Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 11:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927030.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_SRR927030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927030_1.fastq.gz SRR927030_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 11:59:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,709,452
Mapped reads	37,038,309 / 98.22%
Unmapped reads	671,143 / 1.78%
Mapped paired reads	37,038,309 / 98.22%
Mapped reads, first in pair	18,623,839 / 49.39%
Mapped reads, second in pair	18,414,470 / 48.83%
Mapped reads, both in pair	36,641,640 / 97.17%
Mapped reads, singletons	396,669 / 1.05%
Secondary alignments	0
Supplementary alignments	259,876 / 0.69%
Read min/max/mean length	30 / 101 / 101.28
Duplicated reads (estimated)	2,935,983 / 7.79%
Duplication rate	6.22%
Clipped reads	9,467,398 / 25.11%

2.2. ACGT Content

Number/percentage of A's	1,000,760,484 / 28.67%
Number/percentage of C's	696,993,474 / 19.97%
Number/percentage of T's	1,013,005,559 / 29.02%
Number/percentage of G's	779,414,311 / 22.33%
Number/percentage of N's	536,612 / 0.02%

GC Percentage	42.3%

2.3. Coverage

Mean	1.1284
Standard Deviation	4.2366

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	78,822.85
Standard Deviation	2,772,072.8
P25/Median/P75	152 / 194 / 259

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	36,364,250
Insertions	546,802
Mapped reads with at least one insertion	1.45%
Deletions	1,809,490
Mapped reads with at least one deletion	4.76%
Homopolymer indels	53.05%

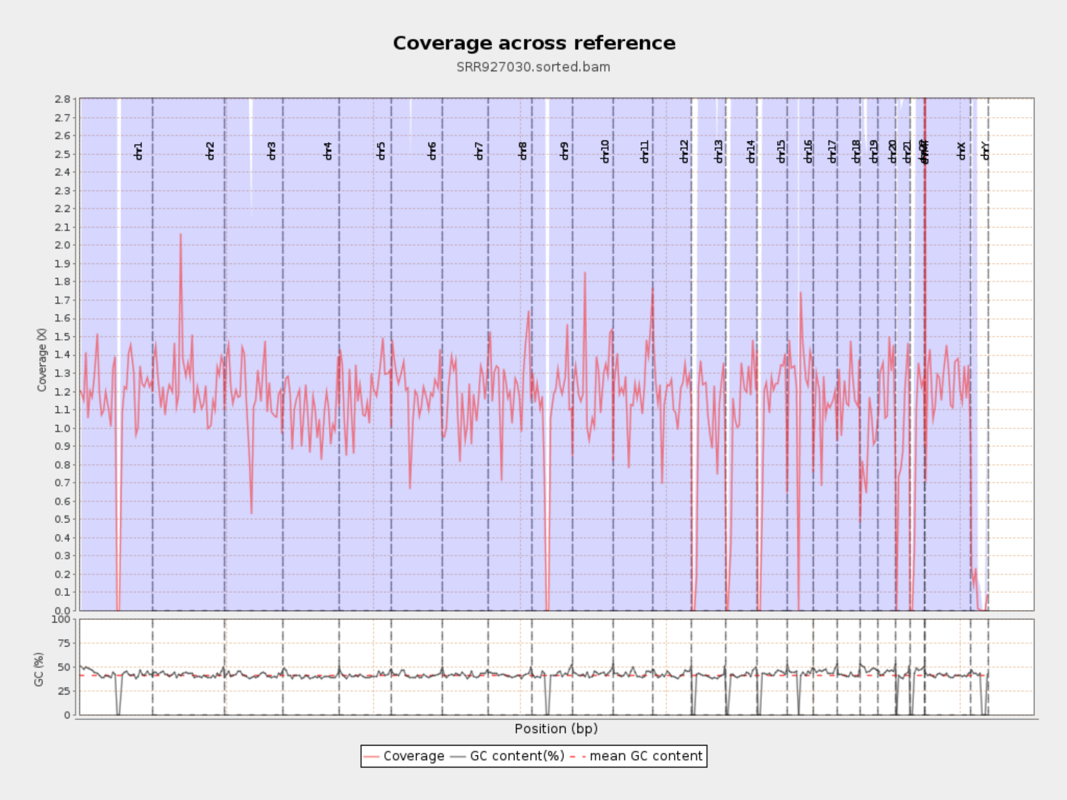
2.7. Chromosome stats

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

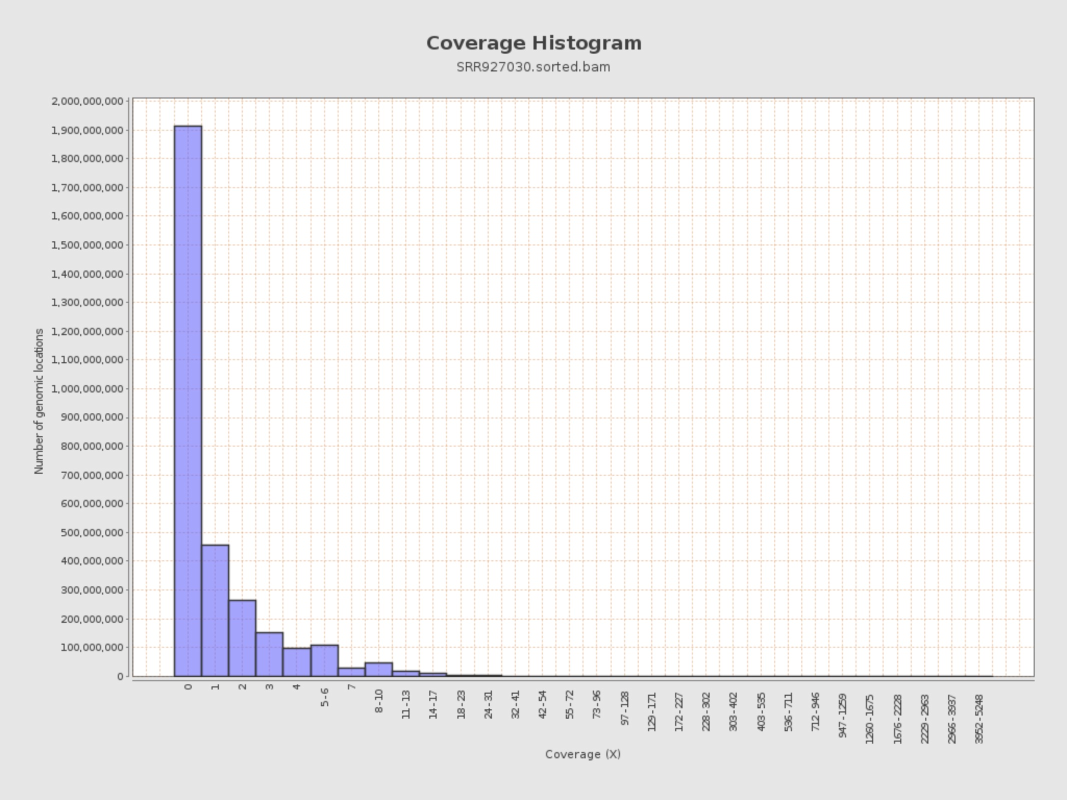
		bases	coverage	deviation
chr1	249250621	285142609	1.144	5.9996
chr2	243199373	306213164	1.2591	6.8031
chr3	198022430	233986717	1.1816	2.2673
chr4	191154276	207797593	1.0871	3.3145
chr5	180915260	217165236	1.2004	2.2612
chr6	171115067	205550280	1.2012	2.3589
chr7	159138663	181345704	1.1395	2.8727
chr8	146364022	181860655	1.2425	2.7247
chr9	141213431	148431448	1.0511	5.1484
chr10	135534747	170458173	1.2577	8.9669
chr11	135006516	165574065	1.2264	3.3441
chr12	133851895	158440944	1.1837	2.2853
chr13	115169878	109755659	0.953	2.0168
chr14	107349540	106504141	0.9921	2.1913
chr15	102531392	105163488	1.0257	2.2304
chr16	90354753	110732782	1.2255	6.0136
chr17	81195210	89481556	1.1021	3.5364
chr18	78077248	94947696	1.2161	5.214
chr19	59128983	52010837	0.8796	3.2331
chr20	63025520	78754924	1.2496	2.5245
chr21	48129895	44931214	0.9335	2.7339
chr22	51304566	42656244	0.8314	2.0934
chrMT	16571	191161	11.5359	8.2698
chrX	155270560	191249405	1.2317	2.702

chrY	59373566	4903470	0.0826	2.4321

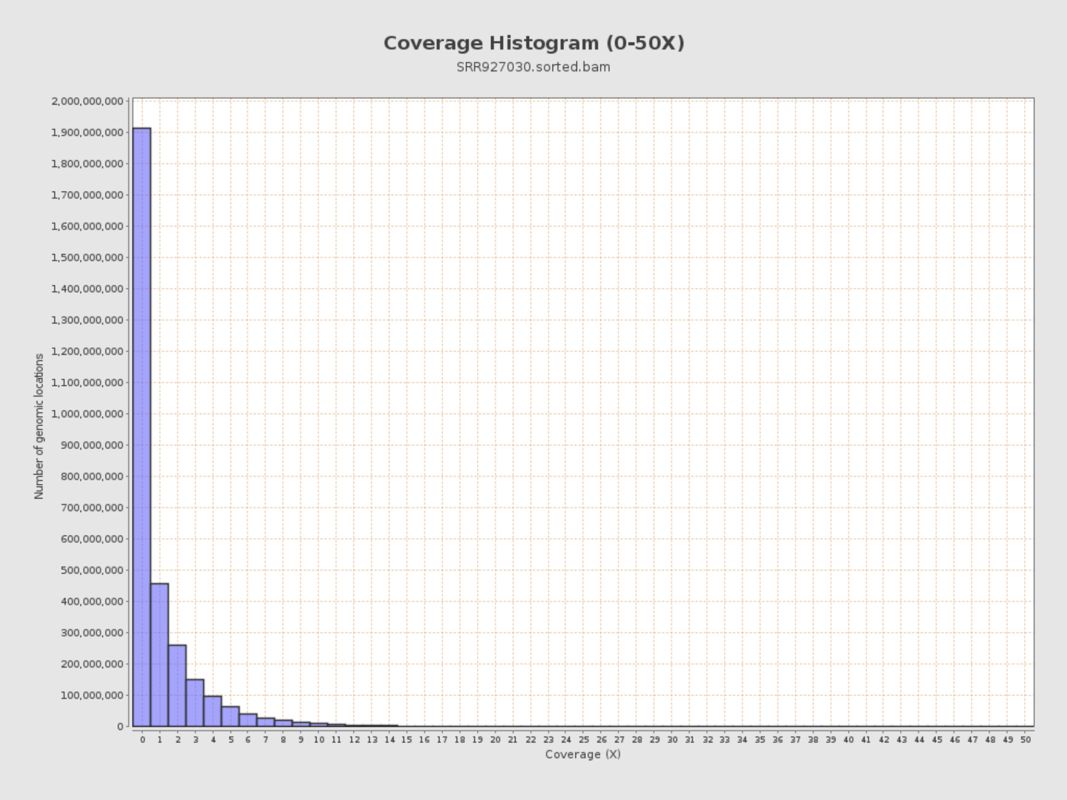
3. Results : Coverage across reference



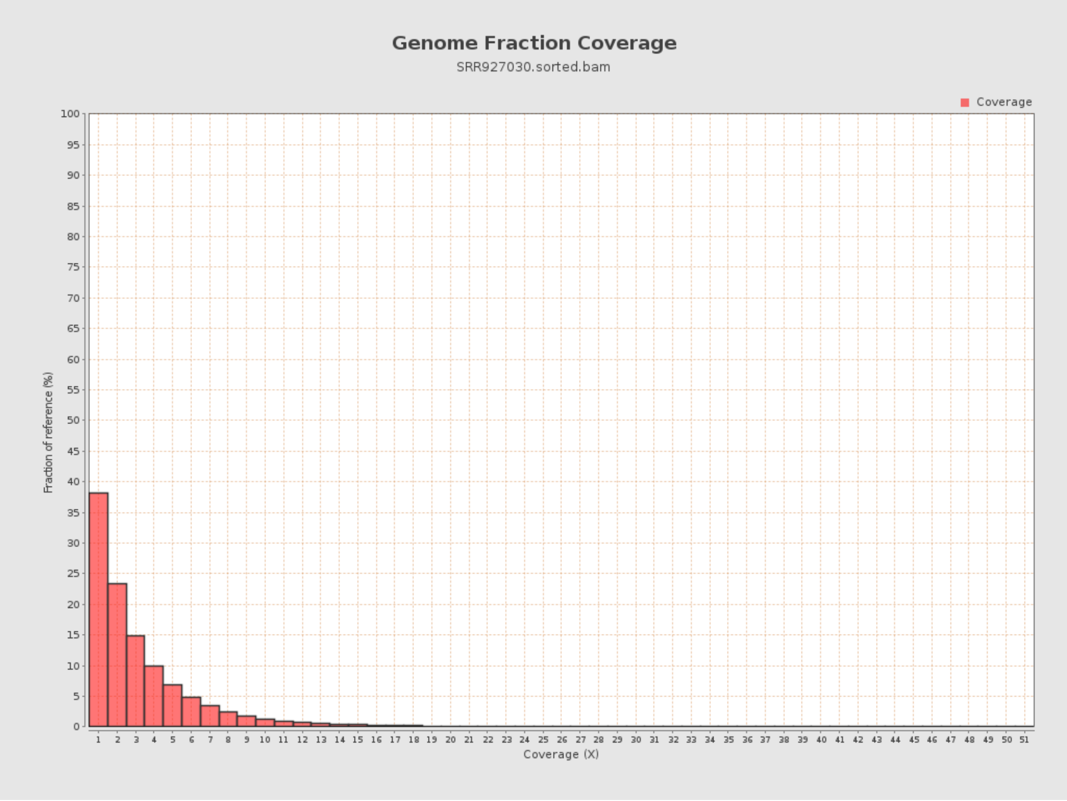
4. Results : Coverage Histogram



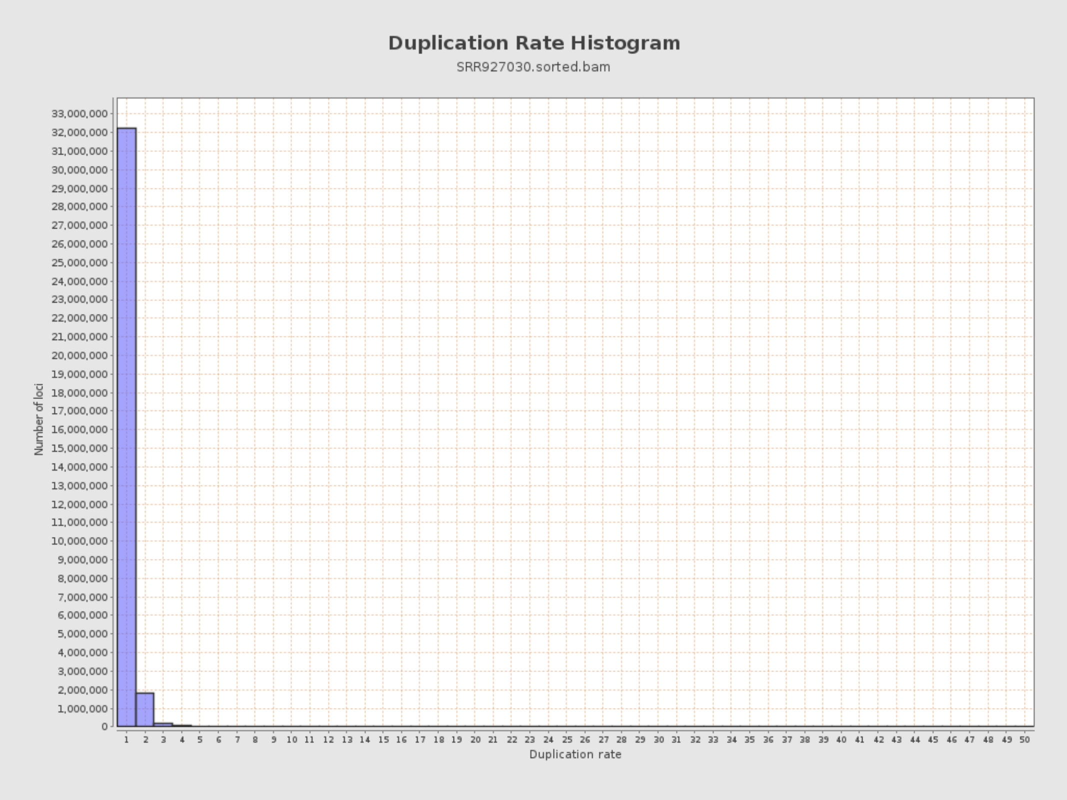
5. Results : Coverage Histogram (0-50X)



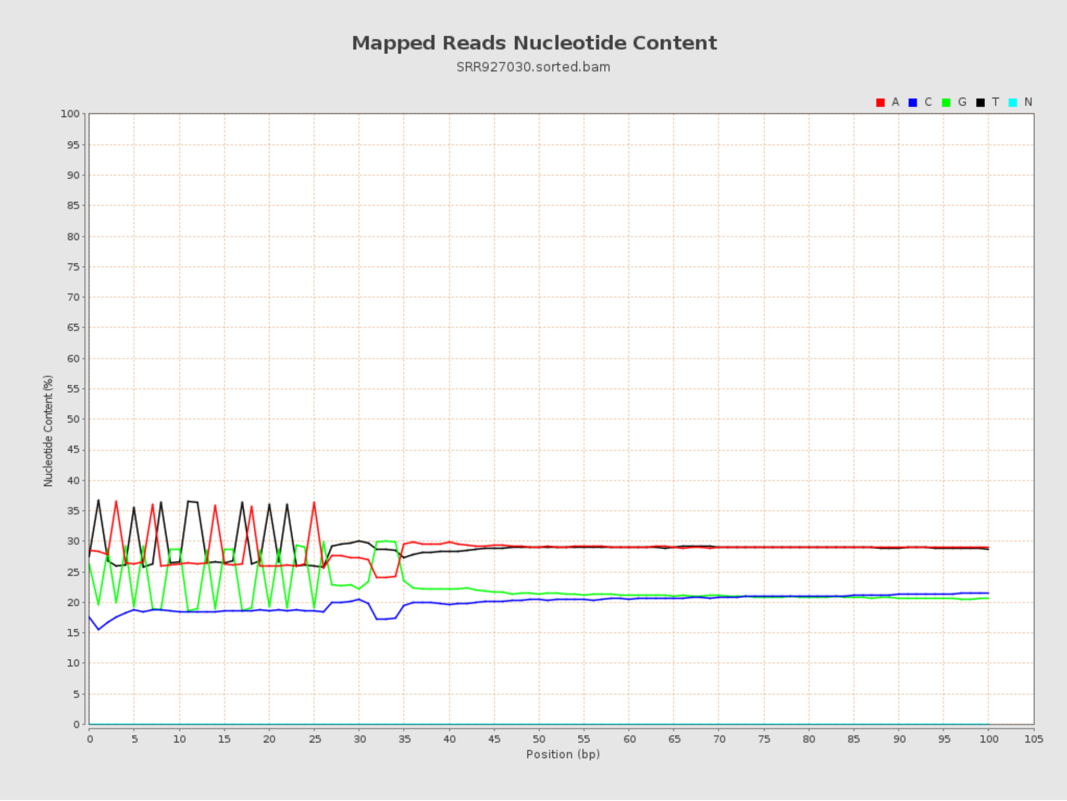
6. Results : Genome Fraction Coverage



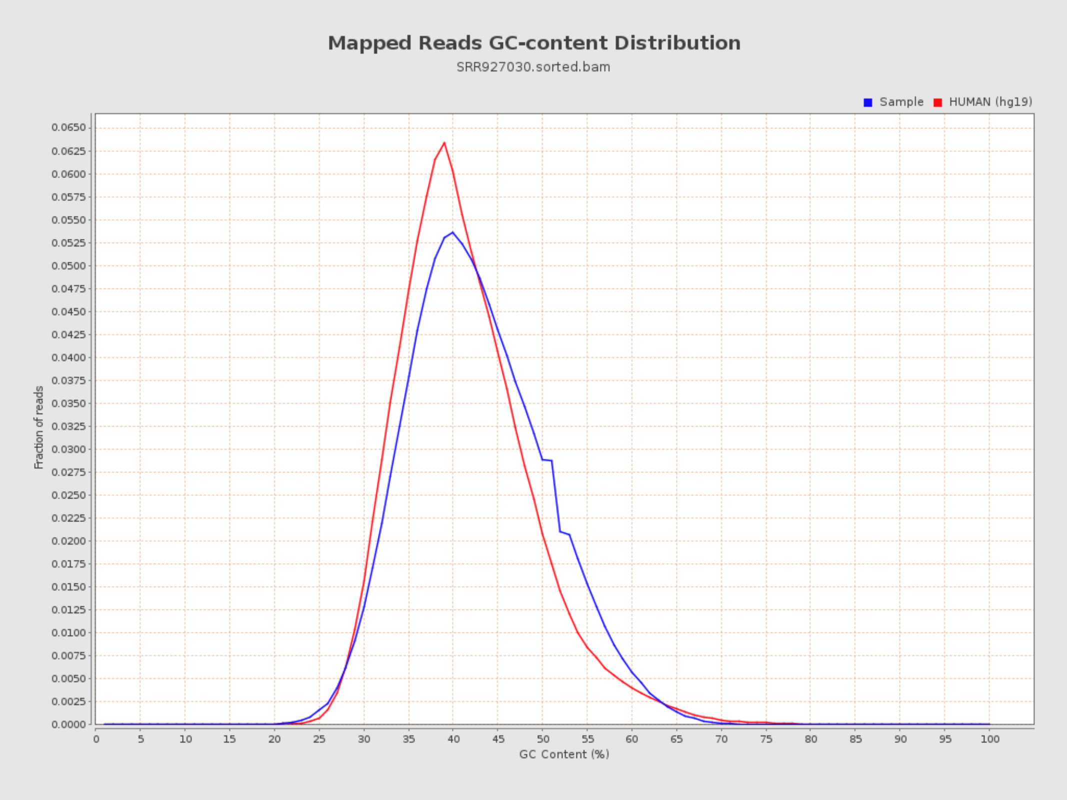
7. Results : Duplication Rate Histogram



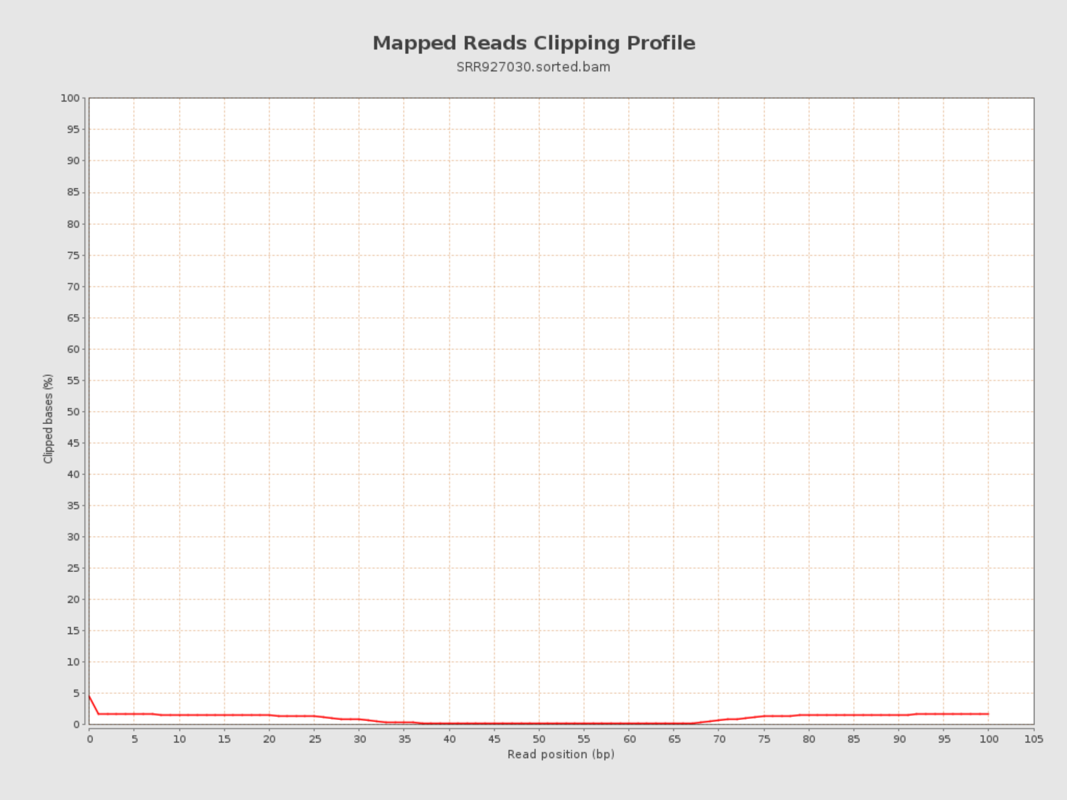
8. Results : Mapped Reads Nucleotide Content



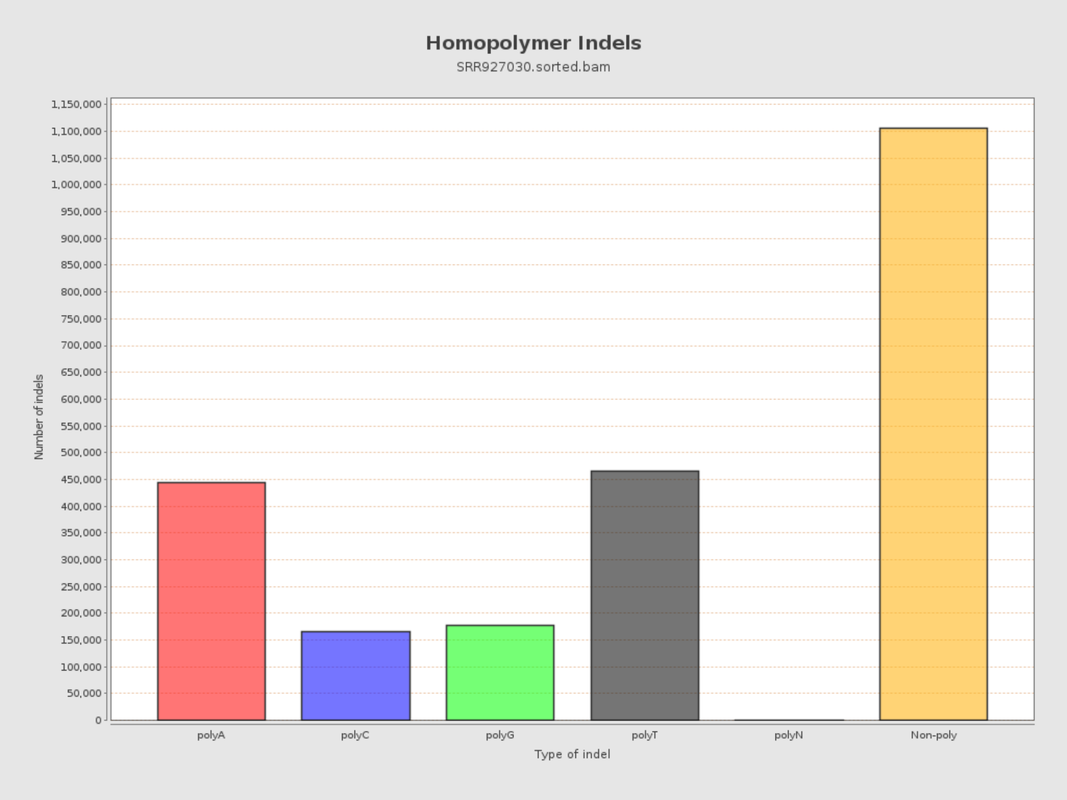
9. Results : Mapped Reads GC-content Distribution



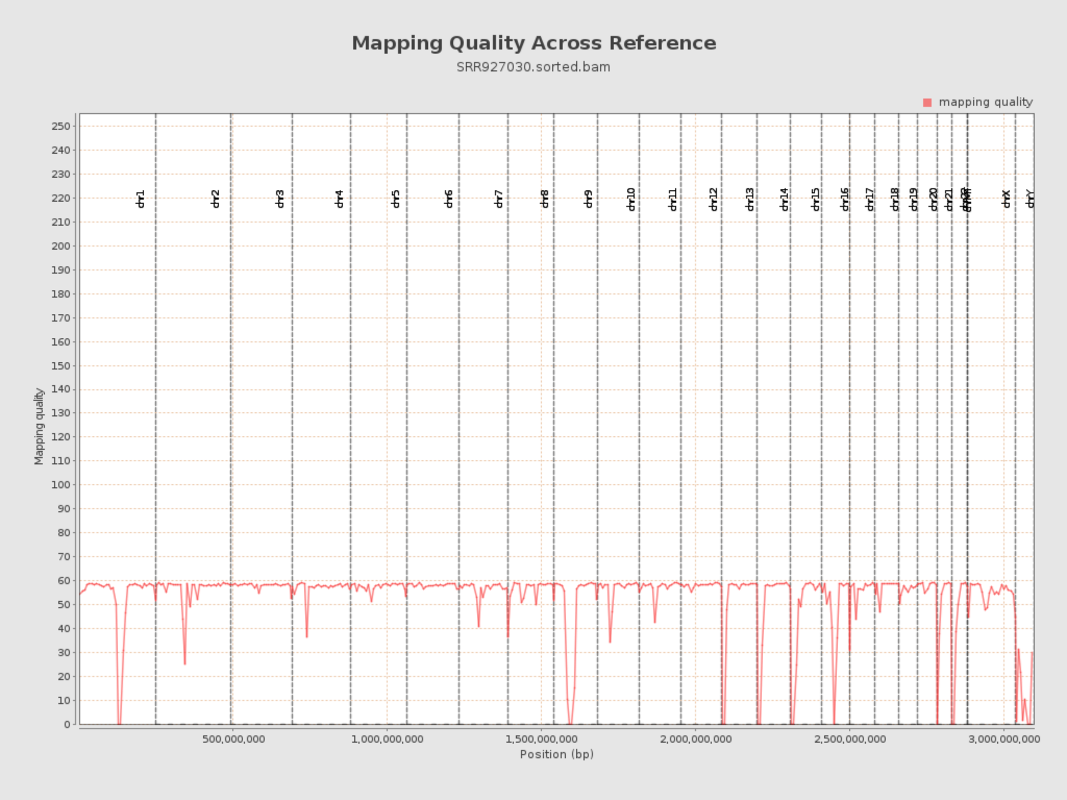
10. Results : Mapped Reads Clipping Profile



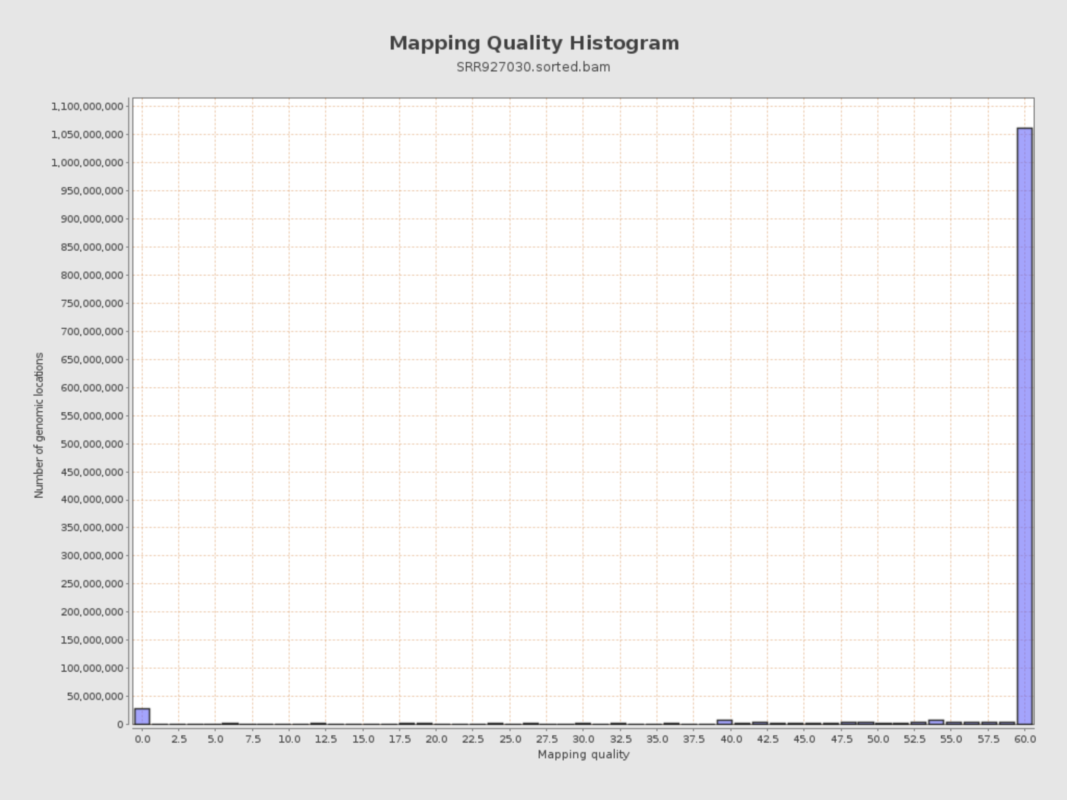
11. Results : Homopolymer Indels



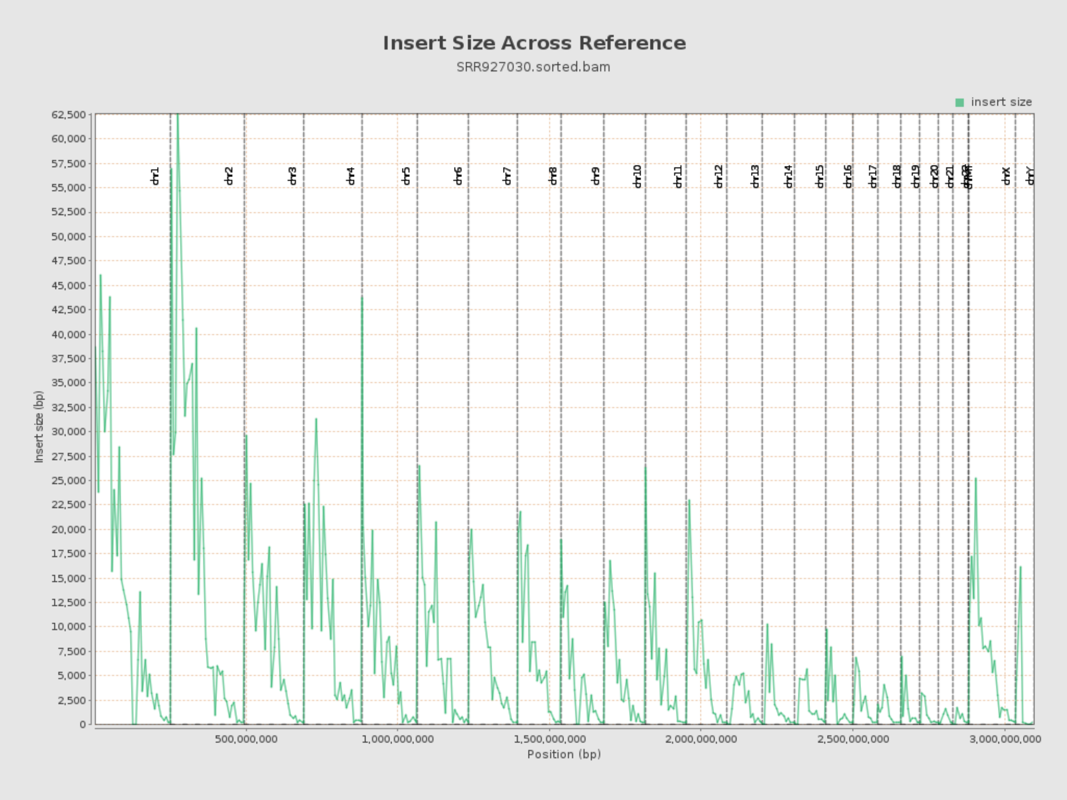
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram