Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 12:51:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961019.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_SRR961019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961019_1.fastq.gz SRR961019_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 12:51:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	307,638,920
Mapped reads	300,522,777 / 97.69%
Unmapped reads	7,116,143 / 2.31%
Mapped paired reads	300,522,777 / 97.69%
Mapped reads, first in pair	150,433,105 / 48.9%
Mapped reads, second in pair	150,089,672 / 48.79%
Mapped reads, both in pair	299,539,418 / 97.37%
Mapped reads, singletons	983,359 / 0.32%
Secondary alignments	0
Supplementary alignments	690,991 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	38,487,537 / 12.51%
Duplication rate	8.4%
Clipped reads	22,892,224 / 7.44%

2.2. ACGT Content

Number/percentage of A's	8,693,007,240 / 29.45%
Number/percentage of C's	6,042,003,144 / 20.47%
Number/percentage of T's	8,671,319,857 / 29.38%
Number/percentage of G's	6,091,693,901 / 20.64%
Number/percentage of N's	14,942,967 / 0.05%

GC Percentage	41.11%

2.3. Coverage

Mean	9.5365
Standard Deviation	104.6401

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	21,824.33
Standard Deviation	1,383,627.98
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	141,508,678
Insertions	3,054,022
Mapped reads with at least one insertion	0.98%
Deletions	3,624,218
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.64%

2.7. Chromosome stats

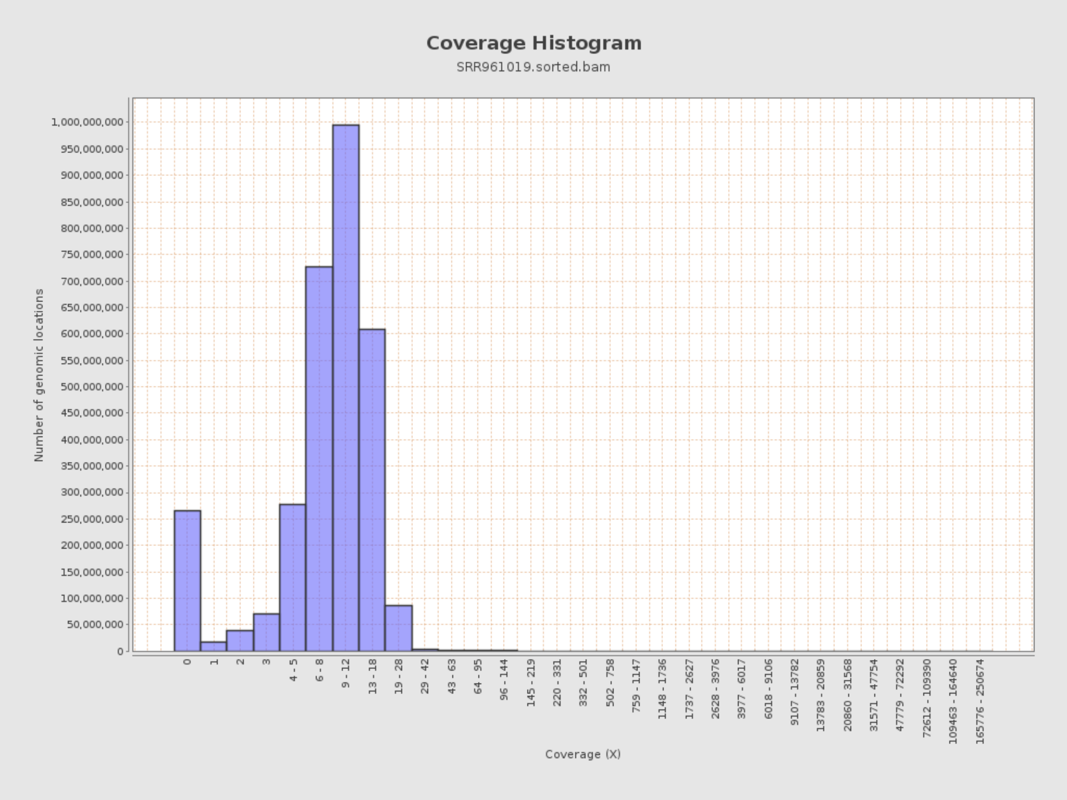
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	2402862638	9.6403	248.8722
chr2	243199373	2527920151	10.3944	65.3529
chr3	198022430	1941252814	9.8032	21.4822
chr4	191154276	1986226641	10.3907	92.0612
chr5	180915260	1770829260	9.7882	10.1799
chr6	171115067	1686899945	9.8583	30.4241
chr7	159138663	1575426478	9.8997	64.4242
chr8	146364022	1481336618	10.1209	101.4937
chr9	141213431	1231834239	8.7232	89.297
chr10	135534747	1544370392	11.3946	246.5672
chr11	135006516	1329778292	9.8497	41.3745
chr12	133851895	1300886406	9.7188	8.0769
chr13	115169878	936460350	8.1311	5.8863
chr14	107349540	869136138	8.0963	9.3683
chr15	102531392	819269581	7.9904	6.0476
chr16	90354753	948894414	10.5019	101.0074
chr17	81195210	791571276	9.749	38.7847
chr18	78077248	803095339	10.2859	107.0048
chr19	59128983	577265655	9.7628	120.6172
chr20	63025520	608732760	9.6585	34.4086
chr21	48129895	405438764	8.4238	46.1309
chr22	51304566	347290373	6.7692	8.1043
chrMT	16571	22709803	1,370.4546	194.1128
chrX	155270560	1513429651	9.747	31.4722

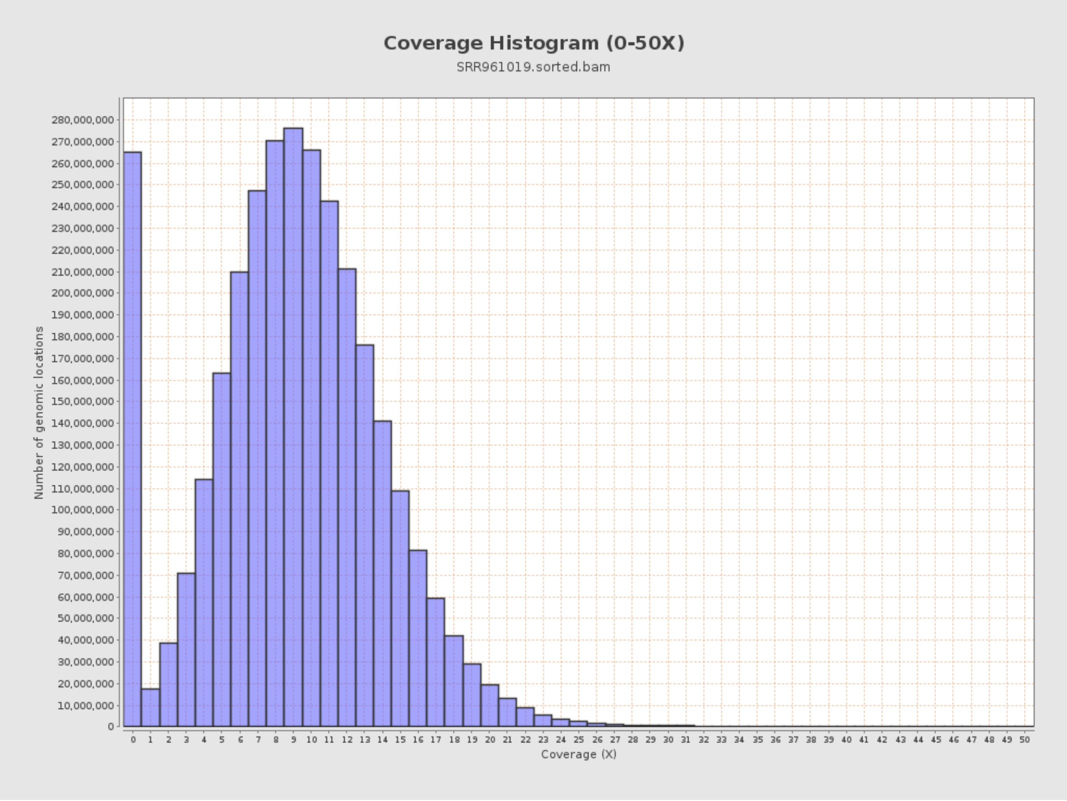
chrY	59373566	99240910	1.6715	98.0157

3. Results : Coverage across reference

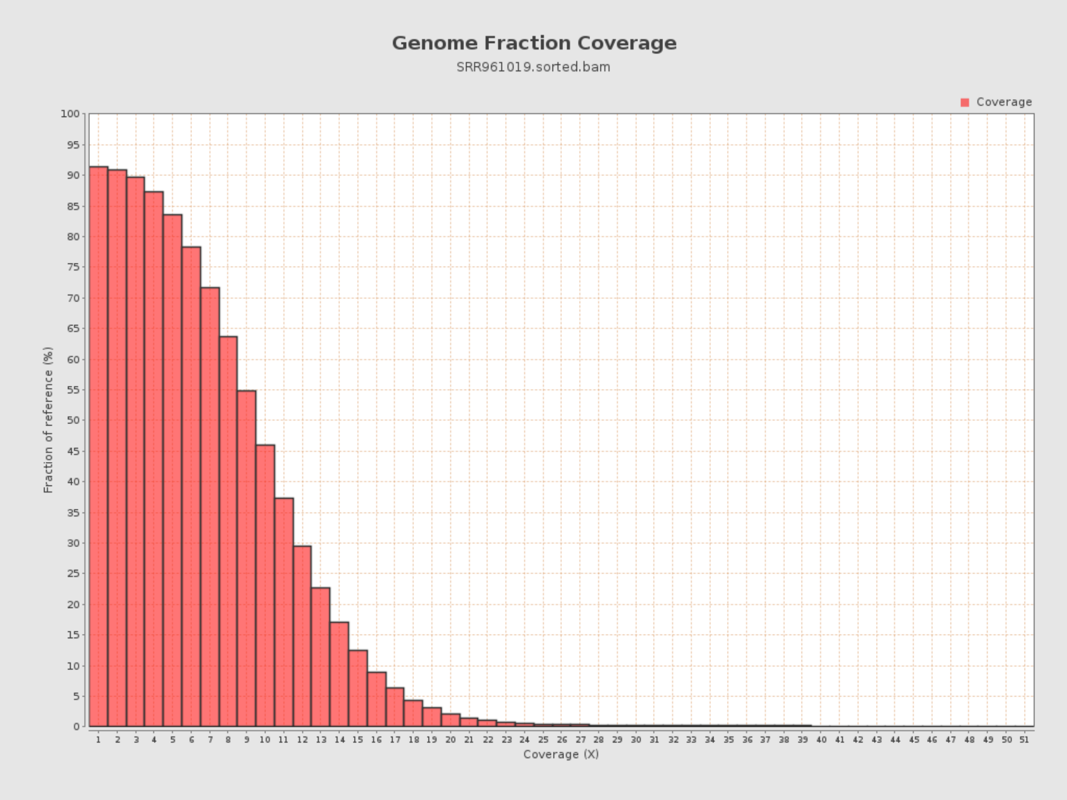
4. Results : Coverage Histogram



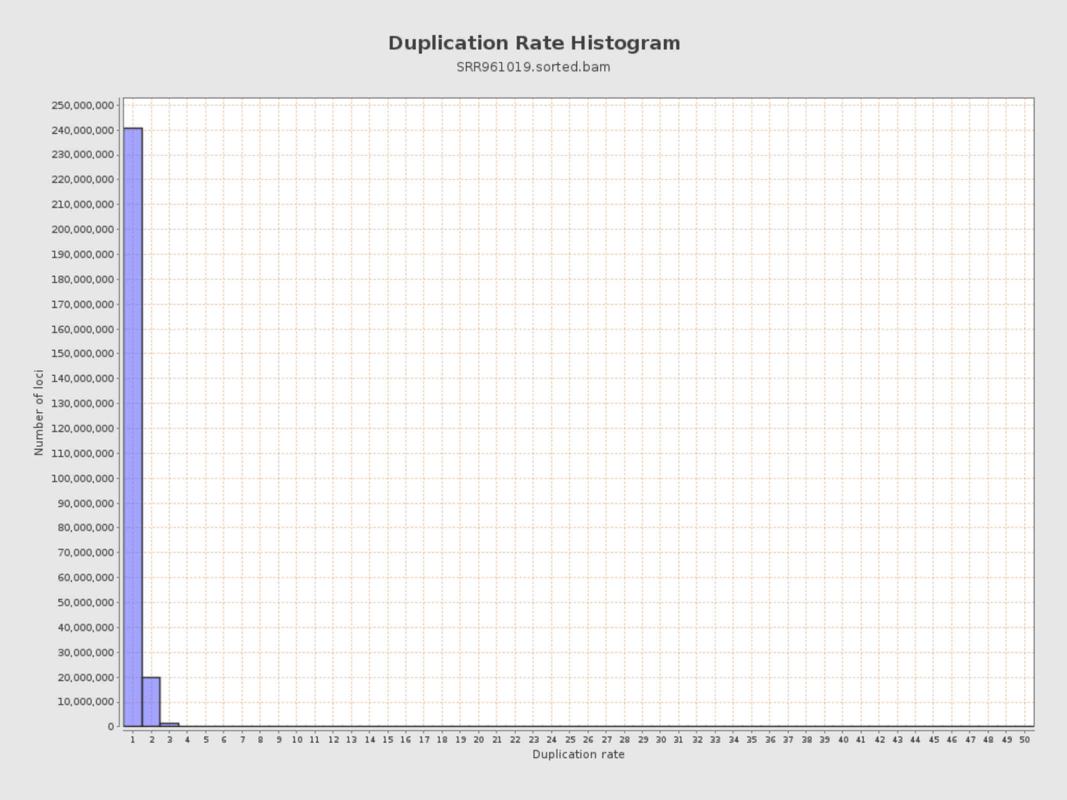
5. Results : Coverage Histogram (0-50X)



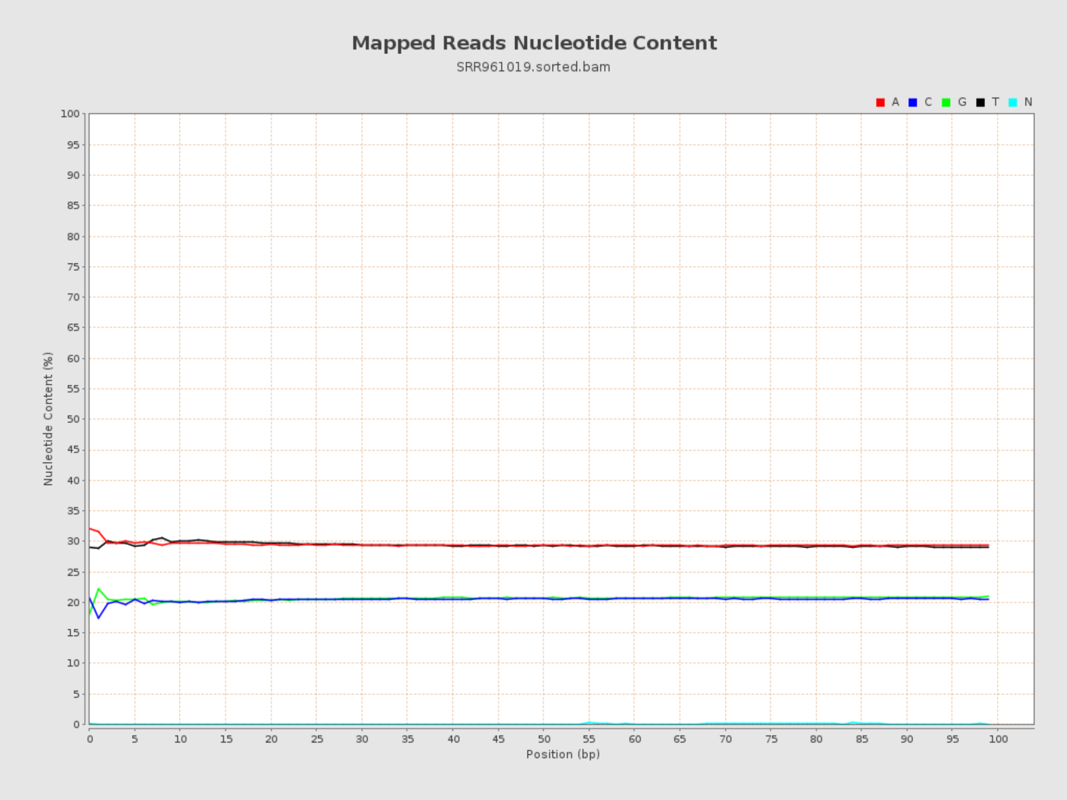
6. Results : Genome Fraction Coverage



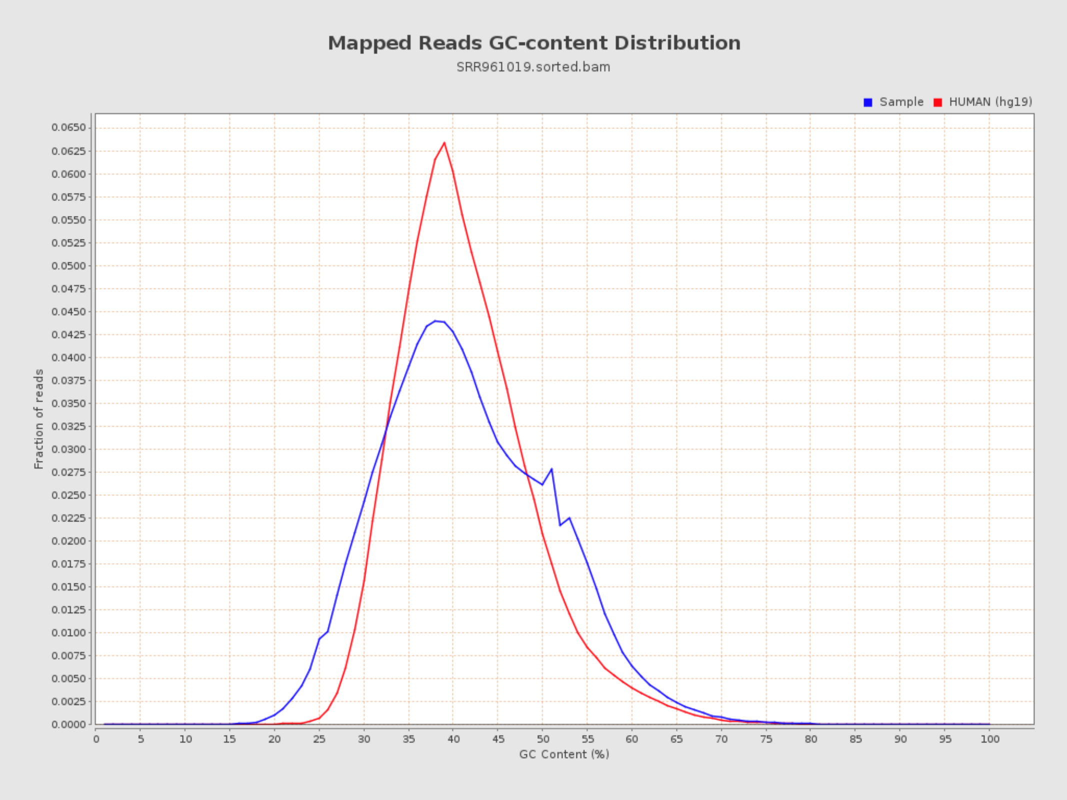
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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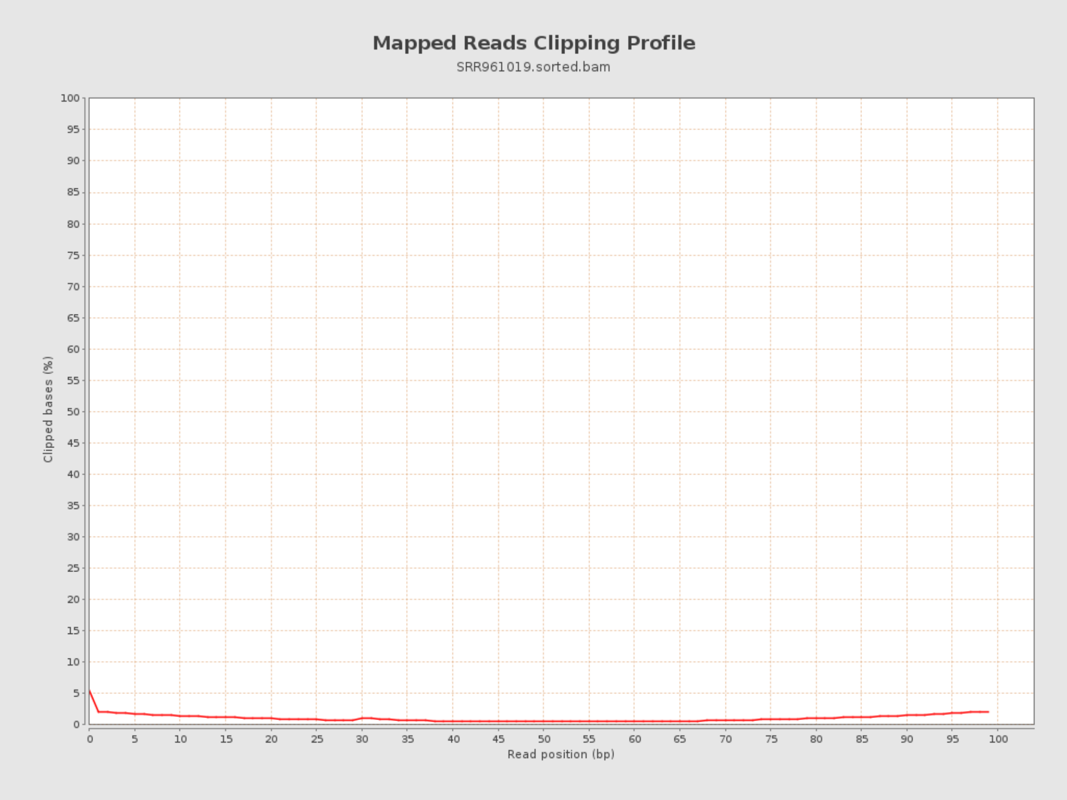
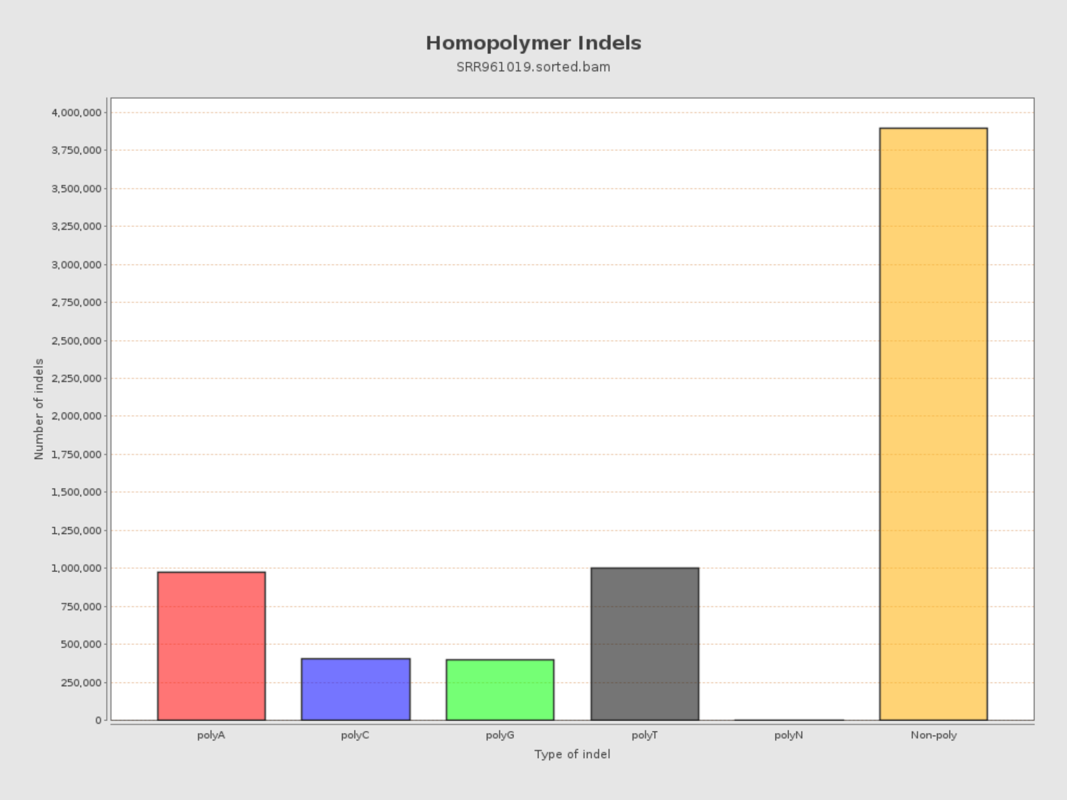
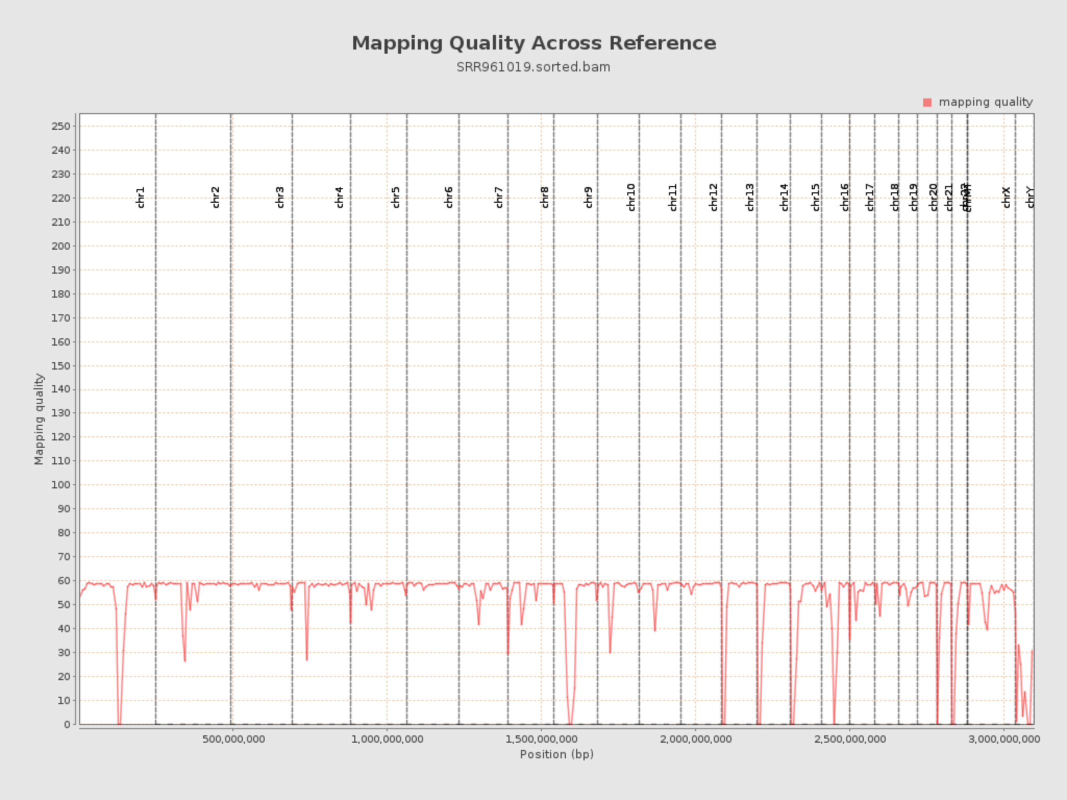
10. Results : Mapped Reads Clipping Profile



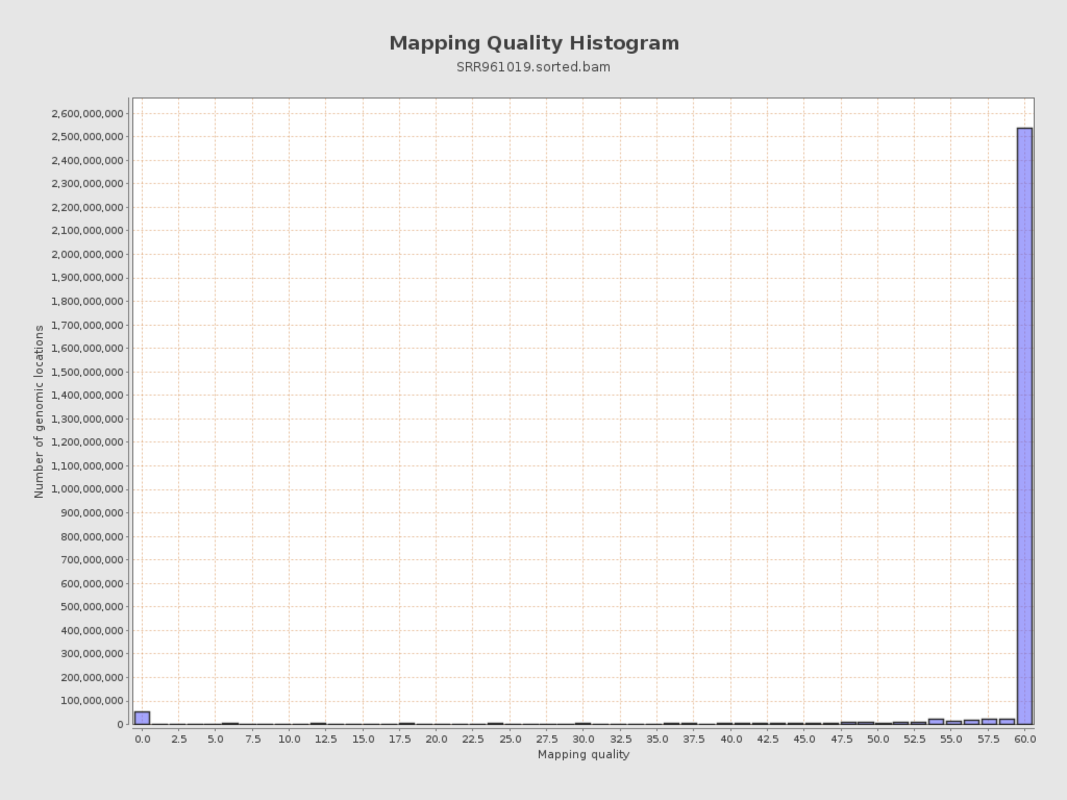
11. Results : Homopolymer Indels



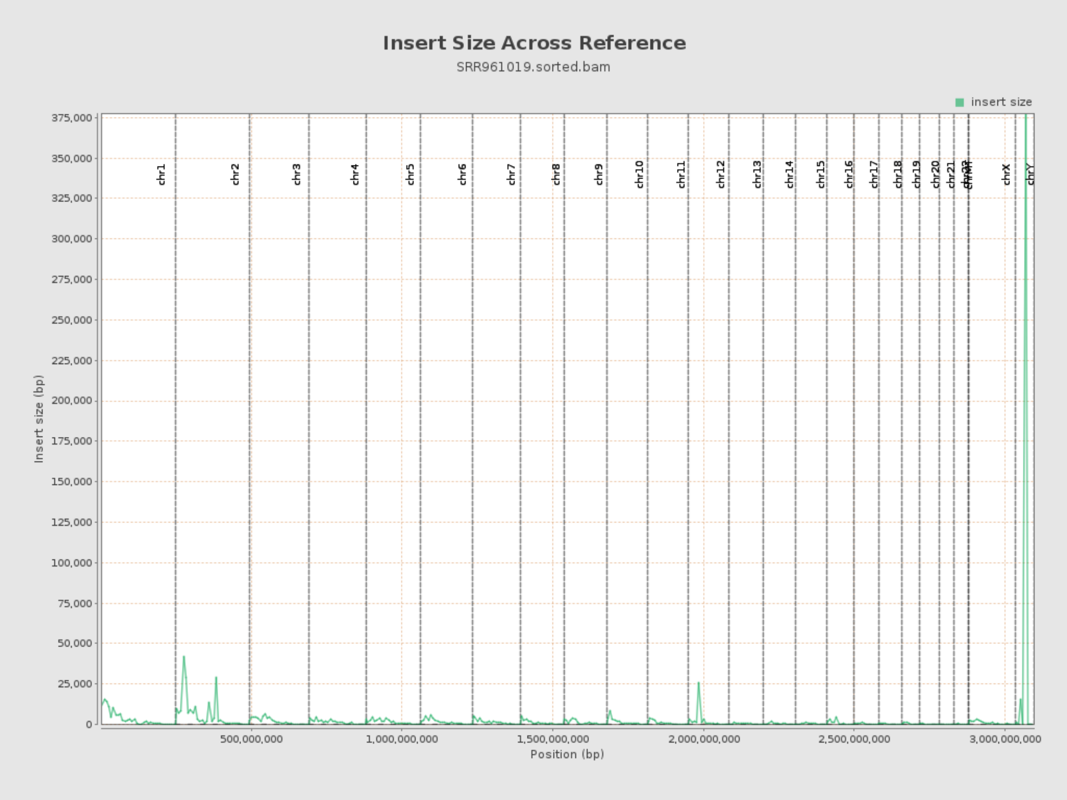
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram