Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 17:38:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927040.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_SRR927040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927040_1.fastq.gz SRR927040_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 17:38:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,499,194
Mapped reads	19,770,824 / 96.45%
Unmapped reads	728,370 / 3.55%
Mapped paired reads	19,770,824 / 96.45%
Mapped reads, first in pair	9,936,504 / 48.47%
Mapped reads, second in pair	9,834,320 / 47.97%
Mapped reads, both in pair	19,335,332 / 94.32%
Mapped reads, singletons	435,492 / 2.12%
Secondary alignments	0
Supplementary alignments	791,361 / 3.86%
Read min/max/mean length	30 / 101 / 102.61
Duplicated reads (estimated)	1,603,120 / 7.82%
Duplication rate	6.4%
Clipped reads	10,190,654 / 49.71%

2.2. ACGT Content

Number/percentage of A's	511,449,489 / 28.76%
Number/percentage of C's	341,825,681 / 19.22%
Number/percentage of T's	525,024,007 / 29.53%
Number/percentage of G's	399,679,036 / 22.48%
Number/percentage of N's	218,321 / 0.01%

GC Percentage	41.7%

2.3. Coverage

Mean	0.5748
Standard Deviation	2.3285

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	415,124.04
Standard Deviation	6,299,466.03
P25/Median/P75	133 / 176 / 241

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	18,787,619
Insertions	308,460
Mapped reads with at least one insertion	1.53%
Deletions	881,111
Mapped reads with at least one deletion	4.34%
Homopolymer indels	51.25%

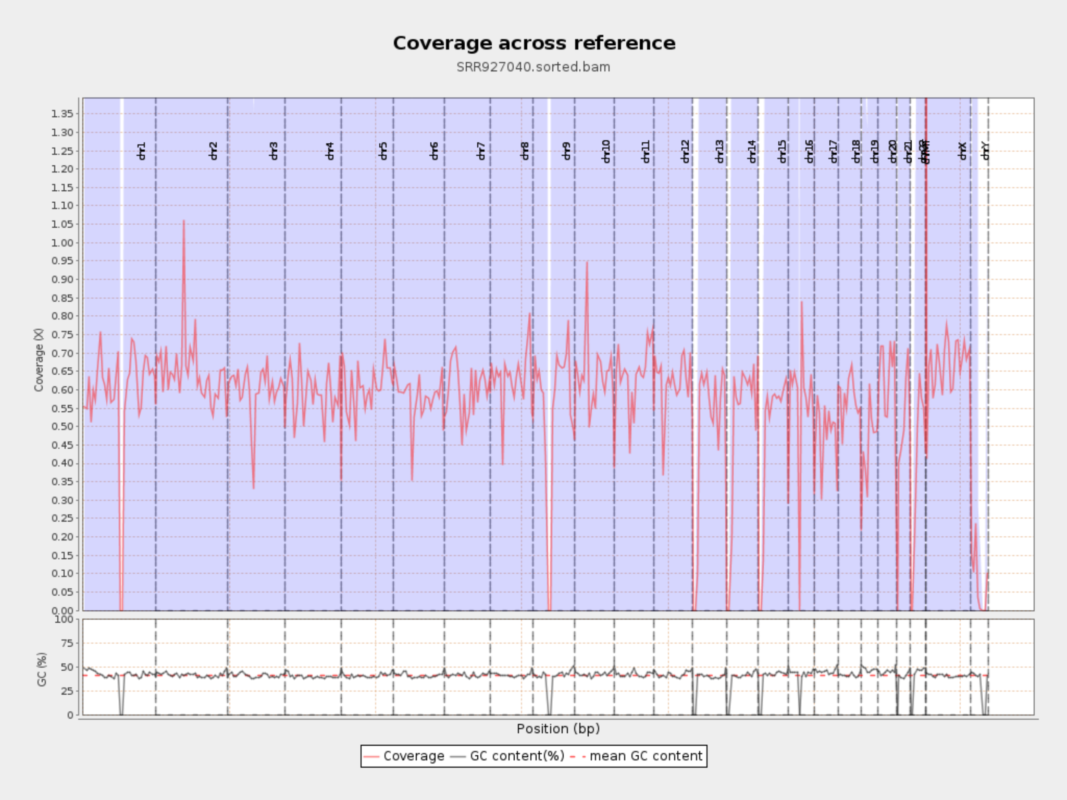
2.7. Chromosome stats

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

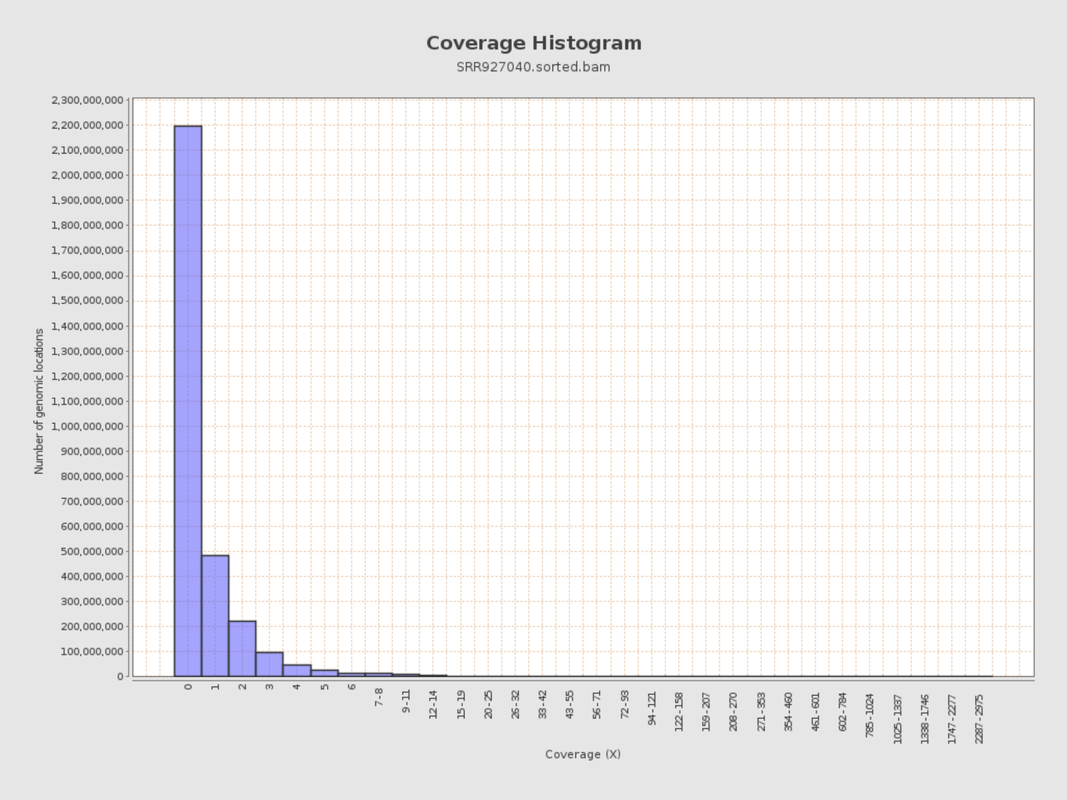
		bases	coverage	deviation
chr1	249250621	146520376	0.5878	3.2562
chr2	243199373	158647865	0.6523	3.9204
chr3	198022430	118567934	0.5988	1.2543
chr4	191154276	113936567	0.596	1.9997
chr5	180915260	110498786	0.6108	1.256
chr6	171115067	99145501	0.5794	1.2972
chr7	159138663	95440517	0.5997	1.8539
chr8	146364022	92771466	0.6338	1.5243
chr9	141213431	77781916	0.5508	2.8391
chr10	135534747	86596840	0.6389	4.2466
chr11	135006516	86109327	0.6378	2.0848
chr12	133851895	83422624	0.6232	1.3084
chr13	115169878	56396485	0.4897	1.1253
chr14	107349540	53508368	0.4984	1.2305
chr15	102531392	47578525	0.464	1.1086
chr16	90354753	49937229	0.5527	3.1757
chr17	81195210	39511091	0.4866	1.5459
chr18	78077248	45018048	0.5766	2.7148
chr19	59128983	26691287	0.4514	1.7874
chr20	63025520	40615271	0.6444	1.396
chr21	48129895	22988781	0.4776	1.6183
chr22	51304566	19791860	0.3858	1.0949
chrMT	16571	106143	6.4053	3.3493
chrX	155270560	103375253	0.6658	1.5112

chrY	59373566	4546943	0.0766	2.8224

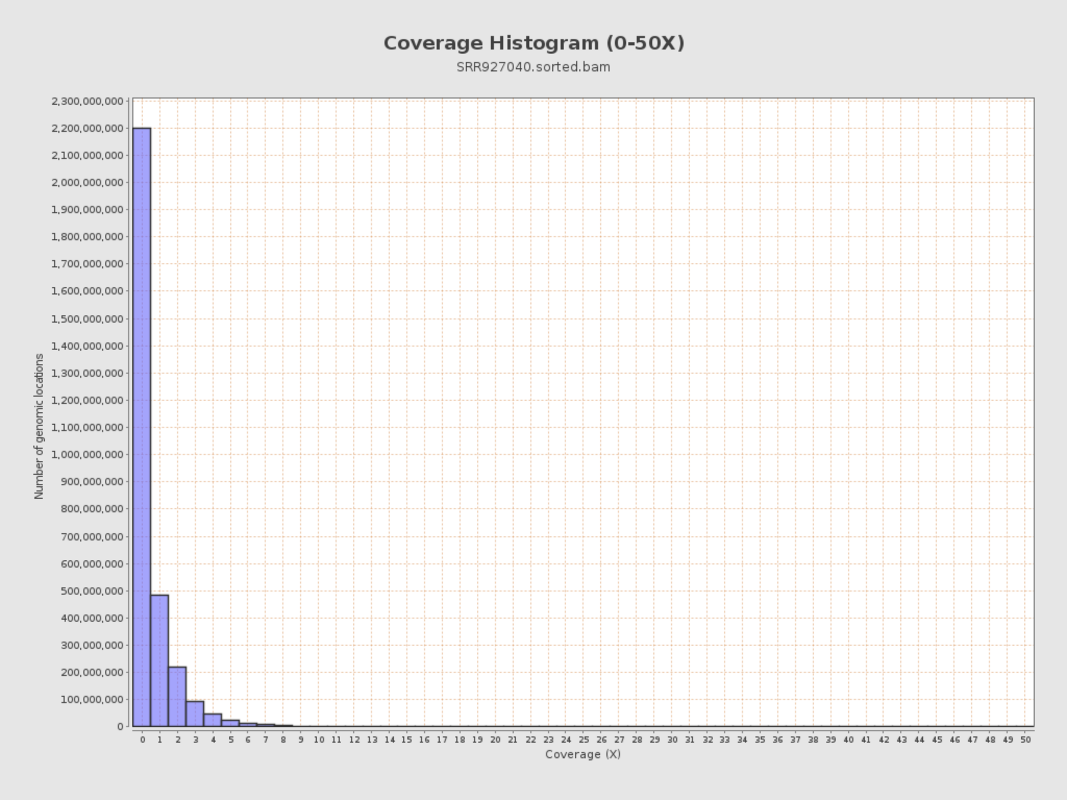
3. Results : Coverage across reference



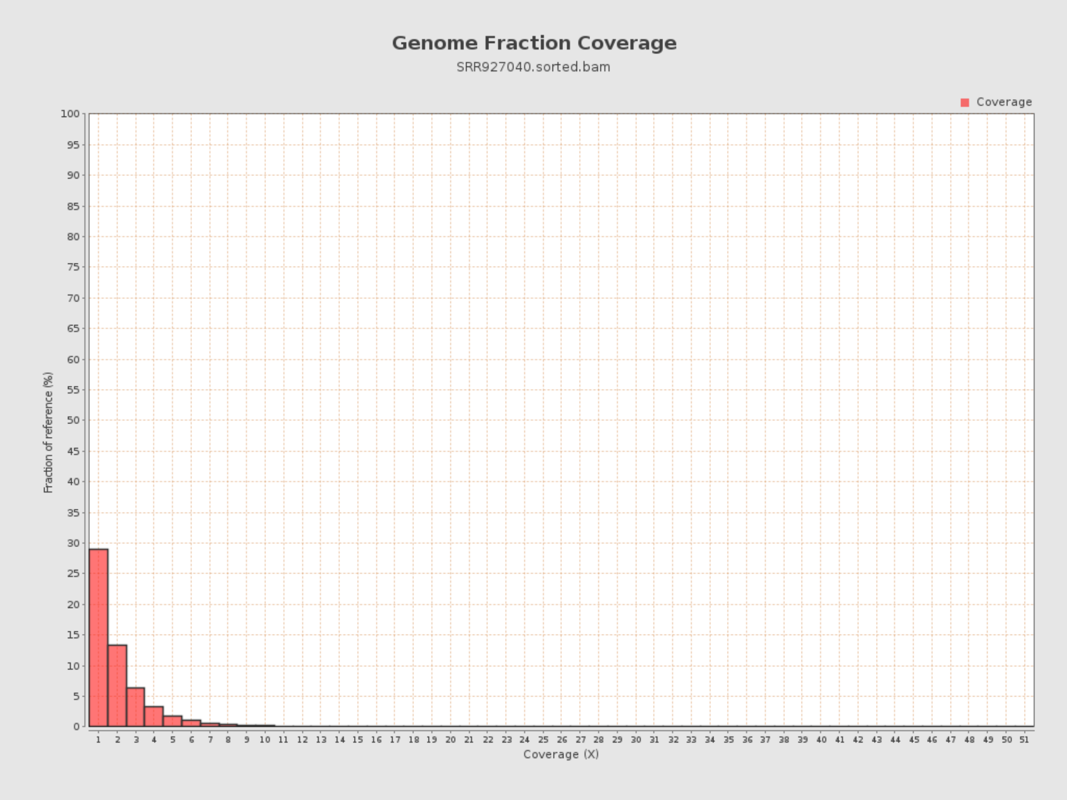
4. Results : Coverage Histogram



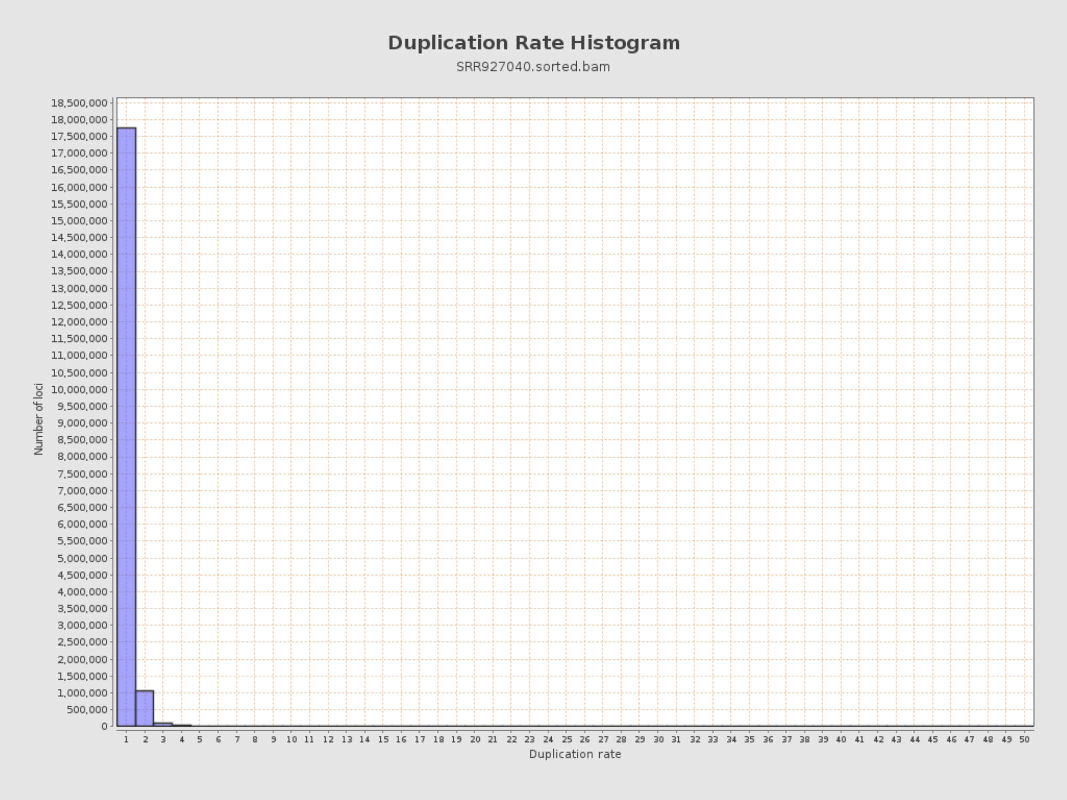
5. Results : Coverage Histogram (0-50X)



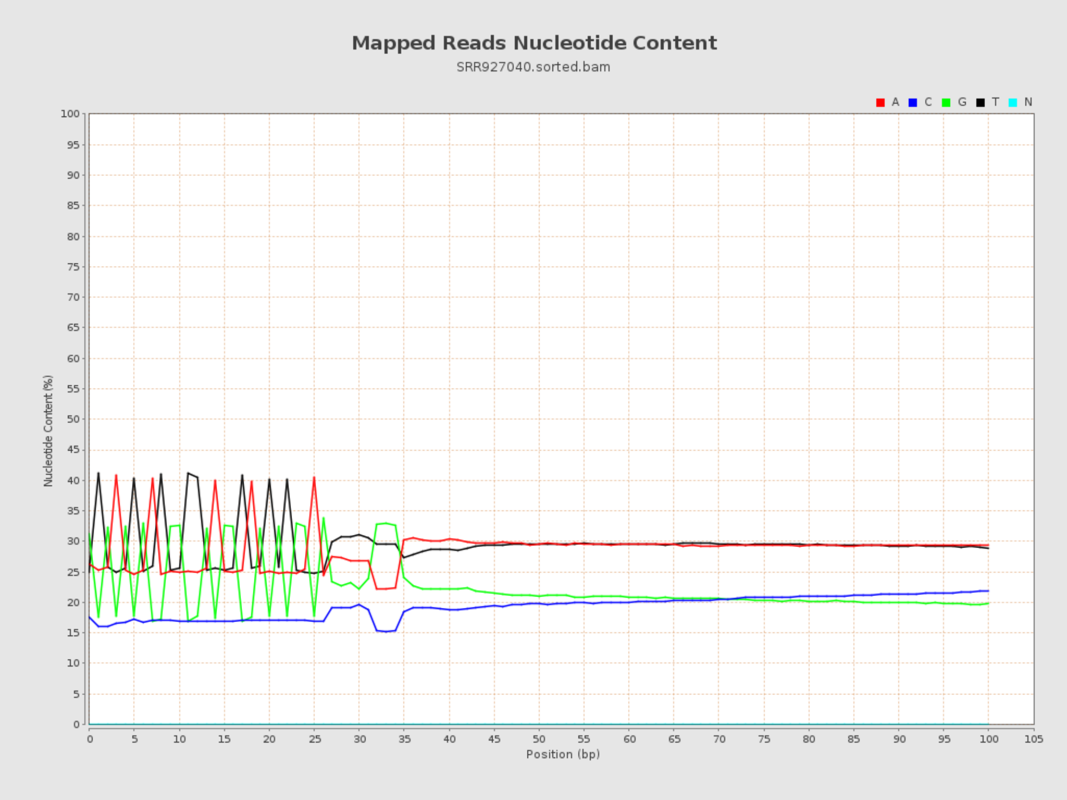
6. Results : Genome Fraction Coverage



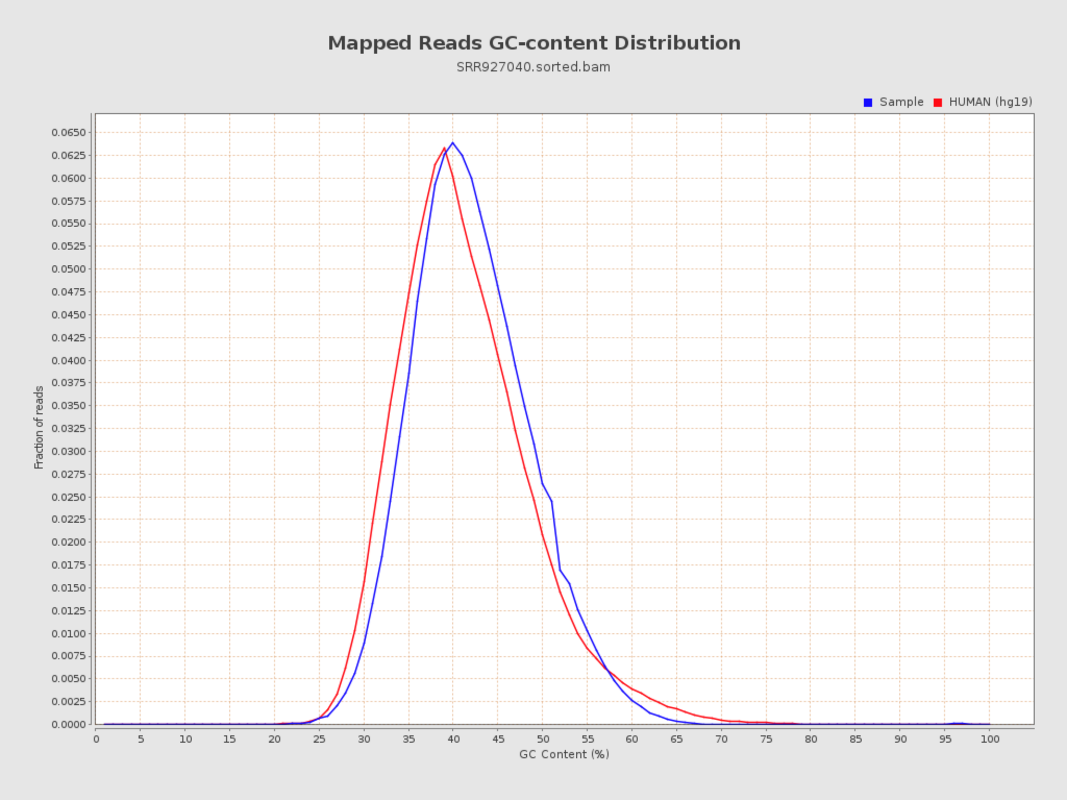
7. Results : Duplication Rate Histogram



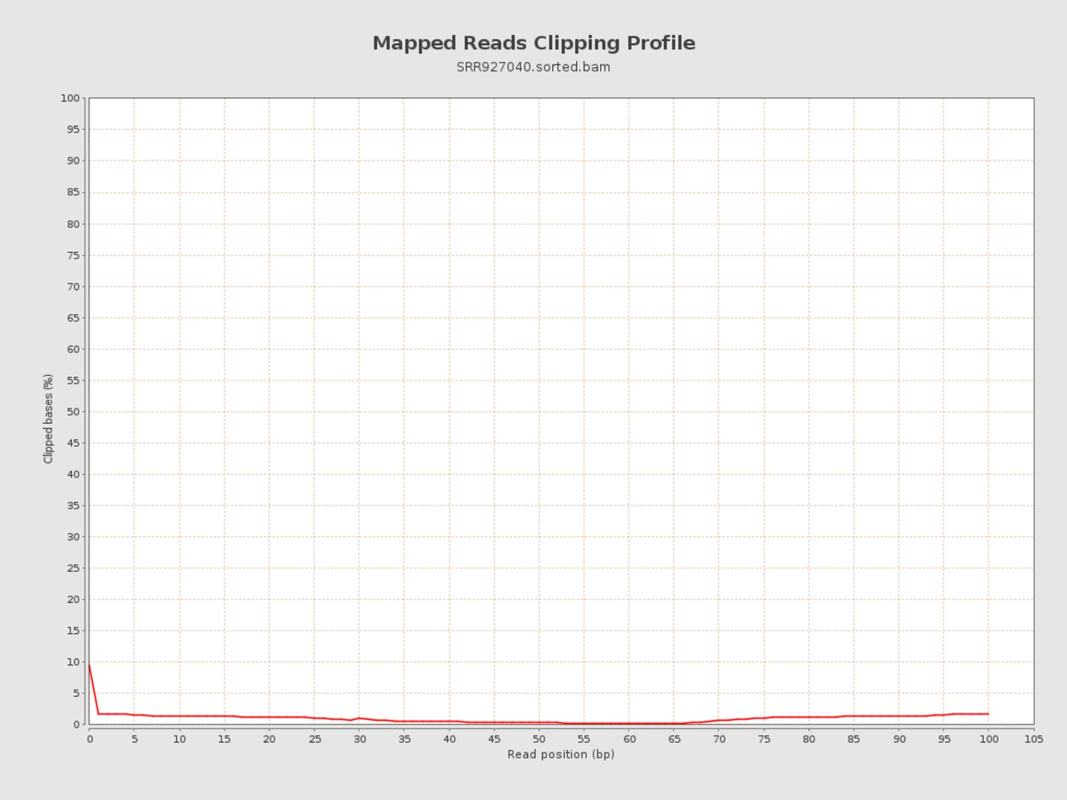
8. Results : Mapped Reads Nucleotide Content



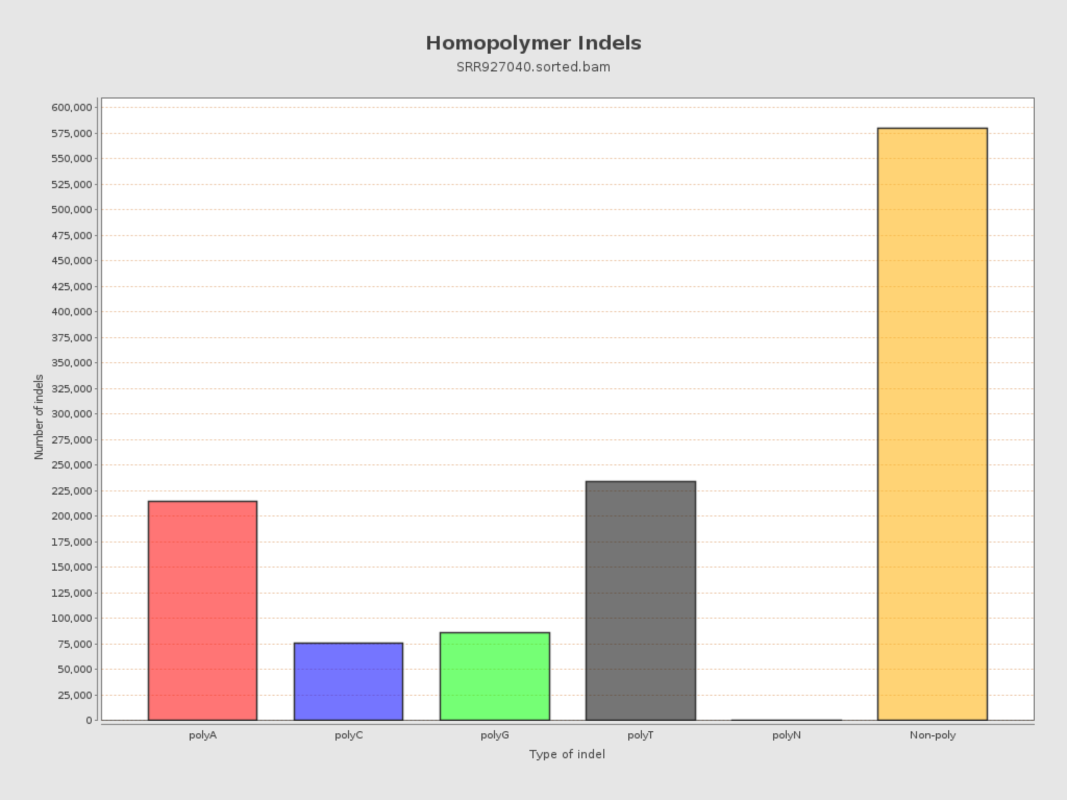
9. Results : Mapped Reads GC-content Distribution



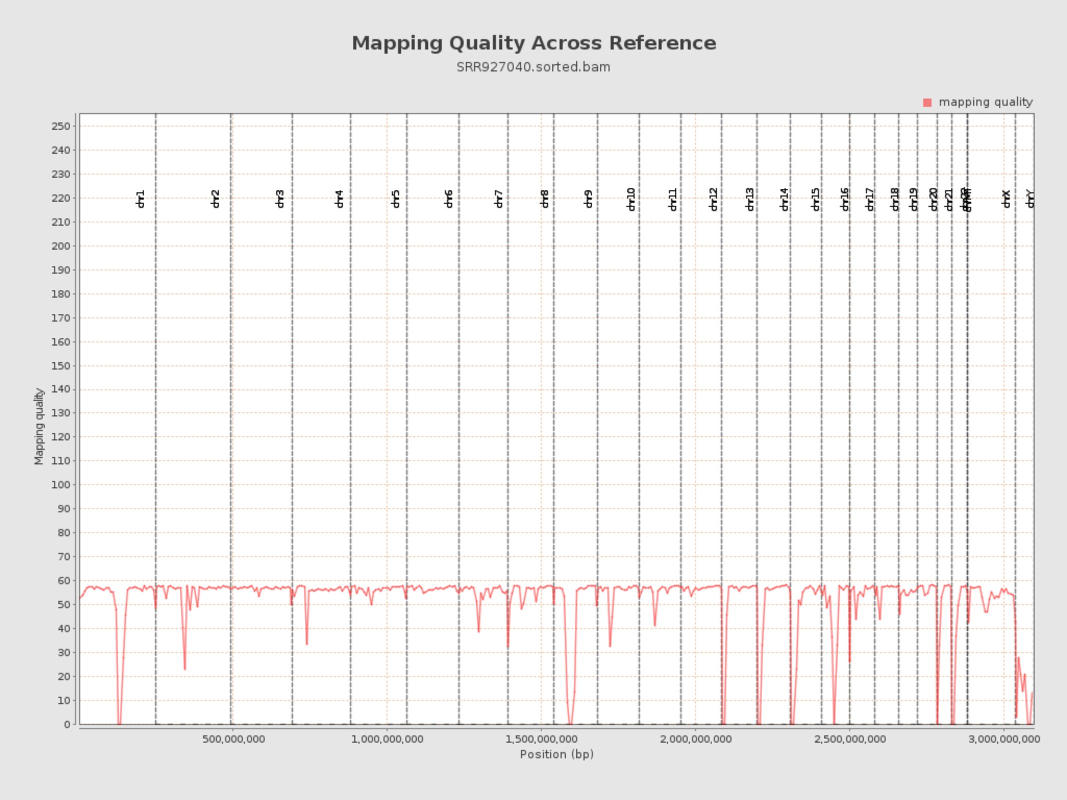
10. Results : Mapped Reads Clipping Profile



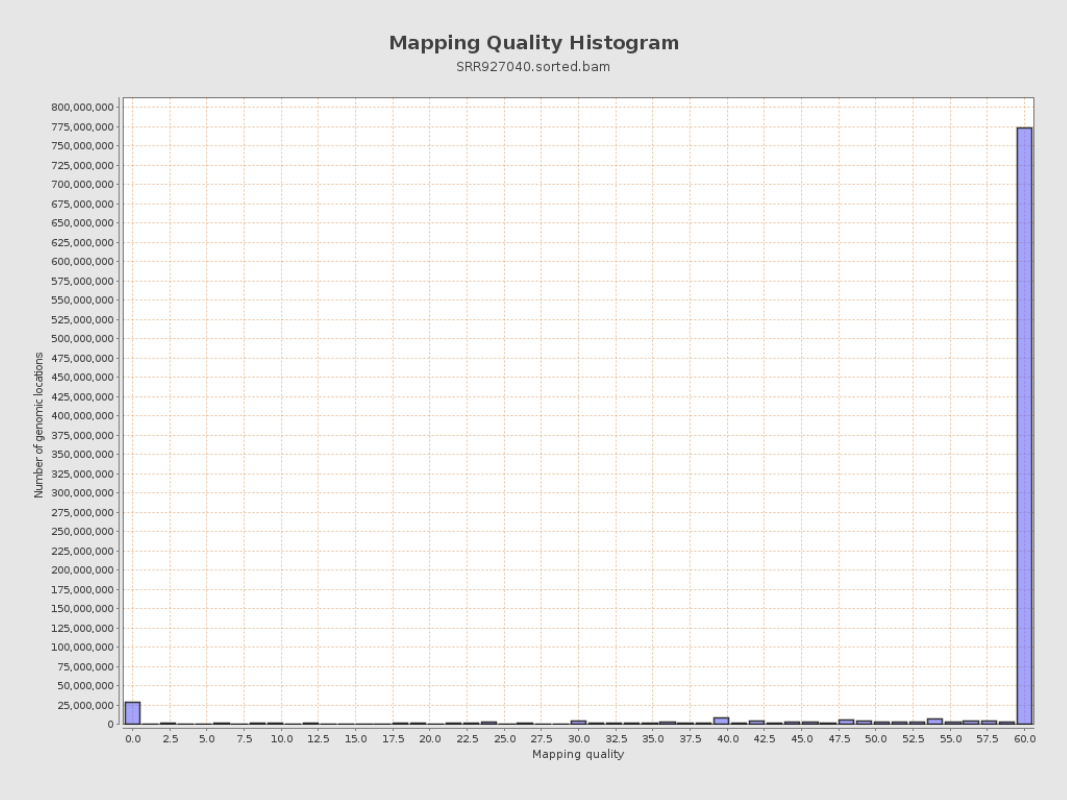
11. Results : Homopolymer Indels



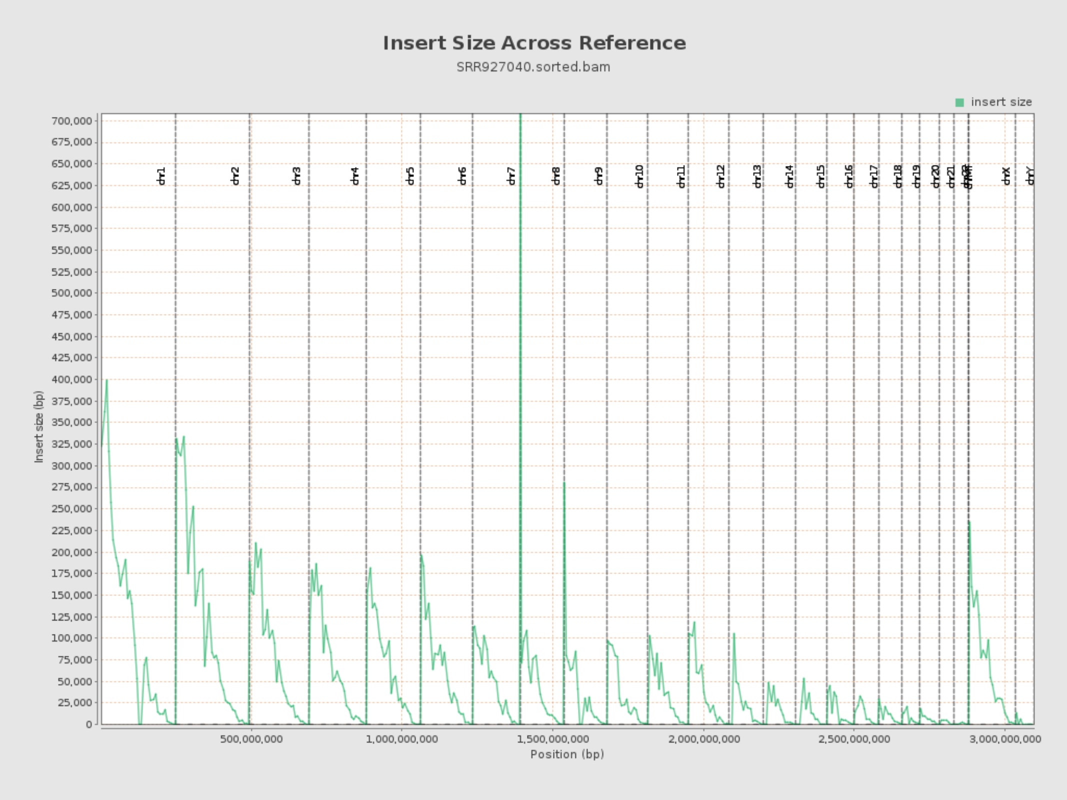
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram