

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 21:07:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438269.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_SRR8438269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438269_1.fastq.gz SRR8438269_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 21:07:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	755,054,160
Mapped reads	752,629,046 / 99.68%
Unmapped reads	2,425,114 / 0.32%
Mapped paired reads	752,629,046 / 99.68%
Mapped reads, first in pair	376,558,952 / 49.87%
Mapped reads, second in pair	376,070,094 / 49.81%
Mapped reads, both in pair	750,937,080 / 99.45%
Mapped reads, singletons	1,691,966 / 0.22%
Secondary alignments	0
Supplementary alignments	12,421,233 / 1.65%
Read min/max/mean length	28 / 151 / 144.56
Duplicated reads (estimated)	292,804,408 / 38.78%
Duplication rate	35.93%
Clipped reads	136,369,938 / 18.06%

2.2. ACGT Content

Number/percentage of A's	32,562,119,319 / 30.2%
Number/percentage of C's	21,609,064,409 / 20.04%
Number/percentage of T's	31,055,253,724 / 28.8%
Number/percentage of G's	22,594,261,173 / 20.96%
Number/percentage of N's	808,946 / 0%

GC Percentage	41%
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2.3. Coverage

Mean	34.8387
Standard Deviation	93.2989

2.4. Mapping Quality

Mean Mapping Quality	55.11
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2.5. Insert size

Mean	43,649.64
Standard Deviation	2,073,739.74
P25/Median/P75	188 / 255 / 376

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	553,539,141
Insertions	13,078,178
Mapped reads with at least one insertion	1.71%
Deletions	11,531,704
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.41%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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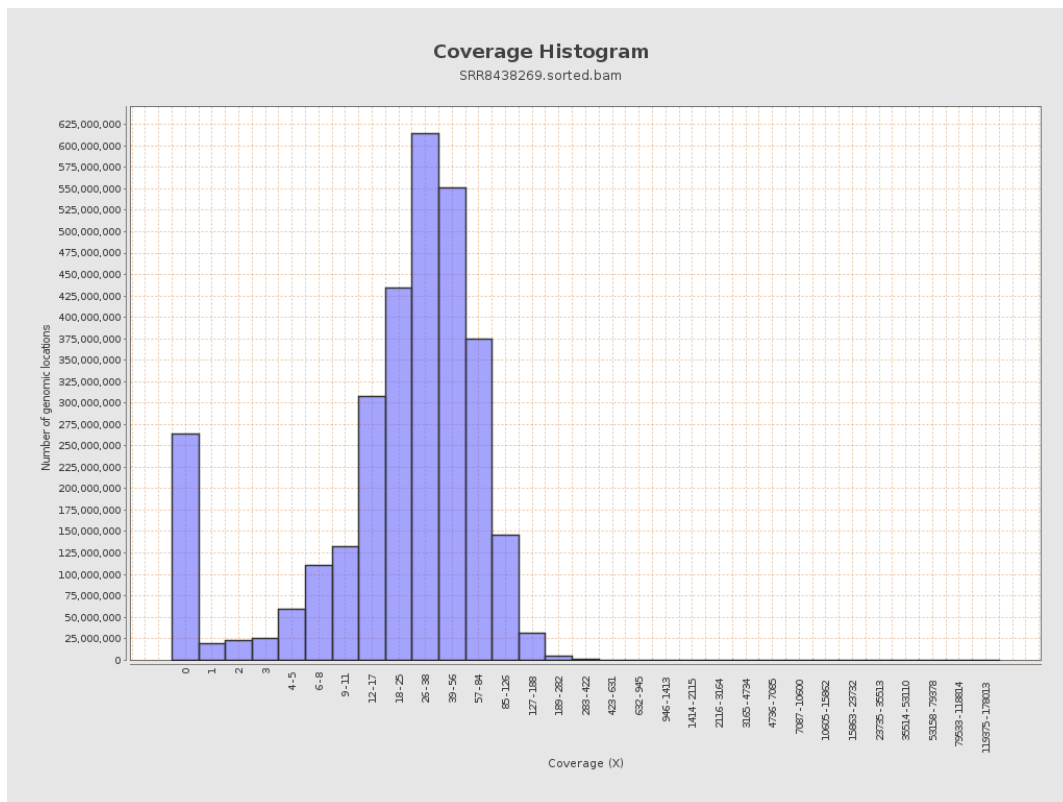
		bases	coverage	deviation
chr1	249250621	9474549543	38.0121	33.7038
chr2	243199373	9837030704	40.4484	151.3712
chr3	198022430	7257111275	36.6479	148.9821
chr4	191154276	7193158287	37.6301	30.2121
chr5	180915260	7019570010	38.8003	32.3342
chr6	171115067	6575510063	38.4274	30.1676
chr7	159138663	5975021159	37.546	30.1559
chr8	146364022	5915356618	40.4154	30.8135
chr9	141213431	4714556058	33.386	34.1352
chr10	135534747	5351267599	39.4826	37.7736
chr11	135006516	4936124178	36.5621	28.8814
chr12	133851895	4977544029	37.187	28.546
chr13	115169878	3798018440	32.9775	29.191
chr14	107349540	3383622379	31.5197	30.3566
chr15	102531392	2828944150	27.591	28.1657
chr16	90354753	2607554432	28.8591	43.0085
chr17	81195210	2446138958	30.1266	33.1238
chr18	78077248	3195061850	40.9218	31.4555
chr19	59128983	1574919022	26.6353	181.2948
chr20	63025520	2204538637	34.9785	29.4533
chr21	48129895	1405695667	29.2063	90.5456
chr22	51304566	1209859450	23.5819	30.0016
chrMT	16571	417355456	25,185.8944	9,431.5597
chrX	155270560	3140742279	20.2275	31.2821

chrY	59373566	410706801	6.9173	19.415
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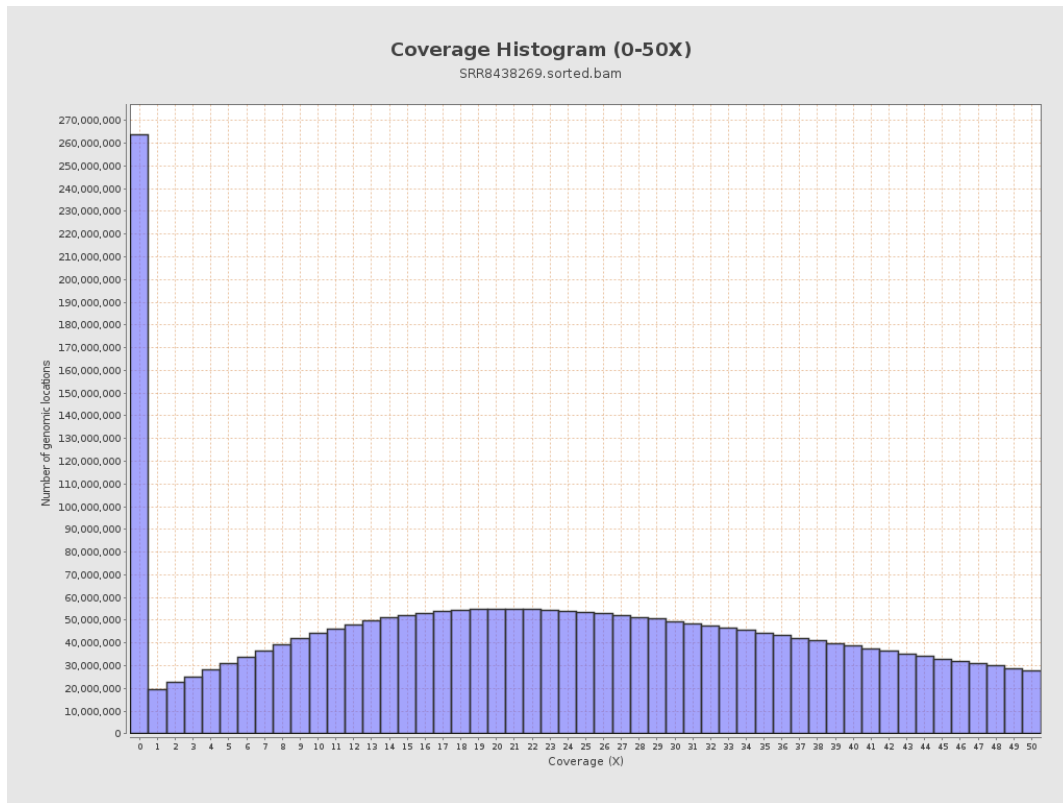
3. Results : Coverage across reference



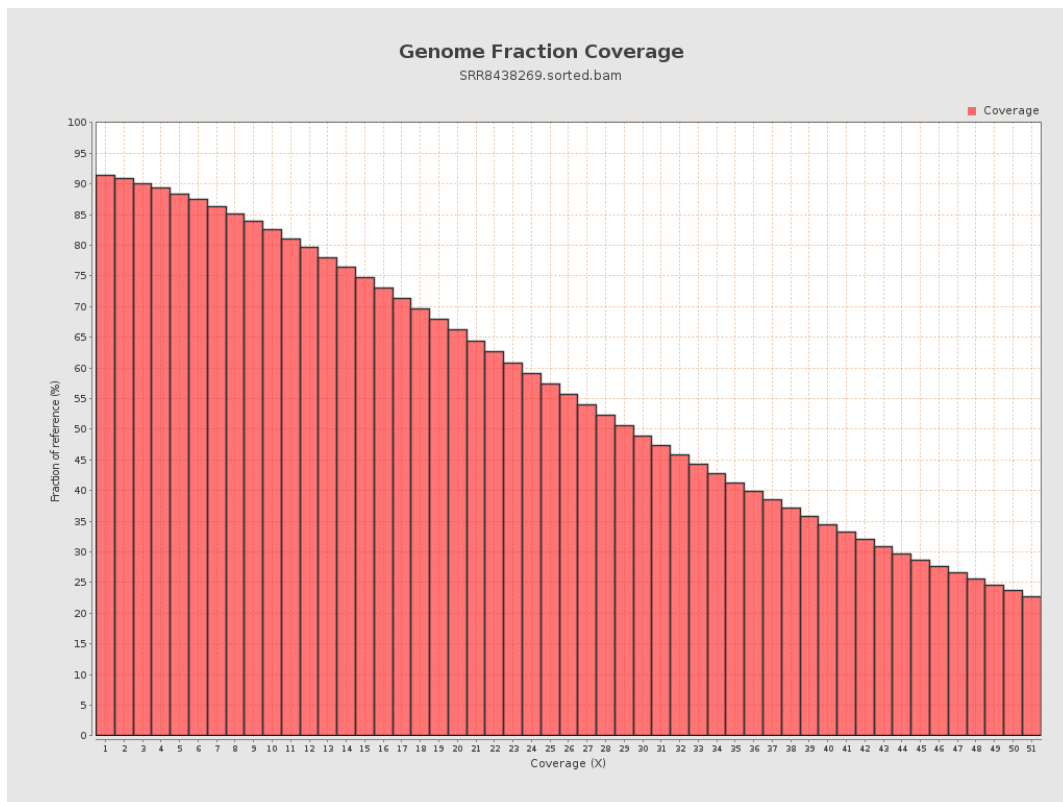
4. Results : Coverage Histogram



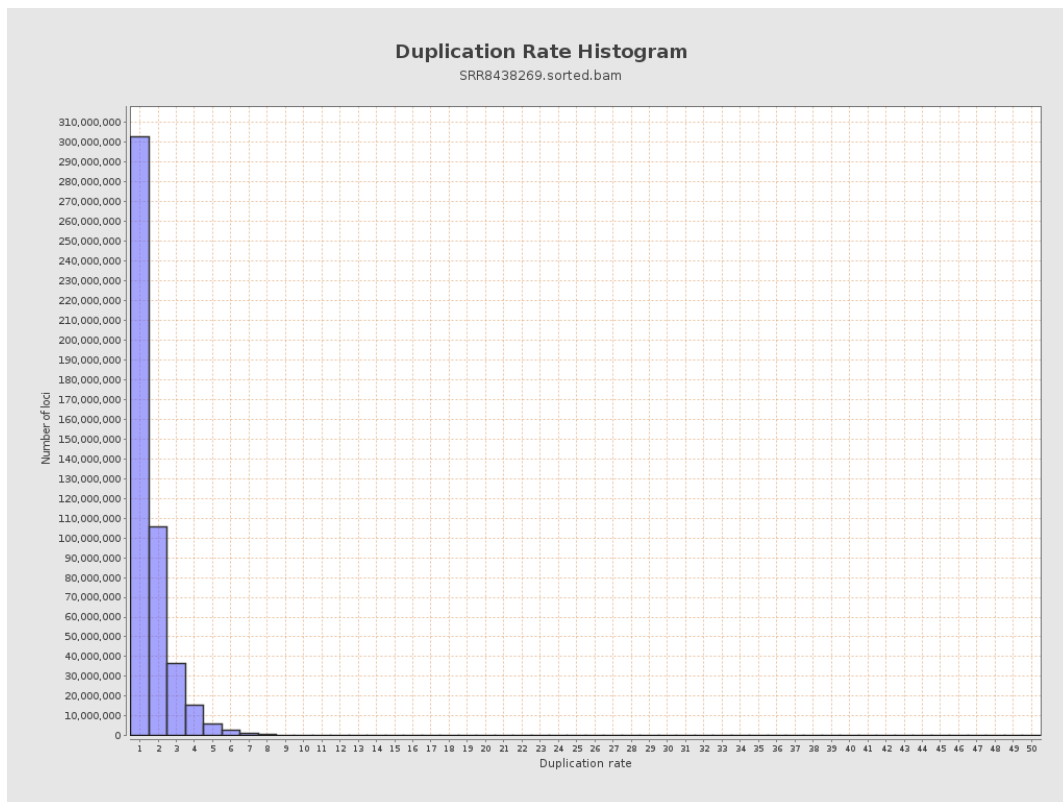
5. Results : Coverage Histogram (0-50X)



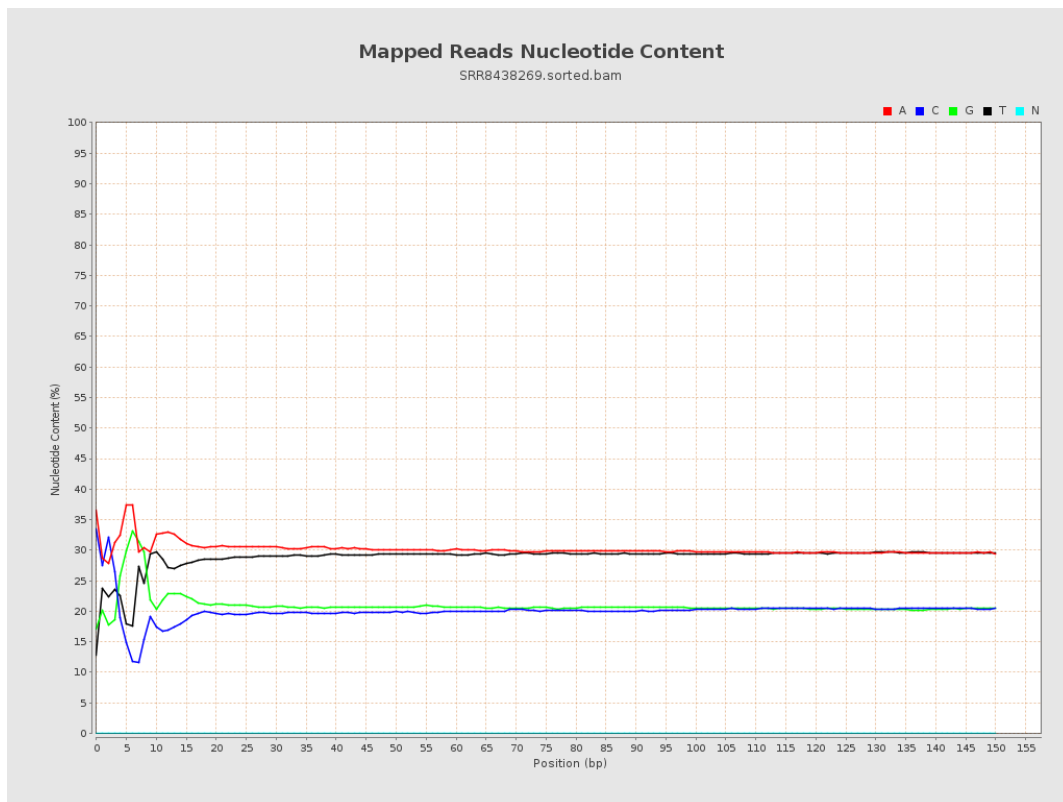
6. Results : Genome Fraction Coverage



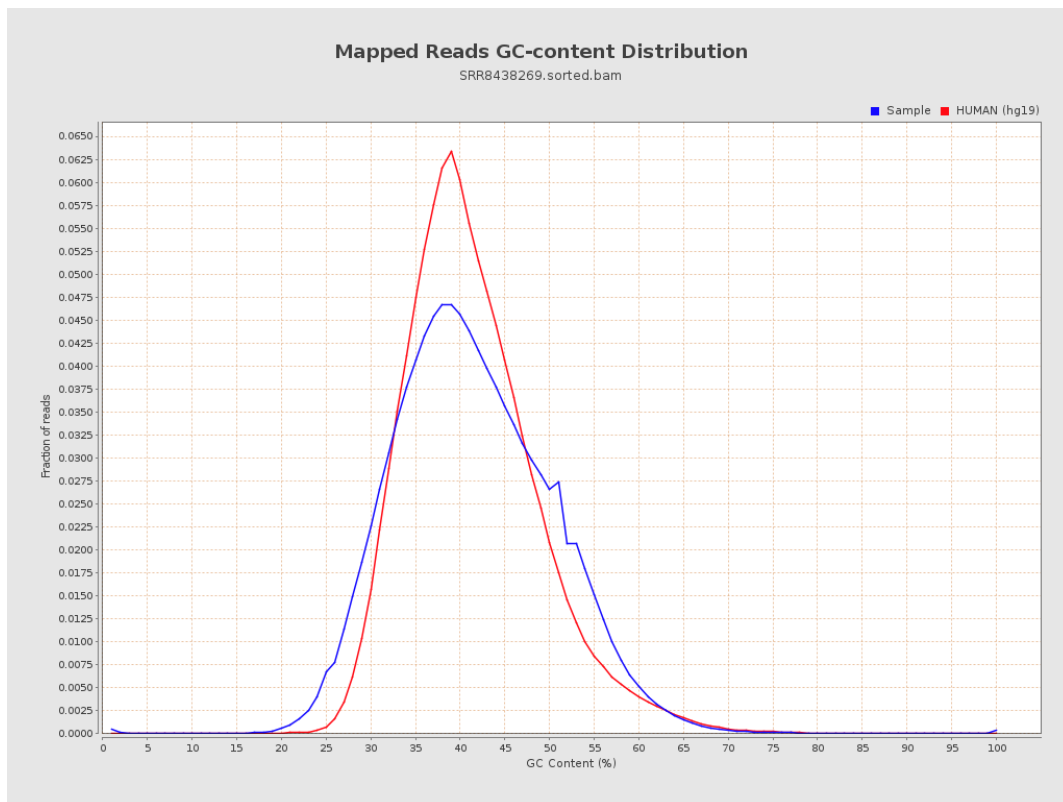
7. Results : Duplication Rate Histogram



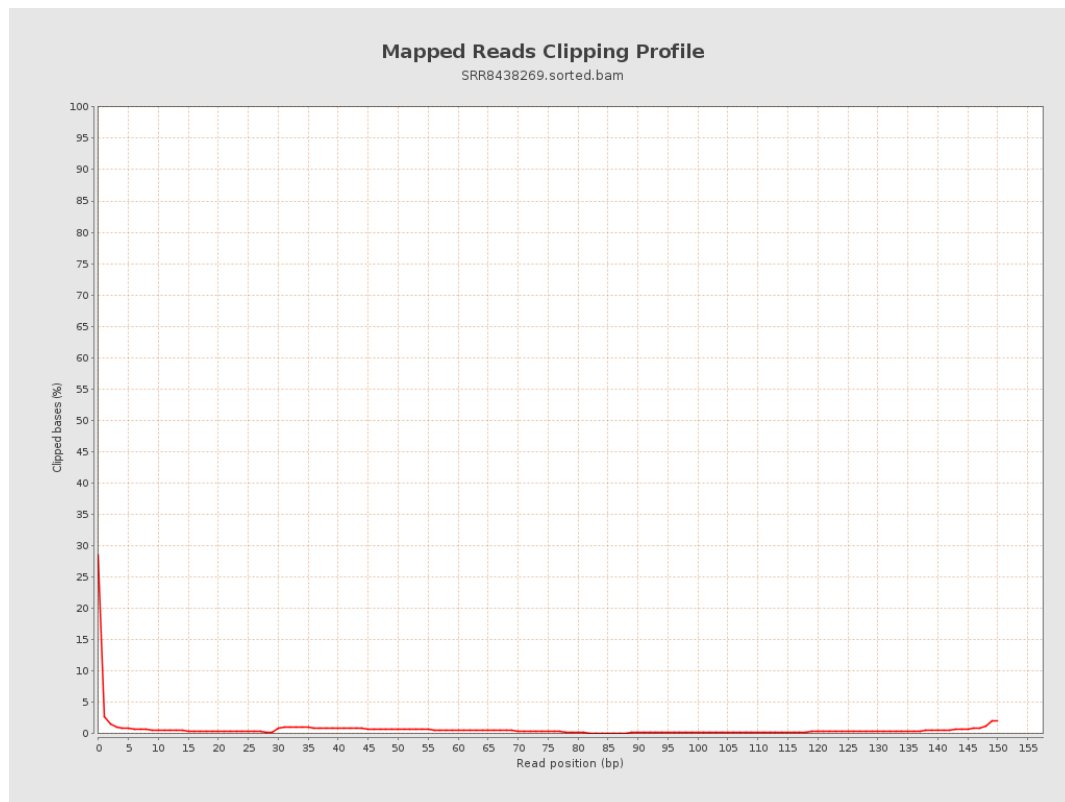
8. Results : Mapped Reads Nucleotide Content



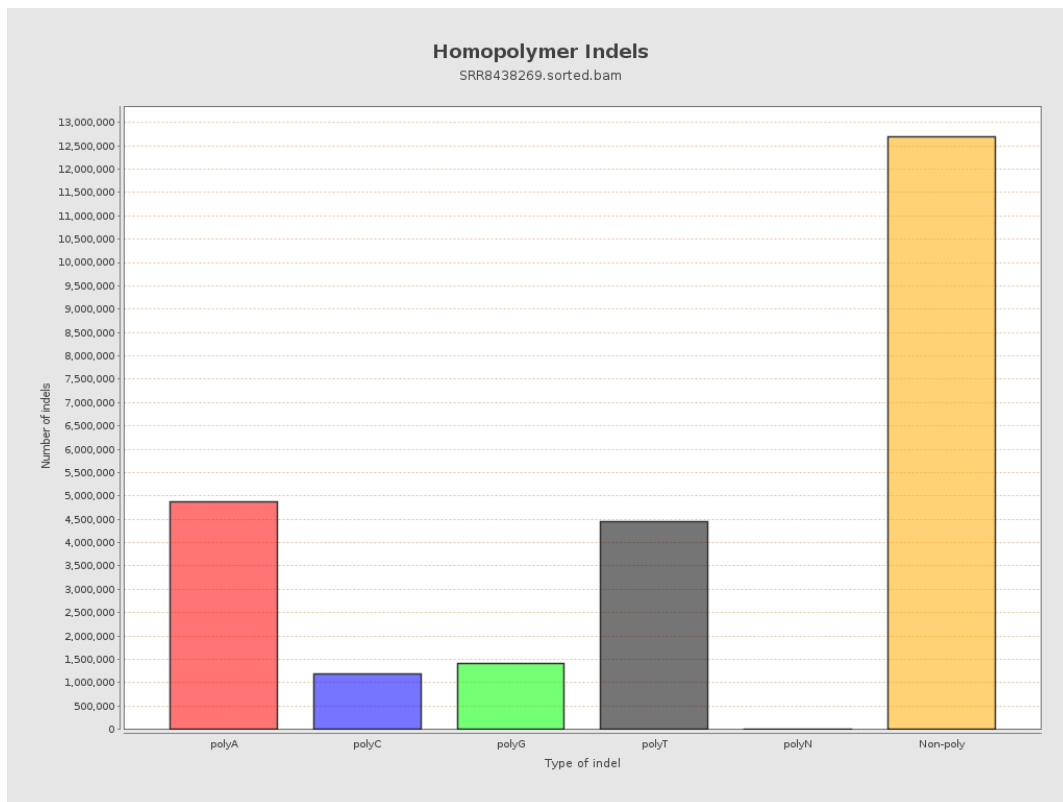
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



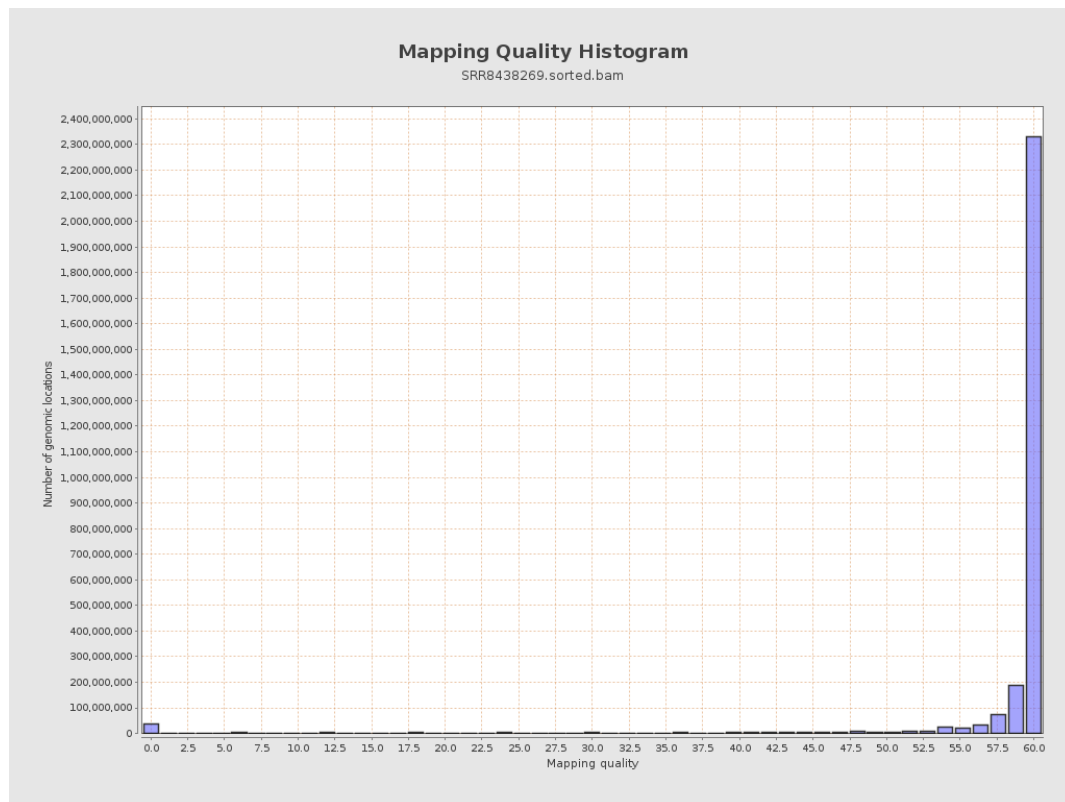
11. Results : Homopolymer Indels



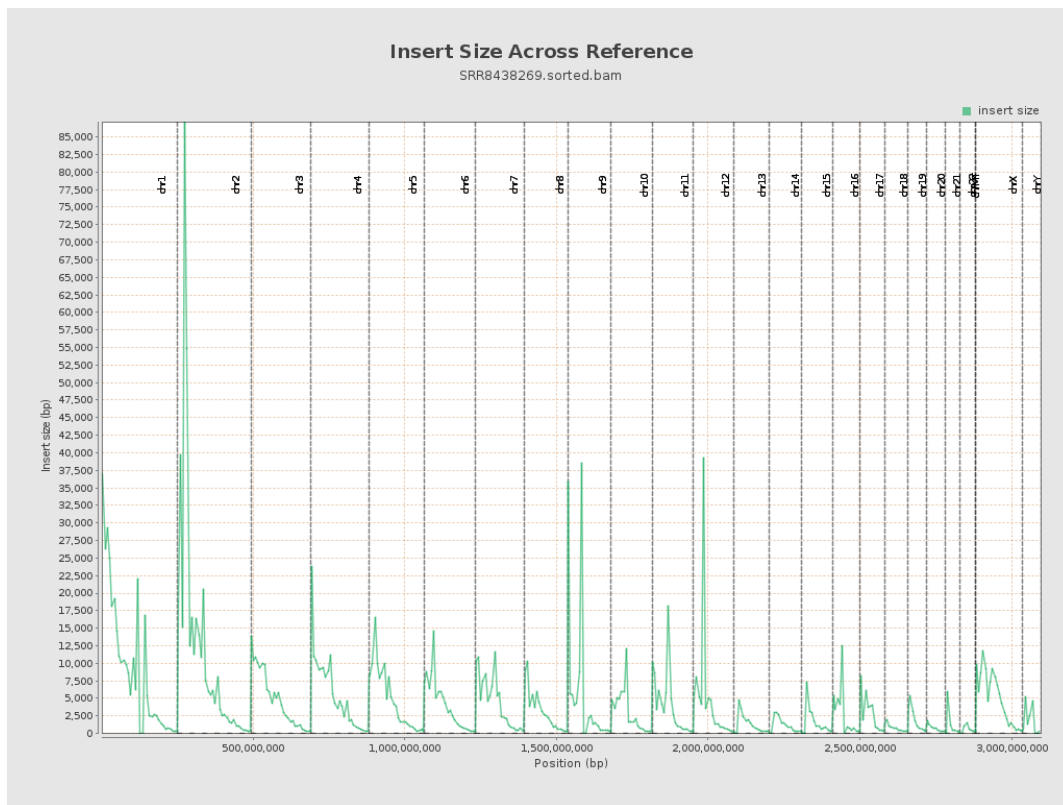
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

