Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 18:55:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926921.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_SRR926921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926921_1.fastq.gz SRR926921_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 18:55:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,402,640
Mapped reads	29,456,945 / 96.89%
Unmapped reads	945,695 / 3.11%
Mapped paired reads	29,456,945 / 96.89%
Mapped reads, first in pair	14,777,454 / 48.61%
Mapped reads, second in pair	14,679,491 / 48.28%
Mapped reads, both in pair	29,032,368 / 95.49%
Mapped reads, singletons	424,577 / 1.4%
Secondary alignments	0
Supplementary alignments	1,019,379 / 3.35%
Read min/max/mean length	30 / 101 / 102.39
Duplicated reads (estimated)	2,785,223 / 9.16%
Duplication rate	7.45%
Clipped reads	12,632,521 / 41.55%

2.2. ACGT Content

Number/percentage of A's	758,886,525 / 28.23%
Number/percentage of C's	533,663,733 / 19.85%
Number/percentage of T's	766,672,081 / 28.52%
Number/percentage of G's	629,112,787 / 23.4%
Number/percentage of N's	226,708 / 0.01%

GC Percentage	43.25%

2.3. Coverage

Mean	0.8692
Standard Deviation	3.3808

2.4. Mapping Quality

Mean Mapping Quality	52.44

2.5. Insert size

Mean	376,698.99
Standard Deviation	6,023,847.53
P25/Median/P75	138 / 178 / 240

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	25,629,654
Insertions	459,244
Mapped reads with at least one insertion	1.53%
Deletions	1,444,830
Mapped reads with at least one deletion	4.78%
Homopolymer indels	51.93%

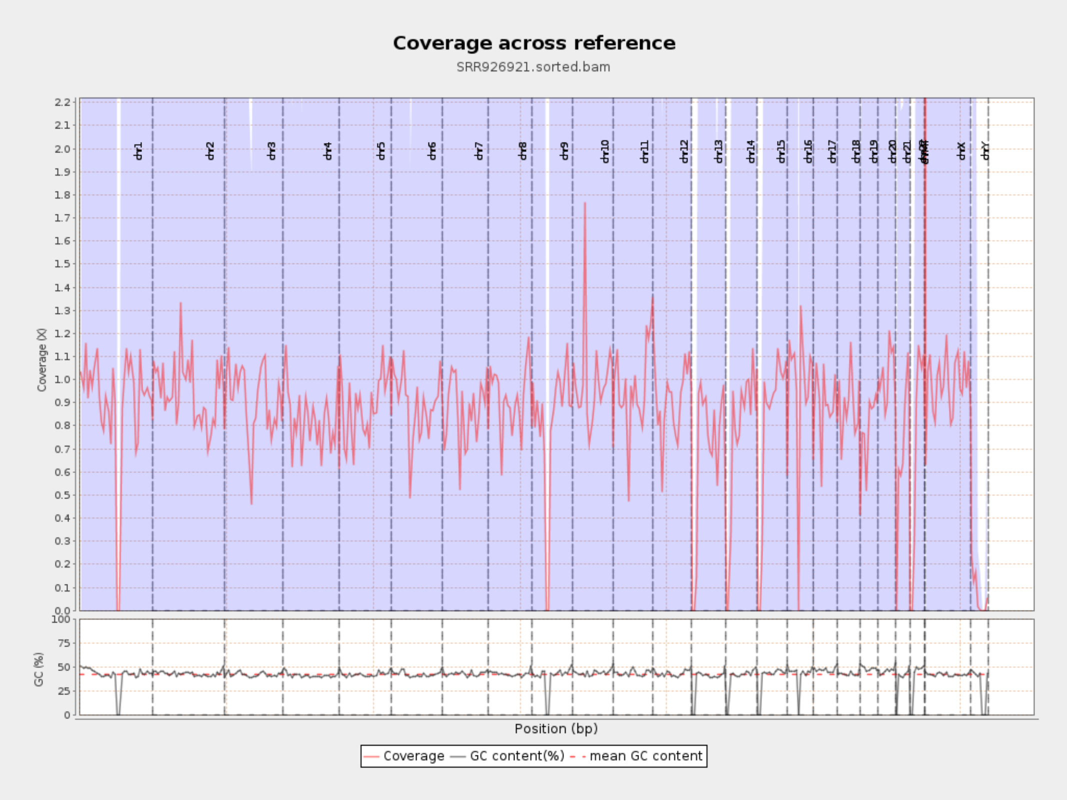
2.7. Chromosome stats

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

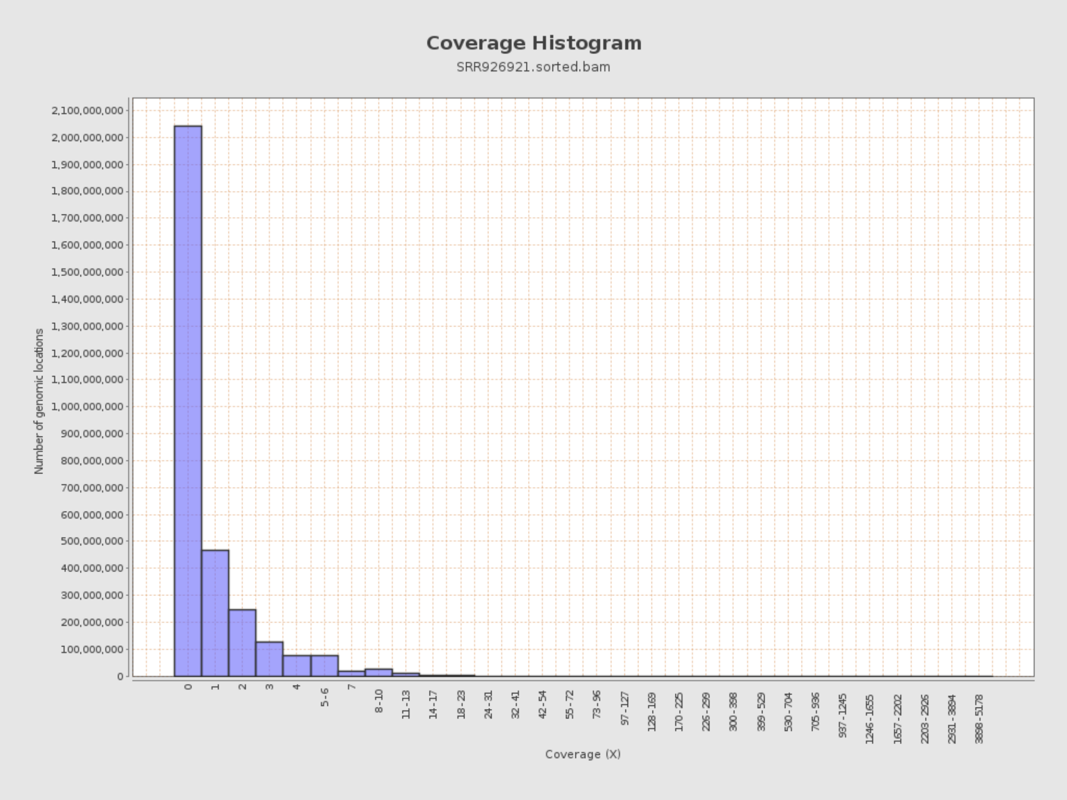
		bases	coverage	deviation
chr1	249250621	222969794	0.8946	2.7306
chr2	243199373	231146631	0.9504	4.5068
chr3	198022430	180614410	0.9121	1.9575
chr4	191154276	158651174	0.83	2.0972
chr5	180915260	161128795	0.8906	1.8551
chr6	171115067	153501409	0.8971	2.1704
chr7	159138663	137971596	0.867	2.2703
chr8	146364022	135058512	0.9228	2.0427
chr9	141213431	114011360	0.8074	3.1196
chr10	135534747	135790101	1.0019	10.5927
chr11	135006516	128798731	0.954	2.4104
chr12	133851895	121987668	0.9114	2.2314
chr13	115169878	79569603	0.6909	1.6911
chr14	107349540	80104372	0.7462	1.7524
chr15	102531392	81100481	0.791	1.8686
chr16	90354753	86495454	0.9573	4.608
chr17	81195210	72445708	0.8922	2.0856
chr18	78077248	70162927	0.8986	3.1234
chr19	59128983	46788375	0.7913	2.1156
chr20	63025520	64363571	1.0212	2.1749
chr21	48129895	34195118	0.7105	2.5259
chr22	51304566	36634138	0.7141	1.872
chrMT	16571	1238061	74.7125	49.5866
chrX	155270560	151847898	0.978	2.0575

chrY	59373566	4108394	0.0692	1.5715

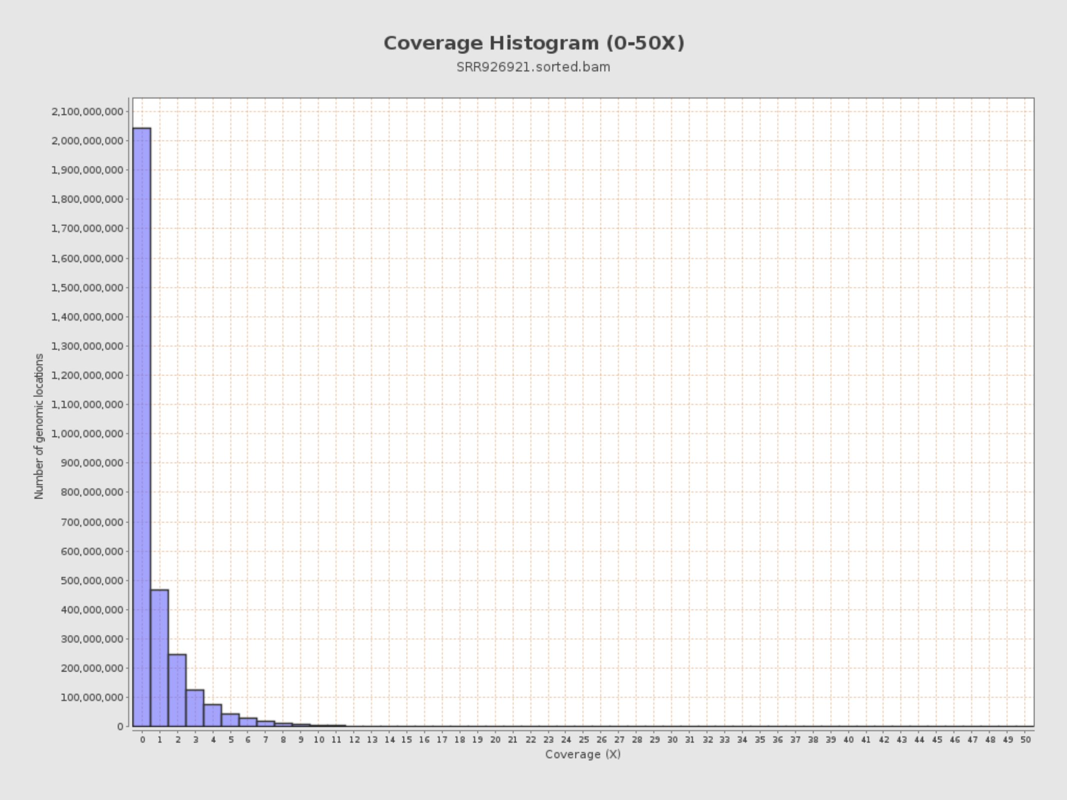
3. Results : Coverage across reference



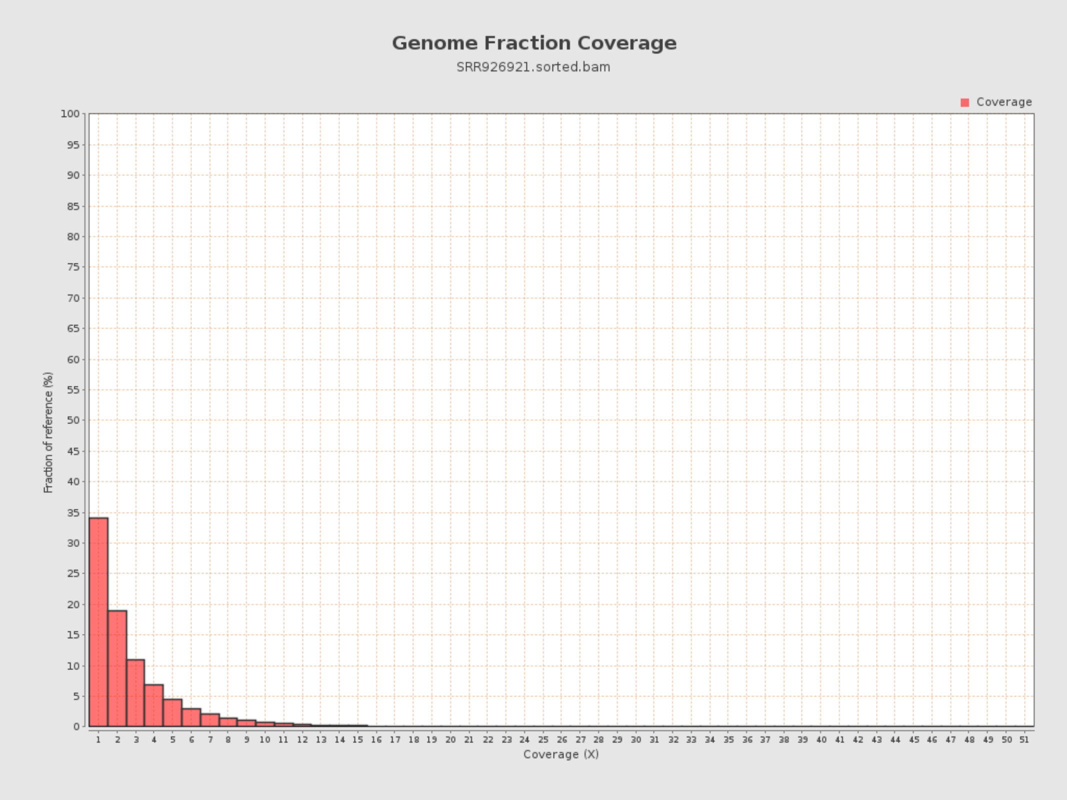
4. Results : Coverage Histogram



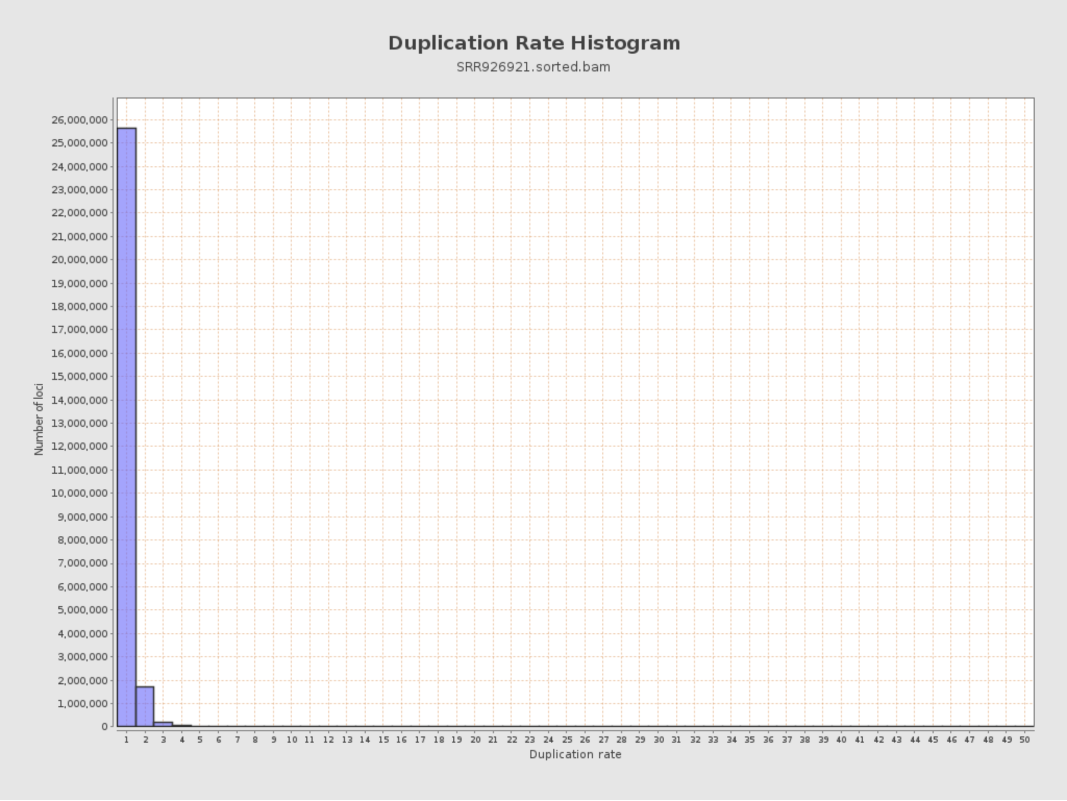
5. Results : Coverage Histogram (0-50X)



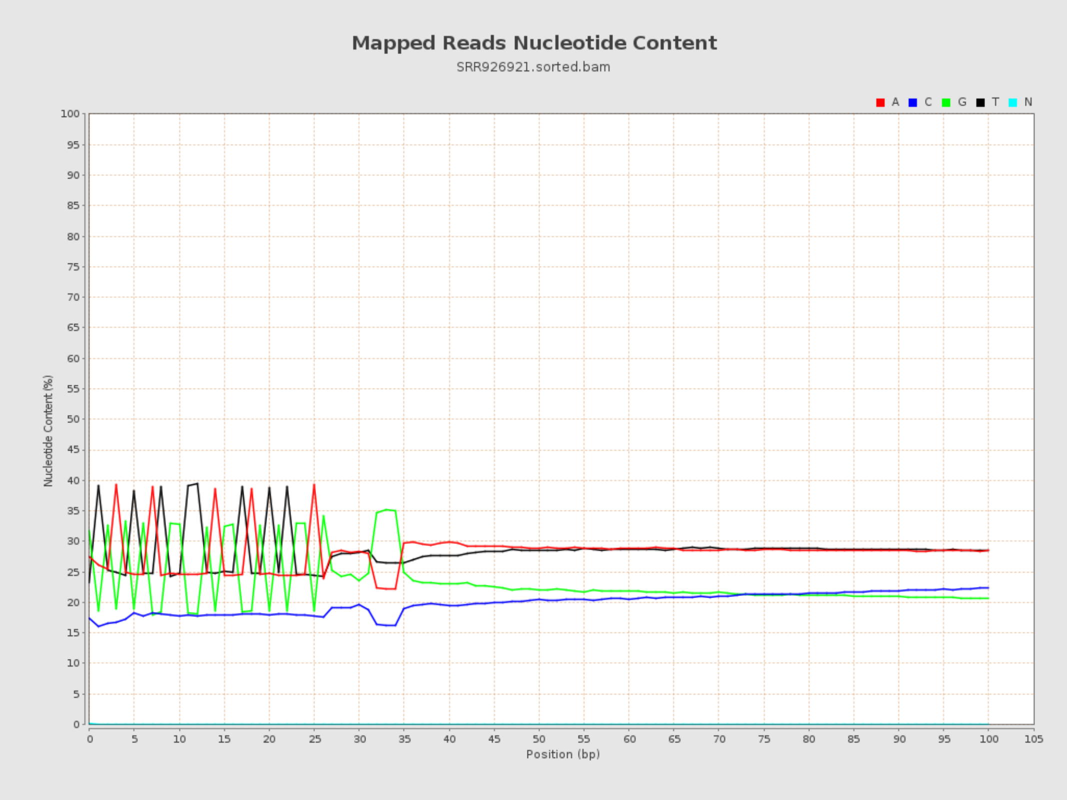
6. Results : Genome Fraction Coverage



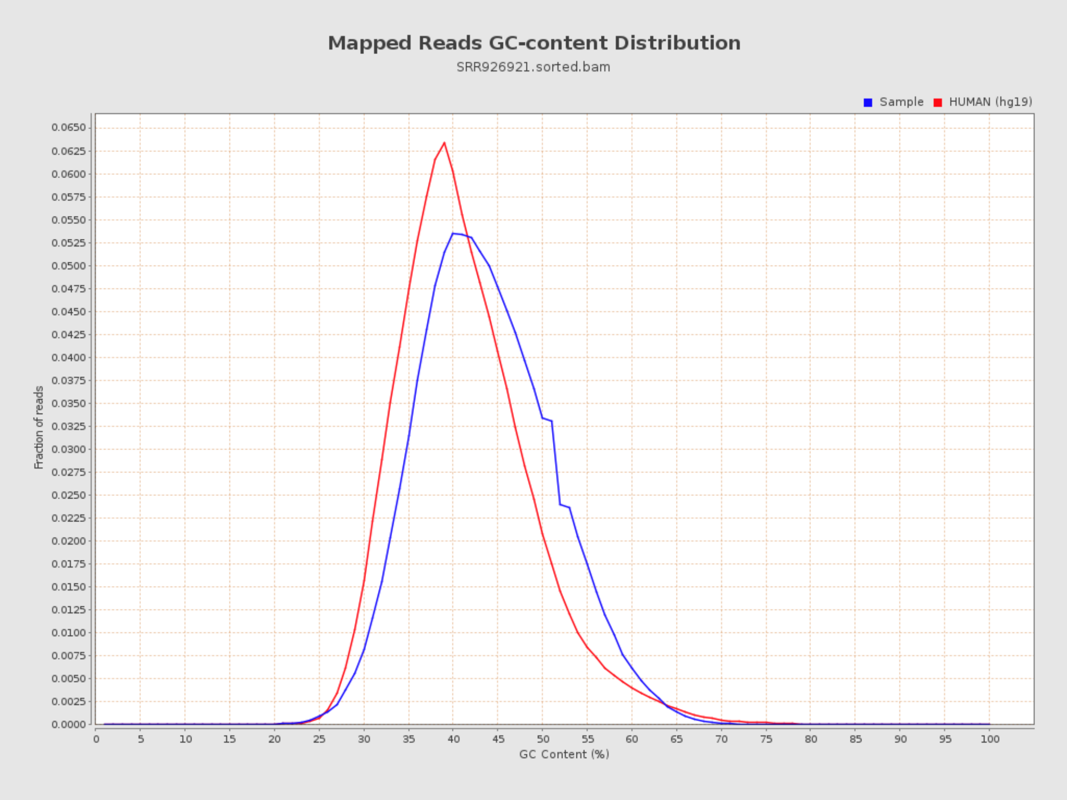
7. Results : Duplication Rate Histogram



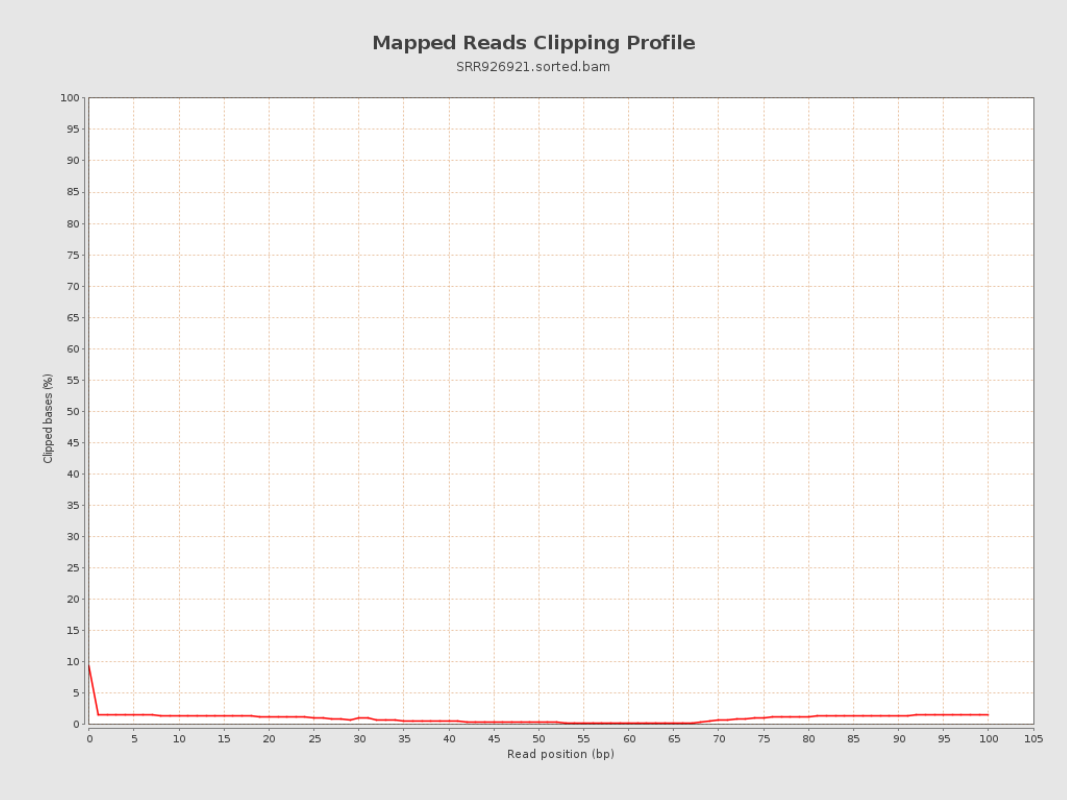
8. Results : Mapped Reads Nucleotide Content



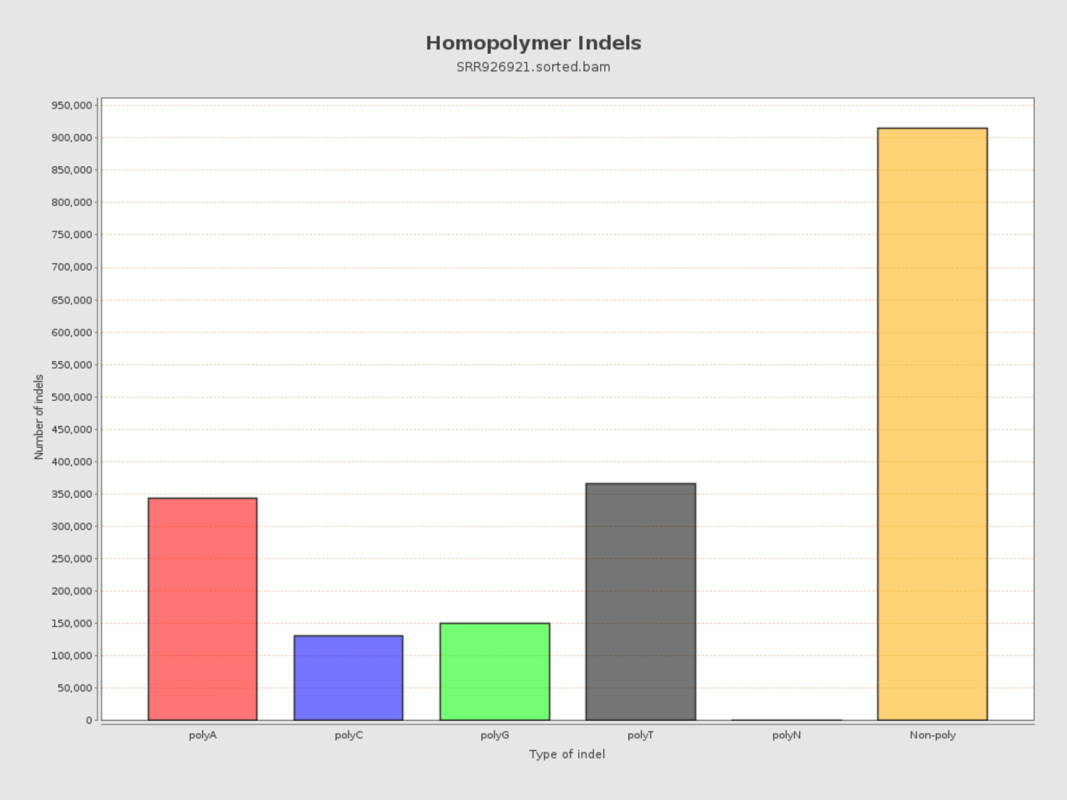
9. Results : Mapped Reads GC-content Distribution



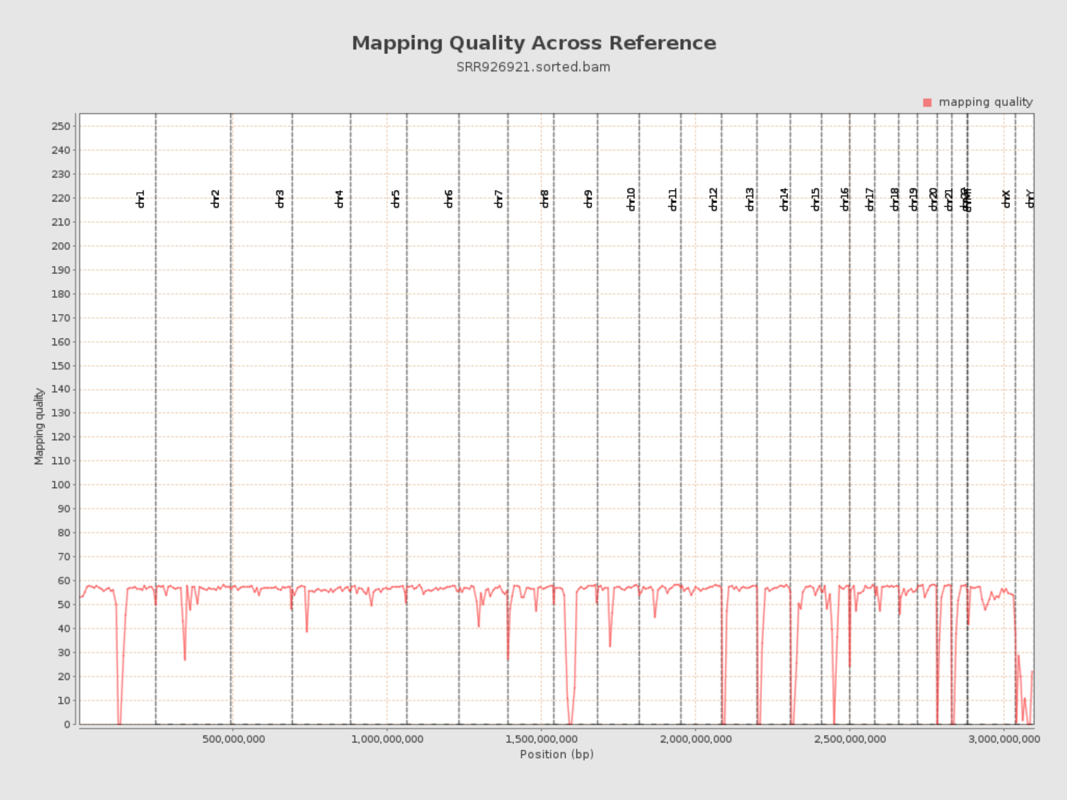
10. Results : Mapped Reads Clipping Profile



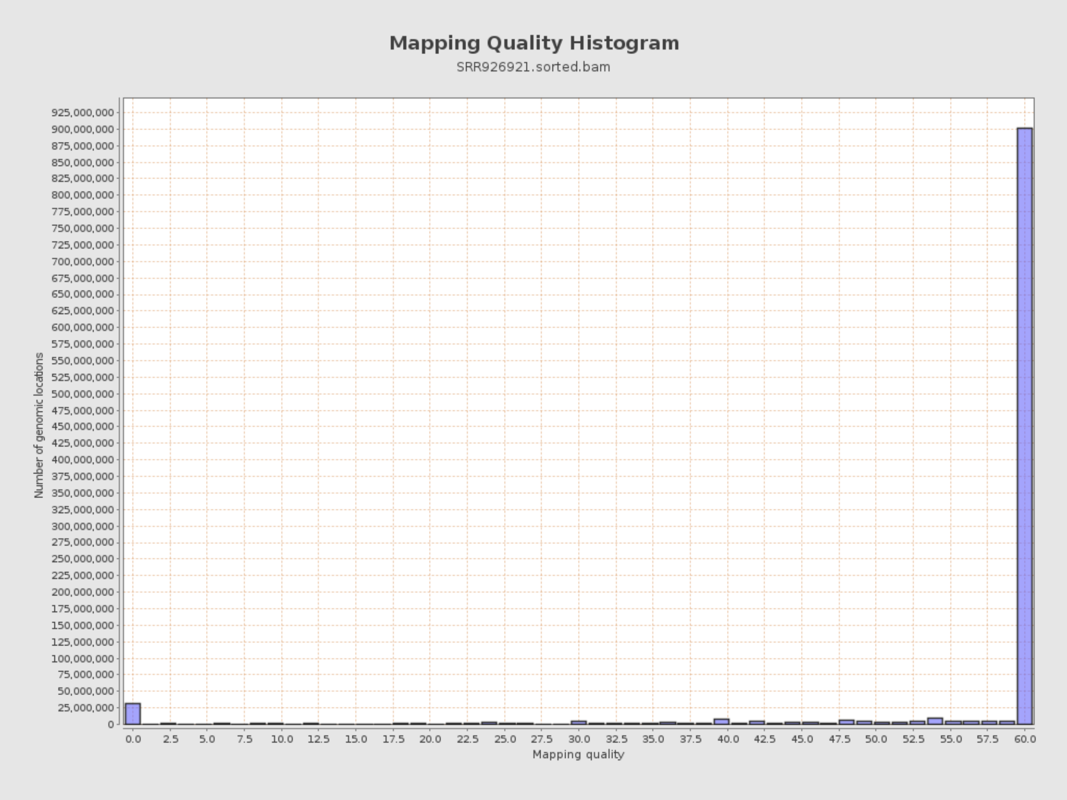
11. Results : Homopolymer Indels



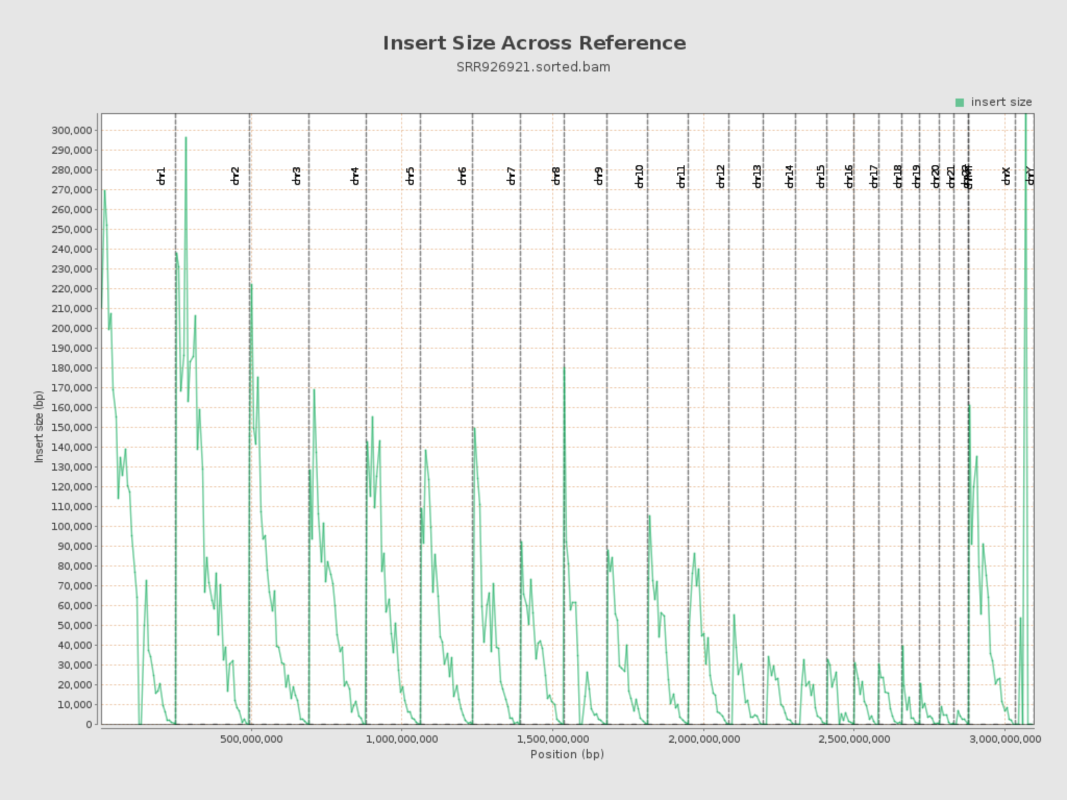
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram