Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 18:24:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926920.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_SRR926920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926920_1.fastq.gz SRR926920_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 18:24:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,155,932
Mapped reads	21,485,426 / 92.79%
Unmapped reads	1,670,506 / 7.21%
Mapped paired reads	21,485,426 / 92.79%
Mapped reads, first in pair	10,818,150 / 46.72%
Mapped reads, second in pair	10,667,276 / 46.07%
Mapped reads, both in pair	21,179,808 / 91.47%
Mapped reads, singletons	305,618 / 1.32%
Secondary alignments	0
Supplementary alignments	245,445 / 1.06%
Read min/max/mean length	30 / 101 / 101.43
Duplicated reads (estimated)	1,308,386 / 5.65%
Duplication rate	4.98%
Clipped reads	5,641,625 / 24.36%

2.2. ACGT Content

Number/percentage of A's	581,479,583 / 28.67%
Number/percentage of C's	406,688,138 / 20.05%
Number/percentage of T's	586,349,693 / 28.91%
Number/percentage of G's	453,704,239 / 22.37%
Number/percentage of N's	195,232 / 0.01%

GC Percentage	42.42%

2.3. Coverage

Mean	0.6557
Standard Deviation	2.6171

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	116,533.6
Standard Deviation	3,346,434.54
P25/Median/P75	151 / 195 / 262

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	20,873,625
Insertions	329,436
Mapped reads with at least one insertion	1.51%
Deletions	1,114,873
Mapped reads with at least one deletion	5.05%
Homopolymer indels	53.04%

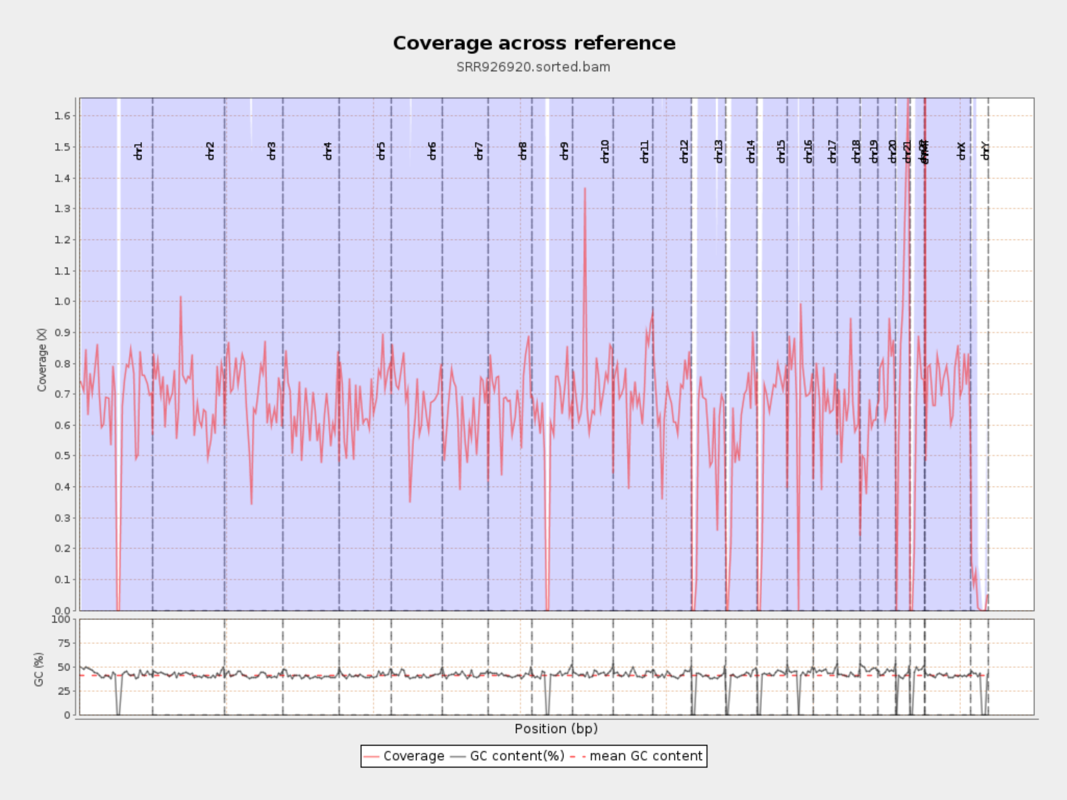
2.7. Chromosome stats

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

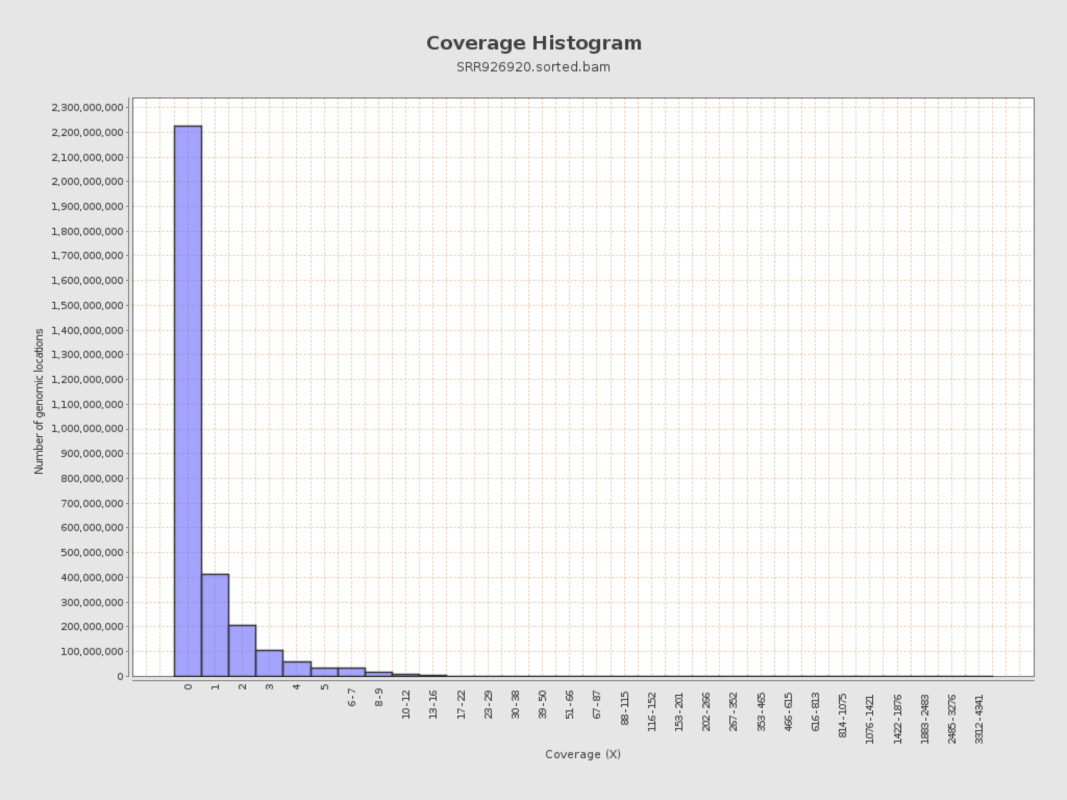
		bases	coverage	deviation
chr1	249250621	166713039	0.6689	2.2887
chr2	243199373	170077466	0.6993	2.988
chr3	198022430	138994267	0.7019	1.5626
chr4	191154276	121834329	0.6374	1.586
chr5	180915260	123398982	0.6821	1.4804
chr6	171115067	116469057	0.6806	1.7791
chr7	159138663	100292103	0.6302	1.6407
chr8	146364022	101847019	0.6958	1.5863
chr9	141213431	83901171	0.5941	2.4723
chr10	135534747	101172624	0.7465	8.4027
chr11	135006516	97175393	0.7198	1.8368
chr12	133851895	90361097	0.6751	1.595
chr13	115169878	58112616	0.5046	1.2999
chr14	107349540	58097503	0.5412	1.3686
chr15	102531392	60052155	0.5857	1.4834
chr16	90354753	63105188	0.6984	3.4424
chr17	81195210	53782192	0.6624	1.6693
chr18	78077248	52725086	0.6753	2.6939
chr19	59128983	32110764	0.5431	1.6684
chr20	63025520	48416491	0.7682	1.7459
chr21	48129895	47733705	0.9918	2.6231
chr22	51304566	26739261	0.5212	1.4352
chrMT	16571	74587	4.5011	3.54
chrX	155270560	113898003	0.7335	1.652

chrY	59373566	2909506	0.049	0.9773

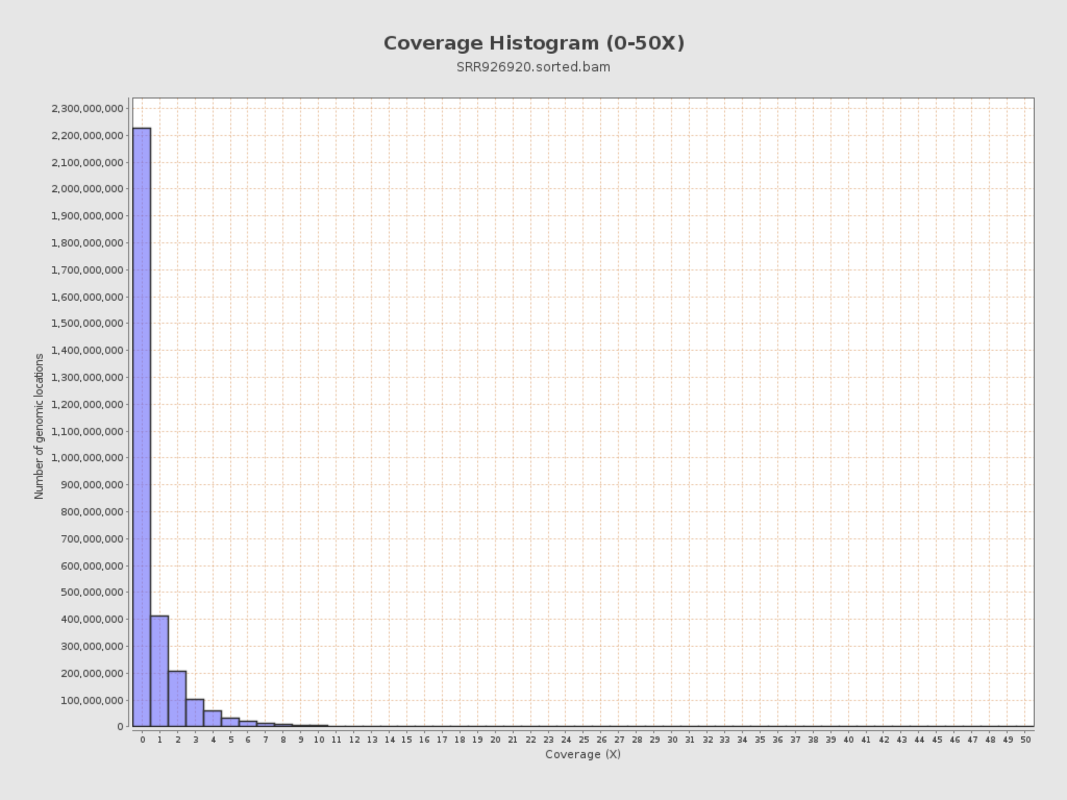
3. Results : Coverage across reference



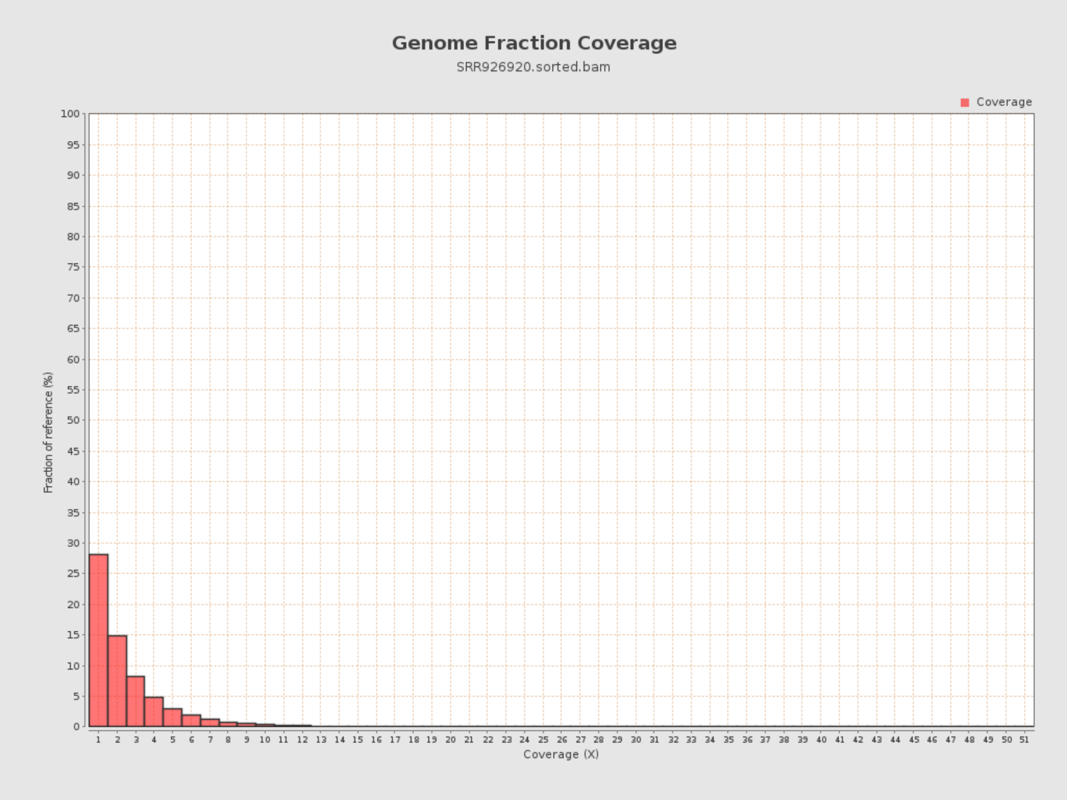
4. Results : Coverage Histogram



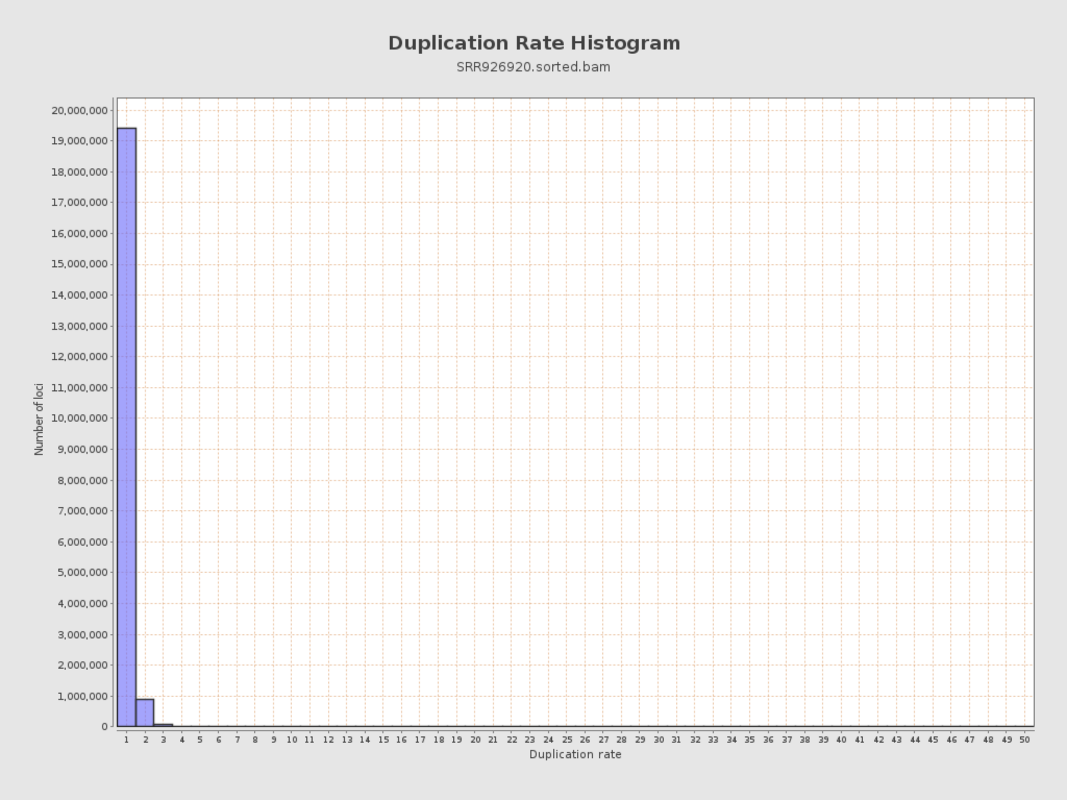
5. Results : Coverage Histogram (0-50X)



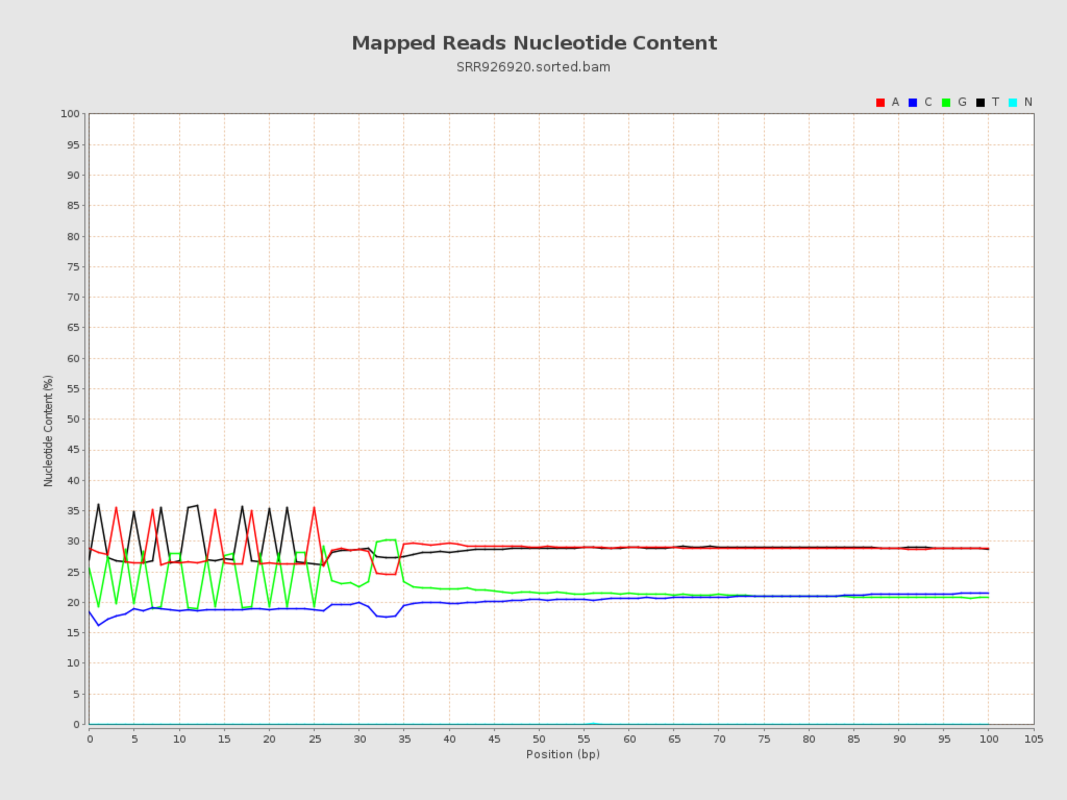
6. Results : Genome Fraction Coverage



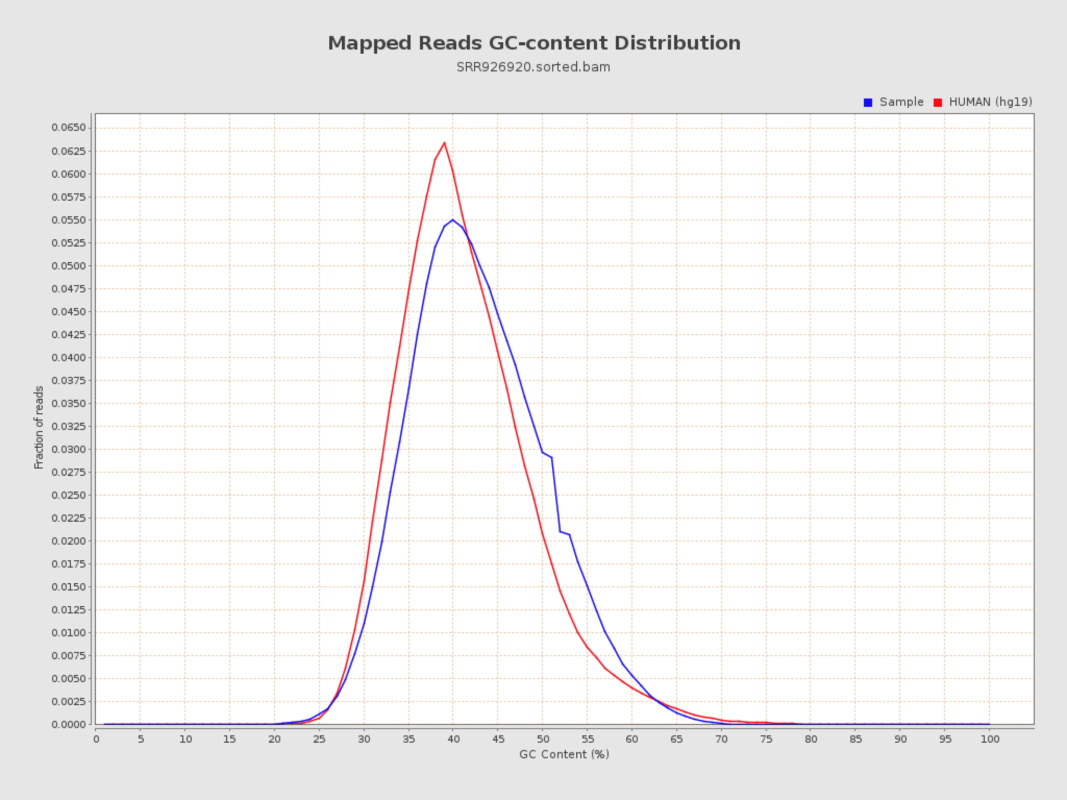
7. Results : Duplication Rate Histogram



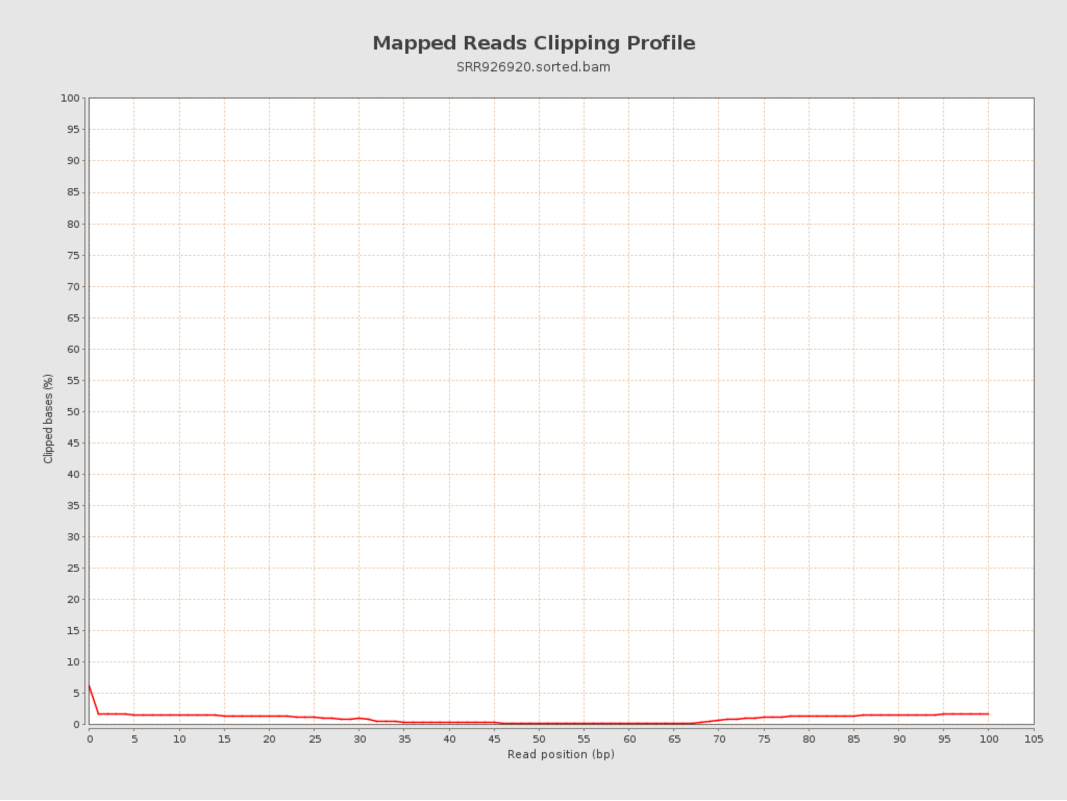
8. Results : Mapped Reads Nucleotide Content



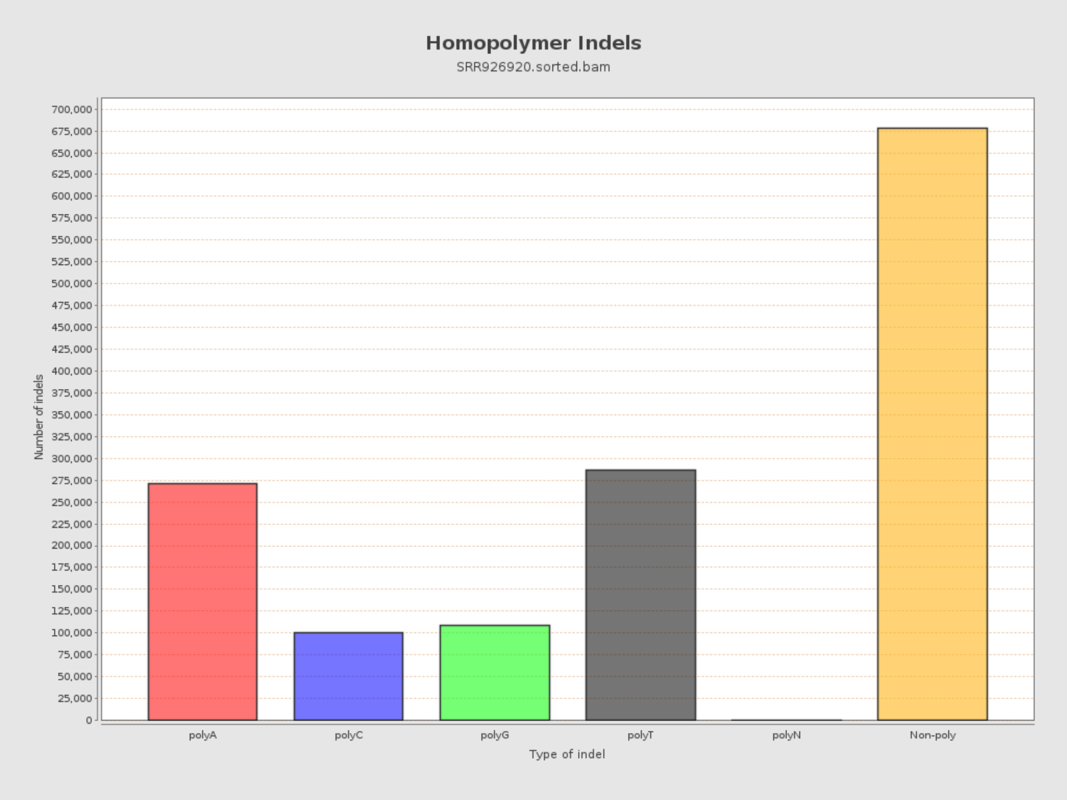
9. Results : Mapped Reads GC-content Distribution



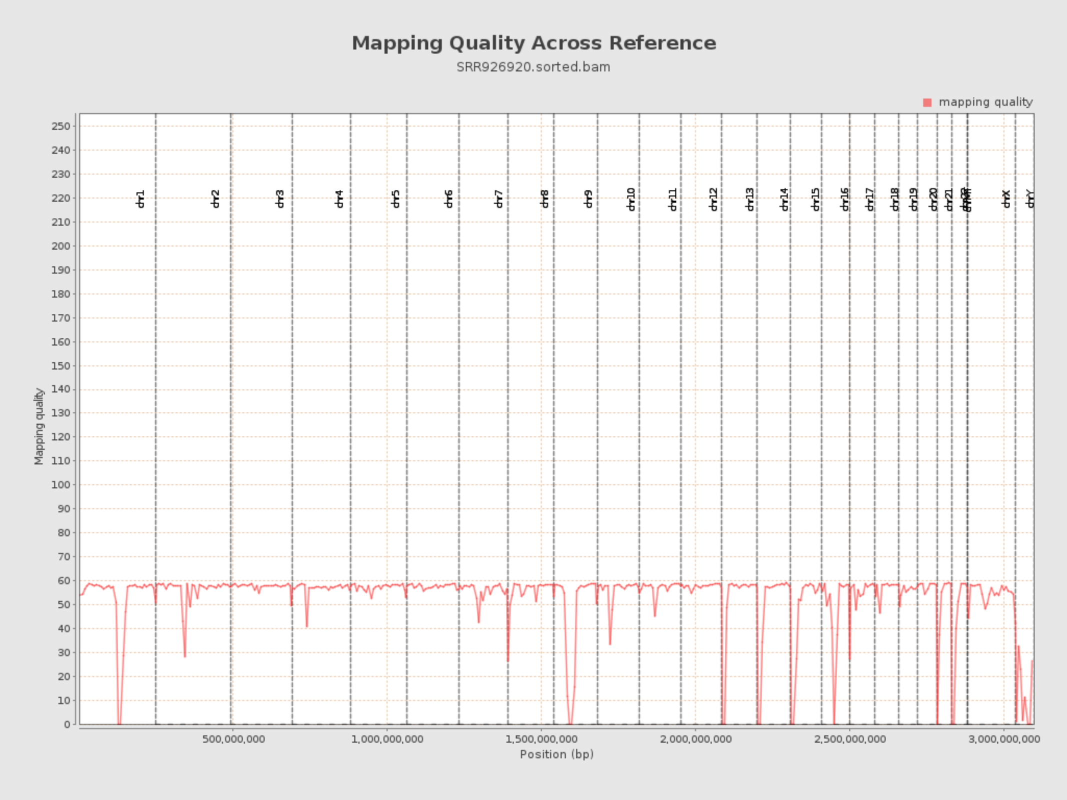
10. Results : Mapped Reads Clipping Profile



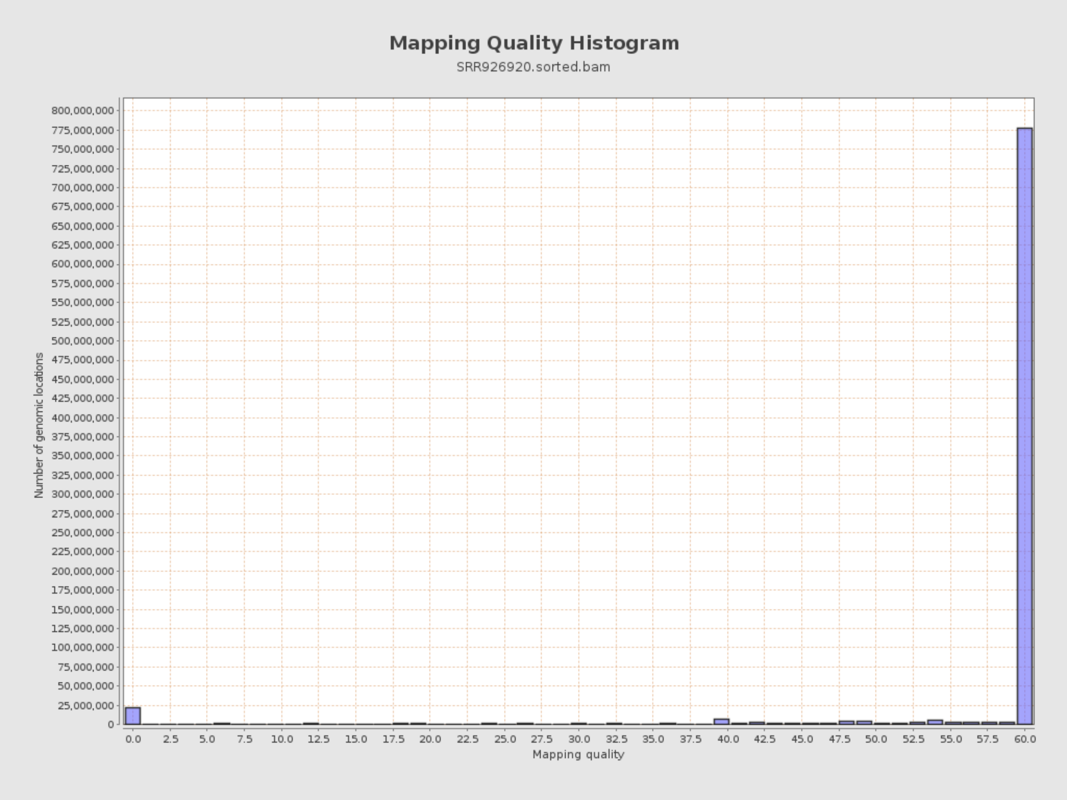
11. Results : Homopolymer Indels



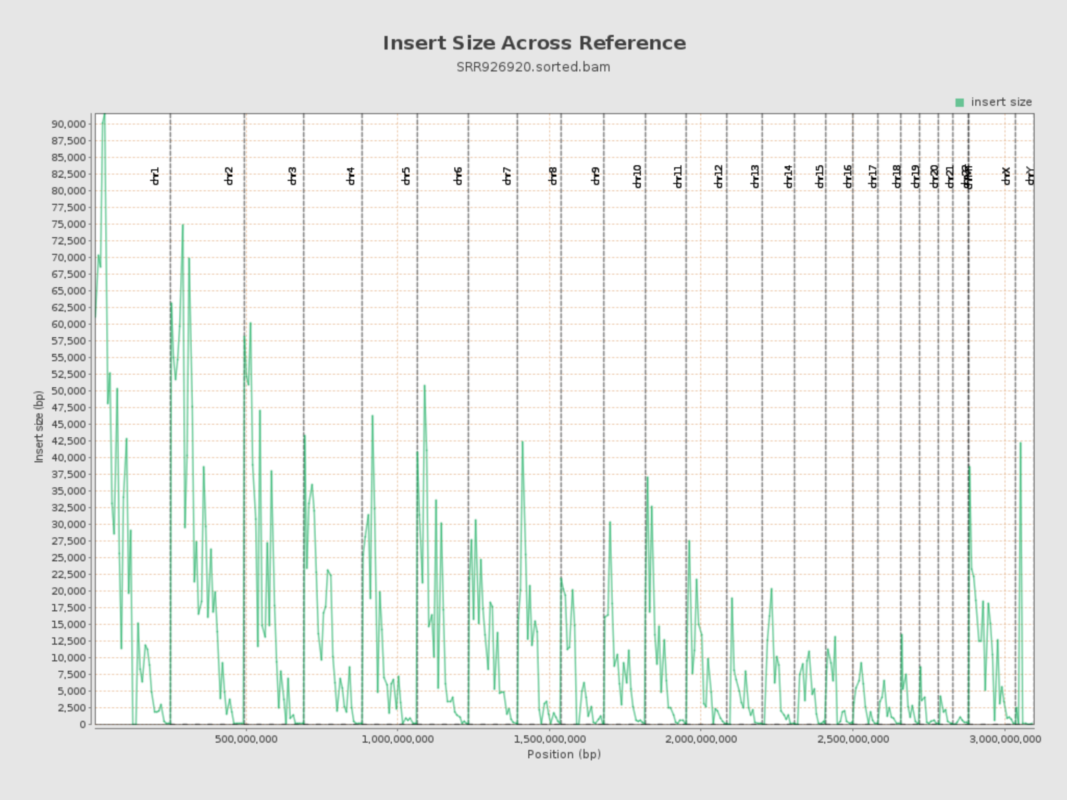
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram