Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 19:54:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926924.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_SRR926924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926924_1.fastq.gz SRR926924_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 19:54:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,355,846
Mapped reads	13,981,932 / 97.4%
Unmapped reads	373,914 / 2.6%
Mapped paired reads	13,981,932 / 97.4%
Mapped reads, first in pair	6,977,785 / 48.61%
Mapped reads, second in pair	7,004,147 / 48.79%
Mapped reads, both in pair	13,774,686 / 95.95%
Mapped reads, singletons	207,246 / 1.44%
Secondary alignments	0
Supplementary alignments	522,456 / 3.64%
Read min/max/mean length	30 / 101 / 102.51
Duplicated reads (estimated)	975,861 / 6.8%
Duplication rate	5.62%
Clipped reads	7,105,062 / 49.49%

2.2. ACGT Content

Number/percentage of A's	358,238,900 / 28.42%
Number/percentage of C's	246,328,061 / 19.54%
Number/percentage of T's	364,659,238 / 28.93%
Number/percentage of G's	291,122,928 / 23.1%
Number/percentage of N's	49,924 / 0%

GC Percentage	42.64%

2.3. Coverage

Mean	0.4075
Standard Deviation	1.6757

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	343,224.43
Standard Deviation	5,621,432.74
P25/Median/P75	134 / 174 / 234

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	12,105,951
Insertions	216,320
Mapped reads with at least one insertion	1.52%
Deletions	646,010
Mapped reads with at least one deletion	4.5%
Homopolymer indels	51.45%

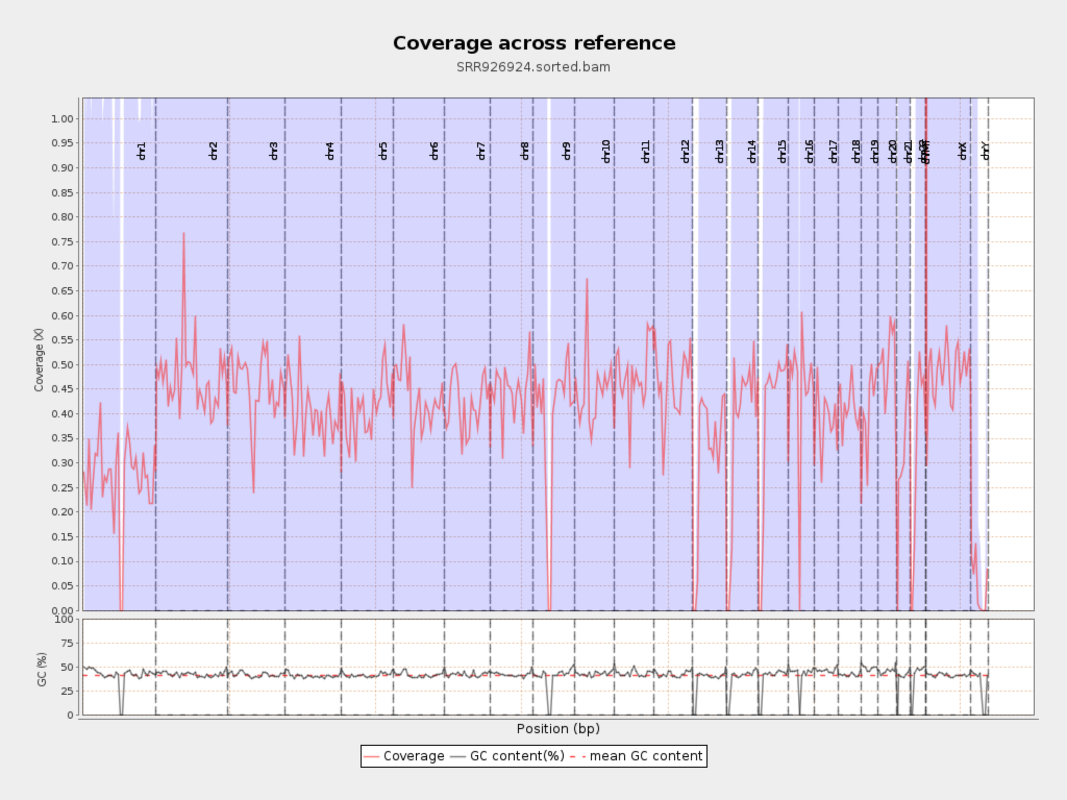
2.7. Chromosome stats

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

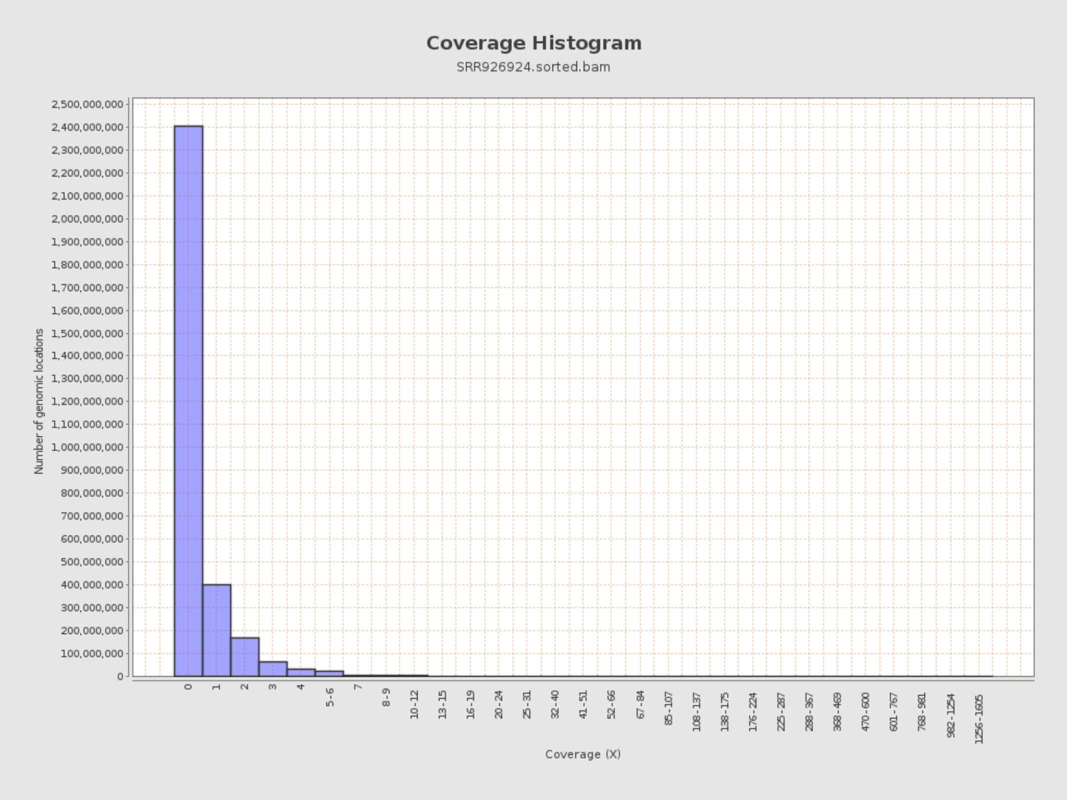
		bases	**coverage**	**deviation**
chr1	249250621	66767025	0.2679	1.6866
chr2	243199373	115579754	0.4752	2.7994
chr3	198022430	90455603	0.4568	1.0566
chr4	191154276	78002723	0.4081	1.8336
chr5	180915260	74961131	0.4143	0.9926
chr6	171115067	73903356	0.4319	1.4892
chr7	159138663	66793916	0.4197	1.4667
chr8	146364022	65085607	0.4447	1.1891
chr9	141213431	55651981	0.3941	2.0154
chr10	135534747	60261559	0.4446	2.8842
chr11	135006516	64388962	0.4769	1.5055
chr12	133851895	62785056	0.4691	1.1463
chr13	115169878	36311316	0.3153	0.8582
chr14	107349540	40057078	0.3731	0.9799
chr15	102531392	39652831	0.3867	1.0073
chr16	90354753	39866351	0.4412	2.2327
chr17	81195210	31651909	0.3898	1.219
chr18	78077248	32299027	0.4137	2.0109
chr19	59128983	24340558	0.4117	1.4328
chr20	63025520	32310318	0.5127	1.2875
chr21	48129895	15563527	0.3234	1.3326
chr22	51304566	16354336	0.3188	0.9504
chrMT	16571	184128	11.1115	7.4991
chrX	155270560	75148678	0.484	1.1891

chrY	59373566	2973789	0.0501	1.5662

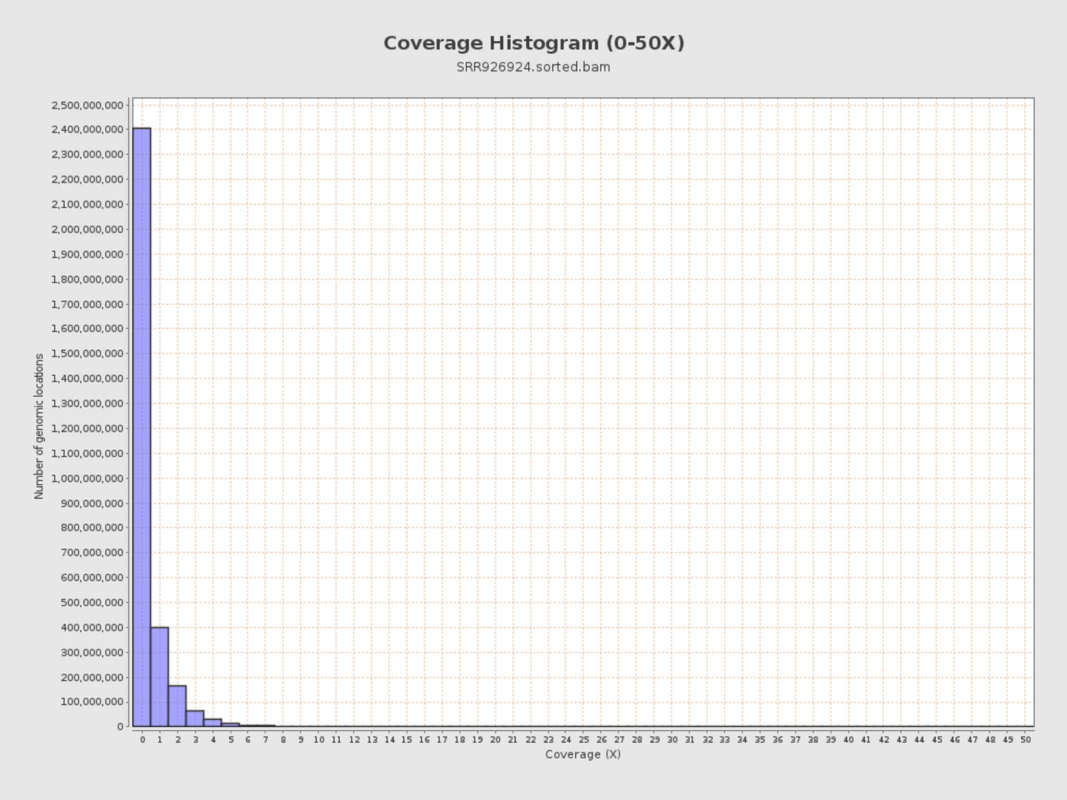
3. Results : Coverage across reference



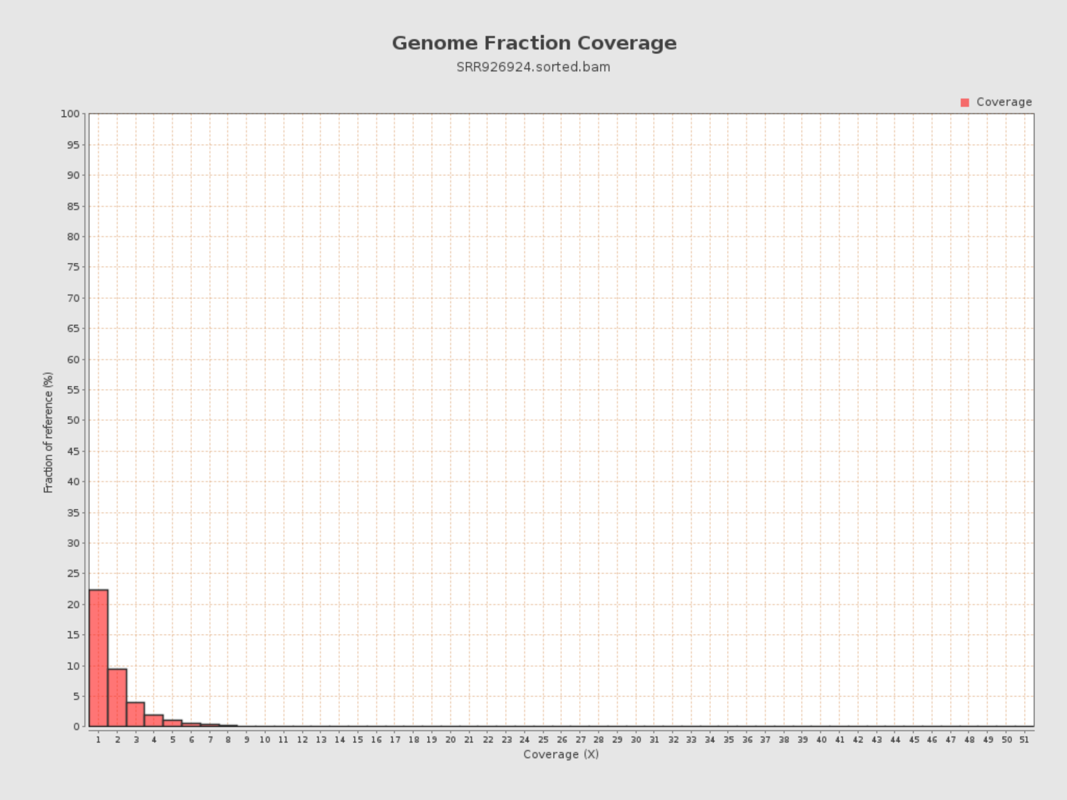
4. Results : Coverage Histogram



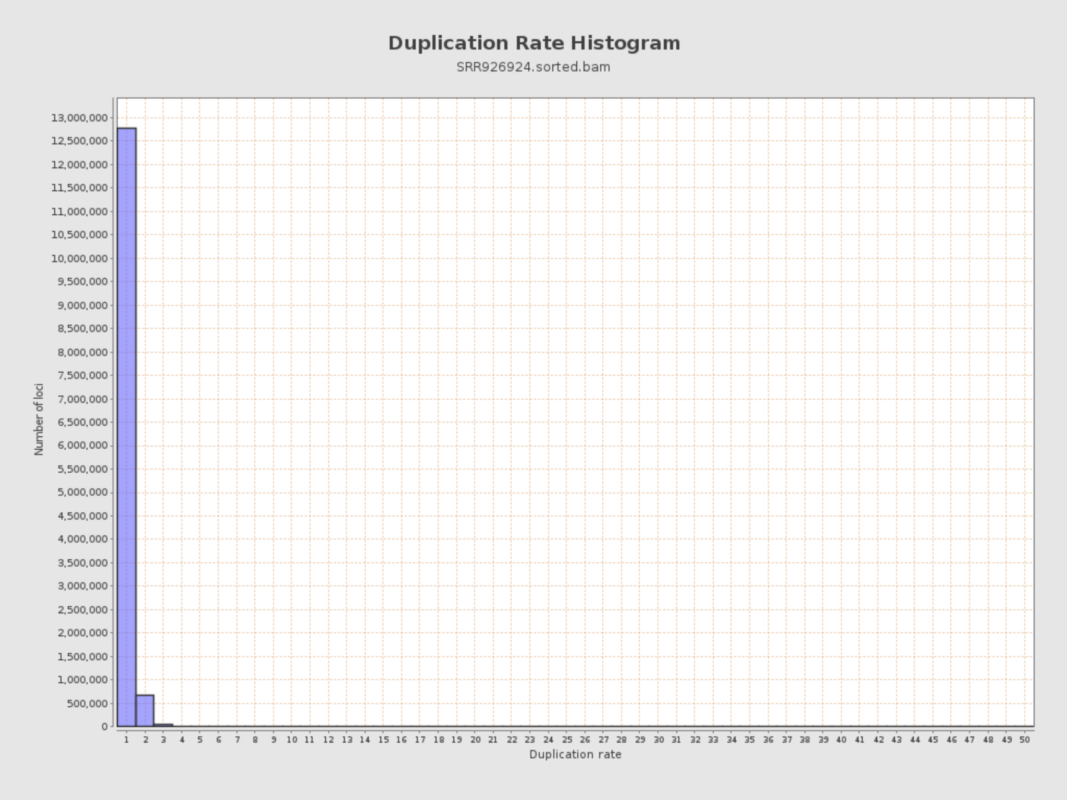
5. Results : Coverage Histogram (0-50X)



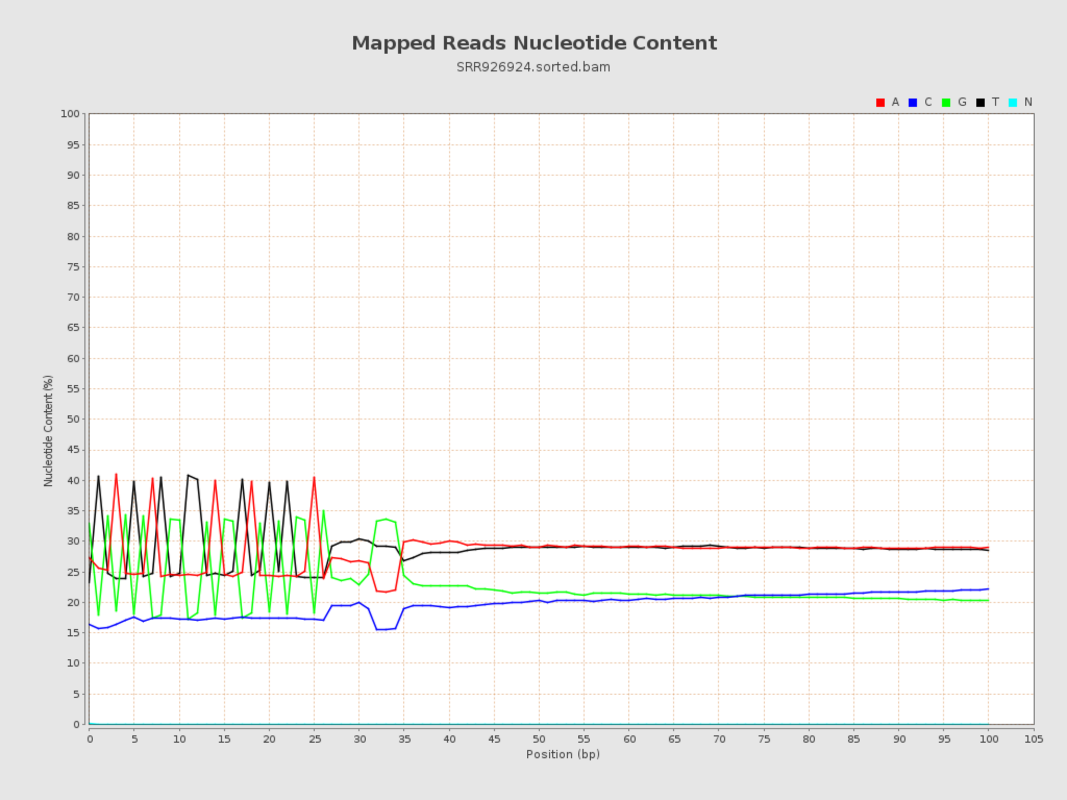
6. Results : Genome Fraction Coverage



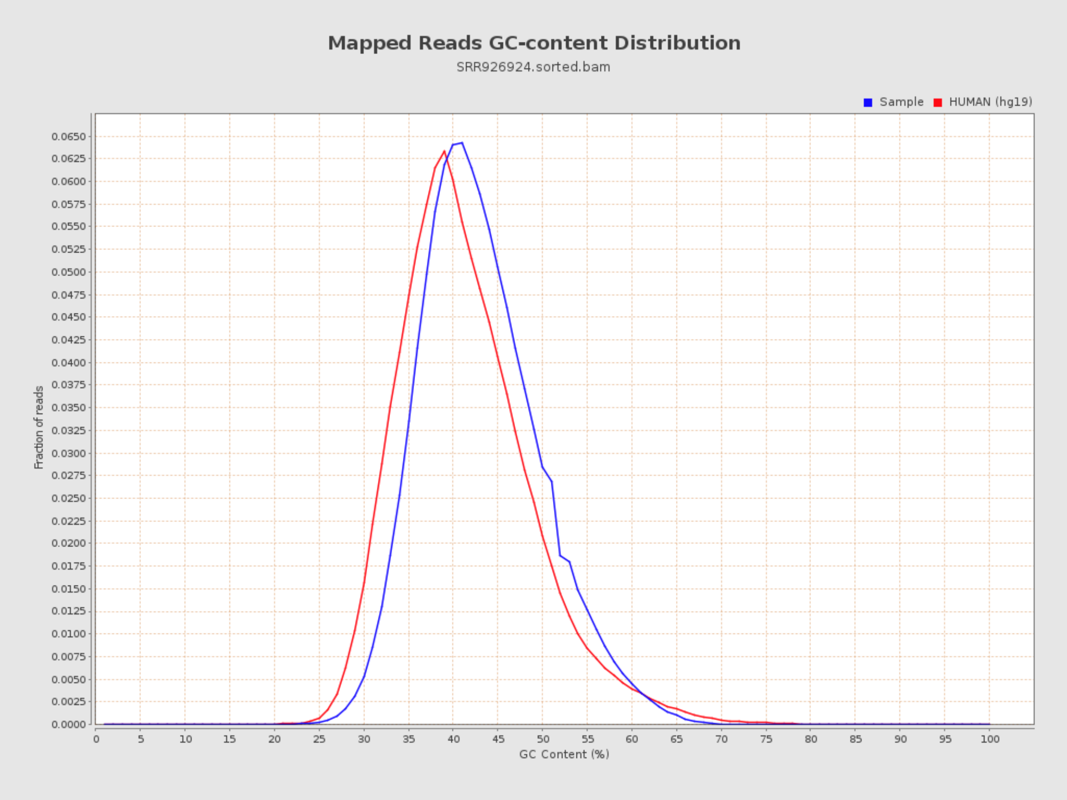
7. Results : Duplication Rate Histogram



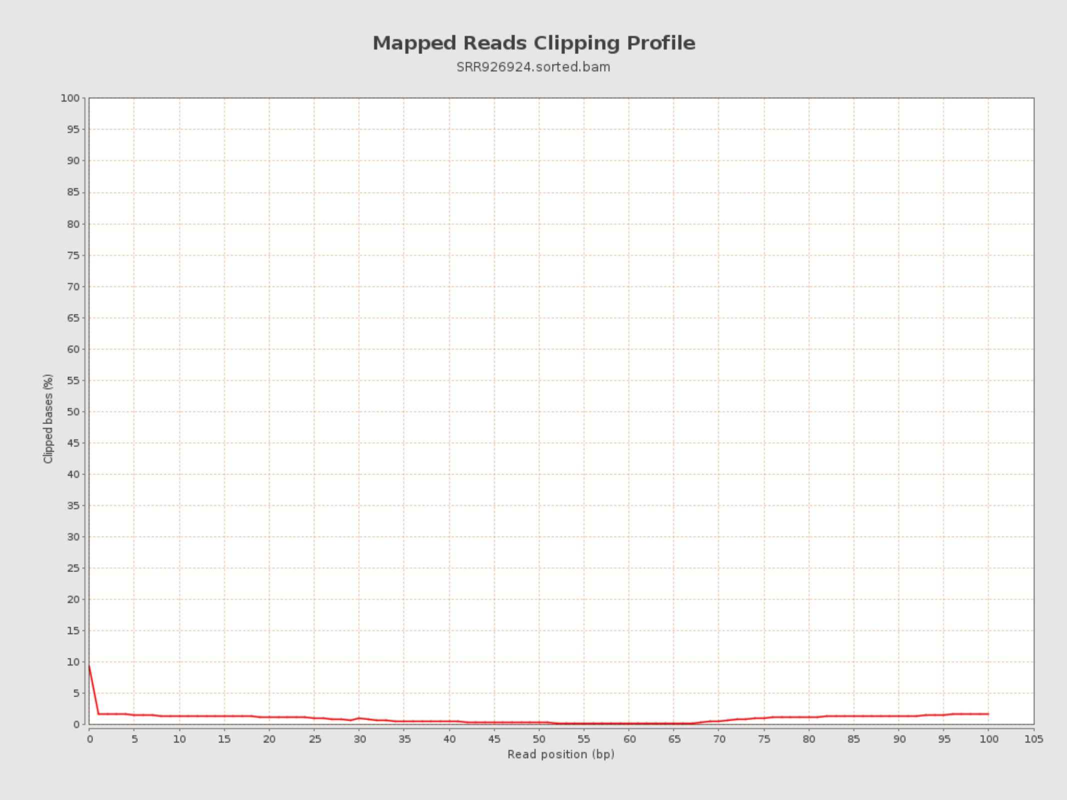
8. Results : Mapped Reads Nucleotide Content



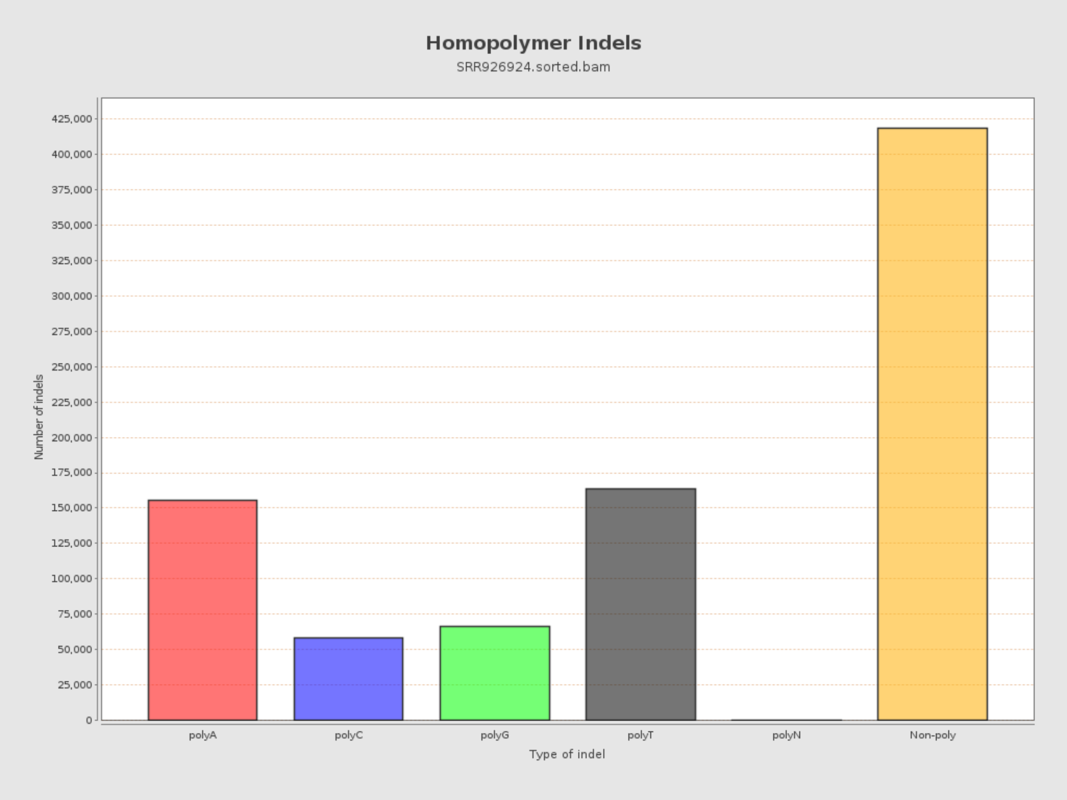
9. Results : Mapped Reads GC-content Distribution



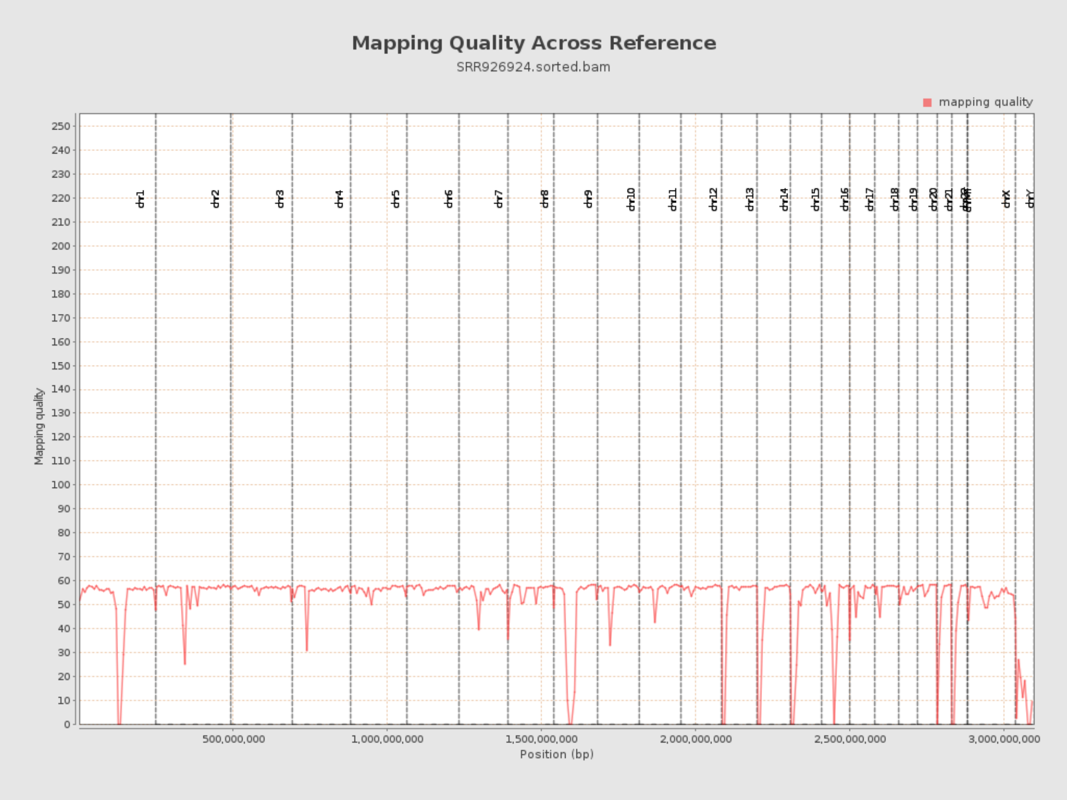
10. Results : Mapped Reads Clipping Profile



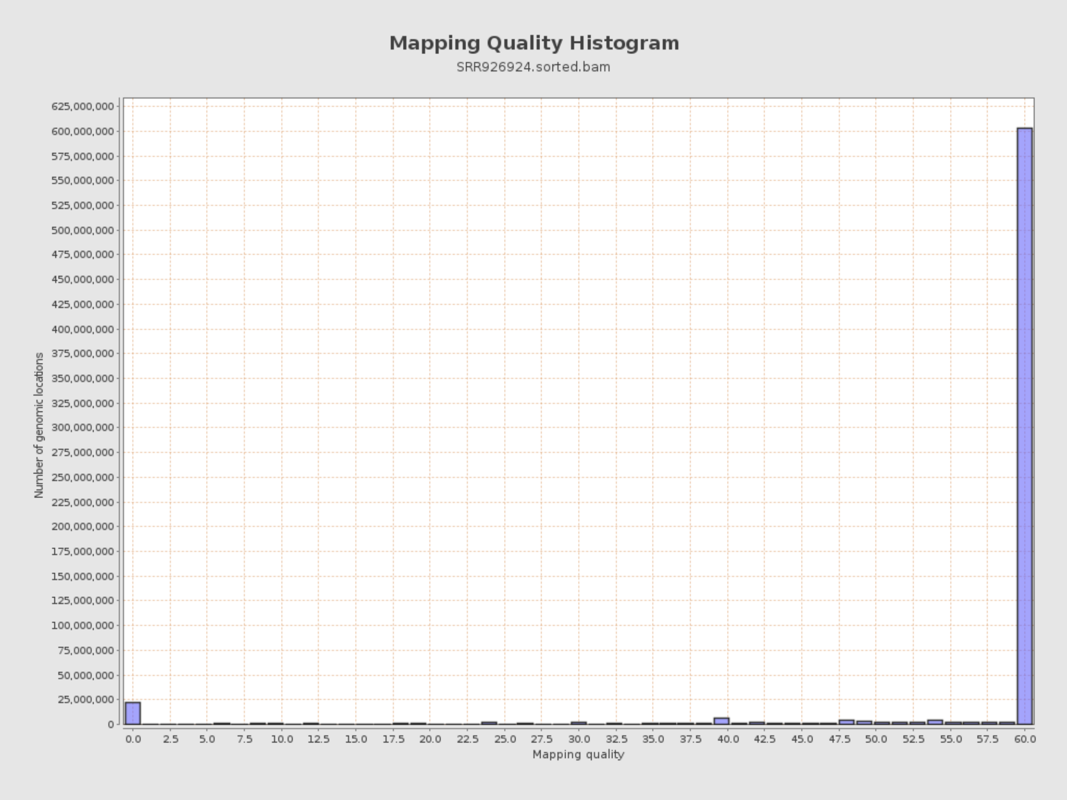
11. Results : Homopolymer Indels



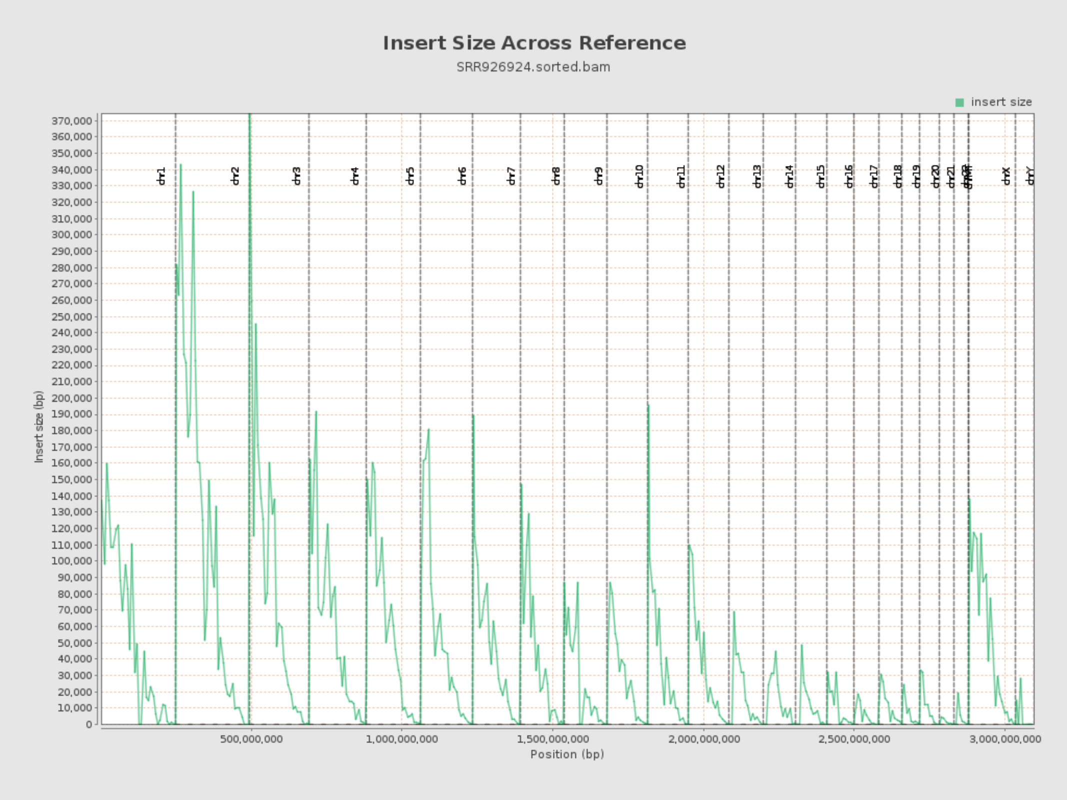
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram