Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/30 23:57:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438290.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_SRR8438290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438290_1.fastq.gz SRR8438290_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 30 23:57:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	834,873,472
Mapped reads	832,320,660 / 99.69%
Unmapped reads	2,552,812 / 0.31%
Mapped paired reads	832,320,660 / 99.69%
Mapped reads, first in pair	416,313,920 / 49.87%
Mapped reads, second in pair	416,006,740 / 49.83%
Mapped reads, both in pair	830,621,128 / 99.49%
Mapped reads, singletons	1,699,532 / 0.2%
Secondary alignments	0
Supplementary alignments	13,456,402 / 1.61%
Read min/max/mean length	28 / 151 / 144.64
Duplicated reads (estimated)	361,374,430 / 43.28%
Duplication rate	40.13%
Clipped reads	154,323,598 / 18.48%

2.2. ACGT Content

Number/percentage of A's	35,687,246,138 / 29.92%
Number/percentage of C's	24,217,937,611 / 20.3%
Number/percentage of T's	34,101,442,398 / 28.59%
Number/percentage of G's	25,273,457,408 / 21.19%
Number/percentage of N's	737,631 / 0%

GC Percentage	41.49%

2.3. Coverage

Mean	38.5415
Standard Deviation	84.1842

2.4. Mapping Quality

Mean Mapping Quality	55.15

2.5. Insert size

Mean	41,891.08
Standard Deviation	2,034,358.16
P25/Median/P75	179 / 238 / 339

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	607,624,659
Insertions	14,829,598
Mapped reads with at least one insertion	1.75%
Deletions	13,075,029
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.51%

2.7. Chromosome stats

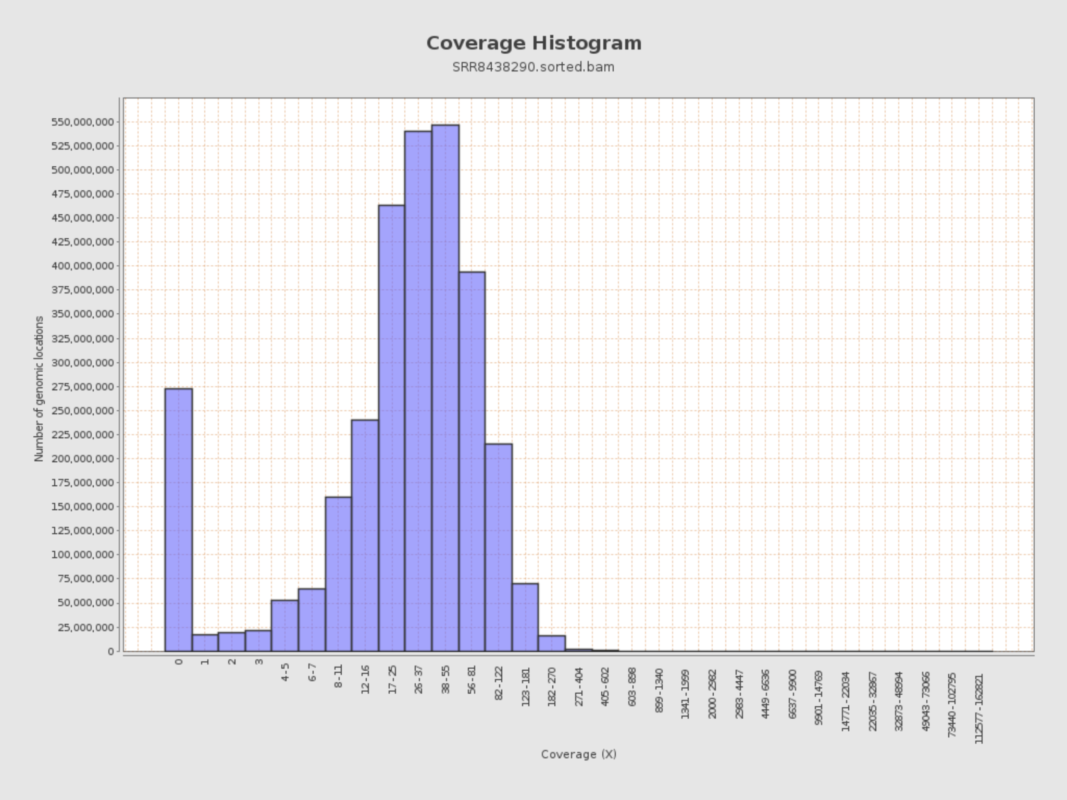
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	10850264424	43.5315	41.0959
chr2	243199373	10531025964	43.302	166.0069
chr3	198022430	8616665000	43.5136	109.4301
chr4	191154276	6868539283	35.9319	31.2456
chr5	180915260	7119714534	39.3539	35.0418
chr6	171115067	6978463534	40.7823	34.5675
chr7	159138663	6288594277	39.5164	34.2739
chr8	146364022	5805018761	39.6615	32.9766
chr9	141213431	5085451882	36.0125	38.5739
chr10	135534747	5852235772	43.1789	45.0586
chr11	135006516	5835939354	43.2271	36.7907
chr12	133851895	5830014641	43.5557	35.5611
chr13	115169878	3721334292	32.3117	31.4379
chr14	107349540	4028170177	37.5239	37.3723
chr15	102531392	3819511256	37.2521	37.8106
chr16	90354753	3446537558	38.1445	52.7101
chr17	81195210	3565142261	43.9083	44.9608
chr18	78077248	2818841037	36.1032	31.3218
chr19	59128983	2102028814	35.5499	153.9322
chr20	63025520	2860628464	45.3884	39.0431
chr21	48129895	1545318115	32.1072	70.913
chr22	51304566	1614018306	31.4595	40.0218
chrMT	16571	333346529	20,116.2591	7,610.3001
chrX	155270560	3349971100	21.5751	26.1059

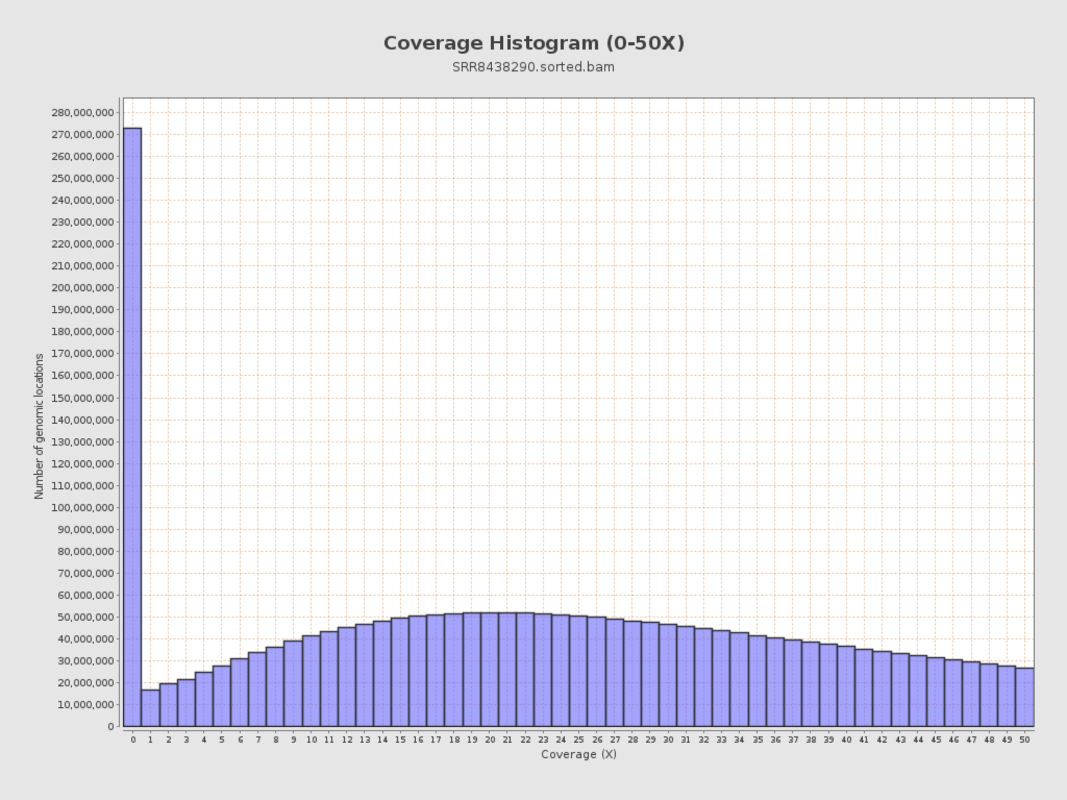
chrY	59373566	445892631	7.51	23.6729

3. Results : Coverage across reference

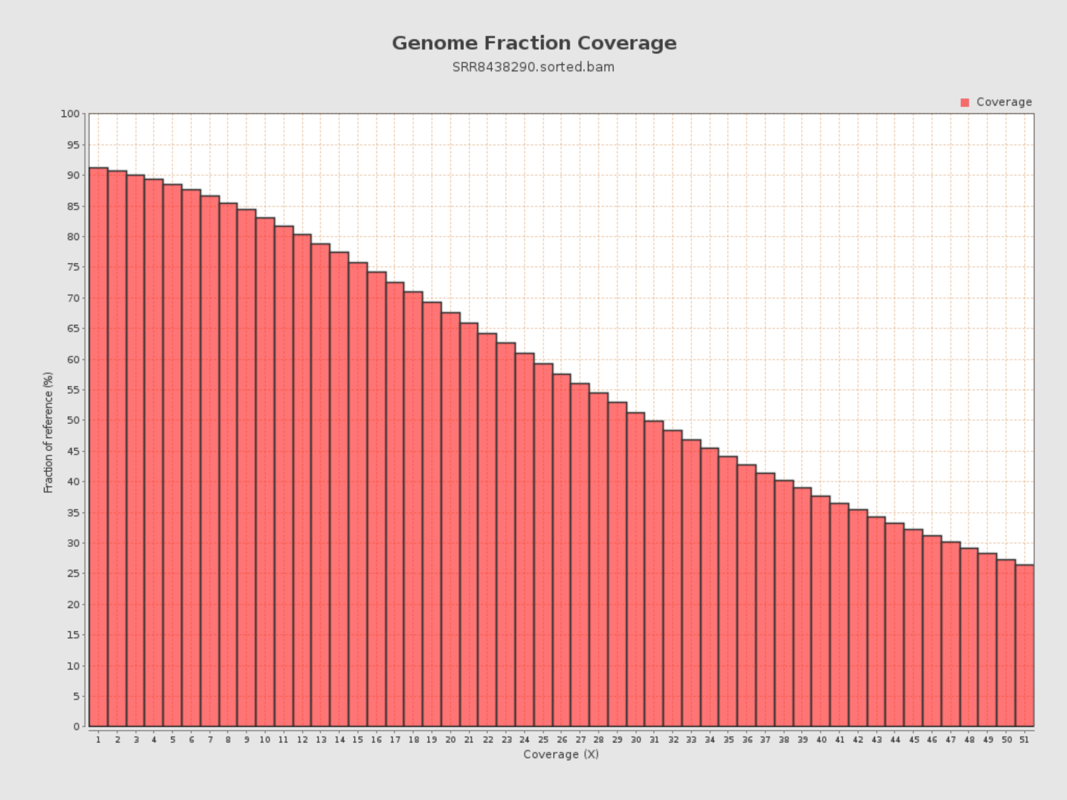
4. Results : Coverage Histogram



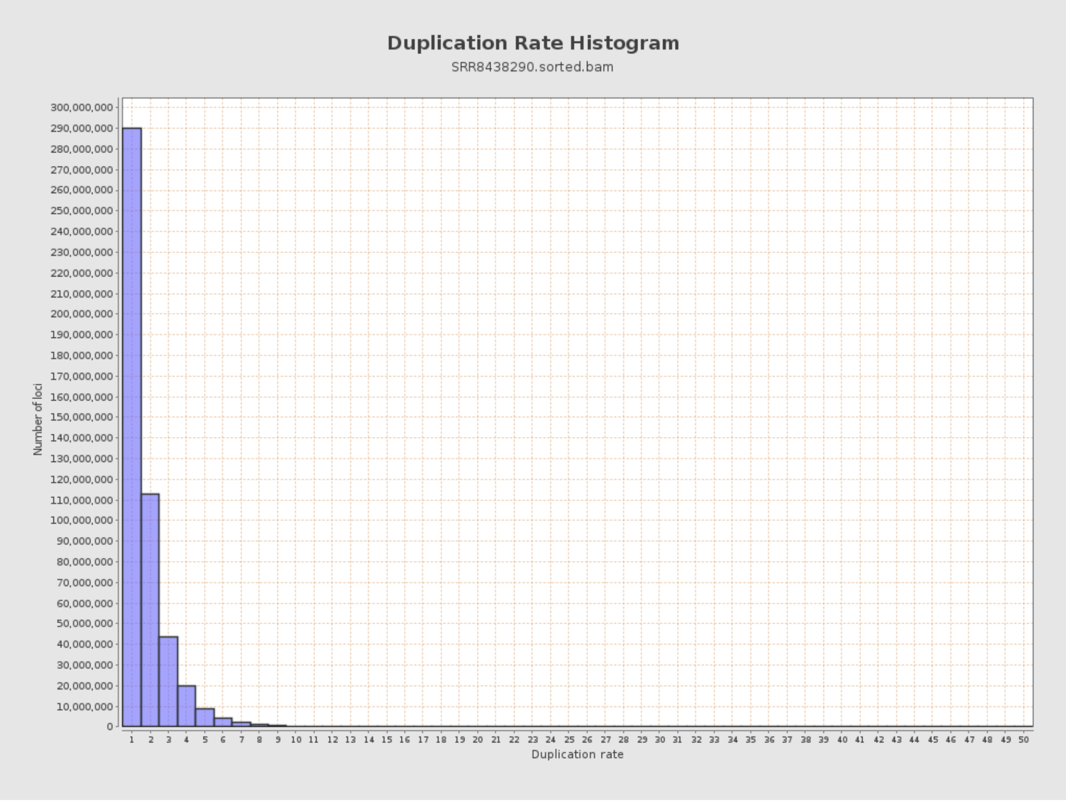
5. Results : Coverage Histogram (0-50X)



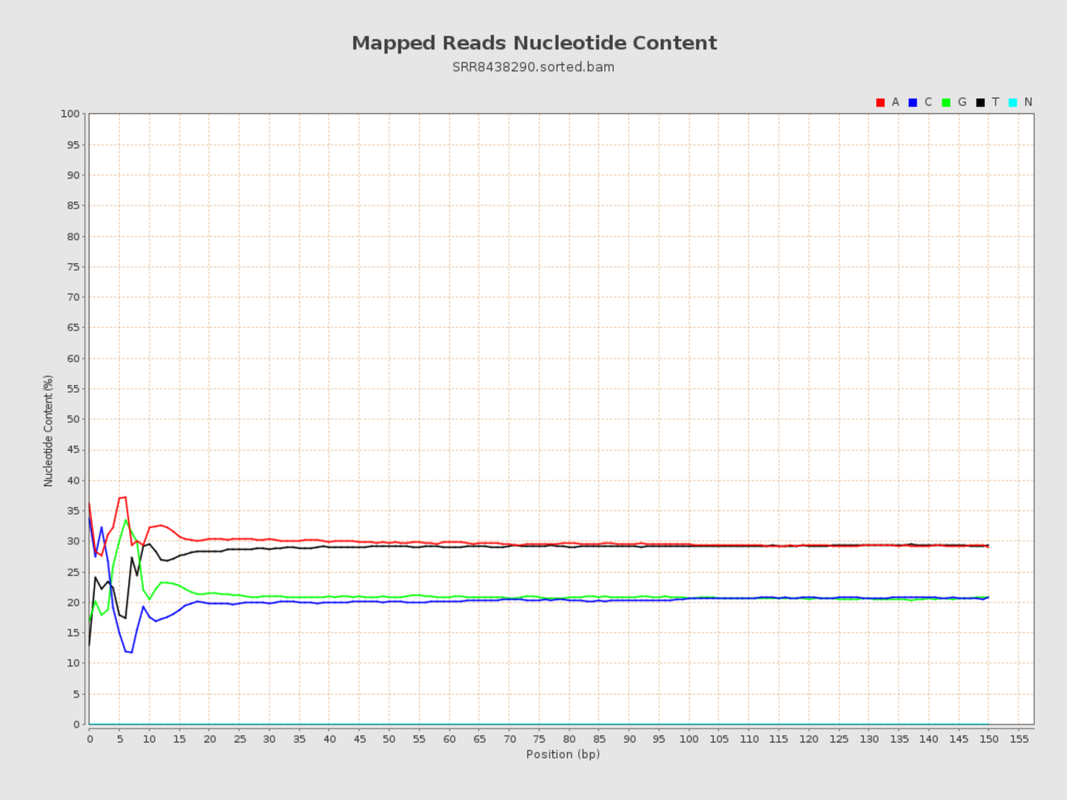
6. Results : Genome Fraction Coverage



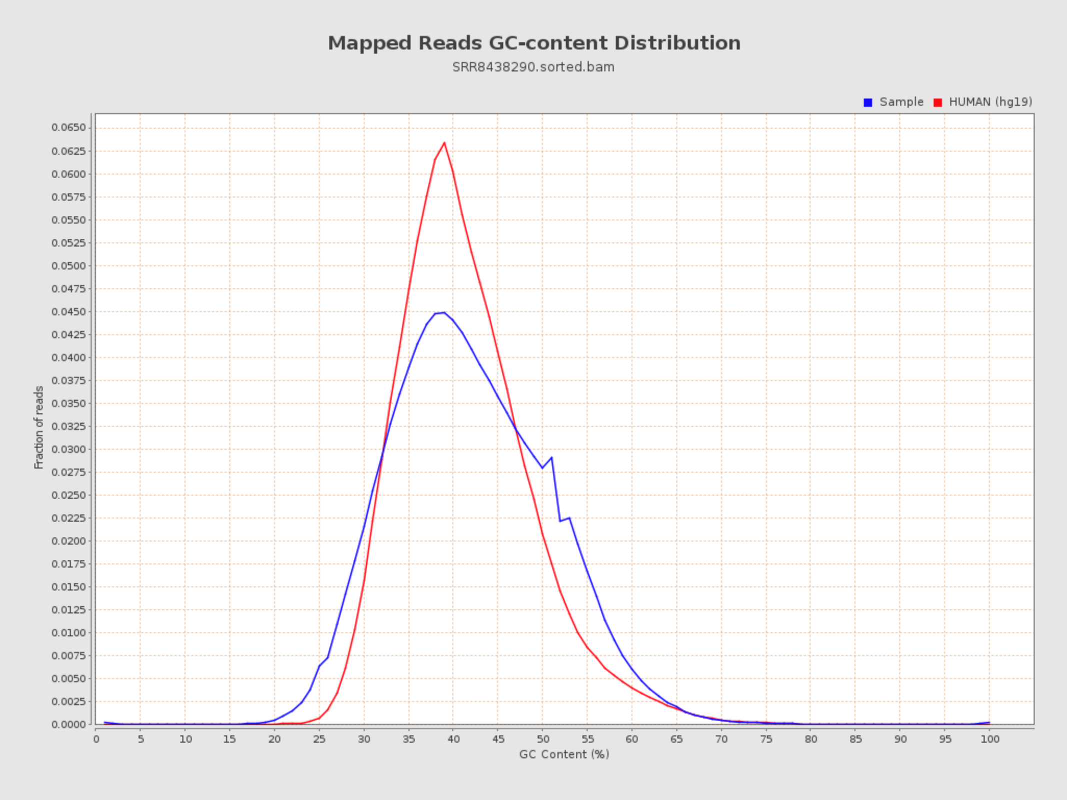
7. Results : Duplication Rate Histogram



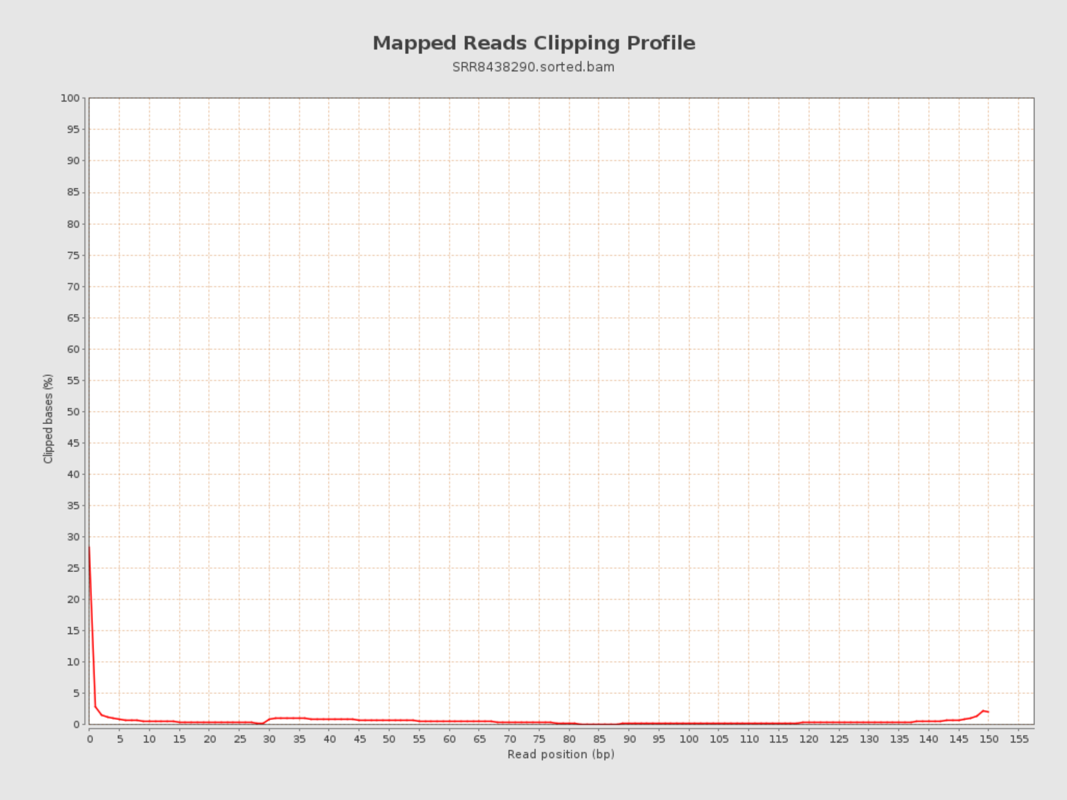
8. Results : Mapped Reads Nucleotide Content



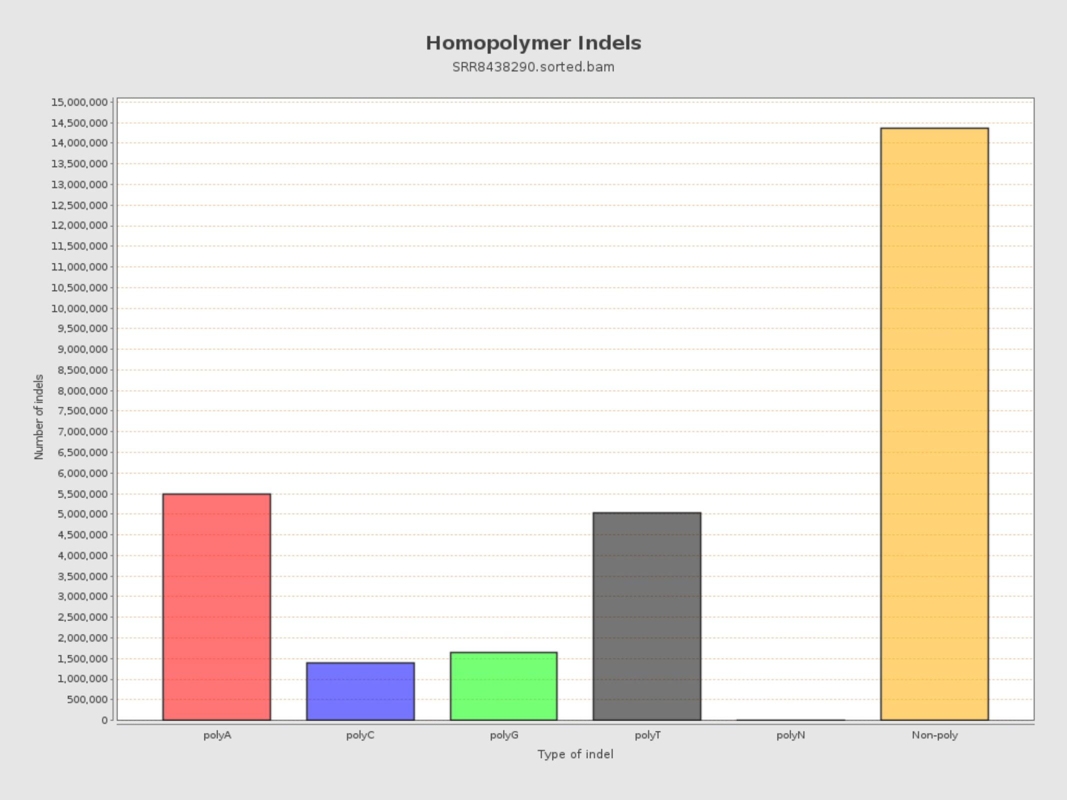
9. Results : Mapped Reads GC-content Distribution



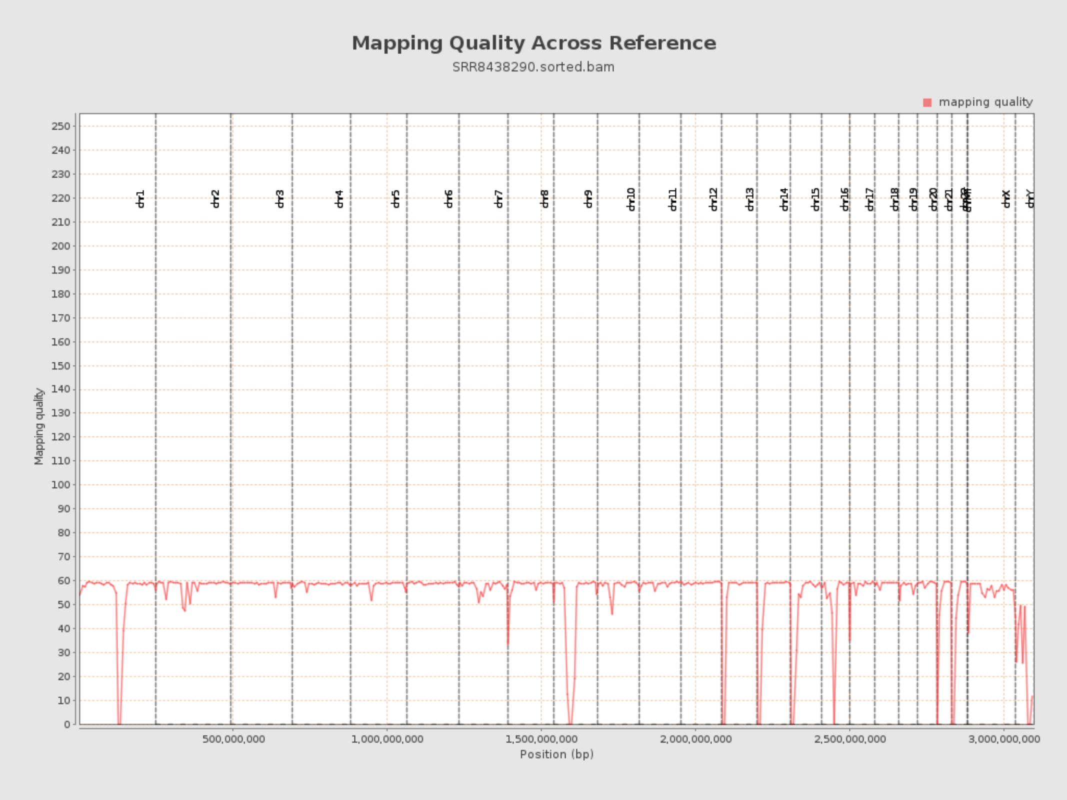
10. Results : Mapped Reads Clipping Profile



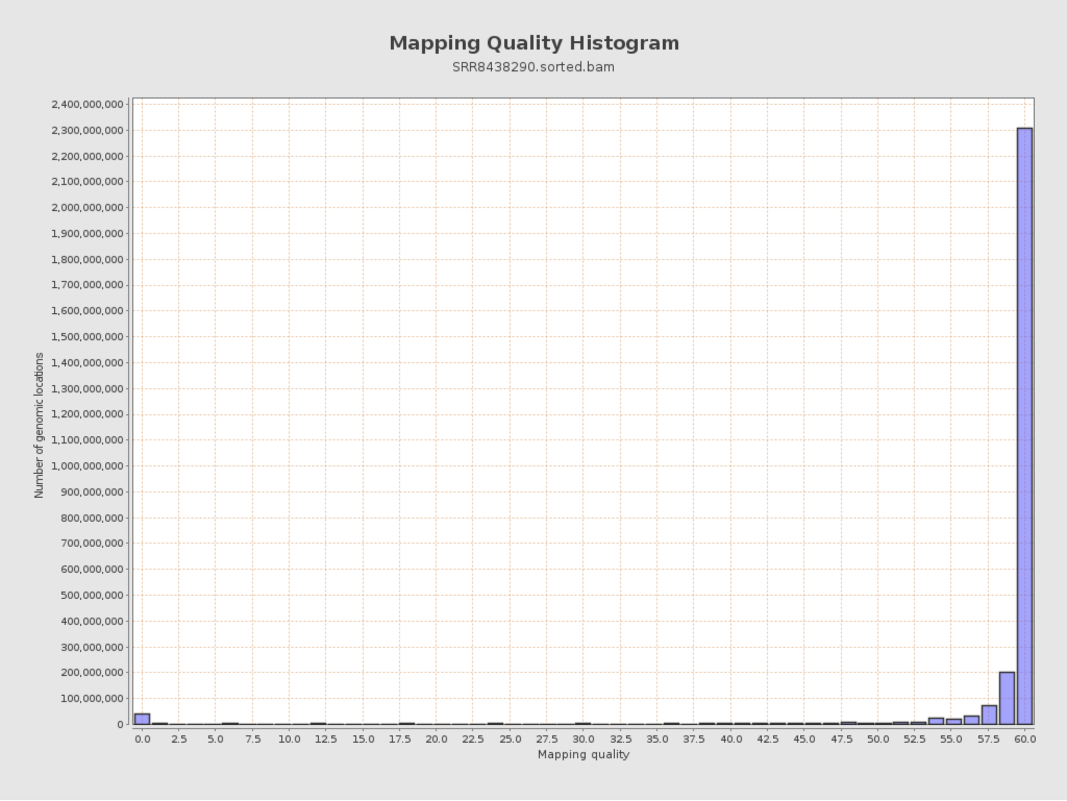
11. Results : Homopolymer Indels



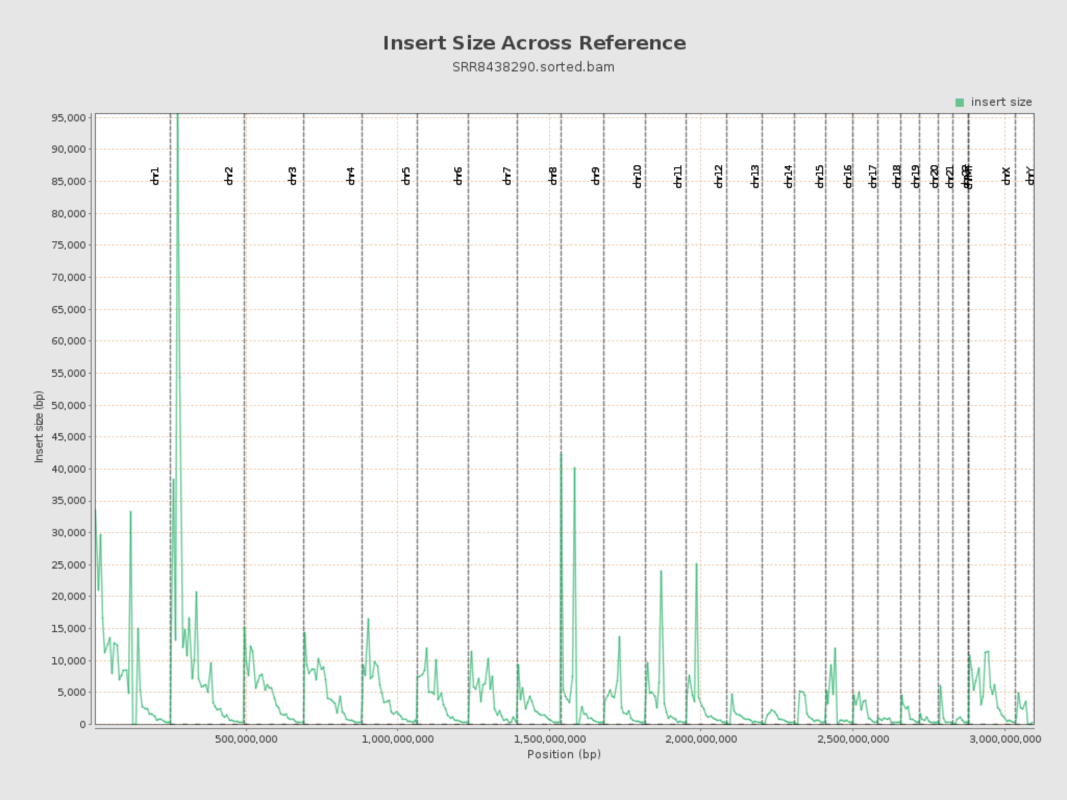
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram