

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:54:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156425.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_SRR10156425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156425_1.fastq.gz SRR10156425_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:54:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,531,104
Mapped reads	2,482,455 / 98.08%
Unmapped reads	48,649 / 1.92%
Mapped paired reads	2,482,455 / 98.08%
Mapped reads, first in pair	1,241,928 / 49.07%
Mapped reads, second in pair	1,240,527 / 49.01%
Mapped reads, both in pair	2,453,562 / 96.94%
Mapped reads, singletons	28,893 / 1.14%
Secondary alignments	0
Supplementary alignments	308,240 / 12.18%
Read min/max/mean length	30 / 133 / 124.08
Duplicated reads (estimated)	1,865,480 / 73.7%
Duplication rate	61.45%
Clipped reads	1,328,910 / 52.5%

2.2. ACGT Content

Number/percentage of A's	83,657,963 / 30.13%
Number/percentage of C's	54,544,027 / 19.64%
Number/percentage of T's	82,940,303 / 29.87%
Number/percentage of G's	56,549,583 / 20.36%
Number/percentage of N's	2,145 / 0%

GC Percentage	40.01%
---------------	--------

2.3. Coverage

Mean	0.0898
Standard Deviation	1.8215

2.4. Mapping Quality

Mean Mapping Quality	52.72
----------------------	-------

2.5. Insert size

Mean	1,004,279.55
Standard Deviation	9,128,390.23
P25/Median/P75	100 / 144 / 215

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	2,258,370
Insertions	29,532
Mapped reads with at least one insertion	1.14%
Deletions	78,451
Mapped reads with at least one deletion	3.08%
Homopolymer indels	41.23%

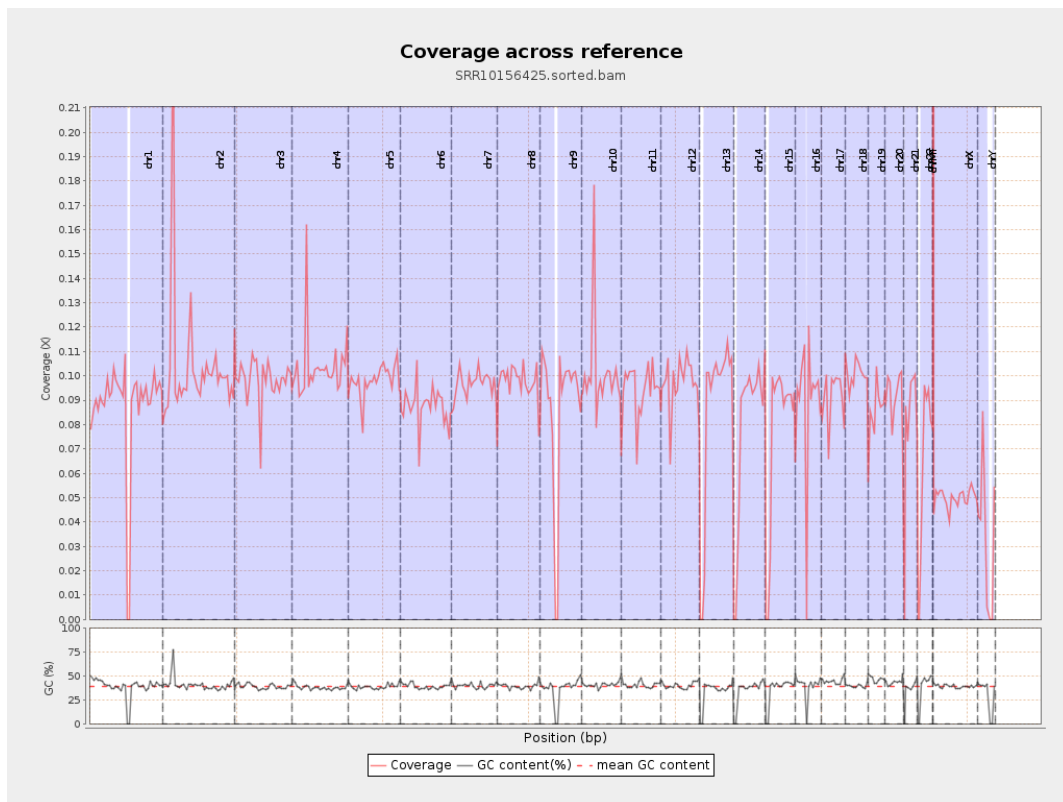
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

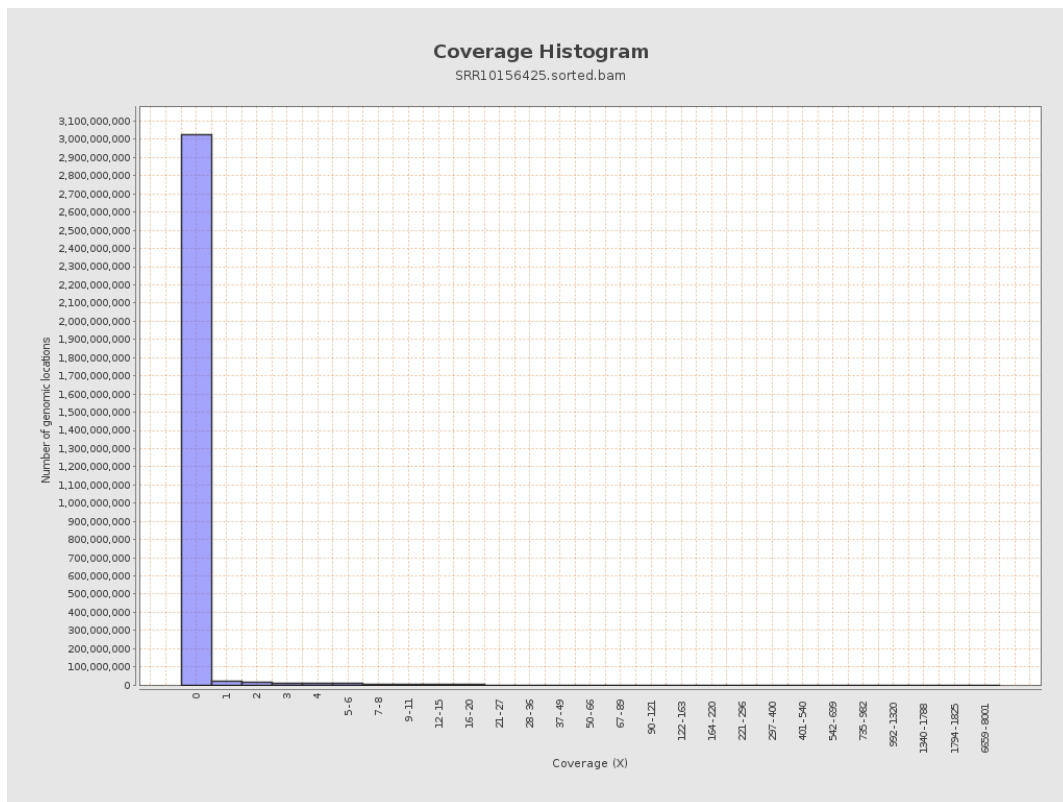
		bases	coverage	deviation
chr1	249250621	21741264	0.0872	1.0054
chr2	243199373	25149505	0.1034	5.6602
chr3	198022430	19503668	0.0985	0.8934
chr4	191154276	19809747	0.1036	1.0321
chr5	180915260	17710729	0.0979	0.8852
chr6	171115067	14976154	0.0875	0.8809
chr7	159138663	15344433	0.0964	0.9708
chr8	146364022	14319617	0.0978	1.1997
chr9	141213431	12273382	0.0869	0.9655
chr10	135534747	13648950	0.1007	1.1958
chr11	135006516	12751684	0.0945	0.8687
chr12	133851895	13058093	0.0976	0.888
chr13	115169878	9890430	0.0859	0.8364
chr14	107349540	8552068	0.0797	0.7988
chr15	102531392	7703631	0.0751	0.7746
chr16	90354753	7975440	0.0883	0.9312
chr17	81195210	7459760	0.0919	0.8791
chr18	78077248	7861910	0.1007	1.088
chr19	59128983	5112765	0.0865	0.8936
chr20	63025520	5816911	0.0923	0.8699
chr21	48129895	3910695	0.0813	0.8903
chr22	51304566	3243807	0.0632	0.7519
chrMT	16571	290540	17.533	16.9766
chrX	155270560	7751188	0.0499	0.6204

chrY	59373566	2027589	0.0341	0.6019
------	----------	---------	--------	--------

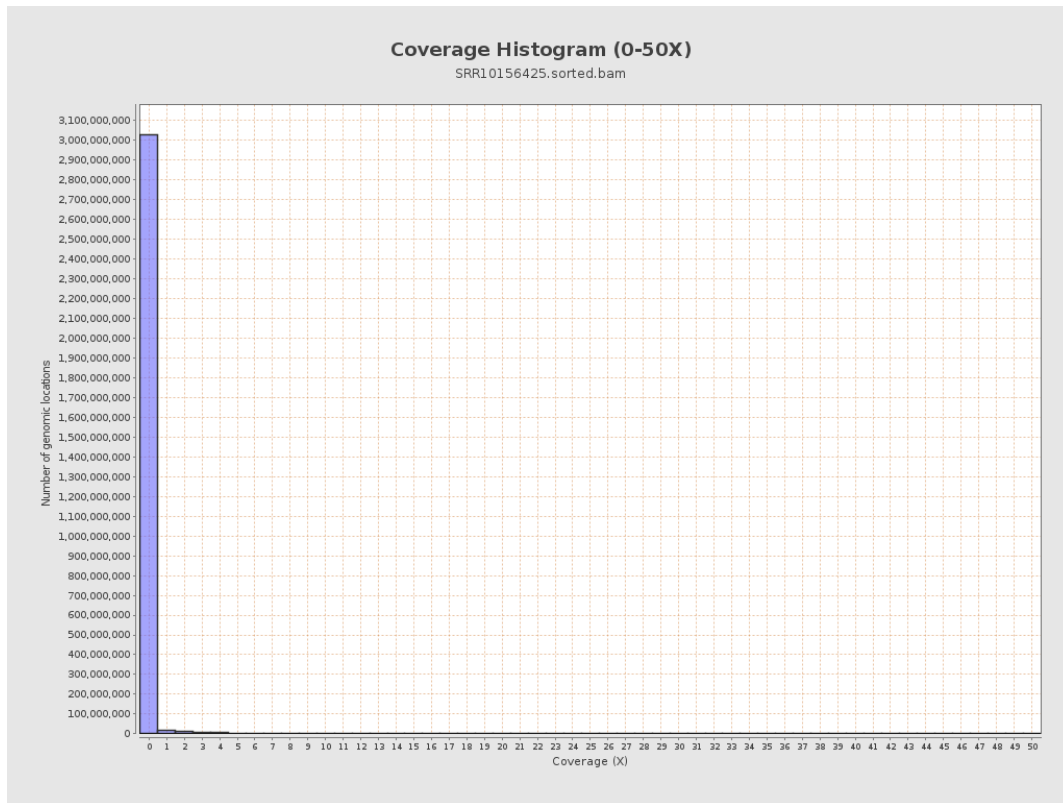
3. Results : Coverage across reference



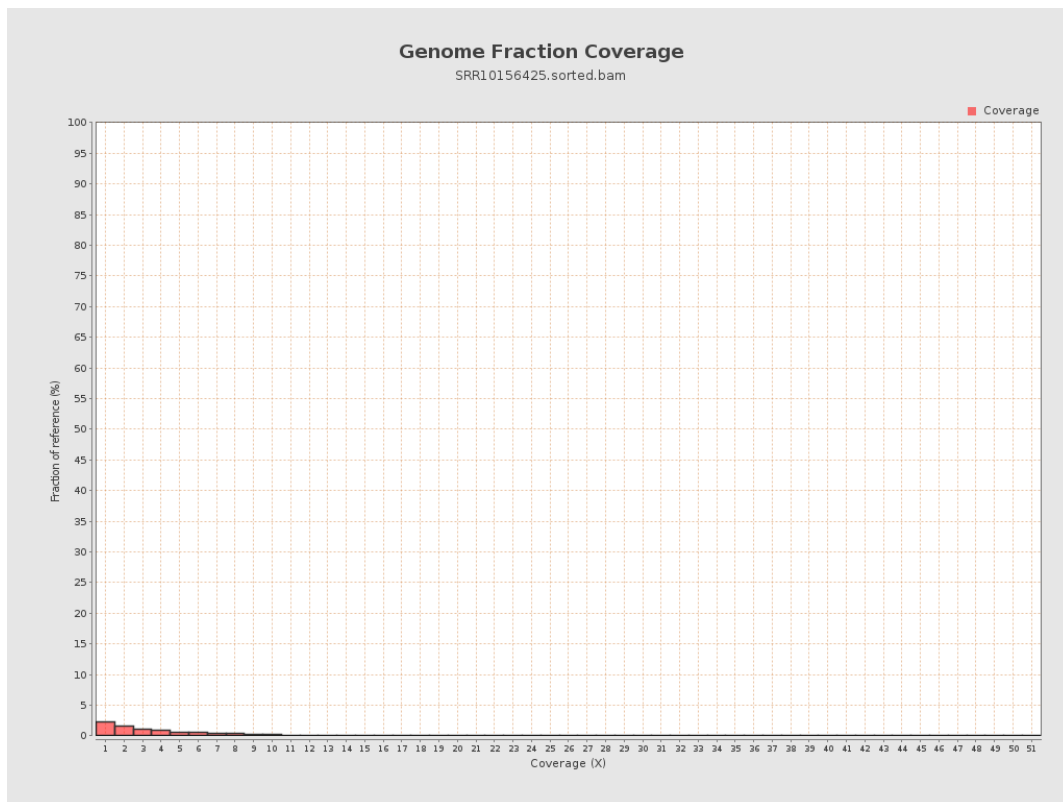
4. Results : Coverage Histogram



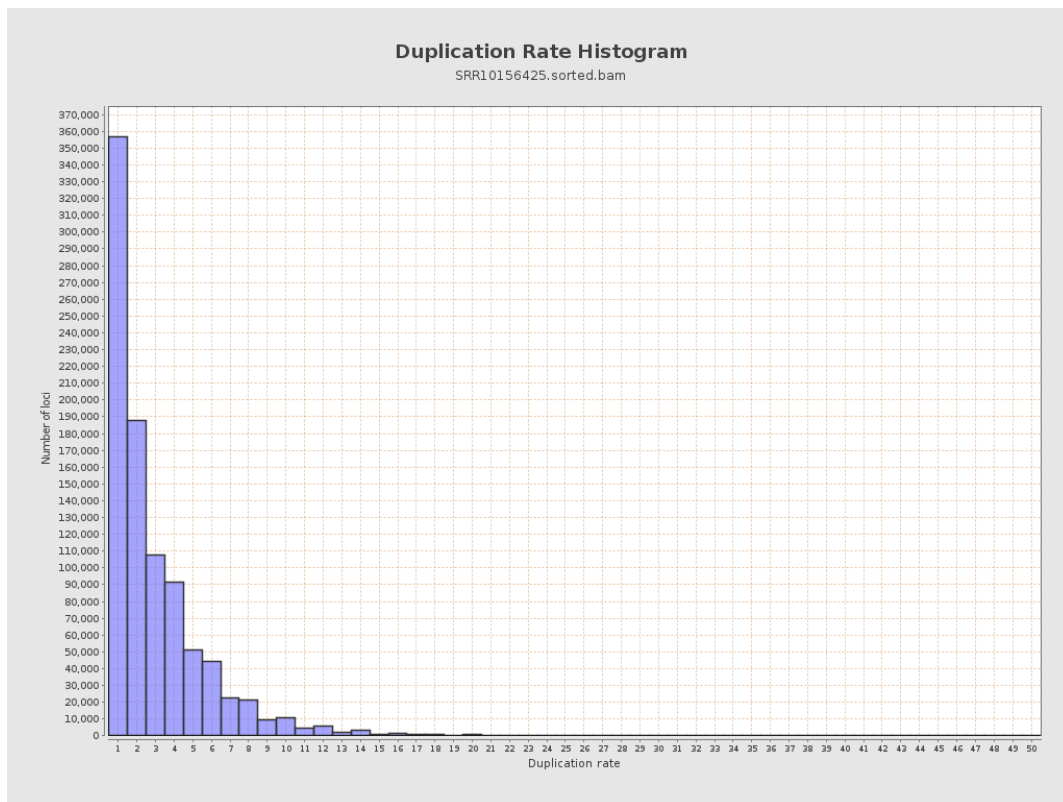
5. Results : Coverage Histogram (0-50X)



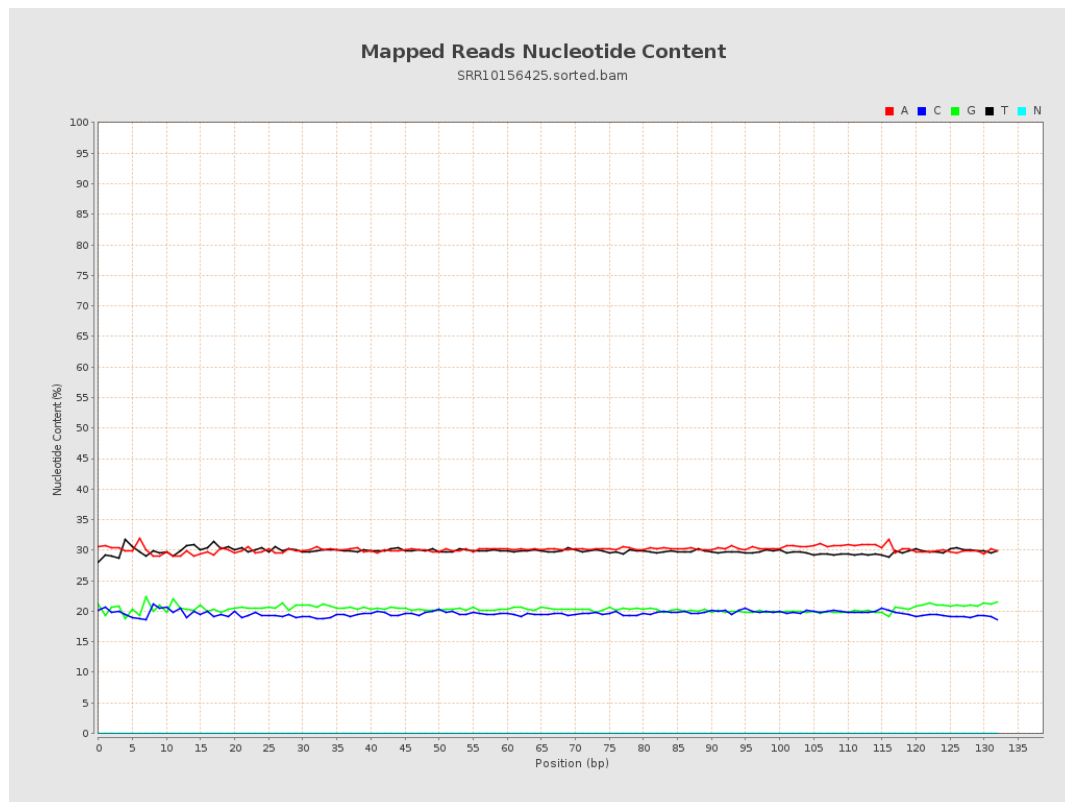
6. Results : Genome Fraction Coverage



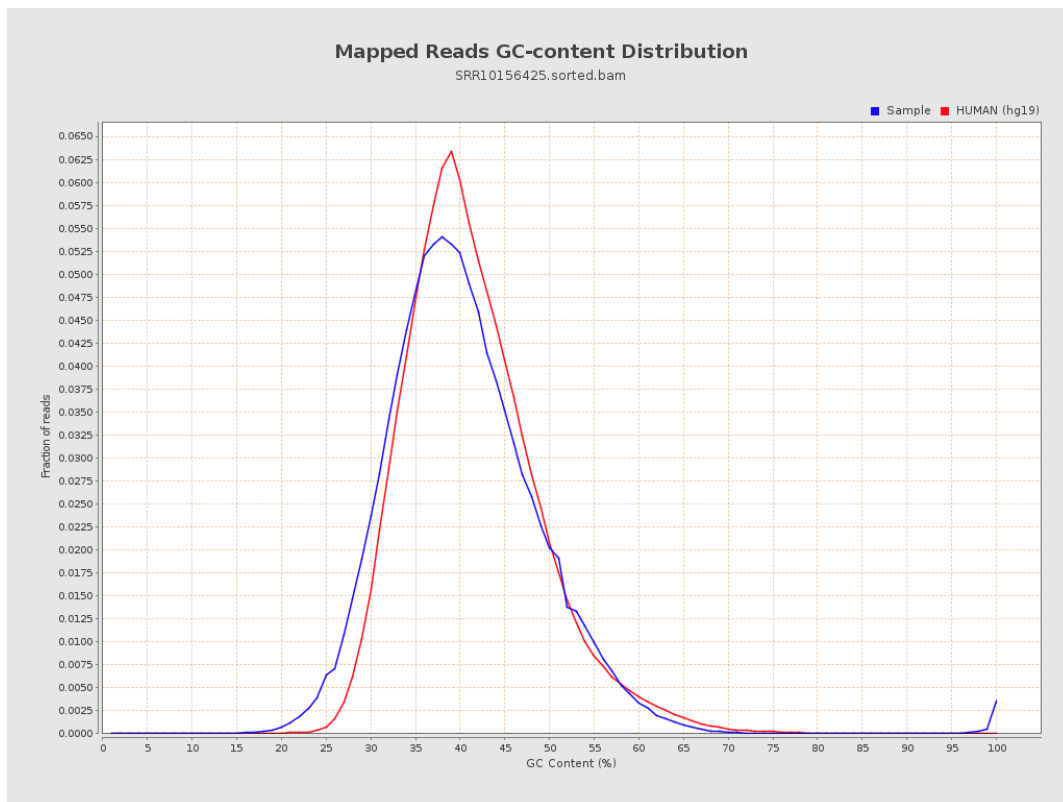
7. Results : Duplication Rate Histogram



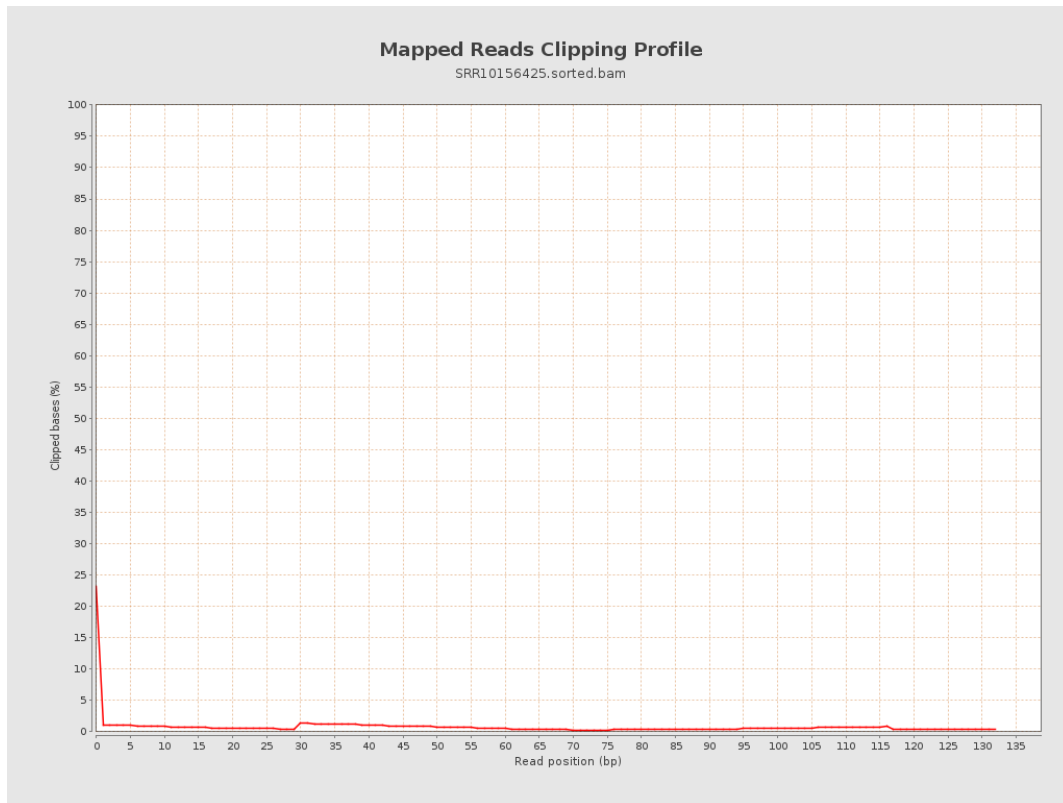
8. Results : Mapped Reads Nucleotide Content



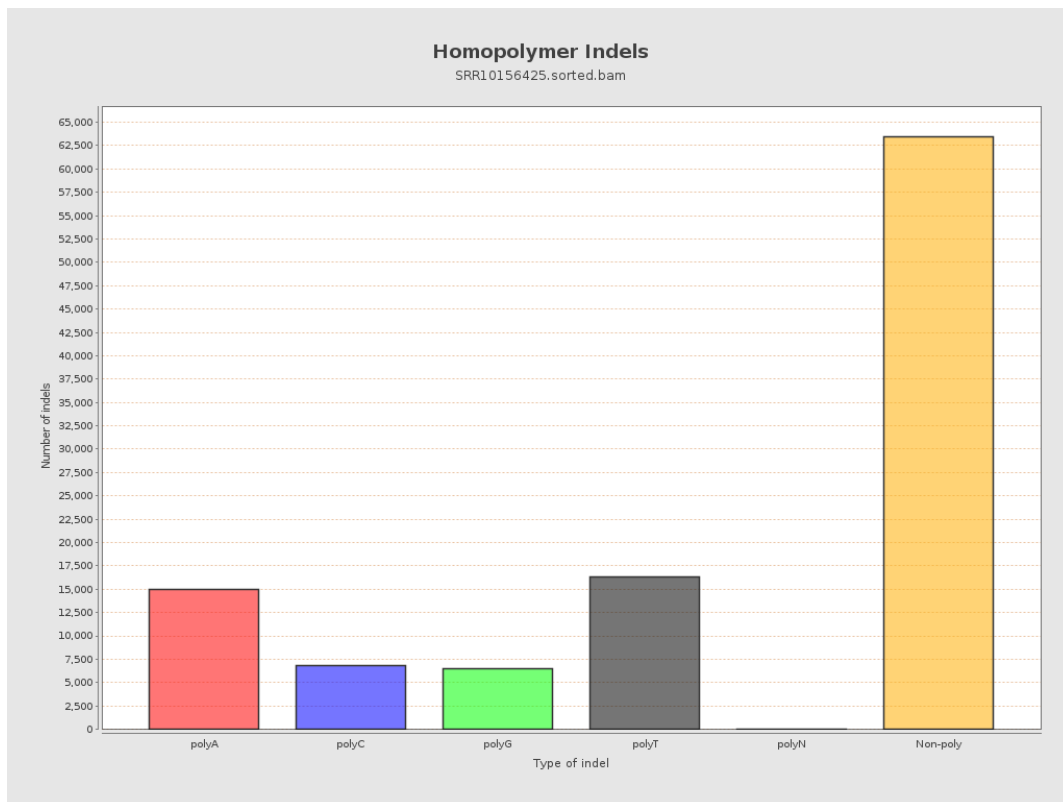
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



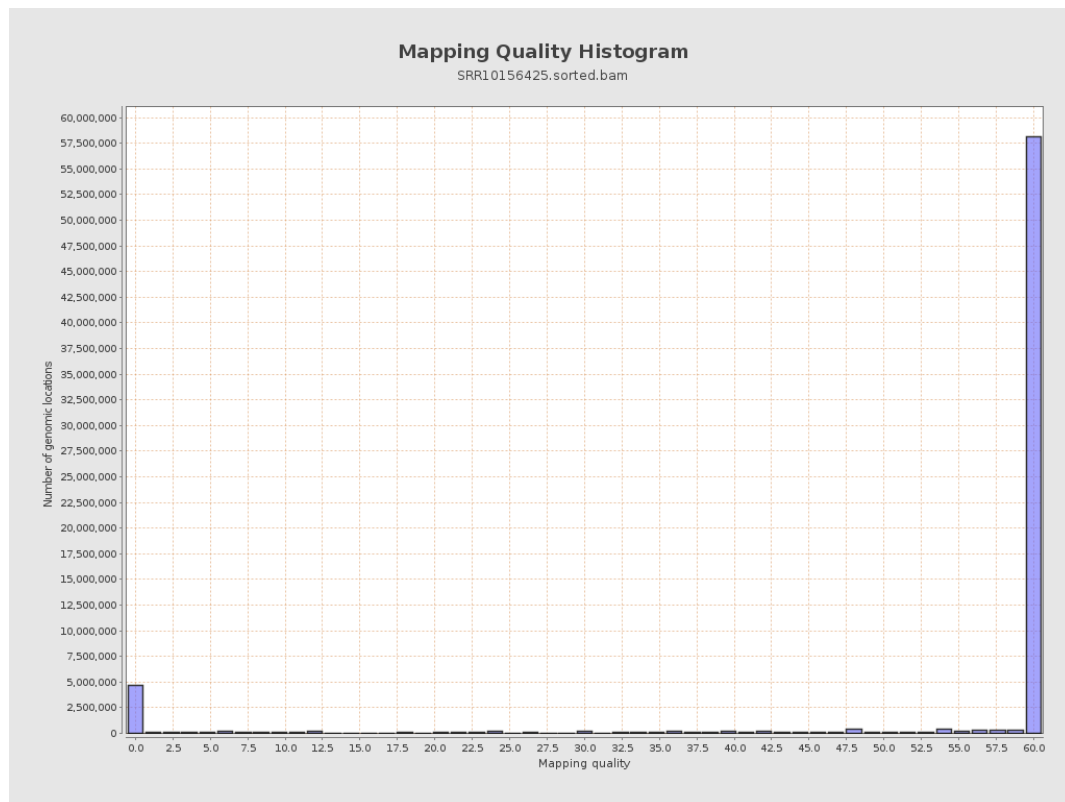
11. Results : Homopolymer Indels



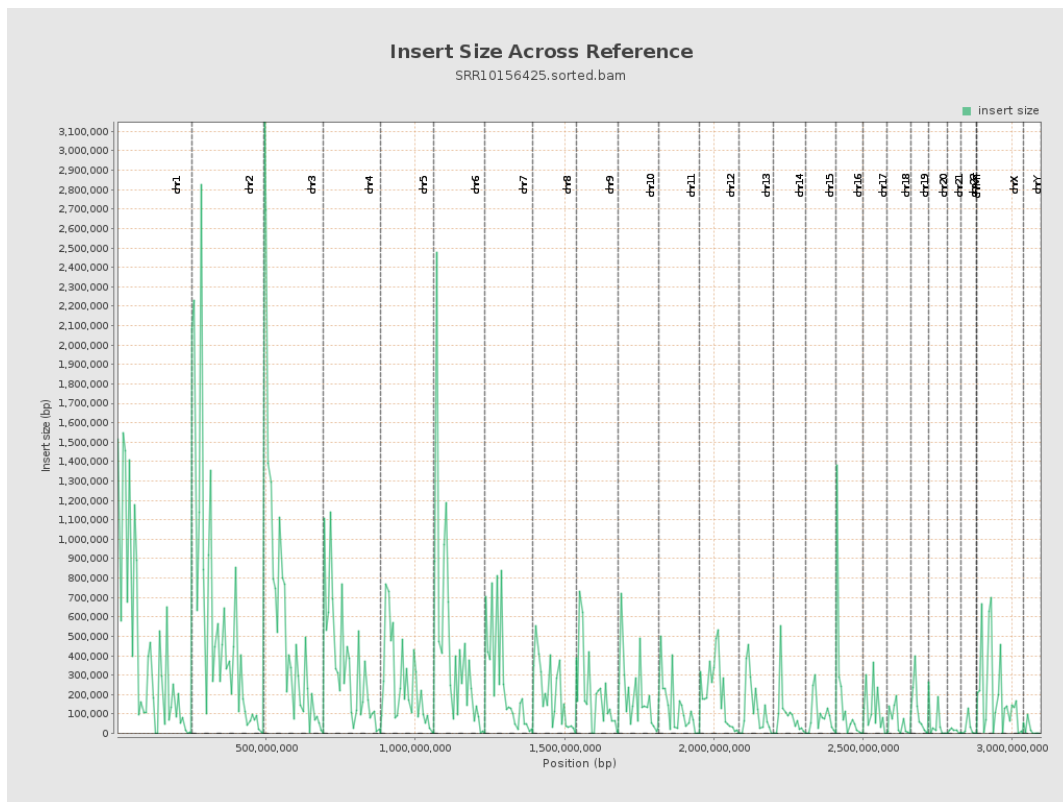
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

