Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 23:24:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926939.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_SRR926939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926939_1.fastq.gz SRR926939_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 23:24:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,091,826
Mapped reads	6,009,836 / 98.65%
Unmapped reads	81,990 / 1.35%
Mapped paired reads	6,009,836 / 98.65%
Mapped reads, first in pair	3,015,004 / 49.49%
Mapped reads, second in pair	2,994,832 / 49.16%
Mapped reads, both in pair	5,962,886 / 97.88%
Mapped reads, singletons	46,950 / 0.77%
Secondary alignments	0
Supplementary alignments	43,609 / 0.72%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	201,451 / 3.31%
Duplication rate	2.82%
Clipped reads	1,486,548 / 24.4%

2.2. ACGT Content

Number/percentage of A's	163,039,680 / 28.72%
Number/percentage of C's	113,054,828 / 19.92%
Number/percentage of T's	164,665,721 / 29.01%
Number/percentage of G's	126,706,535 / 22.32%
Number/percentage of N's	124,290 / 0.02%

GC Percentage	42.24%

2.3. Coverage

Mean	0.1835
Standard Deviation	0.7967

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	72,517.58
Standard Deviation	2,617,361.8
P25/Median/P75	150 / 192 / 255

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	5,102,085
Insertions	89,952
Mapped reads with at least one insertion	1.47%
Deletions	303,822
Mapped reads with at least one deletion	4.92%
Homopolymer indels	53.37%

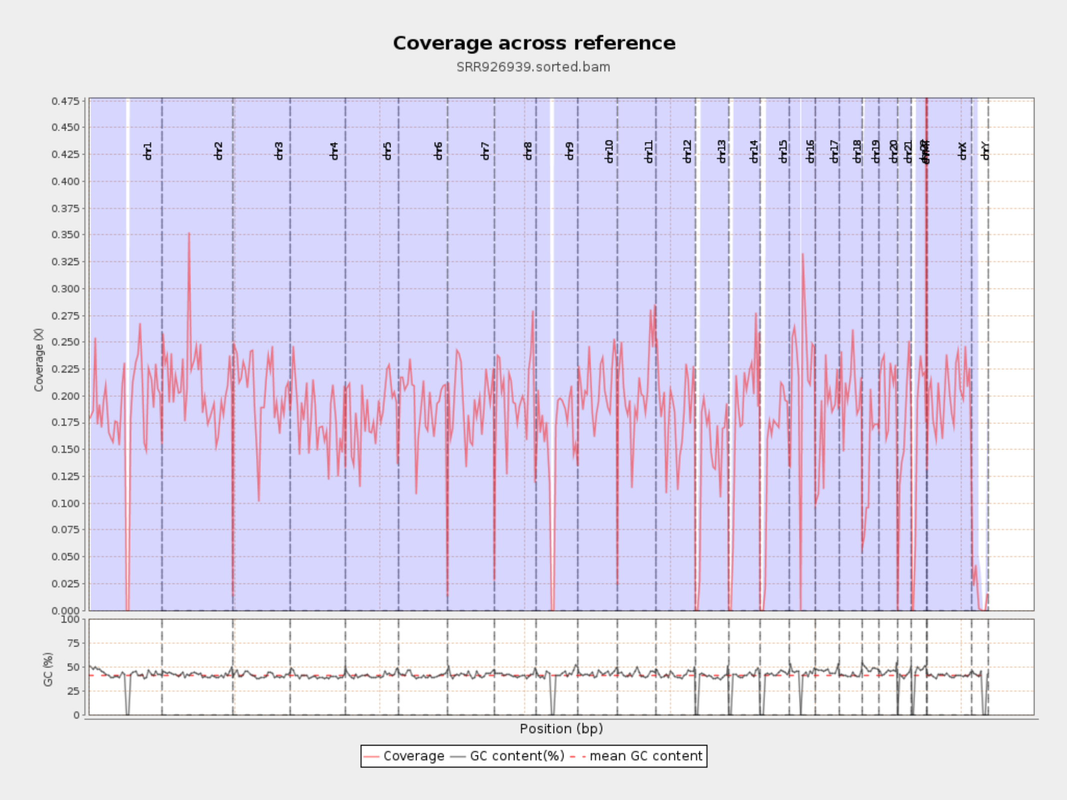
2.7. Chromosome stats

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

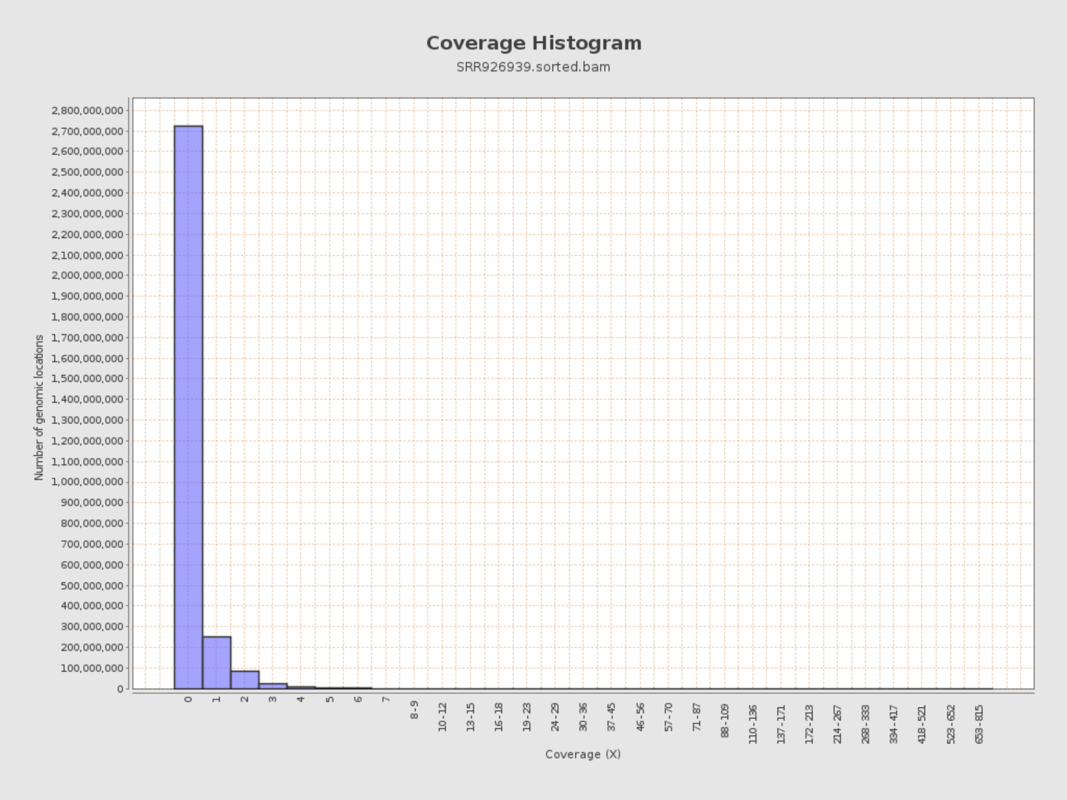
		bases	coverage	deviation
chr1	249250621	46071242	0.1848	1.0158
chr2	243199373	51508566	0.2118	1.2973
chr3	198022430	40153122	0.2028	0.6076
chr4	191154276	34159400	0.1787	0.681
chr5	180915260	32940168	0.1821	0.5754
chr6	171115067	32458943	0.1897	0.6596
chr7	159138663	30572770	0.1921	0.6535
chr8	146364022	29031352	0.1984	0.6336
chr9	141213431	22270647	0.1577	0.9176
chr10	135534747	28215644	0.2082	0.9849
chr11	135006516	27636559	0.2047	0.7278
chr12	133851895	24845923	0.1856	0.5866
chr13	115169878	15706405	0.1364	0.4932
chr14	107349540	18573866	0.173	0.5715
chr15	102531392	14762170	0.144	0.5187
chr16	90354753	20016857	0.2215	1.2461
chr17	81195210	14393827	0.1773	0.6435
chr18	78077248	16191005	0.2074	0.9906
chr19	59128983	8140814	0.1377	0.6687
chr20	63025520	13154681	0.2087	0.6476
chr21	48129895	7641638	0.1588	0.6465
chr22	51304566	7595570	0.148	0.5437
chrMT	16571	36665	2.2126	2.4511
chrX	155270560	31086937	0.2002	0.6283

chrY	59373566	853233	0.0144	0.4772

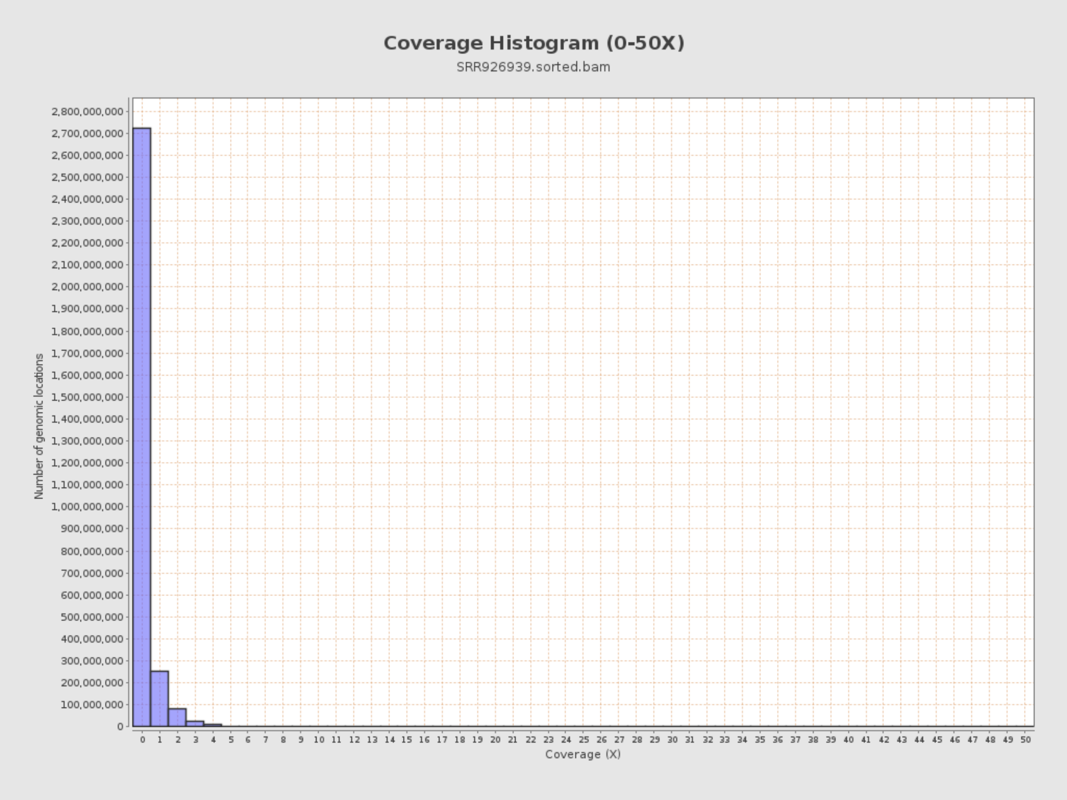
3. Results : Coverage across reference



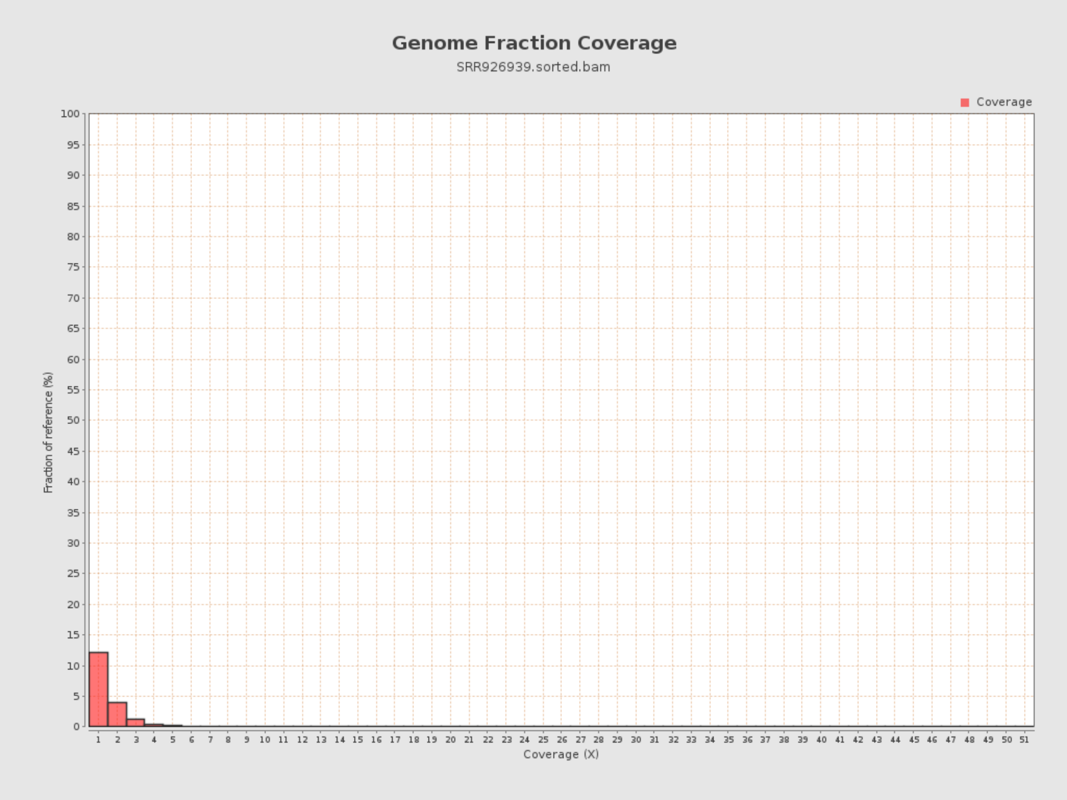
4. Results : Coverage Histogram



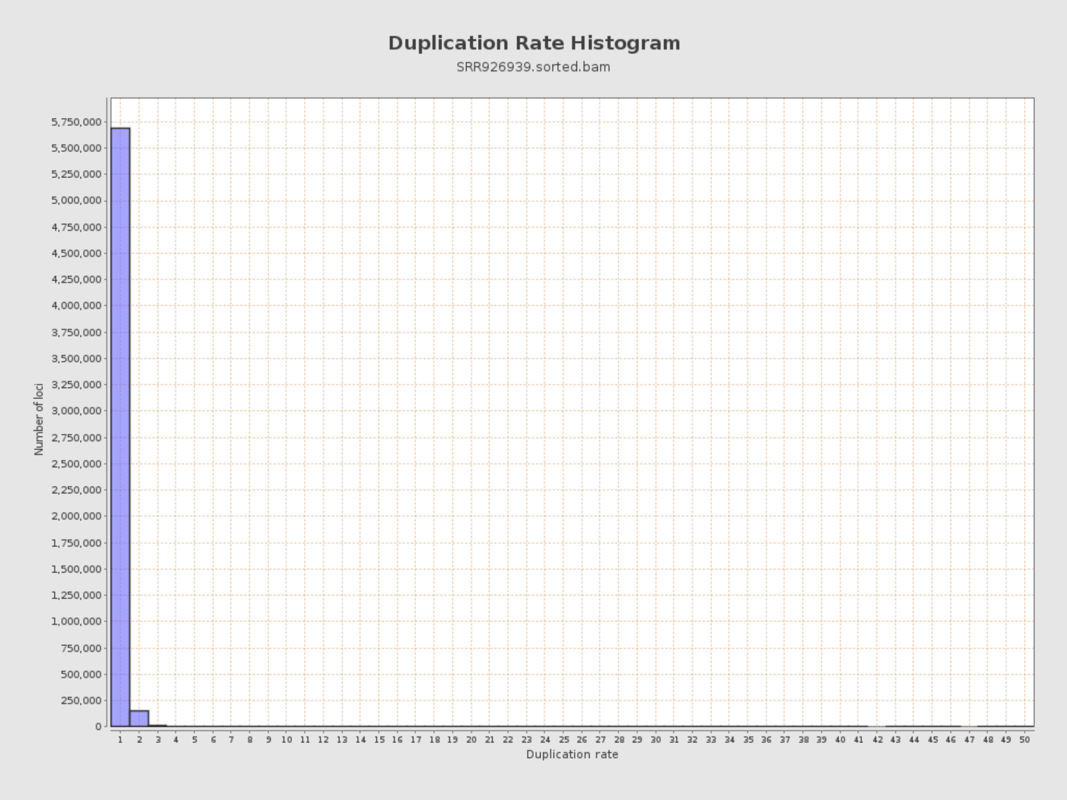
5. Results : Coverage Histogram (0-50X)



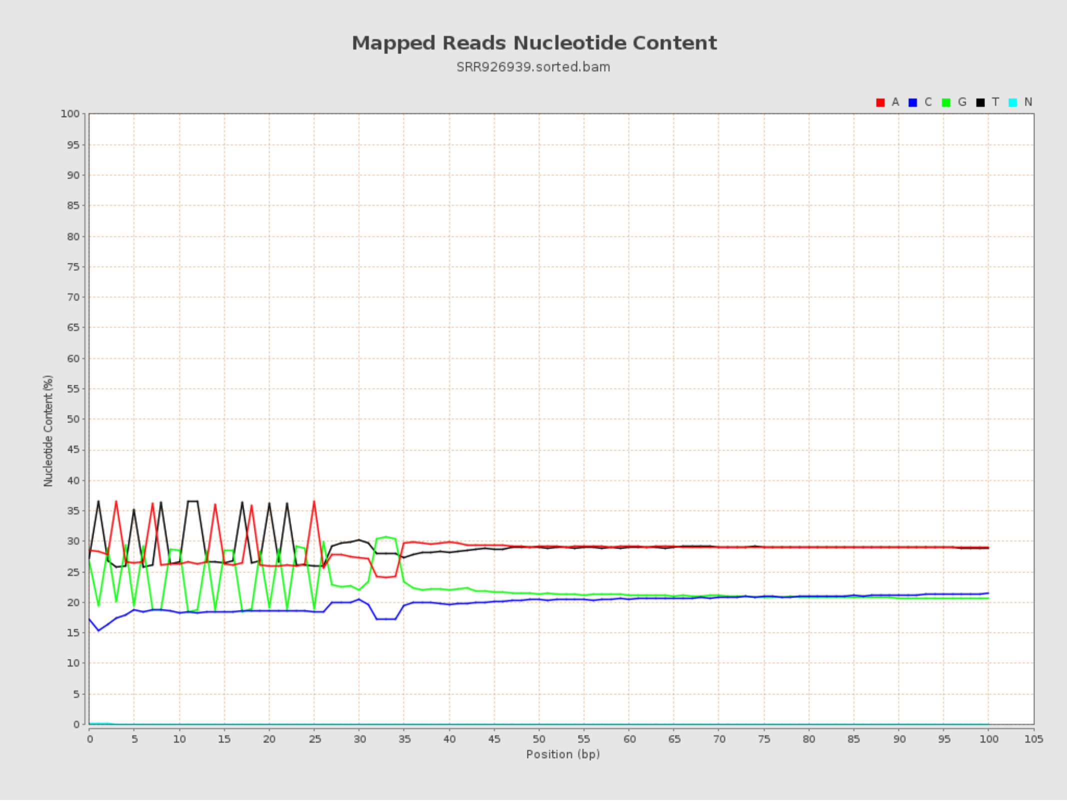
6. Results : Genome Fraction Coverage



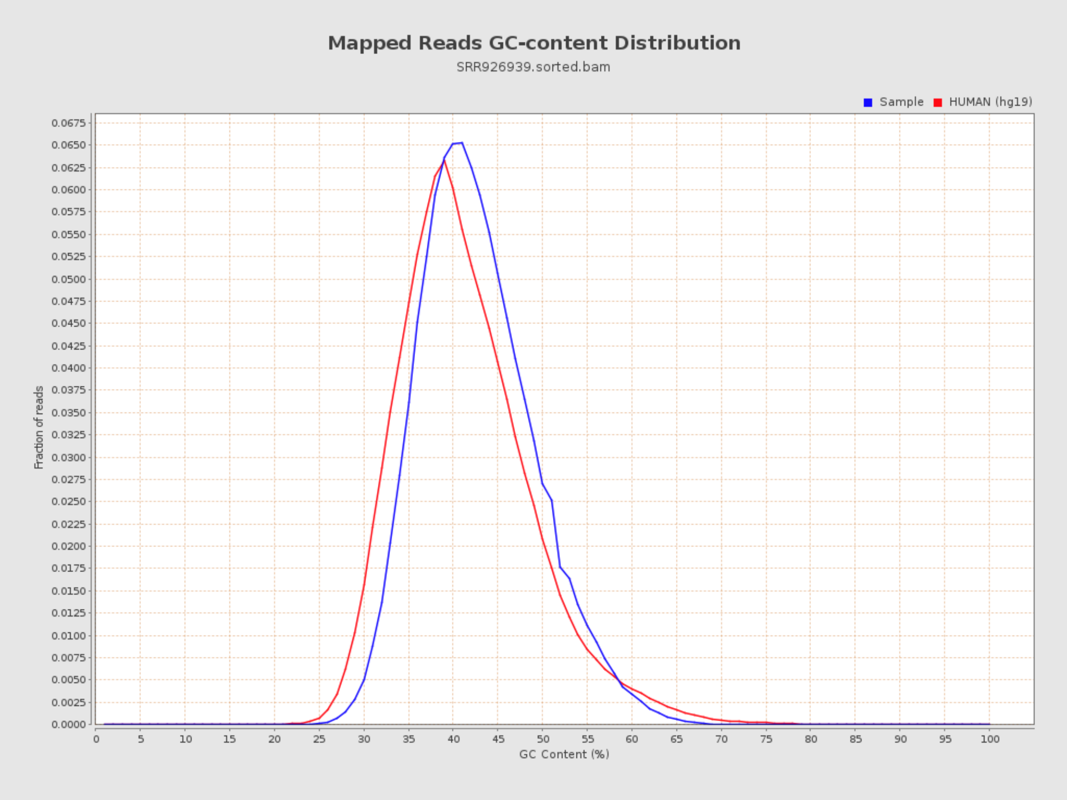
7. Results : Duplication Rate Histogram



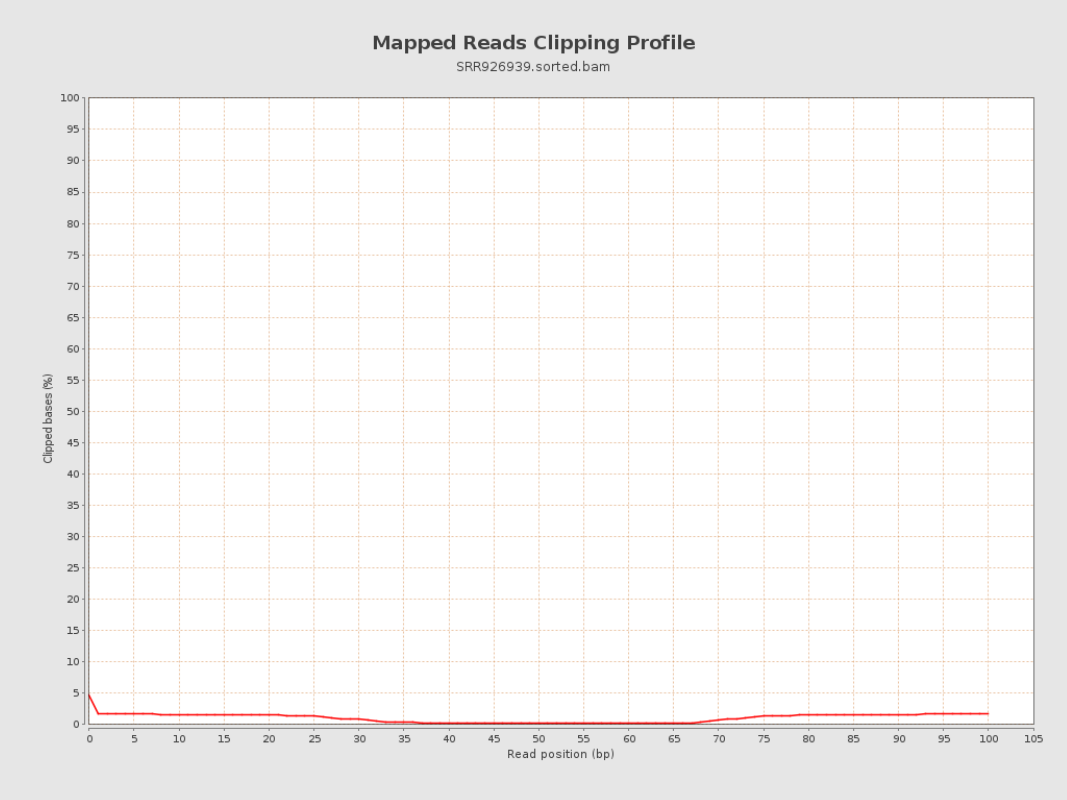
8. Results : Mapped Reads Nucleotide Content



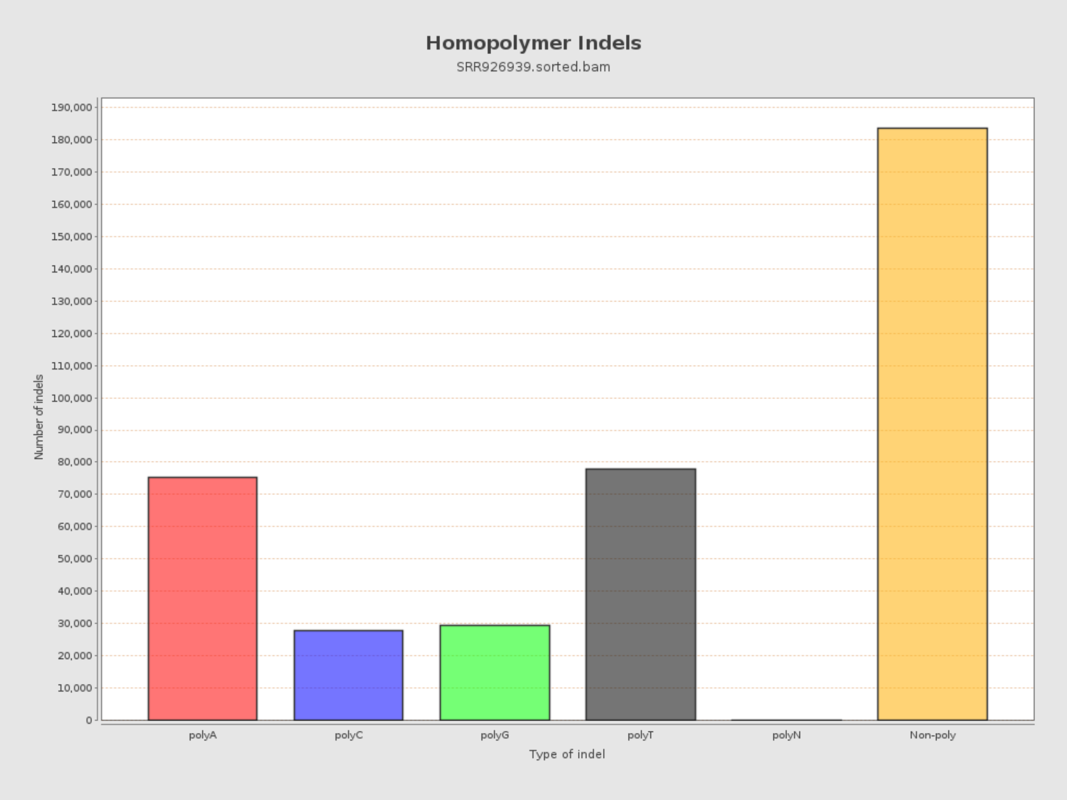
9. Results : Mapped Reads GC-content Distribution



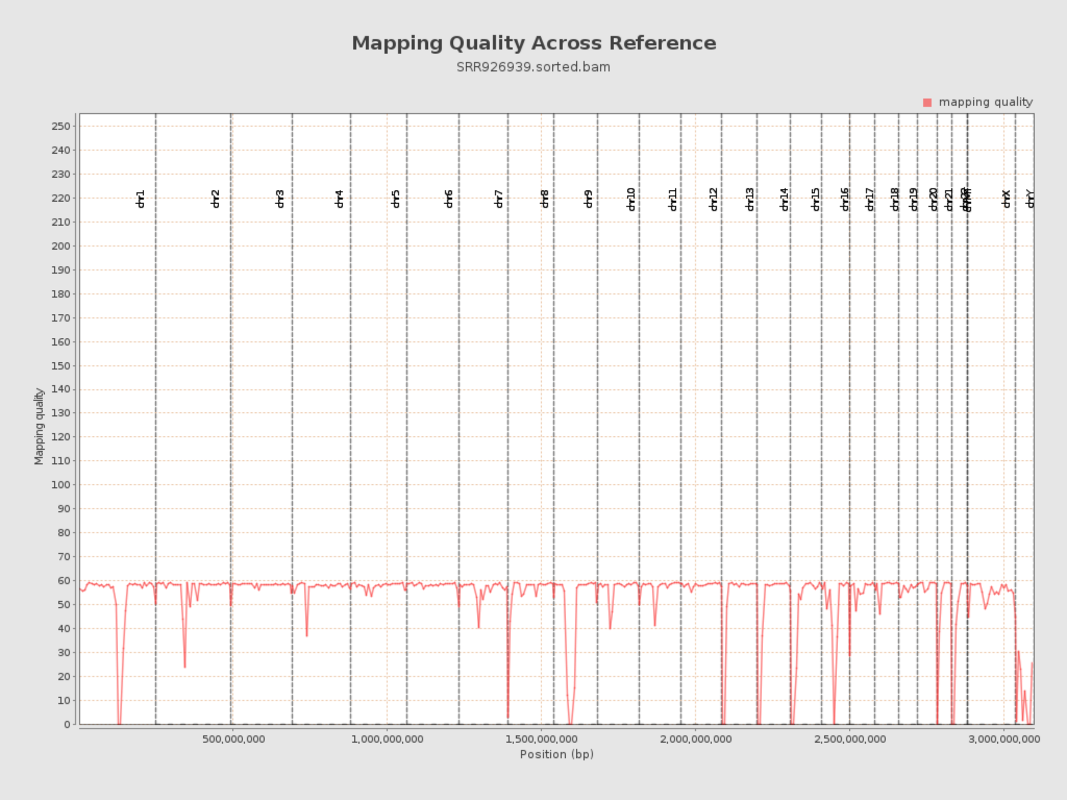
10. Results : Mapped Reads Clipping Profile



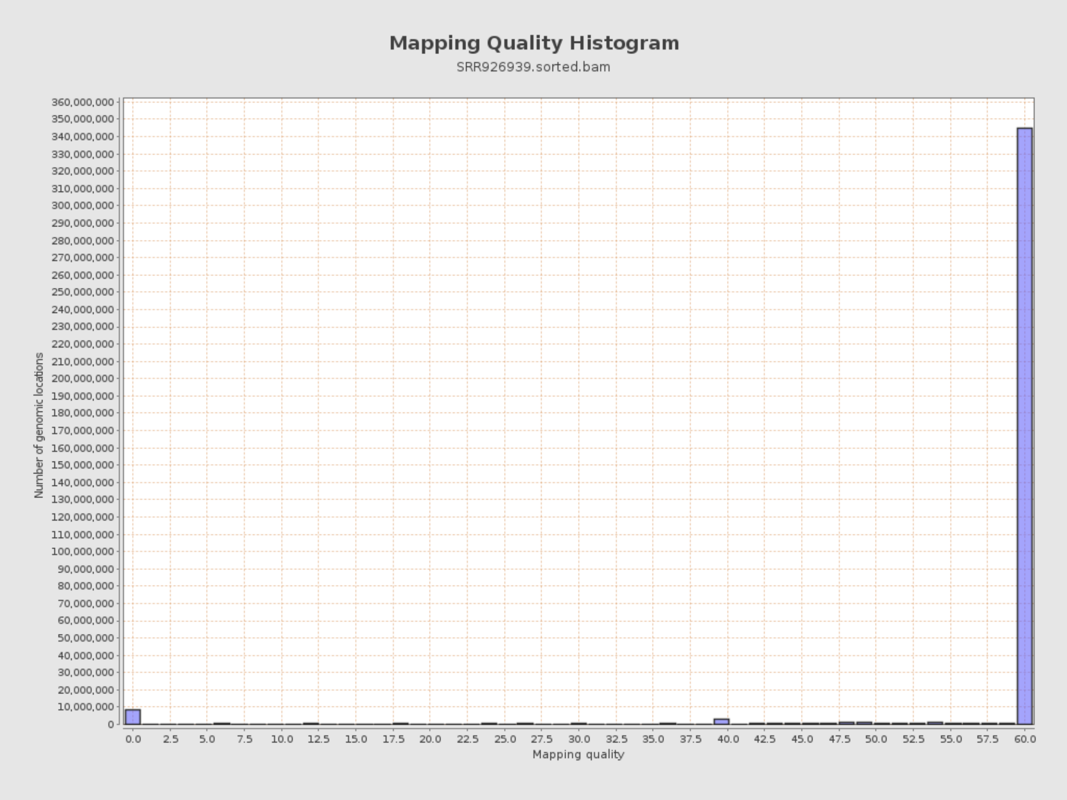
11. Results : Homopolymer Indels



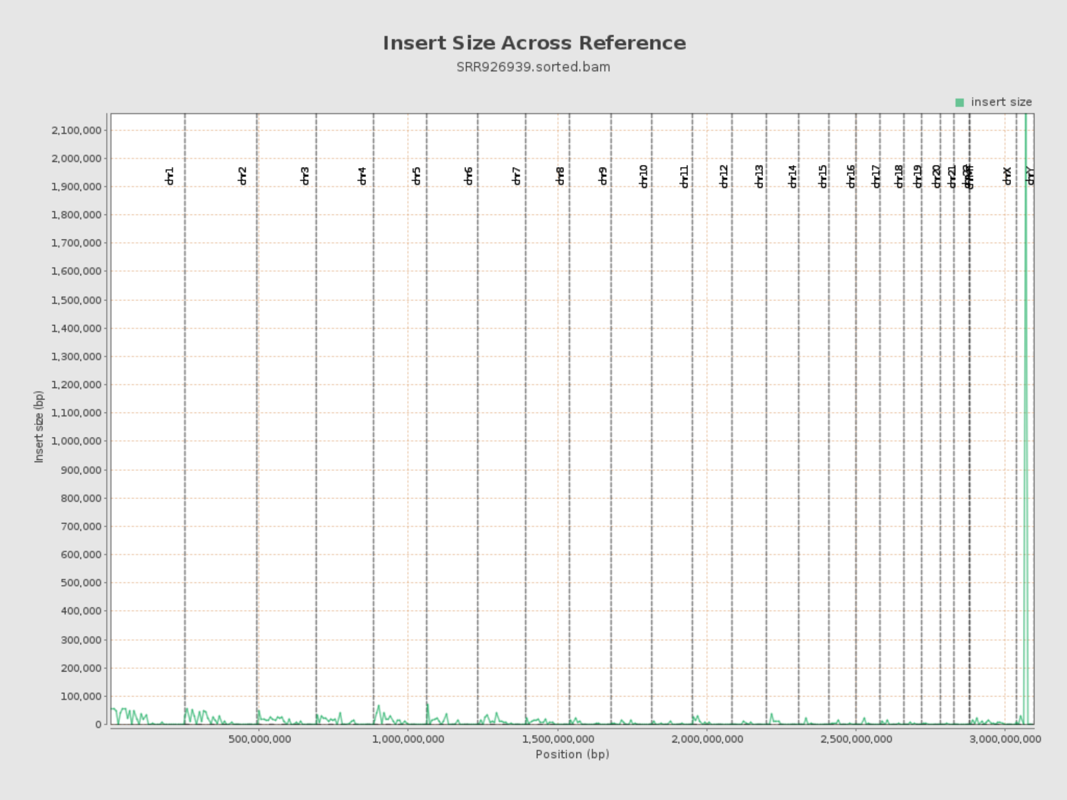
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram