Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 12:27:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926909.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_SRR926909 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926909_1.fastq.gz SRR926909_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 12:27:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926909.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,595,756
Mapped reads	32,608,521 / 97.06%
Unmapped reads	987,235 / 2.94%
Mapped paired reads	32,608,521 / 97.06%
Mapped reads, first in pair	16,383,621 / 48.77%
Mapped reads, second in pair	16,224,900 / 48.29%
Mapped reads, both in pair	32,089,492 / 95.52%
Mapped reads, singletons	519,029 / 1.54%
Secondary alignments	0
Supplementary alignments	1,243,771 / 3.7%
Read min/max/mean length	30 / 101 / 102.52
Duplicated reads (estimated)	3,588,383 / 10.68%
Duplication rate	8.58%
Clipped reads	16,480,892 / 49.06%

2.2. ACGT Content

Number/percentage of A's	822,038,297 / 28.23%
Number/percentage of C's	567,794,195 / 19.5%
Number/percentage of T's	828,925,316 / 28.47%
Number/percentage of G's	693,053,242 / 23.8%
Number/percentage of N's	242,784 / 0.01%

GC Percentage	43.3%

2.3. Coverage

Mean	0.9414
Standard Deviation	2.9997

2.4. Mapping Quality

Mean Mapping Quality	52.35

2.5. Insert size

Mean	435,865.39
Standard Deviation	6,498,383.95
P25/Median/P75	133 / 176 / 240

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	27,077,751
Insertions	483,621
Mapped reads with at least one insertion	1.46%
Deletions	1,491,560
Mapped reads with at least one deletion	4.46%
Homopolymer indels	51.61%

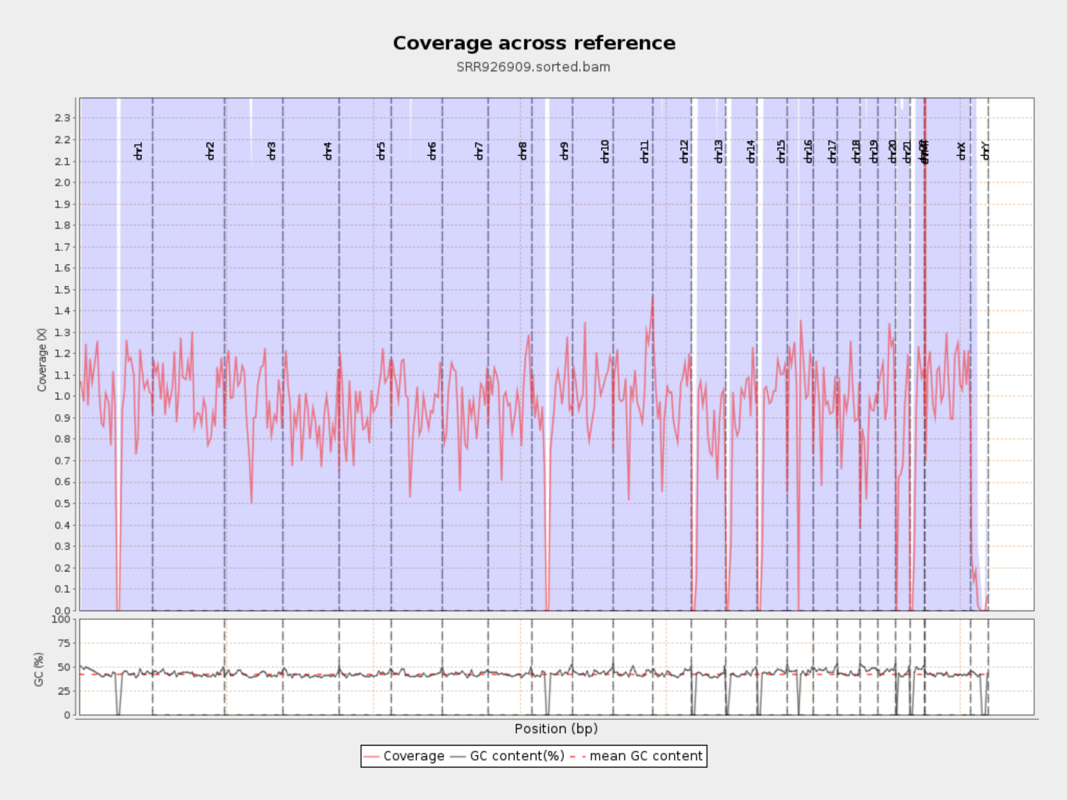
2.7. Chromosome stats

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

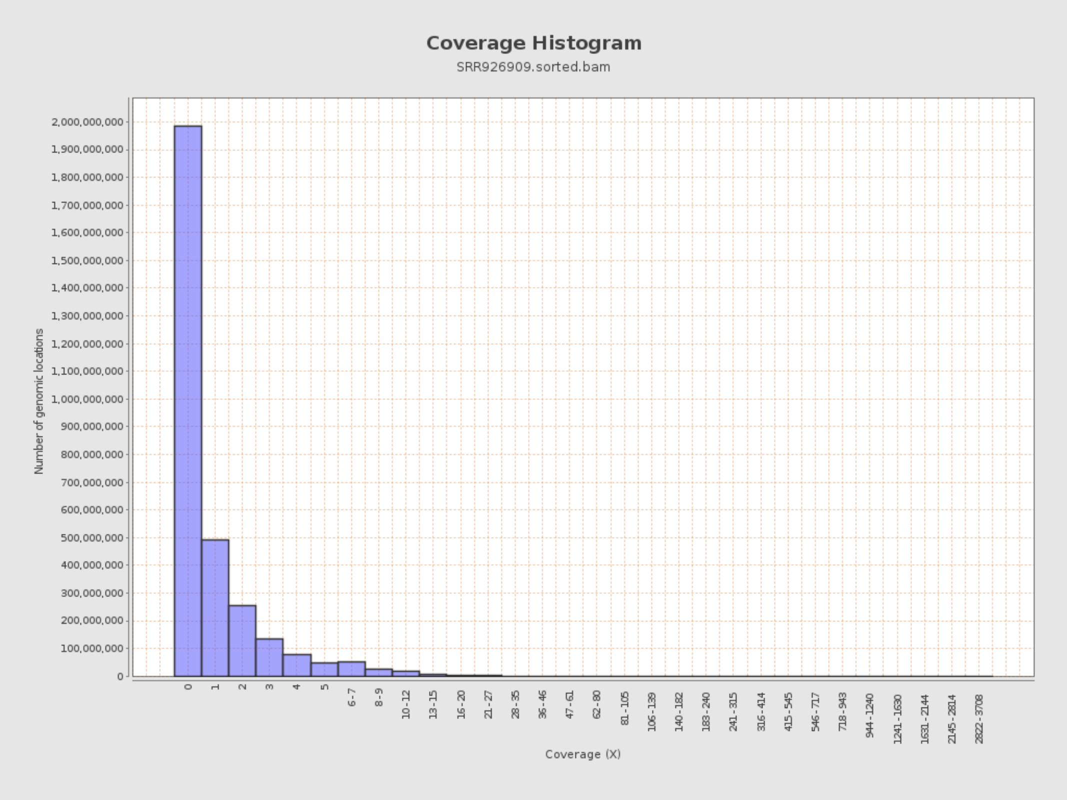
		bases	coverage	deviation
chr1	249250621	242851581	0.9743	2.8419
chr2	243199373	249786069	1.0271	4.8385
chr3	198022430	196965091	0.9947	2.0674
chr4	191154276	172666088	0.9033	2.3284
chr5	180915260	175168394	0.9682	2.013
chr6	171115067	166825945	0.9749	2.1955
chr7	159138663	150252241	0.9442	2.3806
chr8	146364022	146596402	1.0016	2.1782
chr9	141213431	122880776	0.8702	2.8716
chr10	135534747	142097463	1.0484	6.3404
chr11	135006516	140290093	1.0391	2.4361
chr12	133851895	131805594	0.9847	2.387
chr13	115169878	86886622	0.7544	1.8369
chr14	107349540	87470250	0.8148	1.9251
chr15	102531392	87210170	0.8506	2.0159
chr16	90354753	92808951	1.0272	4.8245
chr17	81195210	77935865	0.9599	2.1981
chr18	78077248	76613208	0.9812	2.918
chr19	59128983	49801700	0.8423	2.1978
chr20	63025520	70054293	1.1115	2.337
chr21	48129895	36588824	0.7602	2.696
chr22	51304566	38147093	0.7435	1.9737
chrMT	16571	2046890	123.5224	84.8117
chrX	155270560	165942139	1.0687	2.2031

chrY	59373566	4580814	0.0772	1.8534

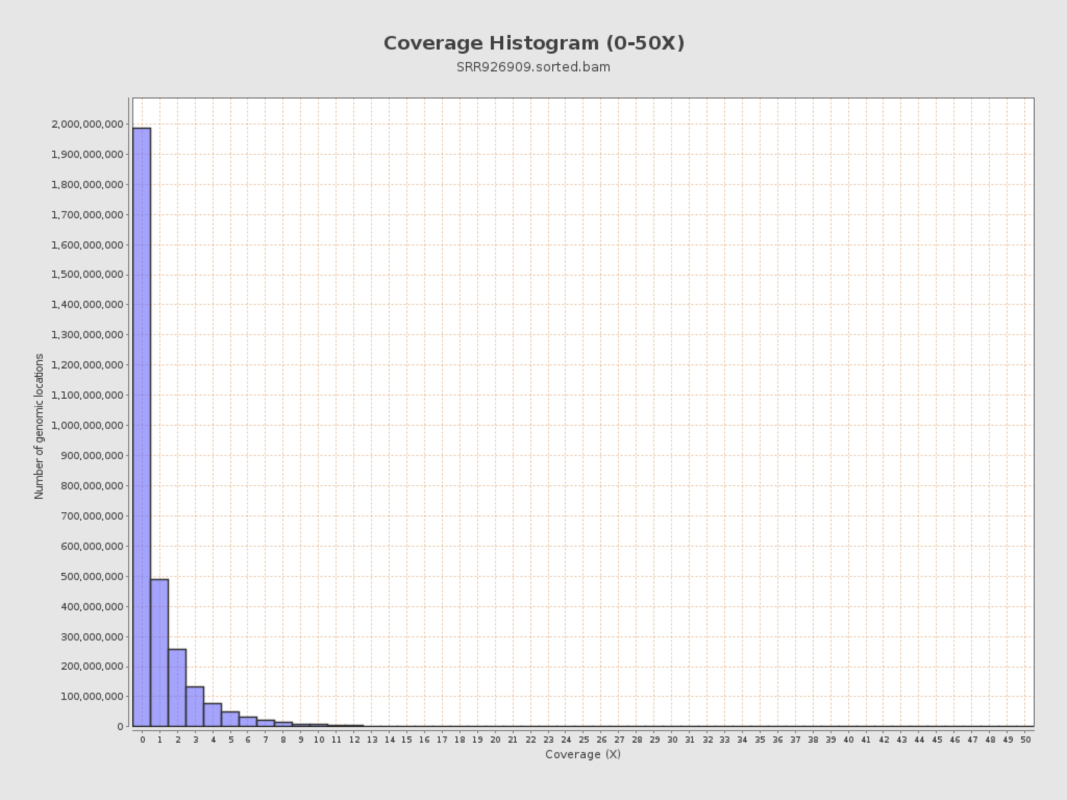
3. Results : Coverage across reference



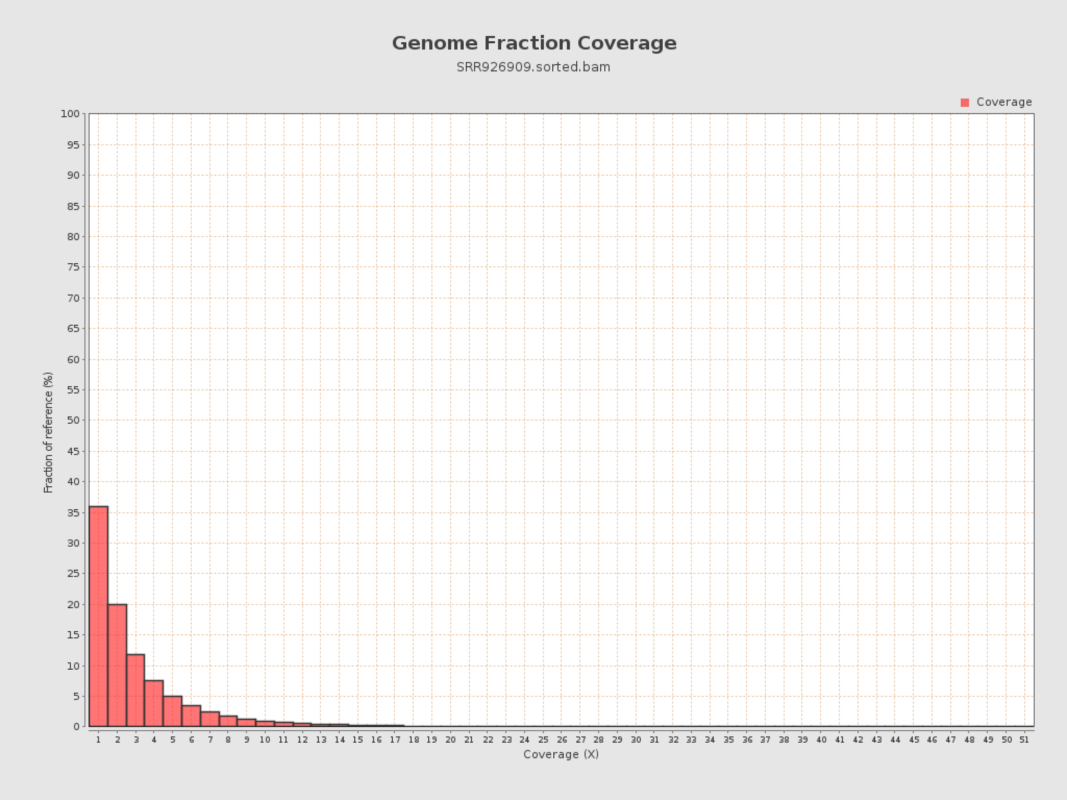
4. Results : Coverage Histogram



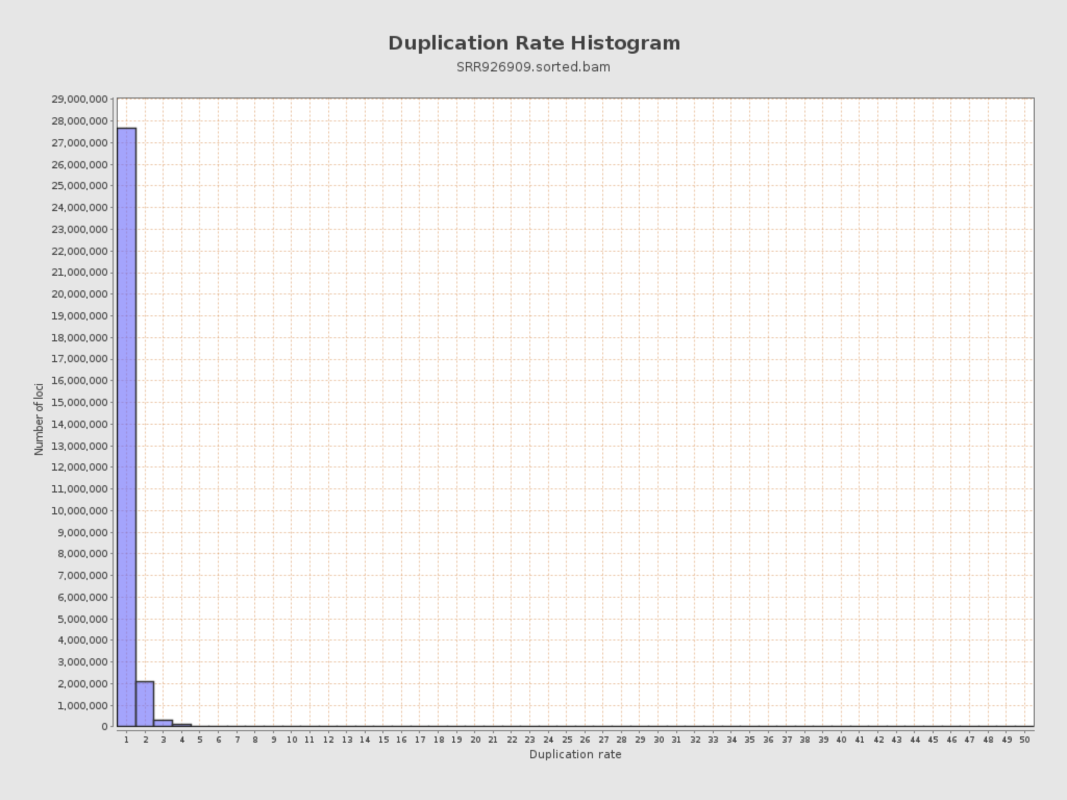
5. Results : Coverage Histogram (0-50X)



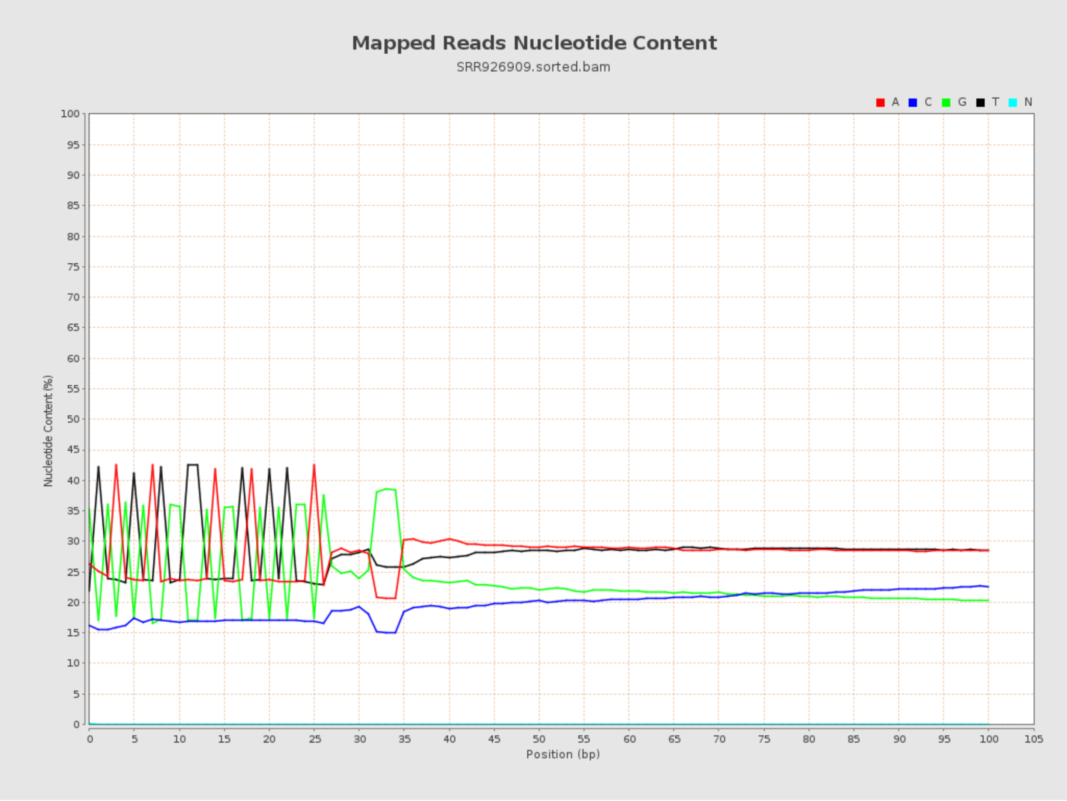
6. Results : Genome Fraction Coverage



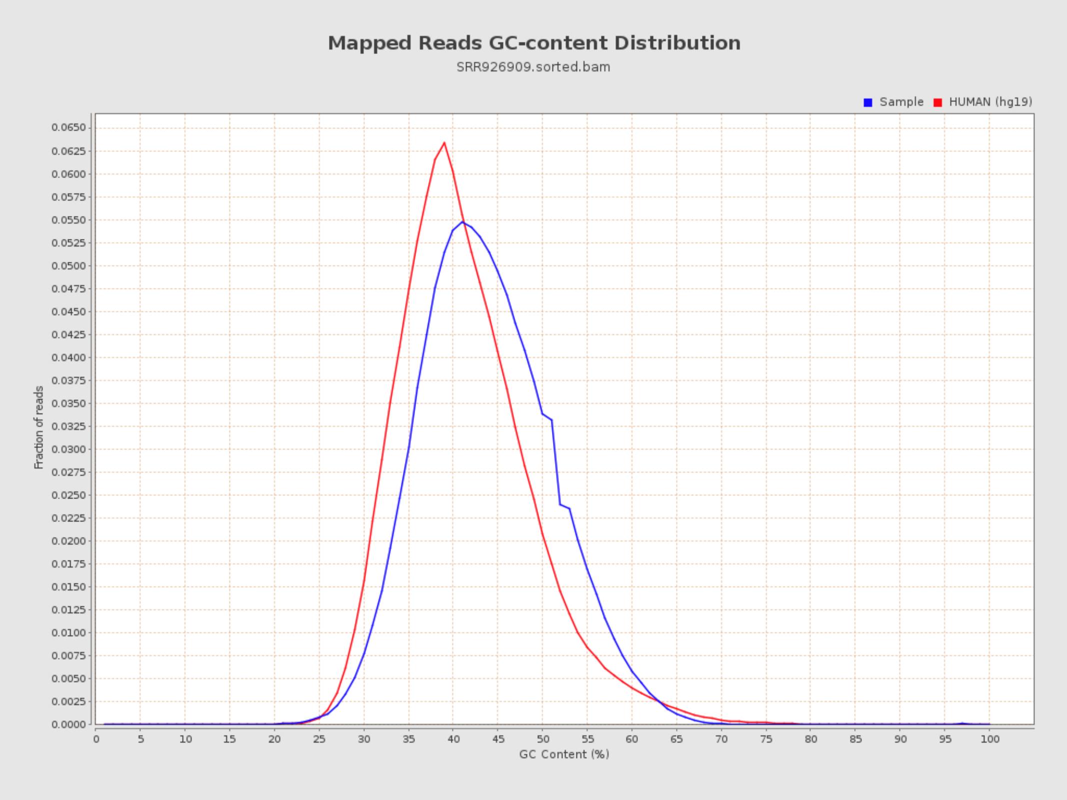
7. Results : Duplication Rate Histogram



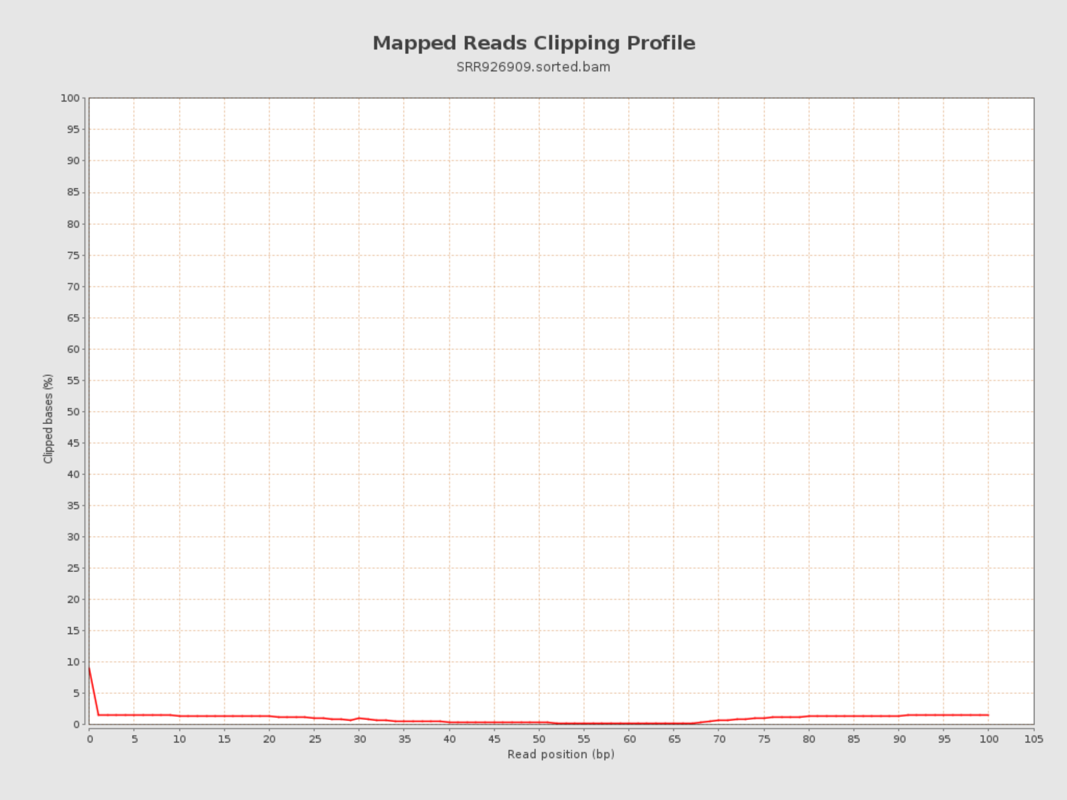
8. Results : Mapped Reads Nucleotide Content



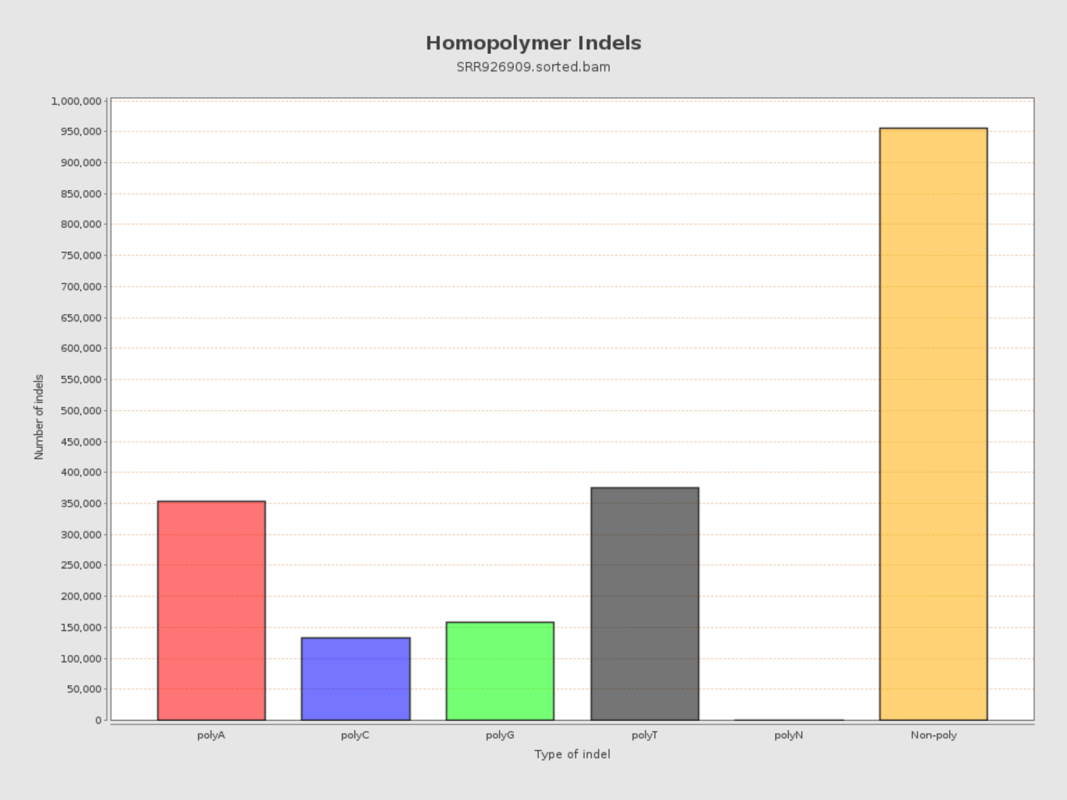
9. Results : Mapped Reads GC-content Distribution



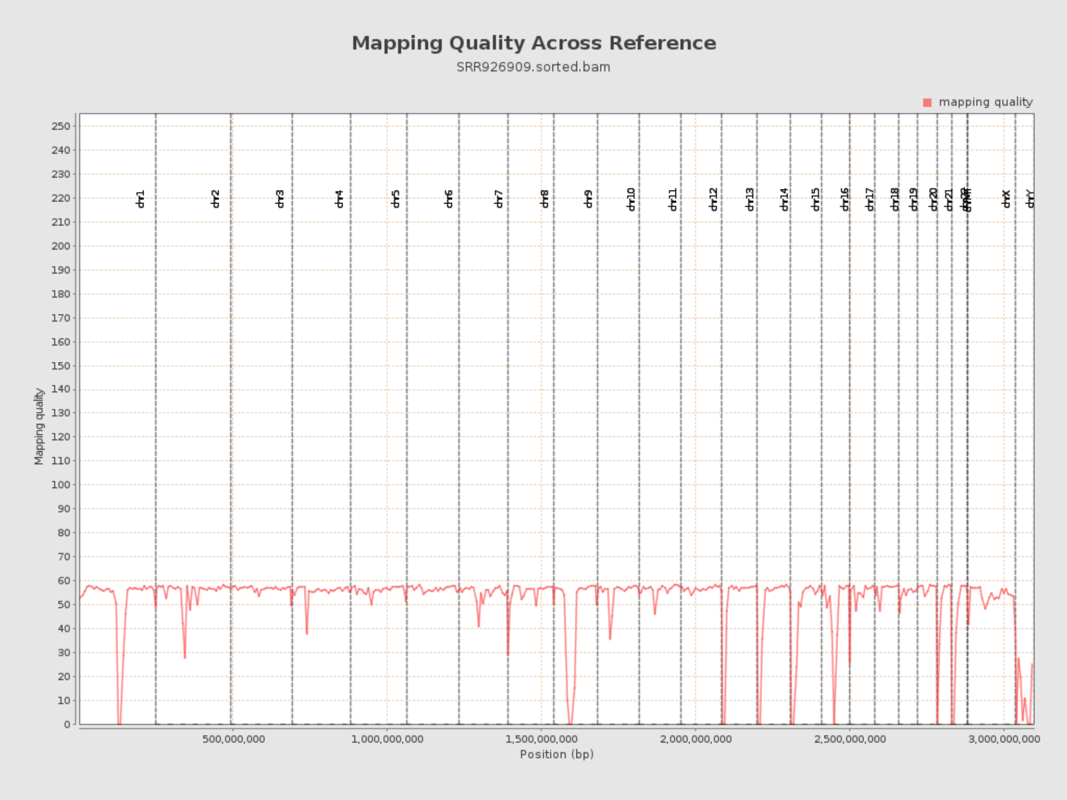
10. Results : Mapped Reads Clipping Profile



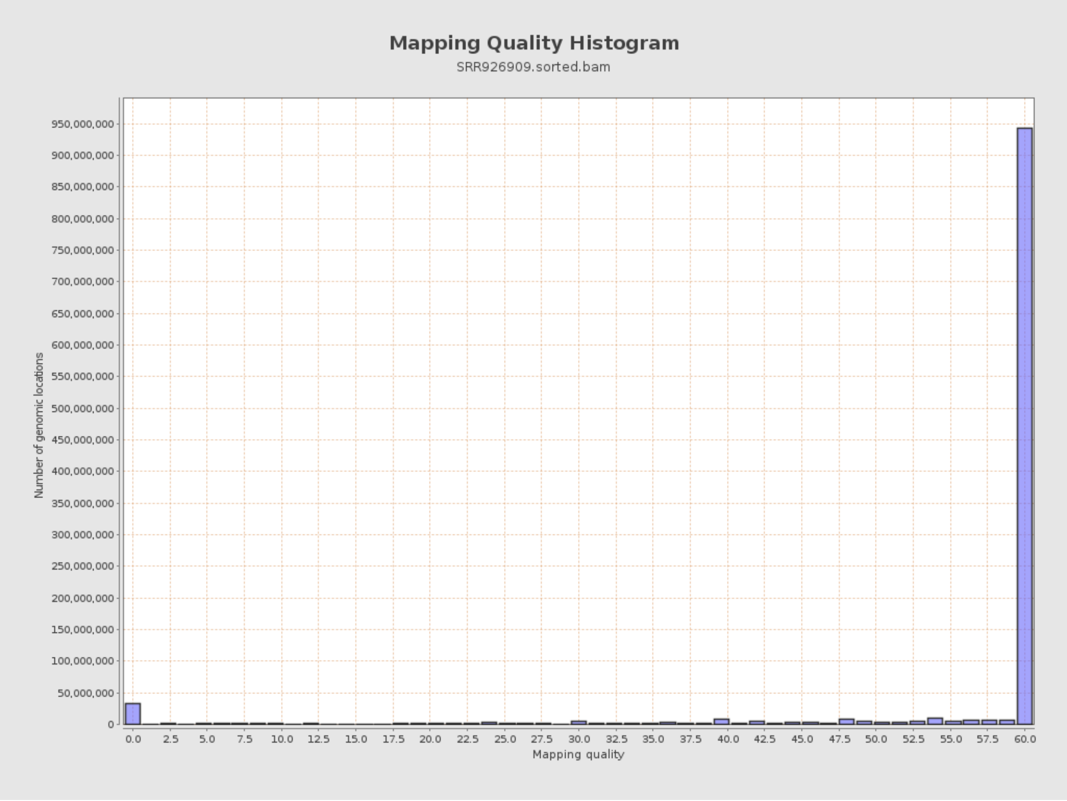
11. Results : Homopolymer Indels



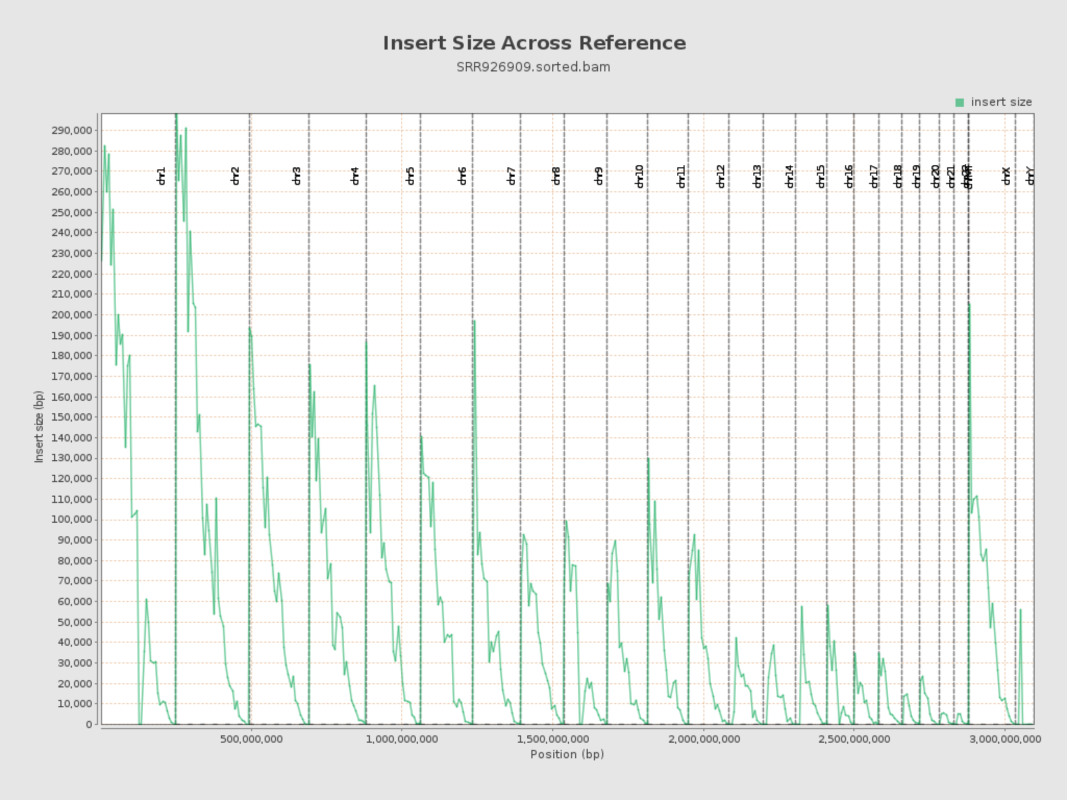
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram