Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 13:04:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926910.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_SRR926910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926910_1.fastq.gz SRR926910_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 13:04:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,697,328
Mapped reads	27,543,768 / 84.24%
Unmapped reads	5,153,560 / 15.76%
Mapped paired reads	27,543,768 / 84.24%
Mapped reads, first in pair	13,833,221 / 42.31%
Mapped reads, second in pair	13,710,547 / 41.93%
Mapped reads, both in pair	27,115,036 / 82.93%
Mapped reads, singletons	428,732 / 1.31%
Secondary alignments	0
Supplementary alignments	493,118 / 1.51%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	2,098,643 / 6.42%
Duplication rate	6.03%
Clipped reads	9,988,521 / 30.55%

2.2. ACGT Content

Number/percentage of A's	712,920,948 / 28.15%
Number/percentage of C's	507,259,788 / 20.03%
Number/percentage of T's	720,873,739 / 28.46%
Number/percentage of G's	591,391,335 / 23.35%
Number/percentage of N's	222,950 / 0.01%

GC Percentage	43.38%

2.3. Coverage

Mean	0.8187
Standard Deviation	3.2268

2.4. Mapping Quality

Mean Mapping Quality	52.88

2.5. Insert size

Mean	191,358.16
Standard Deviation	4,317,693.9
P25/Median/P75	146 / 189 / 253

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	26,428,755
Insertions	409,067
Mapped reads with at least one insertion	1.46%
Deletions	1,319,882
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.27%

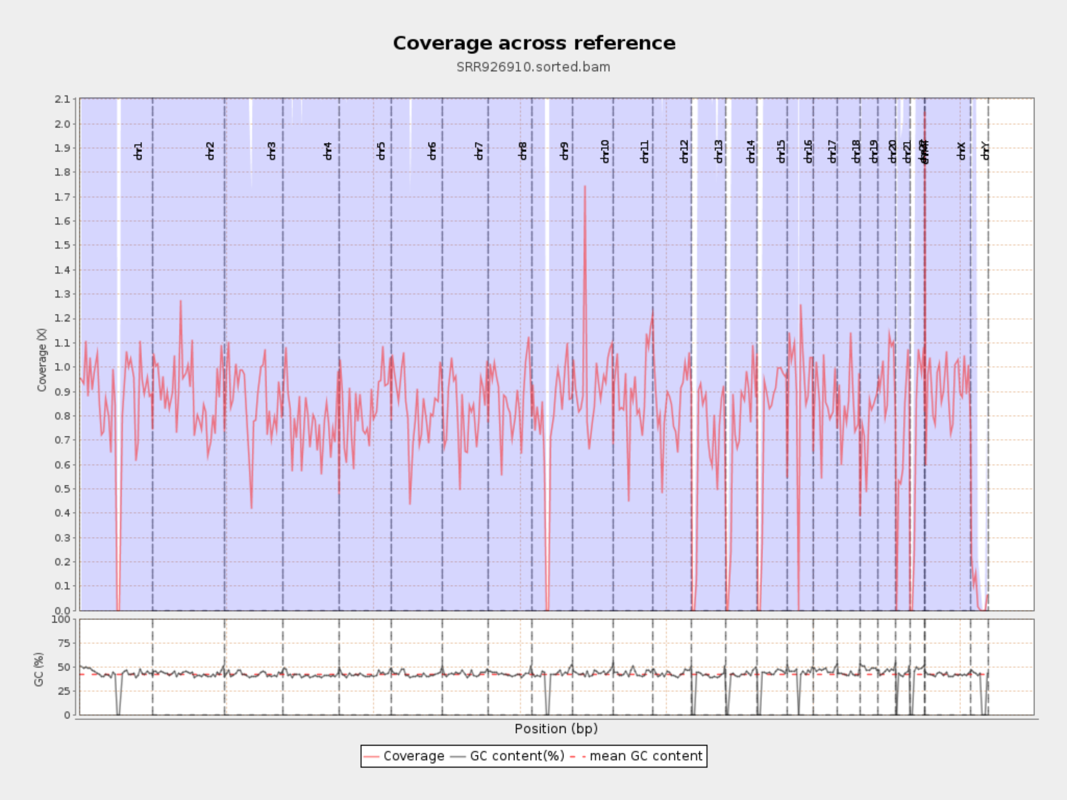
2.7. Chromosome stats

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

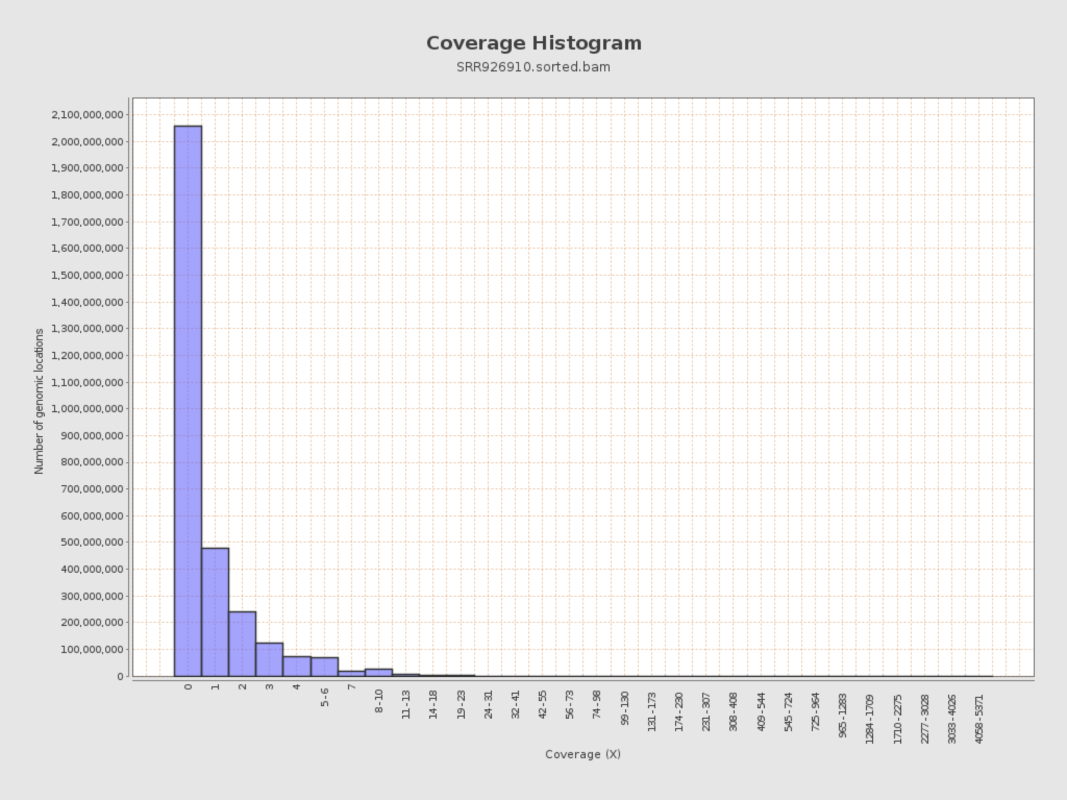
		bases	coverage	deviation
chr1	249250621	210866438	0.846	2.7126
chr2	243199373	218271606	0.8975	3.8292
chr3	198022430	170847200	0.8628	1.805
chr4	191154276	147746866	0.7729	1.8701
chr5	180915260	151039128	0.8349	1.7023
chr6	171115067	143450118	0.8383	1.71
chr7	159138663	130716073	0.8214	1.8806
chr8	146364022	128210343	0.876	1.91
chr9	141213431	107844955	0.7637	2.8518
chr10	135534747	129110995	0.9526	10.8826
chr11	135006516	120405803	0.8919	2.0348
chr12	133851895	113547272	0.8483	1.7924
chr13	115169878	74942599	0.6507	1.5126
chr14	107349540	75492857	0.7032	1.6086
chr15	102531392	76581505	0.7469	1.731
chr16	90354753	82535387	0.9135	4.5224
chr17	81195210	69332751	0.8539	1.9786
chr18	78077248	66315245	0.8494	2.818
chr19	59128983	44694760	0.7559	2.002
chr20	63025520	61283971	0.9724	1.9861
chr21	48129895	32263113	0.6703	2.2158
chr22	51304566	34512117	0.6727	1.7157
chrMT	16571	34001	2.0518	2.0468
chrX	155270560	140725233	0.9063	1.8708

chrY	59373566	3797902	0.064	1.3395

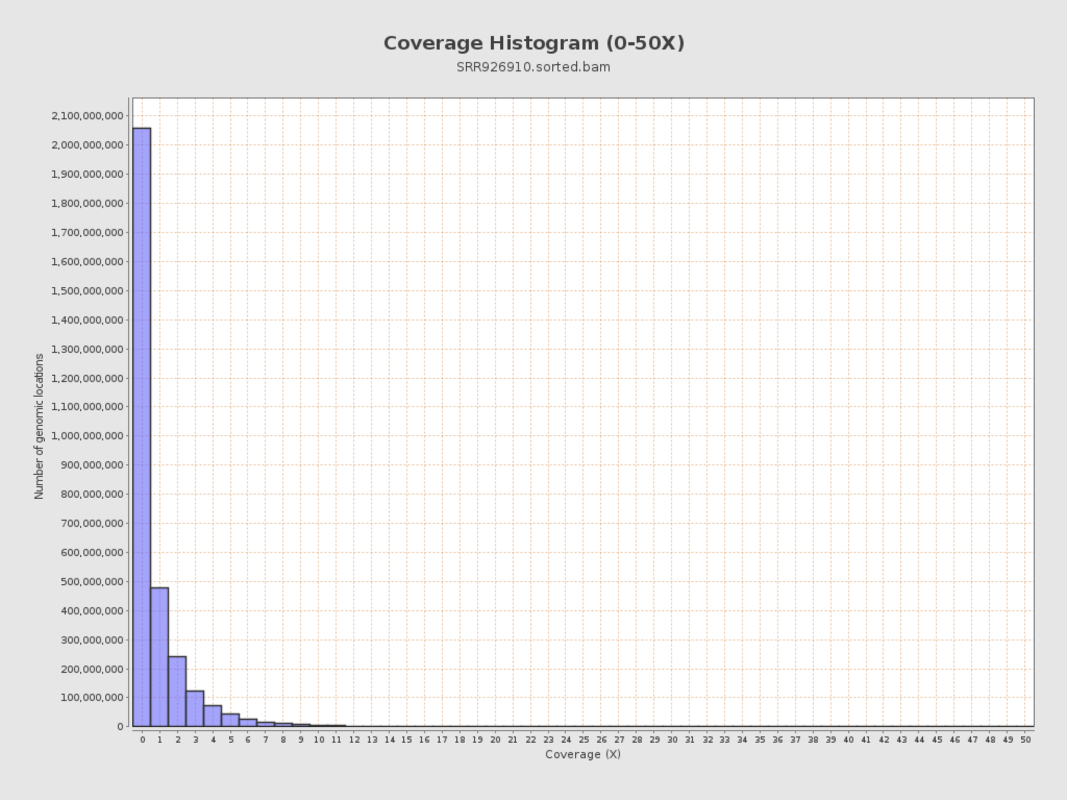
3. Results : Coverage across reference



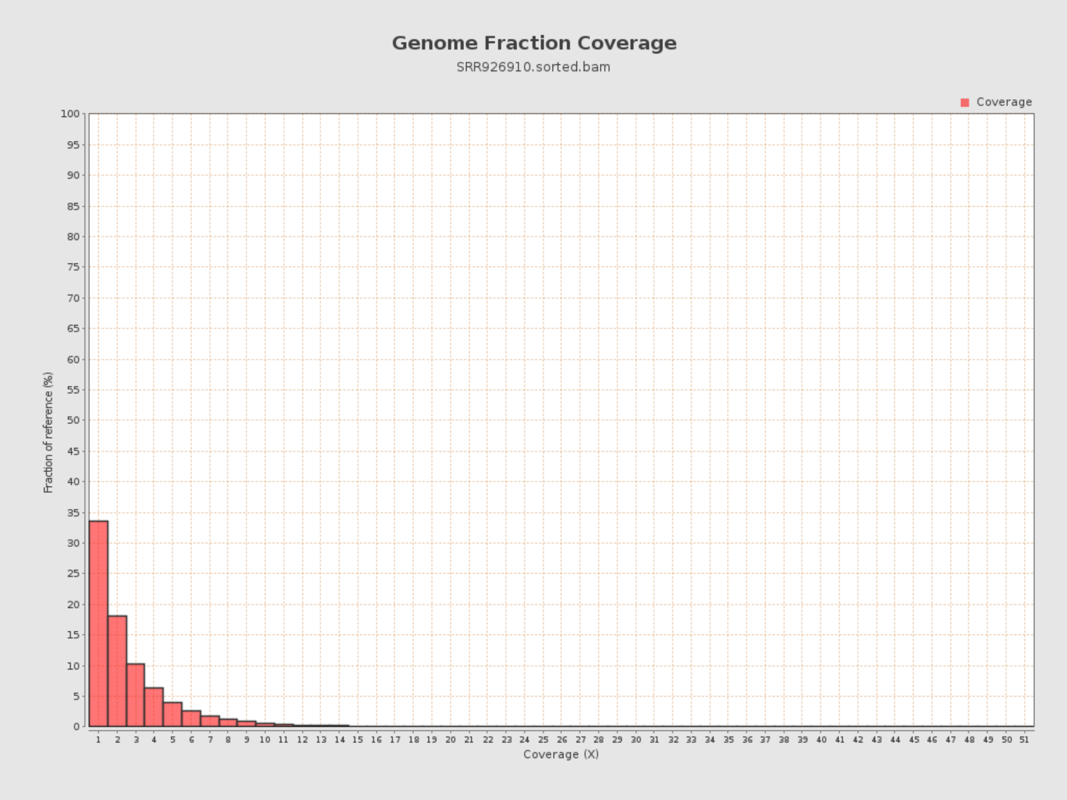
4. Results : Coverage Histogram



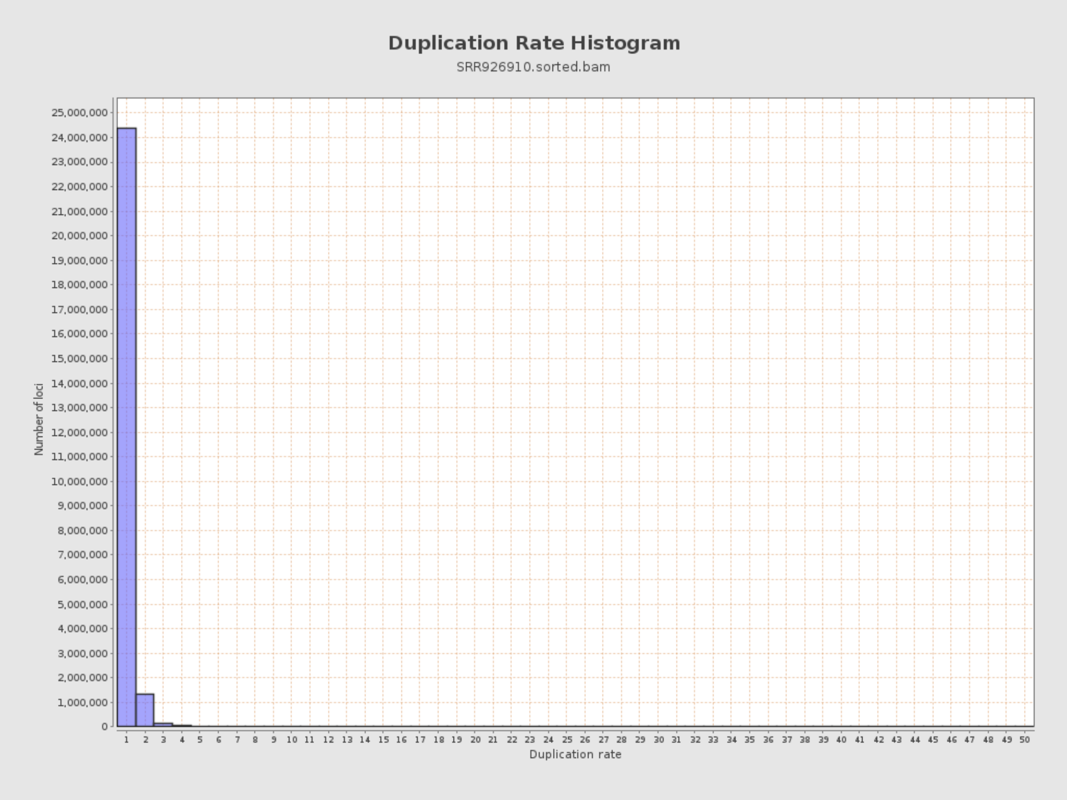
5. Results : Coverage Histogram (0-50X)



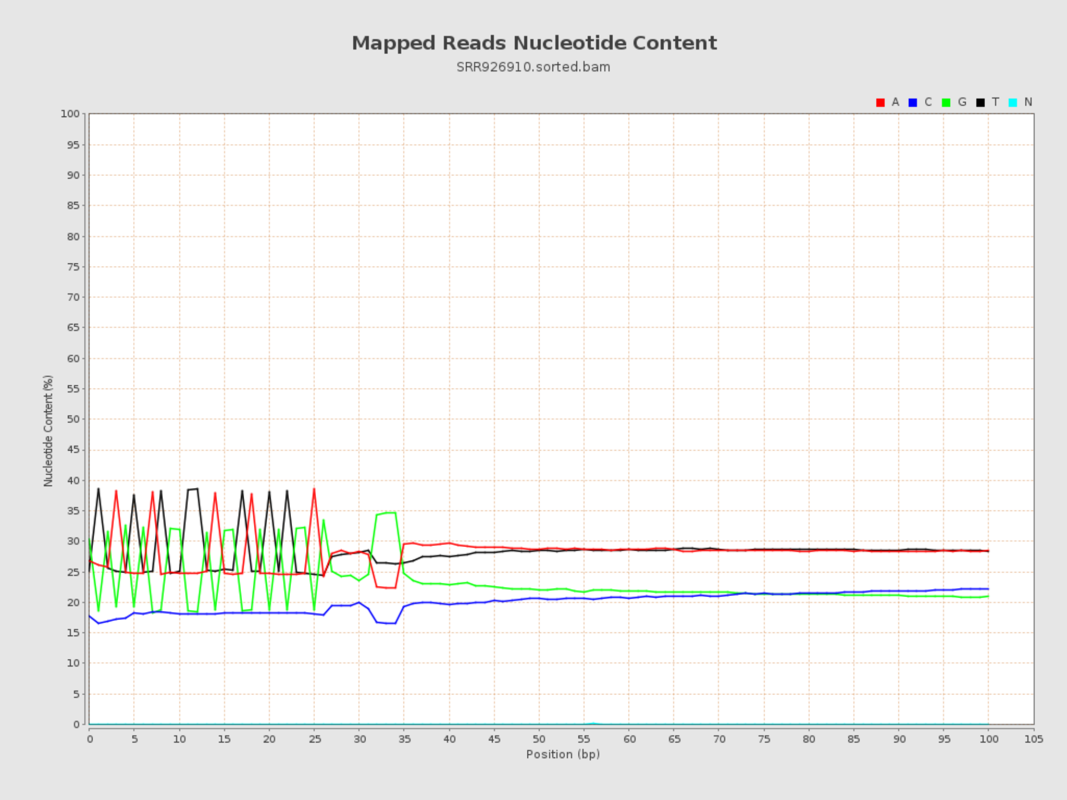
6. Results : Genome Fraction Coverage



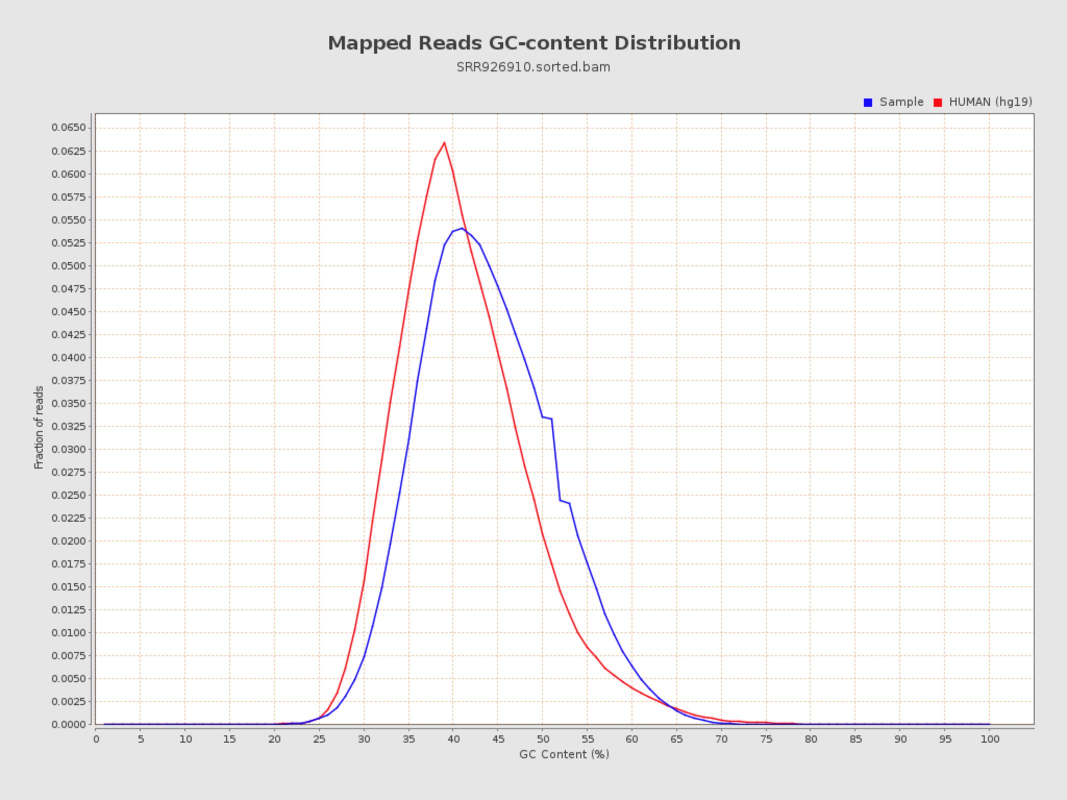
7. Results : Duplication Rate Histogram



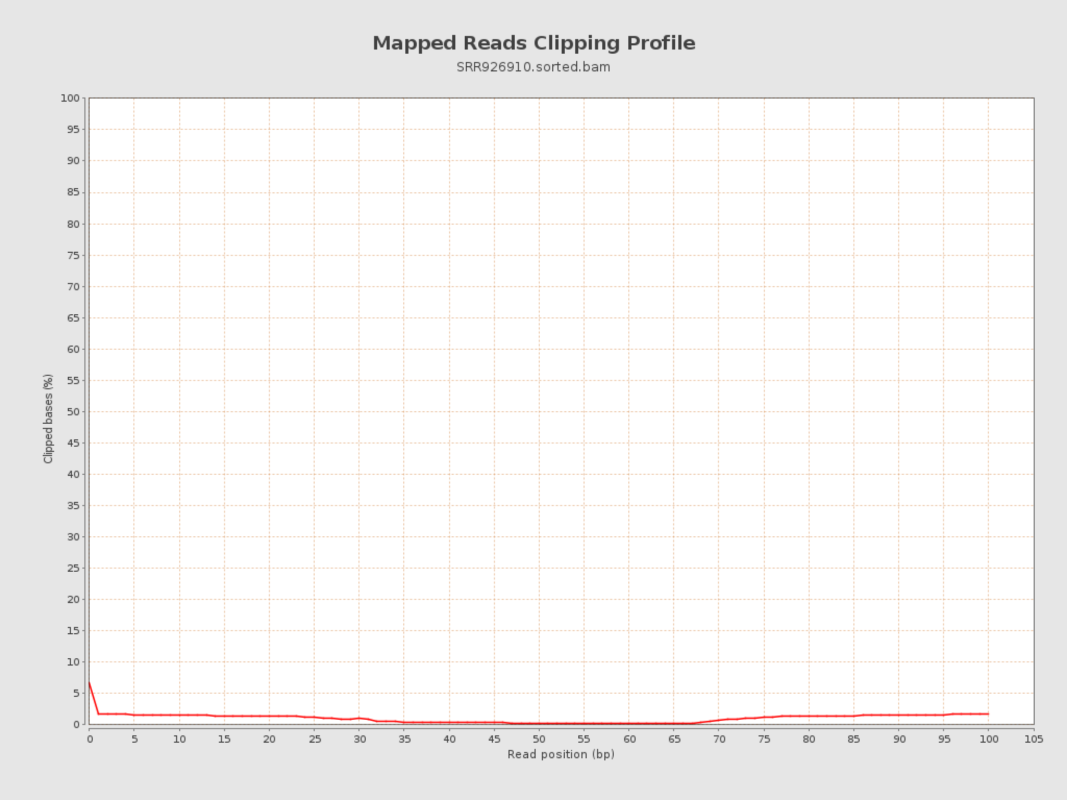
8. Results : Mapped Reads Nucleotide Content



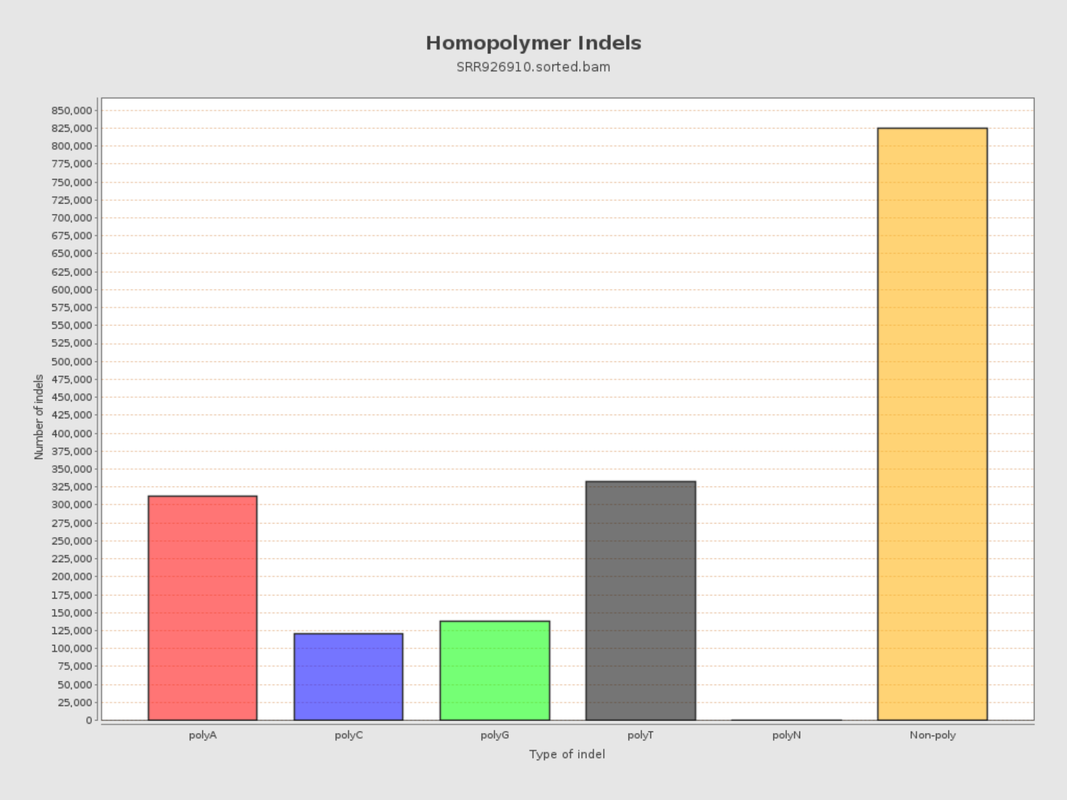
9. Results : Mapped Reads GC-content Distribution



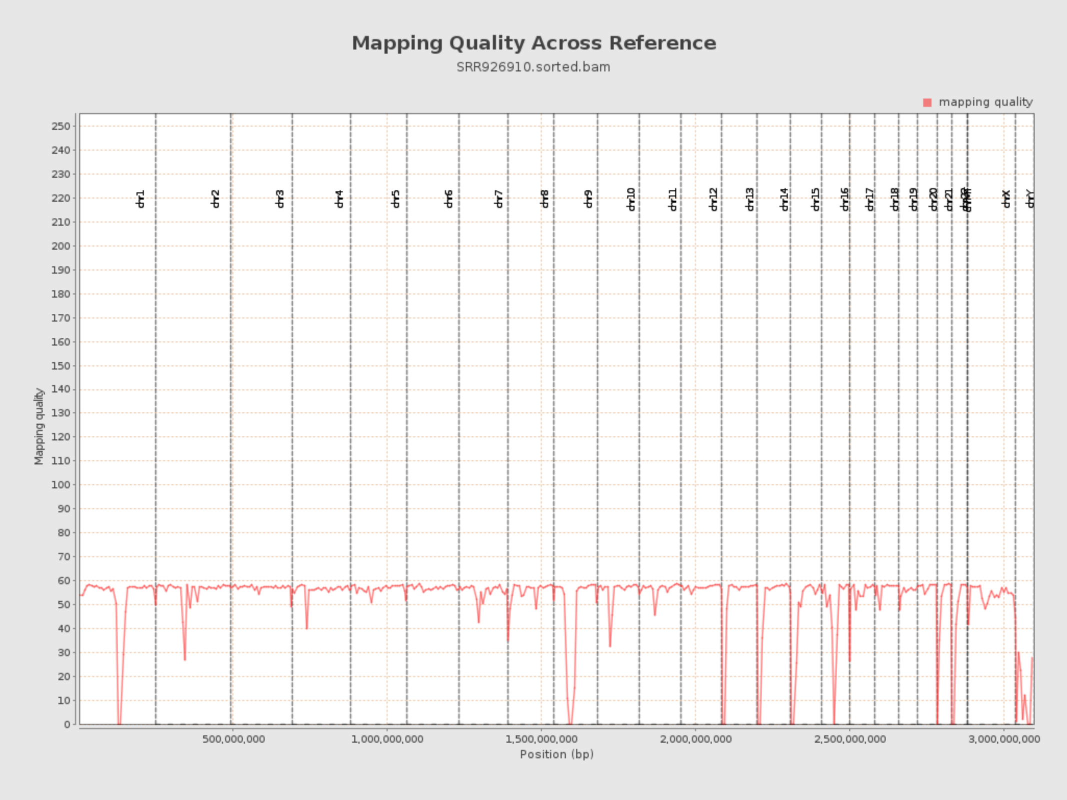
10. Results : Mapped Reads Clipping Profile



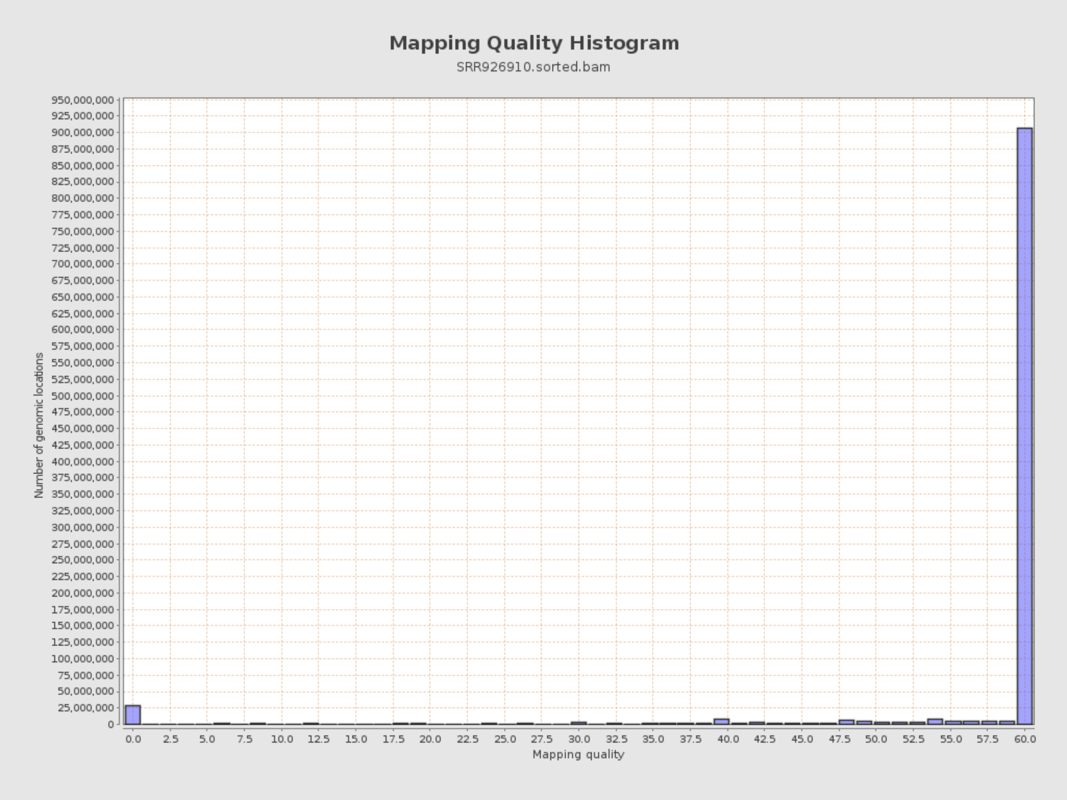
11. Results : Homopolymer Indels



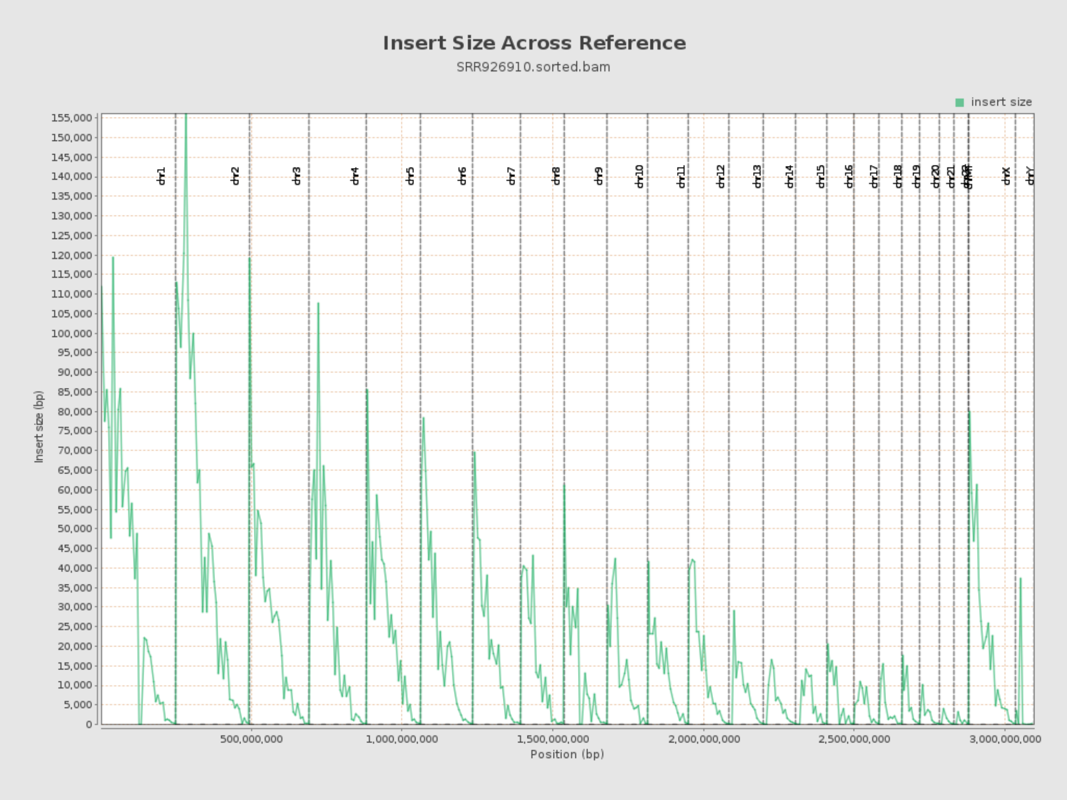
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram