Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 06:33:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927065.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_SRR927065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927065_1.fastq.gz SRR927065_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 06:33:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,309,364
Mapped reads	22,720,781 / 97.47%
Unmapped reads	588,583 / 2.53%
Mapped paired reads	22,720,781 / 97.47%
Mapped reads, first in pair	11,412,690 / 48.96%
Mapped reads, second in pair	11,308,091 / 48.51%
Mapped reads, both in pair	22,379,570 / 96.01%
Mapped reads, singletons	341,211 / 1.46%
Secondary alignments	0
Supplementary alignments	503,308 / 2.16%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	1,598,814 / 6.86%
Duplication rate	5.49%
Clipped reads	9,359,678 / 40.15%

2.2. ACGT Content

Number/percentage of A's	591,472,270 / 28.4%
Number/percentage of C's	413,040,594 / 19.83%
Number/percentage of T's	602,520,302 / 28.93%
Number/percentage of G's	475,358,436 / 22.82%
Number/percentage of N's	310,348 / 0.01%

GC Percentage	42.66%

2.3. Coverage

Mean	0.6732
Standard Deviation	2.8335

2.4. Mapping Quality

Mean Mapping Quality	52.77

2.5. Insert size

Mean	230,753.28
Standard Deviation	4,700,814.98
P25/Median/P75	139 / 181 / 244

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	21,270,642
Insertions	336,217
Mapped reads with at least one insertion	1.45%
Deletions	991,722
Mapped reads with at least one deletion	4.26%
Homopolymer indels	51.65%

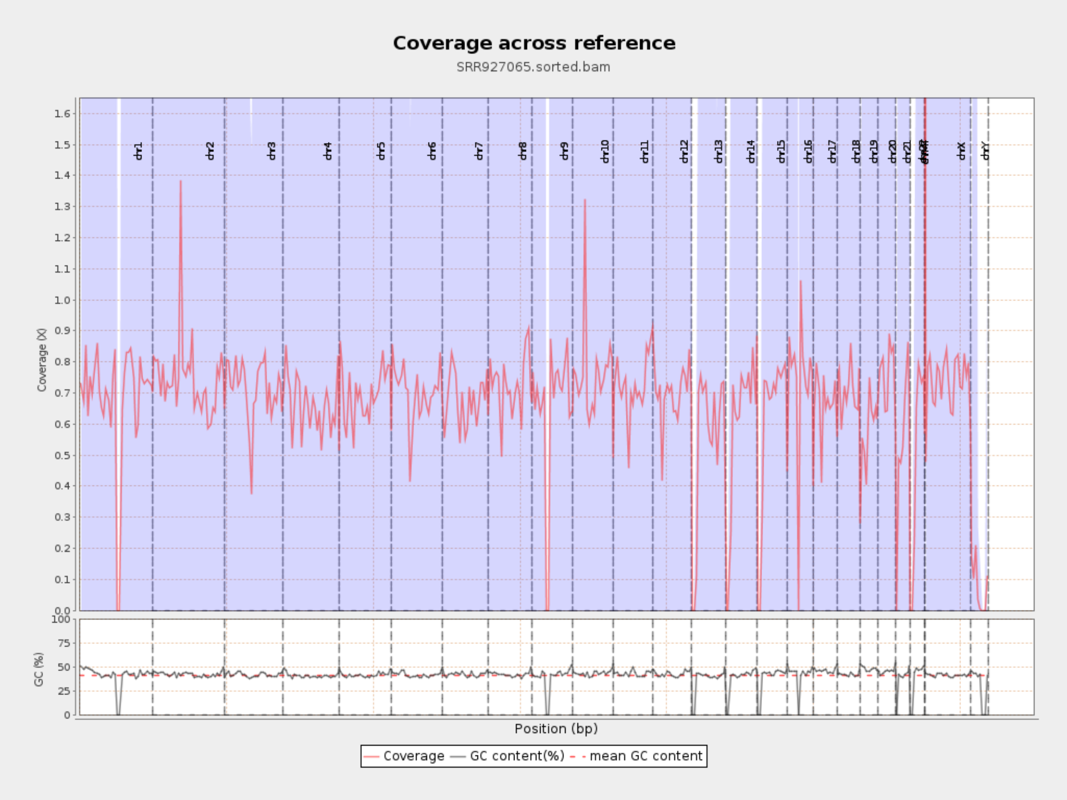
2.7. Chromosome stats

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

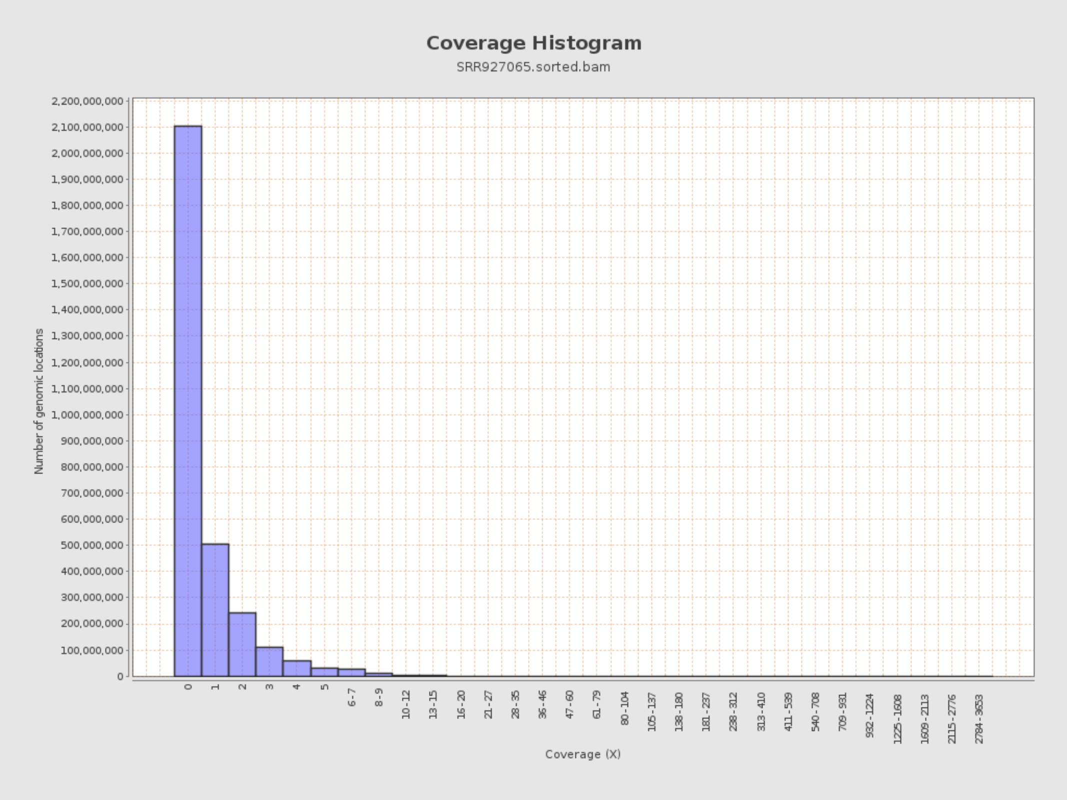
		bases	coverage	deviation
chr1	249250621	170153416	0.6827	3.9467
chr2	243199373	182761559	0.7515	4.5851
chr3	198022430	141526847	0.7147	1.4097
chr4	191154276	126608268	0.6623	2.1403
chr5	180915260	126213046	0.6976	1.367
chr6	171115067	120402641	0.7036	1.4642
chr7	159138663	107786039	0.6773	2.0513
chr8	146364022	106643406	0.7286	1.7717
chr9	141213431	91171555	0.6456	3.4093
chr10	135534747	104109799	0.7681	6.6155
chr11	135006516	97089809	0.7191	2.1321
chr12	133851895	93682383	0.6999	1.387
chr13	115169878	62706805	0.5445	1.2006
chr14	107349540	62758404	0.5846	1.315
chr15	102531392	61607689	0.6009	1.3302
chr16	90354753	65173255	0.7213	3.6018
chr17	81195210	54106691	0.6664	1.9353
chr18	78077248	55835594	0.7151	3.4618
chr19	59128983	34080679	0.5764	2.3055
chr20	63025520	48170533	0.7643	1.5748
chr21	48129895	26926058	0.5594	1.8252
chr22	51304566	25518506	0.4974	1.2577
chrMT	16571	186959	11.2823	6.0596
chrX	155270560	114463962	0.7372	1.6655

chrY	59373566	4468886	0.0753	1.7806

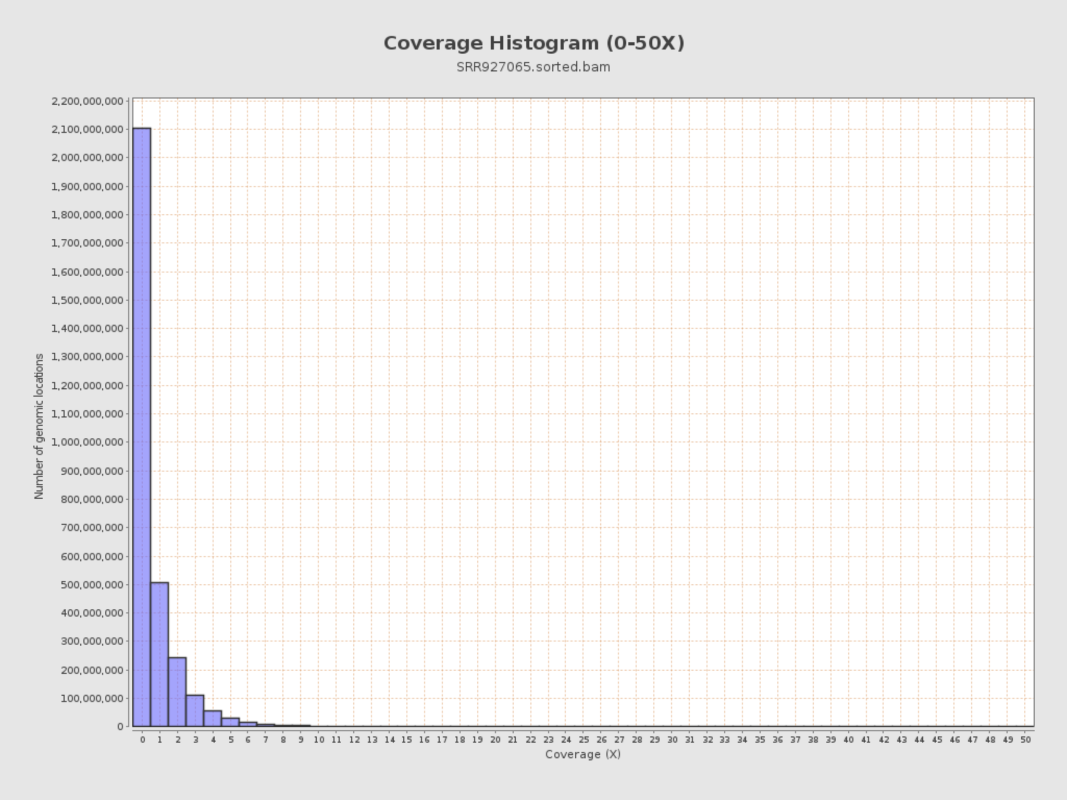
3. Results : Coverage across reference



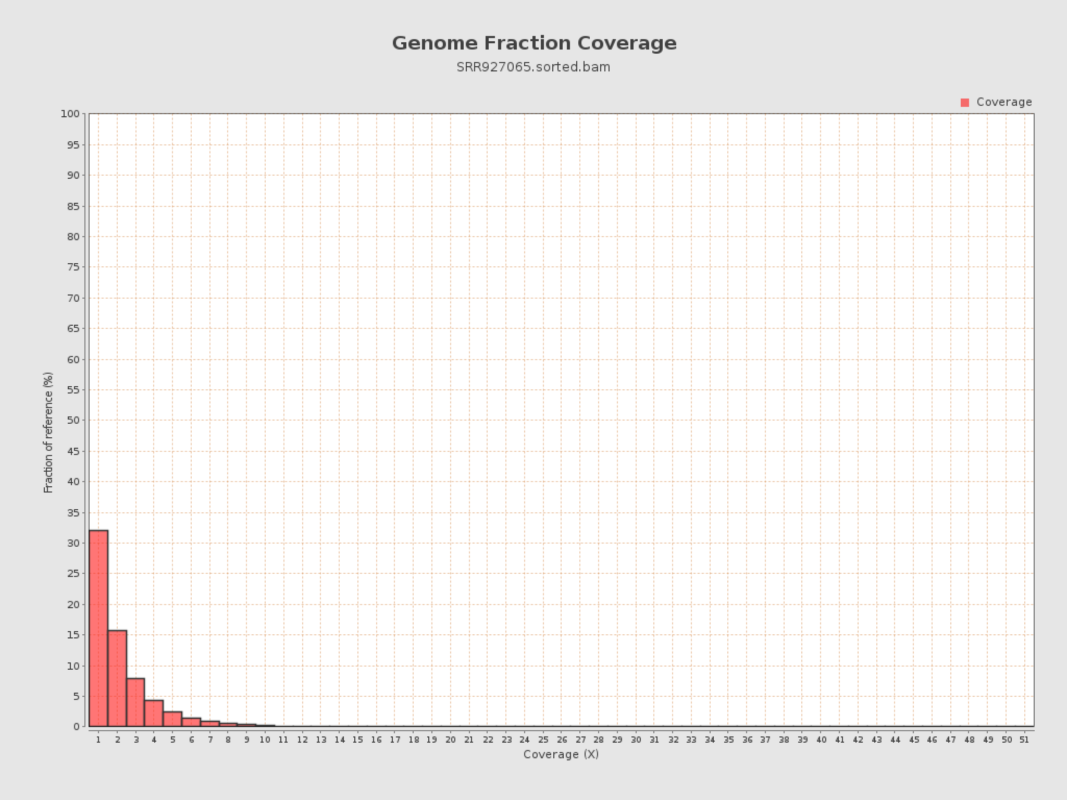
4. Results : Coverage Histogram



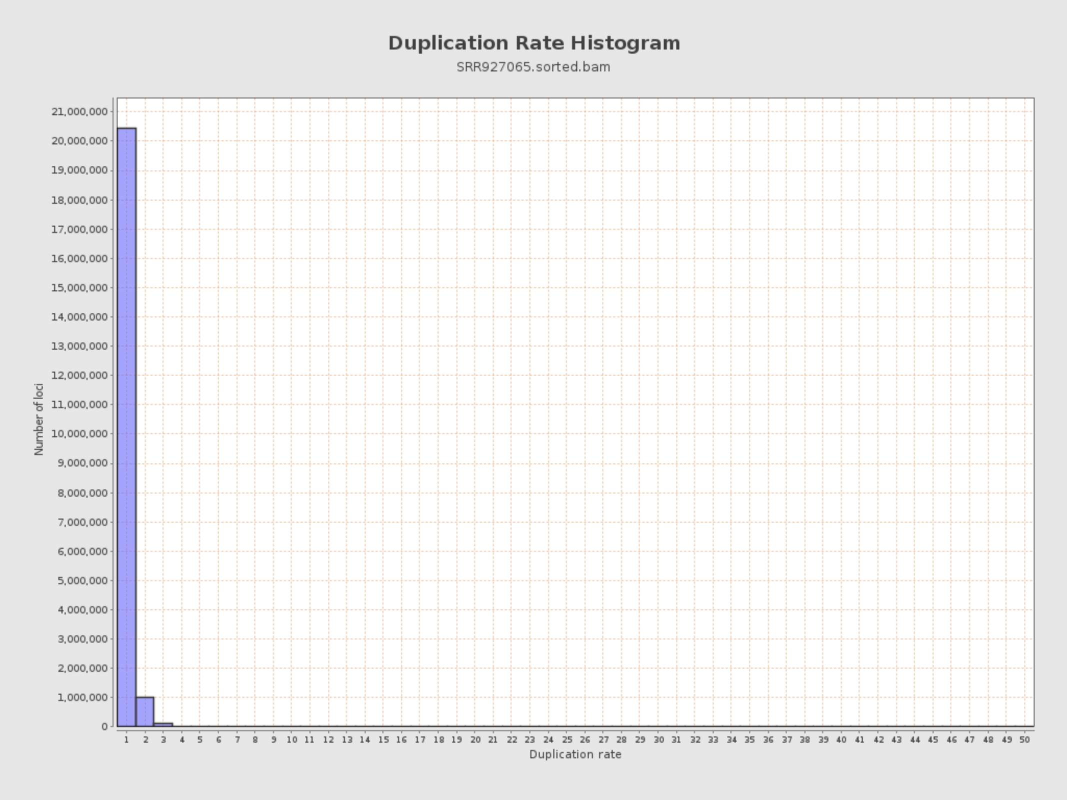
5. Results : Coverage Histogram (0-50X)



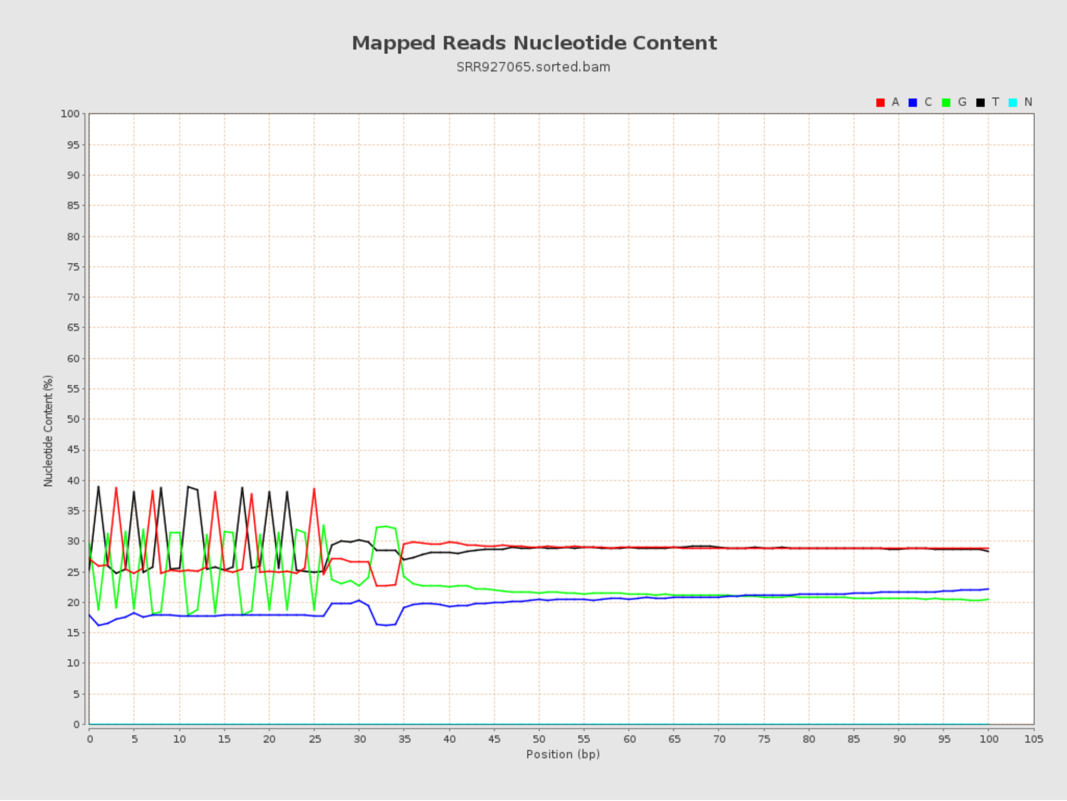
6. Results : Genome Fraction Coverage



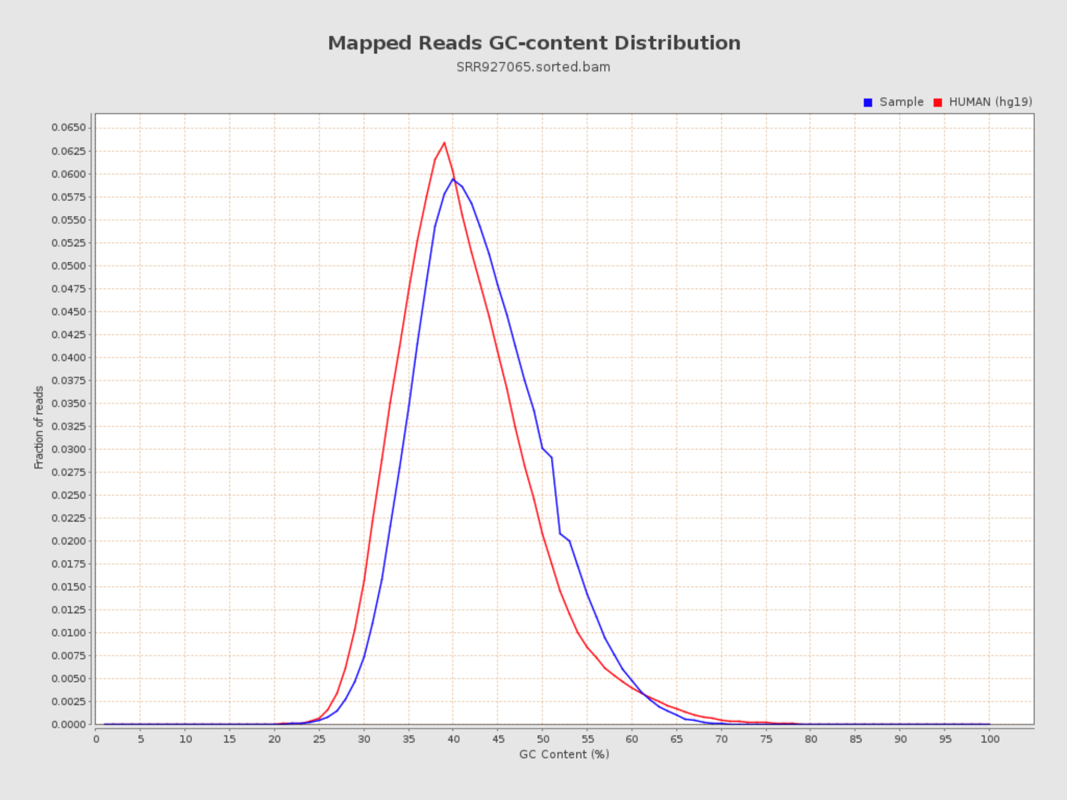
7. Results : Duplication Rate Histogram



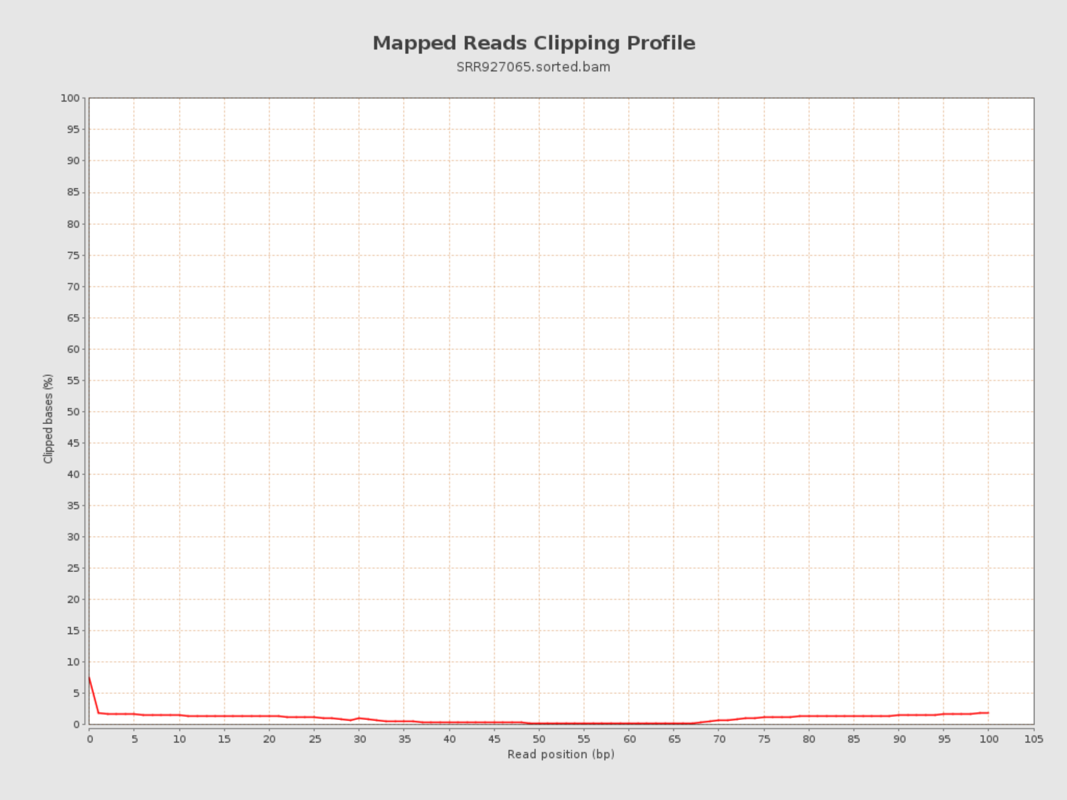
8. Results : Mapped Reads Nucleotide Content



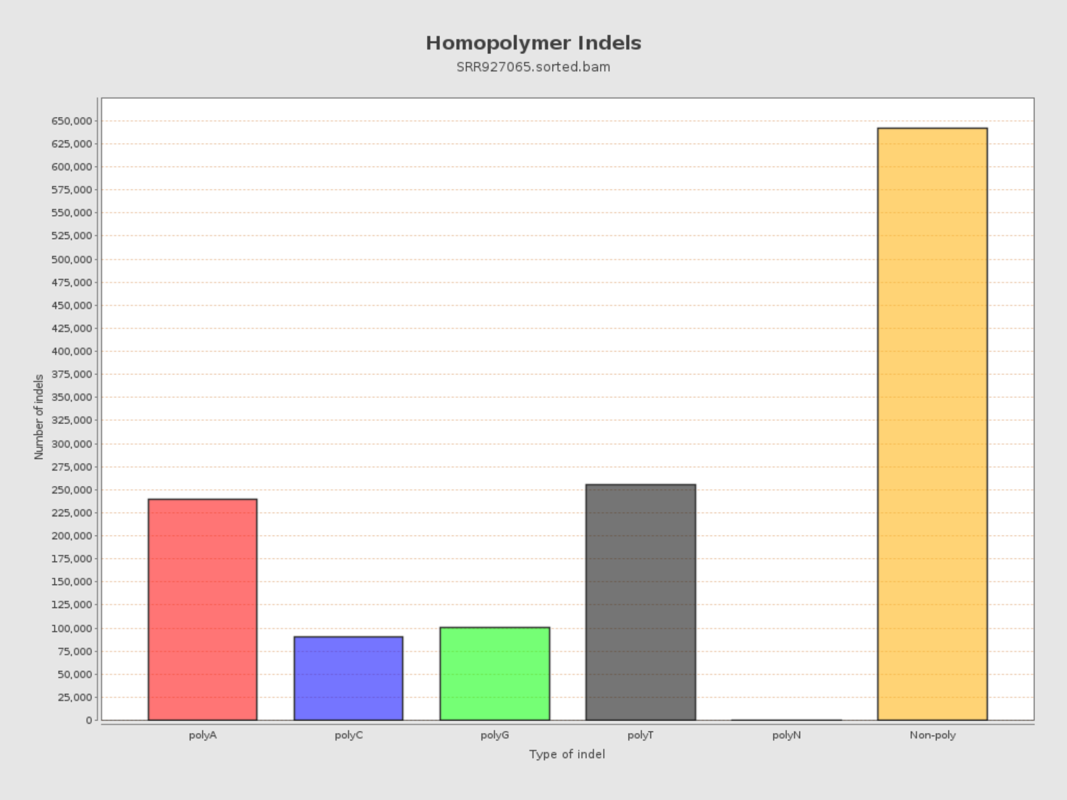
9. Results : Mapped Reads GC-content Distribution



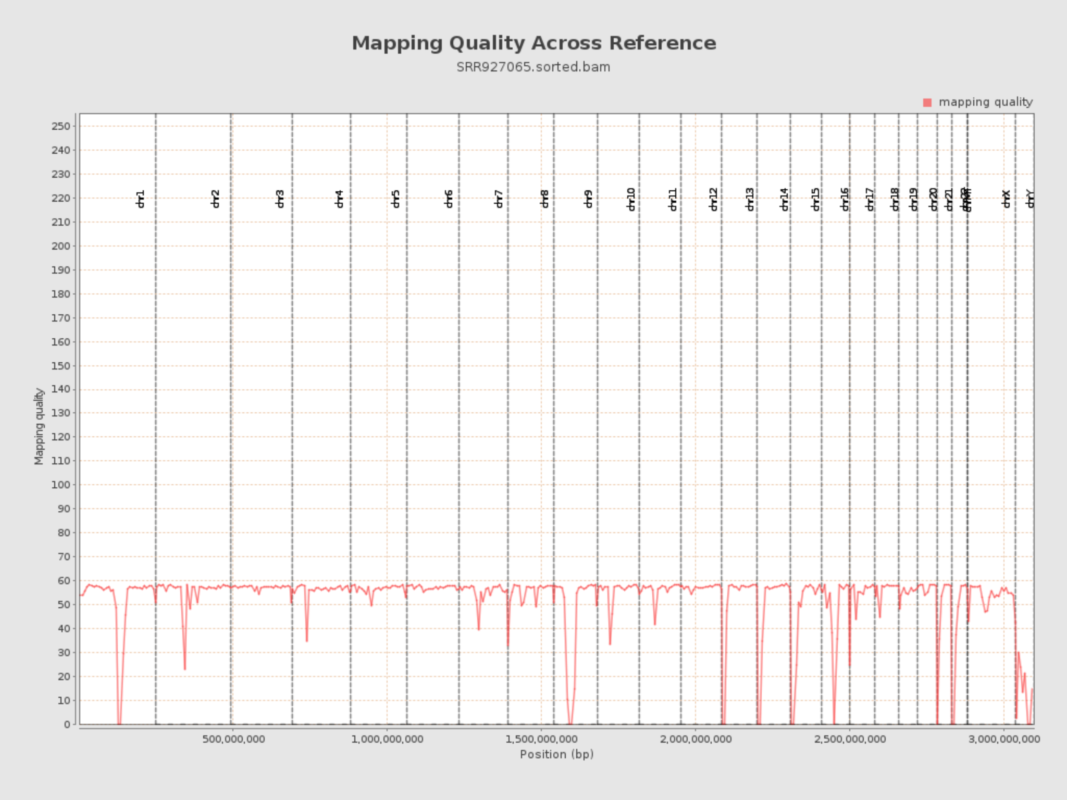
10. Results : Mapped Reads Clipping Profile



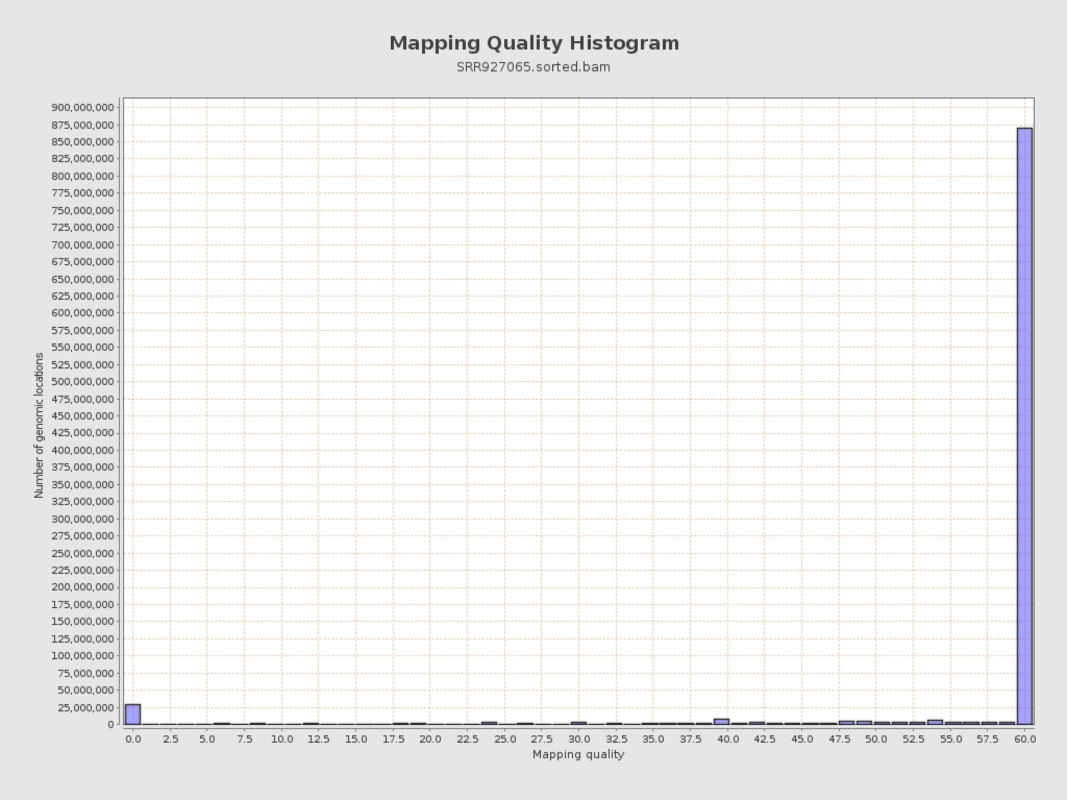
11. Results : Homopolymer Indels



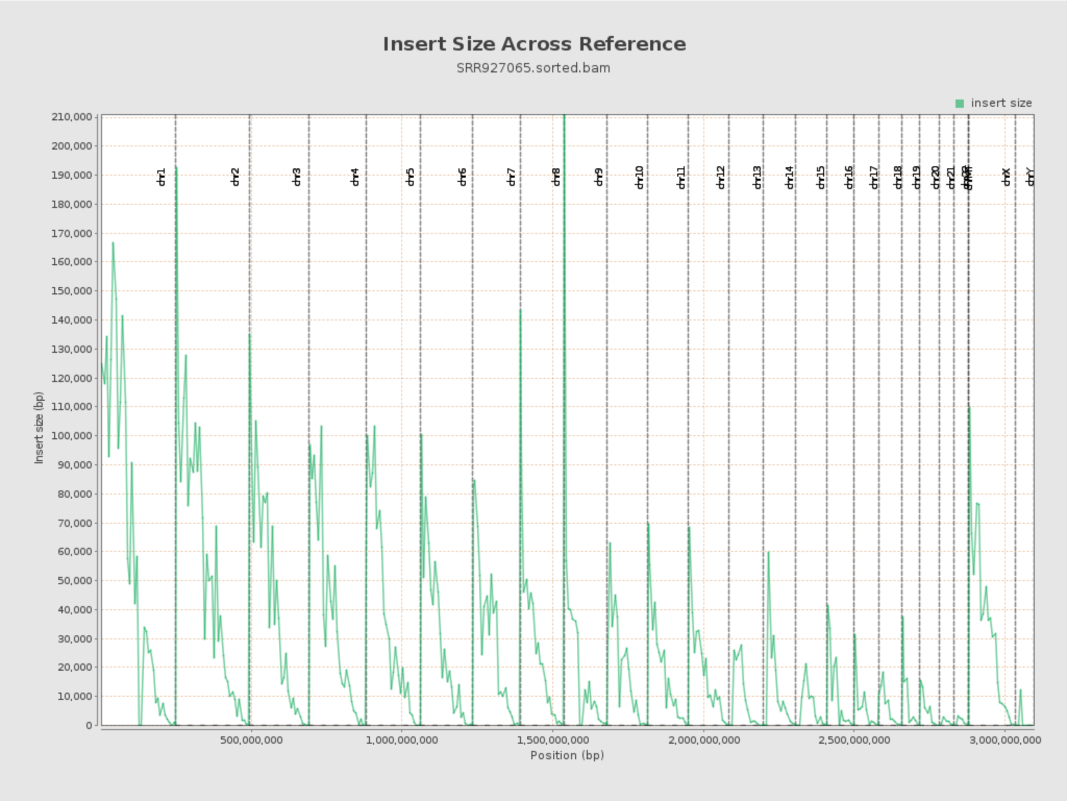
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram