

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:03:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124932.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_SRR3124932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124932_1.fastq.gz SRR3124932_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,153,068
Mapped reads	7,078,208 / 98.95%
Unmapped reads	74,860 / 1.05%
Mapped paired reads	7,078,208 / 98.95%
Mapped reads, first in pair	3,541,468 / 49.51%
Mapped reads, second in pair	3,536,740 / 49.44%
Mapped reads, both in pair	7,054,134 / 98.62%
Mapped reads, singletons	24,074 / 0.34%
Secondary alignments	0
Supplementary alignments	33,916 / 0.47%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	408,614 / 5.71%
Duplication rate	3.1%
Clipped reads	4,229,657 / 59.13%

2.2. ACGT Content

Number/percentage of A's	186,896,435 / 28.95%
Number/percentage of C's	130,919,818 / 20.28%
Number/percentage of T's	186,925,890 / 28.95%
Number/percentage of G's	140,837,628 / 21.82%
Number/percentage of N's	10,580 / 0%

GC Percentage	42.09%
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2.3. Coverage

Mean	0.2087
Standard Deviation	2.0106

2.4. Mapping Quality

Mean Mapping Quality	52.85
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2.5. Insert size

Mean	69,468.47
Standard Deviation	2,516,849.46
P25/Median/P75	136 / 169 / 214

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	4,650,771
Insertions	107,914
Mapped reads with at least one insertion	1.49%
Deletions	204,190
Mapped reads with at least one deletion	2.83%
Homopolymer indels	45.82%

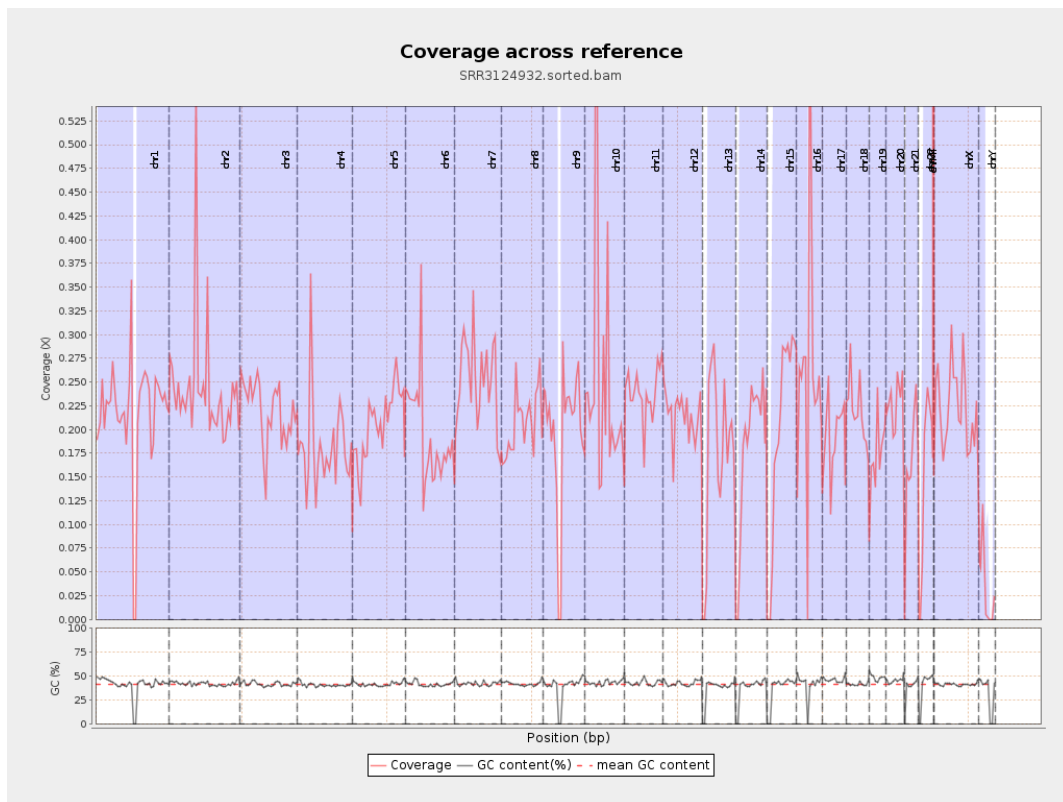
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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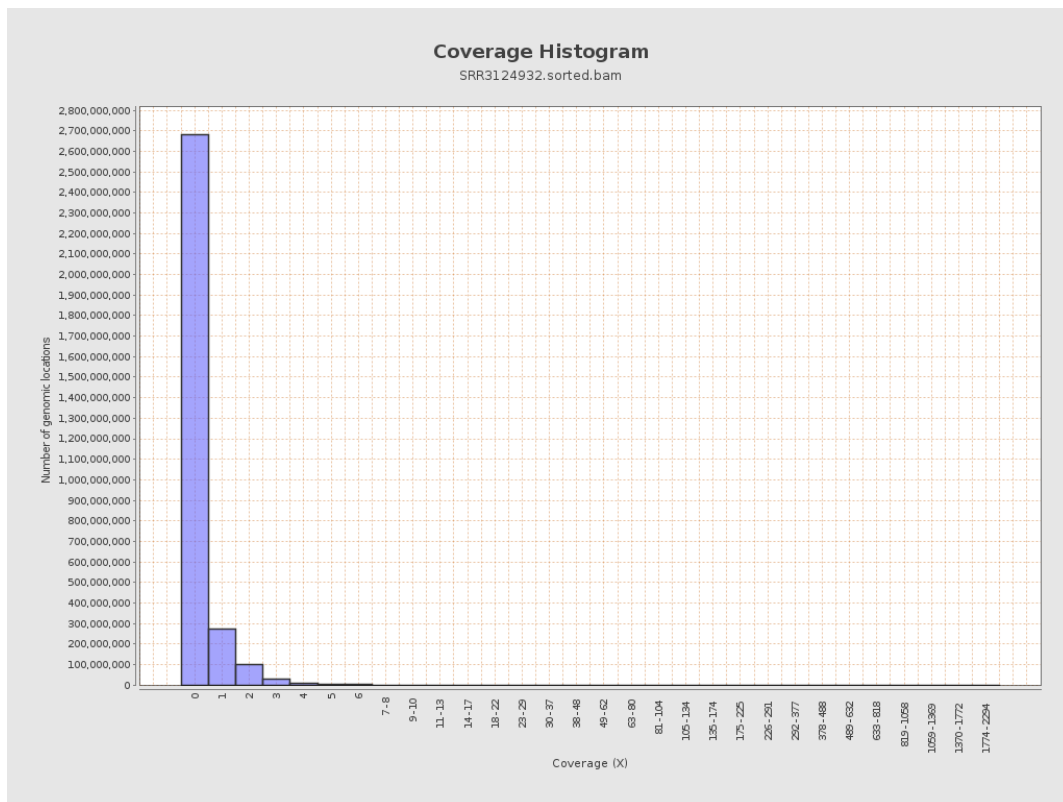
		bases	coverage	deviation
chr1	249250621	53873959	0.2161	2.388
chr2	243199373	59244266	0.2436	2.5349
chr3	198022430	43489753	0.2196	0.663
chr4	191154276	34337124	0.1796	1.355
chr5	180915260	37159753	0.2054	0.6327
chr6	171115067	33176020	0.1939	1.7821
chr7	159138663	40363014	0.2536	2.5469
chr8	146364022	30252553	0.2067	0.86
chr9	141213431	27744977	0.1965	2.913
chr10	135534747	33480867	0.247	4.8455
chr11	135006516	31920299	0.2364	1.5002
chr12	133851895	28654732	0.2141	0.6325
chr13	115169878	19784150	0.1718	0.5563
chr14	107349540	19227094	0.1791	0.6794
chr15	102531392	20374188	0.1987	0.6106
chr16	90354753	23284729	0.2577	3.2039
chr17	81195210	15505736	0.191	1.6422
chr18	78077248	17270177	0.2212	3.072
chr19	59128983	10402339	0.1759	1.4218
chr20	63025520	14200866	0.2253	0.7404
chr21	48129895	7986597	0.1659	0.8414
chr22	51304566	7570466	0.1476	0.566
chrMT	16571	157215	9.4874	5.7042
chrX	155270560	34574822	0.2227	1.1049

chrY	59373566	1907917	0.0321	1.7951
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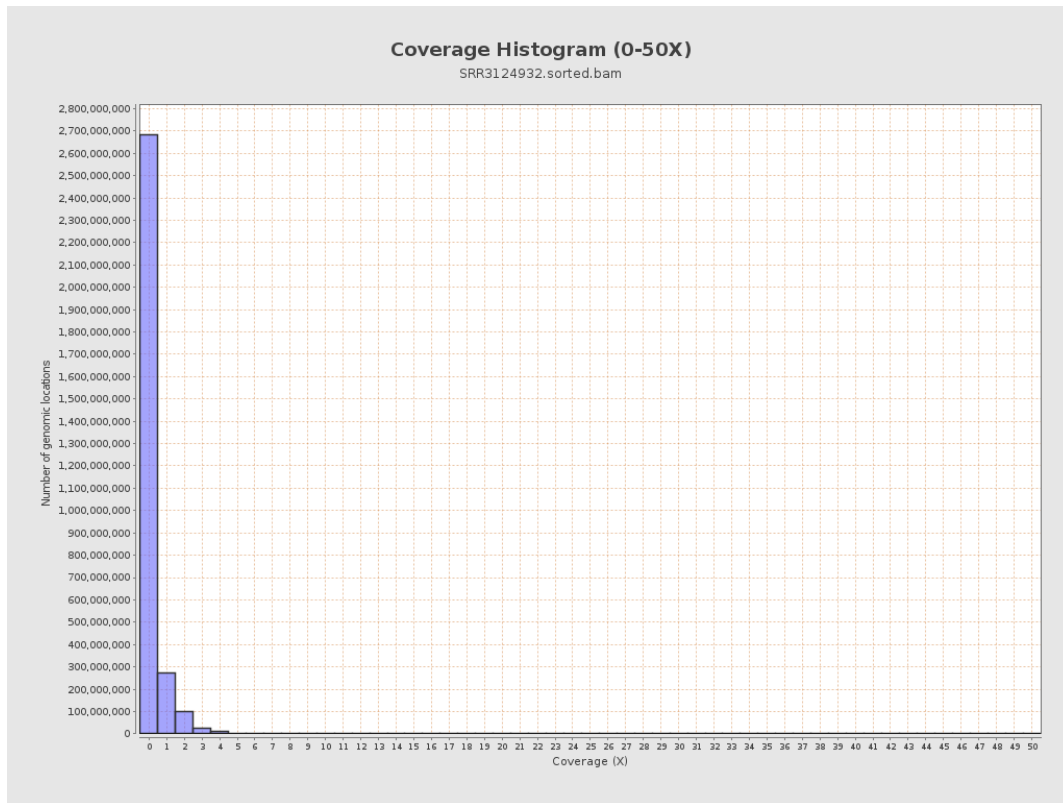
3. Results : Coverage across reference



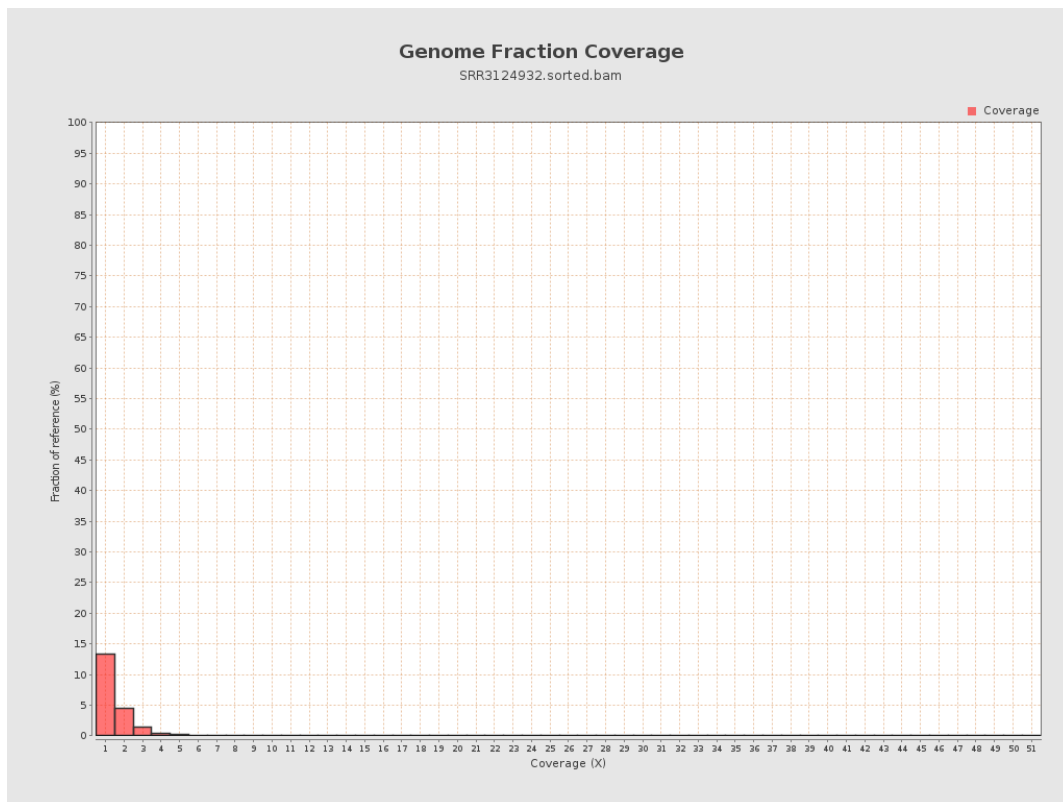
4. Results : Coverage Histogram



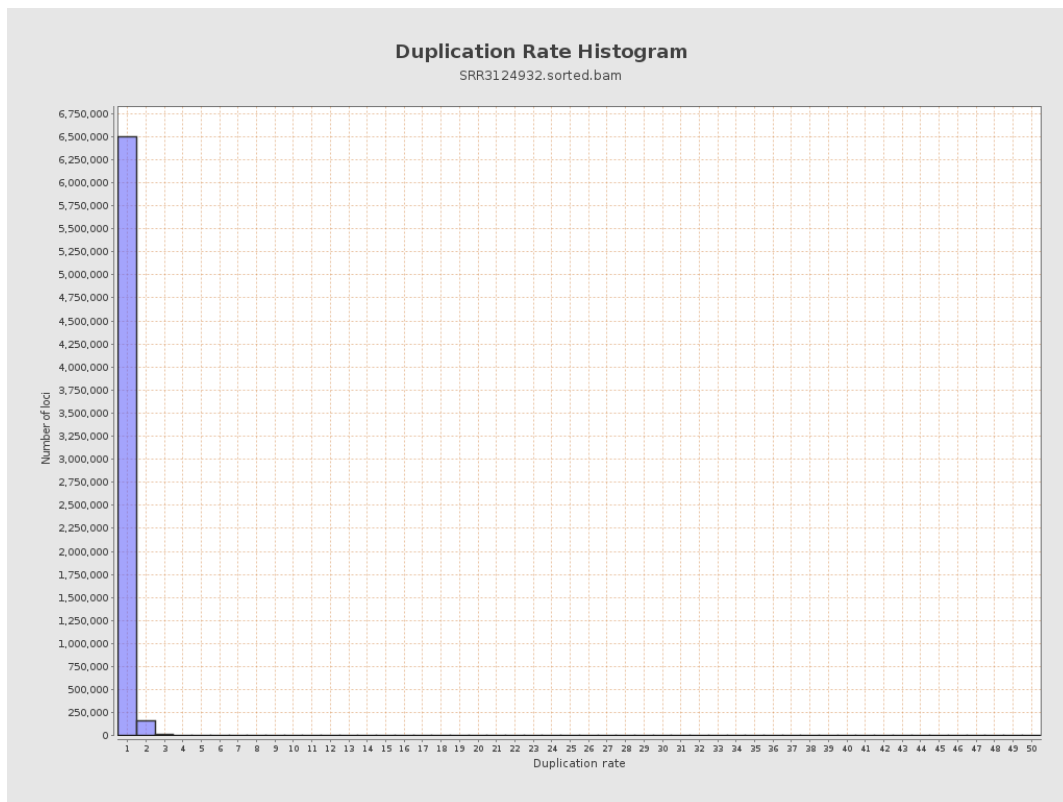
5. Results : Coverage Histogram (0-50X)



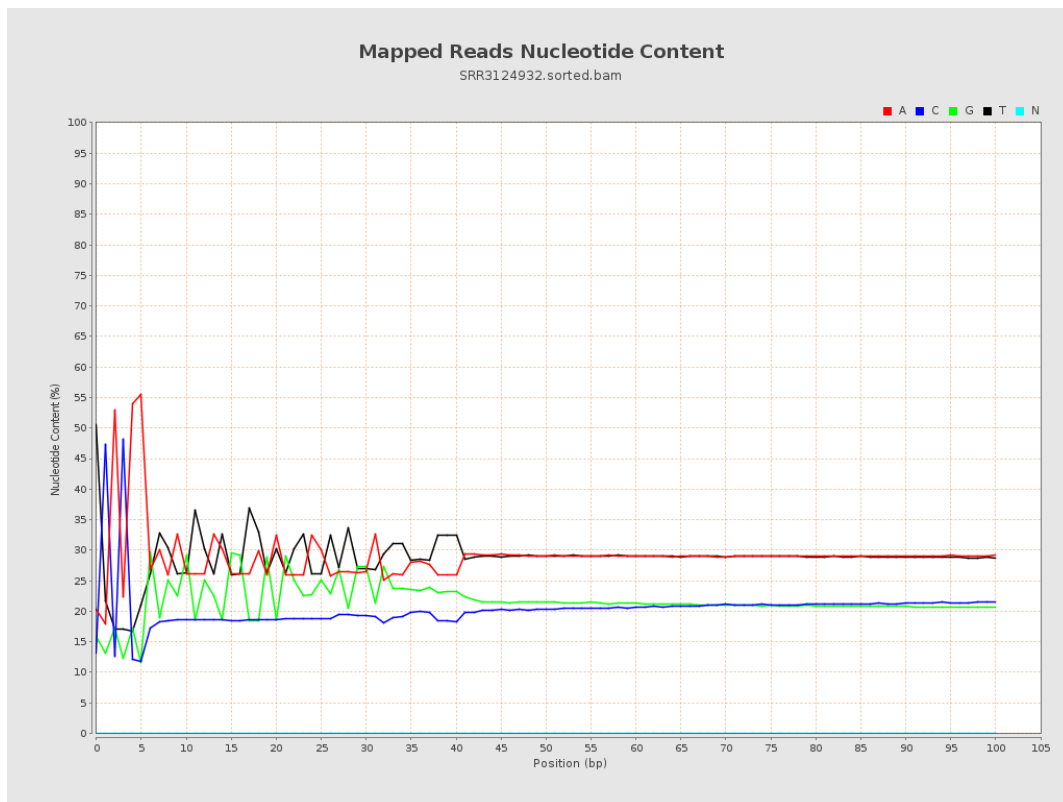
6. Results : Genome Fraction Coverage



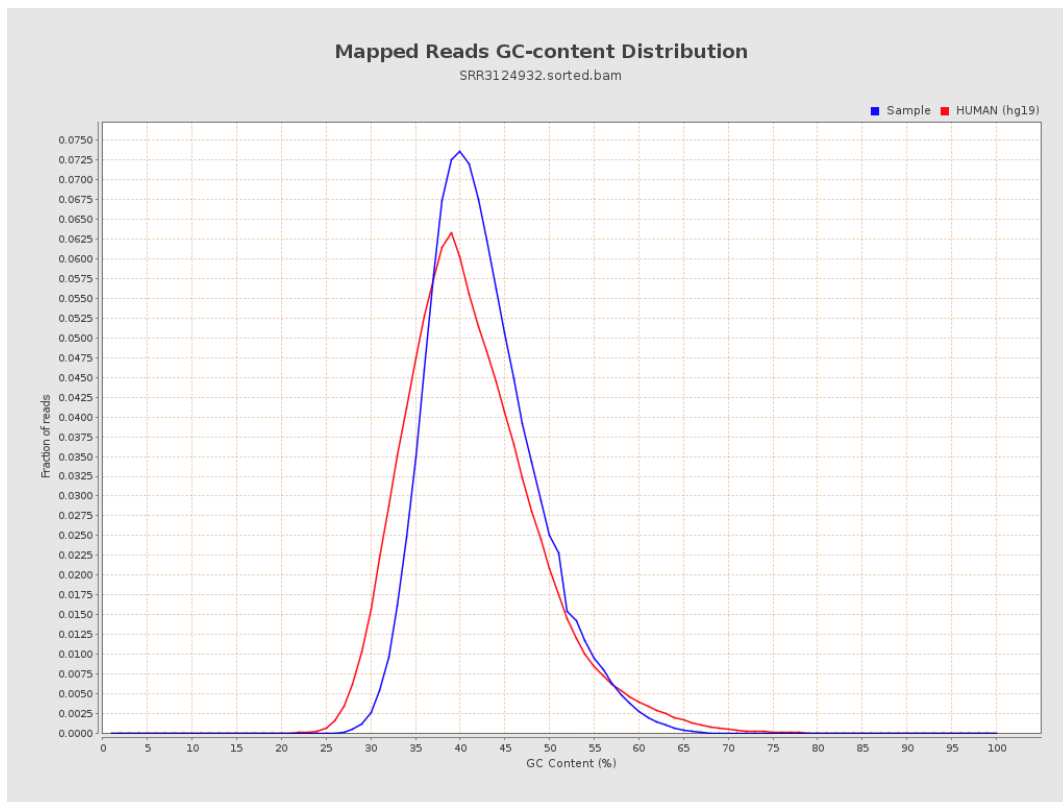
7. Results : Duplication Rate Histogram



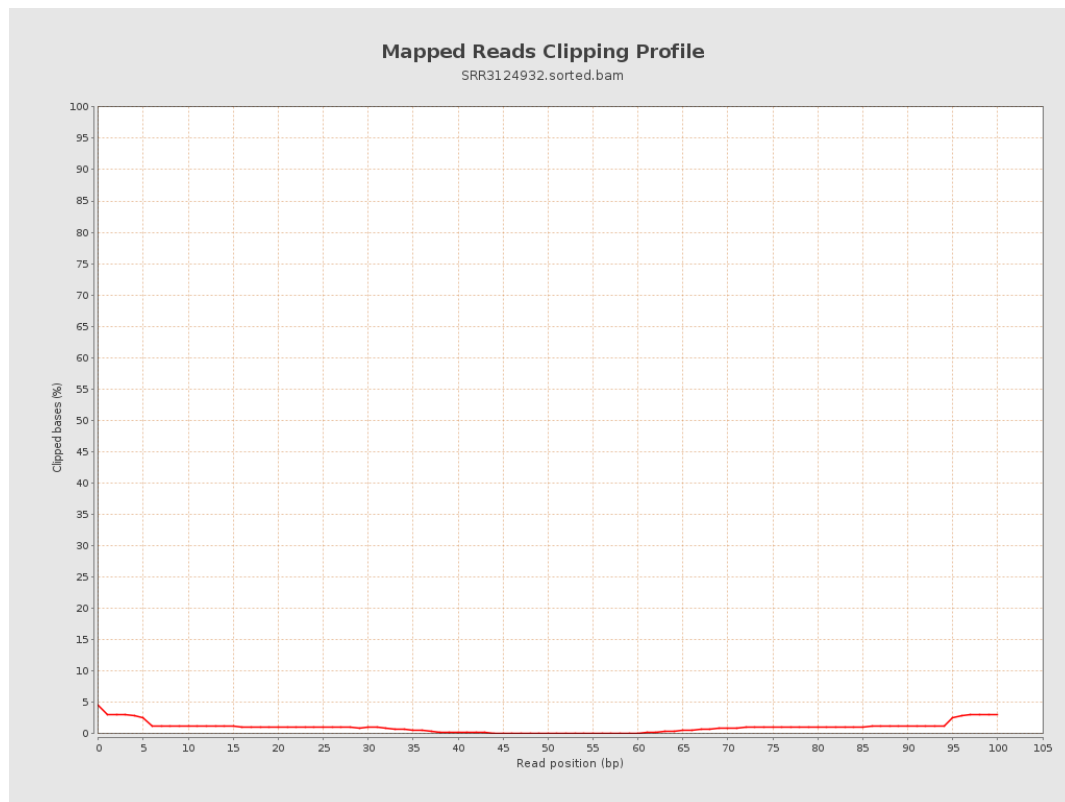
8. Results : Mapped Reads Nucleotide Content



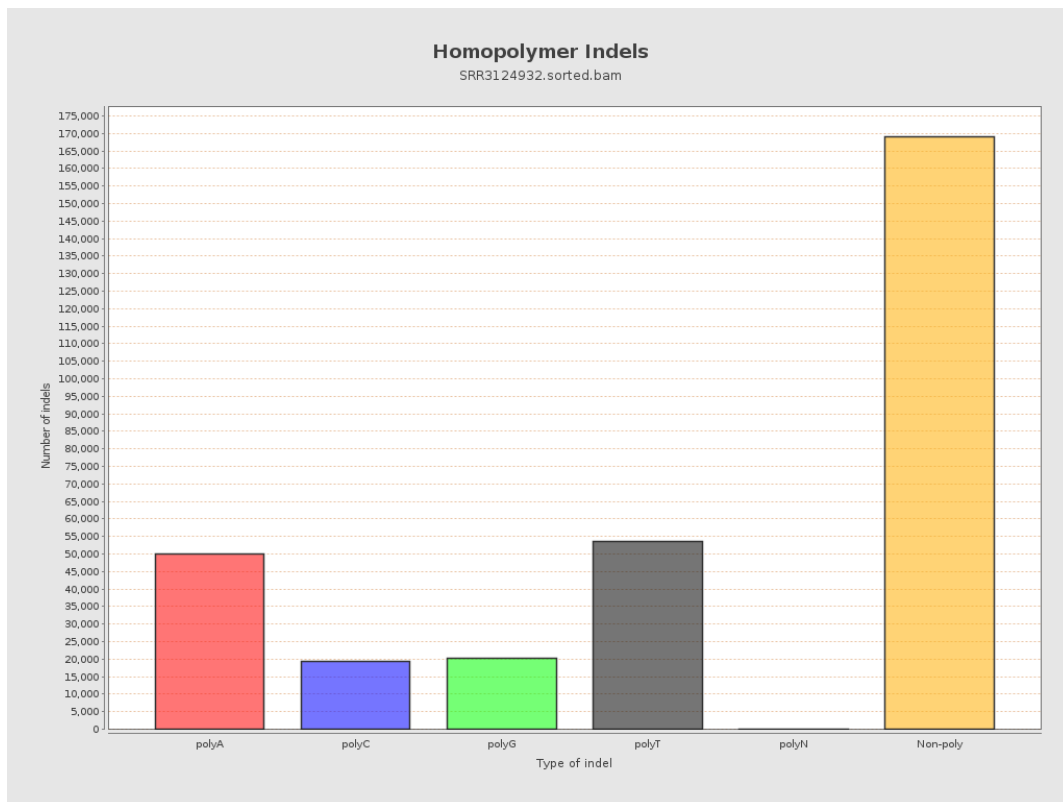
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



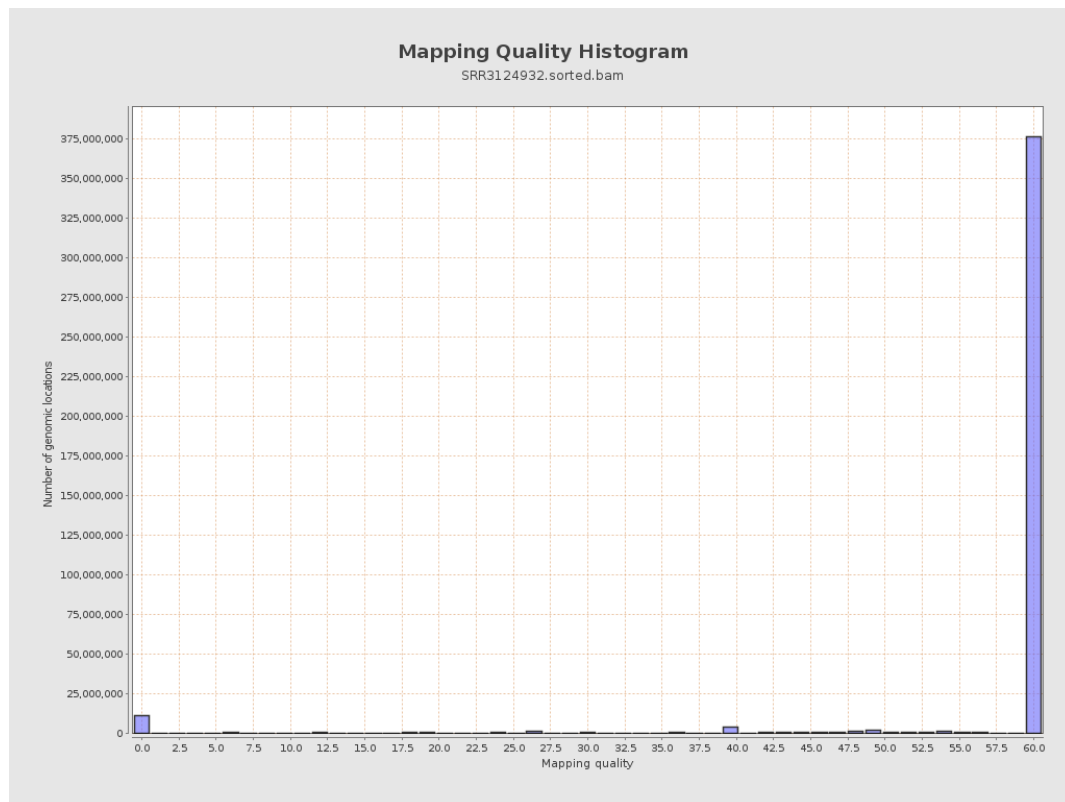
11. Results : Homopolymer Indels



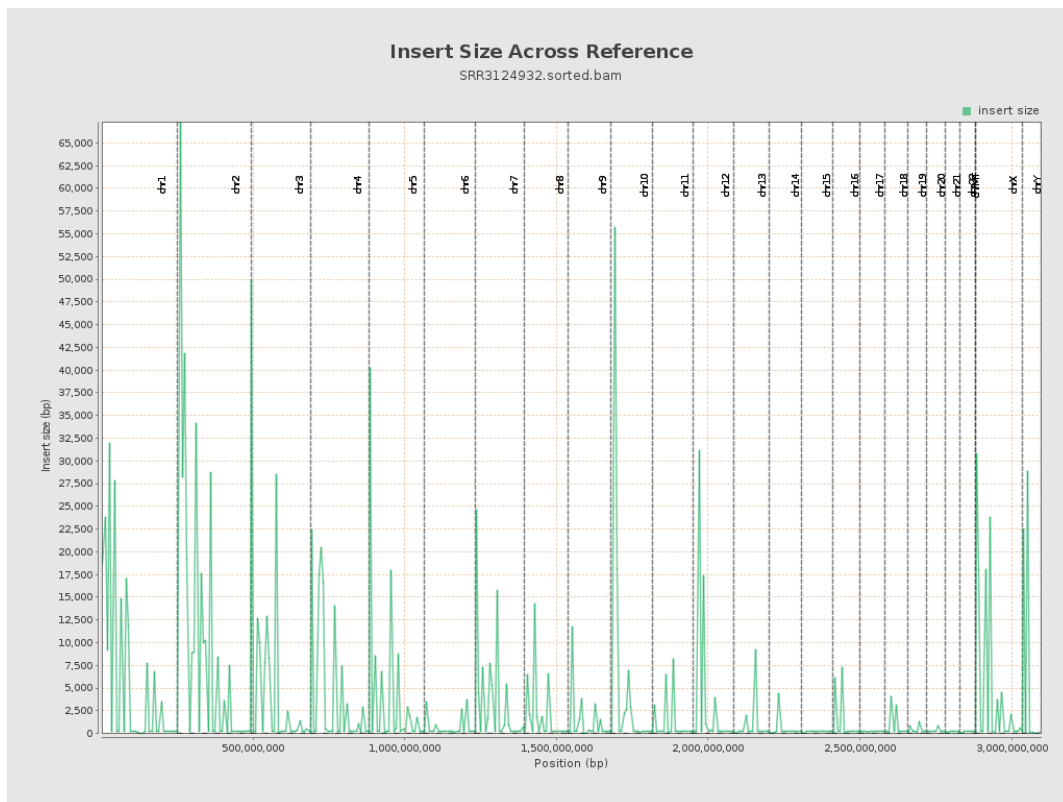
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

