

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:21:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174032.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_SRR10174032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174032_1.fastq.gz SRR10174032_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:21:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,798,912
Mapped reads	3,689,247 / 97.11%
Unmapped reads	109,665 / 2.89%
Mapped paired reads	3,689,247 / 97.11%
Mapped reads, first in pair	1,850,693 / 48.72%
Mapped reads, second in pair	1,838,554 / 48.4%
Mapped reads, both in pair	3,616,986 / 95.21%
Mapped reads, singletons	72,261 / 1.9%
Secondary alignments	0
Supplementary alignments	354,739 / 9.34%
Read min/max/mean length	30 / 133 / 128.11
Duplicated reads (estimated)	2,812,266 / 74.03%
Duplication rate	63.52%
Clipped reads	1,597,330 / 42.05%

2.2. ACGT Content

Number/percentage of A's	130,028,178 / 30.02%
Number/percentage of C's	85,172,761 / 19.67%
Number/percentage of T's	129,775,037 / 29.96%
Number/percentage of G's	88,110,875 / 20.34%
Number/percentage of N's	4,991 / 0%

GC Percentage	40.01%
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2.3. Coverage

Mean	0.14
Standard Deviation	2.0595

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	901,595.41
Standard Deviation	8,521,570.54
P25/Median/P75	146 / 202 / 290

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	4,523,394
Insertions	44,556
Mapped reads with at least one insertion	1.17%
Deletions	92,382
Mapped reads with at least one deletion	2.45%
Homopolymer indels	43.63%

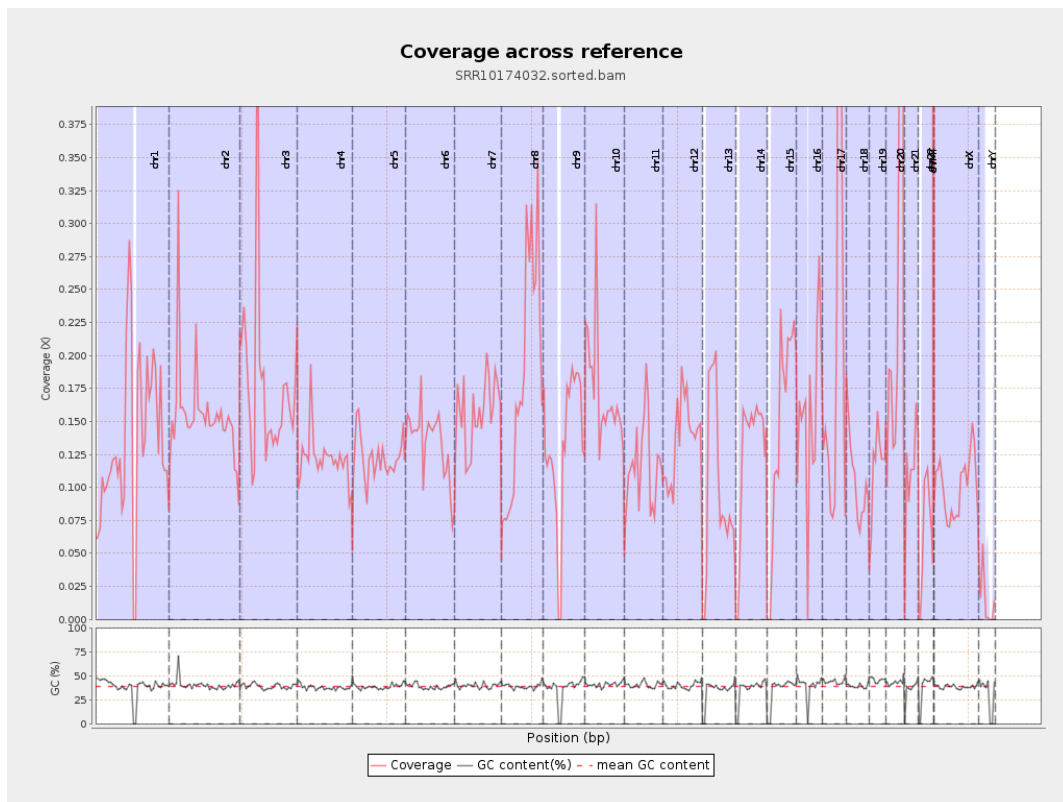
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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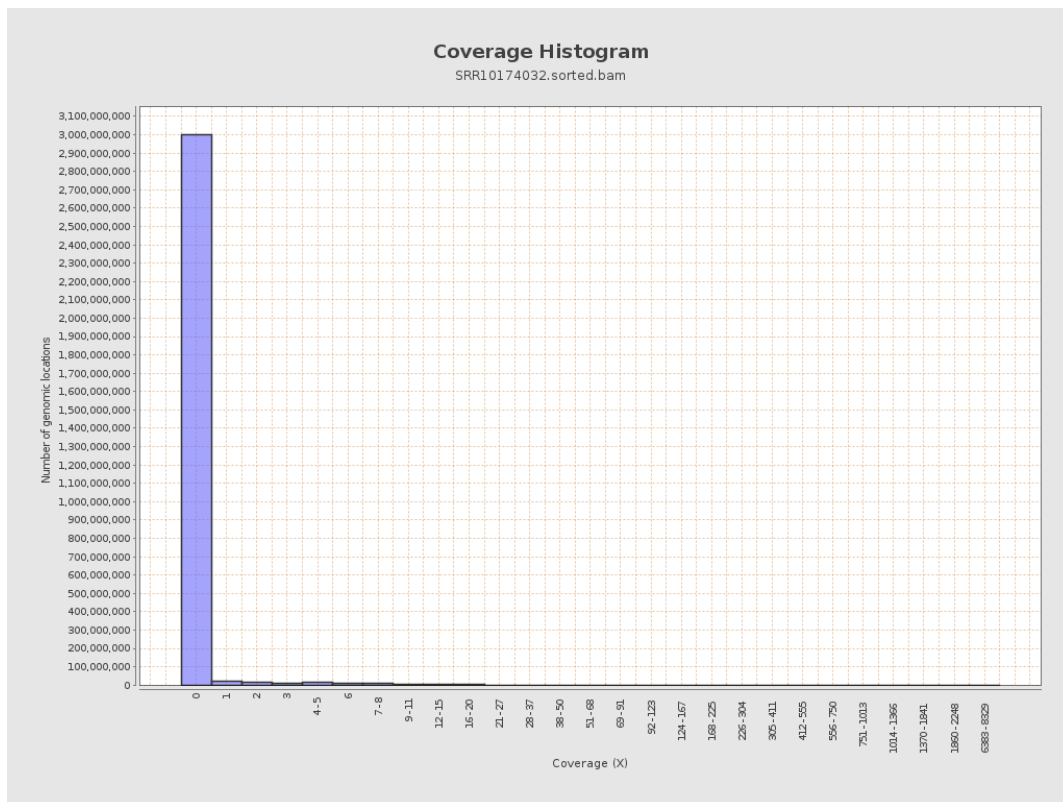
		bases	coverage	deviation
chr1	249250621	33579936	0.1347	1.5103
chr2	243199373	37722964	0.1551	5.892
chr3	198022430	34642126	0.1749	1.2058
chr4	191154276	23163178	0.1212	1.1282
chr5	180915260	22112669	0.1222	0.9895
chr6	171115067	22917344	0.1339	1.155
chr7	159138663	25111257	0.1578	1.4792
chr8	146364022	26641783	0.182	1.5174
chr9	141213431	18384432	0.1302	1.215
chr10	135534747	23396349	0.1726	2.057
chr11	135006516	15747797	0.1166	0.9801
chr12	133851895	18302451	0.1367	1.0536
chr13	115169878	11188895	0.0972	0.8833
chr14	107349540	13376754	0.1246	0.9955
chr15	102531392	14867674	0.145	1.0698
chr16	90354753	14324072	0.1585	1.336
chr17	81195210	17809211	0.2193	1.4083
chr18	78077248	8287941	0.1062	1.6504
chr19	59128983	6958560	0.1177	1.2534
chr20	63025520	18547067	0.2943	1.636
chr21	48129895	5382381	0.1118	0.9681
chr22	51304566	3267681	0.0637	0.6756
chrMT	16571	1062282	64.1049	49.8162
chrX	155270560	15706718	0.1012	0.9003

chrY	59373566	823835	0.0139	0.5568
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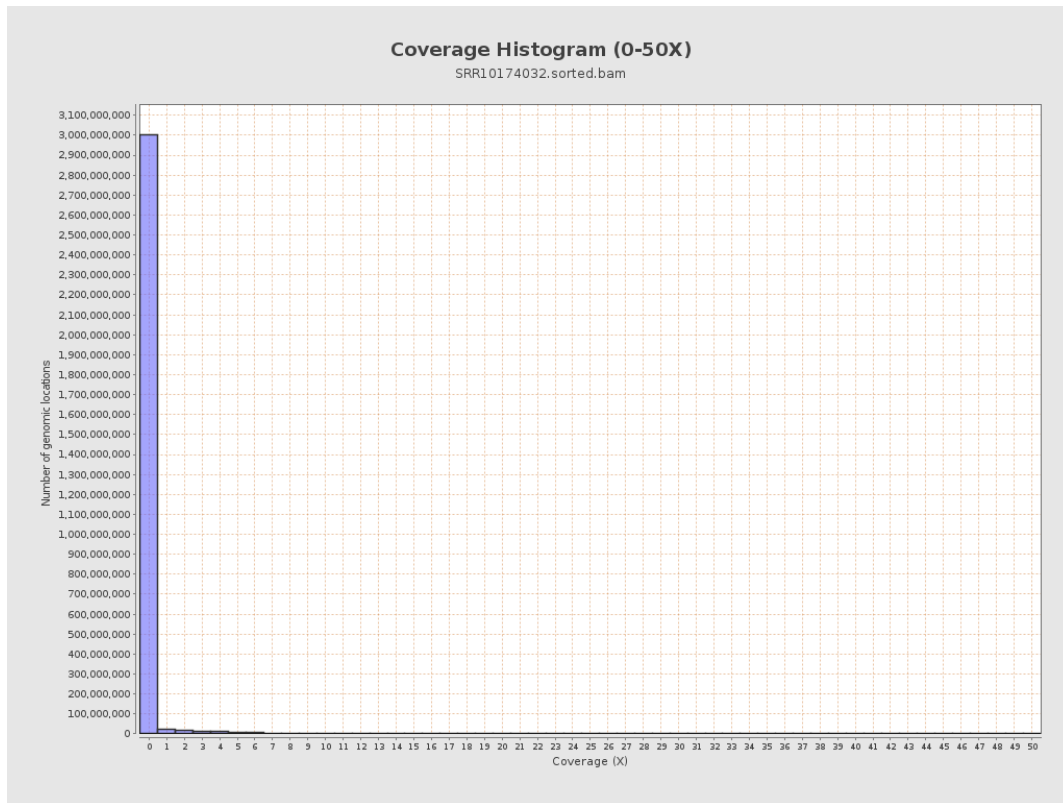
3. Results : Coverage across reference



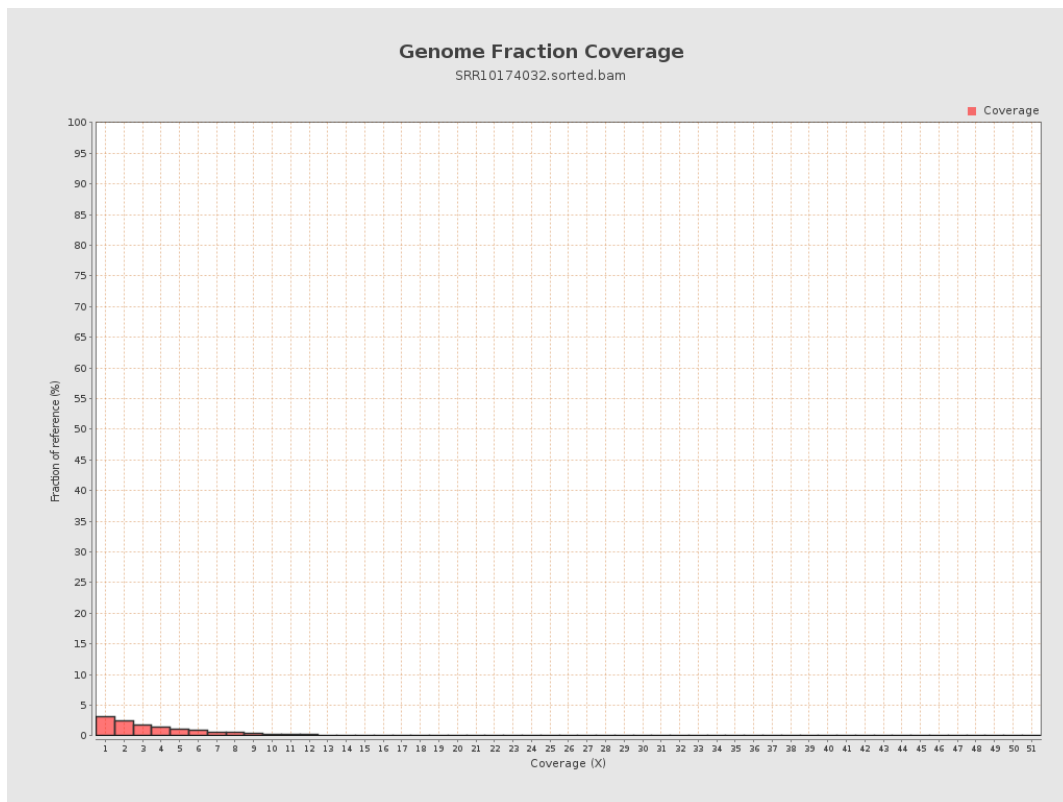
4. Results : Coverage Histogram



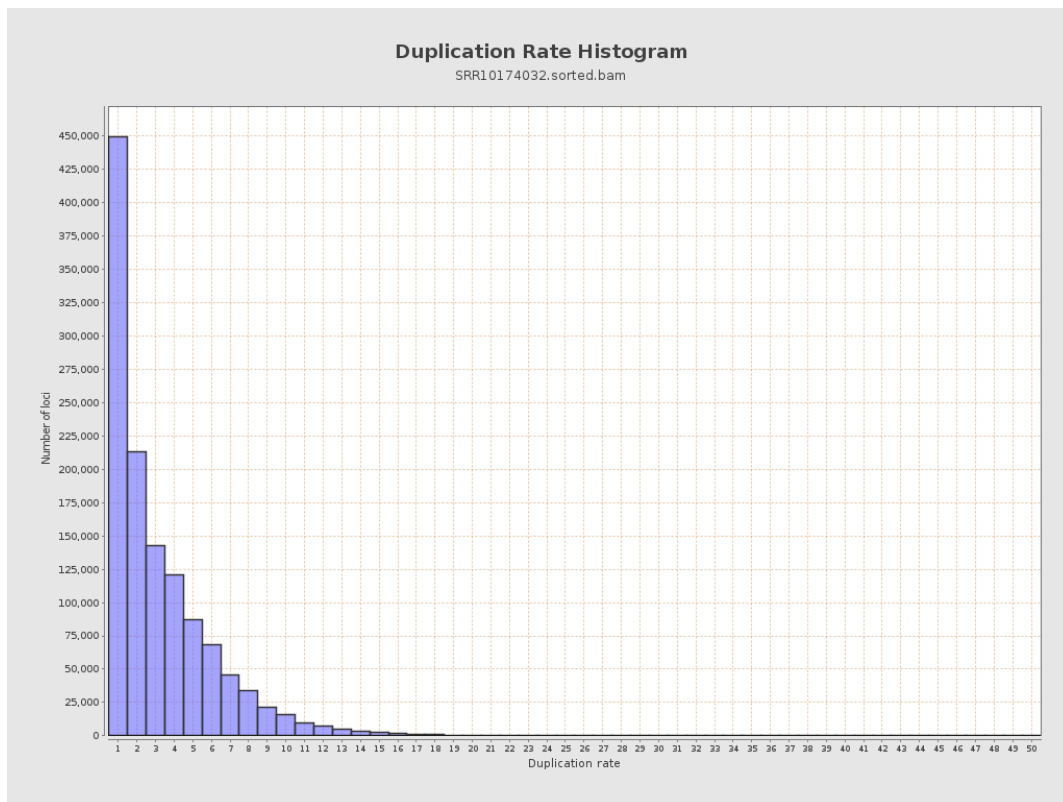
5. Results : Coverage Histogram (0-50X)



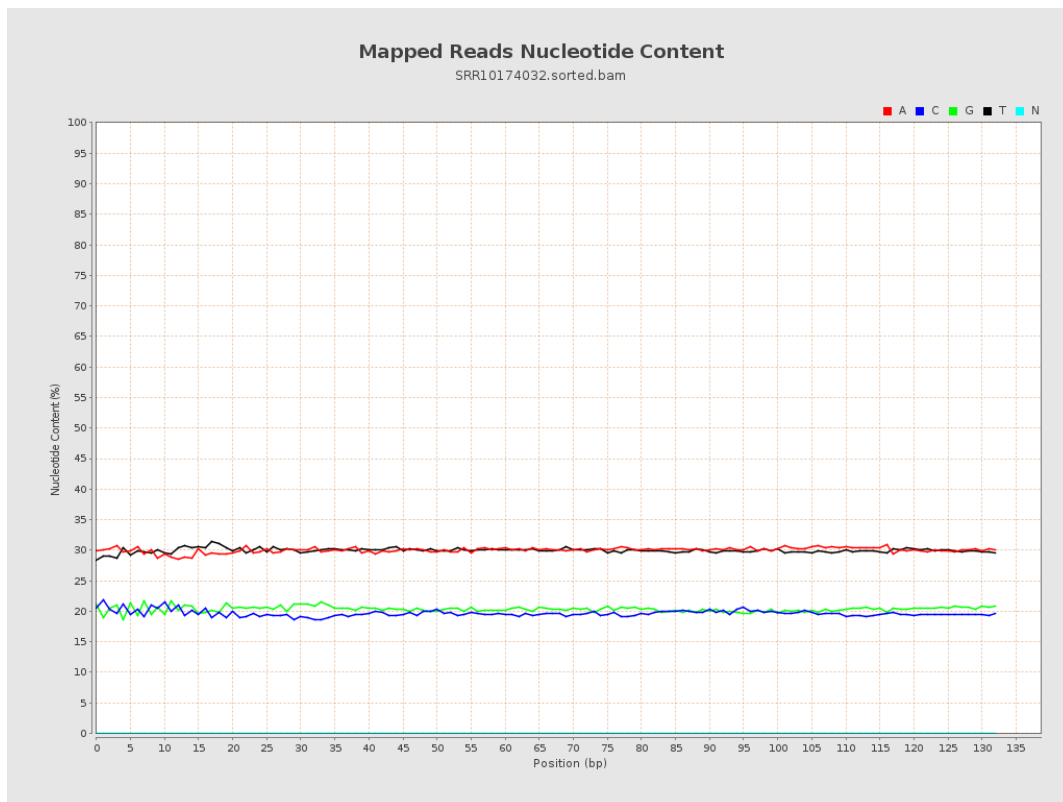
6. Results : Genome Fraction Coverage



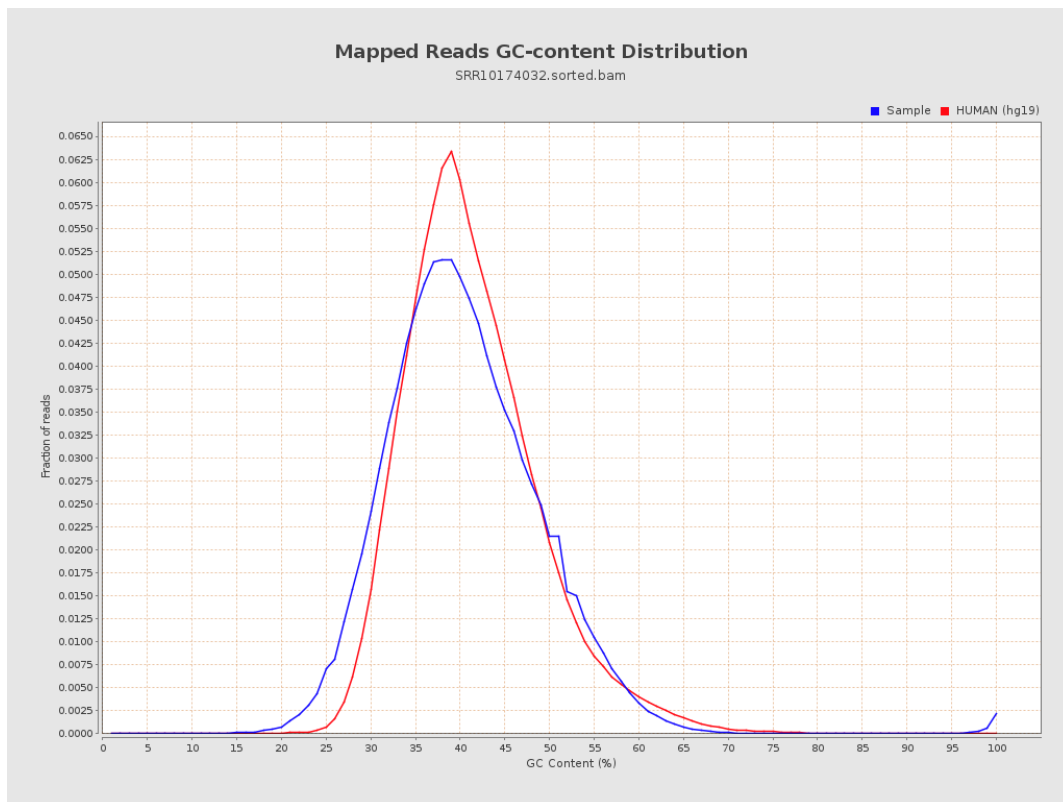
7. Results : Duplication Rate Histogram



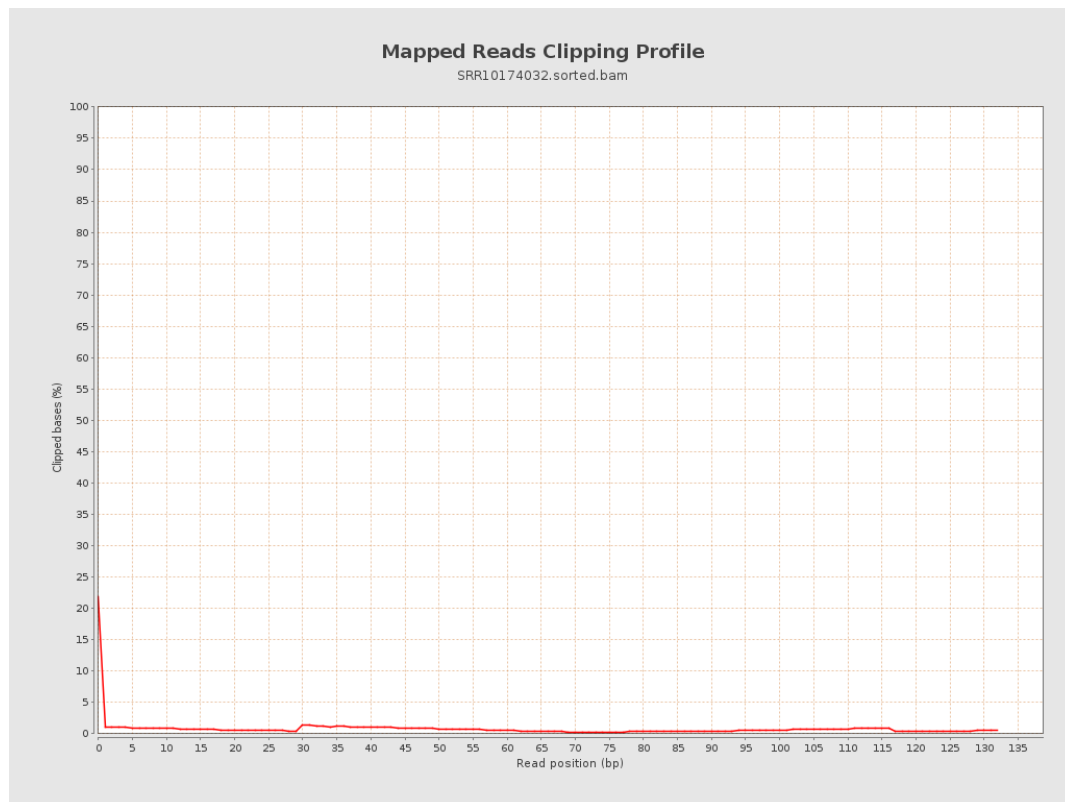
8. Results : Mapped Reads Nucleotide Content



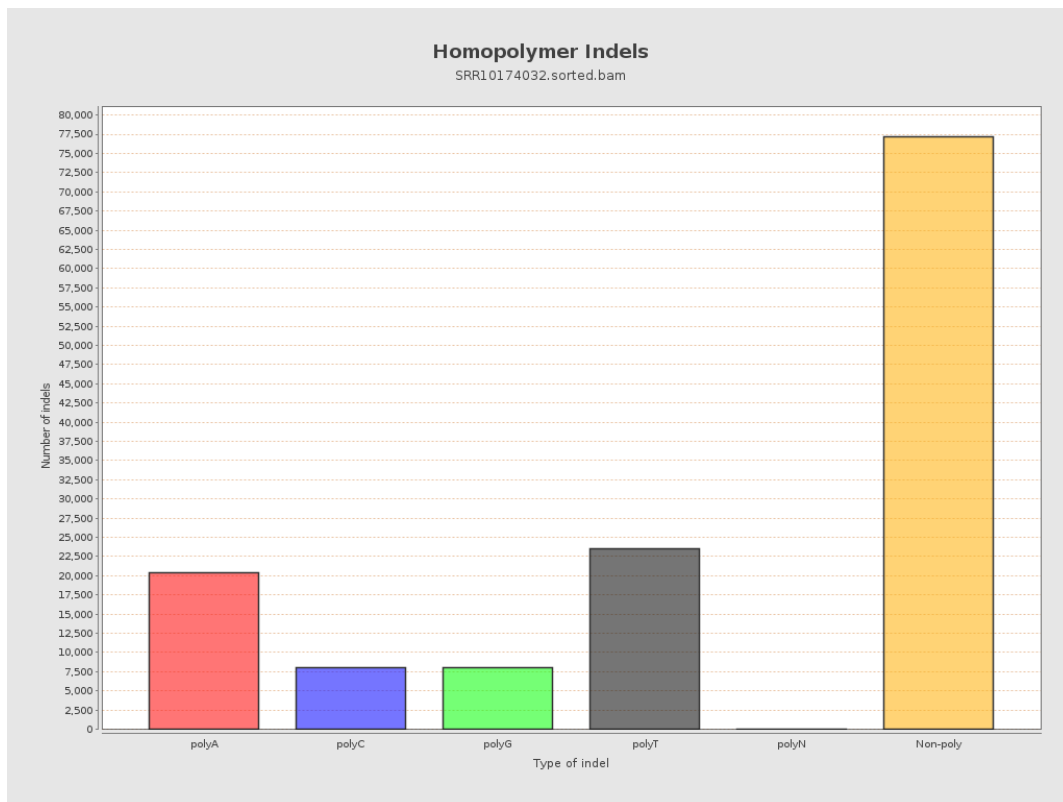
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



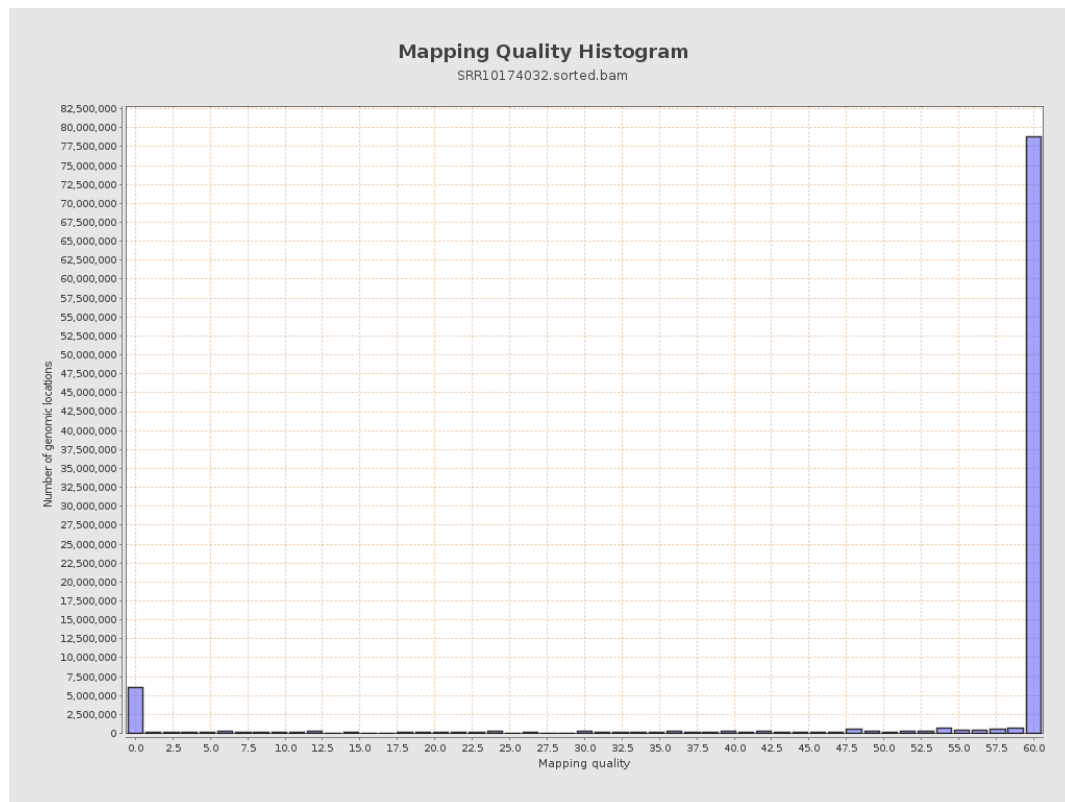
11. Results : Homopolymer Indels



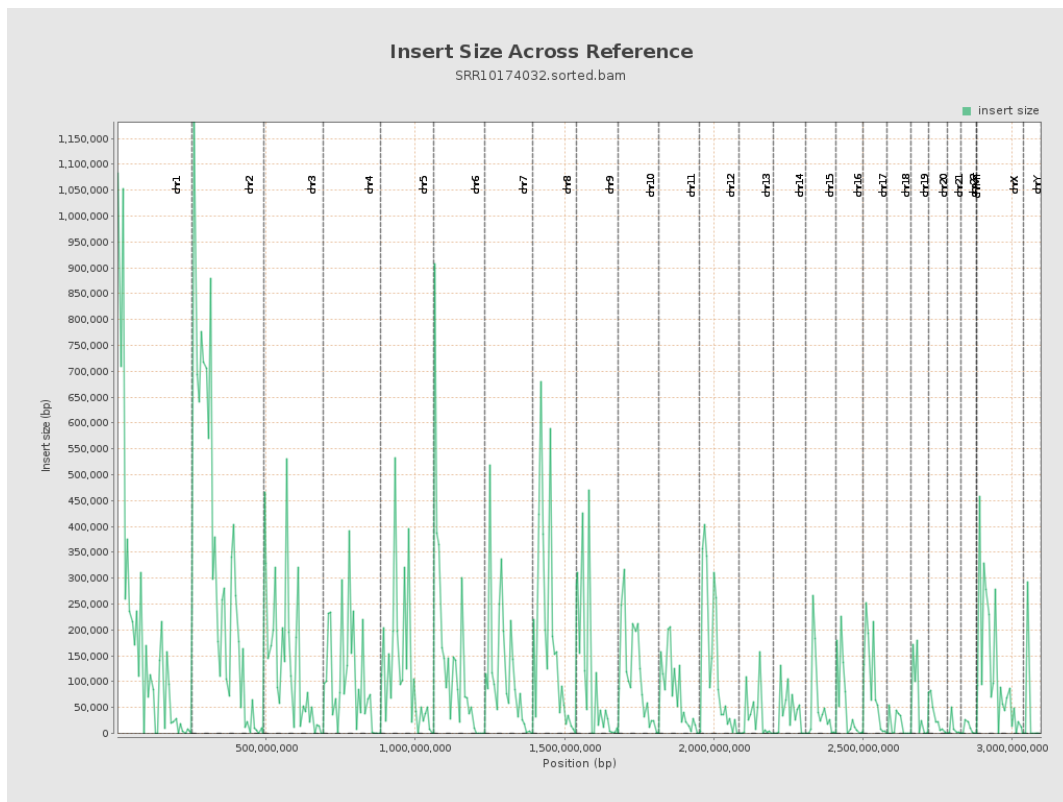
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

