Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 21:16:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926930.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_SRR926930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926930_1.fastq.gz SRR926930_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 21:16:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,245,610
Mapped reads	9,960,504 / 97.22%
Unmapped reads	285,106 / 2.78%
Mapped paired reads	9,960,504 / 97.22%
Mapped reads, first in pair	4,999,921 / 48.8%
Mapped reads, second in pair	4,960,583 / 48.42%
Mapped reads, both in pair	9,801,212 / 95.66%
Mapped reads, singletons	159,292 / 1.55%
Secondary alignments	0
Supplementary alignments	362,091 / 3.53%
Read min/max/mean length	30 / 101 / 102.47
Duplicated reads (estimated)	587,841 / 5.74%
Duplication rate	4.69%
Clipped reads	4,464,303 / 43.57%

2.2. ACGT Content

Number/percentage of A's	257,864,239 / 28.52%
Number/percentage of C's	176,057,508 / 19.47%
Number/percentage of T's	262,693,850 / 29.05%
Number/percentage of G's	207,421,410 / 22.94%
Number/percentage of N's	176,245 / 0.02%

GC Percentage	42.41%

2.3. Coverage

Mean	0.2923
Standard Deviation	1.3205

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	387,126.48
Standard Deviation	6,085,609.28
P25/Median/P75	136 / 177 / 238

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	8,639,755
Insertions	160,754
Mapped reads with at least one insertion	1.58%
Deletions	486,604
Mapped reads with at least one deletion	4.76%
Homopolymer indels	51.64%

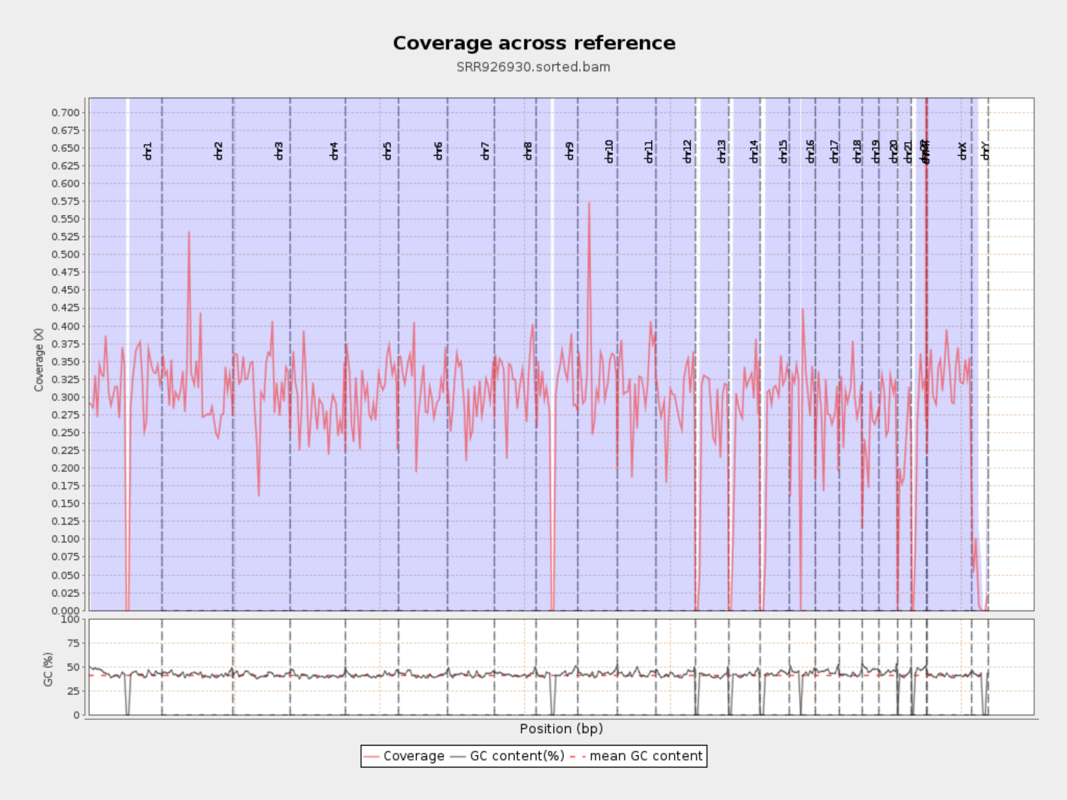
2.7. Chromosome stats

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

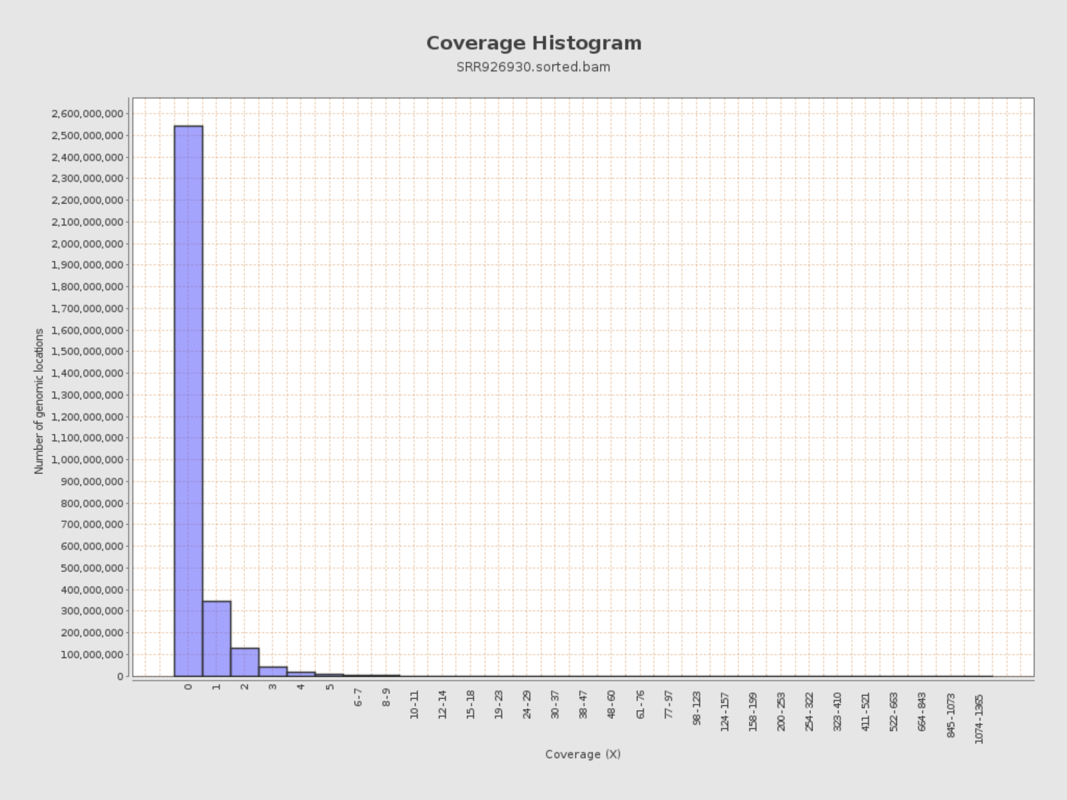
		bases	coverage	deviation
chr1	249250621	75590281	0.3033	1.2491
chr2	243199373	76468947	0.3144	2.2234
chr3	198022430	63057143	0.3184	0.8133
chr4	191154276	54914887	0.2873	1.298
chr5	180915260	55622015	0.3074	0.7897
chr6	171115067	54058966	0.3159	1.4369
chr7	159138663	47659152	0.2995	1.0113
chr8	146364022	47925745	0.3274	0.8797
chr9	141213431	40821340	0.2891	1.4096
chr10	135534747	45479333	0.3356	2.7879
chr11	135006516	43035797	0.3188	0.9917
chr12	133851895	39578740	0.2957	0.8112
chr13	115169878	28193078	0.2448	0.7003
chr14	107349540	27492721	0.2561	0.74
chr15	102531392	26076314	0.2543	0.7279
chr16	90354753	26425152	0.2925	1.7508
chr17	81195210	22160345	0.2729	0.8731
chr18	78077248	23533484	0.3014	1.3379
chr19	59128983	14433421	0.2441	0.9407
chr20	63025520	18539268	0.2942	0.829
chr21	48129895	10031235	0.2084	1.0061
chr22	51304566	10971078	0.2138	0.7125
chrMT	16571	54462	3.2866	3.2248
chrX	155270560	50999781	0.3285	0.8734

chrY	59373566	1812537	0.0305	1.3763

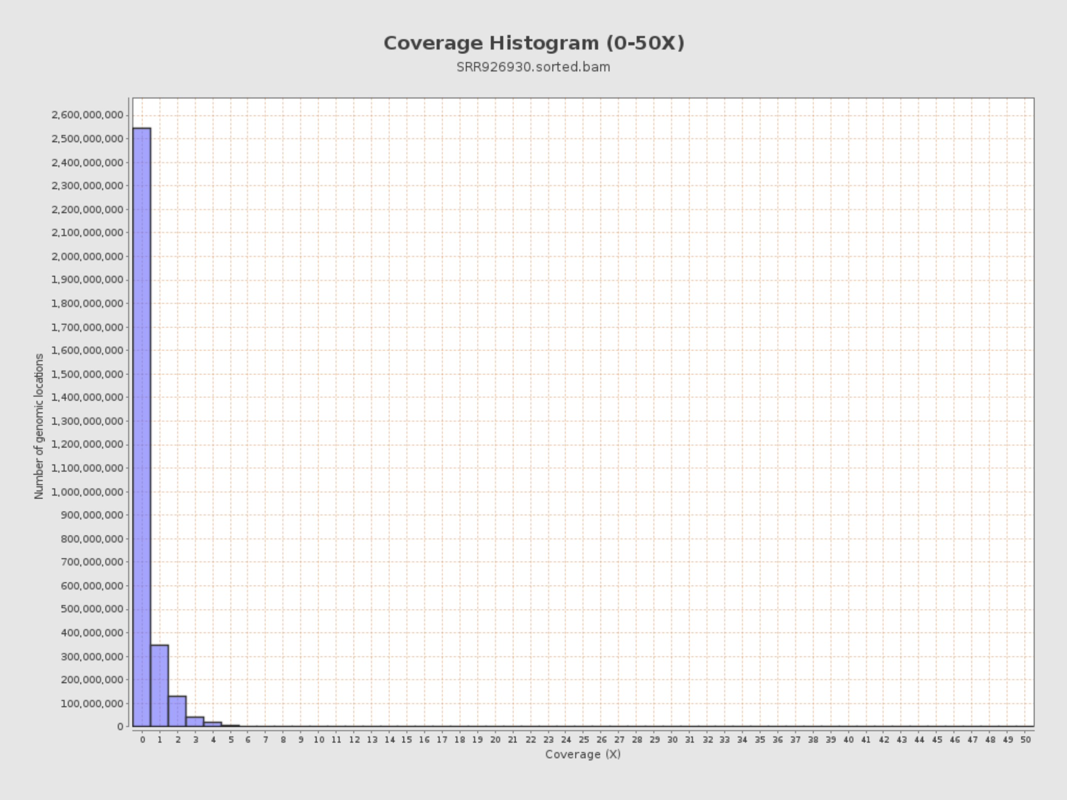
3. Results : Coverage across reference



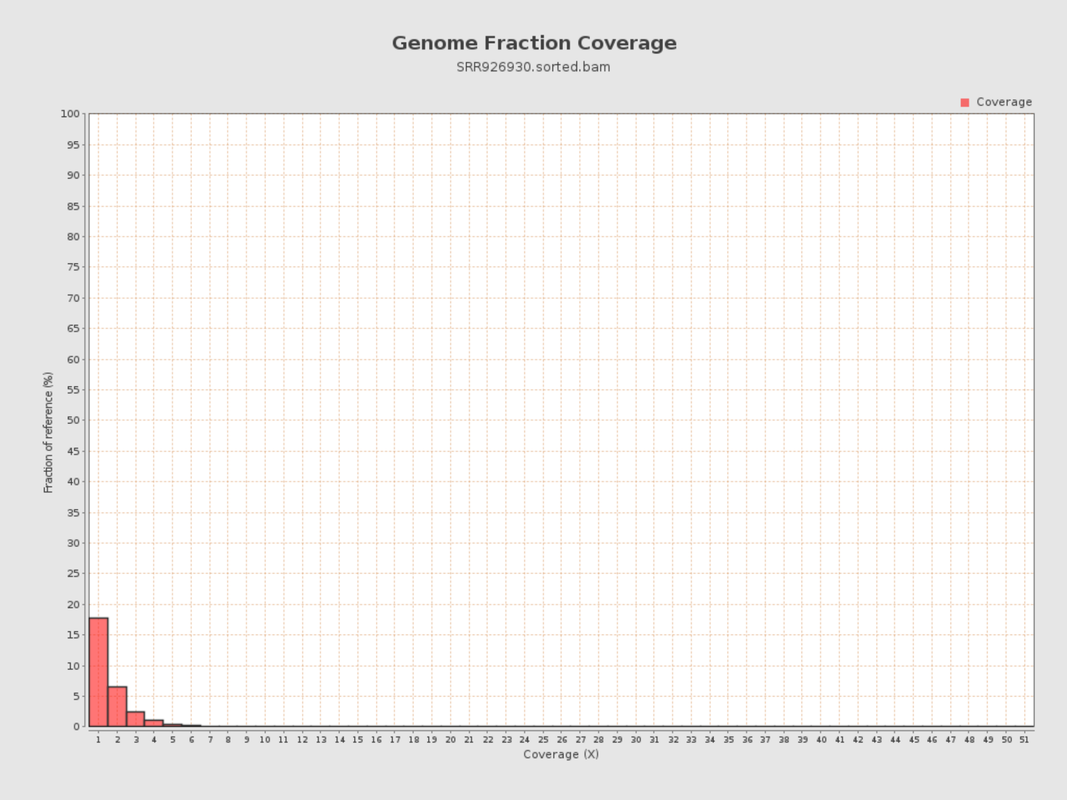
4. Results : Coverage Histogram



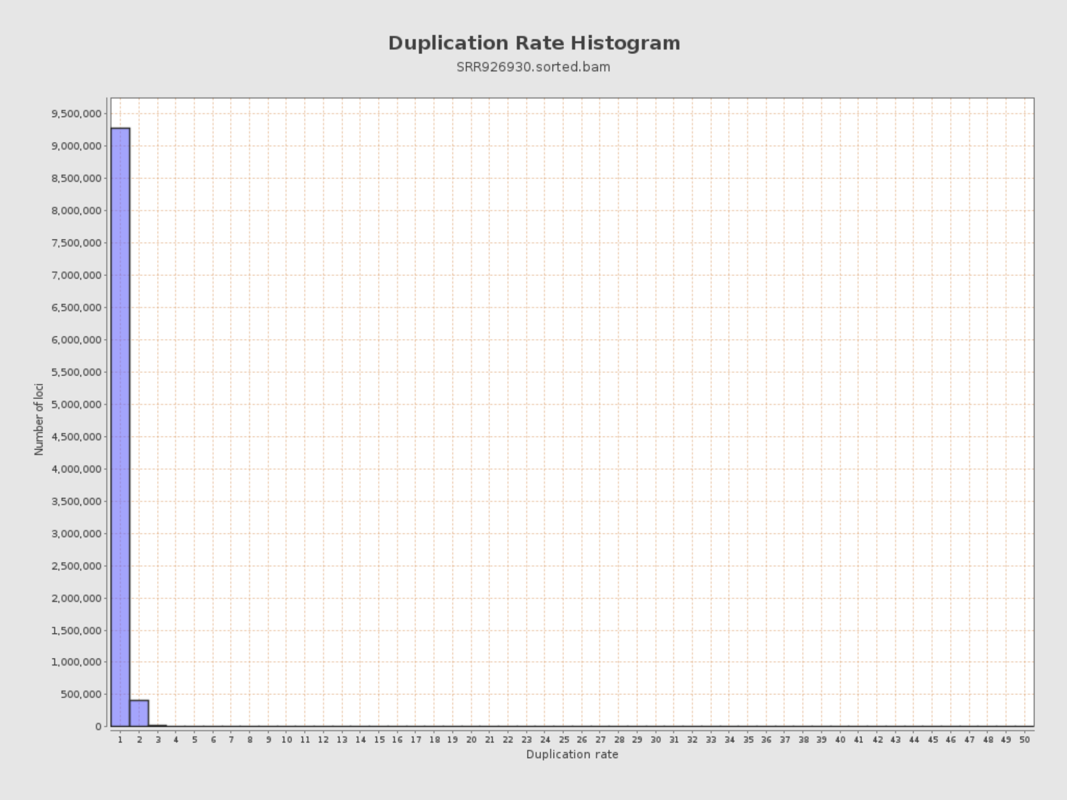
5. Results : Coverage Histogram (0-50X)



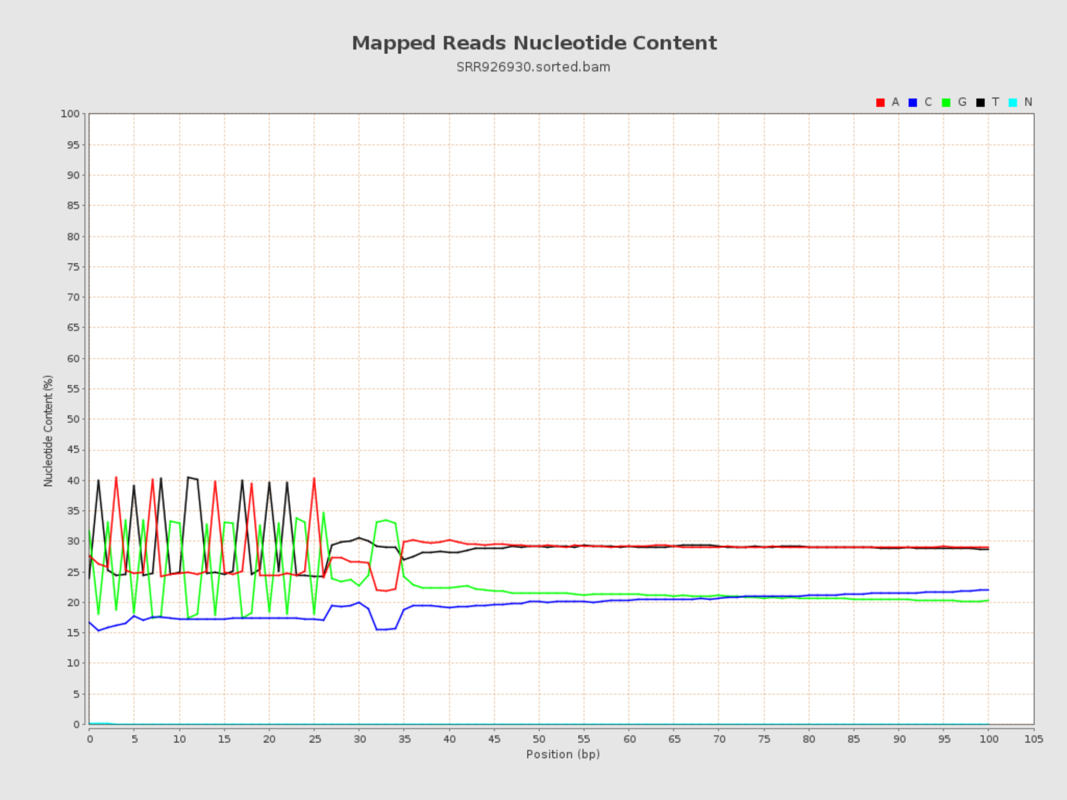
6. Results : Genome Fraction Coverage



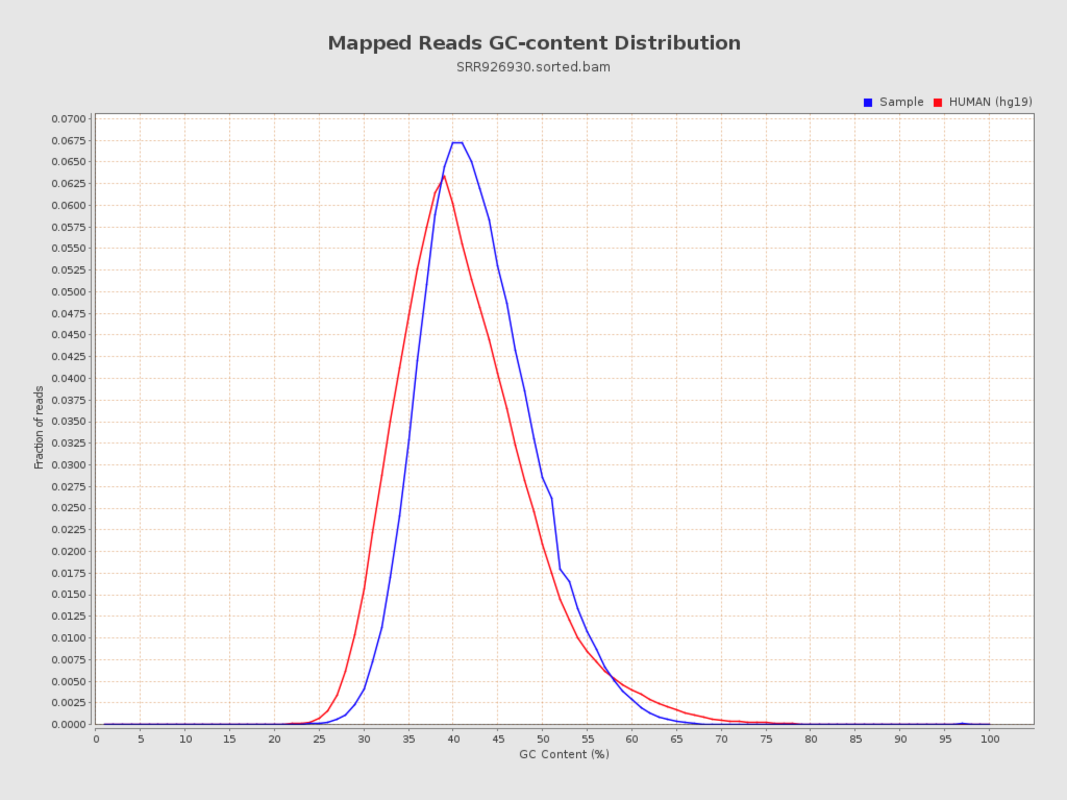
7. Results : Duplication Rate Histogram



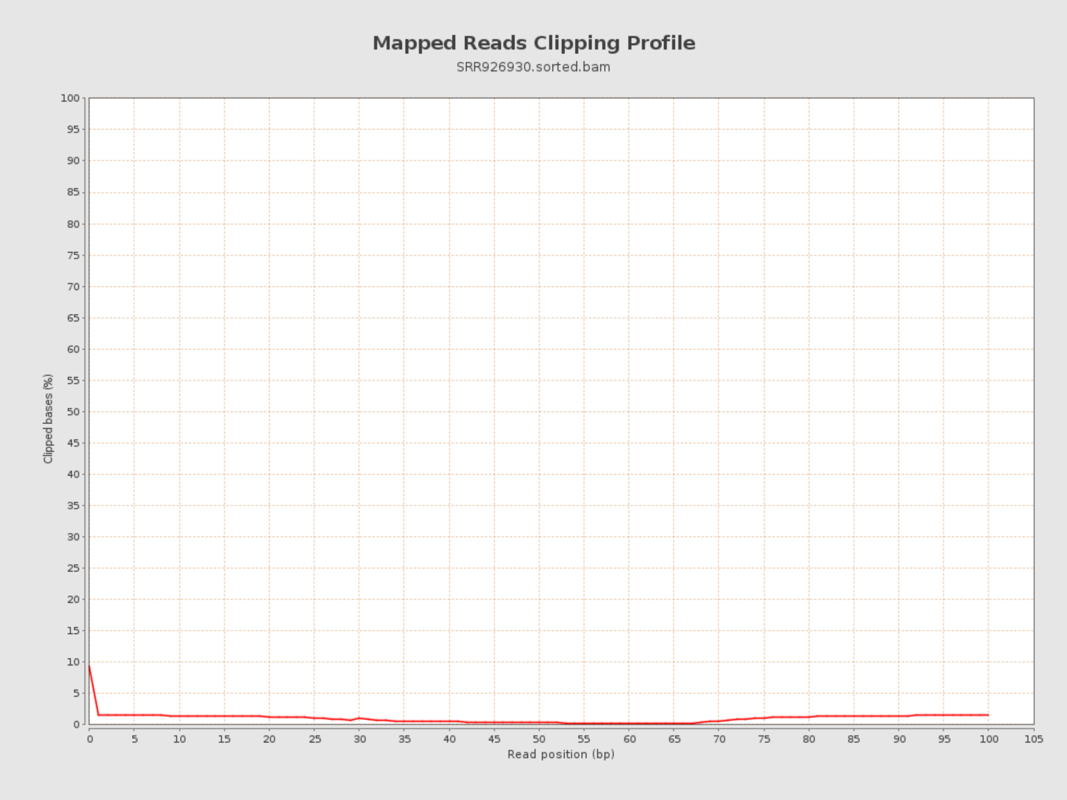
8. Results : Mapped Reads Nucleotide Content



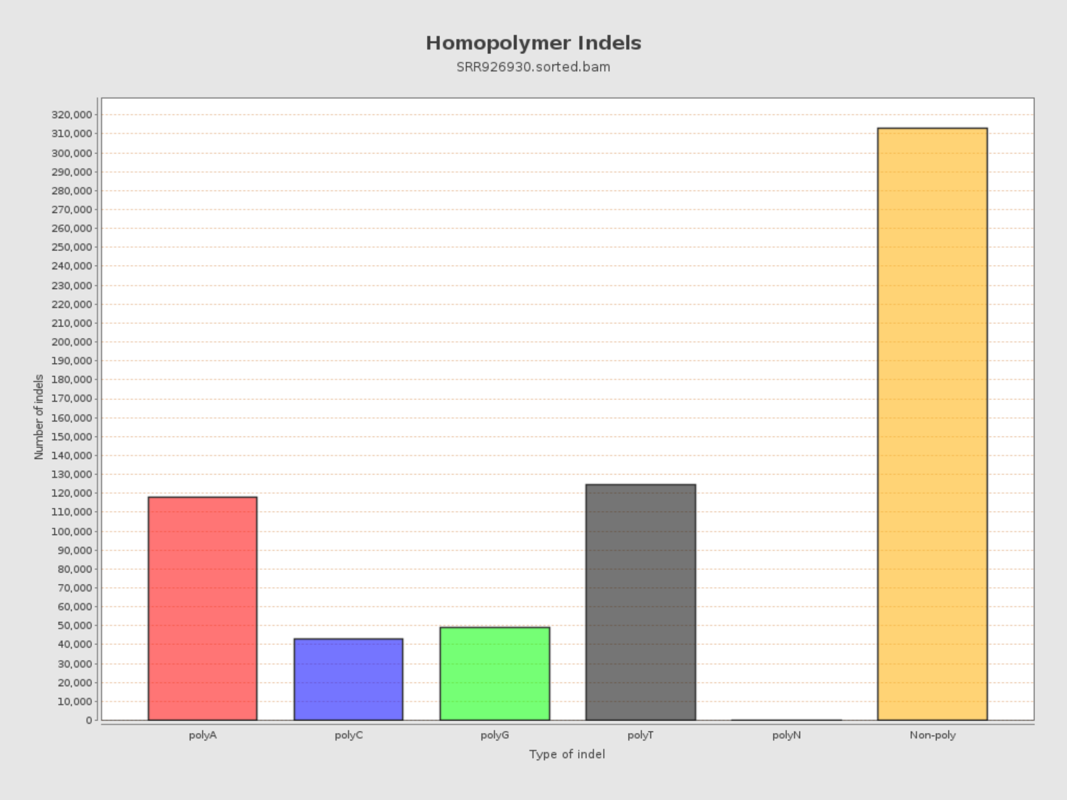
9. Results : Mapped Reads GC-content Distribution



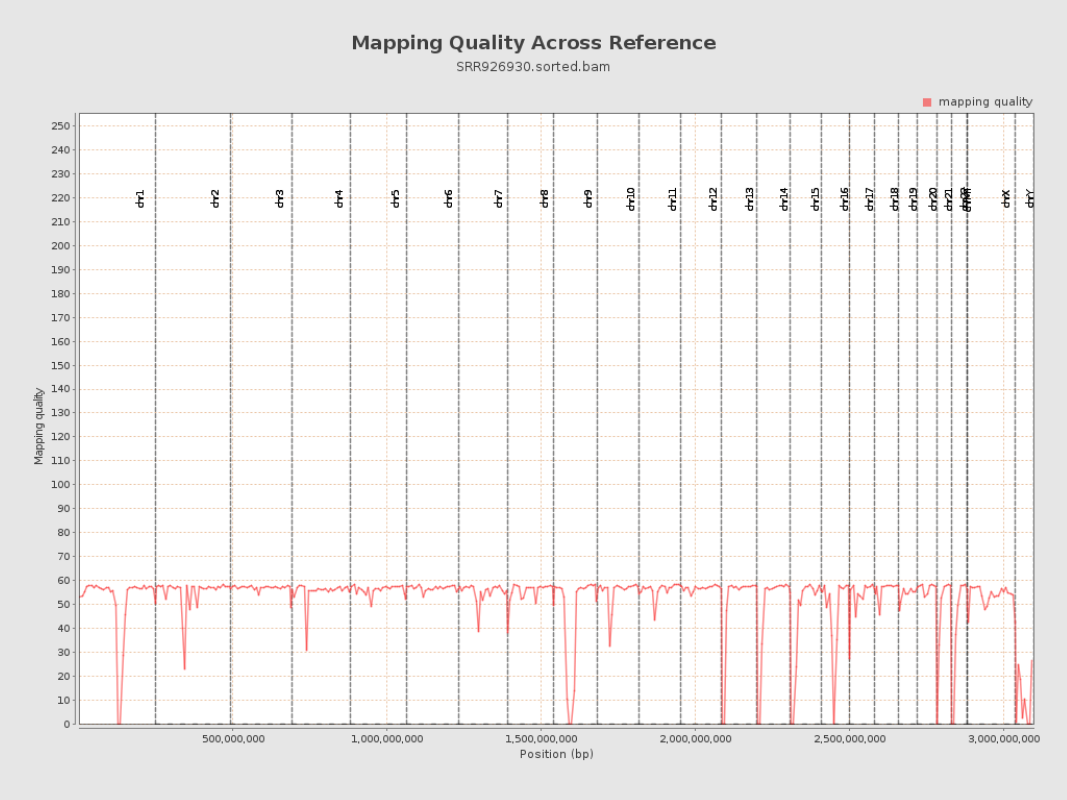
10. Results : Mapped Reads Clipping Profile



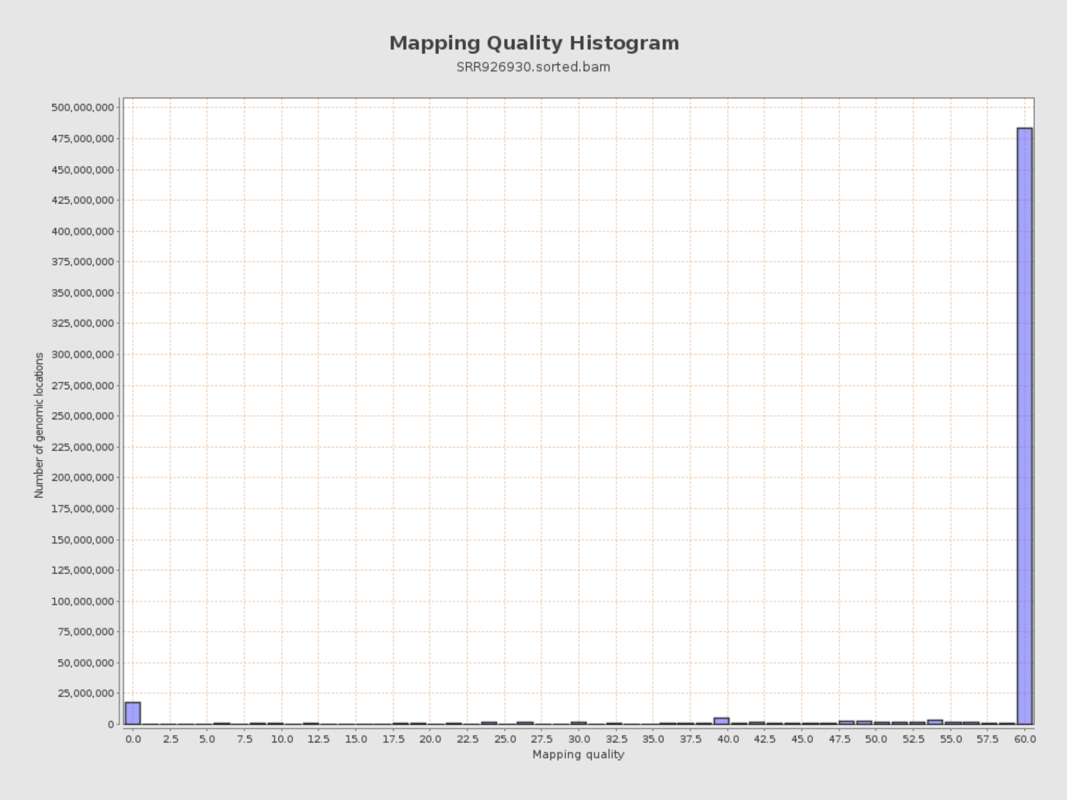
11. Results : Homopolymer Indels



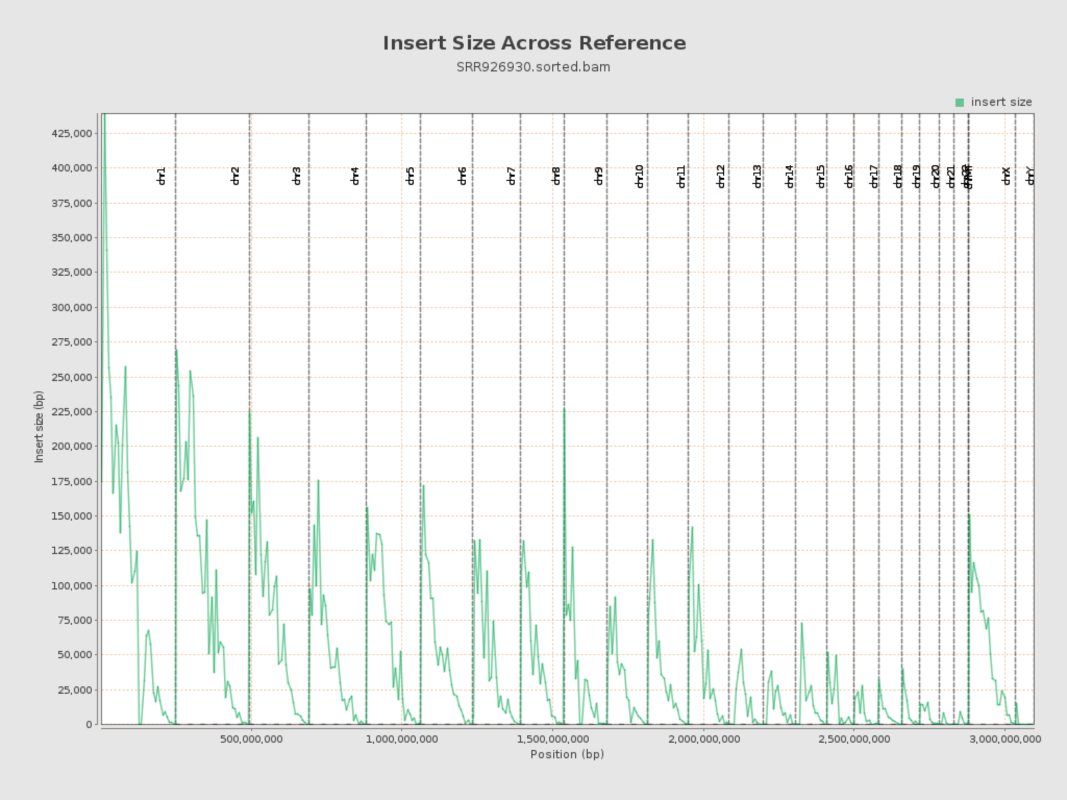
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram