Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 10:11:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927026.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_SRR927026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927026_1.fastq.gz SRR927026_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 10:11:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,335,180
Mapped reads	33,614,167 / 97.9%
Unmapped reads	721,013 / 2.1%
Mapped paired reads	33,614,167 / 97.9%
Mapped reads, first in pair	16,879,900 / 49.16%
Mapped reads, second in pair	16,734,267 / 48.74%
Mapped reads, both in pair	33,216,648 / 96.74%
Mapped reads, singletons	397,519 / 1.16%
Secondary alignments	0
Supplementary alignments	424,616 / 1.24%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	2,819,263 / 8.21%
Duplication rate	6.23%
Clipped reads	10,004,928 / 29.14%

2.2. ACGT Content

Number/percentage of A's	904,320,398 / 28.81%
Number/percentage of C's	615,059,005 / 19.6%
Number/percentage of T's	916,874,718 / 29.21%
Number/percentage of G's	702,264,790 / 22.37%
Number/percentage of N's	161,644 / 0.01%

GC Percentage	41.97%

2.3. Coverage

Mean	1.0147
Standard Deviation	4.8329

2.4. Mapping Quality

Mean Mapping Quality	53.27

2.5. Insert size

Mean	131,738.65
Standard Deviation	3,578,131.24
P25/Median/P75	154 / 199 / 267

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	29,034,239
Insertions	522,682
Mapped reads with at least one insertion	1.53%
Deletions	1,660,152
Mapped reads with at least one deletion	4.81%
Homopolymer indels	53.01%

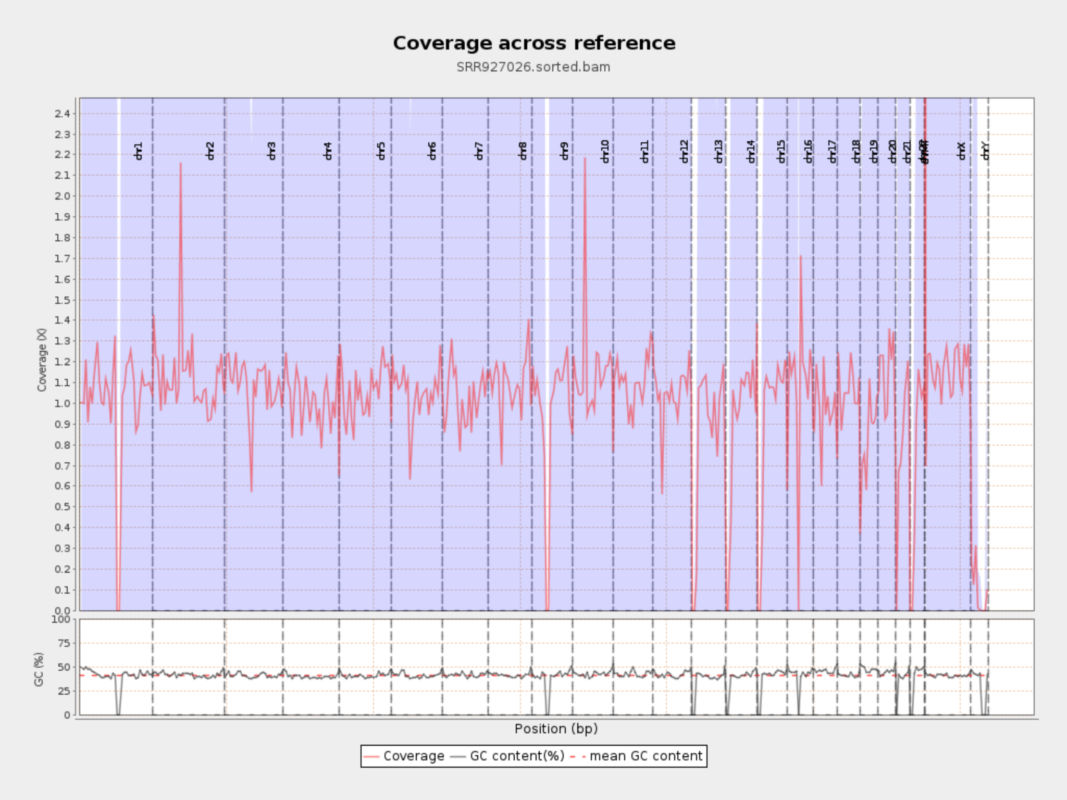
2.7. Chromosome stats

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

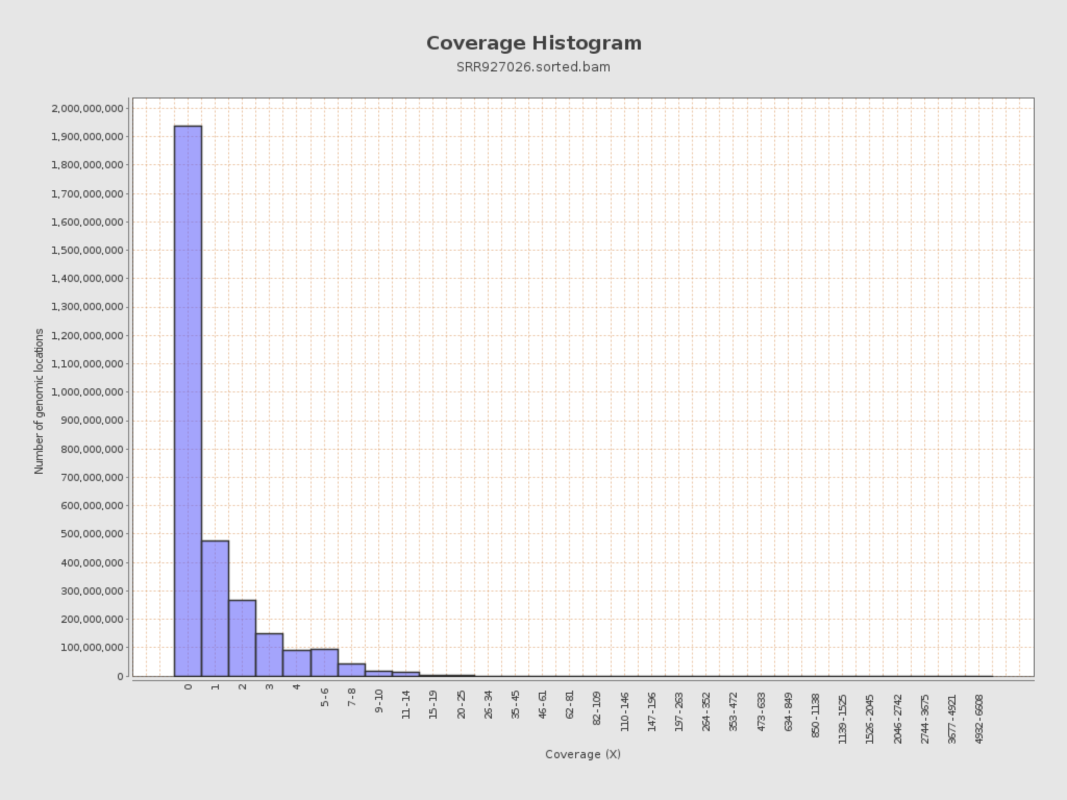
		bases	coverage	deviation
chr1	249250621	252619652	1.0135	7.1046
chr2	243199373	276795537	1.1381	7.9718
chr3	198022430	215195419	1.0867	2.127
chr4	191154276	194715282	1.0186	3.137
chr5	180915260	192117767	1.0619	1.9929
chr6	171115067	180790855	1.0565	2.0809
chr7	159138663	163167387	1.0253	3.2688
chr8	146364022	160147876	1.0942	2.4309
chr9	141213431	132879200	0.941	4.9471
chr10	135534747	158382280	1.1686	11.8022
chr11	135006516	148182781	1.0976	5.1363
chr12	133851895	139732834	1.0439	2.0483
chr13	115169878	97410966	0.8458	1.7888
chr14	107349540	94640625	0.8816	1.9144
chr15	102531392	91713961	0.8945	1.9188
chr16	90354753	97019037	1.0738	6.0918
chr17	81195210	78358810	0.9651	2.4812
chr18	78077248	83938725	1.0751	5.1852
chr19	59128983	48991008	0.8285	4.193
chr20	63025520	72392982	1.1486	2.2646
chr21	48129895	39497660	0.8206	2.8745
chr22	51304566	36897399	0.7192	1.7894
chrMT	16571	1994269	120.3469	90.2033
chrX	155270560	177966419	1.1462	2.6186

chrY	59373566	5514092	0.0929	2.8376

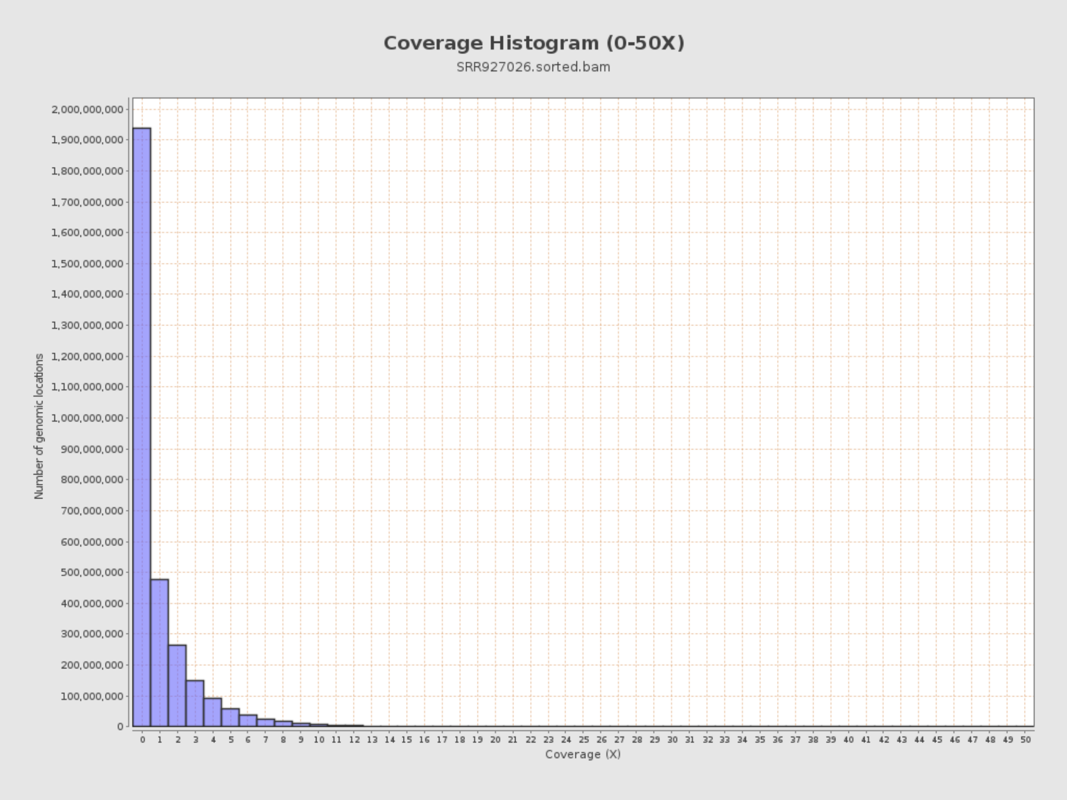
3. Results : Coverage across reference



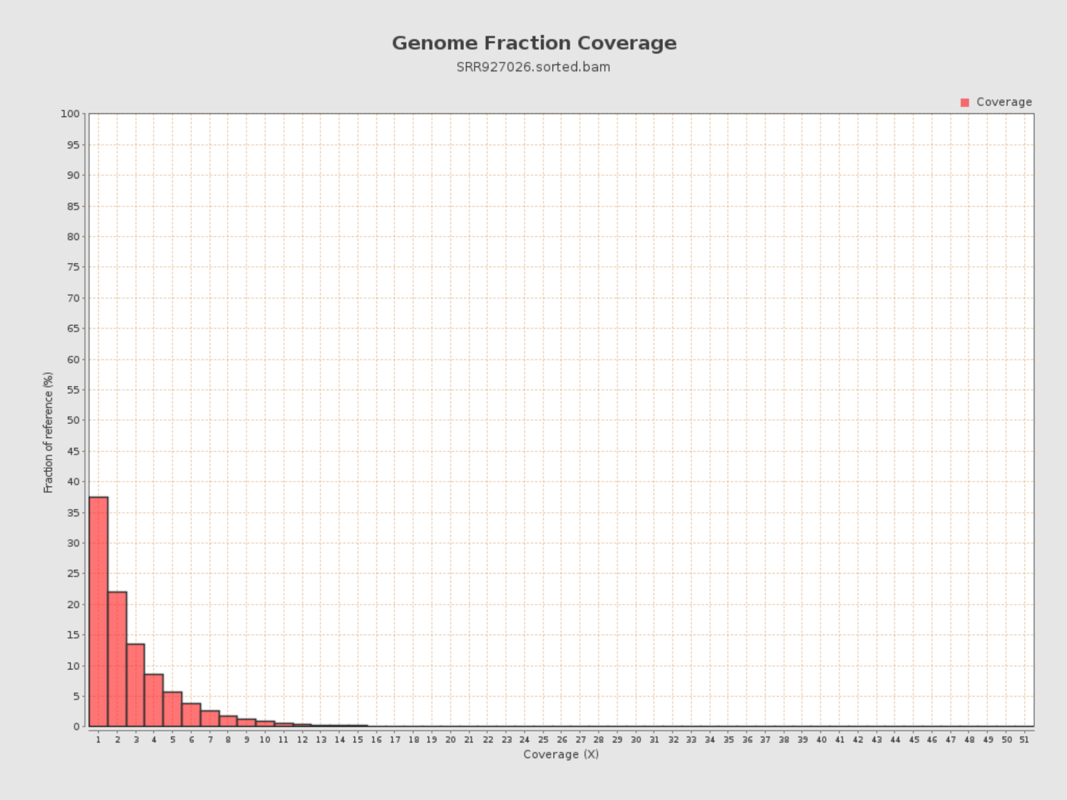
4. Results : Coverage Histogram



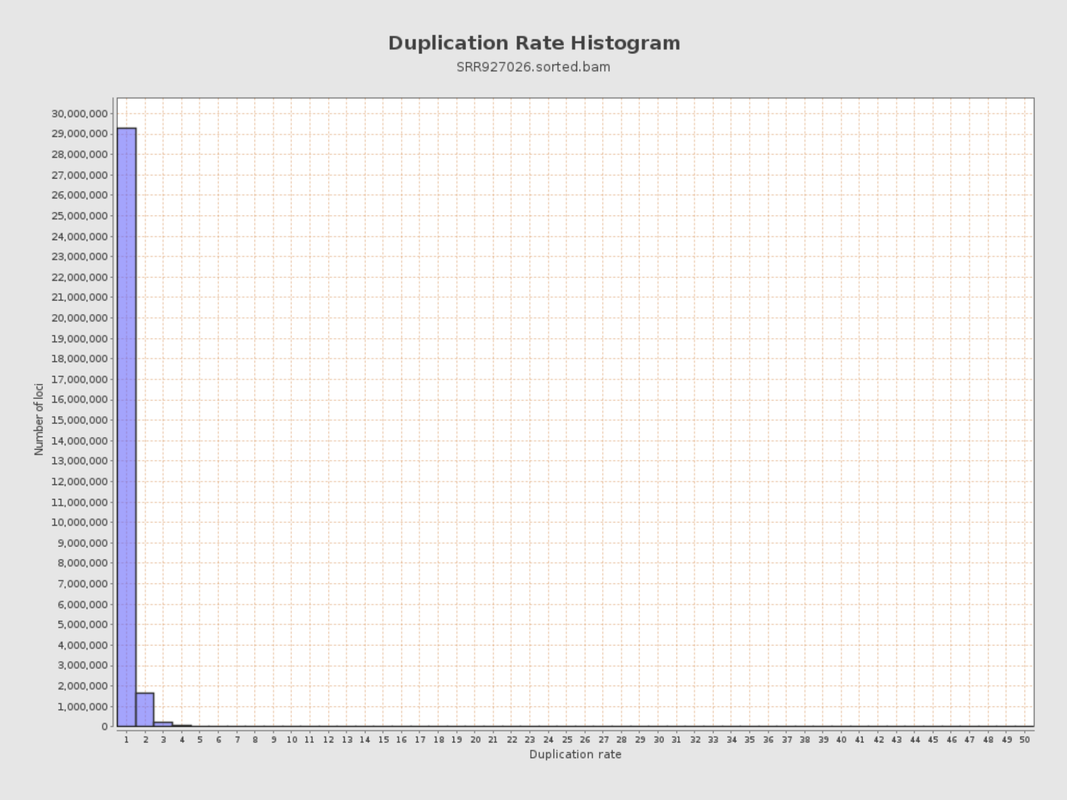
5. Results : Coverage Histogram (0-50X)



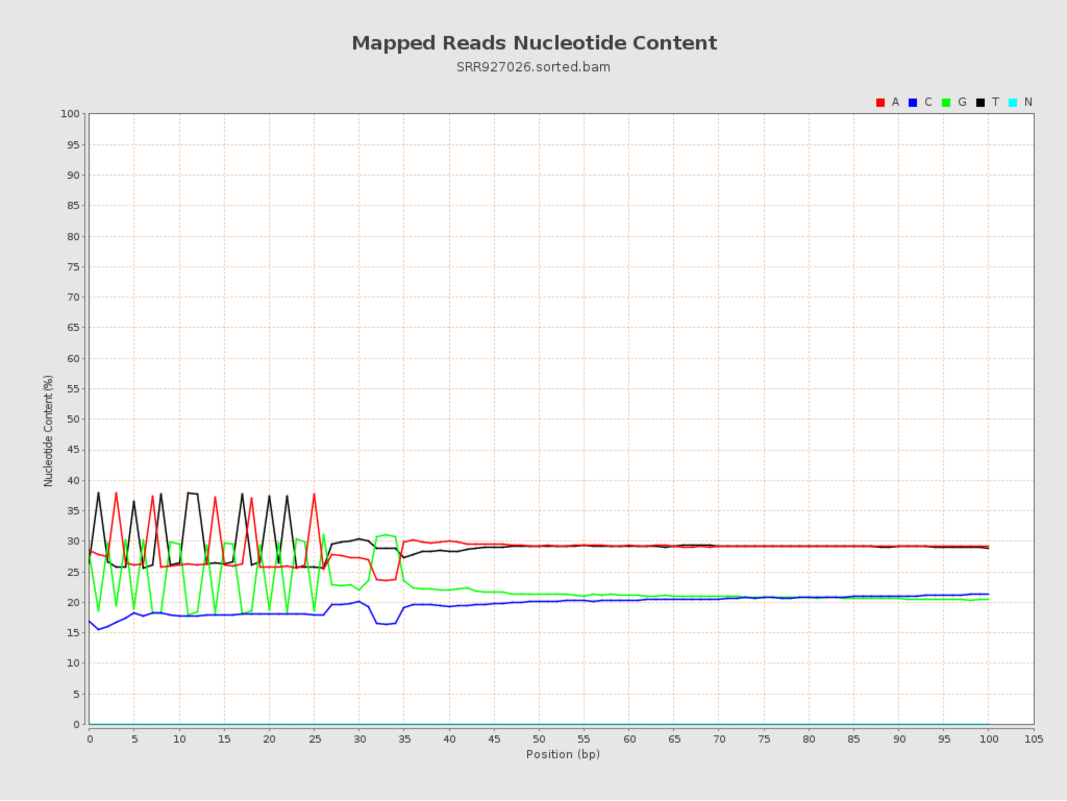
6. Results : Genome Fraction Coverage



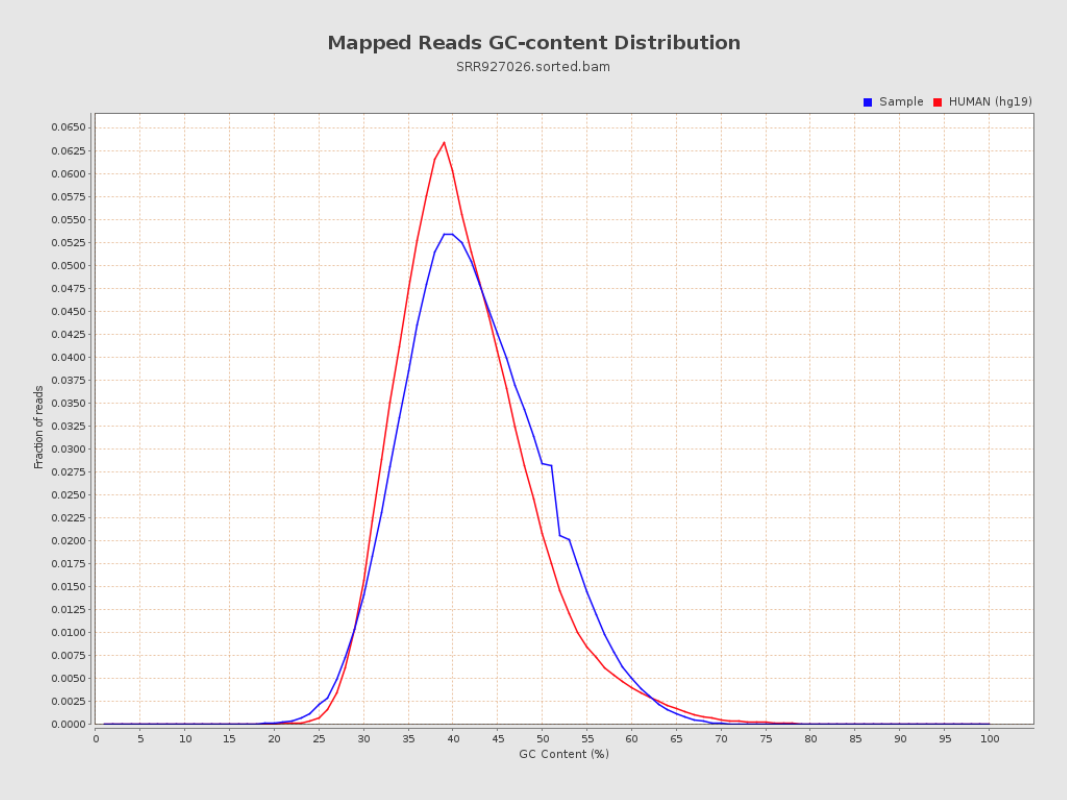
7. Results : Duplication Rate Histogram



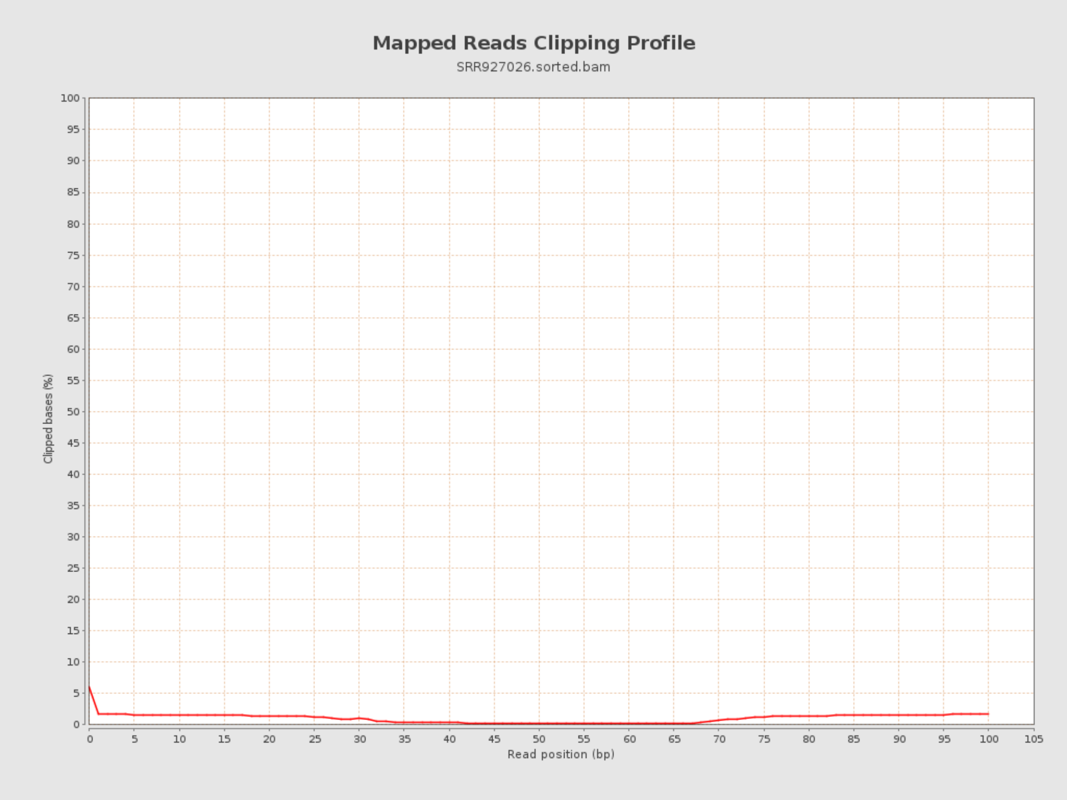
8. Results : Mapped Reads Nucleotide Content



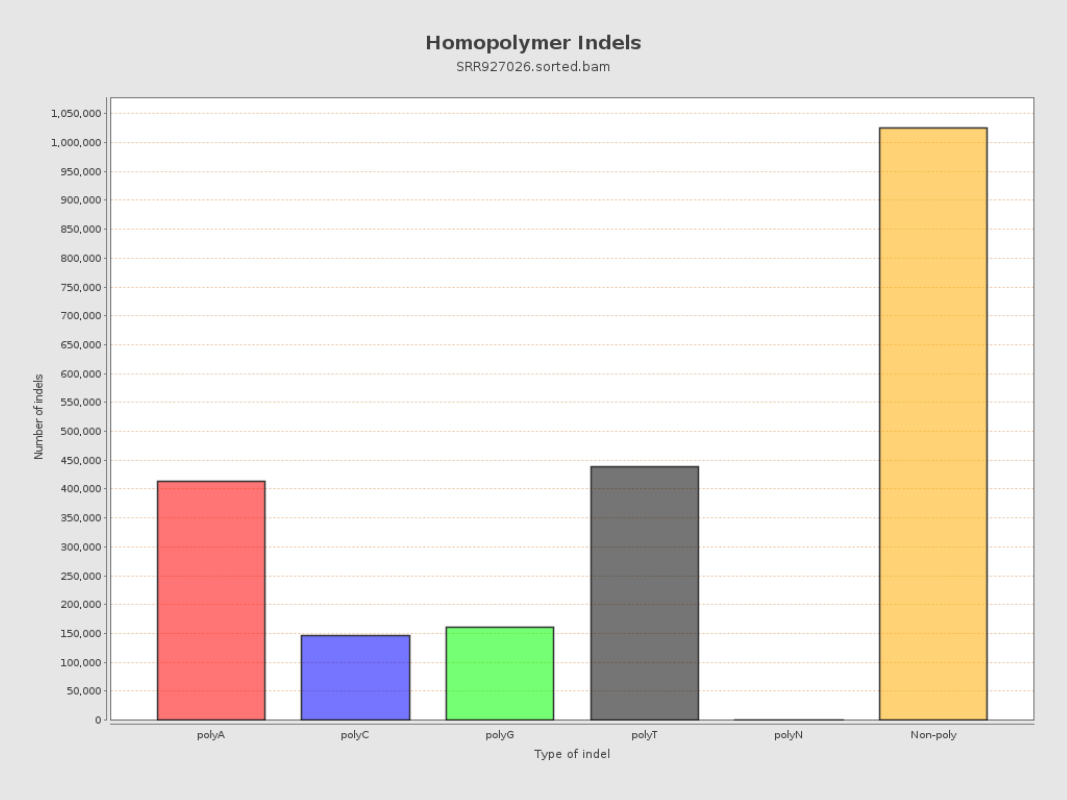
9. Results : Mapped Reads GC-content Distribution



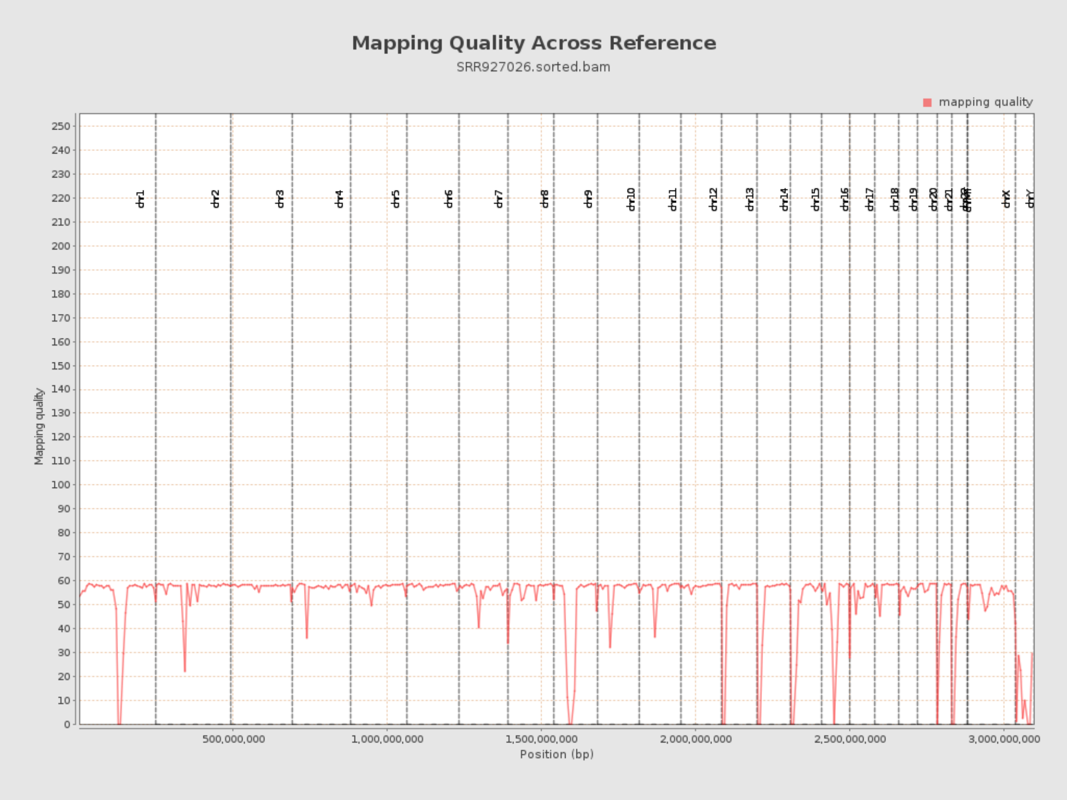
10. Results : Mapped Reads Clipping Profile



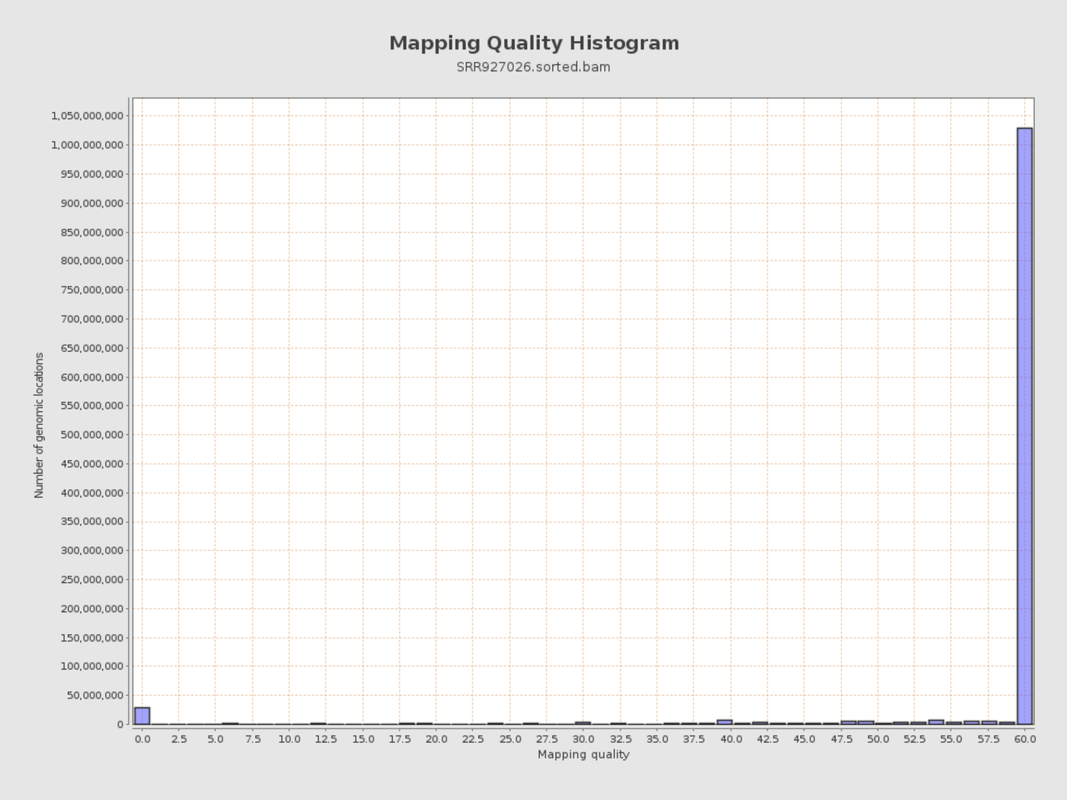
11. Results : Homopolymer Indels



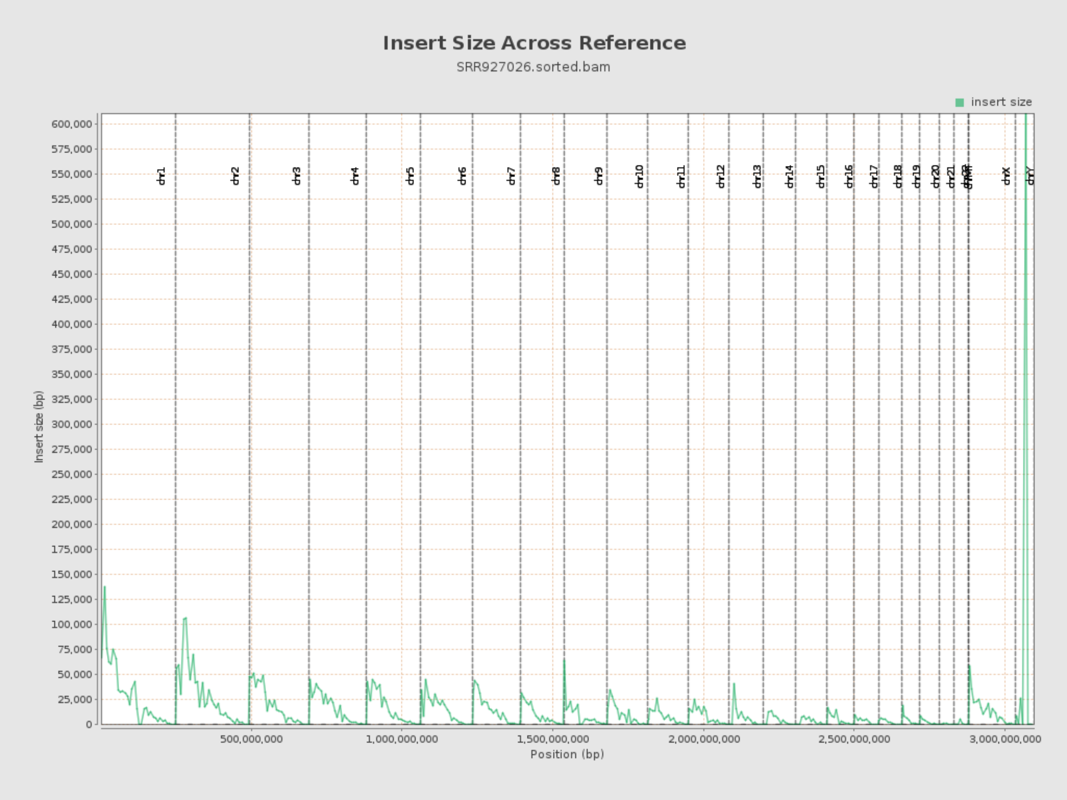
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram