Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/07 23:50:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264622.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_SRR1264622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264622_1.fastq.gz SRR1264622_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 07 23:50:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,616,214
Mapped reads	1,400,307,768 / 99.34%
Unmapped reads	9,308,446 / 0.66%
Mapped paired reads	1,400,307,768 / 99.34%
Mapped reads, first in pair	702,244,418 / 49.82%
Mapped reads, second in pair	698,063,350 / 49.52%
Mapped reads, both in pair	1,394,880,870 / 98.95%
Mapped reads, singletons	5,426,898 / 0.38%
Secondary alignments	0
Supplementary alignments	7,962,194 / 0.56%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	528,815,486 / 37.51%
Duplication rate	37.06%
Clipped reads	58,822,352 / 4.17%

2.2. ACGT Content

Number/percentage of A's	43,477,331,131 / 30.94%
Number/percentage of C's	26,692,747,269 / 18.99%
Number/percentage of T's	43,401,604,386 / 30.88%
Number/percentage of G's	26,964,825,039 / 19.19%
Number/percentage of N's	7,577,328 / 0.01%

GC Percentage	38.18%

2.3. Coverage

Mean	45.4103
Standard Deviation	50.0571

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	66,590.77
Standard Deviation	2,485,015.69
P25/Median/P75	285 / 312 / 345

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	593,087,098
Insertions	15,371,881
Mapped reads with at least one insertion	1.08%
Deletions	14,471,366
Mapped reads with at least one deletion	1.01%
Homopolymer indels	48.47%

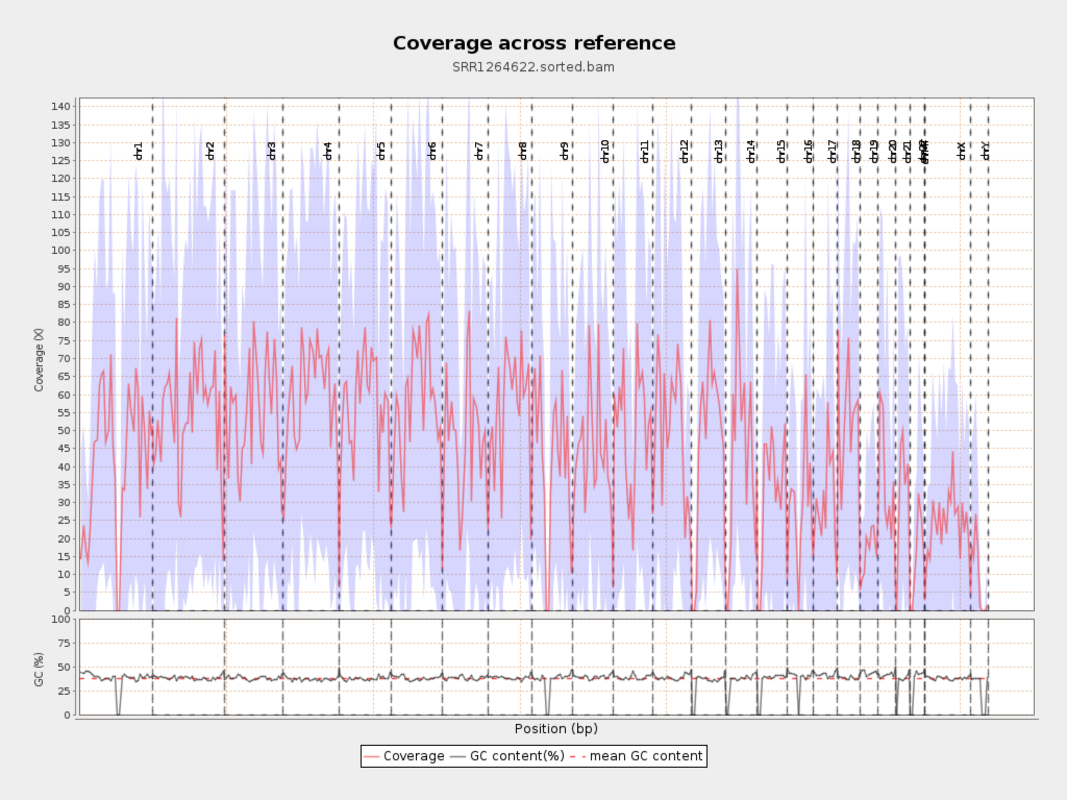
2.7. Chromosome stats

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

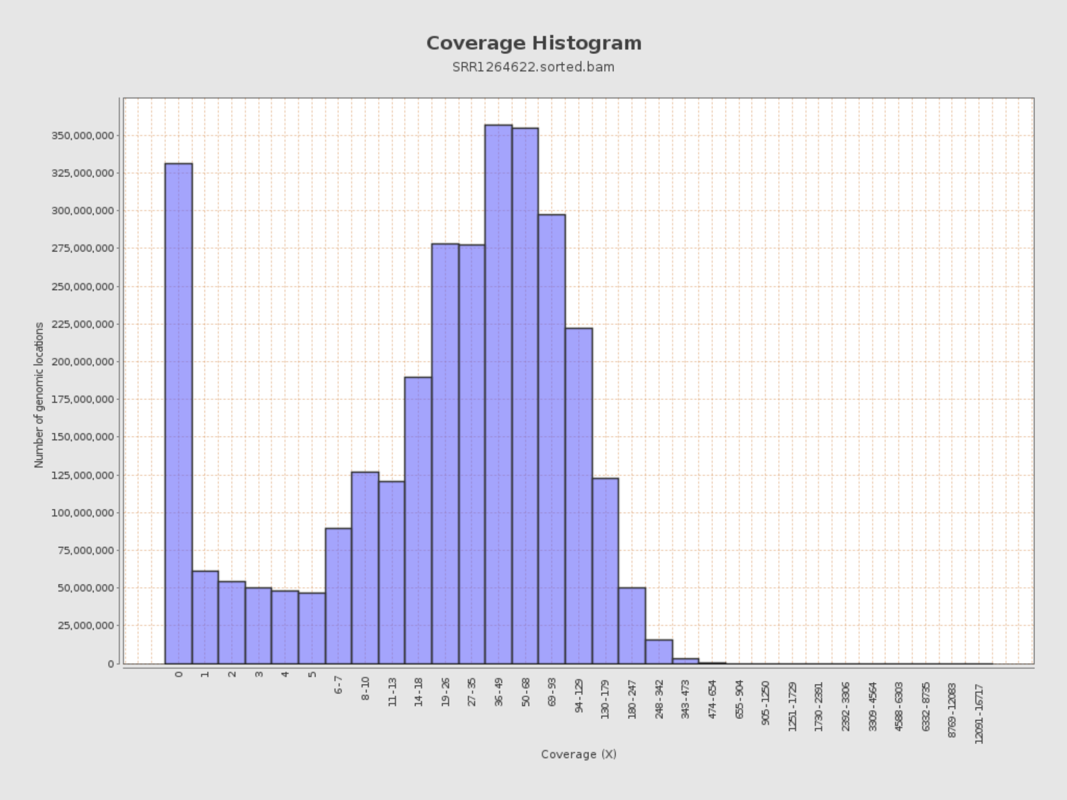
		bases	coverage	deviation
chr1	249250621	10561000074	42.371	49.2584
chr2	243199373	13358663358	54.9289	53.9777
chr3	198022430	10987333761	55.4853	52.8516
chr4	191154276	11542694730	60.3842	53.0206
chr5	180915260	10155104924	56.1318	50.5634
chr6	171115067	10026412579	58.5946	55.0901
chr7	159138663	7500327045	47.1308	50.0186
chr8	146364022	8368005504	57.1726	52.4868
chr9	141213431	5817504306	41.1965	48.6772
chr10	135534747	6042400085	44.5819	46.5104
chr11	135006516	6802066511	50.3832	52.1967
chr12	133851895	6712403166	50.148	52.6915
chr13	115169878	5506174326	47.8092	50.0962
chr14	107349540	4713681230	43.9097	51.7931
chr15	102531392	3382744739	32.9923	41.885
chr16	90354753	2539606547	28.1071	36.541
chr17	81195210	2470427816	30.4258	39.1692
chr18	78077248	4152448805	53.1839	49.3298
chr19	59128983	986872116	16.6902	25.6752
chr20	63025520	2176791007	34.5382	47.2192
chr21	48129895	1613138714	33.5164	48.3811
chr22	51304566	778373212	15.1716	27.4682
chrMT	16571	47423	2.8618	7.7567
chrX	155270560	3813476142	24.5602	31.9541

chrY	59373566	568668697	9.5778	23.708

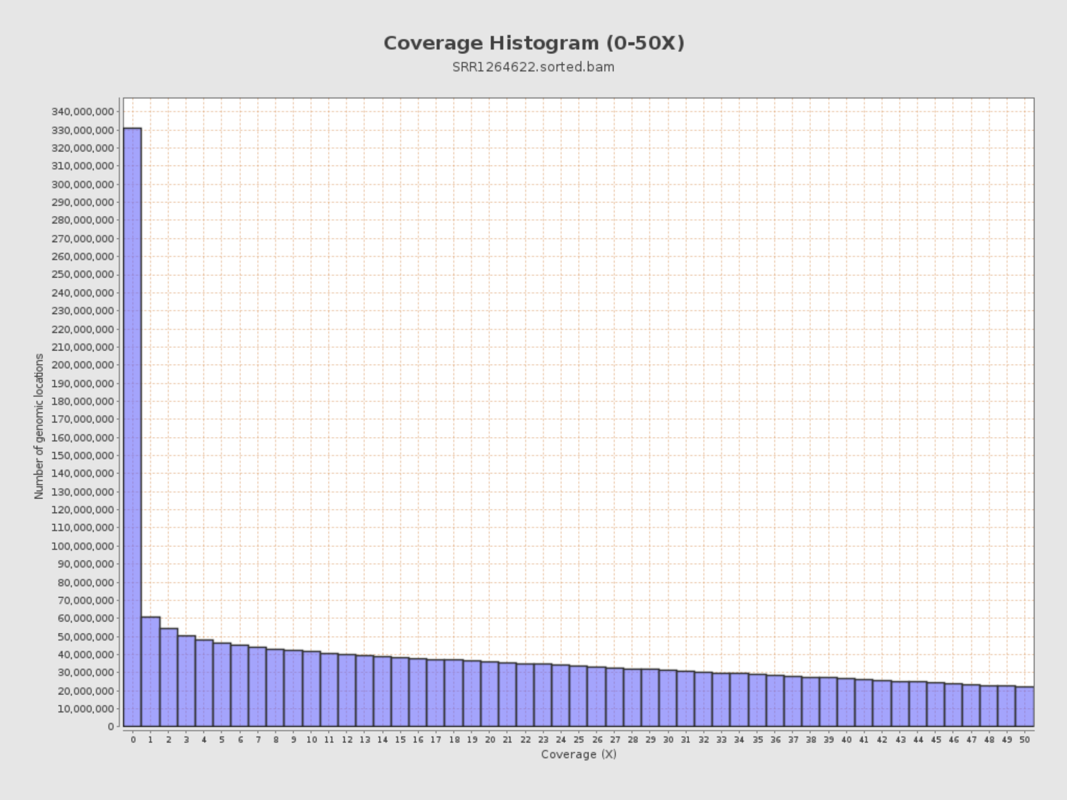
3. Results : Coverage across reference



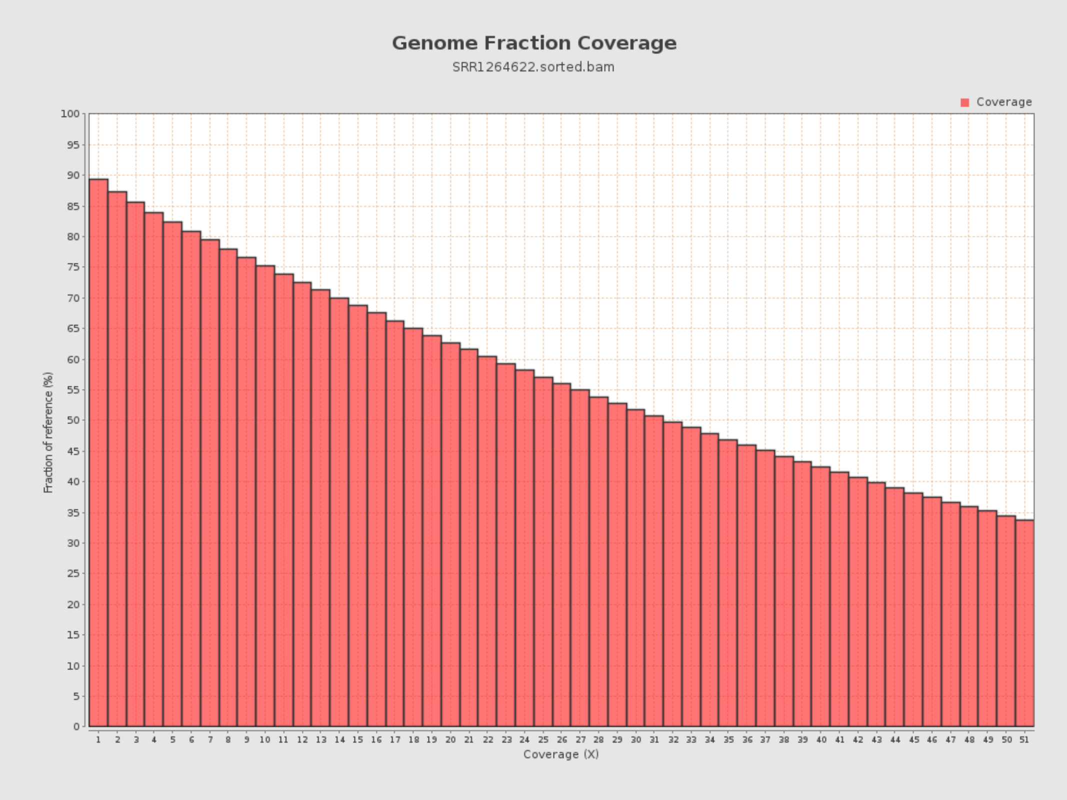
4. Results : Coverage Histogram



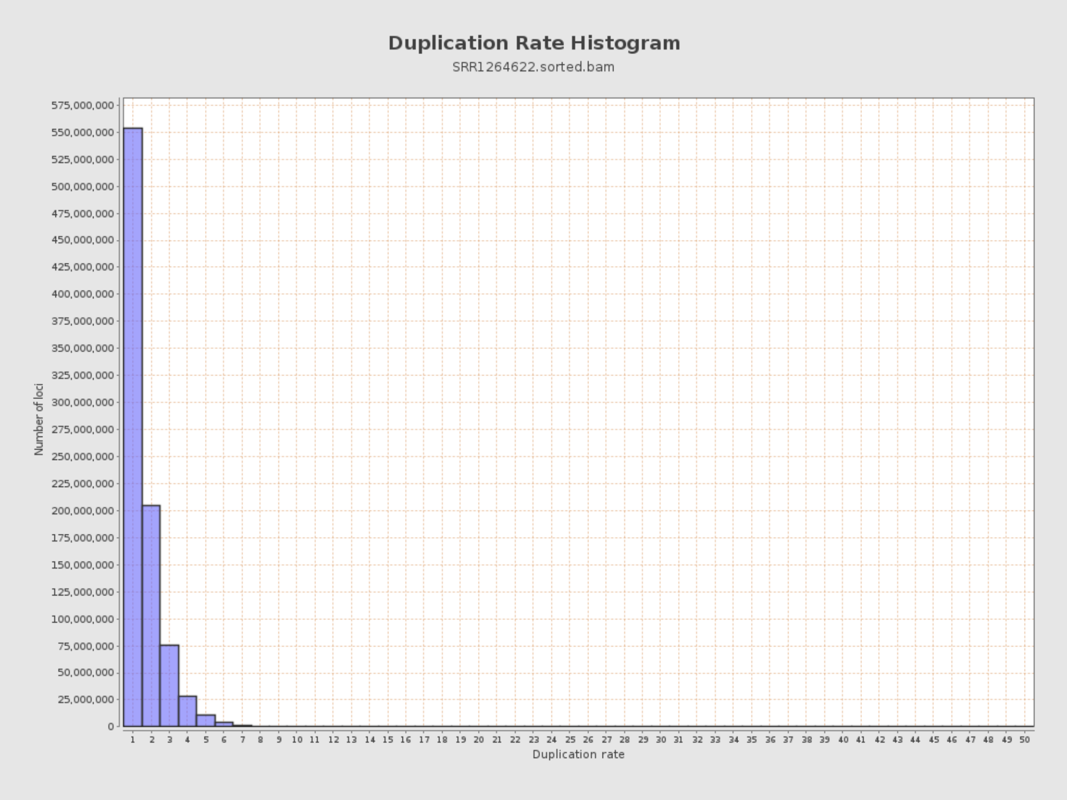
5. Results : Coverage Histogram (0-50X)



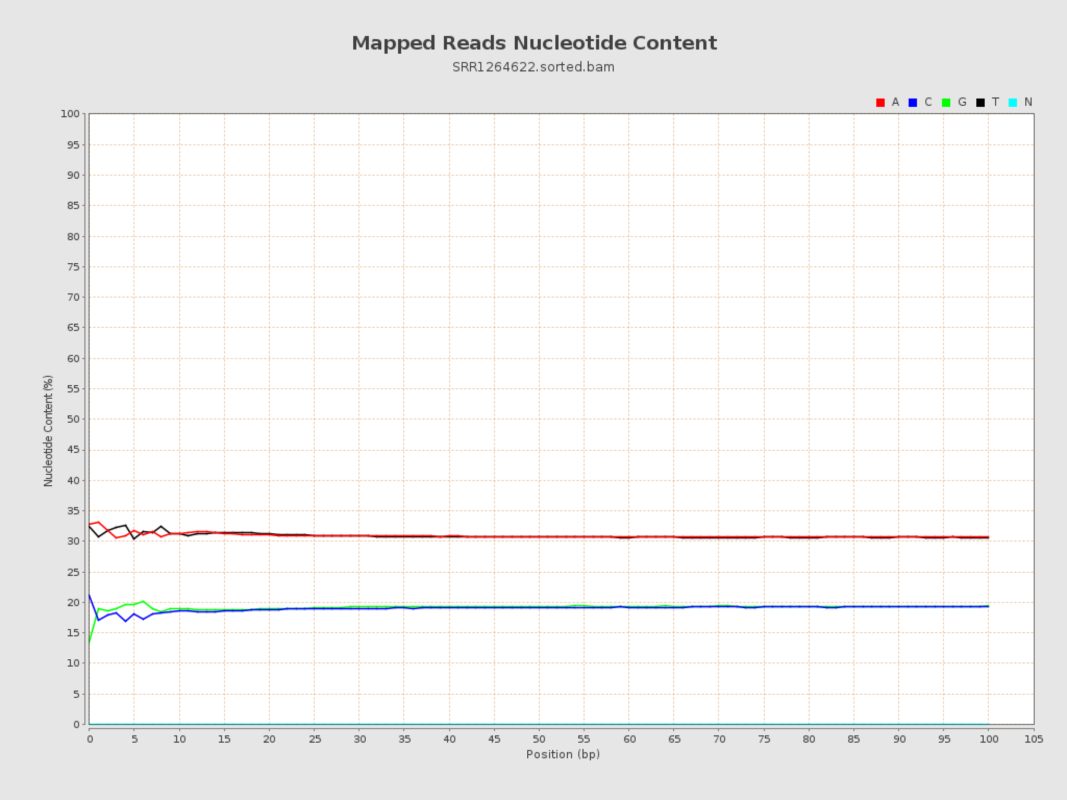
6. Results : Genome Fraction Coverage



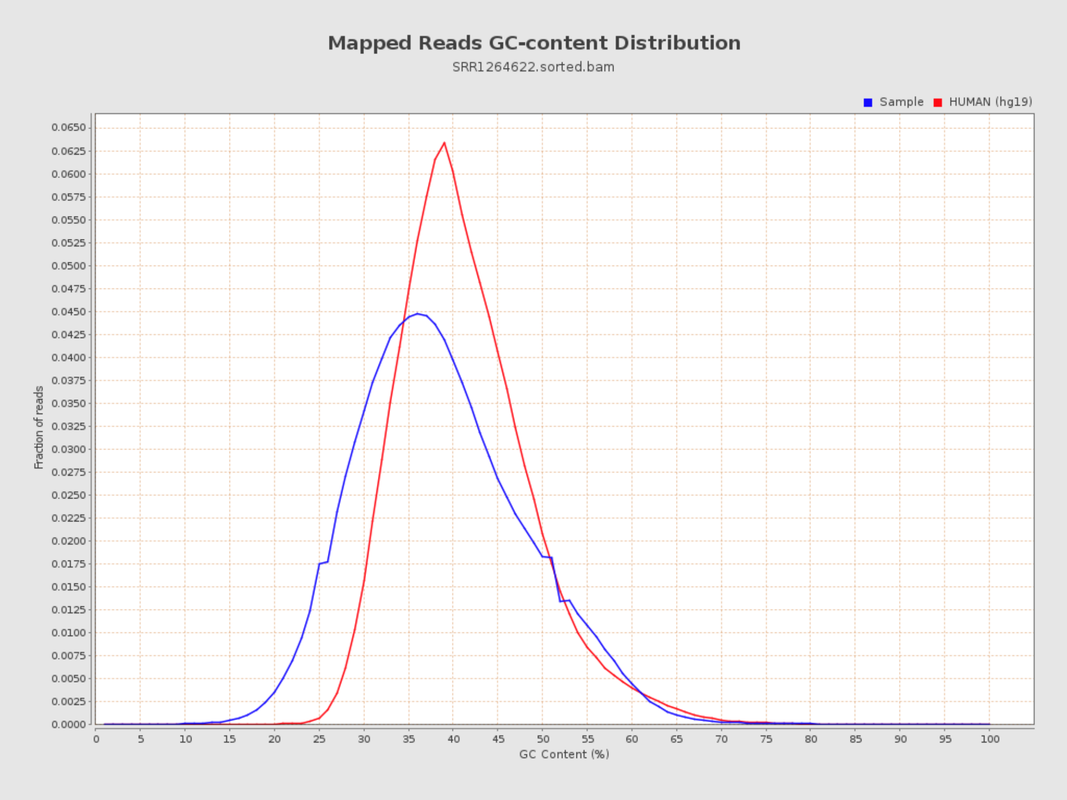
7. Results : Duplication Rate Histogram



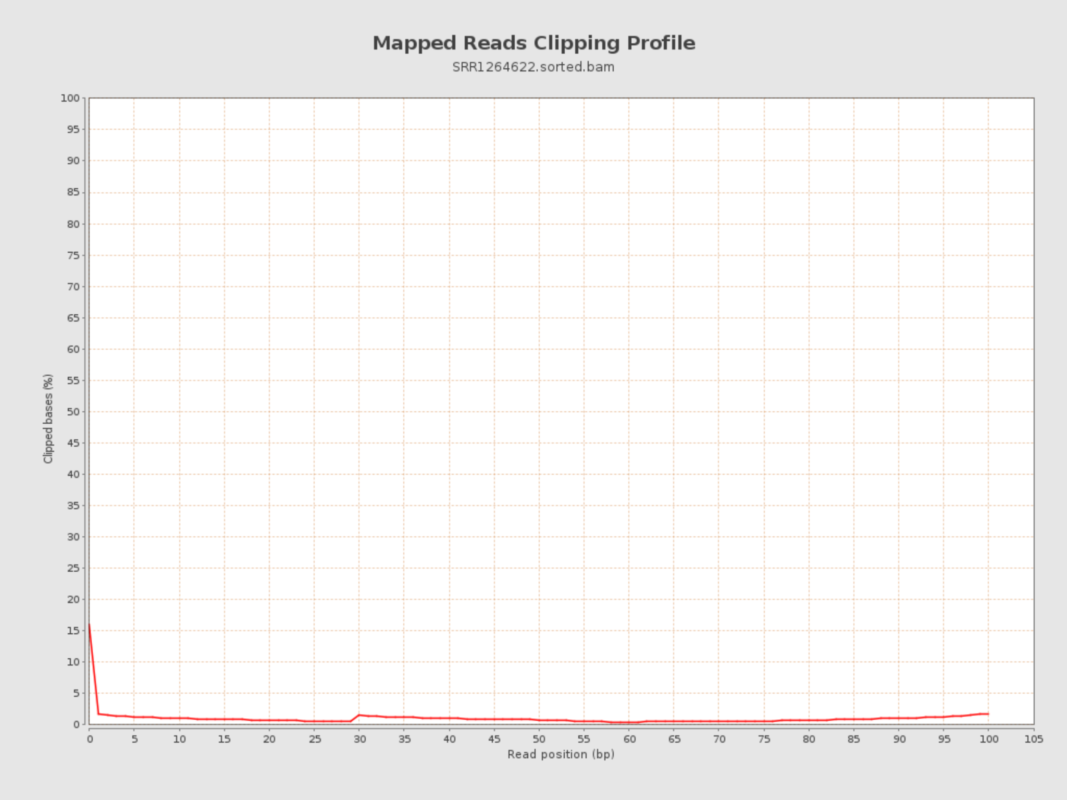
8. Results : Mapped Reads Nucleotide Content



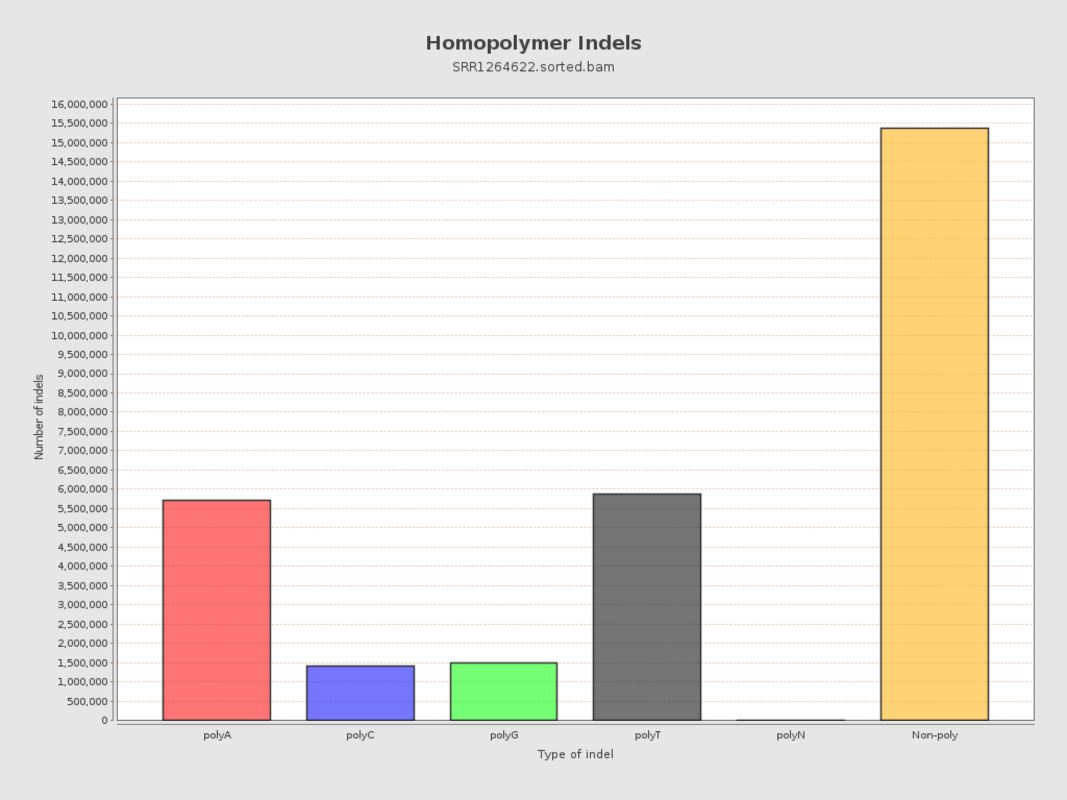
9. Results : Mapped Reads GC-content Distribution



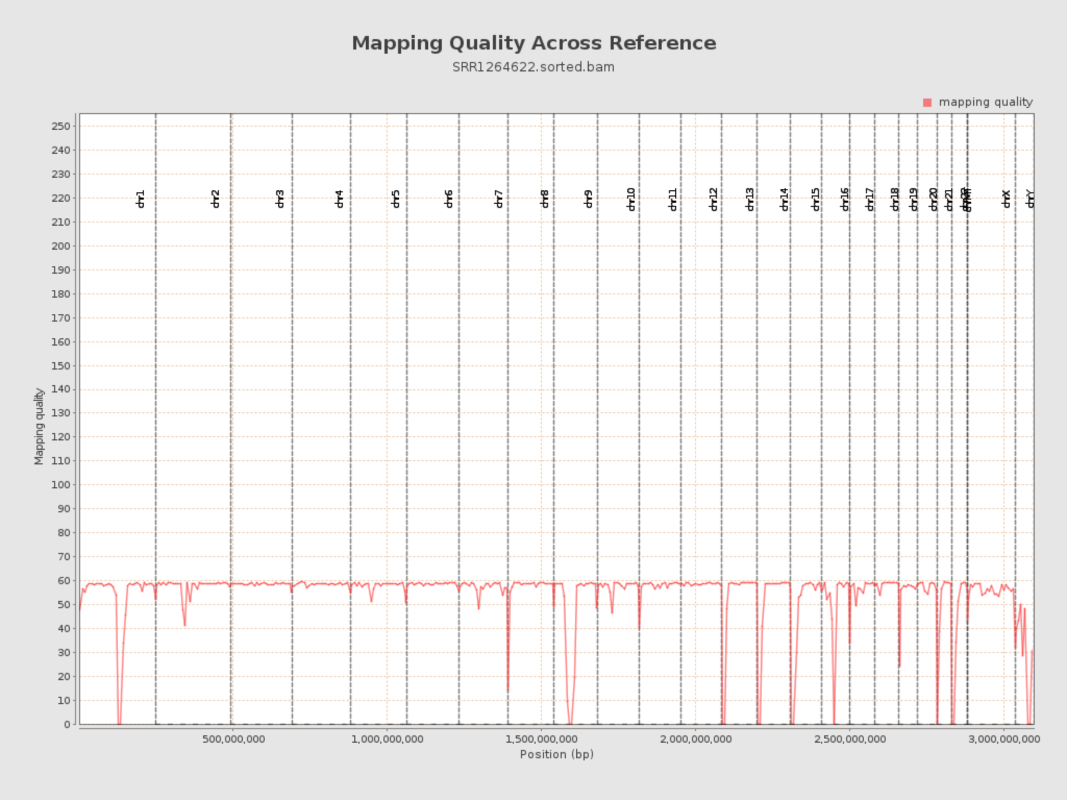
10. Results : Mapped Reads Clipping Profile



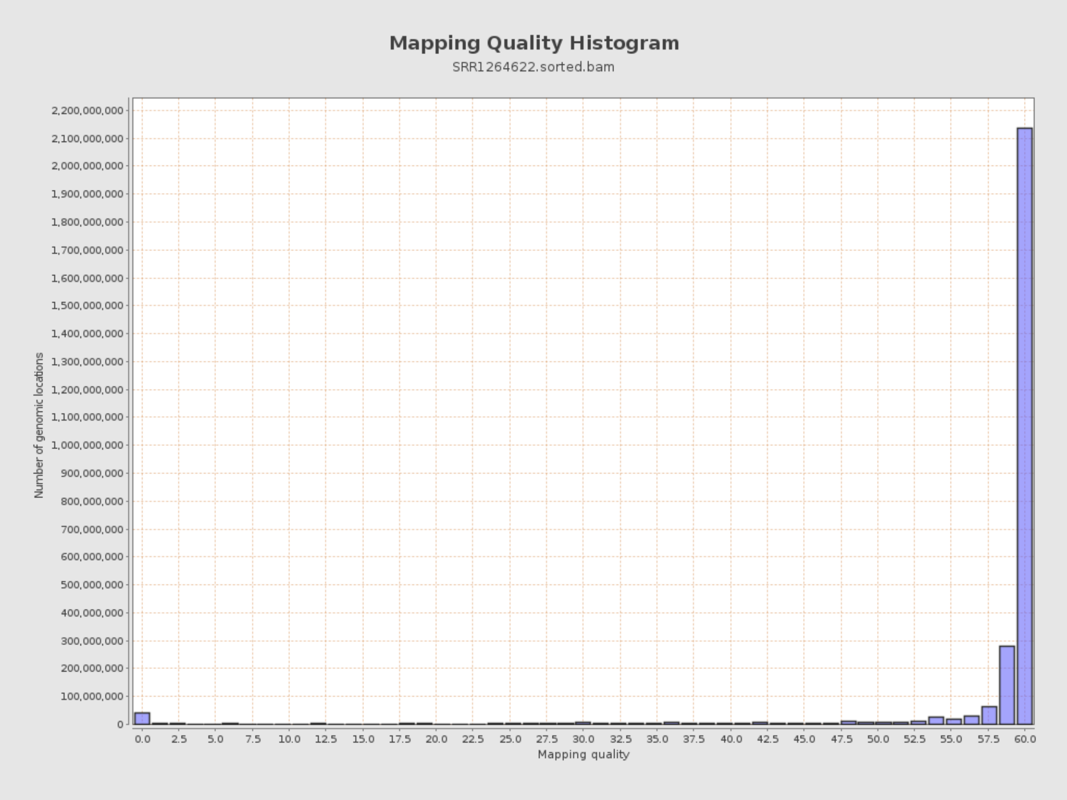
11. Results : Homopolymer Indels



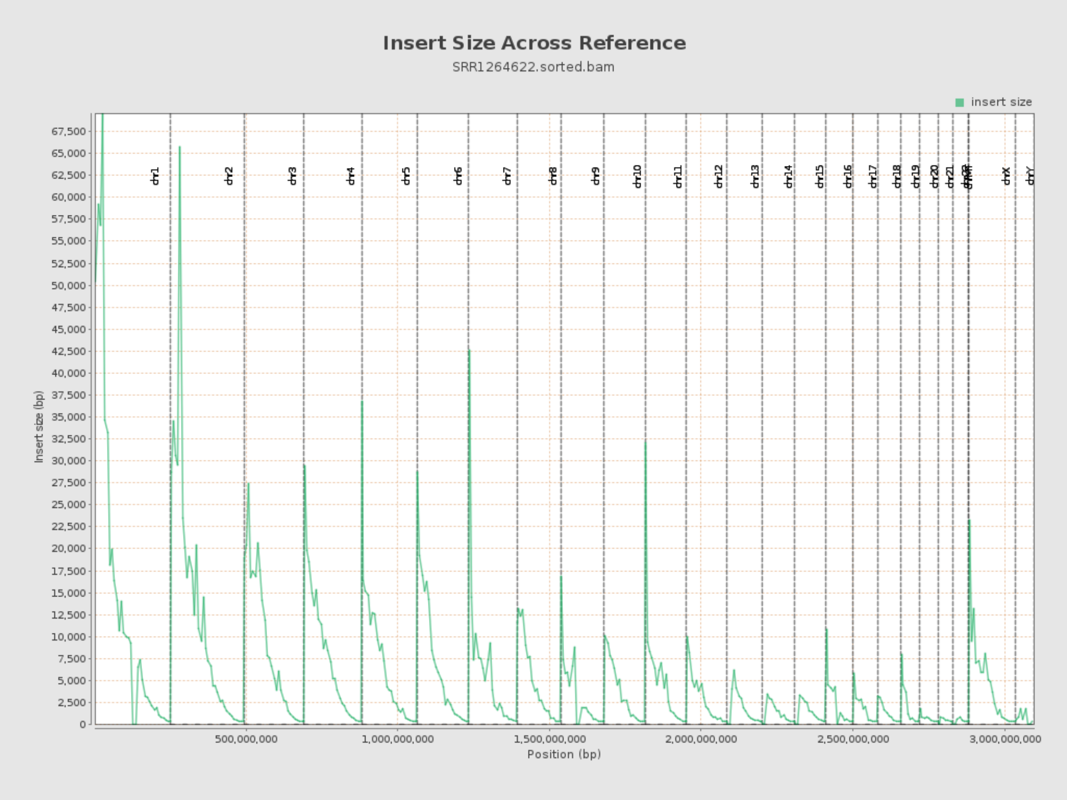
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram