Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 22:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926935.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_SRR926935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926935_1.fastq.gz SRR926935_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 22:26:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,690,538
Mapped reads	12,323,312 / 97.11%
Unmapped reads	367,226 / 2.89%
Mapped paired reads	12,323,312 / 97.11%
Mapped reads, first in pair	6,175,938 / 48.67%
Mapped reads, second in pair	6,147,374 / 48.44%
Mapped reads, both in pair	12,136,332 / 95.63%
Mapped reads, singletons	186,980 / 1.47%
Secondary alignments	0
Supplementary alignments	288,226 / 2.27%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	744,889 / 5.87%
Duplication rate	4.95%
Clipped reads	5,137,344 / 40.48%

2.2. ACGT Content

Number/percentage of A's	315,746,812 / 28.23%
Number/percentage of C's	219,748,072 / 19.65%
Number/percentage of T's	322,778,123 / 28.86%
Number/percentage of G's	259,998,079 / 23.25%
Number/percentage of N's	55,982 / 0.01%

GC Percentage	42.9%

2.3. Coverage

Mean	0.3615
Standard Deviation	1.4247

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	228,176.12
Standard Deviation	4,597,457.85
P25/Median/P75	141 / 183 / 247

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	10,607,795
Insertions	193,459
Mapped reads with at least one insertion	1.54%
Deletions	591,095
Mapped reads with at least one deletion	4.67%
Homopolymer indels	51.98%

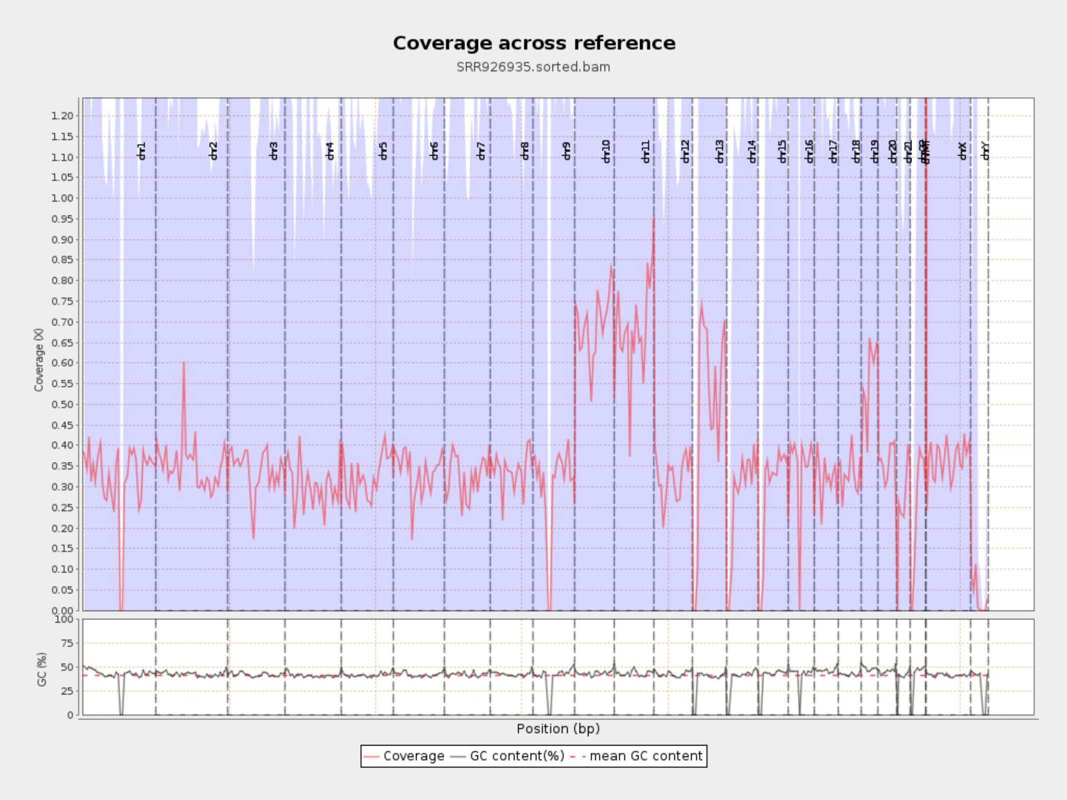
2.7. Chromosome stats

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

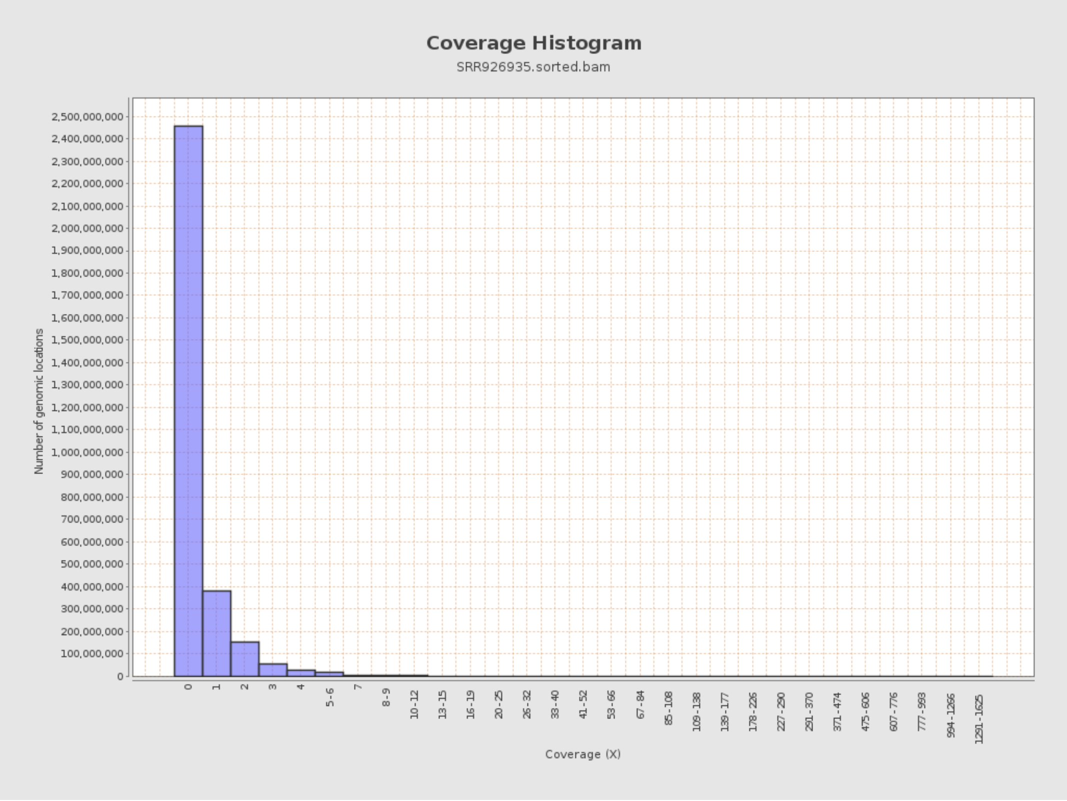
		bases	coverage	deviation
chr1	249250621	79735790	0.3199	1.9071
chr2	243199373	86038427	0.3538	2.1996
chr3	198022430	67082252	0.3388	0.8459
chr4	191154276	58464668	0.3059	1.3573
chr5	180915260	59286809	0.3277	0.8275
chr6	171115067	57353773	0.3352	1.3421
chr7	159138663	51702401	0.3249	1.0325
chr8	146364022	49719520	0.3397	0.9167
chr9	141213431	42464675	0.3007	1.5294
chr10	135534747	93818359	0.6922	2.3538
chr11	135006516	91392419	0.6769	1.7825
chr12	133851895	43875415	0.3278	0.8611
chr13	115169878	56719930	0.4925	1.1491
chr14	107349540	29606000	0.2758	0.7806
chr15	102531392	28823180	0.2811	0.7781
chr16	90354753	30564638	0.3383	1.3783
chr17	81195210	26222761	0.323	0.9763
chr18	78077248	25670727	0.3288	1.5348
chr19	59128983	32896725	0.5564	1.5586
chr20	63025520	22751994	0.361	0.9414
chr21	48129895	12846598	0.2669	1.2151
chr22	51304566	12590670	0.2454	0.7605
chrMT	16571	949718	57.3121	46.0662
chrX	155270560	56625256	0.3647	0.9719

chrY	59373566	1992913	0.0336	1.1594

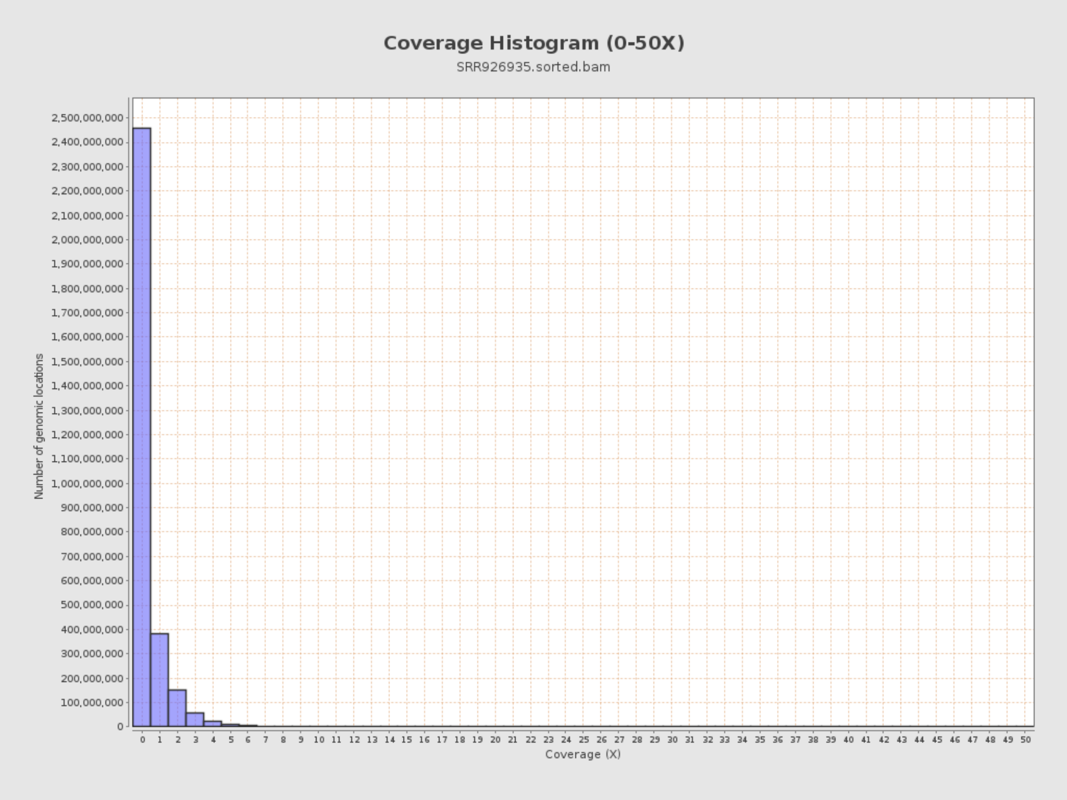
3. Results : Coverage across reference



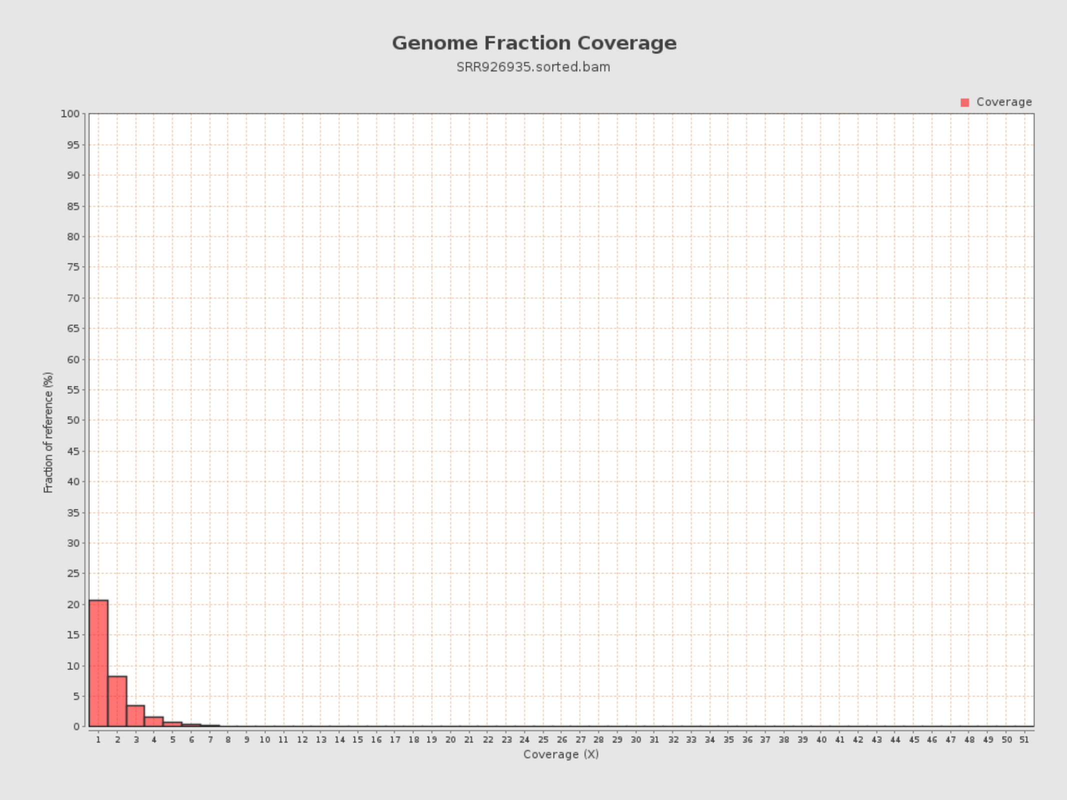
4. Results : Coverage Histogram



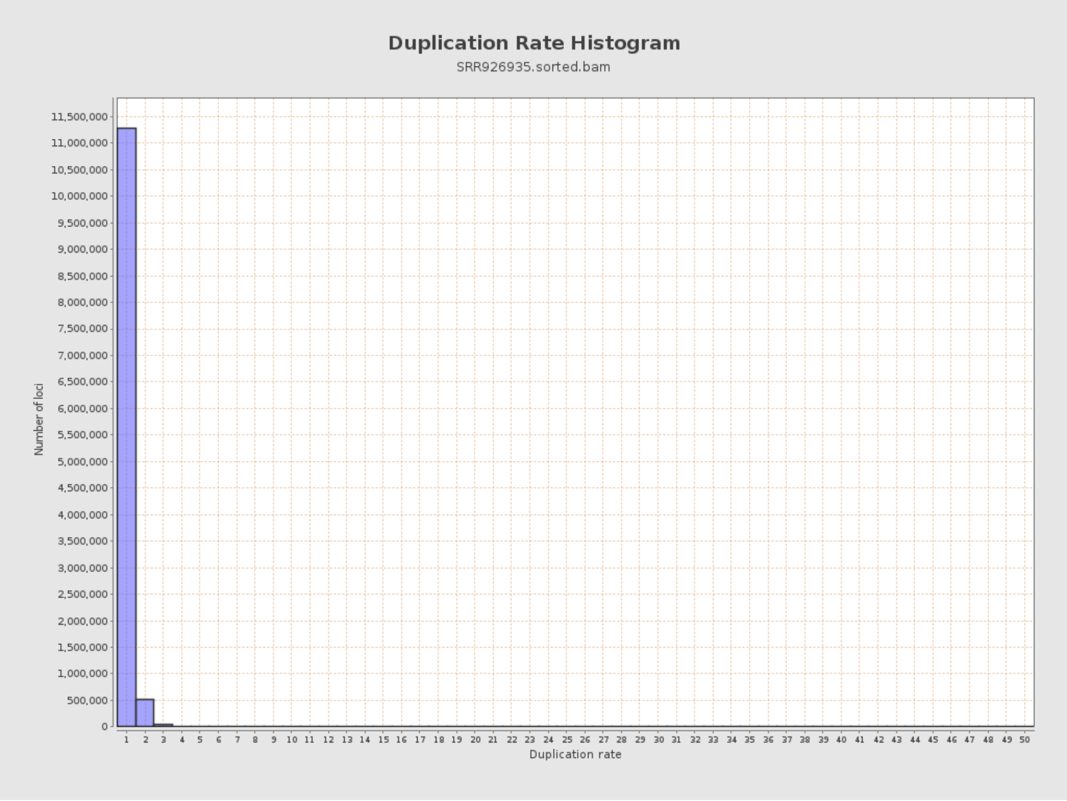
5. Results : Coverage Histogram (0-50X)



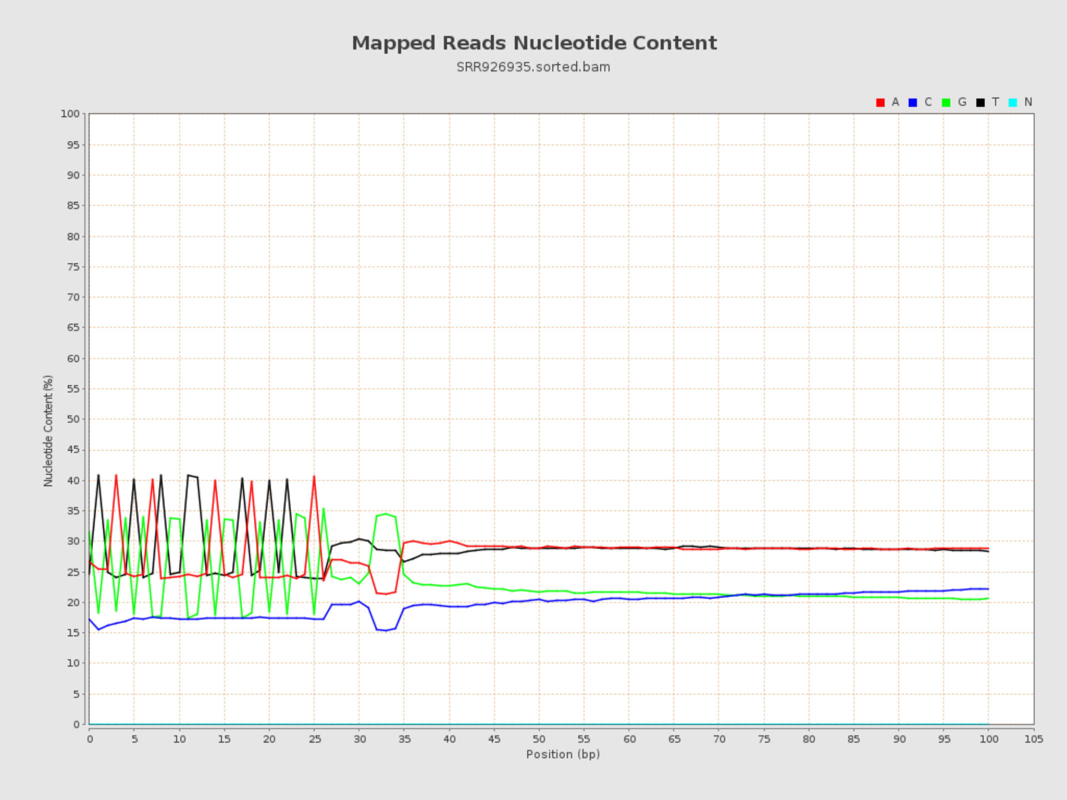
6. Results : Genome Fraction Coverage



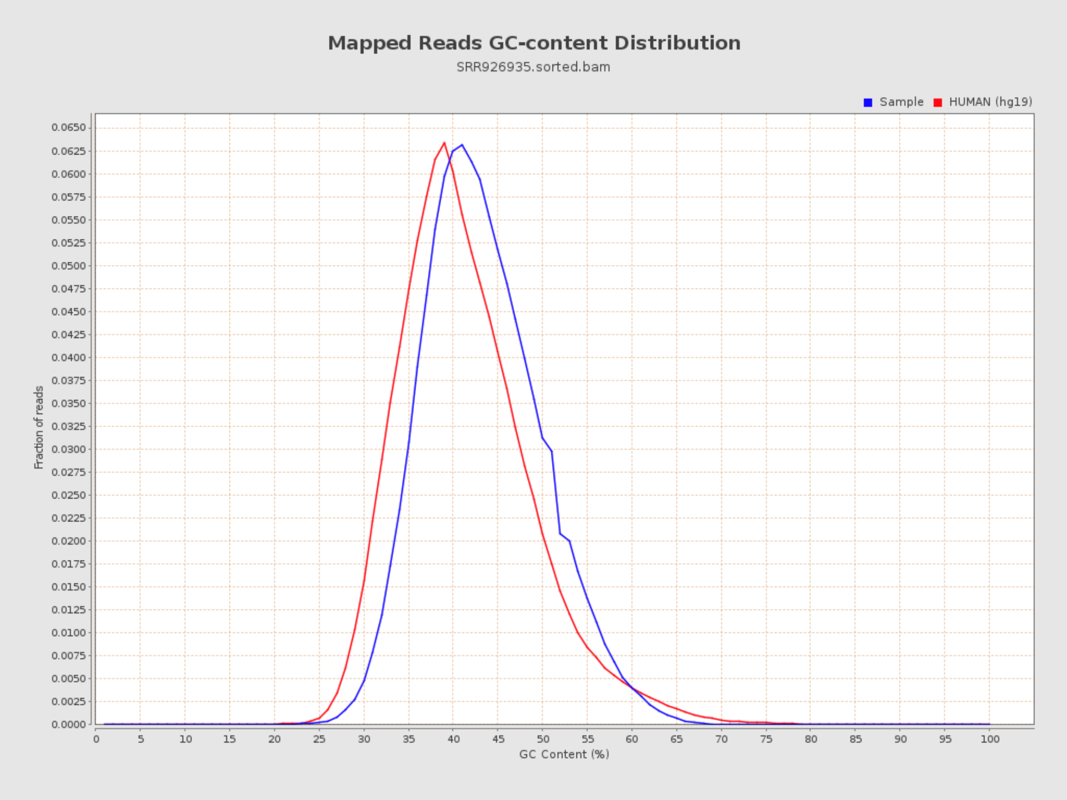
7. Results : Duplication Rate Histogram



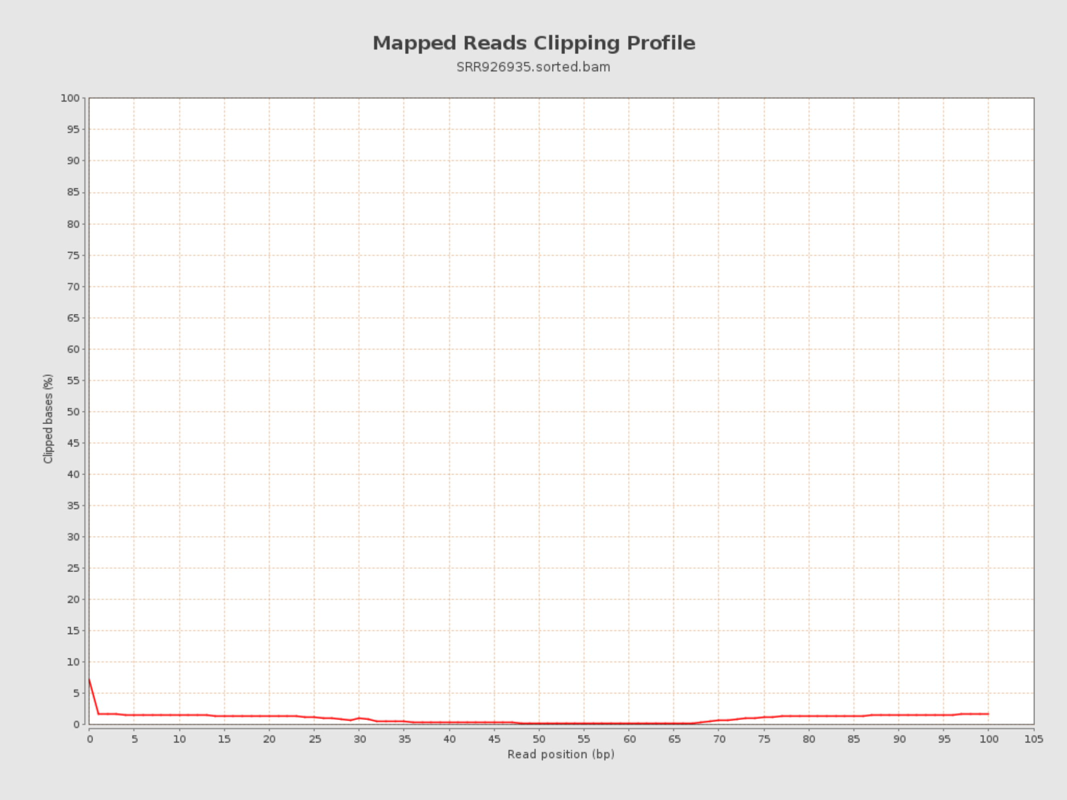
8. Results : Mapped Reads Nucleotide Content



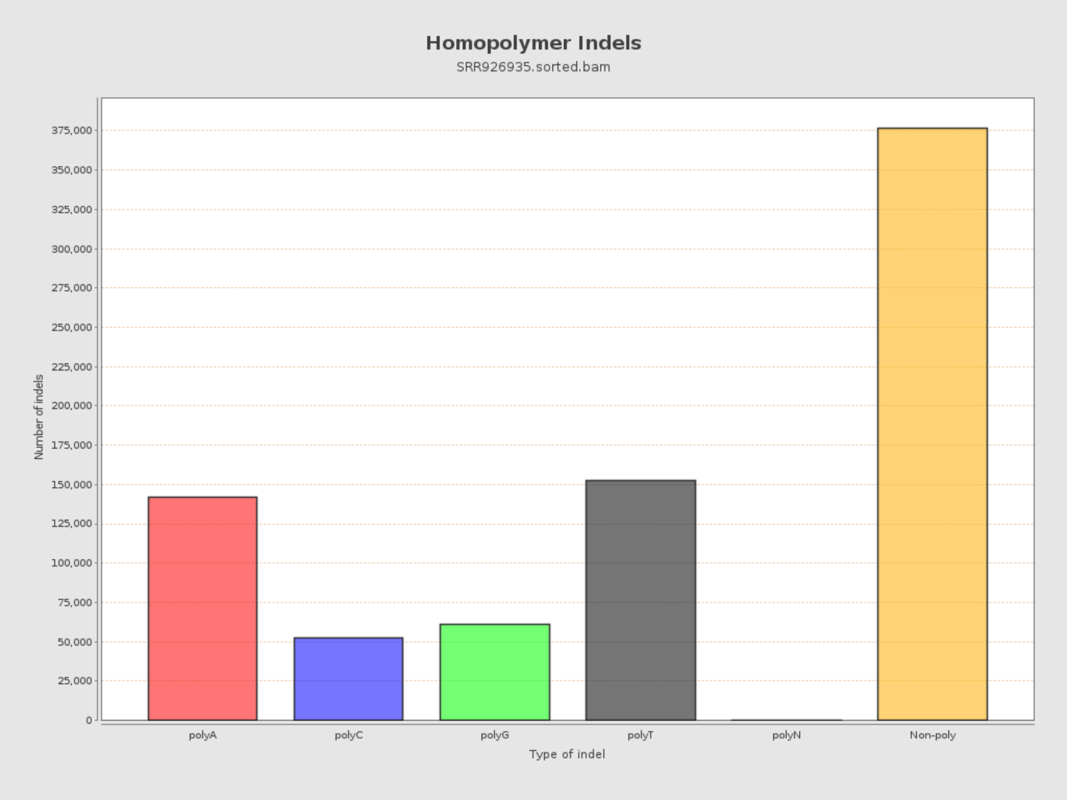
9. Results : Mapped Reads GC-content Distribution



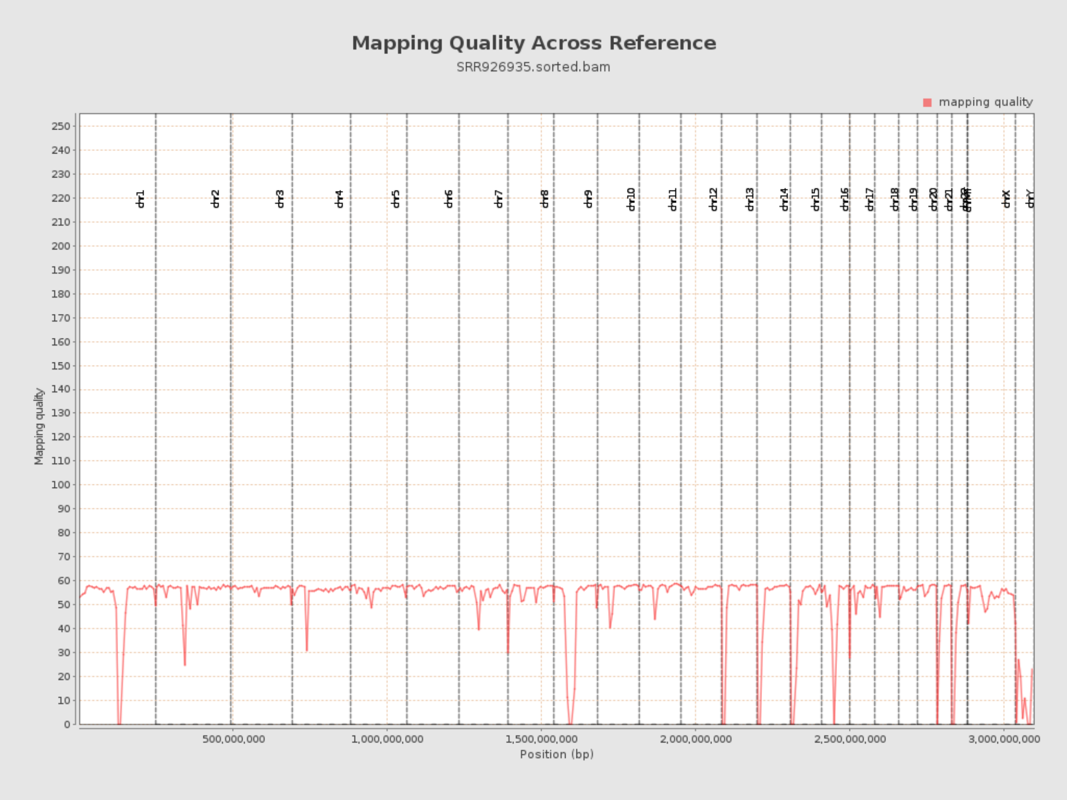
10. Results : Mapped Reads Clipping Profile



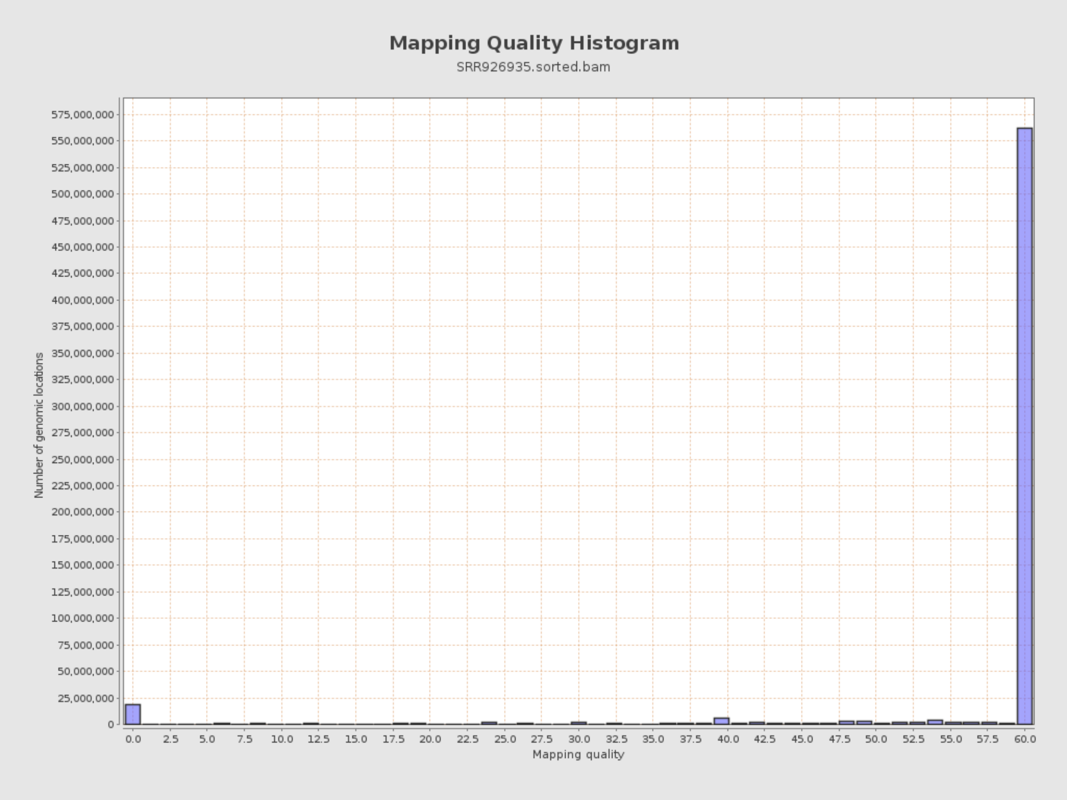
11. Results : Homopolymer Indels



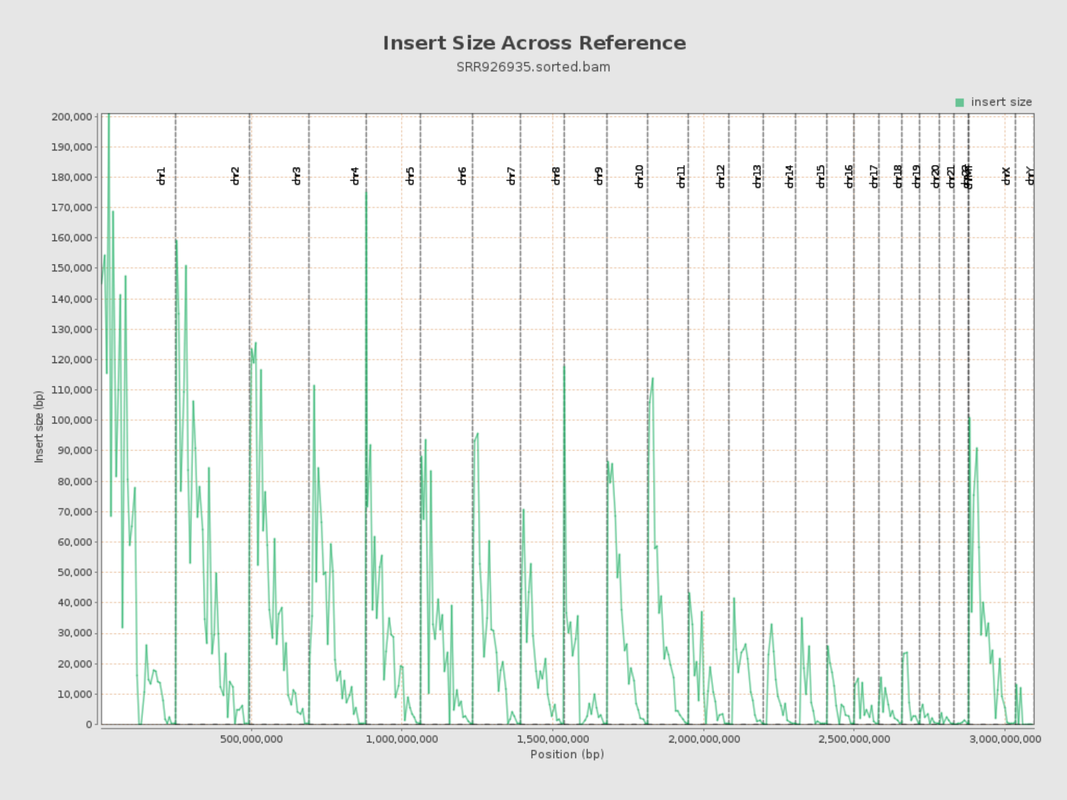
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram