Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 19:20:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472640.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_SRR3472640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472640_1.fastq.gz SRR3472640_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 19:20:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,314,796
Mapped reads	16,208,948 / 99.35%
Unmapped reads	105,848 / 0.65%
Mapped paired reads	16,208,948 / 99.35%
Mapped reads, first in pair	8,125,218 / 49.8%
Mapped reads, second in pair	8,083,730 / 49.55%
Mapped reads, both in pair	16,136,204 / 98.91%
Mapped reads, singletons	72,744 / 0.45%
Secondary alignments	0
Supplementary alignments	77,924 / 0.48%
Read min/max/mean length	30 / 101 / 99.77
Duplicated reads (estimated)	11,491,197 / 70.43%
Duplication rate	48.67%
Clipped reads	1,126,564 / 6.91%

2.2. ACGT Content

Number/percentage of A's	424,927,371 / 26.64%
Number/percentage of C's	374,784,977 / 23.49%
Number/percentage of T's	425,494,499 / 26.67%
Number/percentage of G's	369,831,032 / 23.18%
Number/percentage of N's	303,112 / 0.02%

GC Percentage	46.67%

2.3. Coverage

Mean	0.5154
Standard Deviation	28.6266

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	19,039.95
Standard Deviation	1,323,500.52
P25/Median/P75	155 / 211 / 280

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,522,242
Insertions	99,448
Mapped reads with at least one insertion	0.61%
Deletions	88,790
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.09%

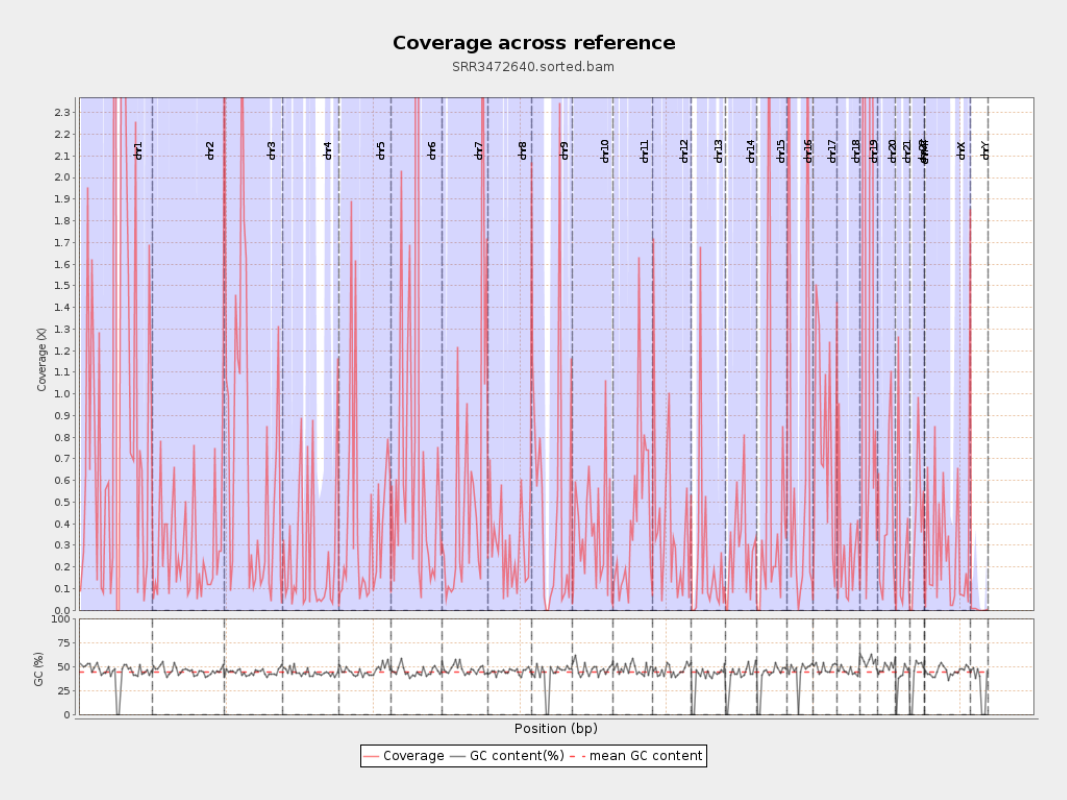
2.7. Chromosome stats

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

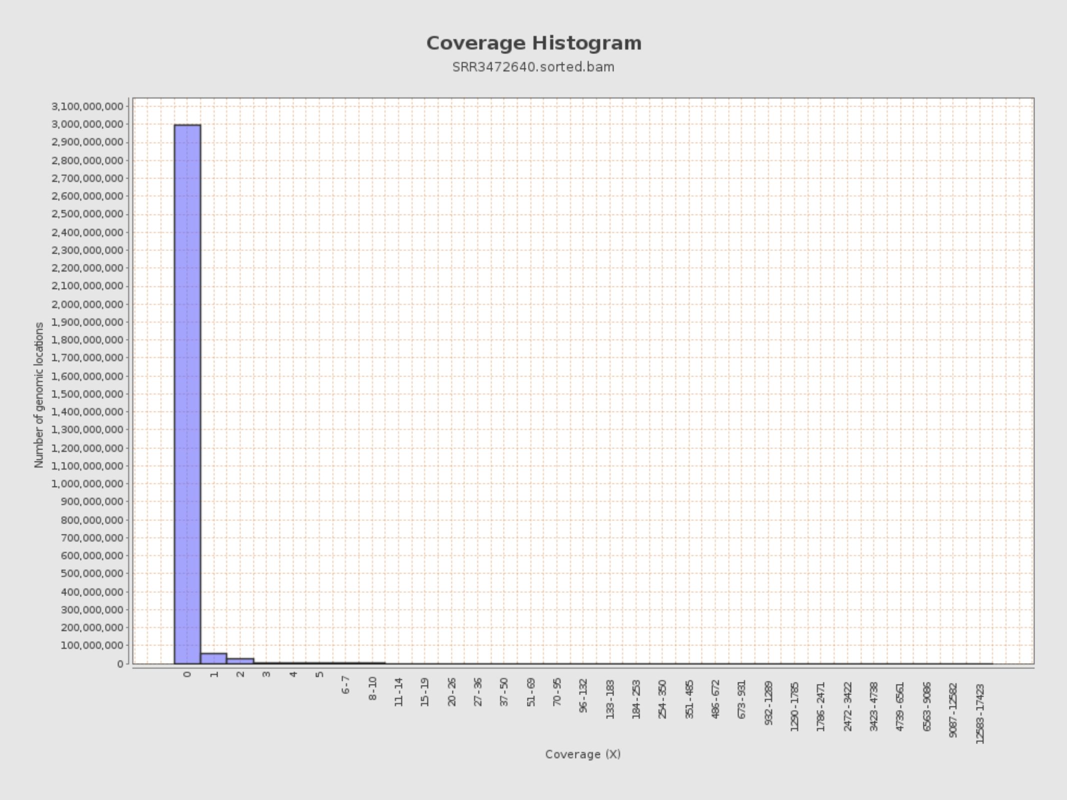
		bases	coverage	deviation
chr1	249250621	251891979	1.0106	40.429
chr2	243199373	69925775	0.2875	11.0484
chr3	198022430	143386586	0.7241	22.3415
chr4	191154276	49115257	0.2569	14.9789
chr5	180915260	76020979	0.4202	18.5629
chr6	171115067	147290484	0.8608	43.7468
chr7	159138663	96341727	0.6054	28.229
chr8	146364022	44690056	0.3053	10.7703
chr9	141213431	70626707	0.5001	21.4557
chr10	135534747	50637579	0.3736	16.9928
chr11	135006516	56594409	0.4192	29.5683
chr12	133851895	54610560	0.408	13.9732
chr13	115169878	26680268	0.2317	13.8943
chr14	107349540	30362169	0.2828	14.327
chr15	102531392	47504469	0.4633	32.806
chr16	90354753	66688092	0.7381	36.2491
chr17	81195210	64173226	0.7904	26.5209
chr18	78077248	21907026	0.2806	11.9837
chr19	59128983	120647269	2.0404	112.0093
chr20	63025520	27548675	0.4371	16.0267
chr21	48129895	15809073	0.3285	28.9107
chr22	51304566	20680811	0.4031	15.7769
chrMT	16571	1852	0.1118	0.4045
chrX	155270560	42250692	0.2721	12.2

chrY	59373566	207114	0.0035	0.1799

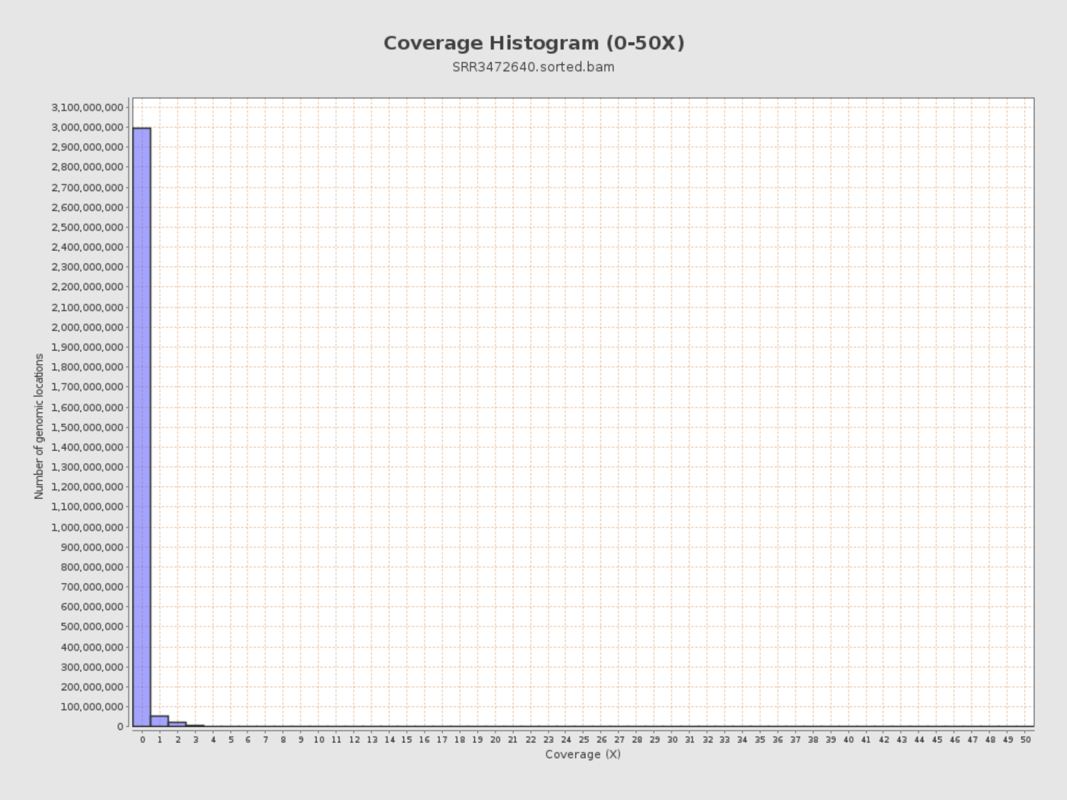
3. Results : Coverage across reference



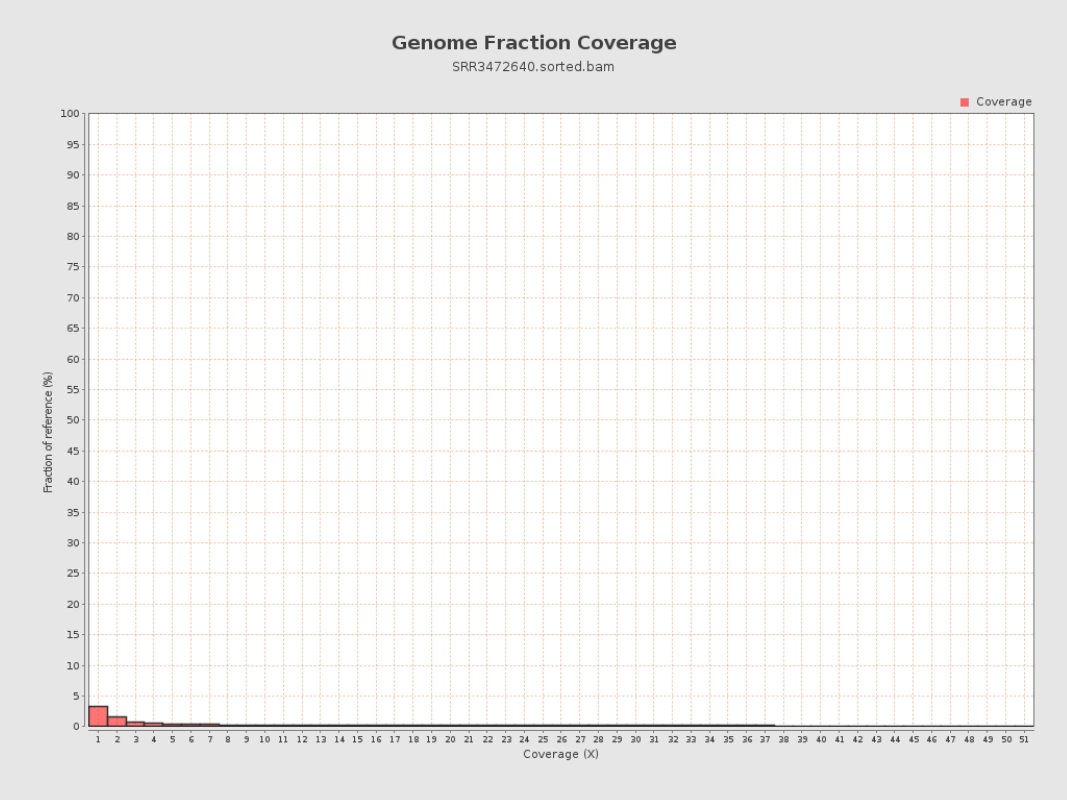
4. Results : Coverage Histogram



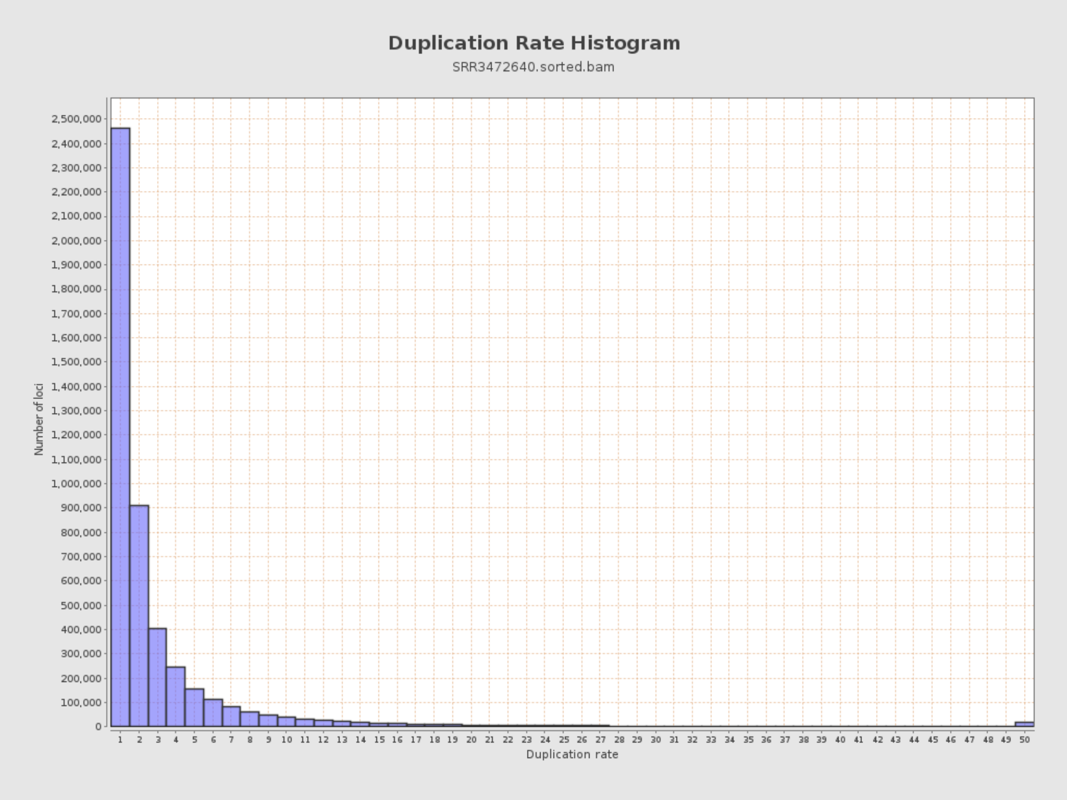
5. Results : Coverage Histogram (0-50X)



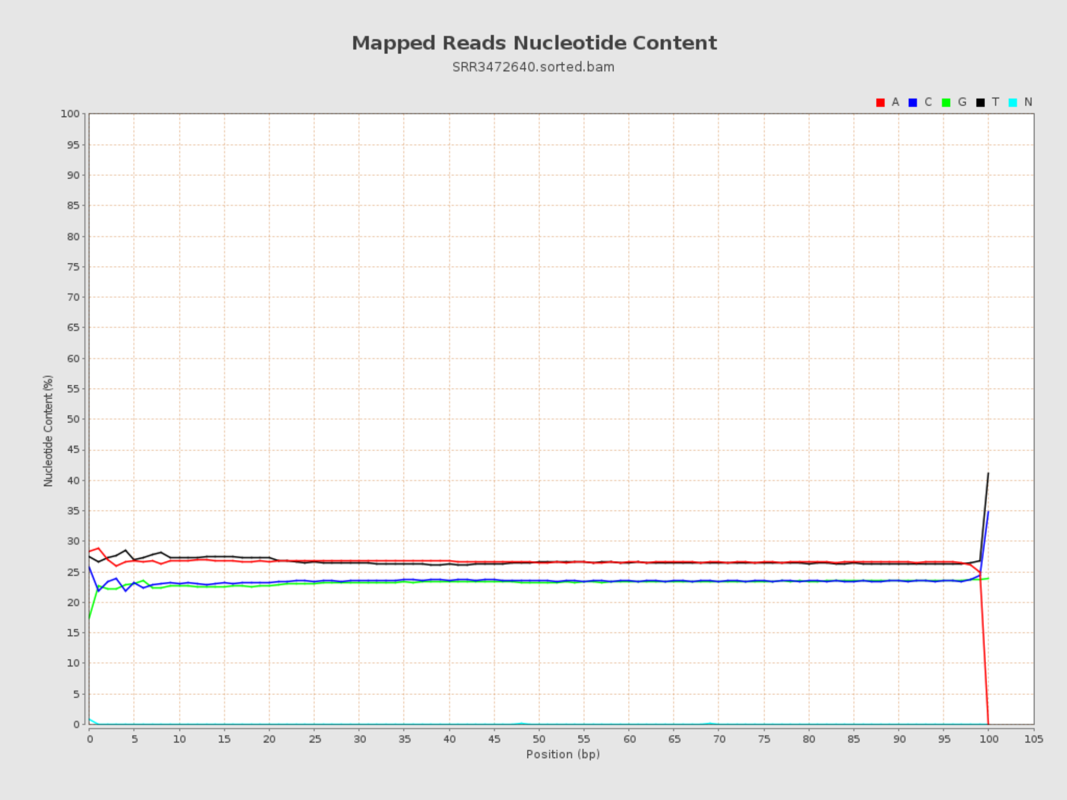
6. Results : Genome Fraction Coverage



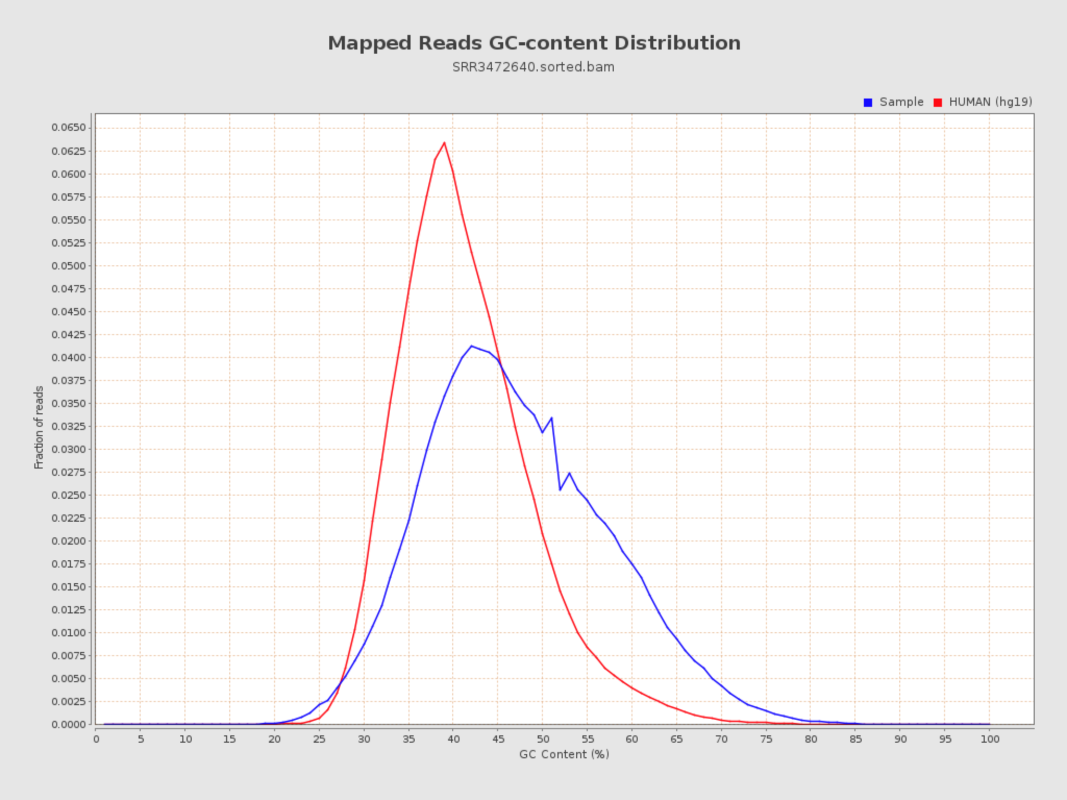
7. Results : Duplication Rate Histogram



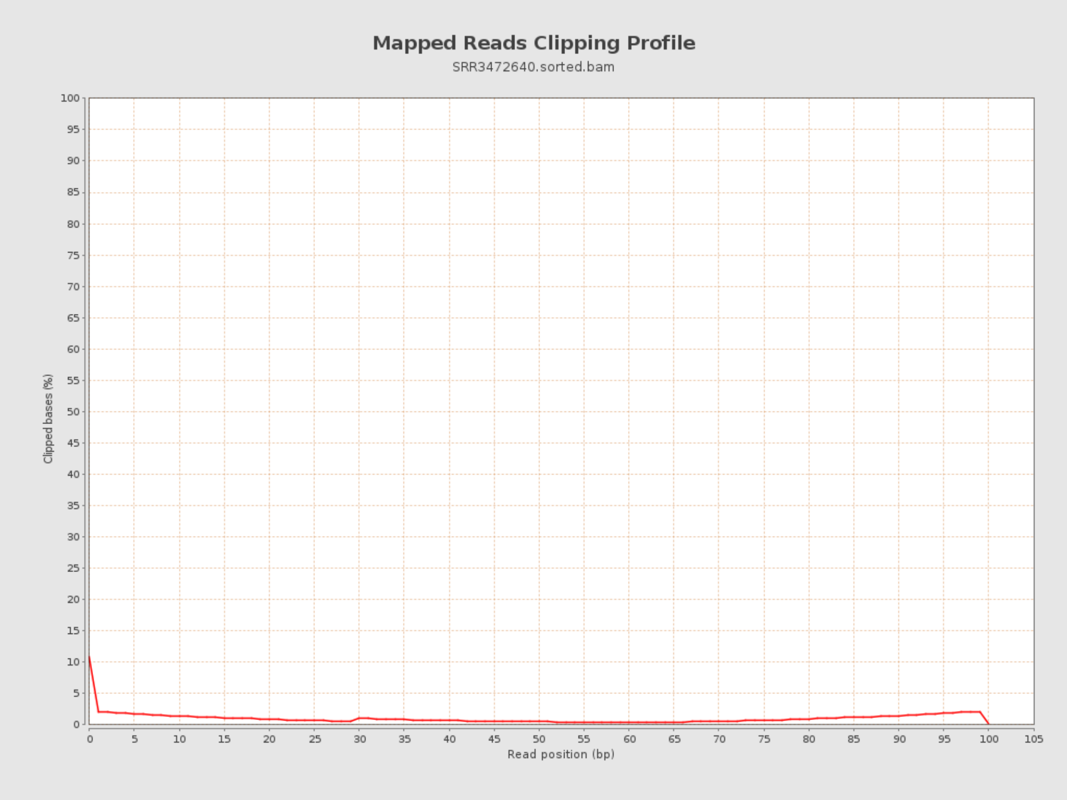
8. Results : Mapped Reads Nucleotide Content



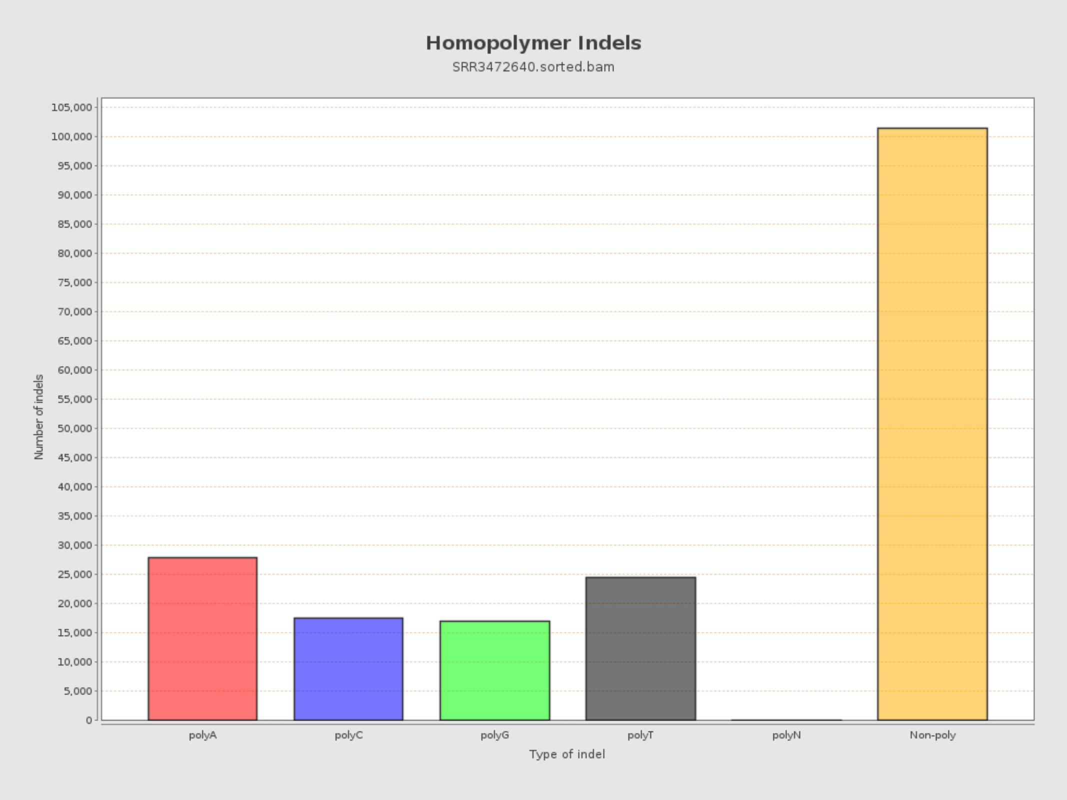
9. Results : Mapped Reads GC-content Distribution



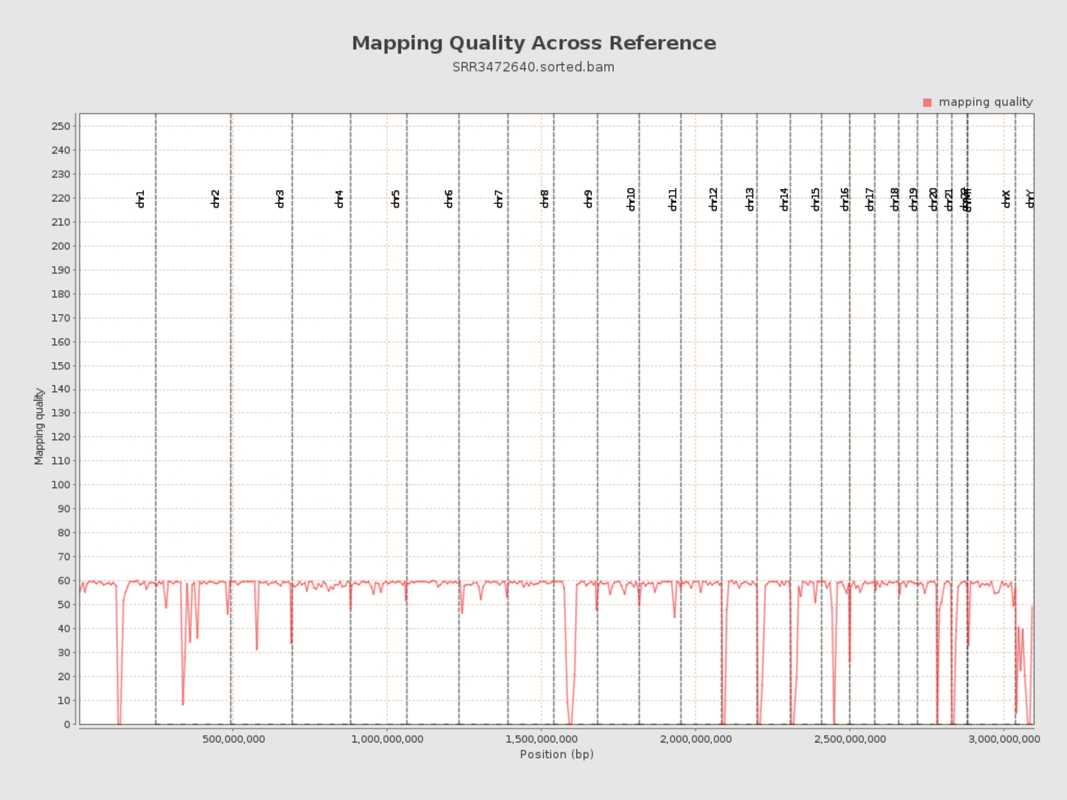
10. Results : Mapped Reads Clipping Profile



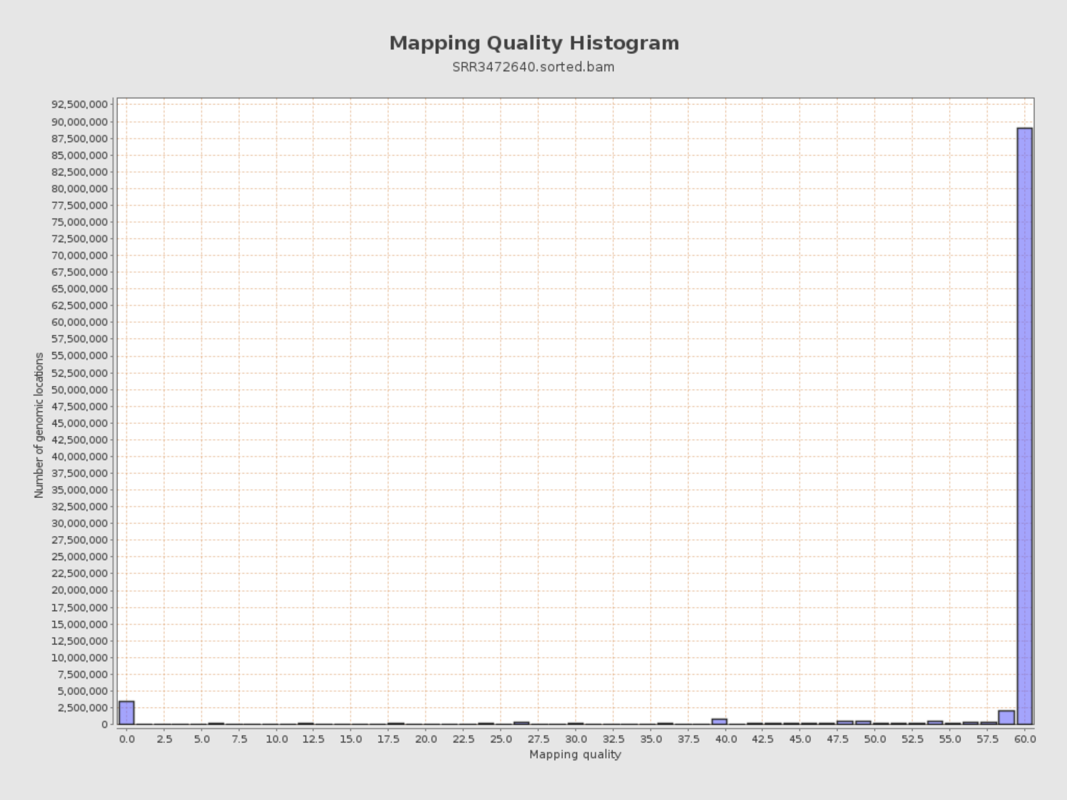
11. Results : Homopolymer Indels



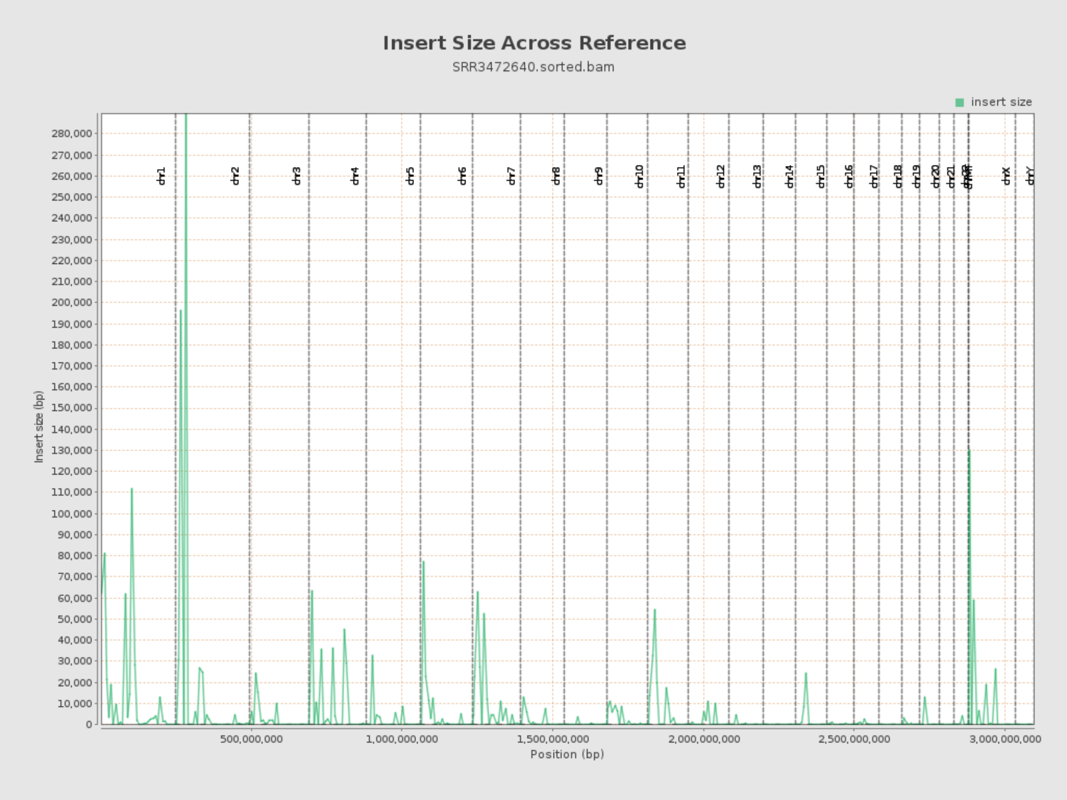
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram