Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 18:08:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927041.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_SRR927041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927041_1.fastq.gz SRR927041_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 18:08:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,413,286
Mapped reads	30,595,649 / 97.4%
Unmapped reads	817,637 / 2.6%
Mapped paired reads	30,595,649 / 97.4%
Mapped reads, first in pair	15,361,988 / 48.9%
Mapped reads, second in pair	15,233,661 / 48.49%
Mapped reads, both in pair	30,109,288 / 95.85%
Mapped reads, singletons	486,361 / 1.55%
Secondary alignments	0
Supplementary alignments	720,274 / 2.29%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	3,185,264 / 10.14%
Duplication rate	7.9%
Clipped reads	12,924,838 / 41.14%

2.2. ACGT Content

Number/percentage of A's	783,052,952 / 28.22%
Number/percentage of C's	546,990,421 / 19.71%
Number/percentage of T's	802,812,283 / 28.93%
Number/percentage of G's	641,511,475 / 23.12%
Number/percentage of N's	347,770 / 0.01%

GC Percentage	42.83%

2.3. Coverage

Mean	0.897
Standard Deviation	4.3066

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	235,756.49
Standard Deviation	4,818,758.41
P25/Median/P75	136 / 178 / 240

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	28,689,373
Insertions	467,624
Mapped reads with at least one insertion	1.5%
Deletions	1,435,404
Mapped reads with at least one deletion	4.57%
Homopolymer indels	51.96%

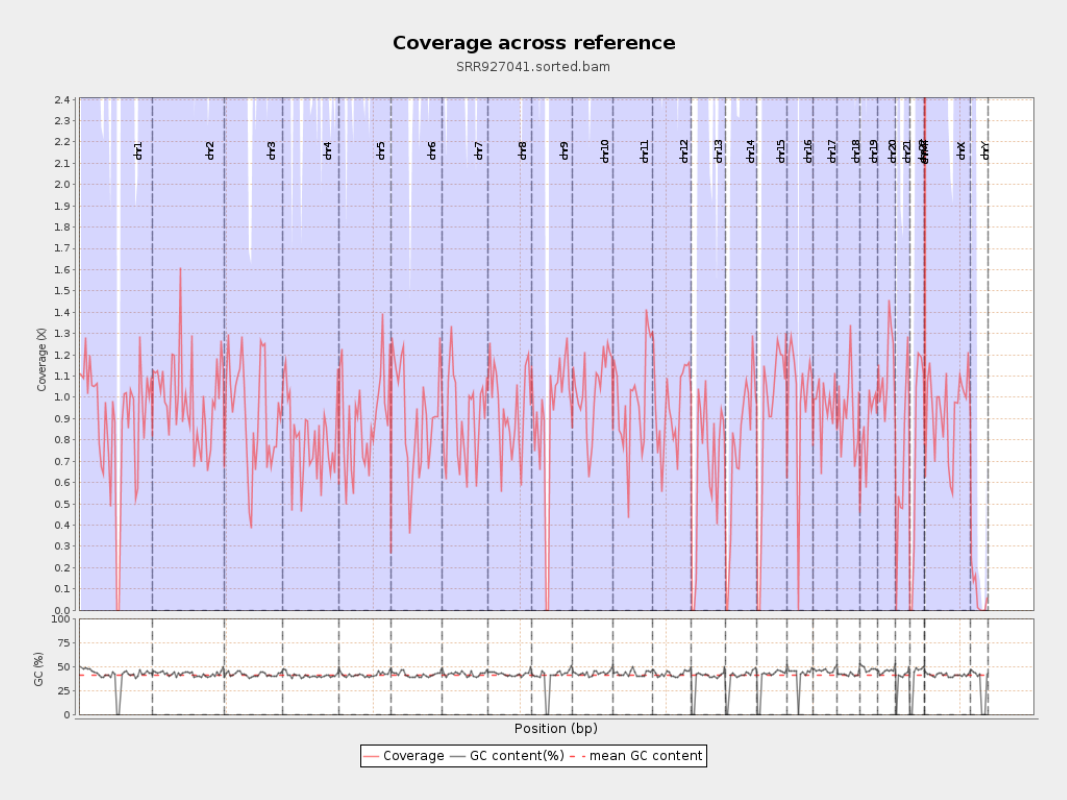
2.7. Chromosome stats

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

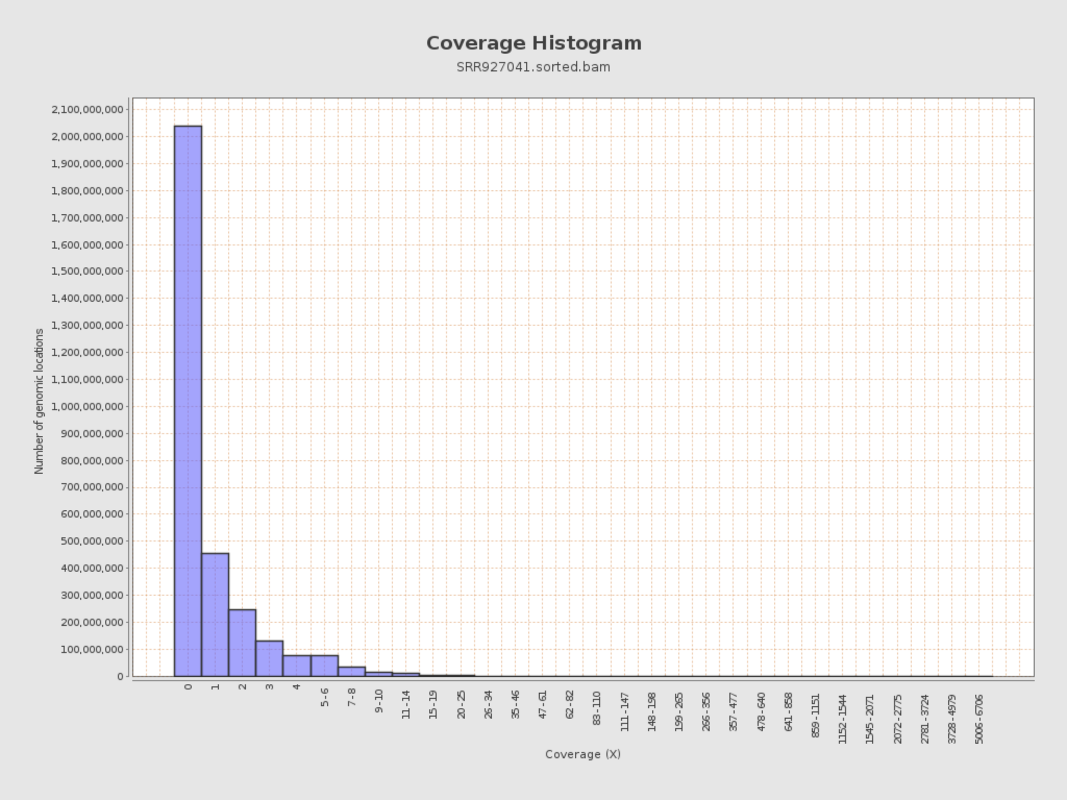
		bases	coverage	deviation
chr1	249250621	220011730	0.8827	3.131
chr2	243199373	241999471	0.9951	5.6756
chr3	198022430	183722490	0.9278	1.9035
chr4	191154276	153122599	0.801	2.1975
chr5	180915260	161237862	0.8912	1.8807
chr6	171115067	156192773	0.9128	1.9021
chr7	159138663	143081158	0.8991	2.2214
chr8	146364022	137496116	0.9394	2.1793
chr9	141213431	126538328	0.8961	3.5529
chr10	135534747	140915795	1.0397	4.4542
chr11	135006516	132925934	0.9846	2.5098
chr12	133851895	126247102	0.9432	1.9547
chr13	115169878	77468849	0.6726	1.6215
chr14	107349540	81301532	0.7574	1.7961
chr15	102531392	92083656	0.8981	1.9956
chr16	90354753	89066685	0.9857	3.5947
chr17	81195210	77998534	0.9606	2.4205
chr18	78077248	74040447	0.9483	3.4211
chr19	59128983	51211285	0.8661	2.3707
chr20	63025520	71539393	1.1351	2.2914
chr21	48129895	33437933	0.6947	2.2528
chr22	51304566	39061451	0.7614	1.943
chrMT	16571	17770162	1,072.3651	857.9872
chrX	155270560	144197090	0.9287	2.0548

chrY	59373566	4126444	0.0695	2.1647

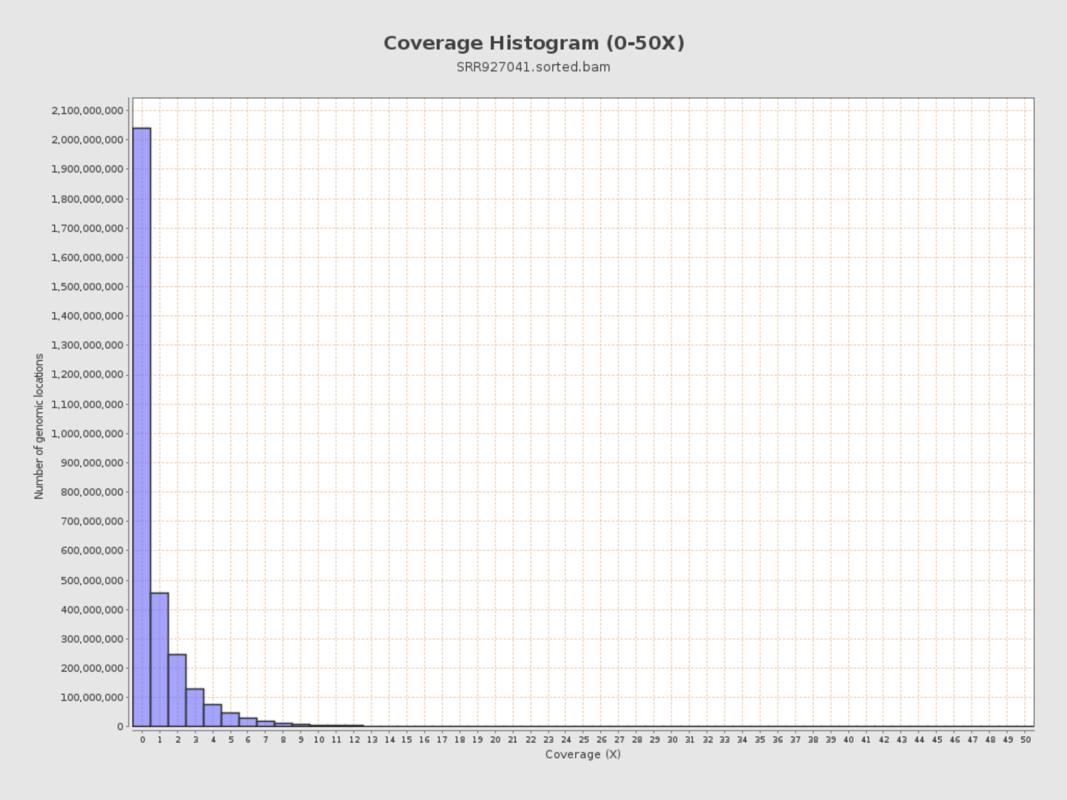
3. Results : Coverage across reference



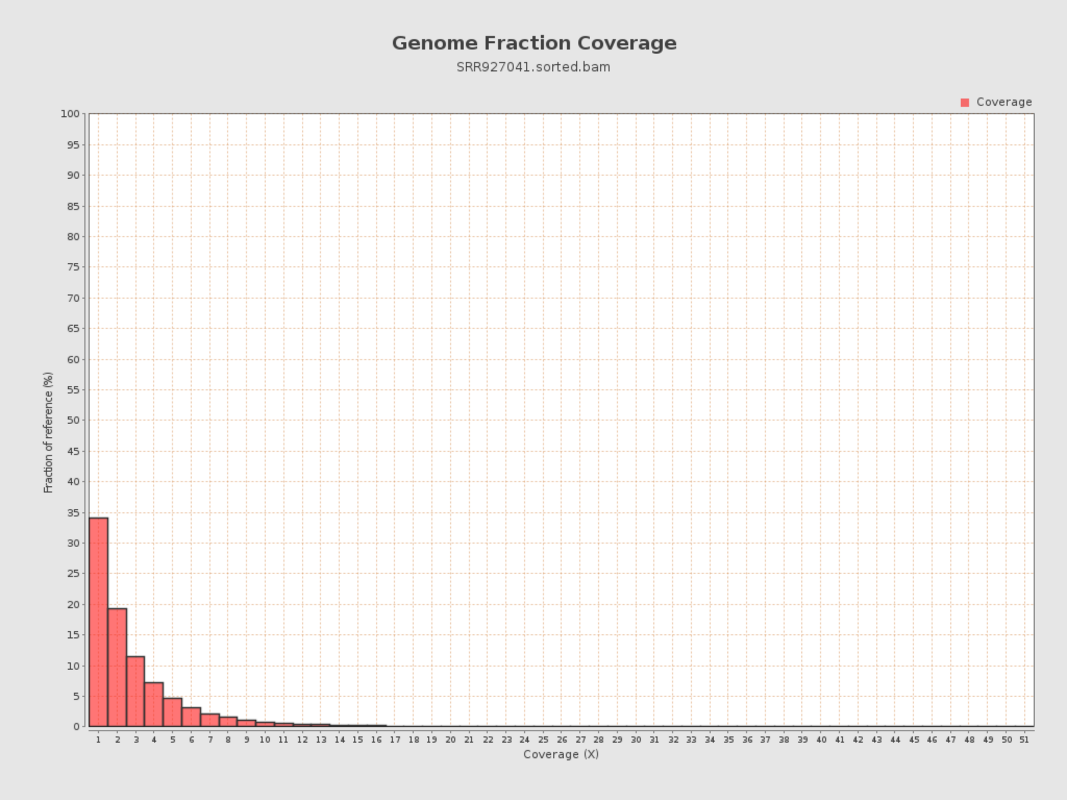
4. Results : Coverage Histogram



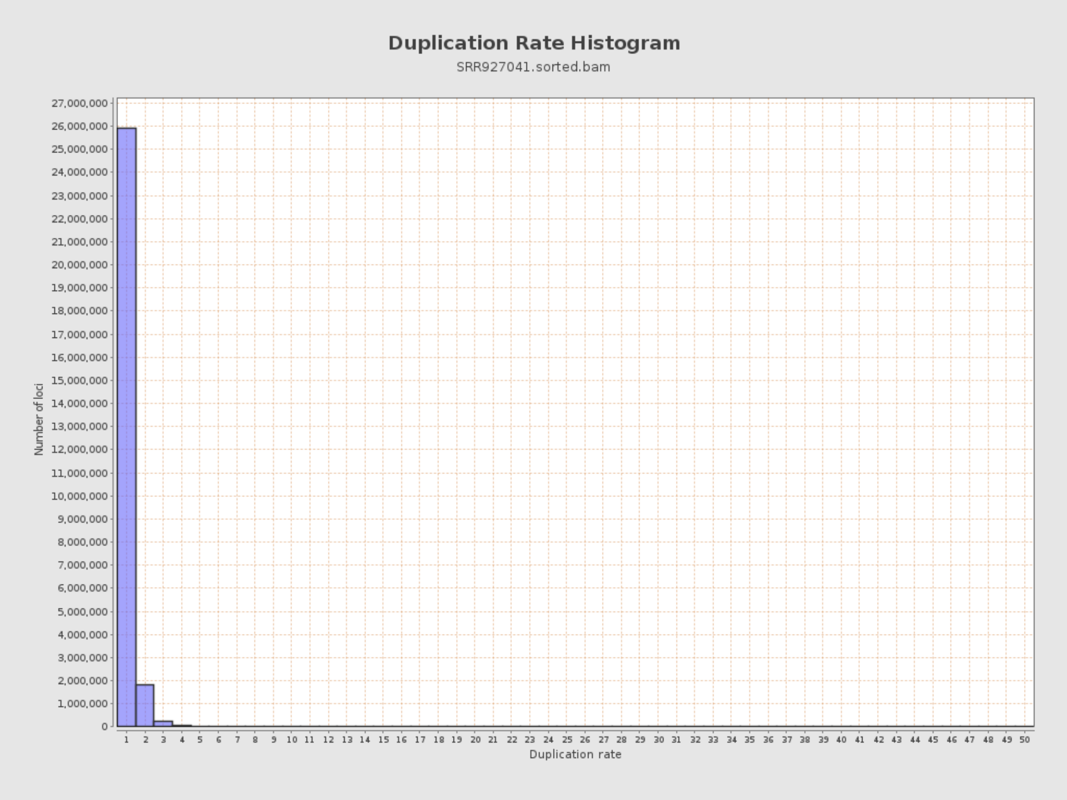
5. Results : Coverage Histogram (0-50X)



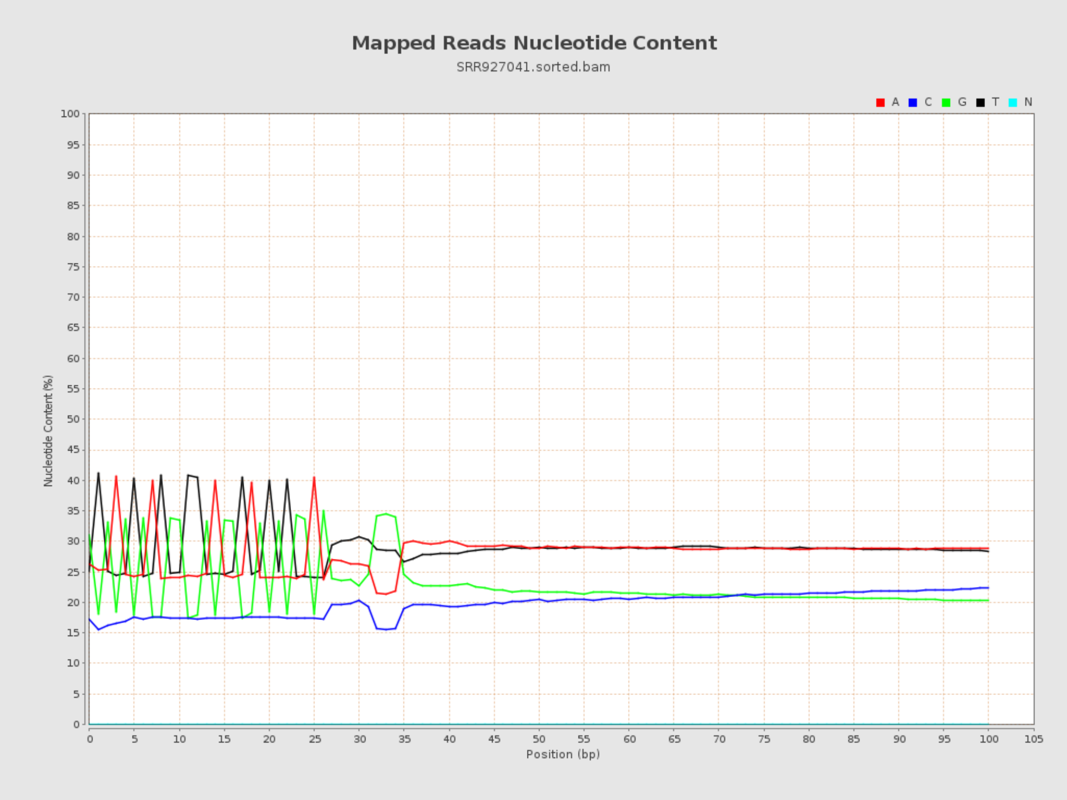
6. Results : Genome Fraction Coverage



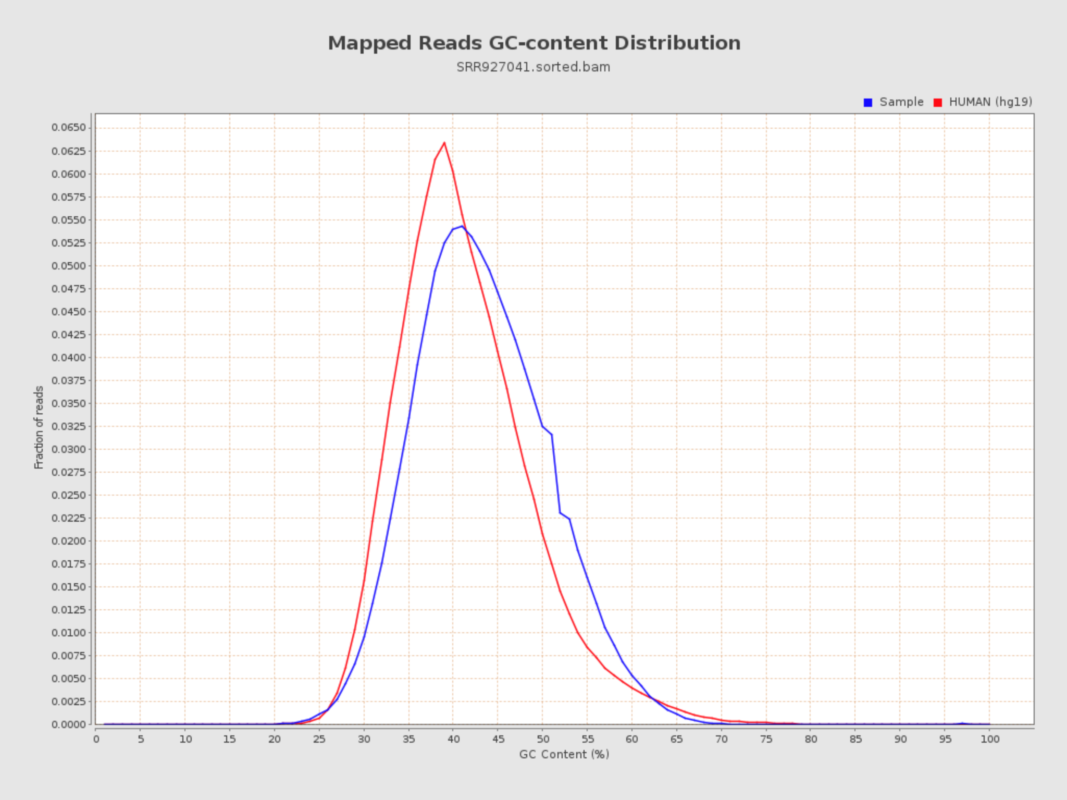
7. Results : Duplication Rate Histogram



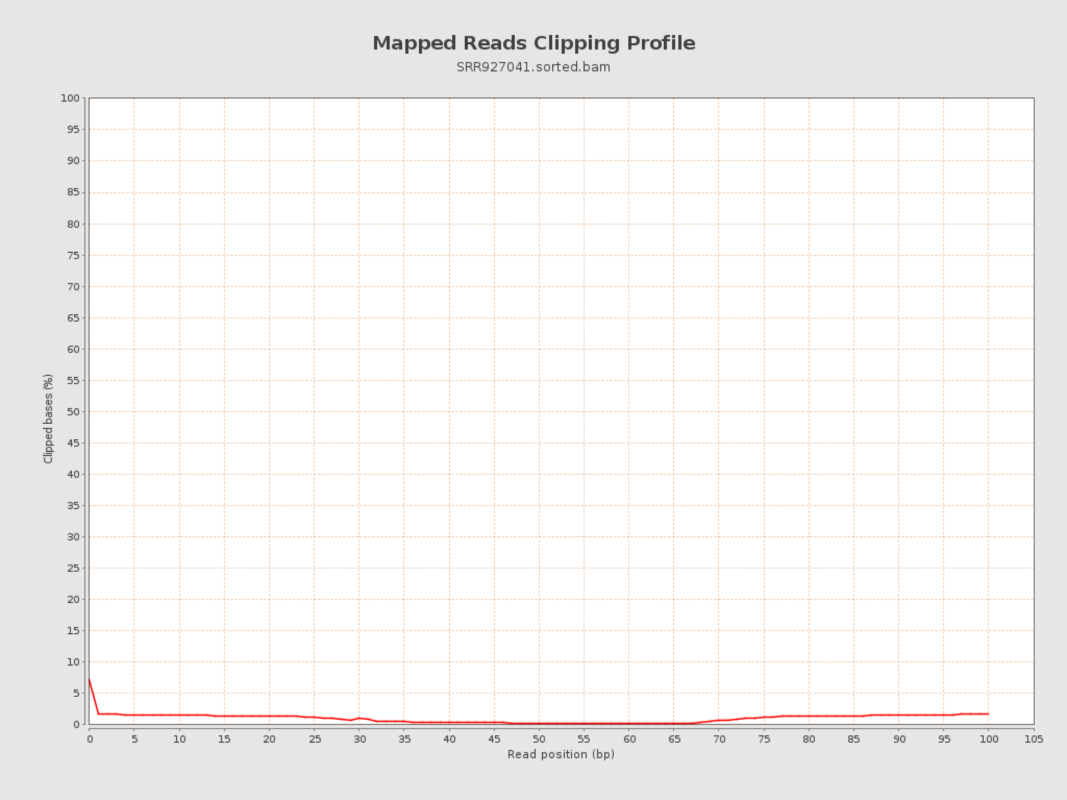
8. Results : Mapped Reads Nucleotide Content



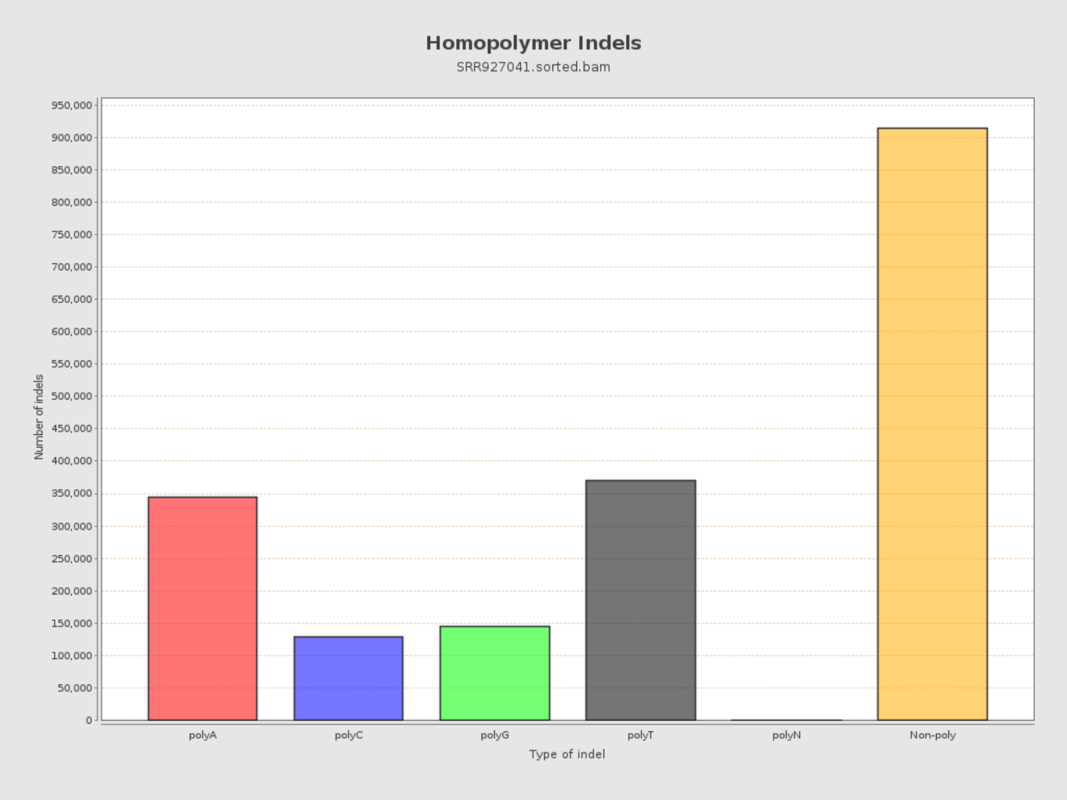
9. Results : Mapped Reads GC-content Distribution



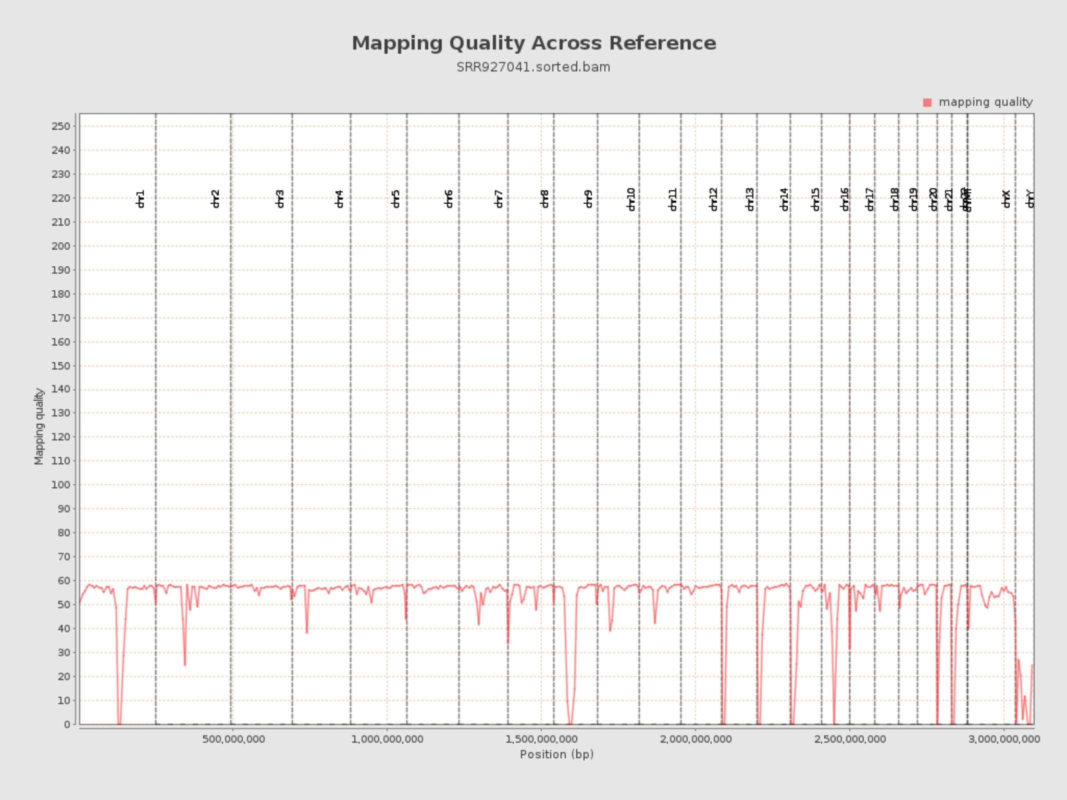
10. Results : Mapped Reads Clipping Profile



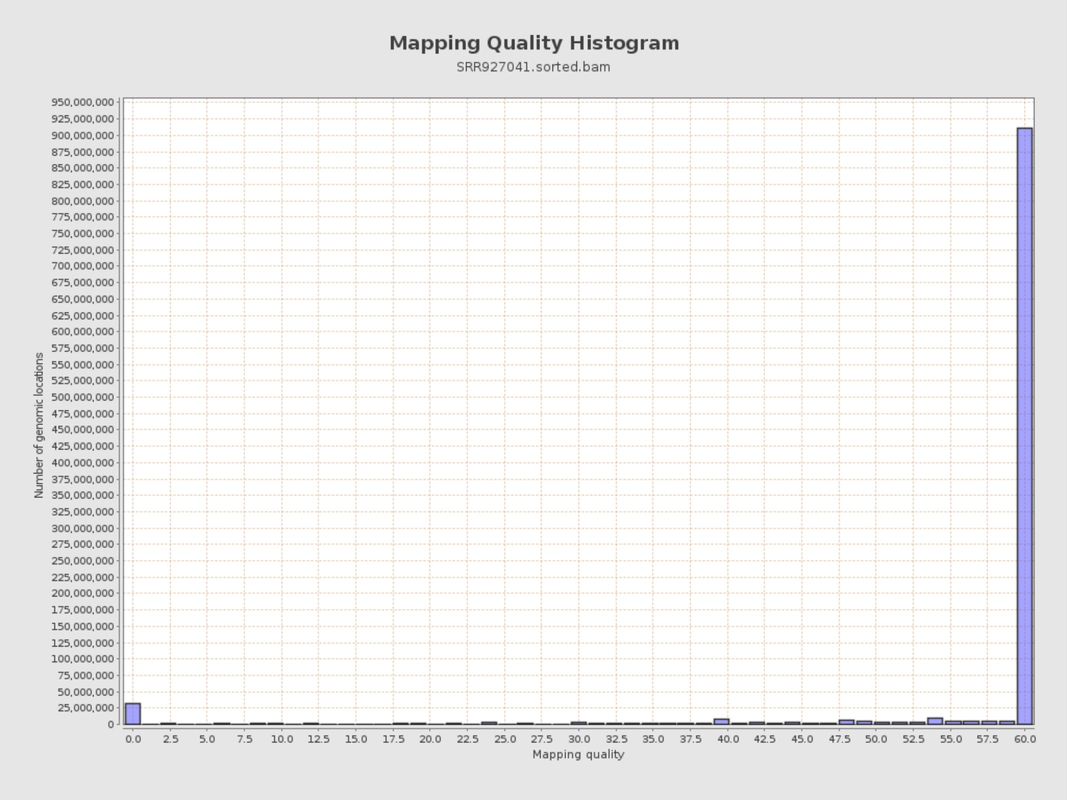
11. Results : Homopolymer Indels



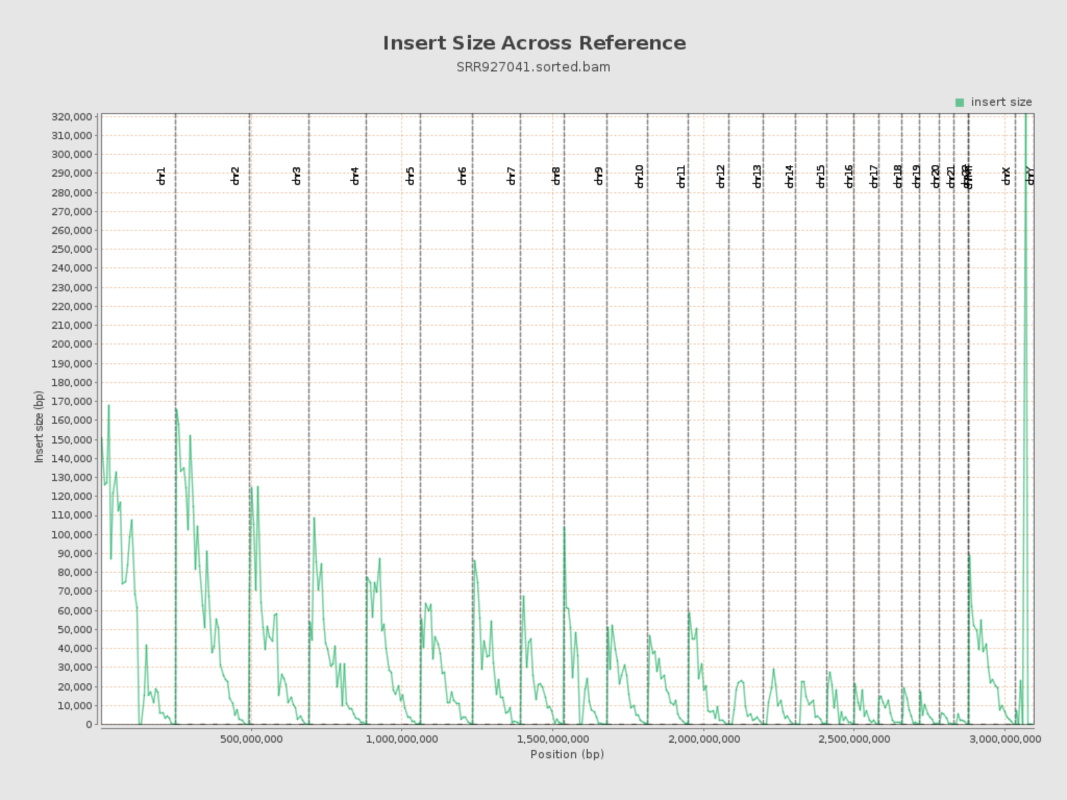
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram