Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 21:45:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438257.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_SRR8438257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438257_1.fastq.gz SRR8438257_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 21:45:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	727,335,368
Mapped reads	723,916,776 / 99.53%
Unmapped reads	3,418,592 / 0.47%
Mapped paired reads	723,916,776 / 99.53%
Mapped reads, first in pair	362,147,785 / 49.79%
Mapped reads, second in pair	361,768,991 / 49.74%
Mapped reads, both in pair	722,534,870 / 99.34%
Mapped reads, singletons	1,381,906 / 0.19%
Secondary alignments	0
Supplementary alignments	29,899,648 / 4.11%
Read min/max/mean length	30 / 149 / 128.65
Duplicated reads (estimated)	342,327,008 / 47.07%
Duplication rate	42.24%
Clipped reads	207,726,554 / 28.56%

2.2. ACGT Content

Number/percentage of A's	26,739,393,393 / 30.35%
Number/percentage of C's	17,512,043,602 / 19.88%
Number/percentage of T's	26,107,296,540 / 29.63%
Number/percentage of G's	17,743,019,390 / 20.14%
Number/percentage of N's	200,833 / 0%

GC Percentage	40.02%

2.3. Coverage

Mean	28.4672
Standard Deviation	194.9445

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	209,005.24
Standard Deviation	4,445,886.26
P25/Median/P75	96 / 163 / 233

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	246,989,590
Insertions	13,763,454
Mapped reads with at least one insertion	1.86%
Deletions	9,331,143
Mapped reads with at least one deletion	1.26%
Homopolymer indels	49.07%

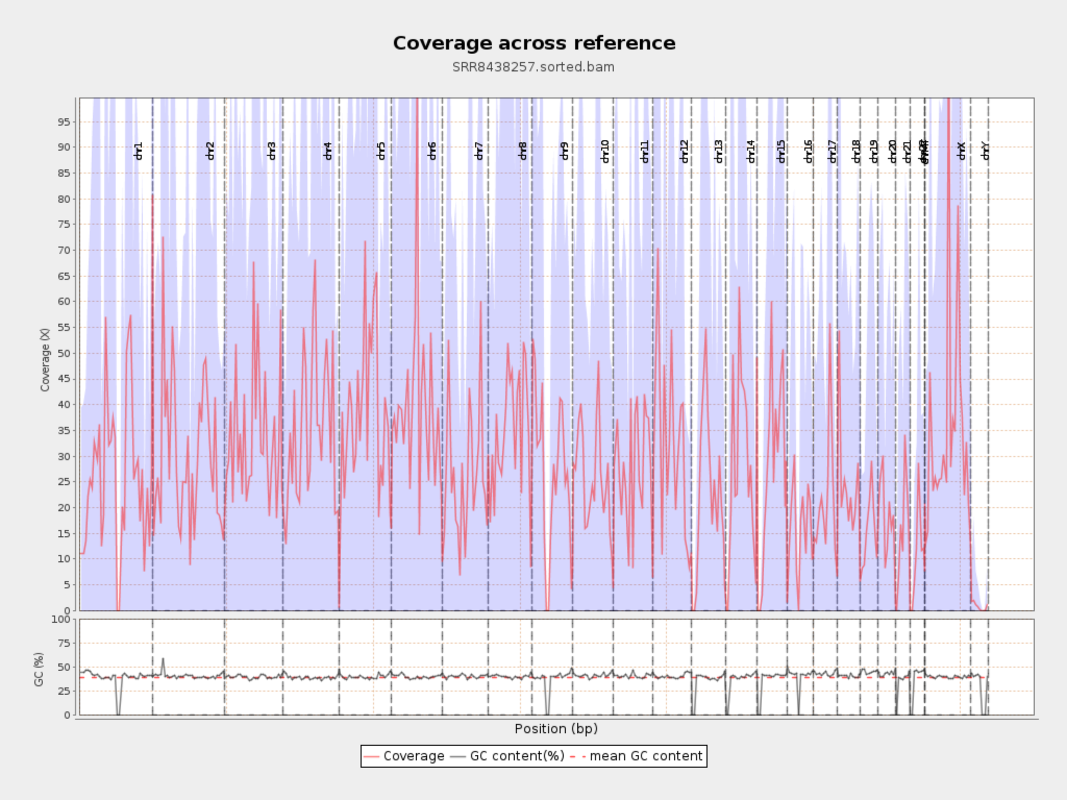
2.7. Chromosome stats

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

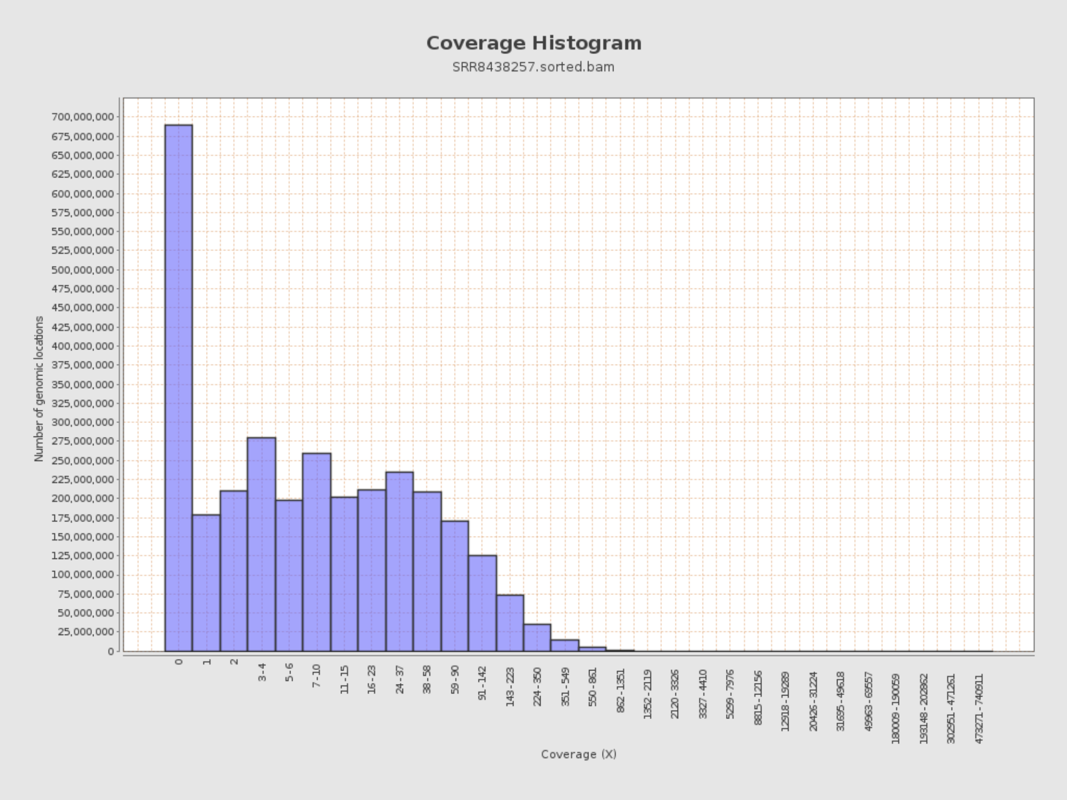
		bases	coverage	deviation
chr1	249250621	6520979198	26.1623	65.8137
chr2	243199373	7321108115	30.1033	661.6068
chr3	198022430	6737519015	34.024	66.6558
chr4	191154276	6787915745	35.5101	66.5505
chr5	180915260	6791367041	37.5389	67.1011
chr6	171115067	6846399875	40.0105	75.2302
chr7	159138663	4160101644	26.1414	61.2539
chr8	146364022	5094258701	34.8054	69.2882
chr9	141213431	3743301867	26.5081	57.9282
chr10	135534747	3606681194	26.6107	55.6563
chr11	135006516	3818163531	28.2813	57.3709
chr12	133851895	4318554729	32.2637	71.0156
chr13	115169878	2619436607	22.7441	53.7705
chr14	107349540	2952902340	27.5074	61.7569
chr15	102531392	2792554284	27.2361	59.7871
chr16	90354753	1388063286	15.3624	37.5541
chr17	81195210	1700815498	20.9472	52.4488
chr18	78077248	2013360559	25.7868	51.9883
chr19	59128983	928228411	15.6984	39.92
chr20	63025520	1135456432	18.0158	41.9562
chr21	48129895	751927203	15.6229	43.857
chr22	51304566	554617020	10.8103	29.0654
chrMT	16571	345736	20.8639	16.0096
chrX	155270560	5493238221	35.3785	83.8958

chrY	59373566	48553962	0.8178	7.2959

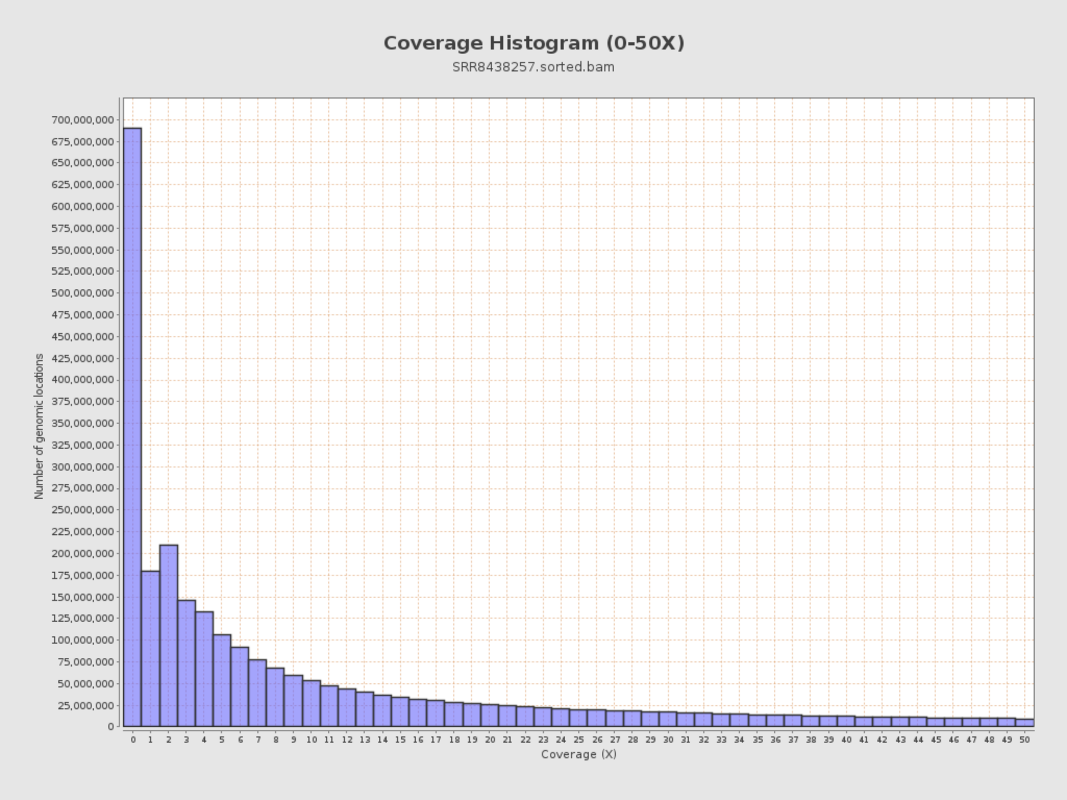
3. Results : Coverage across reference



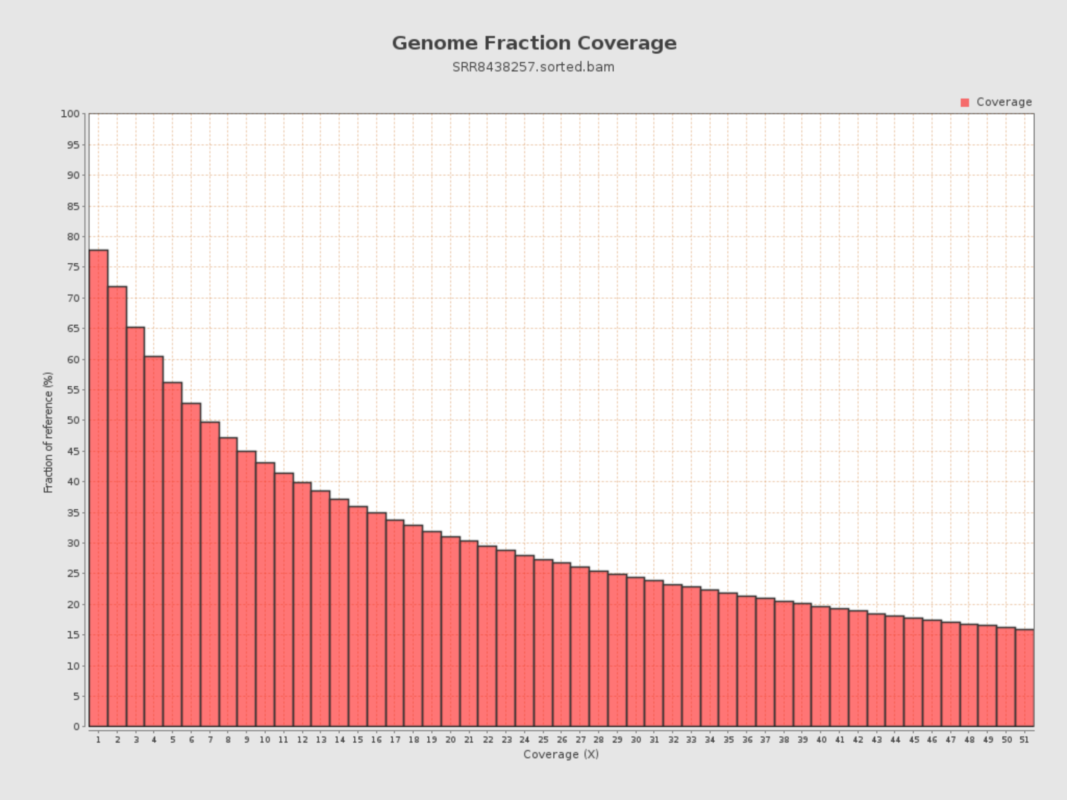
4. Results : Coverage Histogram



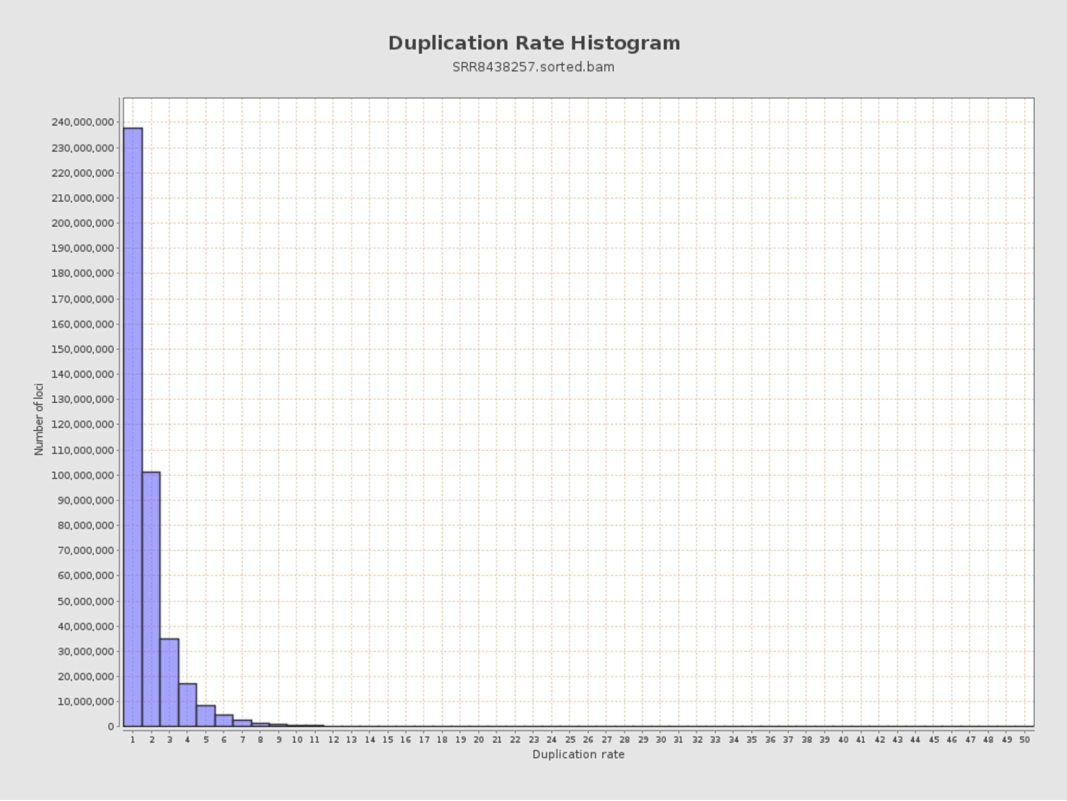
5. Results : Coverage Histogram (0-50X)



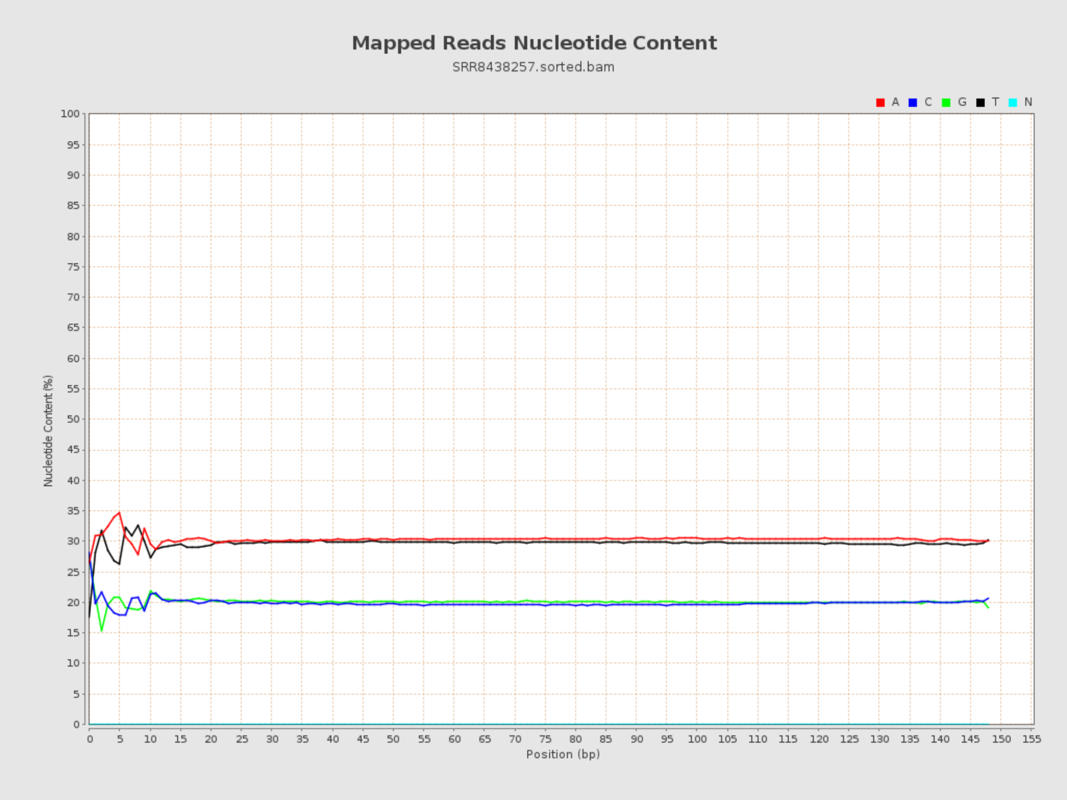
6. Results : Genome Fraction Coverage



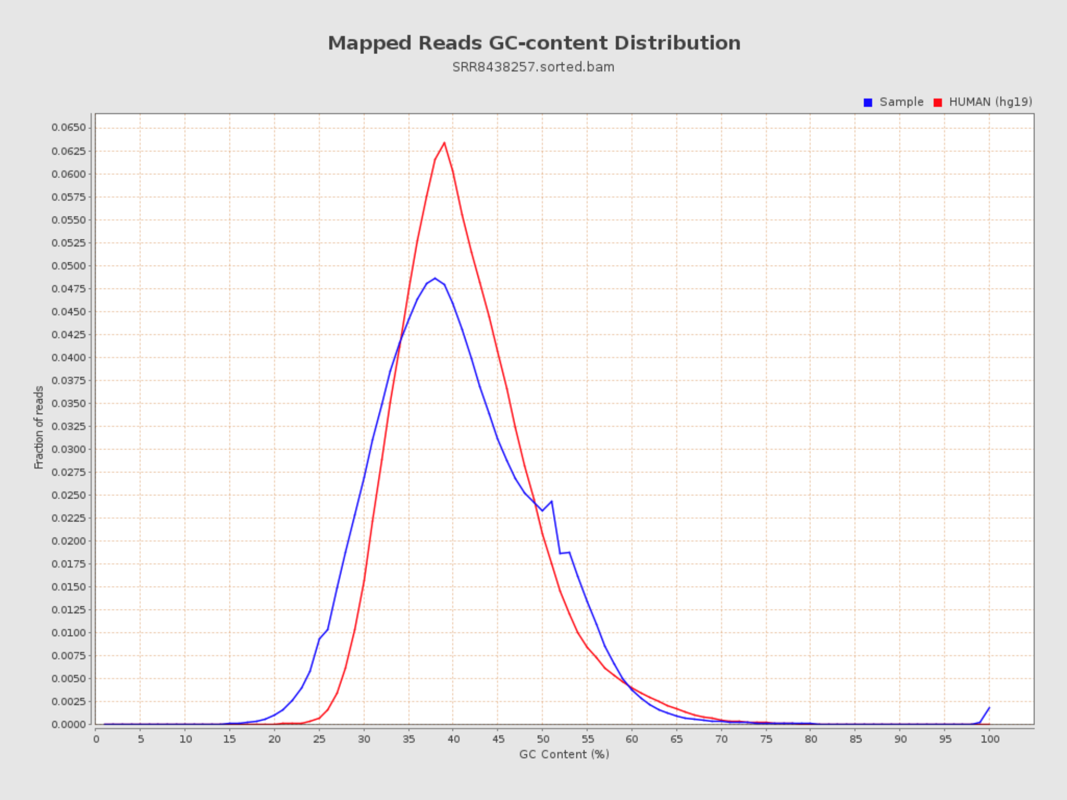
7. Results : Duplication Rate Histogram



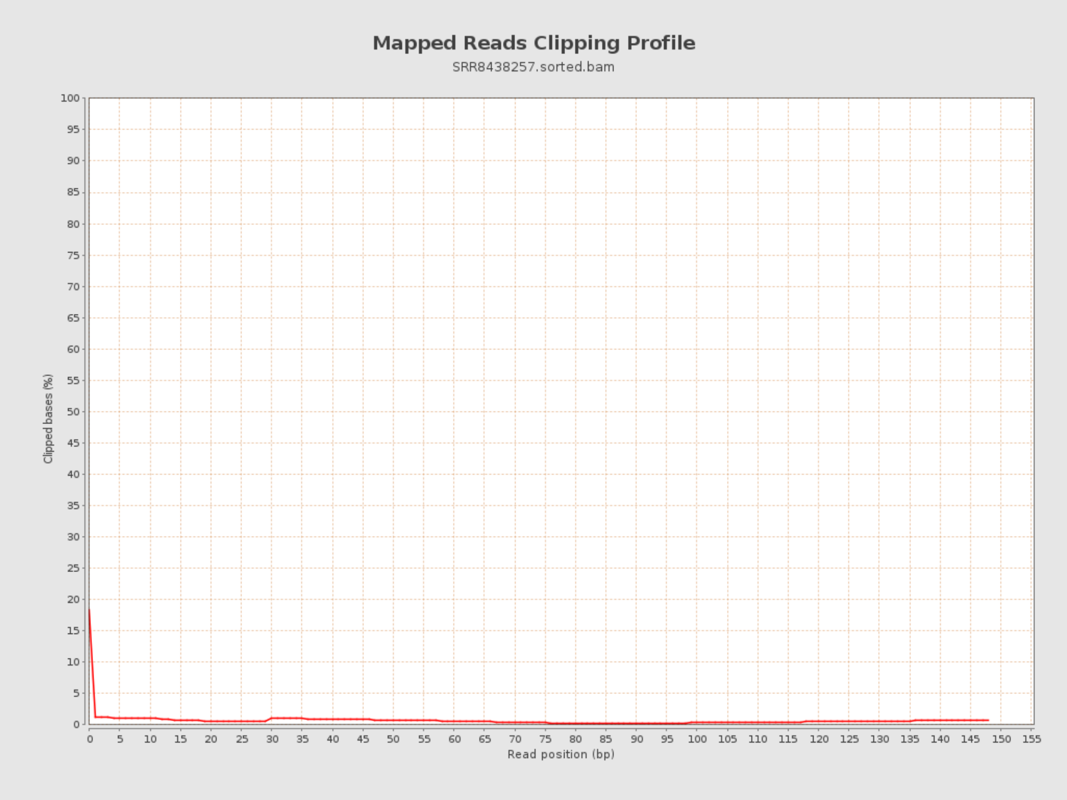
8. Results : Mapped Reads Nucleotide Content



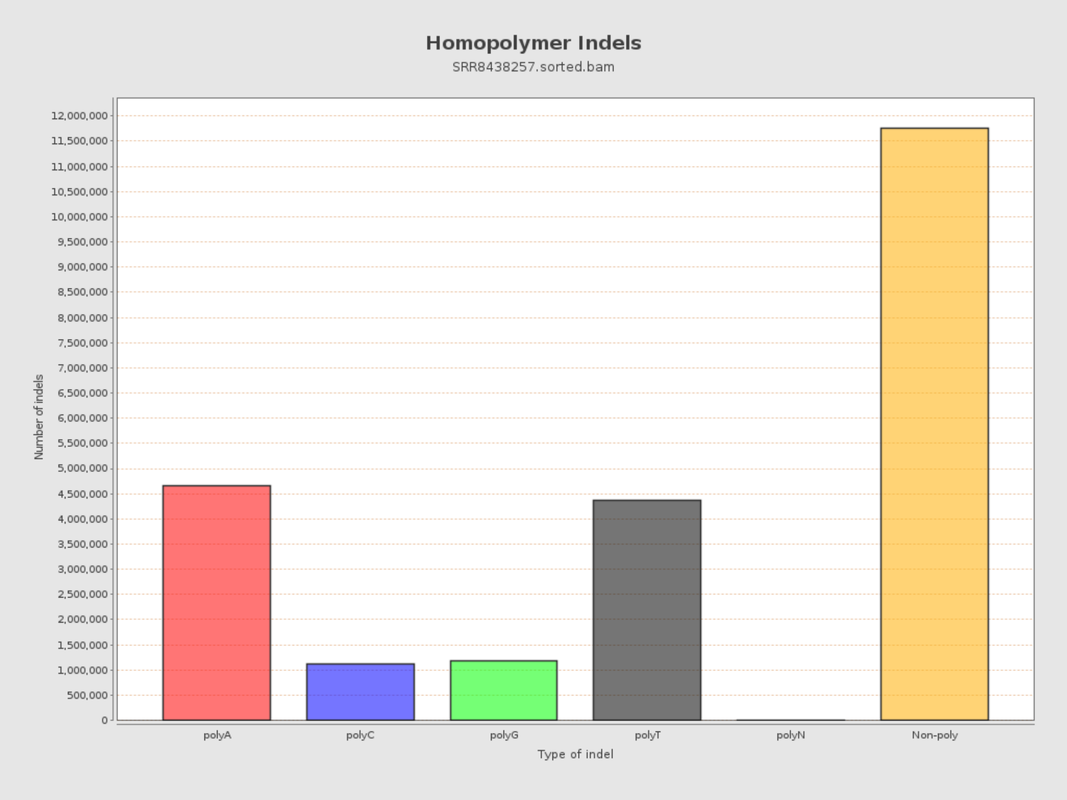
9. Results : Mapped Reads GC-content Distribution



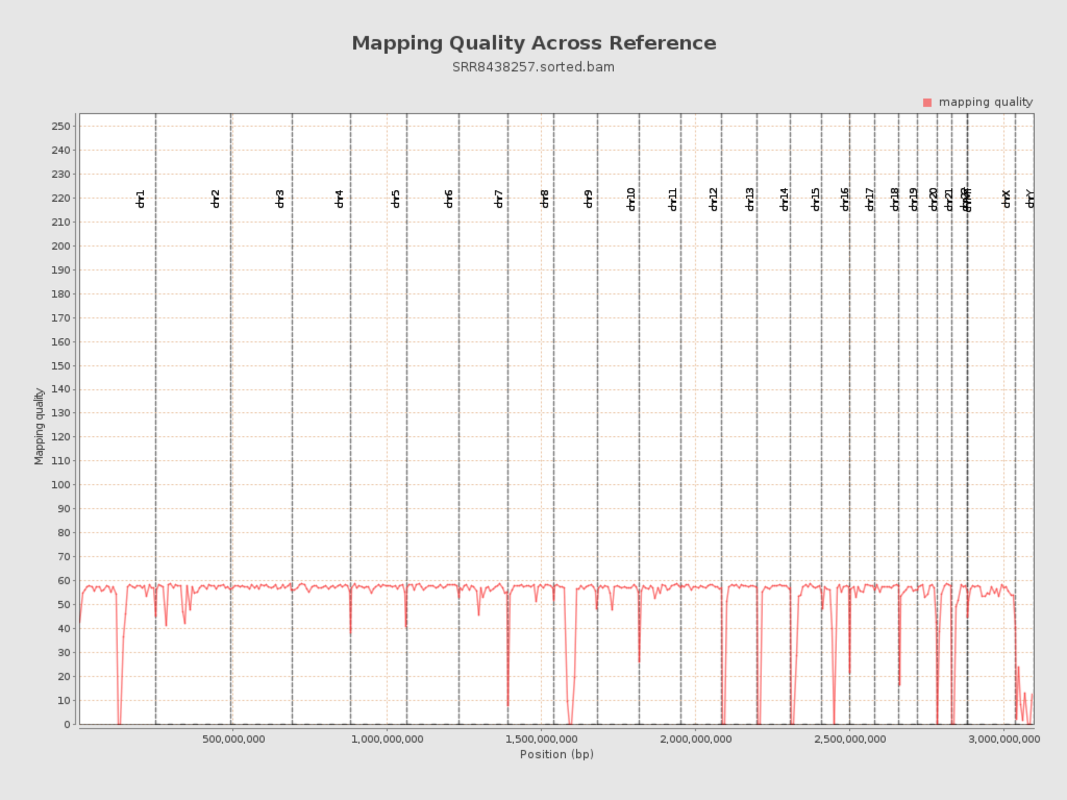
10. Results : Mapped Reads Clipping Profile



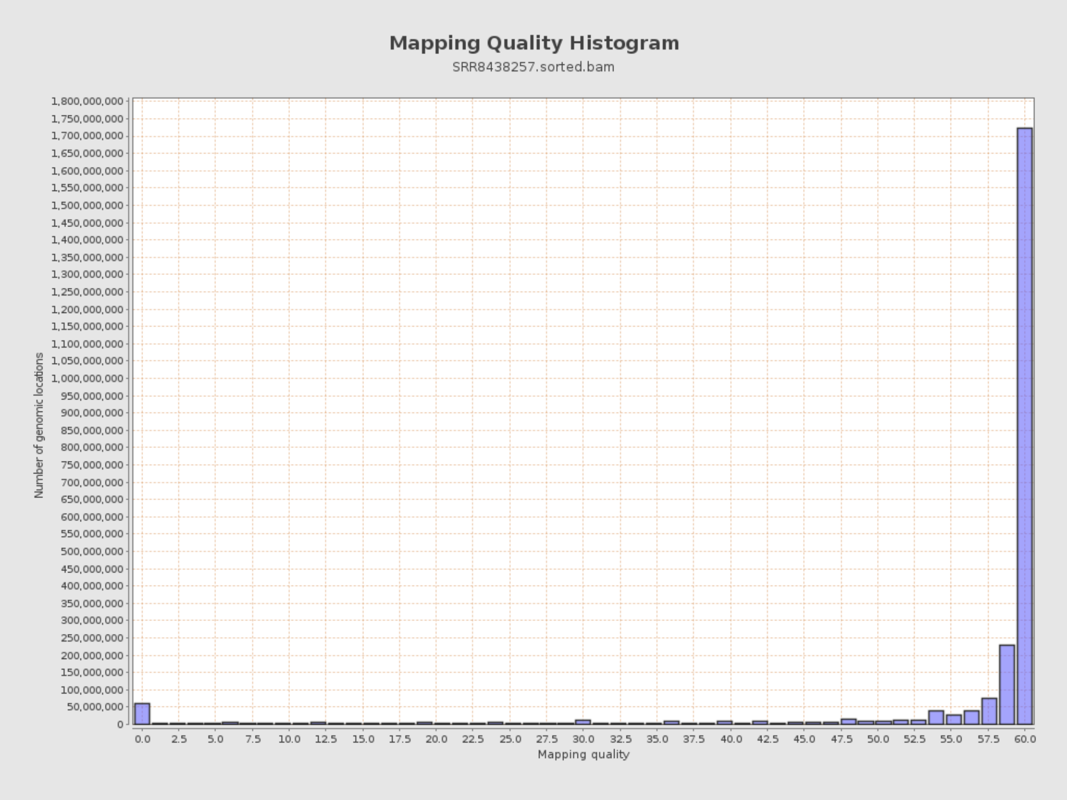
11. Results : Homopolymer Indels



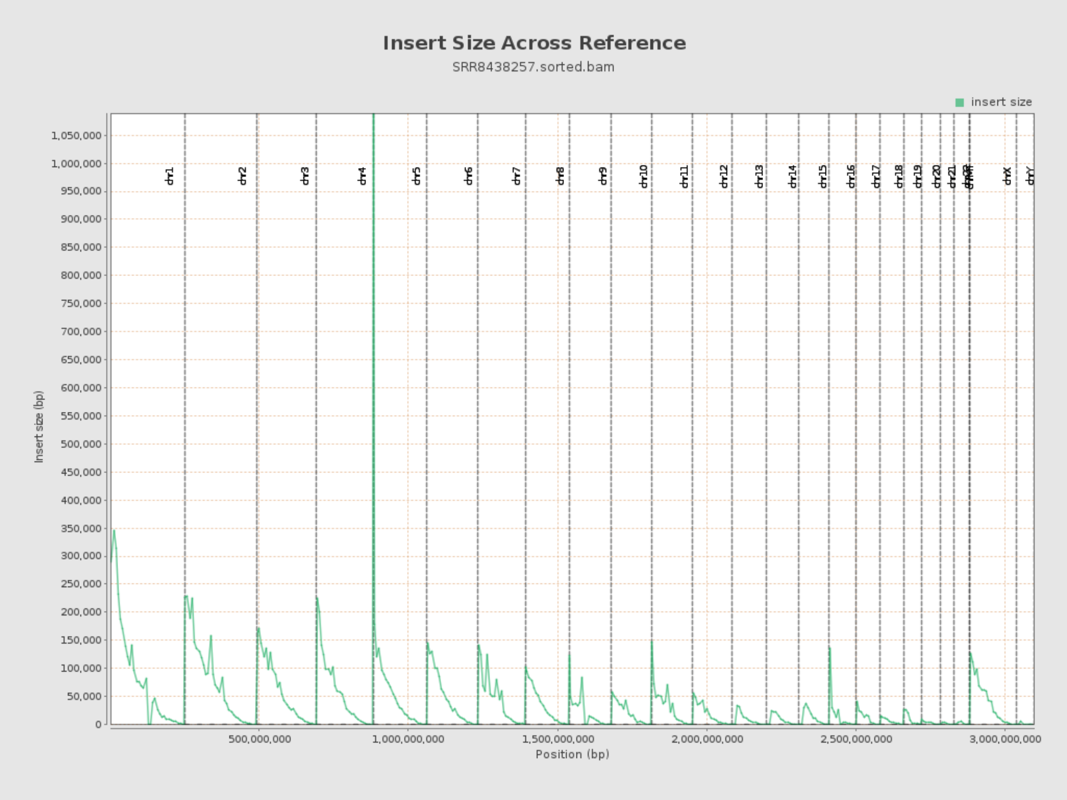
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram