Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 04:24:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926961.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_SRR926961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926961_1.fastq.gz SRR926961_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 04:24:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,290,832
Mapped reads	14,907,392 / 97.49%
Unmapped reads	383,440 / 2.51%
Mapped paired reads	14,907,392 / 97.49%
Mapped reads, first in pair	7,445,159 / 48.69%
Mapped reads, second in pair	7,462,233 / 48.8%
Mapped reads, both in pair	14,682,858 / 96.02%
Mapped reads, singletons	224,534 / 1.47%
Secondary alignments	0
Supplementary alignments	555,156 / 3.63%
Read min/max/mean length	30 / 101 / 102.51
Duplicated reads (estimated)	1,129,950 / 7.39%
Duplication rate	6.06%
Clipped reads	7,056,158 / 46.15%

2.2. ACGT Content

Number/percentage of A's	383,423,118 / 28.28%
Number/percentage of C's	268,405,139 / 19.79%
Number/percentage of T's	389,970,419 / 28.76%
Number/percentage of G's	314,169,091 / 23.17%
Number/percentage of N's	57,066 / 0%

GC Percentage	42.96%

2.3. Coverage

Mean	0.4384
Standard Deviation	1.7737

2.4. Mapping Quality

Mean Mapping Quality	52.67

2.5. Insert size

Mean	383,475.32
Standard Deviation	6,072,523.45
P25/Median/P75	144 / 188 / 256

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	12,938,351
Insertions	239,046
Mapped reads with at least one insertion	1.58%
Deletions	700,871
Mapped reads with at least one deletion	4.58%
Homopolymer indels	51.94%

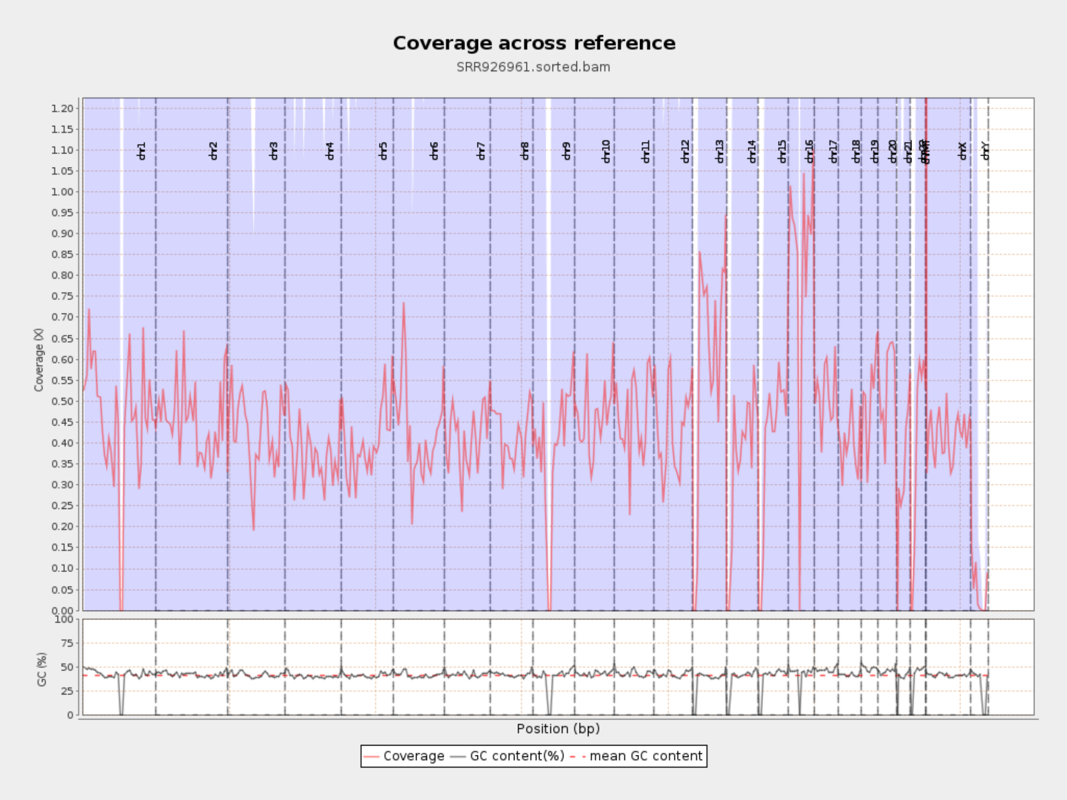
2.7. Chromosome stats

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

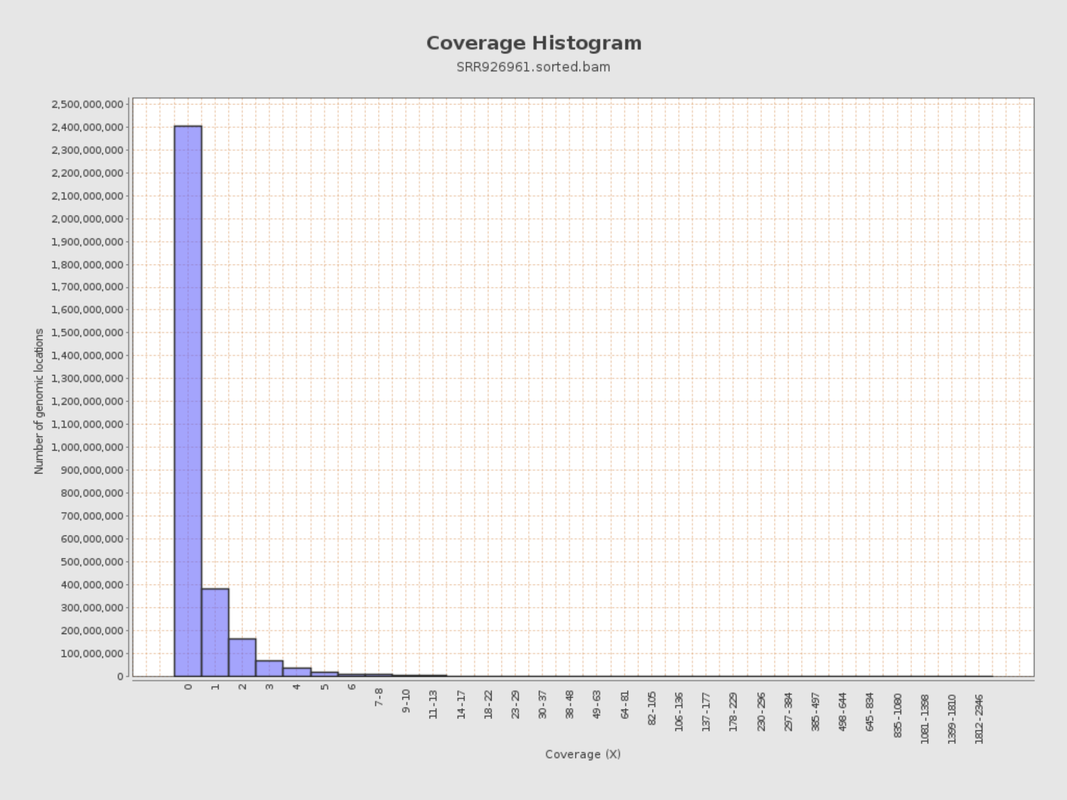
		bases	coverage	deviation
chr1	249250621	113665706	0.456	2.0642
chr2	243199373	110592503	0.4547	2.5135
chr3	198022430	84189959	0.4252	1.0798
chr4	191154276	72256217	0.378	1.563
chr5	180915260	73645158	0.4071	1.0323
chr6	171115067	72501268	0.4237	1.114
chr7	159138663	65512014	0.4117	1.1501
chr8	146364022	61517968	0.4203	1.1106
chr9	141213431	54345547	0.3848	1.5094
chr10	135534747	61975497	0.4573	3.0722
chr11	135006516	62720307	0.4646	1.3648
chr12	133851895	58446910	0.4367	1.1358
chr13	115169878	67652948	0.5874	1.3819
chr14	107349540	39137463	0.3646	1.0062
chr15	102531392	40289396	0.3929	1.067
chr16	90354753	74774175	0.8276	2.0329
chr17	81195210	41832269	0.5152	1.3225
chr18	78077248	30900231	0.3958	1.6231
chr19	59128983	29703873	0.5024	1.6581
chr20	63025520	34045084	0.5402	1.3799
chr21	48129895	16305991	0.3388	1.7043
chr22	51304566	19793234	0.3858	1.0997
chrMT	16571	3540269	213.6424	236.367
chrX	155270560	64811509	0.4174	1.0828

chrY	59373566	2915873	0.0491	1.1684

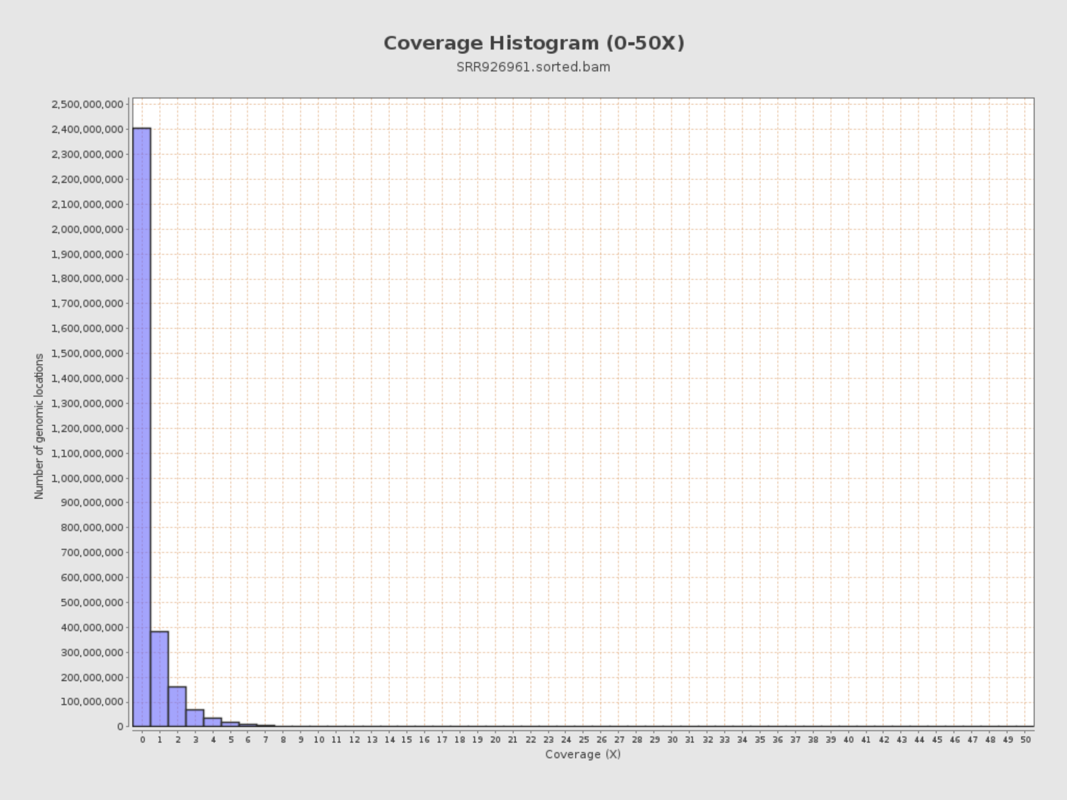
3. Results : Coverage across reference



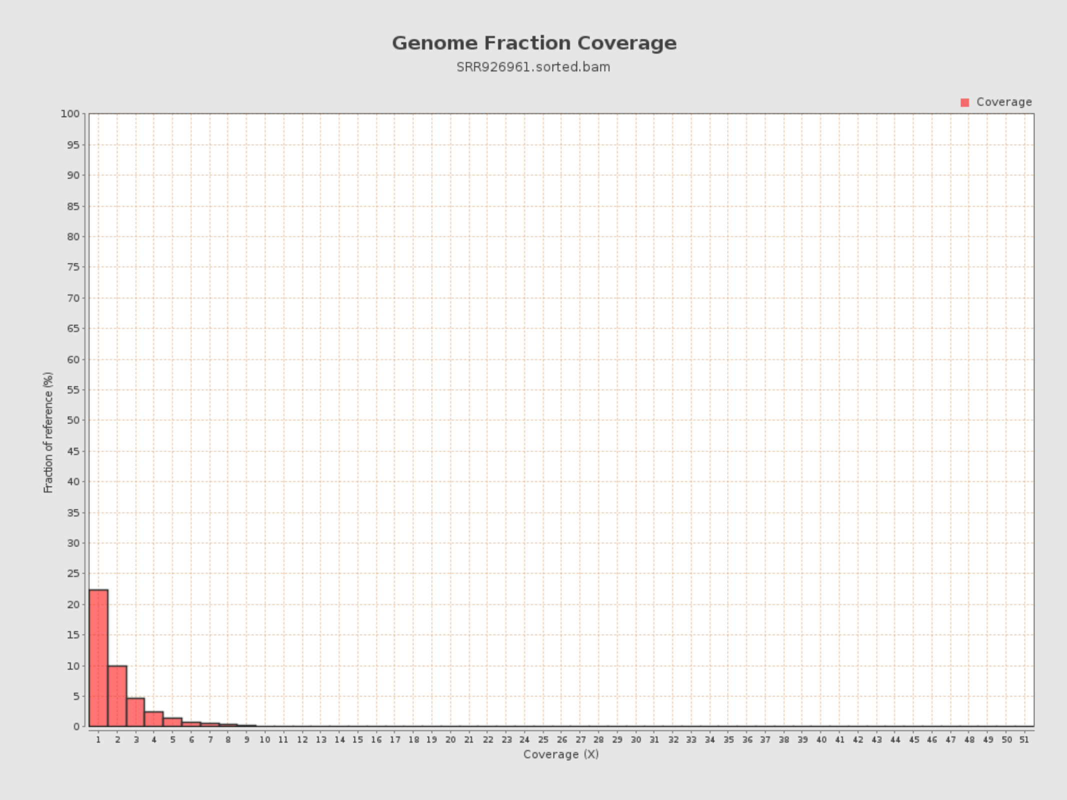
4. Results : Coverage Histogram



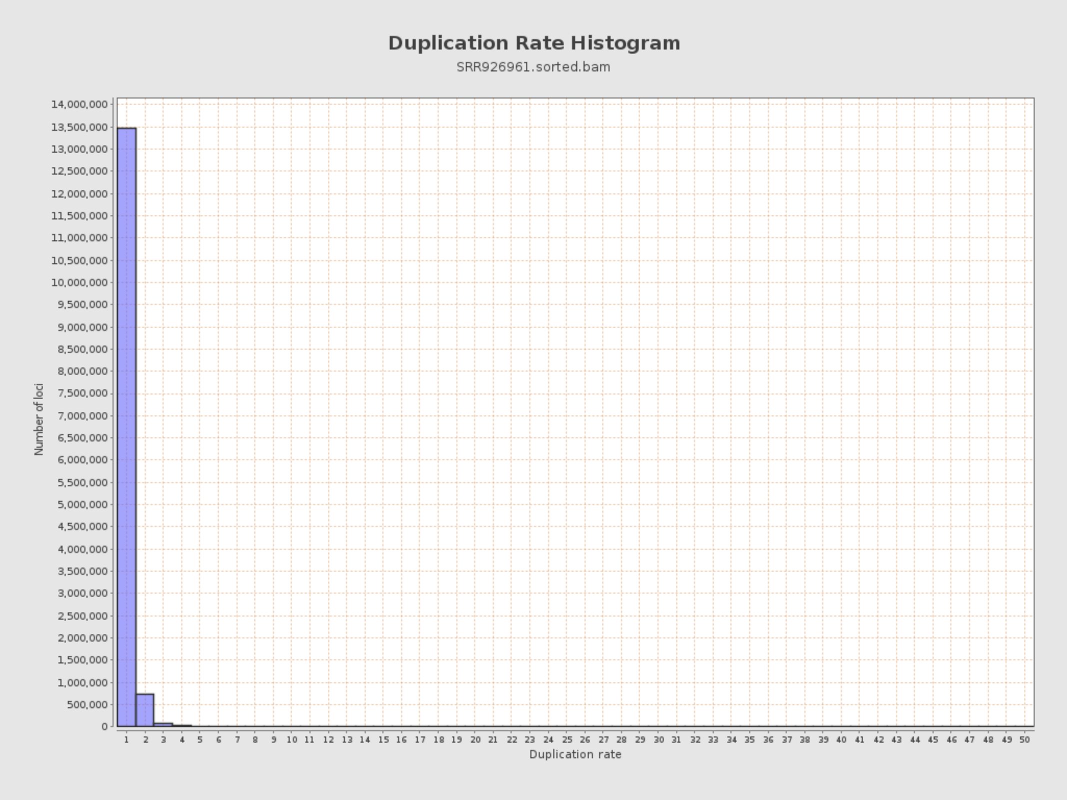
5. Results : Coverage Histogram (0-50X)



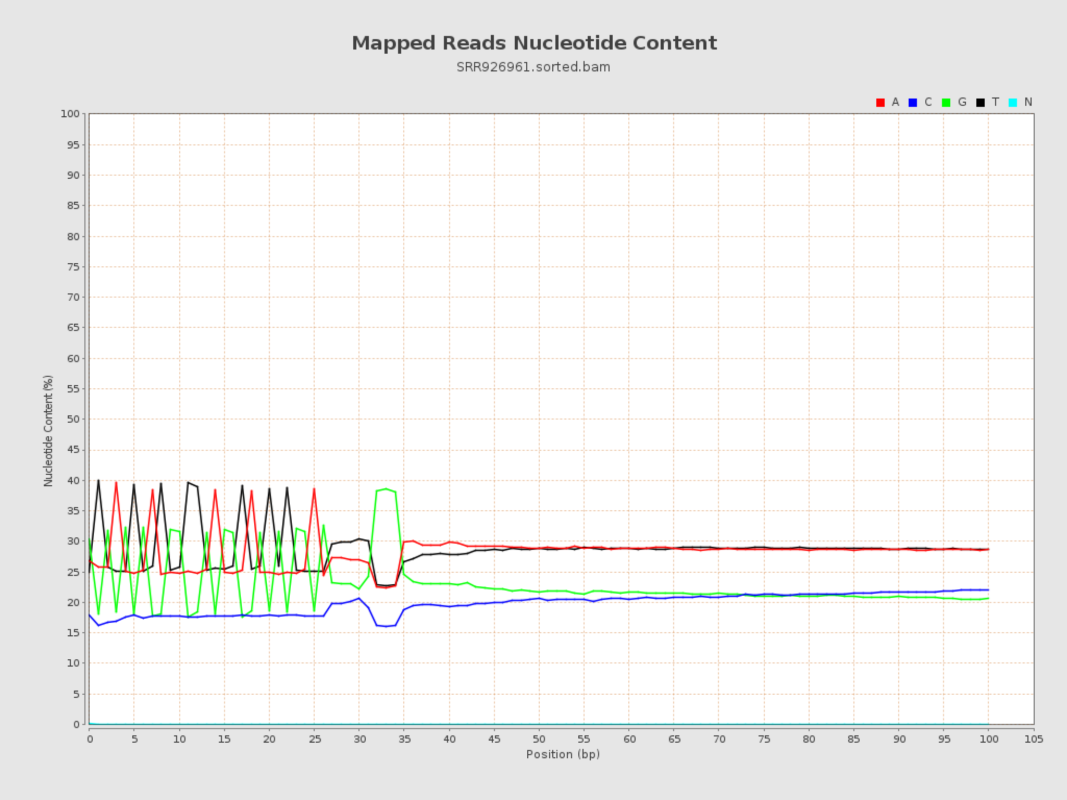
6. Results : Genome Fraction Coverage



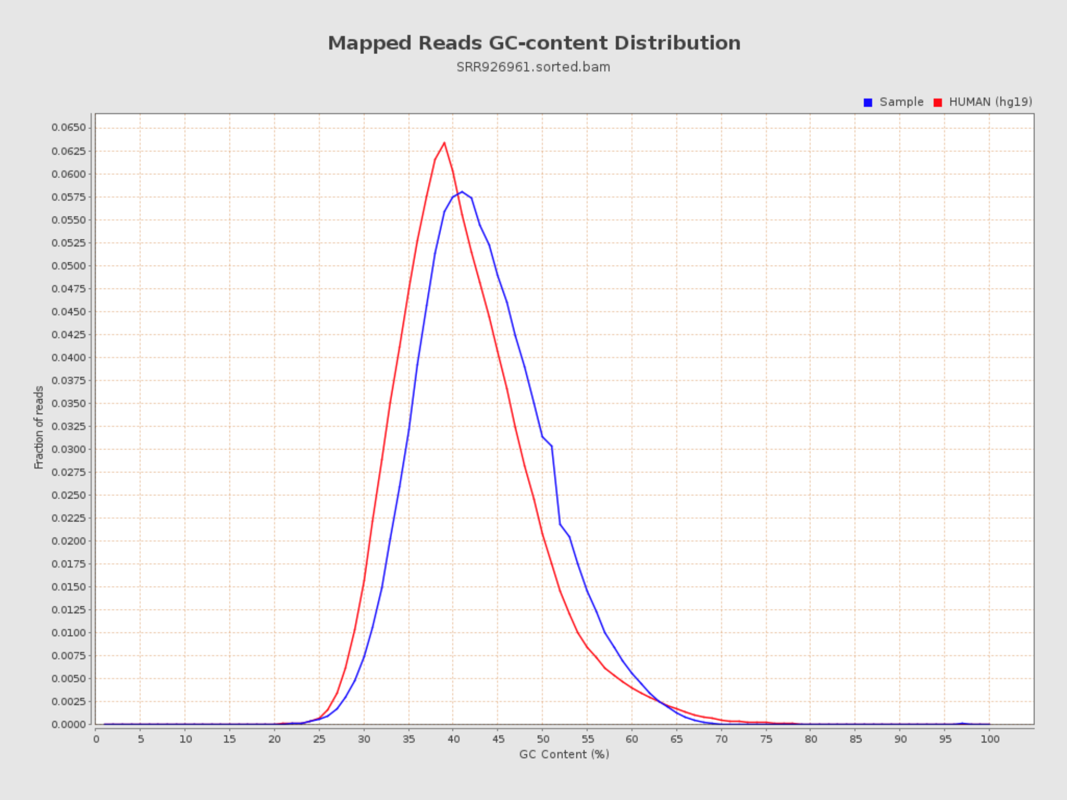
7. Results : Duplication Rate Histogram



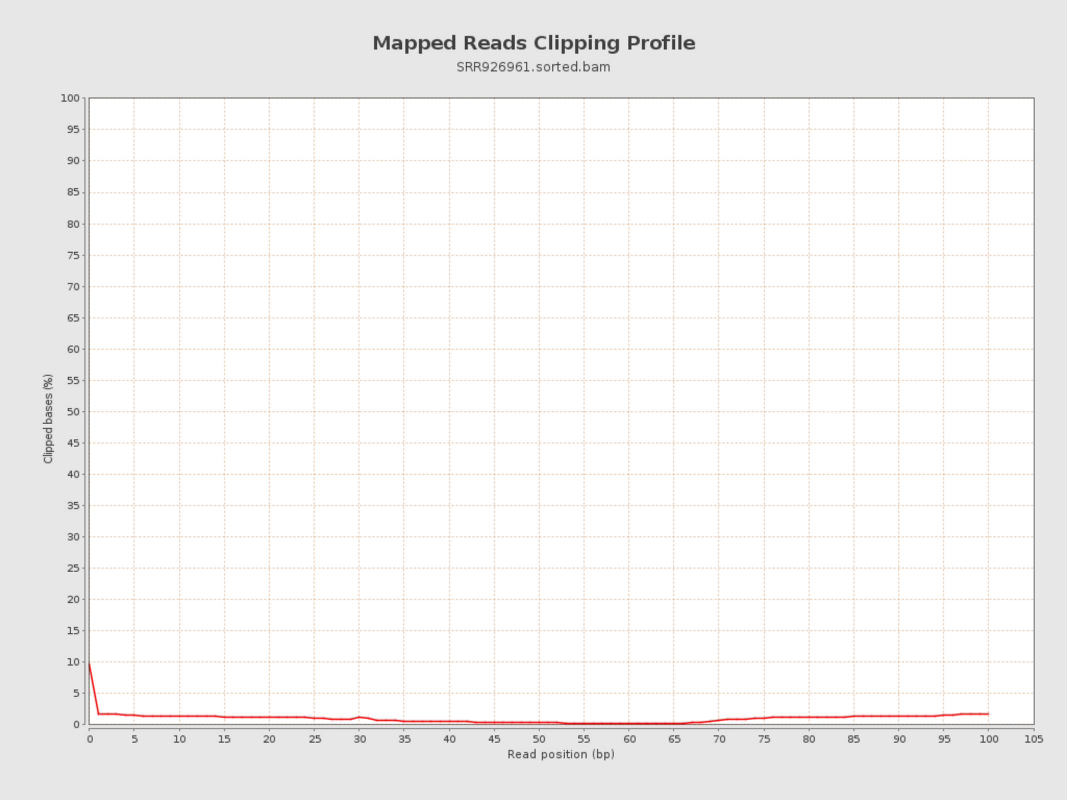
8. Results : Mapped Reads Nucleotide Content



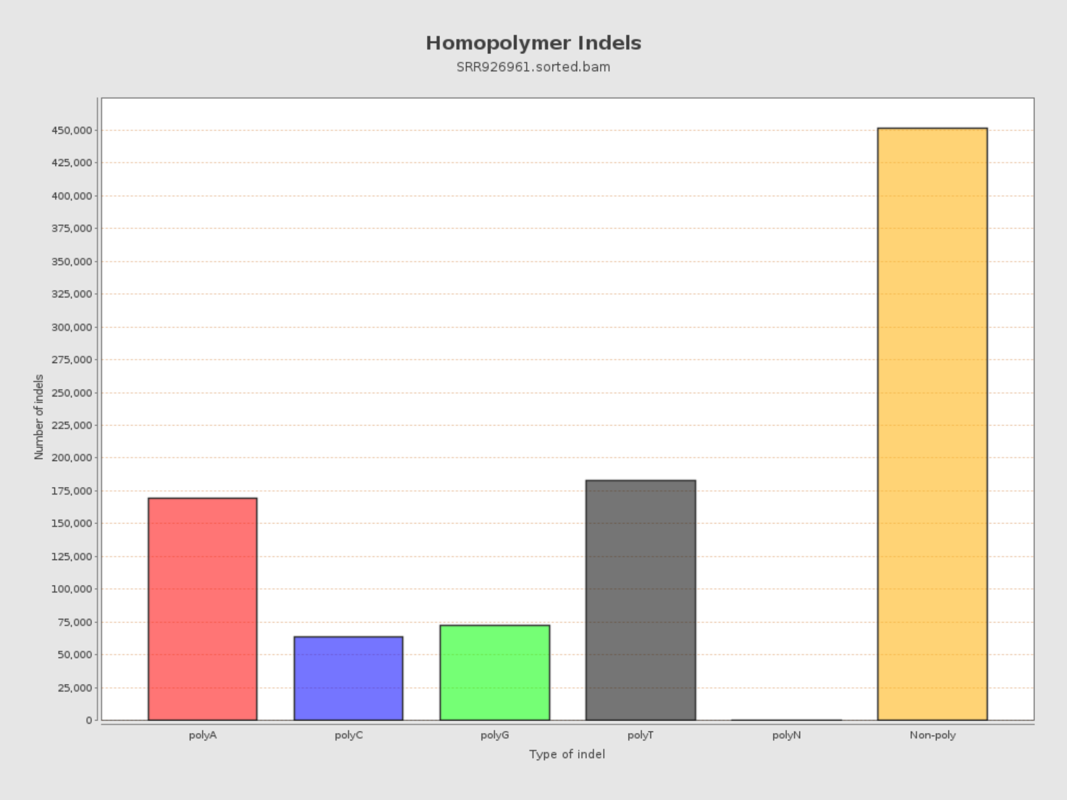
9. Results : Mapped Reads GC-content Distribution



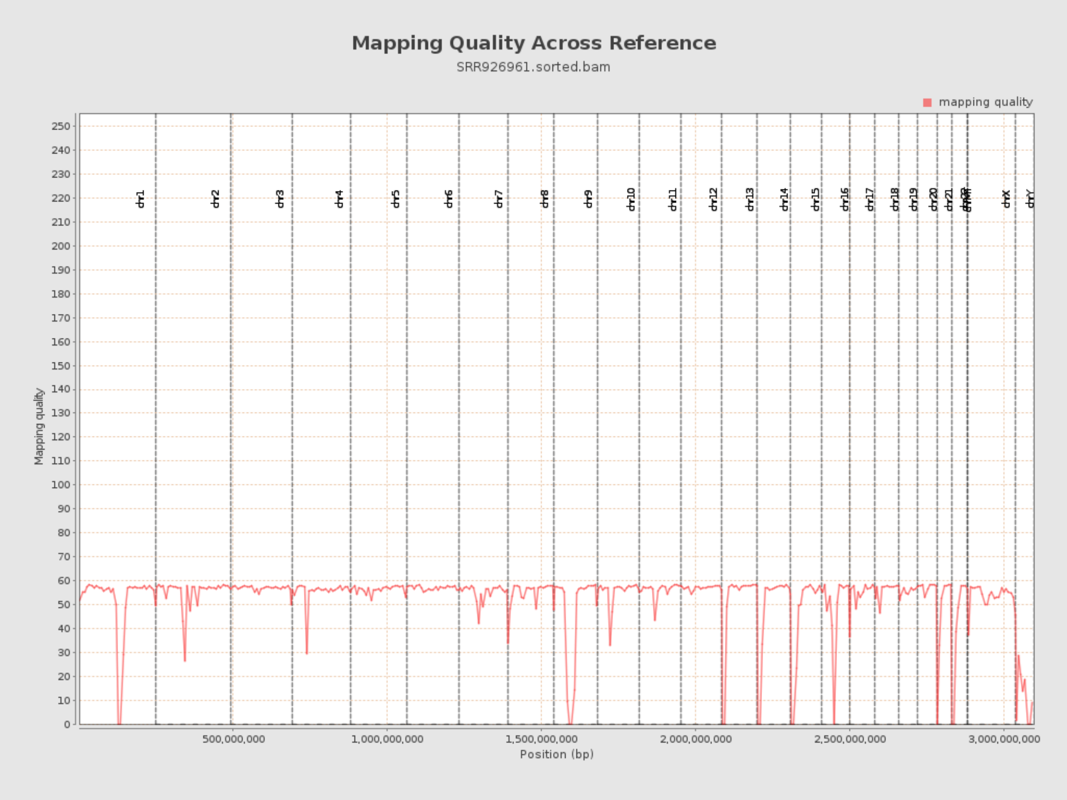
10. Results : Mapped Reads Clipping Profile



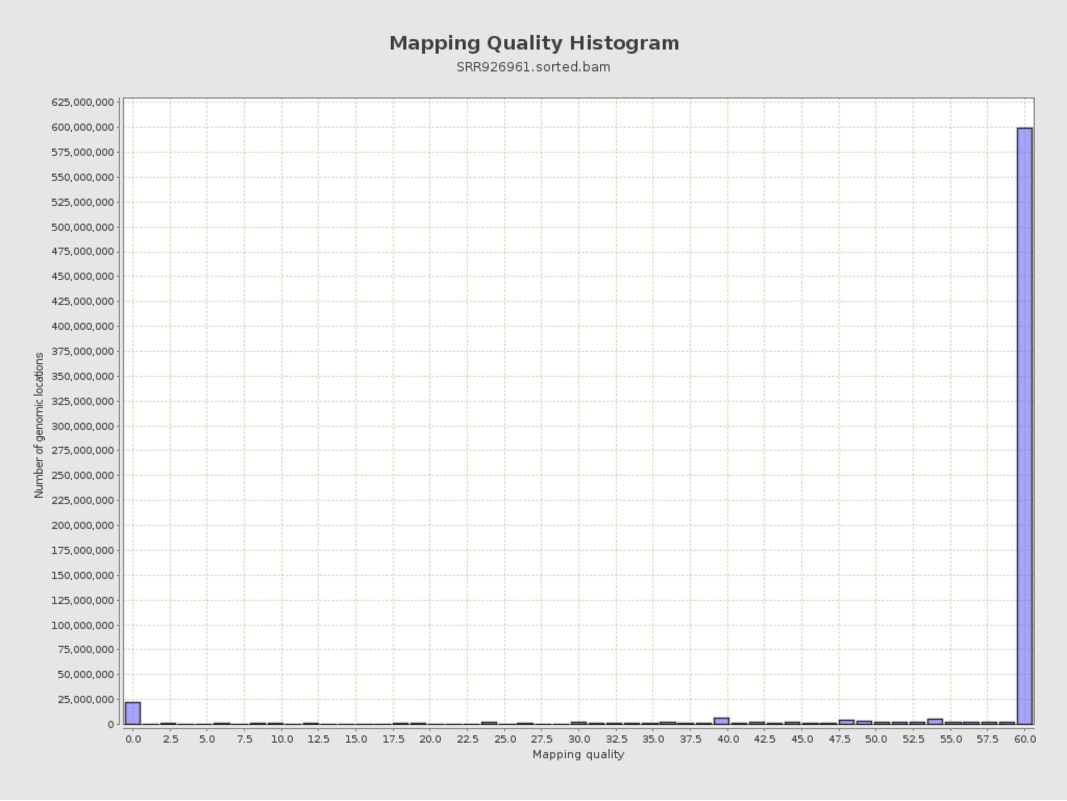
11. Results : Homopolymer Indels



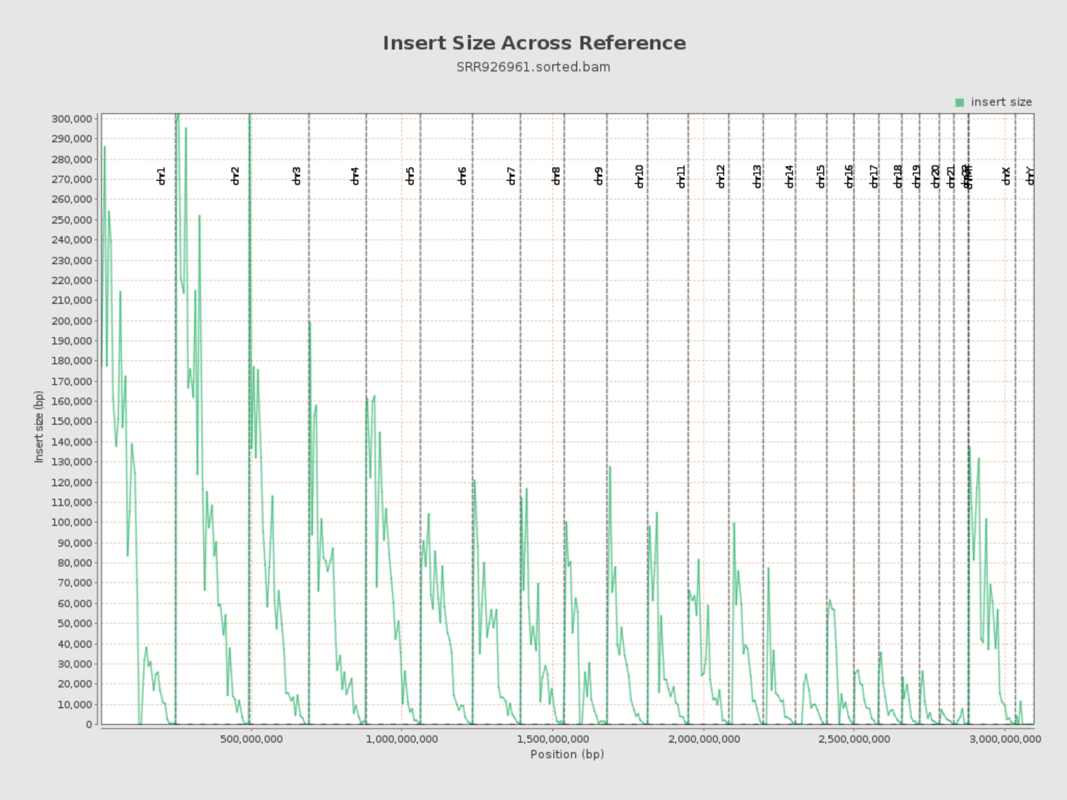
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram