Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 07:11:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438259.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_SRR8438259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438259_1.fastq.gz SRR8438259_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 07:11:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	807,735,190
Mapped reads	803,648,589 / 99.49%
Unmapped reads	4,086,601 / 0.51%
Mapped paired reads	803,648,589 / 99.49%
Mapped reads, first in pair	401,975,684 / 49.77%
Mapped reads, second in pair	401,672,905 / 49.73%
Mapped reads, both in pair	801,118,384 / 99.18%
Mapped reads, singletons	2,530,205 / 0.31%
Secondary alignments	0
Supplementary alignments	21,040,776 / 2.6%
Read min/max/mean length	30 / 149 / 143.39
Duplicated reads (estimated)	349,474,390 / 43.27%
Duplication rate	38.48%
Clipped reads	108,976,654 / 13.49%

2.2. ACGT Content

Number/percentage of A's	35,075,557,392 / 30.78%
Number/percentage of C's	21,576,260,252 / 18.93%
Number/percentage of T's	33,024,738,162 / 28.98%
Number/percentage of G's	24,287,140,229 / 21.31%
Number/percentage of N's	210,694 / 0%

GC Percentage	40.24%

2.3. Coverage

Mean	36.8255
Standard Deviation	100.7546

2.4. Mapping Quality

Mean Mapping Quality	54.28

2.5. Insert size

Mean	99,261.93
Standard Deviation	3,014,425.81
P25/Median/P75	390 / 464 / 584

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	624,226,108
Insertions	15,097,556
Mapped reads with at least one insertion	1.83%
Deletions	13,436,895
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.2%

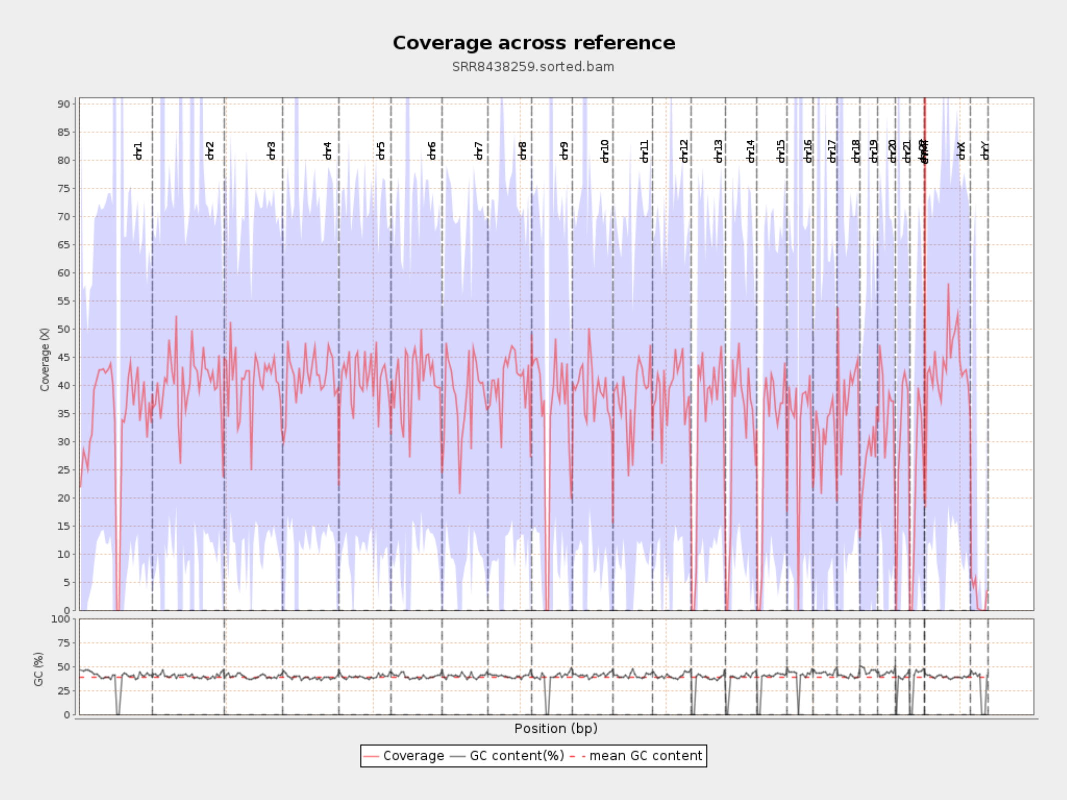
2.7. Chromosome stats

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

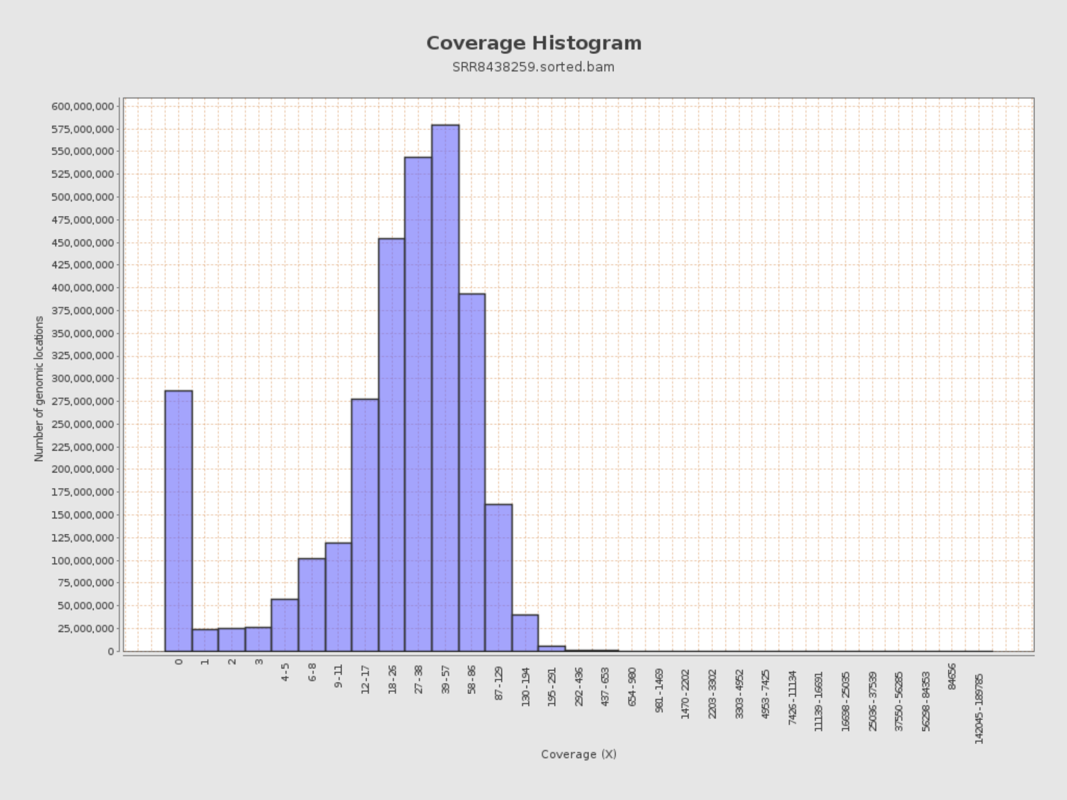
		bases	coverage	deviation
chr1	249250621	8558471663	34.3368	44.811
chr2	243199373	9802916682	40.3081	143.898
chr3	198022430	8086077339	40.8341	30.3852
chr4	191154276	7996882739	41.8347	38.0284
chr5	180915260	7410896383	40.9634	31.1755
chr6	171115067	7020235919	41.0264	39.1436
chr7	159138663	6022328953	37.8433	31.7557
chr8	146364022	5958936516	40.7131	34.2835
chr9	141213431	4865691857	34.4563	56.0399
chr10	135534747	5300301164	39.1066	84.3003
chr11	135006516	5078864356	37.6194	32.5878
chr12	133851895	5190860211	38.7806	32.6372
chr13	115169878	3881024144	33.6983	31.2682
chr14	107349540	3406145341	31.7295	31.5107
chr15	102531392	3121618582	30.4455	30.6714
chr16	90354753	2939390502	32.5317	77.5596
chr17	81195210	2481994628	30.5682	42.5335
chr18	78077248	3040227297	38.9387	61.4845
chr19	59128983	1575620301	26.6472	34.2345
chr20	63025520	2253934844	35.7623	35.2426
chr21	48129895	1512529690	31.426	47.7902
chr22	51304566	1107271631	21.5823	29.9033
chrMT	16571	552777466	33,358.1236	12,474.0334
chrX	155270560	6696091608	43.1253	34.4441

chrY	59373566	139315321	2.3464	34.9822

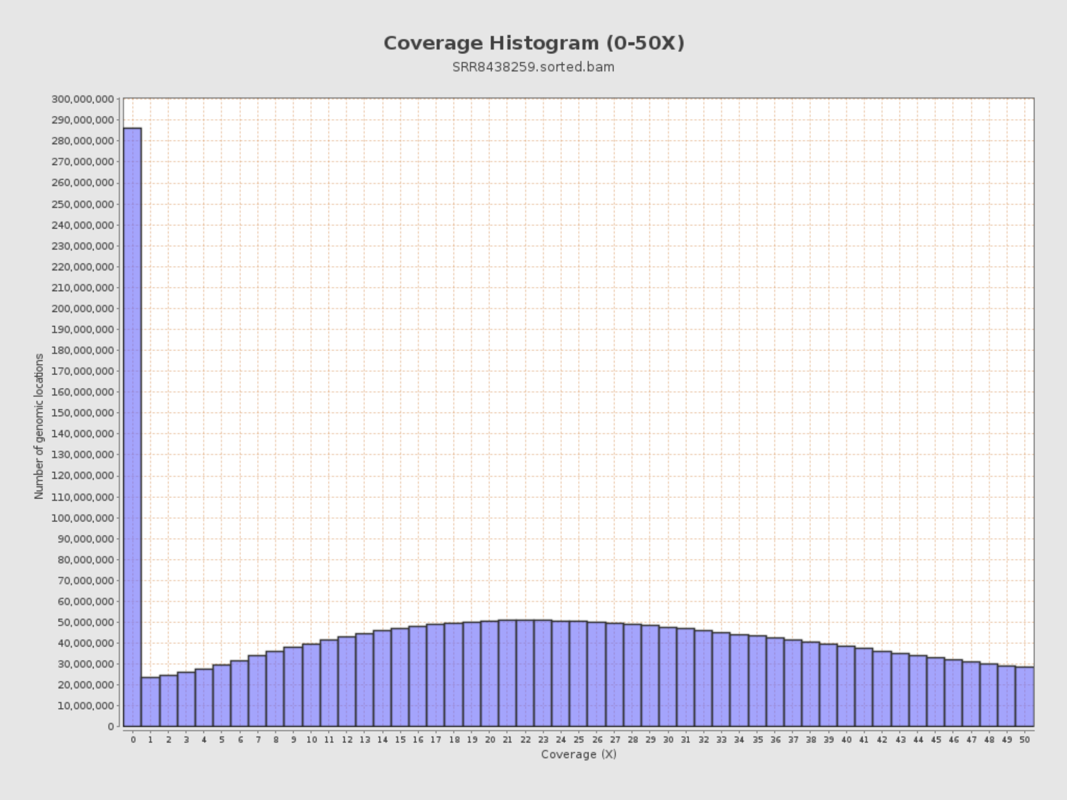
3. Results : Coverage across reference



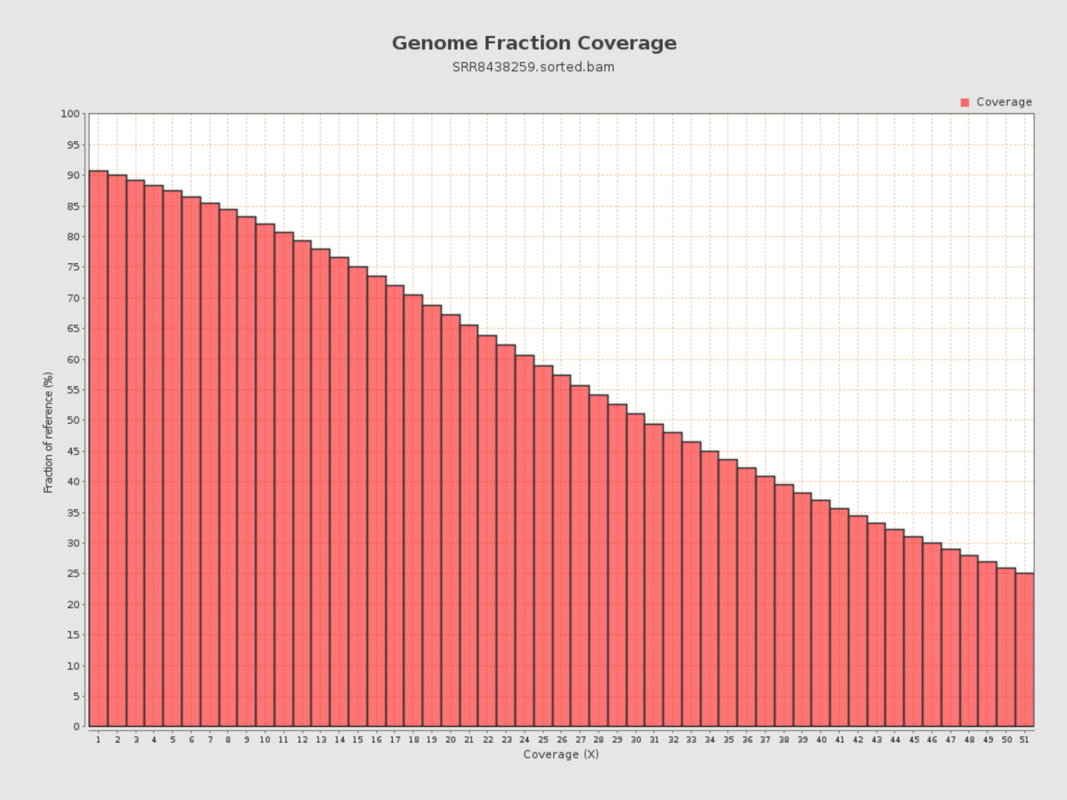
4. Results : Coverage Histogram



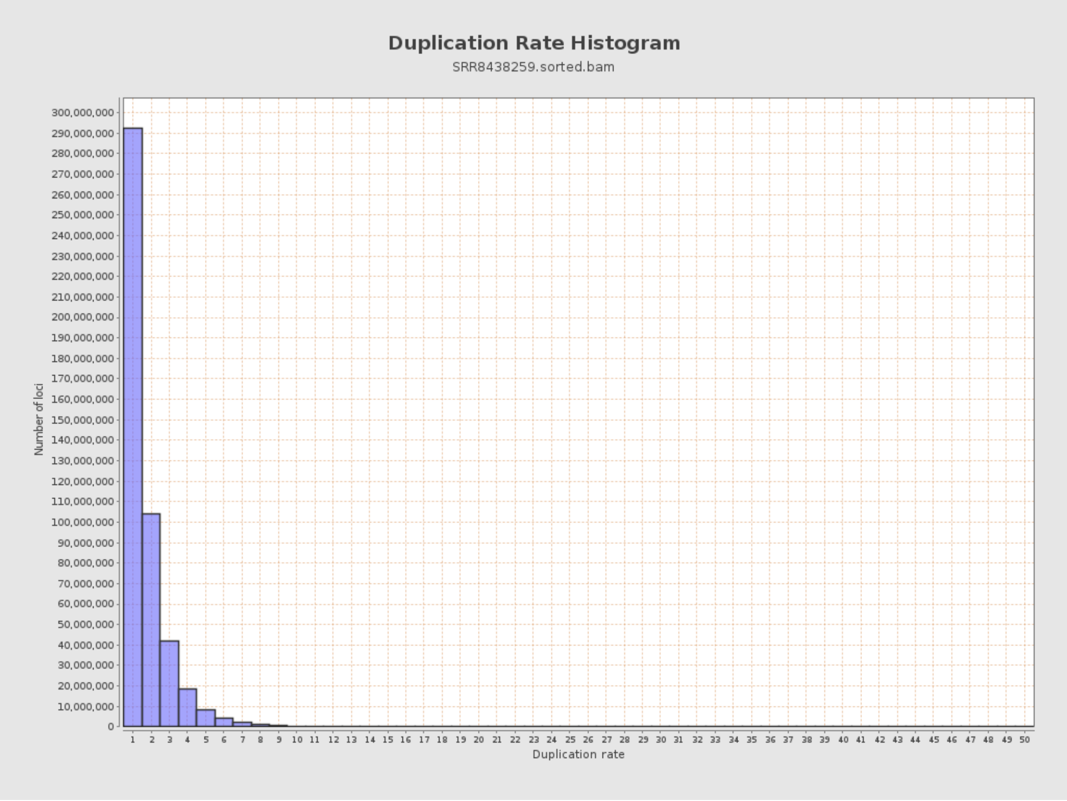
5. Results : Coverage Histogram (0-50X)



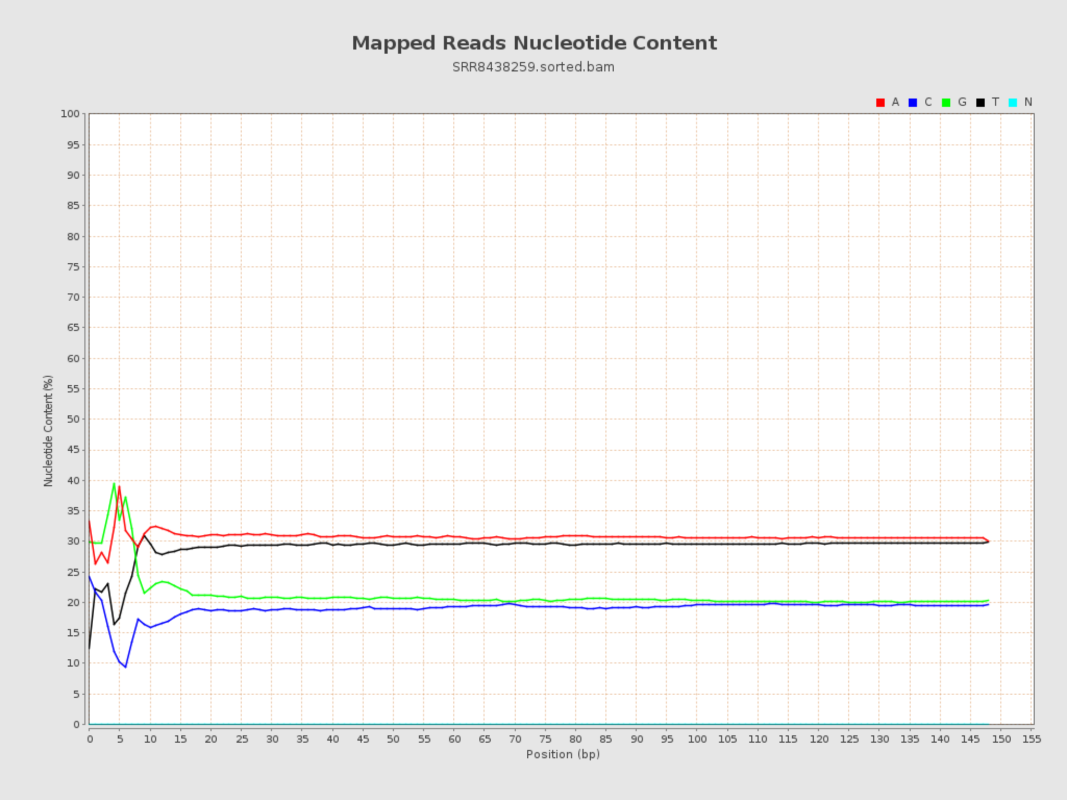
6. Results : Genome Fraction Coverage



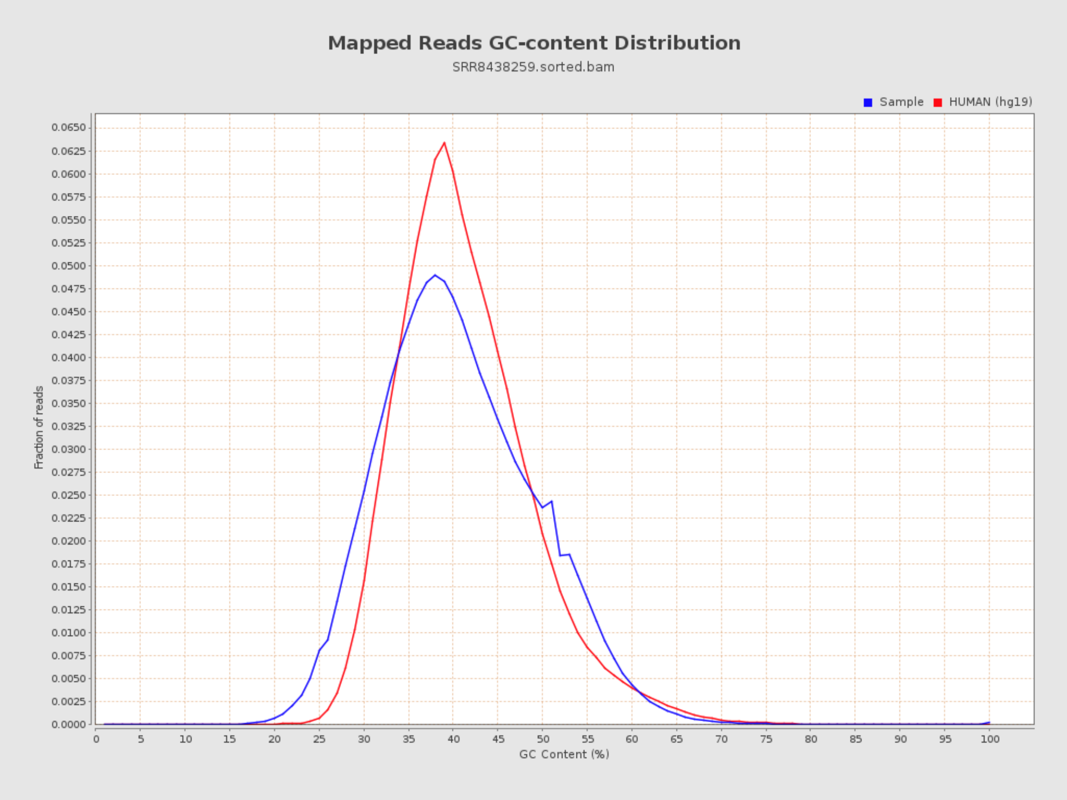
7. Results : Duplication Rate Histogram



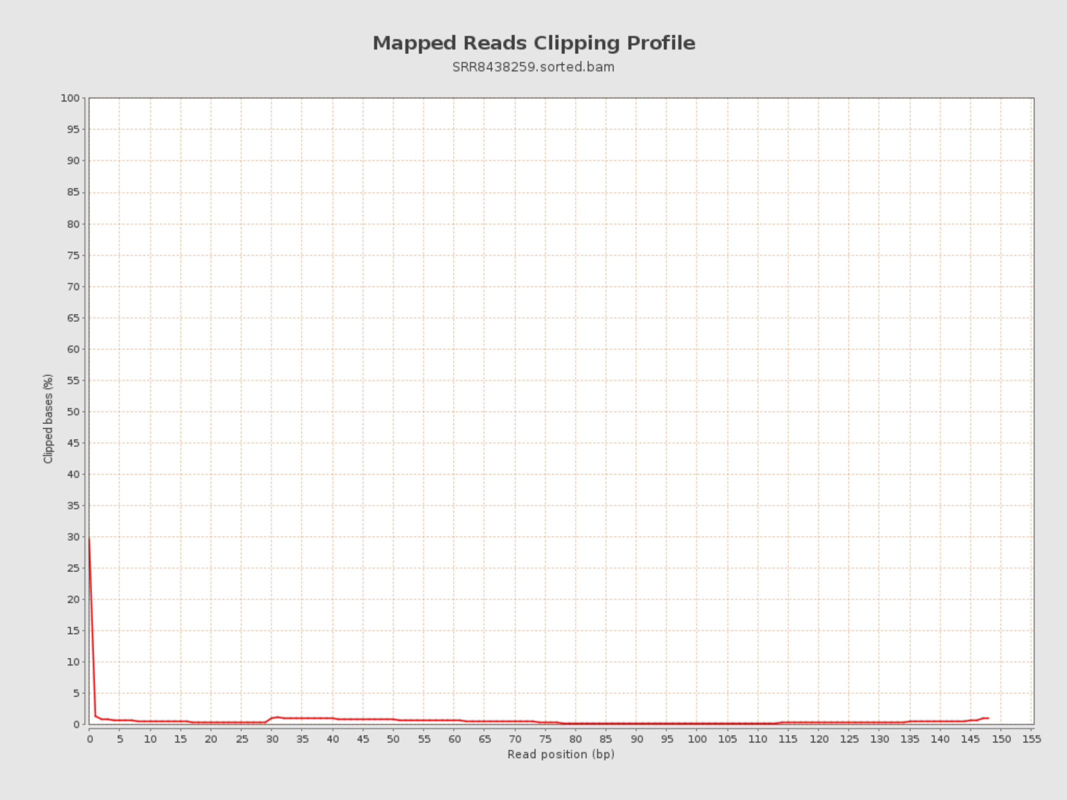
8. Results : Mapped Reads Nucleotide Content



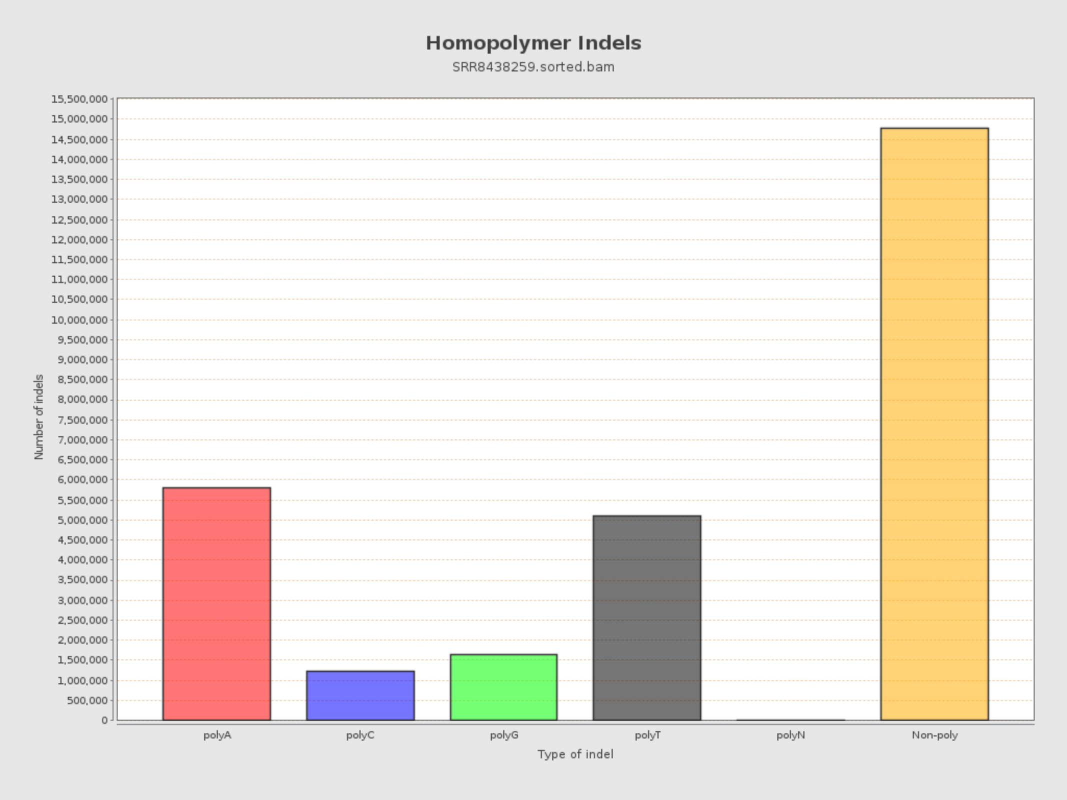
9. Results : Mapped Reads GC-content Distribution



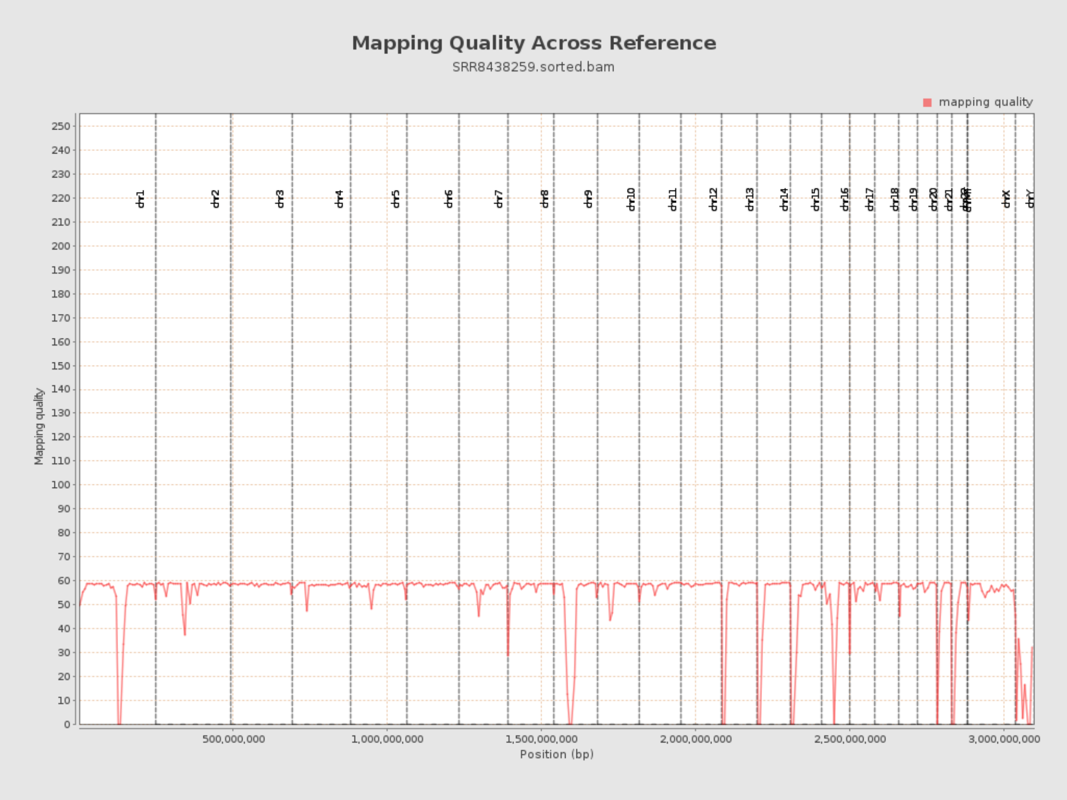
10. Results : Mapped Reads Clipping Profile



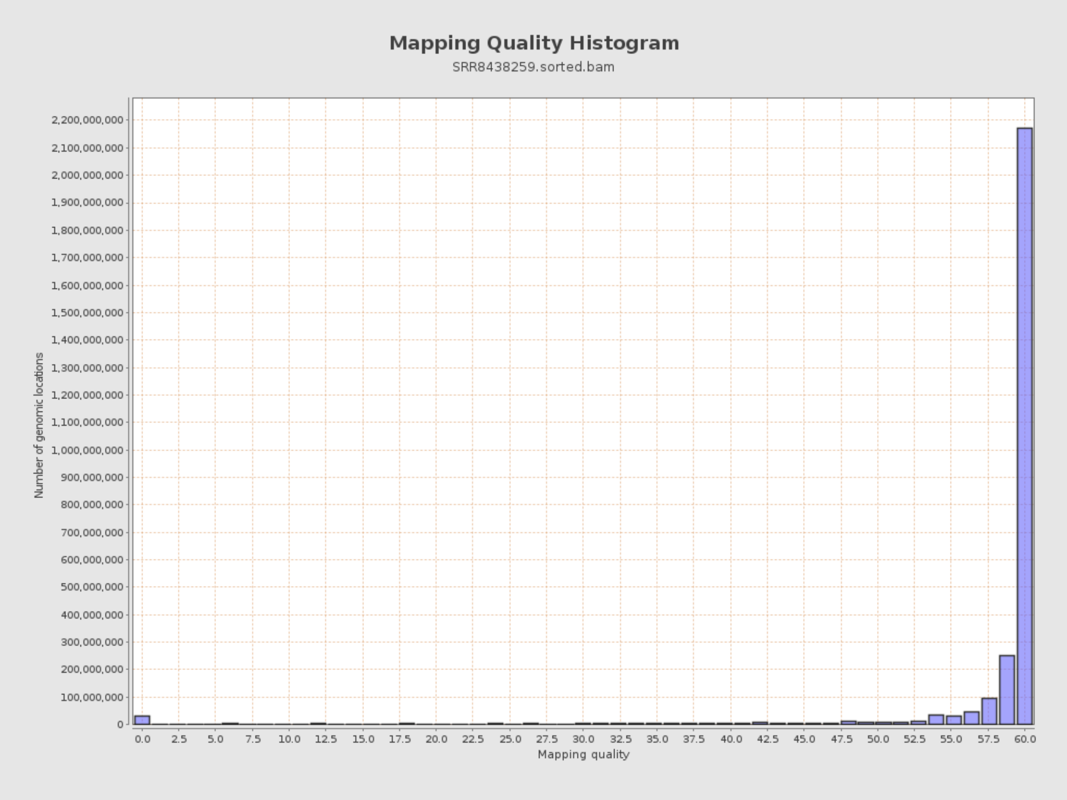
11. Results : Homopolymer Indels



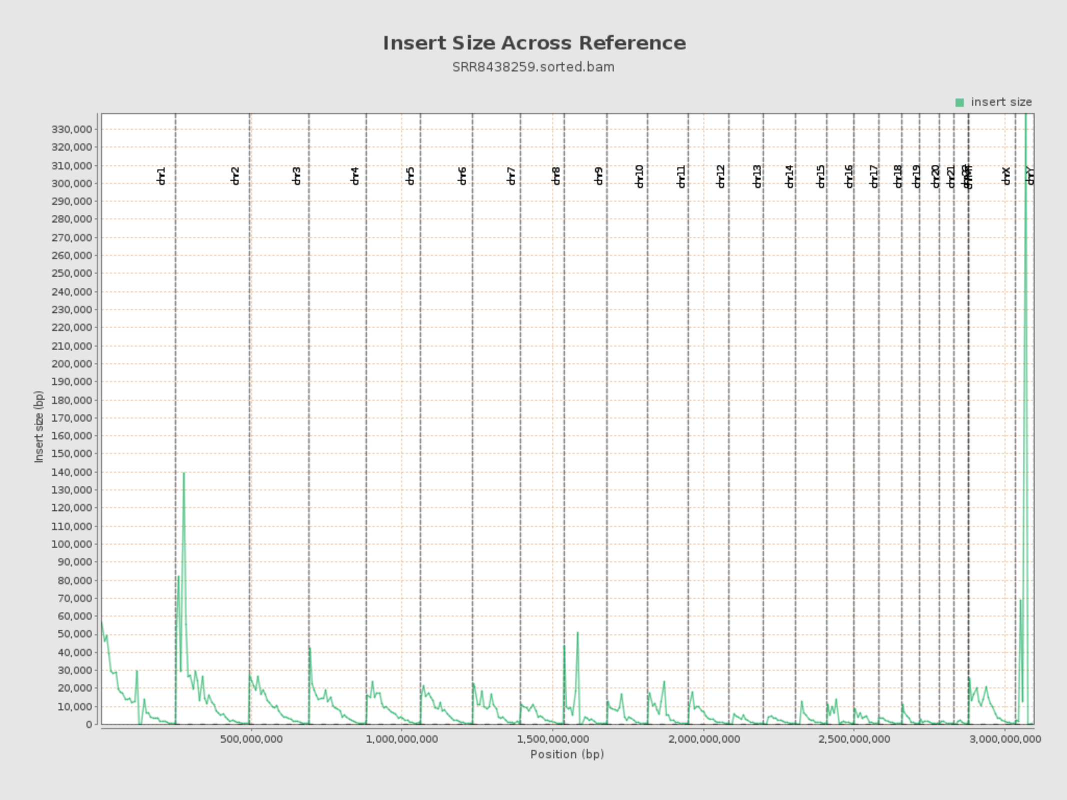
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram