Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 18:34:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927042.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_SRR927042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927042_1.fastq.gz SRR927042_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 18:34:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,912,276
Mapped reads	17,314,706 / 96.66%
Unmapped reads	597,570 / 3.34%
Mapped paired reads	17,314,706 / 96.66%
Mapped reads, first in pair	8,705,739 / 48.6%
Mapped reads, second in pair	8,608,967 / 48.06%
Mapped reads, both in pair	16,970,202 / 94.74%
Mapped reads, singletons	344,504 / 1.92%
Secondary alignments	0
Supplementary alignments	686,990 / 3.84%
Read min/max/mean length	30 / 101 / 102.6
Duplicated reads (estimated)	1,455,051 / 8.12%
Duplication rate	6.85%
Clipped reads	8,787,140 / 49.06%

2.2. ACGT Content

Number/percentage of A's	444,336,825 / 28.7%
Number/percentage of C's	295,272,746 / 19.07%
Number/percentage of T's	457,783,467 / 29.57%
Number/percentage of G's	350,439,808 / 22.64%
Number/percentage of N's	164,195 / 0.01%

GC Percentage	41.71%

2.3. Coverage

Mean	0.5004
Standard Deviation	1.8651

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	392,772.41
Standard Deviation	6,126,300.76
P25/Median/P75	130 / 173 / 237

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	16,861,626
Insertions	267,262
Mapped reads with at least one insertion	1.52%
Deletions	812,191
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.8%

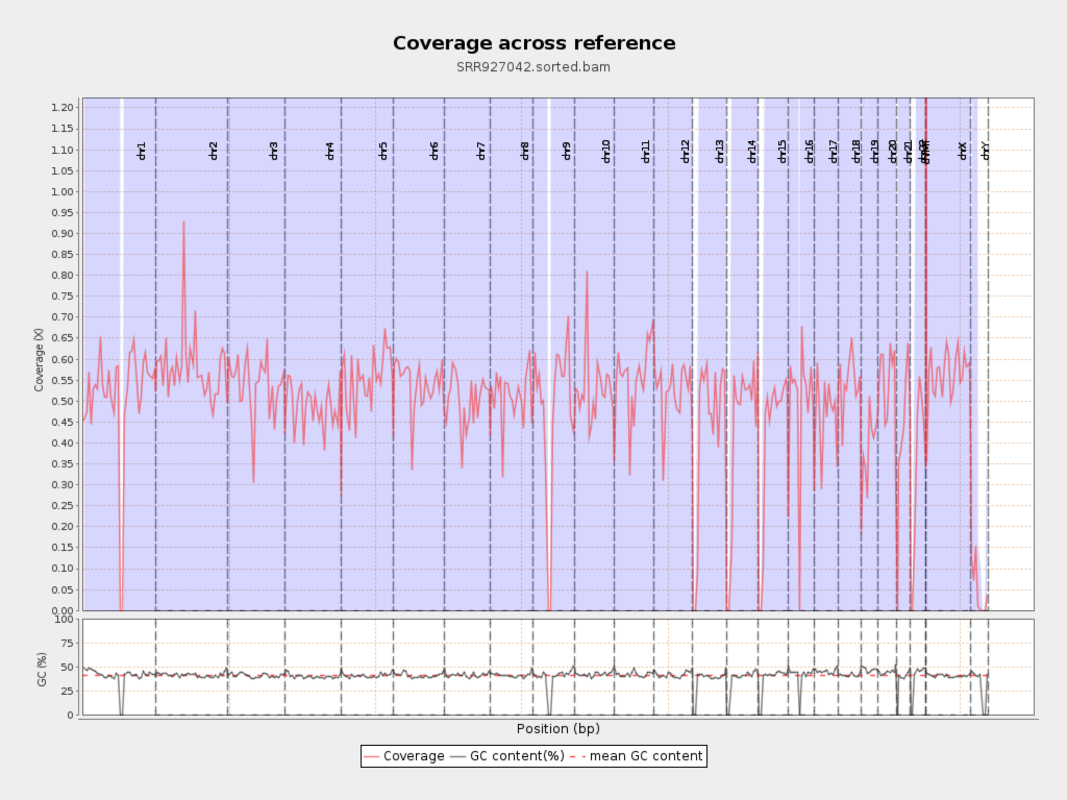
2.7. Chromosome stats

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

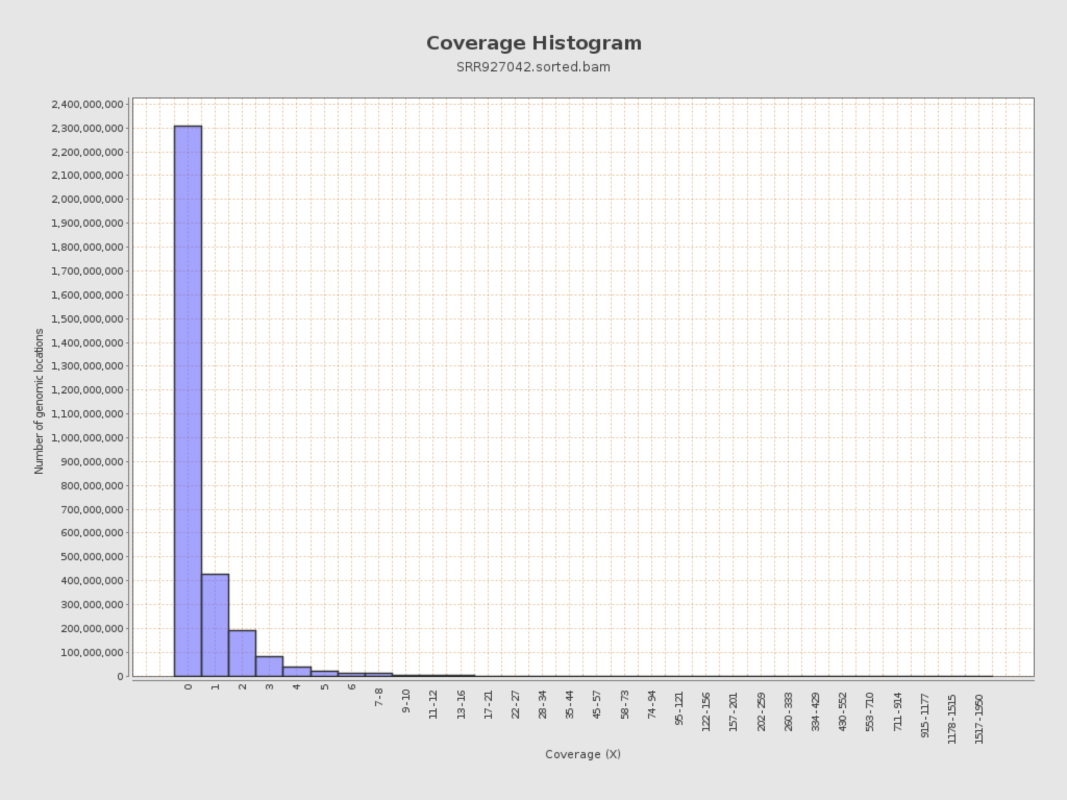
		bases	coverage	deviation
chr1	249250621	127604904	0.512	2.2046
chr2	243199373	141329302	0.5811	3.104
chr3	198022430	106315378	0.5369	1.2165
chr4	191154276	93587572	0.4896	1.5045
chr5	180915260	99977730	0.5526	1.2134
chr6	171115067	92675115	0.5416	1.2217
chr7	159138663	79681116	0.5007	1.4513
chr8	146364022	75014173	0.5125	1.3034
chr9	141213431	67623312	0.4789	2.1781
chr10	135534747	71366605	0.5266	3.7516
chr11	135006516	74910440	0.5549	1.6116
chr12	133851895	70515655	0.5268	1.2002
chr13	115169878	49714199	0.4317	1.0724
chr14	107349540	46370476	0.432	1.1111
chr15	102531392	41445822	0.4042	1.0479
chr16	90354753	43916732	0.486	2.3786
chr17	81195210	38535320	0.4746	1.3251
chr18	78077248	42571170	0.5452	2.0749
chr19	59128983	23076062	0.3903	1.4539
chr20	63025520	34829369	0.5526	1.2891
chr21	48129895	20705994	0.4302	1.4382
chr22	51304566	17106589	0.3334	1.0053
chrMT	16571	82739	4.993	4.8728
chrX	155270560	87434228	0.5631	1.3037

chrY	59373566	2785726	0.0469	1.9597

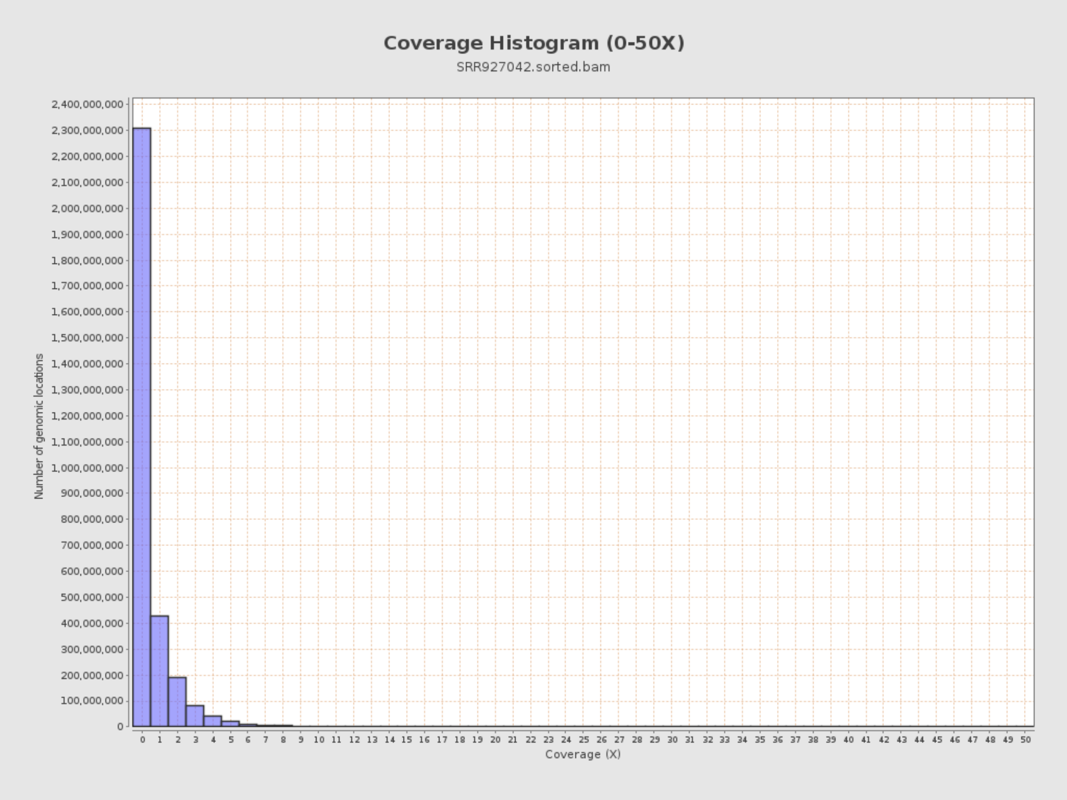
3. Results : Coverage across reference



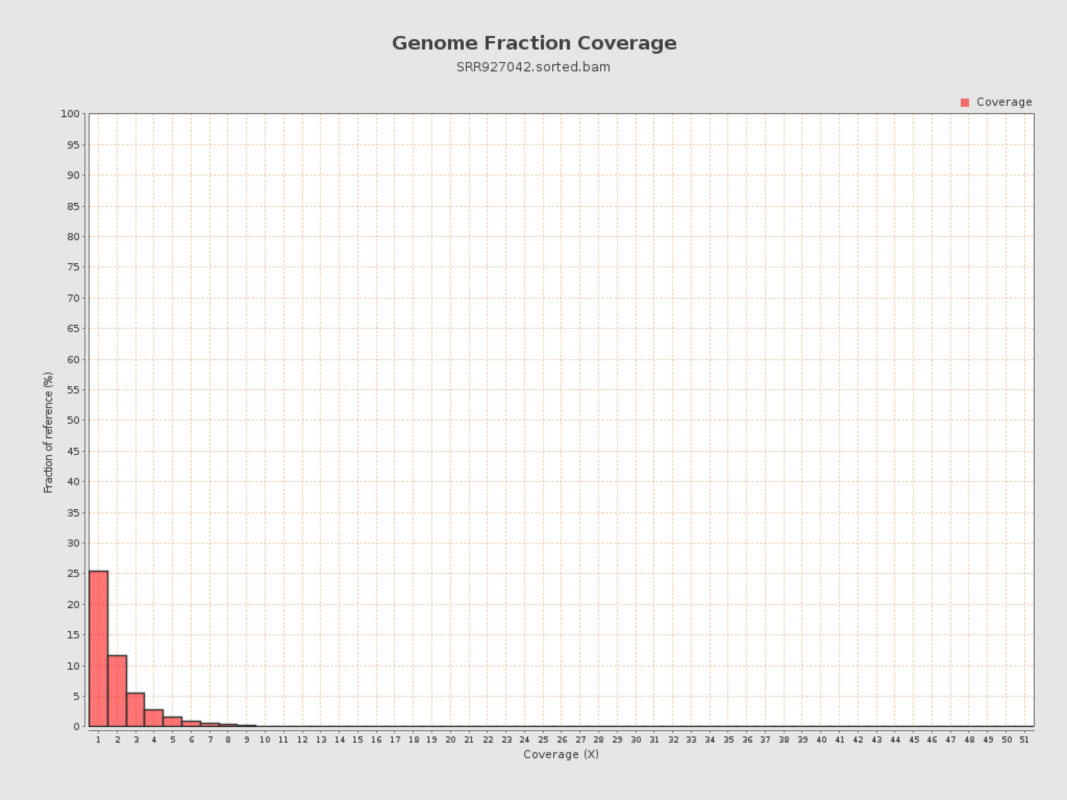
4. Results : Coverage Histogram



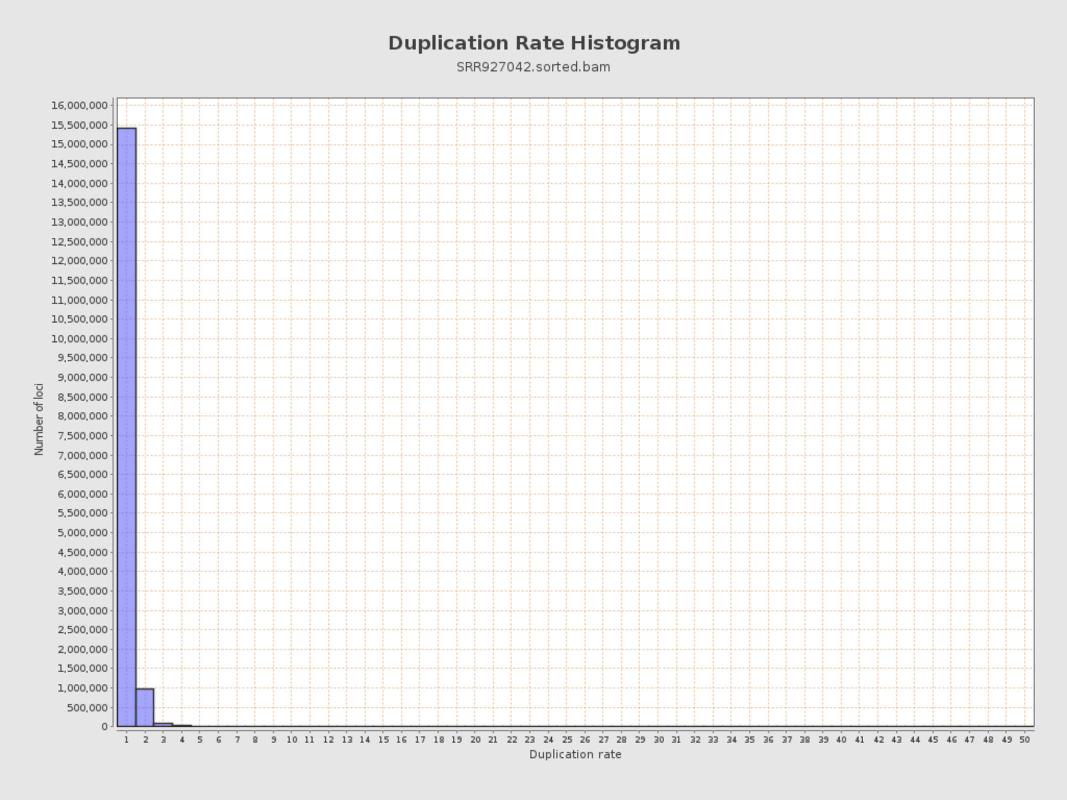
5. Results : Coverage Histogram (0-50X)



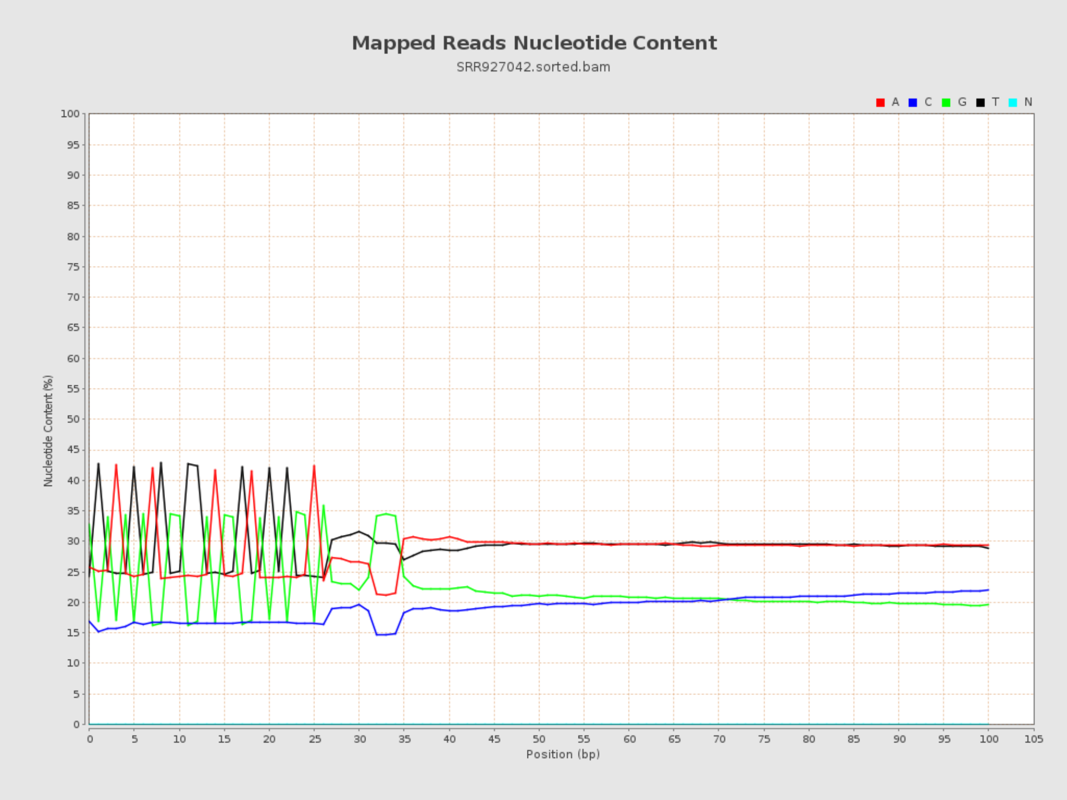
6. Results : Genome Fraction Coverage



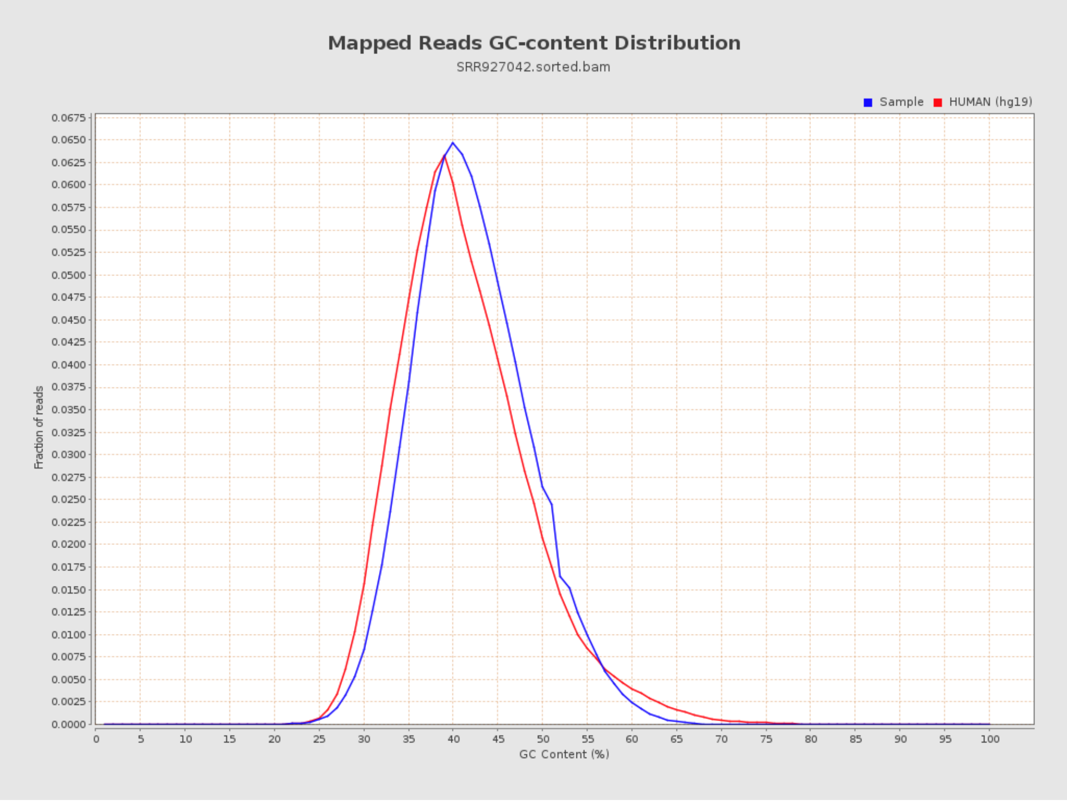
7. Results : Duplication Rate Histogram



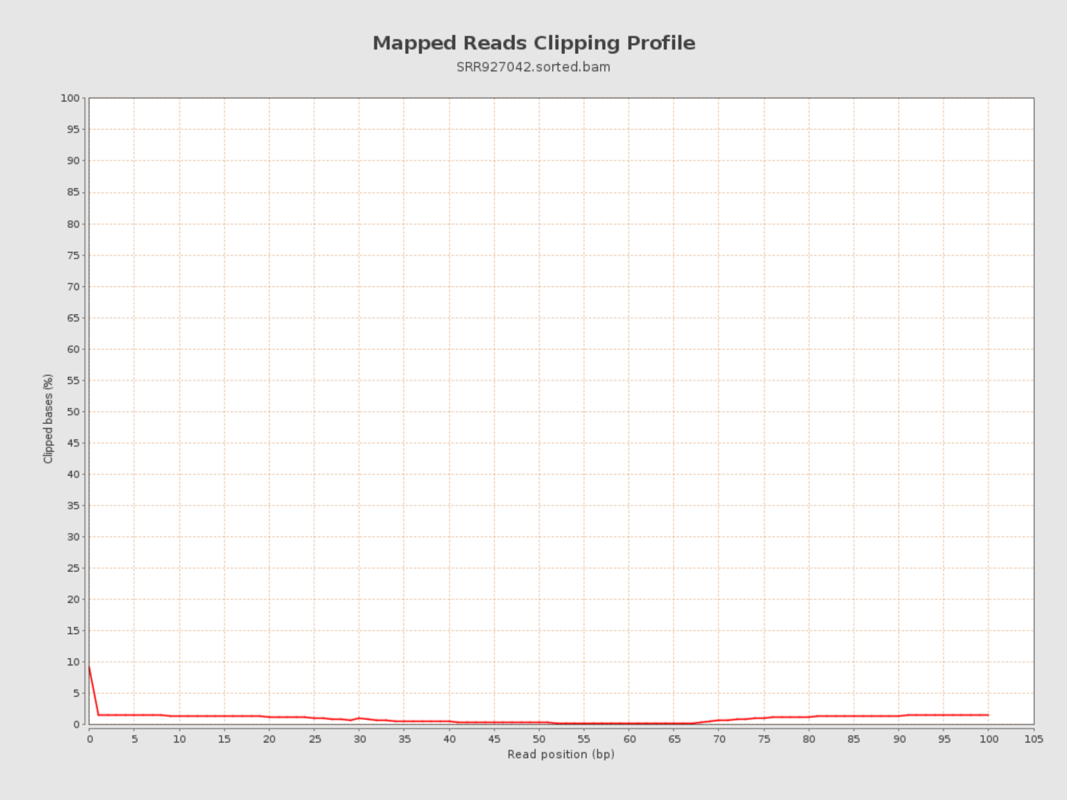
8. Results : Mapped Reads Nucleotide Content



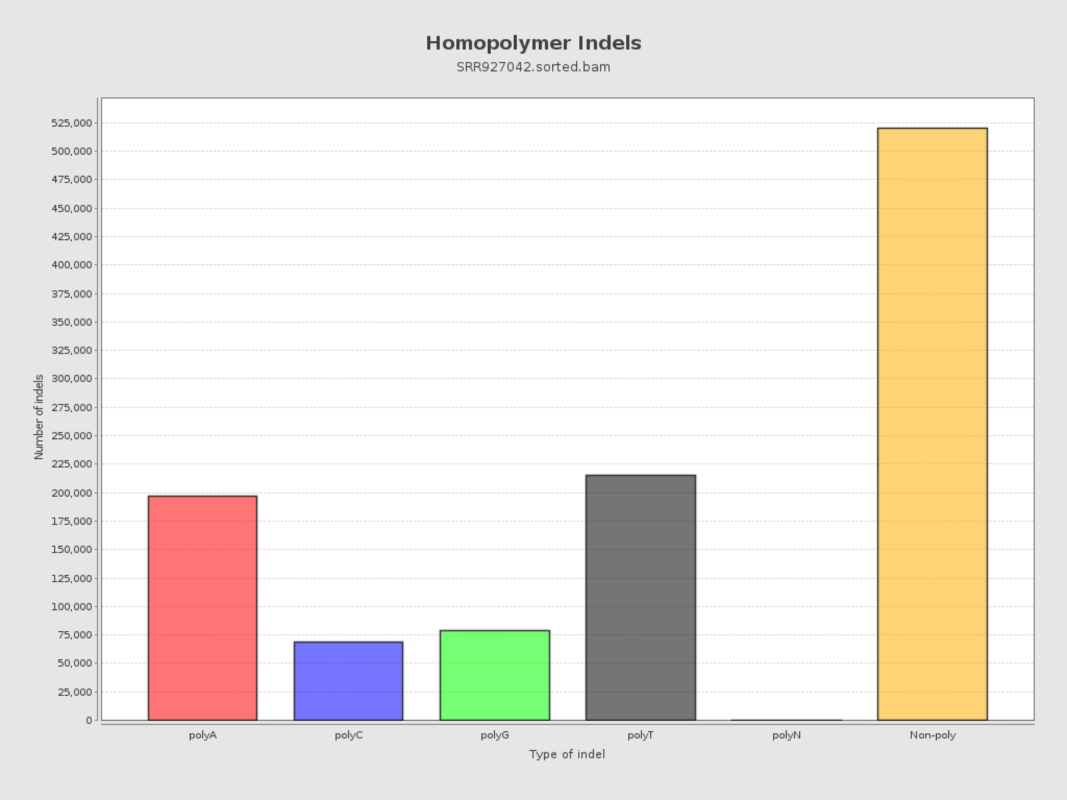
9. Results : Mapped Reads GC-content Distribution



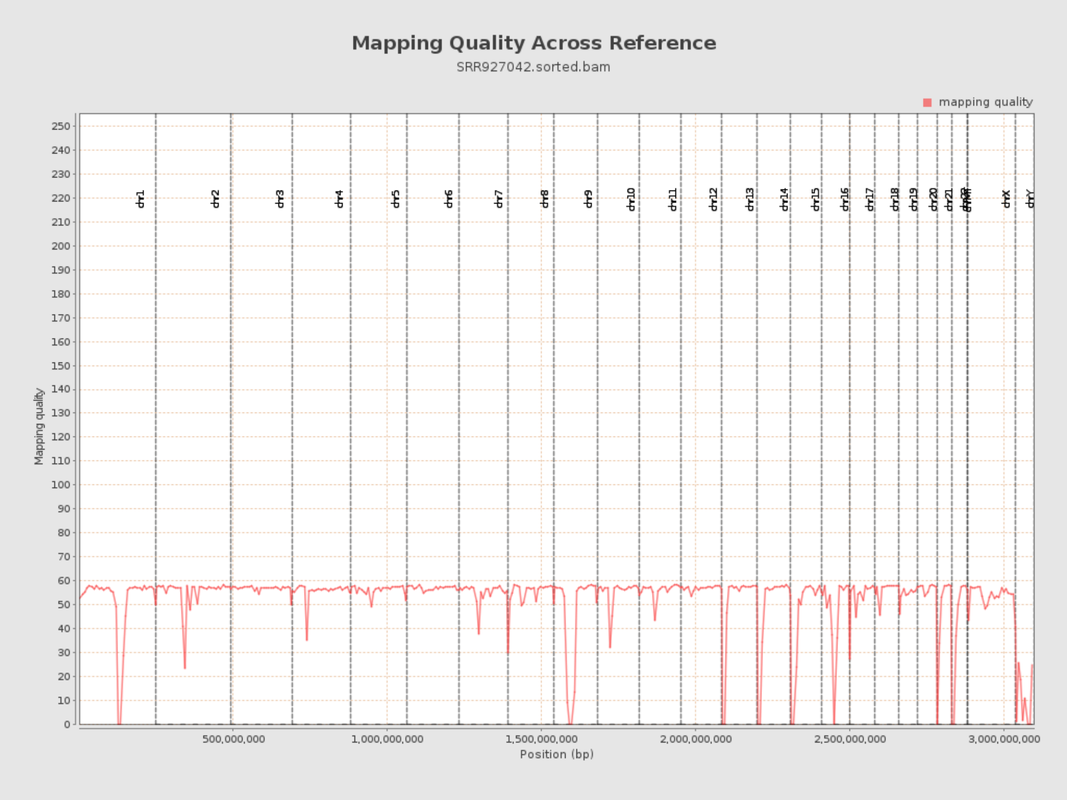
10. Results : Mapped Reads Clipping Profile



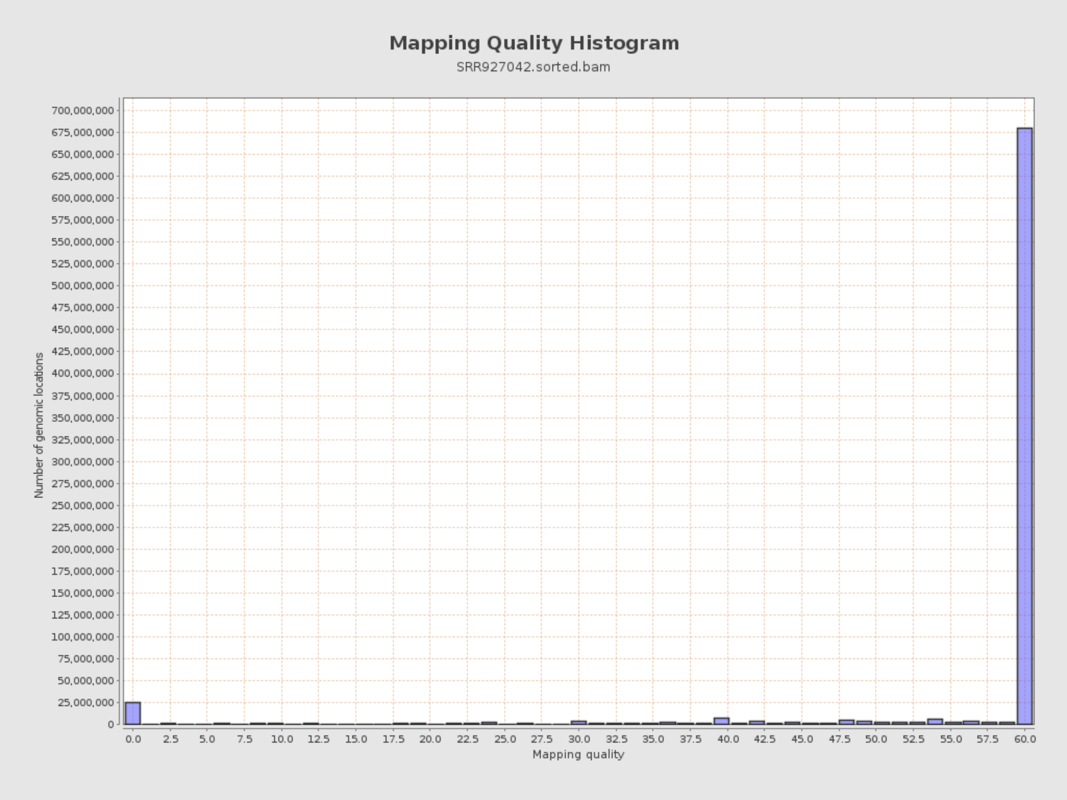
11. Results : Homopolymer Indels



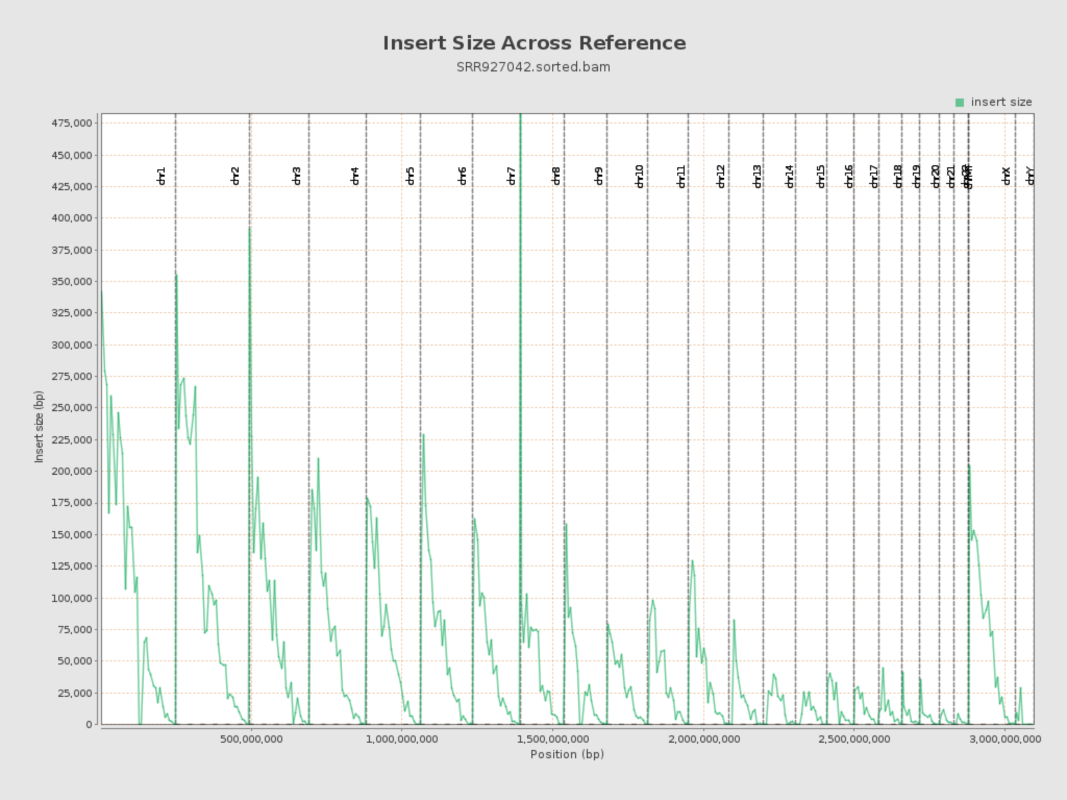
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram