Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 16:51:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960901.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_SRR960901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960901_1.fastq.gz SRR960901_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 16:51:06 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	108,027,796
Mapped reads	106,447,005 / 98.54%
Unmapped reads	1,580,791 / 1.46%
Mapped paired reads	106,447,005 / 98.54%
Mapped reads, first in pair	53,300,624 / 49.34%
Mapped reads, second in pair	53,146,381 / 49.2%
Mapped reads, both in pair	106,026,844 / 98.15%
Mapped reads, singletons	420,161 / 0.39%
Secondary alignments	0
Supplementary alignments	260,054 / 0.24%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	8,926,466 / 8.26%
Duplication rate	4.27%
Clipped reads	11,017,711 / 10.2%

2.2. ACGT Content

Number/percentage of A's	3,105,042,088 / 29.55%
Number/percentage of C's	2,143,870,153 / 20.4%
Number/percentage of T's	3,090,547,154 / 29.41%
Number/percentage of G's	2,168,410,579 / 20.64%
Number/percentage of N's	270,850 / 0%

GC Percentage	41.04%

2.3. Coverage

Mean	3.3955
Standard Deviation	37.3219

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	23,111
Standard Deviation	1,427,905.02
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	68,223,105
Insertions	1,156,257
Mapped reads with at least one insertion	1.05%
Deletions	1,273,277
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.53%

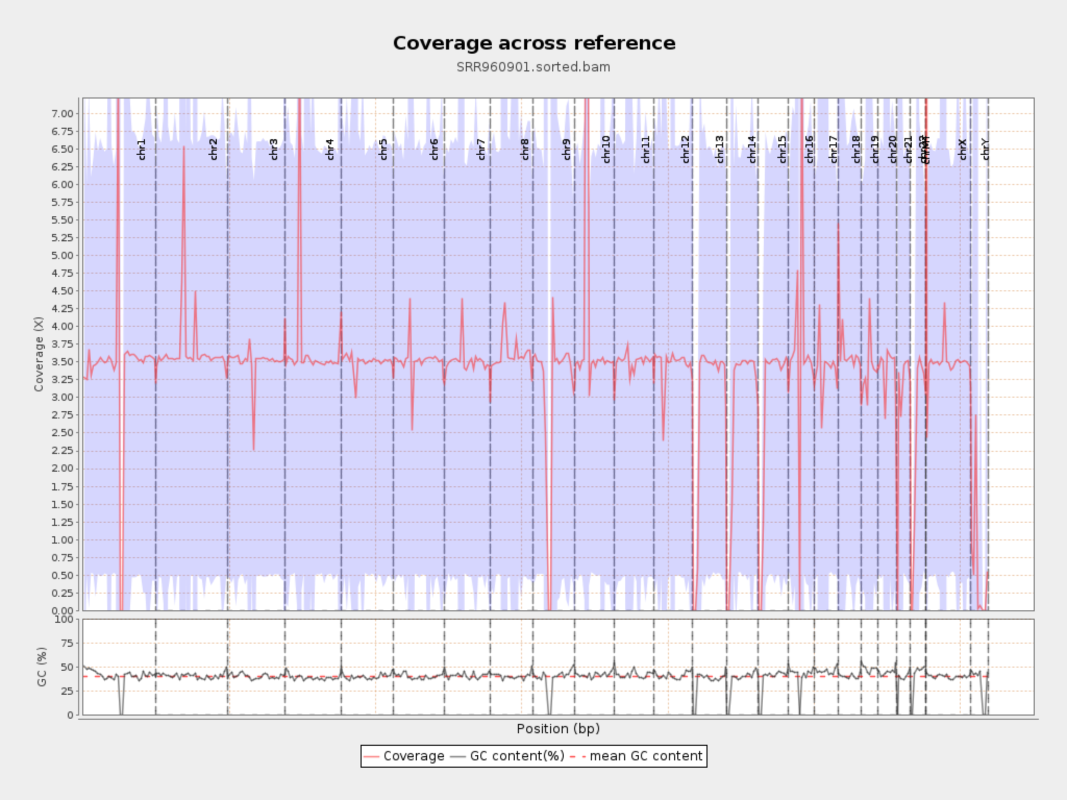
2.7. Chromosome stats

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

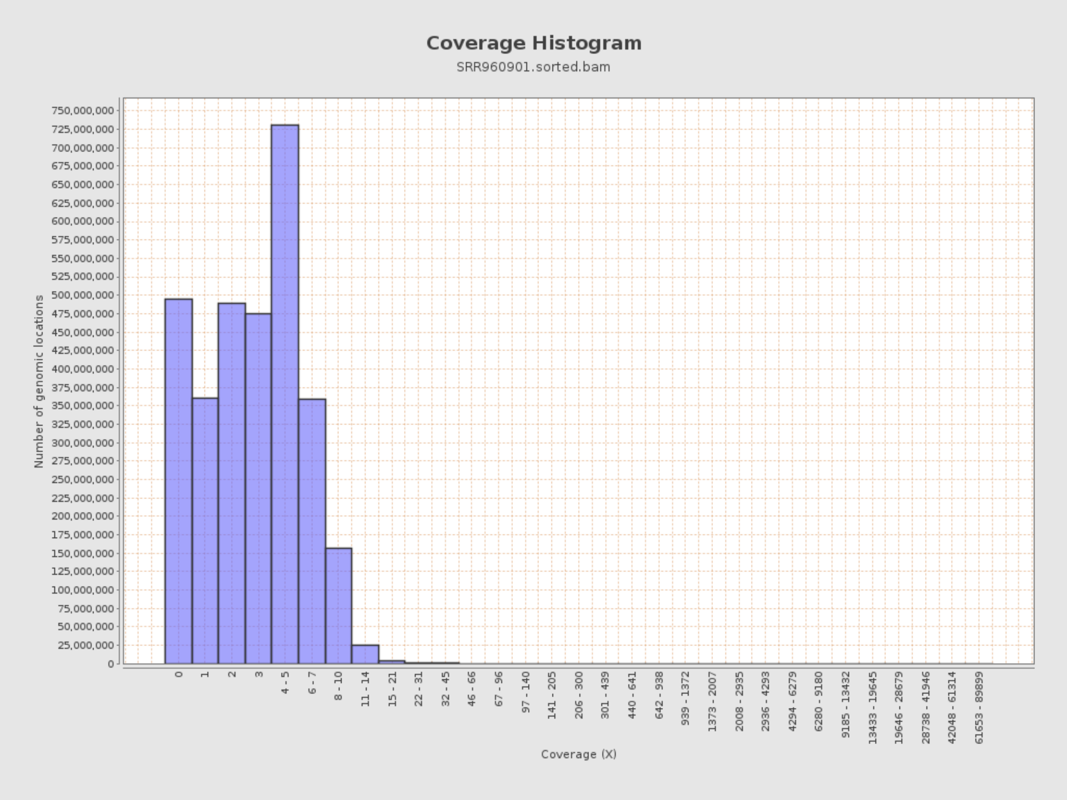
		bases	coverage	deviation
chr1	249250621	855019943	3.4304	89.6504
chr2	243199373	902146398	3.7095	23.5056
chr3	198022430	693607468	3.5027	7.5905
chr4	191154276	709875106	3.7136	32.2775
chr5	180915260	632720984	3.4973	4.0887
chr6	171115067	602253639	3.5196	10.9744
chr7	159138663	560960203	3.525	22.8705
chr8	146364022	529434940	3.6172	38.2514
chr9	141213431	438456581	3.1049	32.3402
chr10	135534747	547860488	4.0422	85.2665
chr11	135006516	472790661	3.502	14.9531
chr12	133851895	463639081	3.4638	5.5708
chr13	115169878	335356414	2.9118	2.6924
chr14	107349540	309692126	2.8849	3.6371
chr15	102531392	291046782	2.8386	2.7306
chr16	90354753	333836231	3.6947	34.8222
chr17	81195210	278188149	3.4262	14.2611
chr18	78077248	287246375	3.679	38.5989
chr19	59128983	201291248	3.4043	43.3627
chr20	63025520	215611866	3.421	12.574
chr21	48129895	144085292	2.9937	16.1898
chr22	51304566	121669484	2.3715	3.2405
chrMT	16571	8129756	490.6014	76.2515
chrX	155270560	541485776	3.4874	11.5202

chrY	59373566	34972481	0.589	34.4073

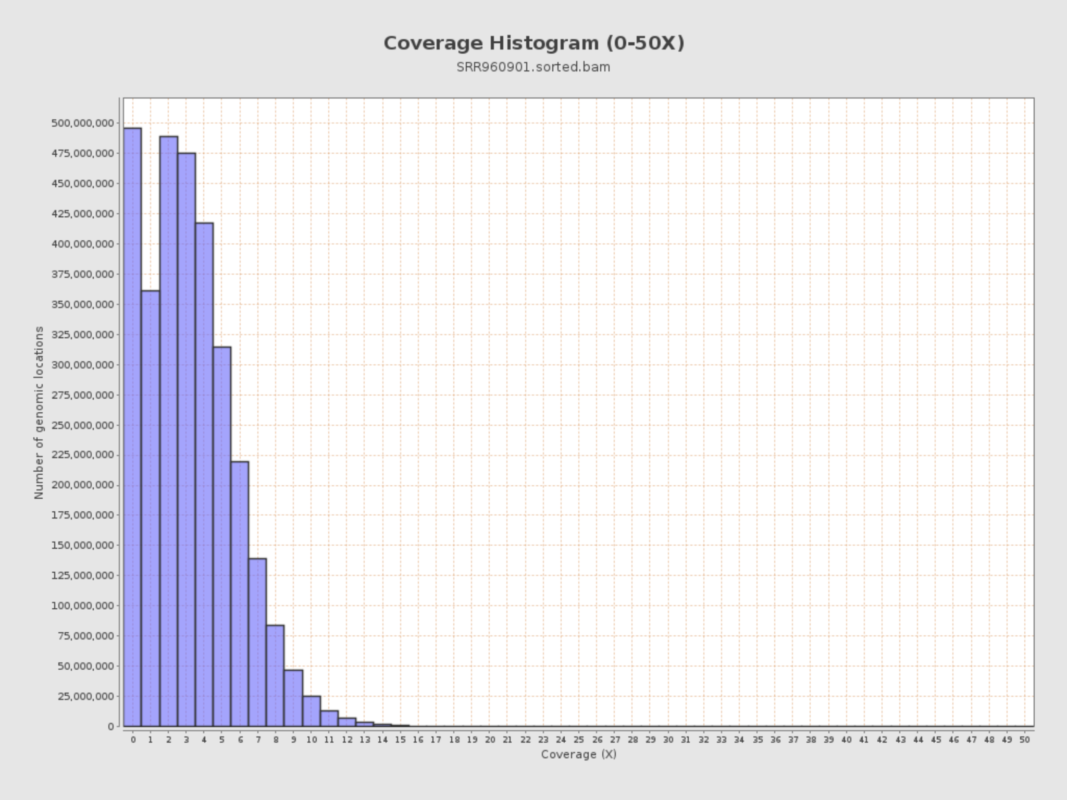
3. Results : Coverage across reference



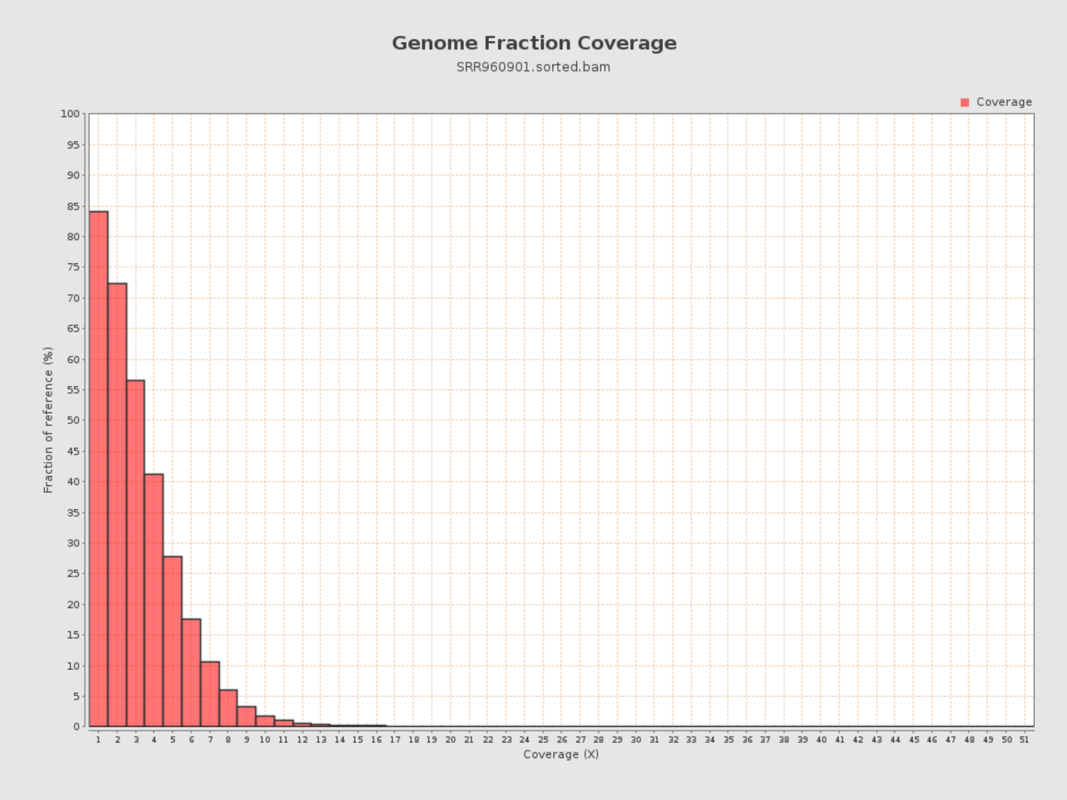
4. Results : Coverage Histogram



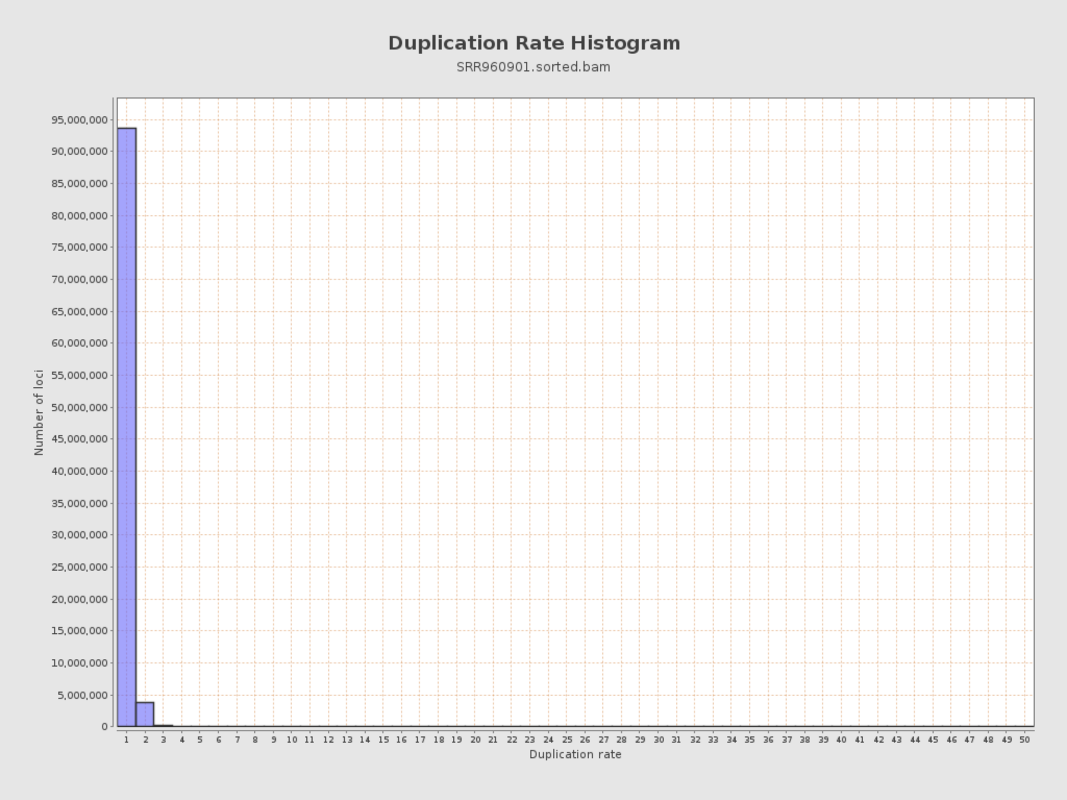
5. Results : Coverage Histogram (0-50X)



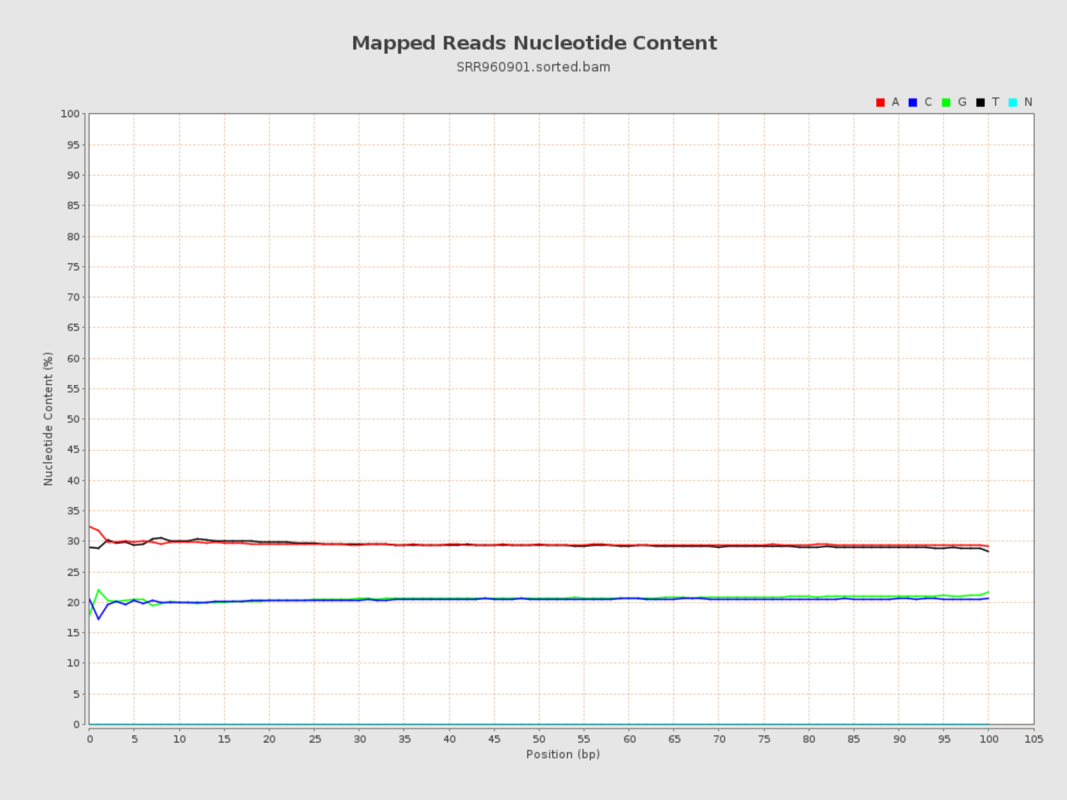
6. Results : Genome Fraction Coverage



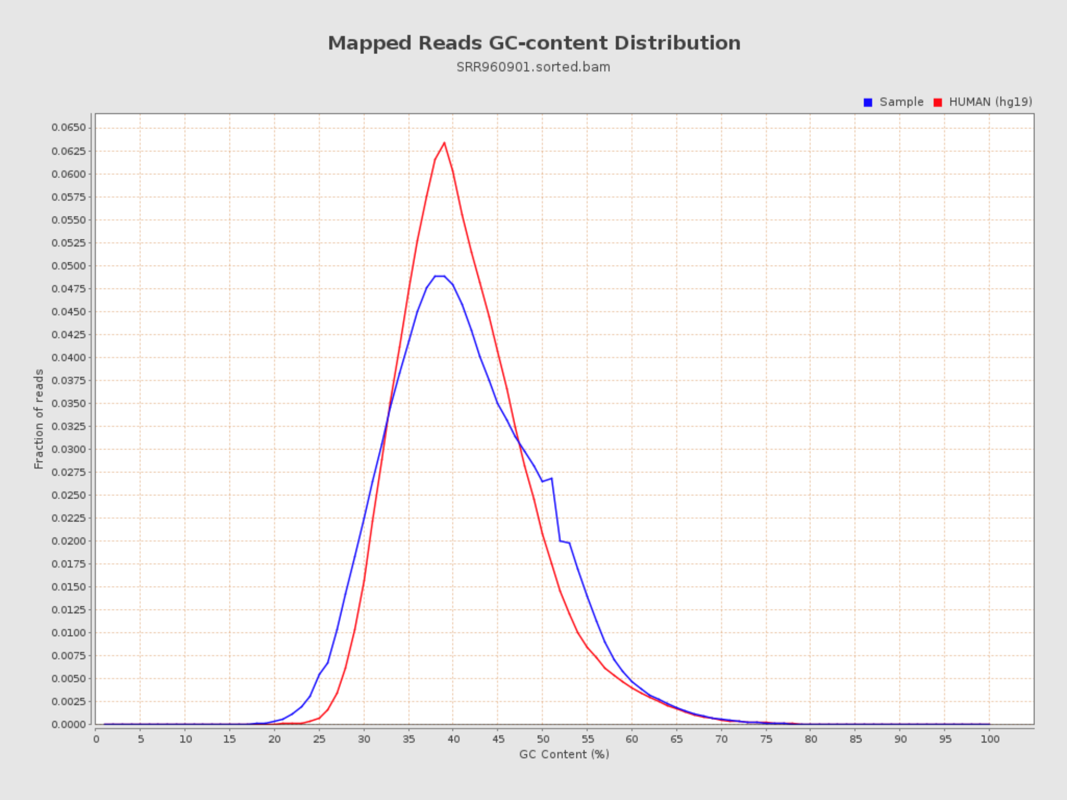
7. Results : Duplication Rate Histogram



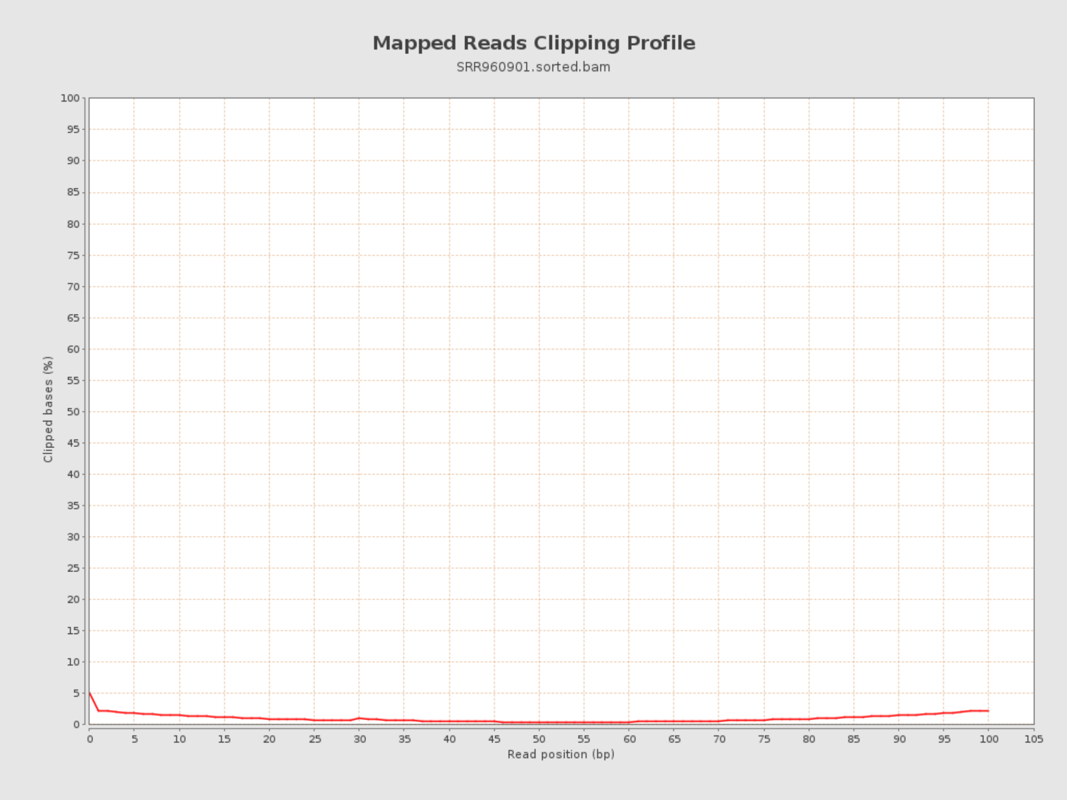
8. Results : Mapped Reads Nucleotide Content



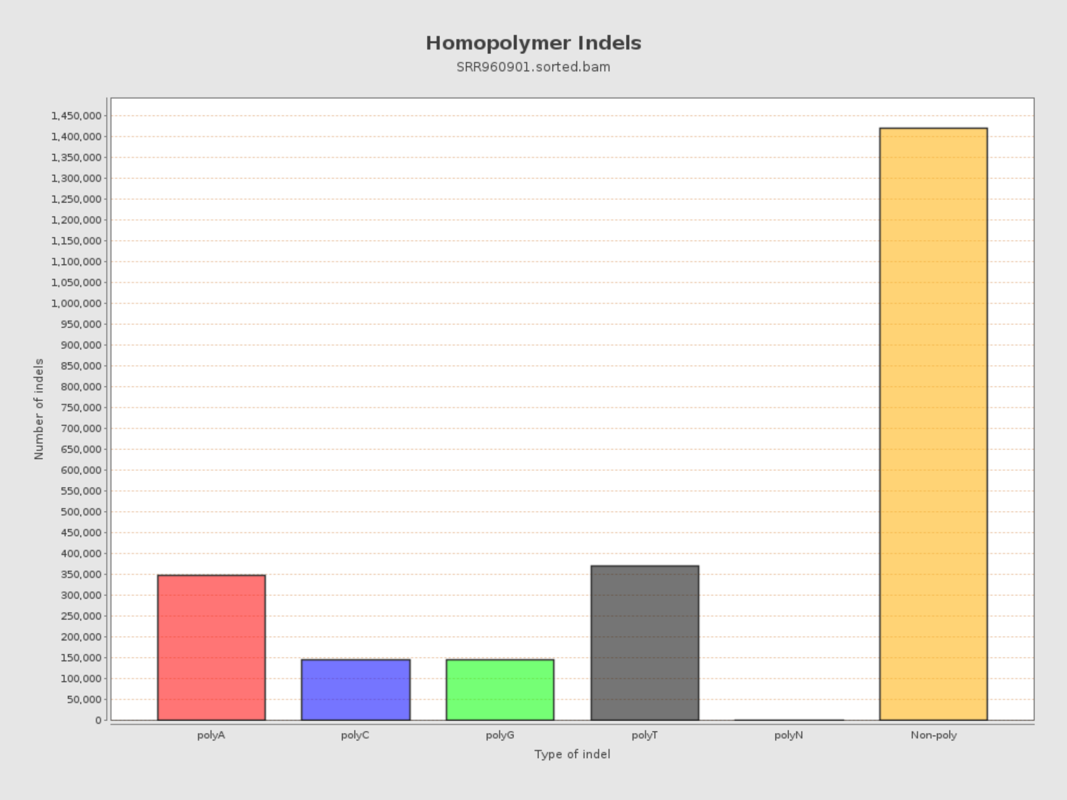
9. Results : Mapped Reads GC-content Distribution



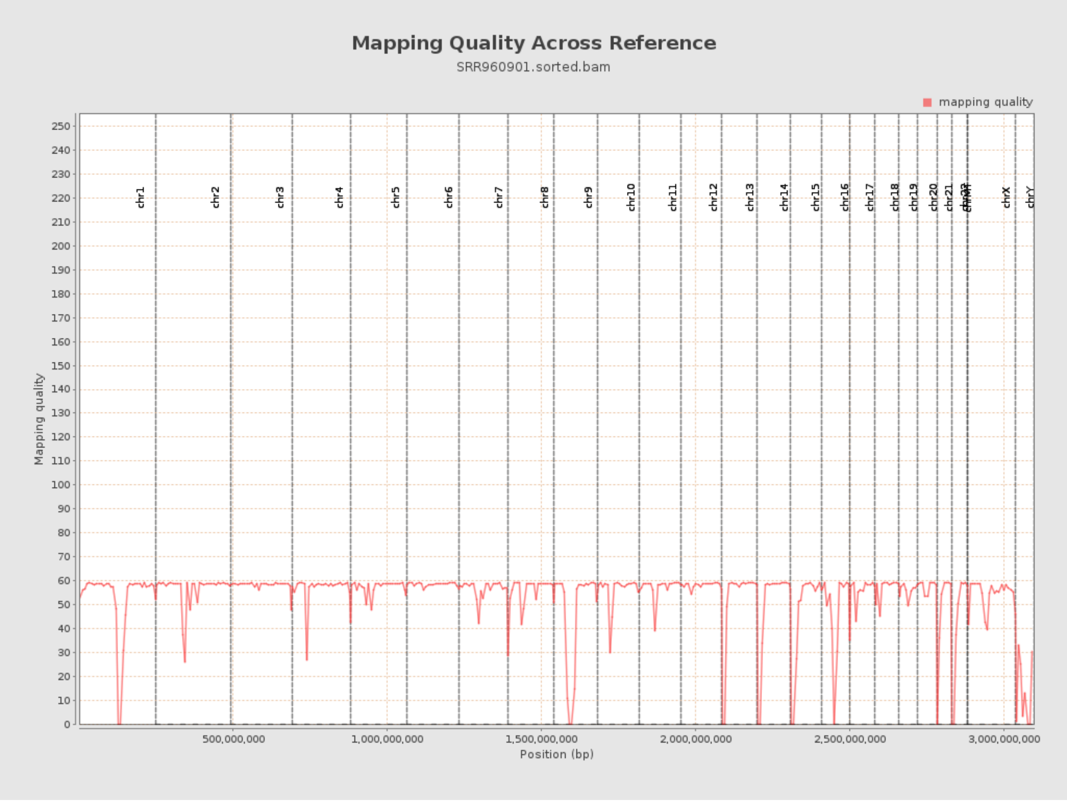
10. Results : Mapped Reads Clipping Profile



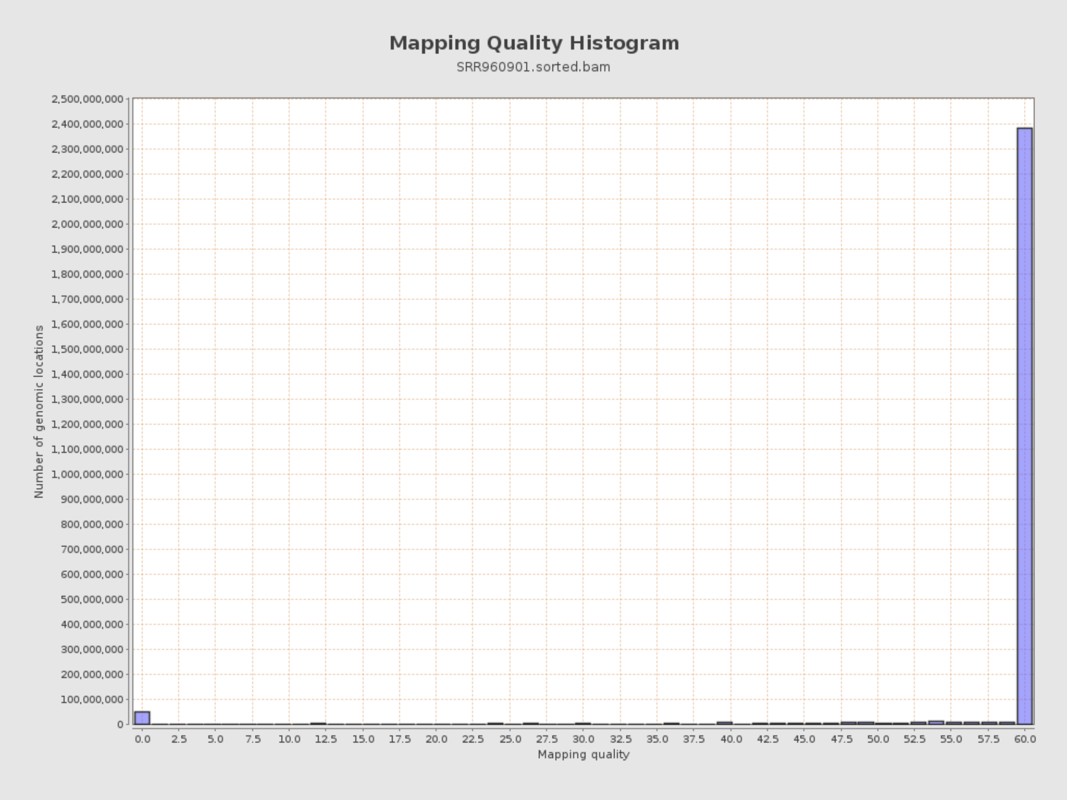
11. Results : Homopolymer Indels



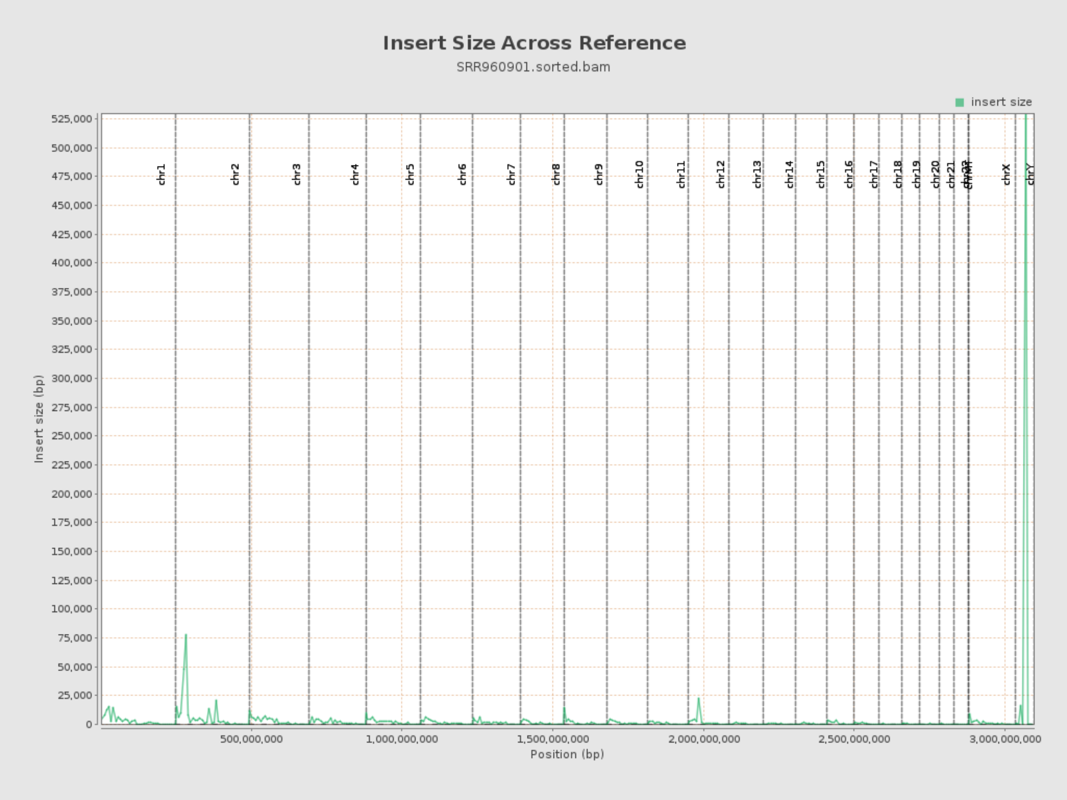
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram