Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 04:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926960.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_SRR926960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926960_1.fastq.gz SRR926960_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 04:07:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,218,966
Mapped reads	13,708,091 / 96.41%
Unmapped reads	510,875 / 3.59%
Mapped paired reads	13,708,091 / 96.41%
Mapped reads, first in pair	6,865,636 / 48.29%
Mapped reads, second in pair	6,842,455 / 48.12%
Mapped reads, both in pair	13,475,708 / 94.77%
Mapped reads, singletons	232,383 / 1.63%
Secondary alignments	0
Supplementary alignments	347,906 / 2.45%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	979,703 / 6.89%
Duplication rate	5.77%
Clipped reads	5,197,597 / 36.55%

2.2. ACGT Content

Number/percentage of A's	361,234,134 / 28.64%
Number/percentage of C's	247,707,419 / 19.64%
Number/percentage of T's	364,361,544 / 28.89%
Number/percentage of G's	287,864,194 / 22.82%
Number/percentage of N's	70,982 / 0.01%

GC Percentage	42.46%

2.3. Coverage

Mean	0.4077
Standard Deviation	2.0426

2.4. Mapping Quality

Mean Mapping Quality	50.39

2.5. Insert size

Mean	287,254.75
Standard Deviation	5,289,460.43
P25/Median/P75	148 / 196 / 268

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	12,635,089
Insertions	213,009
Mapped reads with at least one insertion	1.53%
Deletions	667,700
Mapped reads with at least one deletion	4.74%
Homopolymer indels	52.92%

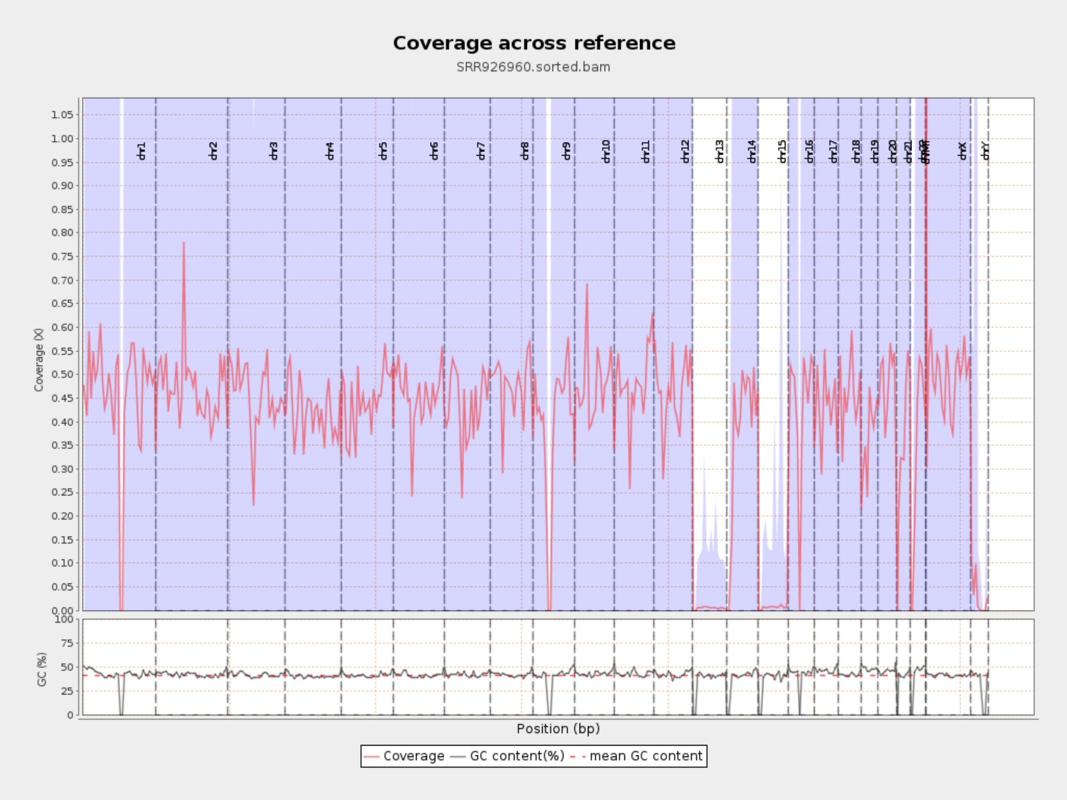
2.7. Chromosome stats

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

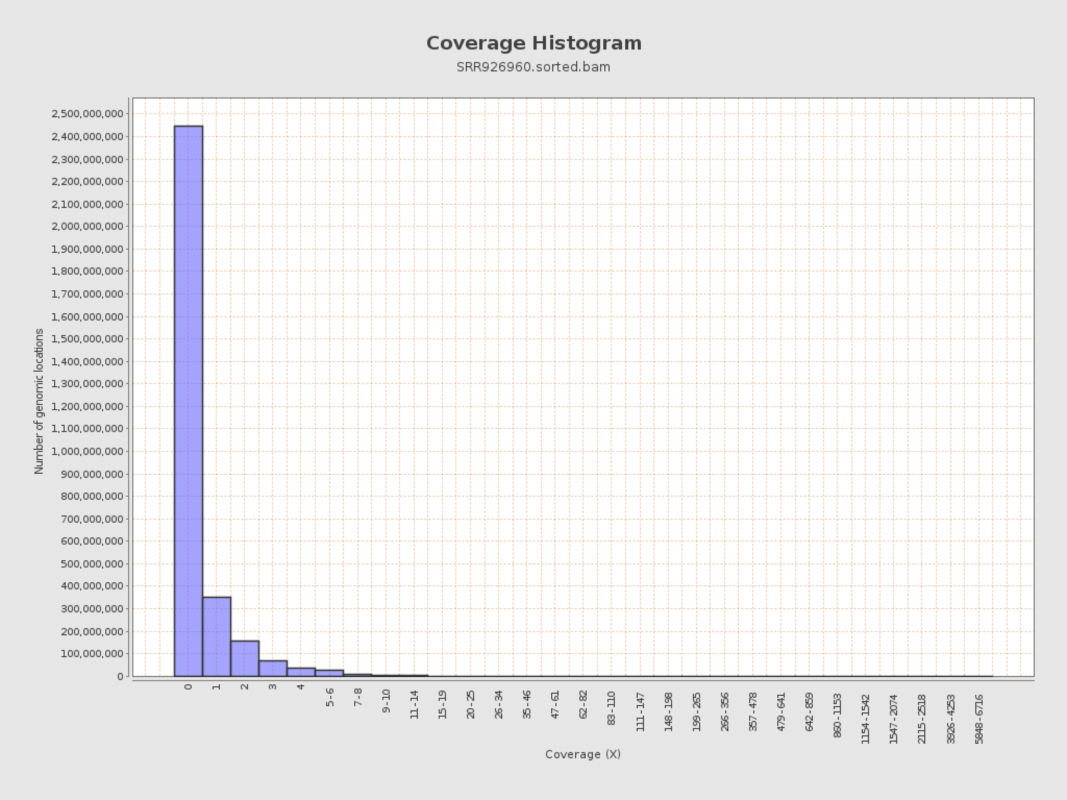
		bases	coverage	deviation
chr1	249250621	114222475	0.4583	2.3377
chr2	243199373	115407986	0.4745	2.8033
chr3	198022430	89711977	0.453	1.1032
chr4	191154276	81035566	0.4239	1.6704
chr5	180915260	80876512	0.447	1.095
chr6	171115067	78248775	0.4573	1.9419
chr7	159138663	69390023	0.436	1.1549
chr8	146364022	69938379	0.4778	1.1742
chr9	141213431	55784446	0.395	1.4418
chr10	135534747	64534479	0.4761	3.7248
chr11	135006516	64710773	0.4793	1.3551
chr12	133851895	62679784	0.4683	5.2378
chr13	115169878	591048	0.0051	0.1453
chr14	107349540	39826062	0.371	1.0023
chr15	102531392	696530	0.0068	0.3092
chr16	90354753	38319456	0.4241	1.1503
chr17	81195210	35238189	0.434	1.1424
chr18	78077248	35789071	0.4584	1.5427
chr19	59128983	21788038	0.3685	1.4832
chr20	63025520	30611699	0.4857	1.1987
chr21	48129895	17060939	0.3545	2.5305
chr22	51304566	17230235	0.3358	0.9704
chrMT	16571	139716	8.4314	9.6722
chrX	155270560	76518126	0.4928	1.2875

chrY	59373566	1851723	0.0312	1.1466

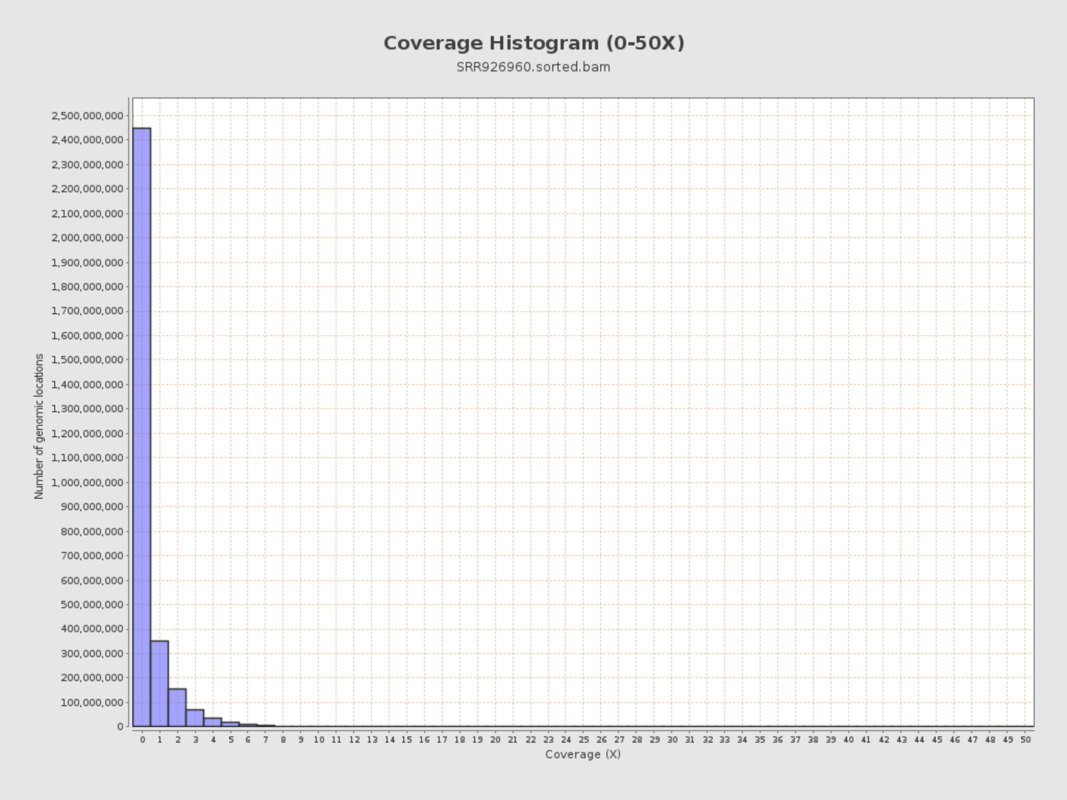
3. Results : Coverage across reference



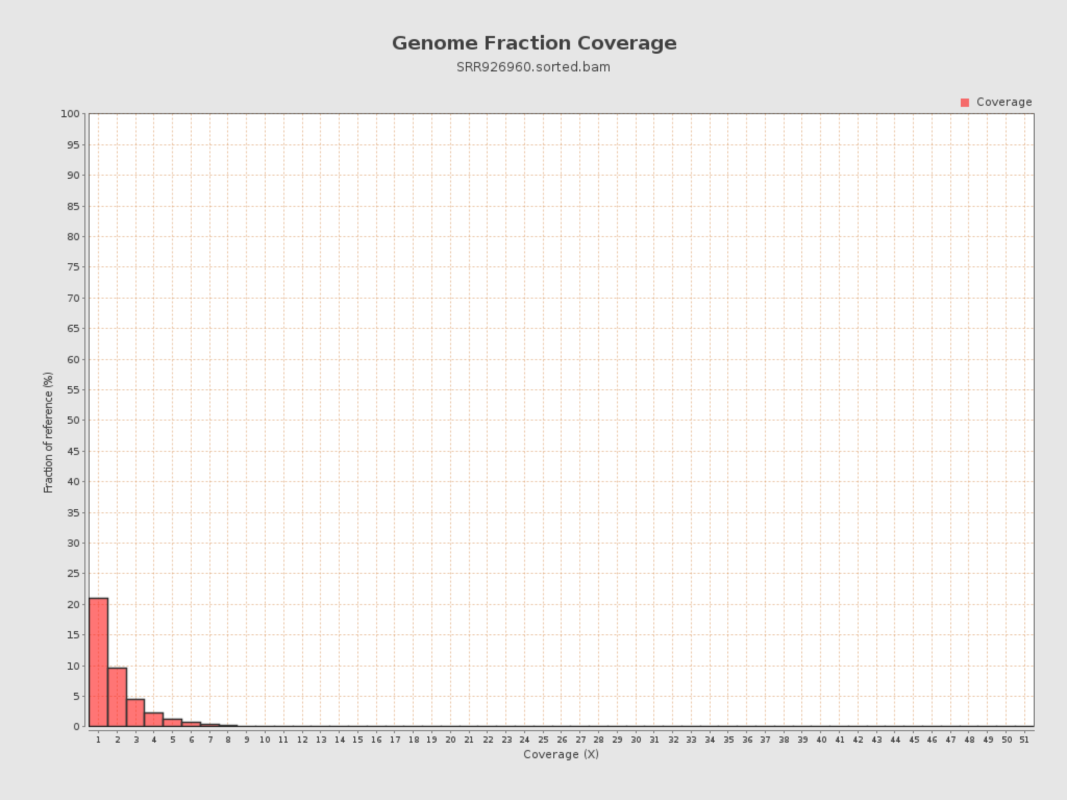
4. Results : Coverage Histogram



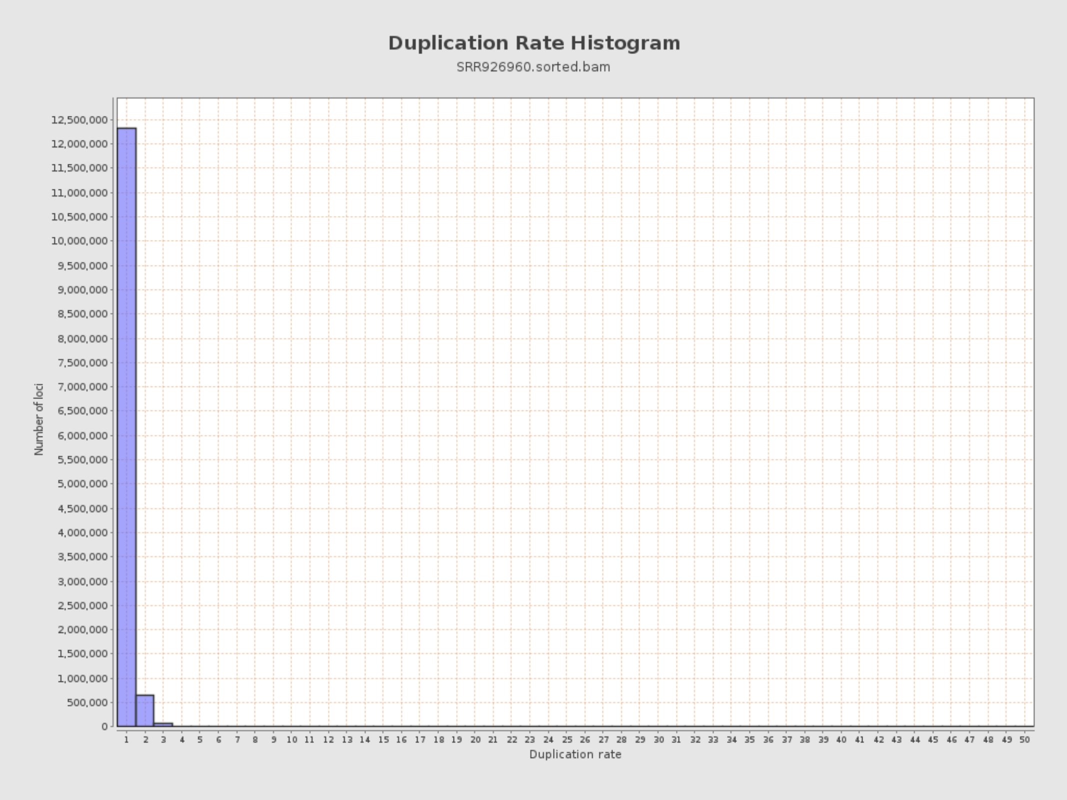
5. Results : Coverage Histogram (0-50X)



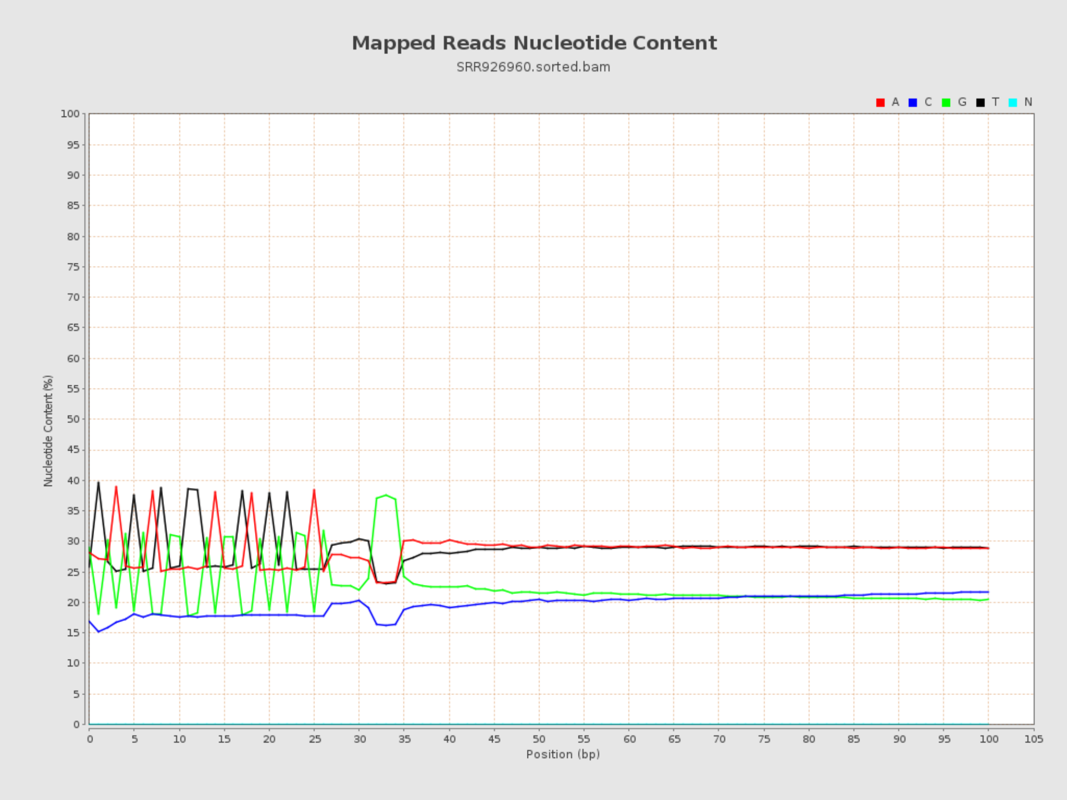
6. Results : Genome Fraction Coverage



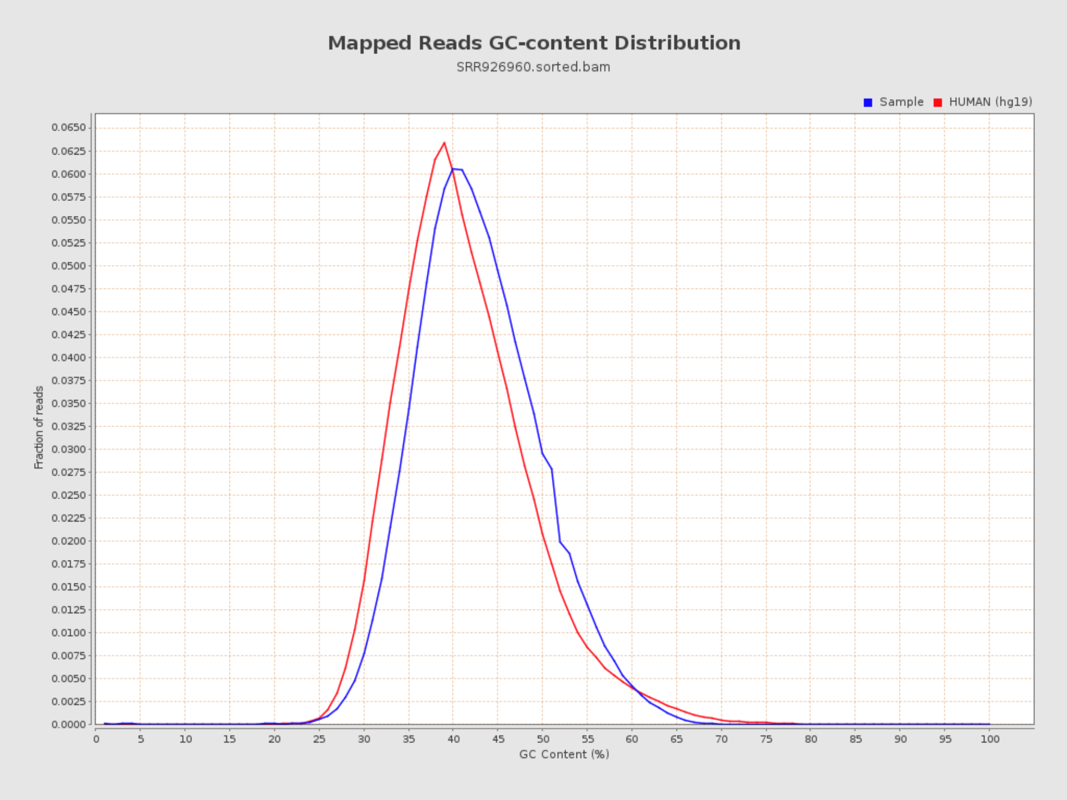
7. Results : Duplication Rate Histogram



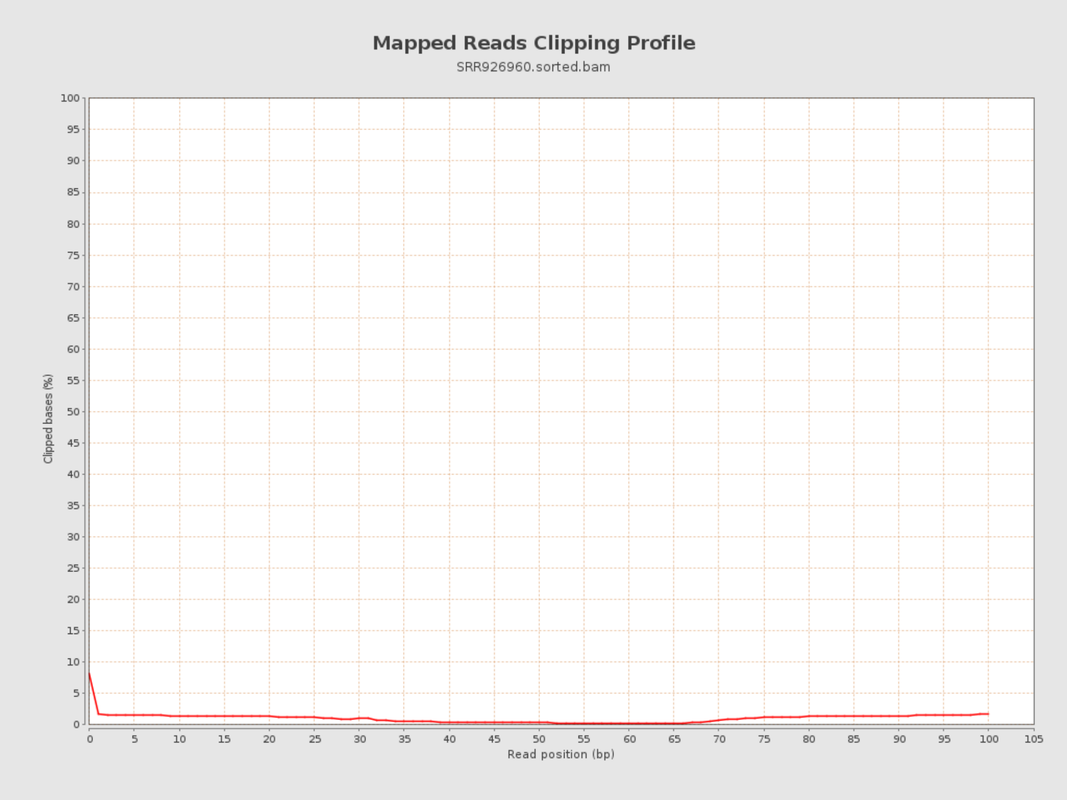
8. Results : Mapped Reads Nucleotide Content



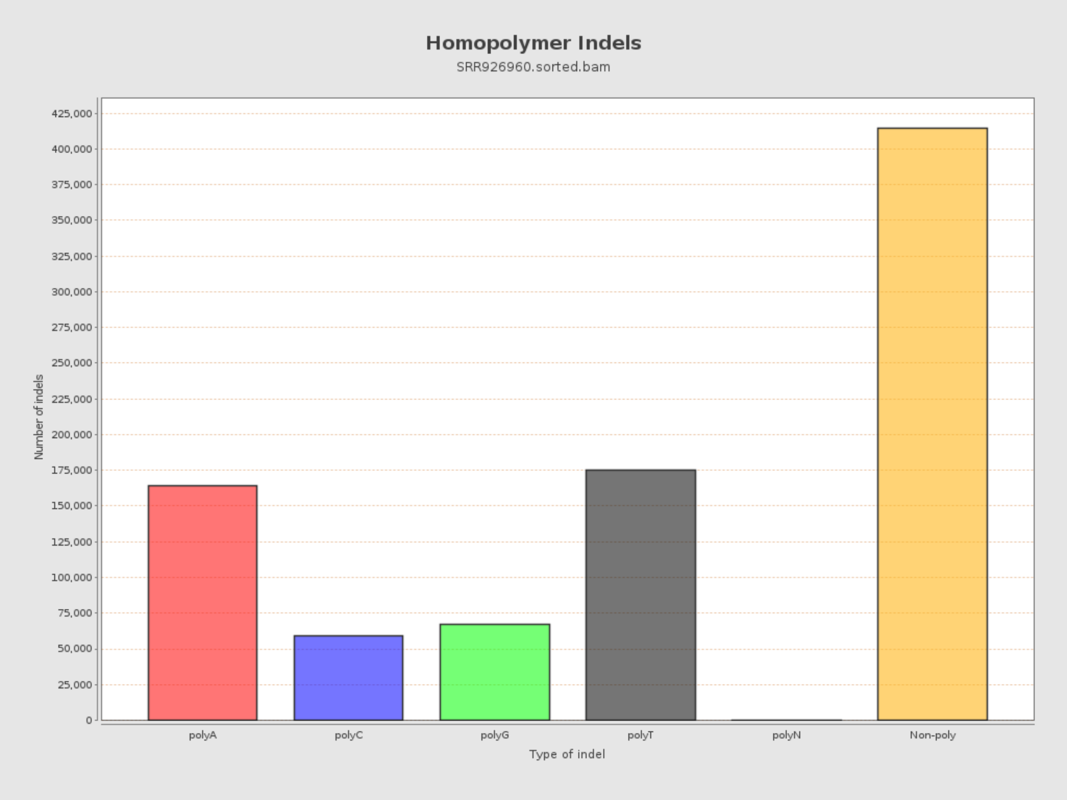
9. Results : Mapped Reads GC-content Distribution



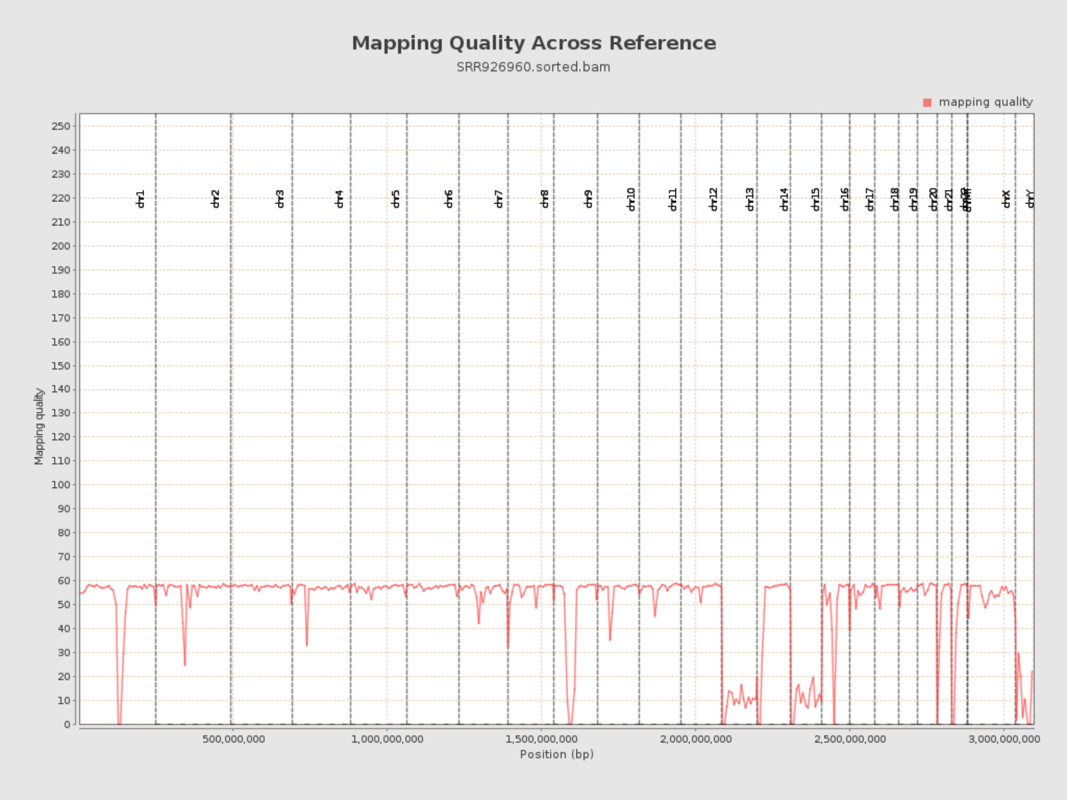
10. Results : Mapped Reads Clipping Profile



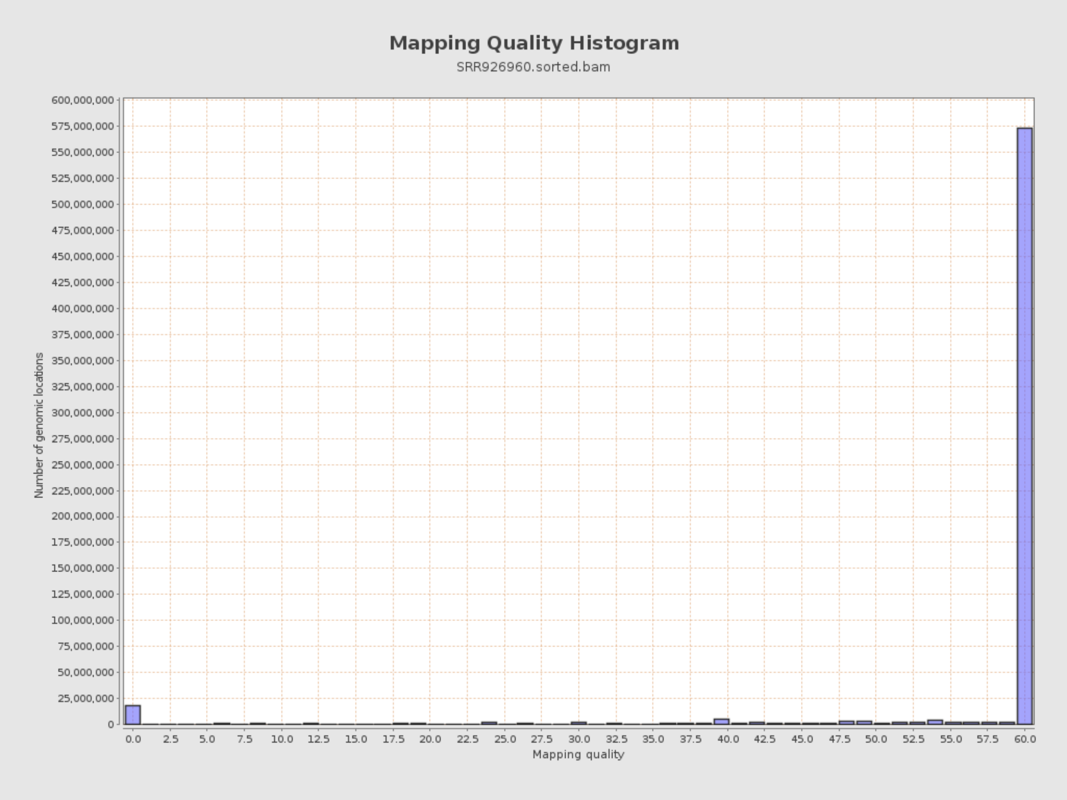
11. Results : Homopolymer Indels



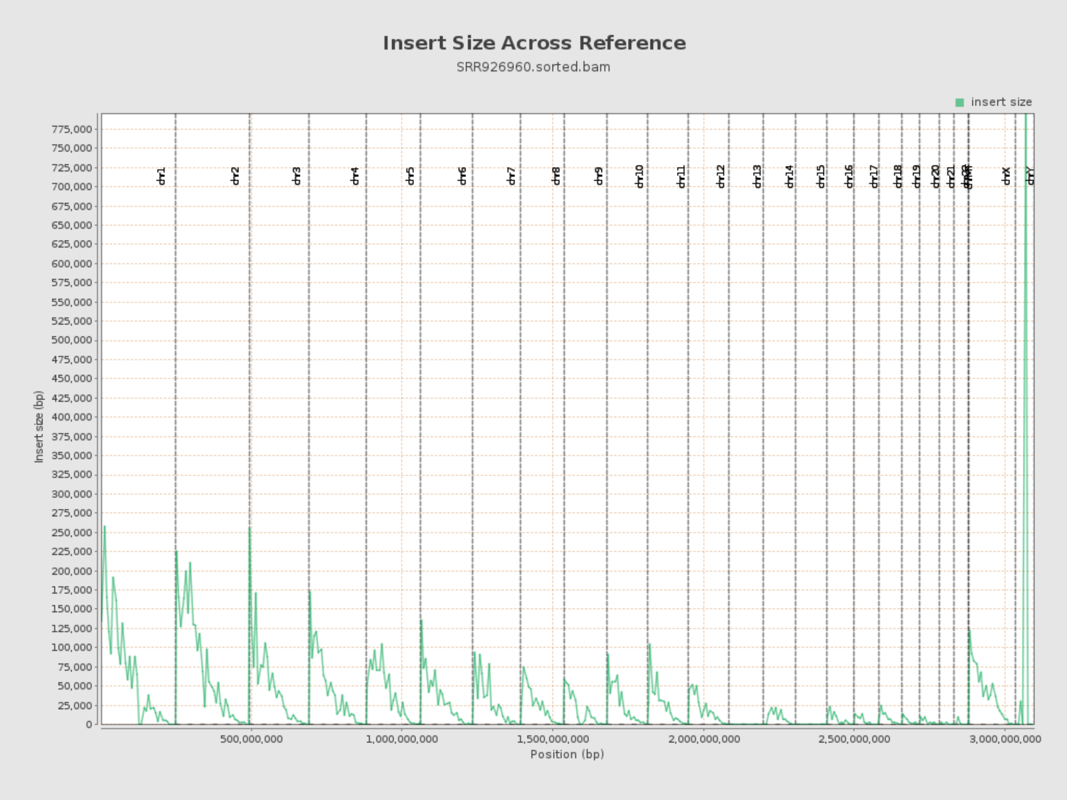
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram