Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 03:56:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927060.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_SRR927060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927060_1.fastq.gz SRR927060_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 03:56:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,861,440
Mapped reads	21,276,264 / 97.32%
Unmapped reads	585,176 / 2.68%
Mapped paired reads	21,276,264 / 97.32%
Mapped reads, first in pair	10,686,980 / 48.89%
Mapped reads, second in pair	10,589,284 / 48.44%
Mapped reads, both in pair	20,919,148 / 95.69%
Mapped reads, singletons	357,116 / 1.63%
Secondary alignments	0
Supplementary alignments	402,553 / 1.84%
Read min/max/mean length	30 / 101 / 101.76
Duplicated reads (estimated)	1,688,127 / 7.72%
Duplication rate	6.23%
Clipped reads	9,728,498 / 44.5%

2.2. ACGT Content

Number/percentage of A's	549,939,765 / 28.72%
Number/percentage of C's	365,672,443 / 19.1%
Number/percentage of T's	563,049,444 / 29.41%
Number/percentage of G's	435,801,976 / 22.76%
Number/percentage of N's	260,837 / 0.01%

GC Percentage	41.86%

2.3. Coverage

Mean	0.619
Standard Deviation	2.4492

2.4. Mapping Quality

Mean Mapping Quality	53.04

2.5. Insert size

Mean	207,198.83
Standard Deviation	4,455,481.32
P25/Median/P75	140 / 182 / 246

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	19,964,217
Insertions	312,730
Mapped reads with at least one insertion	1.45%
Deletions	943,967
Mapped reads with at least one deletion	4.33%
Homopolymer indels	51.82%

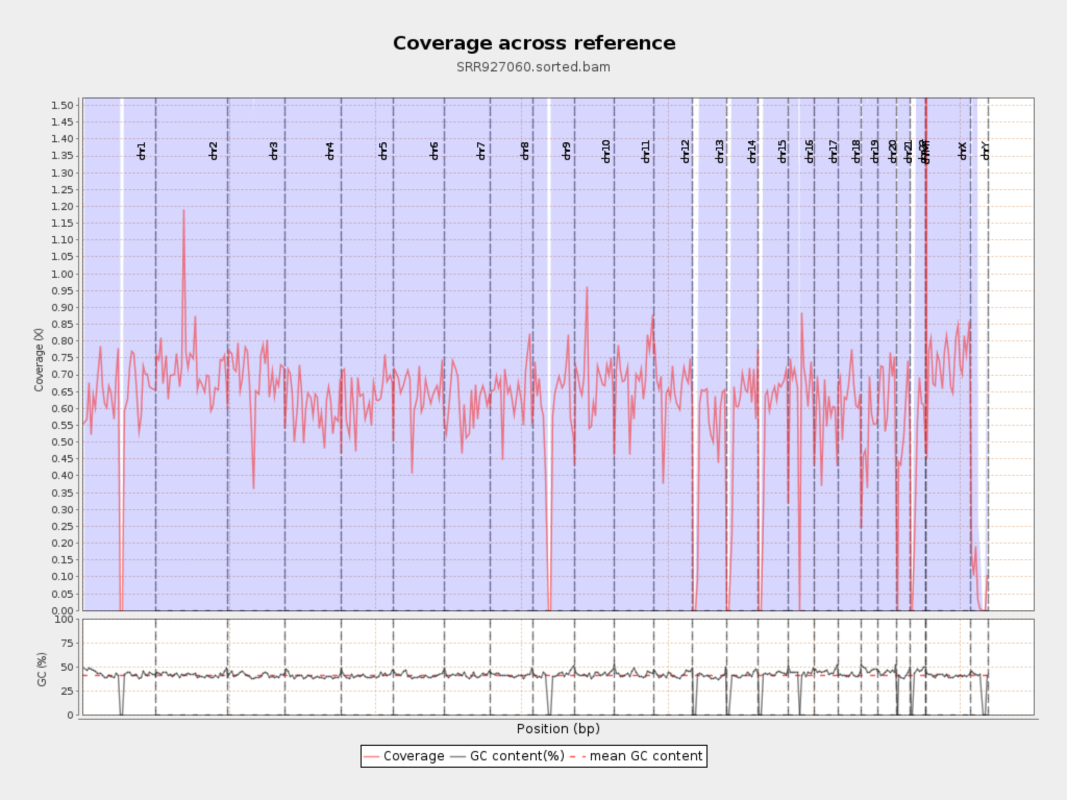
2.7. Chromosome stats

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

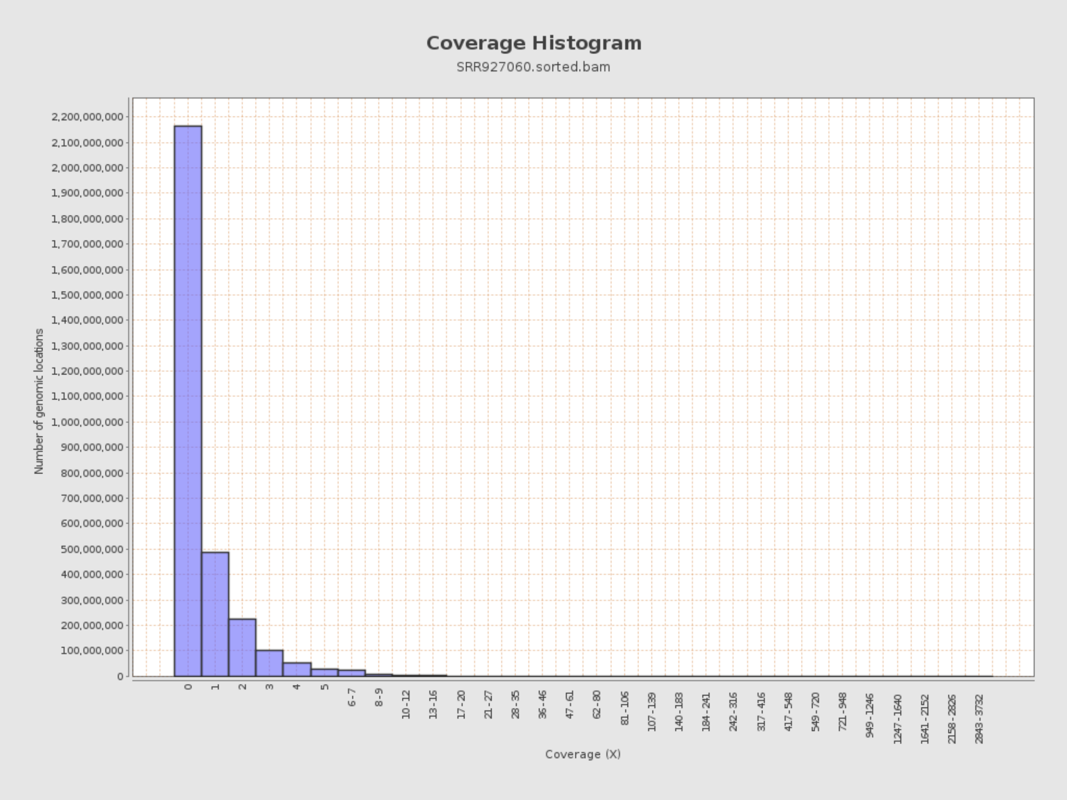
		bases	coverage	deviation
chr1	249250621	153153746	0.6145	3.8472
chr2	243199373	176262549	0.7248	4.0825
chr3	198022430	137196706	0.6928	1.3969
chr4	191154276	116558301	0.6098	2.0913
chr5	180915260	114645423	0.6337	1.3064
chr6	171115067	111474957	0.6515	1.4322
chr7	159138663	97255045	0.6111	1.9516
chr8	146364022	95363793	0.6516	1.631
chr9	141213431	80100998	0.5672	2.9602
chr10	135534747	92291733	0.6809	3.9337
chr11	135006516	93486479	0.6925	2.3482
chr12	133851895	88191574	0.6589	1.3715
chr13	115169878	56797865	0.4932	1.1503
chr14	107349540	57837013	0.5388	1.2904
chr15	102531392	54802435	0.5345	1.255
chr16	90354753	56377471	0.624	2.9482
chr17	81195210	46864777	0.5772	1.9293
chr18	78077248	50288785	0.6441	3.0459
chr19	59128983	30470472	0.5153	2.2165
chr20	63025520	42022521	0.6668	1.4589
chr21	48129895	24020576	0.4991	1.7048
chr22	51304566	21565128	0.4203	1.1568
chrMT	16571	384668	23.2133	16.5418
chrX	155270560	114424424	0.7369	1.7101

chrY	59373566	4253510	0.0716	1.7432

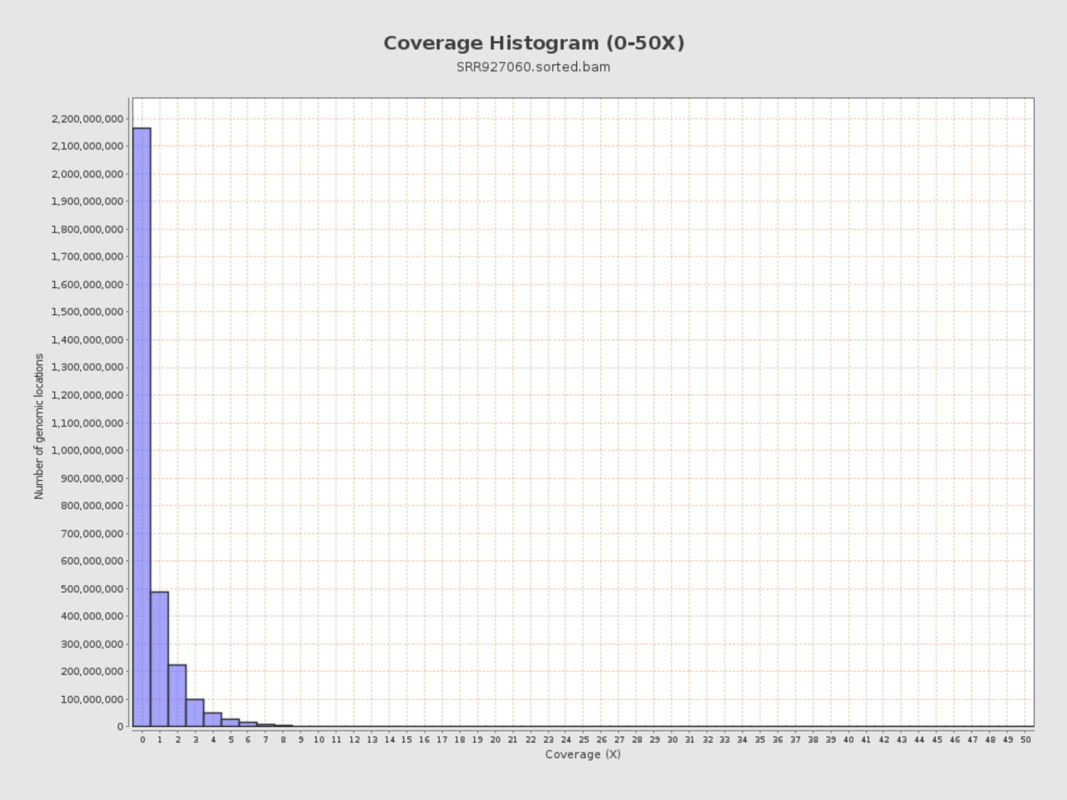
3. Results : Coverage across reference



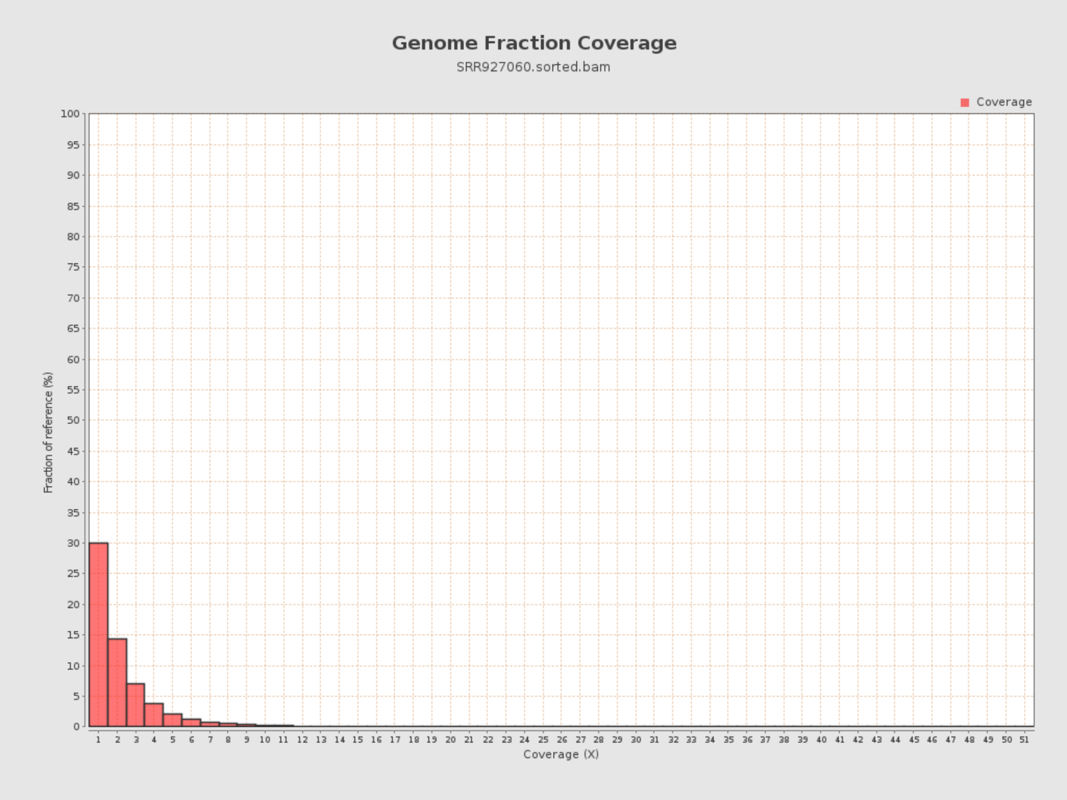
4. Results : Coverage Histogram



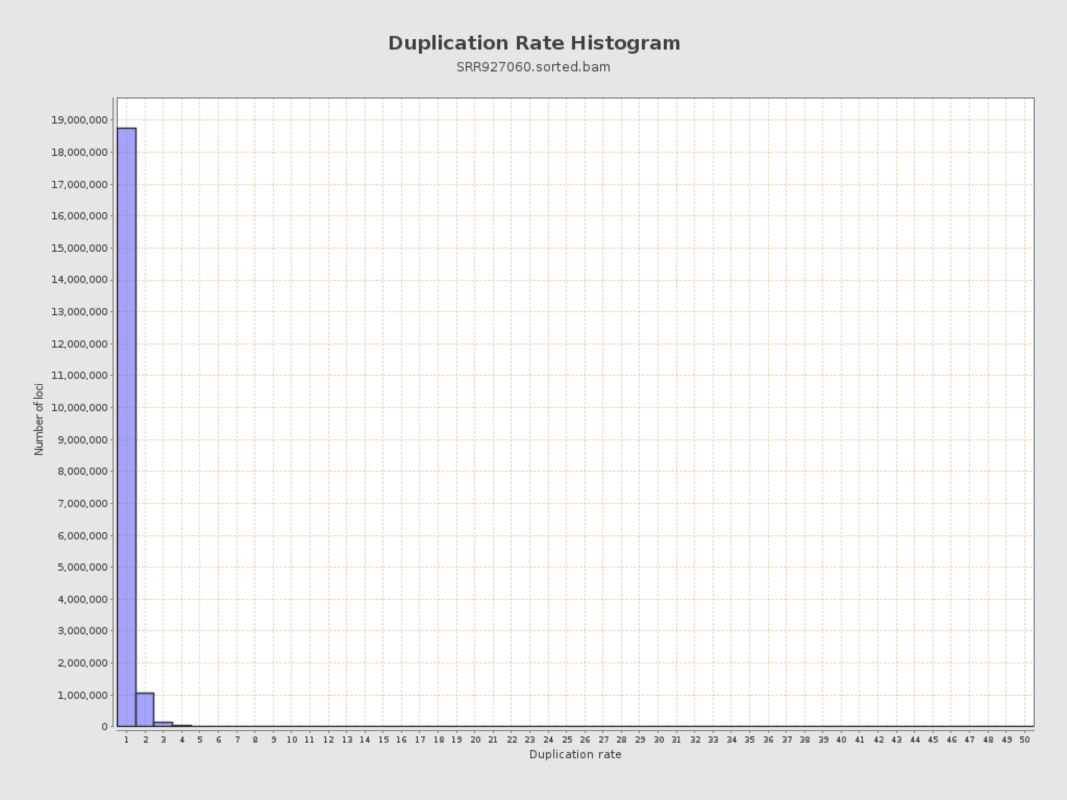
5. Results : Coverage Histogram (0-50X)



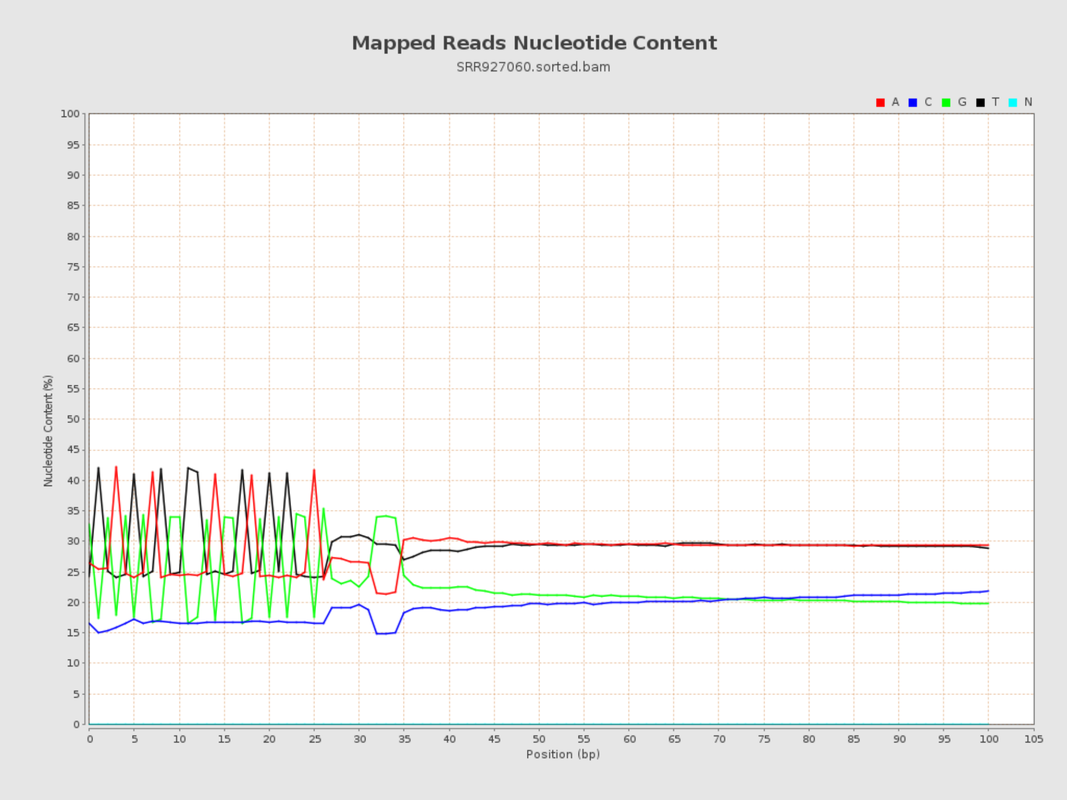
6. Results : Genome Fraction Coverage



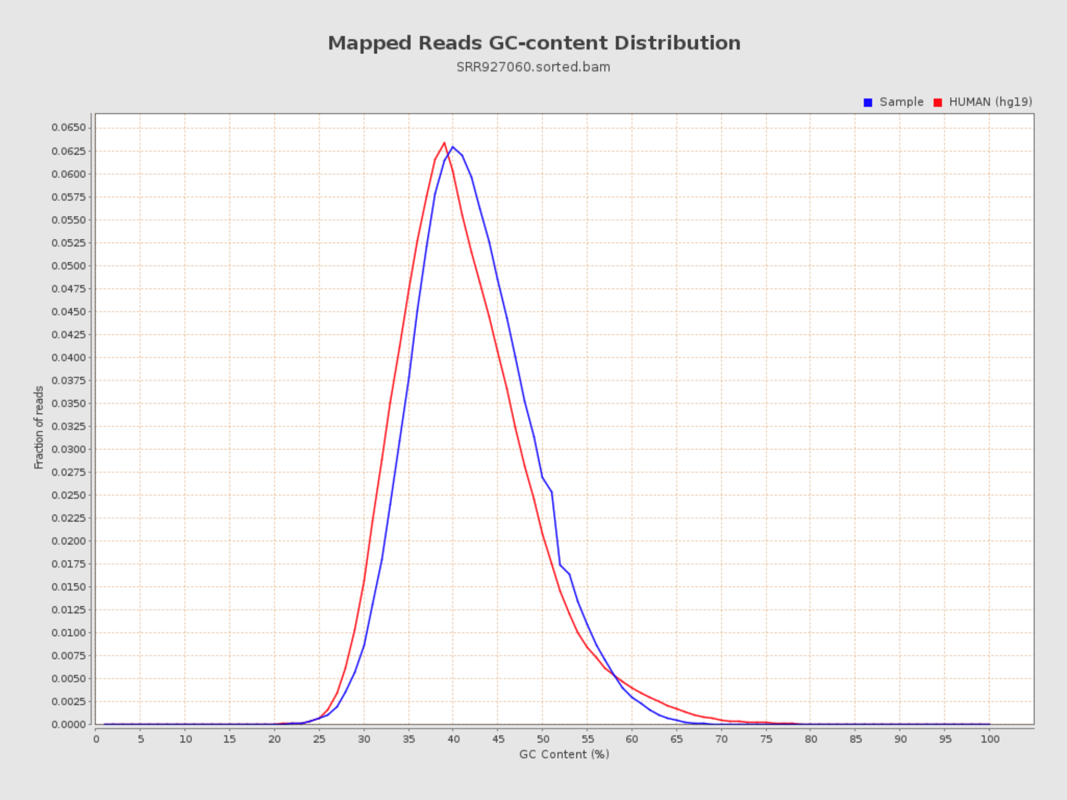
7. Results : Duplication Rate Histogram



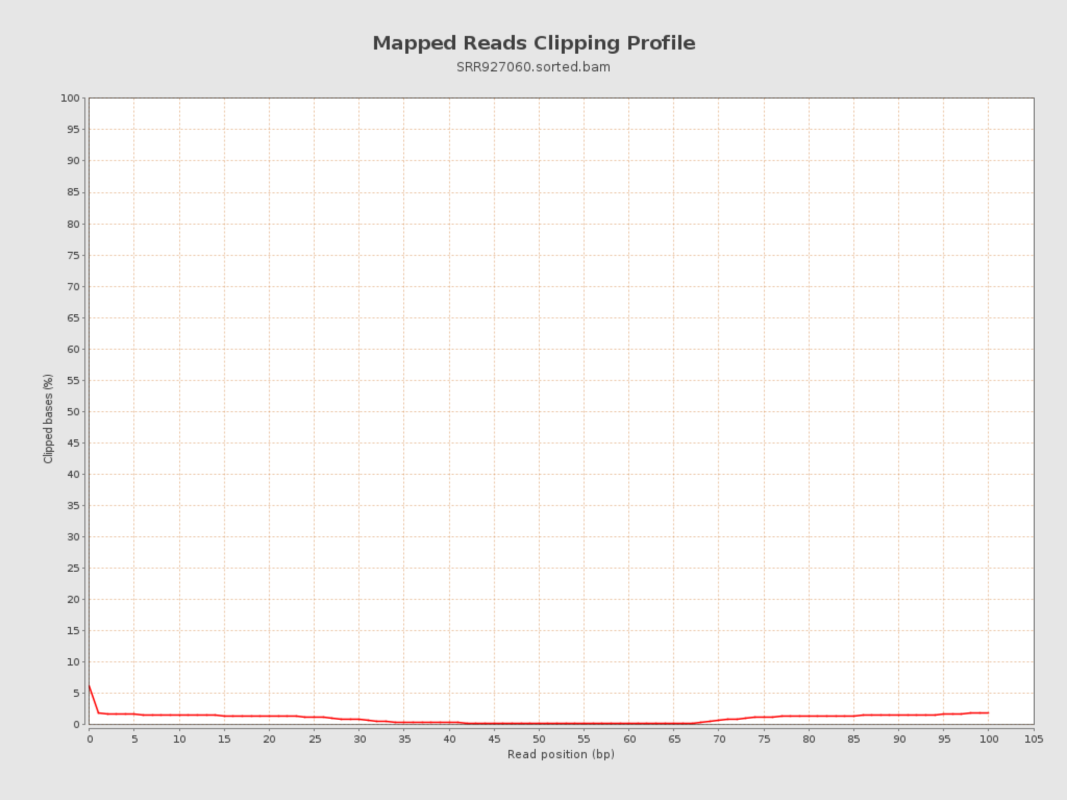
8. Results : Mapped Reads Nucleotide Content



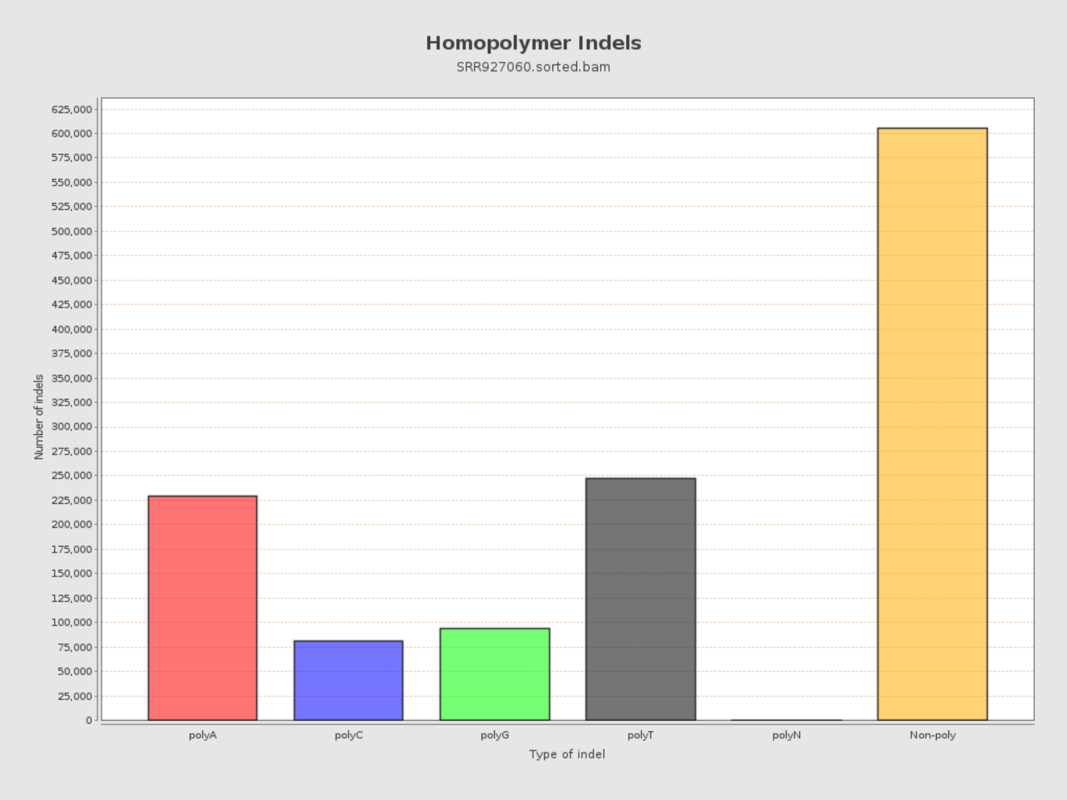
9. Results : Mapped Reads GC-content Distribution



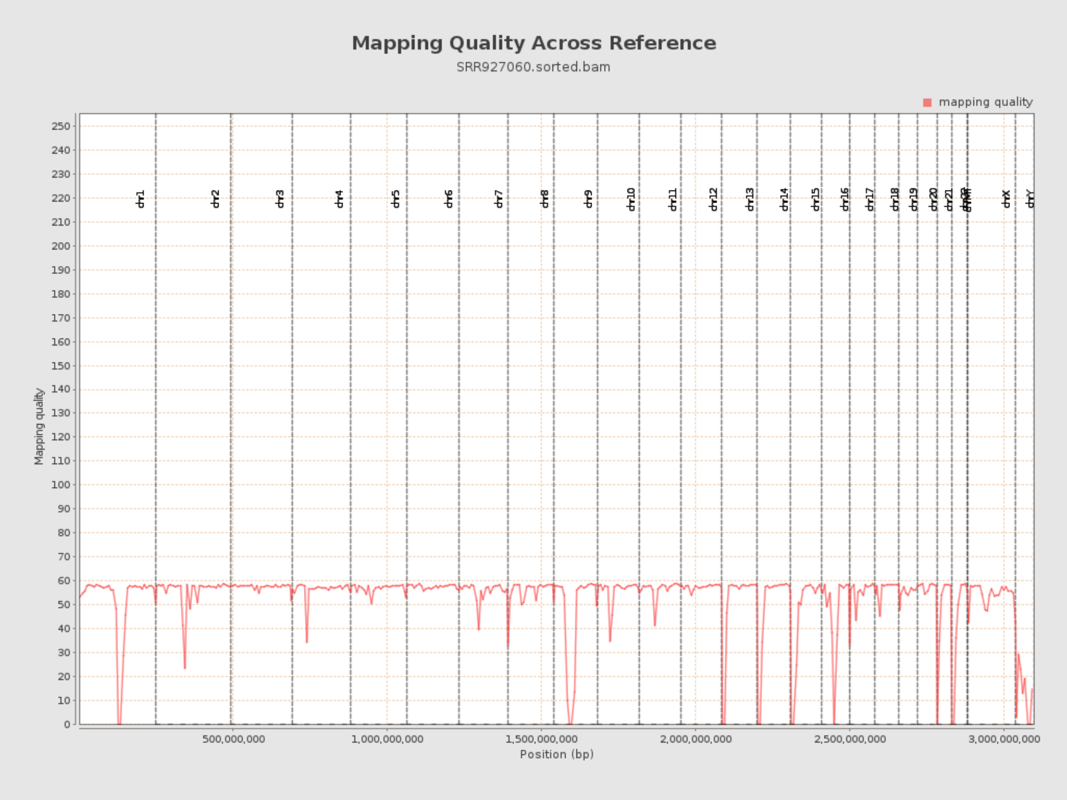
10. Results : Mapped Reads Clipping Profile



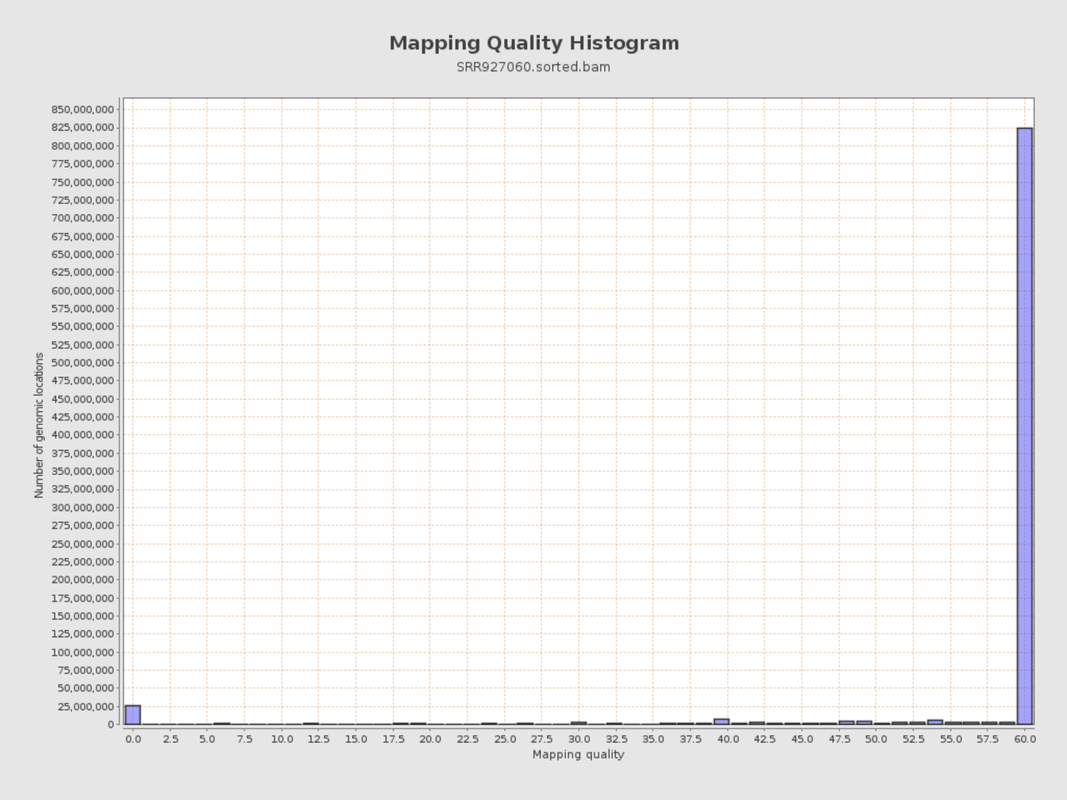
11. Results : Homopolymer Indels



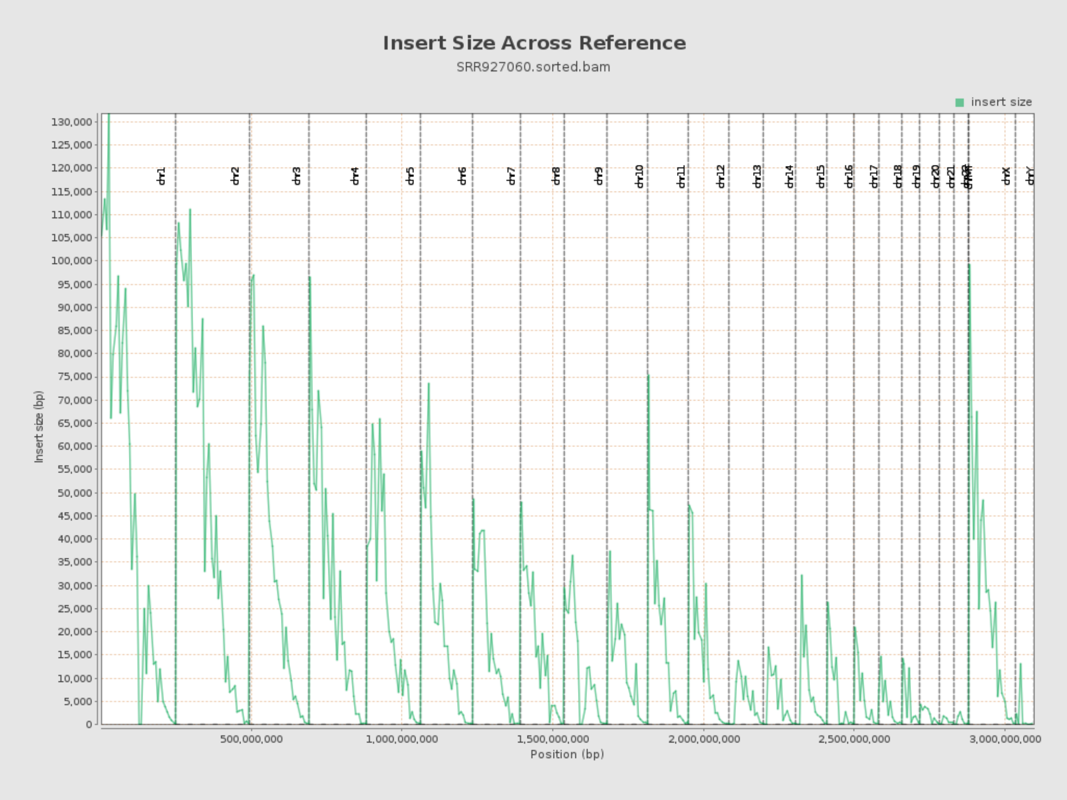
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram