Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 14:02:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926912.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_SRR926912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926912_1.fastq.gz SRR926912_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 14:02:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,946,110
Mapped reads	24,946,532 / 96.15%
Unmapped reads	999,578 / 3.85%
Mapped paired reads	24,946,532 / 96.15%
Mapped reads, first in pair	12,554,883 / 48.39%
Mapped reads, second in pair	12,391,649 / 47.76%
Mapped reads, both in pair	24,446,766 / 94.22%
Mapped reads, singletons	499,766 / 1.93%
Secondary alignments	0
Supplementary alignments	955,428 / 3.68%
Read min/max/mean length	30 / 101 / 102.52
Duplicated reads (estimated)	2,660,428 / 10.25%
Duplication rate	8.71%
Clipped reads	12,774,621 / 49.24%

2.2. ACGT Content

Number/percentage of A's	632,121,804 / 28.45%
Number/percentage of C's	429,042,065 / 19.31%
Number/percentage of T's	644,404,104 / 29.01%
Number/percentage of G's	515,927,746 / 23.22%
Number/percentage of N's	170,466 / 0.01%

GC Percentage	42.53%

2.3. Coverage

Mean	0.7182
Standard Deviation	2.1575

2.4. Mapping Quality

Mean Mapping Quality	52.3

2.5. Insert size

Mean	444,641.85
Standard Deviation	6,546,148.46
P25/Median/P75	130 / 174 / 239

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	23,277,631
Insertions	381,595
Mapped reads with at least one insertion	1.51%
Deletions	1,209,294
Mapped reads with at least one deletion	4.72%
Homopolymer indels	51.86%

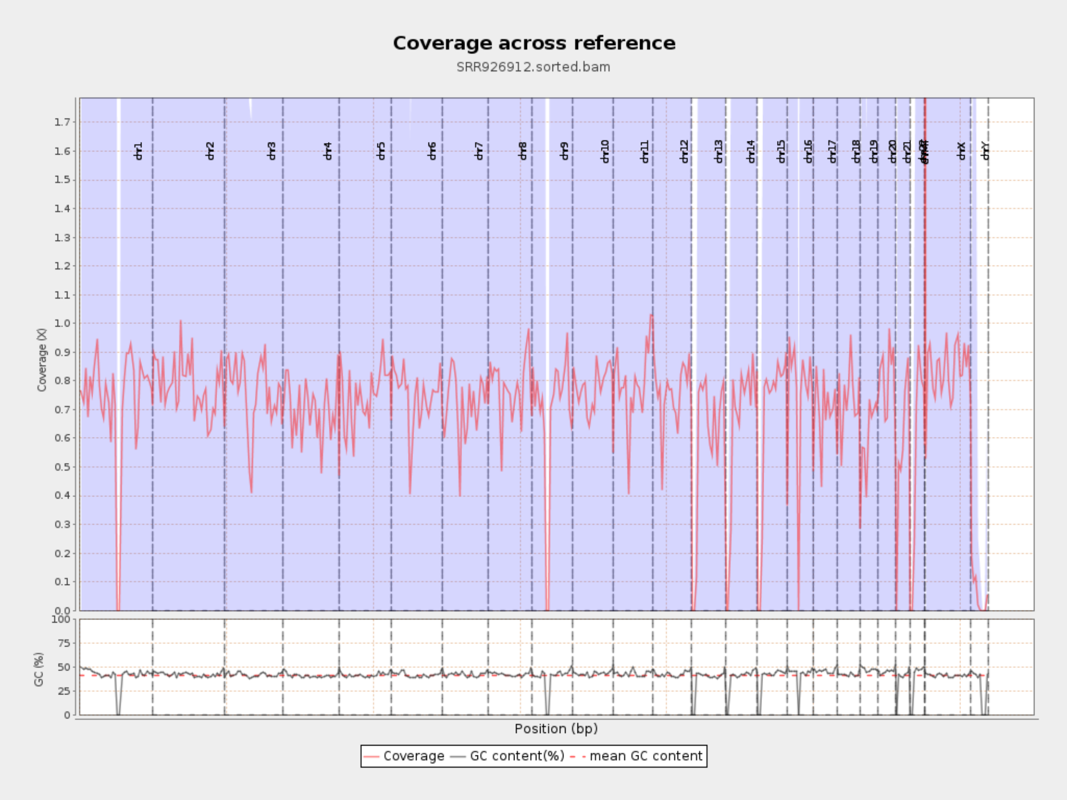
2.7. Chromosome stats

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

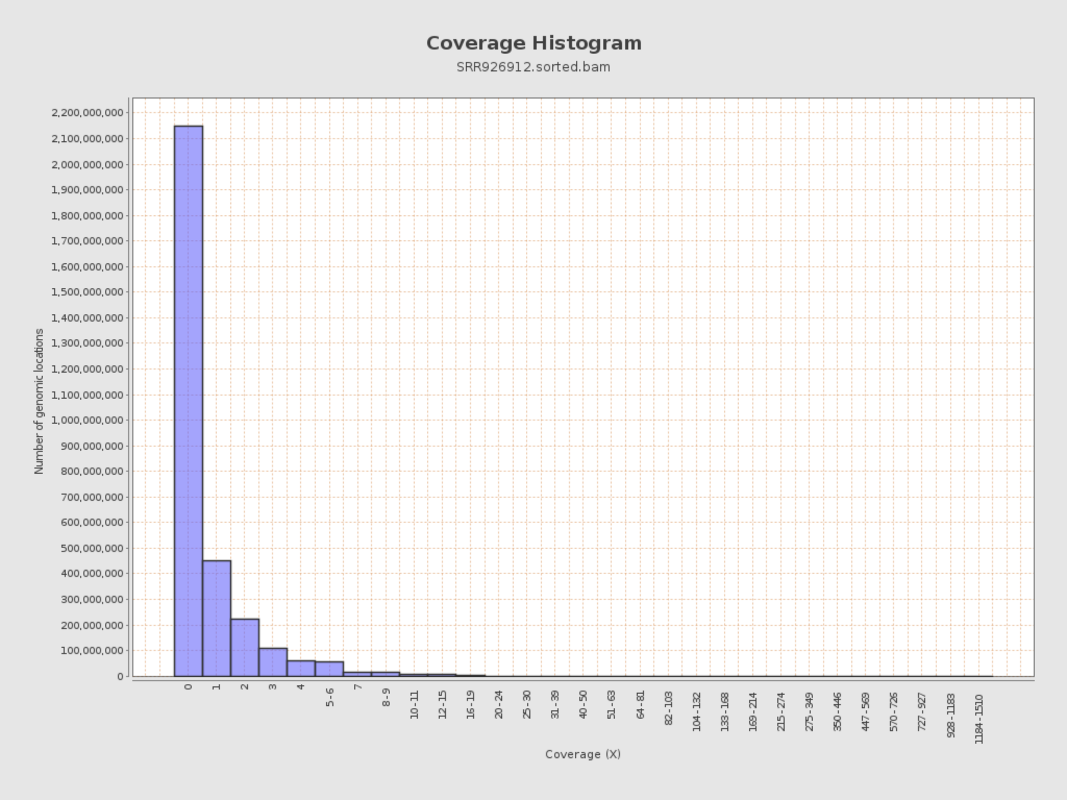
		bases	coverage	deviation
chr1	249250621	181922276	0.7299	2.1222
chr2	243199373	191507174	0.7874	3.1861
chr3	198022430	151266050	0.7639	1.6483
chr4	191154276	134119039	0.7016	1.7367
chr5	180915260	135950044	0.7515	1.6232
chr6	171115067	128382035	0.7503	1.8051
chr7	159138663	114004247	0.7164	1.7508
chr8	146364022	113971652	0.7787	1.7607
chr9	141213431	95809510	0.6785	2.3325
chr10	135534747	106076375	0.7827	2.9959
chr11	135006516	106132175	0.7861	1.9596
chr12	133851895	101535883	0.7586	1.7976
chr13	115169878	66956969	0.5814	1.4346
chr14	107349540	67857715	0.6321	1.5509
chr15	102531392	66748925	0.651	1.6444
chr16	90354753	66271082	0.7335	2.3874
chr17	81195210	56373739	0.6943	1.6393
chr18	78077248	58536369	0.7497	2.1324
chr19	59128983	36012204	0.609	1.6924
chr20	63025520	51169094	0.8119	1.8017
chr21	48129895	28151927	0.5849	2.0364
chr22	51304566	27835939	0.5426	1.5233
chrMT	16571	4280622	258.3201	179.7675
chrX	155270560	129309732	0.8328	1.7772

chrY	59373566	3261695	0.0549	1.1364

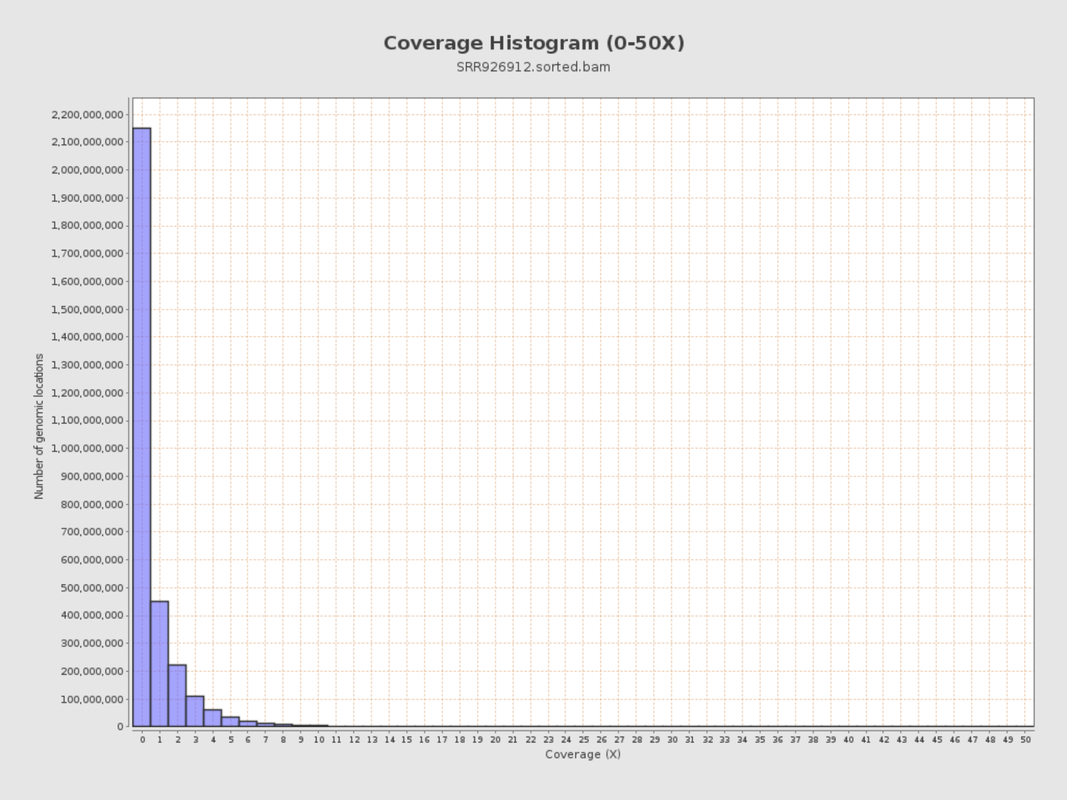
3. Results : Coverage across reference



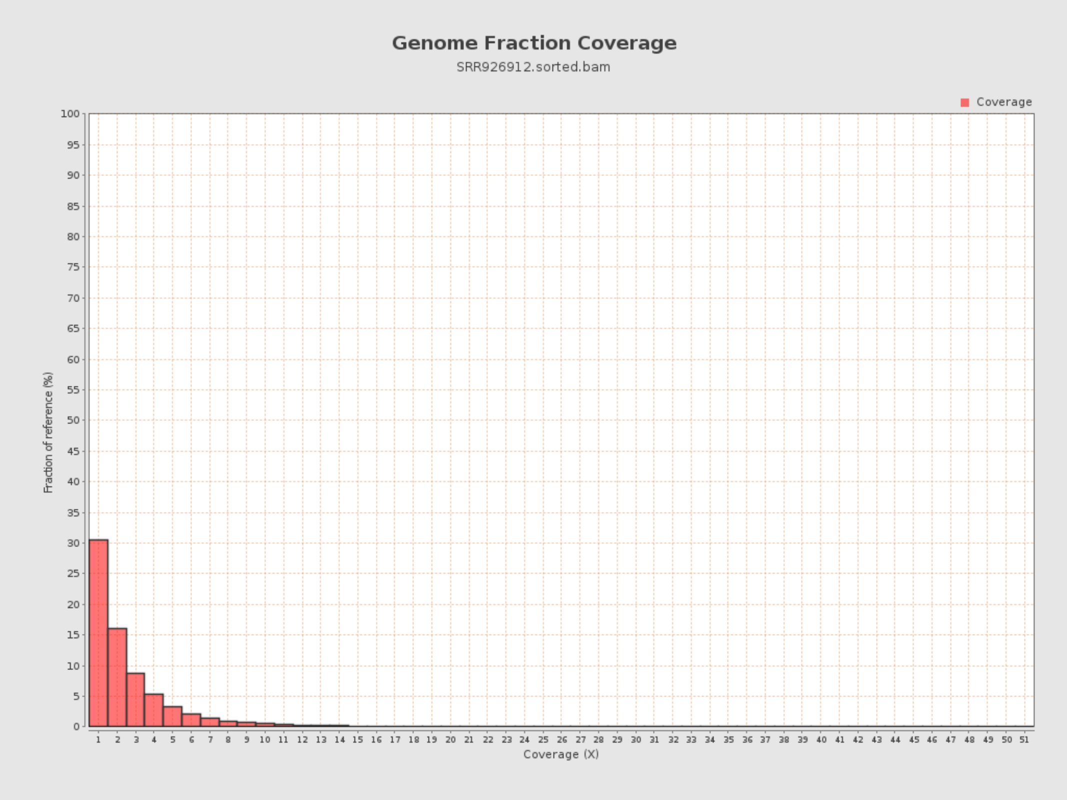
4. Results : Coverage Histogram



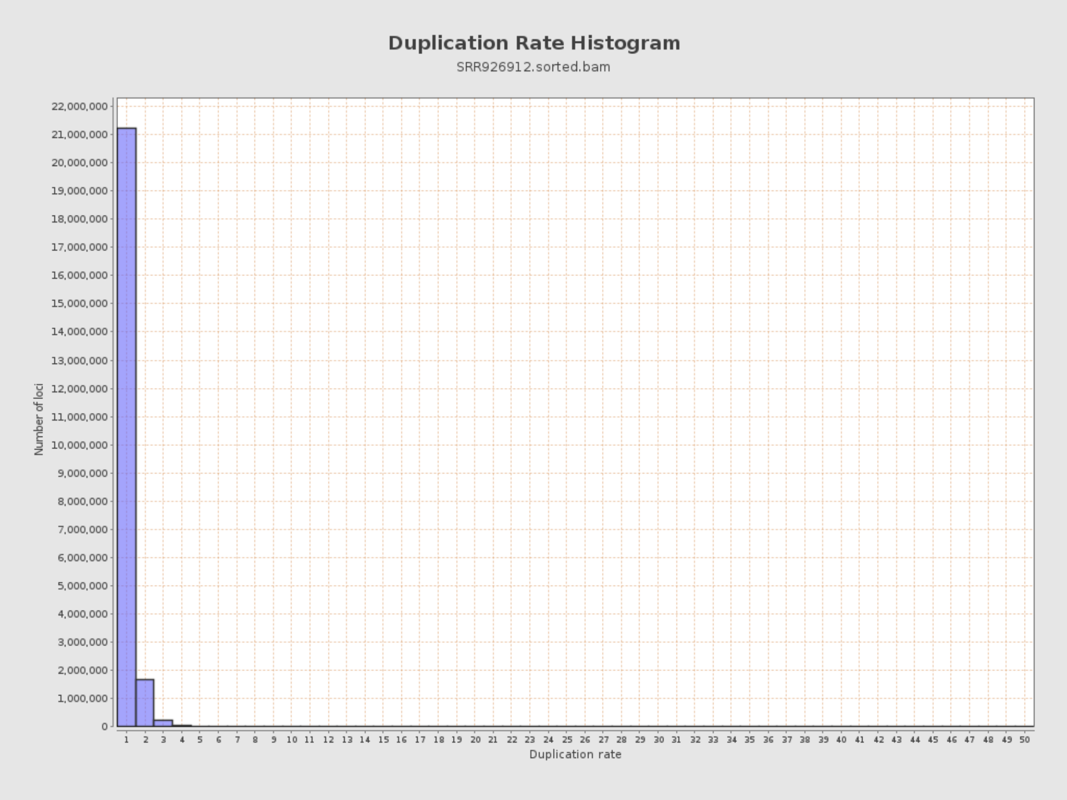
5. Results : Coverage Histogram (0-50X)



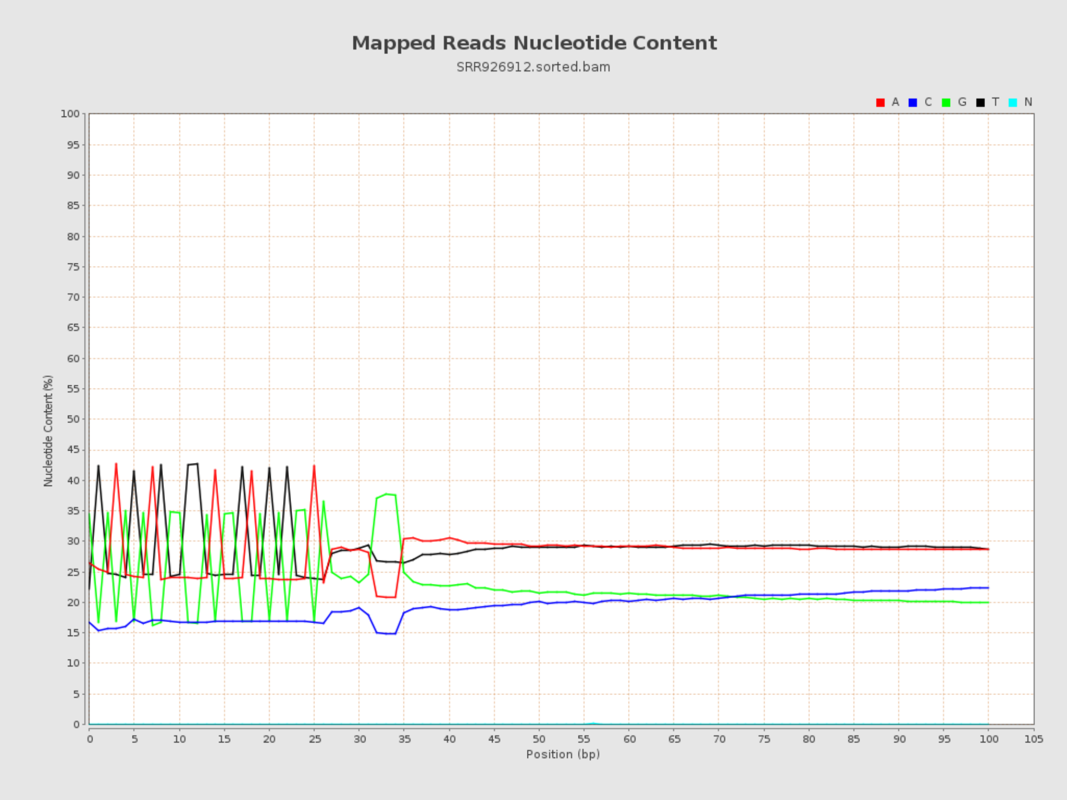
6. Results : Genome Fraction Coverage



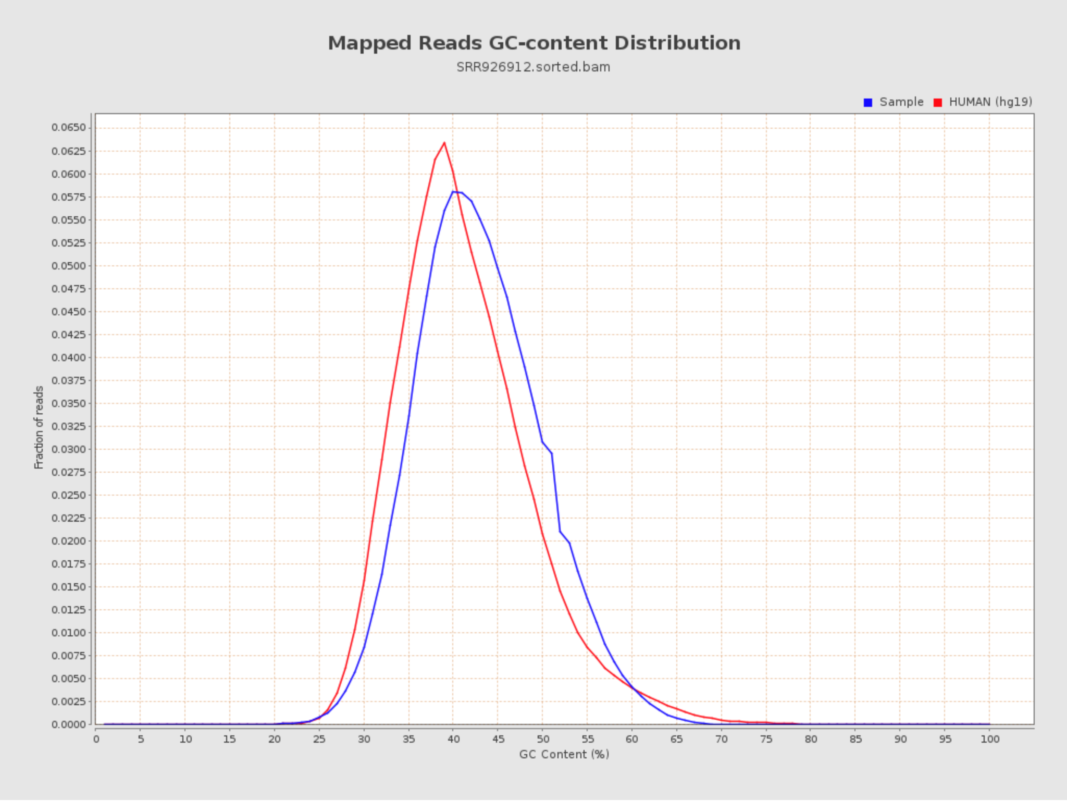
7. Results : Duplication Rate Histogram



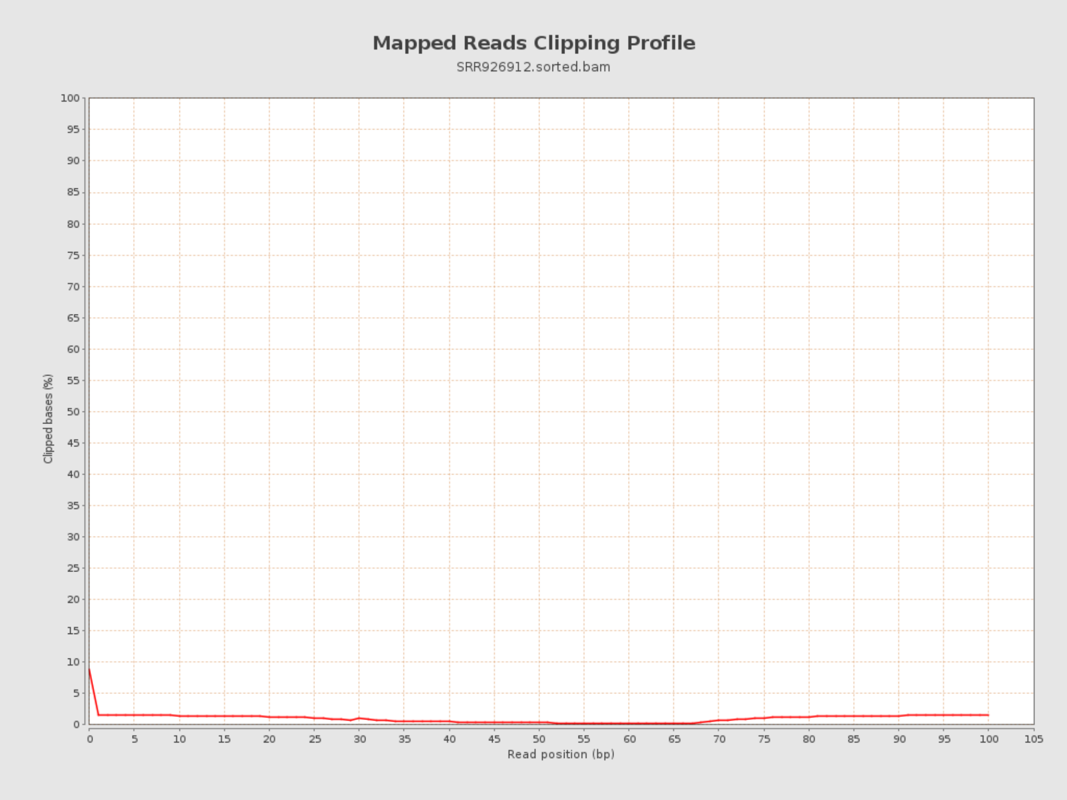
8. Results : Mapped Reads Nucleotide Content



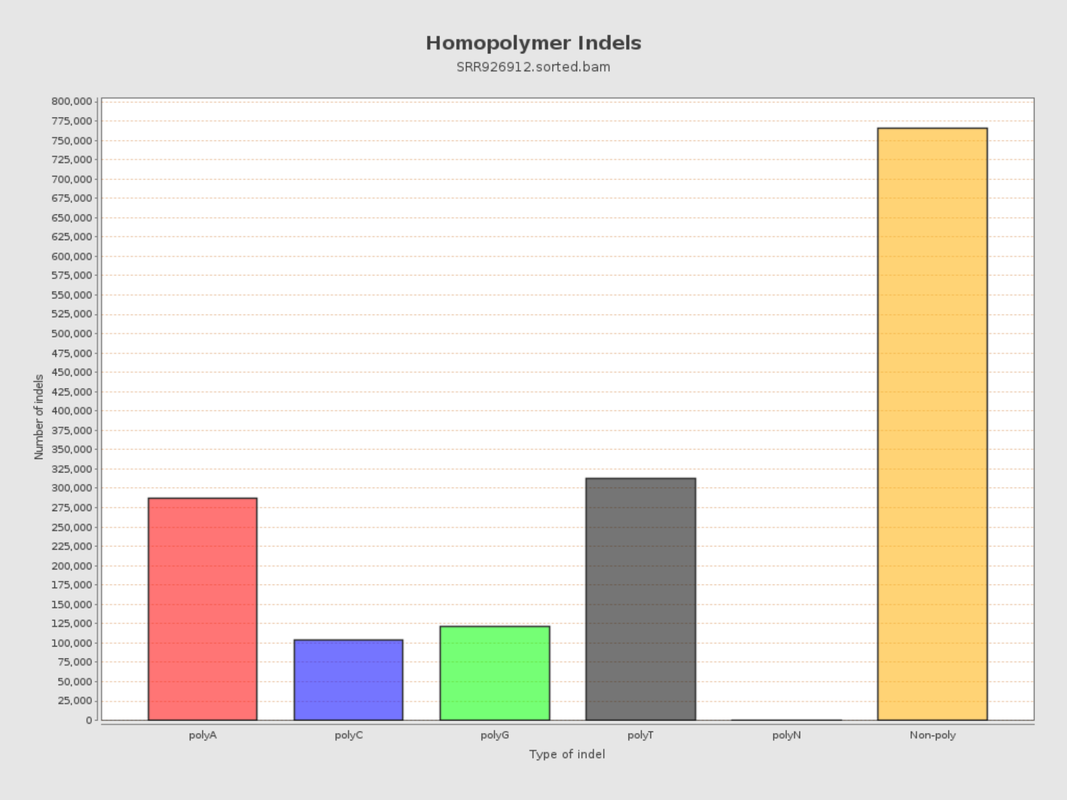
9. Results : Mapped Reads GC-content Distribution



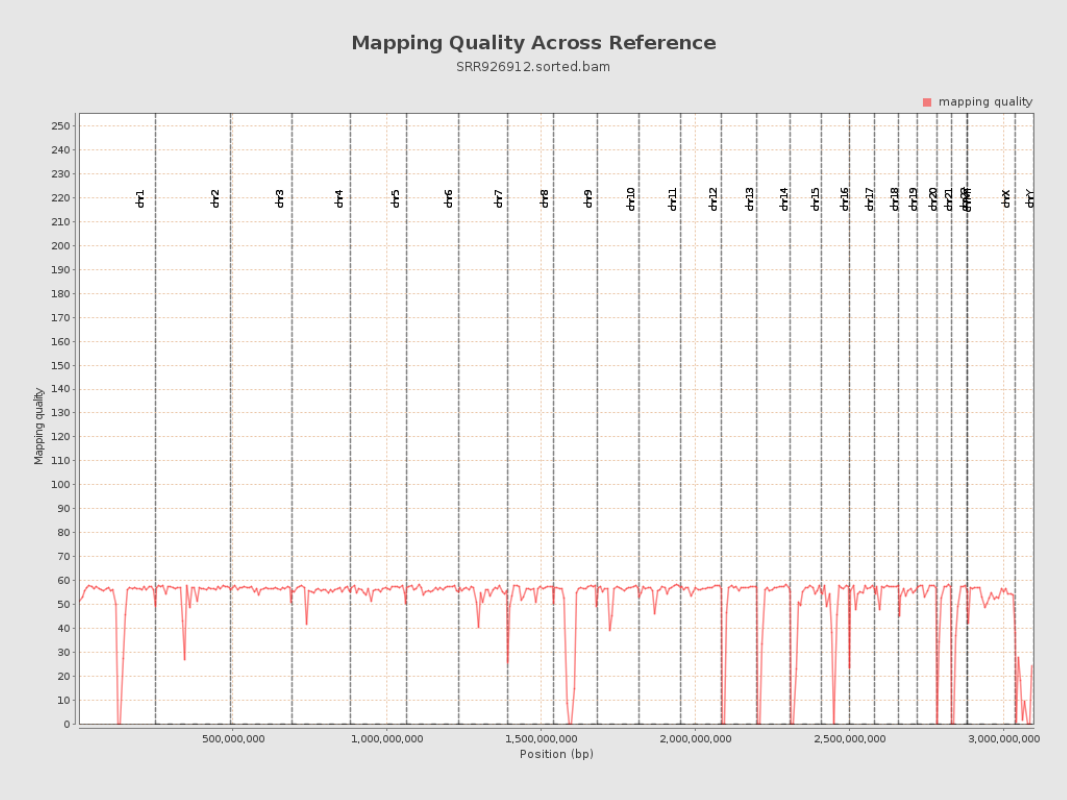
10. Results : Mapped Reads Clipping Profile



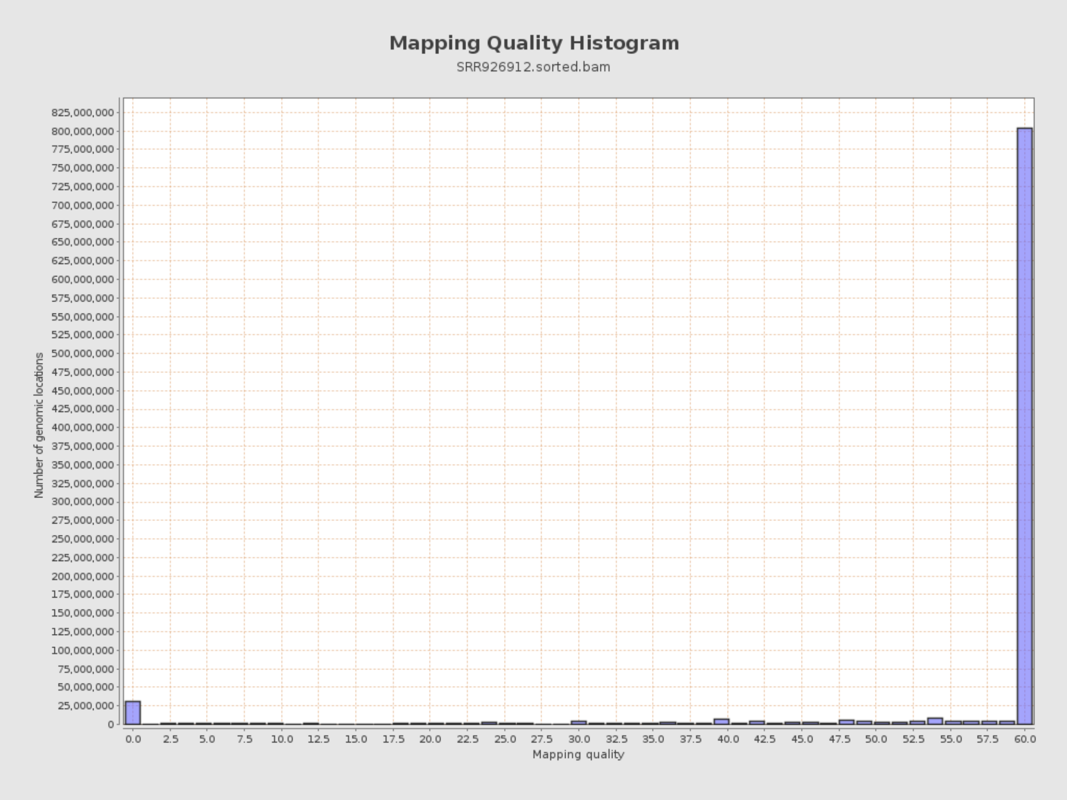
11. Results : Homopolymer Indels



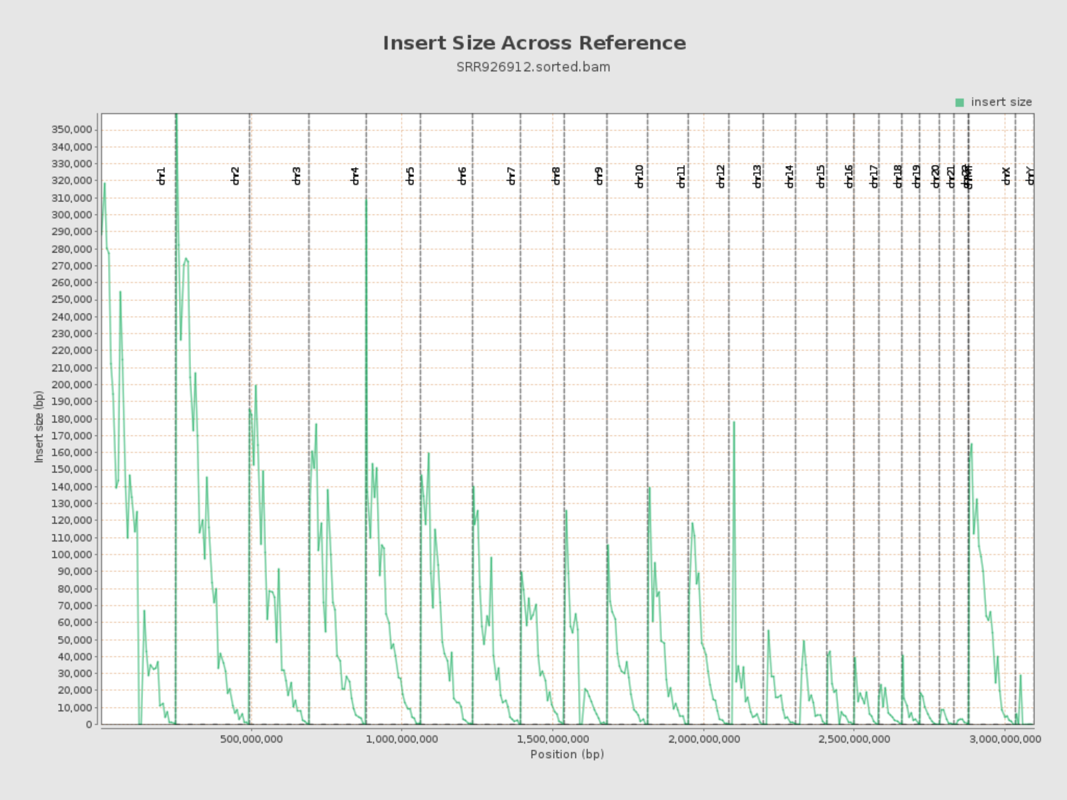
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram