Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 03:00:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961013.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_SRR961013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961013_1.fastq.gz SRR961013_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 03:00:49 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	399,275,520
Mapped reads	384,883,279 / 96.4%
Unmapped reads	14,392,241 / 3.6%
Mapped paired reads	384,883,279 / 96.4%
Mapped reads, first in pair	197,374,704 / 49.43%
Mapped reads, second in pair	187,508,575 / 46.96%
Mapped reads, both in pair	374,022,362 / 93.68%
Mapped reads, singletons	10,860,917 / 2.72%
Secondary alignments	0
Supplementary alignments	6,537,979 / 1.64%
Read min/max/mean length	30 / 100 / 100.68
Duplicated reads (estimated)	63,066,989 / 15.8%
Duplication rate	11.42%
Clipped reads	49,689,729 / 12.44%

2.2. ACGT Content

Number/percentage of A's	11,006,080,302 / 29.19%
Number/percentage of C's	7,793,442,677 / 20.67%
Number/percentage of T's	10,948,089,700 / 29.03%
Number/percentage of G's	7,857,761,373 / 20.84%
Number/percentage of N's	103,186,349 / 0.27%

GC Percentage	41.51%

2.3. Coverage

Mean	12.1845
Standard Deviation	150.6354

2.4. Mapping Quality

Mean Mapping Quality	53.14

2.5. Insert size

Mean	85,883.3
Standard Deviation	2,819,380.02
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	448,852,316
Insertions	3,800,276
Mapped reads with at least one insertion	0.95%
Deletions	4,468,046
Mapped reads with at least one deletion	1.12%
Homopolymer indels	40.55%

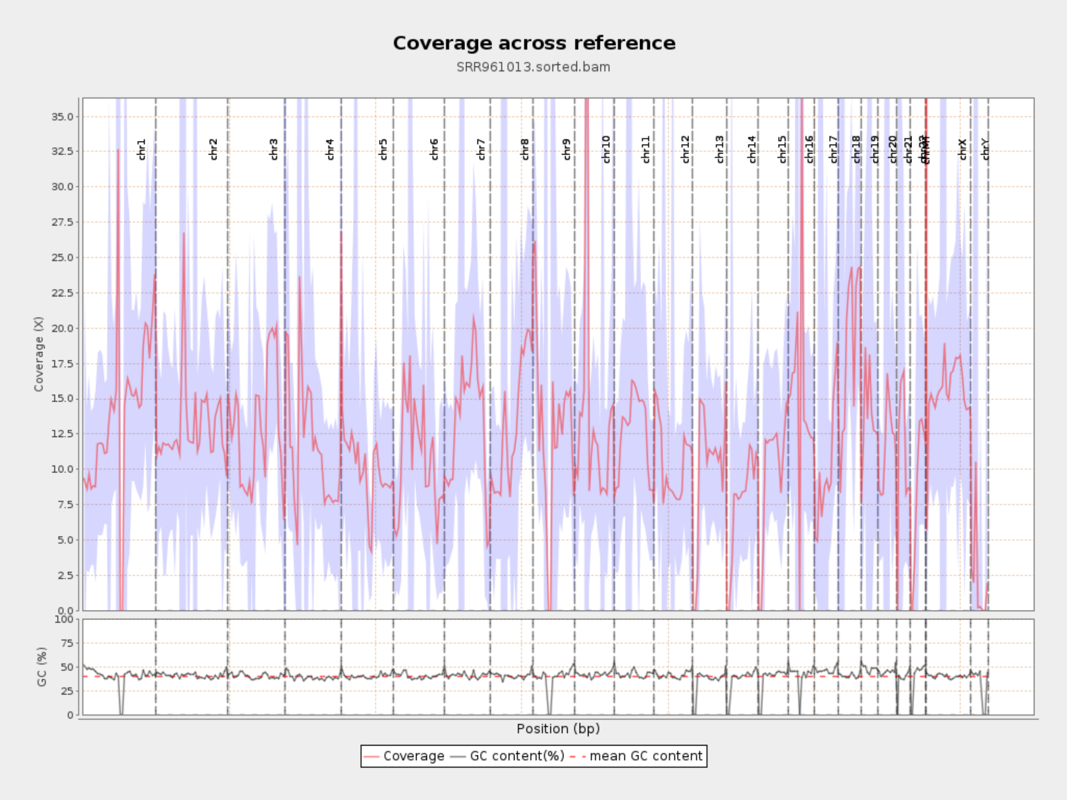
2.7. Chromosome stats

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

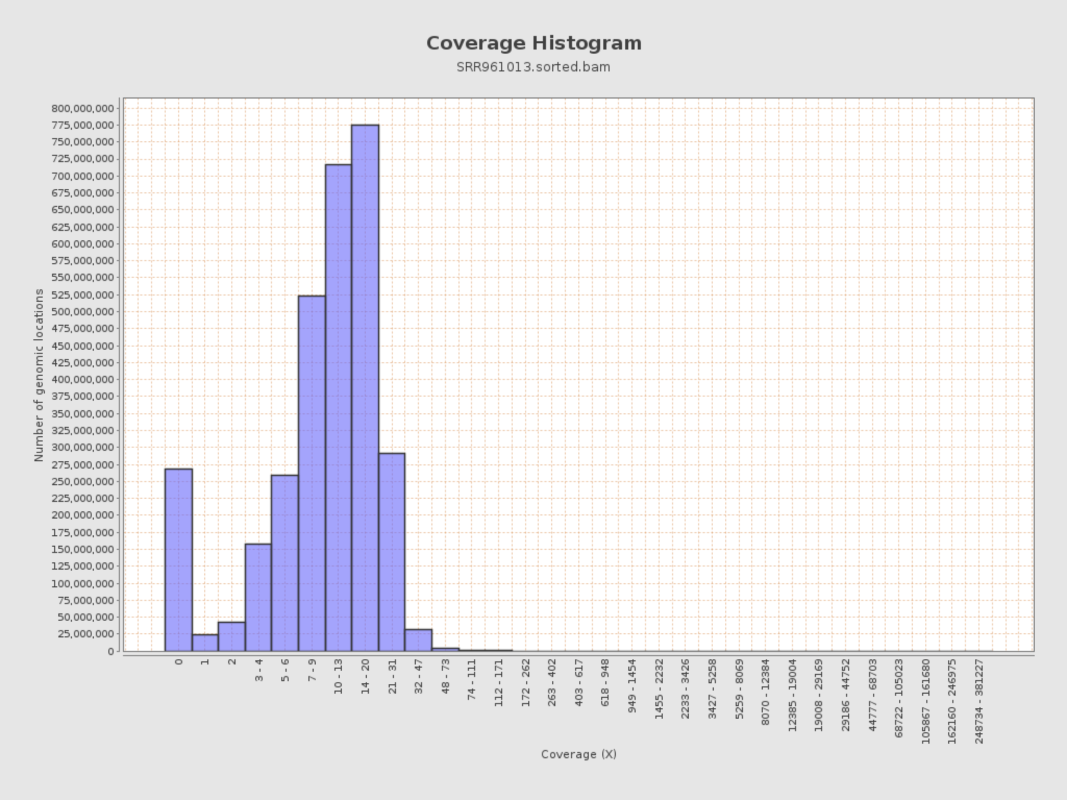
		bases	coverage	deviation
chr1	249250621	3487265992	13.991	383.4696
chr2	243199373	3187971713	13.1085	89.272
chr3	198022430	2556128460	12.9083	33.2405
chr4	191154276	2257349830	11.809	101.0603
chr5	180915260	1813617403	10.0247	14.9453
chr6	171115067	1853035905	10.8292	46.6226
chr7	159138663	2131548176	13.3943	95.2416
chr8	146364022	1939887047	13.2539	131.5638
chr9	141213431	1793966735	12.7039	116.2691
chr10	135534747	1871888070	13.8111	333.2759
chr11	135006516	1710627802	12.6707	64.1972
chr12	133851895	1415806279	10.5774	15.836
chr13	115169878	1154519998	10.0245	7.3939
chr14	107349540	828816520	7.7207	12.3761
chr15	102531392	995216913	9.7065	7.4998
chr16	90354753	1403835659	15.5369	157.0169
chr17	81195210	803465467	9.8955	38.0474
chr18	78077248	1435165898	18.3814	146.1993
chr19	59128983	833430557	14.0951	187.5073
chr20	63025520	734917738	11.6606	36.6078
chr21	48129895	528633649	10.9835	56.0755
chr22	51304566	433920630	8.4577	9.914
chrMT	16571	8536914	515.1719	93.2388
chrX	155270560	2410112231	15.522	49.3544

chrY	59373566	129835920	2.1868	114.3183

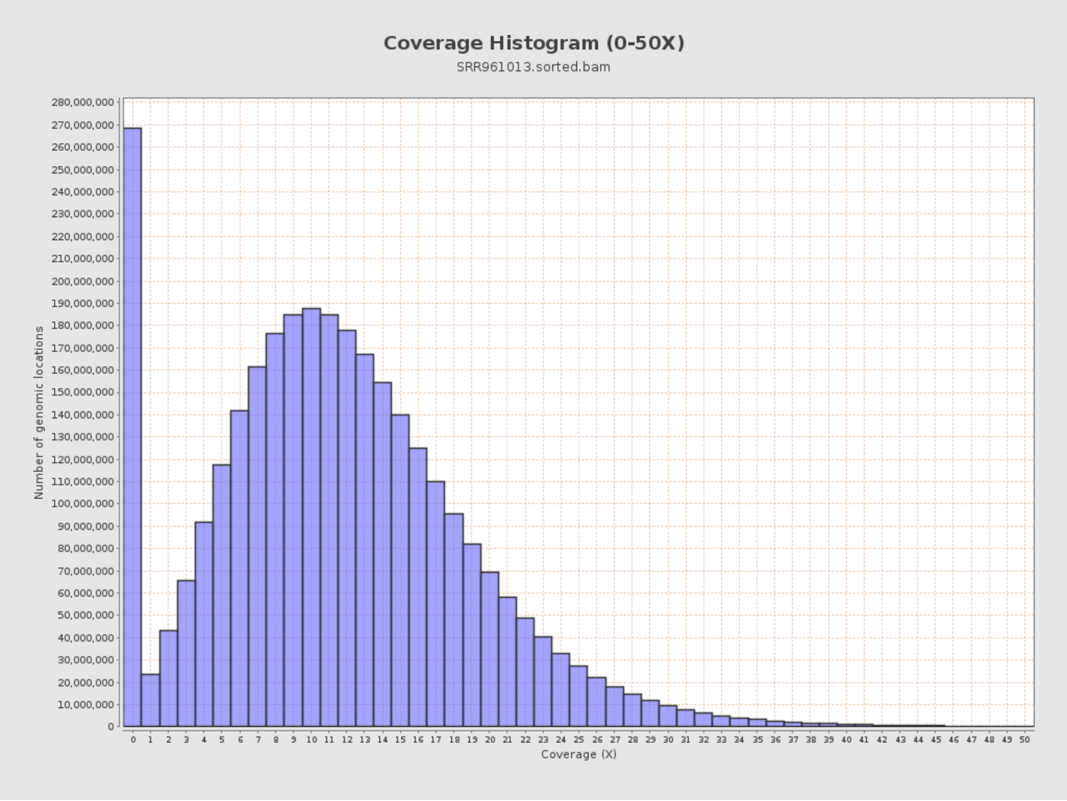
3. Results : Coverage across reference



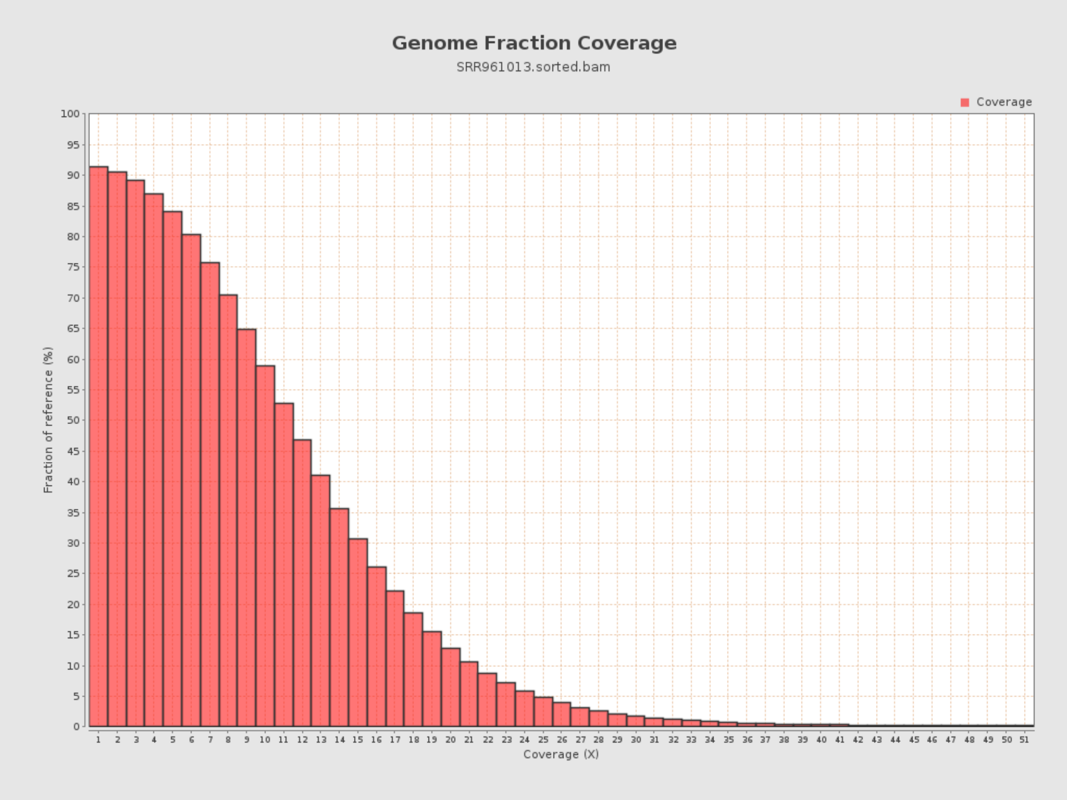
4. Results : Coverage Histogram



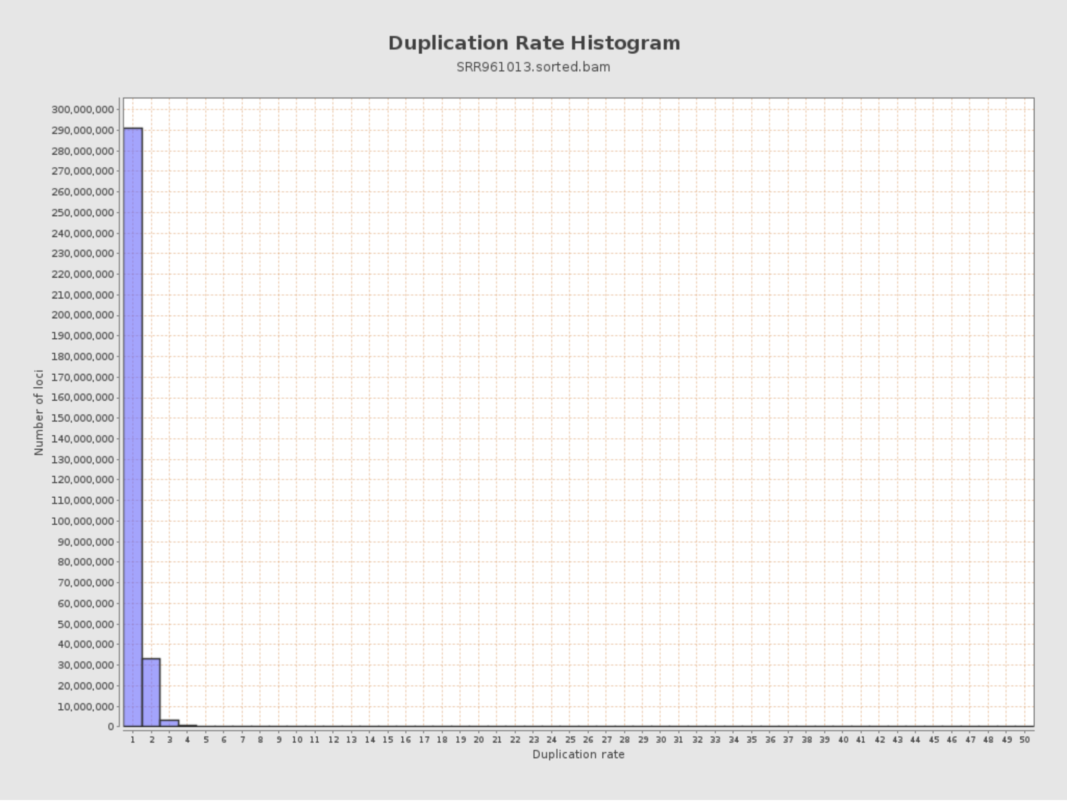
5. Results : Coverage Histogram (0-50X)



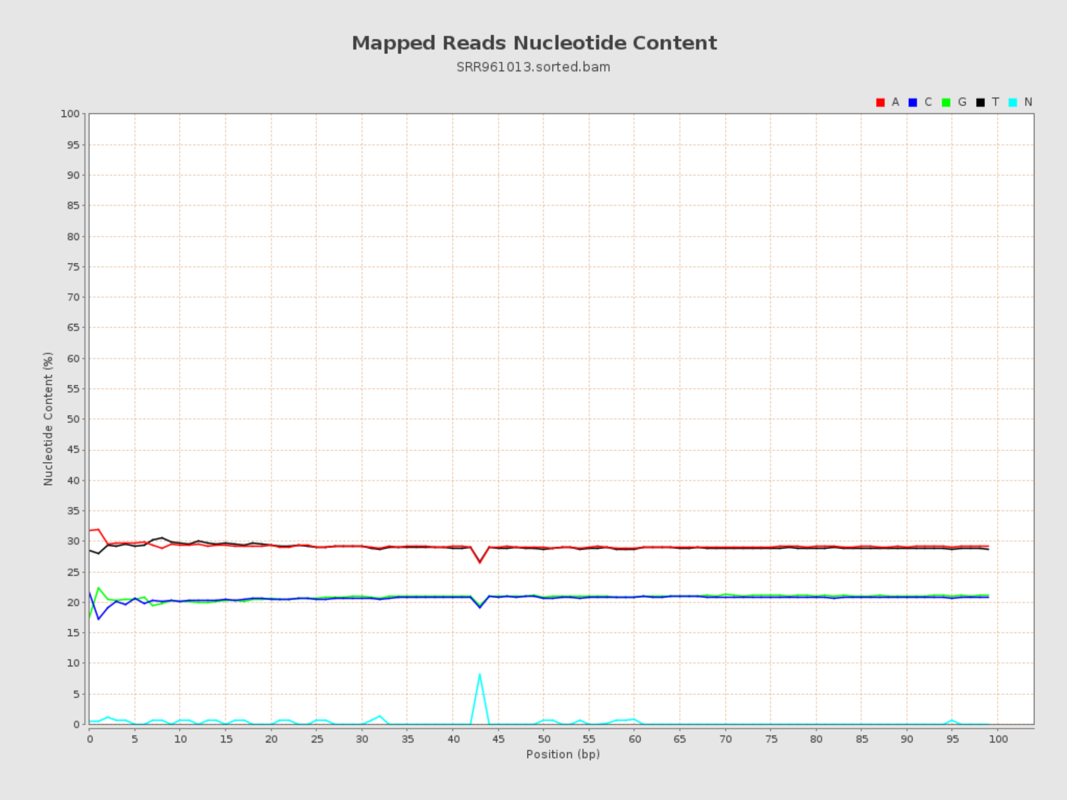
6. Results : Genome Fraction Coverage



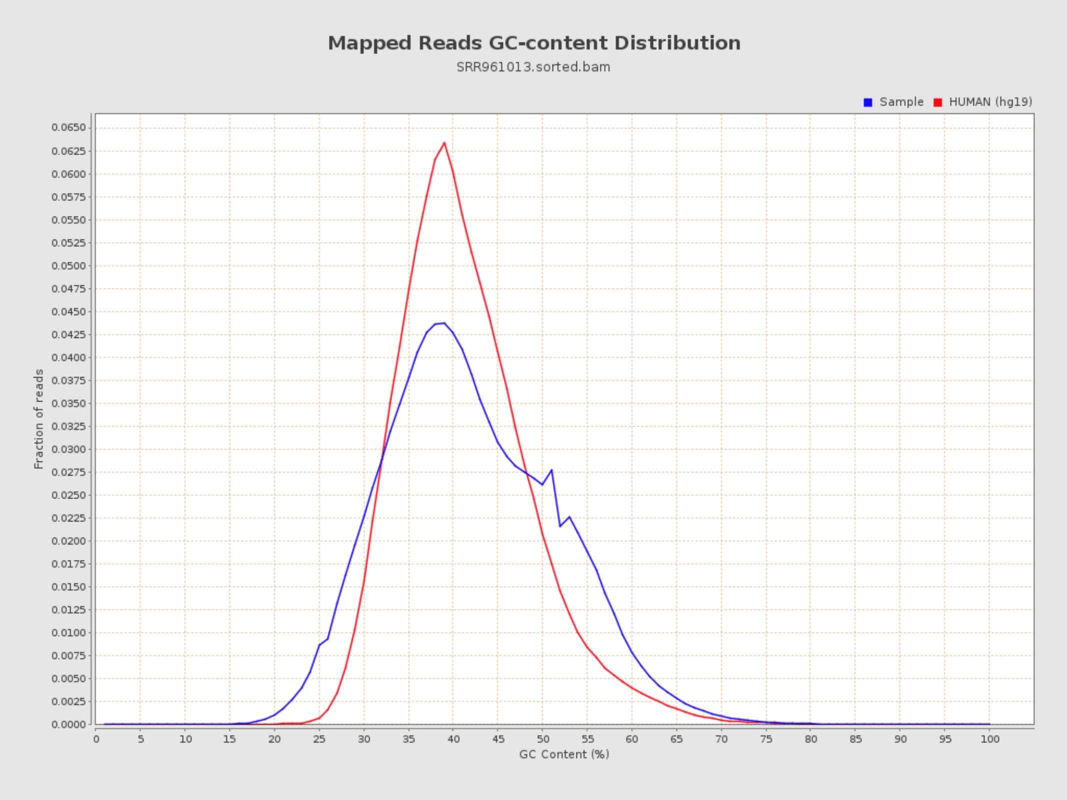
7. Results : Duplication Rate Histogram



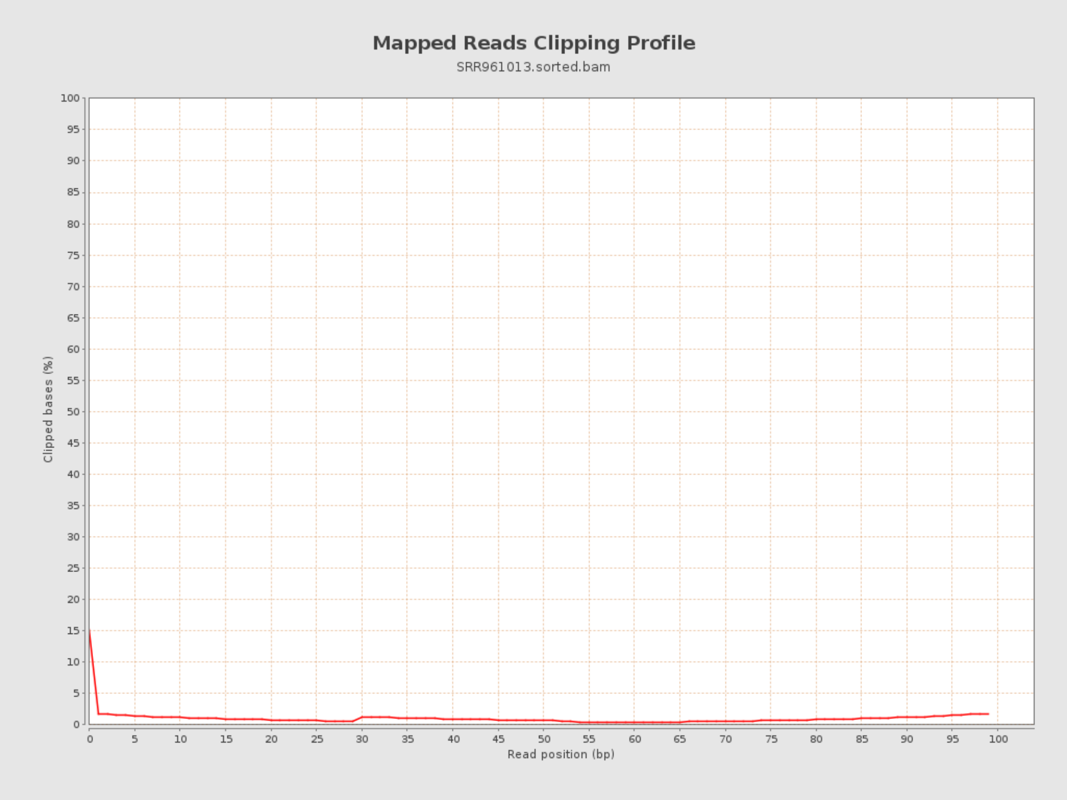
8. Results : Mapped Reads Nucleotide Content



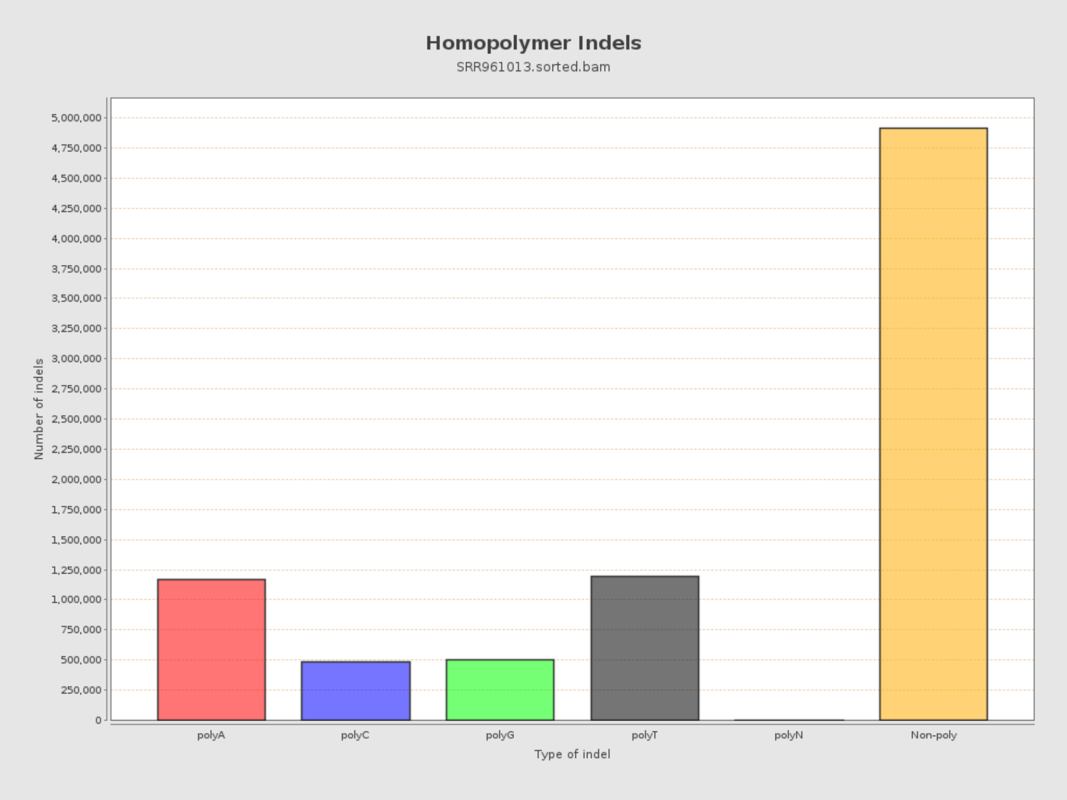
9. Results : Mapped Reads GC-content Distribution



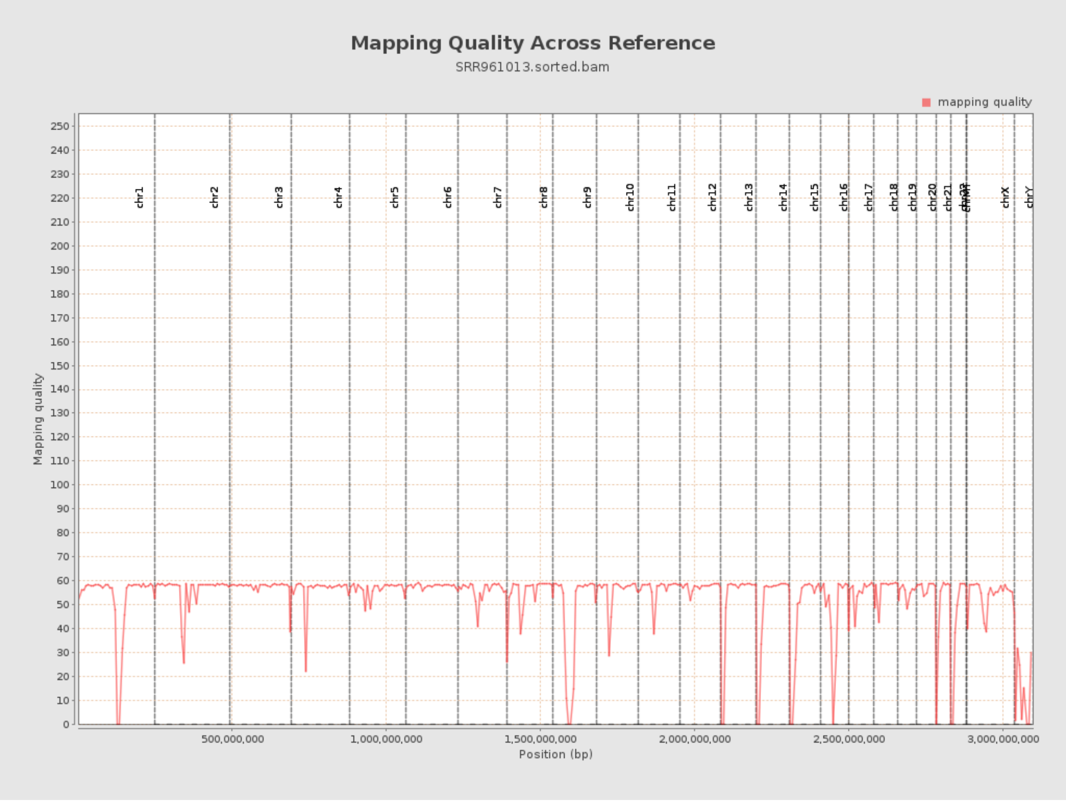
10. Results : Mapped Reads Clipping Profile



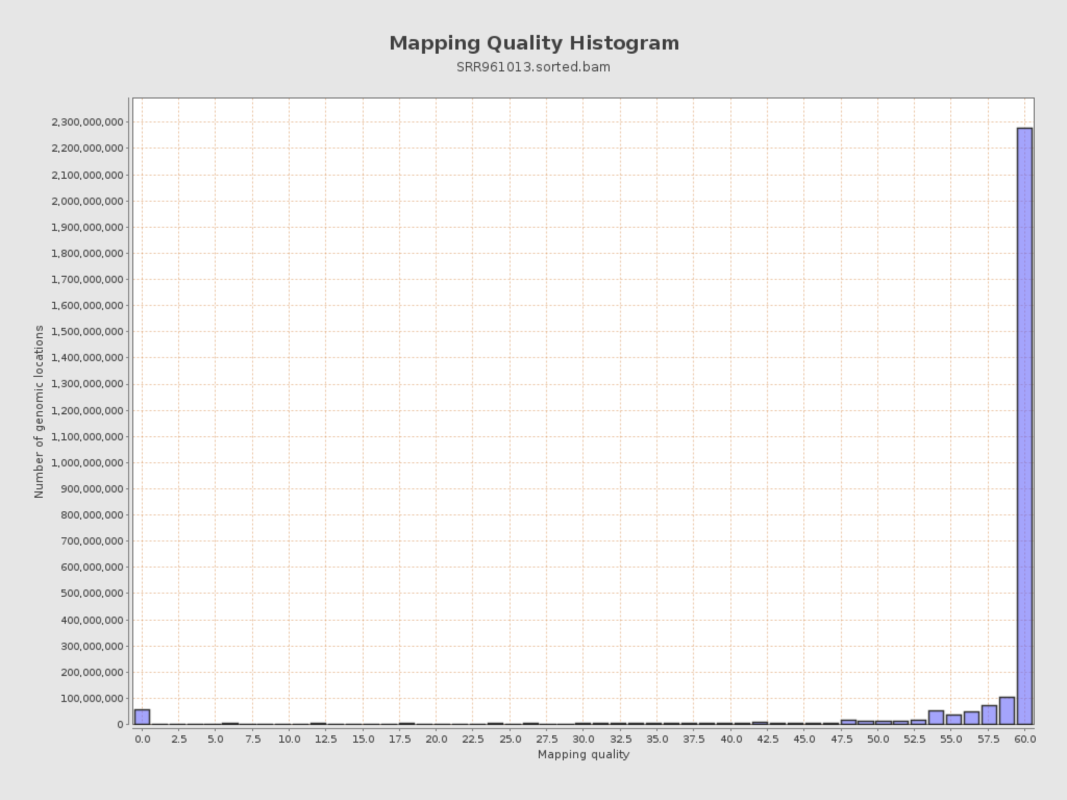
11. Results : Homopolymer Indels



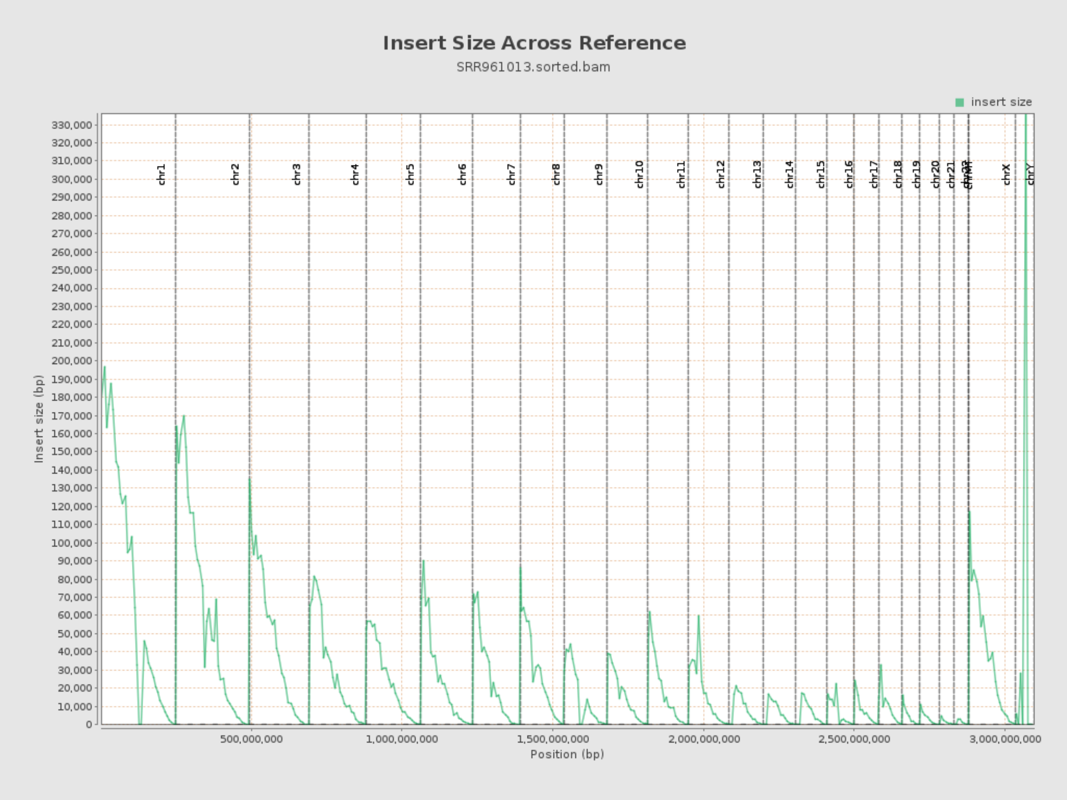
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram