Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 22:57:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926937.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_SRR926937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926937_1.fastq.gz SRR926937_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 22:57:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,630,356
Mapped reads	16,330,632 / 98.2%
Unmapped reads	299,724 / 1.8%
Mapped paired reads	16,330,632 / 98.2%
Mapped reads, first in pair	8,156,938 / 49.05%
Mapped reads, second in pair	8,173,694 / 49.15%
Mapped reads, both in pair	16,156,798 / 97.15%
Mapped reads, singletons	173,834 / 1.05%
Secondary alignments	0
Supplementary alignments	244,887 / 1.47%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	963,075 / 5.79%
Duplication rate	4.58%
Clipped reads	5,685,237 / 34.19%

2.2. ACGT Content

Number/percentage of A's	428,096,573 / 27.99%
Number/percentage of C's	315,896,113 / 20.65%
Number/percentage of T's	434,188,064 / 28.38%
Number/percentage of G's	351,402,045 / 22.97%
Number/percentage of N's	65,580 / 0%

GC Percentage	43.62%

2.3. Coverage

Mean	0.4945
Standard Deviation	2.1733

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	123,577.17
Standard Deviation	3,483,320.28
P25/Median/P75	146 / 185 / 244

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	14,196,174
Insertions	246,987
Mapped reads with at least one insertion	1.48%
Deletions	768,158
Mapped reads with at least one deletion	4.58%
Homopolymer indels	52.04%

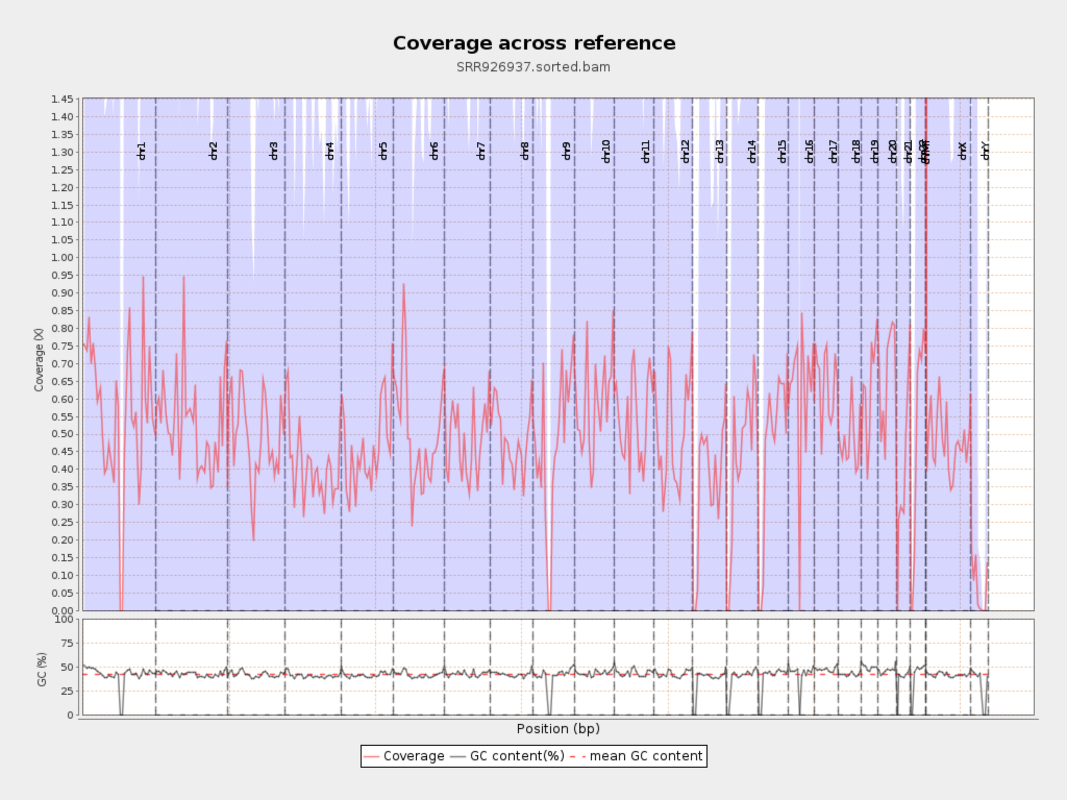
2.7. Chromosome stats

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

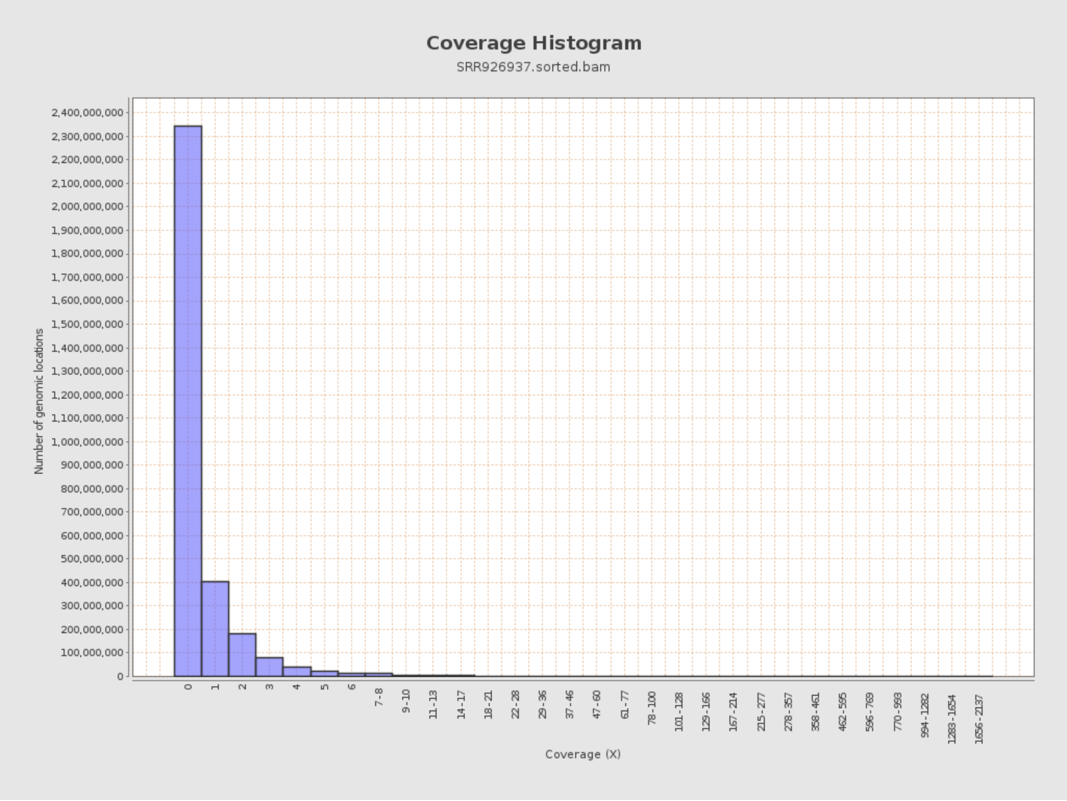
		bases	coverage	deviation
chr1	249250621	138061959	0.5539	2.6487
chr2	243199373	128904455	0.53	3.2695
chr3	198022430	97146802	0.4906	1.2249
chr4	191154276	78321140	0.4097	1.8403
chr5	180915260	84539079	0.4673	1.176
chr6	171115067	85280500	0.4984	1.4176
chr7	159138663	77218470	0.4852	1.6153
chr8	146364022	70727954	0.4832	1.3009
chr9	141213431	65509634	0.4639	2.1979
chr10	135534747	78259471	0.5774	4.1286
chr11	135006516	73266096	0.5427	2.1331
chr12	133851895	67964240	0.5078	1.3266
chr13	115169878	40875711	0.3549	0.9832
chr14	107349540	47462626	0.4421	1.1723
chr15	102531392	46275314	0.4513	1.2001
chr16	90354753	55967076	0.6194	3.1972
chr17	81195210	52347110	0.6447	1.8227
chr18	78077248	37290261	0.4776	2.2178
chr19	59128983	36965936	0.6252	2.1189
chr20	63025520	42061418	0.6674	1.7112
chr21	48129895	19474107	0.4046	1.7402
chr22	51304566	25206411	0.4913	1.3512
chrMT	16571	3237475	195.3699	156.5619
chrX	155270560	74435291	0.4794	1.3512

chrY	59373566	3970421	0.0669	1.9018

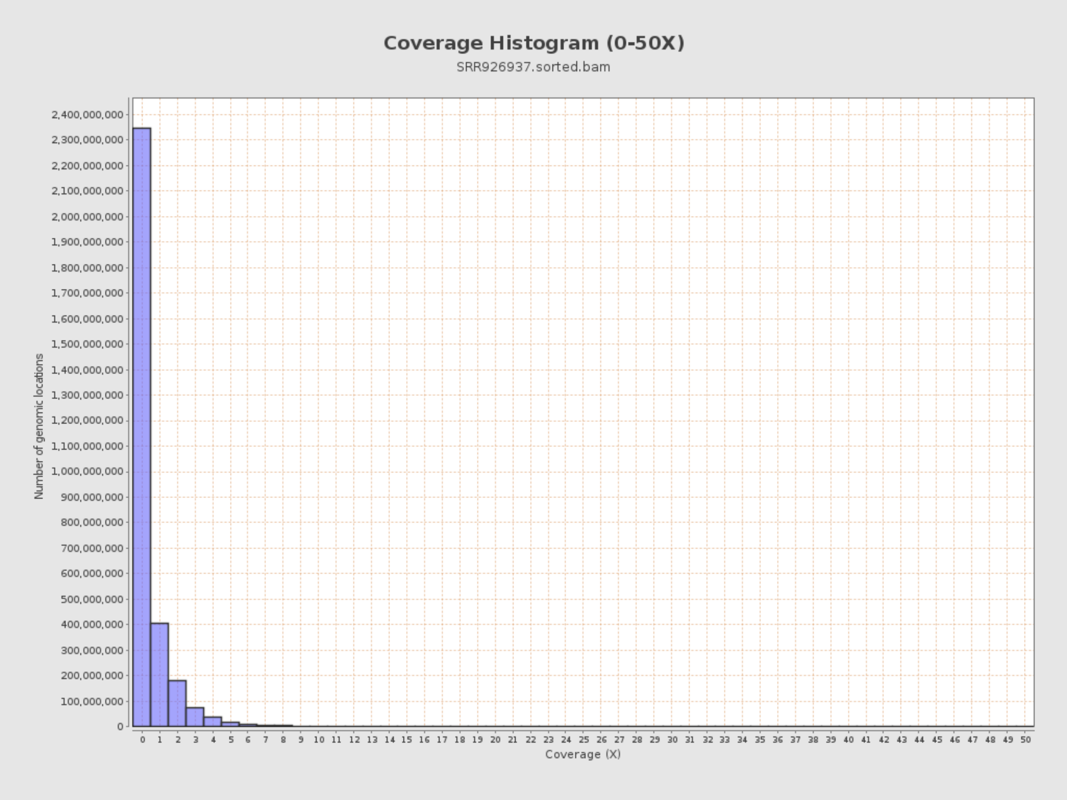
3. Results : Coverage across reference



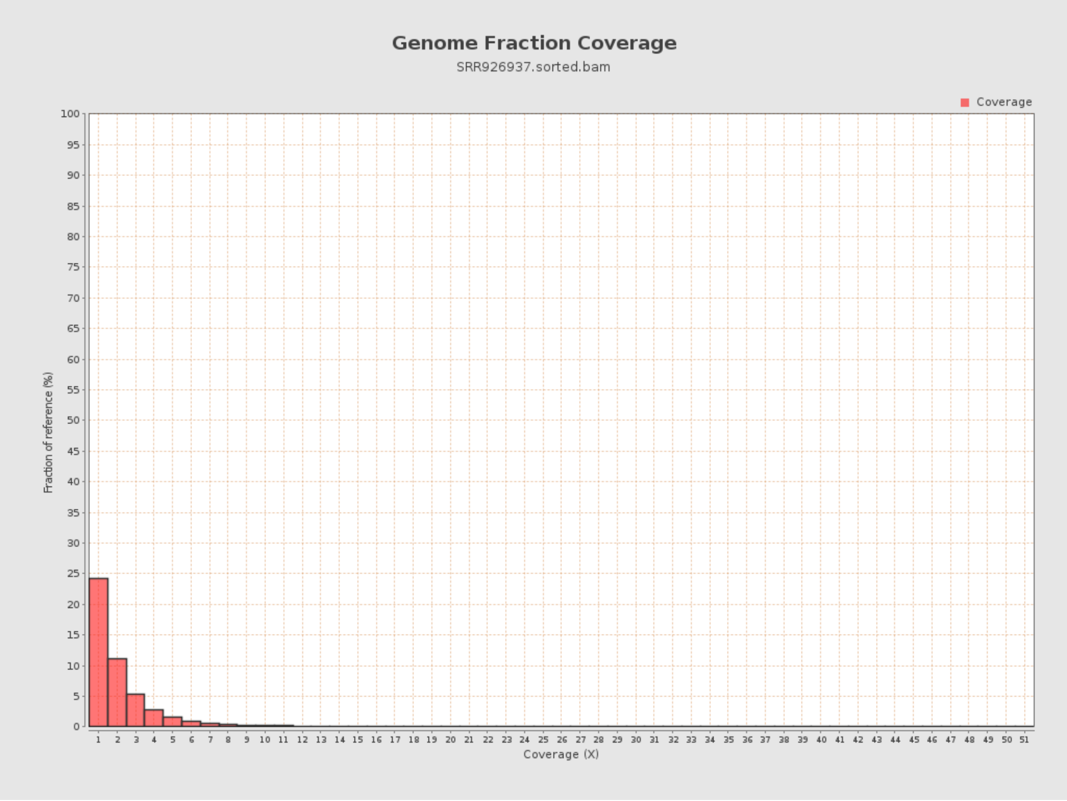
4. Results : Coverage Histogram



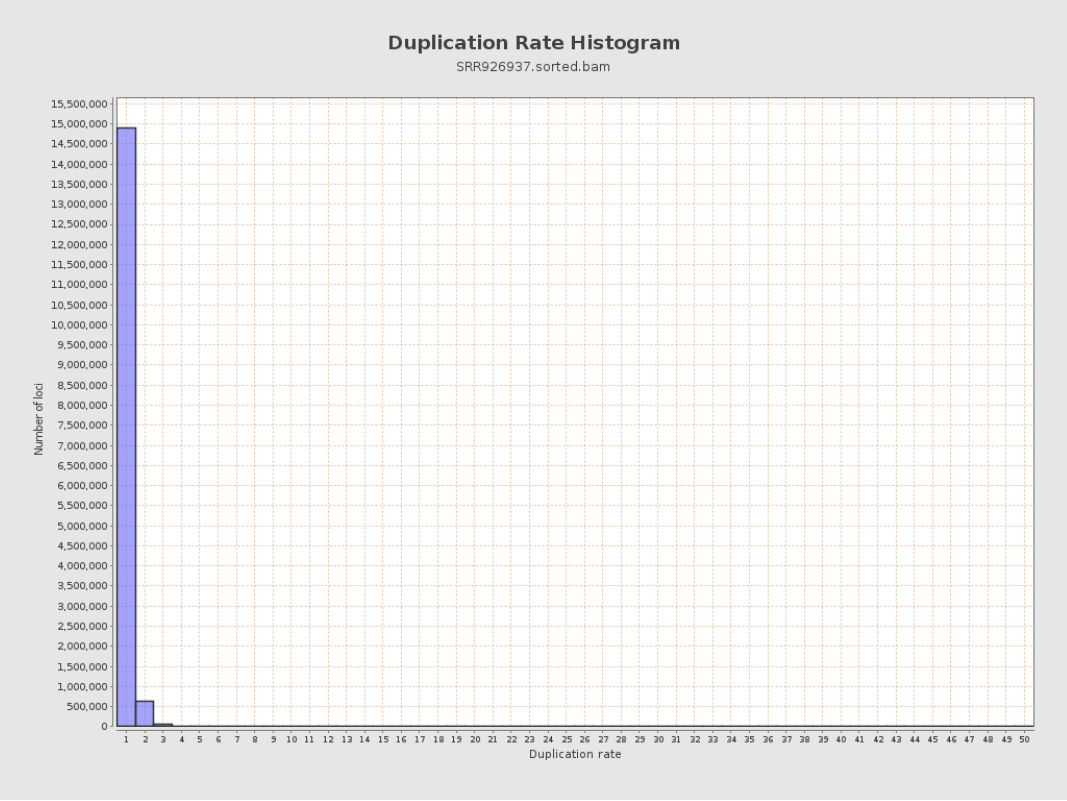
5. Results : Coverage Histogram (0-50X)



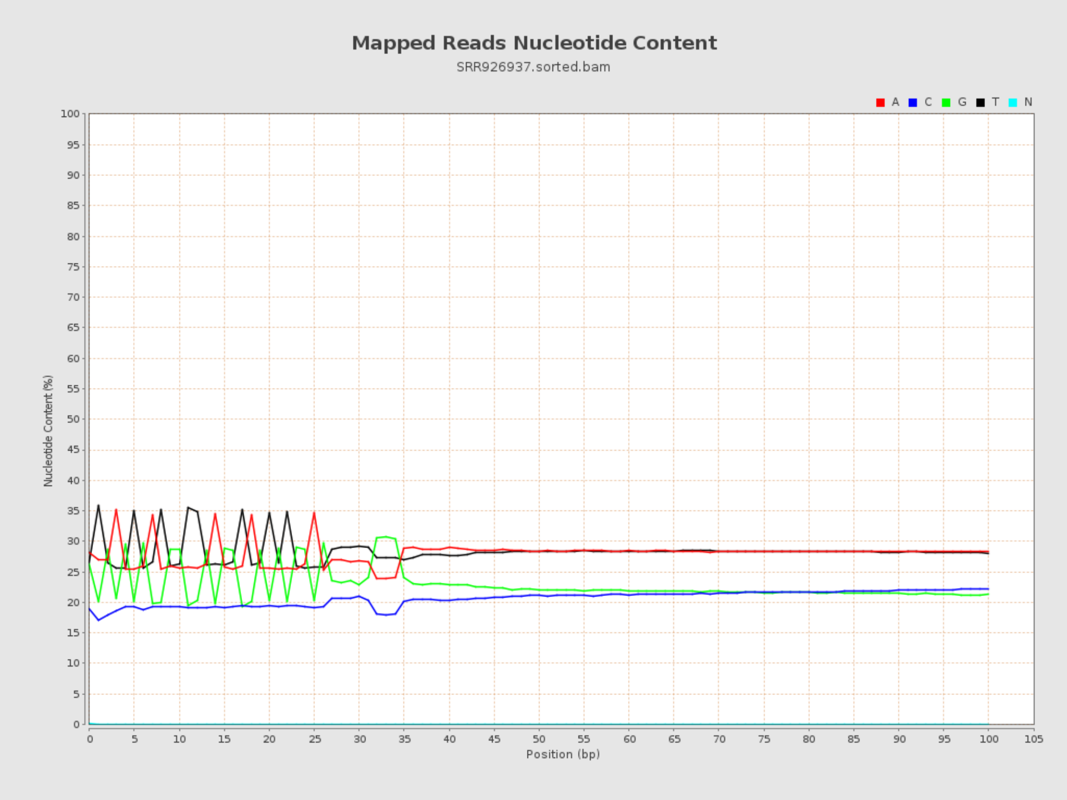
6. Results : Genome Fraction Coverage



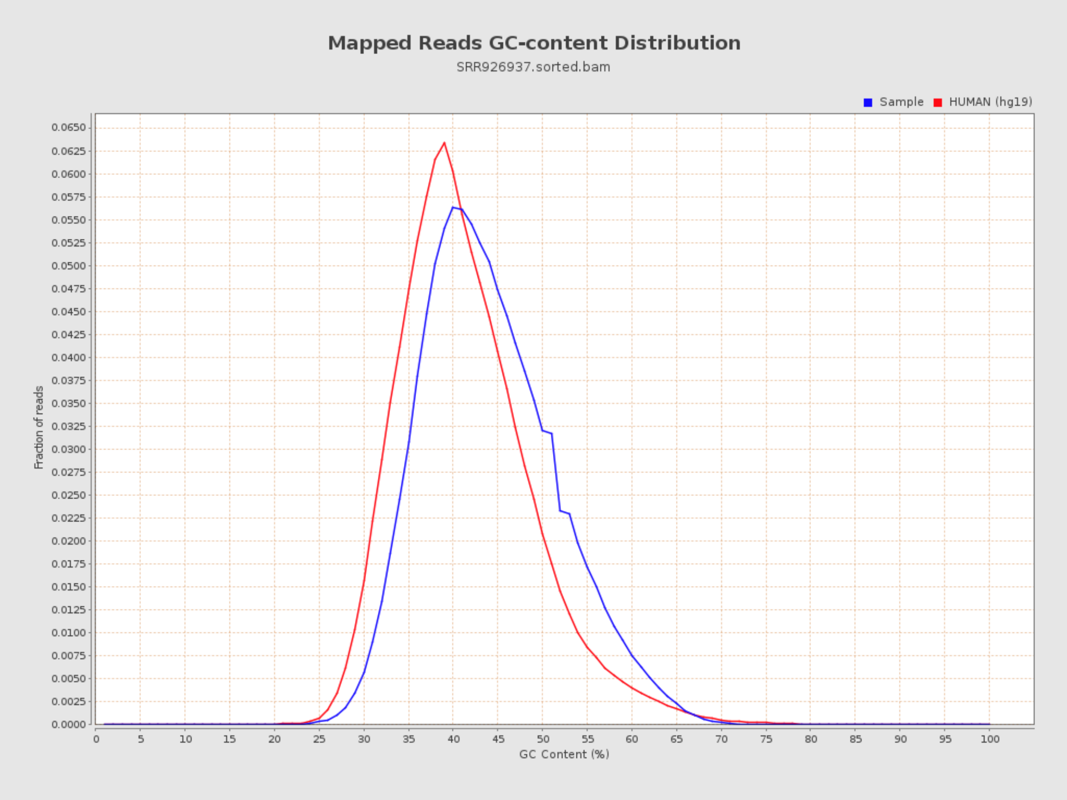
7. Results : Duplication Rate Histogram



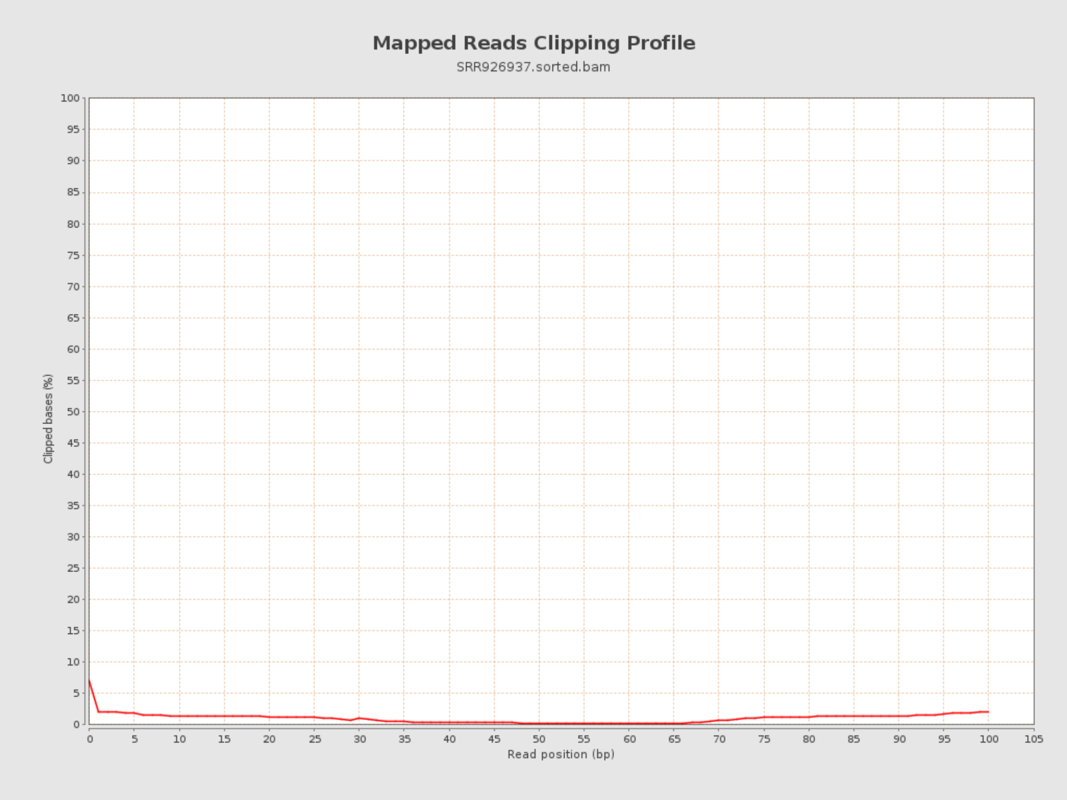
8. Results : Mapped Reads Nucleotide Content



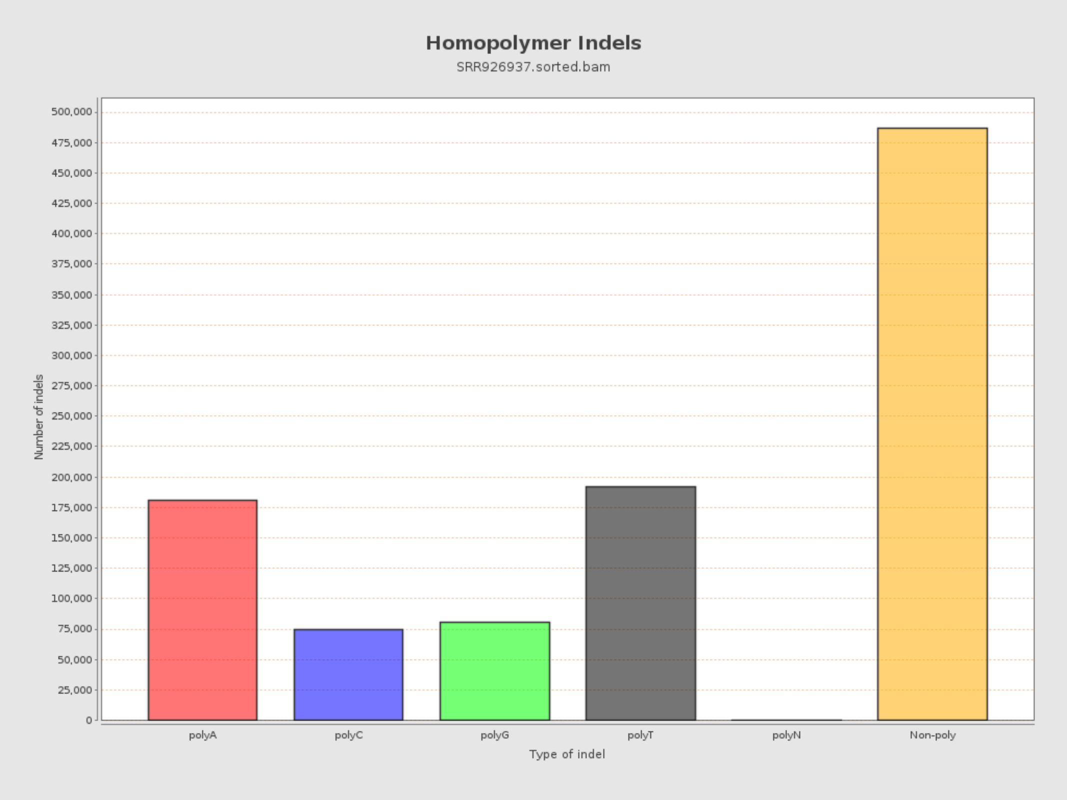
9. Results : Mapped Reads GC-content Distribution



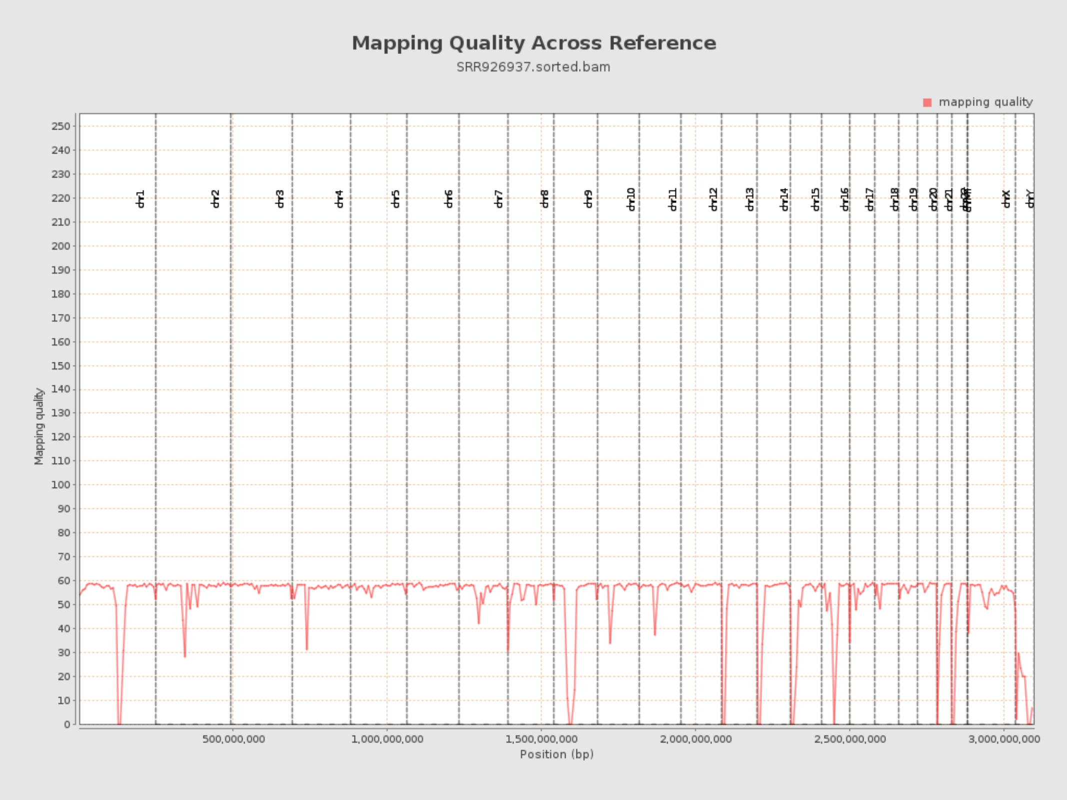
10. Results : Mapped Reads Clipping Profile



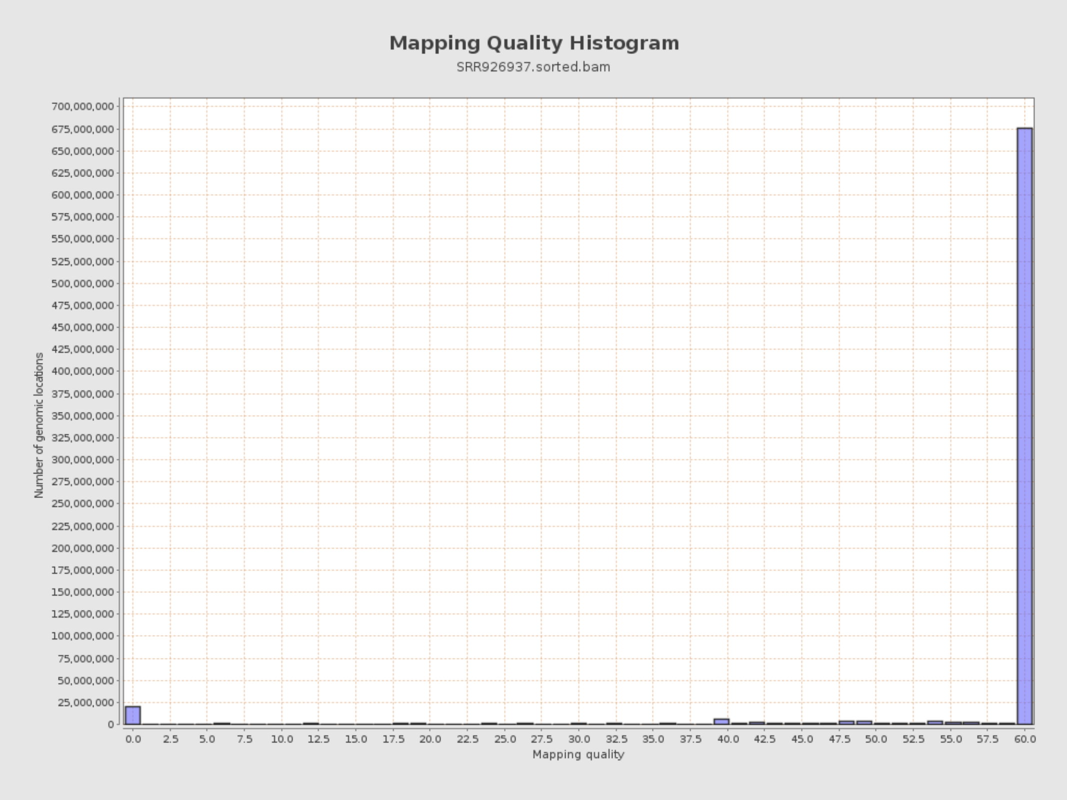
11. Results : Homopolymer Indels



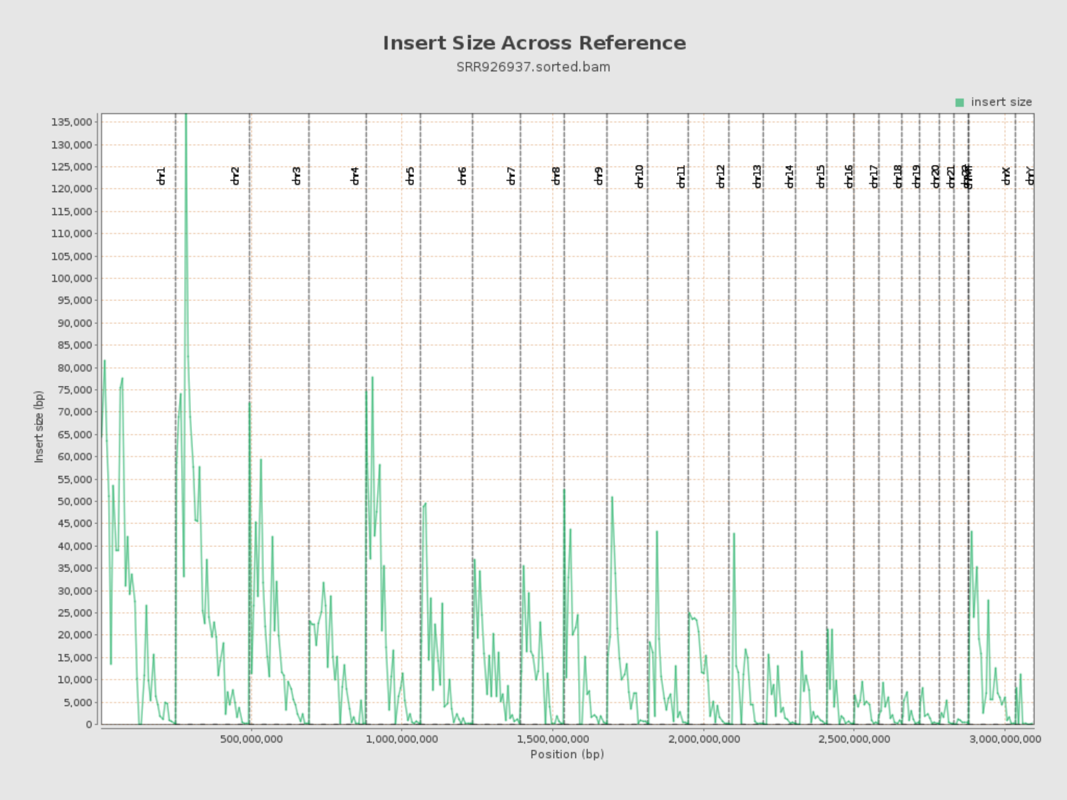
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram