

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 11:24:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173949.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_SRR10173949 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173949_1.fastq.gz SRR10173949_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 11:24:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,559,072
Mapped reads	13,207,738 / 97.41%
Unmapped reads	351,334 / 2.59%
Mapped paired reads	13,207,738 / 97.41%
Mapped reads, first in pair	6,611,210 / 48.76%
Mapped reads, second in pair	6,596,528 / 48.65%
Mapped reads, both in pair	12,981,610 / 95.74%
Mapped reads, singletons	226,128 / 1.67%
Secondary alignments	0
Supplementary alignments	1,814,580 / 13.38%
Read min/max/mean length	30 / 133 / 126.04
Duplicated reads (estimated)	10,774,947 / 79.47%
Duplication rate	65.51%
Clipped reads	6,992,313 / 51.57%

2.2. ACGT Content

Number/percentage of A's	444,442,748 / 29.72%
Number/percentage of C's	298,792,176 / 19.98%
Number/percentage of T's	440,874,303 / 29.48%
Number/percentage of G's	311,266,986 / 20.82%
Number/percentage of N's	10,725 / 0%

GC Percentage	40.8%
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2.3. Coverage

Mean	0.4834
Standard Deviation	8.5319

2.4. Mapping Quality

Mean Mapping Quality	52.48
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2.5. Insert size

Mean	1,149,904.39
Standard Deviation	9,831,559.66
P25/Median/P75	107 / 158 / 247

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	13,139,231
Insertions	170,942
Mapped reads with at least one insertion	1.24%
Deletions	454,833
Mapped reads with at least one deletion	3.36%
Homopolymer indels	40.81%

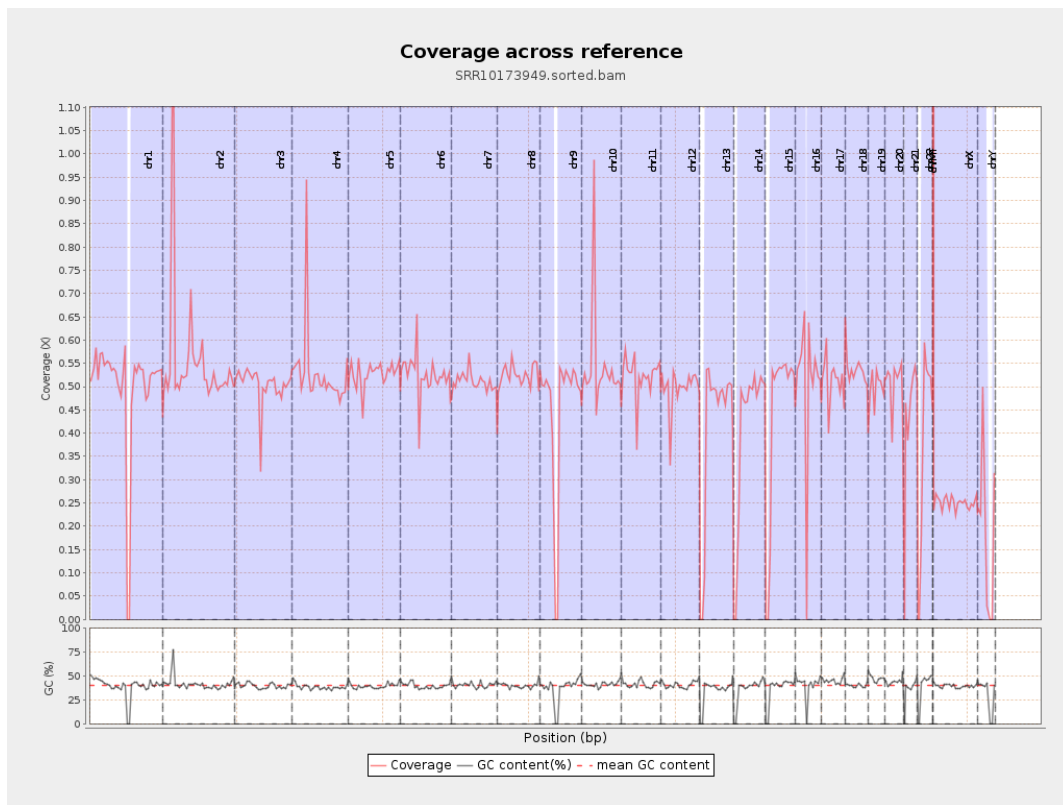
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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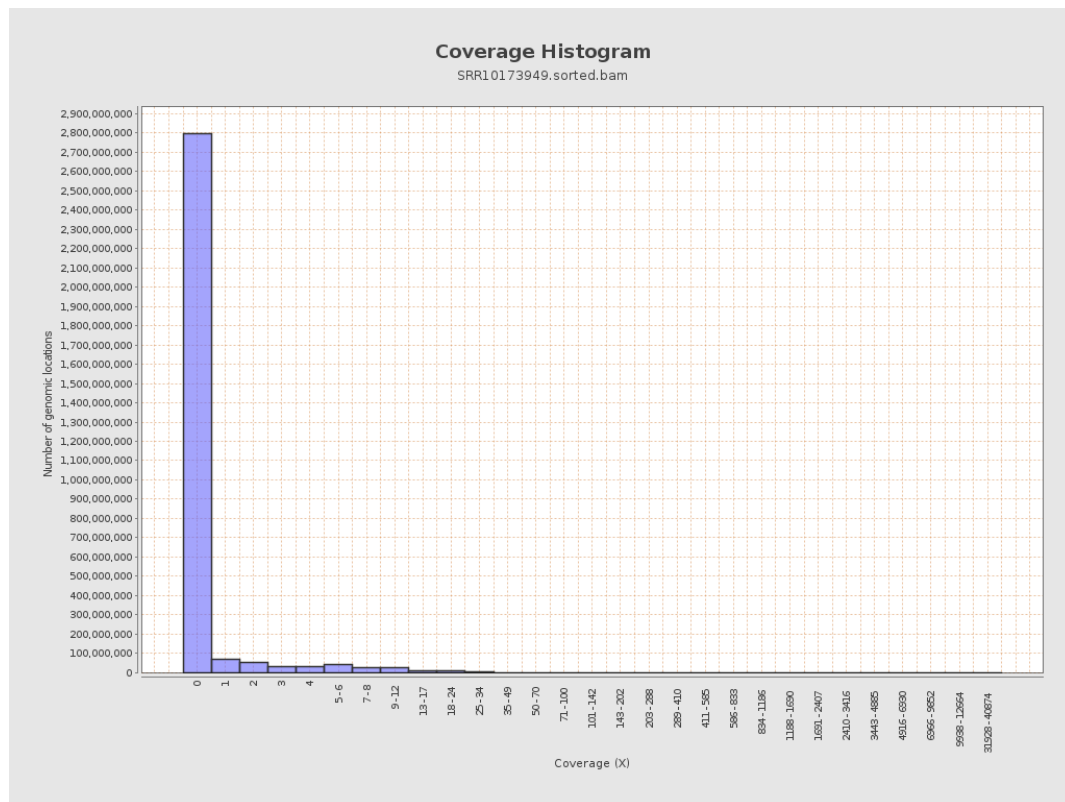
		bases	coverage	deviation
chr1	249250621	124106852	0.4979	3.8565
chr2	243199373	134626418	0.5536	28.4481
chr3	198022430	99890298	0.5044	2.1856
chr4	191154276	101181696	0.5293	3.7655
chr5	180915260	95477241	0.5277	2.2456
chr6	171115067	89891243	0.5253	2.8169
chr7	159138663	81303114	0.5109	3.4287
chr8	146364022	76801165	0.5247	4.8547
chr9	141213431	63729162	0.4513	3.3653
chr10	135534747	73082697	0.5392	4.763
chr11	135006516	70486834	0.5221	2.392
chr12	133851895	66710968	0.4984	2.3116
chr13	115169878	47773875	0.4148	1.9701
chr14	107349540	44342057	0.4131	2.0617
chr15	102531392	44048741	0.4296	2.1213
chr16	90354753	45652111	0.5053	3.1255
chr17	81195210	41876021	0.5157	2.6316
chr18	78077248	41784000	0.5352	4.6453
chr19	59128983	29431104	0.4977	3.0119
chr20	63025520	32050155	0.5085	2.5216
chr21	48129895	21066966	0.4377	3.0473
chr22	51304566	19155867	0.3734	2.6266
chrMT	16571	1604058	96.7991	69.4126
chrX	155270560	38886161	0.2504	1.5682

chrY	59373566	11500848	0.1937	3.0273
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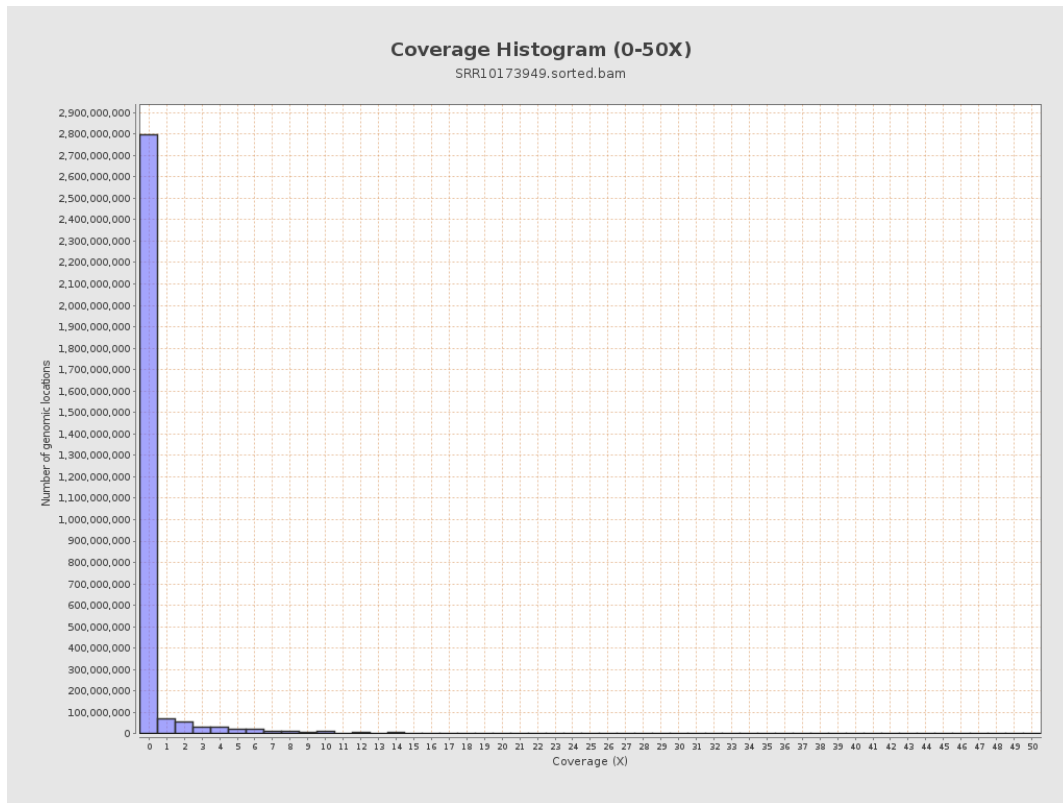
3. Results : Coverage across reference



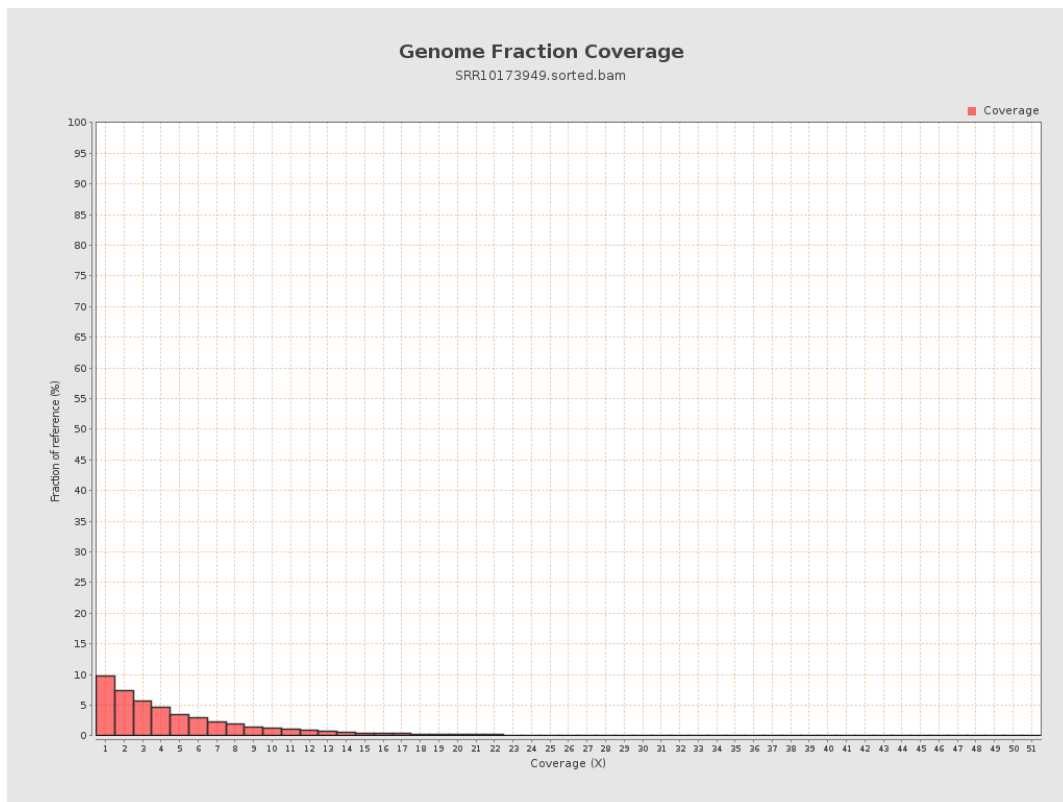
4. Results : Coverage Histogram



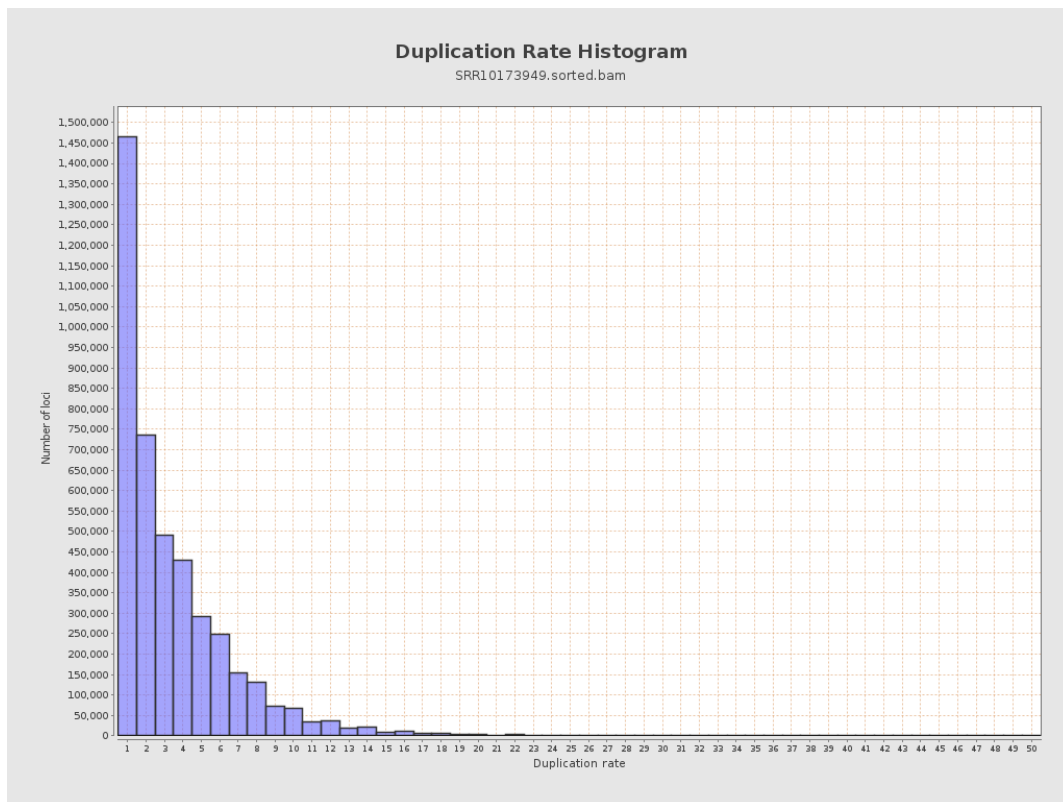
5. Results : Coverage Histogram (0-50X)



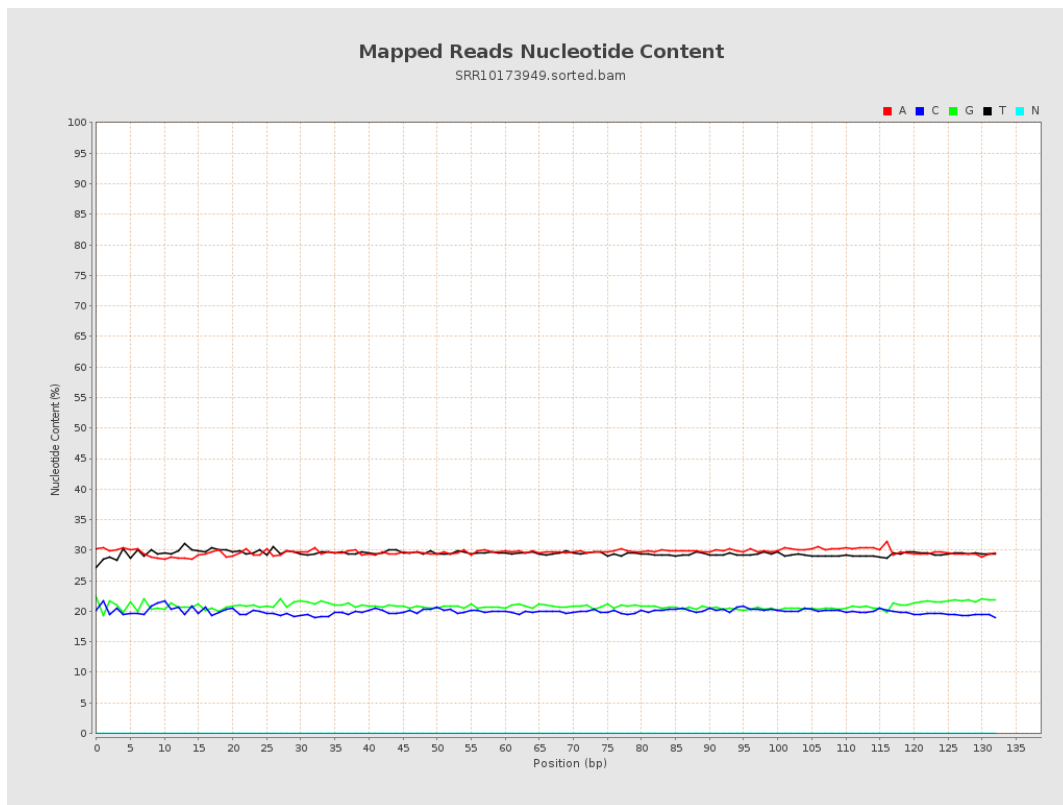
6. Results : Genome Fraction Coverage



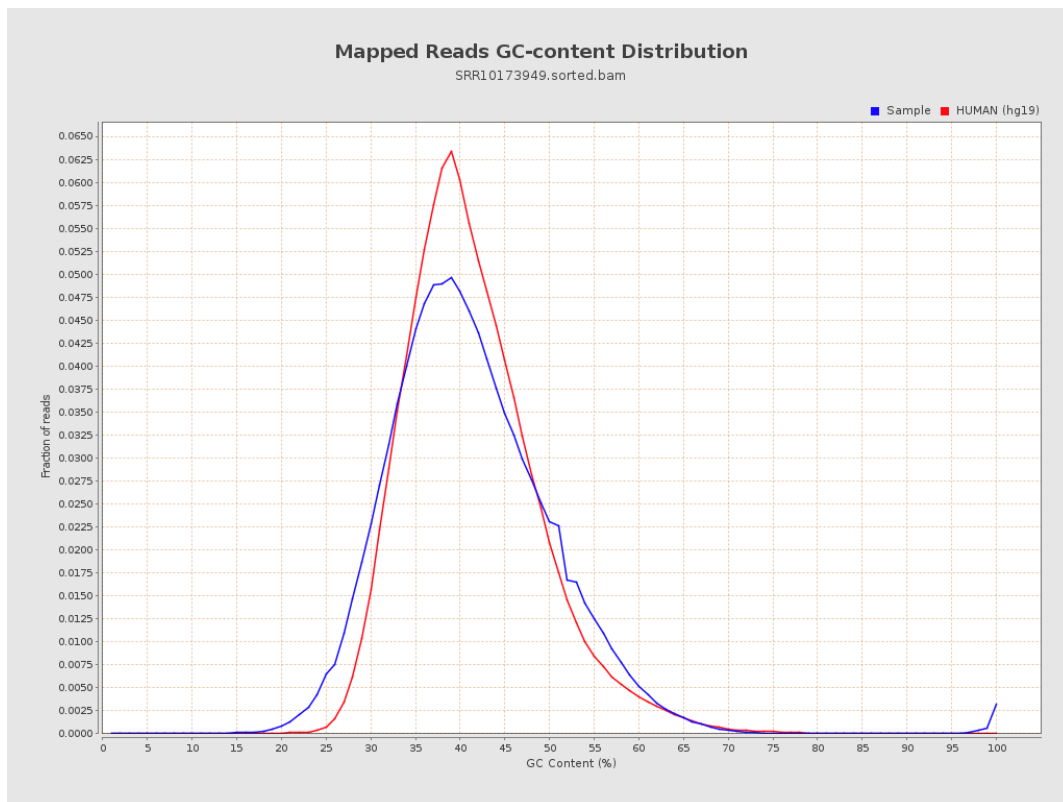
7. Results : Duplication Rate Histogram



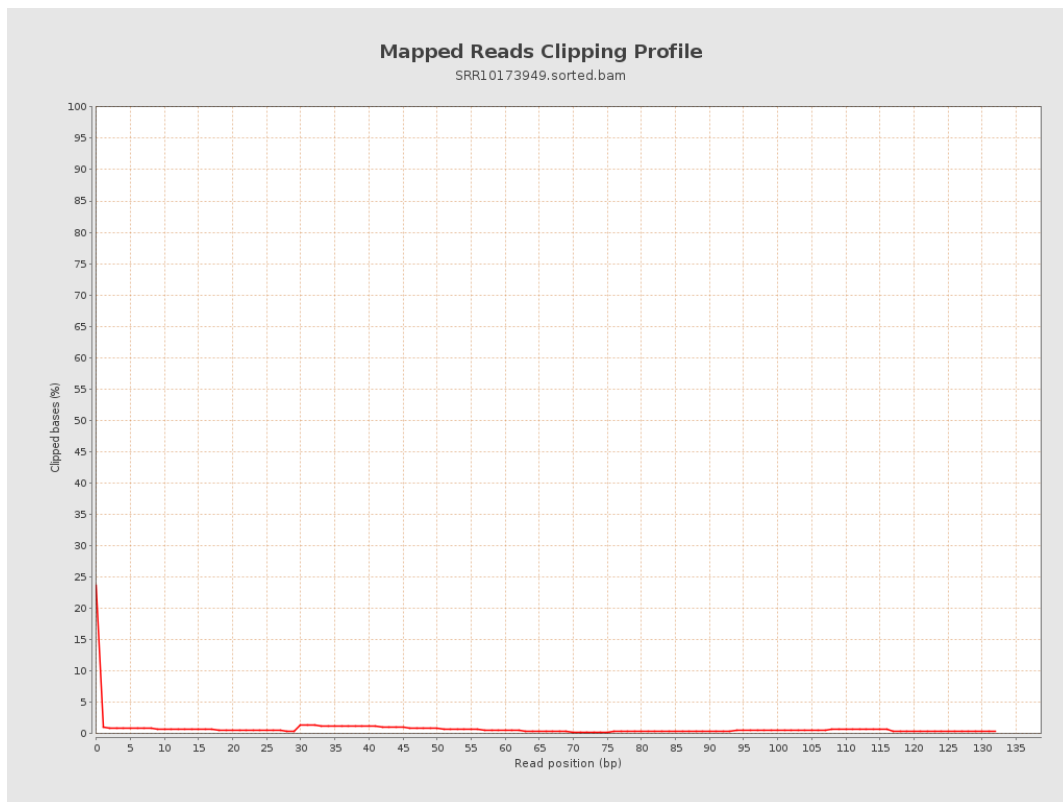
8. Results : Mapped Reads Nucleotide Content



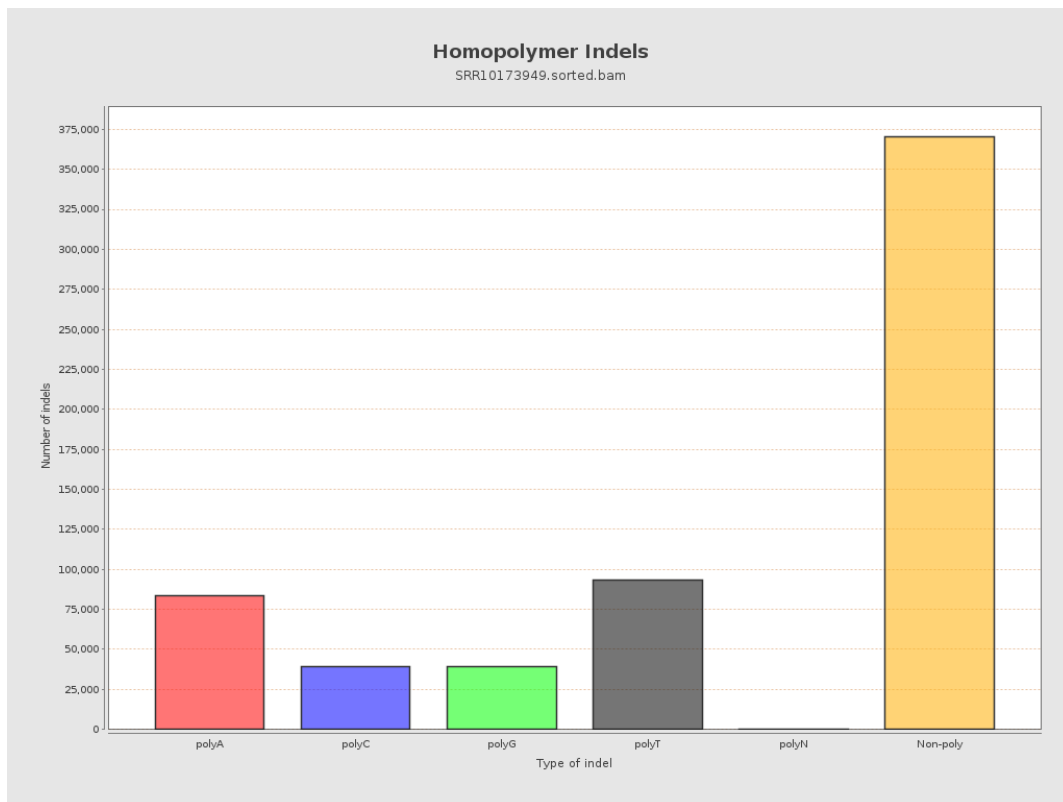
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



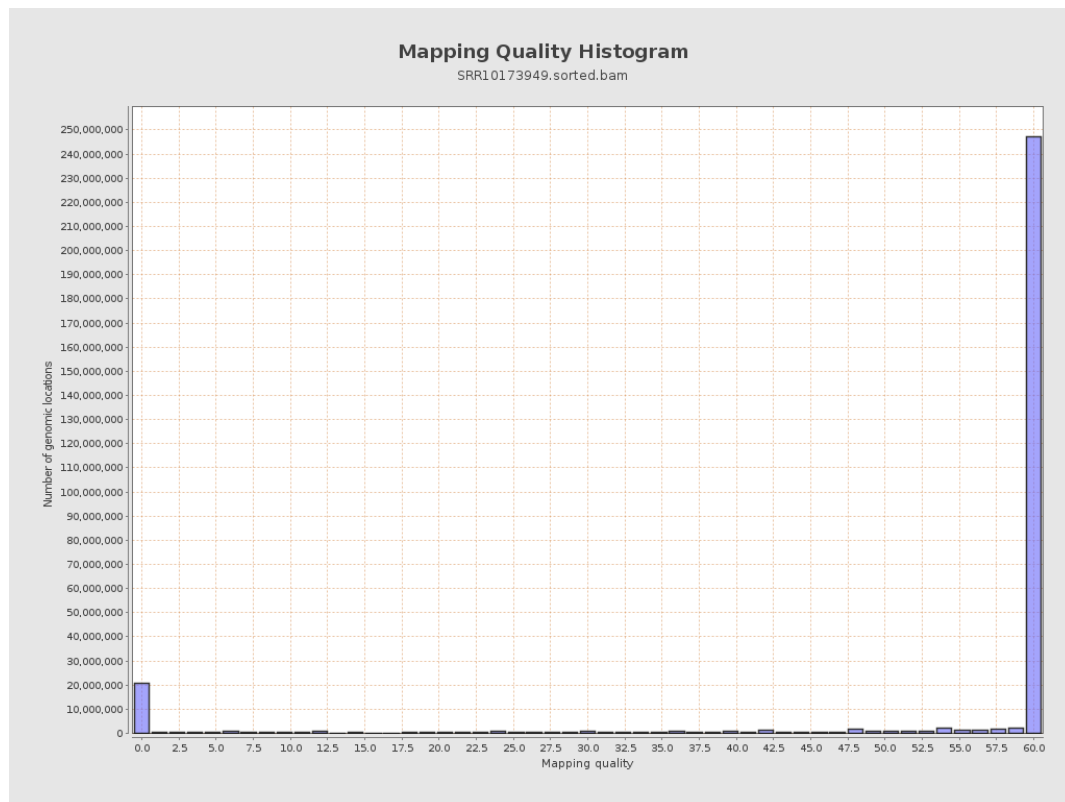
11. Results : Homopolymer Indels



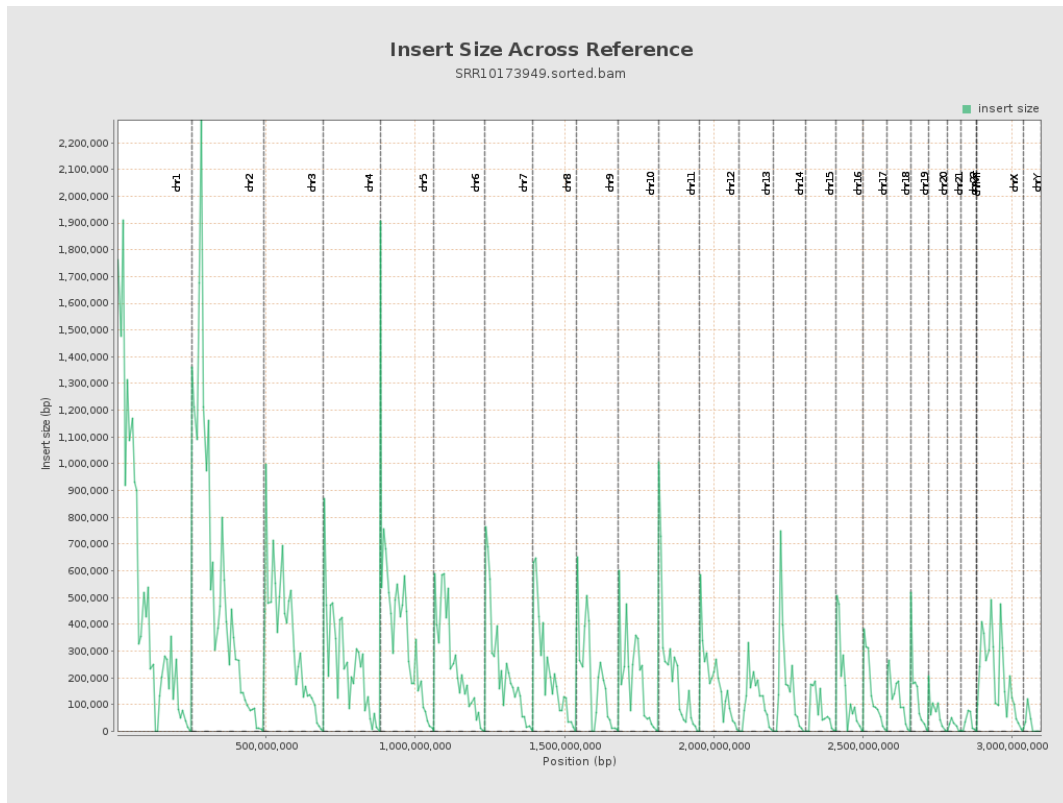
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

