

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:27:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251052.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_SRR10251052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251052_1.fastq.gz SRR10251052_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:27:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,364,962
Mapped reads	1,303,492 / 95.5%
Unmapped reads	61,470 / 4.5%
Mapped paired reads	1,303,492 / 95.5%
Mapped reads, first in pair	654,012 / 47.91%
Mapped reads, second in pair	649,480 / 47.58%
Mapped reads, both in pair	1,296,282 / 94.97%
Mapped reads, singletons	7,210 / 0.53%
Secondary alignments	0
Supplementary alignments	36,308 / 2.66%
Read min/max/mean length	30 / 127 / 128.21
Duplicated reads (estimated)	243,276 / 17.82%
Duplication rate	17.02%
Clipped reads	308,319 / 22.59%

2.2. ACGT Content

Number/percentage of A's	47,828,572 / 29.76%
Number/percentage of C's	32,227,761 / 20.05%
Number/percentage of T's	47,803,213 / 29.74%
Number/percentage of G's	32,864,110 / 20.45%
Number/percentage of N's	5,457 / 0%

GC Percentage	40.5%
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2.3. Coverage

Mean	0.052
Standard Deviation	0.6833

2.4. Mapping Quality

Mean Mapping Quality	53.29
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2.5. Insert size

Mean	74,855.62
Standard Deviation	2,535,826.43
P25/Median/P75	151 / 192 / 260

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	1,233,154
Insertions	26,483
Mapped reads with at least one insertion	1.92%
Deletions	69,254
Mapped reads with at least one deletion	5.1%
Homopolymer indels	44.73%

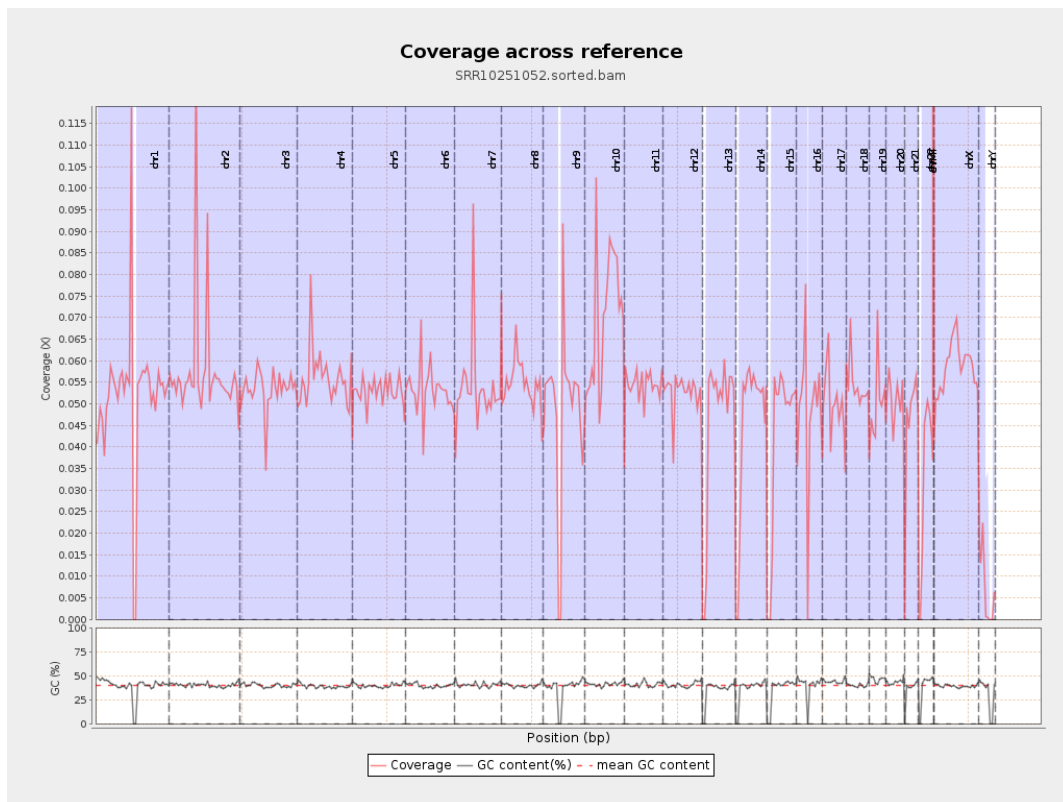
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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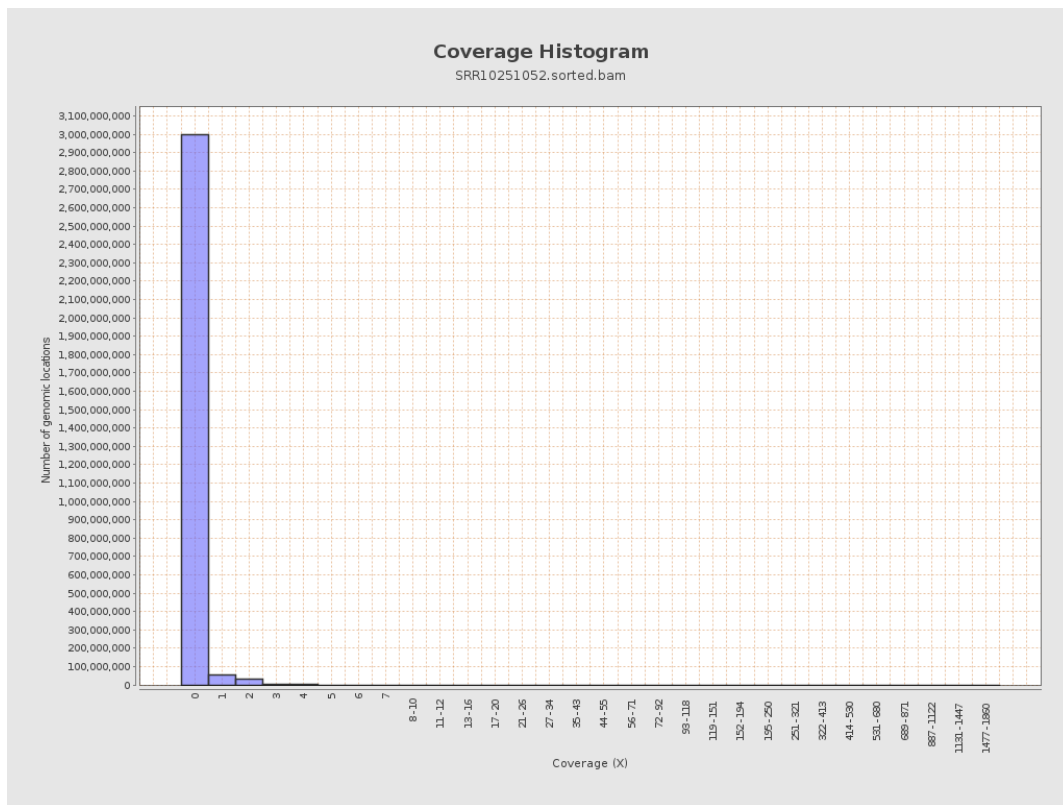
		bases	coverage	deviation
chr1	249250621	12894126	0.0517	1.5062
chr2	243199373	14073066	0.0579	0.8125
chr3	198022430	10576785	0.0534	0.3422
chr4	191154276	10686085	0.0559	0.4373
chr5	180915260	9584292	0.053	0.3423
chr6	171115067	9102998	0.0532	0.402
chr7	159138663	8572663	0.0539	0.9775
chr8	146364022	8007245	0.0547	0.4978
chr9	141213431	6871158	0.0487	0.9023
chr10	135534747	9457793	0.0698	0.7412
chr11	135006516	7326260	0.0543	0.4558
chr12	133851895	7027889	0.0525	0.3444
chr13	115169878	5201570	0.0452	0.3149
chr14	107349540	4803313	0.0447	0.3233
chr15	102531392	4357870	0.0425	0.3034
chr16	90354753	4376983	0.0484	0.4731
chr17	81195210	4017703	0.0495	0.4385
chr18	78077248	4258668	0.0545	0.6954
chr19	59128983	2970030	0.0502	0.7525
chr20	63025520	3207872	0.0509	0.3455
chr21	48129895	2192441	0.0456	0.3497
chr22	51304566	1645486	0.0321	0.2673
chrMT	16571	195834	11.8179	7.1962
chrX	155270560	9048157	0.0583	0.3745

chrY	59373566	413718	0.007	0.3624
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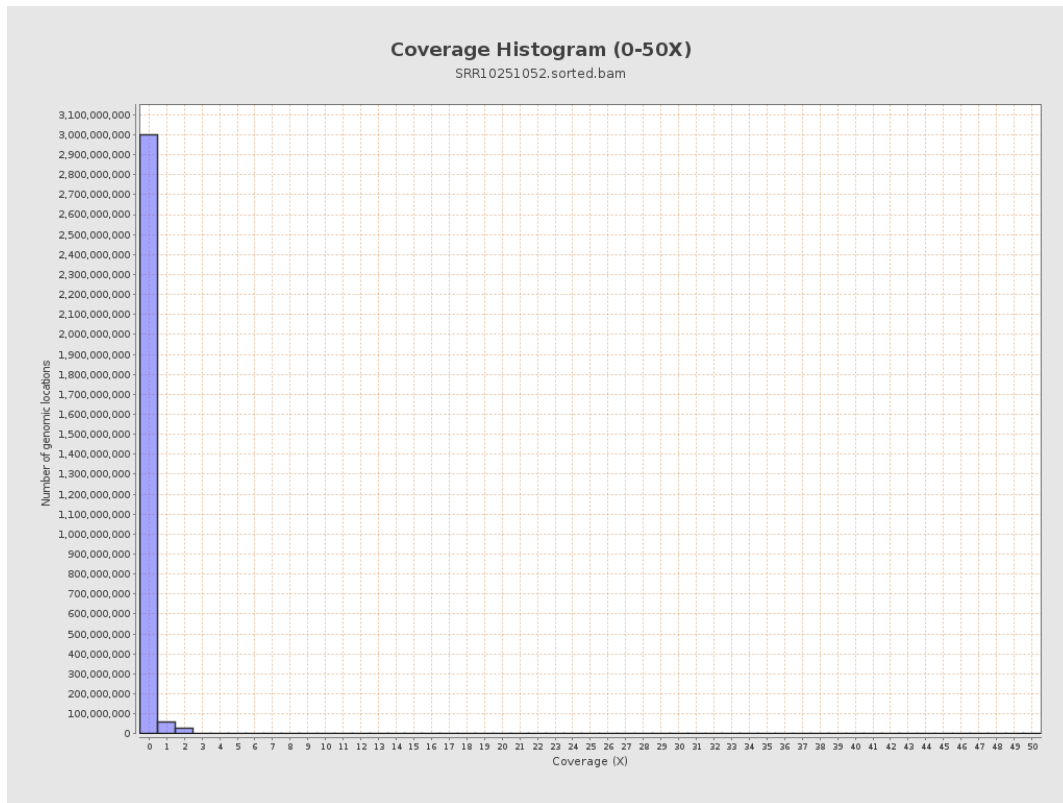
3. Results : Coverage across reference



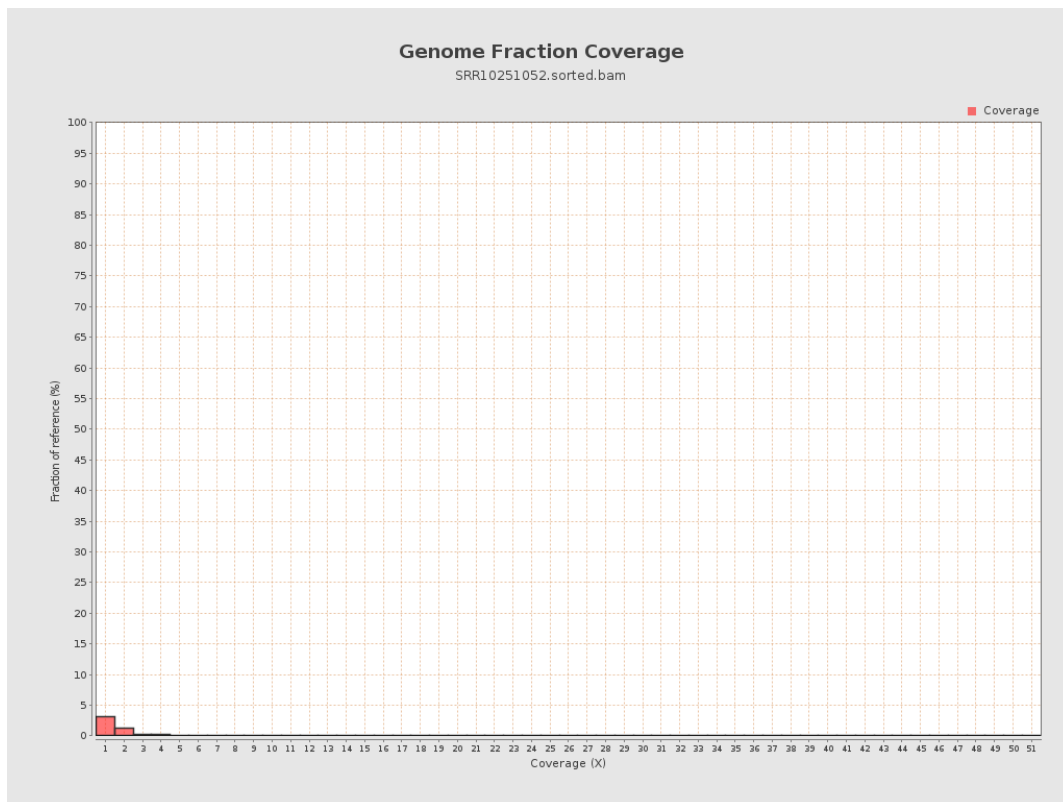
4. Results : Coverage Histogram



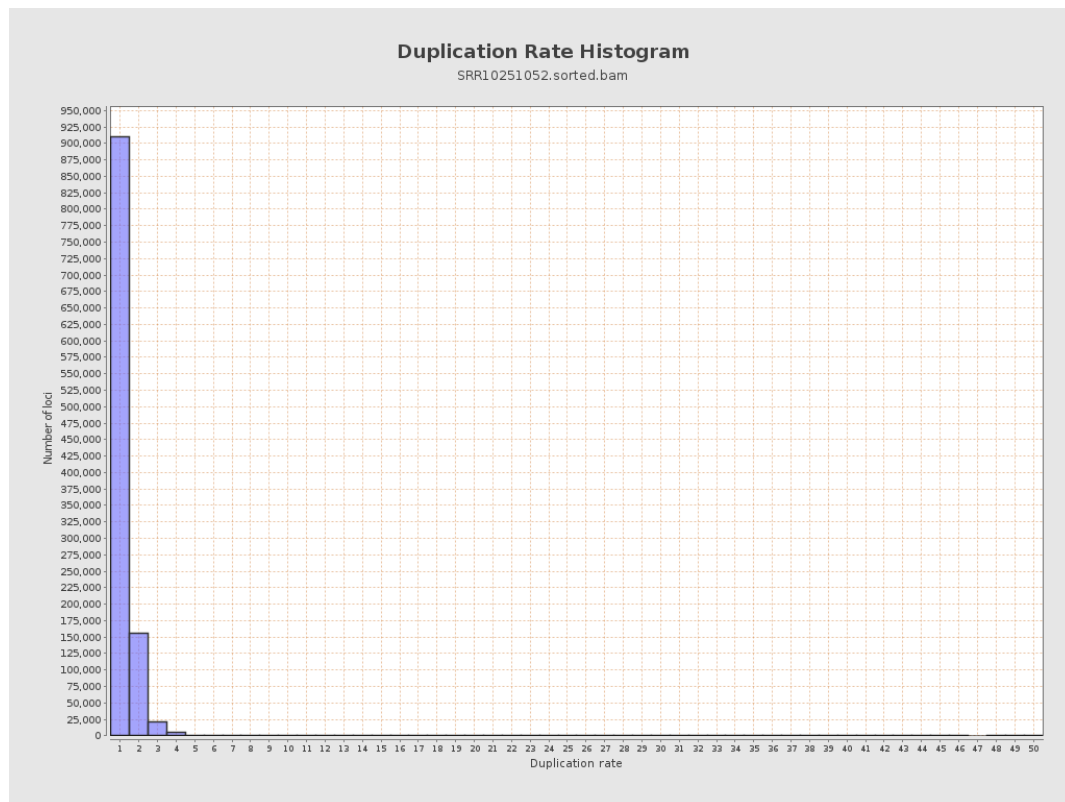
5. Results : Coverage Histogram (0-50X)



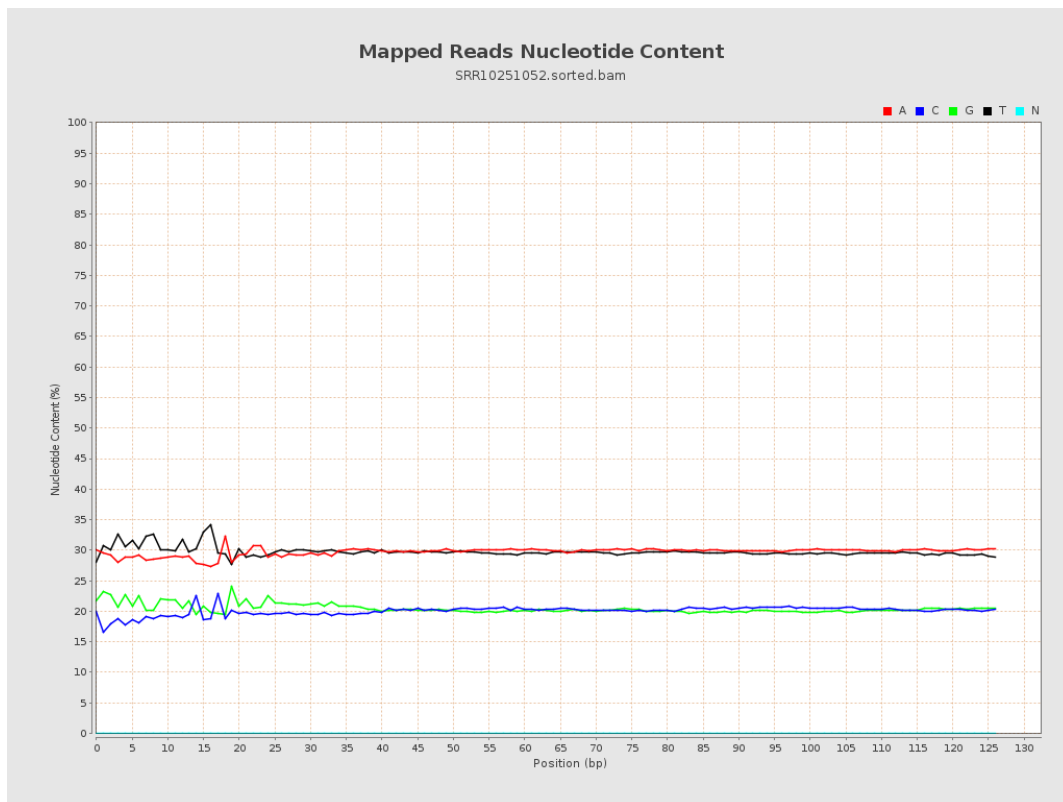
6. Results : Genome Fraction Coverage



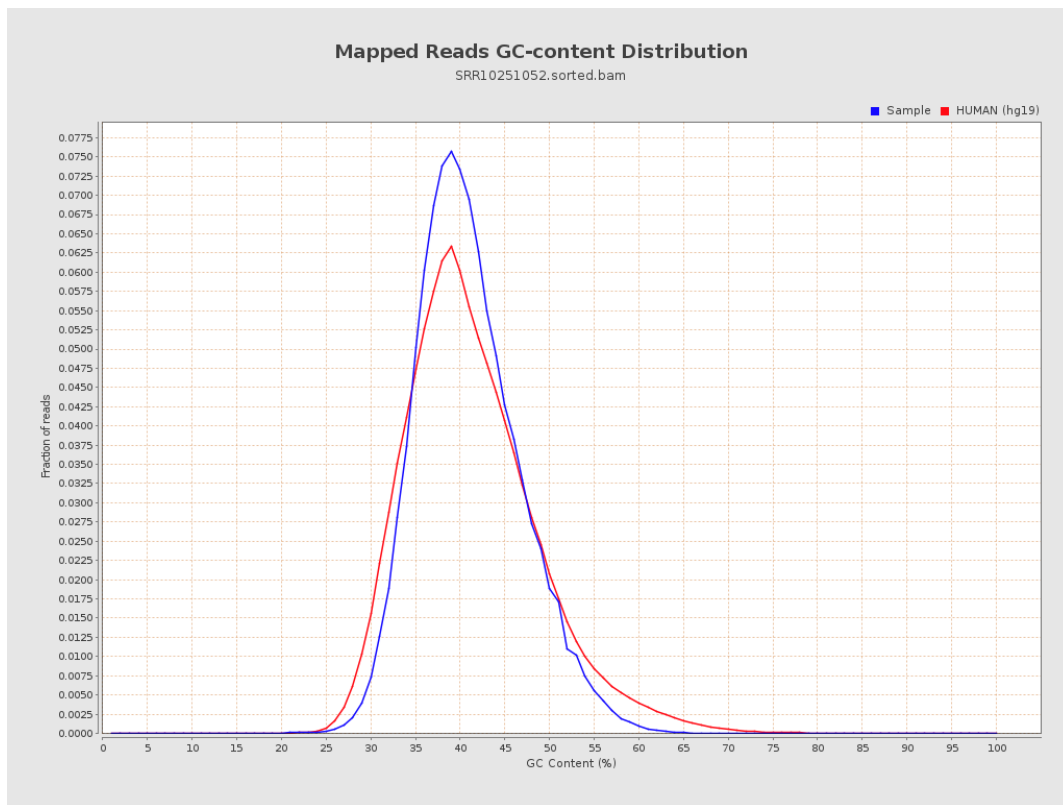
7. Results : Duplication Rate Histogram



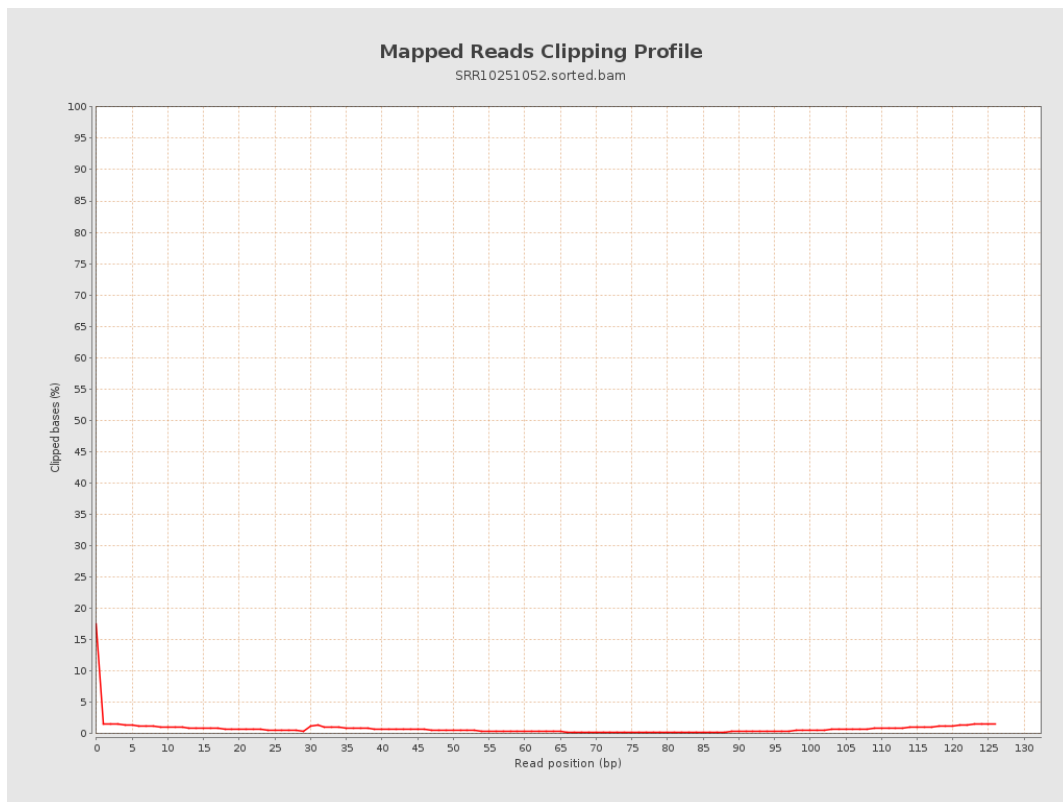
8. Results : Mapped Reads Nucleotide Content



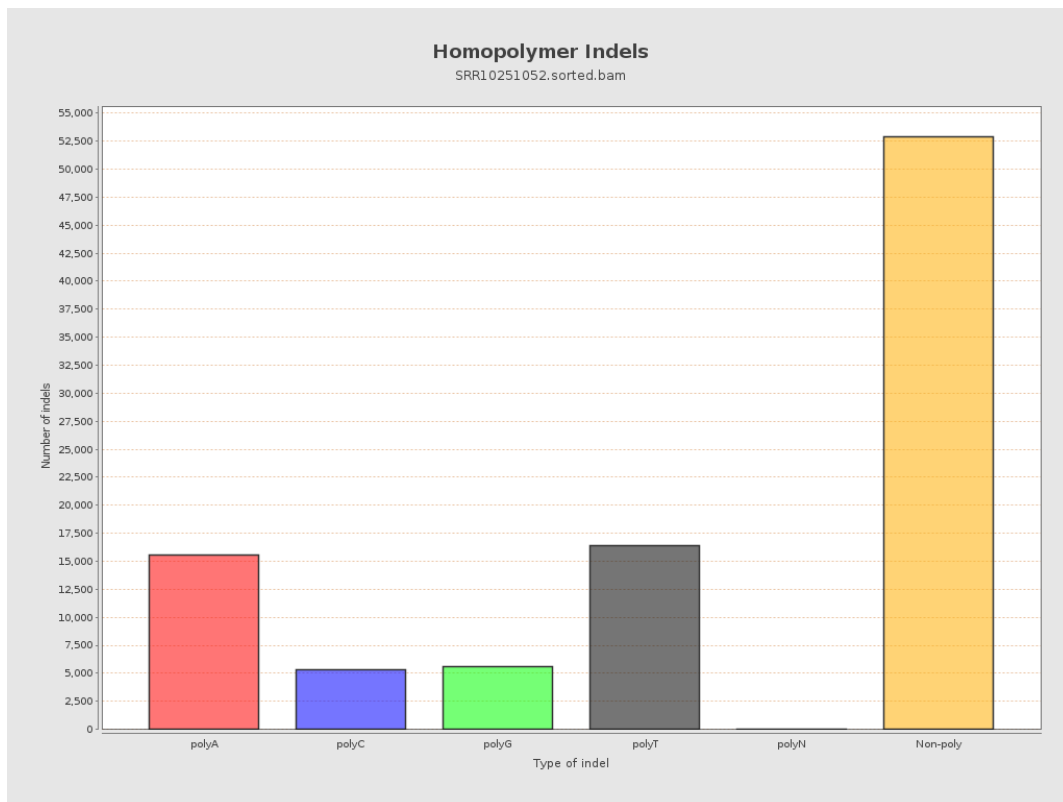
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



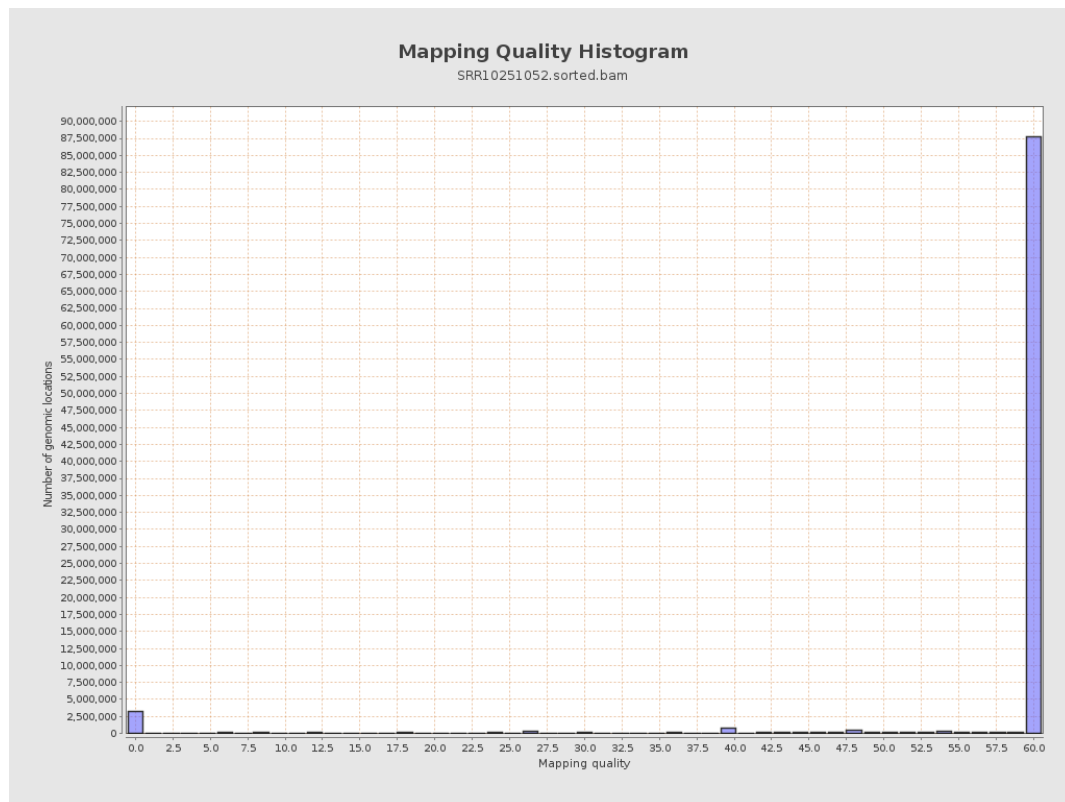
11. Results : Homopolymer Indels



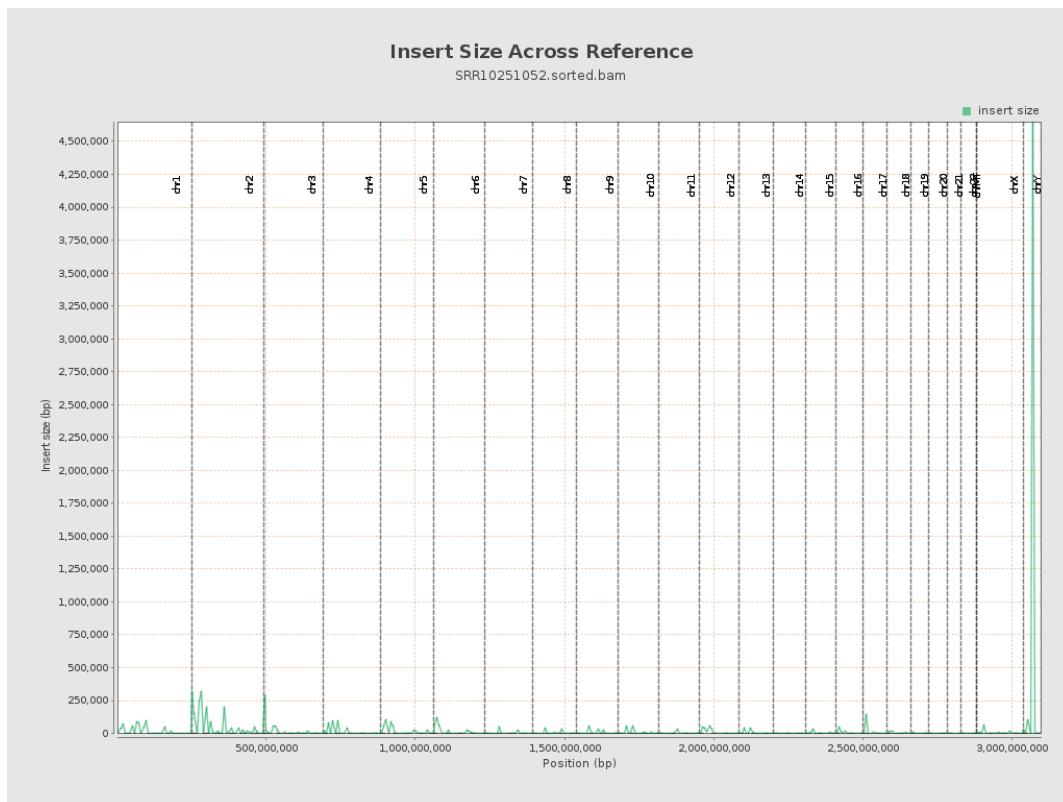
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

