Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 00:58:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927054.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_SRR927054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927054_1.fastq.gz SRR927054_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 00:58:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,347,374
Mapped reads	21,735,158 / 97.26%
Unmapped reads	612,216 / 2.74%
Mapped paired reads	21,735,158 / 97.26%
Mapped reads, first in pair	10,896,152 / 48.76%
Mapped reads, second in pair	10,839,006 / 48.5%
Mapped reads, both in pair	21,371,884 / 95.63%
Mapped reads, singletons	363,274 / 1.63%
Secondary alignments	0
Supplementary alignments	452,044 / 2.02%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	1,733,145 / 7.76%
Duplication rate	6.28%
Clipped reads	9,936,658 / 44.46%

2.2. ACGT Content

Number/percentage of A's	561,575,553 / 28.68%
Number/percentage of C's	375,031,111 / 19.15%
Number/percentage of T's	575,338,361 / 29.38%
Number/percentage of G's	445,740,613 / 22.77%
Number/percentage of N's	250,662 / 0.01%

GC Percentage	41.92%

2.3. Coverage

Mean	0.6329
Standard Deviation	2.5239

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	209,075.43
Standard Deviation	4,446,390.53
P25/Median/P75	141 / 184 / 249

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	20,480,536
Insertions	319,023
Mapped reads with at least one insertion	1.44%
Deletions	963,476
Mapped reads with at least one deletion	4.32%
Homopolymer indels	51.66%

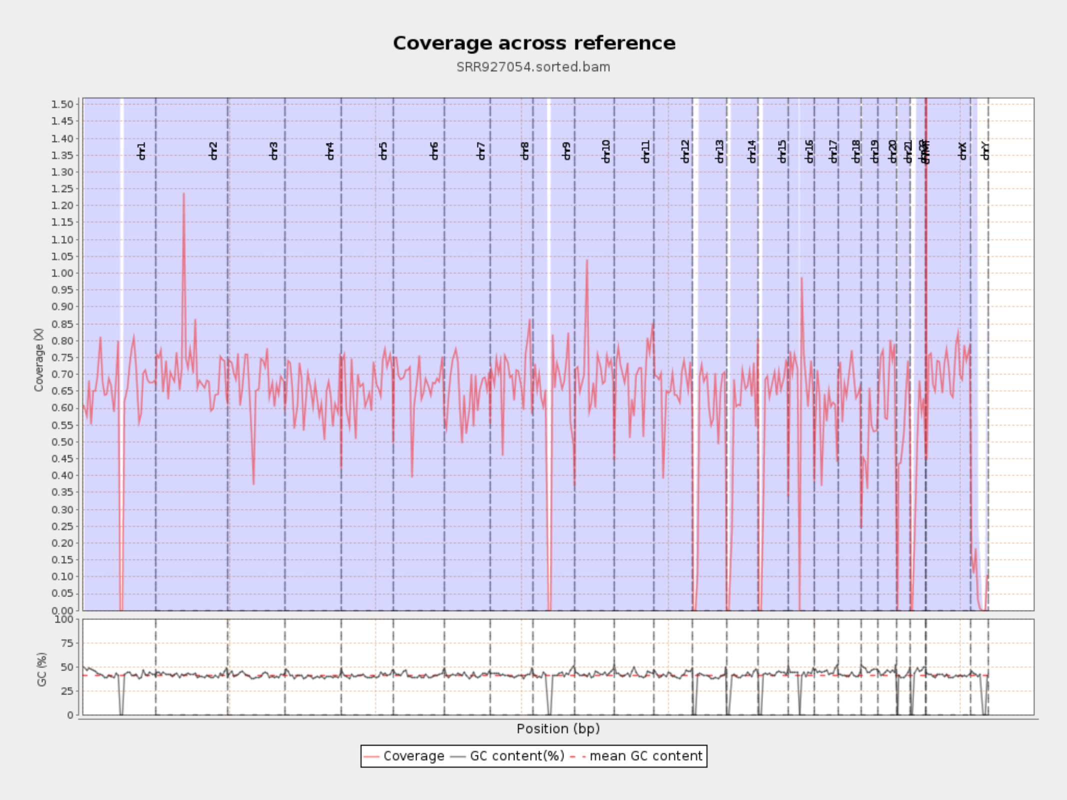
2.7. Chromosome stats

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

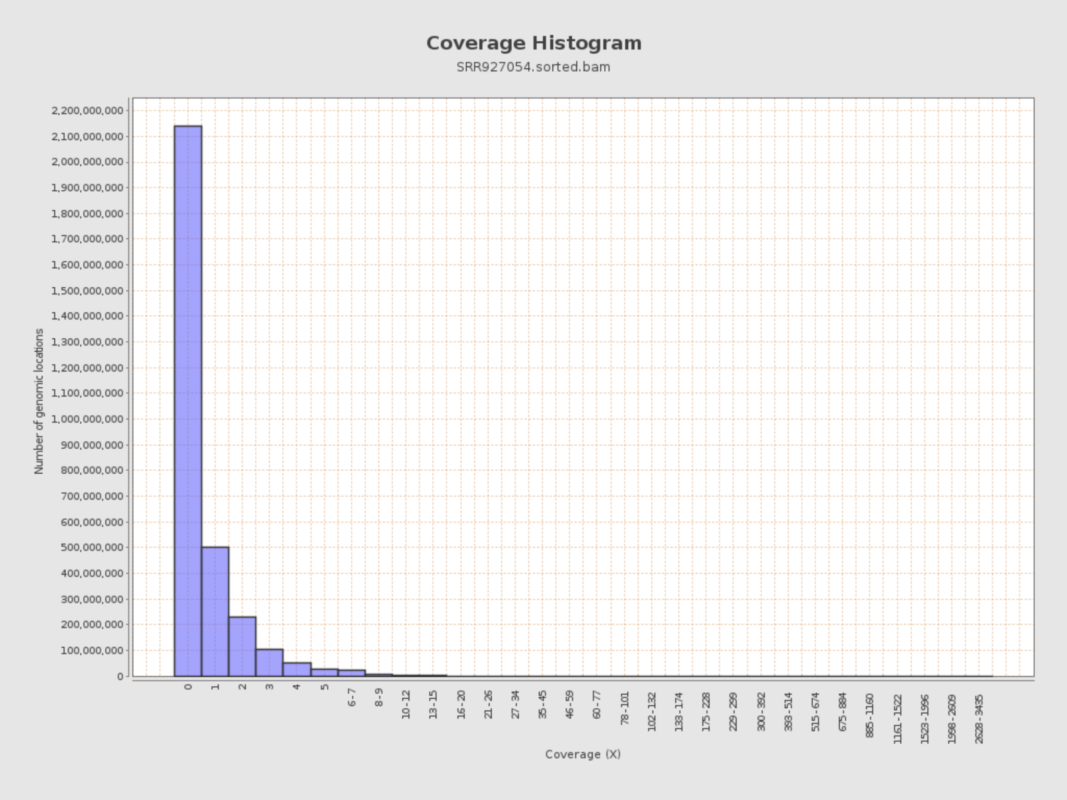
		bases	coverage	deviation
chr1	249250621	157567590	0.6322	3.679
chr2	243199373	174384762	0.717	4.1303
chr3	198022430	133139060	0.6723	1.3494
chr4	191154276	121597449	0.6361	2.0249
chr5	180915260	120740390	0.6674	1.3362
chr6	171115067	115715596	0.6762	1.4053
chr7	159138663	102429288	0.6436	1.9853
chr8	146364022	101964782	0.6967	1.6695
chr9	141213431	84933794	0.6015	3.2455
chr10	135534747	95770817	0.7066	4.4888
chr11	135006516	93386987	0.6917	2.4683
chr12	133851895	88385272	0.6603	1.3438
chr13	115169878	61825749	0.5368	1.2015
chr14	107349540	58118696	0.5414	1.2902
chr15	102531392	57210547	0.558	1.2737
chr16	90354753	58757471	0.6503	3.5881
chr17	81195210	47702817	0.5875	2.0298
chr18	78077248	52412368	0.6713	3.3283
chr19	59128983	29267774	0.495	2.0851
chr20	63025520	43976896	0.6978	1.4954
chr21	48129895	24204719	0.5029	1.6708
chr22	51304566	20956115	0.4085	1.1263
chrMT	16571	81562	4.922	2.6394
chrX	155270560	110603623	0.7123	1.5894

chrY	59373566	4204410	0.0708	1.7362

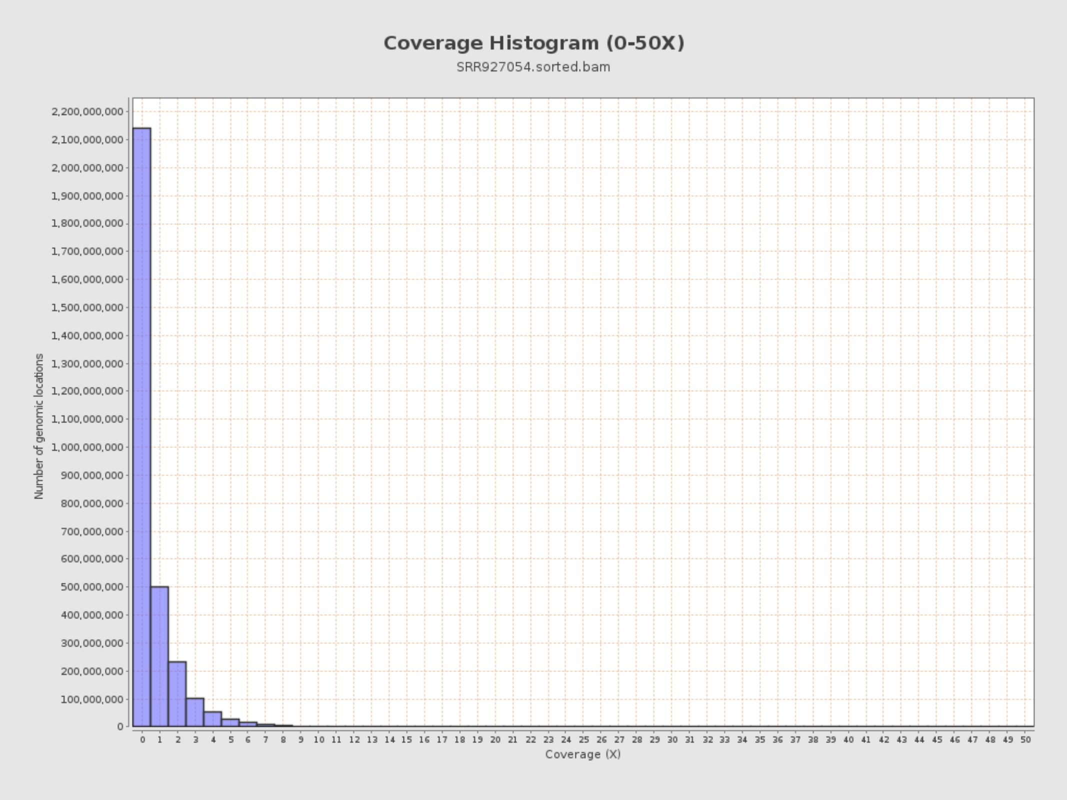
3. Results : Coverage across reference



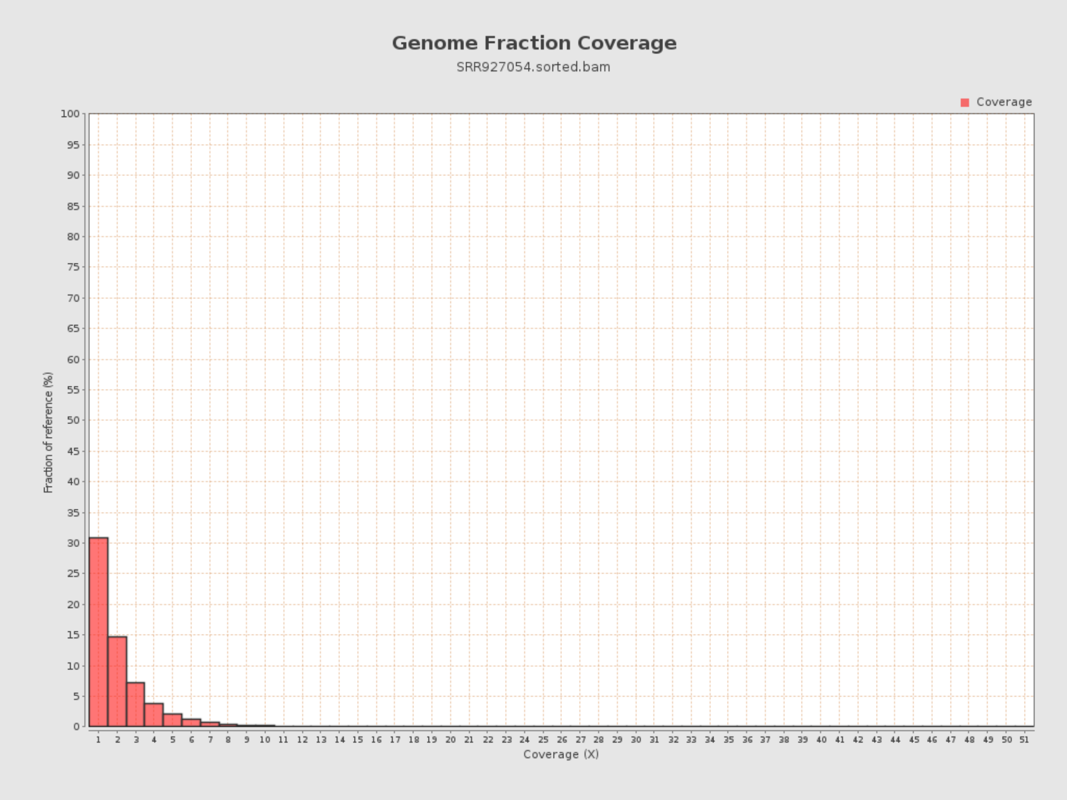
4. Results : Coverage Histogram



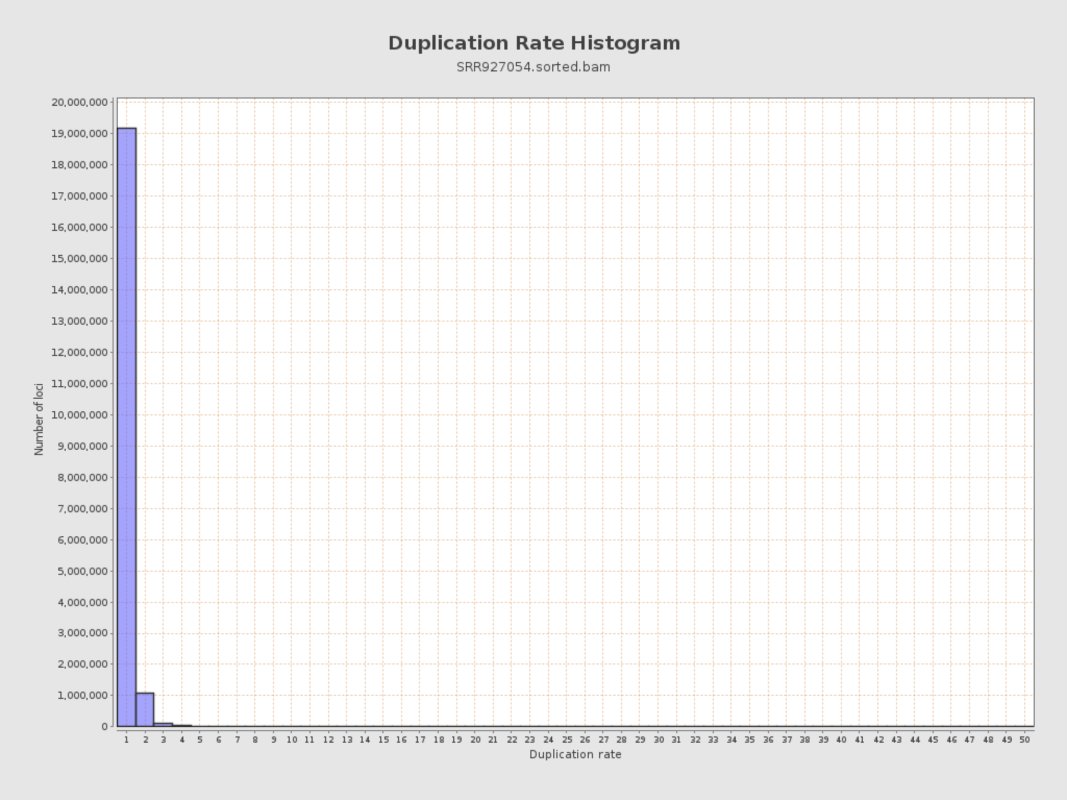
5. Results : Coverage Histogram (0-50X)



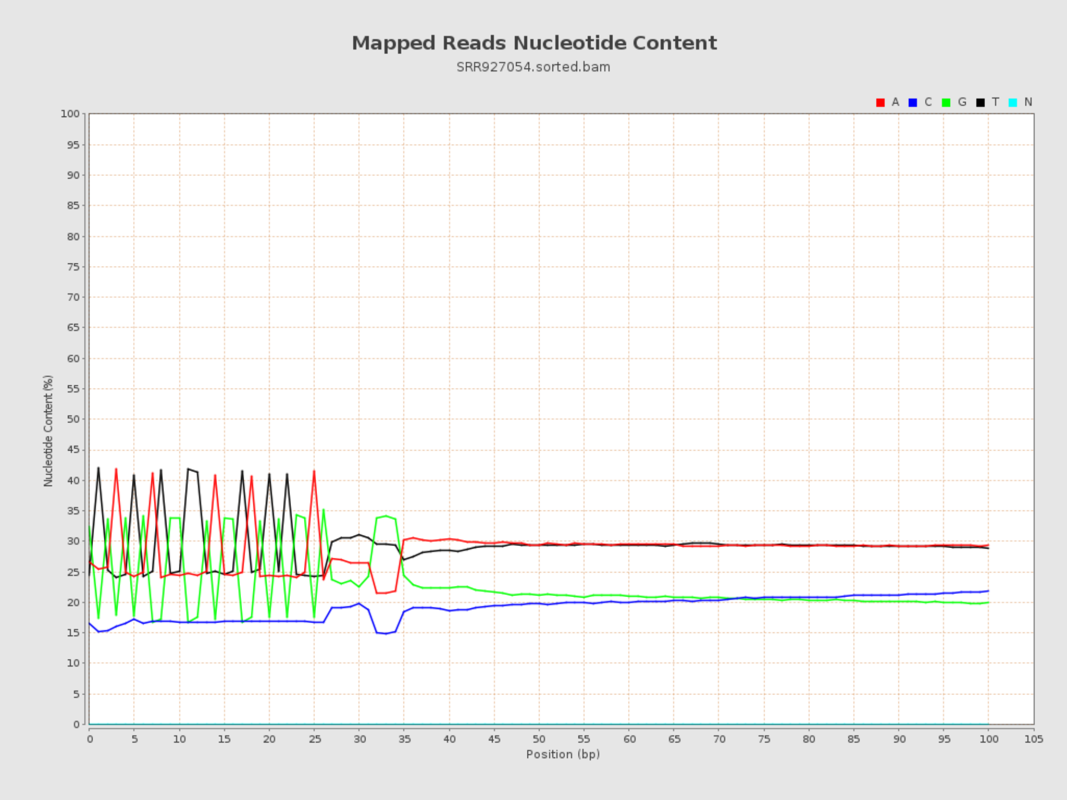
6. Results : Genome Fraction Coverage



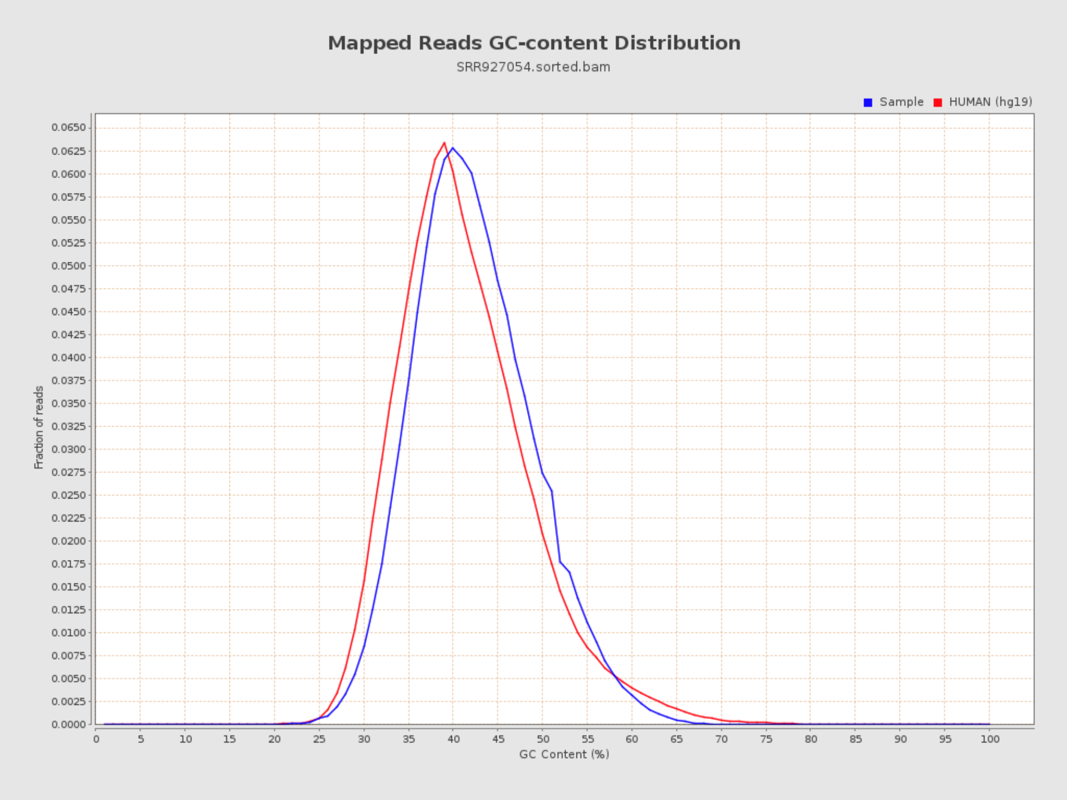
7. Results : Duplication Rate Histogram



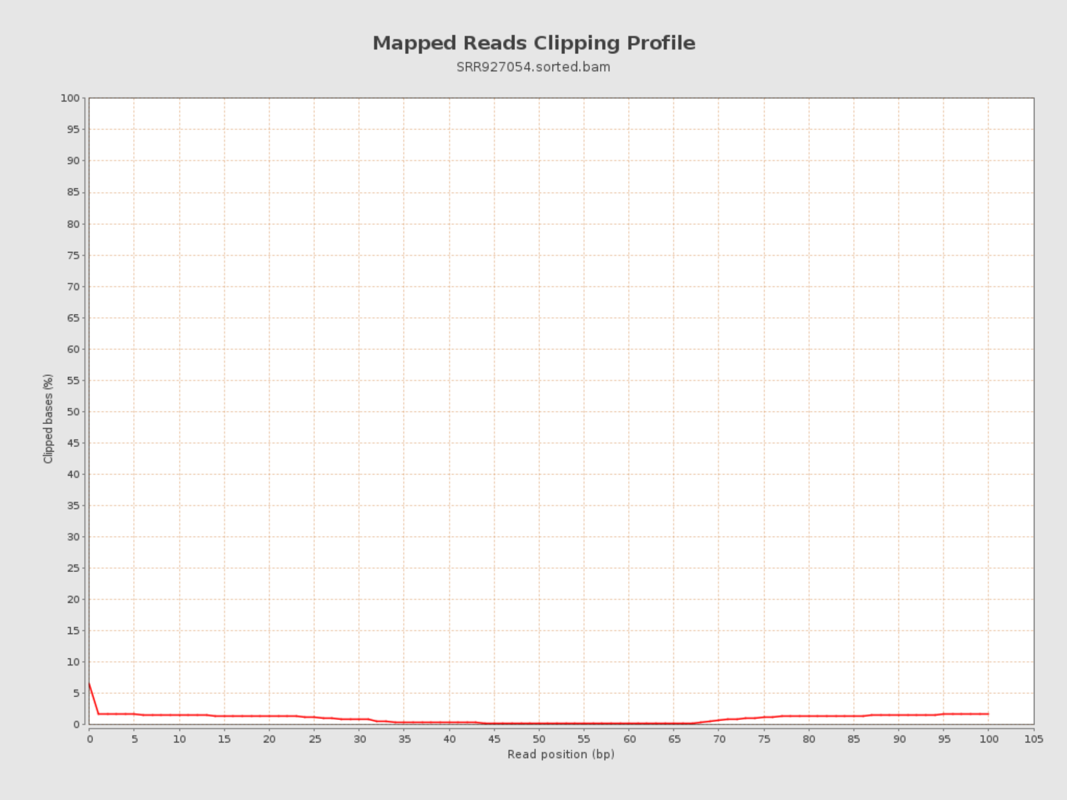
8. Results : Mapped Reads Nucleotide Content



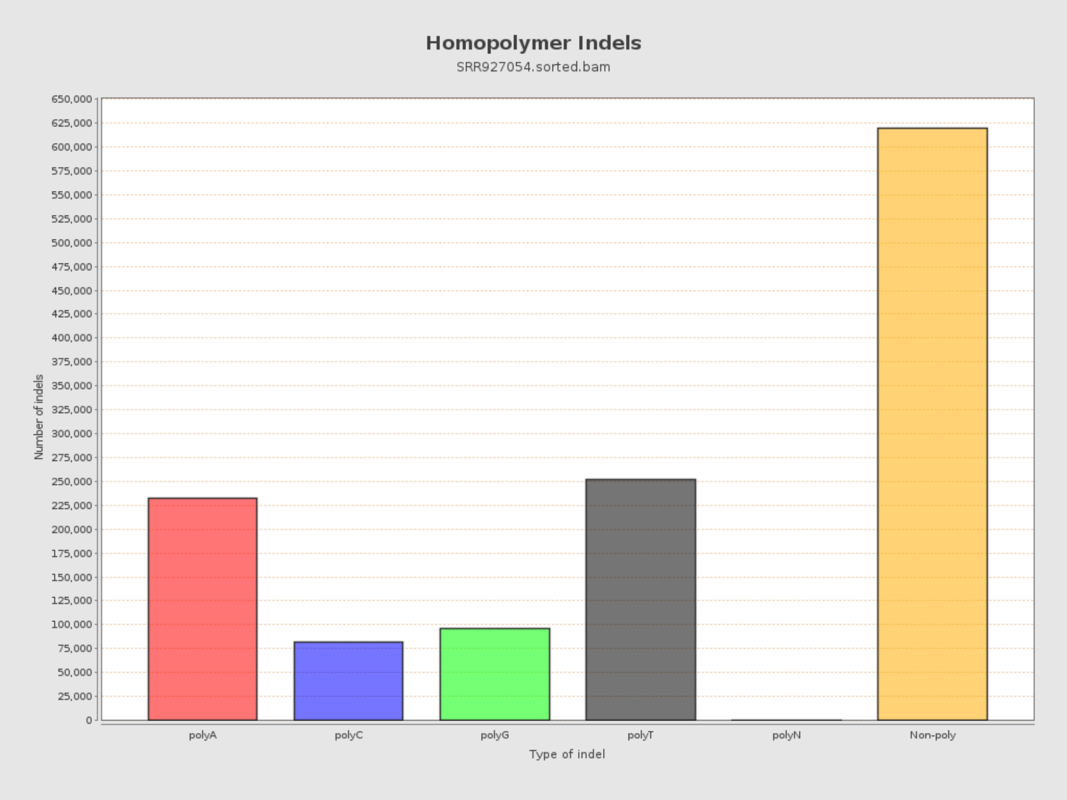
9. Results : Mapped Reads GC-content Distribution



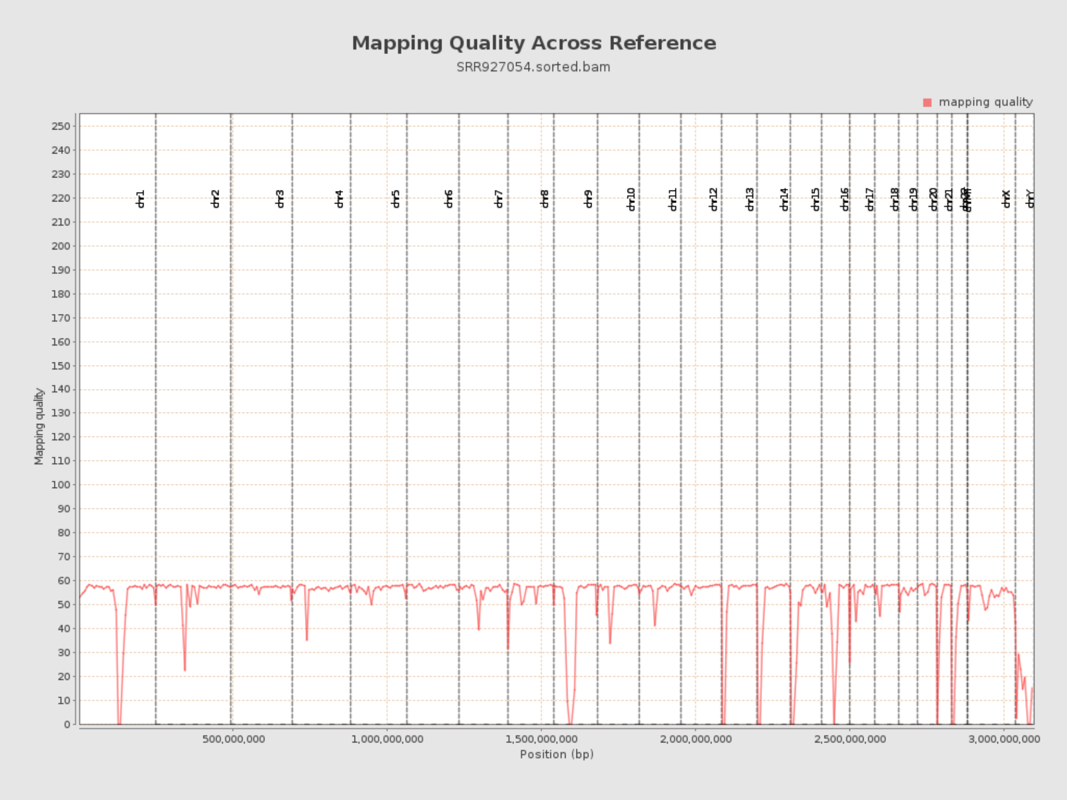
10. Results : Mapped Reads Clipping Profile



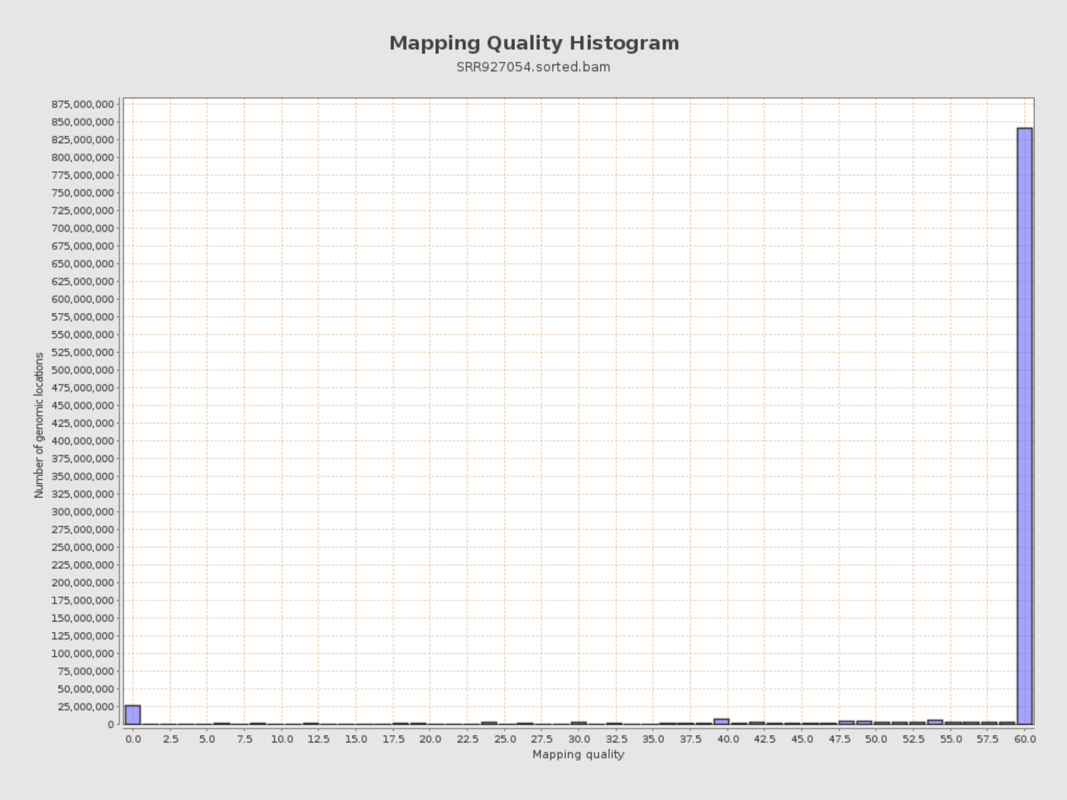
11. Results : Homopolymer Indels



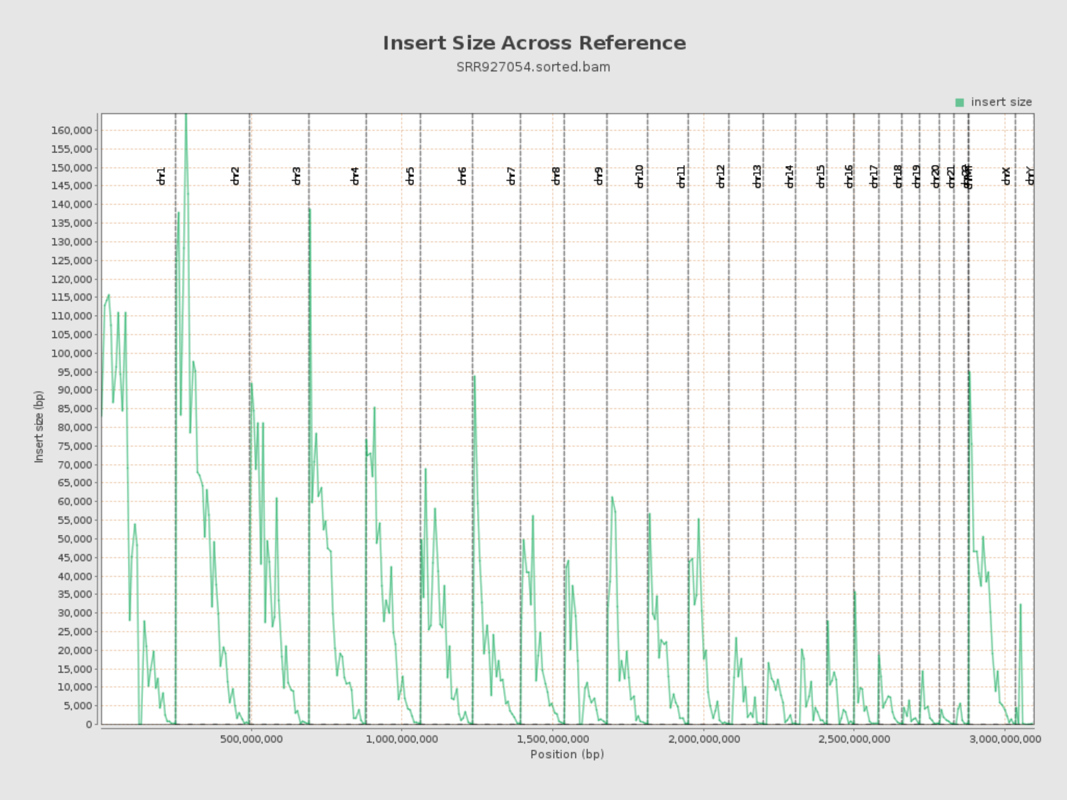
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram