Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 09:50:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926904.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_SRR926904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926904_1.fastq.gz SRR926904_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 09:50:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,046,832
Mapped reads	20,085,920 / 87.15%
Unmapped reads	2,960,912 / 12.85%
Mapped paired reads	20,085,920 / 87.15%
Mapped reads, first in pair	10,084,420 / 43.76%
Mapped reads, second in pair	10,001,500 / 43.4%
Mapped reads, both in pair	19,768,300 / 85.77%
Mapped reads, singletons	317,620 / 1.38%
Secondary alignments	0
Supplementary alignments	353,579 / 1.53%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	1,632,415 / 7.08%
Duplication rate	6.52%
Clipped reads	7,158,163 / 31.06%

2.2. ACGT Content

Number/percentage of A's	528,954,651 / 28.58%
Number/percentage of C's	364,422,385 / 19.69%
Number/percentage of T's	535,623,715 / 28.94%
Number/percentage of G's	421,877,277 / 22.79%
Number/percentage of N's	156,018 / 0.01%

GC Percentage	42.48%

2.3. Coverage

Mean	0.5984
Standard Deviation	2.7678

2.4. Mapping Quality

Mean Mapping Quality	49.07

2.5. Insert size

Mean	295,889.83
Standard Deviation	5,449,860.01
P25/Median/P75	144 / 187 / 252

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	19,255,507
Insertions	310,269
Mapped reads with at least one insertion	1.52%
Deletions	1,010,044
Mapped reads with at least one deletion	4.89%
Homopolymer indels	52.64%

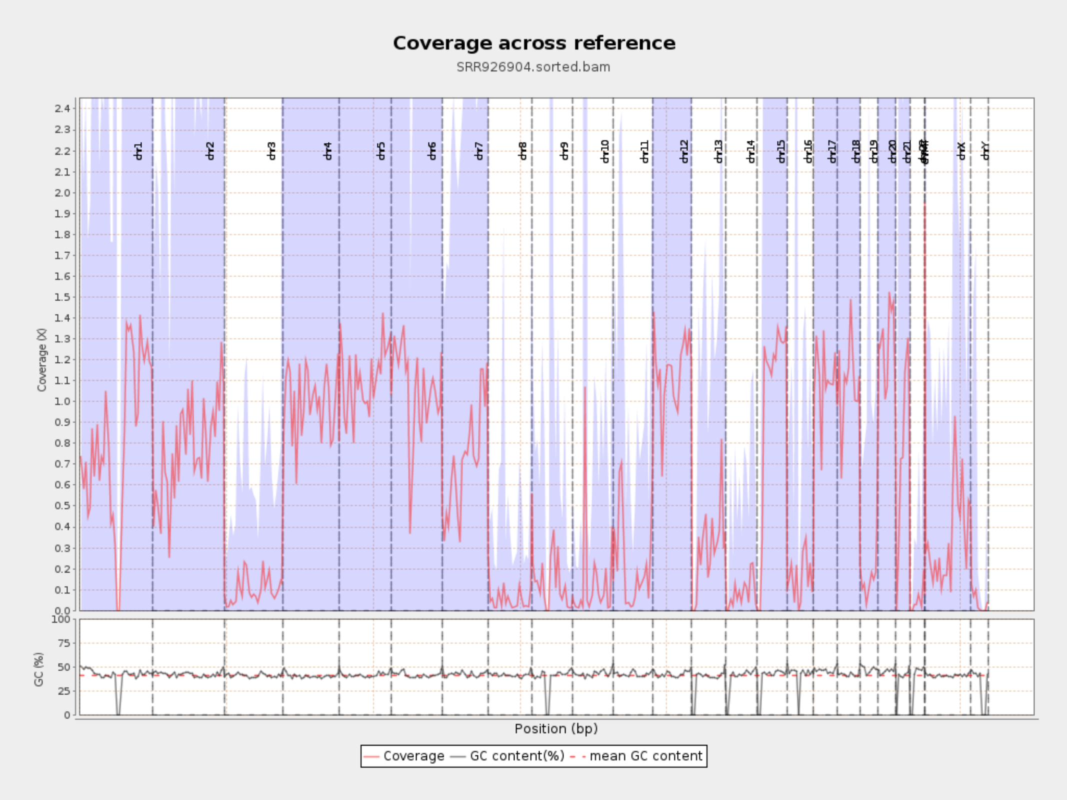
2.7. Chromosome stats

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

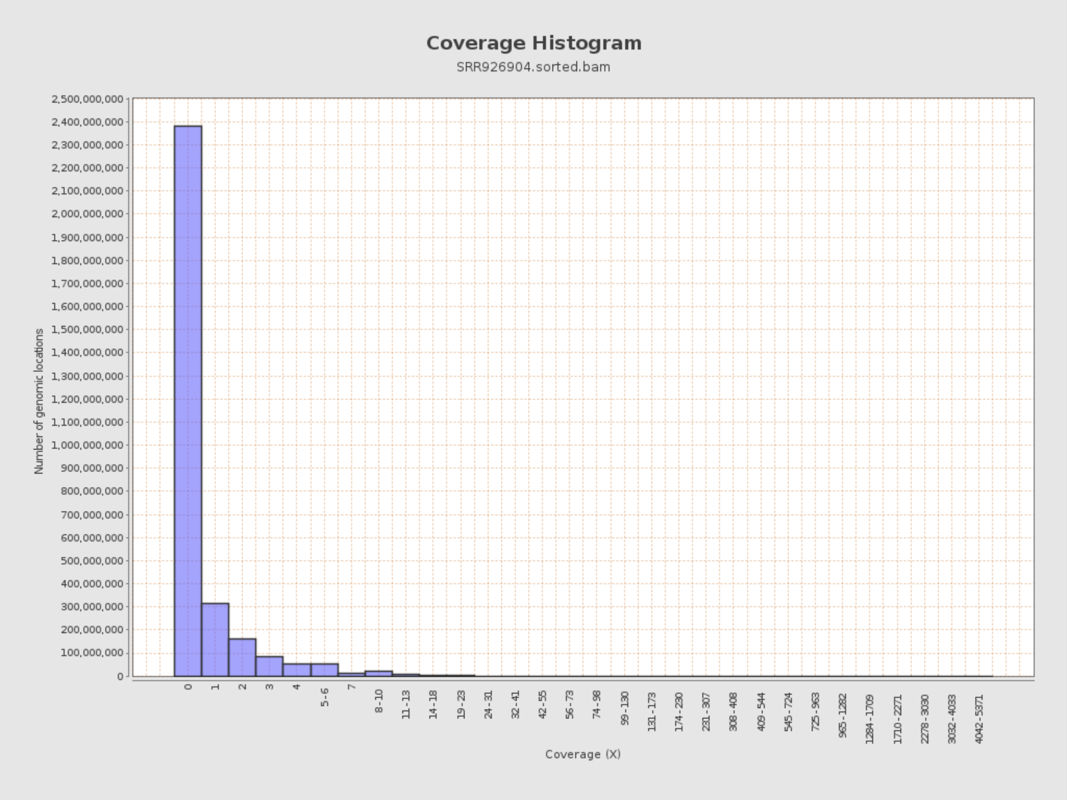
		bases	coverage	deviation
chr1	249250621	206489138	0.8284	2.2761
chr2	243199373	190269570	0.7824	3.011
chr3	198022430	20191382	0.102	0.7523
chr4	191154276	191823261	1.0035	2.0044
chr5	180915260	201228082	1.1123	2.1165
chr6	171115067	180533111	1.055	2.5569
chr7	159138663	115084225	0.7232	1.7196
chr8	146364022	7200392	0.0492	0.5597
chr9	141213431	17974233	0.1273	1.6038
chr10	135534747	18884483	0.1393	9.6401
chr11	135006516	29415835	0.2179	0.9197
chr12	133851895	152829116	1.1418	2.2193
chr13	115169878	34263769	0.2975	1.0023
chr14	107349540	8896229	0.0829	0.5559
chr15	102531392	102435565	0.9991	2.1281
chr16	90354753	14063340	0.1556	1.3976
chr17	81195210	89312270	1.1	2.4242
chr18	78077248	86473374	1.1075	2.442
chr19	59128983	8344239	0.1411	1.1156
chr20	63025520	80818543	1.2823	2.422
chr21	48129895	37493720	0.779	1.9461
chr22	51304566	2861536	0.0558	0.4844
chrMT	16571	32404	1.9555	2.2436
chrX	155270560	53234788	0.3429	1.1359

chrY	59373566	2326589	0.0392	0.8284

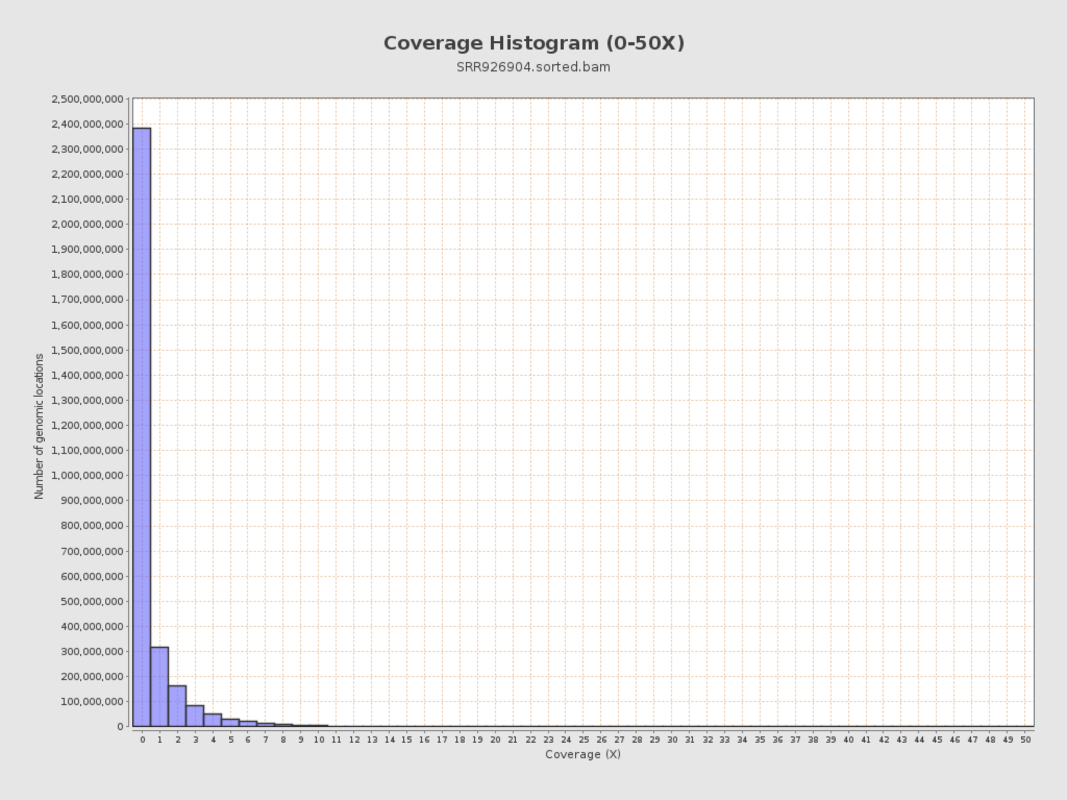
3. Results : Coverage across reference



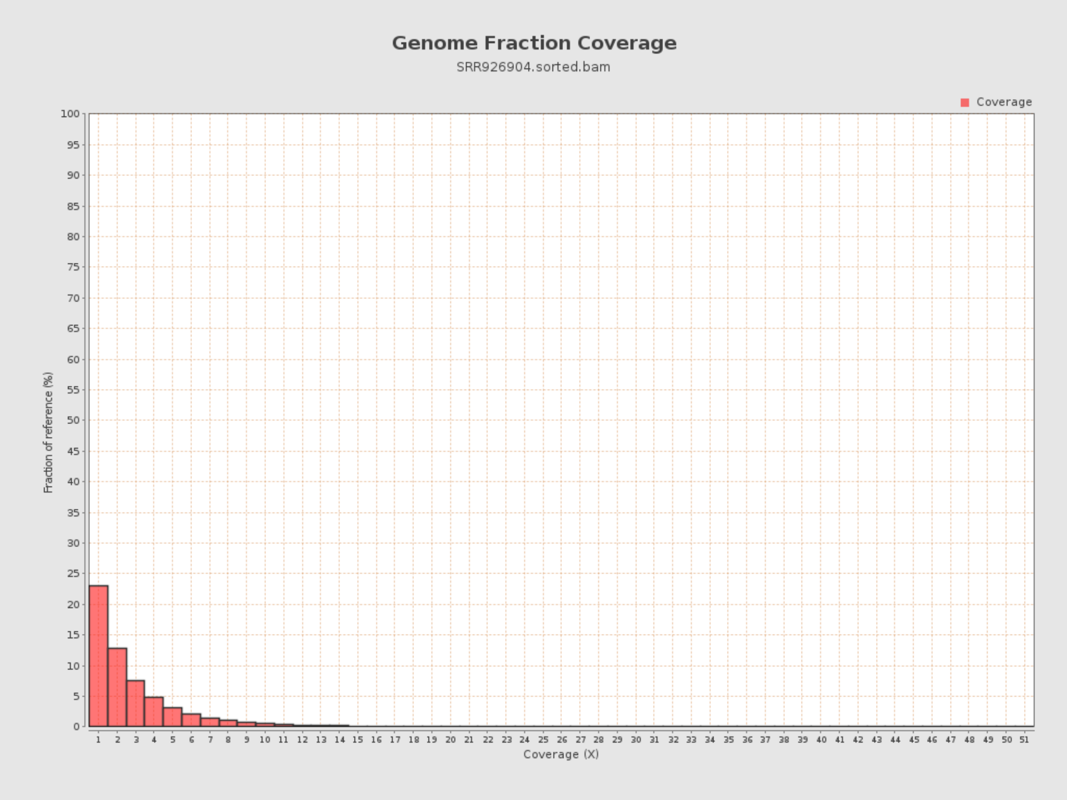
4. Results : Coverage Histogram



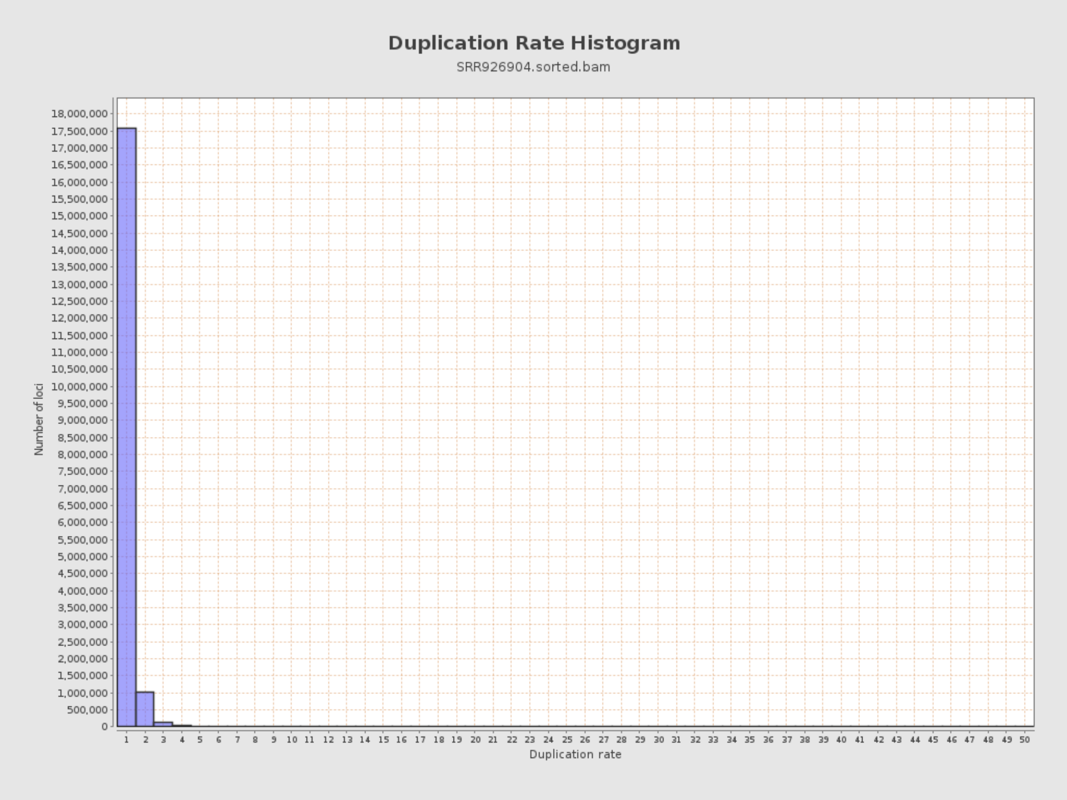
5. Results : Coverage Histogram (0-50X)



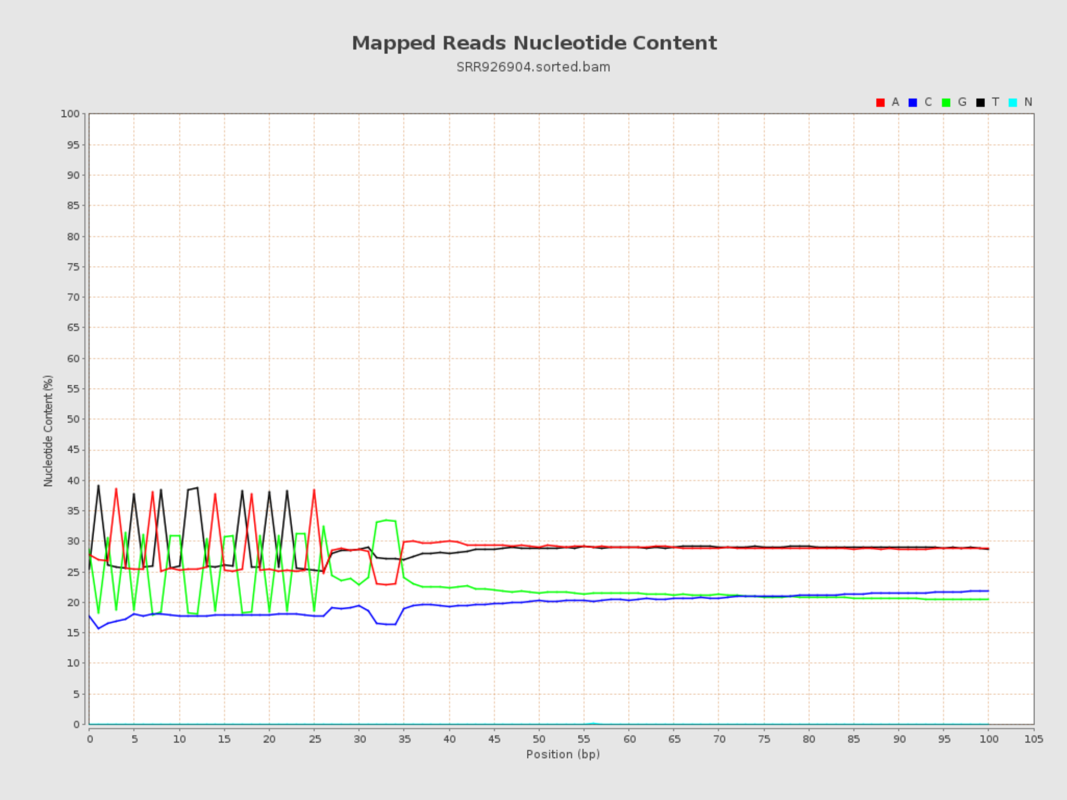
6. Results : Genome Fraction Coverage



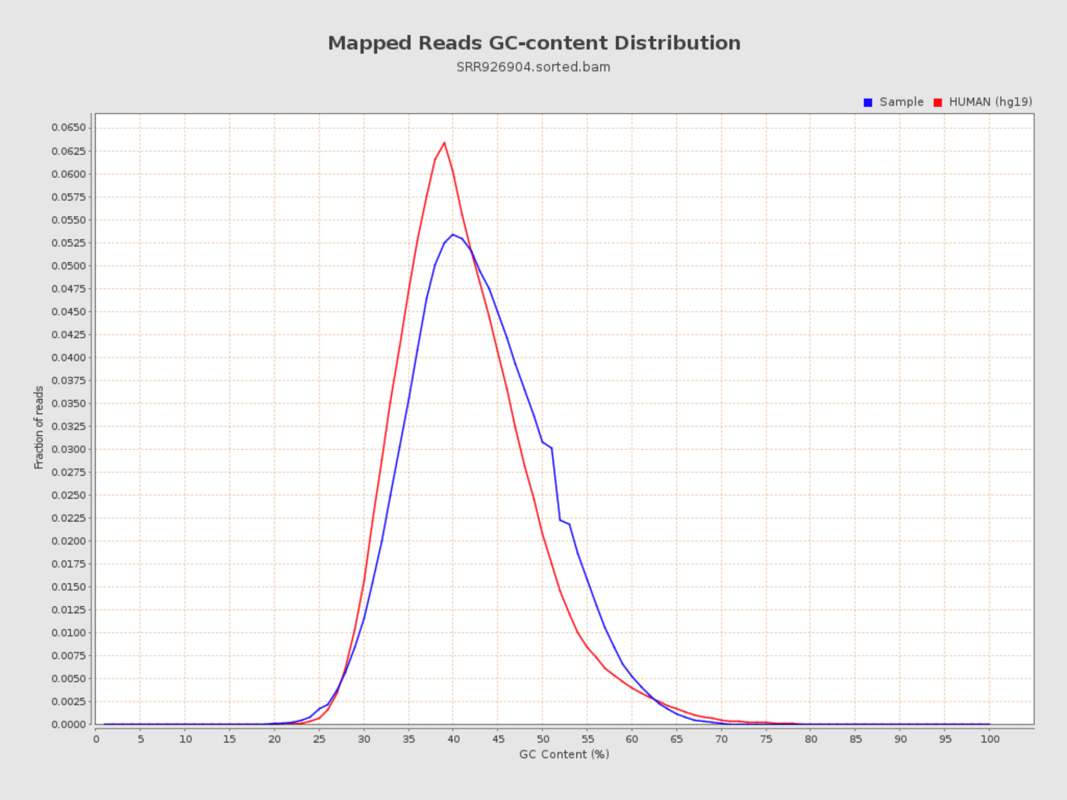
7. Results : Duplication Rate Histogram



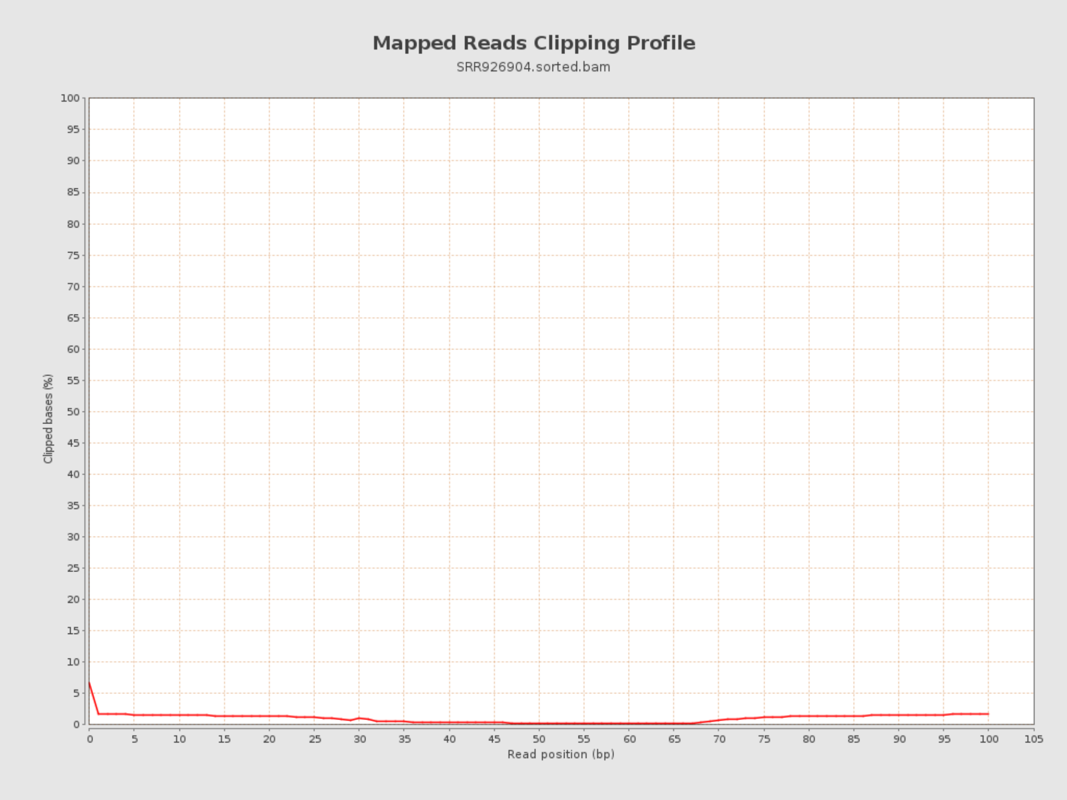
8. Results : Mapped Reads Nucleotide Content



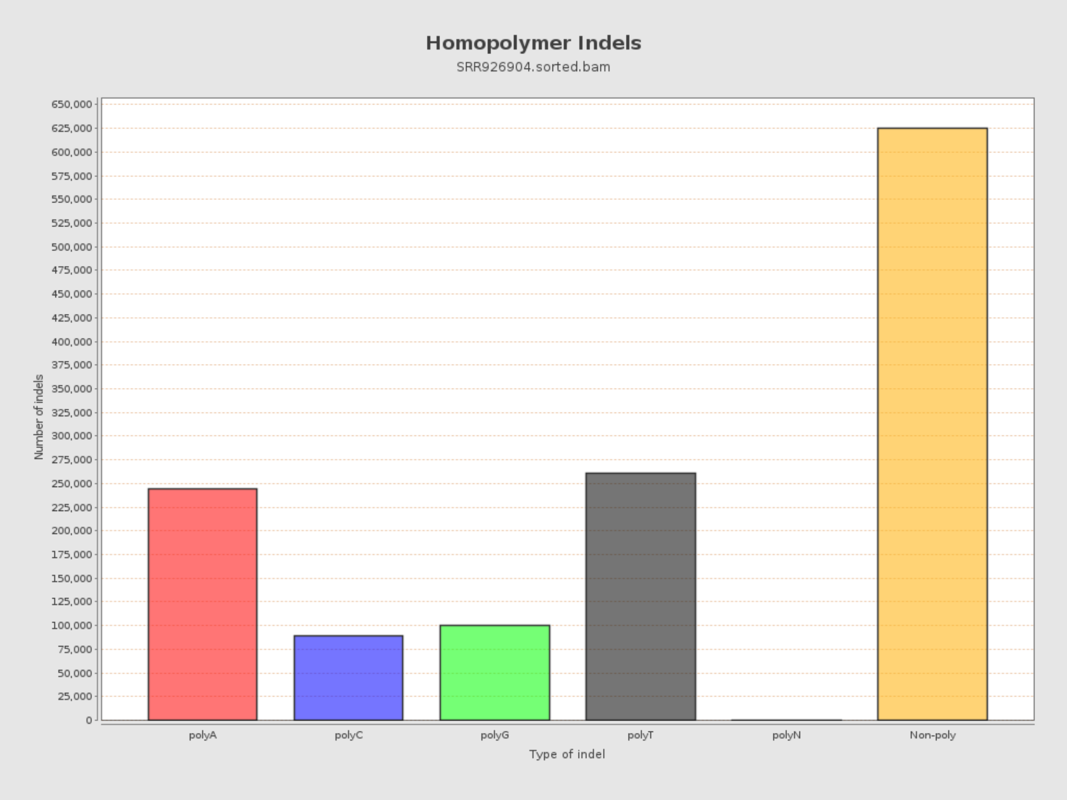
9. Results : Mapped Reads GC-content Distribution



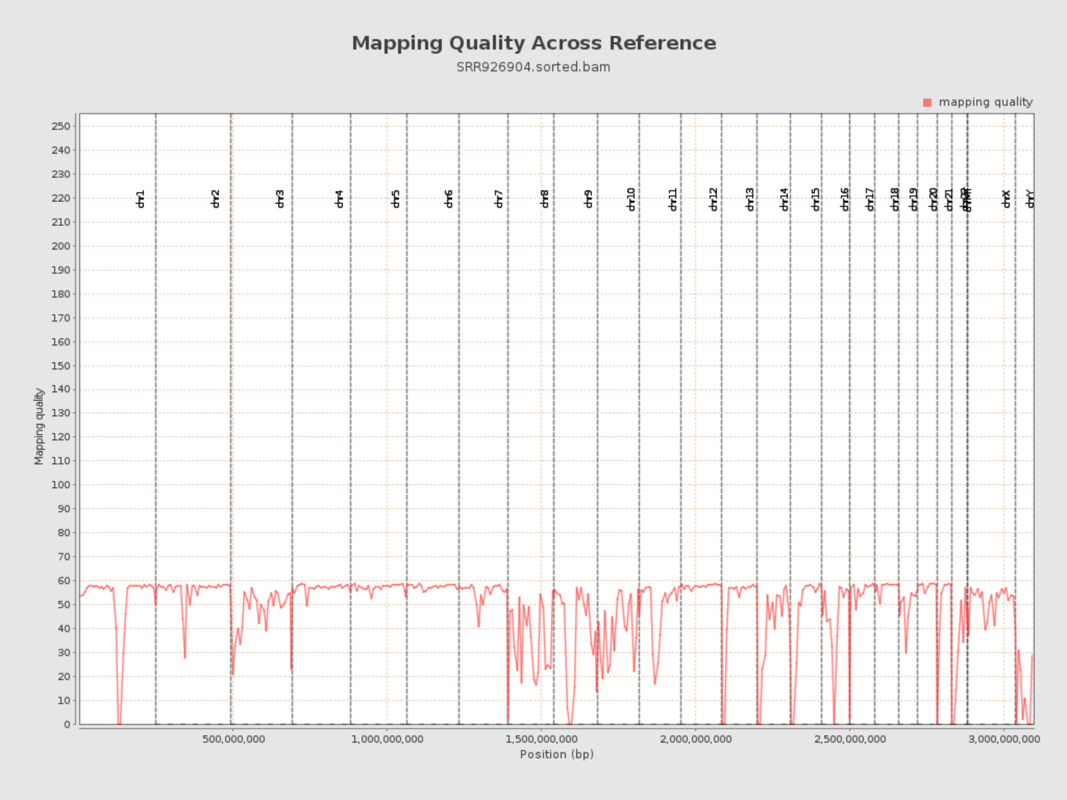
10. Results : Mapped Reads Clipping Profile



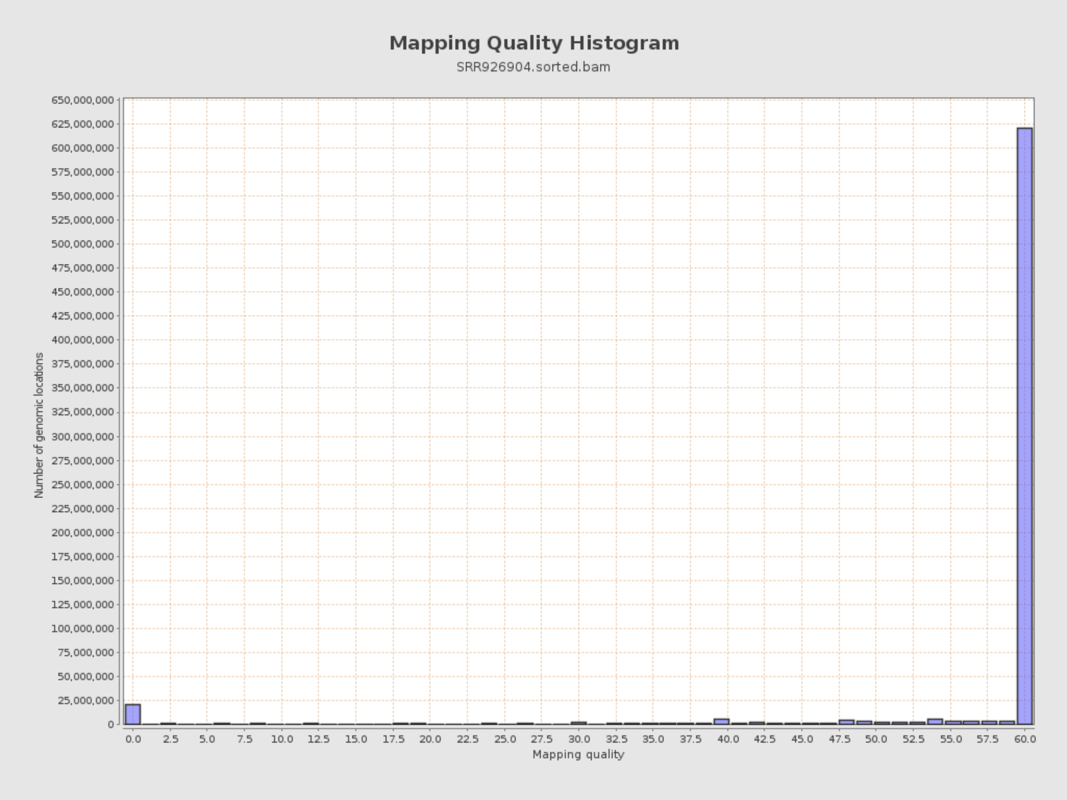
11. Results : Homopolymer Indels



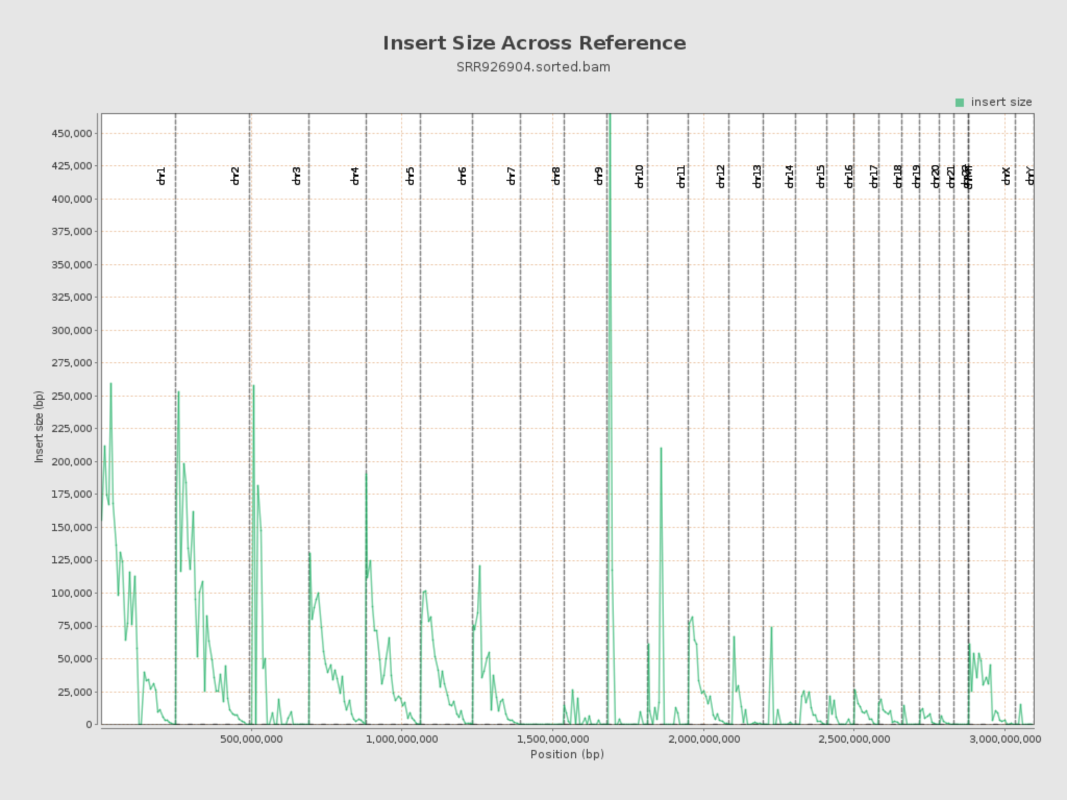
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram