Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 00:52:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926946.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_SRR926946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926946_1.fastq.gz SRR926946_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 00:52:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,032,546
Mapped reads	11,794,230 / 98.02%
Unmapped reads	238,316 / 1.98%
Mapped paired reads	11,794,230 / 98.02%
Mapped reads, first in pair	5,918,809 / 49.19%
Mapped reads, second in pair	5,875,421 / 48.83%
Mapped reads, both in pair	11,648,688 / 96.81%
Mapped reads, singletons	145,542 / 1.21%
Secondary alignments	0
Supplementary alignments	247,274 / 2.06%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	687,588 / 5.71%
Duplication rate	4.55%
Clipped reads	4,640,874 / 38.57%

2.2. ACGT Content

Number/percentage of A's	308,373,879 / 28.68%
Number/percentage of C's	207,049,127 / 19.26%
Number/percentage of T's	314,082,137 / 29.21%
Number/percentage of G's	245,498,603 / 22.83%
Number/percentage of N's	214,604 / 0.02%

GC Percentage	42.09%

2.3. Coverage

Mean	0.3476
Standard Deviation	1.5677

2.4. Mapping Quality

Mean Mapping Quality	53.16

2.5. Insert size

Mean	229,829.99
Standard Deviation	4,722,154.99
P25/Median/P75	146 / 189 / 253

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	9,554,371
Insertions	176,575
Mapped reads with at least one insertion	1.47%
Deletions	550,468
Mapped reads with at least one deletion	4.55%
Homopolymer indels	52.47%

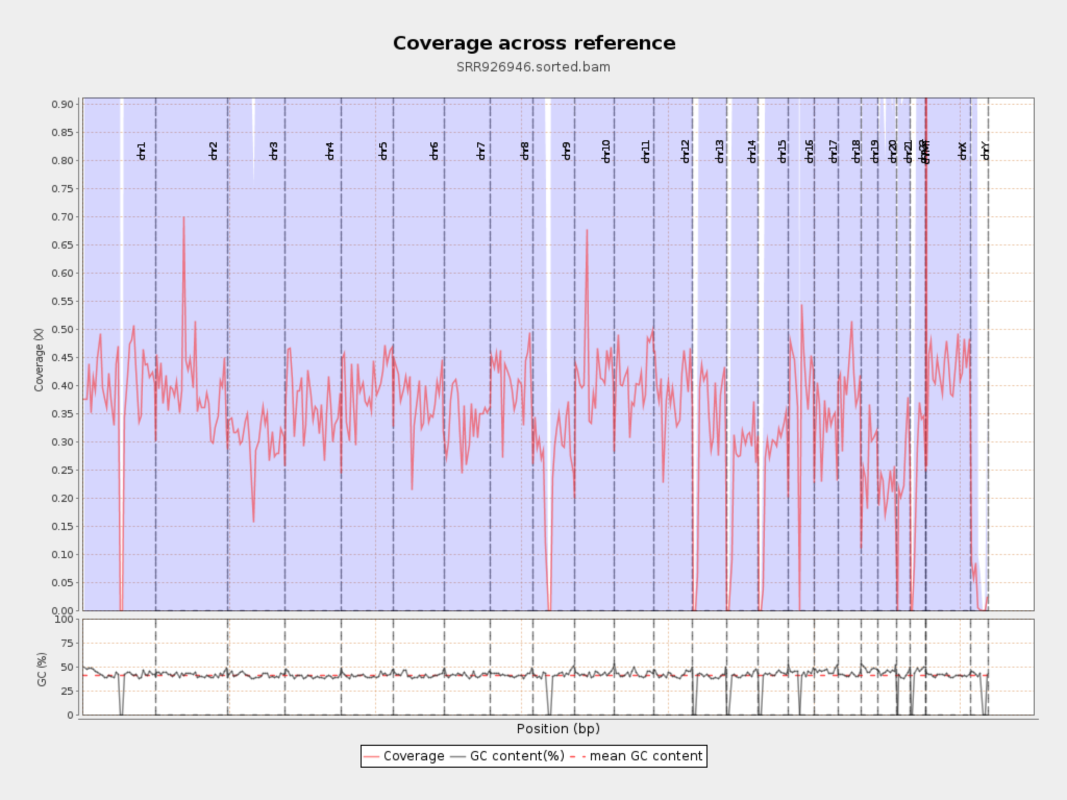
2.7. Chromosome stats

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

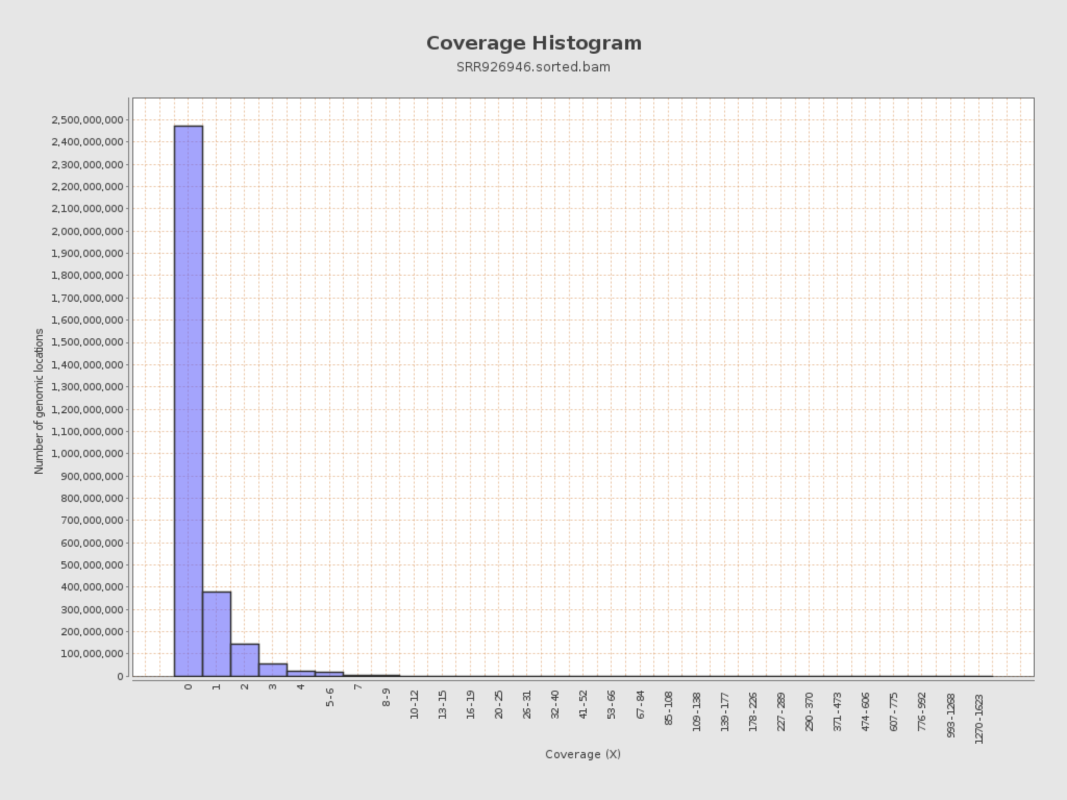
		bases	coverage	deviation
chr1	249250621	96180621	0.3859	1.9557
chr2	243199373	96826406	0.3981	2.6637
chr3	198022430	60162468	0.3038	0.8066
chr4	191154276	69934721	0.3659	1.1511
chr5	180915260	72316071	0.3997	0.935
chr6	171115067	64203863	0.3752	1.0408
chr7	159138663	53379810	0.3354	1.0917
chr8	146364022	59977197	0.4098	1.0886
chr9	141213431	36324512	0.2572	1.4999
chr10	135534747	57380796	0.4234	3.378
chr11	135006516	55519939	0.4112	1.7944
chr12	133851895	51884181	0.3876	0.9461
chr13	115169878	35951153	0.3122	0.826
chr14	107349540	26606044	0.2478	0.7428
chr15	102531392	24867923	0.2425	0.7234
chr16	90354753	35030355	0.3877	2.0787
chr17	81195210	27036381	0.333	1.2014
chr18	78077248	31405707	0.4022	1.5871
chr19	59128983	16042999	0.2713	1.4814
chr20	63025520	13619322	0.2161	0.7035
chr21	48129895	11551951	0.24	1.1187
chr22	51304566	11537323	0.2249	0.751
chrMT	16571	84461	5.0969	4.9837
chrX	155270560	66418183	0.4278	1.0835

chrY	59373566	1776163	0.0299	1.1245

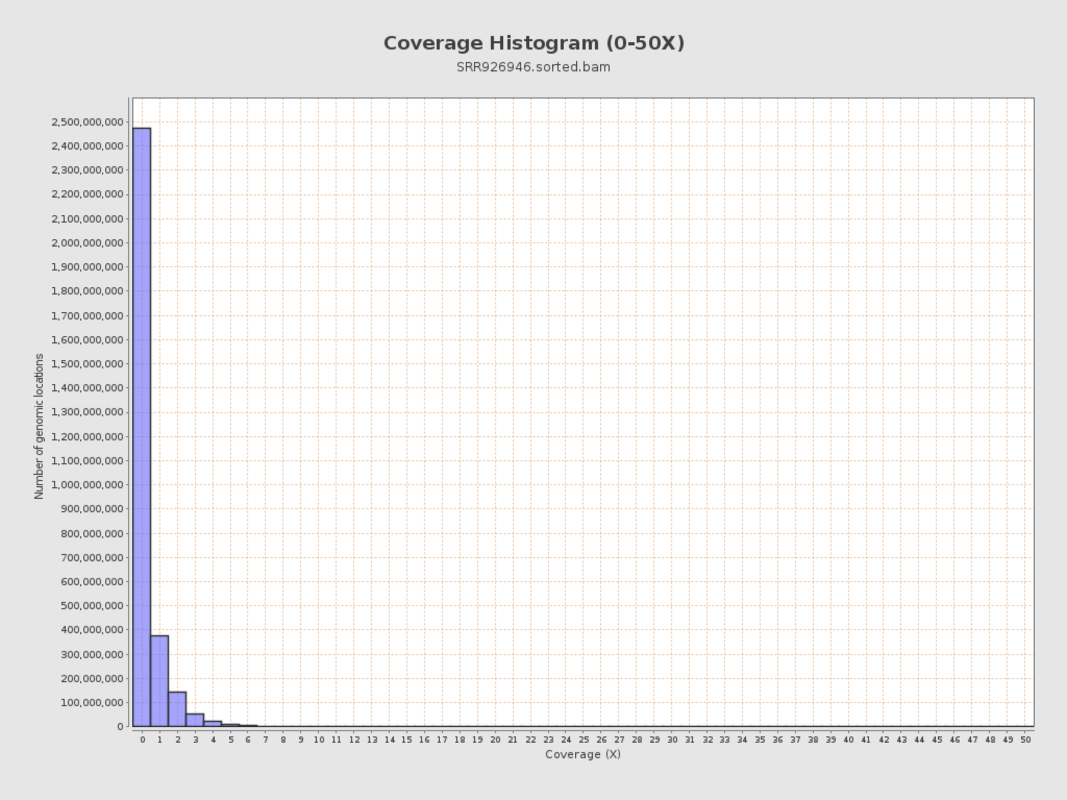
3. Results : Coverage across reference



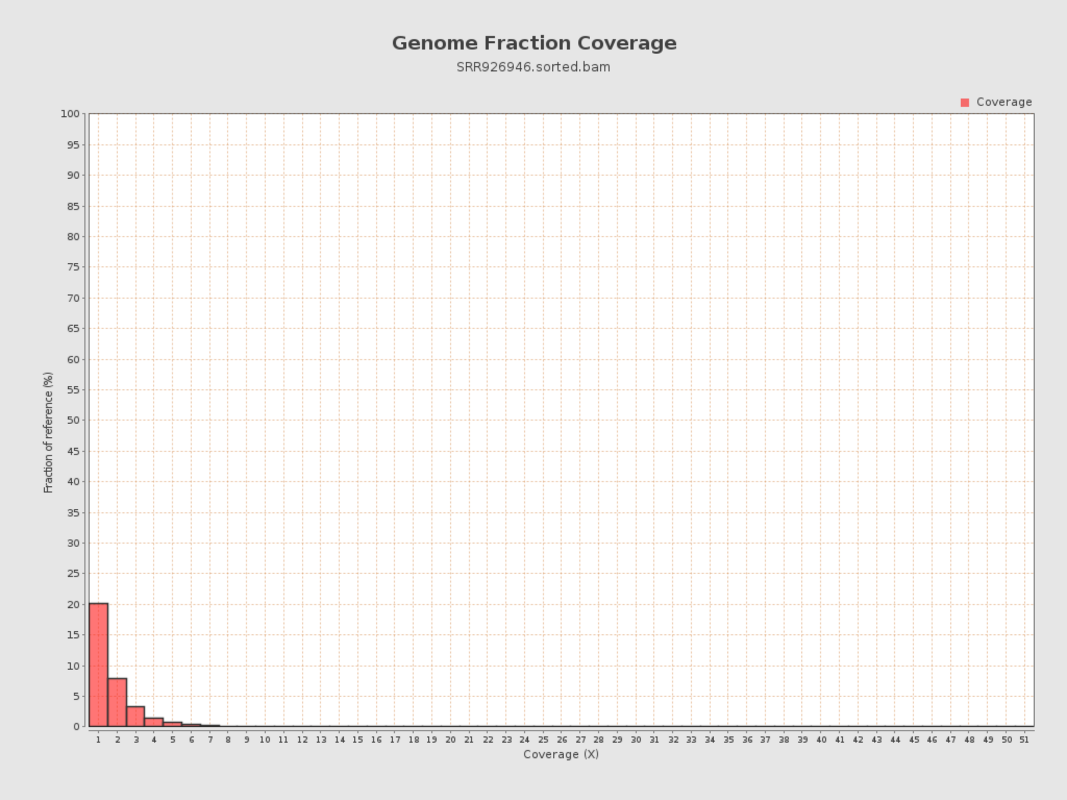
4. Results : Coverage Histogram



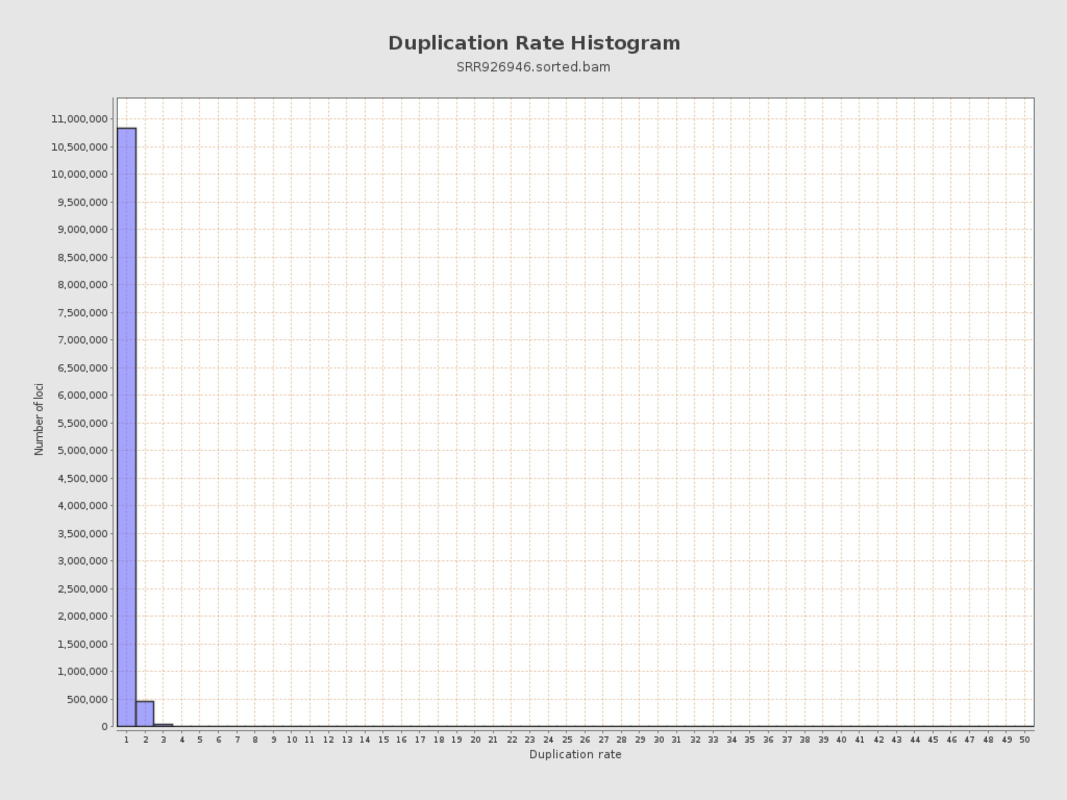
5. Results : Coverage Histogram (0-50X)



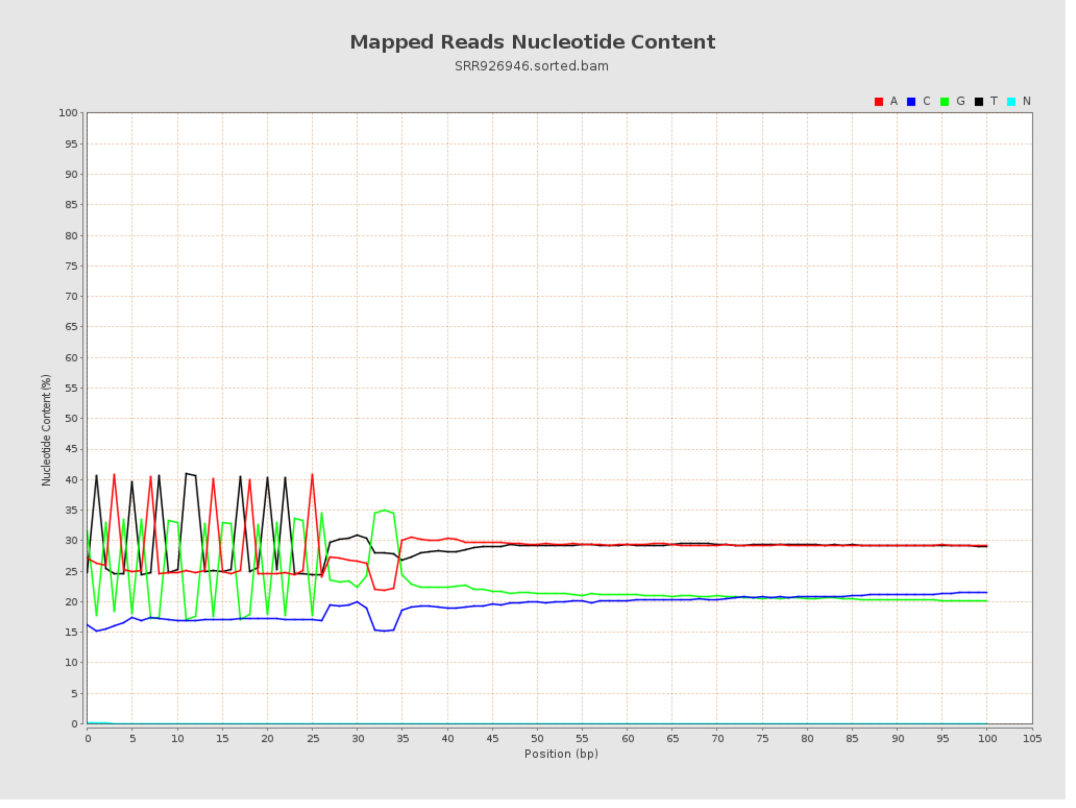
6. Results : Genome Fraction Coverage



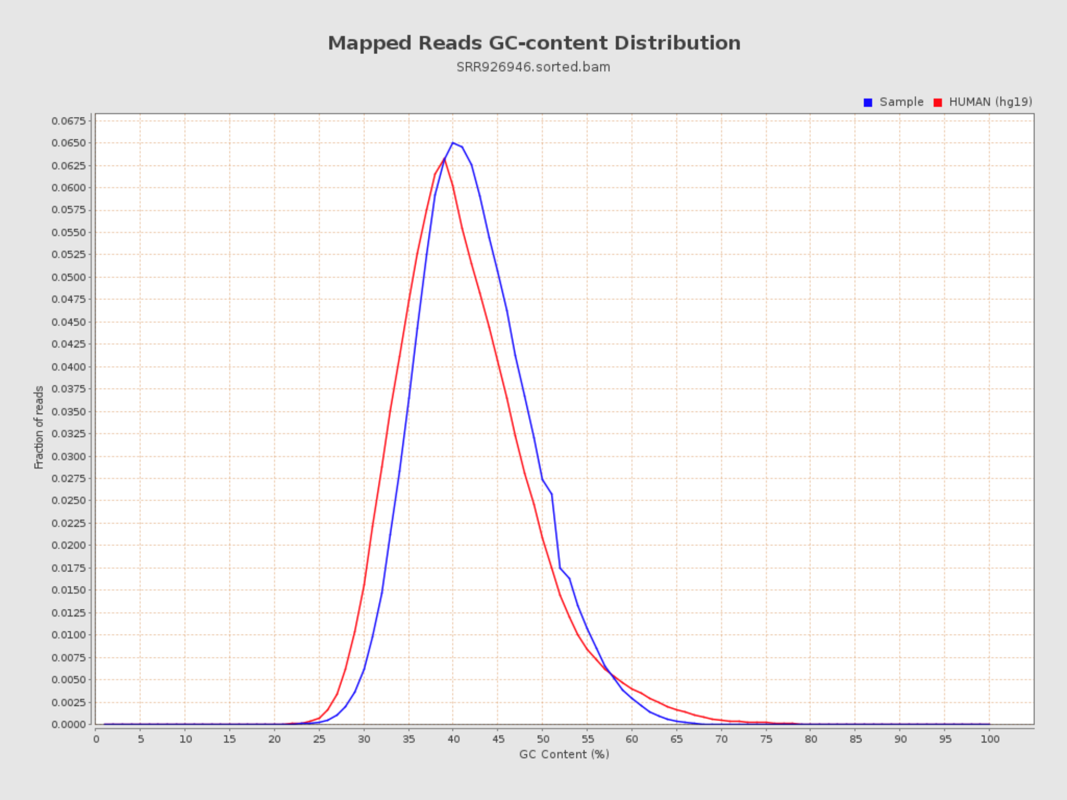
7. Results : Duplication Rate Histogram



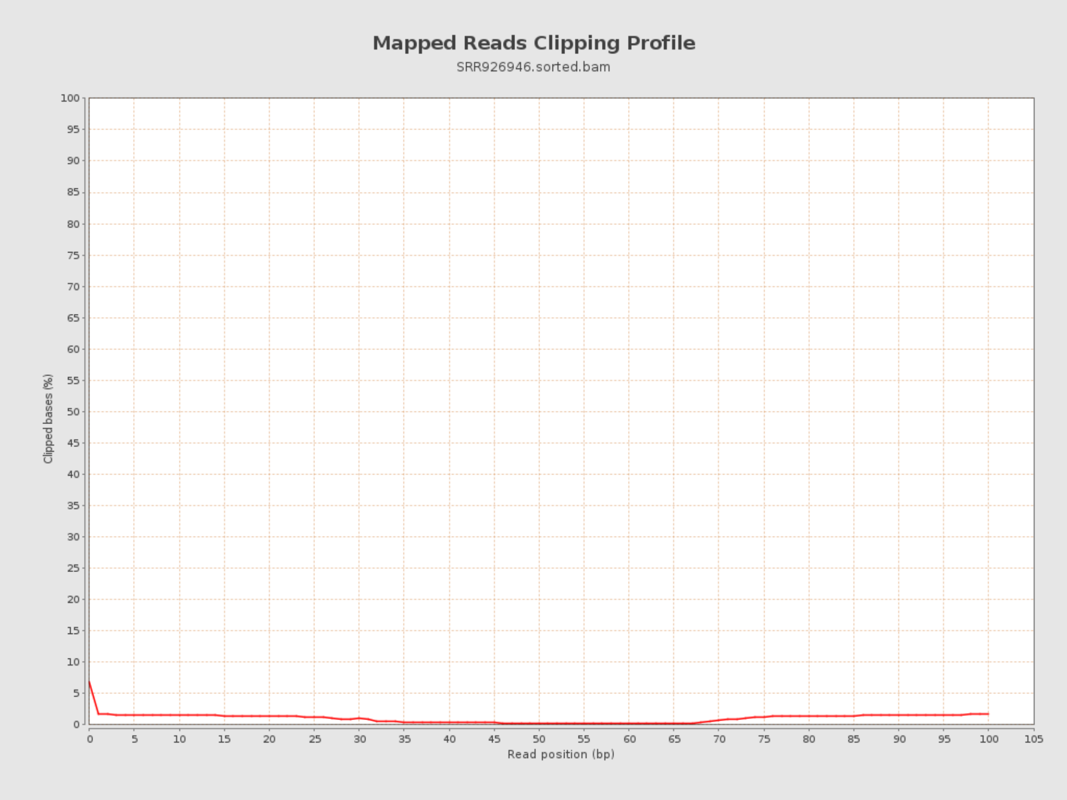
8. Results : Mapped Reads Nucleotide Content



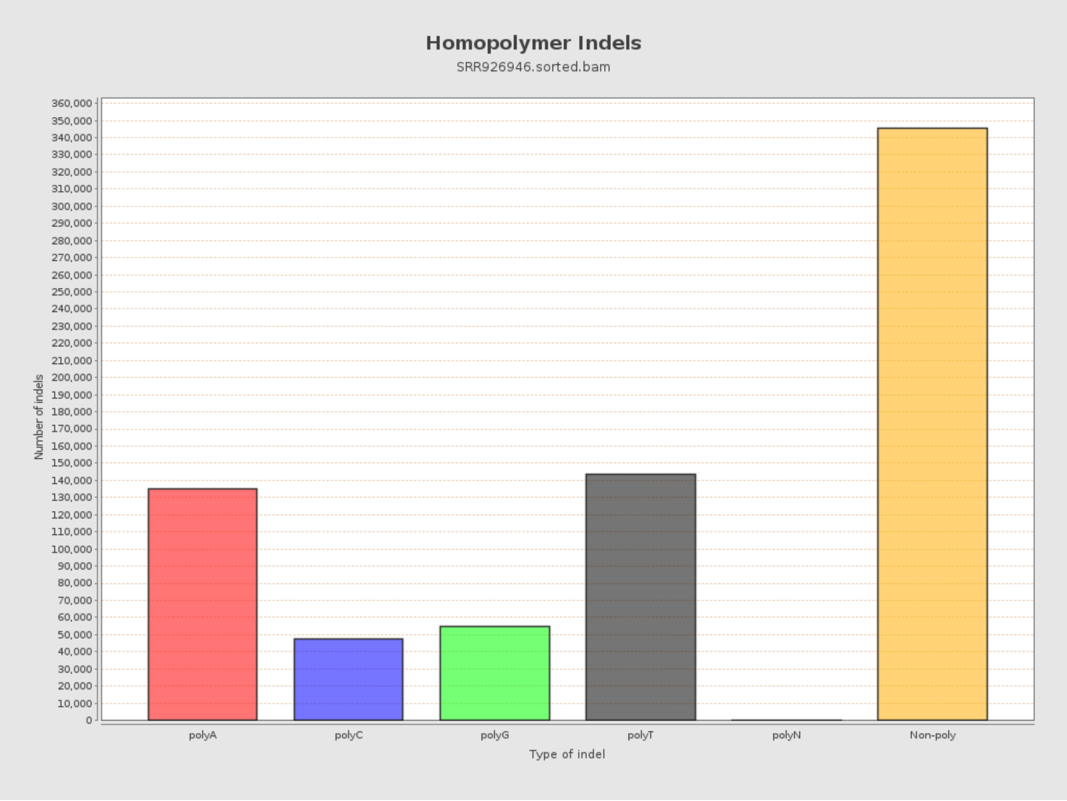
9. Results : Mapped Reads GC-content Distribution



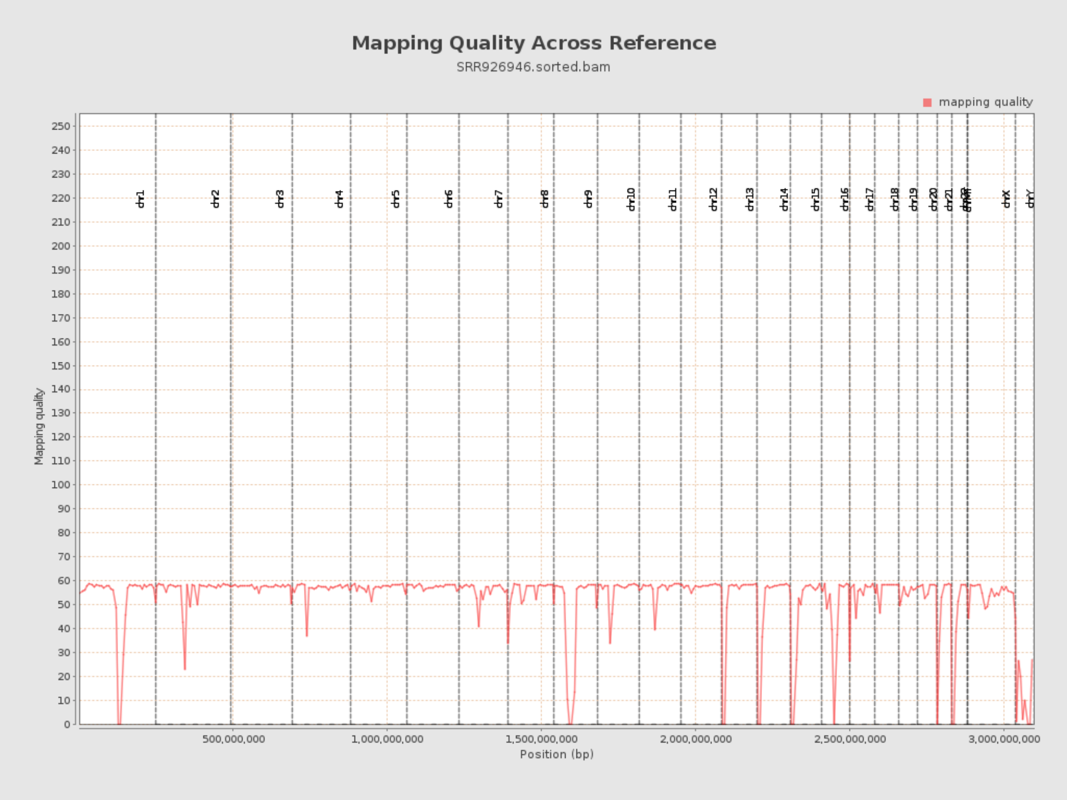
10. Results : Mapped Reads Clipping Profile



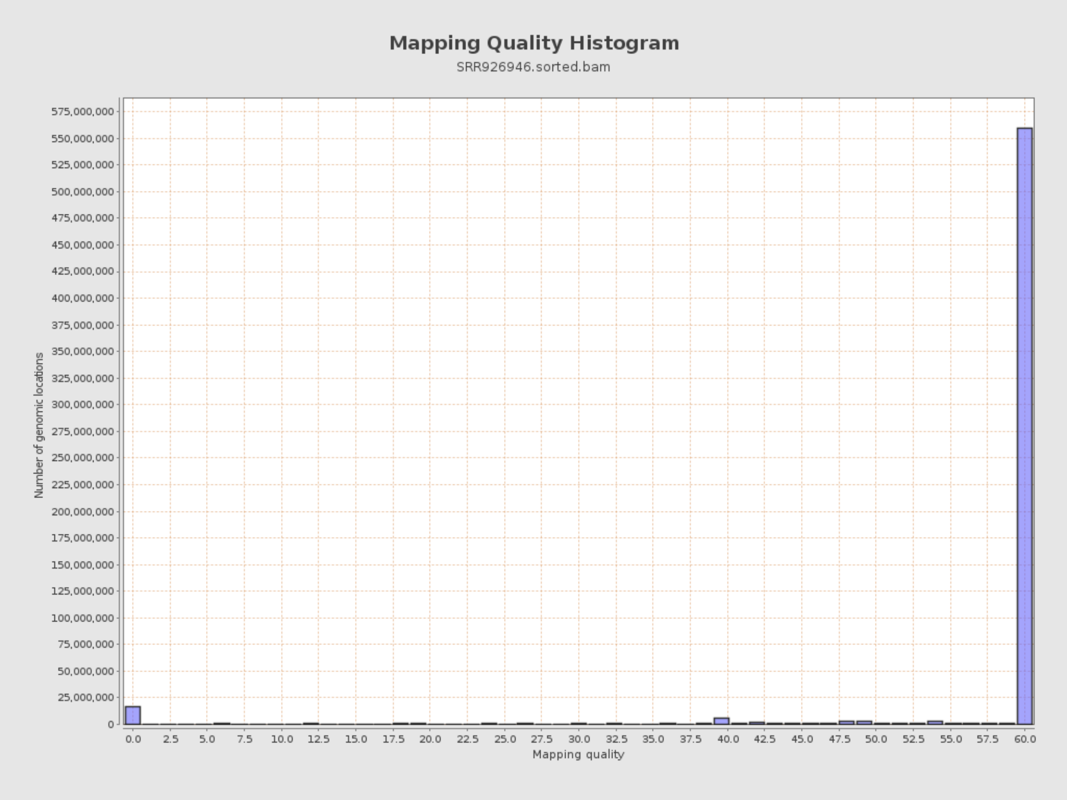
11. Results : Homopolymer Indels



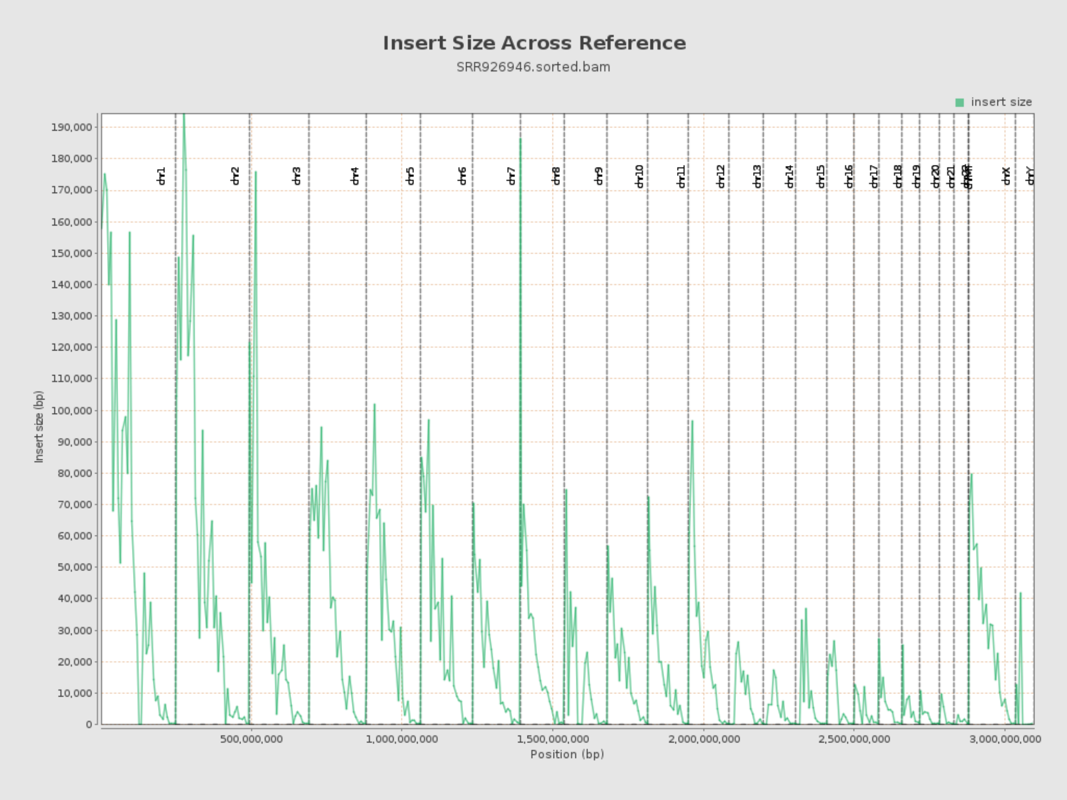
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram