Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 16:50:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961015.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_SRR961015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961015_1.fastq.gz SRR961015_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 16:50:47 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	409,951,378
Mapped reads	394,753,162 / 96.29%
Unmapped reads	15,198,216 / 3.71%
Mapped paired reads	394,753,162 / 96.29%
Mapped reads, first in pair	202,747,693 / 49.46%
Mapped reads, second in pair	192,005,469 / 46.84%
Mapped reads, both in pair	383,057,660 / 93.44%
Mapped reads, singletons	11,695,502 / 2.85%
Secondary alignments	0
Supplementary alignments	6,803,862 / 1.66%
Read min/max/mean length	30 / 100 / 100.69
Duplicated reads (estimated)	65,738,063 / 16.04%
Duplication rate	11.65%
Clipped reads	50,021,407 / 12.2%

2.2. ACGT Content

Number/percentage of A's	11,304,395,001 / 29.23%
Number/percentage of C's	7,999,961,250 / 20.68%
Number/percentage of T's	11,248,392,591 / 29.08%
Number/percentage of G's	8,048,307,853 / 20.81%
Number/percentage of N's	76,107,069 / 0.2%

GC Percentage	41.49%

2.3. Coverage

Mean	12.4975
Standard Deviation	155.9641

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	87,858.26
Standard Deviation	2,854,165.78
P25/Median/P75	127 / 142 / 155

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	399,711,726
Insertions	3,946,846
Mapped reads with at least one insertion	0.97%
Deletions	4,646,948
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.75%

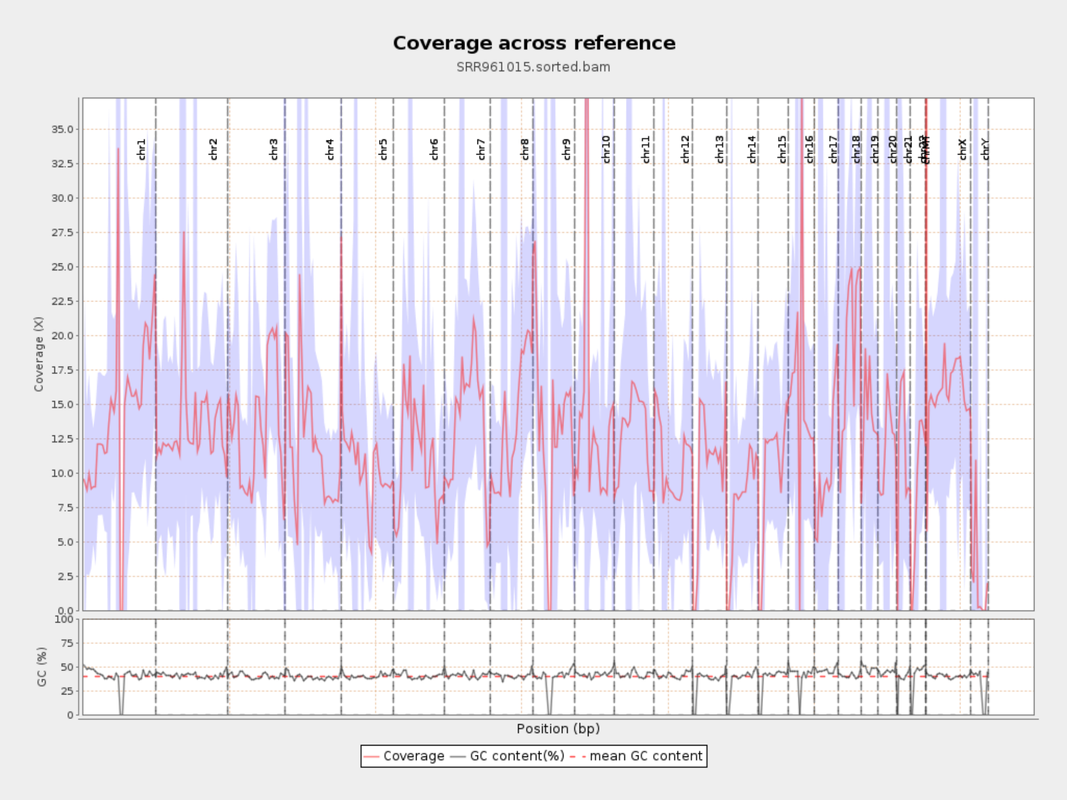
2.7. Chromosome stats

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

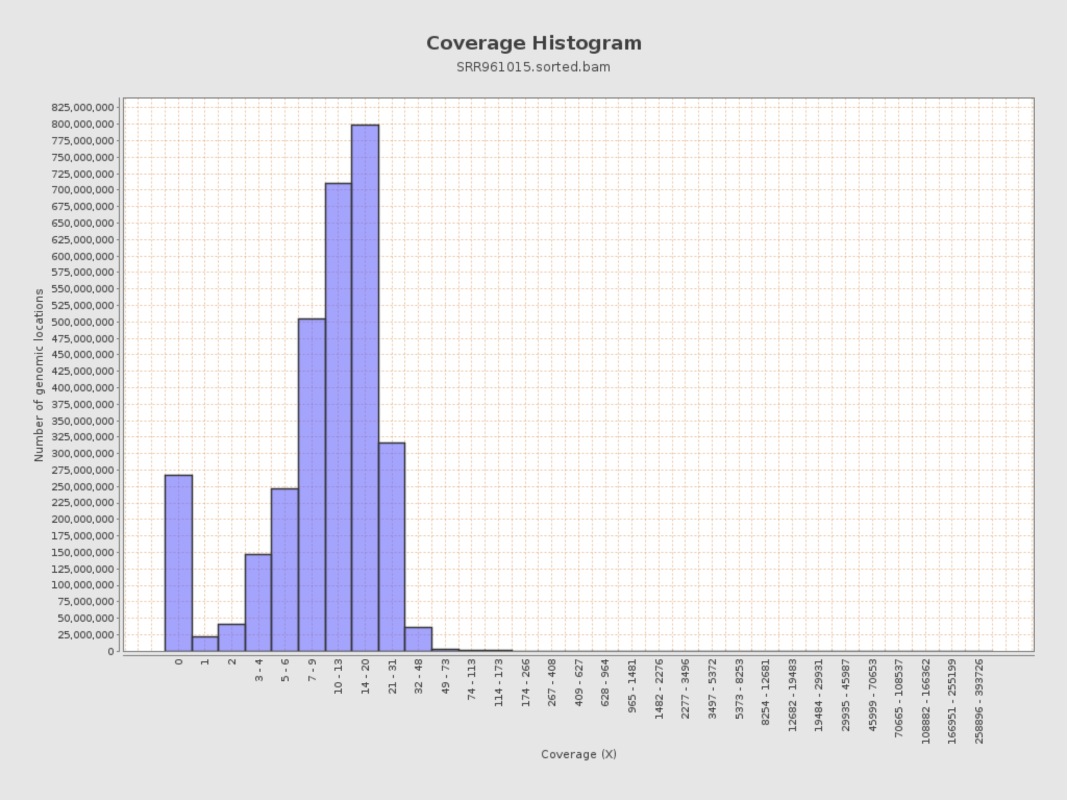
		bases	coverage	deviation
chr1	249250621	3576360879	14.3485	395.4136
chr2	243199373	3268950787	13.4414	92.9322
chr3	198022430	2619887290	13.2303	34.5926
chr4	191154276	2317031091	12.1213	106.6537
chr5	180915260	1858842182	10.2747	15.4153
chr6	171115067	1899272039	11.0994	48.2729
chr7	159138663	2183886279	13.7232	97.993
chr8	146364022	1990278492	13.5981	140.0606
chr9	141213431	1843193300	13.0525	122.3562
chr10	135534747	1921976691	14.1807	345.2004
chr11	135006516	1753591579	12.9889	66.6659
chr12	133851895	1450781790	10.8387	13.3104
chr13	115169878	1184210759	10.2823	7.5908
chr14	107349540	850034243	7.9184	12.6768
chr15	102531392	1021792943	9.9657	7.646
chr16	90354753	1439090575	15.9271	161.0158
chr17	81195210	824516154	10.1547	39.5839
chr18	78077248	1473695909	18.8748	151.7887
chr19	59128983	855057009	14.4609	193.8395
chr20	63025520	754089890	11.9648	38.4372
chr21	48129895	542686419	11.2755	57.1627
chr22	51304566	444794058	8.6697	10.2471
chrMT	16571	8743511	527.6393	94.1104
chrX	155270560	2470923891	15.9137	51.0728

chrY	59373566	134840280	2.271	121.978

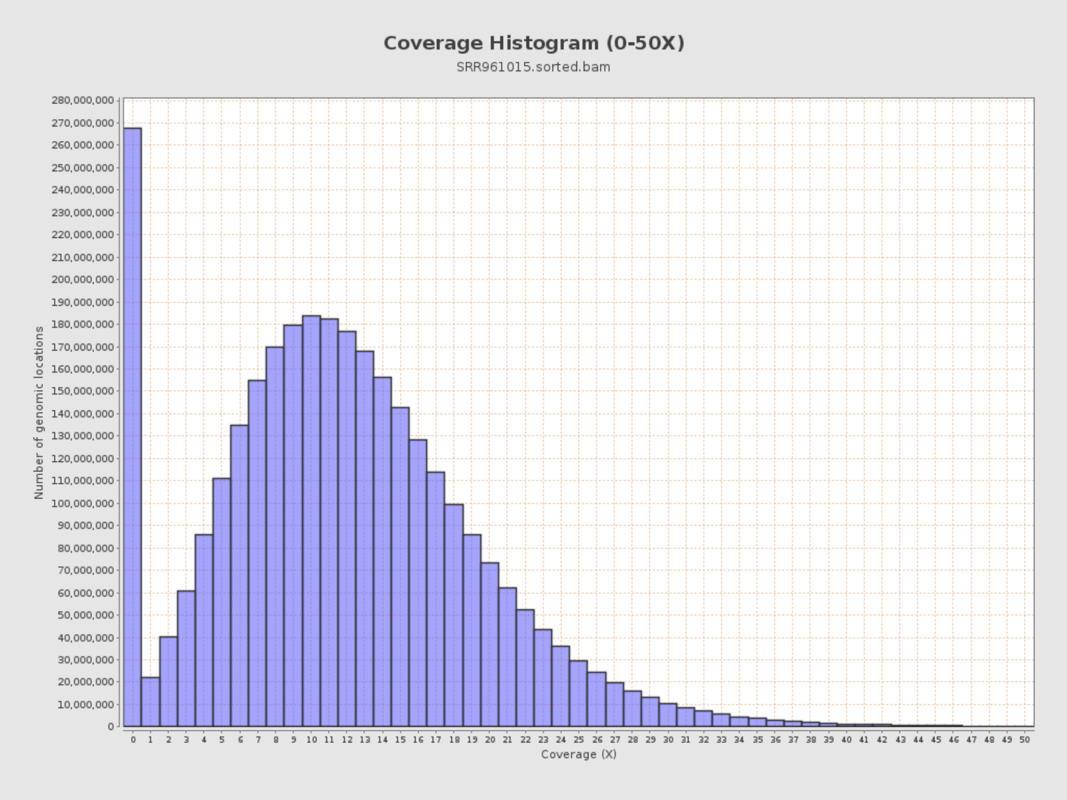
3. Results : Coverage across reference



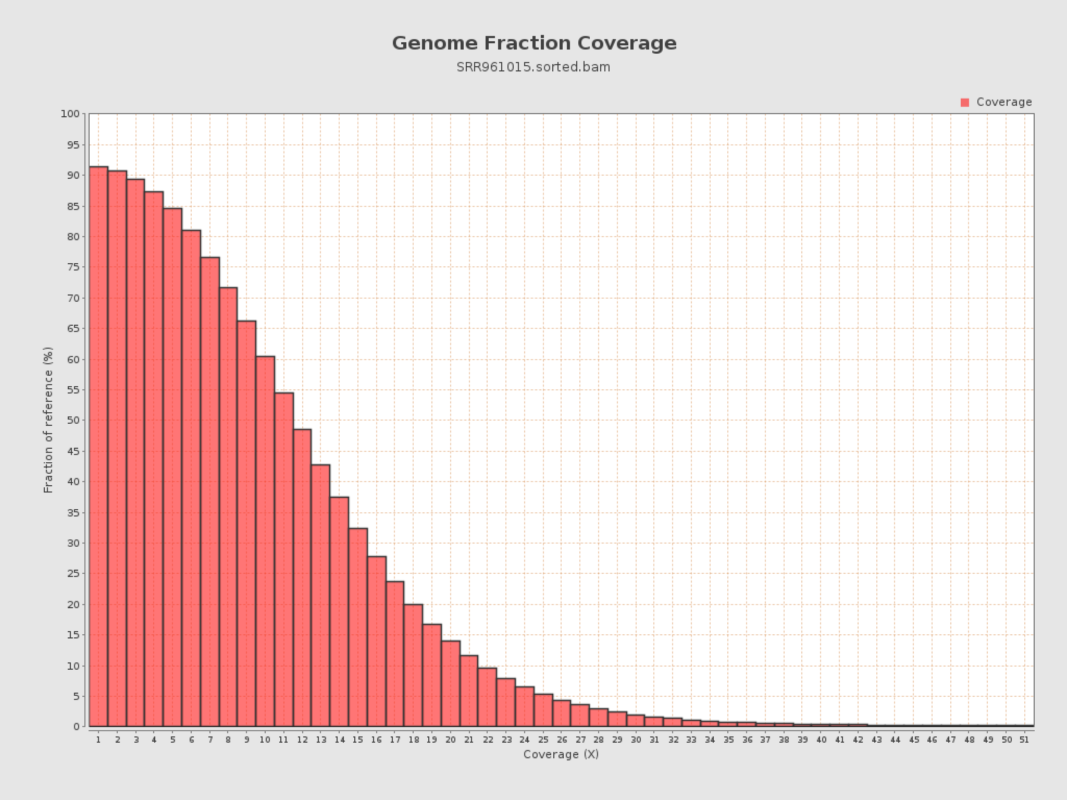
4. Results : Coverage Histogram



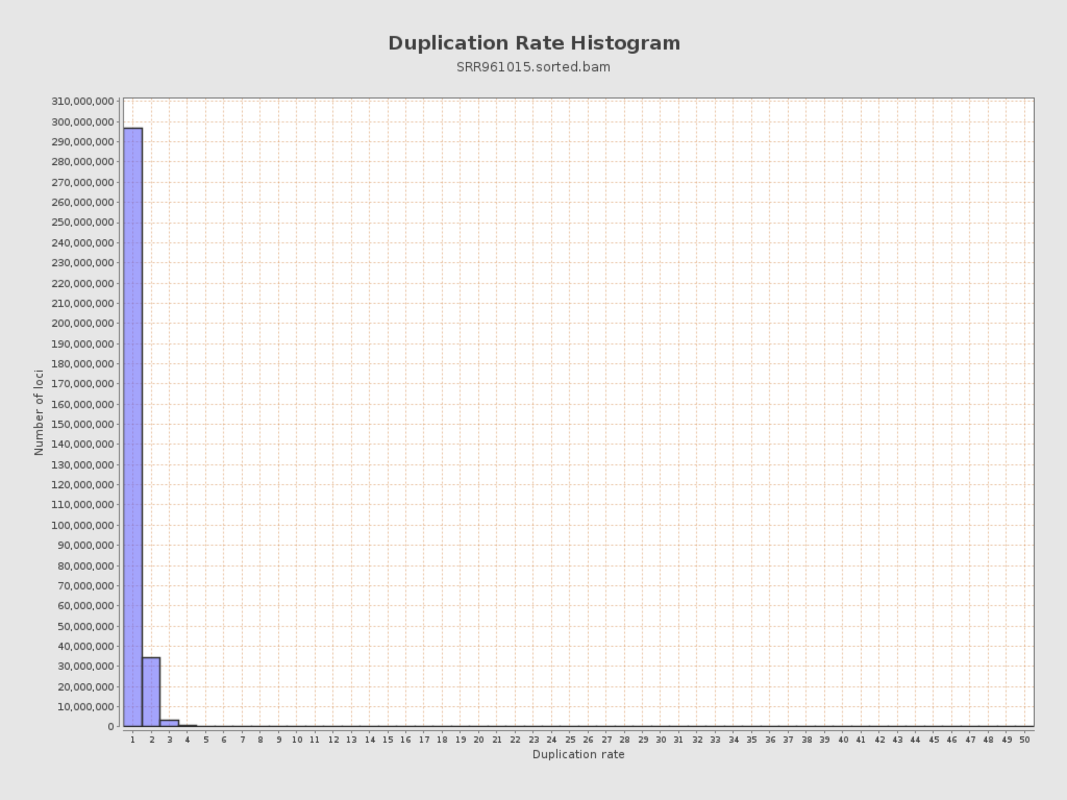
5. Results : Coverage Histogram (0-50X)



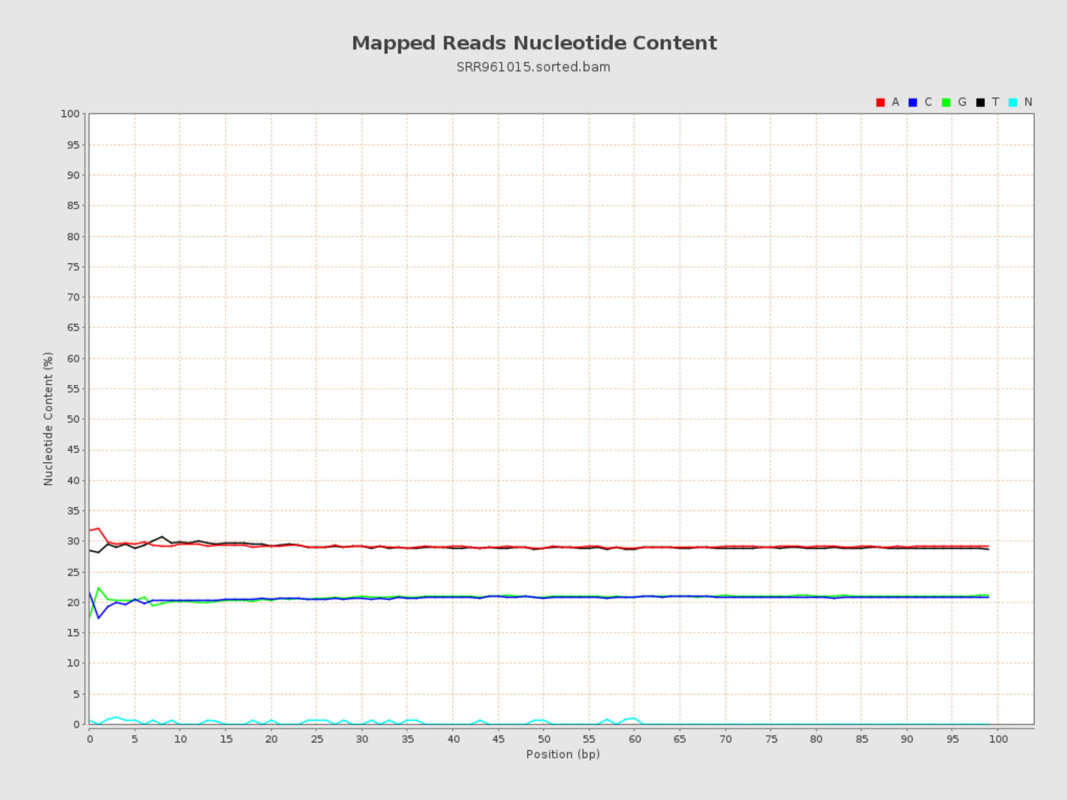
6. Results : Genome Fraction Coverage



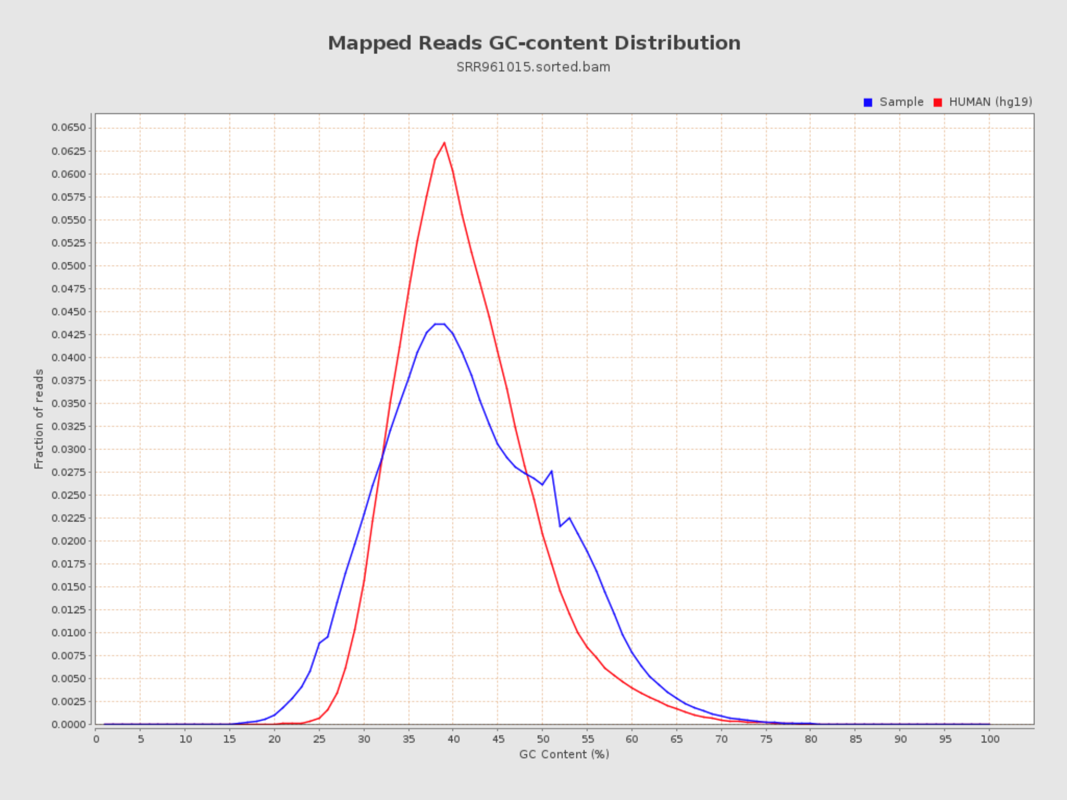
7. Results : Duplication Rate Histogram



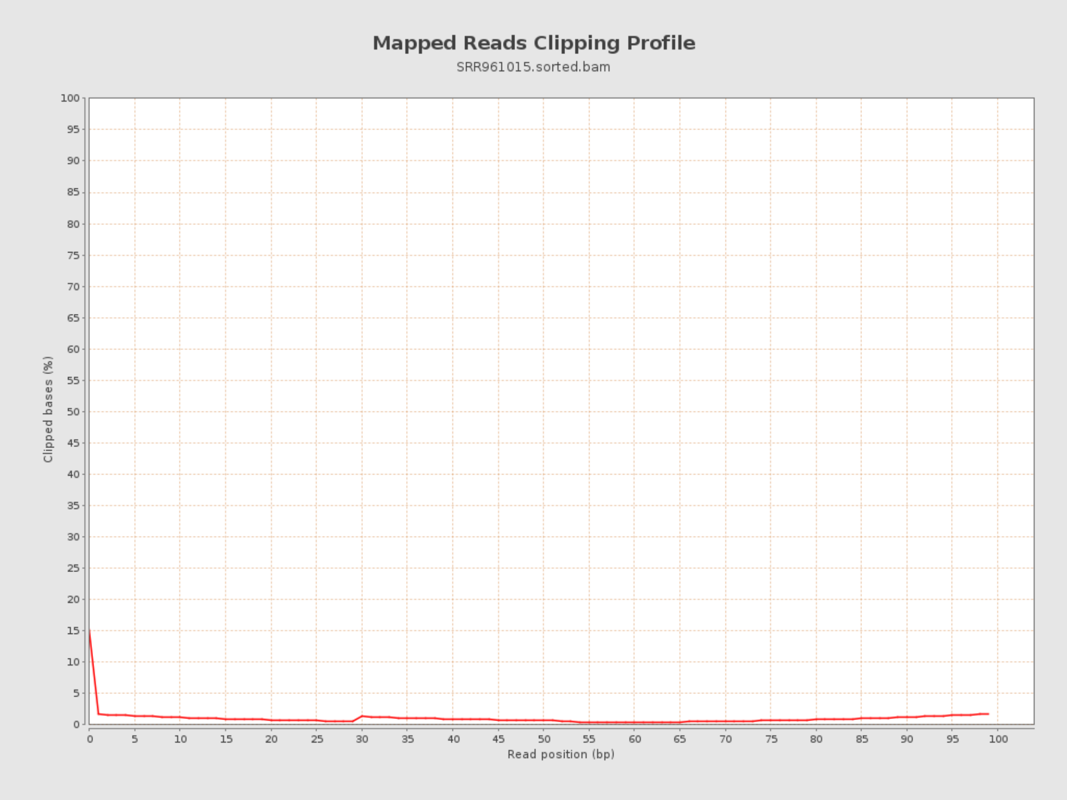
8. Results : Mapped Reads Nucleotide Content



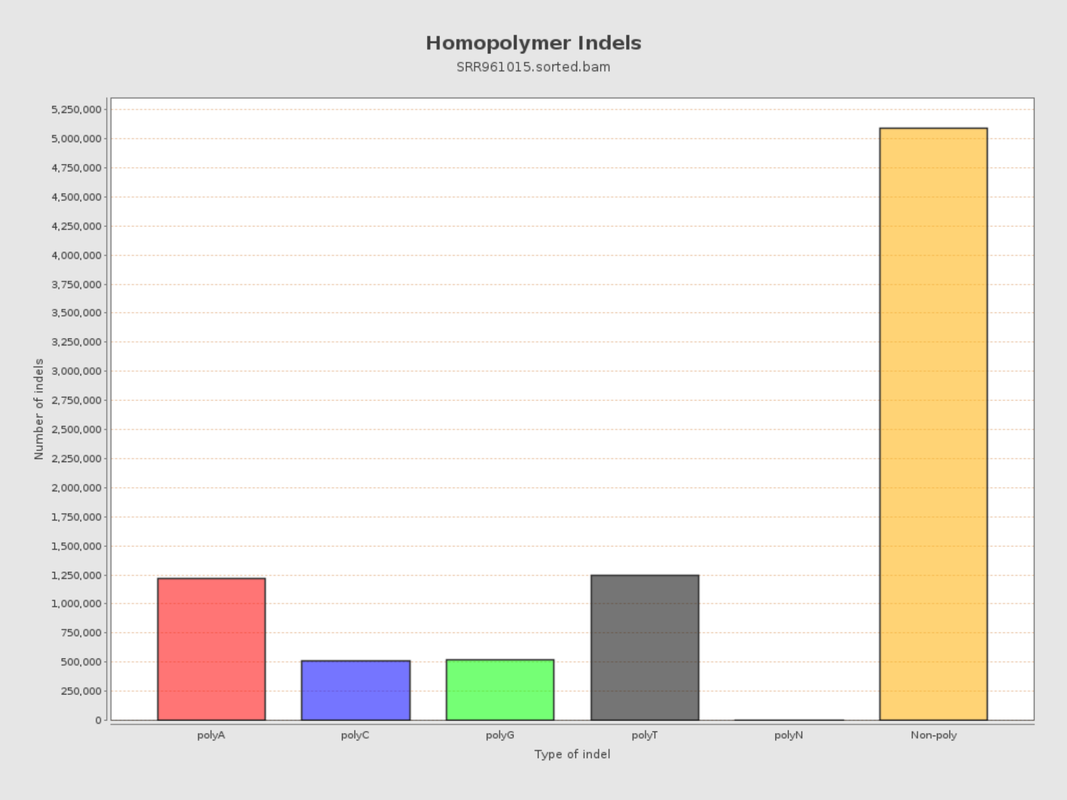
9. Results : Mapped Reads GC-content Distribution



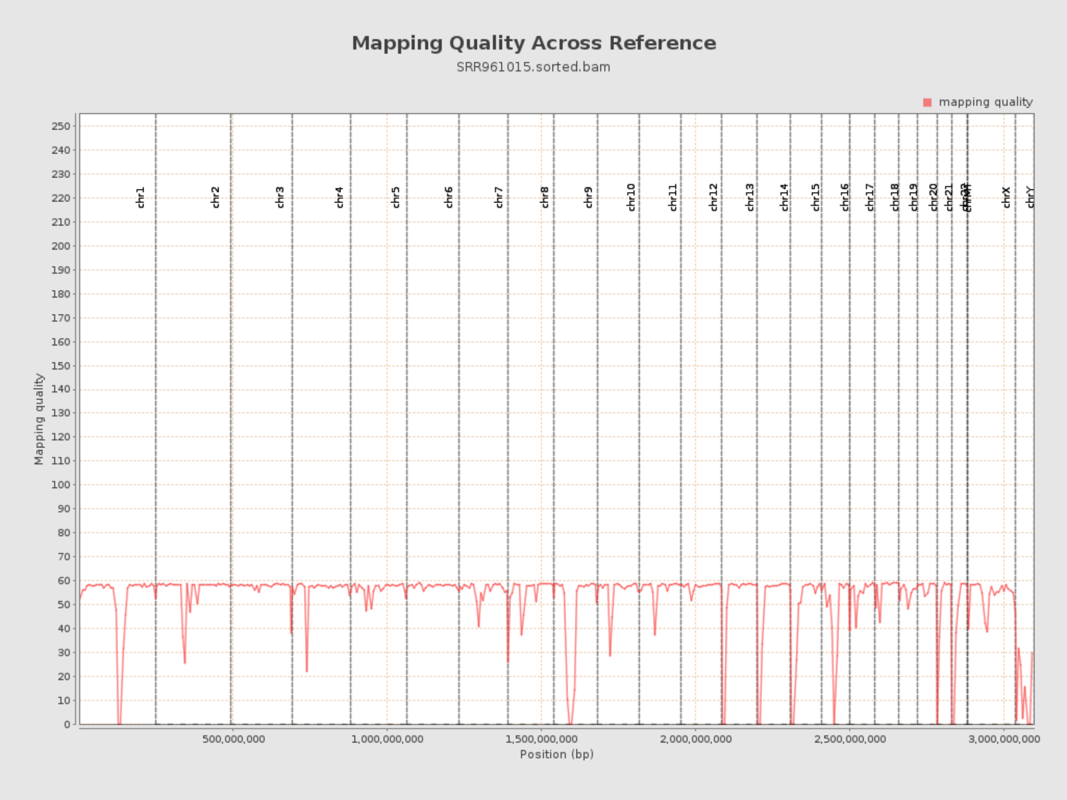
10. Results : Mapped Reads Clipping Profile



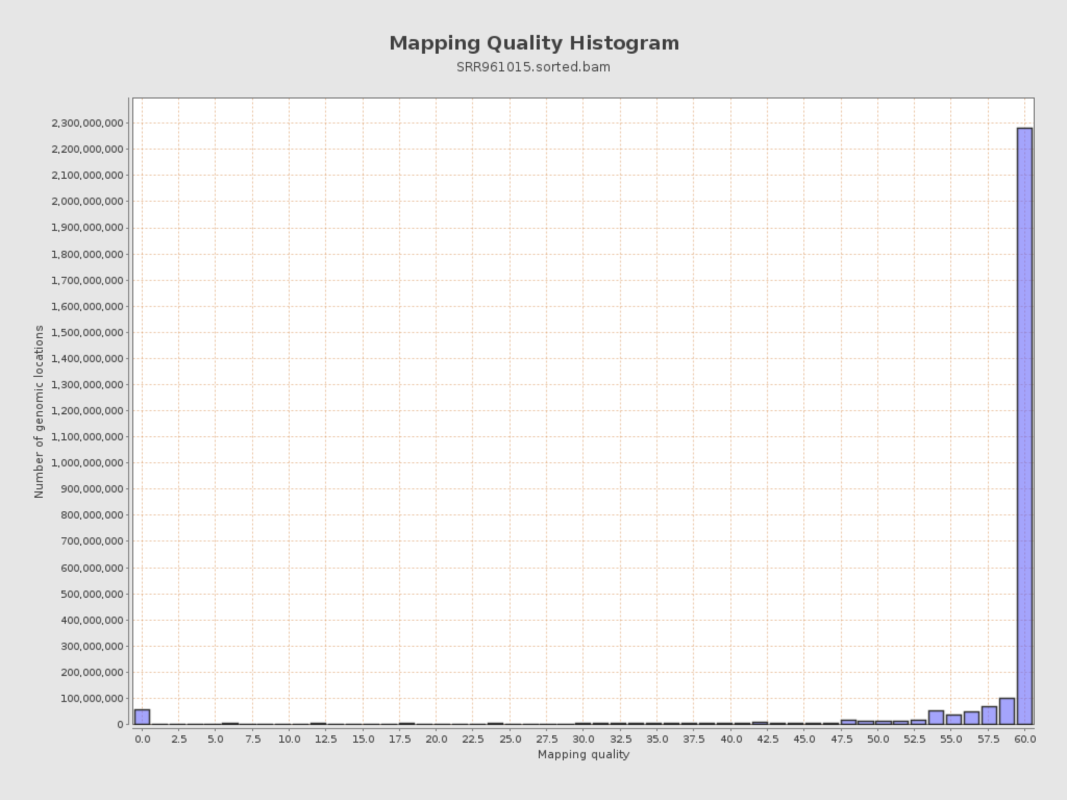
11. Results : Homopolymer Indels



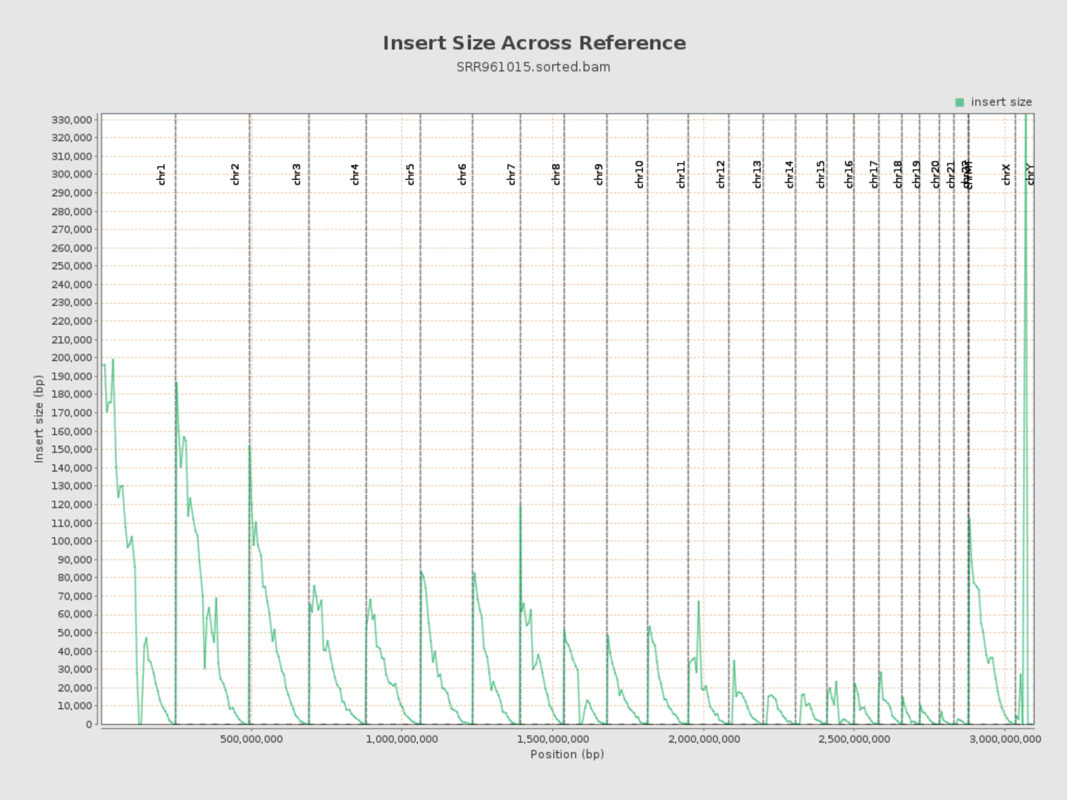
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram