Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/12 16:58:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438264.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_SRR8438264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438264_1.fastq.gz SRR8438264_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 12 16:58:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	593,284,296
Mapped reads	591,560,069 / 99.71%
Unmapped reads	1,724,227 / 0.29%
Mapped paired reads	591,560,069 / 99.71%
Mapped reads, first in pair	295,903,514 / 49.88%
Mapped reads, second in pair	295,656,555 / 49.83%
Mapped reads, both in pair	590,372,400 / 99.51%
Mapped reads, singletons	1,187,669 / 0.2%
Secondary alignments	0
Supplementary alignments	9,136,384 / 1.54%
Read min/max/mean length	28 / 151 / 145.06
Duplicated reads (estimated)	260,265,421 / 43.87%
Duplication rate	41.24%
Clipped reads	111,982,783 / 18.88%

2.2. ACGT Content

Number/percentage of A's	25,726,186,076 / 30.25%
Number/percentage of C's	16,975,672,213 / 19.96%
Number/percentage of T's	24,577,492,897 / 28.9%
Number/percentage of G's	17,754,882,753 / 20.88%
Number/percentage of N's	522,750 / 0%

GC Percentage	40.84%

2.3. Coverage

Mean	27.4765
Standard Deviation	114.7352

2.4. Mapping Quality

Mean Mapping Quality	54.89

2.5. Insert size

Mean	39,896.19
Standard Deviation	1,947,526.02
P25/Median/P75	183 / 238 / 324

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	437,501,084
Insertions	11,056,230
Mapped reads with at least one insertion	1.84%
Deletions	9,794,355
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.38%

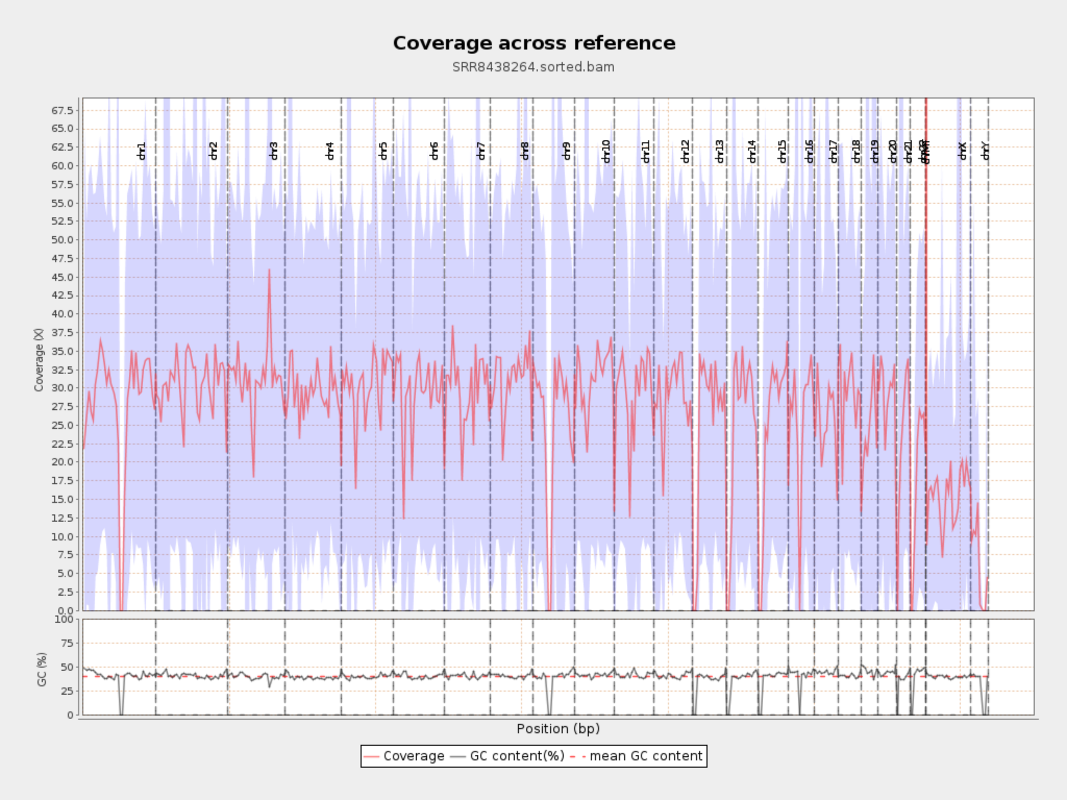
2.7. Chromosome stats

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

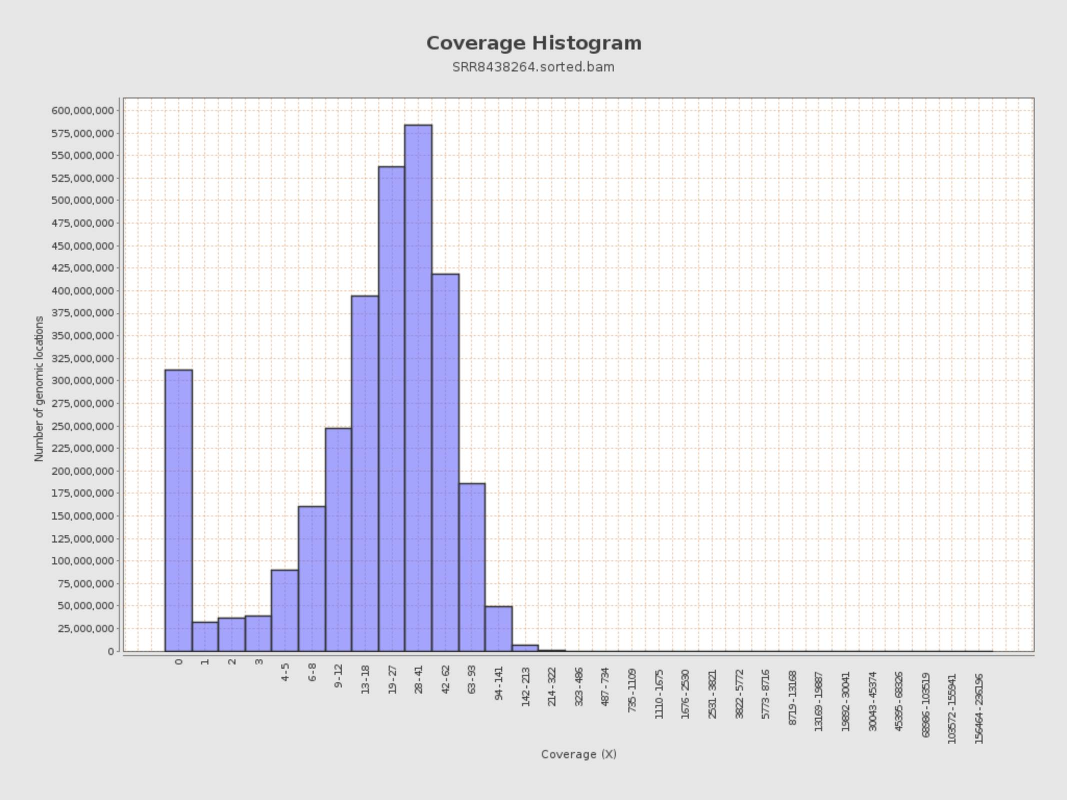
		bases	coverage	deviation
chr1	249250621	6981882928	28.0115	29.3883
chr2	243199373	7431044572	30.5554	110.2188
chr3	198022430	6202350039	31.3215	267.0649
chr4	191154276	5655978470	29.5886	36.4705
chr5	180915260	5474222869	30.2585	68.0405
chr6	171115067	5054361126	29.5378	29.1597
chr7	159138663	4706920271	29.5775	34.6482
chr8	146364022	4556681401	31.1325	29.8474
chr9	141213431	3556658888	25.1864	35.8767
chr10	135534747	4279410971	31.5743	49.146
chr11	135006516	3968893890	29.3978	25.9818
chr12	133851895	3902431239	29.1548	25.6794
chr13	115169878	2919719027	25.3514	25.865
chr14	107349540	2723322469	25.3687	32.8106
chr15	102531392	2477326813	24.1616	26.8133
chr16	90354753	2287902292	25.3213	46.5552
chr17	81195210	2101024809	25.8762	32.0428
chr18	78077248	2300351929	29.4625	27.4997
chr19	59128983	1450025304	24.5231	378.6657
chr20	63025520	1850559097	29.3621	28.1933
chr21	48129895	1096605145	22.7843	110.6353
chr22	51304566	902662147	17.5942	23.4726
chrMT	16571	398908181	24,072.668	9,701.7776
chrX	155270560	2414170431	15.5482	37.1738

chrY	59373566	365480346	6.1556	23.8693

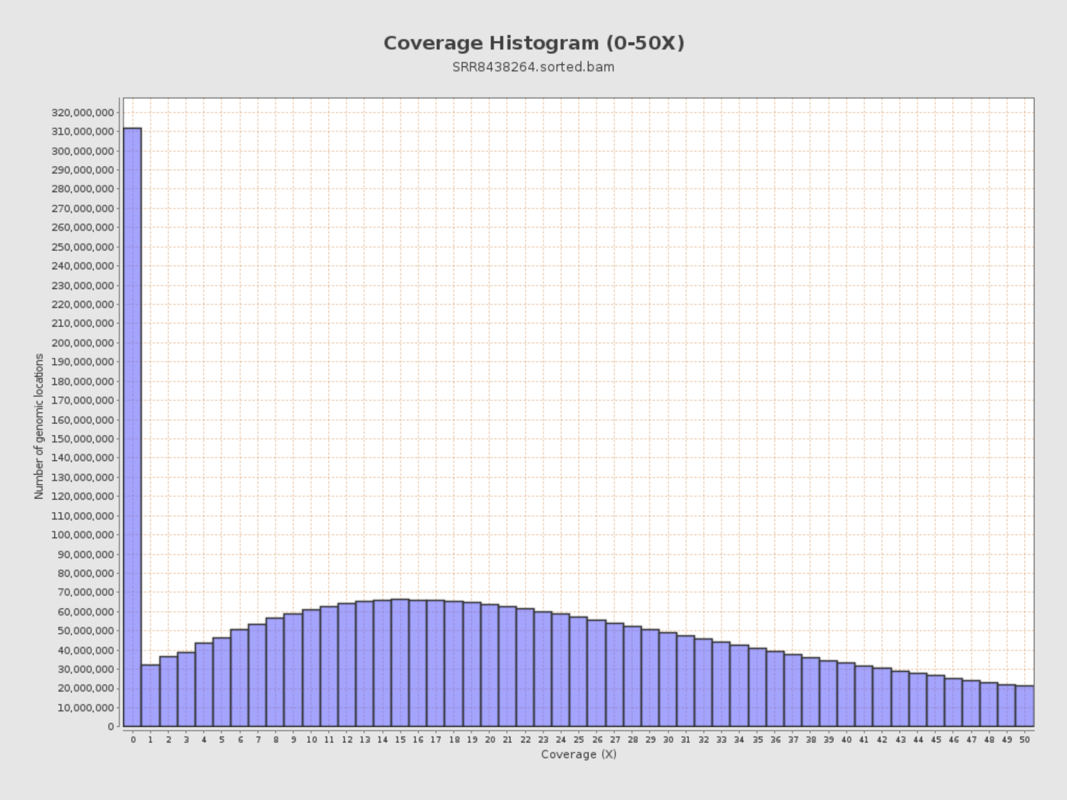
3. Results : Coverage across reference



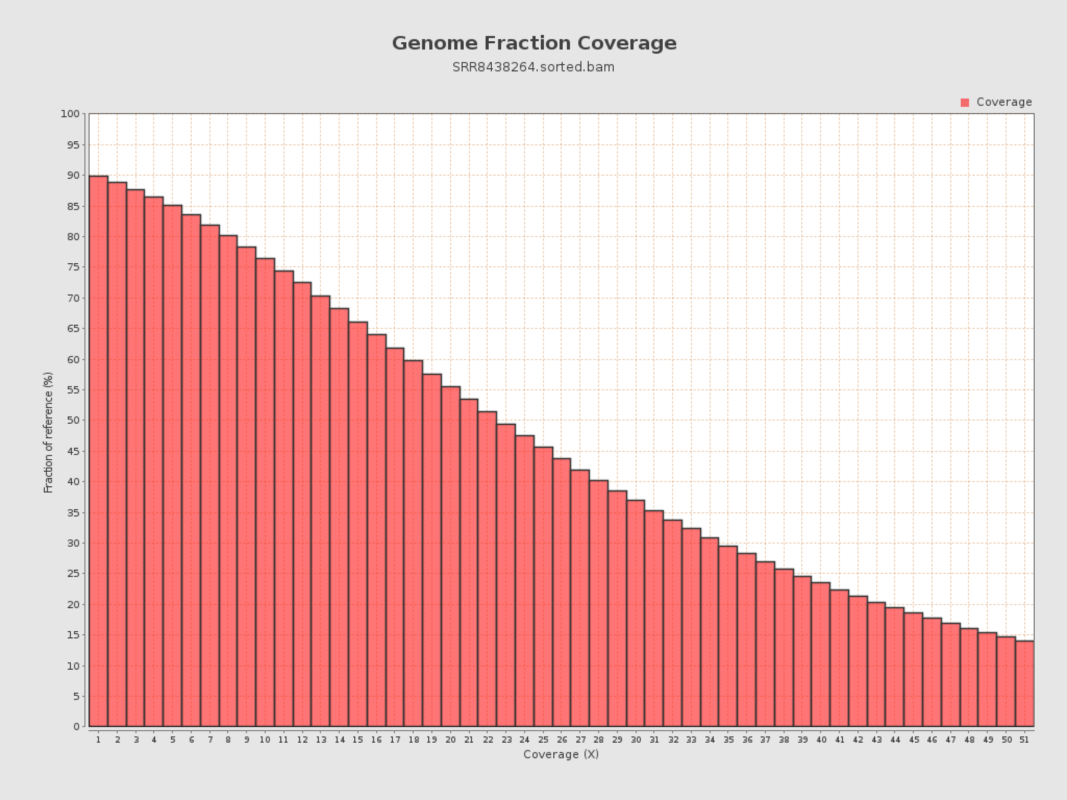
4. Results : Coverage Histogram



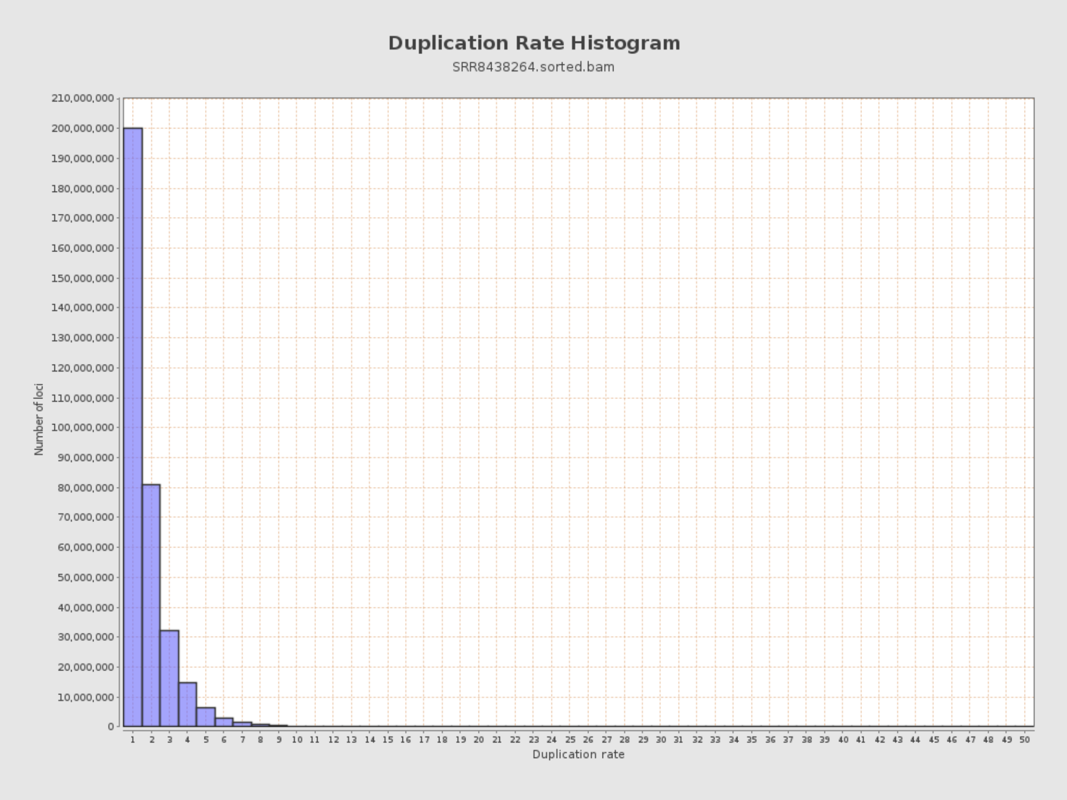
5. Results : Coverage Histogram (0-50X)



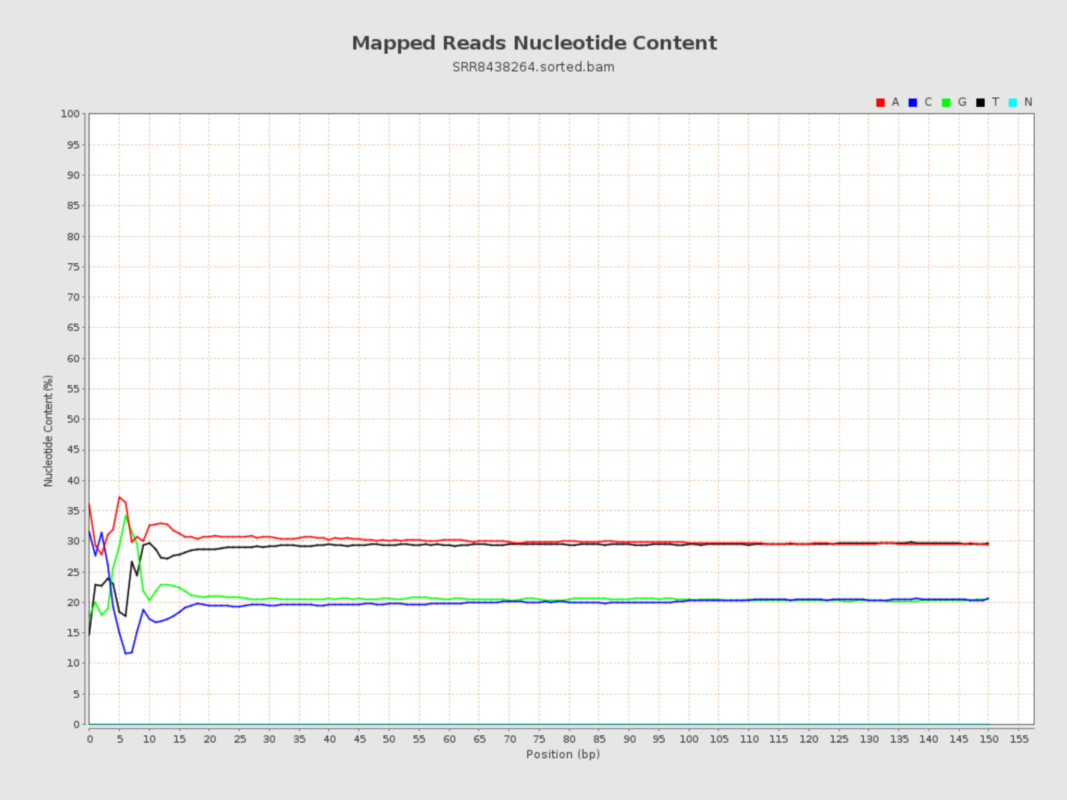
6. Results : Genome Fraction Coverage



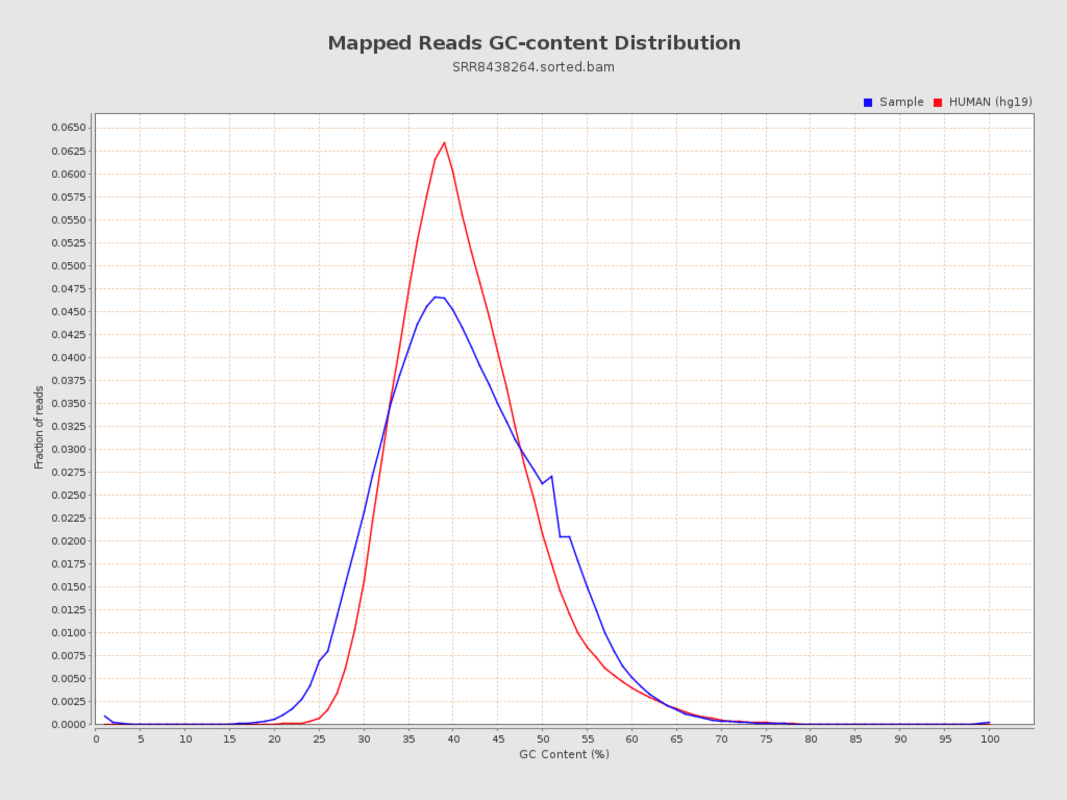
7. Results : Duplication Rate Histogram



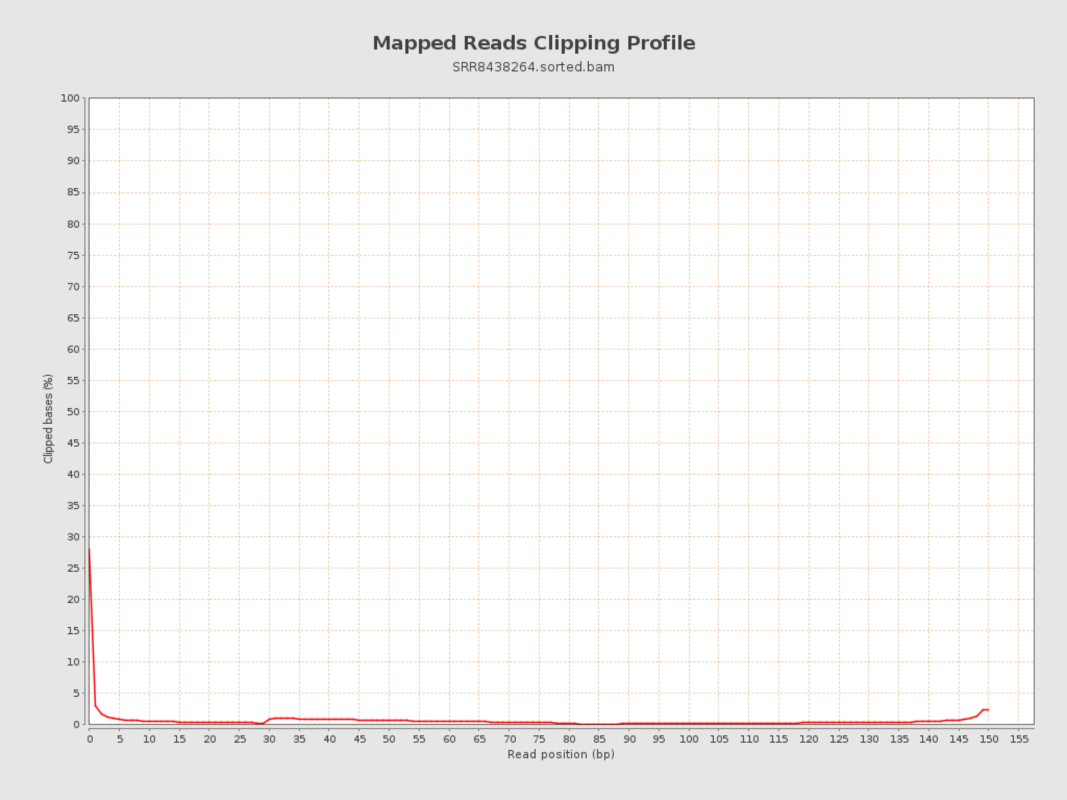
8. Results : Mapped Reads Nucleotide Content



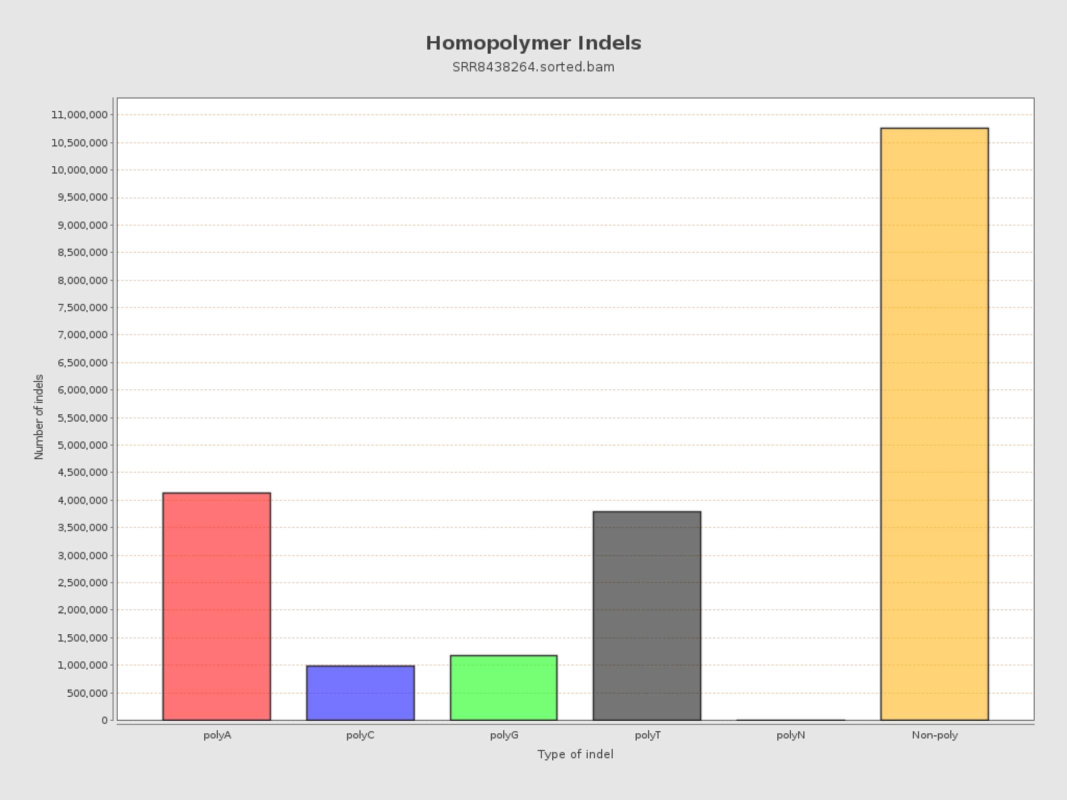
9. Results : Mapped Reads GC-content Distribution



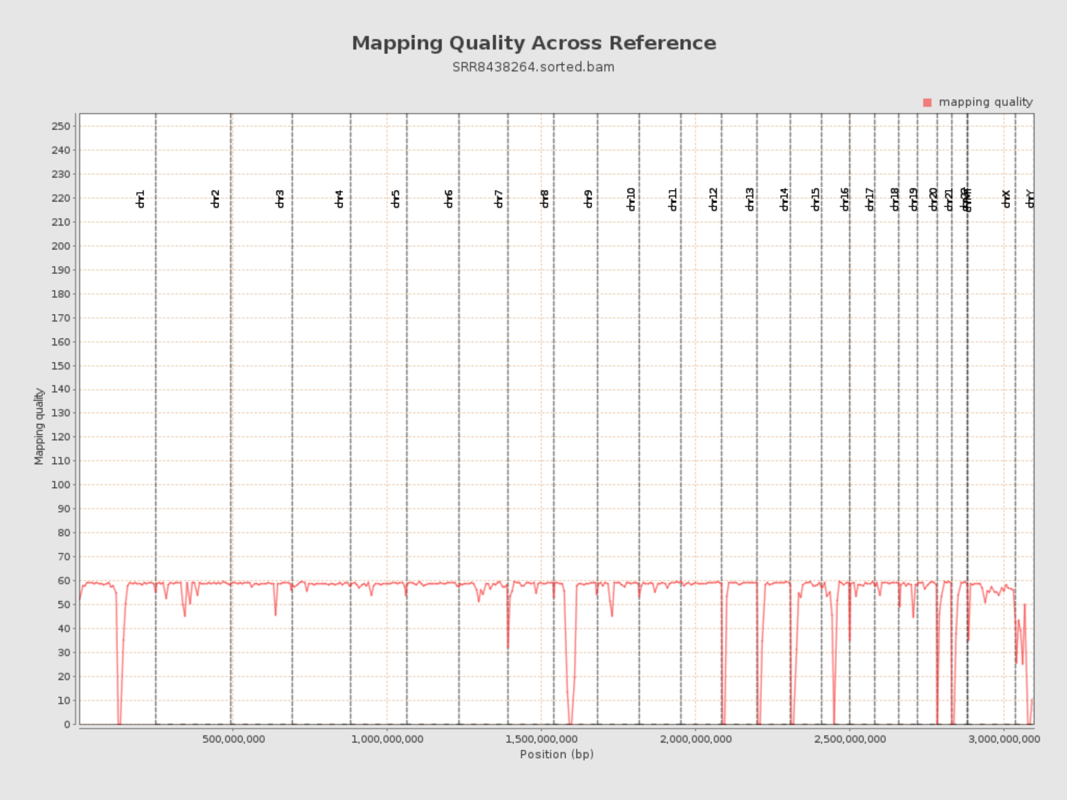
10. Results : Mapped Reads Clipping Profile



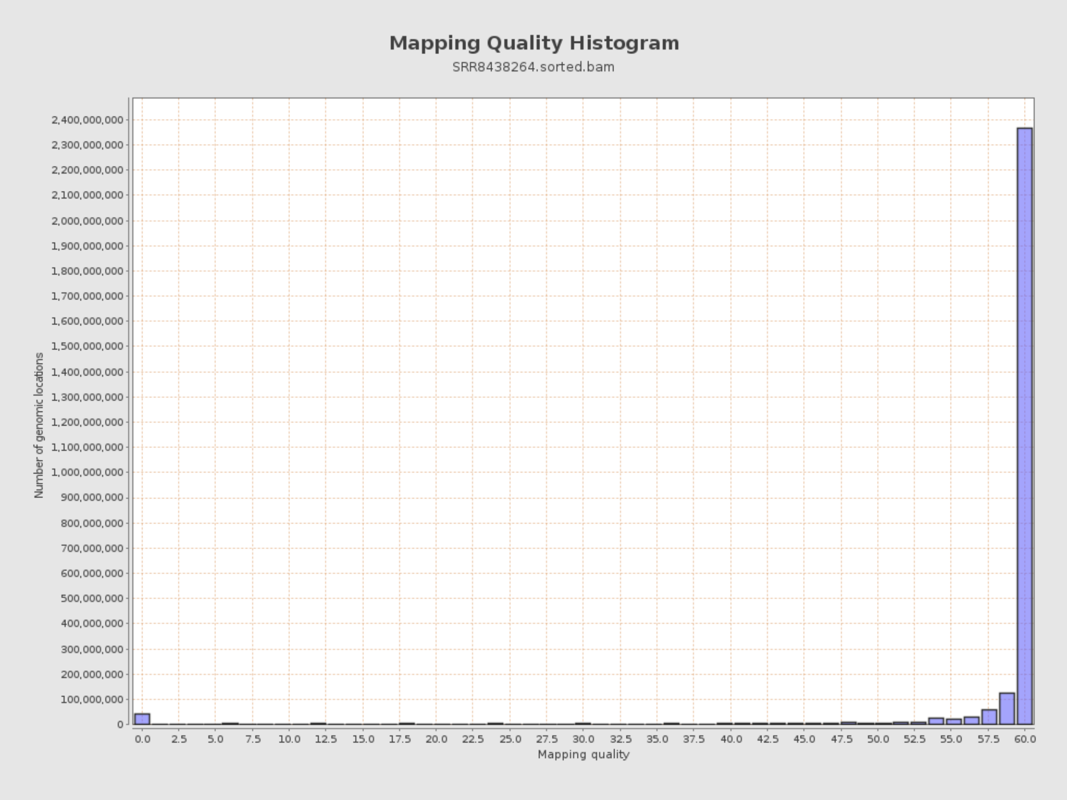
11. Results : Homopolymer Indels



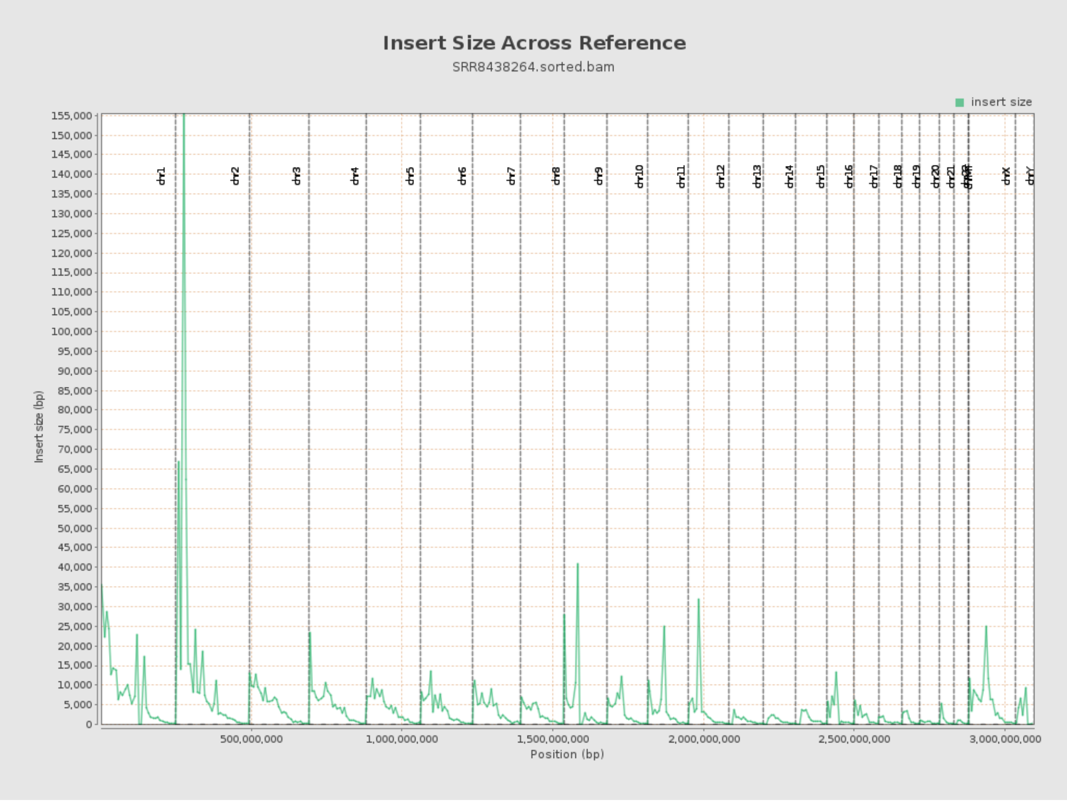
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram