Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 08:06:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961018.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_SRR961018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961018_1.fastq.gz SRR961018_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 08:06:30 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	310,749,478
Mapped reads	303,558,512 / 97.69%
Unmapped reads	7,190,966 / 2.31%
Mapped paired reads	303,558,512 / 97.69%
Mapped reads, first in pair	151,952,705 / 48.9%
Mapped reads, second in pair	151,605,807 / 48.79%
Mapped reads, both in pair	302,551,870 / 97.36%
Mapped reads, singletons	1,006,642 / 0.32%
Secondary alignments	0
Supplementary alignments	695,503 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	39,039,852 / 12.56%
Duplication rate	8.46%
Clipped reads	23,242,589 / 7.48%

2.2. ACGT Content

Number/percentage of A's	8,779,402,787 / 29.46%
Number/percentage of C's	6,099,206,576 / 20.46%
Number/percentage of T's	8,757,155,774 / 29.38%
Number/percentage of G's	6,149,642,425 / 20.63%
Number/percentage of N's	19,377,458 / 0.07%

GC Percentage	41.1%

2.3. Coverage

Mean	9.6308
Standard Deviation	105.7738

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	21,799.76
Standard Deviation	1,374,739.67
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	145,695,938
Insertions	3,075,201
Mapped reads with at least one insertion	0.98%
Deletions	3,653,403
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.64%

2.7. Chromosome stats

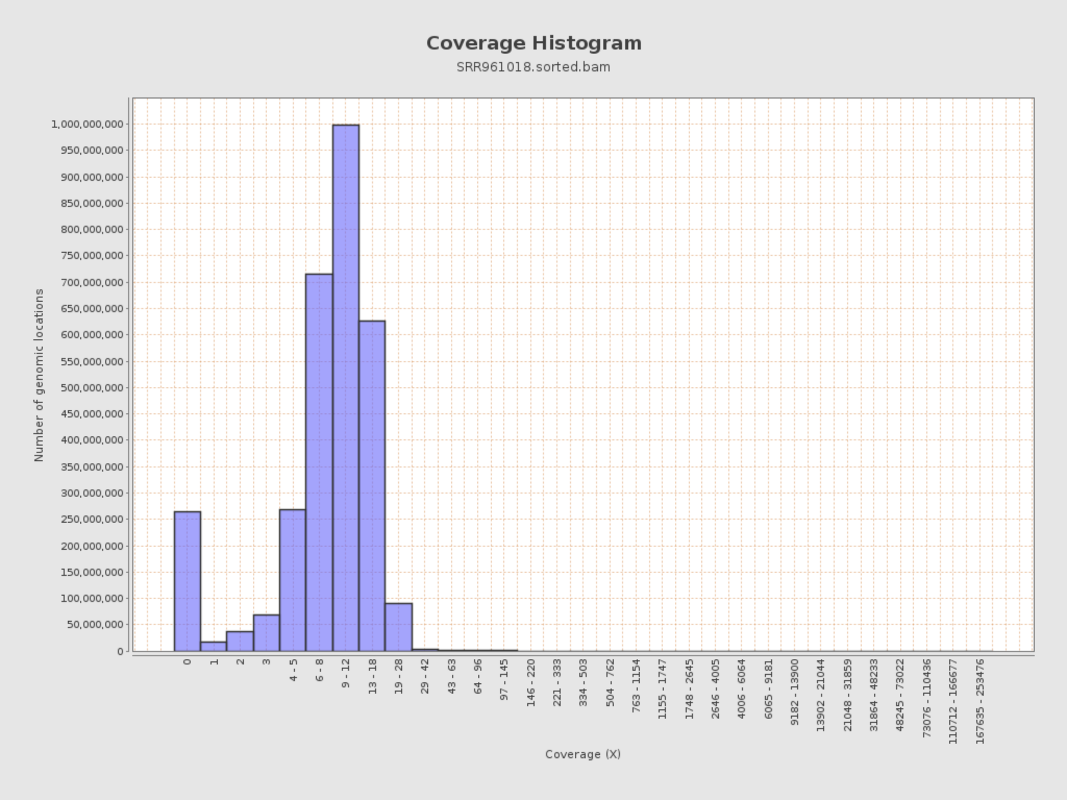
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	2426762001	9.7362	251.6543
chr2	243199373	2554177876	10.5024	66.0891
chr3	198022430	1960445723	9.9001	21.4096
chr4	191154276	2006024520	10.4943	93.2358
chr5	180915260	1788658475	9.8867	10.2999
chr6	171115067	1703312485	9.9542	30.6505
chr7	159138663	1591166809	9.9986	64.4492
chr8	146364022	1498113327	10.2355	103.1532
chr9	141213431	1243674256	8.8071	90.5381
chr10	135534747	1560016937	11.5101	249.0843
chr11	135006516	1343537706	9.9517	41.7069
chr12	133851895	1313250791	9.8112	8.126
chr13	115169878	945436552	8.2091	5.9412
chr14	107349540	877764564	8.1767	9.3338
chr15	102531392	826153579	8.0576	6.0915
chr16	90354753	957853198	10.601	102.184
chr17	81195210	799207087	9.843	39.2476
chr18	78077248	810713556	10.3835	108.137
chr19	59128983	581586655	9.8359	122.0458
chr20	63025520	614501152	9.75	34.9743
chr21	48129895	409824142	8.515	46.4948
chr22	51304566	350128373	6.8245	8.0717
chrMT	16571	22900675	1,381.973	196.1632
chrX	155270560	1528721779	9.8455	31.7484

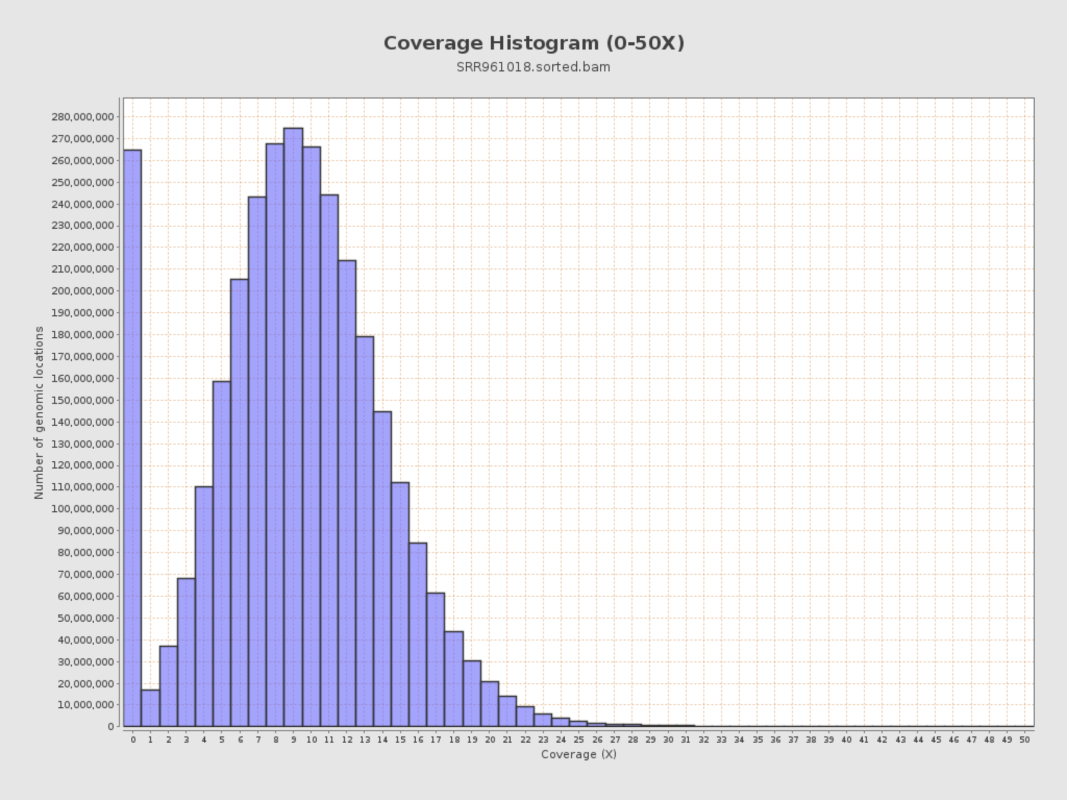
chrY	59373566	100118659	1.6862	97.829

3. Results : Coverage across reference

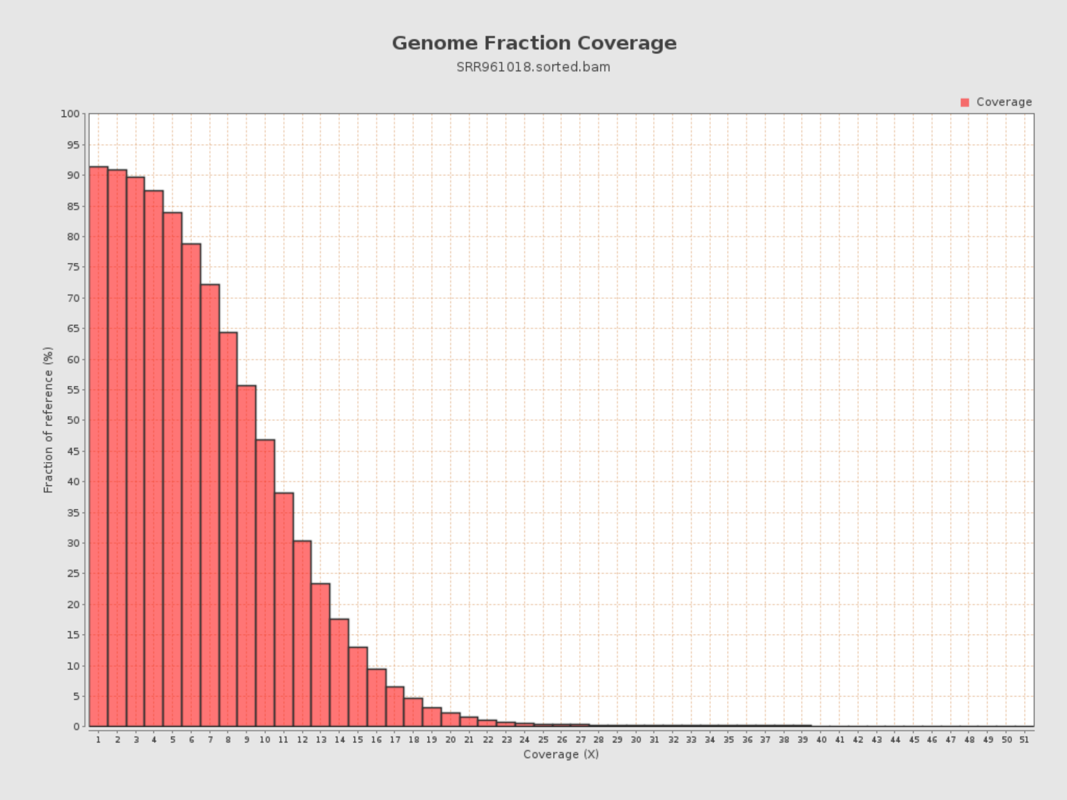
4. Results : Coverage Histogram



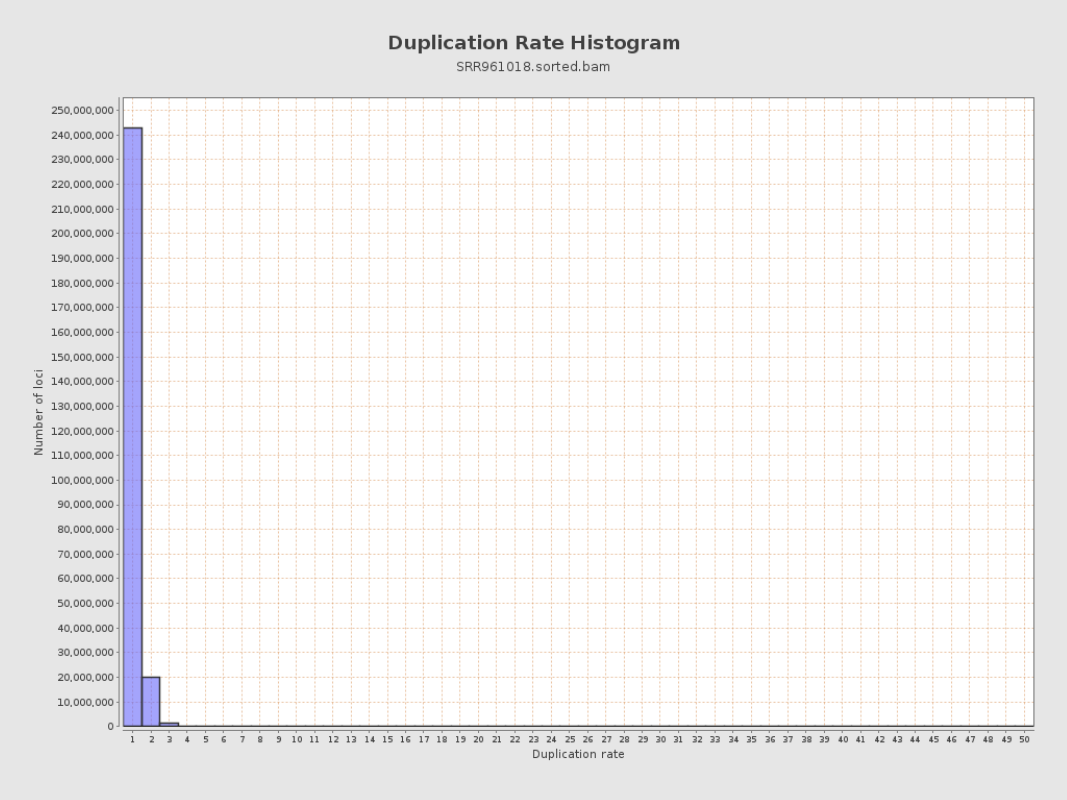
5. Results : Coverage Histogram (0-50X)



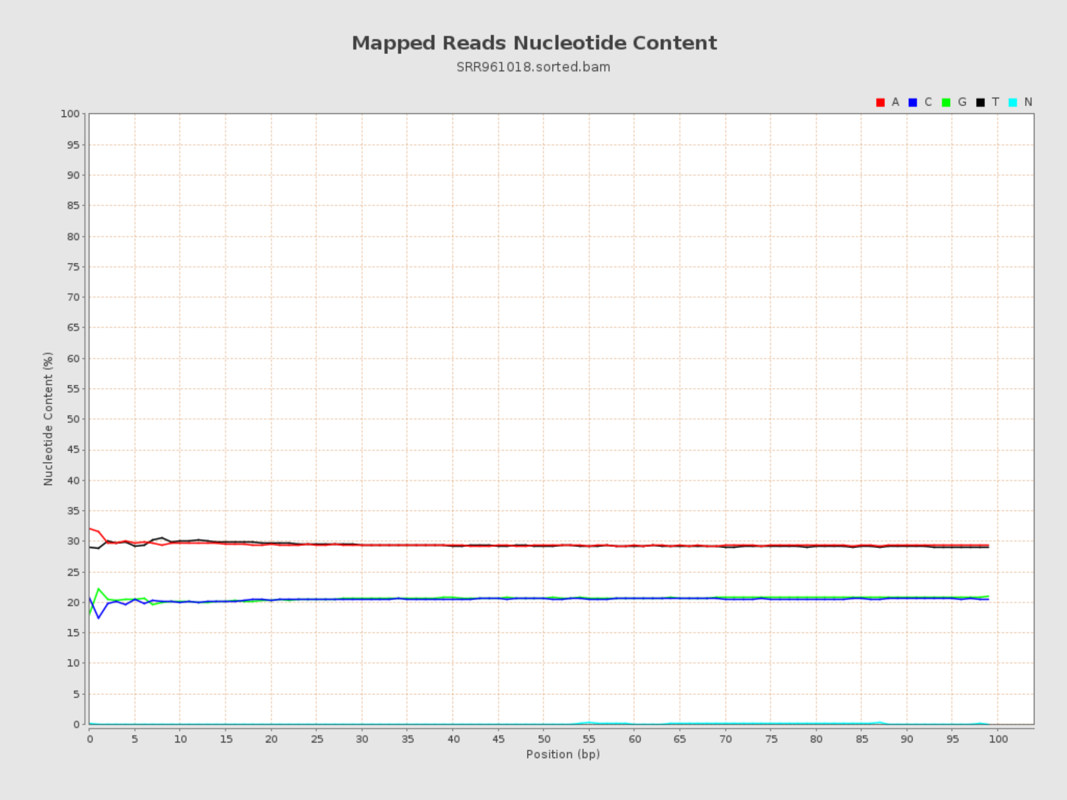
6. Results : Genome Fraction Coverage



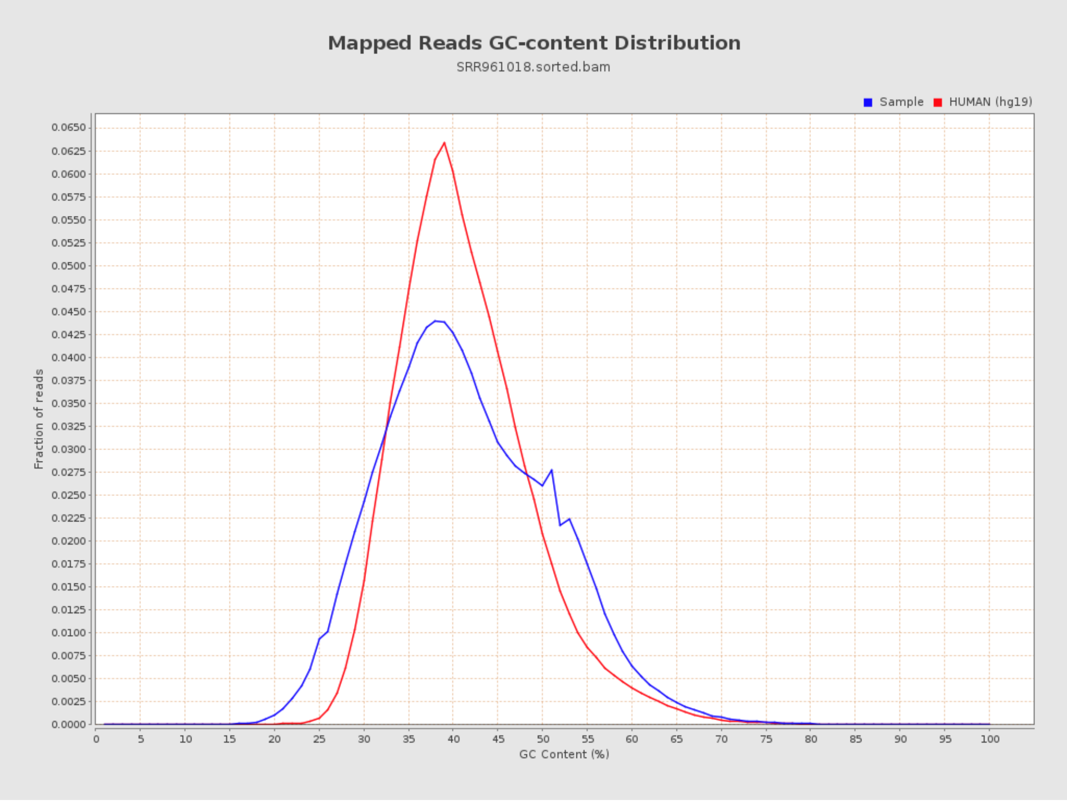
7. Results : Duplication Rate Histogram



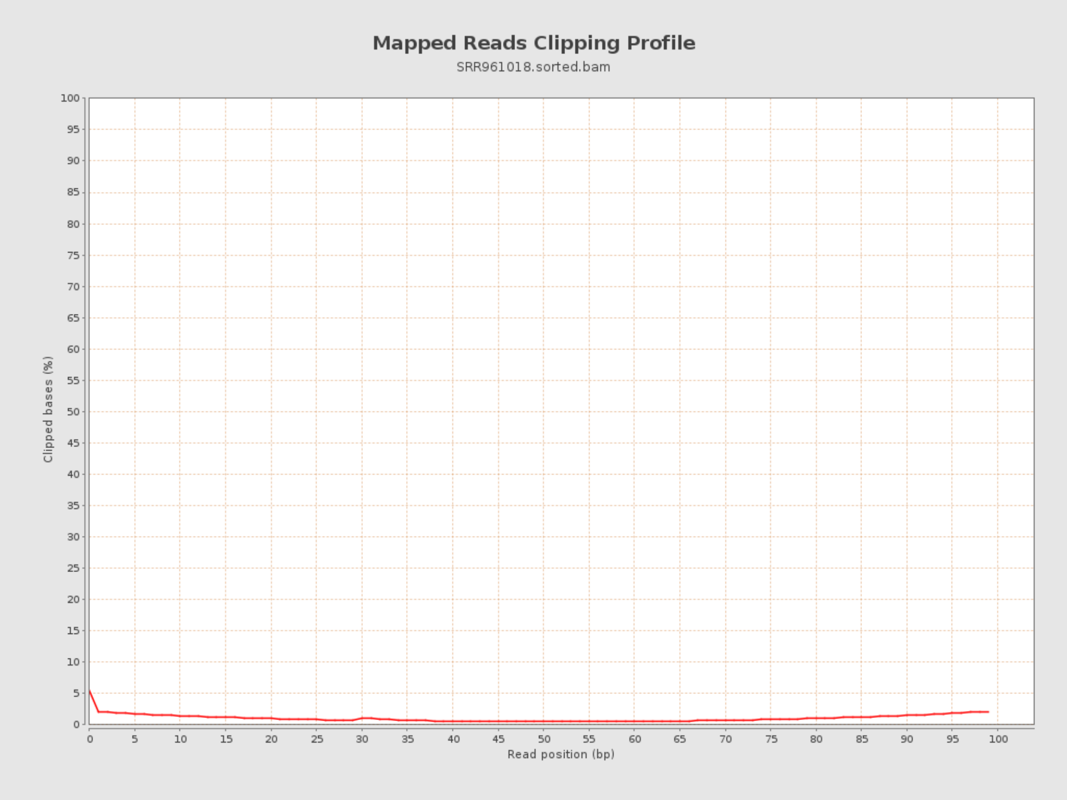
8. Results : Mapped Reads Nucleotide Content



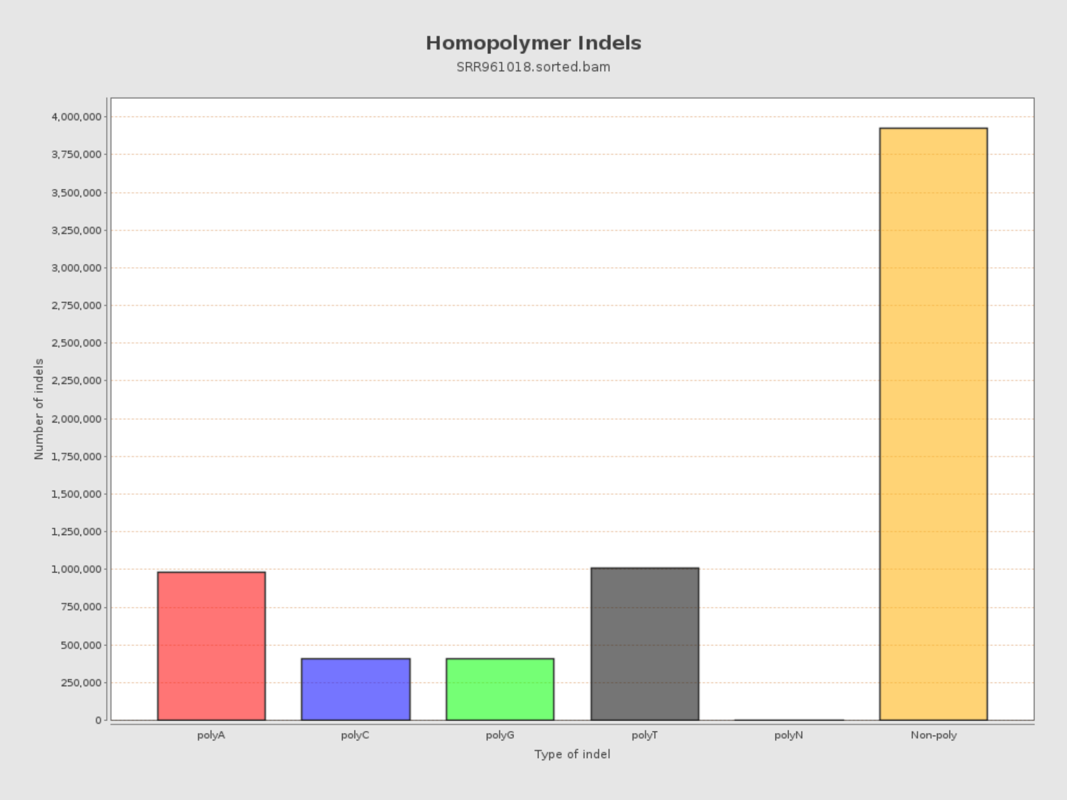
9. Results : Mapped Reads GC-content Distribution



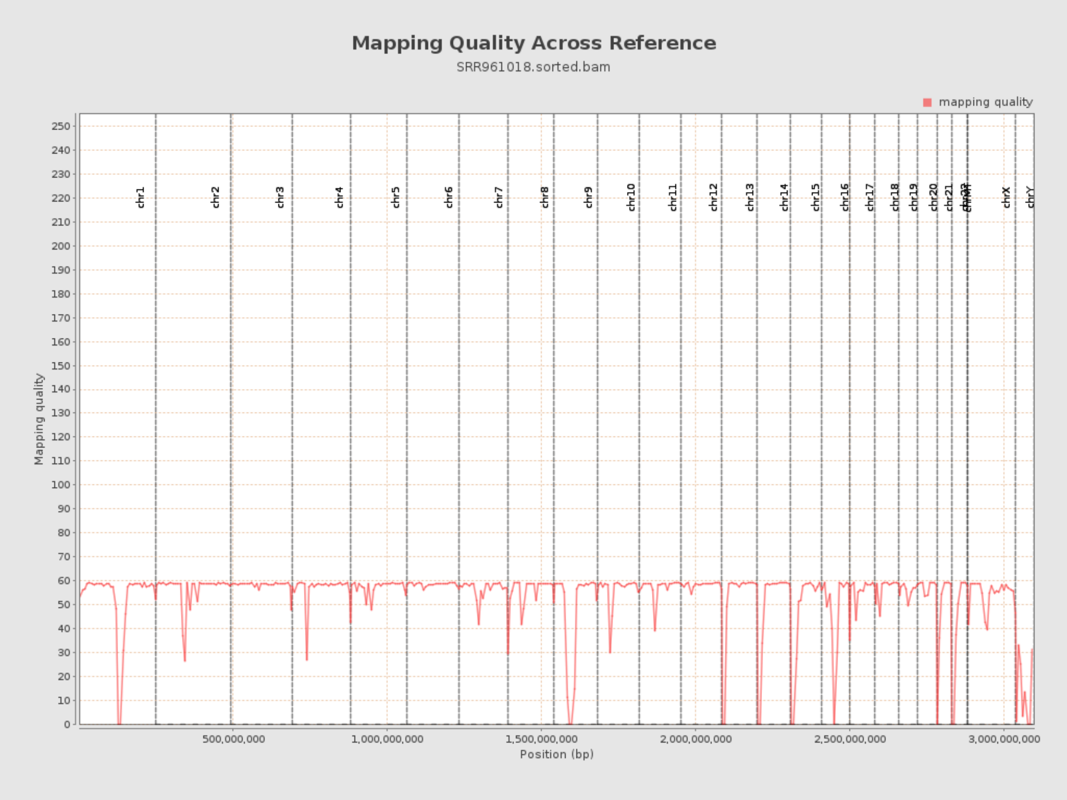
10. Results : Mapped Reads Clipping Profile



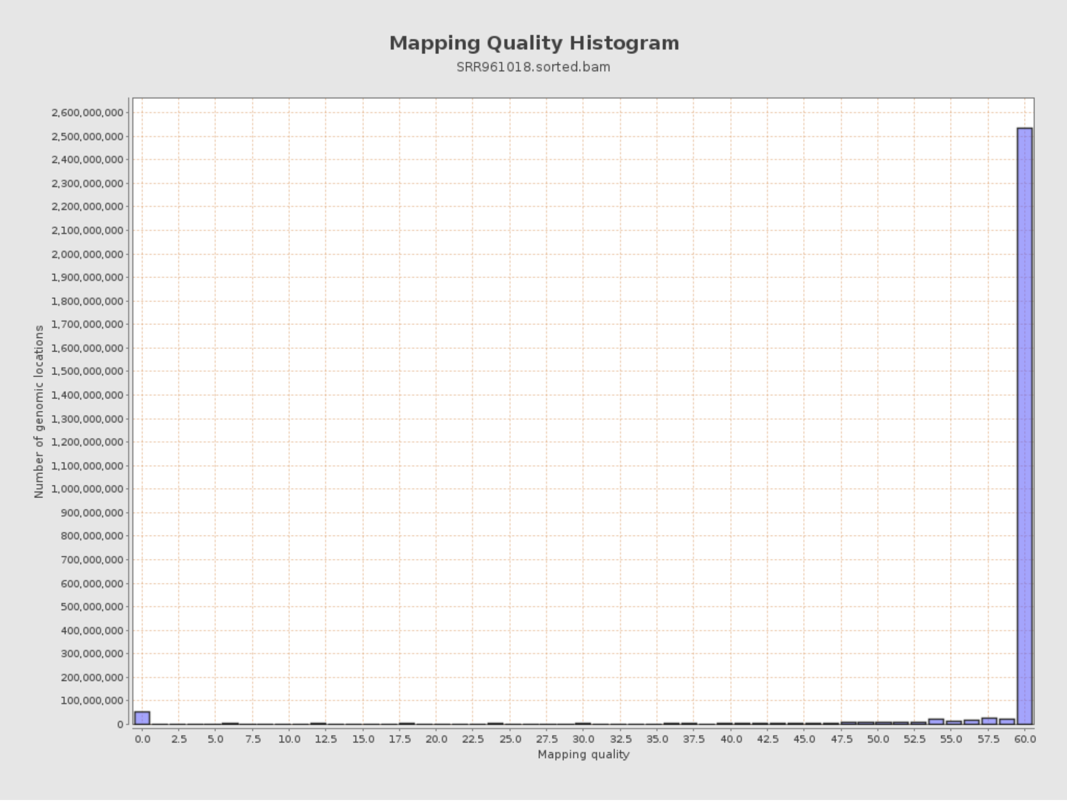
11. Results : Homopolymer Indels



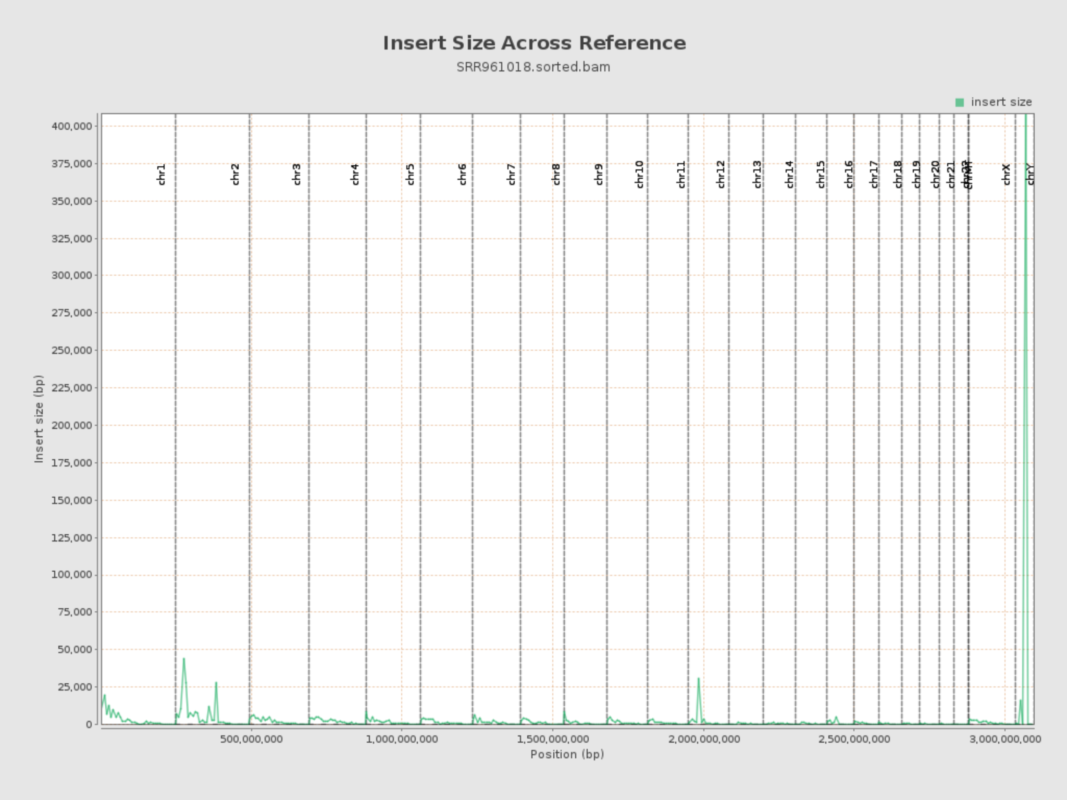
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram