Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 00:34:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472660.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_SRR3472660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472660_1.fastq.gz SRR3472660_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 00:34:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,247,194
Mapped reads	16,117,328 / 99.2%
Unmapped reads	129,866 / 0.8%
Mapped paired reads	16,117,328 / 99.2%
Mapped reads, first in pair	8,082,573 / 49.75%
Mapped reads, second in pair	8,034,755 / 49.45%
Mapped reads, both in pair	16,026,060 / 98.64%
Mapped reads, singletons	91,268 / 0.56%
Secondary alignments	0
Supplementary alignments	101,899 / 0.63%
Read min/max/mean length	30 / 101 / 99.93
Duplicated reads (estimated)	10,856,422 / 66.82%
Duplication rate	49%
Clipped reads	1,076,572 / 6.63%

2.2. ACGT Content

Number/percentage of A's	438,247,835 / 27.57%
Number/percentage of C's	358,651,567 / 22.56%
Number/percentage of T's	439,488,697 / 27.64%
Number/percentage of G's	353,082,384 / 22.21%
Number/percentage of N's	296,325 / 0.02%

GC Percentage	44.77%

2.3. Coverage

Mean	0.5136
Standard Deviation	22.1963

2.4. Mapping Quality

Mean Mapping Quality	54.74

2.5. Insert size

Mean	23,425.55
Standard Deviation	1,498,571.69
P25/Median/P75	172 / 234 / 307

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,971,345
Insertions	107,716
Mapped reads with at least one insertion	0.66%
Deletions	82,339
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.45%

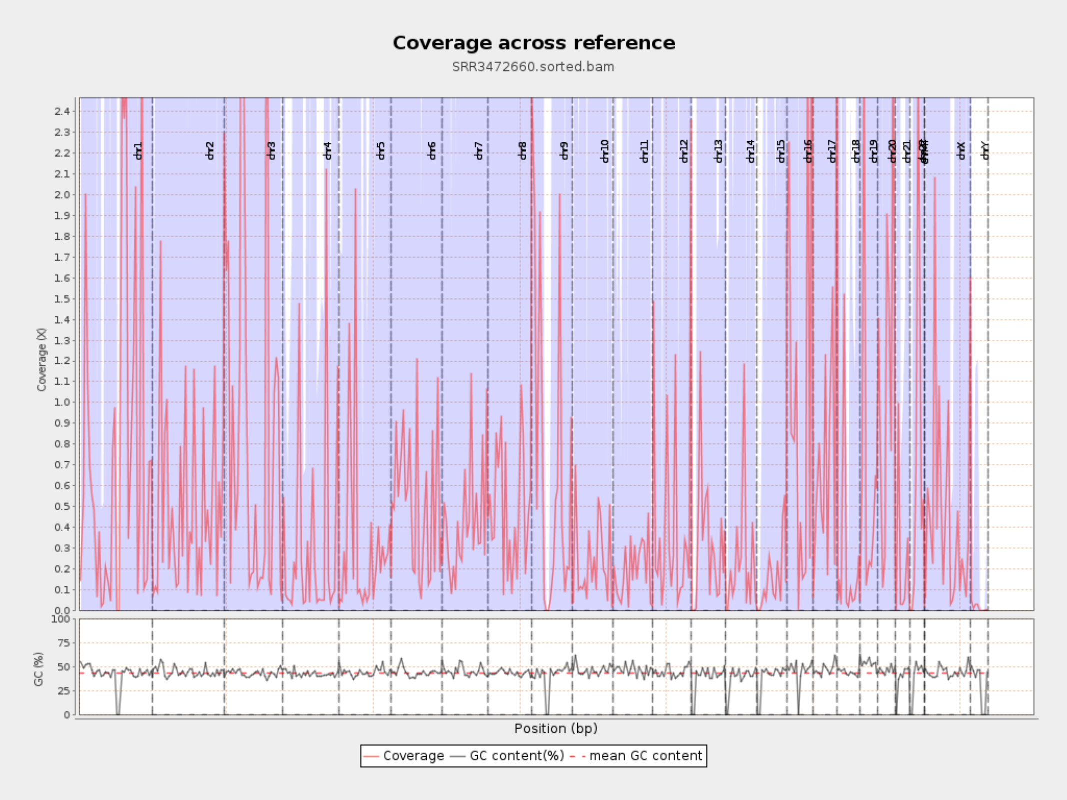
2.7. Chromosome stats

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

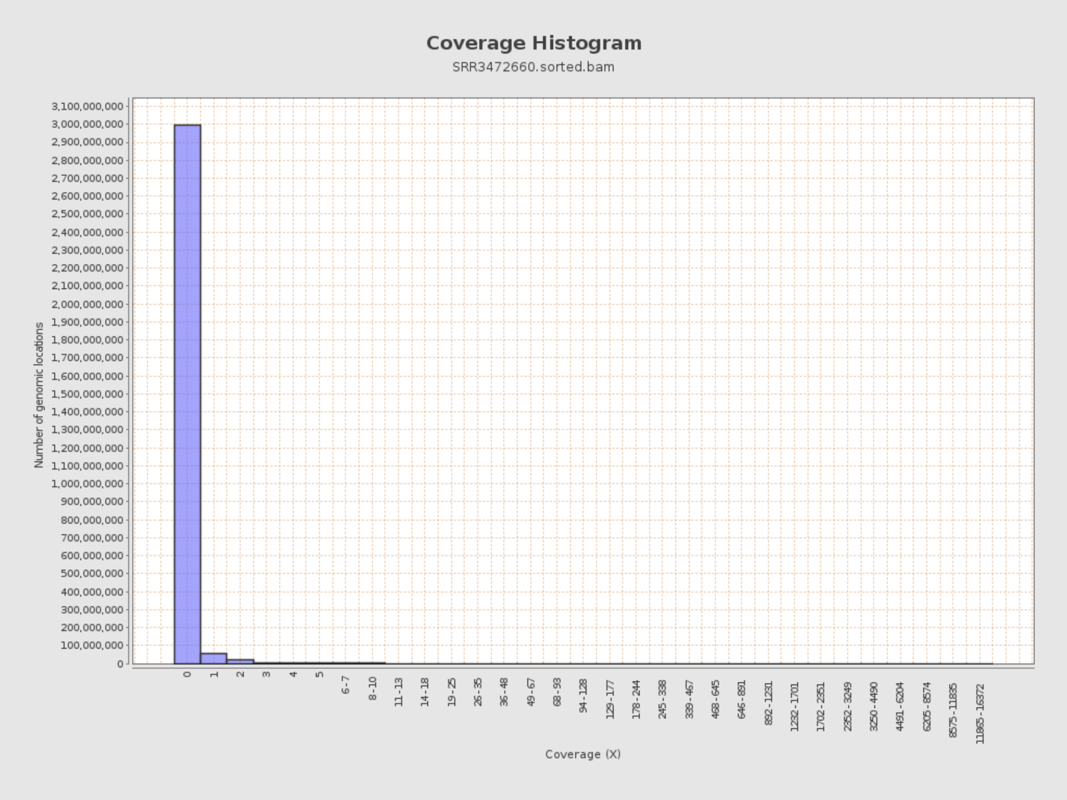
		bases	coverage	deviation
chr1	249250621	196455530	0.7882	30.919
chr2	243199373	119777473	0.4925	18.5267
chr3	198022430	205486773	1.0377	40.4718
chr4	191154276	60436003	0.3162	18.5536
chr5	180915260	59211384	0.3273	13.0106
chr6	171115067	89542388	0.5233	13.94
chr7	159138663	69005093	0.4336	13.8196
chr8	146364022	72597448	0.496	16.3214
chr9	141213431	102492863	0.7258	19.0436
chr10	135534747	31552383	0.2328	12.8381
chr11	135006516	26254915	0.1945	7.1772
chr12	133851895	55177908	0.4122	14.8104
chr13	115169878	36931528	0.3207	11.6815
chr14	107349540	24309368	0.2265	10.2078
chr15	102531392	16368057	0.1596	6.1617
chr16	90354753	111118892	1.2298	46.7484
chr17	81195210	62569843	0.7706	23.2154
chr18	78077248	17870754	0.2289	20.9744
chr19	59128983	40129248	0.6787	19.7094
chr20	63025520	74093804	1.1756	44.2943
chr21	48129895	11710070	0.2433	18.0199
chr22	51304566	34393684	0.6704	36.5764
chrMT	16571	6795	0.4101	0.8164
chrX	155270560	71667912	0.4616	14.4882

chrY	59373566	804711	0.0136	0.8098

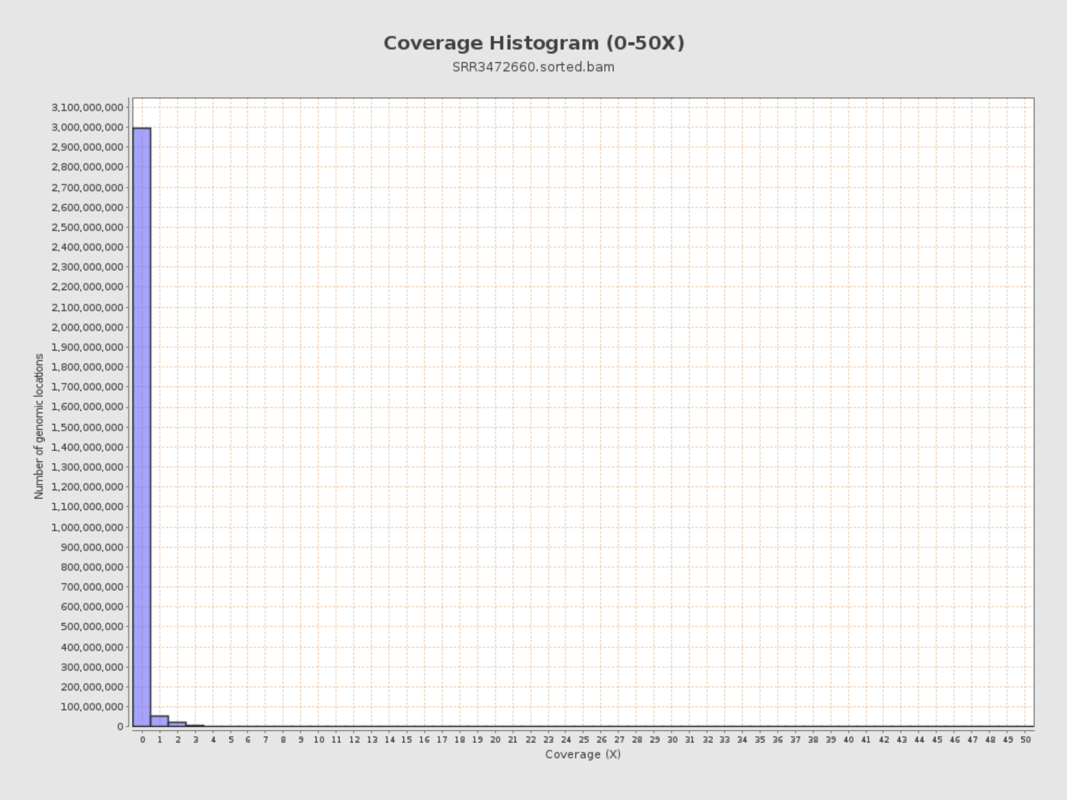
3. Results : Coverage across reference



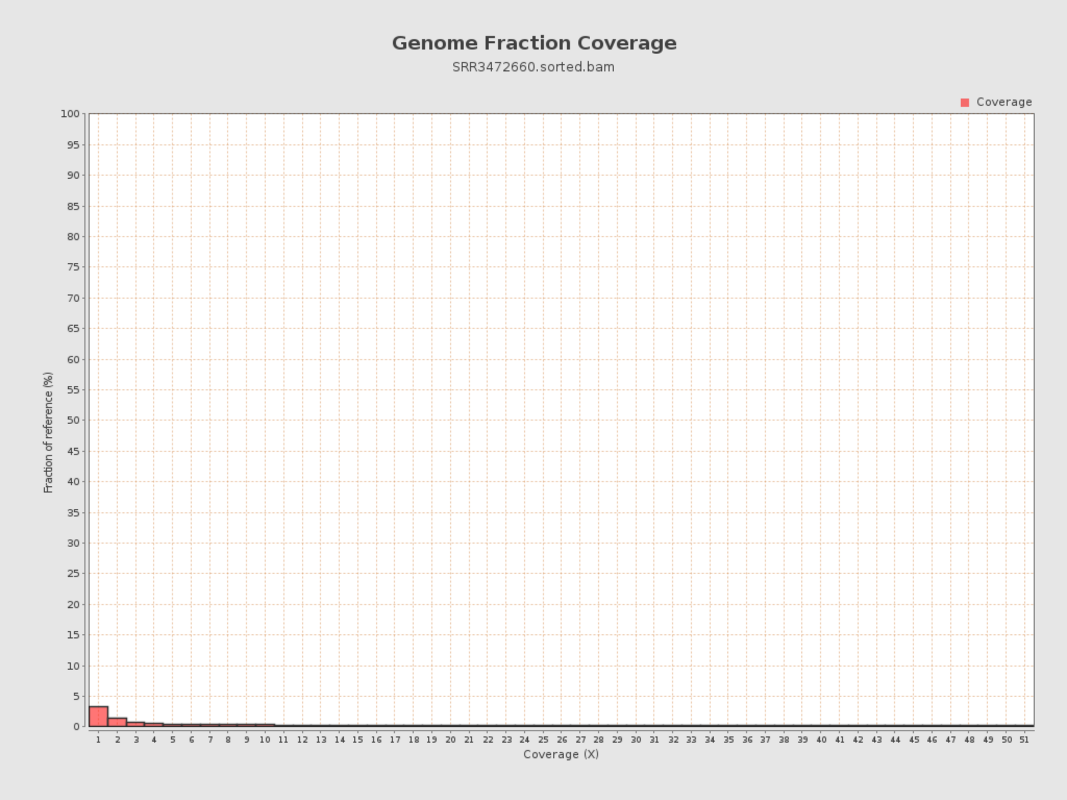
4. Results : Coverage Histogram



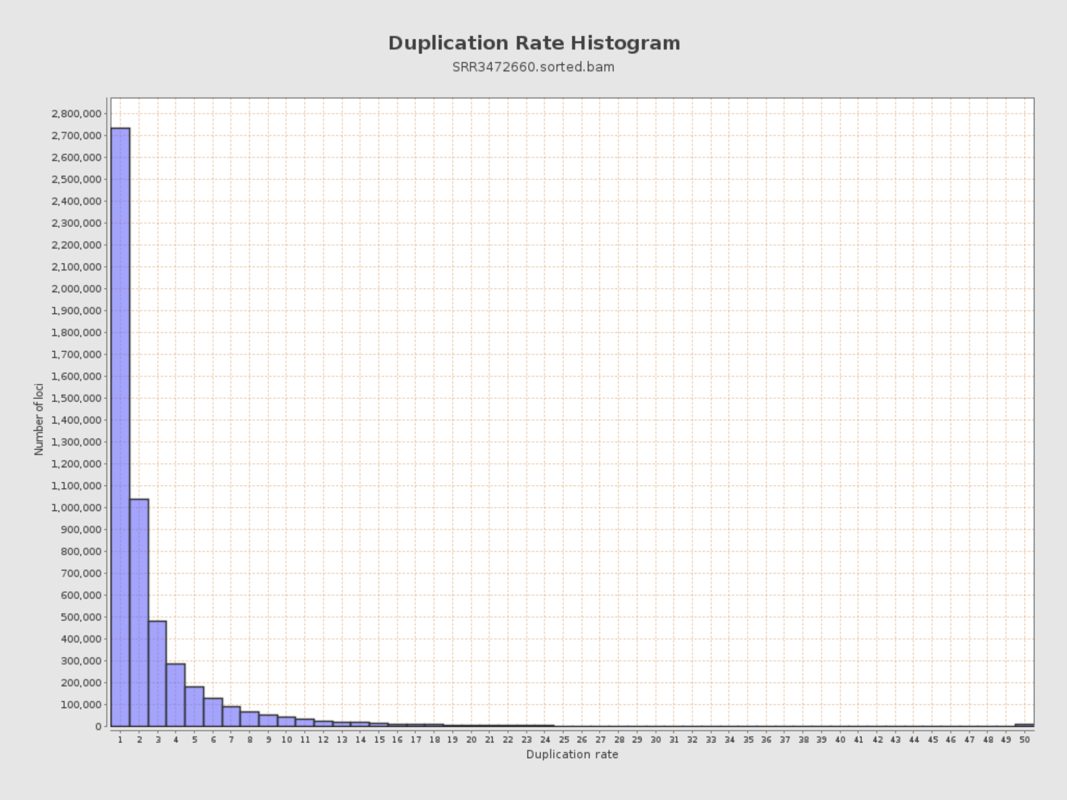
5. Results : Coverage Histogram (0-50X)



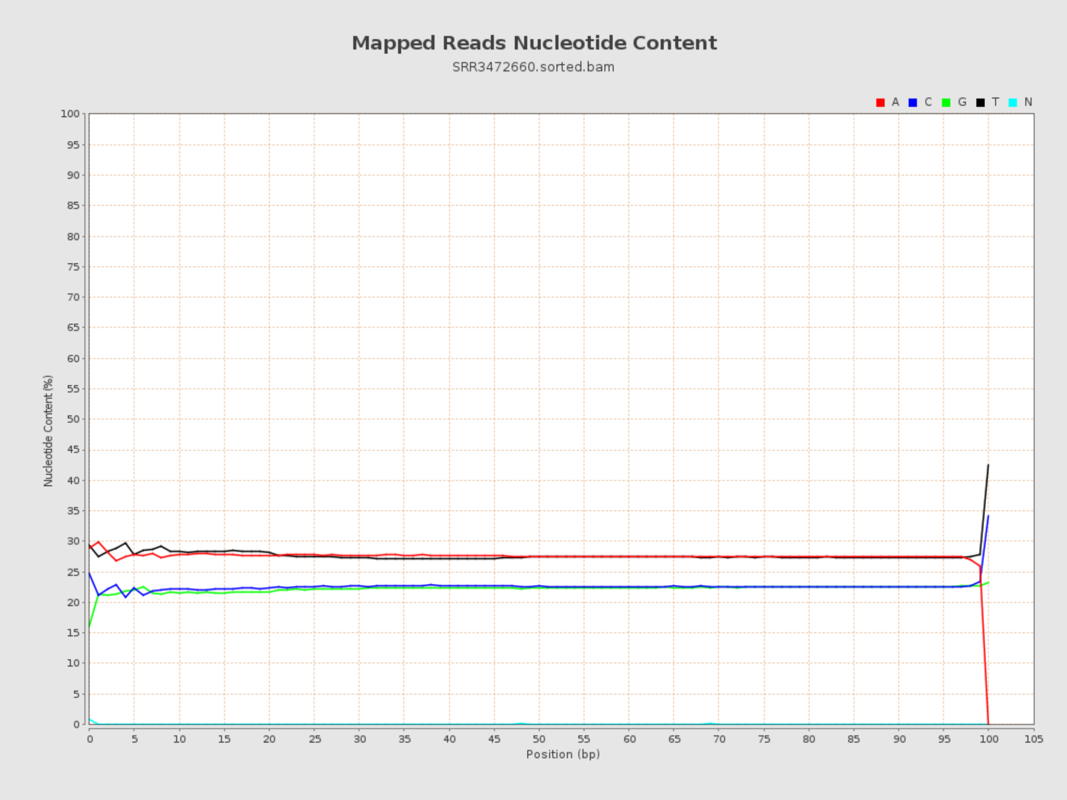
6. Results : Genome Fraction Coverage



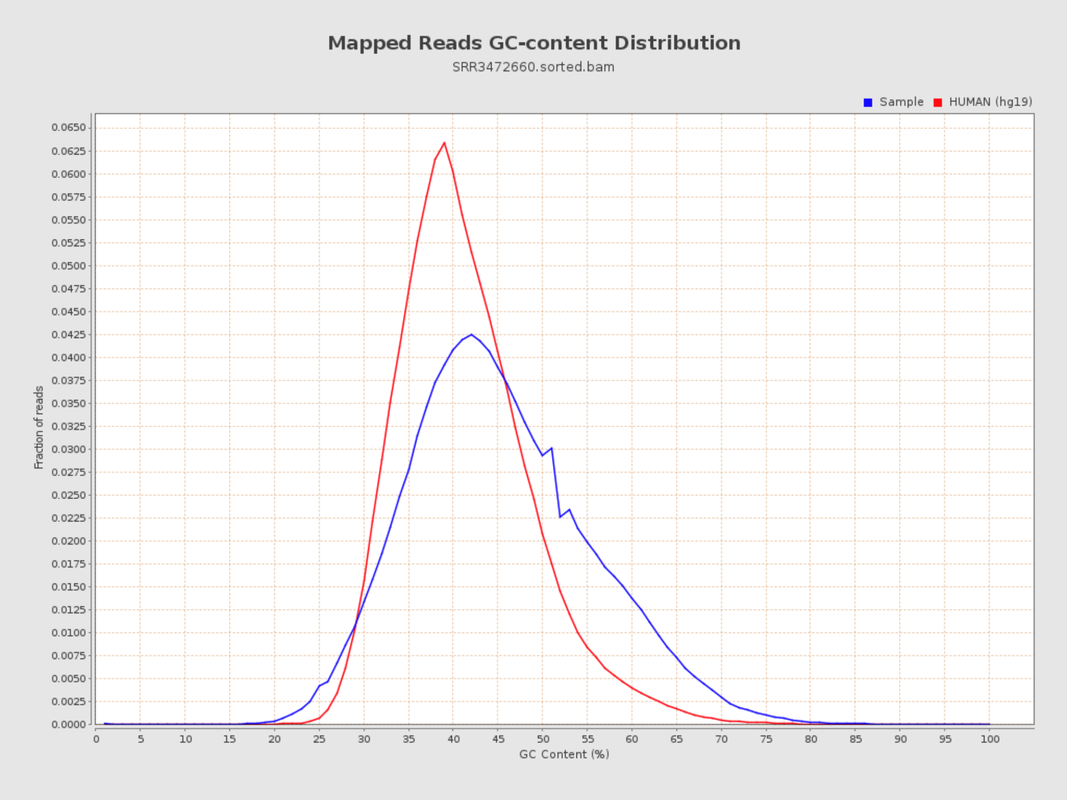
7. Results : Duplication Rate Histogram



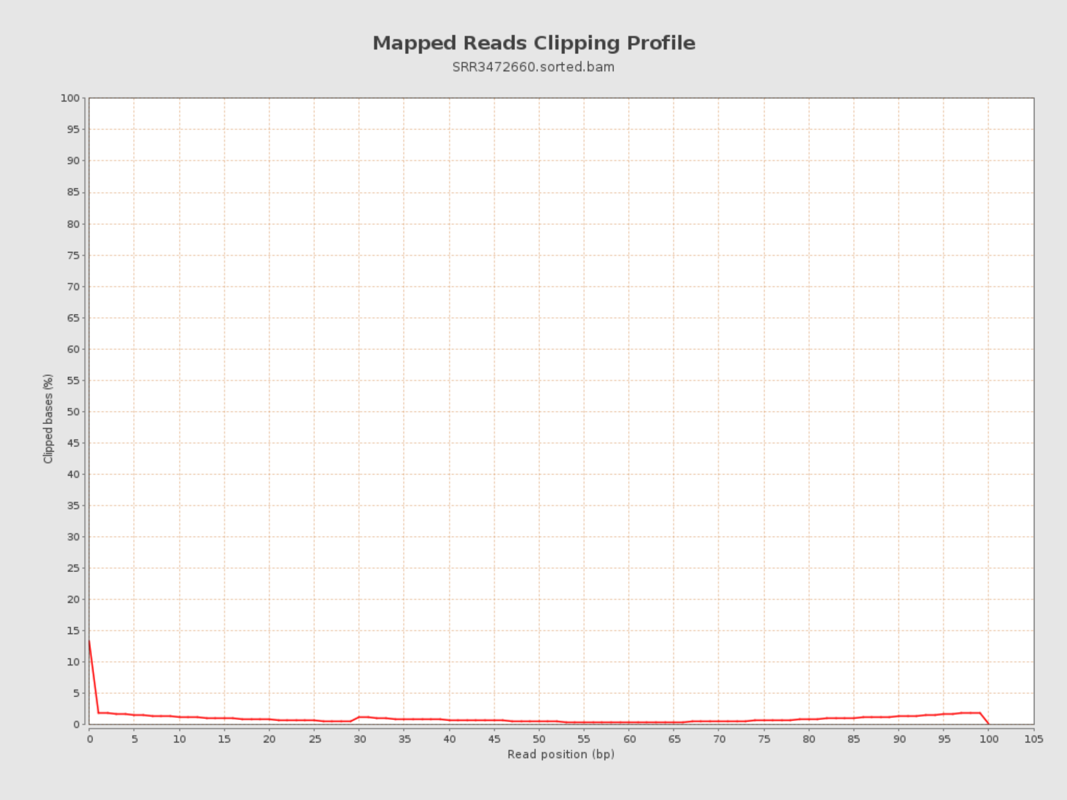
8. Results : Mapped Reads Nucleotide Content



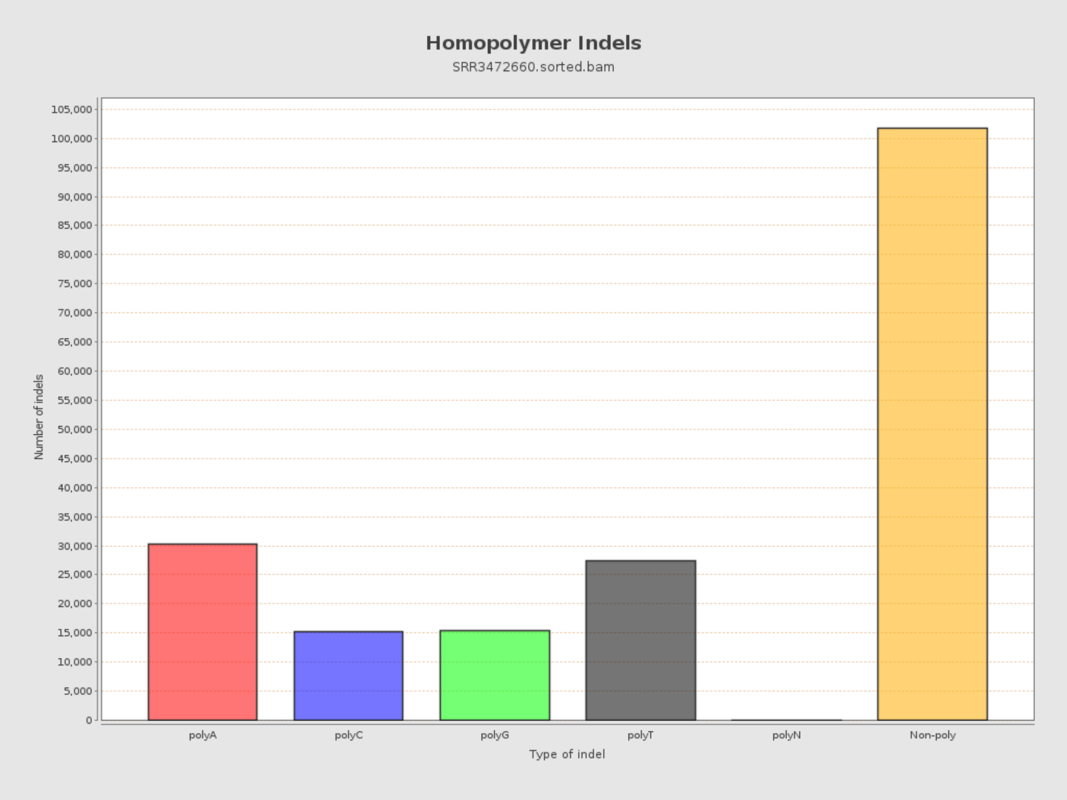
9. Results : Mapped Reads GC-content Distribution



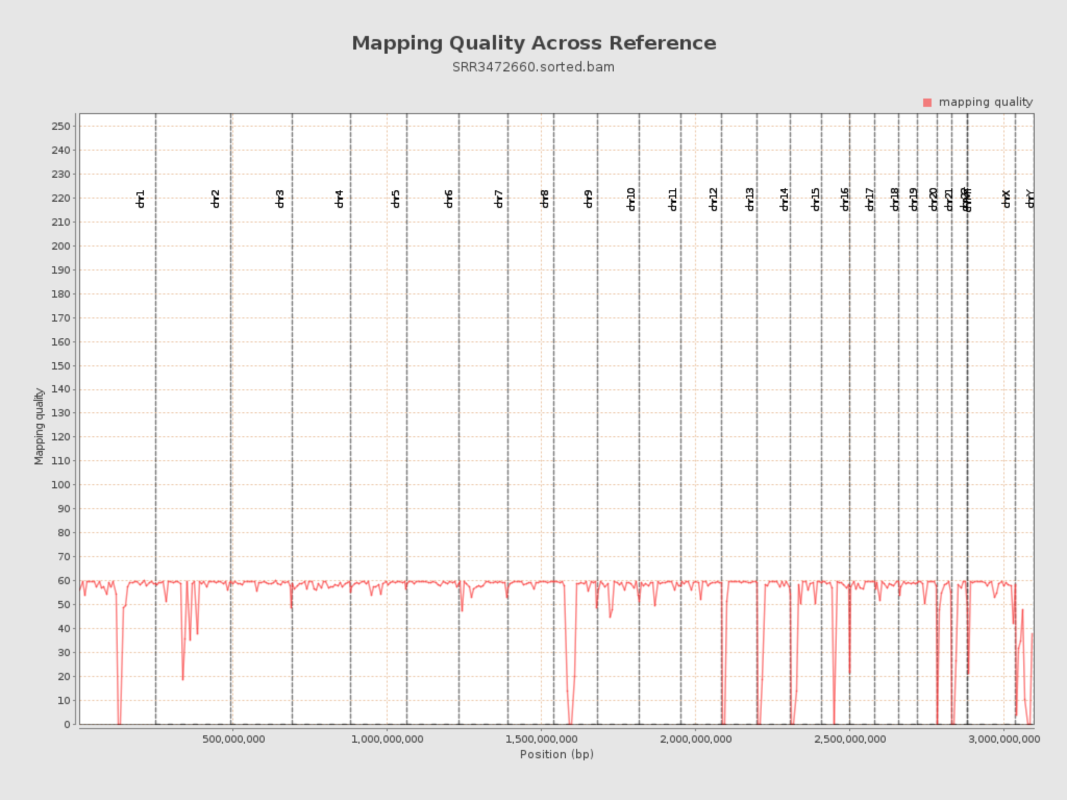
10. Results : Mapped Reads Clipping Profile



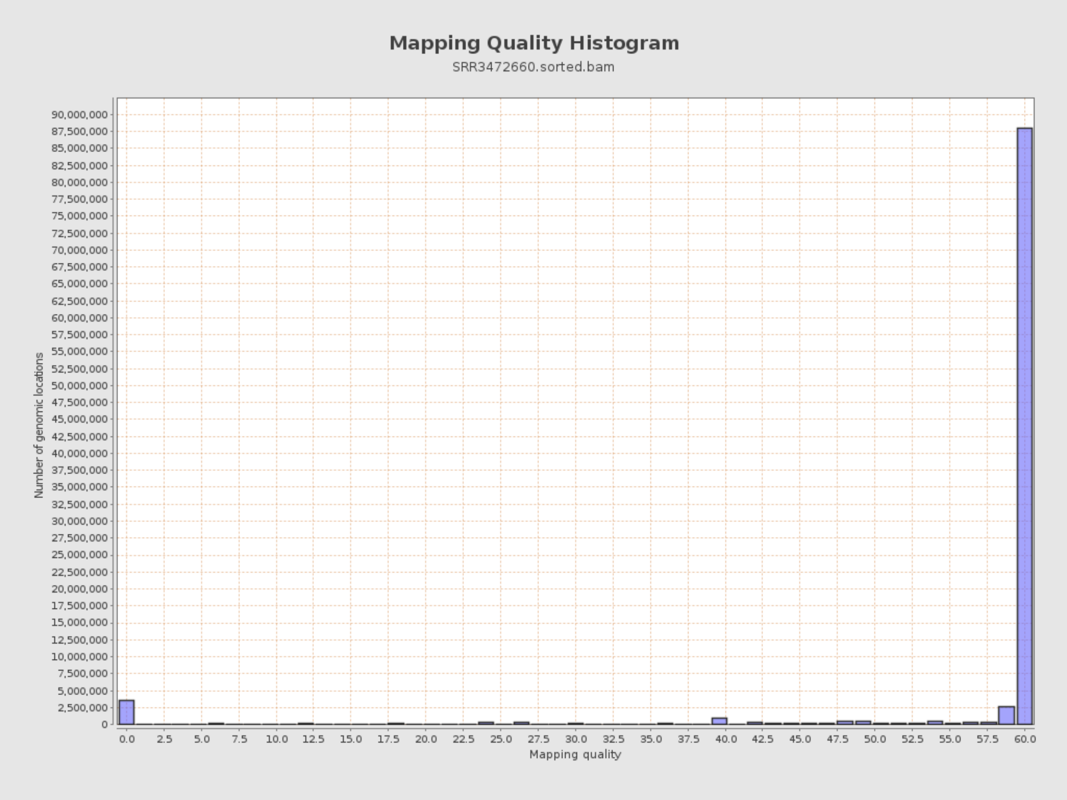
11. Results : Homopolymer Indels



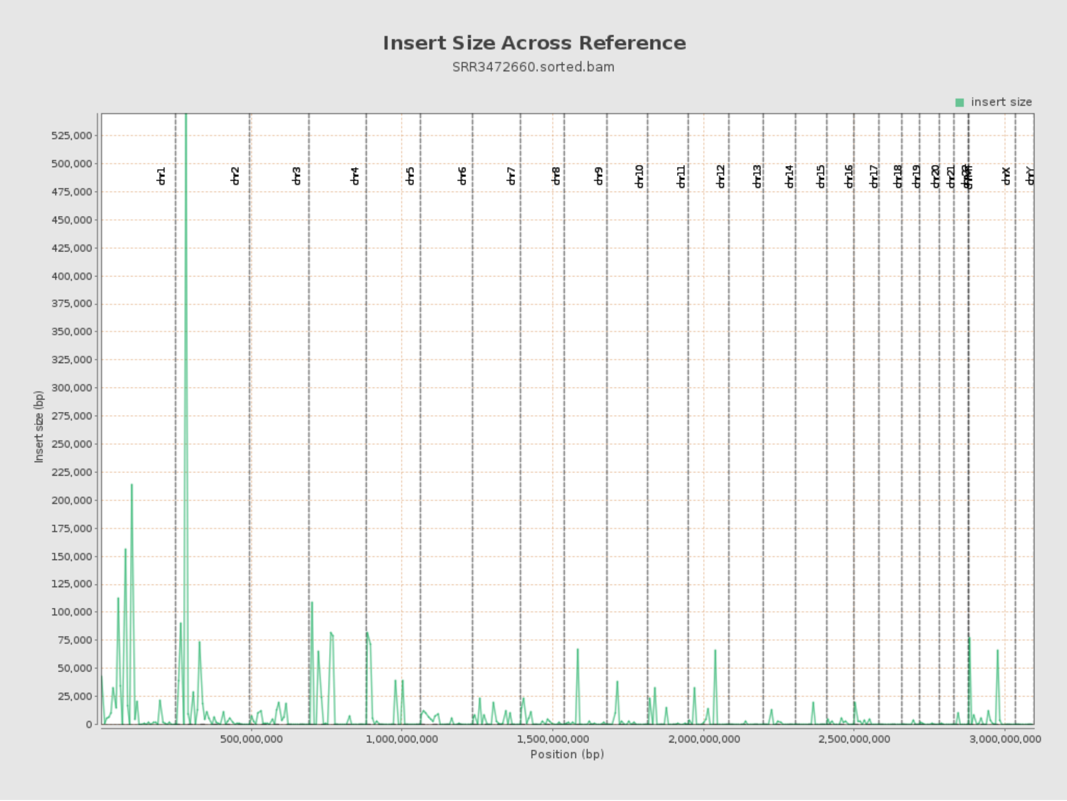
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram