Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 02:01:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264628.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_SRR1264628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264628_1.fastq.gz SRR1264628_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 02:01:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264628.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,225,488,472
Mapped reads	1,217,642,116 / 99.36%
Unmapped reads	7,846,356 / 0.64%
Mapped paired reads	1,217,642,116 / 99.36%
Mapped reads, first in pair	610,212,176 / 49.79%
Mapped reads, second in pair	607,429,940 / 49.57%
Mapped reads, both in pair	1,213,771,056 / 99.04%
Mapped reads, singletons	3,871,060 / 0.32%
Secondary alignments	0
Supplementary alignments	6,803,858 / 0.56%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	427,868,429 / 34.91%
Duplication rate	34.86%
Clipped reads	47,207,810 / 3.85%

2.2. ACGT Content

Number/percentage of A's	37,847,978,075 / 30.95%
Number/percentage of C's	23,254,309,179 / 19.02%
Number/percentage of T's	37,731,069,597 / 30.86%
Number/percentage of G's	23,421,429,933 / 19.16%
Number/percentage of N's	15,318,532 / 0.01%

GC Percentage	38.17%

2.3. Coverage

Mean	39.5059
Standard Deviation	39.962

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	69,215.91
Standard Deviation	2,523,721.96
P25/Median/P75	285 / 310 / 341

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	425,840,868
Insertions	13,540,100
Mapped reads with at least one insertion	1.1%
Deletions	12,633,394
Mapped reads with at least one deletion	1.02%
Homopolymer indels	48.48%

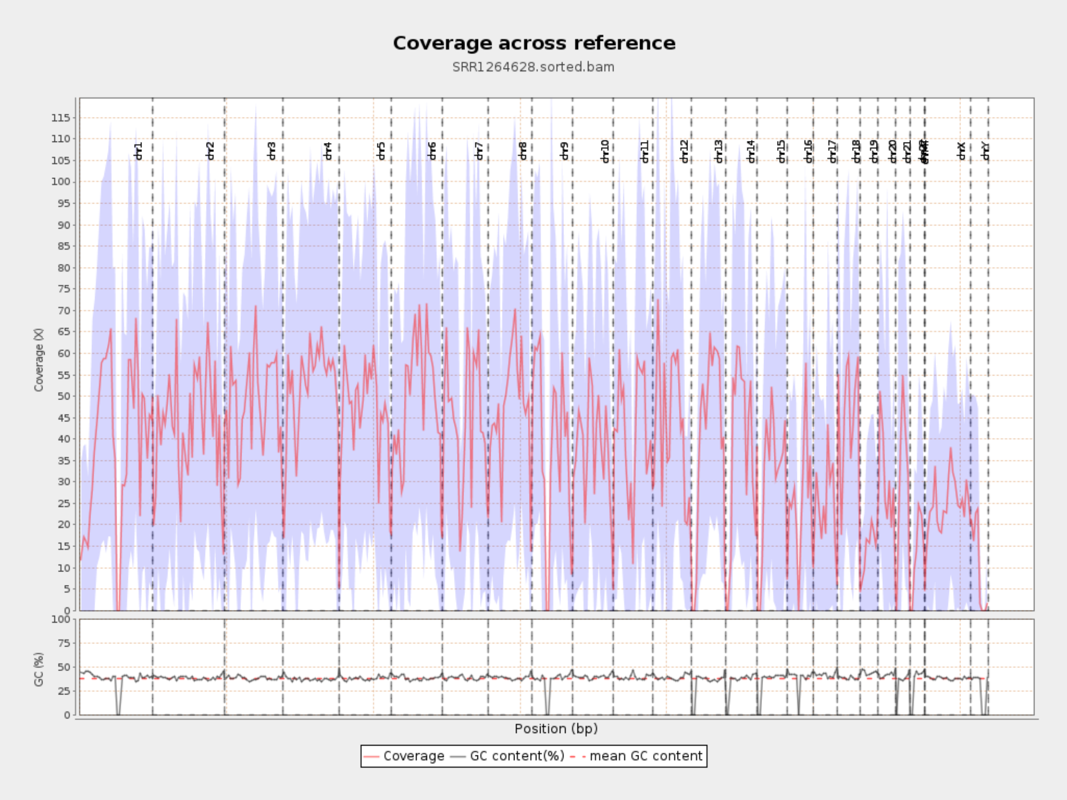
2.7. Chromosome stats

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

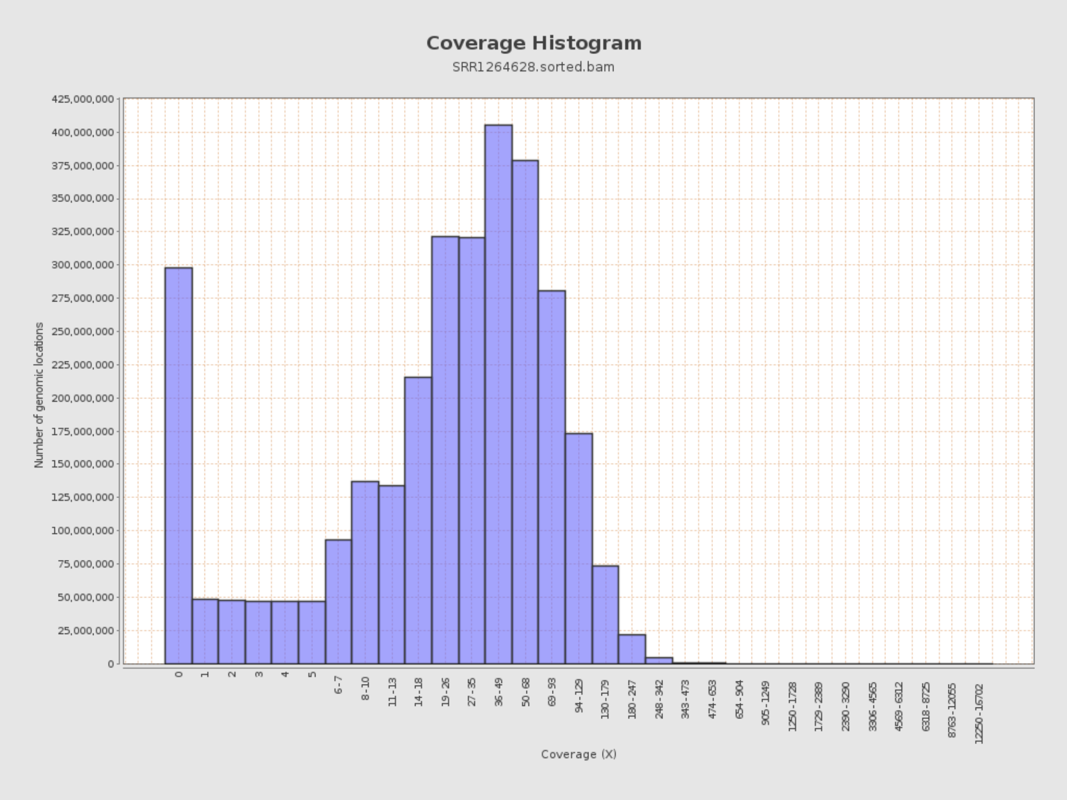
		bases	coverage	deviation
chr1	249250621	9763091833	39.1698	41.5147
chr2	243199373	10505096381	43.1954	40.4984
chr3	198022430	9663571216	48.8004	39.7685
chr4	191154276	10071978795	52.6903	40.9886
chr5	180915260	8424967701	46.5686	38.5775
chr6	171115067	8654274418	50.5758	43.1122
chr7	159138663	7047160449	44.2831	41.3018
chr8	146364022	7021711934	47.9743	40.4849
chr9	141213431	5321375787	37.6832	43.5539
chr10	135534747	5219234905	38.5085	36.7108
chr11	135006516	5575337539	41.2968	41.3138
chr12	133851895	5800606518	43.336	41.9657
chr13	115169878	4785592909	41.5525	39.7918
chr14	107349540	4065458294	37.8712	40.605
chr15	102531392	3178432298	30.9996	36.2306
chr16	90354753	2209929180	24.4584	30.6928
chr17	81195210	1994405816	24.5631	30.6716
chr18	78077248	3539354124	45.3314	38.8534
chr19	59128983	851750035	14.4049	21.7316
chr20	63025520	1869488883	29.6624	40.1706
chr21	48129895	1542667361	32.0522	42.0045
chr22	51304566	680837605	13.2705	22.5126
chrMT	16571	73506	4.4358	7.7886
chrX	155270560	3892936217	25.072	26.2466

chrY	59373566	618879513	10.4235	22.7523

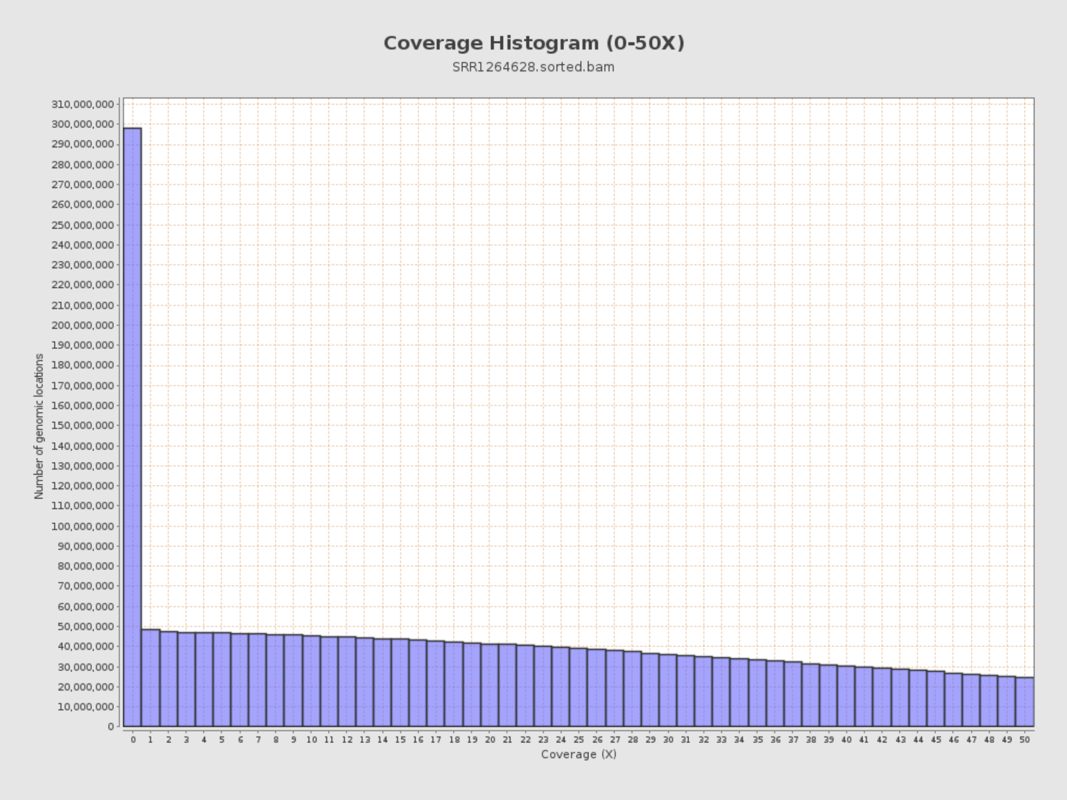
3. Results : Coverage across reference



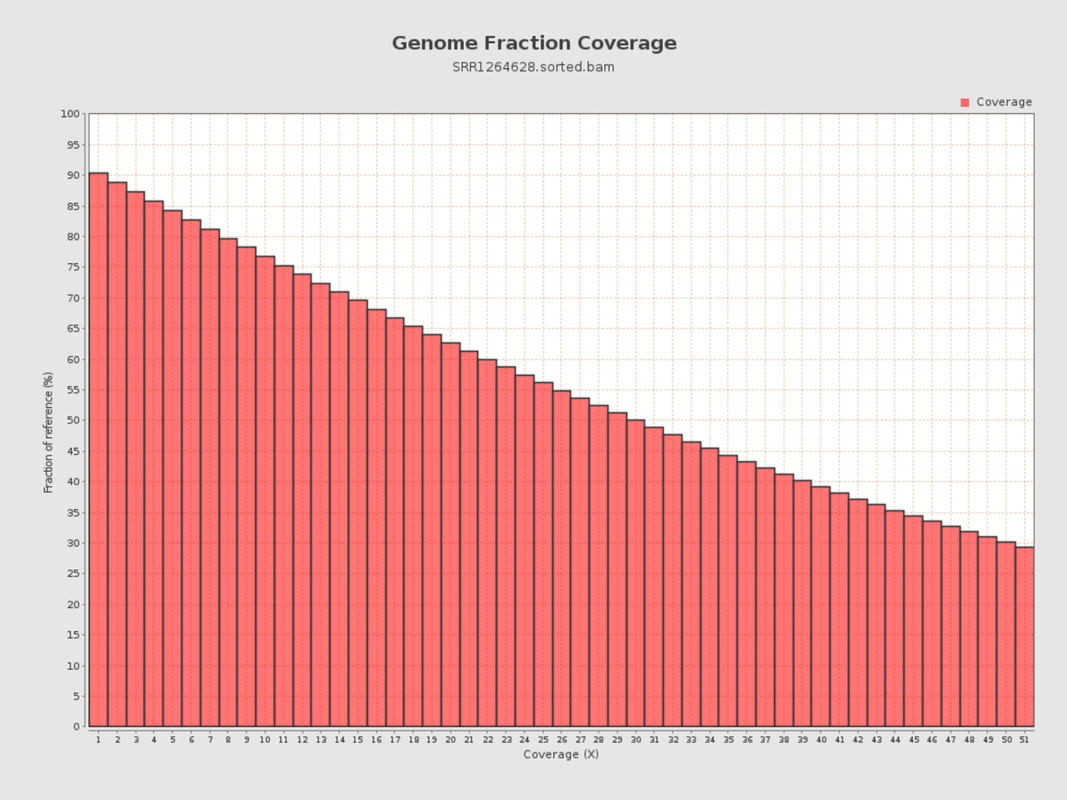
4. Results : Coverage Histogram



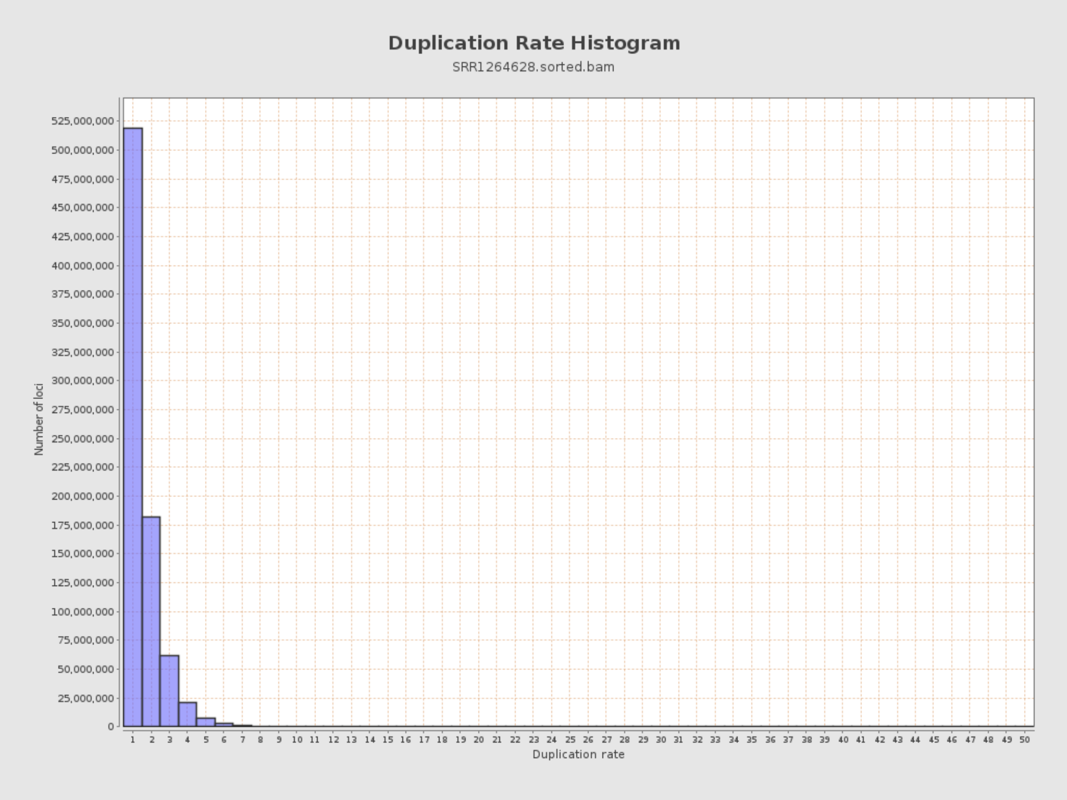
5. Results : Coverage Histogram (0-50X)



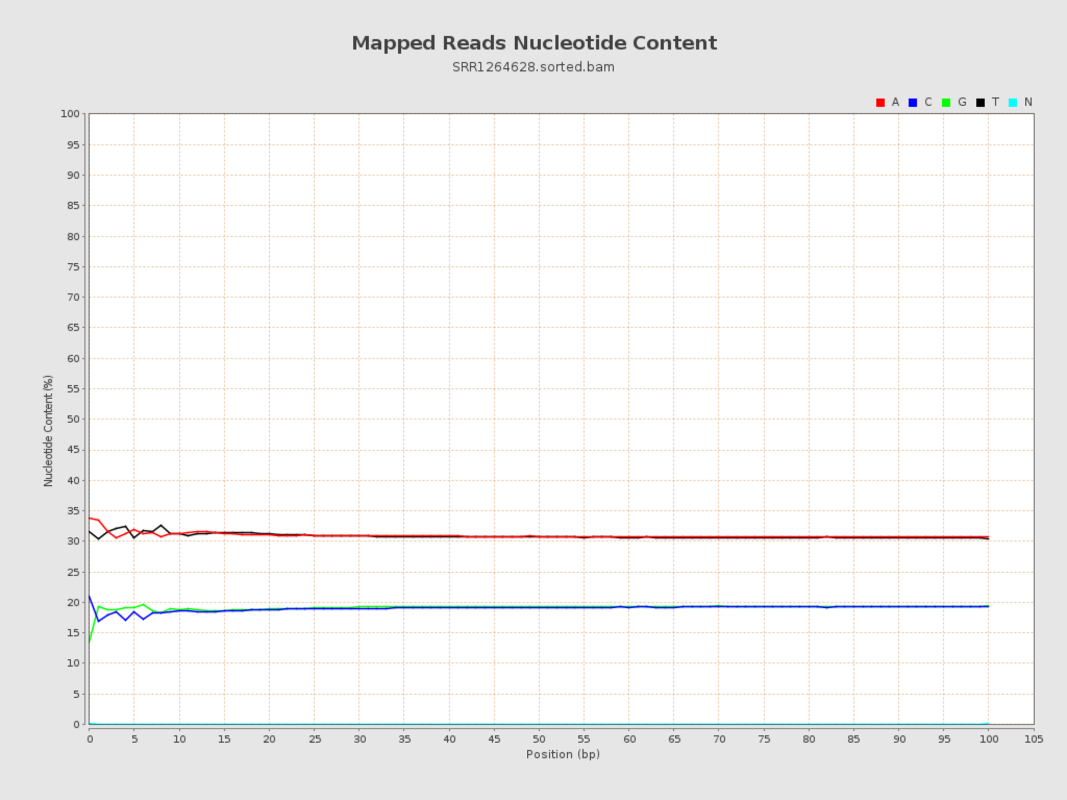
6. Results : Genome Fraction Coverage



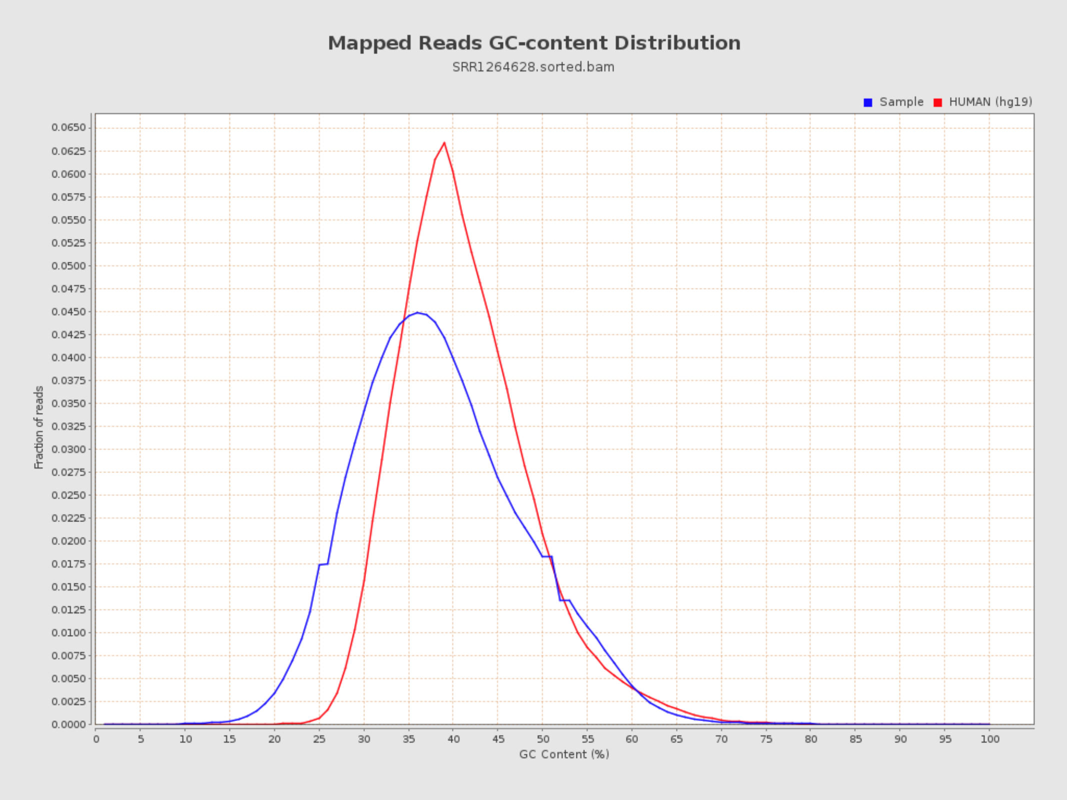
7. Results : Duplication Rate Histogram



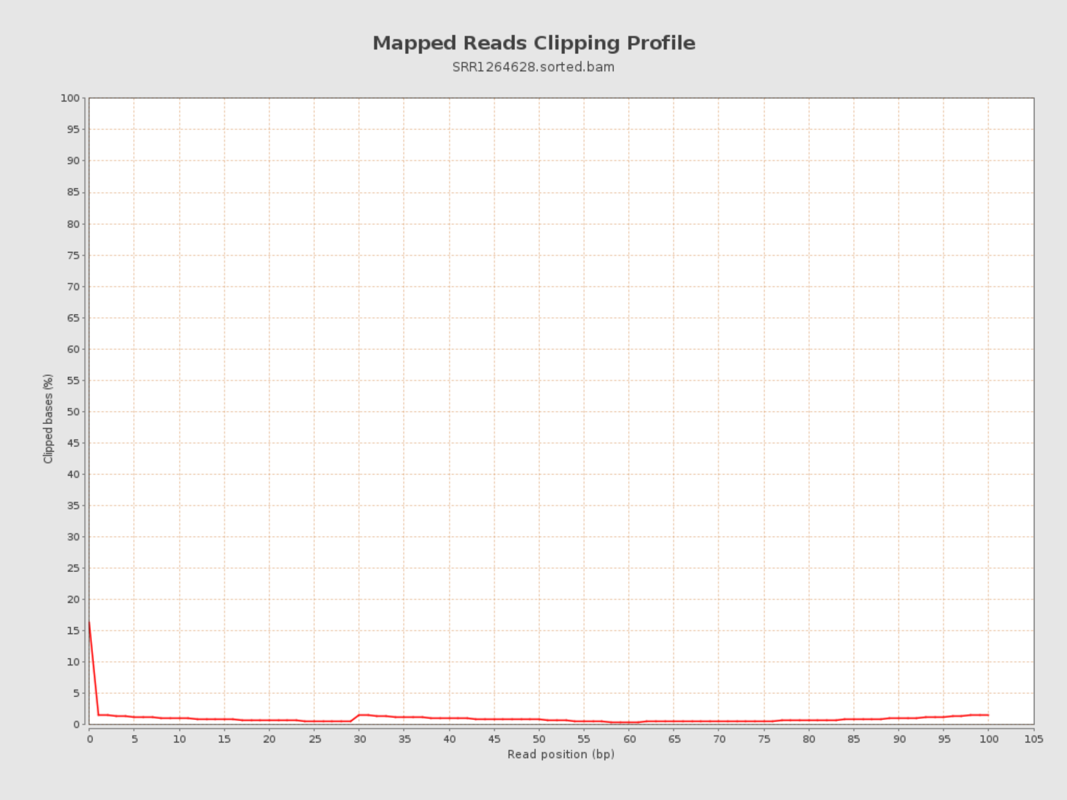
8. Results : Mapped Reads Nucleotide Content



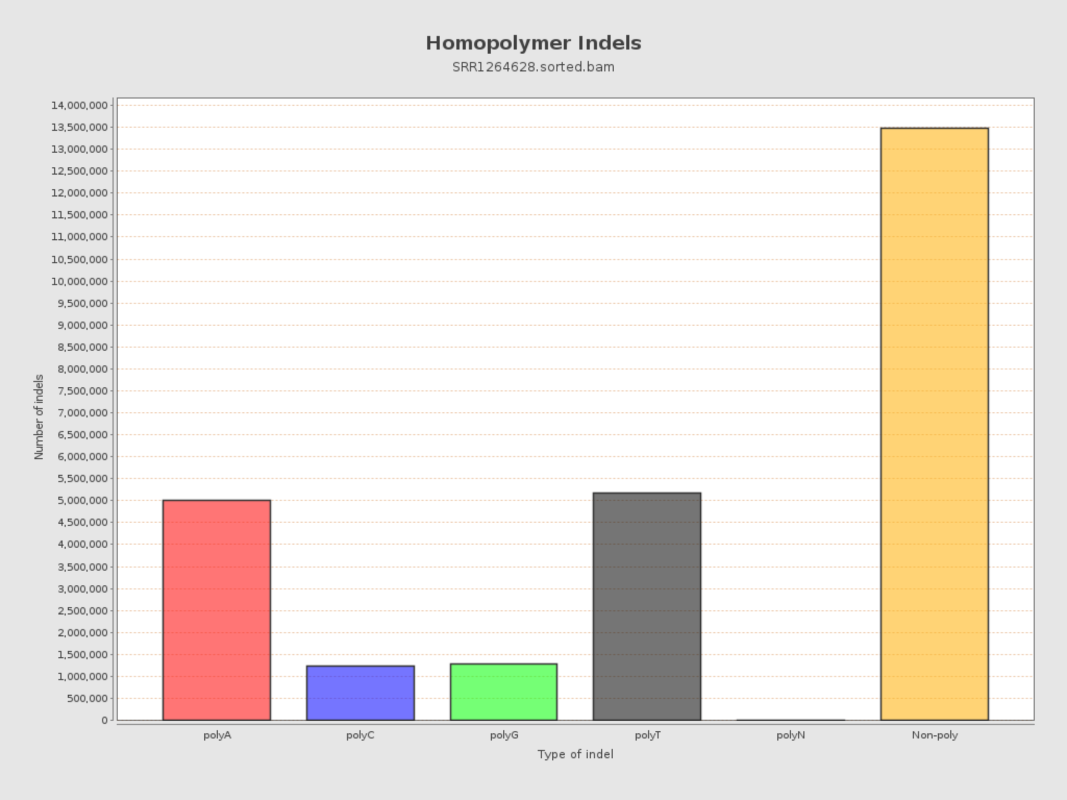
9. Results : Mapped Reads GC-content Distribution



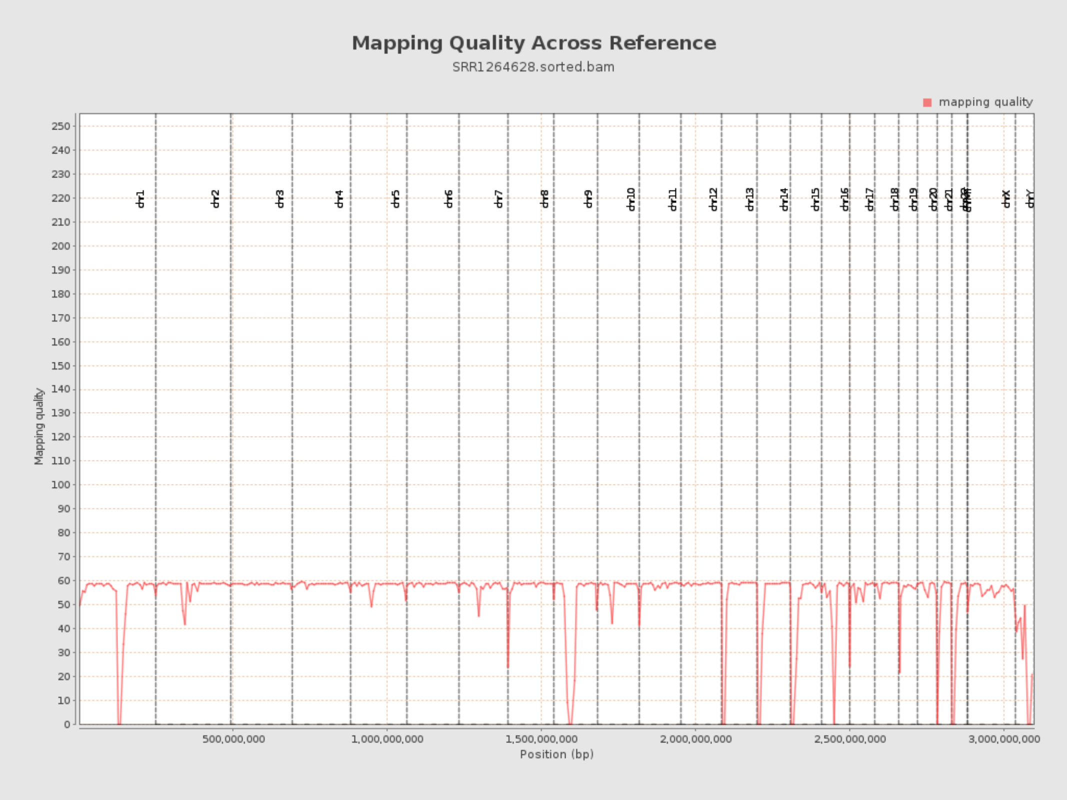
10. Results : Mapped Reads Clipping Profile



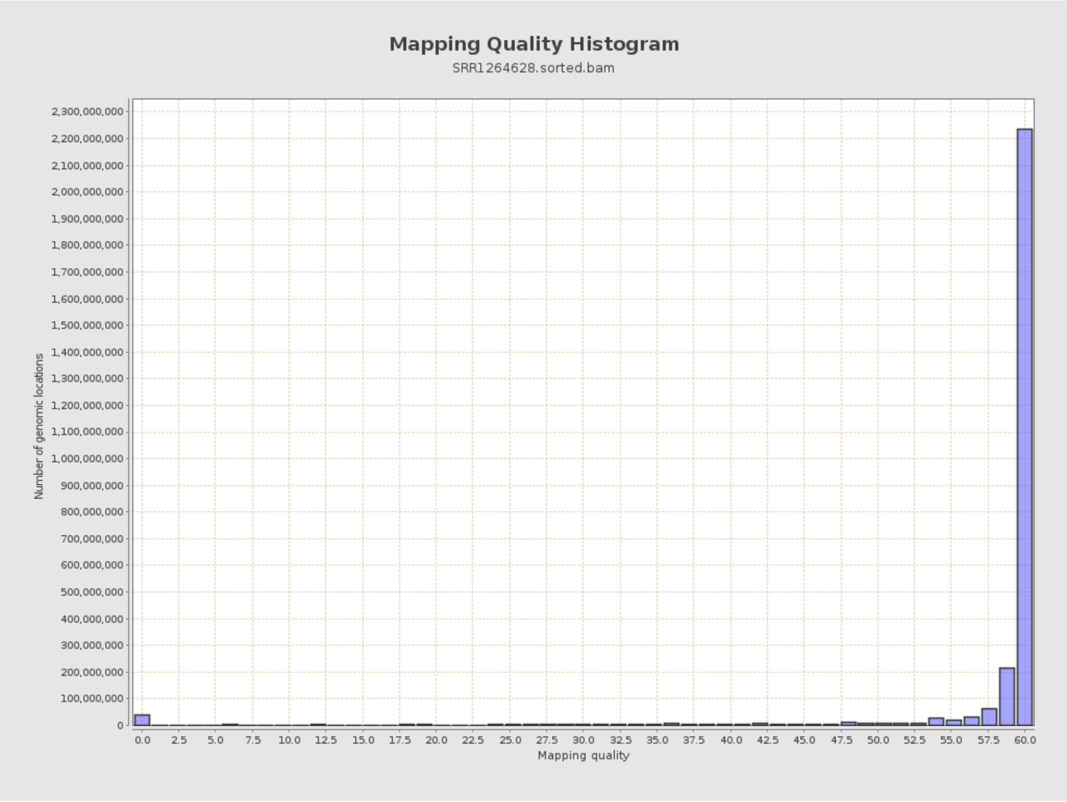
11. Results : Homopolymer Indels



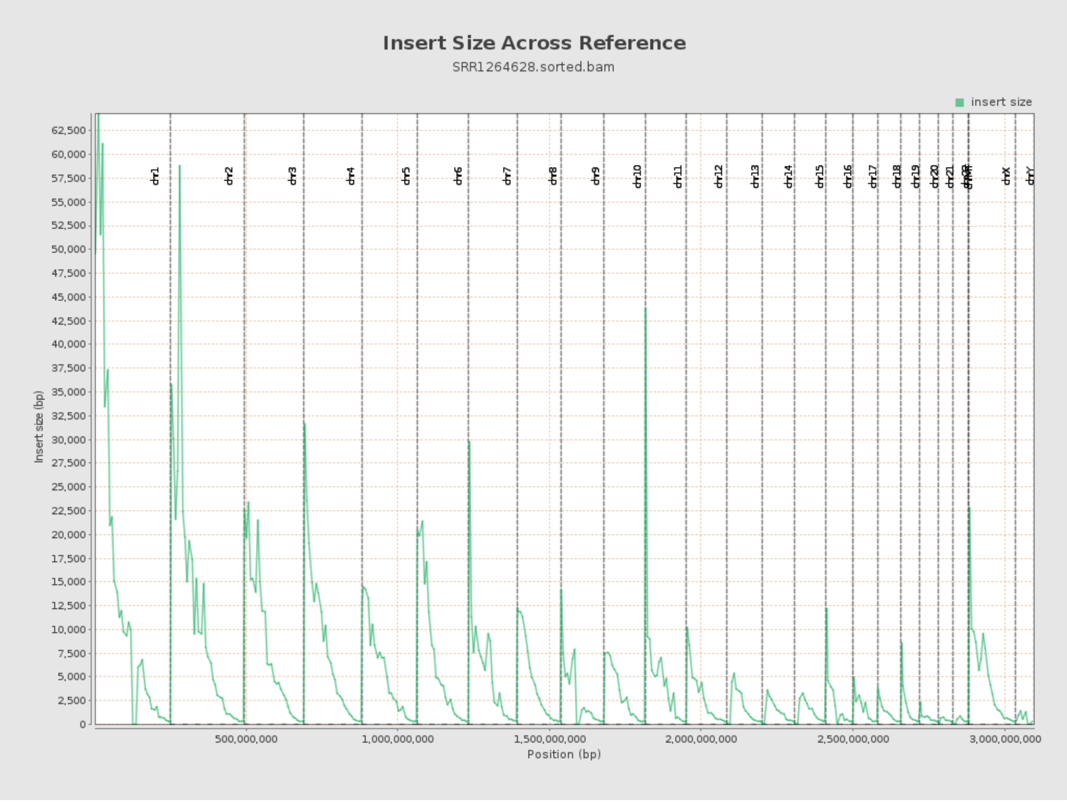
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram