Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 22:20:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927049.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_SRR927049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927049_1.fastq.gz SRR927049_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 22:20:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,483,148
Mapped reads	31,760,492 / 97.78%
Unmapped reads	722,656 / 2.22%
Mapped paired reads	31,760,492 / 97.78%
Mapped reads, first in pair	15,943,211 / 49.08%
Mapped reads, second in pair	15,817,281 / 48.69%
Mapped reads, both in pair	31,333,476 / 96.46%
Mapped reads, singletons	427,016 / 1.31%
Secondary alignments	0
Supplementary alignments	457,588 / 1.41%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	2,477,102 / 7.63%
Duplication rate	6.28%
Clipped reads	9,186,806 / 28.28%

2.2. ACGT Content

Number/percentage of A's	837,132,529 / 28.1%
Number/percentage of C's	608,897,250 / 20.44%
Number/percentage of T's	849,293,398 / 28.51%
Number/percentage of G's	683,037,894 / 22.93%
Number/percentage of N's	463,365 / 0.02%

GC Percentage	43.37%

2.3. Coverage

Mean	0.963
Standard Deviation	3.0402

2.4. Mapping Quality

Mean Mapping Quality	53.4

2.5. Insert size

Mean	134,900.69
Standard Deviation	3,586,715.5
P25/Median/P75	150 / 193 / 258

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	30,446,708
Insertions	474,044
Mapped reads with at least one insertion	1.47%
Deletions	1,553,846
Mapped reads with at least one deletion	4.77%
Homopolymer indels	52.62%

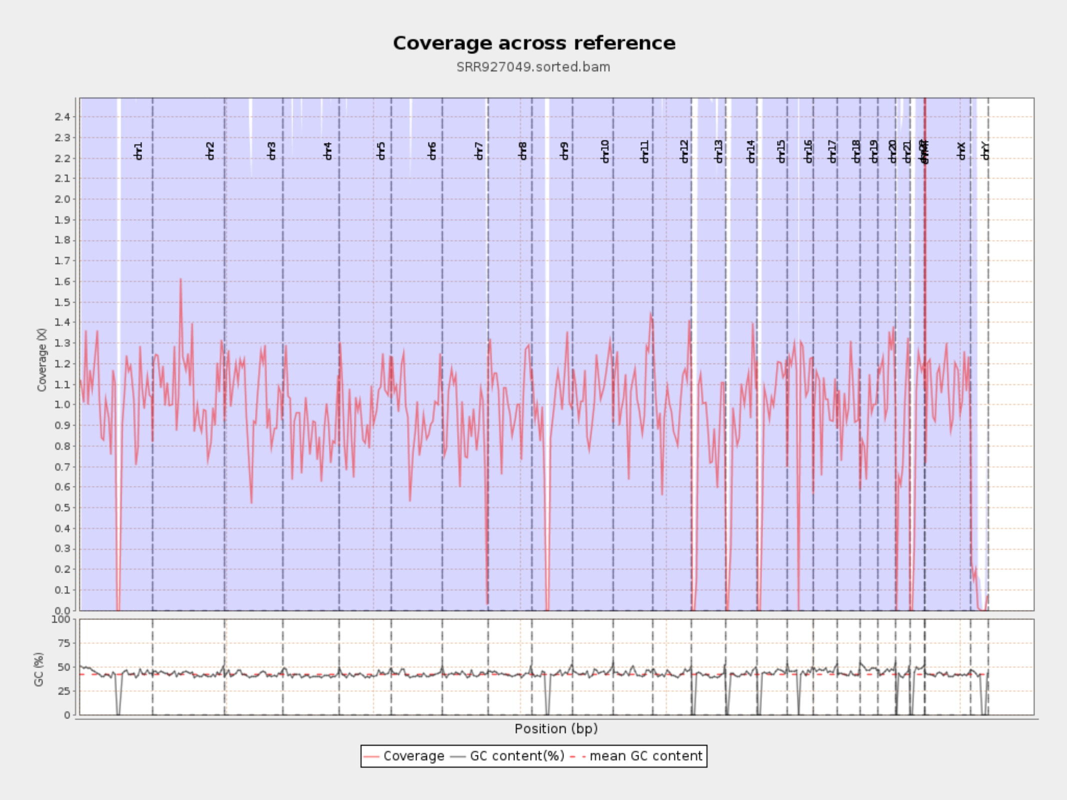
2.7. Chromosome stats

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

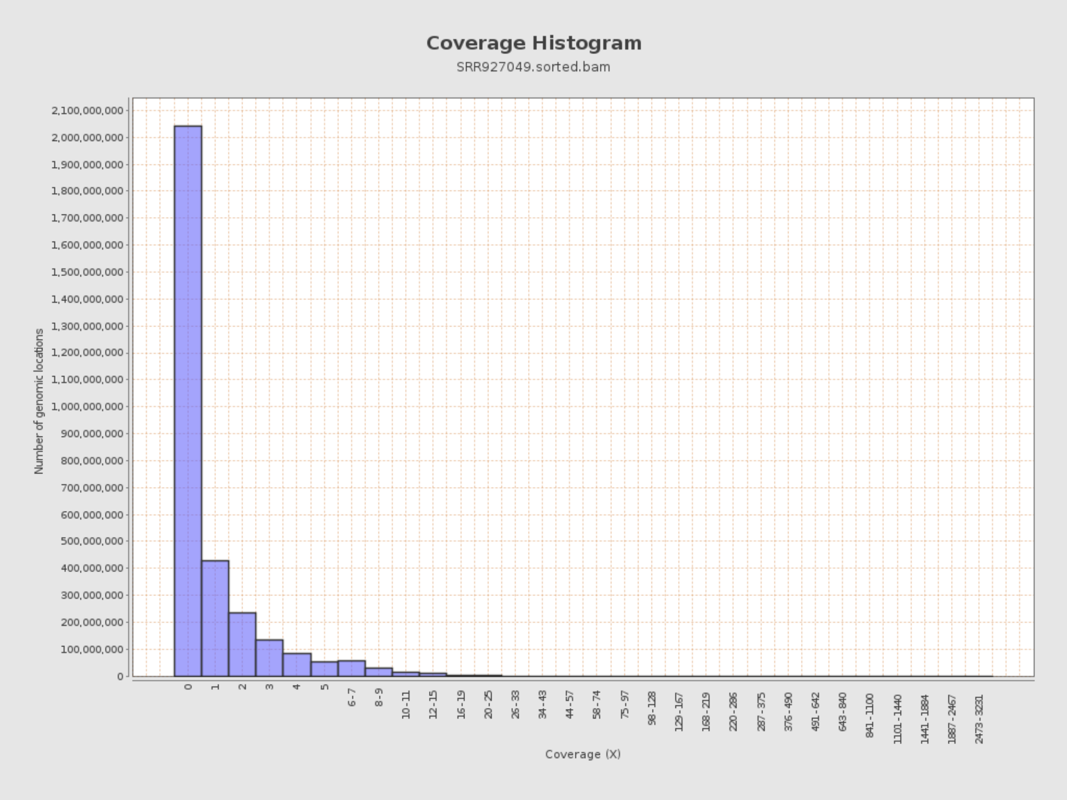
		bases	**coverage**	**deviation**
chr1	249250621	246136858	0.9875	4.0377
chr2	243199373	264545987	1.0878	4.9362
chr3	198022430	204026263	1.0303	2.1056
chr4	191154276	171812541	0.8988	2.7047
chr5	180915260	177549760	0.9814	2.0565
chr6	171115067	164992643	0.9642	2.0369
chr7	159138663	138654450	0.8713	2.2846
chr8	146364022	152970182	1.0451	2.3856
chr9	141213431	127301220	0.9015	3.4286
chr10	135534747	145056698	1.0703	4.0523
chr11	135006516	144648596	1.0714	3.2268
chr12	133851895	134898172	1.0078	2.1136
chr13	115169878	89114673	0.7738	1.8037
chr14	107349540	90981677	0.8475	1.9833
chr15	102531392	91141915	0.8889	2.0723
chr16	90354753	96889451	1.0723	4.377
chr17	81195210	81264125	1.0008	2.9158
chr18	78077248	79406031	1.017	3.4841
chr19	59128983	53288530	0.9012	2.7498
chr20	63025520	74127122	1.1761	2.4837
chr21	48129895	38598889	0.802	2.632
chr22	51304566	40834287	0.7959	2.0877
chrMT	16571	183472	11.0719	9.1338
chrX	155270560	168077315	1.0825	2.4748

chrY	59373566	4530581	0.0763	2.2138

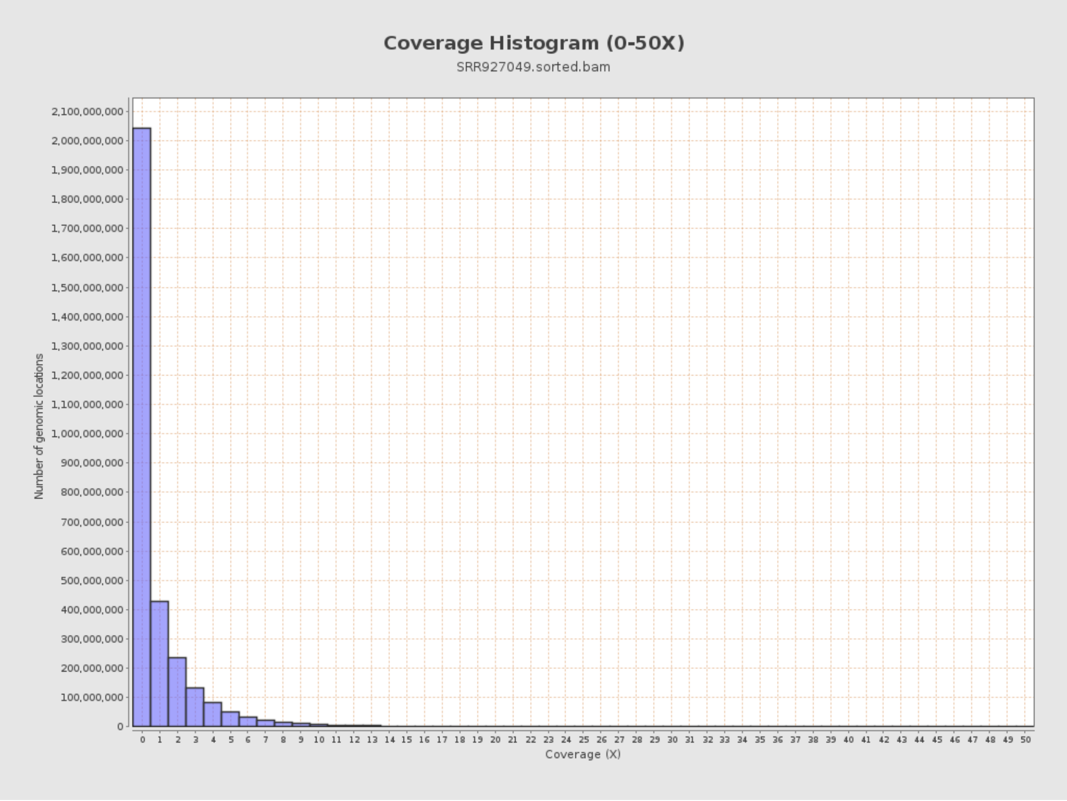
3. Results : Coverage across reference



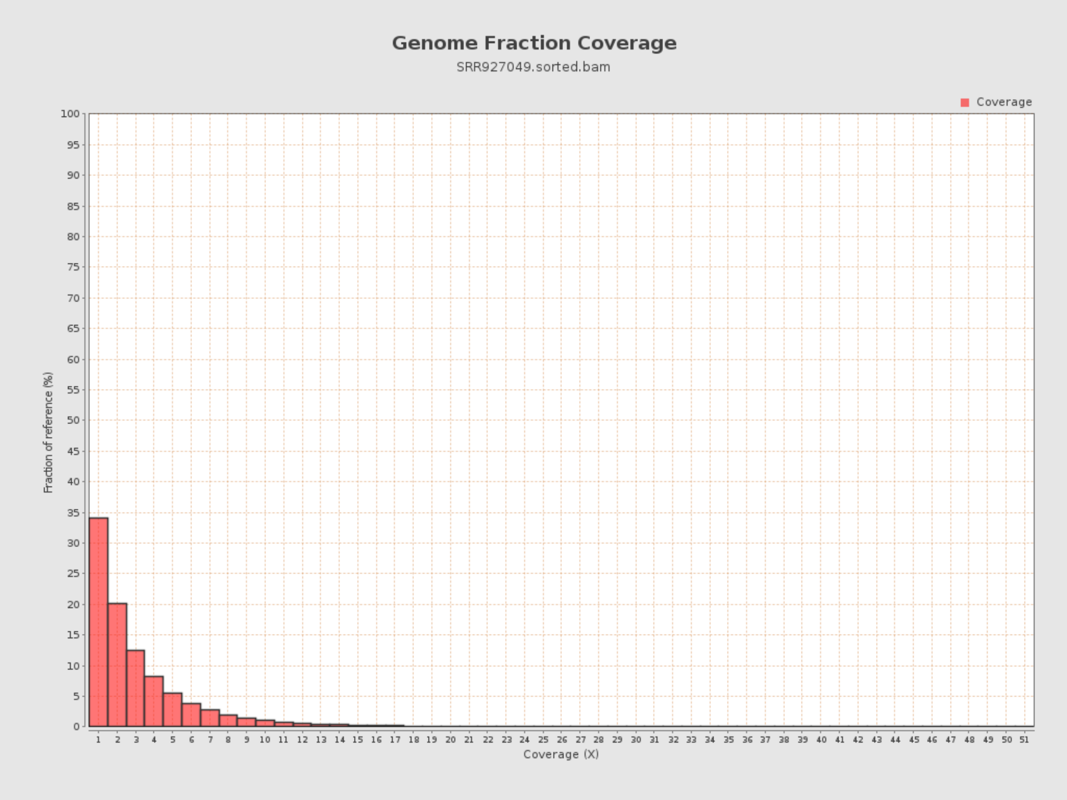
4. Results : Coverage Histogram



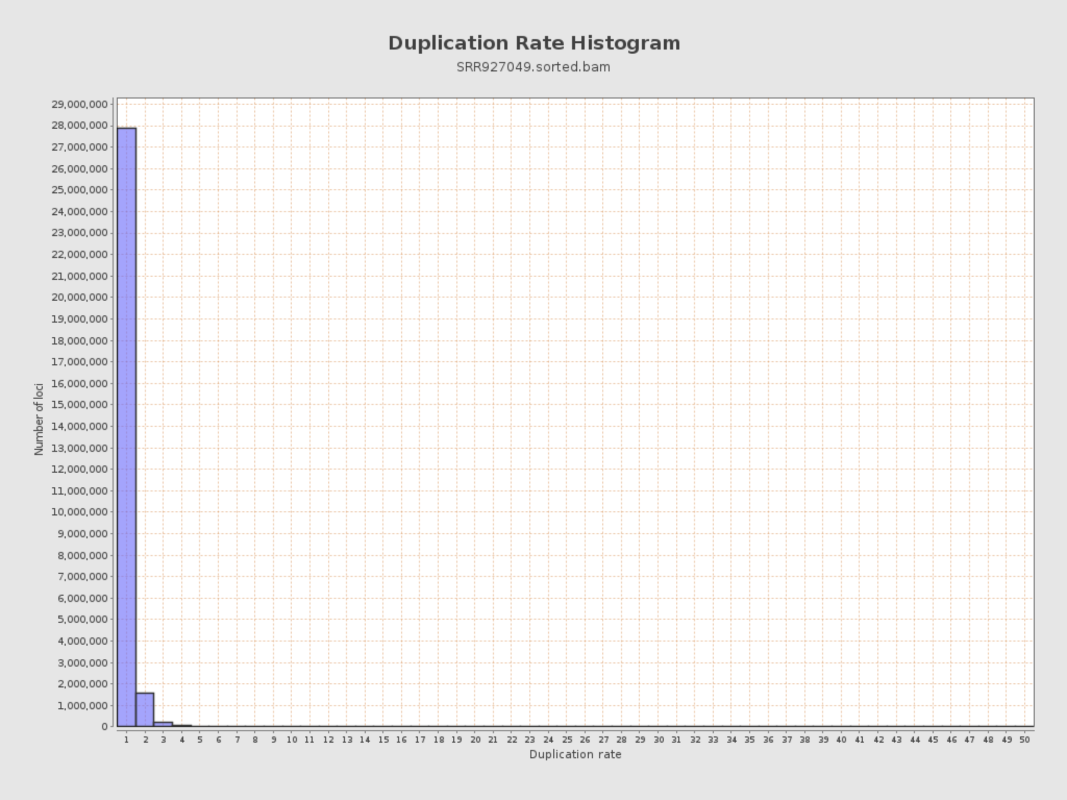
5. Results : Coverage Histogram (0-50X)



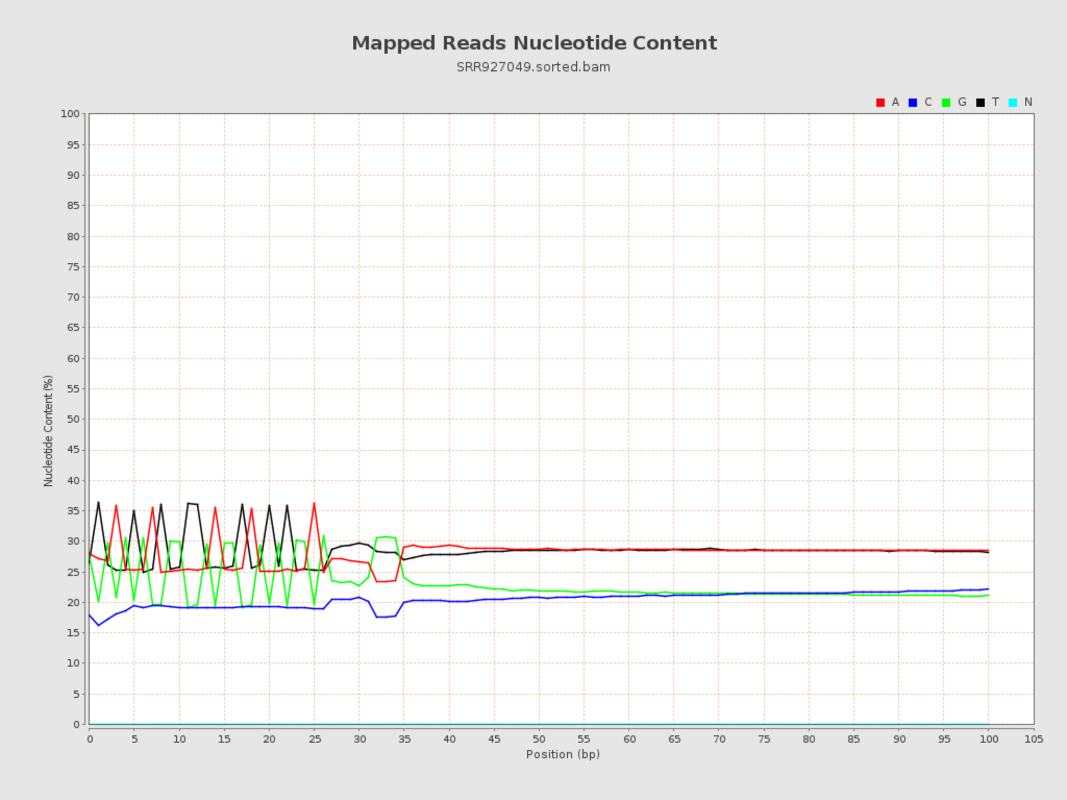
6. Results : Genome Fraction Coverage



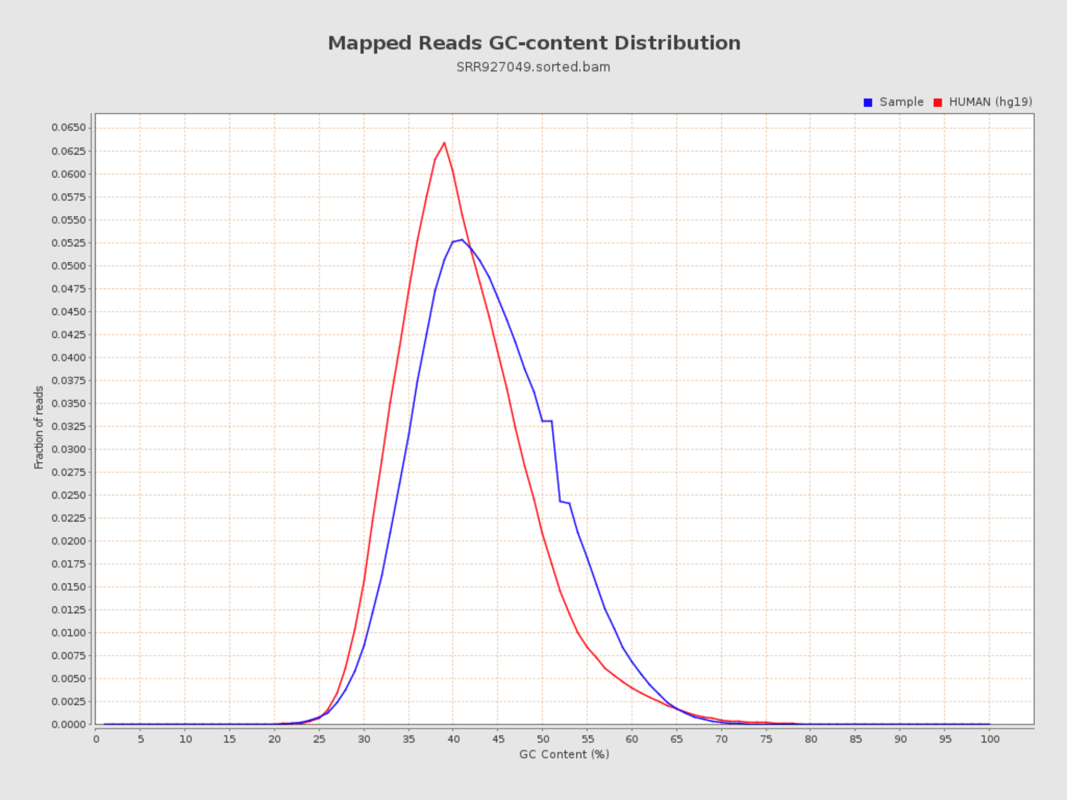
7. Results : Duplication Rate Histogram



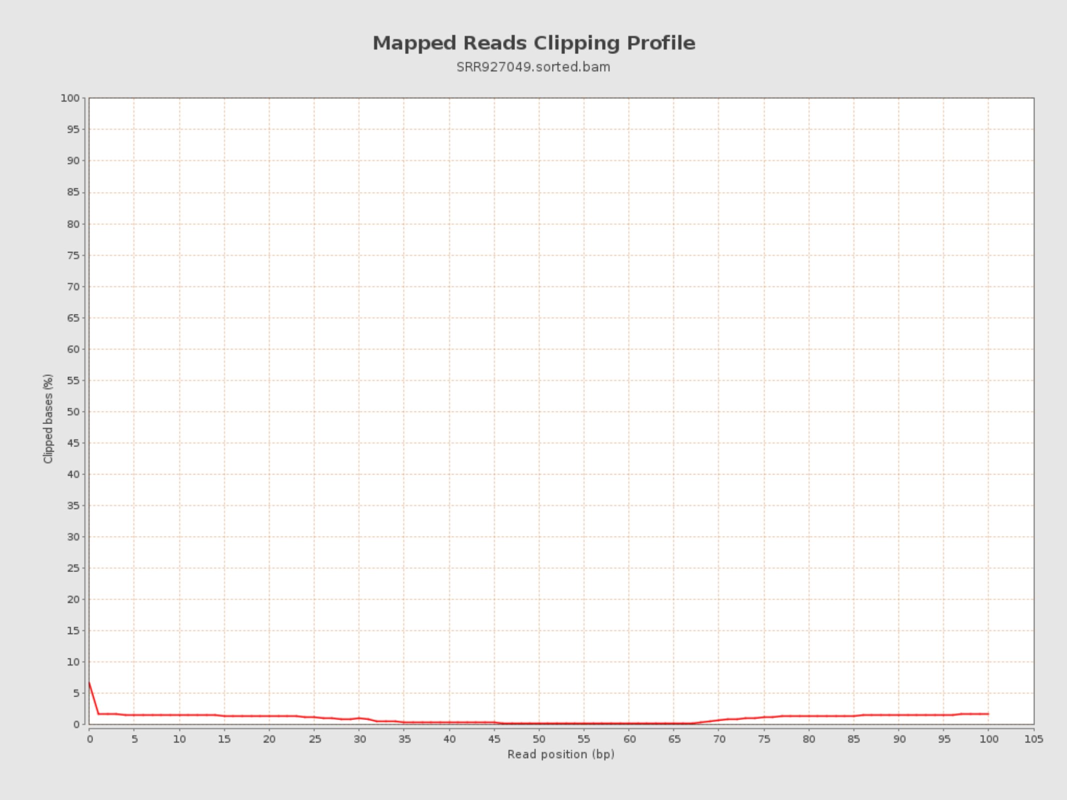
8. Results : Mapped Reads Nucleotide Content



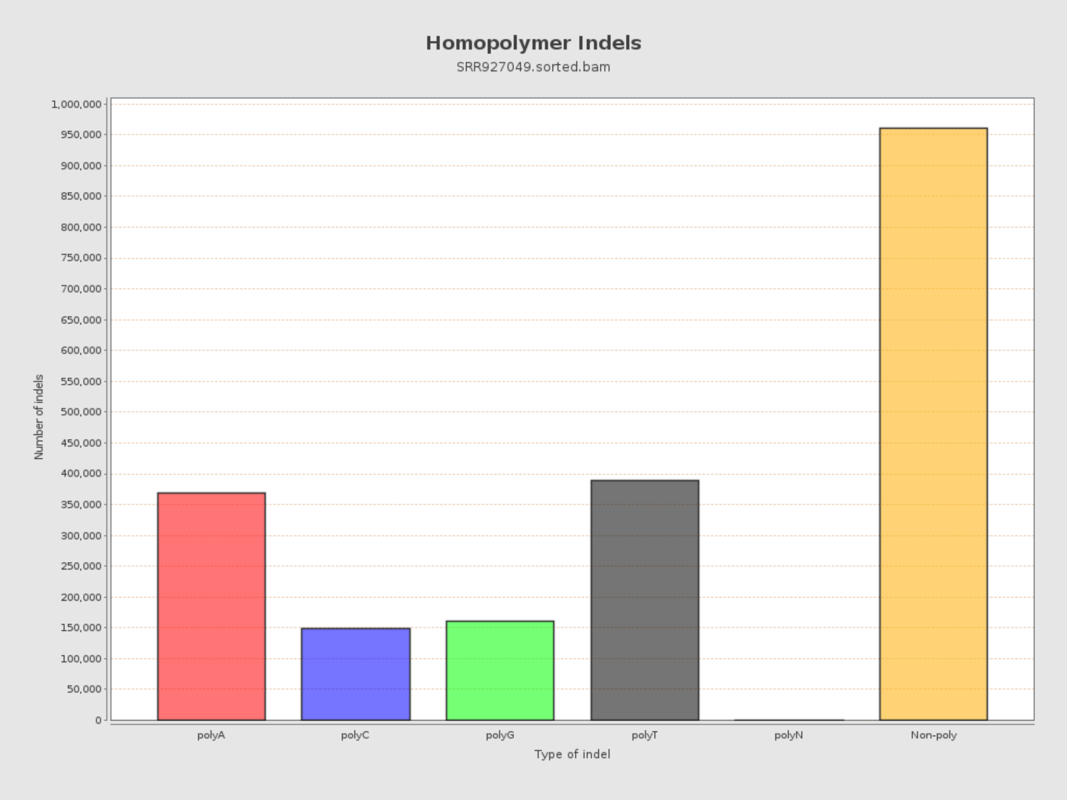
9. Results : Mapped Reads GC-content Distribution



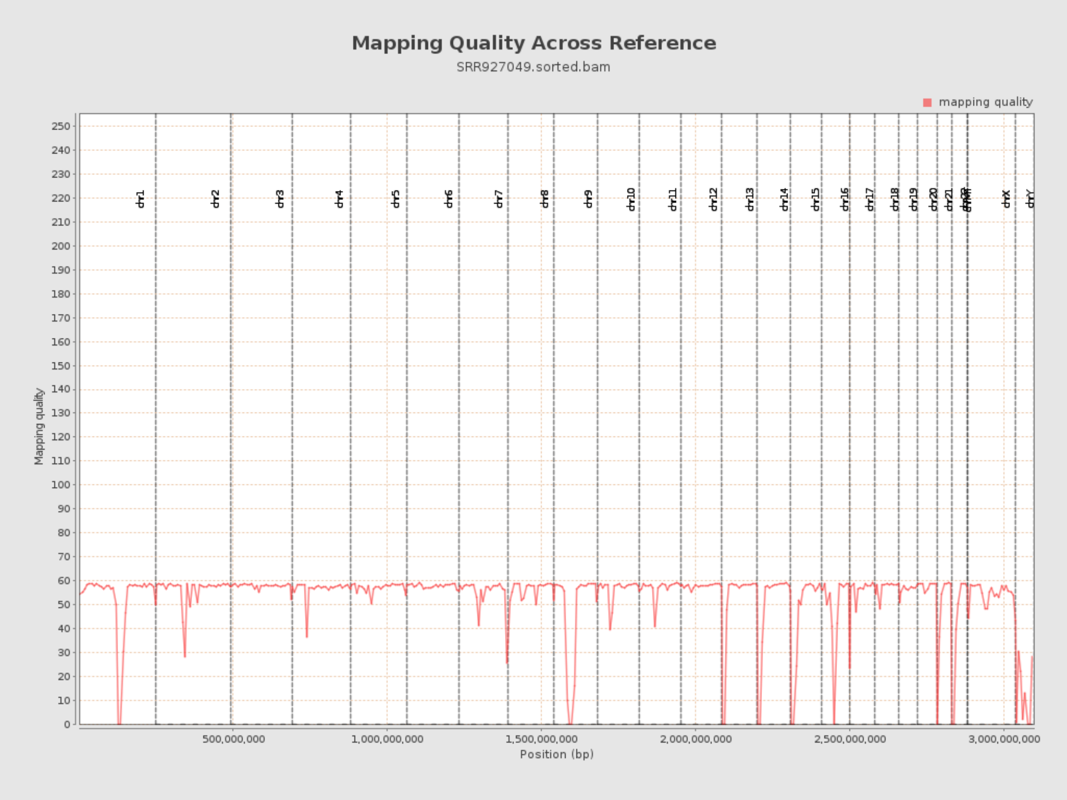
10. Results : Mapped Reads Clipping Profile



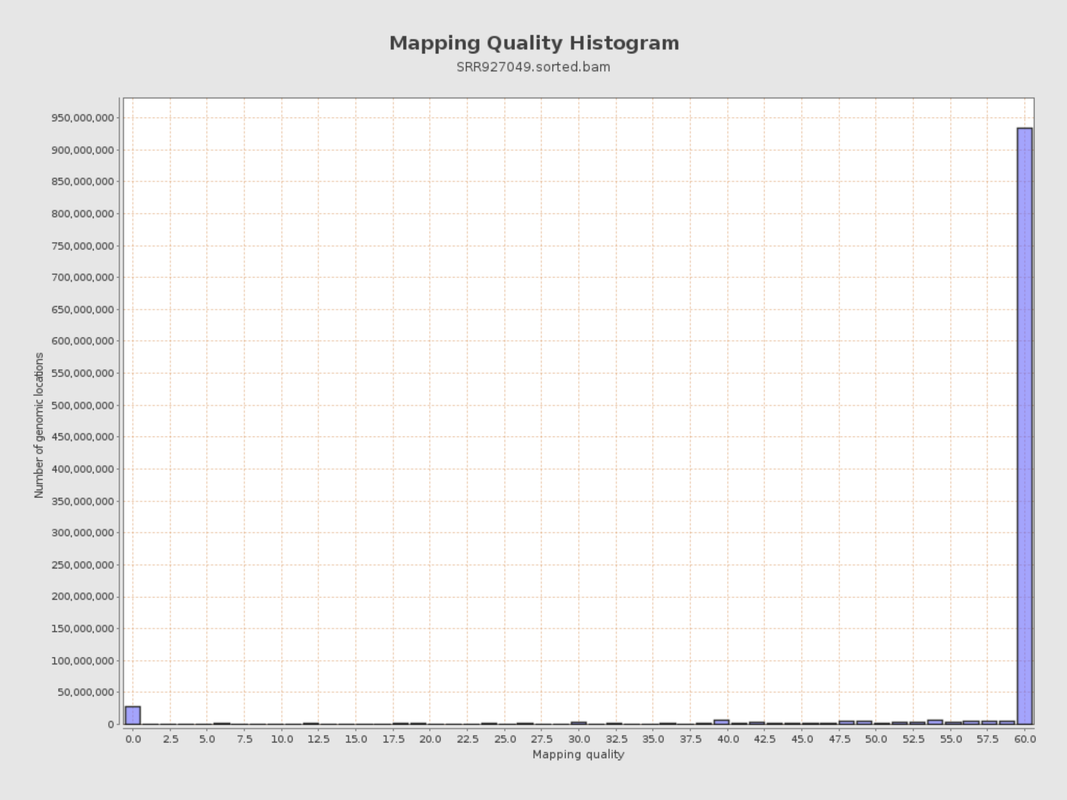
11. Results : Homopolymer Indels



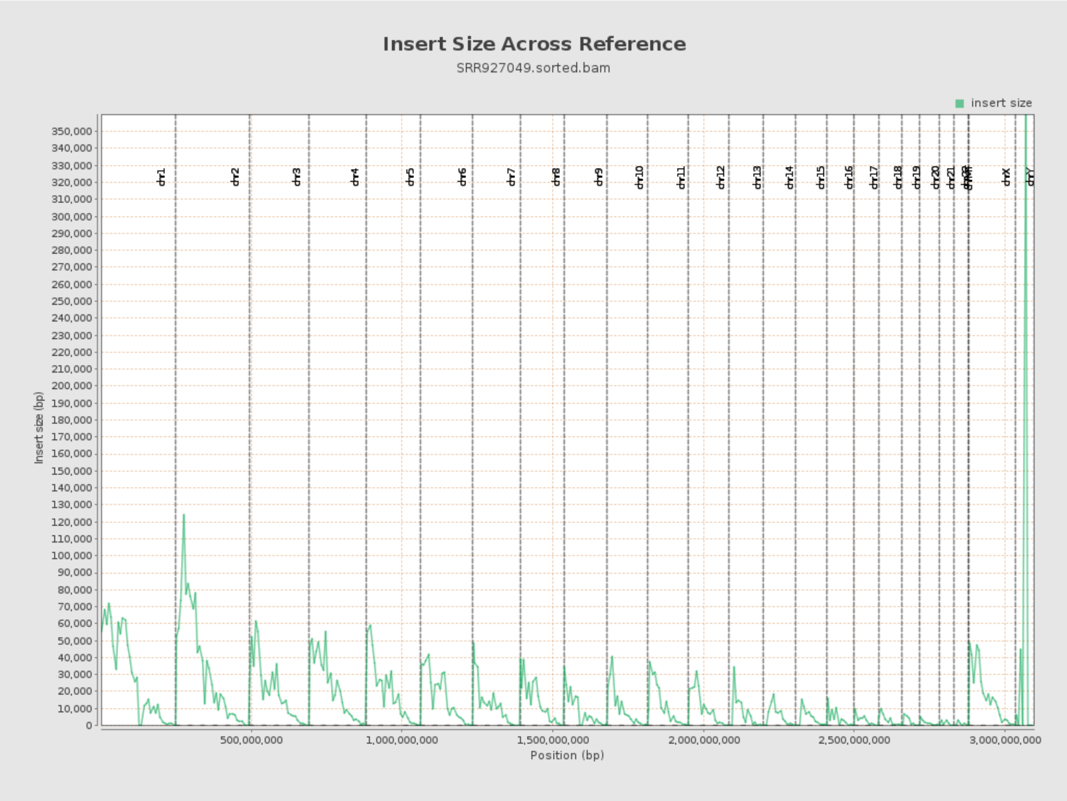
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram