

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:08:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173928.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_SRR10173928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173928_1.fastq.gz SRR10173928_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:08:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,037,652
Mapped reads	3,952,732 / 97.9%
Unmapped reads	84,920 / 2.1%
Mapped paired reads	3,952,732 / 97.9%
Mapped reads, first in pair	1,973,780 / 48.88%
Mapped reads, second in pair	1,978,952 / 49.01%
Mapped reads, both in pair	3,898,272 / 96.55%
Mapped reads, singletons	54,460 / 1.35%
Secondary alignments	0
Supplementary alignments	569,817 / 14.11%
Read min/max/mean length	30 / 133 / 125.67
Duplicated reads (estimated)	3,219,122 / 79.73%
Duplication rate	64.98%
Clipped reads	2,100,690 / 52.03%

2.2. ACGT Content

Number/percentage of A's	133,186,396 / 29.79%
Number/percentage of C's	89,159,474 / 19.94%
Number/percentage of T's	132,052,044 / 29.54%
Number/percentage of G's	92,664,088 / 20.73%
Number/percentage of N's	3,847 / 0%

GC Percentage	40.67%
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2.3. Coverage

Mean	0.1445
Standard Deviation	2.8048

2.4. Mapping Quality

Mean Mapping Quality	52.38
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2.5. Insert size

Mean	1,050,706.08
Standard Deviation	9,539,879.94
P25/Median/P75	103 / 152 / 237

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	3,773,656
Insertions	50,762
Mapped reads with at least one insertion	1.23%
Deletions	123,663
Mapped reads with at least one deletion	3.06%
Homopolymer indels	41.4%

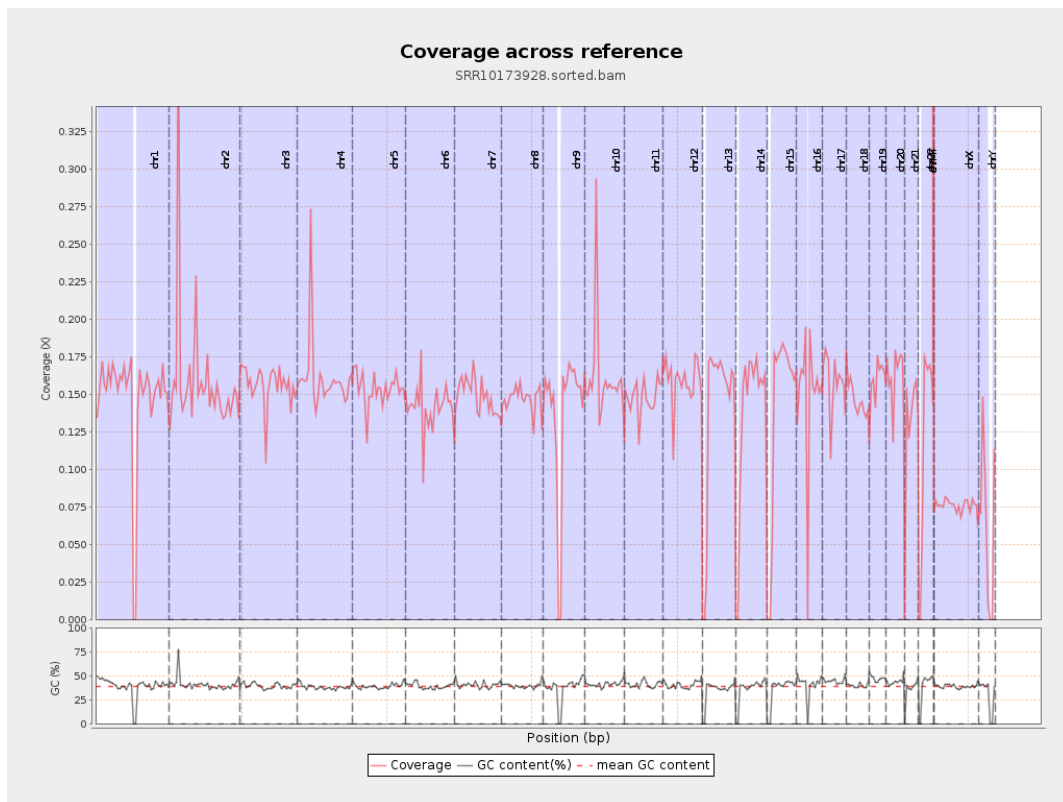
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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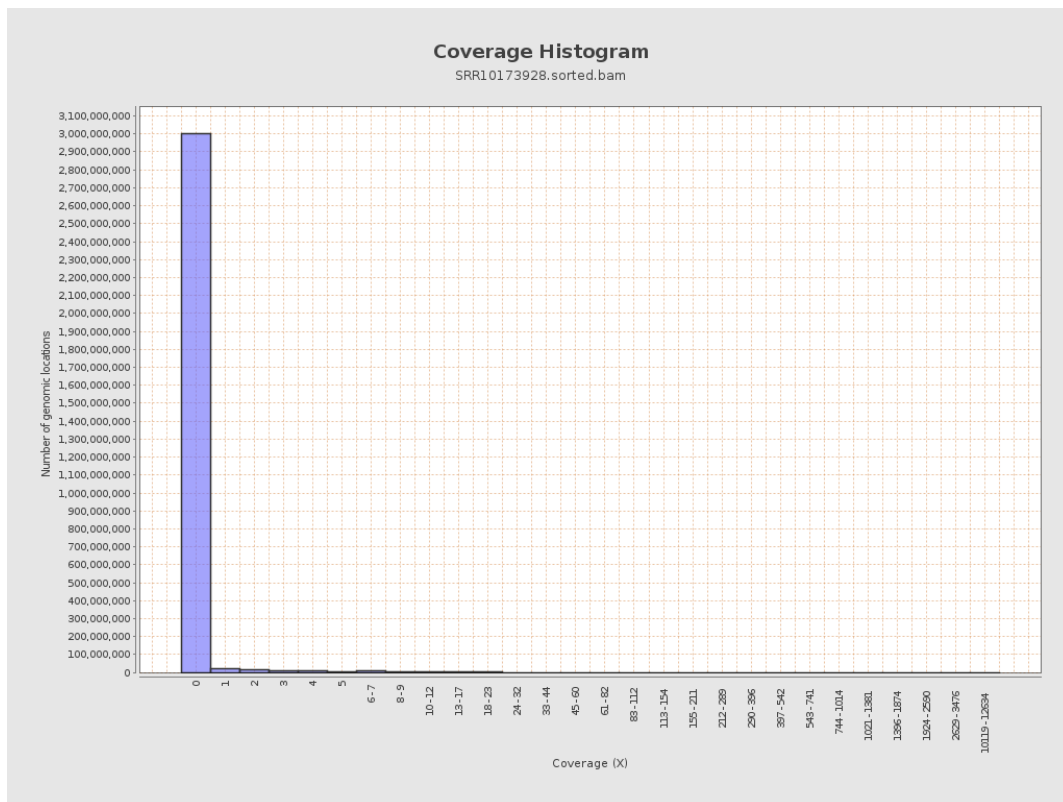
		bases	coverage	deviation
chr1	249250621	36698091	0.1472	1.5111
chr2	243199373	38953838	0.1602	8.8739
chr3	198022430	30938348	0.1562	1.2082
chr4	191154276	30638919	0.1603	1.4725
chr5	180915260	27766056	0.1535	1.1924
chr6	171115067	24166115	0.1412	1.2205
chr7	159138663	23782573	0.1494	1.4251
chr8	146364022	21460818	0.1466	1.6379
chr9	141213431	19314241	0.1368	1.452
chr10	135534747	21786955	0.1607	1.7061
chr11	135006516	19957927	0.1478	1.1897
chr12	133851895	21202312	0.1584	1.2389
chr13	115169878	15855019	0.1377	1.1488
chr14	107349540	14631171	0.1363	1.1233
chr15	102531392	14303493	0.1395	1.1407
chr16	90354753	13456015	0.1489	1.3222
chr17	81195210	12726482	0.1567	1.2464
chr18	78077248	11493562	0.1472	1.8777
chr19	59128983	9445790	0.1597	1.4065
chr20	63025520	10197769	0.1618	1.2586
chr21	48129895	6269174	0.1303	1.3322
chr22	51304566	5978061	0.1165	1.1429
chrMT	16571	930531	56.1542	49.7732
chrX	155270560	11805007	0.076	0.8234

chrY	59373566	3607011	0.0608	1.0325
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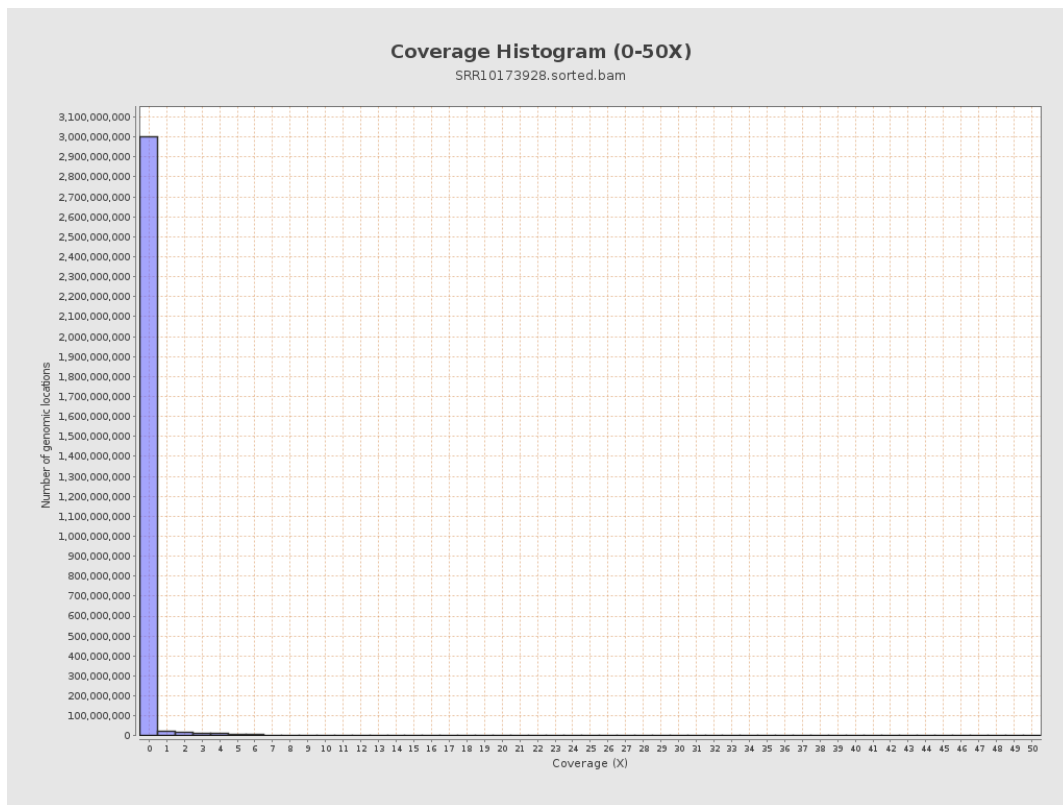
3. Results : Coverage across reference



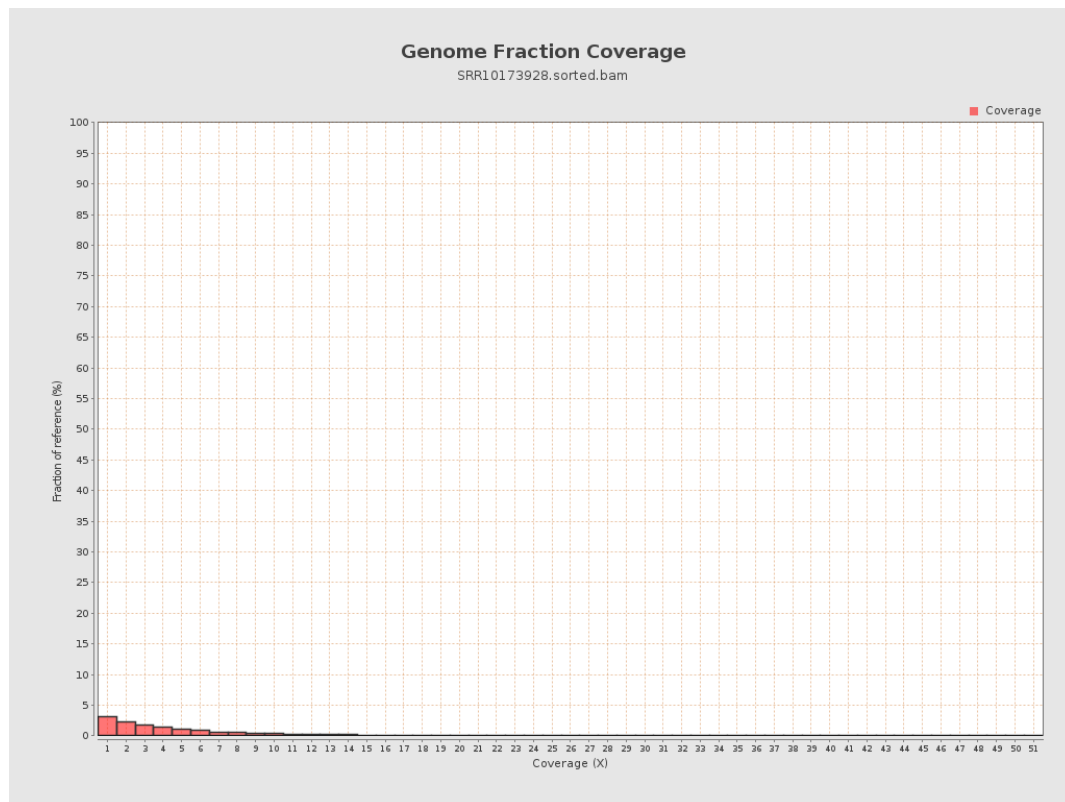
4. Results : Coverage Histogram



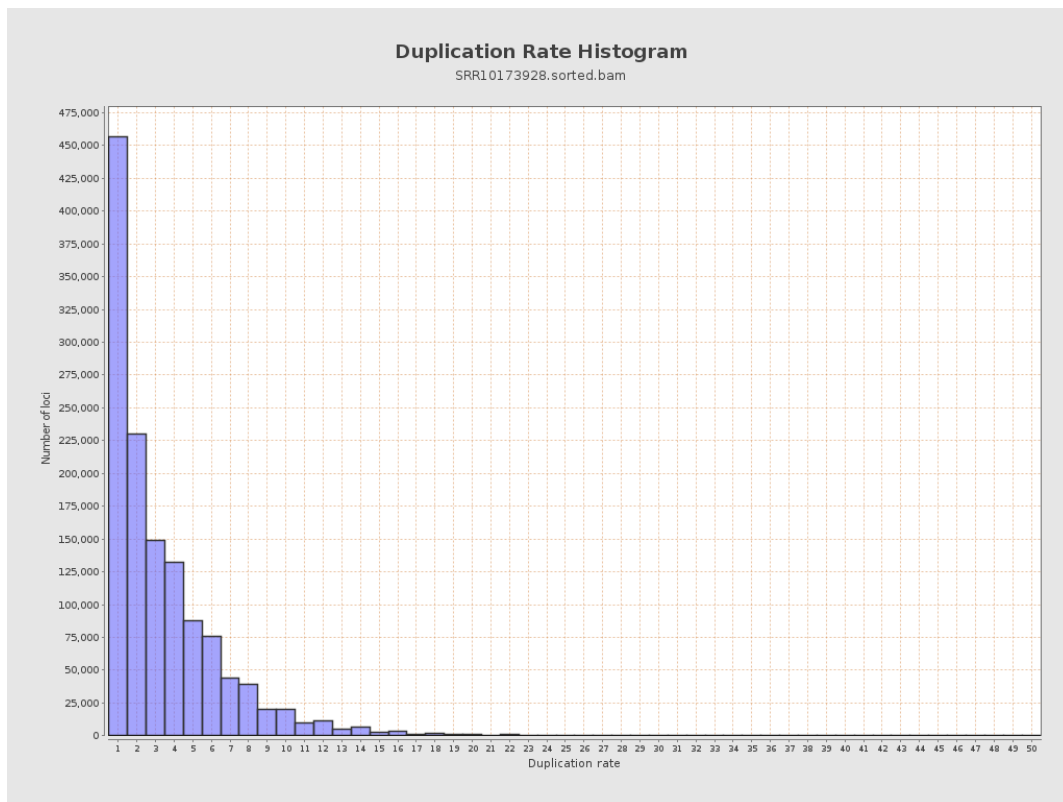
5. Results : Coverage Histogram (0-50X)



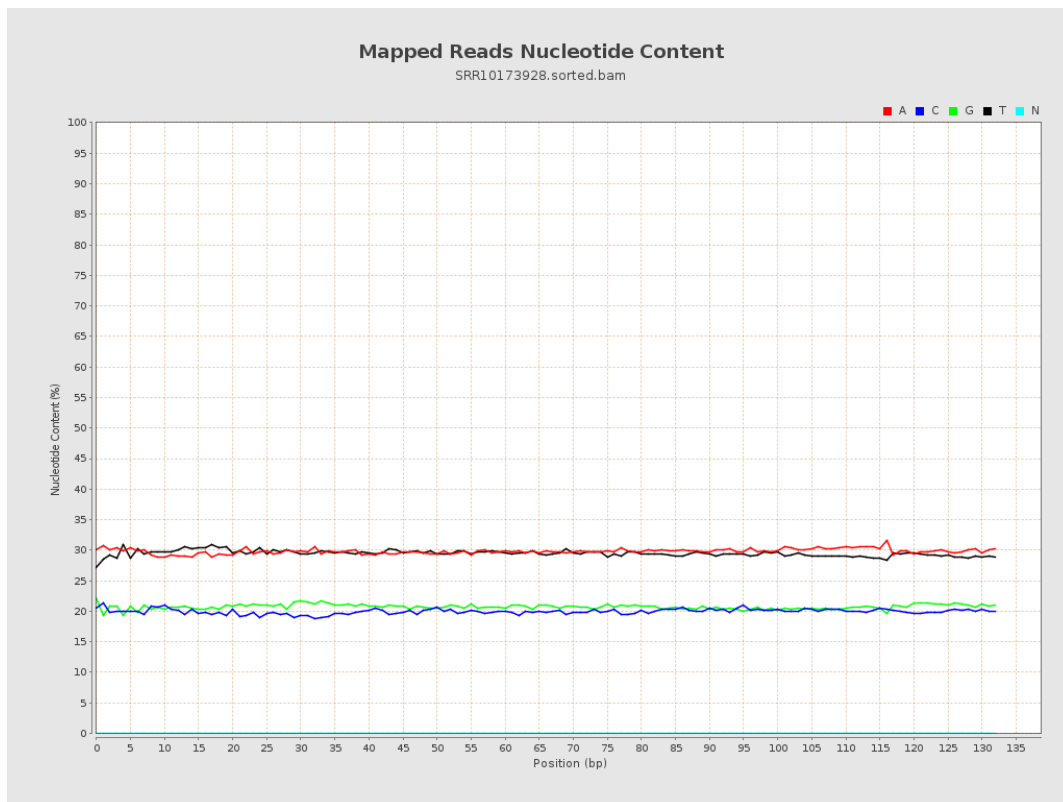
6. Results : Genome Fraction Coverage



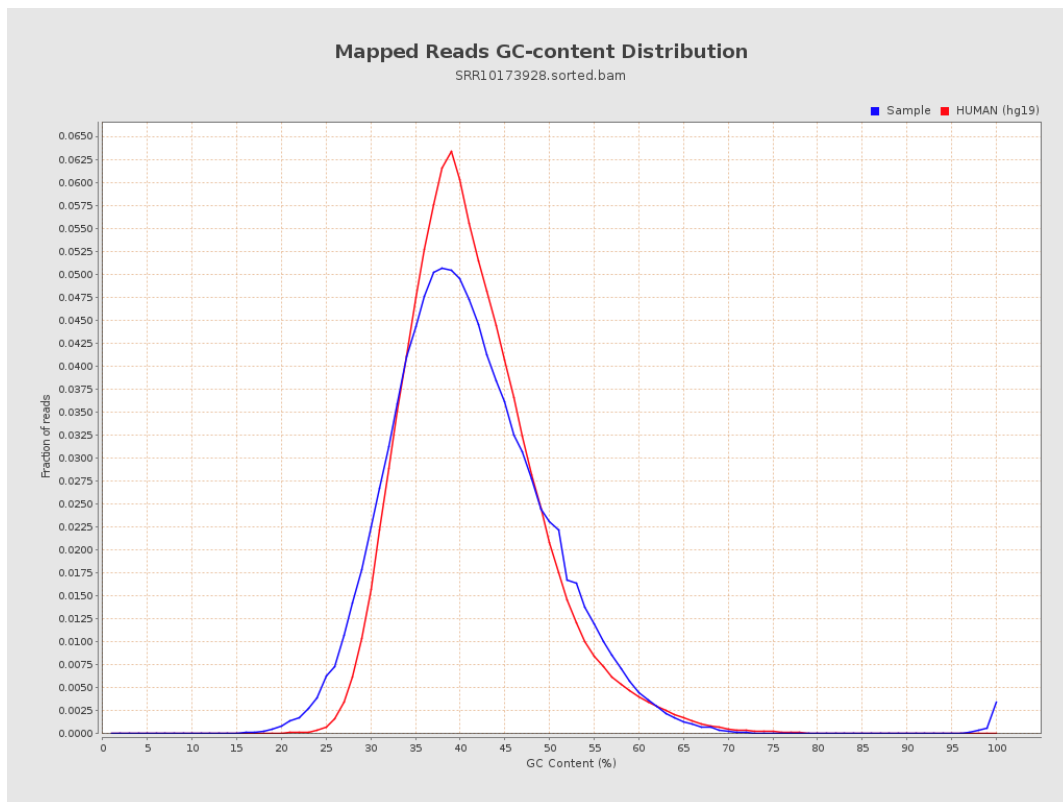
7. Results : Duplication Rate Histogram



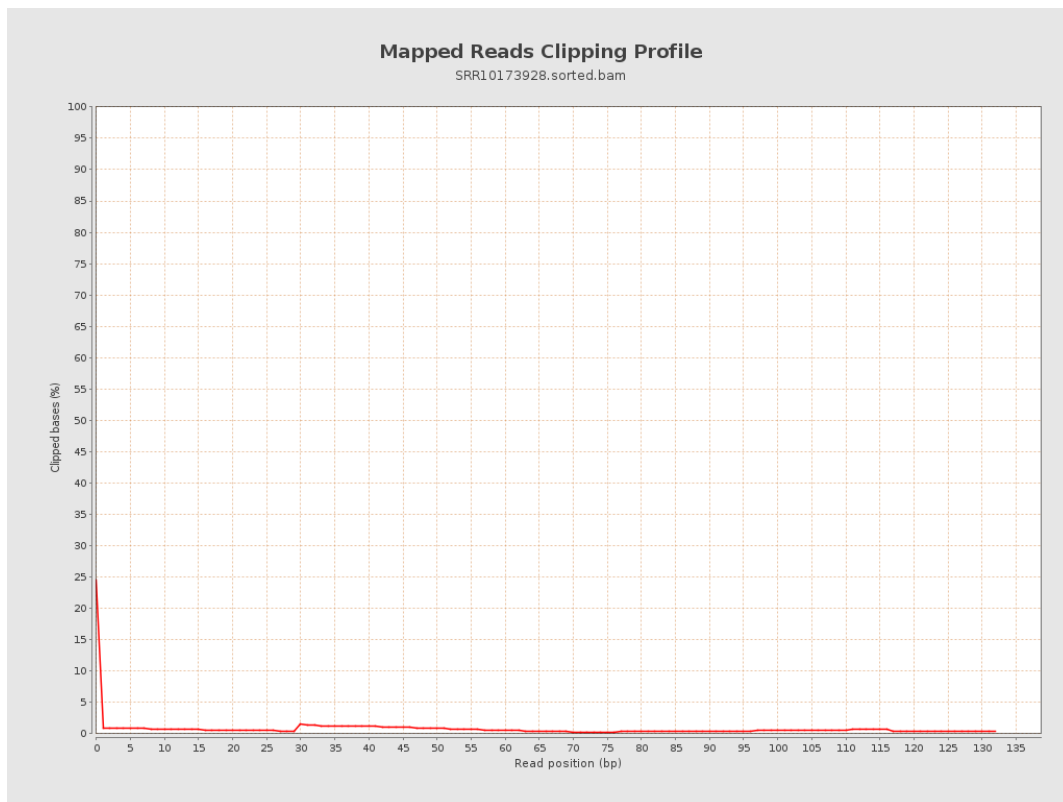
8. Results : Mapped Reads Nucleotide Content



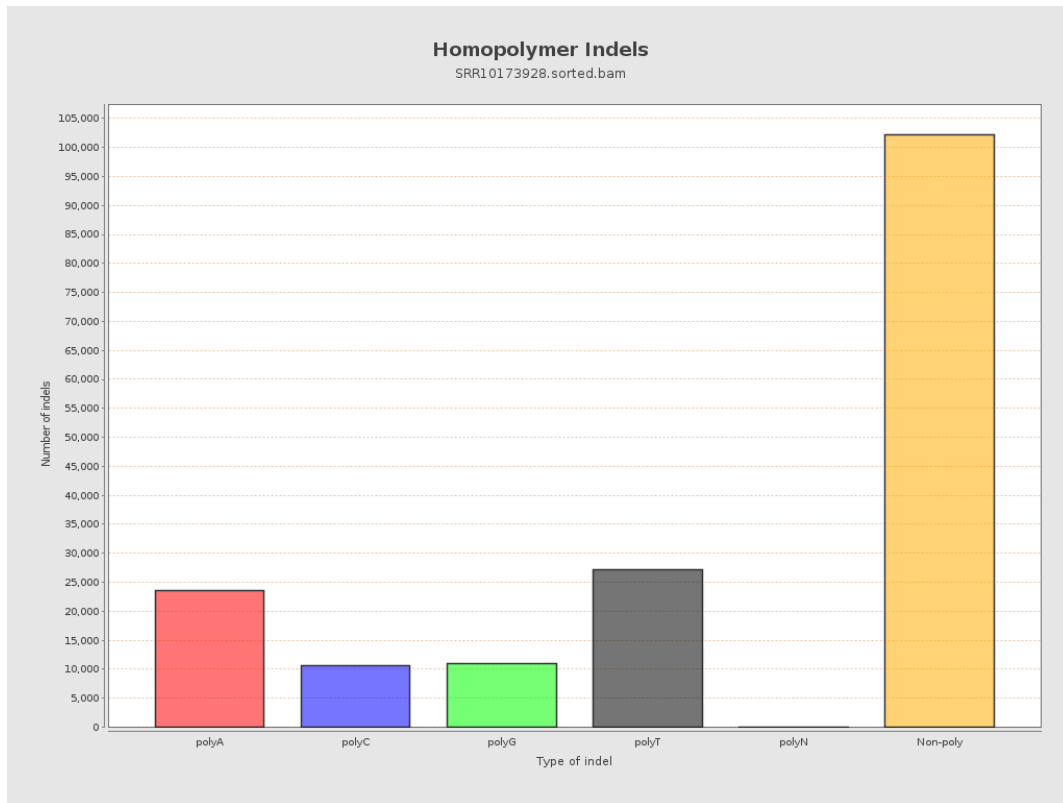
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



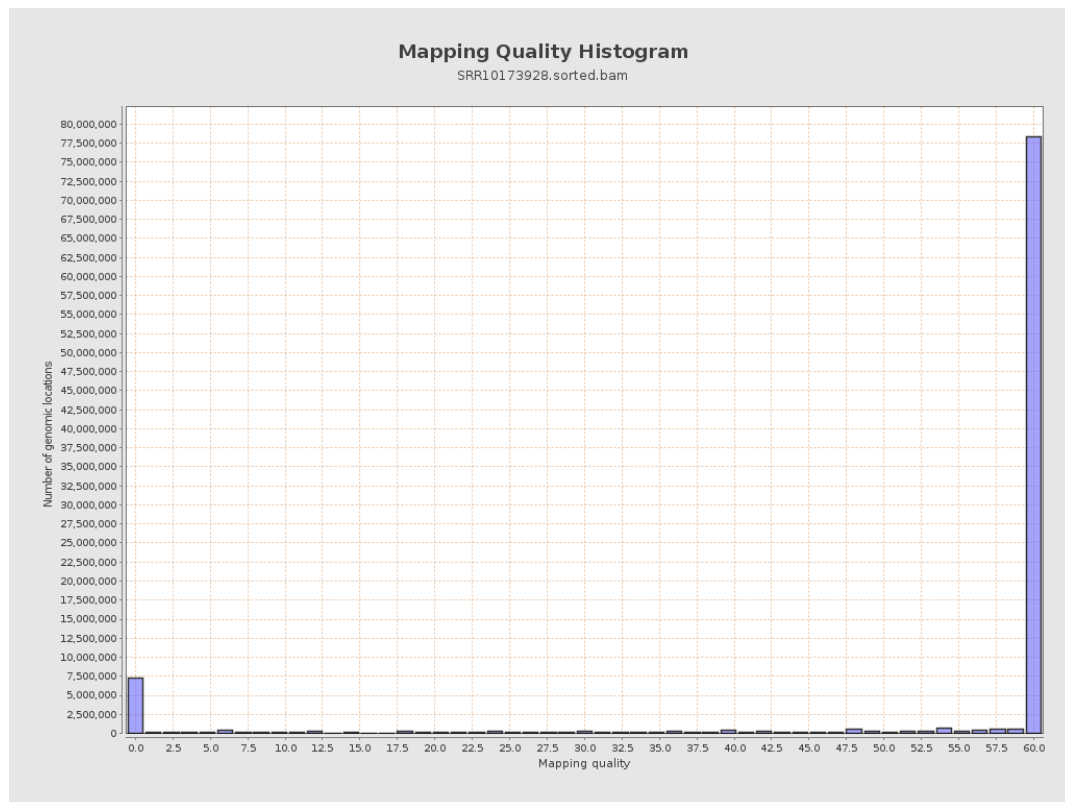
11. Results : Homopolymer Indels



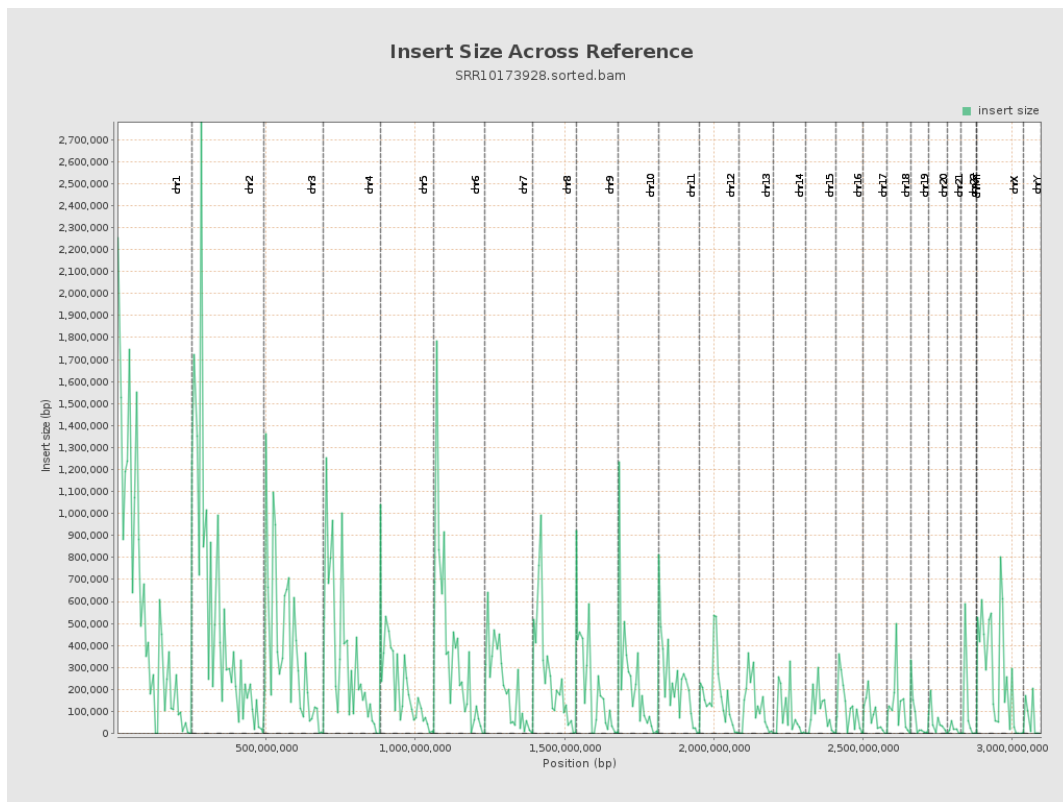
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

