Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 01:41:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926949.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_SRR926949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926949_1.fastq.gz SRR926949_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 01:41:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,783,760
Mapped reads	13,565,659 / 98.42%
Unmapped reads	218,101 / 1.58%
Mapped paired reads	13,565,659 / 98.42%
Mapped reads, first in pair	6,781,952 / 49.2%
Mapped reads, second in pair	6,783,707 / 49.22%
Mapped reads, both in pair	13,428,780 / 97.42%
Mapped reads, singletons	136,879 / 0.99%
Secondary alignments	0
Supplementary alignments	279,023 / 2.02%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	799,321 / 5.8%
Duplication rate	4.72%
Clipped reads	5,280,449 / 38.31%

2.2. ACGT Content

Number/percentage of A's	357,564,974 / 28.59%
Number/percentage of C's	246,022,622 / 19.67%
Number/percentage of T's	364,506,399 / 29.15%
Number/percentage of G's	282,485,579 / 22.59%
Number/percentage of N's	54,273 / 0%

GC Percentage	42.26%

2.3. Coverage

Mean	0.4043
Standard Deviation	1.7097

2.4. Mapping Quality

Mean Mapping Quality	53.22

2.5. Insert size

Mean	202,929.35
Standard Deviation	4,400,697.52
P25/Median/P75	142 / 183 / 245

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	11,438,158
Insertions	204,714
Mapped reads with at least one insertion	1.48%
Deletions	645,494
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.52%

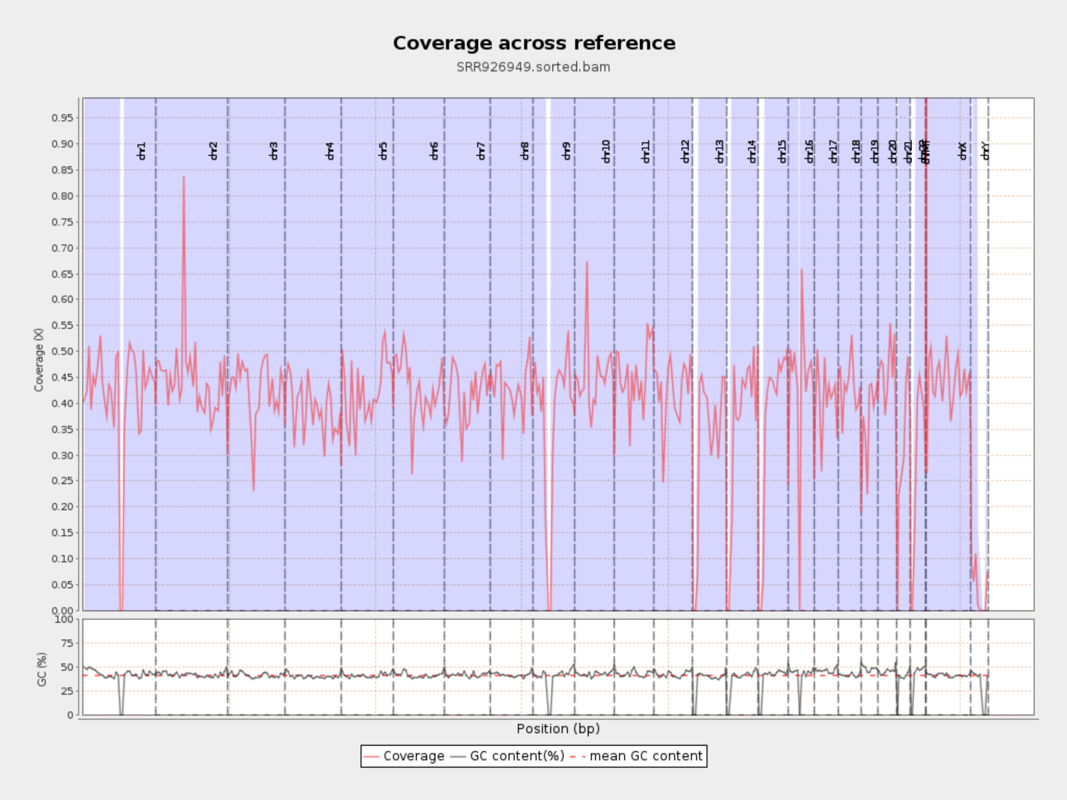
2.7. Chromosome stats

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

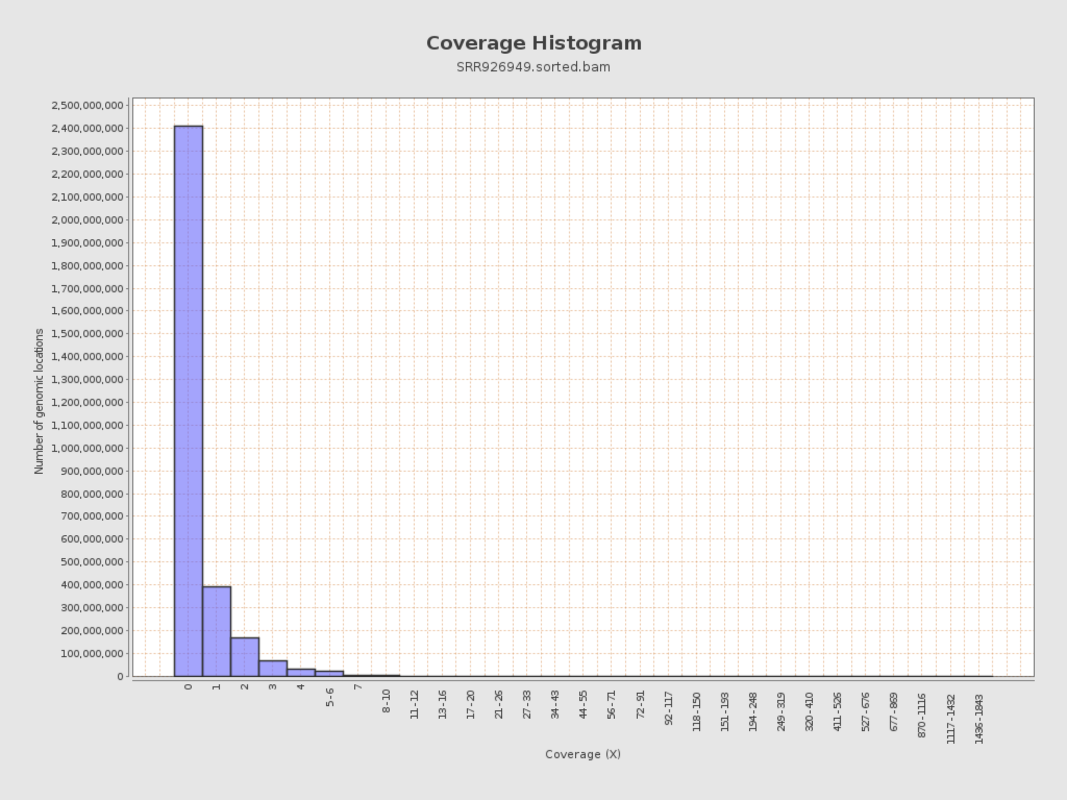
		bases	**coverage**	**deviation**
chr1	249250621	103309436	0.4145	2.1498
chr2	243199373	109095266	0.4486	3.0005
chr3	198022430	83923152	0.4238	1.0039
chr4	191154276	75097641	0.3929	1.2826
chr5	180915260	76494190	0.4228	0.9871
chr6	171115067	73422691	0.4291	1.1929
chr7	159138663	65970118	0.4145	1.2471
chr8	146364022	62590885	0.4276	1.1175
chr9	141213431	52624961	0.3727	1.9229
chr10	135534747	61188123	0.4515	3.169
chr11	135006516	60751363	0.45	1.9448
chr12	133851895	57119870	0.4267	1.047
chr13	115169878	37575770	0.3263	0.8663
chr14	107349540	38159623	0.3555	0.9361
chr15	102531392	36410718	0.3551	0.9346
chr16	90354753	38859761	0.4301	2.2778
chr17	81195210	33419326	0.4116	1.2905
chr18	78077248	33690561	0.4315	1.9626
chr19	59128983	21807040	0.3688	1.5865
chr20	63025520	29378067	0.4661	1.1513
chr21	48129895	14996228	0.3116	1.083
chr22	51304566	14522493	0.2831	0.8667
chrMT	16571	179236	10.8162	8.234
chrX	155270560	68554605	0.4415	1.1722

chrY	59373566	2417428	0.0407	1.1012

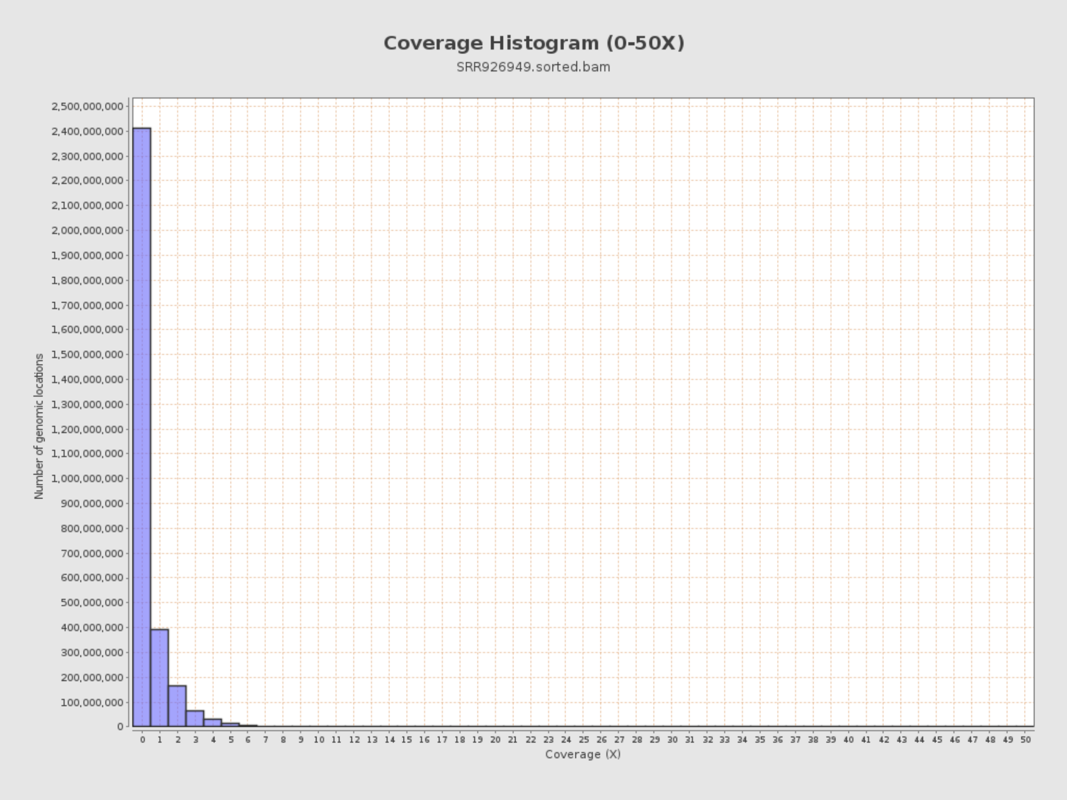
3. Results : Coverage across reference



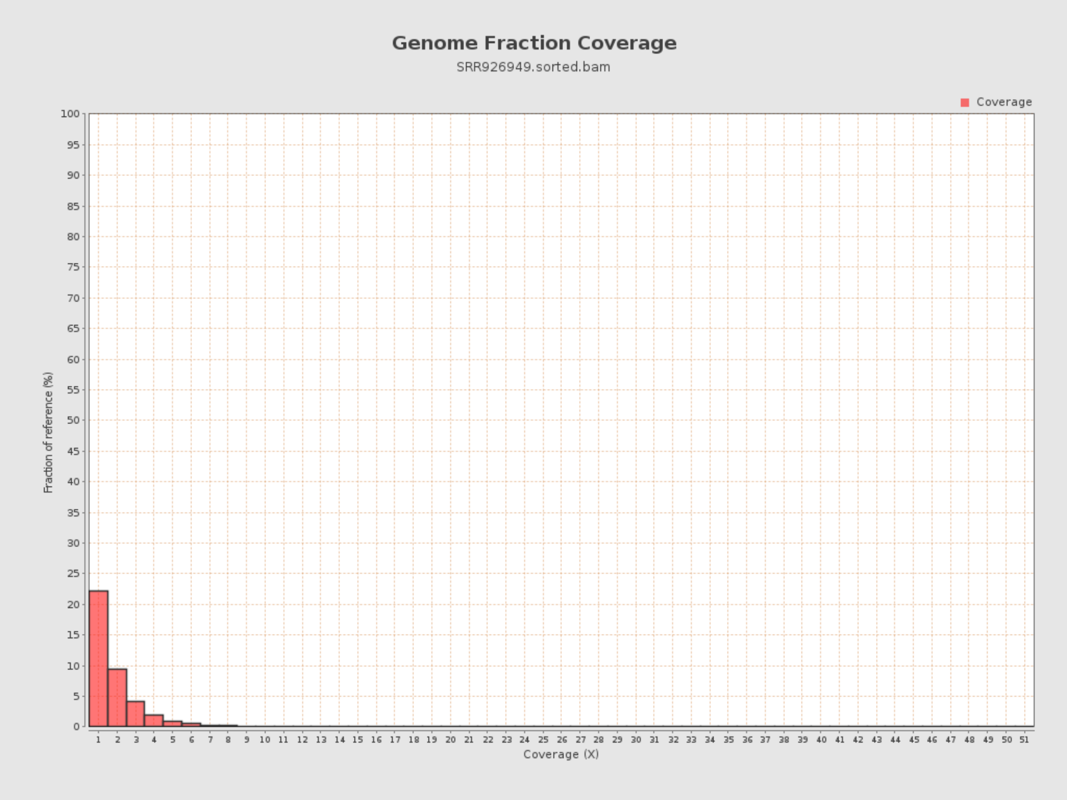
4. Results : Coverage Histogram



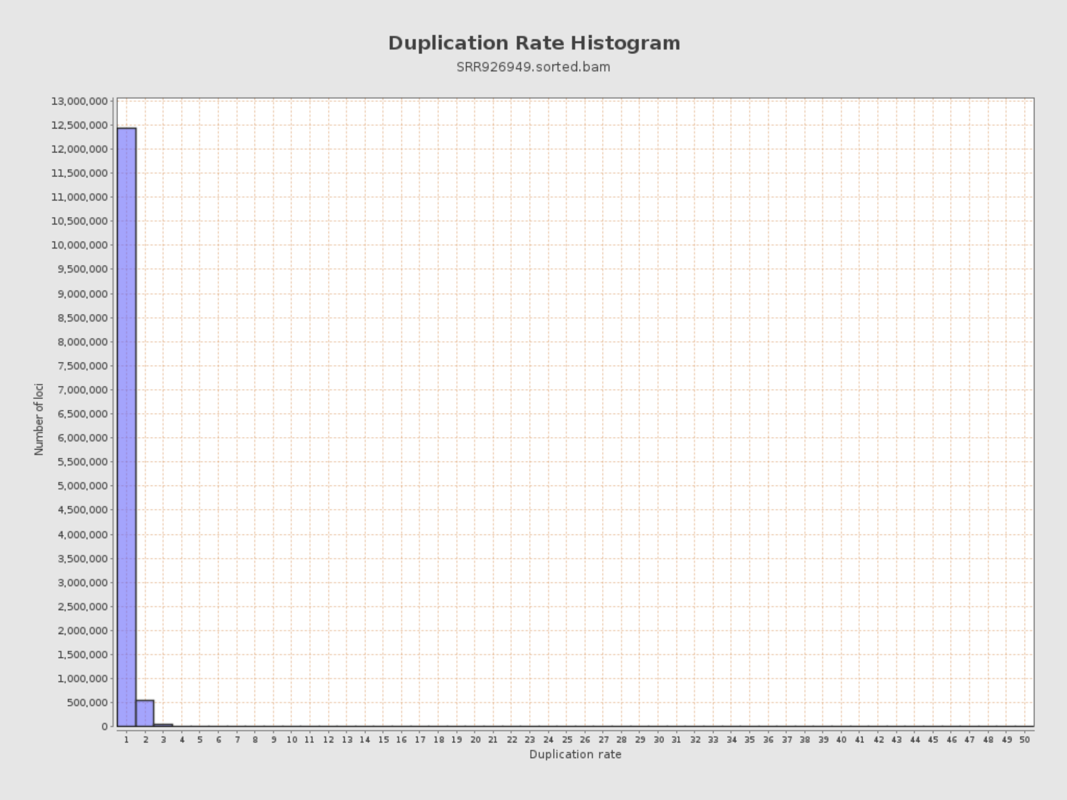
5. Results : Coverage Histogram (0-50X)



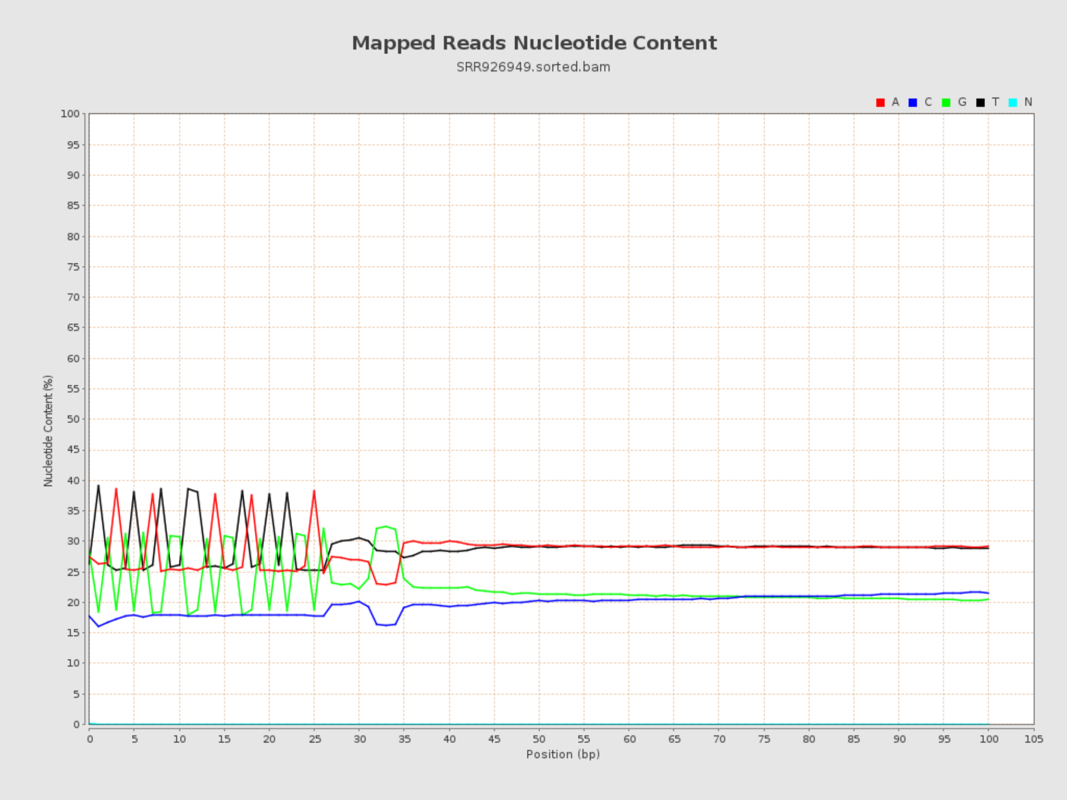
6. Results : Genome Fraction Coverage



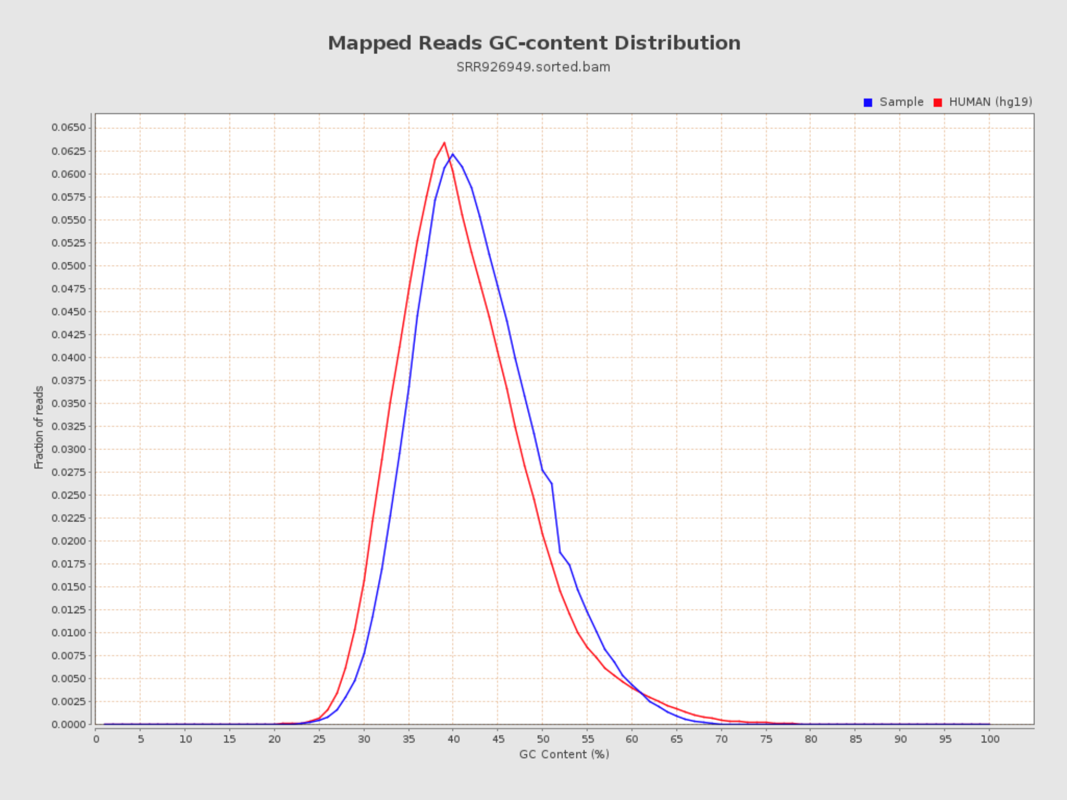
7. Results : Duplication Rate Histogram



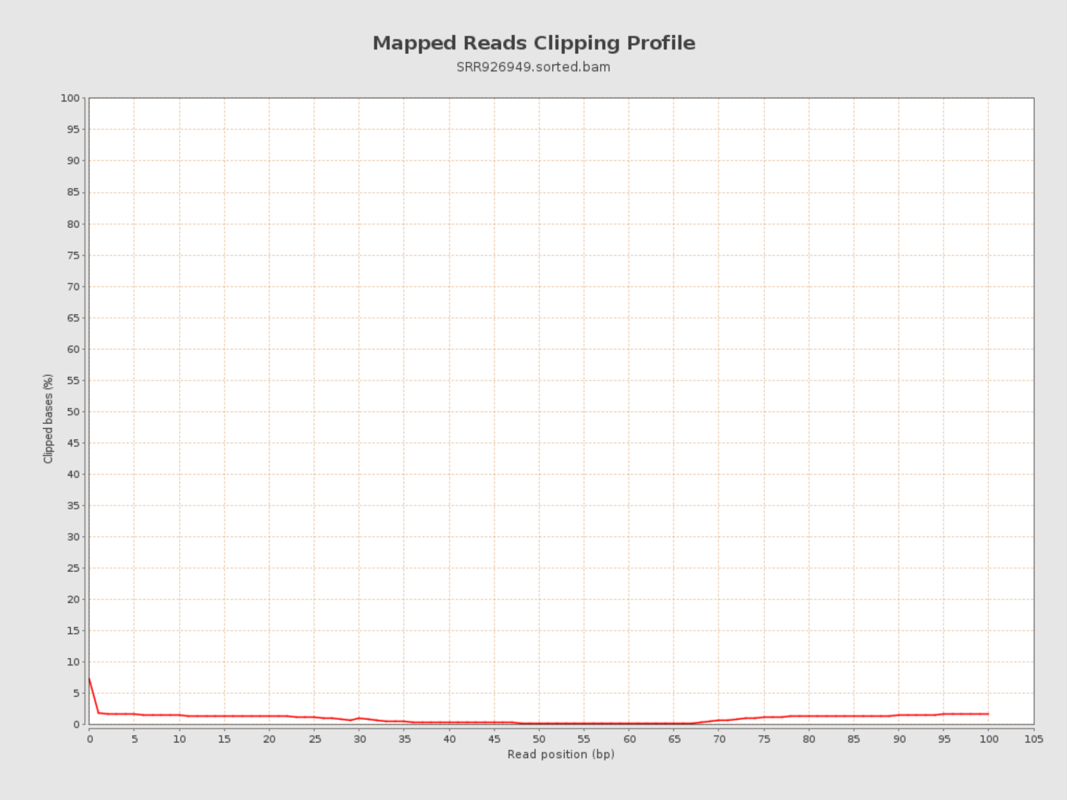
8. Results : Mapped Reads Nucleotide Content



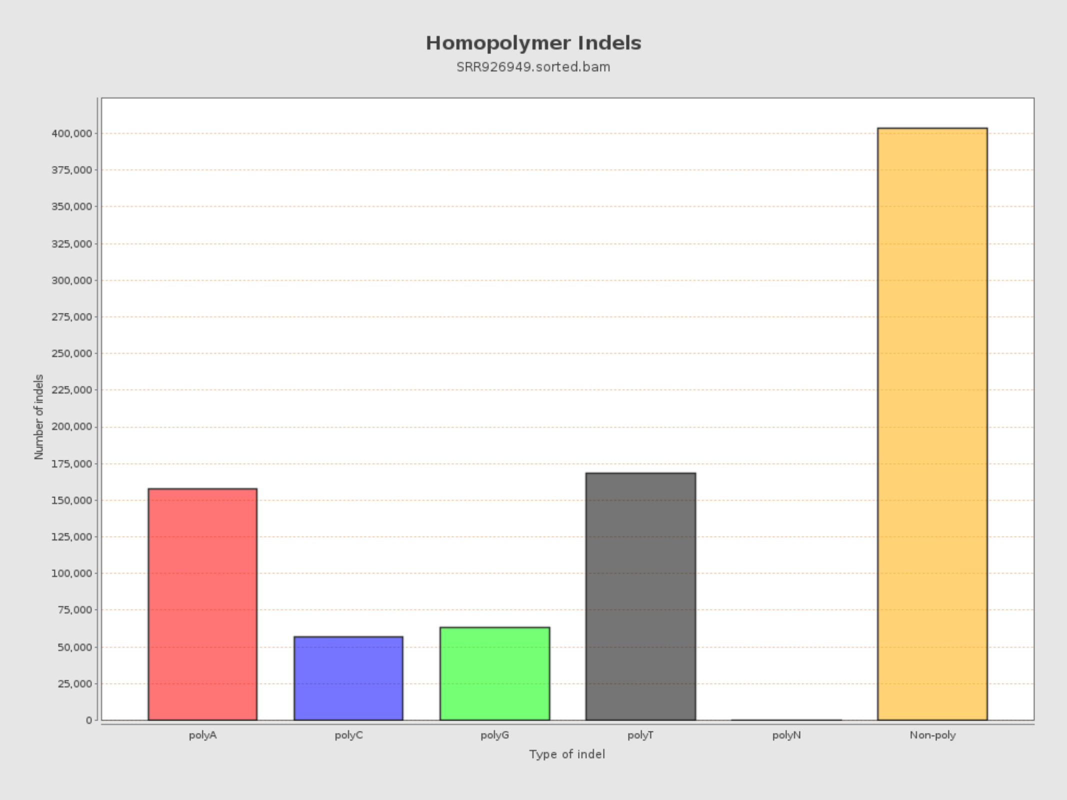
9. Results : Mapped Reads GC-content Distribution



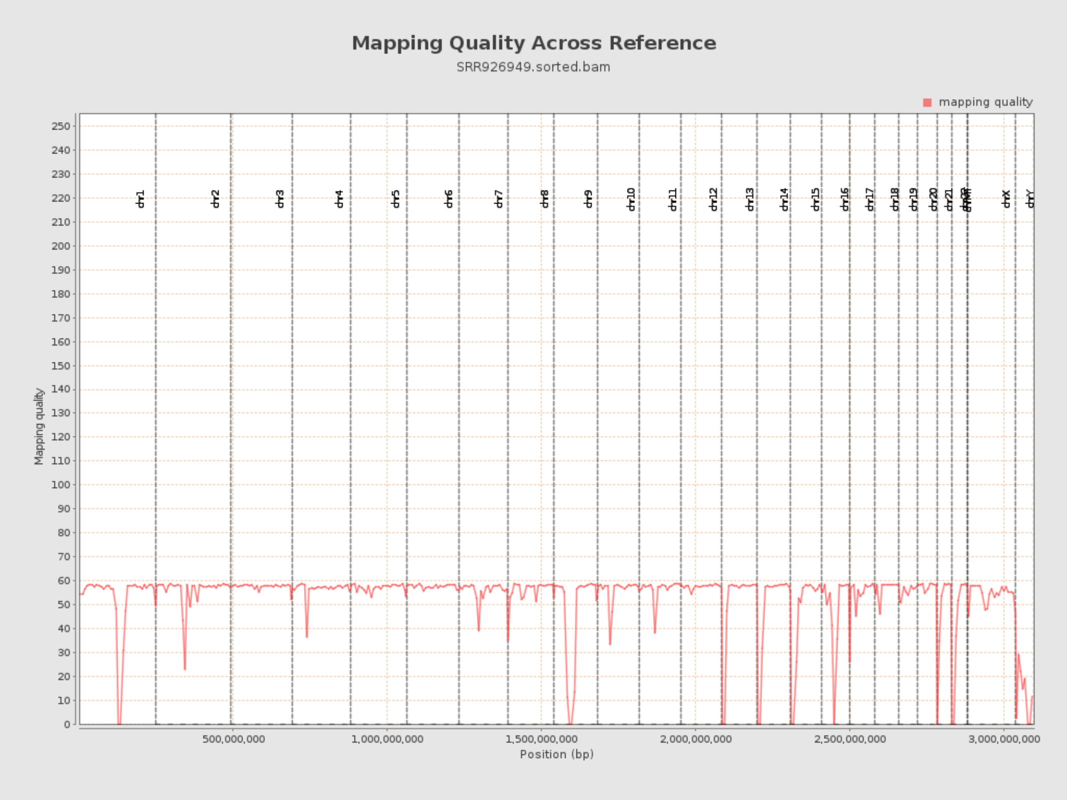
10. Results : Mapped Reads Clipping Profile



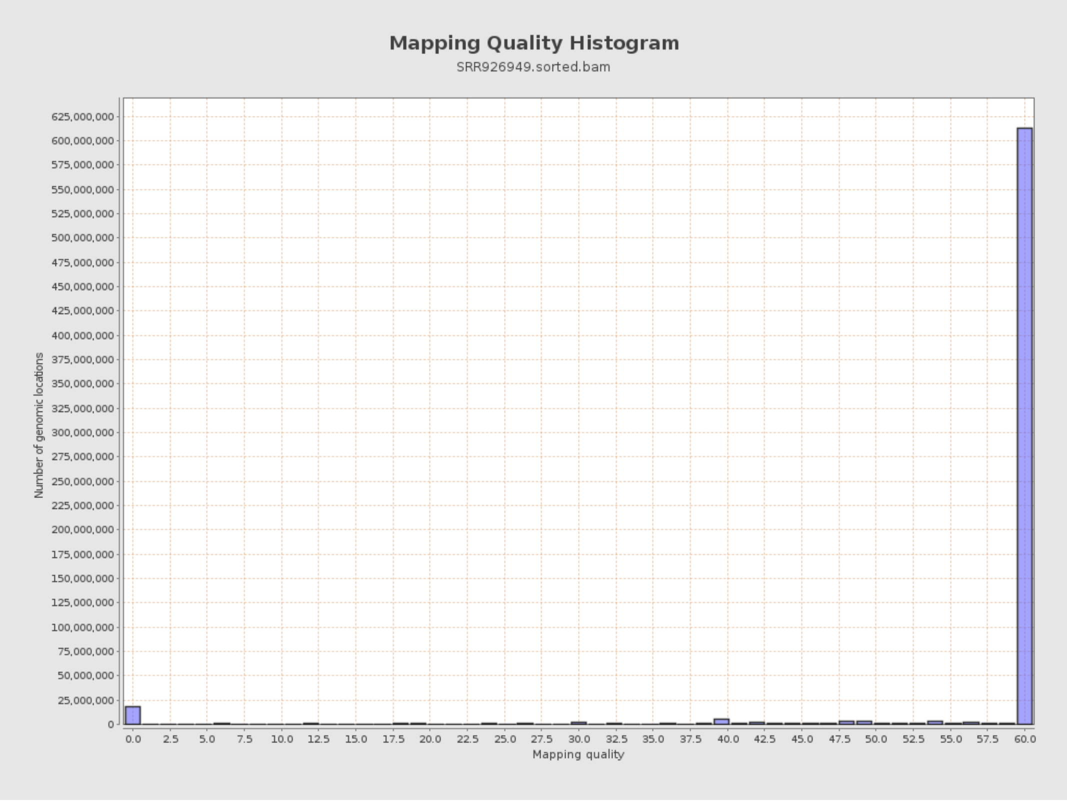
11. Results : Homopolymer Indels



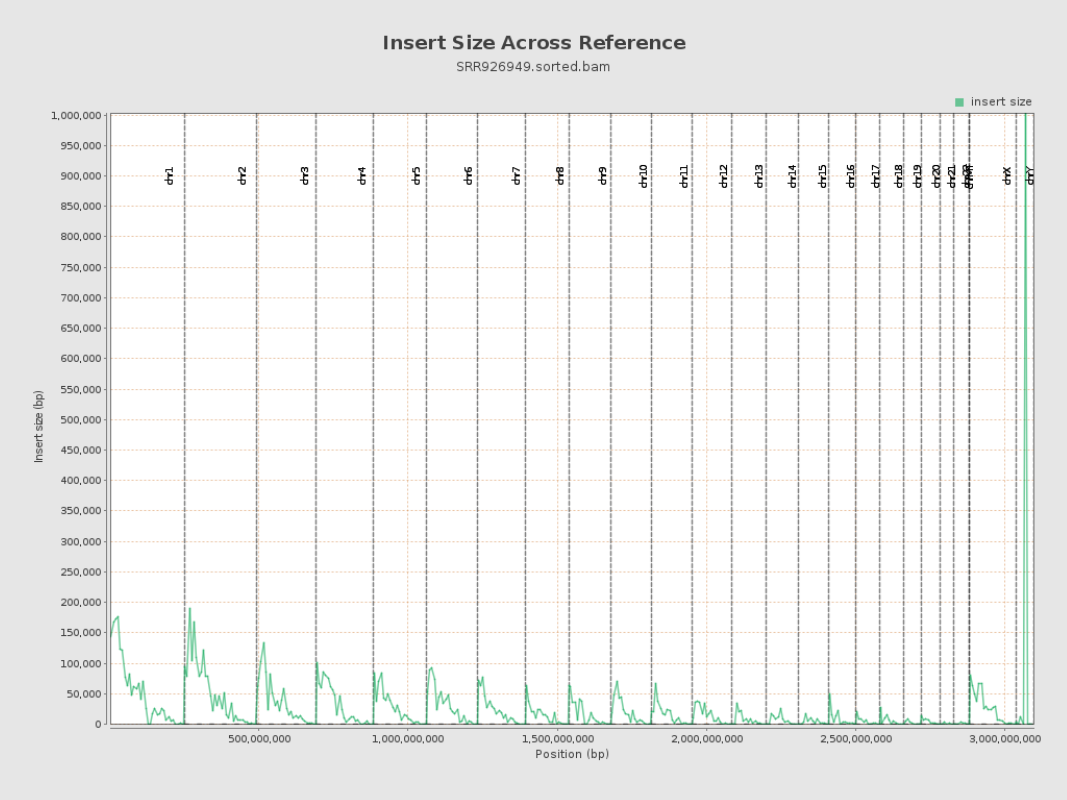
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram