Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 10:42:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472766.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_SRR3472766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472766_1.fastq.gz SRR3472766_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 10:42:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,960,098
Mapped reads	13,816,720 / 98.97%
Unmapped reads	143,378 / 1.03%
Mapped paired reads	13,816,720 / 98.97%
Mapped reads, first in pair	6,936,867 / 49.69%
Mapped reads, second in pair	6,879,853 / 49.28%
Mapped reads, both in pair	13,727,772 / 98.34%
Mapped reads, singletons	88,948 / 0.64%
Secondary alignments	0
Supplementary alignments	49,312 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,458,992 / 60.59%
Duplication rate	46.54%
Clipped reads	980,104 / 7.02%

2.2. ACGT Content

Number/percentage of A's	382,510,470 / 28.06%
Number/percentage of C's	301,097,713 / 22.09%
Number/percentage of T's	380,700,683 / 27.92%
Number/percentage of G's	298,745,369 / 21.91%
Number/percentage of N's	259,855 / 0.02%

GC Percentage	44%

2.3. Coverage

Mean	0.4405
Standard Deviation	16.2257

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	21,286.55
Standard Deviation	1,420,020.32
P25/Median/P75	188 / 262 / 351

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	8,899,264
Insertions	80,927
Mapped reads with at least one insertion	0.58%
Deletions	77,350
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.26%

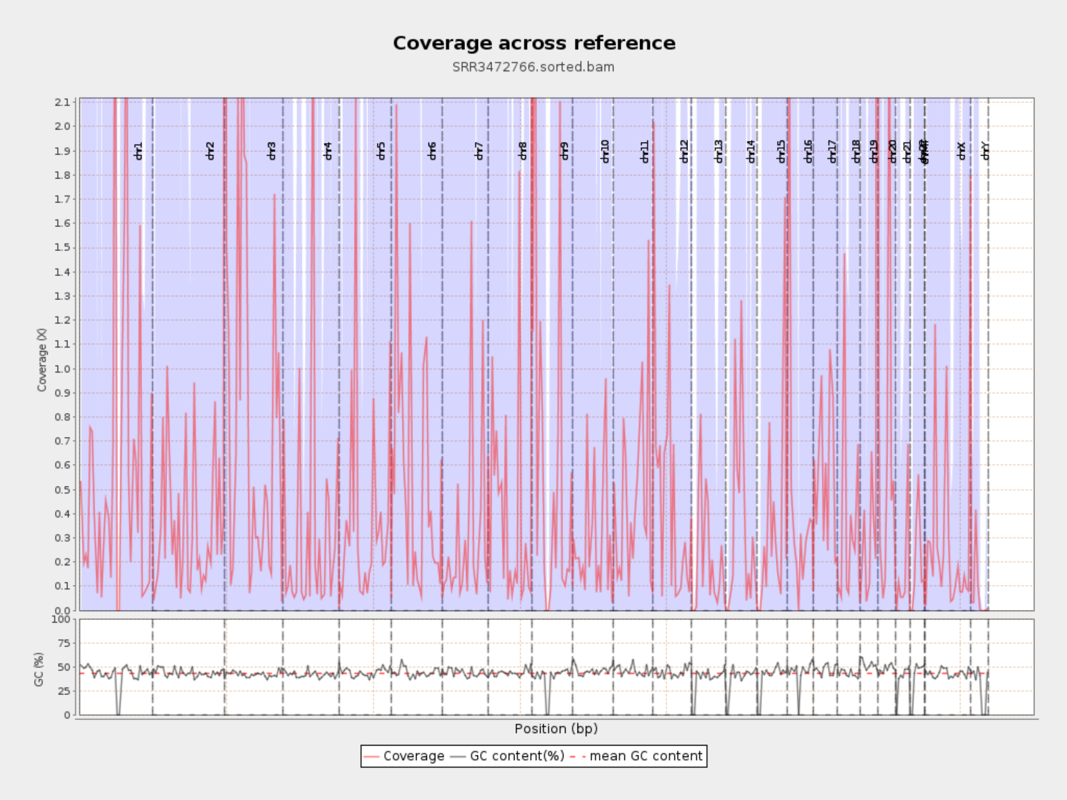
2.7. Chromosome stats

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

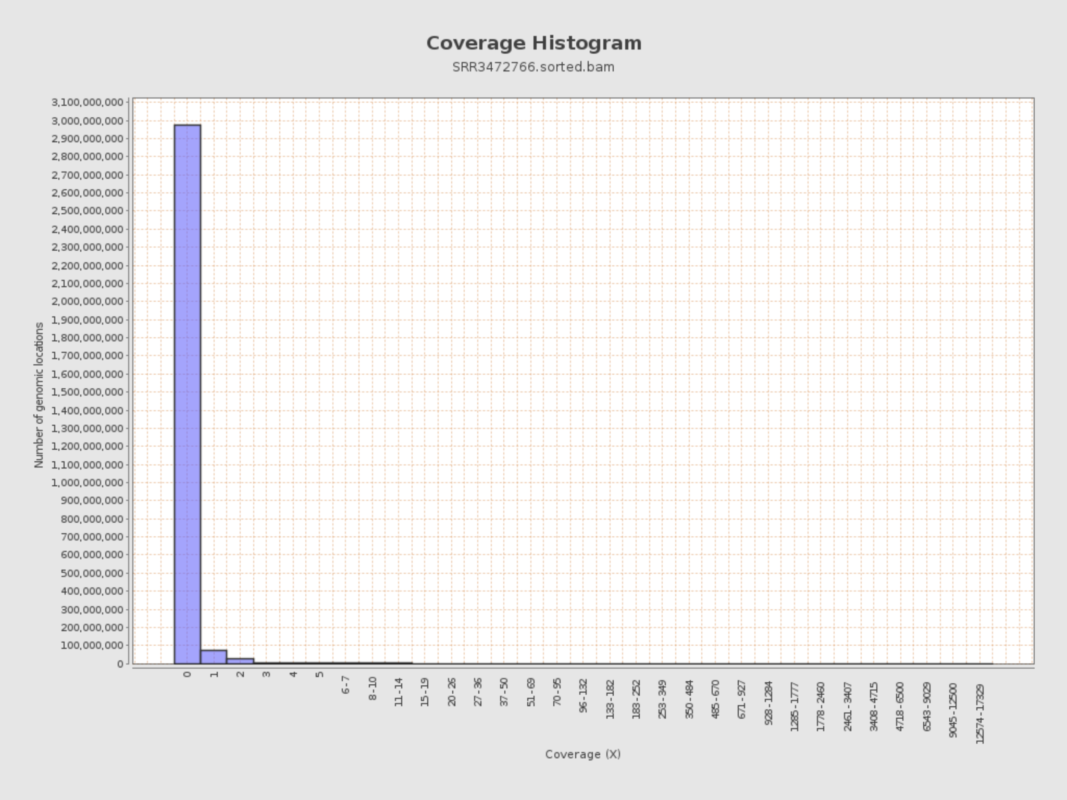
		bases	coverage	deviation
chr1	249250621	150617701	0.6043	28.7286
chr2	243199373	84782658	0.3486	11.1644
chr3	198022430	171222749	0.8647	20.8672
chr4	191154276	63783923	0.3337	16.7552
chr5	180915260	71492757	0.3952	12.8746
chr6	171115067	94496782	0.5522	15.1975
chr7	159138663	50362144	0.3165	10.477
chr8	146364022	56944150	0.3891	13.4839
chr9	141213431	92920540	0.658	16.7762
chr10	135534747	42738589	0.3153	12.8683
chr11	135006516	62448343	0.4626	15.3309
chr12	133851895	65384800	0.4885	16.2868
chr13	115169878	25851714	0.2245	8.1954
chr14	107349540	37132018	0.3459	12.6242
chr15	102531392	40341769	0.3935	13.8179
chr16	90354753	43235523	0.4785	12.5106
chr17	81195210	47091570	0.58	13.9896
chr18	78077248	27231451	0.3488	17.4616
chr19	59128983	28710394	0.4856	27.1913
chr20	63025520	42026979	0.6668	24.2939
chr21	48129895	8034690	0.1669	8.597
chr22	51304566	9979017	0.1945	6.4405
chrMT	16571	4444	0.2682	1.0142
chrX	155270560	42015833	0.2706	7.9675

chrY	59373566	4649370	0.0783	4.6295

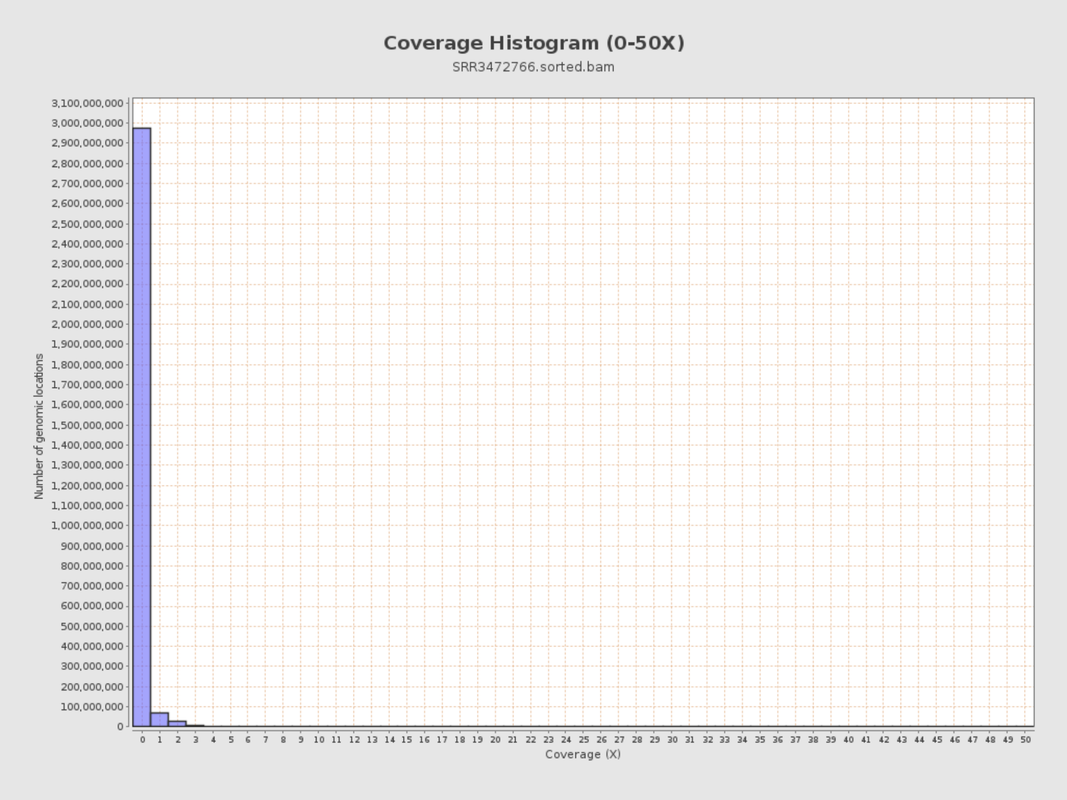
3. Results : Coverage across reference



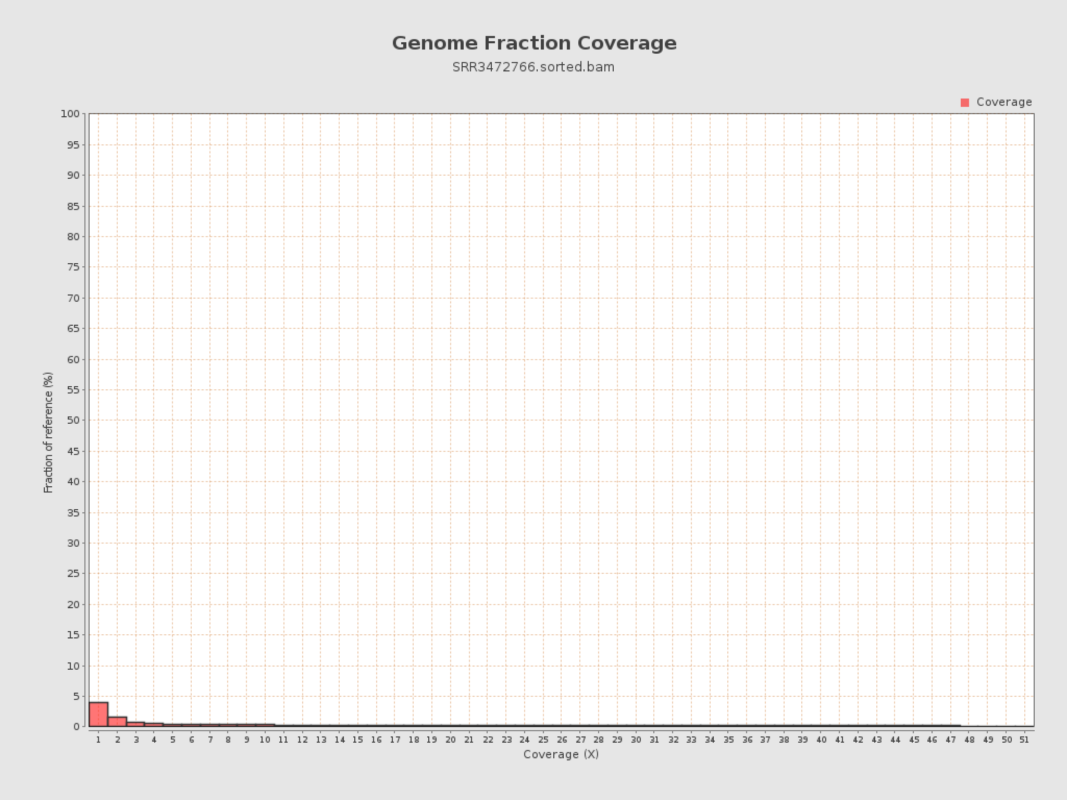
4. Results : Coverage Histogram



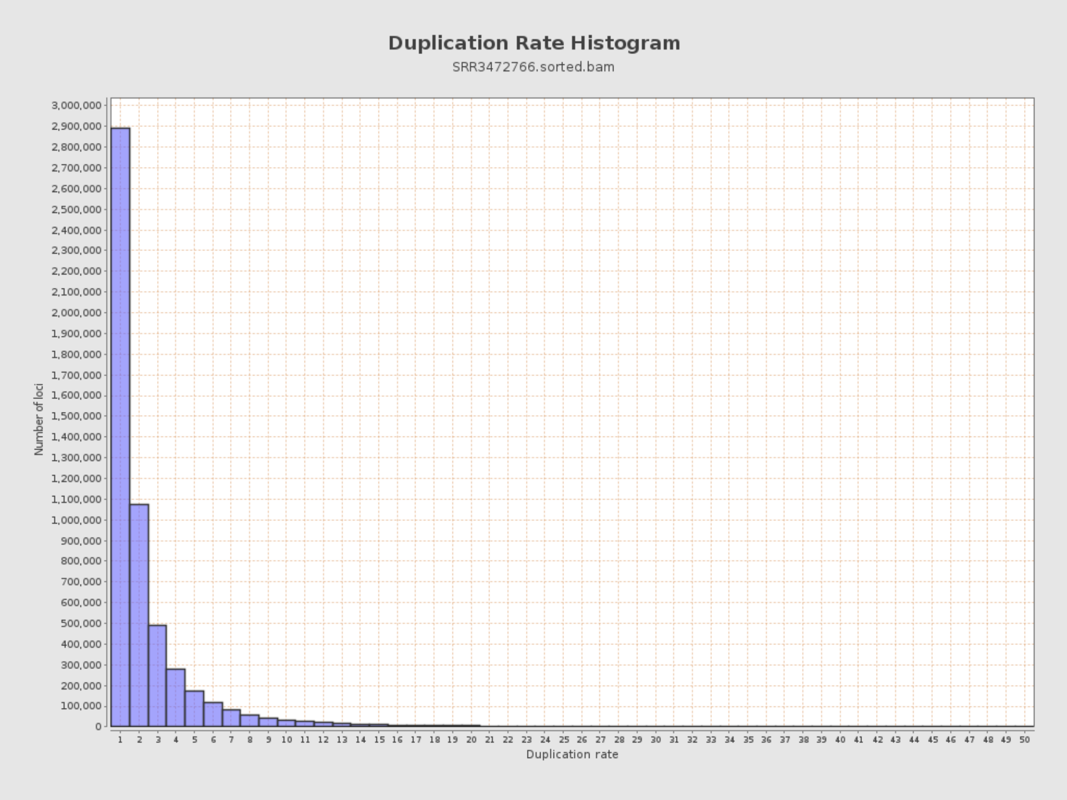
5. Results : Coverage Histogram (0-50X)



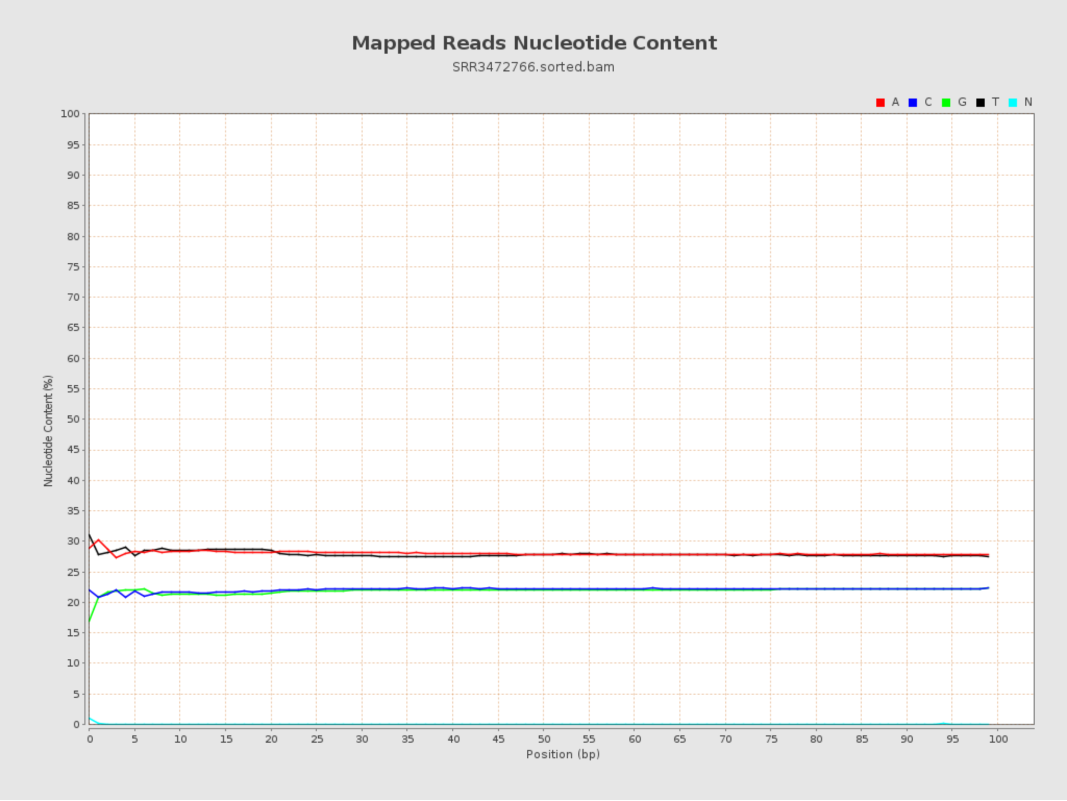
6. Results : Genome Fraction Coverage



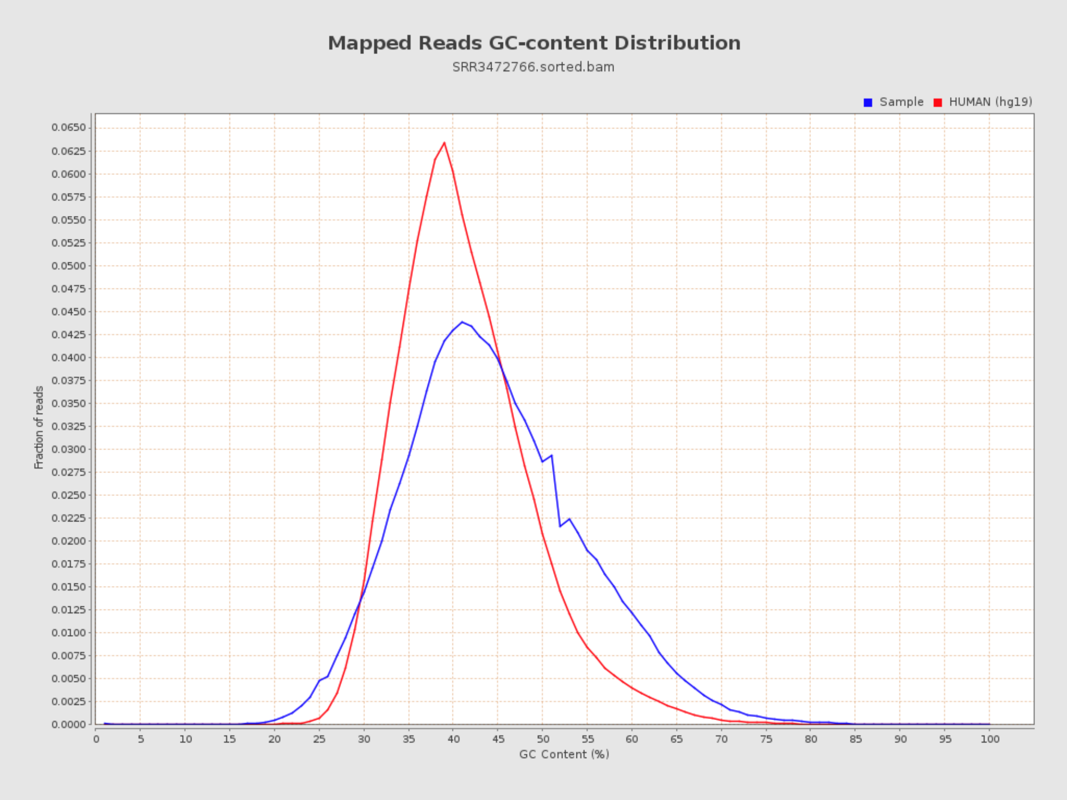
7. Results : Duplication Rate Histogram



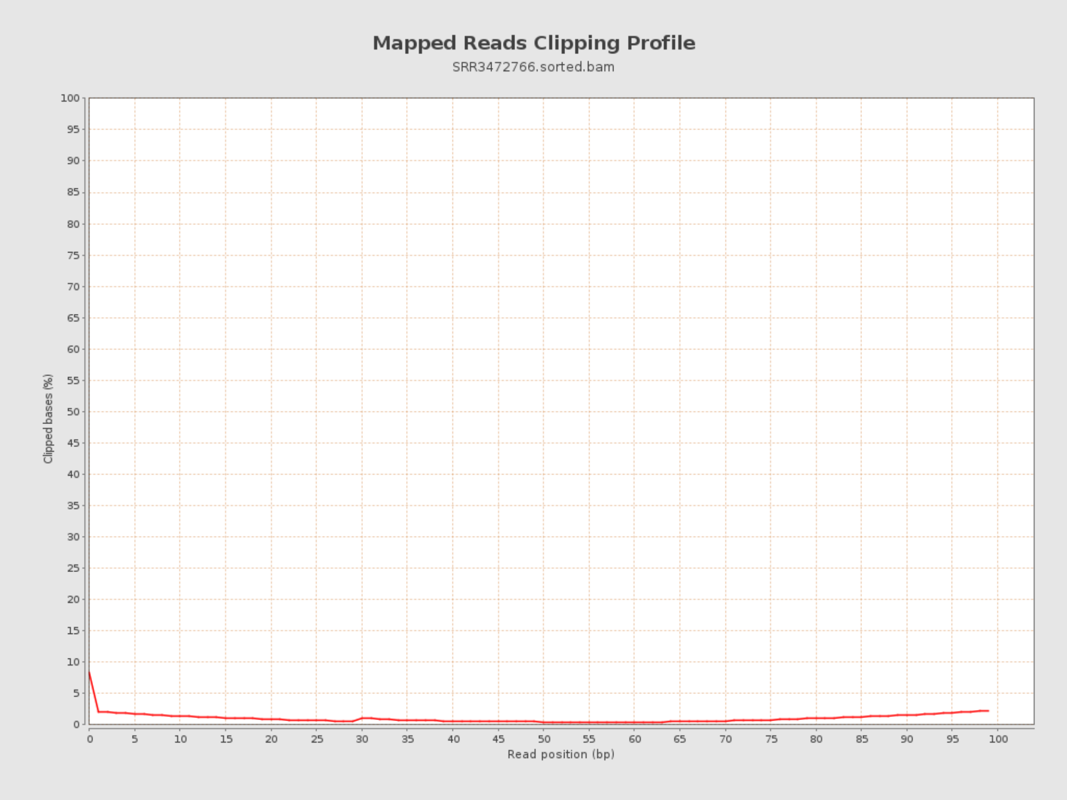
8. Results : Mapped Reads Nucleotide Content



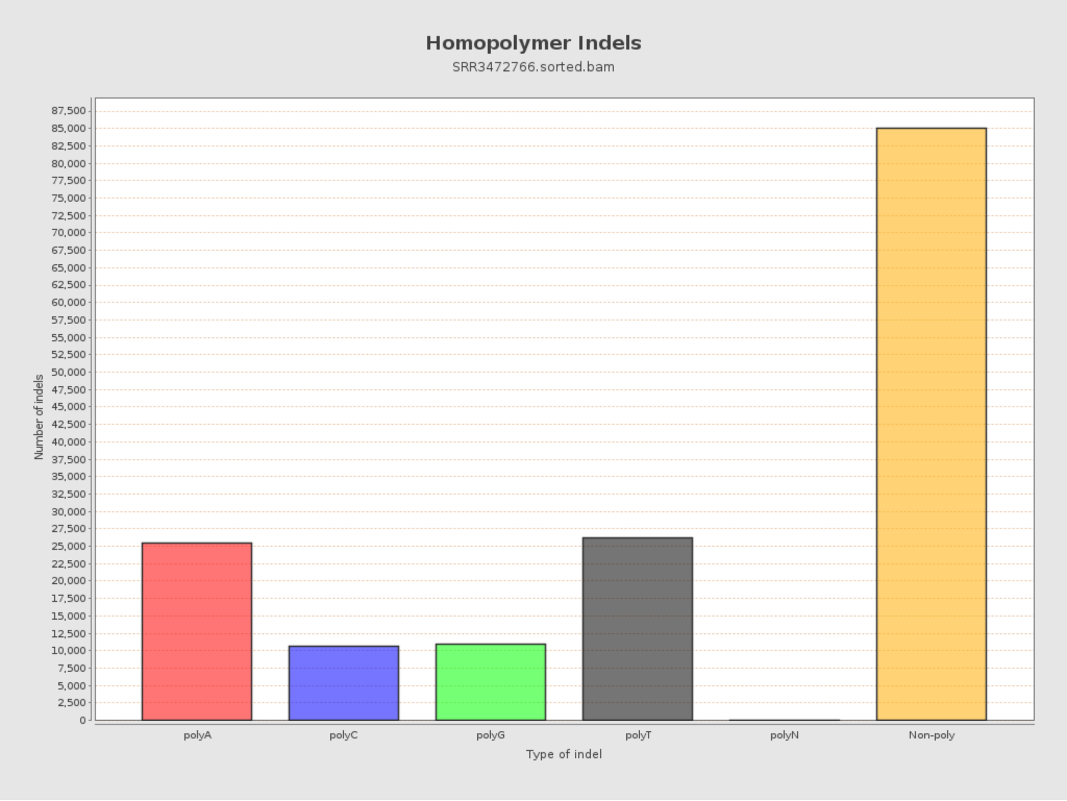
9. Results : Mapped Reads GC-content Distribution



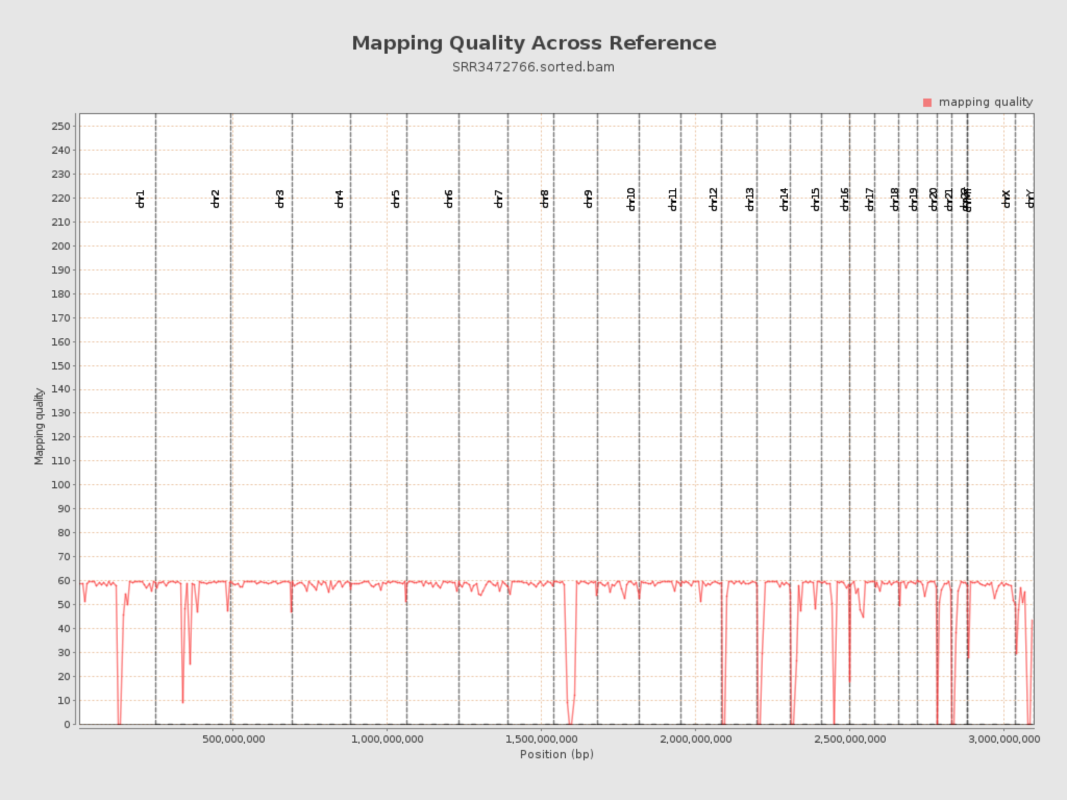
10. Results : Mapped Reads Clipping Profile



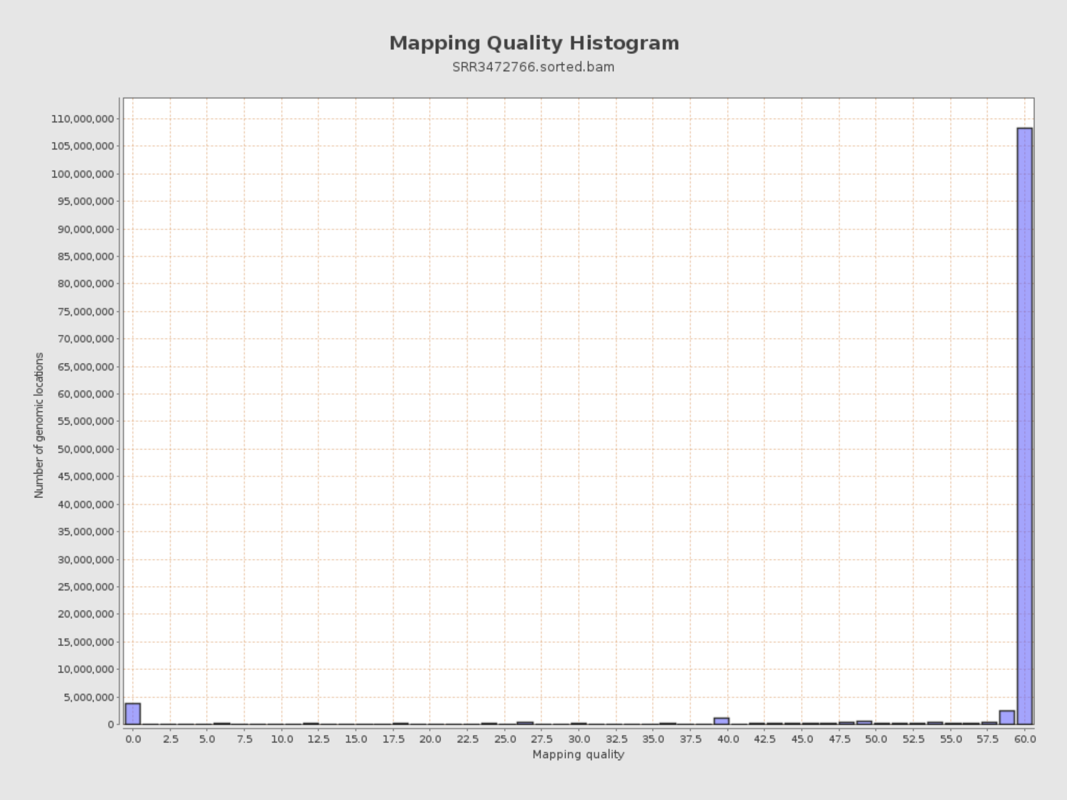
11. Results : Homopolymer Indels



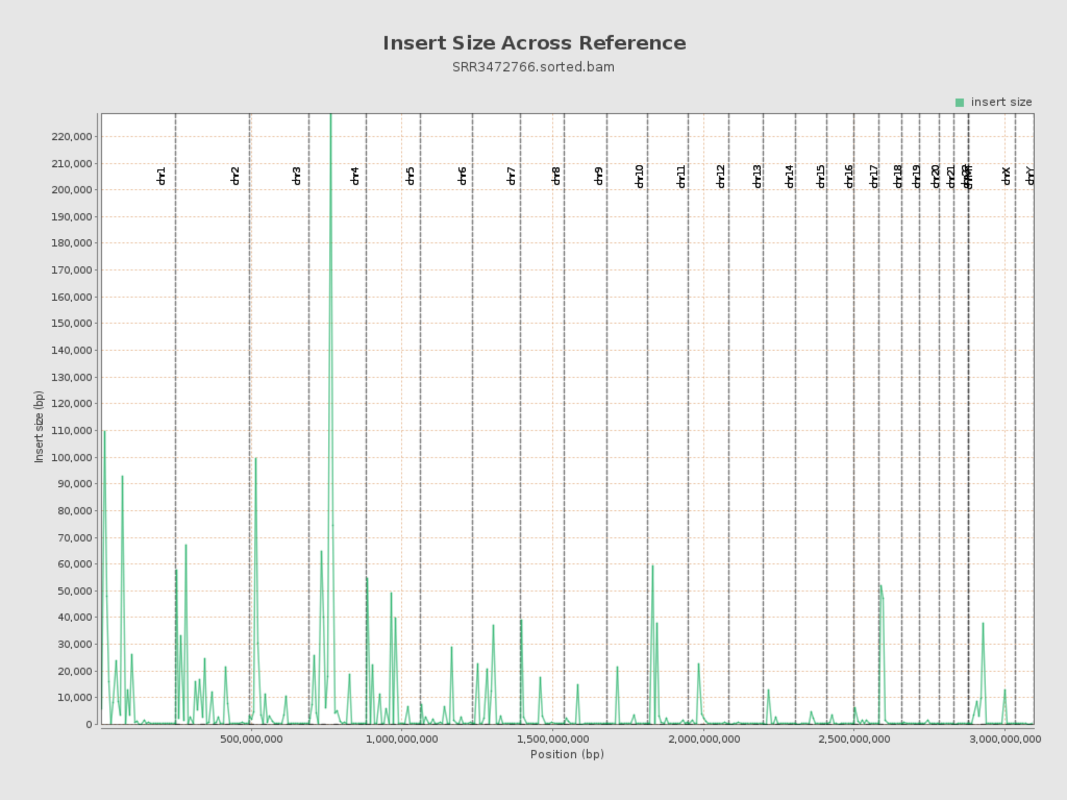
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram