

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:29:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173846.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_SRR10173846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173846_1.fastq.gz SRR10173846_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:29:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,680,618
Mapped reads	6,512,311 / 97.48%
Unmapped reads	168,307 / 2.52%
Mapped paired reads	6,512,311 / 97.48%
Mapped reads, first in pair	3,258,126 / 48.77%
Mapped reads, second in pair	3,254,185 / 48.71%
Mapped reads, both in pair	6,401,858 / 95.83%
Mapped reads, singletons	110,453 / 1.65%
Secondary alignments	0
Supplementary alignments	681,183 / 10.2%
Read min/max/mean length	30 / 133 / 128.58
Duplicated reads (estimated)	5,092,576 / 76.23%
Duplication rate	64.68%
Clipped reads	2,669,355 / 39.96%

2.2. ACGT Content

Number/percentage of A's	230,003,112 / 29.78%
Number/percentage of C's	153,428,385 / 19.86%
Number/percentage of T's	229,631,351 / 29.73%
Number/percentage of G's	159,332,525 / 20.63%
Number/percentage of N's	10,301 / 0%

GC Percentage	40.49%
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2.3. Coverage

Mean	0.2497
Standard Deviation	3.4259

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	976,525.04
Standard Deviation	9,089,019.85
P25/Median/P75	149 / 207 / 298

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	8,081,056
Insertions	78,902
Mapped reads with at least one insertion	1.17%
Deletions	192,775
Mapped reads with at least one deletion	2.89%
Homopolymer indels	42.43%

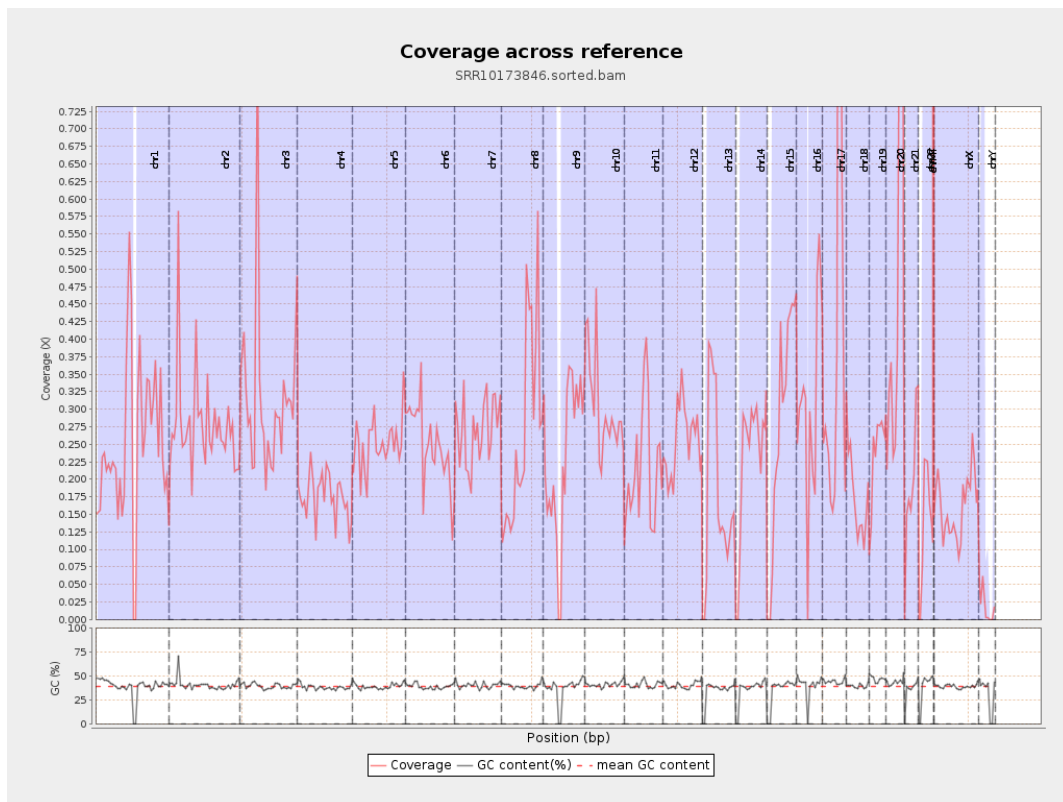
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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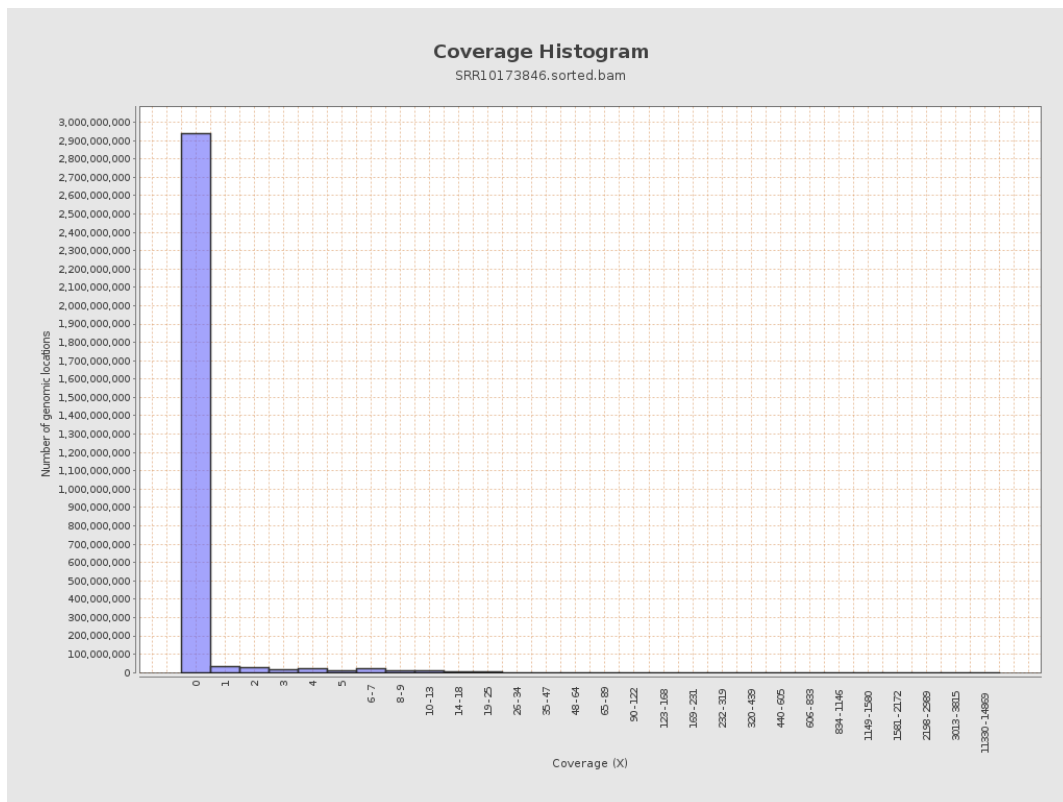
		bases	coverage	deviation
chr1	249250621	61967975	0.2486	2.6092
chr2	243199373	67604608	0.278	10.4223
chr3	198022430	61529843	0.3107	1.6436
chr4	191154276	33278399	0.1741	1.4471
chr5	180915260	45291242	0.2503	1.4428
chr6	171115067	42734686	0.2497	1.7674
chr7	159138663	42923815	0.2697	2.1366
chr8	146364022	38887477	0.2657	1.7765
chr9	141213431	31541954	0.2234	1.9101
chr10	135534747	40904005	0.3018	2.7456
chr11	135006516	29340030	0.2173	1.3942
chr12	133851895	34373085	0.2568	1.4623
chr13	115169878	20031805	0.1739	1.2161
chr14	107349540	24305384	0.2264	1.3685
chr15	102531392	28681004	0.2797	1.5329
chr16	90354753	28166215	0.3117	1.9352
chr17	81195210	33805047	0.4163	2.0904
chr18	78077248	13595412	0.1741	2.8134
chr19	59128983	14236972	0.2408	2.0105
chr20	63025520	36139880	0.5734	2.4912
chr21	48129895	9480258	0.197	1.3229
chr22	51304566	6661489	0.1298	0.9894
chrMT	16571	1271413	76.7252	59.994
chrX	155270560	25049395	0.1613	1.1602

chrY	59373566	1072424	0.0181	0.6734
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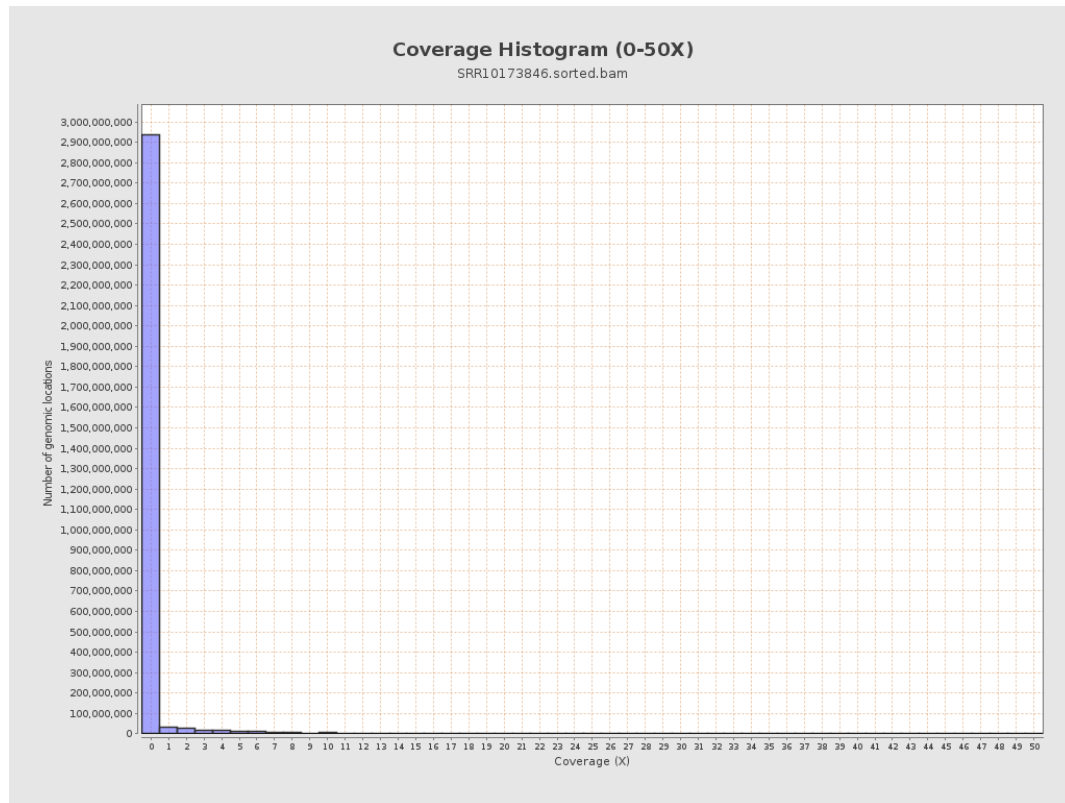
3. Results : Coverage across reference



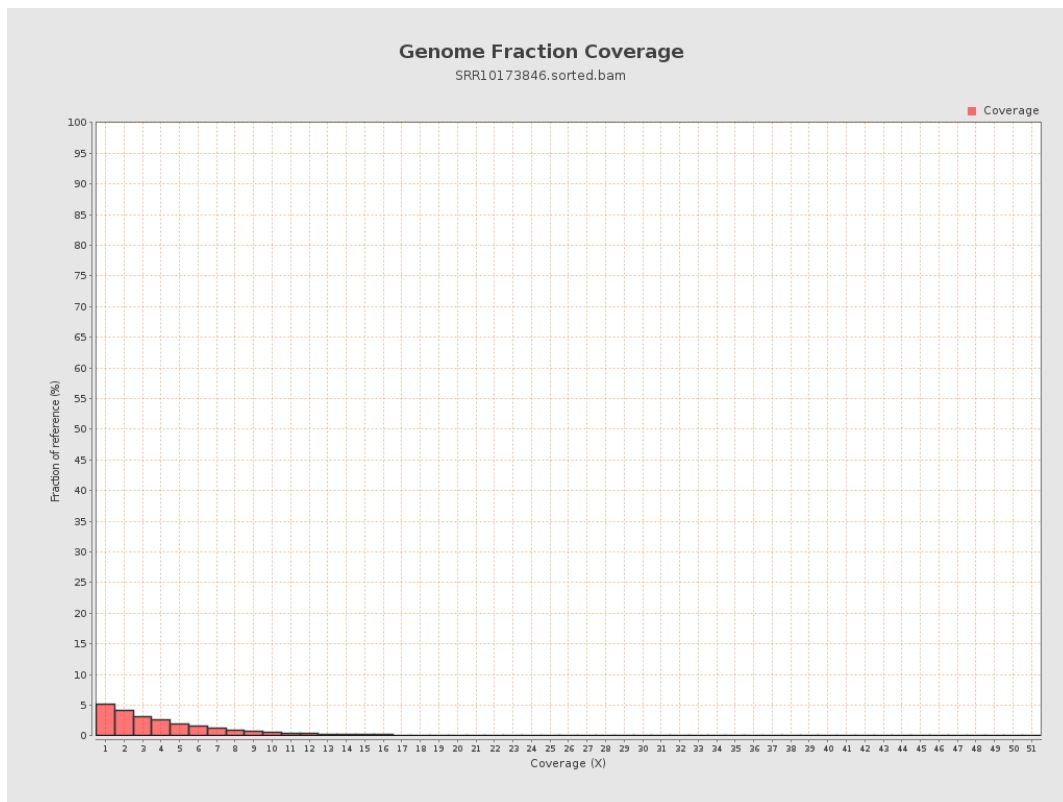
4. Results : Coverage Histogram



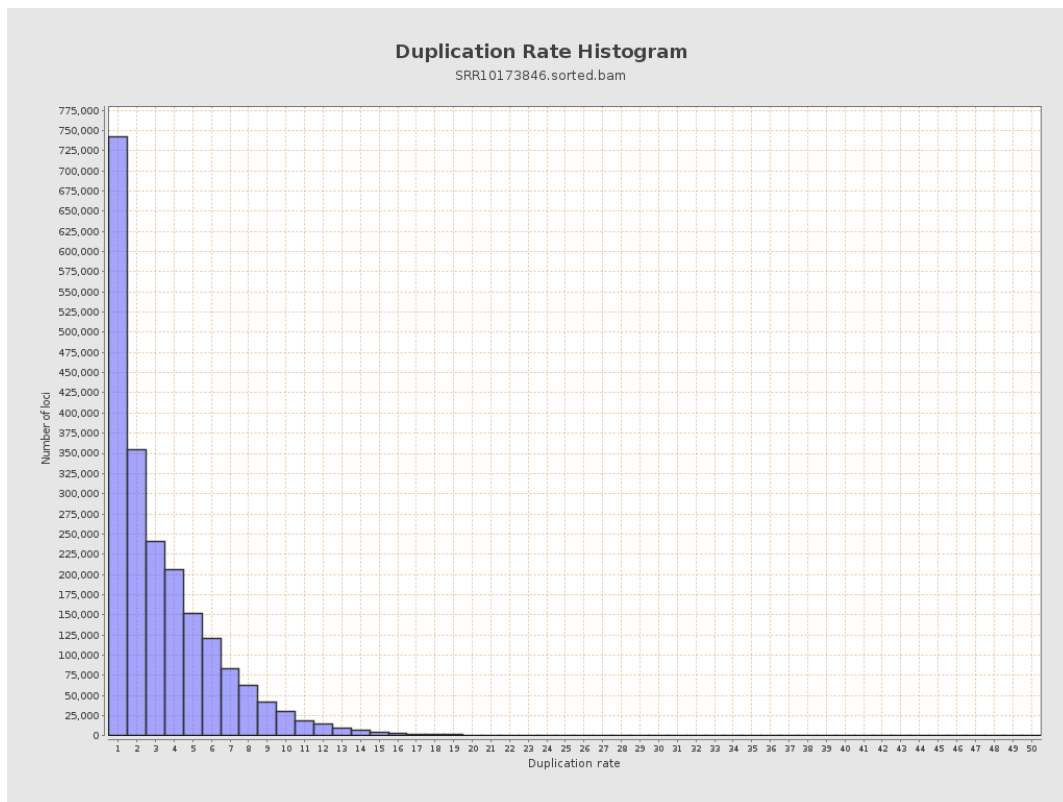
5. Results : Coverage Histogram (0-50X)



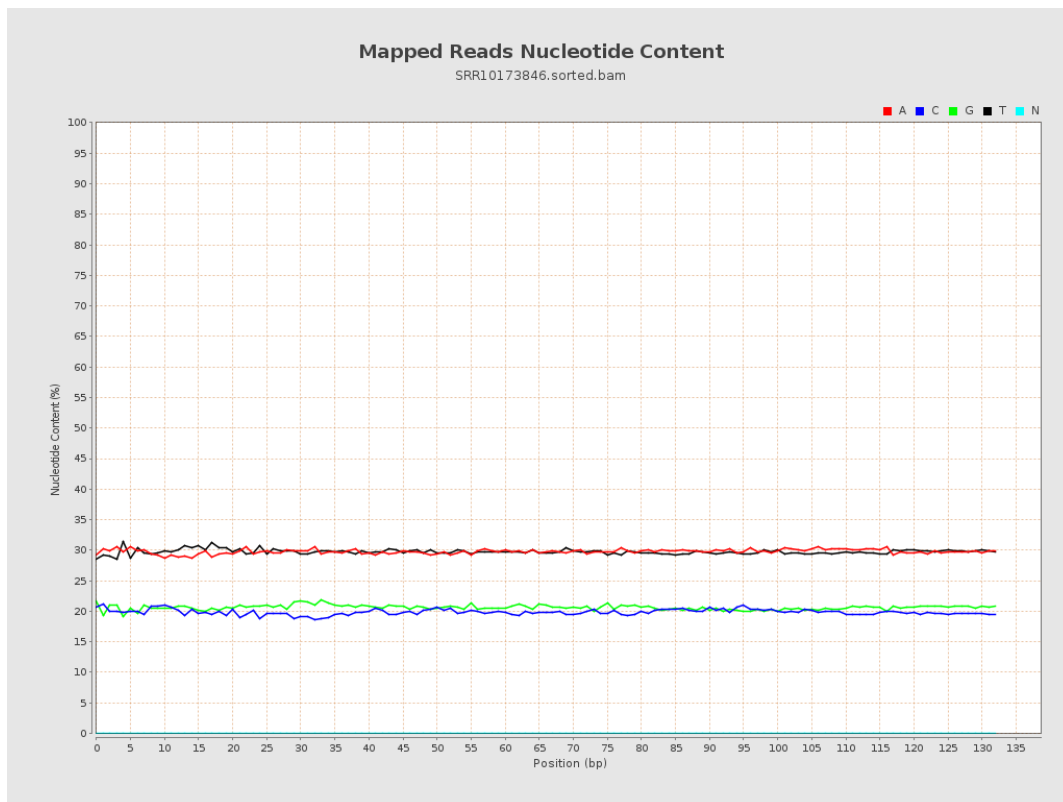
6. Results : Genome Fraction Coverage



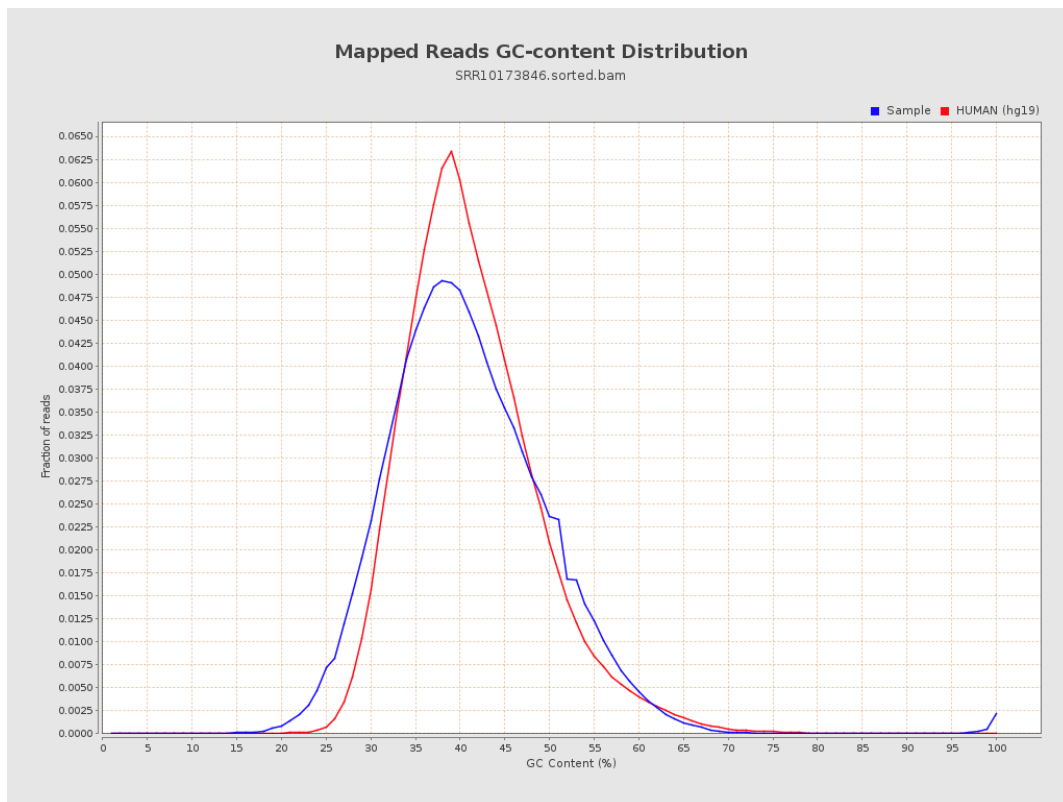
7. Results : Duplication Rate Histogram



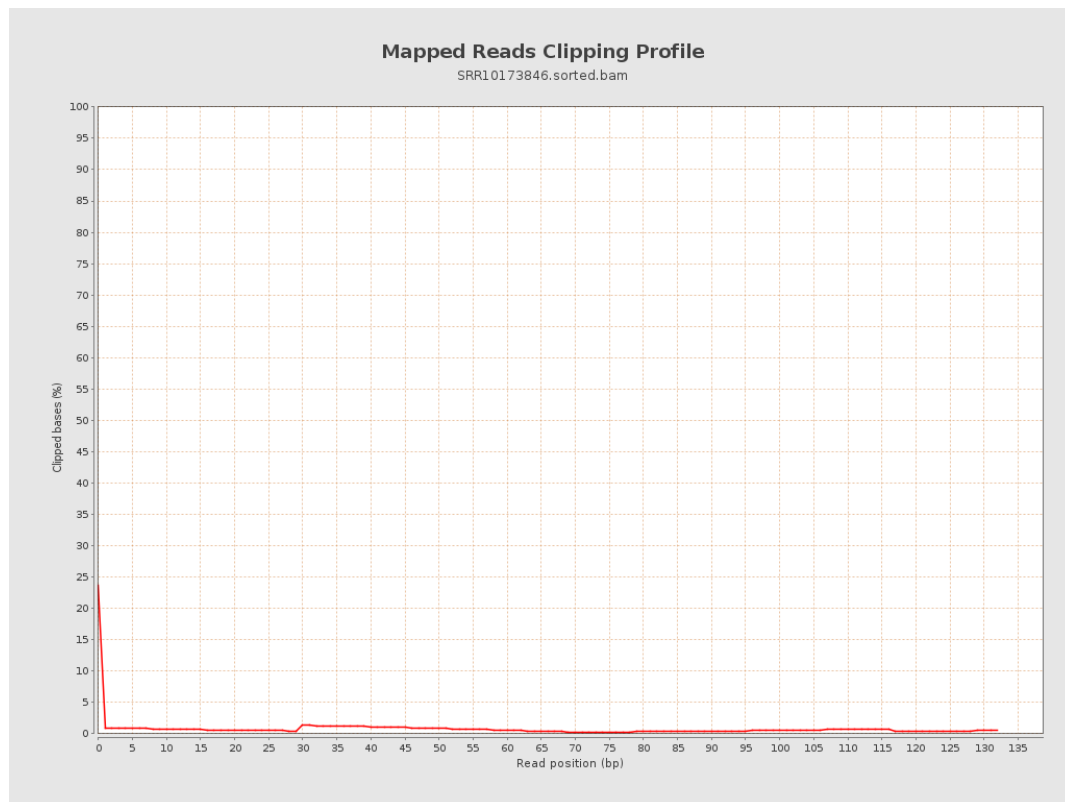
8. Results : Mapped Reads Nucleotide Content



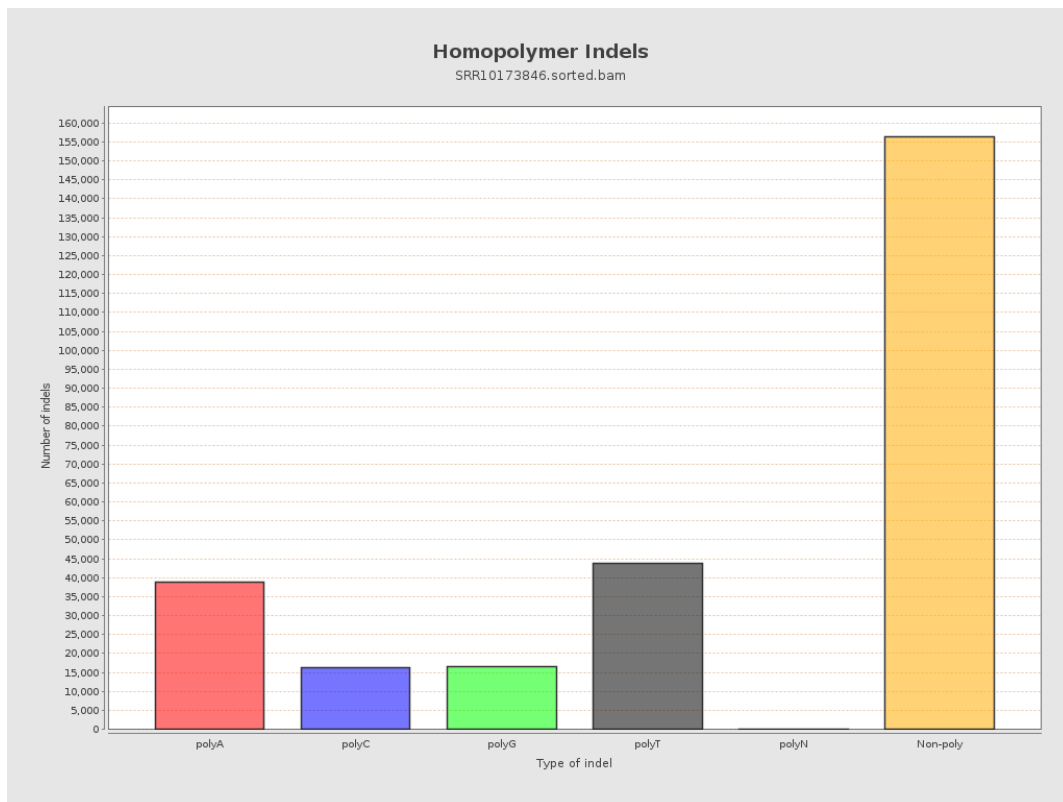
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



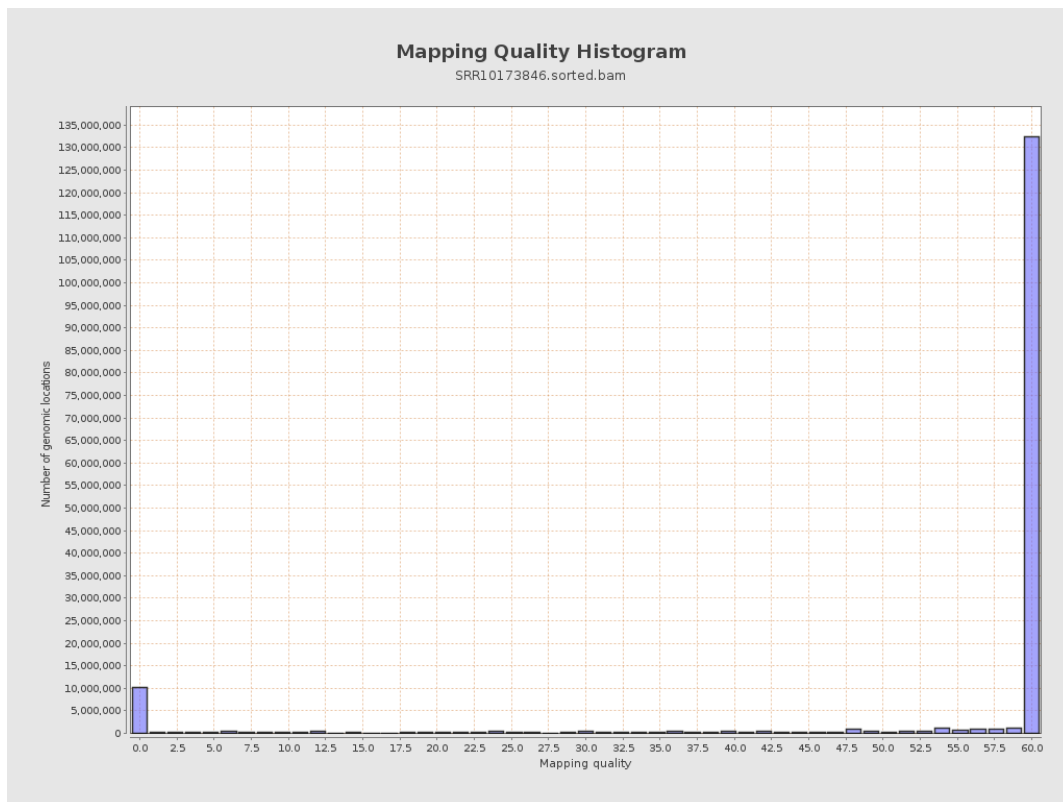
11. Results : Homopolymer Indels



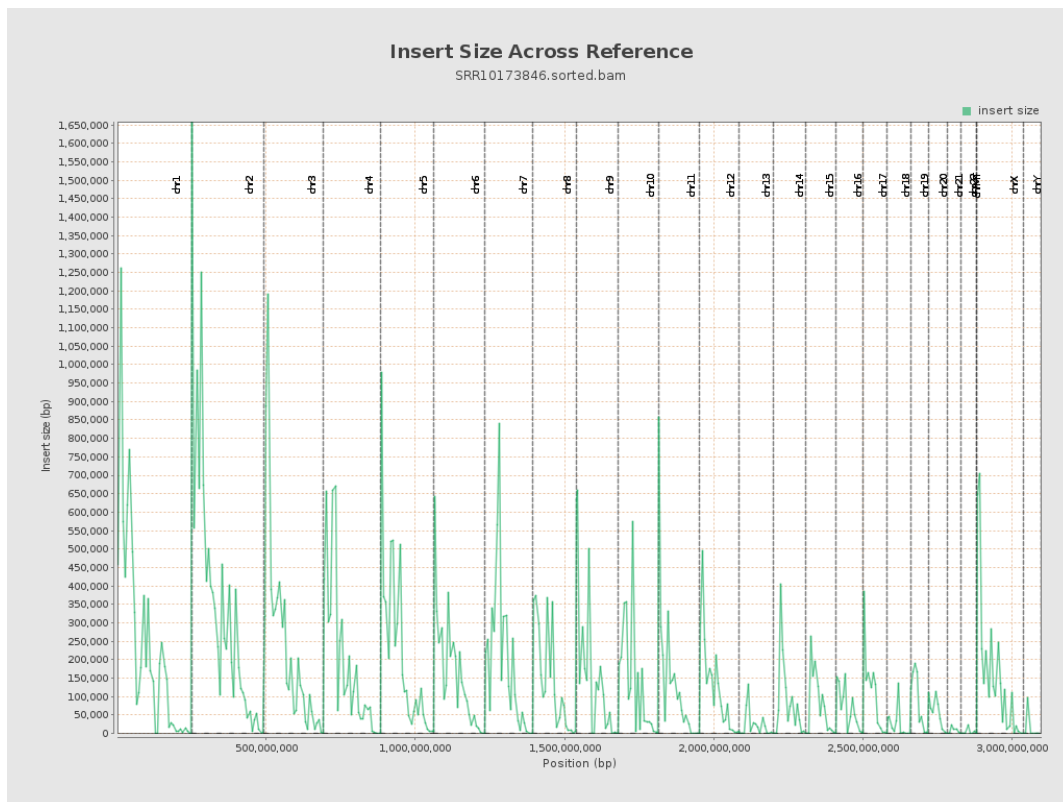
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

