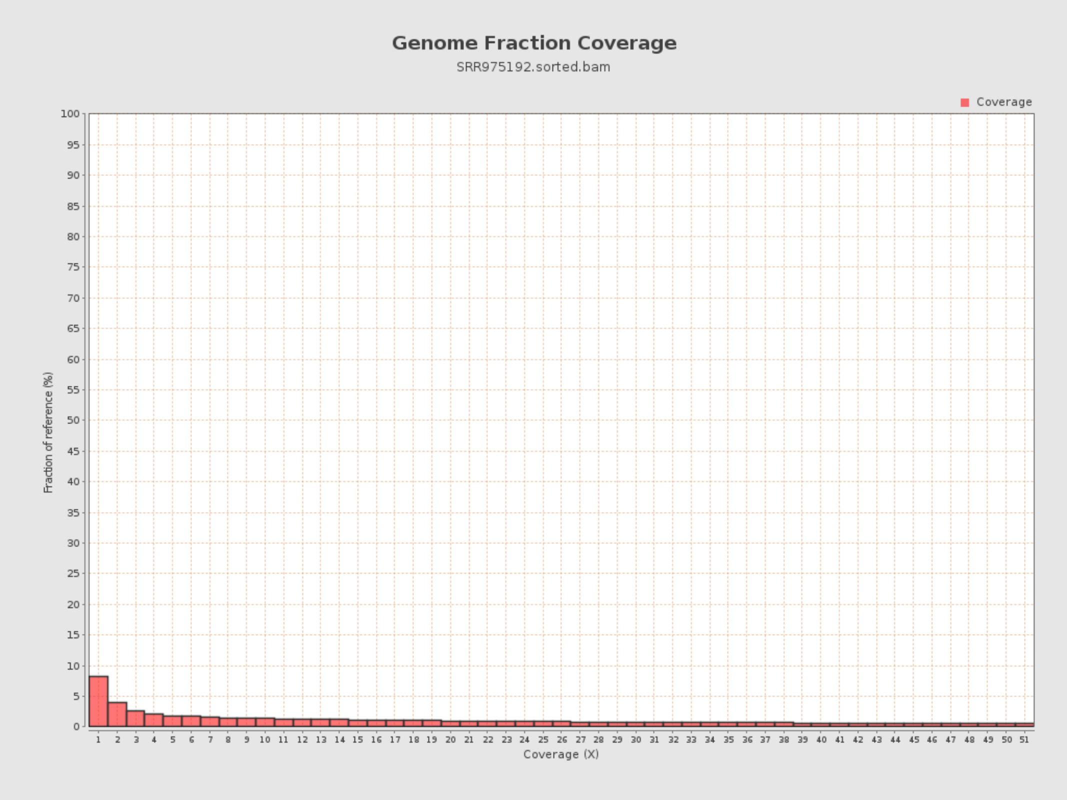
4. Results : Coverage Histogram



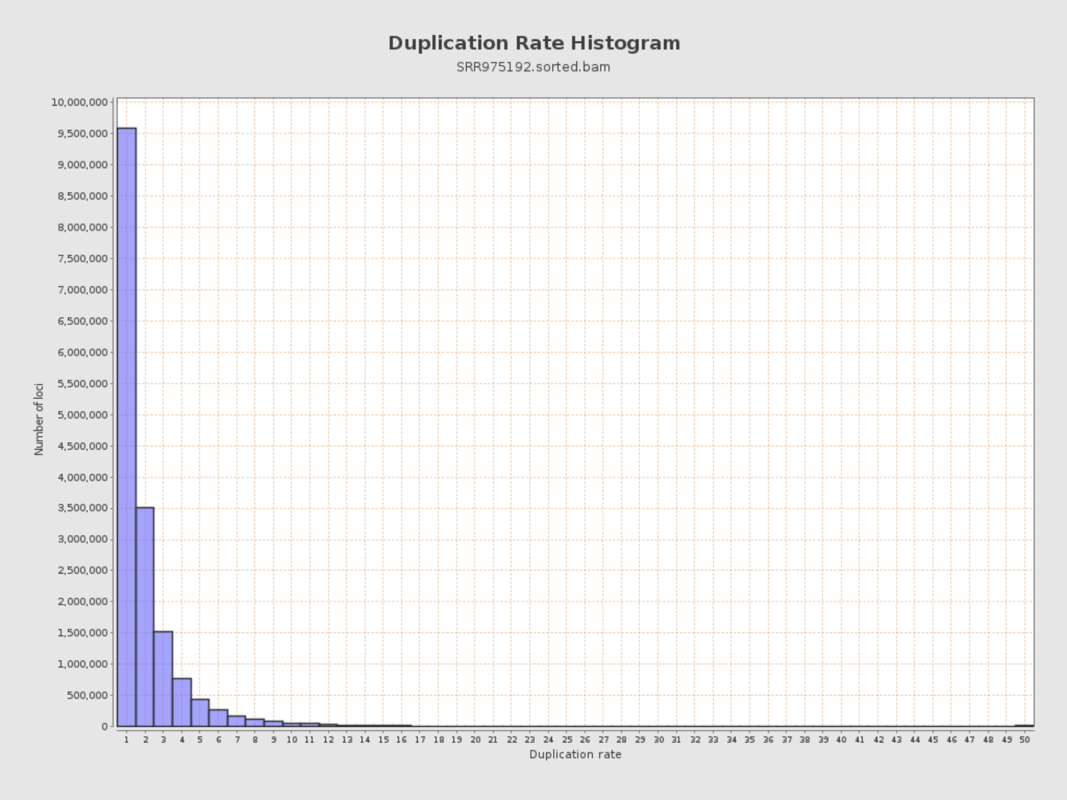
5. Results : Coverage Histogram (0-50X)



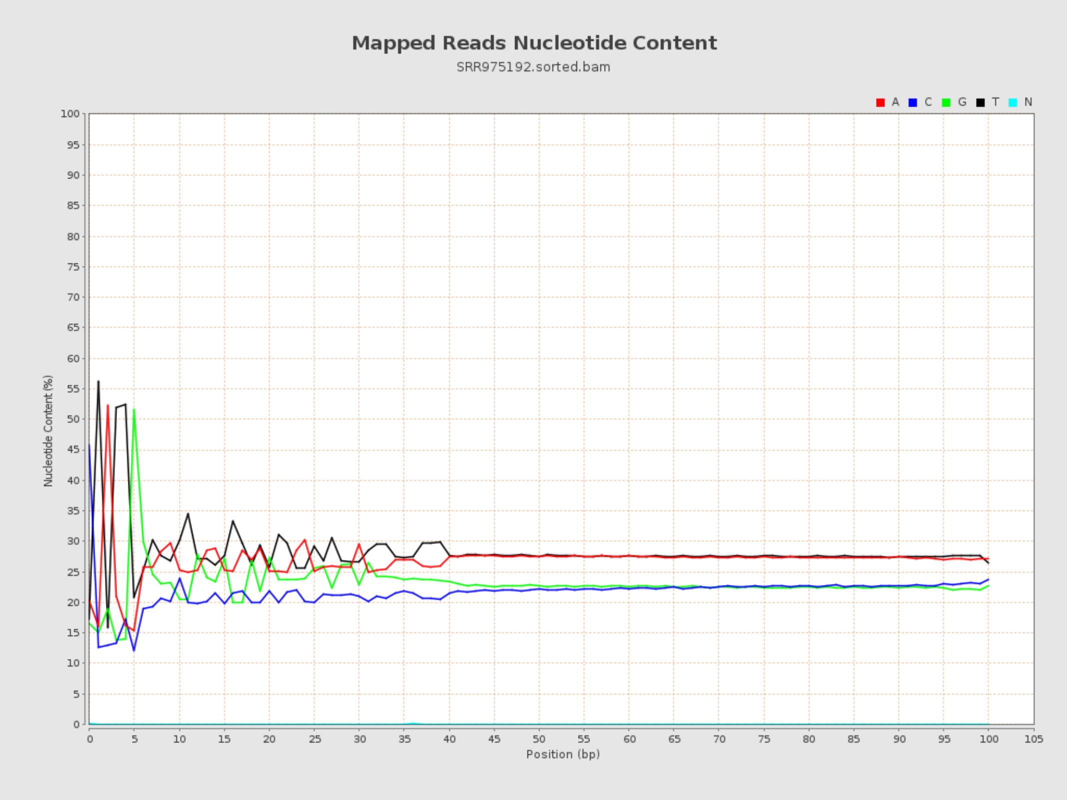
6. Results : Genome Fraction Coverage



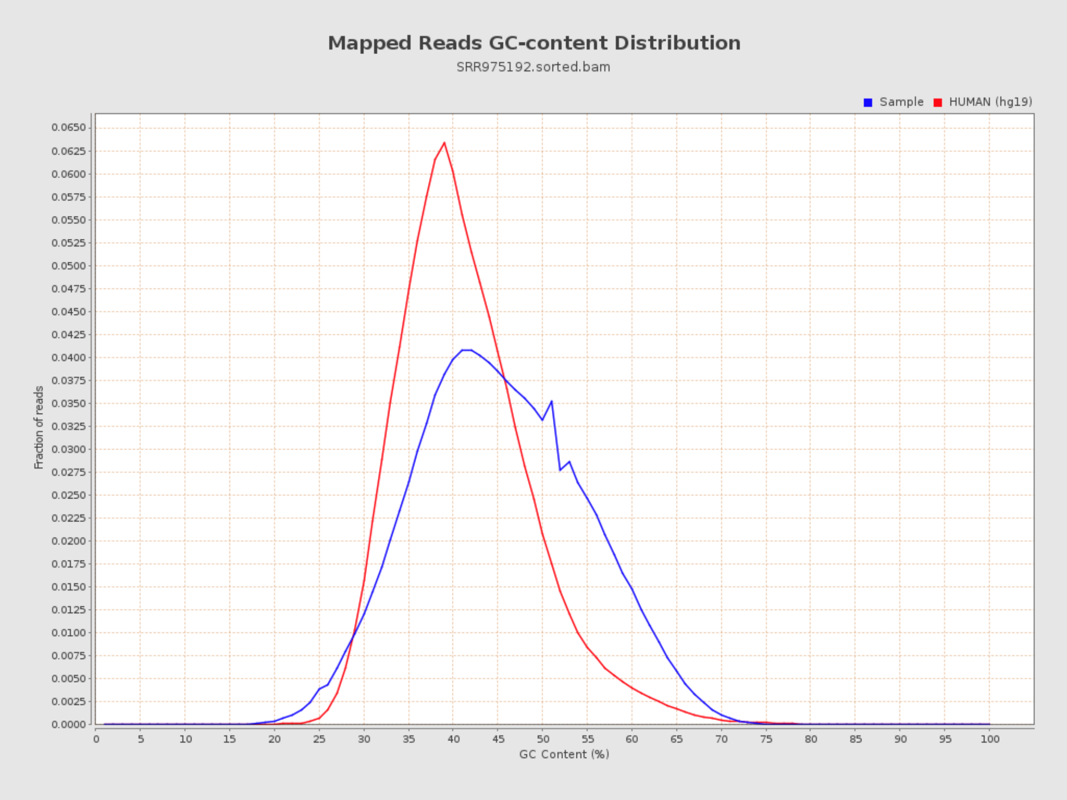
7. Results : Duplication Rate Histogram



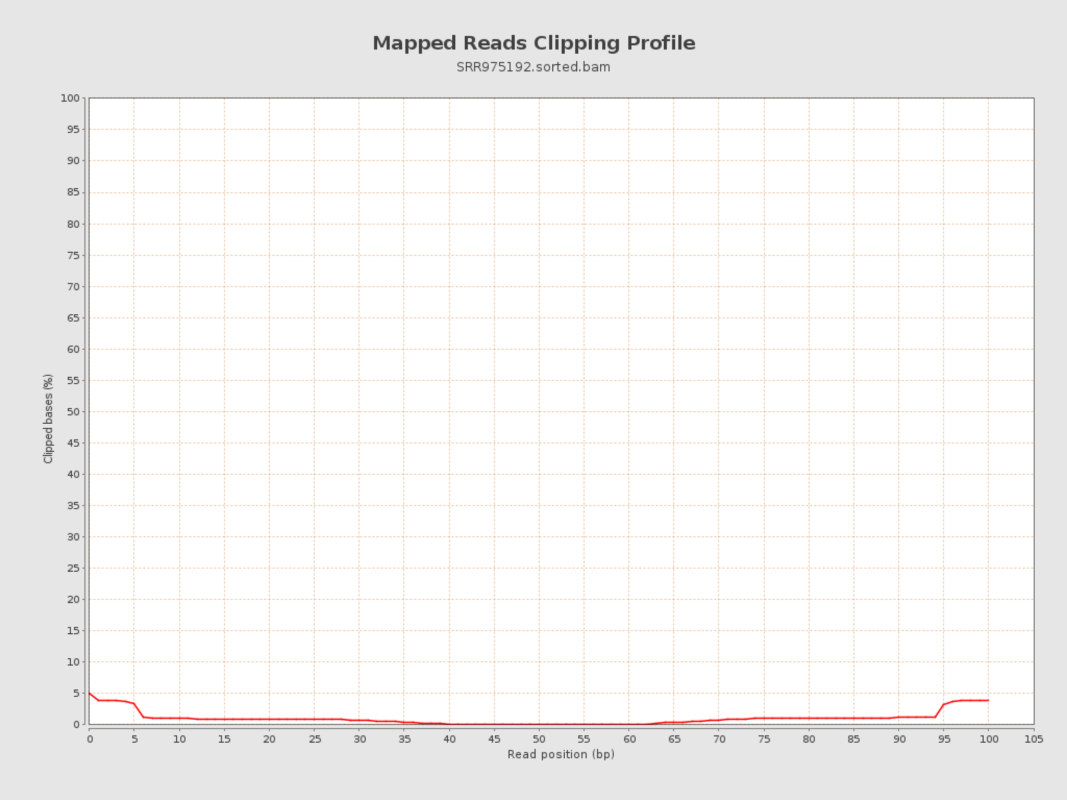
8. Results : Mapped Reads Nucleotide Content



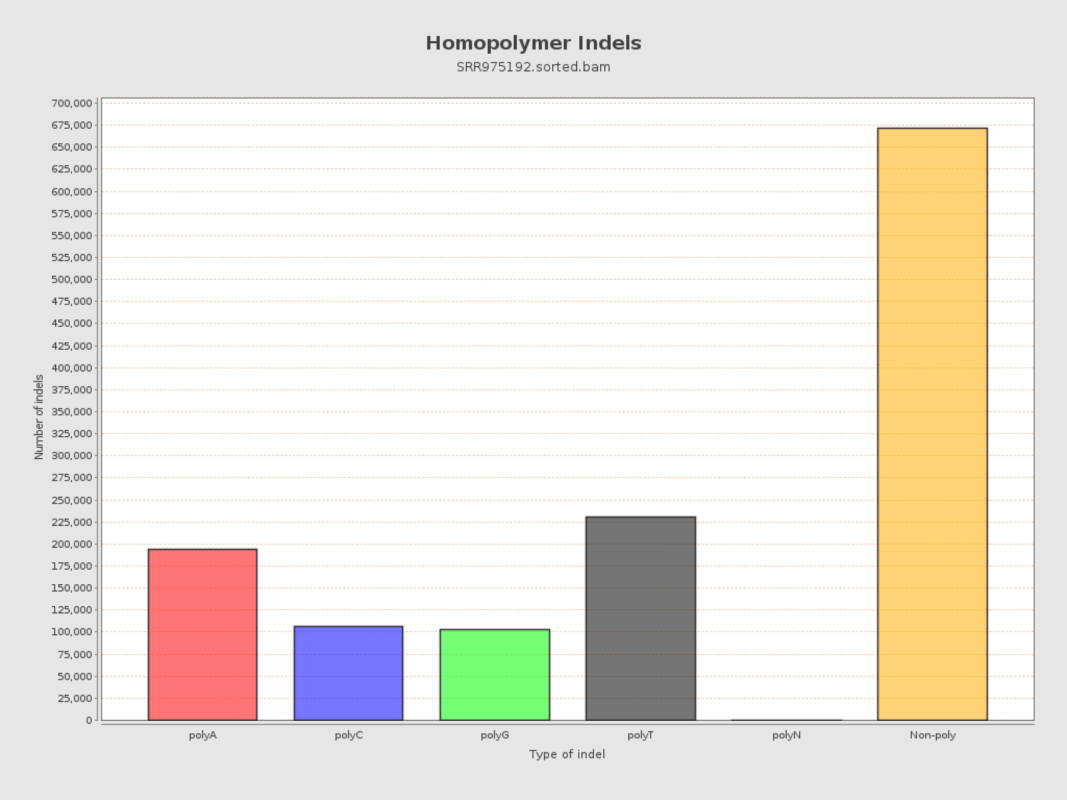
9. Results : Mapped Reads GC-content Distribution



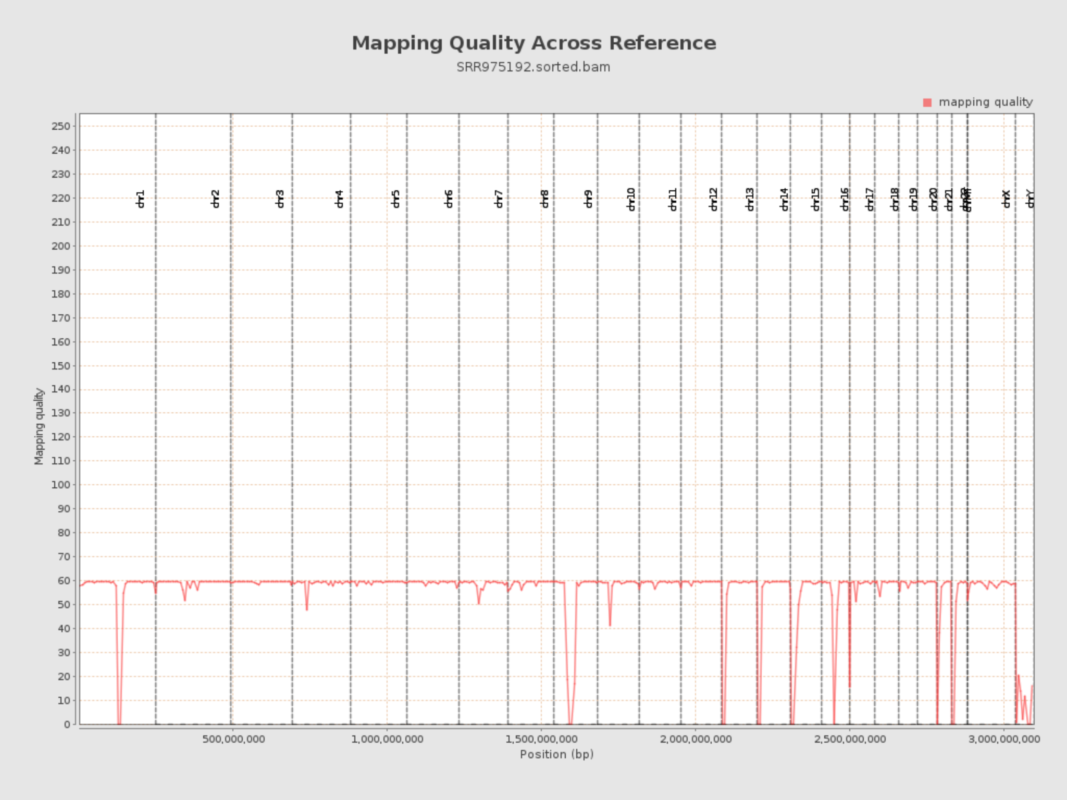
10. Results : Mapped Reads Clipping Profile



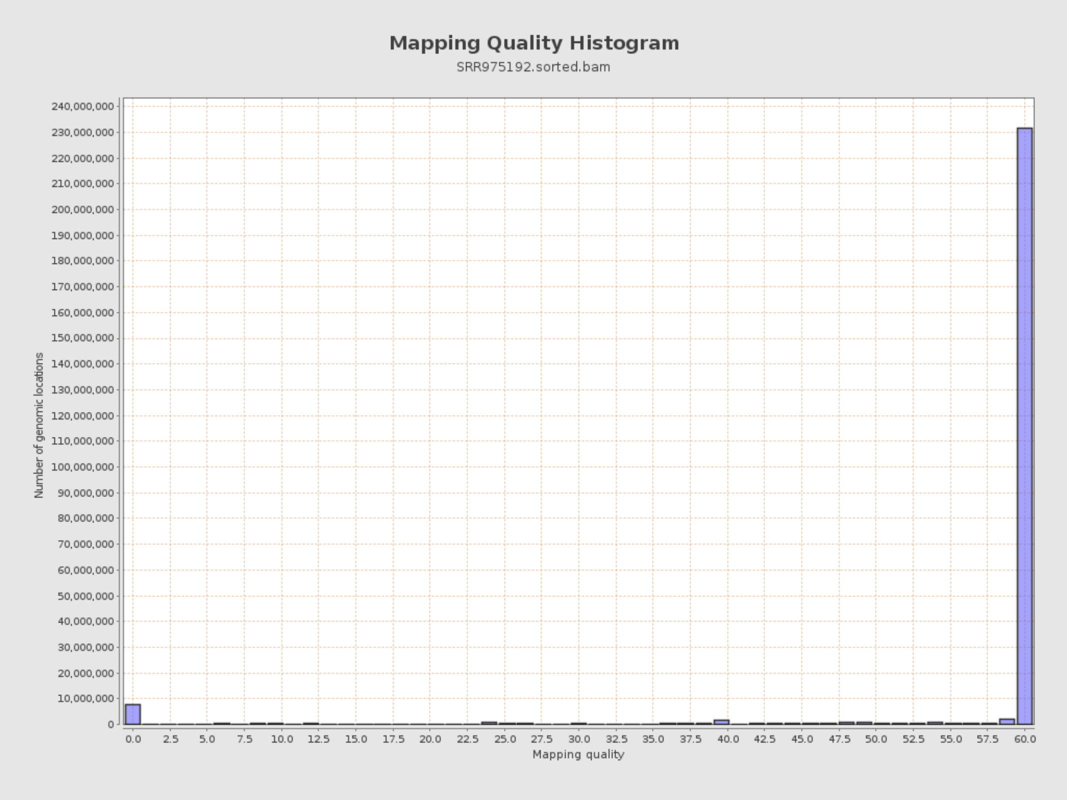
11. Results : Homopolymer Indels



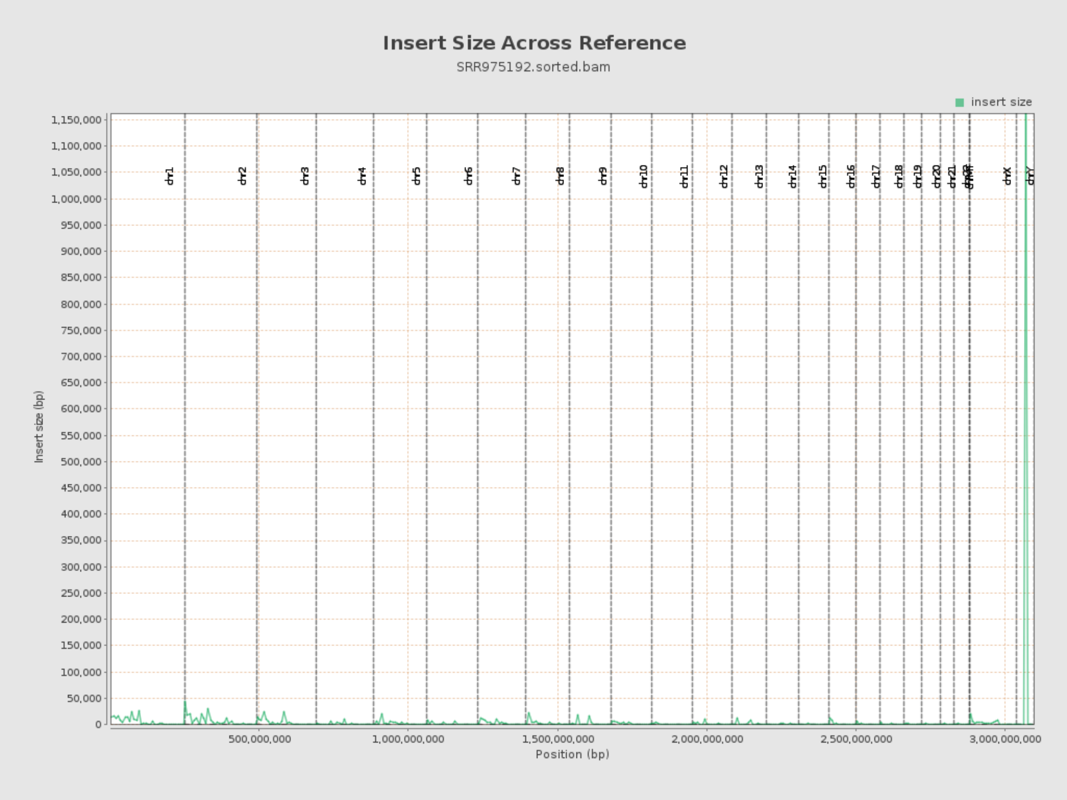
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram