Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 01:59:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927056.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_SRR927056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927056_1.fastq.gz SRR927056_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 01:59:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,346,944
Mapped reads	31,664,430 / 97.89%
Unmapped reads	682,514 / 2.11%
Mapped paired reads	31,664,430 / 97.89%
Mapped reads, first in pair	15,884,678 / 49.11%
Mapped reads, second in pair	15,779,752 / 48.78%
Mapped reads, both in pair	31,252,976 / 96.62%
Mapped reads, singletons	411,454 / 1.27%
Secondary alignments	0
Supplementary alignments	813,326 / 2.51%
Read min/max/mean length	30 / 101 / 102.04
Duplicated reads (estimated)	6,297,465 / 19.47%
Duplication rate	6.24%
Clipped reads	11,924,437 / 36.86%

2.2. ACGT Content

Number/percentage of A's	819,097,561 / 28.1%
Number/percentage of C's	586,159,846 / 20.11%
Number/percentage of T's	834,647,932 / 28.64%
Number/percentage of G's	674,280,145 / 23.13%
Number/percentage of N's	409,795 / 0.01%

GC Percentage	43.25%

2.3. Coverage

Mean	0.9422
Standard Deviation	60.7672

2.4. Mapping Quality

Mean Mapping Quality	52.92

2.5. Insert size

Mean	219,674.88
Standard Deviation	4,690,221.57
P25/Median/P75	146 / 189 / 253

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	29,705,781
Insertions	451,298
Mapped reads with at least one insertion	1.4%
Deletions	1,451,361
Mapped reads with at least one deletion	4.47%
Homopolymer indels	52.31%

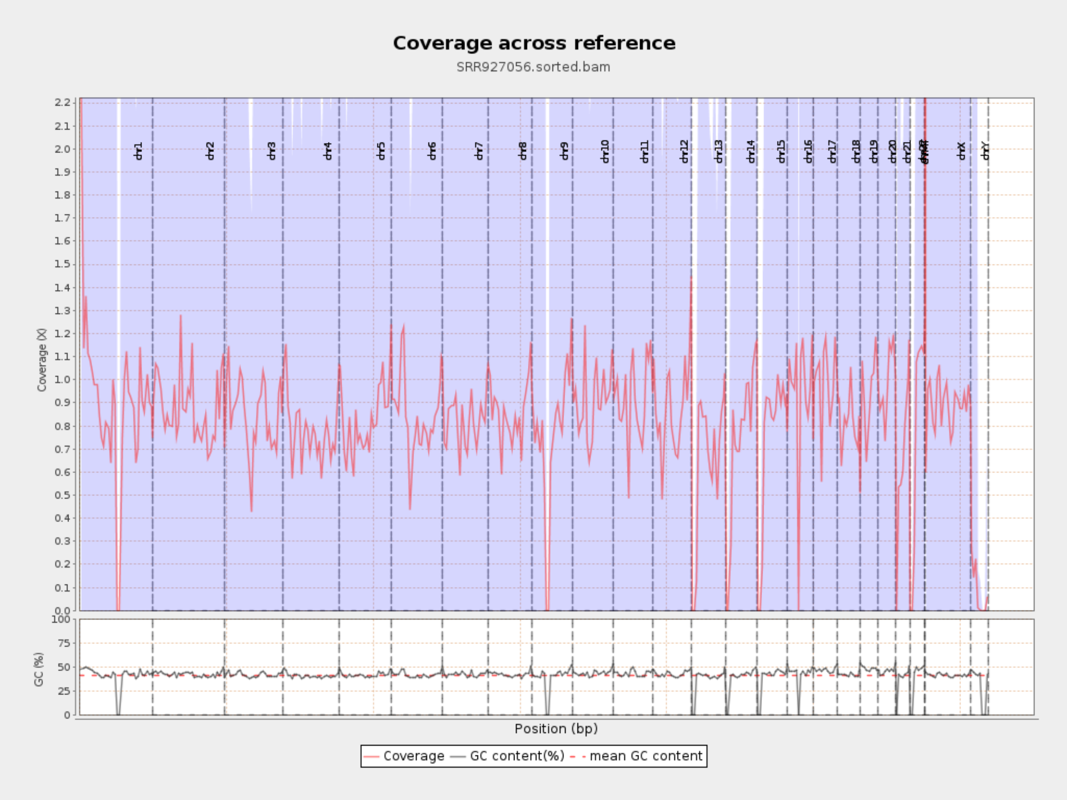
2.7. Chromosome stats

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

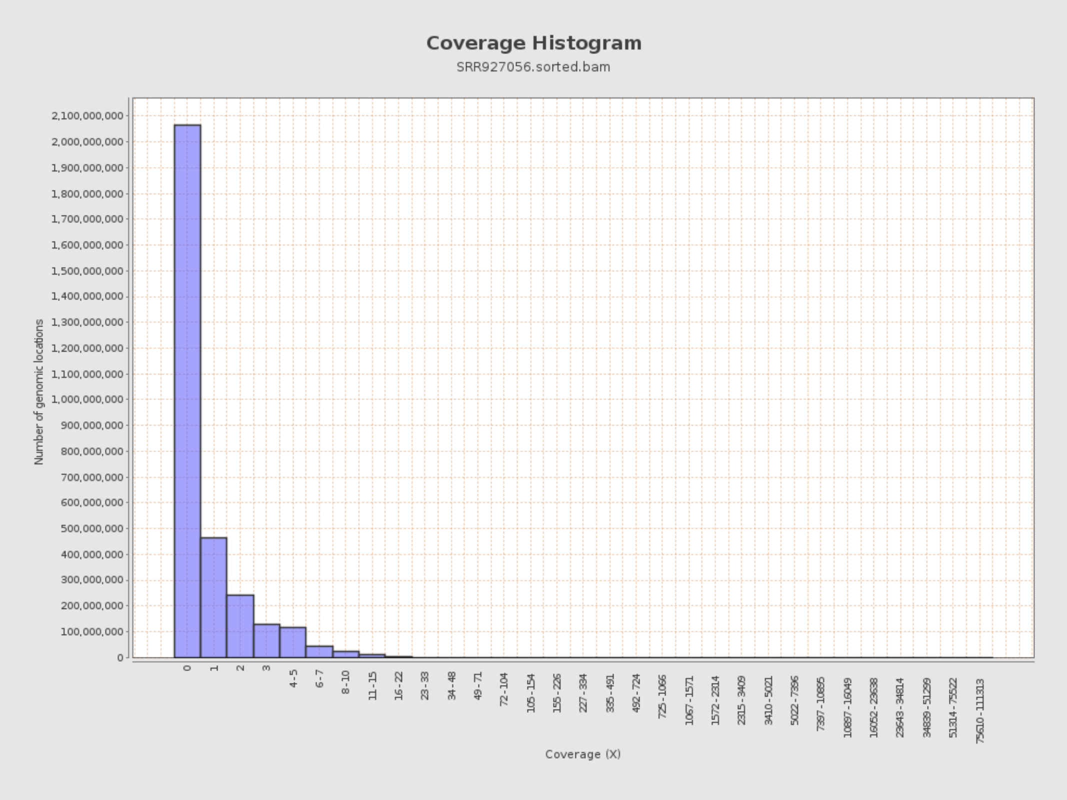
		bases	coverage	deviation
chr1	249250621	228145913	0.9153	13.4561
chr2	243199373	213792118	0.8791	4.4104
chr3	198022430	168720634	0.852	1.7378
chr4	191154276	148189233	0.7752	2.2897
chr5	180915260	149789018	0.828	1.9209
chr6	171115067	143195908	0.8368	1.7425
chr7	159138663	130919089	0.8227	2.1234
chr8	146364022	124945685	0.8537	1.9997
chr9	141213431	107265983	0.7596	2.9729
chr10	135534747	123003750	0.9075	5.3486
chr11	135006516	124481410	0.922	2.4134
chr12	133851895	115733361	0.8646	1.7974
chr13	115169878	73723335	0.6401	5.0472
chr14	107349540	77496486	0.7219	1.665
chr15	102531392	73644810	0.7183	1.6357
chr16	90354753	84304412	0.933	4.1072
chr17	81195210	80494474	0.9914	9.0564
chr18	78077248	64468691	0.8257	2.9685
chr19	59128983	55712413	0.9422	2.5553
chr20	63025520	62217024	0.9872	2.0605
chr21	48129895	32792229	0.6813	2.6321
chr22	51304566	39123649	0.7626	1.9616
chrMT	16571	351871618	21,234.1813	15,323.3805
chrX	155270560	137860413	0.8879	1.9386

chrY	59373566	4768987	0.0803	3.1532

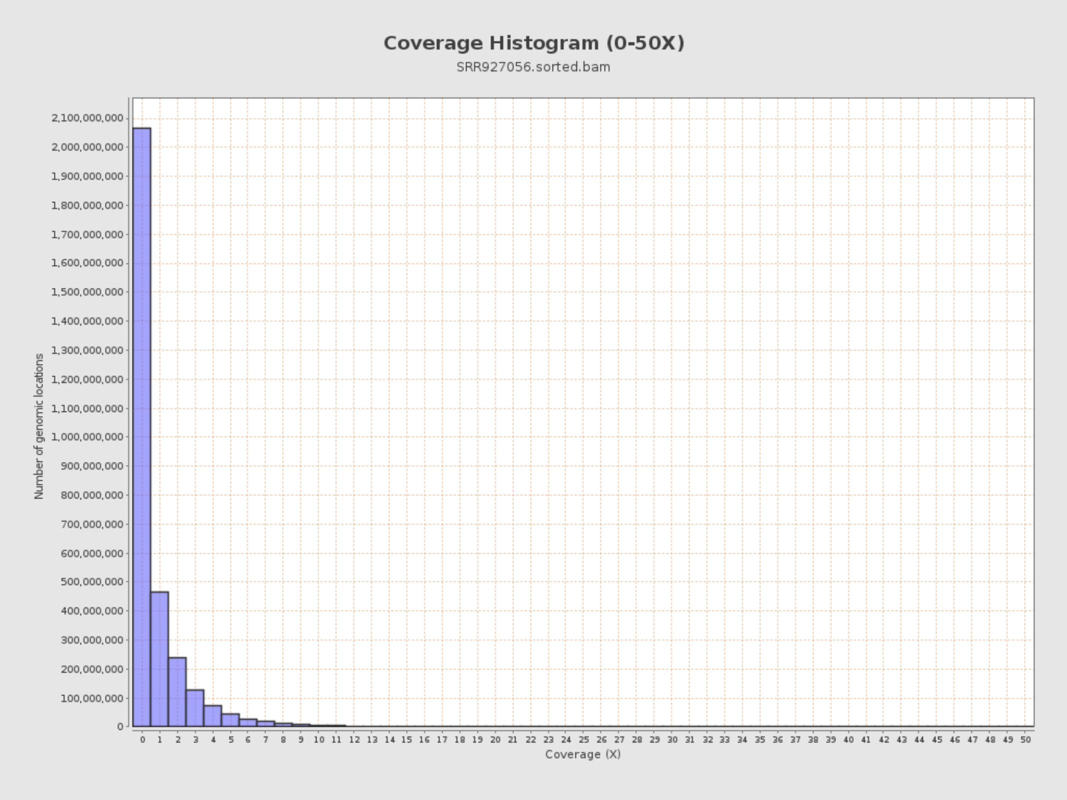
3. Results : Coverage across reference



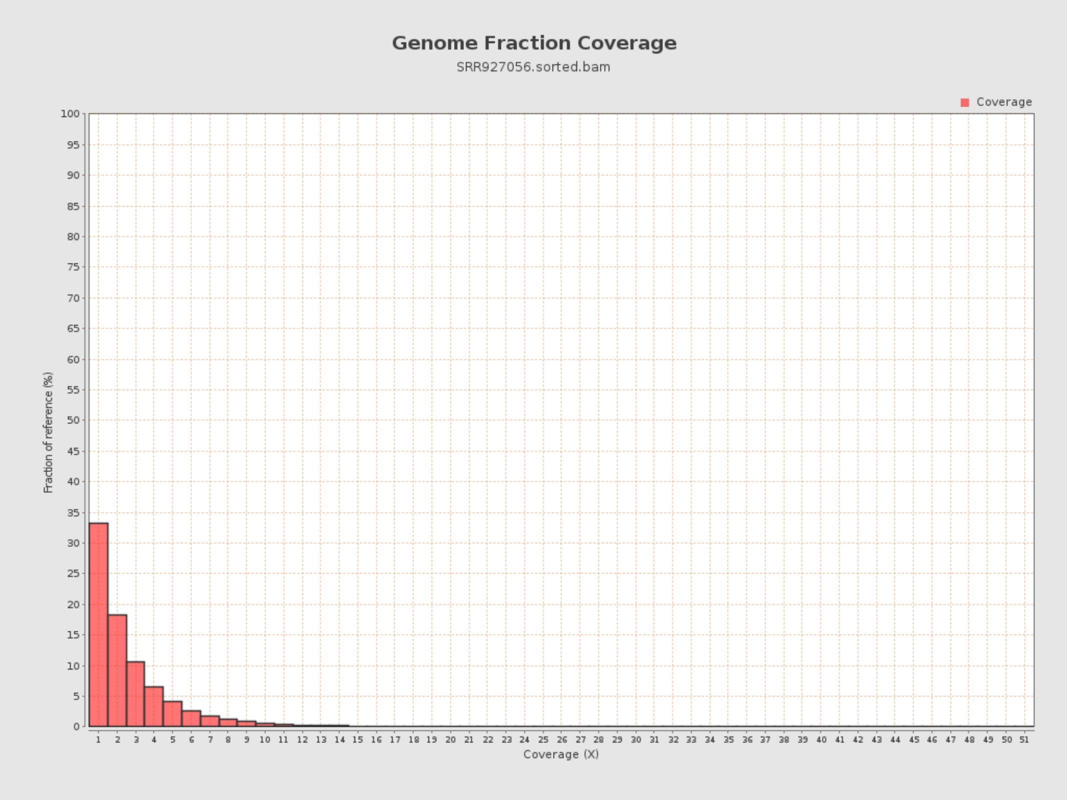
4. Results : Coverage Histogram



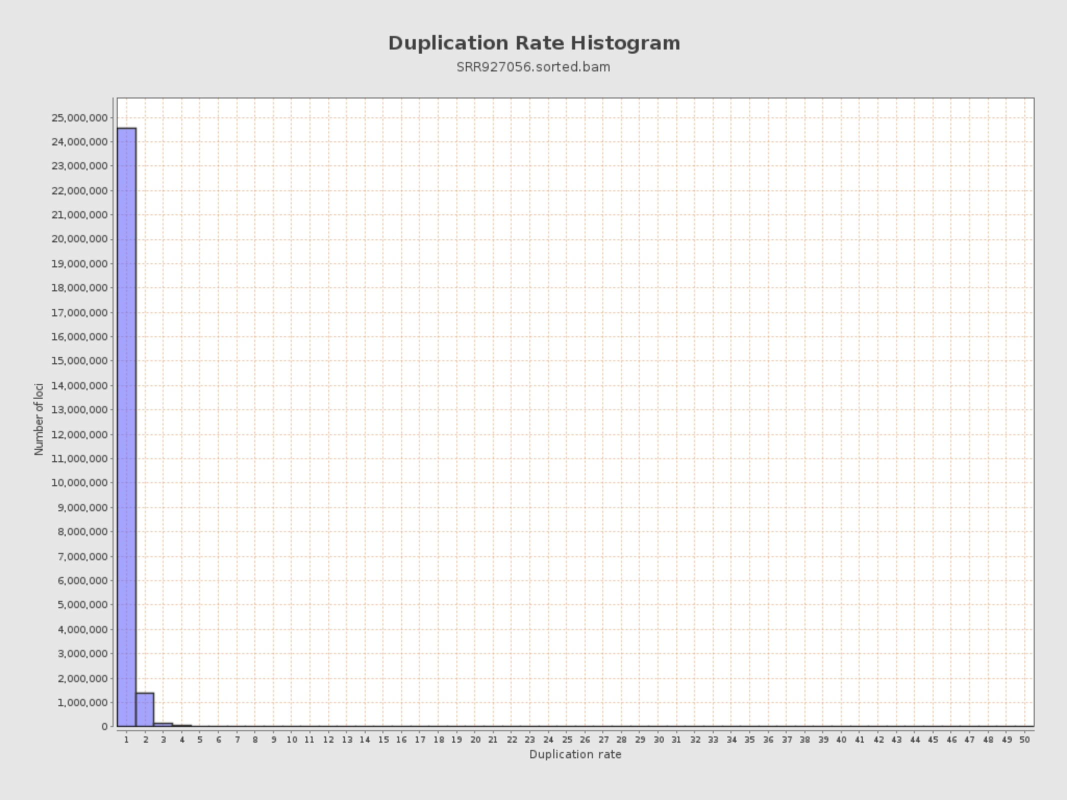
5. Results : Coverage Histogram (0-50X)



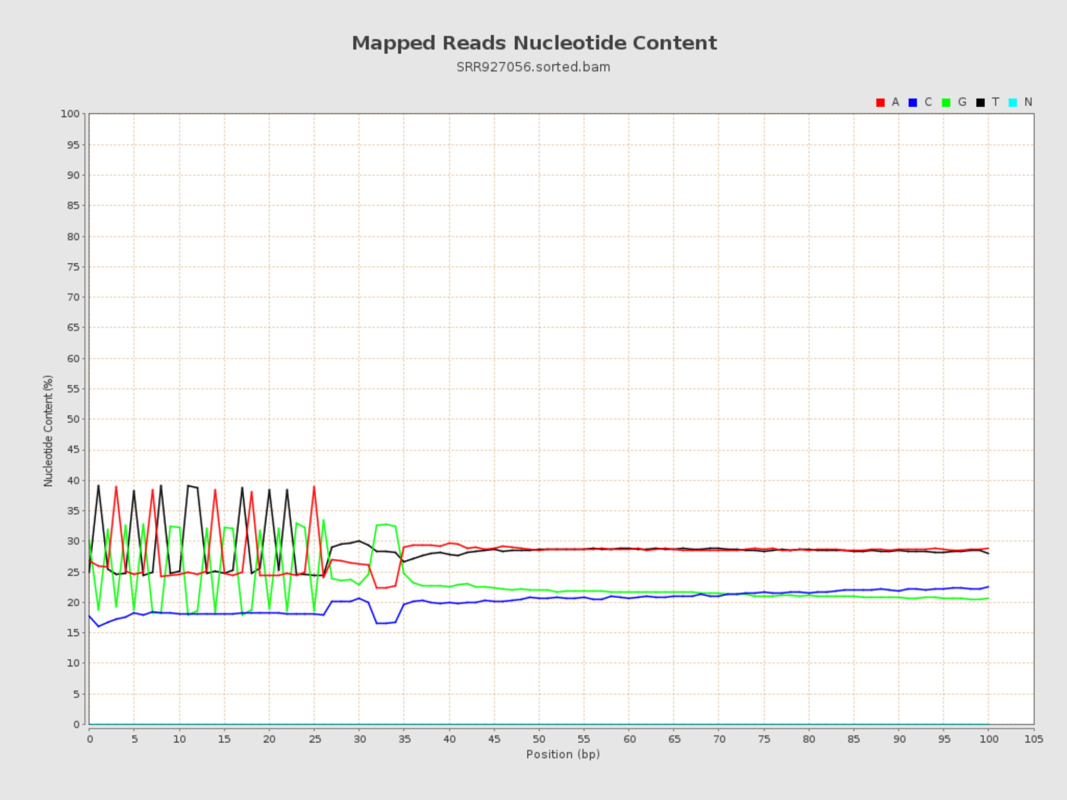
6. Results : Genome Fraction Coverage



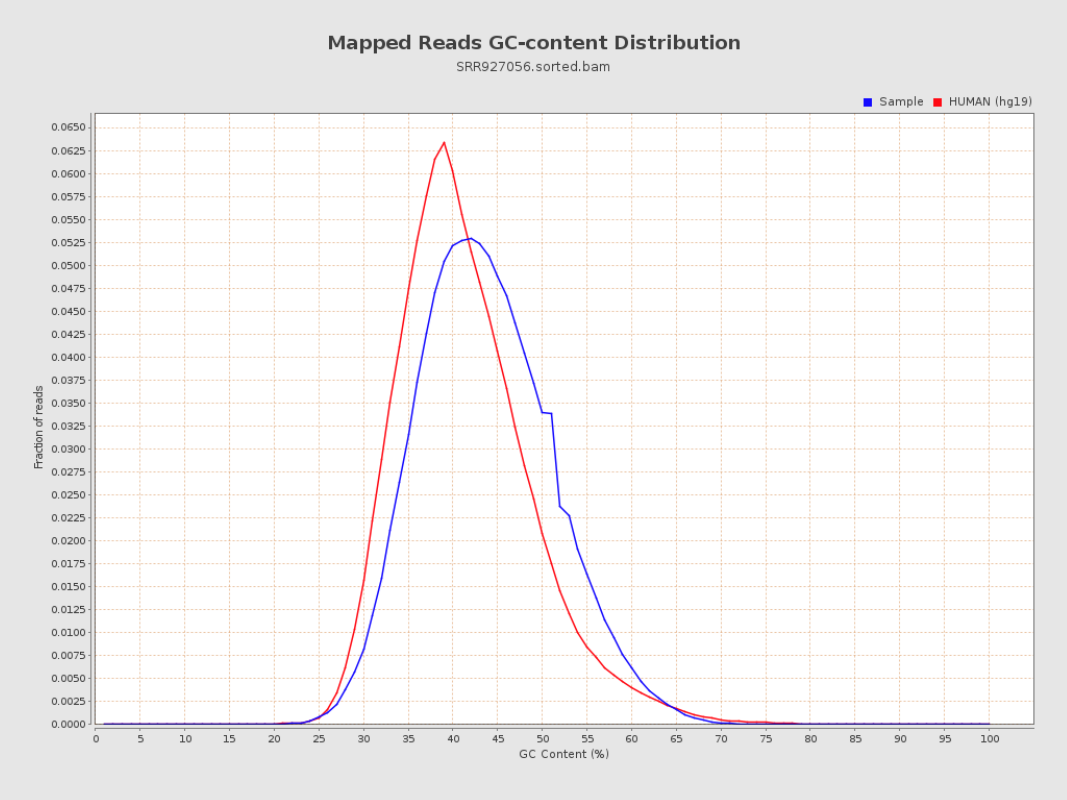
7. Results : Duplication Rate Histogram



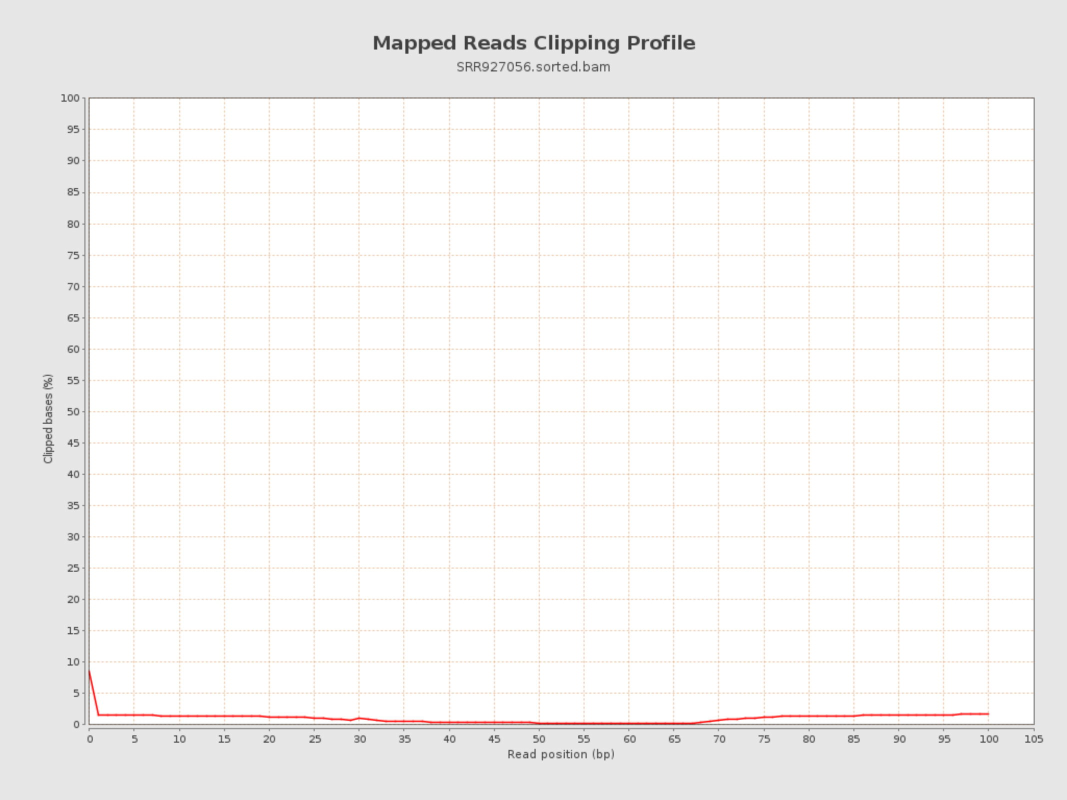
8. Results : Mapped Reads Nucleotide Content



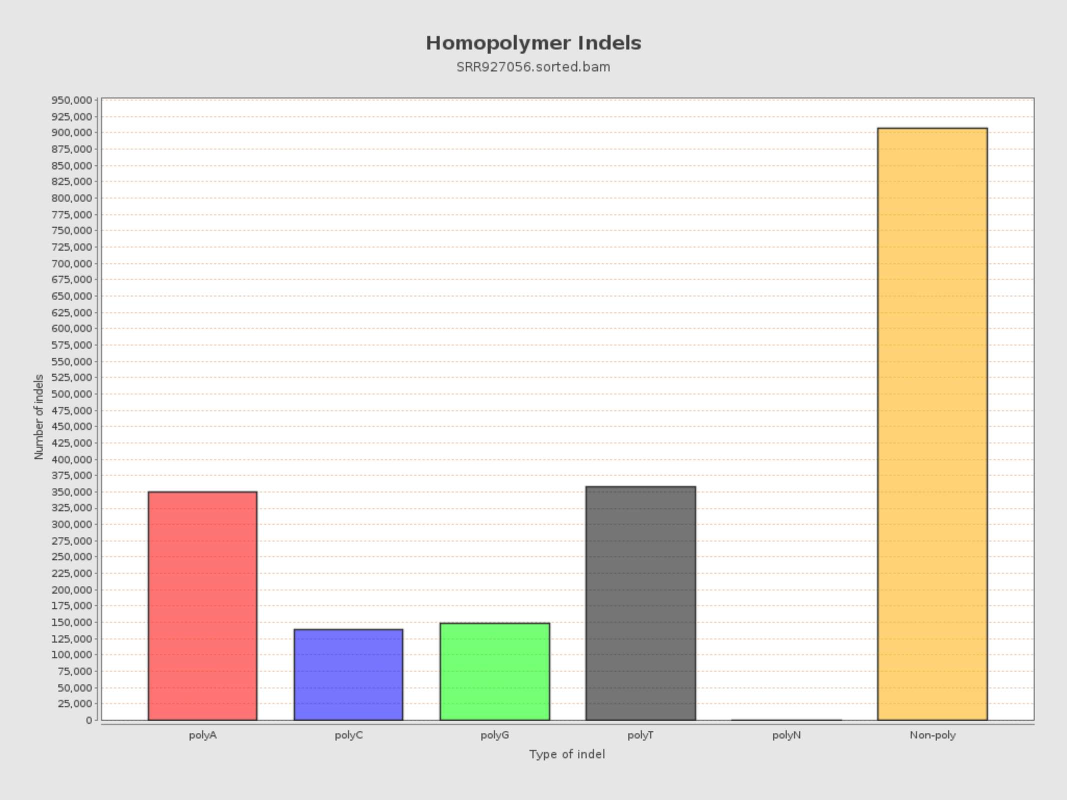
9. Results : Mapped Reads GC-content Distribution



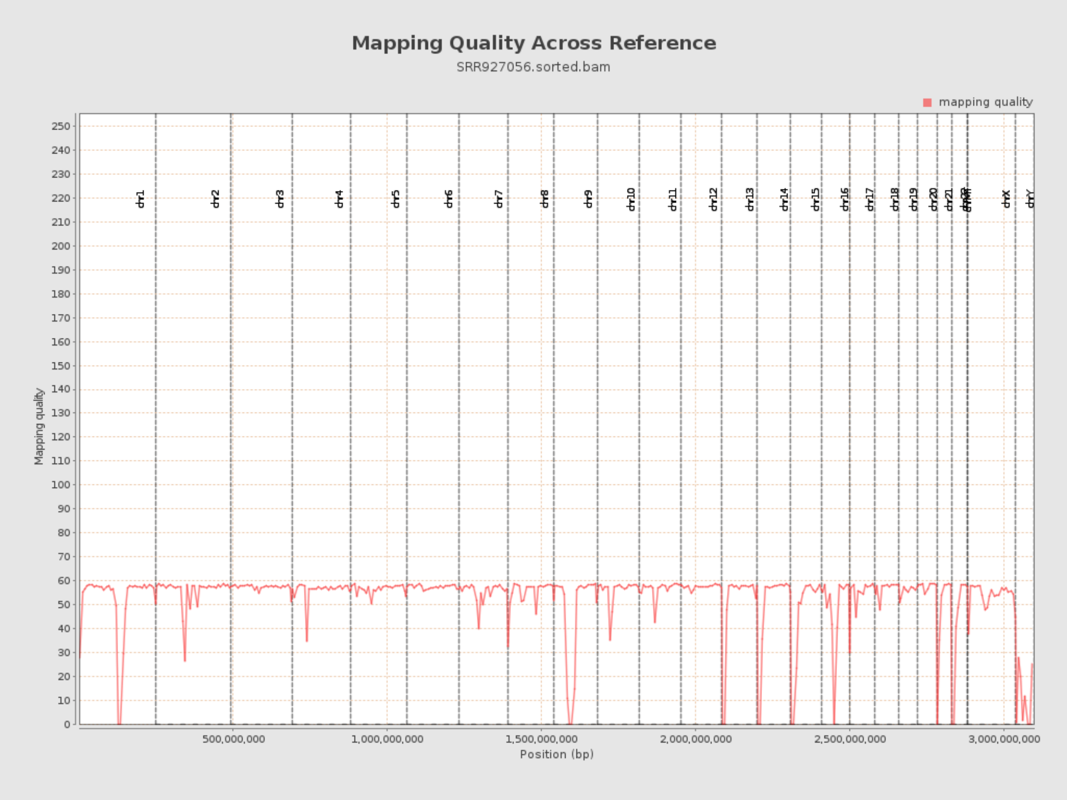
10. Results : Mapped Reads Clipping Profile



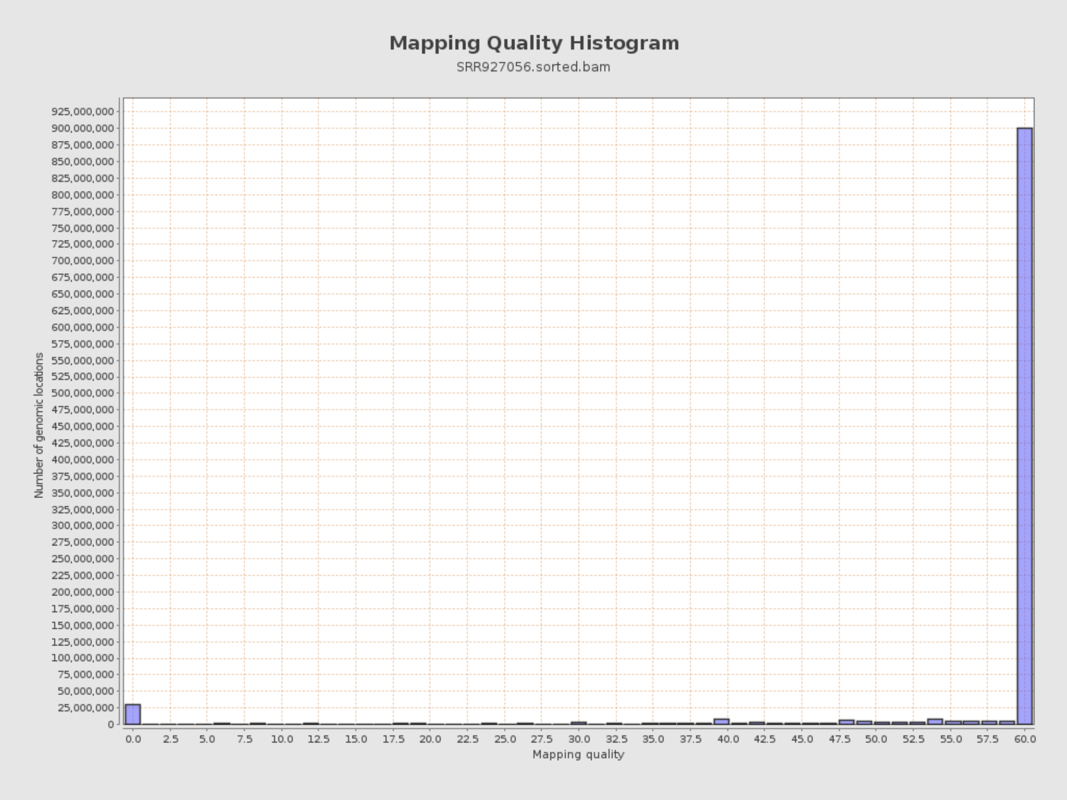
11. Results : Homopolymer Indels



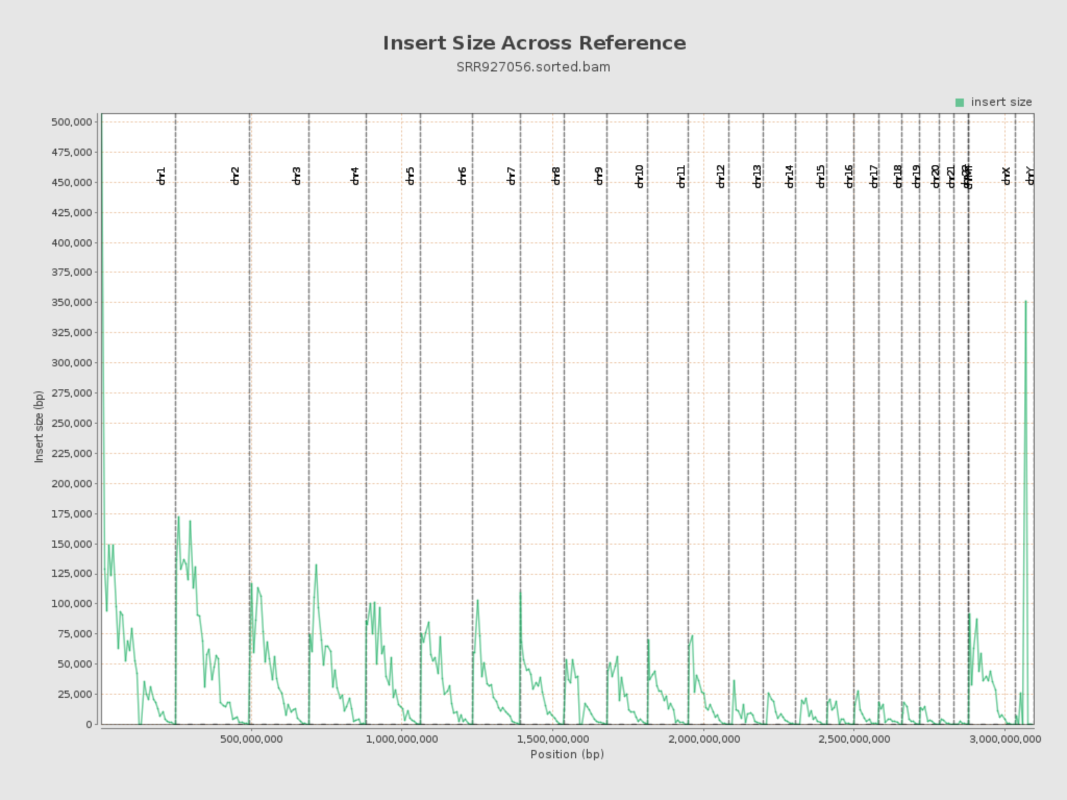
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram