Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 11:53:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472616.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_SRR3472616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472616_1.fastq.gz SRR3472616_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 11:53:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,447,326
Mapped reads	15,306,908 / 99.09%
Unmapped reads	140,418 / 0.91%
Mapped paired reads	15,306,908 / 99.09%
Mapped reads, first in pair	7,668,760 / 49.64%
Mapped reads, second in pair	7,638,148 / 49.45%
Mapped reads, both in pair	15,222,078 / 98.54%
Mapped reads, singletons	84,830 / 0.55%
Secondary alignments	0
Supplementary alignments	80,020 / 0.52%
Read min/max/mean length	30 / 101 / 99.7
Duplicated reads (estimated)	10,621,105 / 68.76%
Duplication rate	48.71%
Clipped reads	1,165,233 / 7.54%

2.2. ACGT Content

Number/percentage of A's	401,585,577 / 26.72%
Number/percentage of C's	352,437,775 / 23.45%
Number/percentage of T's	401,559,459 / 26.72%
Number/percentage of G's	347,238,744 / 23.1%
Number/percentage of N's	272,945 / 0.02%

GC Percentage	46.55%

2.3. Coverage

Mean	0.4856
Standard Deviation	24.8105

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	20,569.12
Standard Deviation	1,356,336.38
P25/Median/P75	154 / 211 / 282

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,432,913
Insertions	84,759
Mapped reads with at least one insertion	0.55%
Deletions	76,410
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.01%

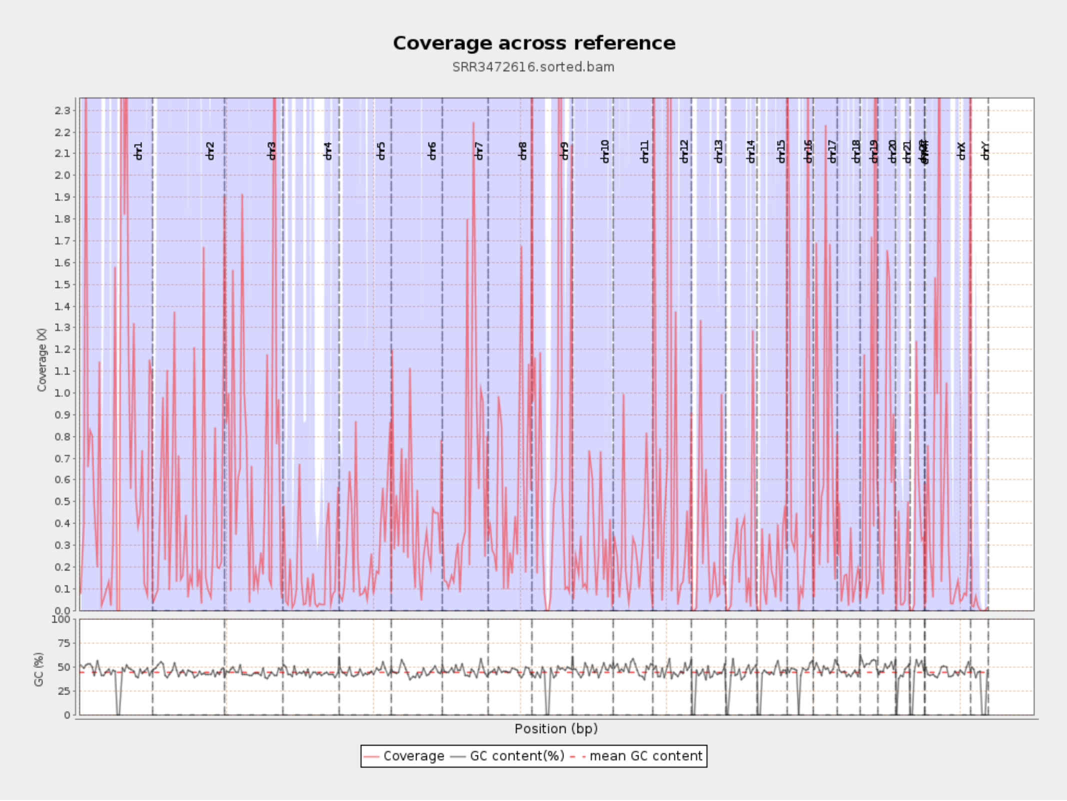
2.7. Chromosome stats

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

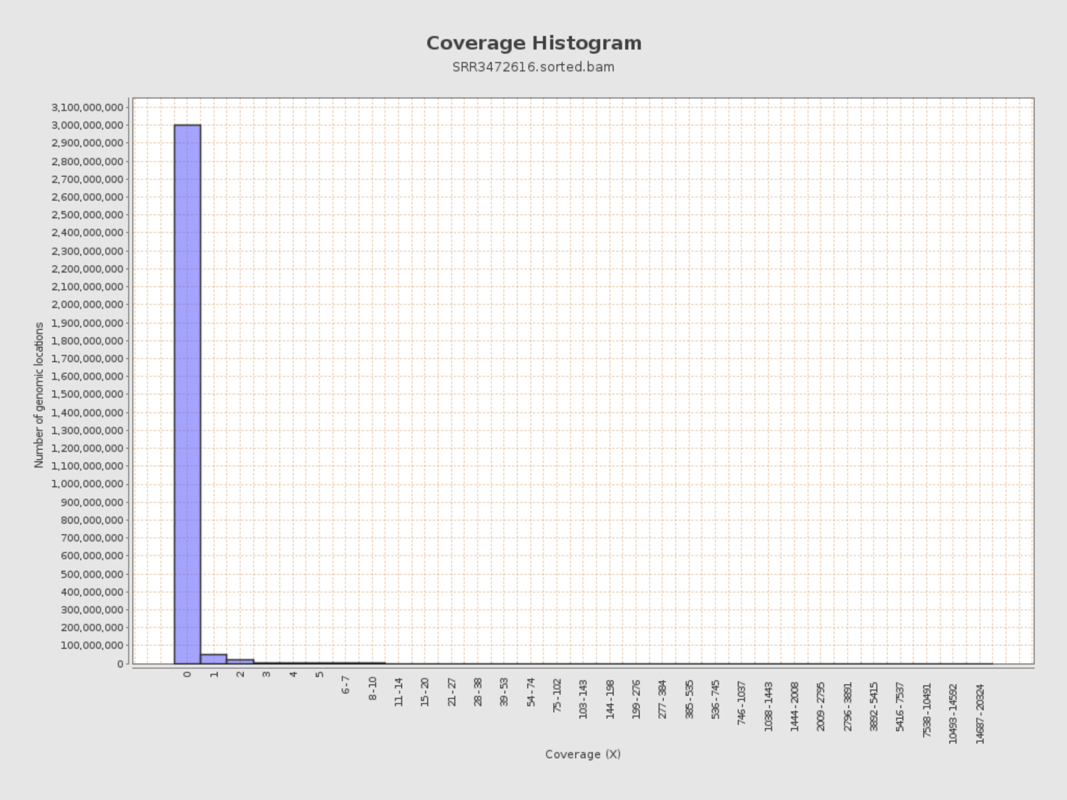
		bases	coverage	deviation
chr1	249250621	195918221	0.786	26.6939
chr2	243199373	101762982	0.4184	16.538
chr3	198022430	139997707	0.707	29.682
chr4	191154276	29182111	0.1527	7.3229
chr5	180915260	52611728	0.2908	11.5198
chr6	171115067	70936742	0.4146	12.9444
chr7	159138663	91356721	0.5741	23.7485
chr8	146364022	76732299	0.5243	17.4546
chr9	141213431	106205415	0.7521	42.9717
chr10	135534747	37065059	0.2735	13.916
chr11	135006516	41129035	0.3046	13.3506
chr12	133851895	117665029	0.8791	48.1608
chr13	115169878	36506740	0.317	13.869
chr14	107349540	26804067	0.2497	14.3509
chr15	102531392	20559651	0.2005	8.4041
chr16	90354753	64173916	0.7102	26.2465
chr17	81195210	64043269	0.7888	33.1649
chr18	78077248	14181659	0.1816	7.8871
chr19	59128983	62489778	1.0568	65.1142
chr20	63025520	45667659	0.7246	25.0389
chr21	48129895	8373874	0.174	11.174
chr22	51304566	19769938	0.3853	38.6447
chrMT	16571	9631	0.5812	1.0872
chrX	155270560	79153415	0.5098	23.7003

chrY	59373566	1050069	0.0177	0.8052

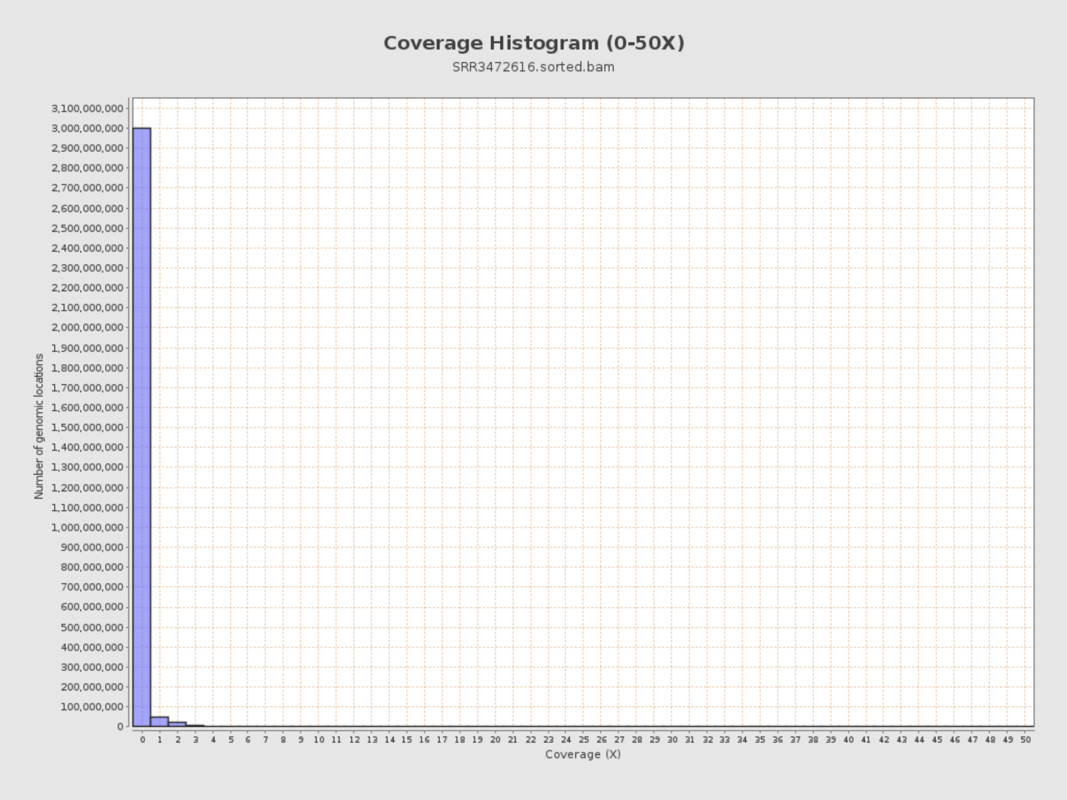
3. Results : Coverage across reference



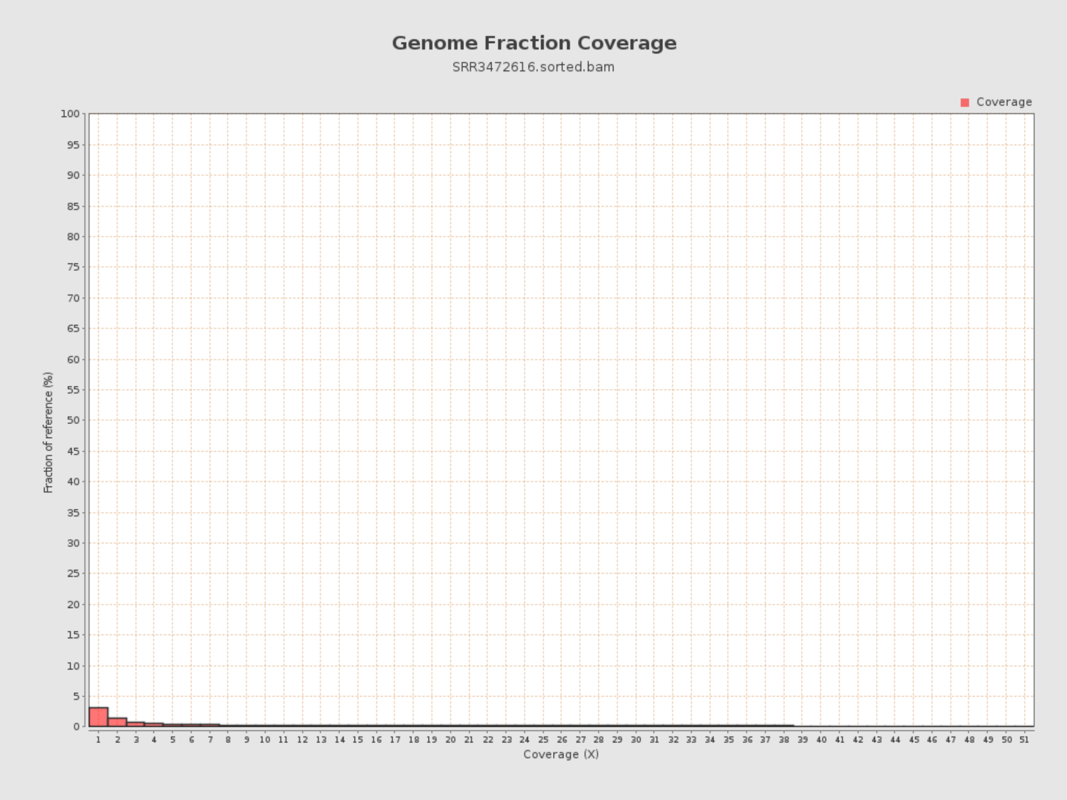
4. Results : Coverage Histogram



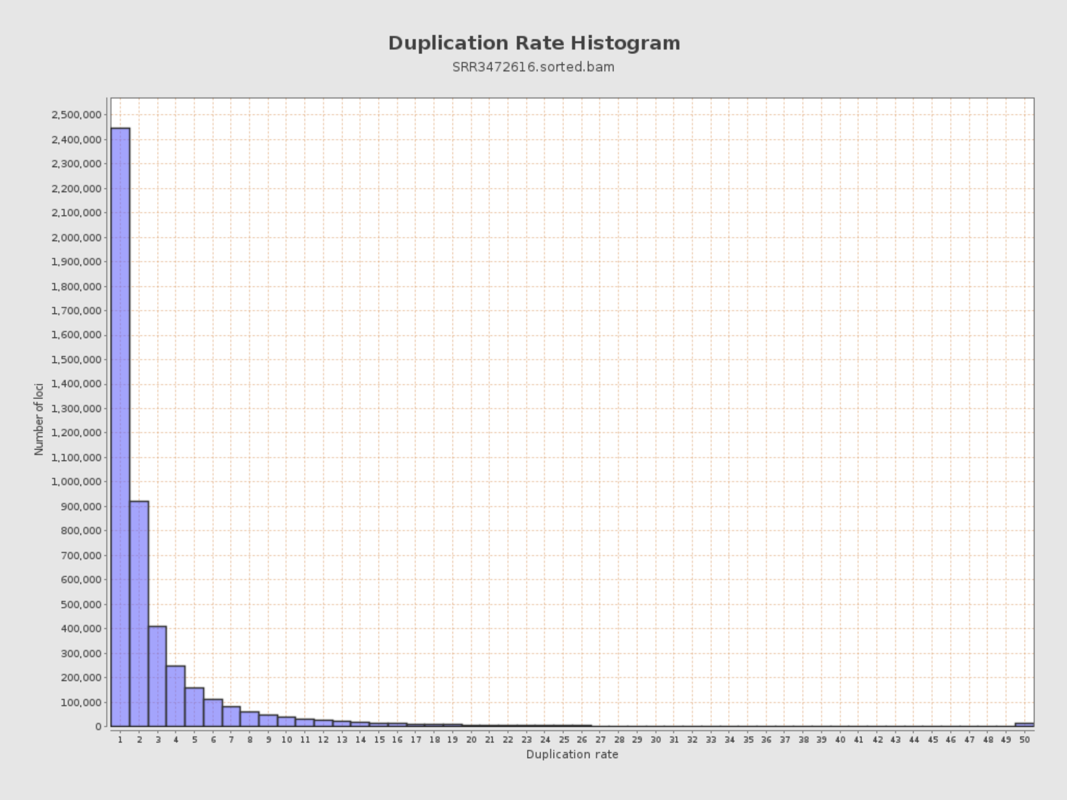
5. Results : Coverage Histogram (0-50X)



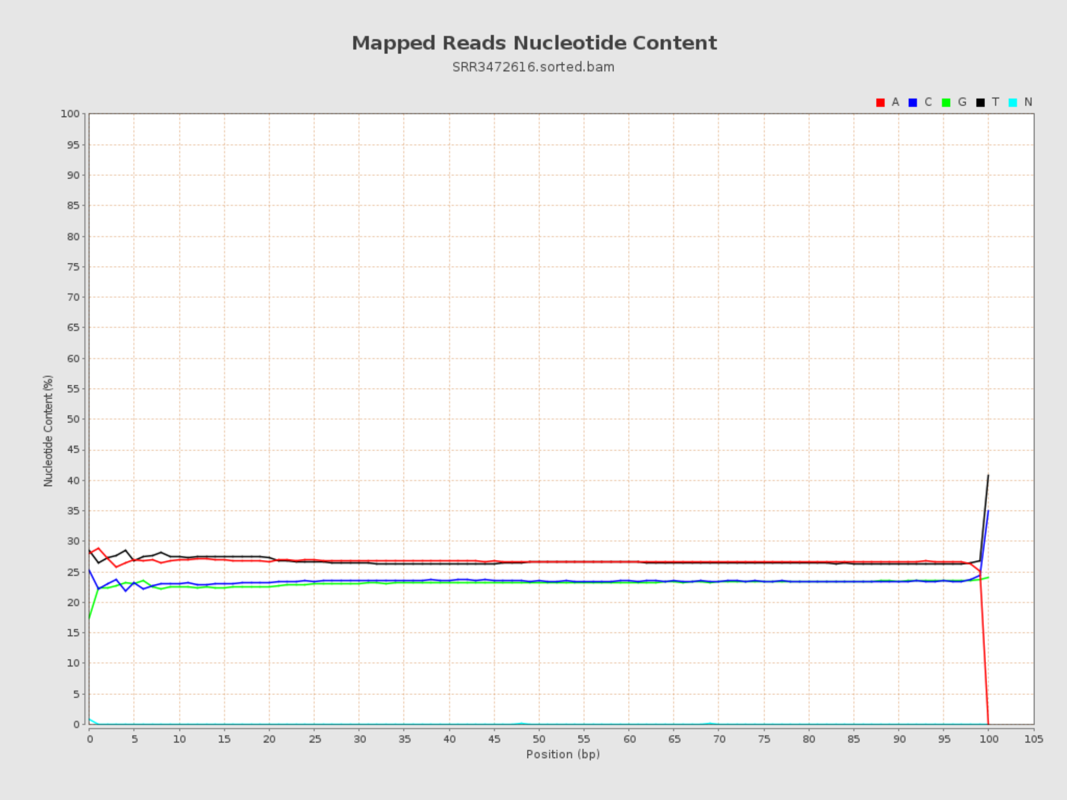
6. Results : Genome Fraction Coverage



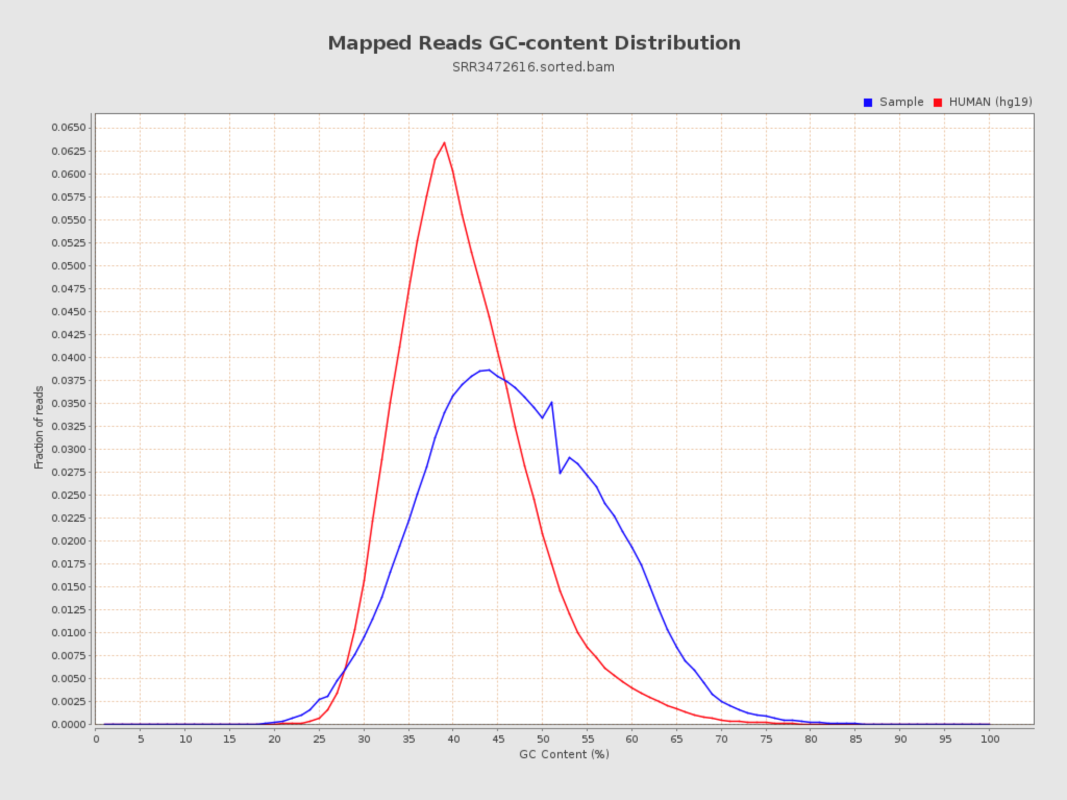
7. Results : Duplication Rate Histogram



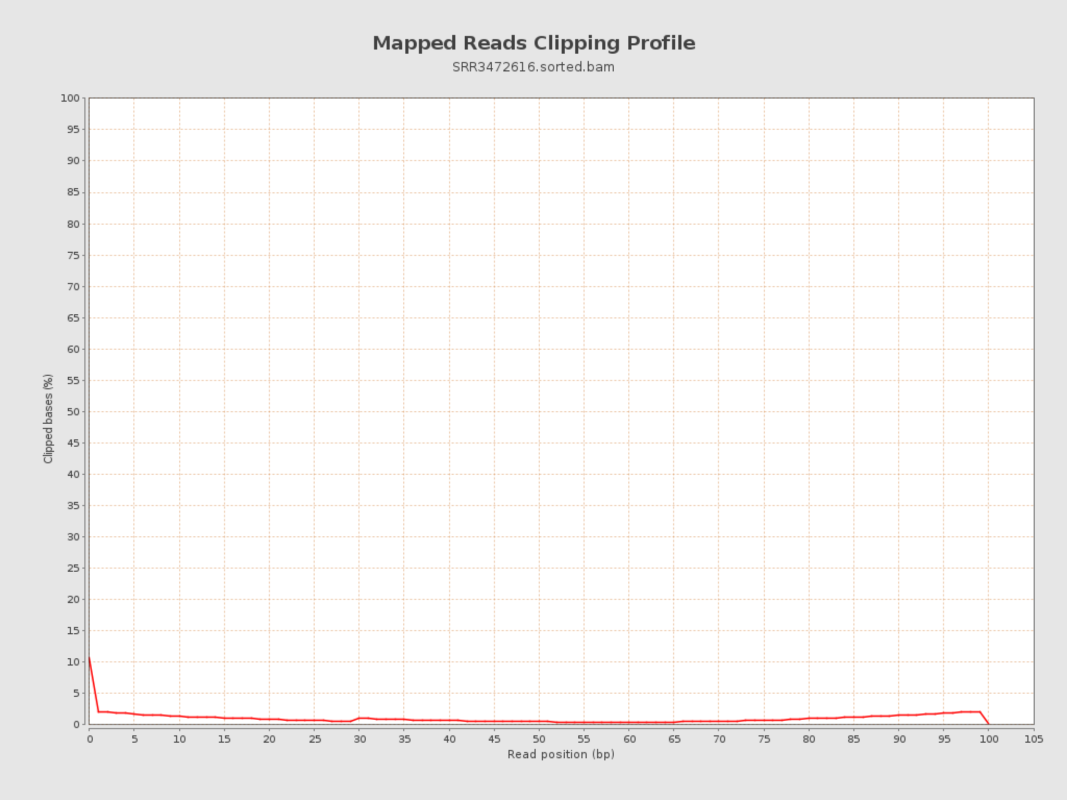
8. Results : Mapped Reads Nucleotide Content



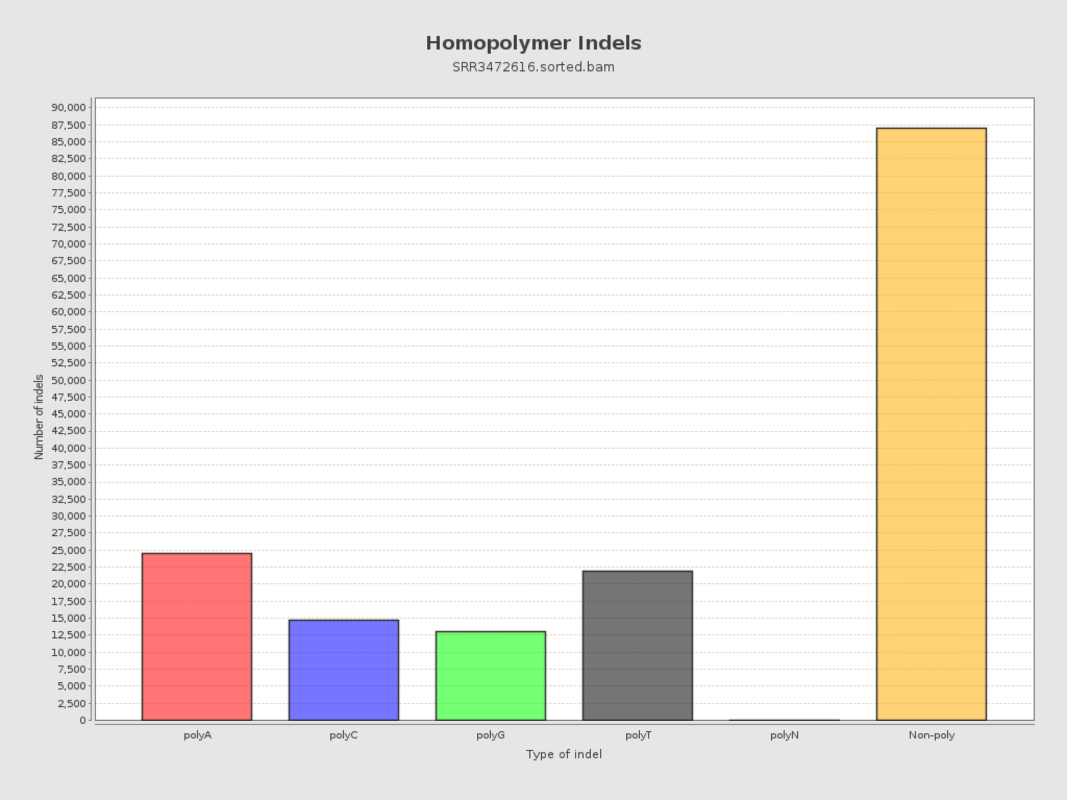
9. Results : Mapped Reads GC-content Distribution



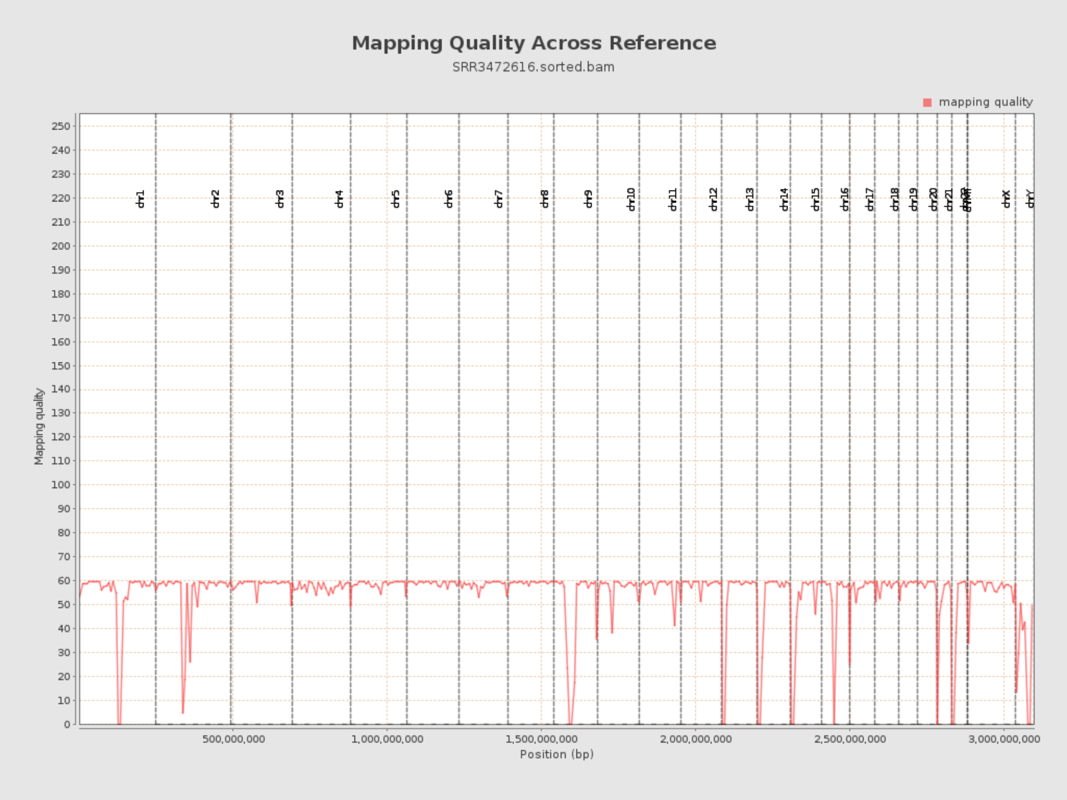
10. Results : Mapped Reads Clipping Profile



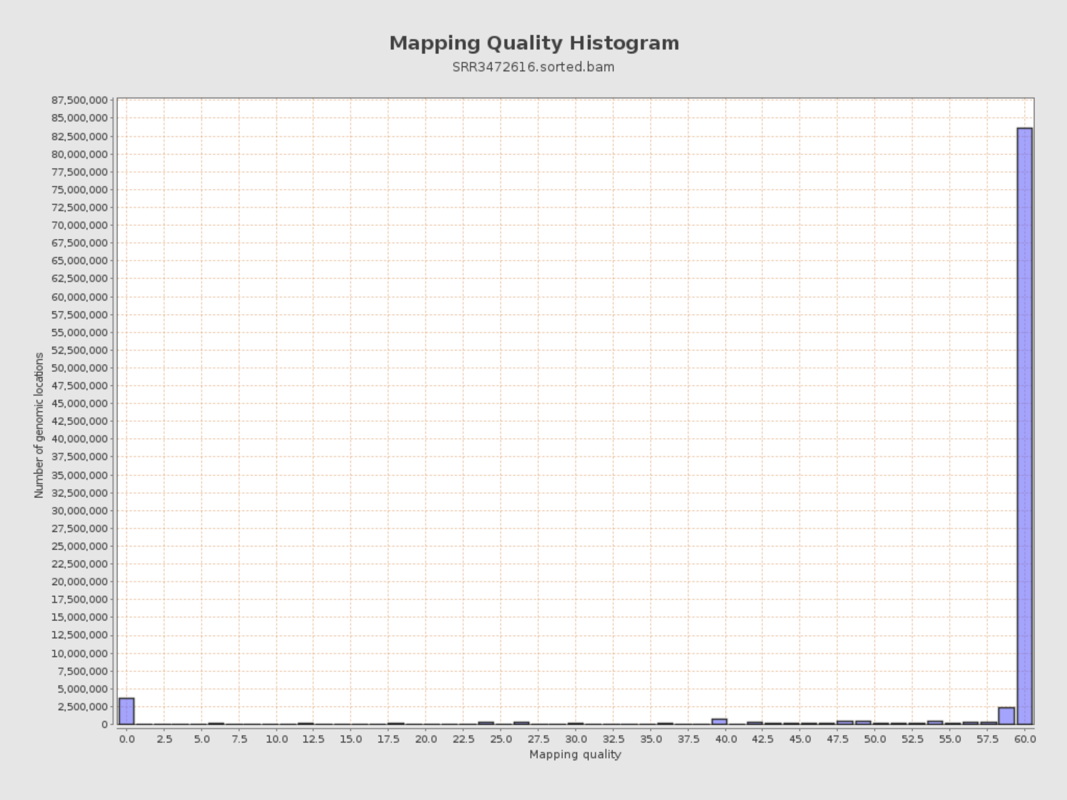
11. Results : Homopolymer Indels



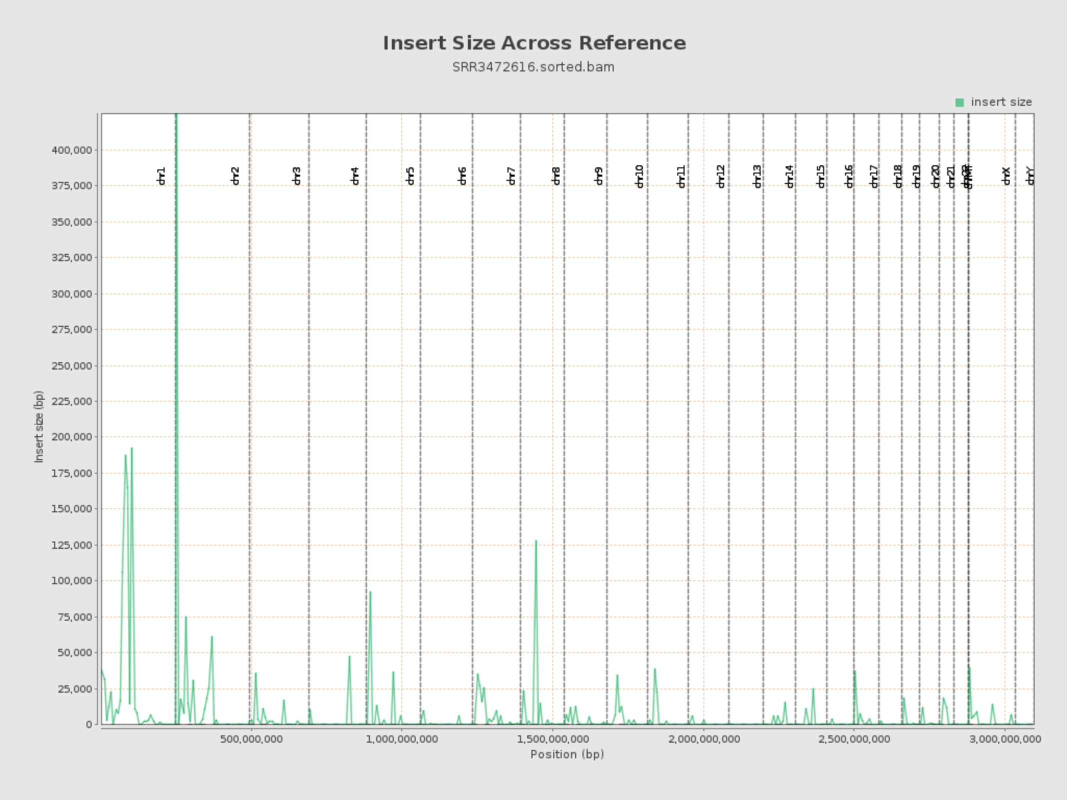
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram