Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 20:49:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926928.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_SRR926928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926928_1.fastq.gz SRR926928_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 20:49:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,170,900
Mapped reads	11,900,970 / 97.78%
Unmapped reads	269,930 / 2.22%
Mapped paired reads	11,900,970 / 97.78%
Mapped reads, first in pair	5,966,033 / 49.02%
Mapped reads, second in pair	5,934,937 / 48.76%
Mapped reads, both in pair	11,807,722 / 97.02%
Mapped reads, singletons	93,248 / 0.77%
Secondary alignments	0
Supplementary alignments	84,736 / 0.7%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	511,481 / 4.2%
Duplication rate	3.2%
Clipped reads	2,674,308 / 21.97%

2.2. ACGT Content

Number/percentage of A's	325,373,544 / 28.75%
Number/percentage of C's	226,572,680 / 20.02%
Number/percentage of T's	328,849,055 / 29.06%
Number/percentage of G's	250,536,523 / 22.14%
Number/percentage of N's	250,257 / 0.02%

GC Percentage	42.16%

2.3. Coverage

Mean	0.3658
Standard Deviation	1.7423

2.4. Mapping Quality

Mean Mapping Quality	53.71

2.5. Insert size

Mean	74,182.42
Standard Deviation	2,648,629.61
P25/Median/P75	155 / 196 / 258

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	10,626,829
Insertions	187,000
Mapped reads with at least one insertion	1.54%
Deletions	623,476
Mapped reads with at least one deletion	5.1%
Homopolymer indels	53.02%

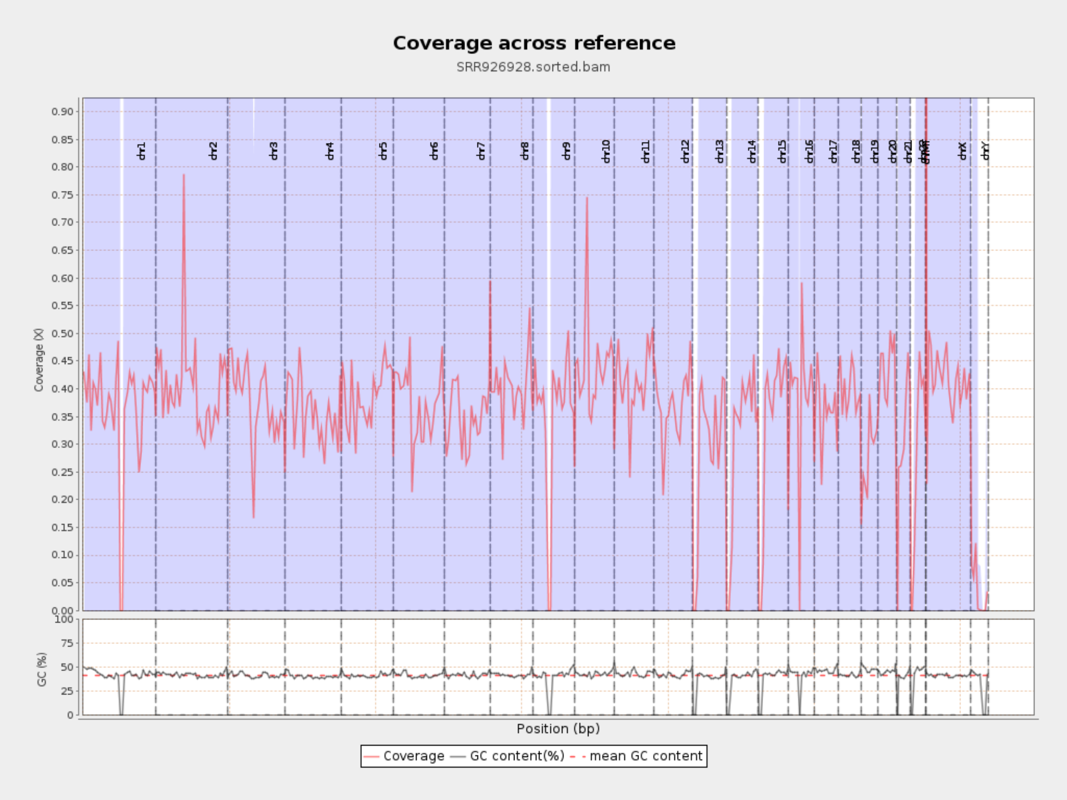
2.7. Chromosome stats

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

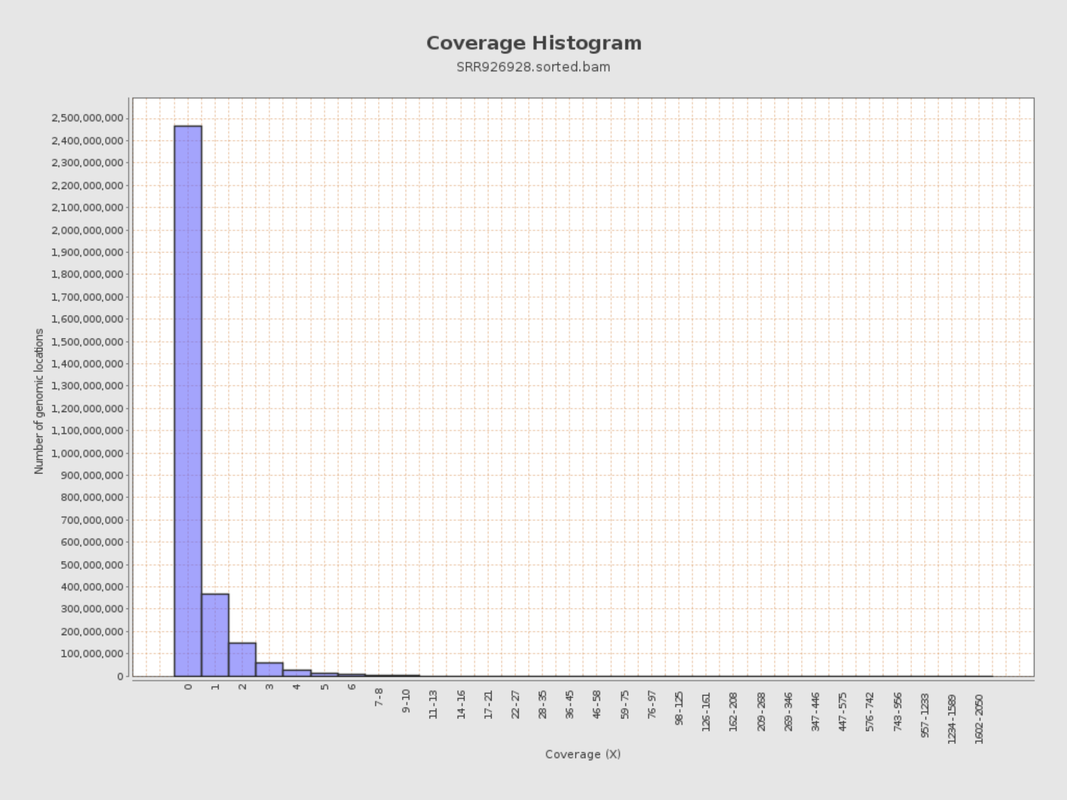
		bases	coverage	deviation
chr1	249250621	90545634	0.3633	2.4165
chr2	243199373	98689446	0.4058	2.7227
chr3	198022430	74681300	0.3771	0.9312
chr4	191154276	68701091	0.3594	1.5899
chr5	180915260	70292817	0.3885	0.9361
chr6	171115067	64017454	0.3741	1.5417
chr7	159138663	55328223	0.3477	1.2398
chr8	146364022	58978155	0.403	1.109
chr9	141213431	50083257	0.3547	2.0463
chr10	135534747	59739283	0.4408	3.5876
chr11	135006516	55507549	0.4111	1.2199
chr12	133851895	49827399	0.3723	0.9339
chr13	115169878	33317304	0.2893	0.7965
chr14	107349540	33541124	0.3124	0.8623
chr15	102531392	34048360	0.3321	0.8896
chr16	90354753	34396451	0.3807	2.1892
chr17	81195210	29614357	0.3647	1.2704
chr18	78077248	31167209	0.3992	2.2445
chr19	59128983	16650368	0.2816	1.4169
chr20	63025520	27609987	0.4381	1.0997
chr21	48129895	14829125	0.3081	1.3366
chr22	51304566	14171547	0.2762	0.8534
chrMT	16571	283017	17.0791	13.5158
chrX	155270560	64327691	0.4143	1.0654

chrY	59373566	2123546	0.0358	1.5117

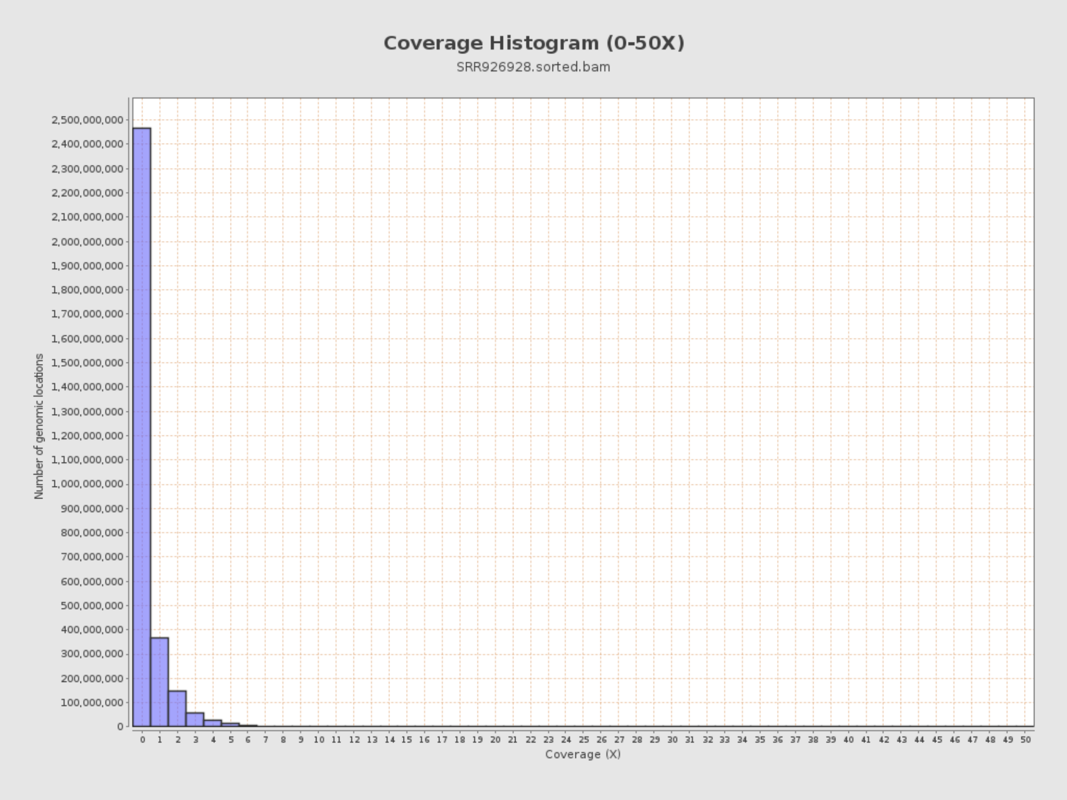
3. Results : Coverage across reference



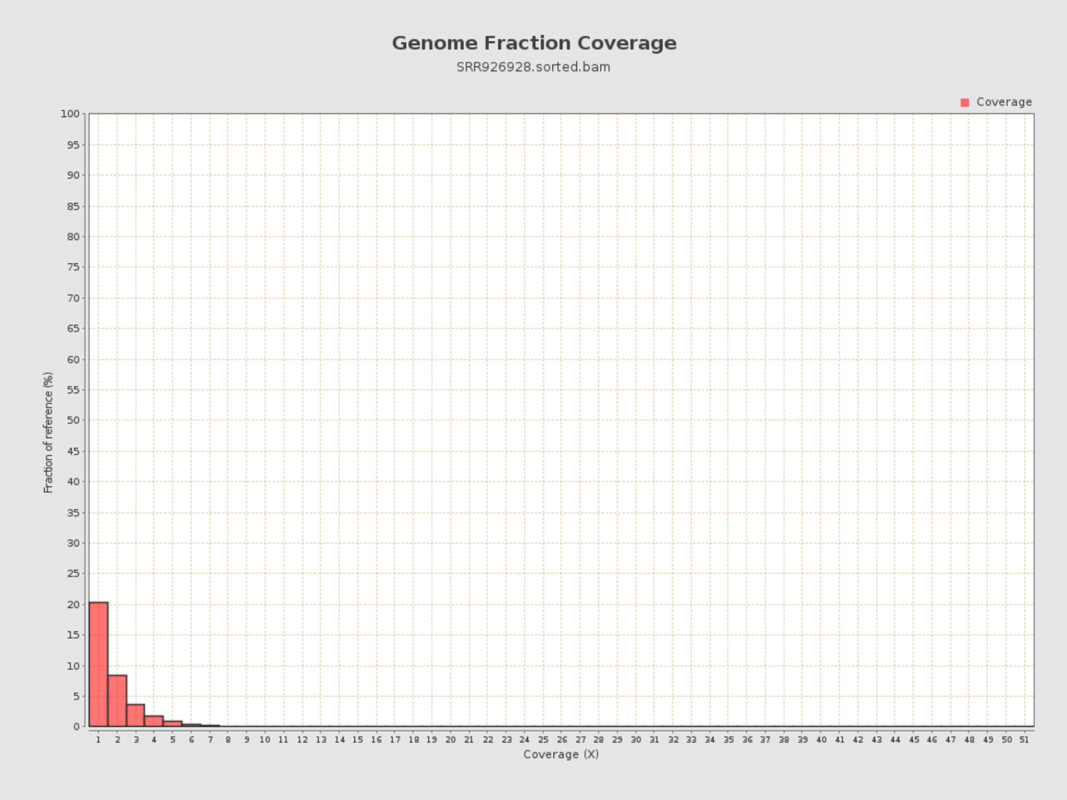
4. Results : Coverage Histogram



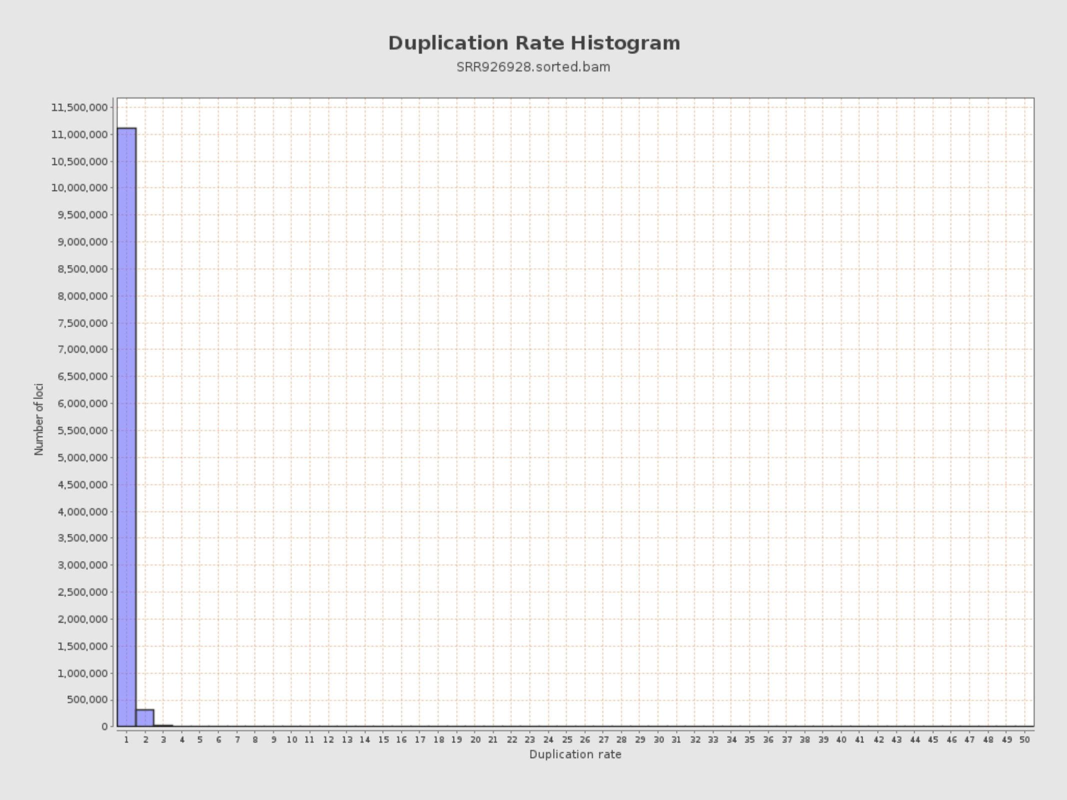
5. Results : Coverage Histogram (0-50X)



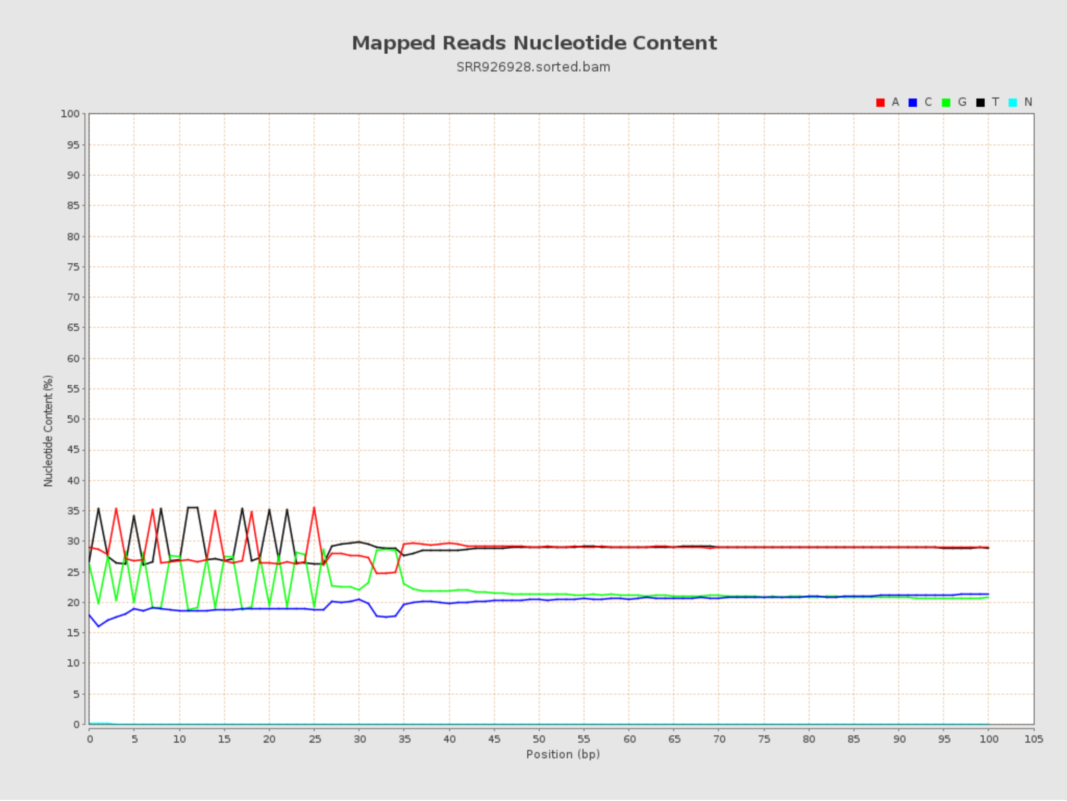
6. Results : Genome Fraction Coverage



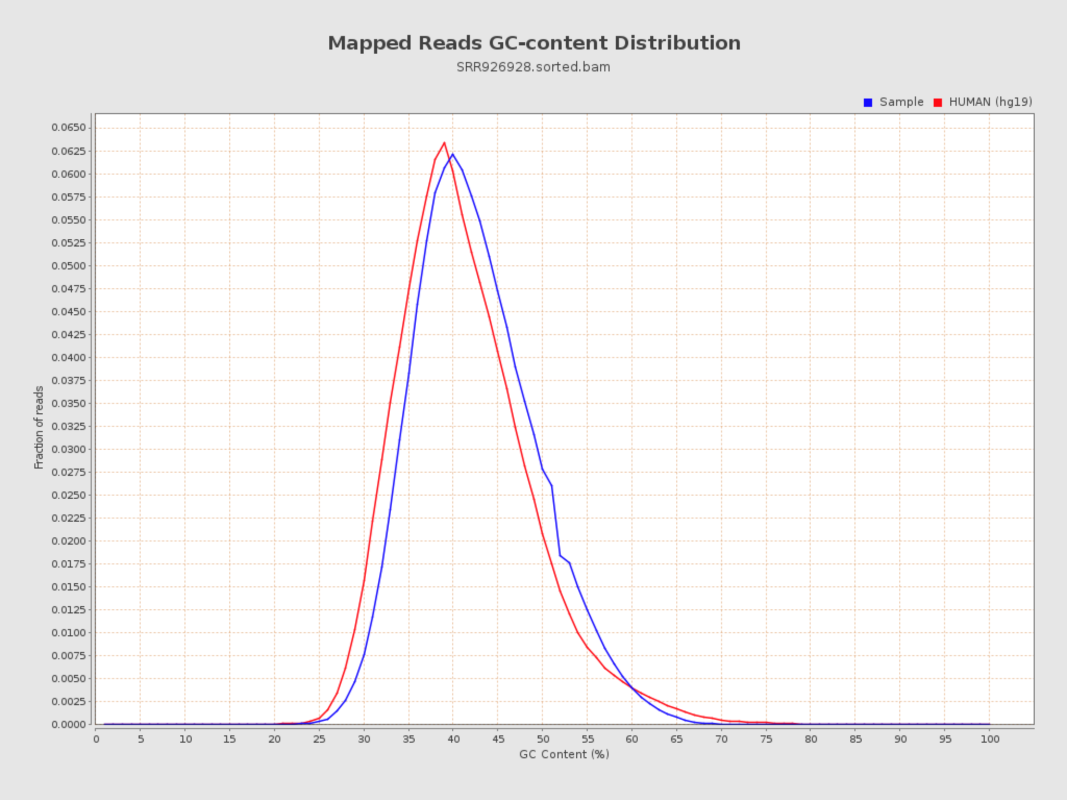
7. Results : Duplication Rate Histogram



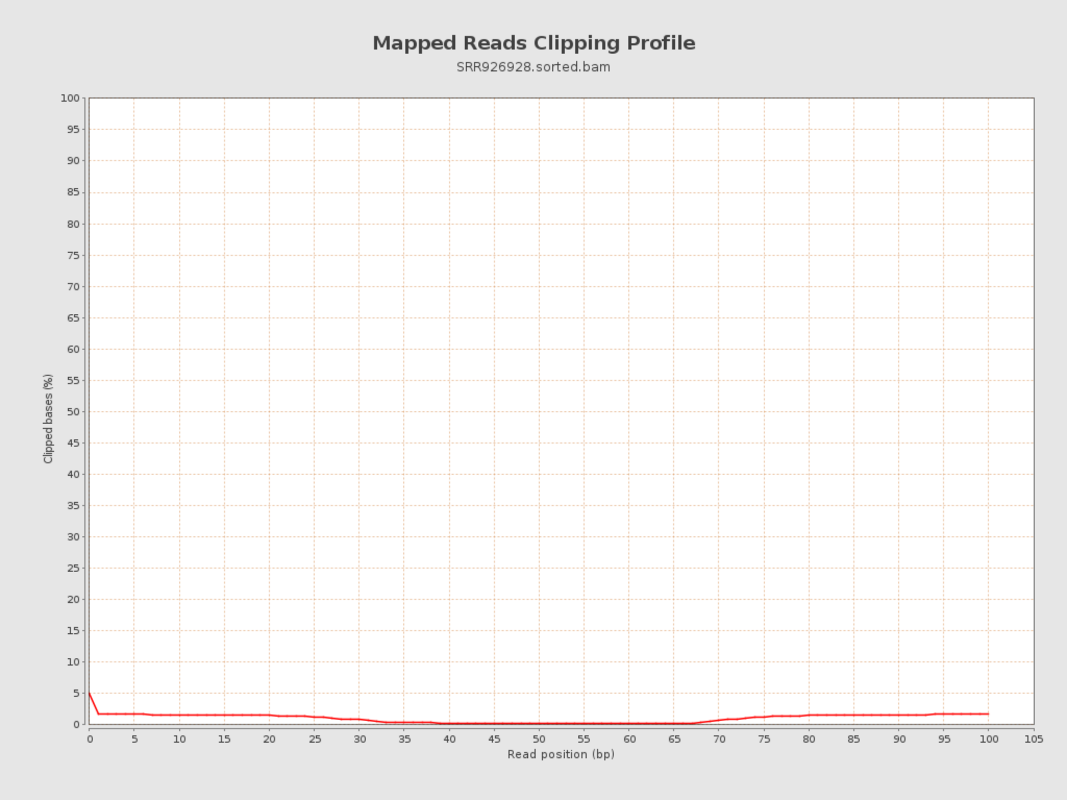
8. Results : Mapped Reads Nucleotide Content



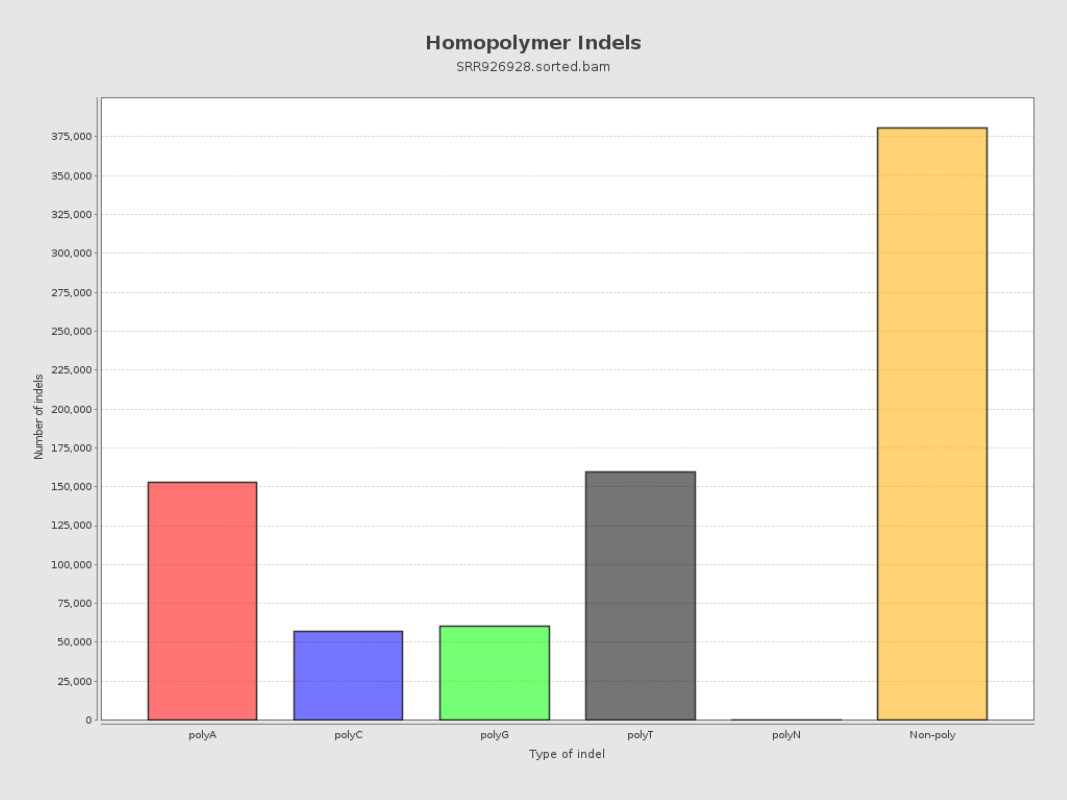
9. Results : Mapped Reads GC-content Distribution



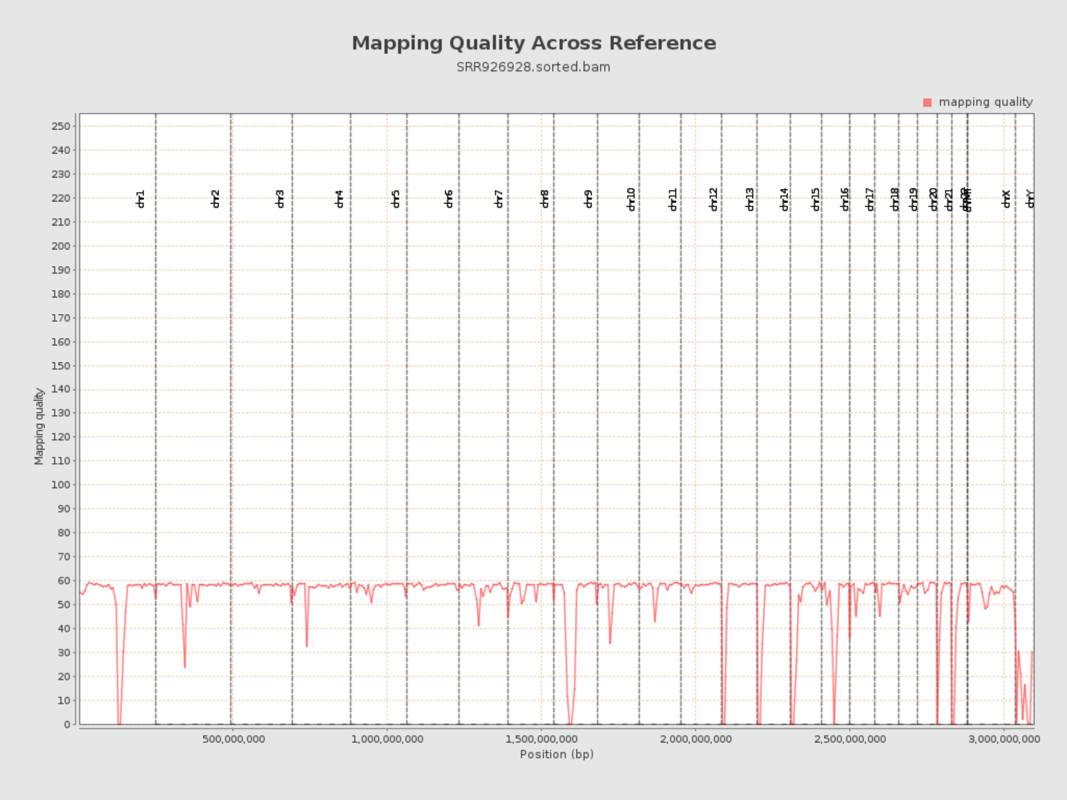
10. Results : Mapped Reads Clipping Profile



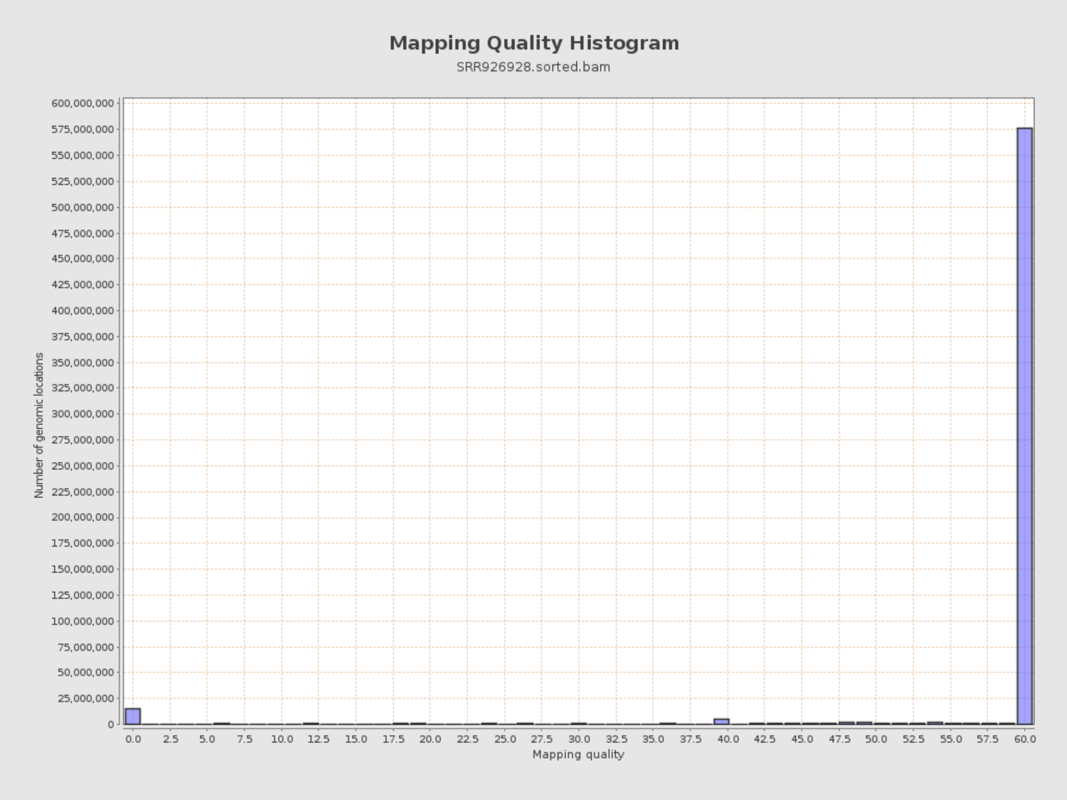
11. Results : Homopolymer Indels



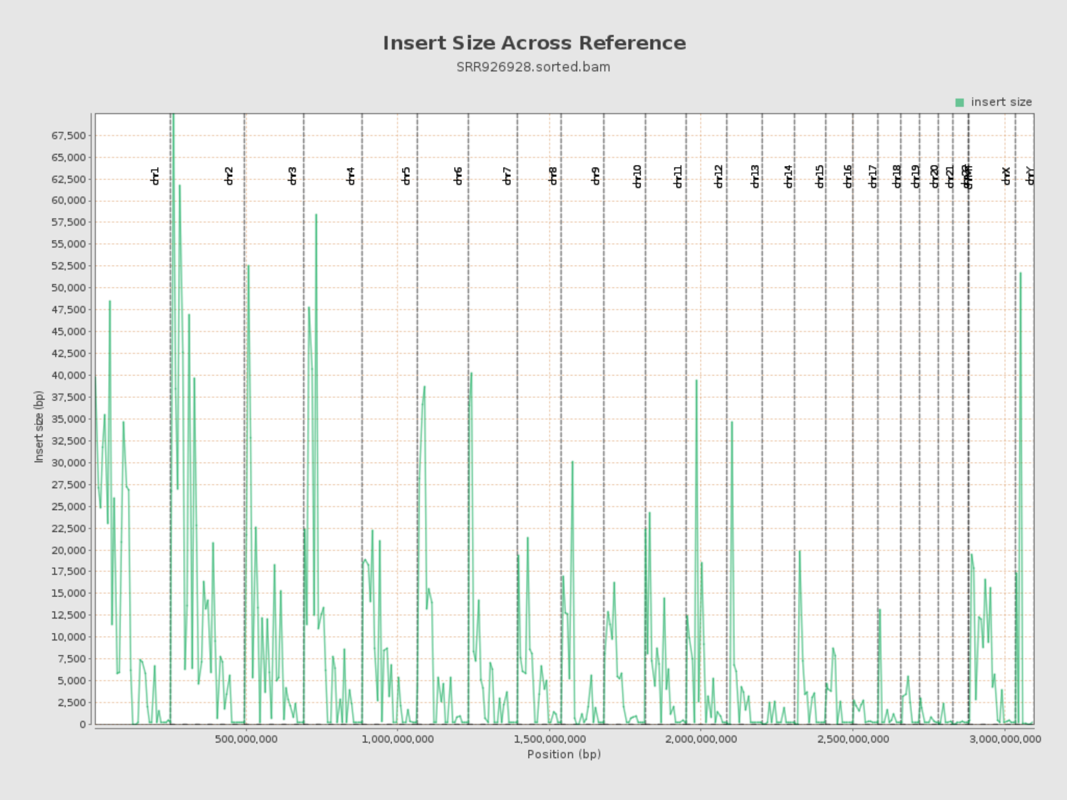
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram