Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 01:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926948.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_SRR926948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926948_1.fastq.gz SRR926948_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 01:24:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,140,640
Mapped reads	14,885,767 / 98.32%
Unmapped reads	254,873 / 1.68%
Mapped paired reads	14,885,767 / 98.32%
Mapped reads, first in pair	7,449,083 / 49.2%
Mapped reads, second in pair	7,436,684 / 49.12%
Mapped reads, both in pair	14,737,092 / 97.33%
Mapped reads, singletons	148,675 / 0.98%
Secondary alignments	0
Supplementary alignments	363,503 / 2.4%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	933,030 / 6.16%
Duplication rate	4.77%
Clipped reads	6,703,878 / 44.28%

2.2. ACGT Content

Number/percentage of A's	388,690,761 / 28.32%
Number/percentage of C's	276,154,699 / 20.12%
Number/percentage of T's	394,492,897 / 28.74%
Number/percentage of G's	313,001,517 / 22.81%
Number/percentage of N's	51,047 / 0%

GC Percentage	42.93%

2.3. Coverage

Mean	0.4436
Standard Deviation	2.2053

2.4. Mapping Quality

Mean Mapping Quality	53.24

2.5. Insert size

Mean	260,253.28
Standard Deviation	5,014,282.56
P25/Median/P75	139 / 177 / 234

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	12,107,847
Insertions	229,022
Mapped reads with at least one insertion	1.51%
Deletions	661,319
Mapped reads with at least one deletion	4.33%
Homopolymer indels	51.41%

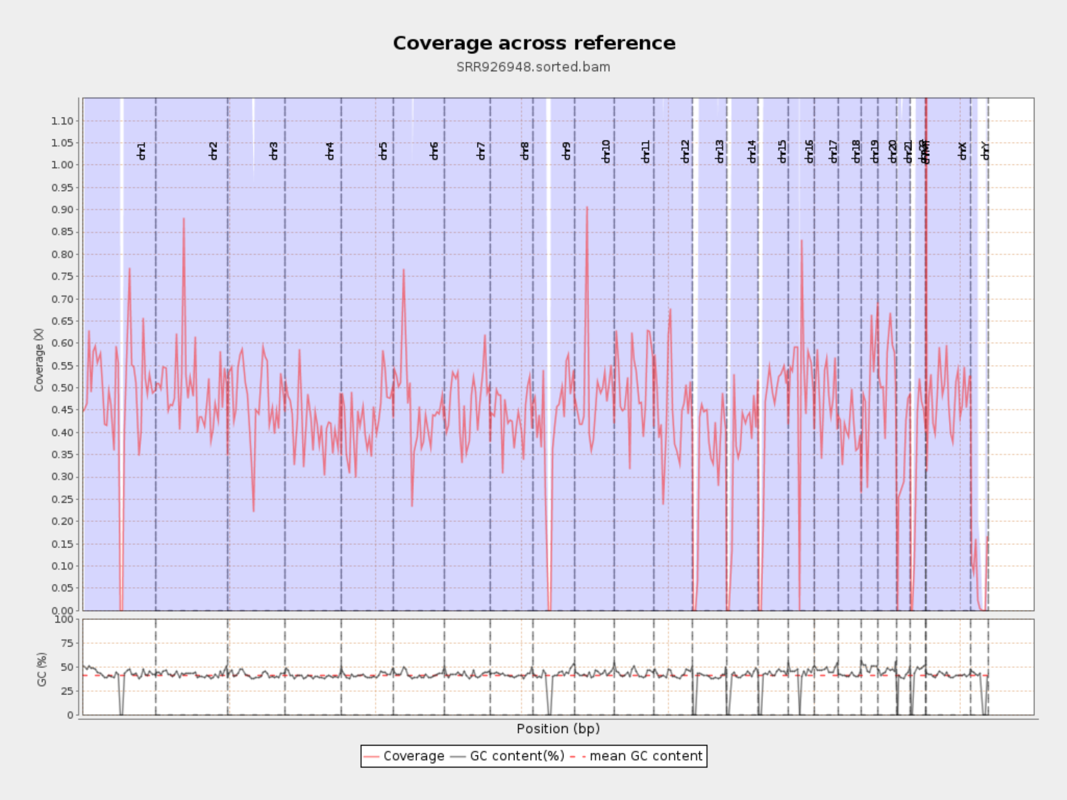
2.7. Chromosome stats

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

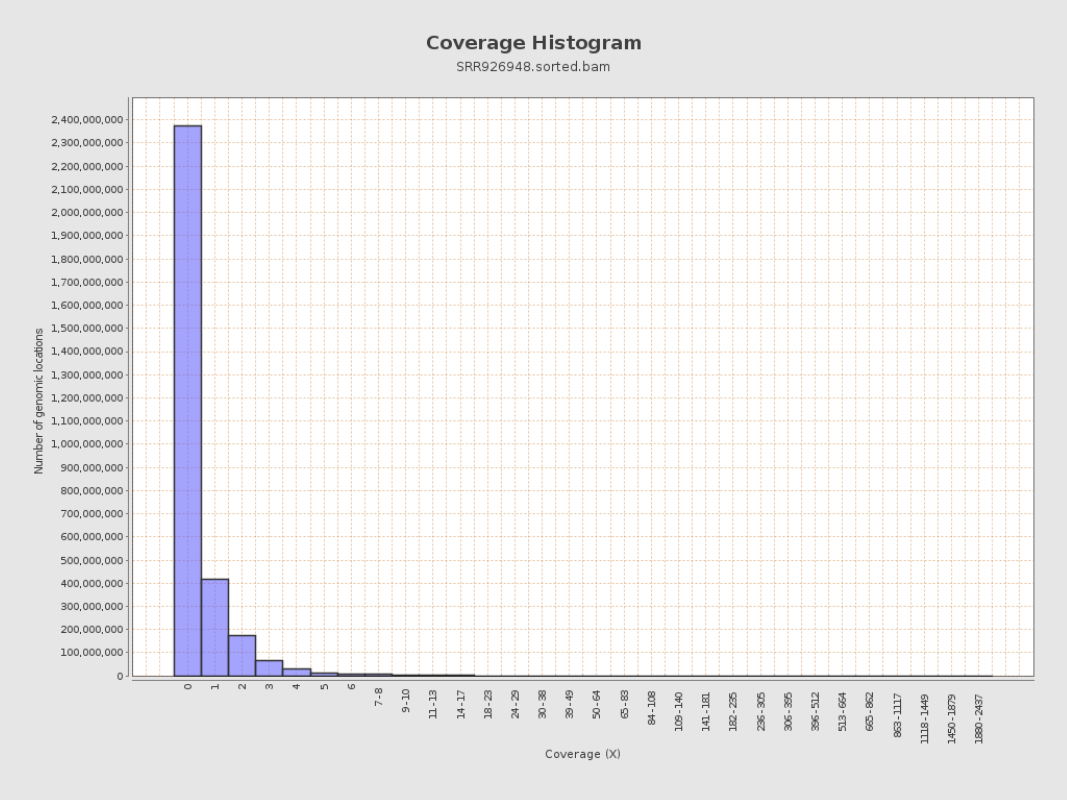
		bases	coverage	deviation
chr1	249250621	120730344	0.4844	2.5895
chr2	243199373	121252142	0.4986	3.5239
chr3	198022430	93771948	0.4735	1.2436
chr4	191154276	80377991	0.4205	1.9156
chr5	180915260	77994351	0.4311	1.152
chr6	171115067	78049075	0.4561	1.4868
chr7	159138663	74212188	0.4663	1.7299
chr8	146364022	63733058	0.4354	1.2823
chr9	141213431	57190683	0.405	2.2566
chr10	135534747	65777035	0.4853	4.9616
chr11	135006516	69023360	0.5113	1.838
chr12	133851895	60552799	0.4524	1.349
chr13	115169878	38815209	0.337	0.9705
chr14	107349540	37384893	0.3483	1.0512
chr15	102531392	42411017	0.4136	1.2005
chr16	90354753	46498939	0.5146	3.4656
chr17	81195210	39974247	0.4923	1.7432
chr18	78077248	31412662	0.4023	2.196
chr19	59128983	29769858	0.5035	2.2291
chr20	63025520	34093888	0.541	1.7095
chr21	48129895	15665916	0.3255	1.4386
chr22	51304566	16204945	0.3159	1.0897
chrMT	16571	130557	7.8786	5.2713
chrX	155270560	74377260	0.479	1.3522

chrY	59373566	3966812	0.0668	2.0167

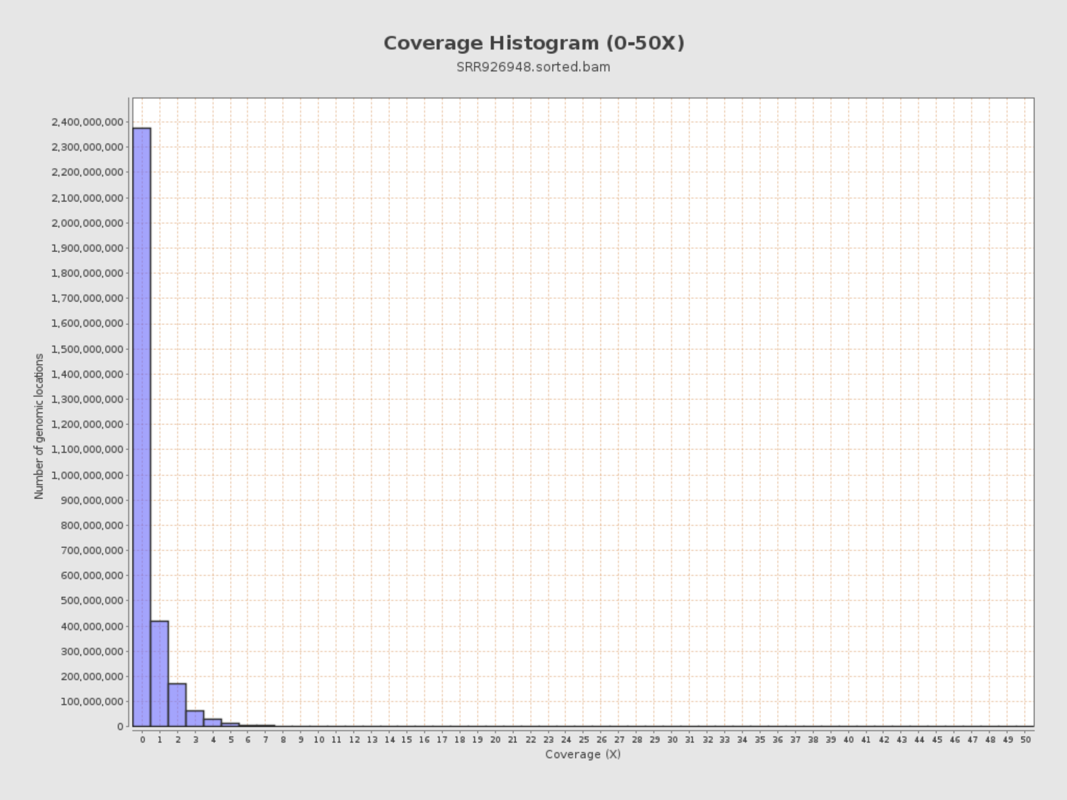
3. Results : Coverage across reference



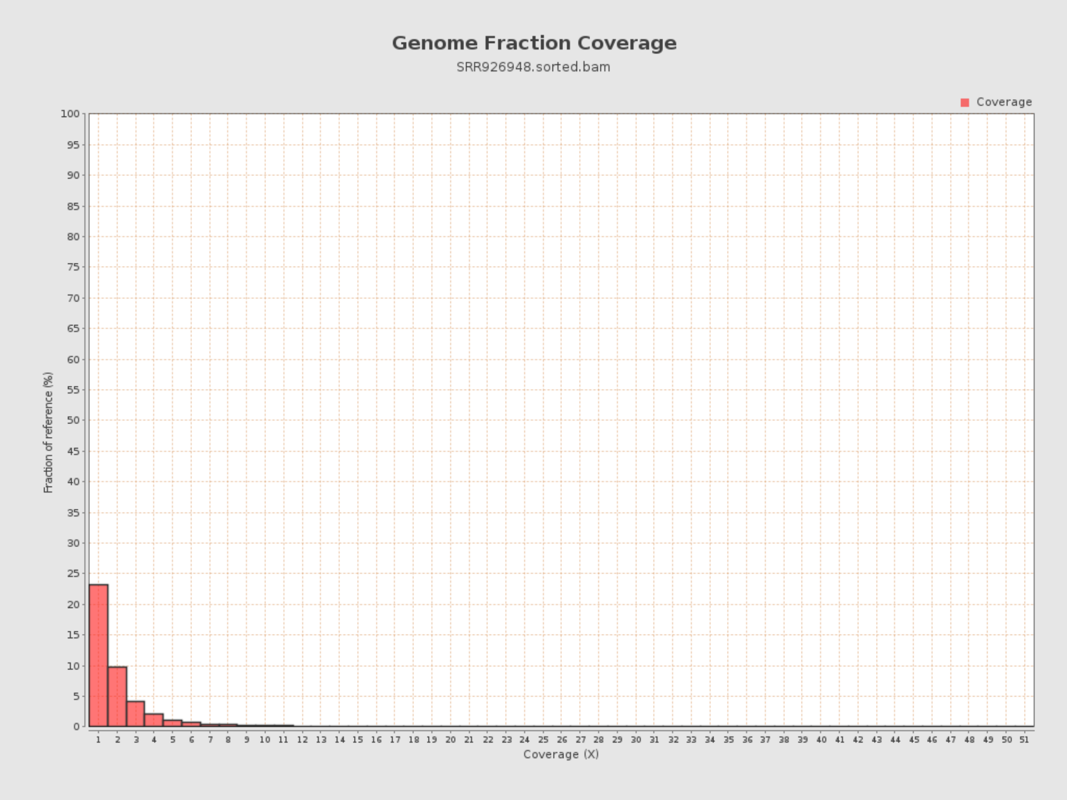
4. Results : Coverage Histogram



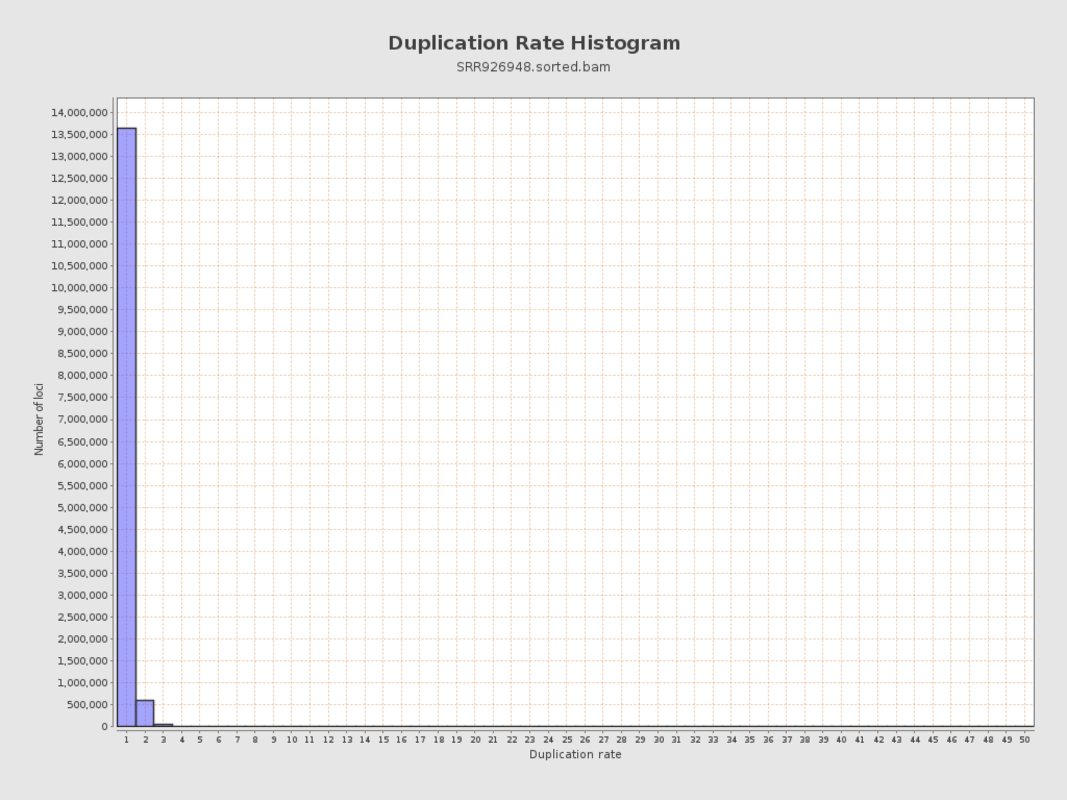
5. Results : Coverage Histogram (0-50X)



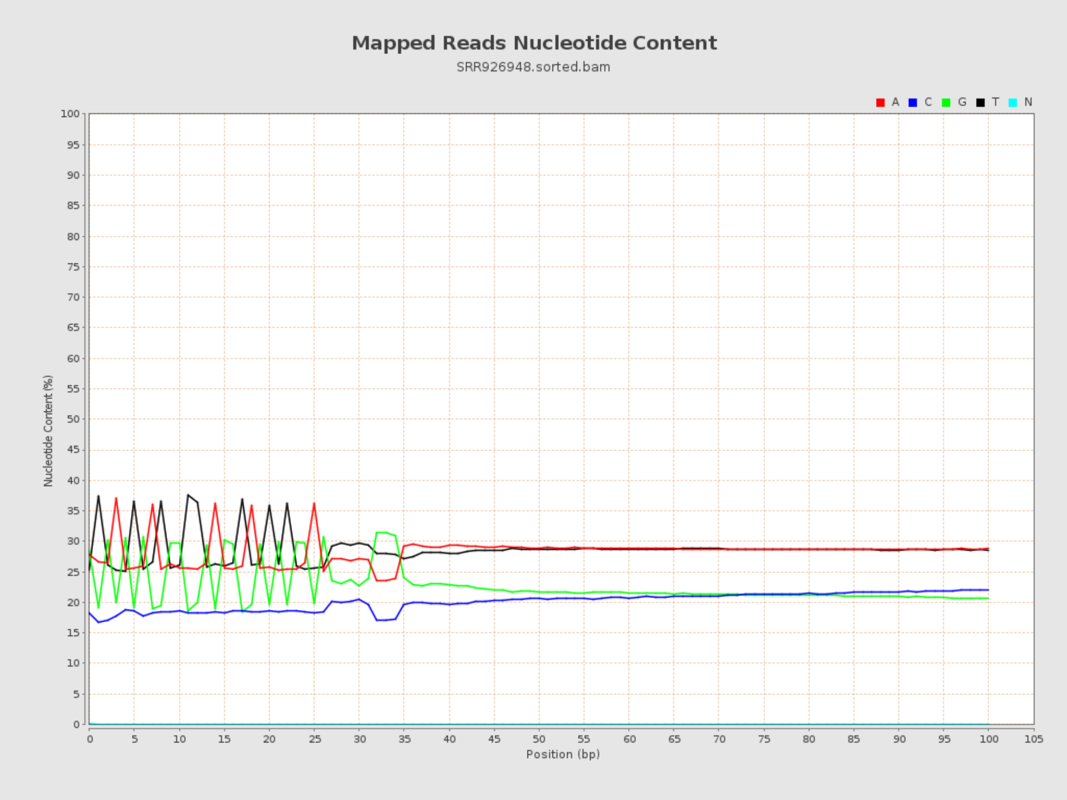
6. Results : Genome Fraction Coverage



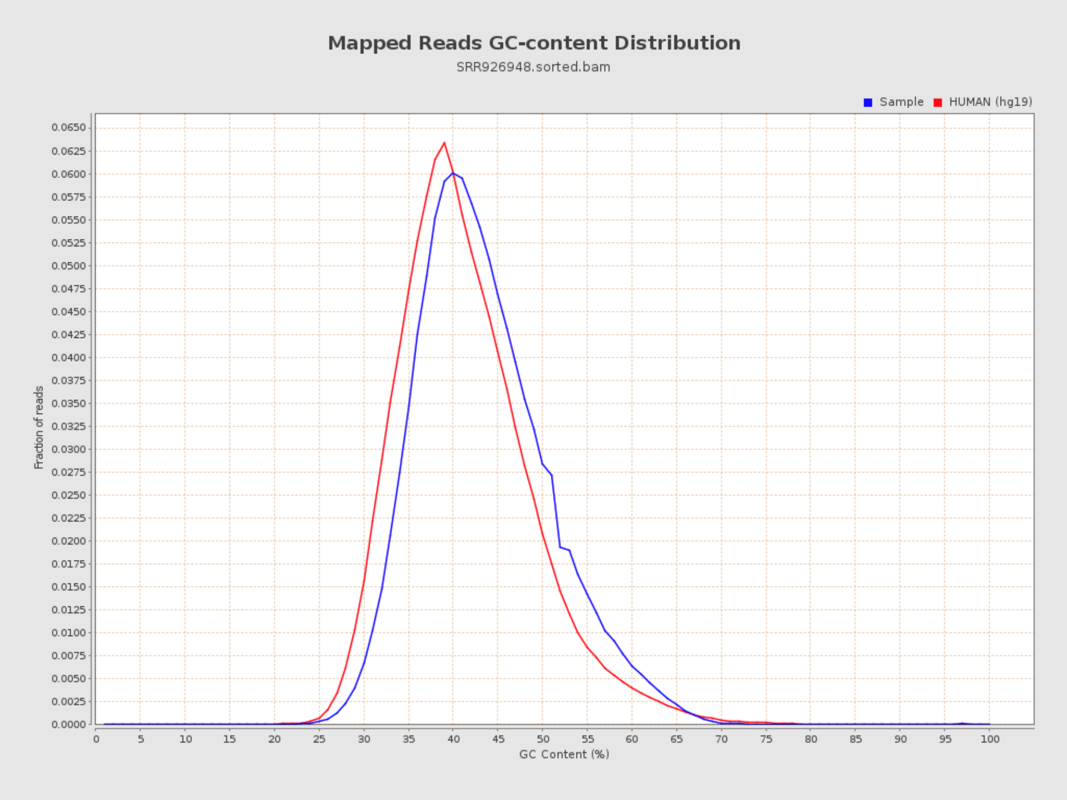
7. Results : Duplication Rate Histogram



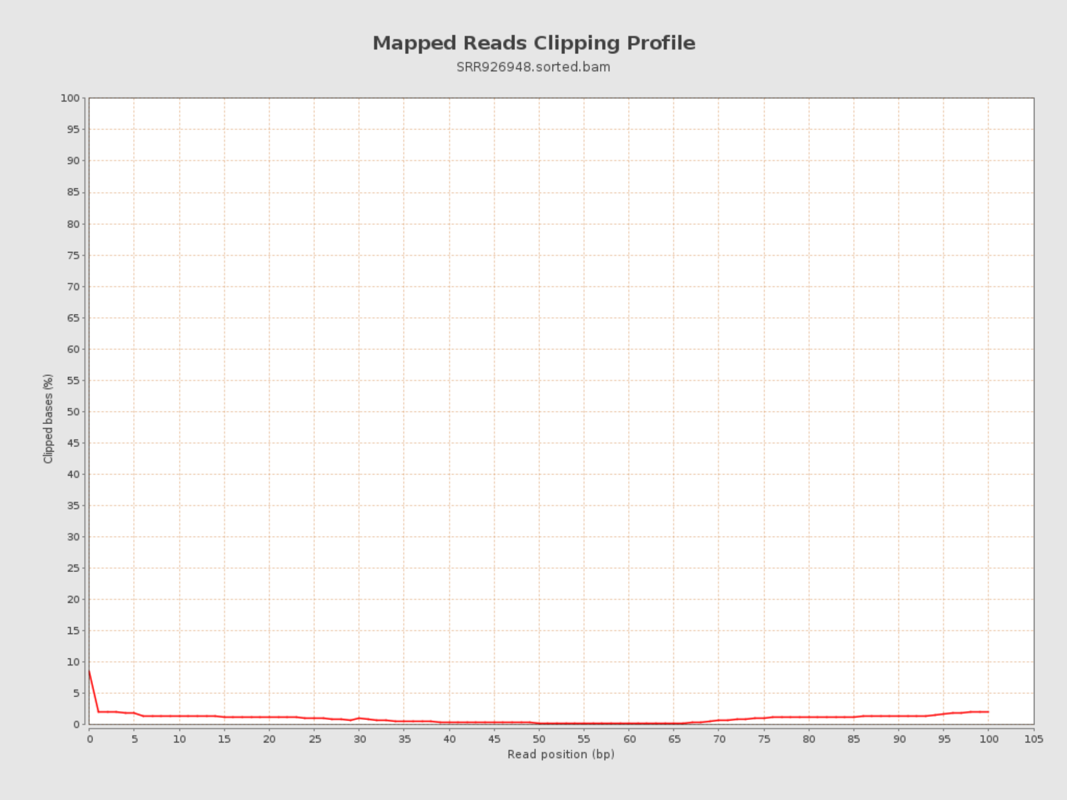
8. Results : Mapped Reads Nucleotide Content



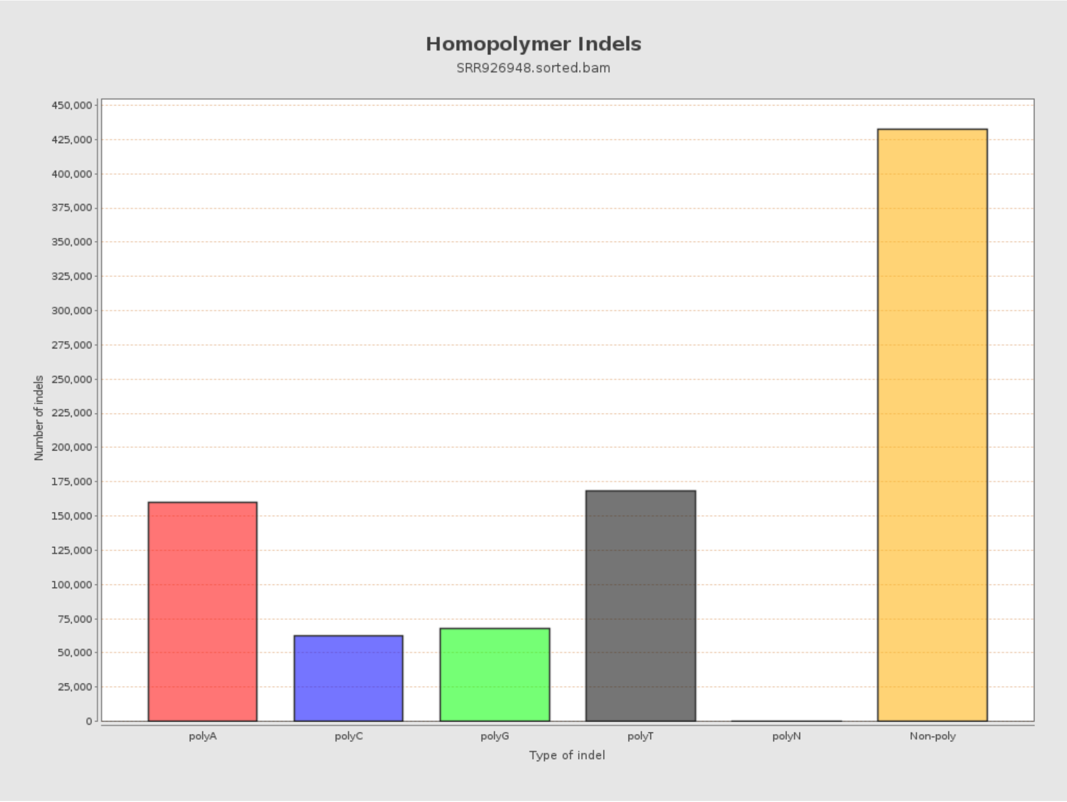
9. Results : Mapped Reads GC-content Distribution



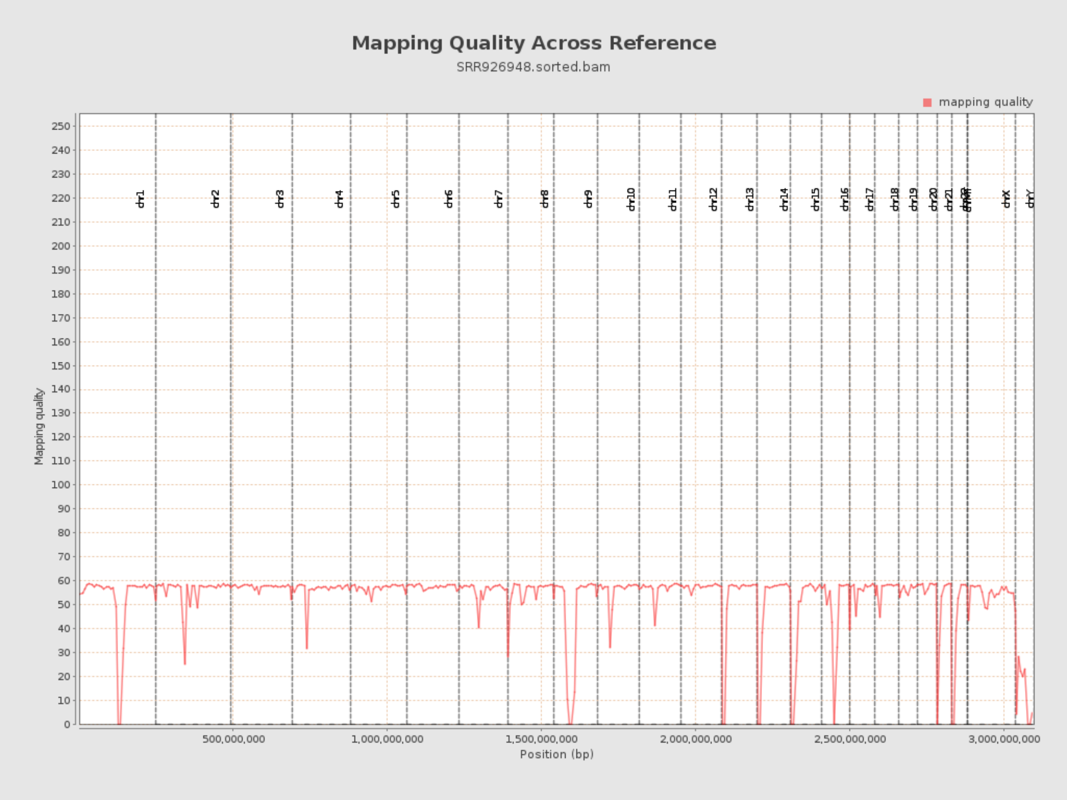
10. Results : Mapped Reads Clipping Profile



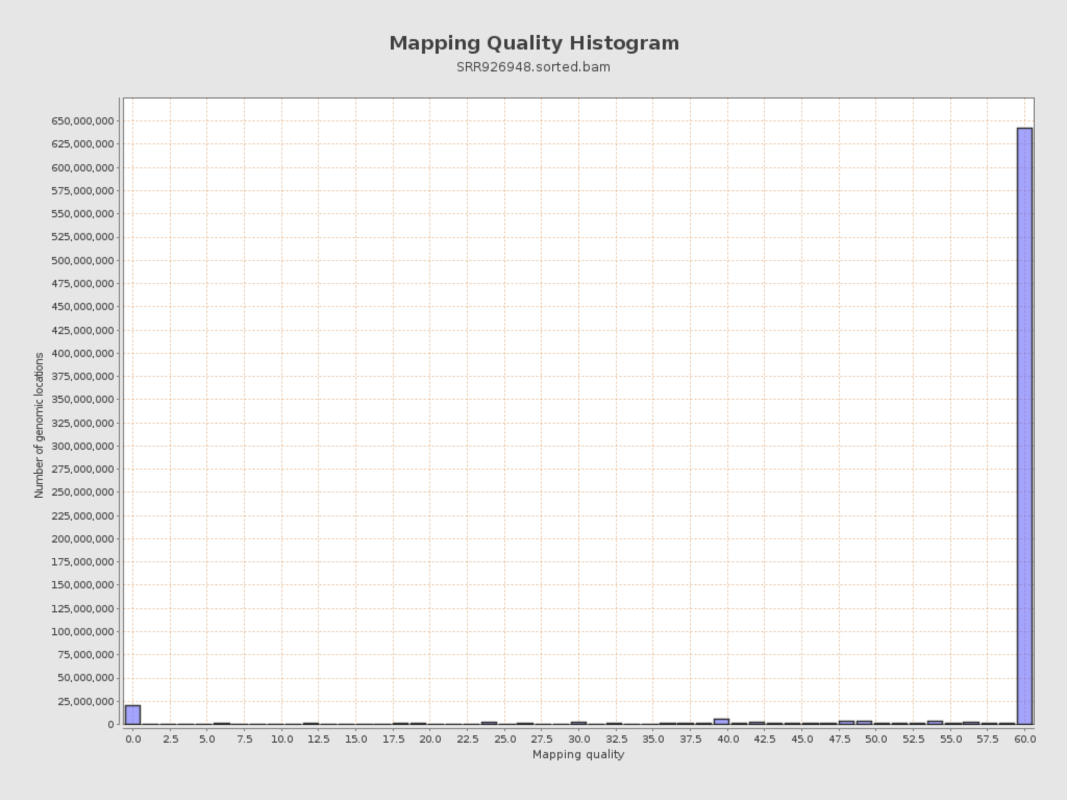
11. Results : Homopolymer Indels



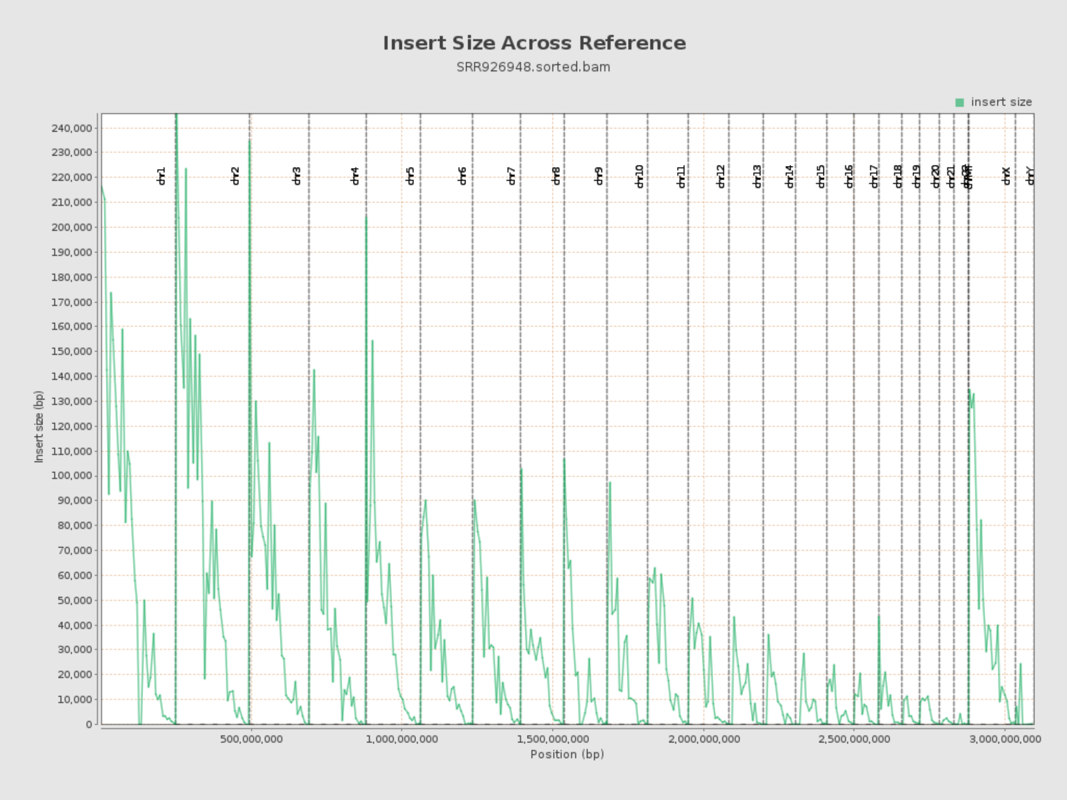
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram