Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 00:29:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927053.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_SRR927053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927053_1.fastq.gz SRR927053_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 00:29:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,665,140
Mapped reads	31,043,332 / 98.04%
Unmapped reads	621,808 / 1.96%
Mapped paired reads	31,043,332 / 98.04%
Mapped reads, first in pair	15,587,410 / 49.23%
Mapped reads, second in pair	15,455,922 / 48.81%
Mapped reads, both in pair	30,727,166 / 97.04%
Mapped reads, singletons	316,166 / 1%
Secondary alignments	0
Supplementary alignments	376,182 / 1.19%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	2,358,722 / 7.45%
Duplication rate	6.02%
Clipped reads	8,586,007 / 27.12%

2.2. ACGT Content

Number/percentage of A's	821,589,313 / 28.14%
Number/percentage of C's	598,294,022 / 20.49%
Number/percentage of T's	833,152,859 / 28.54%
Number/percentage of G's	666,266,123 / 22.82%
Number/percentage of N's	441,999 / 0.02%

GC Percentage	43.31%

2.3. Coverage

Mean	0.9438
Standard Deviation	3.4709

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	122,387.76
Standard Deviation	3,426,879.2
P25/Median/P75	146 / 188 / 251

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	31,070,068
Insertions	452,543
Mapped reads with at least one insertion	1.43%
Deletions	1,489,029
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.6%

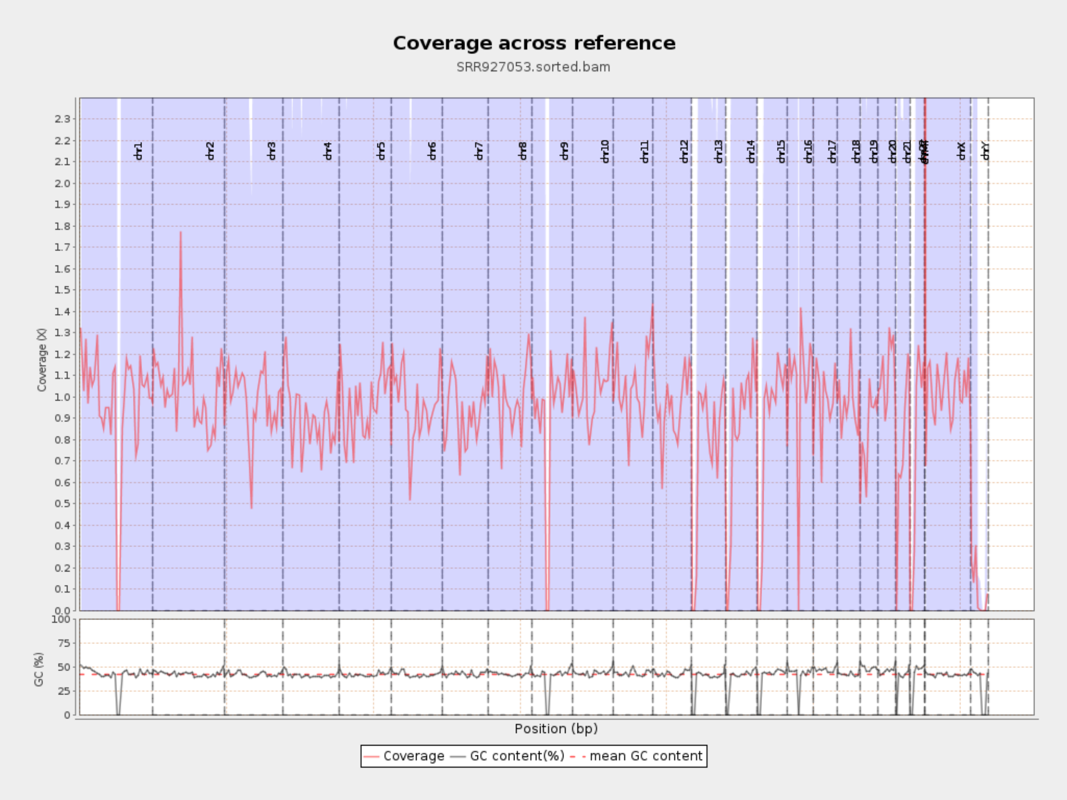
2.7. Chromosome stats

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

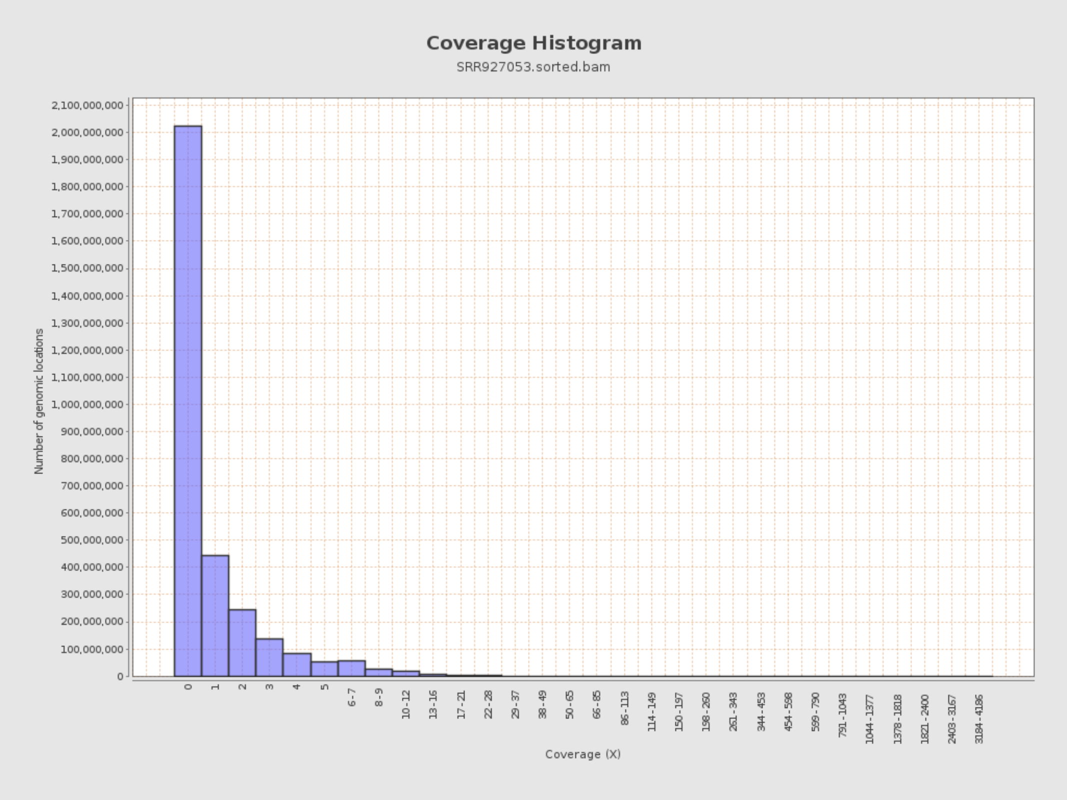
		bases	coverage	deviation
chr1	249250621	241829712	0.9702	4.894
chr2	243199373	252933728	1.04	5.5787
chr3	198022430	195543794	0.9875	1.9595
chr4	191154276	172331531	0.9015	2.7982
chr5	180915260	175696749	0.9712	1.9346
chr6	171115067	165630078	0.9679	1.9642
chr7	159138663	148126378	0.9308	2.6539
chr8	146364022	148894063	1.0173	2.3993
chr9	141213431	129710648	0.9185	4.5815
chr10	135534747	143127803	1.056	5.23
chr11	135006516	140985167	1.0443	3.6134
chr12	133851895	128934939	0.9633	1.9712
chr13	115169878	87366227	0.7586	1.7172
chr14	107349540	87883682	0.8187	1.887
chr15	102531392	86218071	0.8409	1.8835
chr16	90354753	94660034	1.0476	4.8902
chr17	81195210	80800850	0.9951	2.654
chr18	78077248	77349883	0.9907	4.7849
chr19	59128983	50050130	0.8465	3.1098
chr20	63025520	70381733	1.1167	2.3629
chr21	48129895	37365215	0.7763	2.8503
chr22	51304566	38947455	0.7591	1.9562
chrMT	16571	2471041	149.1184	108.1258
chrX	155270560	159332036	1.0262	2.3125

chrY	59373566	5274465	0.0888	3.3686

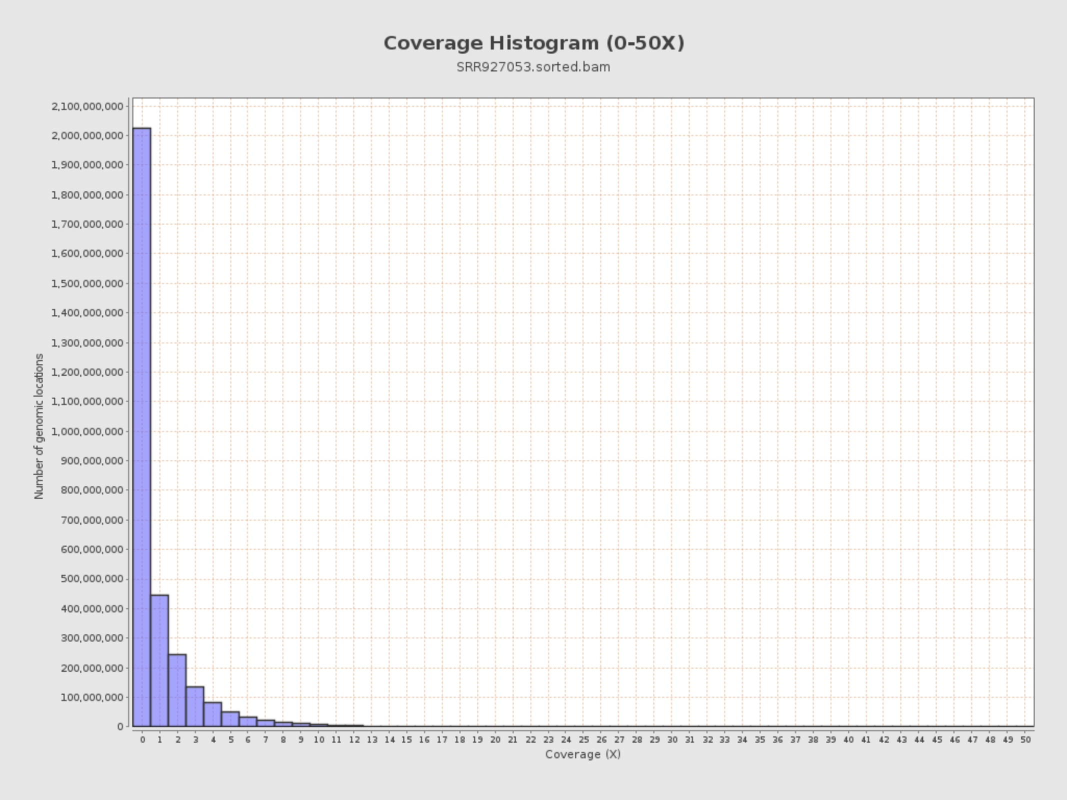
3. Results : Coverage across reference



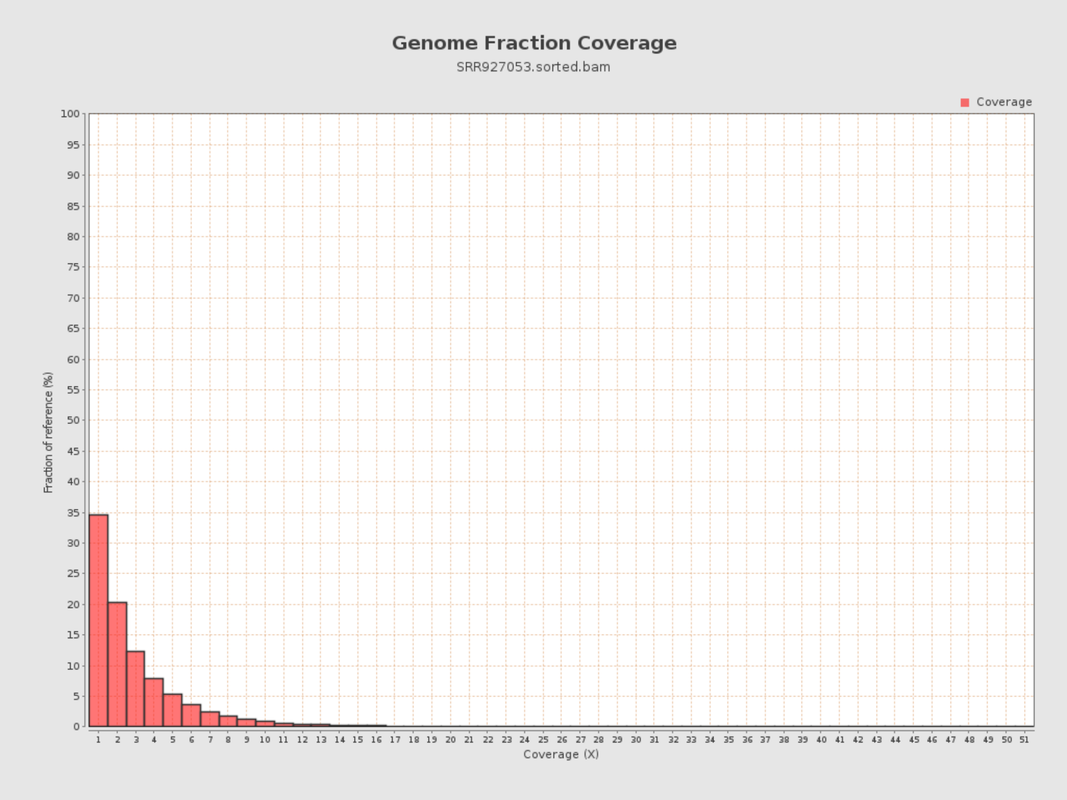
4. Results : Coverage Histogram



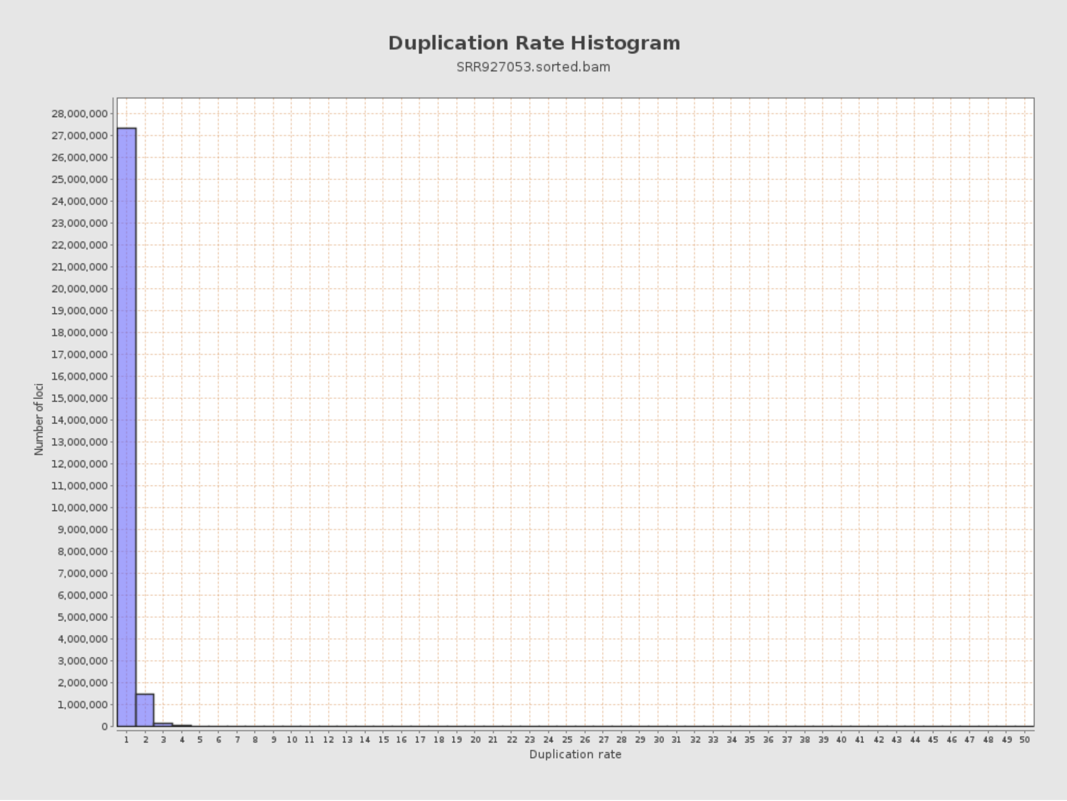
5. Results : Coverage Histogram (0-50X)



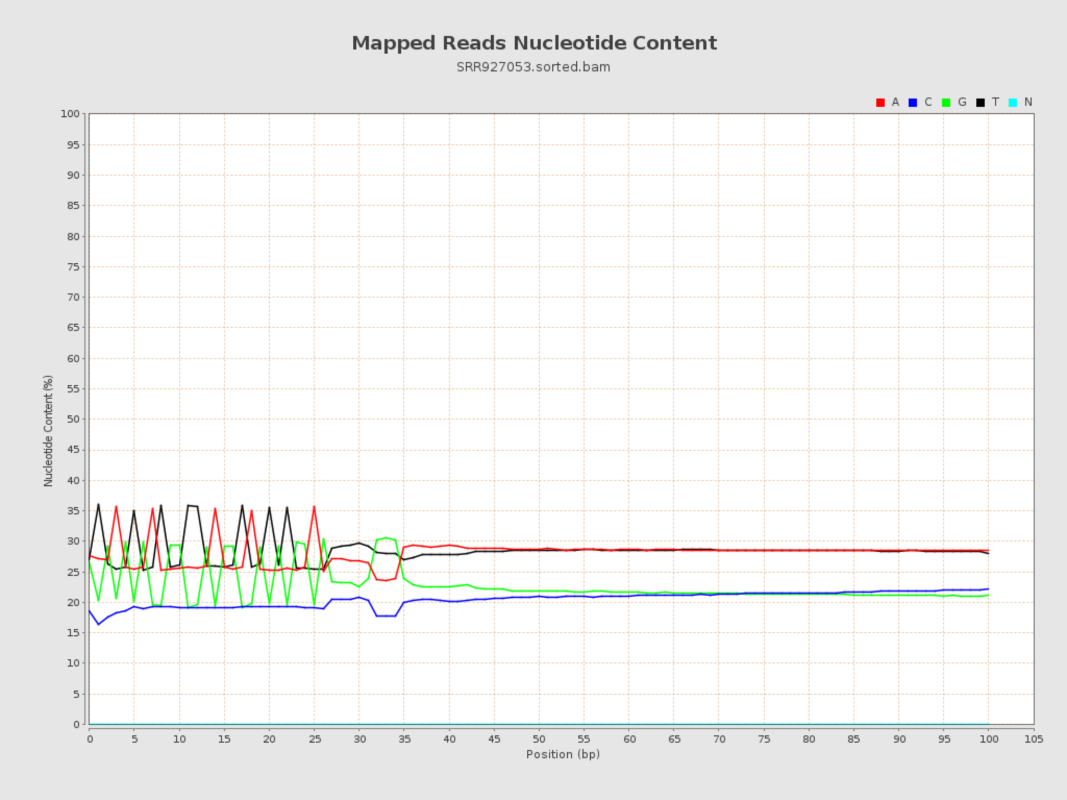
6. Results : Genome Fraction Coverage



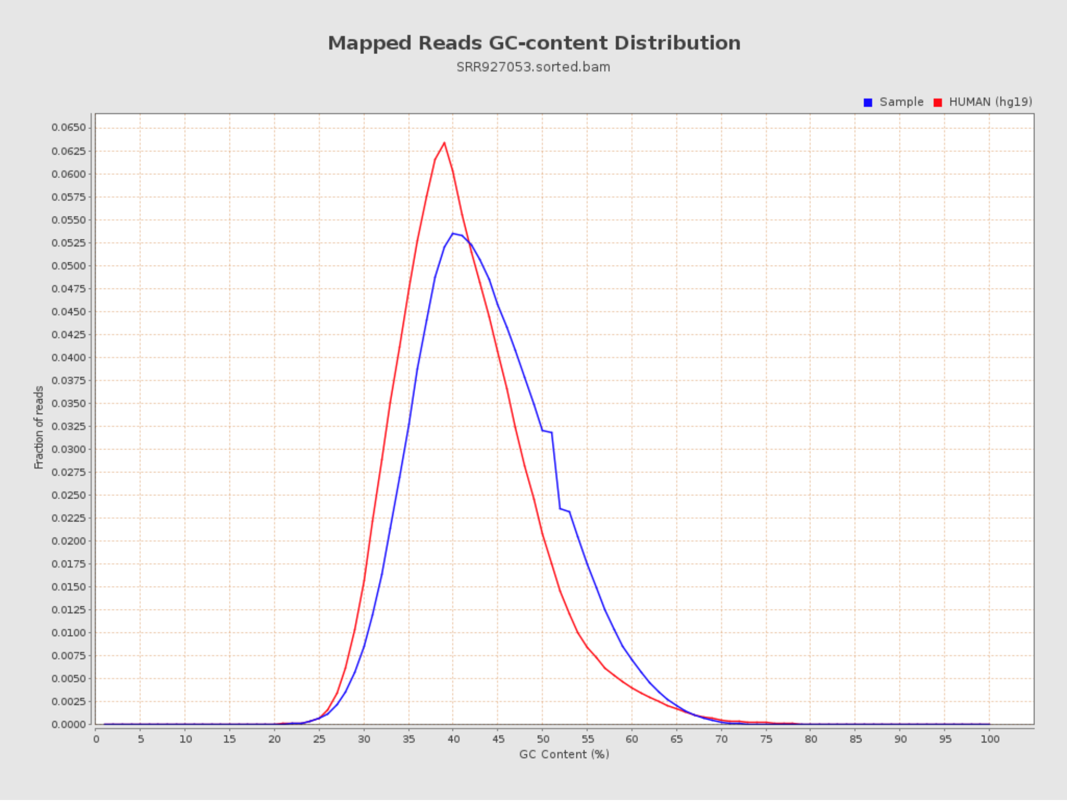
7. Results : Duplication Rate Histogram



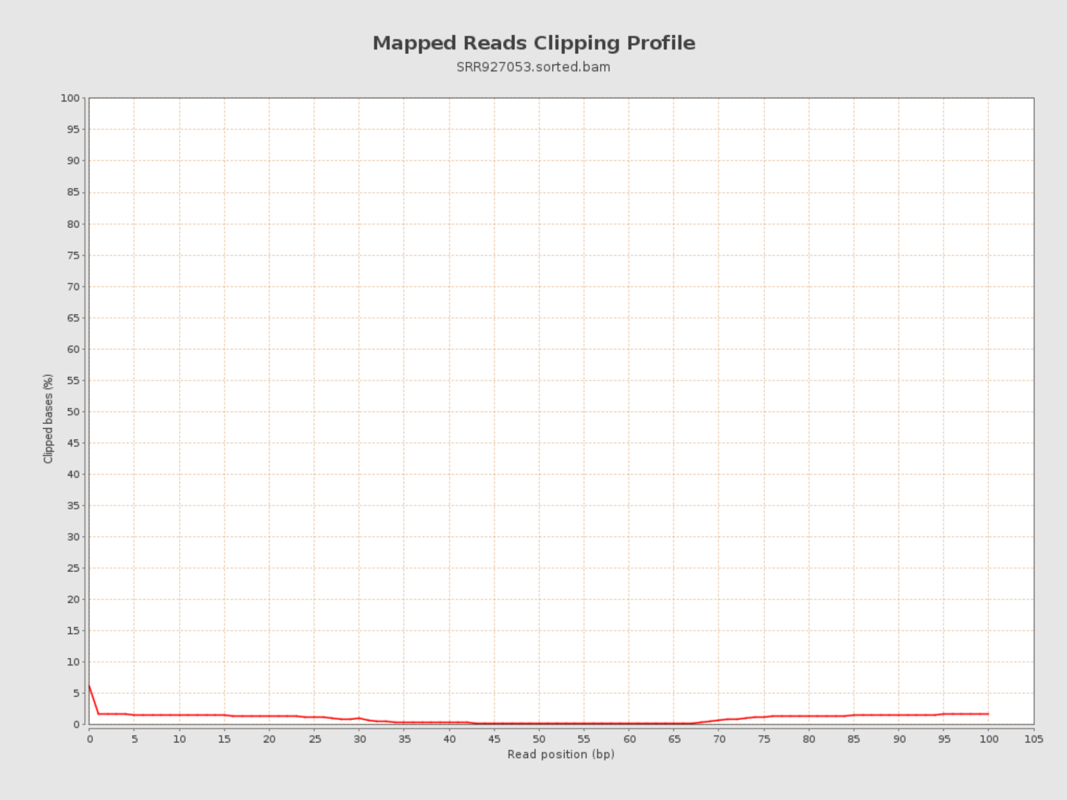
8. Results : Mapped Reads Nucleotide Content



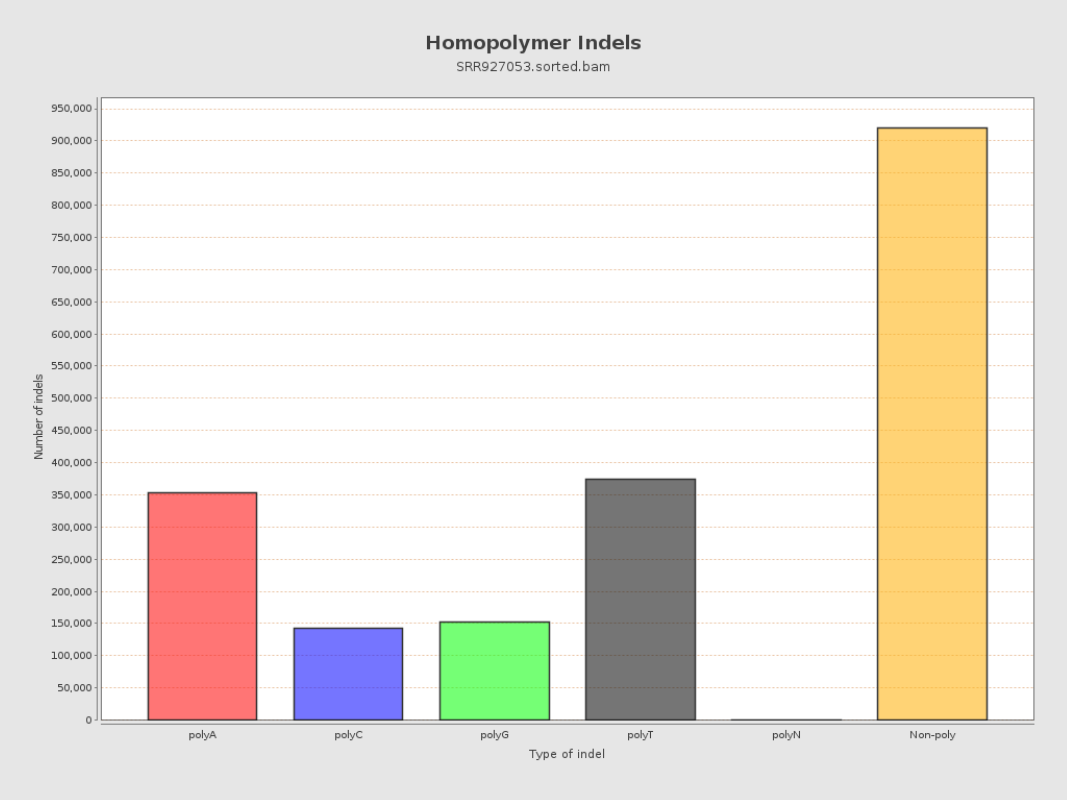
9. Results : Mapped Reads GC-content Distribution



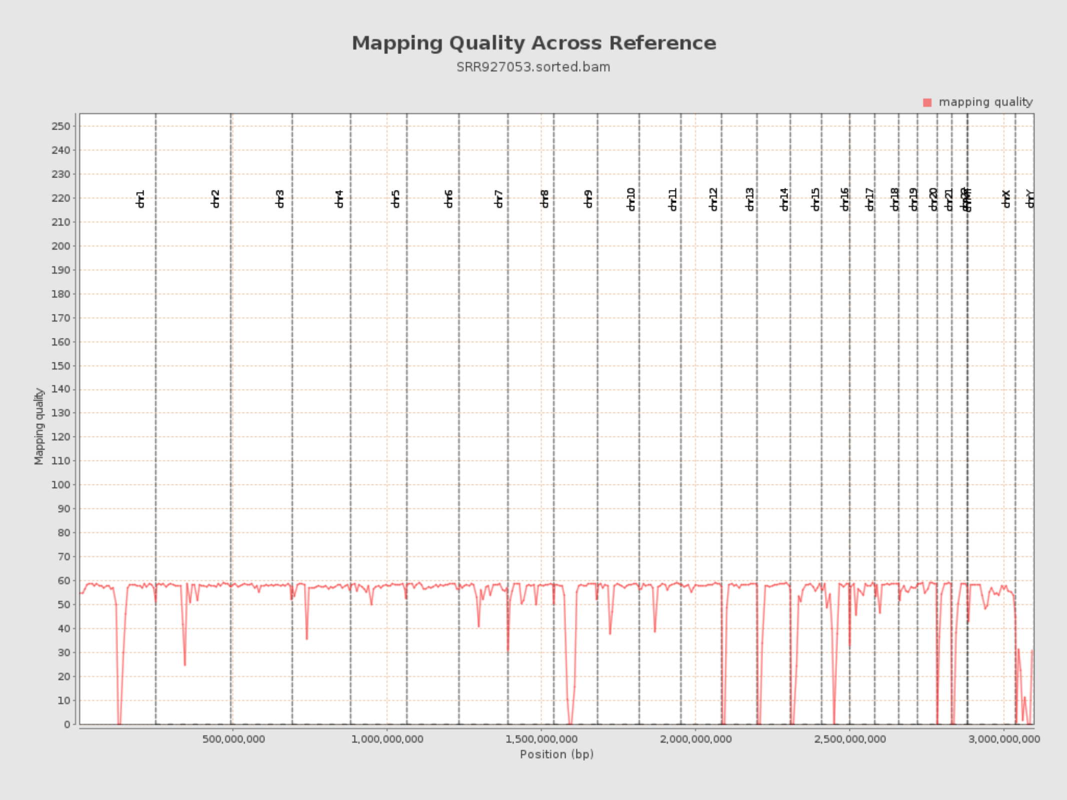
10. Results : Mapped Reads Clipping Profile



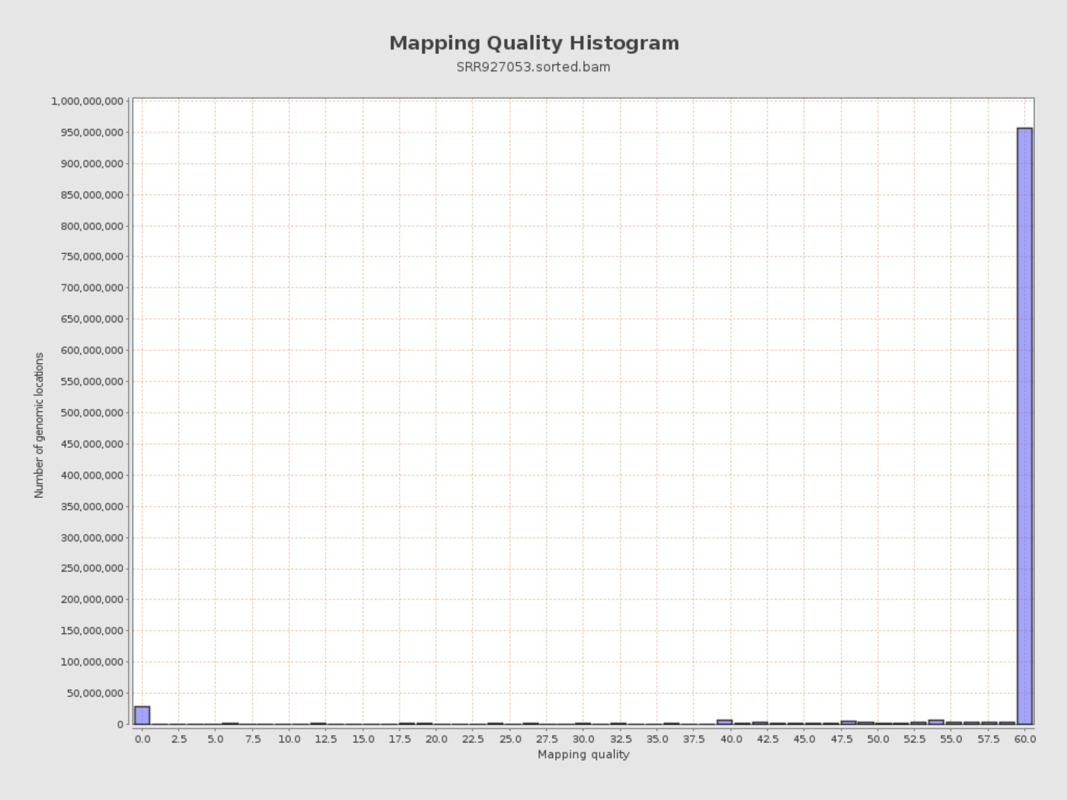
11. Results : Homopolymer Indels



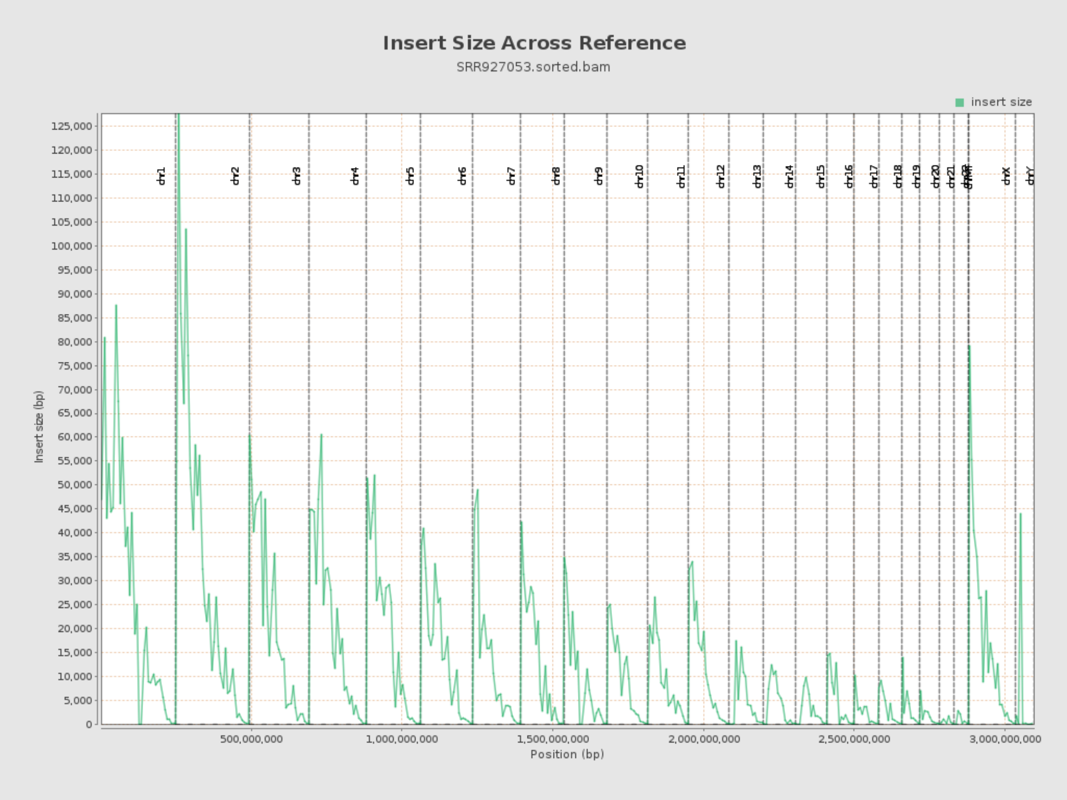
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram