Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 00:24:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438254.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_SRR8438254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438254_1.fastq.gz SRR8438254_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 00:24:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	787,637,176
Mapped reads	783,615,491 / 99.49%
Unmapped reads	4,021,685 / 0.51%
Mapped paired reads	783,615,491 / 99.49%
Mapped reads, first in pair	391,967,796 / 49.77%
Mapped reads, second in pair	391,647,695 / 49.72%
Mapped reads, both in pair	781,220,936 / 99.19%
Mapped reads, singletons	2,394,555 / 0.3%
Secondary alignments	0
Supplementary alignments	20,435,650 / 2.59%
Read min/max/mean length	30 / 149 / 143.62
Duplicated reads (estimated)	356,378,508 / 45.25%
Duplication rate	40.48%
Clipped reads	106,248,753 / 13.49%

2.2. ACGT Content

Number/percentage of A's	34,227,725,155 / 30.76%
Number/percentage of C's	21,093,965,141 / 18.95%
Number/percentage of T's	32,256,701,107 / 28.99%
Number/percentage of G's	23,707,871,934 / 21.3%
Number/percentage of N's	206,150 / 0%

GC Percentage	40.26%

2.3. Coverage

Mean	35.9604
Standard Deviation	109.3692

2.4. Mapping Quality

Mean Mapping Quality	54.33

2.5. Insert size

Mean	93,799.68
Standard Deviation	2,955,157.76
P25/Median/P75	368 / 440 / 555

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	600,869,034
Insertions	14,791,961
Mapped reads with at least one insertion	1.84%
Deletions	13,093,453
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.18%

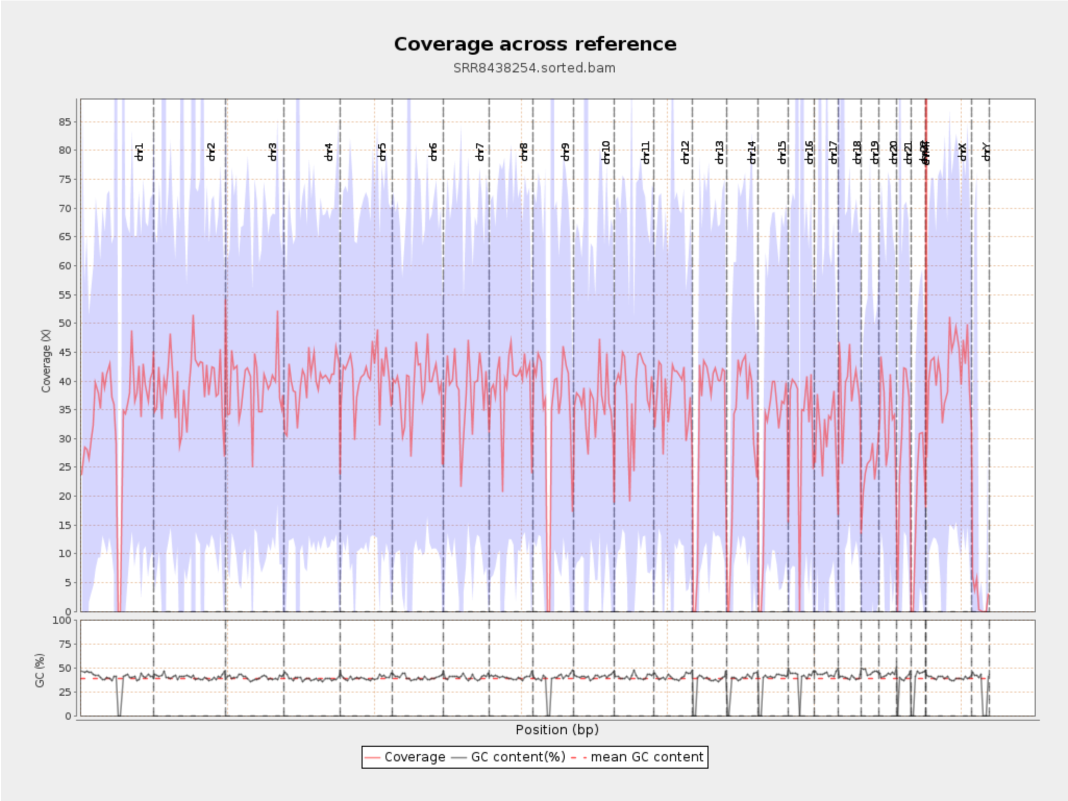
2.7. Chromosome stats

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

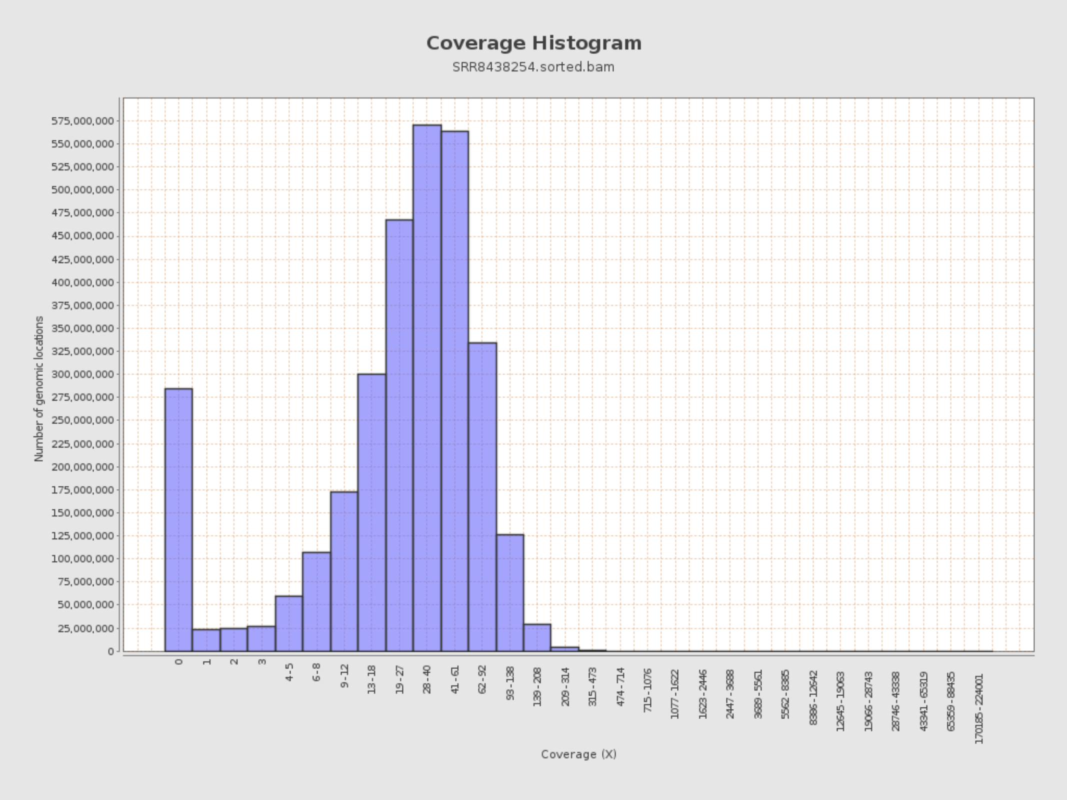
		bases	coverage	deviation
chr1	249250621	8524968513	34.2024	44.1654
chr2	243199373	9535775252	39.2097	170.81
chr3	198022430	7779442234	39.2857	30.1614
chr4	191154276	7630076882	39.9158	38.3138
chr5	180915260	7382014805	40.8037	31.4777
chr6	171115067	6703232779	39.1738	37.8099
chr7	159138663	6069765979	38.1414	33.1106
chr8	146364022	5793609902	39.5836	33.7007
chr9	141213431	4788512354	33.9098	55.3883
chr10	135534747	4917642238	36.2833	82.0541
chr11	135006516	5143335242	38.0969	33.6692
chr12	133851895	5034513610	37.6126	31.9648
chr13	115169878	3901776621	33.8784	31.572
chr14	107349540	3351646709	31.2218	31.5671
chr15	102531392	2989343264	29.1554	29.6592
chr16	90354753	2923210457	32.3526	85.2753
chr17	81195210	2479444628	30.5368	46.6504
chr18	78077248	3062268729	39.221	59.8274
chr19	59128983	1452837963	24.5707	31.5858
chr20	63025520	2133073800	33.8446	33.7848
chr21	48129895	1484396374	30.8415	47.4762
chr22	51304566	975522883	19.0143	27.205
chrMT	16571	597450261	36,053.9654	13,479.9189
chrX	155270560	6536485109	42.0974	33.4187

chrY	59373566	131895580	2.2215	36.4262

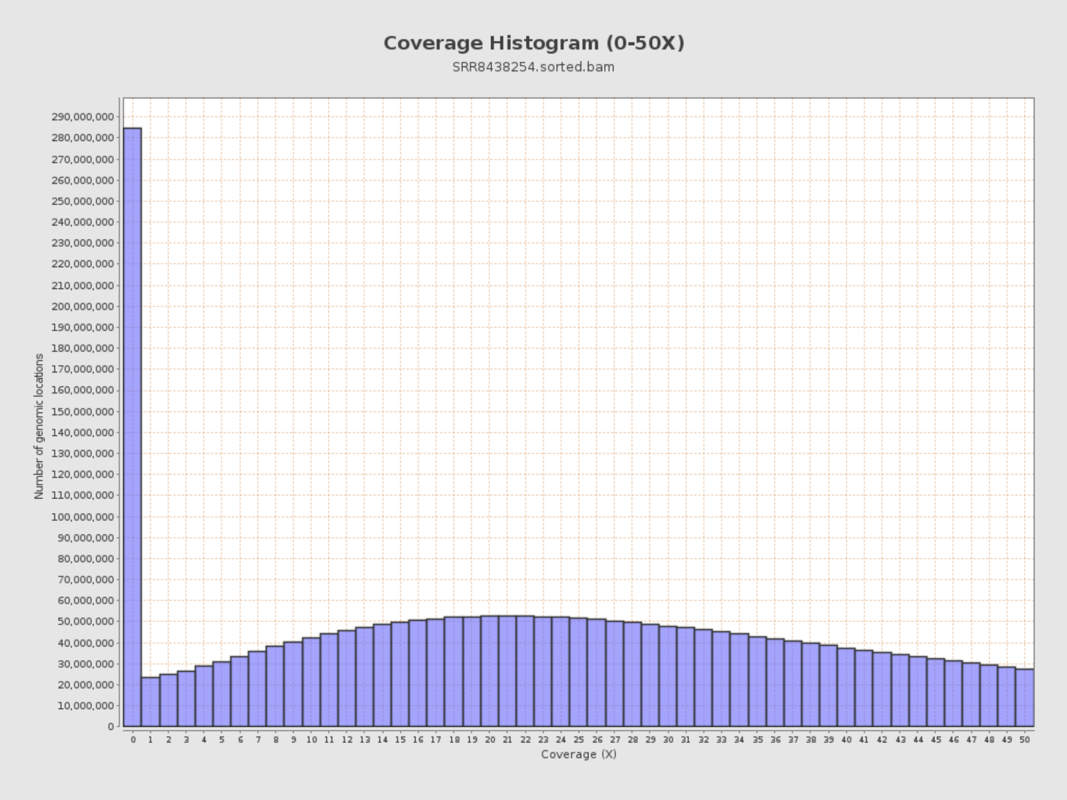
3. Results : Coverage across reference



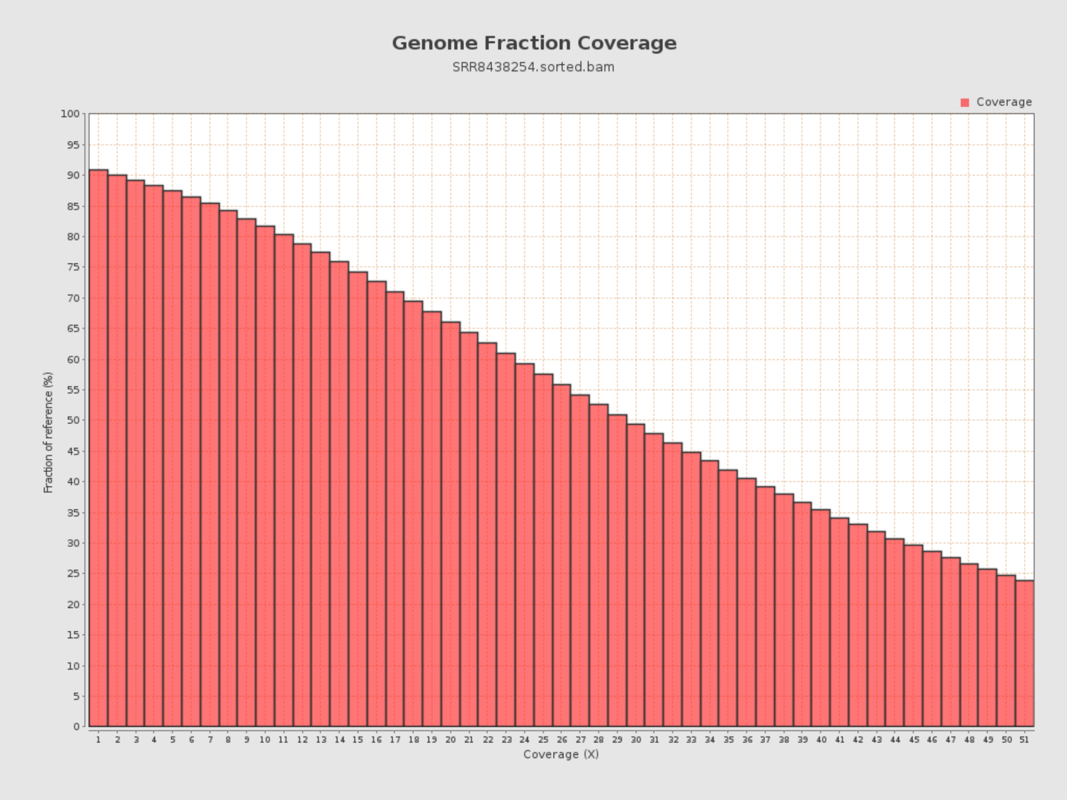
4. Results : Coverage Histogram



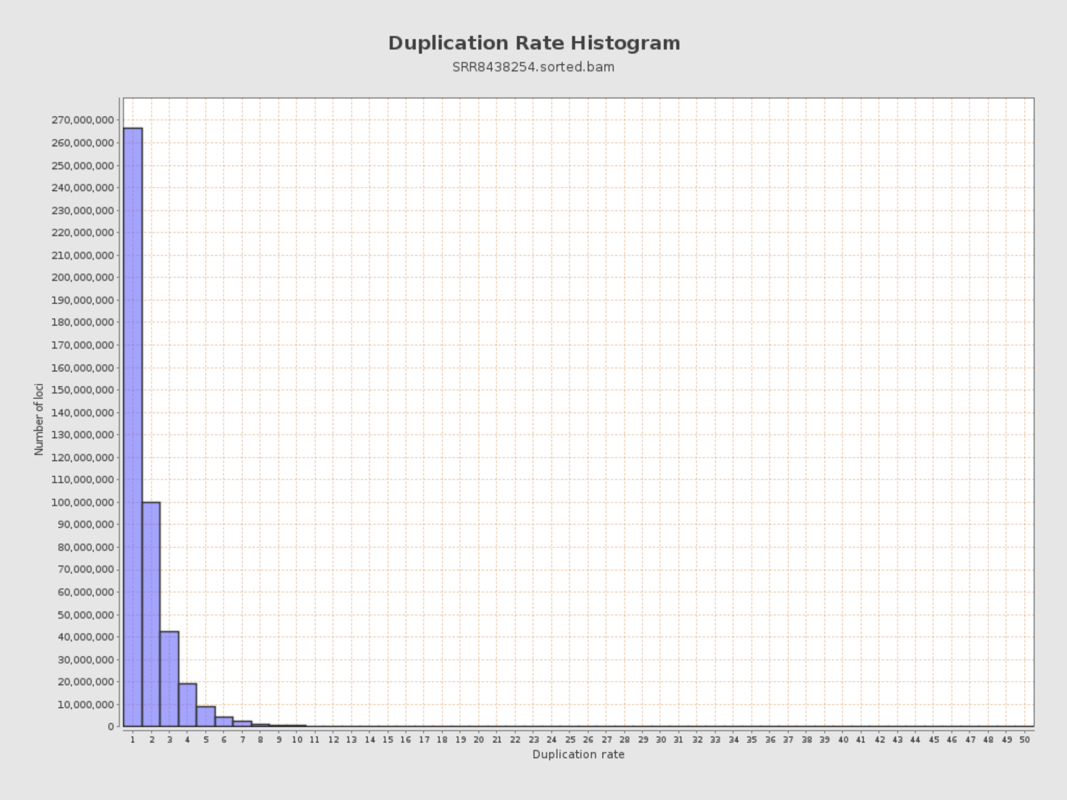
5. Results : Coverage Histogram (0-50X)



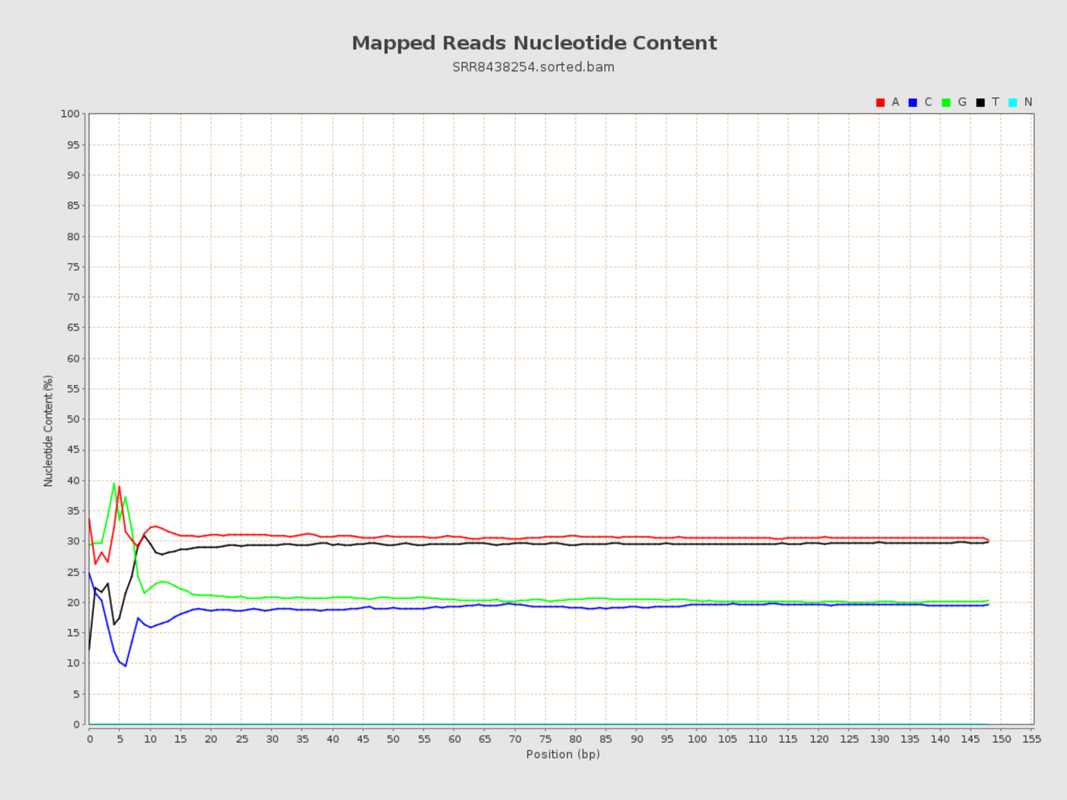
6. Results : Genome Fraction Coverage



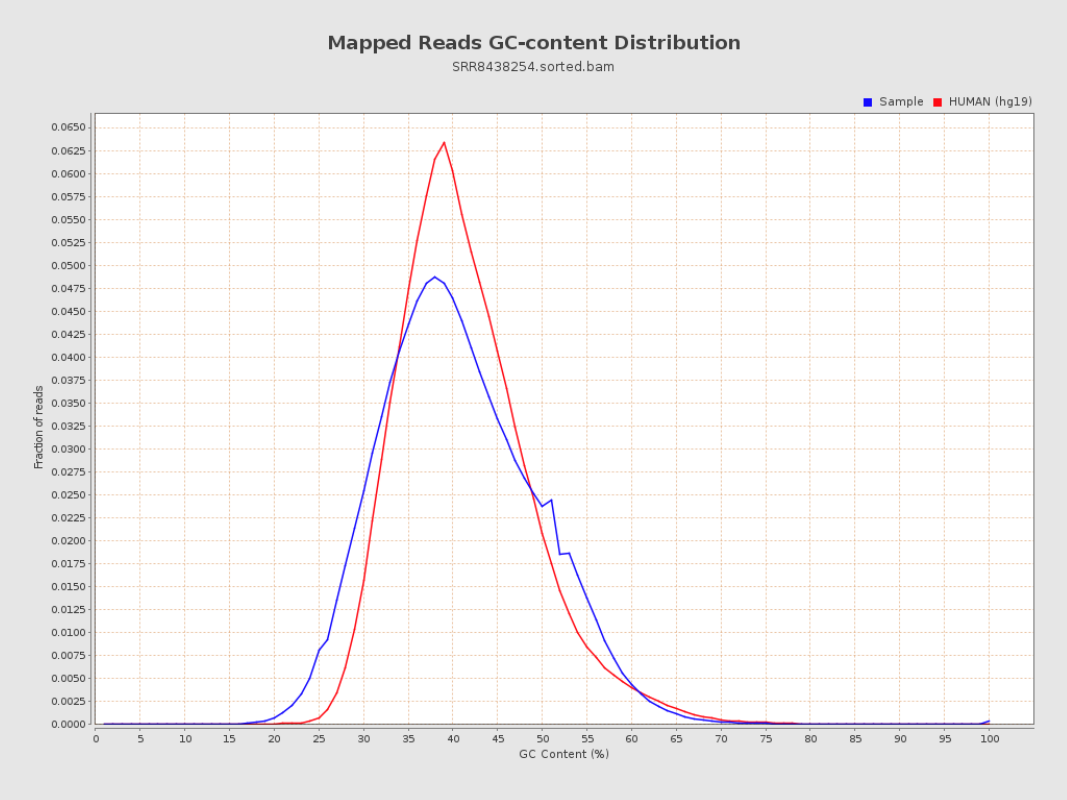
7. Results : Duplication Rate Histogram



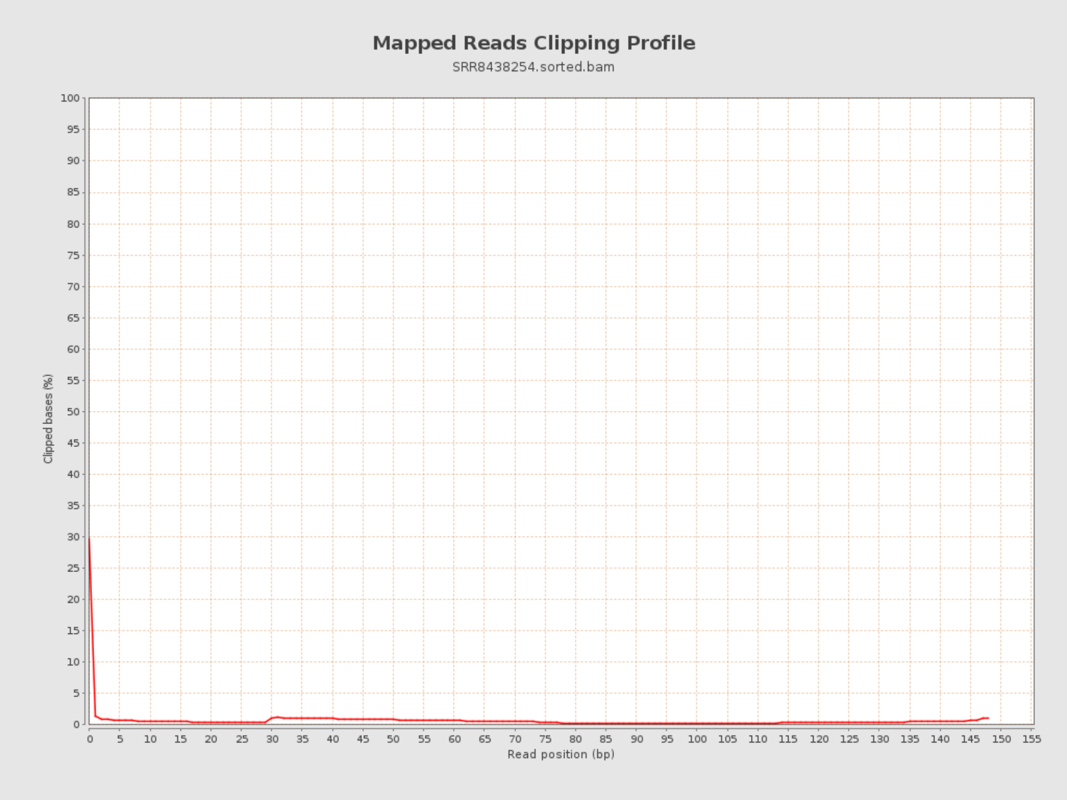
8. Results : Mapped Reads Nucleotide Content



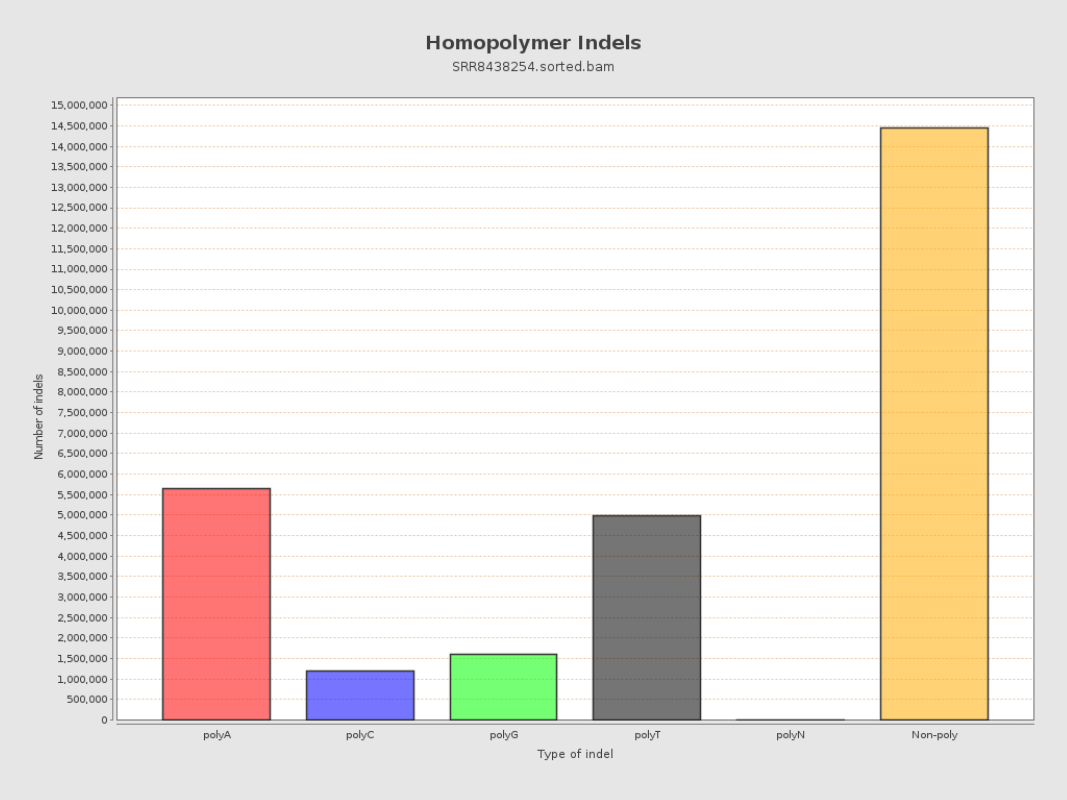
9. Results : Mapped Reads GC-content Distribution



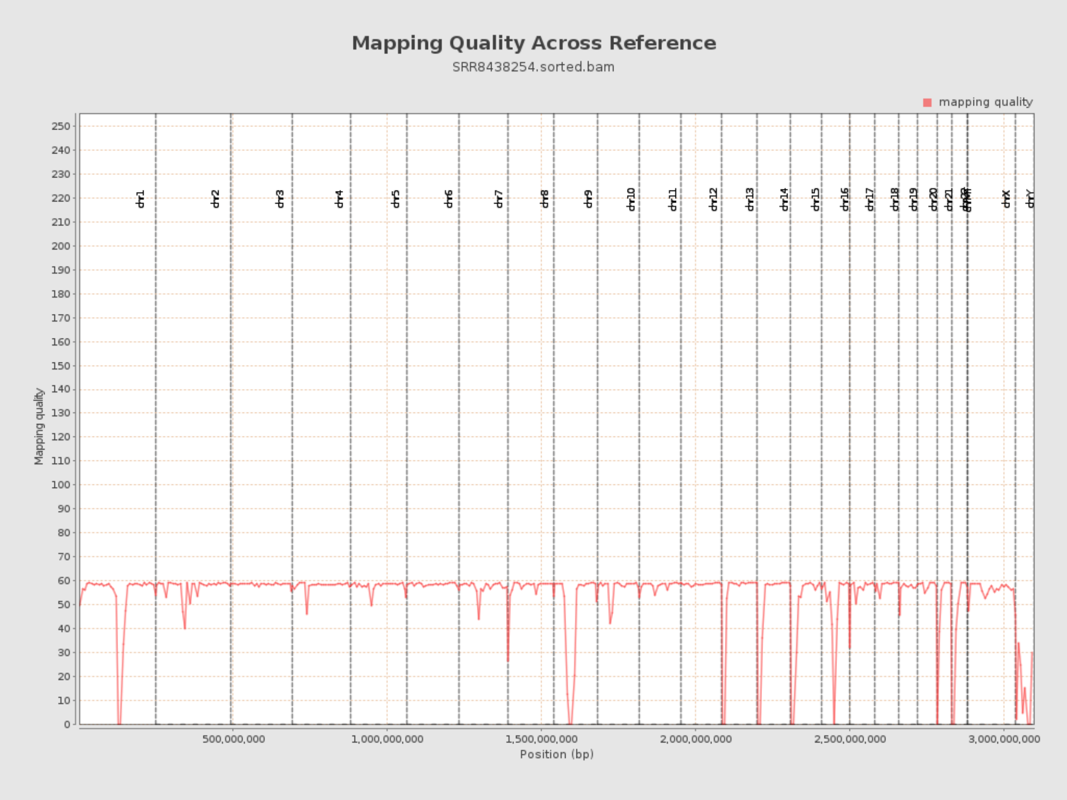
10. Results : Mapped Reads Clipping Profile



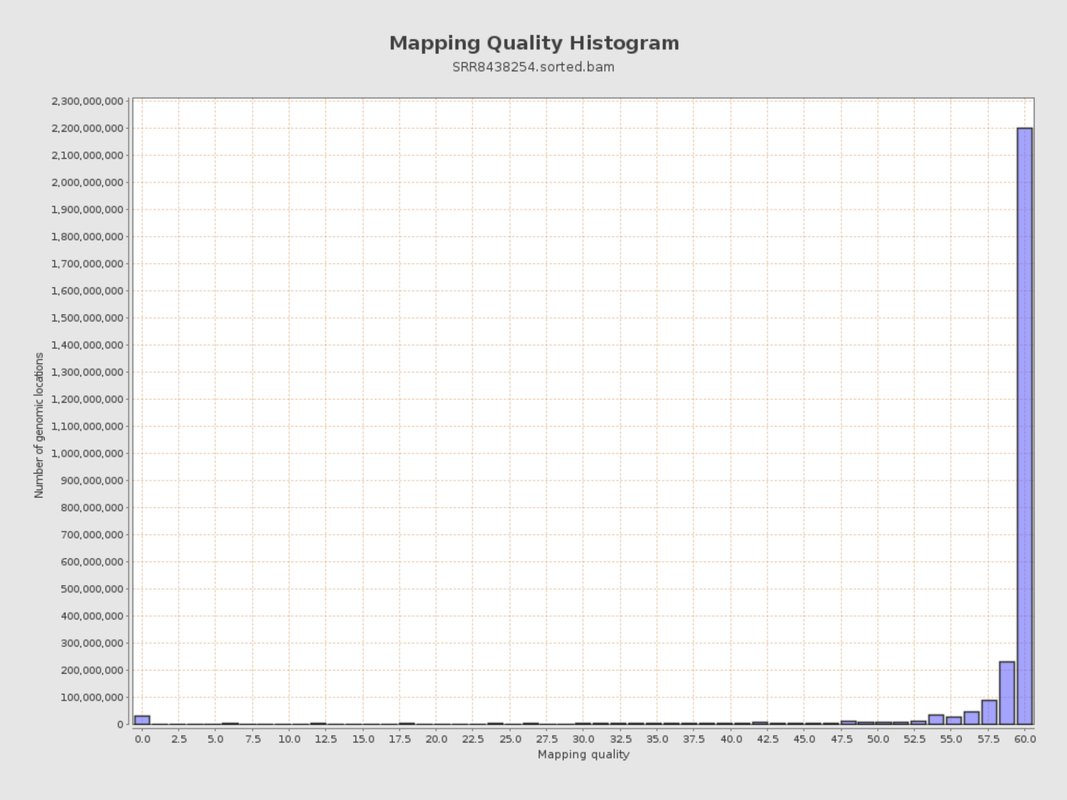
11. Results : Homopolymer Indels



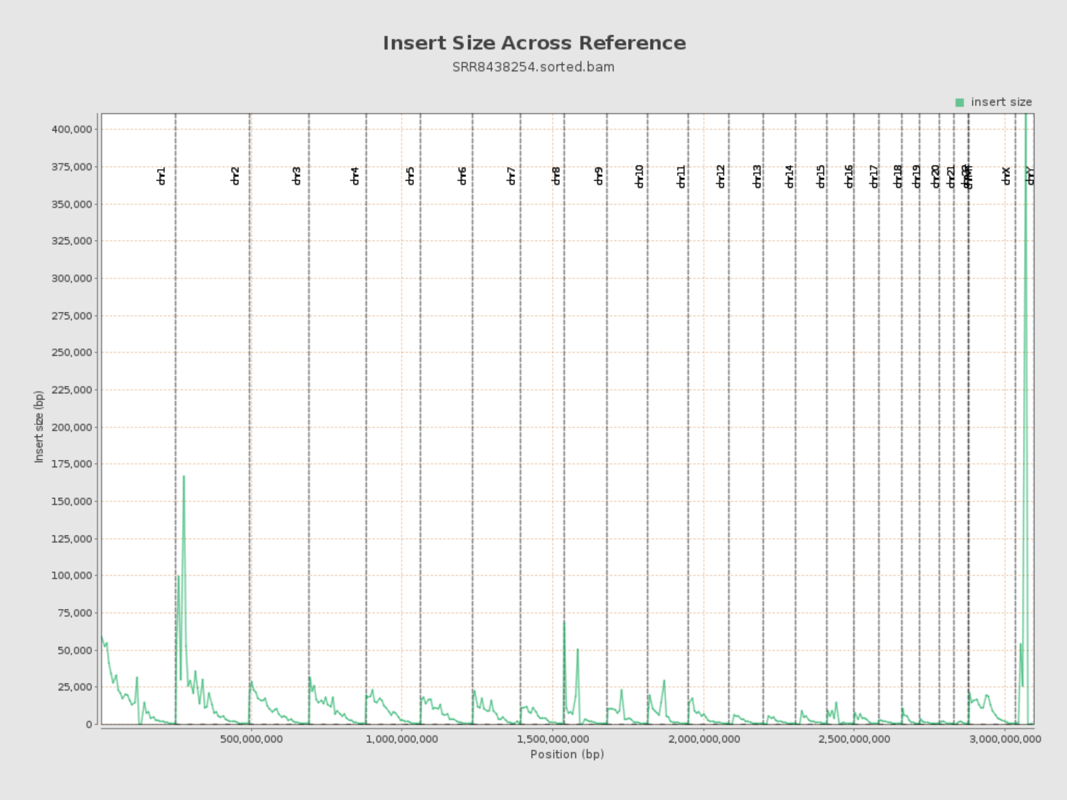
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram