Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 16:04:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927037.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_SRR927037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927037_1.fastq.gz SRR927037_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 16:04:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,119,132
Mapped reads	34,258,867 / 97.55%
Unmapped reads	860,265 / 2.45%
Mapped paired reads	34,258,867 / 97.55%
Mapped reads, first in pair	17,169,870 / 48.89%
Mapped reads, second in pair	17,088,997 / 48.66%
Mapped reads, both in pair	33,771,800 / 96.16%
Mapped reads, singletons	487,067 / 1.39%
Secondary alignments	0
Supplementary alignments	842,739 / 2.4%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	3,667,872 / 10.44%
Duplication rate	8.28%
Clipped reads	14,271,713 / 40.64%

2.2. ACGT Content

Number/percentage of A's	875,722,155 / 28.11%
Number/percentage of C's	618,912,400 / 19.87%
Number/percentage of T's	896,274,395 / 28.77%
Number/percentage of G's	723,881,213 / 23.24%
Number/percentage of N's	388,483 / 0.01%

GC Percentage	43.1%

2.3. Coverage

Mean	1.007
Standard Deviation	3.7897

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	232,113.76
Standard Deviation	4,768,457.26
P25/Median/P75	138 / 181 / 244

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	32,228,844
Insertions	516,082
Mapped reads with at least one insertion	1.48%
Deletions	1,590,815
Mapped reads with at least one deletion	4.53%
Homopolymer indels	52.16%

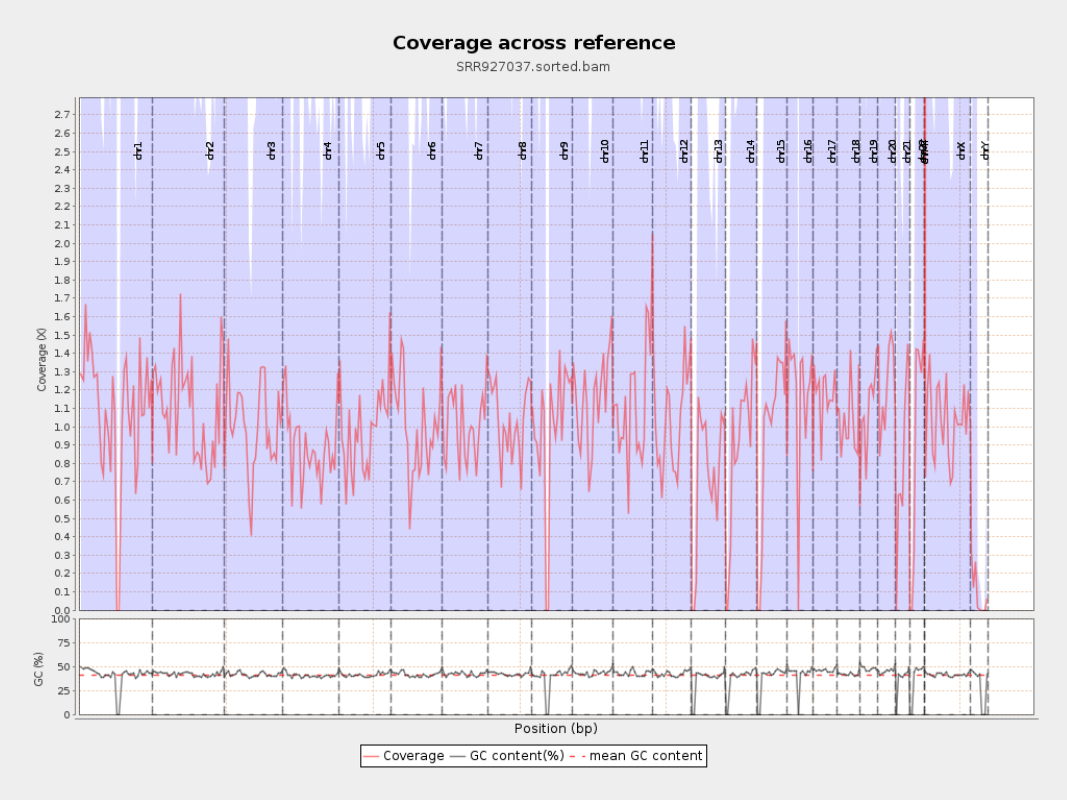
2.7. Chromosome stats

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

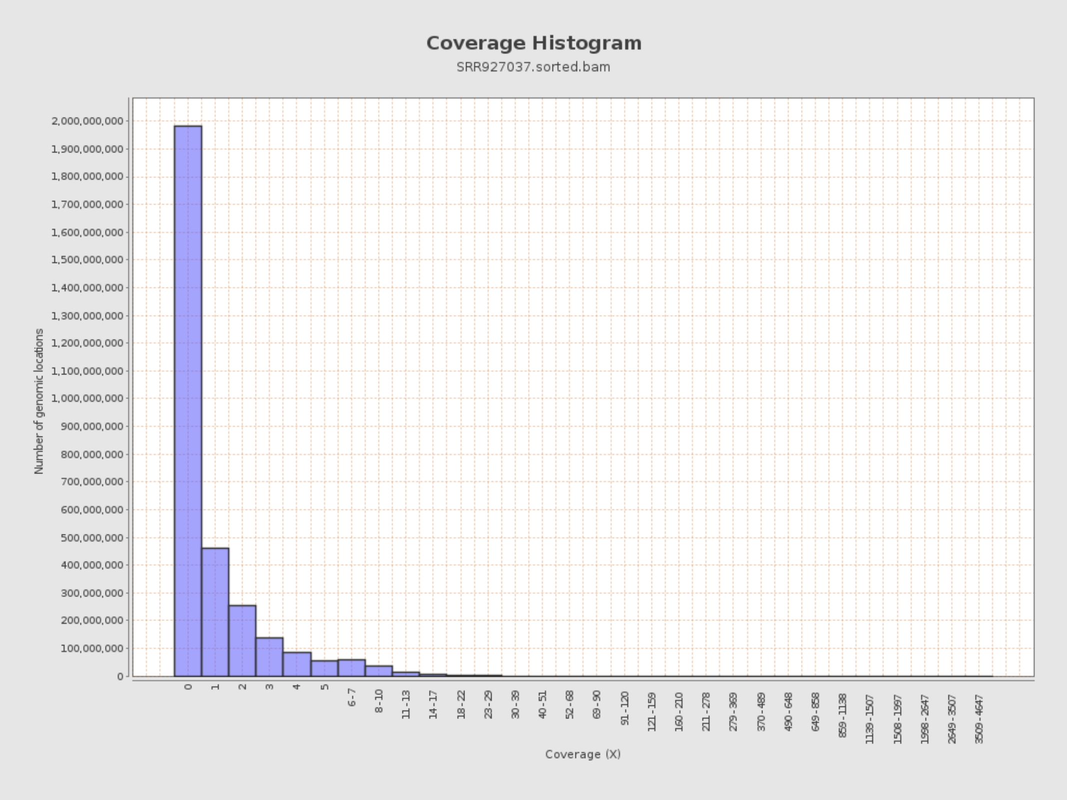
		bases	coverage	deviation
chr1	249250621	268684891	1.078	3.7511
chr2	243199373	267245532	1.0989	4.8007
chr3	198022430	199325306	1.0066	2.0745
chr4	191154276	169590766	0.8872	2.4995
chr5	180915260	178677083	0.9876	2.0355
chr6	171115067	171408442	1.0017	2.0717
chr7	159138663	160572962	1.009	2.4272
chr8	146364022	151159022	1.0328	2.3397
chr9	141213431	139140482	0.9853	4.1187
chr10	135534747	156717295	1.1563	5.0991
chr11	135006516	148944308	1.1032	2.8989
chr12	133851895	137694662	1.0287	2.136
chr13	115169878	84152648	0.7307	1.7202
chr14	107349540	96744905	0.9012	2.0621
chr15	102531392	98082531	0.9566	2.1317
chr16	90354753	104600224	1.1577	3.8062
chr17	81195210	95671008	1.1783	2.757
chr18	78077248	81107371	1.0388	3.8029
chr19	59128983	64336806	1.0881	2.7571
chr20	63025520	77854872	1.2353	2.5525
chr21	48129895	40495222	0.8414	2.8288
chr22	51304566	48403892	0.9435	2.3028
chrMT	16571	12417664	749.3612	594.0909
chrX	155270560	159136581	1.0249	2.2596

chrY	59373566	5315048	0.0895	3.1347

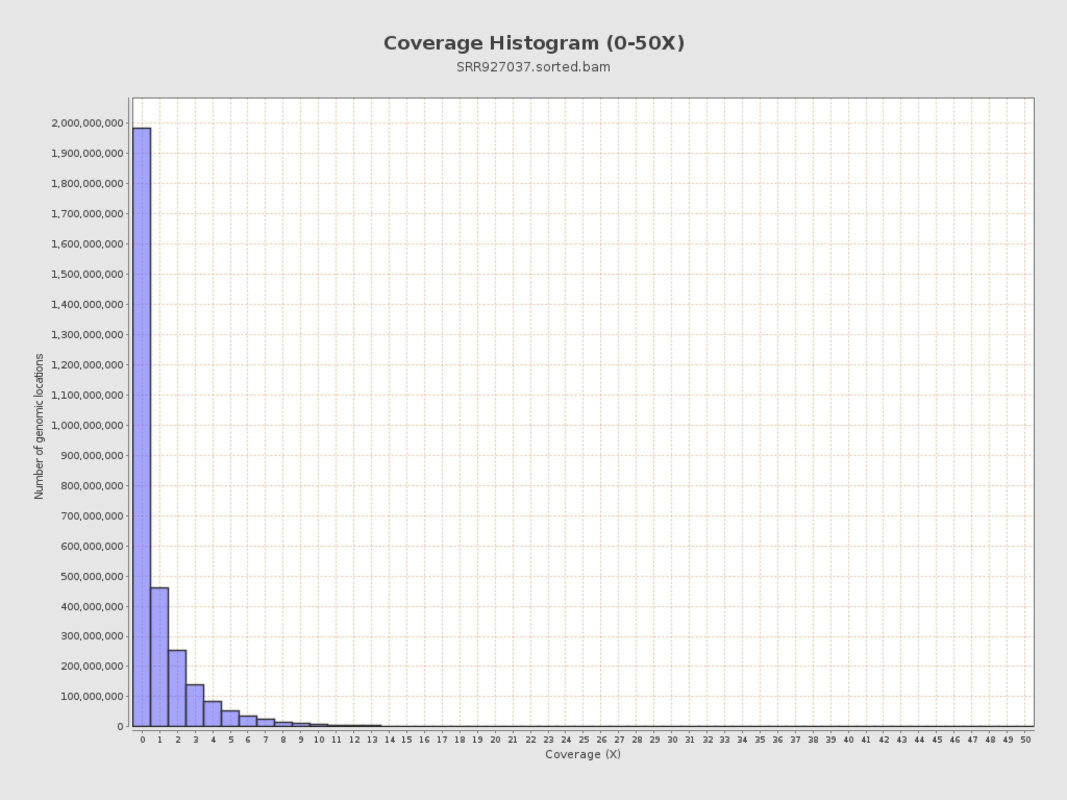
3. Results : Coverage across reference



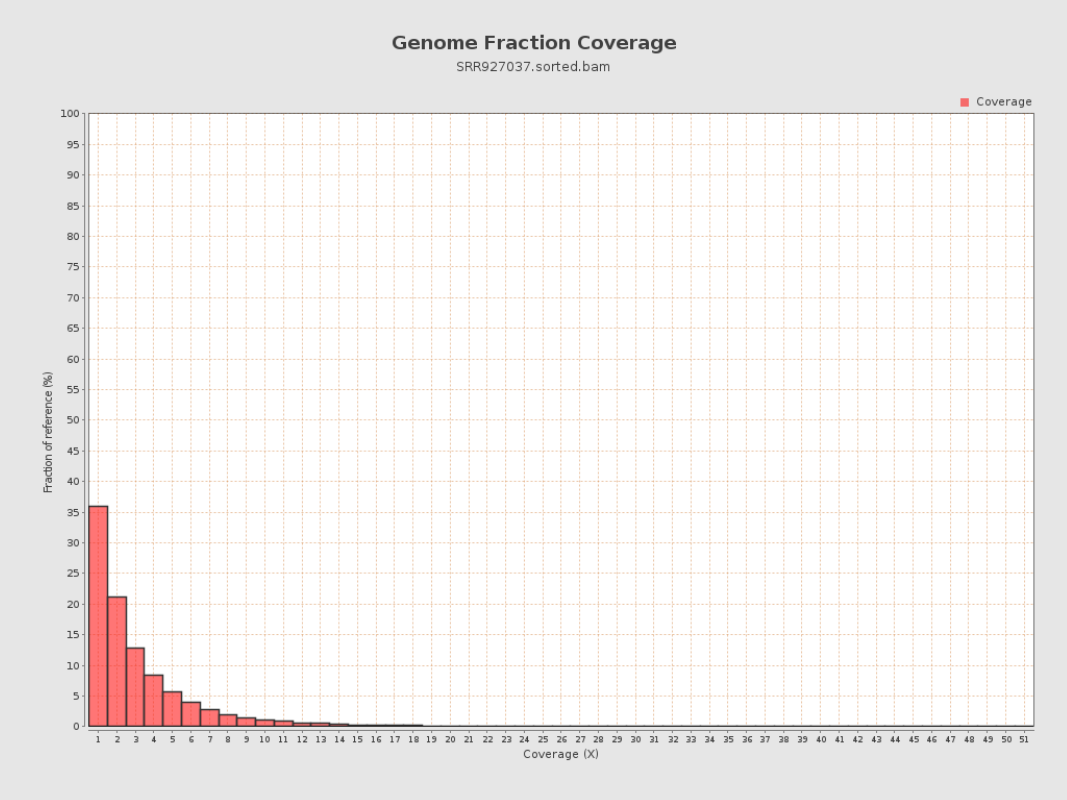
4. Results : Coverage Histogram



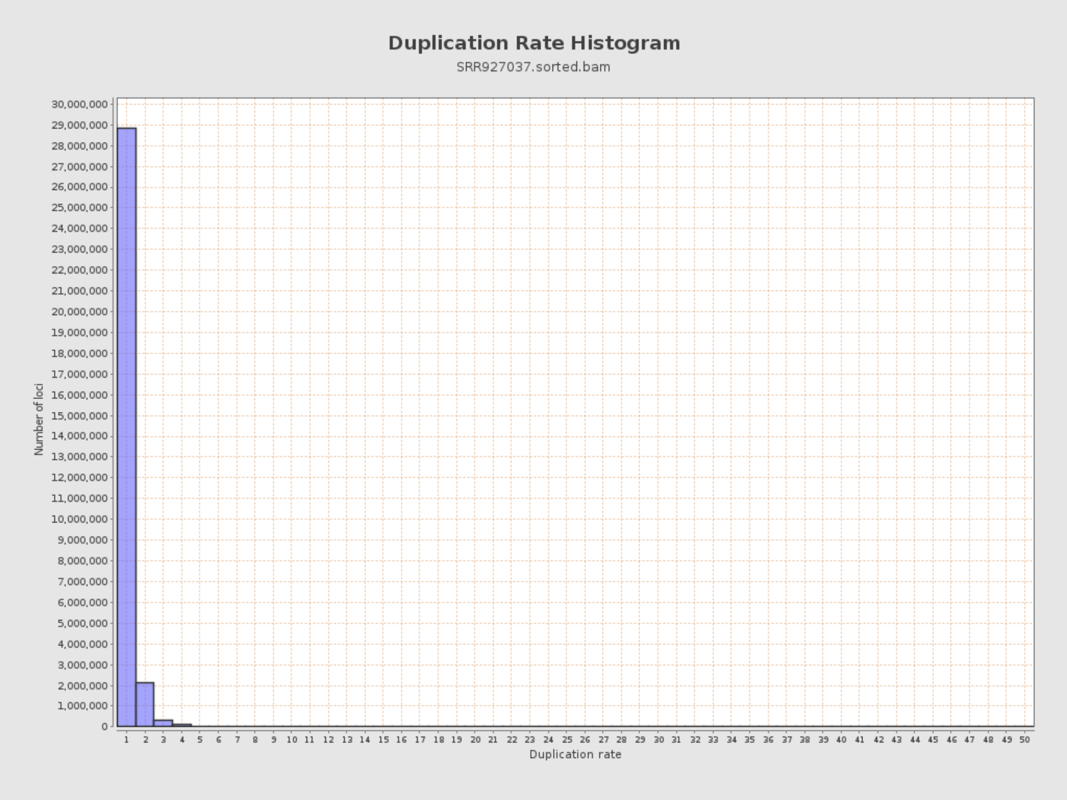
5. Results : Coverage Histogram (0-50X)



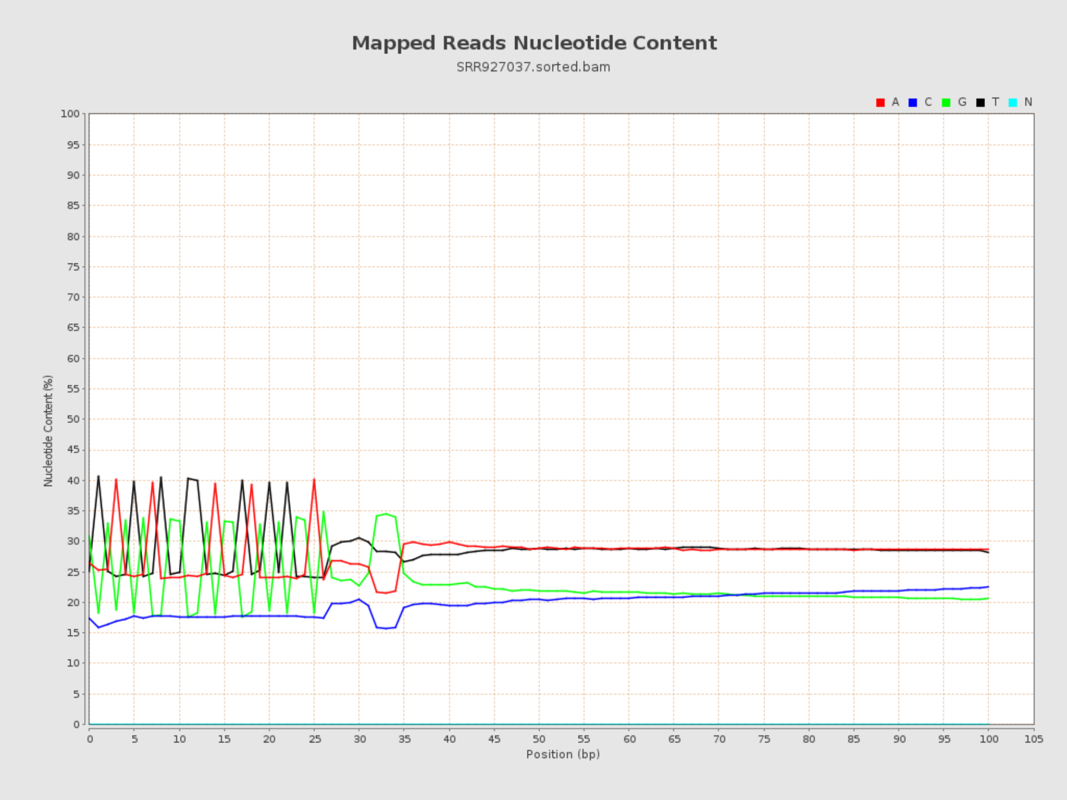
6. Results : Genome Fraction Coverage



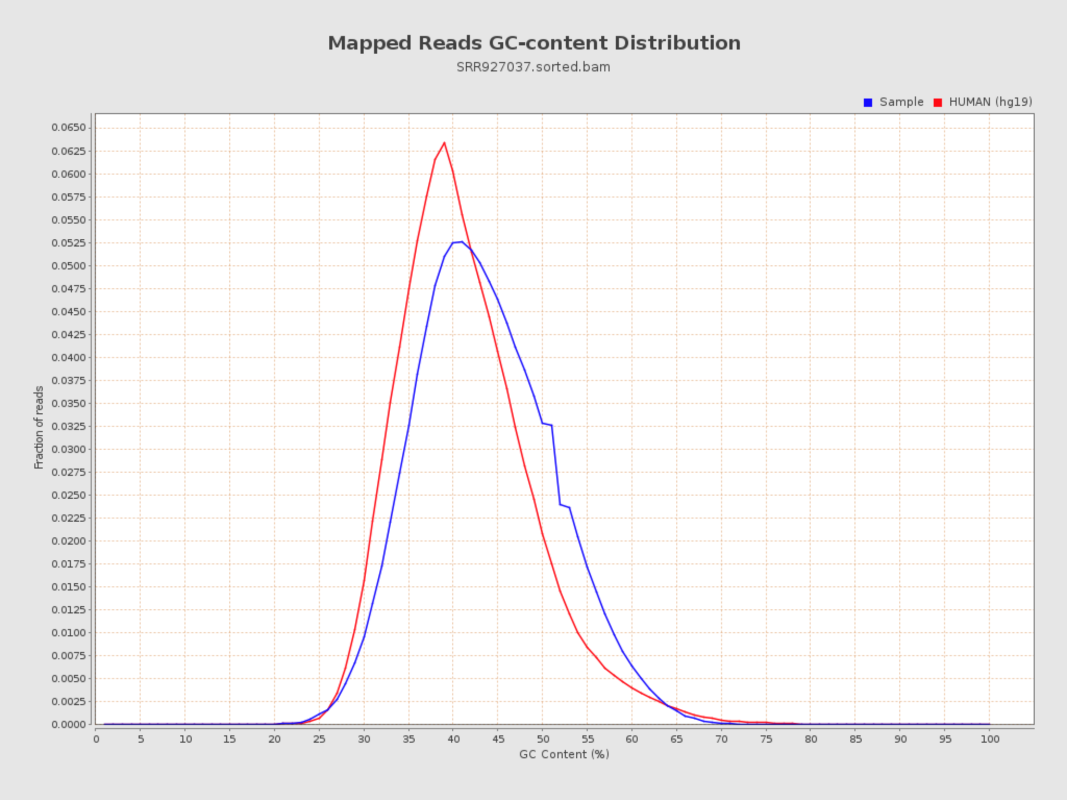
7. Results : Duplication Rate Histogram



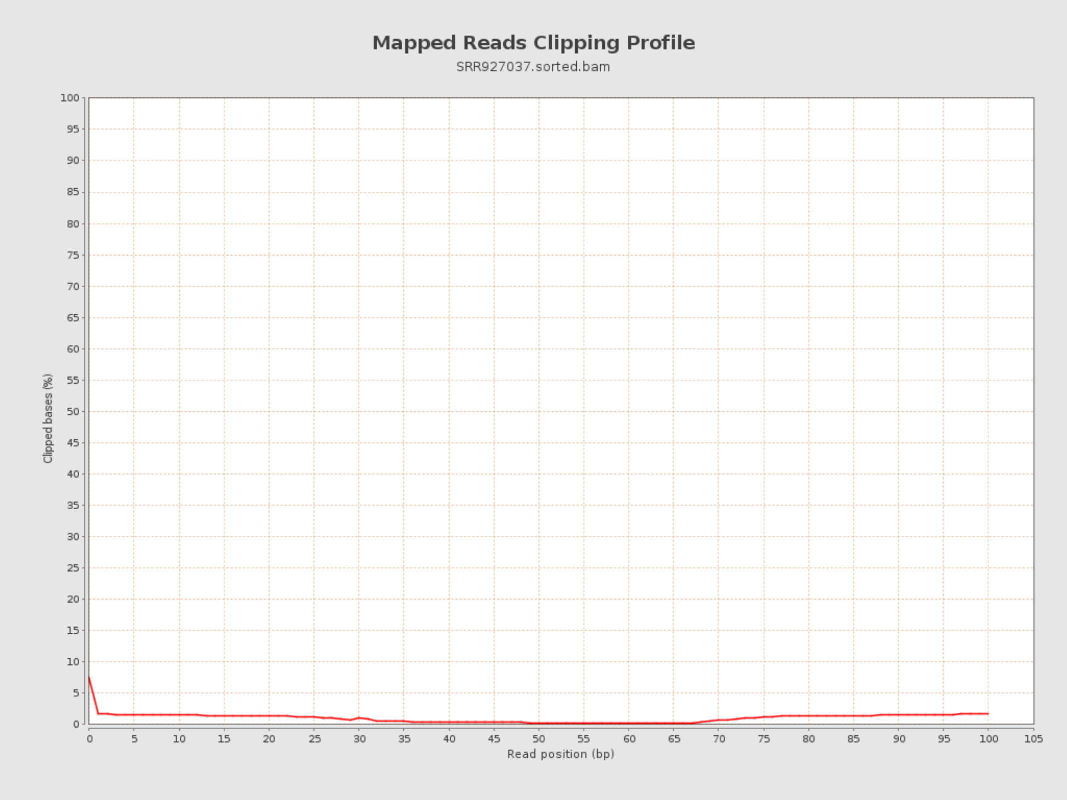
8. Results : Mapped Reads Nucleotide Content



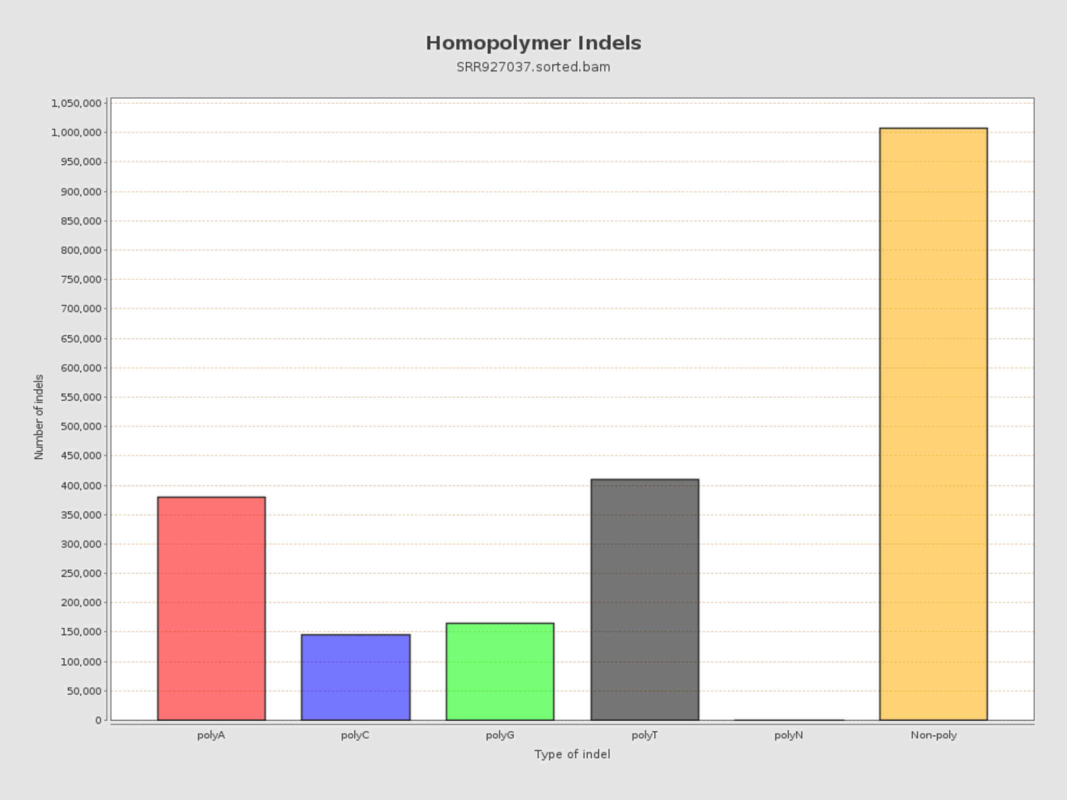
9. Results : Mapped Reads GC-content Distribution



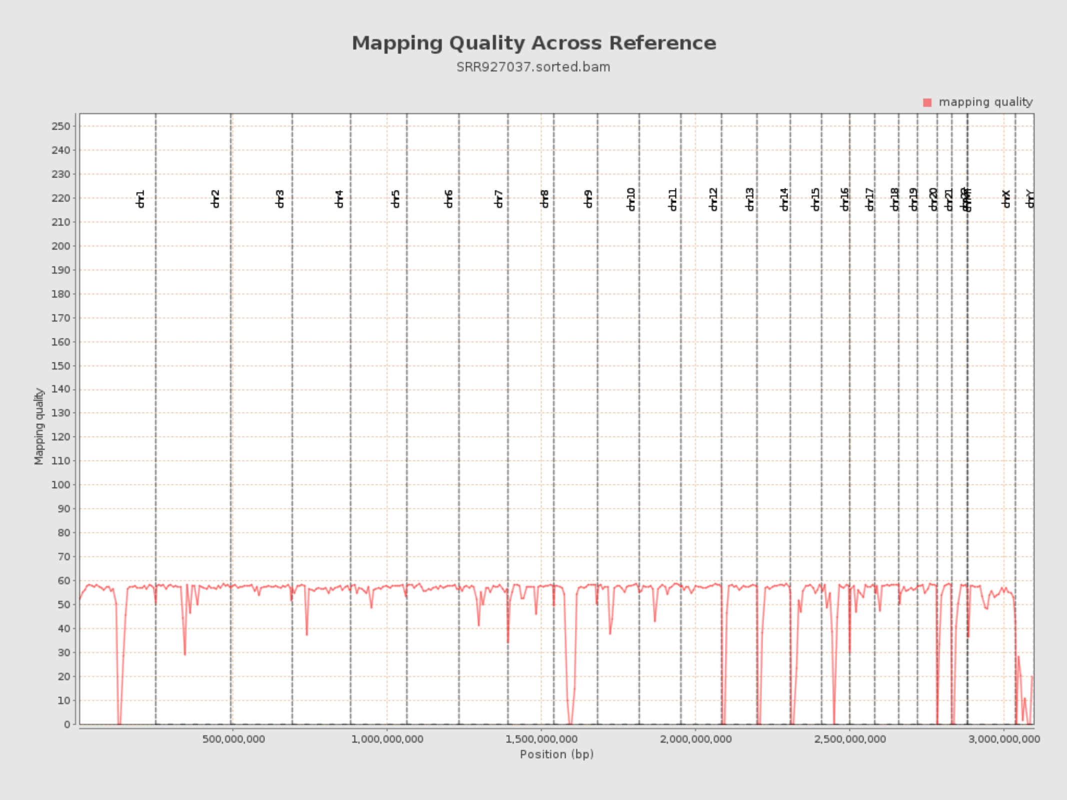
10. Results : Mapped Reads Clipping Profile



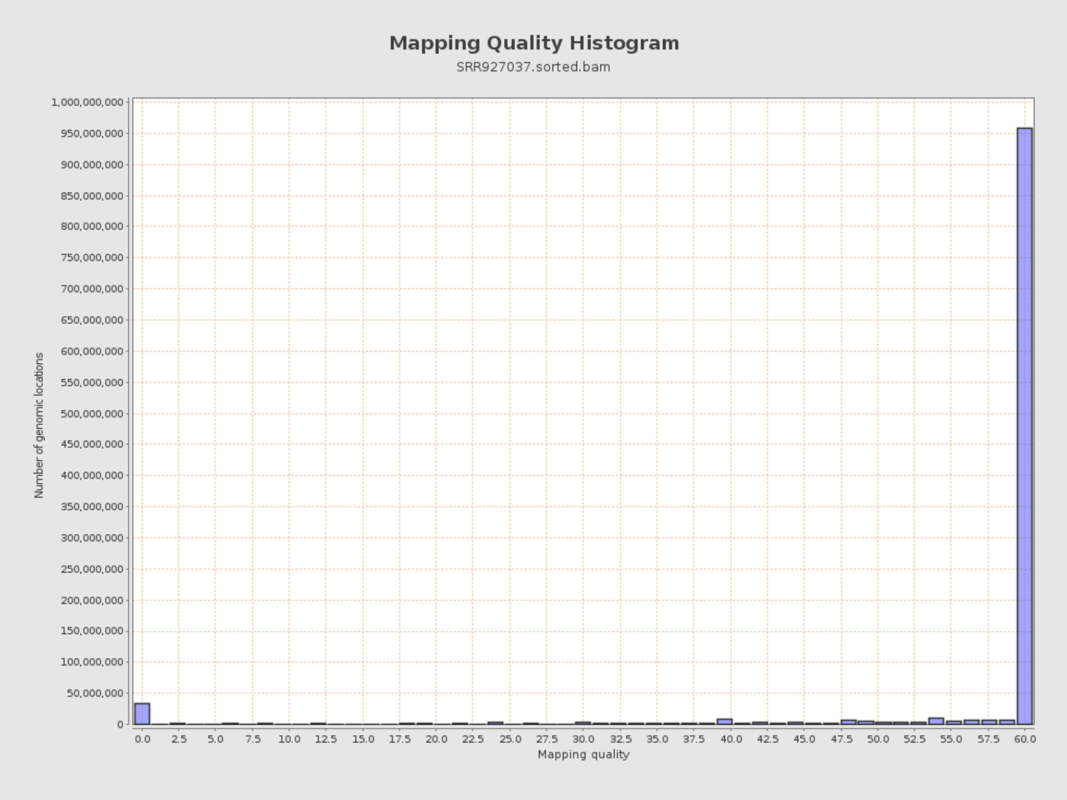
11. Results : Homopolymer Indels



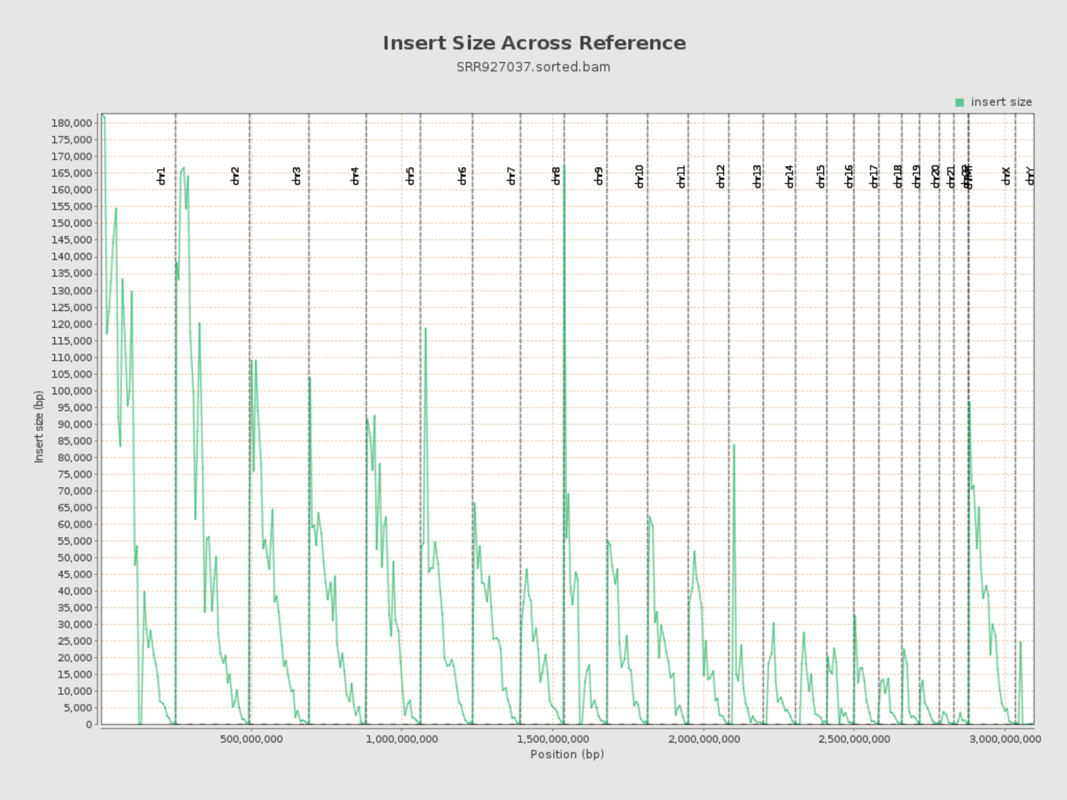
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram