Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 13:05:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927032.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_SRR927032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927032_1.fastq.gz SRR927032_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 13:05:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,823,768
Mapped reads	20,181,443 / 96.92%
Unmapped reads	642,325 / 3.08%
Mapped paired reads	20,181,443 / 96.92%
Mapped reads, first in pair	10,125,522 / 48.62%
Mapped reads, second in pair	10,055,921 / 48.29%
Mapped reads, both in pair	19,831,554 / 95.24%
Mapped reads, singletons	349,889 / 1.68%
Secondary alignments	0
Supplementary alignments	846,989 / 4.07%
Read min/max/mean length	30 / 101 / 102.7
Duplicated reads (estimated)	1,839,423 / 8.83%
Duplication rate	7.25%
Clipped reads	10,614,478 / 50.97%

2.2. ACGT Content

Number/percentage of A's	510,580,266 / 28.4%
Number/percentage of C's	348,284,487 / 19.37%
Number/percentage of T's	524,665,341 / 29.18%
Number/percentage of G's	414,101,797 / 23.03%
Number/percentage of N's	184,054 / 0.01%

GC Percentage	42.41%

2.3. Coverage

Mean	0.5812
Standard Deviation	2.4183

2.4. Mapping Quality

Mean Mapping Quality	52.06

2.5. Insert size

Mean	433,794.89
Standard Deviation	6,446,937.8
P25/Median/P75	128 / 169 / 231

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	19,878,558
Insertions	314,415
Mapped reads with at least one insertion	1.53%
Deletions	923,911
Mapped reads with at least one deletion	4.46%
Homopolymer indels	51.15%

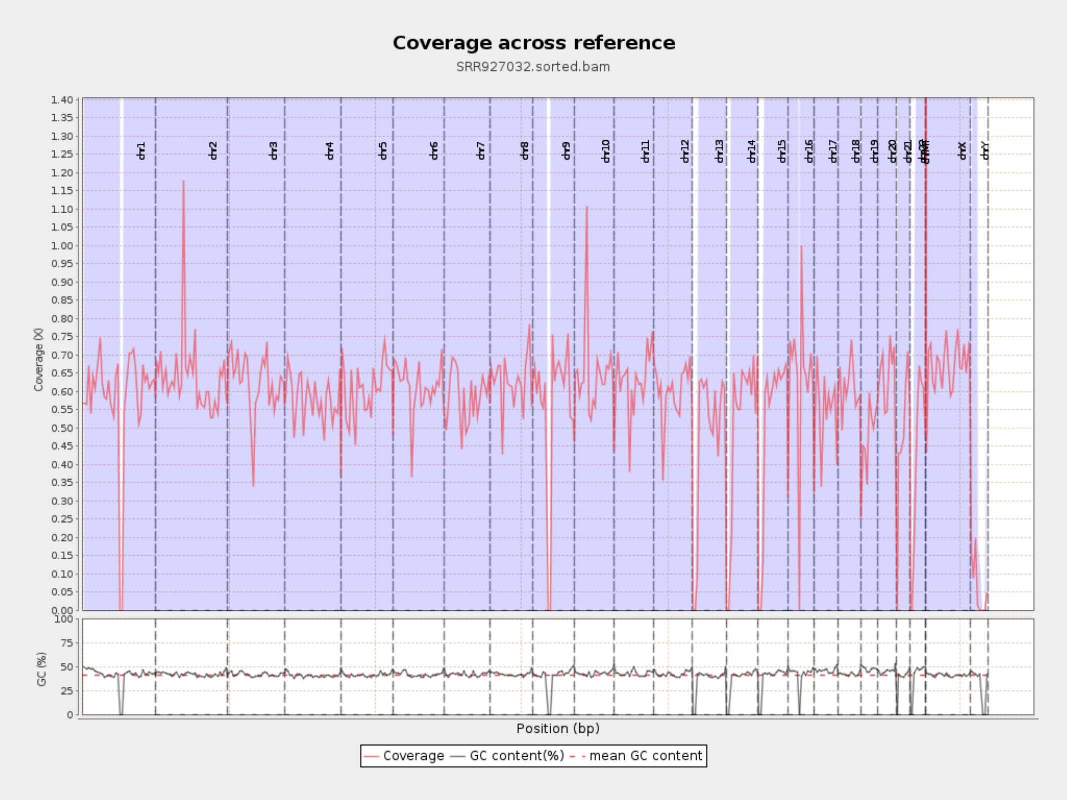
2.7. Chromosome stats

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

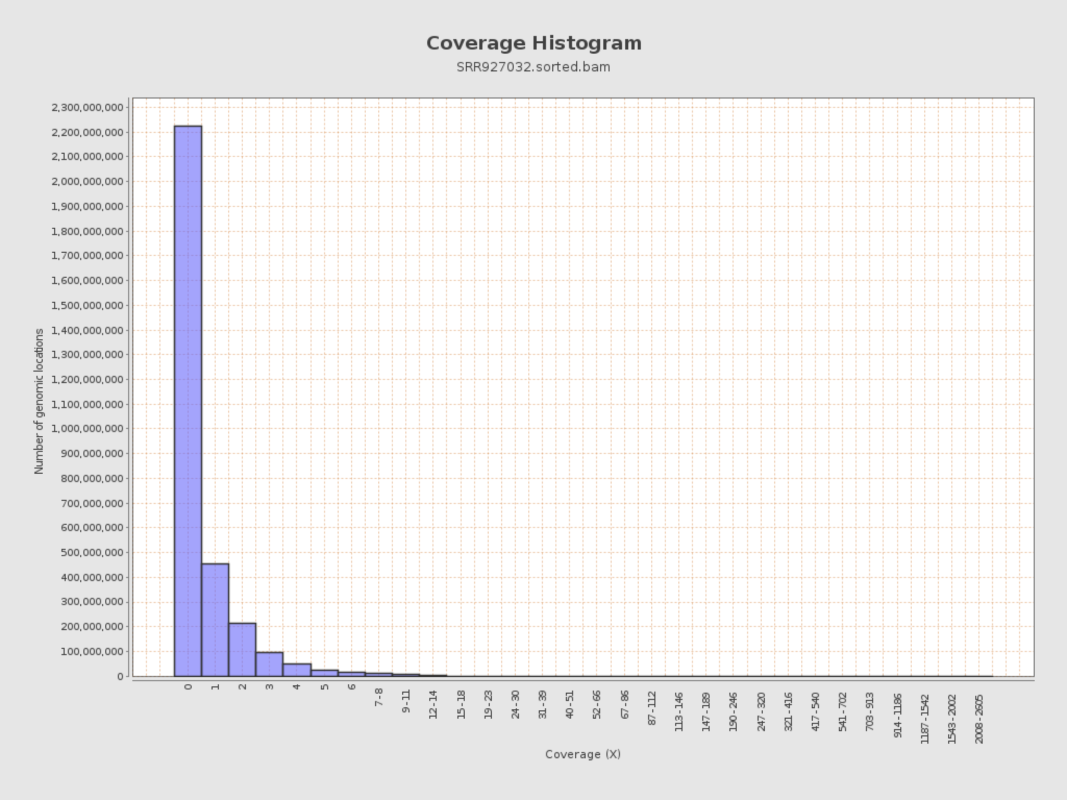
		bases	coverage	deviation
chr1	249250621	145390095	0.5833	2.8612
chr2	243199373	155748441	0.6404	3.9741
chr3	198022430	123261560	0.6225	1.3669
chr4	191154276	111310650	0.5823	1.7385
chr5	180915260	109920112	0.6076	1.2983
chr6	171115067	104948777	0.6133	1.3416
chr7	159138663	92945289	0.5841	1.7909
chr8	146364022	91932672	0.6281	1.6266
chr9	141213431	79663986	0.5641	2.9316
chr10	135534747	88089435	0.6499	5.4129
chr11	135006516	84461226	0.6256	1.8654
chr12	133851895	80667117	0.6027	1.3187
chr13	115169878	54519805	0.4734	1.1352
chr14	107349540	54419286	0.5069	1.2596
chr15	102531392	51577065	0.503	1.207
chr16	90354753	56280343	0.6229	3.7174
chr17	81195210	45124028	0.5557	1.5383
chr18	78077248	47870290	0.6131	2.9965
chr19	59128983	28427866	0.4808	1.7691
chr20	63025520	40628477	0.6446	1.4394
chr21	48129895	23334483	0.4848	1.7108
chr22	51304566	21169717	0.4126	1.1681
chrMT	16571	122807	7.411	7.2691
chrX	155270560	103841183	0.6688	1.5244

chrY	59373566	3524764	0.0594	2.4358

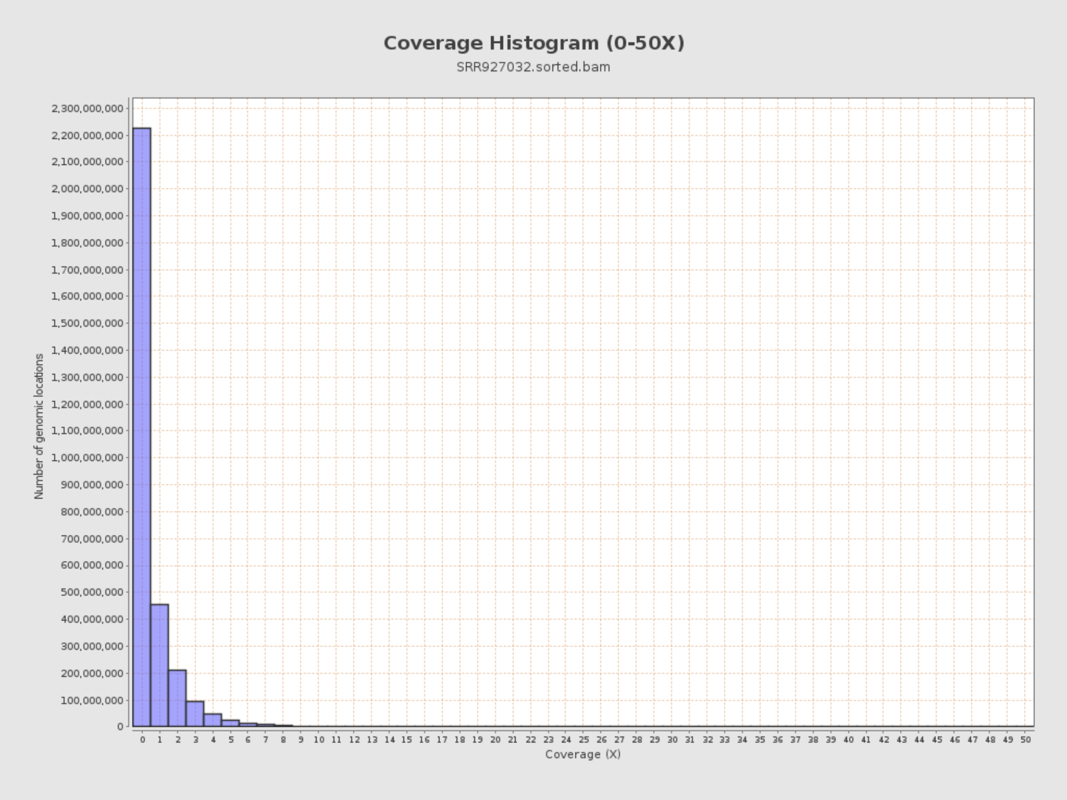
3. Results : Coverage across reference



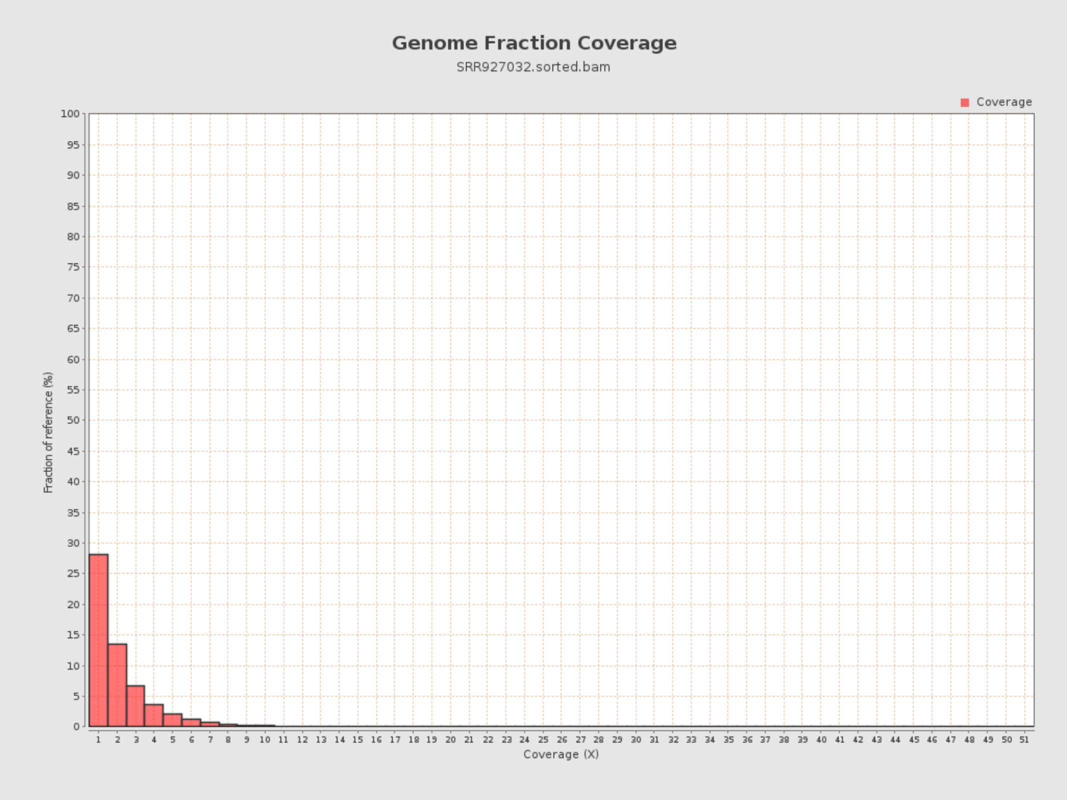
4. Results : Coverage Histogram



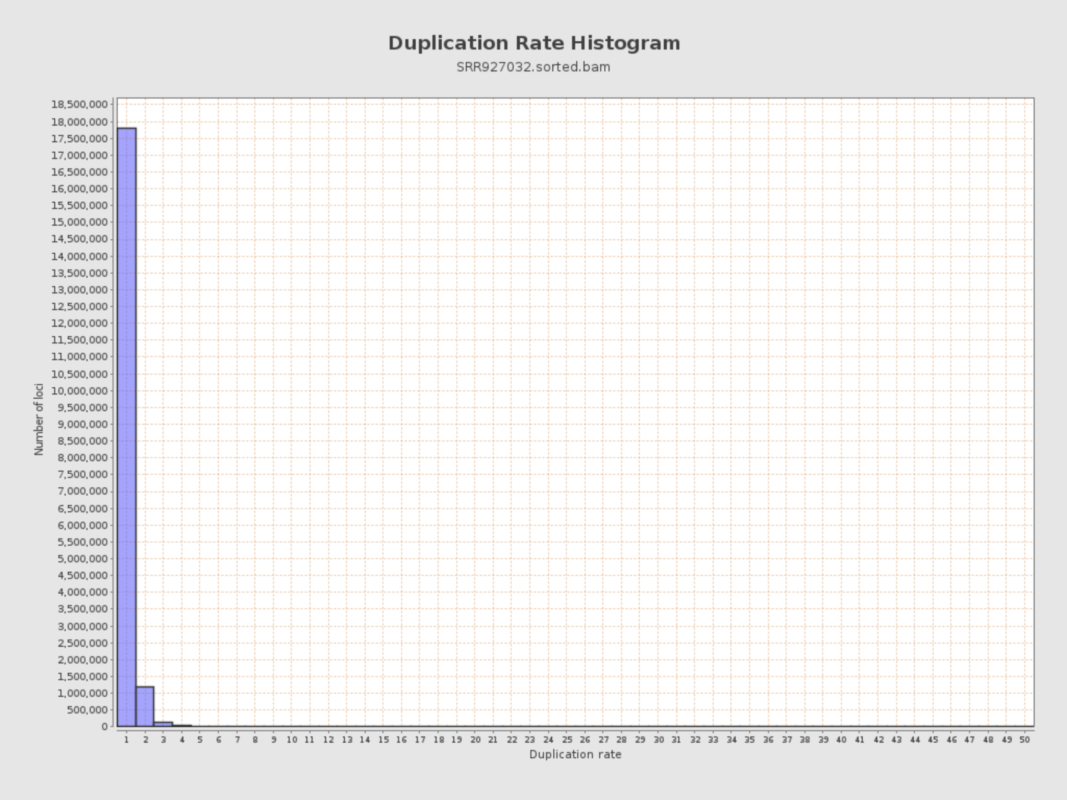
5. Results : Coverage Histogram (0-50X)



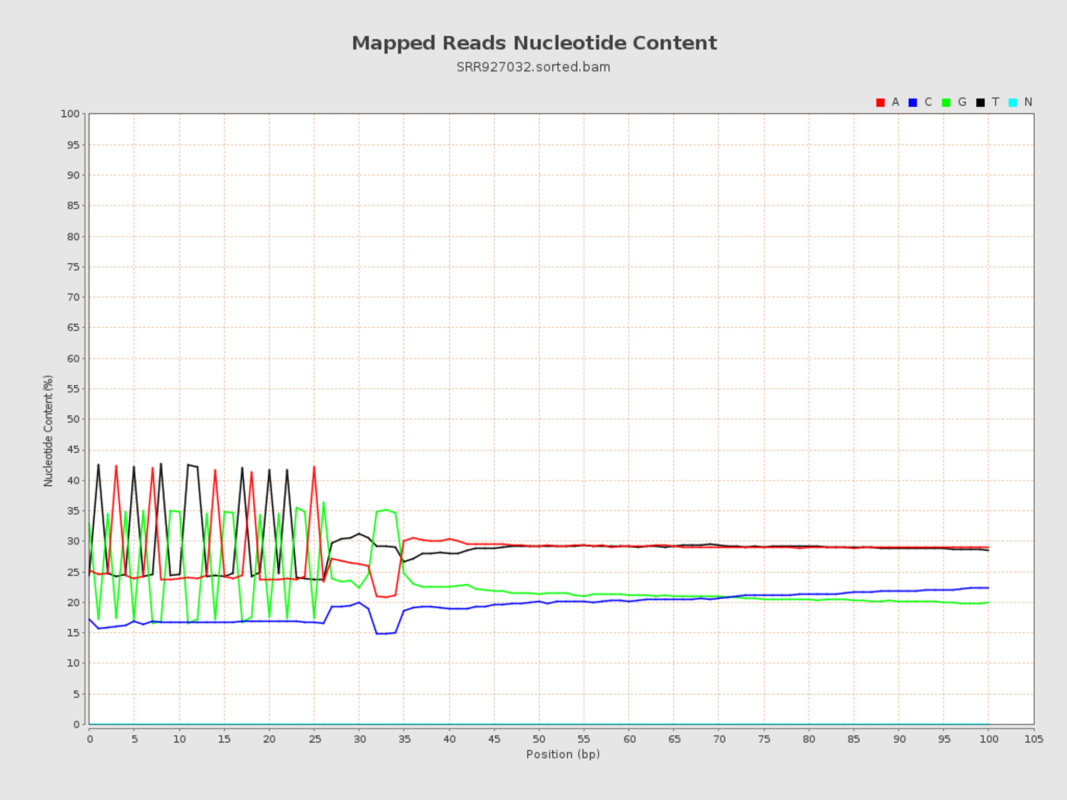
6. Results : Genome Fraction Coverage



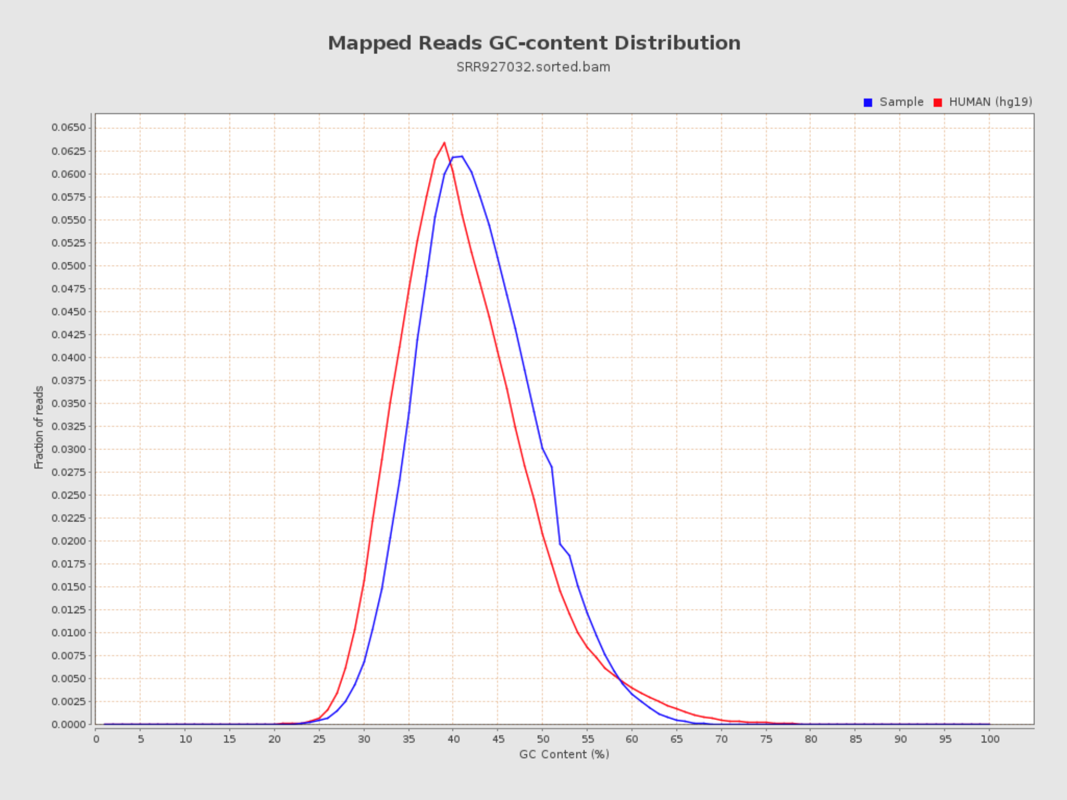
7. Results : Duplication Rate Histogram



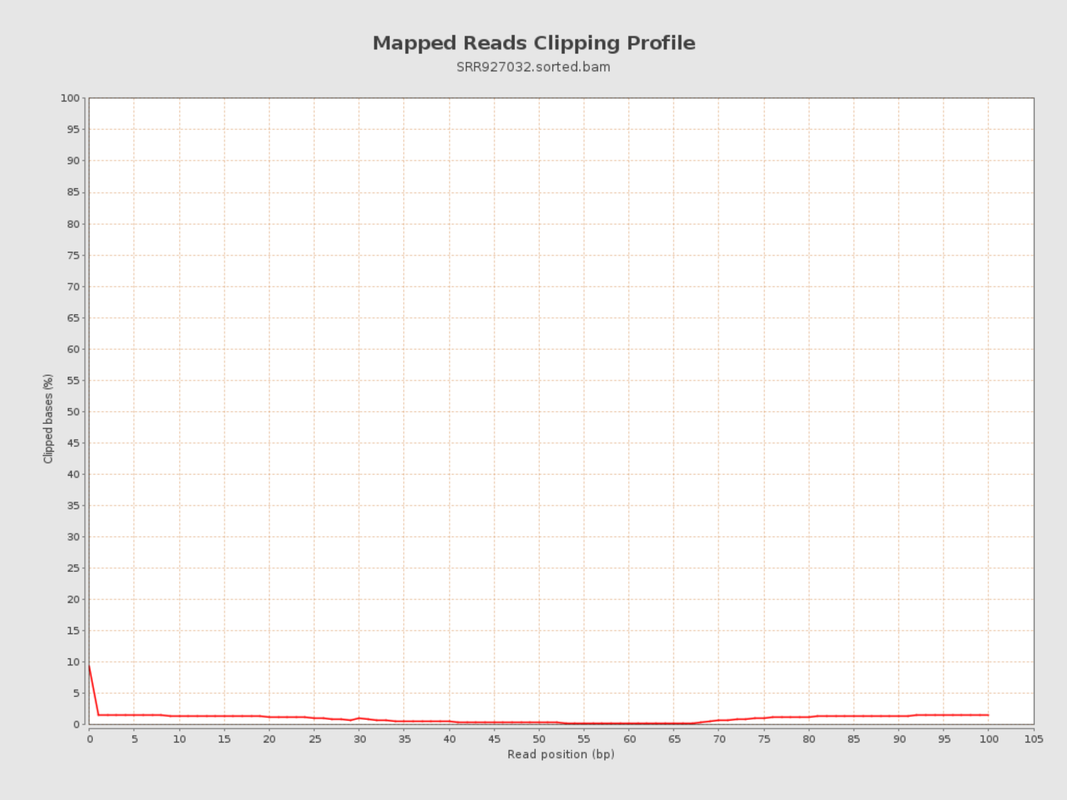
8. Results : Mapped Reads Nucleotide Content



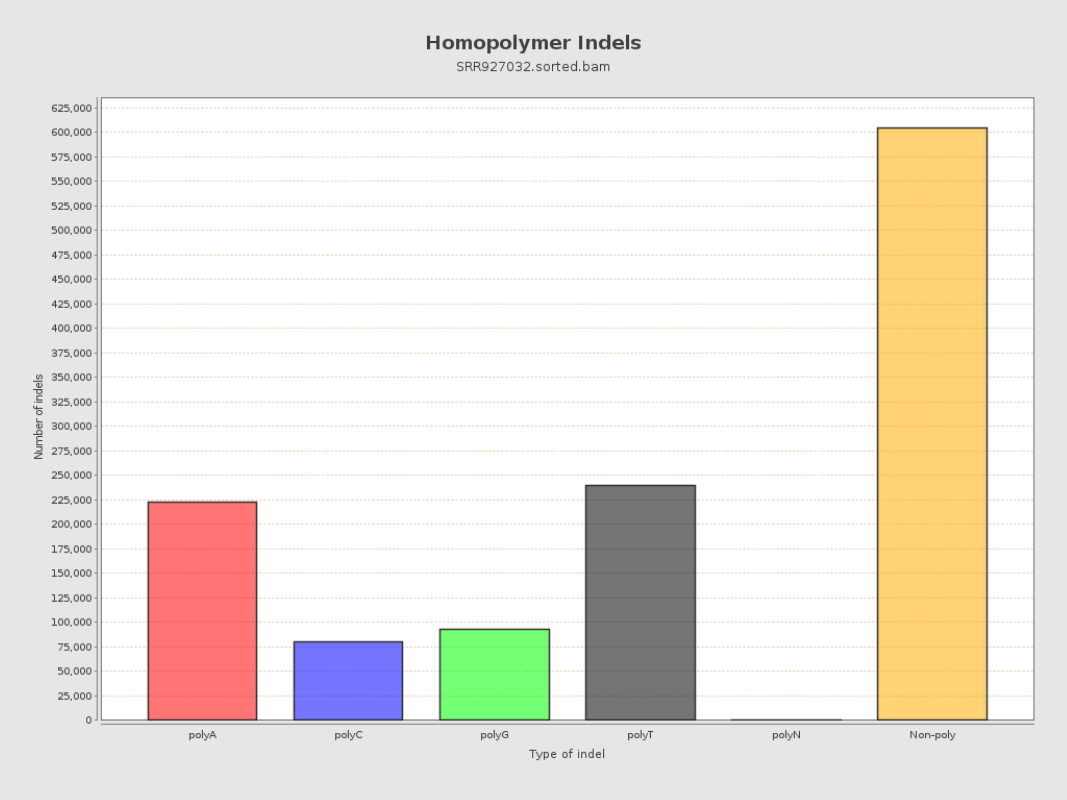
9. Results : Mapped Reads GC-content Distribution



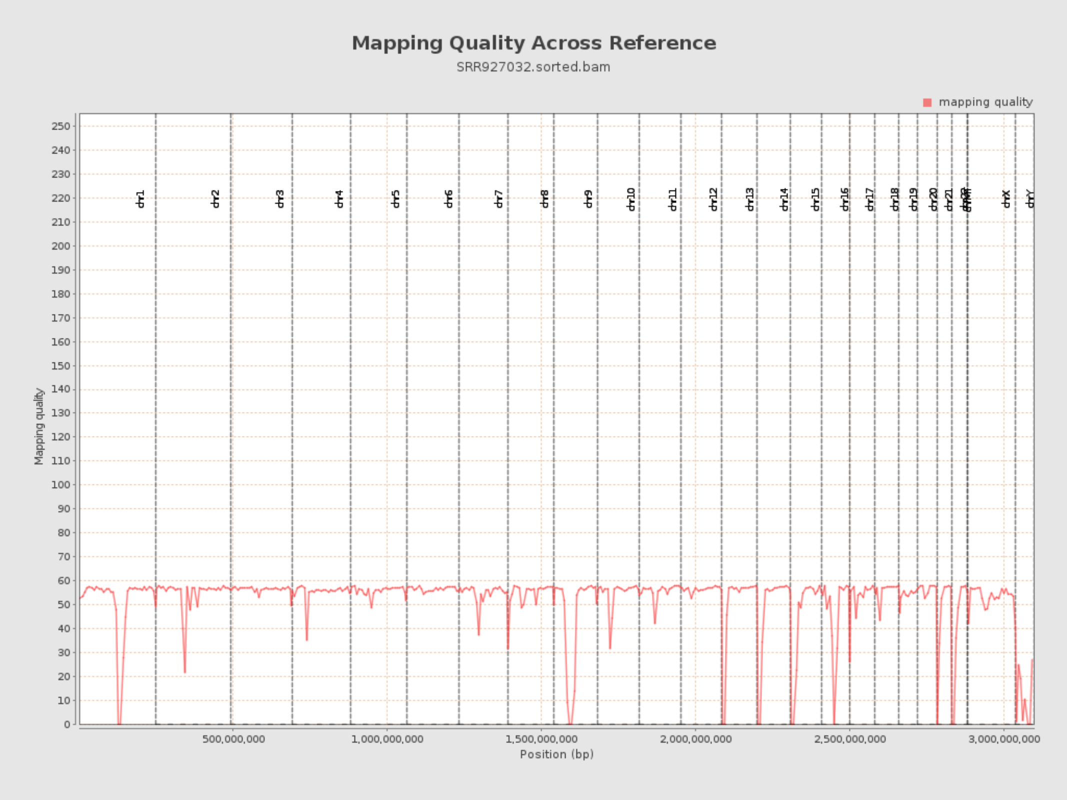
10. Results : Mapped Reads Clipping Profile



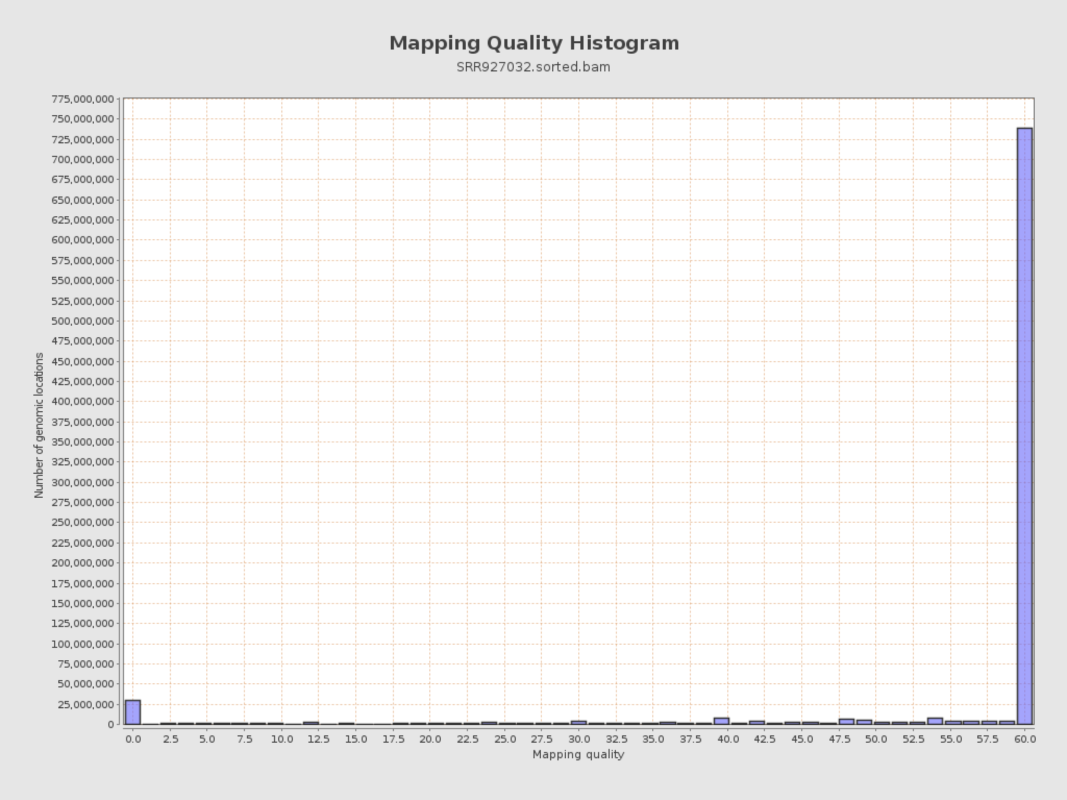
11. Results : Homopolymer Indels



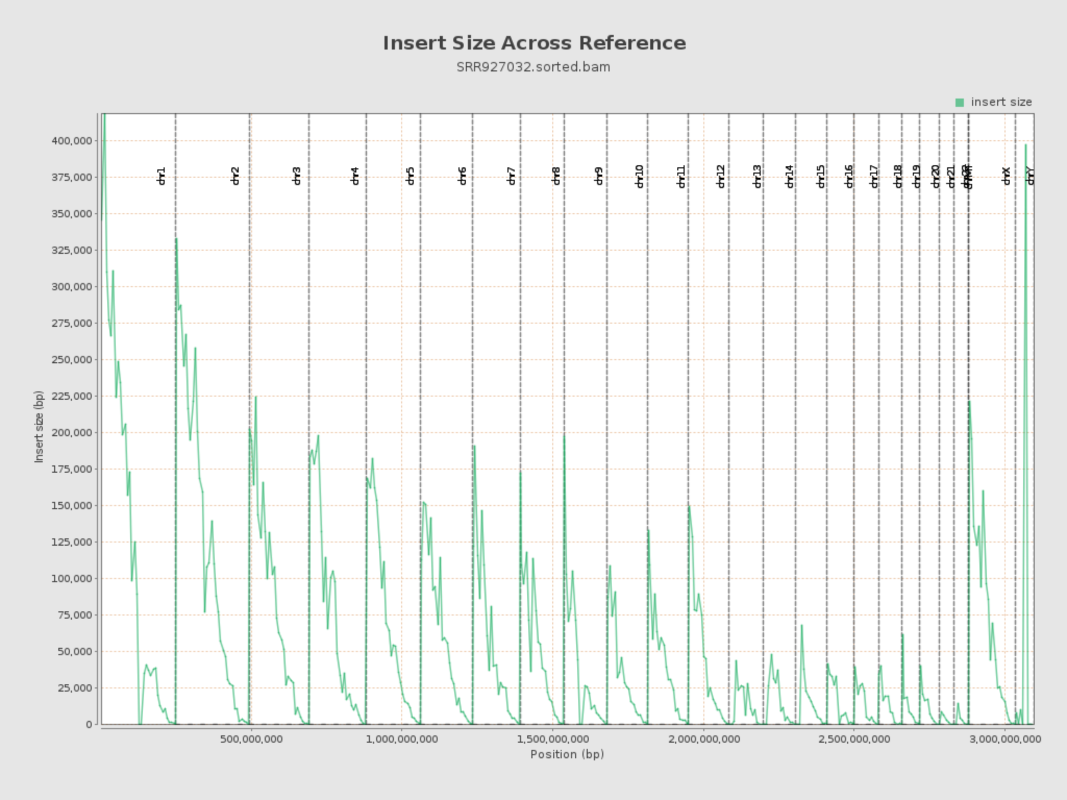
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram