Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 03:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927012.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_SRR927012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927012_1.fastq.gz SRR927012_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 03:58:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,054,690
Mapped reads	22,181,953 / 96.21%
Unmapped reads	872,737 / 3.79%
Mapped paired reads	22,181,953 / 96.21%
Mapped reads, first in pair	11,069,403 / 48.01%
Mapped reads, second in pair	11,112,550 / 48.2%
Mapped reads, both in pair	21,613,550 / 93.75%
Mapped reads, singletons	568,403 / 2.47%
Secondary alignments	0
Supplementary alignments	811,660 / 3.52%
Read min/max/mean length	30 / 101 / 102.46
Duplicated reads (estimated)	1,961,798 / 8.51%
Duplication rate	7.06%
Clipped reads	9,962,308 / 43.21%

2.2. ACGT Content

Number/percentage of A's	583,948,567 / 29.06%
Number/percentage of C's	375,691,585 / 18.69%
Number/percentage of T's	599,001,000 / 29.81%
Number/percentage of G's	450,709,753 / 22.43%
Number/percentage of N's	356,402 / 0.02%

GC Percentage	41.12%

2.3. Coverage

Mean	0.6497
Standard Deviation	2.3312

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	426,819.05
Standard Deviation	6,345,085.48
P25/Median/P75	175 / 230 / 298

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	20,599,214
Insertions	352,732
Mapped reads with at least one insertion	1.56%
Deletions	1,096,063
Mapped reads with at least one deletion	4.81%
Homopolymer indels	52.65%

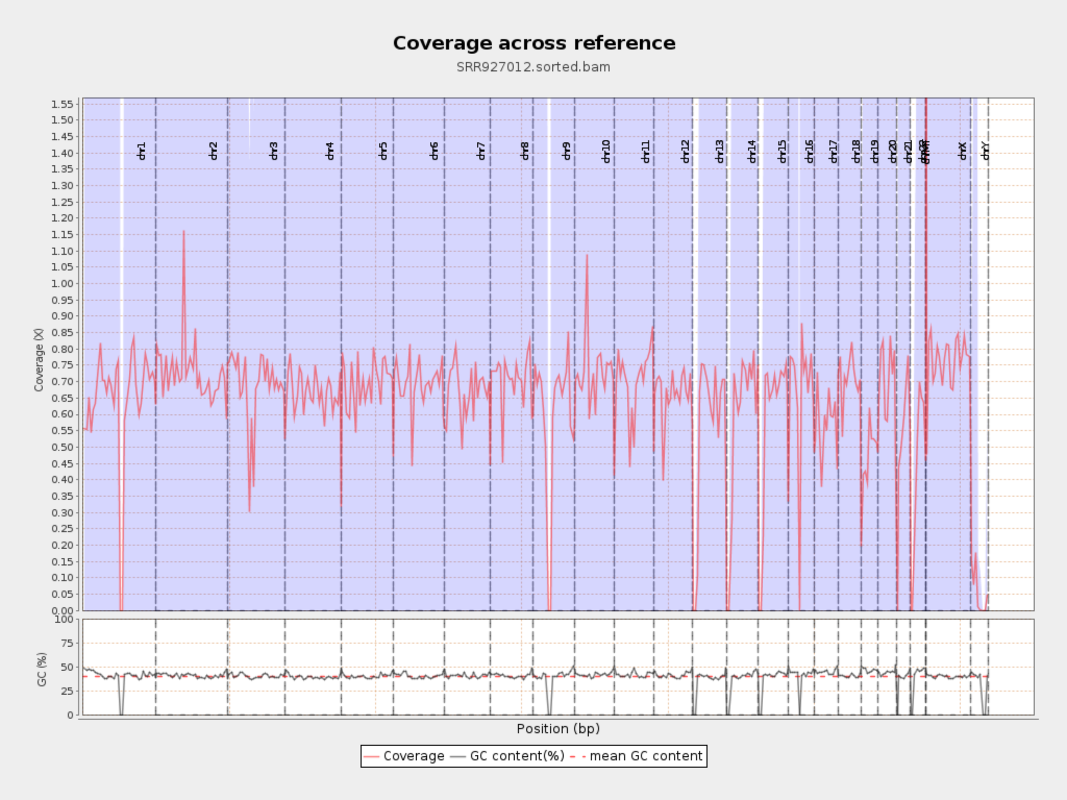
2.7. Chromosome stats

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

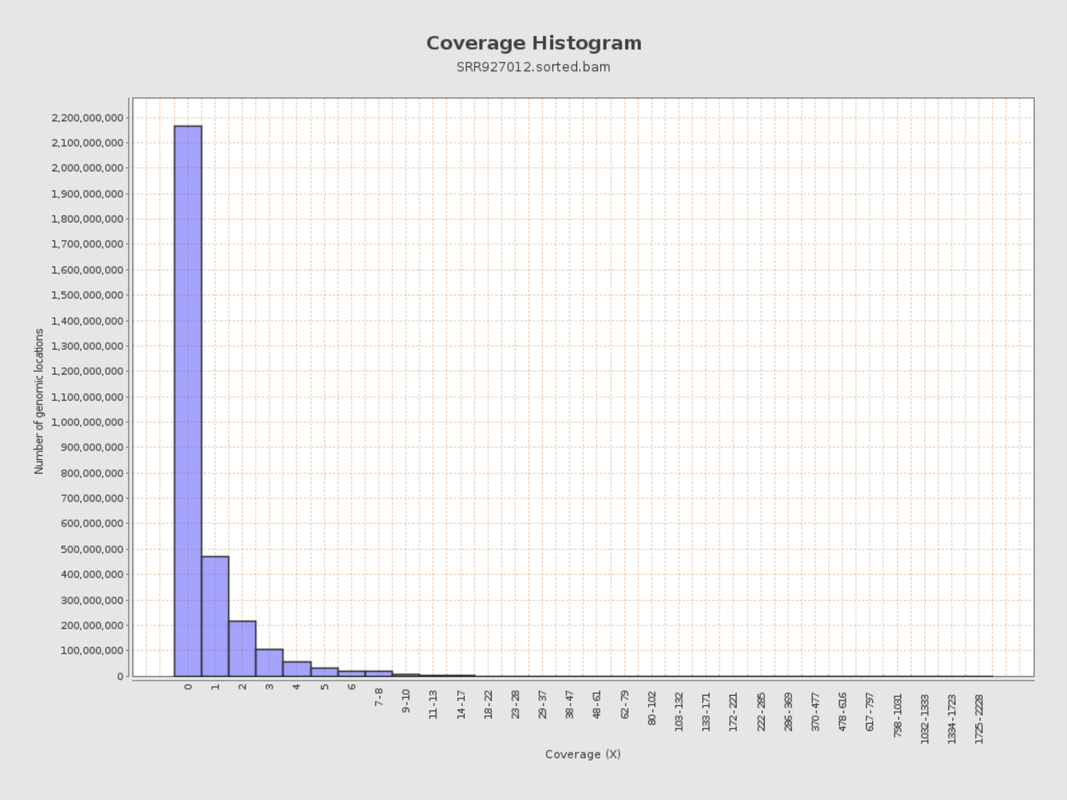
		bases	coverage	deviation
chr1	249250621	160383976	0.6435	2.7752
chr2	243199373	177567903	0.7301	3.7364
chr3	198022430	135148591	0.6825	1.4293
chr4	191154276	128601026	0.6728	1.8995
chr5	180915260	125577146	0.6941	1.4142
chr6	171115067	119271501	0.697	1.8984
chr7	159138663	106592543	0.6698	1.9879
chr8	146364022	103671058	0.7083	1.6376
chr9	141213431	84117273	0.5957	2.9332
chr10	135534747	98835214	0.7292	4.6577
chr11	135006516	94405933	0.6993	2.0621
chr12	133851895	89024680	0.6651	1.4204
chr13	115169878	64279843	0.5581	1.28
chr14	107349540	62193527	0.5794	1.3741
chr15	102531392	58176940	0.5674	1.3506
chr16	90354753	58976660	0.6527	2.8943
chr17	81195210	46760980	0.5759	1.571
chr18	78077248	55400335	0.7096	2.8422
chr19	59128983	28027771	0.474	1.8929
chr20	63025520	44958205	0.7133	1.5407
chr21	48129895	25762799	0.5353	1.8449
chr22	51304566	21976698	0.4284	1.1872
chrMT	16571	111942	6.7553	7.6092
chrX	155270560	118222972	0.7614	1.6468

chrY	59373566	3224632	0.0543	1.8032

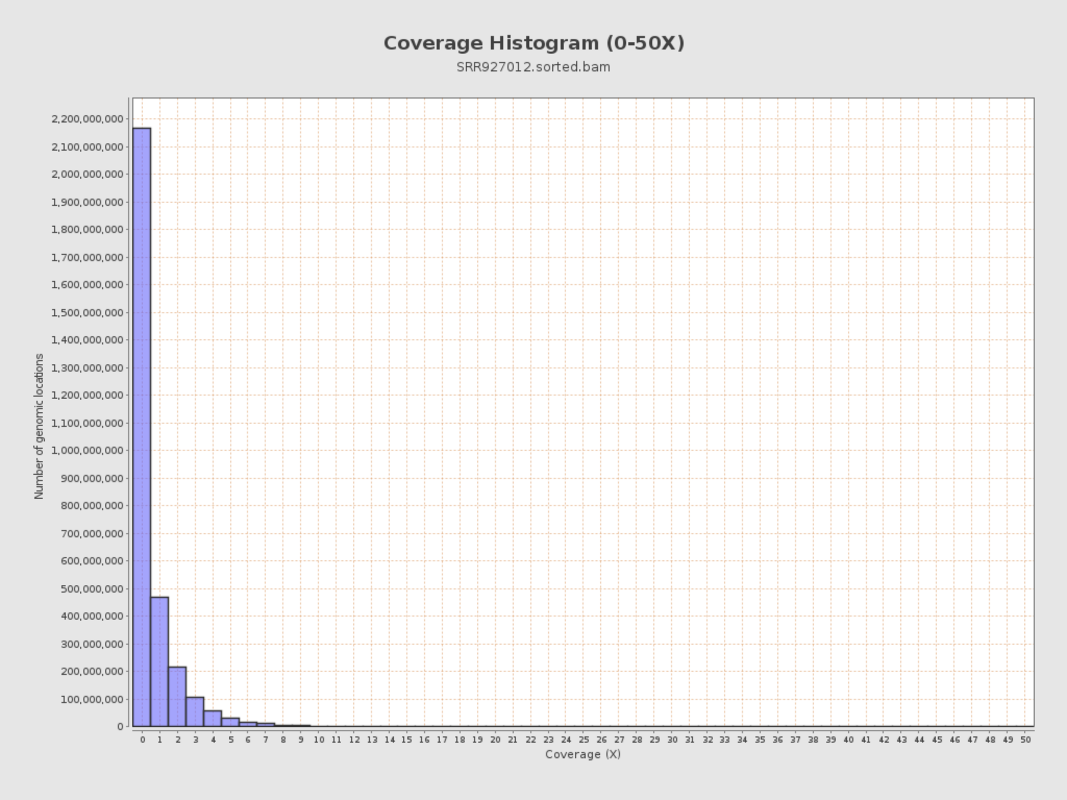
3. Results : Coverage across reference



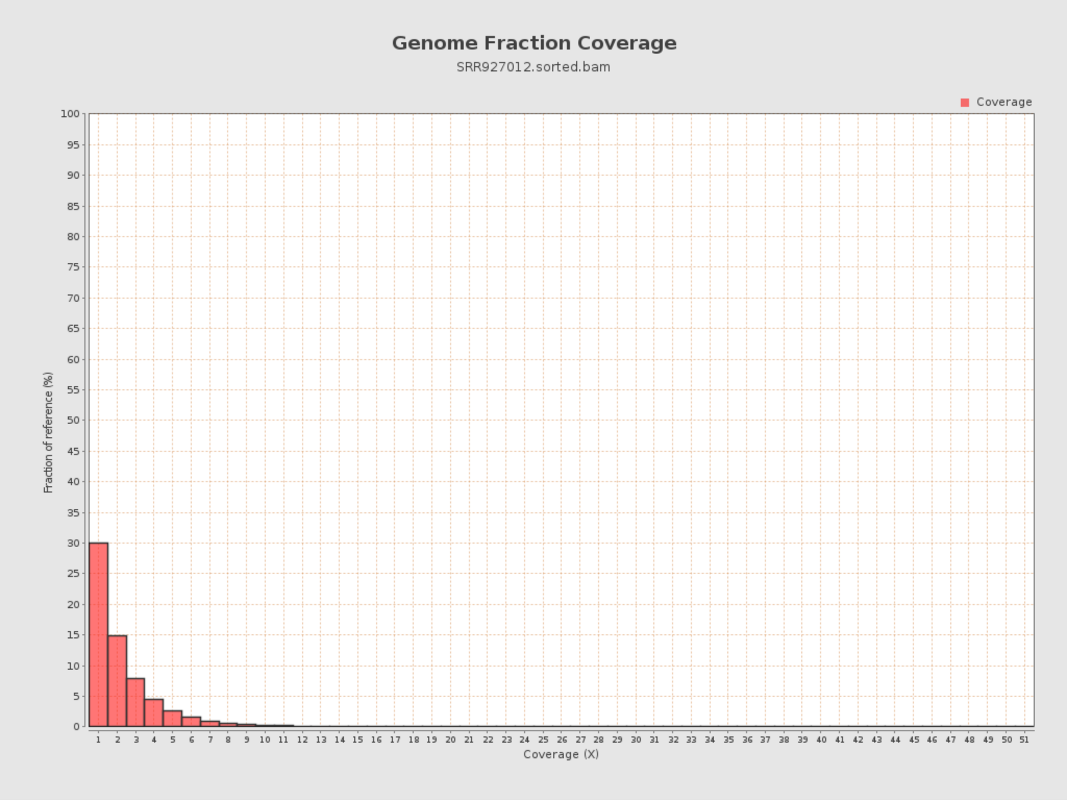
4. Results : Coverage Histogram



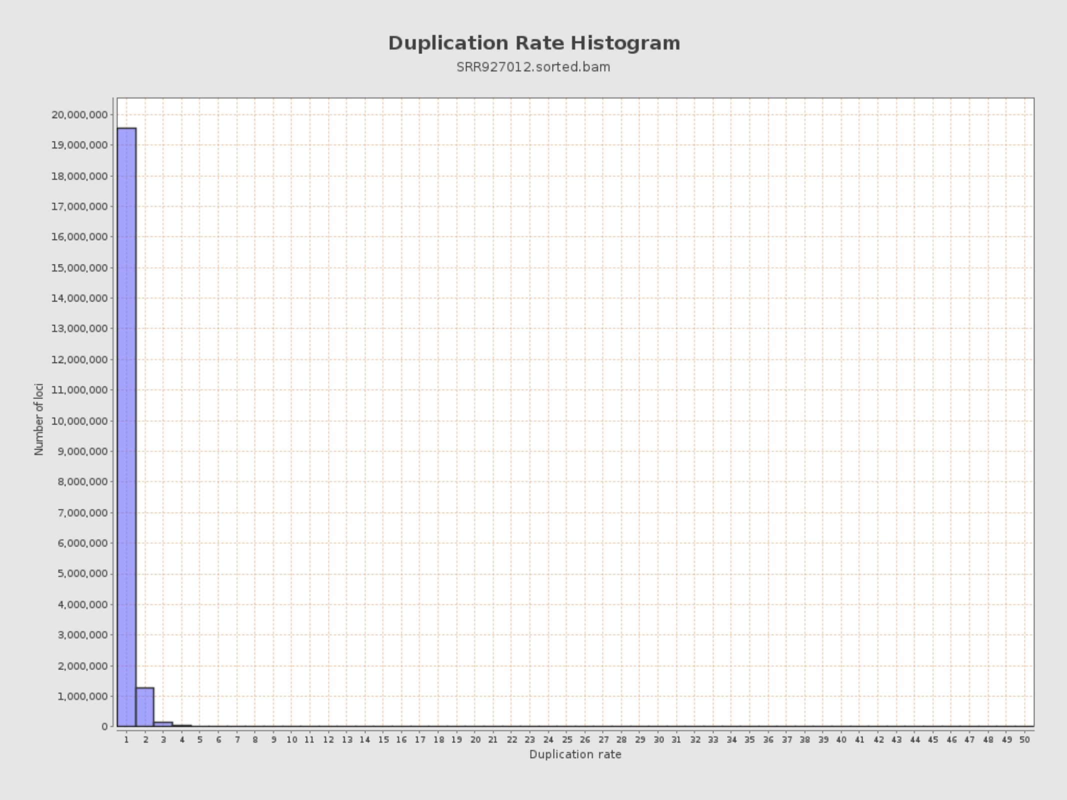
5. Results : Coverage Histogram (0-50X)



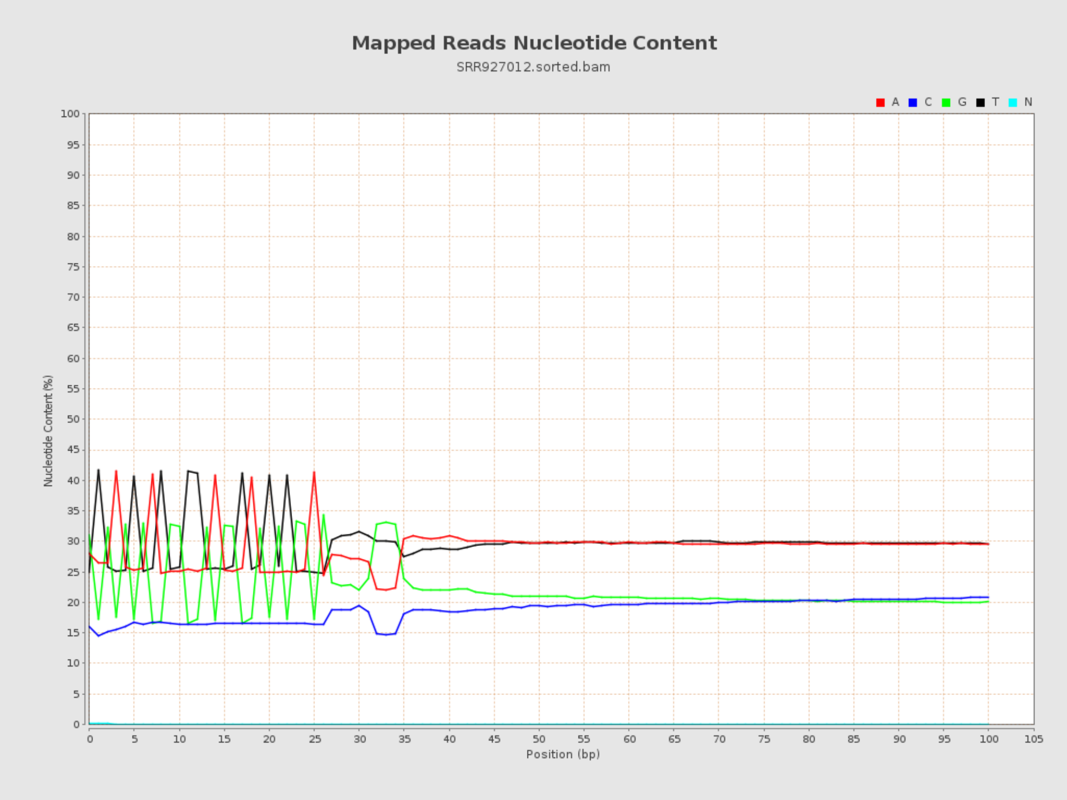
6. Results : Genome Fraction Coverage



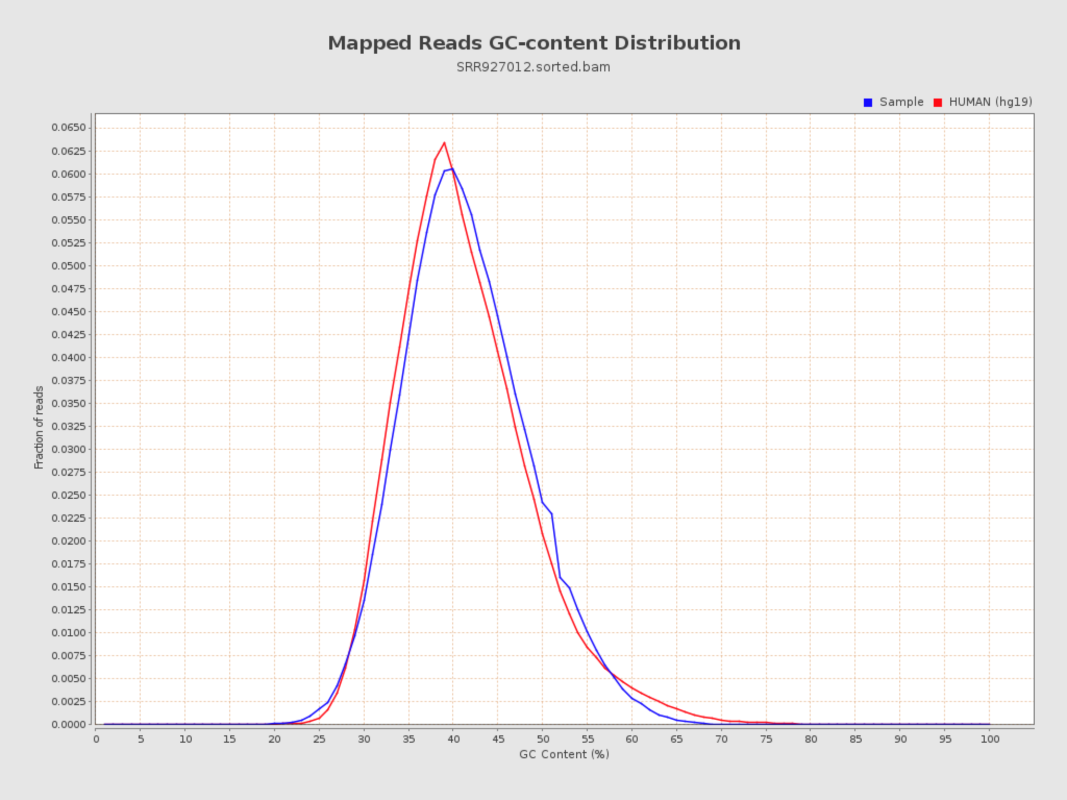
7. Results : Duplication Rate Histogram



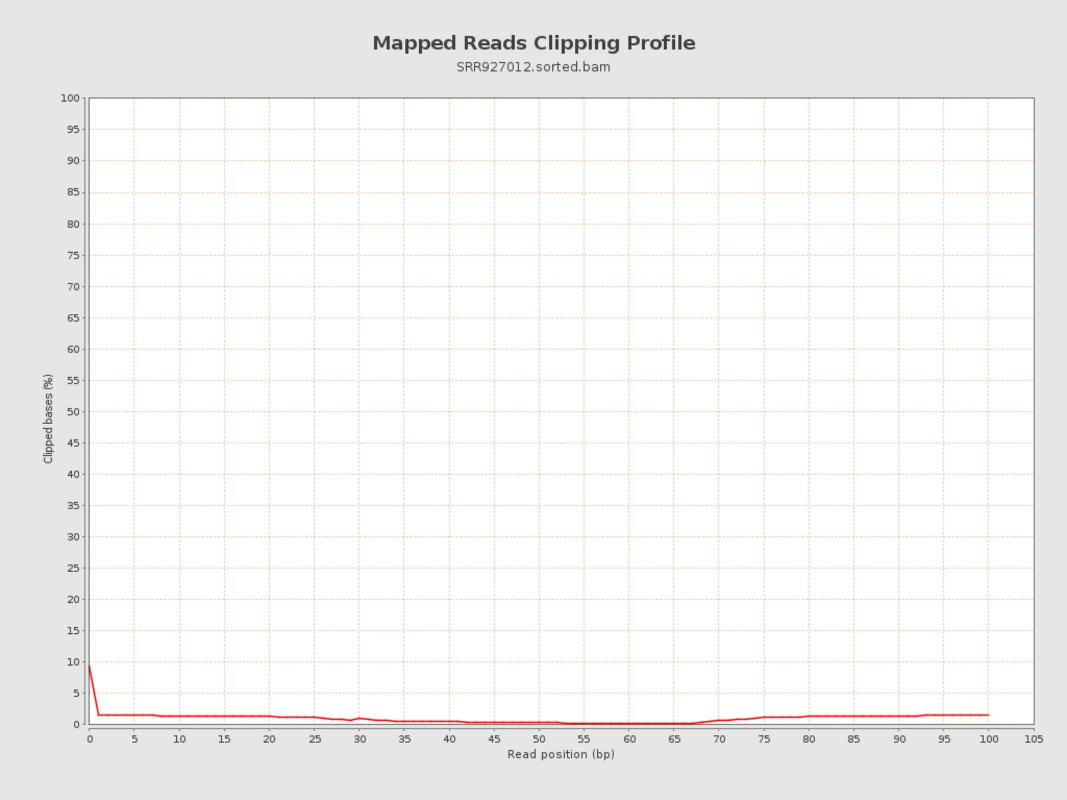
8. Results : Mapped Reads Nucleotide Content



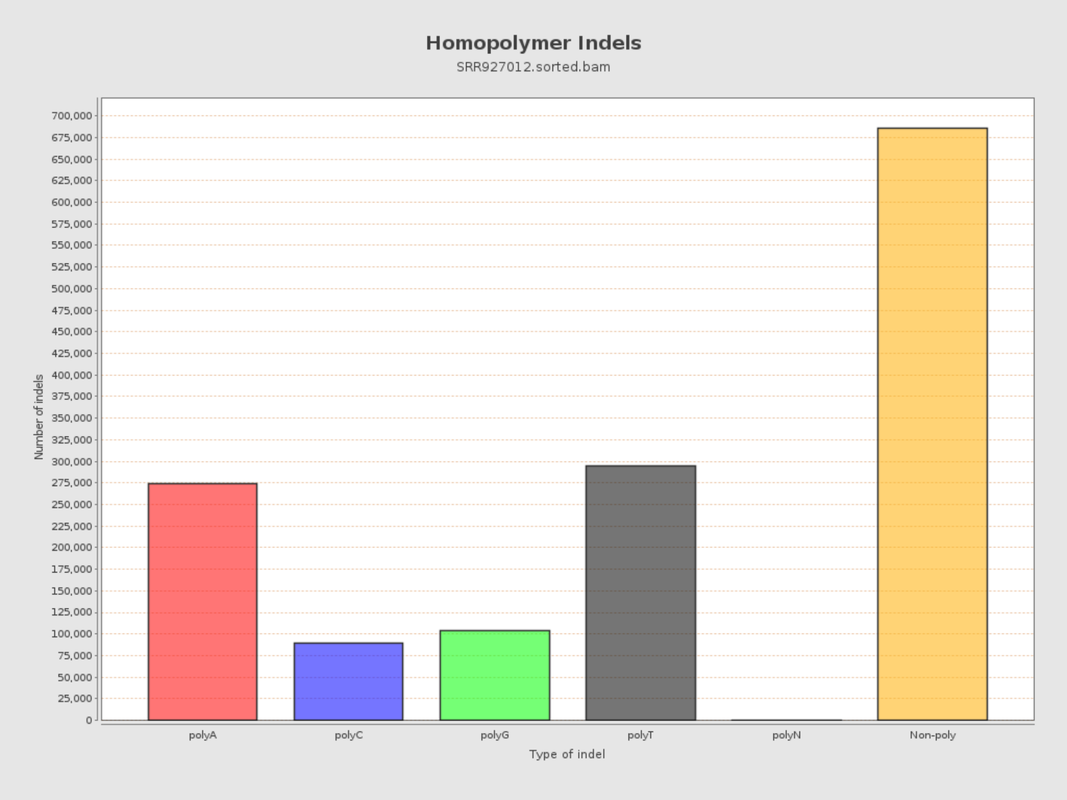
9. Results : Mapped Reads GC-content Distribution



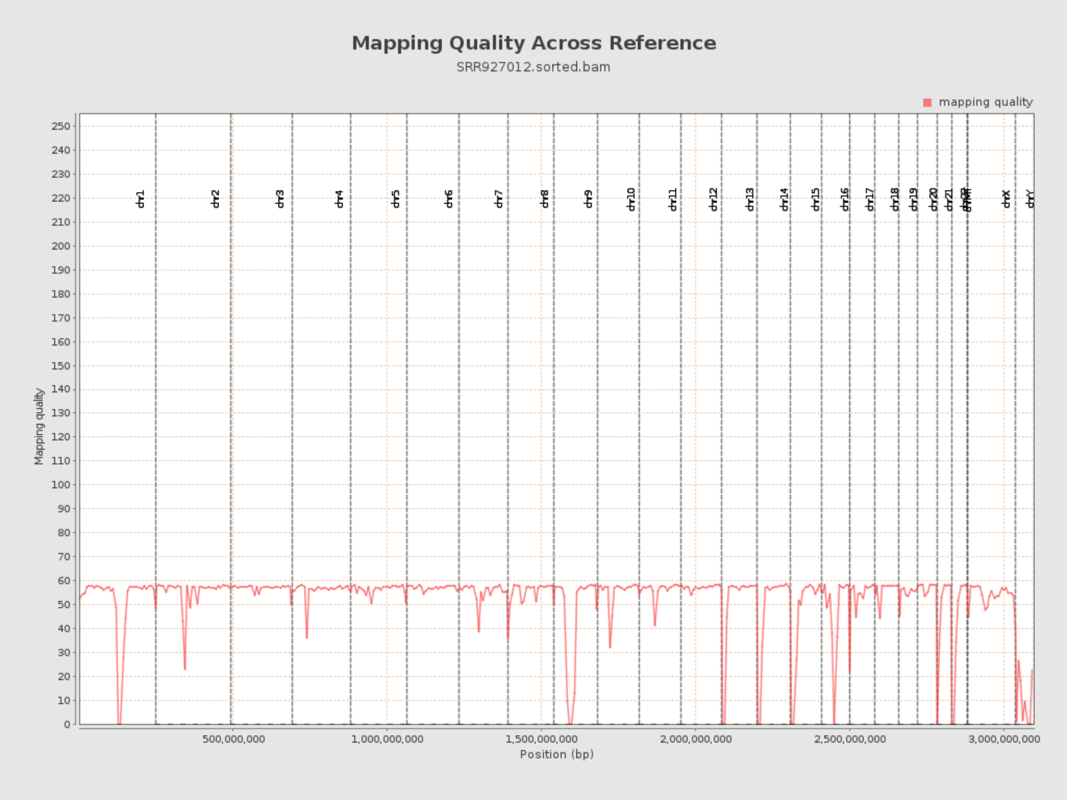
10. Results : Mapped Reads Clipping Profile



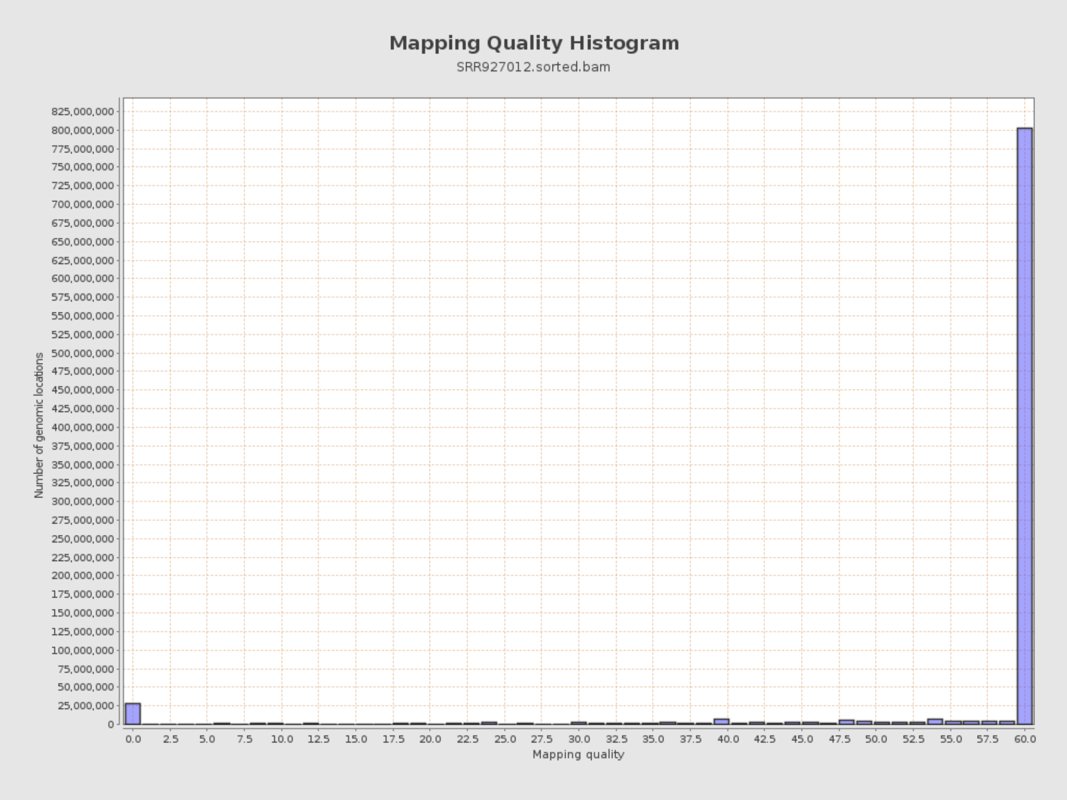
11. Results : Homopolymer Indels



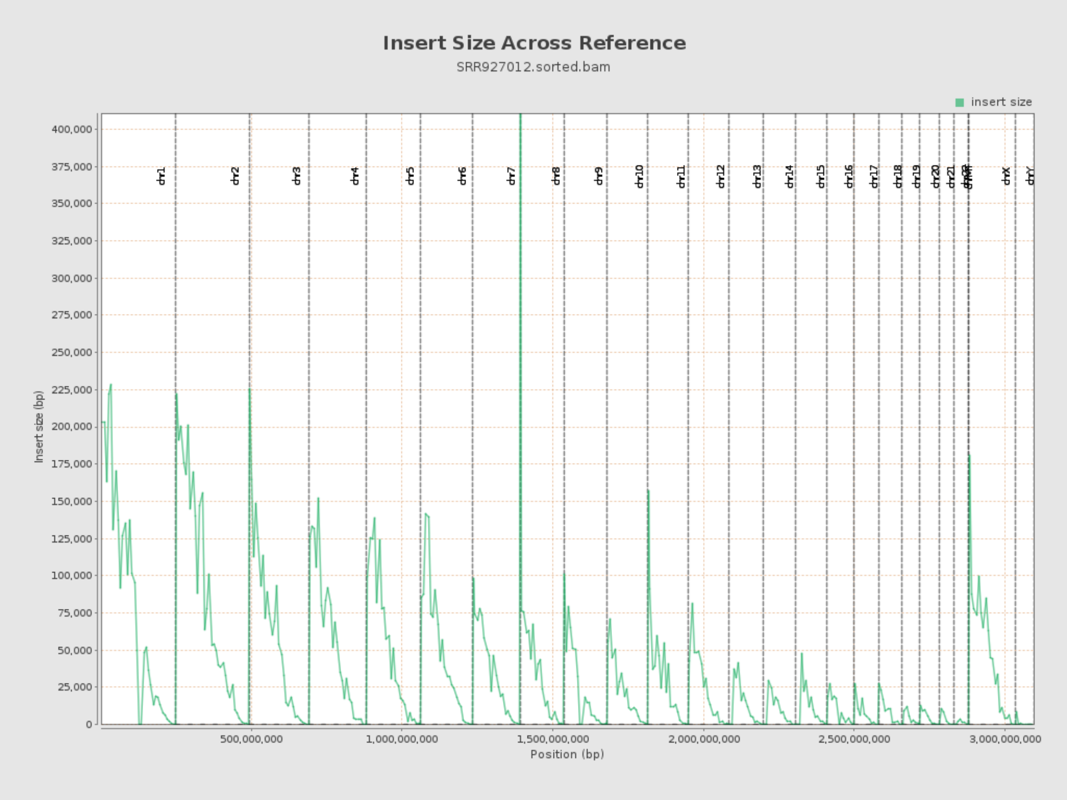
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram