

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/13 16:35:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438266.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_SRR8438266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438266_1.fastq.gz SRR8438266_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 13 16:35:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	741,482,424
Mapped reads	739,174,889 / 99.69%
Unmapped reads	2,307,535 / 0.31%
Mapped paired reads	739,174,889 / 99.69%
Mapped reads, first in pair	369,804,743 / 49.87%
Mapped reads, second in pair	369,370,146 / 49.82%
Mapped reads, both in pair	737,537,242 / 99.47%
Mapped reads, singletons	1,637,647 / 0.22%
Secondary alignments	0
Supplementary alignments	12,399,987 / 1.67%
Read min/max/mean length	28 / 151 / 145.5
Duplicated reads (estimated)	322,257,316 / 43.46%
Duplication rate	40.88%
Clipped reads	135,569,482 / 18.28%

2.2. ACGT Content

Number/percentage of A's	32,237,633,285 / 30.25%
Number/percentage of C's	21,297,944,294 / 19.98%
Number/percentage of T's	30,756,354,162 / 28.86%
Number/percentage of G's	22,284,670,323 / 20.91%
Number/percentage of N's	659,769 / 0%

GC Percentage	40.89%
---------------	--------

2.3. Coverage

Mean	34.4373
Standard Deviation	109.1335

2.4. Mapping Quality

Mean Mapping Quality	55.07
----------------------	-------

2.5. Insert size

Mean	43,834.69
Standard Deviation	2,049,933.21
P25/Median/P75	188 / 247 / 347

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	547,772,792
Insertions	13,568,966
Mapped reads with at least one insertion	1.81%
Deletions	12,107,129
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.47%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

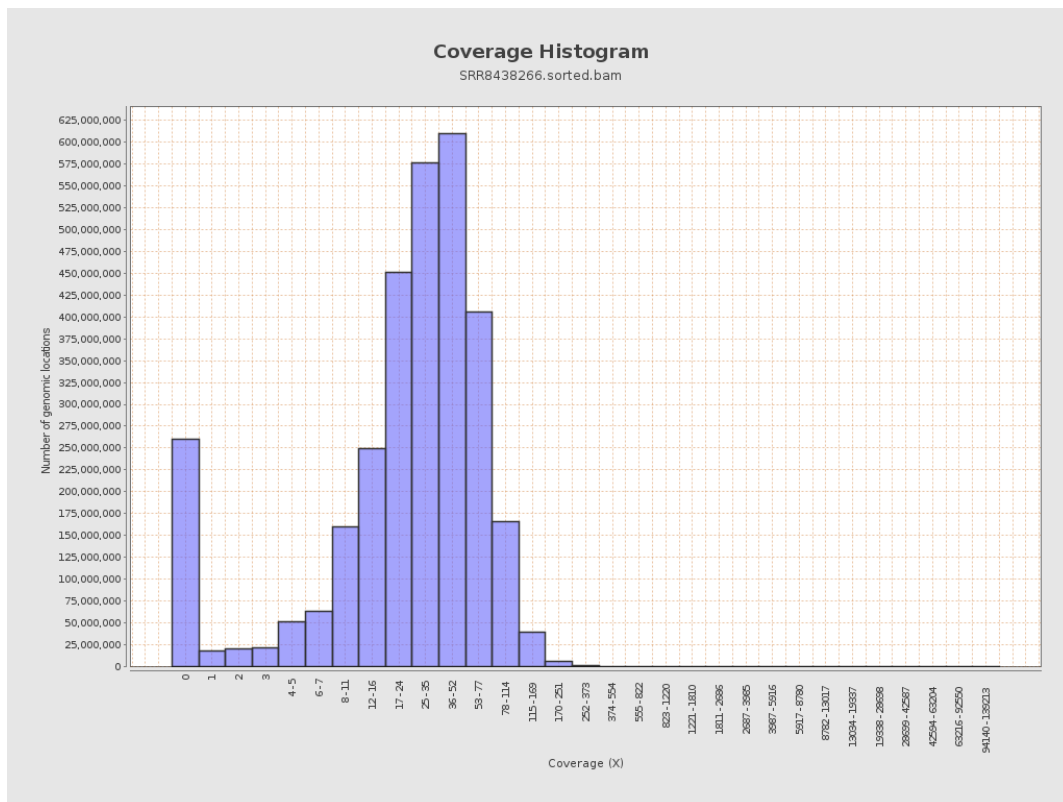
		bases	coverage	deviation
chr1	249250621	8664544994	34.7624	33.7487
chr2	243199373	9442568621	38.8265	140.2909
chr3	198022430	7719677819	38.9839	39.0262
chr4	191154276	7264428782	38.003	26.4039
chr5	180915260	6948641645	38.4083	27.1513
chr6	171115067	6363972328	37.1912	28.3439
chr7	159138663	5826470866	36.6125	27.2517
chr8	146364022	5428873705	37.0916	27.3145
chr9	141213431	4646225774	32.9022	34.6377
chr10	135534747	5083043626	37.5036	39.4718
chr11	135006516	4885337297	36.1859	27.8088
chr12	133851895	4939307245	36.9013	26.6378
chr13	115169878	3733521786	32.4175	27.7767
chr14	107349540	3307132225	30.8071	28.552
chr15	102531392	3123653398	30.4653	29.7507
chr16	90354753	2922249791	32.342	45.0495
chr17	81195210	2552235144	31.4333	34.4625
chr18	78077248	2917295667	37.3642	29.0766
chr19	59128983	1622477017	27.4396	48.8523
chr20	63025520	2360976659	37.4606	30.8052
chr21	48129895	1300581243	27.0223	36.6382
chr22	51304566	1146245401	22.342	28.7653
chrMT	16571	648856629	39,156.1541	15,175.899
chrX	155270560	3210521683	20.677	17.2473

chrY	59373566	548416490	9.2367	25.8033
------	----------	-----------	--------	---------

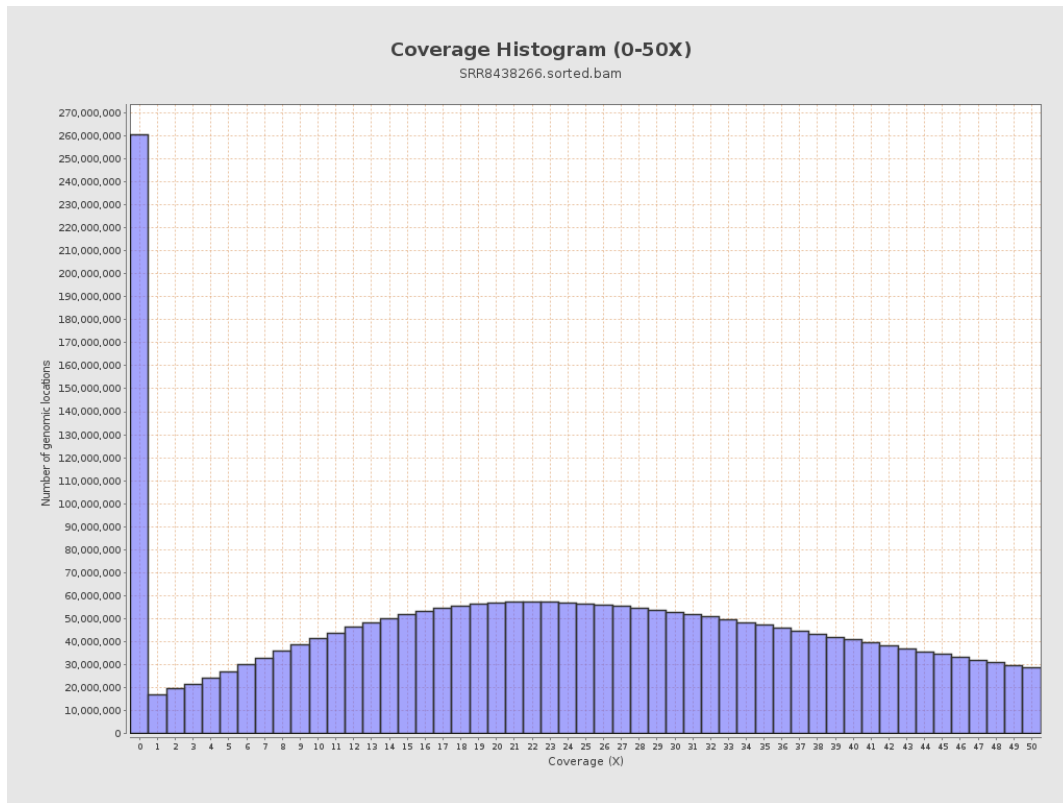
3. Results : Coverage across reference



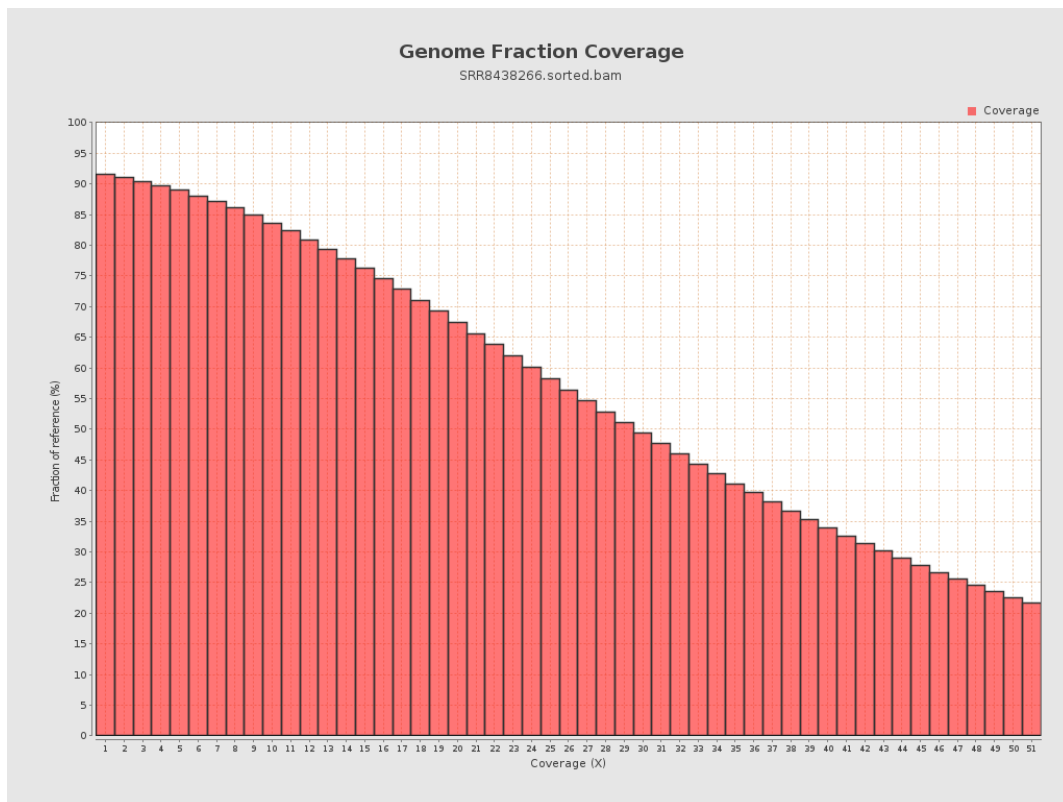
4. Results : Coverage Histogram



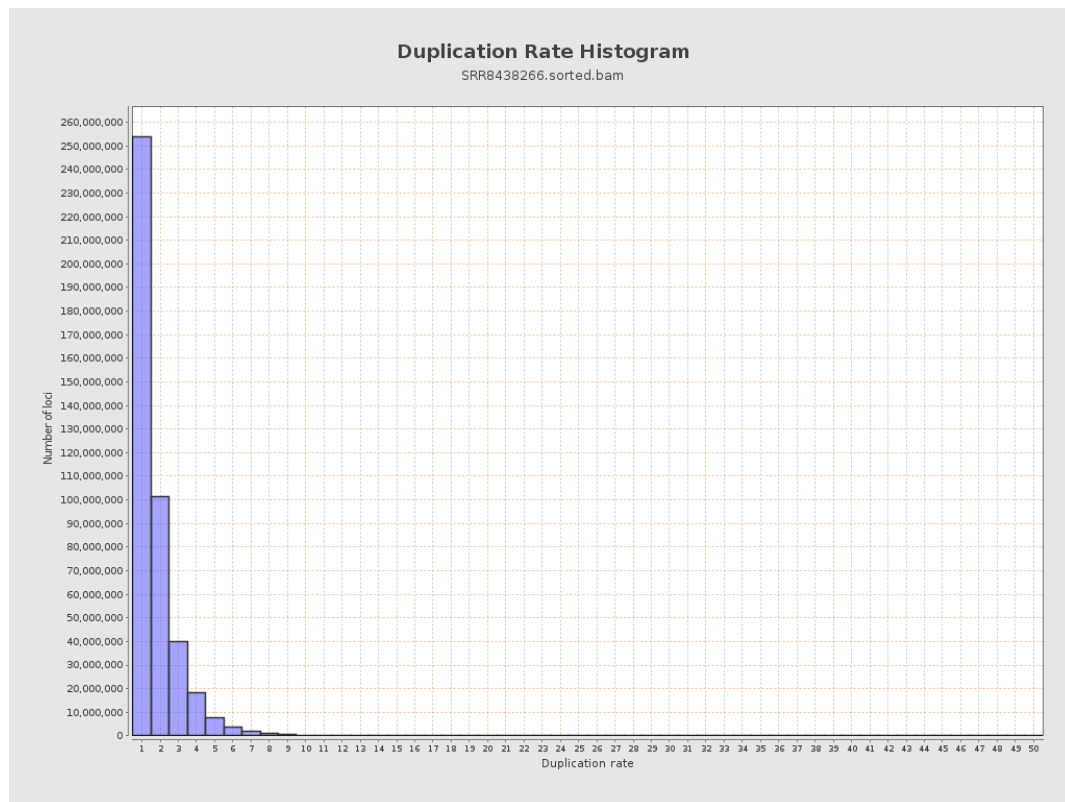
5. Results : Coverage Histogram (0-50X)



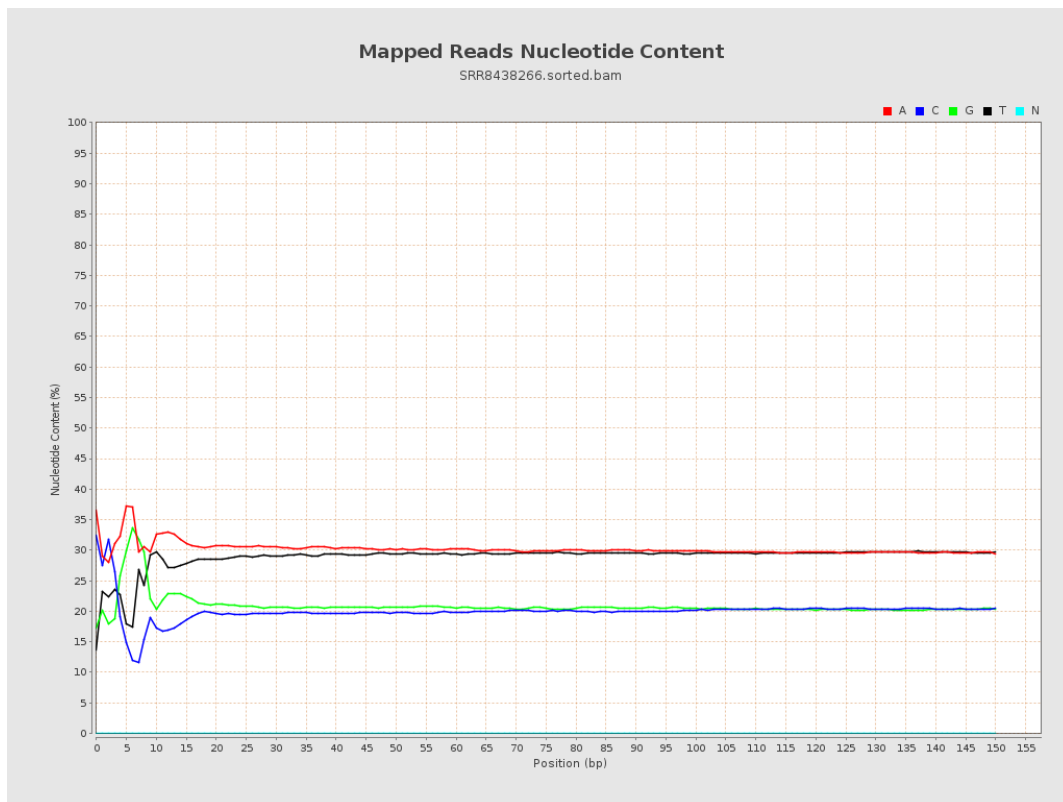
6. Results : Genome Fraction Coverage



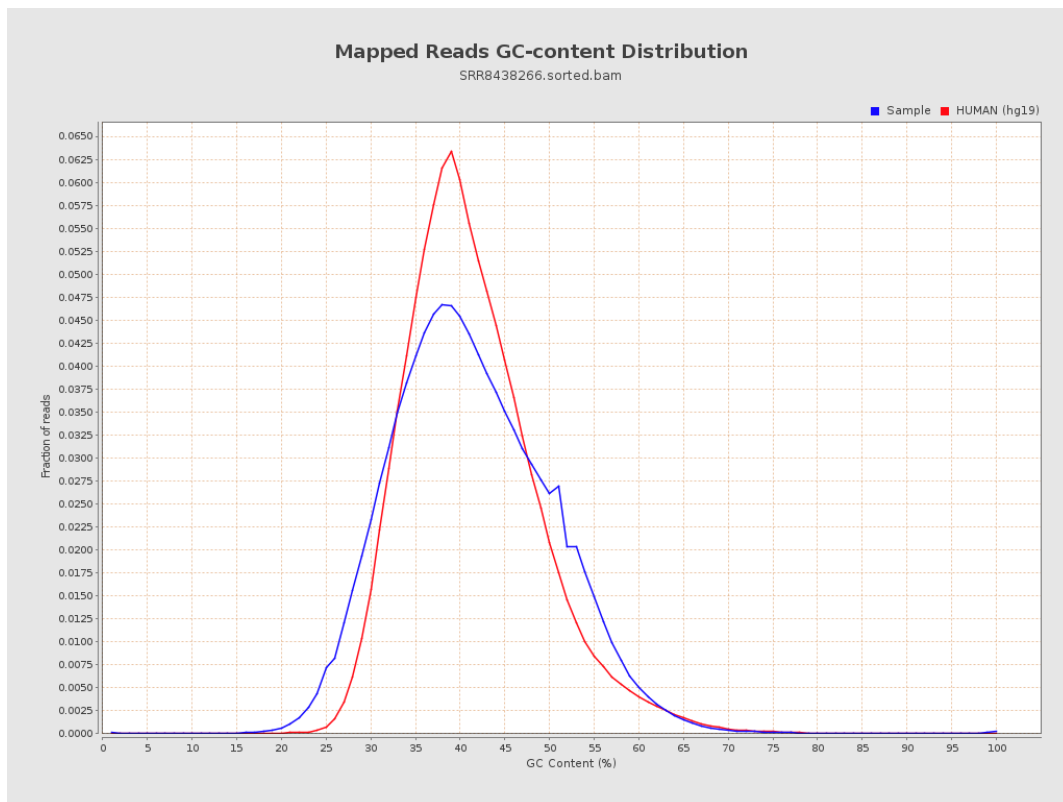
7. Results : Duplication Rate Histogram



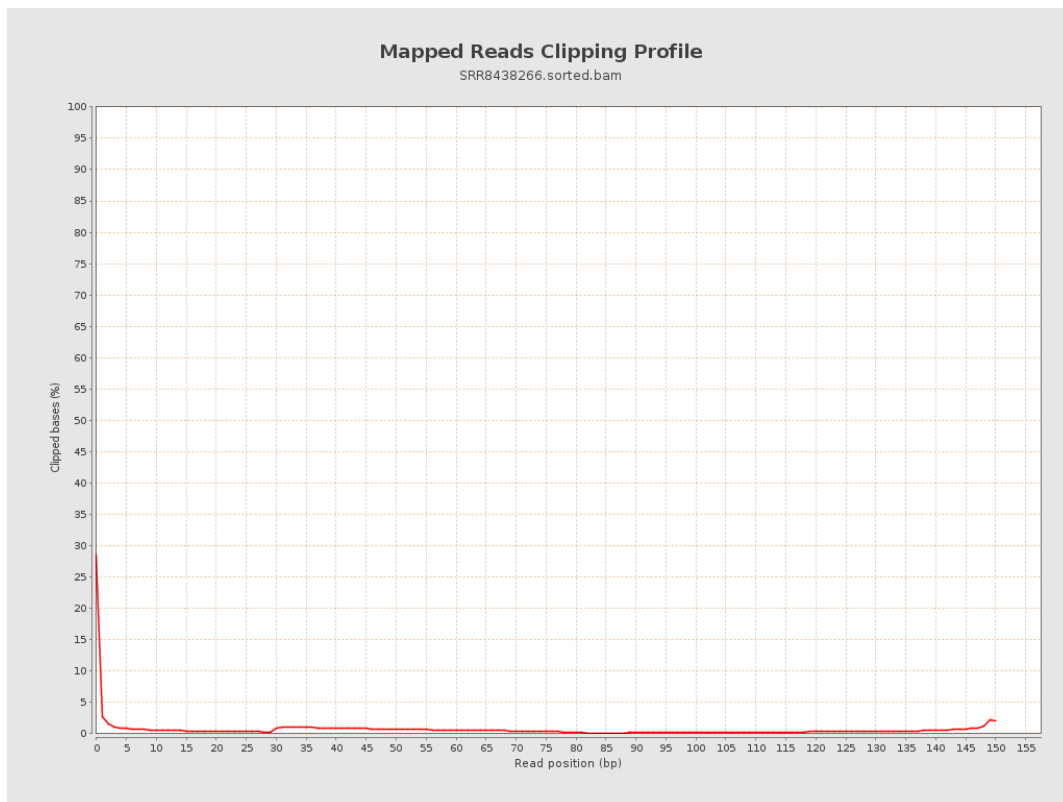
8. Results : Mapped Reads Nucleotide Content



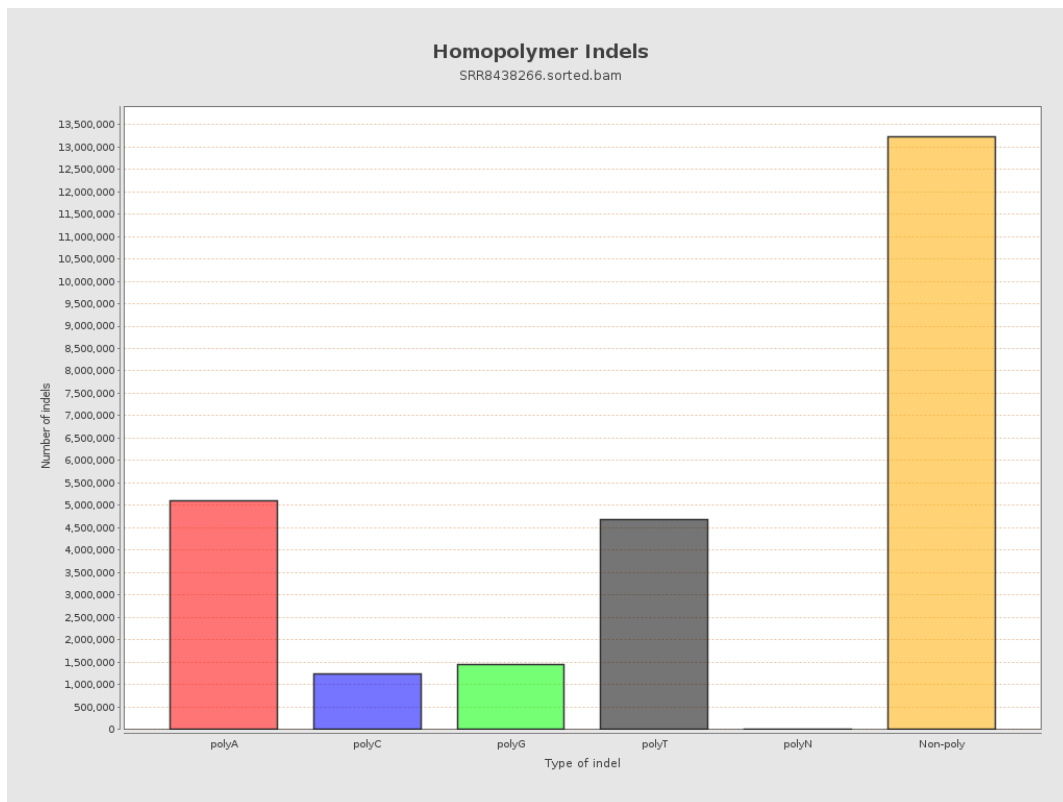
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



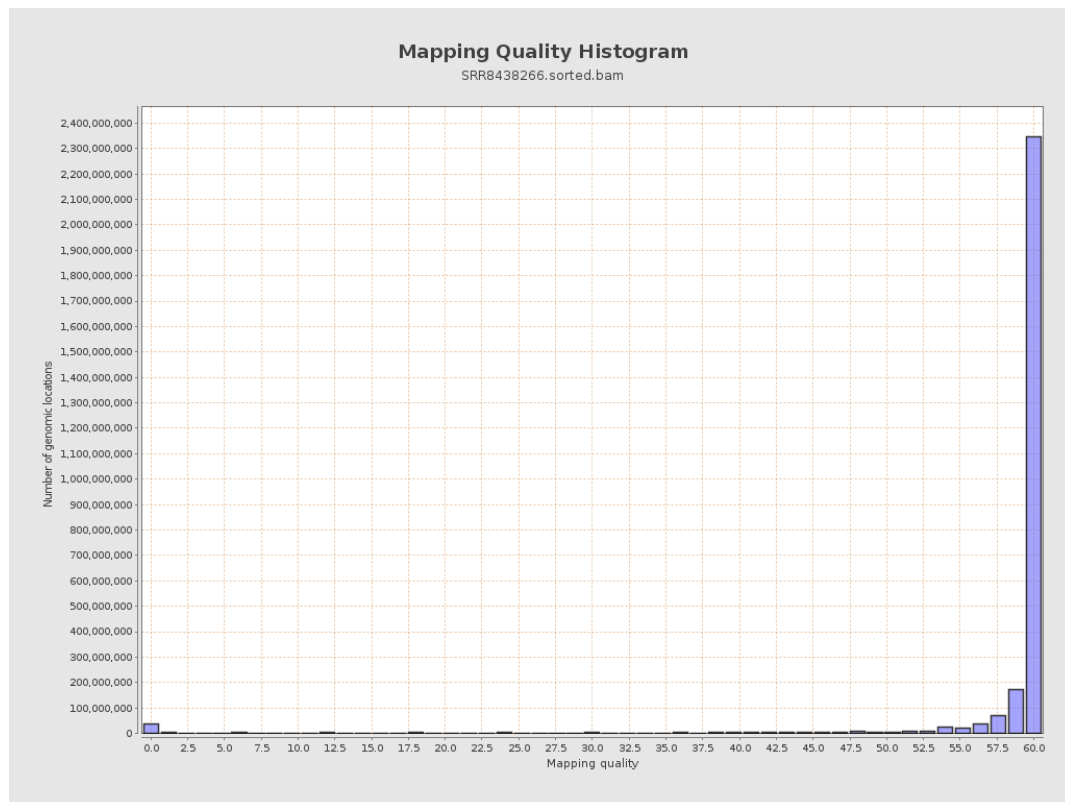
11. Results : Homopolymer Indels



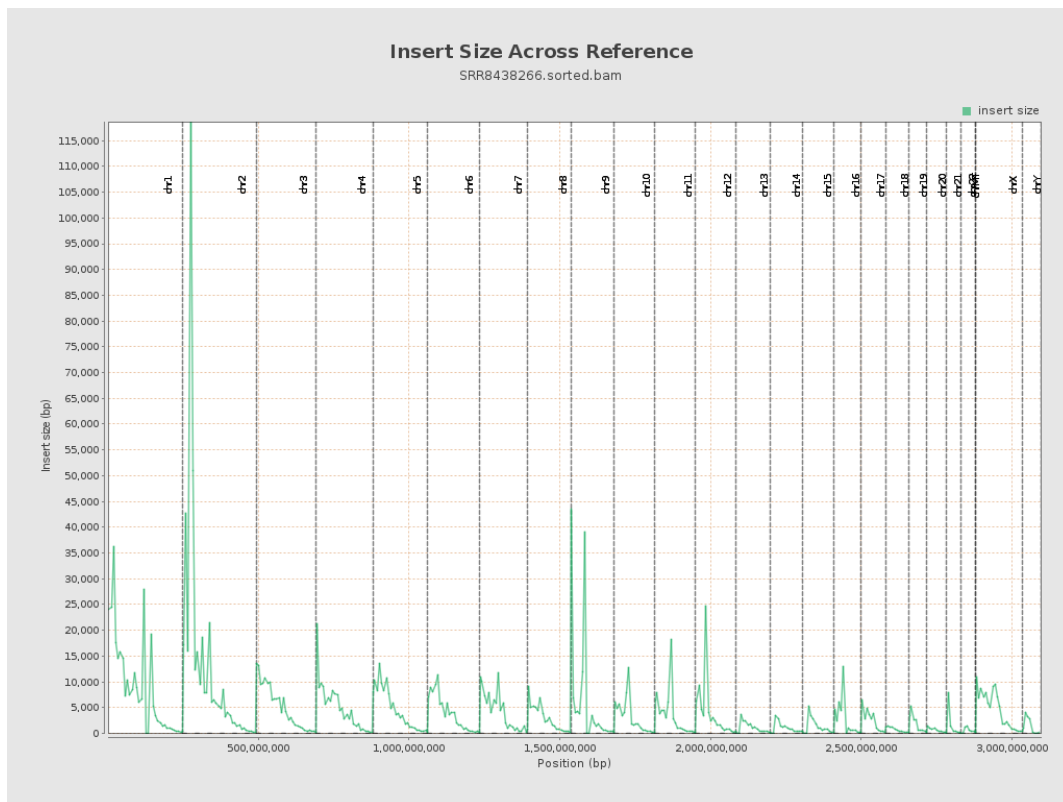
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

