Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:54:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438260.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_SRR8438260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438260_1.fastq.gz SRR8438260_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:54:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,521,325,884
Mapped reads	1,510,180,186 / 99.27%
Unmapped reads	11,145,698 / 0.73%
Mapped paired reads	1,510,180,186 / 99.27%
Mapped reads, first in pair	755,412,933 / 49.65%
Mapped reads, second in pair	754,767,253 / 49.61%
Mapped reads, both in pair	1,507,042,962 / 99.06%
Mapped reads, singletons	3,137,224 / 0.21%
Secondary alignments	0
Supplementary alignments	45,952,591 / 3.02%
Read min/max/mean length	30 / 149 / 115.03
Duplicated reads (estimated)	875,948,222 / 57.58%
Duplication rate	52.78%
Clipped reads	378,379,188 / 24.87%

2.2. ACGT Content

Number/percentage of A's	50,658,987,343 / 30.53%
Number/percentage of C's	32,656,061,858 / 19.68%
Number/percentage of T's	49,481,411,024 / 29.82%
Number/percentage of G's	33,131,081,510 / 19.97%
Number/percentage of N's	457,858 / 0%

GC Percentage	39.65%

2.3. Coverage

Mean	53.6149
Standard Deviation	502.6955

2.4. Mapping Quality

Mean Mapping Quality	52.07

2.5. Insert size

Mean	122,709.68
Standard Deviation	3,546,286.54
P25/Median/P75	75 / 121 / 195

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	575,892,599
Insertions	25,268,830
Mapped reads with at least one insertion	1.64%
Deletions	18,133,119
Mapped reads with at least one deletion	1.18%
Homopolymer indels	47.59%

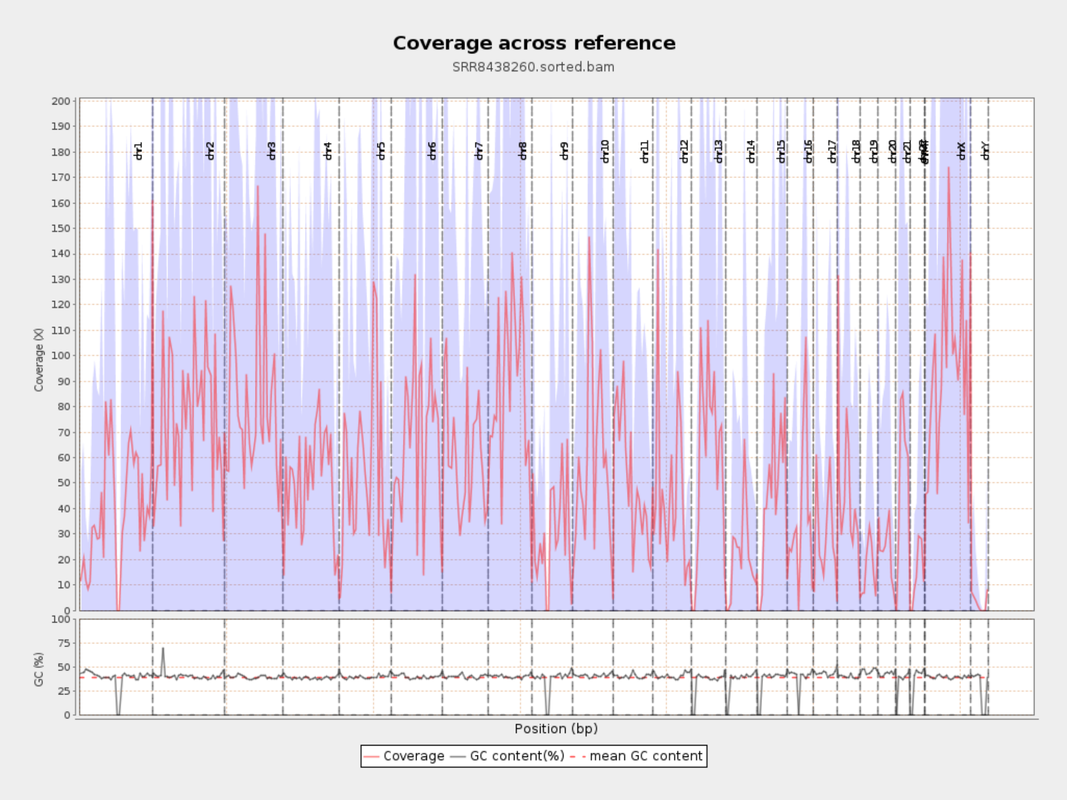
2.7. Chromosome stats

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

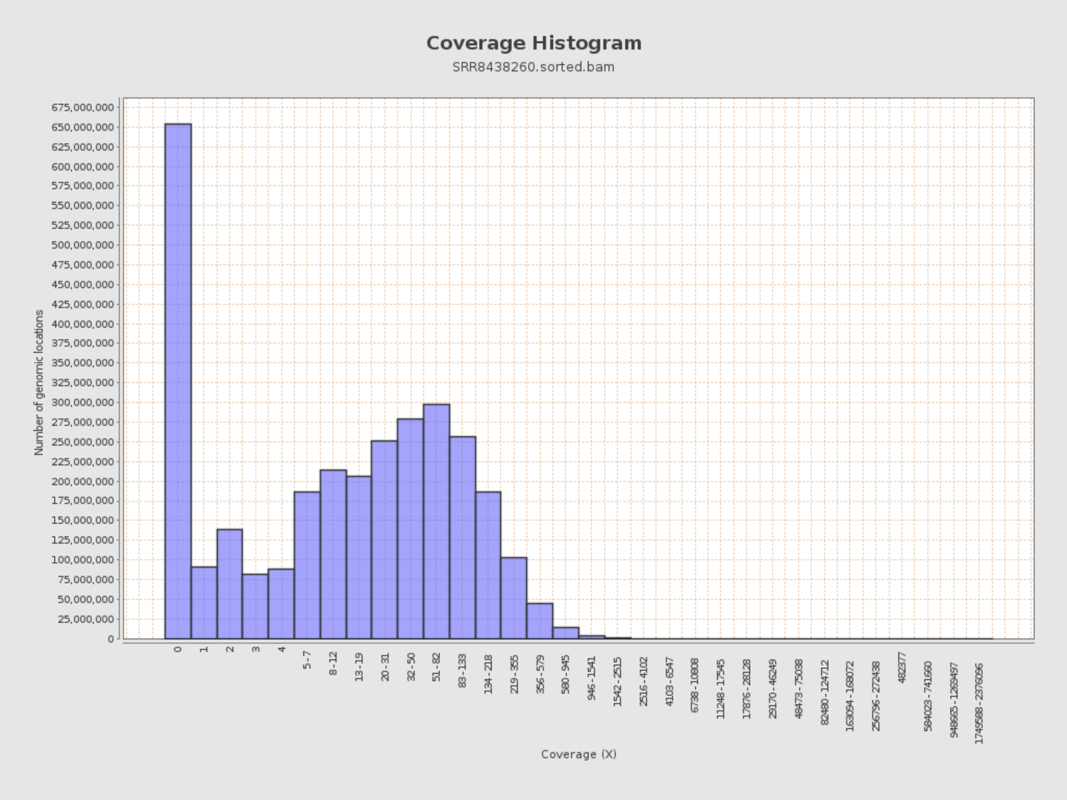
		bases	coverage	deviation
chr1	249250621	9994957715	40.1	86.0653
chr2	243199373	18118062038	74.4988	1,759.8502
chr3	198022430	15860587642	80.0949	123.993
chr4	191154276	9907696333	51.8309	93.3897
chr5	180915260	9336634201	51.6078	98.4414
chr6	171115067	11602152342	67.8032	118.7341
chr7	159138663	9446099527	59.3577	104.3184
chr8	146364022	13080884185	89.3723	124.4732
chr9	141213431	4128407071	29.2352	76.9303
chr10	135534747	7884873047	58.176	103.7221
chr11	135006516	6780409699	50.2228	89.891
chr12	133851895	5938803983	44.3685	93.8268
chr13	115169878	6977296025	60.5826	102.8549
chr14	107349540	2335702821	21.7579	59.2029
chr15	102531392	4657209860	45.4223	93.9945
chr16	90354753	3149800620	34.8604	73.4407
chr17	81195210	2324135368	28.624	62.8796
chr18	78077248	3588905517	45.9661	85.1604
chr19	59128983	929650700	15.7224	40.39
chr20	63025520	1486602675	23.5873	62.6127
chr21	48129895	2664129207	55.3529	102.8587
chr22	51304566	732072047	14.2691	44.8266
chrMT	16571	340481	20.5468	15.8284
chrX	155270560	14860411232	95.7066	149.1655

chrY	59373566	189438892	3.1906	25.6224

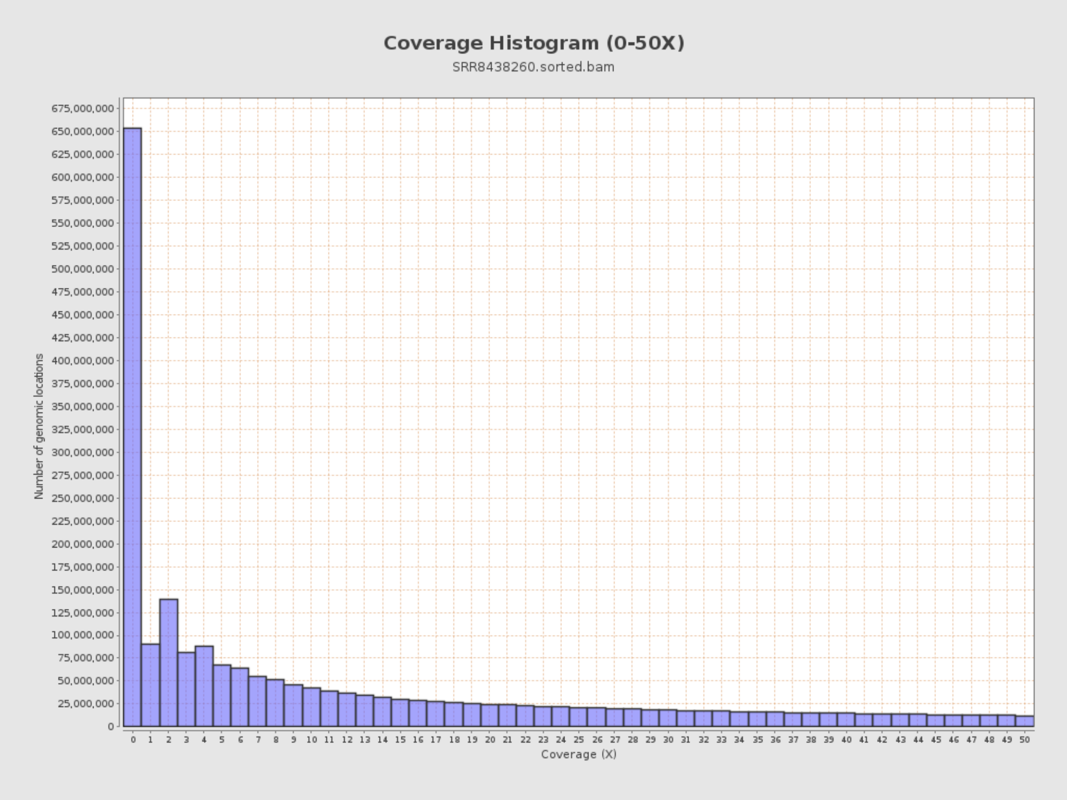
3. Results : Coverage across reference



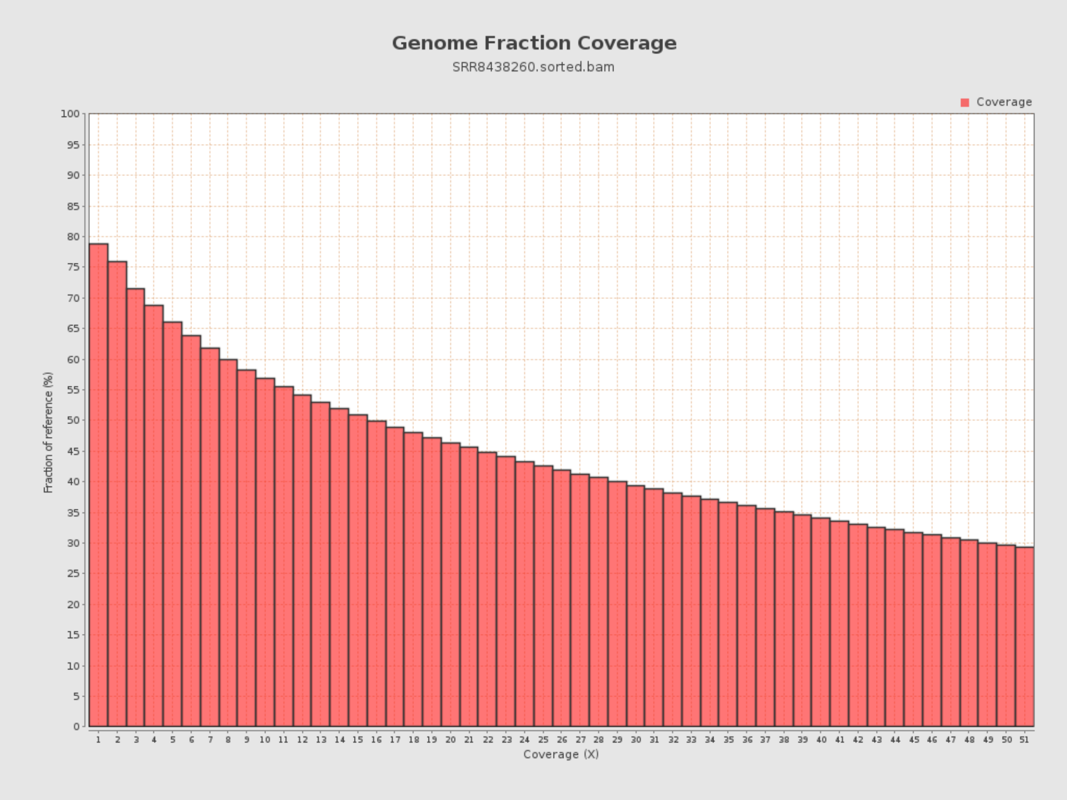
4. Results : Coverage Histogram



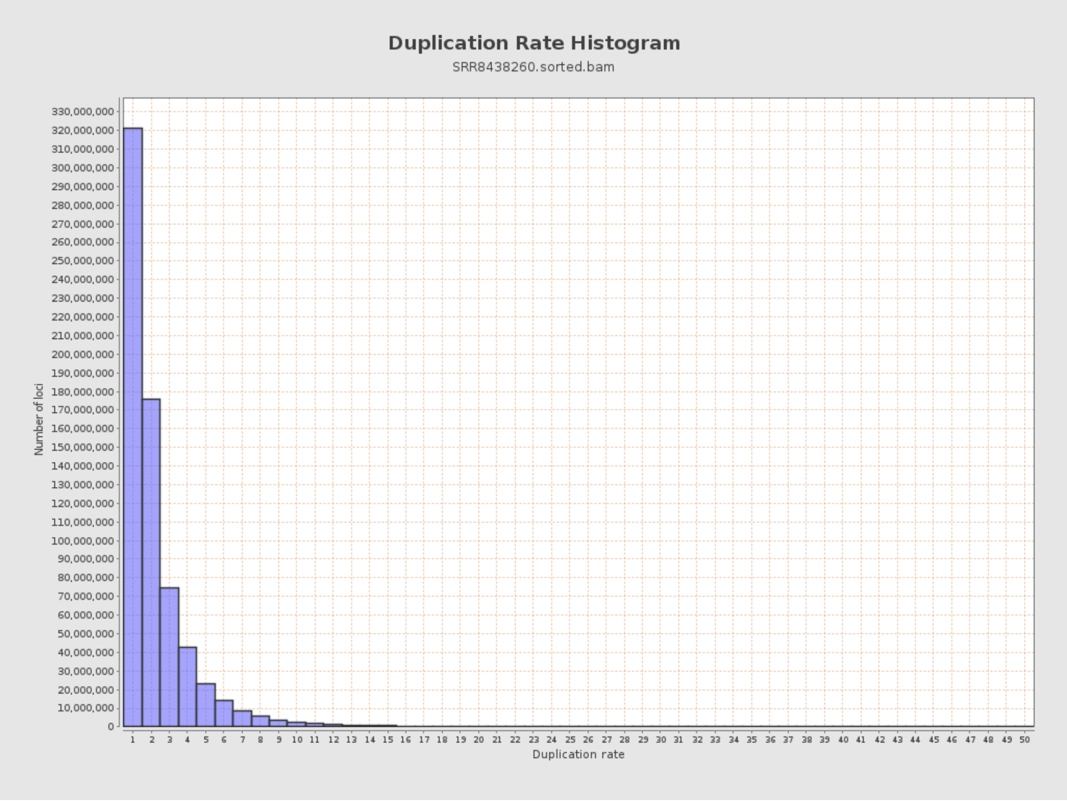
5. Results : Coverage Histogram (0-50X)



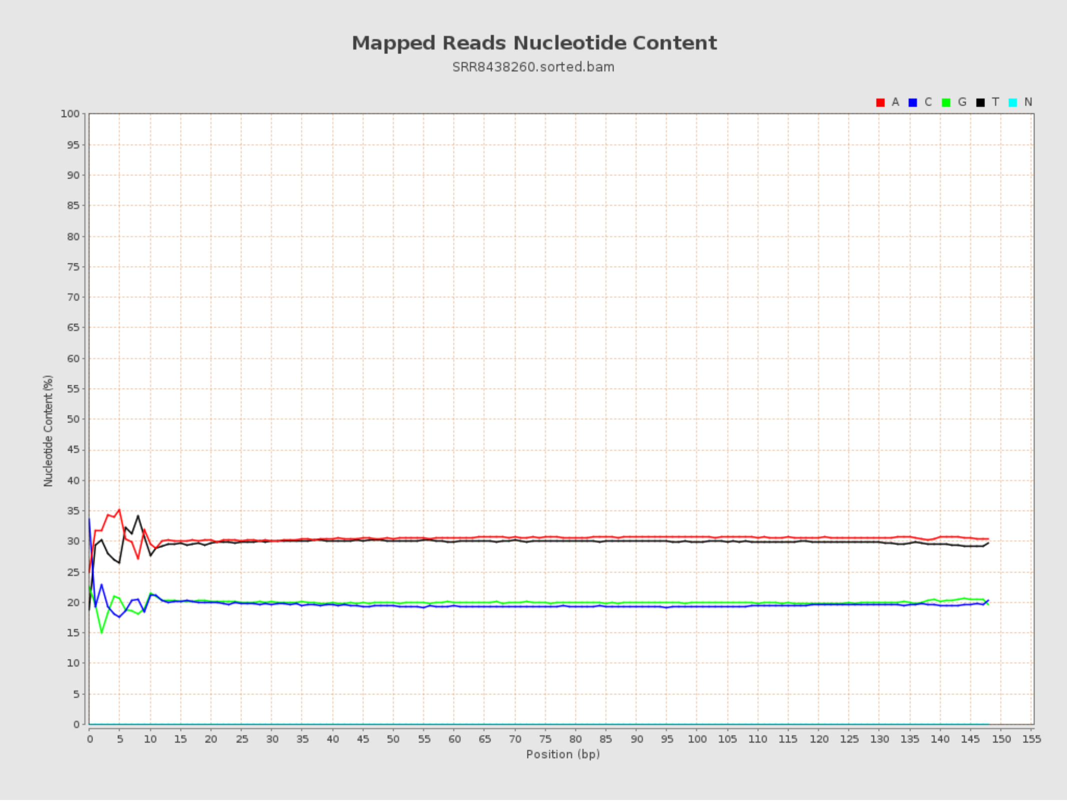
6. Results : Genome Fraction Coverage



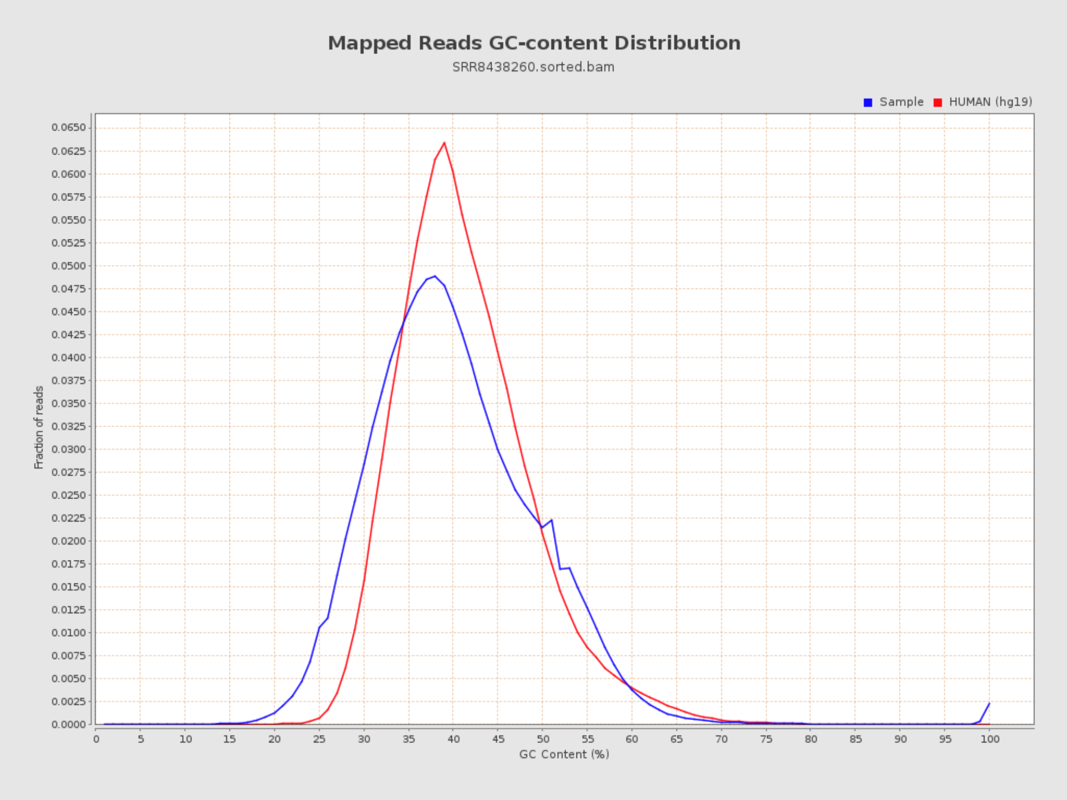
7. Results : Duplication Rate Histogram



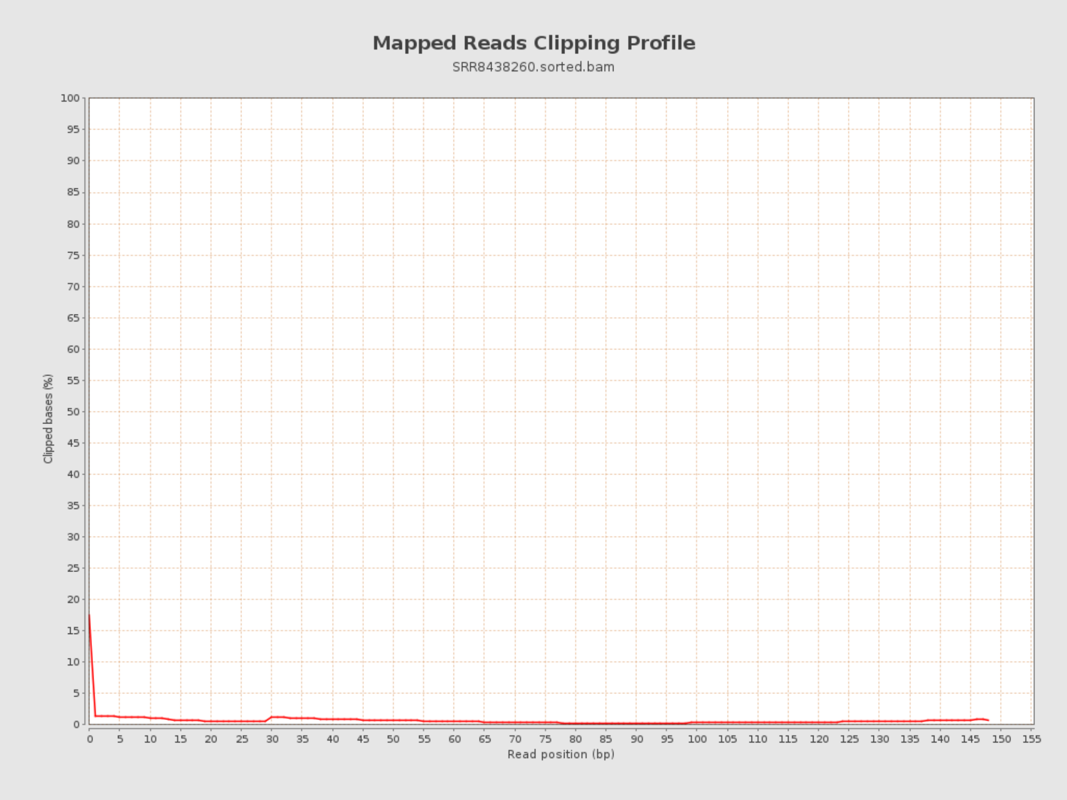
8. Results : Mapped Reads Nucleotide Content



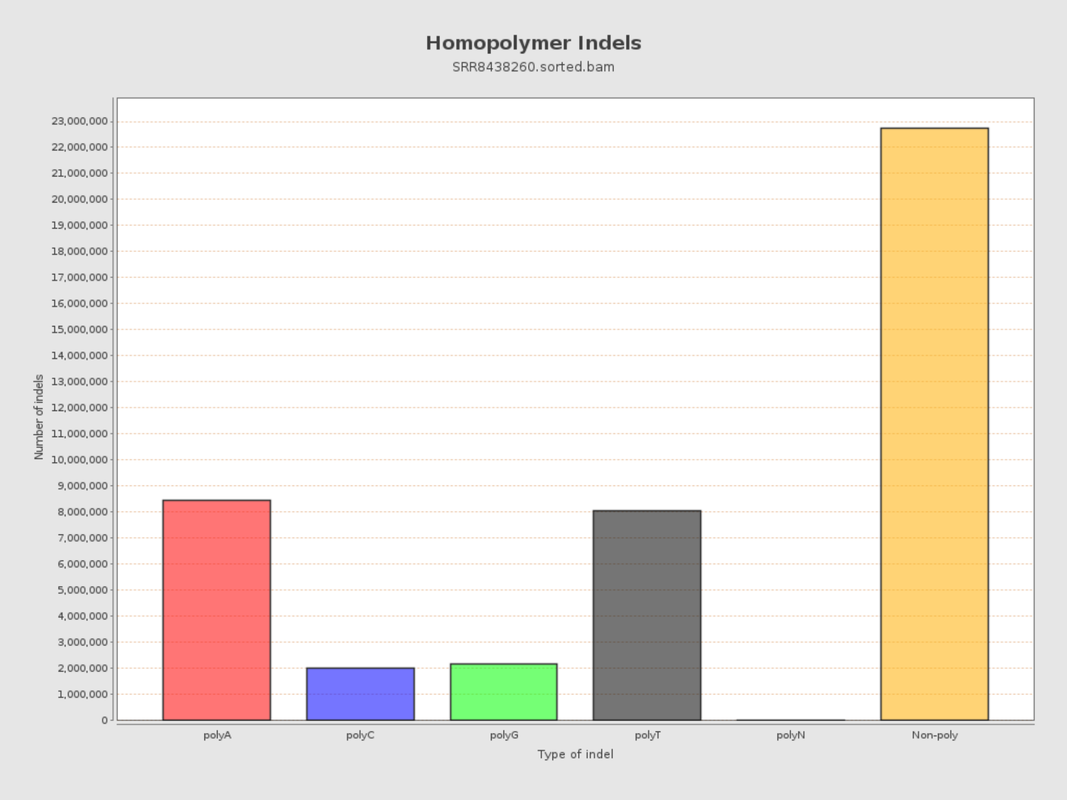
9. Results : Mapped Reads GC-content Distribution



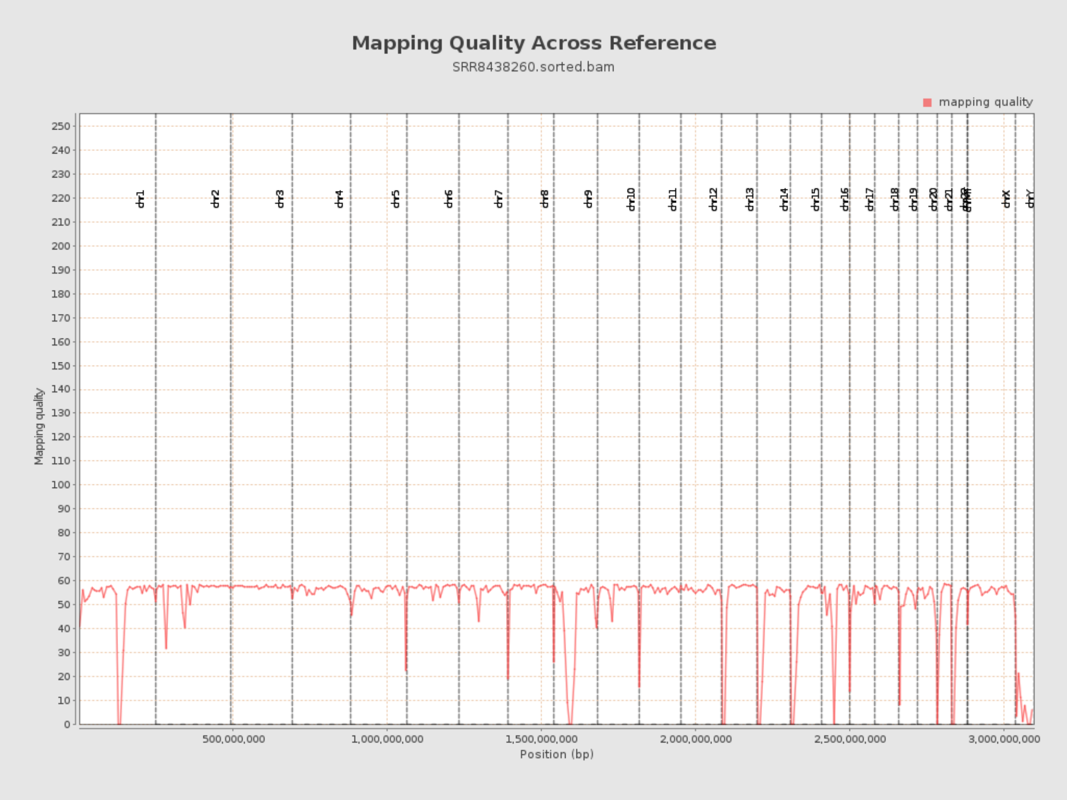
10. Results : Mapped Reads Clipping Profile



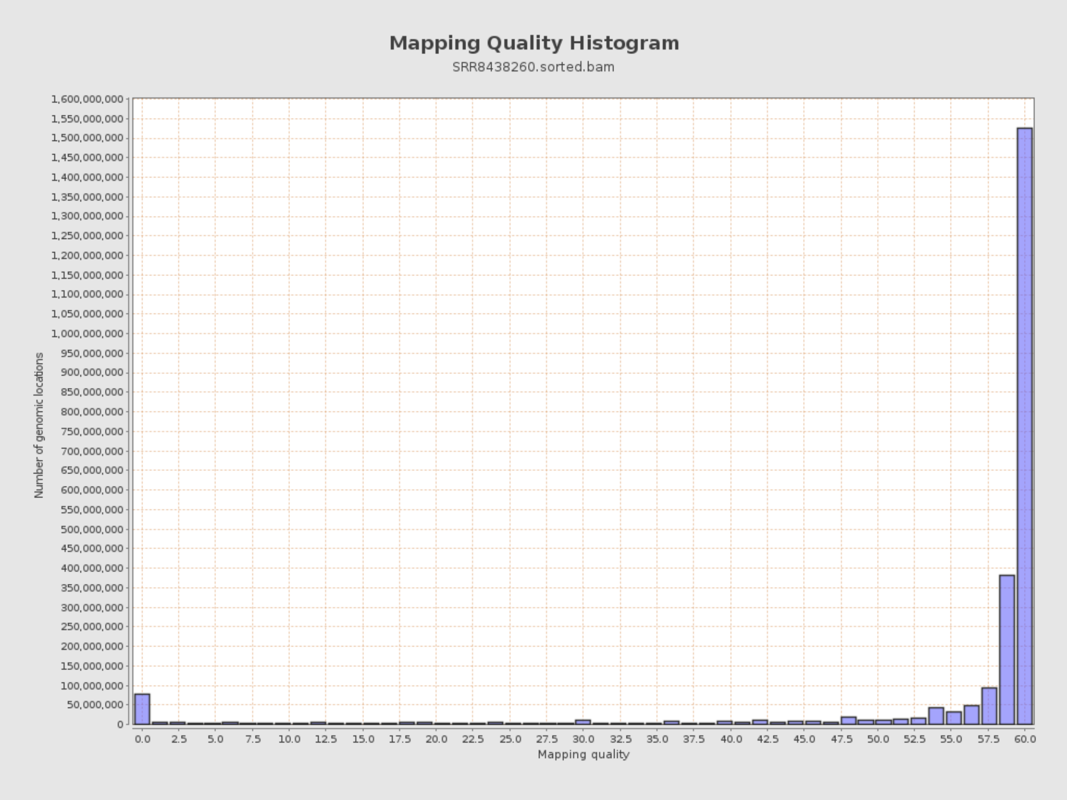
11. Results : Homopolymer Indels



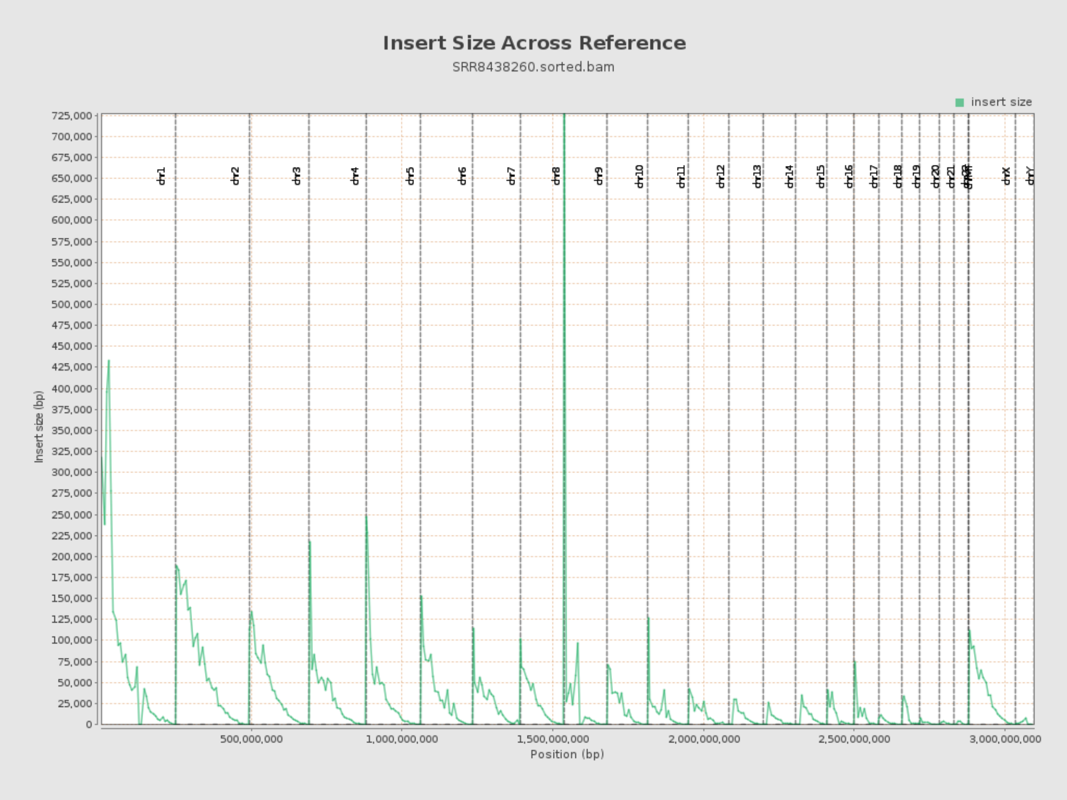
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram