Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 08:32:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926969.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_SRR926969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926969_1.fastq.gz SRR926969_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 08:32:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,317,738
Mapped reads	27,844,815 / 98.33%
Unmapped reads	472,923 / 1.67%
Mapped paired reads	27,844,815 / 98.33%
Mapped reads, first in pair	13,983,306 / 49.38%
Mapped reads, second in pair	13,861,509 / 48.95%
Mapped reads, both in pair	27,583,476 / 97.41%
Mapped reads, singletons	261,339 / 0.92%
Secondary alignments	0
Supplementary alignments	553,903 / 1.96%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	2,216,759 / 7.83%
Duplication rate	6.11%
Clipped reads	6,935,714 / 24.49%

2.2. ACGT Content

Number/percentage of A's	741,482,628 / 27.93%
Number/percentage of C's	557,092,554 / 20.98%
Number/percentage of T's	749,046,722 / 28.21%
Number/percentage of G's	607,126,460 / 22.87%
Number/percentage of N's	239,590 / 0.01%

GC Percentage	43.85%

2.3. Coverage

Mean	0.8583
Standard Deviation	3.8969

2.4. Mapping Quality

Mean Mapping Quality	52.14

2.5. Insert size

Mean	211,397.02
Standard Deviation	4,609,838.38
P25/Median/P75	142 / 179 / 233

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	24,893,509
Insertions	431,716
Mapped reads with at least one insertion	1.52%
Deletions	1,388,938
Mapped reads with at least one deletion	4.86%
Homopolymer indels	52.57%

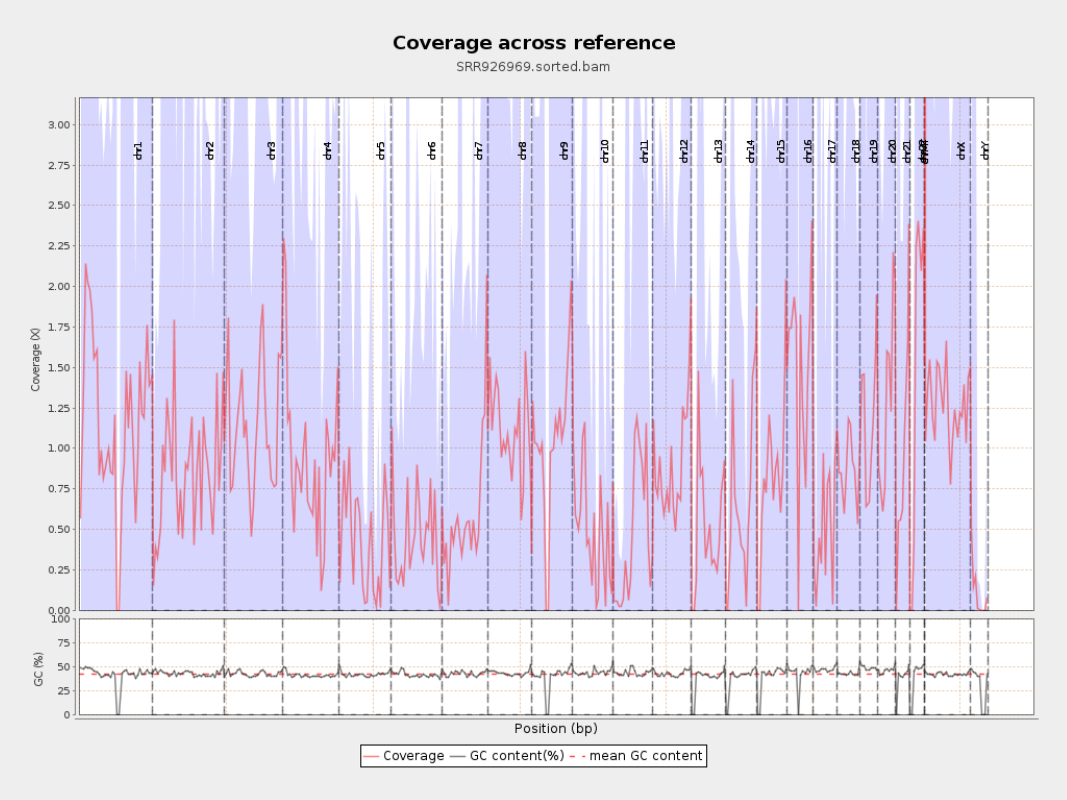
2.7. Chromosome stats

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

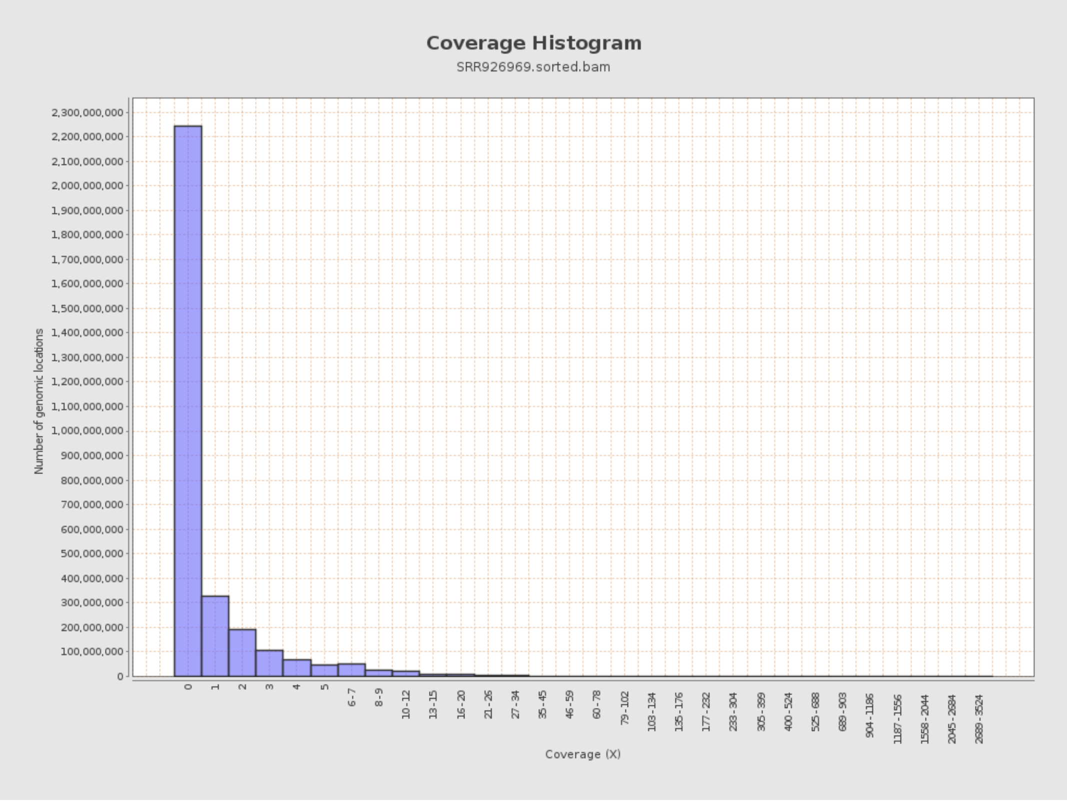
		bases	coverage	deviation
chr1	249250621	290155155	1.1641	4.1172
chr2	243199373	207452855	0.853	4.1461
chr3	198022430	226501966	1.1438	2.4585
chr4	191154276	178769998	0.9352	2.9092
chr5	180915260	75824816	0.4191	1.4576
chr6	171115067	75498580	0.4412	1.9377
chr7	159138663	96803579	0.6083	2.8902
chr8	146364022	162028423	1.107	2.8169
chr9	141213431	149012835	1.0552	5.1983
chr10	135534747	67098906	0.4951	4.3818
chr11	135006516	64167471	0.4753	2.0854
chr12	133851895	120171176	0.8978	2.4309
chr13	115169878	59548172	0.517	1.6816
chr14	107349540	70561773	0.6573	1.9668
chr15	102531392	81817150	0.798	2.2301
chr16	90354753	136697476	1.5129	6.3912
chr17	81195210	41740055	0.5141	3.1564
chr18	78077248	67914024	0.8698	5.3565
chr19	59128983	68465819	1.1579	3.3508
chr20	63025520	79745132	1.2653	2.9757
chr21	48129895	46710169	0.9705	3.7601
chr22	51304566	77052900	1.5019	3.4303
chrMT	16571	11736269	708.2414	485.2518
chrX	155270560	195427433	1.2586	2.7237

chrY	59373566	6091621	0.1026	2.2824

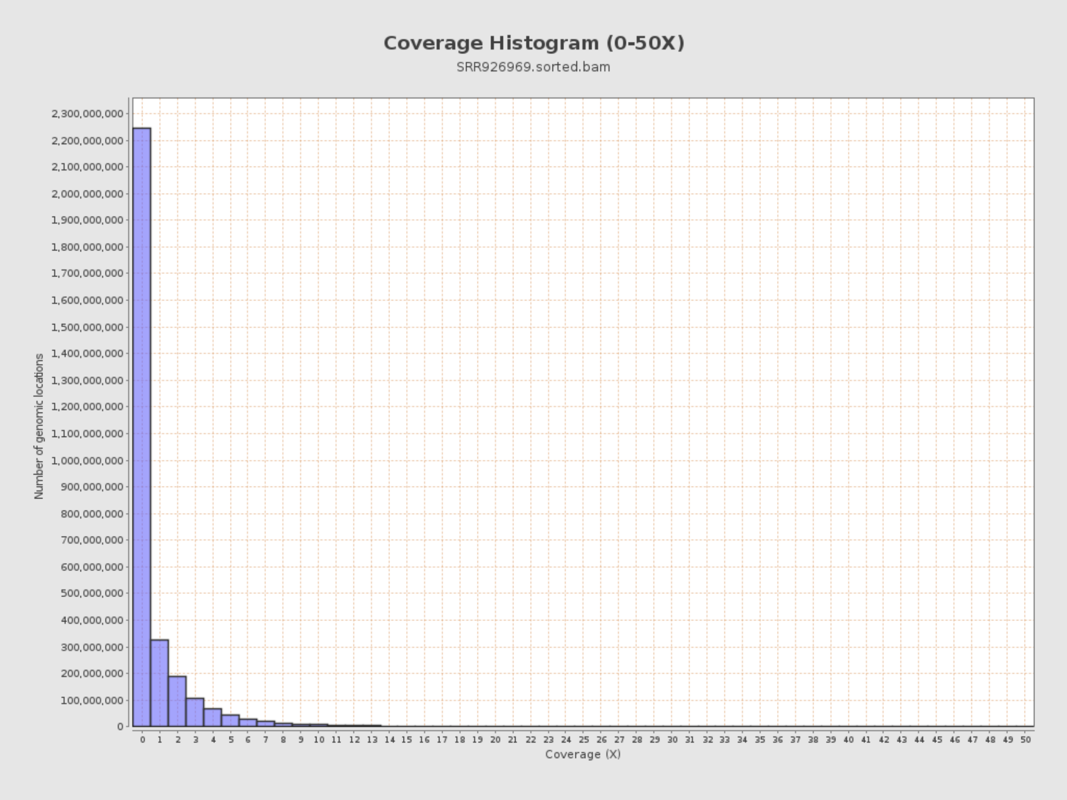
3. Results : Coverage across reference



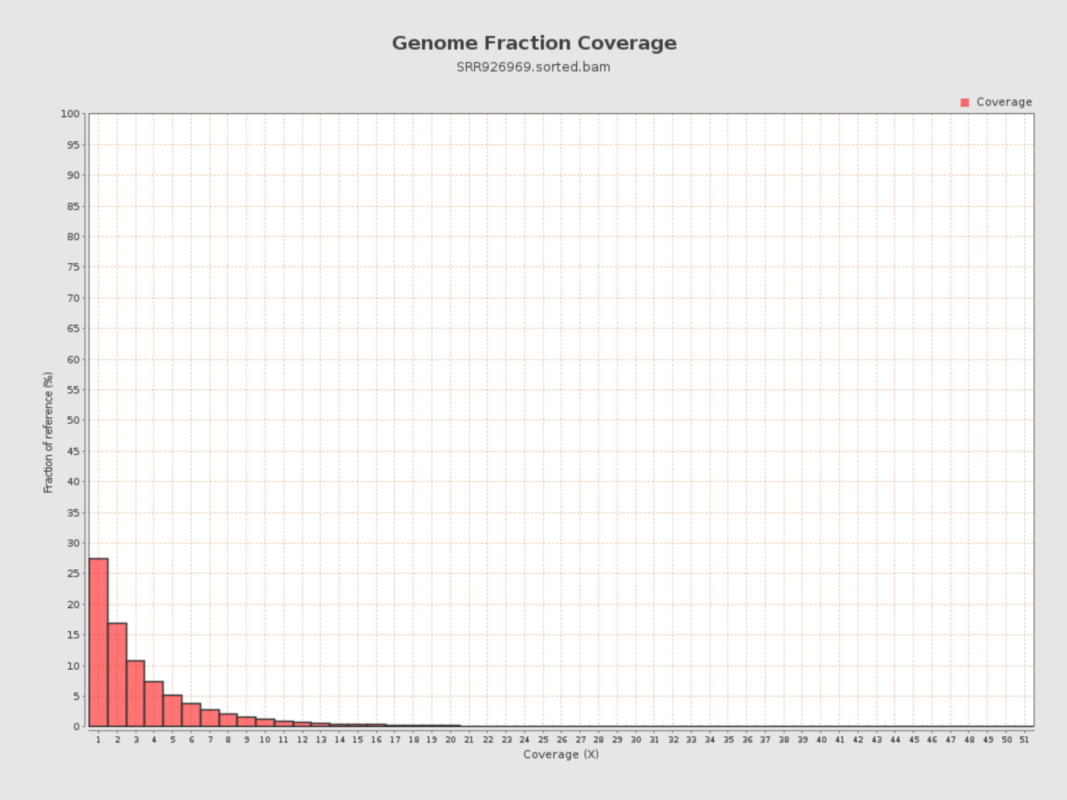
4. Results : Coverage Histogram



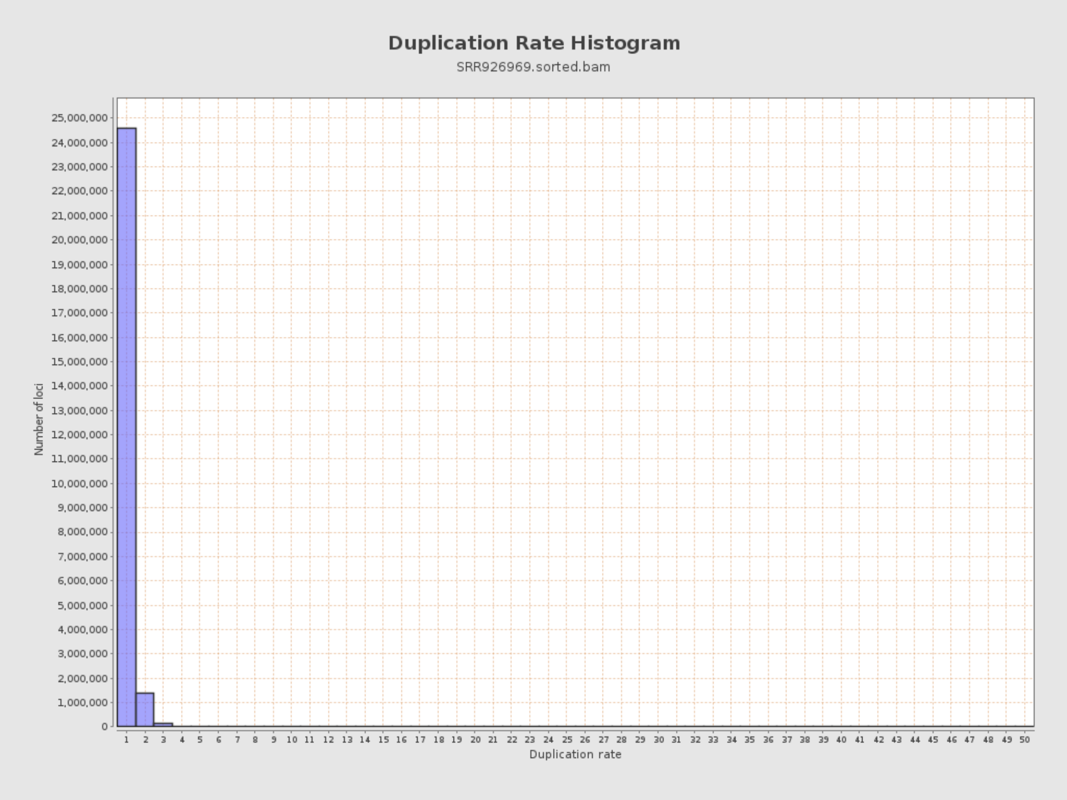
5. Results : Coverage Histogram (0-50X)



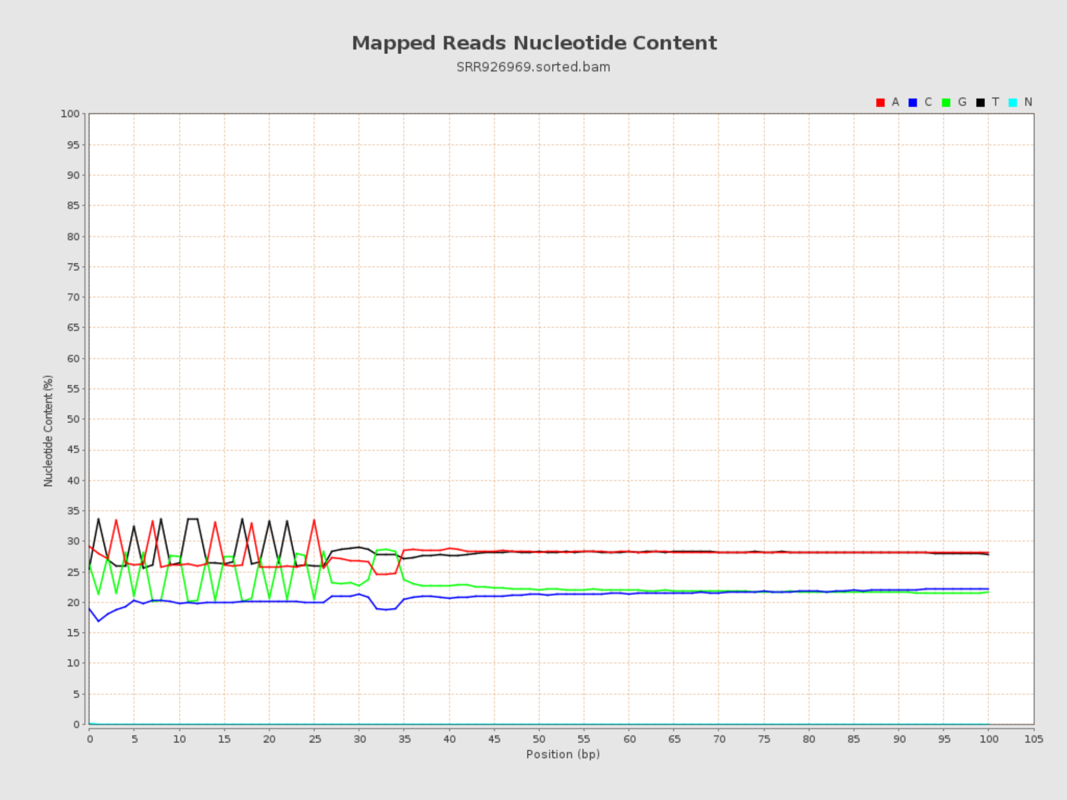
6. Results : Genome Fraction Coverage



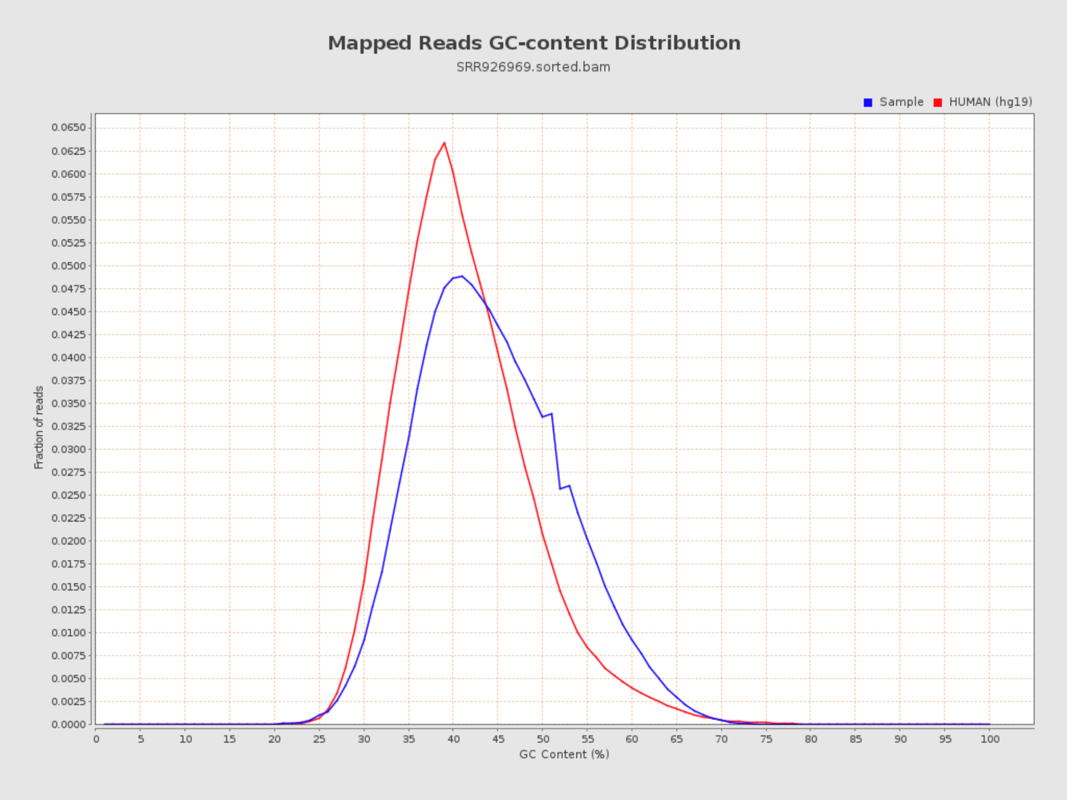
7. Results : Duplication Rate Histogram



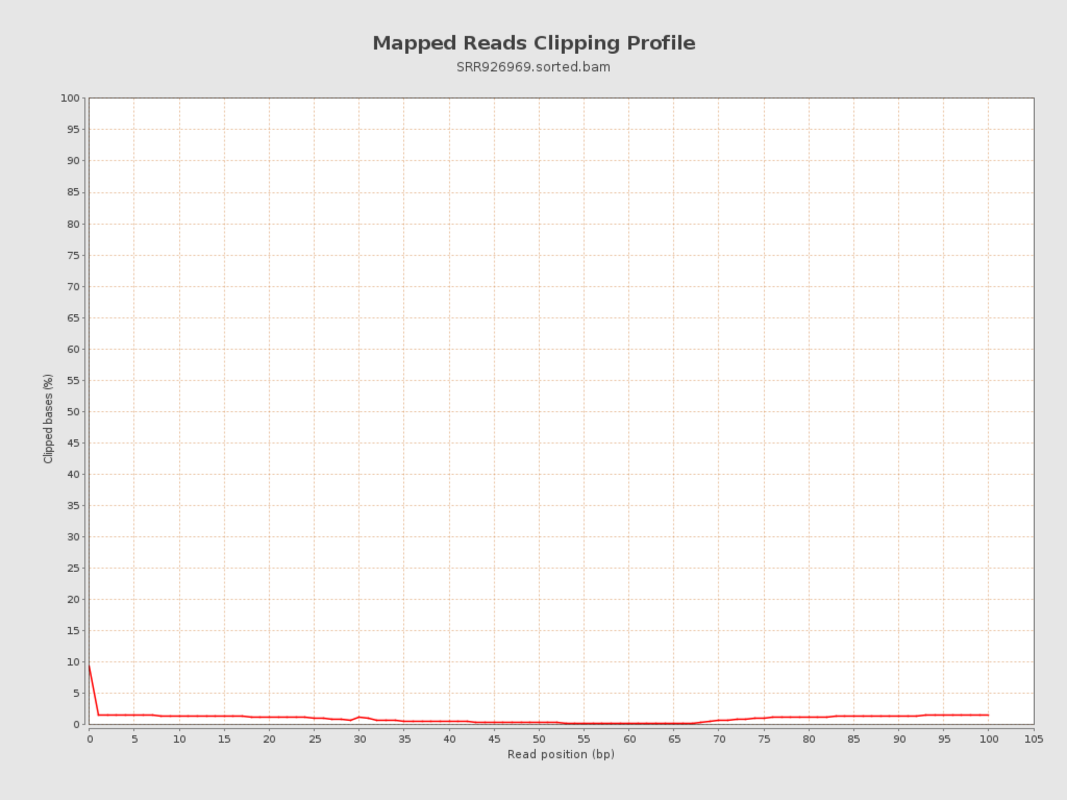
8. Results : Mapped Reads Nucleotide Content



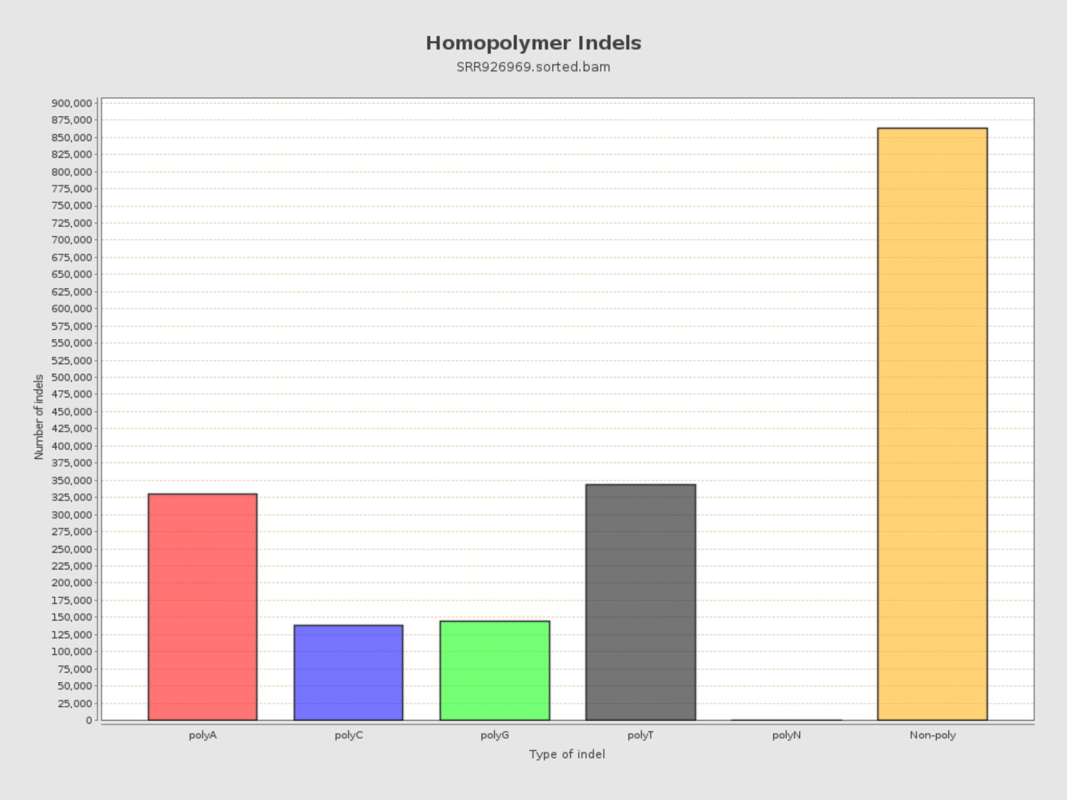
9. Results : Mapped Reads GC-content Distribution



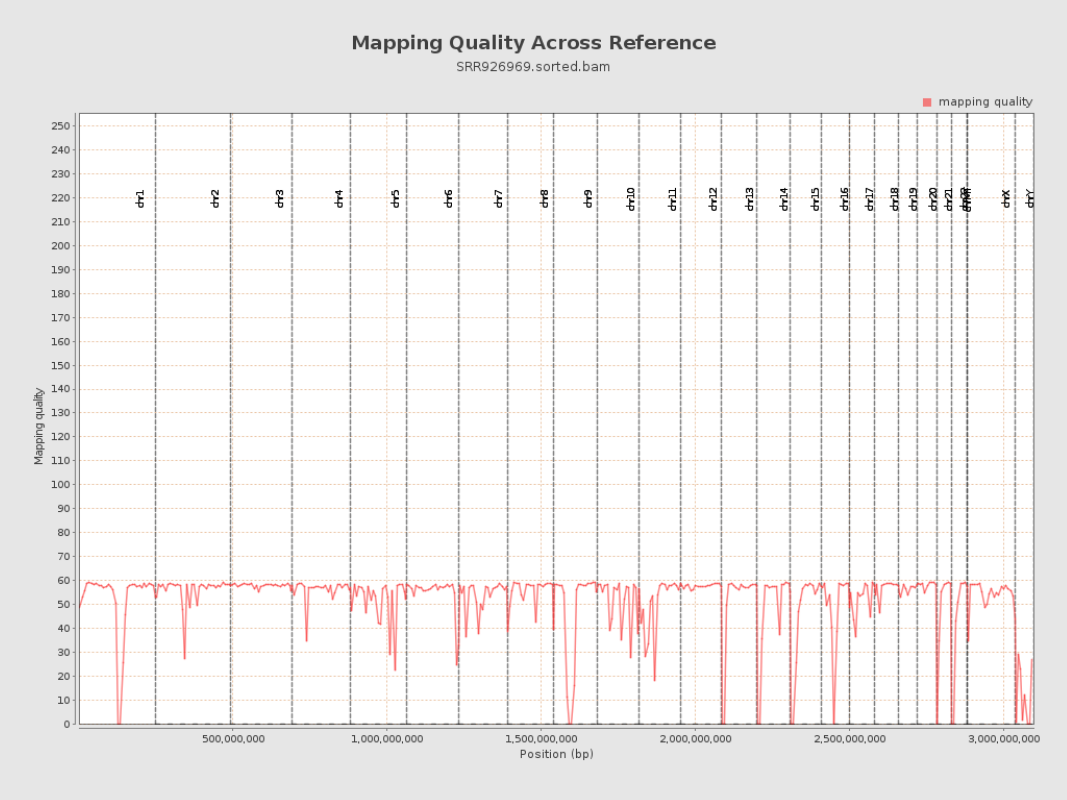
10. Results : Mapped Reads Clipping Profile



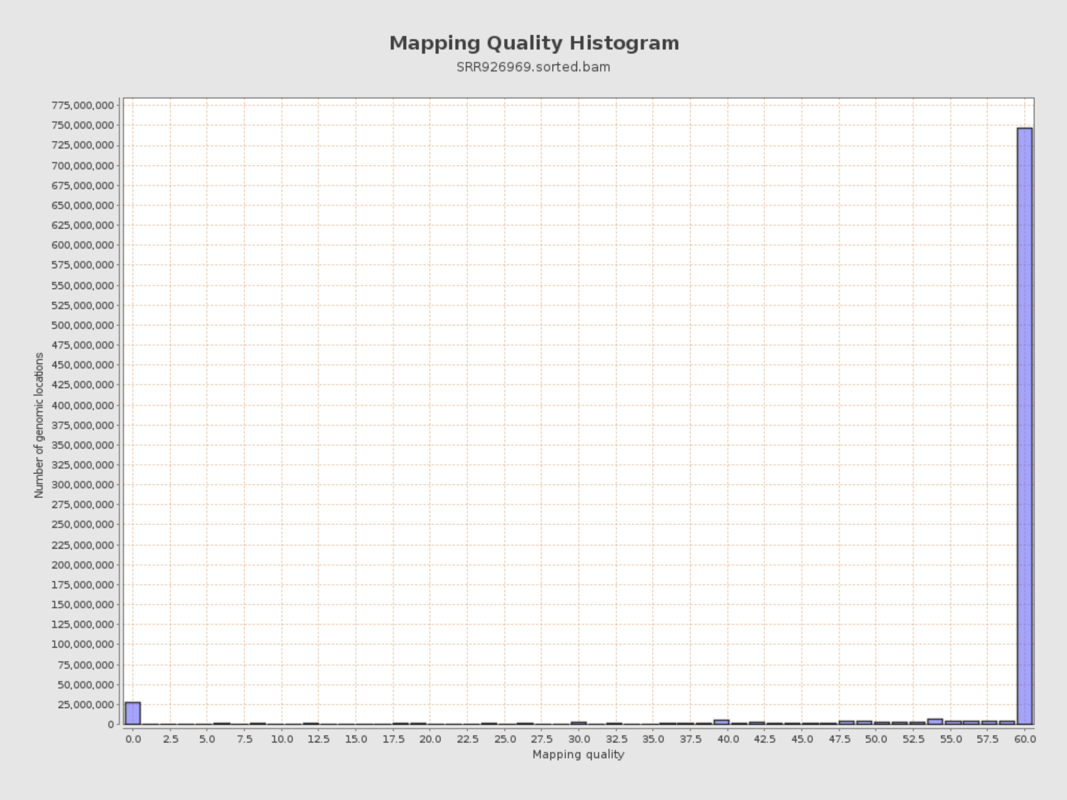
11. Results : Homopolymer Indels



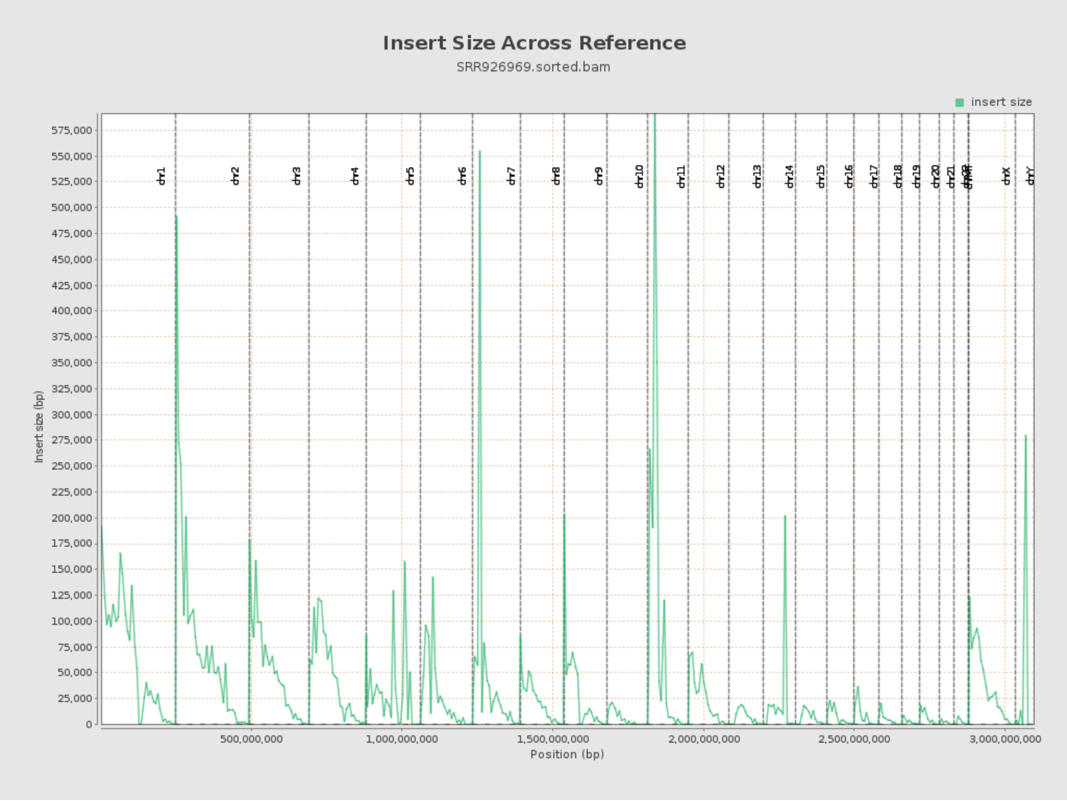
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram