Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 04:53:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926962.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_SRR926962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926962_1.fastq.gz SRR926962_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 04:53:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,315,202
Mapped reads	31,319,332 / 96.92%
Unmapped reads	995,870 / 3.08%
Mapped paired reads	31,319,332 / 96.92%
Mapped reads, first in pair	15,628,701 / 48.36%
Mapped reads, second in pair	15,690,631 / 48.55%
Mapped reads, both in pair	30,722,492 / 95.07%
Mapped reads, singletons	596,840 / 1.85%
Secondary alignments	0
Supplementary alignments	1,189,324 / 3.68%
Read min/max/mean length	30 / 101 / 102.52
Duplicated reads (estimated)	4,165,842 / 12.89%
Duplication rate	10.6%
Clipped reads	16,708,242 / 51.7%

2.2. ACGT Content

Number/percentage of A's	784,471,968 / 28.33%
Number/percentage of C's	534,056,622 / 19.29%
Number/percentage of T's	816,169,776 / 29.47%
Number/percentage of G's	634,228,492 / 22.9%
Number/percentage of N's	306,099 / 0.01%

GC Percentage	42.19%

2.3. Coverage

Mean	0.8953
Standard Deviation	3.4441

2.4. Mapping Quality

Mean Mapping Quality	52.34

2.5. Insert size

Mean	359,183.59
Standard Deviation	5,856,512.51
P25/Median/P75	124 / 167 / 230

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	28,636,325
Insertions	485,393
Mapped reads with at least one insertion	1.52%
Deletions	1,485,212
Mapped reads with at least one deletion	4.62%
Homopolymer indels	51.55%

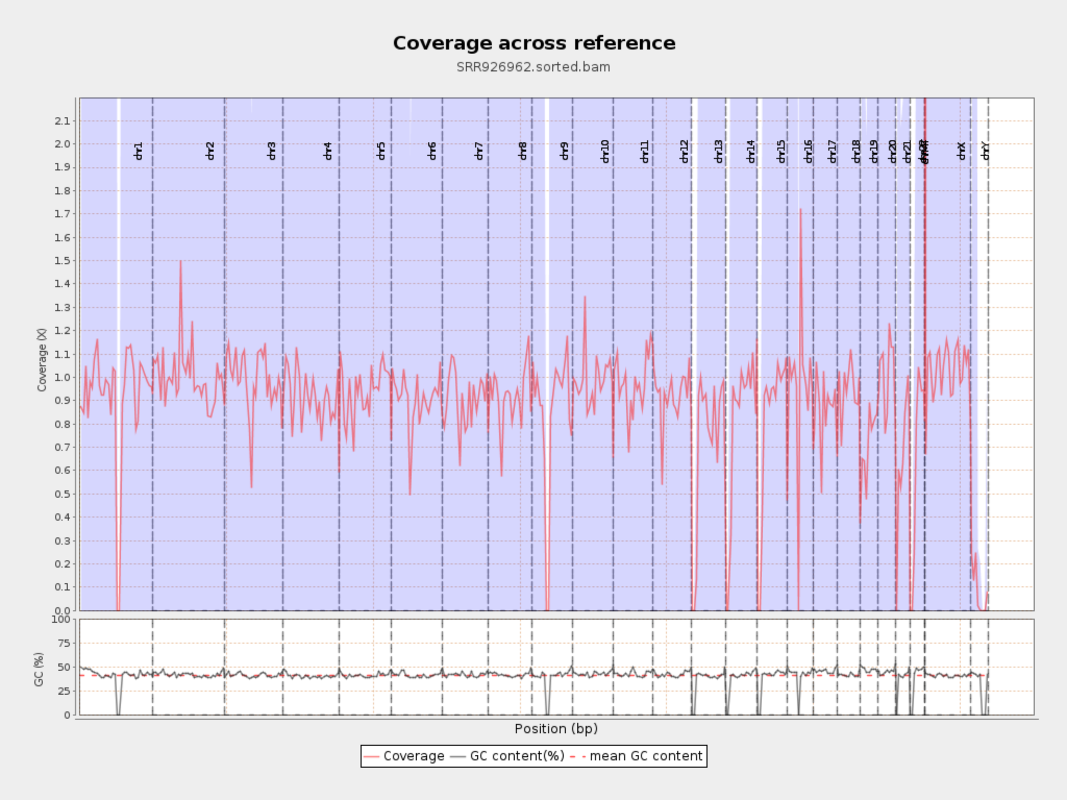
2.7. Chromosome stats

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

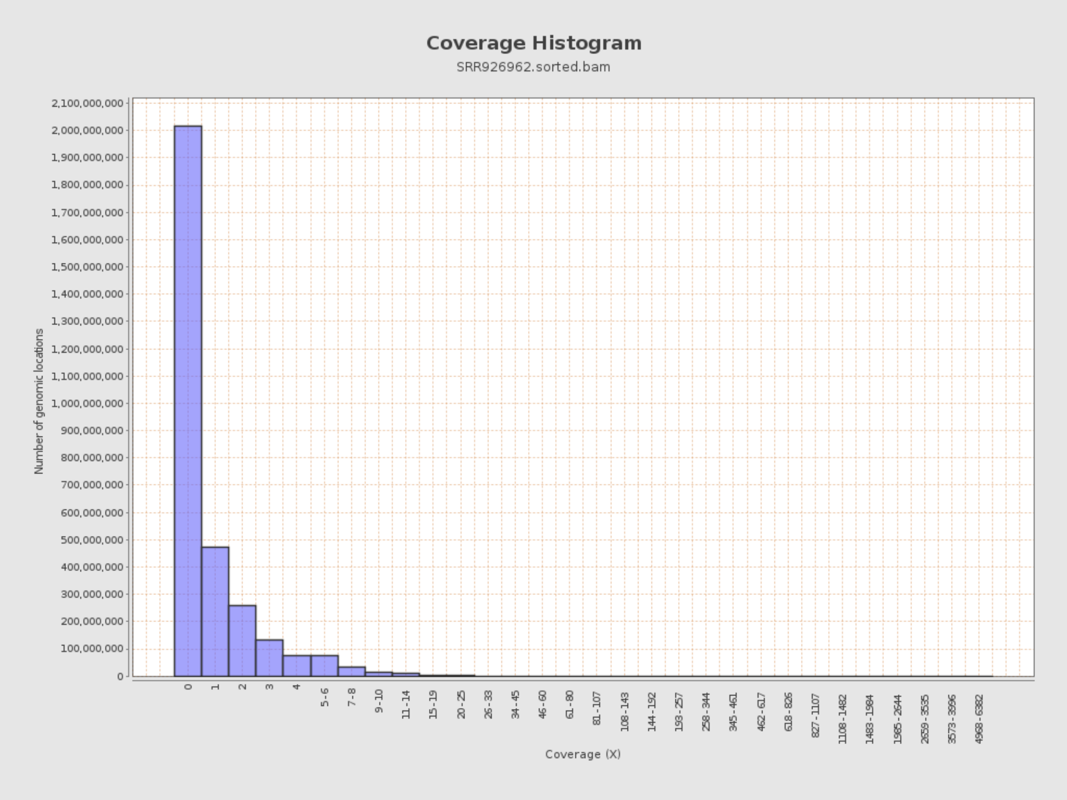
		bases	coverage	deviation
chr1	249250621	228609110	0.9172	3.3238
chr2	243199373	244317587	1.0046	6.341
chr3	198022430	195797765	0.9888	2
chr4	191154276	175615866	0.9187	2.9128
chr5	180915260	170233665	0.941	1.9053
chr6	171115067	155424158	0.9083	2.5218
chr7	159138663	144045296	0.9052	2.614
chr8	146364022	134937971	0.9219	2.1834
chr9	141213431	117644062	0.8331	3.9077
chr10	135534747	134615001	0.9932	5.3917
chr11	135006516	130724278	0.9683	4.1756
chr12	133851895	123368958	0.9217	2.0002
chr13	115169878	83129793	0.7218	1.6826
chr14	107349540	85129839	0.793	1.8771
chr15	102531392	81228932	0.7922	1.8589
chr16	90354753	85764801	0.9492	6.7502
chr17	81195210	69551201	0.8566	2.2009
chr18	78077248	75107157	0.962	3.9102
chr19	59128983	42159805	0.713	2.399
chr20	63025520	63897097	1.0138	2.198
chr21	48129895	32262299	0.6703	2.7648
chr22	51304566	32599801	0.6354	1.7418
chrMT	16571	440638	26.5909	24.4286
chrX	155270560	159866660	1.0296	2.3454

chrY	59373566	4974883	0.0838	2.5533

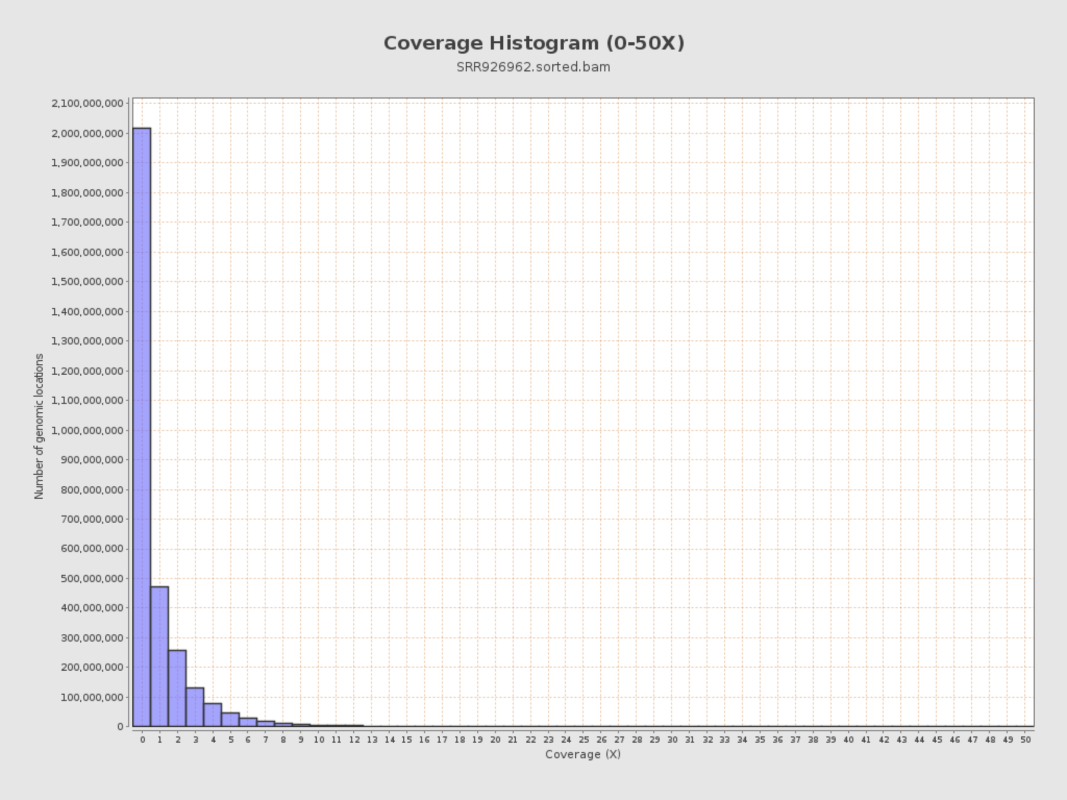
3. Results : Coverage across reference



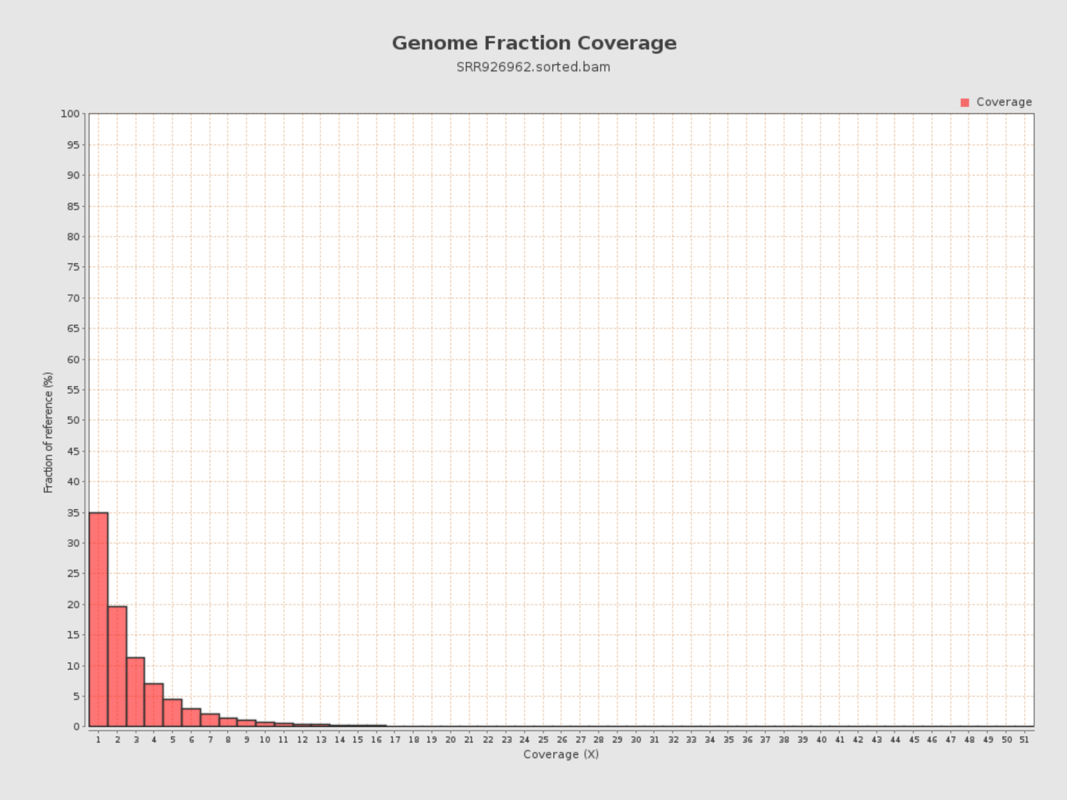
4. Results : Coverage Histogram



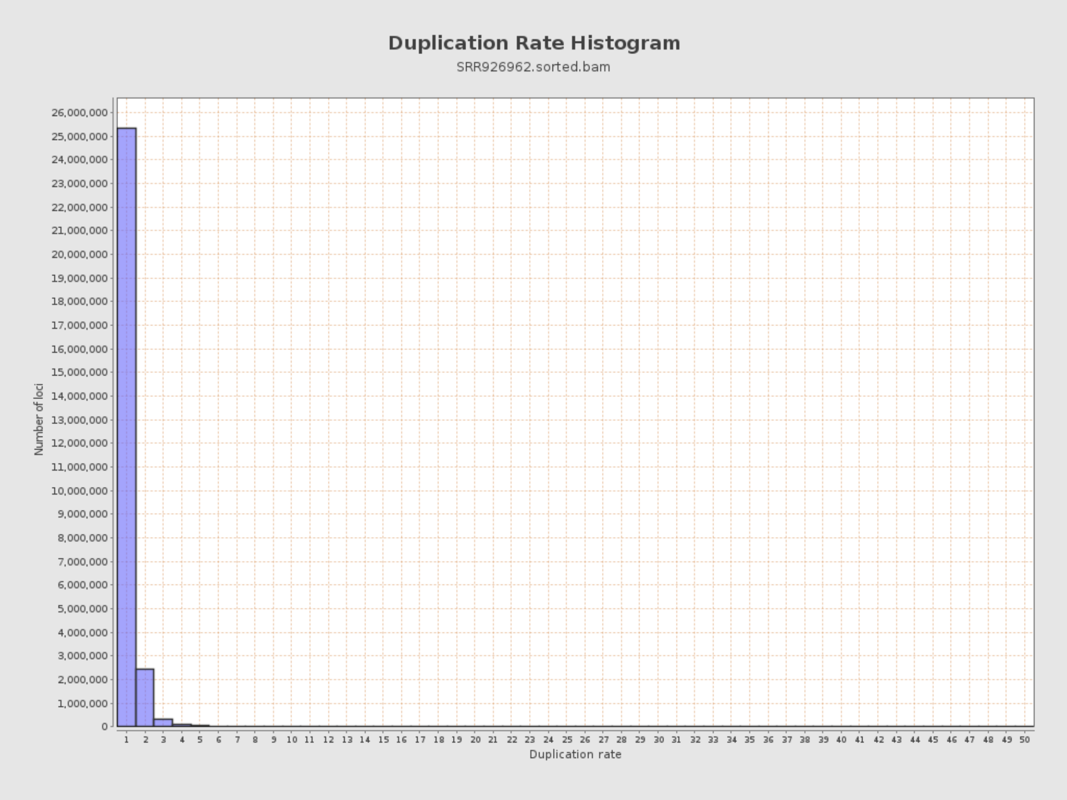
5. Results : Coverage Histogram (0-50X)



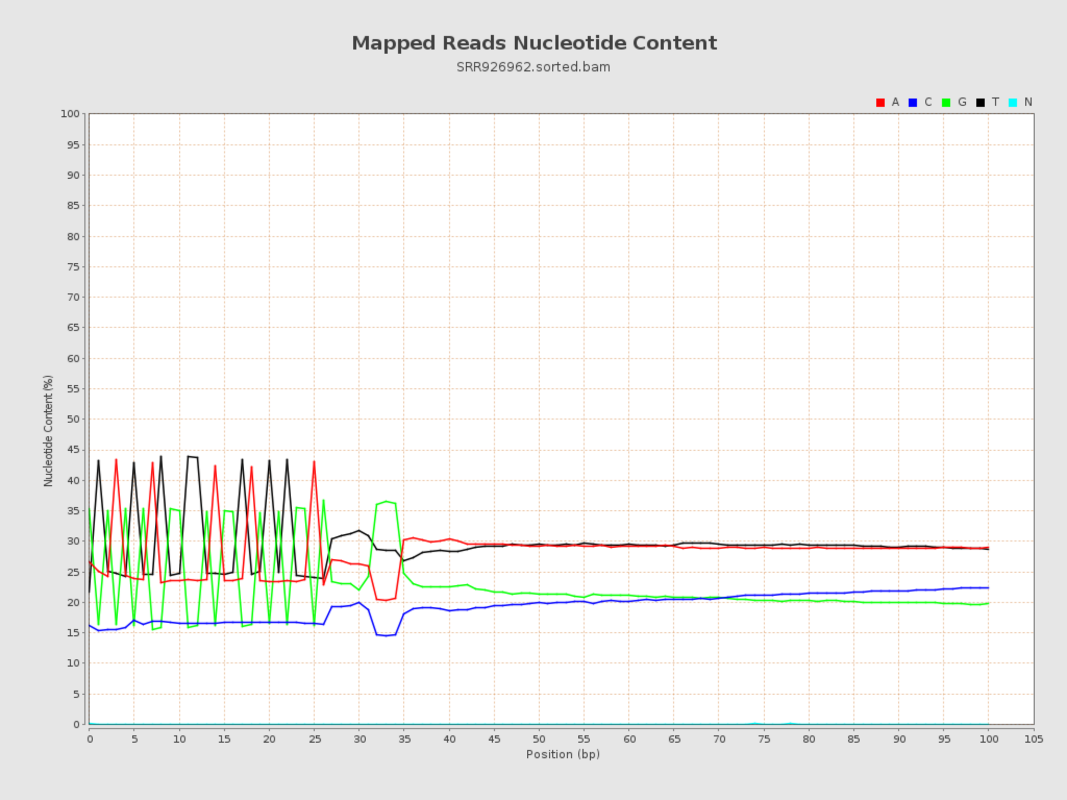
6. Results : Genome Fraction Coverage



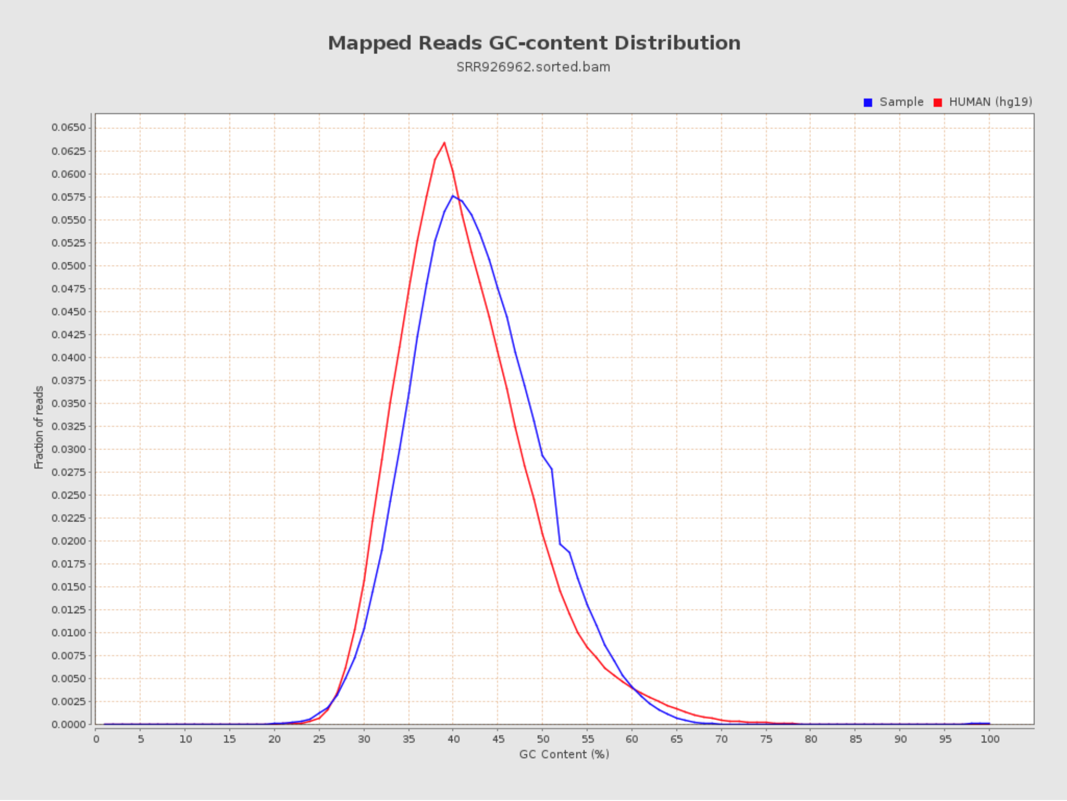
7. Results : Duplication Rate Histogram



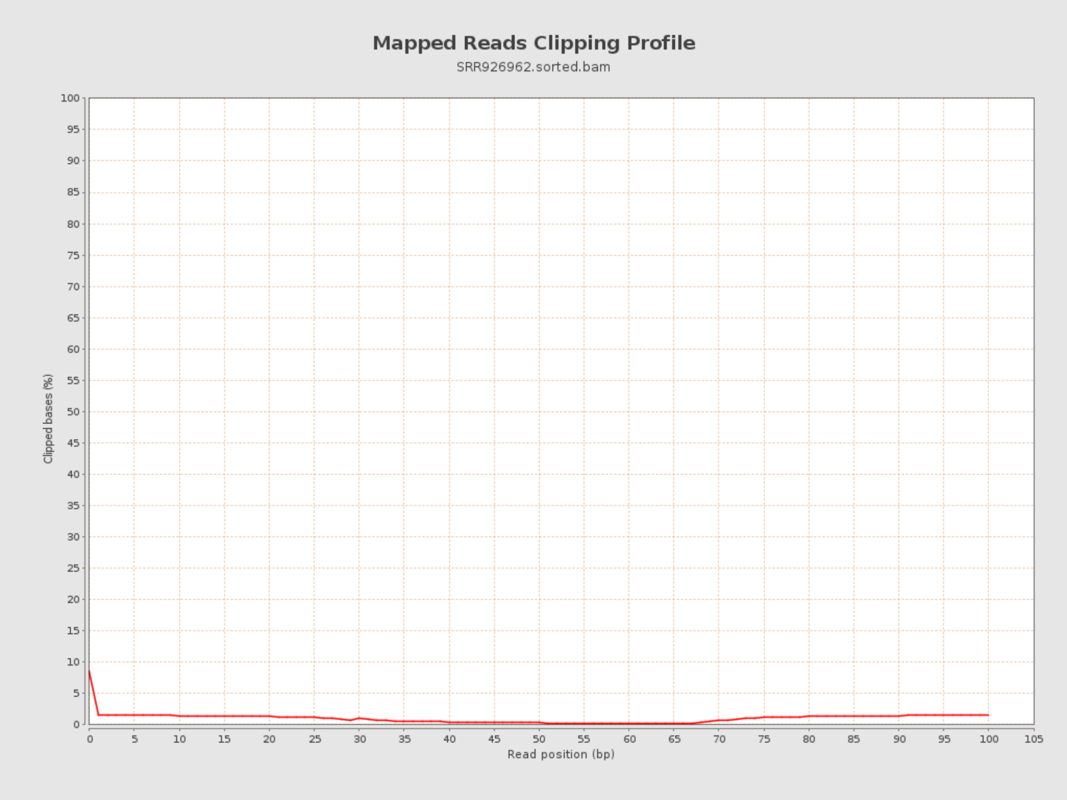
8. Results : Mapped Reads Nucleotide Content



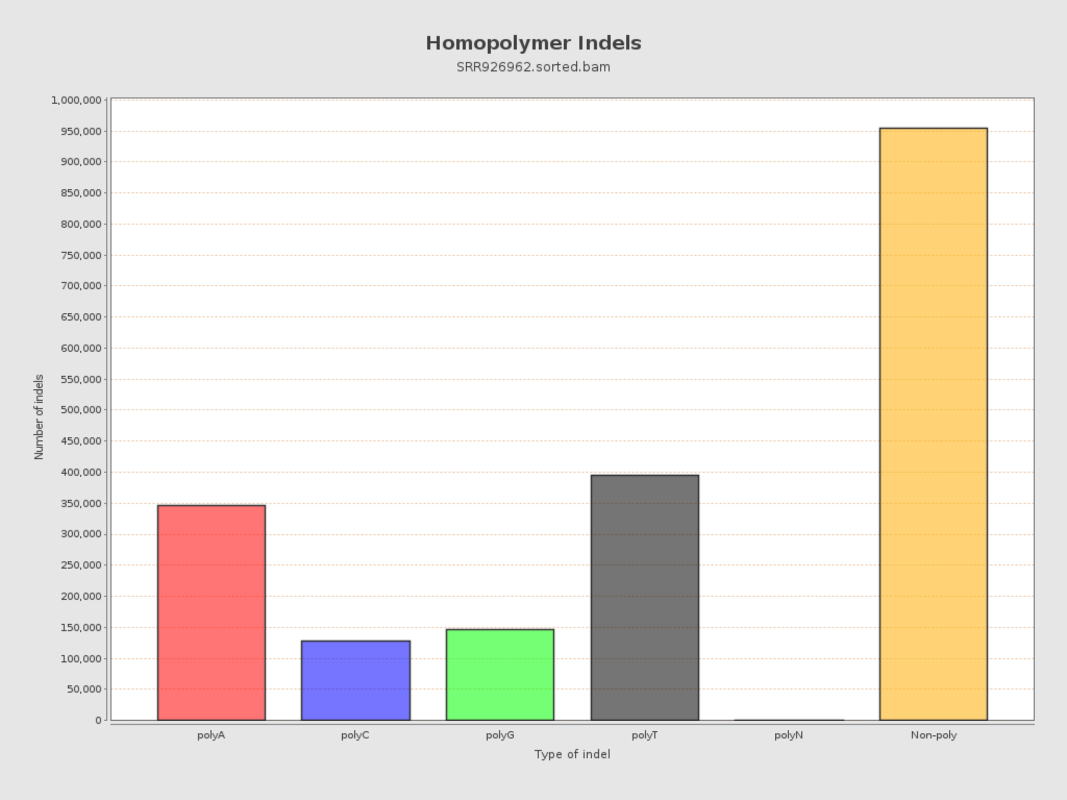
9. Results : Mapped Reads GC-content Distribution



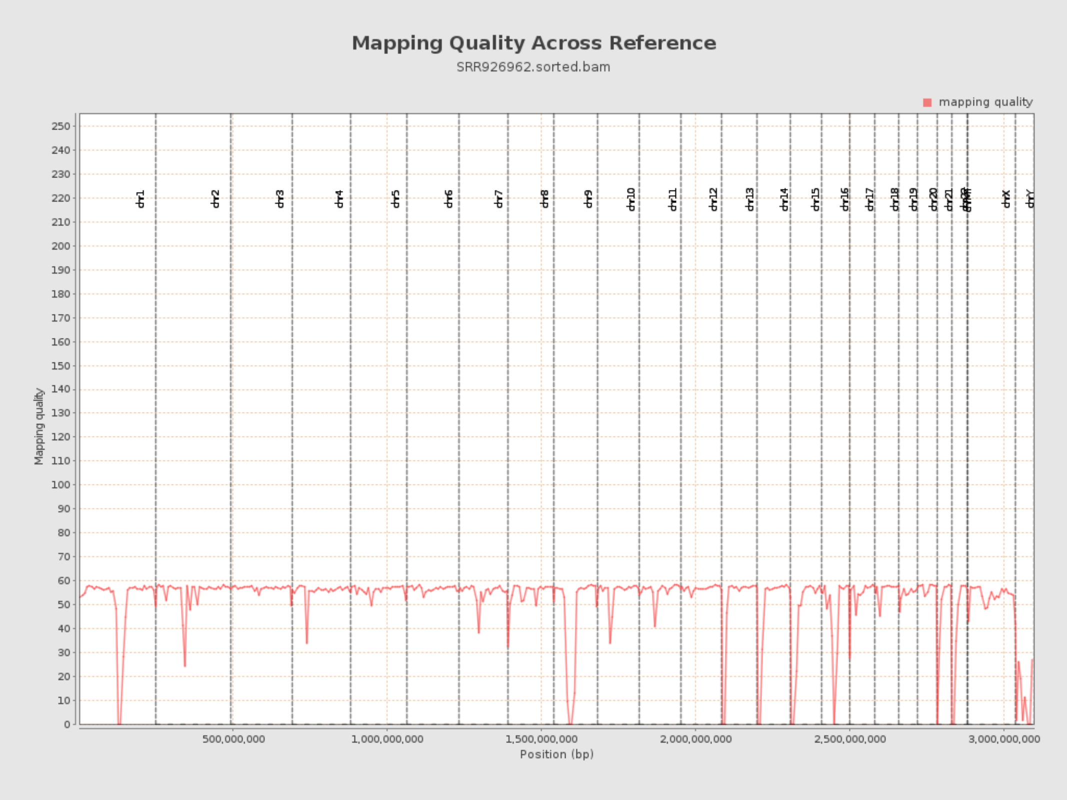
10. Results : Mapped Reads Clipping Profile



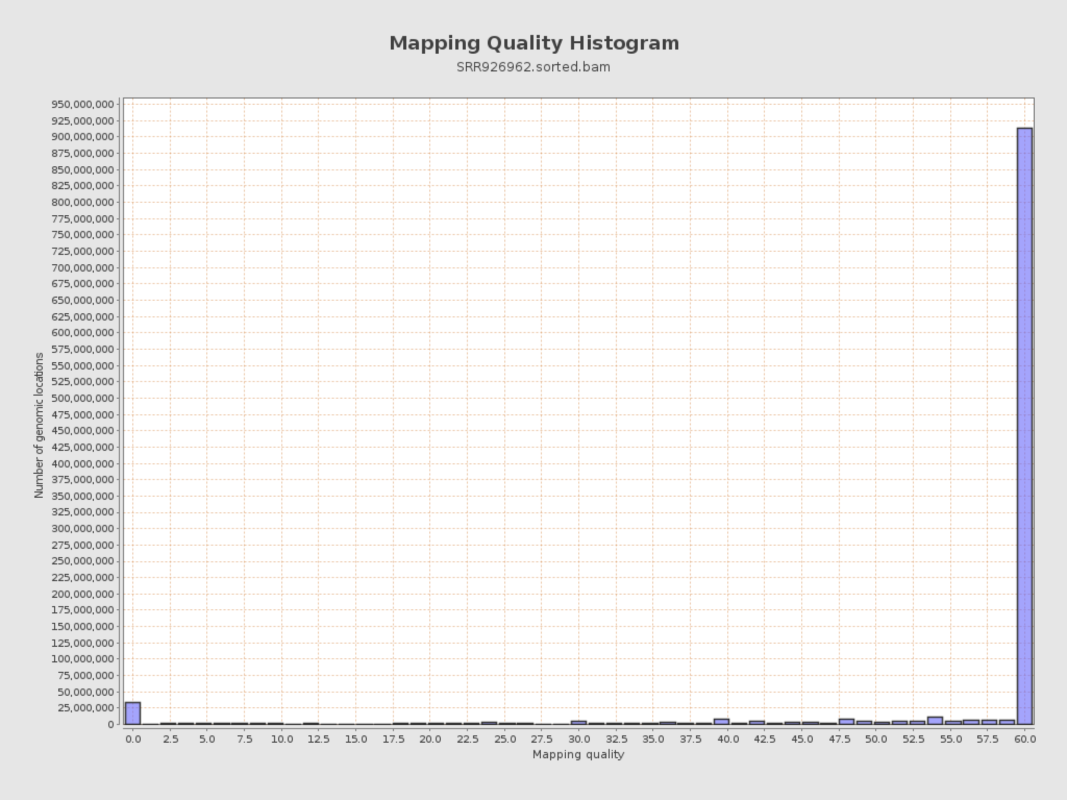
11. Results : Homopolymer Indels



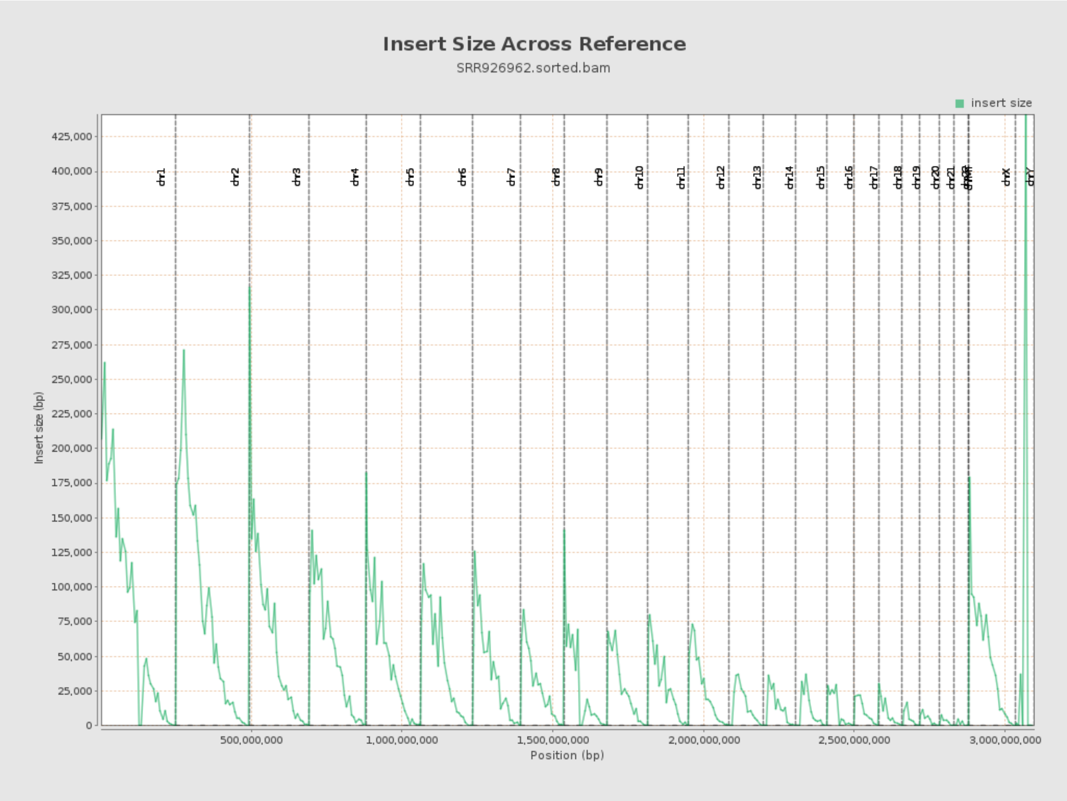
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram