Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 09:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927024.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_SRR927024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927024_1.fastq.gz SRR927024_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 09:13:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,207,806
Mapped reads	8,980,839 / 97.54%
Unmapped reads	226,967 / 2.46%
Mapped paired reads	8,980,839 / 97.54%
Mapped reads, first in pair	4,509,481 / 48.97%
Mapped reads, second in pair	4,471,358 / 48.56%
Mapped reads, both in pair	8,842,506 / 96.03%
Mapped reads, singletons	138,333 / 1.5%
Secondary alignments	0
Supplementary alignments	294,003 / 3.19%
Read min/max/mean length	30 / 101 / 102.33
Duplicated reads (estimated)	500,634 / 5.44%
Duplication rate	4.41%
Clipped reads	3,829,291 / 41.59%

2.2. ACGT Content

Number/percentage of A's	235,439,545 / 28.71%
Number/percentage of C's	159,191,742 / 19.41%
Number/percentage of T's	240,013,416 / 29.26%
Number/percentage of G's	185,398,067 / 22.6%
Number/percentage of N's	153,017 / 0.02%

GC Percentage	42.01%

2.3. Coverage

Mean	0.2652
Standard Deviation	1.3523

2.4. Mapping Quality

Mean Mapping Quality	52.35

2.5. Insert size

Mean	350,480.68
Standard Deviation	5,811,399.08
P25/Median/P75	138 / 181 / 247

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	8,075,274
Insertions	144,831
Mapped reads with at least one insertion	1.58%
Deletions	429,254
Mapped reads with at least one deletion	4.66%
Homopolymer indels	51.75%

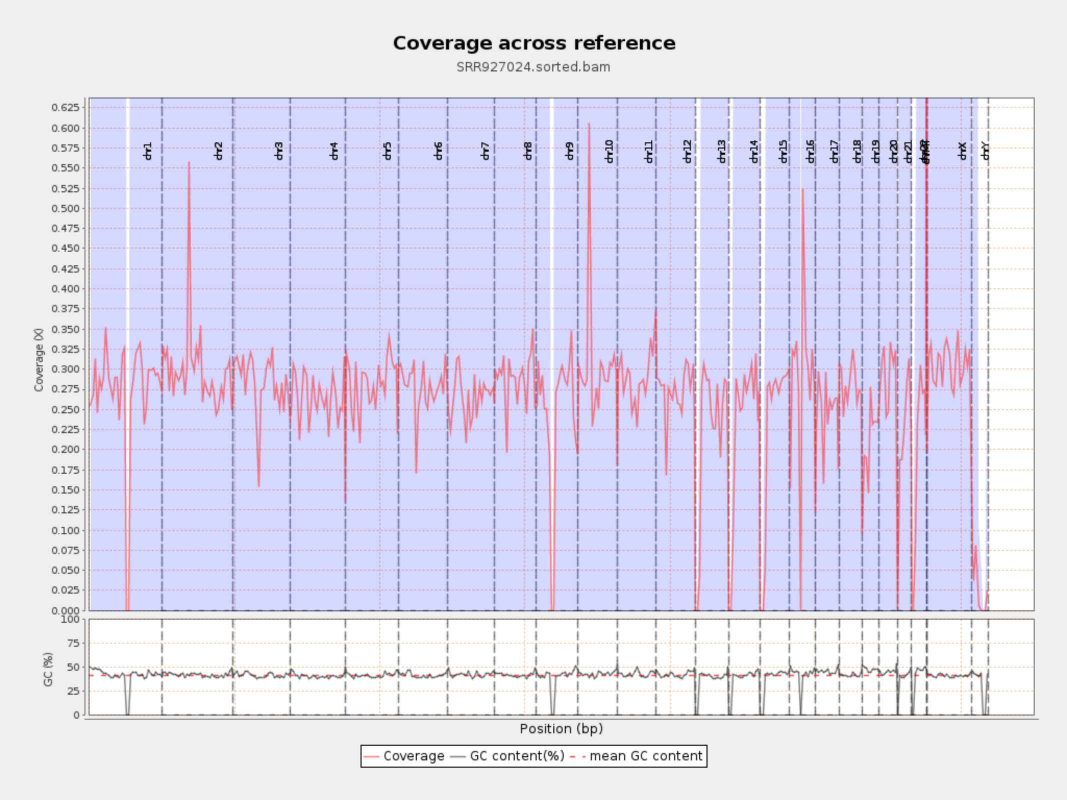
2.7. Chromosome stats

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

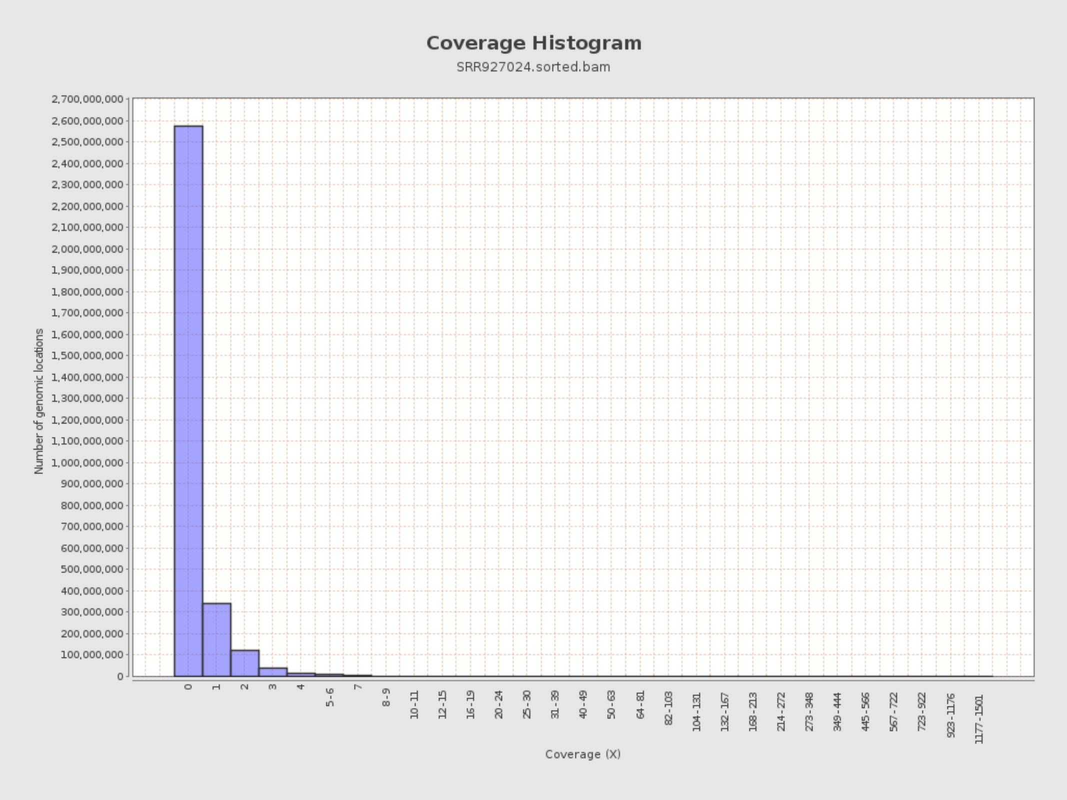
		bases	coverage	deviation
chr1	249250621	67428819	0.2705	1.4667
chr2	243199373	72860218	0.2996	1.986
chr3	198022430	55921190	0.2824	0.75
chr4	191154276	50573857	0.2646	0.9391
chr5	180915260	50899195	0.2813	0.7248
chr6	171115067	47656951	0.2785	0.8039
chr7	159138663	42177333	0.265	0.975
chr8	146364022	42289684	0.2889	0.8338
chr9	141213431	34408928	0.2437	1.6535
chr10	135534747	41206628	0.304	3.3327
chr11	135006516	38821905	0.2876	1.5788
chr12	133851895	36512149	0.2728	0.7206
chr13	115169878	25160165	0.2185	0.6341
chr14	107349540	24469733	0.2279	0.6748
chr15	102531392	23162465	0.2259	0.6579
chr16	90354753	26062858	0.2885	2.0673
chr17	81195210	20037653	0.2468	0.7698
chr18	78077248	22030684	0.2822	1.7515
chr19	59128983	12468659	0.2109	0.9934
chr20	63025520	18321694	0.2907	0.7777
chr21	48129895	10356218	0.2152	0.8091
chr22	51304566	9471940	0.1846	0.6217
chrMT	16571	27211	1.6421	2.0246
chrX	155270560	46991393	0.3026	0.8898

chrY	59373566	1511630	0.0255	0.8125

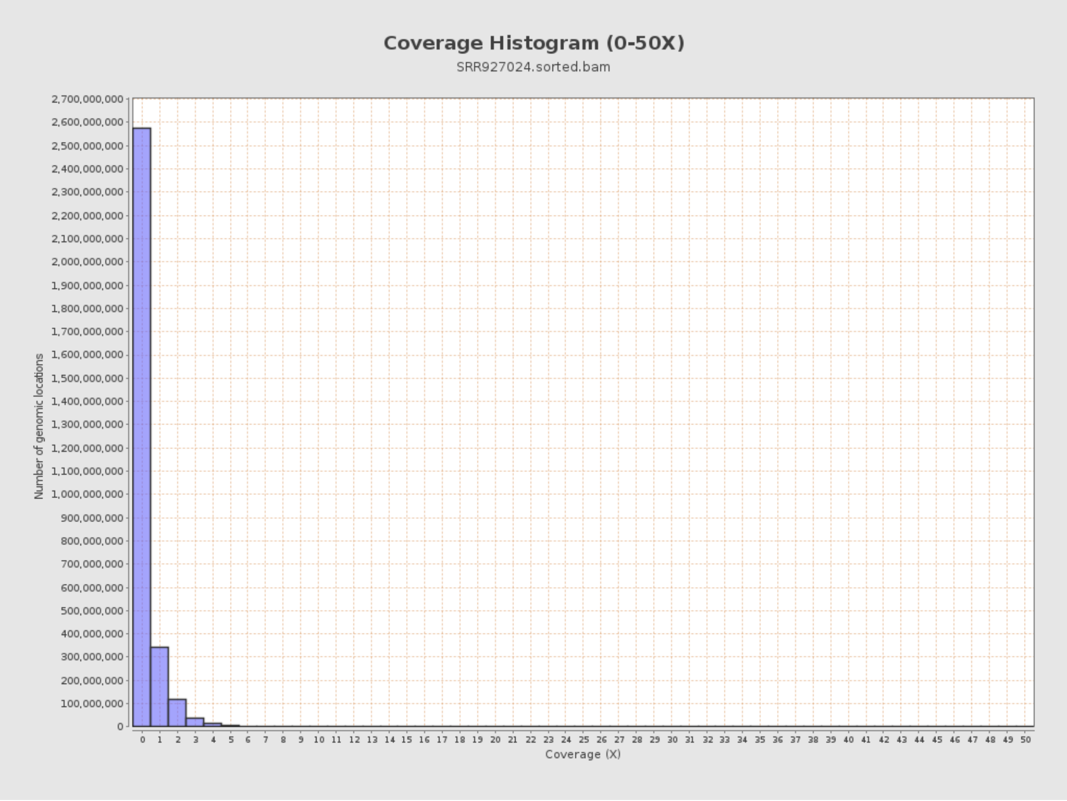
3. Results : Coverage across reference



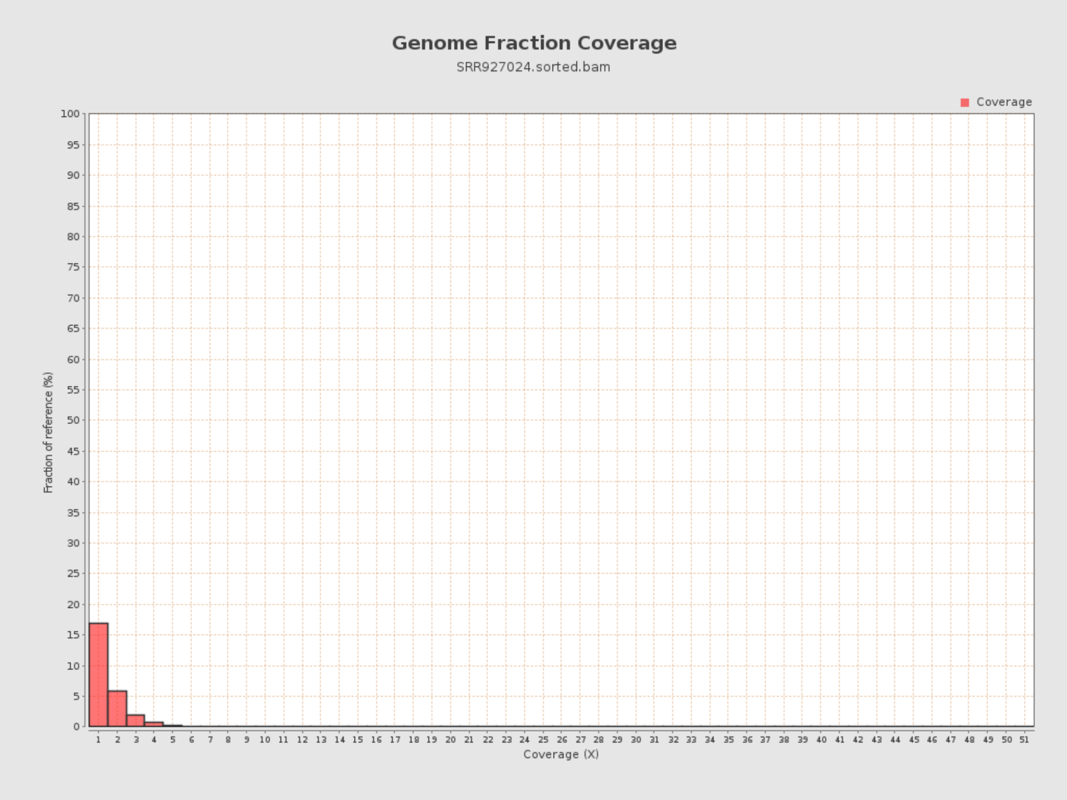
4. Results : Coverage Histogram



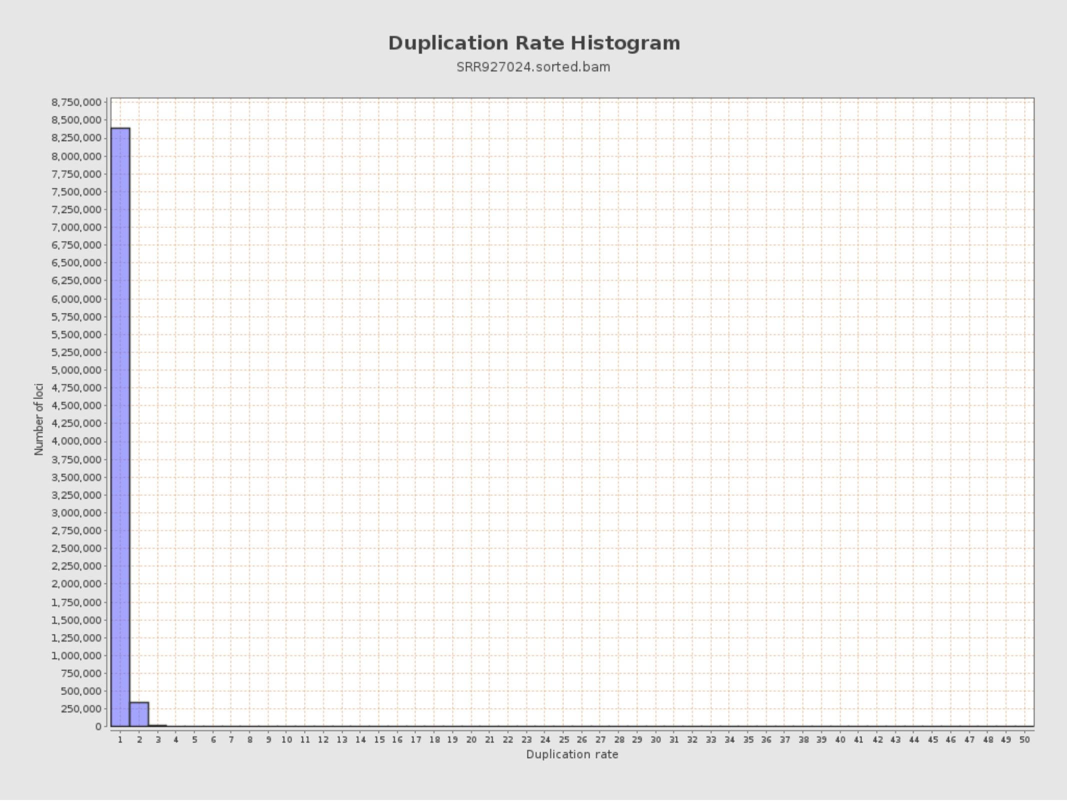
5. Results : Coverage Histogram (0-50X)



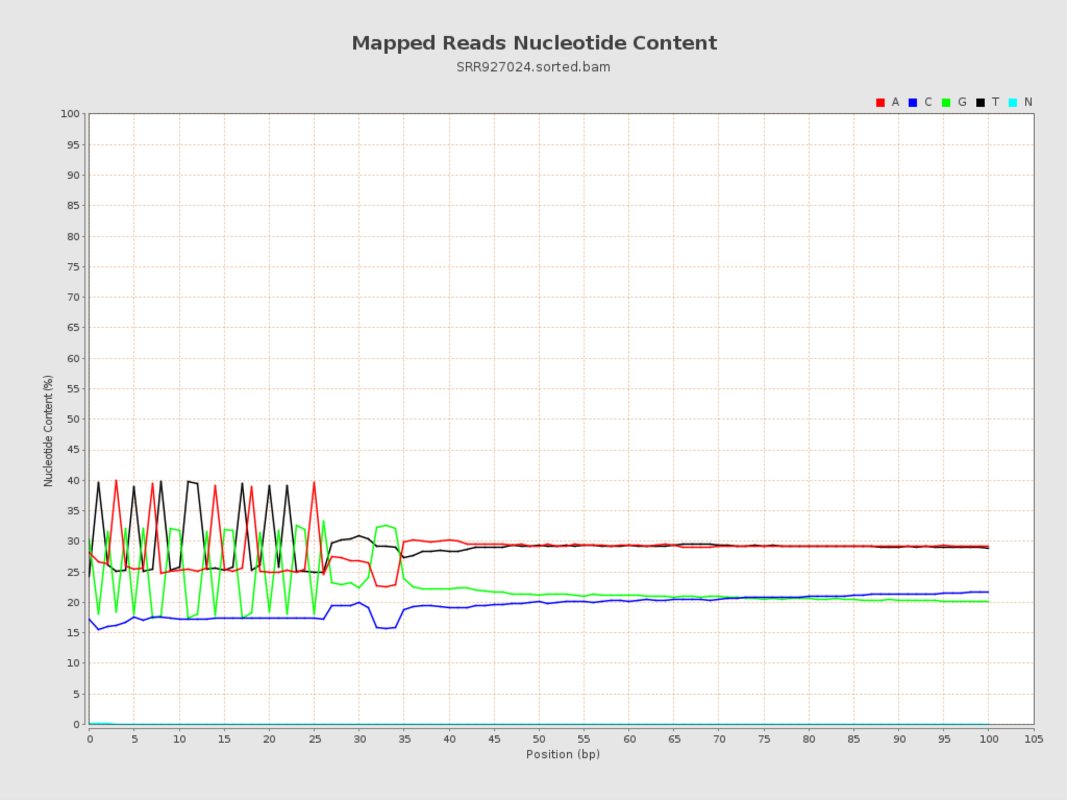
6. Results : Genome Fraction Coverage



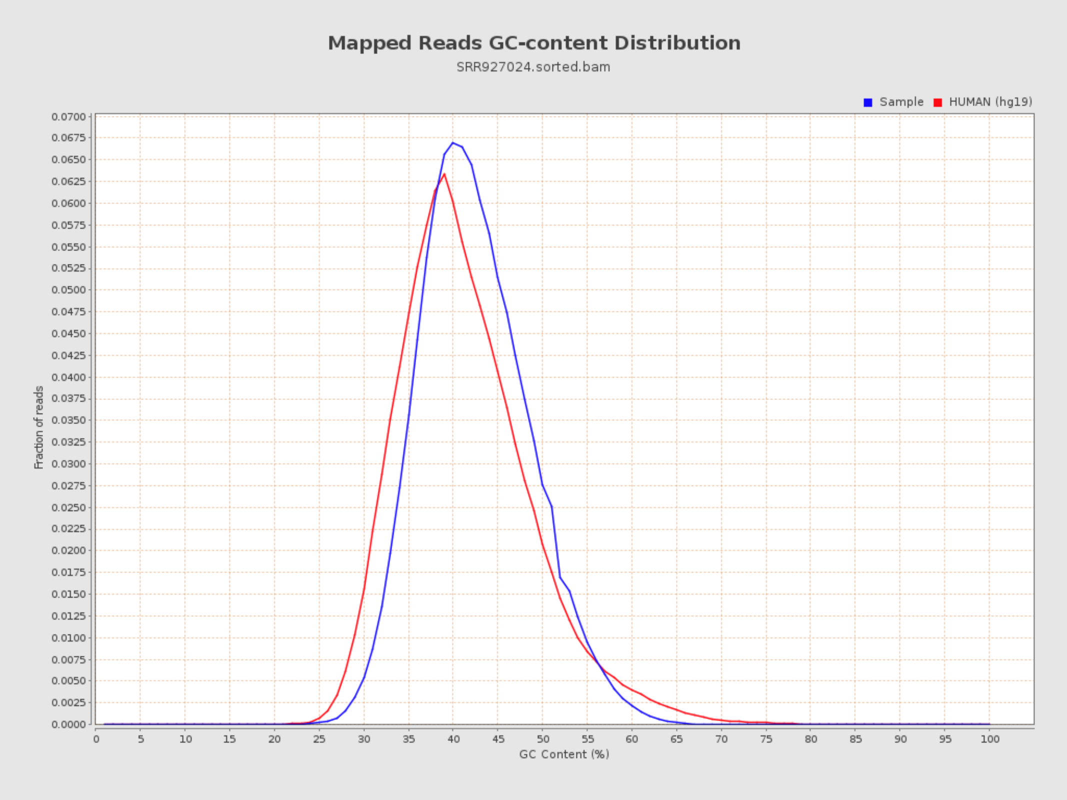
7. Results : Duplication Rate Histogram



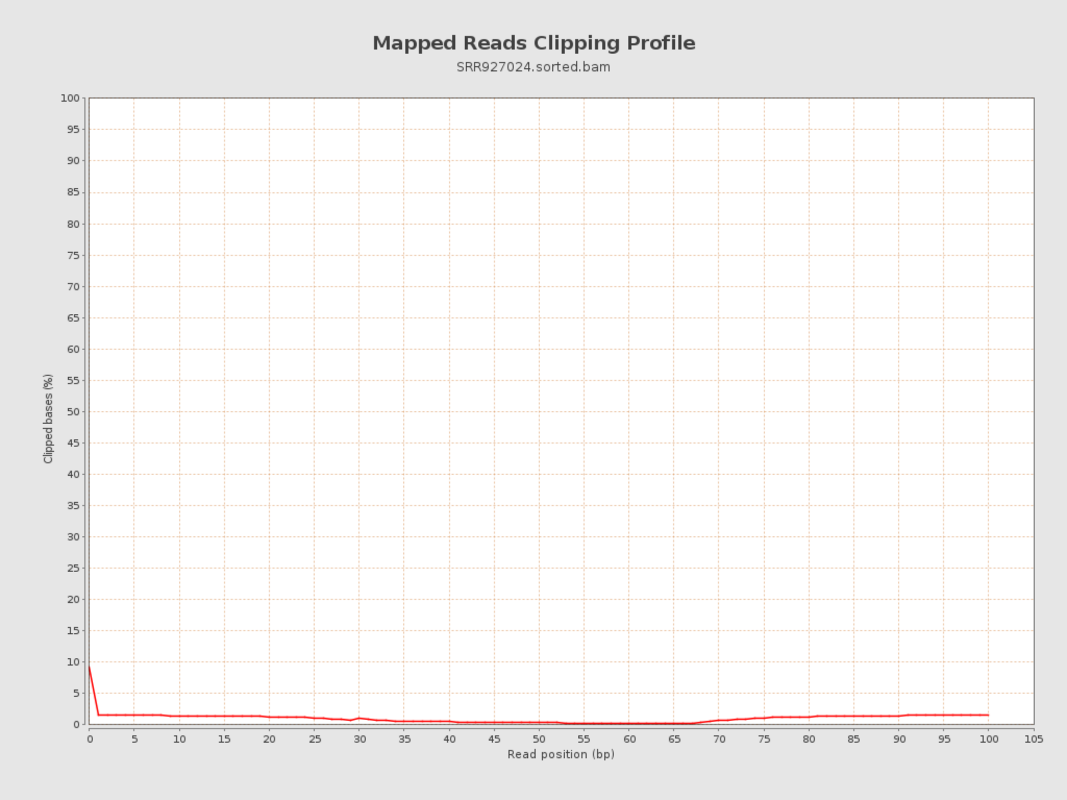
8. Results : Mapped Reads Nucleotide Content



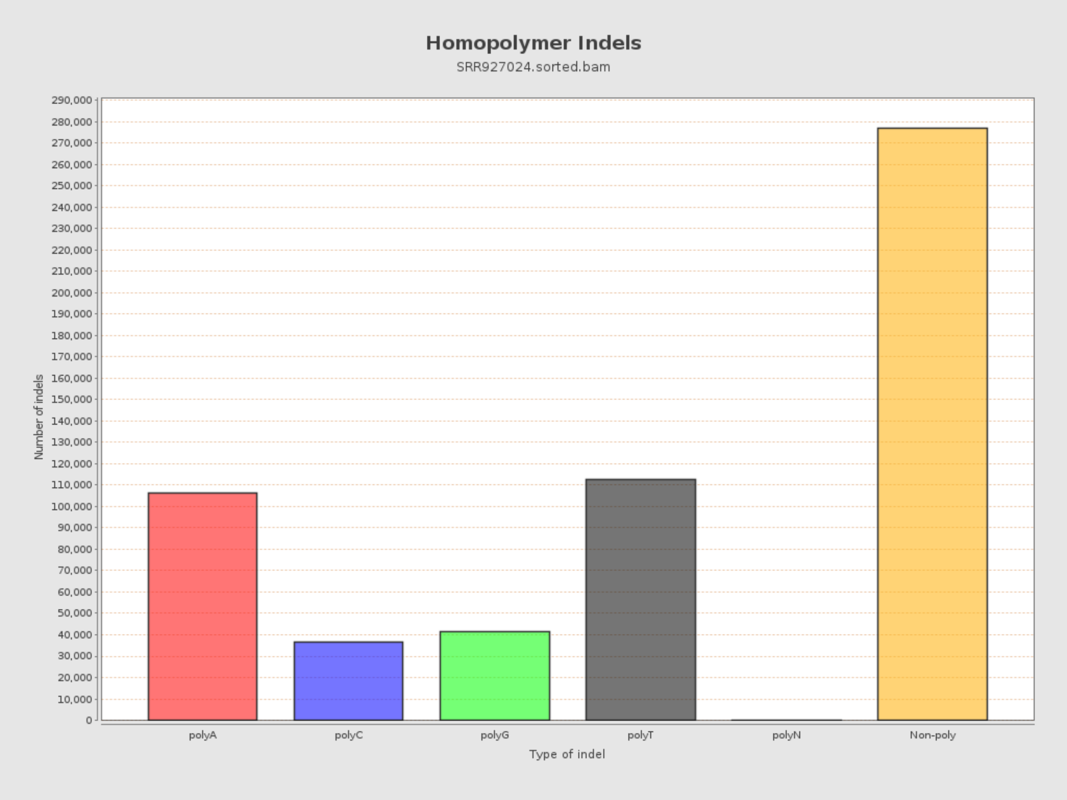
9. Results : Mapped Reads GC-content Distribution



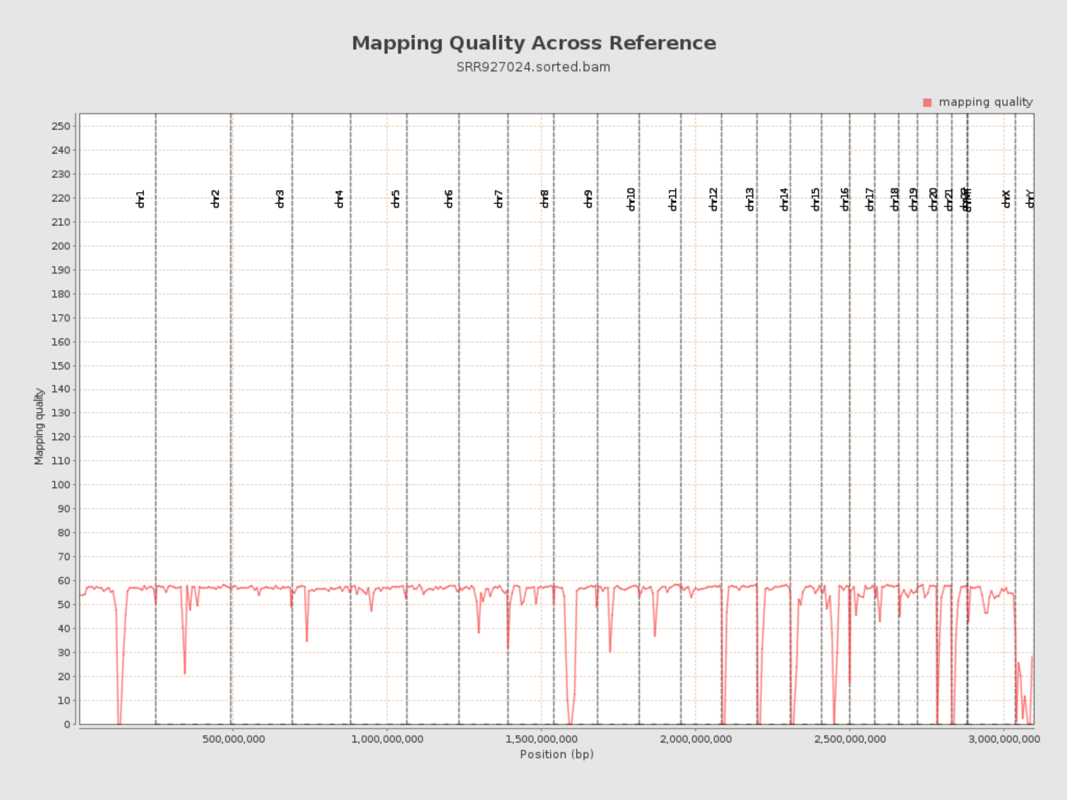
10. Results : Mapped Reads Clipping Profile



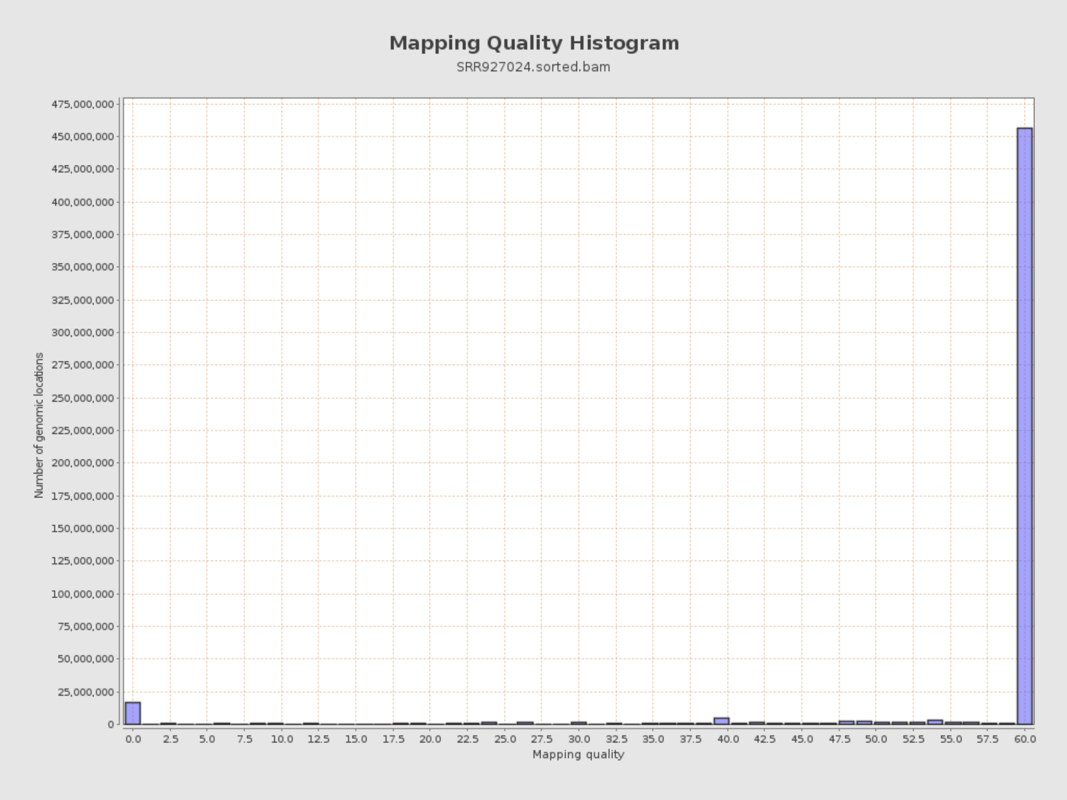
11. Results : Homopolymer Indels



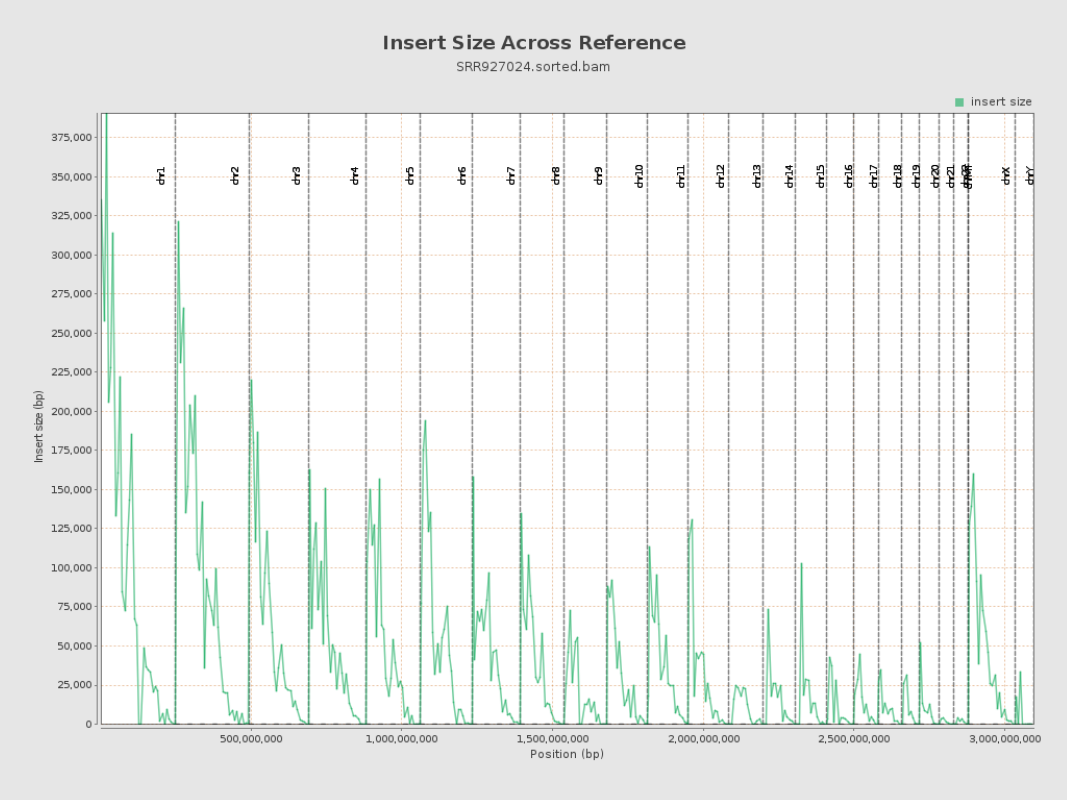
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram