Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 07:06:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927066.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_SRR927066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927066_1.fastq.gz SRR927066_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 07:06:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,561,946
Mapped reads	34,136,436 / 98.77%
Unmapped reads	425,510 / 1.23%
Mapped paired reads	34,136,436 / 98.77%
Mapped reads, first in pair	17,130,378 / 49.56%
Mapped reads, second in pair	17,006,058 / 49.2%
Mapped reads, both in pair	33,892,950 / 98.06%
Mapped reads, singletons	243,486 / 0.7%
Secondary alignments	0
Supplementary alignments	230,130 / 0.67%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	2,278,930 / 6.59%
Duplication rate	5.25%
Clipped reads	6,934,728 / 20.06%

2.2. ACGT Content

Number/percentage of A's	951,644,521 / 29.11%
Number/percentage of C's	649,076,294 / 19.85%
Number/percentage of T's	961,225,030 / 29.4%
Number/percentage of G's	706,614,544 / 21.61%
Number/percentage of N's	579,713 / 0.02%

GC Percentage	41.47%

2.3. Coverage

Mean	1.0568
Standard Deviation	3.9444

2.4. Mapping Quality

Mean Mapping Quality	53.83

2.5. Insert size

Mean	66,843.83
Standard Deviation	2,507,118.14
P25/Median/P75	151 / 194 / 259

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	32,833,954
Insertions	530,830
Mapped reads with at least one insertion	1.53%
Deletions	1,776,032
Mapped reads with at least one deletion	5.06%
Homopolymer indels	53.35%

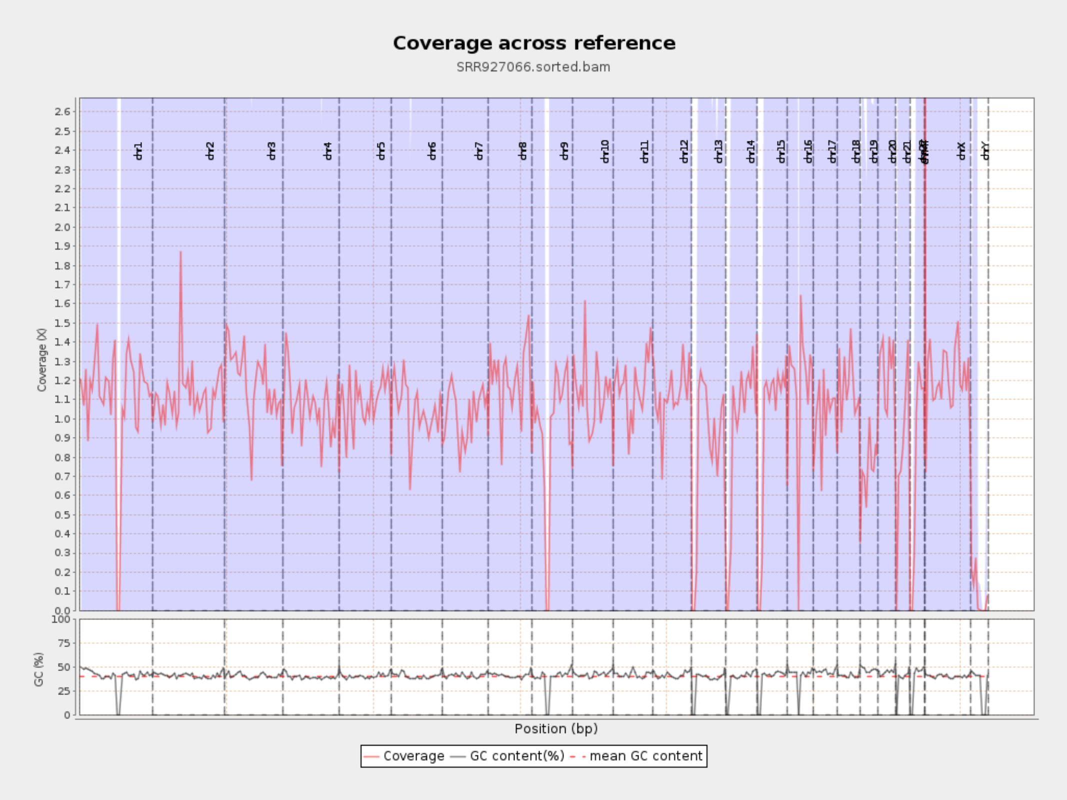
2.7. Chromosome stats

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

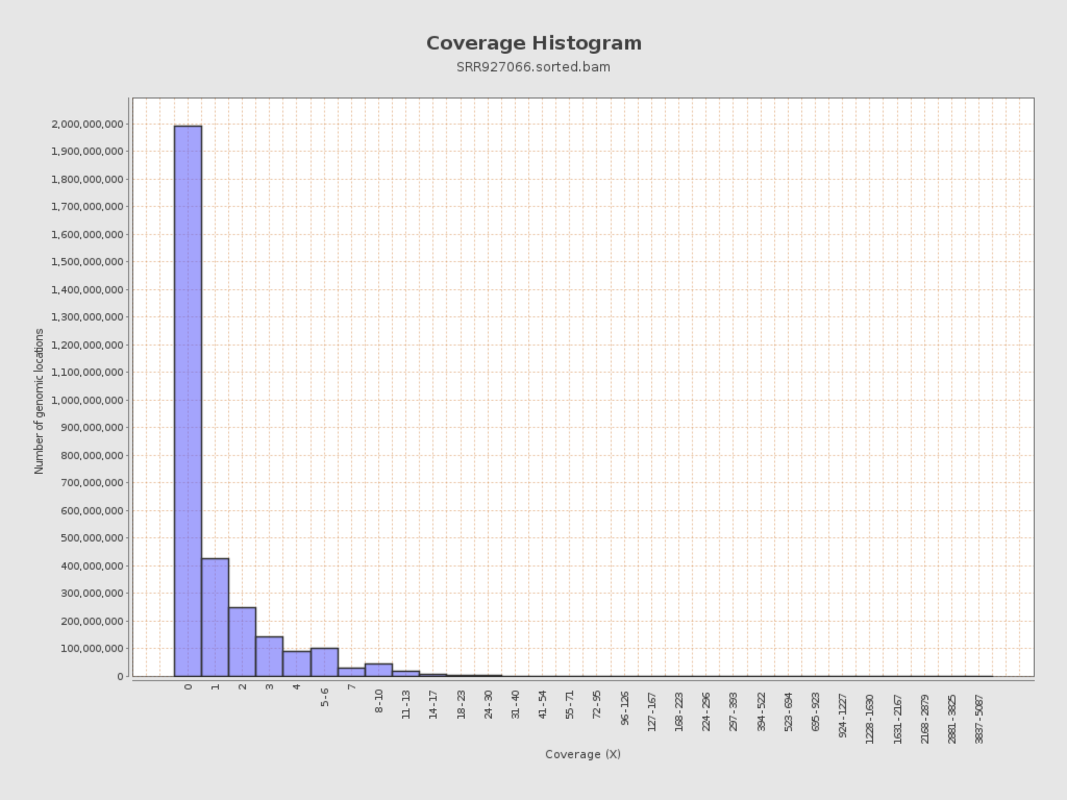
		bases	**coverage**	**deviation**
chr1	249250621	276011405	1.1074	5.9625
chr2	243199373	274370291	1.1282	6.1949
chr3	198022430	235968451	1.1916	2.301
chr4	191154276	205306855	1.074	2.9445
chr5	180915260	197313491	1.0906	2.183
chr6	171115067	180209393	1.0531	2.1754
chr7	159138663	162739907	1.0226	3.0794
chr8	146364022	177585868	1.2133	2.7646
chr9	141213431	131726176	0.9328	5.3748
chr10	135534747	154828354	1.1424	5.8696
chr11	135006516	157266125	1.1649	4.2308
chr12	133851895	150956447	1.1278	2.2541
chr13	115169878	97117474	0.8433	1.8955
chr14	107349540	100663679	0.9377	2.126
chr15	102531392	96091015	0.9372	2.1036
chr16	90354753	103997871	1.151	5.4818
chr17	81195210	82294647	1.0135	3.5802
chr18	78077248	92419890	1.1837	5.5441
chr19	59128983	43746475	0.7398	3.2774
chr20	63025520	78242325	1.2414	2.5588
chr21	48129895	40924292	0.8503	2.6979
chr22	51304566	39903248	0.7778	2.0104
chrMT	16571	84110	5.0757	4.4657
chrX	155270560	186864252	1.2035	2.7391

chrY	59373566	4975433	0.0838	3.5317

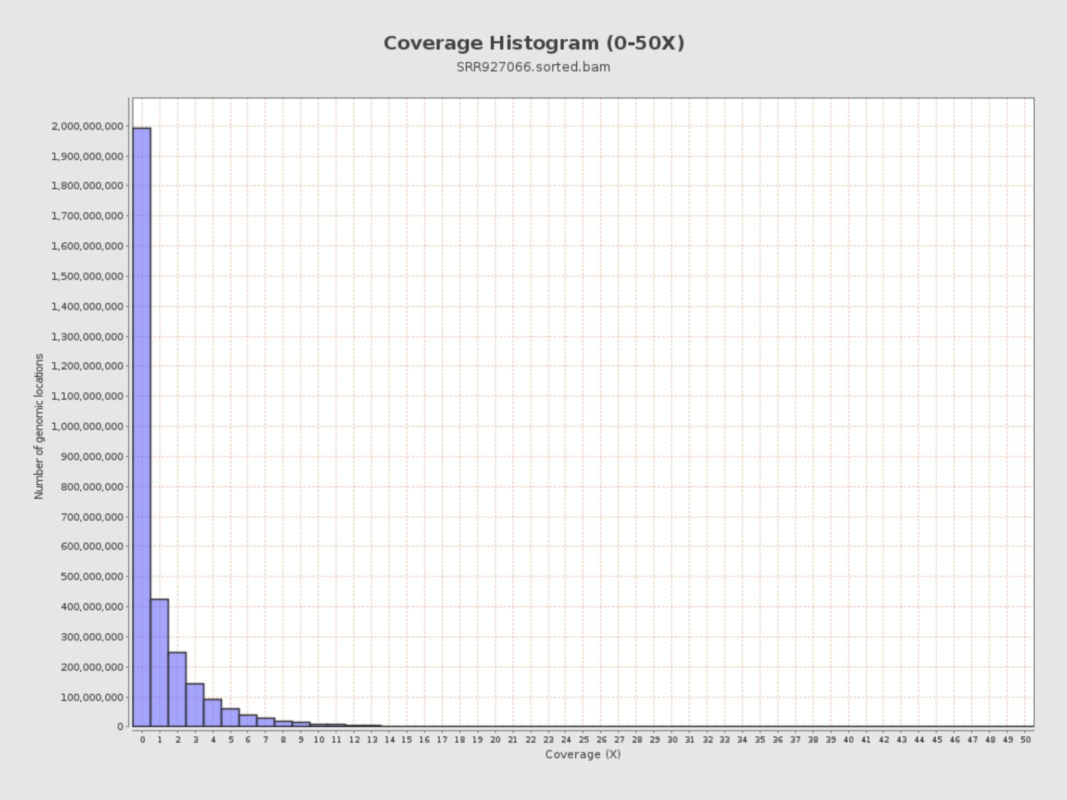
3. Results : Coverage across reference



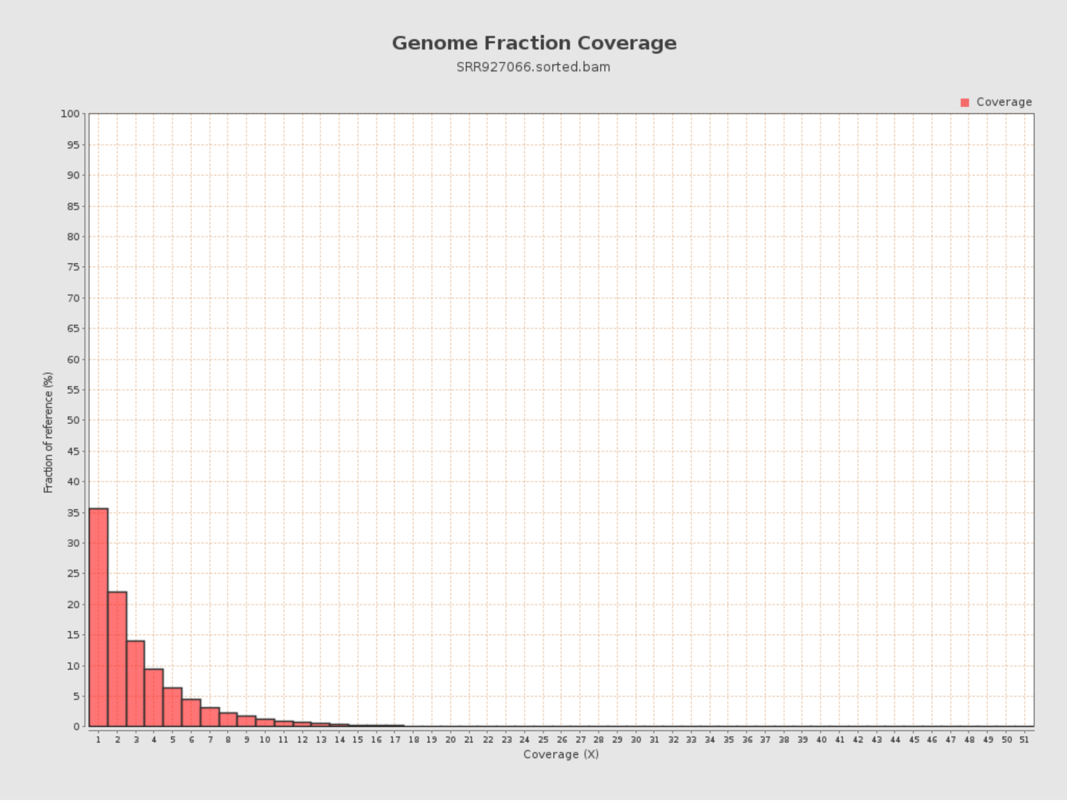
4. Results : Coverage Histogram



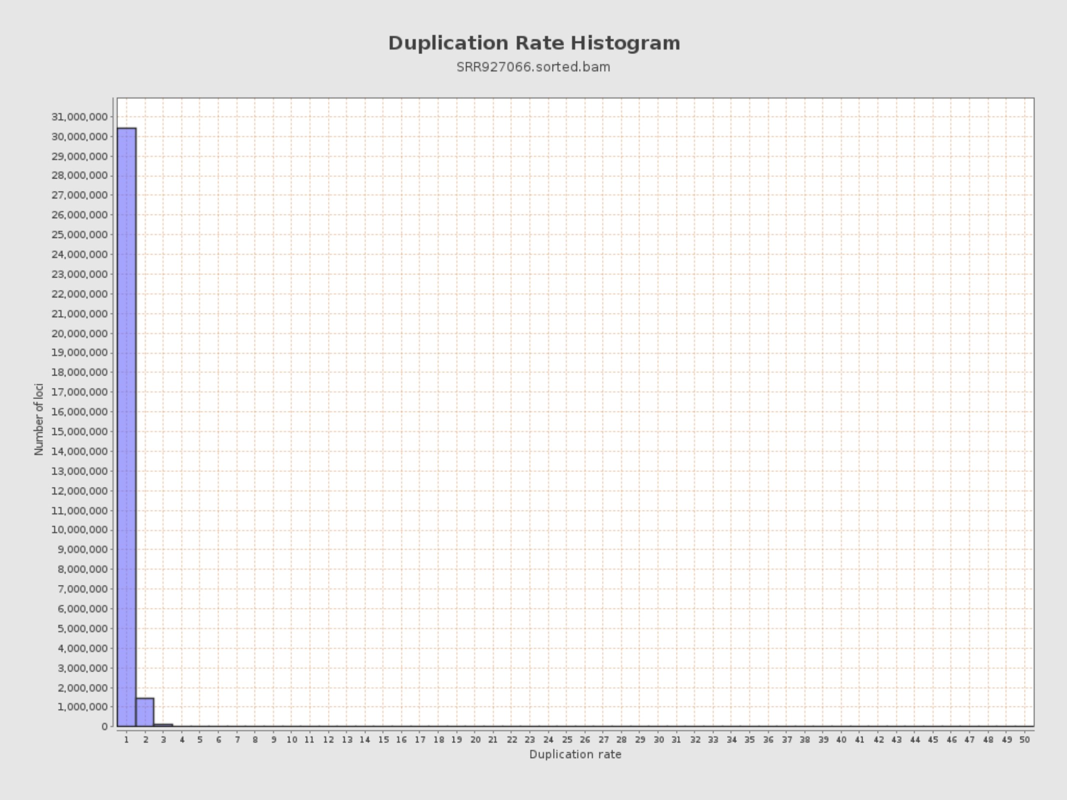
5. Results : Coverage Histogram (0-50X)



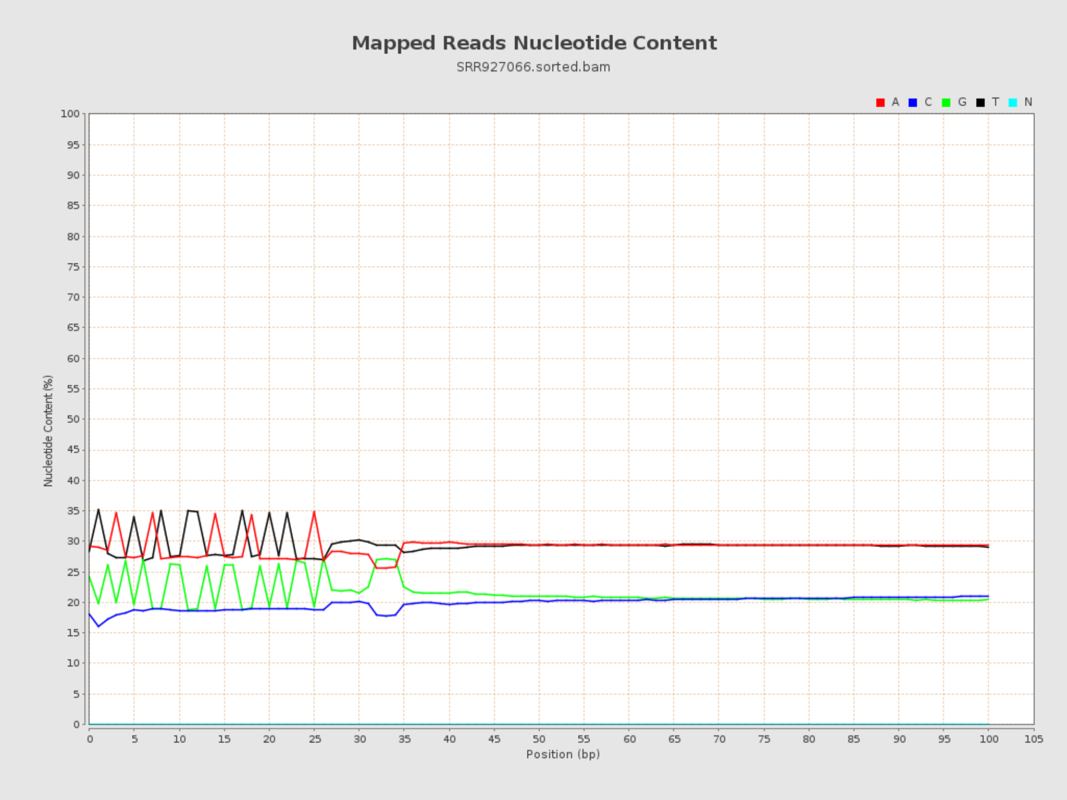
6. Results : Genome Fraction Coverage



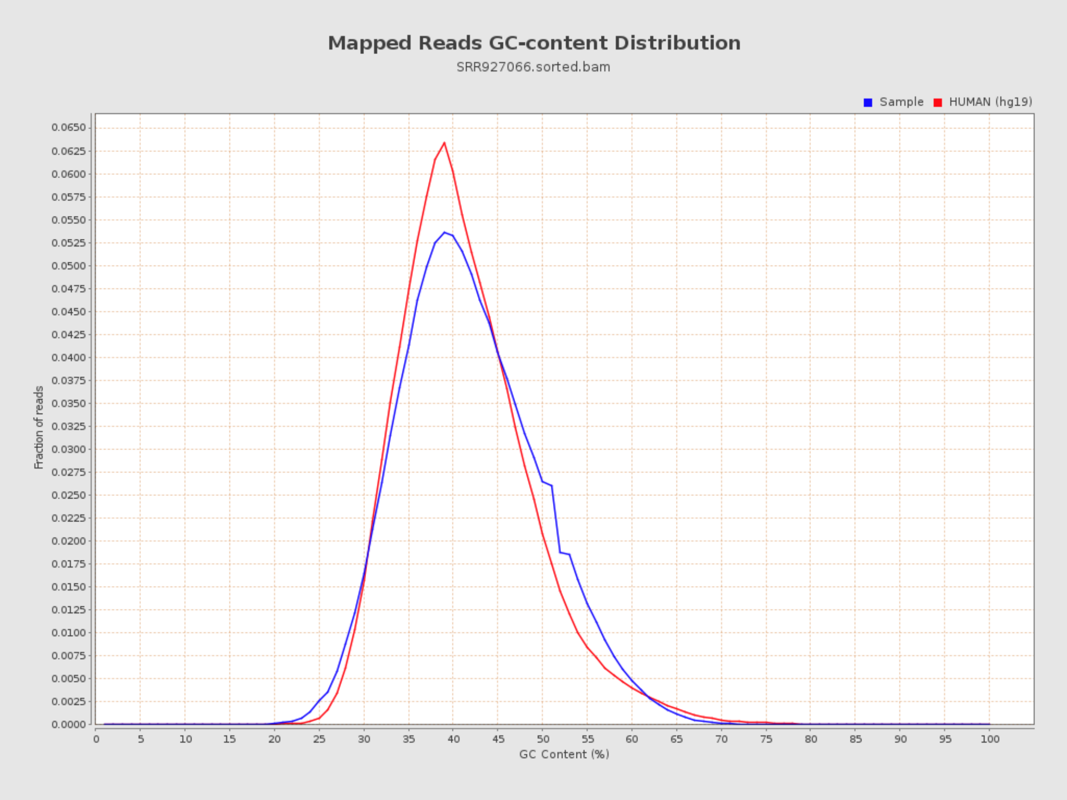
7. Results : Duplication Rate Histogram



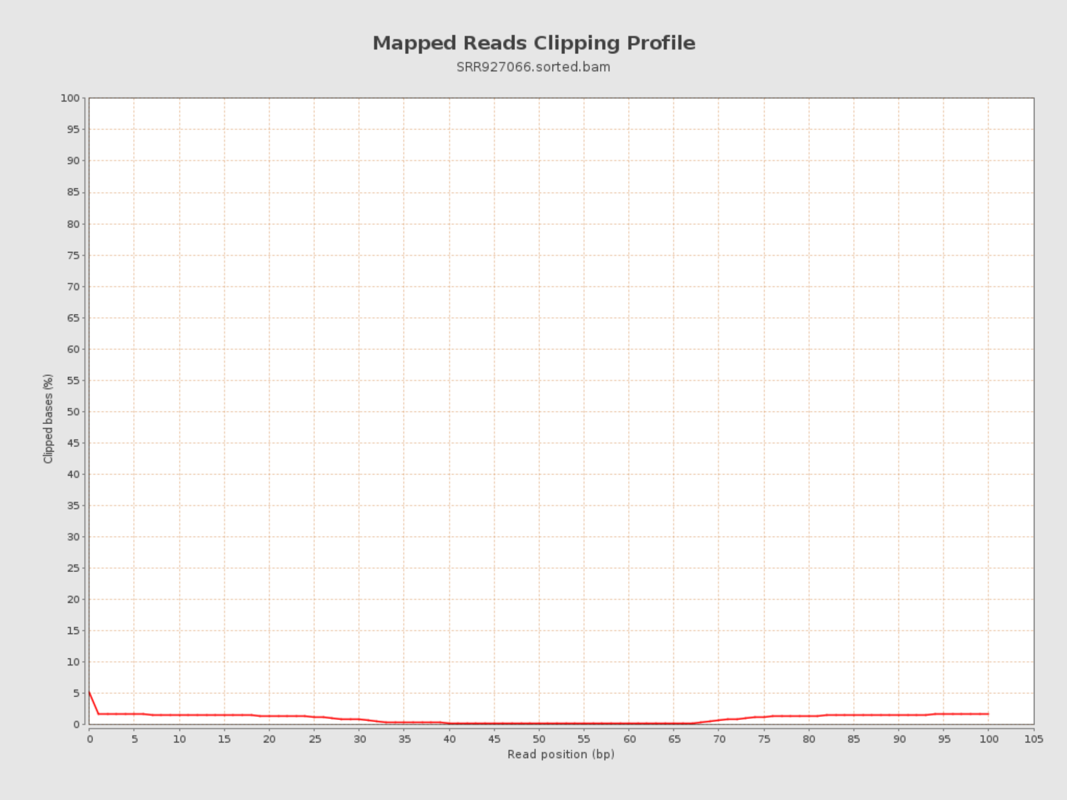
8. Results : Mapped Reads Nucleotide Content



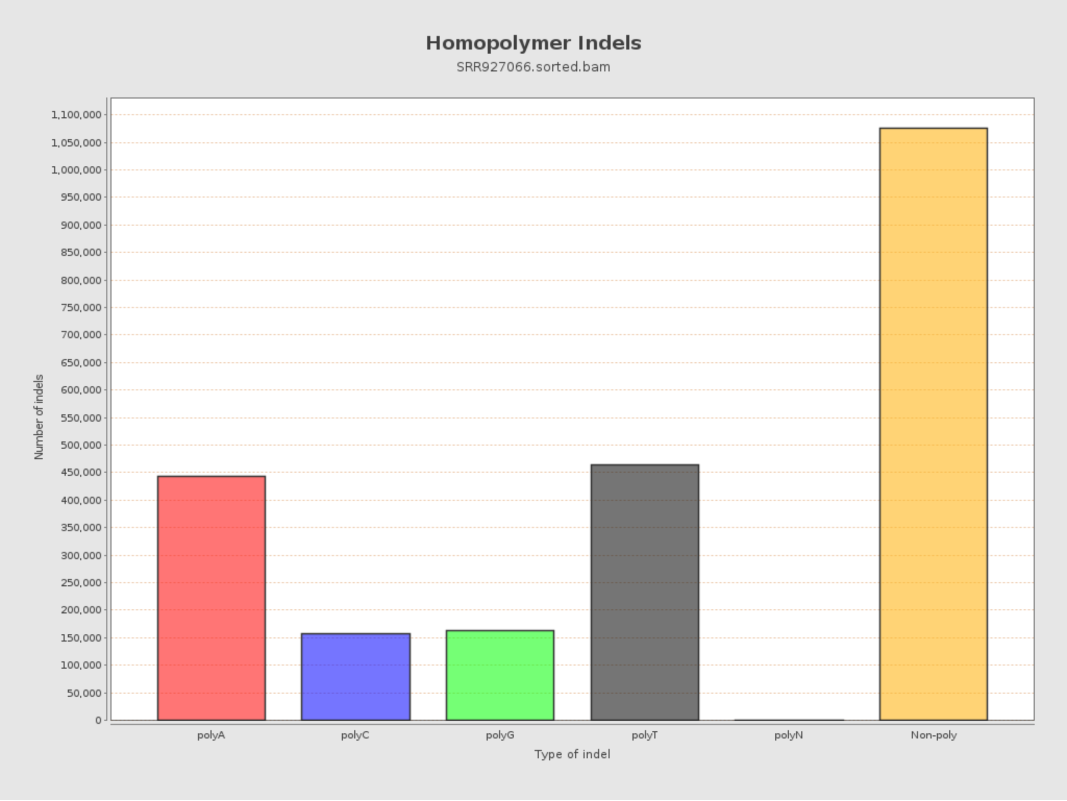
9. Results : Mapped Reads GC-content Distribution



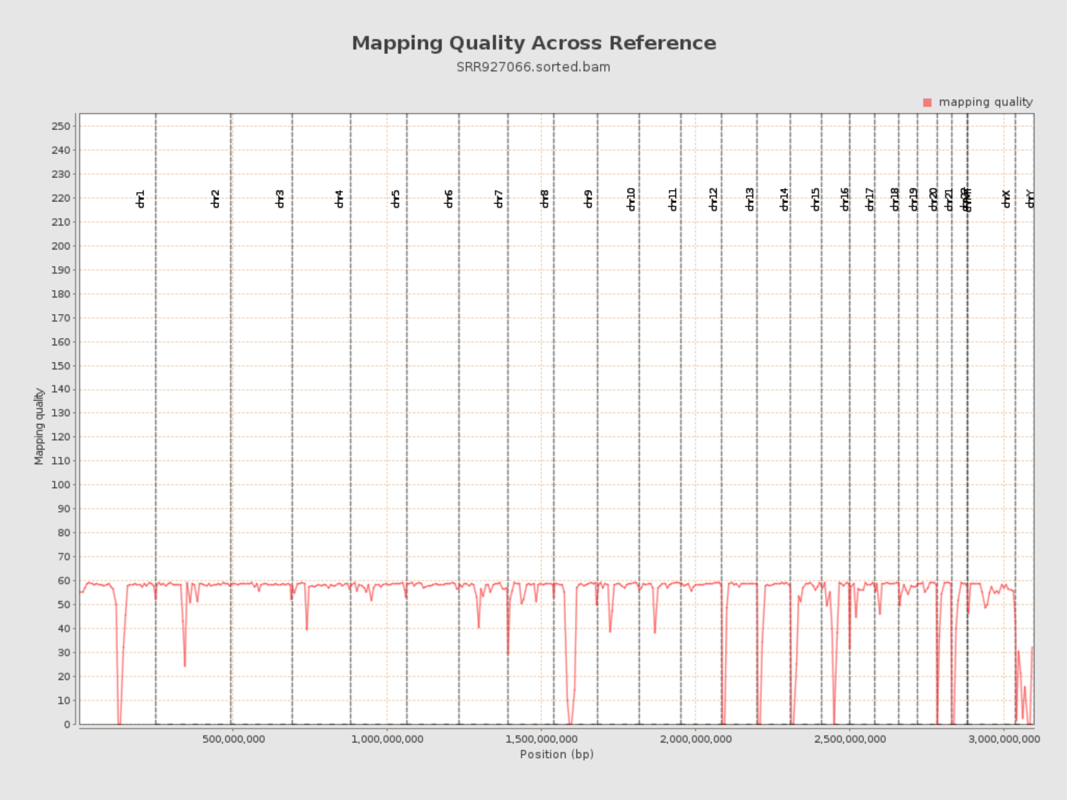
10. Results : Mapped Reads Clipping Profile



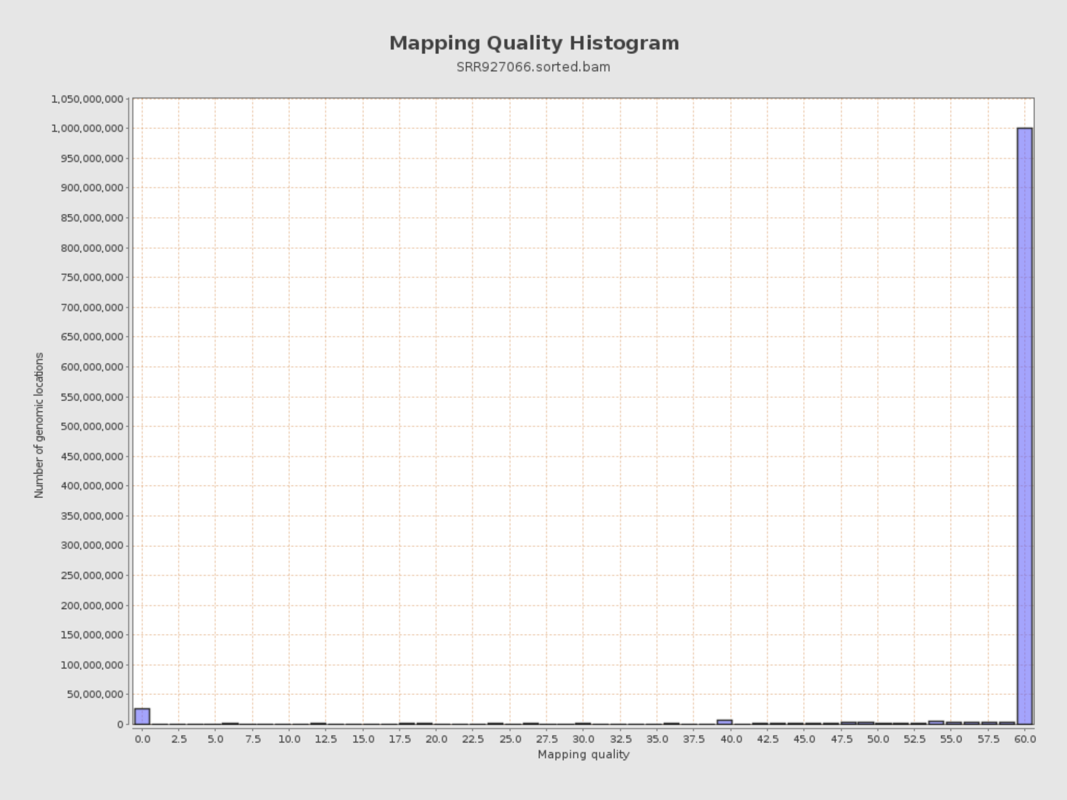
11. Results : Homopolymer Indels



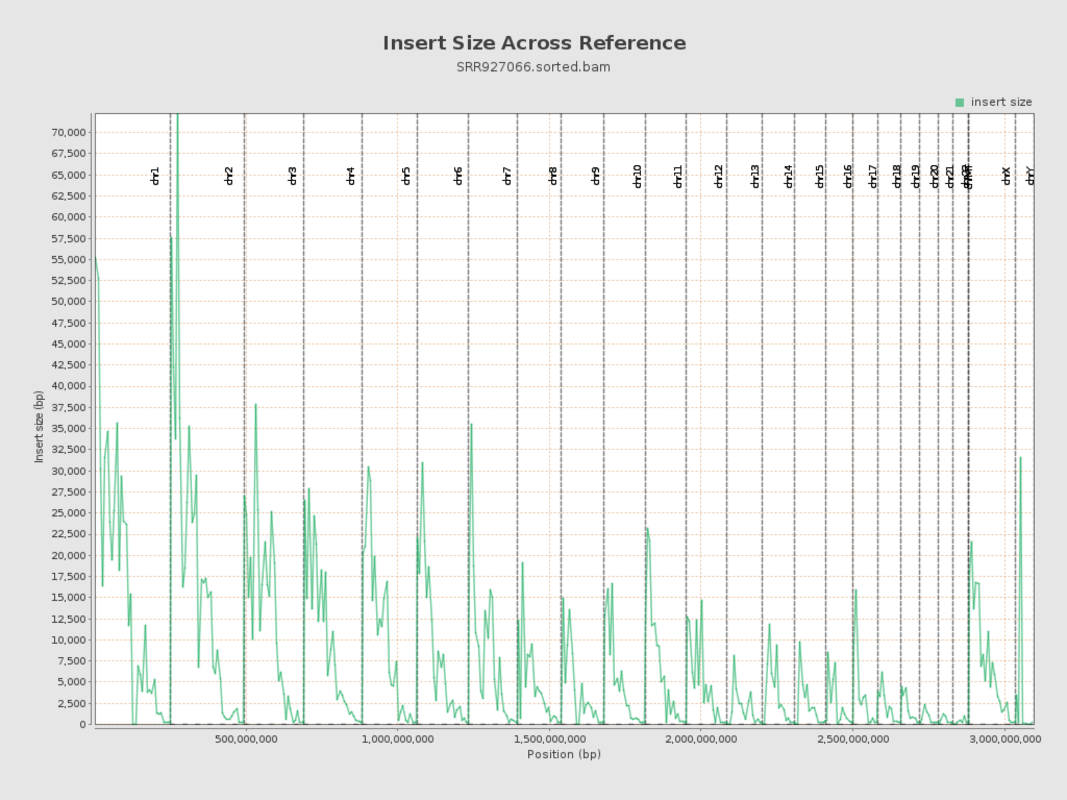
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram