Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 11:23:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926907.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_SRR926907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926907_1.fastq.gz SRR926907_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 11:23:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,148,160
Mapped reads	23,433,299 / 89.62%
Unmapped reads	2,714,861 / 10.38%
Mapped paired reads	23,433,299 / 89.62%
Mapped reads, first in pair	11,757,344 / 44.96%
Mapped reads, second in pair	11,675,955 / 44.65%
Mapped reads, both in pair	23,106,824 / 88.37%
Mapped reads, singletons	326,475 / 1.25%
Secondary alignments	0
Supplementary alignments	367,333 / 1.4%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	1,473,245 / 5.63%
Duplication rate	5.05%
Clipped reads	7,469,554 / 28.57%

2.2. ACGT Content

Number/percentage of A's	613,193,360 / 28.13%
Number/percentage of C's	442,035,491 / 20.28%
Number/percentage of T's	618,774,235 / 28.38%
Number/percentage of G's	505,886,855 / 23.2%
Number/percentage of N's	205,254 / 0.01%

GC Percentage	43.48%

2.3. Coverage

Mean	0.7048
Standard Deviation	2.9762

2.4. Mapping Quality

Mean Mapping Quality	52.95

2.5. Insert size

Mean	179,895.84
Standard Deviation	4,176,074.12
P25/Median/P75	150 / 192 / 254

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	22,108,480
Insertions	344,960
Mapped reads with at least one insertion	1.45%
Deletions	1,134,227
Mapped reads with at least one deletion	4.72%
Homopolymer indels	52.61%

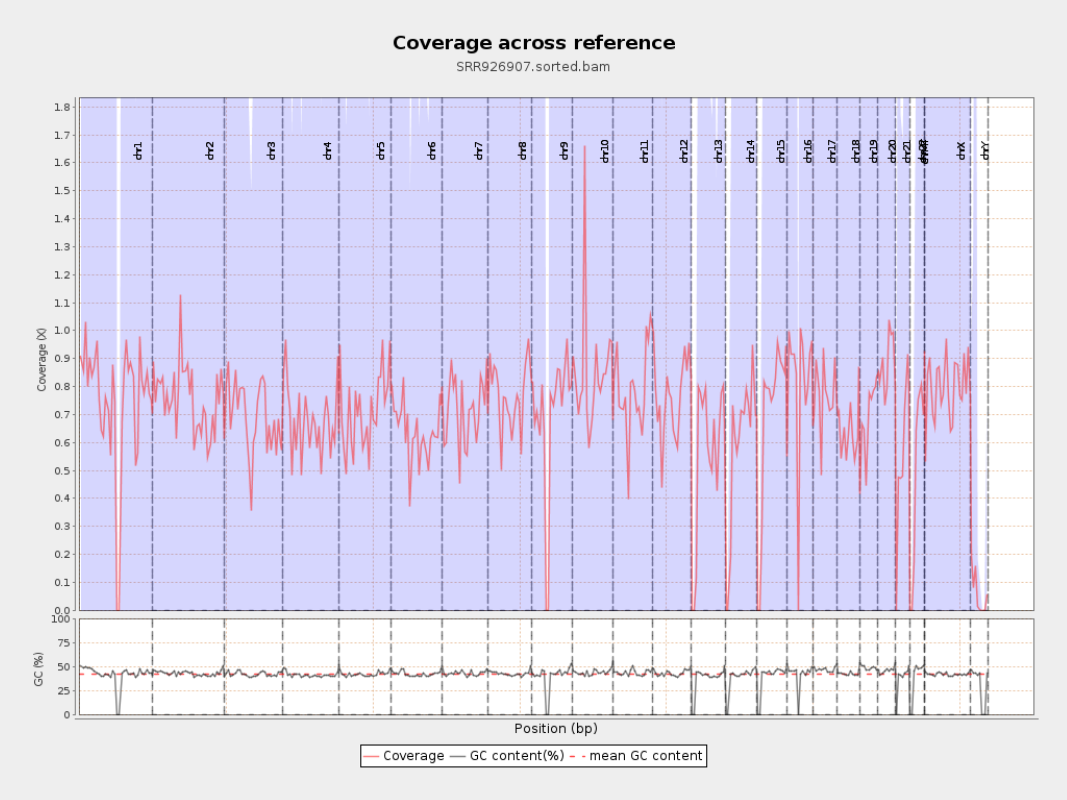
2.7. Chromosome stats

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

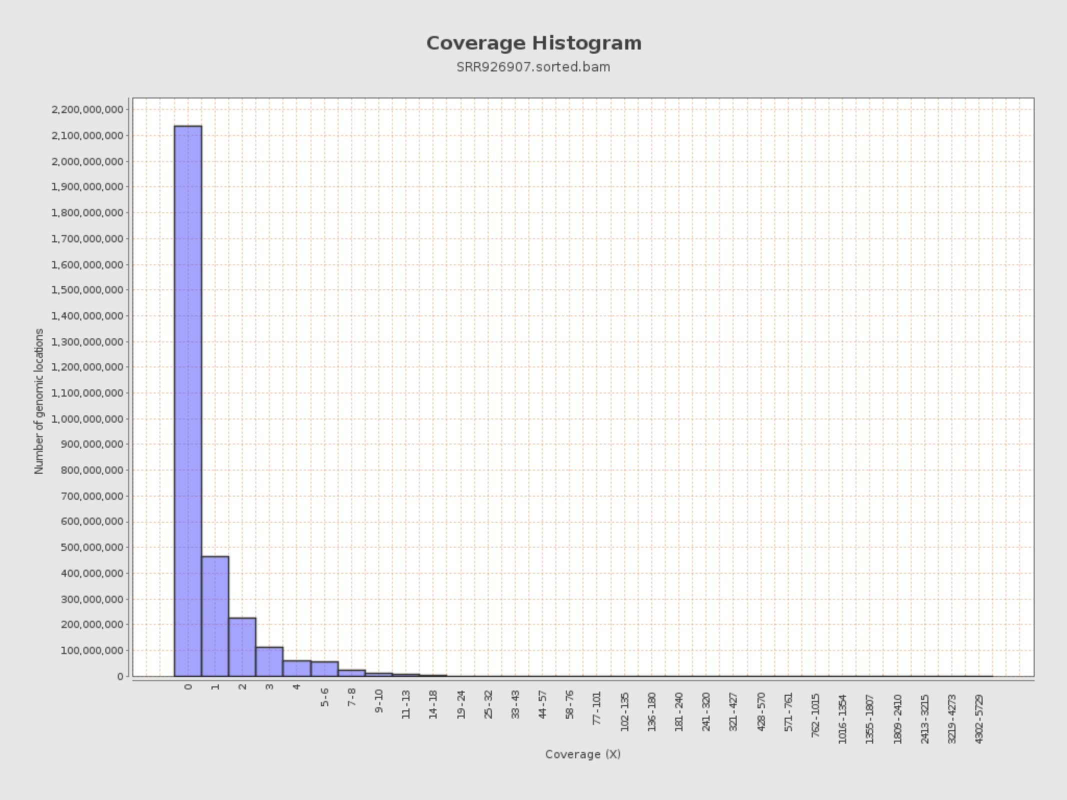
		bases	coverage	deviation
chr1	249250621	186560678	0.7485	2.3297
chr2	243199373	184089757	0.7569	3.2894
chr3	198022430	136936267	0.6915	1.5437
chr4	191154276	129302253	0.6764	1.6163
chr5	180915260	129514613	0.7159	1.4991
chr6	171115067	109139325	0.6378	1.6072
chr7	159138663	113959372	0.7161	1.7086
chr8	146364022	112262351	0.767	1.6909
chr9	141213431	97902190	0.6933	2.7567
chr10	135534747	116196011	0.8573	10.6411
chr11	135006516	106016681	0.7853	1.8652
chr12	133851895	101767548	0.7603	1.6088
chr13	115169878	64581382	0.5607	1.3255
chr14	107349540	62429220	0.5816	1.3776
chr15	102531392	69414794	0.677	1.5723
chr16	90354753	72912651	0.807	2.9949
chr17	81195210	62331089	0.7677	1.7784
chr18	78077248	49965217	0.6399	2.532
chr19	59128983	40738078	0.689	1.795
chr20	63025520	55824312	0.8857	1.8642
chr21	48129895	27642166	0.5743	1.9148
chr22	51304566	25401285	0.4951	1.3297
chrMT	16571	15375	0.9278	1.2056
chrX	155270560	123399501	0.7947	1.6769

chrY	59373566	3417204	0.0576	1.3748

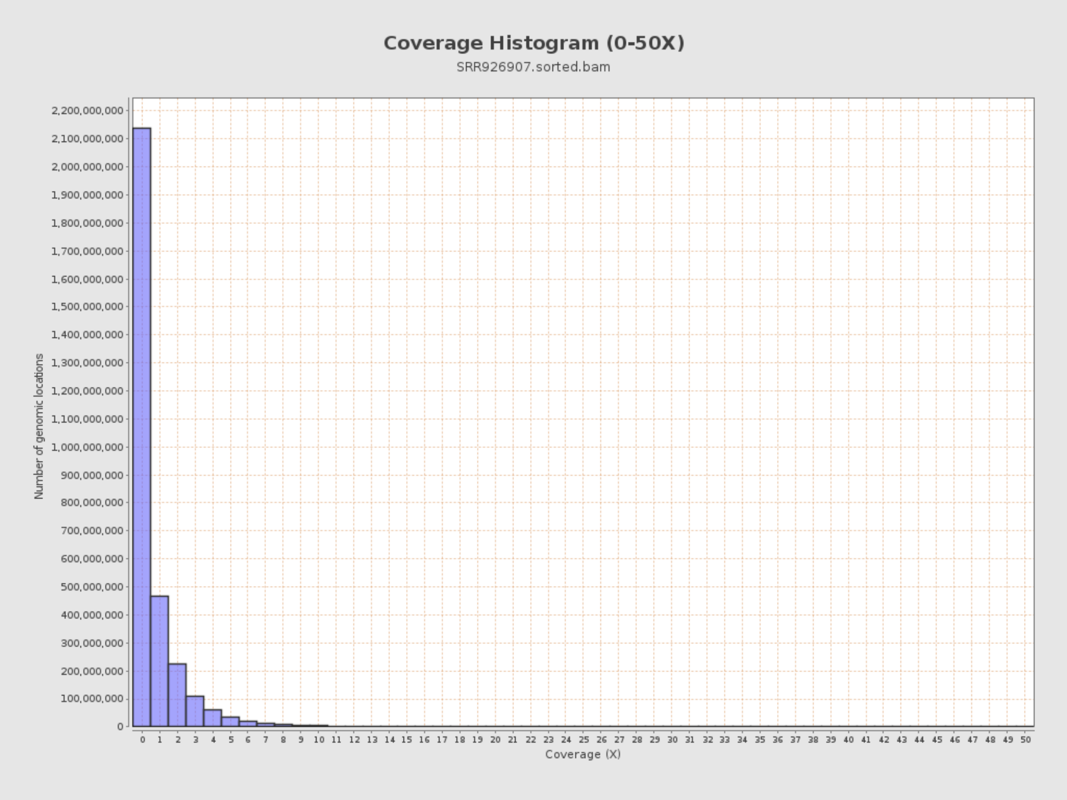
3. Results : Coverage across reference



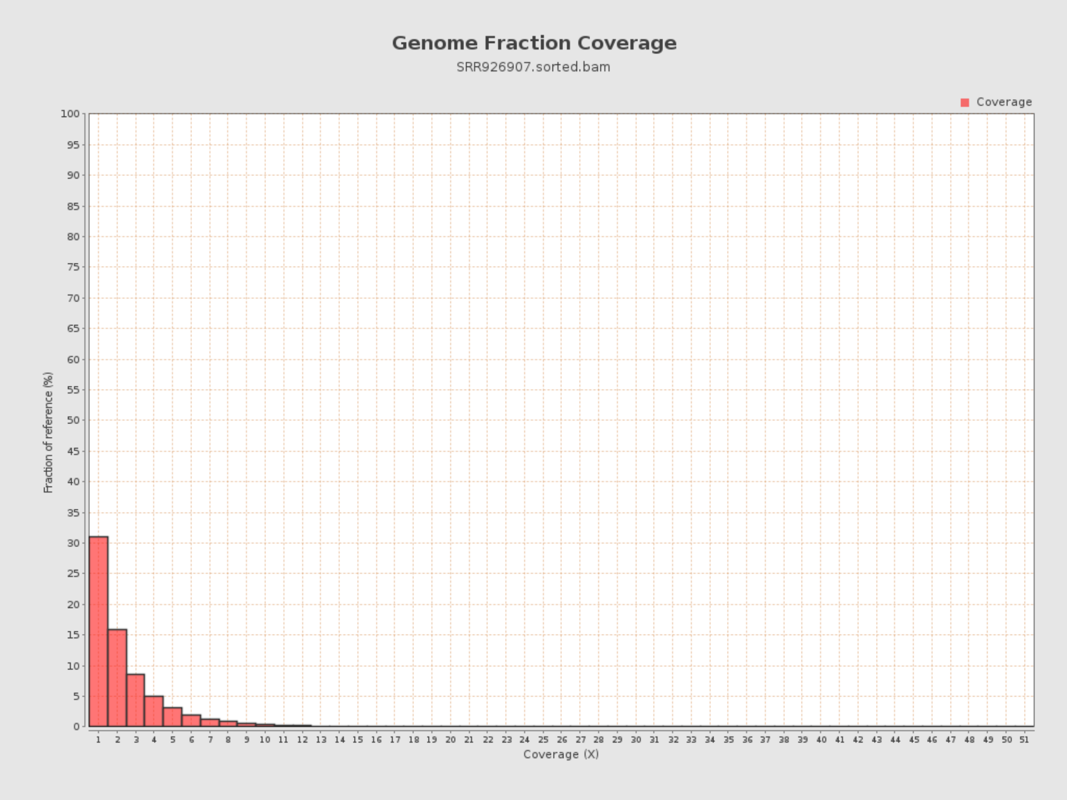
4. Results : Coverage Histogram



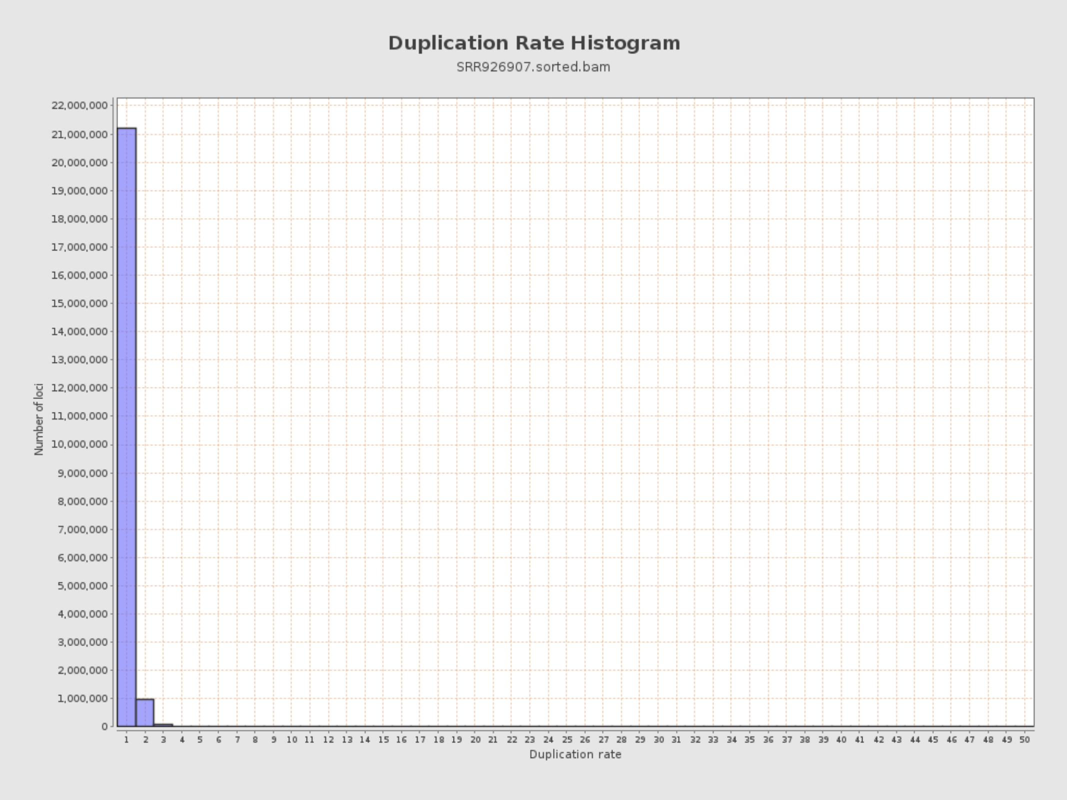
5. Results : Coverage Histogram (0-50X)



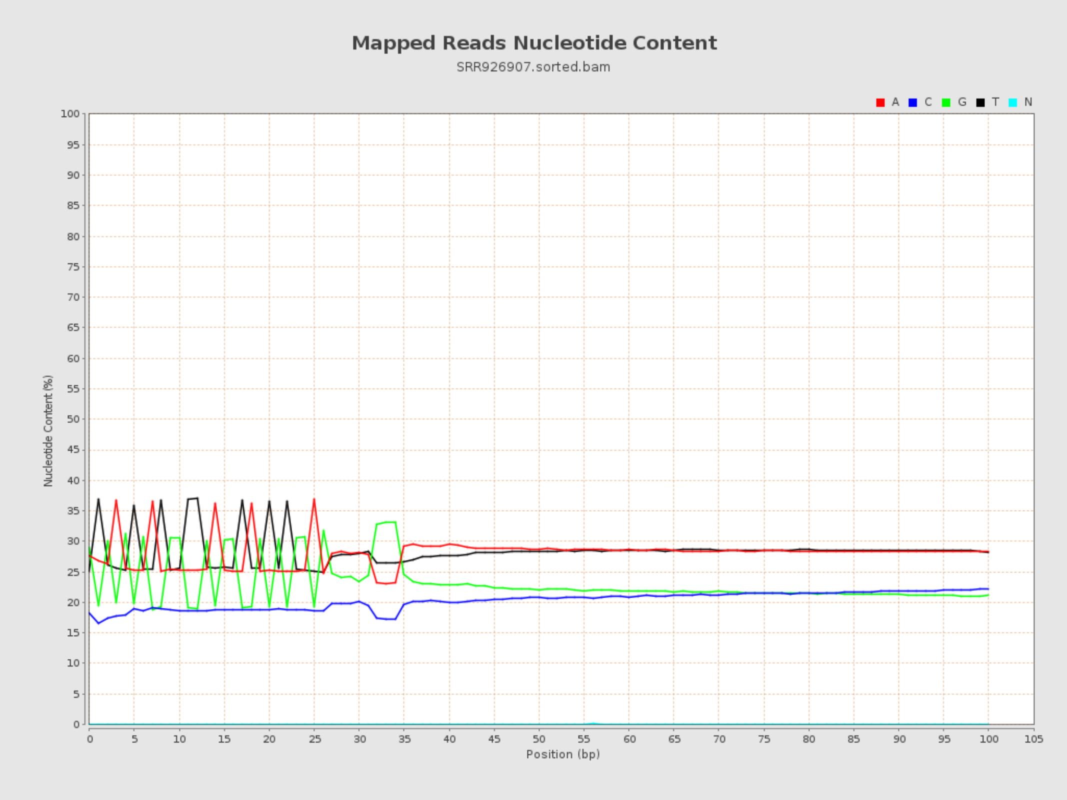
6. Results : Genome Fraction Coverage



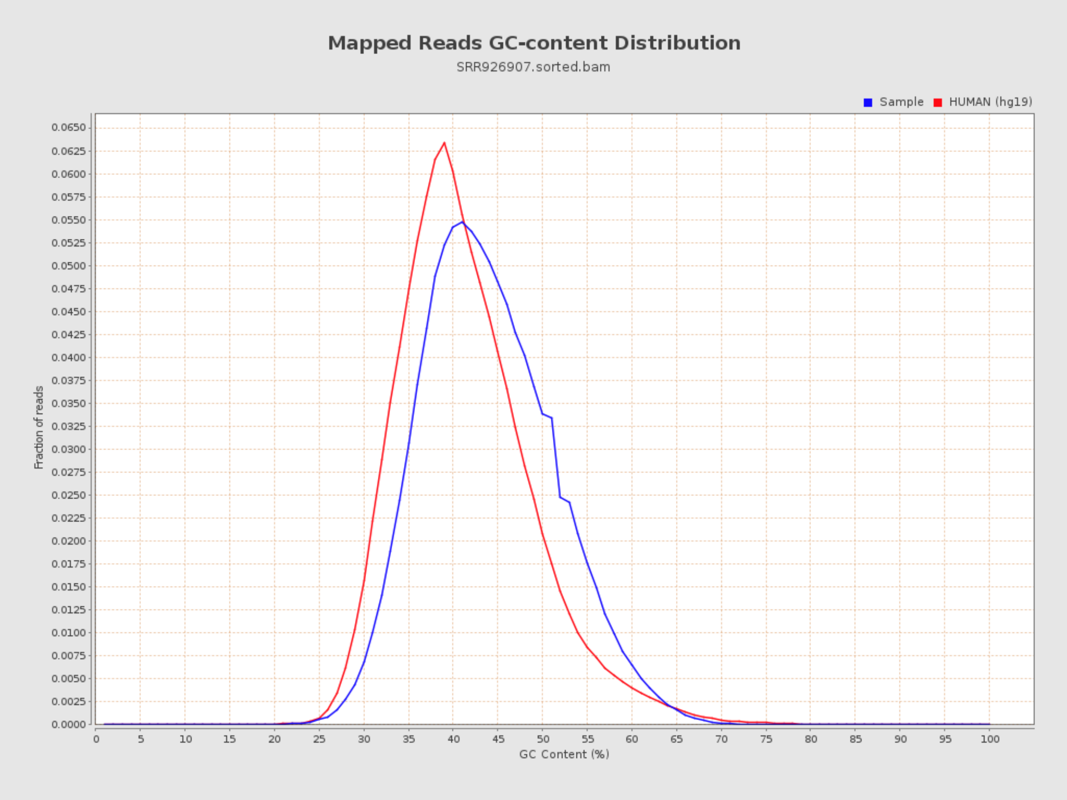
7. Results : Duplication Rate Histogram



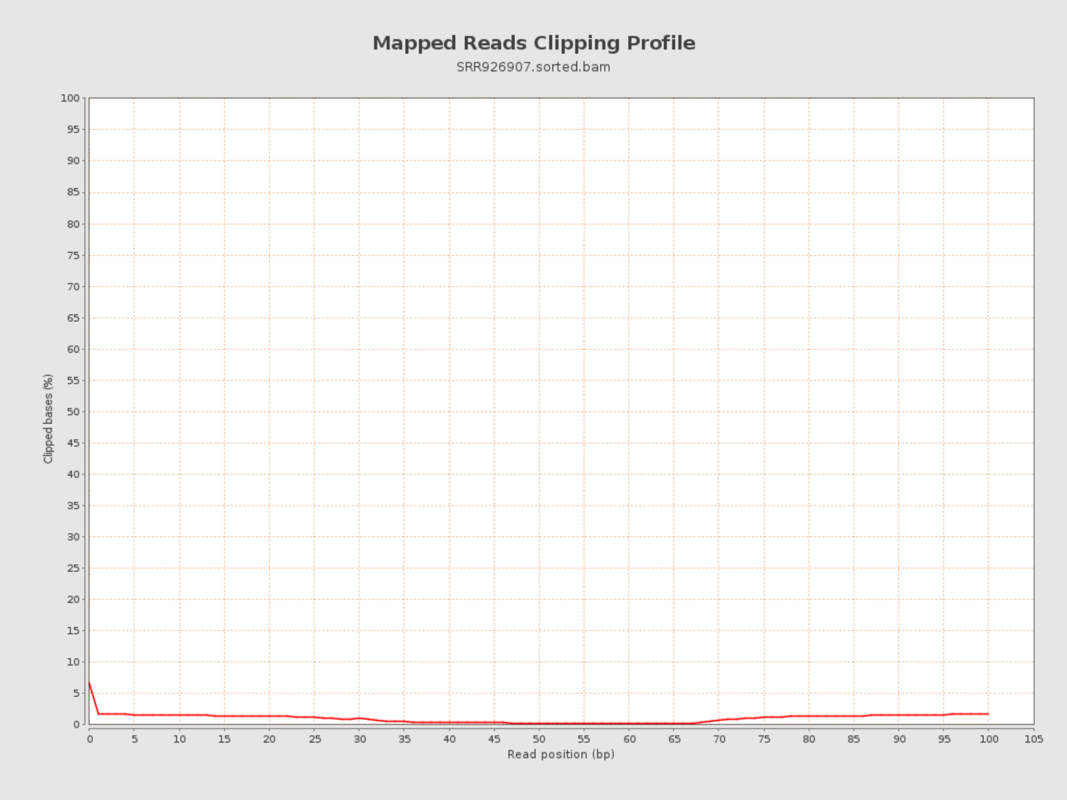
8. Results : Mapped Reads Nucleotide Content



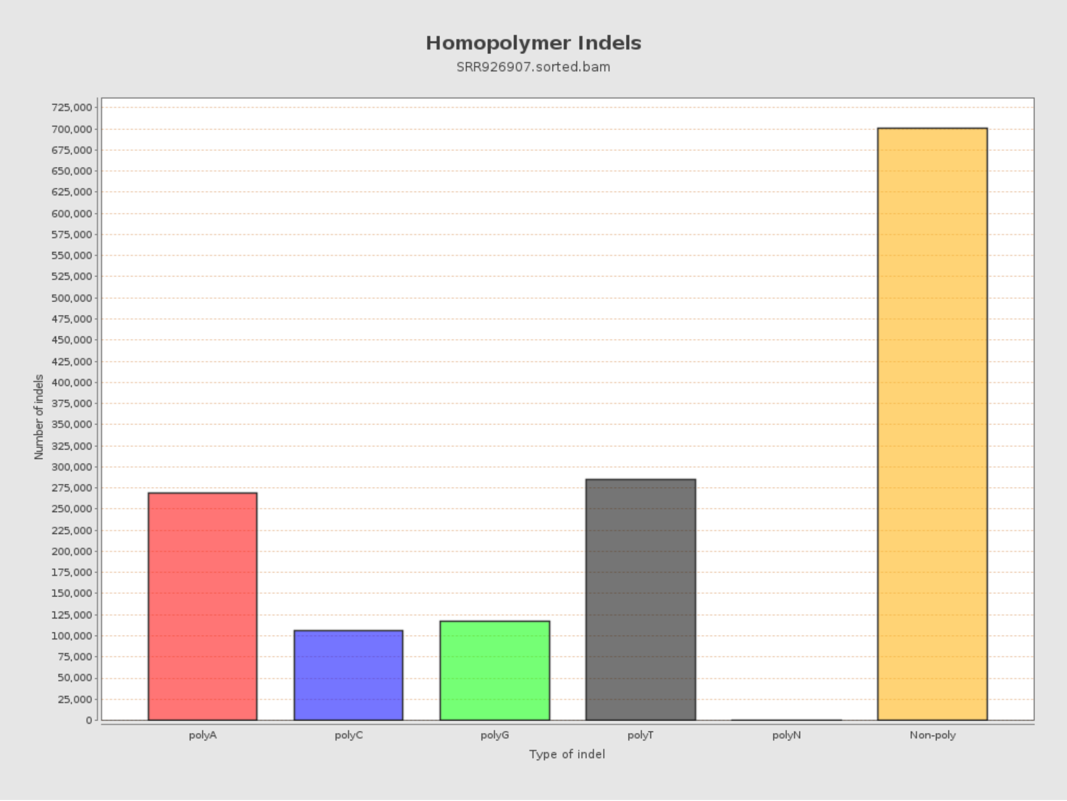
9. Results : Mapped Reads GC-content Distribution



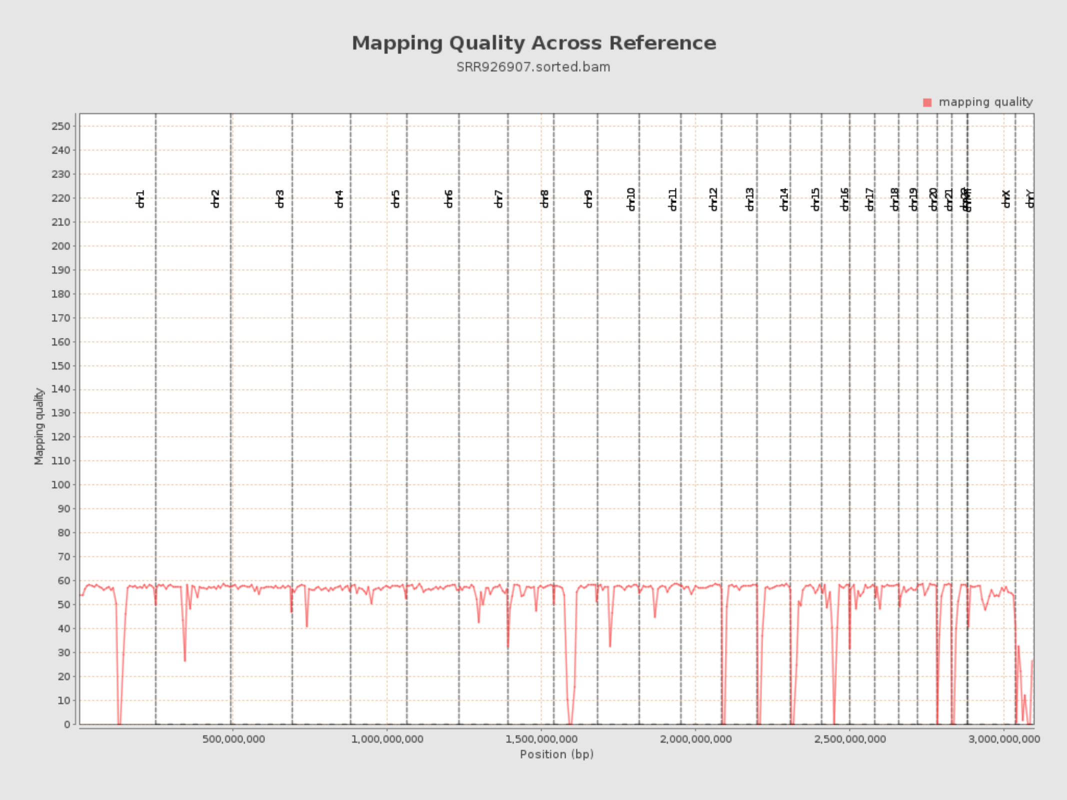
10. Results : Mapped Reads Clipping Profile



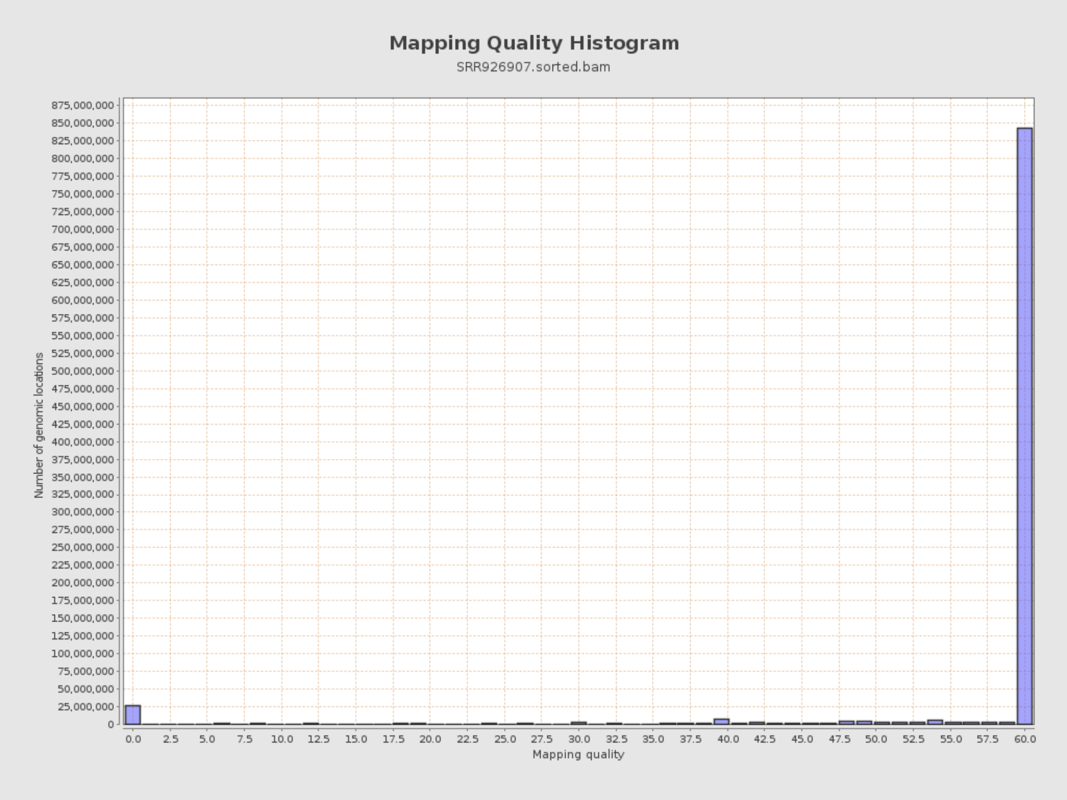
11. Results : Homopolymer Indels



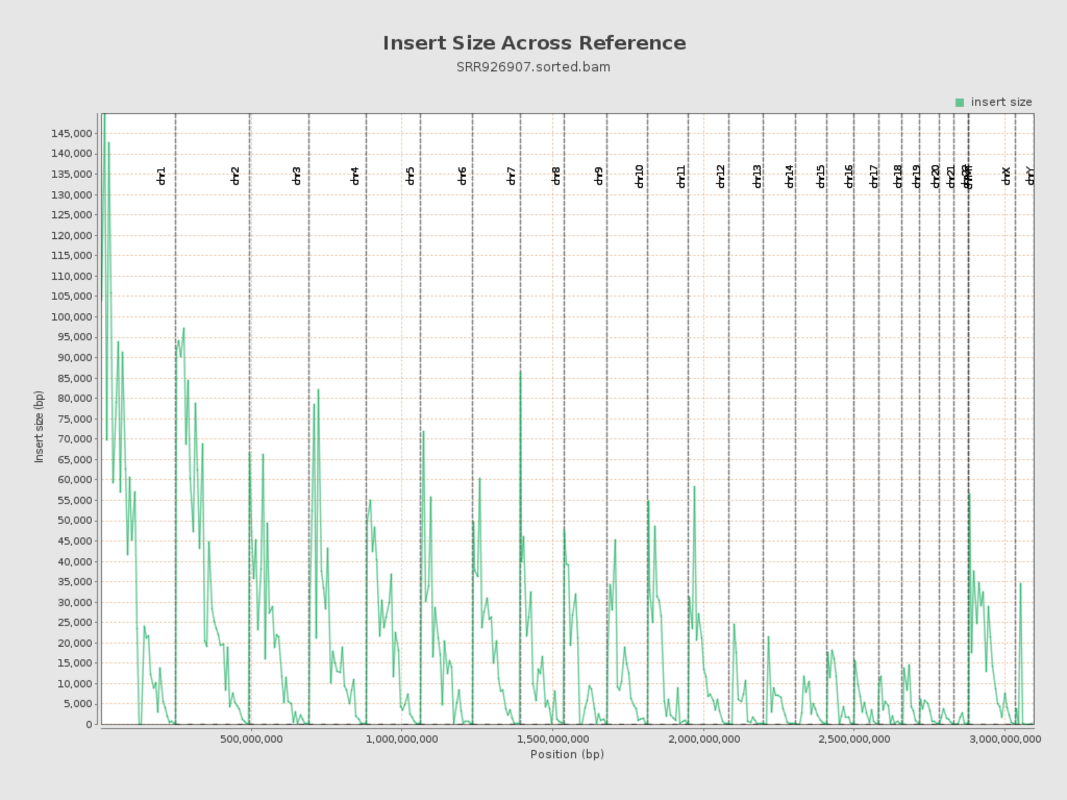
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram