

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:56:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173934.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_SRR10173934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173934_1.fastq.gz SRR10173934_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:56:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,415,316
Mapped reads	7,236,592 / 97.59%
Unmapped reads	178,724 / 2.41%
Mapped paired reads	7,236,592 / 97.59%
Mapped reads, first in pair	3,620,733 / 48.83%
Mapped reads, second in pair	3,615,859 / 48.76%
Mapped reads, both in pair	7,124,110 / 96.07%
Mapped reads, singletons	112,482 / 1.52%
Secondary alignments	0
Supplementary alignments	1,018,552 / 13.74%
Read min/max/mean length	30 / 133 / 126.13
Duplicated reads (estimated)	5,803,029 / 78.26%
Duplication rate	64.12%
Clipped reads	4,045,309 / 54.55%

2.2. ACGT Content

Number/percentage of A's	243,791,494 / 29.84%
Number/percentage of C's	161,966,355 / 19.82%
Number/percentage of T's	242,191,467 / 29.64%
Number/percentage of G's	169,093,518 / 20.7%
Number/percentage of N's	6,046 / 0%

GC Percentage	40.52%
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2.3. Coverage

Mean	0.2641
Standard Deviation	4.8657

2.4. Mapping Quality

Mean Mapping Quality	52.39
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2.5. Insert size

Mean	965,417.8
Standard Deviation	9,228,494.73
P25/Median/P75	105 / 155 / 238

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	7,274,999
Insertions	91,195
Mapped reads with at least one insertion	1.21%
Deletions	270,156
Mapped reads with at least one deletion	3.64%
Homopolymer indels	40.22%

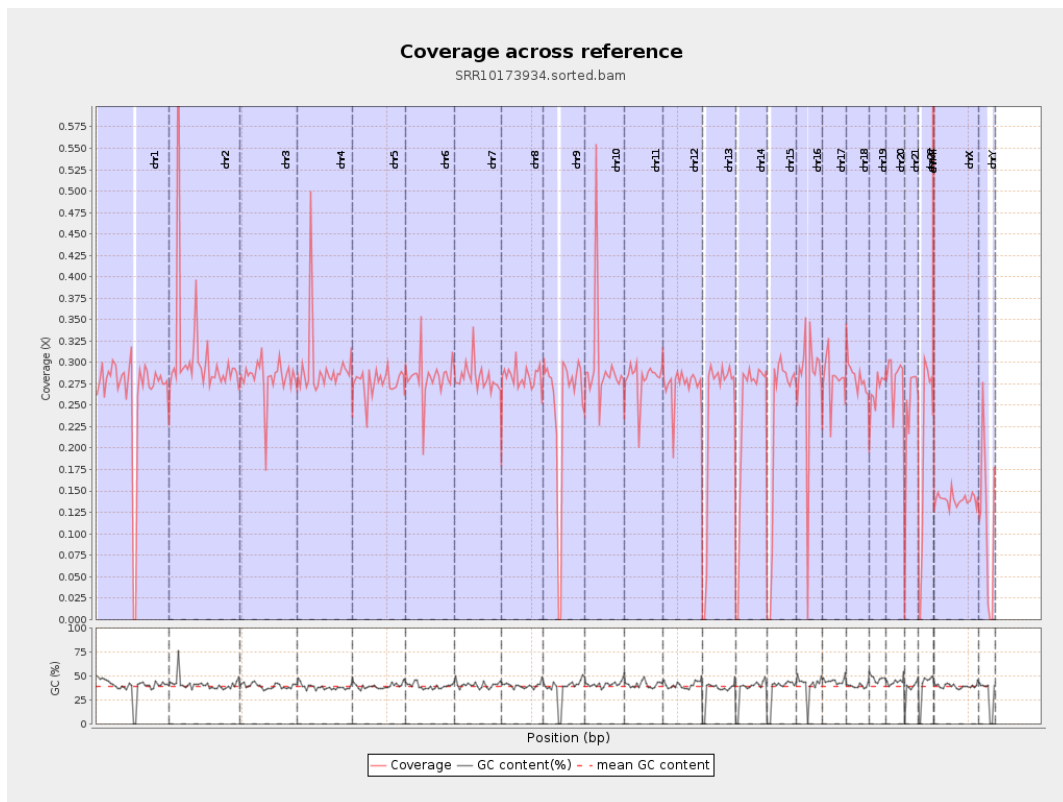
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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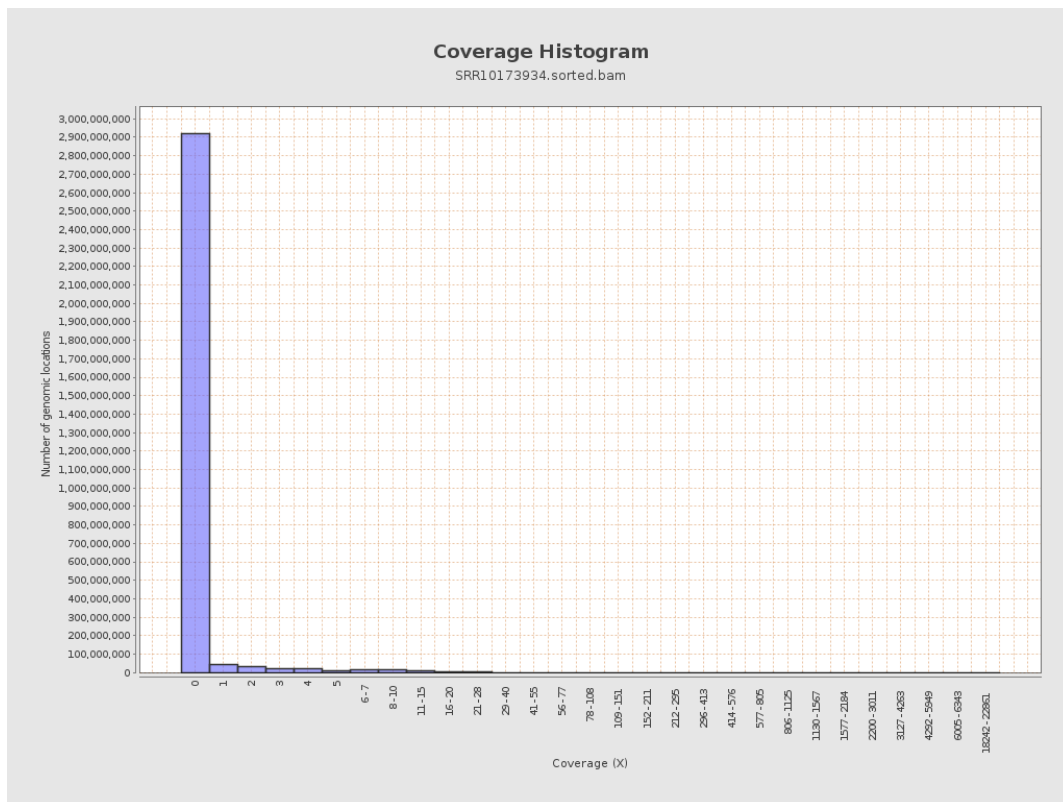
		bases	coverage	deviation
chr1	249250621	65781256	0.2639	2.3577
chr2	243199373	75048003	0.3086	15.9689
chr3	198022430	55910692	0.2823	1.5941
chr4	191154276	56056130	0.2933	2.2374
chr5	180915260	50044057	0.2766	1.5692
chr6	171115067	48423687	0.283	1.9048
chr7	159138663	44990282	0.2827	2.368
chr8	146364022	41377131	0.2827	2.5791
chr9	141213431	35107856	0.2486	2.0124
chr10	135534747	39996365	0.2951	2.876
chr11	135006516	38035778	0.2817	1.6509
chr12	133851895	36513295	0.2728	1.6375
chr13	115169878	27379354	0.2377	1.4655
chr14	107349540	25571776	0.2382	1.4877
chr15	102531392	23623999	0.2304	1.4856
chr16	90354753	24829155	0.2748	1.9819
chr17	81195210	22711243	0.2797	1.7059
chr18	78077248	22145349	0.2836	2.852
chr19	59128983	15797134	0.2672	1.8641
chr20	63025520	17741560	0.2815	1.6687
chr21	48129895	11513789	0.2392	1.9291
chr22	51304566	10177241	0.1984	1.5751
chrMT	16571	807598	48.7356	41.4344
chrX	155270560	21683149	0.1396	1.1256

chrY	59373566	6412441	0.108	1.7522
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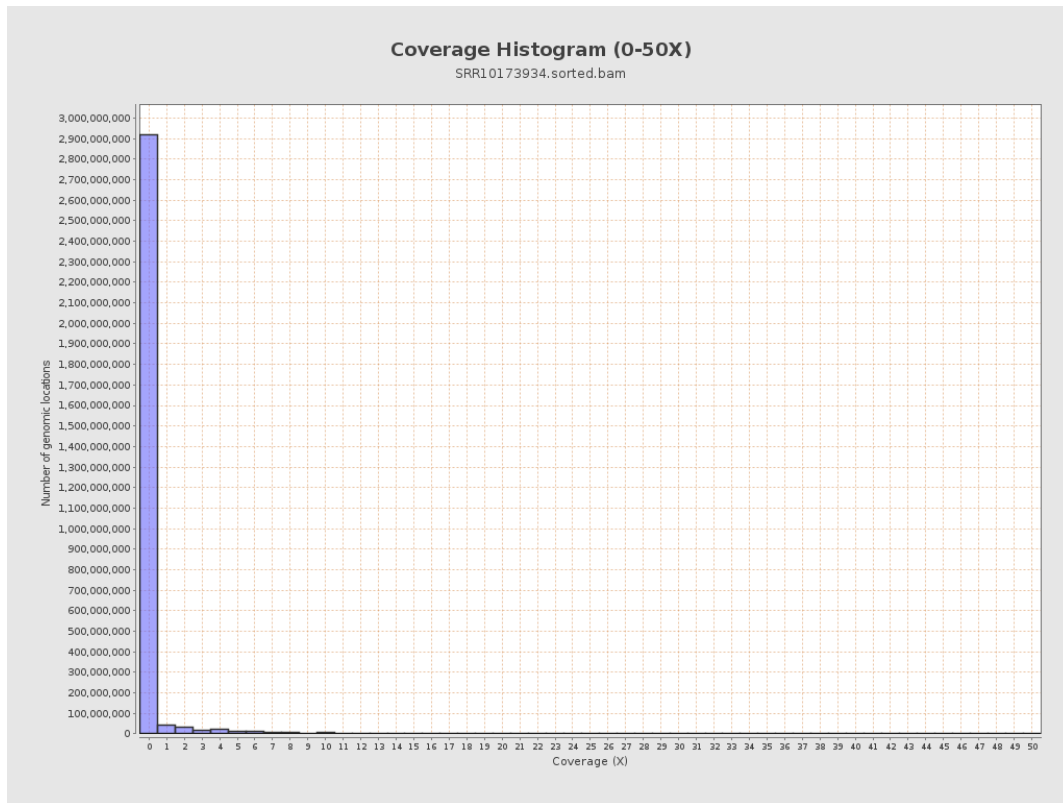
3. Results : Coverage across reference



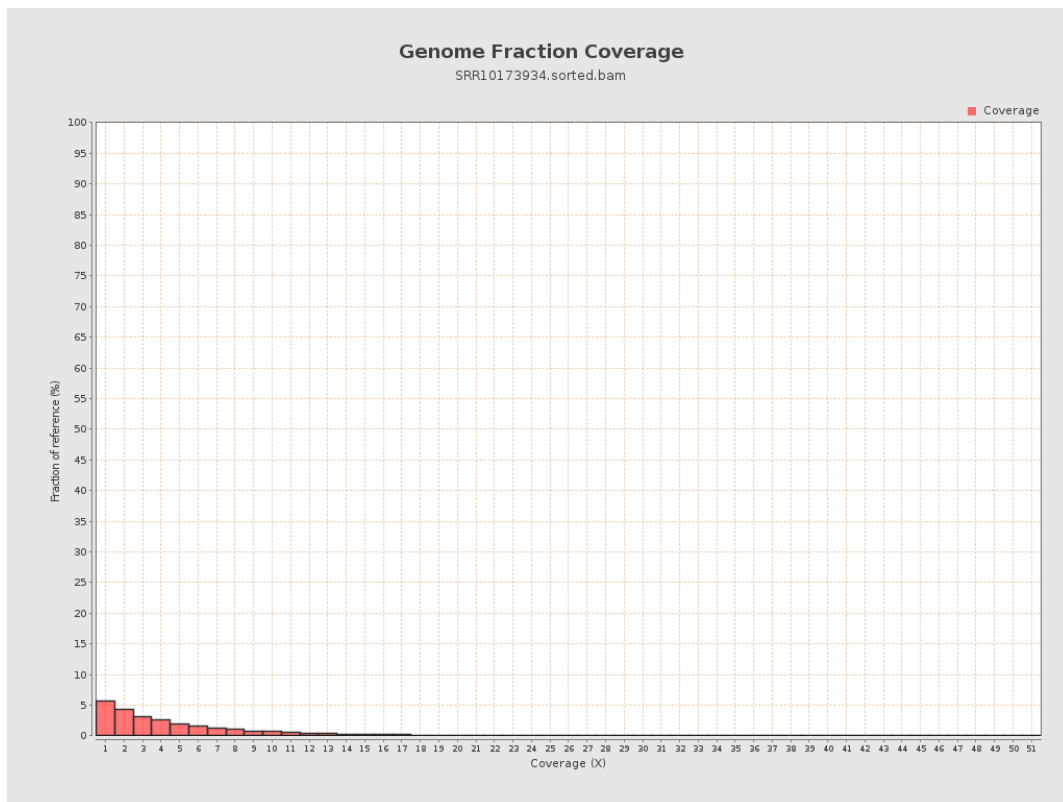
4. Results : Coverage Histogram



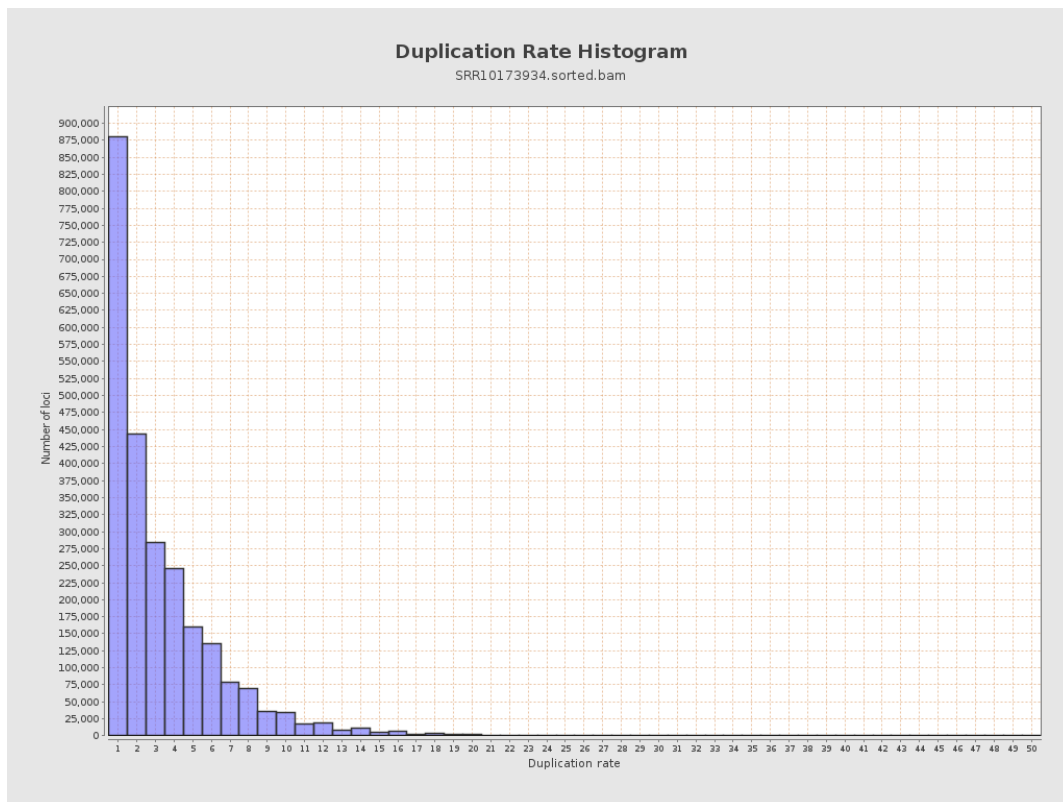
5. Results : Coverage Histogram (0-50X)



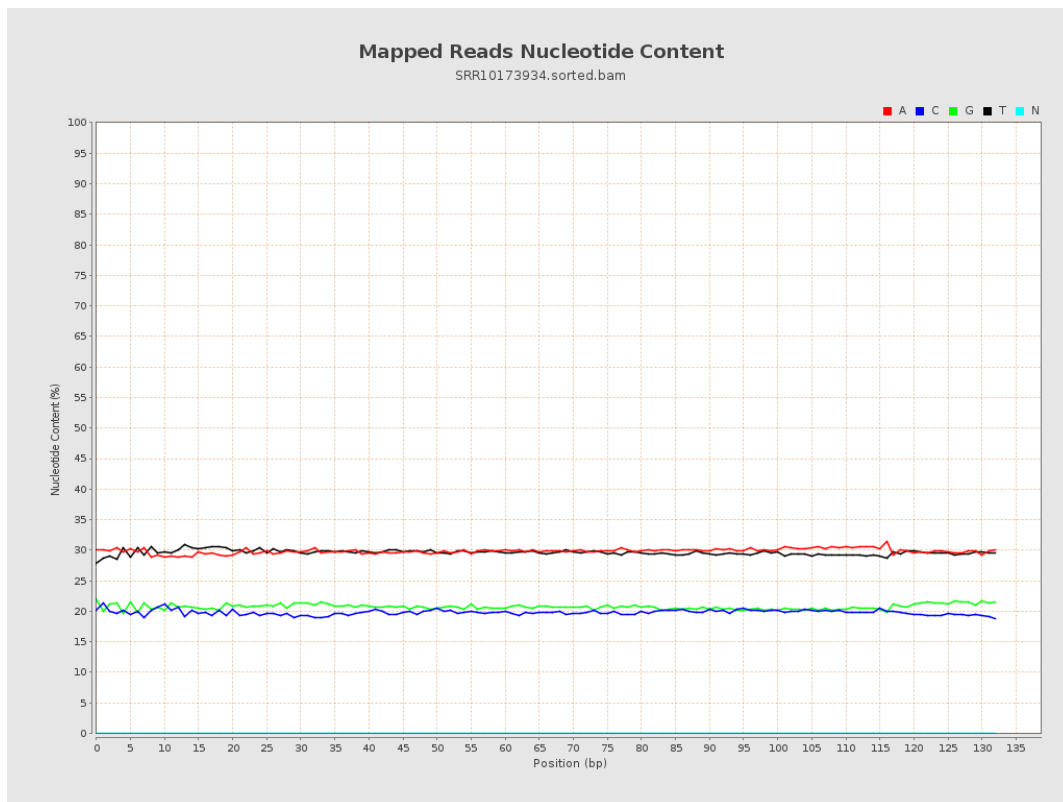
6. Results : Genome Fraction Coverage



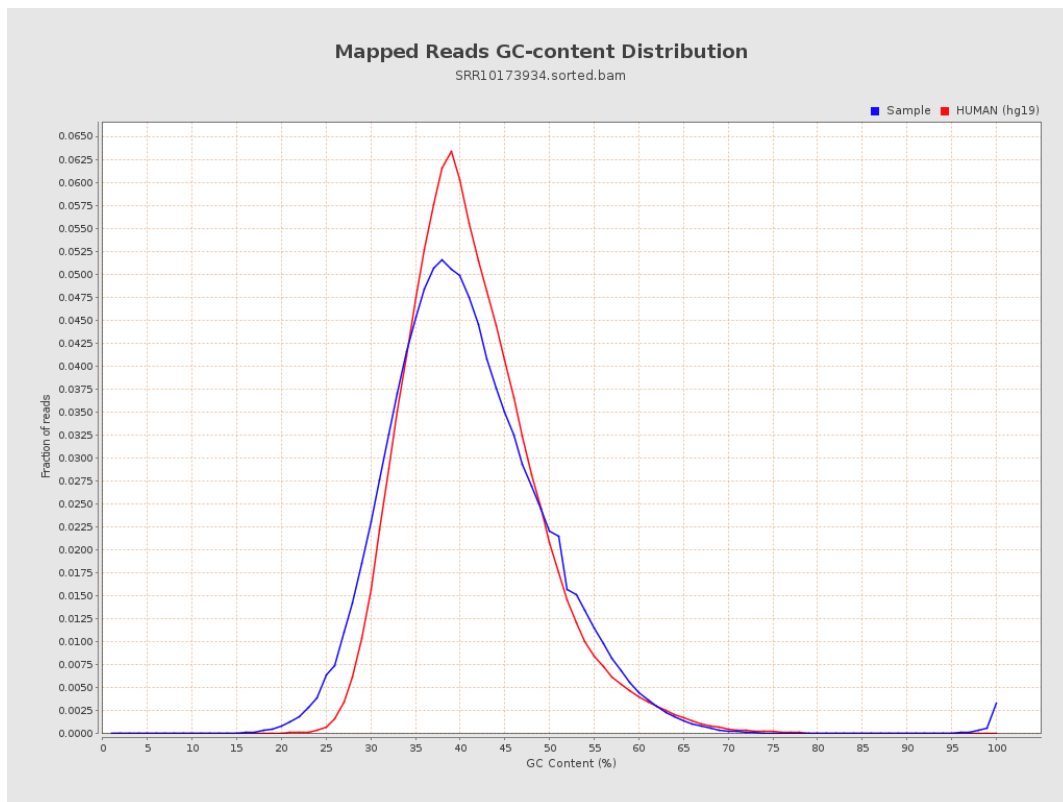
7. Results : Duplication Rate Histogram



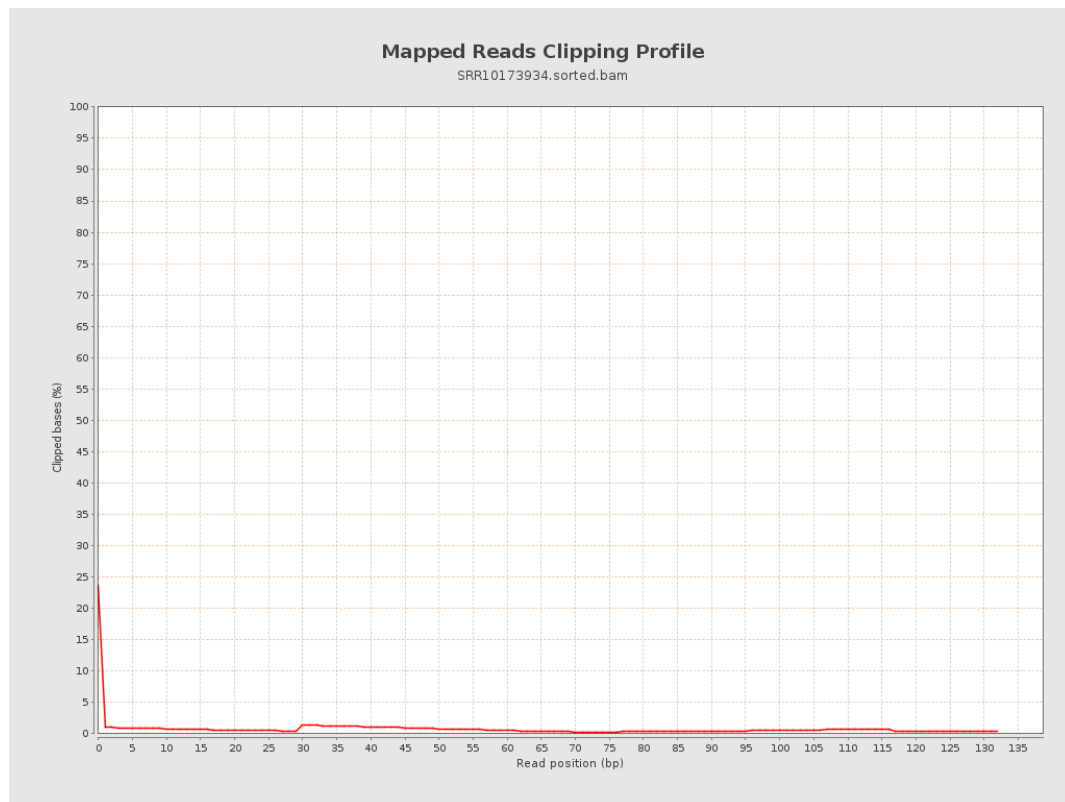
8. Results : Mapped Reads Nucleotide Content



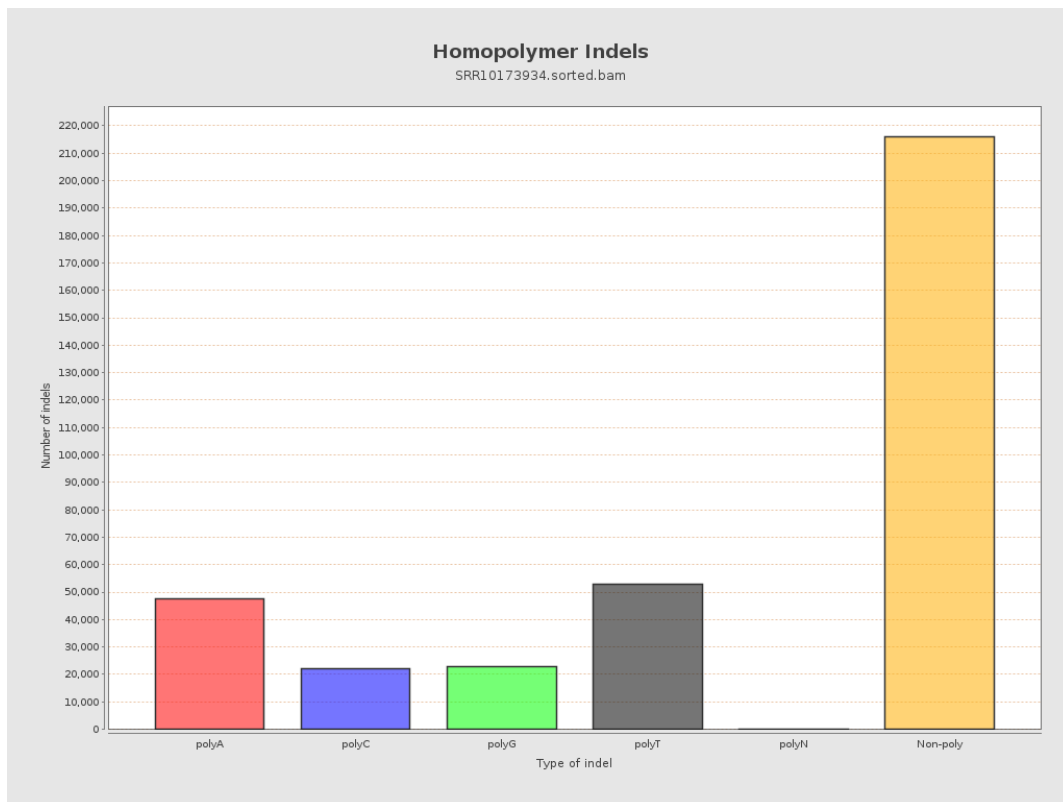
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



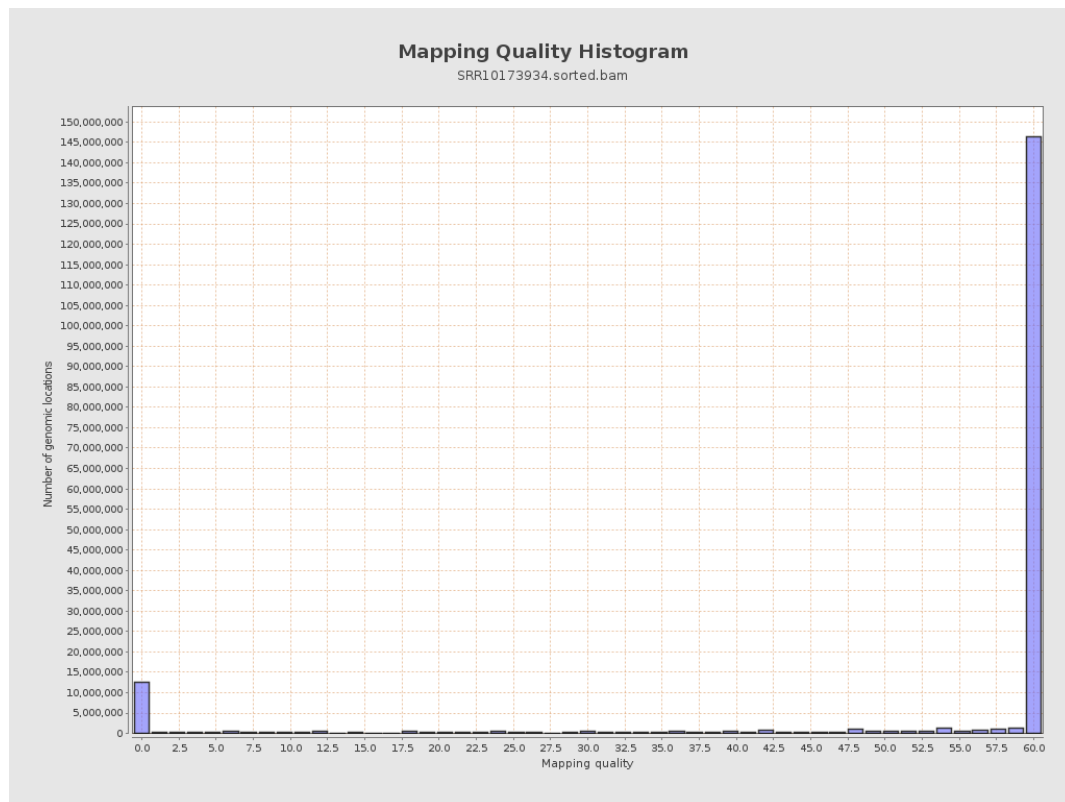
11. Results : Homopolymer Indels



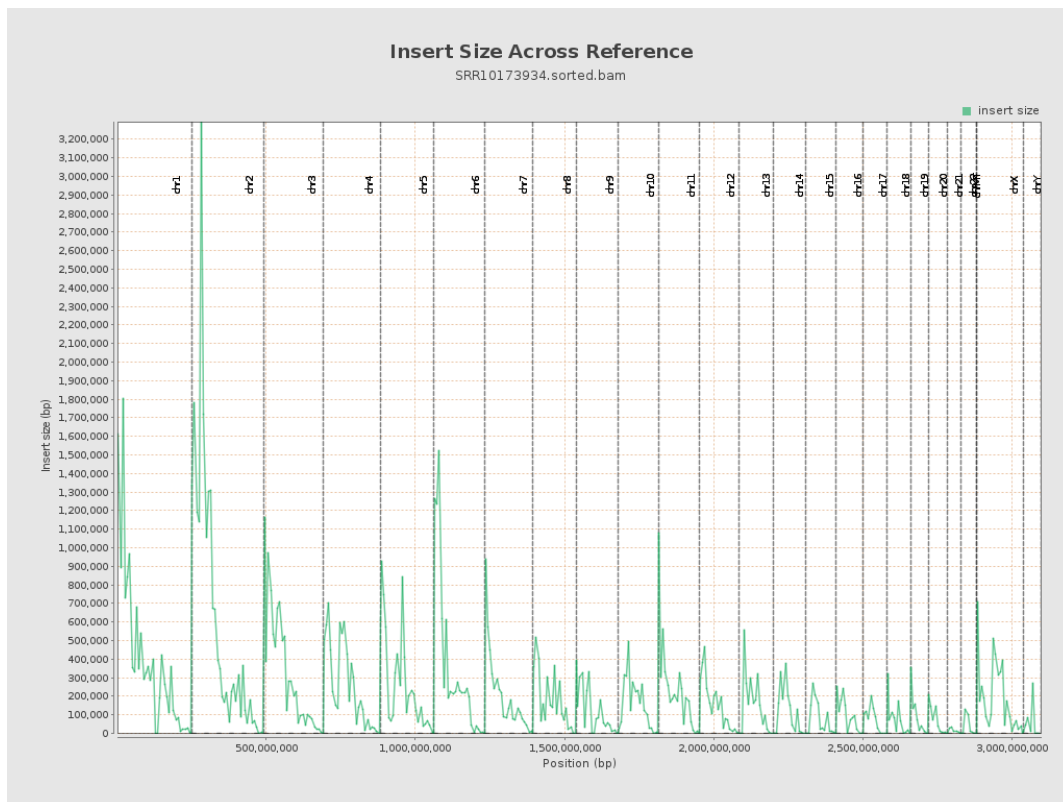
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

