Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 23:36:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926940.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_SRR926940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926940_1.fastq.gz SRR926940_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 23:36:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,777,492
Mapped reads	12,504,977 / 97.87%
Unmapped reads	272,515 / 2.13%
Mapped paired reads	12,504,977 / 97.87%
Mapped reads, first in pair	6,252,427 / 48.93%
Mapped reads, second in pair	6,252,550 / 48.93%
Mapped reads, both in pair	12,339,724 / 96.57%
Mapped reads, singletons	165,253 / 1.29%
Secondary alignments	0
Supplementary alignments	281,419 / 2.2%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	742,334 / 5.81%
Duplication rate	4.72%
Clipped reads	5,553,219 / 43.46%

2.2. ACGT Content

Number/percentage of A's	320,058,102 / 27.92%
Number/percentage of C's	232,913,620 / 20.31%
Number/percentage of T's	326,925,040 / 28.51%
Number/percentage of G's	266,594,884 / 23.25%
Number/percentage of N's	47,209 / 0%

GC Percentage	43.57%

2.3. Coverage

Mean	0.3706
Standard Deviation	1.607

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	236,723.95
Standard Deviation	4,856,631.91
P25/Median/P75	142 / 183 / 243

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	10,899,923
Insertions	198,064
Mapped reads with at least one insertion	1.55%
Deletions	573,453
Mapped reads with at least one deletion	4.47%
Homopolymer indels	51.18%

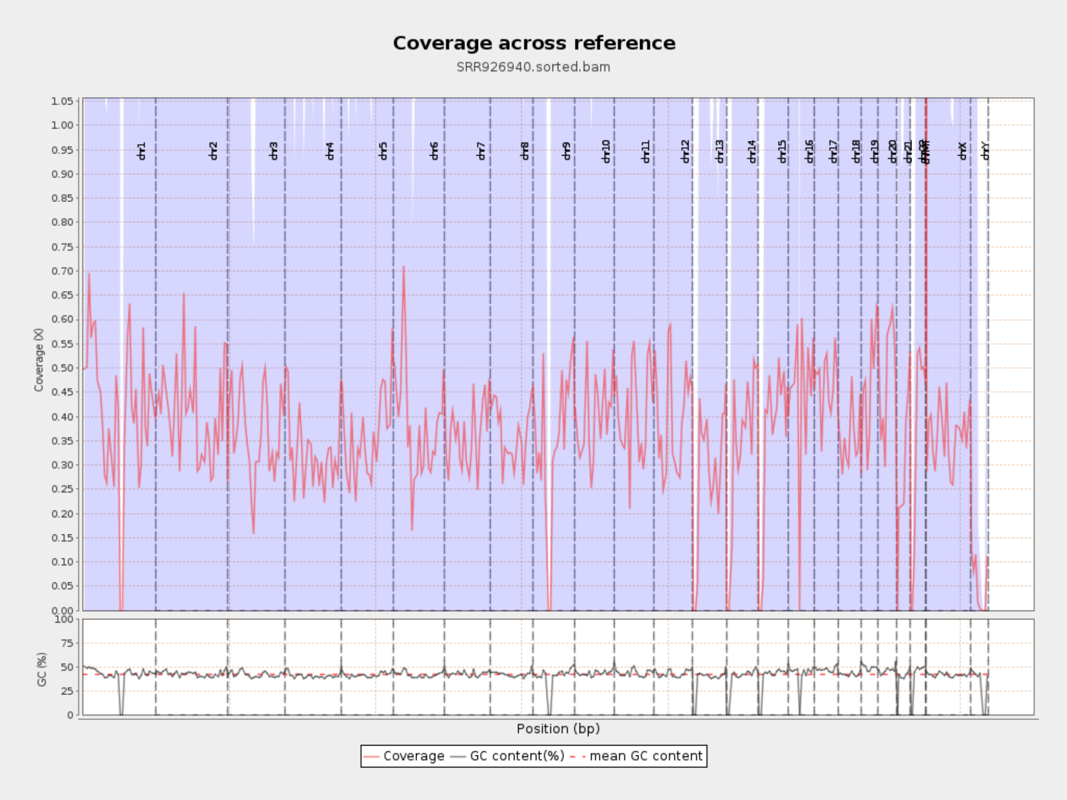
2.7. Chromosome stats

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

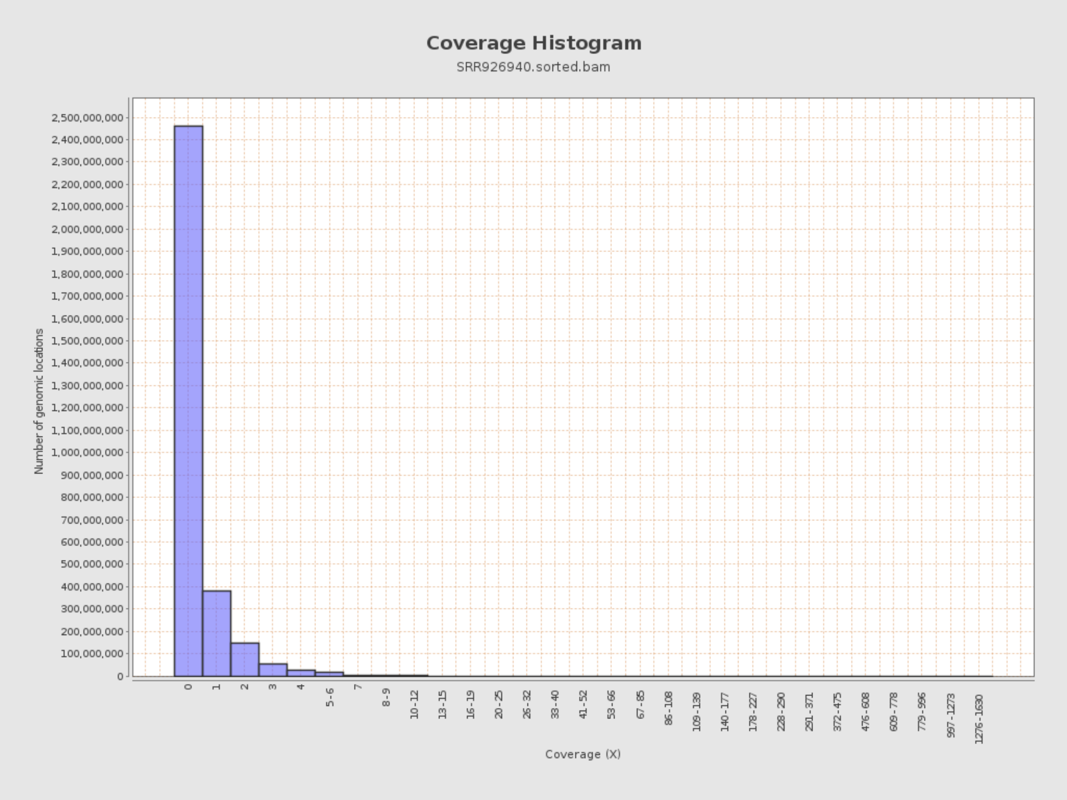
		bases	coverage	deviation
chr1	249250621	102417553	0.4109	1.8298
chr2	243199373	99234406	0.408	2.8131
chr3	198022430	72167327	0.3644	0.984
chr4	191154276	61901677	0.3238	1.4061
chr5	180915260	65636932	0.3628	0.9718
chr6	171115067	64796873	0.3787	1.1459
chr7	159138663	57710112	0.3626	1.1937
chr8	146364022	52985029	0.362	1.0195
chr9	141213431	48768690	0.3454	1.6913
chr10	135534747	53590387	0.3954	2.6005
chr11	135006516	55042223	0.4077	1.383
chr12	133851895	53764817	0.4017	1.1303
chr13	115169878	31830162	0.2764	0.8211
chr14	107349540	35804383	0.3335	0.9512
chr15	102531392	35109881	0.3424	0.9787
chr16	90354753	40346861	0.4465	2.7264
chr17	81195210	38263574	0.4713	1.3762
chr18	78077248	27566268	0.3531	1.6367
chr19	59128983	27743866	0.4692	1.6057
chr20	63025520	30623660	0.4859	1.3918
chr21	48129895	14138450	0.2938	1.3581
chr22	51304566	17848380	0.3479	1.0583
chrMT	16571	866117	52.267	43.5832
chrX	155270560	56059644	0.361	1.0573

chrY	59373566	3184490	0.0536	1.5954

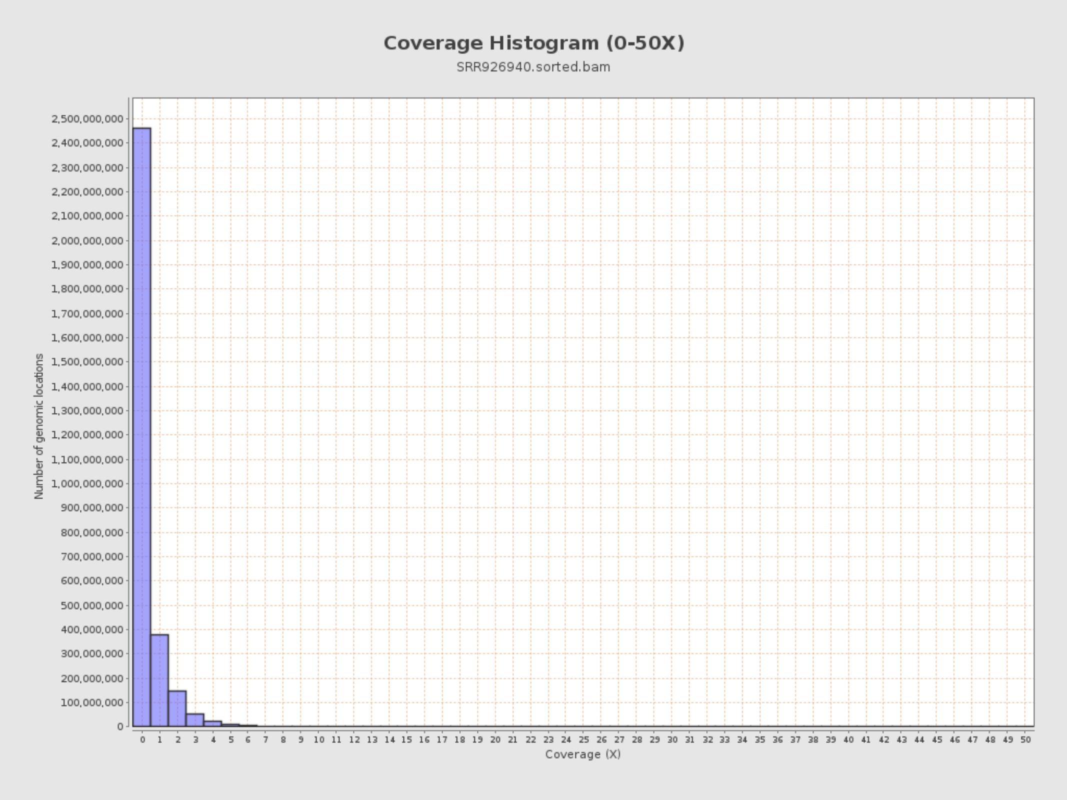
3. Results : Coverage across reference



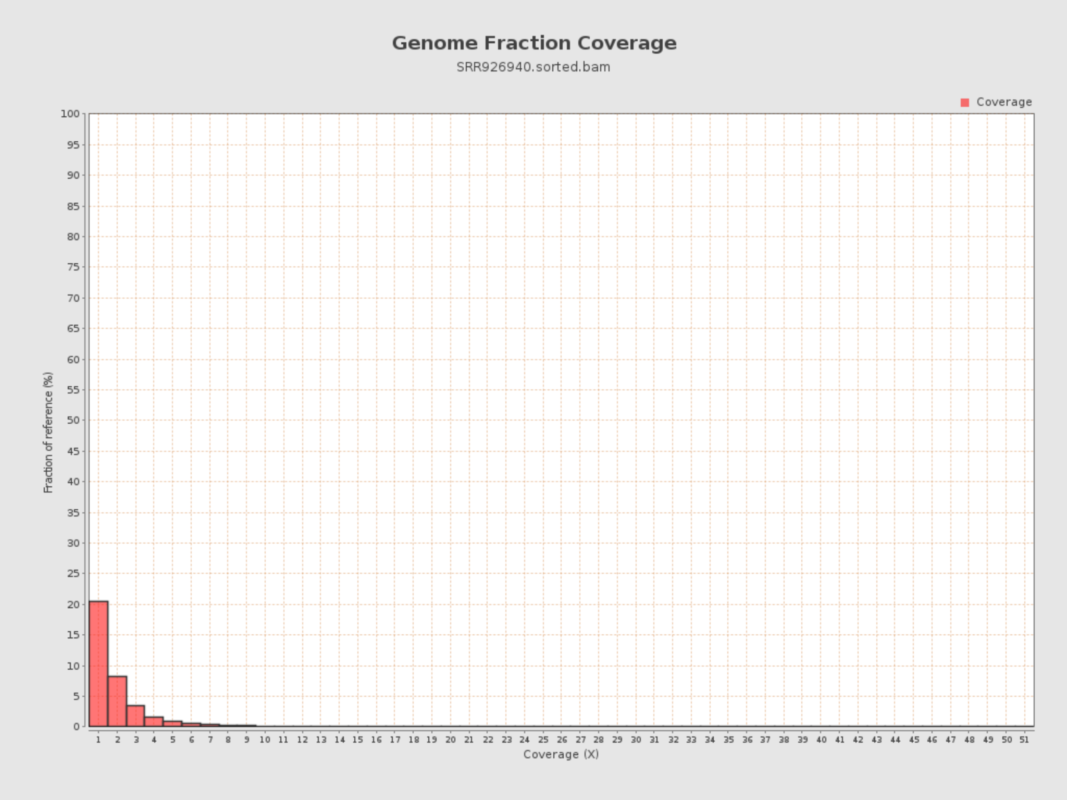
4. Results : Coverage Histogram



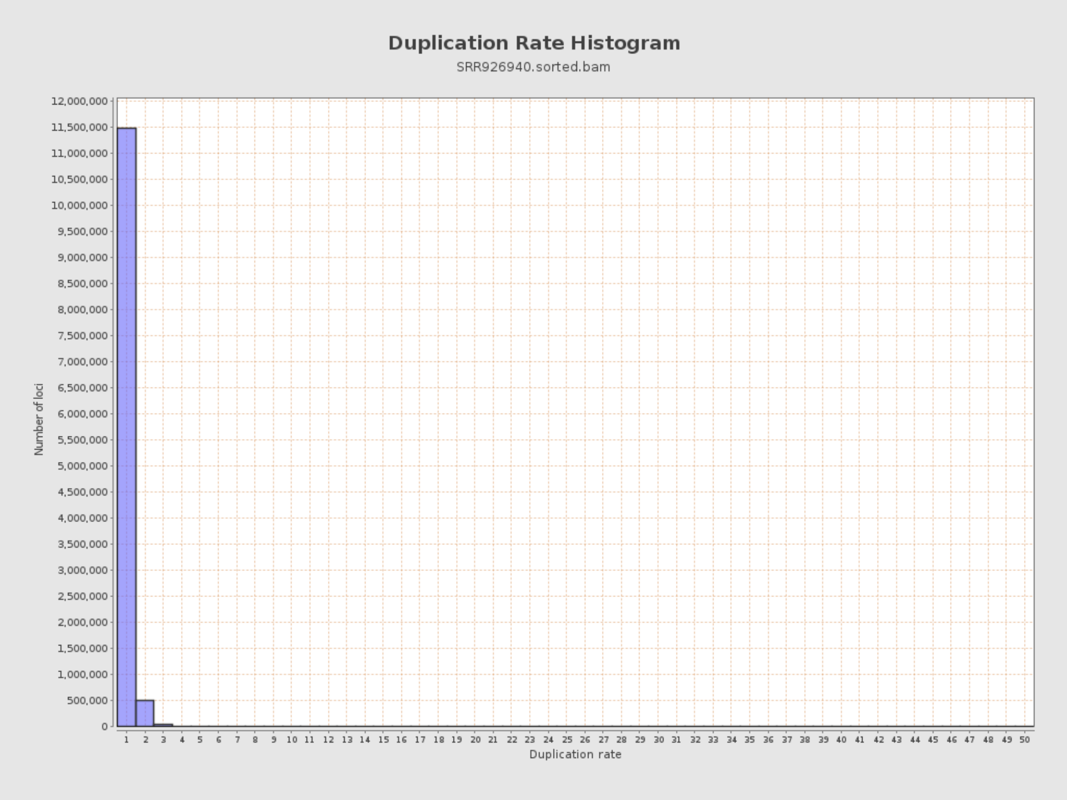
5. Results : Coverage Histogram (0-50X)



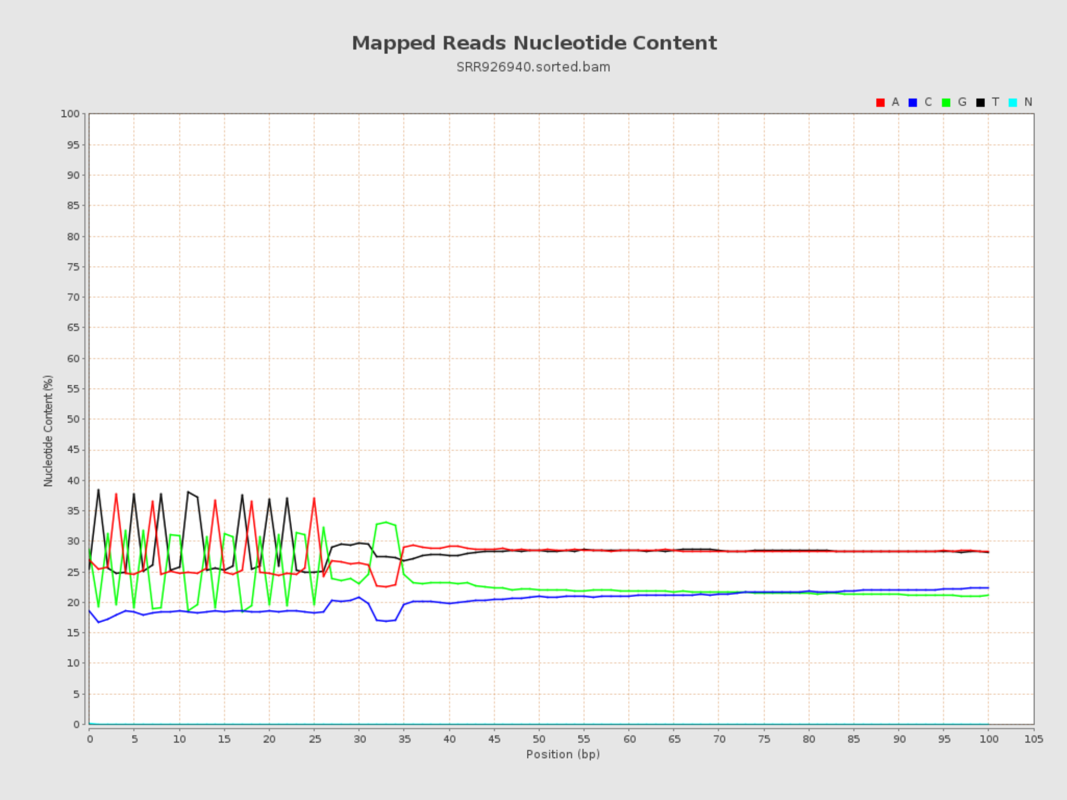
6. Results : Genome Fraction Coverage



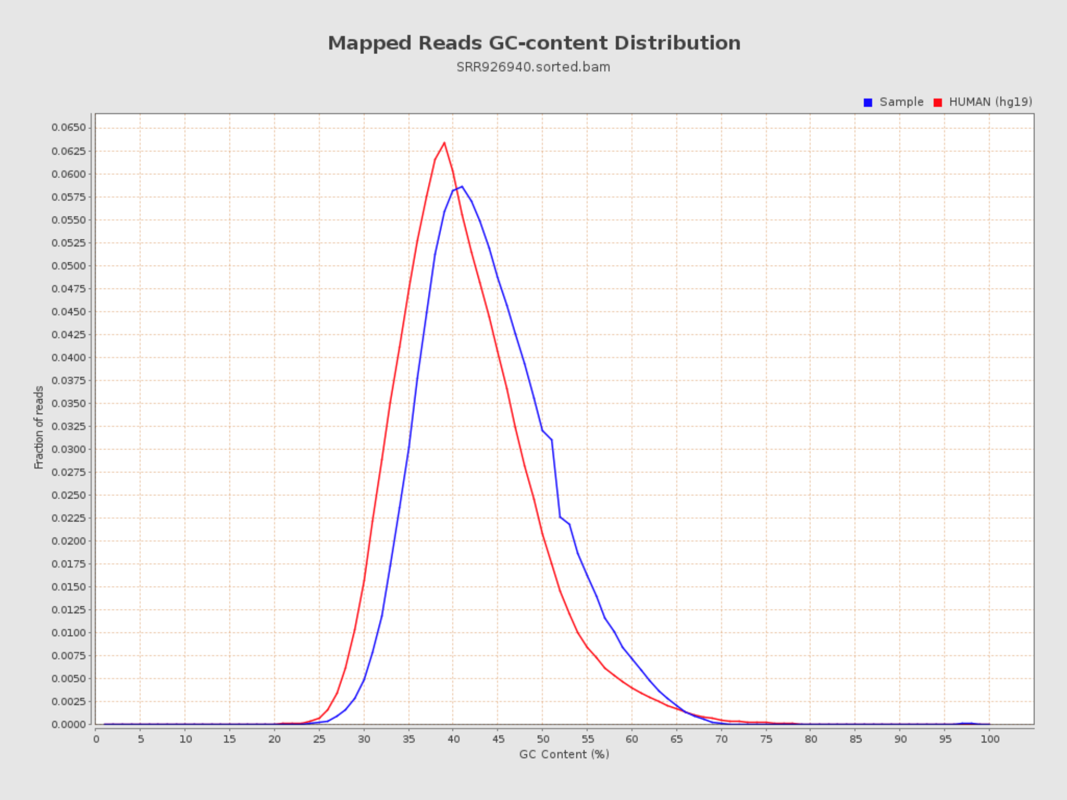
7. Results : Duplication Rate Histogram



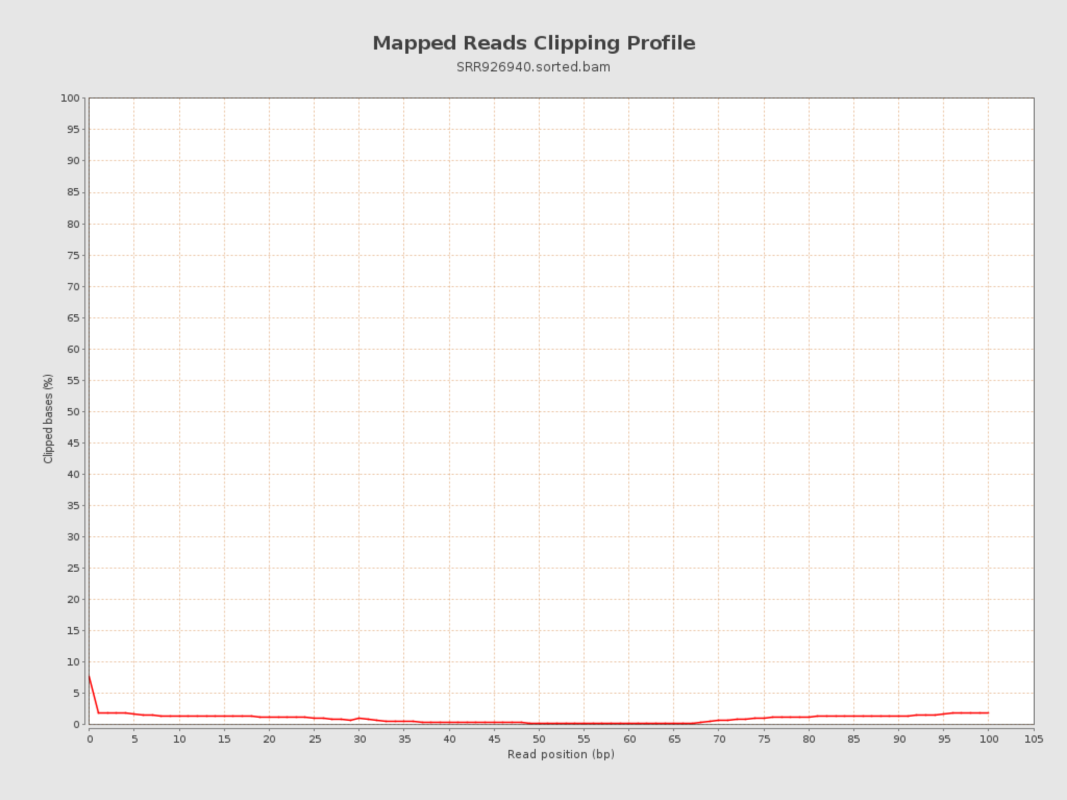
8. Results : Mapped Reads Nucleotide Content



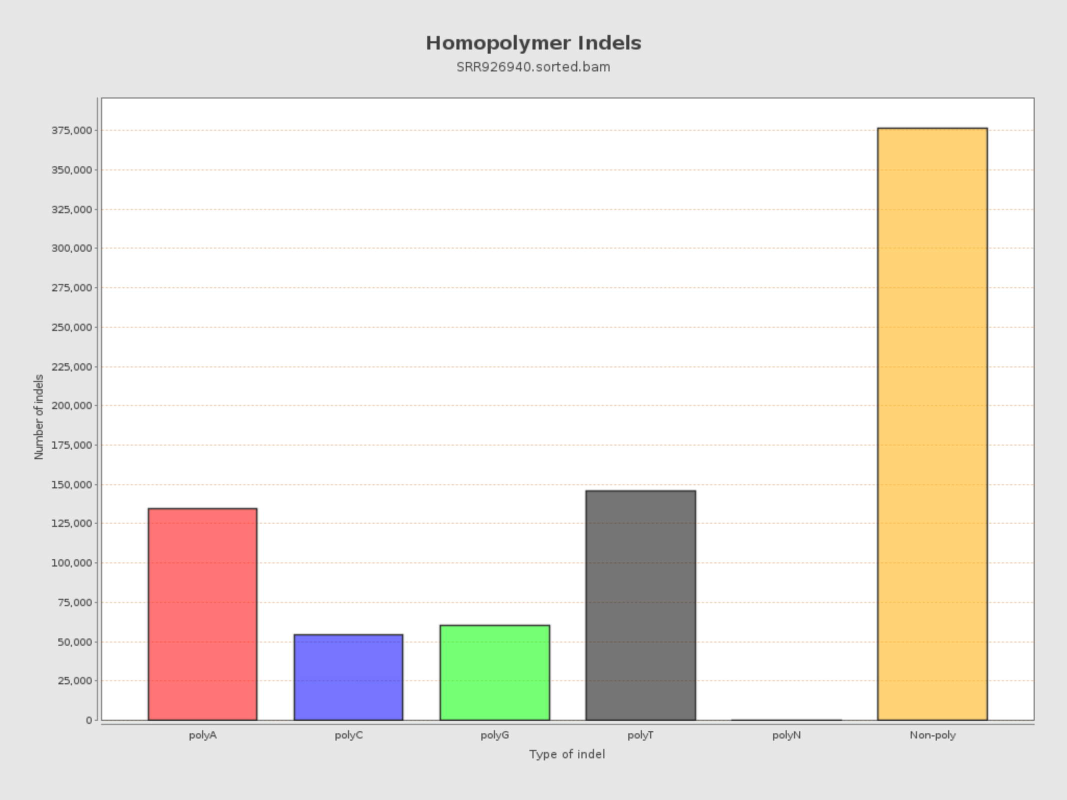
9. Results : Mapped Reads GC-content Distribution



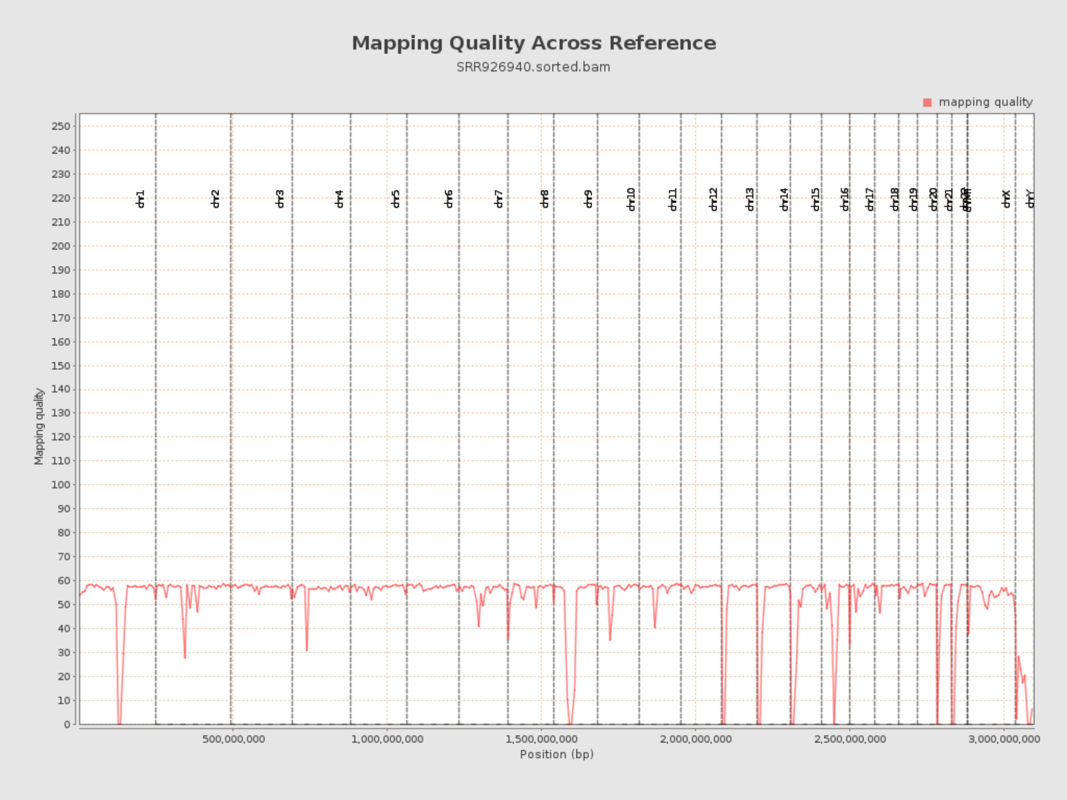
10. Results : Mapped Reads Clipping Profile



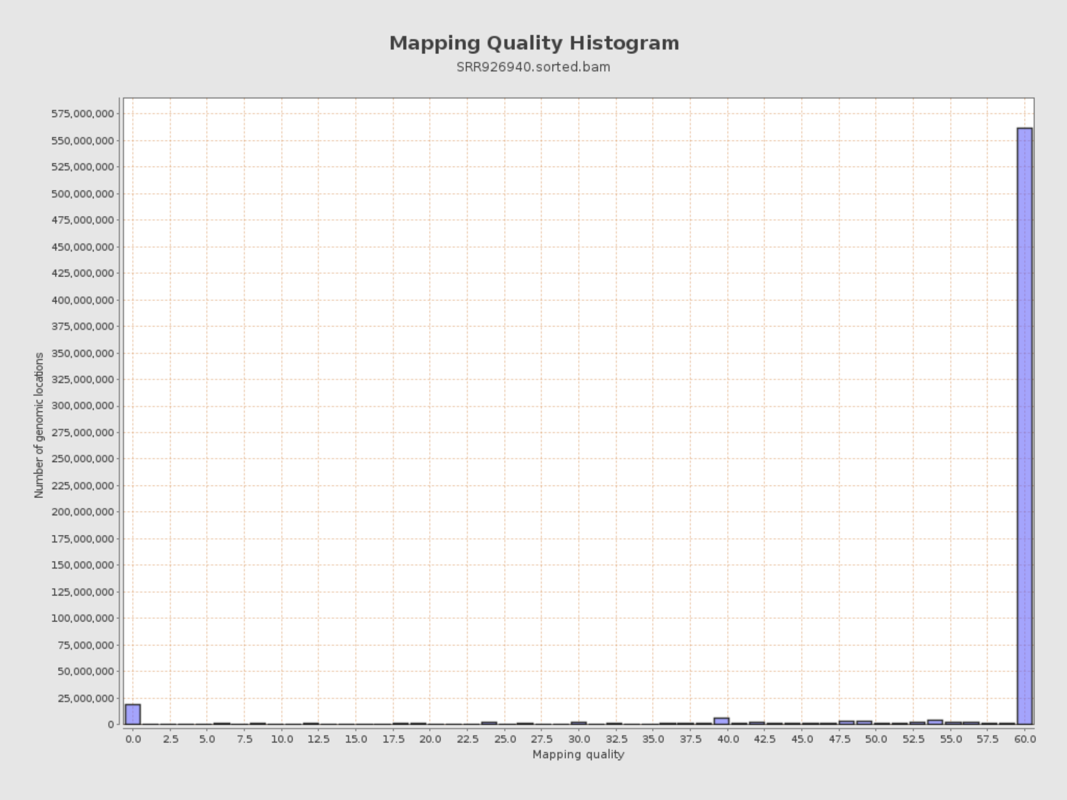
11. Results : Homopolymer Indels



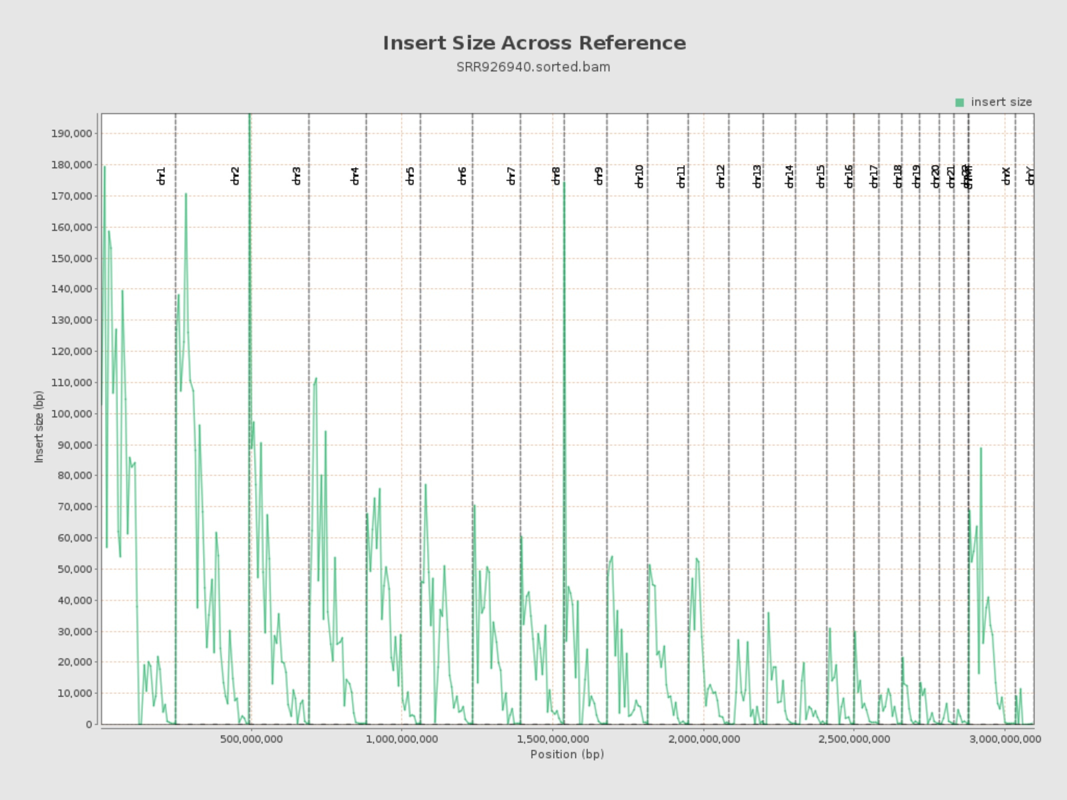
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram