Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 12:56:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438279.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_SRR8438279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438279_1.fastq.gz SRR8438279_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 12:56:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	680,728,418
Mapped reads	678,760,781 / 99.71%
Unmapped reads	1,967,637 / 0.29%
Mapped paired reads	678,760,781 / 99.71%
Mapped reads, first in pair	339,508,334 / 49.87%
Mapped reads, second in pair	339,252,447 / 49.84%
Mapped reads, both in pair	677,423,194 / 99.51%
Mapped reads, singletons	1,337,587 / 0.2%
Secondary alignments	0
Supplementary alignments	10,312,512 / 1.51%
Read min/max/mean length	28 / 151 / 144.92
Duplicated reads (estimated)	313,990,348 / 46.13%
Duplication rate	43.56%
Clipped reads	125,867,704 / 18.49%

2.2. ACGT Content

Number/percentage of A's	29,470,100,758 / 30.23%
Number/percentage of C's	19,484,043,671 / 19.99%
Number/percentage of T's	28,210,325,783 / 28.94%
Number/percentage of G's	20,316,086,235 / 20.84%
Number/percentage of N's	604,398 / 0%

GC Percentage	40.83%

2.3. Coverage

Mean	31.4975
Standard Deviation	70.0131

2.4. Mapping Quality

Mean Mapping Quality	55.15

2.5. Insert size

Mean	39,104.67
Standard Deviation	1,931,722.09
P25/Median/P75	174 / 225 / 308

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	498,217,774
Insertions	11,835,939
Mapped reads with at least one insertion	1.72%
Deletions	10,519,382
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.24%

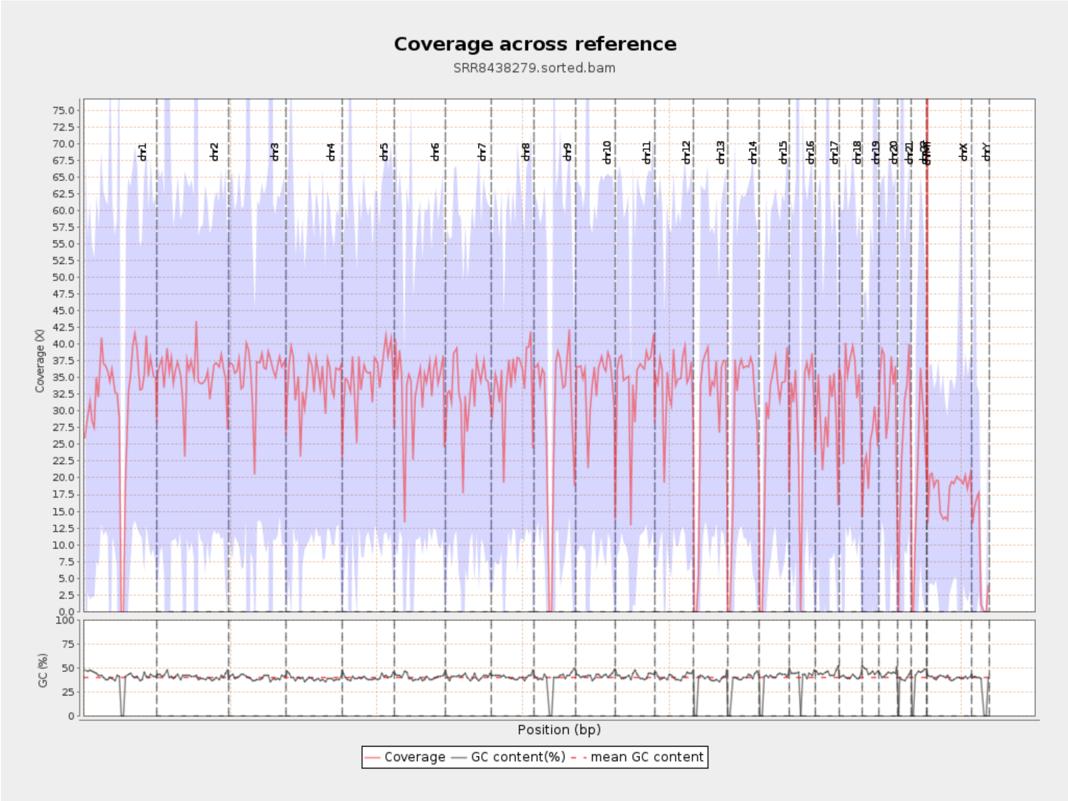
2.7. Chromosome stats

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

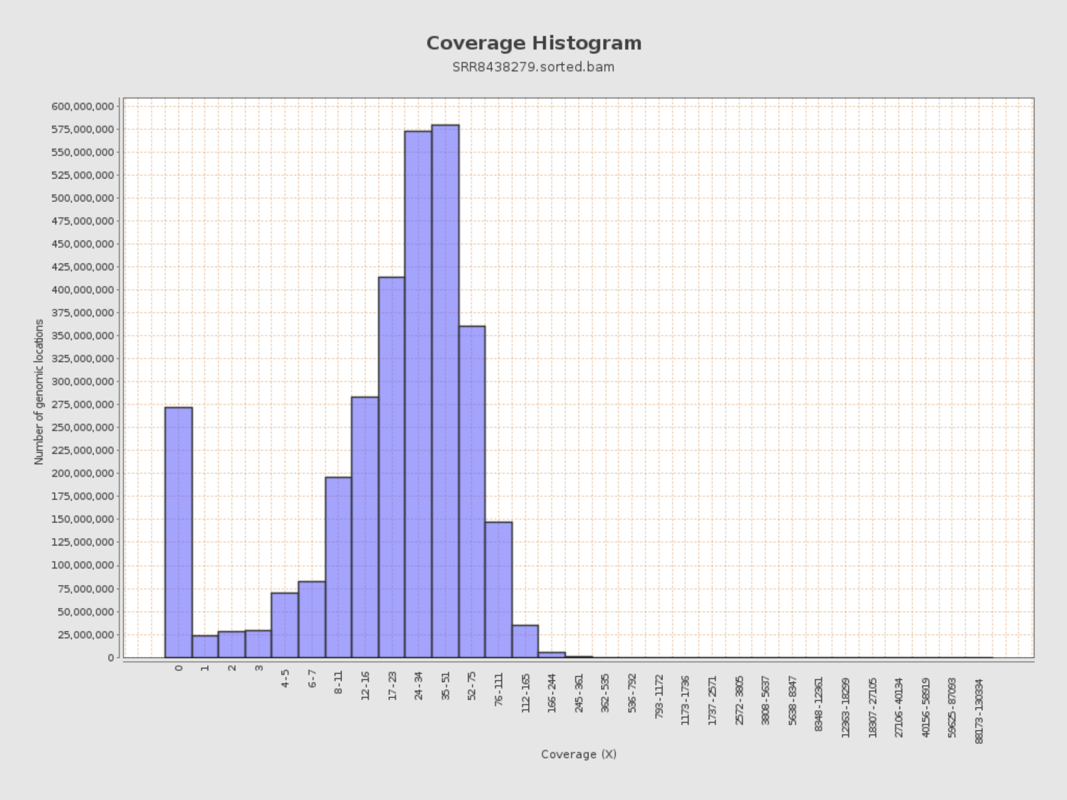
		bases	coverage	deviation
chr1	249250621	7950122486	31.8961	30.4165
chr2	243199373	8625370840	35.4663	126.4128
chr3	198022430	7121749558	35.9644	79.6914
chr4	191154276	6607779322	34.5678	25.8006
chr5	180915260	6365567073	35.1854	28.0856
chr6	171115067	5758242711	33.6513	26.1208
chr7	159138663	5237631626	32.9124	26.1854
chr8	146364022	5040541397	34.4384	26.378
chr9	141213431	4240202821	30.0269	30.951
chr10	135534747	4713178464	34.7747	33.0636
chr11	135006516	4663473889	34.5426	27.1845
chr12	133851895	4618397921	34.5038	26.1134
chr13	115169878	3383539405	29.3787	26.3173
chr14	107349540	3159362102	29.4306	28.5513
chr15	102531392	2850673372	27.8029	28.3527
chr16	90354753	2617071377	28.9644	49.8681
chr17	81195210	2376407173	29.2678	35.5417
chr18	78077248	2700238523	34.5842	27.2317
chr19	59128983	1437278043	24.3075	117.2405
chr20	63025520	2127453411	33.7554	29.7021
chr21	48129895	1214404340	25.2318	50.892
chr22	51304566	1052287606	20.5106	27.4946
chrMT	16571	314925068	19,004.5904	7,377.5546
chrX	155270560	2833711192	18.2502	19.9087

chrY	59373566	496907152	8.3692	26.0705

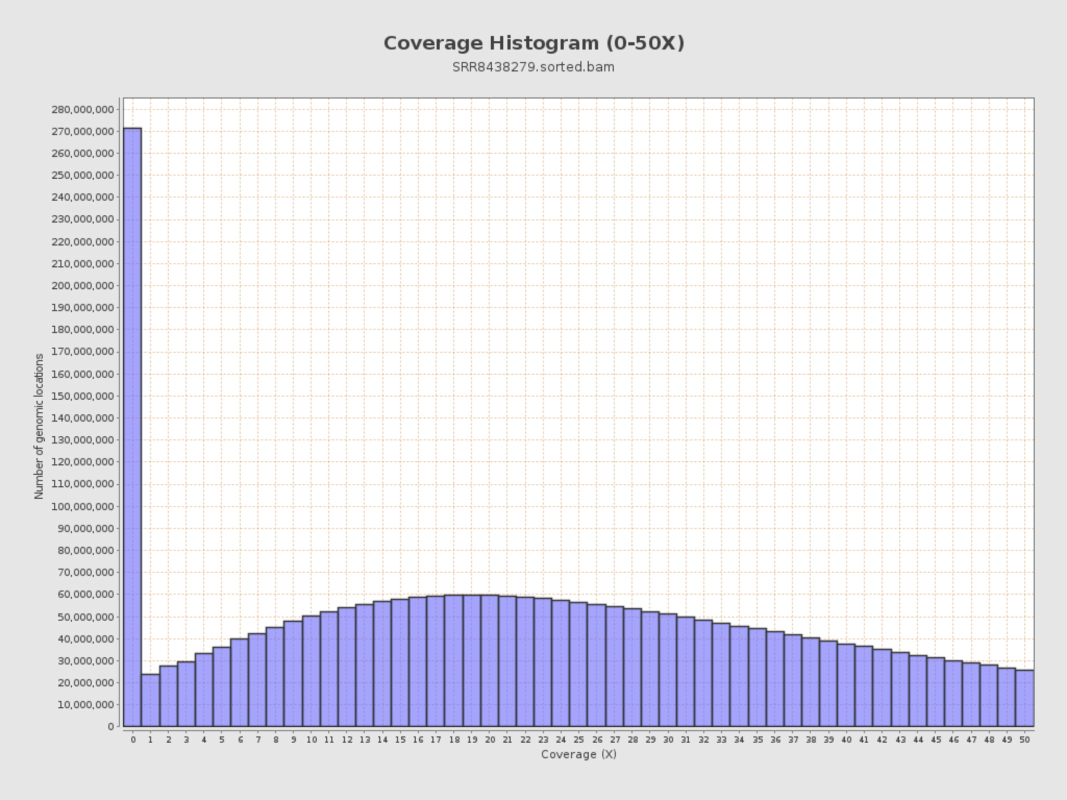
3. Results : Coverage across reference



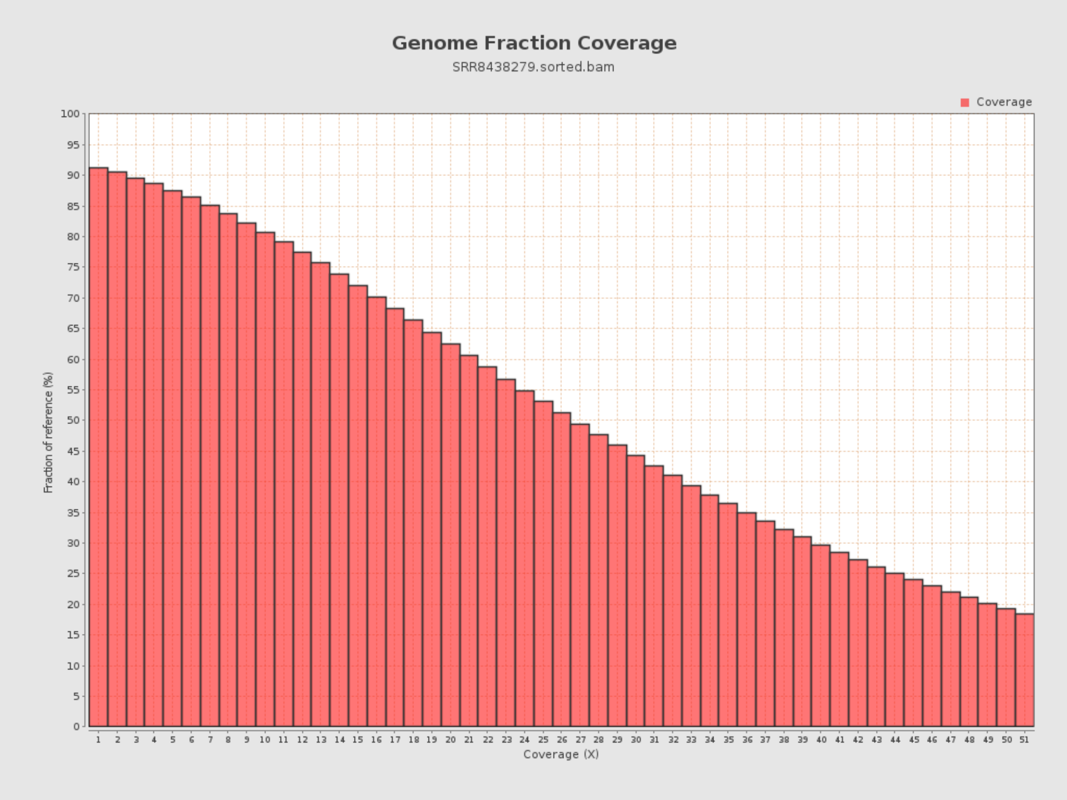
4. Results : Coverage Histogram



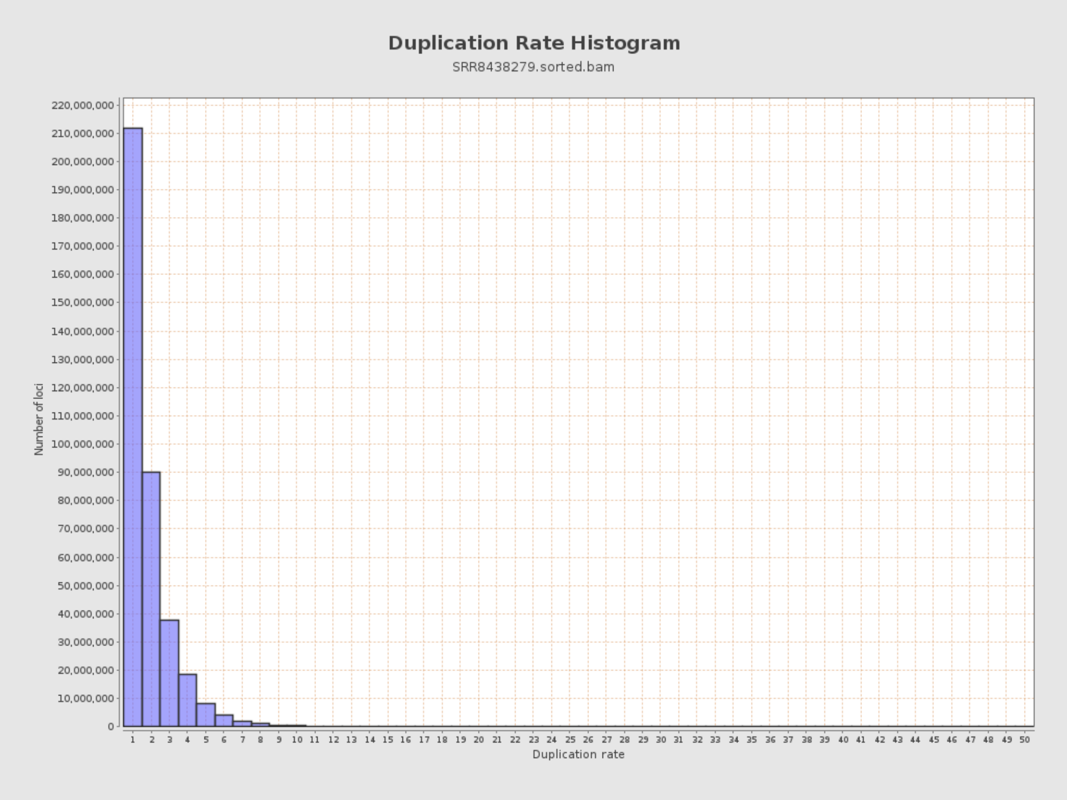
5. Results : Coverage Histogram (0-50X)



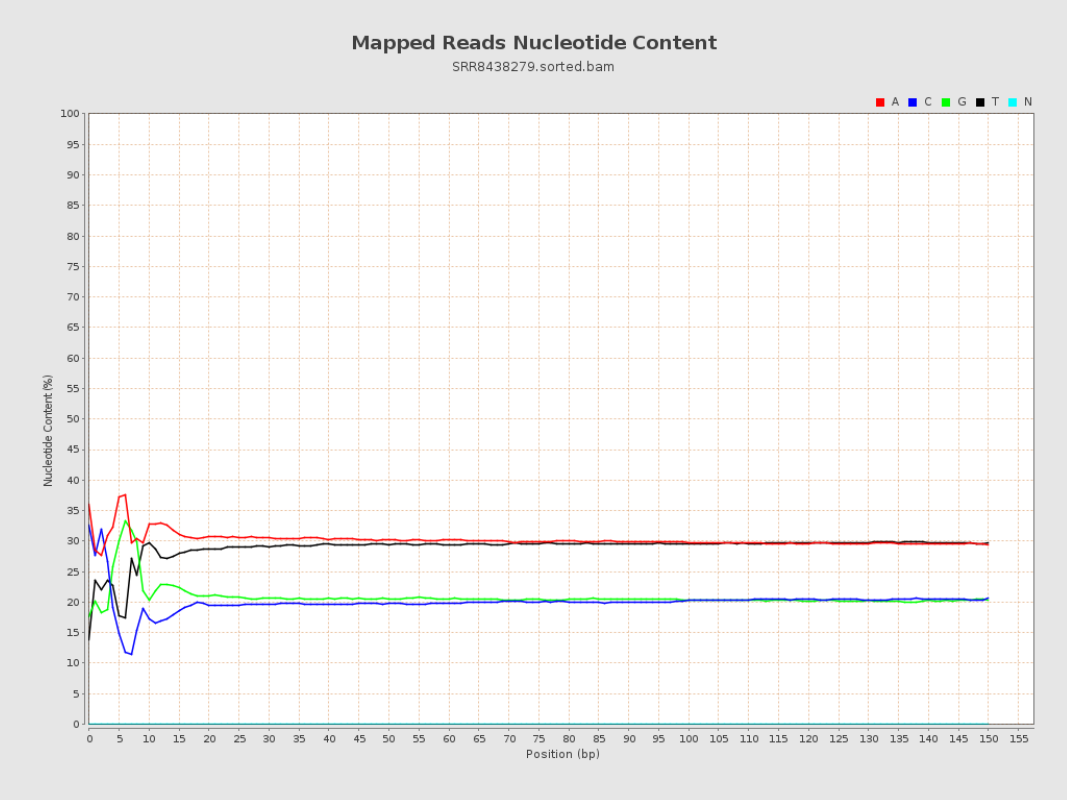
6. Results : Genome Fraction Coverage



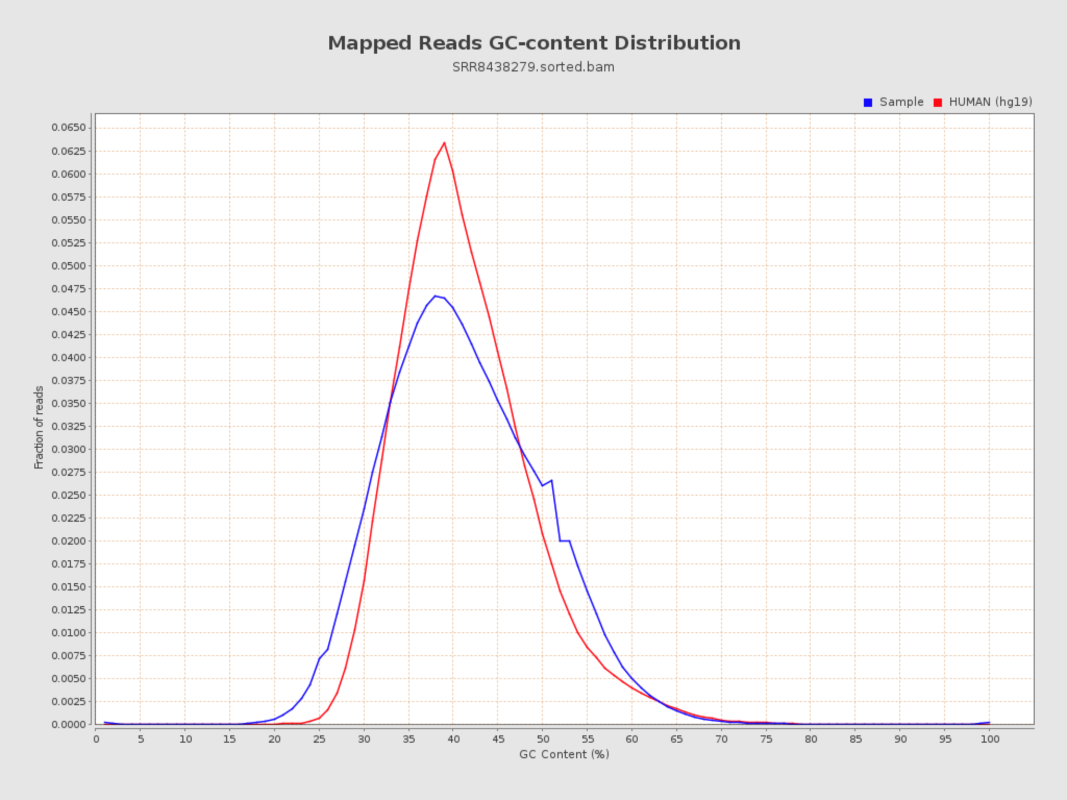
7. Results : Duplication Rate Histogram



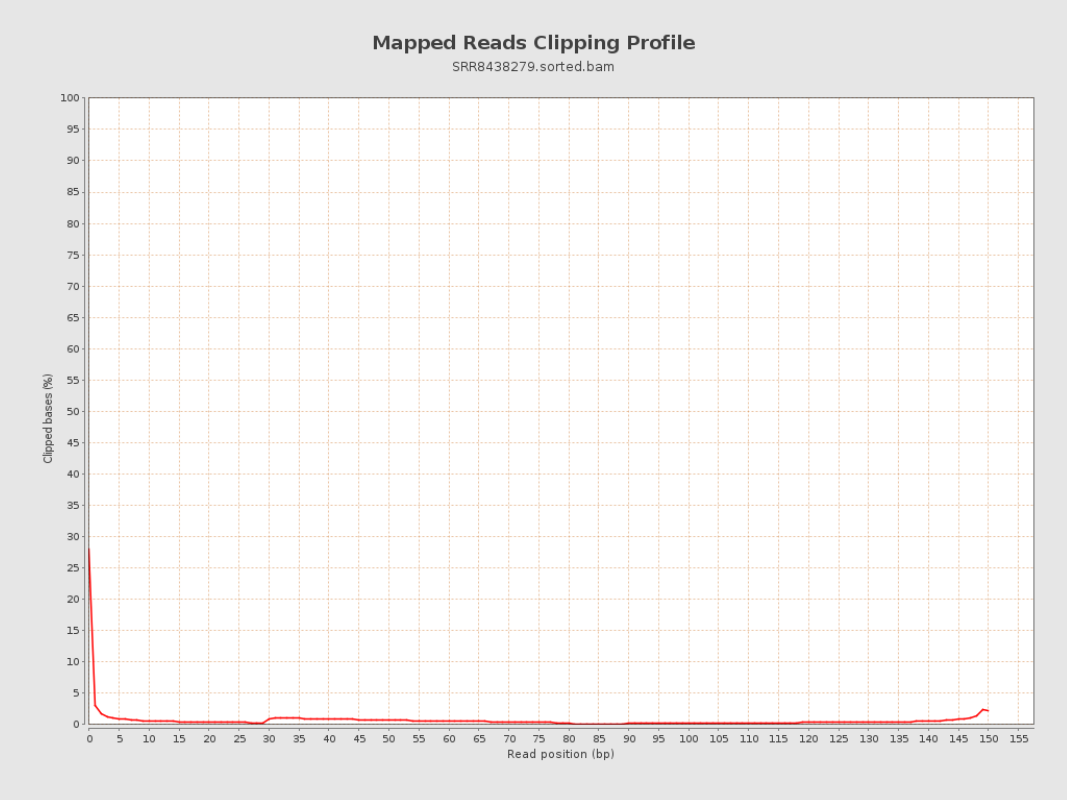
8. Results : Mapped Reads Nucleotide Content



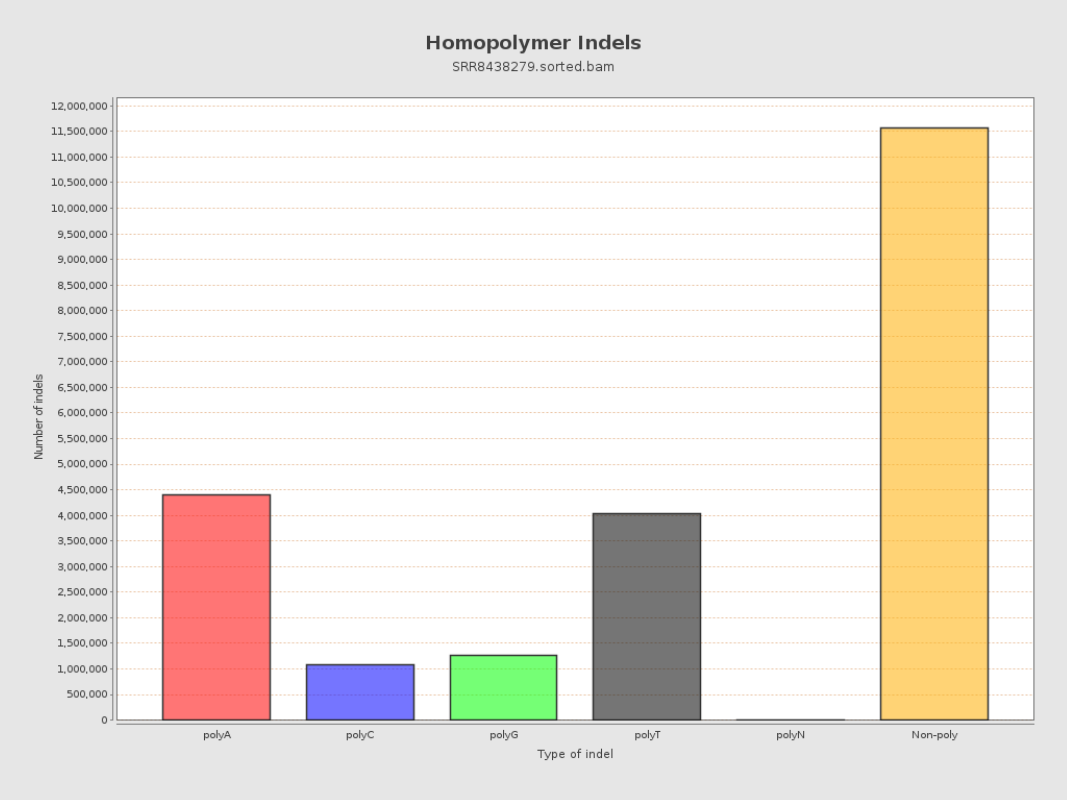
9. Results : Mapped Reads GC-content Distribution



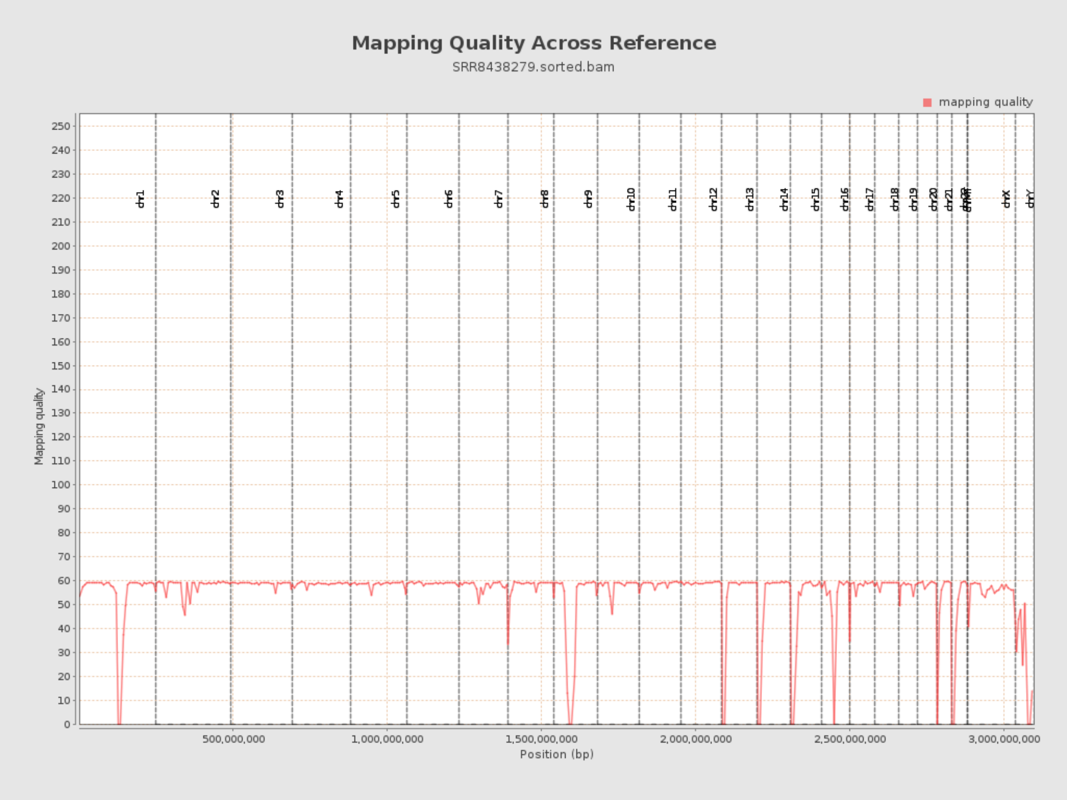
10. Results : Mapped Reads Clipping Profile



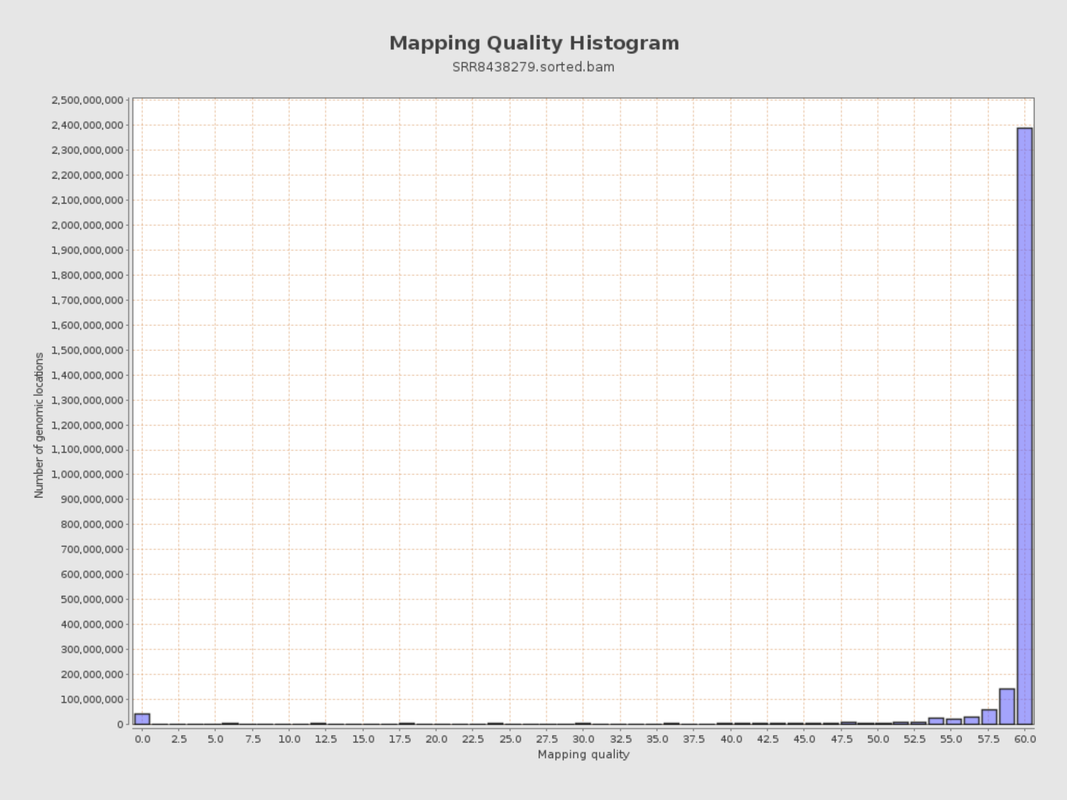
11. Results : Homopolymer Indels



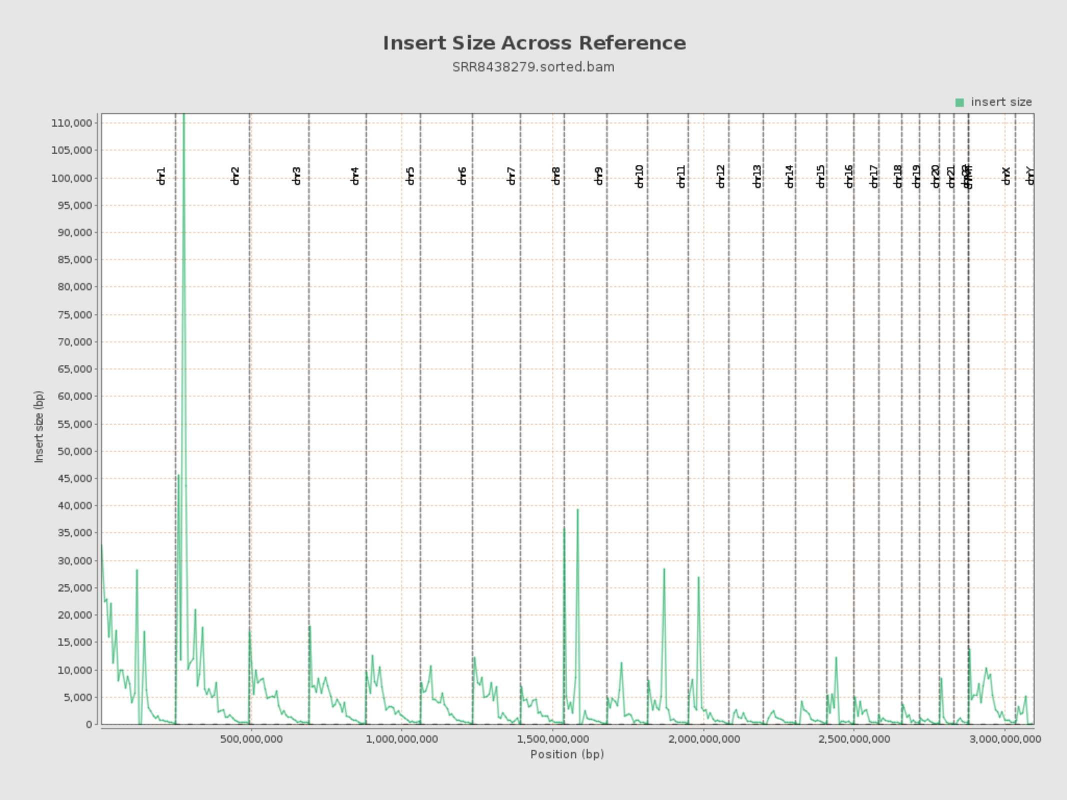
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram