

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:31:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251053.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_SRR10251053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251053_1.fastq.gz SRR10251053_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:31:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,402,546
Mapped reads	1,338,475 / 95.43%
Unmapped reads	64,071 / 4.57%
Mapped paired reads	1,338,475 / 95.43%
Mapped reads, first in pair	671,694 / 47.89%
Mapped reads, second in pair	666,781 / 47.54%
Mapped reads, both in pair	1,330,922 / 94.89%
Mapped reads, singletons	7,553 / 0.54%
Secondary alignments	0
Supplementary alignments	37,869 / 2.7%
Read min/max/mean length	30 / 127 / 128.23
Duplicated reads (estimated)	253,821 / 18.1%
Duplication rate	17.3%
Clipped reads	317,227 / 22.62%

2.2. ACGT Content

Number/percentage of A's	49,145,307 / 29.78%
Number/percentage of C's	33,054,005 / 20.03%
Number/percentage of T's	49,114,415 / 29.76%
Number/percentage of G's	33,713,391 / 20.43%
Number/percentage of N's	5,334 / 0%

GC Percentage	40.46%
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2.3. Coverage

Mean	0.0534
Standard Deviation	0.7073

2.4. Mapping Quality

Mean Mapping Quality	53.3
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2.5. Insert size

Mean	79,566.52
Standard Deviation	2,637,865.89
P25/Median/P75	151 / 192 / 260

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	1,256,359
Insertions	26,951
Mapped reads with at least one insertion	1.9%
Deletions	70,480
Mapped reads with at least one deletion	5.07%
Homopolymer indels	44.82%

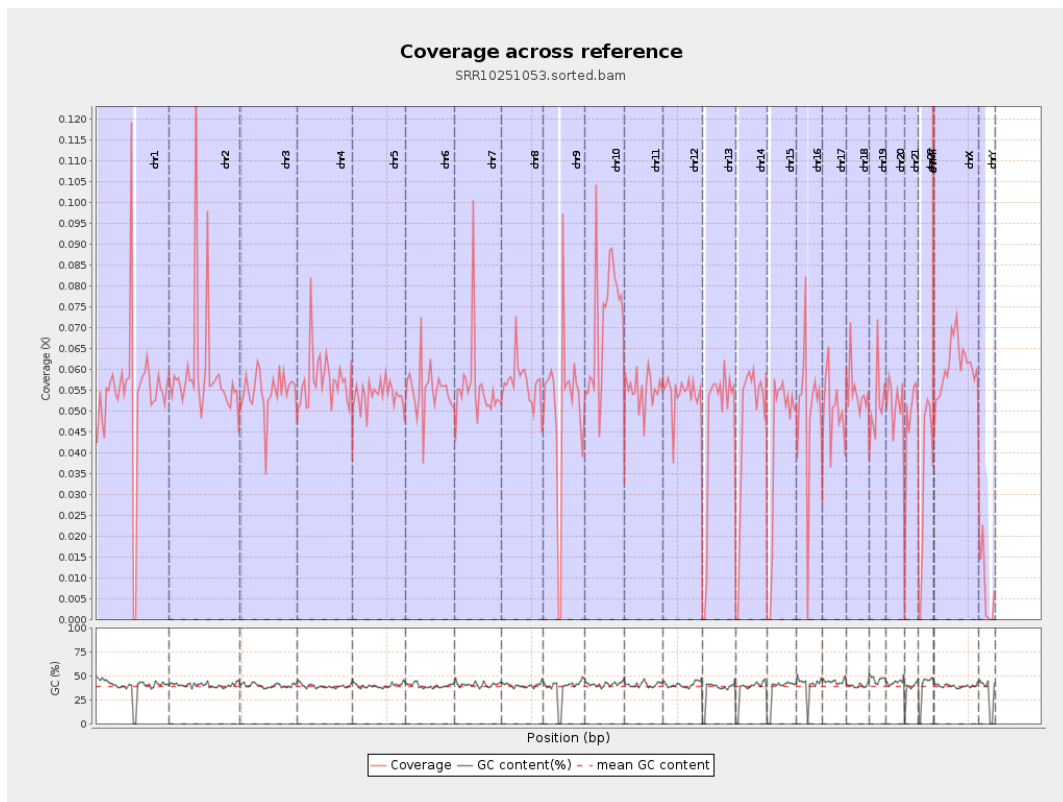
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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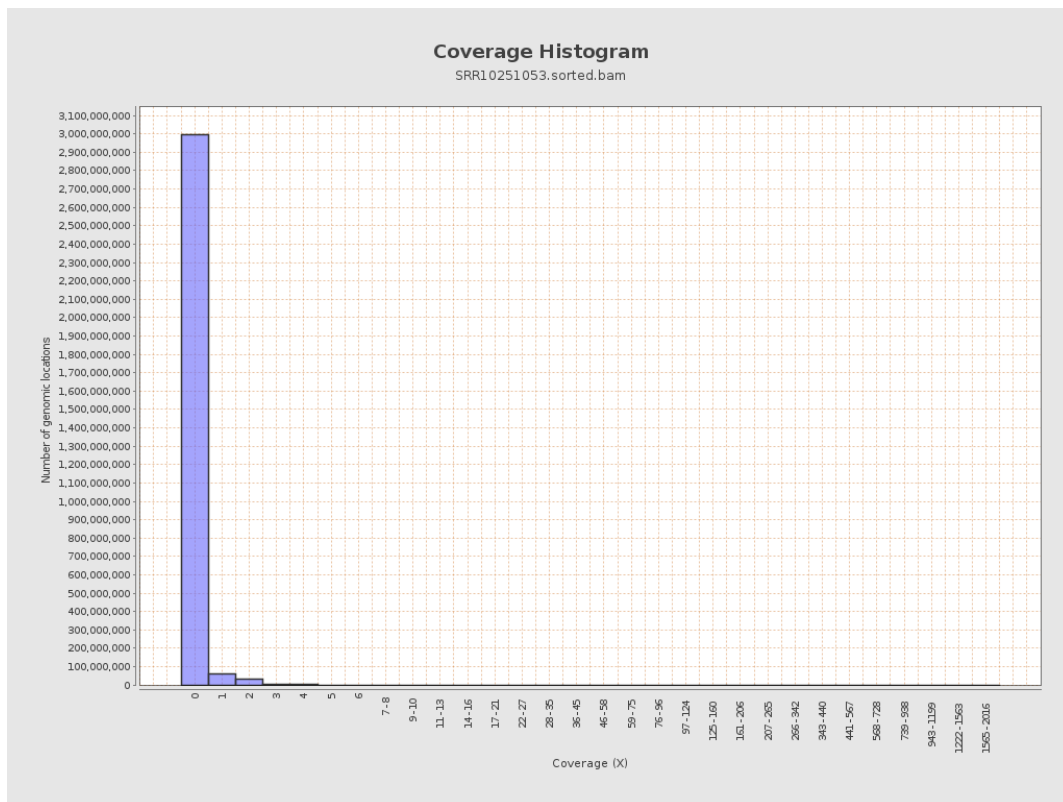
		bases	coverage	deviation
chr1	249250621	13315889	0.0534	1.5853
chr2	243199373	14454951	0.0594	0.8269
chr3	198022430	10830815	0.0547	0.3465
chr4	191154276	10969228	0.0574	0.4562
chr5	180915260	9742736	0.0539	0.3475
chr6	171115067	9393758	0.0549	0.4046
chr7	159138663	8885116	0.0558	0.9841
chr8	146364022	8310926	0.0568	0.5123
chr9	141213431	7149357	0.0506	0.9632
chr10	135534747	9627822	0.071	0.7584
chr11	135006516	7379718	0.0547	0.4655
chr12	133851895	7217739	0.0539	0.3496
chr13	115169878	5284845	0.0459	0.3165
chr14	107349540	4971644	0.0463	0.335
chr15	102531392	4410187	0.043	0.3051
chr16	90354753	4560522	0.0505	0.4826
chr17	81195210	4059011	0.05	0.4368
chr18	78077248	4293802	0.055	0.6913
chr19	59128983	3064202	0.0518	0.7701
chr20	63025520	3264408	0.0518	0.3466
chr21	48129895	2242247	0.0466	0.351
chr22	51304566	1733683	0.0338	0.2737
chrMT	16571	213402	12.878	7.5913
chrX	155270560	9375590	0.0604	0.3849

chrY	59373566	424391	0.0071	0.3964
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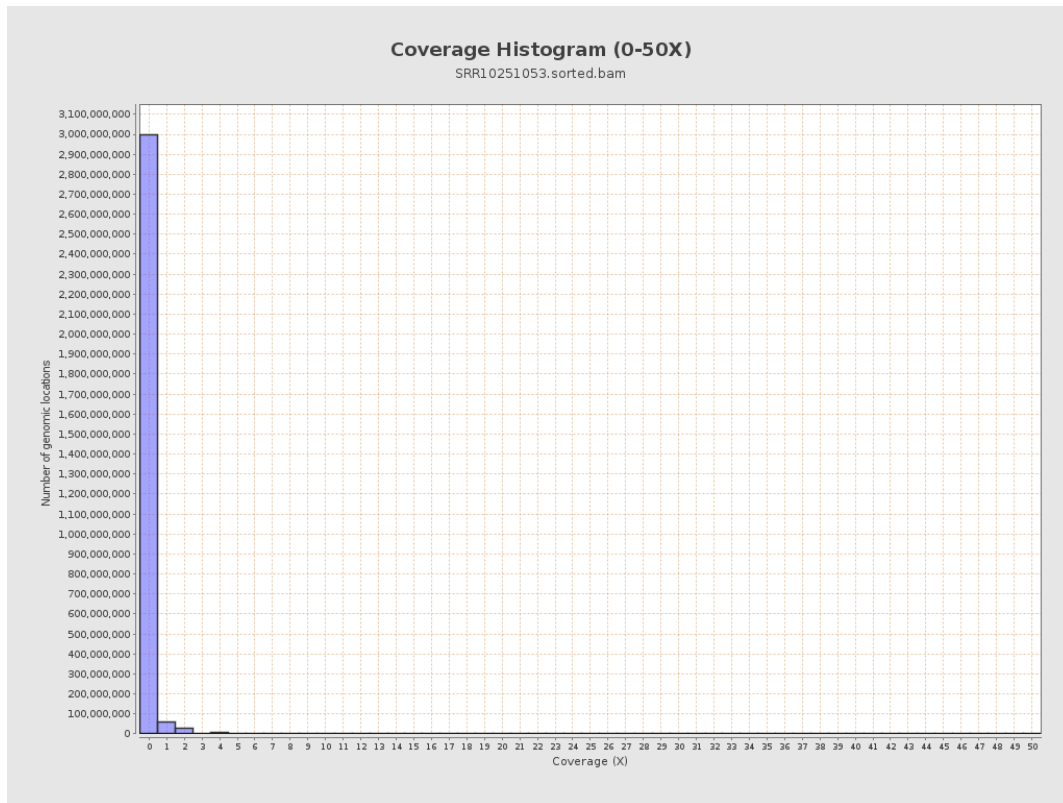
3. Results : Coverage across reference



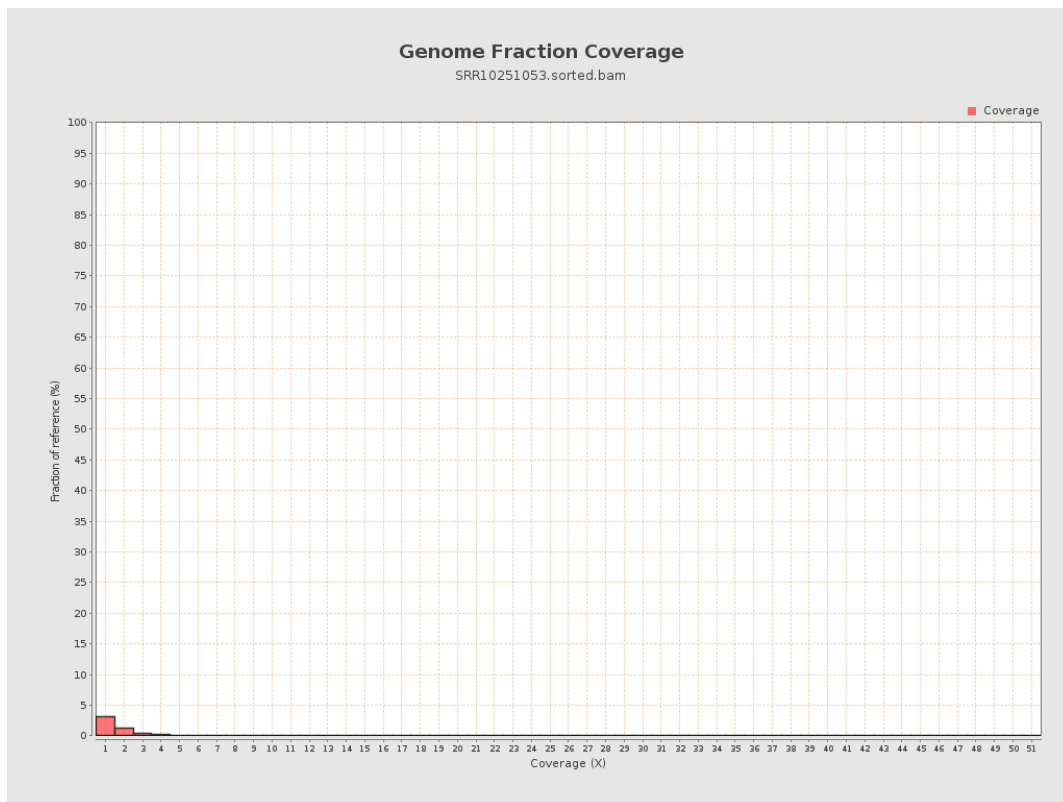
4. Results : Coverage Histogram



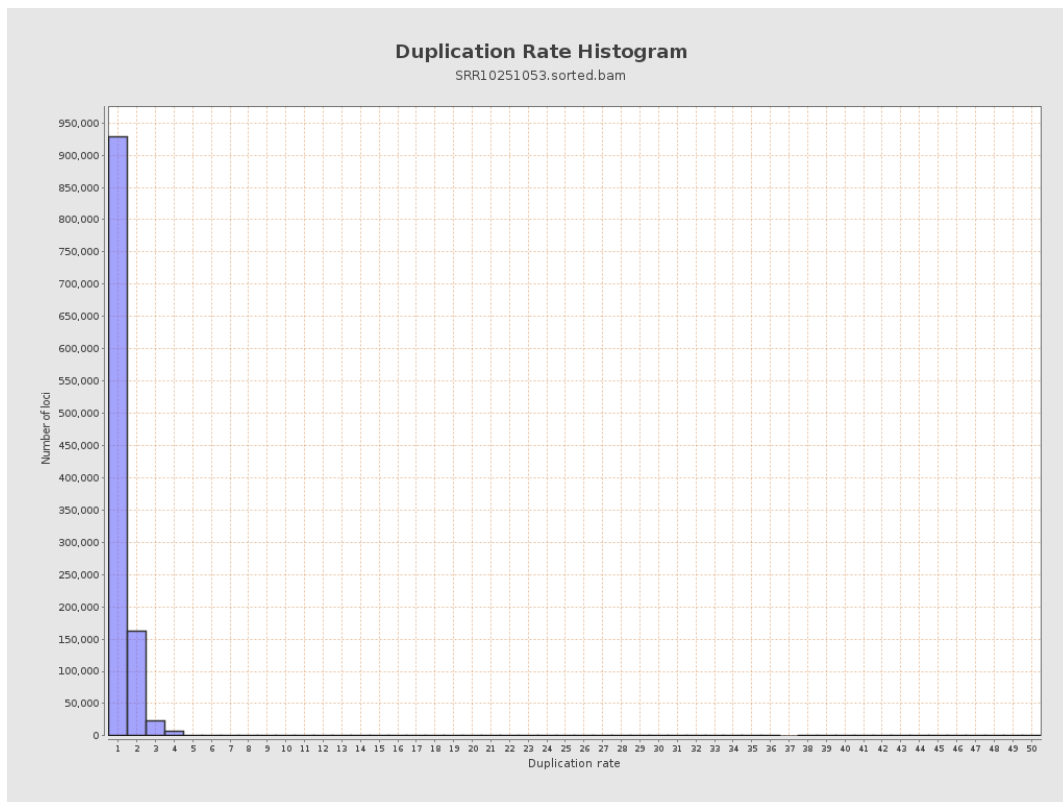
5. Results : Coverage Histogram (0-50X)



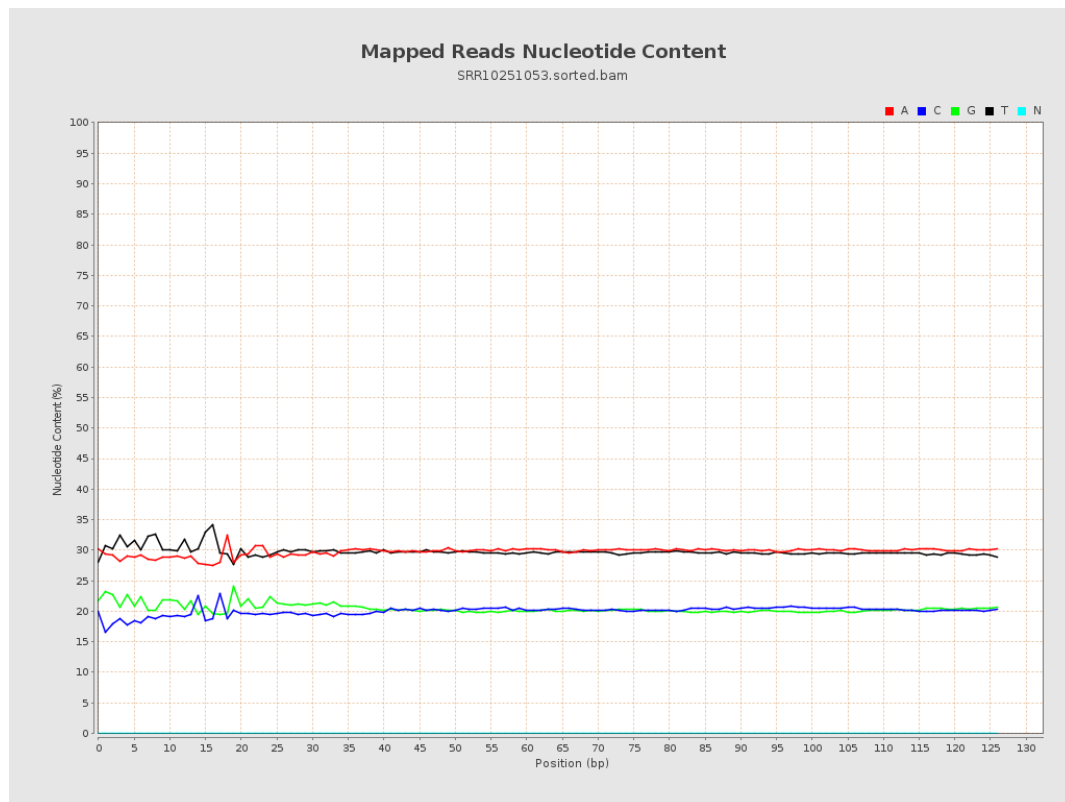
6. Results : Genome Fraction Coverage



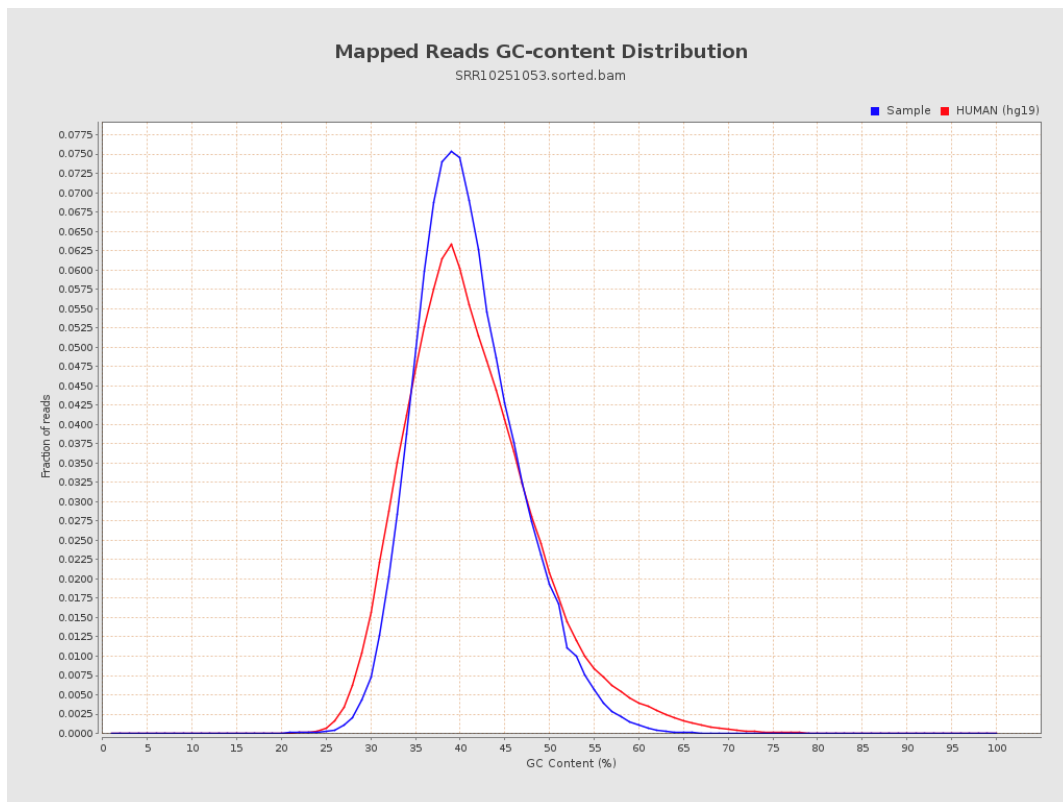
7. Results : Duplication Rate Histogram



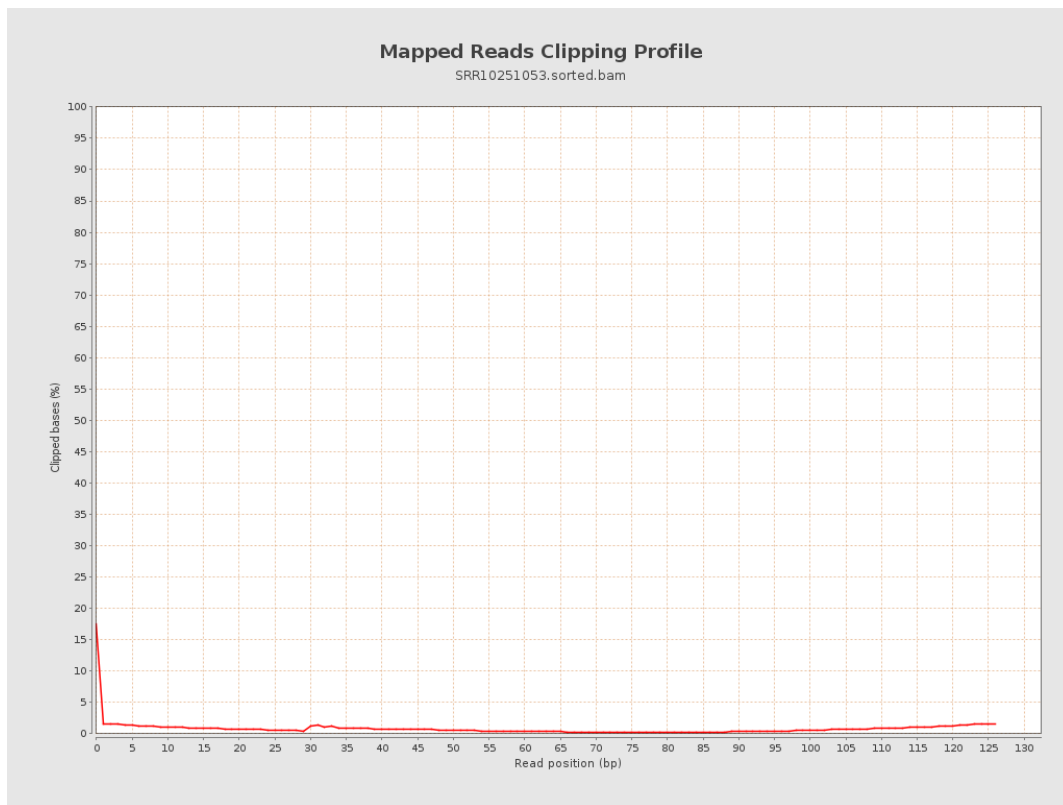
8. Results : Mapped Reads Nucleotide Content



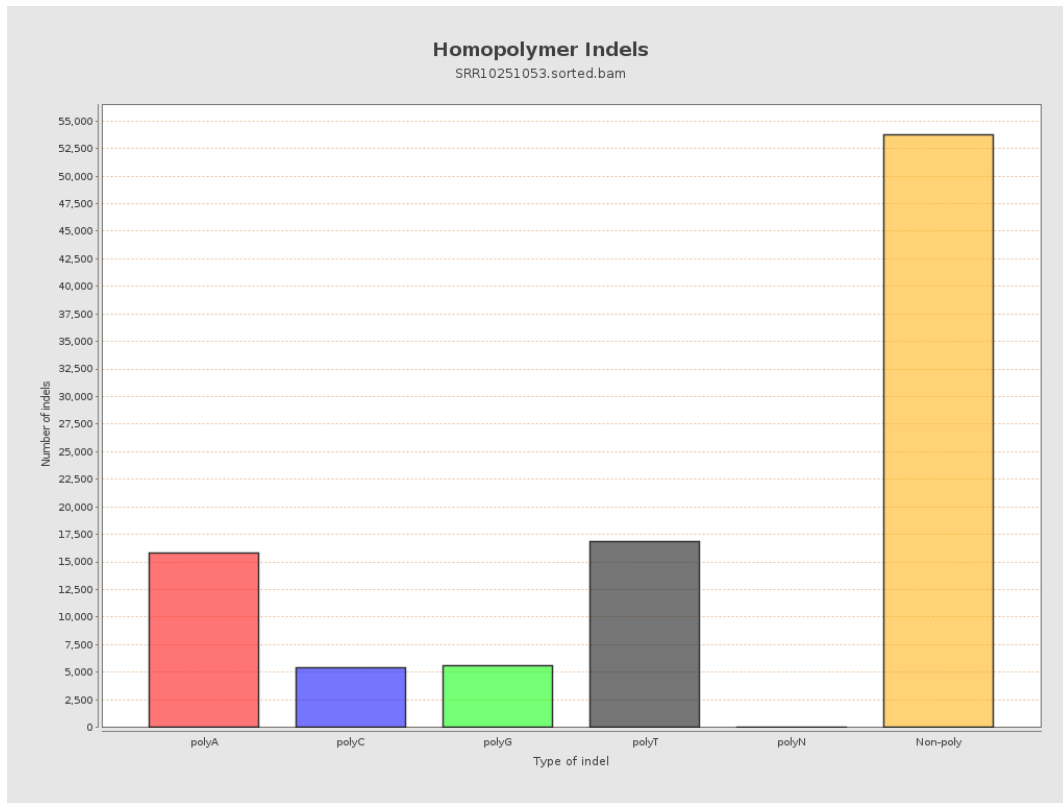
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



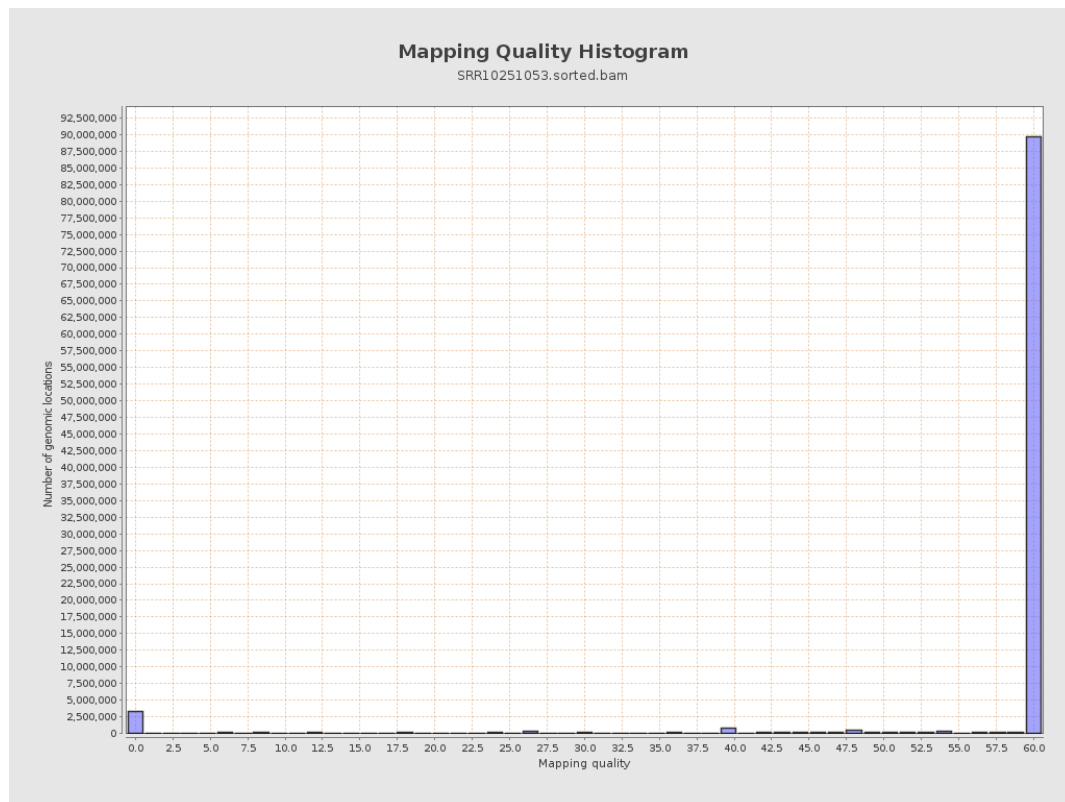
11. Results : Homopolymer Indels



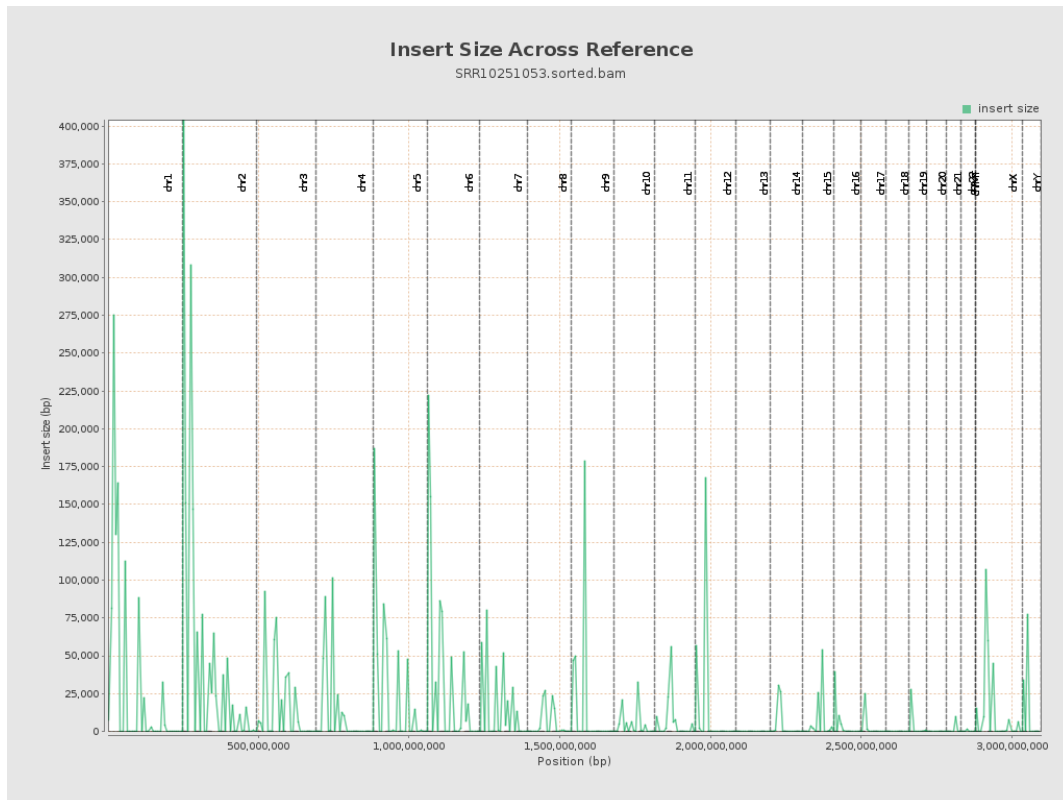
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

