Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 10:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926905.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_SRR926905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926905_1.fastq.gz SRR926905_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 10:19:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,317,546
Mapped reads	27,440,296 / 93.6%
Unmapped reads	1,877,250 / 6.4%
Mapped paired reads	27,440,296 / 93.6%
Mapped reads, first in pair	13,801,120 / 47.07%
Mapped reads, second in pair	13,639,176 / 46.52%
Mapped reads, both in pair	27,108,136 / 92.46%
Mapped reads, singletons	332,160 / 1.13%
Secondary alignments	0
Supplementary alignments	238,620 / 0.81%
Read min/max/mean length	30 / 101 / 101.33
Duplicated reads (estimated)	1,822,286 / 6.22%
Duplication rate	5.27%
Clipped reads	6,899,366 / 23.53%

2.2. ACGT Content

Number/percentage of A's	735,620,812 / 28.4%
Number/percentage of C's	523,773,531 / 20.22%
Number/percentage of T's	740,998,406 / 28.61%
Number/percentage of G's	589,784,715 / 22.77%
Number/percentage of N's	246,586 / 0.01%

GC Percentage	42.99%

2.3. Coverage

Mean	0.8374
Standard Deviation	3.3048

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	102,717.53
Standard Deviation	3,170,201.68
P25/Median/P75	160 / 203 / 267

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	26,961,177
Insertions	411,014
Mapped reads with at least one insertion	1.48%
Deletions	1,426,878
Mapped reads with at least one deletion	5.06%
Homopolymer indels	53.18%

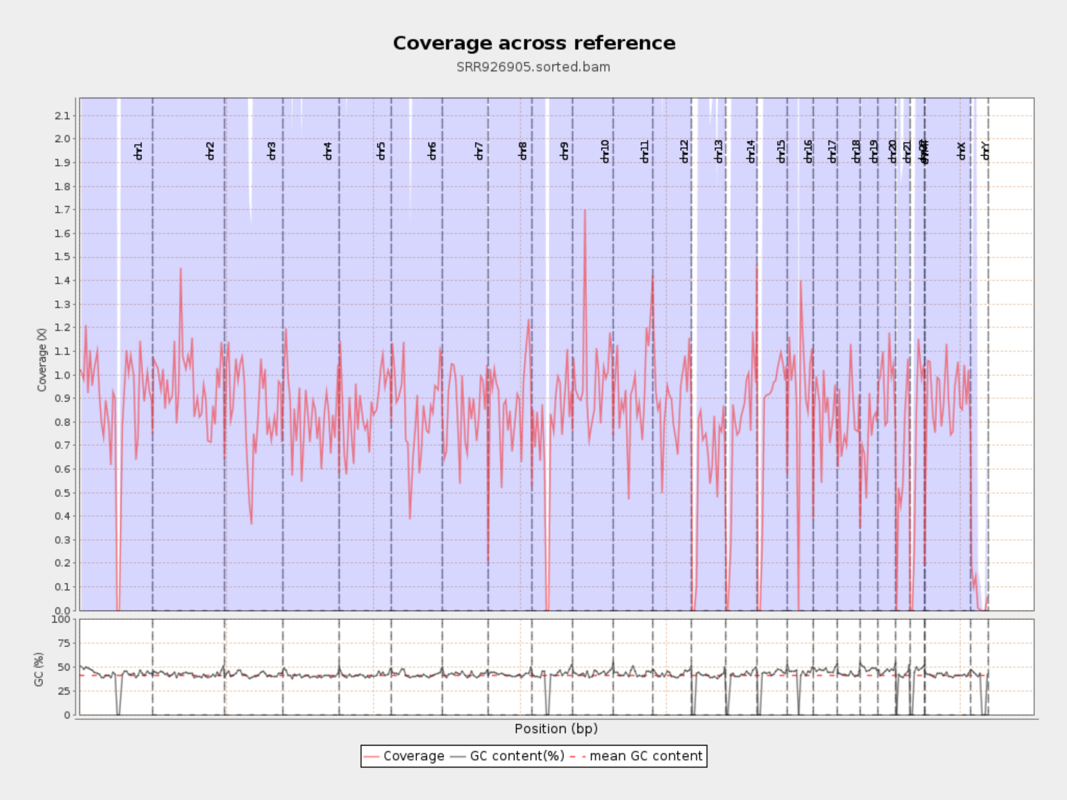
2.7. Chromosome stats

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

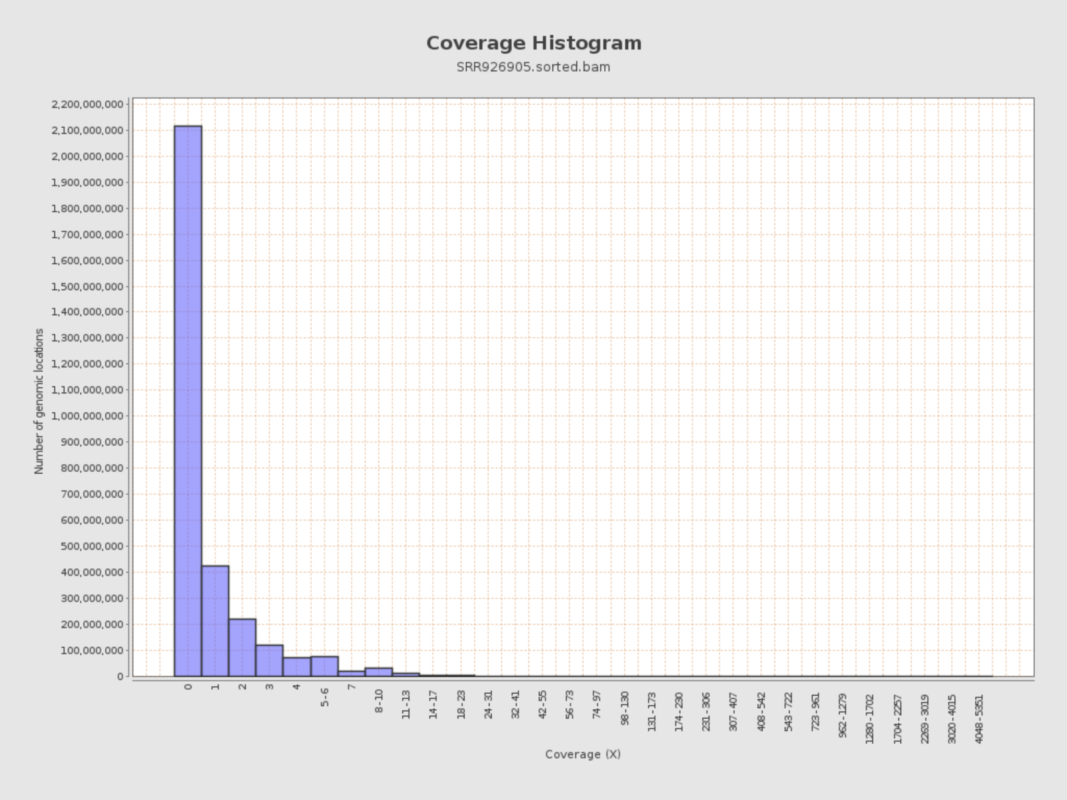
		bases	coverage	deviation
chr1	249250621	218410326	0.8763	3.0405
chr2	243199373	234553464	0.9644	4.3579
chr3	198022430	169746077	0.8572	1.8855
chr4	191154276	157966847	0.8264	1.9559
chr5	180915260	155610954	0.8601	1.8263
chr6	171115067	144556097	0.8448	1.8368
chr7	159138663	135458078	0.8512	2.1988
chr8	146364022	130751154	0.8933	2.0354
chr9	141213431	106194903	0.752	3.4805
chr10	135534747	134431584	0.9919	10.1419
chr11	135006516	124693808	0.9236	2.2691
chr12	133851895	119728915	0.8945	1.949
chr13	115169878	69393353	0.6025	1.5401
chr14	107349540	79336832	0.7391	1.7764
chr15	102531392	80695307	0.787	1.8898
chr16	90354753	84686815	0.9373	4.6299
chr17	81195210	68484086	0.8434	2.1386
chr18	78077248	64416513	0.825	3.4152
chr19	59128983	42675088	0.7217	2.1631
chr20	63025520	61294679	0.9725	2.1668
chr21	48129895	30459801	0.6329	2.5952
chr22	51304566	34926375	0.6808	1.8264
chrMT	16571	3177	0.1917	0.5249
chrX	155270560	140522242	0.905	1.9879

chrY	59373566	3425423	0.0577	1.2985

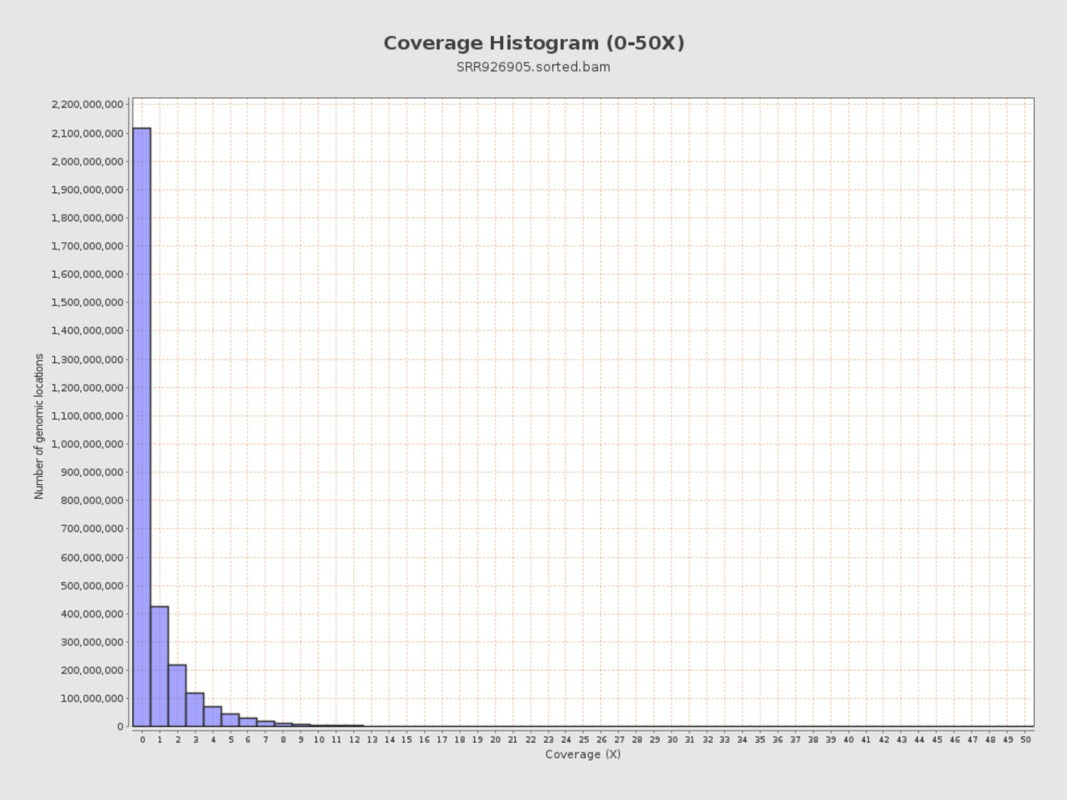
3. Results : Coverage across reference



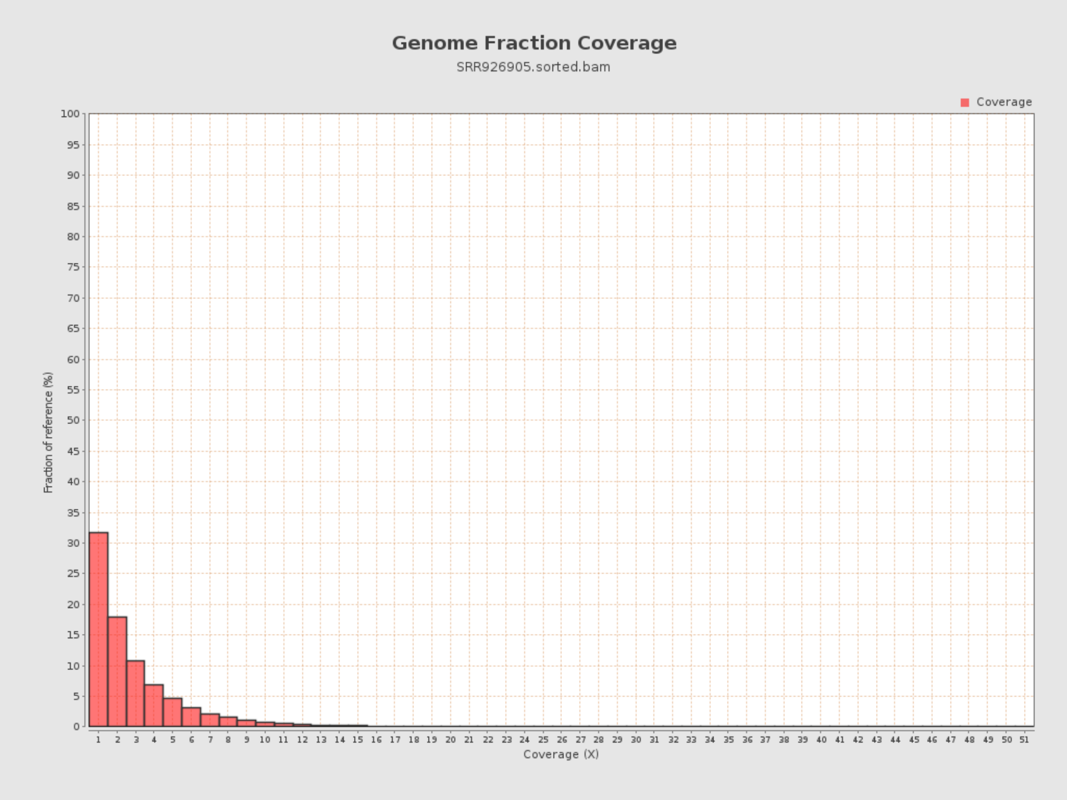
4. Results : Coverage Histogram



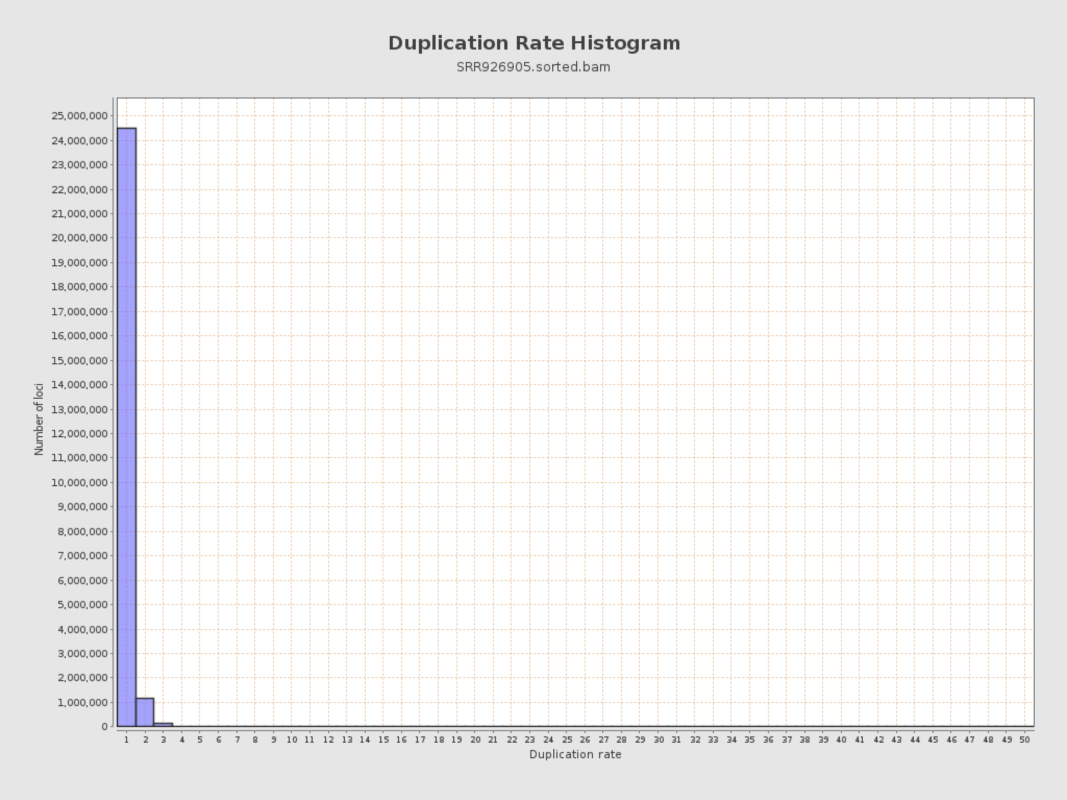
5. Results : Coverage Histogram (0-50X)



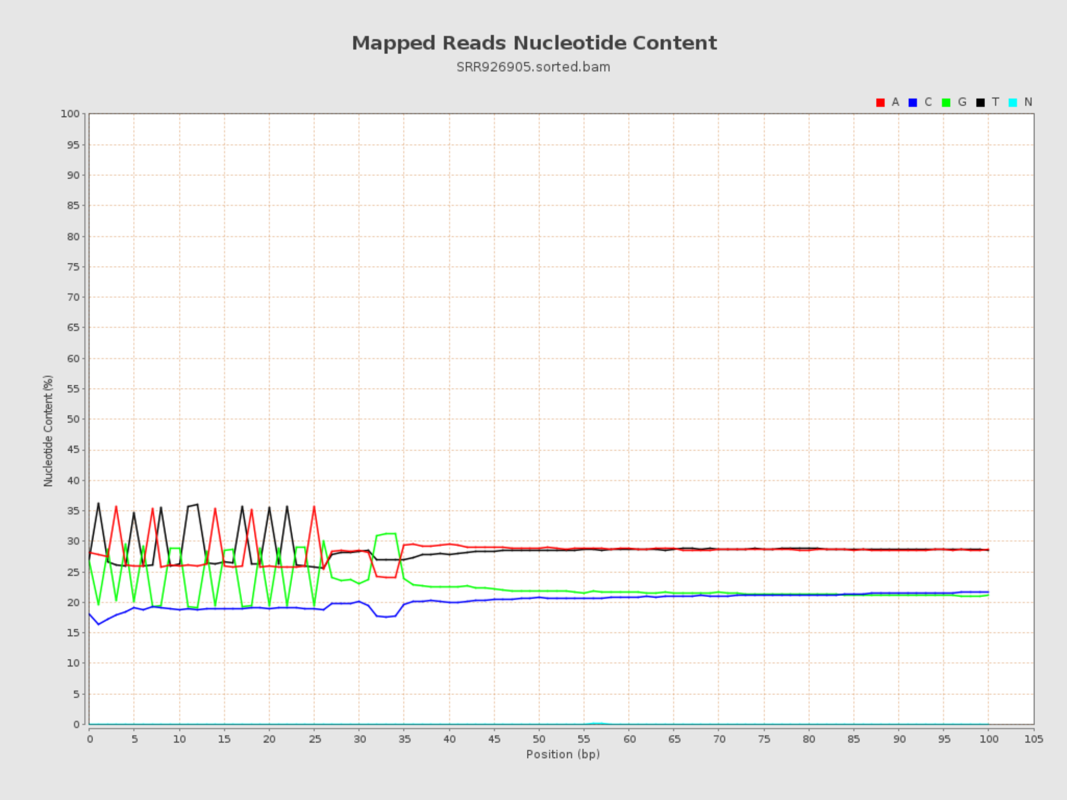
6. Results : Genome Fraction Coverage



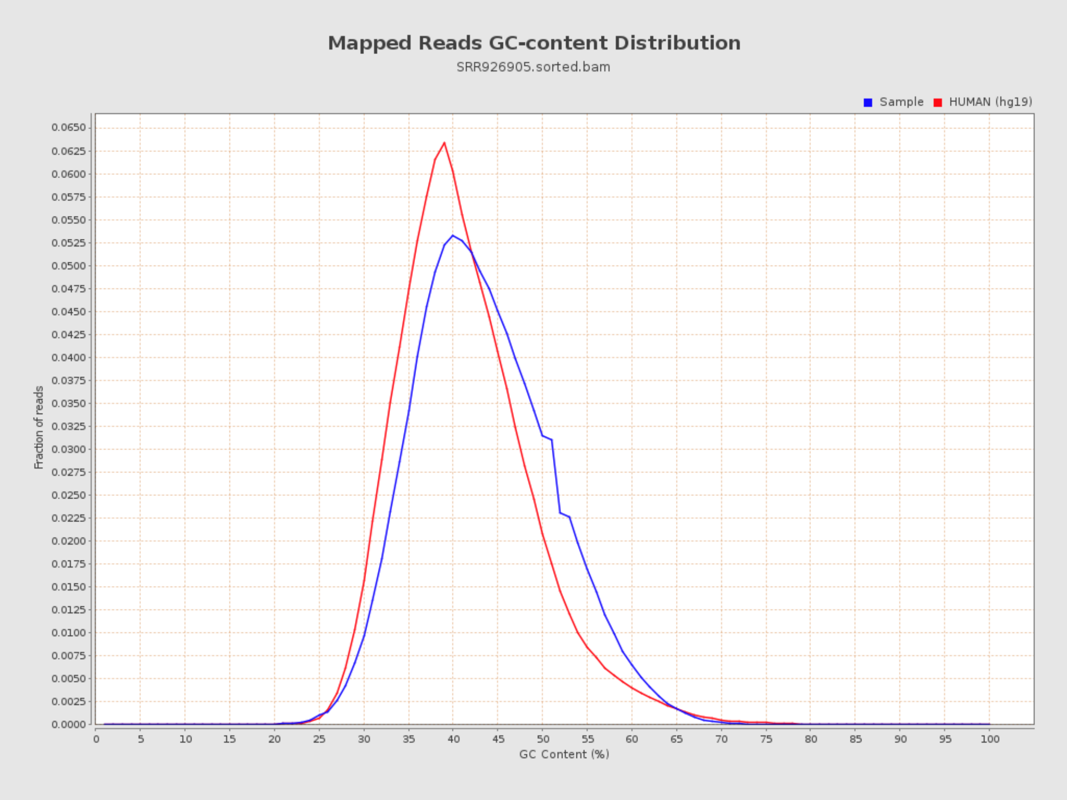
7. Results : Duplication Rate Histogram



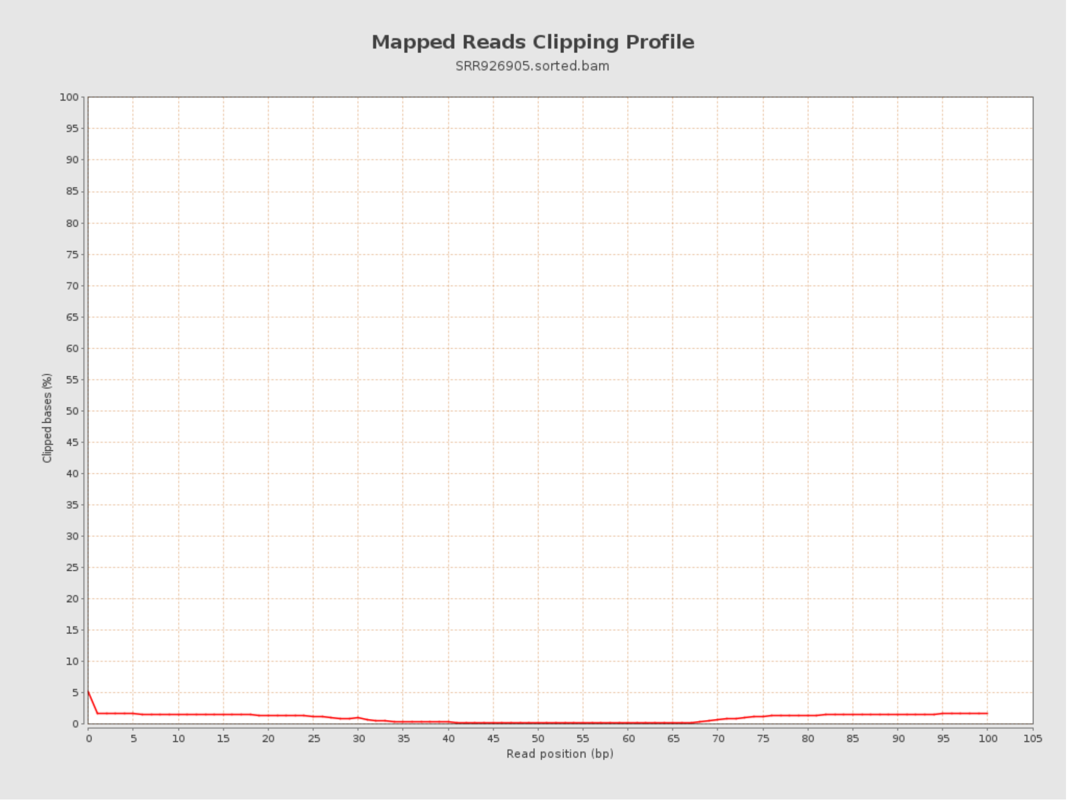
8. Results : Mapped Reads Nucleotide Content



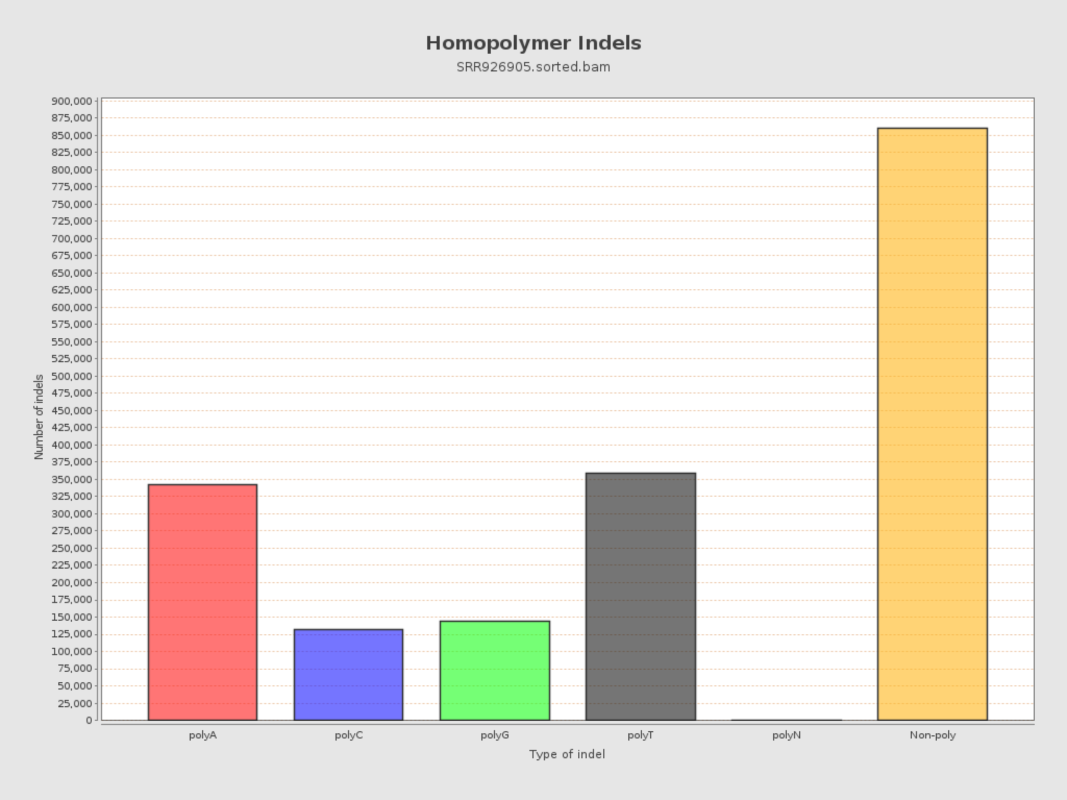
9. Results : Mapped Reads GC-content Distribution



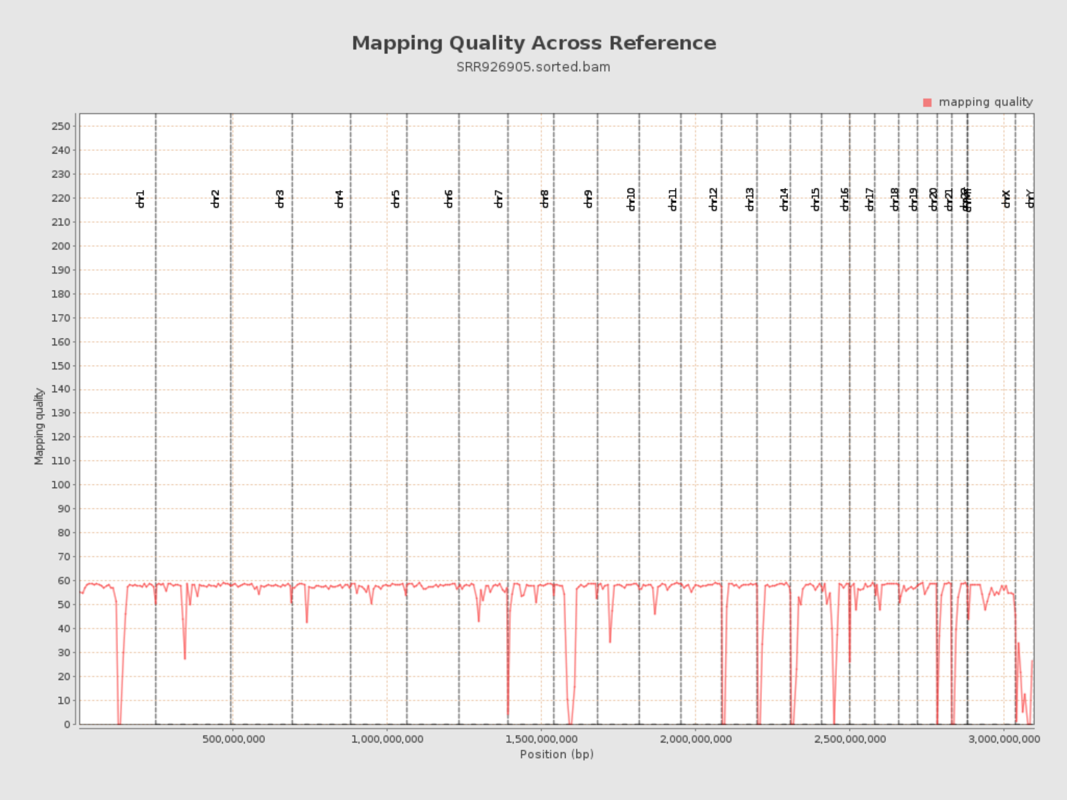
10. Results : Mapped Reads Clipping Profile



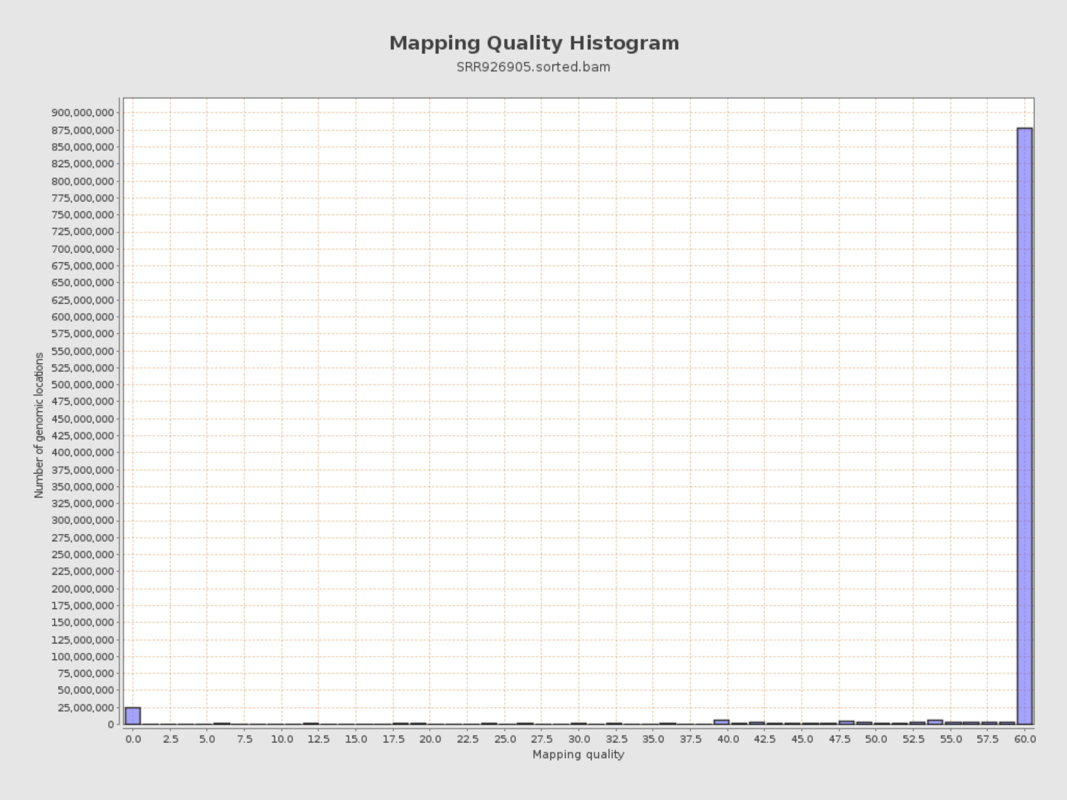
11. Results : Homopolymer Indels



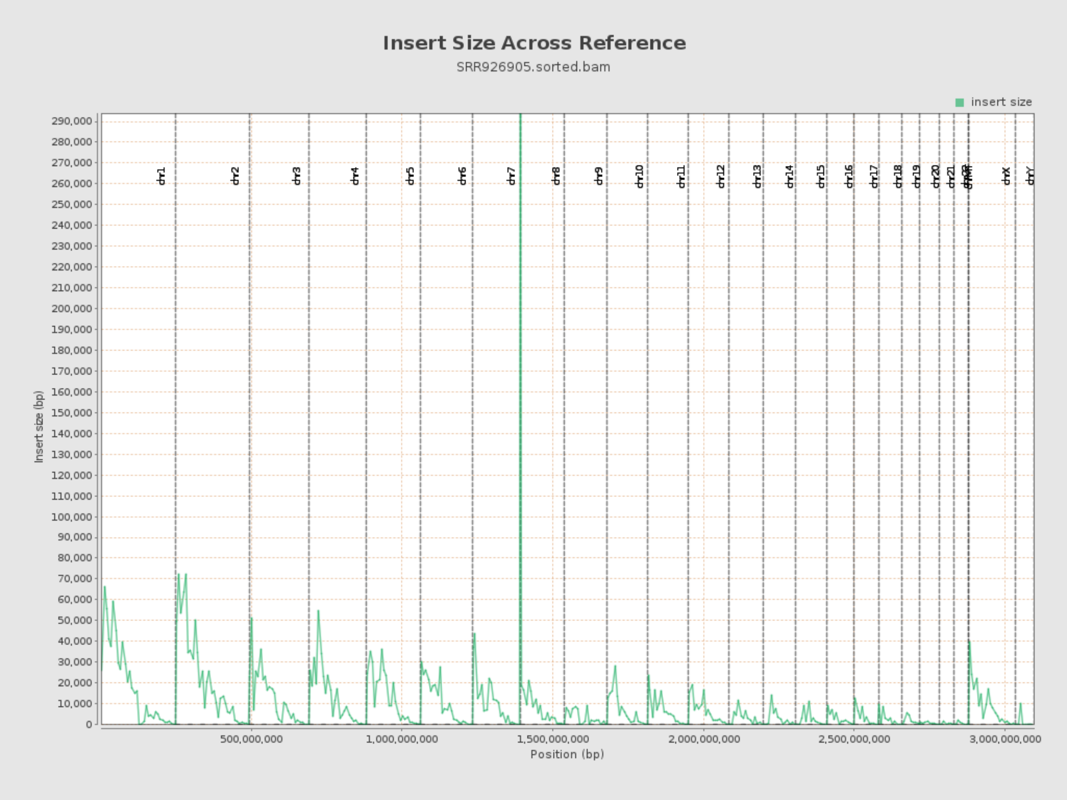
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram