Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 10:26:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472765.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_SRR3472765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472765_1.fastq.gz SRR3472765_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 10:26:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,264,274
Mapped reads	18,102,937 / 99.12%
Unmapped reads	161,337 / 0.88%
Mapped paired reads	18,102,937 / 99.12%
Mapped reads, first in pair	9,083,979 / 49.74%
Mapped reads, second in pair	9,018,958 / 49.38%
Mapped reads, both in pair	18,002,488 / 98.57%
Mapped reads, singletons	100,449 / 0.55%
Secondary alignments	0
Supplementary alignments	68,227 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,475,774 / 62.83%
Duplication rate	46.25%
Clipped reads	1,353,014 / 7.41%

2.2. ACGT Content

Number/percentage of A's	490,254,157 / 27.45%
Number/percentage of C's	405,976,206 / 22.73%
Number/percentage of T's	487,107,647 / 27.27%
Number/percentage of G's	402,292,299 / 22.53%
Number/percentage of N's	344,610 / 0.02%

GC Percentage	45.26%

2.3. Coverage

Mean	0.577
Standard Deviation	21.6315

2.4. Mapping Quality

Mean Mapping Quality	55.23

2.5. Insert size

Mean	28,955.88
Standard Deviation	1,675,540.71
P25/Median/P75	179 / 248 / 332

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	11,264,873
Insertions	106,167
Mapped reads with at least one insertion	0.58%
Deletions	103,777
Mapped reads with at least one deletion	0.57%
Homopolymer indels	44.97%

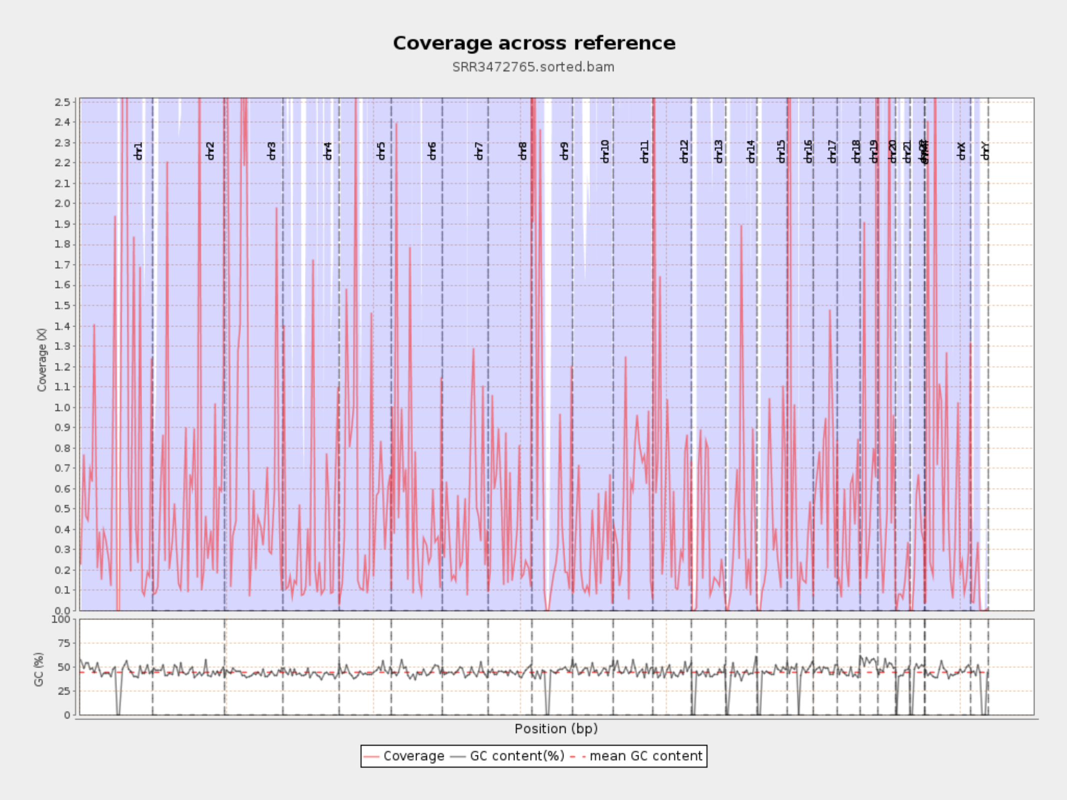
2.7. Chromosome stats

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

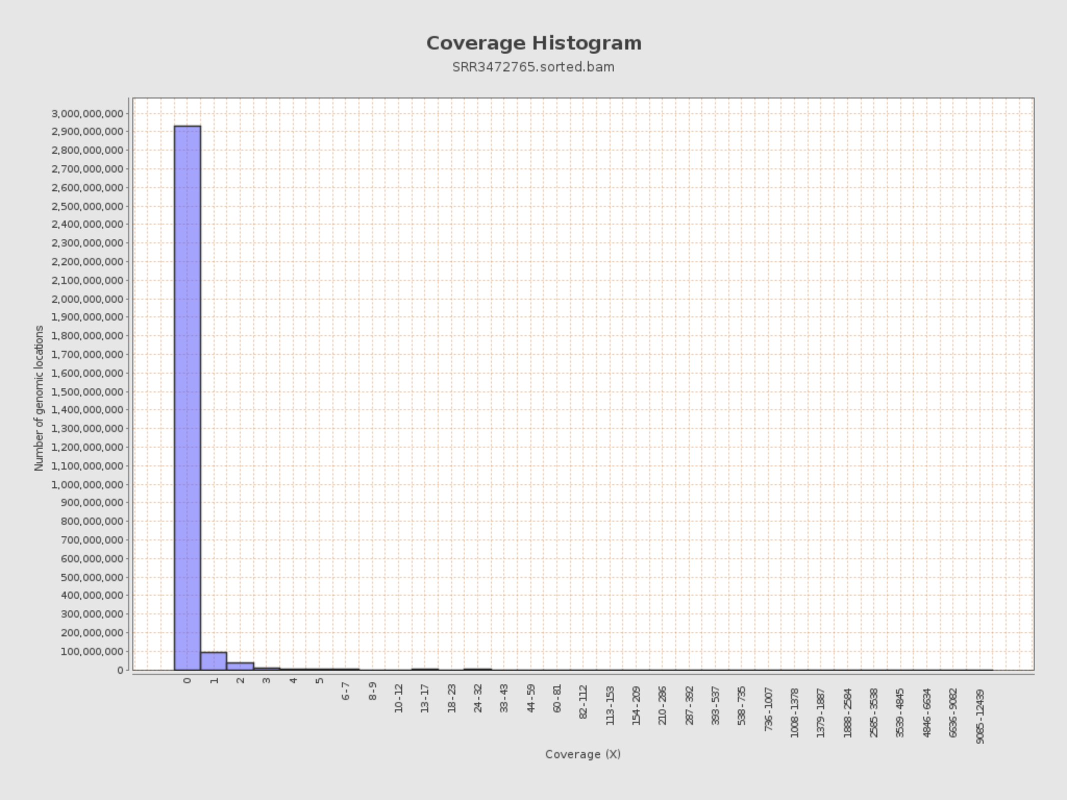
		bases	coverage	deviation
chr1	249250621	222892284	0.8942	42.4988
chr2	243199373	132973064	0.5468	28.0664
chr3	198022430	198027918	1	21.9906
chr4	191154276	67099231	0.351	12.5966
chr5	180915260	109949260	0.6077	24.7987
chr6	171115067	97641573	0.5706	15.3601
chr7	159138663	73975029	0.4648	13.5319
chr8	146364022	64135345	0.4382	13.5873
chr9	141213431	101912723	0.7217	18.3439
chr10	135534747	40724936	0.3005	9.8684
chr11	135006516	77515357	0.5742	16.9237
chr12	133851895	93667487	0.6998	19.2733
chr13	115169878	34403485	0.2987	11.3928
chr14	107349540	44793376	0.4173	14.576
chr15	102531392	40047597	0.3906	12.1236
chr16	90354753	62041316	0.6866	21.8716
chr17	81195210	56756863	0.699	15.0111
chr18	78077248	30609785	0.392	13.0227
chr19	59128983	53310895	0.9016	31.6484
chr20	63025520	50255079	0.7974	26.7014
chr21	48129895	6165193	0.1281	3.7325
chr22	51304566	16695190	0.3254	9.8807
chrMT	16571	7686	0.4638	1.4784
chrX	155270560	105960463	0.6824	23.3607

chrY	59373566	4677996	0.0788	5.0057

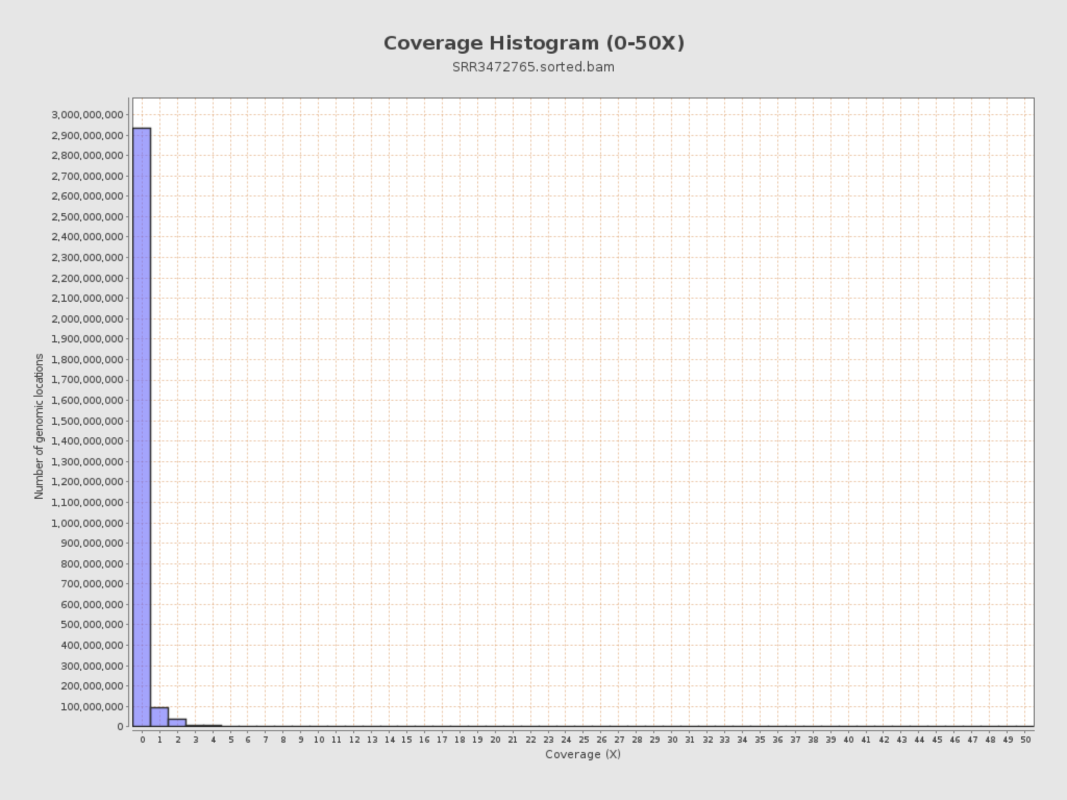
3. Results : Coverage across reference



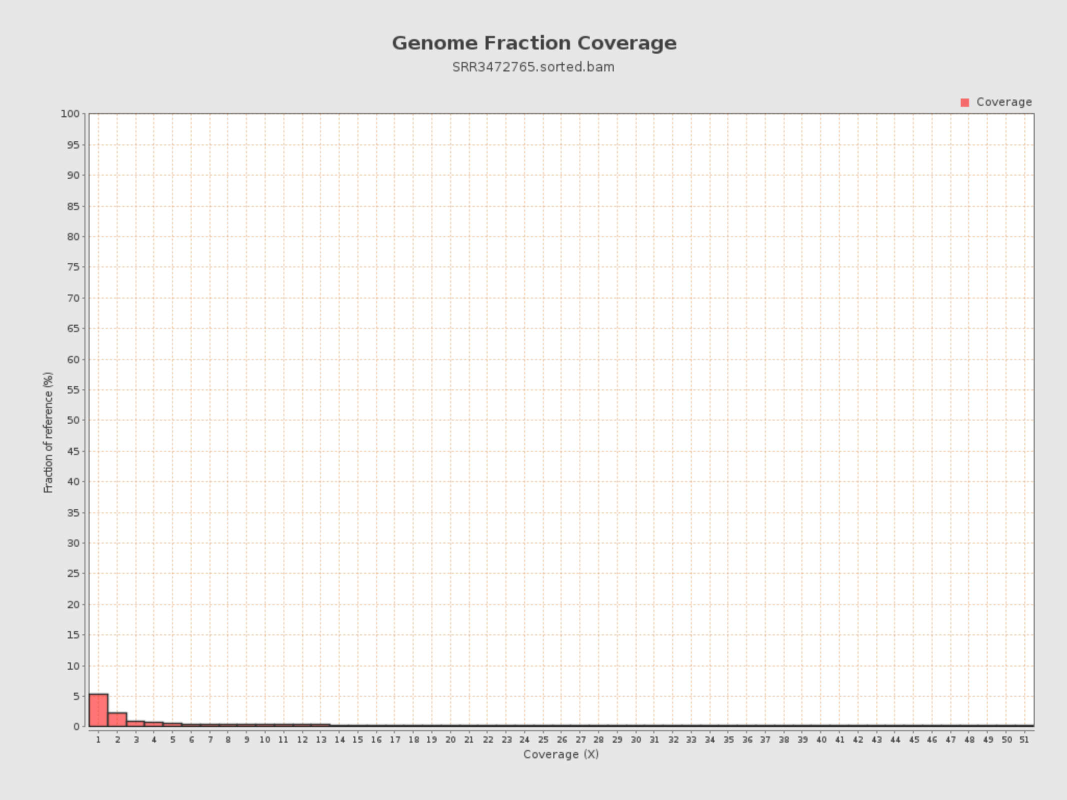
4. Results : Coverage Histogram



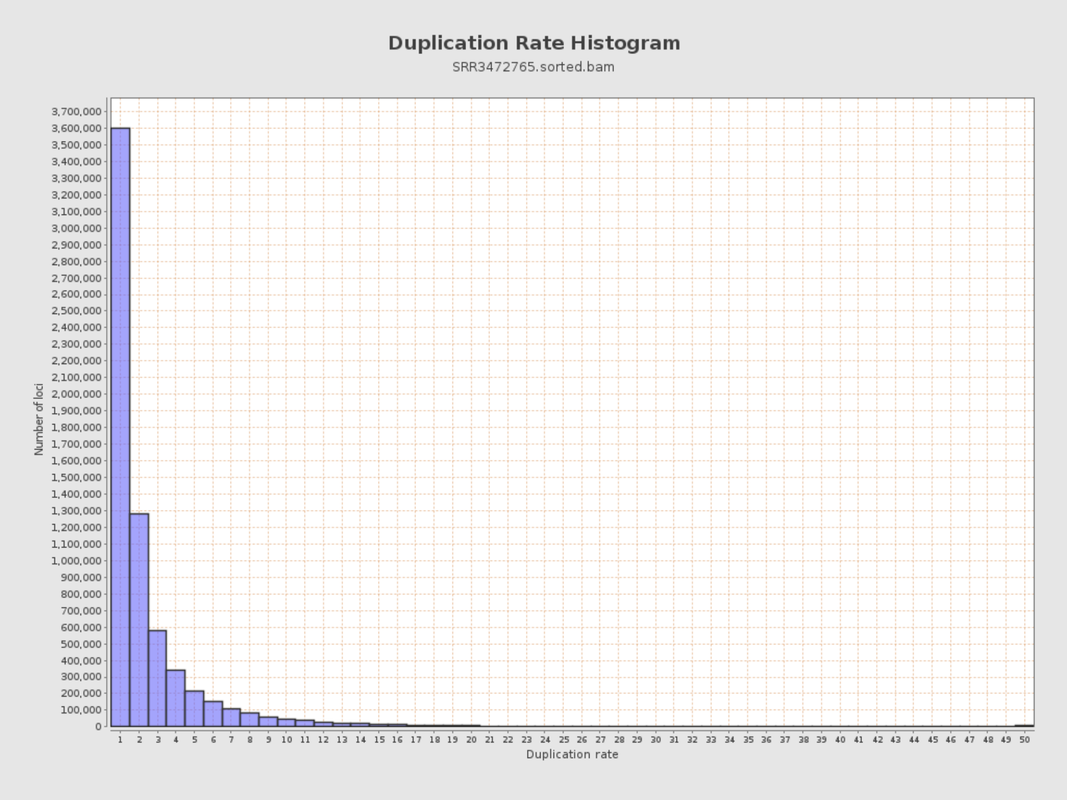
5. Results : Coverage Histogram (0-50X)



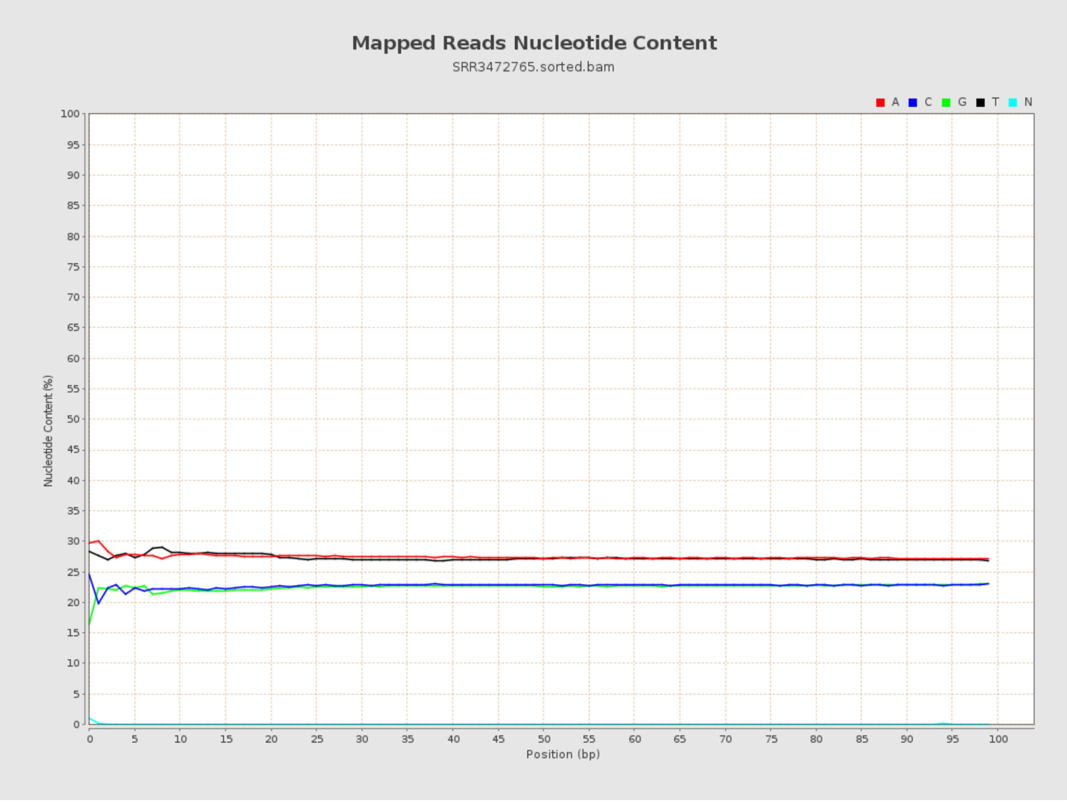
6. Results : Genome Fraction Coverage



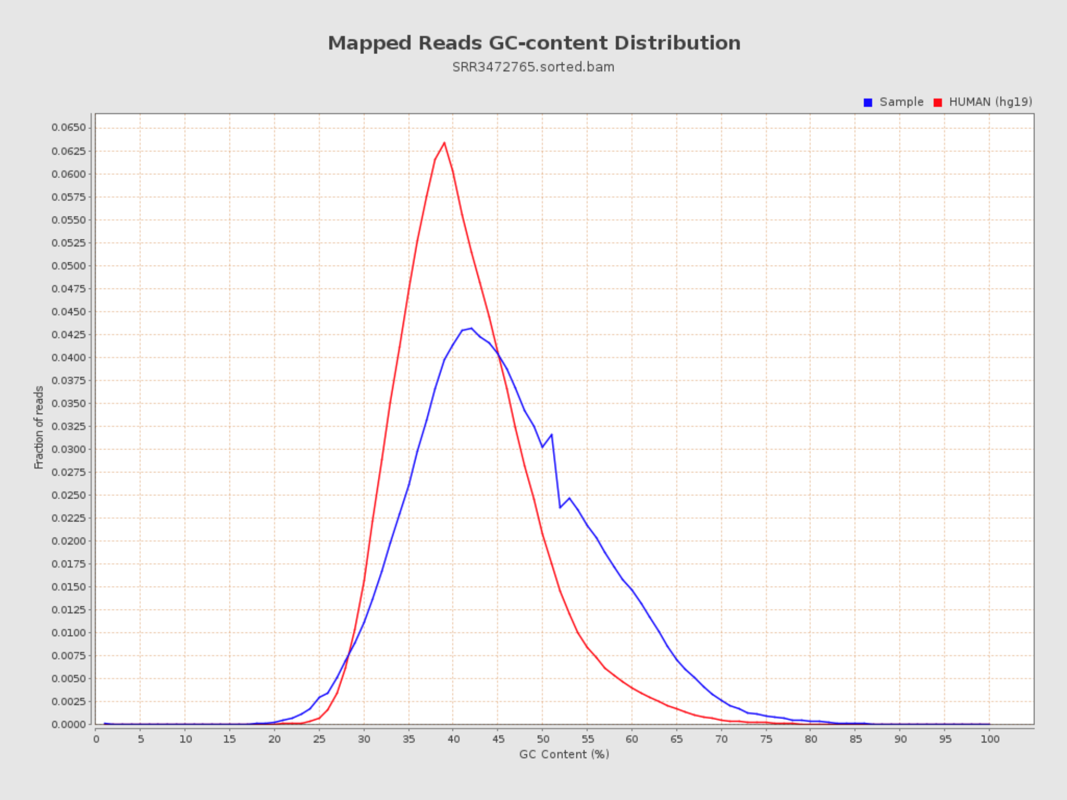
7. Results : Duplication Rate Histogram



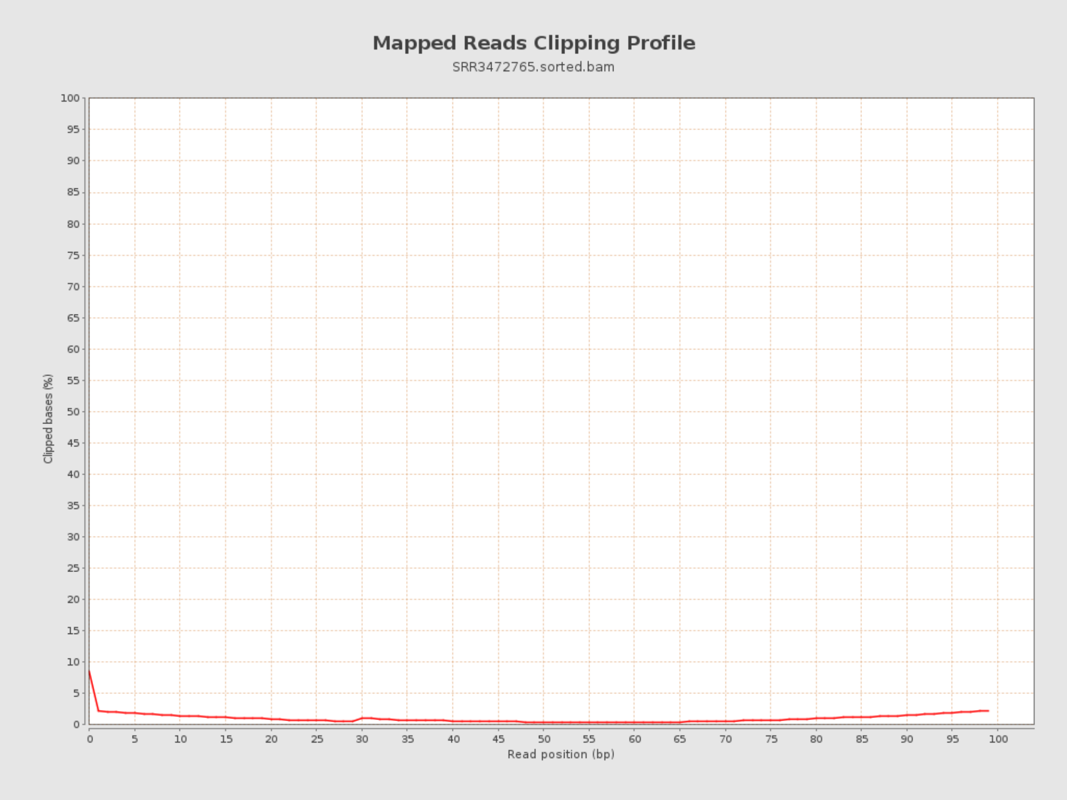
8. Results : Mapped Reads Nucleotide Content



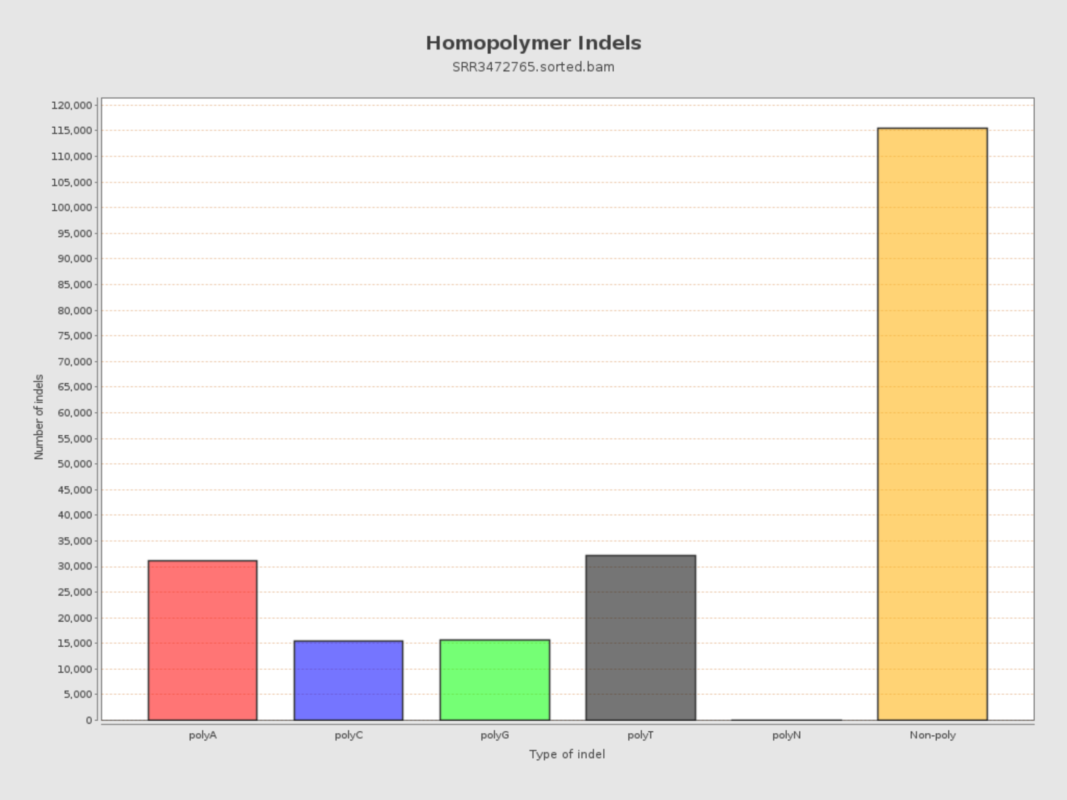
9. Results : Mapped Reads GC-content Distribution



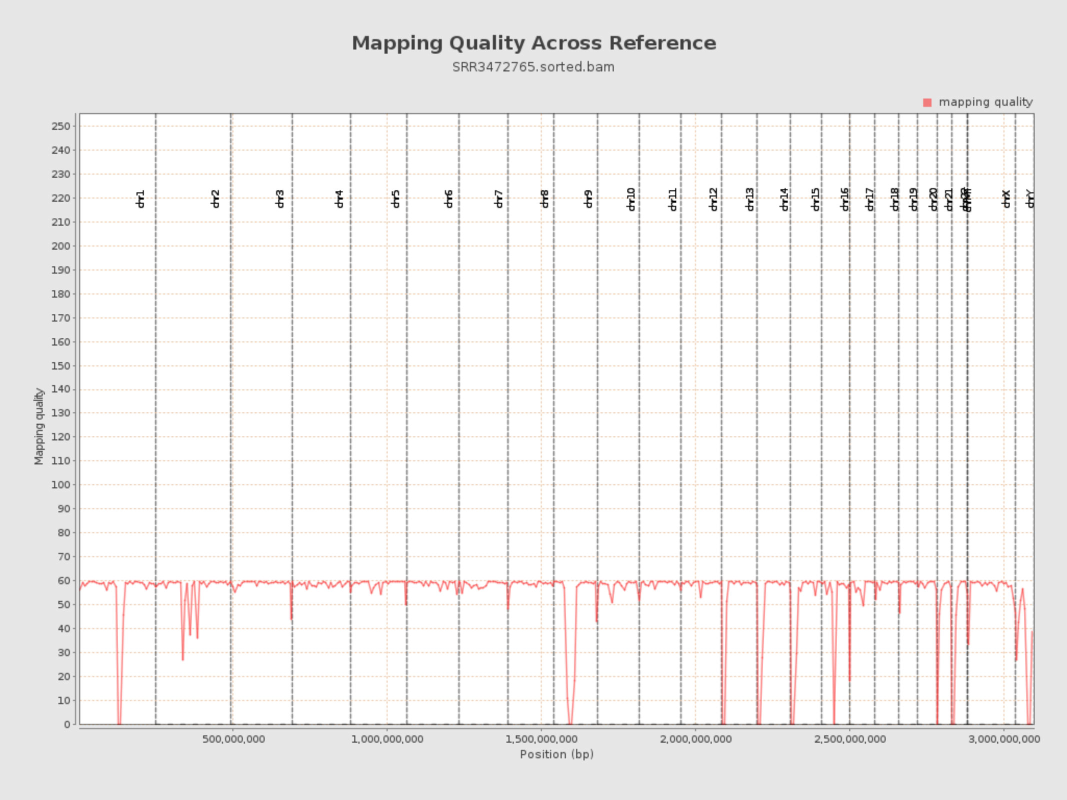
10. Results : Mapped Reads Clipping Profile



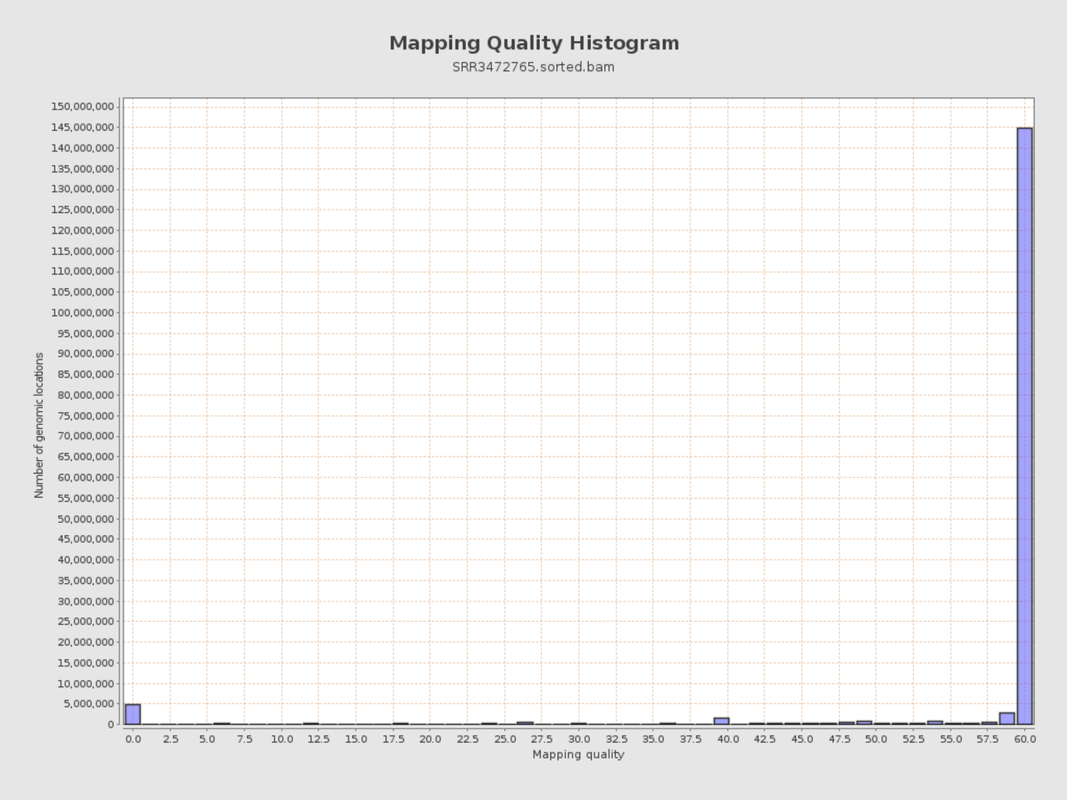
11. Results : Homopolymer Indels



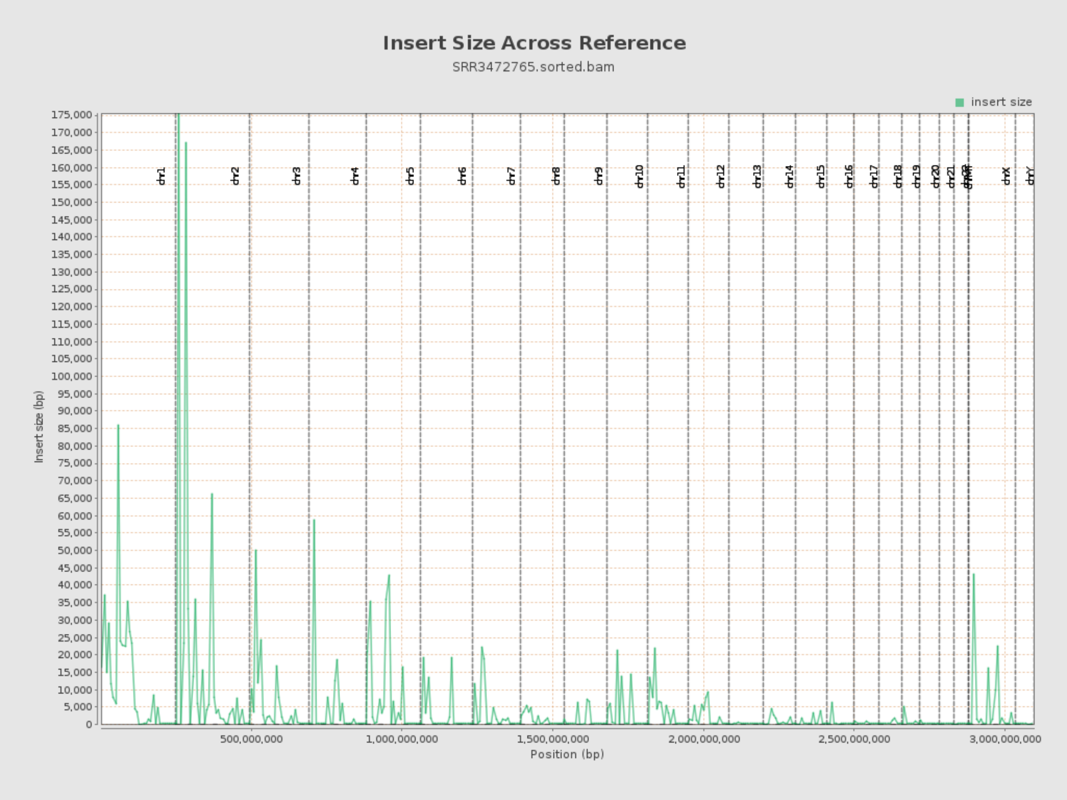
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram