Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 04:28:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927061.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_SRR927061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927061_1.fastq.gz SRR927061_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 04:28:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,802,858
Mapped reads	32,328,032 / 98.55%
Unmapped reads	474,826 / 1.45%
Mapped paired reads	32,328,032 / 98.55%
Mapped reads, first in pair	16,217,252 / 49.44%
Mapped reads, second in pair	16,110,780 / 49.11%
Mapped reads, both in pair	32,055,272 / 97.72%
Mapped reads, singletons	272,760 / 0.83%
Secondary alignments	0
Supplementary alignments	268,982 / 0.82%
Read min/max/mean length	30 / 101 / 101.34
Duplicated reads (estimated)	2,147,961 / 6.55%
Duplication rate	5.19%
Clipped reads	7,145,108 / 21.78%

2.2. ACGT Content

Number/percentage of A's	892,587,662 / 28.95%
Number/percentage of C's	614,594,892 / 19.94%
Number/percentage of T's	902,564,208 / 29.28%
Number/percentage of G's	672,551,242 / 21.82%
Number/percentage of N's	543,687 / 0.02%

GC Percentage	41.75%

2.3. Coverage

Mean	0.9966
Standard Deviation	3.8337

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	83,402.87
Standard Deviation	2,814,293.88
P25/Median/P75	150 / 193 / 257

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	31,305,819
Insertions	503,201
Mapped reads with at least one insertion	1.53%
Deletions	1,665,141
Mapped reads with at least one deletion	5.01%
Homopolymer indels	53.09%

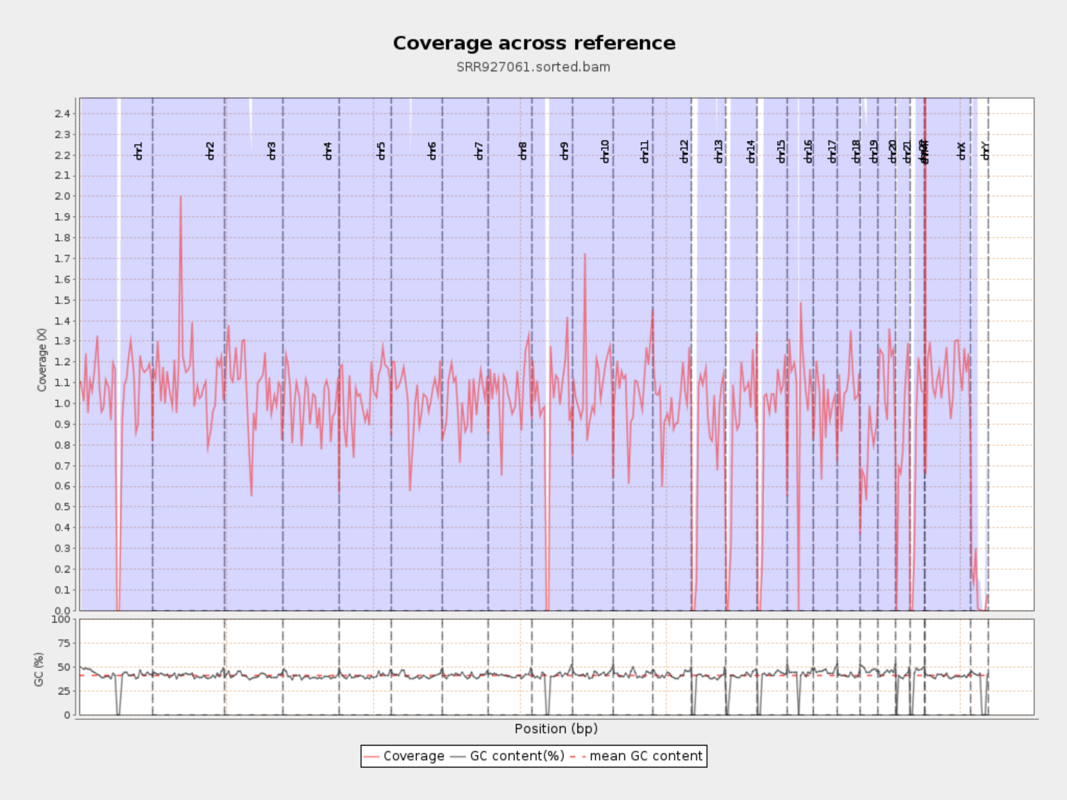
2.7. Chromosome stats

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

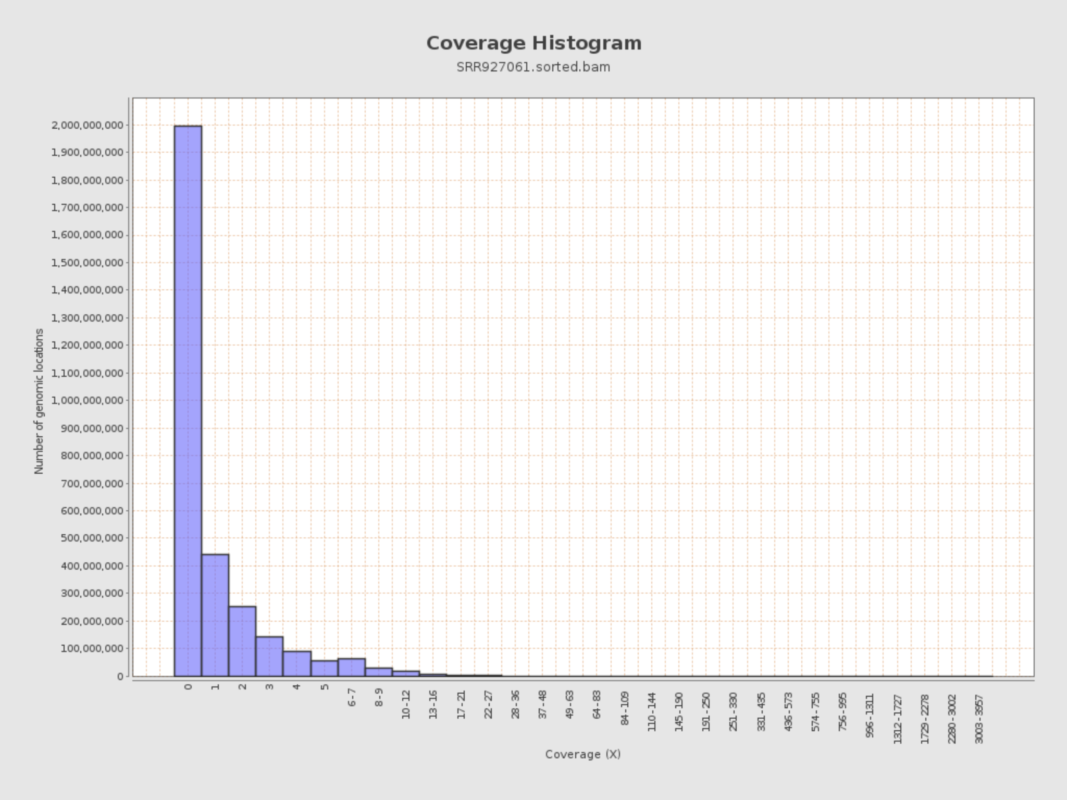
		bases	coverage	deviation
chr1	249250621	257031421	1.0312	4.5669
chr2	243199373	274062945	1.1269	6.4843
chr3	198022430	213624046	1.0788	2.1235
chr4	191154276	191626354	1.0025	3.0972
chr5	180915260	188353094	1.0411	2.0345
chr6	171115067	176742900	1.0329	2.0658
chr7	159138663	160427604	1.0081	2.6566
chr8	146364022	155104628	1.0597	2.4002
chr9	141213431	136116537	0.9639	5.1143
chr10	135534747	148797266	1.0979	8.3423
chr11	135006516	144324660	1.069	2.7875
chr12	133851895	133652117	0.9985	2.0271
chr13	115169878	95557450	0.8297	1.8235
chr14	107349540	91929552	0.8564	1.9483
chr15	102531392	86702991	0.8456	1.8974
chr16	90354753	93750744	1.0376	5.0107
chr17	81195210	78556832	0.9675	2.6448
chr18	78077248	84795383	1.086	5.0646
chr19	59128983	44719417	0.7563	2.742
chr20	63025520	72806618	1.1552	2.4193
chr21	48129895	39745366	0.8258	2.7562
chr22	51304566	36850990	0.7183	1.8564
chrMT	16571	223317	13.4764	10.1917
chrX	155270560	174593575	1.1244	2.3651

chrY	59373566	5080557	0.0856	3.8251

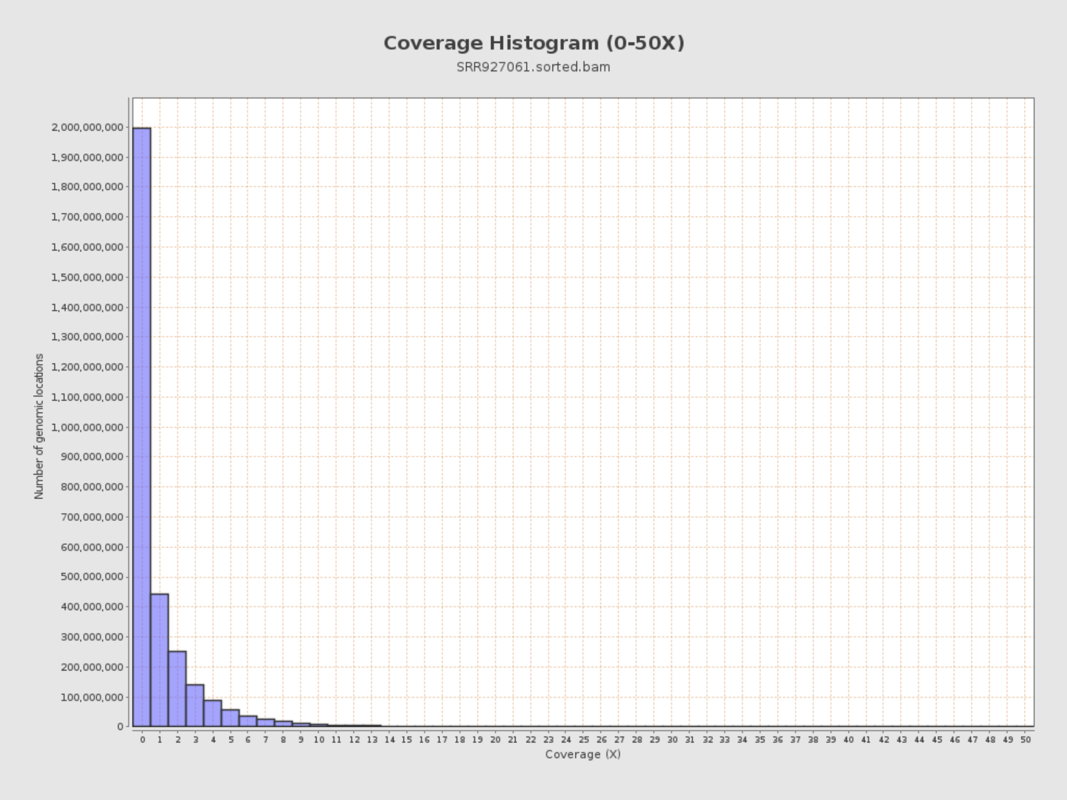
3. Results : Coverage across reference



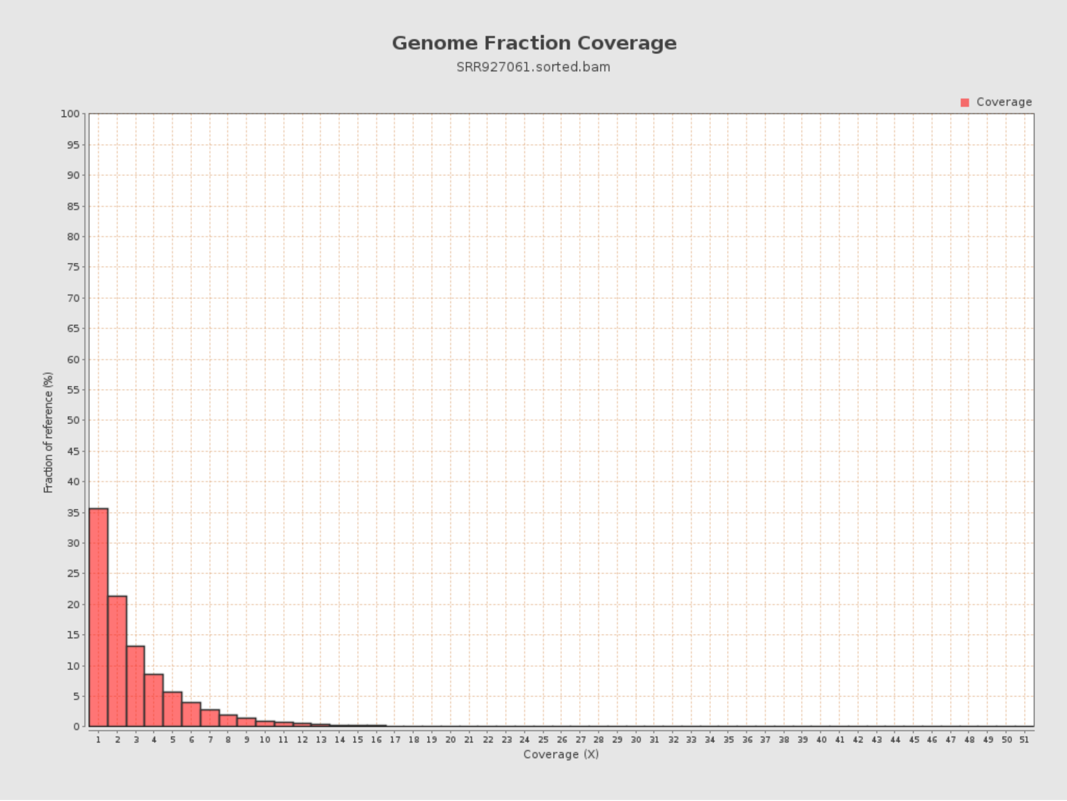
4. Results : Coverage Histogram



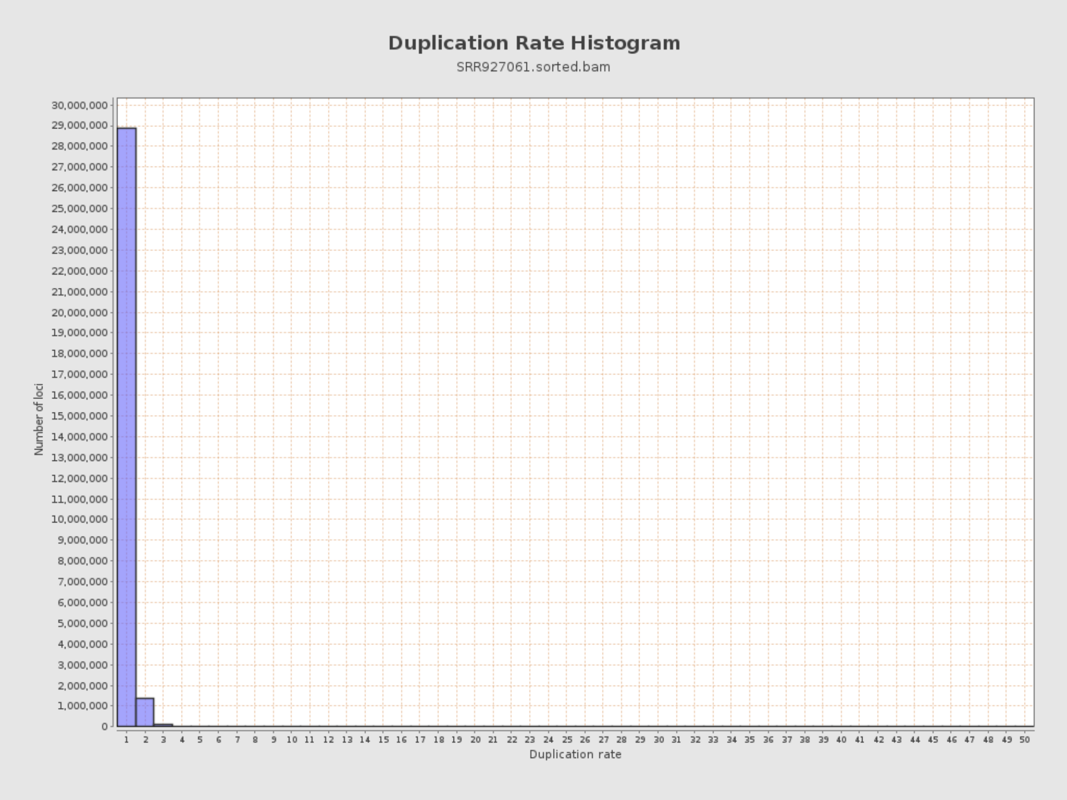
5. Results : Coverage Histogram (0-50X)



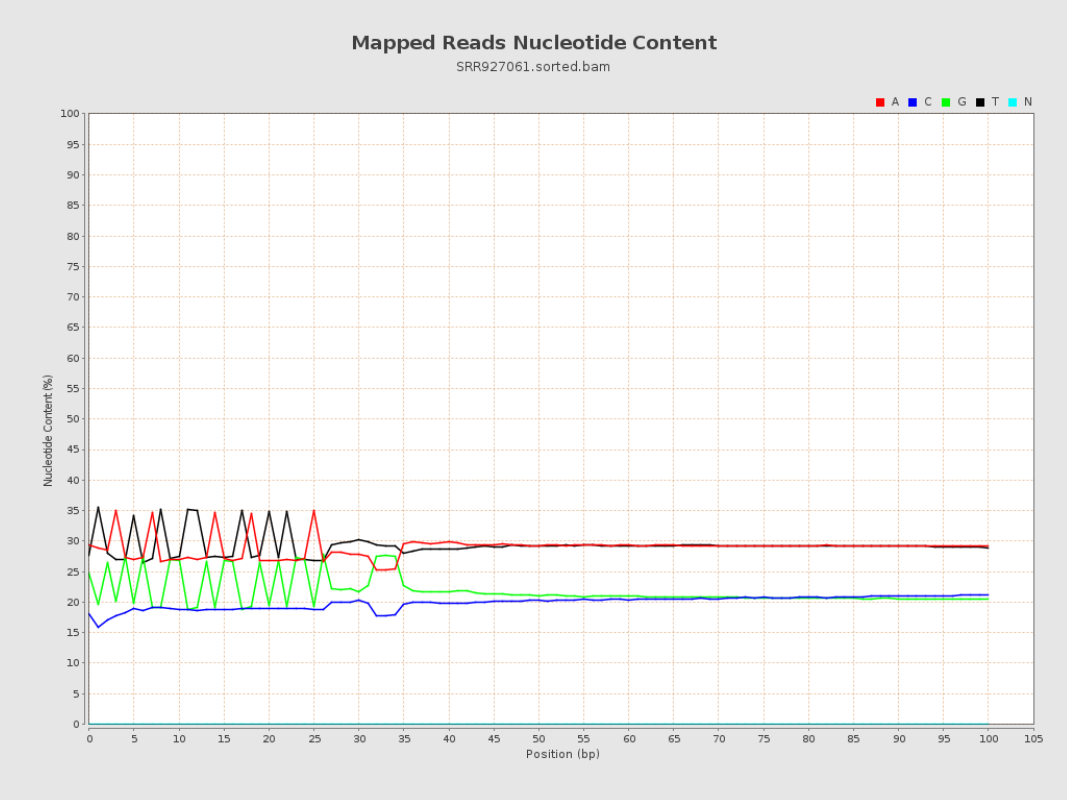
6. Results : Genome Fraction Coverage



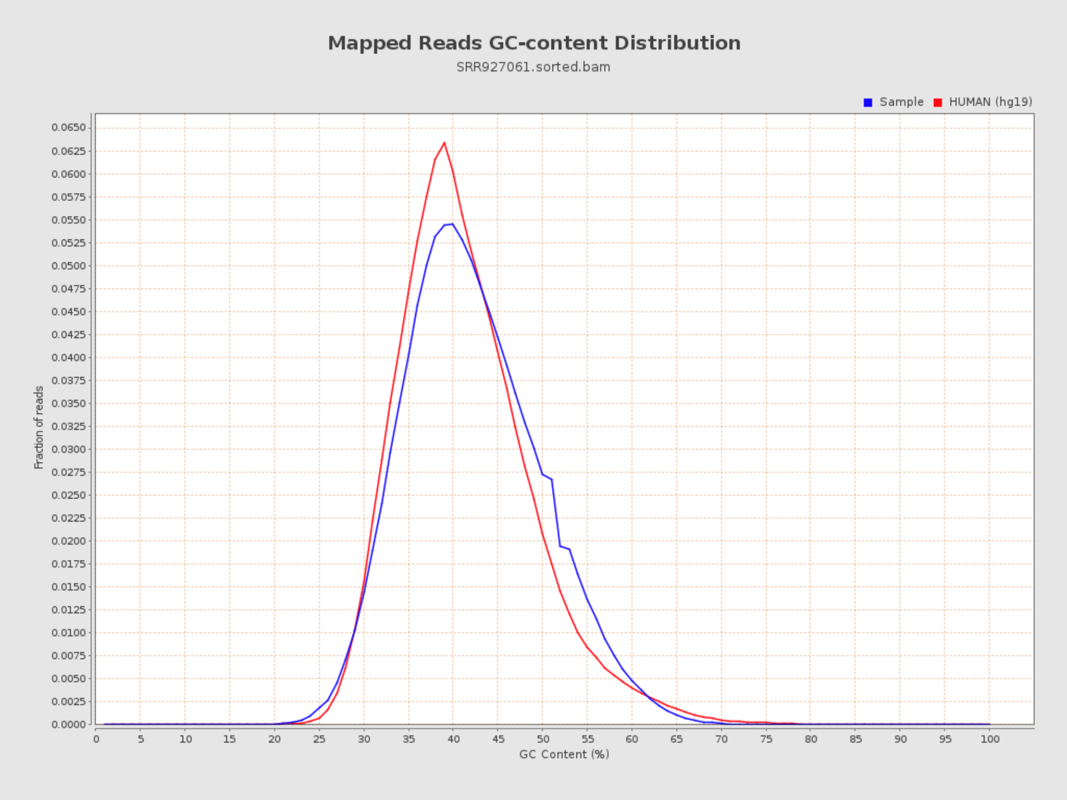
7. Results : Duplication Rate Histogram



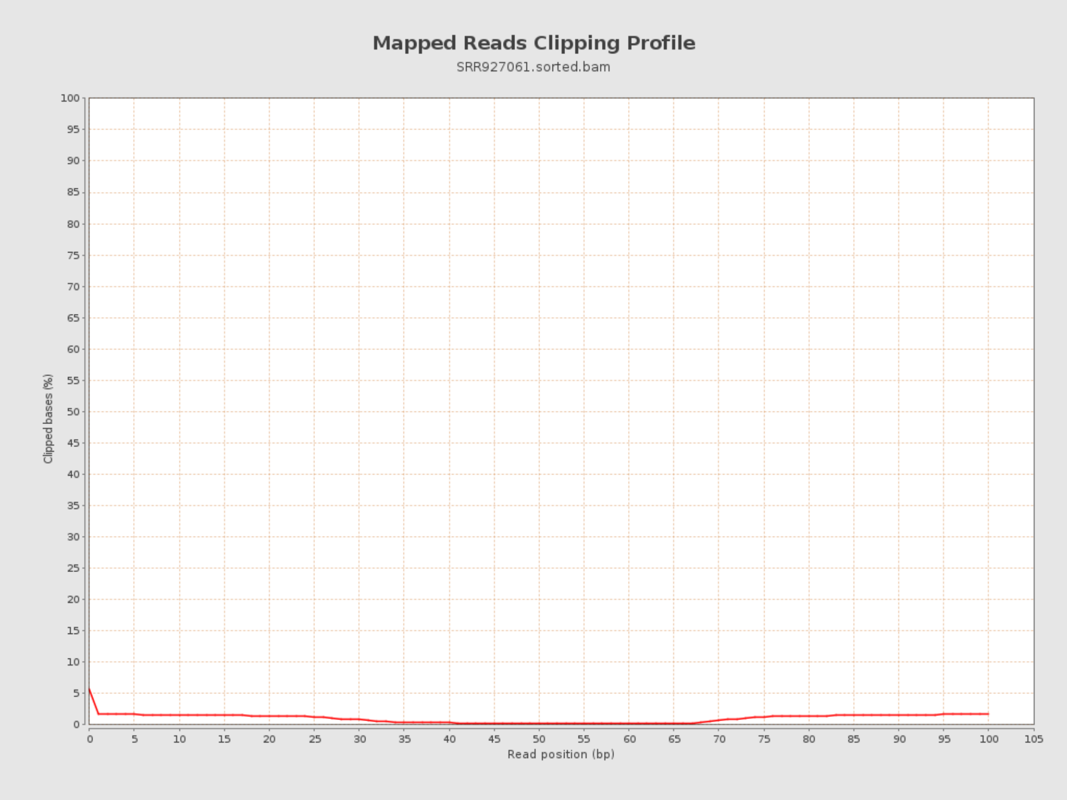
8. Results : Mapped Reads Nucleotide Content



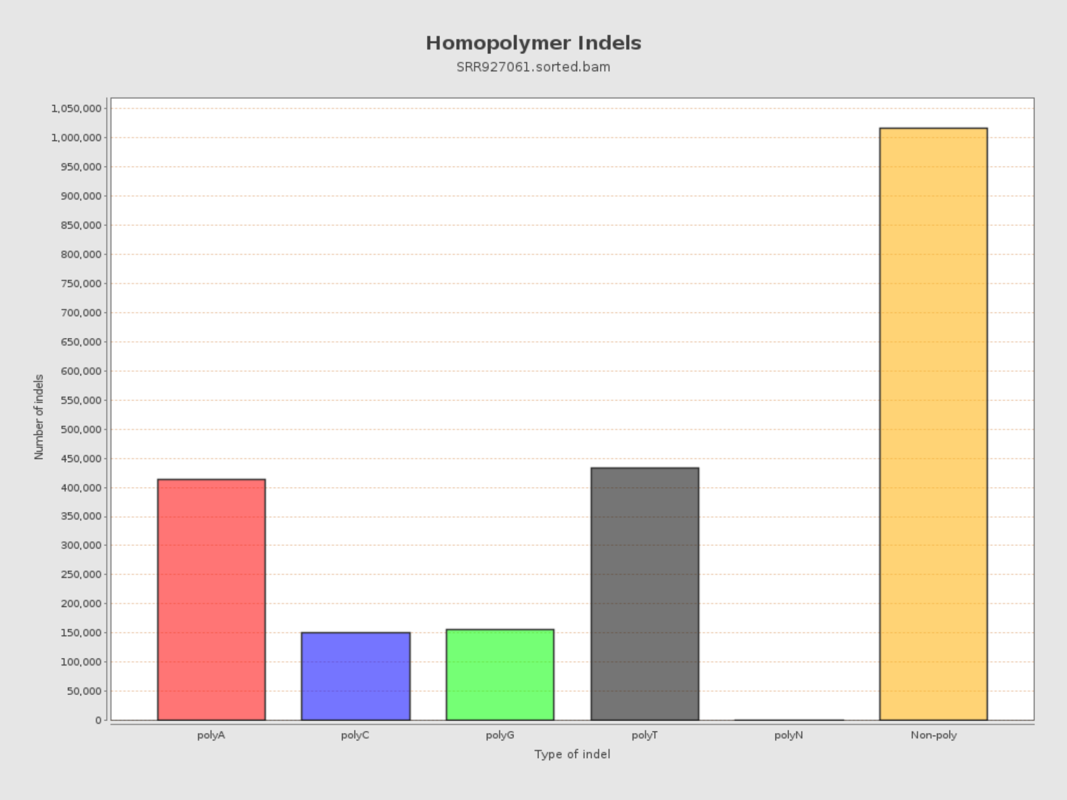
9. Results : Mapped Reads GC-content Distribution



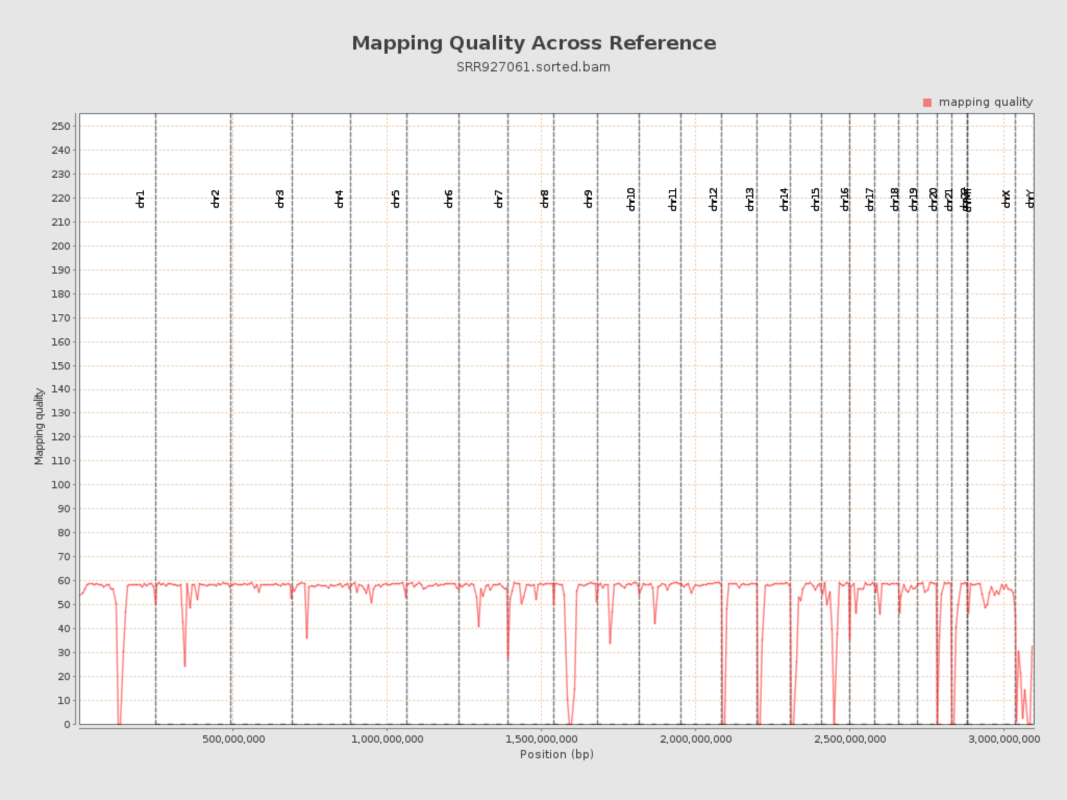
10. Results : Mapped Reads Clipping Profile



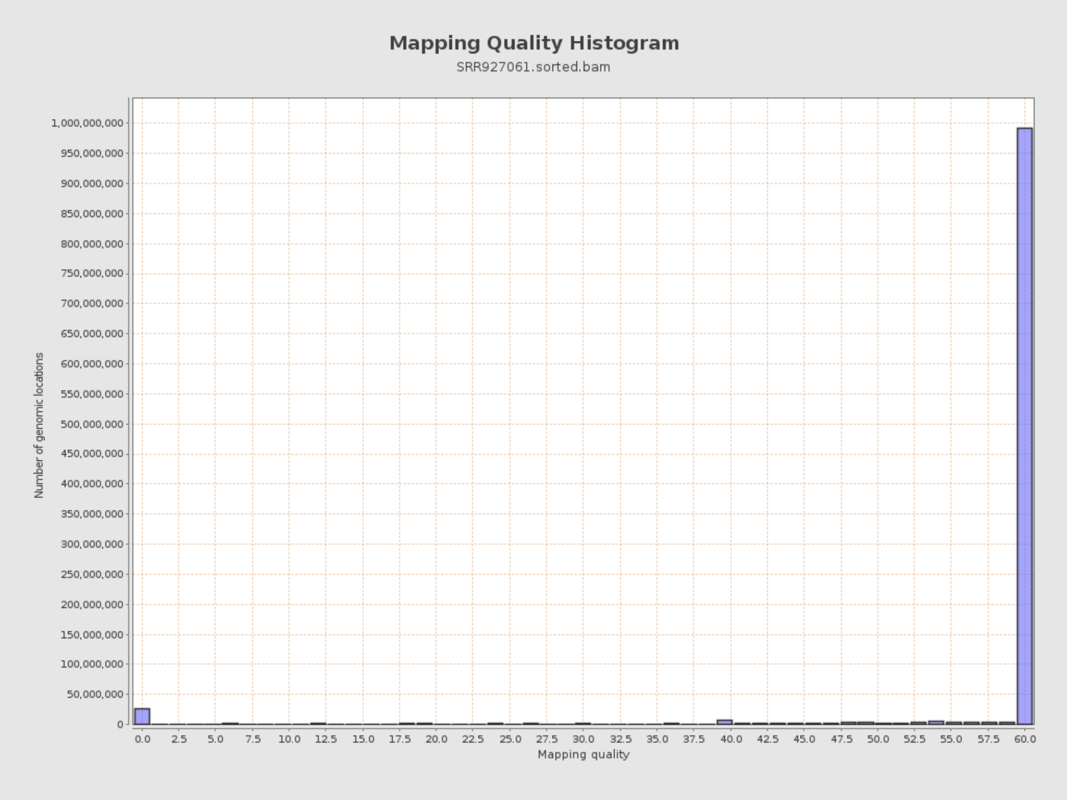
11. Results : Homopolymer Indels



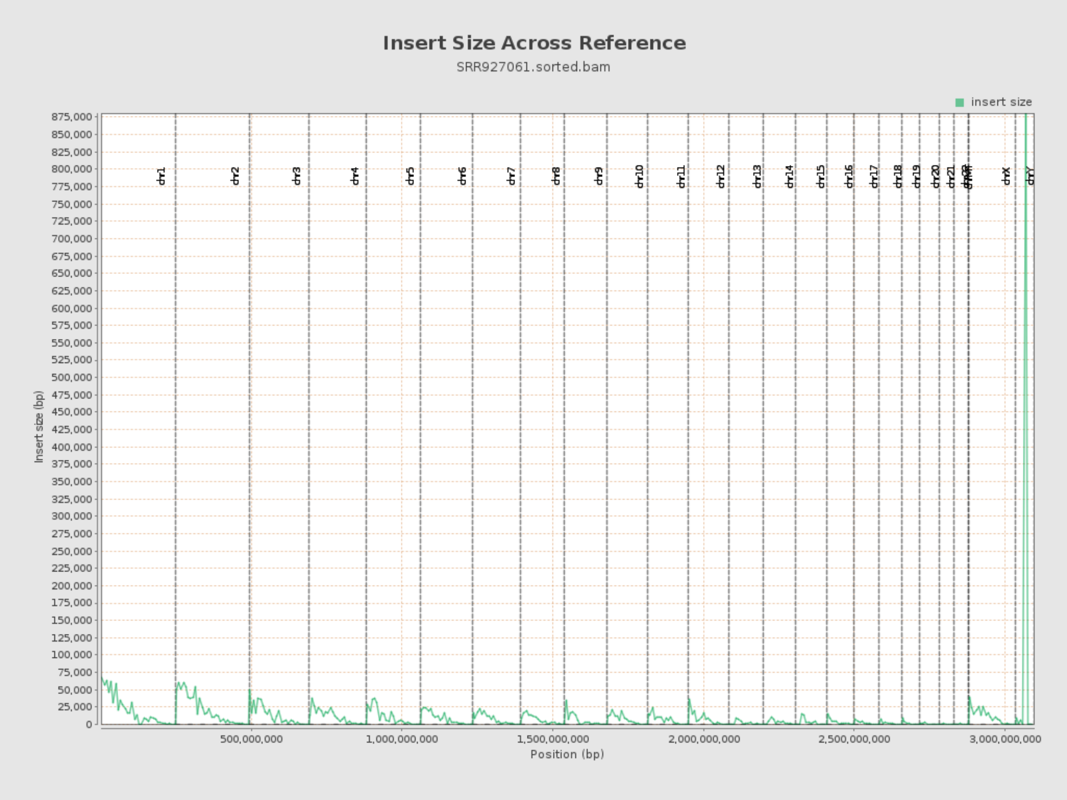
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram