Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 10:29:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926973.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_SRR926973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926973_1.fastq.gz SRR926973_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 10:29:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,356,400
Mapped reads	19,934,921 / 97.93%
Unmapped reads	421,479 / 2.07%
Mapped paired reads	19,934,921 / 97.93%
Mapped reads, first in pair	10,006,169 / 49.15%
Mapped reads, second in pair	9,928,752 / 48.77%
Mapped reads, both in pair	19,665,408 / 96.61%
Mapped reads, singletons	269,513 / 1.32%
Secondary alignments	0
Supplementary alignments	692,186 / 3.4%
Read min/max/mean length	30 / 101 / 102.41
Duplicated reads (estimated)	1,926,365 / 9.46%
Duplication rate	7.77%
Clipped reads	9,697,639 / 47.64%

2.2. ACGT Content

Number/percentage of A's	511,018,712 / 28.65%
Number/percentage of C's	339,547,513 / 19.04%
Number/percentage of T's	525,502,404 / 29.47%
Number/percentage of G's	407,160,865 / 22.83%
Number/percentage of N's	134,226 / 0.01%

GC Percentage	41.87%

2.3. Coverage

Mean	0.5765
Standard Deviation	2.1627

2.4. Mapping Quality

Mean Mapping Quality	52.51

2.5. Insert size

Mean	373,177.86
Standard Deviation	5,986,098.14
P25/Median/P75	128 / 166 / 222

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	17,024,375
Insertions	318,617
Mapped reads with at least one insertion	1.57%
Deletions	954,458
Mapped reads with at least one deletion	4.67%
Homopolymer indels	51.67%

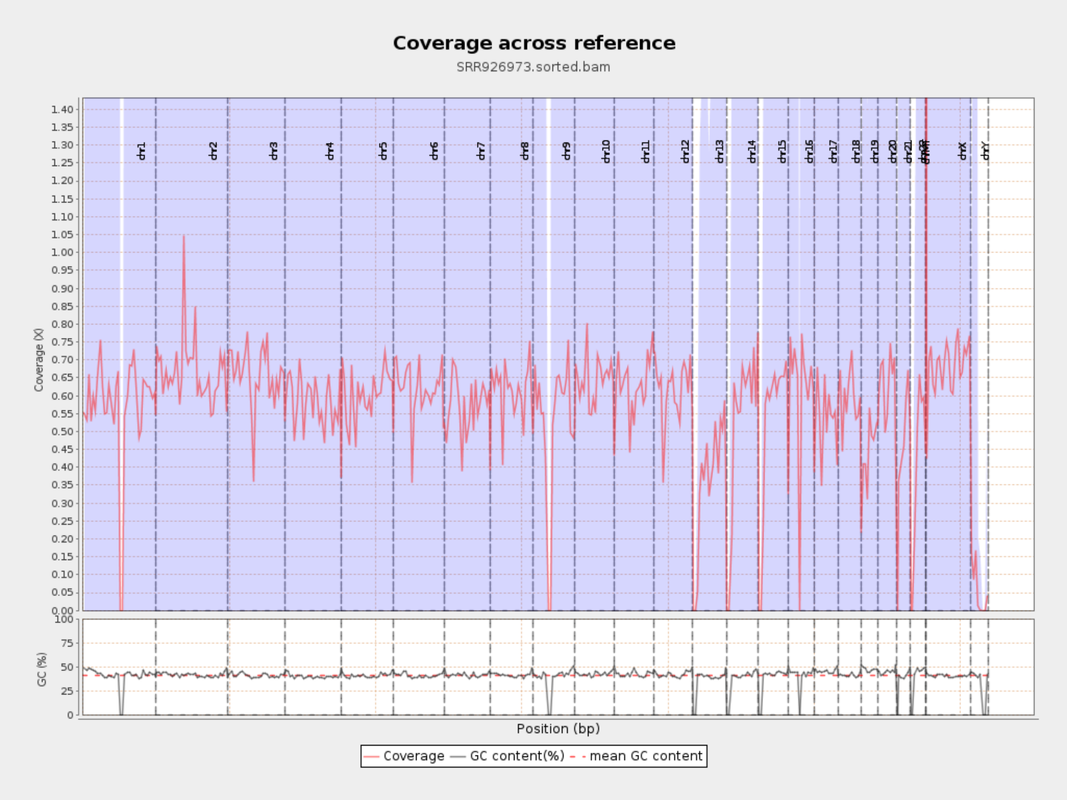
2.7. Chromosome stats

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

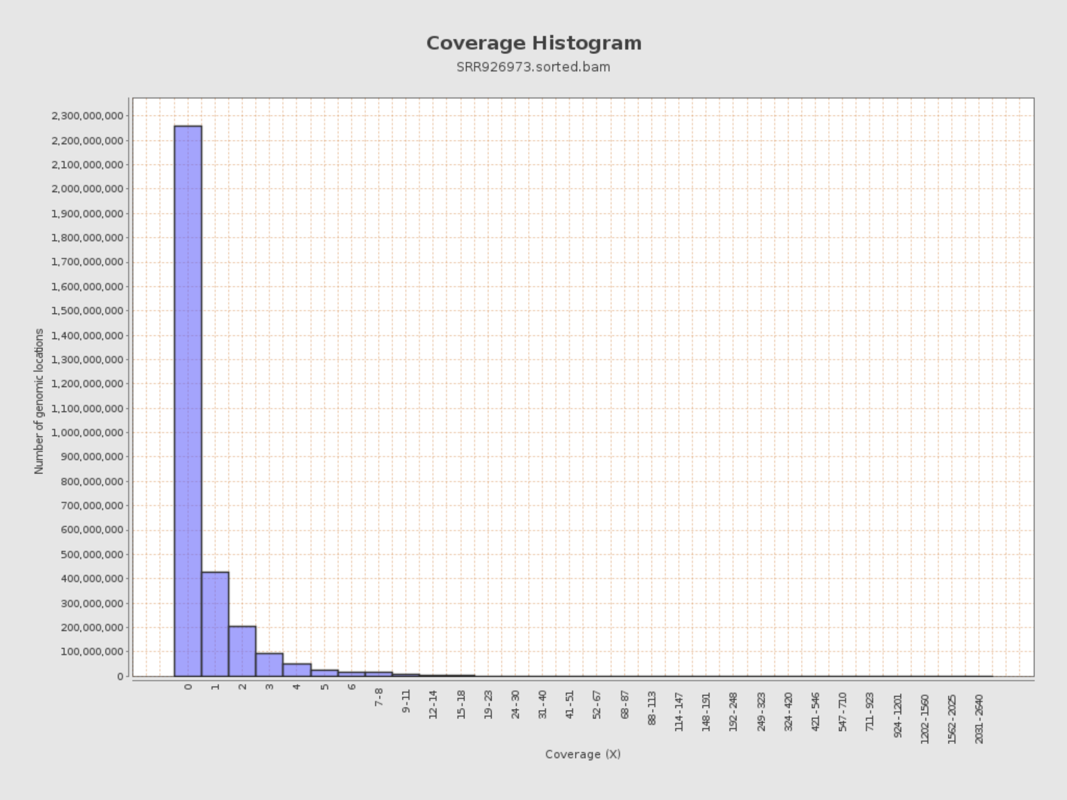
		bases	coverage	deviation
chr1	249250621	141725335	0.5686	2.351
chr2	243199373	162844334	0.6696	3.7566
chr3	198022430	130052909	0.6568	1.4289
chr4	191154276	112279561	0.5874	2.0252
chr5	180915260	109420457	0.6048	1.352
chr6	171115067	106360260	0.6216	1.6613
chr7	159138663	90961044	0.5716	2.027
chr8	146364022	90219121	0.6164	1.654
chr9	141213431	73815225	0.5227	2.437
chr10	135534747	87096492	0.6426	2.857
chr11	135006516	84731923	0.6276	2.8556
chr12	133851895	83093738	0.6208	1.6686
chr13	115169878	41511622	0.3604	1.0911
chr14	107349540	55488841	0.5169	1.3235
chr15	102531392	52722415	0.5142	1.3614
chr16	90354753	54411050	0.6022	2.8286
chr17	81195210	44038304	0.5424	1.6013
chr18	78077248	46248779	0.5923	2.5845
chr19	59128983	26392764	0.4464	1.6606
chr20	63025520	39965129	0.6341	1.5149
chr21	48129895	21772862	0.4524	1.712
chr22	51304566	20478765	0.3992	1.1971
chrMT	16571	371960	22.4464	20.991
chrX	155270560	105540859	0.6797	1.7108

chrY	59373566	3229968	0.0544	1.8897

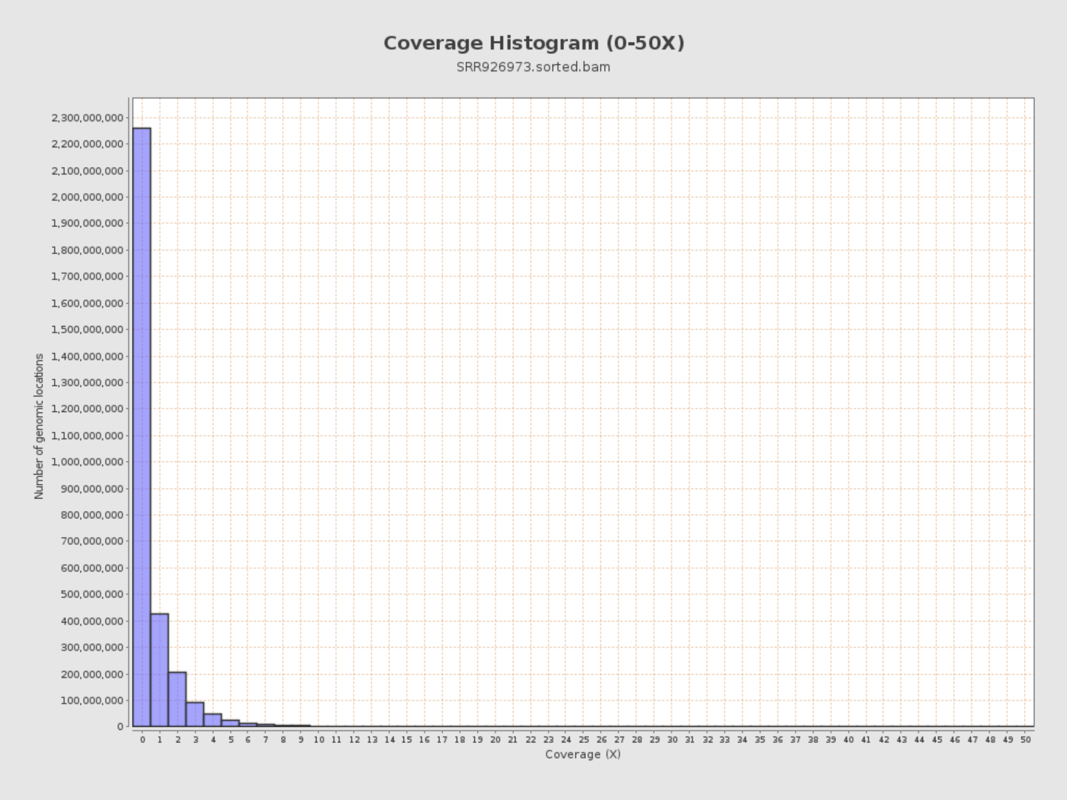
3. Results : Coverage across reference



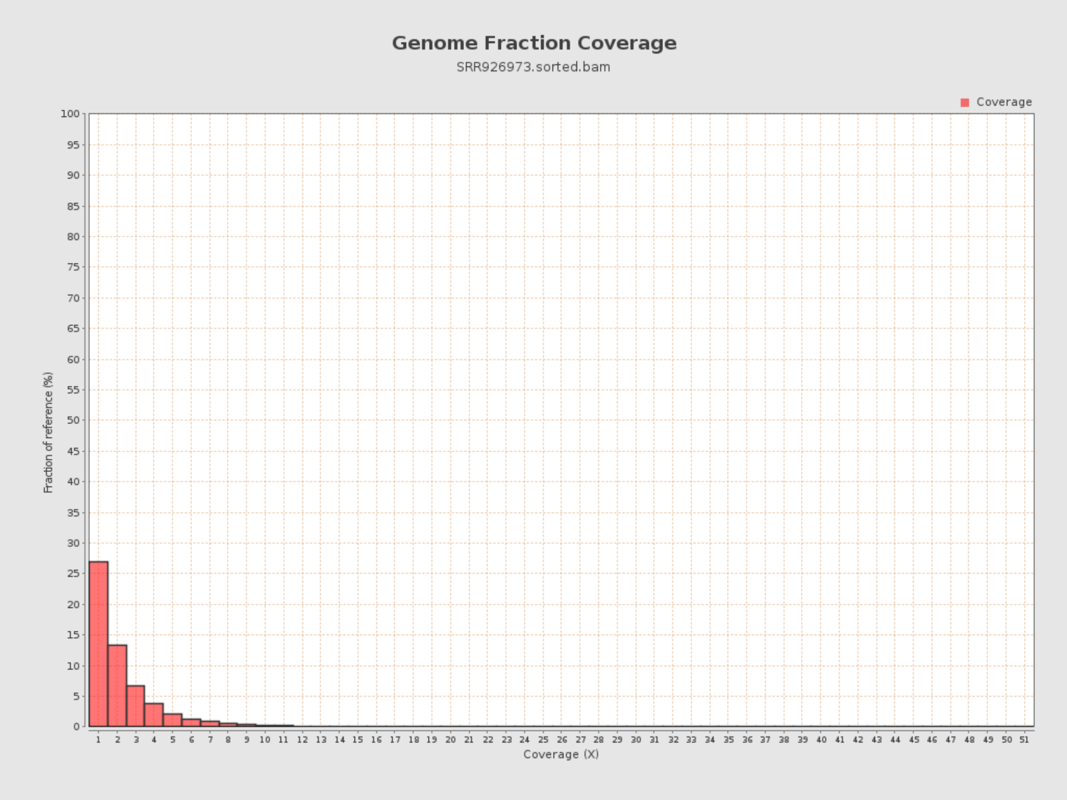
4. Results : Coverage Histogram



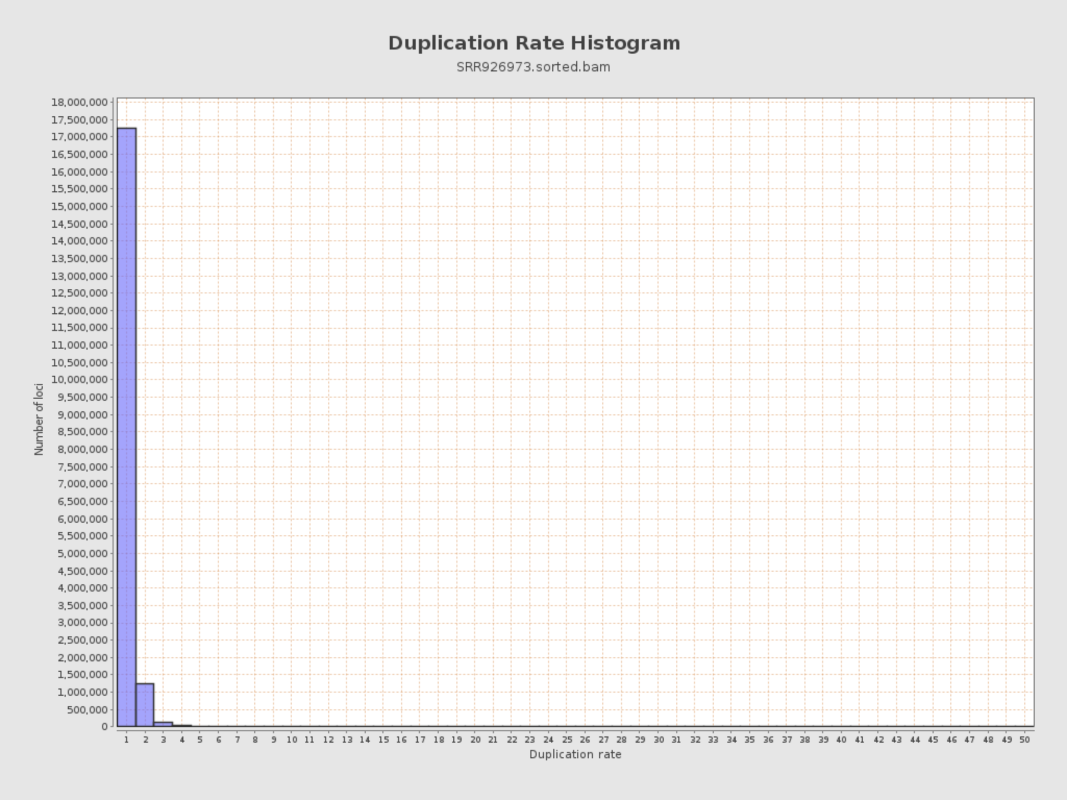
5. Results : Coverage Histogram (0-50X)



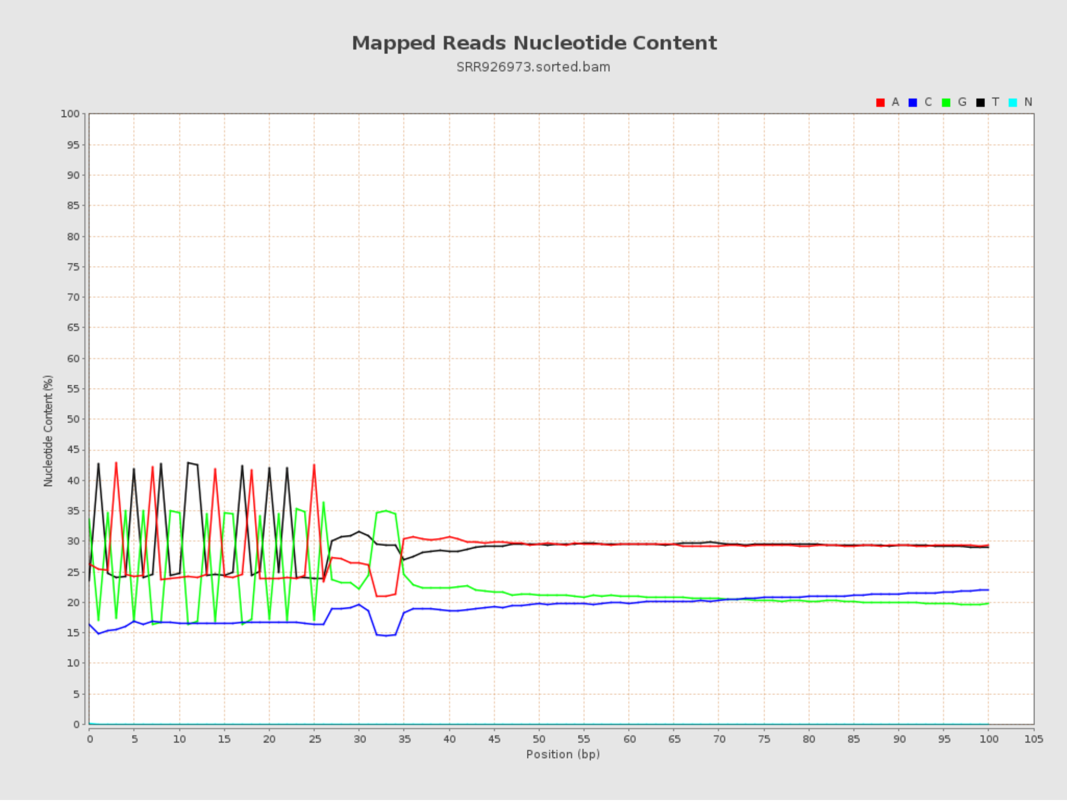
6. Results : Genome Fraction Coverage



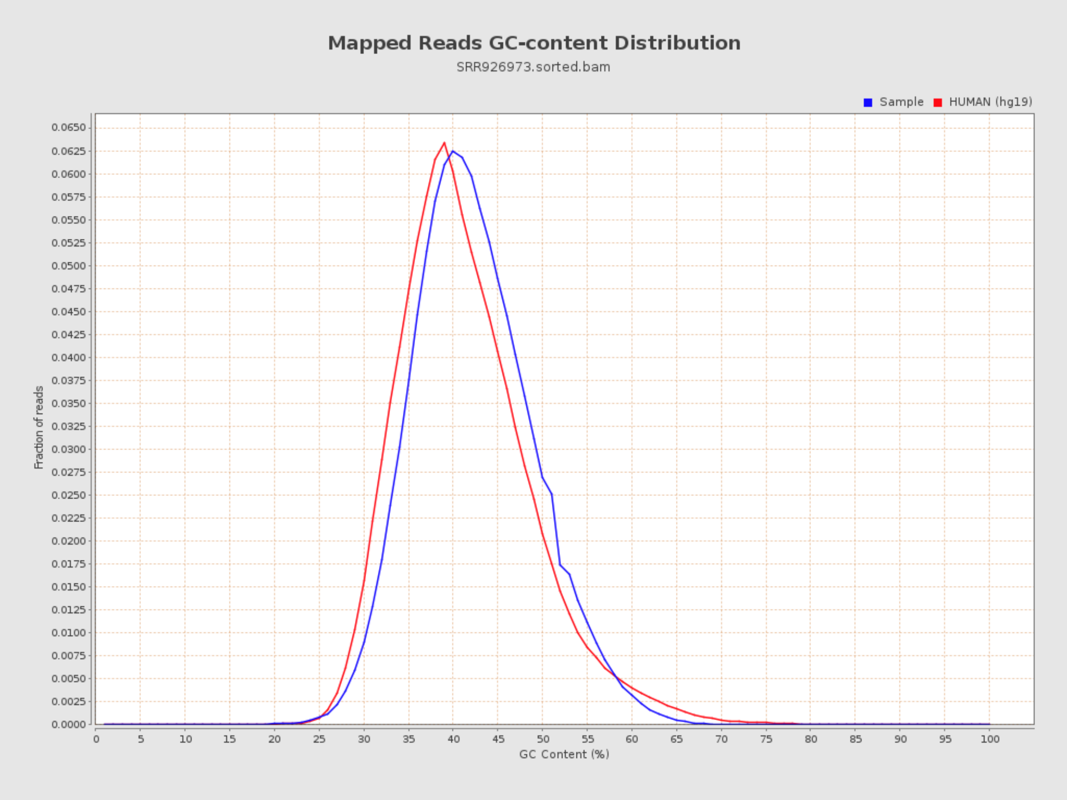
7. Results : Duplication Rate Histogram



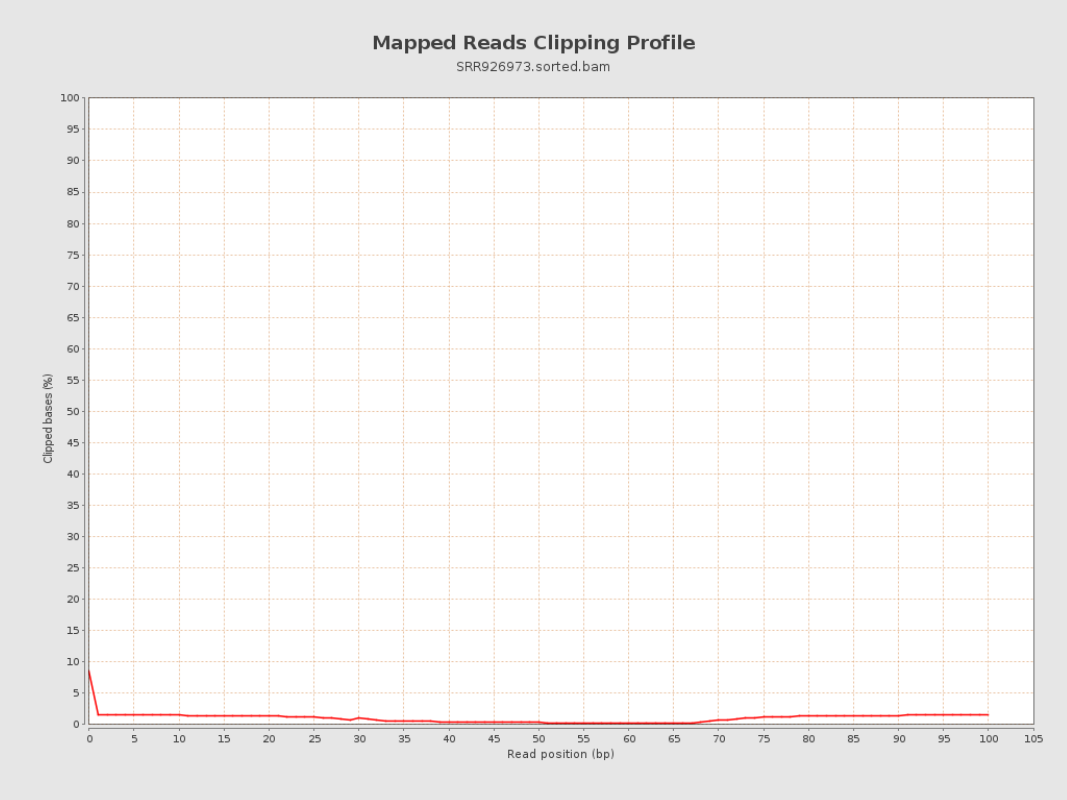
8. Results : Mapped Reads Nucleotide Content



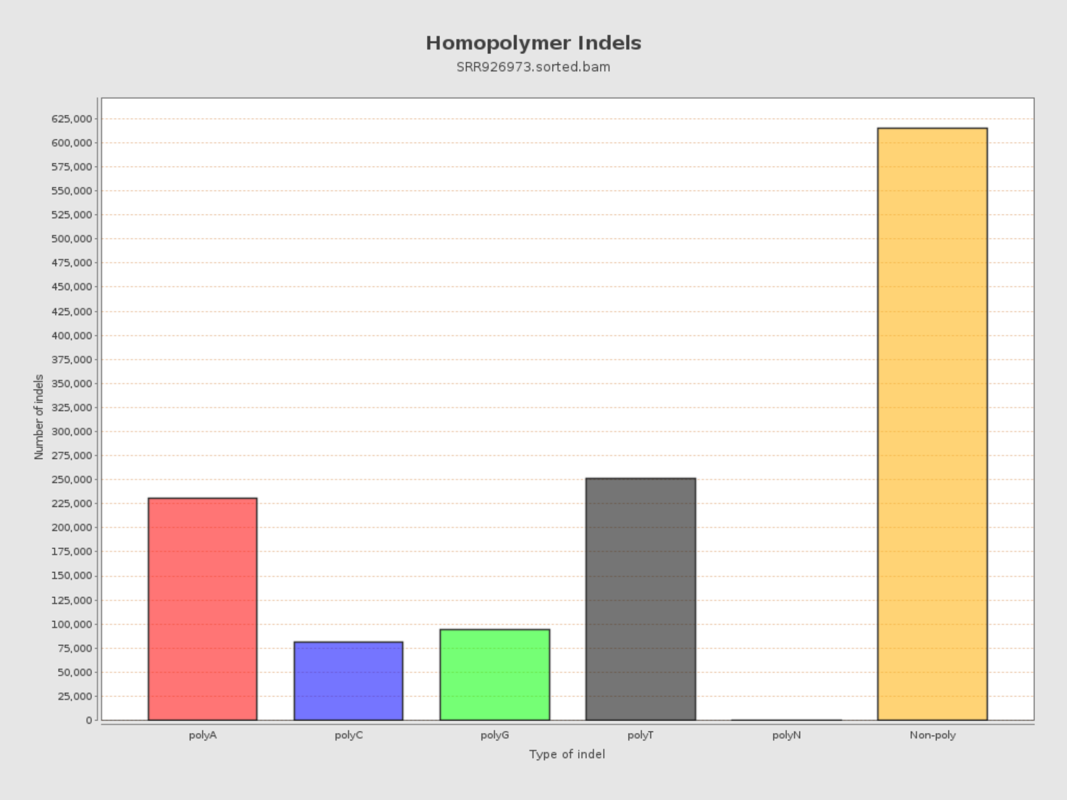
9. Results : Mapped Reads GC-content Distribution



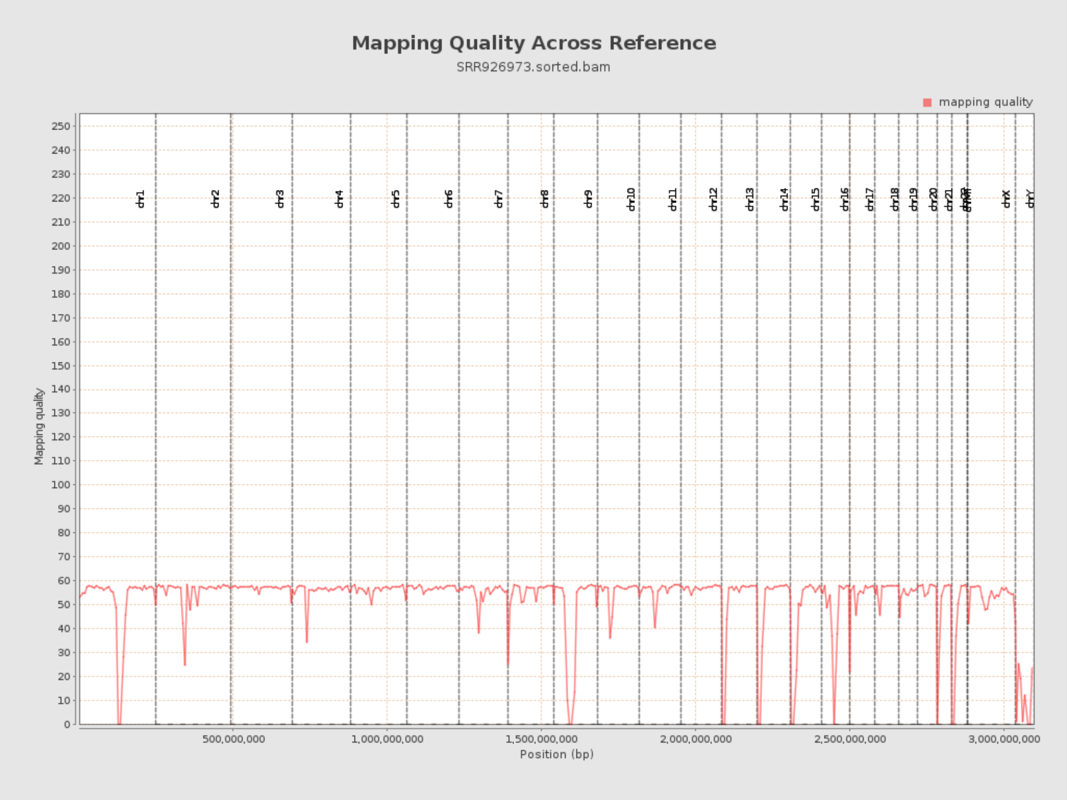
10. Results : Mapped Reads Clipping Profile



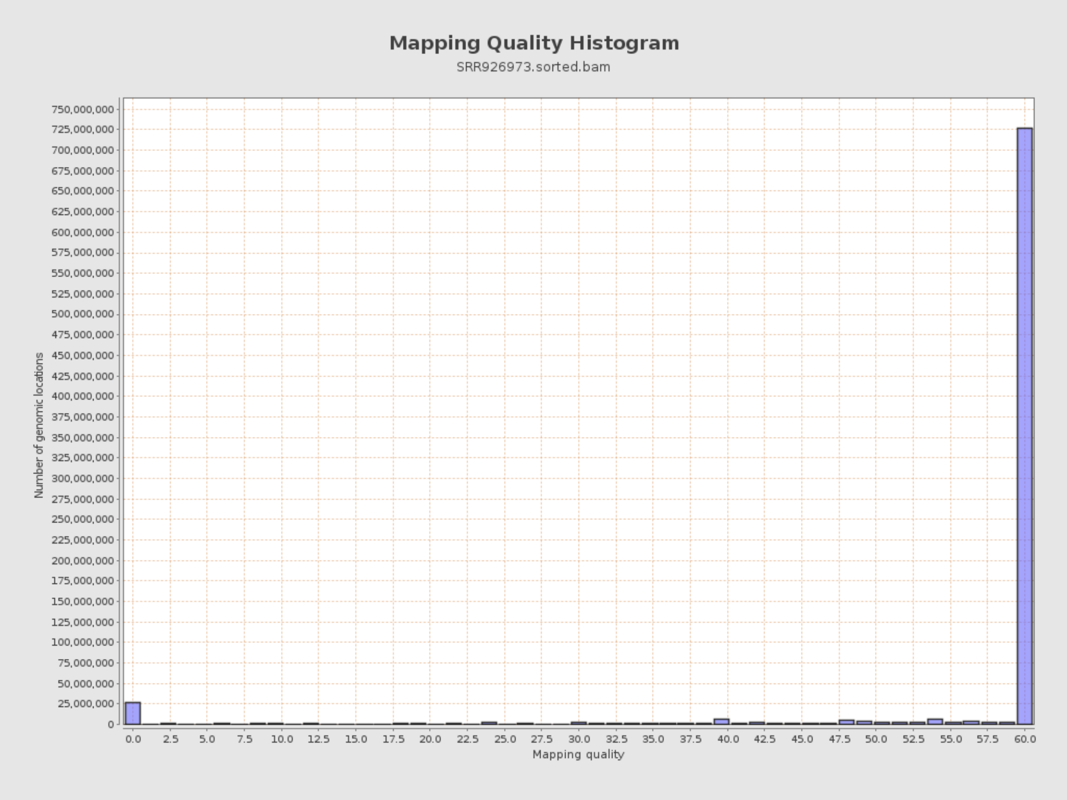
11. Results : Homopolymer Indels



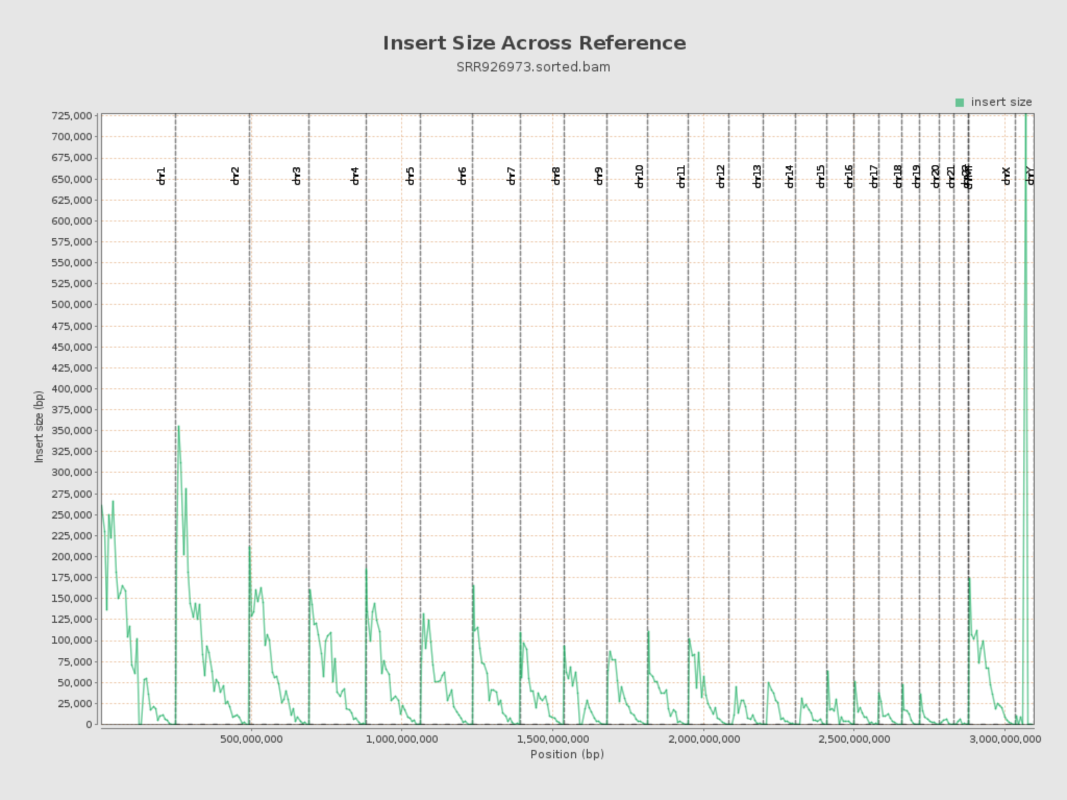
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram