Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 14:43:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927035.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_SRR927035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927035_1.fastq.gz SRR927035_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 14:43:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,242,400
Mapped reads	16,643,361 / 96.53%
Unmapped reads	599,039 / 3.47%
Mapped paired reads	16,643,361 / 96.53%
Mapped reads, first in pair	8,361,795 / 48.5%
Mapped reads, second in pair	8,281,566 / 48.03%
Mapped reads, both in pair	16,306,574 / 94.57%
Mapped reads, singletons	336,787 / 1.95%
Secondary alignments	0
Supplementary alignments	684,057 / 3.97%
Read min/max/mean length	30 / 101 / 102.65
Duplicated reads (estimated)	1,441,692 / 8.36%
Duplication rate	7.12%
Clipped reads	8,897,868 / 51.6%

2.2. ACGT Content

Number/percentage of A's	423,103,471 / 28.67%
Number/percentage of C's	280,461,123 / 19%
Number/percentage of T's	436,136,470 / 29.55%
Number/percentage of G's	335,997,493 / 22.77%
Number/percentage of N's	148,148 / 0.01%

GC Percentage	41.77%

2.3. Coverage

Mean	0.4771
Standard Deviation	1.7218

2.4. Mapping Quality

Mean Mapping Quality	52.33

2.5. Insert size

Mean	409,787.73
Standard Deviation	6,250,468.78
P25/Median/P75	127 / 170 / 233

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	16,086,556
Insertions	256,800
Mapped reads with at least one insertion	1.52%
Deletions	769,691
Mapped reads with at least one deletion	4.51%
Homopolymer indels	51.62%

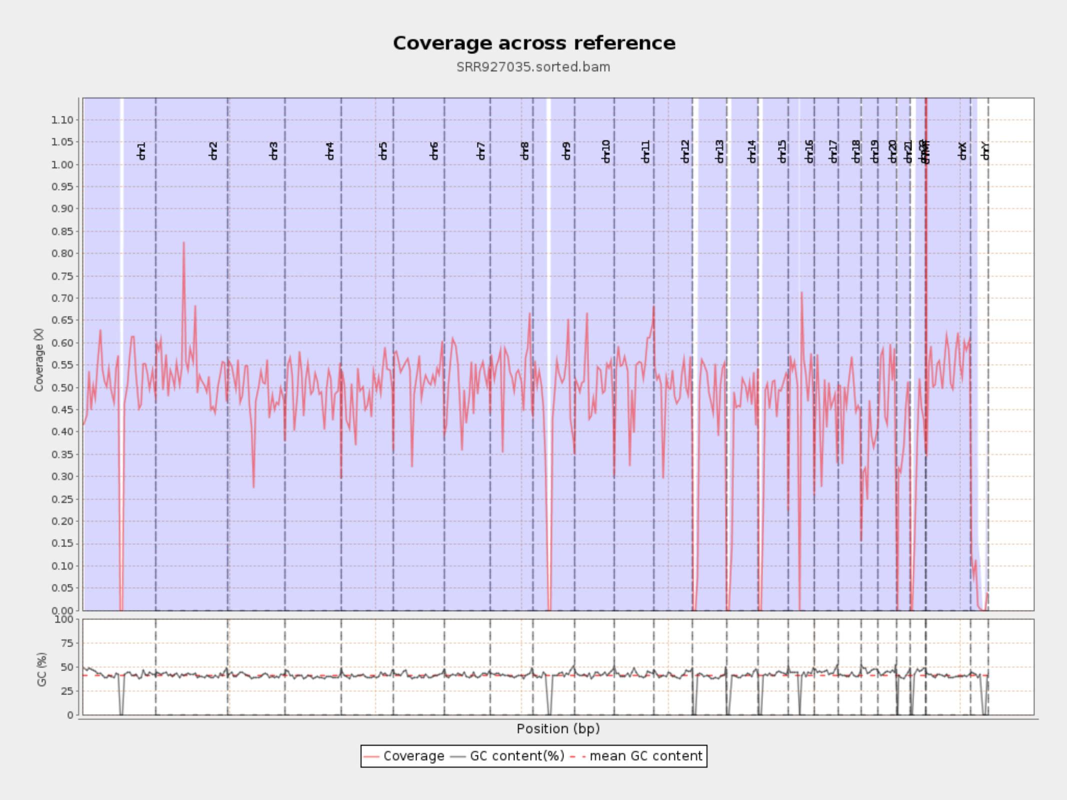
2.7. Chromosome stats

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

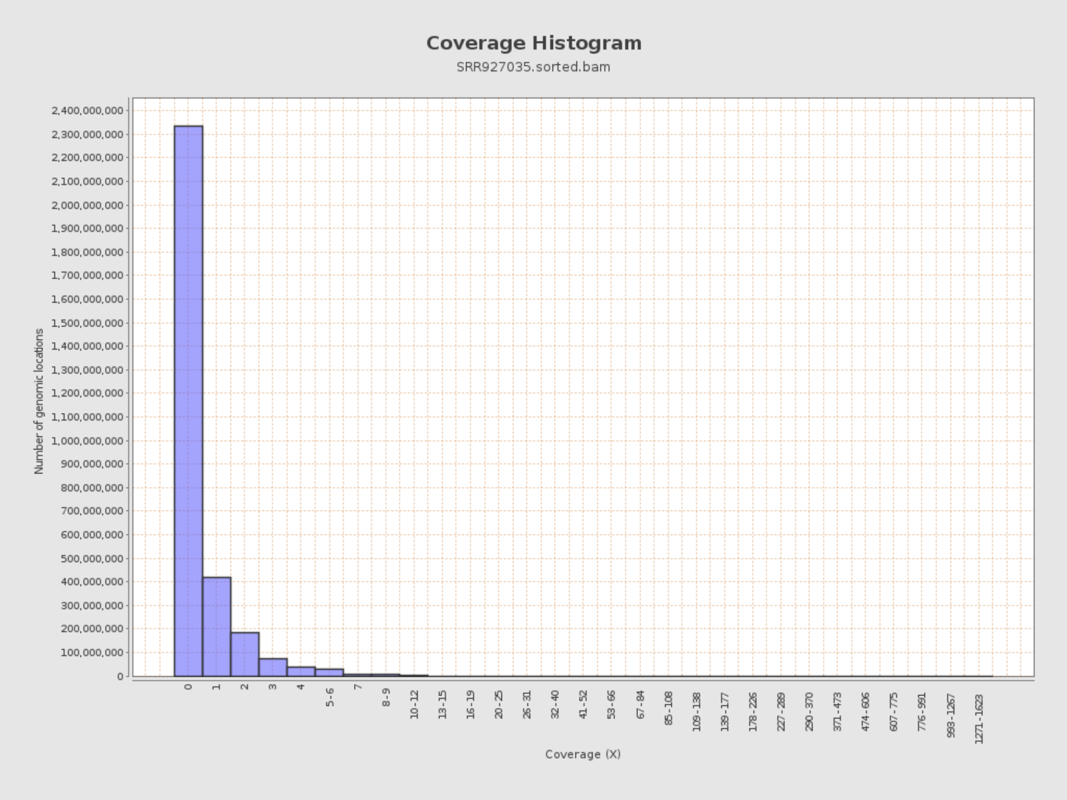
		bases	**coverage**	**deviation**
chr1	249250621	121101737	0.4859	1.9576
chr2	243199373	131441937	0.5405	3.0459
chr3	198022430	96735546	0.4885	1.1301
chr4	191154276	96009359	0.5023	1.612
chr5	180915260	88556945	0.4895	1.1262
chr6	171115067	90156085	0.5269	1.2128
chr7	159138663	80358859	0.505	1.442
chr8	146364022	78254980	0.5347	1.3474
chr9	141213431	62539992	0.4429	1.8164
chr10	135534747	69135369	0.5101	2.7196
chr11	135006516	72198005	0.5348	1.529
chr12	133851895	66742689	0.4986	1.1664
chr13	115169878	48388526	0.4201	1.0573
chr14	107349540	42561369	0.3965	1.0572
chr15	102531392	41535340	0.4051	1.061
chr16	90354753	43823376	0.485	2.7401
chr17	81195210	36645732	0.4513	1.276
chr18	78077248	37133428	0.4756	1.7882
chr19	59128983	20703813	0.3501	1.4025
chr20	63025520	32367021	0.5136	1.2419
chr21	48129895	17041855	0.3541	1.3307
chr22	51304566	15605006	0.3042	0.9703
chrMT	16571	344793	20.807	18.1627
chrX	155270560	85050588	0.5478	1.2842

chrY	59373566	2541202	0.0428	1.3805

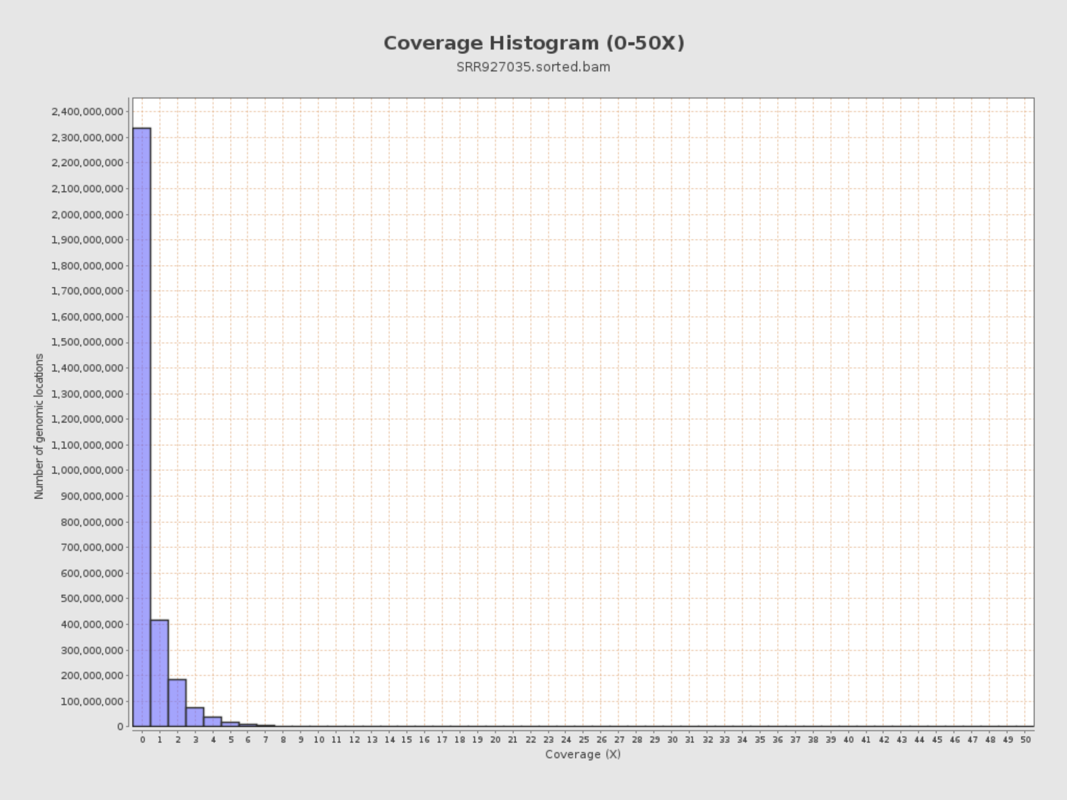
3. Results : Coverage across reference



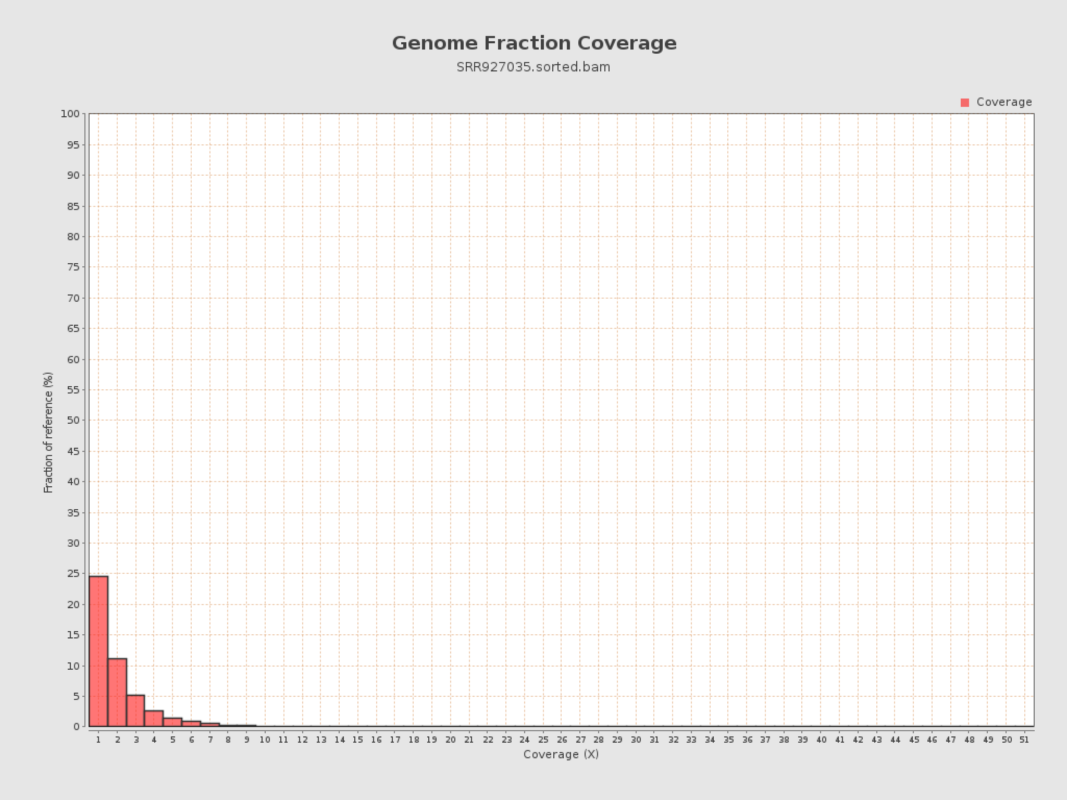
4. Results : Coverage Histogram



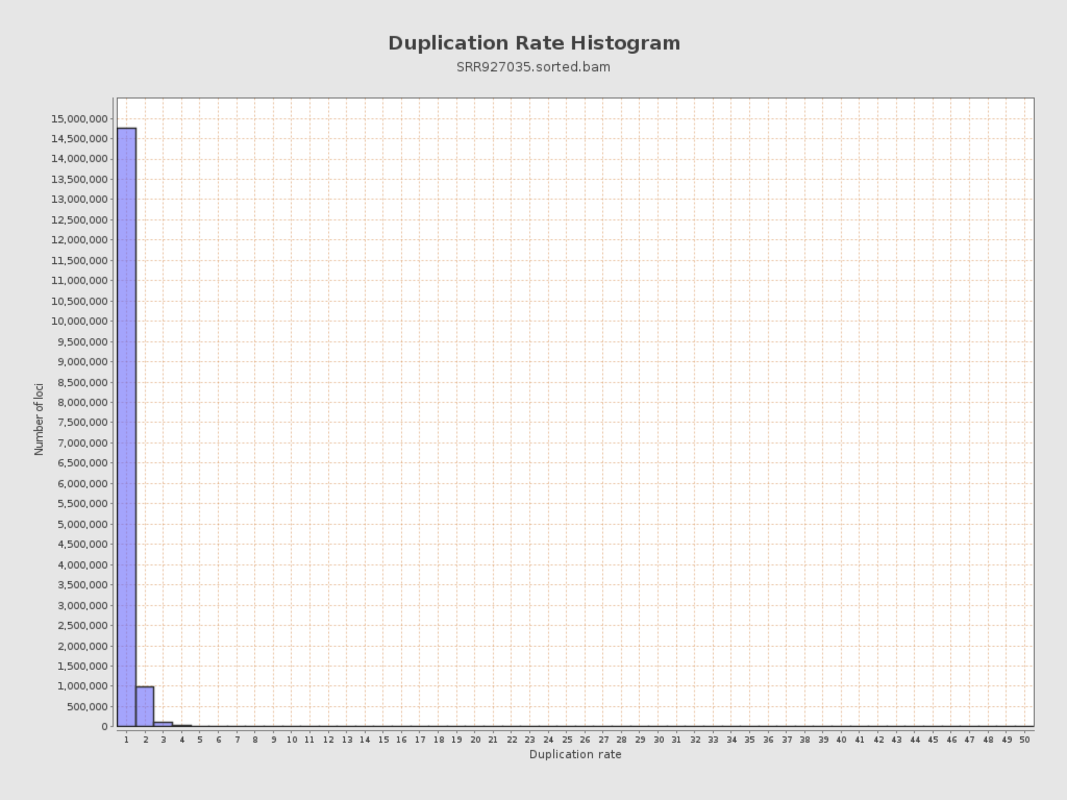
5. Results : Coverage Histogram (0-50X)



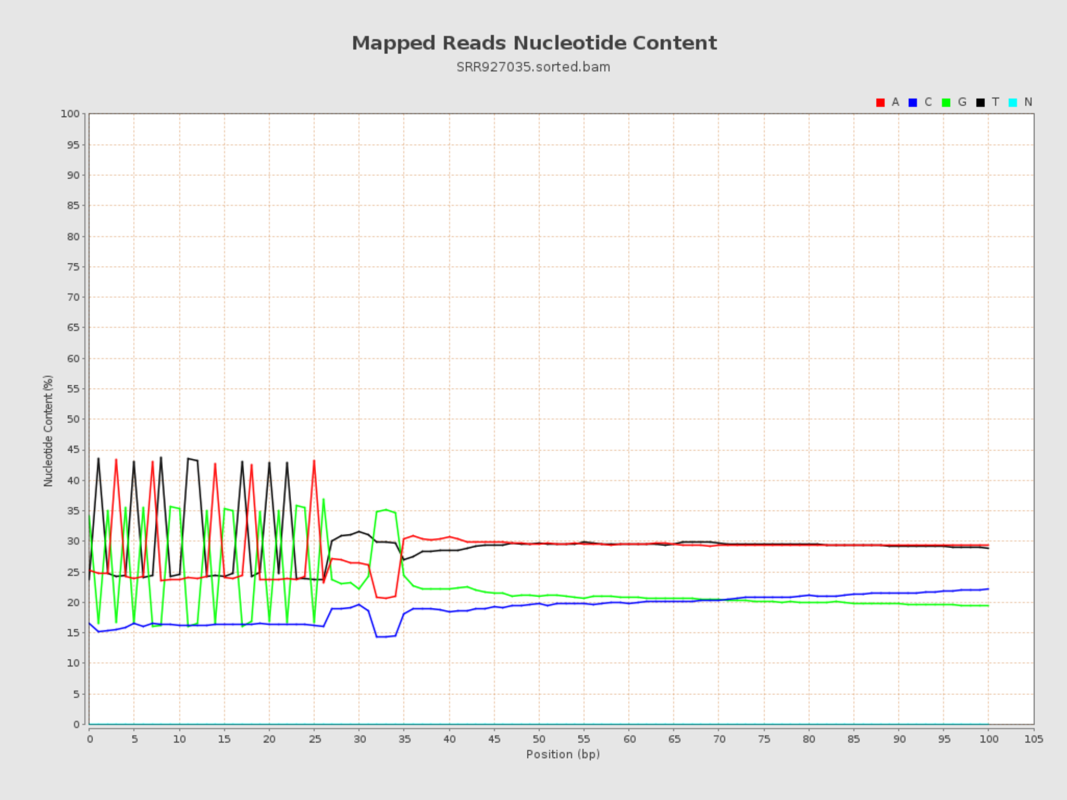
6. Results : Genome Fraction Coverage



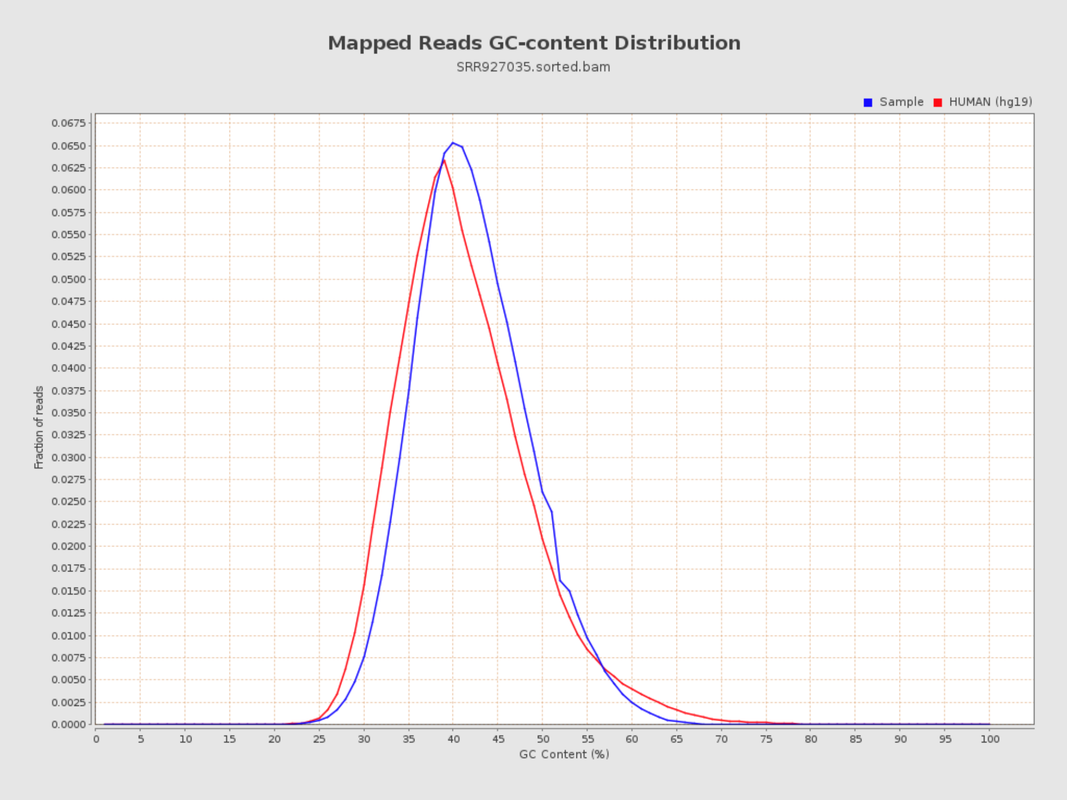
7. Results : Duplication Rate Histogram



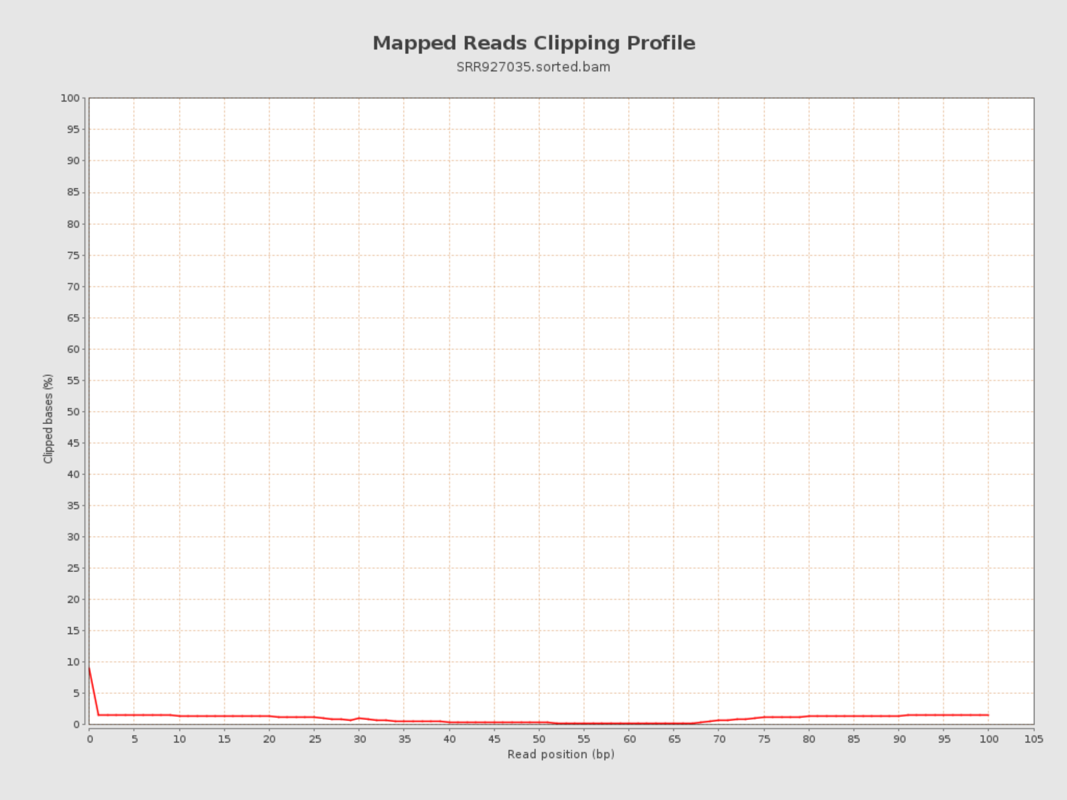
8. Results : Mapped Reads Nucleotide Content



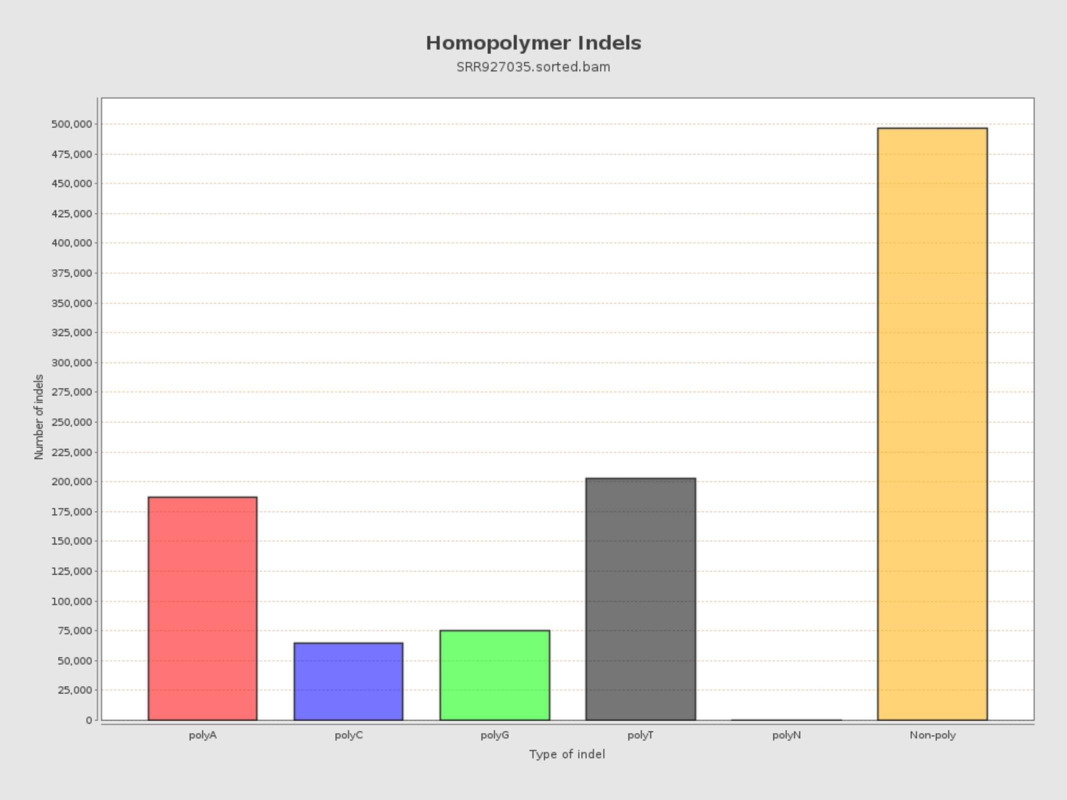
9. Results : Mapped Reads GC-content Distribution



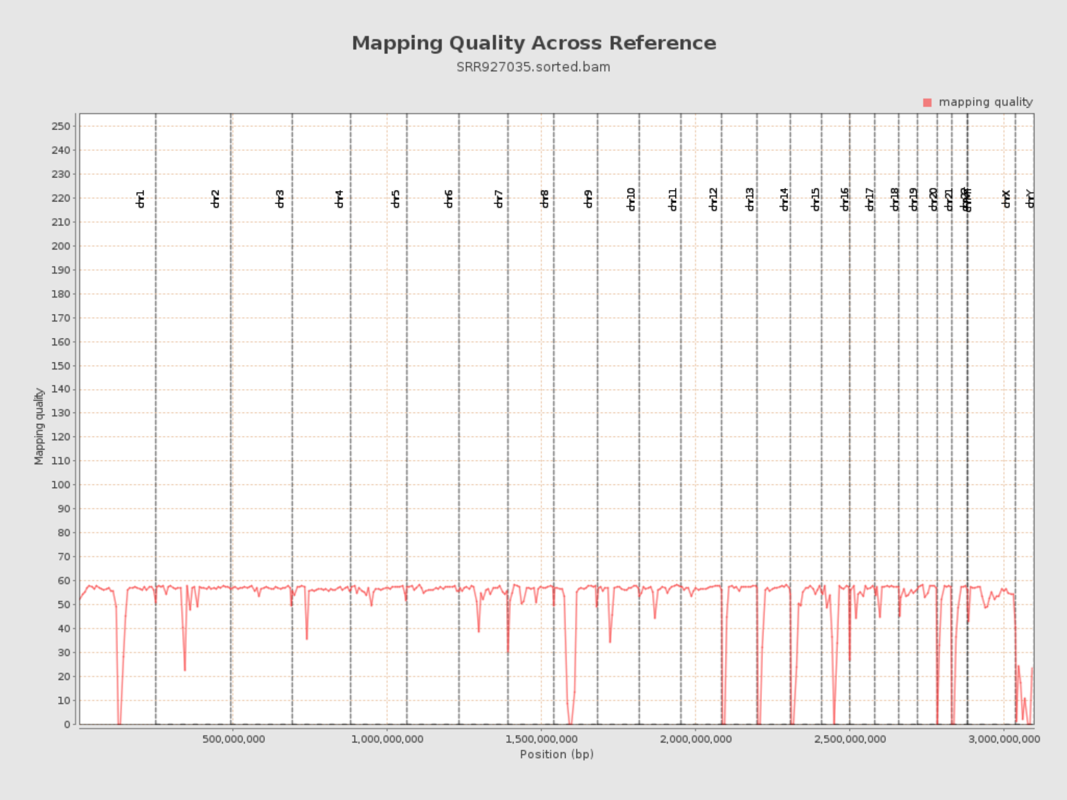
10. Results : Mapped Reads Clipping Profile



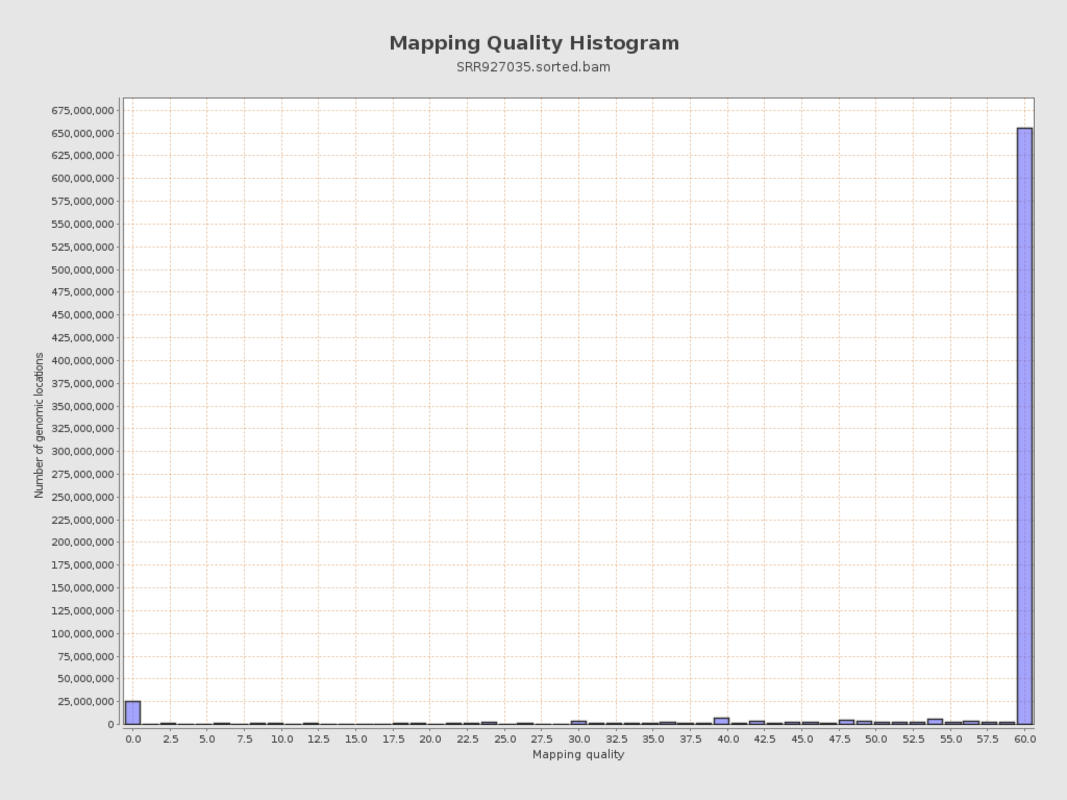
11. Results : Homopolymer Indels



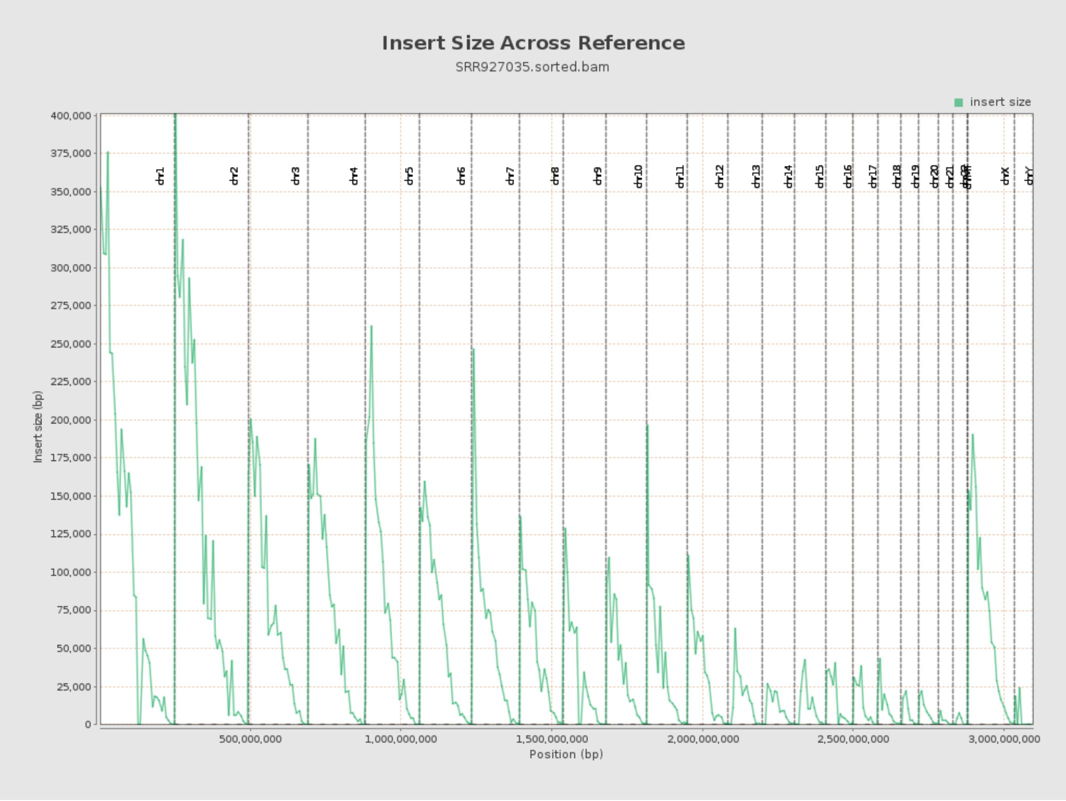
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram