Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 14:15:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927034.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_SRR927034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927034_1.fastq.gz SRR927034_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 14:15:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,794,008
Mapped reads	36,056,457 / 98%
Unmapped reads	737,551 / 2%
Mapped paired reads	36,056,457 / 98%
Mapped reads, first in pair	18,086,661 / 49.16%
Mapped reads, second in pair	17,969,796 / 48.84%
Mapped reads, both in pair	35,633,504 / 96.85%
Mapped reads, singletons	422,953 / 1.15%
Secondary alignments	0
Supplementary alignments	790,103 / 2.15%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	3,504,766 / 9.53%
Duplication rate	7.67%
Clipped reads	13,618,417 / 37.01%

2.2. ACGT Content

Number/percentage of A's	927,935,482 / 28.03%
Number/percentage of C's	665,575,559 / 20.1%
Number/percentage of T's	948,368,340 / 28.65%
Number/percentage of G's	768,242,896 / 23.21%
Number/percentage of N's	452,966 / 0.01%

GC Percentage	43.31%

2.3. Coverage

Mean	1.0702
Standard Deviation	3.3224

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	228,175.19
Standard Deviation	4,730,554.19
P25/Median/P75	141 / 183 / 245

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	33,381,105
Insertions	546,544
Mapped reads with at least one insertion	1.49%
Deletions	1,693,249
Mapped reads with at least one deletion	4.58%
Homopolymer indels	52.06%

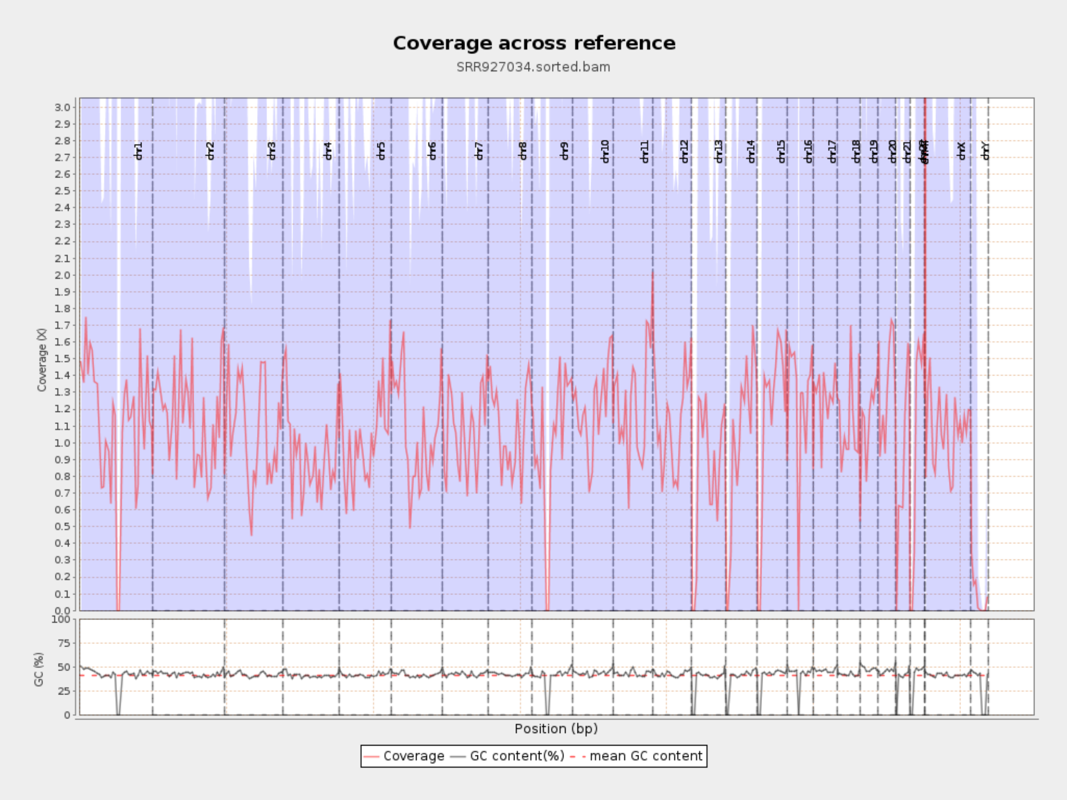
2.7. Chromosome stats

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

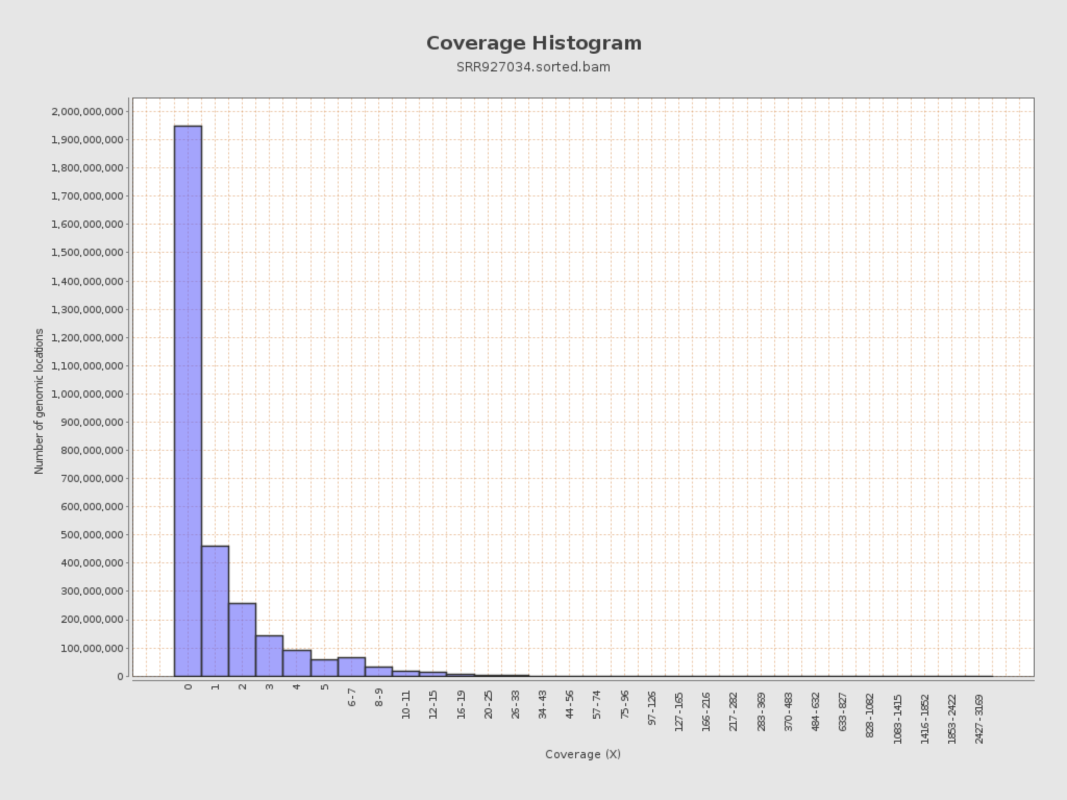
		bases	coverage	deviation
chr1	249250621	276910385	1.111	4.0402
chr2	243199373	280850323	1.1548	5.292
chr3	198022430	213187917	1.0766	2.186
chr4	191154276	177041112	0.9262	2.6197
chr5	180915260	186658880	1.0317	2.1229
chr6	171115067	180485711	1.0548	2.1769
chr7	159138663	171023883	1.0747	2.4432
chr8	146364022	158680146	1.0841	2.3572
chr9	141213431	141553971	1.0024	3.6903
chr10	135534747	164221241	1.2117	4.1317
chr11	135006516	164053736	1.2152	3.1245
chr12	133851895	149758480	1.1188	2.268
chr13	115169878	94409438	0.8197	1.8944
chr14	107349540	107234800	0.9989	2.211
chr15	102531392	116869115	1.1398	2.4355
chr16	90354753	112197291	1.2417	4.4596
chr17	81195210	103580271	1.2757	2.9248
chr18	78077248	87921507	1.1261	3.3265
chr19	59128983	67977682	1.1497	3.0356
chr20	63025520	85262362	1.3528	2.698
chr21	48129895	43369904	0.9011	2.9094
chr22	51304566	53242004	1.0378	2.4549
chrMT	16571	5956160	359.4327	287.006
chrX	155270560	165497999	1.0659	2.3394

chrY	59373566	5086189	0.0857	2.4168

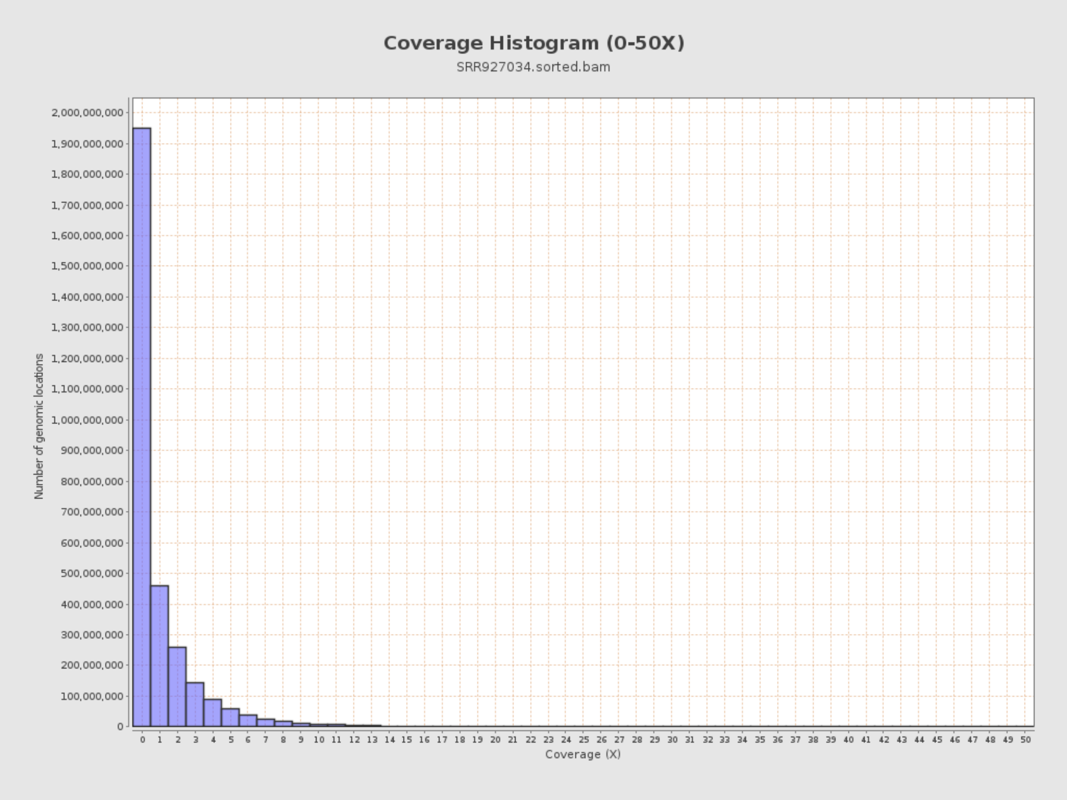
3. Results : Coverage across reference



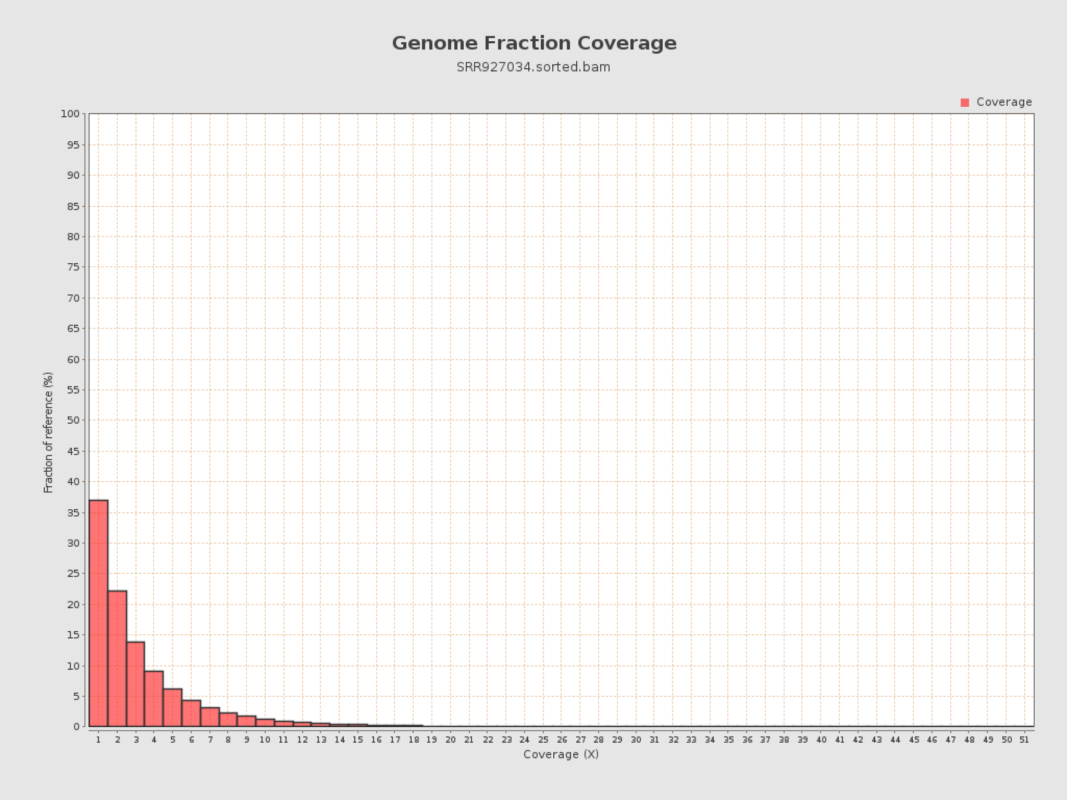
4. Results : Coverage Histogram



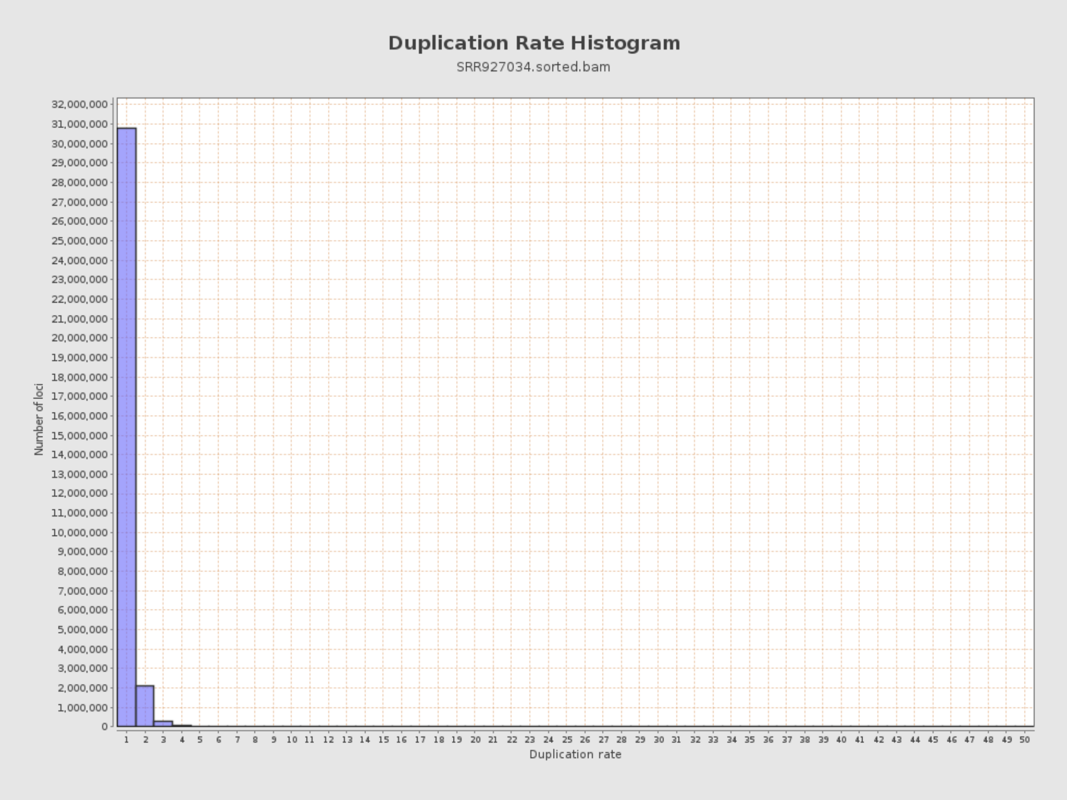
5. Results : Coverage Histogram (0-50X)



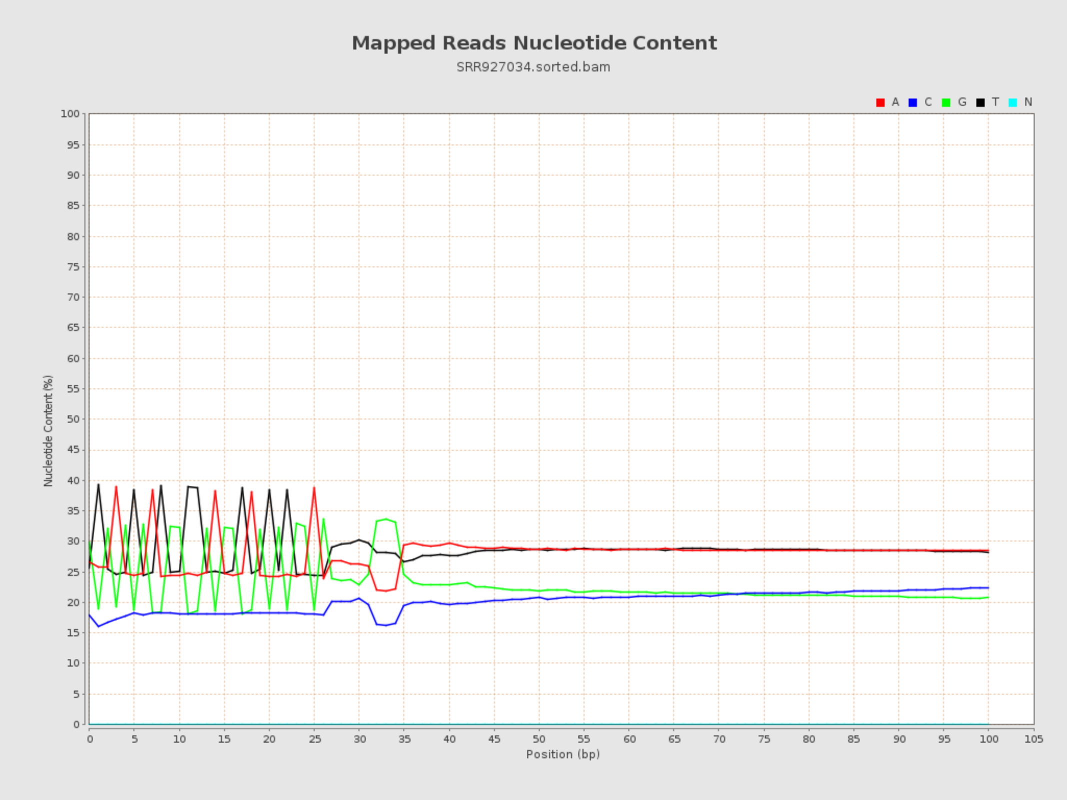
6. Results : Genome Fraction Coverage



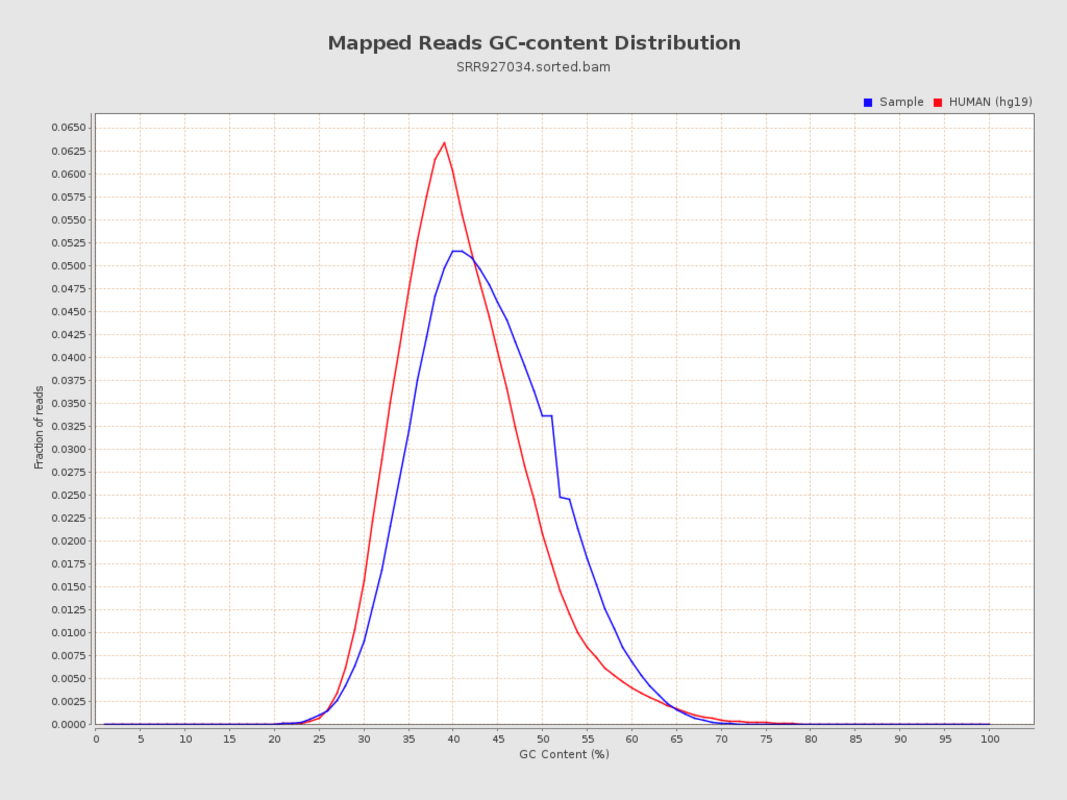
7. Results : Duplication Rate Histogram



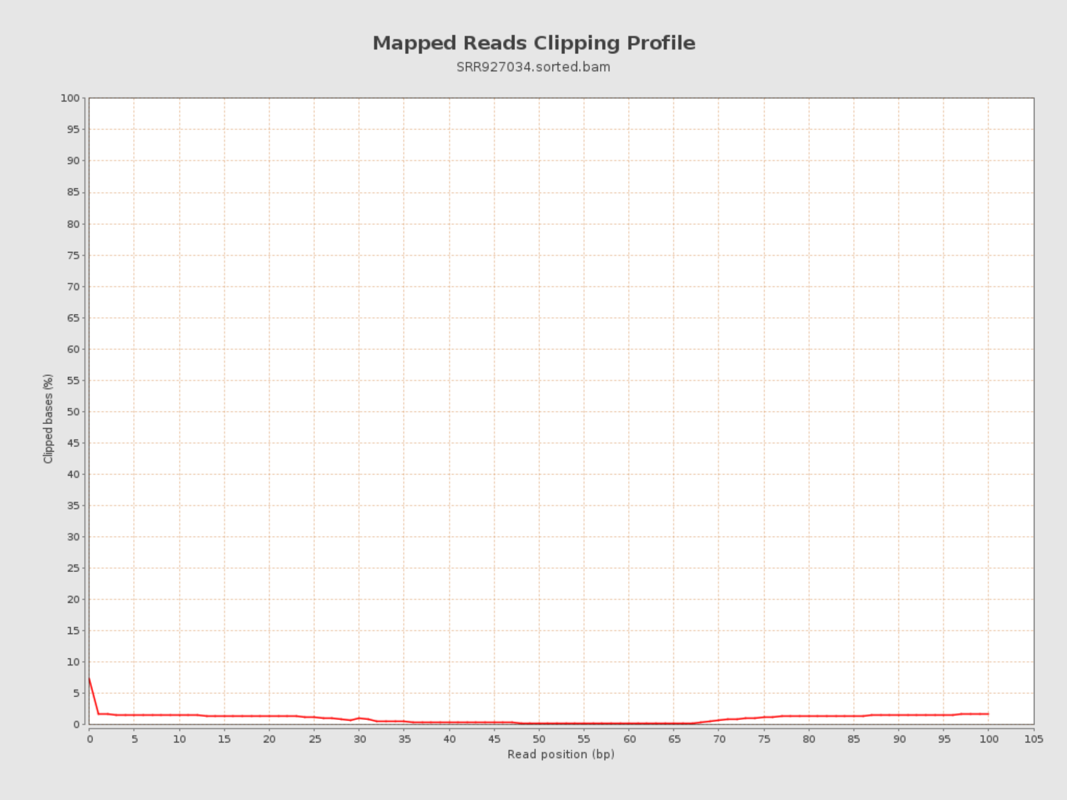
8. Results : Mapped Reads Nucleotide Content



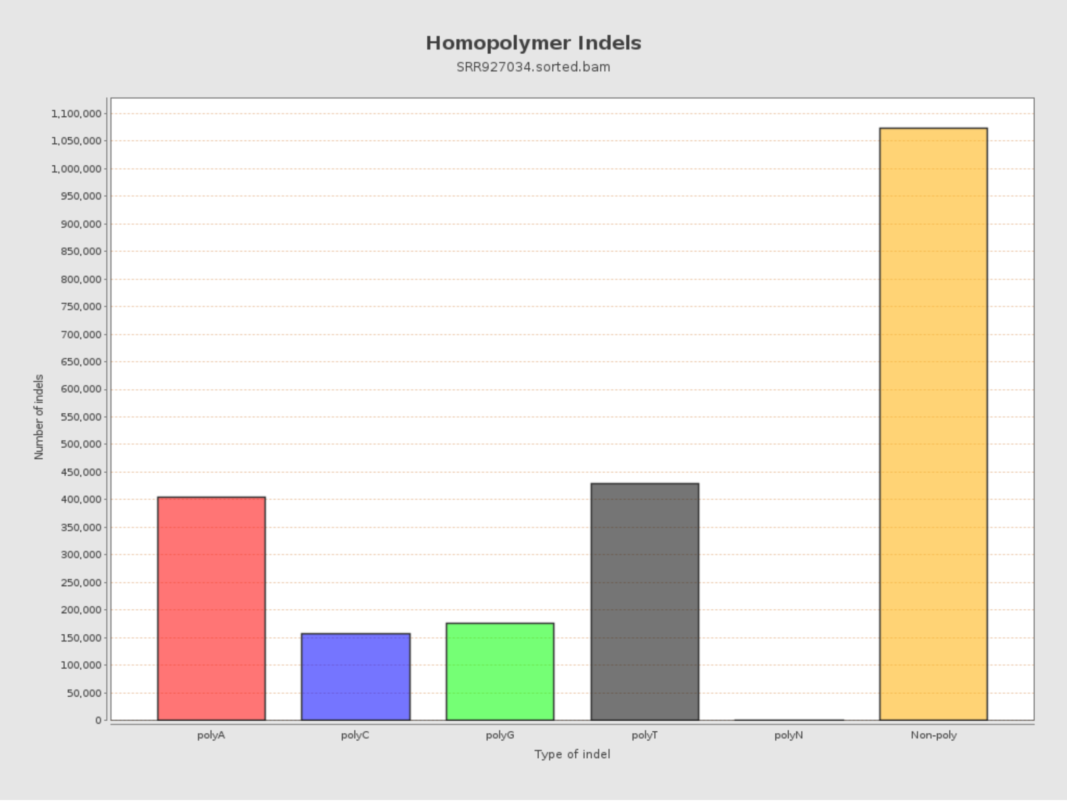
9. Results : Mapped Reads GC-content Distribution



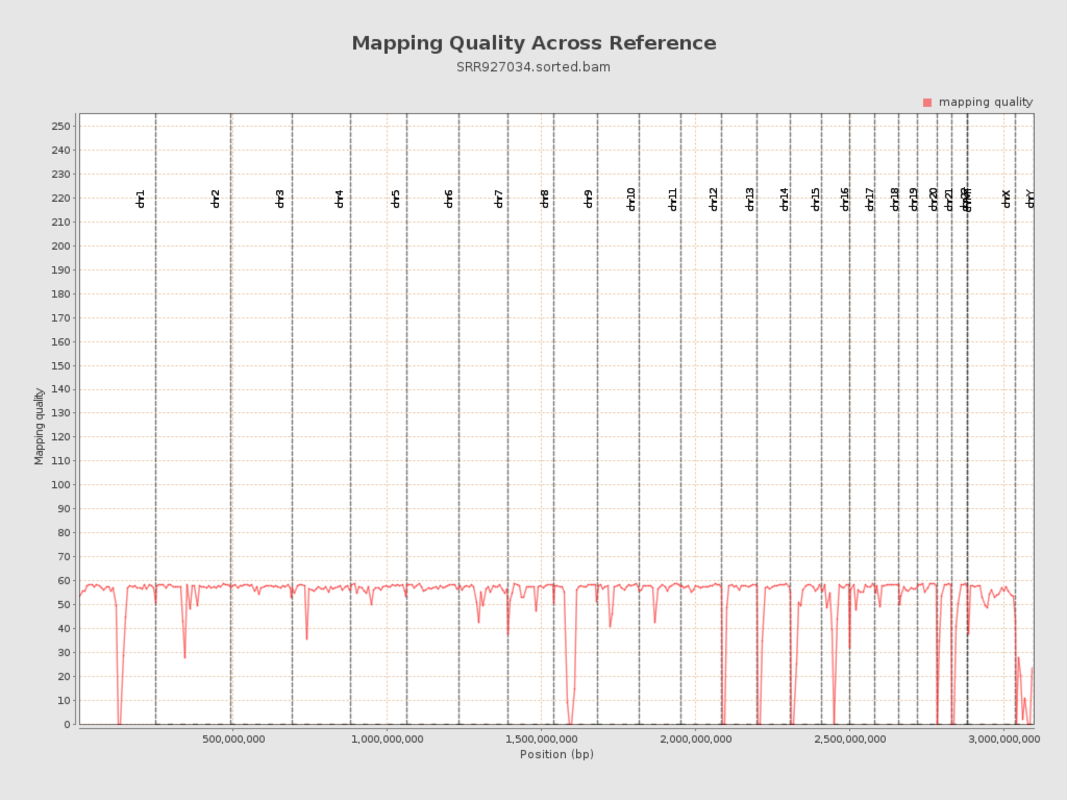
10. Results : Mapped Reads Clipping Profile



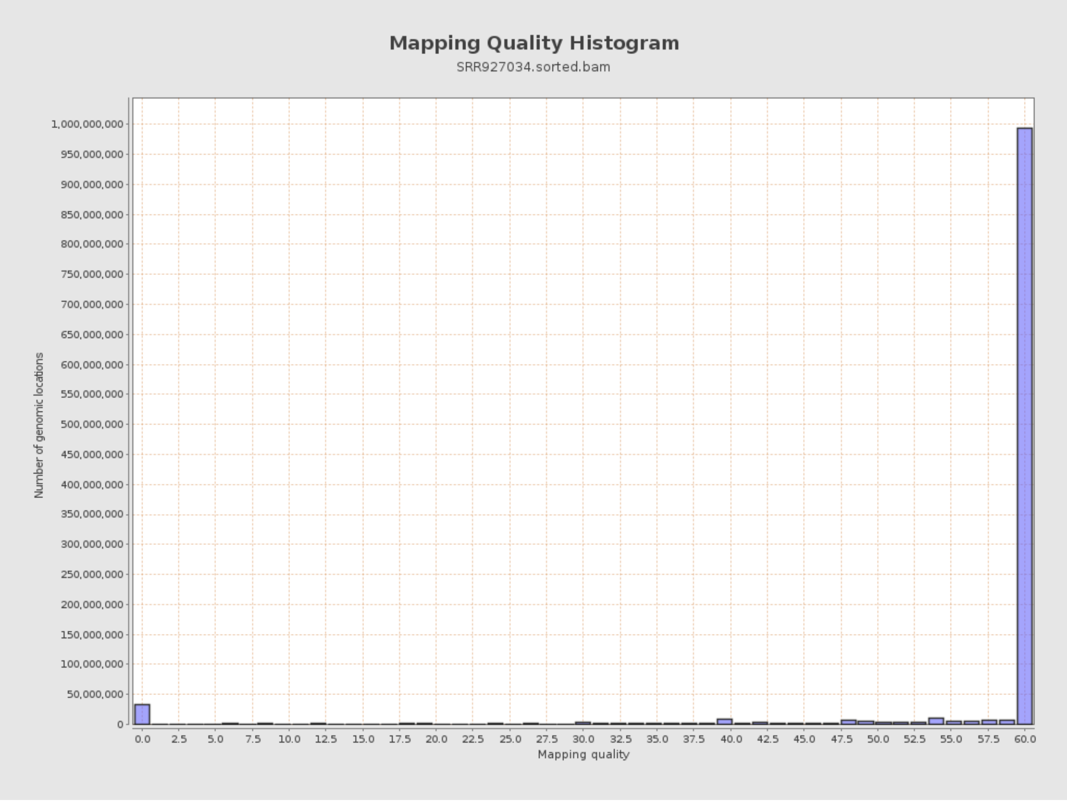
11. Results : Homopolymer Indels



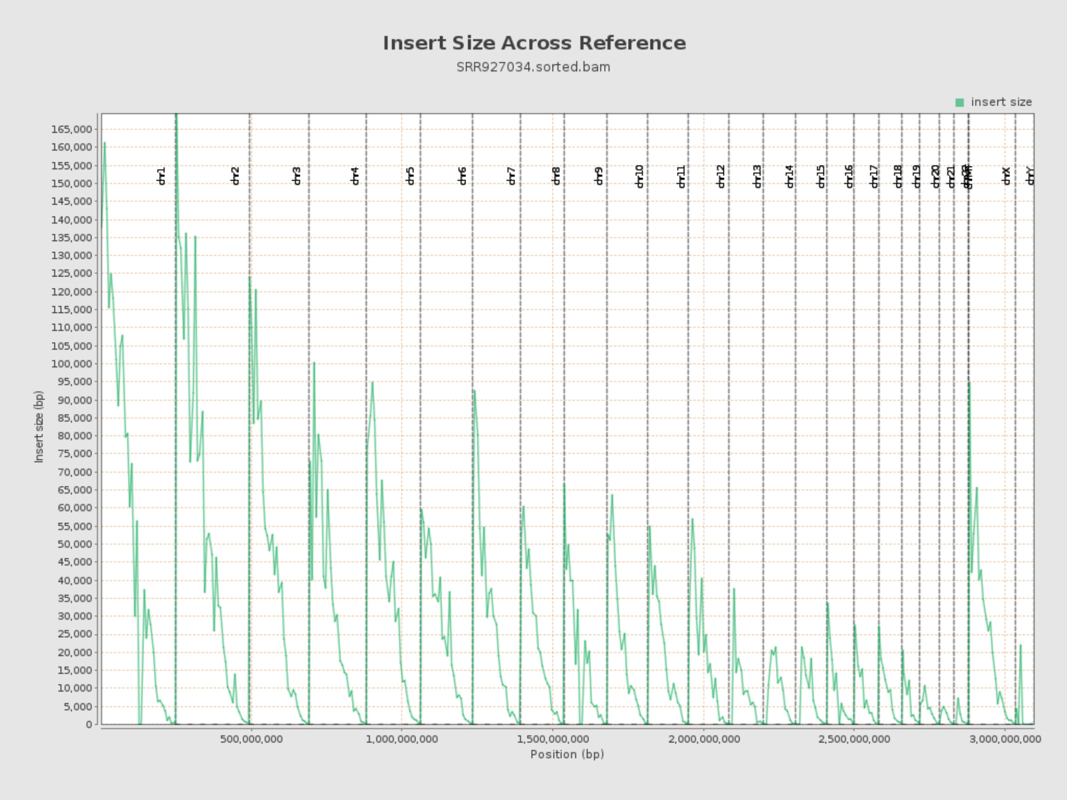
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram